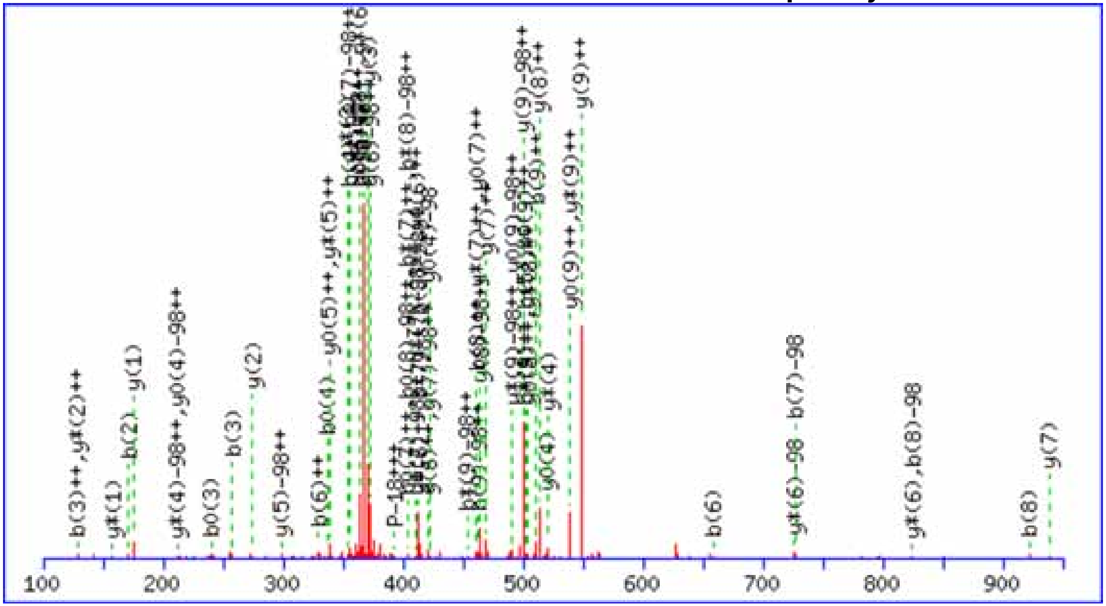
Peptide No.1

AASPFRSPVR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of AASPFRSPVR
Found in BAG3_MOUSE, BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=1

Match to Query 1189: 1194.591150 from(399.204326,3+)
Title: Elution from: 27.507 to 27.507 scan no 1962 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1194.5910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.016

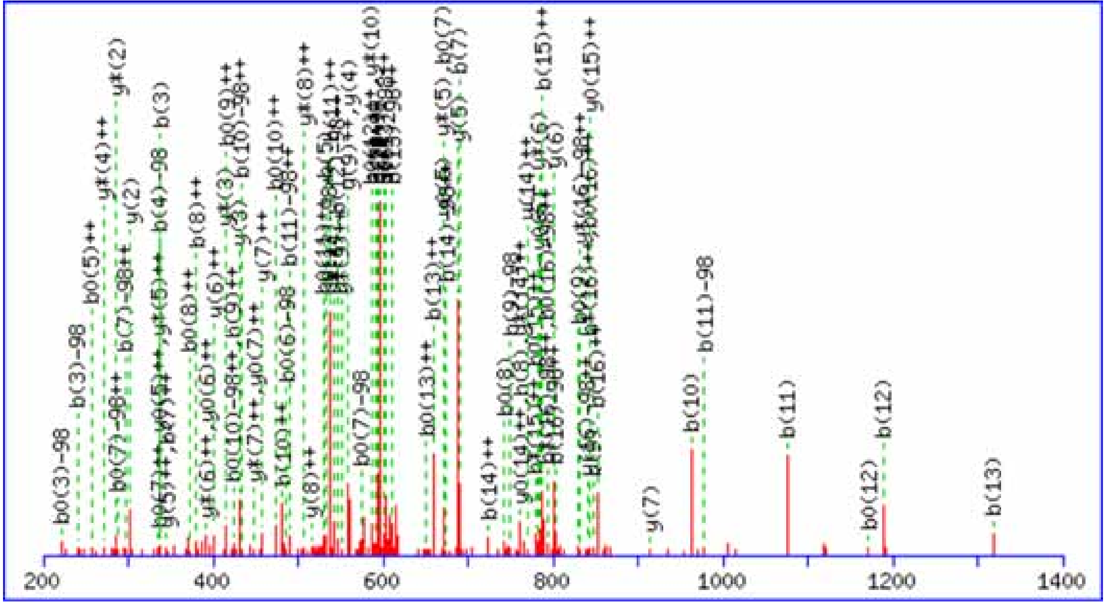
Matched b ions: b(2), b(3)++, b(3), b(4), b(5), b(6), b(6)++, b(7)-98, b(7)-98++, b(7)++, b(8), b(8)-98, b(8)-98++, b(8)++, b(9)++, b(9)-98++
Matched y ions: y(1), y(2), y(3), y(5)-98++, y(6)-98++, y(6)++, y(7), y(7)++, y(7)-98++, y(8)++, y(8)-98++, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.2

AASPPASASDLIEQQQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AASPPASASDLIEQQQK
Found in FA40A_MOUSE, Protein FAM40A OS=Mus musculus GN=Fam40a PE=1 SV=2

Match to Query 4893: 1875.898605 from(626.306811,3+)
Title: Elution from: 42.289 to 42.289 scan no 3964 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1875.8979
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 58 Expect: 0.00012

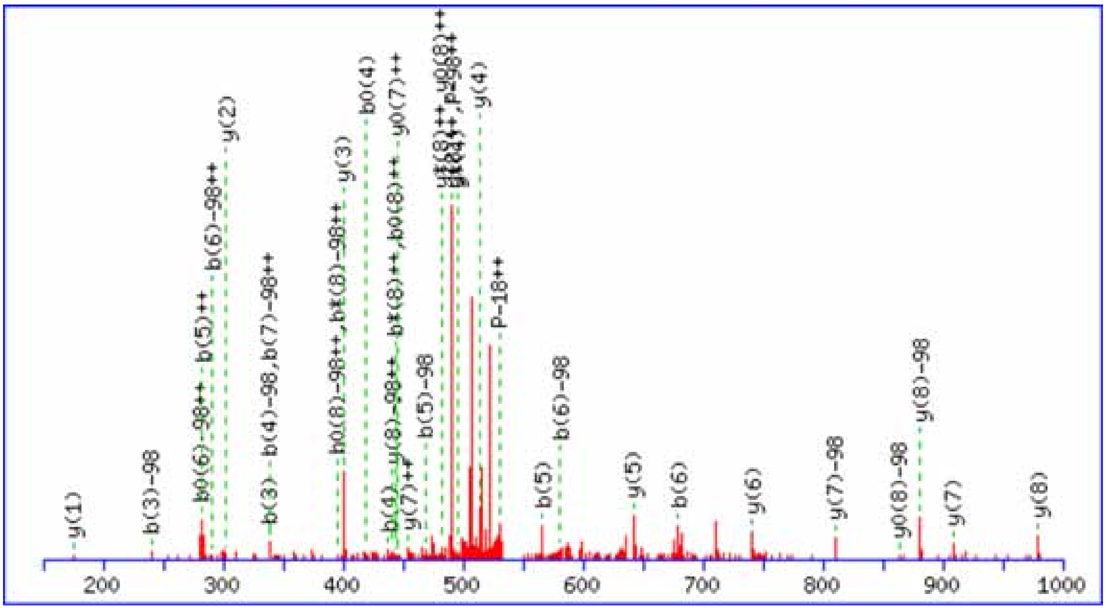
Matched b ions: b(3), b(3)-98, b(4)-98, b(5), b(6), b(7), b(7)-98++, b(7)++, b(7)-98, b(8), b(8)++, b(9), b(9)++, b(9)-98, b(10), b(10)++, b(10)-98++, b(11), b(11)++, b(11)-98, b(11)-98++, b(12)++, b(12), b(12)-98++, b(13), b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7)++, y(7), y(8)++, y(9)++, y(10)++, y(14)++, y(16)-98++
Precursor origin neutral loss:

Peptide No.3

AASVELPQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AASVELPQR
Found in SPEG_MOUSE, Striated muscle-specific serine/threonine-protein kinase OS=Mus musculus GN=Speg PE=1 SV=2

Match to Query 511: 1077.523190 from(539.768871,2+)
Title: Elution from: 32.193 to 32.193 scan no 2395 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1077.5219
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.018

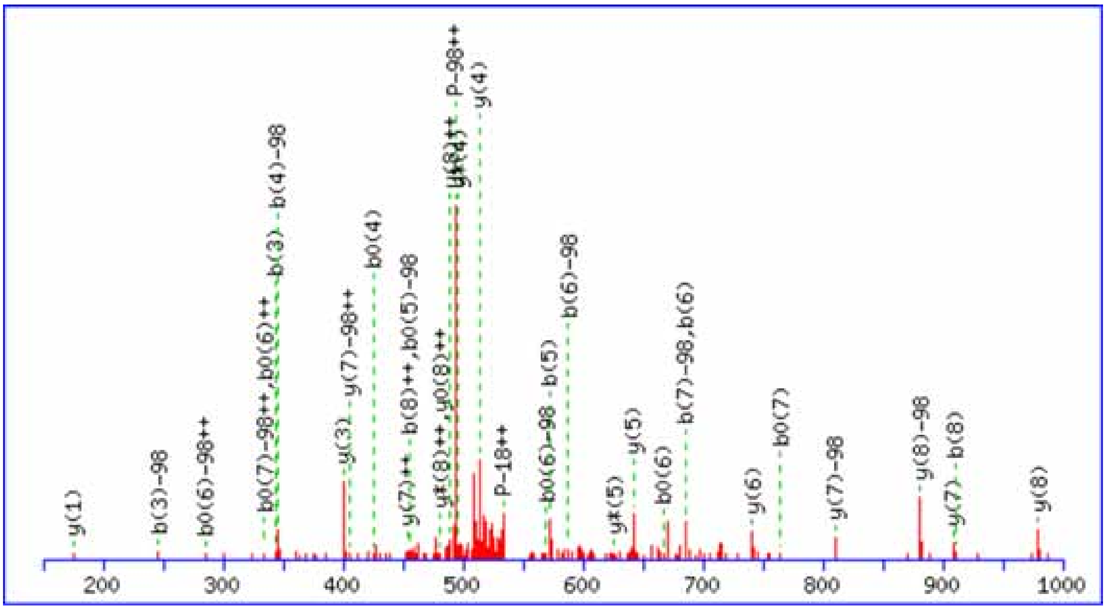
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)++, b(5)-98, b(5), b(6), b(6)-98++, b(6)-98, b(7)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(7)++, y(8)++, y(8)-98, y(8), y(8)-98++
Precursor origin neutral loss: +

Peptide No.4

AASVELPQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AASVELPQR
Found in SPEG_MOUSE, Striated muscle-specific serine/threonine-protein kinase OS=Mus musculus GN=Speg PE=1 SV=2

Match to Query 598: 1083.554478 from(542.784515,2+)
Title: Elution from: 32.102 to 32.102 scan no 2389 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1083.5538
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 0.0002

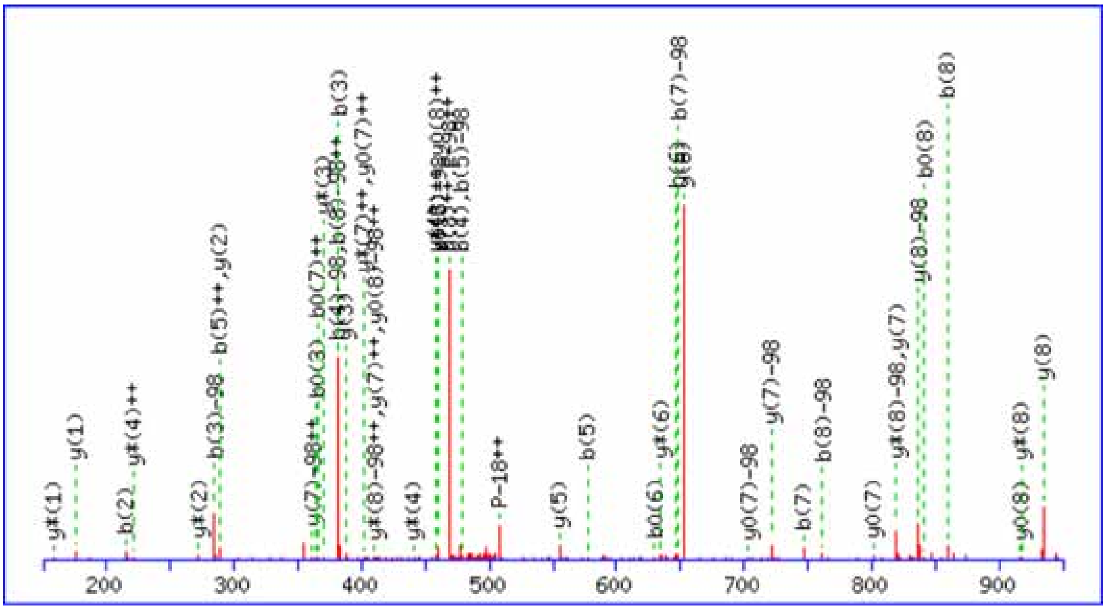
Matched b ions: b(3)-98, b(3), b(4)-98, b(5), b(6), b(6)-98, b(7)-98, b(8), b(8)++
Matched y ions: y(1), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(7)-98++, y(7)++, y(8)-98, y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.5

ADSPPAVIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ADSPPAVIR
Found in NACAM_MOUSE, Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1

Match to Query 561: 1032.500770 from(517.257661,2+)
Title: Elution from: 31.598 to 31.598 scan no 2525 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1032.5005
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 2.1e-005

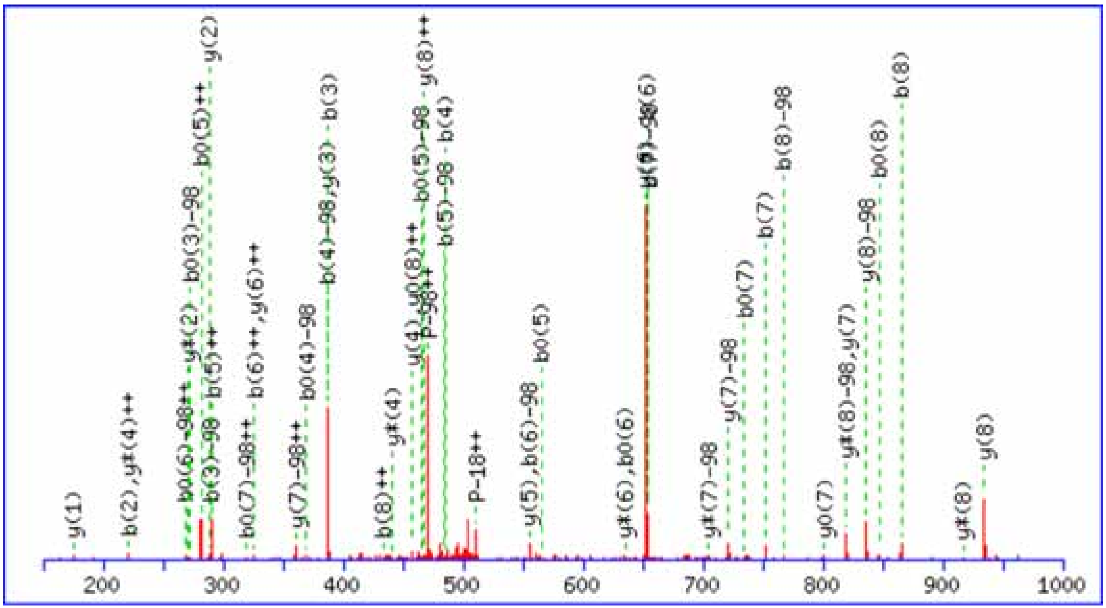
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)++, b(5)-98, b(5), b(6), b(7), b(7)-98, b(8), b(8)-98++, b(8)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(7)++, y(7)-98++, y(8)++, y(8)-98, y(8)
Precursor origin neutral loss: +

Peptide No.6

ADSPPAVIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ADSPPAVIR
Found in NACAM_MOUSE, Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1

Match to Query 392: 1038.532808 from(520.273680,2+)
Title: Elution from: 31.903 to 31.903 scan no 2258 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1038.5323
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 **Expect:** 0.0014

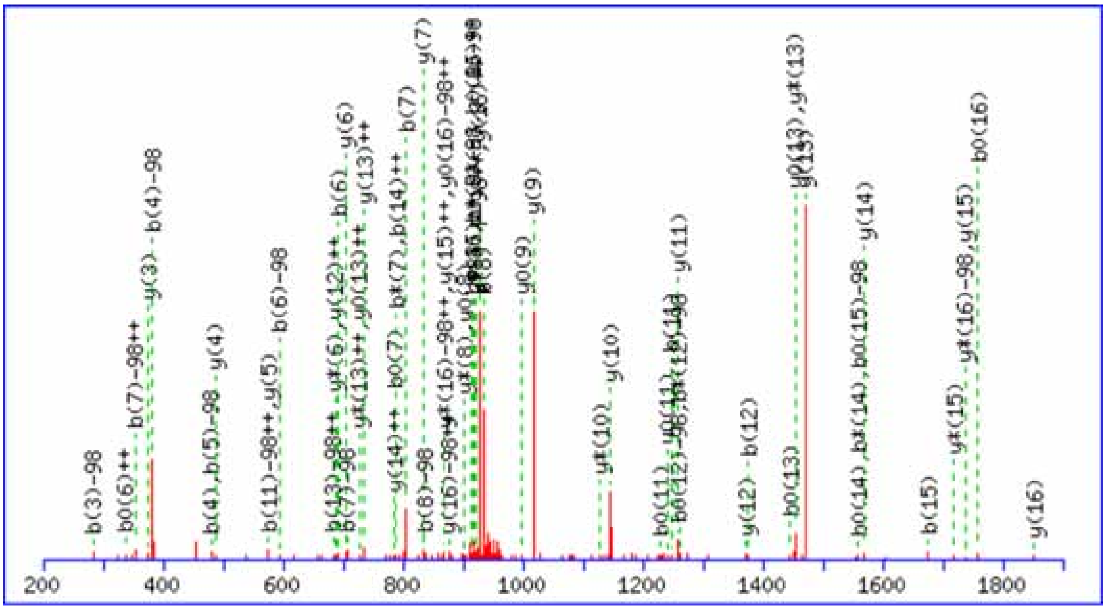
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)++, b(5)-98, b(6), b(6)-98, b(6)++, b(7), b(7)-98, b(8), b(8)-98, b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)-98, y(7), y(7)-98++, y(8)-98, y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.7

ADSVPNLEPSEESLVTK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ADSVPNLEPSEESLVTK
Found in LNP_MOUSE, Protein lunapark OS=Mus musculus GN=Lnp PE=1 SV=1

Match to Query 6269: 1949.925358 from(975.969955,2+)
Title: Elution from: 49.821 to 49.821 scan no 4936 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1949.9234
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 69 Expect: 8.3e-006

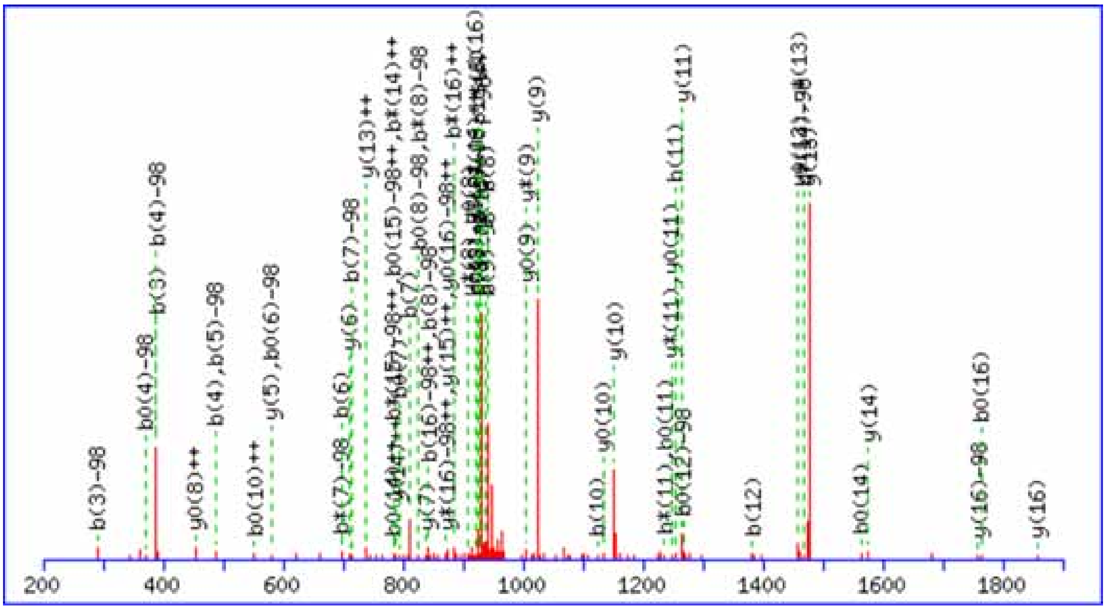
Matched b ions: b(3)-98, b(4)-98, b(4), b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(7)-98++, b(8)-98, b(8), b(11)-98++, b(11), b(12), b(13)-98++, b(14)++, b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(13)++, y(13), y(14), y(14)++, y(15), y(15)++, y(16)++, y(16), y(16)-98++
Precursor origin neutral loss: +

Peptide No.8

ADSVPNLEPSEESLVTK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ADSVPNLEPSEESLVTK
Found in LNP_MOUSE, Protein lunapark OS=Mus musculus GN=Lnp PE=1 SV=1

Match to Query 4843: 1961.988840 from(982.001696,2+)
Title: Elution from: 49.896 to 49.896 scan no 4716 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1961.9871
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 38 **Expect:** 0.0094

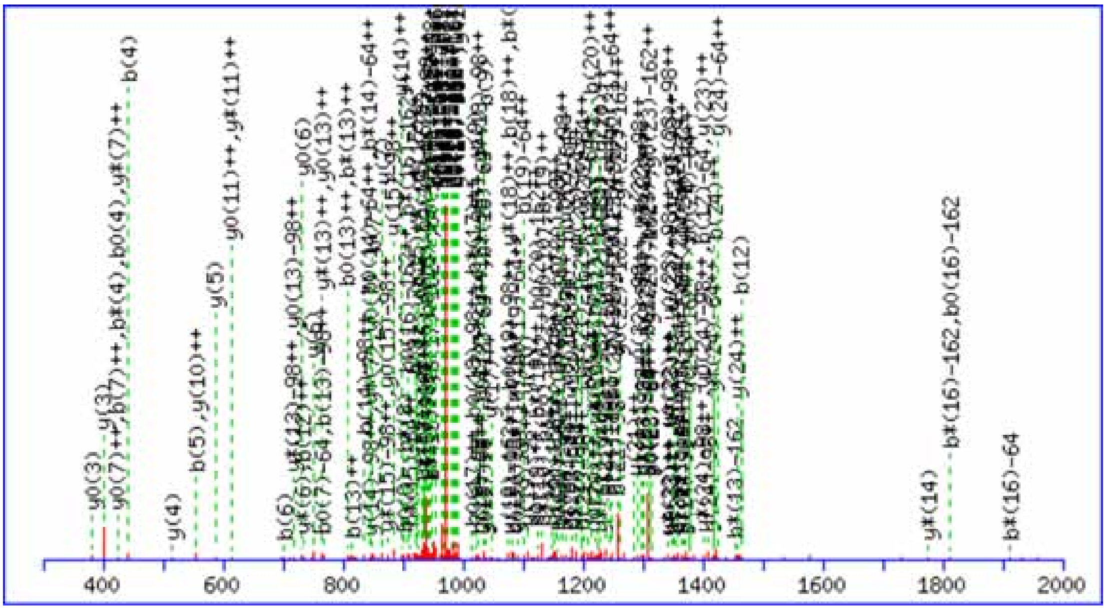
Matched b ions: b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(10), b(11), b(12), b(16)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13)++, y(13), y(14), y(14)++, y(15)++, y(16), y(16)-98, y(16)++
Precursor origin neutral loss: +

Peptide No.9

ADVQLFMADDAYSHHSGVDYADPEK
Confirmed sites: @Y:12,@S:13
Ambiguous sites:

MS/MS Fragmentation of ADVQLFMADDAYSHHSGVDYADPEK
Found in CAV2_MOUSE, Caveolin-2 OS=Mus musculus GN=Cav2 PE=1 SV=1

Match to Query 8585: 3012.193872 from(1005.071900,3+)
Title: Elution from: 50.669 to 50.669 scan no 4990 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3012.1926
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y12 : Phospho (Y)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K25 : Dimethyl (K)
Ions Score: 68 **Expect:** 7.3e-006

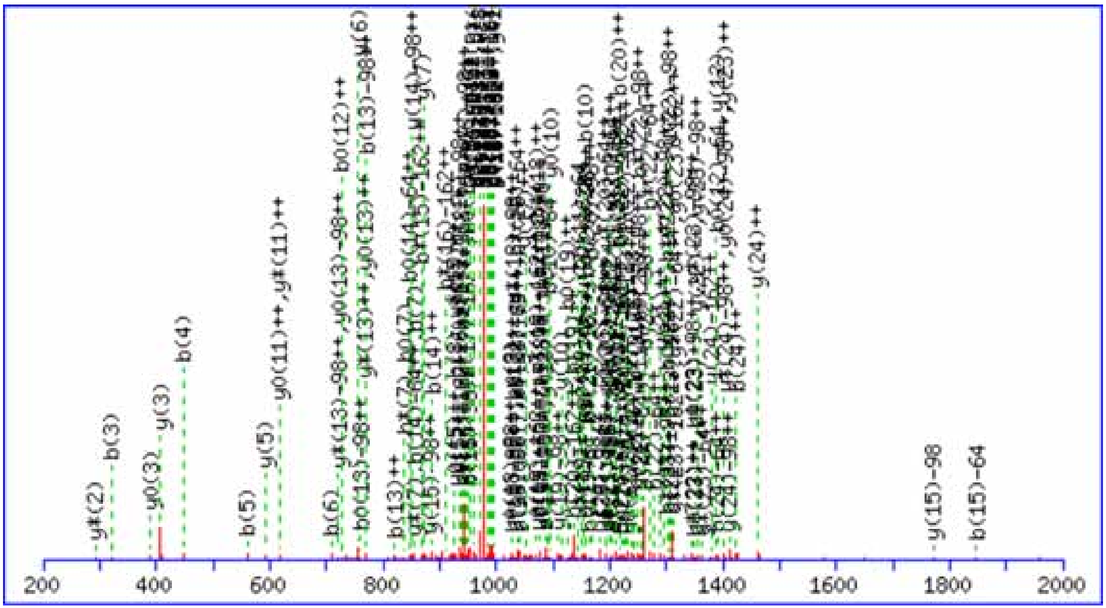
Matched b ions: b(4), b(5), b(6), b(7), b(7)++, b(8), b(9), b(10), b(11), b(12)++, b(12), b(13)-98++, b(13)++, b(14)-98++, b(15)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(23)-98++, b(23)++, b(24)-98++, b(24)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(23)++, y(23)-98++, y(24)-98++, y(24)++
Precursor origin neutral loss: +

Peptide No.10

ADVQLFMADDAYSHHSGVDYADPEK
Confirmed sites: @Y:12,@S:13
Ambiguous sites:

MS/MS Fragmentation of ADVQLFMADDAYSHHSGVDYADPEK
Found in CAV2_MOUSE, Caveolin-2 OS=Mus musculus GN=Cav2 PE=1 SV=1

Match to Query 6681: 3024.256263 from(1009.092697,3+)
Title: Elution from: 50.439 to 50.439 scan no 4592 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3024.2562
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y12 : Phospho (Y)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K25 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 60 **Expect:** 5.7e-005

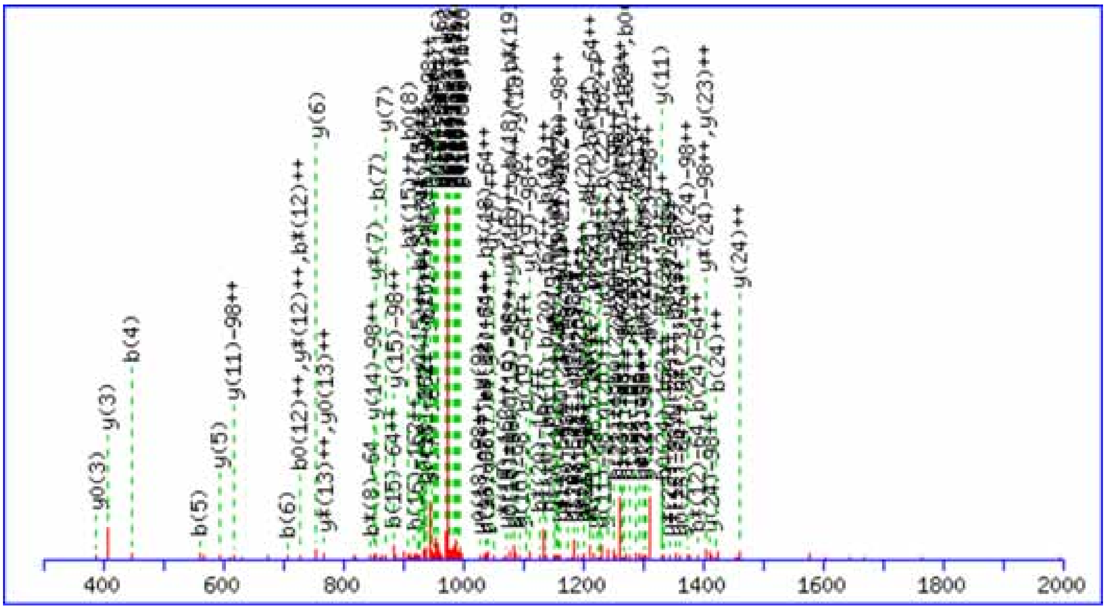
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(13)-98++, b(13)++, b(14)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(24)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14)-98++, y(15)-98++, y(15)-98, y(15)++, y(16)-98++, y(16)++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(23)-98++, y(23)++, y(24)-98++, y(24)++
Precursor origin neutral loss: +

Peptide No.11

ADVQLFMADDAYSHHSGVDYADPEK
Confirmed sites: @S:16
Ambiguous sites: @Y:12orS:13

MS/MS Fragmentation of **ADVQLFMADDAYSHHSGVDYADPEK**
Found in **CAV2_MOUSE**, Caveolin-2 OS=Mus musculus GN=Cav2 PE=1 SV=1

Match to Query 7237: 3024.260232 from(1009.094020,3+)
Title: Elution from: 50.538 to 50.538 scan no 4735 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3024.2562
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y12 : Phospho (Y)
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K25 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 45 Expect: 0.0022

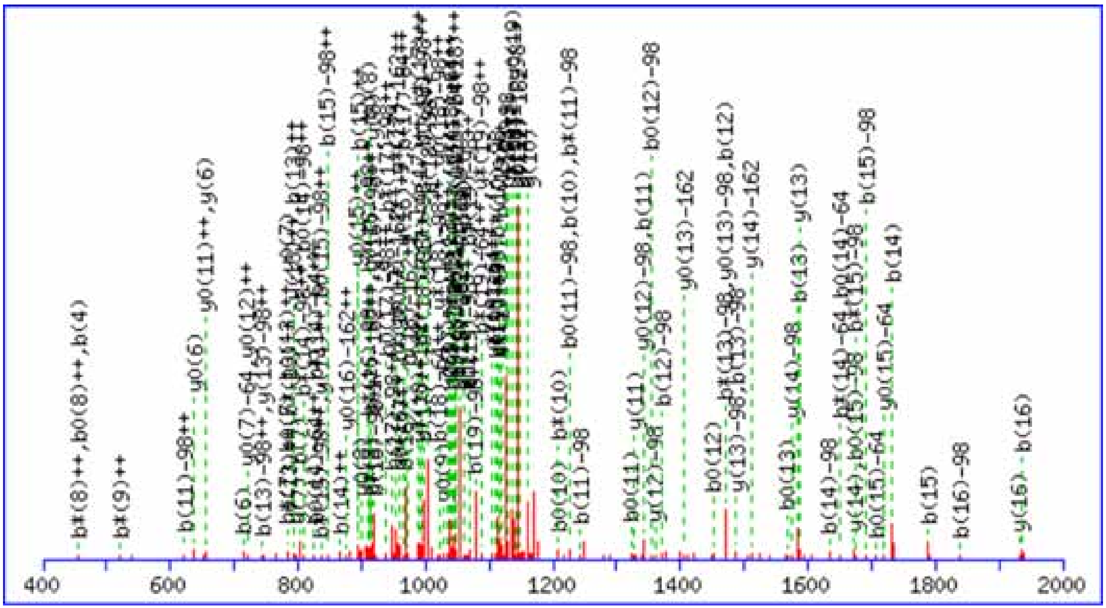
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(16)-98++, b(17)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(24)-98++, b(24)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(11)-98++, y(11)-98, y(11), y(14)-98++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(23)++, y(23)-98++, y(24)-98++, y(24)++
Precursor origin neutral loss: +

Peptide No.12

AEAKEESEESDEDMGFGLFD
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of AEAKEESEESDEDMGFGLFD
Found in RLA0_MOUSE, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 7265: 2385.910824 from(1193.962688,2+)
Title: Elution from: 58.578 to 58.578 scan no 5806 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2385.9083
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K4 : Dimethyl (K)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 47 Expect: 0.00055

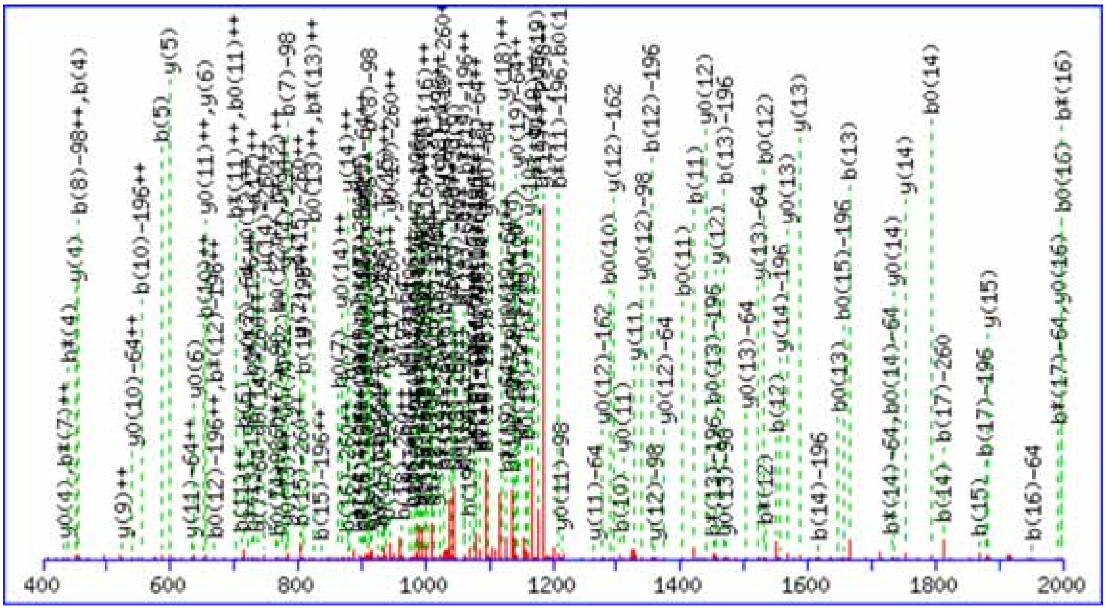
Matched b ions: b(4), b(6), b(7), b(9), b(10), b(10)-98, b(11), b(11)-98++, b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(13)-98++, b(13)++, b(14), b(14)-98, b(14)++, b(15), b(15)-98, b(15)++, b(15)-98++, b(16)-98++, b(16), b(16)-98, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(19)-98++
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(13)-98, y(13), y(13)-98++, y(13)++, y(14), y(14)++, y(14)-98, y(16)-98++, y(16), y(16)++, y(17)++, y(17)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.13

AEAKEESEESDEDMGFGLFD
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of AEAKEESEESDEDMGFGLFD
Found in RLA0_MOUSE, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 7426: 2465.874656 from(1233.944604,2+)
Title: Elution from: 65.275 to 65.275 scan no 6363 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2465.8746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K4 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 60 Expect: 1.7e-005

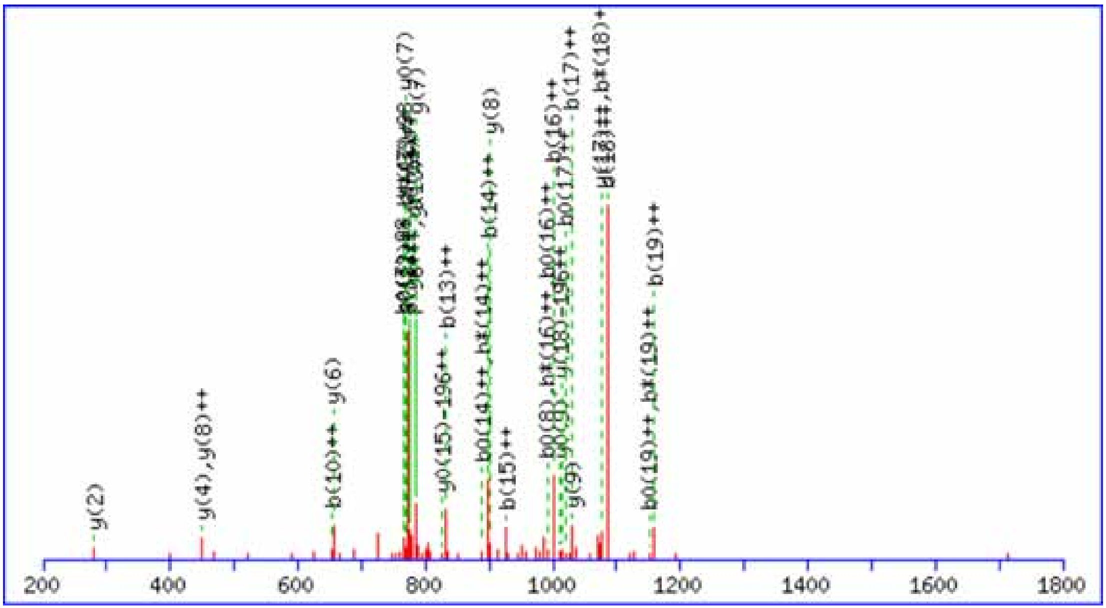
Matched b ions: b(4), b(5), b(6), b(7)-98, b(7), b(8)-98++, b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)++, b(10)-196++, b(10)-98, b(11)-98, b(11), b(11)++, b(12), b(12)-98, b(12)-196, b(12)-98++, b(12)++, b(13), b(13)-98, b(13)-98++, b(13)-196, b(14)-98, b(14), b(14)++, b(14)-196, b(14)-98++, b(14)-196++, b(15)-98++, b(15), b(15)-98, b(15)++, b(15)-196++, b(16)++, b(16)-98, b(16)-98++, b(16)-196++, b(17)-98++, b(17)++, b(17)-196, b(17)-196++, b(18)++, b(18)-98++, b(18)-196++, b(19)++, b(19)-98++, b(19)-196++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11), y(12), y(12)-98, y(12)++, y(13), y(14), y(14)-196++, y(14)++, y(14)-98, y(14)-196, y(15), y(16)-98, y(17)++, y(17)-98++, y(17)-196++, y(18)-196++, y(18)-98++, y(18)++, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.14

AEAKEESEESDEDMGFGLFD
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of AEAKEESEESDEDMGFGLFD
Found in RLA0_MOUSE, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 6377: 2449.883667 from(817.635165,3+)
Title: Elution from: 72.702 to 72.702 scan no 6718 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2449.8797
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K4 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 Expect: 8.1e-006

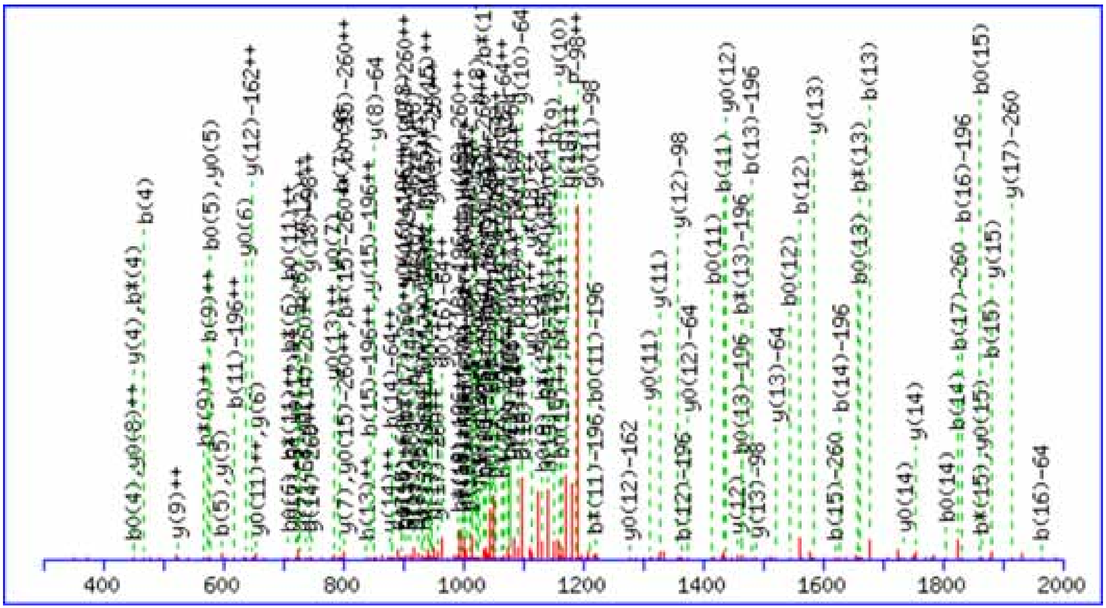
Matched b ions: b(10)++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++
Matched y ions: y(2), y(4), y(6), y(7), y(8)++, y(8), y(9), y(13)++, y(17)++, y(18)-196++
Precursor origin neutral loss: +

Peptide No.15

AEAKEESEESDEDMGFGLFD
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of AEAKEESEESDEDMGFGLFD
Found in RLA0_MOUSE, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 5864: 2477.938486 from(1239.976519,2+)
Title: Elution from: 65.062 to 65.062 scan no 5804 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2477.9383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K4 : Dimethyl:2H(4)13C(2) (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 61 **Expect:** 2.1e-005

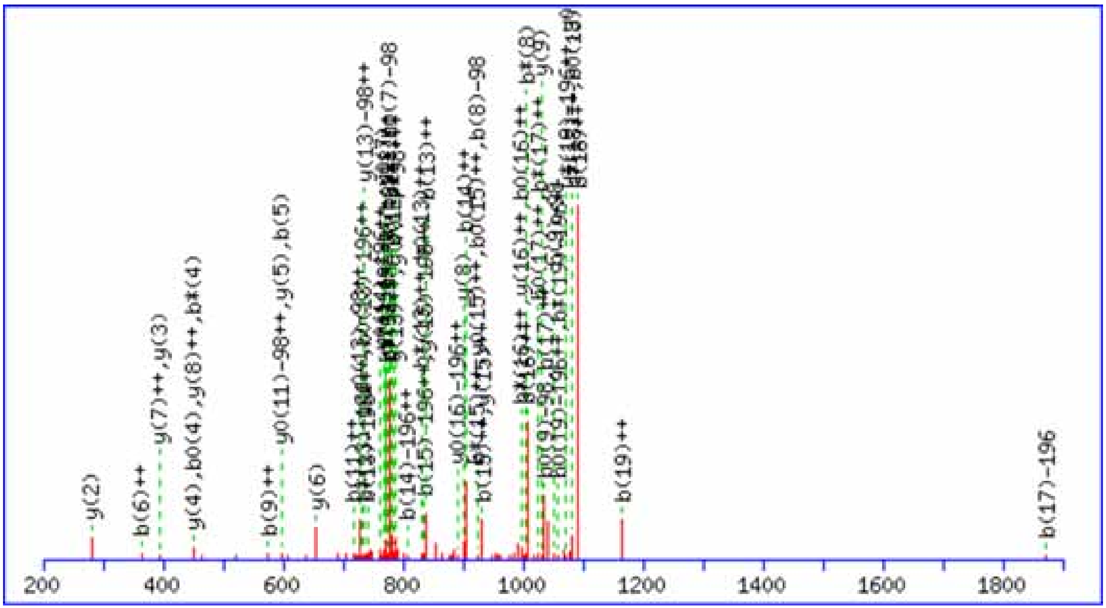
Matched b ions: b(4), b(5), b(6), b(7)-98, b(8)-98, b(8), b(9), b(9)++, b(9)-98, b(10)-98, b(11)-98, b(11), b(11)-196++, b(12)-98, b(12), b(12)-196, b(13), b(13)-98, b(13)++, b(13)-196, b(13)-98++, b(14), b(14)-98, b(14)-98++, b(14)-196, b(14)++, b(15), b(15)-98++, b(15)-98, b(15)++, b(15)-196++, b(16)-196++, b(16)-98, b(16)++, b(16)-98++, b(16)-196, b(17)++, b(17)-98, b(17)-98++, b(17)-196++, b(18)-98++, b(18)++, b(18)-196++, b(19)++, b(19)-98++, b(19)-196++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11), y(12), y(12)-98, y(12)++, y(13)-98, y(13)-98++, y(13), y(14), y(14)-98, y(14)++, y(15)-98++, y(15), y(15)++, y(15)-196++, y(16)-98, y(16)++, y(16)-98++, y(18)-196++, y(18)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.16

AEAKEESEESDEDMGFGLFD
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of AEAKEESEESDEDMGFGLFD
Found in RLA0_MOUSE, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 5889: 2461.947447 from(821.656425,3+)
Title: Elution from: 72.182 to 72.182 scan no 6558 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2461.9433
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K4 : Dimethyl:2H(4)13C(2) (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 **Expect:** 4.3e-006

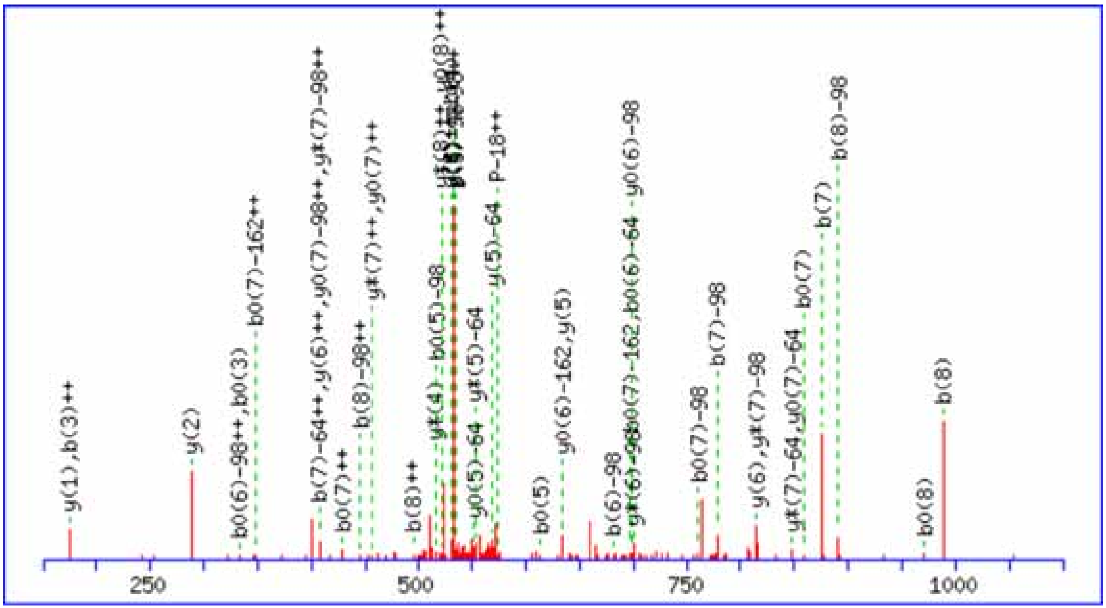
Matched b ions: b(5), b(6)++, b(8)-98, b(9)++, b(9)-98, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-98++, b(14)-196++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-98++, b(17)-196, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(13)++, y(13)-98++, y(14)-196++, y(15)++, y(15)-98++, y(15)-196++, y(16)++, y(17)-98++
Precursor origin neutral loss:

Peptide No.17

AEDTTMPIR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of AEDTTMPIR
Found in HP1B3_MOUSE, Heterochromatin protein 1-binding protein 3 OS=Mus musculus GN=Hp1bp3 PE=1 SV=1

Match to Query 946: 1162.516550 from(582.265551,2+)
Title: Elution from: 44.296 to 44.296 scan no 4054 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1162.5153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 Expect: 0.046

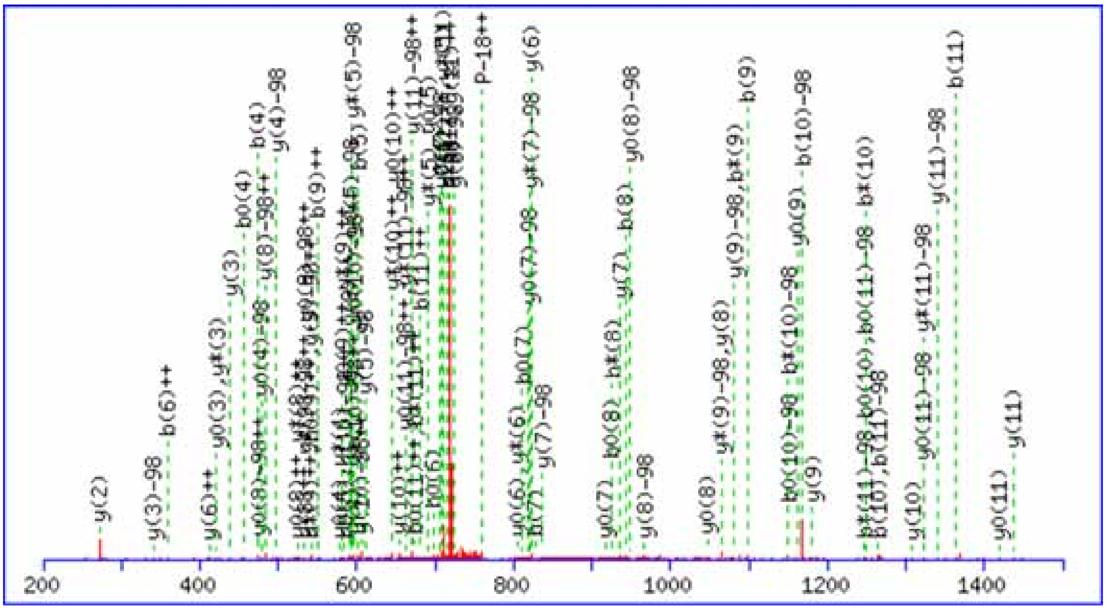
Matched b ions: b(3)++, b(4), b(5)-98, b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(8)-98++, b(8)++
Matched y ions: y(1), y(2), y(4), y(5), y(6), y(6)++, y(8)++
Precursor origin neutral loss: +

Peptide No.18

AEEDEILNRSPR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of AEEDEILNRSPR
Found in CALX_MOUSE, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 2048: 1535.698294 from(768.856423,2+)
Title: Elution from: 31.462 to 31.462 scan no 2302 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1535.6980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.0017

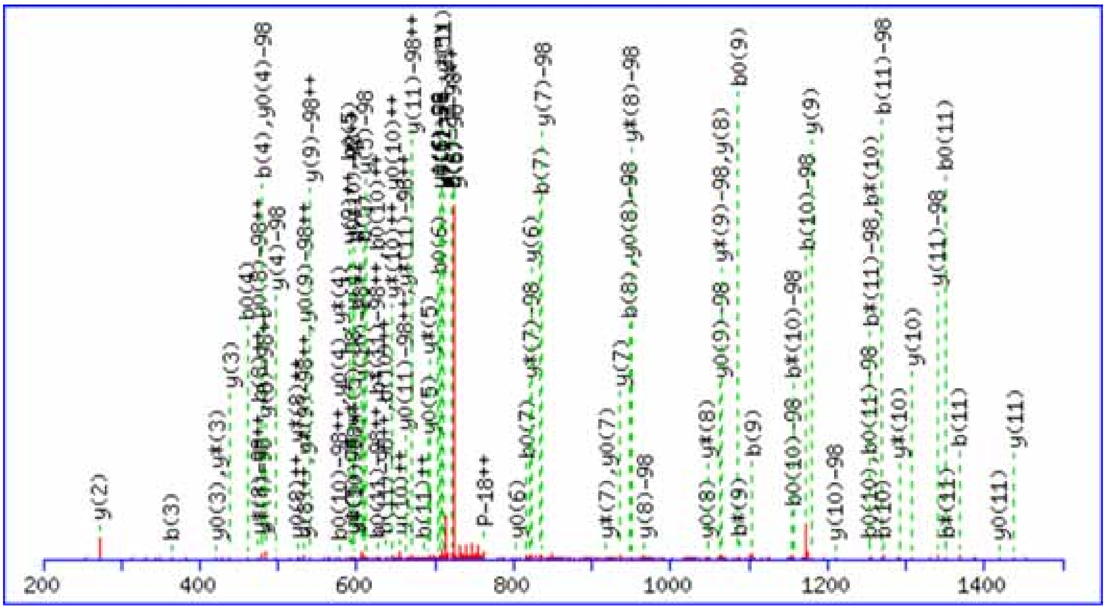
Matched b ions: b(3), b(4), b(5), b(6)++, b(6), b(7), b(8), b(9), b(9)++, b(10)-98, b(10), b(10)-98++, b(11)-98, b(11), b(11)++
Matched y ions: y(2), y(3), y(3)-98, y(4), y(4)-98, y(5), y(5)-98, y(6), y(6)++, y(6)-98, y(7), y(7)-98, y(8)-98++, y(8)-98, y(8), y(8)++, y(9)-98++, y(9)++, y(9), y(9)-98, y(10)-98++, y(10), y(10)++, y(11)++, y(11)-98, y(11), y(11)-98++
Precursor origin neutral loss: +

Peptide No.19

AEEDEILNRSPR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of AEEDEILNRSPR
Found in CALX_MOUSE, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 2451: 1541.729622 from(771.872087,2+)
Title: Elution from: 31.508 to 31.508 scan no 2345 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1541.7299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.013

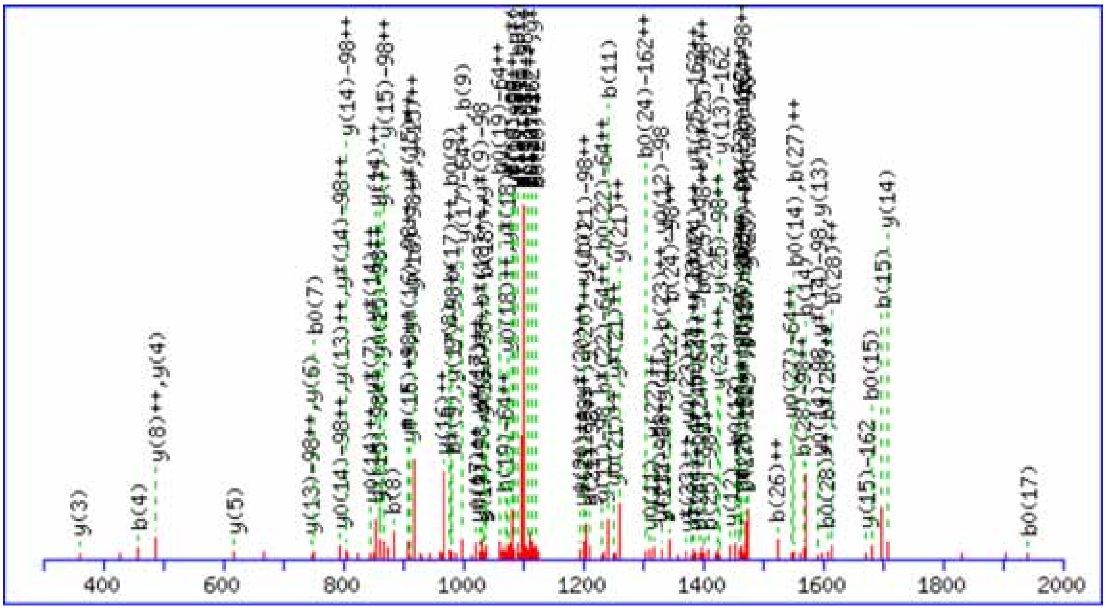
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(8)++, b(9), b(10)-98, b(10), b(10)++, b(11), b(11)-98, b(11)-98++, b(11)++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(8)-98++, y(8)-98, y(8)++, y(8), y(9)-98++, y(9), y(9)++, y(10)-98++, y(10), y(10)++, y(10)-98, y(11)-98, y(11), y(11)-98++
Precursor origin neutral loss: +

Peptide No.20

AEETPSQLDQDTQVQDMDEGSDDEEEGQK
Confirmed sites: @S:21
Ambiguous sites:

MS/MS Fragmentation of AEETPSQLDQDTQVQDMDEGSDDEEEGQK
Found in SF3A1_MOUSE, Splicing factor 3A subunit 1 OS=Mus musculus GN=Sf3a1 PE=1 SV=1

Match to Query 8775: 3404.328186 from(1135.783338,3+)
Title: Elution from: 37.755 to 37.755 scan no 3366 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3404.3246
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K29 : Dimethyl (K)
Ions Score: 83 Expect: 2.4e-007

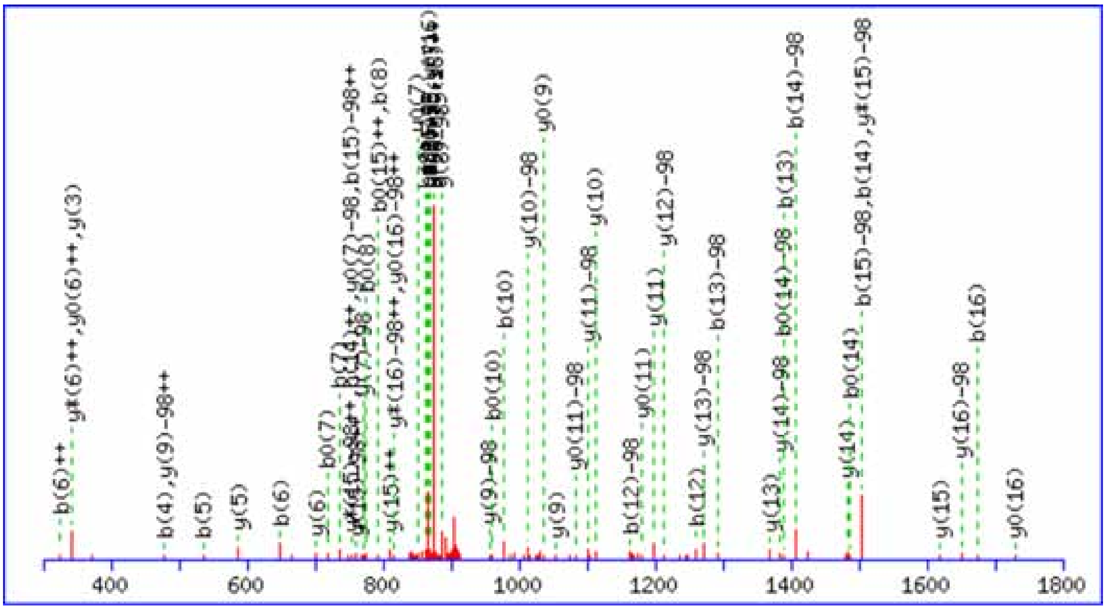
Matched b ions: b(4), b(8), b(9), b(11), b(12), b(13), b(14), b(15), b(17)++, b(18)++, b(19)++, b(23)++, b(24)-98++, b(24)++, b(25)-98++, b(26)-98++, b(26)++, b(27)++, b(28)++, b(28)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(10)-98, y(10), y(11), y(11)-98, y(12), y(13)++, y(13)-98++, y(13), y(14)++, y(14), y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(23)-98++, y(23)++, y(24)++, y(25)++, y(25)-98++
Precursor origin neutral loss: +

Peptide No.21

AEHLGLSGADSDEDPAK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of AEHLGLSGADSDEDPAK
Found in COBL_MOUSE, Protein cordon-bleu OS=Mus musculus GN=Cobl PE=1 SV=1

Match to Query 4067: 1846.798390 from(924.406471,2+)
Title: Elution from: 33.951 to 33.951 scan no 2676 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1846.7986
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K17 : Dimethyl (K)
Ions Score: 87 Expect: 7.9e-008

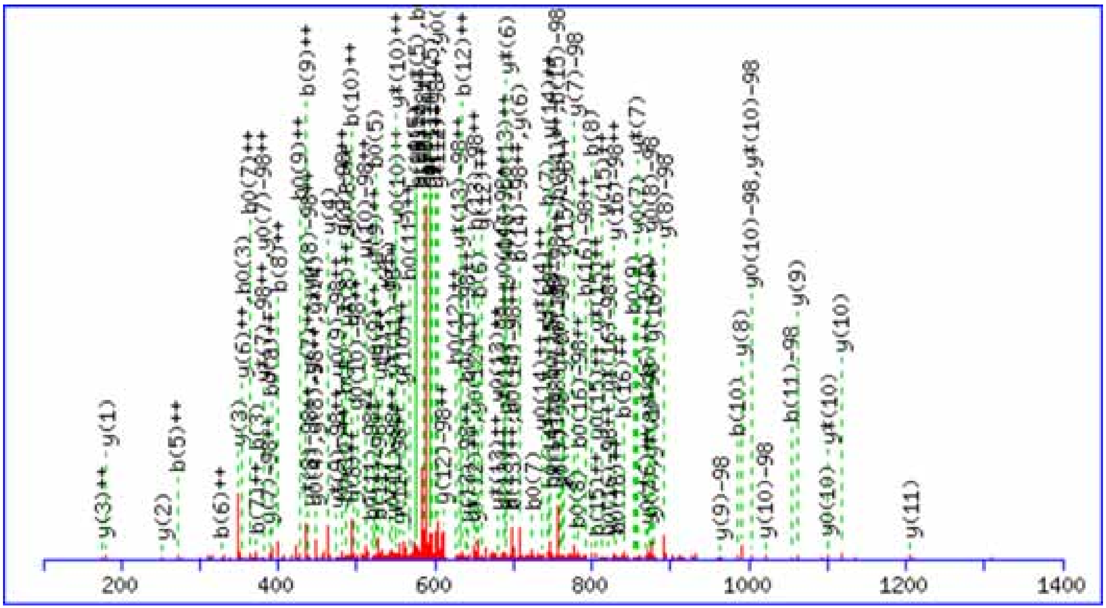
Matched b ions: b(4), b(5), b(6), b(6)++, b(7), b(8), b(9), b(10), b(12)-98, b(12), b(13)-98, b(13), b(14)-98, b(14), b(14)++, b(15)-98, b(15)-98++, b(16)
Matched y ions: y(3), y(5), y(6), y(7)-98, y(7), y(8)-98, y(9)-98++, y(9), y(9)-98, y(10)-98, y(10), y(11)-98, y(11), y(12)-98, y(13)-98, y(13), y(14), y(14)-98, y(15), y(15)++, y(15)-98++, y(16)++, y(16)-98
Precursor origin neutral loss: +

Peptide No.22

AEHLGLSGADSDEDPAK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of AEHLGLSGADSDEDPAK
Found in COBL_MOUSE, Protein cordon-bleu OS=Mus musculus GN=Cobl PE=1 SV=1

Match to Query 5427: 1858.862997 from(620.628275,3+)
Title: Elution from: 33.756 to 33.756 scan no 2745 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1858.8622
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 63 Expect: 2.7e-005

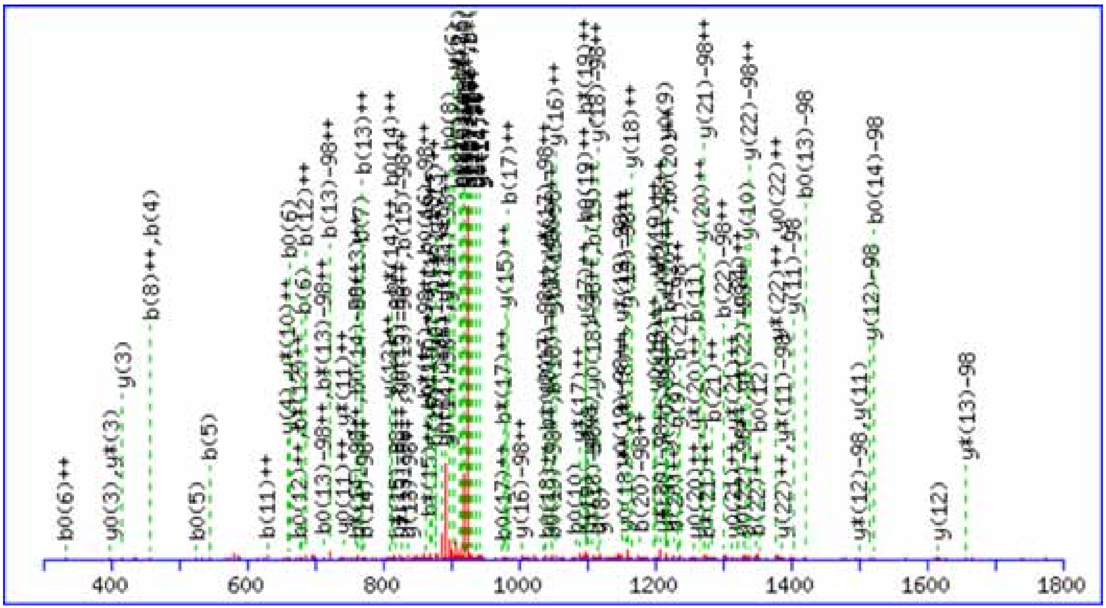
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)-98++, b(11)-98, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(5), y(6), y(6)++, y(7)-98, y(7), y(7)-98++, y(7)++, y(8)-98, y(8), y(8)-98++, y(8)++, y(9), y(9)++, y(9)-98, y(9)-98++, y(10), y(10)-98, y(10)++, y(10)-98++, y(11), y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.23

AEIDSHSFGEKNSTLSEEDYIER
Confirmed sites: @S:13,@Y:20
Ambiguous sites:

MS/MS Fragmentation of AEIDSHSFGEKNSTLSEEDYIER
Found in BNIP3_MOUSE, BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 OS=Mus musculus GN=Bnip3 PE=1 SV=1

Match to Query 8707: 2871.190947 from(958.070925,3+)
Title: Elution from: 46.988 to 46.988 scan no 4571 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2871.1888
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K11 : Dimethyl (K)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y20 : Phospho (Y)
Ions Score: 35 **Expect:** 0.018

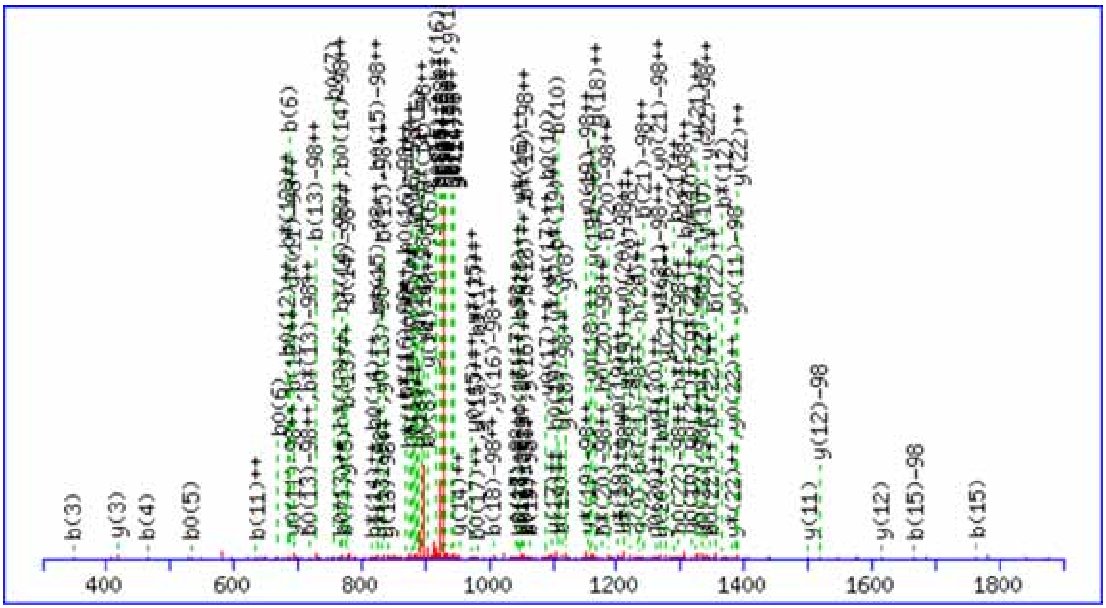
Matched b ions: b(4), b(5), b(6), b(7), b(8)++, b(8), b(10), b(11)++, b(11), b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)-98++, b(22)++
Matched y ions: y(3), y(4), y(6), y(8), y(9), y(10), y(11), y(11)-98, y(12)-98, y(12), y(12)++, y(13)++, y(13)-98++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(22)++
Precursor origin neutral loss: +

Peptide No.24

AEIDSHSFGEKNSTLSEEDYIER
Confirmed sites: @S:13,@Y:20
Ambiguous sites:

MS/MS Fragmentation of AEIDSHSFGEKNSTLSEEDYIER
Found in BNIP3_MOUSE, BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 OS=Mus musculus GN=Bnip3 PE=1 SV=1

Match to Query 6774: 2883.253077 from(962.091635,3+)
Title: Elution from: 47.045 to 47.045 scan no 4250 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2883.2525
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K11 : Dimethyl:2H(4)13C(2) (K)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y20 : Phospho (Y)
Ions Score: 46 **Expect:** 0.0021

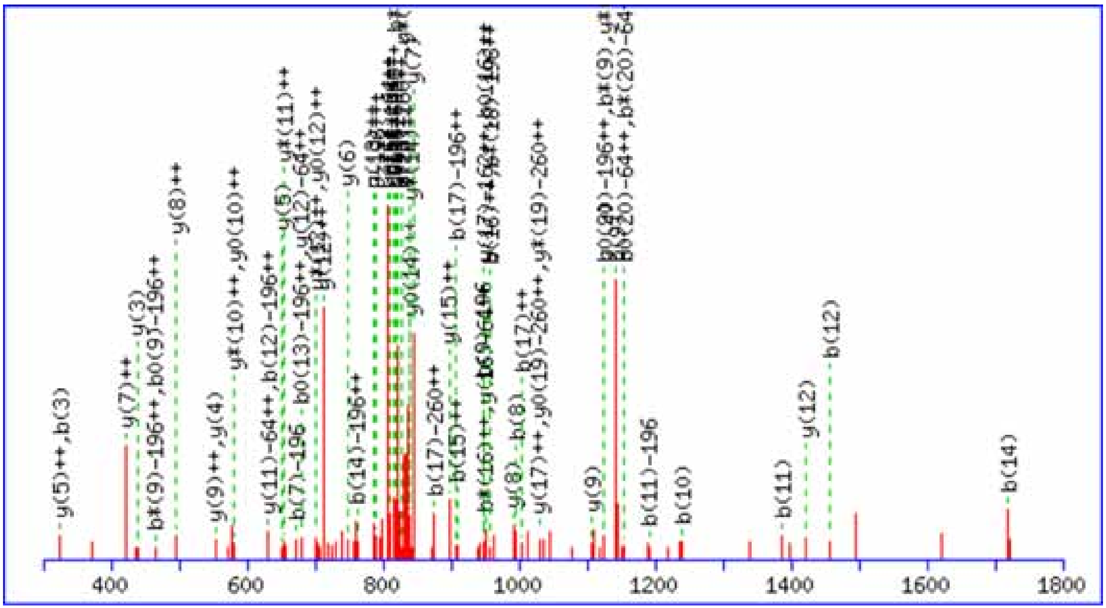
Matched b ions: b(3), b(4), b(6), b(7), b(8), b(10), b(11)++, b(11), b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15)-98, b(15), b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(22)++
Matched y ions: y(3), y(5), y(6), y(8), y(9), y(10), y(11), y(12)-98, y(12), y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)++, y(22)-98++
Precursor origin neutral loss: +

Peptide No.25

AEPTPSPQFPFADMPPPDTYK
Confirmed sites: @T:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of AEPTPSPQFPFADMPPPDTYK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 7780: 2564.062380 from(855.694736,3+)
Title: Elution from: 60.454 to 60.454 scan no 5983 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2564.0623
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K21 : Dimethyl (K)
Ions Score: 32 Expect: 0.031

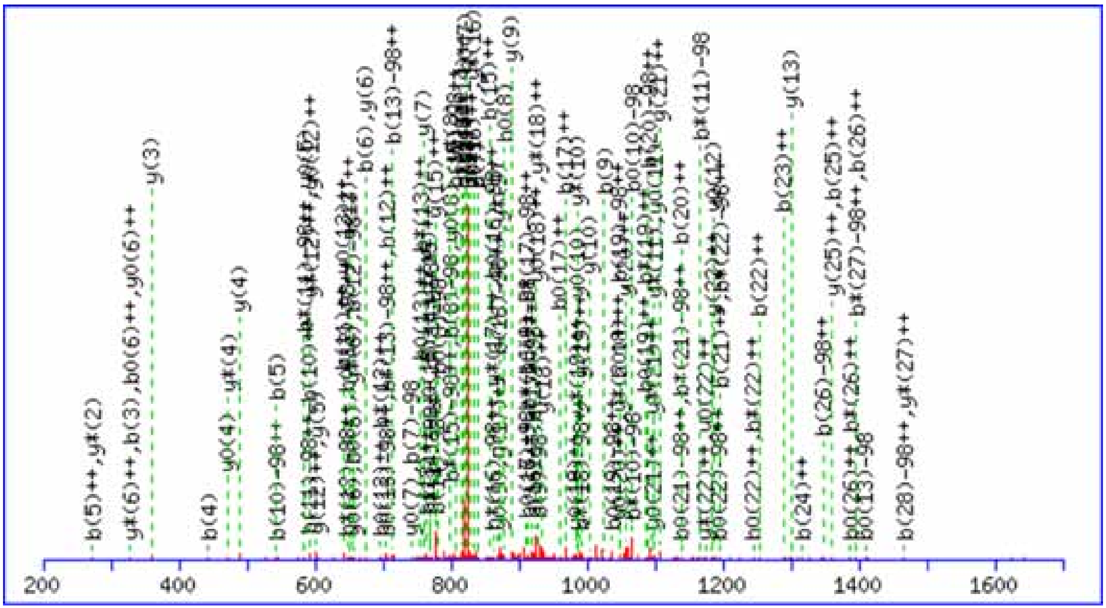
Matched b ions: b(3), b(6)-98, b(7)-196, b(8), b(8)-98, b(9), b(9)-98, b(9)-196, b(10)-98, b(10), b(11), b(11)-196, b(12), b(12)-196++, b(13)-98++, b(14)-98, b(14), b(14)-98++, b(14)-196++, b(15)-98, b(15)-196++, b(15)++, b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(12)++, y(12), y(13)++, y(15)++, y(17)++
Precursor origin neutral loss: +

Peptide No.26

AEVDTESGEKVEDQGEPRPSLDAGSAIEANK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of AEVDTESGEKVEDQGEPRPSLDAGSAIEANK
Found in SRCA_MOUSE, Sarcalumenin OS=Mus musculus GN=Srl PE=1 SV=1

Match to Query 8770: 3391.569368 from(848.899618,4+)
Title: Elution from: 39.952 to 39.952 scan no 3659 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3391.5668
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K10 : Dimethyl (K)
K31 : Dimethyl (K)
Ions Score: 70 Expect: 1.2e-005

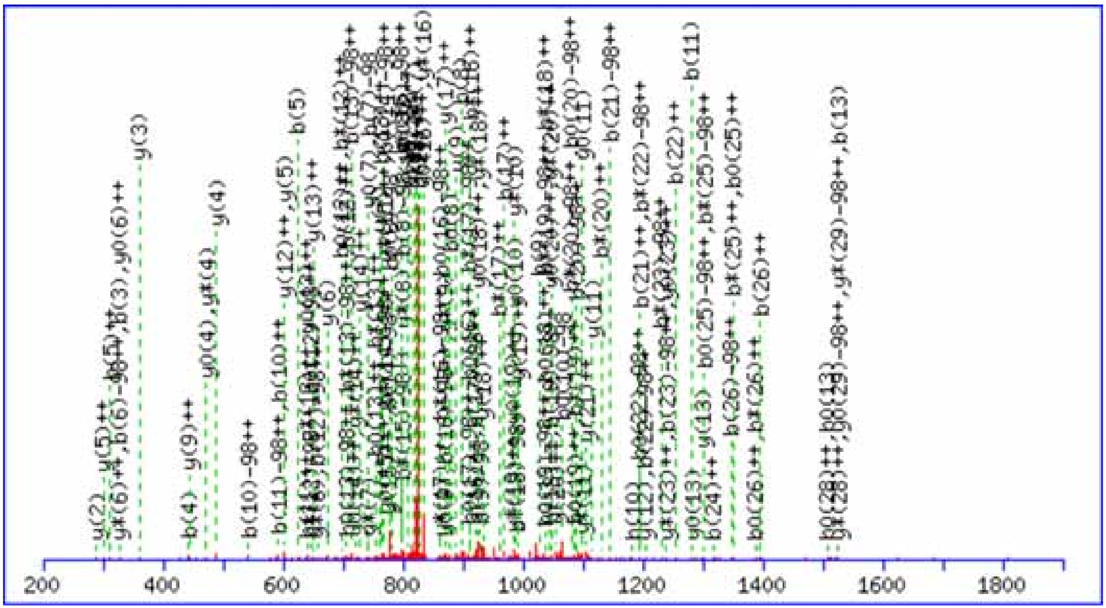
Matched b ions: b(3), b(4), b(5)++, b(5), b(6), b(7)-98, b(7), b(8)-98, b(9)-98, b(9), b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(22)++, b(23)++, b(24)++, b(25)++, b(26)-98++, b(26)++, b(28)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12)++, y(13), y(13)++, y(15)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)++, y(25)++
Precursor origin neutral loss: +

Peptide No.27

AEVDTESGEKVEDQGEPRPSLDAGSAIEANK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of AEVDTESGEKVEDQGEPRPSLDAGSAIEANK
Found in SRCA_MOUSE, Sarcalumenin OS=Mus musculus GN=Srl PE=1 SV=1

Match to Query 8769: 3391.568428 from(848.899383,4+)
Title: Elution from: 40.391 to 40.391 scan no 3718 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3391.5668
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K10 : Dimethyl (K)
K31 : Dimethyl (K)
Ions Score: 45 Expect: 0.0038

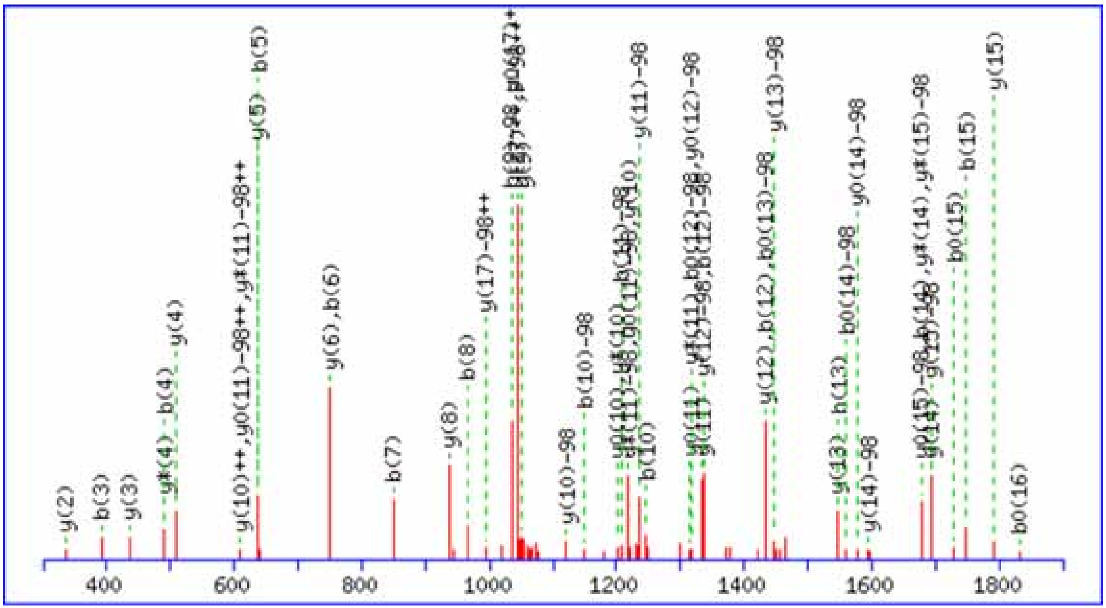
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)-98++, b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(10)-98++, b(10)++, b(10), b(11)-98++, b(11)++, b(11), b(12)-98++, b(12)++, b(13)++, b(13), b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(19)-98++, b(20)-98++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(23)-98++, b(24)++, b(26)++, b(26)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7), y(8), y(9)++, y(9), y(11), y(12)++, y(12), y(13), y(13)++, y(14)++, y(15)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)++
Precursor origin neutral loss: +

Peptide No.28

AEYVFIVDSDGEDEATCR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of AEYVFIVDSDGEDEATCR
Found in CF142_MOUSE, Uncharacterized protein C6orf142 homolog OS=Mus musculus PE=2 SV=1

Match to Query 5867: 2182.879220 from(1092.446886,2+)
Title: Elution from: 54.591 to 54.591 scan no 5238 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2182.8766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 98 Expect: 5e-009

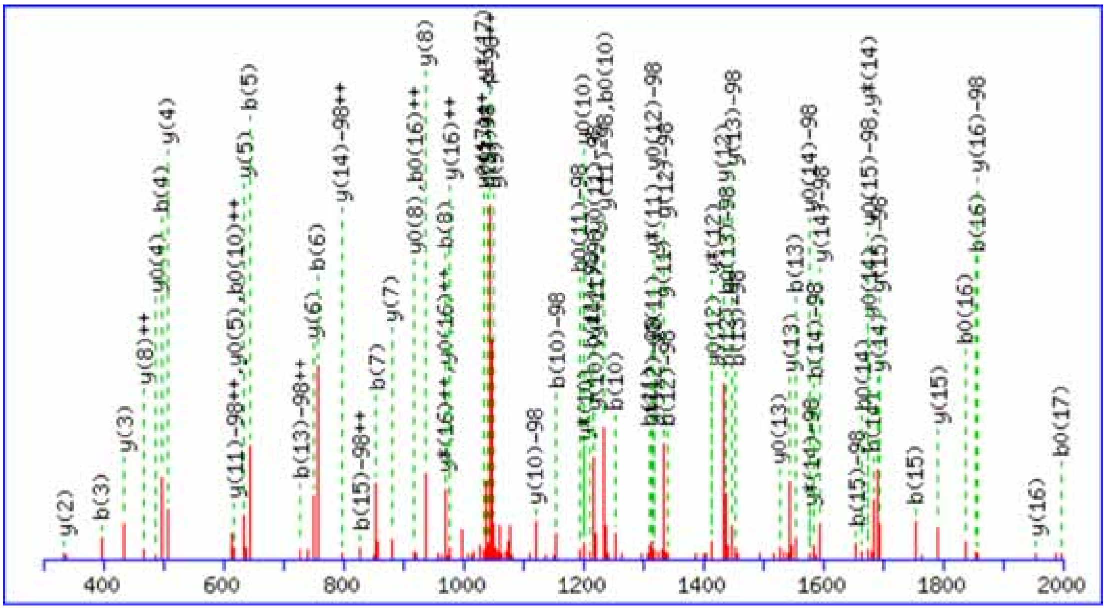
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10), b(10)-98, b(11)-98, b(12), b(12)-98, b(13), b(14), b(15)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10)++, y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(14), y(14)-98, y(15)-98, y(15), y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.29

AEYVFIVDSDGEDEATCR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of AEYVFIVDSDGEDEATCR
Found in CF142_MOUSE, Uncharacterized protein C6orf142 homolog OS=Mus musculus PE=2 SV=1

Match to Query 5643: 2188.911308 from(1095.462930,2+)
Title: Elution from: 54.214 to 54.214 scan no 5183 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2188.9084
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 98 Expect: 6.4e-009

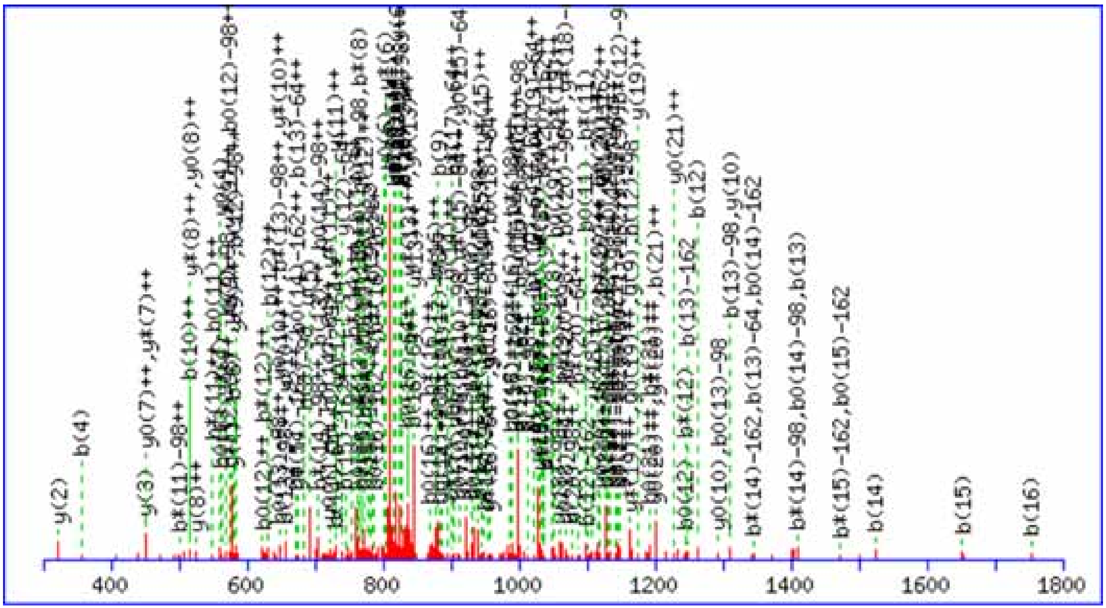
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98++, b(13)-98, b(14), b(14)-98, b(15), b(15)-98++, b(15)-98, b(16)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(10)-98, y(11)-98, y(11)-98++, y(11), y(12), y(12)-98, y(13), y(13)-98, y(14), y(14)-98, y(14)-98++, y(15), y(15)-98, y(16), y(16)-98, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.30

AGAEGSSNVFSMFDQTQIQEFK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of AGAEGSSNVFSMFDQTQIQEFK
Found in MLRS_MOUSE, Myosin regulatory light chain 2, skeletal muscle isoform OS=Mus musculus GN=Mylpf PE=1 SV=3

Match to Query 6763: 2572.119876 from(858.380568,3+)
Title: Elution from: 63.316 to 63.316 scan no 5991 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2572.1193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K22 : Dimethyl (K)
Ions Score: 62 Expect: 4.9e-005

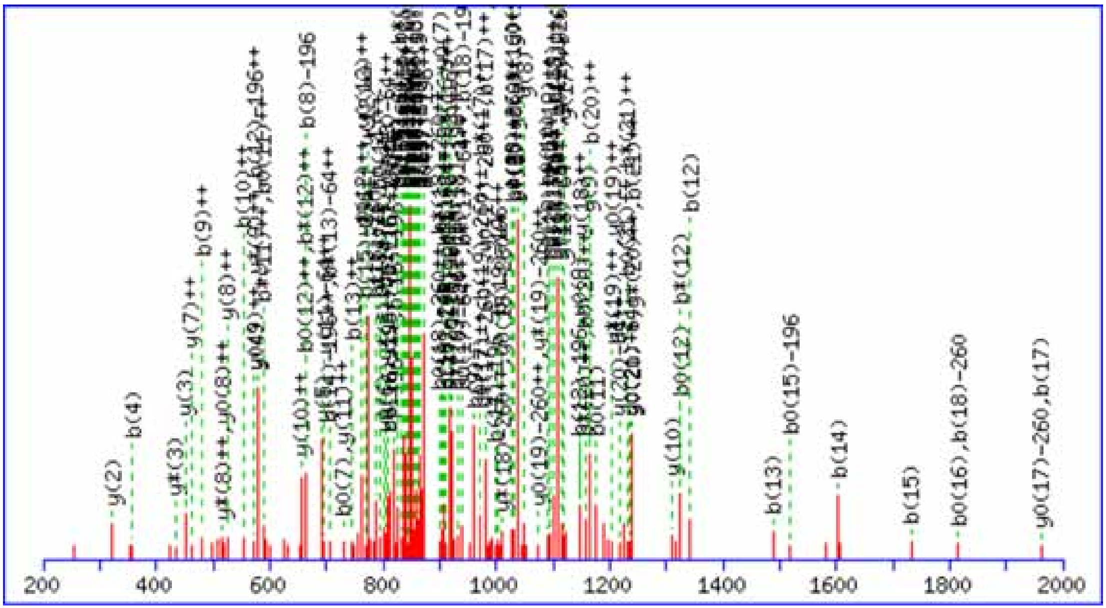
Matched b ions: b(4), b(6), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)++, b(10)-98, b(12), b(12)-98++, b(12)-98, b(12)++, b(13), b(13)++, b(13)-98, b(13)-98++, b(14), b(14)++, b(15), b(15)++, b(15)-98++, b(16), b(16)++, b(16)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++
Precursor origin neutral loss: +

Peptide No.31

AGAEGSSNVFSMFDQTQIQEFK
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of AGAEGSSNVFSMFDQTQIQEFK
Found in MLRS_MOUSE, Myosin regulatory light chain 2, skeletal muscle isoform OS=Mus musculus GN=Mylpf PE=1 SV=3

Match to Query 6948: 2652.088818 from(885.036882,3+)
Title: Elution from: 68.955 to 68.955 scan no 6441 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2652.0856
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K22 : Dimethyl (K)
Ions Score: 66 Expect: 1.3e-005

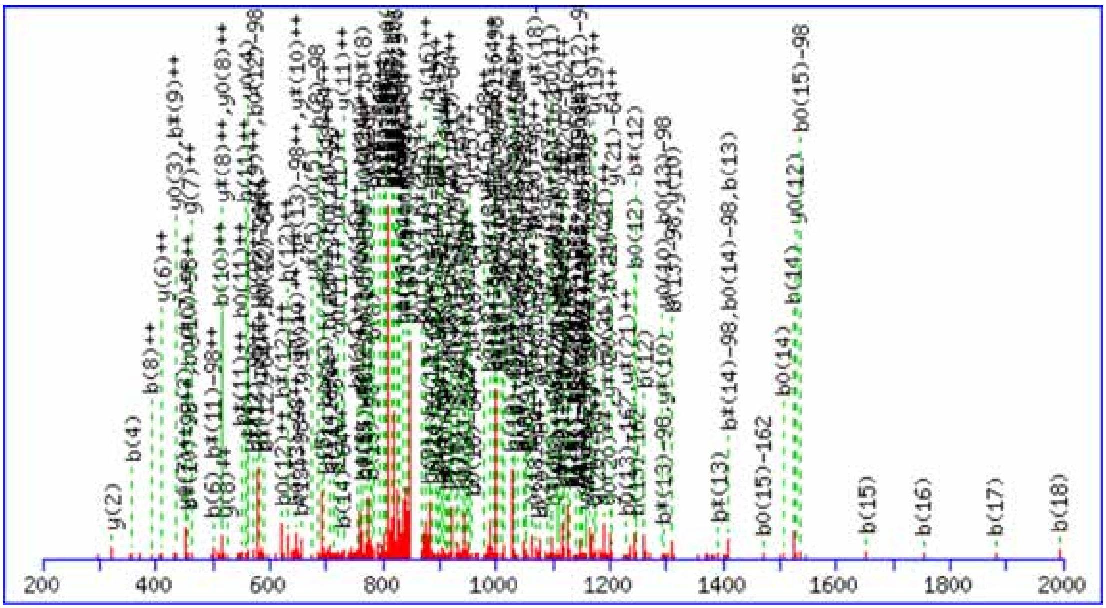
Matched b ions: b(4), b(8)-196, b(8)-98, b(8), b(9), b(9)++, b(9)-98, b(10), b(10)++, b(10)-98, b(10)-196, b(11)-196, b(12), b(12)-196, b(12)-196++, b(13), b(13)++, b(14), b(14)-196++, b(14)++, b(15), b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-196++, b(16)-98++, b(17), b(17)++, b(17)-98++, b(18)++, b(18)-196++, b(18)-98++, b(19)++, b(19)-196++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9), y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(17)++, y(18)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.32

AGAEGSSNVFSMFDQTQIQEFK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of AGAEGSSNVFSMFDQTQIQEFK
Found in MLRS_MOUSE, Myosin regulatory light chain 2, skeletal muscle isoform OS=Mus musculus GN=Mylpf PE=1 SV=3

Match to Query 6260: 2572.122237 from(858.381355,3+)
Title: Elution from: 63.278 to 63.278 scan no 5838 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2572.1193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K22 : Dimethyl (K)
Ions Score: 65 Expect: 2.1e-005

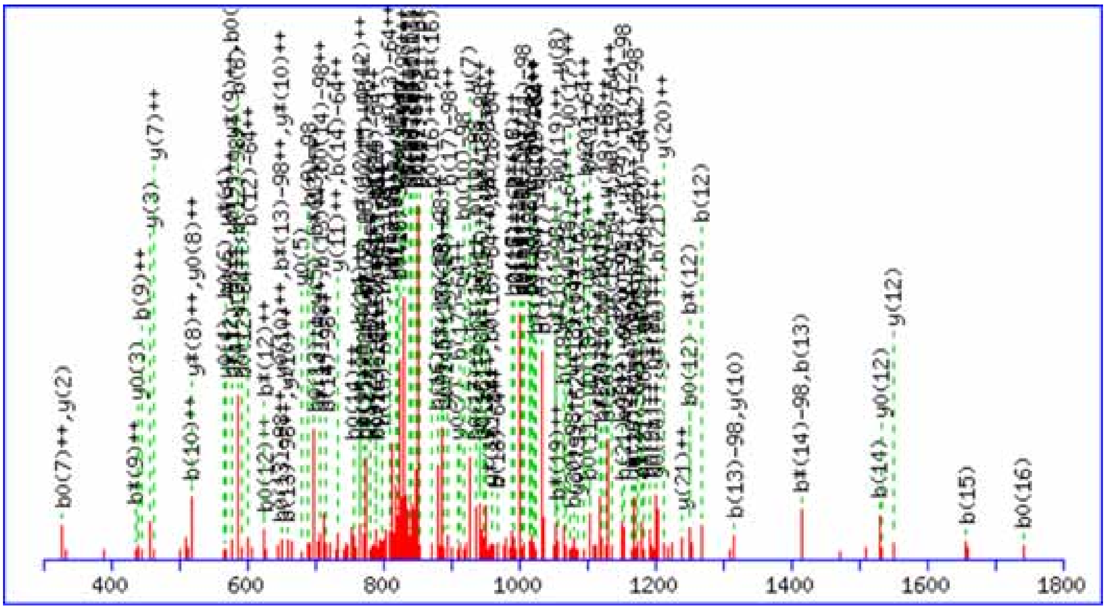
Matched b ions: b(4), b(6), b(8)++, b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)++, b(10)-98, b(11)++, b(11), b(12), b(12)++, b(12)-98, b(12)-98++, b(13)-98, b(13), b(13)-98++, b(13)++, b(14), b(14)++, b(14)-98++, b(15), b(15)-98++, b(15)++, b(16), b(16)-98++, b(16)++, b(17), b(17)++, b(17)-98++, b(18)++, b(18), b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(18)++, y(19)++
Precursor origin neutral loss: +

Peptide No.33

AGAEGSSNVFSMFDQTQIQEFK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of AGAEGSSNVFSMFDQTQIQEFK
Found in MLRS_MOUSE, Myosin regulatory light chain 2, skeletal muscle isoform OS=Mus musculus GN=Mylpf PE=1 SV=3

Match to Query 6294: 2584.187475 from(862.403101,3+)
Title: Elution from: 63.620 to 63.620 scan no 5869 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2584.1829
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K22 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 66 Expect: 2.2e-005

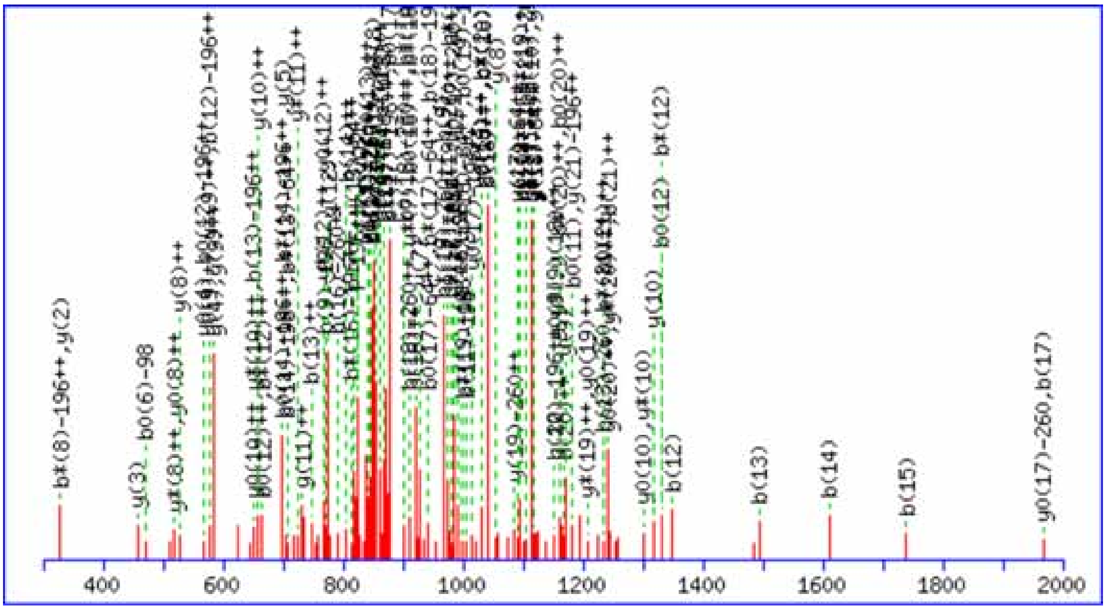
Matched b ions: b(6), b(7)-98, b(8)-98, b(8), b(9), b(9)++, b(9)-98, b(10), b(10)++, b(10)-98, b(11), b(12)-98++, b(12), b(12)-98, b(13), b(13)++, b(13)-98, b(13)-98++, b(14), b(14)++, b(14)-98++, b(15), b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(12), y(12)++, y(13)++, y(16)++, y(17)-98++, y(19)++, y(19)-98++, y(20)++, y(21)++
Precursor origin neutral loss: +

Peptide No.34

AGAEGSSNVFSMFDQTQIQEFK
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of AGAEGSSNVFSMFDQTQIQEFK
Found in MLRS_MOUSE, Myosin regulatory light chain 2, skeletal muscle isoform OS=Mus musculus GN=Mylpf PE=1 SV=3

Match to Query 6981: 2664.151233 from(889.057687,3+)
Title: Elution from: 69.003 to 69.003 scan no 6447 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2664.1492
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K22 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 67 Expect: 1.4e-005

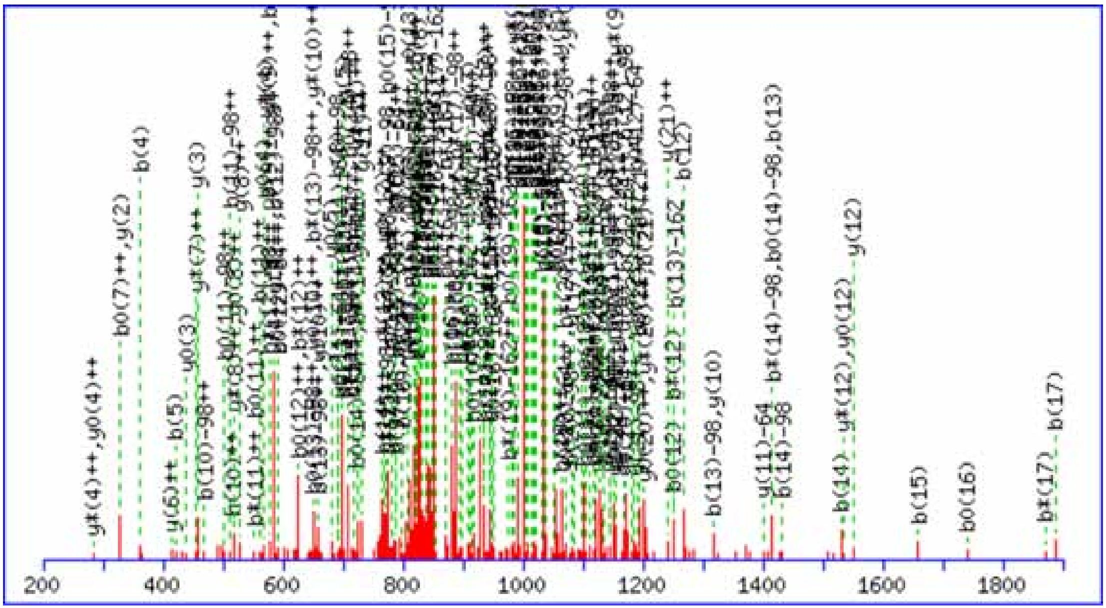
Matched b ions: b(7)-98++, b(8)-98, b(8), b(9), b(9)-98, b(9)-196, b(10), b(10)-98, b(11)-196, b(11)-98, b(12), b(12)-196++, b(12)-98++, b(12)-196, b(13)-98++, b(13), b(13)-196++, b(13)++, b(14), b(14)-196++, b(14)-98++, b(14)++, b(15), b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17), b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(16)-98++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++, y(20)-196++, y(21)-196++
Precursor origin neutral loss: +

Peptide No.35

AGAEGSSNVFSMFDQTQIQEFK
Confirmed sites:
Ambiguous sites: @S:6orS:7

MS/MS Fragmentation of AGAEGSSNVFSMFDQTQIQEFK
Found in MLRS_MOUSE, Myosin regulatory light chain 2, skeletal muscle isoform OS=Mus musculus GN=Mylpf PE=1 SV=3

Match to Query 6795: 2584.184064 from(862.401964,3+)
Title: Elution from: 63.361 to 63.361 scan no 5995 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2584.1829
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K22 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 71 **Expect:** 7.9e-006

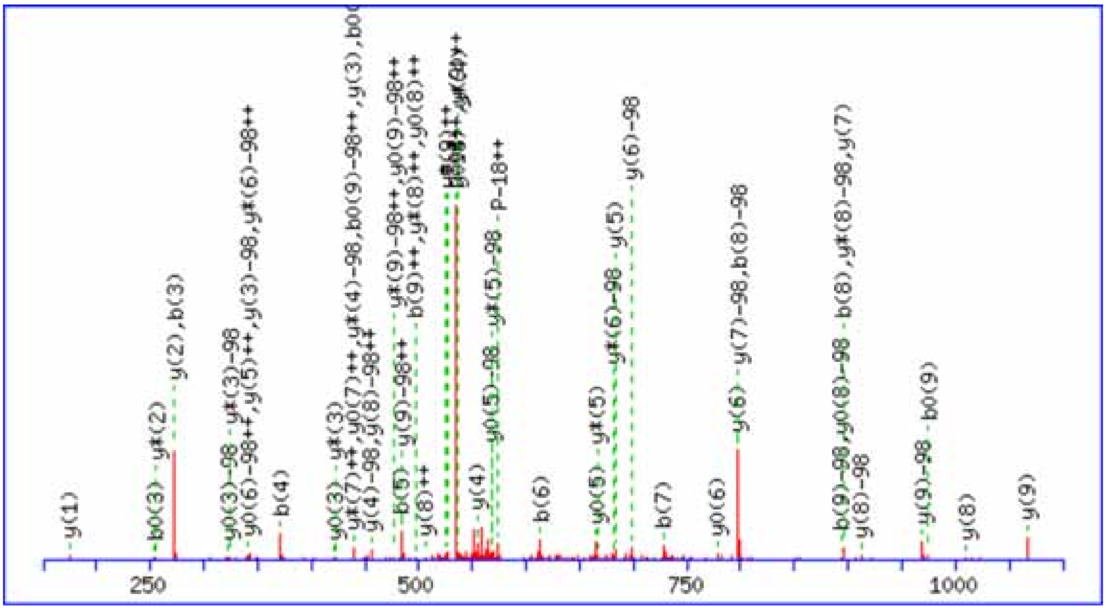
Matched b ions: b(4), b(5), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10)++, b(10), b(10)-98++, b(10)-98, b(11)-98++, b(11)++, b(11), b(12)-98++, b(12)-98, b(12), b(13)-98, b(13), b(13)++, b(13)-98++, b(14), b(14)++, b(14)-98, b(14)-98++, b(15), b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17), b(17)++, b(17)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(12)++, y(12), y(13)++, y(14)++, y(17)-98++, y(17)++, y(18)++, y(19)-98++, y(21)++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.36

AGDVLEDSPK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of AGDVLEDSPK
Found in HDGF_MOUSE, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 1086: 1165.526868 from(583.770710,2+)
Title: Elution from: 28.519 to 28.519 scan no 2100 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1165.5268
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K10 : Dimethyl (K)
Ions Score: 58 Expect: 3.8e-005

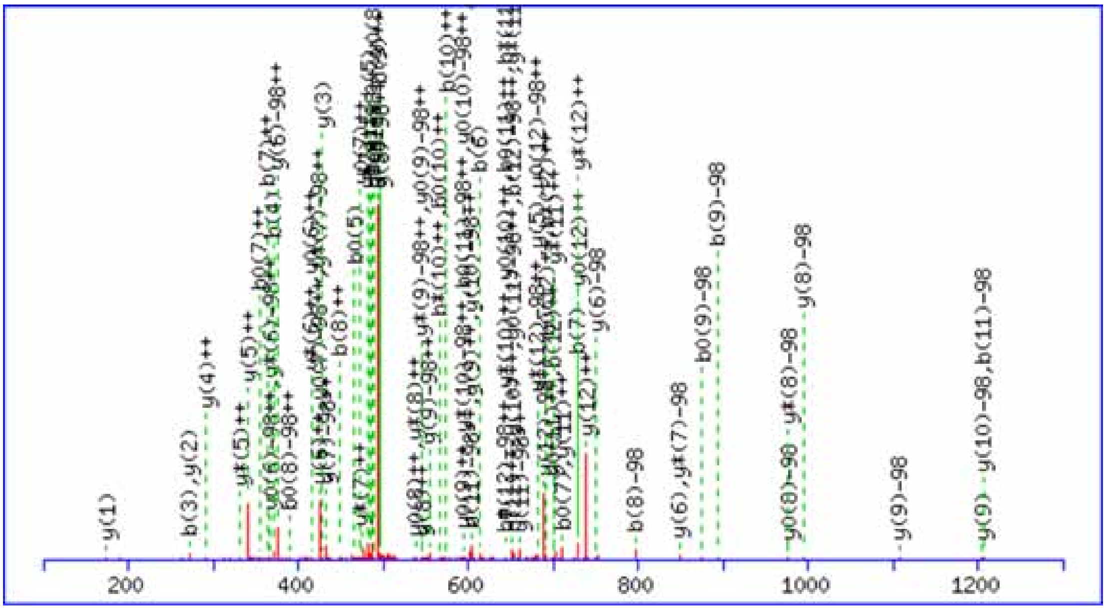
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)-98, b(8), b(9)-98, b(9)++
Matched y ions: y(1), y(2), y(3), y(3)-98, y(4)-98, y(4), y(5)++, y(5), y(6)-98, y(6), y(7)-98, y(7), y(8)-98++, y(8), y(8)-98, y(8)++, y(9)++, y(9)-98, y(9), y(9)-98++
Precursor origin neutral loss: +

Peptide No.37

AGDVLEDSPKRPK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of AGDVLEDSPKRPK
Found in HDGF_MOUSE, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 2909: 1574.807304 from(525.943044,3+)
Title: Elution from: 23.937 to 23.937 scan no 1490 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1574.8069
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K10 : Dimethyl (K)
K13 : Dimethyl (K)
Ions Score: 56 **Expect:** 0.00013

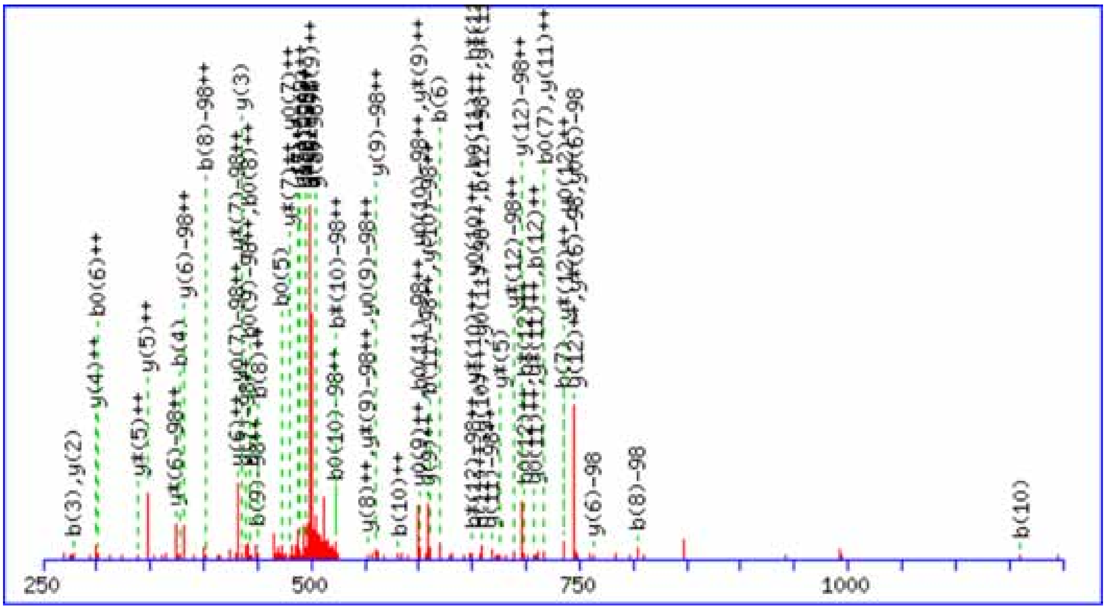
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(7)++, b(8)-98, b(8)++, b(9)-98, b(9)++, b(10)++, b(11)-98++, b(11)++, b(11)-98, b(12)-98++, b(12)++
Matched y ions: y(1), y(2), y(3), y(4)++, y(5)++, y(5), y(6)++, y(6)-98++, y(6), y(6)-98, y(7)++, y(7)-98++, y(8)-98, y(8)-98++, y(8)++, y(9)++, y(9)-98, y(9), y(9)-98++, y(10)-98++, y(10)++, y(10)-98, y(11)-98++, y(11)++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.38

AGDVLEDSPKRPK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of AGDVLEDSPKRPK
Found in HDGF_MOUSE, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 2603: 1592.903106 from(531.974978,3+)
Title: Elution from: 23.906 to 23.906 scan no 1363 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1592.9023
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K10 : Dimethyl:2H(4)13C(2) (K)
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 31 Expect: 0.028

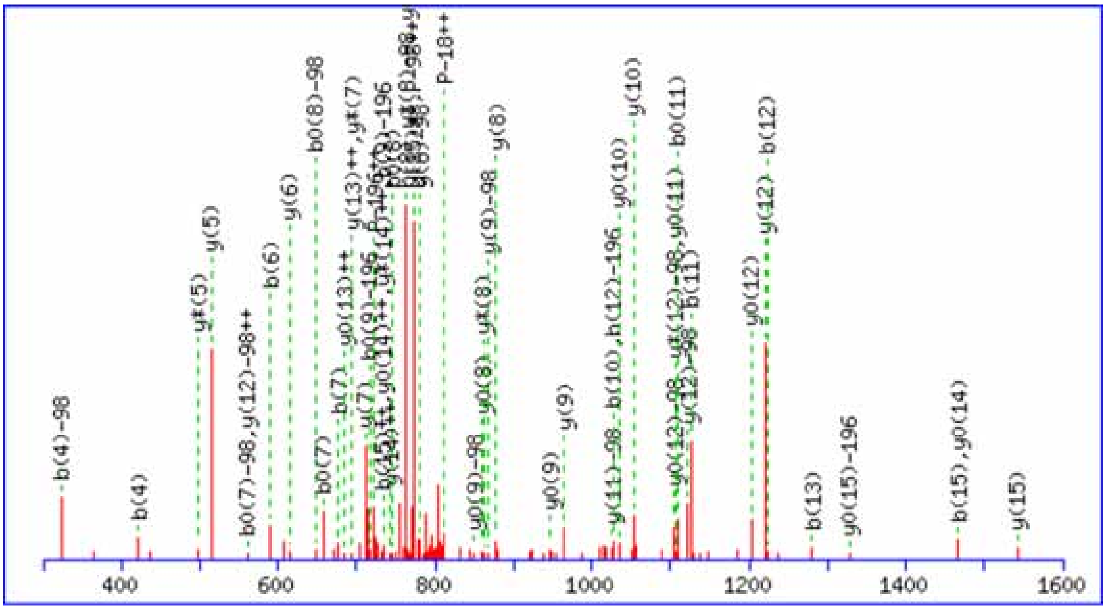
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)-98, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10), b(10)++, b(11)++, b(11)-98++, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4)++, y(5)++, y(6)++, y(6)-98++, y(6)-98, y(7)-98++, y(7)++, y(8)-98++, y(8)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.39

AGPSPASSSPVPGGER
Confirmed sites: @S:4,@S:9
Ambiguous sites:

MS/MS Fragmentation of AGPSPASSSPVPGGER
Found in SRPK3_MOUSE, Serine/threonine-protein kinase SRPK3 OS=Mus musculus GN=Srpk3 PE=2 SV=1

Match to Query 3362: 1639.664430 from(820.839491,2+)
Title: Elution from: 28.351 to 28.351 scan no 2078 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1639.6644
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 0.00018

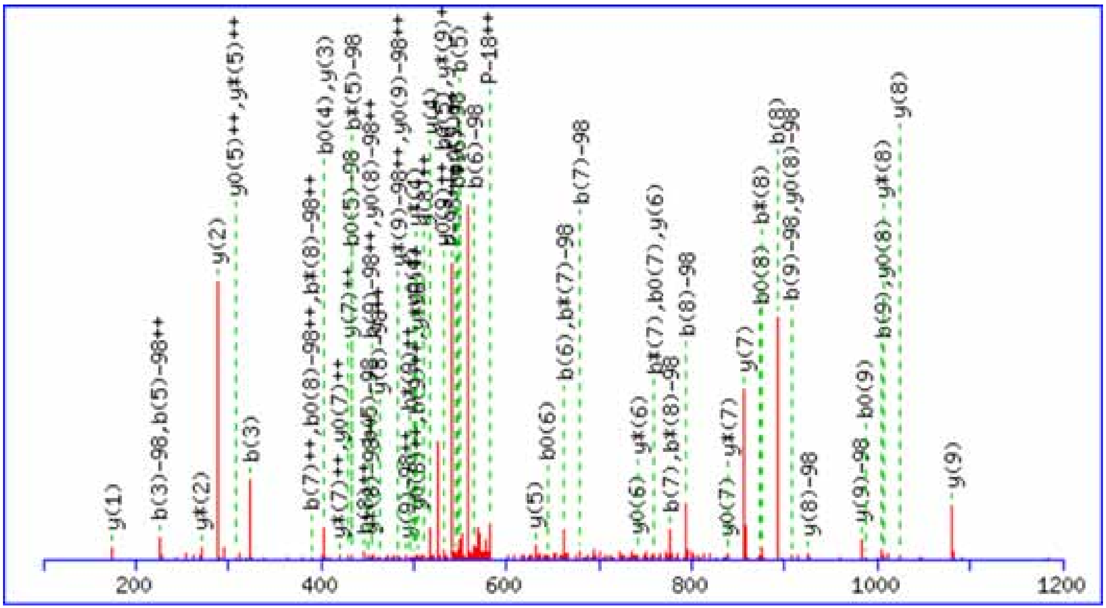
Matched b ions: b(4)-98, b(4), b(6), b(7), b(8), b(9)-98, b(9)-196, b(10), b(11)-98++, b(11), b(11)-98, b(12), b(12)-196, b(13), b(15), b(15)-98++, b(15)++
Matched y ions: y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(11)-98, y(12)-98, y(12), y(12)-98++, y(13)++, y(14)++, y(15), y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.40

AGSPQLDDIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AGSPQLDDIR
Found in EI2BE_MOUSE, Translation initiation factor eIF-2B subunit epsilon OS=Mus musculus GN=Eif2b5 PE=1 SV=1

Match to Query 1134: 1178.533948 from(590.274250,2+)
Title: Elution from: 35.473 to 35.473 scan no 3053 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1178.5332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00039

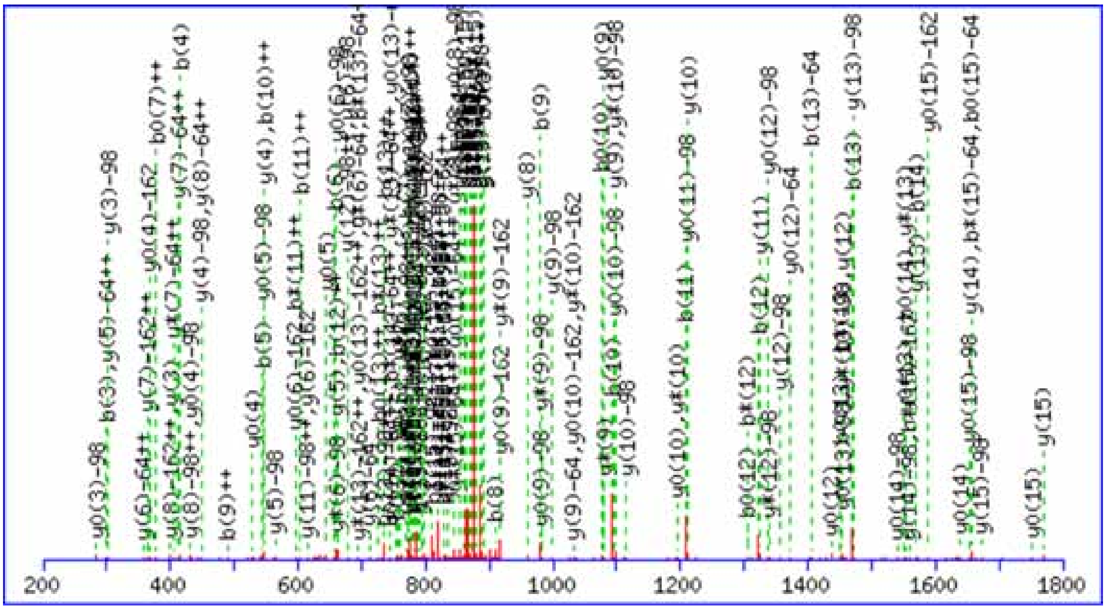
Matched b ions: b(3)-98, b(3), b(5)-98++, b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7), b(7)++, b(8), b(8)++, b(8)-98, b(9), b(9)-98, b(9)-98++, b(9)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)-98, y(8), y(8)-98++, y(8)++, y(9)-98, y(9), y(9)++, y(9)-98++
Precursor origin neutral loss: +

Peptide No.41

AISDELDHALNDMTSI
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AISDELDHALNDMTSI
Found in TPM3_MOUSE, Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2

Match to Query 3823: 1867.792852 from(934.903702,2+)
Title: Elution from: 57.570 to 57.570 scan no 5252 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1867.7910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 88 **Expect:** 5.5e-008

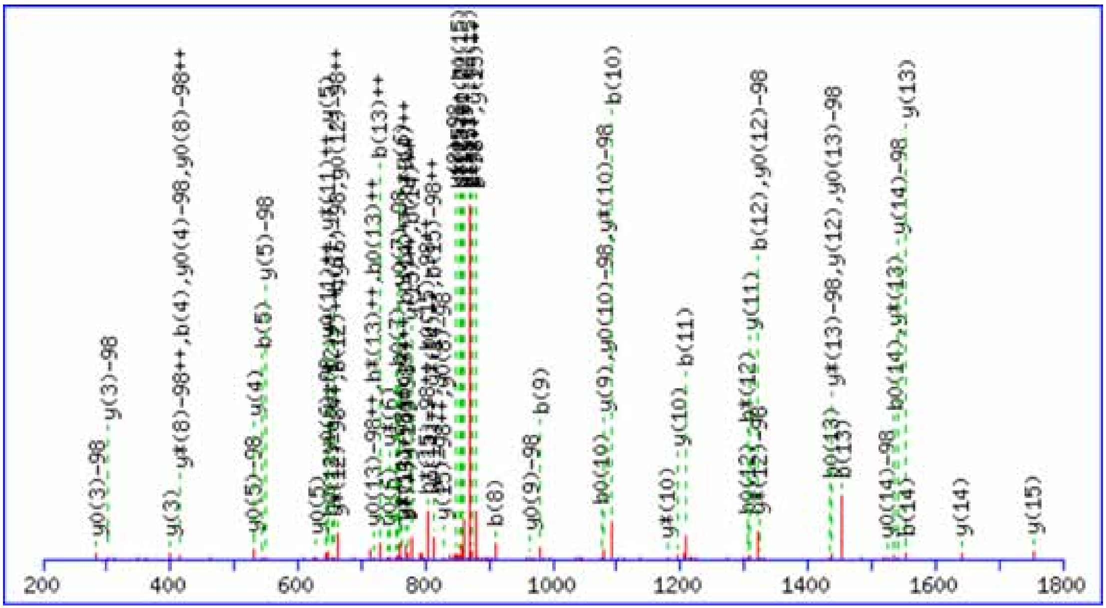
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(9)++, b(10), b(10)++, b(11), b(11)++, b(12), b(12)++, b(13), b(13)++, b(14), b(14)++, b(15)-98++, b(15)++
Matched y ions: y(3), y(3)-98, y(4), y(4)-98, y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)-98++, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)-98++, y(12), y(12)-98, y(12)-98++, y(13), y(13)++, y(13)-98, y(13)-98++, y(14), y(14)-98++, y(14)-98, y(14)++, y(15)++, y(15), y(15)-98, y(15)-98++
Precursor origin neutral loss: +

Peptide No.42

AISDELDHALNDMTSI
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AISDELDHALNDMTSI
Found in TPM3_MOUSE, Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2

Match to Query 4691: 1851.796798 from(926.905675,2+)
Title: Elution from: 67.381 to 67.381 scan no 6535 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1851.7961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 99 Expect: 5.2e-009

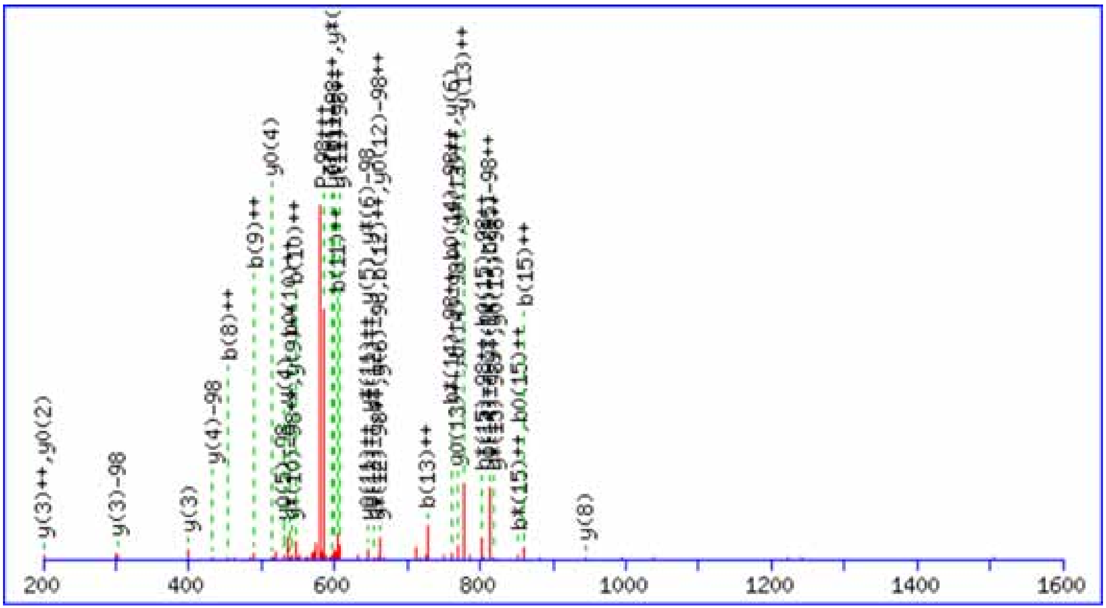
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12)++, b(12), b(13), b(13)++, b(14)++, b(14), b(15)-98++, b(15)++
Matched y ions: y(3), y(3)-98, y(4), y(5), y(5)-98, y(6)-98, y(6), y(7), y(8)-98, y(9), y(10), y(11), y(12), y(13)++, y(13), y(14), y(14)-98, y(14)-98++, y(15), y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.43

AISDELDHALNDMTSI
Confirmed sites: @T:14
Ambiguous sites:

MS/MS Fragmentation of AISDELDHALNDMTSI
Found in TPM3_MOUSE, Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2

Match to Query 3998: 1851.796413 from(618.272747,3+)
Title: Elution from: 67.170 to 67.170 scan no 6306 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1851.7961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.011

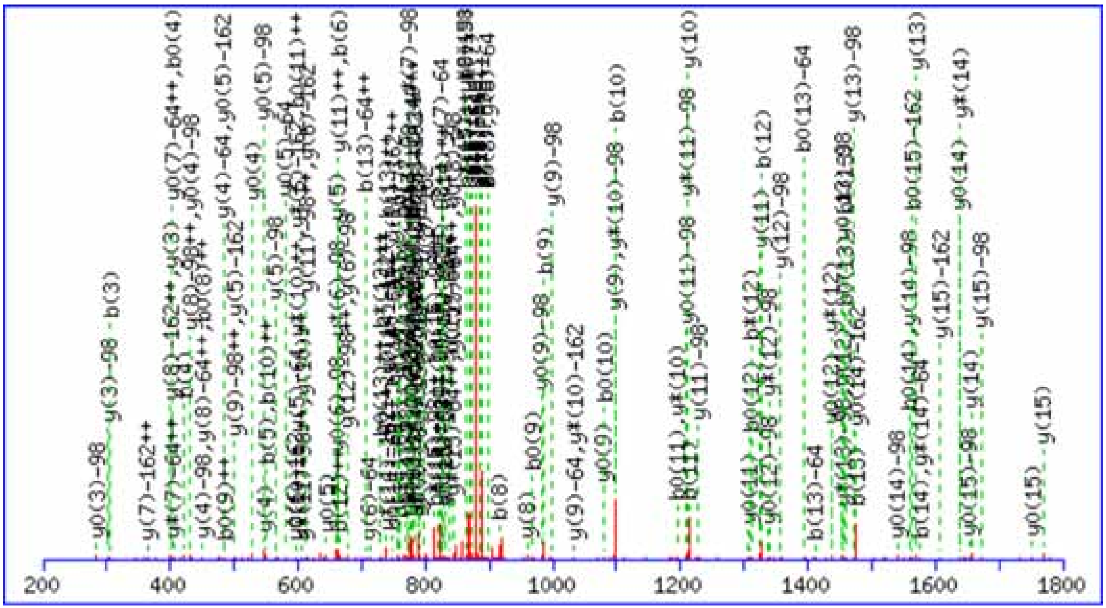
Matched b ions: b(8)++, b(9)++, b(10)++, b(11)++, b(12)++, b(13)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(3), y(3)++, y(3)-98, y(4)-98, y(4), y(5), y(6)-98, y(6), y(8), y(9)++, y(10)++, y(11)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.44

AISDELDHALNDMTSI
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of **AISDELDHALNDMTSI**
Found in **TPM3_MOUSE**, Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2

Match to Query 3588: 1873.823372 from(937.918962,2+)
Title: Elution from: 57.677 to 57.677 scan no 5365 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1873.8229
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 87 Expect: 8.7e-008

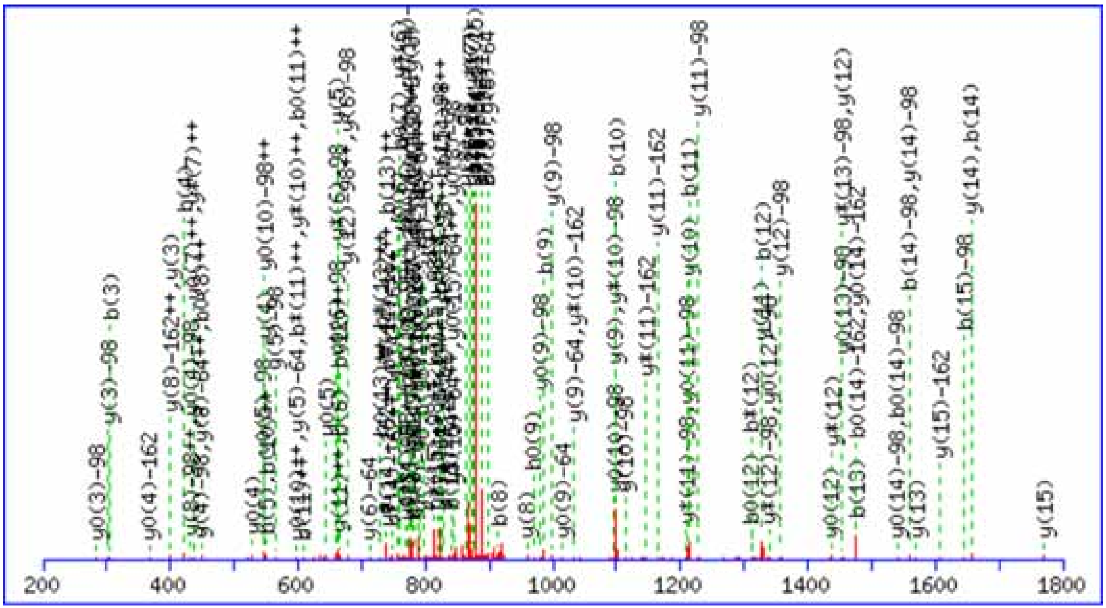
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(10)++, b(11), b(12), b(12)++, b(13), b(13)++, b(14), b(14)++, b(15)-98++, b(15)++
Matched y ions: y(3), y(3)-98, y(4), y(4)-98, y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)-98++, y(8), y(8)-98, y(9), y(9)-98, y(9)-98++, y(10), y(10)++, y(11), y(11)++, y(11)-98++, y(11)-98, y(12), y(12)-98++, y(12)-98, y(13), y(13)-98, y(14), y(14)-98++, y(14)-98, y(14)++, y(15), y(15)-98, y(15)++
Precursor origin neutral loss: +

Peptide No.45

AISDELDHALNDMTSI
Confirmed sites: @T:14
Ambiguous sites:

MS/MS Fragmentation of AISDELDHALNDMTSI
Found in TPM3_MOUSE, Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2

Match to Query 4218: 1873.822996 from(937.918774,2+)
Title: Elution from: 57.944 to 57.944 scan no 5517 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1873.8229
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 Expect: 3.8e-007

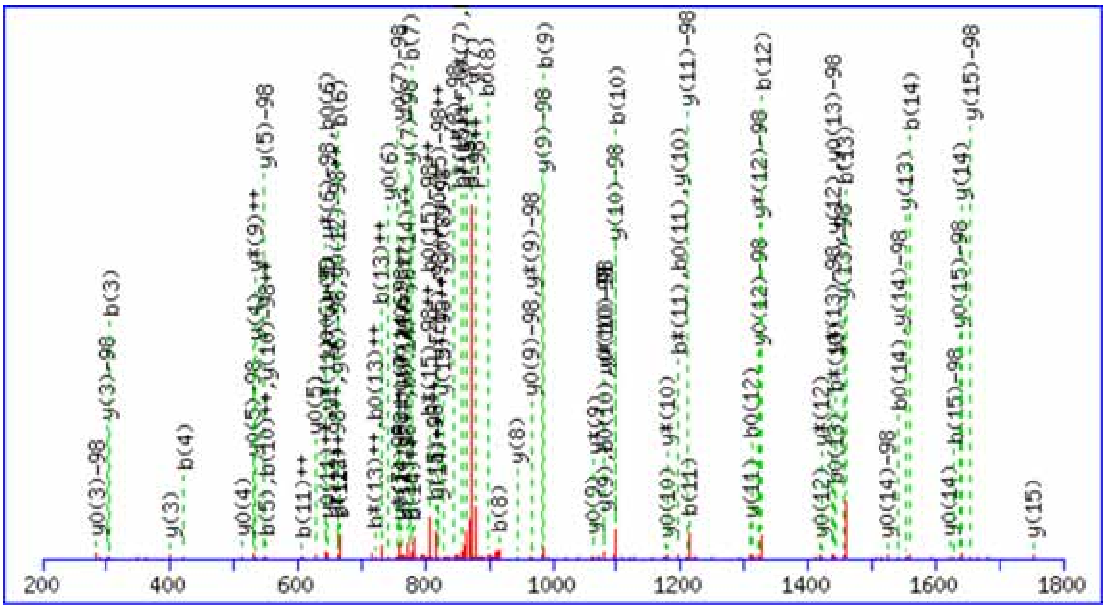
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(10)++, b(11), b(11)++, b(12), b(12)++, b(13), b(13)++, b(14)-98, b(14), b(14)-98++, b(14)++, b(15)-98++, b(15)-98, b(15)++
Matched y ions: y(3), y(3)-98, y(4), y(4)-98, y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)-98++, y(8)-98, y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)++, y(11)-98, y(12)-98++, y(12), y(12)-98, y(13), y(14)-98, y(14), y(14)-98++, y(14)++, y(15)
Precursor origin neutral loss: +

Peptide No.46

AISDELDHALNDMTSI
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AISDELDHALNDMTSI
Found in TPM3_MOUSE, Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2

Match to Query 5416: 1857.828868 from(929.921710,2+)
Title: Elution from: 67.391 to 67.391 scan no 6668 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1857.8279
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 92 Expect: 2.9e-008

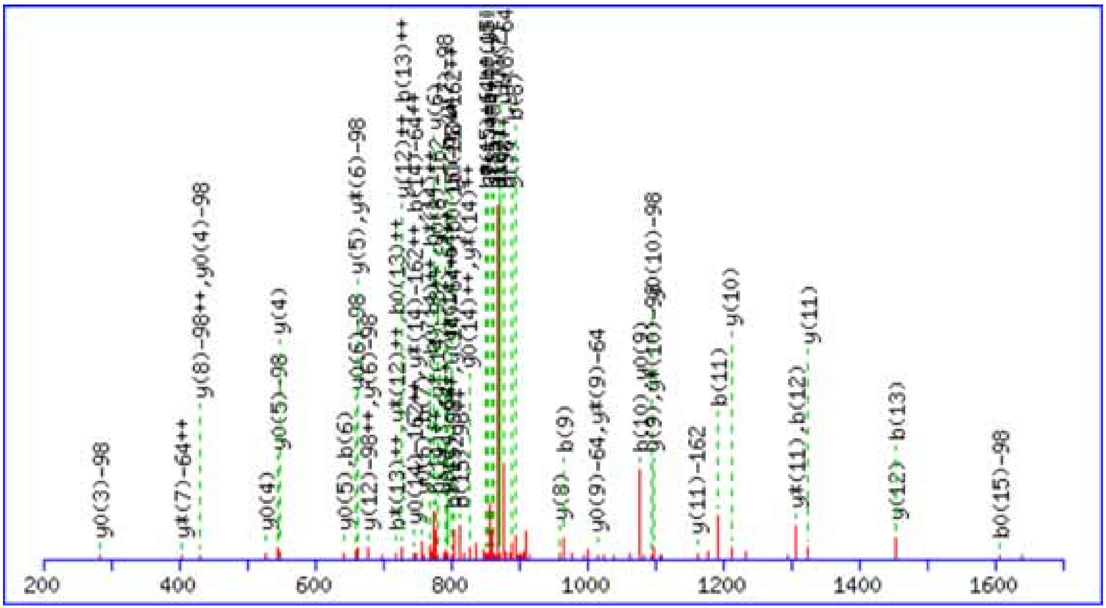
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(10)++, b(11), b(11)++, b(12)++, b(12), b(13), b(13)++, b(14)++, b(14), b(15)-98++, b(15)-98, b(15)++
Matched y ions: y(3), y(3)-98, y(4), y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)-98, y(8), y(9), y(9)-98, y(10)-98, y(10), y(10)-98++, y(11), y(11)-98, y(12), y(13), y(13)-98, y(14), y(14)-98++, y(14)-98, y(14)++, y(15), y(15)-98, y(15)-98++
Precursor origin neutral loss: +

Peptide No.47

AISEELDHALNDMTSI
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AISEELDHALNDMTSI
Found in TPM1_MOUSE, Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1

Match to Query 4703: 1853.776852 from(927.895702,2+)
Title: Elution from: 59.038 to 59.038 scan no 5853 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1853.7754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0025

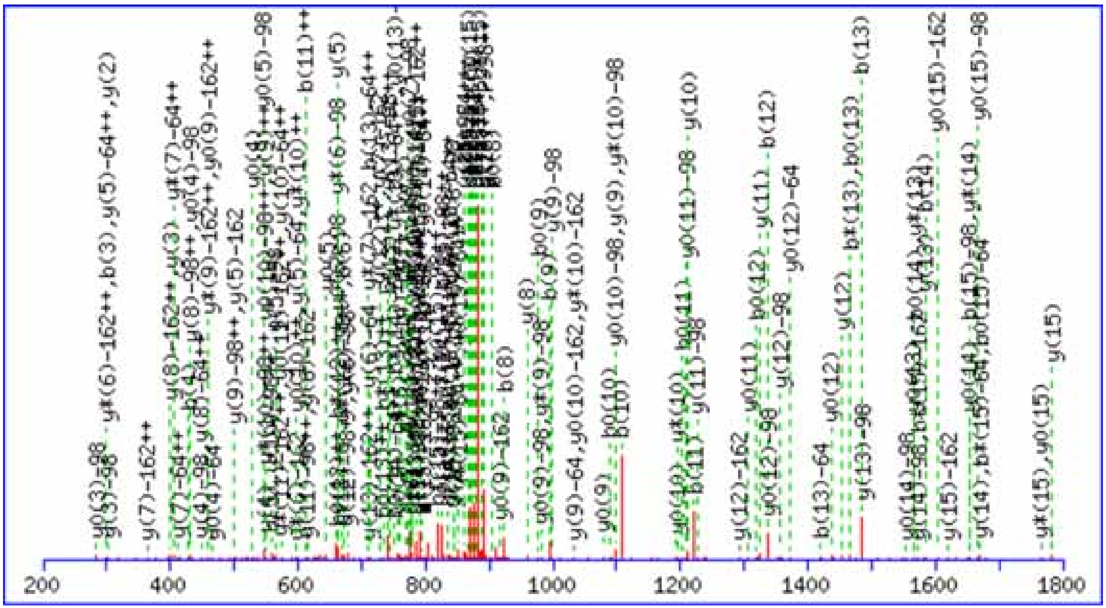
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13), b(13)++, b(14)++, b(15)-98++, b(15)++
Matched y ions: y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8)-98++, y(8)-98, y(8), y(9), y(10), y(11), y(12)-98++, y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.48

AISEELDHALNDMTSI
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AISEELDHALNDMTSI
Found in TPM1_MOUSE, Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1

Match to Query 5713: 1881.808188 from(941.911370,2+)
Title: Elution from: 55.938 to 55.938 scan no 5592 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1881.8067
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 88 **Expect:** 8e-008

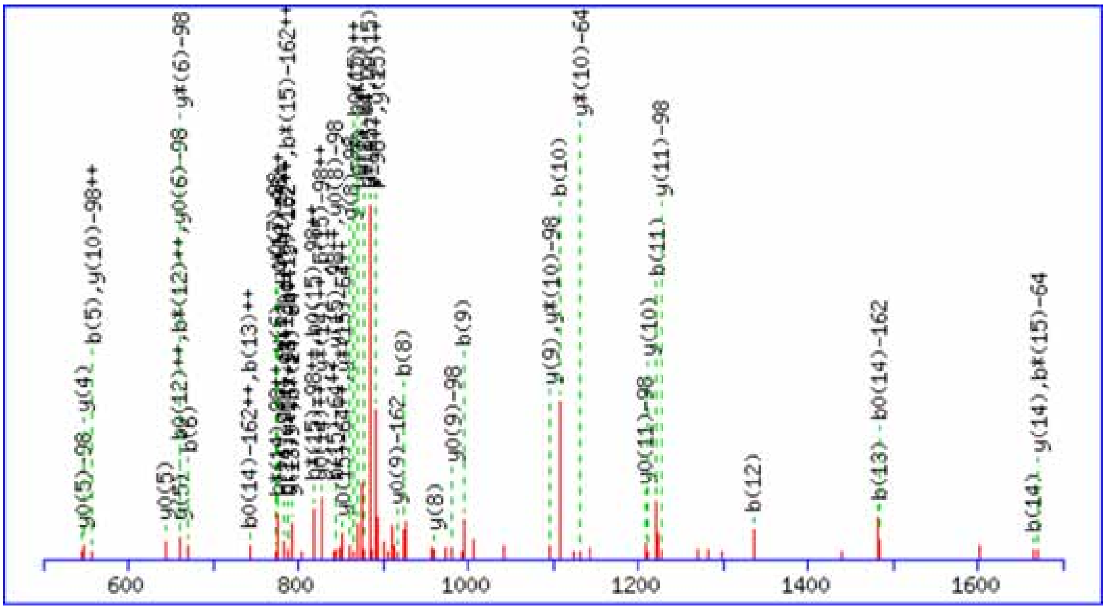
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(11)++, b(12), b(12)++, b(13), b(13)++, b(14), b(14)++, b(15)-98++, b(15)-98, b(15)++
Matched y ions: y(2), y(3), y(3)-98, y(4), y(4)-98, y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)-98++, y(8), y(8)-98, y(9), y(9)-98, y(9)++, y(9)-98++, y(10)-98++, y(10), y(11), y(11)-98++, y(11)-98, y(12)-98++, y(12), y(12)++, y(12)-98, y(13), y(13)++, y(13)-98, y(13)-98++, y(14)-98, y(14), y(14)-98++, y(14)++, y(15)++, y(15), y(15)-98++
Precursor origin neutral loss: +

Peptide No.49

AISEELDHALNDMTSI
Confirmed sites: @T:14
Ambiguous sites:

MS/MS Fragmentation of AISEELDHALNDMTSI
Found in TPM1_MOUSE, Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1

Match to Query 3970: 1881.810788 from(941.912670,2+)
Title: Elution from: 81.186 to 81.186 scan no 7225 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1881.8067
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.0025

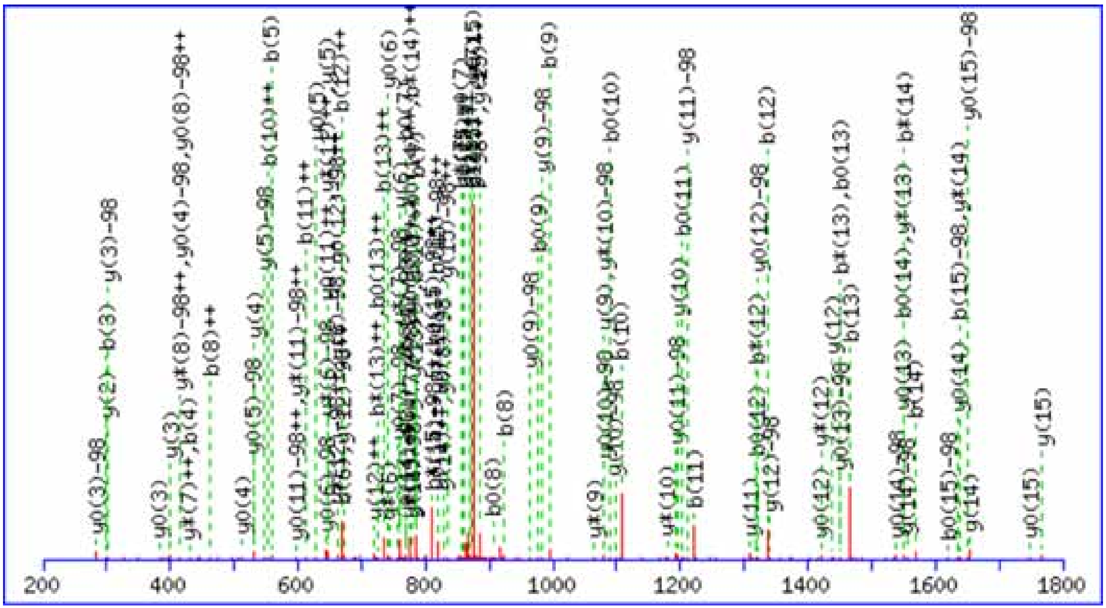
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13), b(13)++, b(14), b(14)-98++, b(15)-98++
Matched y ions: y(4), y(5), y(6), y(8), y(8)-98, y(9), y(10)-98++, y(10), y(11)-98, y(13)++, y(14), y(14)-98++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.50

AISEELDHALNDMTSI
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AISEELDHALNDMTSI
Found in TPM1_MOUSE, Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1

Match to Query 5493: 1865.813482 from(933.914017,2+)
Title: Elution from: 65.326 to 65.326 scan no 6484 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1865.8118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 89 **Expect:** 5.8e-008

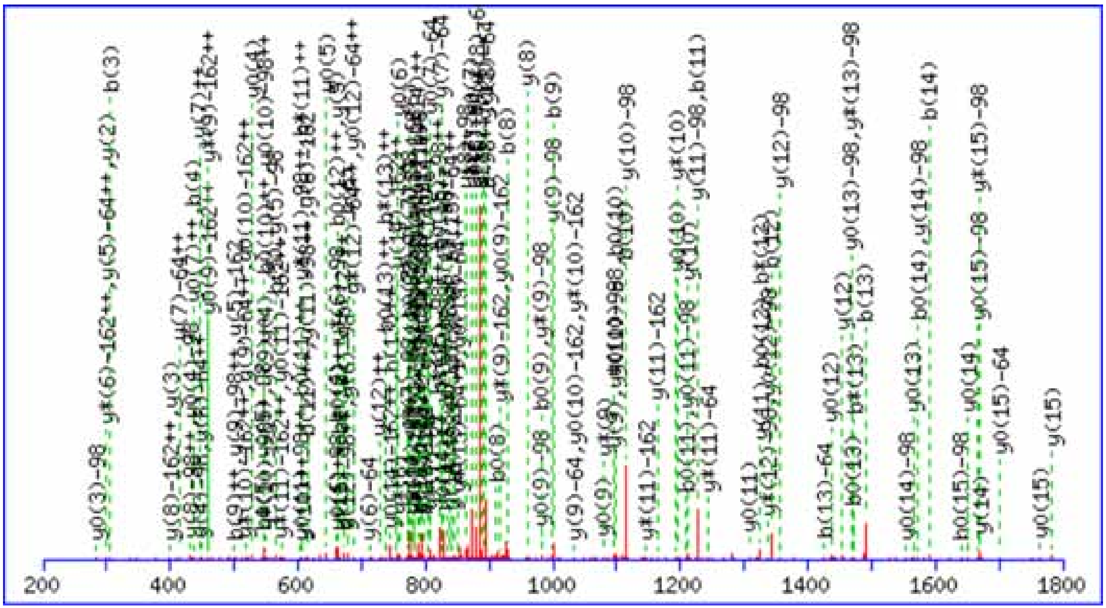
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(8)++, b(9), b(10), b(10)++, b(11), b(11)++, b(12)++, b(12), b(13)++, b(13), b(14), b(14)++, b(15)-98, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(3)-98, y(4), y(5), y(5)-98, y(6), y(6)-98, y(7)-98, y(7), y(9), y(9)-98, y(10)-98, y(10), y(11), y(11)-98, y(12)++, y(12)-98++, y(12), y(12)-98, y(13)++, y(14), y(14)-98, y(14)-98++, y(14)++, y(15)++, y(15), y(15)-98++
Precursor origin neutral loss: +

Peptide No.51

AISEELDHALNDMTSI
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AISEELDHALNDMTSI
Found in TPM1_MOUSE, Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1

Match to Query 4108: 1887.839806 from(944.927179,2+)
Title: Elution from: 56.310 to 56.310 scan no 5306 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1887.8385
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 78 Expect: 7.9e-007

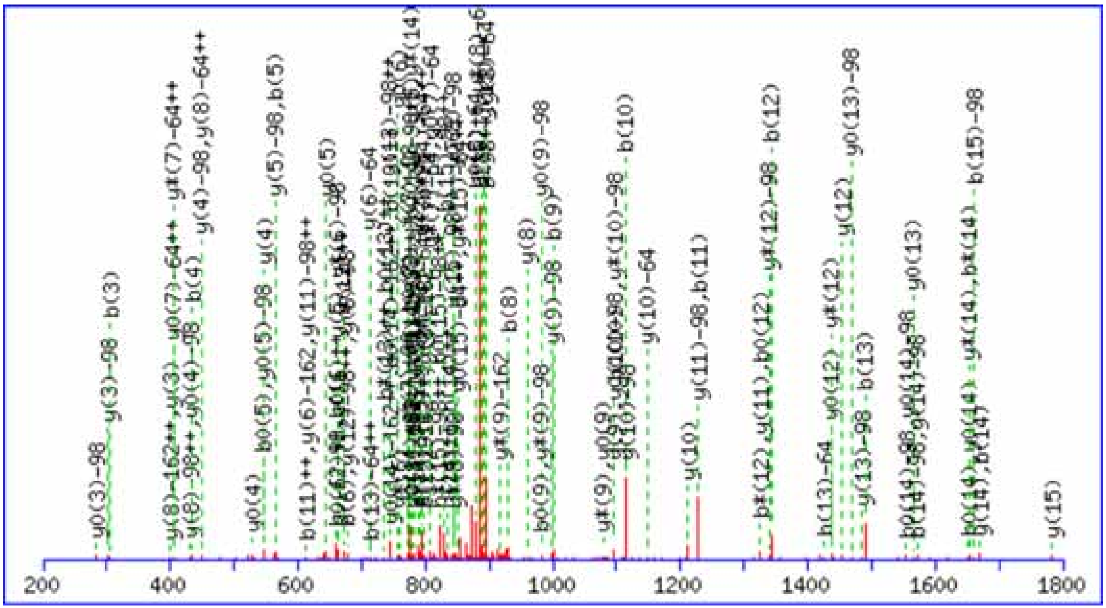
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(9)++, b(10), b(11), b(11)++, b(12), b(12)++, b(13), b(13)++, b(14), b(14)++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)++, y(7)-98, y(8)-98++, y(8)-98, y(8), y(9)-98, y(9), y(9)-98++, y(9)++, y(10), y(10)++, y(10)-98, y(11)-98, y(11), y(11)-98++, y(11)++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13)++, y(14), y(14)-98, y(14)-98++, y(14)++, y(15), y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.52

AISEELDHALNDMTSI
Confirmed sites: @T:14
Ambiguous sites:

MS/MS Fragmentation of AISEELDHALNDMTSI
Found in TPM1_MOUSE, Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1

Match to Query 4270: 1887.839582 from(944.927067,2+)
Title: Elution from: 55.646 to 55.646 scan no 5257 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1887.8385
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 1.2e-005

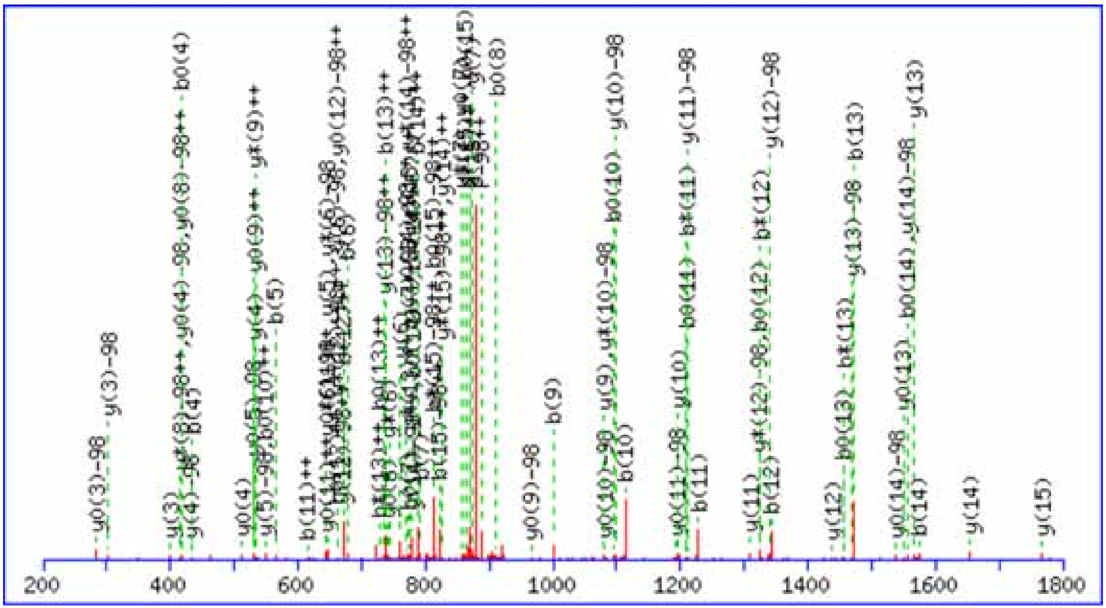
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(11)++, b(12), b(12)++, b(13), b(13)++, b(14), b(14)-98, b(14)-98++, b(14)++, b(15)-98, b(15)-98++, b(15)++
Matched y ions: y(3)-98, y(3), y(4), y(4)-98, y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(8)-98++, y(8), y(9)-98, y(9), y(10), y(10)-98, y(11)-98, y(11), y(11)++, y(11)-98++, y(12), y(12)-98++, y(13)-98, y(13)-98++, y(13)++, y(14), y(14)-98, y(14)-98++, y(14)++, y(15), y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.53

AISEELDHALNDMTSI
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AISEELDHALNDMTSI
Found in TPM1_MOUSE, Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1

Match to Query 4309: 1871.843634 from(936.929093,2+)
Title: Elution from: 65.501 to 65.501 scan no 6160 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1871.8436
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 2.9e-006

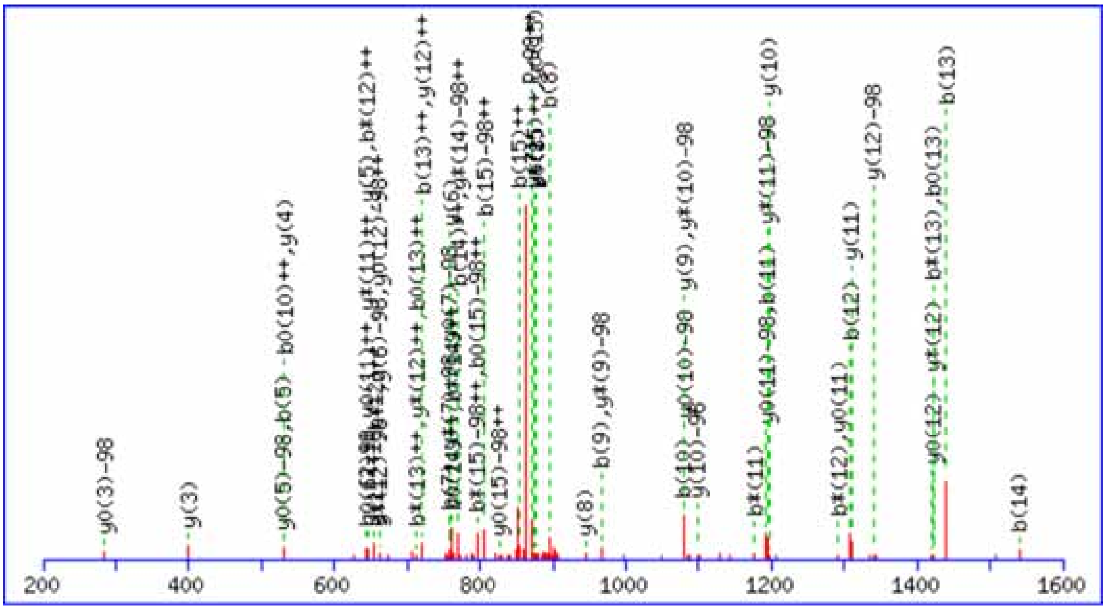
Matched b ions: b(4), b(5), b(6), b(7), b(9), b(10), b(11), b(11)++, b(12)++, b(12), b(13)++, b(13), b(14), b(14)++, b(15)-98++, b(15)++
Matched y ions: y(3), y(3)-98, y(4), y(4)-98, y(5)-98, y(5), y(6), y(6)-98, y(7)-98, y(7), y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98++, y(12)-98, y(13), y(13)-98++, y(13)-98, y(14), y(14)-98++, y(14)-98, y(14)++, y(15)
Precursor origin neutral loss:

Peptide No.54

AISEELDHALNDMTSI
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AISEELDHALNDMTSI
Found in TPM1_MOUSE, Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1

Match to Query 3258: 1837.783732 from(919.899142,2+)
Title: Elution from: 68.516 to 68.516 scan no 6265 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1837.7805
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 0.00013

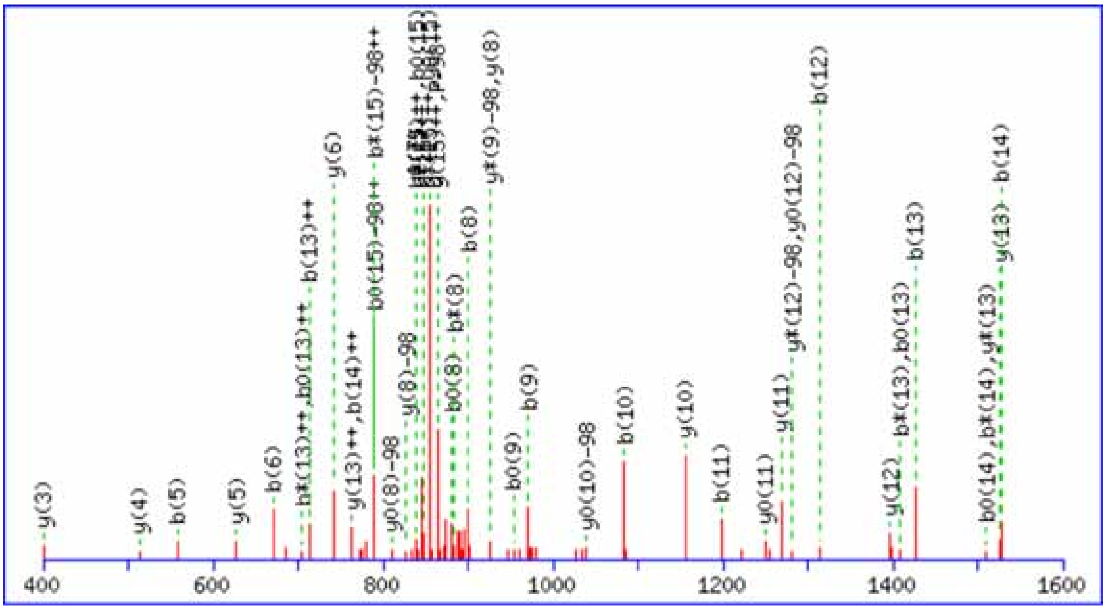
Matched b ions: b(5), b(7), b(8), b(9), b(10), b(11), b(12)++, b(12), b(13), b(13)++, b(14), b(14)++, b(15)-98++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)-98, y(7), y(8), y(9), y(10), y(10)-98, y(11)++, y(11), y(12)++, y(12)-98
Precursor origin neutral loss: +

Peptide No.55

AISEELDNALNDITSL
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AISEELDNALNDITSL
Found in TPM2_MOUSE, Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=1

Match to Query 3581: 1824.841560 from(913.428056,2+)
Title: Elution from: 67.695 to 67.695 scan no 6329 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1824.8394
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 92 Expect: 3.4e-008

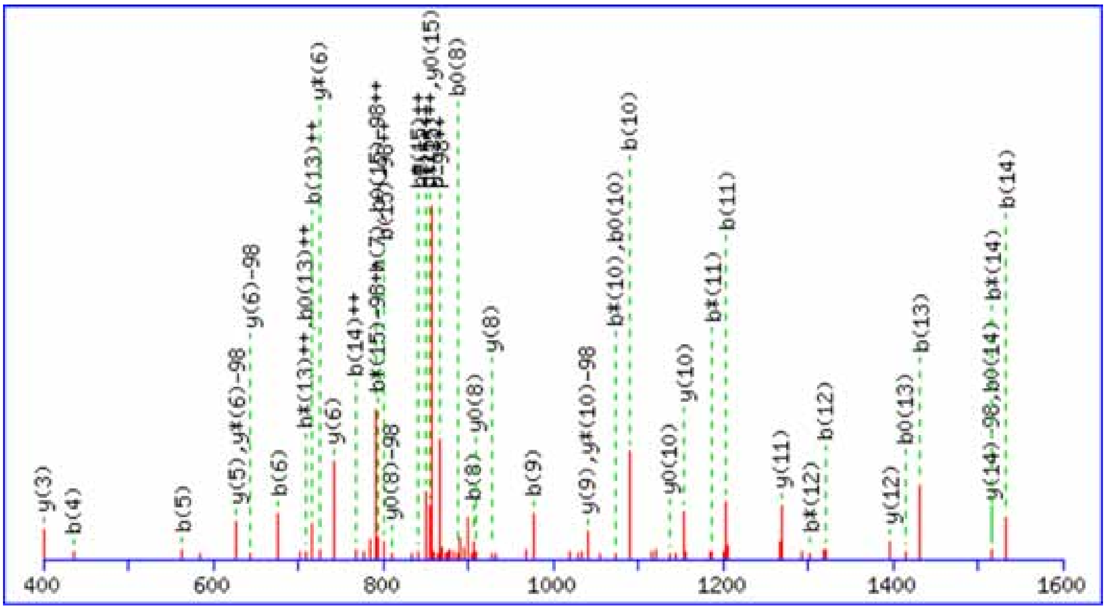
Matched b ions: b(5), b(6), b(8), b(9), b(10), b(11), b(12), b(13), b(13)++, b(14), b(14)++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(10), y(11), y(12), y(13), y(13)++, y(15)++
Precursor origin neutral loss: +

Peptide No.56

AISEELDNALNDITSL
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of AISEELDNALNDITSL
Found in TPM2_MOUSE, Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=1

Match to Query 3859: 1830.872790 from(916.443671,2+)
Title: Elution from: 75.687 to 75.687 scan no 6935 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1830.8712
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 84 Expect: 2.6e-007

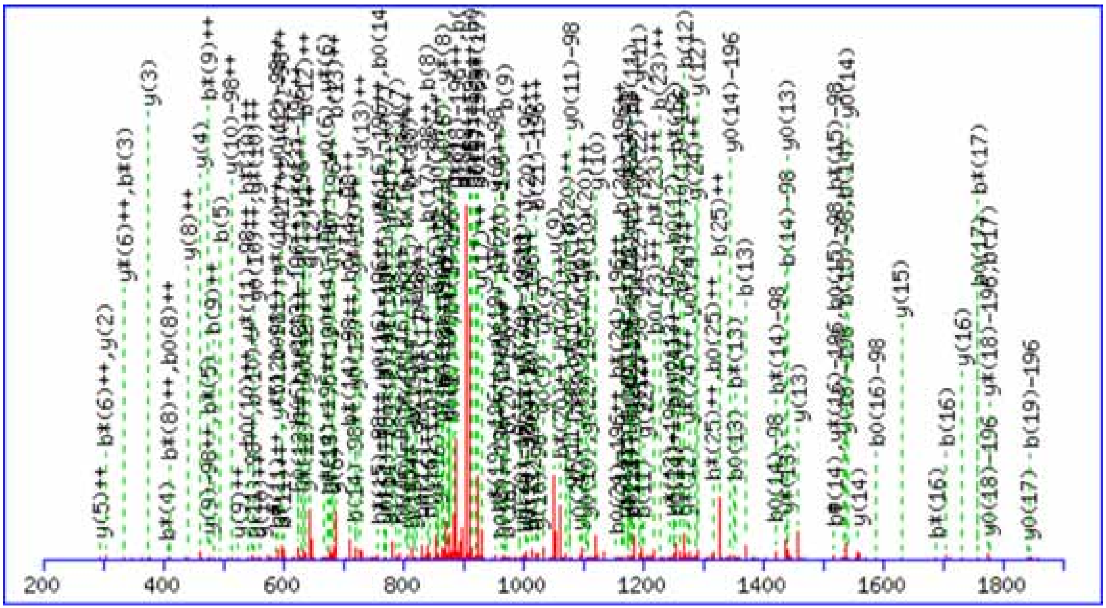
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13), b(13)++, b(14), b(14)++, b(15)++, b(15)-98++
Matched y ions: y(3), y(5), y(6), y(6)-98, y(7), y(8), y(9), y(10), y(11), y(12), y(14)-98
Precursor origin neutral loss: +

Peptide No.57

AKPAAQSEEETATSPAASPTPQSAER
Confirmed sites: @S:14,@S:18
Ambiguous sites:

MS/MS Fragmentation of AKPAAQSEEETATSPAASPTPQSAER
Found in EIF3B_MOUSE, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 8345: 2827.232226 from(943.418018,3+)
Title: Elution from: 26.740 to 26.740 scan no 1857 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2827.2314
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 **Expect:** 4e-007

Matched b ions: b(5), b(6), b(8), b(9)++, b(9), b(10)++, b(10), b(11), b(11)++, b(12), b(12)++, b(13), b(13)++, b(14), b(14)-98, b(14)-98++, b(14)++, b(15)-98, b(15)-98++, b(15)++, b(16), b(16)++, b(16)-98++, b(17)++, b(17), b(17)-98++, b(18)-98, b(18)-98++, b(18)-196++, b(18)++, b(19)-196, b(19)-196++, b(19)-98++, b(20)-98++, b(20)++, b(20)-196++, b(21)-196++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++, b(23)++, b(24)++, b(24)-196++, b(24)-98++, b(25)++, b(25)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7), y(8), y(8)++, y(9), y(9)-98++, y(9)++, y(9)-98, y(10), y(10)-98++, y(10)-98, y(10)++, y(11)-98++, y(11)++, y(11), y(12)++, y(12)-98++, y(12), y(12)-98, y(13), y(13)++, y(13)-196, y(13)-196++, y(13)-98++, y(13)-98, y(14)++, y(14), y(14)-98++, y(14)-98, y(14)-196++, y(15), y(15)-98++, y(15)++, y(15)-98, y(16), y(16)++, y(16)-196++, y(16)-98++, y(16)-196, y(17)++, y(17)-98++, y(18)++, y(20)-196++, y(20)-98++, y(20)++, y(21)++, y(22)-196++, y(22)++, y(24)++
Precursor origin neutral loss: +

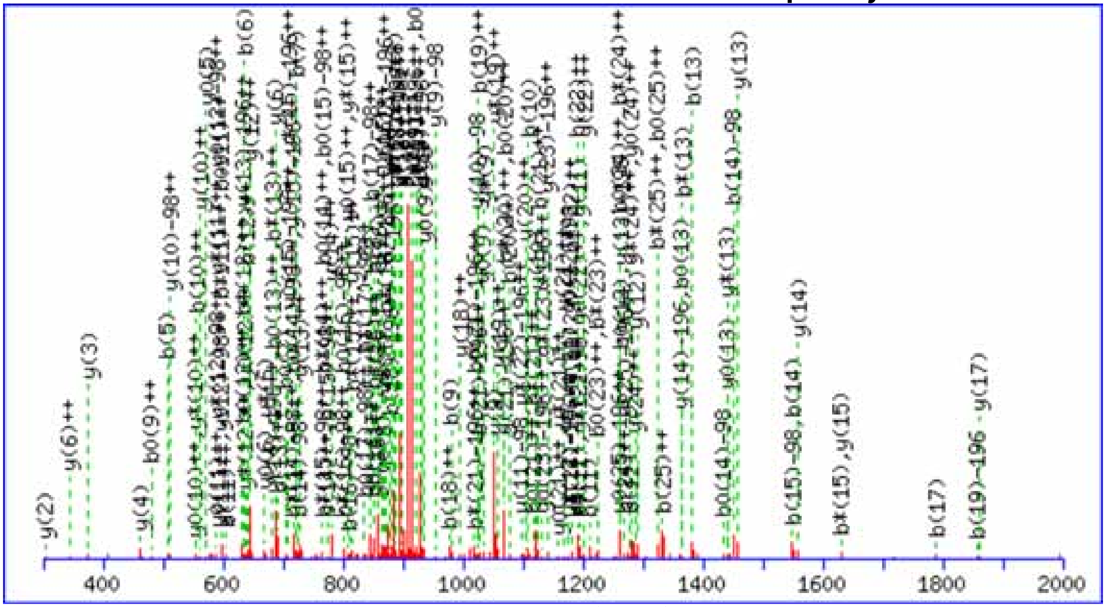
Peptide No.58

AKPAAQSEEETATSPAASPTPQSAER
Confirmed sites: @S:14,@S:18
Ambiguous sites:

MS/MS Fragmentation of AKPAAQSEEETATSPAASPTPQSAER
Found in EIF3B_MOUSE, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 6513: 2839.295949 from(947.439259,3+)

Title: Elution from: 26.612 to 26.612 scan no 1700 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2839.2950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K2 : Dimethyl:2H(4)13C(2) (K)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 78 Expect: 1.3e-006

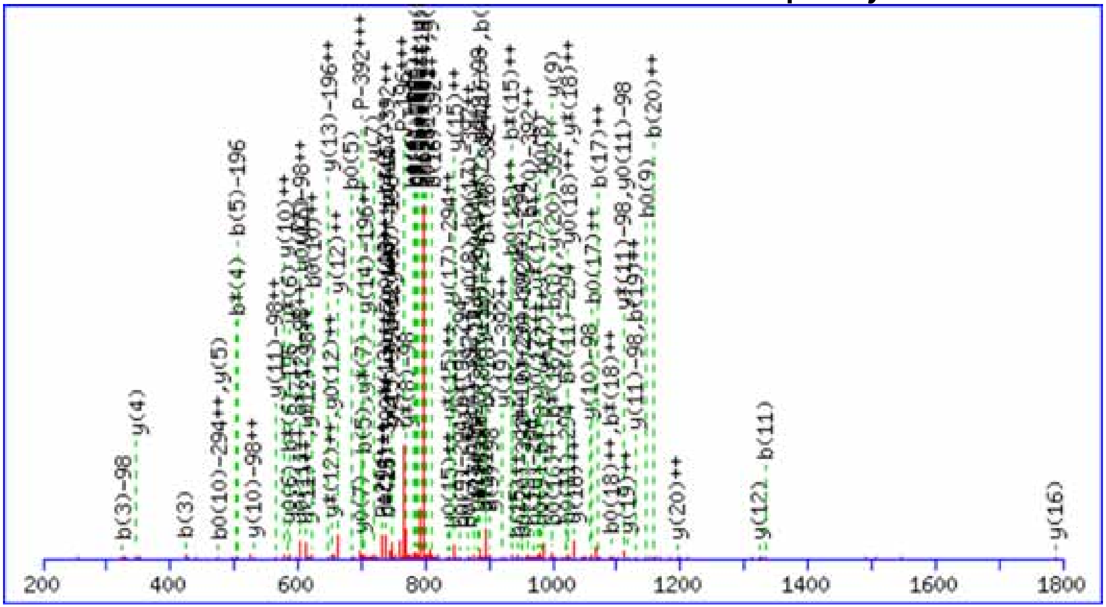
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10)++, b(10), b(11), b(11)++, b(12), b(12)++, b(13)++, b(13), b(14)-98, b(14), b(14)-98++, b(14)++, b(15)-98, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17), b(17)-98++, b(18)-98, b(18)-98++, b(18)++, b(18)-196++, b(19)-196, b(19)-196++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(21)-196++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(24)-98++, b(24)++, b(25)++, b(25)-98++
Matched y ions: y(2), y(3), y(4), y(6), y(6)++, y(8), y(9), y(9)-98, y(10), y(10)-98++, y(10)++, y(10)-98, y(11)++, y(11), y(11)-98, y(12)-98++, y(12)++, y(12), y(12)-98, y(13), y(13)++, y(13)-196++, y(13)-98++, y(13)-98, y(13)-196, y(14)++, y(14), y(14)-196++, y(14)-98++, y(14)-196, y(15), y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(17), y(17)++, y(17)-98++, y(18)-196++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(21)-196++, y(21)++, y(22)++, y(23)-98++, y(23)-196++, y(24)++, y(25)-196++
Precursor origin neutral loss: +

Peptide No.59

AKSPTPSLSPARNSDQEGGGK
Confirmed sites: @S:3,@T:5,@S:9,@S:14
Ambiguous sites:

MS/MS Fragmentation of AKSPTPSLSPARNSDQEGGGK
Found in SRRM1_MOUSE, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=1

Match to Query 7502: 2486.991195 from(830.004341,3+)
Title: Elution from: 27.178 to 27.178 scan no 1918 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2486.9886
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl (K)
Ions Score: 46 **Expect:** 0.00094

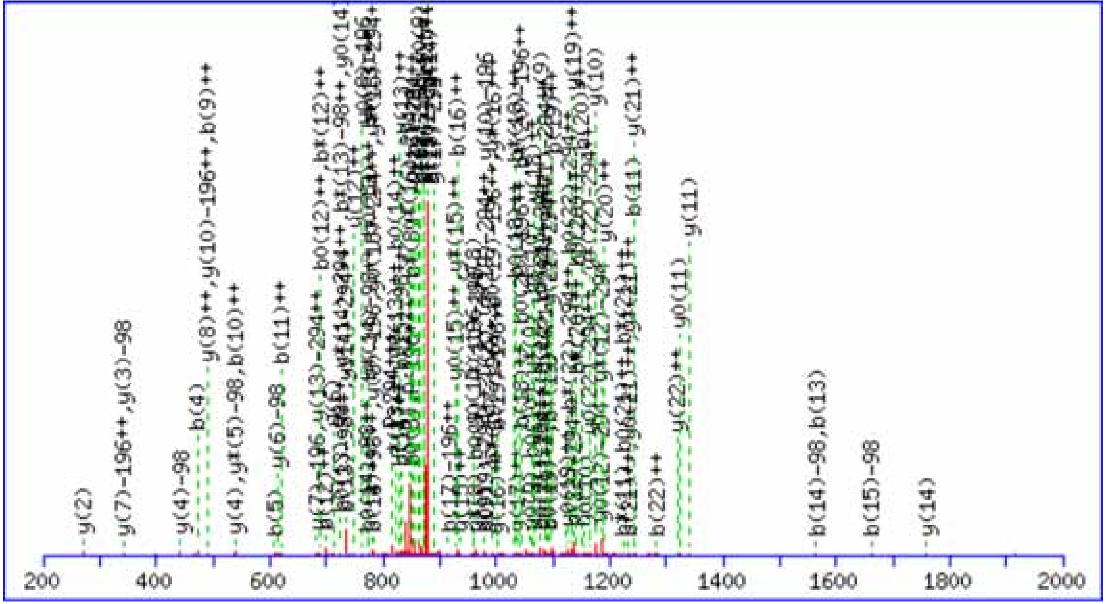
Matched b ions: b(3), b(3)-98, b(5)-98, b(5)-196, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(8)-196, b(9)-98, b(9)-196, b(10)-196, b(10)-294, b(11), b(11)-98++, b(12)++, b(12)-98++, b(12)-196++, b(13)-98, b(13)-98++, b(13)-196++, b(13)++, b(14)-294++, b(14)++, b(14)-196++, b(14)-98++, b(15)-98++, b(15)-98, b(15)-196++, b(15)-392++, b(15)++, b(16)-392++, b(16)-98++, b(17)++, b(17)-392++, b(17)-196++, b(17)-98++, b(18)-294++, b(19)-294++, b(19)++, b(20)++, b(20)-392++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-98++, y(10)++, y(10)-98, y(11)++, y(11)-98++, y(11)-98, y(12)-98++, y(12)++, y(12), y(13)++, y(13)-98++, y(13)-196++, y(14)-98, y(14)-98++, y(14)-196++, y(14)++, y(15)-98++, y(15)++, y(15)-196++, y(16)++, y(16), y(16)-98++, y(17)++, y(17)-196++, y(17)-98++, y(17)-294++, y(18)++, y(18)-98++, y(18)-294++, y(18)-196++, y(19)-98++, y(19)-392++, y(19)-294++, y(19)-196++, y(19)++, y(20)-392++, y(20)++
Precursor origin neutral loss: +

Peptide No.60

AKTDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @S:13,@S:17,@S:21
Ambiguous sites:

MS/MS Fragmentation of AKTDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 8593: 2737.217061 from(913.412963,3+)
Title: Elution from: 33.901 to 33.901 scan no 2767 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2737.2166
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
K12 : Dimethyl (K)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S21 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.0017

Matched b ions: b(4), b(5), b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(13)-98++, b(13), b(13)++, b(14)-98, b(14)-98++, b(14)++, b(15)++, b(15)-98, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)-196++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(19)-196++, b(20)-98++, b(20)++, b(21)-196++, b(21)-98++, b(21)++, b(21)-294++, b(22)-294++, b(22)-196++, b(22)++, b(22)-98++
Matched y ions: y(2), y(3)-98, y(4)-98, y(4), y(6), y(6)-98, y(7)-196++, y(7)-98, y(7), y(7)-196, y(8)-98, y(8)++, y(8), y(8)-196, y(9)-196, y(9)-98++, y(9)-98, y(9), y(10), y(10)-196++, y(10)-196, y(10)-98, y(11)-98++, y(11), y(11)-98, y(11)-196, y(12)-98++, y(12)++, y(13)-98++, y(13)-294++, y(13)++, y(14)-294++, y(14)++, y(14)-196, y(14), y(14)-196++, y(14)-98++, y(15)-98++, y(15)++, y(16)-294++, y(16)++, y(17)-294++, y(17)++, y(18)++, y(19)++, y(19)-98++, y(20)-196++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(21)-294++, y(21)-196++, y(22)++, y(22)-98++
Precursor origin neutral loss: +

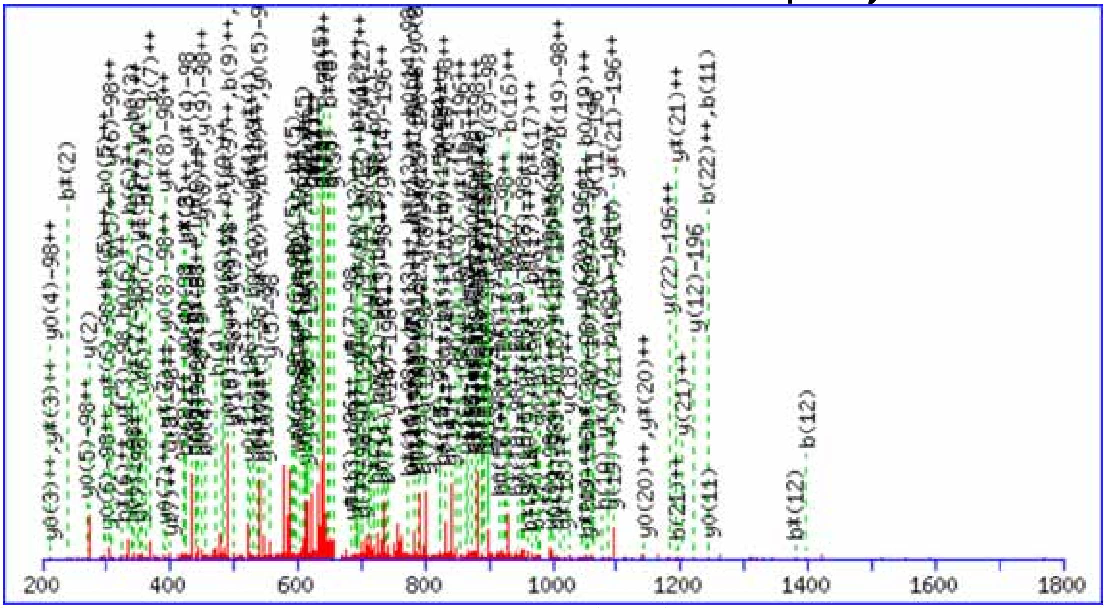
Peptide No.61

AKTDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @S:13,@S:21

Ambiguous sites:

MS/MS Fragmentation of AKTDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 7017: 2657.252824 from(665.320482,4+)
Title: Elution from: 32.277 to 32.277 scan no 2410 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2657.2503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
K12 : Dimethyl (K)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 75 Expect: 3.1e-006

Matched b ions: b(4), b(5)++, b(5), b(6)++, b(7)++, b(7), b(8)++, b(8), b(9)++, b(10)++, b(10), b(11)++, b(11), b(12), b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(21)++, b(22)++, b(22)-98++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5)-98, y(5), y(6)++, y(6), y(6)-98++, y(6)-98, y(7), y(7)++, y(7)-98++, y(7)-98, y(8)-98++, y(8), y(8)-98, y(8)++, y(9)-98++, y(9)-98, y(9), y(9)++, y(10), y(10)-98, y(10)++, y(10)-98++, y(11)-98, y(11)-98++, y(11)++, y(11)-196, y(12)-196, y(12)-196++, y(12)++, y(13)++, y(13)-196++, y(13)-98++, y(14)-98++, y(14)++, y(14)-196++, y(15)-196++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)++, y(17)-196++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-196++, y(20)-196++, y(21)++, y(22)-196++
Precursor origin neutral loss: +

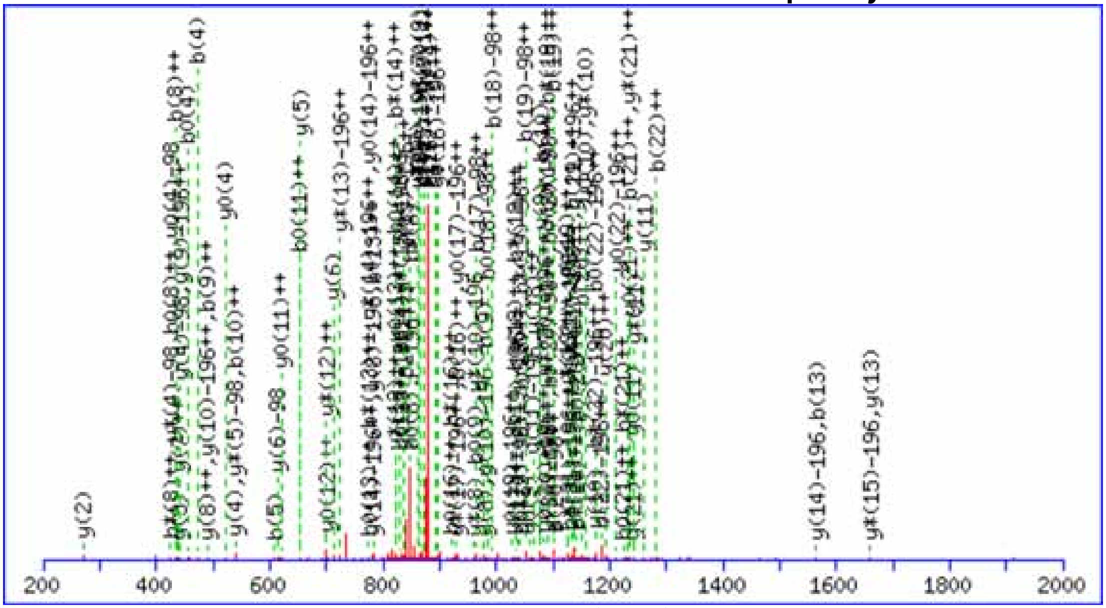
Peptide No.62

AKTDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @Y:11,@S:17,@S:21

Ambiguous sites:

MS/MS Fragmentation of AKTDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 6598: 2737.218300 from(913.413376,3+)
Title: Elution from: 33.892 to 33.892 scan no 2525 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2737.2166
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
Y11 : Phospho (Y)
K12 : Dimethyl (K)
S17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S21 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 0.00043

Matched b ions: b(4), b(5), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(13), b(13)++, b(14)++, b(15)++, b(16)++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-196++, b(21)-98++, b(21)++, b(22)-196++, b(22)++, b(22)-98++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5), y(6), y(6)-98, y(7), y(7)++, y(7)-98, y(8)-98, y(8)++, y(8), y(8)-98++, y(8)-196, y(9)-196, y(9)-196++, y(9)-98++, y(9)-98, y(9), y(10), y(10)-196++, y(10)-98, y(10)-196, y(11)-196, y(11)-98, y(11), y(13), y(13)-98++, y(13)++, y(14)++, y(14)-196, y(14)-196++, y(14)-98++, y(15)-196++, y(15)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-196++, y(19)++, y(19)-98++, y(20)-196++, y(20)-98++, y(20)++, y(21)-98++, y(21)++
Precursor origin neutral loss: +

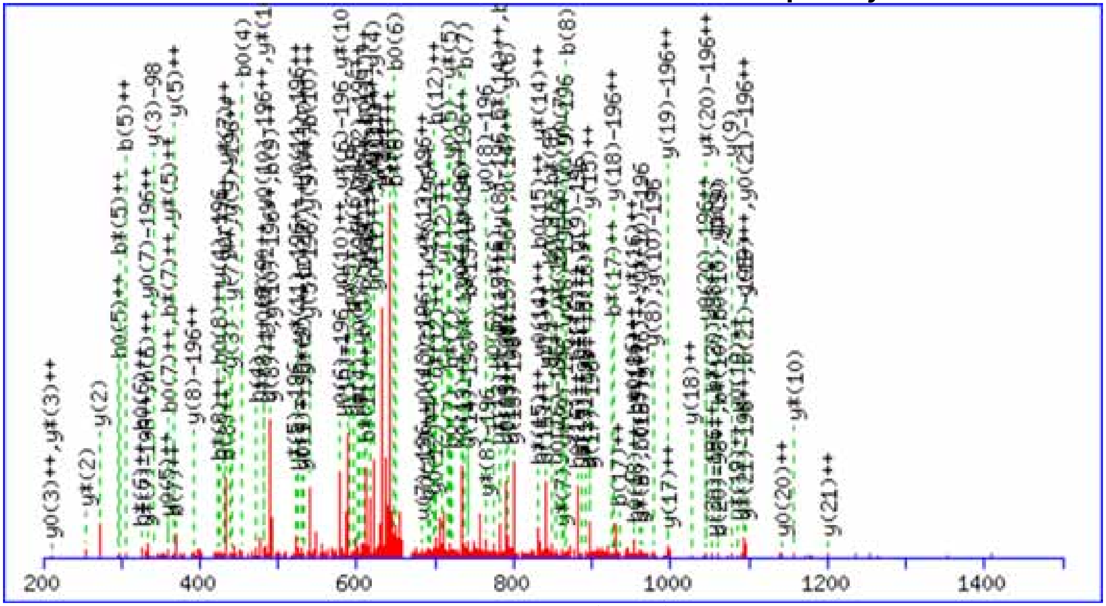
Peptide No.63

AKTDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @T:20,@S:21

Ambiguous sites:

MS/MS Fragmentation of AKTDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 6966: 2657.252460 from(665.320391,4+)
Title: Elution from: 32.091 to 32.091 scan no 2388 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2657.2503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
K12 : Dimethyl (K)
T20 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S21 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 0.001

Matched b ions: b(4), b(5)++, b(5), b(6)++, b(7)++, b(7), b(8)++, b(8), b(9)++, b(10)++, b(11)++, b(12)++, b(13)++, b(14)++, b(15)++, b(16)++, b(17)++, b(18)++, b(20)-98++, b(21)-196++
Matched y ions: y(2), y(3)-98, y(3), y(4), y(4)-98, y(4)-196, y(5)-196, y(5)-98, y(5)++, y(6), y(6)-98++, y(6)-196, y(6)-98, y(7)-98++, y(7)++, y(7)-196, y(7)-98, y(8)++, y(8)-98, y(8)-196, y(8)-196++, y(8)-98++, y(8), y(9)-98++, y(9)-196, y(9)++, y(9), y(9)-196++, y(10)-196++, y(10)++, y(10)-98++, y(10)-196, y(11)-196++, y(11)-98++, y(11)++, y(12)-196++, y(12)++, y(13)++, y(13)-98++, y(13)-196++, y(14)++, y(14)-98++, y(14)-196++, y(15)-196++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(16)-196++, y(17)-196++, y(17)++, y(17)-98++, y(18)++, y(18)-196++, y(18)-98++, y(19)++, y(19)-98++, y(19)-196++, y(20)-196++, y(21)++
Precursor origin neutral loss: +

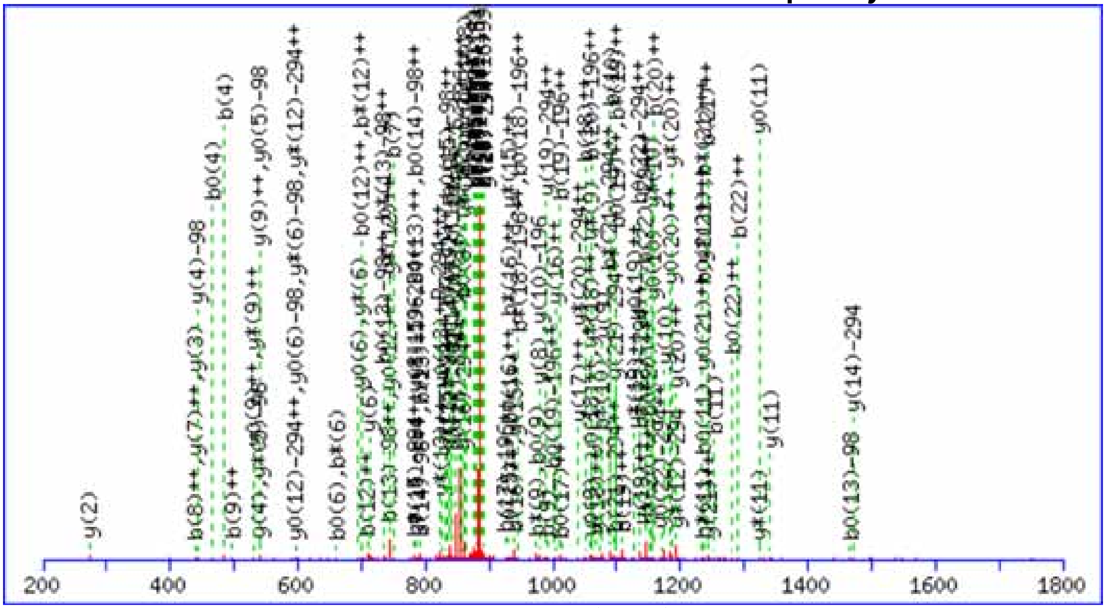
Peptide No.64

AKTDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @S:13,@S:17,@S:21

Ambiguous sites:

MS/MS Fragmentation of AKTDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 7301: 2755.312416 from(919.444748,3+)
Title: Elution from: 33.974 to 33.974 scan no 2679 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2755.3121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K2 : Dimethyl:2H(4)13C(2) (K)
K12 : Dimethyl:2H(4)13C(2) (K)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.022

Matched b ions: b(4), b(7), b(8)++, b(8), b(9)++, b(9), b(10), b(11), b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)-196++, b(18)++, b(19)-98++, b(19)++, b(19)-196++, b(20)-196++, b(20)-98++, b(20)++, b(21)-196++, b(21)-98++, b(21)++, b(21)-294++, b(22)-294++, b(22)-196++, b(22)++, b(22)-98++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(6), y(7)++, y(7), y(7)-98, y(8)-98, y(8), y(8)-196, y(9)-196, y(9)++, y(9), y(10), y(10)-196, y(10)-98, y(11)-196, y(11), y(11)-98, y(12)-98++, y(13)-98, y(13)-98++, y(13)++, y(14)-294, y(14)-196, y(14)-196++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(15)-196++, y(16)-294++, y(16)-196++, y(16)++, y(17)-98++, y(17)++, y(17)-294++, y(18)++, y(19)-98++, y(19)++, y(19)-294++, y(19)-196++, y(20)-98++, y(20)++, y(20)-196++, y(21)-294++, y(21)-196++, y(21)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.65

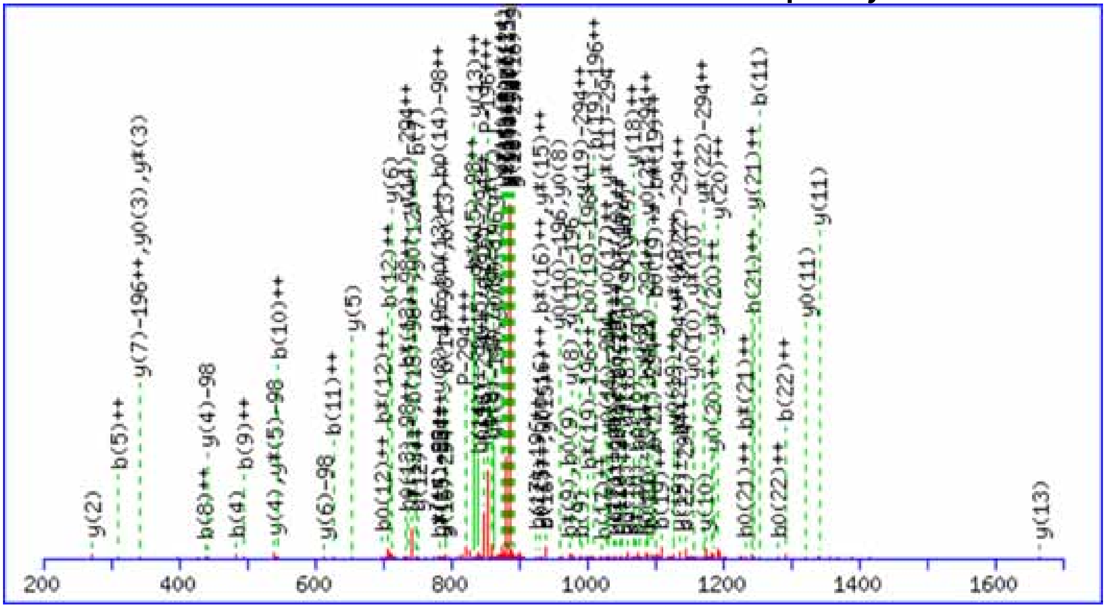
AKTDHGAEIVYKSPVVSGDTSPR

Confirmed sites: @S:13,@S:17,@T:20

Ambiguous sites:

MS/MS Fragmentation of AKTDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 7113: 2755.313565 from(919.445131,3+)
Title: Elution from: 33.796 to 33.796 scan no 2620 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2755.3121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K2 : Dimethyl:2H(4)13C(2) (K)
K12 : Dimethyl:2H(4)13C(2) (K)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 6e-005

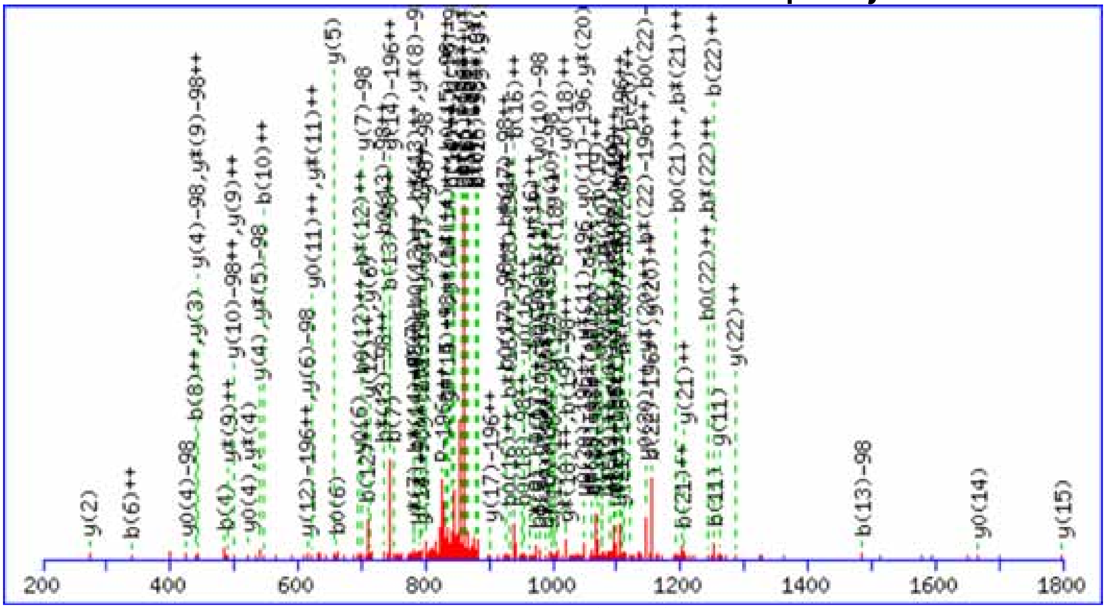
Matched b ions: b(4), b(5)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)-196++, b(17)++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(19)-196++, b(20)-196++, b(20)-98++, b(21)-196++, b(21)-98++, b(21)++, b(21)-294++, b(22)++, b(22)-294++, b(22)-196++, b(22)-98++
Matched y ions: y(2), y(4)-98, y(4), y(5), y(6)-98, y(6), y(7)-196++, y(7), y(7)-98, y(8)-98, y(8), y(8)-196, y(9)-196, y(9)-98, y(9), y(10), y(10)-196, y(10)-98, y(11)-196, y(11), y(11)-98, y(11)-294, y(12)-196++, y(12)-98++, y(12)++, y(13), y(13)-196++, y(13)-98++, y(13)++, y(14)-98, y(14)-294++, y(14)-196++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(15)-196++, y(15)-294++, y(16)-196++, y(17)++, y(17)-294++, y(17)-98++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(19)-196++, y(19)-294++, y(20)-98++, y(20)++, y(20)-196++, y(20)-294++, y(21)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.66

AKTDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @S:13,@S:21
Ambiguous sites:

MS/MS Fragmentation of AKTDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 7008: 2675.347974 from(892.789934,3+)
Title: Elution from: 32.142 to 32.142 scan no 2395 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2675.3457
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K2 : Dimethyl:2H(4)13C(2) (K)
K12 : Dimethyl:2H(4)13C(2) (K)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.0035

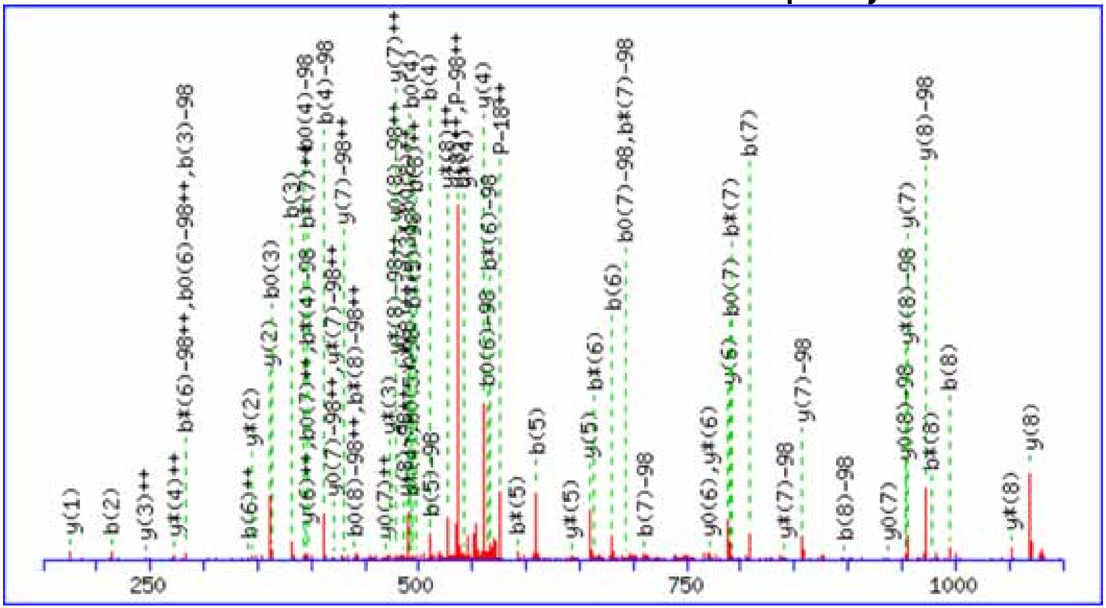
Matched b ions: b(4), b(6)++, b(7), b(8)++, b(8), b(10)++, b(10), b(11), b(12)++, b(13)-98++, b(13)-98, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(16)++, b(19)++, b(19)-98++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(21)-196++, b(22)-196++, b(22)++, b(22)-98++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5), y(6)-98, y(6), y(7)-98, y(7), y(8)-98, y(9)++, y(10), y(10)-98++, y(10)-98, y(11), y(11)-98, y(12)-98++, y(12)-98, y(12)-196++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-196++, y(14)-98++, y(15), y(15)-98++, y(16)-196++, y(16)++, y(17)-196++, y(17)++, y(18)-196++, y(18)-98++, y(19)-98++, y(19)++, y(19)-196++, y(20)++, y(20)-98++, y(21)++, y(21)-196++, y(21)-98++, y(22)++
Precursor origin neutral loss: +

Peptide No.67

ANSEVAQWR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ANSEVAQWR
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 846: 1167.507932 from(584.761242,2+)
Title: Elution from: 33.915 to 33.915 scan no 2634 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1167.5074
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 3.2e-006

Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)++, b(7), b(7)-98, b(8), b(8)-98, b(8)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(5), y(6), y(6)++, y(7)-98, y(7), y(7)-98++, y(7)++, y(8)++, y(8)-98, y(8), y(8)-98++
Precursor origin neutral loss: +

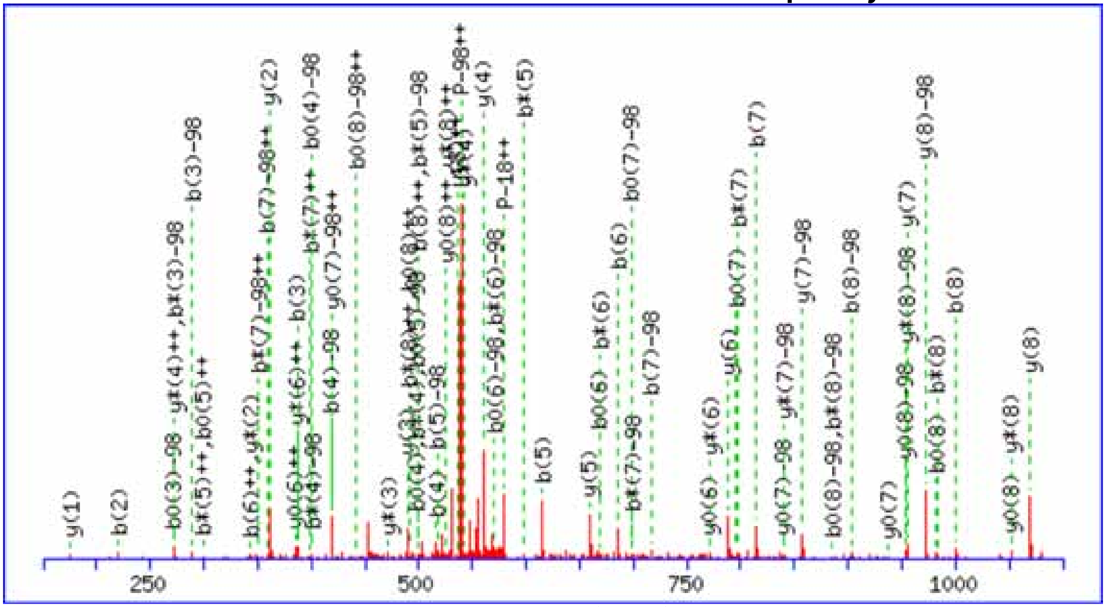
Peptide No.68

ANSEVAQWR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ANSEVAQWR
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 980: 1173.539082 from(587.776817,2+)

Title: Elution from: 33.938 to 33.938 scan no 2674 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1173.5392
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 0.00027

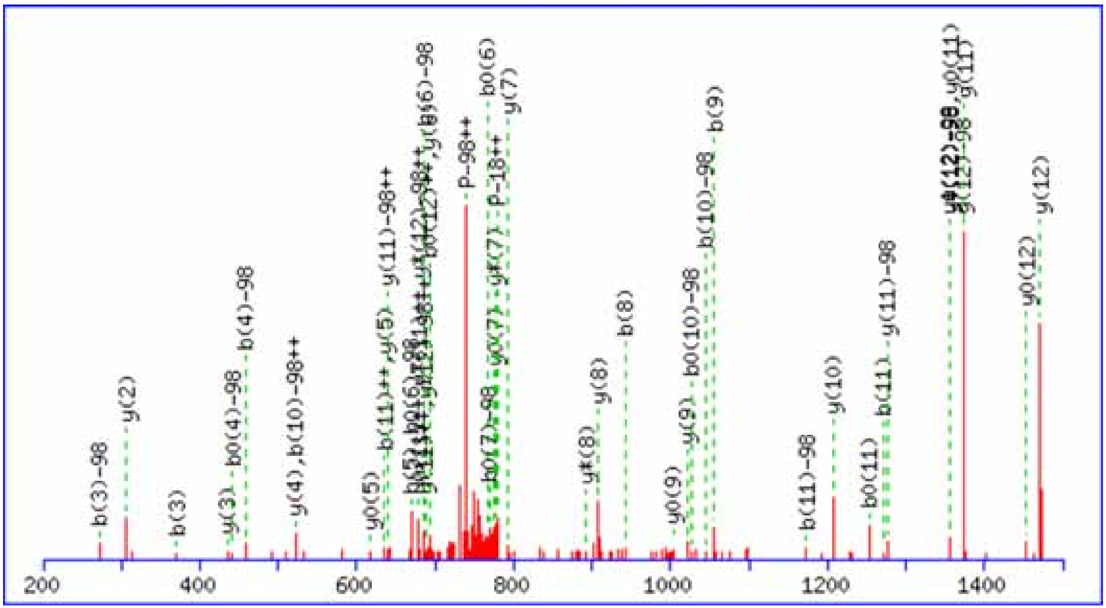
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)++, b(7)-98, b(7), b(7)-98++, b(8), b(8)++, b(8)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8)-98, y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.69

APSWIDTGLSEMR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of APSWIDTGLSEMR
Found in CRYAB_MOUSE, Alpha-crystallin B chain OS=Mus musculus GN=Cryab PE=1 SV=2

Match to Query 2238: 1575.722424 from(788.868488,2+)
Title: Elution from: 60.009 to 60.009 scan no 5695 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1575.7216
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 0.00013

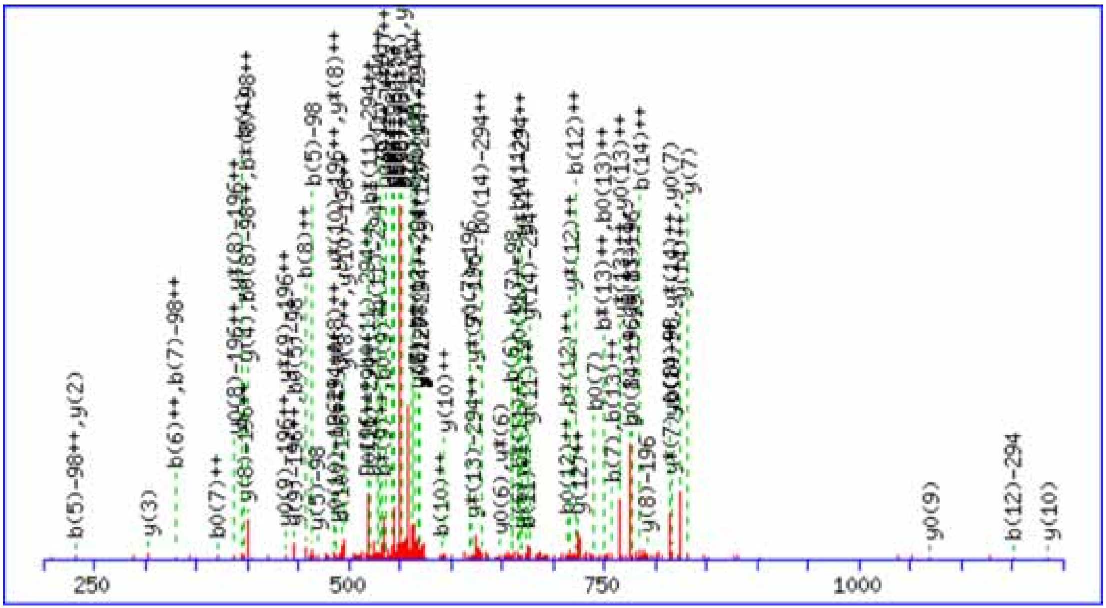
Matched b ions: b(3)-98, b(3), b(4)-98, b(5), b(6)-98, b(8), b(9), b(10)-98++, b(10)-98, b(11)++, b(11)-98, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11), y(11)-98++, y(11)++, y(12)-98, y(12), y(12)-98++
Precursor origin neutral loss: +

Peptide No.70

APTPSPVRSVSPAGR
Confirmed sites: @S:5,@S:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of APTPSPVRSVSPAGR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4015: 1745.730819 from(582.917549,3+)
Title: Elution from: 29.666 to 29.666 scan no 2259 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1745.7304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.0025

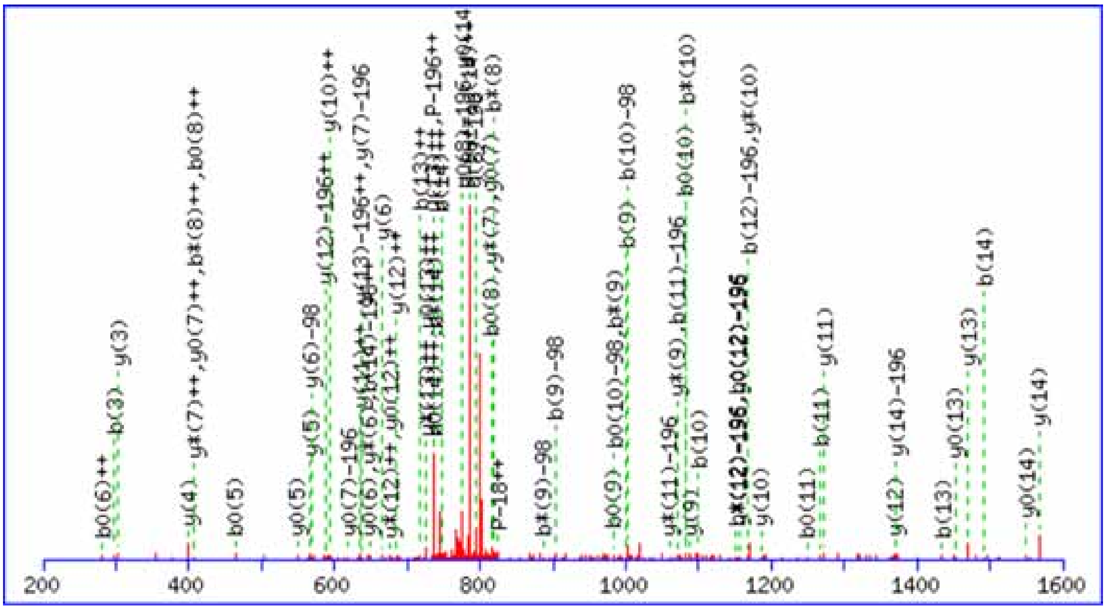
Matched b ions: b(4), b(5)-98++, b(5)-98, b(5), b(6)++, b(6)-98, b(6), b(7)-98++, b(7)-98, b(7), b(8)-98, b(8)++, b(9)-98++, b(9)++, b(10)-196++, b(10)-98++, b(10)++, b(11)-98++, b(11)-196, b(11)-294++, b(11)++, b(12)-196++, b(12)-294, b(12)-98++, b(12)++, b(13)-196++, b(13)-98++, b(13)++, b(14)++, b(14)-196++, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(8)++, y(8)-98++, y(8)-196++, y(8)-196, y(9)-98++, y(9)-196++, y(9)++, y(10)-196++, y(10), y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(11)-294++, y(12)-98++, y(12)++, y(12)-196++, y(13)++, y(13)-196++, y(13)-98++, y(14)-98++, y(14)++, y(14)-294++, y(14)-196++
Precursor origin neutral loss: +

Peptide No.71

APTPSPVRSVSPAGR
Confirmed sites: @S:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of APTPSPVRSVSPAGR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4202: 1665.765298 from(833.889925,2+)
Title: Elution from: 28.371 to 28.371 scan no 1993 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1665.7641
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.005

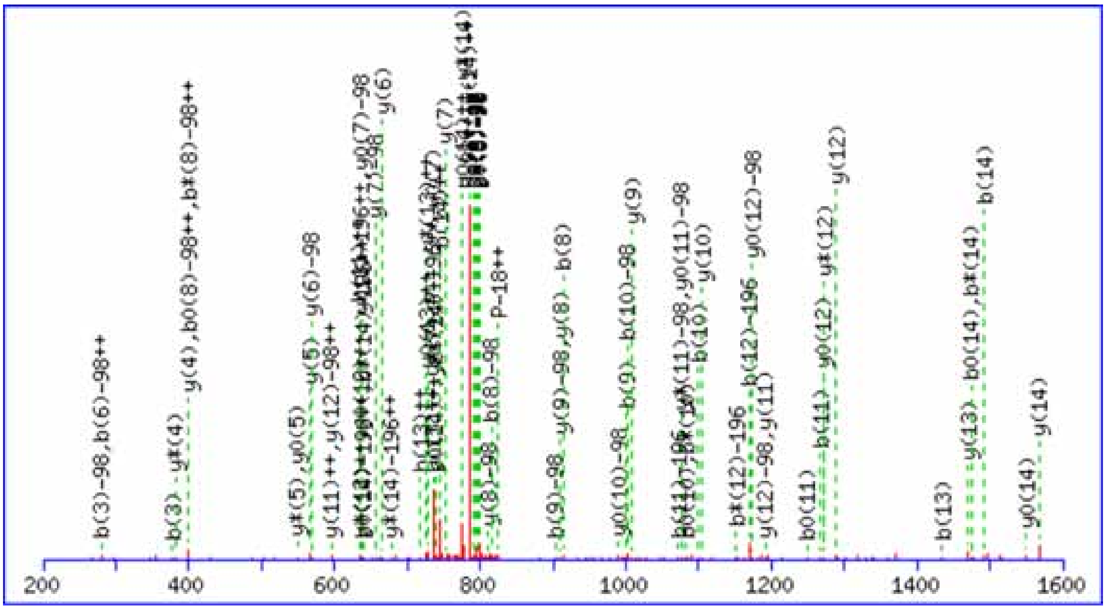
Matched b ions: b(3), b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(11)-196, b(12)-196, b(13), b(13)++, b(14)-196++, b(14), b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)-98, y(7)-98, y(7)-196, y(8)-196, y(9), y(9)-98, y(10)++, y(10), y(11)++, y(11), y(11)-98++, y(12)-98++, y(12)-98, y(12), y(12)-196++, y(12)++, y(13)++, y(13), y(13)-98, y(13)-196++, y(13)-98++, y(14)-98++, y(14)++, y(14)-98, y(14), y(14)-196
Precursor origin neutral loss: +

Peptide No.72

APTPSPVRSVSPAGR
Confirmed sites: @T:3,@S:11
Ambiguous sites:

MS/MS Fragmentation of APTPSPVRSVSPAGR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3512: 1665.764392 from(833.889472,2+)
Title: Elution from: 28.526 to 28.526 scan no 2101 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1665.7641
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.0048

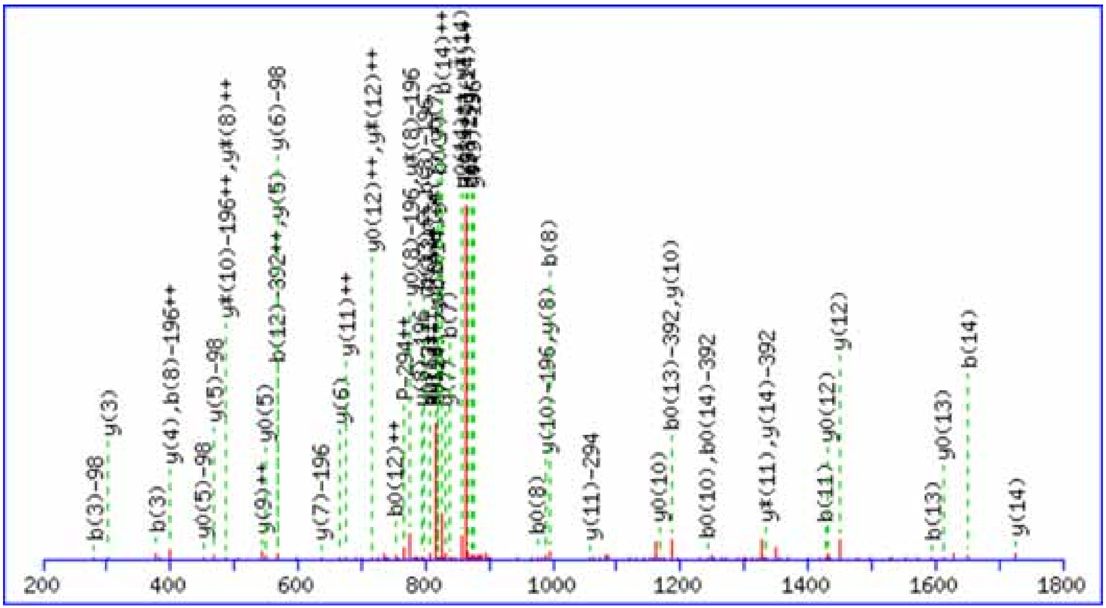
Matched b ions: b(3)-98, b(3), b(6)-98++, b(8), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11)-196, b(11)++, b(11), b(12)-196, b(12)-98++, b(12)-98, b(13), b(13)-98, b(13)++, b(14), b(14)++
Matched y ions: y(4), y(5), y(6)-98, y(6), y(7)-98, y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(11)++, y(11), y(12), y(12)-98++, y(12)-98, y(13)++, y(13)-196++, y(13), y(14)-98++, y(14)++, y(14)-98, y(14)
Precursor origin neutral loss: +

Peptide No.73

APTPSPVRSVSPAGR
Confirmed sites: @T:3,@S:5,@S:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of APTPSPVRSVSPAGR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4521: 1825.696938 from(913.855745,2+)
Title: Elution from: 31.166 to 31.166 scan no 2466 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1825.6967
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 0.00017

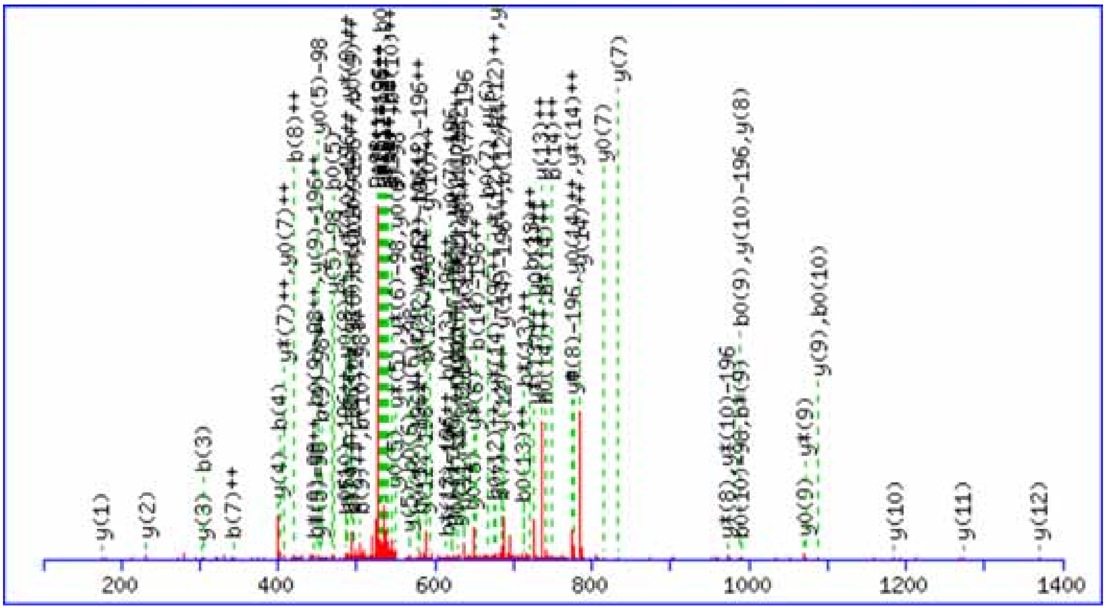
Matched b ions: b(3), b(3)-98, b(5)-98, b(7), b(8)-196++, b(8)-98, b(8), b(8)-196, b(9)-98, b(9)-294, b(9)-196, b(10)-98, b(10)-196, b(11)-98, b(11)-294++, b(11)-196, b(11), b(12)-196, b(12)-392++, b(13)-98, b(13), b(13)-196, b(13)-196++, b(13)++, b(14), b(14)-98, b(14)++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6), y(6)-98, y(7)-196, y(7)-98, y(7), y(8), y(8)-196, y(9)++, y(10)-98++, y(10), y(10)-196, y(10)-98, y(11)++, y(11)-294, y(12), y(12)-98++, y(12)-98, y(12)-196, y(13)-98++, y(13)++, y(13)-98, y(14)++, y(14)-196, y(14)-98, y(14), y(14)-196++, y(14)-98++, y(14)-294, y(14)-392, y(14)-294++
Precursor origin neutral loss: +

Peptide No.74

APTPSPVRSVSPAGR
Confirmed sites: @S:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of APTPSPVRSVSPAGR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2969: 1671.796431 from(558.272753,3+)
Title: Elution from: 28.418 to 28.418 scan no 1898 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1671.7959
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.017

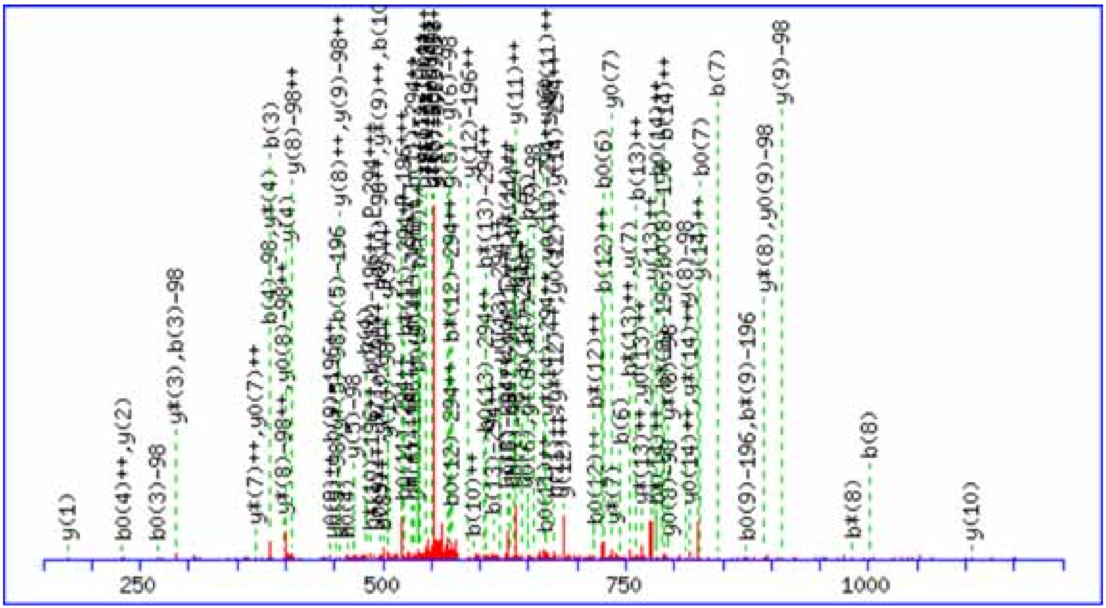
Matched b ions: b(3), b(4), b(5), b(7)++, b(7), b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(11)-98++, b(11)++, b(11)-196++, b(12)-196++, b(12)++, b(12)-98, b(12)-98++, b(13)-98++, b(13)++, b(14)-196++, b(14)-98++, b(14)++
Matched y ions: y(1), y(2), y(3), y(4), y(5)-98, y(5), y(6), y(6)-98, y(7)-98, y(7), y(7)-196, y(8), y(8)-98++, y(8)++, y(9), y(9)-98, y(9)++, y(9)-196++, y(9)-98++, y(10)-196, y(10), y(10)-98++, y(10)-196++, y(10)++, y(11)-98++, y(11), y(11)++, y(11)-196++, y(12), y(12)-98++, y(12)++, y(12)-196++, y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++
Precursor origin neutral loss: +

Peptide No.75

APTPSPVRSVSPAGR
Confirmed sites: @T:3,@S:5,@S:11
Ambiguous sites:

MS/MS Fragmentation of APTPSPVRSVSPAGR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3338: 1751.763603 from(584.928477,3+)
Title: Elution from: 30.150 to 30.150 scan no 2126 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1751.7622
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.018

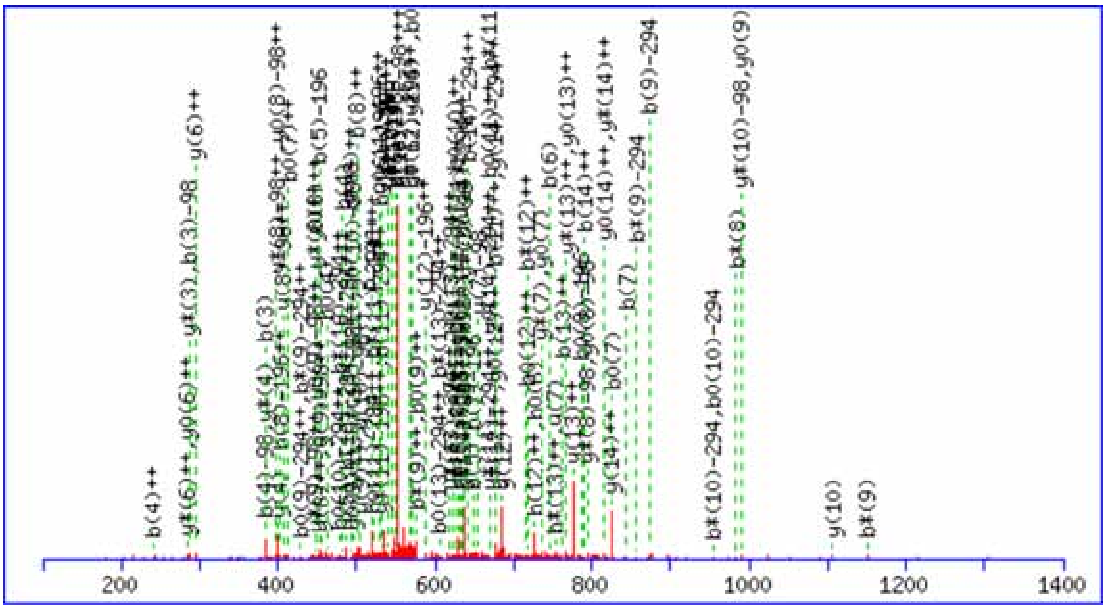
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-196, b(5)-98, b(5), b(6)-196, b(6), b(7)-196, b(7)-98, b(7), b(8), b(8)-98++, b(8)++, b(9)-196++, b(9)-98++, b(9)++, b(10)-196++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(11)-294++, b(12)-196++, b(12)++, b(12)-98++, b(13)-294++, b(13)-196++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(14)-294++, b(14)-196++
Matched y ions: y(1), y(2), y(4), y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)-98++, y(8)++, y(8)-98, y(9)-98, y(9)-98++, y(9)++, y(10)++, y(10), y(10)-98++, y(11)++, y(11)-196++, y(11)-98++, y(12)-98++, y(12)++, y(12)-196++, y(13)++, y(13)-294++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++, y(14)-294++
Precursor origin neutral loss: +

Peptide No.76

APTPSPVRSVSPAGR
Confirmed sites: @T:3,@S:5,@S:9
Ambiguous sites:

MS/MS Fragmentation of APTPSPVRSVSPAGR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3024: 1751.764077 from(584.928635,3+)
Title: Elution from: 30.676 to 30.676 scan no 2196 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1751.7622
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.045

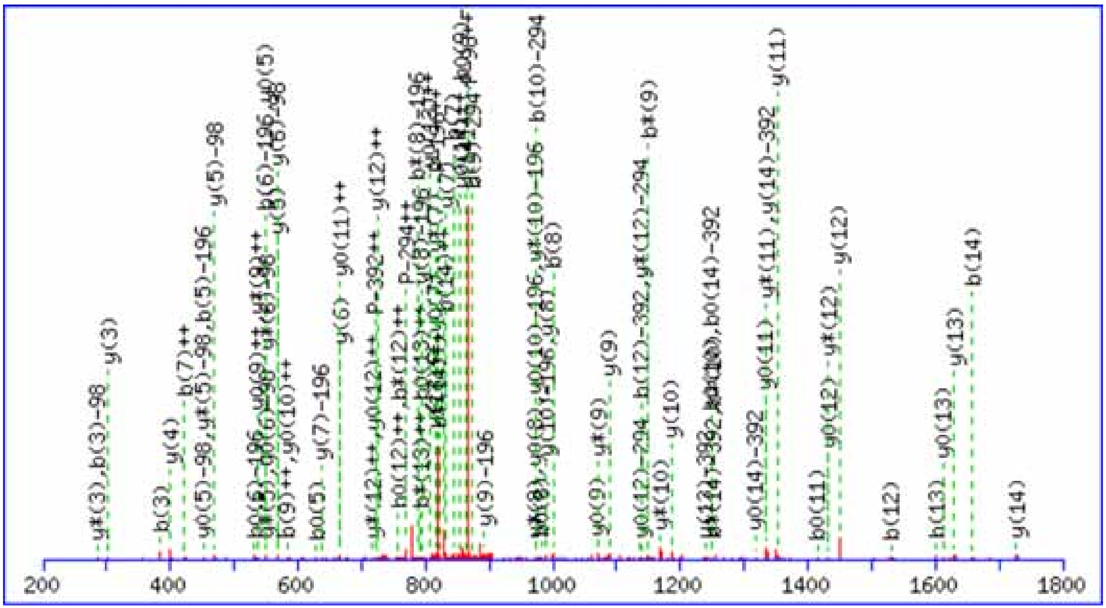
Matched b ions: b(3)-98, b(3), b(4)-98, b(4)++, b(4), b(5)-196, b(5)-98, b(5), b(6)-196, b(6)-98, b(6), b(7)-196, b(7)-98, b(7), b(8)-98++, b(8)-196++, b(8)++, b(9)-98++, b(9)-196++, b(9)-294, b(10)-196++, b(10)-294++, b(10)++, b(11)-98++, b(11)++, b(11)-294++, b(12)-196++, b(12)-98++, b(12)++, b(13)-196++, b(13)-98++, b(13)++, b(14)-294++, b(14)-196++, b(14)-98++, b(14)++
Matched y ions: y(4), y(5), y(6)++, y(7), y(7)-98, y(8)++, y(8)-98++, y(9)-98++, y(9)++, y(10)++, y(10), y(10)-98++, y(11)++, y(11)-196++, y(11)-98++, y(12)-98++, y(12)++, y(12)-196++, y(13)++, y(13)-294++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++, y(14)-294++
Precursor origin neutral loss: +

Peptide No.77

APTPSPVRSVSPAGR
Confirmed sites: @T:3,@S:5,@S:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of APTPSPVRSVSPAGR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3862: 1831.729912 from(916.872232,2+)
Title: Elution from: 30.937 to 30.937 scan no 2233 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1831.7285
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 0.00019

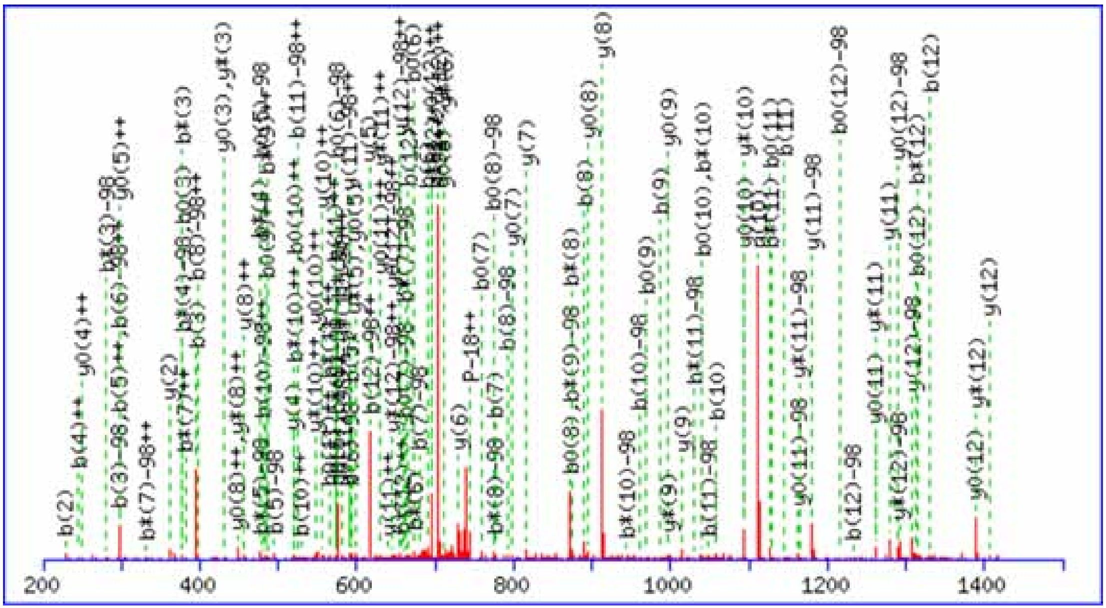
Matched b ions: b(3), b(3)-98, b(5)-98, b(5)-196, b(6)-196, b(7)++, b(7), b(8), b(8)-98++, b(8)-98, b(9)-98, b(9)++, b(9)-98++, b(9)-294, b(9)-196, b(10)-98, b(10)-196, b(10)-196++, b(10)-294, b(11)-98, b(11)-196, b(11)-294, b(12)-196, b(12)-196++, b(12), b(12)-98, b(12)-294, b(12)-98++, b(12)-392, b(13)-98, b(13), b(13)-196++, b(14), b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5), y(5)-98, y(6), y(6)-98, y(7)-196, y(7)-98, y(7), y(8), y(8)-98, y(8)-196, y(9)-196, y(9), y(9)-98, y(10), y(10)-196, y(10)-98, y(11), y(11)-98, y(11)-98++, y(12), y(12)-98, y(12)-196++, y(12)++, y(13), y(13)-294, y(13)-98++, y(13)++, y(13)-392, y(14)-392, y(14)-98, y(14), y(14)-196, y(14)-196++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.78

AQSPTPSLPASWK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AQSPTPSLPASWK
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 2124: 1504.733350 from(753.373951,2+)
Title: Elution from: 45.885 to 45.885 scan no 4234 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1504.7327
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
Ions Score: 78 Expect: 7.9e-007

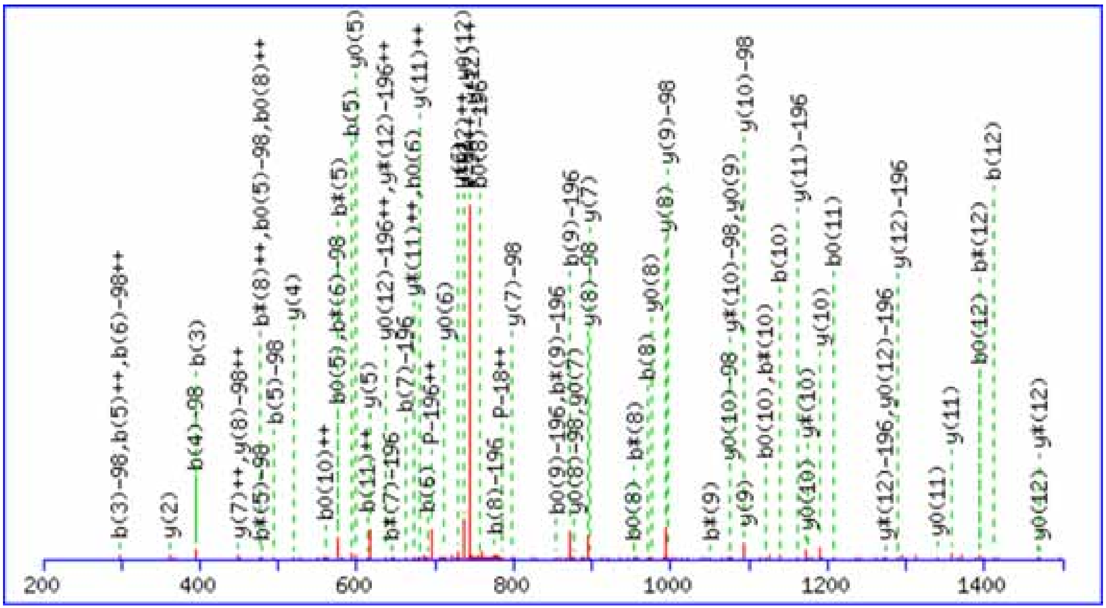
Matched b ions: b(2), b(3)-98, b(3), b(4)++, b(5)++, b(5)-98, b(5), b(6)-98++, b(6)-98, b(6), b(7)-98, b(7), b(8), b(8)-98++, b(8)-98, b(9), b(10), b(10)-98++, b(10)++, b(10)-98, b(11)++, b(11)-98++, b(11)-98, b(11), b(12)-98++, b(12), b(12)++, b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(10)++, y(11)-98, y(11), y(11)-98++, y(11)++, y(12)++, y(12)-98, y(12), y(12)-98++
Precursor origin neutral loss: +

Peptide No.79

AQSPTPSLPASWK
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of AQSPTPSLPASWK
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 2572: 1584.699770 from(793.357161,2+)
Title: Elution from: 49.958 to 49.958 scan no 4742 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1584.6990
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 67 **Expect:** 7.2e-006

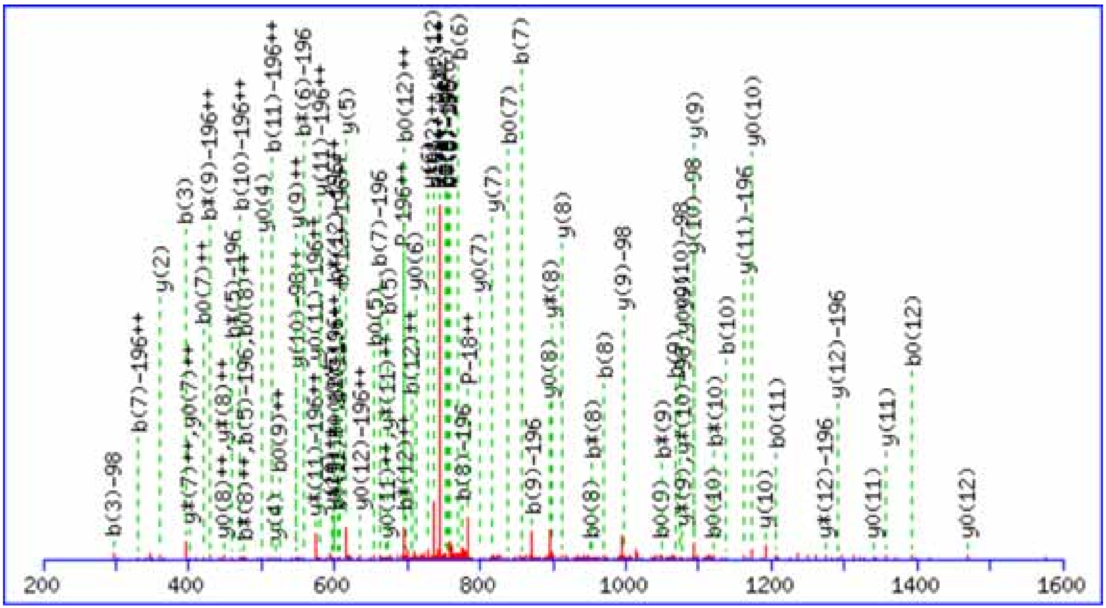
Matched b ions: b(3), b(3)-98, b(4)-98, b(5)++, b(5)-98, b(5), b(6)-98++, b(6), b(7)-98, b(7)-196, b(8)-98, b(8), b(8)-196, b(9)-196, b(9)-98, b(10)-98, b(10), b(11)-98, b(11)-98++, b(11)++, b(12)-98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(7)-98, y(8)-98++, y(8), y(8)-98, y(9), y(9)-98, y(10)-98, y(10), y(11), y(11)-98, y(11)-196, y(11)++, y(12)++, y(12)-98++, y(12)-196, y(12)-98
Precursor origin neutral loss: +

Peptide No.80

AQSPTPSLPASWK
Confirmed sites: @S:3,@T:5
Ambiguous sites:

MS/MS Fragmentation of AQSPTPSLPASWK
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 2266: 1584.700278 from(793.357415,2+)
Title: Elution from: 49.574 to 49.574 scan no 4634 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1584.6990
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
Ions Score: 31 Expect: 0.027

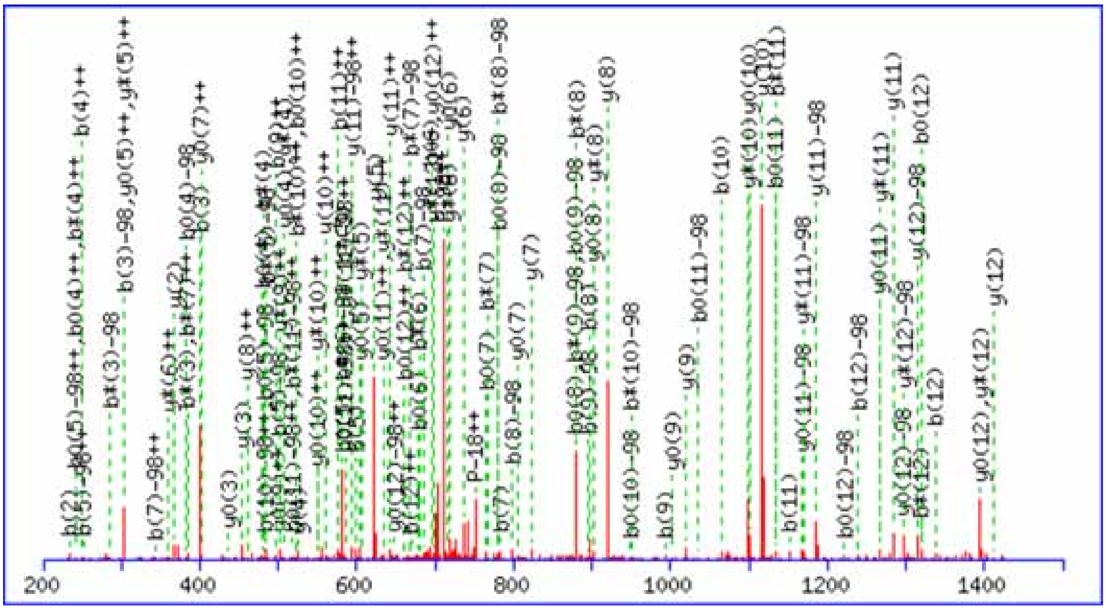
Matched b ions: b(3), b(3)-98, b(5)-98, b(5)-196, b(5), b(6)-98, b(6), b(7)-98, b(7)-196++, b(7)-196, b(7), b(8)-98, b(8)-196, b(8), b(9)-196, b(9)-98, b(9), b(10)-98, b(10), b(10)-196++, b(11)-196++, b(12)-98, b(12)-196++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(9)-98, y(10)-98, y(10), y(10)-98++, y(10)++, y(11)-98, y(11), y(11)-196, y(11)-196++, y(11)-98++, y(12)++, y(12)-98++, y(12)-196
Precursor origin neutral loss: +

Peptide No.81

AQSPTPSLPASWK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of AQSPTPSLPASWK
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 3295: 1516.796734 from(759.405643,2+)
Title: Elution from: 45.828 to 45.828 scan no 4417 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1516.7963
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 65 Expect: 1.4e-005

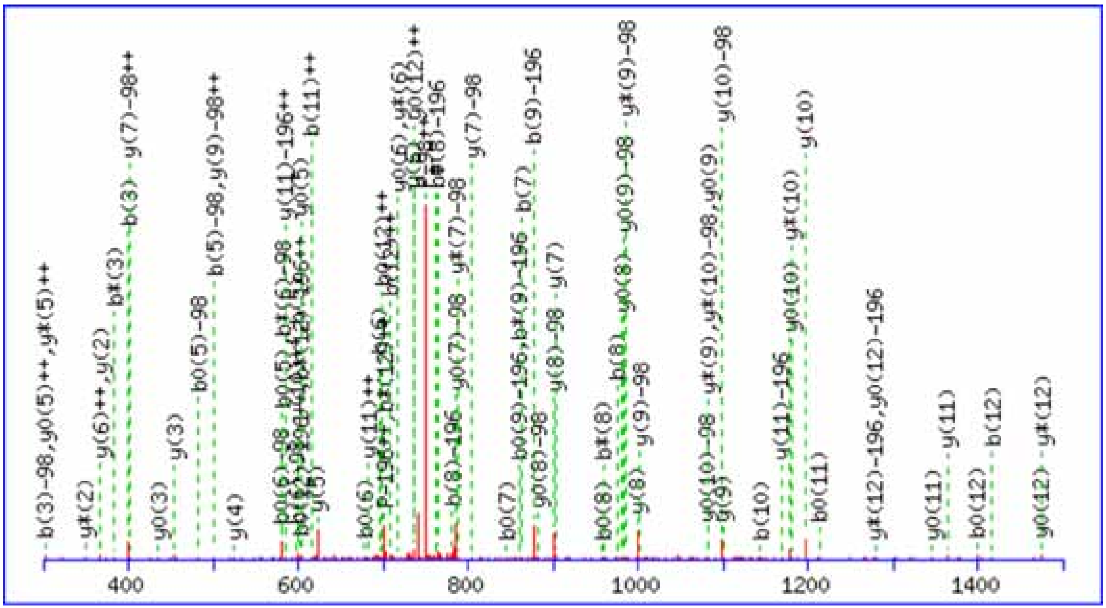
Matched b ions: b(2), b(3)-98, b(3), b(4)++, b(5)-98, b(5), b(5)-98++, b(6), b(7), b(7)-98++, b(7)-98, b(8), b(8)-98, b(9), b(9)++, b(9)-98, b(10)-98++, b(10), b(11), b(11)++, b(12), b(12)++, b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(10)++, y(11)-98, y(11), y(11)-98++, y(11)++, y(12)-98, y(12)
Precursor origin neutral loss: +

Peptide No.82

AQSPTPSLPASWK
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of AQSPTPSLPASWK
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 2271: 1596.764178 from(799.389365,2+)
Title: Elution from: 49.930 to 49.930 scan no 4665 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1596.7626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 41 **Expect:** 0.0046

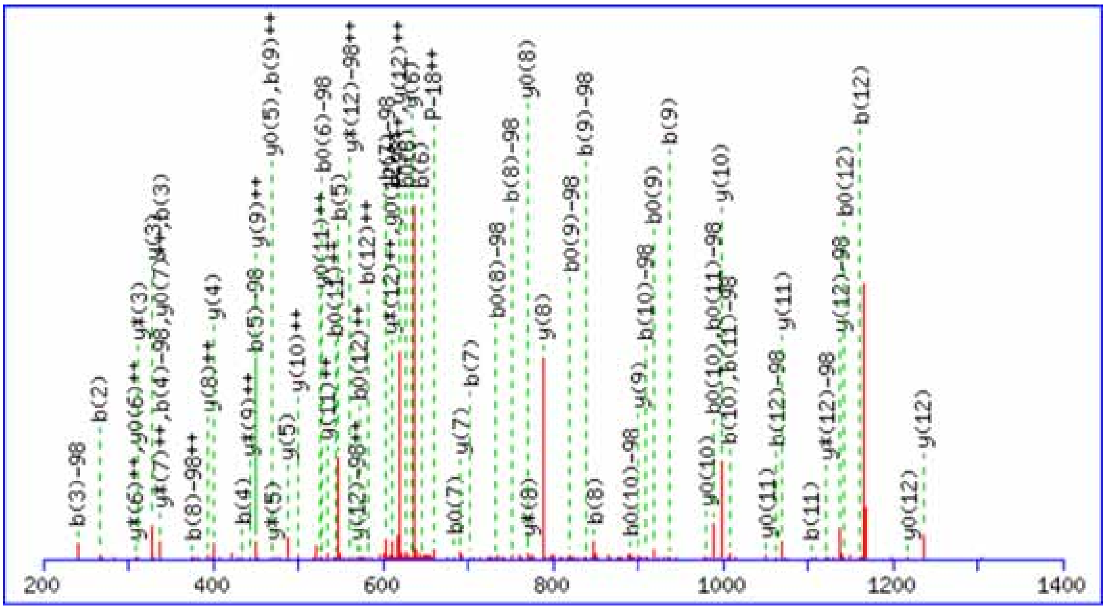
Matched b ions: b(3), b(3)-98, b(5), b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(8)-196, b(9)-98, b(9)-196, b(10)-98, b(10)-98++, b(10), b(11)-98, b(11)++, b(12), b(12)-98, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(7)-98++, y(7)-98, y(8), y(8)-98, y(9)-98++, y(9), y(9)-98, y(10)-98, y(10), y(10)++, y(11)-98, y(11), y(11)-196, y(11)-196++, y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.83

ASAPLPGFSAPGR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of ASAPLPGFSAPGR
Found in HSPB6_MOUSE, Heat shock protein beta-6 OS=Mus musculus GN=Hspb6 PE=1 SV=1

Match to Query 1761: 1334.638612 from(668.326582,2+)
Title: Elution from: 45.555 to 45.555 scan no 4369 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1334.6384
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 **Expect:** 4.2e-005

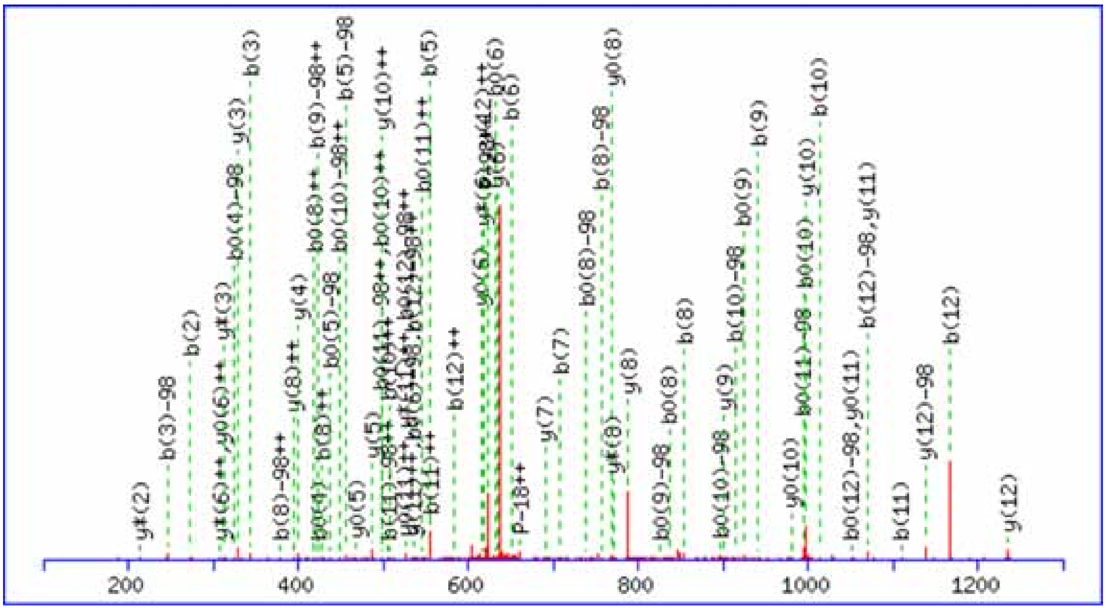
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6), b(7)-98, b(7), b(8), b(8)-98, b(8)-98++, b(9)++, b(9)-98, b(9), b(10), b(10)-98, b(11)-98, b(11), b(12), b(12)++, b(12)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12)-98, y(12)++, y(12), y(12)-98++
Precursor origin neutral loss: +

Peptide No.84

ASAPLPGFSAPGR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of ASAPLPGFSAPGR
Found in HSPB6_MOUSE, Heat shock protein beta-6 OS=Mus musculus GN=Hspb6 PE=1 SV=1

Match to Query 1130: 1340.671252 from(671.342902,2+)
Title: Elution from: 45.484 to 45.484 scan no 4058 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1340.6702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 8.4e-005

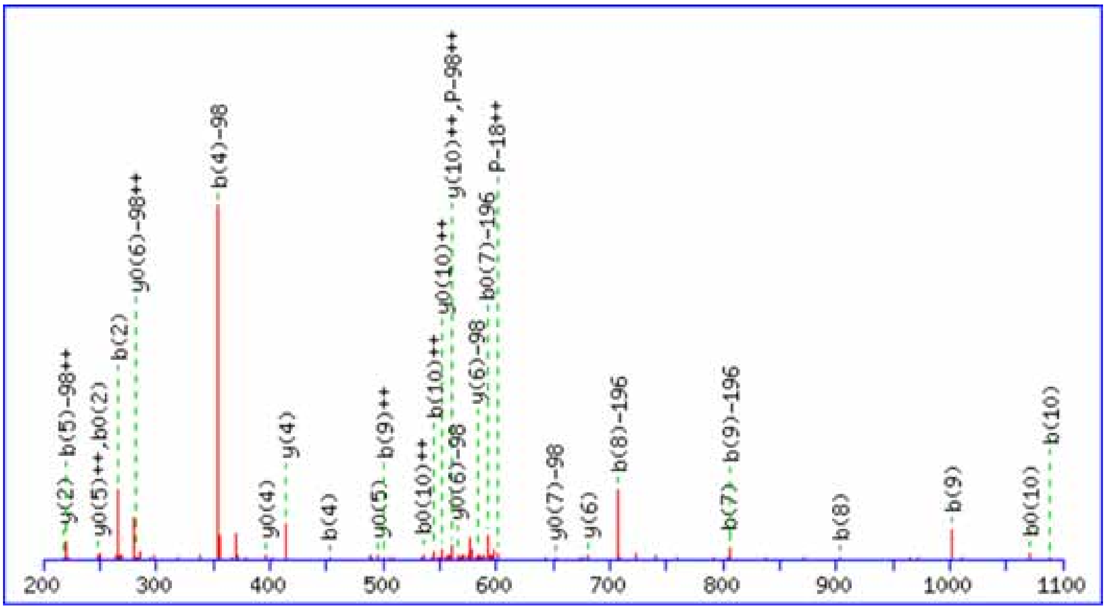
Matched b ions: b(2), b(3)-98, b(3), b(5), b(5)-98, b(6), b(7), b(8), b(8)++, b(8)-98, b(8)-98++, b(9), b(9)-98++, b(10), b(10)++, b(10)-98, b(11)++, b(11), b(11)-98++, b(12)-98, b(12), b(12)-98++, b(12)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)-98, y(12)++
Precursor origin neutral loss: +

Peptide No.85

ASSVSSVPVSI
Confirmed sites: @S:2,@S:6
Ambiguous sites:

MS/MS Fragmentation of ASSVSSVPVSI
Found in KLH31_MOUSE, Kelch-like protein 31 OS=Mus musculus GN=Klhl31 PE=1 SV=1

Match to Query 896: 1219.514830 from(610.764691,2+)
Title: Elution from: 54.567 to 54.567 scan no 5159 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1219.5138
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.043

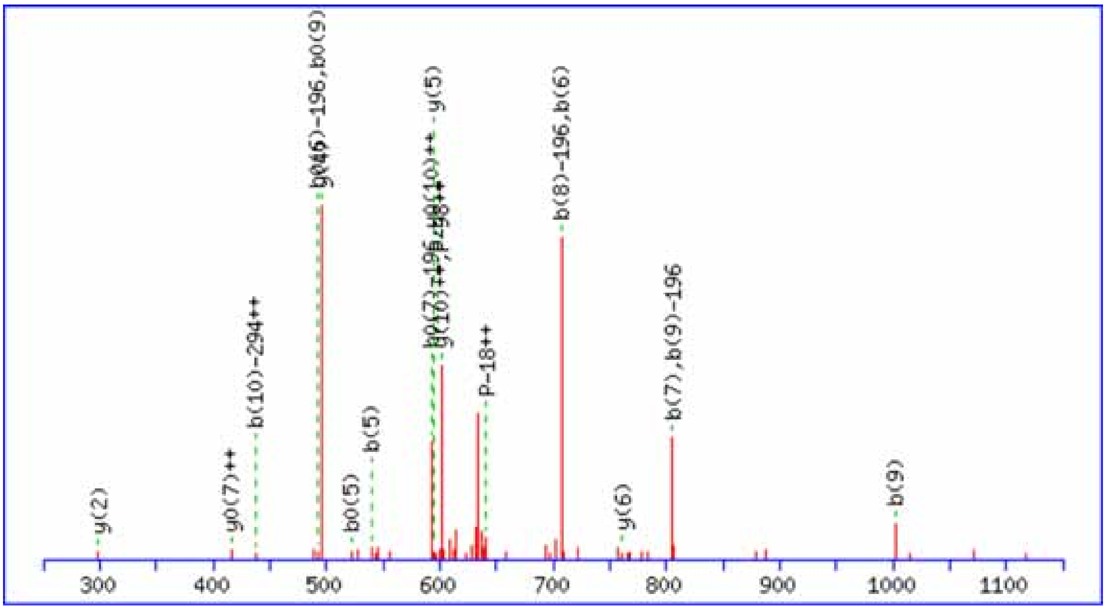
Matched b ions: b(2), b(4)-98, b(4), b(5)-98++, b(7)-98++, b(7)-98, b(7), b(8)-196, b(8)-98, b(8), b(9), b(9)-196, b(9)++, b(9)-98++, b(10)-98++, b(10), b(10)++
Matched y ions: y(2), y(4), y(6), y(6)-98, y(10)++
Precursor origin neutral loss:

Peptide No.86

ASSVSSVPVSI
Confirmed sites: @S:6,@S:10
Ambiguous sites: @S:2orS:3orS:5

MS/MS Fragmentation of ASSVSSVPVSI
Found in KLH31_MOUSE, Kelch-like protein 31 OS=Mus musculus GN=Klhl31 PE=1 SV=1

Match to Query 1628: 1299.481048 from(650.747800,2+)
Title: Elution from: 57.001 to 57.001 scan no 5655 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1299.4802
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.014

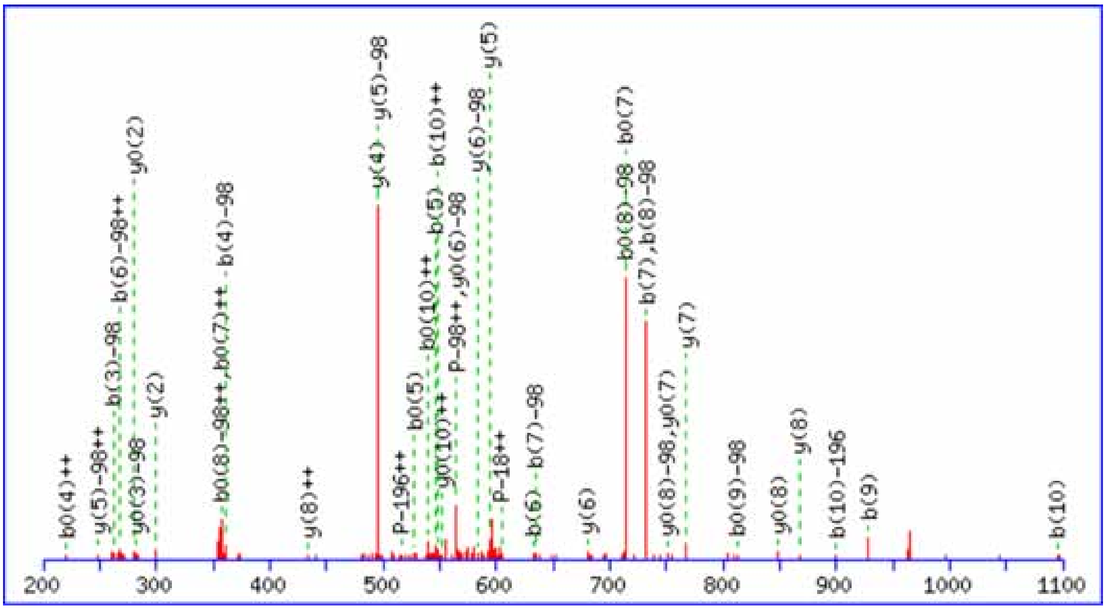
Matched b ions: b(5), b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(8)-196, b(9)-196, b(9), b(10)-98, b(10)-294++
Matched y ions: y(2), y(4), y(5), y(6), y(10)++
Precursor origin neutral loss: +

Peptide No.87

ASSVSSVPVSI
Confirmed sites: @S:10
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of **ASSVSSVPVSI**
Found in **KLH31_MOUSE**, Kelch-like protein 31 OS=Mus musculus GN=Klhl31 PE=1 SV=1

Match to Query 1153: 1225.545810 from(613.780181,2+)
Title: Elution from: 53.436 to 53.436 scan no 5113 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1225.5457
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0038

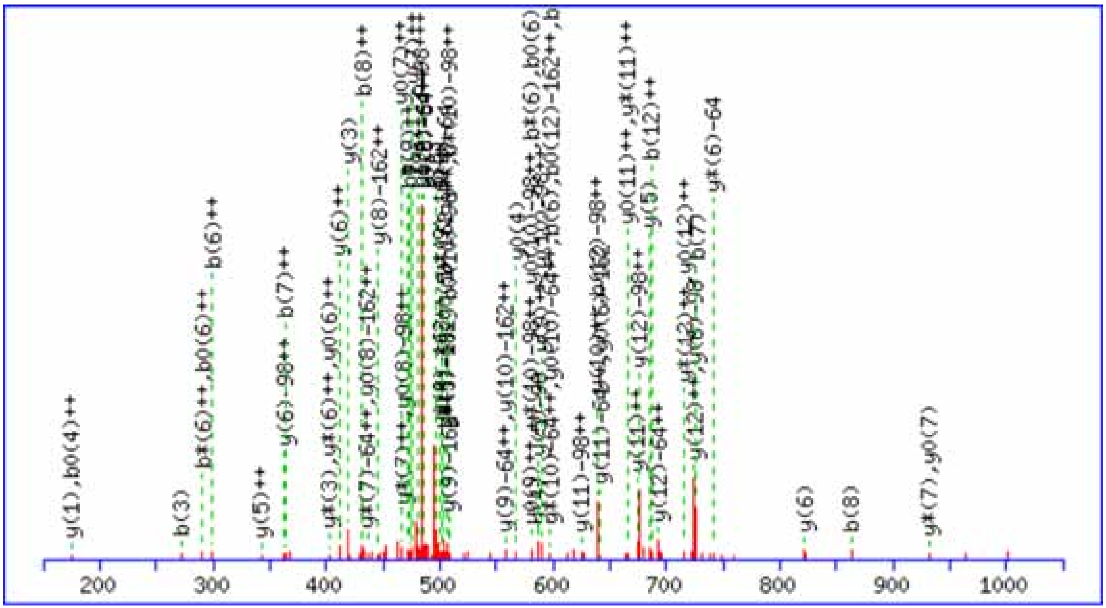
Matched b ions: b(3)-98, b(4)-98, b(5), b(6)-98++, b(6), b(7), b(7)-98, b(8)-98, b(9), b(10), b(10)-196, b(10)-98, b(10)-98++, b(10)++
Matched y ions: y(2), y(4), y(5)-98, y(5), y(5)-98++, y(6), y(6)-98, y(7), y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.88

ATAPQTQHVSPMR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ATAPQTQHVSPMR
Found in EF1D_MOUSE, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 2108: 1546.696851 from(516.572893,3+)
Title: Elution from: 21.291 to 21.291 scan no 1064 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1546.6963
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 40 Expect: 0.0039

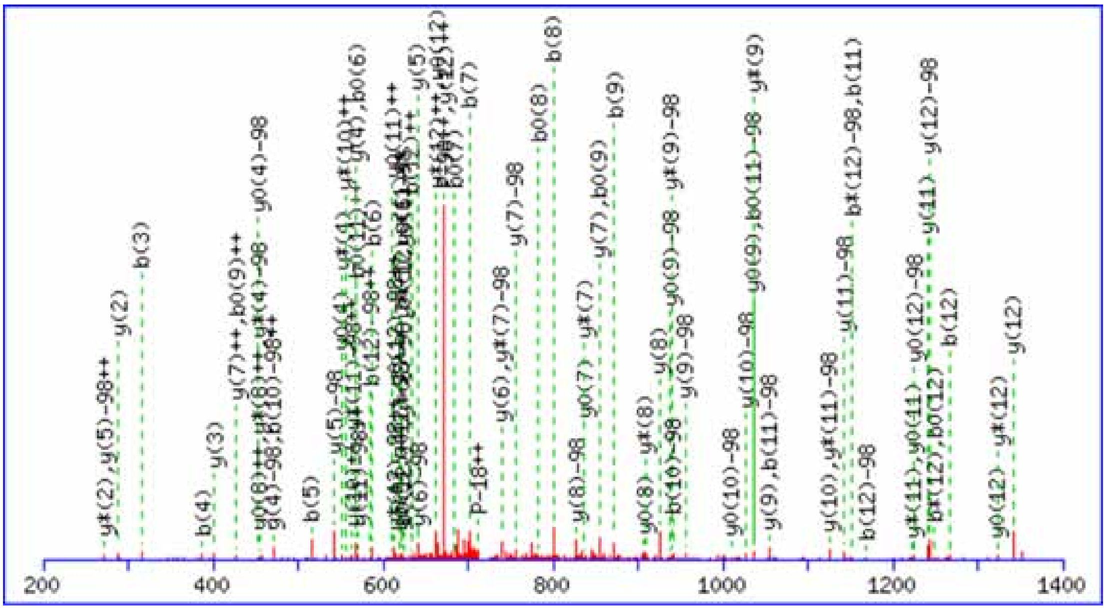
Matched b ions: b(3), b(5), b(6)++, b(6), b(7)++, b(7), b(8), b(8)++, b(9)++, b(12)-98++, b(12)++
Matched y ions: y(1), y(3), y(4), y(5)-98, y(5)++, y(5), y(6)-98, y(6), y(6)++, y(6)-98++, y(7)++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.89

ATDAEADVASLNR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ATDAEADVASLNR
Found in TPM2_MOUSE, Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=1

Match to Query 2204: 1439.629504 from(720.822028,2+)
Title: Elution from: 33.513 to 33.513 scan no 2784 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1439.6293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 7.4e-007

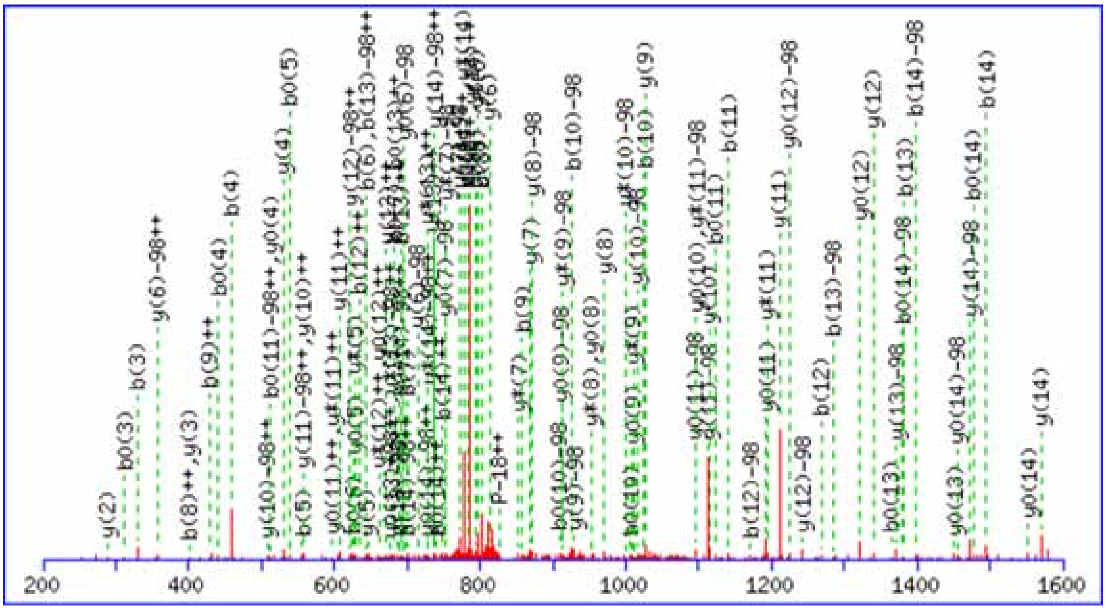
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10)-98++, b(10)-98, b(11)-98, b(11), b(12), b(12)-98, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5)-98++, y(5), y(6)-98, y(6), y(7), y(7)++, y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(10)++, y(11)-98, y(11), y(11)-98++, y(11)++, y(12)++, y(12)-98, y(12), y(12)-98++
Precursor origin neutral loss: +

Peptide No.90

ATEEPSGTGSDELIK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of ATEEPSGTGSDELIK
Found in PTRF_MOUSE, Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1

Match to Query 4228: 1668.750606 from(835.382579,2+)
Title: Elution from: 35.661 to 35.661 scan no 3019 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1668.7495
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K15 : Dimethyl (K)
Ions Score: 87 Expect: 7.5e-008

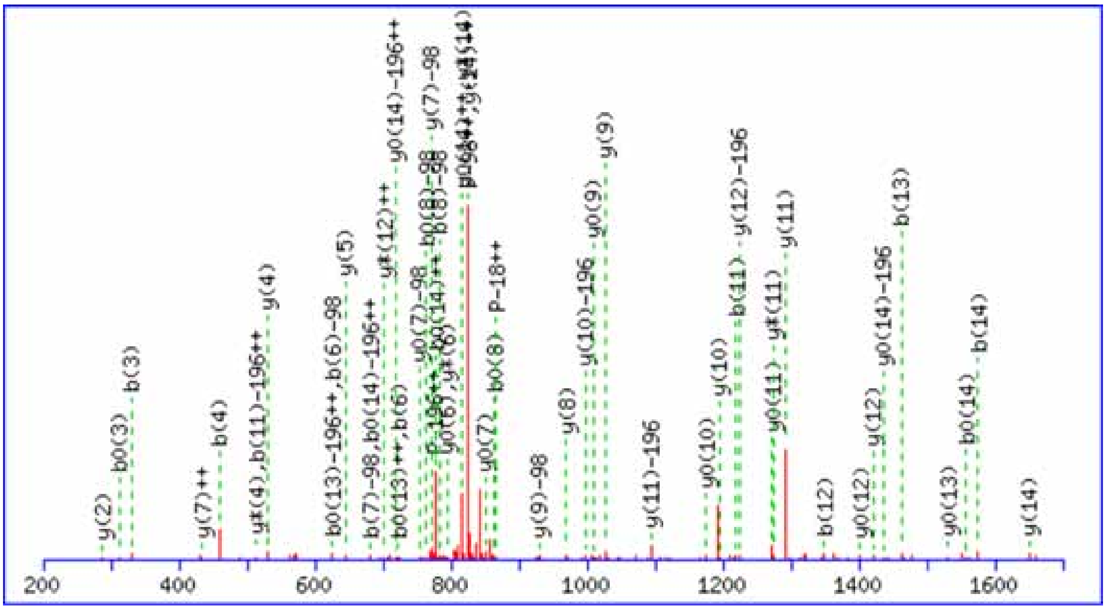
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)++, b(8), b(9)++, b(9), b(10)-98, b(10), b(11), b(12), b(12)-98, b(12)++, b(13)-98++, b(13)-98, b(13)++, b(13), b(14), b(14)++, b(14)-98, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98++, y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10)++, y(10), y(10)-98, y(10)-98++, y(11)++, y(11)-98, y(11), y(11)-98++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13)-98, y(13)++, y(13)-98++, y(14)++, y(14)-98, y(14), y(14)-98++
Precursor origin neutral loss: +

Peptide No.91

ATEEPSGTGSDELIK
Confirmed sites: @S:6,@S:10
Ambiguous sites:

MS/MS Fragmentation of ATEEPSGTGSDELIK
Found in PTRF_MOUSE, Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1

Match to Query 4032: 1748.715664 from(875.365108,2+)
Title: Elution from: 39.877 to 39.877 scan no 3649 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1748.7158
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 40 Expect: 0.0027

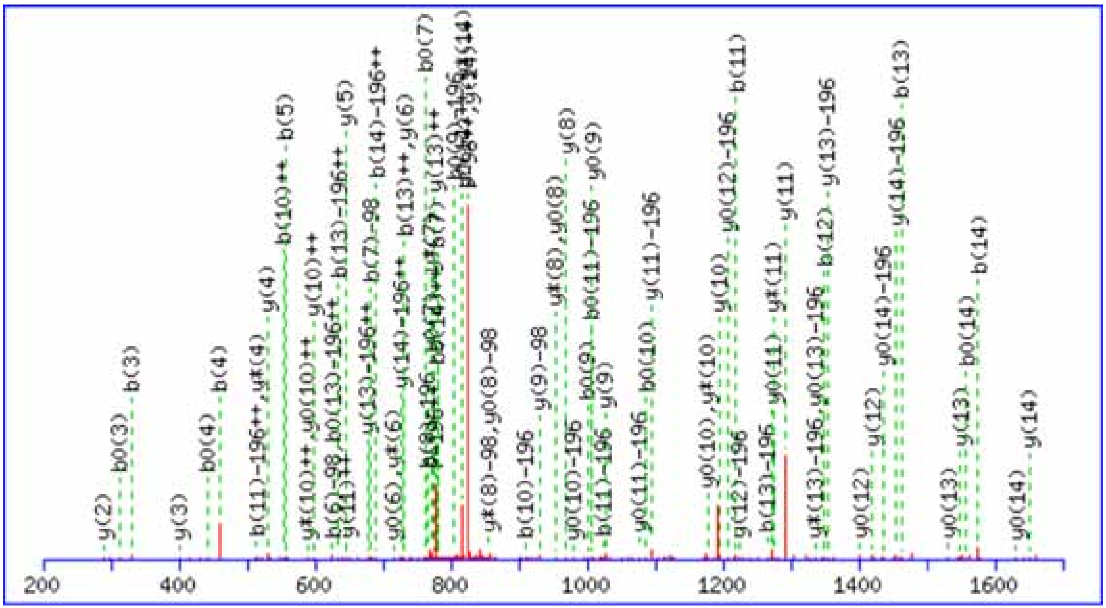
Matched b ions: b(3), b(4), b(6)-98, b(6), b(7)-98, b(8)-98, b(11)-98++, b(11)-98, b(11), b(11)-196++, b(12), b(13), b(13)-98, b(13)-98++, b(14), b(14)-98
Matched y ions: y(2), y(4), y(5), y(7)-98, y(7)++, y(8), y(9), y(9)-98, y(10)-196, y(10)-98, y(10), y(11)-196, y(11)-98, y(11), y(12)-196, y(12)-98, y(12), y(13)-98++, y(14)-98++, y(14)++, y(14), y(14)-98
Precursor origin neutral loss: +

Peptide No.92

ATEEPSGTGSDELIK
Confirmed sites: @S:6,@T:8
Ambiguous sites:

MS/MS Fragmentation of ATEEPSGTGSDELIK
Found in PTRF_MOUSE, Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1

Match to Query 4034: 1748.716896 from(875.365724,2+)
Title: Elution from: 39.522 to 39.522 scan no 3602 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1748.7158
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 59 **Expect:** 3.2e-005

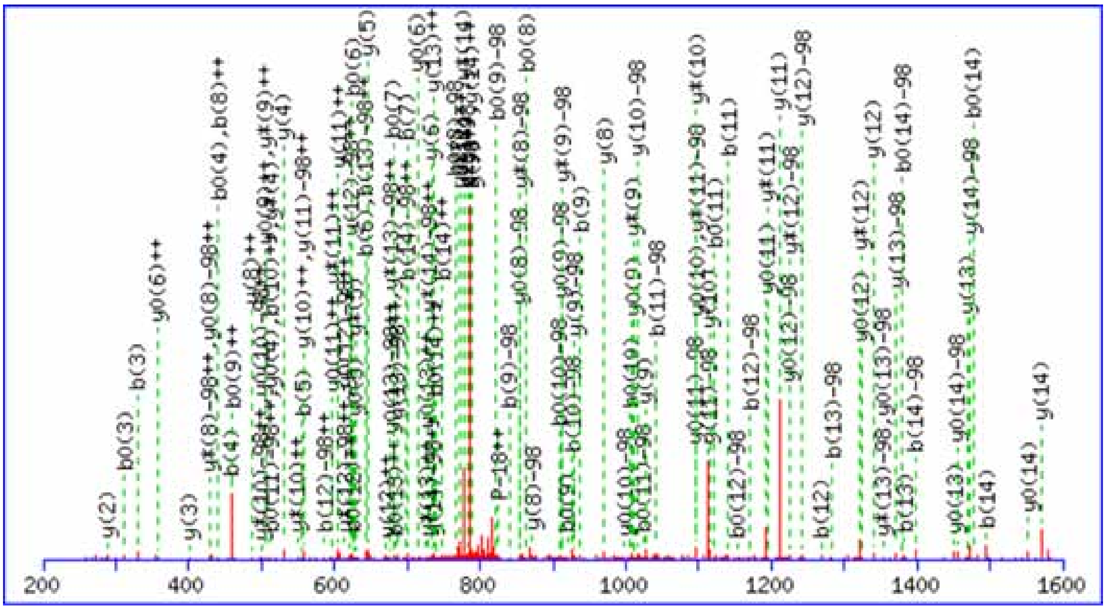
Matched b ions: b(3), b(4), b(5), b(6)-98, b(7)-98, b(7), b(8)-196, b(8)-98, b(9)-98, b(10)++, b(10)-196, b(10)-98, b(11)-98, b(11)-196++, b(11), b(11)-196, b(12)-98, b(12), b(13)-196++, b(13)-98, b(13), b(13)-98++, b(13)-196, b(13)++, b(14)-98, b(14), b(14)-196++, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9)-98, y(9), y(10)++, y(10), y(10)-98, y(11)-196, y(11)-98, y(11), y(11)-98++, y(11)++, y(12)-98, y(12), y(12)-98++, y(12)-196, y(13)-196, y(13), y(13)-98++, y(13)-196++, y(13)++, y(13)-98, y(14)-98++, y(14)++, y(14)-98, y(14), y(14)-196, y(14)-196++
Precursor origin neutral loss: +

Peptide No.93

ATEEPSGTGSDELIK
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of ATEEPSGTGSDELIK
Found in PTRF_MOUSE, Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1

Match to Query 2724: 1668.750426 from(835.382489,2+)
Title: Elution from: 35.672 to 35.672 scan no 2881 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1668.7495
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K15 : Dimethyl (K)
Ions Score: 82 Expect: 2.3e-007

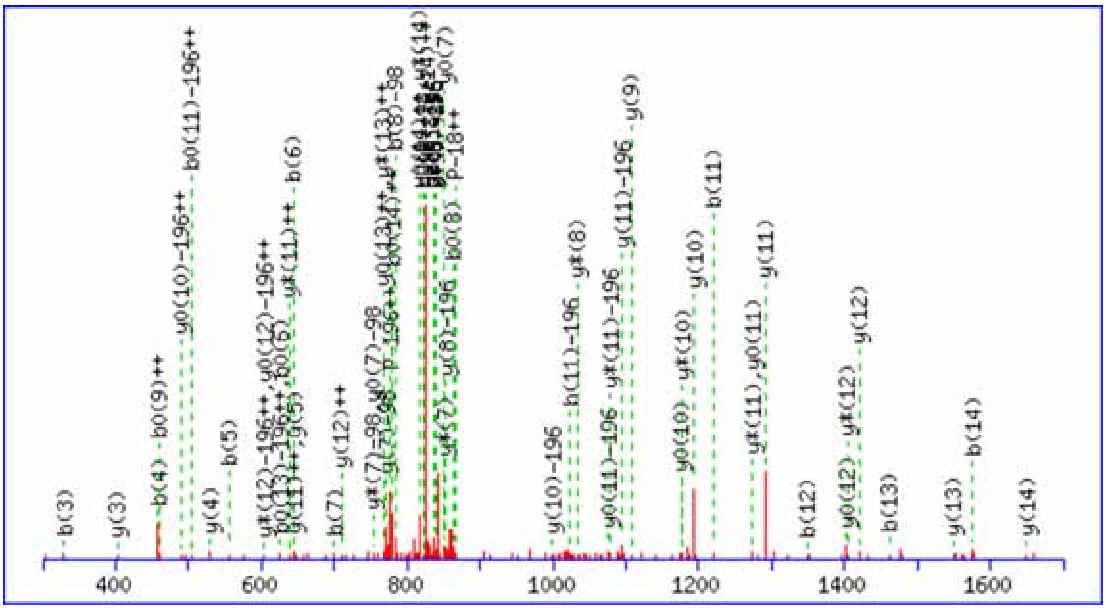
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)++, b(8)-98, b(9)-98, b(9), b(10)-98, b(10)++, b(11)-98, b(11), b(12), b(12)-98, b(12)-98++, b(13)-98++, b(13)-98, b(13), b(14)-98, b(14), b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(8)++, y(9), y(9)-98, y(10)++, y(10)-98, y(10), y(11)-98, y(11), y(11)++, y(11)-98++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13)++, y(13)-98, y(13)-98++, y(13), y(14)-98++, y(14)++, y(14)-98, y(14)
Precursor origin neutral loss: +

Peptide No.94

ATEEPSGTGSDELIK
Confirmed sites: @T:8,@S:10
Ambiguous sites:

MS/MS Fragmentation of ATEEPSGTGSDELIK
Found in PTRF_MOUSE, Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1

Match to Query 3450: 1748.717998 from(875.366275,2+)
Title: Elution from: 38.741 to 38.741 scan no 3335 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1748.7158
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 39 Expect: 0.004

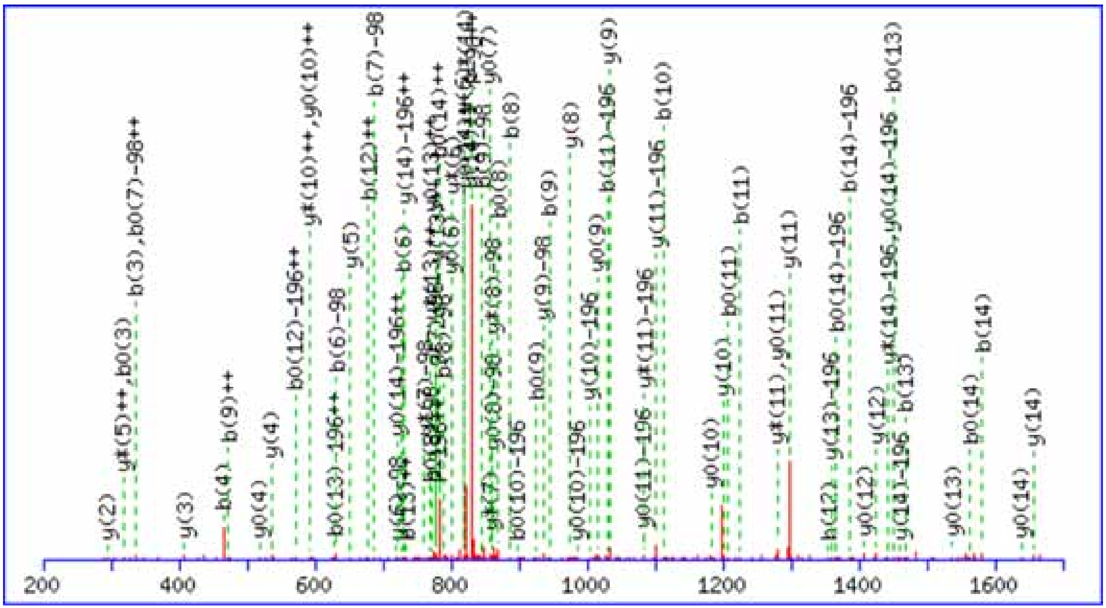
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)-98, b(9)-98, b(10)-98++, b(10)-98, b(11), b(11)-98, b(11)-196, b(12), b(13), b(14)-98, b(14)
Matched y ions: y(3), y(4), y(5), y(7)-98, y(8)-98, y(8)-196, y(9), y(9)-98, y(10), y(10)-196, y(10)-98, y(11)++, y(11)-196, y(11)-98, y(11), y(12), y(12)-98, y(12)++, y(13), y(13)-98++, y(14)-98++, y(14)++, y(14)-98, y(14)
Precursor origin neutral loss: +

Peptide No.95

ATEEPSGTGSDELIK
Confirmed sites: @S:6,@S:10
Ambiguous sites:

MS/MS Fragmentation of ATEEPSGTGSDELIK
Found in PTRF_MOUSE, Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1

Match to Query 3062: 1760.780712 from(881.397632,2+)
Title: Elution from: 39.459 to 39.459 scan no 3383 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1760.7794
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 45 **Expect:** 0.0012

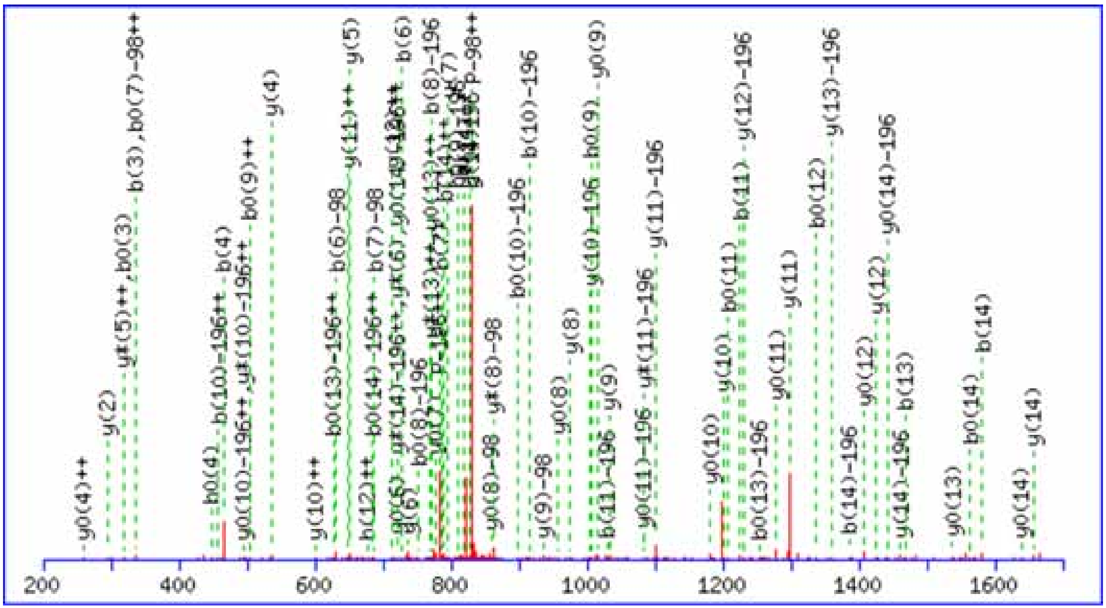
Matched b ions: b(3), b(4), b(6)-98, b(6), b(7)-98, b(8)-98, b(8), b(9), b(9)++, b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(11)-196, b(12)-98, b(12), b(12)++, b(12)-98++, b(13), b(13)-98, b(13)++, b(14)-98, b(14), b(14)-196
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(8), y(9)-98, y(9), y(10), y(10)-98, y(10)-196, y(11)-196, y(11)-98, y(11), y(12), y(12)-98++, y(12)-98, y(13)-98++, y(13)-196, y(13)-98, y(13)++, y(14)-98, y(14), y(14)-196, y(14)-98++, y(14)-196++, y(14)++
Precursor origin neutral loss: +

Peptide No.96

ATEEPSGTGSDELIK
Confirmed sites: @S:6,@T:8
Ambiguous sites:

MS/MS Fragmentation of ATEEPSGTGSDELIK
Found in PTRF_MOUSE, Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1

Match to Query 4713: 1760.779816 from(881.397184,2+)
Title: Elution from: 39.067 to 39.067 scan no 3507 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1760.7794
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 37 **Expect:** 0.009

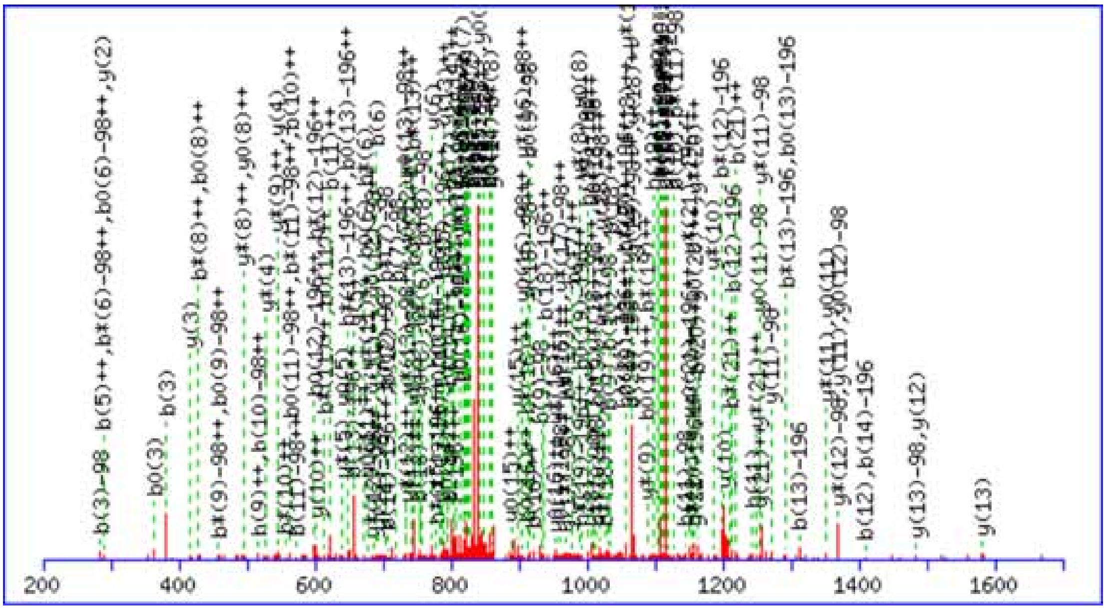
Matched b ions: b(3), b(4), b(6)-98, b(6), b(7)-98, b(7), b(8)-196, b(8)-98, b(9)-98++, b(9)-196, b(10)-196++, b(10)-98, b(10)-196, b(11), b(11)-98, b(11)-196, b(12)-98, b(12)++, b(12)-98++, b(13), b(13)-98++, b(14), b(14)-98, b(14)-196, b(14)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10)-98, y(10), y(10)++, y(10)-196, y(11)-196, y(11)-98, y(11), y(11)++, y(11)-98++, y(12), y(12)-98, y(12)-196, y(12)++, y(13)-98++, y(13)-196, y(14)-98, y(14)-196, y(14), y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.97

ATTPPNQGRPDSPVYANLQELK
Confirmed sites: @T:2,@S:12
Ambiguous sites:

MS/MS Fragmentation of ATTPPNQGRPDSPVYANLQELK
Found in RHG12_MOUSE, Rho GTPase-activating protein 12 OS=Mus musculus GN=Arhgap12 PE=1 SV=2

Match to Query 8377: 2611.211223 from(871.411017,3+)
Title: Elution from: 49.618 to 49.618 scan no 4910 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2611.2084
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K22 : Dimethyl (K)
Ions Score: 36 **Expect:** 0.021

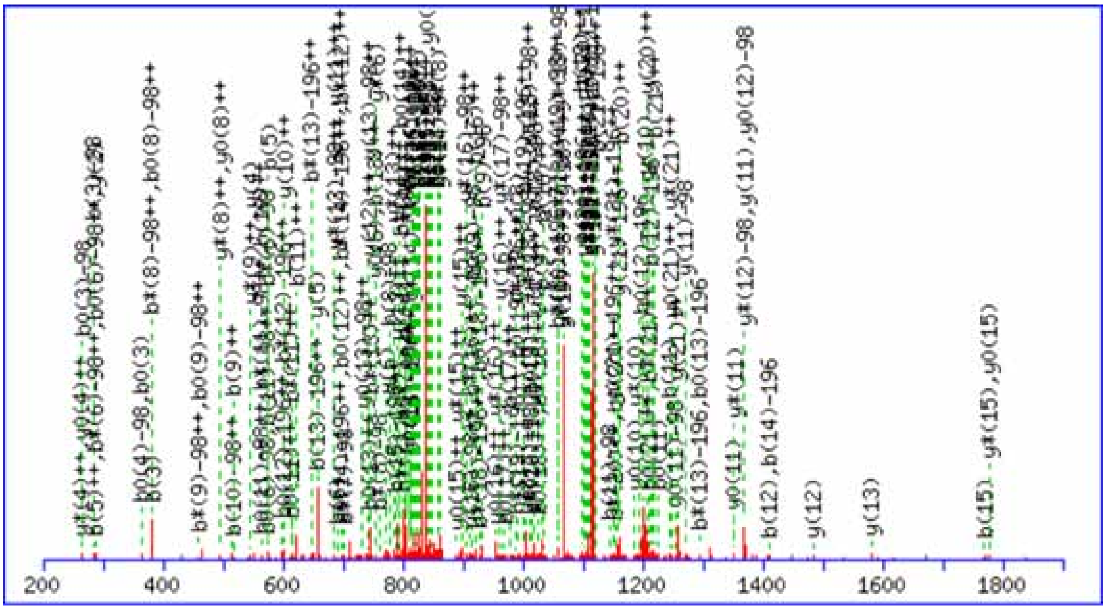
Matched b ions: b(3), b(3)-98, b(5)++, b(6), b(7)-98, b(7), b(9)++, b(9), b(9)-98, b(10)-98++, b(10)++, b(10)-98, b(10), b(11)++, b(11)-98, b(11)-98++, b(11), b(12)-98++, b(12)-98, b(12), b(12)++, b(12)-196, b(13)-196++, b(13)-196, b(13)-98, b(13)-98++, b(13)++, b(14)-196, b(14)-98++, b(14)-196++, b(14)++, b(15)-196++, b(15)-98++, b(16)-196++, b(16)++, b(17)++, b(18)-196++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(19)-196++, b(20)++, b(20)-98++, b(20)-196++, b(21)++, b(21)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)-98, y(11)++, y(12), y(12)-98++, y(12)++, y(13), y(13)-98, y(13)-98++, y(13)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(21)++, y(21)-98++, y(21)-196++
Precursor origin neutral loss: +

Peptide No.98

ATTPPNQGRPDSPVYANLQELK
Confirmed sites: @T:3,@S:12
Ambiguous sites:

MS/MS Fragmentation of ATTPPNQGRPDSPVYANLQELK
Found in RHG12_MOUSE, Rho GTPase-activating protein 12 OS=Mus musculus GN=Arhgap12 PE=1 SV=2

Match to Query 7914: 2611.210029 from(871.410619,3+)
Title: Elution from: 49.758 to 49.758 scan no 4889 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2611.2084
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K22 : Dimethyl (K)
Ions Score: 38 **Expect:** 0.014

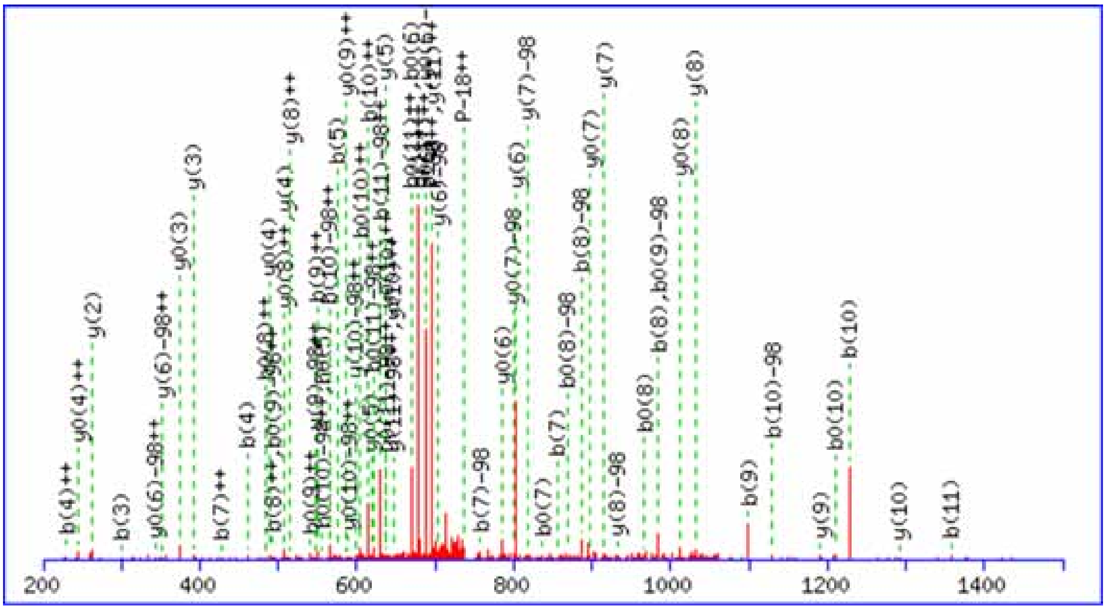
Matched b ions: b(3)-98, b(3), b(5)++, b(5), b(6), b(7), b(8)-98, b(9)++, b(9), b(9)-98, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(11)-98, b(11), b(12)-98++, b(12)-98, b(12), b(12)-196, b(13)-196++, b(13)-98, b(13)++, b(14)-196, b(14)-98++, b(14)++, b(15)-98, b(15), b(15)-196++, b(15)-98++, b(16)++, b(16)-196++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-196++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-196++, b(21)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)-98, y(11)++, y(12), y(12)++, y(13), y(13)++, y(13)-98++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-196++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(21)-196++
Precursor origin neutral loss: +

Peptide No.99

AVTCDISEDEED
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of AVTCDISEDEED
Found in PCY1A_MOUSE, Choline-phosphate cytidylyltransferase A OS=Mus musculus GN=Pcyt1a PE=1 SV=1

Match to Query 1535: 1489.518708 from(745.766630,2+)
Title: Elution from: 36.057 to 36.057 scan no 2820 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1489.5167
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0018

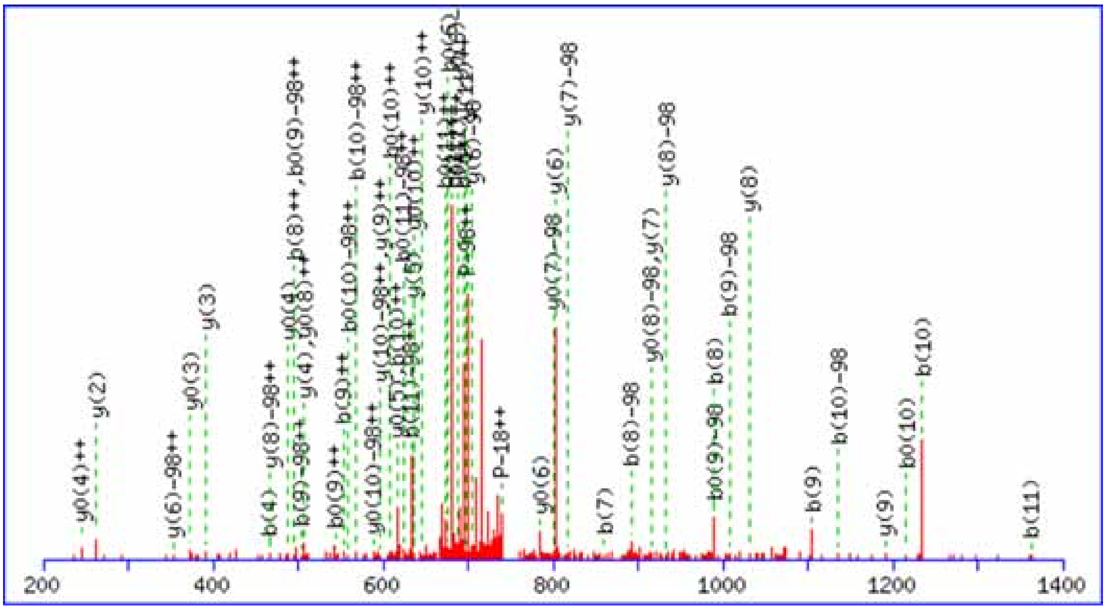
Matched b ions: b(3), b(4), b(4)++, b(5), b(6), b(7)++, b(7)-98, b(7), b(8)-98, b(8), b(8)++, b(9), b(9)++, b(10)++, b(10), b(10)-98++, b(10)-98, b(11)++, b(11), b(11)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98++, y(6)-98, y(7), y(7)-98, y(8), y(8)++, y(8)-98, y(9), y(9)-98++, y(10), y(10)-98++, y(10)++, y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.100

AVTCDISEDEED
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of AVTCDISEDEED
Found in PCY1A_MOUSE, Choline-phosphate cytidylyltransferase A OS=Mus musculus GN=Pcyt1a PE=1 SV=1

Match to Query 2091: 1495.550056 from(748.782304,2+)
Title: Elution from: 36.411 to 36.411 scan no 3014 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1495.5486
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.027

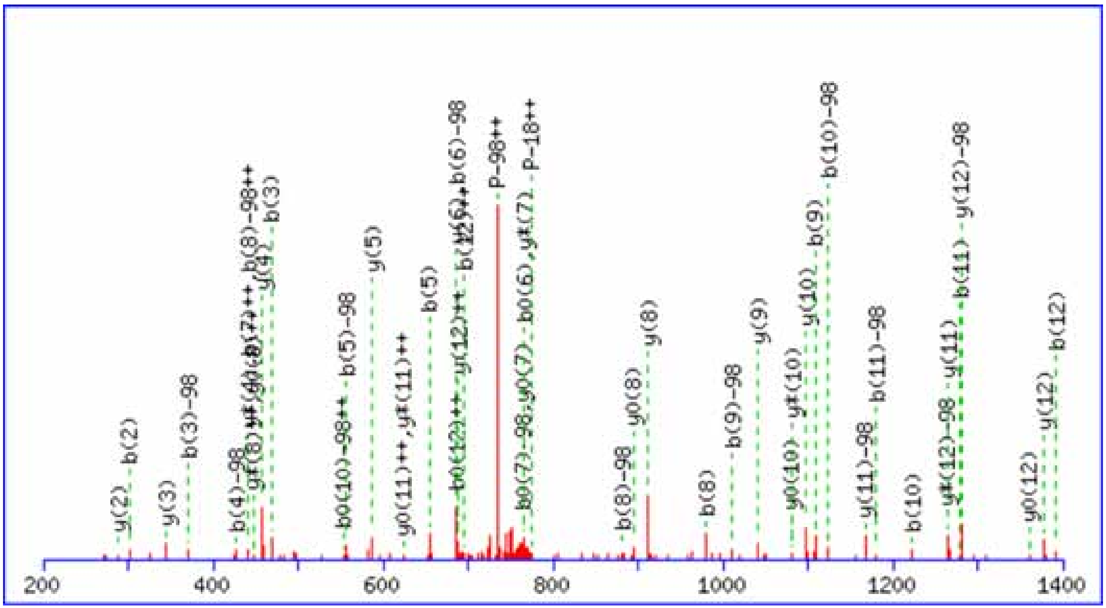
Matched b ions: b(4), b(6), b(7), b(8)-98, b(8), b(8)++, b(9), b(9)-98++, b(9)++, b(9)-98, b(10), b(10)++, b(10)-98++, b(10)-98, b(11)-98++, b(11)++, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98++, y(6)-98, y(7)-98, y(7), y(8)-98++, y(8)-98, y(8), y(9), y(9)++, y(10)-98++, y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.101

CLSGEEPVELGLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of CLSGEEPVELGLR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 2848: 1565.717008 from(783.865780,2+)
Title: Elution from: 51.155 to 51.155 scan no 5049 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1565.7160
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 6.5e-005

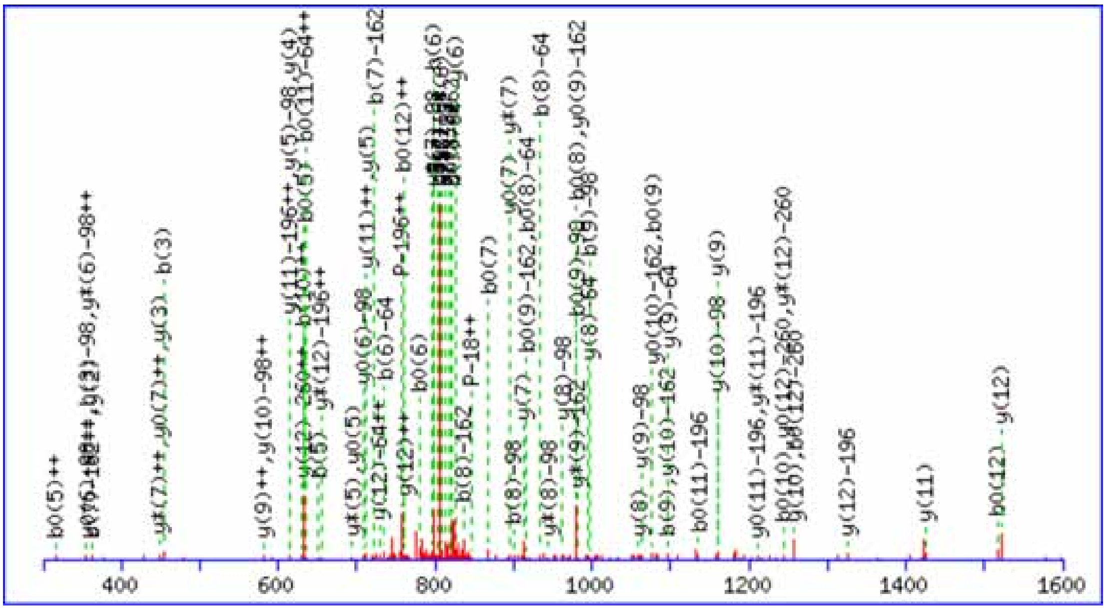
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(7)++, b(8), b(8)-98++, b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(11)-98, y(12)-98, y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.102

CPSPTMSLPSSWK
Confirmed sites: @S:3,@S:10
Ambiguous sites:

MS/MS Fragmentation of CPSPTMSLPSSWK
Found in SYNPO_MOUSE, Synaptopodin OS=Mus musculus GN=Synpo PE=1 SV=2

Match to Query 3775: 1708.665438 from(855.339995,2+)
Title: Elution from: 47.216 to 47.216 scan no 4571 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1708.6643
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 46 Expect: 0.00049

Matched b ions: b(3), b(3)-98, b(5), b(6), b(8)-98, b(9), b(9)-98, b(10)++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9)++, y(9), y(9)-98, y(10), y(10)-98++, y(10)-98, y(11)-196++, y(11)++, y(11), y(12)-196, y(12)-98, y(12), y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.103

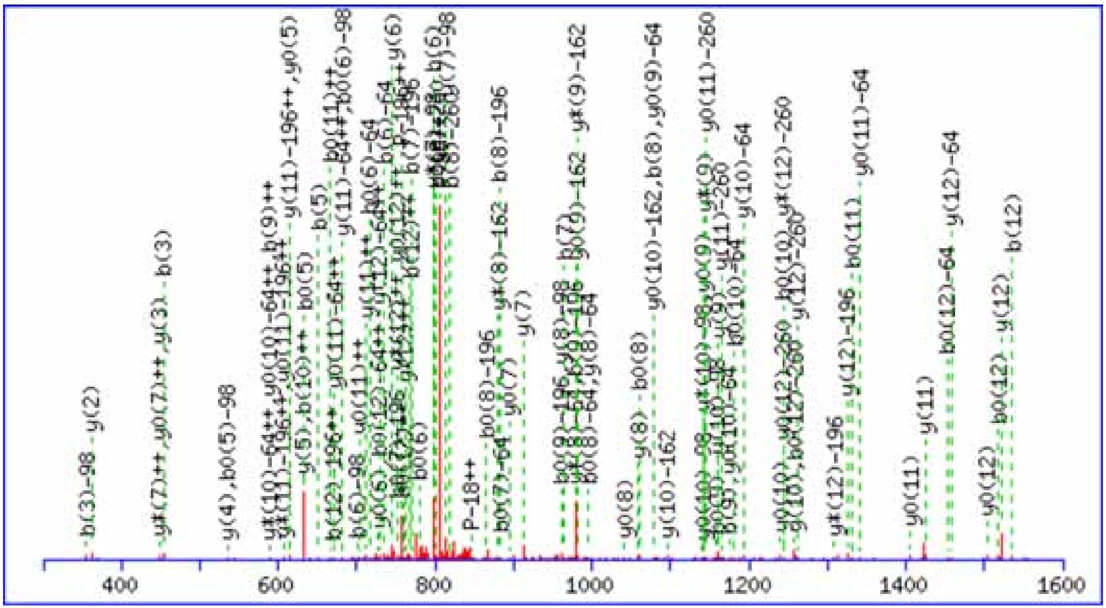
CPSPTMSLPSSWK

Confirmed sites: @S:3,@S:7

Ambiguous sites:

MS/MS Fragmentation of CPSPTMSLPSSWK
Found in SYNPO_MOUSE, Synaptopodin OS=Mus musculus GN=Synpo PE=1 SV=2

Match to Query 3777: 1708.665672 from(855.340112,2+)
Title: Elution from: 46.862 to 46.862 scan no 4527 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1708.6643
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 45 Expect: 0.00059

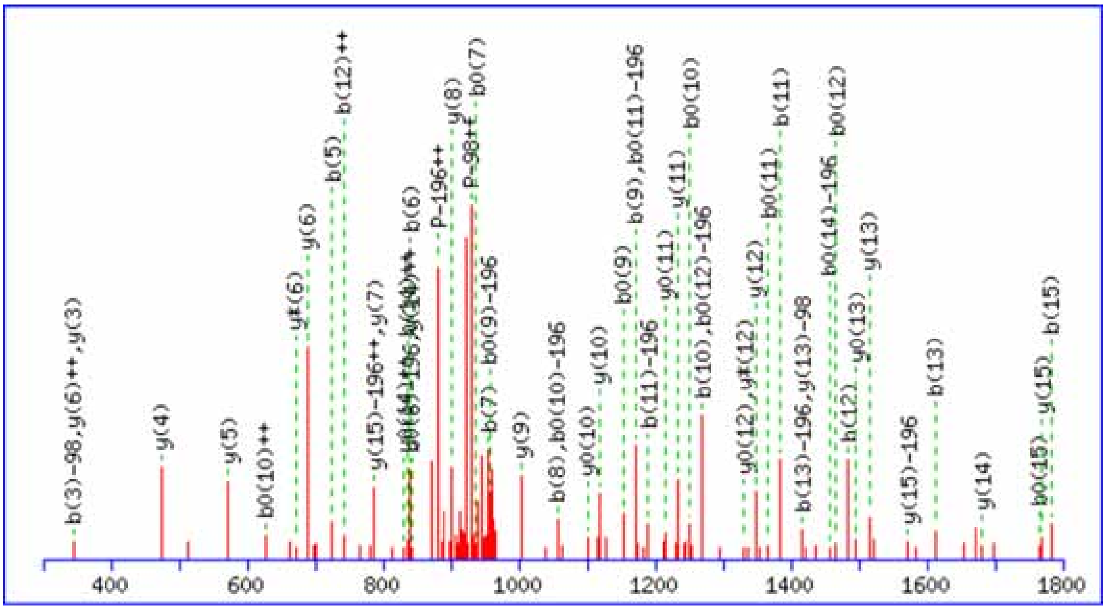
Matched b ions: b(3), b(3)-98, b(5), b(6)-98, b(6), b(7)-98, b(7)-196, b(7), b(8)-98, b(8)-196, b(8), b(9)-196, b(9)++, b(9), b(9)-98, b(10)++, b(10)-98, b(12), b(12)-196++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8)-98, y(8), y(9), y(10)-98, y(10), y(11), y(11)-196++, y(11)-98, y(11)++, y(12)-98, y(12), y(12)-196, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.104

CSSSDDDTDVDVEGLR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of CSSSDDDTDVDVEGLR
Found in PBIP1_MOUSE, Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Mus musculus GN=Pbxip1 PE=1 SV=2

Match to Query 4608: 1956.672380 from(979.343466,2+)
Title: Elution from: 45.931 to 45.931 scan no 4200 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1956.6697
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 91 **Expect:** 5.8e-009

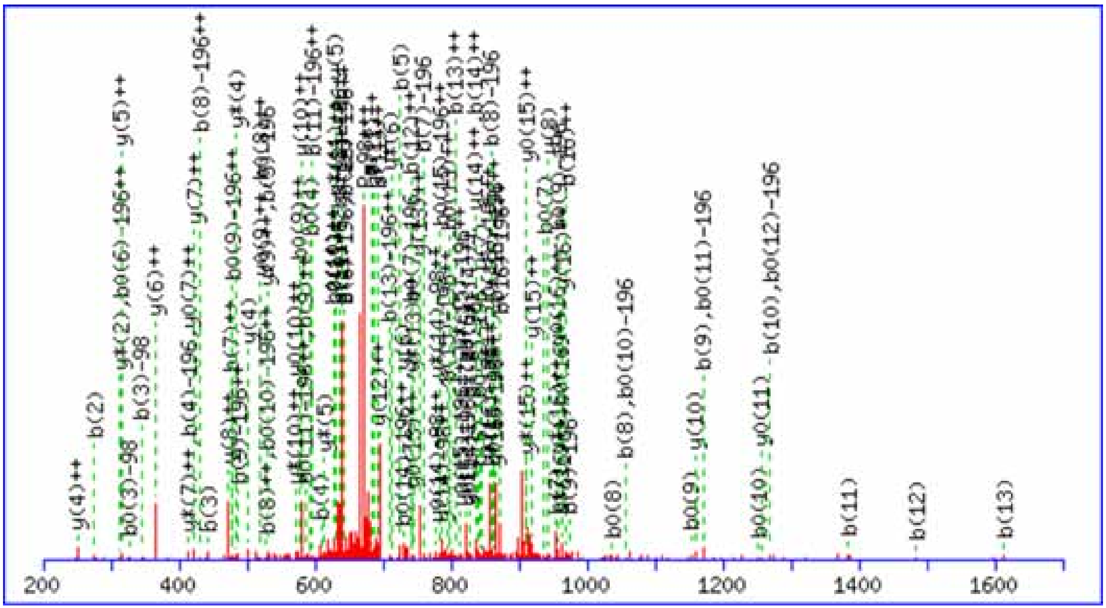
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7), b(8), b(8)-98, b(9), b(10), b(11), b(11)-196, b(12), b(12)++, b(13), b(13)-98, b(13)-196, b(14)-98++, b(14)-98, b(14)++, b(15)
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)-98, y(14)-98, y(14), y(14)++, y(15)-98, y(15)-196++, y(15)-196, y(15)
Precursor origin neutral loss: +

Peptide No.105

CSSSDDDTDVDVEGLRR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of **CSSSDDDTDVDVEGLRR**
Found in **PBIP1_MOUSE**, Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Mus musculus GN=Pbxip1 PE=1 SV=2

Match to Query 6196: 2112.772944 from(705.264924,3+)
Title: Elution from: 39.807 to 39.807 scan no 3640 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2112.7708
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 Expect: 6.3e-007

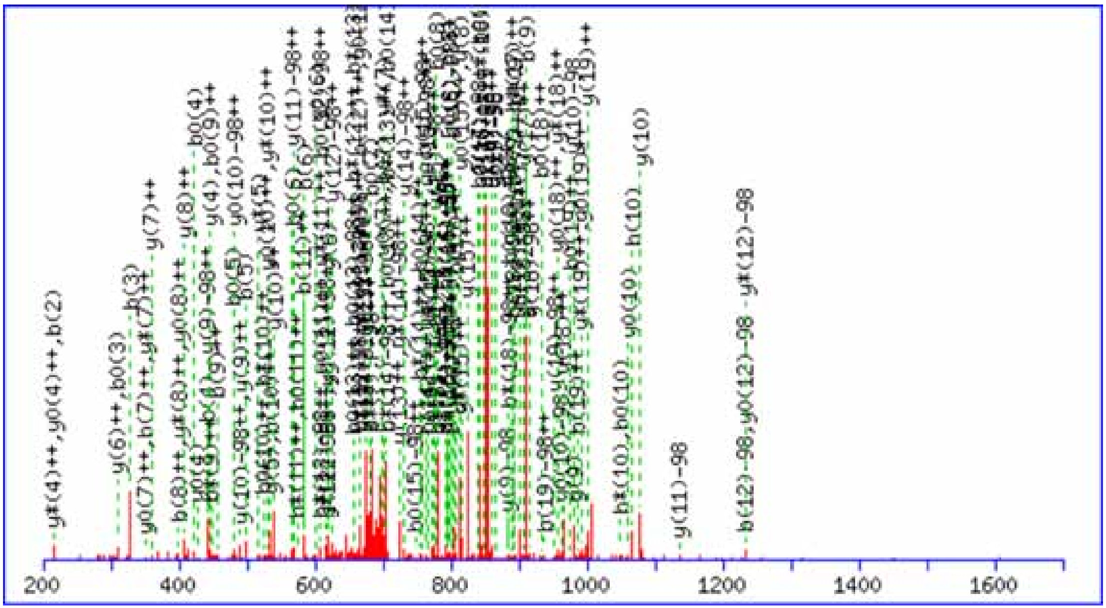
Matched b ions: b(2), b(3), b(3)-98, b(4)-196, b(4)-98, b(4), b(5)-196, b(5)-98++, b(5)-98, b(5), b(6), b(6)-196, b(6)-98, b(7), b(7)-98, b(7)++, b(7)-196, b(8)-98++, b(8), b(8)-196++, b(8)++, b(8)-196, b(8)-98, b(9), b(9)-196++, b(9)++, b(9)-196, b(10), b(10)-98, b(10)-98++, b(10)++, b(11), b(11)-196++, b(11)-98++, b(11)++, b(12), b(12)-98, b(12)-196++, b(12)-98++, b(12)++, b(13), b(13)-196++, b(13)++, b(14)++, b(14)-98++, b(15)-196++, b(16)++, b(16)-196++, b(16)-98++
Matched y ions: y(4)++, y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(14)-98++, y(15)-196++, y(15)-98++, y(15)++, y(16)-196++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.106

DALLGSNPNKPSPPSSPSSR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of DALLGSNPNKPSPPSSPSSR
Found in MYOM1_MOUSE, Myomesin-1 OS=Mus musculus GN=Myom1 PE=1 SV=2

Match to Query 6278: 2143.033767 from(715.351865,3+)
Title: Elution from: 35.949 to 35.949 scan no 3118 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2143.0310
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K10 : Dimethyl (K)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 2.8e-005

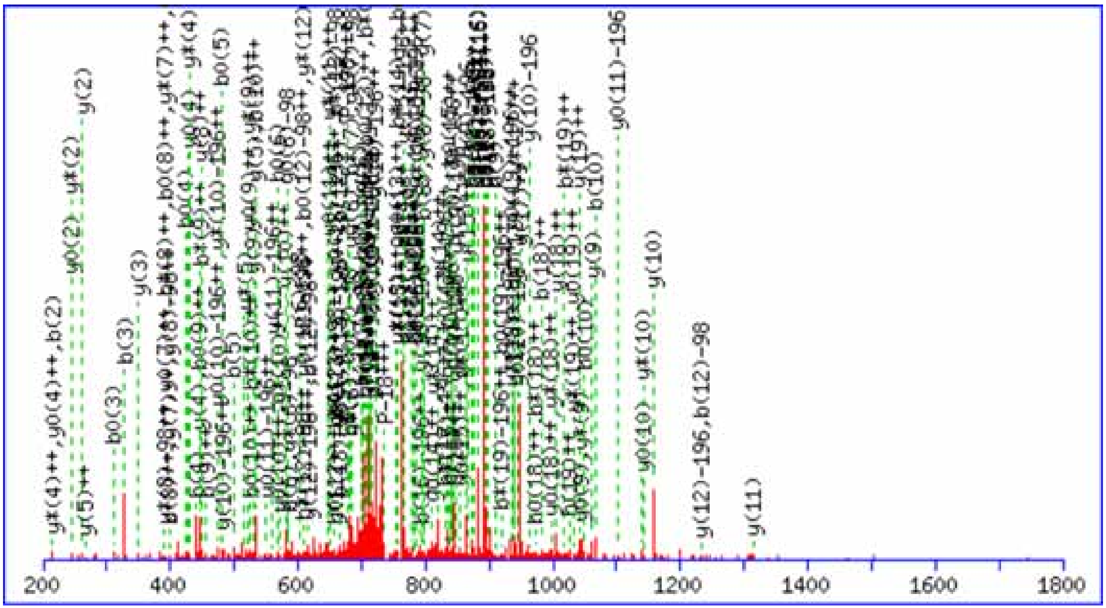
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(7)++, b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(12)-98, b(12)-98++, b(12)++, b(13)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(17)-98++, b(18)-98++, b(19)-98++, b(19)++
Matched y ions: y(4), y(5), y(6)++, y(6), y(7)++, y(8)++, y(8), y(9)++, y(9), y(9)-98++, y(9)-98, y(10)++, y(10), y(10)-98++, y(10)-98, y(11)-98, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.107

DALLGSNPNKPSPPSSPSSR
Confirmed sites: @S:12,@S:15
Ambiguous sites:

MS/MS Fragmentation of DALLGSNPNKPSPPSSPSSR
Found in MYOM1_MOUSE, Myomesin-1 OS=Mus musculus GN=Myom1 PE=1 SV=2

Match to Query 5832: 2222.998857 from(742.006895,3+)
Title: Elution from: 36.870 to 36.870 scan no 3046 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2222.9973
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K10 : Dimethyl (K)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00059

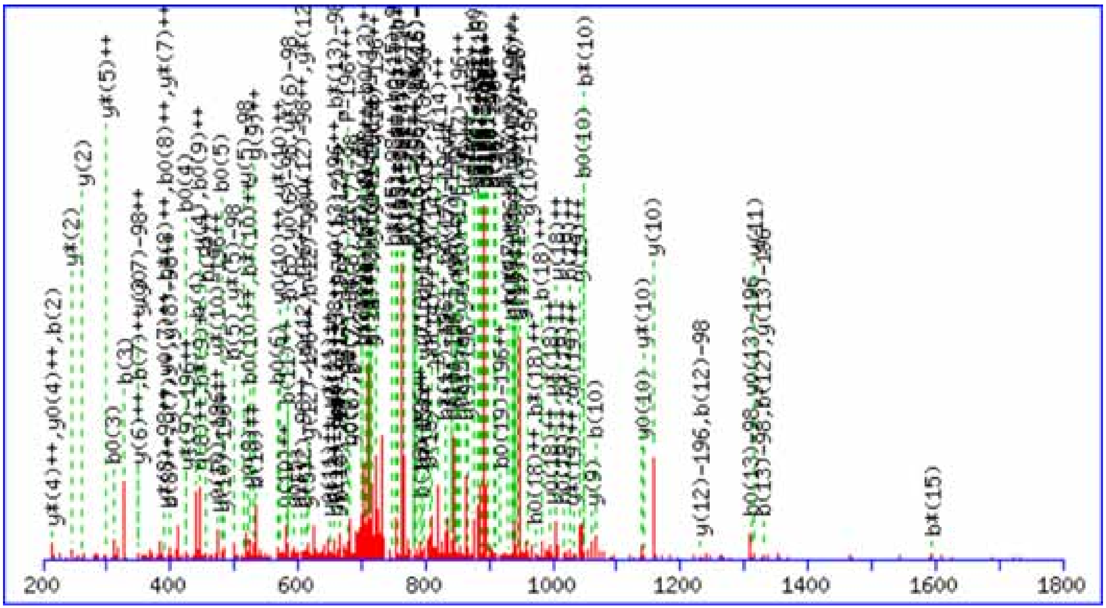
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(12)-98, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-196++, b(16)-98++, b(16)++, b(17)-196++, b(17)++, b(18)-196++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6)-98, y(6), y(7)++, y(7)-98, y(7), y(8), y(8)++, y(8)-98++, y(8)-98, y(9)++, y(9)-196, y(9)-98, y(9), y(10), y(10)++, y(10)-98, y(10)-98++, y(10)-196++, y(10)-196, y(11), y(11)-196++, y(11)-98++, y(11)++, y(12)++, y(12)-196, y(12)-196++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)-196++, y(14)++, y(14)-98++, y(15)++, y(15)-196++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.108

DALLGSNPNKPSPPSSPSSR
Confirmed sites: @S:12,@S:16
Ambiguous sites:

MS/MS Fragmentation of DALLGSNPNKPSPPSSPSSR
Found in MYOM1_MOUSE, Myomesin-1 OS=Mus musculus GN=Myom1 PE=1 SV=2

Match to Query 6696: 2223.001740 from(742.007856,3+)
Title: Elution from: 37.269 to 37.269 scan no 3299 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2222.9973
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K10 : Dimethyl (K)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 0.00053

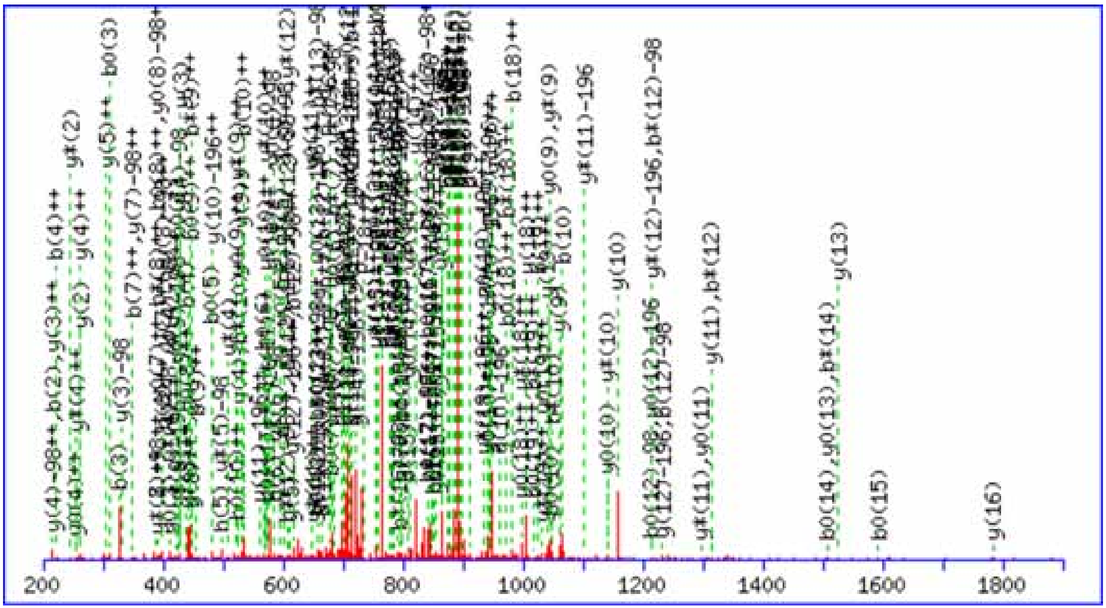
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(7)++, b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(12), b(12)-98, b(12)-98++, b(12)++, b(13)++, b(13)-98, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-196++, b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)++, b(18)-196++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6)++, y(6), y(7)++, y(7)-98, y(7)-98++, y(7), y(8)++, y(8)-98++, y(8), y(8)-98, y(9)++, y(9)-98++, y(9)-196, y(9), y(10), y(10)++, y(10)-98, y(10)-98++, y(10)-196++, y(10)-196, y(11), y(11)-98++, y(11)++, y(12)++, y(12)-98, y(12)-196, y(12)-196++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196, y(13)-196++, y(14)-196++, y(14)++, y(14)-98++, y(15)-196++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)++, y(17)-196++, y(17)-98++, y(18)++, y(18)-98++, y(18)-196++, y(19)++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.109

DALLGSNPNKPSPPSSPSSR
Confirmed sites: @S:12,@S:18
Ambiguous sites:

MS/MS Fragmentation of DALLGSNPNKPSPPSSPSSR
Found in MYOM1_MOUSE, Myomesin-1 OS=Mus musculus GN=Myom1 PE=1 SV=2

Match to Query 5930: 2222.998890 from(742.006906,3+)
Title: Elution from: 37.577 to 37.577 scan no 3146 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2222.9973
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K10 : Dimethyl (K)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 **Expect:** 7.1e-005

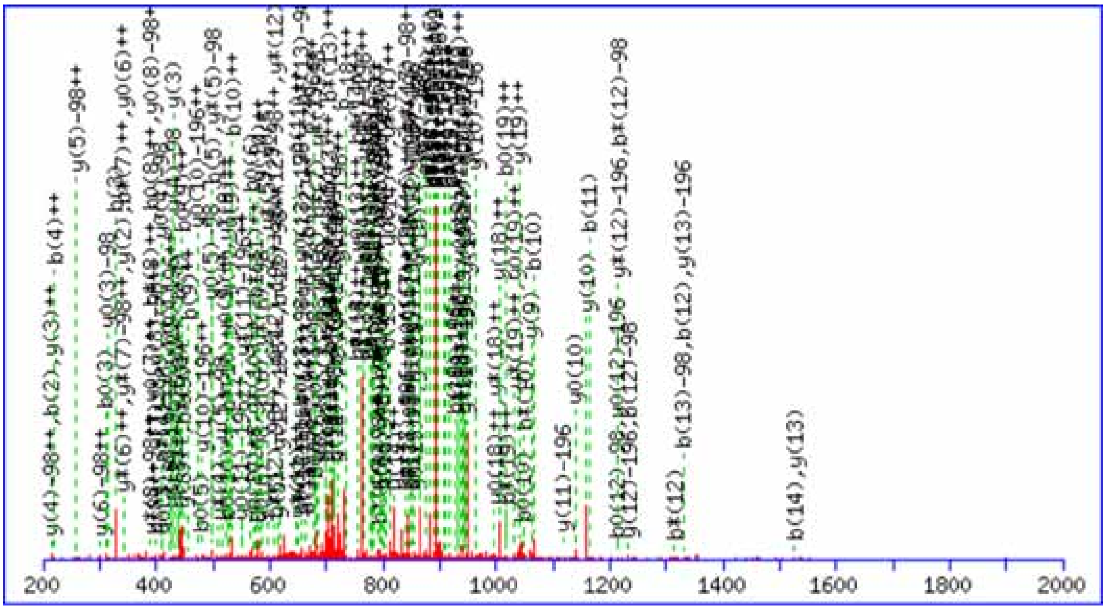
Matched b ions: b(2), b(3), b(4), b(4)++, b(5), b(6), b(7), b(7)++, b(8)++, b(8), b(9)++, b(9), b(10), b(10)++, b(12)-98, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(17)-98++, b(17)++, b(18)-196++, b(18)++, b(18)-98++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3)++, y(3), y(3)-98, y(4)-98++, y(4)-98, y(4)++, y(4), y(5)++, y(5), y(6)-98, y(6), y(7)++, y(7)-98, y(7)-98++, y(7), y(8)-98++, y(8)++, y(8), y(8)-98, y(9)++, y(9)-196, y(9), y(9)-98++, y(9)-98, y(10)++, y(10), y(10)-98++, y(10)-98, y(10)-196++, y(10)-196, y(11), y(11)-196++, y(11)-98++, y(11)++, y(12)++, y(12)-196, y(12)-196++, y(12)-98++, y(13)++, y(13)-98++, y(13), y(13)-196++, y(14)-196++, y(14)++, y(14)-98++, y(15)++, y(15)-196++, y(15)-98++, y(16)++, y(16), y(16)-98++, y(16)-196++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(18)-98++, y(19)++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.110

DALLGSNPNKPSPPSSPSSR
Confirmed sites: @S:12,@S:19
Ambiguous sites:

MS/MS Fragmentation of DALLGSNPNKPSPPSSPSSR
Found in MYOM1_MOUSE, Myomesin-1 OS=Mus musculus GN=Myom1 PE=1 SV=2

Match to Query 5833: 2222.998926 from(742.006918,3+)
Title: Elution from: 37.294 to 37.294 scan no 3108 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2222.9973
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K10 : Dimethyl (K)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 0.00029

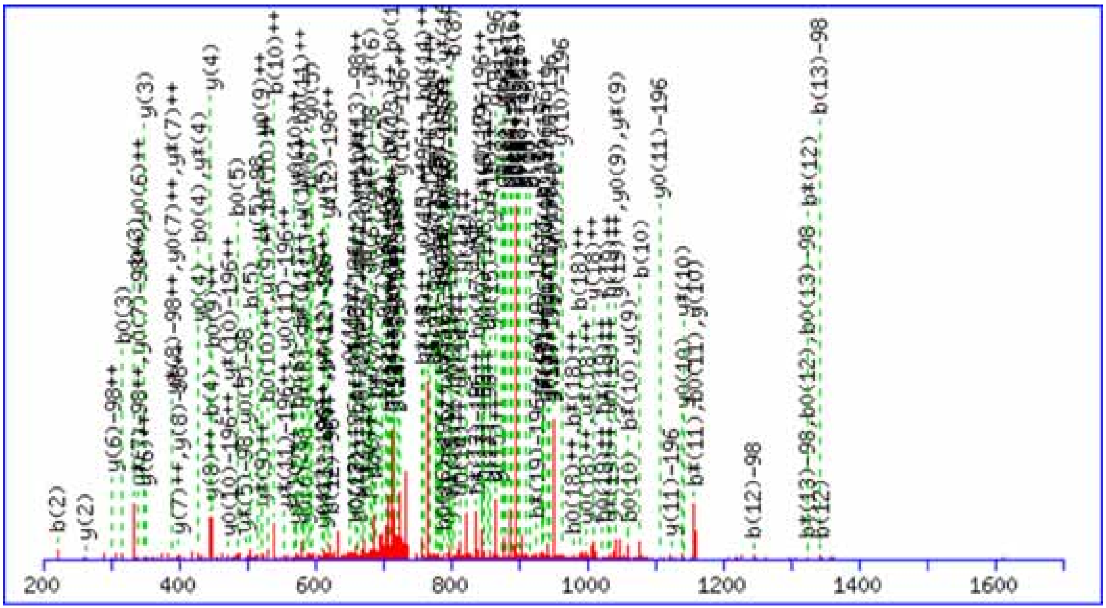
Matched b ions: b(2), b(3), b(4), b(4)++, b(5), b(6), b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11), b(12)-98, b(12), b(12)-98++, b(12)++, b(13)++, b(13)-98, b(13)-98++, b(14)++, b(14), b(14)-98++, b(15)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-196++
Matched y ions: y(2), y(3)++, y(3), y(4)-98++, y(4)-98, y(4), y(5)-98, y(5)-98++, y(5), y(6)-98++, y(6), y(7)-98, y(7)++, y(7), y(8)++, y(8), y(8)-98++, y(8)-98, y(9), y(9)++, y(9)-196, y(9)-98, y(10), y(10)++, y(10)-98, y(10)-98++, y(10)-196++, y(10)-196, y(11)-98++, y(11)++, y(11)-196, y(11)-98, y(12)-196, y(12)++, y(12)-98, y(12)-196++, y(12)-98++, y(13)++, y(13), y(13)-98++, y(13)-196, y(13)-196++, y(14)++, y(14)-196++, y(14)-98++, y(15)++, y(15)-196++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(18)-98++, y(18)-196++, y(19)++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.111

DALLGSNPNKPSPPSSPSSR
Confirmed sites: @S:12,@S:16
Ambiguous sites:

MS/MS Fragmentation of DALLGSNPNKPSPPSSPSSR
Found in MYOM1_MOUSE, Myomesin-1 OS=Mus musculus GN=Myom1 PE=1 SV=2

Match to Query 7438: 2235.062976 from(746.028268,3+)
Title: Elution from: 37.024 to 37.024 scan no 3216 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2235.0610
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K10 : Dimethyl:2H(4)13C(2) (K)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 **Expect:** 0.00019

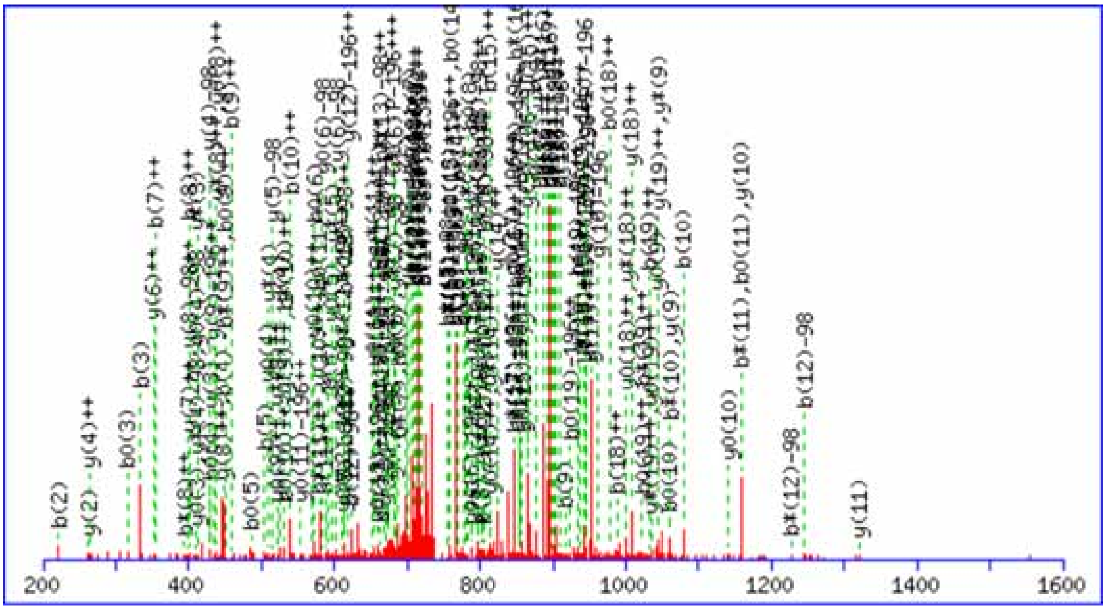
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10)++, b(10), b(11)++, b(12), b(12)-98, b(12)-98++, b(12)++, b(13)-98, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(16)++, b(16)-98++, b(16)-196++, b(17)-98++, b(17)-196++, b(17)++, b(18)-196++, b(18)-98++, b(18)++, b(19)-196++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6)-98++, y(6)++, y(6), y(7)++, y(7)-98, y(7), y(8)++, y(8), y(8)-98++, y(8)-98, y(9)++, y(9)-196, y(9)-98, y(9), y(10), y(10)++, y(10)-98++, y(10)-98, y(10)-196, y(11)-196, y(11)-98, y(11)-98++, y(11)++, y(12)++, y(12)-196++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)++, y(14)-196++, y(14)-98++, y(15)++, y(15)-196++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(18)-196++, y(18)-98++, y(19)++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.112

DALLGSNPNKPSPPSSPSSR
Confirmed sites: @S:12,@S:18
Ambiguous sites:

MS/MS Fragmentation of DALLGSNPNKPSPPSSPSSR
Found in MYOM1_MOUSE, Myomesin-1 OS=Mus musculus GN=Myom1 PE=1 SV=2

Match to Query 6132: 2235.061317 from(746.027715,3+)
Title: Elution from: 37.210 to 37.210 scan no 3127 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2235.0610
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K10 : Dimethyl:2H(4)13C(2) (K)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 **Expect:** 5.4e-006

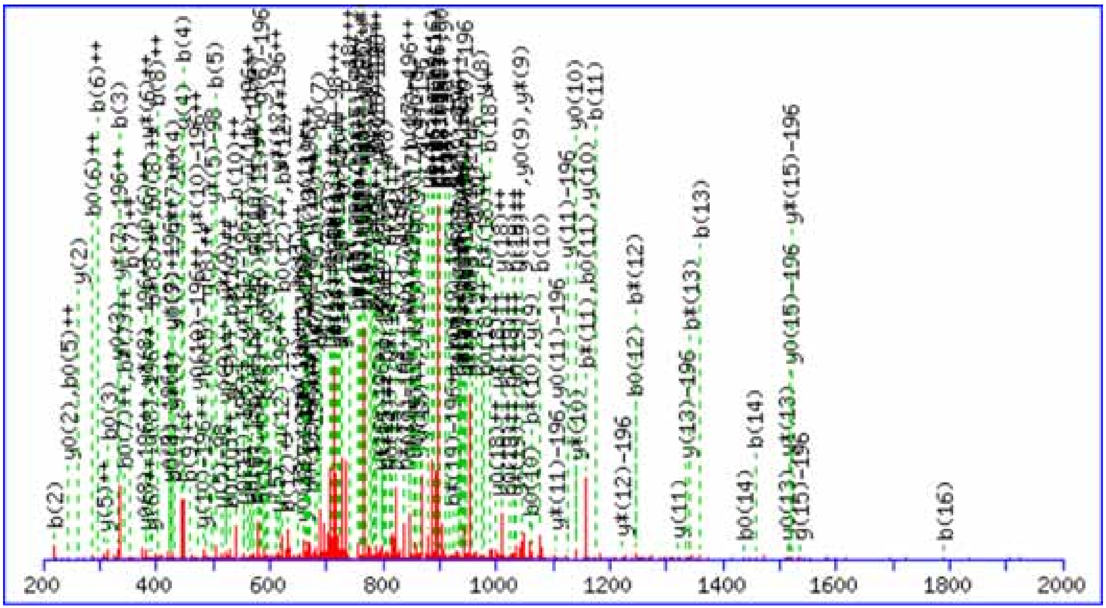
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(7)++, b(8)++, b(8), b(9)++, b(9), b(10), b(10)++, b(11)++, b(12)-98, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-196++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(4)++, y(4)-98, y(4), y(5), y(5)-98, y(6)++, y(6)-98, y(6), y(7)++, y(7)-98, y(7), y(8)++, y(8), y(8)-98++, y(8)-98, y(9)-98++, y(9)++, y(9), y(9)-196++, y(9)-196, y(9)-98, y(10)++, y(10), y(10)-98, y(10)-98++, y(10)-196, y(11), y(11)-98++, y(11)++, y(12)++, y(12)-196++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)++, y(14)-98++, y(15)++, y(15)-196++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(18)-98++, y(18)-196++, y(19)++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.113

DALLGSNPNKPSPPSSPSSR
Confirmed sites: @S:15,@S:16
Ambiguous sites:

MS/MS Fragmentation of DALLGSNPNKPSPPSSPSSR
Found in MYOM1_MOUSE, Myomesin-1 OS=Mus musculus GN=Myom1 PE=1 SV=2

Match to Query 7437: 2235.062595 from(746.028141,3+)
Title: Elution from: 37.467 to 37.467 scan no 3282 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2235.0610
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K10 : Dimethyl:2H(4)13C(2) (K)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 0.00034

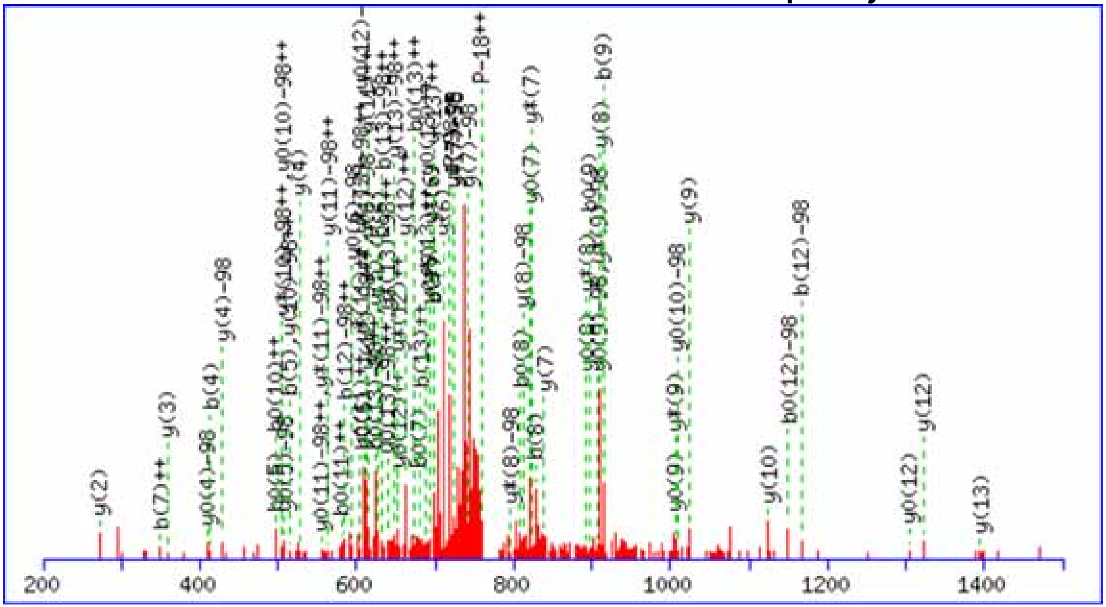
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(6)++, b(7), b(7)++, b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11), b(11)++, b(12)++, b(13), b(13)++, b(14), b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98, b(16), b(16)-98++, b(16)-196++, b(17)-98++, b(17)++, b(17)-196++, b(18)++, b(18)-196++, b(18)-98++, b(19)-196++, b(19)-98++, b(19)++
Matched y ions: y(2), y(4), y(5), y(5)++, y(5)-98, y(6)++, y(6)-196, y(6)-98, y(6), y(7)-98++, y(7)-196, y(7)-98, y(7), y(8)-196++, y(8)++, y(8)-196, y(8)-98, y(8), y(9)-98++, y(9)++, y(9), y(9)-196, y(9)-98, y(10)++, y(10), y(10)-98, y(10)-196++, y(10)-98++, y(10)-196, y(11), y(11)-196++, y(11)-98++, y(11)++, y(11)-196, y(11)-98, y(12)++, y(12)-98, y(12)-196++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196, y(13)-196++, y(14)++, y(14)-196++, y(14)-98++, y(15)-196, y(15)++, y(15)-98++, y(15)-196++, y(16)++, y(16)-98++, y(16)-196++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(18)-196++, y(18)-98++, y(19)++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.114

DAPTTLAESPSSPK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of DAPTTLAESPSSPK
Found in NACAM_MOUSE, Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1

Match to Query 2050: 1535.713712 from(768.864132,2+)
Title: Elution from: 33.252 to 33.252 scan no 2537 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1535.7120
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
Ions Score: 41 Expect: 0.0027

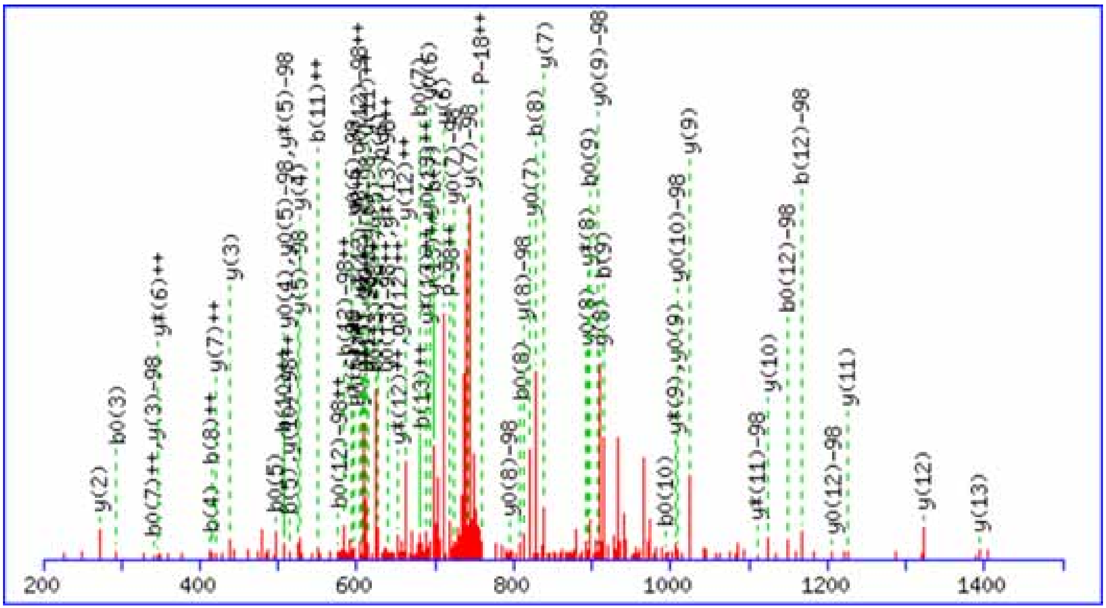
Matched b ions: b(4), b(5), b(6), b(7)++, b(7), b(8), b(9), b(12)-98, b(12)-98++, b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(10), y(10)-98++, y(11)++, y(11)-98++, y(12), y(12)++, y(12)-98++, y(13), y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.115

DAPTTLAESPSSPK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of DAPTTLAESPSSPK
Found in NACAM_MOUSE, Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1

Match to Query 2746: 1535.712600 from(768.863576,2+)
Title: Elution from: 33.215 to 33.215 scan no 2743 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1535.7120
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
Ions Score: 66 **Expect:** 8.6e-006

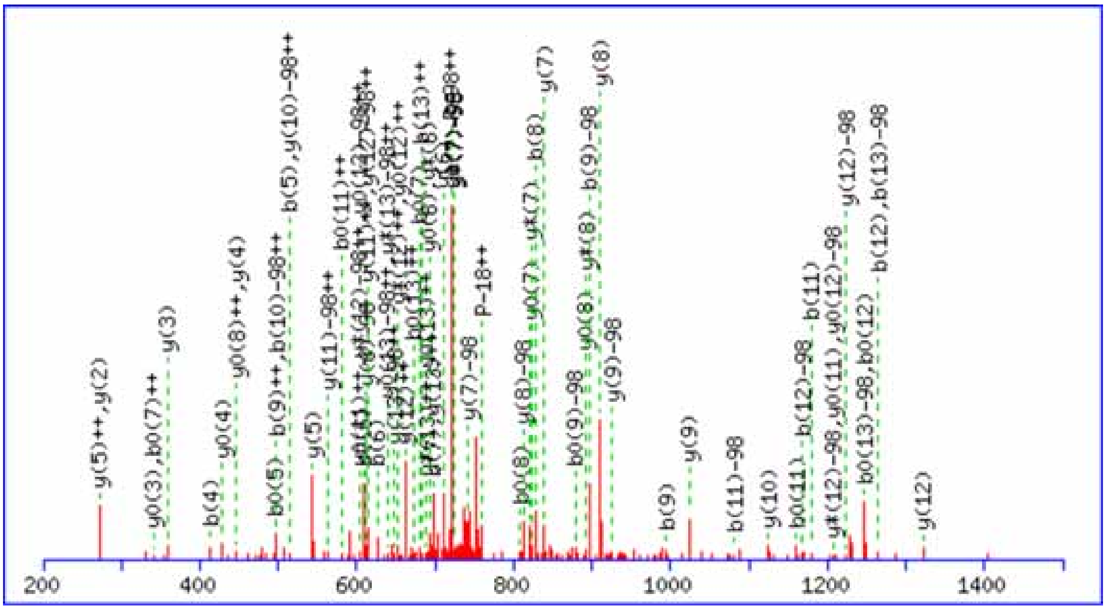
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(8)++, b(9), b(10)++, b(11)++, b(12)-98, b(12)-98++, b(13)++
Matched y ions: y(2), y(3), y(3)-98, y(4), y(5), y(5)-98, y(6), y(6)-98, y(7)++, y(7), y(7)-98, y(8), y(8)-98, y(9), y(10), y(10)-98++, y(11), y(11)++, y(12), y(12)-98++, y(12)++, y(13), y(13)++
Precursor origin neutral loss:

Peptide No.116

DAPTTLAESPSSPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of DAPTTLAESPSSPK
Found in NACAM_MOUSE, Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1

Match to Query 2747: 1535.712908 from(768.863730,2+)
Title: Elution from: 32.246 to 32.246 scan no 2613 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1535.7120
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
Ions Score: 57 Expect: 6.6e-005

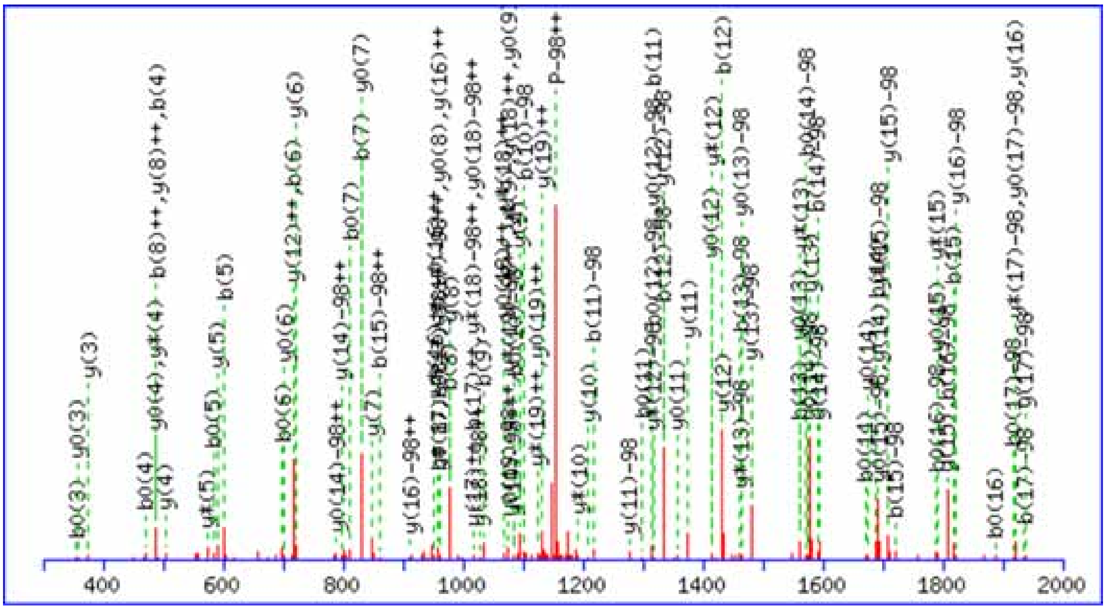
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)-98, b(9), b(9)++, b(10)-98++, b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12), y(12)-98++, y(12)-98, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.117

DDDDIDLFGSDDEEESEEAK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DDDDIDLFGSDDEEESEEAK
Found in EF1B_MOUSE, Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5

Match to Query 7305: 2407.895940 from(1204.955246,2+)
Title: Elution from: 58.060 to 58.060 scan no 5756 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2407.8952
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
Ions Score: 82 Expect: 1.6e-007

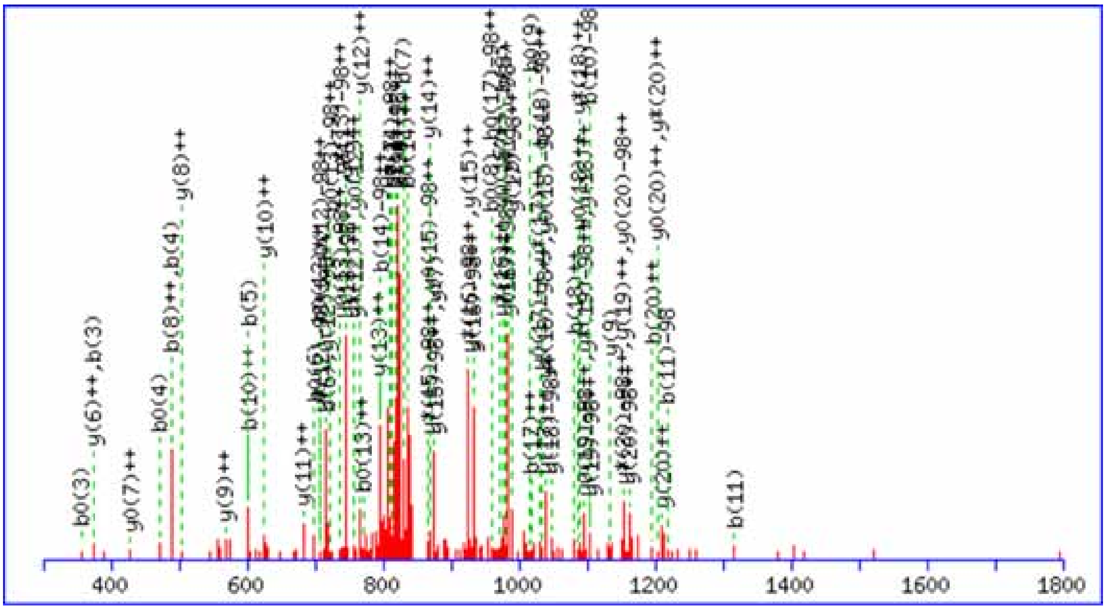
Matched b ions: b(4), b(5), b(6), b(7), b(8)++, b(8), b(9), b(10)-98, b(11)-98, b(11), b(12)-98, b(12), b(13)-98, b(13), b(14), b(14)-98, b(15), b(15)-98, b(15)-98++, b(16)-98, b(17)++, b(17)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11), y(11)-98, y(12)++, y(12)-98, y(12), y(13)-98, y(13), y(14), y(14)-98, y(14)-98++, y(15), y(15)-98, y(16), y(16)++, y(16)-98, y(16)-98++, y(17)-98, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.118

DDDDIDLFGSDDEEESEEAKK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of DDDDIDLFGSDDEEESEEAKK
Found in EF1B_MOUSE, Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5

Match to Query 7779: 2564.022744 from(855.681524,3+)
Title: Elution from: 51.719 to 51.719 scan no 5110 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2564.0214
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl (K)
K21 : Dimethyl (K)
Ions Score: 58 **Expect:** 7.5e-005

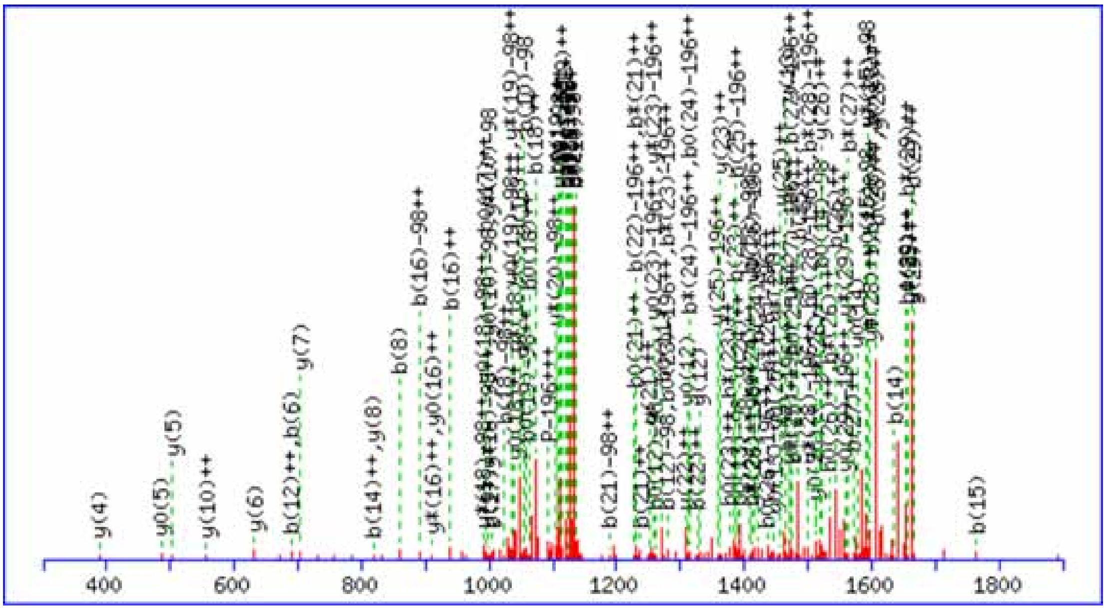
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)++, b(8), b(10)++, b(10)-98, b(11), b(11)-98, b(14)-98++, b(17)++, b(18)++, b(18)-98++, b(20)++
Matched y ions: y(6)++, y(6), y(7), y(8)++, y(9)++, y(9), y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++
Precursor origin neutral loss: +

Peptide No.119

DDGDEEGLLTHSEEELEHSQDTDAEDGALQ
Confirmed sites: @T:10,@T:22
Ambiguous sites:

MS/MS Fragmentation of DDGDEEGLLTHSEEELEHSQDTDAEDGALQ
Found in RALY_MOUSE, RNA-binding protein Raly OS=Mus musculus GN=Raly PE=1 SV=2

Match to Query 8791: 3471.304299 from(1158.108709,3+)
Title: Elution from: 53.604 to 53.604 scan no 5310 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3471.3036
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T22 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00085

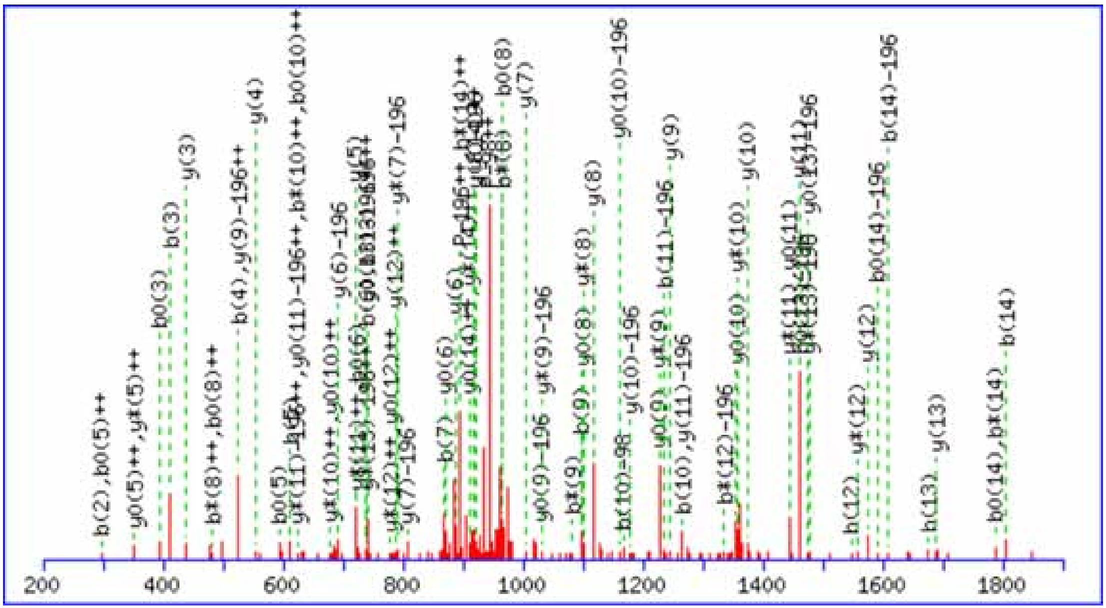
Matched b ions: b(6), b(8), b(10)-98, b(12)++, b(12)-98, b(13)-98, b(14)++, b(14), b(15), b(16)++, b(16)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(20)-98++, b(21)++, b(21)-98++, b(22)-196++, b(22)-98++, b(22)++, b(23)++, b(23)-98++, b(24)++, b(24)-98++, b(25)++, b(25)-98++, b(25)-196++, b(26)++, b(26)-98++, b(27)-196++, b(27)-98++, b(27)++, b(28)++, b(28)-98++, b(29)++, b(29)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(12), y(13), y(18)++, y(18)-98++, y(20)-98++, y(21)++, y(22)++, y(22)-98++, y(23)++, y(24)++, y(24)-98++, y(25)-196++, y(25)-98++, y(25)++, y(26)-98++, y(26)++, y(28)++, y(28)-98++, y(29)++
Precursor origin neutral loss: +

Peptide No.120

DFDISEQNDSSDEEK
Confirmed sites: @S:10,@S:11
Ambiguous sites:

MS/MS Fragmentation of DFDISEQNDSSDEEK
Found in DNJC1_MOUSE, DnaJ homolog subfamily C member 1 OS=Mus musculus GN=Dnajc1 PE=1 SV=1

Match to Query 5124: 1984.750530 from(993.382541,2+)
Title: Elution from: 46.584 to 46.584 scan no 4340 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1984.7500
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 54 Expect: 6e-005

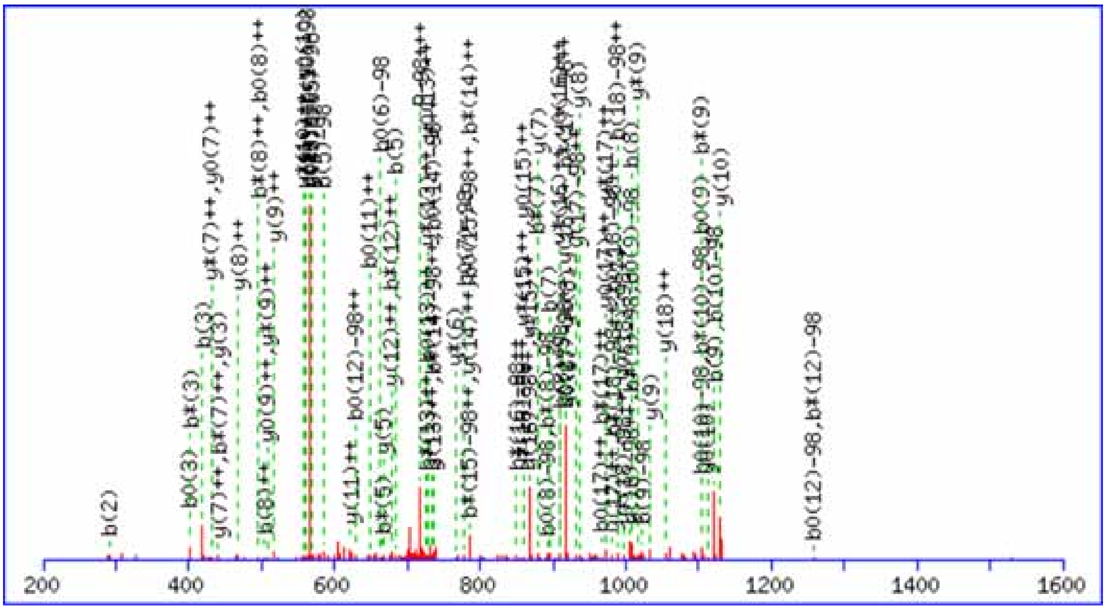
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(9), b(10), b(10)-98, b(11)-196, b(11)-98, b(12), b(12)-98, b(13)-196++, b(13), b(13)-98++, b(14), b(14)-98, b(14)-196
Matched y ions: y(3), y(4), y(5), y(6)-196, y(6), y(6)-98, y(7)-98, y(7), y(7)-196, y(8)-98, y(8), y(8)-196, y(9)-196++, y(9), y(9)-98, y(10), y(10)-98, y(10)-196, y(11)-98, y(11), y(11)-196, y(11)-98++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13), y(13)-98, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.121

DFQPSPDLIPPGPDVQHQR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DFQPSPDLIPPGPDVQHQR
Found in XIRP1_MOUSE, Xin actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 PE=1 SV=2

Match to Query 6874: 2250.049638 from(751.023822,3+)
Title: Elution from: 49.975 to 49.975 scan no 4914 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2250.0471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.0017

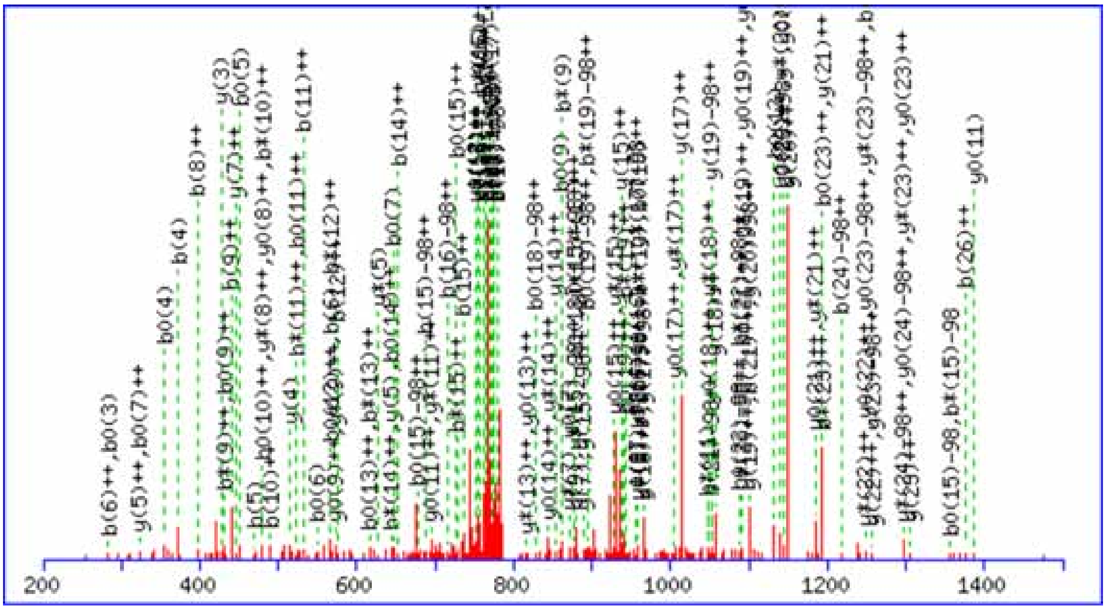
Matched b ions: b(2), b(3), b(5)-98, b(5), b(7), b(8), b(8)++, b(8)-98, b(9), b(9)-98, b(9)++, b(10)-98, b(10)-98++, b(13)++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(7), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.122

DGTAPPPQSPSSPGSGQDEDWSDEESPRK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of DGTAPPPQSPSSPGSGQDEDWSDEESPRK
Found in PACN3_MOUSE, Protein kinase C and casein kinase II substrate protein 3 OS=Mus musculus GN=Pacsin3 PE=1 SV=1

Match to Query 8665: 3175.330400 from(794.839876,4+)
Title: Elution from: 35.717 to 35.717 scan no 3087 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3175.3255
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K29 : Dimethyl (K)
Ions Score: 36 Expect: 0.022

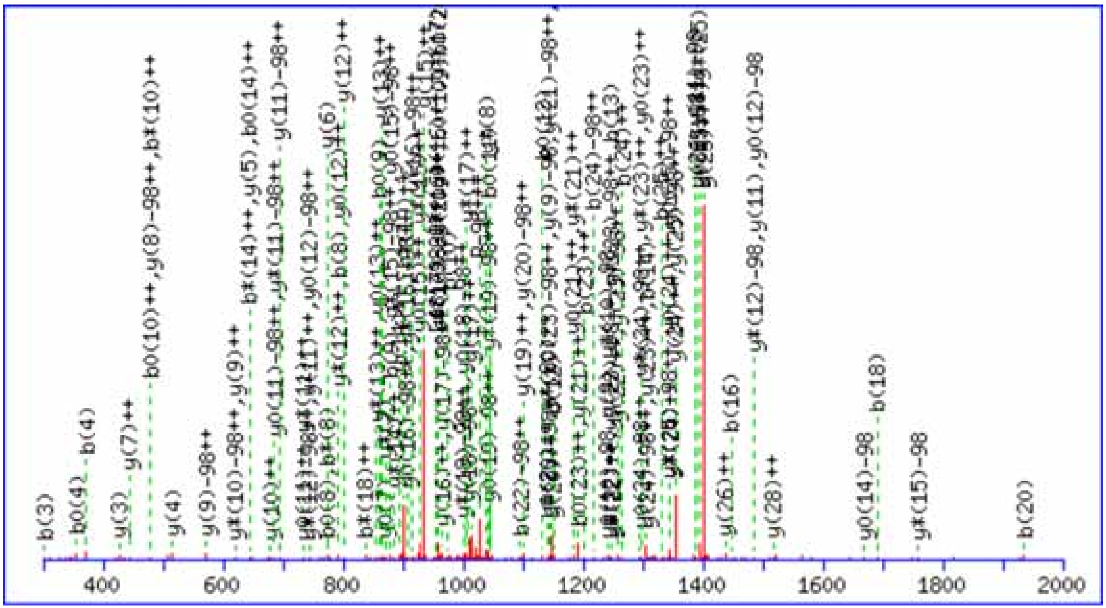
Matched b ions: b(4), b(5), b(6), b(6)++, b(8)++, b(9)++, b(9), b(10)++, b(11)++, b(12)++, b(13), b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(20)-98++, b(21)++, b(21)-98++, b(24)-98++, b(26)++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(12)++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.123

DGTAPPPQSPSSPGSGQDEDWSDEESPRK
Confirmed sites: @S:22
Ambiguous sites:

MS/MS Fragmentation of DGTAPPPQSPSSPGSGQDEDWSDEESPRK
Found in PACN3_MOUSE, Protein kinase C and casein kinase II substrate protein 3 OS=Mus musculus GN=Pacsin3 PE=1 SV=1

Match to Query 7627: 3175.325838 from(1059.449222,3+)
Title: Elution from: 35.834 to 35.834 scan no 2935 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3175.3255
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S22 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K29 : Dimethyl (K)
Ions Score: 100 **Expect:** 9.1e-009

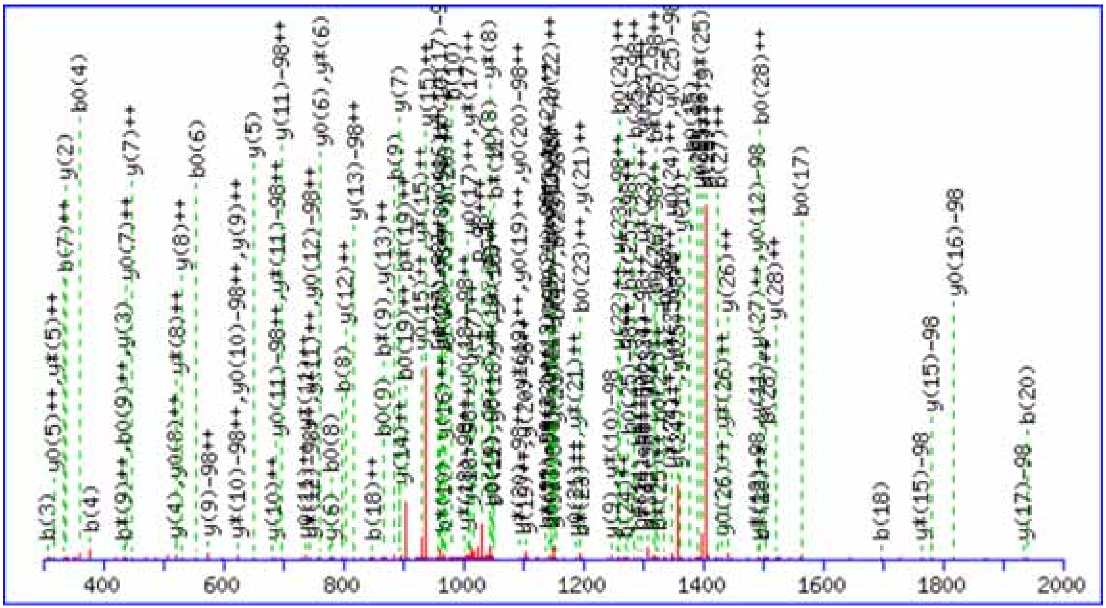
Matched b ions: b(3), b(4), b(8), b(9), b(10), b(12), b(13), b(14), b(16), b(18), b(20), b(22)++, b(22)-98++, b(23)++, b(24)-98++, b(24)++, b(25)++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(8)-98++, y(8)-98, y(9)-98++, y(9)++, y(9), y(9)-98, y(10)++, y(11)-98++, y(11)++, y(11), y(11)-98, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(23)-98++, y(23)++, y(24)++, y(24)-98++, y(25)-98++, y(25)++, y(26)++, y(26)-98++, y(28)++
Precursor origin neutral loss: +

Peptide No.124

DGTAPPPQSPSSPGSGQDEDWSDEESPRK
Confirmed sites: @S:22
Ambiguous sites:

MS/MS Fragmentation of DGTAPPPQSPSSPGSGQDEDWSDEESPRK
Found in PACN3_MOUSE, Protein kinase C and casein kinase II substrate protein 3 OS=Mus musculus GN=Pacsin3 PE=1 SV=1

Match to Query 8920: 3187.389282 from(1063.470370,3+)
Title: Elution from: 35.589 to 35.589 scan no 3008 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3187.3891
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S22 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K29 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 111 **Expect:** 7.5e-010

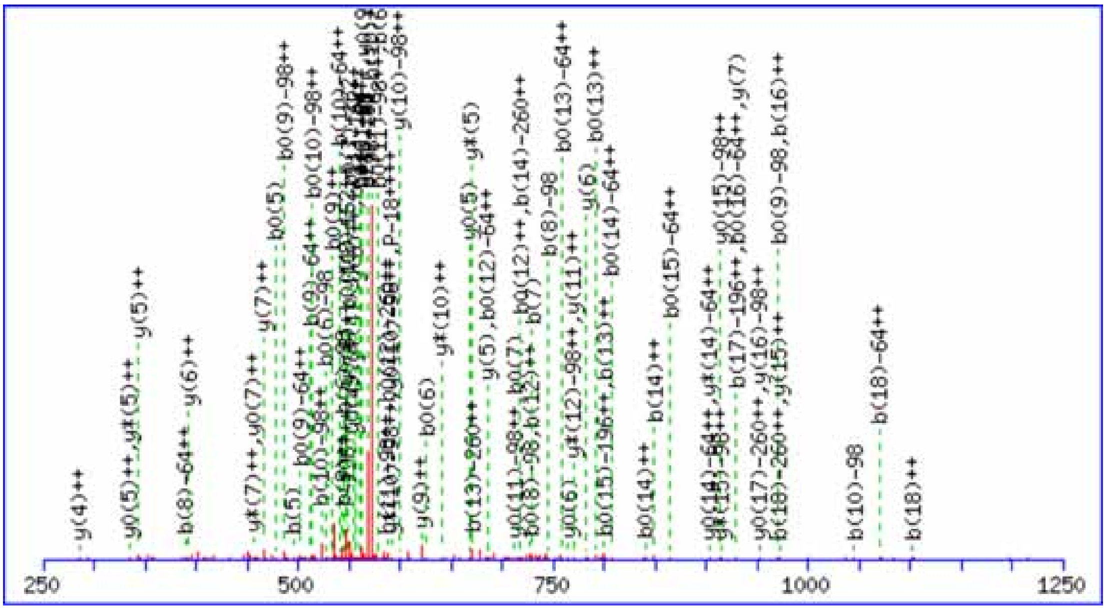
Matched b ions: b(3), b(4), b(7)++, b(8), b(9), b(10), b(12), b(18), b(18)++, b(20), b(20)++, b(22)++, b(23)-98++, b(24)++, b(25)-98++, b(25)++, b(27)++, b(28)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8)-98, y(9)-98++, y(9)++, y(9), y(9)-98, y(10)++, y(10), y(11), y(11)-98++, y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(15)-98, y(15)++, y(16)++, y(17)-98, y(17)-98++, y(17)++, y(18)-98++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(23)-98++, y(23)++, y(24)++, y(24)-98++, y(25)++, y(25)-98++, y(26)++, y(26)-98++, y(27)++, y(28)++
Precursor origin neutral loss: +

Peptide No.125

DGTGGMSIYGETFPDENFK
Confirmed sites: @T:3,@Y:9,@T:12
Ambiguous sites:

MS/MS Fragmentation of DGTGGMSIYGETFPDENFK
Found in PPIC_MOUSE, Peptidyl-prolyl cis-trans isomerase C OS=Mus musculus GN=Ppic PE=1 SV=1

Match to Query 6533: 2381.867272 from(596.474094,4+)
Title: Elution from: 37.159 to 37.159 scan no 3119 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2381.8665
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y9 : Phospho (Y)
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 33 Expect: 0.0097

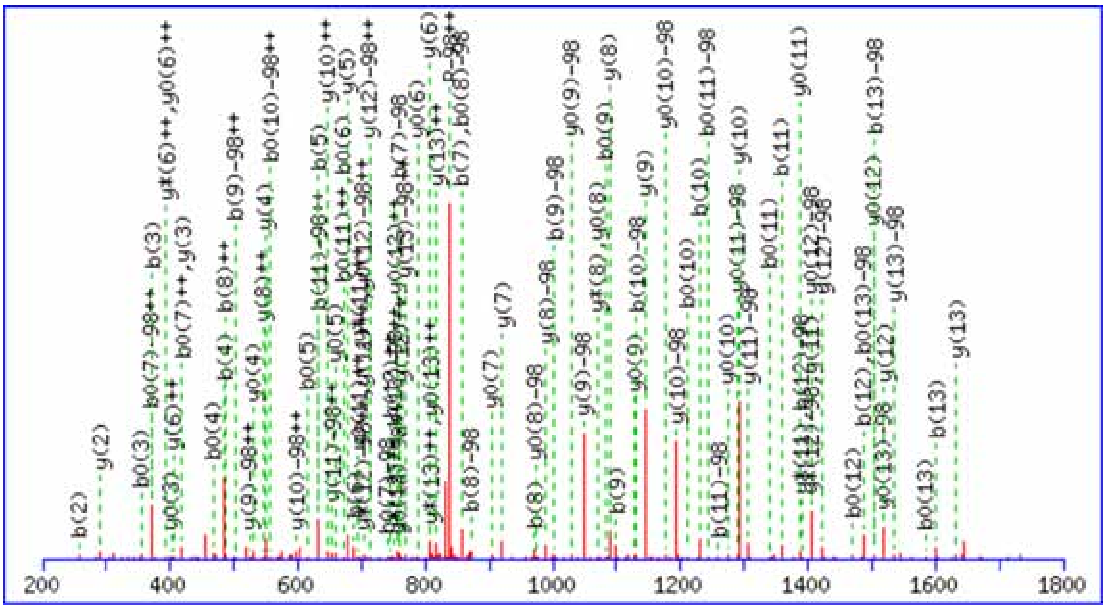
Matched b ions: b(5), b(6)-98, b(7), b(8)-98, b(9)++, b(10)++, b(10)-98, b(10)-98++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(14)-98++, b(14)++, b(16)++, b(17)-196++, b(18)++
Matched y ions: y(4)++, y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(9)-98++, y(9)++, y(10)-98++, y(11)++, y(15)++, y(16)-98++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.126

DIDLFGSDEEEEDK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DIDLFGSDEEEEDK
Found in EF1D_MOUSE, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 4162: 1775.703718 from(888.859135,2+)
Title: Elution from: 58.489 to 58.489 scan no 5796 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1775.7026
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
Ions Score: 88 Expect: 3.2e-008

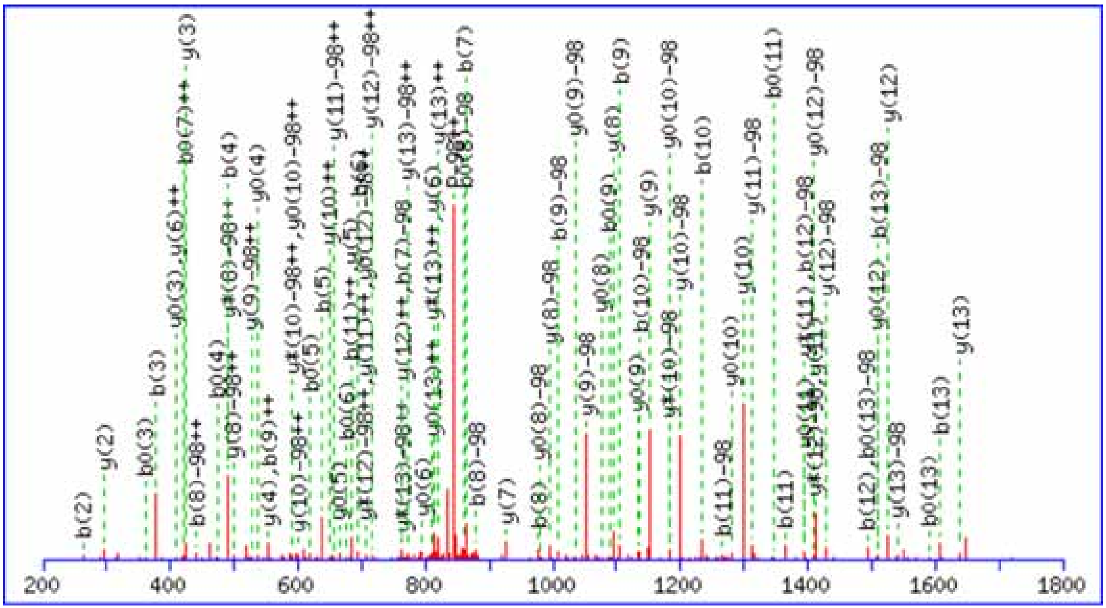
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)-98, b(7), b(8)-98, b(8), b(8)++, b(9), b(9)-98, b(9)-98++, b(10), b(10)-98, b(11), b(11)-98++, b(11)-98, b(12), b(12)-98, b(12)++, b(13), b(13)-98++, b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8)-98, y(8), y(8)++, y(9)-98, y(9), y(9)-98++, y(10)-98, y(10), y(10)++, y(10)-98++, y(11), y(11)-98, y(11)++, y(11)-98++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13), y(13)++, y(13)-98, y(13)-98++
Precursor origin neutral loss: +

Peptide No.127

DIDLFGSDEEEEDK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DIDLFGSDEEEEDK
Found in EF1D_MOUSE, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 4859: 1787.766226 from(894.890389,2+)
Title: Elution from: 57.968 to 57.968 scan no 5806 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1787.7662
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 85 Expect: 1.3e-007

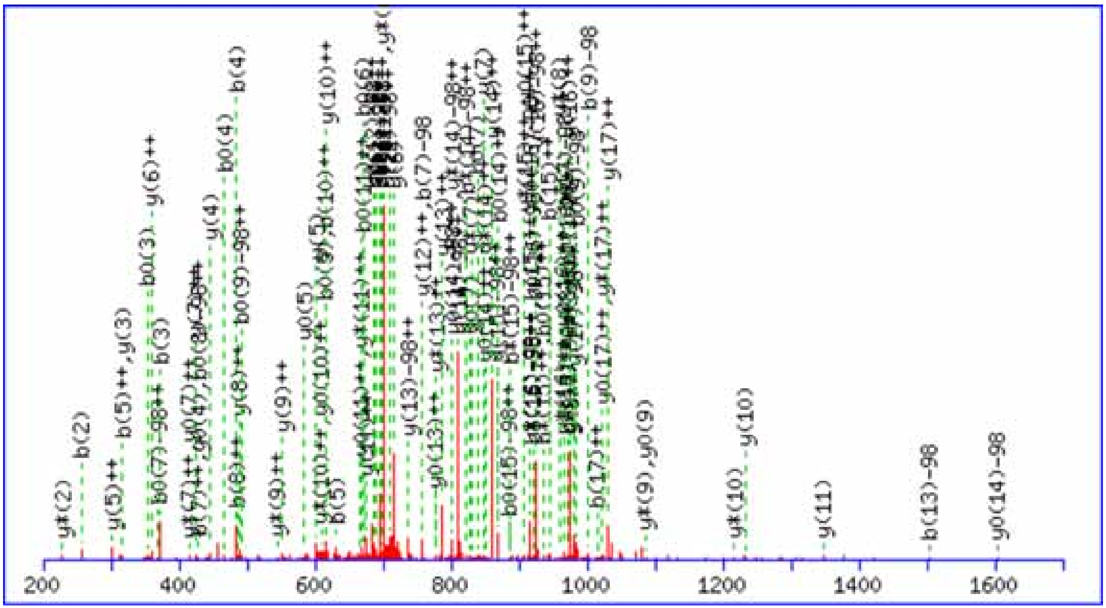
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)-98, b(7), b(8)-98++, b(8)-98, b(8), b(9)++, b(9), b(9)-98, b(10), b(10)-98, b(11)++, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8)-98, y(8), y(8)-98++, y(9)-98, y(9), y(9)-98++, y(10)-98, y(10), y(10)-98++, y(10)++, y(11), y(11)-98, y(11)++, y(11)-98++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13), y(13)++, y(13)-98, y(13)-98++
Precursor origin neutral loss: +

Peptide No.128

DIDLFGSDEEEEDKEAAR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DIDLFGSDEEEEDKEAAR
Found in EF1D_MOUSE, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 5566: 2202.923127 from(735.314985,3+)
Title: Elution from: 52.209 to 52.209 scan no 4925 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2202.9205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
Ions Score: 67 Expect: 9.4e-006

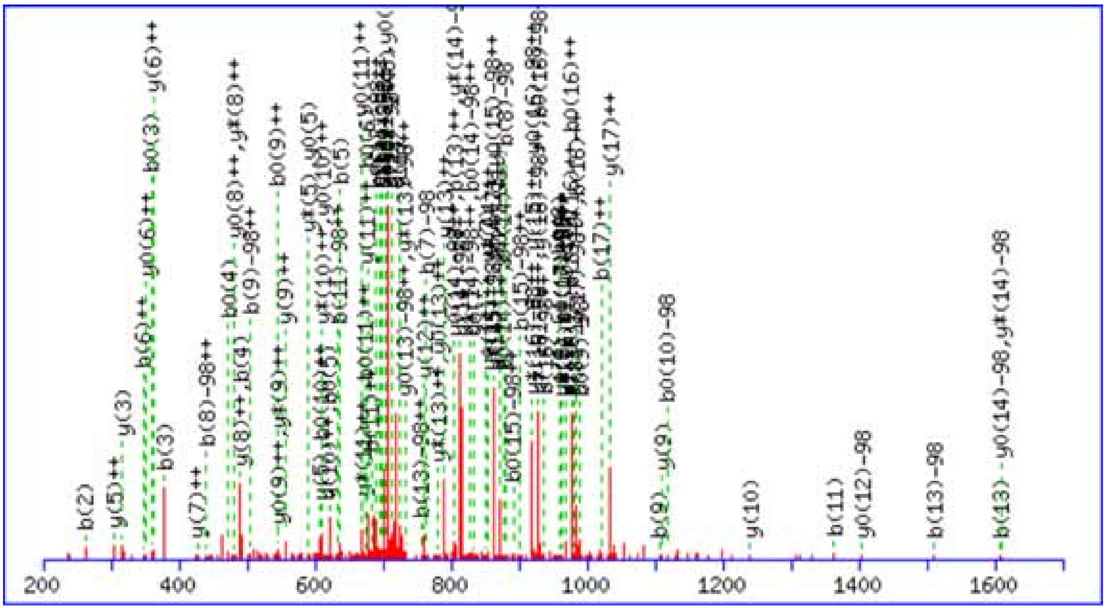
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6), b(7)-98, b(7)++, b(8)++, b(8), b(9)-98, b(10)++, b(12)-98++, b(13)-98, b(15)++, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(10), y(11), y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.129

DIDLFGSDEEEEDKEAAR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DIDLFGSDEEEEDKEAAR
Found in EF1D_MOUSE, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 5639: 2214.986958 from(739.336262,3+)
Title: Elution from: 52.130 to 52.130 scan no 4915 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2214.9841
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 61 Expect: 5e-005

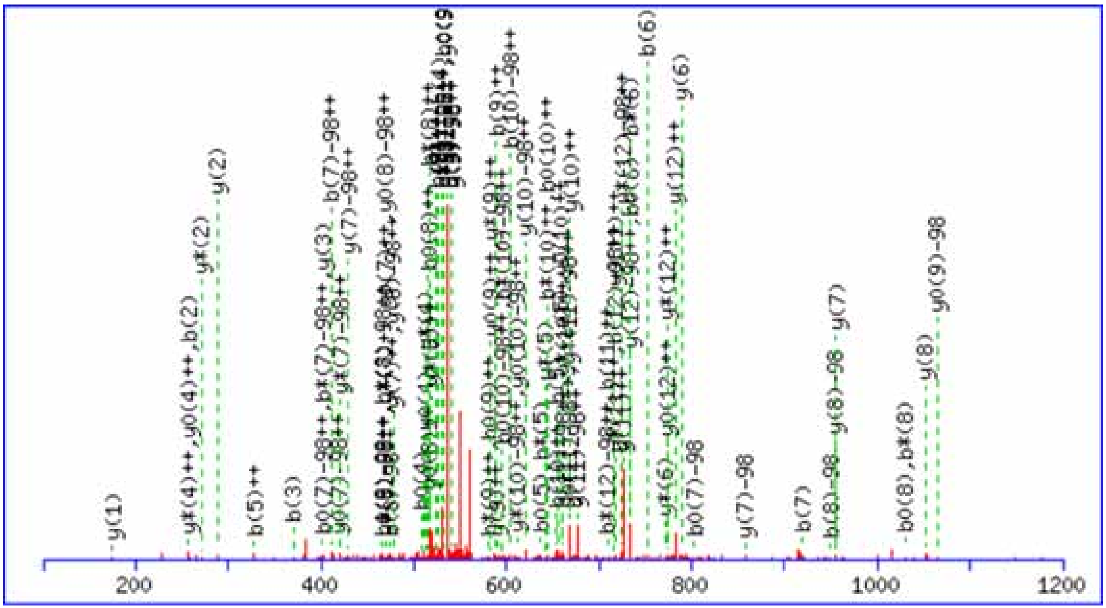
Matched b ions: b(2), b(3), b(4), b(5), b(6)++, b(6), b(7)-98, b(7), b(8), b(8)-98++, b(8)-98, b(9)-98++, b(9), b(11), b(11)-98++, b(11)++, b(12)-98++, b(13)-98, b(13), b(13)++, b(13)-98++, b(15)-98++, b(16)++, b(16)-98++, b(17)++
Matched y ions: y(3), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)++, y(12)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.130

DIIRQPSEEEIIK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DIIRQPSEEEIIK
Found in PEA15_MOUSE, Astrocytic phosphoprotein PEA-15 OS=Mus musculus GN=Pea15 PE=1 SV=1

Match to Query 3093: 1704.871677 from(569.297835,3+)
Title: Elution from: 44.838 to 44.838 scan no 4103 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1704.8699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
Ions Score: 31 Expect: 0.034

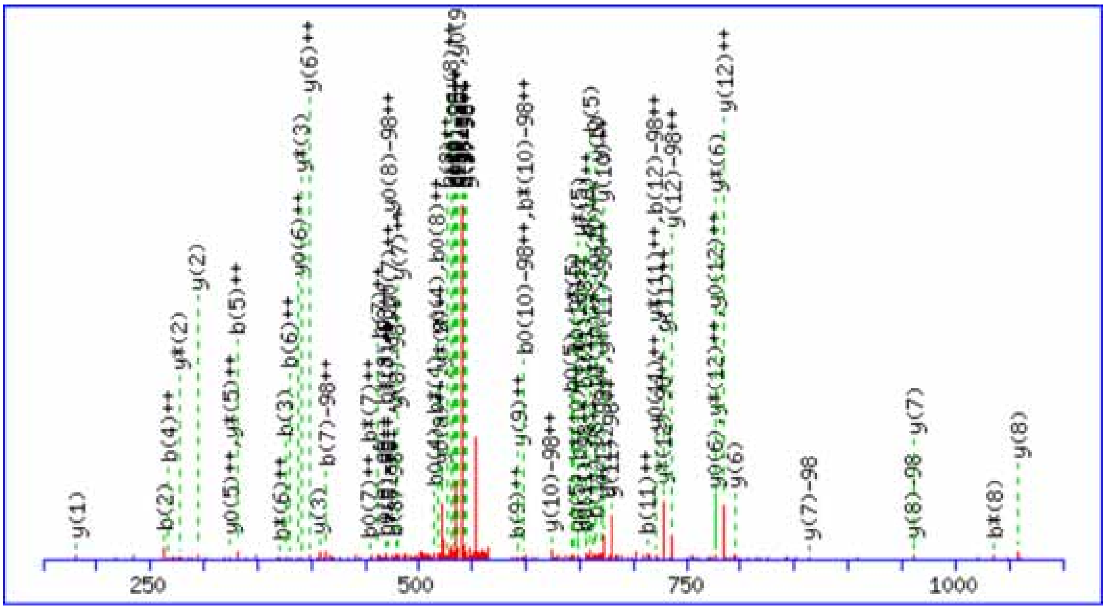
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6), b(7)-98++, b(7), b(8)-98, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98++, y(7)-98, y(7)++, y(8), y(8)-98, y(8)-98++, y(8)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.131

DIIRQPSEEEIIK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of DIIRQPSEEEIIK
Found in PEA15_MOUSE, Astrocytic phosphoprotein PEA-15 OS=Mus musculus GN=Pea15 PE=1 SV=1

Match to Query 2961: 1716.934353 from(573.318727,3+)
Title: Elution from: 44.801 to 44.801 scan no 4073 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1716.9335
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 31 Expect: 0.037

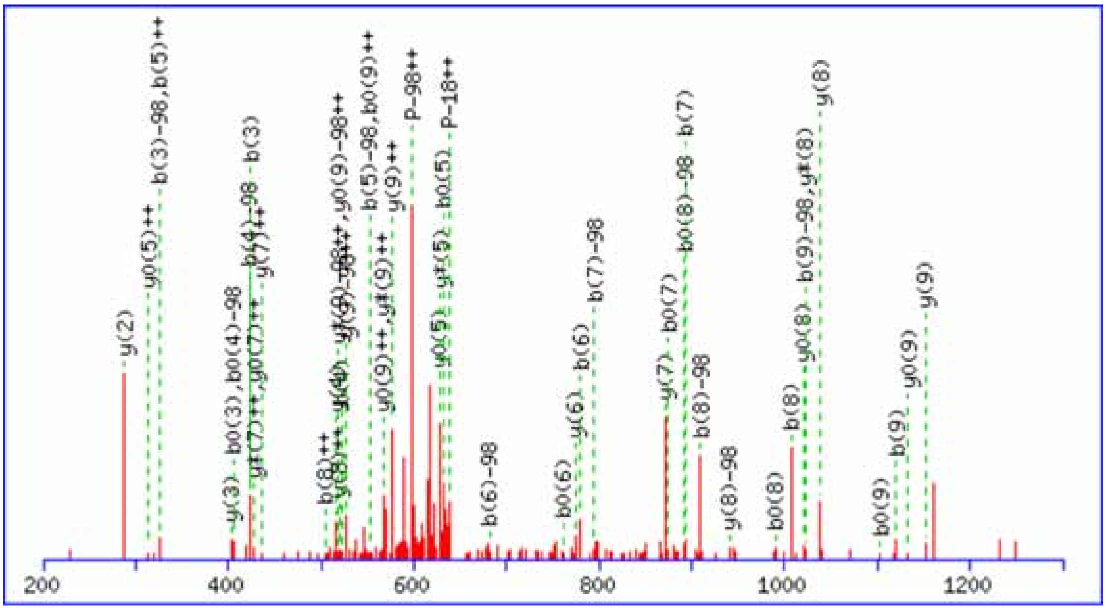
Matched b ions: b(2), b(3), b(4)++, b(4), b(5)++, b(5), b(6)++, b(7)-98++, b(7)++, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)++, b(11)++, b(11)-98++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)-98, y(7)++, y(8), y(8)-98, y(8)-98++, y(8)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.132

DISPEEIDLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DISPEEIDLK
Found in SRBS1_MOUSE, Sorbin and SH3 domain-containing protein 1 OS=Mus musculus GN=Sorbs1 PE=1 SV=2

Match to Query 1010: 1293.610008 from(647.812280,2+)
Title: Elution from: 48.890 to 48.890 scan no 4459 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1293.6105
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K10 : Dimethyl (K)
Ions Score: 51 Expect: 0.00027

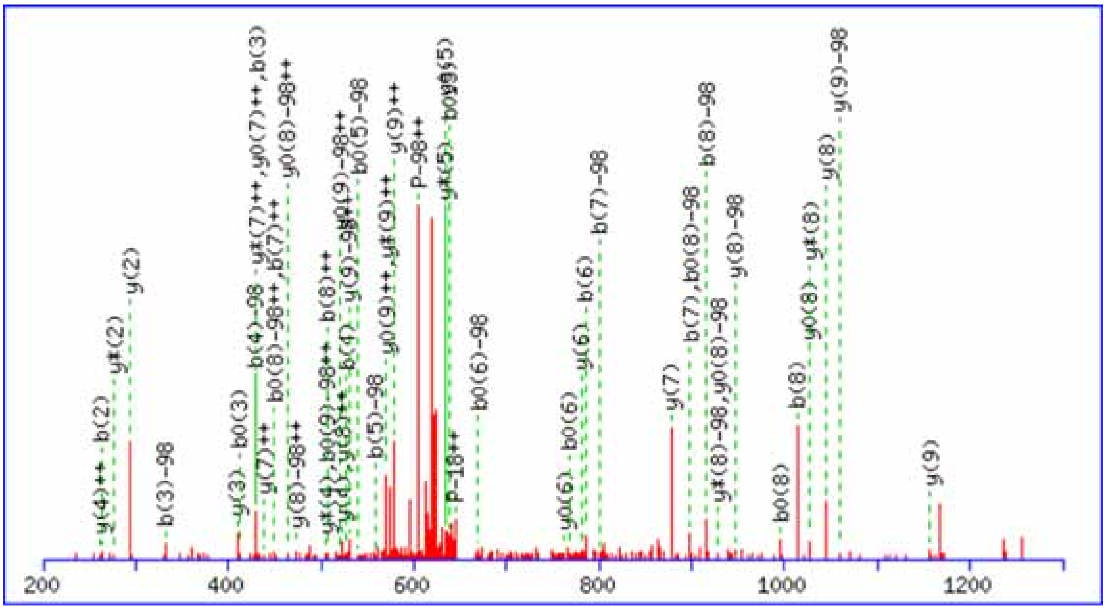
Matched b ions: b(3), b(3)-98, b(4)-98, b(4), b(5)++, b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(8)++, b(9), b(9)-98
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(7)++, y(8), y(8)++, y(8)-98, y(9)-98++, y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.133

DISPEEIDLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DISPEEIDLK
Found in SRBS1_MOUSE, Sorbin and SH3 domain-containing protein 1 OS=Mus musculus GN=Sorbs1 PE=1 SV=2

Match to Query 1284: 1305.674388 from(653.844470,2+)
Title: Elution from: 48.958 to 48.958 scan no 4561 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1305.6741
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K10 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 31 **Expect:** 0.026

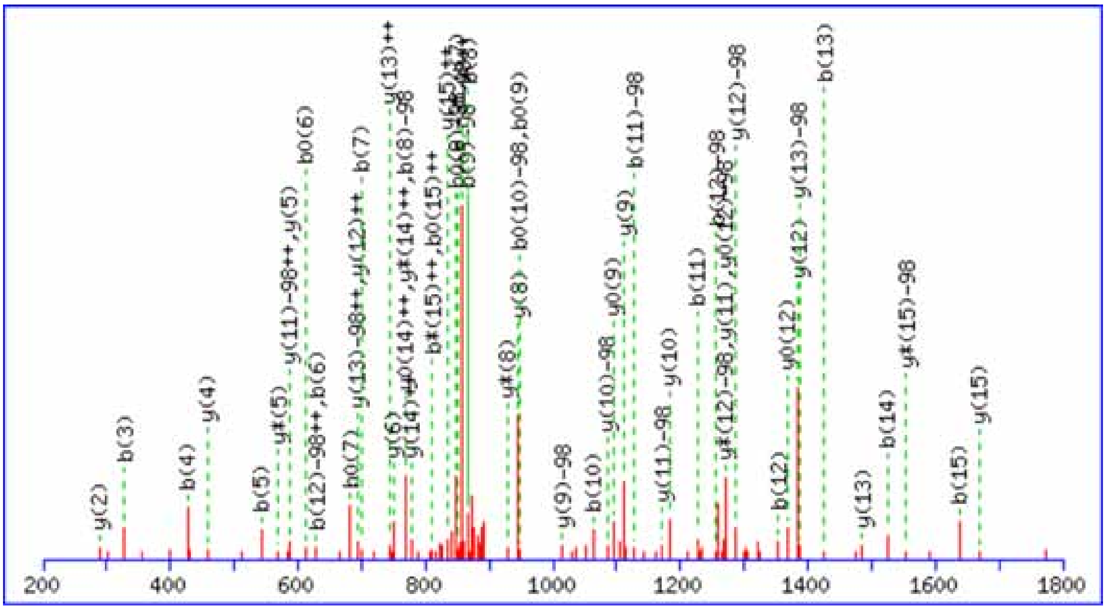
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(6), b(7), b(7)++, b(7)-98, b(8), b(8)-98, b(8)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(6), y(7), y(7)++, y(8), y(8)++, y(8)-98++, y(8)-98, y(9)-98++, y(9), y(9)-98, y(9)++
Precursor origin neutral loss: +

Peptide No.134

DLAVDSASPVYQAVIK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **DLAVDSASPVYQAVIK**
Found in **LDB3_MOUSE**, LIM domain-binding protein 3 OS=Mus musculus GN=Ldb3 PE=1 SV=1

Match to Query 5058: 1810.911610 from(906.463081,2+)
Title: Elution from: 57.005 to 57.005 scan no 5710 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1810.9118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl (K)
Ions Score: 85 Expect: 1.6e-007

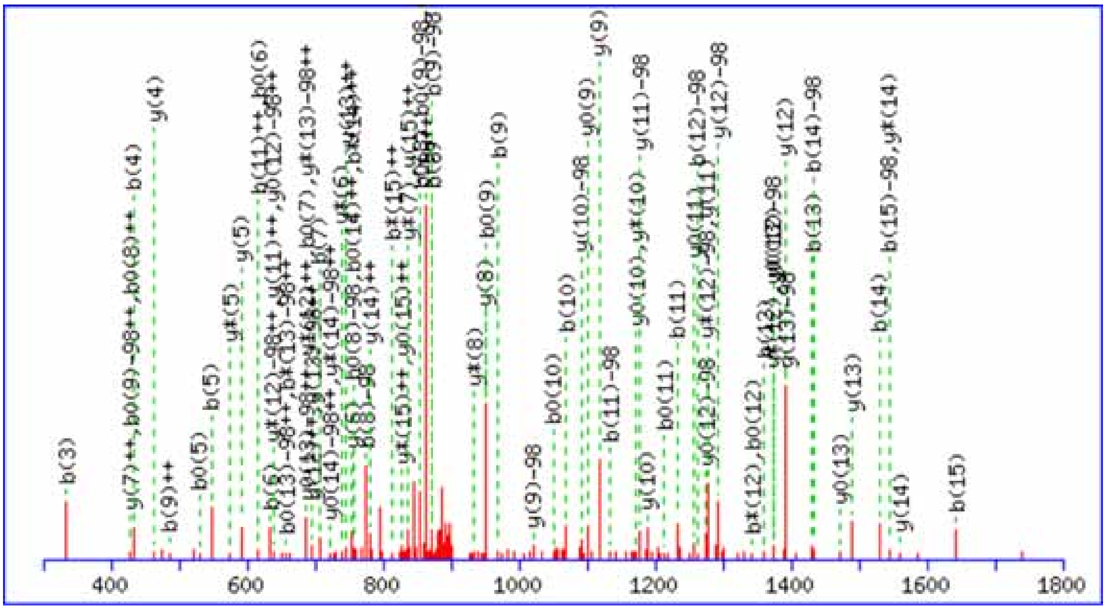
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)-98, b(8), b(9)-98, b(10), b(11), b(11)-98, b(12)-98++, b(12), b(12)-98, b(13), b(14), b(15)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10)-98, y(10), y(11), y(11)-98++, y(11)-98, y(12), y(12)-98, y(12)++, y(13), y(13)-98++, y(13)++, y(13)-98, y(14)++, y(15), y(15)++
Precursor origin neutral loss: +

Peptide No.135

DLAVDSASPVYQAVIK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DLAVDSASPVYQAVIK
Found in LDB3_MOUSE, LIM domain-binding protein 3 OS=Mus musculus GN=Ldb3 PE=1 SV=1

Match to Query 5156: 1822.976674 from(912.495613,2+)
Title: Elution from: 57.044 to 57.044 scan no 5715 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1822.9754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 85 Expect: 1.7e-007

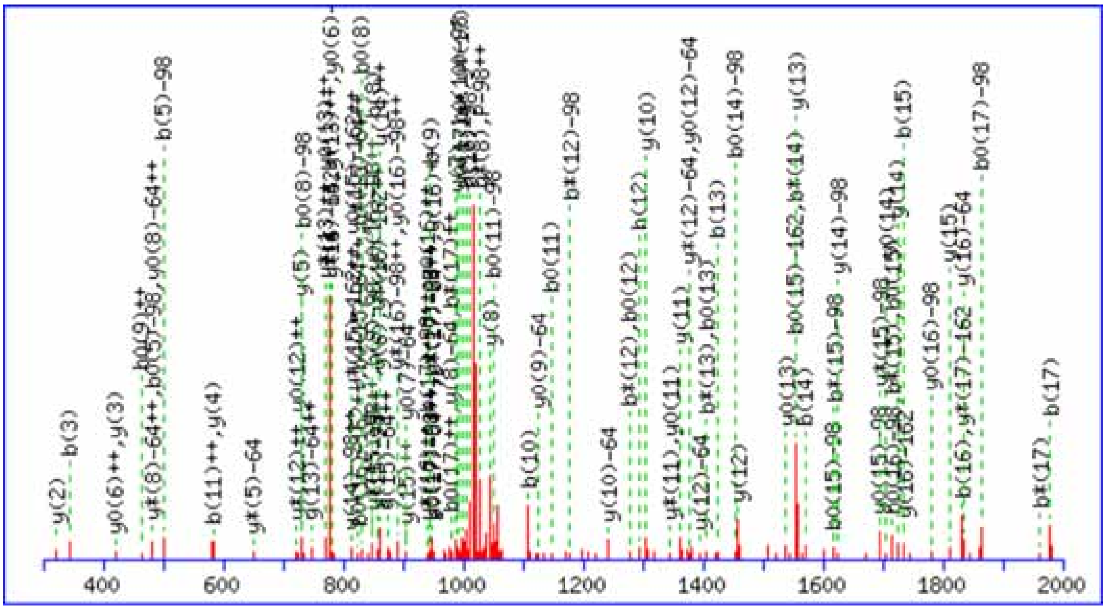
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)-98, b(8), b(9)++, b(9), b(9)-98, b(10), b(11), b(11)++, b(11)-98, b(12), b(12)-98, b(13), b(14), b(14)-98, b(15)-98, b(15)
Matched y ions: y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(11)++, y(12), y(12)-98, y(12)++, y(13), y(13)-98++, y(13)-98, y(13)++, y(14), y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.136

DLSSSPPGPYGQEMYVFR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DLSSSPPGPYGQEMYVFR
Found in AAKB2_MOUSE, 5'-AMP-activated protein kinase subunit beta-2 OS=Mus musculus GN=Prkab2 PE=2 SV=1

Match to Query 5734: 2152.919216 from(1077.466884,2+)
Title: Elution from: 55.295 to 55.295 scan no 5293 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2152.9177
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 72 Expect: 3.1e-006

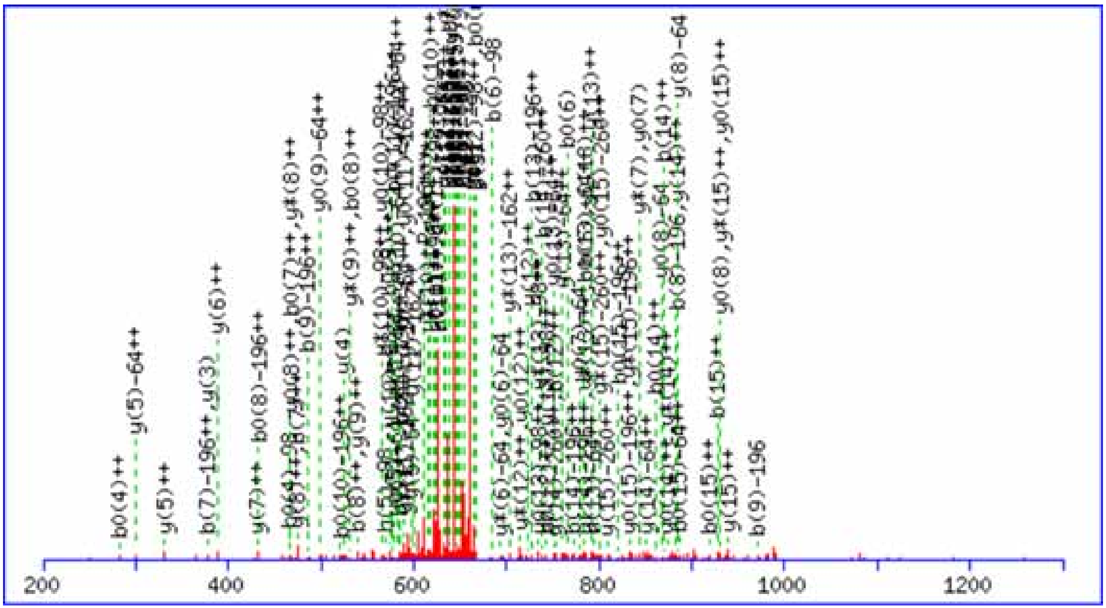
Matched b ions: b(3), b(5)-98, b(8), b(9)-98, b(9), b(10), b(10)-98, b(11)++, b(12), b(13), b(14), b(15), b(16), b(17), b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(12), y(13)++, y(13), y(14)++, y(14), y(14)-98++, y(14)-98, y(15), y(15)-98++, y(15)++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.137

DLTHSDSESSLHMSDR
Confirmed sites: @T:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of DLTHSDSESSLHMSDR
Found in STIM1_MOUSE, Stromal interaction molecule 1 OS=Mus musculus GN=Stim1 PE=1 SV=1

Match to Query 5117: 2025.762588 from(676.261472,3+)
Title: Elution from: 27.034 to 27.034 scan no 1718 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2025.7600
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 Expect: 0.053

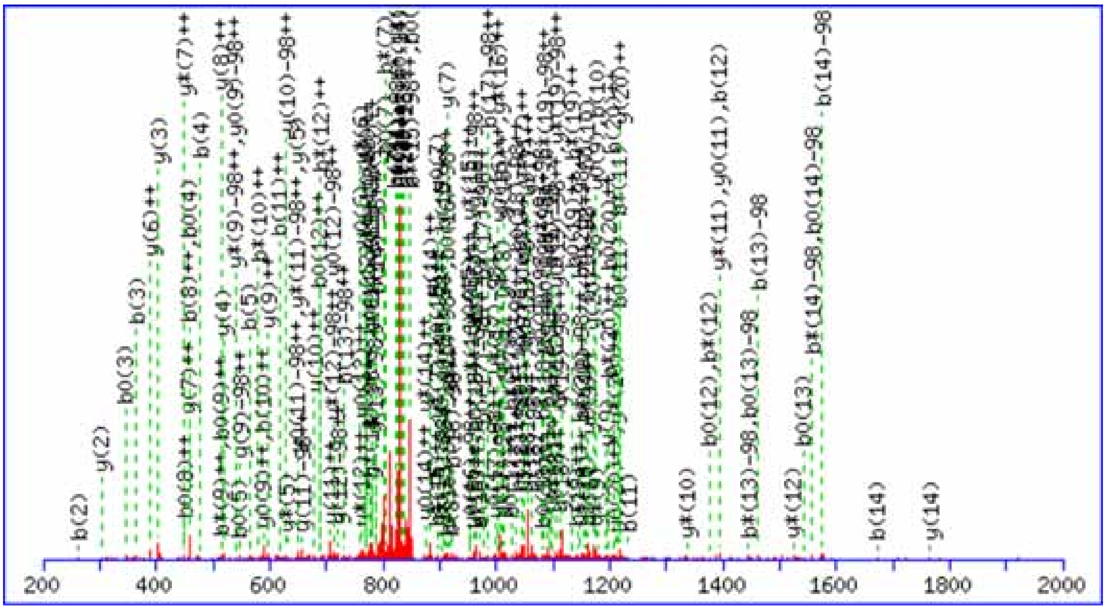
Matched b ions: b(5)-98, b(5), b(6), b(6)-98, b(7)++, b(7)-196++, b(7)-98, b(8)++, b(8)-98, b(8)-196, b(9)-196, b(9)-196++, b(9)++, b(10)++, b(11)-196++, b(11)-98++, b(12)-196++, b(12)++, b(12)-98++, b(13)-196++, b(13)-98++, b(14)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(7)++, y(8)++, y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)-196++, y(14)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.138

DLTLSTRPEEGCSLHEEDTQR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of DLTLSTRPEEGCSLHEEDTQR
Found in TELT_MOUSE, Telethonin OS=Mus musculus GN=Tcap PE=2 SV=1

Match to Query 6976: 2586.146661 from(863.056163,3+)
Title: Elution from: 38.874 to 38.874 scan no 3353 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2586.1481
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 Expect: 5.6e-005

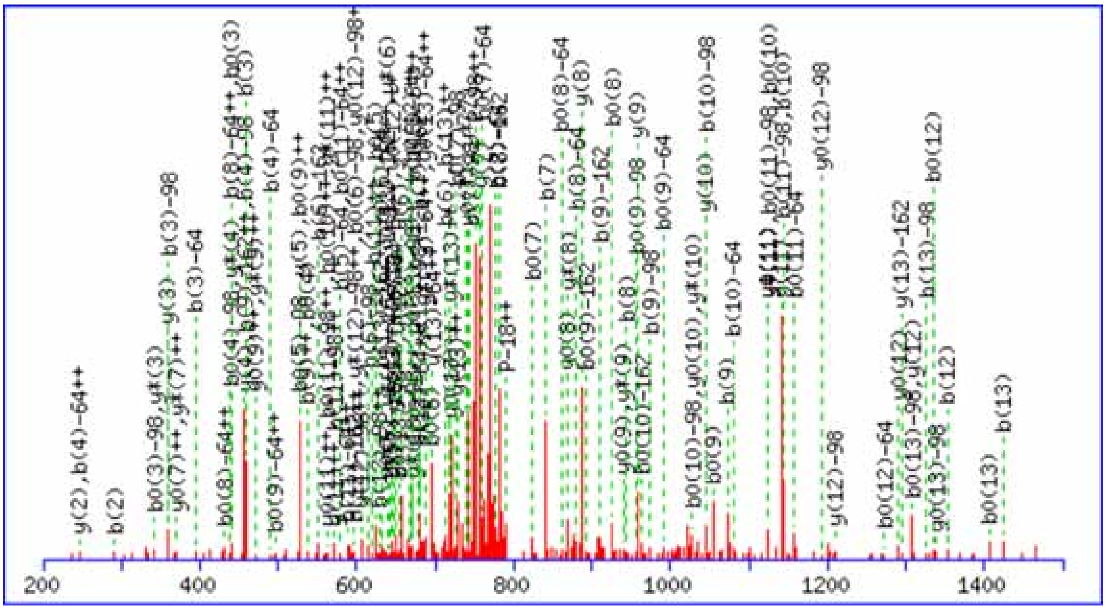
Matched b ions: b(2), b(3), b(4), b(5), b(7), b(8)++, b(8), b(9), b(10)++, b(10), b(11)++, b(11), b(12), b(13)-98, b(13)-98++, b(13)++, b(14)-98, b(14), b(14)-98++, b(14)++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(9)-98++, y(9)++, y(9), y(9)-98, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14), y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)-98++, y(20)++
Precursor origin neutral loss: +

Peptide No.139

DMSPSAETEAPLAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DMSPSAETEAPLAK
Found in MAP4_MOUSE, Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3

Match to Query 3087: 1597.695932 from(799.855242,2+)
Title: Elution from: 33.064 to 33.064 scan no 2723 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1597.6946
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
Ions Score: 77 Expect: 5.8e-007

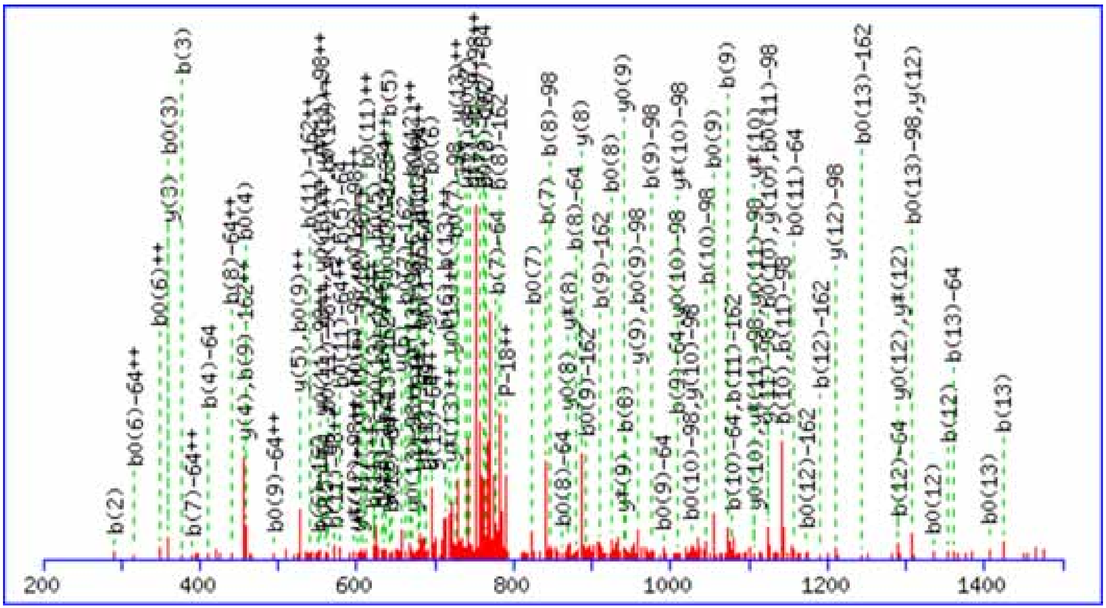
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8), b(9), b(9)++, b(9)-98, b(10), b(10)-98, b(11)-98, b(11)-98++, b(11)++, b(12), b(12)-98++, b(12)++, b(13), b(13)-98, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)-98++, y(12)++, y(12)-98, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.140

DMSPSAETEAPLAK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DMSPSAETEAPLAK
Found in MAP4_MOUSE, Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3

Match to Query 2667: 1597.696576 from(799.855564,2+)
Title: Elution from: 32.936 to 32.936 scan no 2536 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1597.6946
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
Ions Score: 52 Expect: 0.00021

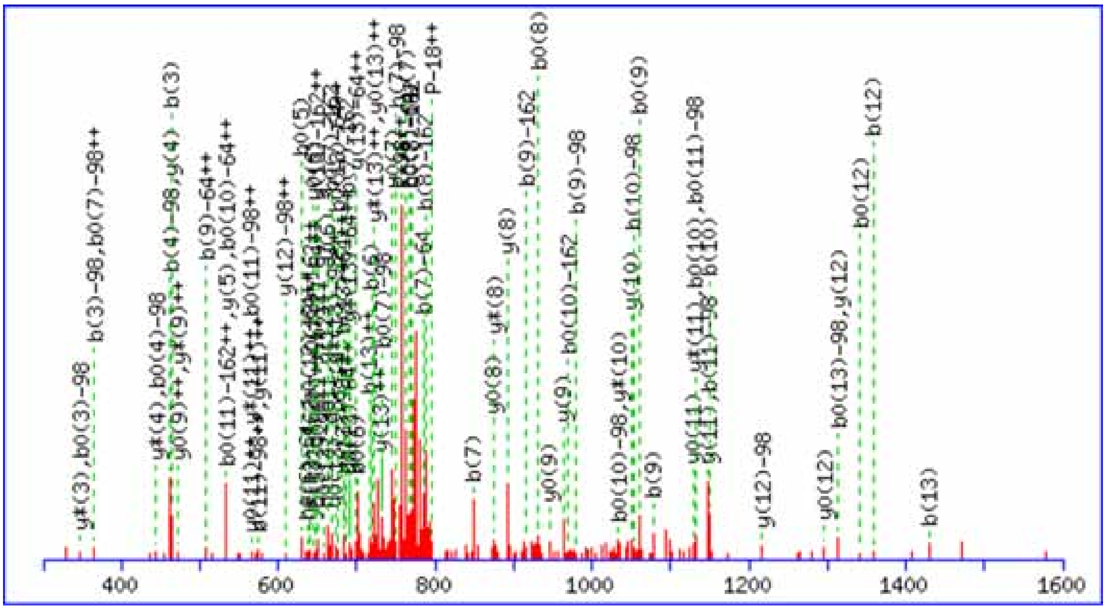
Matched b ions: b(2), b(3), b(5), b(6), b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11)-98, b(11)-98++, b(11)++, b(12), b(12)++, b(13), b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(10)++, y(11)-98, y(12), y(12)-98, y(12)-98++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.141

DMSPSAETEAPLAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of DMSPSAETEAPLAK
Found in MAP4_MOUSE, Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3

Match to Query 2470: 1609.757806 from(805.886179,2+)
Title: Elution from: 32.930 to 32.930 scan no 2500 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1609.7582
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 61 **Expect:** 3.3e-005

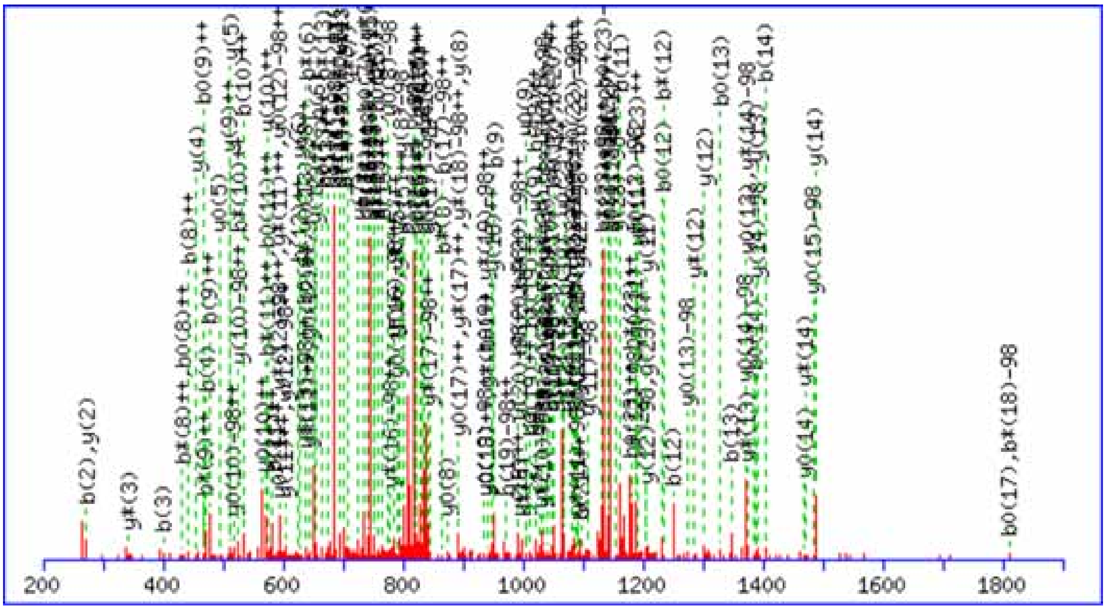
Matched b ions: b(3)-98, b(3), b(4)-98, b(5), b(6), b(7), b(7)-98, b(9), b(9)-98, b(10), b(10)-98, b(11)-98, b(11)-98++, b(12), b(13), b(13)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.142

DQEAPSPEALPSPGQESPDGPSPR
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of DQEAPSPEALPSPGQESPDGPSPR
Found in SPEG_MOUSE, Striated muscle-specific serine/threonine-protein kinase OS=Mus musculus GN=Speg PE=1 SV=2

Match to Query 6877: 2552.109636 from(851.710488,3+)
Title: Elution from: 42.102 to 42.102 scan no 3787 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2552.1068
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0045

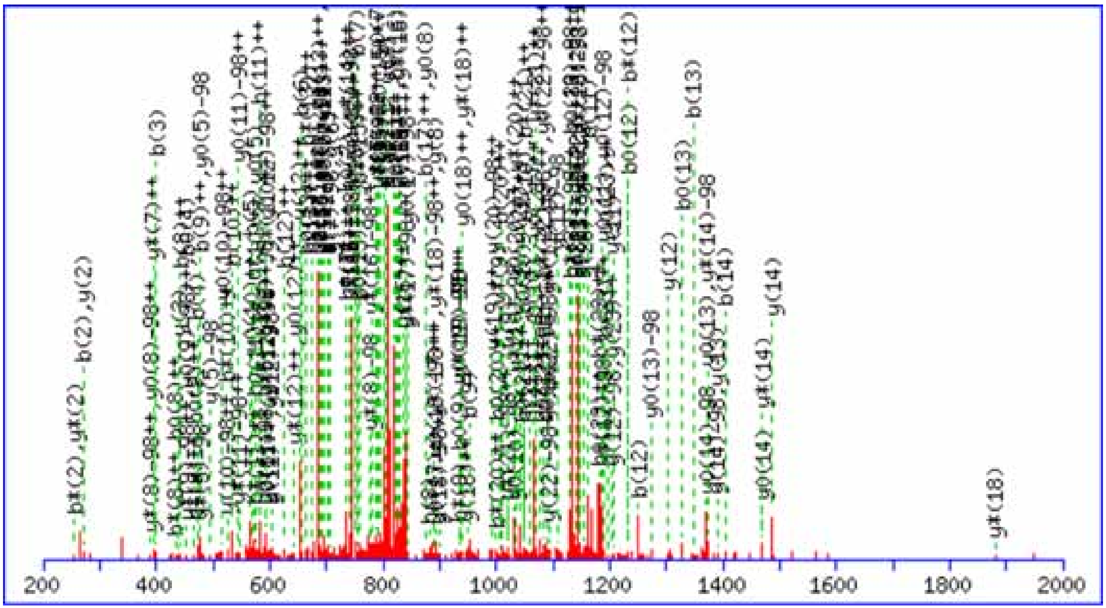
Matched b ions: b(2), b(3), b(4), b(6), b(7), b(8)++, b(9), b(9)++, b(10), b(10)++, b(11)++, b(11), b(12), b(12)++, b(13), b(13)++, b(14)++, b(14), b(15)++, b(16)++, b(17)-98++, b(19)++, b(19)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(23)-98++, b(23)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)++, y(10)-98++, y(10)-98, y(10)++, y(11)++, y(11), y(11)-98, y(12)++, y(12), y(12)-98++, y(12)-98, y(13), y(13)++, y(14), y(14)++, y(14)-98, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(18)++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(22)-98++, y(22)++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.143

DQEAPSPEALPSPGQESPDGPSPR
Confirmed sites: @S:22
Ambiguous sites:

MS/MS Fragmentation of DQEAPSPEALPSPGQESPDGPSPR
Found in SPEG_MOUSE, Striated muscle-specific serine/threonine-protein kinase OS=Mus musculus GN=Speg PE=1 SV=2

Match to Query 6201: 2552.110101 from(851.710643,3+)
Title: Elution from: 42.140 to 42.140 scan no 3640 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2552.1068
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S22 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 **Expect:** 0.0078

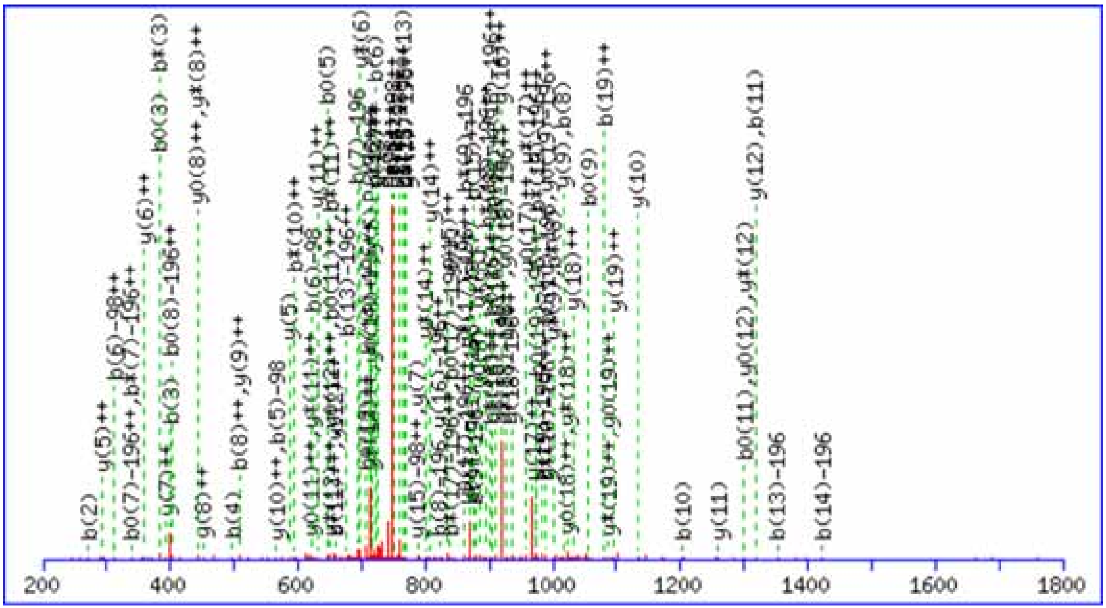
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)++, b(8), b(9), b(9)++, b(10)++, b(10), b(11)++, b(11), b(12), b(12)++, b(13)++, b(13), b(14), b(14)++, b(16)++, b(17)++, b(20)++, b(21)++, b(22)-98++, b(22)++, b(23)-98++, b(23)++
Matched y ions: y(2), y(3), y(5)-98, y(5), y(6), y(7)-98, y(7), y(8), y(8)-98, y(9), y(10)-98++, y(10)++, y(11)++, y(11)-98, y(11), y(12)++, y(12), y(12)-98++, y(12)-98, y(13)++, y(13), y(14), y(14)++, y(14)-98++, y(14)-98, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(18)++, y(18)-98++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(22)-98++, y(22)++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.144

DQQPSGSEGEDDDAEAALKK
Confirmed sites: @S:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of DQQPSGSEGEDDDAEAALKK
Found in THUM1_MOUSE, THUMP domain-containing protein 1 OS=Mus musculus GN=Thumpd1 PE=1 SV=1

Match to Query 7139: 2332.936521 from(778.652783,3+)
Title: Elution from: 36.118 to 36.118 scan no 3141 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2332.9349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K19 : Dimethyl (K)
K20 : Dimethyl (K)
Ions Score: 40 Expect: 0.0039

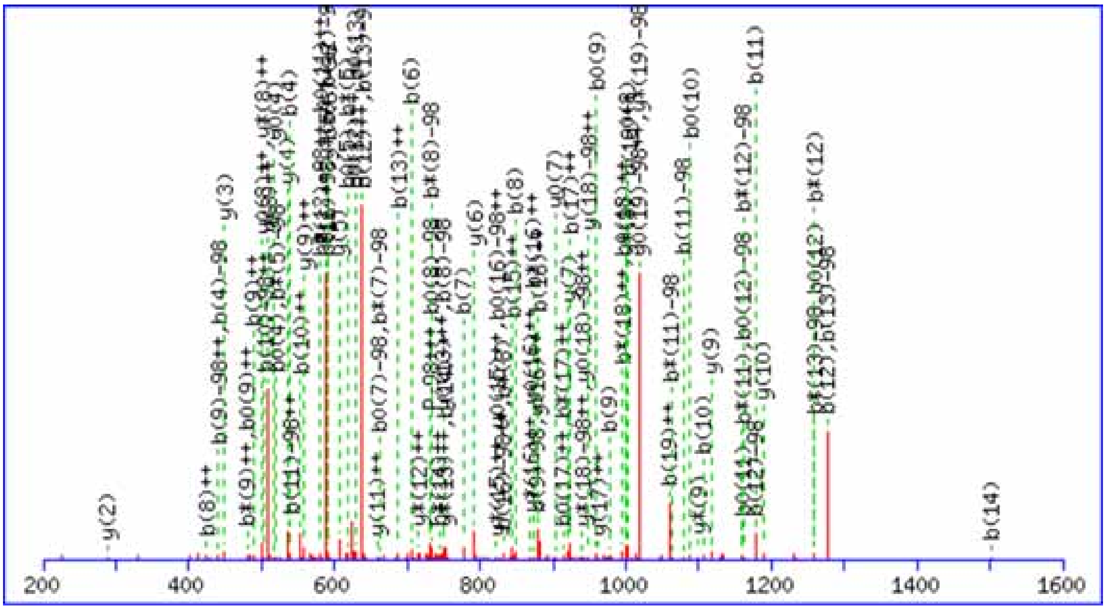
Matched b ions: b(2), b(3), b(4), b(5)-98, b(6)-98, b(6)-98++, b(6), b(7)-196, b(7)-98, b(8)-98, b(8)++, b(8)-196, b(8), b(9)-196, b(10), b(11), b(11)++, b(12)++, b(13)-196, b(13)-98++, b(13)-196++, b(14)-196, b(14)-98++, b(14)-196++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(18)-196++, b(19)-196++, b(19)++, b(19)-98++
Matched y ions: y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12), y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)-98++, y(17)++, y(17)-196++, y(18)-98++, y(18)-196++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.145

DRASPAAAEEAVPEWASCLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DRASPAAAEEAVPEWASCLK
Found in SYNPO_MOUSE, Synaptopodin OS=Mus musculus GN=Synpo PE=1 SV=2

Match to Query 7030: 2293.046700 from(765.356176,3+)
Title: Elution from: 56.169 to 56.169 scan no 5567 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2293.0449
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl (K)
Ions Score: 73 Expect: 3.2e-006

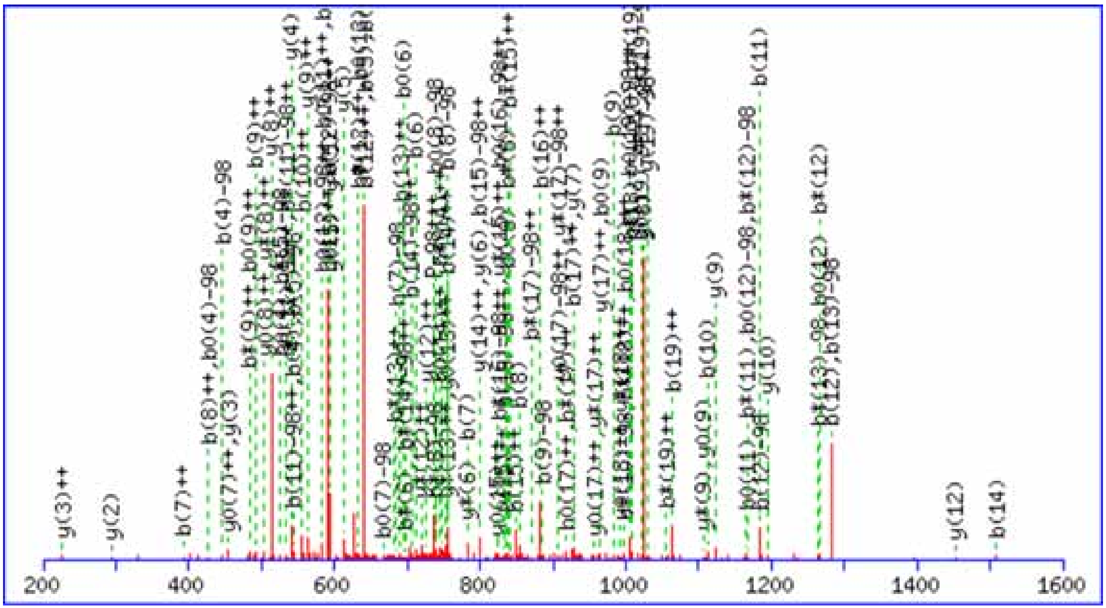
Matched b ions: b(4)-98, b(4), b(6), b(7), b(8)++, b(8), b(8)-98, b(9)++, b(9)-98++, b(9), b(9)-98, b(10), b(10)++, b(10)-98++, b(11)++, b(11), b(11)-98, b(11)-98++, b(12)-98++, b(12)++, b(12), b(12)-98, b(13)-98++, b(13)-98, b(13)++, b(14), b(14)++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(11)++, y(16)++, y(17)++, y(18)-98++
Precursor origin neutral loss:

Peptide No.146

DRASPAAAEEAVPEWASCLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DRASPAAAEEAVPEWASCLK
Found in SYNPO_MOUSE, Synaptopodin OS=Mus musculus GN=Synpo PE=1 SV=2

Match to Query 7661: 2305.109436 from(769.377088,3+)
Title: Elution from: 56.209 to 56.209 scan no 5619 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2305.1086
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 78 **Expect:** 1.2e-006

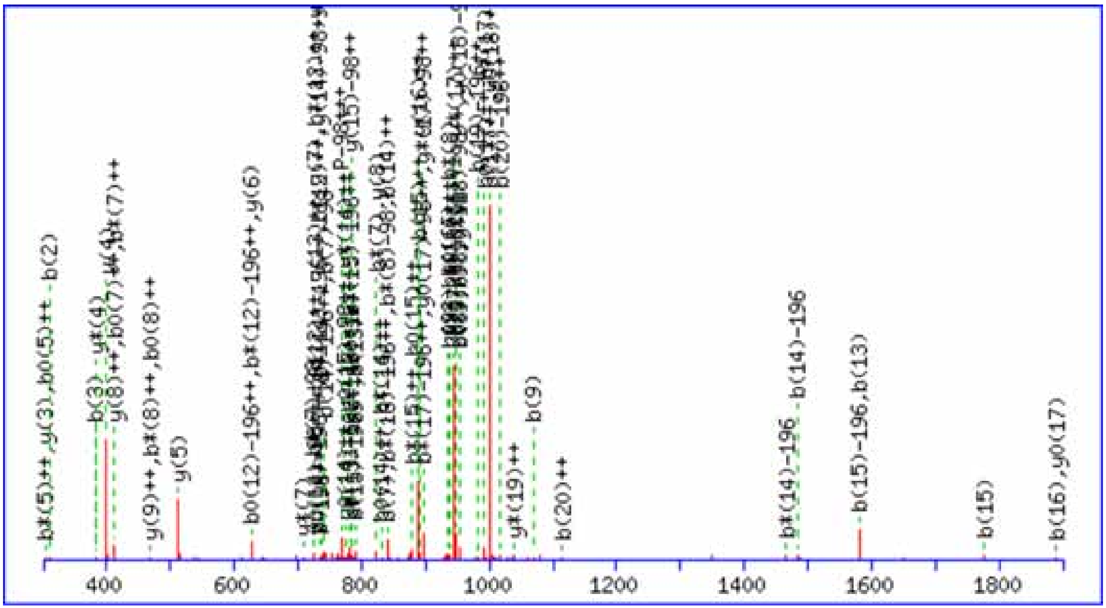
Matched b ions: b(4)-98, b(4), b(5), b(5)-98, b(6), b(7)++, b(7), b(7)-98, b(8), b(8)-98, b(8)++, b(9)++, b(9)-98, b(9), b(10)++, b(10), b(11)++, b(11), b(11)-98++, b(12)-98++, b(12)++, b(12), b(12)-98, b(13)-98++, b(13)-98, b(13)++, b(14), b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(19)++
Matched y ions: y(2), y(3)++, y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(12), y(12)++, y(14)++, y(15)++, y(17)++, y(19)-98++
Precursor origin neutral loss:

Peptide No.147

DSALQDTDDSDDDPVLIPGAR
Confirmed sites: @S:2,@S:10
Ambiguous sites:

MS/MS Fragmentation of DSALQDTDDSDDDPVLIPGAR
Found in DCAF6_MOUSE, DDB1- and CUL4-associated factor 6 OS=Mus musculus GN=Dcaf6 PE=1 SV=1

Match to Query 7280: 2401.958529 from(801.660119,3+)
Title: Elution from: 59.847 to 59.847 scan no 5928 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2401.9564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.011

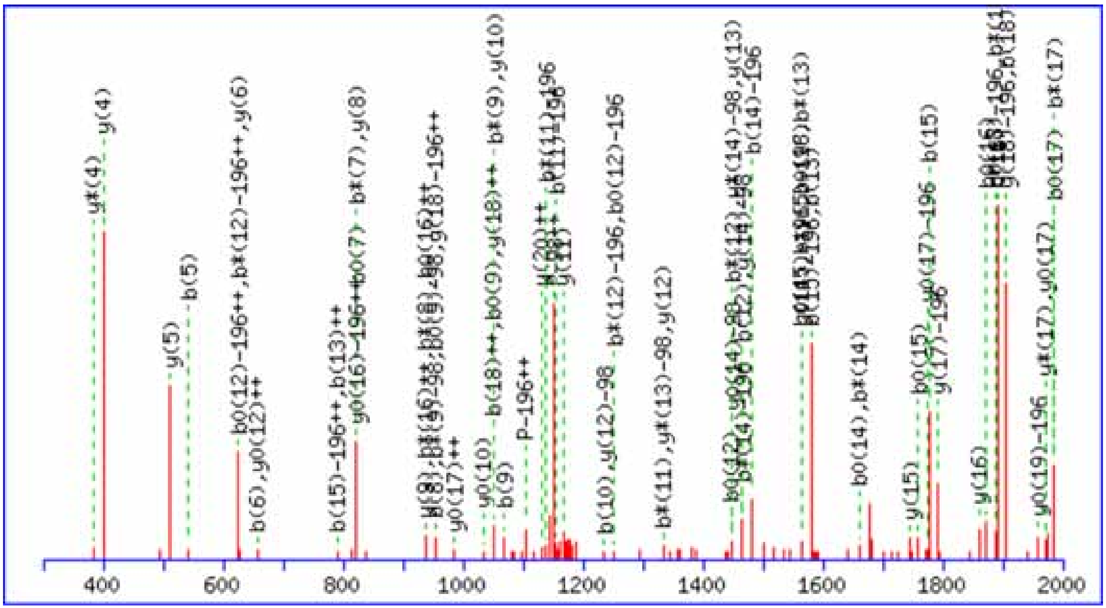
Matched b ions: b(2), b(3), b(7)-98, b(7), b(8), b(9), b(11)-98++, b(12)++, b(13)-98, b(13), b(13)-98++, b(13)++, b(14)-196, b(14)-98, b(14)-196++, b(14)++, b(14)-98++, b(15)++, b(15)-196, b(15), b(15)-98++, b(15)-196++, b(16), b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)-98++, b(18)-196++, b(19)-196++, b(20)++, b(20)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.148

DSALQDTDDSDDDPVLIPGAR
Confirmed sites: @T:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of DSALQDTDDSDDDPVLIPGAR
Found in DCAF6_MOUSE, DDB1- and CUL4-associated factor 6 OS=Mus musculus GN=Dcaf6 PE=1 SV=1

Match to Query 6143: 2401.958858 from(1201.986705,2+)
Title: Elution from: 59.875 to 59.875 scan no 5645 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2401.9564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 3.1e-005

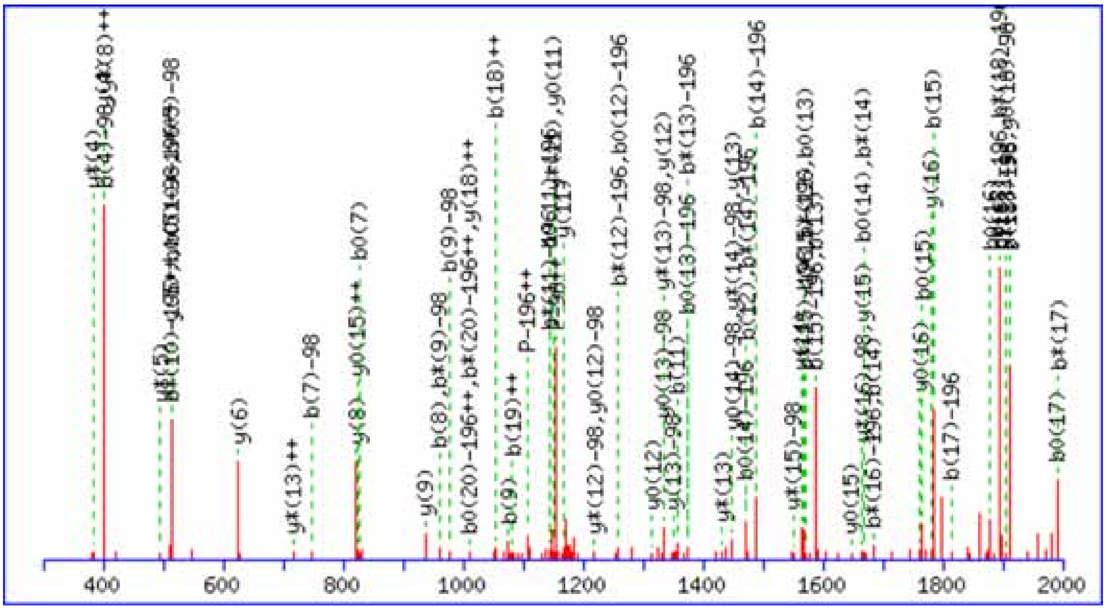
Matched b ions: b(5), b(6), b(8), b(9), b(10), b(10)-98, b(11)-98++, b(11)-98, b(11)-196, b(12), b(13)-98, b(13), b(13)++, b(14)-196, b(14)-98, b(14)-98++, b(15)-196, b(15)-98, b(15), b(15)-196++, b(16)-98, b(16), b(17)-98++, b(17)-98, b(18)++, b(18)-196
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(12), y(12)-98, y(13), y(14)-98, y(14), y(15), y(16), y(17)-196, y(17)-98, y(18)++, y(18)-196++, y(18)-196, y(20)++
Precursor origin neutral loss: +

Peptide No.149

DSALQDTDDSDDDPVLIPGAR
Confirmed sites: @S:2,@S:10
Ambiguous sites:

MS/MS Fragmentation of DSALQDTDDSDDDPVLIPGAR
Found in DCAF6_MOUSE, DDB1- and CUL4-associated factor 6 OS=Mus musculus GN=Dcaf6 PE=1 SV=1

Match to Query 5797: 2407.990002 from(1205.002277,2+)
Title: Elution from: 59.824 to 59.824 scan no 5558 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2407.9882
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 7.4e-005

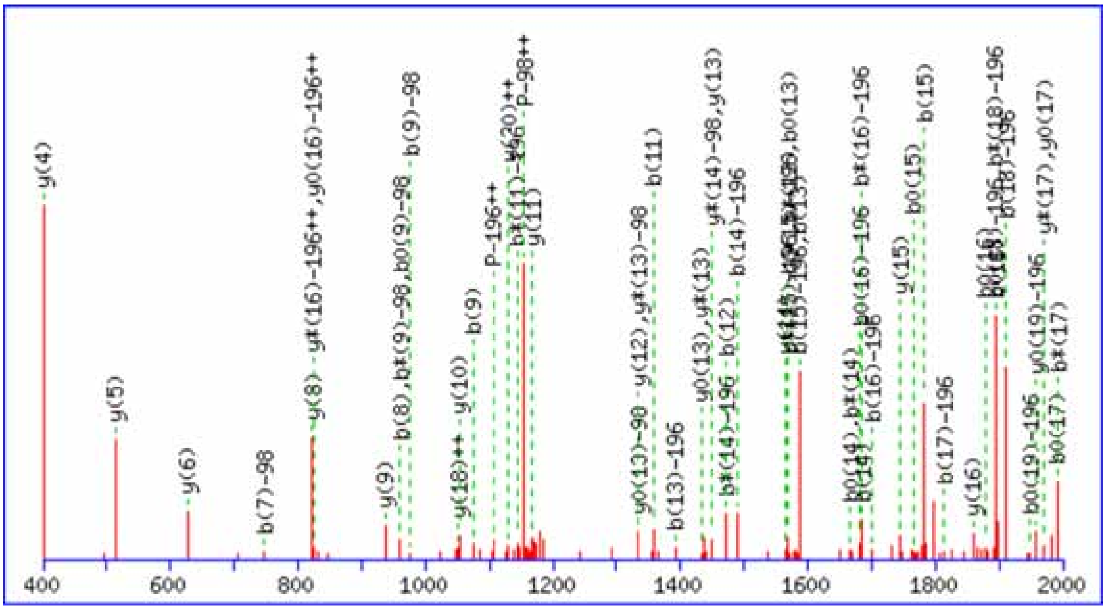
Matched b ions: b(4)-98, b(7)-98, b(8), b(9), b(9)-98, b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13), b(14)-196, b(14)-98, b(14), b(15)-196, b(15), b(15)-98, b(16), b(16)-98, b(17)-98, b(17)-196, b(18)++, b(18)-196, b(19)++
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(11), y(12), y(13), y(13)-98, y(14), y(15), y(16), y(18)++, y(20)-98++
Precursor origin neutral loss: +

Peptide No.150

DSALQDTDDSDDDPVLIPGAR
Confirmed sites: @T:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of DSALQDTDDSDDDPVLIPGAR
Found in DCAF6_MOUSE, DDB1- and CUL4-associated factor 6 OS=Mus musculus GN=Dcaf6 PE=1 SV=1

Match to Query 6553: 2407.990668 from(1205.002610,2+)
Title: Elution from: 59.742 to 59.742 scan no 5710 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2407.9882
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 **Expect:** 2.6e-005

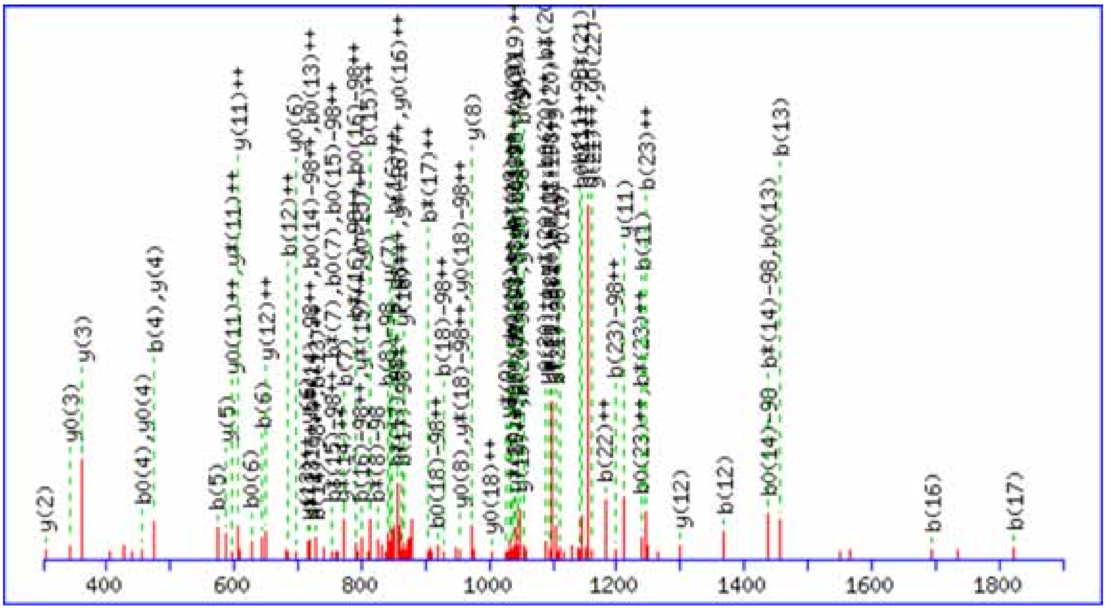
Matched b ions: b(7)-98, b(8), b(9), b(9)-98, b(10)-98, b(11), b(12), b(13), b(13)-98, b(13)-196, b(14)-98, b(14), b(14)-196, b(15)-196, b(15)-98, b(15), b(16), b(16)-98, b(16)-196, b(17)-98, b(17)-196, b(18)-196
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15)-98++, y(15), y(16), y(16)-98, y(18)++, y(20)++
Precursor origin neutral loss: +

Peptide No.151

DSDQVAQSDGEESPAAEEQLLGER
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DSDQVAQSDGEESPAAEEQLLGER
Found in SC31A_MOUSE, Protein transport protein Sec31A OS=Mus musculus GN=Sec31a PE=1 SV=2

Match to Query 8070: 2667.118362 from(890.046730,3+)
Title: Elution from: 50.692 to 50.692 scan no 4993 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2667.1185
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 79 Expect: 7e-007

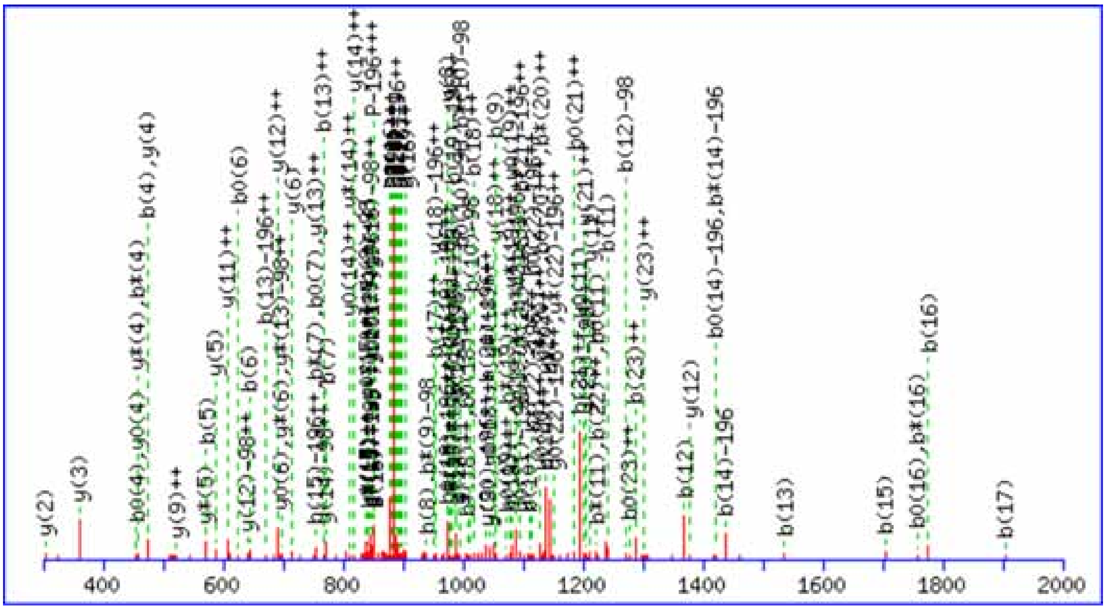
Matched b ions: b(4), b(5), b(6), b(7), b(8)-98, b(9), b(10), b(11), b(11)-98, b(12), b(12)++, b(13)++, b(13), b(14)-98++, b(15)++, b(16), b(16)-98++, b(16)++, b(17), b(17)-98++, b(18)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(23)++, b(23)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11)++, y(11), y(12)++, y(12), y(13)++, y(16)++, y(19)++, y(20)++, y(20)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.152

DSDQVAQSDGEESPAAEEQLLGER
Confirmed sites: @S:8,@S:13
Ambiguous sites:

MS/MS Fragmentation of DSDQVAQSDGEESPAAEEQLLGER
Found in SC31A_MOUSE, Protein transport protein Sec31A OS=Mus musculus GN=Sec31a PE=1 SV=2

Match to Query 8221: 2747.089476 from(916.703768,3+)
Title: Elution from: 52.945 to 52.945 scan no 5243 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2747.0848
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 Expect: 1.1e-005

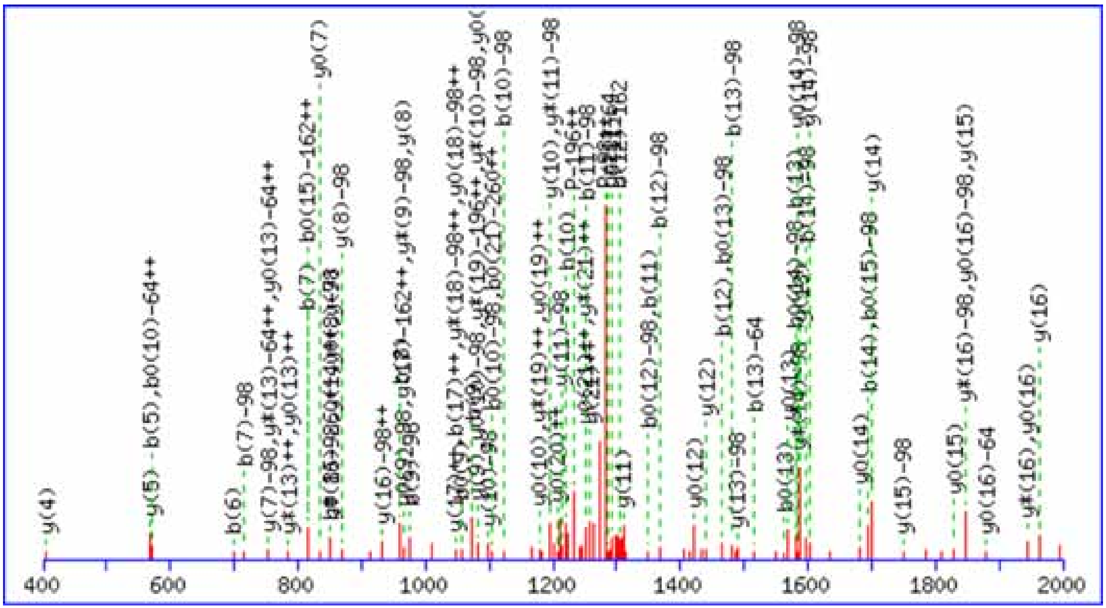
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(8)-98, b(9), b(10)-98, b(10), b(11), b(12), b(12)-98, b(13)-98, b(13), b(13)++, b(13)-196++, b(14)-196, b(14)-98, b(14)-98++, b(15), b(15)-196++, b(15)-98++, b(15)++, b(16), b(16)++, b(16)-98++, b(17), b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-196++, b(19)-98++, b(20)-98++, b(20)++, b(20)-196++, b(21)++, b(21)-98++, b(21)-196++, b(22)++, b(22)-98++, b(23)++, b(23)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(11)++, y(11), y(12)++, y(12), y(12)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(16)++, y(17)++, y(17)-196++, y(17)-98++, y(18)++, y(18)-98++, y(18)-196++, y(19)++, y(19)-196++, y(19)-98++, y(20)-98++, y(20)++, y(20)-196++, y(21)++, y(21)-98++, y(22)-98++, y(23)-196++, y(23)++
Precursor origin neutral loss: +

Peptide No.153

DSGSDEDFLMEDDDDSDYGSSK
Confirmed sites: @S:4,@S:16
Ambiguous sites:

MS/MS Fragmentation of DSGSDEDFLMEDDDDSDYGSSK
Found in NUCKS_MOUSE, Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Mus musculus GN=Nucks1 PE=1 SV=1

Match to Query 8035: 2659.858810 from(1330.936681,2+)
Title: Elution from: 53.153 to 53.153 scan no 5262 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2659.8558
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K22 : Dimethyl (K)
Ions Score: 67 Expect: 1.6e-006

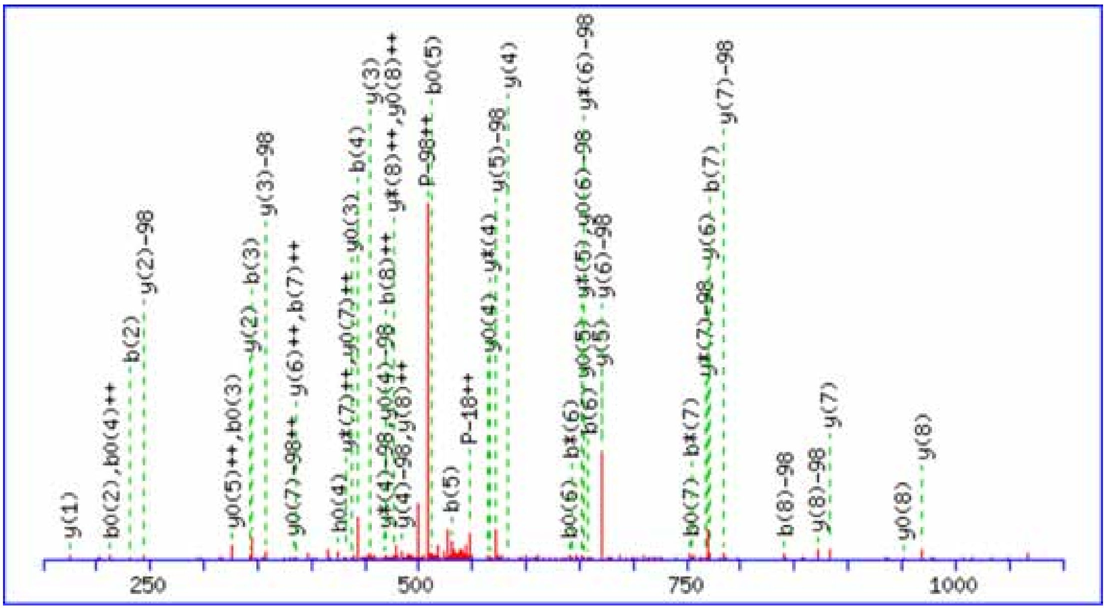
Matched b ions: b(5), b(6), b(7), b(7)-98, b(8), b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13), b(14), b(14)-98, b(16)-98, b(17)-98, b(17)++
Matched y ions: y(4), y(5), y(7)-98, y(7), y(8)-98, y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(13), y(13)-98, y(14), y(14)++, y(14)-98, y(15), y(15)-98, y(16), y(16)-98++, y(17)++, y(20)-98++, y(21)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.154

DSLVSQLSR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DSLVSQLSR
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 745: 1111.527320 from(556.770936,2+)
Title: Elution from: 39.062 to 39.062 scan no 3379 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1111.5274
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 0.00015

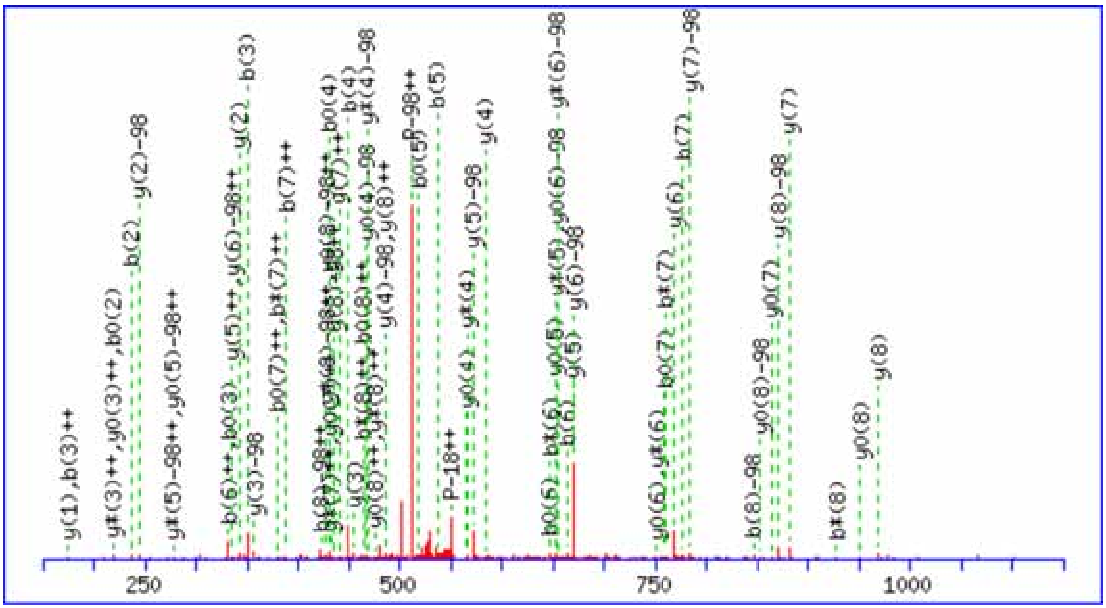
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(7)++, b(8)-98, b(8)++
Matched y ions: y(1), y(2)-98, y(2), y(3)-98, y(3), y(4)-98, y(4), y(5), y(5)-98, y(6), y(6)-98, y(6)++, y(7)-98, y(7), y(8)-98, y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.155

DSLVSQLSR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of DSLVSQLSR
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 542: 1117.559784 from(559.787168,2+)
Title: Elution from: 38.918 to 38.918 scan no 3216 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1117.5593
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00051

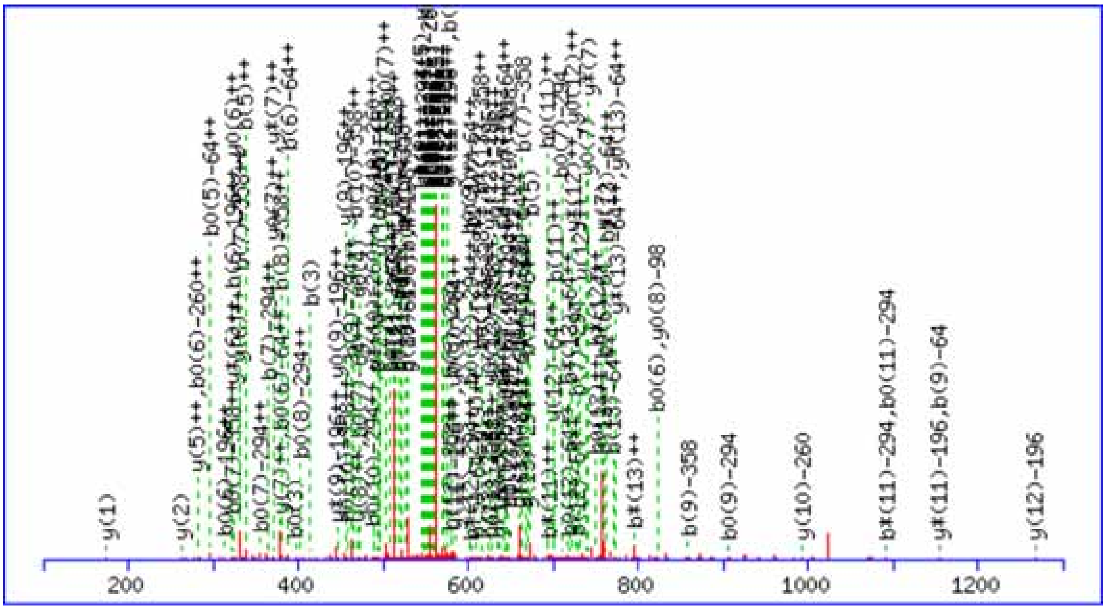
Matched b ions: b(2), b(3), b(3)++, b(4), b(5), b(6)++, b(6), b(7), b(7)++, b(8)-98, b(8)-98++
Matched y ions: y(1), y(2)-98, y(2), y(3)-98, y(3), y(4)-98, y(4), y(5), y(5)-98, y(5)++, y(6), y(6)-98, y(6)-98++, y(7), y(7)-98, y(7)++, y(8)-98, y(8), y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.156

DSPLMSTPVANDSR
Confirmed sites: @S:2,@S:6,@T:7
Ambiguous sites:

MS/MS Fragmentation of DSPLMSTPVANDSR
Found in TMM71_MOUSE, Transmembrane protein 71 OS=Mus musculus GN=Tmem71 PE=2 SV=1

Match to Query 3582: 1778.646003 from(593.889277,3+)
Title: Elution from: 29.719 to 29.719 scan no 2106 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1778.6449
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.052

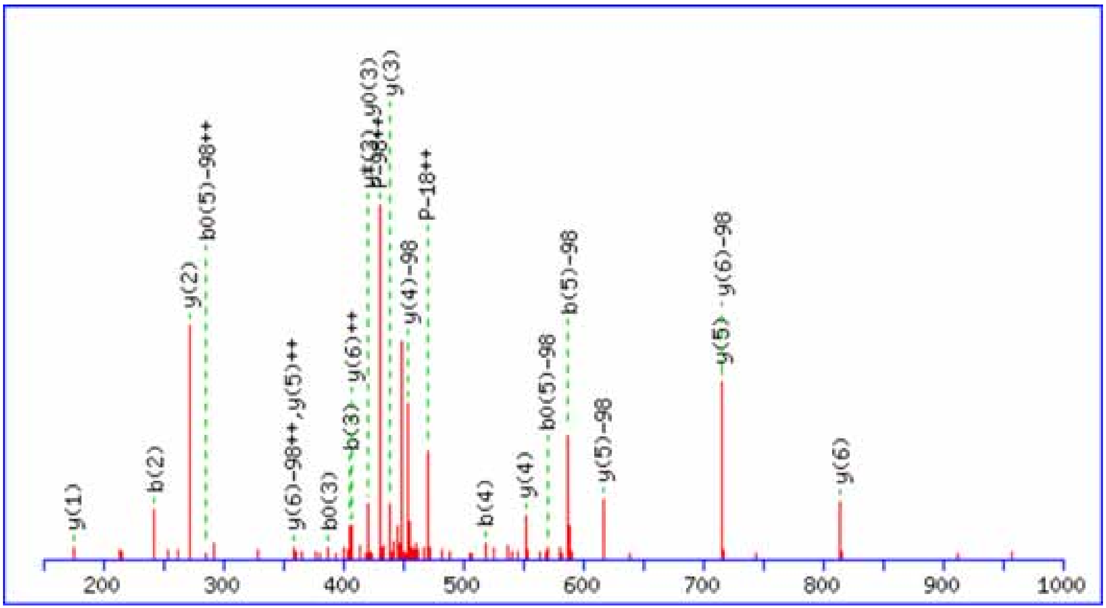
Matched b ions: b(3), b(4), b(5)++, b(5), b(5)-98, b(6)-196++, b(7)-98++, b(7)++, b(7)-294++, b(7)-294, b(8)-98++, b(8)++, b(9)-294++, b(9)-196++, b(9)++, b(10)-196++, b(10)++, b(11)-294++, b(11)-196++, b(11)-98++, b(11)++, b(12)++, b(12)-196++, b(12)-98++, b(13)-98++, b(13)-196++
Matched y ions: y(1), y(2), y(5), y(5)++, y(6)++, y(6), y(7)++, y(7), y(8)++, y(9)-196++, y(9)-98++, y(9)++, y(10)-196++, y(10)-98++, y(11)-196++, y(11)-98++, y(12)-196, y(12)-196++, y(12)++, y(13)-98++, y(13)-294++, y(13)-196++
Precursor origin neutral loss: +

Peptide No.157

DVYLSPR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of DVYLSPR
Found in HNRPG_MOUSE, Heterogeneous nuclear ribonucleoprotein G OS=Mus musculus GN=Rbmx PE=1 SV=1

Match to Query 368: 956.436066 from(479.225309,2+)
Title: Elution from: 34.627 to 34.627 scan no 2937 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 956.4368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 **Expect:** 0.043

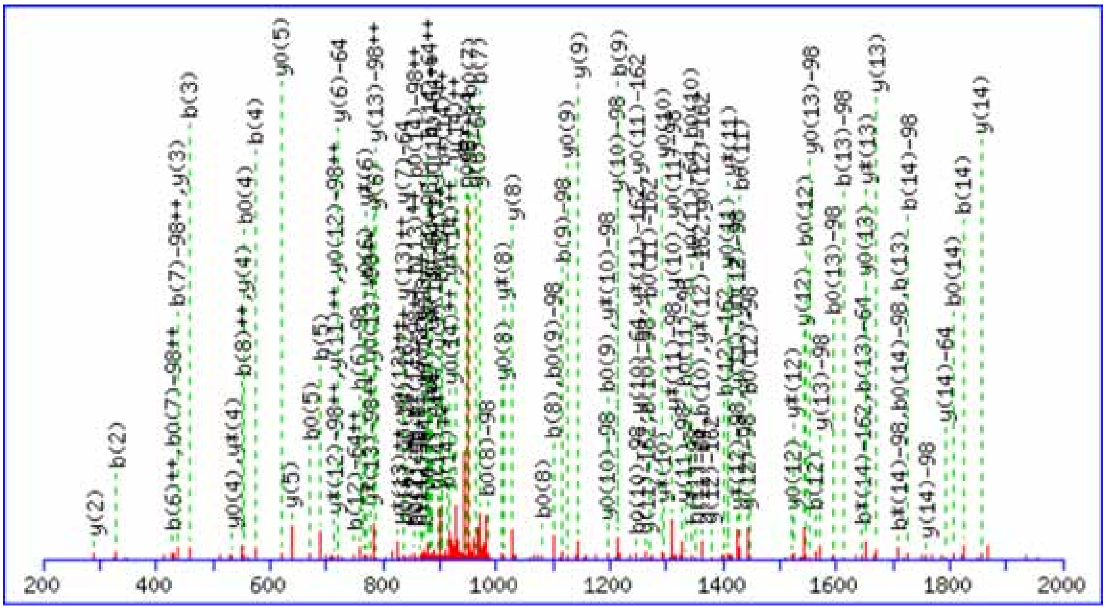
Matched b ions: b(2), b(3), b(4), b(5)-98
Matched y ions: y(1), y(2), y(3), y(4), y(4)-98, y(5), y(5)++, y(5)-98, y(6), y(6)-98++, y(6)-98, y(6)++
Precursor origin neutral loss: +

Peptide No.158

DWEDDSDEDMSNFDR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of DWEDDSDEDMSNFDR
Found in TEBP_MOUSE, Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=1 SV=1

Match to Query 5577: 1998.646292 from(1000.330422,2+)
Title: Elution from: 43.452 to 43.452 scan no 4111 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1998.6463
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 84 Expect: 1.9e-008

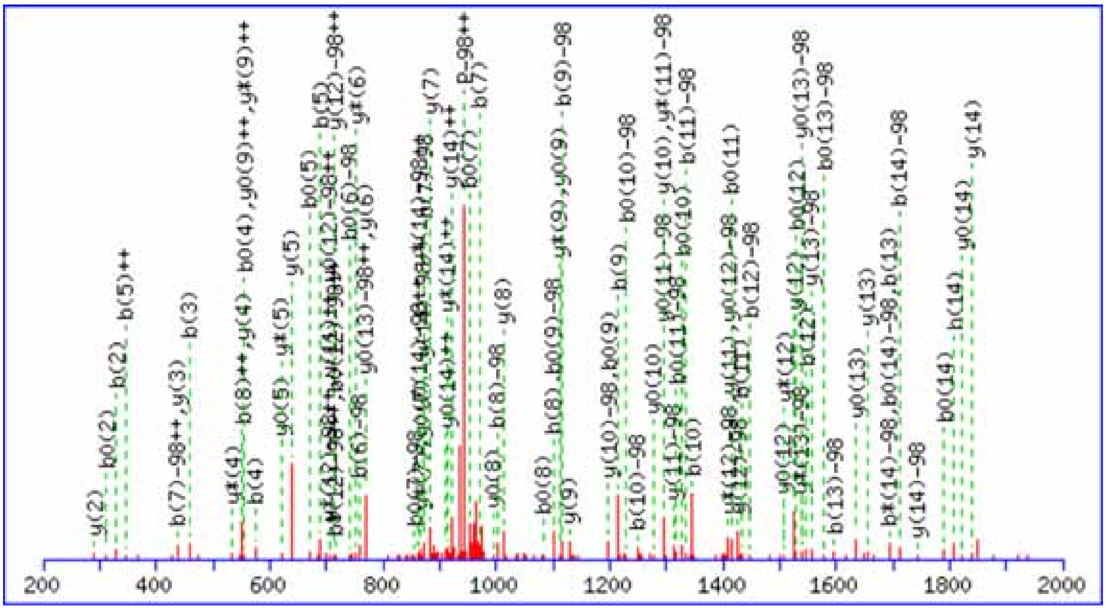
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(6)++, b(7)-98++, b(7)-98, b(7), b(8)++, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11)-98, b(12), b(13), b(13)++, b(13)-98, b(14), b(14)-98, b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(11)++, y(12)-98, y(12), y(13)-98, y(13), y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(14)-98, y(14)
Precursor origin neutral loss: +

Peptide No.159

DWEDDSDEDMSNFDR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of DWEDDSDEDMSNFDR
Found in TEBP_MOUSE, Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=1 SV=1

Match to Query 6422: 1982.650324 from(992.332438,2+)
Title: Elution from: 51.660 to 51.660 scan no 5157 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1982.6513
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 98 **Expect:** 8.1e-010

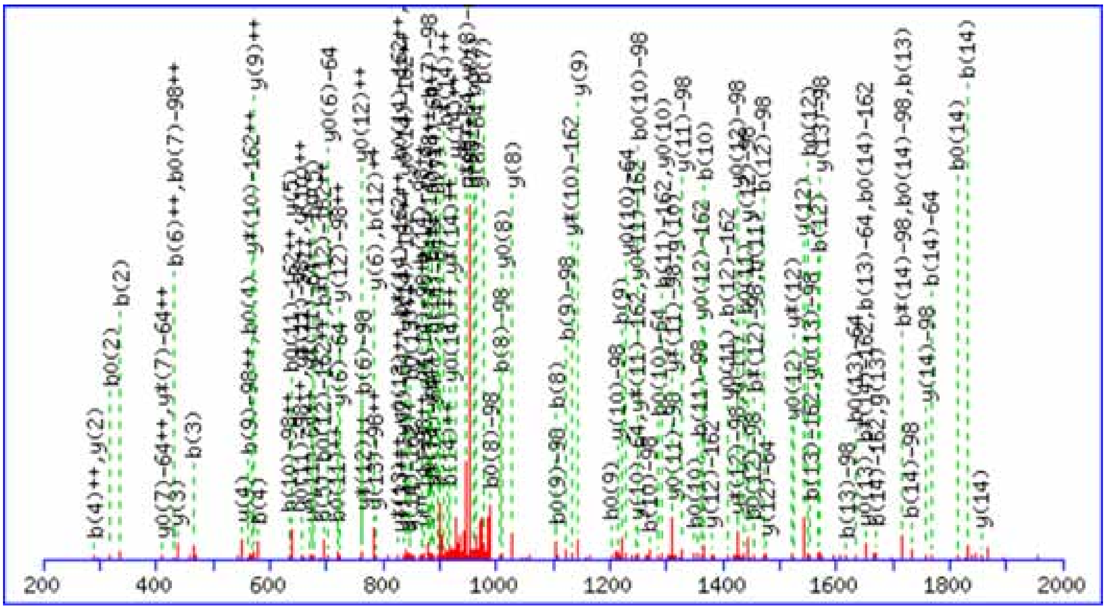
Matched b ions: b(2), b(3), b(4), b(5), b(5)++, b(6)-98, b(7)-98++, b(7)-98, b(7), b(8)++, b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(14)-98, b(14)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11), y(11)-98, y(11)++, y(12)-98, y(12), y(12)-98++, y(13), y(13)-98, y(14)-98++, y(14)-98, y(14)++, y(14)
Precursor origin neutral loss: +

Peptide No.160

DWEDDSDEDMSNFDR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **DWEDDSDEDMSNFDR**
Found in **TEBP_MOUSE**, Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=1 SV=1

Match to Query 6519: 2004.678404 from(1003.346478,2+)
Title: Elution from: 43.610 to 43.610 scan no 4116 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2004.6781
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 88 Expect: 1.2e-008

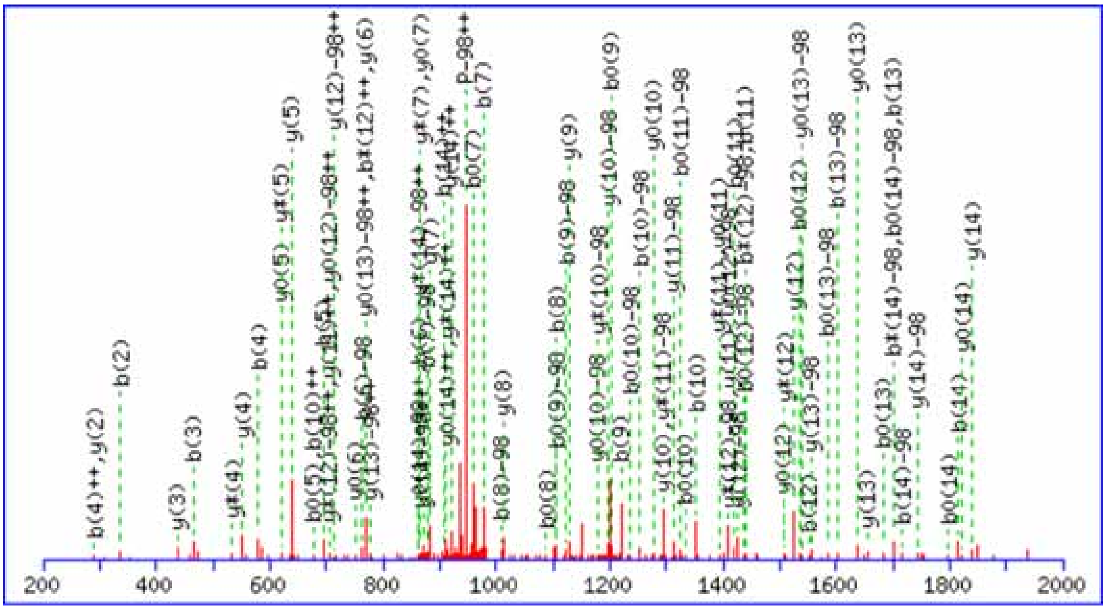
Matched b ions: b(2), b(3), b(4)++, b(4), b(5), b(6)-98, b(6)++, b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(9)-98++, b(10)-98, b(10), b(10)-98++, b(11)-98, b(11), b(12)++, b(12), b(12)-98, b(13), b(13)-98, b(14), b(14)-98, b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)-98, y(10)++, y(11), y(11)-98, y(12), y(12)-98, y(12)-98++, y(13)-98, y(13), y(13)-98++, y(13)++, y(14)-98++, y(14)-98, y(14), y(14)++
Precursor origin neutral loss: +

Peptide No.161

DWEDDSDEDMSNFDR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of DWEDDSDEDMSNFDR
Found in TEBP_MOUSE, Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=1 SV=1

Match to Query 6441: 1988.684952 from(995.349752,2+)
Title: Elution from: 51.616 to 51.616 scan no 5151 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1988.6832
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 96 Expect: 2e-009

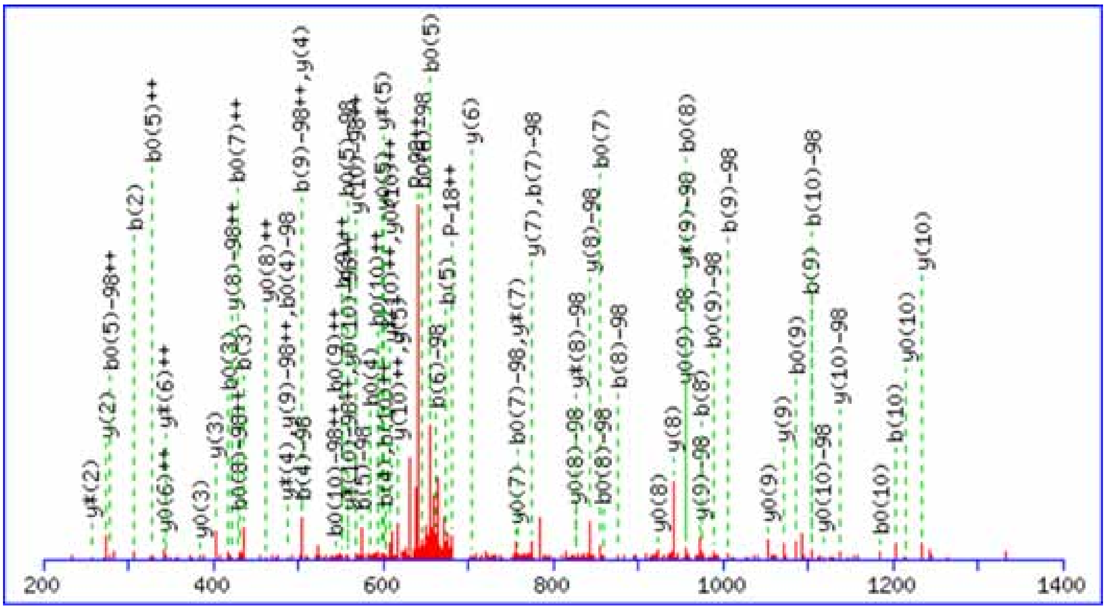
Matched b ions: b(2), b(3), b(4)++, b(4), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)++, b(10)-98, b(11), b(12), b(13), b(13)-98, b(14), b(14)-98, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(11)++, y(12), y(12)-98, y(12)-98++, y(13)-98, y(13), y(13)-98++, y(14)-98++, y(14)-98, y(14), y(14)++
Precursor origin neutral loss: +

Peptide No.162

DYESASLTEVR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of DYESASLTEVR
Found in ACTN2_MOUSE, Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1

Match to Query 1481: 1376.586928 from(689.300740,2+)
Title: Elution from: 40.152 to 40.152 scan no 3496 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1376.5861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 5e-005

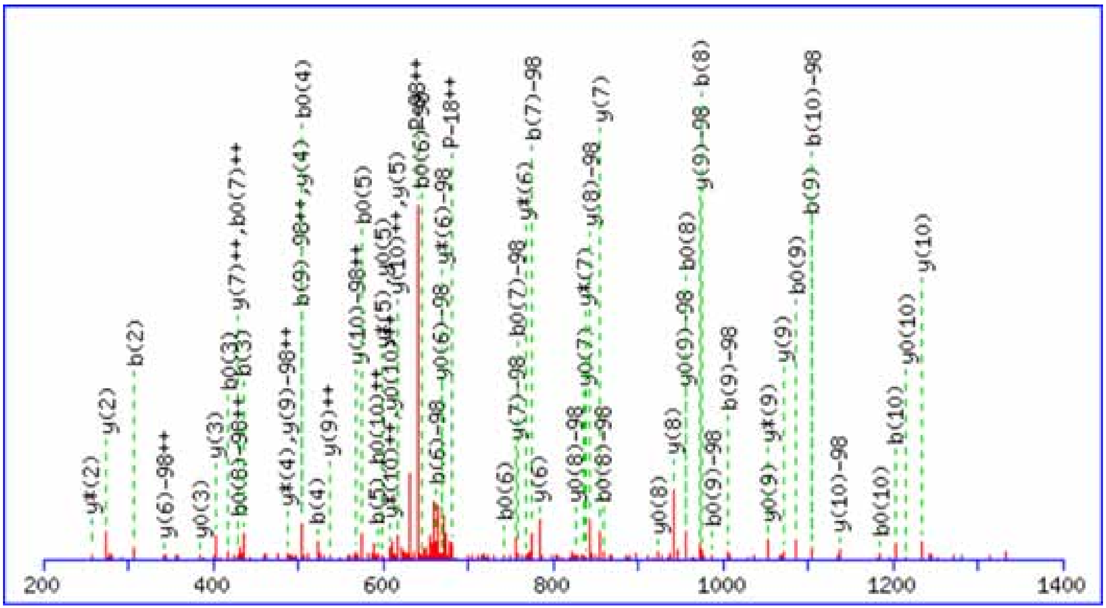
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(7)-98, b(8), b(8)-98, b(9)-98++, b(9), b(9)-98, b(9)++, b(10), b(10)-98, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(8)-98++, y(9)-98, y(9), y(9)-98++, y(10), y(10)++, y(10)-98, y(10)-98++
Precursor origin neutral loss: +

Peptide No.163

DYESASLTEVR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of DYESASLTEVR
Found in ACTN2_MOUSE, Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1

Match to Query 1927: 1376.587462 from(689.301007,2+)
Title: Elution from: 40.258 to 40.258 scan no 3700 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1376.5861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00073

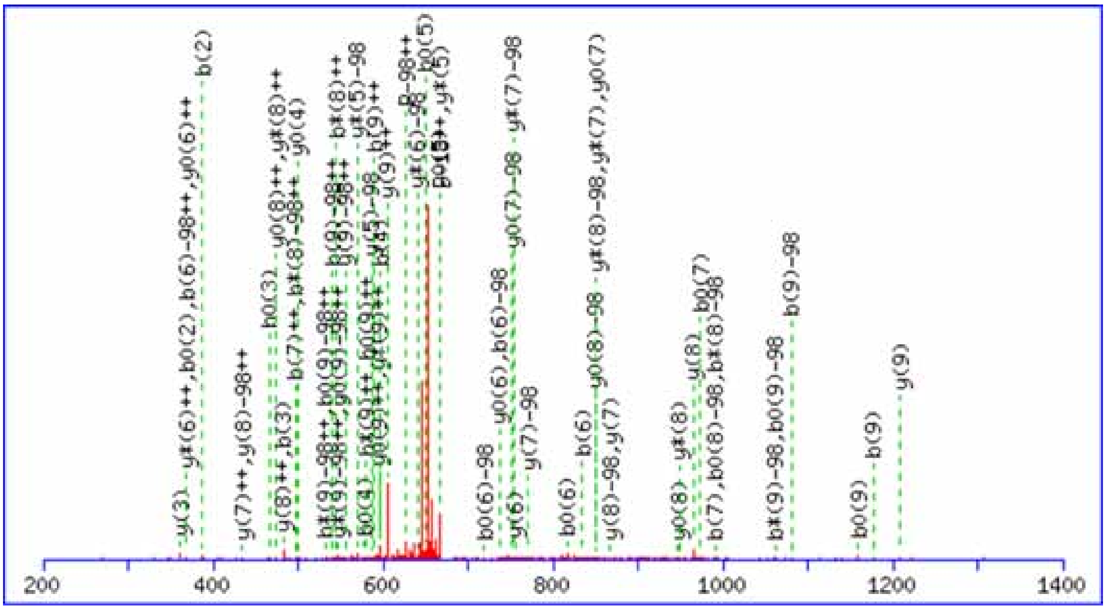
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(7)-98, b(8), b(9)-98++, b(9), b(9)-98, b(10), b(10)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98++, y(7), y(7)-98, y(7)++, y(8)-98, y(8), y(9)-98, y(9), y(9)-98++, y(9)++, y(10), y(10)-98, y(10)++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.164

DYPLASKDAK
Confirmed sites: @Y:2,@S:6
Ambiguous sites:

MS/MS Fragmentation of DYPLASKDAK
Found in IMDH2_MOUSE, Inosine-5'-monophosphate dehydrogenase 2 OS=Mus musculus GN=Impdh2 PE=1 SV=2

Match to Query 1269: 1350.586238 from(676.300395,2+)
Title: Elution from: 42.036 to 42.036 scan no 3716 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1350.5873
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y2 : Phospho (Y)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K7 : Dimethyl (K)
K10 : Dimethyl (K)
Ions Score: 27 Expect: 0.043

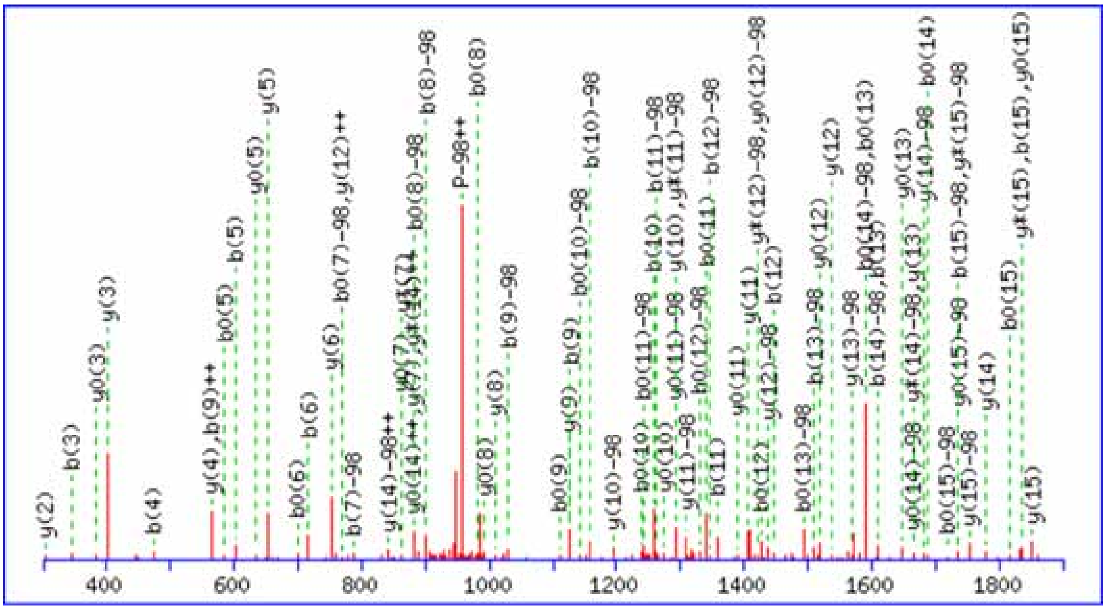
Matched b ions: b(2), b(3), b(4), b(6)-98++, b(6)-98, b(6), b(7), b(7)++, b(9), b(9)-98, b(9)-98++, b(9)++
Matched y ions: y(3), y(5)-98, y(6), y(7)++, y(7)-98, y(7), y(8)++, y(8), y(8)-98++, y(8)-98, y(9), y(9)++, y(9)-98++
Precursor origin neutral loss: +

Peptide No.165

EADEEDSDEETSYPER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EADEEDSDEETSYPER
Found in CF203_MOUSE, Uncharacterized protein C6orf203 homolog OS=Mus musculus PE=1 SV=1

Match to Query 5646: 2007.710610 from(1004.862581,2+)
Title: Elution from: 28.748 to 28.748 scan no 2131 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2007.7106
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 90 Expect: 1.3e-008

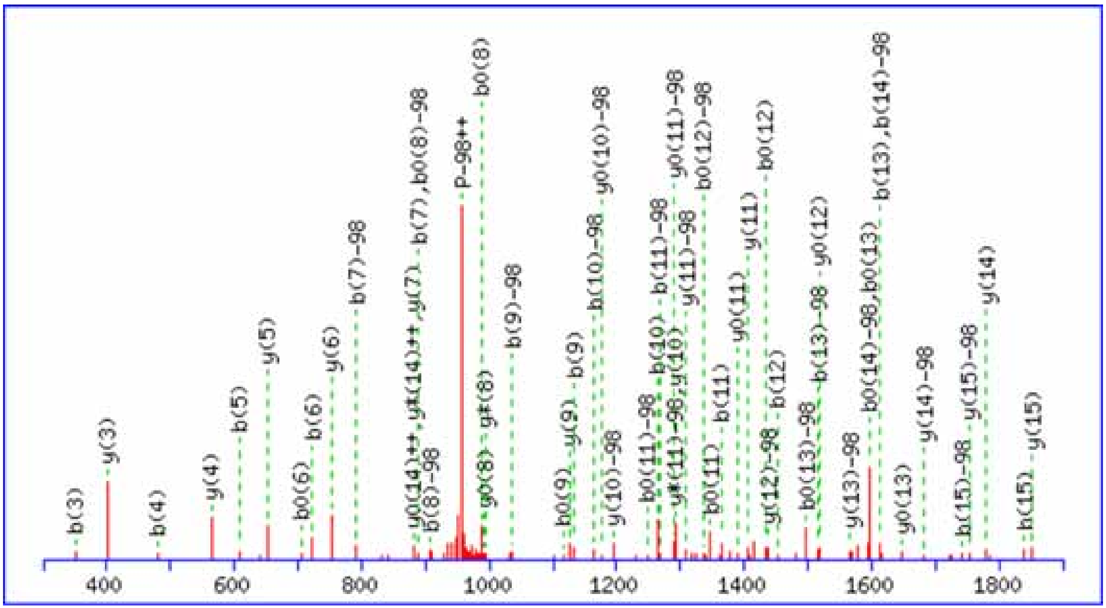
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(8)-98, b(9)++, b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(12)-98, b(12), b(13), b(13)-98, b(14)-98, b(15)-98, b(15)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(11), y(12)-98, y(12)++, y(12), y(13), y(13)-98, y(14)-98++, y(14), y(14)-98, y(15)-98, y(15)
Precursor origin neutral loss: +

Peptide No.166

EADEEDSDEETSYPER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of EADEEDSDEETSYPER
Found in CF203_MOUSE, Uncharacterized protein C6orf203 homolog OS=Mus musculus PE=1 SV=1

Match to Query 6566: 2013.742288 from(1007.878420,2+)
Title: Elution from: 28.410 to 28.410 scan no 1998 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2013.7424
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 **Expect:** 1.6e-007

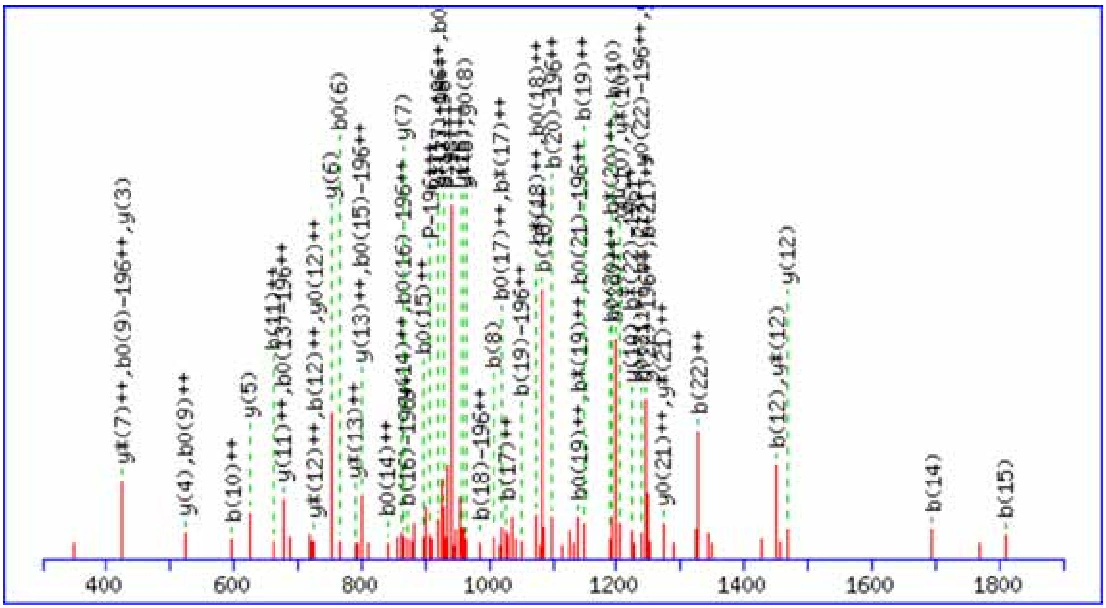
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(7), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12), b(13)-98, b(13), b(14)-98, b(15)-98, b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10)-98, y(10), y(11), y(11)-98, y(12)-98, y(13)-98, y(14)-98, y(14), y(15), y(15)-98
Precursor origin neutral loss: +

Peptide No.167

EAEEESSGGEEEDEDENIEVVYSK
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of EAEEESSGGEEEDEDENIEVVYSK
Found in IF5_MOUSE, Eukaryotic translation initiation factor 5 OS=Mus musculus GN=Eif5 PE=1 SV=1

Match to Query 8461: 2917.084425 from(973.368751,3+)
Title: Elution from: 50.902 to 50.902 scan no 5018 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2917.0838
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K24 : Dimethyl (K)
Ions Score: 32 **Expect:** 0.019

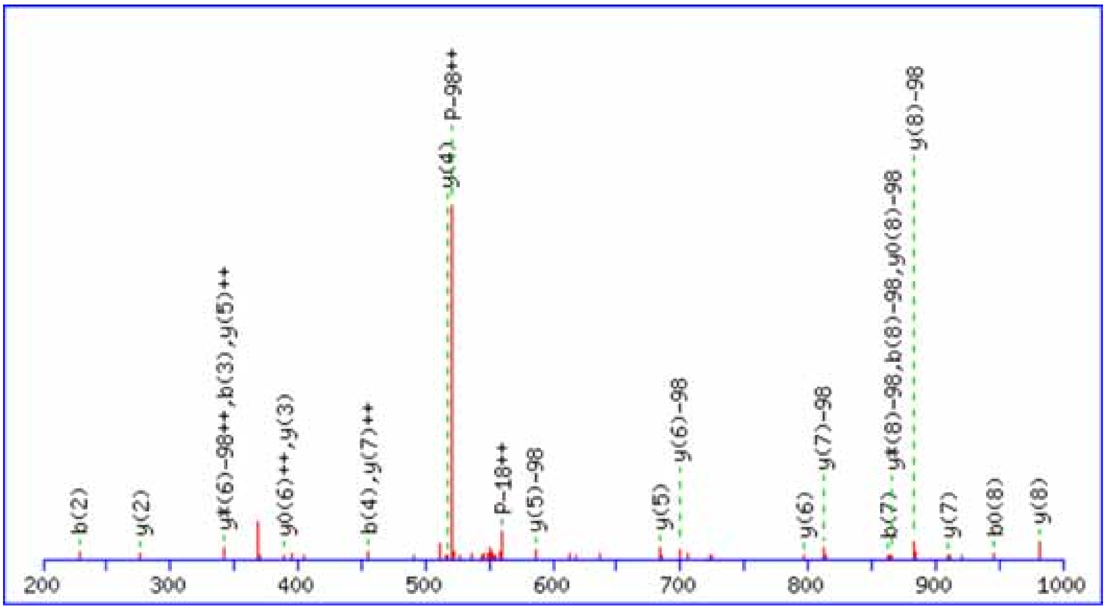
Matched b ions: b(8), b(8)-98, b(10)++, b(10), b(11)++, b(12)-98++, b(12), b(12)++, b(13)-98, b(14), b(14)-98++, b(15), b(15)-98++, b(16)-98++, b(16)-196++, b(17)-196++, b(17)++, b(18)++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)++, b(19)-196++, b(20)++, b(20)-98++, b(20)-196++, b(21)-98++, b(21)++, b(22)++, b(23)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(10), y(11)++, y(12), y(13)++, y(14)++, y(16)++, y(22)-196++
Precursor origin neutral loss: +

Peptide No.168

EALISQLTR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of EALISQLTR
Found in MYH7_MOUSE, Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1

Match to Query 961: 1137.580088 from(569.797320,2+)
Title: Elution from: 52.953 to 52.953 scan no 5244 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1137.5795
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.017

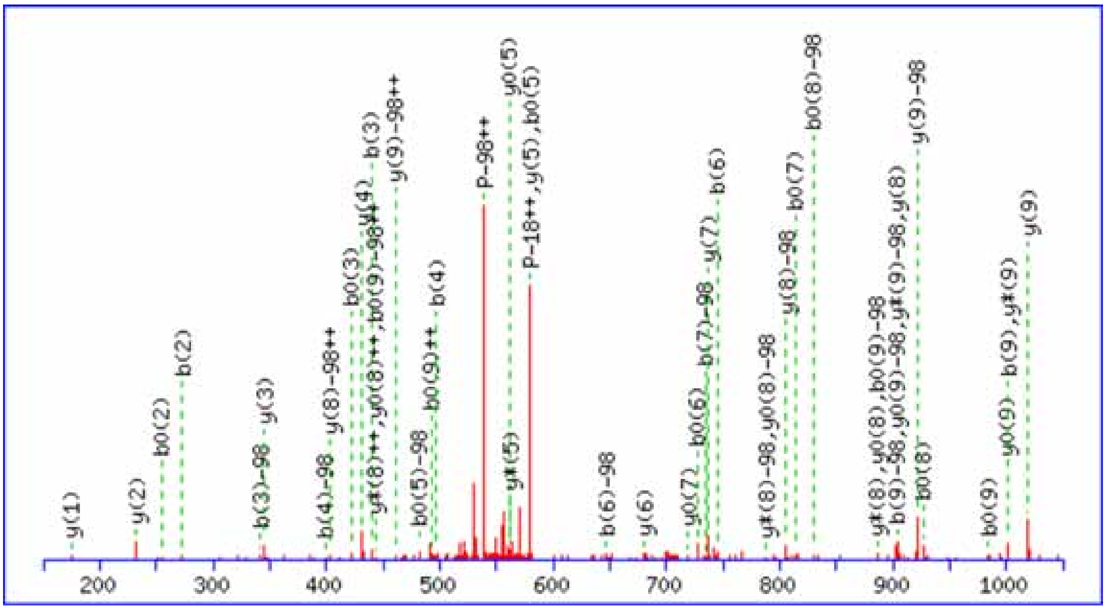
Matched b ions: b(2), b(3), b(4), b(7), b(8)-98
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(5)-98, y(6)-98, y(6), y(7)-98, y(7)++, y(7), y(8)-98, y(8)
Precursor origin neutral loss: +

Peptide No.169

EDSGTFSLGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EDSGTFSLGK
Found in PRKRA_MOUSE, Interferon-inducible double stranded RNA-dependent protein kinase activator A OS=Mus musculus GN=Prkra PE=1 SV=1

Match to Query 1121: 1175.511470 from(588.763011,2+)
Title: Elution from: 39.125 to 39.125 scan no 3549 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1175.5111
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K10 : Dimethyl (K)
Ions Score: 66 Expect: 4.7e-006

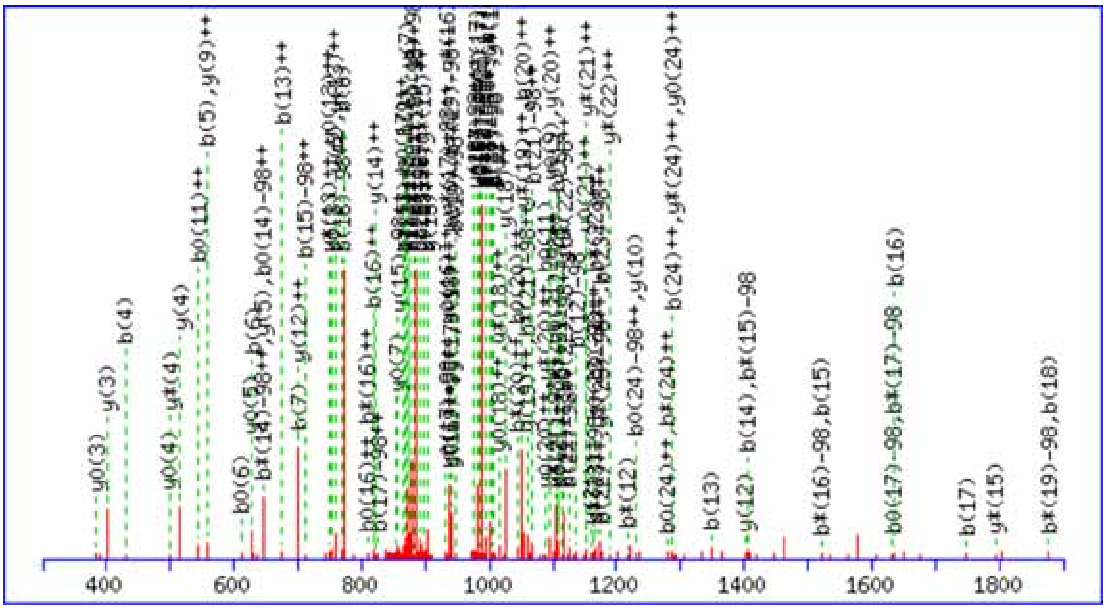
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(6)-98, b(6), b(7)-98, b(9)-98, b(9)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(8)-98++, y(9)-98, y(9), y(9)-98++
Precursor origin neutral loss: +

Peptide No.170

EEAAEAAAPASQNGDDLENLEDPEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of EEAAEAAAPASQNGDDLENLEDPEK
Found in ABEC2_MOUSE, Probable C->U-editing enzyme APOBEC-2 OS=Mus musculus GN=Apobec2 PE=1 SV=1

Match to Query 8225: 2748.165369 from(917.062399,3+)
Title: Elution from: 46.527 to 46.527 scan no 4487 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2748.1650
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K25 : Dimethyl (K)
Ions Score: 86 **Expect:** 1.7e-007

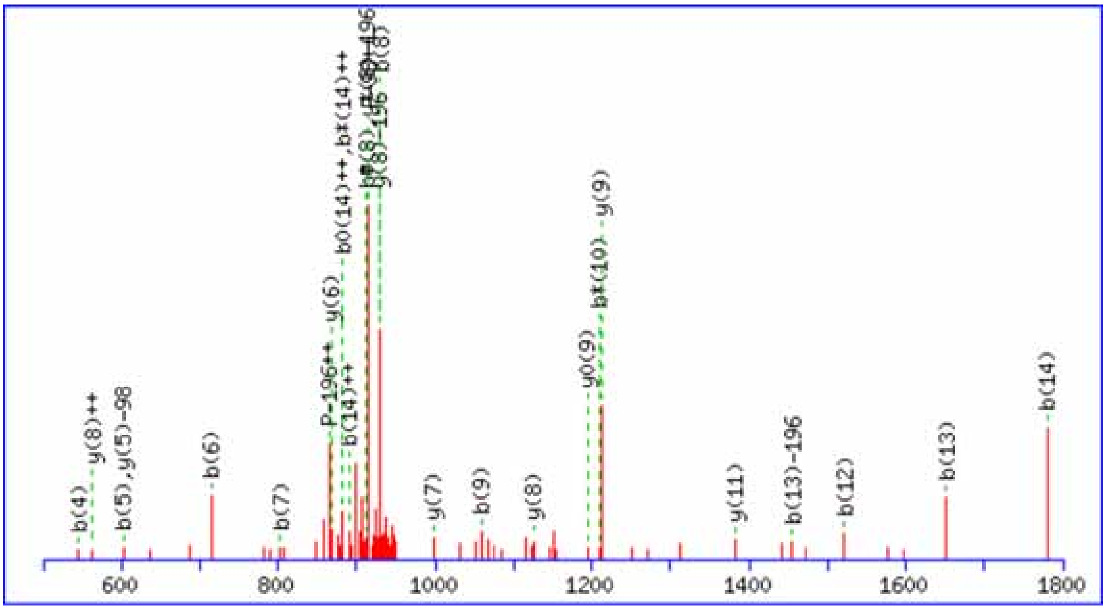
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(11)-98, b(12)-98, b(13), b(13)++, b(14), b(15), b(15)-98++, b(16), b(16)-98++, b(16)++, b(17), b(17)++, b(17)-98++, b(18), b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++, b(24)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(12)++, y(12), y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(20)++, y(21)++
Precursor origin neutral loss: +

Peptide No.171

EEEEGISQESSEEEQ
Confirmed sites: @S:10,@S:11
Ambiguous sites:

MS/MS Fragmentation of EEEEGISQESSEEEQ
Found in HMGA1_MOUSE, High mobility group protein HMG-I/HMG-Y OS=Mus musculus GN=Hmga1 PE=1 SV=4

Match to Query 4646: 1925.633792 from(963.824172,2+)
Title: Elution from: 31.238 to 31.238 scan no 2274 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1925.6340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00016

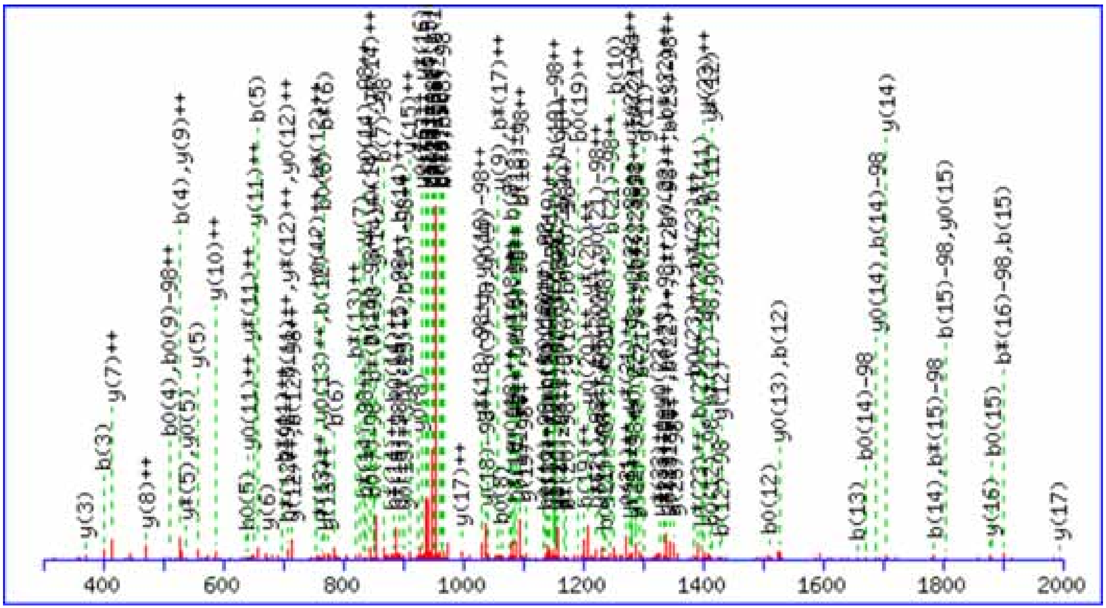
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(12), b(13), b(13)-196, b(14), b(14)++
Matched y ions: y(5)-98, y(6), y(7), y(7)-98, y(8)++, y(8), y(8)-196, y(9), y(9)-98, y(11)
Precursor origin neutral loss: +

Peptide No.172

EELEQQTDGDCDEEDDDKDGEVPK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of EELEQQTDGDCDEEDDDKDGEVPK
Found in SEC62_MOUSE, Translocation protein SEC62 OS=Mus musculus GN=Sec62 PE=1 SV=1

Match to Query 8524: 2958.149829 from(987.057219,3+)
Title: Elution from: 32.344 to 32.344 scan no 2626 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2958.1485
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl (K)
K24 : Dimethyl (K)
Ions Score: 71 **Expect:** 3e-006

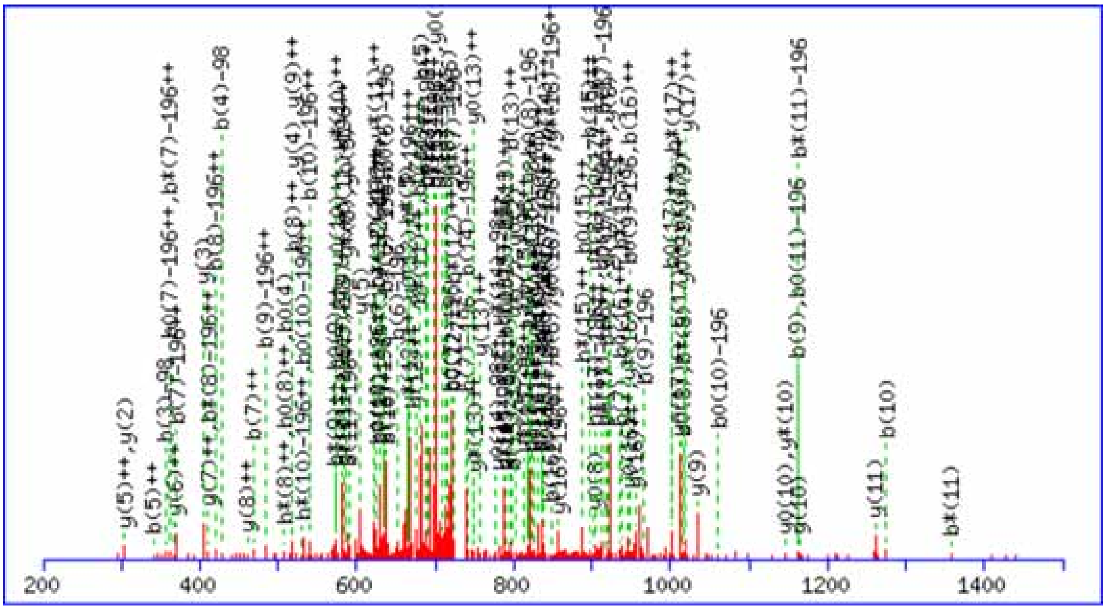
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(7), b(8), b(9)-98, b(9), b(10), b(10)-98, b(11)++, b(11), b(12)-98++, b(12), b(12)-98, b(12)++, b(13), b(14), b(14)-98++, b(14)-98, b(14)++, b(15)-98, b(15), b(15)-98++, b(15)++, b(16)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++, b(23)++
Matched y ions: y(3), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13)++, y(14)++, y(14), y(15)++, y(16)++, y(16), y(17), y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)-98++, y(21)-98++, y(21)++, y(22)++, y(22)-98++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.173

EESARSSPELTSESLTQR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of EESARSSPELTSESLTQR
Found in SVIL_MOUSE, Supervillin OS=Mus musculus GN=Svil PE=1 SV=1

Match to Query 5220: 2193.919122 from(732.313650,3+)
Title: Elution from: 36.883 to 36.883 scan no 3018 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2193.9191
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.023

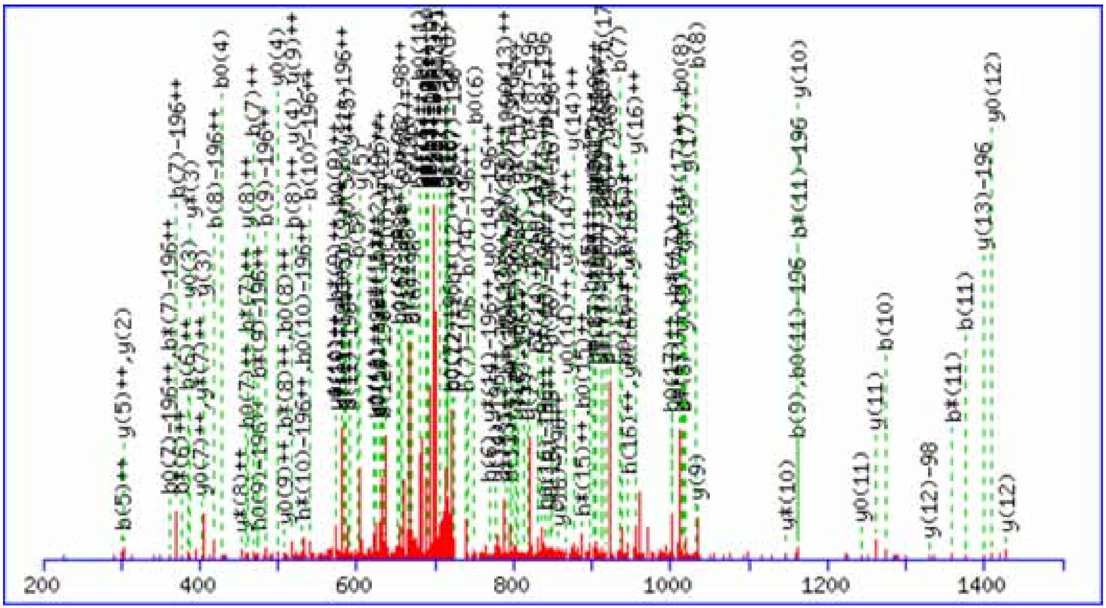
Matched b ions: b(3)-98, b(4)-98, b(5)++, b(5)-98, b(5), b(6)-196, b(6)-98, b(6), b(7)-196++, b(7)-98, b(7)++, b(7)-98++, b(7)-196, b(7), b(8)-196, b(8)-98++, b(8)-196++, b(8)++, b(8)-98, b(9)++, b(9), b(9)-196++, b(9)-98++, b(9)-196, b(10)-98++, b(10), b(10)++, b(10)-196++, b(10)-98, b(11)-196++, b(11)-98++, b(11)++, b(12)-98++, b(12)-196++, b(13)-196++, b(13)++, b(13)-98++, b(14)++, b(14)-196++, b(14)-98++, b(15)-196++, b(15)++, b(16)-196++, b(16)++, b(17)++, b(17)-98++, b(17)-196++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(10), y(11), y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(16)-196++, y(16)++, y(16)-98++, y(17)-196++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.174

EESARSSPELTSESLTQR
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of EESARSSPELTSESLTQR
Found in SVIL_MOUSE, Supervillin OS=Mus musculus GN=Svil PE=1 SV=1

Match to Query 5924: 2193.922062 from(732.314630,3+)
Title: Elution from: 36.975 to 36.975 scan no 3093 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2193.9191
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00096

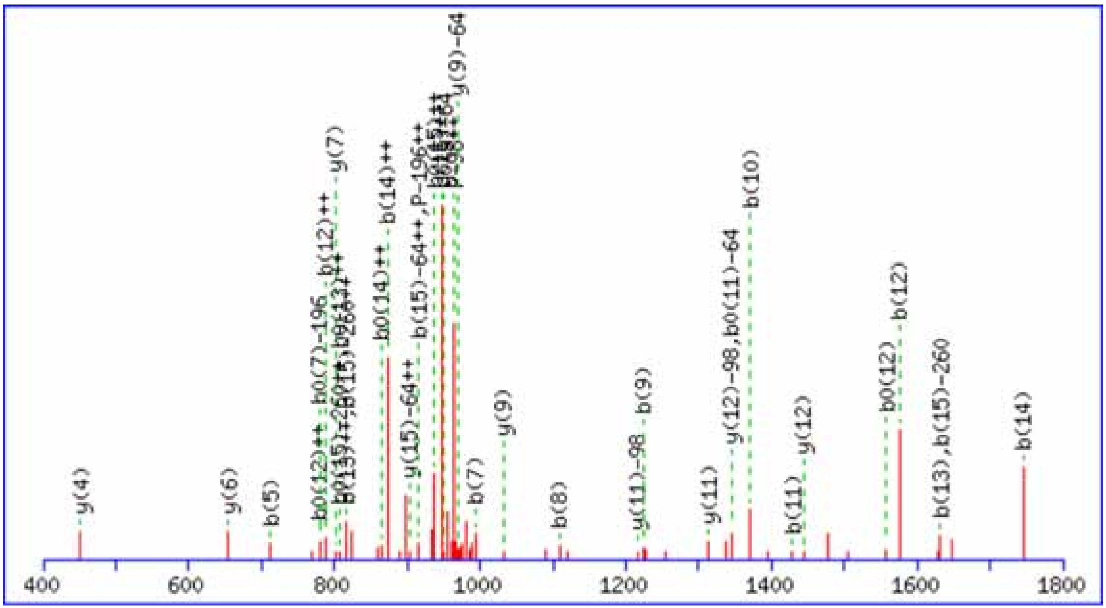
Matched b ions: b(5)++, b(5), b(6)++, b(6)-98, b(6), b(7)-196++, b(7)-98++, b(7)-98, b(7)-196, b(7)++, b(7), b(8)++, b(8)-196++, b(8), b(8)-98++, b(8)-196, b(9)++, b(9), b(9)-196++, b(9)-98++, b(10), b(10)-98++, b(10)++, b(10)-196++, b(11), b(11)++, b(11)-196++, b(11)-98++, b(12)-98++, b(12)-196++, b(13)++, b(13)-196++, b(13)-98++, b(14)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-196++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(17)-196++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(7), y(8), y(8)++, y(9)++, y(9), y(10)++, y(10), y(11), y(11)++, y(12), y(12)-98, y(12)++, y(12)-98++, y(13)-196++, y(13)-196, y(13)++, y(14)++, y(14)-196++, y(14)-98++, y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(16)-196++, y(17)-196++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.175

EESEEESDDDMGFGLFD
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of EESEEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5732: 2024.616358 from(1013.315455,2+)
Title: Elution from: 80.827 to 80.827 scan no 7422 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2024.6159
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 49 Expect: 3.6e-005

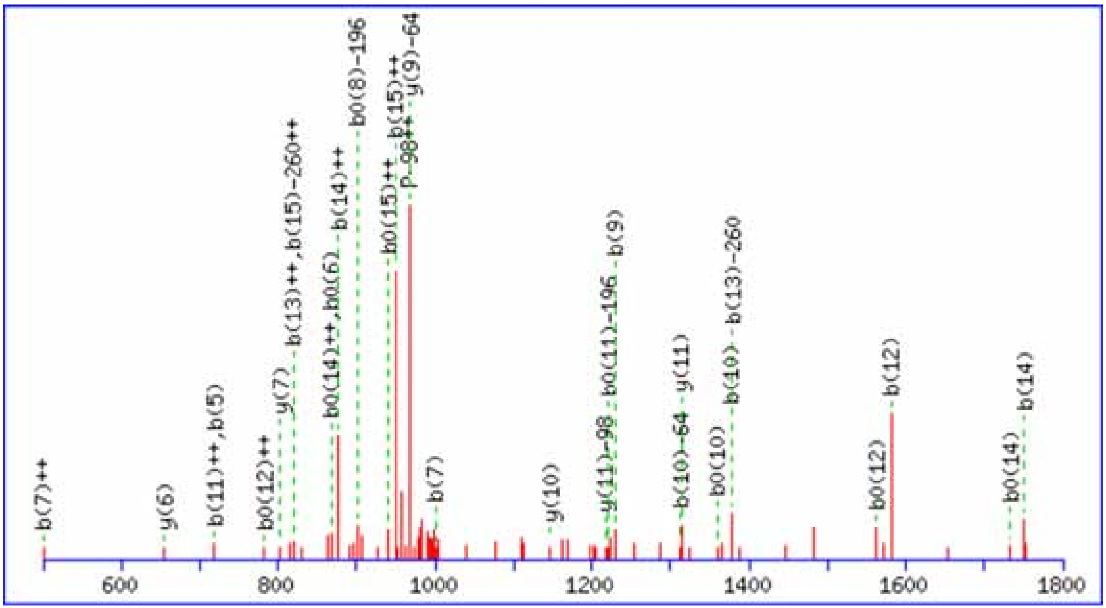
Matched b ions: b(5), b(7), b(8), b(9), b(10), b(11), b(12)-98, b(12), b(12)++, b(13)++, b(13), b(14), b(14)-98++, b(14)++, b(14)-98, b(15)++, b(15)-98++
Matched y ions: y(4), y(6), y(7), y(9), y(11)-98, y(11), y(12)-98, y(12)
Precursor origin neutral loss: +

Peptide No.176

EESEESDDDMGFGLFD
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of EESEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 6634: 2030.651400 from(1016.332976,2+)
Title: Elution from: 80.995 to 80.995 scan no 7681 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2030.6478
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 **Expect:** 0.006

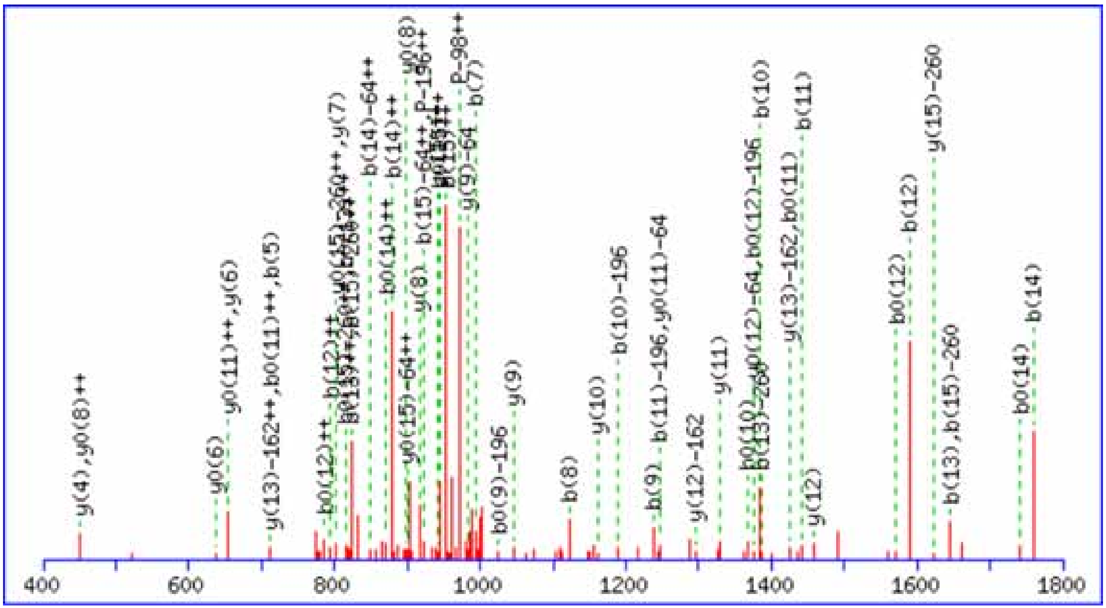
Matched b ions: b(5), b(7)++, b(7), b(9), b(10), b(11)++, b(12)-98, b(12), b(13)++, b(14)++, b(14)-98, b(14), b(15)-98++, b(15)++
Matched y ions: y(6), y(7), y(10), y(11), y(11)-98
Precursor origin neutral loss: +

Peptide No.177

EESEESDEDMGFGLFD
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of EESEESDEDMGFGLFD
Found in RLA0_MOUSE, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 4576: 2038.635246 from(1020.324899,2+)
Title: Elution from: 81.108 to 81.108 scan no 7185 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2038.6316
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 44 Expect: 0.00014

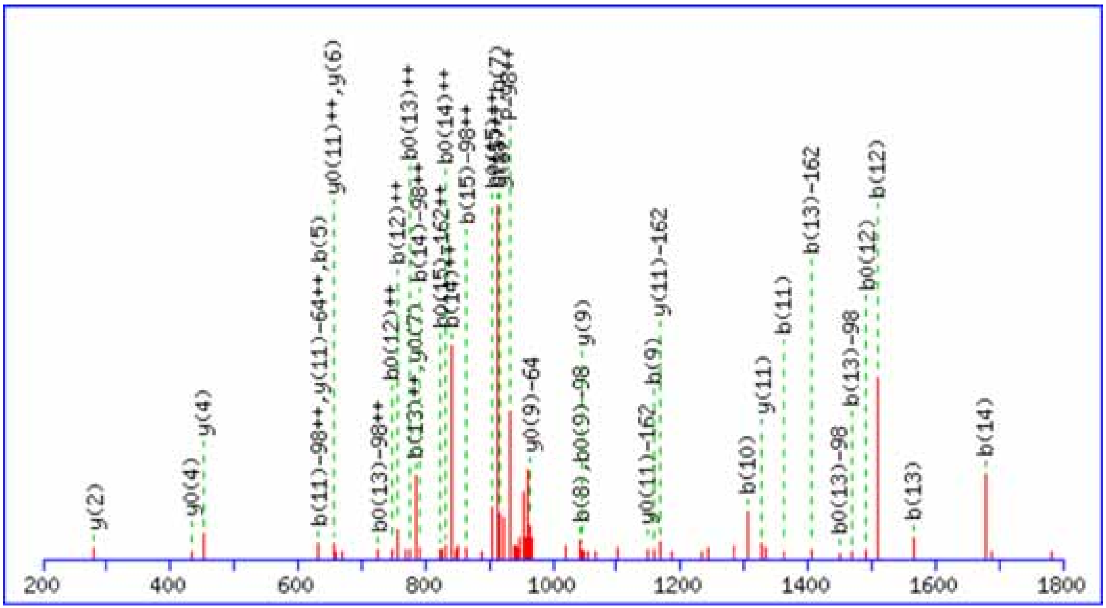
Matched b ions: b(5), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(9), b(10)-98, b(10), b(10)-196, b(11)-196, b(11), b(12)-98, b(12), b(12)++, b(13)++, b(13), b(13)-98++, b(14)++, b(14)-98, b(14), b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(15)++
Precursor origin neutral loss: +

Peptide No.178

EESEESDEDMGFGLFD
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of EESEESDEDMGFGLFD
Found in RLA0_MOUSE, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 6300: 1958.666190 from(980.340371,2+)
Title: Elution from: 68.837 to 68.837 scan no 6802 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1958.6653
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 39 Expect: 0.00092

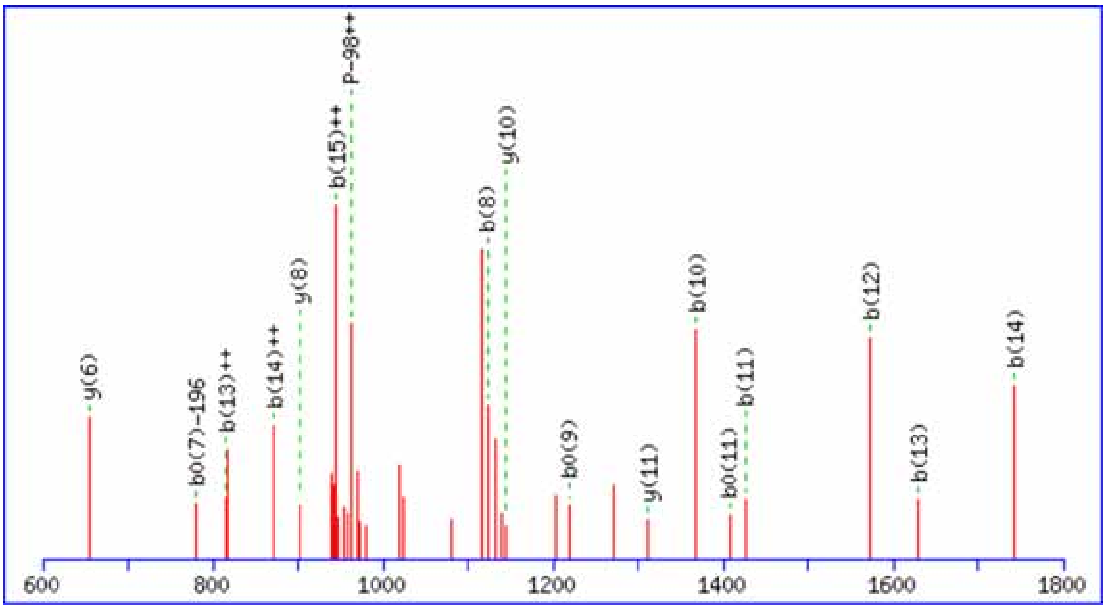
Matched b ions: b(5), b(7), b(8), b(9), b(10), b(11)-98++, b(11), b(12)++, b(12), b(13)++, b(13)-98, b(13), b(14)++, b(14), b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(4), y(6), y(8), y(9), y(11)
Precursor origin neutral loss: +

Peptide No.179

EESEESDEDMGFGLFD
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of EESEESDEDMGFGLFD
Found in RLA0_MOUSE, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 4532: 2022.637752 from(1012.326152,2+)
Title: Elution from: 95.378 to 95.378 scan no 7962 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2022.6367
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.0013

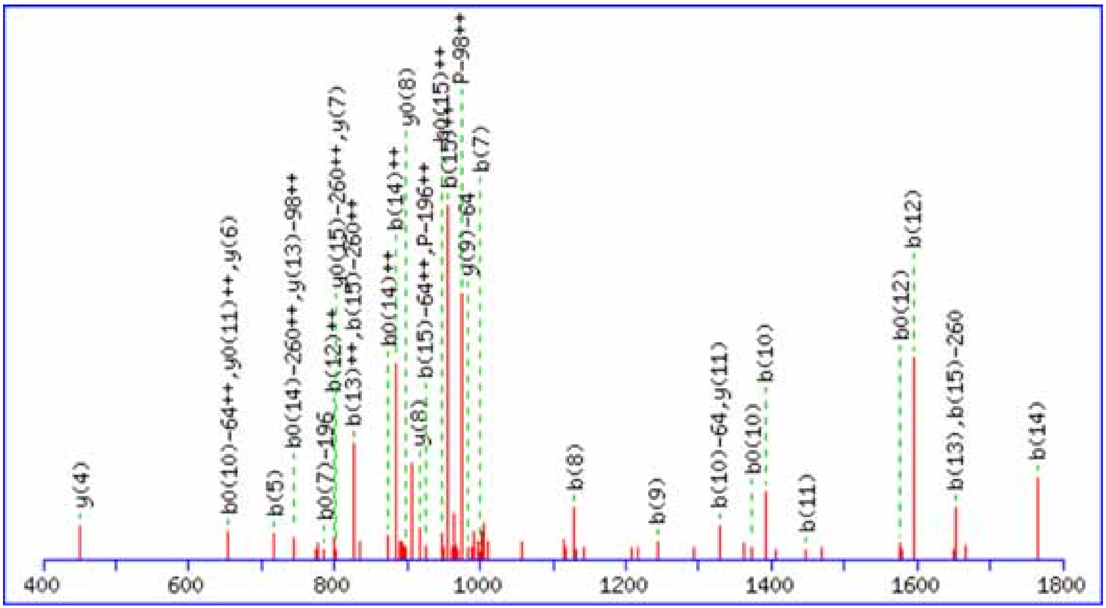
Matched b ions: b(6)-98, b(8), b(8)-98, b(9)-98, b(10)-98, b(10), b(11), b(12), b(13)++, b(13), b(14), b(14)++, b(15)++
Matched y ions: y(6), y(8), y(10), y(11)
Precursor origin neutral loss: +

Peptide No.180

EESEESDEDMGFGLFD
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of EESEESDEDMGFGLFD
Found in RLA0_MOUSE, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 5347: 2044.664950 from(1023.339751,2+)
Title: Elution from: 81.071 to 81.071 scan no 7201 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2044.6634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 49 **Expect:** 8.9e-005

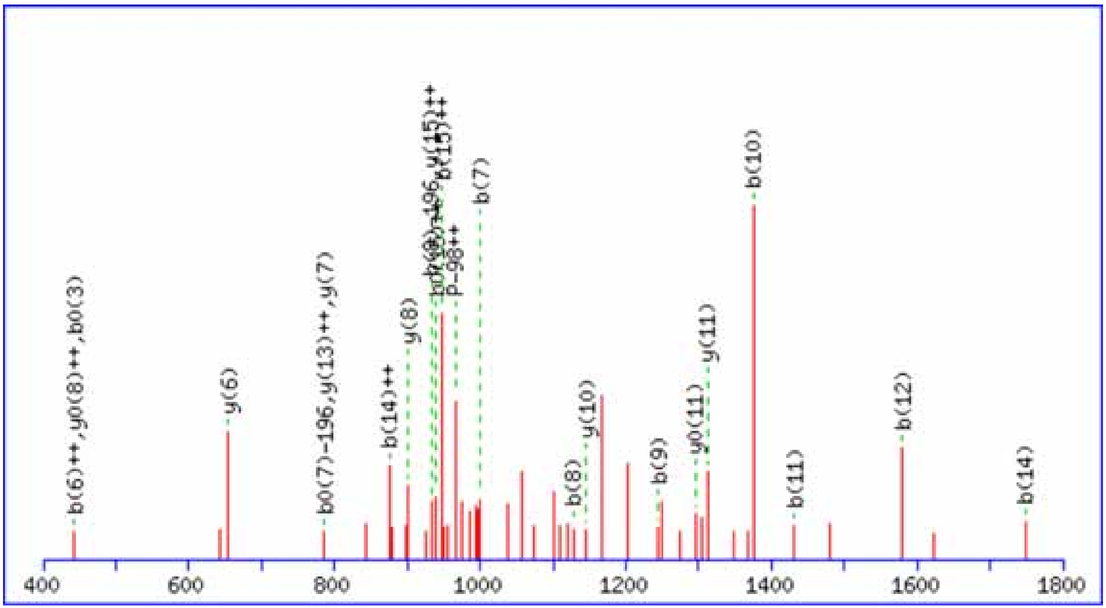
Matched b ions: b(5), b(6)-98, b(7)-98++, b(7), b(8), b(9), b(10), b(10)-98, b(11), b(12), b(12)++, b(13)++, b(13), b(13)-98++, b(14)++, b(14), b(14)-98, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(4), y(6), y(7), y(8), y(11), y(13)-98++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.181

EESEESDEDMGFGLFD
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of EESEESDEDMGFGLFD
Found in RLA0_MOUSE, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 4553: 2028.668814 from(1015.341683,2+)
Title: Elution from: 95.398 to 95.398 scan no 7964 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2028.6685
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0055

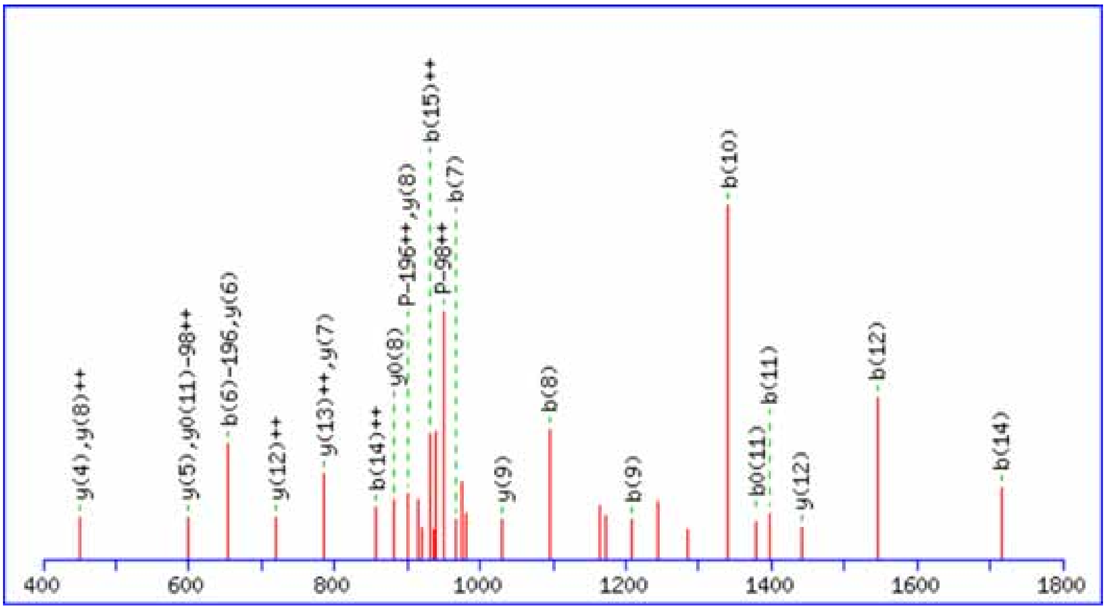
Matched b ions: b(6)++, b(7), b(8)-196, b(8), b(9), b(10), b(11), b(12)-98, b(12), b(14)++, b(14), b(15)++, b(15)-98++
Matched y ions: y(6), y(7), y(8), y(10), y(11), y(13)++, y(15)++
Precursor origin neutral loss: +

Peptide No.182

EESEESDEDMGFGLFD
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of EESEESDEDMGFGLFD
Found in RLA0_MOUSE, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 4773: 1994.607844 from(998.311198,2+)
Title: Elution from: 96.155 to 96.155 scan no 8036 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1994.6054
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 **Expect:** 1.6e-005

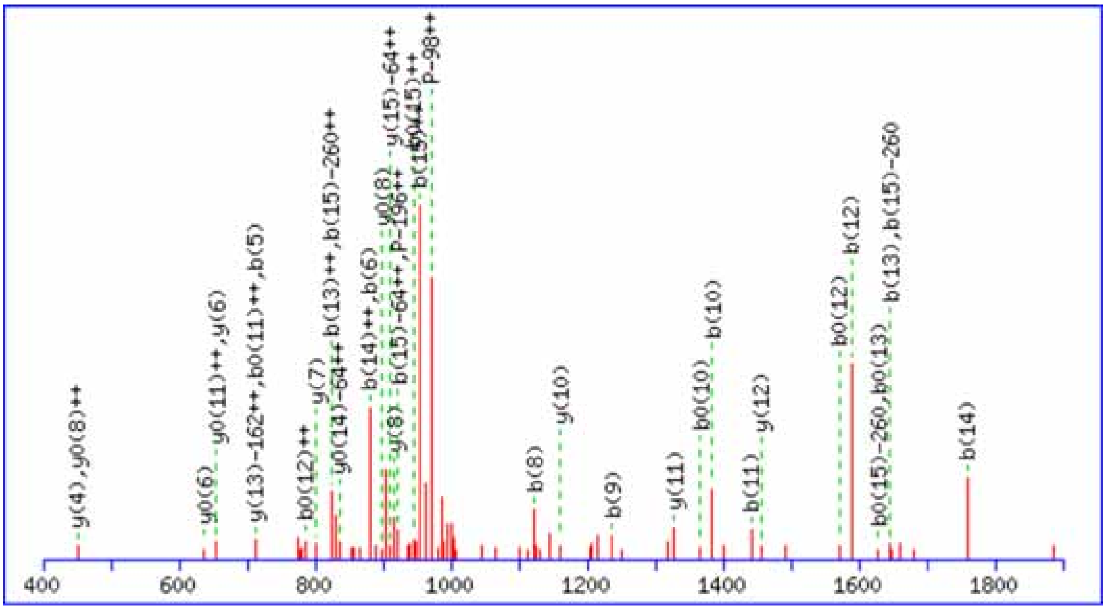
Matched b ions: b(6)-196, b(7), b(8), b(9), b(10)-98, b(10), b(11), b(12), b(14), b(14)++, b(15)++, b(15)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(12)++, y(12), y(13)++
Precursor origin neutral loss: +

Peptide No.183

EESEEESEDDMGFGLFD
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of EESEEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 5148: 2038.631962 from(1020.323257,2+)
Title: Elution from: 81.227 to 81.227 scan no 7301 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2038.6316
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 56 Expect: 9.4e-006

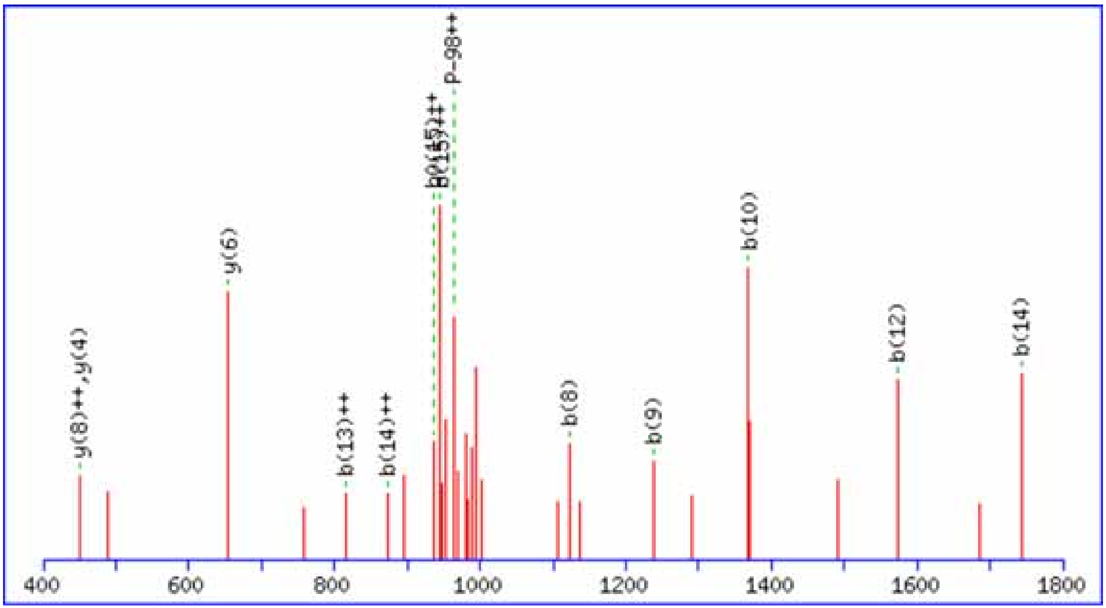
Matched b ions: b(5), b(6), b(6)-98, b(7)-98, b(8), b(9), b(10), b(11), b(12)-98, b(12), b(13)++, b(13), b(13)-98++, b(14)++, b(14)-98, b(14), b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(4), y(6), y(7), y(8), y(10), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.184

EESEESEDDMGFGLFD
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of EESEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 5091: 2022.638650 from(1012.326601,2+)
Title: Elution from: 95.492 to 95.492 scan no 8046 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2022.6367
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.003

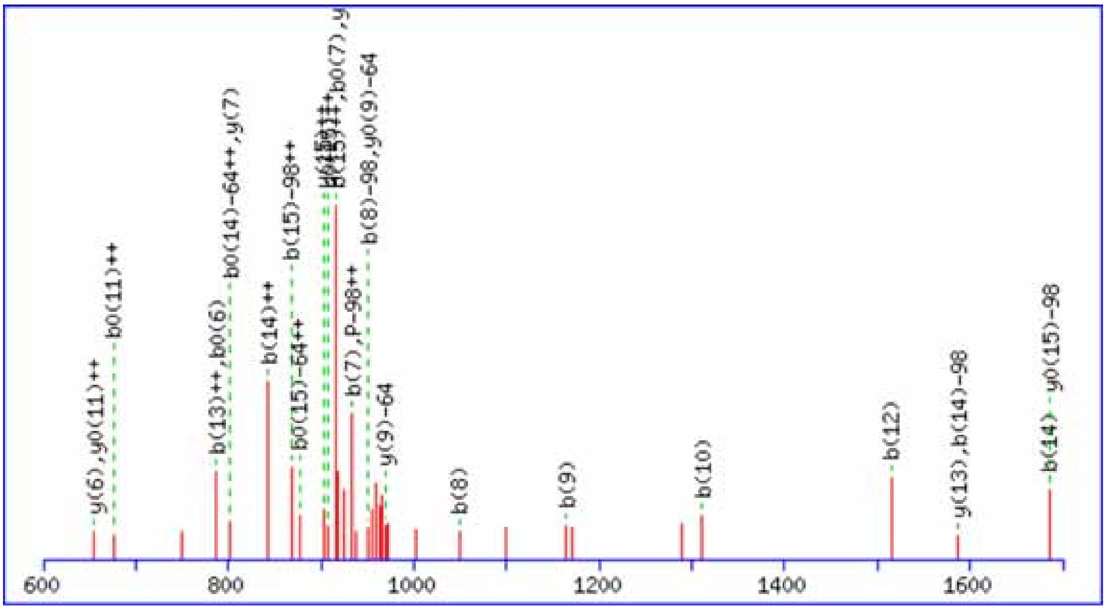
Matched b ions: b(8), b(9), b(10), b(12), b(13)++, b(14), b(14)++, b(15)++, b(15)-98++
Matched y ions: y(4), y(6), y(8)++
Precursor origin neutral loss: +

Peptide No.185

EESEESEDDMGFGLFD
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of EESEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 4407: 1964.698086 from(983.356319,2+)
Title: Elution from: 68.972 to 68.972 scan no 6103 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1964.6971
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 30 **Expect:** 0.013

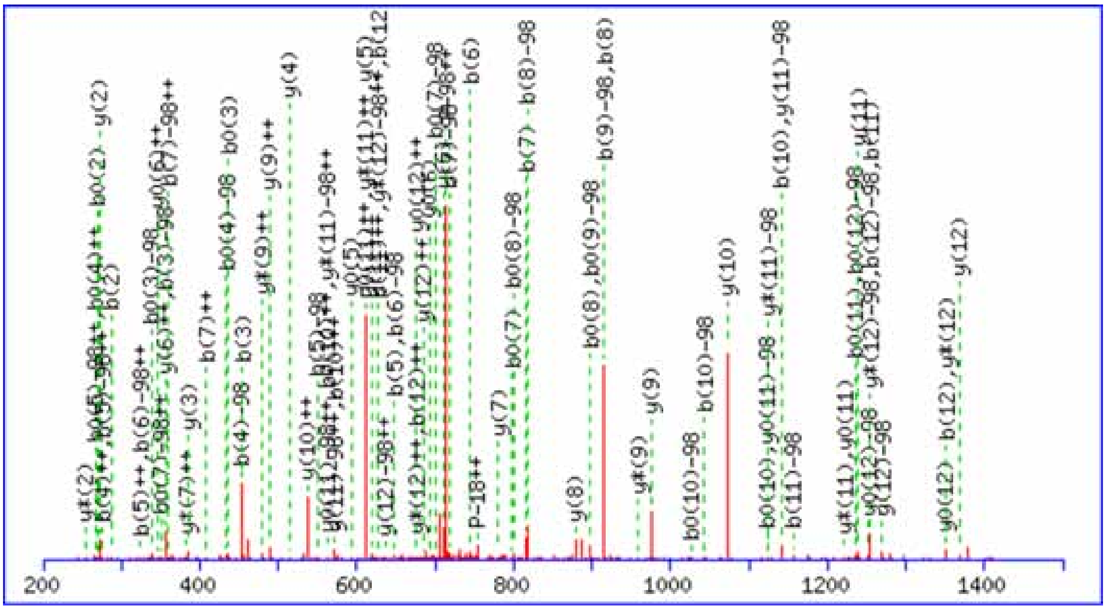
Matched b ions: b(7), b(8), b(8)-98, b(9), b(10), b(12), b(13)++, b(14)++, b(14)-98, b(14), b(15)++, b(15)-98++
Matched y ions: y(6), y(7), y(8), y(13), y(15)++
Precursor origin neutral loss: +

Peptide No.186

EESPPPAVPEIPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EESPPPAVPEIPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2089: 1524.748810 from(763.381681,2+)
Title: Elution from: 42.469 to 42.469 scan no 3722 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1524.7476
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
Ions Score: 64 Expect: 1.9e-005

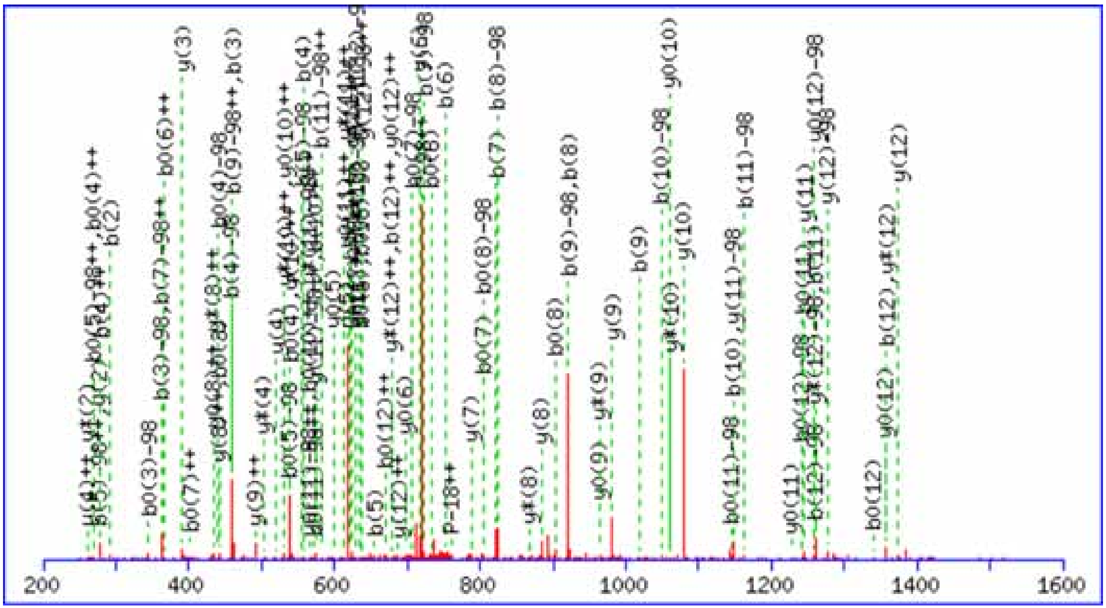
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4)++, b(5)++, b(5)-98++, b(5)-98, b(5), b(6), b(6)-98++, b(6)-98, b(7), b(7)++, b(7)-98, b(7)-98++, b(8)-98, b(8), b(9)-98, b(10)++, b(10), b(10)-98, b(11), b(11)-98, b(11)++, b(12)-98, b(12), b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)-98++, y(11)-98, y(11)++, y(12)-98, y(12), y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.187

EESPPPAVPEIPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EESPPPAVPEIPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2068: 1536.812602 from(769.413577,2+)
Title: Elution from: 42.615 to 42.615 scan no 3791 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1536.8113
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 72 Expect: 3.1e-006

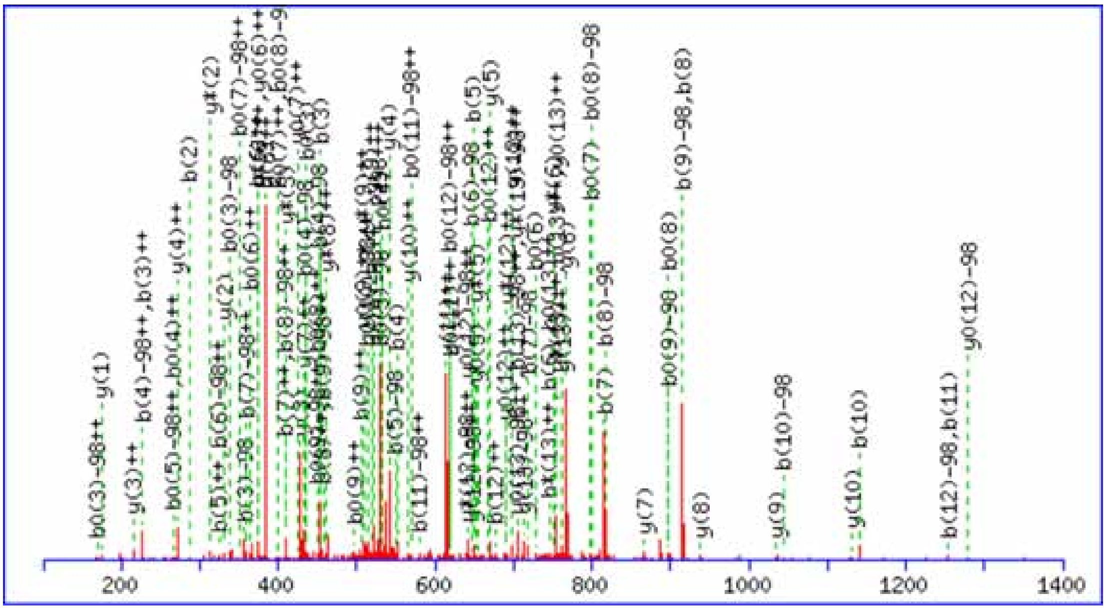
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4)++, b(4), b(5)-98++, b(5)-98, b(5), b(6), b(7)-98++, b(7), b(7)-98, b(8)-98, b(8), b(9)-98++, b(9)-98, b(9), b(10), b(10)-98, b(10)++, b(11), b(11)-98, b(11)-98++, b(11)++, b(12)-98, b(12), b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)-98, y(11)++, y(11)-98++, y(12)-98, y(12), y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.188

EESPPPAVPEIPKK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EESPPPAVPEIPKK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2800: 1680.874116 from(561.298648,3+)
Title: Elution from: 36.115 to 36.115 scan no 2918 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1680.8739
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
K14 : Dimethyl (K)
Ions Score: 52 Expect: 0.00036

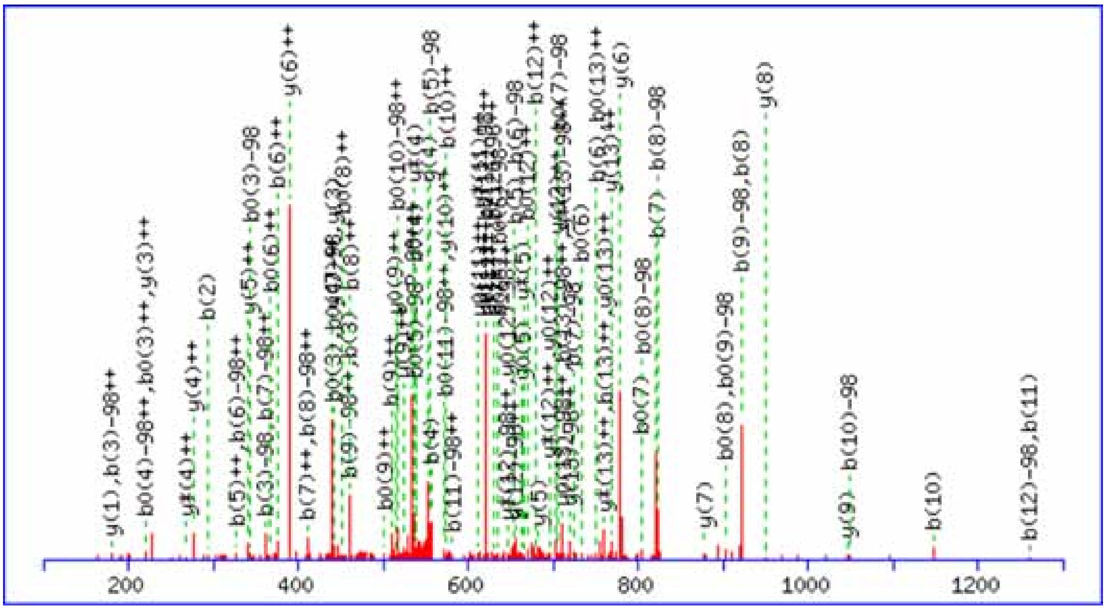
Matched b ions: b(2), b(3)++, b(3)-98, b(3), b(4)-98++, b(4), b(4)-98, b(5), b(5)++, b(5)-98, b(6)++, b(6)-98++, b(6)-98, b(6), b(7), b(7)-98++, b(7)-98, b(7)++, b(8), b(8)-98, b(8)-98++, b(8)++, b(9)-98, b(9)-98++, b(9)++, b(10), b(10)-98++, b(10)-98, b(11), b(11)-98++, b(12)-98, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(1), y(2), y(3)++, y(3), y(4)++, y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.189

EESPPPAVPEIPKK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of EESPPPAVPEIPKK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2848: 1698.969867 from(567.330565,3+)
Title: Elution from: 35.812 to 35.812 scan no 2883 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1698.9693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl:2H(4)13C(2) (K)
K14 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 50 Expect: 0.00039

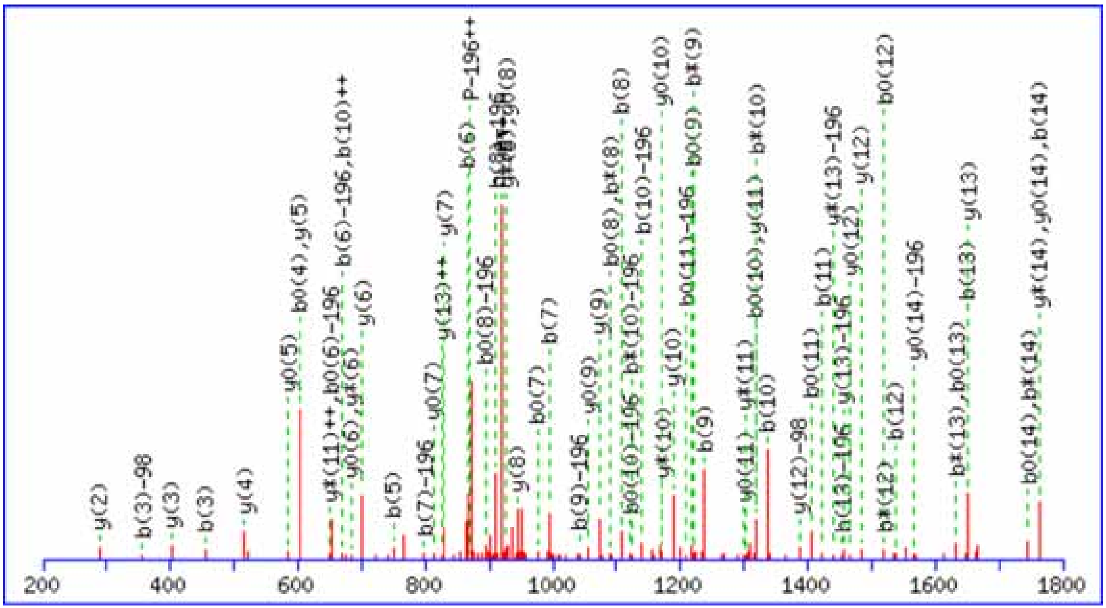
Matched b ions: b(2), b(3)-98, b(3)-98++, b(3), b(4), b(5), b(5)++, b(5)-98, b(6)-98, b(6)-98++, b(6)++, b(6), b(7)-98++, b(7), b(7)++, b(7)-98, b(8), b(8)-98, b(8)-98++, b(8)++, b(9)-98, b(9)-98++, b(9)++, b(10), b(10)-98, b(10)++, b(11), b(11)-98++, b(11)++, b(12)-98, b(12)-98++, b(12)++, b(13)-98++, b(13)++
Matched y ions: y(1), y(3)++, y(3), y(4)++, y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(9), y(9)++, y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.190

EESSEDENEVSNILR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of EESSEDENEVSNILR
Found in OTUD4_MOUSE, OTU domain-containing protein 4 OS=Mus musculus GN=Otud4 PE=1 SV=1

Match to Query 4860: 1936.735846 from(969.375199,2+)
Title: Elution from: 56.583 to 56.583 scan no 5414 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1936.7340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 82 Expect: 1.2e-007

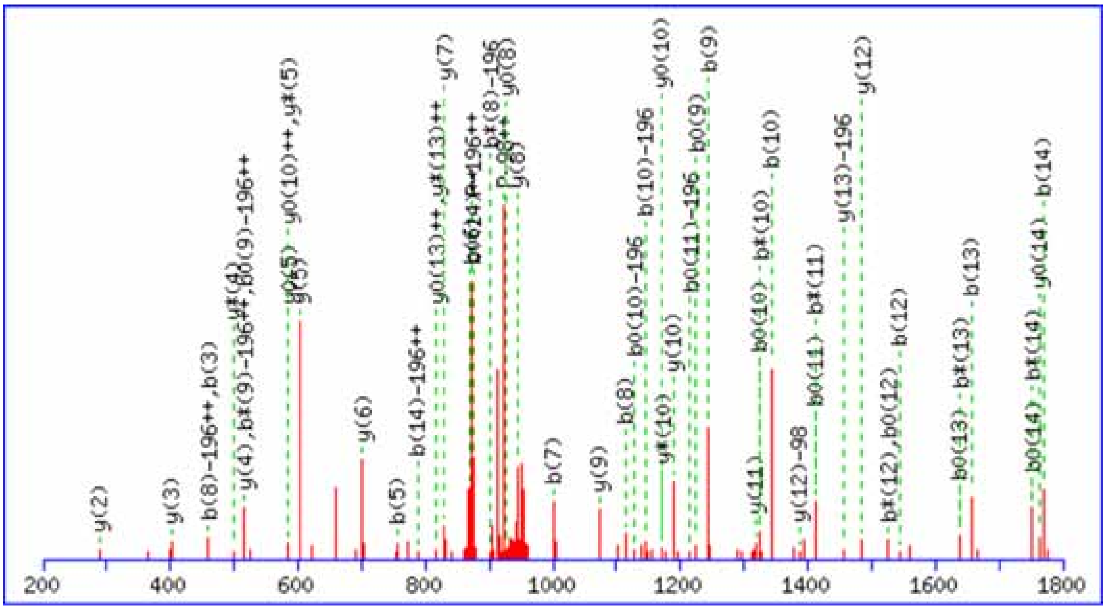
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(6)-196, b(7), b(7)-196, b(7)-98, b(8), b(8)-196, b(8)-98, b(9), b(9)-98, b(9)-196, b(10), b(10)-98, b(10)++, b(10)-196, b(11), b(12)-98, b(12), b(13)-98, b(13), b(13)-196, b(14), b(14)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98, y(13), y(13)-196, y(13)++
Precursor origin neutral loss: +

Peptide No.191

EESSEDENEVSNILR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of EESSEDENEVSNILR
Found in OTUD4_MOUSE, OTU domain-containing protein 4 OS=Mus musculus GN=Otud4 PE=1 SV=1

Match to Query 4286: 1942.768394 from(972.391473,2+)
Title: Elution from: 56.571 to 56.571 scan no 5151 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1942.7658
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 7.6e-005

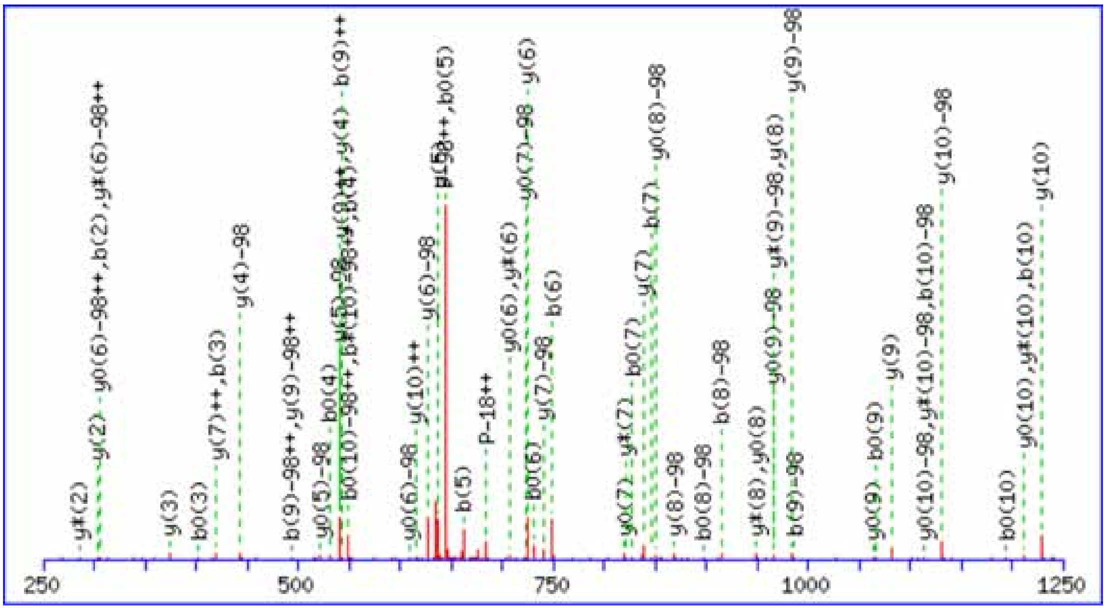
Matched b ions: b(3), b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-196++, b(8), b(9), b(9)-98, b(10), b(10)-196, b(10)-98, b(10)-98++, b(12), b(13), b(13)-98, b(14), b(14)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98, y(13)-196
Precursor origin neutral loss: +

Peptide No.192

EFDELSPSAQR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of EFDELSPSAQR
Found in AT2A2_MOUSE, Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2

Match to Query 1507: 1385.586986 from(693.800769,2+)
Title: Elution from: 39.240 to 39.240 scan no 3369 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1385.5864
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 Expect: 1e-006

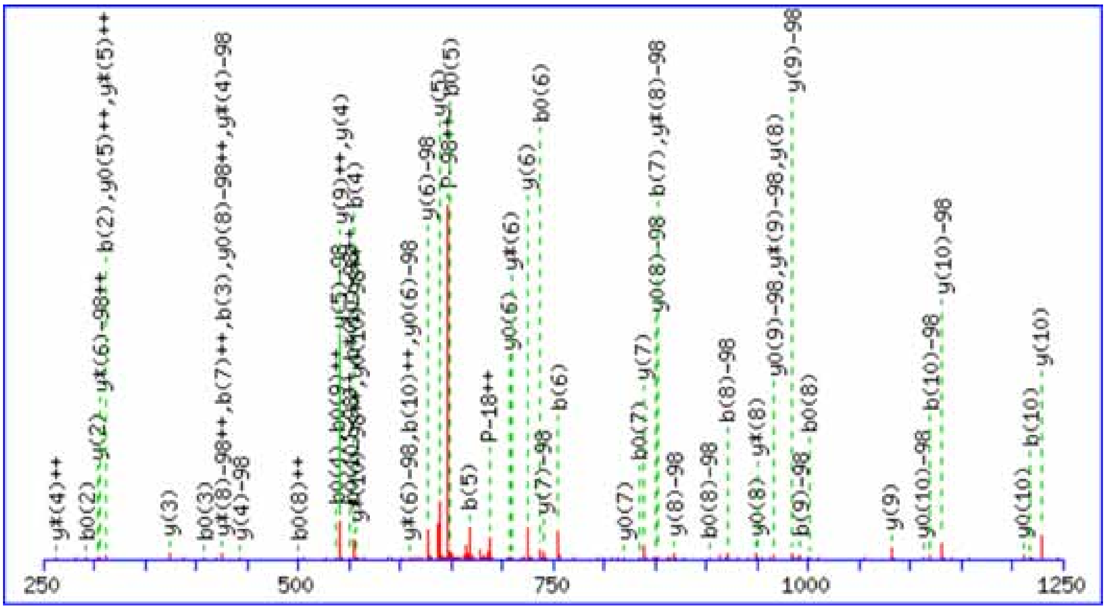
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)-98, b(9)-98, b(9)++, b(9)-98++, b(10), b(10)-98
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)++, y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(9)++, y(9)-98++, y(10)-98, y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.193

EFDELSPSAQR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of EFDELSPSAQR
Found in AT2A2_MOUSE, Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2

Match to Query 1802: 1391.618470 from(696.816511,2+)
Title: Elution from: 39.282 to 39.282 scan no 3409 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1391.6182
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 1.7e-006

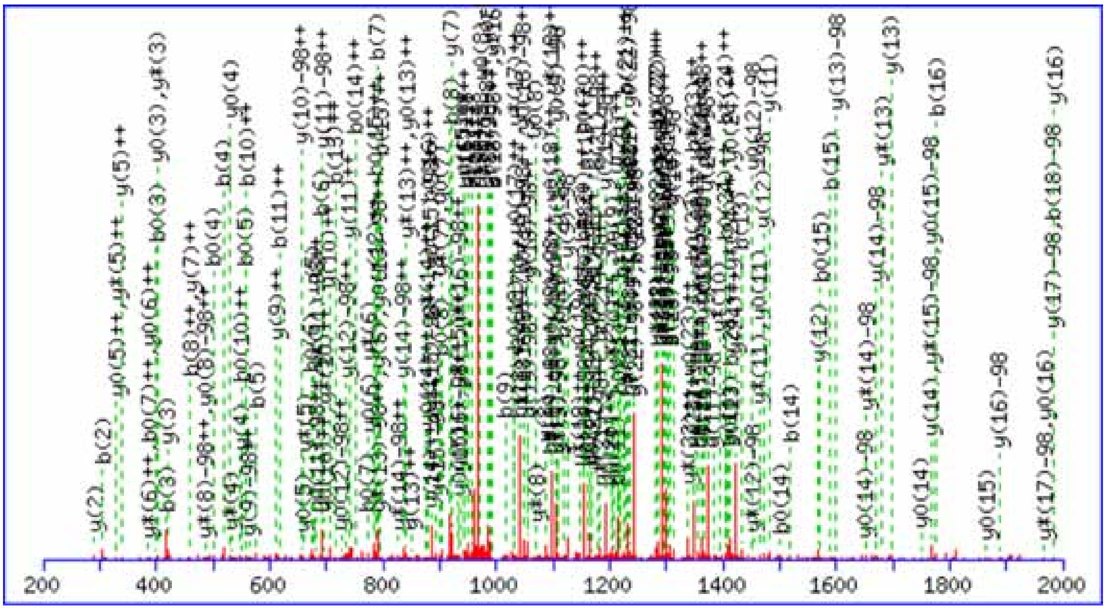
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)++, b(7), b(8)-98, b(9)-98, b(10)-98, b(10), b(10)++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(9)++, y(10)-98, y(10)
Precursor origin neutral loss: +

Peptide No.194

EFITGDVEPTDAESAWHSENEEEDK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of EFITGDVEPTDAESAWHSENEEEDK
Found in NP1L4_MOUSE, Nucleosome assembly protein 1-like 4 OS=Mus musculus GN=Nap1l4 PE=1 SV=1

Match to Query 7563: 2999.223180 from(1000.748336,3+)
Title: Elution from: 50.555 to 50.555 scan no 4810 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2999.2233
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K25 : Dimethyl (K)
Ions Score: 78 Expect: 8.4e-007

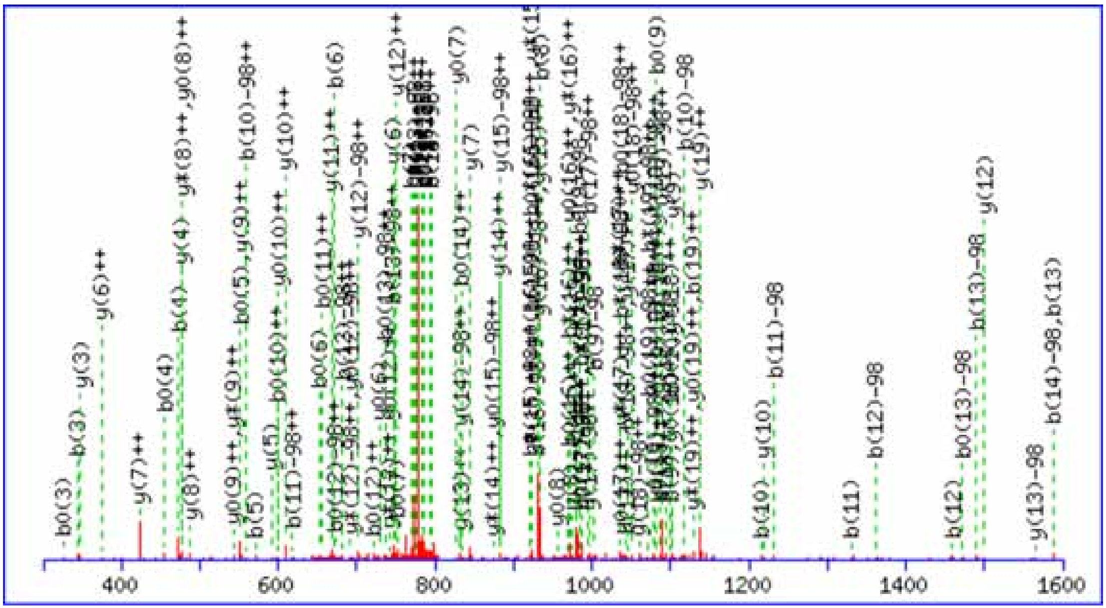
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(8)++, b(9), b(10)++, b(10), b(11), b(11)++, b(12), b(13), b(13)++, b(14), b(15), b(15)++, b(16), b(17)++, b(18)++, b(18)-98++, b(18)-98, b(19)-98++, b(19)++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(23)-98++, b(23)++, b(24)++, b(24)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(7)++, y(8), y(8)-98, y(9)++, y(9)-98, y(9)-98++, y(9), y(10)-98++, y(10)++, y(10), y(10)-98, y(11)++, y(11)-98++, y(11), y(11)-98, y(12), y(12)++, y(12)-98, y(12)-98++, y(13)-98, y(13), y(13)++, y(14)++, y(14), y(14)-98, y(14)-98++, y(15)-98++, y(15)++, y(16)-98, y(16), y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(17)-98, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)-98++, y(22)++, y(23)-98++, y(23)++, y(24)++, y(24)-98++
Precursor origin neutral loss: +

Peptide No.195

EGEEPTVYSDDEEPKDETAR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EGEEPTVYSDDEEPKDETAR
Found in PGRC1_MOUSE, Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4

Match to Query 7853: 2430.995868 from(811.339232,3+)
Title: Elution from: 32.058 to 32.058 scan no 2507 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2430.9951
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K15 : Dimethyl (K)
Ions Score: 77 **Expect:** 9.7e-007

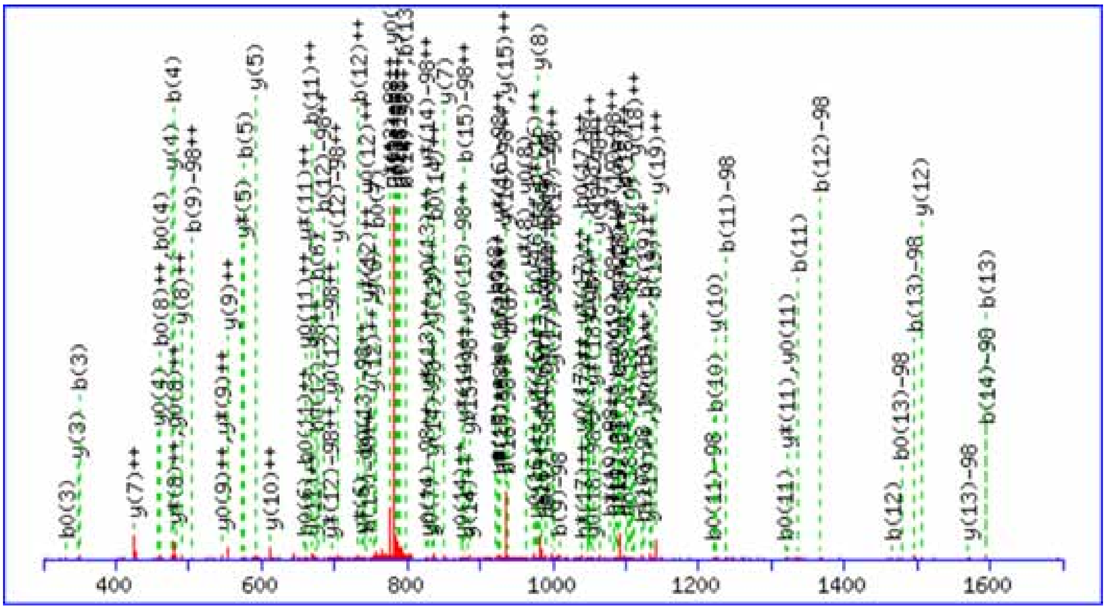
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(9), b(10), b(10)-98, b(10)-98++, b(11)-98, b(11), b(11)-98++, b(12), b(12)-98, b(12)-98++, b(13)-98, b(13), b(13)-98++, b(13)++, b(14)-98, b(14)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)-98++, y(12), y(12)++, y(13)-98, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.196

EGEEPTVYSDDEEPKDETAR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EGEEPTVYSDDEEPKDETAR
Found in PGRC1_MOUSE, Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4

Match to Query 6183: 2443.061124 from(815.360984,3+)
Title: Elution from: 32.022 to 32.022 scan no 2371 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2443.0588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 62 Expect: 4.4e-005

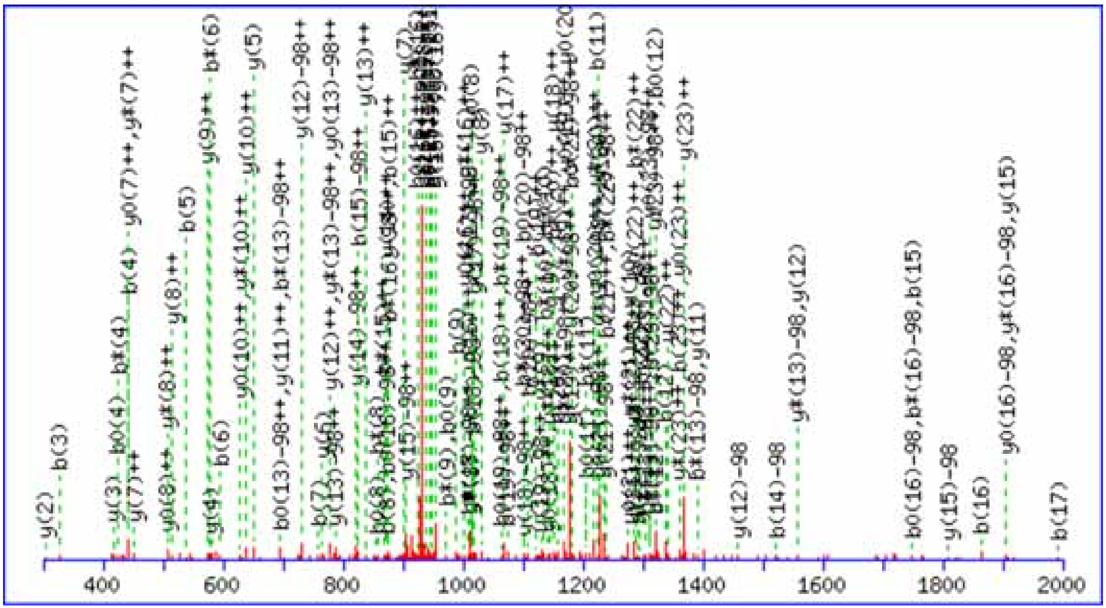
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(9), b(9)-98++, b(10), b(10)-98, b(11)-98, b(11), b(11)++, b(12), b(12)-98, b(12)-98++, b(12)++, b(13)-98, b(13), b(13)-98++, b(13)++, b(14)-98, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12), y(12)-98++, y(12)++, y(13)++, y(13)-98, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.197

EGINPGYDDYADSDEDQHDAYLER
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of EGINPGYDDYADSDEDQHDAYLER
Found in SSRP1_MOUSE, FACT complex subunit SSRP1 OS=Mus musculus GN=Ssrp1 PE=1 SV=2

Match to Query 8425: 2894.121063 from(965.714297,3+)
Title: Elution from: 45.693 to 45.693 scan no 4385 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2894.1192
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 1.2e-006

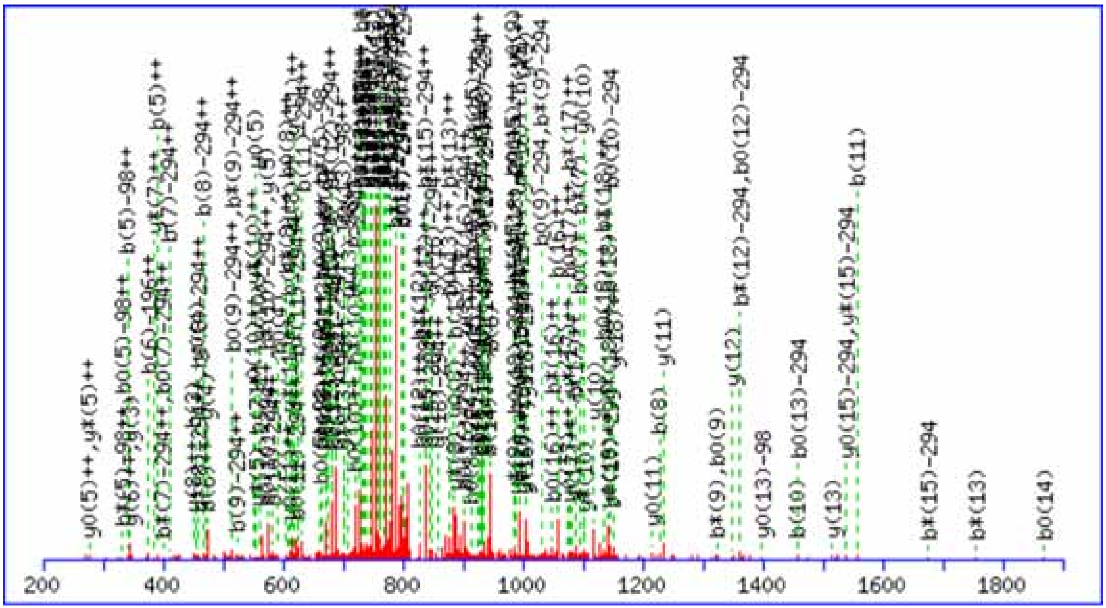
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(11), b(12), b(14)-98, b(15), b(15)-98++, b(15)++, b(16)++, b(16), b(17), b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(22)++, b(23)++, b(23)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(8)++, y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)-98++, y(12)-98, y(12)++, y(12), y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15), y(15)++, y(15)-98++, y(15)-98, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.198

EHRCSSSDDDTDVDVEGLR
Confirmed sites: @S:5,@S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of EHRCSSSDDDTDVDVEGLR
Found in PBIP1_MOUSE, Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Mus musculus GN=Pbxip1 PE=1 SV=2

Match to Query 6461: 2458.841718 from(820.621182,3+)
Title: Elution from: 39.567 to 39.567 scan no 3415 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2458.8387
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 5.4e-005

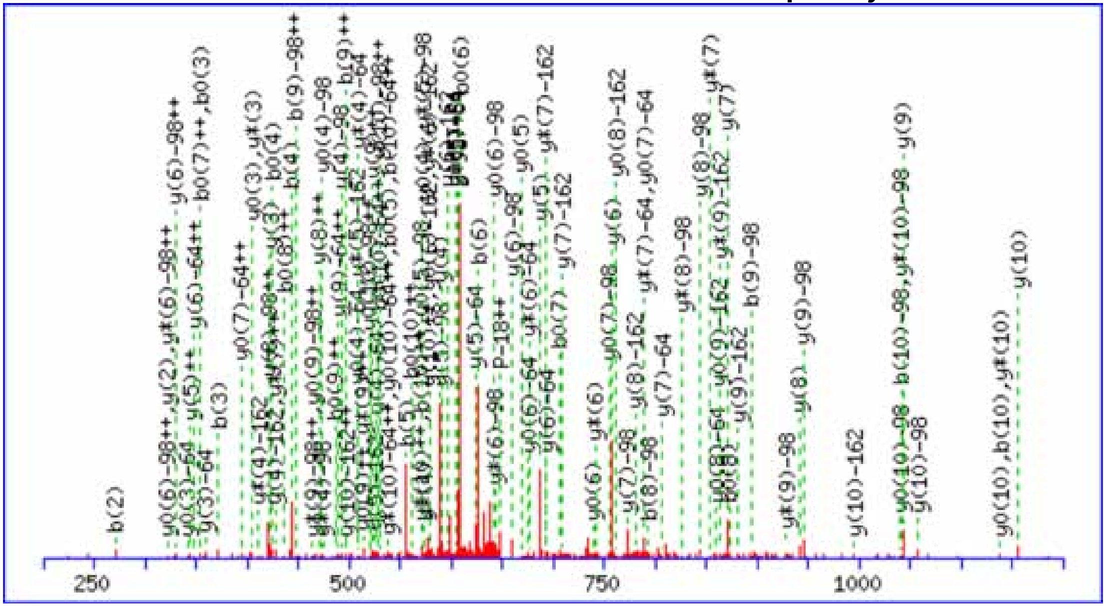
Matched b ions: b(3), b(4), b(5)-98++, b(5)++, b(5)-98, b(5), b(6)-196++, b(6)-196, b(6)-98++, b(6)++, b(6)-98, b(6), b(7)-196++, b(7)-294++, b(7)-98++, b(7)++, b(7)-196, b(7)-98, b(8)-294++, b(8)-98++, b(8)-196++, b(8)++, b(8)-98, b(8), b(8)-294, b(8)-196, b(9)++, b(9)-196++, b(9)-98++, b(9)-294++, b(9)-196, b(10), b(10)-196++, b(10)++, b(10)-98++, b(10)-294++, b(11)-196, b(11)-98, b(11), b(11)++, b(11)-294++, b(11)-196++, b(11)-98++, b(12)-98++, b(12)++, b(12)-294++, b(12)-196++, b(13)-196++, b(13)++, b(13)-98++, b(13)-294++, b(14)++, b(14)-98++, b(14)-294++, b(14)-196++, b(15)-98++, b(15)++, b(15)-196++, b(15)-294++, b(16)++, b(16)-98++, b(16)-196++, b(17)++, b(17)-196++, b(17)-98++, b(18)++, b(18)-294++, b(18)-196++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8)++, y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(13)-98++, y(14)-196++, y(14)-98++, y(15)-294++, y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(16)-294++, y(16)-196++, y(17)-196++, y(17)++, y(17)-294++, y(17)-98++, y(18)++, y(18)-294++, y(18)-98++, y(18)-196++
Precursor origin neutral loss: +

Peptide No.199

EITALAPSTMK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of EITALAPSTMK
Found in ACTS_MOUSE, Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1

Match to Query 1165: 1312.636520 from(657.325536,2+)
Title: Elution from: 34.407 to 34.407 scan no 2689 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1312.6349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K11 : Dimethyl (K)
Ions Score: 43 Expect: 0.0014

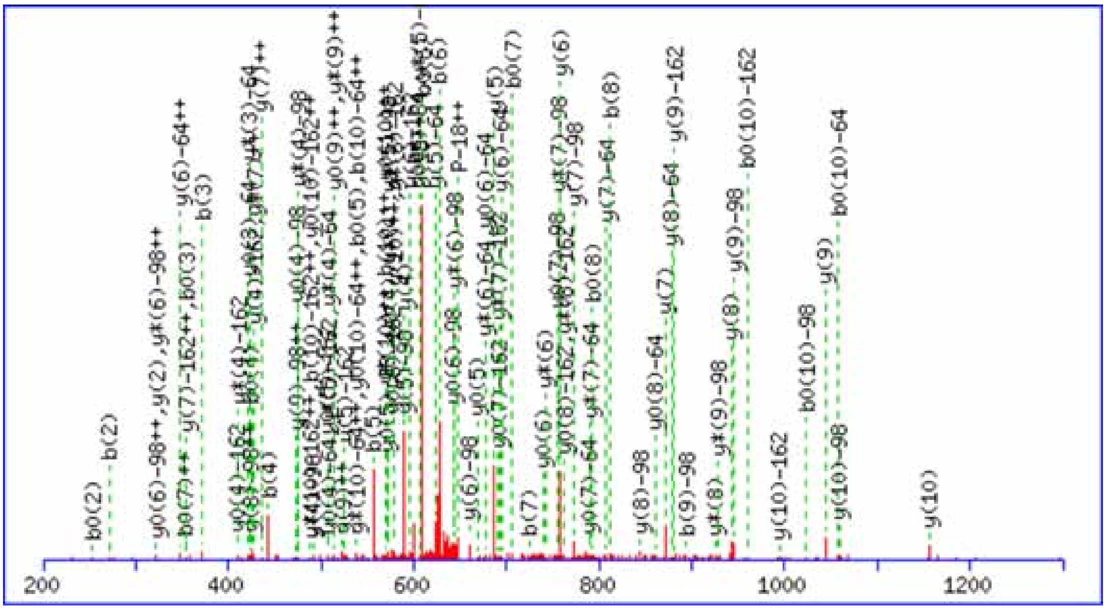
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(8)-98, b(9)-98++, b(9)++, b(9)-98, b(10), b(10)-98, b(10)++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5), y(5)++, y(6), y(6)-98++, y(6)-98, y(7), y(7)-98, y(8)-98++, y(8)-98, y(8), y(8)++, y(9)-98, y(9), y(9)++, y(10), y(10)-98, y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.200

EITALAPSTMK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of EITALAPSTMK
Found in ACTS_MOUSE, Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1

Match to Query 1511: 1312.634954 from(657.324753,2+)
Title: Elution from: 34.324 to 34.324 scan no 2728 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1312.6349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K11 : Dimethyl (K)
Ions Score: 50 Expect: 0.00032

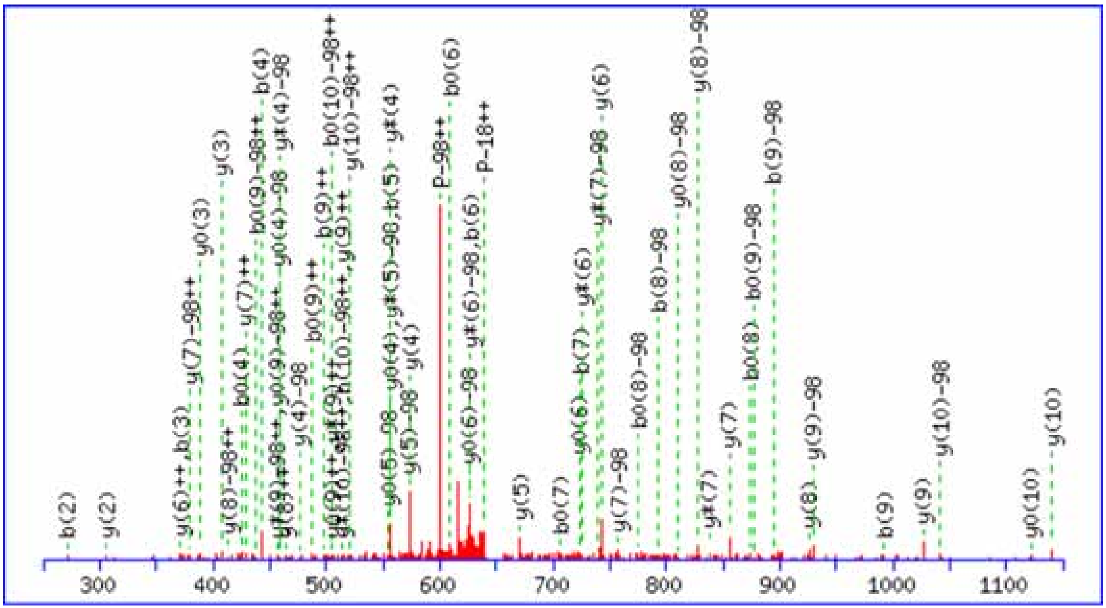
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10)++
Matched y ions: y(2), y(4)-98, y(4), y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(7)++, y(8), y(8)-98, y(8)-98++, y(9), y(9)++, y(9)-98, y(9)-98++, y(10), y(10)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.201

EITALAPSTMK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of EITALAPSTMK
Found in ACTA_MOUSE, Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1

Match to Query 1387: 1296.640212 from(649.327382,2+)
Title: Elution from: 42.720 to 42.720 scan no 3844 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1296.6400
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K11 : Dimethyl (K)
Ions Score: 45 Expect: 0.0011

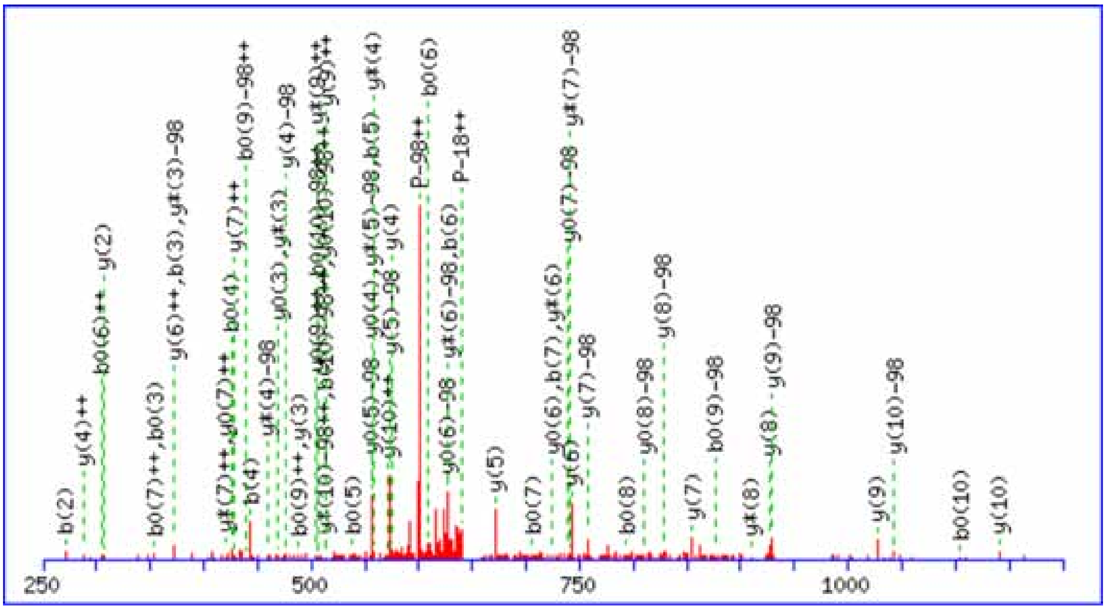
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)-98, b(9), b(9)-98, b(9)++, b(10)-98++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5), y(6), y(6)++, y(7), y(7)-98, y(7)++, y(7)-98++, y(8)-98, y(8), y(8)-98++, y(8)++, y(9)-98, y(9), y(9)++, y(10), y(10)-98, y(10)-98++
Precursor origin neutral loss: +

Peptide No.202

EITALAPSTMK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of EITALAPSTMK
Found in ACTA_MOUSE, Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1

Match to Query 1020: 1296.641112 from(649.327832,2+)
Title: Elution from: 42.848 to 42.848 scan no 3739 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1296.6400
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K11 : Dimethyl (K)
Ions Score: 37 Expect: 0.0071

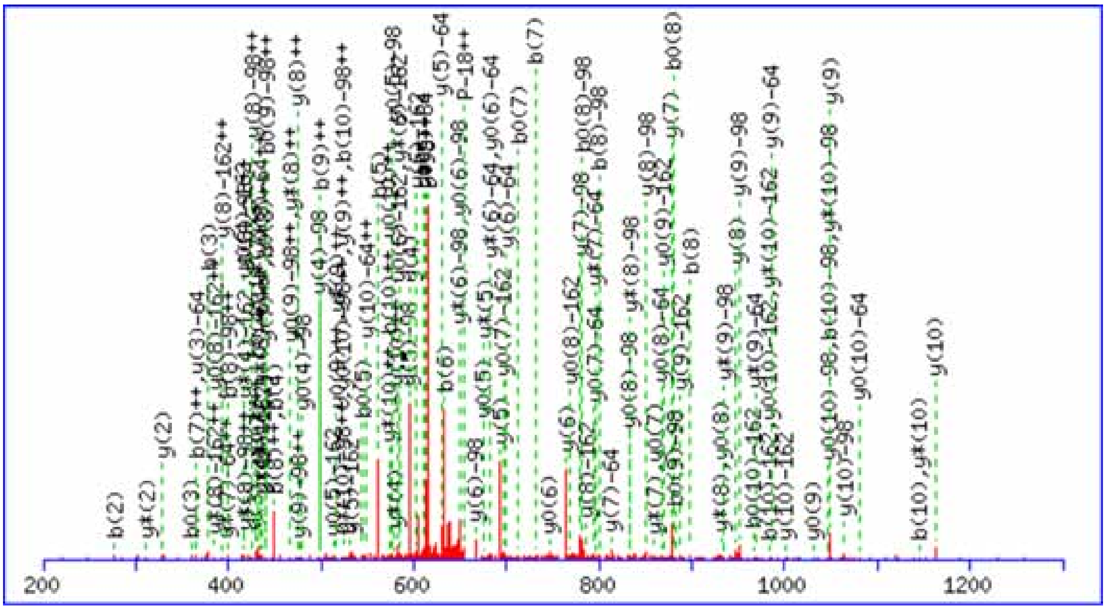
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(10)-98++
Matched y ions: y(2), y(3), y(4)++, y(4)-98, y(4), y(5)-98, y(5), y(6), y(6)++, y(7), y(7)-98, y(7)++, y(8), y(8)-98, y(9)-98, y(9), y(9)++, y(10), y(10)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.203

EITALAPSTMK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of EITALAPSTMK
Found in ACTA_MOUSE, Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1

Match to Query 1091: 1324.699060 from(663.356806,2+)
Title: Elution from: 34.280 to 34.280 scan no 2578 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1324.6985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K11 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 42 Expect: 0.0024

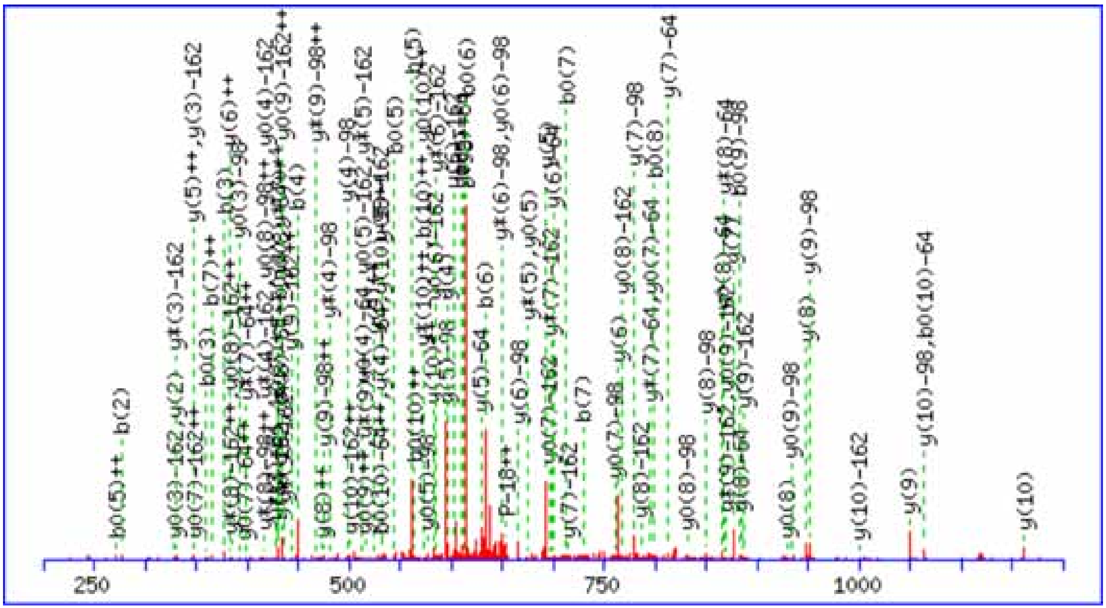
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)++, b(7), b(8)++, b(8)-98++, b(8), b(8)-98, b(9)++, b(10)-98, b(10), b(10)-98++, b(10)++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(7)++, y(8)-98, y(8), y(8)-98++, y(8)++, y(9)-98, y(9), y(9)-98++, y(9)++, y(10), y(10)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.204

EITALAPSTMK
Confirmed sites:
Ambiguous sites: @S:8orT:9

MS/MS Fragmentation of EITALAPSTMK
Found in ACTS_MOUSE, Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1

Match to Query 1197: 1324.699438 from(663.356995,2+)
Title: Elution from: 34.387 to 34.387 scan no 2686 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1324.6985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K11 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 41 Expect: 0.0031

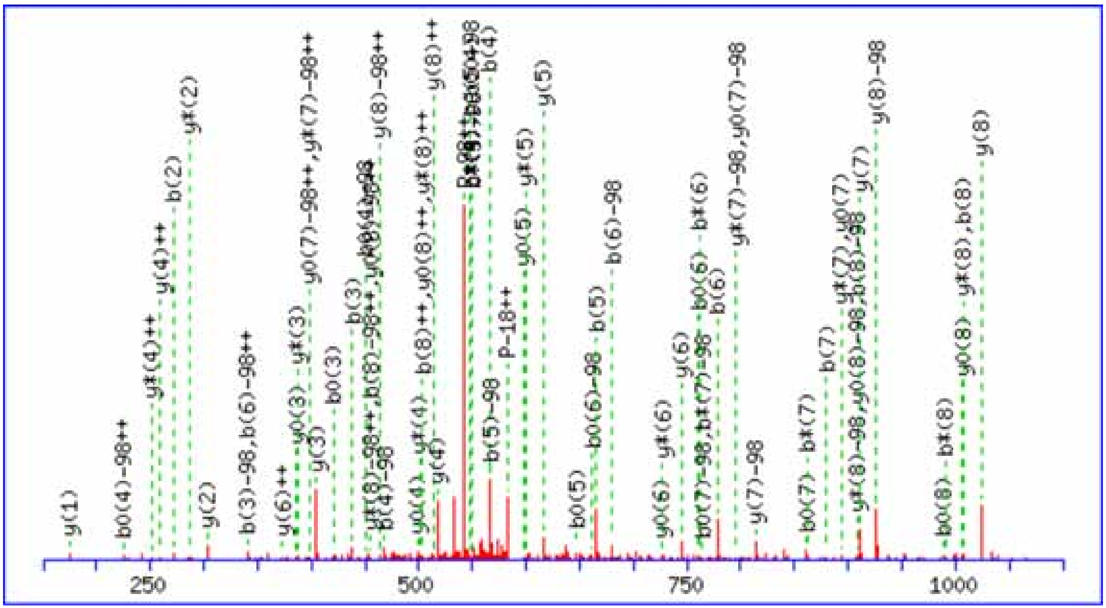
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)++, b(7), b(10)++
Matched y ions: y(2), y(4), y(4)-98, y(5)-98, y(5), y(5)++, y(6), y(6)++, y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(8)++, y(9)-98, y(9), y(9)-98++, y(9)++, y(10), y(10)-98, y(10)++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.205

ELSQVLTQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ELSQVLTQR
Found in CAPZB_MOUSE, F-actin-capping protein subunit beta OS=Mus musculus GN=Capzb PE=1 SV=3

Match to Query 880: 1180.586054 from(591.300303,2+)
Title: Elution from: 42.317 to 42.317 scan no 3780 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1180.5853
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 6.1e-005

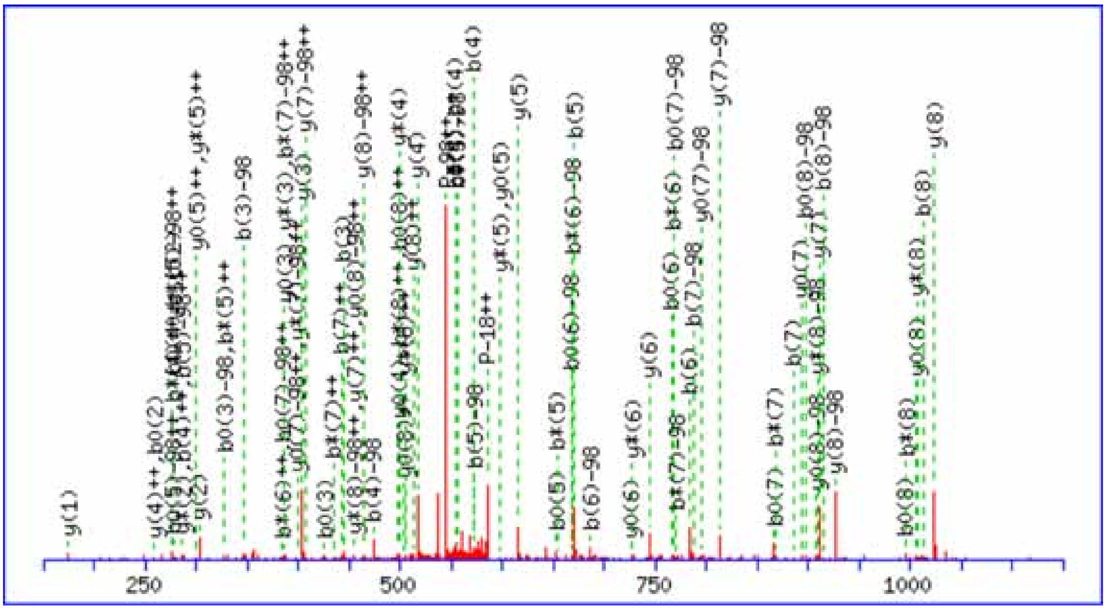
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98++, b(6)-98, b(7), b(8), b(8)-98, b(8)-98++, b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5), y(6), y(6)++, y(7)-98, y(7), y(8)-98, y(8), y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.206

ELSQVLTQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ELSQVLTQR
Found in CAPZB_MOUSE, F-actin-capping protein subunit beta OS=Mus musculus GN=Capzb PE=1 SV=3

Match to Query 998: 1186.617896 from(594.316224,2+)
Title: Elution from: 42.175 to 42.175 scan no 3770 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1186.6171
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 0.00038

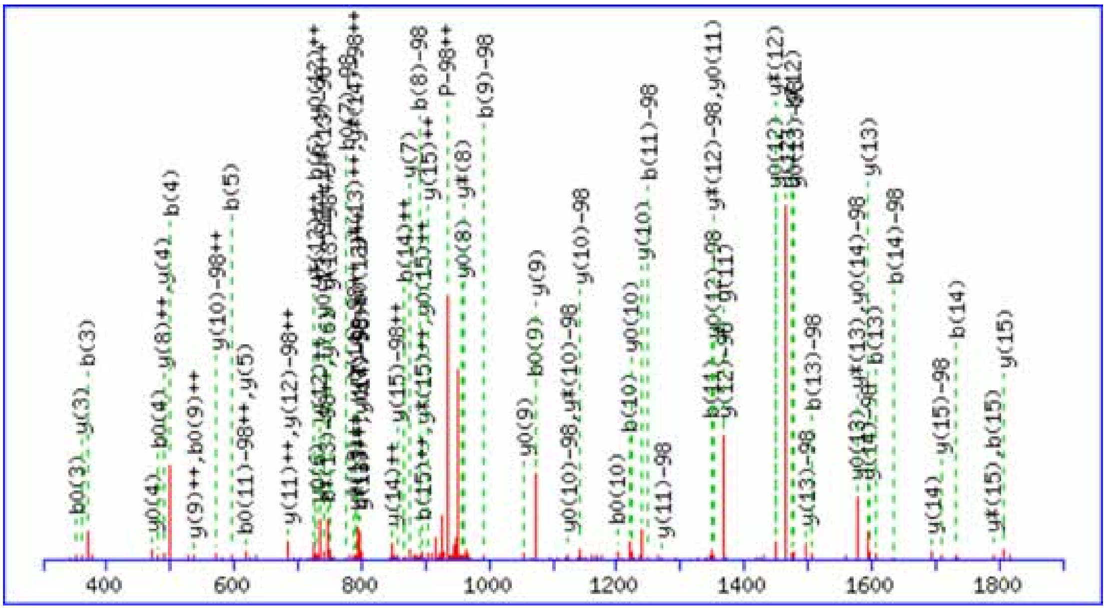
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4)++, b(4), b(5), b(5)-98++, b(5)-98, b(6), b(6)-98, b(7)++, b(7)-98, b(7), b(8), b(8)-98
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5), y(6), y(7)-98, y(7), y(7)++, y(7)-98++, y(8)-98, y(8), y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.207

ELVEPESPTEEQEQGK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ELVEPESPTEEQEQGK
Found in SMTL1_MOUSE, Smoothelin-like protein 1 OS=Mus musculus GN=Smtnl1 PE=1 SV=1

Match to Query 5442: 1963.866434 from(982.940493,2+)
Title: Elution from: 33.723 to 33.723 scan no 2813 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1963.8663
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K16 : Dimethyl (K)
Ions Score: 72 Expect: 3.3e-006

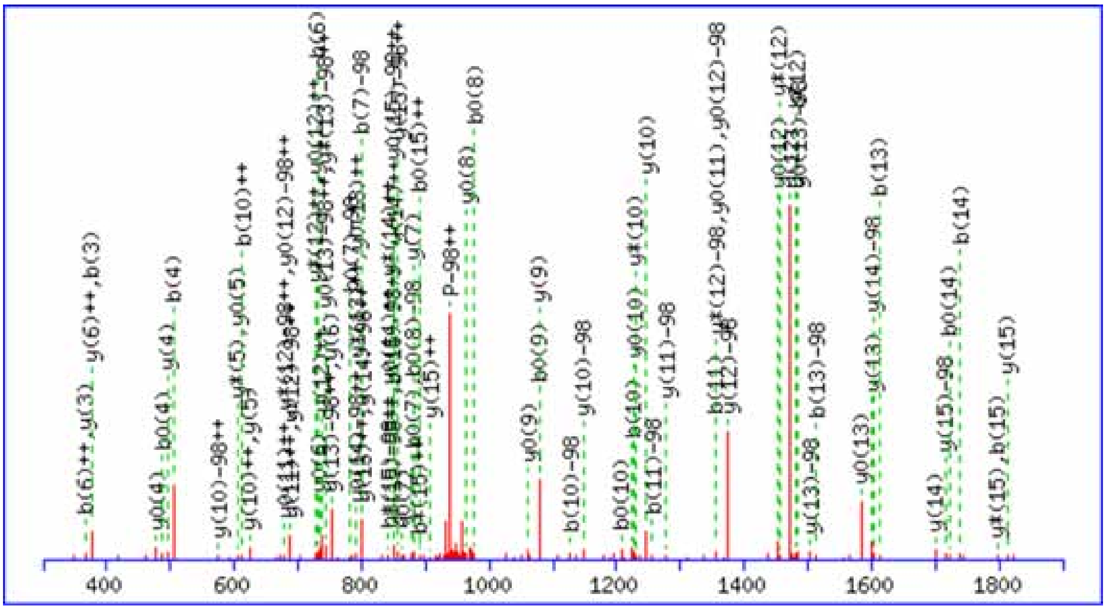
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(8)-98, b(9)-98, b(10), b(11), b(11)-98, b(12), b(13), b(13)-98, b(14), b(14)-98, b(14)++, b(15), b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(9), y(9)++, y(10), y(10)-98++, y(10)-98, y(11)++, y(11)-98, y(11), y(12)++, y(12)-98, y(12), y(12)-98++, y(13), y(13)++, y(13)-98, y(13)-98++, y(14), y(14)-98++, y(14)-98, y(14)++, y(15), y(15)-98, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.208

ELVEPESPTEEQEQGK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ELVEPESPTEEQEQGK
Found in SMTL1_MOUSE, Smoothelin-like protein 1 OS=Mus musculus GN=Smtnl1 PE=1 SV=1

Match to Query 5092: 1975.930366 from(988.972459,2+)
Title: Elution from: 33.630 to 33.630 scan no 2632 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1975.9299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 81 Expect: 4.8e-007

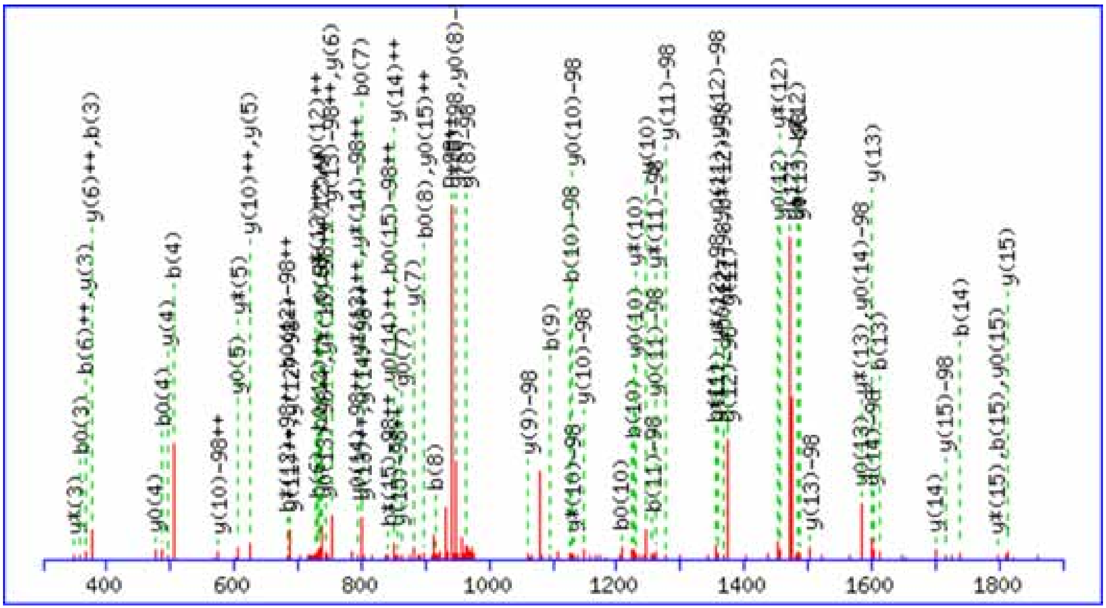
Matched b ions: b(3), b(4), b(6)++, b(6), b(7)-98, b(10), b(10)-98, b(10)++, b(11)-98, b(11), b(12), b(13), b(13)-98, b(14), b(15), b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(9), y(10)++, y(10), y(10)-98++, y(10)-98, y(11)++, y(11)-98, y(12)++, y(12)-98, y(12), y(12)-98++, y(13)-98++, y(13), y(13)++, y(13)-98, y(14), y(14)-98++, y(14)++, y(14)-98, y(15)-98, y(15), y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.209

ELVEPESPTEEQEQGK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of ELVEPESPTEEQEQGK
Found in SMTL1_MOUSE, Smoothelin-like protein 1 OS=Mus musculus GN=Smtnl1 PE=1 SV=1

Match to Query 4886: 1975.930396 from(988.972474,2+)
Title: Elution from: 33.565 to 33.565 scan no 2586 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1975.9299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 80 Expect: 7.1e-007

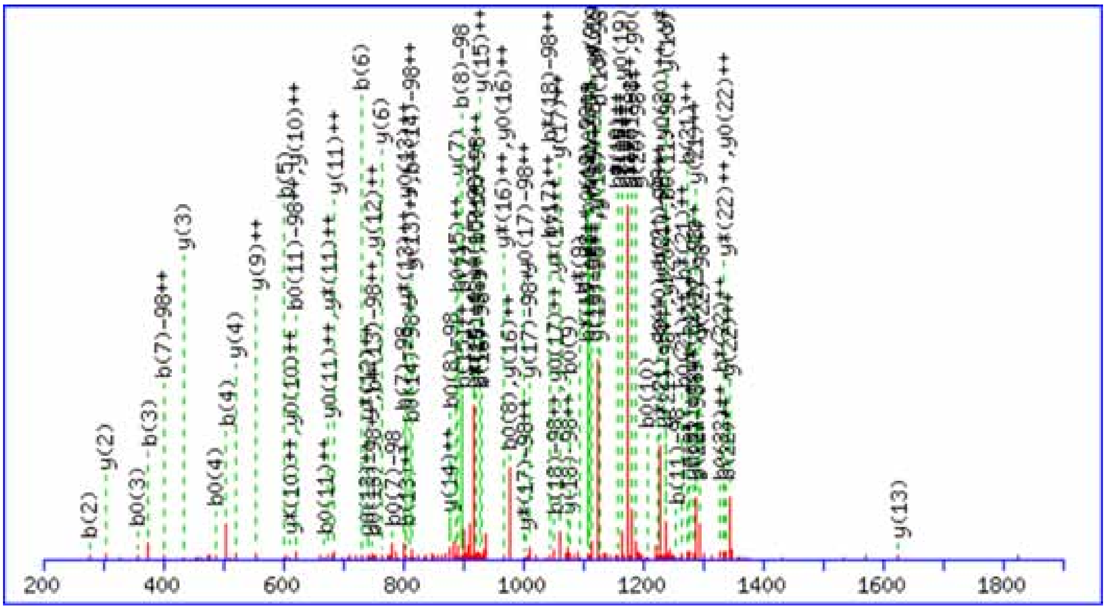
Matched b ions: b(3), b(4), b(6)++, b(6), b(8), b(9), b(10), b(10)-98, b(11)-98, b(11), b(12), b(13), b(14), b(15)
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8)-98, y(9)-98, y(10)++, y(10), y(10)-98++, y(10)-98, y(11)++, y(11), y(11)-98, y(12)++, y(12)-98, y(12), y(12)-98++, y(13)-98++, y(13)++, y(13), y(13)-98, y(14), y(14)-98++, y(14)-98, y(14)++, y(15), y(15)-98, y(15)-98++
Precursor origin neutral loss: +

Peptide No.210

ELVEPESPTEEQEQGKENESEER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ELVEPESPTEEQEQGKENESEER
Found in SMTL1_MOUSE, Smoothelin-like protein 1 OS=Mus musculus GN=Smtnl1 PE=1 SV=1

Match to Query 7379: 2849.277885 from(950.766571,3+)
Title: Elution from: 32.632 to 32.632 scan no 2495 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2849.2763
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 61 Expect: 7.1e-005

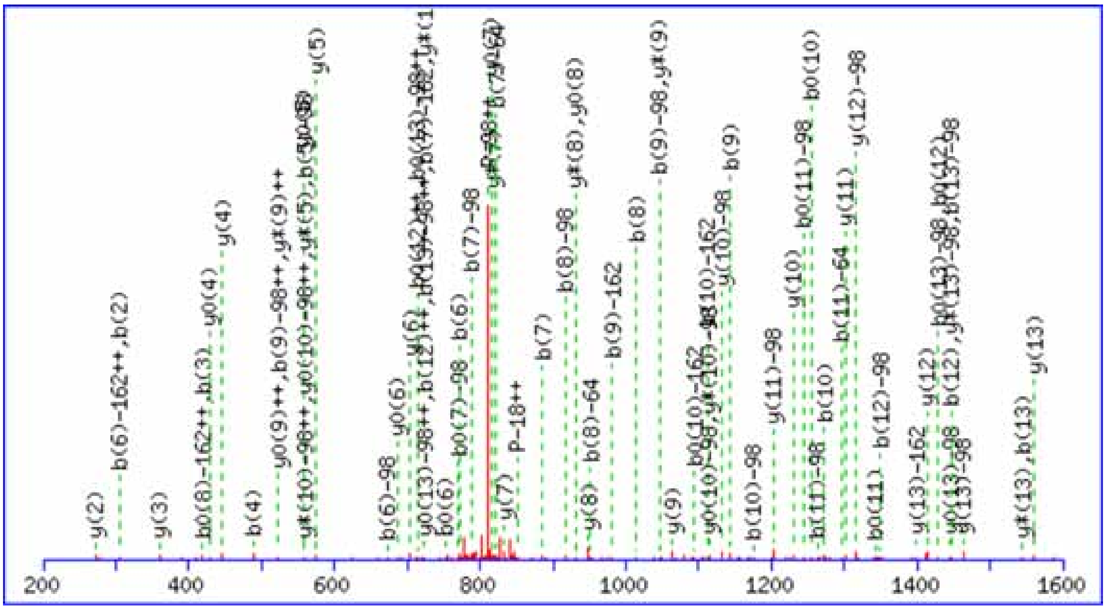
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)-98, b(7)-98++, b(7), b(8)-98, b(10)-98, b(10), b(11)-98, b(13)++, b(15)++, b(16)-98++, b(17)++, b(18)-98++, b(19)-98++, b(19)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)++, y(13), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(22)-98++
Precursor origin neutral loss: +

Peptide No.211

EMLASDDEEESSPK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of EMLASDDEEESSPK
Found in NEXN_MOUSE, Nexilin OS=Mus musculus GN=Nexn PE=1 SV=2

Match to Query 3846: 1717.664984 from(859.839768,2+)
Title: Elution from: 27.111 to 27.111 scan no 1909 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1717.6641
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
Ions Score: 83 Expect: 1.2e-007

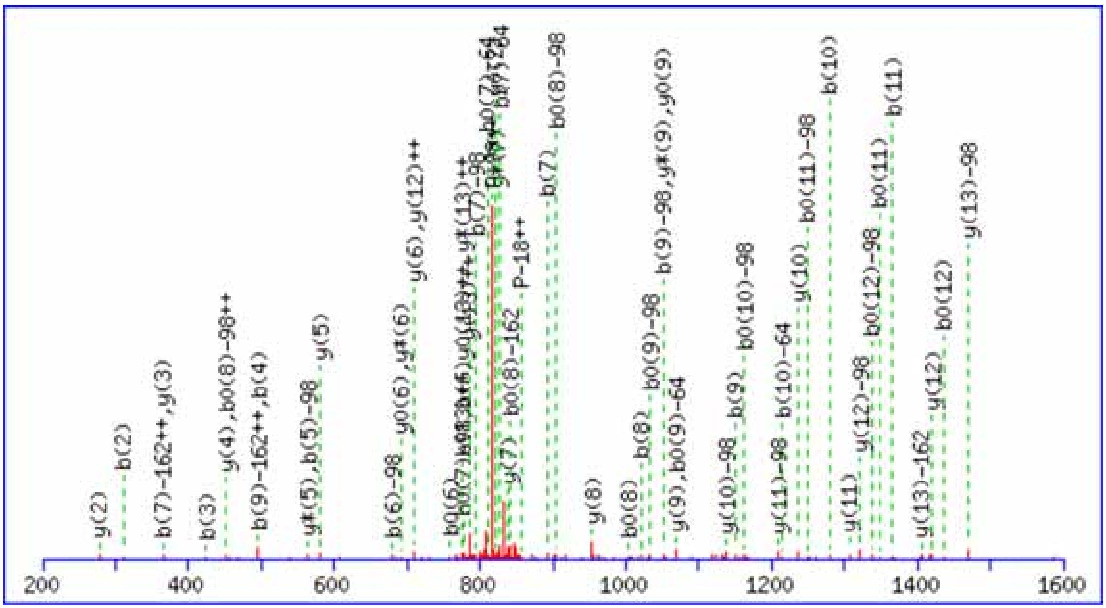
Matched b ions: b(2), b(3), b(4), b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(9), b(9)-98++, b(9)-98, b(10), b(10)-98, b(11)-98, b(12), b(12)-98, b(12)++, b(13), b(13)-98, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)-98, y(11), y(12)-98, y(12), y(13)-98, y(13)
Precursor origin neutral loss: +

Peptide No.212

EMLASDDEEESSPK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of EMLASDDEEESSPK
Found in NEXN_MOUSE, Nexilin OS=Mus musculus GN=Nexn PE=1 SV=2

Match to Query 2907: 1729.727946 from(865.871249,2+)
Title: Elution from: 26.713 to 26.713 scan no 1677 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1729.7277
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 94 Expect: 1.1e-008

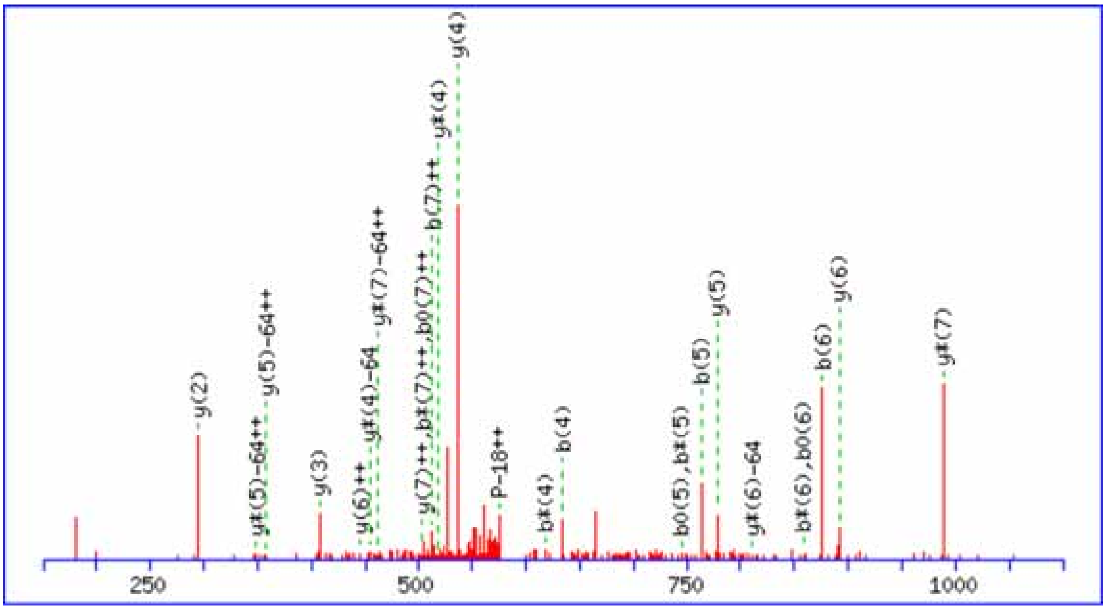
Matched b ions: b(2), b(3), b(4), b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(8), b(9)-98, b(9), b(10), b(11), b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)-98, y(11), y(12)++, y(12)-98, y(12), y(13)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.213

ENLYQLMK
Confirmed sites: @Y:4
Ambiguous sites:

MS/MS Fragmentation of ENLYQLMK
Found in MAK_MOUSE, Serine/threonine-protein kinase MAK OS=Mus musculus GN=Mak PE=2 SV=1

Match to Query 686: 1167.546936 from(584.780744,2+)
Title: Elution from: 44.233 to 44.233 scan no 3896 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1167.5459
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y4 : Phospho (Y)
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 30 **Expect:** 0.023

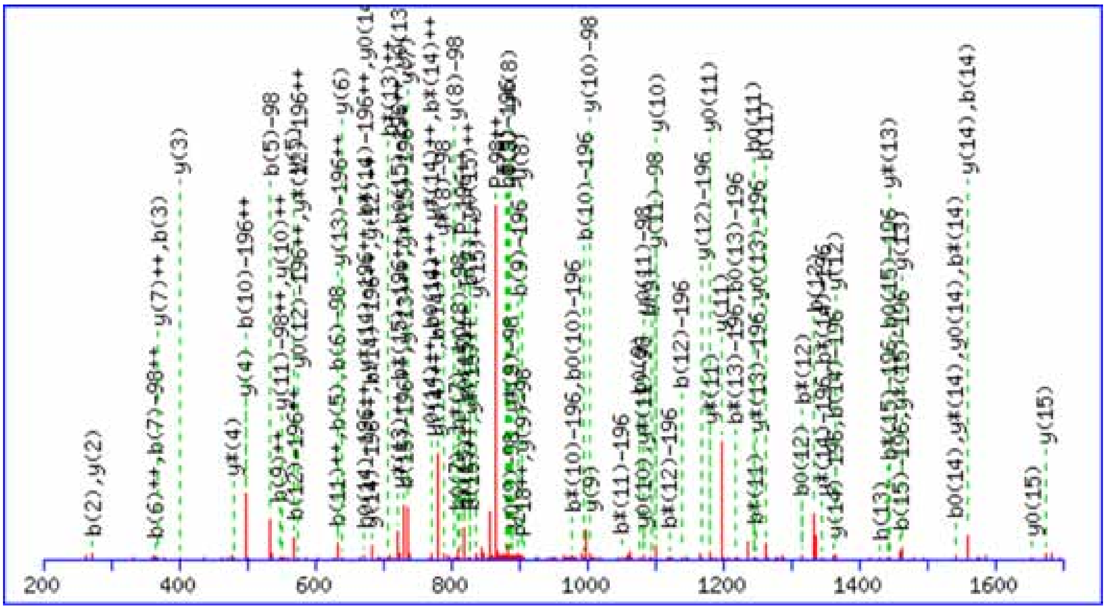
Matched b ions: b(4), b(5), b(6), b(7)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)++
Precursor origin neutral loss: +

Peptide No.214

ENPPSPPTSPAAPQPR
Confirmed sites: @S:5,@S:9
Ambiguous sites:

MS/MS Fragmentation of ENPPSPPTSPAAPQPR
Found in SFR1_MOUSE, Swi5-dependent recombination DNA repair protein 1 homolog OS=Mus musculus GN=Meir5 PE=1 SV=2

Match to Query 4546: 1829.775230 from(915.894891,2+)
Title: Elution from: 33.506 to 33.506 scan no 2783 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1829.7750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 Expect: 1.6e-005

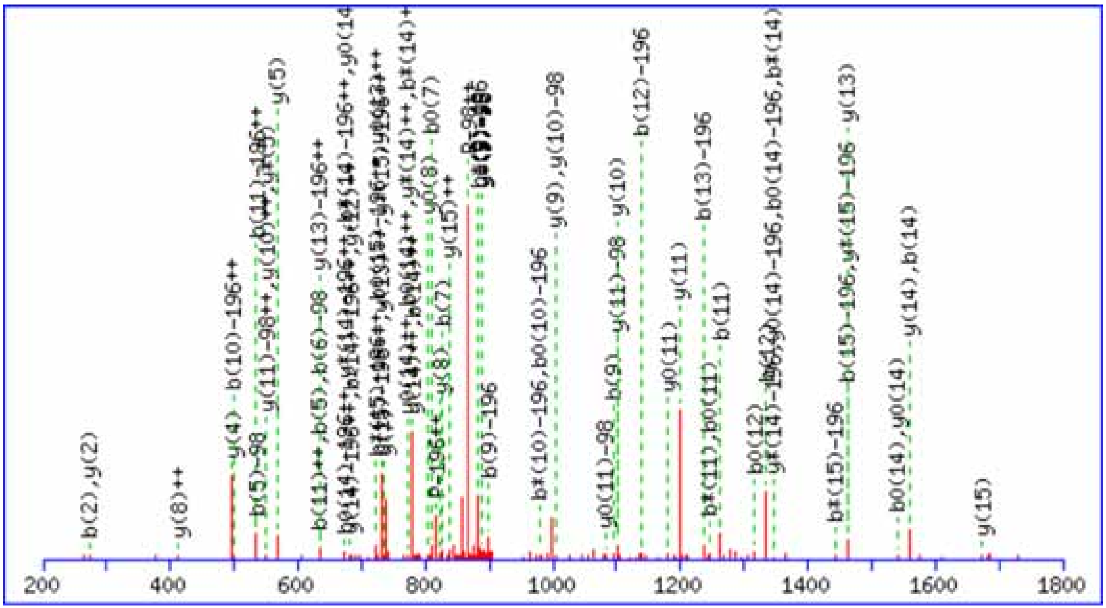
Matched b ions: b(2), b(3), b(5)-98, b(5), b(6)-98, b(6)++, b(7)-98++, b(7), b(9)-98, b(9)-98++, b(9), b(9)-196, b(9)++, b(10)-196++, b(10)-98, b(10)-98++, b(10)-196, b(11)++, b(11), b(11)-98, b(12), b(12)-98, b(12)-196++, b(12)-196, b(13)-98, b(13), b(14)-98++, b(14)++, b(14)-98, b(14), b(14)-196, b(14)-196++, b(15)-196++, b(15)-98++, b(15)-196, b(15)-98, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)-98, y(8), y(9), y(9)-98, y(10), y(10)++, y(10)-98, y(11)-98, y(11), y(11)-98++, y(12)-98++, y(12), y(12)++, y(12)-196, y(12)-98, y(13)++, y(13), y(13)-196++, y(13)-98, y(13)-98++, y(14)-98++, y(14)++, y(14)-98, y(14), y(14)-196, y(14)-196++, y(15), y(15)-98, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.215

ENPPSPPTSPAAPQPR
Confirmed sites: @S:5,@T:8
Ambiguous sites:

MS/MS Fragmentation of ENPPSPPTSPAAPQPR
Found in SFR1_MOUSE, Swi5-dependent recombination DNA repair protein 1 homolog OS=Mus musculus GN=Meir5 PE=1 SV=2

Match to Query 4547: 1829.775566 from(915.895059,2+)
Title: Elution from: 33.163 to 33.163 scan no 2736 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1829.7750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0079

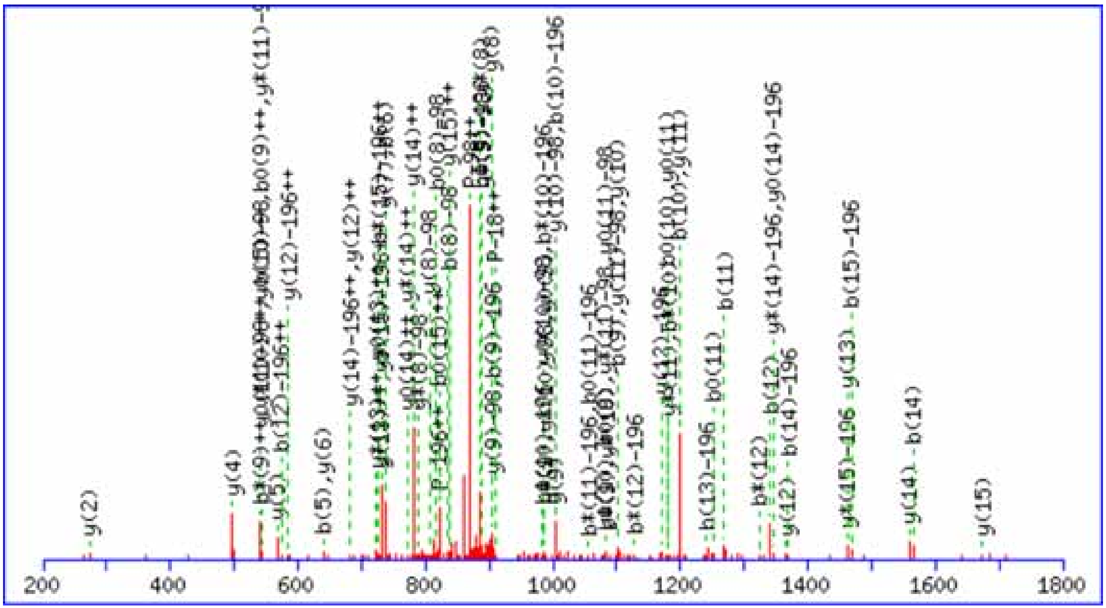
Matched b ions: b(2), b(5)-98, b(5), b(6)-98, b(7), b(9)-98, b(9)-196, b(9), b(10)-196++, b(11), b(11)-196++, b(11)++, b(11)-98, b(12), b(12)-196, b(12)-98, b(13)-98, b(13)-196, b(14)-98++, b(14)++, b(14), b(14)-98, b(14)-196++, b(15)-196++, b(15)-98++, b(15)-98, b(15)-196
Matched y ions: y(2), y(4), y(5), y(7), y(8)++, y(8), y(9), y(10)++, y(10)-98, y(10), y(11)-98, y(11), y(11)-98++, y(12)-98++, y(12)-98, y(12)++, y(13)++, y(13), y(13)-196++, y(13)-98, y(13)-98++, y(14)-98++, y(14)++, y(14)-98, y(14), y(14)-196++, y(15)-98, y(15), y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.216

ENPPSPPTSPAAPQPR
Confirmed sites: @S:5,@S:9
Ambiguous sites:

MS/MS Fragmentation of ENPPSPPTSPAAPQPR
Found in SFR1_MOUSE, Swi5-dependent recombination DNA repair protein 1 homolog OS=Mus musculus GN=Meir5 PE=1 SV=2

Match to Query 3252: 1835.808502 from(918.911527,2+)
Title: Elution from: 32.902 to 32.902 scan no 2392 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1835.8068
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 78 Expect: 6.8e-007

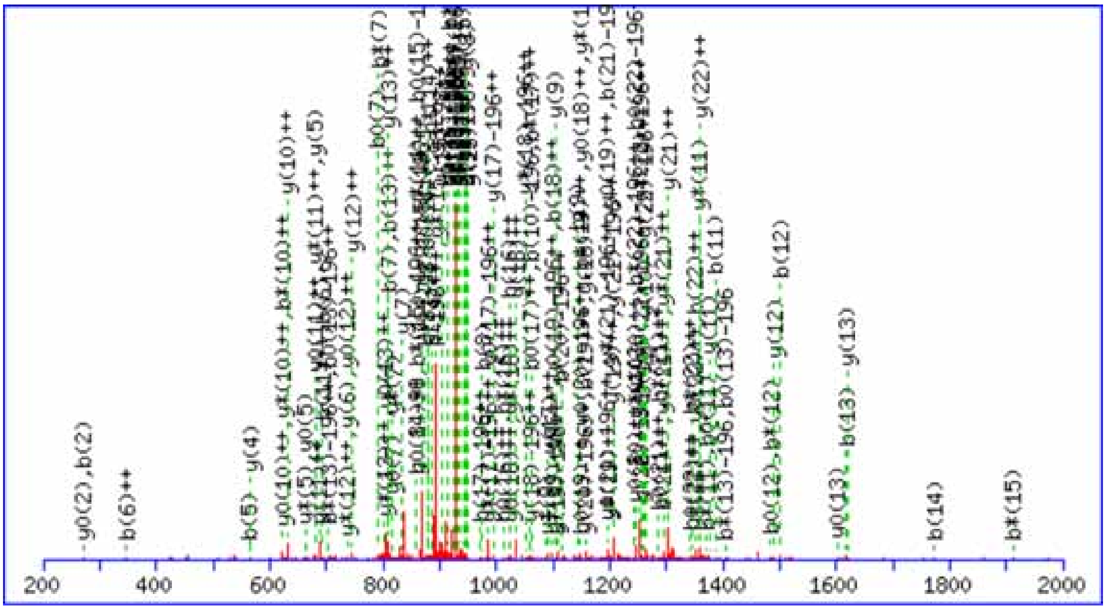
Matched b ions: b(5)-98, b(5), b(6), b(8)-98, b(9)-98, b(9), b(9)-196, b(10)-196, b(10)-98, b(10), b(11), b(11)-98++, b(11)-98, b(12), b(12)-98, b(12)-196++, b(13)-98, b(13)-196, b(14), b(14)-98, b(14)-196, b(15)-98, b(15)-196
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-98, y(10), y(11)-98, y(11), y(12), y(12)-196++, y(12)-98, y(12)-196, y(12)++, y(13)++, y(13), y(13)-98++, y(14)-98++, y(14)++, y(14)-98, y(14), y(14)-196++, y(15), y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.217

ENPPVEDSSDEDDKRNPGNLYDK
Confirmed sites: @S:8,@S:9
Ambiguous sites:

MS/MS Fragmentation of ENPPVEDSSDEDDKRNPGNLYDK
Found in STT3B_MOUSE, Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Mus musculus GN=Stt3b PE=1 SV=2

Match to Query 6759: 2876.183904 from(959.735244,3+)
Title: Elution from: 35.182 to 35.182 scan no 2701 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2876.1790
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
K23 : Dimethyl (K)
Ions Score: 34 Expect: 0.024

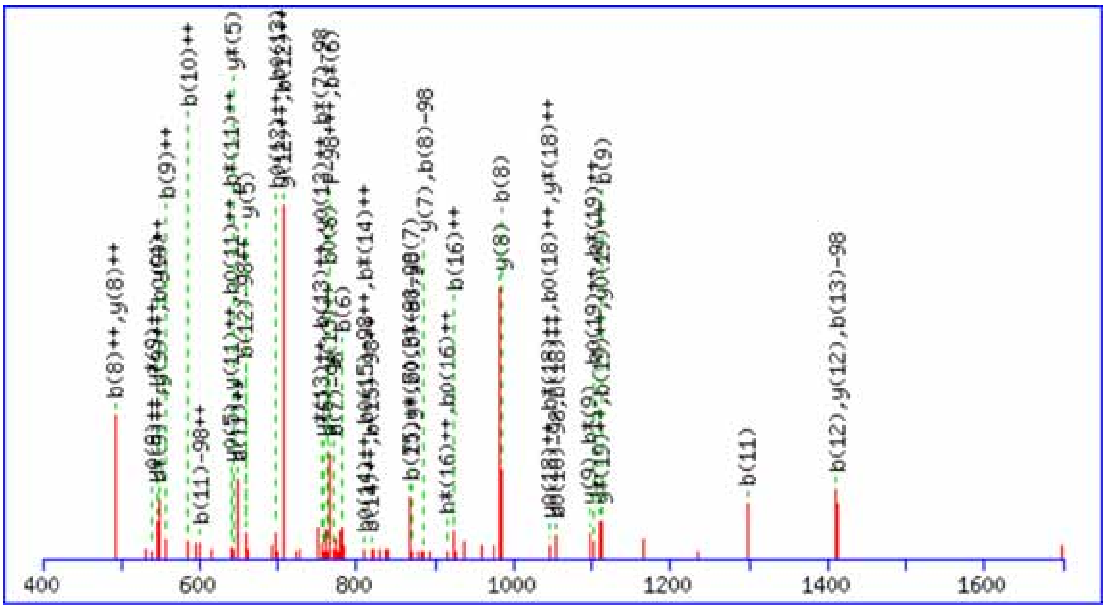
Matched b ions: b(2), b(5), b(6)++, b(6), b(7), b(8)-98, b(8), b(9)-196, b(9), b(10)-196, b(10)-98, b(10), b(11), b(11)++, b(12), b(12)-98, b(12)-98++, b(13), b(13)-98, b(13)++, b(14), b(14)-98++, b(14)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-196++, b(16)-98++, b(17)-98++, b(17)-196++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)-196++, b(21)-98++, b(21)-196++, b(21)++, b(22)-98++, b(22)-196++, b(22)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13)++, y(13), y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(16)-196++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(18)-98++, y(18)-196++, y(19)-98++, y(19)-196++, y(19)++, y(20)-196++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(21)-196++, y(22)++, y(22)-98++, y(22)-196++
Precursor origin neutral loss: +

Peptide No.218

EQEGTESDEGQLPQVLEELK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of EQEGTESDEGQLPQVLEELK
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 7274: 2393.091591 from(798.704473,3+)
Title: Elution from: 64.600 to 64.600 scan no 6306 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2393.0887
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl (K)
Ions Score: 64 Expect: 2.8e-005

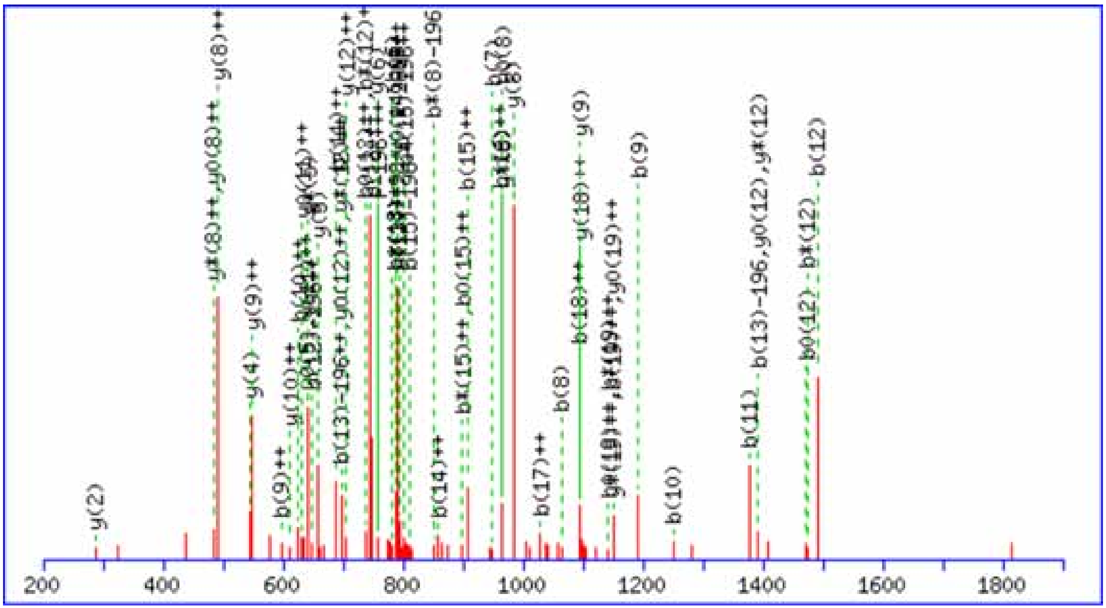
Matched b ions: b(6), b(7), b(7)-98, b(8)++, b(8), b(8)-98, b(9), b(9)++, b(10)++, b(11)++, b(11), b(11)-98++, b(12)++, b(12), b(12)-98++, b(13)-98++, b(13)-98, b(13)++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(18)++, b(19)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(11)++, y(12)++, y(12), y(13)++
Precursor origin neutral loss: +

Peptide No.219

EQEGTESDEGQLPQVLEELK
Confirmed sites: @T:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of EQEGTESDEGQLPQVLEELK
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6511: 2473.058322 from(825.360050,3+)
Title: Elution from: 71.009 to 71.009 scan no 6600 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2473.0550
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl (K)
Ions Score: 60 Expect: 5.5e-005

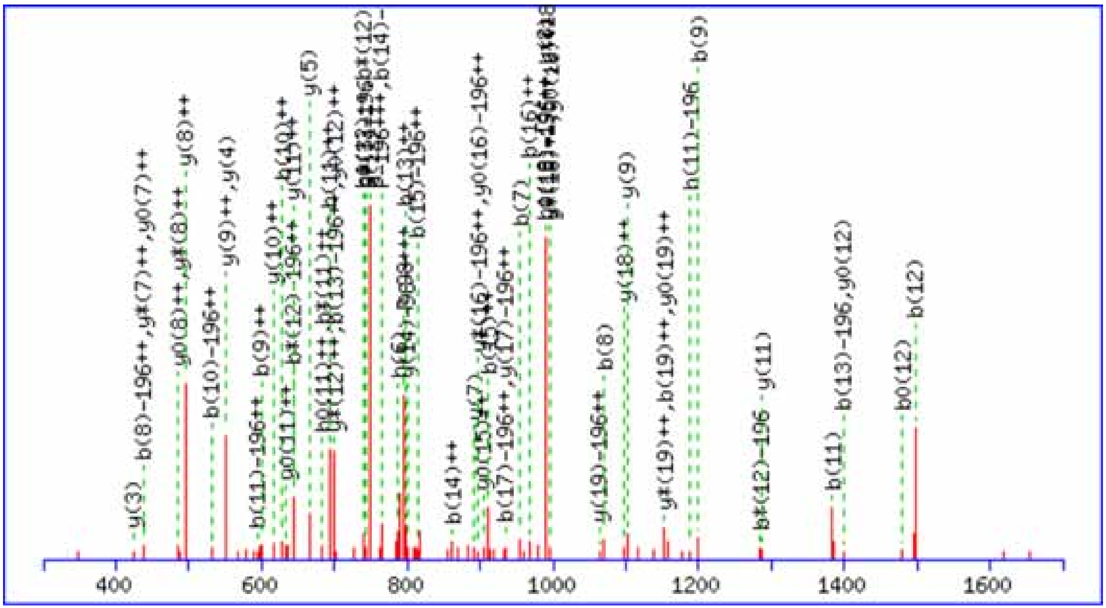
Matched b ions: b(6), b(7), b(7)-98, b(8)-98++, b(8), b(8)-98, b(9), b(9)-98, b(9)++, b(10), b(10)-98++, b(10)++, b(11)-98++, b(11), b(11)++, b(11)-98, b(12)++, b(12)-98, b(12), b(12)-98++, b(12)-196++, b(13)-98++, b(13)-196, b(13)-98, b(13)++, b(13)-196++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(17)++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(8)++, y(8), y(9), y(9)++, y(10)++, y(11)++, y(12)++, y(18)++
Precursor origin neutral loss: +

Peptide No.220

EQEGTESDEGQLPQVLEELK
Confirmed sites: @T:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of EQEGTESDEGQLPQVLEELK
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6696: 2485.121829 from(829.381219,3+)
Title: Elution from: 71.162 to 71.162 scan no 6591 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2485.1186
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 49 Expect: 0.0011

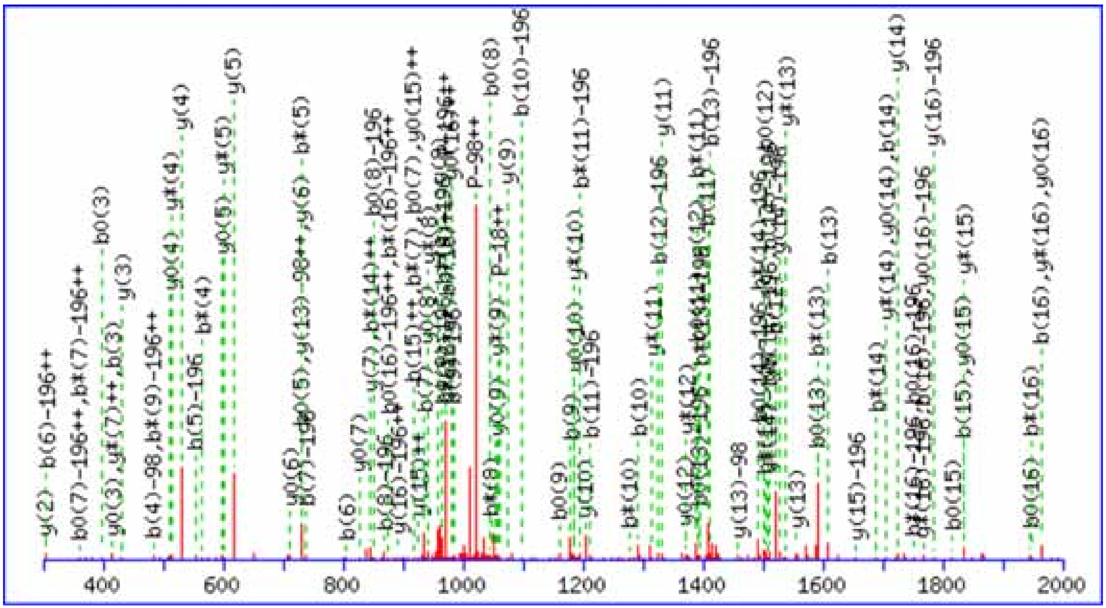
Matched b ions: b(6), b(7), b(8)-196++, b(8), b(8)-98++, b(9)-98++, b(9), b(9)++, b(10)-98, b(10)-196++, b(10)++, b(11)++, b(11), b(11)-98++, b(11)-98, b(11)-196, b(11)-196++, b(12)++, b(12), b(12)-98++, b(12)-98, b(13)-98++, b(13)-98, b(13)-196++, b(13)-196, b(13)++, b(14)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-98++, b(17)-196++, b(19)++, b(19)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(11)++, y(11), y(14)-98++, y(16)-98++, y(17)-196++, y(18)++, y(19)-196++
Precursor origin neutral loss: +

Peptide No.221

EQESSGEEDNDLSPEER
Confirmed sites: @S:4,@S:5
Ambiguous sites:

MS/MS Fragmentation of EQESSGEEDNDLSPEER
Found in IPP2_MOUSE, Protein phosphatase inhibitor 2 OS=Mus musculus GN=Ppp1r2 PE=1 SV=3

Match to Query 6993: 2136.741574 from(1069.378063,2+)
Title: Elution from: 33.030 to 33.030 scan no 2643 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2136.7409
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 **Expect:** 3.7e-006

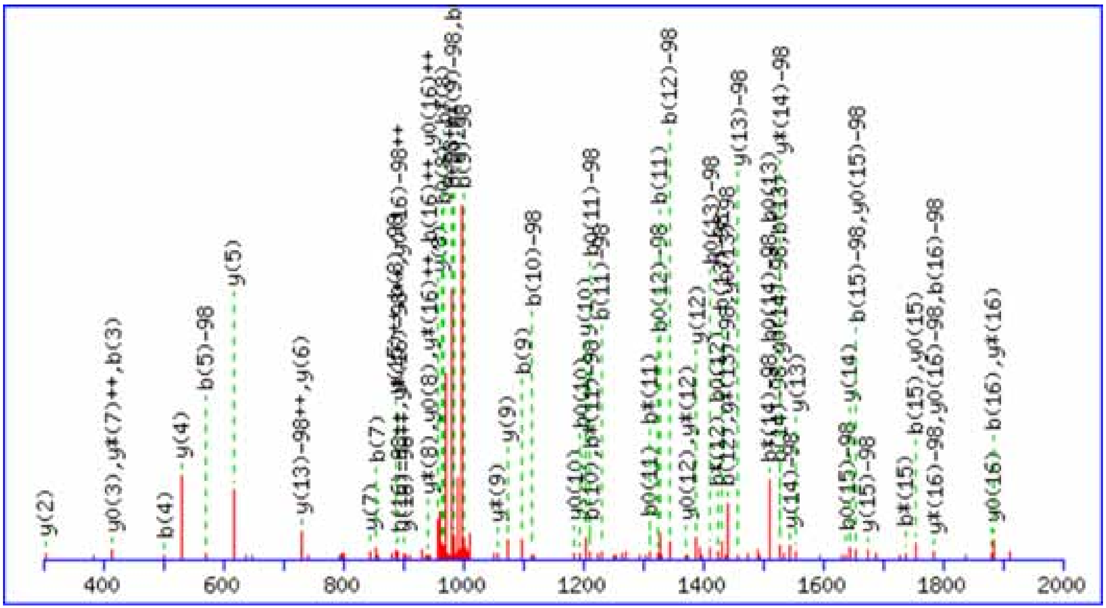
Matched b ions: b(3), b(4)-98, b(5)-98, b(5)-196, b(6)-98, b(6)-196++, b(6), b(7)-98, b(7)-196, b(7), b(8)-98++, b(8)-196, b(8)-98, b(9), b(9)-98, b(9)-196, b(10), b(10)-98, b(10)-196, b(11), b(11)-98, b(11)-196, b(12), b(12)-98++, b(12)-98, b(12)-196, b(13), b(13)-196, b(13)-98, b(14)-98, b(14), b(14)-196, b(15), b(15)-98, b(15)-98++, b(15)++, b(16), b(16)-98, b(16)-196, b(16)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)-98++, y(13)-98, y(13), y(14), y(14)-98, y(14)-196, y(15)-196, y(15)++, y(16)-196++, y(16)-196, y(16)-98++
Precursor origin neutral loss: +

Peptide No.222

EQESSGEEDNDLSPEER
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of EQESSGEEDNDLSPEER
Found in IPP2_MOUSE, Protein phosphatase inhibitor 2 OS=Mus musculus GN=Ppp1r2 PE=1 SV=3

Match to Query 5914: 2056.775892 from(1029.395222,2+)
Title: Elution from: 29.927 to 29.927 scan no 2295 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2056.7746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 1.3e-006

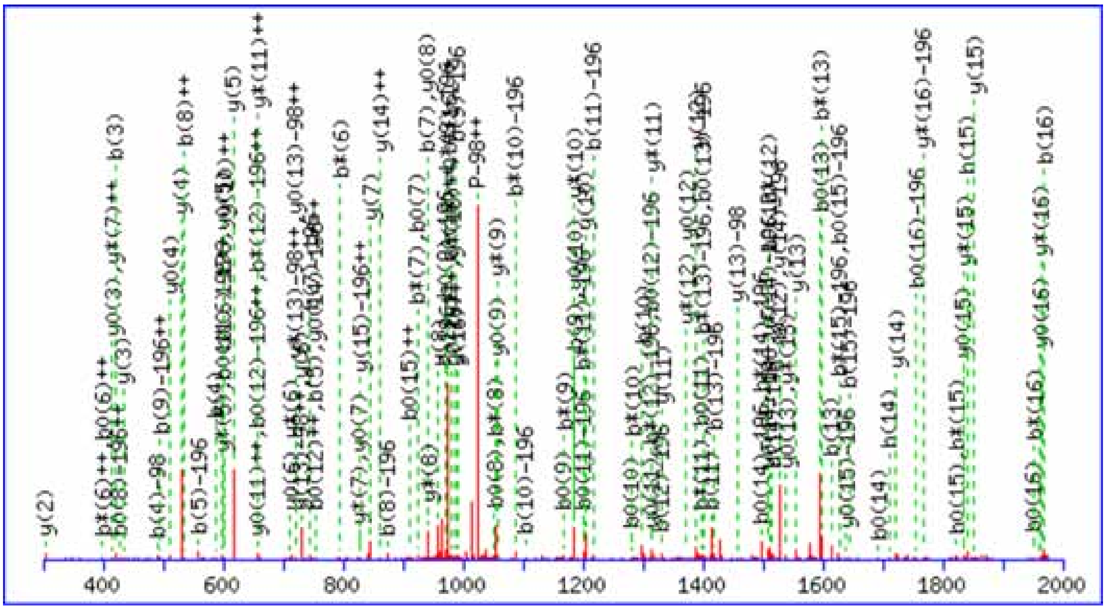
Matched b ions: b(3), b(4), b(5)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(13)-98, b(13), b(14)-98, b(15), b(15)-98, b(16), b(16)-98, b(16)-98++, b(16)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12), y(13)-98++, y(13), y(13)-98, y(14), y(14)-98, y(15)++, y(15)-98, y(16)-98++
Precursor origin neutral loss: +

Peptide No.223

EQESSGEEDNDLSPEER
Confirmed sites: @S:4,@S:5
Ambiguous sites:

MS/MS Fragmentation of EQESSGEEDNDLSPEER
Found in IPP2_MOUSE, Protein phosphatase inhibitor 2 OS=Mus musculus GN=Ppp1r2 PE=1 SV=3

Match to Query 5533: 2142.773024 from(1072.393788,2+)
Title: Elution from: 33.175 to 33.175 scan no 2532 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2142.7727
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 68 Expect: 2.1e-006

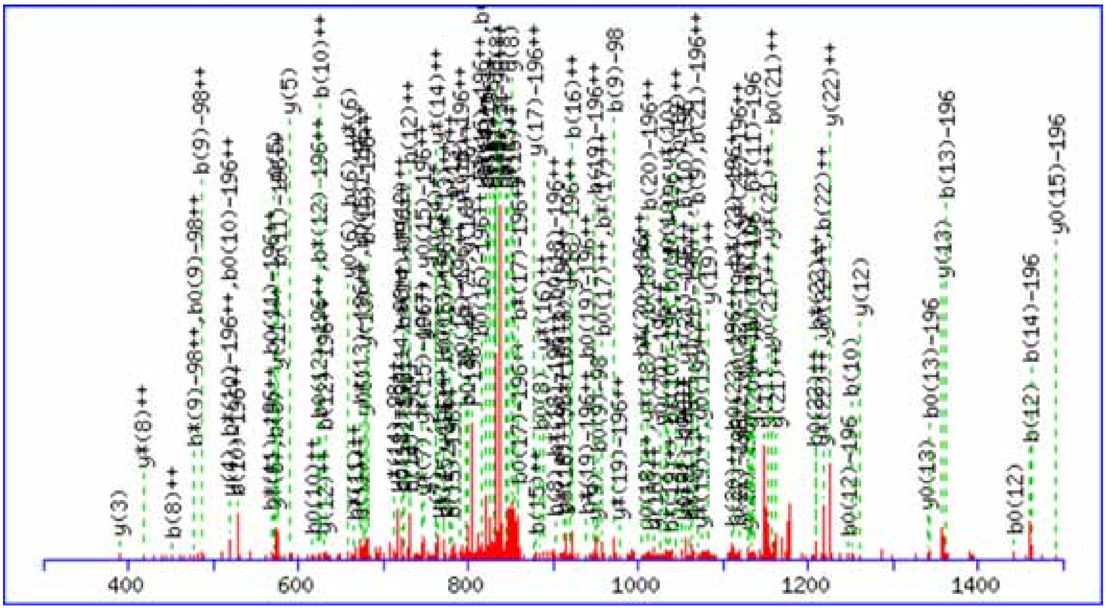
Matched b ions: b(3), b(4)-98, b(4), b(5)-196, b(5)-98, b(5), b(6)-98, b(7)-98++, b(7)-98, b(7)-196, b(7), b(8)-196, b(8)-98, b(8)++, b(9), b(9)-98, b(9)-196++, b(9)-196, b(10), b(10)-98, b(10)-196, b(11), b(11)-98, b(11)-98++, b(11)-196, b(12)-98, b(12), b(12)-196, b(13), b(13)-196, b(13)-98, b(14)-98, b(14), b(14)-196, b(15), b(15)-98, b(15)-196, b(16), b(16)-98, b(16)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(10)++, y(11), y(12), y(13)-98++, y(13), y(13)-98, y(14), y(14)-196, y(14)-98, y(14)++, y(15)-196++, y(15), y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.224

EQGTESRSSTPLPTVSSSAENTR
Confirmed sites: @S:9,@T:10
Ambiguous sites:

MS/MS Fragmentation of EQGTESRSSTPLPTVSSSAENTR
Found in LAP2A_MOUSE, Lamina-associated polypeptide 2, isoforms alpha/zeta OS=Mus musculus GN=Tmpo PE=1 SV=3

Match to Query 6661: 2608.110933 from(870.377587,3+)
Title: Elution from: 32.683 to 32.683 scan no 2464 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2608.1055
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.025

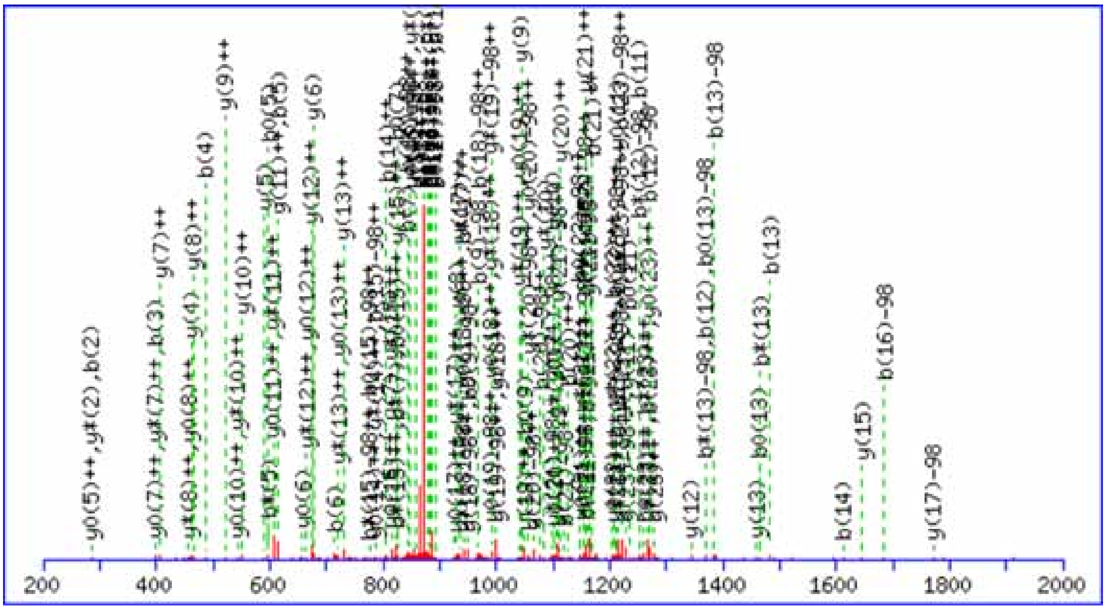
Matched b ions: b(5), b(6), b(7), b(8)++, b(8), b(9)-98++, b(9)-98, b(9), b(10)-196++, b(10)-196, b(10)-98++, b(10)-98, b(10)++, b(10), b(11)-196++, b(11)++, b(11)-98++, b(11)-98, b(12)-98++, b(12), b(12)++, b(12)-98, b(12)-196++, b(13)-98, b(13)-98++, b(13)-196++, b(13)-196, b(13)++, b(14)-196++, b(14)-196, b(14)-98++, b(14)++, b(15)-196++, b(15)-98++, b(15)++, b(16)++, b(16)-196++, b(17)-98++, b(18)-196++, b(18)++, b(19)-196++, b(19)-98++, b(19)++, b(20)-196++, b(20)-98++, b(20)++, b(21)-196++, b(22)++, b(22)-98++, b(22)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)++, y(12), y(13), y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-196++, y(17)-196++, y(18)++, y(18)-98++, y(18)-196++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)-196++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(22)-196++
Precursor origin neutral loss: +

Peptide No.225

EQLSEVEGSGEDDQGDDHSESAQK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EQLSEVEGSGEDDQGDDHSESAQK
Found in UBP4_MOUSE, Ubiquitin carboxyl-terminal hydrolase 4 OS=Mus musculus GN=Usp4 PE=1 SV=2

Match to Query 8161: 2711.072922 from(904.698250,3+)
Title: Elution from: 29.476 to 29.476 scan no 2233 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2711.0719
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K24 : Dimethyl (K)
Ions Score: 108 Expect: 7.5e-010

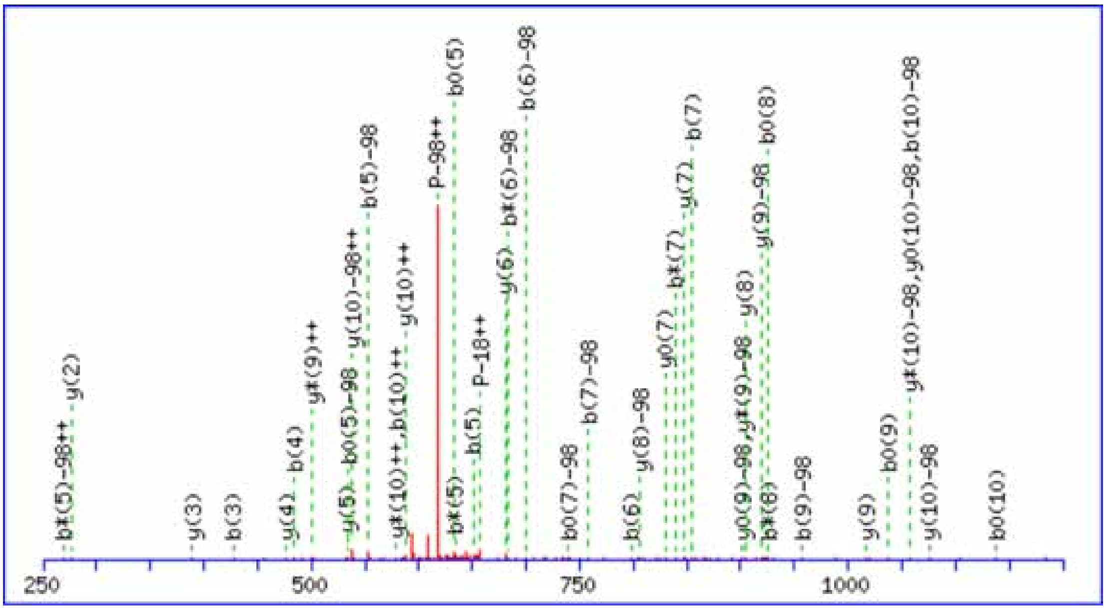
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(9)-98, b(11)-98, b(11), b(12), b(12)-98, b(13)-98, b(13), b(14), b(14)++, b(15)-98++, b(16)-98, b(16)-98++, b(16)++, b(18)-98++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(23)++, b(23)-98++
Matched y ions: y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13)++, y(13), y(15), y(15)++, y(16)-98++, y(17)-98++, y(17)-98, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.226

ERLGSFGSITR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of ERLGSFGSITR
Found in FLNC_MOUSE, Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3

Match to Query 1744: 1329.645386 from(665.829969,2+)
Title: Elution from: 41.377 to 41.377 scan no 3847 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1329.6442
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.014

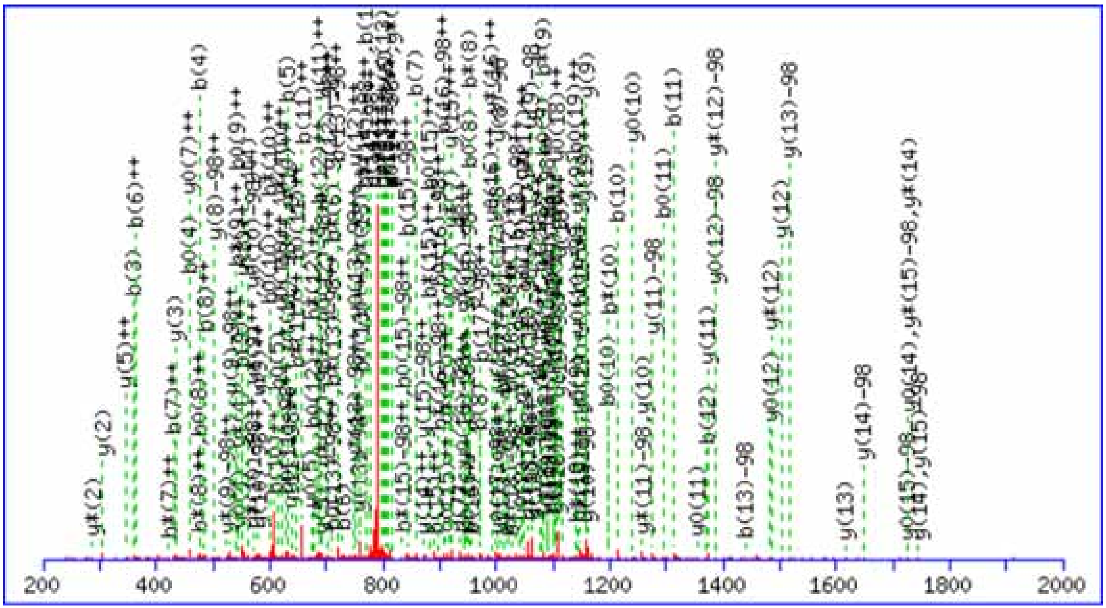
Matched b ions: b(3), b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(9)-98, b(10)-98, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98, y(10)-98++, y(10)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.227

ESDDKPEIEDVGSDEEEEEK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of ESDDKPEIEDVGSDEEEEEK
Found in HS90A_MOUSE, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 5847: 2471.004051 from(824.675293,3+)
Title: Elution from: 36.085 to 36.085 scan no 2914 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2470.9999
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K5 : Dimethyl (K)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
Ions Score: 54 **Expect:** 0.00017

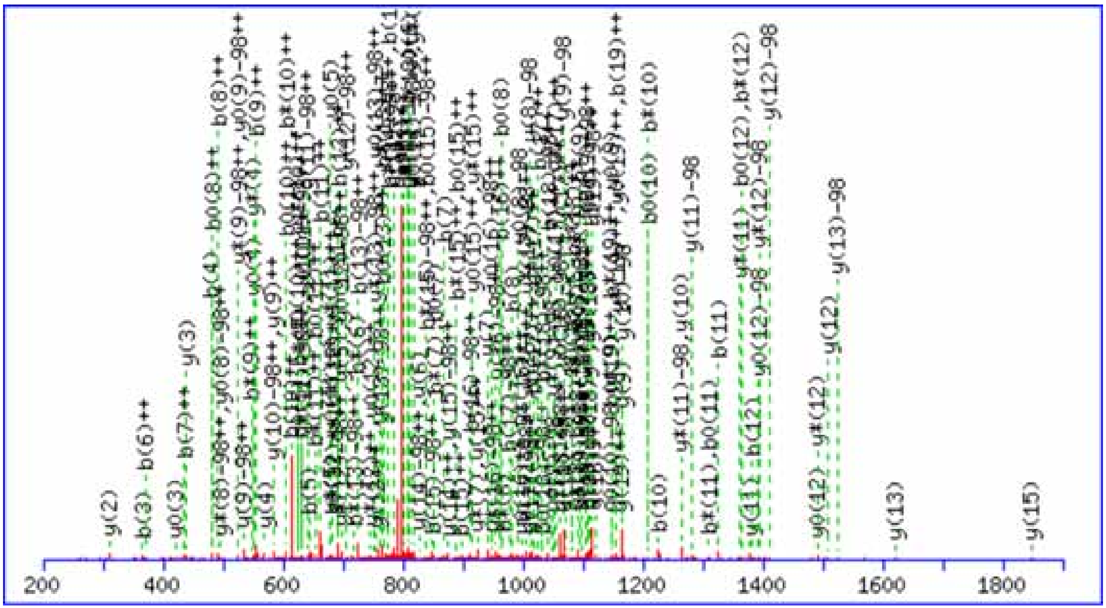
Matched b ions: b(3), b(4), b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(12), b(13)-98++, b(13)++, b(13)-98, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(7), y(8), y(8)-98++, y(8)++, y(8)-98, y(9)-98++, y(9)-98, y(9), y(9)++, y(10), y(10)-98, y(10)++, y(10)-98++, y(11), y(11)-98, y(11)++, y(11)-98++, y(12), y(12)-98++, y(12)++, y(13), y(13)-98++, y(13)-98, y(13)++, y(14)-98, y(14), y(14)++, y(15)++, y(15)-98, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.228

ESDDKPEIEDVGSDEEEEEK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of ESDDKPEIEDVGSDEEEEEK
Found in HS90A_MOUSE, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 5895: 2489.097660 from(830.706496,3+)
Title: Elution from: 36.077 to 36.077 scan no 2913 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2489.0954
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K5 : Dimethyl:2H(4)13C(2) (K)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 75 Expect: 2.3e-006

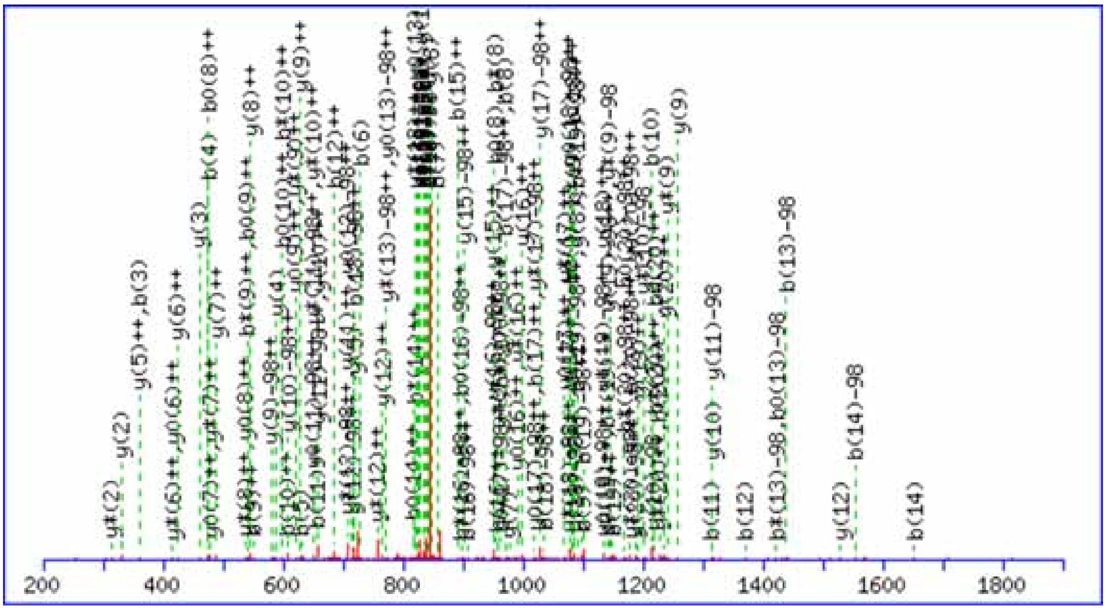
Matched b ions: b(3), b(4), b(5), b(6)++, b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(12), b(13)-98++, b(13)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98++, y(9)++, y(9)-98, y(10), y(10)-98++, y(10)-98, y(10)++, y(11), y(11)-98, y(11)++, y(11)-98++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13), y(13)-98, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15), y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.229

ESDDKPEIEDVGSDEEEEEKK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of ESDDKPEIEDVGSDEEEEEKK
Found in HS90A_MOUSE, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 7960: 2627.128107 from(876.716645,3+)
Title: Elution from: 34.037 to 34.037 scan no 2856 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2627.1262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K5 : Dimethyl (K)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
K21 : Dimethyl (K)
Ions Score: 74 Expect: 2.5e-006

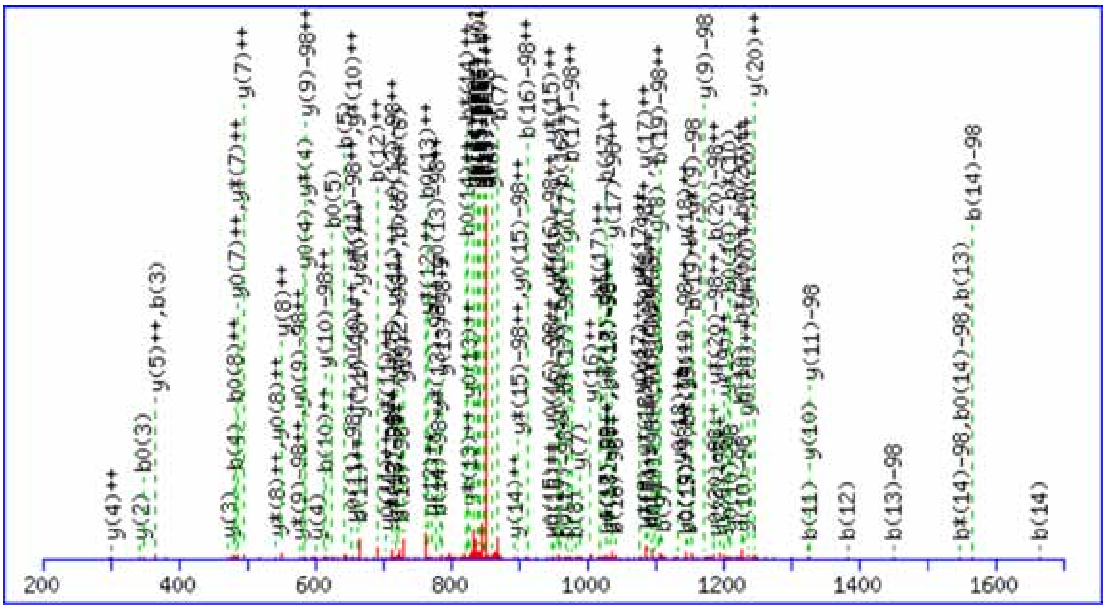
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)++, b(9), b(10), b(10)++, b(11), b(11)++, b(12)++, b(12), b(13)-98, b(13)-98++, b(14), b(14)-98, b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-98++, b(20)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(9)-98++, y(9)++, y(10)-98++, y(10)++, y(10), y(10)-98, y(11)++, y(11)-98++, y(11)-98, y(12), y(12)-98++, y(12)++, y(13)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)-98++, y(20)++
Precursor origin neutral loss: +

Peptide No.230

ESDDKPEIEDVGSDEEEEEKK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of ESDDKPEIEDVGSDEEEEEKK
Found in HS90A_MOUSE, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 6999: 2651.255343 from(884.759057,3+)
Title: Elution from: 33.987 to 33.987 scan no 2644 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2651.2534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K5 : Dimethyl:2H(4)13C(2) (K)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl:2H(4)13C(2) (K)
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 83 **Expect:** 5.2e-007

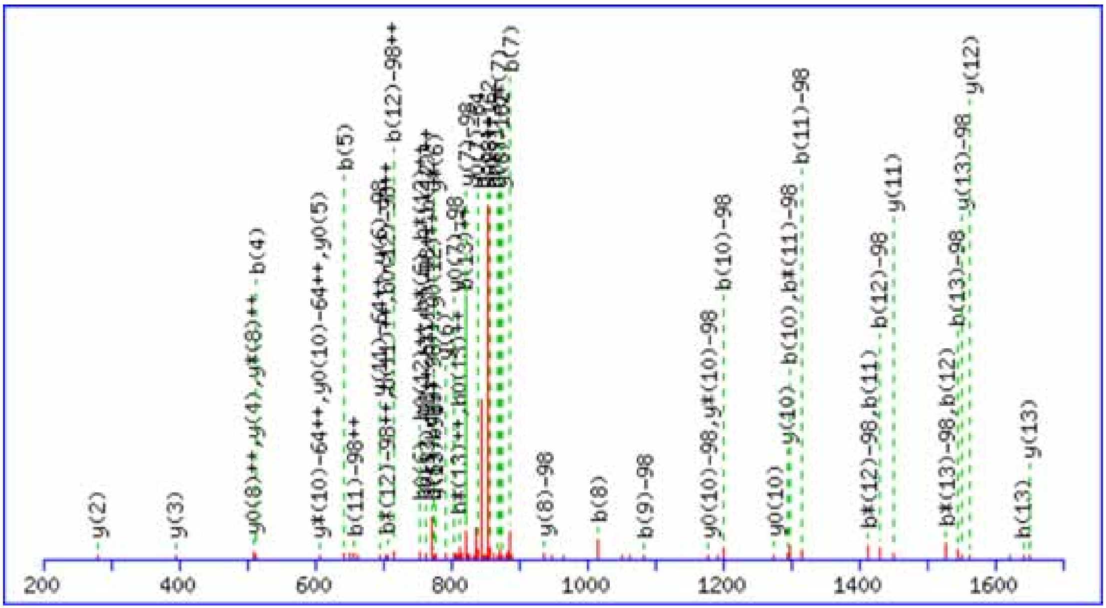
Matched b ions: b(3), b(4), b(5), b(7), b(8), b(9), b(10), b(10)++, b(11), b(11)++, b(12)++, b(12), b(13)-98, b(13), b(13)-98++, b(14)-98, b(14), b(14)-98++, b(14)++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)-98++, y(9)-98, y(10)++, y(10), y(10)-98, y(10)-98++, y(11)-98++, y(11)-98, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(20)-98++, y(20)++
Precursor origin neutral loss: +

Peptide No.231

ESLKEEDESDDDNM
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ESLKEEDESDDDNM
Found in PSA3_MOUSE, Proteasome subunit alpha type-3 OS=Mus musculus GN=Psma3 PE=1 SV=3

Match to Query 3456: 1806.640228 from(904.327390,2+)
Title: Elution from: 24.227 to 24.227 scan no 1373 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1806.6390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K4 : Dimethyl (K)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 82 Expect: 5.1e-008

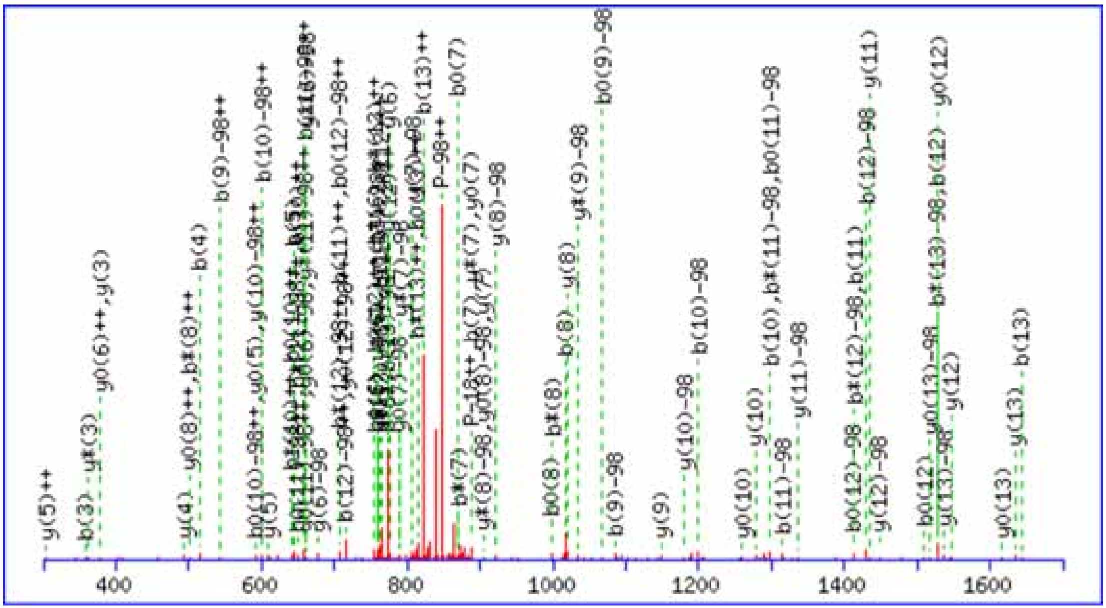
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10)-98, b(10), b(11), b(11)-98++, b(11)-98, b(11)++, b(12), b(12)-98, b(12)-98++, b(12)++, b(13)-98++, b(13), b(13)-98, b(13)++
Matched y ions: y(2), y(3), y(4), y(6)-98, y(6), y(7)-98, y(8)-98, y(10), y(11), y(12), y(13), y(13)-98, y(13)-98++
Precursor origin neutral loss: +

Peptide No.232

ESLKEEDESDDDNM
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ESLKEEDESDDDNM
Found in PSA3_MOUSE, Proteasome subunit alpha type-3 OS=Mus musculus GN=Psma3 PE=1 SV=3

Match to Query 4252: 1790.643736 from(896.329144,2+)
Title: Elution from: 30.964 to 30.964 scan no 2438 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1790.6441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K4 : Dimethyl (K)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 Expect: 6.6e-005

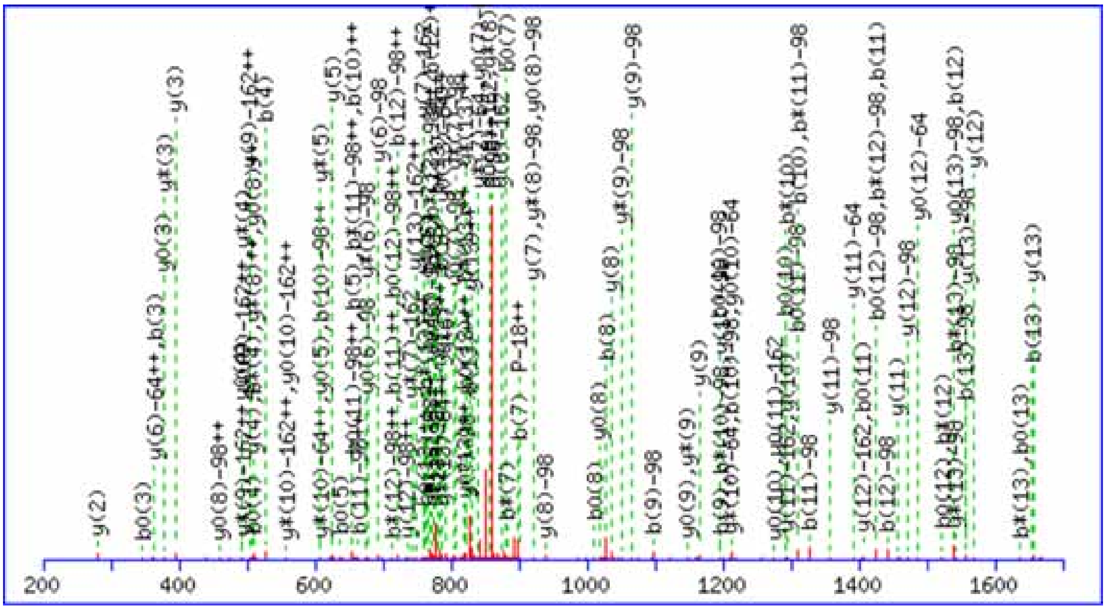
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(9)-98++, b(10)-98, b(10), b(10)-98++, b(10)++, b(11)-98++, b(11)-98, b(11), b(11)++, b(12)-98, b(12), b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(13)
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)-98, y(6), y(7), y(7)-98, y(8)-98, y(8), y(9), y(10)-98++, y(10), y(10)-98, y(11)-98, y(11), y(12)-98, y(12), y(12)++, y(13), y(13)-98
Precursor origin neutral loss: +

Peptide No.233

ESLKEEDESDDDNM
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ESLKEEDESDDDNM
Found in PSA3_MOUSE, Proteasome subunit alpha type-3 OS=Mus musculus GN=Psma3 PE=1 SV=3

Match to Query 3433: 1818.703136 from(910.358844,2+)
Title: Elution from: 24.251 to 24.251 scan no 1402 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1818.7026
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K4 : Dimethyl:2H(4)13C(2) (K)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 72 **Expect:** 1.1e-006

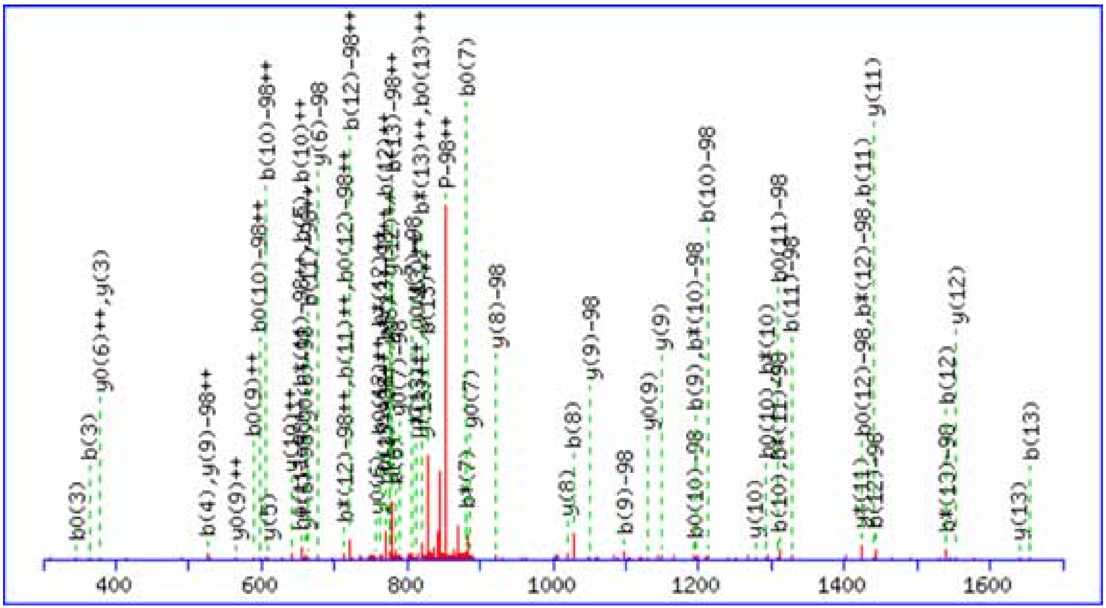
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(9), b(10)++, b(10)-98, b(10), b(10)-98++, b(11)-98, b(11), b(11)-98++, b(11)++, b(12)-98, b(12), b(12)++, b(12)-98++, b(13)-98++, b(13), b(13)-98, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(12)++, y(12)-98++, y(13), y(13)++, y(13)-98, y(13)-98++
Precursor origin neutral loss: +

Peptide No.234

ESLKEEDESDDDNM
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of ESLKEEDESDDDNM
Found in PSA3_MOUSE, Proteasome subunit alpha type-3 OS=Mus musculus GN=Psma3 PE=1 SV=3

Match to Query 3413: 1802.708916 from(902.361734,2+)
Title: Elution from: 30.854 to 30.854 scan no 2222 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1802.7077
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K4 : Dimethyl:2H(4)13C(2) (K)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 0.00026

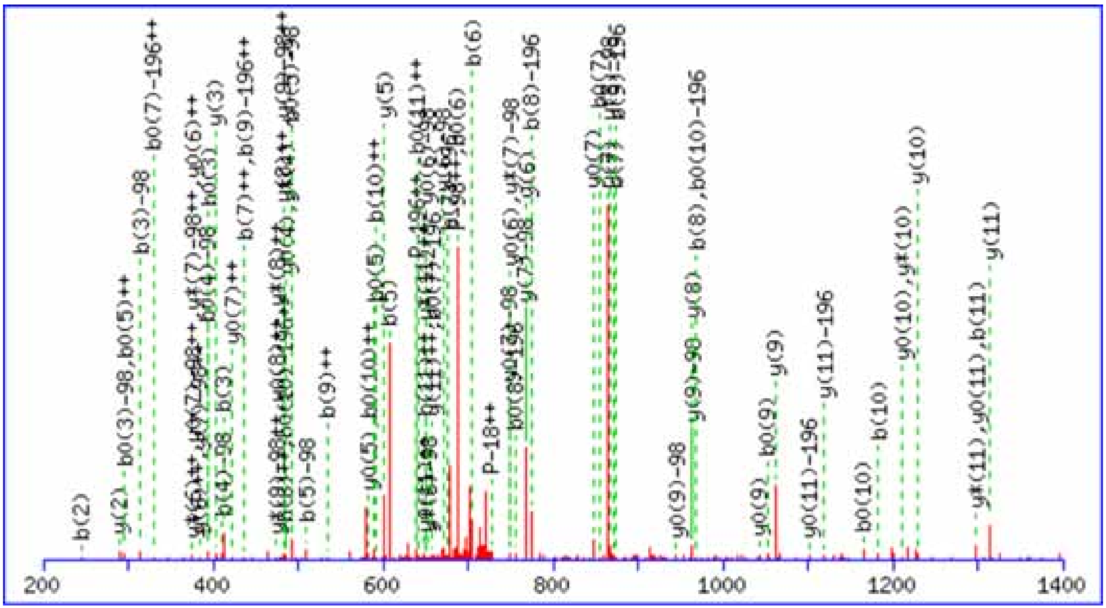
Matched b ions: b(3), b(4), b(5), b(6), b(8), b(9)-98, b(9), b(10)++, b(10), b(10)-98, b(10)-98++, b(11), b(11)-98, b(11)-98++, b(11)++, b(12), b(12)-98, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(13)
Matched y ions: y(3), y(5), y(6)-98, y(6), y(7)-98, y(8)-98, y(8), y(9)-98++, y(9), y(9)-98, y(10)++, y(10), y(11), y(12), y(12)++, y(13), y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.235

ESSPVPSPTLDR
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of ESSPVPSPTLDR
Found in SPTB2_MOUSE, Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2

Match to Query 2308: 1471.599896 from(736.807224,2+)
Title: Elution from: 35.201 to 35.201 scan no 3017 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1471.5997
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0012

Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(5), b(5)-98, b(6), b(7)-98, b(7), b(7)++, b(7)-196, b(8)-196, b(8)++, b(8)-98++, b(8), b(9)++, b(9)-196++, b(9)-98++, b(9)-196, b(10), b(10)++, b(10)-98, b(11)-98++, b(11), b(11)-98, b(11)++
Matched y ions: y(2), y(3), y(5), y(6), y(6)++, y(6)-98, y(7)-98, y(7), y(7)-98++, y(8)-98, y(8), y(8)++, y(9)-98, y(9), y(9)-98++, y(10)-98, y(10), y(11), y(11)-98, y(11)-196, y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.236

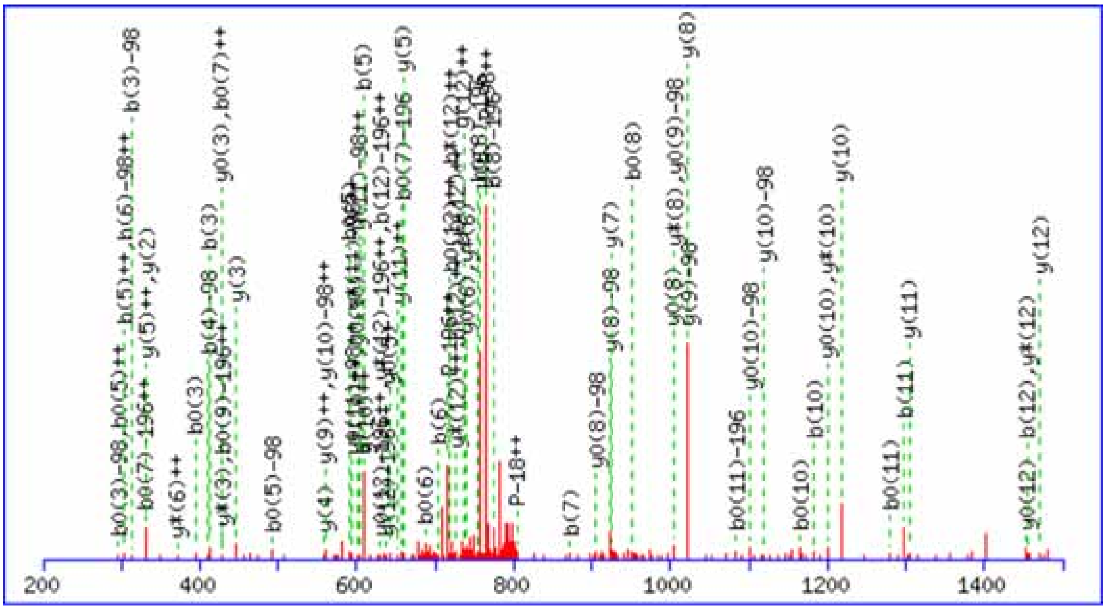
ESSPVPSPTLDRK

Confirmed sites: @S:2,@S:7

Ambiguous sites:

MS/MS Fragmentation of ESSPVPSPTLDRK
Found in SPTB2_MOUSE, Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2

Match to Query 2838: 1627.726670 from(814.870611,2+)
Title: Elution from: 30.847 to 30.847 scan no 2256 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1627.7259
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 37 Expect: 0.0075

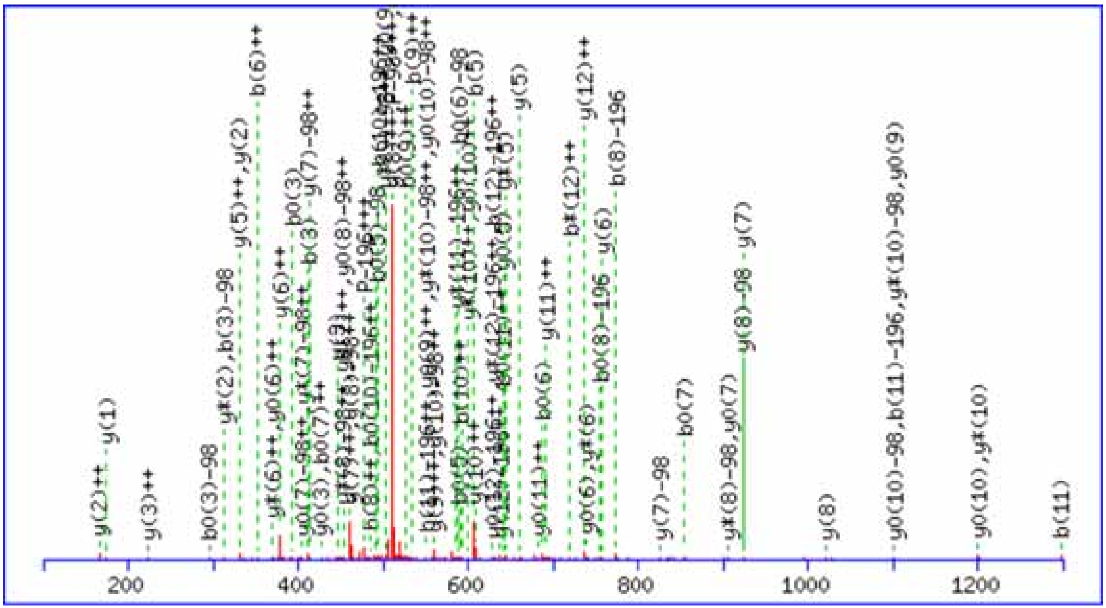
Matched b ions: b(3), b(3)-98, b(4)-98, b(5), b(5)++, b(6)-98++, b(6), b(7)-98, b(7), b(8)-98, b(8)-196, b(10), b(11), b(11)-98, b(11)-98++, b(12)-98++, b(12), b(12)-196++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(8)-98, y(8), y(9)++, y(9)-98, y(10), y(10)-98++, y(10)++, y(10)-98, y(11), y(11)-98++, y(11)++, y(12)-98++, y(12), y(12)-196++, y(12)++
Precursor origin neutral loss: +

Peptide No.237

ESSPVPSPTLDRK
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of ESSPVPSPTLDRK
Found in SPTB2_MOUSE, Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2

Match to Query 3291: 1627.726161 from(543.582663,3+)
Title: Elution from: 30.864 to 30.864 scan no 2423 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1627.7259
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 64 Expect: 1.3e-005

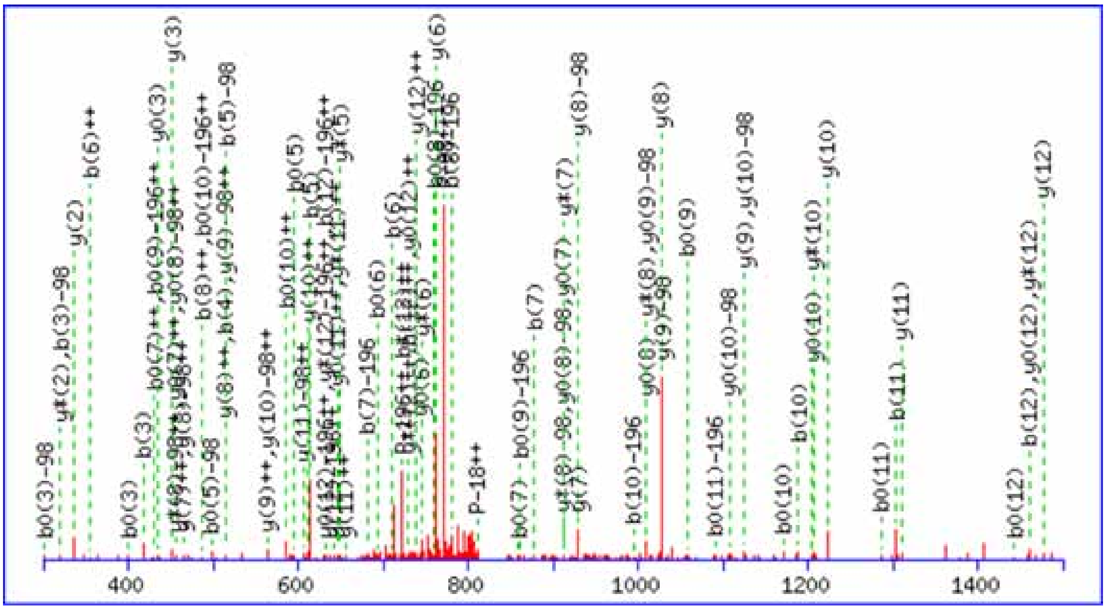
Matched b ions: b(3), b(3)-98, b(5), b(6)++, b(7)-98, b(8)-196, b(8)++, b(9)++, b(10)-196++, b(10)++, b(11)-196, b(11)-98, b(11), b(11)-196++, b(11)-98++, b(12)-98++, b(12)-196++
Matched y ions: y(1), y(2)++, y(2), y(3)++, y(3), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(7)-98++, y(7)-98, y(8)-98++, y(8)++, y(8)-98, y(8), y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(12)-196++
Precursor origin neutral loss: +

Peptide No.238

ESSPVPSPTLDRK
Confirmed sites: @S:2,@S:7
Ambiguous sites:

MS/MS Fragmentation of ESSPVPSPTLDRK
Found in SPTB2_MOUSE, Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2

Match to Query 2926: 1639.790572 from(820.902562,2+)
Title: Elution from: 30.813 to 30.813 scan no 2251 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1639.7896
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 50 **Expect:** 0.00047

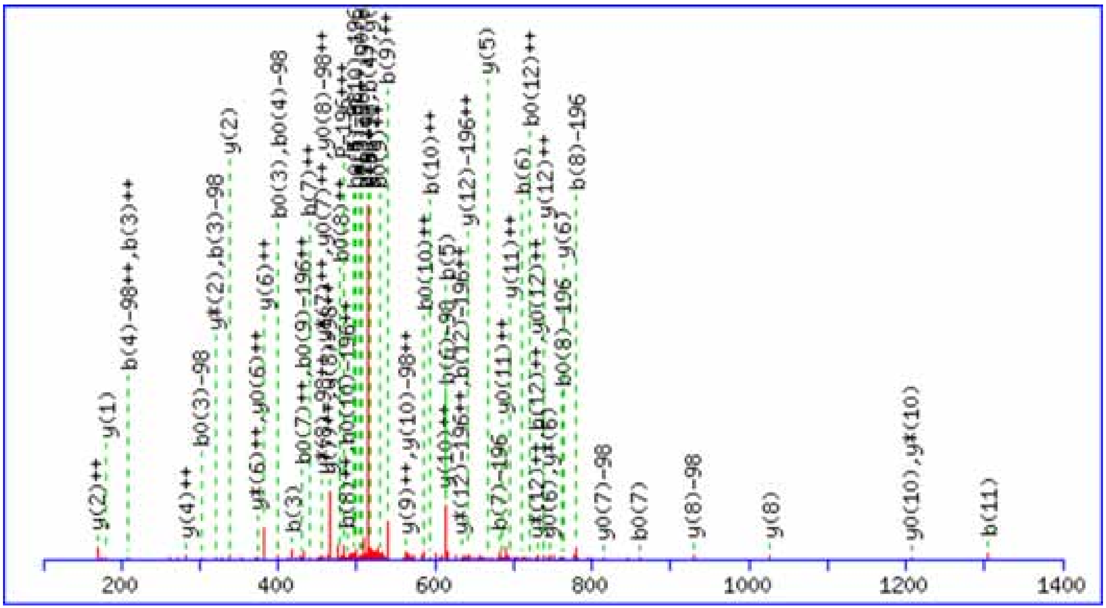
Matched b ions: b(3), b(3)-98, b(4), b(5), b(5)-98, b(6)++, b(6), b(7)-196, b(7)-98, b(7), b(8)++, b(8)-196, b(9)-98, b(10), b(10)-98, b(10)-196, b(11), b(11)-98, b(12), b(12)-98++, b(12)-98, b(12)-196++, b(12)++
Matched y ions: y(2), y(3), y(6), y(7), y(7)++, y(8)-98, y(8), y(8)-98++, y(8)++, y(9)++, y(9), y(9)-98, y(9)-98++, y(10), y(10)-98++, y(10)-98, y(10)++, y(11), y(11)-98++, y(11)++, y(12)-98++, y(12), y(12)-98, y(12)-196++, y(12)++
Precursor origin neutral loss: +

Peptide No.239

ESSPVPSPTLDRK
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of ESSPVPSPTLDRK
Found in SPTB2_MOUSE, Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2

Match to Query 2927: 1639.790829 from(547.604219,3+)
Title: Elution from: 30.855 to 30.855 scan no 2257 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1639.7896
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 47 Expect: 0.00083

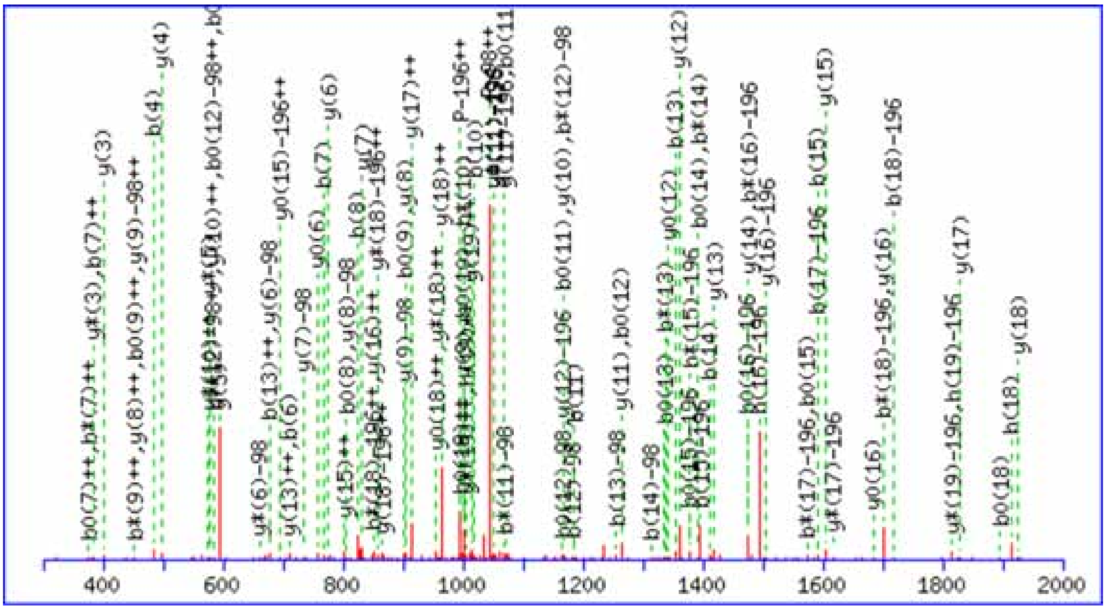
Matched b ions: b(3)++, b(3), b(3)-98, b(4), b(4)-98++, b(5), b(5)-98, b(6)-98, b(6), b(7)-98, b(7)-196, b(7)++, b(8)-196, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)-196++, b(10)++, b(11)-98, b(11), b(12)-98++, b(12)++, b(12)-196++
Matched y ions: y(1), y(2)++, y(2), y(4)++, y(5), y(6)++, y(6), y(7)++, y(8)-98++, y(8)-98, y(8), y(8)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(12)-98++, y(12)++, y(12)-196++
Precursor origin neutral loss: +

Peptide No.240

ETPQPEGGPPSPAGTPPQPK
Confirmed sites: @S:11,@T:15
Ambiguous sites:

MS/MS Fragmentation of ETPQPEGGPPSPAGTPPQPK
Found in JPH2_MOUSE, Junctophilin-2 OS=Mus musculus GN=Jph2 PE=1 SV=2

Match to Query 5630: 2183.952412 from(1092.983482,2+)
Title: Elution from: 32.726 to 32.726 scan no 2478 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2183.9541
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl (K)
Ions Score: 85 **Expect:** 1.6e-007

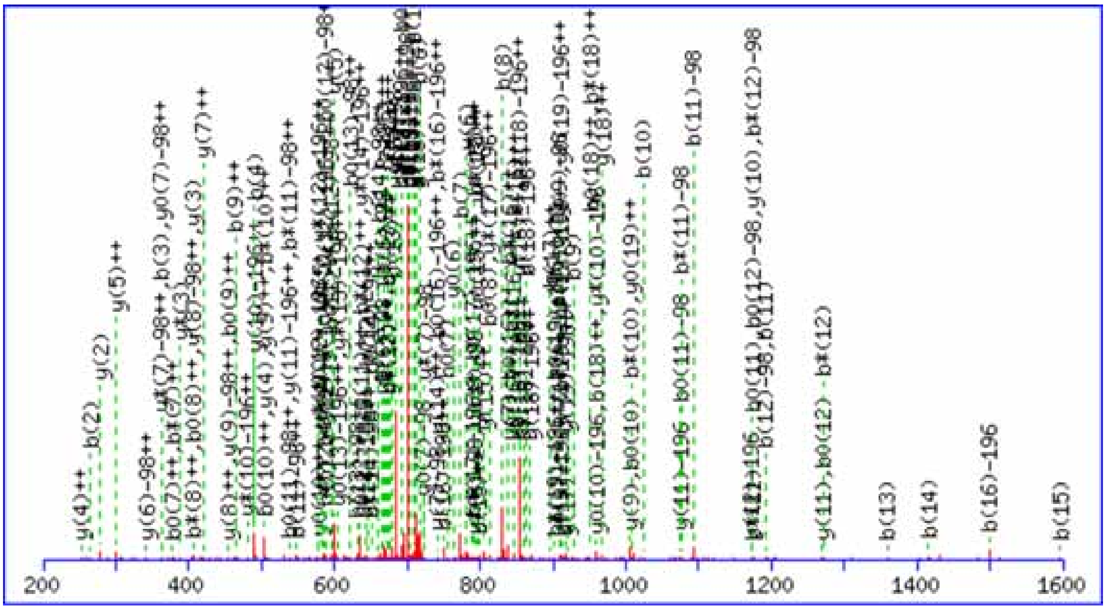
Matched b ions: b(4), b(6), b(7)++, b(7), b(8), b(10), b(11), b(12)-98, b(13)++, b(13)-98, b(13), b(14)-98, b(14), b(15)-196, b(15)-98, b(15), b(16)-196, b(16)-98, b(17)-196, b(18)-98, b(18), b(18)-196, b(19)-196, b(19)-98, b(19)-98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8)++, y(8)-98, y(8), y(9)-98++, y(9), y(9)-98, y(10), y(10)-98, y(10)++, y(11)-98, y(11)-196, y(11), y(11)-98++, y(12)-98, y(12), y(12)-196, y(13)++, y(13), y(13)-98++, y(13)-98, y(14), y(14)-98, y(15)++, y(15), y(15)-98, y(16)-98++, y(16)-98, y(16), y(16)++, y(16)-196, y(17)++, y(17), y(17)-98++, y(18)-98++, y(18)++, y(18), y(18)-98, y(18)-196++, y(19)-98, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.241

ETPQPEGGPPSPAGTPPQPK
Confirmed sites: @S:11,@T:15
Ambiguous sites:

MS/MS Fragmentation of ETPQPEGGPPSPAGTPPQPK
Found in JPH2_MOUSE, Junctophilin-2 OS=Mus musculus GN=Jph2 PE=1 SV=2

Match to Query 5939: 2196.018810 from(733.013546,3+)
Title: Elution from: 33.055 to 33.055 scan no 2552 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2196.0177
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 80 **Expect:** 6.7e-007

Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9)++, b(9), b(10), b(11)-98, b(11), b(11)-98++, b(11)++, b(12)-98, b(12)-98++, b(12)++, b(13), b(13)-98++, b(13)++, b(14), b(14)-98++, b(14)++, b(15)-98, b(15), b(15)-196++, b(15)-98++, b(15)++, b(16)-196, b(16)-98, b(16)-196++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)-196++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5)++, y(5), y(6)-98++, y(6), y(6)-98, y(7)++, y(7), y(7)-98, y(8)-98++, y(8), y(8)++, y(9), y(9)++, y(9)-98, y(9)-98++, y(10), y(10)-196++, y(10)++, y(10)-98, y(10)-98++, y(11), y(11)++, y(11)-98, y(11)-196, y(11)-98++, y(11)-196++, y(12)-98, y(12)-98++, y(12)++, y(12)-196, y(12)-196++, y(13)++, y(13)-98++, y(14)-98++, y(14)-196++, y(14)++, y(15)-98, y(15)++, y(15)-196++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(18)-196++, y(19)-196++
Precursor origin neutral loss: +

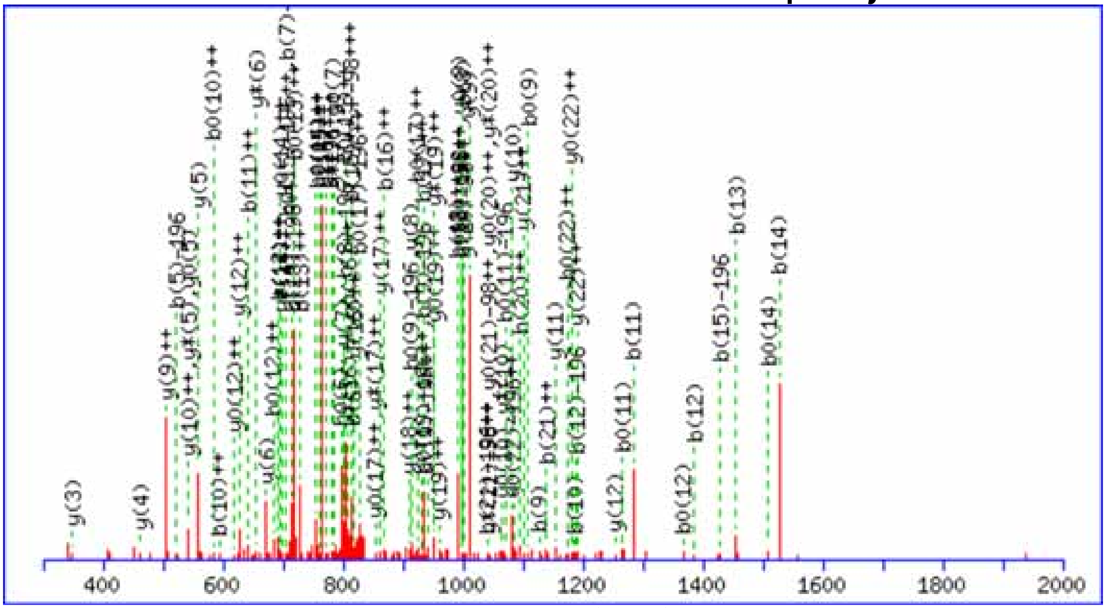
Peptide No.242

ETPTTPSPEGVTAAPLEIPISSK
Confirmed sites: @T:2,@T:4
Ambiguous sites:

MS/MS Fragmentation of ETPTTPSPEGVTAAPLEIPISSK
Found in NACAM_MOUSE, Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1

Match to Query 6155: 2537.198352 from(846.740060,3+)

Title: Elution from: 61.779 to 61.779 scan no 5723 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2537.1955
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K23 : Dimethyl (K)
Ions Score: 47 Expect: 0.0016

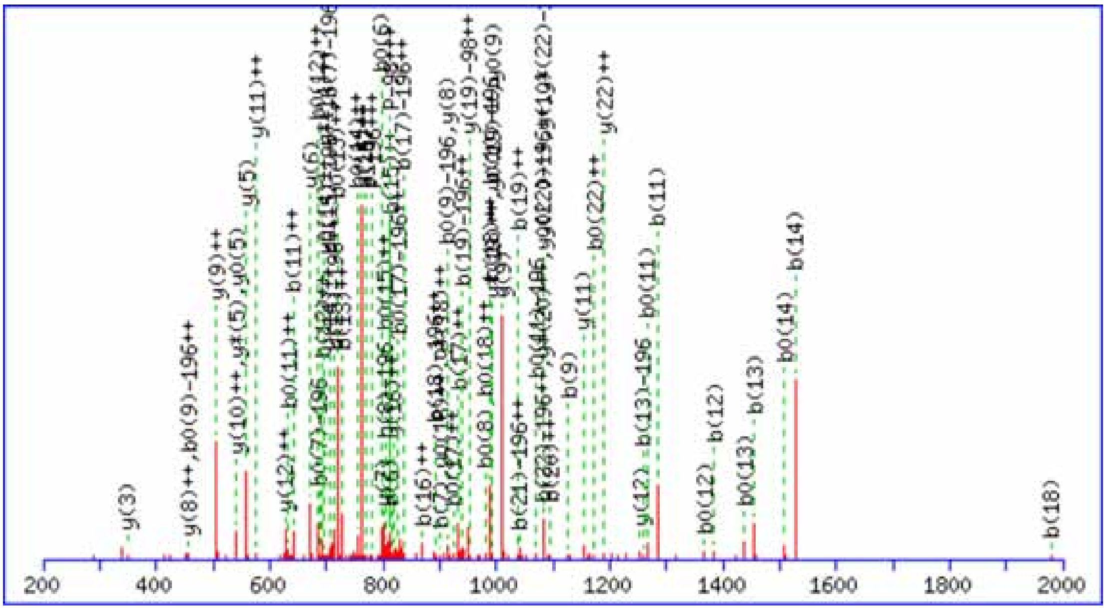
Matched b ions: b(5)-196, b(6), b(7)-98, b(7)-196, b(8)-196, b(8), b(9), b(9)-196, b(10)++, b(10), b(11), b(11)-98++, b(11)++, b(12), b(12)++, b(12)-196, b(13)++, b(13), b(13)-98++, b(14)++, b(14), b(14)-98, b(14)-98++, b(15)-98++, b(15)-98, b(15)-196, b(15)-196++, b(15)++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)-196++, b(20)++, b(20)-196++, b(21)++, b(21)-98++, b(21)-196++, b(22)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(12)++, y(12), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)-98++, y(21)++, y(22)++, y(22)-98++
Precursor origin neutral loss:

Peptide No.243

ETPTTPSPEGVTAAPLEIPISSK
Confirmed sites:
Ambiguous sites: @T:2orT:4, @T:5

MS/MS Fragmentation of ETPTTPSPEGVTAAPLEIPISSK
Found in NACAM_MOUSE, Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1

Match to Query 6657: 2537.199780 from(846.740536,3+)
Title: Elution from: 61.449 to 61.449 scan no 5847 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2537.1955
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K23 : Dimethyl (K)
Ions Score: 62 Expect: 6.3e-005

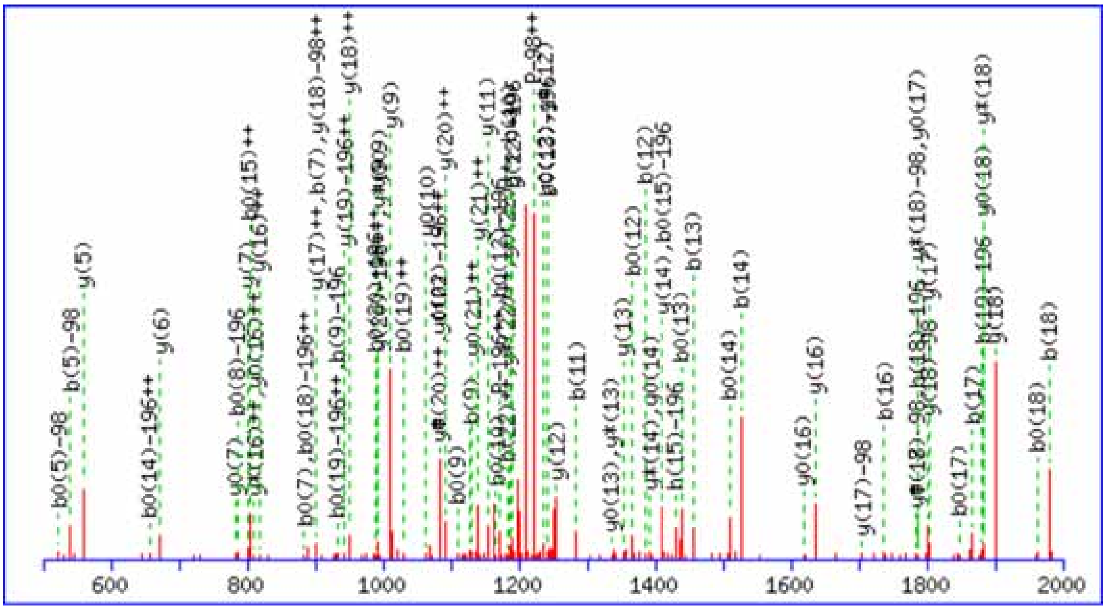
Matched b ions: b(6), b(7)-196, b(7)-98, b(7), b(8)-196, b(8)-98, b(9), b(10)-196, b(11), b(11)++, b(12), b(12)++, b(13), b(13)++, b(13)-196, b(14)++, b(14), b(14)-98++, b(15)-98++, b(15)-98, b(15)-196++, b(15)++, b(16)++, b(17)++, b(17)-196++, b(18), b(18)++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)-196++, b(19)++, b(20)++, b(21)-196++, b(21)-98++, b(22)-196++
Matched y ions: y(3), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11), y(11)++, y(12)++, y(12), y(14)++, y(15)++, y(16)++, y(19)-98++, y(22)++
Precursor origin neutral loss:

Peptide No.244

ETPTTPSPEGVTAAPLEIPISSK
Confirmed sites: @T:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of ETPTTPSPEGVTAAPLEIPISSK
Found in NACAM_MOUSE, Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1

Match to Query 7692: 2537.196838 from(1269.605695,2+)
Title: Elution from: 61.327 to 61.327 scan no 6057 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2537.1955
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K23 : Dimethyl (K)
Ions Score: 67 **Expect:** 1.5e-005

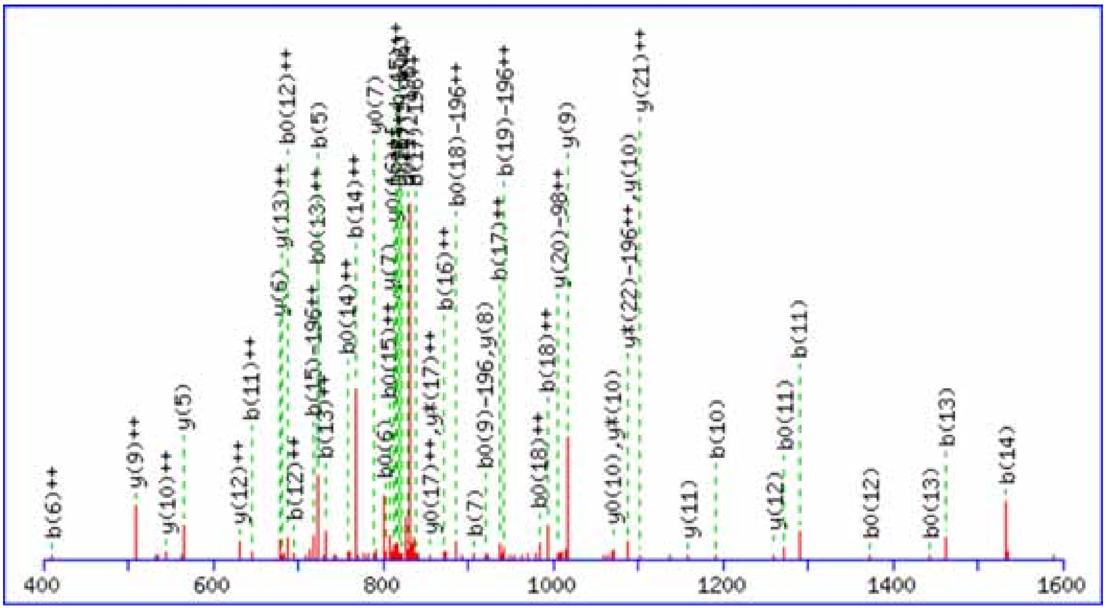
Matched b ions: b(5)-98, b(7)-98, b(7), b(8)-98, b(9)-98, b(9)-196, b(9), b(10), b(11), b(11)-98, b(12)-196, b(12), b(13), b(13)-98, b(14), b(14)-98, b(15)-98, b(15)-196, b(16), b(17)-98++, b(17), b(17)-98, b(18), b(18)-196, b(18)-98, b(19)-98, b(19)-196, b(22)++
Matched y ions: y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(14), y(16), y(16)++, y(17)++, y(17), y(17)-98, y(18)-98++, y(18)-98, y(18), y(18)++, y(19)-98++, y(19)-98, y(19)-196++, y(20)++, y(20)-196++, y(21)-98++, y(21)++, y(22)-98++, y(22)++
Precursor origin neutral loss: +

Peptide No.245

ETPTTPSPEGVTAAPLEIPISSK
Confirmed sites: @T:2
Ambiguous sites: @T:4orT:5

MS/MS Fragmentation of ETPTTPSPEGVTAAPLEIPISSK
Found in NACAM_MOUSE, Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1

Match to Query 6073: 2549.262828 from(850.761552,3+)
Title: Elution from: 61.066 to 61.066 scan no 5538 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2549.2591
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K23 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 37 **Expect:** 0.018

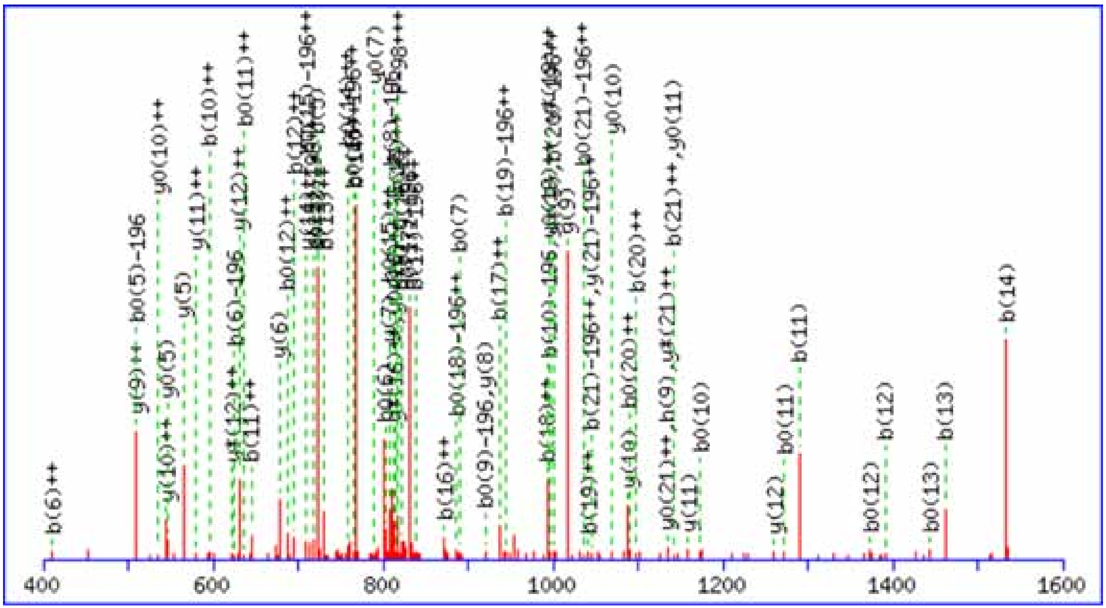
Matched b ions: b(5), b(6)++, b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(10), b(11), b(11)-98, b(11)++, b(12)++, b(13), b(13)++, b(13)-98++, b(14)++, b(14), b(14)-98++, b(15)-98++, b(15)-98, b(15)-196++, b(15)++, b(16)++, b(17)++, b(17)-196++, b(18)++, b(19)-98++, b(19)-196++, b(22)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(11), y(12)++, y(12), y(13)++, y(16)++, y(20)-98++, y(21)++
Precursor origin neutral loss:

Peptide No.246

ETPTTPSPEGVTAAPLEIPISSK
Confirmed sites:
Ambiguous sites: @T:4orT:5, @T:4orT:5

MS/MS Fragmentation of ETPTTPSPEGVTAAPLEIPISSK
Found in NACAM_MOUSE, Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1

Match to Query 6197: 2549.262867 from(850.761565,3+)
Title: Elution from: 61.409 to 61.409 scan no 5689 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2549.2591
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K23 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 53 Expect: 0.00042

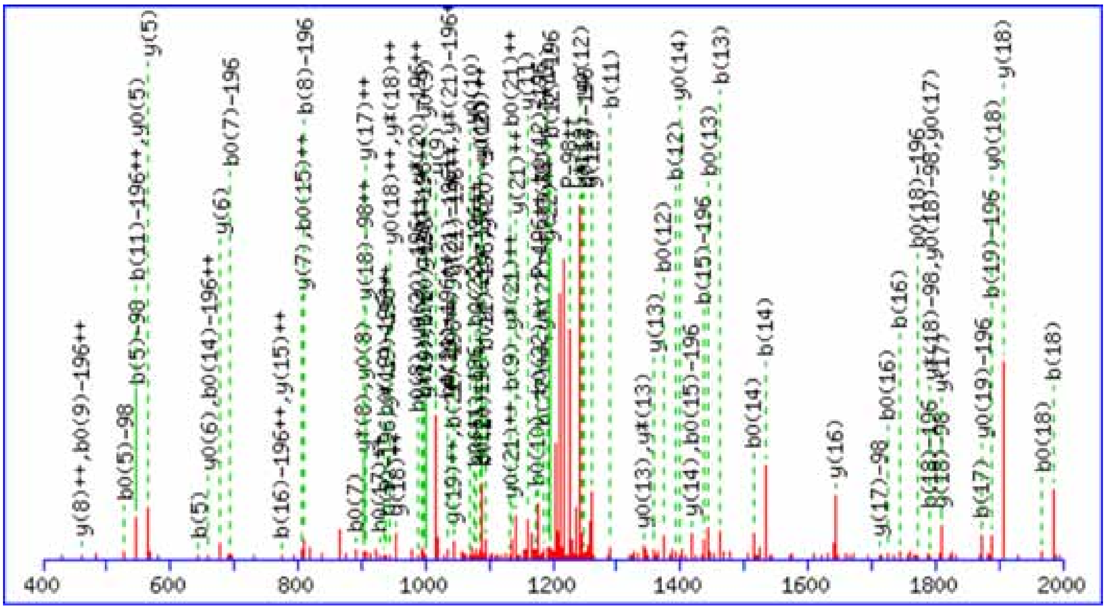
Matched b ions: b(5), b(5)-98, b(6)-98, b(6)++, b(6), b(6)-196, b(7)-98, b(8)-196, b(9), b(9)-98, b(10)++, b(10)-196, b(10)-98++, b(11), b(11)++, b(11)-98++, b(12), b(12)++, b(13), b(13)-98, b(13)++, b(14)++, b(14), b(14)-98++, b(15)-98++, b(15)-98, b(15)-196++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-196++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)-196++, b(19)++, b(20)-196++, b(20)++, b(21)++, b(21)-196++
Matched y ions: y(5), y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(11), y(11)++, y(12)++, y(12), y(14)++, y(16)++, y(21)-196++
Precursor origin neutral loss:

Peptide No.247

ETPTTPSPEGVTAAPLEIPISSK
Confirmed sites: @T:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of ETPTTPSPEGVTAAPLEIPISSK
Found in NACAM_MOUSE, Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1

Match to Query 6686: 2549.261666 from(1275.638109,2+)
Title: Elution from: 61.217 to 61.217 scan no 5828 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2549.2591
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K23 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 50 Expect: 0.0009

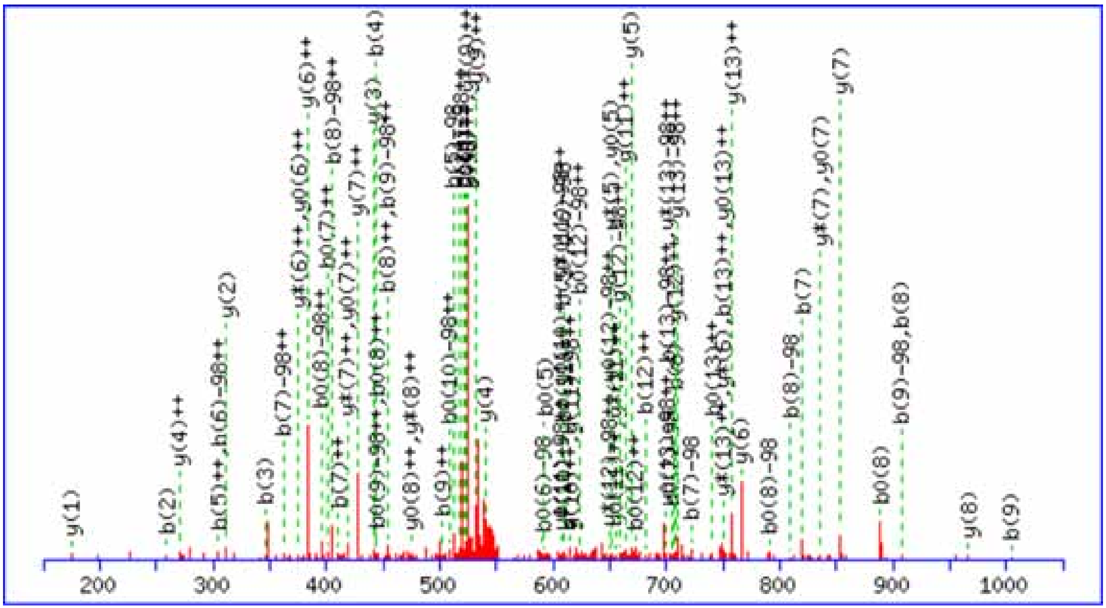
Matched b ions: b(5)-98, b(5), b(7)-98, b(8)-196, b(9)-98, b(9)-196, b(9), b(10)-196, b(10)-98++, b(10)-98, b(10), b(11)-196, b(11)-196++, b(11)-98, b(11), b(12)-196, b(12), b(13), b(13)-98, b(14), b(14)-98, b(15)-98, b(15)-196, b(16), b(16)-196++, b(17), b(18), b(18)-98, b(18)-196, b(19)-98, b(19)-196, b(20)-196++, b(21)-196++, b(21)-98++, b(22)-196++, b(22)++
Matched y ions: y(5), y(6), y(7), y(8)++, y(9), y(10), y(11), y(12), y(13), y(14), y(15)++, y(16), y(17), y(17)++, y(17)-98, y(18)-98, y(18), y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(19)-98, y(20)++, y(20)-98++, y(20)-196++, y(21)-98++, y(21)-196++, y(21)++, y(22)++
Precursor origin neutral loss: +

Peptide No.248

ETSPSPLSPEVEHR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of ETSPSPLSPEVEHR
Found in CMYA5_MOUSE, Cardiomyopathy-associated protein 5 OS=Mus musculus GN=Cmya5 PE=1 SV=2

Match to Query 3551: 1671.750270 from(558.257366,3+)
Title: Elution from: 31.058 to 31.058 scan no 2451 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1671.7505
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0026

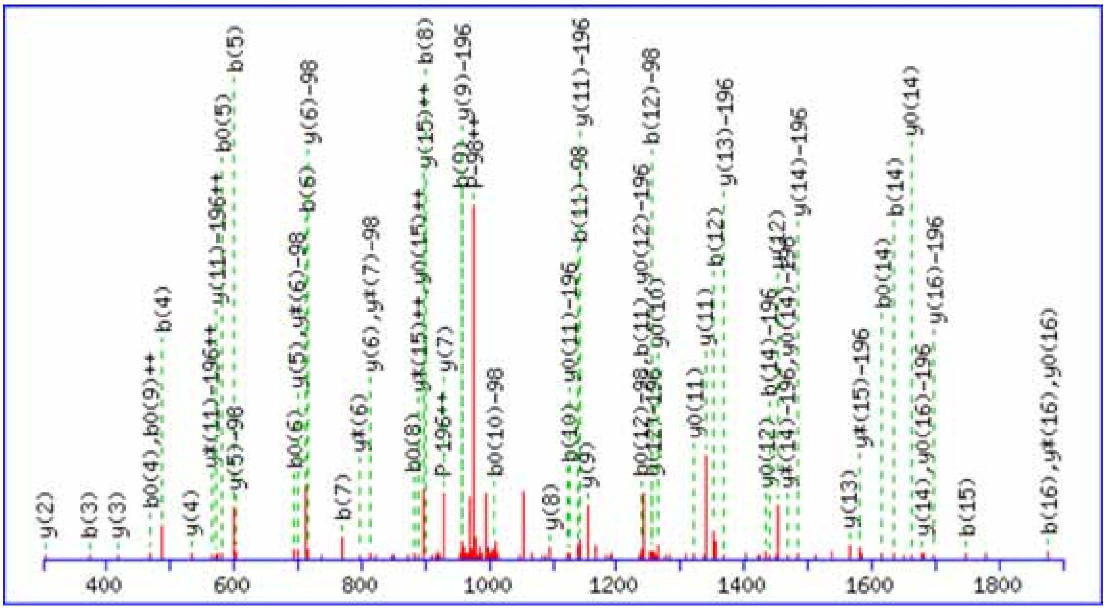
Matched b ions: b(2), b(3), b(4), b(5)++, b(5)-98, b(5), b(6)-98++, b(6)-98, b(6), b(7), b(7)-98++, b(7)++, b(7)-98, b(8)-98++, b(8), b(8)++, b(8)-98, b(9), b(9)-98, b(9)-98++, b(9)++, b(10)-98++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(9)++, y(10)++, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.249

EVDDILGEGSDDSDIEK
Confirmed sites: @S:10,@S:13
Ambiguous sites:

MS/MS Fragmentation of EVDDILGEGSDDSDIEK
Found in CTDP1_MOUSE, RNA polymerase II subunit A C-terminal domain phosphatase OS=Mus musculus GN=Ctdp1 PE=1 SV=1

Match to Query 5811: 2050.790932 from(1026.402742,2+)
Title: Elution from: 53.572 to 53.572 scan no 5306 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2050.7908
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 74 Expect: 9.9e-007

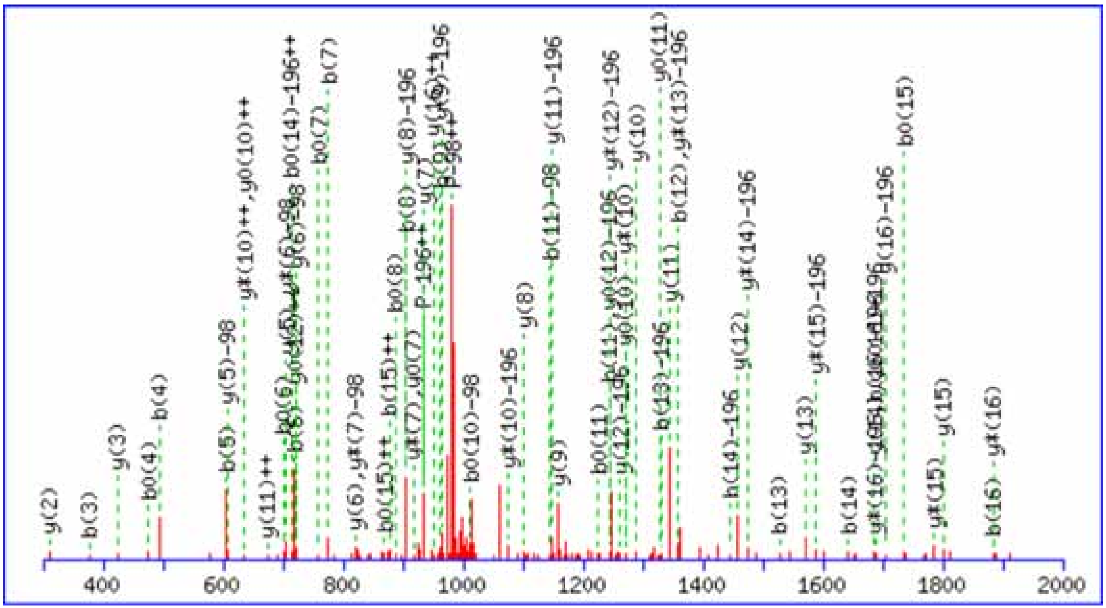
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11)-98, b(11), b(12), b(12)-98, b(13)-98, b(14)-98, b(14), b(14)-196, b(15), b(15)-98, b(16)-98, b(16)
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6), y(6)-98, y(7), y(8), y(8)-98, y(9)-98, y(9), y(9)-196, y(10)-98, y(11)-98, y(11), y(11)-196, y(11)-196++, y(12), y(12)-98, y(12)-196, y(13), y(13)-98, y(13)-196, y(14), y(14)-98, y(14)-196, y(15)++, y(15)-98, y(16)-98++, y(16)-196
Precursor origin neutral loss: +

Peptide No.250

EVDDILGEGSDDSDIEK
Confirmed sites: @S:10,@S:13
Ambiguous sites:

MS/MS Fragmentation of EVDDILGEGSDDSDIEK
Found in CTDP1_MOUSE, RNA polymerase II subunit A C-terminal domain phosphatase OS=Mus musculus GN=Ctdp1 PE=1 SV=1

Match to Query 5305: 2062.856282 from(1032.435417,2+)
Title: Elution from: 53.442 to 53.442 scan no 5062 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2062.8545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 56 Expect: 9e-005

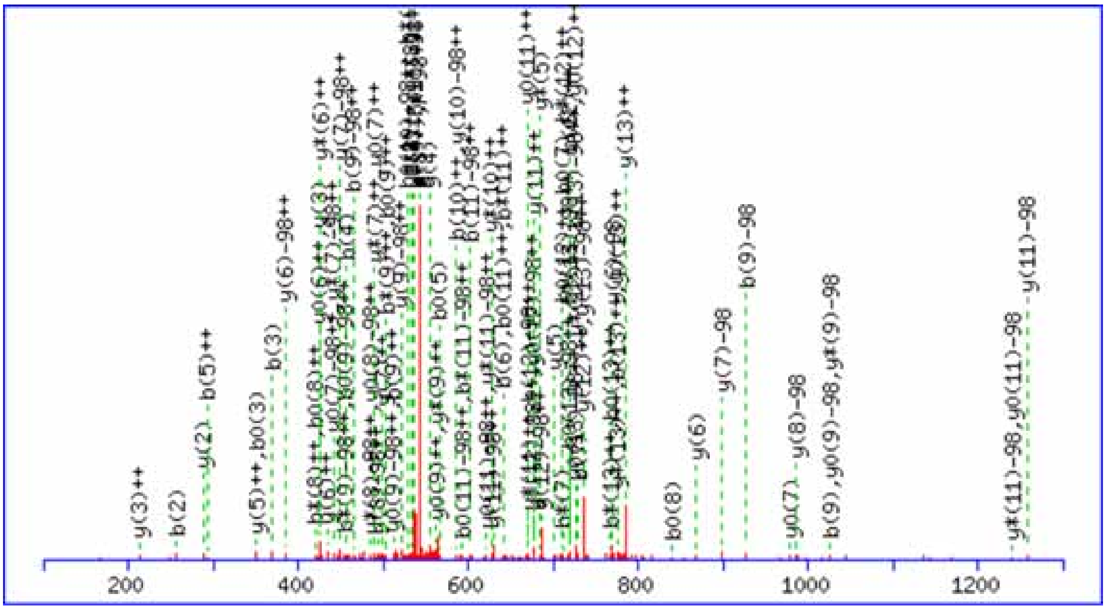
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(11), b(11)-98, b(12), b(13)-98++, b(13), b(13)-196, b(14), b(14)-98, b(14)-196, b(15)-98, b(15)++, b(15)-98++, b(16)-98, b(16), b(16)-196
Matched y ions: y(2), y(3), y(5), y(5)-98, y(6), y(6)-98, y(7), y(8)-196, y(8)-98, y(8), y(9)-98, y(9), y(9)-196, y(10), y(10)-98, y(11)-98, y(11), y(11)-196, y(11)++, y(12), y(12)-98, y(12)-196, y(13), y(13)-98, y(14), y(14)-98, y(15), y(16)-98, y(16)-196, y(16)++
Precursor origin neutral loss: +

Peptide No.251

EVLSQGSESFEHIR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of EVLSQGSESFEHIR
Found in CMYA5_MOUSE, Cardiomyopathy-associated protein 5 OS=Mus musculus GN=Cmya5 PE=1 SV=2

Match to Query 3893: 1724.777952 from(575.933260,3+)
Title: Elution from: 39.982 to 39.982 scan no 3663 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1724.7771
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00065

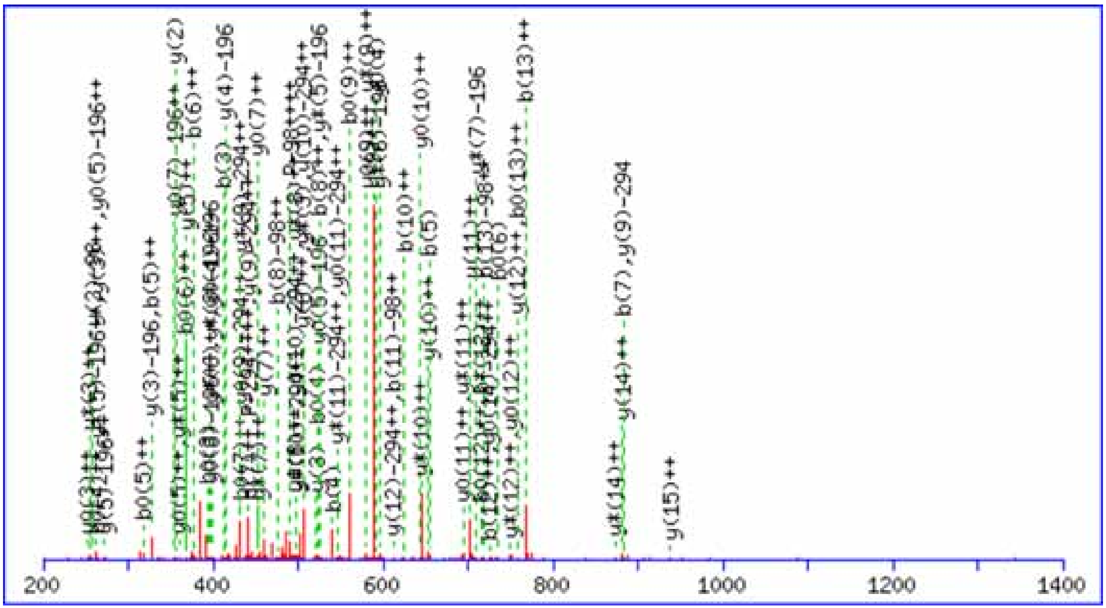
Matched b ions: b(2), b(3), b(4), b(5)++, b(6), b(7), b(9), b(9)-98, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++
Matched y ions: y(2), y(3), y(3)++, y(4), y(5)++, y(5), y(6)-98, y(6)++, y(6), y(6)-98++, y(7)-98, y(7)-98++, y(7)++, y(8)++, y(8)-98, y(8)-98++, y(9)-98++, y(10)-98++, y(11)-98++, y(11)-98, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.252

FDDELVESSLAKSSTR
Confirmed sites: @S:8,@S:14,@T:15
Ambiguous sites:

MS/MS Fragmentation of FDDELVESSLAKSSTR
Found in MCRS1_MOUSE, Microspherule protein 1 OS=Mus musculus GN=Mcrs1 PE=1 SV=1

Match to Query 5918: 2056.820076 from(515.212295,4+)
Title: Elution from: 34.759 to 34.759 scan no 2955 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2056.8256
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.031

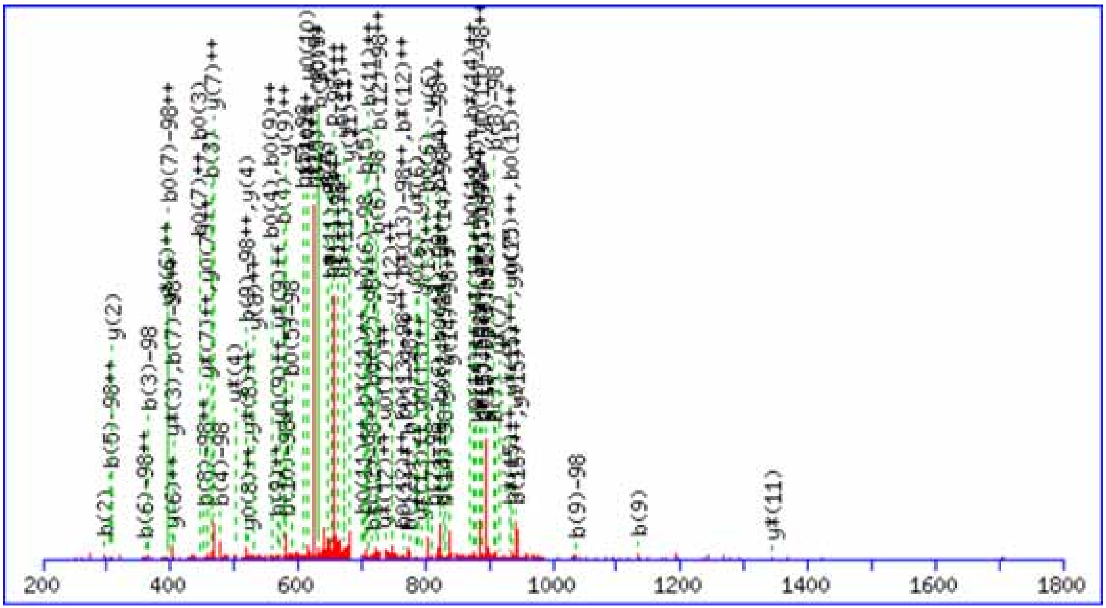
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)++, b(7)++, b(7), b(8)-98++, b(8)++, b(10)++, b(11)-98++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(2)-98, y(2), y(3)++, y(3)-196, y(3), y(4)-196, y(5)-196++, y(5)++, y(6)-98++, y(7)++, y(7)-98++, y(8)++, y(8)-98++, y(9)-294++, y(9)++, y(9)-98++, y(9)-294, y(9)-196++, y(10)-294++, y(10)++, y(11)++, y(11)-98++, y(12)-294++, y(12)++, y(13)-98++, y(14)++, y(15)++
Precursor origin neutral loss:

Peptide No.253

FDSLEDSPEEREPLQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of FDSLEDSPEEREPLQK
Found in CF057_MOUSE, UPF0369 protein C6orf57 homolog OS=Mus musculus PE=2 SV=2

Match to Query 6809: 2065.989147 from(689.670325,3+)
Title: Elution from: 38.891 to 38.891 scan no 3481 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2065.9881
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 32 Expect: 0.045

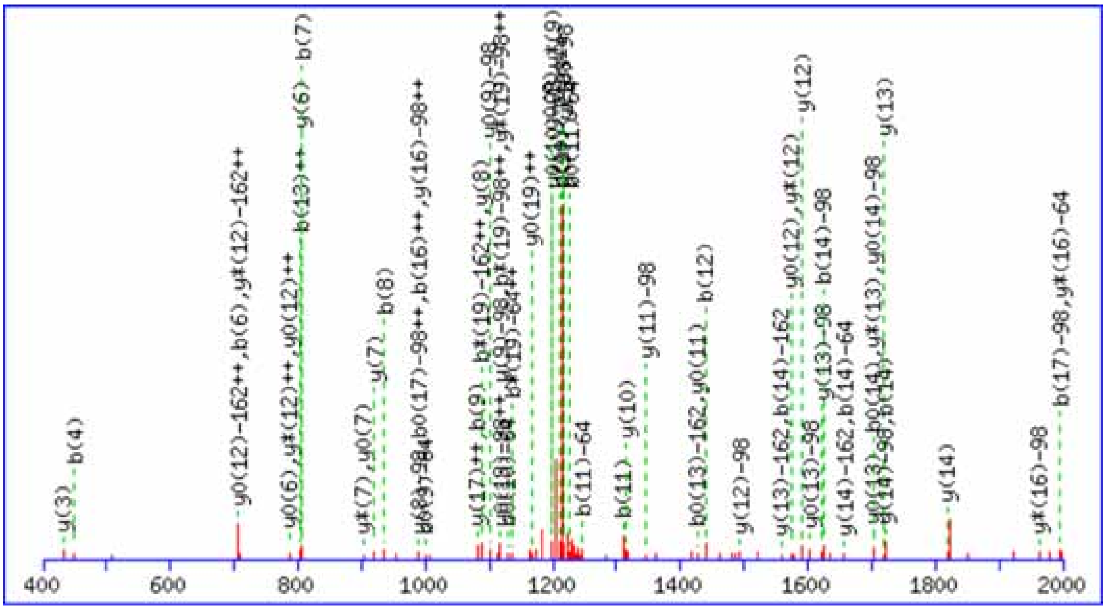
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98++, b(5)-98, b(5), b(6), b(6)-98++, b(6)-98, b(7), b(7)-98++, b(7)-98, b(8)-98, b(8)-98++, b(9), b(9)-98++, b(9)-98, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(15)++
Matched y ions: y(2), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.254

FGESEEVEMEVESDEEDQEK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of FGESEEVEMEVESDEEDQEK
Found in SF3A1_MOUSE, Splicing factor 3A subunit 1 OS=Mus musculus GN=Sf3a1 PE=1 SV=1

Match to Query 7633: 2524.959946 from(1263.487249,2+)
Title: Elution from: 48.396 to 48.396 scan no 4718 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2524.9564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
Ions Score: 38 Expect: 0.0042

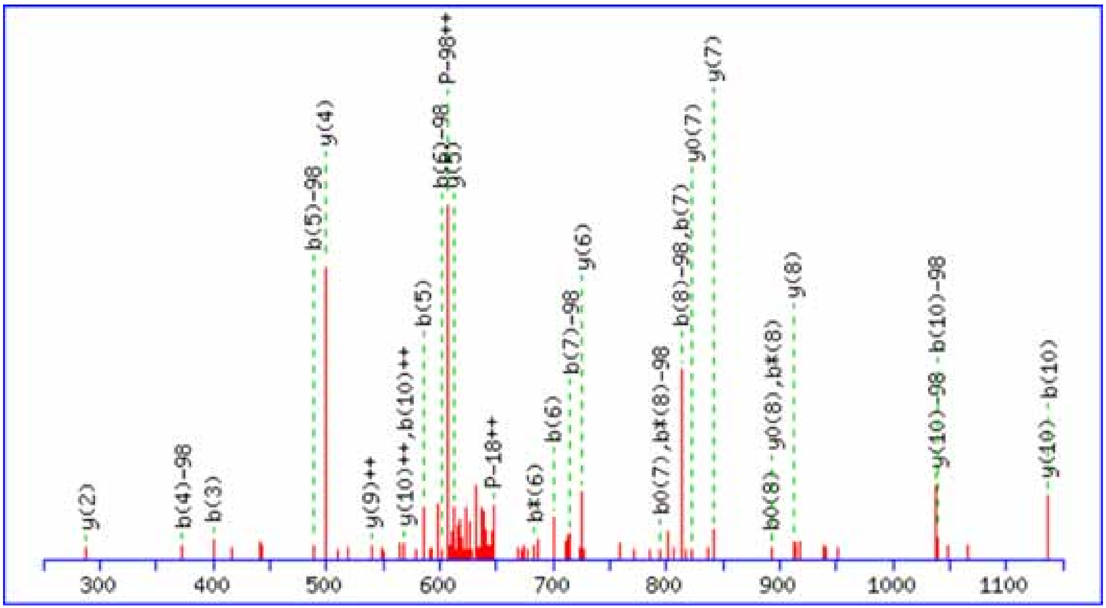
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13)++, b(14)-98, b(14), b(16)++, b(17)-98
Matched y ions: y(3), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(11)-98, y(12), y(12)-98, y(13)-98, y(13), y(14)-98, y(14), y(16)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.255

FGSADNIPNLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of FGSADNIPNLK
Found in TMCC1_MOUSE, Transmembrane and coiled-coil domains protein 1 OS=Mus musculus GN=Tmcc1 PE=1 SV=2

Match to Query 1668: 1310.627544 from(656.321048,2+)
Title: Elution from: 46.886 to 46.886 scan no 4530 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1310.6271
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K11 : Dimethyl (K)
Ions Score: 37 **Expect:** 0.0055

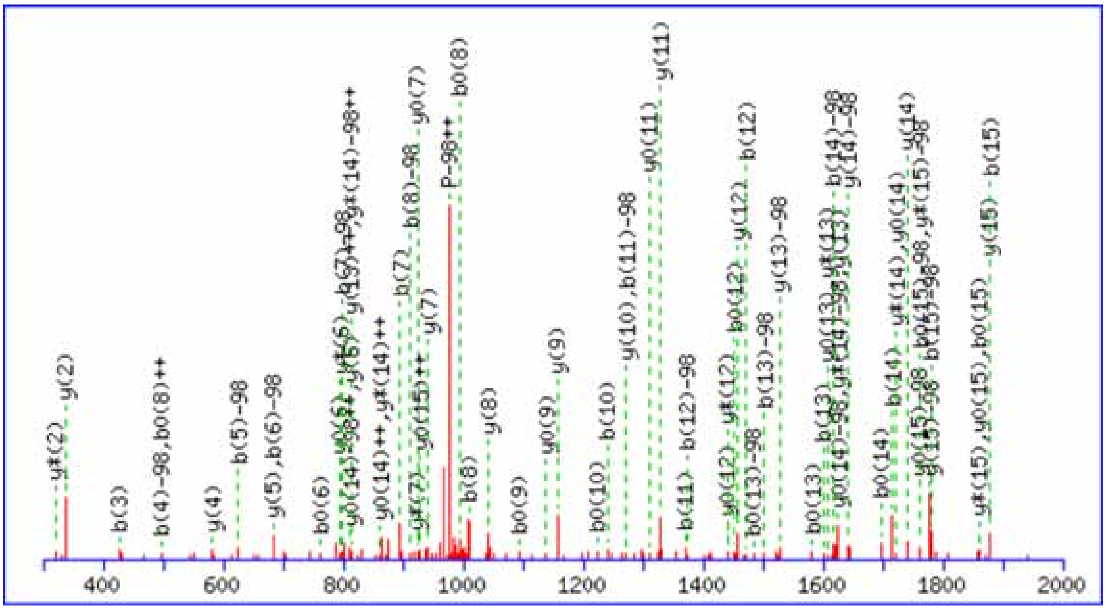
Matched b ions: b(3), b(4)-98, b(5), b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(10)-98, b(10), b(10)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9)++, y(10)-98, y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.256

FHDSEGDDTEETEDYR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **FHDSEGDDTEETEDYR**
Found in **BCLF1_MOUSE**, Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 PE=1 SV=2

Match to Query 5813: 2051.729240 from(1026.871896,2+)
Title: Elution from: 30.942 to 30.942 scan no 2435 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2051.7269
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 3.6e-005

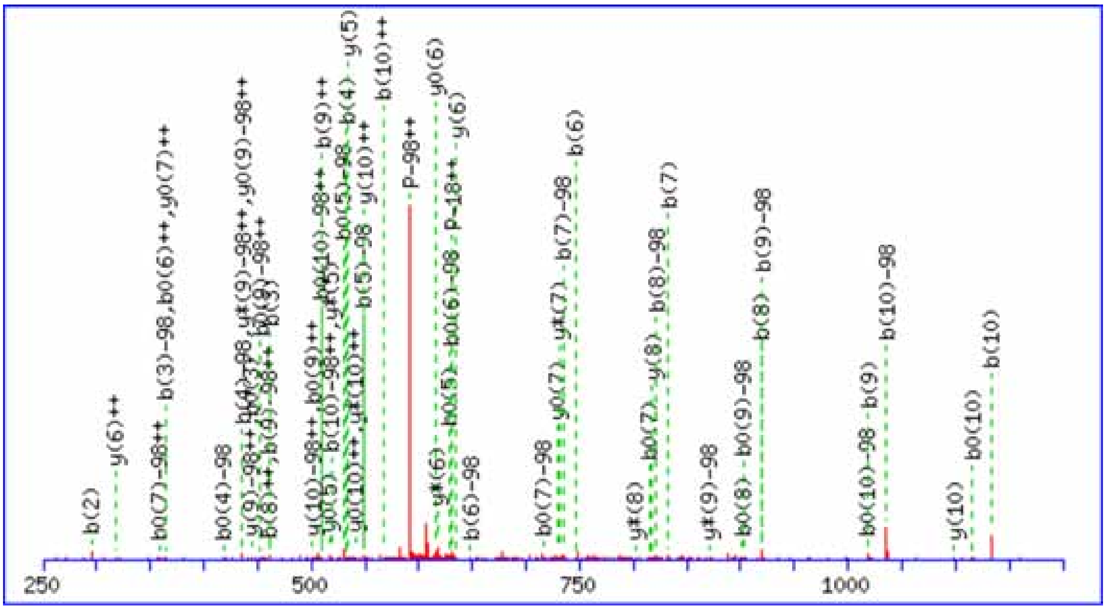
Matched b ions: b(3), b(4)-98, b(5)-98, b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13), b(14), b(14)-98, b(15), b(15)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)-98, y(13)++, y(14), y(14)-98, y(15)-98, y(15)
Precursor origin neutral loss: +

Peptide No.257

FLSAIVSSVDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of FLSAIVSSVDK
Found in IQGA1_MOUSE, Ras GTPase-activating-like protein IQGAP1 OS=Mus musculus GN=Iqgap1 PE=1 SV=1

Match to Query 1200: 1278.667116 from(640.340834,2+)
Title: Elution from: 35.049 to 35.049 scan no 2782 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1278.6685
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 **Expect:** 0.023

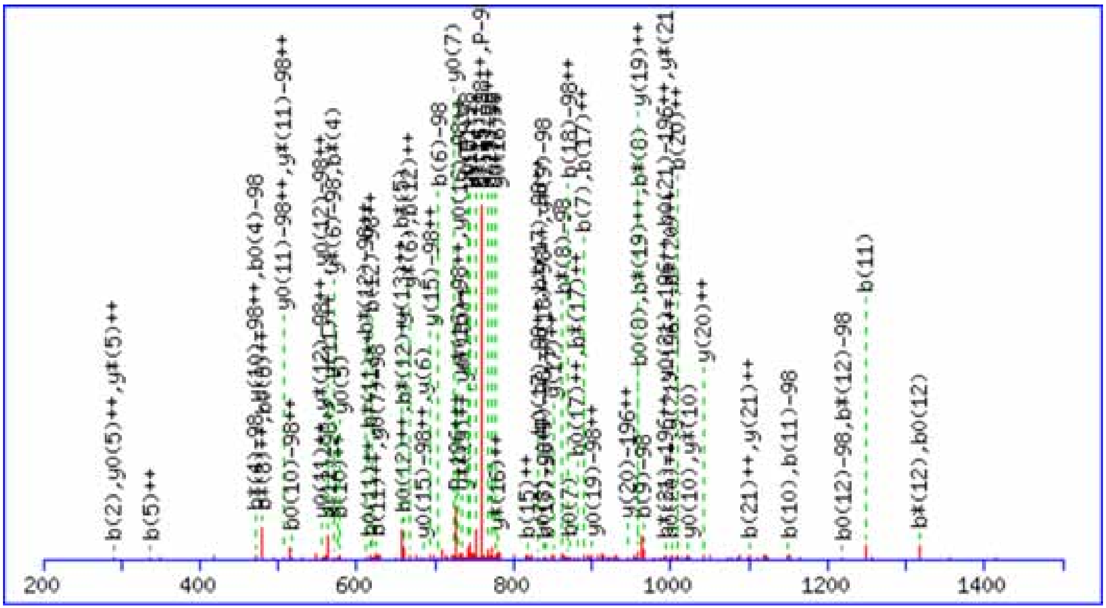
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(8)++, b(9)-98, b(9), b(9)++, b(9)-98++, b(10)-98, b(10), b(10)-98++, b(10)++
Matched y ions: y(5), y(6)++, y(6), y(8), y(9)-98++, y(10), y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.258

FNSESESSSSPSSPDGSGPSTK
Confirmed sites: @S:3,@T:21
Ambiguous sites:

MS/MS Fragmentation of FNSESESSSSPSSPDGSGPSTK
Found in HIRP3_MOUSE, HIRA-interacting protein 3 OS=Mus musculus GN=Hirip3 PE=1 SV=1

Match to Query 7243: 2372.895696 from(791.972508,3+)
Title: Elution from: 44.941 to 44.941 scan no 4297 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2372.8934
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K22 : Dimethyl (K)
Ions Score: 27 **Expect:** 0.049

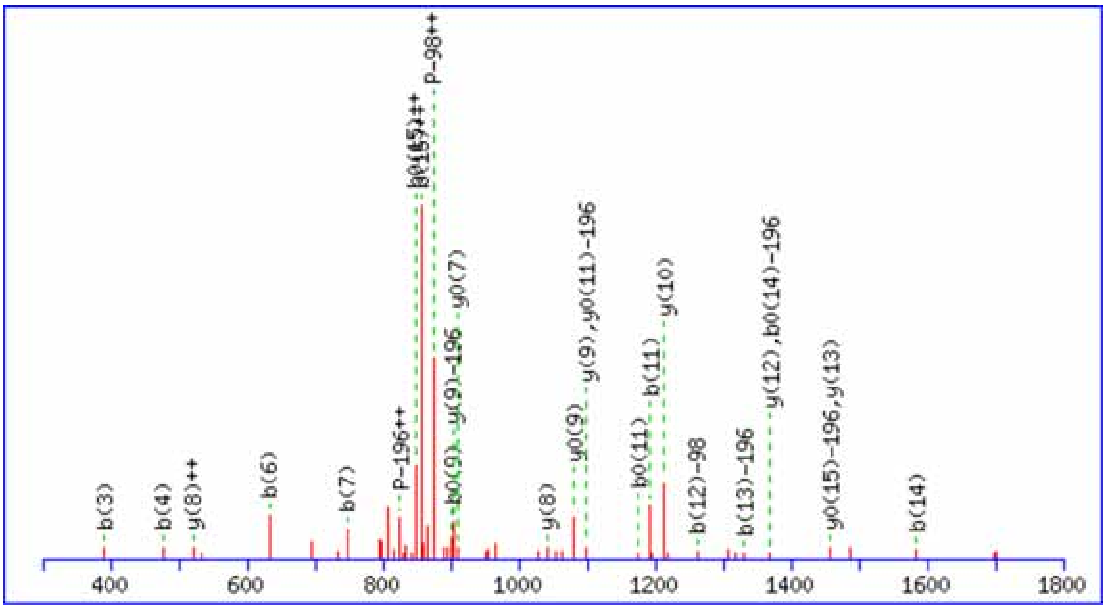
Matched b ions: b(2), b(5)++, b(6)-98, b(7), b(9)-98, b(10), b(10)++, b(11), b(11)++, b(11)-98, b(12)++, b(12)-98++, b(14)++, b(15)++, b(15)-98++, b(17)++, b(17)-98++, b(18)-98++, b(20)++, b(21)-98++, b(21)++
Matched y ions: y(6), y(8)-98, y(10)-98++, y(11)++, y(12)-98++, y(13)++, y(15)++, y(15)-98++, y(17)++, y(19)++, y(20)++, y(20)-98++, y(20)-196++, y(21)-98++, y(21)++, y(21)-196++
Precursor origin neutral loss: +

Peptide No.259

FTLSGVDGDSWSSGED
Confirmed sites: @S:12,@S:13
Ambiguous sites:

MS/MS Fragmentation of FTLSGVDGDSWSSGED
Found in NEST_MOUSE, Nestin OS=Mus musculus GN=Nes PE=1 SV=1

Match to Query 4627: 1845.639526 from(923.827039,2+)
Title: Elution from: 71.337 to 71.337 scan no 6852 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1845.6384
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.0013

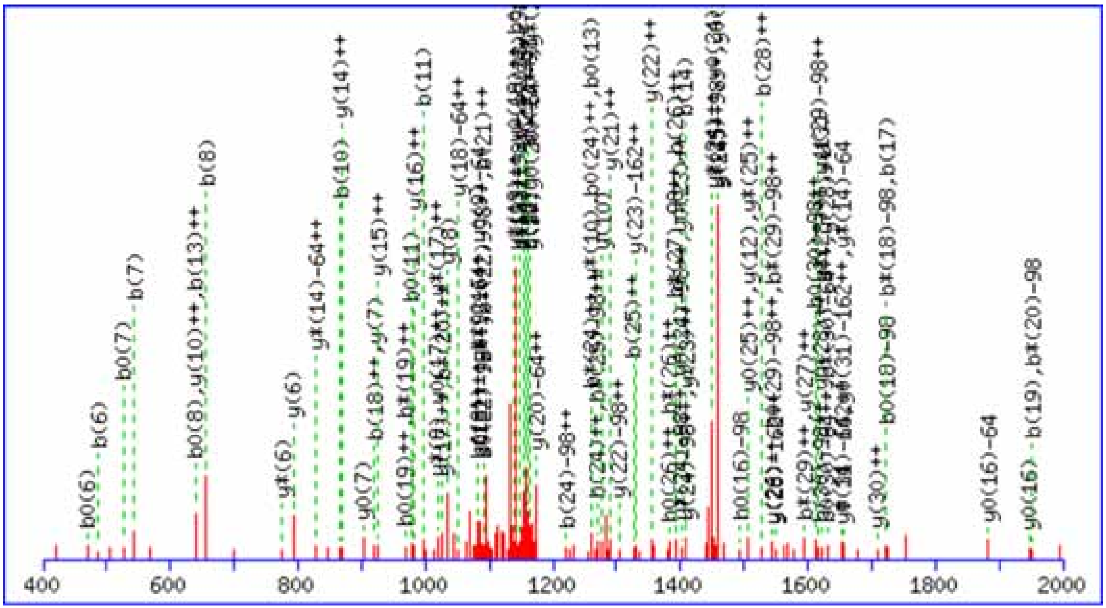
Matched b ions: b(3), b(4), b(6), b(7), b(11), b(12)-98, b(13)-196, b(14)-98, b(14), b(15)++, b(15)-98++
Matched y ions: y(7)-98, y(8)++, y(8), y(9), y(9)-196, y(10), y(12), y(13)
Precursor origin neutral loss: +

Peptide No.260

GASAATGIPLESDEDSNDNDNDLENENCMHTN
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **GASAATGIPLESDEDSNDNDNDLENENCMHTN**
Found in **UBP15_MOUSE**, Ubiquitin carboxyl-terminal hydrolase 15 OS=Mus musculus GN=Usp15 PE=2 SV=1

Match to Query 8822: 3572.346030 from(1191.789286,3+)
Title: Elution from: 44.786 to 44.786 scan no 4279 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3572.3464
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M29 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 53 **Expect:** 0.00019

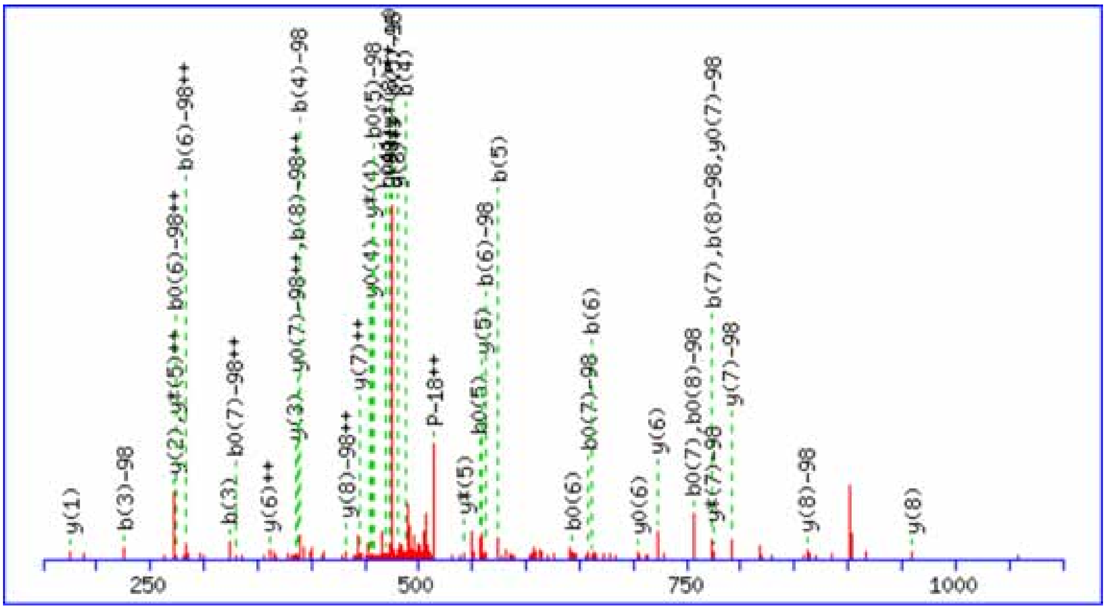
Matched b ions: b(6), b(7), b(8), b(10), b(11), b(12), b(13)++, b(14), b(17), b(18)++, b(19), b(21)++, b(23)-98++, b(24)++, b(24)-98++, b(25)++, b(26)++, b(28)++, b(30)-98++
Matched y ions: y(6), y(7), y(8), y(9), y(10)++, y(10), y(12), y(13), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(21)++, y(22)++, y(22)-98++, y(23)++, y(24)-98++, y(24)++, y(26)++, y(27)++, y(28)++, y(29)-98++, y(30)++
Precursor origin neutral loss: +

Peptide No.261

GASYSSIPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GASYSSIPK
Found in FLNC_MOUSE, Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3

Match to Query 588: 1044.489054 from(523.251803,2+)
Title: Elution from: 31.151 to 31.151 scan no 2464 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1044.4892
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K9 : Dimethyl (K)
Ions Score: 29 **Expect:** 0.034

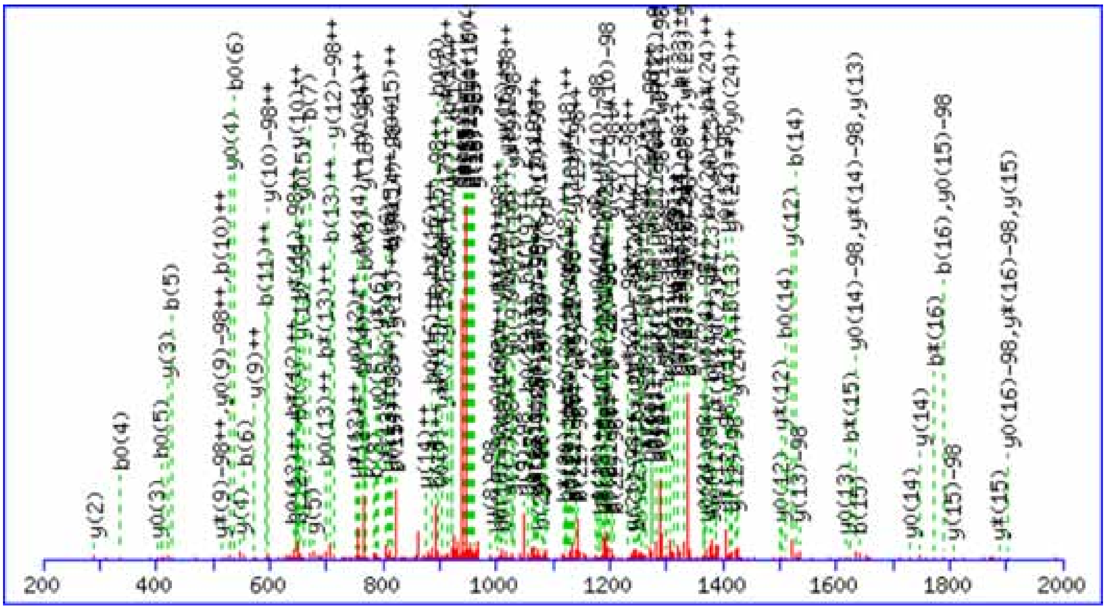
Matched b ions: b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6)-98++, b(6)-98, b(6), b(7), b(8)-98, b(8)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)-98, y(7)++, y(8)-98, y(8), y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.262

GATPAEDDEDKDIDLFGSDEEEEDK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of GATPAEDDEDKDIDLFGSDEEEEDK
Found in **EF1D_MOUSE**, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 8493: 2932.192737 from(978.404855,3+)
Title: Elution from: 49.569 to 49.569 scan no 4865 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2932.1910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K11 : Dimethyl (K)
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K25 : Dimethyl (K)
Ions Score: 80 **Expect:** 5.6e-007

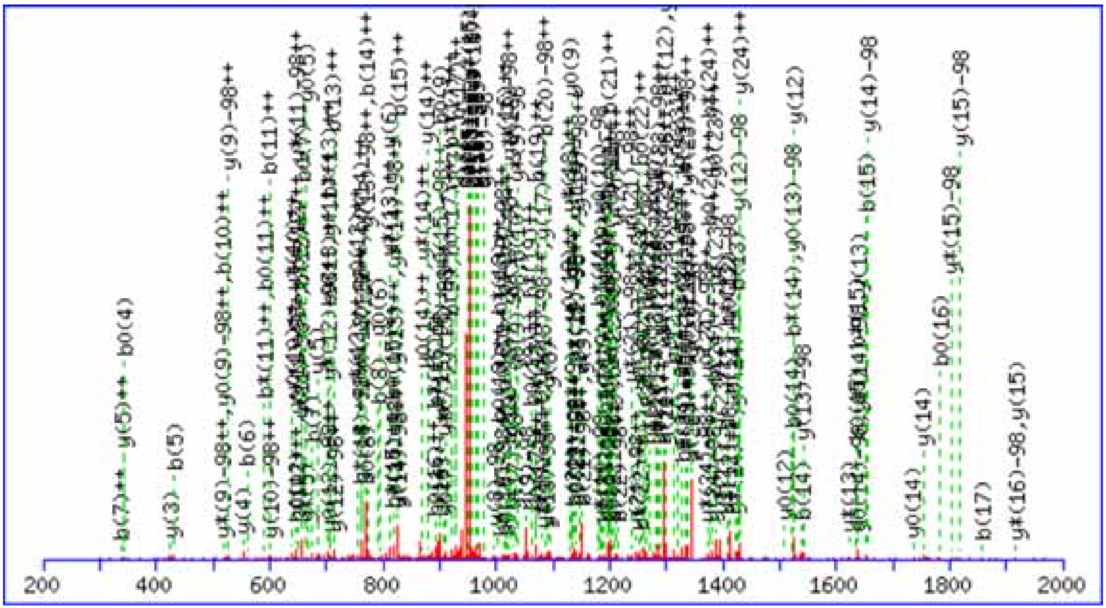
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(12), b(13)++, b(13), b(14)++, b(14), b(15)++, b(15), b(16)++, b(16), b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(23)++, b(23)-98++, b(24)++, b(24)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(9)++, y(10), y(10)-98, y(10)-98++, y(10)++, y(11), y(11)-98, y(11)-98++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13), y(13)-98, y(13)-98++, y(13)++, y(14), y(14)++, y(15)-98, y(15), y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)-98++, y(22)++, y(23)-98++, y(23)++, y(24)++, y(24)-98++
Precursor origin neutral loss: +

Peptide No.263

GATPAEDDEDKDIDLFGSDEEEEDK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of GATPAEDDEDKDIDLFGSDEEEEDK
Found in EF1D_MOUSE, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 7147: 2950.288527 from(984.436785,3+)
Title: Elution from: 49.465 to 49.465 scan no 4613 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2950.2865
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K11 : Dimethyl:2H(4)13C(2) (K)
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K25 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 68 **Expect:** 1.4e-005

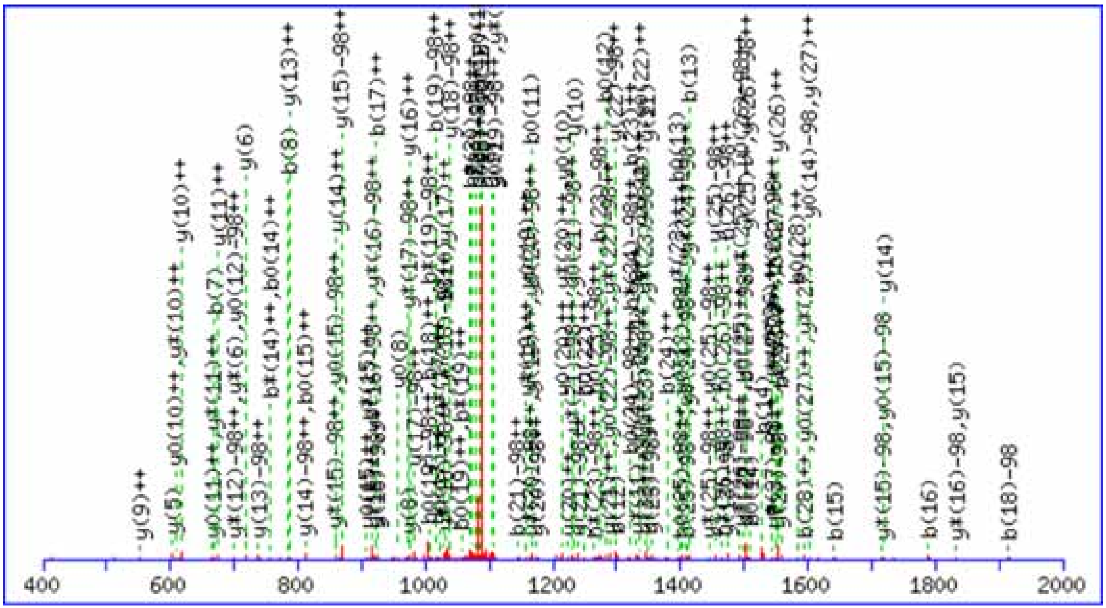
Matched b ions: b(5), b(6), b(7)++, b(7), b(8), b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(12), b(13)++, b(13), b(14)++, b(14), b(15)++, b(15), b(16)++, b(17)++, b(17), b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(24)++, b(24)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(9)-98++, y(10)-98, y(10), y(10)-98++, y(10)++, y(11)-98++, y(11), y(11)-98, y(11)++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13)-98++, y(13), y(13)-98, y(13)++, y(14), y(14)-98++, y(14)-98, y(14)++, y(15)-98, y(15), y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)-98++, y(22)++, y(23)++, y(23)-98++, y(24)++, y(24)-98++
Precursor origin neutral loss: +

Peptide No.264

GATPAEDDEDKDIDLFGSDEEEEDKEAAR
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of GATPAEDDEDKDIDLFGSDEEEEDKEAAR
Found in EF1D_MOUSE, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 6771: 3359.410785 from(1120.810871,3+)
Title: Elution from: 46.580 to 46.580 scan no 4181 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3359.4089
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K11 : Dimethyl (K)
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K25 : Dimethyl (K)
Ions Score: 88 **Expect:** 1.3e-007

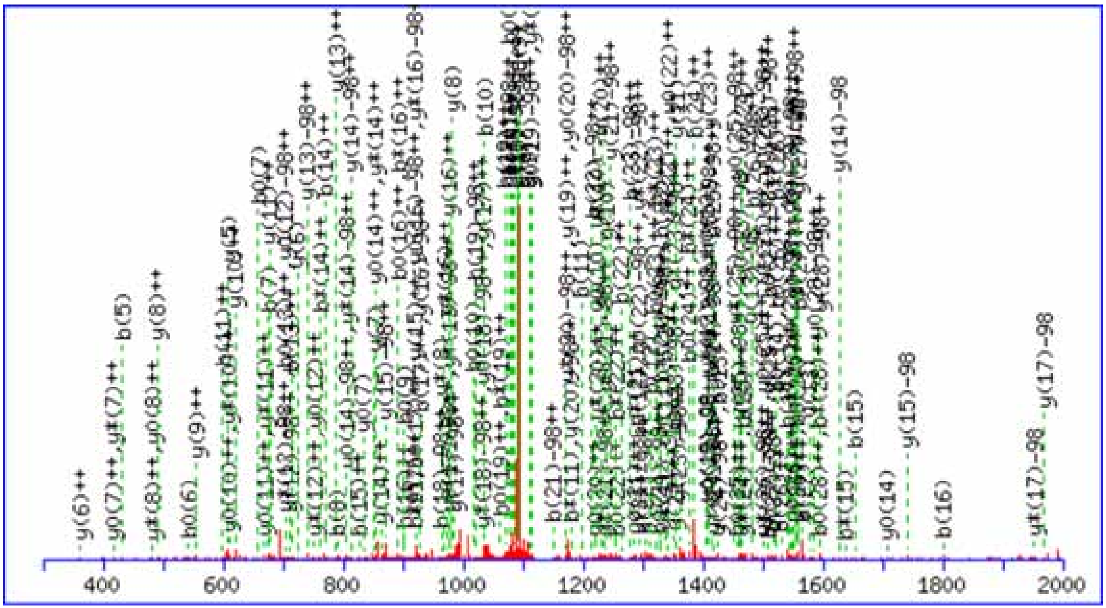
Matched b ions: b(7), b(8), b(10), b(12), b(13), b(14), b(15), b(16), b(17)++, b(18)-98, b(18)++, b(19)-98++, b(20)-98++, b(21)-98++, b(23)-98++, b(23)++, b(24)-98++, b(24)++, b(25)-98++, b(26)-98++, b(27)++, b(28)++, b(28)-98++
Matched y ions: y(5), y(6), y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(13)-98++, y(13)-98, y(13)++, y(14)-98++, y(14)++, y(14), y(15)-98++, y(15), y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(23)-98++, y(23)++, y(25)++, y(25)-98++, y(26)-98++, y(26)++, y(27)-98++, y(27)++
Precursor origin neutral loss: +

Peptide No.265

GATPAEDDEDKDIDLFGSDEEEEDKEAAR
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of GATPAEDDEDKDIDLFGSDEEEEDKEAAR
Found in EF1D_MOUSE, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 7544: 3377.510436 from(1126.844088,3+)
Title: Elution from: 46.713 to 46.713 scan no 4310 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3377.5044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K11 : Dimethyl:2H(4)13C(2) (K)
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K25 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 35 Expect: 0.038

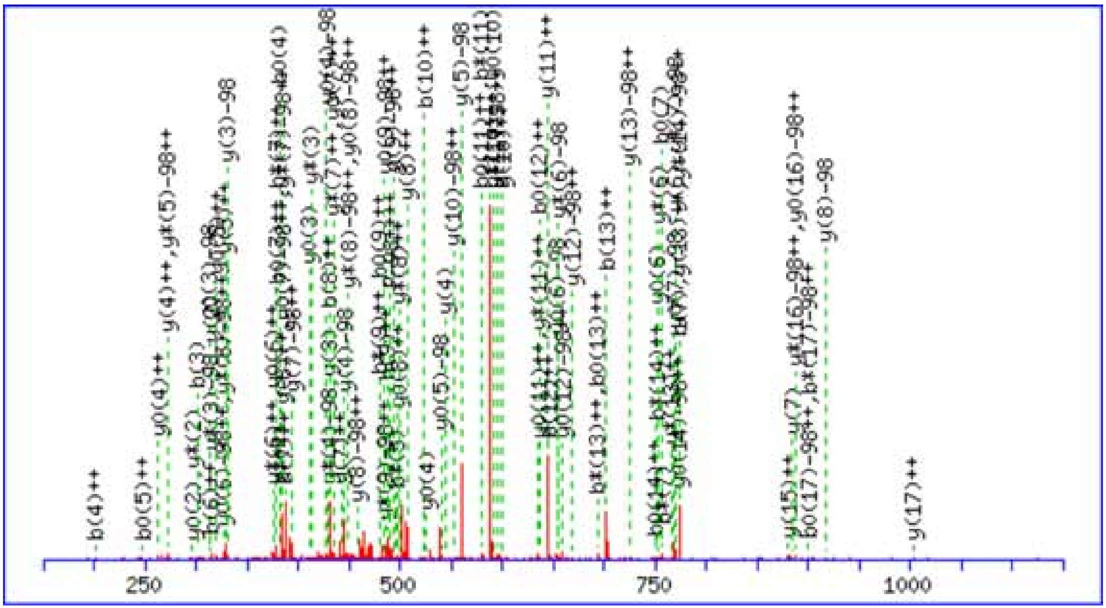
Matched b ions: b(5), b(7), b(8), b(9), b(10), b(11)++, b(11), b(12), b(13), b(13)++, b(14), b(14)++, b(15), b(15)++, b(16), b(16)++, b(17)++, b(18)-98++, b(19)-98++, b(19)++, b(20)-98++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(23)++, b(24)++, b(24)-98++, b(25)++, b(25)-98++, b(26)-98++, b(26)++, b(27)++, b(27)-98++, b(28)-98++
Matched y ions: y(5), y(6)++, y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)-98++, y(13)-98++, y(13)-98, y(13)++, y(13), y(14)-98, y(14)-98++, y(14)++, y(15)-98++, y(15)-98, y(15)++, y(16)-98++, y(16)++, y(17)-98, y(17)++, y(17)-98++, y(18)++, y(19)++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(23)-98++, y(23)++, y(24)-98++, y(25)-98++, y(25)++, y(26)++, y(26)-98++, y(27)-98++, y(28)-98++
Precursor origin neutral loss: +

Peptide No.266

GDQVLNFSDAEDLIDDSK
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of GDQVLNFSDAEDLIDDSK
Found in MCRS1_MOUSE, Microspherule protein 1 OS=Mus musculus GN=Mcrs1 PE=1 SV=1

Match to Query 4814: 2059.863672 from(515.973194,4+)
Title: Elution from: 33.726 to 33.726 scan no 2604 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2059.8623
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.0021

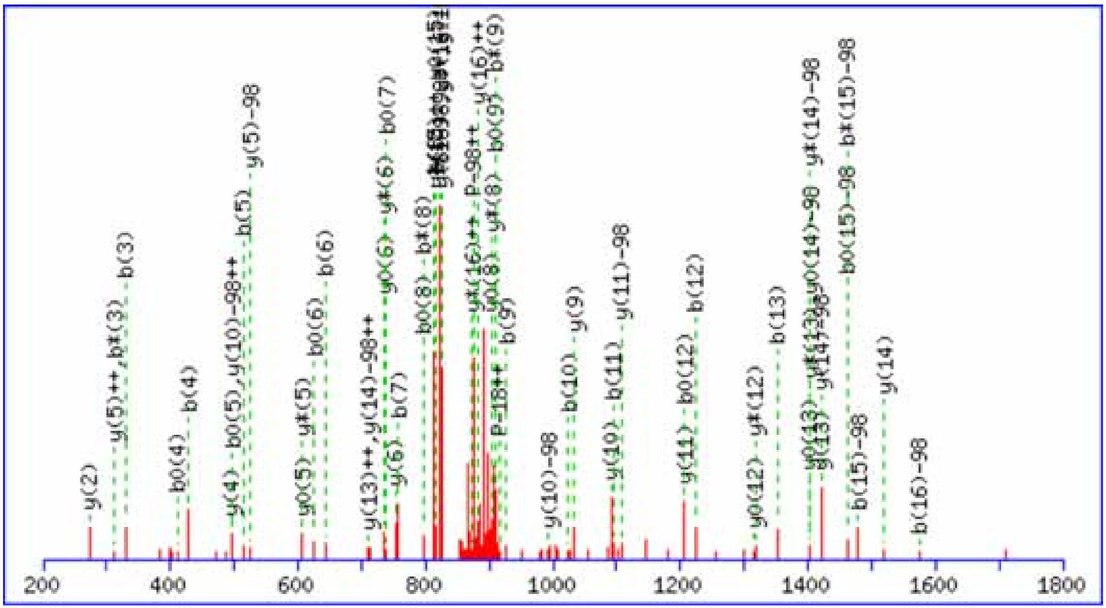
Matched b ions: b(3), b(4)++, b(6)++, b(7)++, b(7), b(8)++, b(9)++, b(10)++, b(11)++, b(12)++, b(13)++
Matched y ions: y(2), y(3)-98, y(3), y(4)++, y(4)-98, y(4), y(5)-98, y(5)++, y(6)++, y(6), y(7), y(7)-98++, y(7)++, y(8)++, y(8)-98, y(8)-98++, y(9)-98++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(13)++, y(13)-98++, y(15)++, y(17)++
Precursor origin neutral loss:

Peptide No.267

GDQVSQNGLPAEQGSPR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of GDQVSQNGLPAEQGSPR
Found in SPTB2_MOUSE, Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2

Match to Query 4656: 1846.819956 from(924.417254,2+)
Title: Elution from: 30.687 to 30.687 scan no 2399 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1846.8211
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 5.1e-006

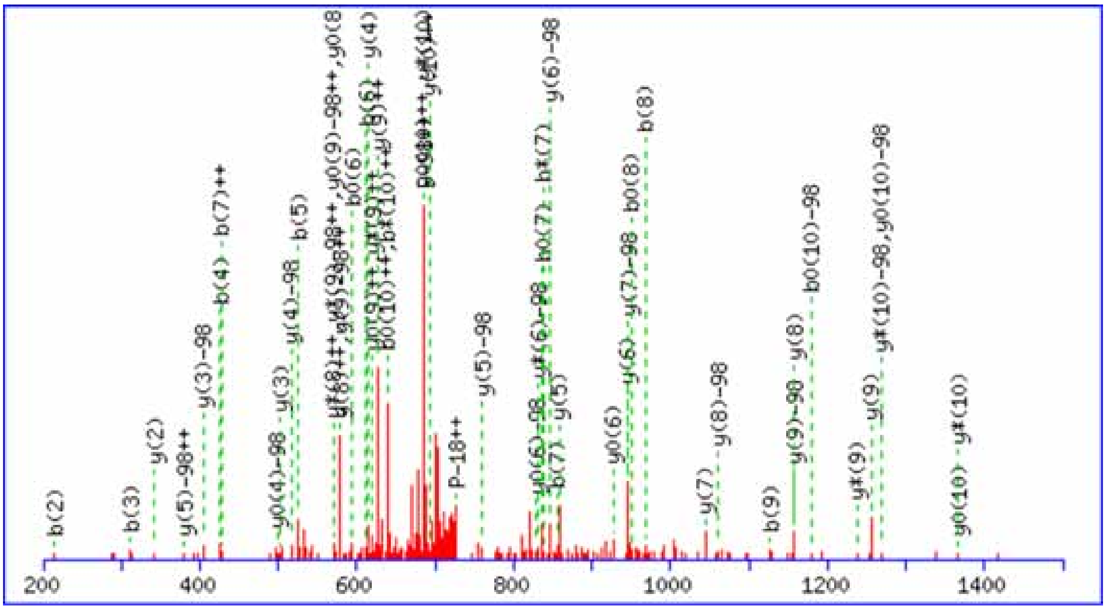
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13), b(15)-98, b(16)-98
Matched y ions: y(2), y(4), y(5)++, y(5)-98, y(6), y(7), y(8)-98, y(9), y(10), y(10)-98++, y(10)-98, y(11), y(11)-98, y(13), y(13)++, y(14)-98, y(14), y(14)-98++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.268

GEPNVSYICSR
Confirmed sites: @Y:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of GEPNVSYICSR
Found in GSK3B_MOUSE, Glycogen synthase kinase-3 beta OS=Mus musculus GN=Gsk3b PE=1 SV=2

Match to Query 2295: 1468.546020 from(735.280286,2+)
Title: Elution from: 37.177 to 37.177 scan no 3286 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1468.5459
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y7 : Phospho (Y)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.028

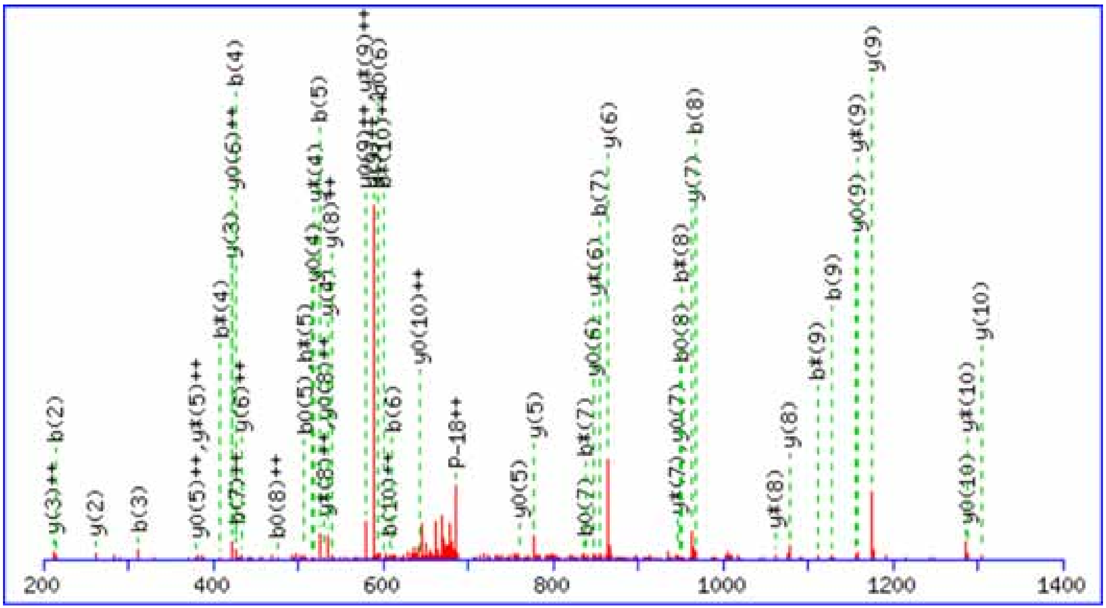
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)++, b(7), b(8), b(9)
Matched y ions: y(2), y(3)-98, y(3), y(4)-98, y(4), y(5), y(5)-98++, y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)++, y(8), y(8)-98, y(9)-98++, y(9)-98, y(9), y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.269

GEPNVSYICSR
Confirmed sites: @Y:7
Ambiguous sites:

MS/MS Fragmentation of GEPNVSYICSR
Found in GSK3A_MOUSE, Glycogen synthase kinase-3 alpha OS=Mus musculus GN=Gsk3a PE=1 SV=2

Match to Query 1547: 1388.580054 from(695.297303,2+)
Title: Elution from: 35.762 to 35.762 scan no 2876 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1388.5795
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y7 : Phospho (Y)
Ions Score: 54 Expect: 6.3e-005

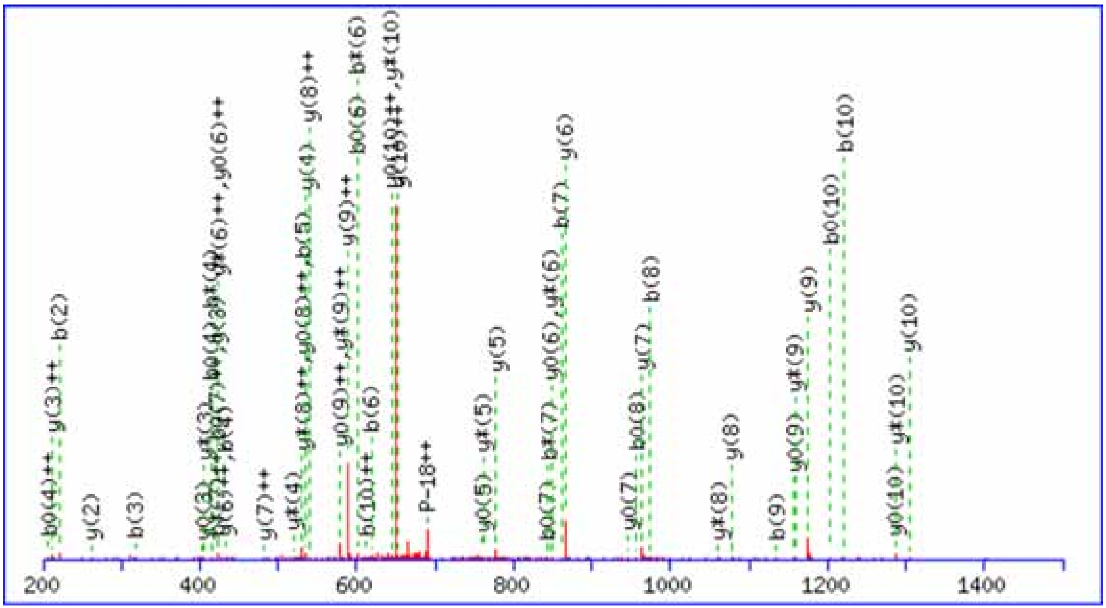
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(7)++, b(8), b(9), b(10)++
Matched y ions: y(2), y(3), y(3)++, y(4), y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(9)++, y(9), y(10)
Precursor origin neutral loss: +

Peptide No.270

GEPNVSYICSR
Confirmed sites: @Y:7
Ambiguous sites:

MS/MS Fragmentation of GEPNVSYICSR
Found in GSK3A_MOUSE, Glycogen synthase kinase-3 alpha OS=Mus musculus GN=Gsk3a PE=1 SV=2

Match to Query 1321: 1394.612264 from(698.313408,2+)
Title: Elution from: 35.458 to 35.458 scan no 2737 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1394.6114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y7 : Phospho (Y)
Ions Score: 57 Expect: 4.1e-005

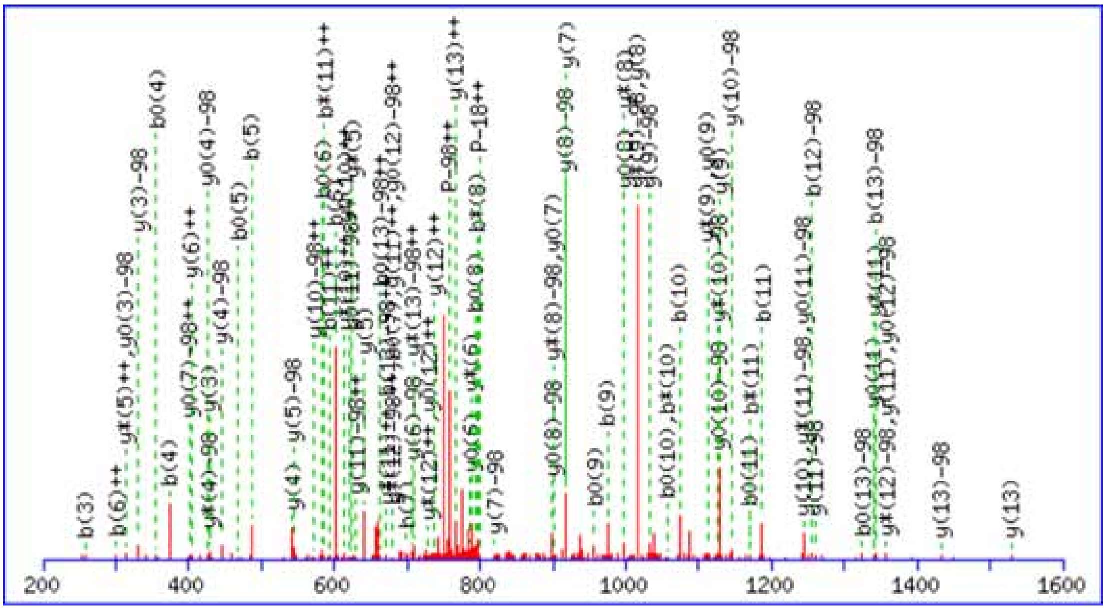
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(10)++
Matched y ions: y(2), y(3), y(3)++, y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9)++, y(9), y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.271

GGDDLDPNYVLSSR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of GGDDLDPNYVLSSR
Found in KCRM_MOUSE, Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1

Match to Query 2762: 1614.693672 from(808.354112,2+)
Title: Elution from: 46.674 to 46.674 scan no 4353 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1614.6927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 **Expect:** 7.5e-006

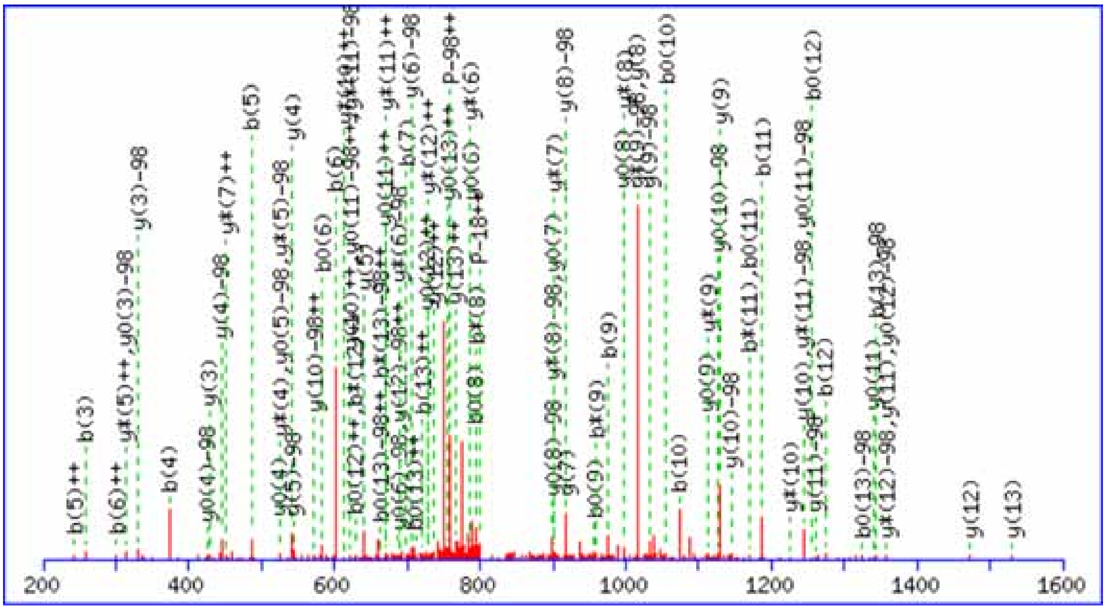
Matched b ions: b(3), b(4), b(5), b(6), b(6)++, b(7), b(9), b(10), b(11), b(11)++, b(12)-98, b(13)-98, b(13)-98++
Matched y ions: y(3)-98, y(3), y(4)-98, y(4), y(5), y(5)-98, y(6)++, y(6)-98, y(7), y(7)-98, y(8)-98, y(8), y(9), y(9)-98, y(10), y(10)-98, y(10)-98++, y(11), y(11)-98, y(11)-98++, y(11)++, y(12)++, y(13), y(13)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.272

GGDDLDPNYVLSSR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of GGDDLDPNYVLSSR
Found in KCRM_MOUSE, Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1

Match to Query 2688: 1614.694522 from(808.354537,2+)
Title: Elution from: 46.513 to 46.513 scan no 4311 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1614.6927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 78 Expect: 4.4e-007

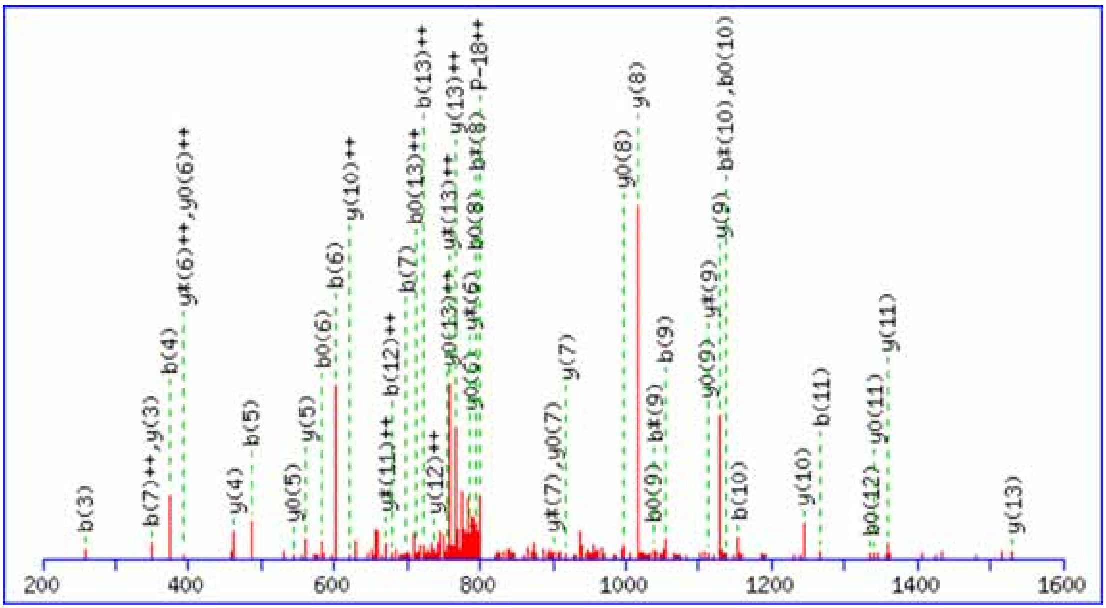
Matched b ions: b(3), b(4), b(5), b(5)++, b(6), b(6)++, b(7), b(9), b(10), b(11), b(12), b(13)-98, b(13)++
Matched y ions: y(3)-98, y(3), y(4), y(4)-98, y(5), y(5)-98, y(6)-98, y(7), y(8)-98, y(8), y(9), y(9)-98, y(10), y(10)-98, y(10)-98++, y(10)++, y(11), y(11)-98, y(12), y(12)++, y(12)-98++, y(13), y(13)++
Precursor origin neutral loss: +

Peptide No.273

GGDDLDPNYVLSSR
Confirmed sites: @Y:9
Ambiguous sites:

MS/MS Fragmentation of GGDDLDPNYVLSSR
Found in KCRM_MOUSE, Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1

Match to Query 2687: 1614.691986 from(808.353269,2+)
Title: Elution from: 49.727 to 49.727 scan no 4695 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1614.6927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y9 : Phospho (Y)
Ions Score: 51 Expect: 0.00023

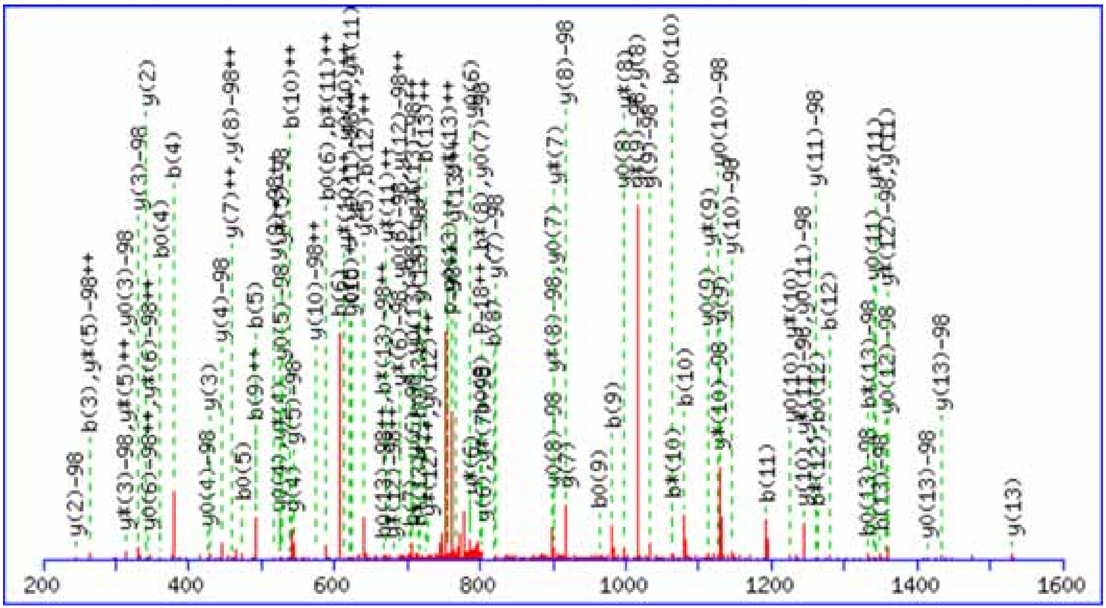
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(9), b(10), b(11), b(12)++, b(13)++
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(9), y(10), y(10)++, y(11), y(12)++, y(13)++, y(13)
Precursor origin neutral loss: +

Peptide No.274

GGDDLDPNYVLSSR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of GGDDLDPNYVLSSR
Found in KCRM_MOUSE, Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1

Match to Query 2717: 1620.726136 from(811.370344,2+)
Title: Elution from: 46.551 to 46.551 scan no 4316 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1620.7245
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 Expect: 2.9e-006

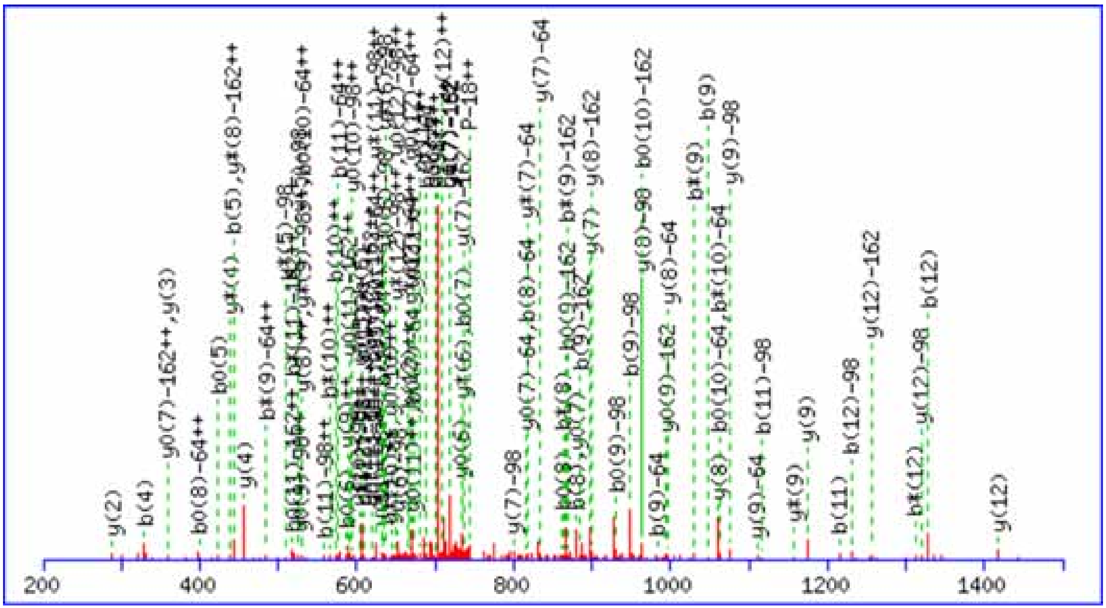
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(9)++, b(10), b(10)++, b(11), b(12)++, b(12), b(13)-98, b(13)++
Matched y ions: y(2)-98, y(2), y(3)-98, y(3), y(4), y(4)-98, y(5), y(5)-98, y(6)-98, y(6), y(7), y(7)++, y(7)-98, y(8)-98, y(8), y(8)-98++, y(9), y(9)-98, y(9)-98++, y(10), y(10)-98, y(10)-98++, y(10)++, y(11), y(11)-98, y(12)-98++, y(13), y(13)-98, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.275

GGGELYMQSPALR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of GGGELYMQSPALR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 2442: 1501.664712 from(751.839632,2+)
Title: Elution from: 36.994 to 36.994 scan no 3262 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1501.6636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.031

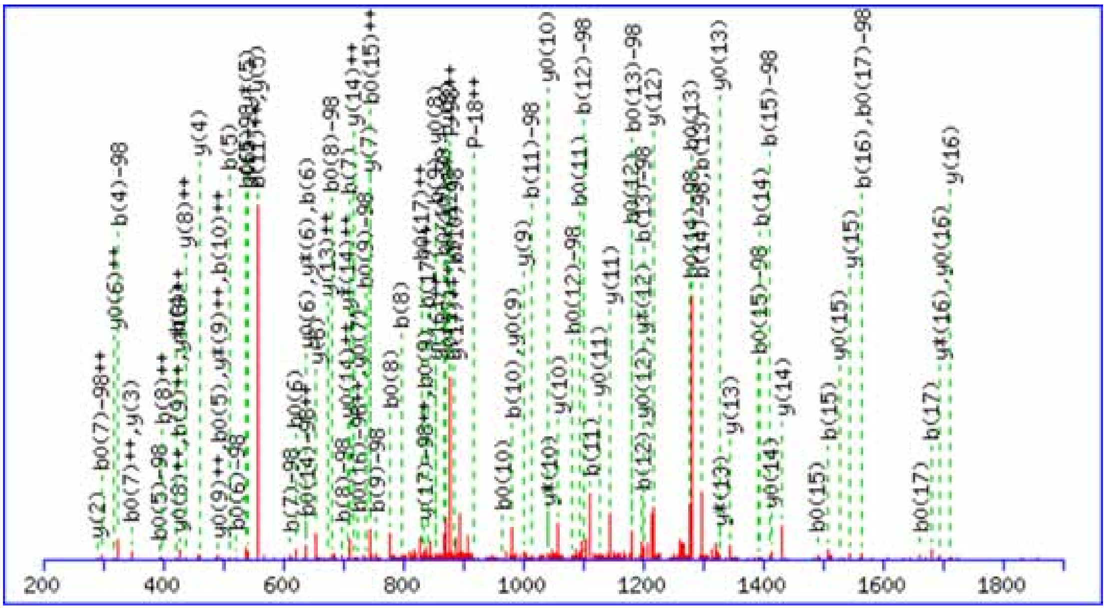
Matched b ions: b(4), b(5), b(6), b(8), b(9)-98, b(9), b(10)++, b(11), b(11)-98, b(11)-98++, b(11)++, b(12)-98, b(12), b(12)++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(8)++, y(9), y(9)-98, y(9)++, y(10)-98++, y(11)-98++, y(11)++, y(12), y(12)-98, y(12)++
Precursor origin neutral loss: +

Peptide No.276

GGSISEASGEESVPLGDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 4015: 1853.805080 from(927.909816,2+)
Title: Elution from: 39.340 to 39.340 scan no 3387 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1853.8044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 97 Expect: 8e-009

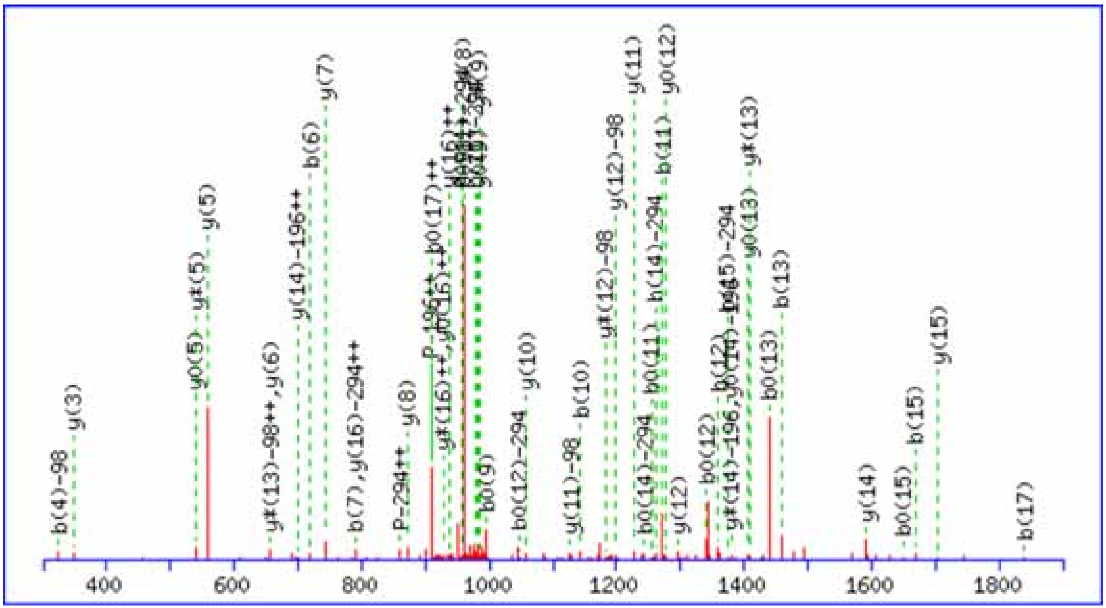
Matched b ions: b(4)-98, b(4), b(5), b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(8)++, b(8), b(9)++, b(9)-98, b(9), b(10), b(10)++, b(10)-98, b(11)++, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(14)-98, b(14), b(15), b(15)-98, b(16), b(17), b(17)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(11), y(12), y(13), y(13)++, y(14), y(14)++, y(15), y(16), y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.277

GGSISEASGEESVPLGDR
Confirmed sites: @S:3,@S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 5061: 2013.738608 from(1007.876580,2+)
Title: Elution from: 44.847 to 44.847 scan no 4080 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2013.7370
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.00031

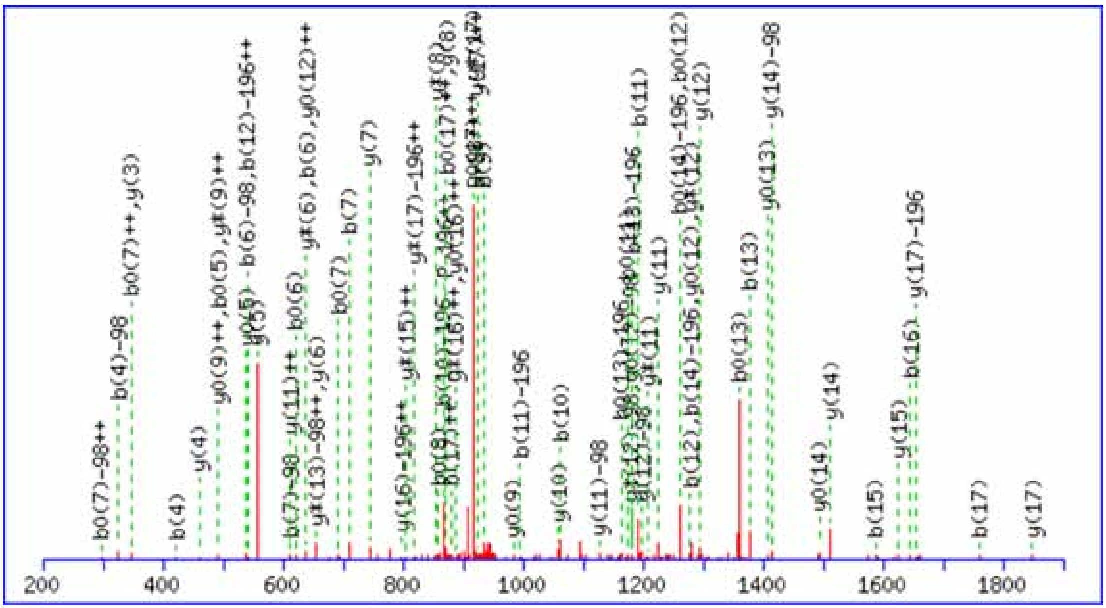
Matched b ions: b(4)-98, b(6), b(7)-98++, b(7), b(7)-98, b(8)-196, b(8)-98, b(8), b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(11)-196++, b(11)-294, b(12), b(12)-98, b(13)-98, b(13), b(13)-196, b(14)-196, b(14)-98, b(14)-294, b(15), b(15)-98, b(15)-98++, b(15)-294, b(17), b(17)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(10), y(11), y(11)-98, y(12), y(12)-98, y(14), y(14)-98, y(14)-196++, y(15)-98, y(15), y(16)-294++, y(16)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.278

GGSISEASGEESVPLGDR
Confirmed sites: @S:3,@S:8
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 5285: 1933.770570 from(967.892561,2+)
Title: Elution from: 41.803 to 41.803 scan no 3904 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1933.7707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 79 Expect: 3.2e-007

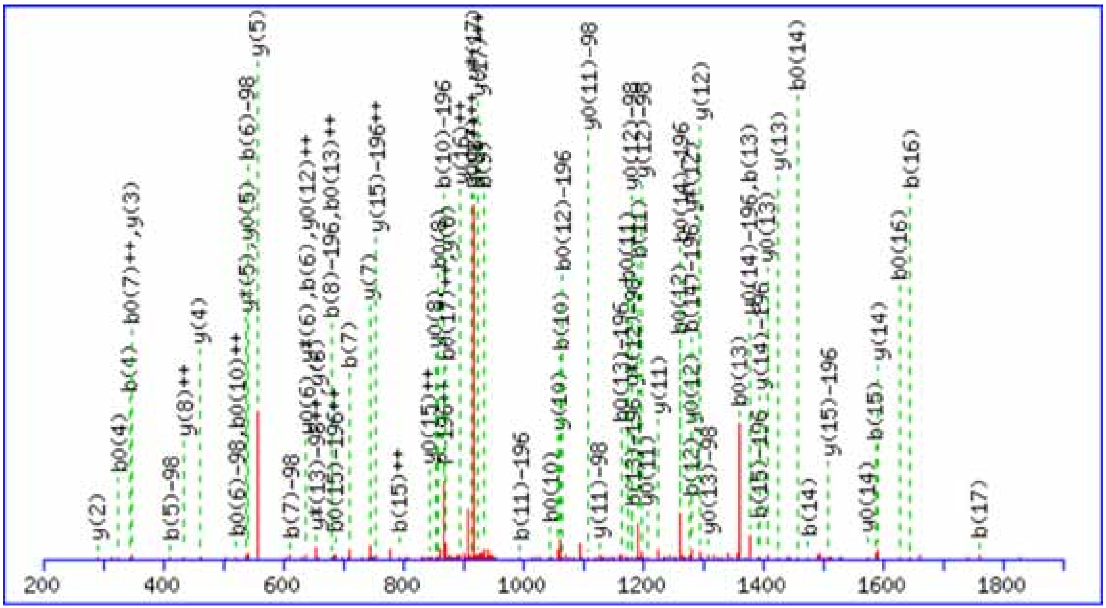
Matched b ions: b(4)-98, b(4), b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(9), b(10), b(10)-196, b(11), b(11)-98, b(11)-196, b(12)-196++, b(12)-98, b(12), b(13), b(13)-98, b(13)-196, b(14)-98, b(14)-196, b(15), b(15)-98, b(16), b(17), b(17)-98, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11)-98, y(11), y(11)++, y(12), y(12)-98, y(14)-98, y(14), y(15), y(16)-196++, y(17), y(17)-196, y(17)++
Precursor origin neutral loss: +

Peptide No.279

GGSISEASGEESVPLGDR
Confirmed sites: @S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 4109: 1933.771816 from(967.893184,2+)
Title: Elution from: 41.850 to 41.850 scan no 3602 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1933.7707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 1.7e-005

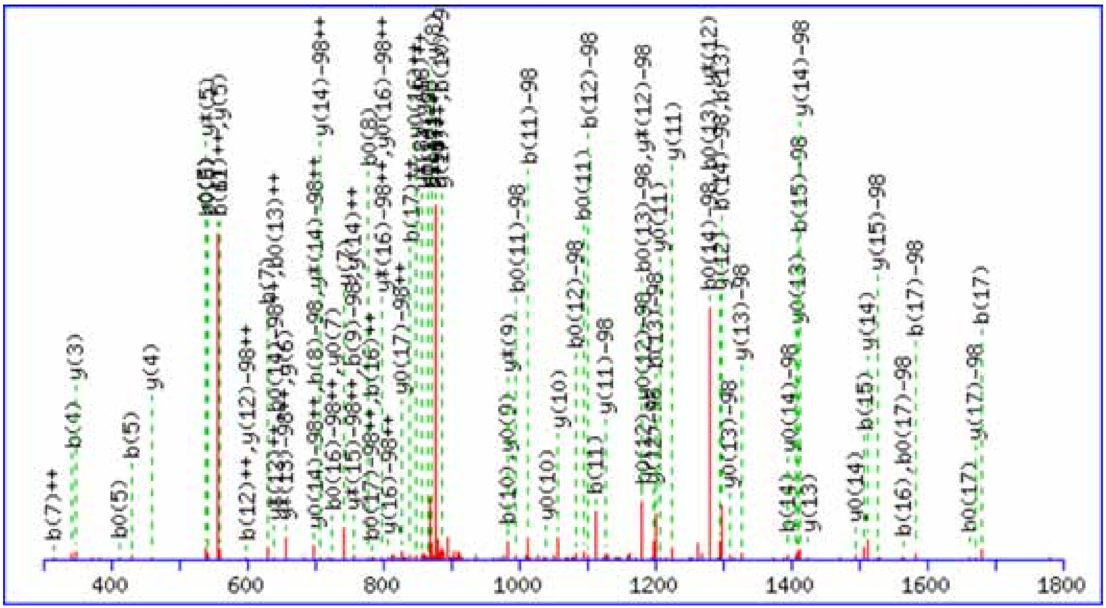
Matched b ions: b(4), b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8)-196, b(9), b(9)-98, b(10), b(10)-196, b(11)-98, b(11), b(11)-196, b(12), b(12)-98, b(13), b(13)-98, b(13)-196, b(14)-98, b(14)-196, b(14), b(15)-98, b(15), b(15)++, b(15)-196, b(16), b(17), b(17)-98, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(10), y(11)-98, y(11), y(12), y(12)-98, y(13), y(14), y(14)-98, y(14)-196, y(14)-98++, y(15)-196++, y(15)-196, y(15)-98++, y(16)-98++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.280

GGSISEASGEESVPLGDR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 4707: 1853.805322 from(927.909937,2+)
Title: Elution from: 38.671 to 38.671 scan no 3488 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1853.8044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 Expect: 5.8e-009

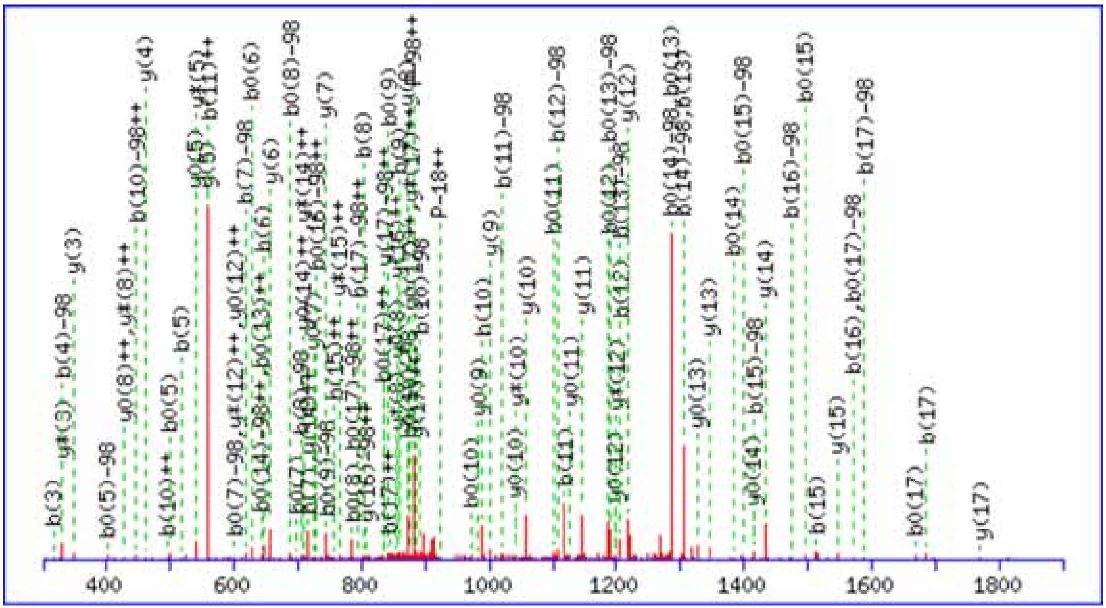
Matched b ions: b(4), b(5), b(6), b(7), b(7)++, b(8)-98, b(9)-98, b(10), b(10)-98, b(11)++, b(11)-98, b(11), b(12)-98, b(12)++, b(13)-98, b(13), b(14)-98, b(14), b(15)-98, b(15), b(16), b(16)++, b(17)-98, b(17), b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11)-98, y(11), y(12), y(12)-98, y(12)-98++, y(13)-98, y(13), y(14)-98, y(14), y(14)++, y(14)-98++, y(15)-98, y(16)-98++, y(16)++, y(17)-98, y(17)++
Precursor origin neutral loss: +

Peptide No.281

GGSISEASGEESVPLGDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 4184: 1859.836320 from(930.925436,2+)
Title: Elution from: 39.436 to 39.436 scan no 3428 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1859.8362
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 99 **Expect:** 5.9e-009

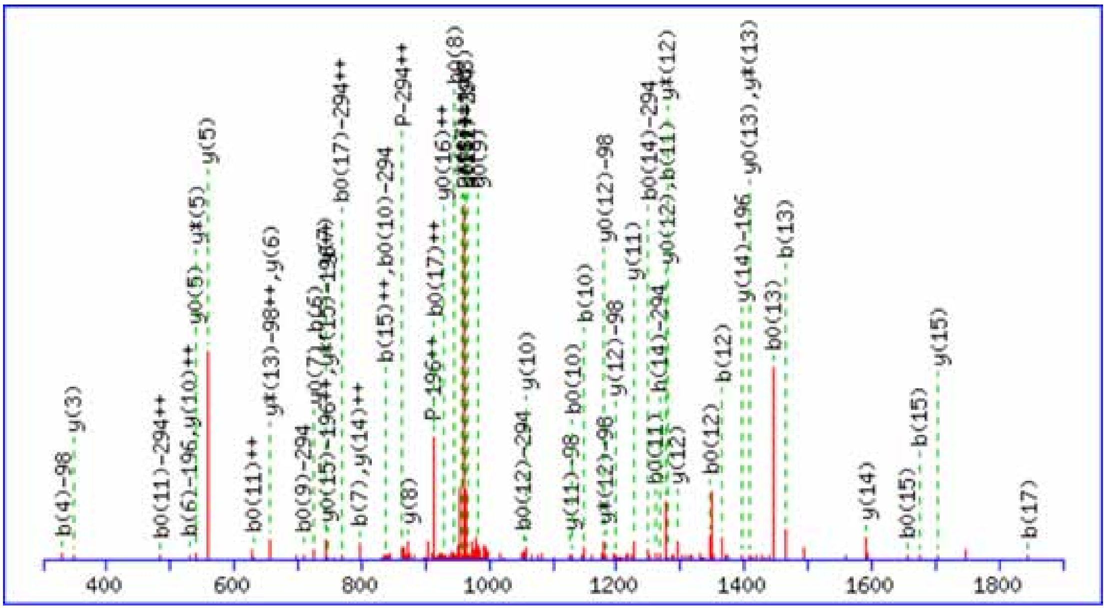
Matched b ions: b(3), b(4)-98, b(5), b(6), b(7), b(7)-98, b(8), b(8)-98, b(9), b(10), b(10)-98++, b(10)++, b(10)-98, b(11), b(11)-98, b(11)++, b(12)-98, b(12), b(13), b(13)-98, b(14)-98, b(15), b(15)-98, b(15)++, b(16), b(16)-98, b(17), b(17)-98, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)++, y(14), y(15), y(16)-98++, y(16)++, y(17), y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.282

GGSISEASGEESVPLGDR
Confirmed sites: @S:3,@S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 5091: 2019.770088 from(1010.892320,2+)
Title: Elution from: 44.696 to 44.696 scan no 4063 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2019.7689
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 4.6e-005

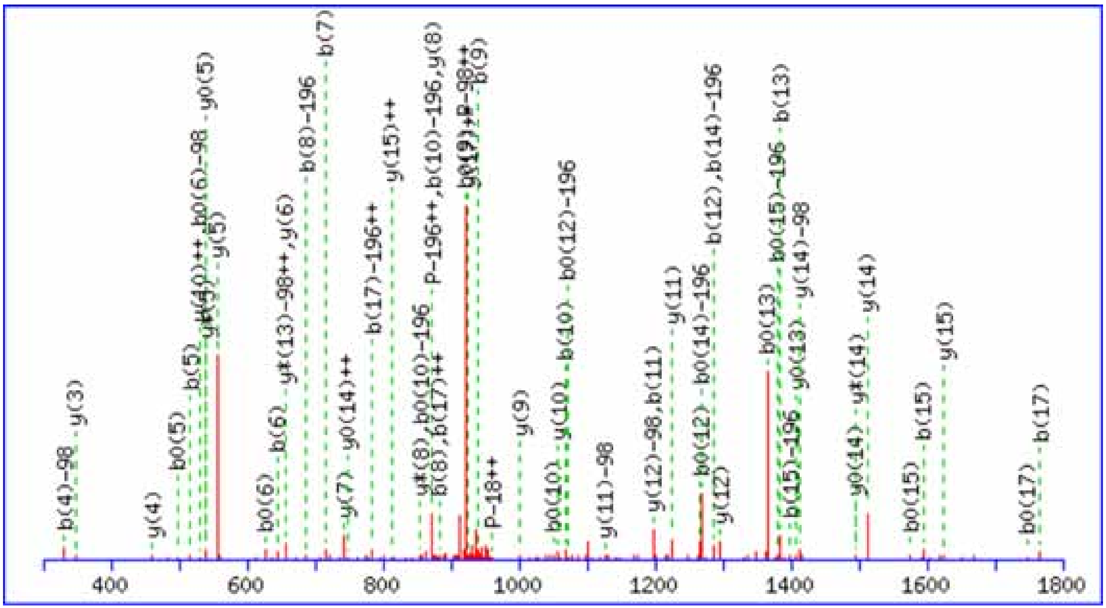
Matched b ions: b(4)-98, b(6)-196, b(6), b(6)-98, b(7), b(7)-98, b(8), b(8)-196, b(8)-98, b(9)-98, b(10)-196, b(10)-98, b(10), b(11)-98, b(11), b(11)-196, b(12), b(12)-98, b(13), b(13)-98, b(14)-98, b(14)-196, b(14)-294, b(15), b(15)++, b(16)-196++, b(17)-98, b(17), b(17)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(10)++, y(10), y(11), y(11)-98, y(12), y(12)-98, y(14), y(14)++, y(14)-98, y(14)-196, y(15), y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.283

GGSISEASGEESVPLGDR
Confirmed sites: @S:3,@S:8
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 4501: 1939.802324 from(970.908438,2+)
Title: Elution from: 41.508 to 41.508 scan no 3648 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1939.8025
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 79 Expect: 3.5e-007

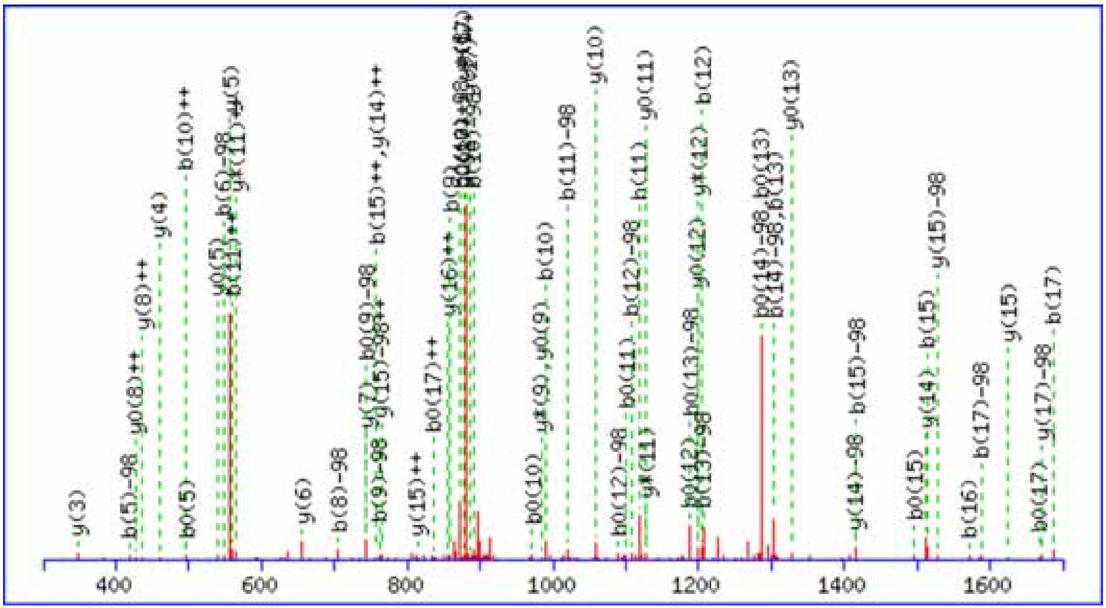
Matched b ions: b(4)-98, b(5), b(6), b(7), b(8)-98, b(8)-196, b(8), b(9), b(9)-98, b(10)-196, b(10), b(11)-98, b(11), b(12), b(13), b(13)-98, b(14)-196, b(15), b(15)-98, b(15)-196, b(17)-98, b(17), b(17)-196++, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(11)-98, y(12)-98, y(12), y(14), y(14)-98, y(15), y(15)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.284

GGSISEASGEESVPLGDR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 3716: 1859.836802 from(930.925677,2+)
Title: Elution from: 38.422 to 38.422 scan no 3239 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1859.8362
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 91 Expect: 3.4e-008

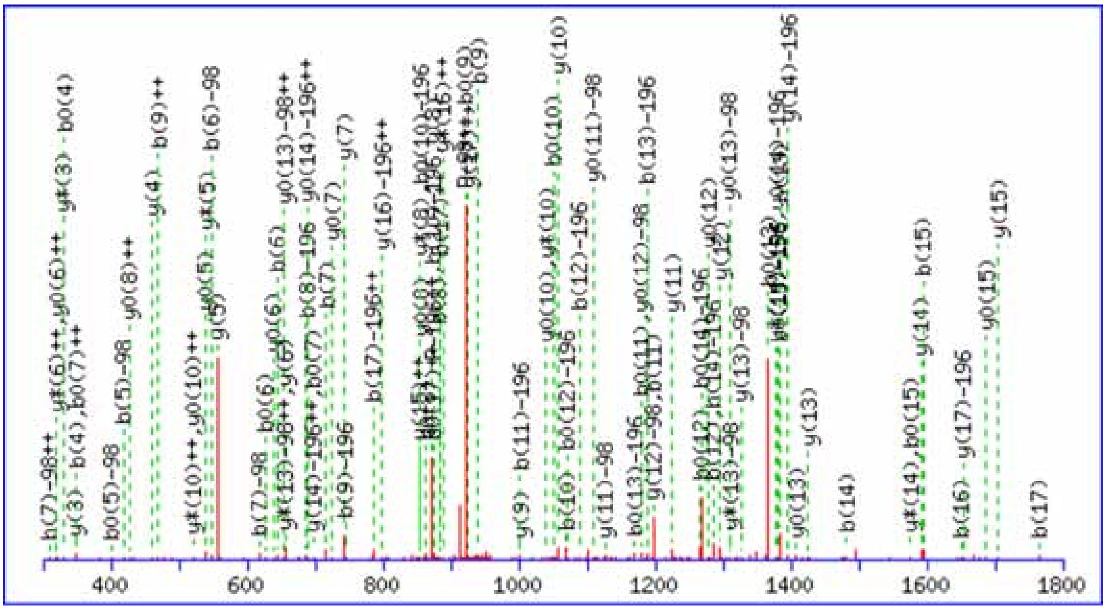
Matched b ions: b(5)-98, b(6)-98, b(8)-98, b(9)-98, b(9), b(10), b(10)++, b(10)-98, b(11), b(11)++, b(11)-98, b(12)-98, b(12), b(13)-98, b(13), b(14)-98, b(15)-98, b(15), b(15)++, b(16), b(17)-98, b(17)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(10), y(14)-98, y(14), y(14)++, y(15)-98++, y(15)-98, y(15), y(15)++, y(16)++, y(17)-98, y(17)++
Precursor origin neutral loss: +

Peptide No.285

GGSISEASGEESVPLGDR
Confirmed sites: @S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 4673: 1939.803002 from(970.908777,2+)
Title: Elution from: 41.850 to 41.850 scan no 3718 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1939.8025
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 **Expect:** 2.4e-006

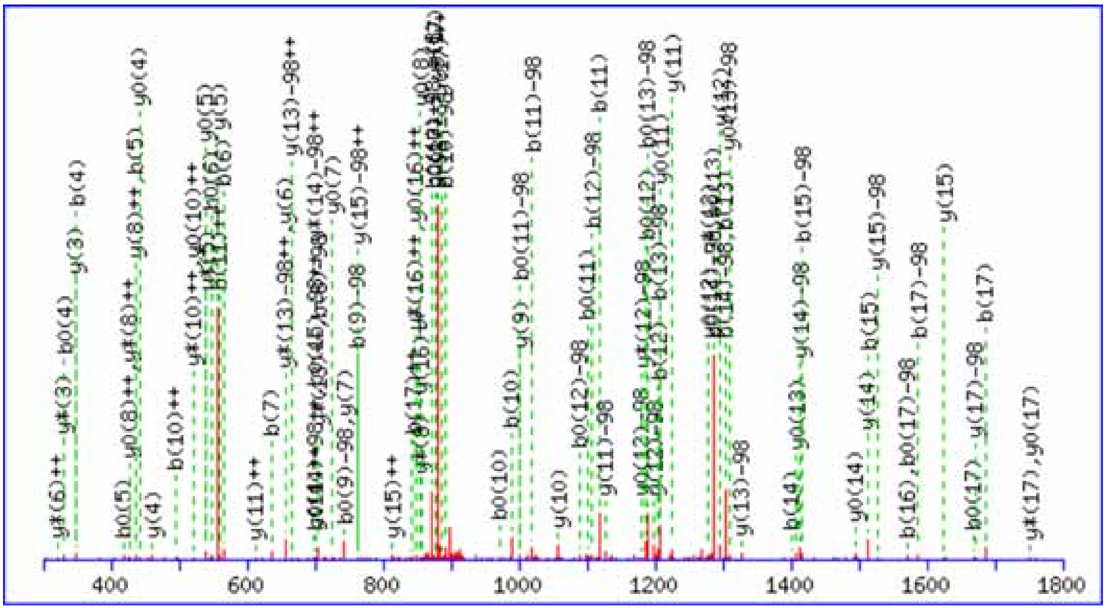
Matched b ions: b(4), b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(7)-98++, b(8)-98, b(8)-196, b(8), b(9)++, b(9)-98, b(9)-196, b(9), b(10)-196, b(10), b(11), b(11)-98, b(11)-196, b(12), b(12)-196, b(12)-98, b(13)-98, b(13), b(13)-196, b(14)-98, b(14)-196, b(14), b(15), b(15)-98, b(16), b(17)-98, b(17), b(17)-196++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12)-98, y(12), y(13), y(13)-98, y(14)-98, y(14), y(14)-196, y(14)-196++, y(15), y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(17)-196, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.286

GGSISEASGEESVPLGDR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 4185: 1859.836510 from(930.925531,2+)
Title: Elution from: 38.448 to 38.448 scan no 3296 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1859.8362
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 86 Expect: 1.2e-007

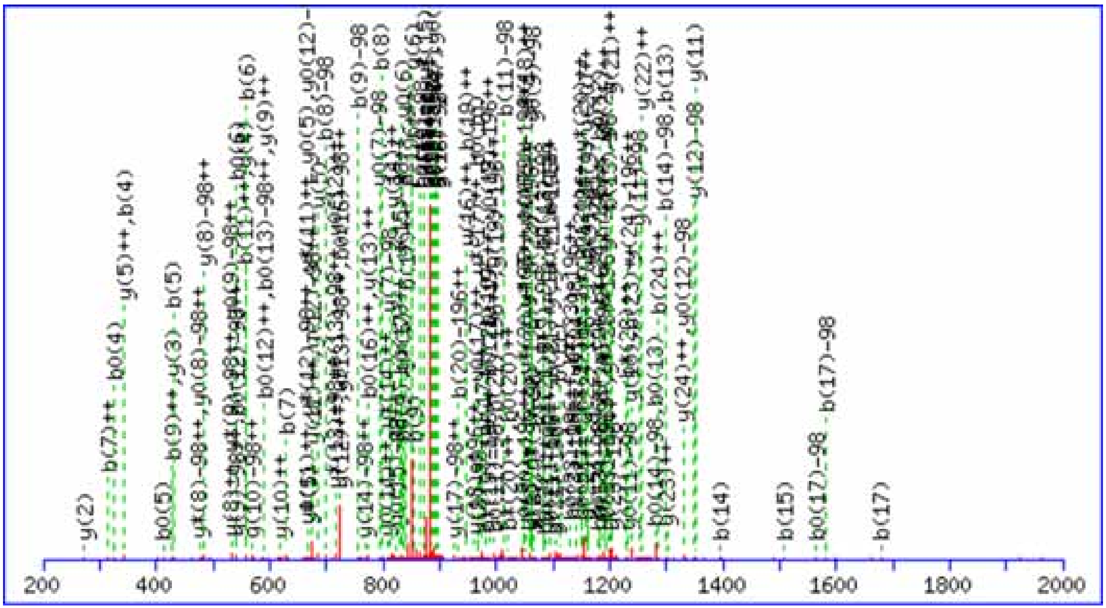
Matched b ions: b(4), b(5), b(6), b(7), b(8)-98, b(9)-98, b(10), b(10)++, b(10)-98, b(11), b(11)-98, b(11)++, b(12), b(12)-98, b(13), b(13)-98, b(14)-98, b(14), b(14)++, b(15), b(15)-98, b(16), b(17), b(17)-98, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11)-98, y(11)++, y(11), y(12)-98, y(12), y(13)-98, y(13)-98++, y(14)-98, y(14), y(15), y(15)-98, y(15)-98++, y(15)++, y(16)++, y(17)-98, y(17)++
Precursor origin neutral loss: +

Peptide No.287

GGSISEASGEESVPLGDRGSQEKPR
Confirmed sites: @S:8,@S:20
Ambiguous sites:

MS/MS Fragmentation of GGSISEASGEESVPLGDRGSQEKPR
Found in JSPR1_MOUSE, Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2

Match to Query 7149: 2744.207292 from(915.743040,3+)
Title: Elution from: 34.626 to 34.626 scan no 2732 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2744.2055
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K23 : Dimethyl (K)
Ions Score: 62 **Expect:** 5.2e-005

Matched b ions: b(4), b(5), b(6), b(7), b(7)++, b(8)-98, b(8), b(9)++, b(9)-98, b(9), b(10)-98, b(10), b(11), b(11)++, b(11)-98, b(13), b(13)-98, b(14), b(14)-98, b(15), b(17)-98, b(17), b(17)++, b(19)++, b(20)-98++, b(20)-196++, b(21)-98++, b(21)-196++, b(21)++, b(22)-98++, b(22)-196++, b(22)++, b(23)++, b(23)-98++, b(23)-196++, b(24)-98++, b(24)-196++, b(24)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7)-98, y(8)++, y(8)-98++, y(8)-98, y(8), y(9)++, y(9)-98++, y(9)-98, y(9), y(10)++, y(10), y(10)-98++, y(10)-98, y(11)++, y(11)-98, y(11), y(12)++, y(12)-98++, y(12)-98, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(18)-196++, y(19)-98++, y(19)++, y(19)-196++, y(20)-196++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(21)-196++, y(22)-98++, y(22)-196++, y(22)++, y(23)++, y(23)-98++, y(23)-196++, y(24)-98++, y(24)++, y(24)-196++
Precursor origin neutral loss: +

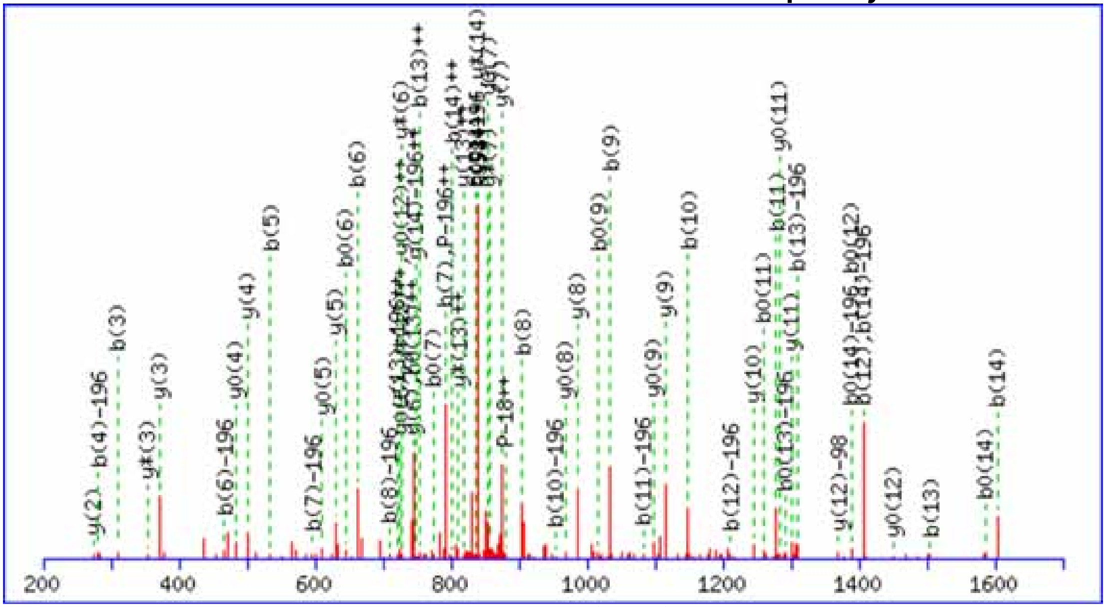
Peptide No.288

GGSSGEELEDEEPVK
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of GGSSGEELEDEEPVK
Found in HDGR2_MOUSE, Hepatoma-derived growth factor-related protein 2 OS=Mus musculus GN=Hdgfrp2 PE=1 SV=1

Match to Query 4167: 1776.674490 from(889.344521,2+)

Title: Elution from: 39.734 to 39.734 scan no 3630 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1776.6743
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 79 Expect: 2e-007

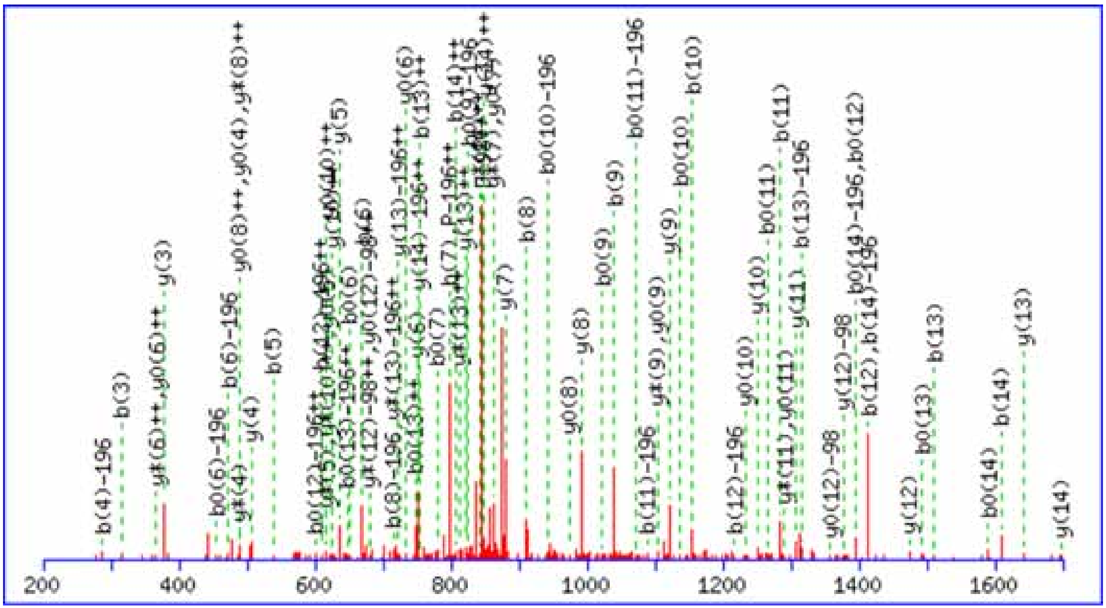
Matched b ions: b(3), b(4)-196, b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(6)-196, b(7), b(7)-98, b(7)-196, b(8), b(8)-196, b(8)-98, b(9), b(9)-98, b(9)-196, b(10), b(10)-98, b(10)-196, b(11), b(11)-98, b(11)-196, b(12), b(12)-98, b(12)-196, b(13)-98, b(13), b(13)-196, b(13)++, b(14)-196, b(14)-98, b(14), b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(13)-196++, y(13)++, y(14)-196++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.289

GGSSGEELEDEEPVK
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of GGSSGEELEDEEPVK
Found in HDGR2_MOUSE, Hepatoma-derived growth factor-related protein 2 OS=Mus musculus GN=Hdgfrp2 PE=1 SV=1

Match to Query 3297: 1788.738290 from(895.376421,2+)
Title: Elution from: 39.619 to 39.619 scan no 3422 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1788.7380
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 80 **Expect:** 2.7e-007

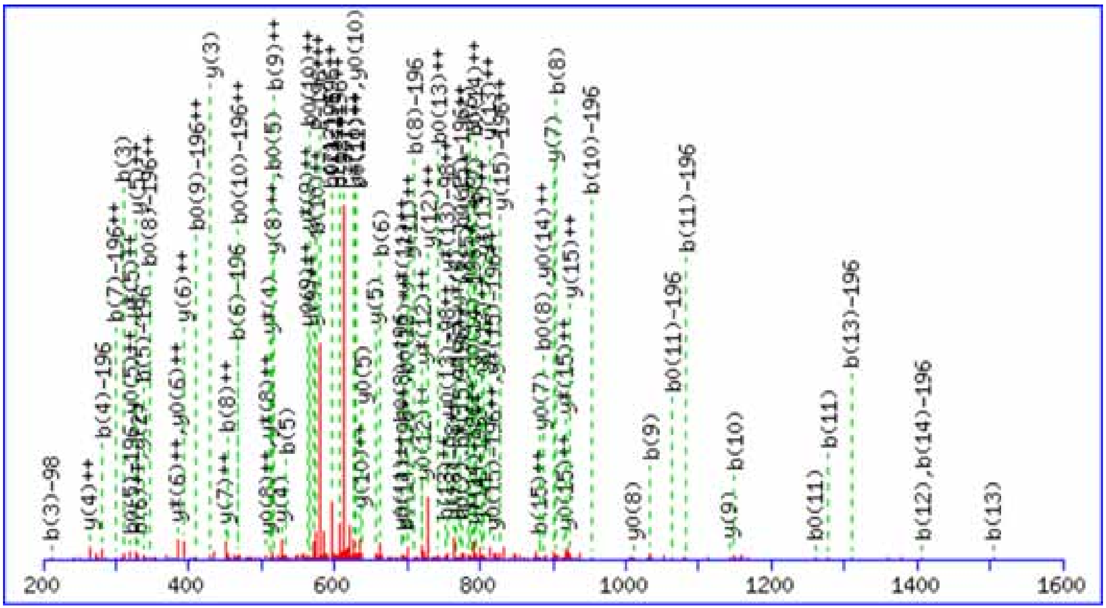
Matched b ions: b(3), b(4)-196, b(4)-98, b(5)-98, b(5), b(6), b(6)-196, b(6)-98, b(7), b(7)-98, b(8), b(8)-196, b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-196, b(11)-98++, b(12), b(12)-98, b(12)-196++, b(12)-196, b(13)-98, b(13), b(13)-196, b(13)++, b(14)-196, b(14), b(14)-98, b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(12), y(12)-98, y(13), y(13)-196++, y(13)++, y(14), y(14)-196++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.290

GGSSGEELEDEEPVKK
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of GGSSGEELEDEEPVKK
Found in HDGR2_MOUSE, Hepatoma-derived growth factor-related protein 2 OS=Mus musculus GN=Hdgfrp2 PE=1 SV=1

Match to Query 5282: 1932.801447 from(645.274425,3+)
Title: Elution from: 34.341 to 34.341 scan no 2898 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1932.8006
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K15 : Dimethyl (K)
K16 : Dimethyl (K)
Ions Score: 48 Expect: 0.00056

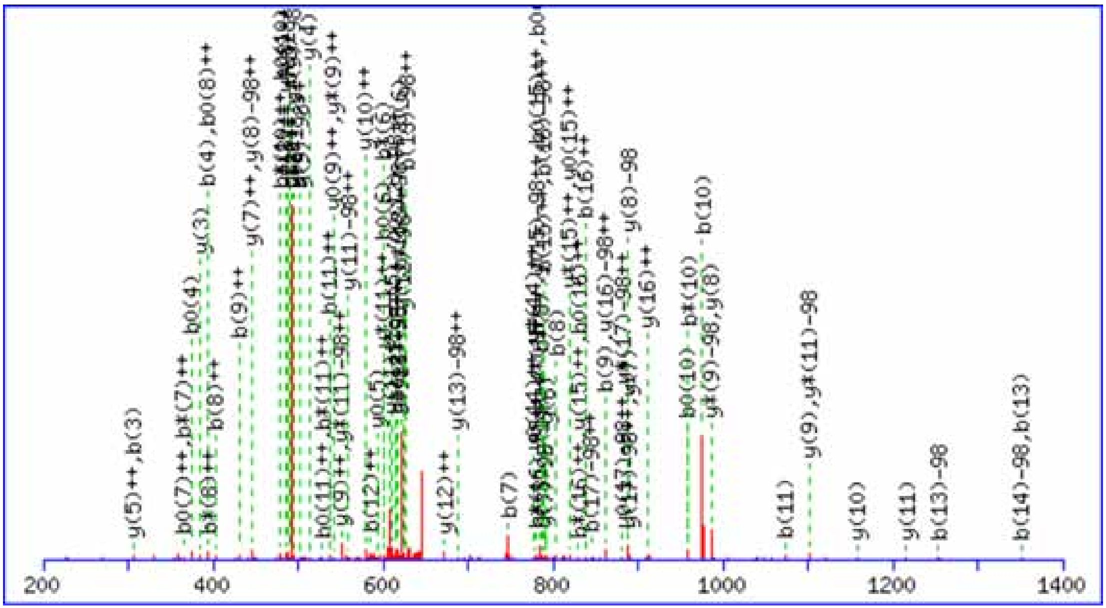
Matched b ions: b(3), b(3)-98, b(4)-196, b(4)-98, b(5)-98, b(5)-196, b(5), b(6), b(6)++, b(6)-196, b(6)-98, b(7)-196, b(7), b(7)-196++, b(7)-98, b(8)++, b(8)-196, b(8)-98, b(8), b(9), b(9)-98++, b(9)-98, b(9)++, b(10), b(10)-98, b(10)-98++, b(10)++, b(10)-196, b(11), b(11)-196, b(11)-98++, b(12), b(12)-196++, b(12)-98, b(13), b(13)-196, b(13)++, b(14)-196, b(14)-98, b(15)-98++, b(15)-196++, b(15)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(9), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)-196++, y(14)-98++, y(15)-98++, y(15)++, y(15)-196++
Precursor origin neutral loss: +

Peptide No.291

GGYSPQEGGDPPTPEPLK
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of GGYSPQEGGDPPTPEPLK
Found in MURC_MOUSE, Muscle-related coiled-coil protein OS=Mus musculus GN=Murc PE=2 SV=1

Match to Query 5431: 1960.883508 from(654.635112,3+)
Title: Elution from: 38.406 to 38.406 scan no 3453 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1960.8819
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl (K)
Ions Score: 53 Expect: 0.00029

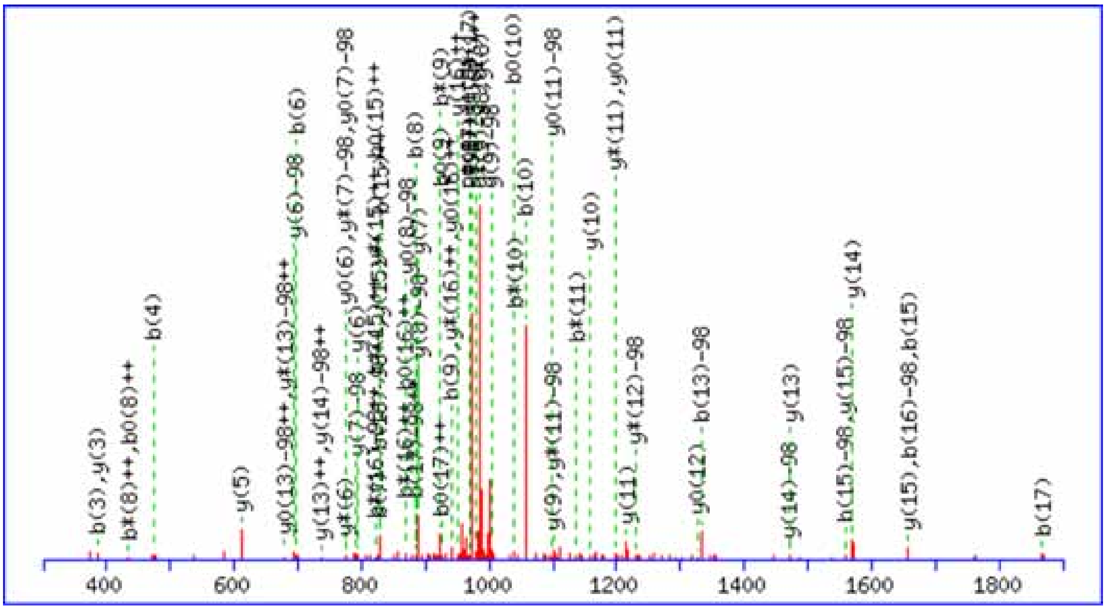
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)++, b(8), b(9), b(9)++, b(10), b(10)++, b(11), b(11)++, b(12)++, b(13), b(13)-98, b(13)-98++, b(14)-98, b(15)++, b(16)-98++, b(16)++, b(17)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6), y(7), y(7)++, y(7)-98, y(8)++, y(8)-98++, y(8), y(8)-98, y(9), y(9)++, y(9)-98++, y(10), y(10)++, y(11)++, y(11), y(11)-98++, y(12)++, y(12)-98++, y(13)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.292

GGYSPQEGGDPPTPEPLK
Confirmed sites: @Y:3,@T:13
Ambiguous sites:

MS/MS Fragmentation of GGYSPQEGGDPPTPEPLK
Found in MURC_MOUSE, Muscle-related coiled-coil protein OS=Mus musculus GN=Murc PE=2 SV=1

Match to Query 5775: 2040.849910 from(1021.432231,2+)
Title: Elution from: 41.779 to 41.779 scan no 3901 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2040.8483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y3 : Phospho (Y)
T13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl (K)
Ions Score: 43 Expect: 0.0018

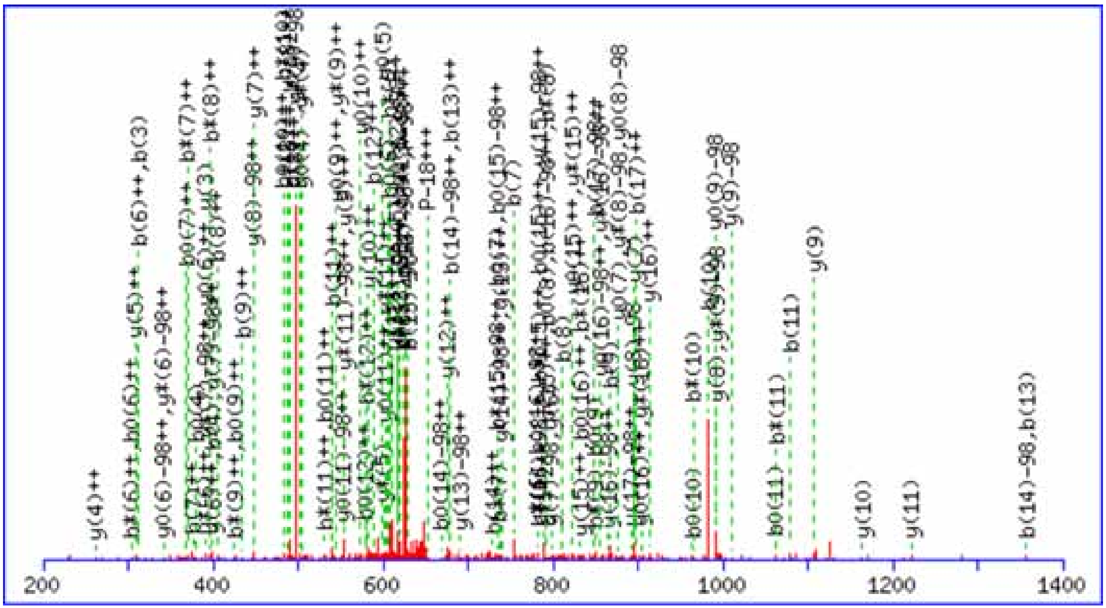
Matched b ions: b(3), b(4), b(6), b(7), b(8), b(9), b(10), b(13)-98, b(15), b(15)-98, b(15)++, b(16)-98, b(16)-98++, b(17), b(17)-98++
Matched y ions: y(3), y(5), y(6)-98, y(6), y(7)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(11), y(13), y(13)++, y(14)-98, y(14), y(14)-98++, y(15), y(15)-98, y(15)++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.293

GGYSPQEGGDPPTPEPLK
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of GGYSPQEGGDPPTPEPLK
Found in MURC_MOUSE, Muscle-related coiled-coil protein OS=Mus musculus GN=Murc PE=2 SV=1

Match to Query 6375: 1972.945854 from(658.655894,3+)
Title: Elution from: 38.120 to 38.120 scan no 3374 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1972.9456
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 36 Expect: 0.016

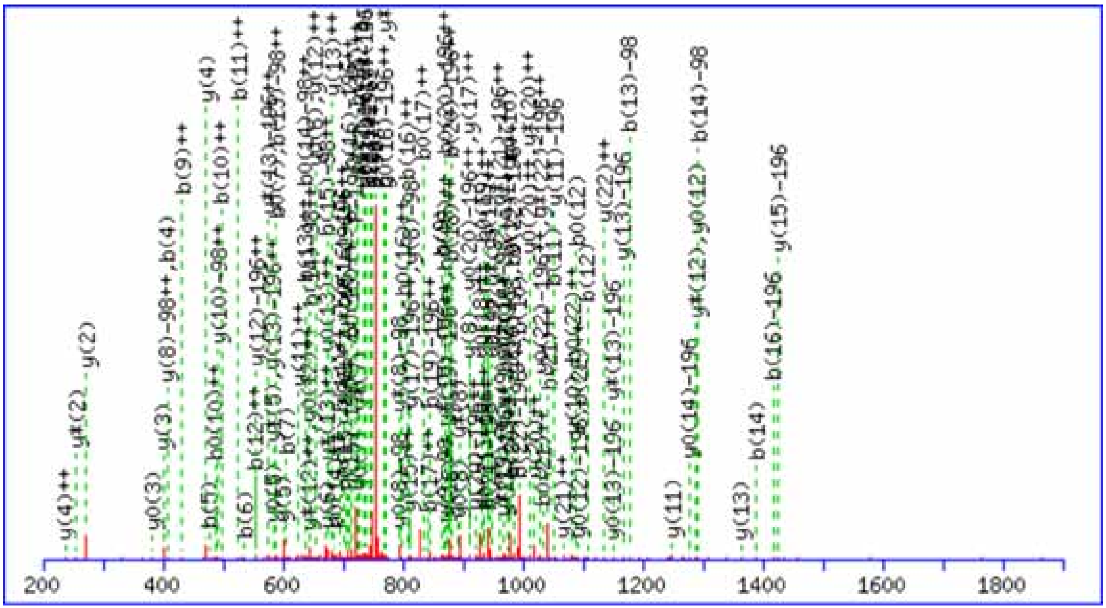
Matched b ions: b(3), b(4), b(5), b(6)++, b(6), b(7), b(7)++, b(8)++, b(8), b(9), b(9)++, b(10), b(10)++, b(11), b(11)++, b(12)++, b(13), b(13)-98++, b(13)++, b(14)-98, b(14)-98++, b(14)++, b(15)++, b(16)-98++, b(17)-98++, b(17)++
Matched y ions: y(3), y(4)++, y(5)++, y(5), y(6)++, y(6), y(7)-98++, y(7), y(7)++, y(7)-98, y(8)++, y(8), y(8)-98++, y(8)-98, y(9), y(9)++, y(9)-98, y(10), y(10)++, y(11), y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.294

GHPSAGAEEEGGSDGSAAEAEPR
Confirmed sites: @S:13,@S:16
Ambiguous sites:

MS/MS Fragmentation of GHPSAGAEEEGGSDGSAAEAEPR
Found in EIF3B_MOUSE, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 6315: 2354.869476 from(785.963768,3+)
Title: Elution from: 24.937 to 24.937 scan no 1459 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2354.8689
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 1.4e-005

Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)++, b(9), b(10), b(10)++, b(11)++, b(11), b(12)++, b(12), b(13)-98, b(13)-98++, b(13)++, b(14), b(14)-98++, b(14)-98, b(14)++, b(15)-98++, b(15)++, b(16)-196, b(16)-196++, b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(19)-196++, b(20)-98++, b(20)++, b(20)-196++, b(21)-98++, b(21)++, b(21)-196++, b(22)-196++, b(22)-98++, b(22)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(7), y(8)-98++, y(8)-98, y(8), y(9)-98, y(9), y(10), y(10)-98, y(10)-98++, y(11), y(11)-98++, y(11)-98, y(11)++, y(11)-196, y(12)-98, y(12)-196++, y(12)-98++, y(12)++, y(13), y(13)-196, y(13)-98++, y(13)++, y(13)-98, y(13)-196++, y(14)++, y(15)-196, y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-196++, y(17)++, y(18)-98++, y(18)++, y(19)-196++, y(19)-98++, y(19)++, y(20)++, y(20)-196++, y(20)-98++, y(21)-98++, y(21)++, y(21)-196++, y(22)-98++, y(22)++
Precursor origin neutral loss: +

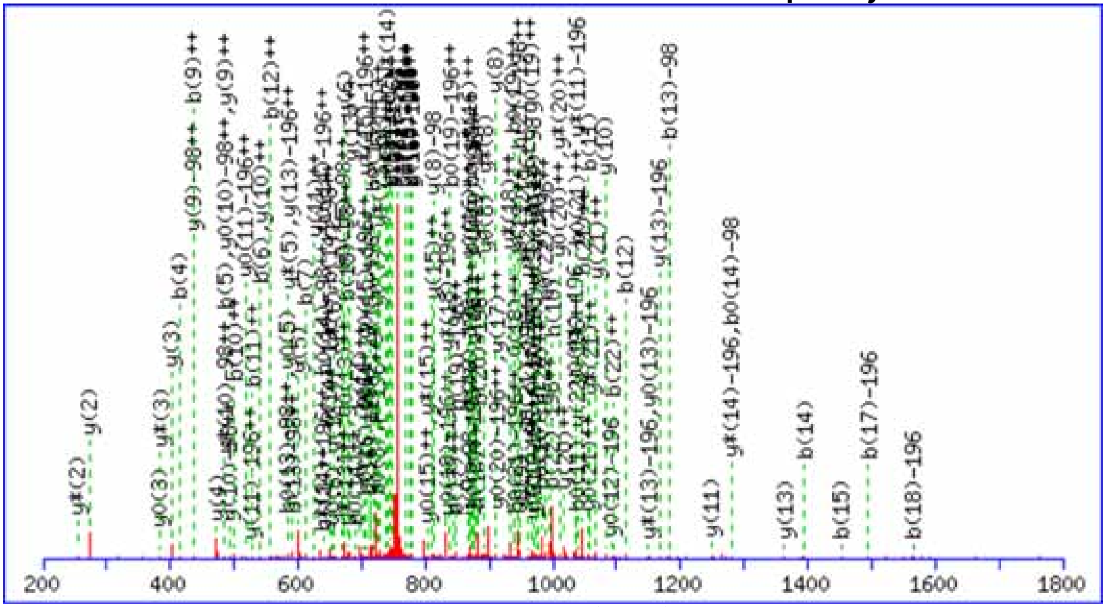
Peptide No.295

GHPSAGAEEEGGSDGSAAEAEPR
Confirmed sites: @S:13,@S:16
Ambiguous sites:

MS/MS Fragmentation of GHPSAGAEEEGGSDGSAAEAEPR
Found in EIF3B_MOUSE, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 7785: 2360.902485 from(787.974771,3+)

Title: Elution from: 24.847 to 24.847 scan no 1519 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2360.9007
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 Expect: 3.8e-005

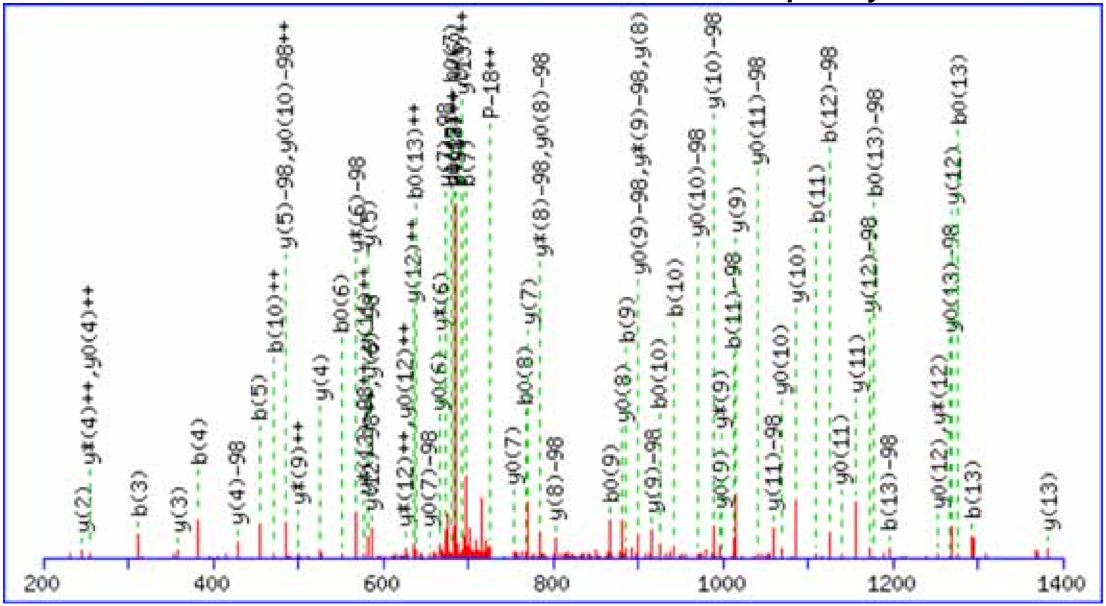
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(9)++, b(10)++, b(10), b(11), b(11)++, b(12), b(12)++, b(13)-98, b(13)-98++, b(13)++, b(14), b(14)-98++, b(14)++, b(15), b(15)++, b(15)-98++, b(16)-98, b(16)-98++, b(16)-196++, b(17)-98, b(17)-196, b(17)-98++, b(17)-196++, b(17)++, b(18)-98, b(18)-196, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(19)-196++, b(20)-98++, b(20)++, b(20)-196++, b(21)-98++, b(21)++, b(21)-196++, b(22)-98++, b(22)-196++, b(22)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9)++, y(9)-98++, y(9), y(9)-98, y(10), y(10)-98++, y(10)++, y(11), y(11)-196++, y(11)-98, y(11)-98++, y(11)++, y(12)-98, y(12)-98++, y(12)++, y(13)-196, y(13)-98, y(13), y(13)-98++, y(13)-196++, y(13)++, y(14)-98, y(14)-196++, y(14)-98++, y(14)++, y(15)-98++, y(15)-196++, y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-196++, y(19)-98++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(21)-196++, y(22)-196++
Precursor origin neutral loss: +

Peptide No.296

GILAADESTGSIAK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGSIAK
Found in ALDOA_MOUSE, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 2291: 1467.723068 from(734.868810,2+)
Title: Elution from: 38.746 to 38.746 scan no 3498 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1467.7222
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
Ions Score: 96 Expect: 1.3e-008

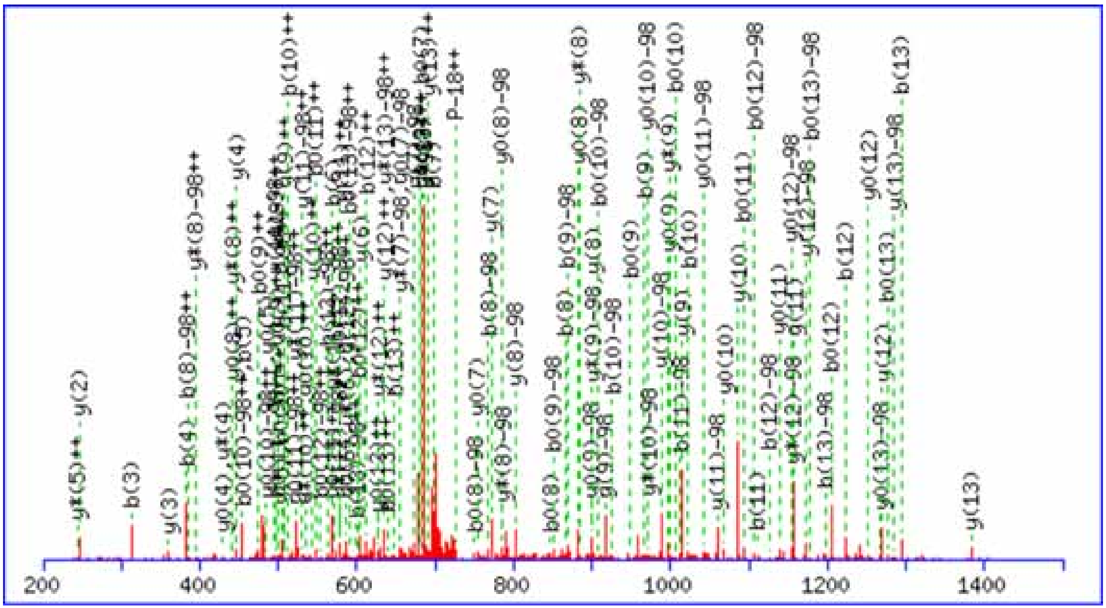
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(10)++, b(11)-98, b(11), b(12)-98, b(13)-98, b(13)
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5), y(6)-98, y(6), y(7), y(7)-98, y(8)-98, y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(11)++, y(12), y(12)-98++, y(12)-98, y(12)++, y(13), y(13)++
Precursor origin neutral loss: +

Peptide No.297

GILAADESTGSIAK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGSIAK
Found in ALDOA_MOUSE, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 1670: 1467.723256 from(734.868904,2+)
Title: Elution from: 40.102 to 40.102 scan no 3469 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1467.7222
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
Ions Score: 67 Expect: 1.1e-005

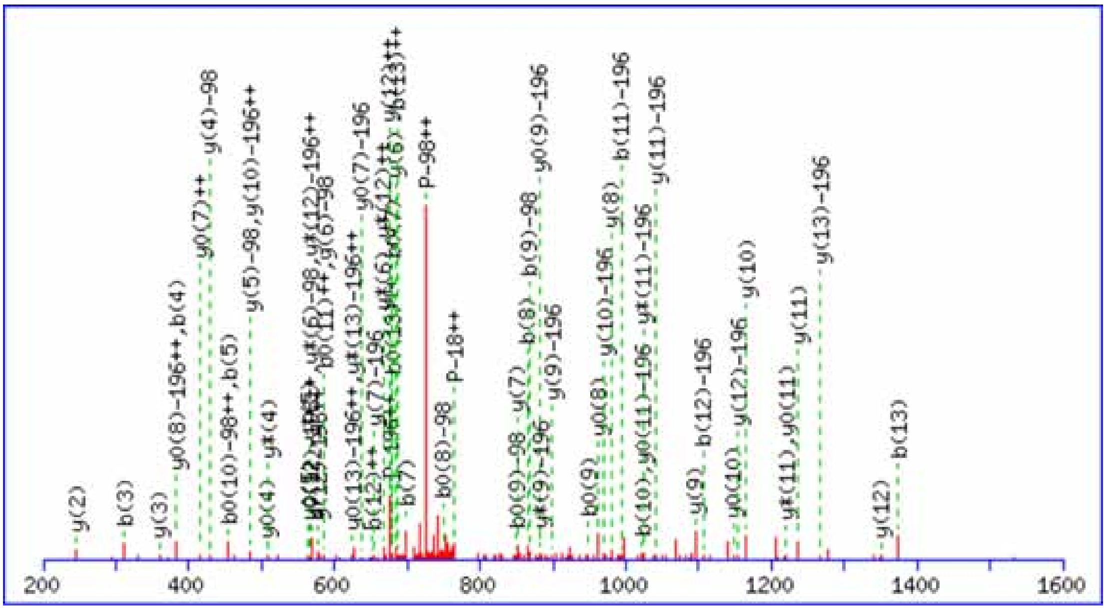
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)-98, b(8)-98++, b(8), b(9)-98, b(9), b(10), b(10)++, b(10)-98, b(11)-98, b(11)-98++, b(11), b(12), b(12)++, b(12)-98++, b(12)-98, b(13), b(13)-98++, b(13)++, b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(9)++, y(10), y(10)-98, y(10)-98++, y(10)++, y(11), y(11)-98, y(11)++, y(11)-98++, y(12), y(12)++, y(12)-98, y(12)-98++, y(13), y(13)++, y(13)-98
Precursor origin neutral loss: +

Peptide No.298

GILAADESTGSIAK
Confirmed sites: @S:8,@S:11
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGSIAK
Found in ALDOA_MOUSE, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 2809: 1547.688880 from(774.851716,2+)
Title: Elution from: 43.765 to 43.765 scan no 4148 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1547.6885
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
Ions Score: 42 Expect: 0.0023

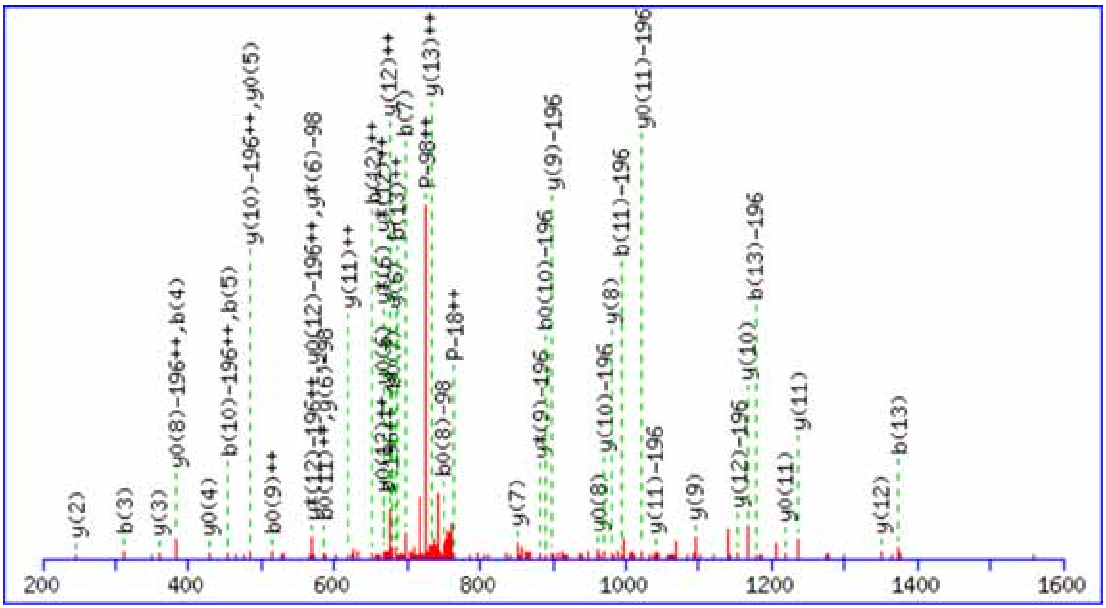
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10), b(11)-98, b(11)-196, b(12)-98, b(12)-196, b(12)++, b(13)-98, b(13), b(13)++
Matched y ions: y(2), y(3), y(4)-98, y(5)-98, y(6)-98, y(6), y(7)-98, y(7), y(7)-196, y(8), y(8)-98, y(9), y(9)-98, y(9)-196, y(10), y(10)-196++, y(10)-98, y(10)-196, y(11)-98, y(11), y(11)-196, y(12)-98++, y(12), y(12)-196++, y(12)-196, y(12)++, y(13)-196
Precursor origin neutral loss: +

Peptide No.299

GILAADESTGSIAK
Confirmed sites: @S:8,@T:9
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGSIAK
Found in ALDOA_MOUSE, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 2229: 1547.688892 from(774.851722,2+)
Title: Elution from: 43.617 to 43.617 scan no 3845 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1547.6885
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
Ions Score: 42 Expect: 0.0025

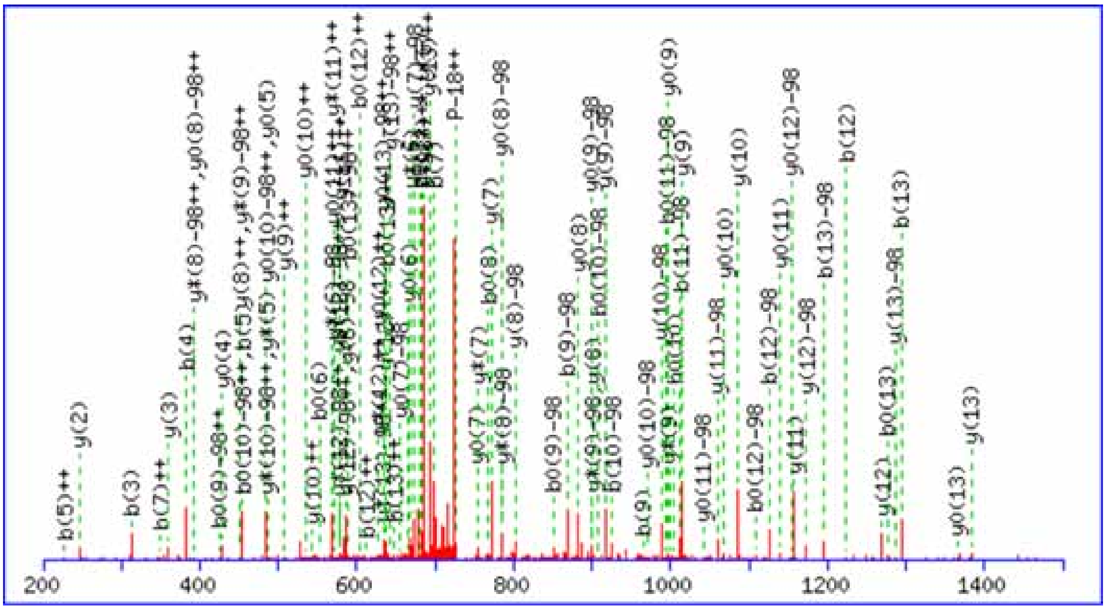
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9)-98, b(9)-98++, b(10)-196++, b(10)-98, b(11)-98, b(11)-196, b(12)-98, b(12)++, b(13)-98, b(13), b(13)-196, b(13)++
Matched y ions: y(2), y(3), y(6)-98, y(6), y(7), y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(9)-196, y(10)-196++, y(10), y(10)-98, y(10)-196, y(11)-98, y(11), y(11)++, y(11)-196, y(12)-98++, y(12), y(12)-196, y(12)++, y(13)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.300

GILAADESTGSIAK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGSIAK
Found in ALDOA_MOUSE, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 2000: 1467.722990 from(734.868771,2+)
Title: Elution from: 38.619 to 38.619 scan no 3288 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1467.7222
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
Ions Score: 81 **Expect:** 3.6e-007

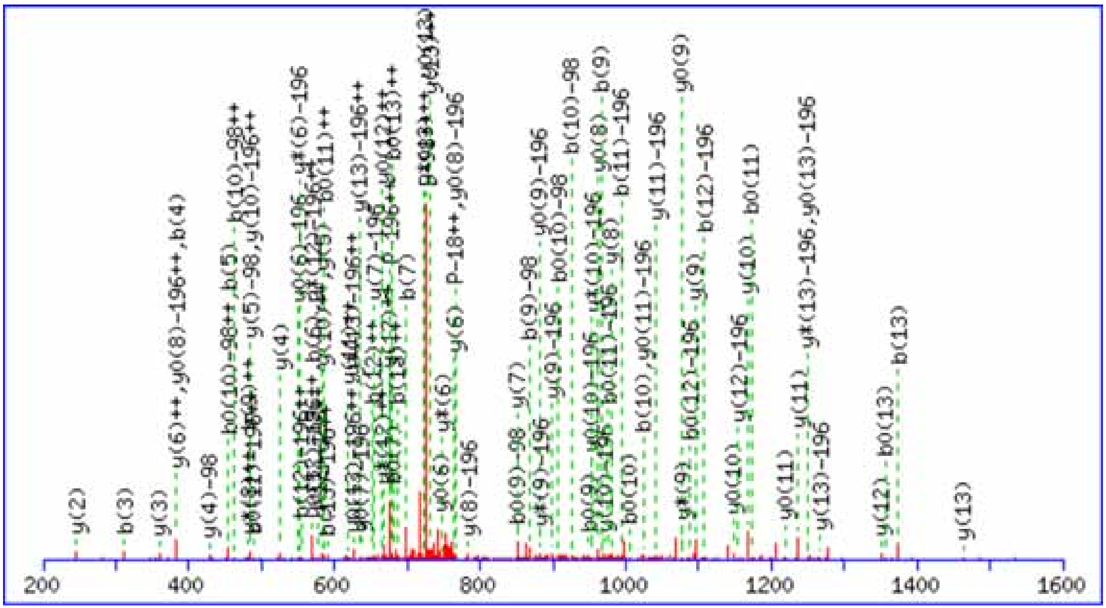
Matched b ions: b(3), b(4), b(5), b(5)++, b(6), b(7), b(7)++, b(8), b(8)++, b(9)-98, b(9), b(10)-98, b(11)-98, b(12)-98, b(12), b(12)++, b(13), b(13)-98, b(13)++
Matched y ions: y(2), y(3), y(6)-98, y(6), y(7), y(7)-98, y(8)-98, y(8), y(8)++, y(9), y(9)-98, y(9)++, y(10), y(10)-98, y(10)++, y(11), y(11)-98, y(11)++, y(12)-98++, y(12), y(12)-98, y(12)++, y(13), y(13)++, y(13)-98++, y(13)-98
Precursor origin neutral loss: +

Peptide No.301

GILAADESTGSIAK
Confirmed sites: @T:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGSIAK
Found in ALDOA_MOUSE, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 2111: 1547.688488 from(774.851520,2+)
Title: Elution from: 43.603 to 43.603 scan no 3911 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1547.6885
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
Ions Score: 65 **Expect:** 1.1e-005

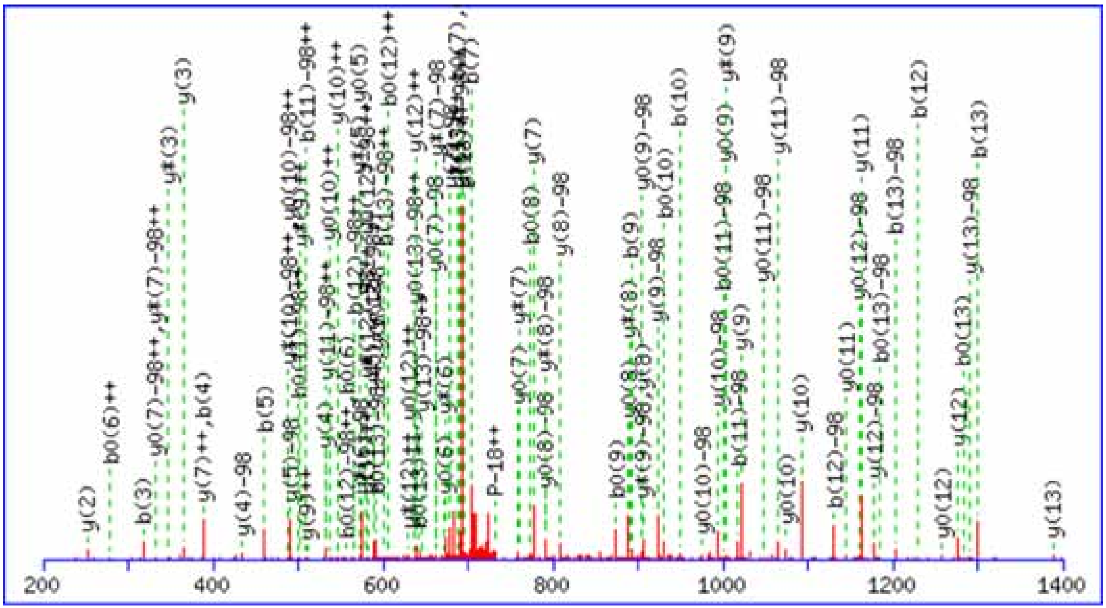
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9)-98, b(9)++, b(9), b(10), b(10)-98++, b(10)-98, b(11)-98, b(11)-196, b(12)-98, b(12)-196, b(12)-196++, b(12)++, b(13)-98, b(13), b(13)-196++, b(13)++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5), y(6)++, y(6), y(6)-98, y(7)-98, y(7), y(7)-196, y(8), y(8)-98, y(8)-196, y(9)-98, y(9), y(9)-196, y(9)-98++, y(10)-98, y(10), y(10)-196++, y(10)++, y(10)-196, y(11), y(11)-98, y(11)-196, y(11)-98++, y(11)++, y(12)-98++, y(12)-98, y(12), y(12)-196++, y(12)++, y(12)-196, y(13), y(13)-98, y(13)-196, y(13)-196++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.302

GILAADESTGSIAK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGSIAK
Found in ALDOA_MOUSE, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 2025: 1479.786292 from(740.900422,2+)
Title: Elution from: 38.630 to 38.630 scan no 3290 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1479.7858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 99 Expect: 4.9e-009

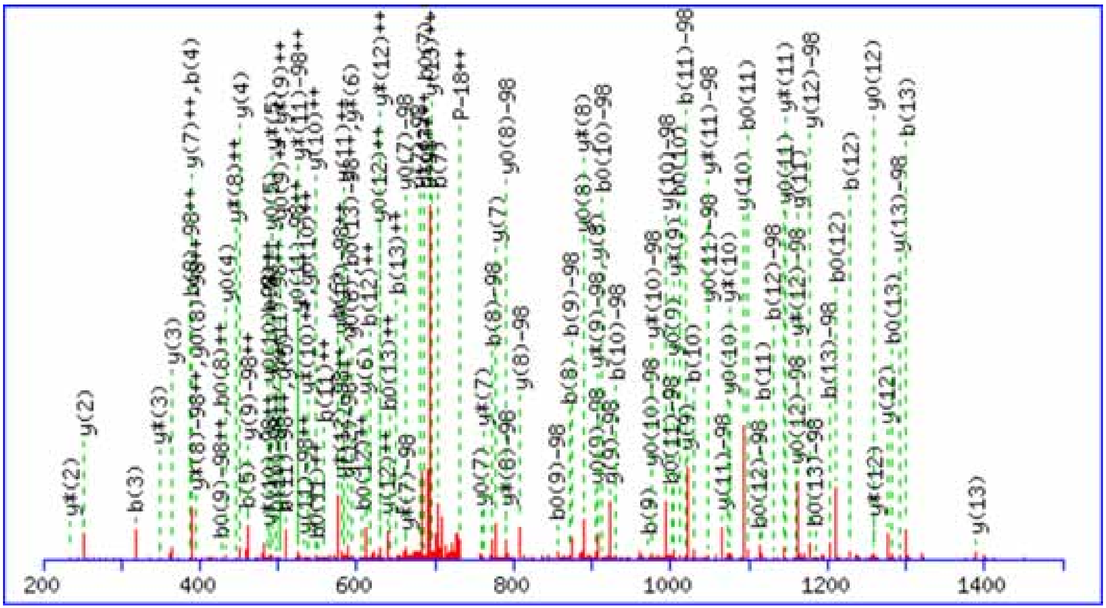
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11)-98, b(11)-98++, b(12)-98, b(12), b(12)-98++, b(13), b(13)-98, b(13)-98++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5), y(6)-98, y(6), y(7)++, y(7), y(7)-98, y(8)-98, y(8), y(9), y(9)-98, y(9)++, y(10), y(10)-98, y(10)++, y(11), y(11)-98, y(11)-98++, y(11)++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13), y(13)-98, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.303

GILAADESTGSIAK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGSIAK
Found in ALDOA_MOUSE, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 1697: 1479.787208 from(740.900880,2+)
Title: Elution from: 40.136 to 40.136 scan no 3474 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1479.7858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 90 Expect: 4.8e-008

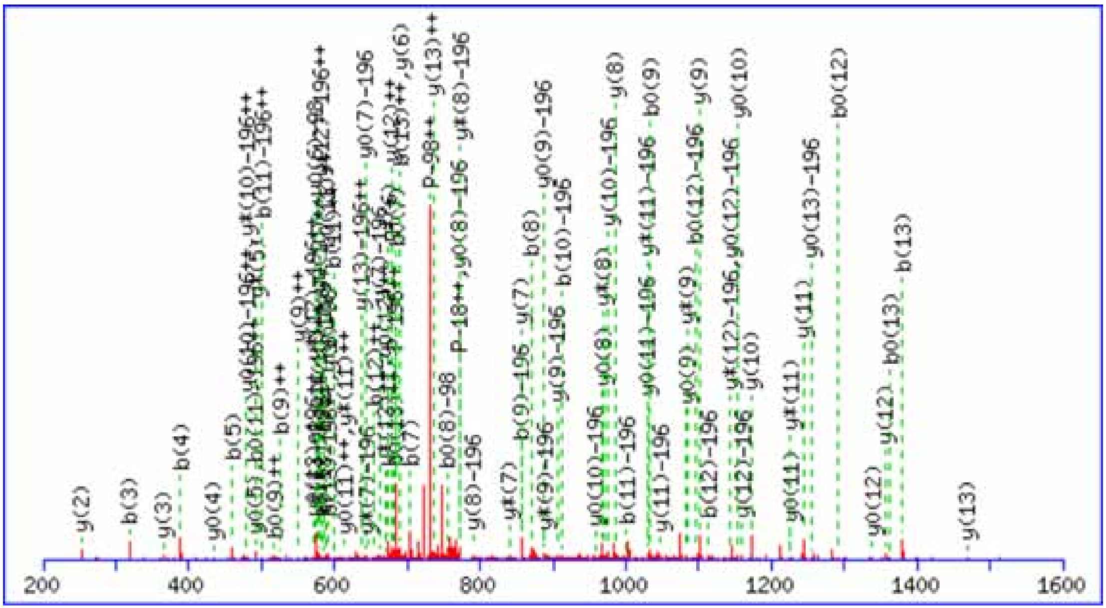
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)-98, b(8)-98++, b(8), b(9)-98, b(9)++, b(9), b(10), b(10)-98, b(11)-98++, b(11), b(11)++, b(11)-98, b(12), b(12)++, b(12)-98, b(13), b(13)-98, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(9)-98++, y(10), y(10)-98, y(10)-98++, y(10)++, y(11), y(11)-98, y(11)-98++, y(11)++, y(12), y(12)-98++, y(12)-98, y(12)++, y(13), y(13)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.304

GILAADESTGSIAK
Confirmed sites: @S:8,@T:9
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGSIAK
Found in ALDOA_MOUSE, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 2193: 1559.752824 from(780.883688,2+)
Title: Elution from: 43.581 to 43.581 scan no 3927 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1559.7521
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 33 **Expect:** 0.023

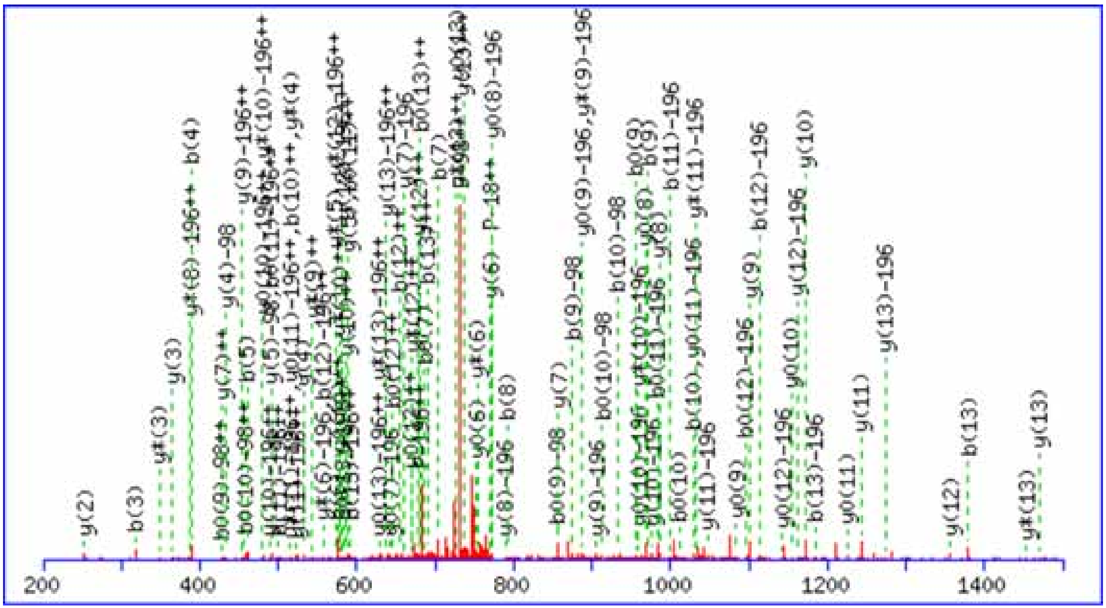
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)-98, b(8), b(9)++, b(9)-196, b(10)-196, b(10)-98, b(11)-98, b(11)-196++, b(11)-98++, b(11)++, b(11)-196, b(12)-98, b(12)-196, b(12)++, b(13)-98, b(13), b(13)-196++, b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(6)-98, y(6), y(7)-98, y(7), y(7)-98++, y(7)-196, y(8)-98, y(8), y(8)-196, y(9)-98, y(9), y(9)-196, y(9)++, y(10)-98, y(10), y(10)-196, y(10)-98++, y(10)++, y(11), y(11)-98, y(11)-98++, y(11)-196, y(12)-98++, y(12)-98, y(12), y(12)-196++, y(12)-196, y(12)++, y(13), y(13)-196++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.305

GILAADESTGSIAK
Confirmed sites: @T:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of GILAADESTGSIAK
Found in ALDOA_MOUSE, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 1906: 1559.752640 from(780.883596,2+)
Title: Elution from: 43.589 to 43.589 scan no 3820 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1559.7521
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 46 Expect: 0.00098

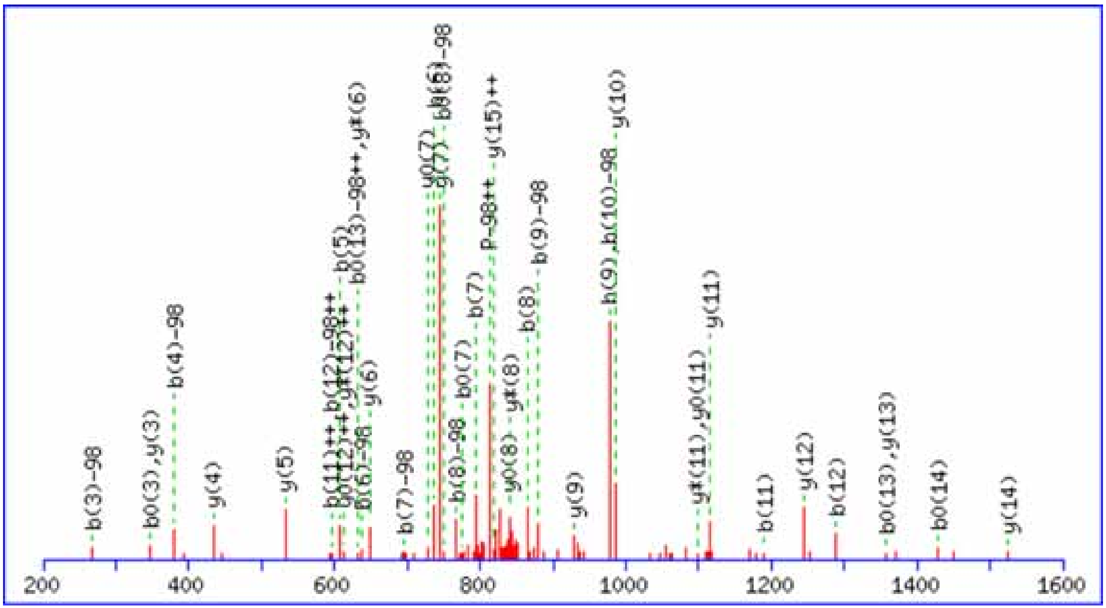
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(9), b(10), b(10)++, b(10)-98, b(11)-98, b(11)-196++, b(11)-98++, b(11)-196, b(12)-98, b(12)-196, b(12)-196++, b(12)++, b(13)-98, b(13), b(13)-196++, b(13)-196, b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5)-98, y(5), y(6), y(7), y(7)-98, y(7)++, y(7)-196, y(8)-98, y(8), y(8)-196, y(9)-98, y(9), y(9)-196, y(9)-196++, y(9)-98++, y(10)-98, y(10), y(10)-196, y(10)-196++, y(10)-98++, y(10)++, y(11), y(11)-98, y(11)-196++, y(11)-98++, y(11)-196, y(12)-98++, y(12)-98, y(12), y(12)-196++, y(12)++, y(12)-196, y(13), y(13)-196, y(13)-98, y(13)-196++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.306

GISLEEGALPDVSATR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GISLEEGALPDVSATR
Found in XIRP1_MOUSE, Xin actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 PE=1 SV=2

Match to Query 3871: 1721.823730 from(861.919141,2+)
Title: Elution from: 54.297 to 54.297 scan no 5381 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1721.8237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 91 **Expect:** 4e-008

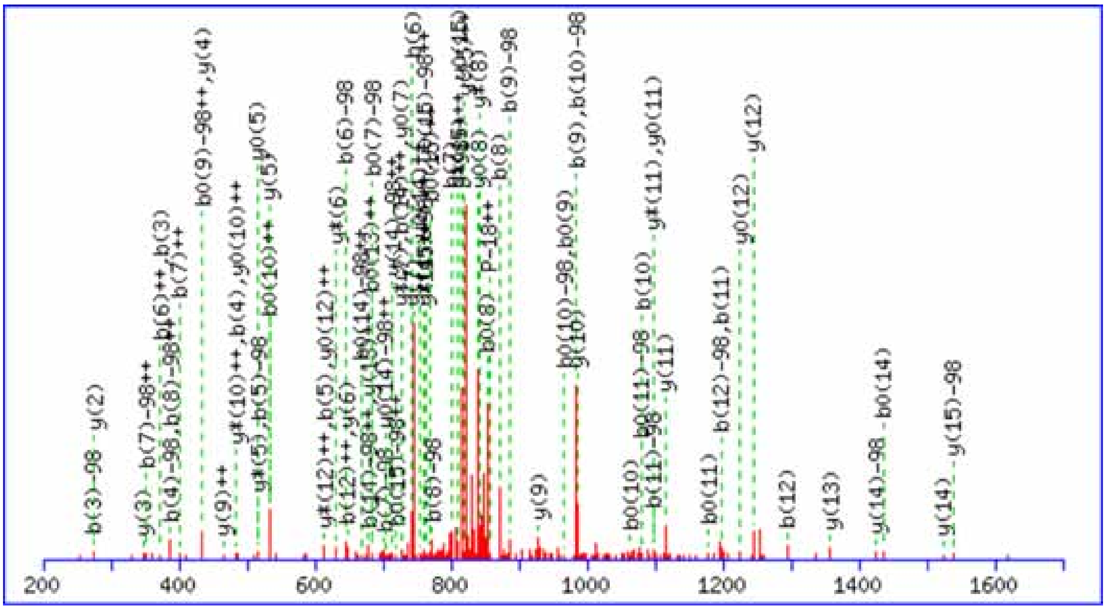
Matched b ions: b(3)-98, b(4)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(11), b(11)++, b(12), b(12)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(14), y(15)++
Precursor origin neutral loss: +

Peptide No.307

GISLEEGALPDVSATR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GISLEEGALPDVSATR
Found in XIRP1_MOUSE, Xin actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 PE=1 SV=2

Match to Query 3345: 1727.855720 from(864.935136,2+)
Title: Elution from: 54.229 to 54.229 scan no 5199 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1727.8555
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 91 Expect: 4.6e-008

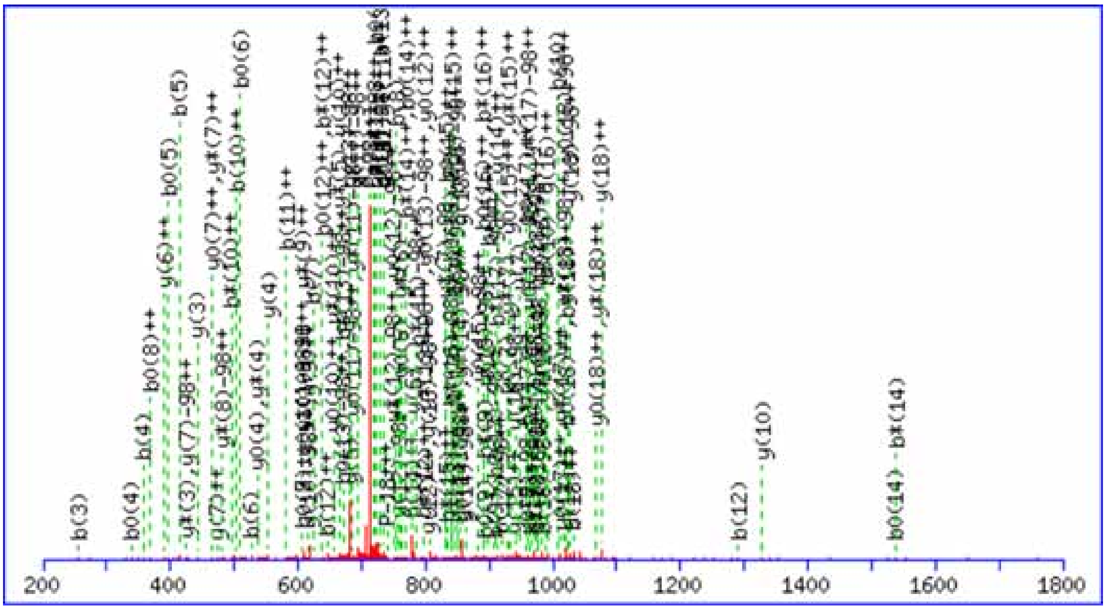
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(6)++, b(7)-98++, b(7)++, b(7)-98, b(7), b(8)-98++, b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(12), b(12)++, b(12)-98, b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9), y(9)++, y(10), y(11), y(12), y(13), y(13)++, y(14), y(14)-98, y(14)-98++, y(14)++, y(15)-98, y(15)++
Precursor origin neutral loss: +

Peptide No.308

GLGTGLPERPRESPQLHER
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of GLGTGLPERPRESPQLHER
Found in JPH2_MOUSE, Junctophilin-2 OS=Mus musculus GN=Jph2 PE=1 SV=2

Match to Query 6755: 2236.113252 from(746.378360,3+)
Title: Elution from: 32.841 to 32.841 scan no 2693 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2236.1113
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.024

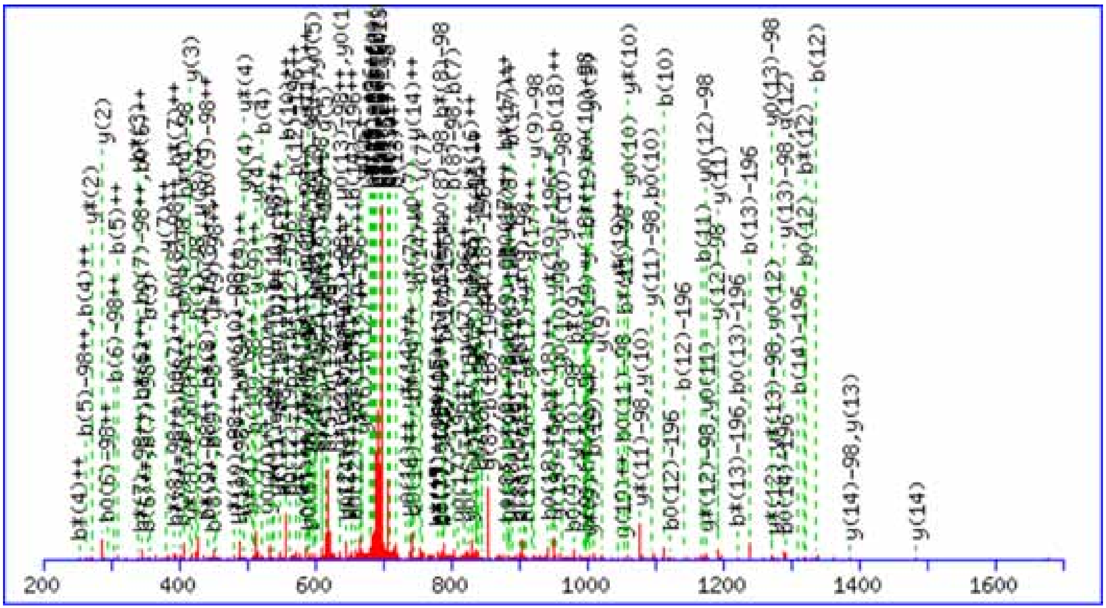
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10)++, b(10), b(11)++, b(12)++, b(12), b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)-98++, y(7)++, y(7)-98, y(8)-98, y(9)++, y(10), y(10)-98++, y(10)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.309

GNKSPSPPPDGSPAATPEIR
Confirmed sites: @S:4,@S:12
Ambiguous sites:

MS/MS Fragmentation of GNKSPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 5891: 2189.977566 from(730.999798,3+)
Title: Elution from: 31.969 to 31.969 scan no 2404 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2189.9759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K3 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 **Expect:** 1.2e-005

Matched b ions: b(3), b(4)-98, b(4)++, b(4), b(5), b(5)++, b(5)-98++, b(6), b(6)-98++, b(6)-98, b(6)++, b(7), b(7)-98, b(7)++, b(7)-98++, b(8)++, b(8)-98, b(8)-98++, b(8), b(9)-98++, b(9), b(10)++, b(10), b(10)-98++, b(11)++, b(11), b(11)-98++, b(12)-98++, b(12)-98, b(12), b(12)-196++, b(12)++, b(12)-196, b(13)-196++, b(13)-196, b(13)-98++, b(13)++, b(14)-196, b(14)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)-196++, b(17)++, b(18)-196++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(19)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9), y(9)++, y(9)-98, y(10)-98, y(10), y(10)-98++, y(10)++, y(11), y(11)-98++, y(11)-98, y(11)++, y(12), y(12)-98, y(12)++, y(12)-98++, y(13)-98, y(13), y(13)++, y(13)-98++, y(14), y(14)-98, y(14)-98++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)-196++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-196++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

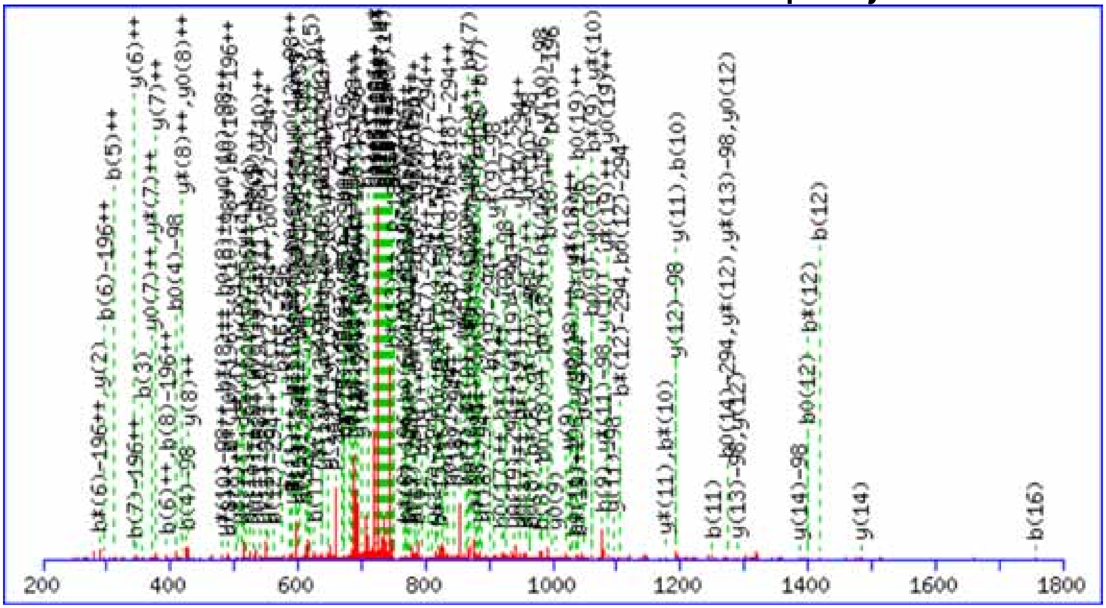
Peptide No.310

GNKSPSPPPDGSPAATPEIR
Confirmed sites: @S:4,@S:6,@S:12
Ambiguous sites:

MS/MS Fragmentation of GNKSPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 5522: 2269.943355 from(757.655061,3+)

Title: Elution from: 34.160 to 34.160 scan no 2562 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2269.9422
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K3 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0074

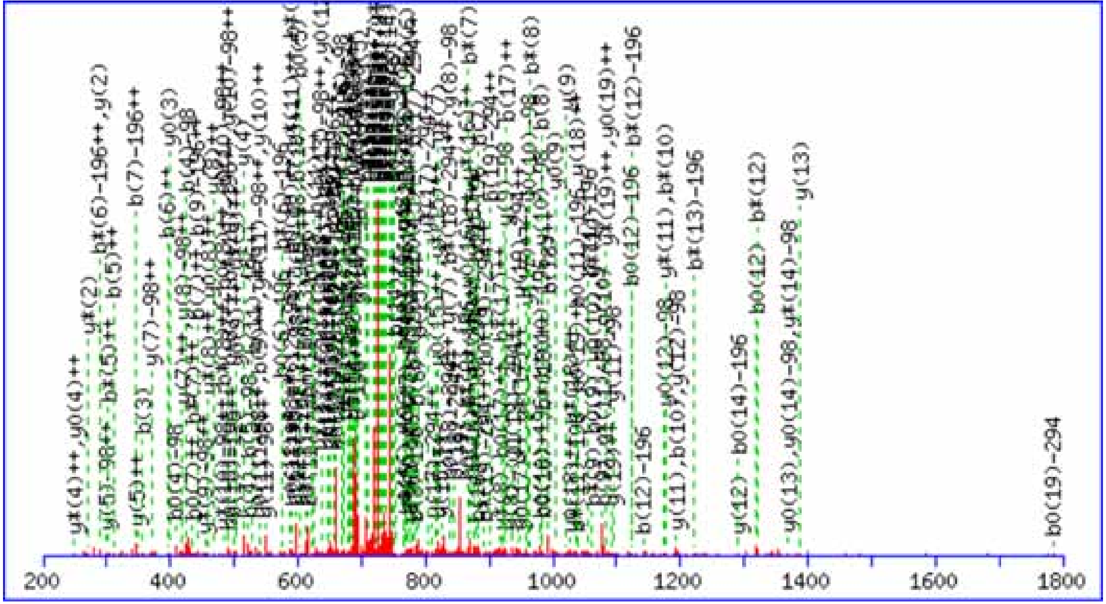
Matched b ions: b(3), b(4)-98, b(4), b(5)++, b(5), b(6), b(6)-98++, b(6)-98, b(6)++, b(6)-196, b(6)-196++, b(7)-98, b(7)-196++, b(7)-98++, b(7), b(7)-196, b(8)++, b(8), b(8)-196++, b(8)-196, b(8)-98, b(9), b(9)-98, b(9)-98++, b(9)++, b(9)-196, b(10)++, b(10), b(10)-98++, b(10)-196, b(10)-98, b(11), b(11)++, b(11)-98++, b(12)-98, b(12), b(12)-196++, b(12)-98++, b(12)-196, b(12)-294++, b(12)++, b(13)-294++, b(13)-196++, b(13)-98++, b(14)-294++, b(14)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(15)-294++, b(15)-196++, b(16), b(16)-294++, b(16)-196++, b(16)-98++, b(16)++, b(17)-98, b(17)-196++, b(17)-294++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(18)-294++, b(18)-196++, b(19)-294++, b(19)-196++, b(19)++
Matched y ions: y(2), y(4), y(5), y(6), y(6)++, y(7)++, y(8), y(8)++, y(9), y(9)++, y(9)-98, y(10), y(10)-98, y(10)-98++, y(10)++, y(11)++, y(11), y(11)-98++, y(11)-98, y(12)-98++, y(12)-98, y(12), y(12)++, y(13)++, y(13)-98, y(13)-98++, y(14)++, y(14), y(14)-98++, y(14)-98, y(15)++, y(15)-196++, y(15)-98++, y(16)-98++, y(16)++, y(16)-196++, y(17)++, y(17)-294++, y(17)-196++, y(17)-98++, y(18)-294++, y(18)-196++, y(18)-98++, y(18)++, y(19)-294++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.311

GNKSPSPPPDGSPAATPEIR
Confirmed sites: @S:4,@S:6,@T:16
Ambiguous sites:

MS/MS Fragmentation of GNKSPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 6036: 2269.944681 from(757.655503,3+)
Title: Elution from: 34.168 to 34.168 scan no 2672 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2269.9422
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K3 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.035

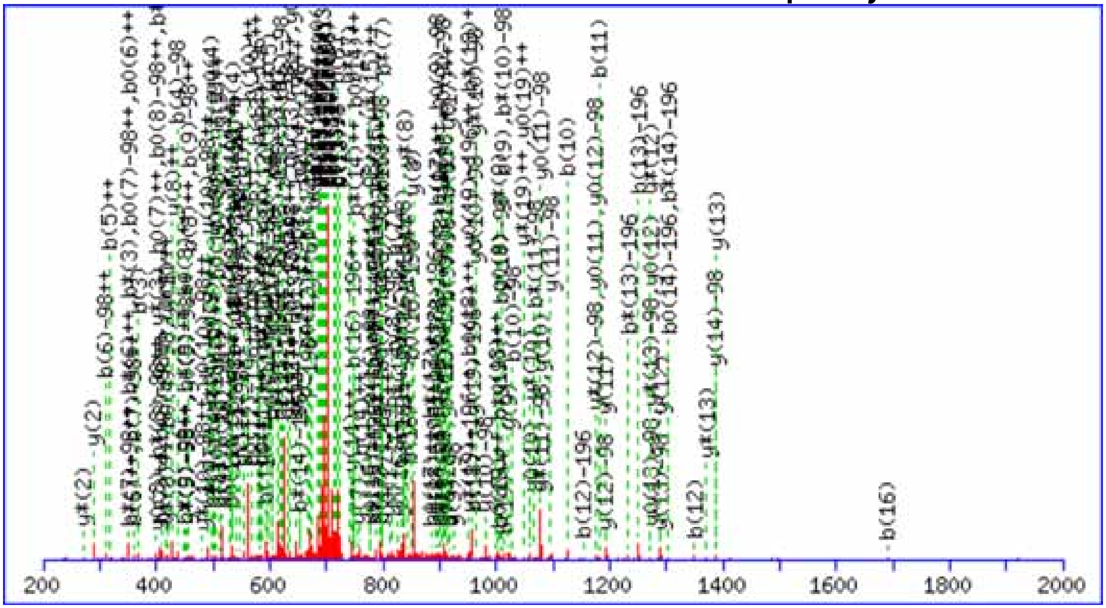
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5)++, b(5), b(6)-98++, b(6), b(6)-98, b(6)-196, b(6)++, b(7)-196++, b(7)-98, b(7), b(7)++, b(7)-196, b(8)++, b(8)-98, b(8)-98++, b(8)-196, b(8), b(9), b(9)-98, b(9)-98++, b(9)-196++, b(9)++, b(9)-196, b(10)++, b(10), b(10)-98++, b(10)-196++, b(10)-98, b(11)-196++, b(11)-98++, b(11)++, b(11)-196, b(12)-196, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-196++, b(14)-98++, b(14)++, b(15)-196++, b(15)-98++, b(15)++, b(16)-294++, b(16)-196++, b(16)-98++, b(16)++, b(17)-294++, b(17)-196++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(18)-294++, b(18)-196++, b(19)-294++, b(19)-196++, b(19)-98++
Matched y ions: y(2), y(4), y(5)-98, y(5)++, y(5), y(5)-98++, y(6)-98, y(6), y(7)-98++, y(7)++, y(7)-98, y(7), y(8)-98++, y(8), y(8)++, y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(10)-98++, y(10)++, y(11)++, y(11), y(11)-98++, y(11)-98, y(12)-98++, y(12)-98, y(12)++, y(12), y(13), y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-196++, y(16)++, y(16)-98++, y(16)-196++, y(17)++, y(17)-294++, y(17)-98++, y(18)++, y(18)-98++, y(19)-294++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.312

GNKSPSPPPDGSPAATPEIR
Confirmed sites: @S:4,@S:12
Ambiguous sites:

MS/MS Fragmentation of GNKSPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 5729: 2202.040914 from(735.020914,3+)
Title: Elution from: 31.428 to 31.428 scan no 2300 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2202.0395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K3 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 0.00012

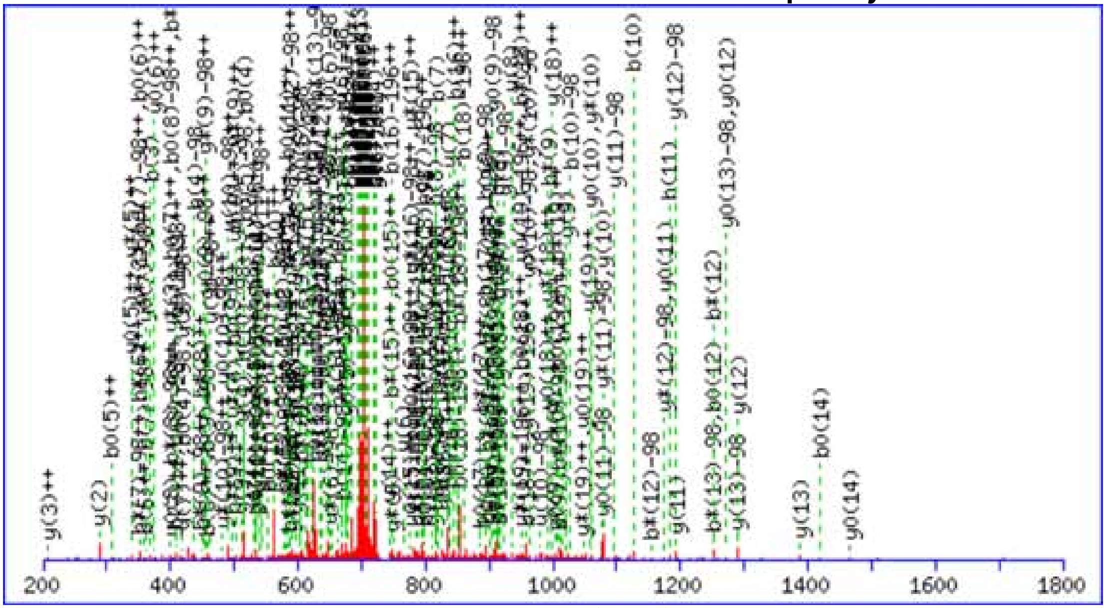
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5)++, b(5), b(6)-98++, b(6), b(6)-98, b(6)++, b(7)++, b(7), b(7)-98++, b(7)-98, b(8)-98++, b(8)++, b(8)-98, b(8), b(9)-98++, b(9)++, b(9)-98, b(9), b(10)-98++, b(10)++, b(10), b(10)-98, b(11)++, b(11), b(12)-98++, b(12)-98, b(12), b(12)-196++, b(12)++, b(12)-196, b(13)-196++, b(13)-196, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-196++, b(15)-98++, b(15)++, b(16), b(16)-196++, b(16)-98++, b(16)++, b(17)-98, b(17)++, b(17)-196++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(9)-98, y(10), y(10)-98, y(10)-98++, y(10)++, y(11), y(11)++, y(11)-98, y(11)-98++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13), y(13)-98, y(13)++, y(13)-98++, y(14)-98, y(14)-98++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)-196++, y(18)++, y(19)-196++
Precursor origin neutral loss: +

Peptide No.313

GNKSPSPPPDGSPAATPEIR
Confirmed sites: @S:4,@T:16
Ambiguous sites:

MS/MS Fragmentation of GNKSPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 5563: 2202.041172 from(735.021000,3+)
Title: Elution from: 31.581 to 31.581 scan no 2316 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2202.0395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K3 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.012

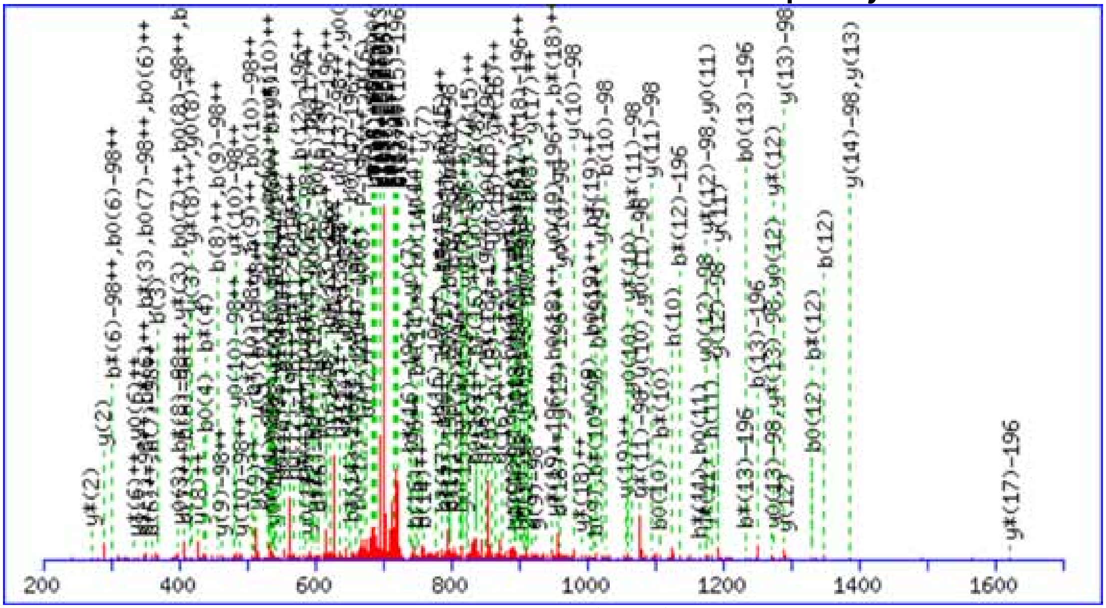
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6), b(6)++, b(6)-98, b(7)-98, b(7)++, b(7)-98++, b(7), b(8)-98++, b(8)++, b(8)-98, b(8), b(9), b(9)-98++, b(9)-98, b(10)++, b(10), b(10)-98++, b(10)-98, b(11)++, b(11), b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(16)++, b(16)-196++, b(16)-98++, b(17)++, b(17)-196++, b(17)-98++, b(18)-98++, b(18)++, b(18)-196++, b(19)-196++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3)++, y(4), y(5), y(5)-98, y(6)-98, y(6), y(7)++, y(7), y(8)-98, y(8)-98++, y(8), y(9)-98, y(9)-98++, y(9)++, y(9), y(10)-98++, y(10), y(10)-98, y(10)++, y(11), y(11)++, y(11)-98, y(12), y(12)-98, y(12)-98++, y(12)++, y(13), y(13)-98, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(18)-98++, y(18)-196++, y(18)++, y(19)-196++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.314

GNKSPSPPPDGSPAATPEIR
Confirmed sites: @S:6,@S:12
Ambiguous sites:

MS/MS Fragmentation of GNKSPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 5808: 2202.040584 from(735.020804,3+)
Title: Elution from: 32.127 to 32.127 scan no 2389 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2202.0395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K3 : Dimethyl:2H(4)13C(2) (K)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00076

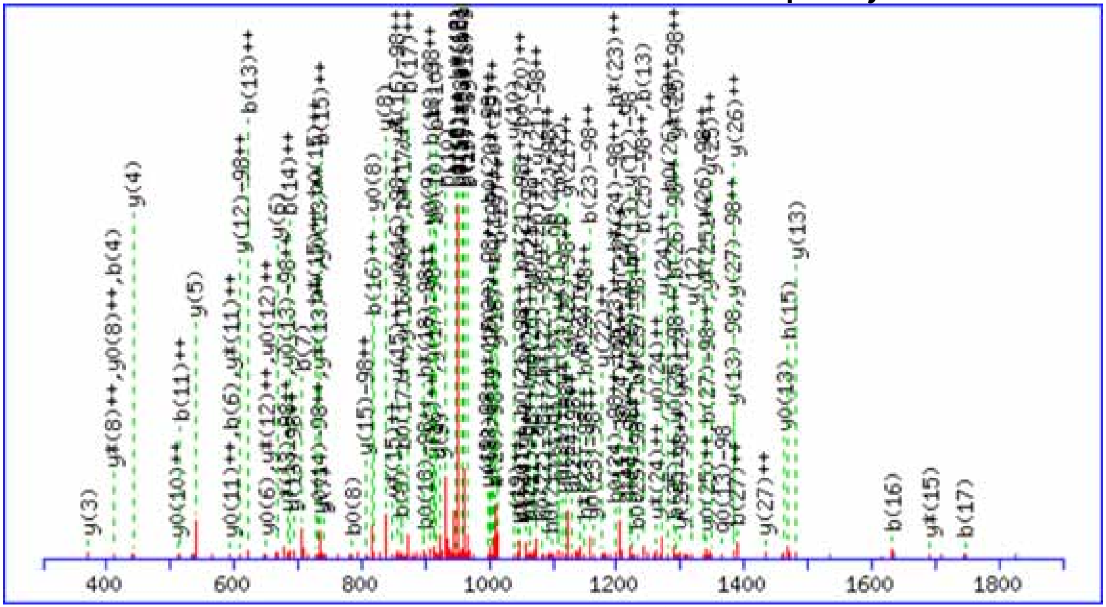
Matched b ions: b(3), b(6), b(6)-98, b(6)++, b(7)++, b(7), b(7)-98++, b(7)-98, b(8)-98++, b(8)++, b(8)-98, b(8), b(9)-98++, b(9)++, b(9)-98, b(9), b(10)-98++, b(10)++, b(10), b(10)-98, b(11), b(11)++, b(11)-98++, b(12)-98++, b(12)-98, b(12), b(12)-196++, b(12)++, b(13)-196++, b(13)-98, b(13)-196, b(13)++, b(13)-98++, b(14)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-196++, b(16)-98++, b(17)-98++, b(17)++, b(17)-196++, b(18)++, b(18)-98++, b(18)-196++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)-98++, y(9)++, y(9)-98, y(9), y(10), y(10)-98, y(10)-98++, y(10)++, y(11), y(11)-98++, y(11)++, y(11)-98, y(12)-98, y(12), y(12)-98++, y(12)++, y(13), y(13)++, y(13)-98, y(13)-98++, y(14)-98, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)-196++, y(17)-98++, y(17)++, y(18)-98++, y(18)-196++, y(19)-196++, y(19)++
Precursor origin neutral loss: +

Peptide No.315

GPARPSLPGAPPDEVYLSDSPAEPAPVK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of GPARPSLPGAPPDEVYLSDSPAEPAPVK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 7491: 2949.455871 from(984.159233,3+)
Title: Elution from: 48.838 to 48.838 scan no 4613 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2949.4525
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K28 : Dimethyl (K)
Ions Score: 89 Expect: 1.3e-007

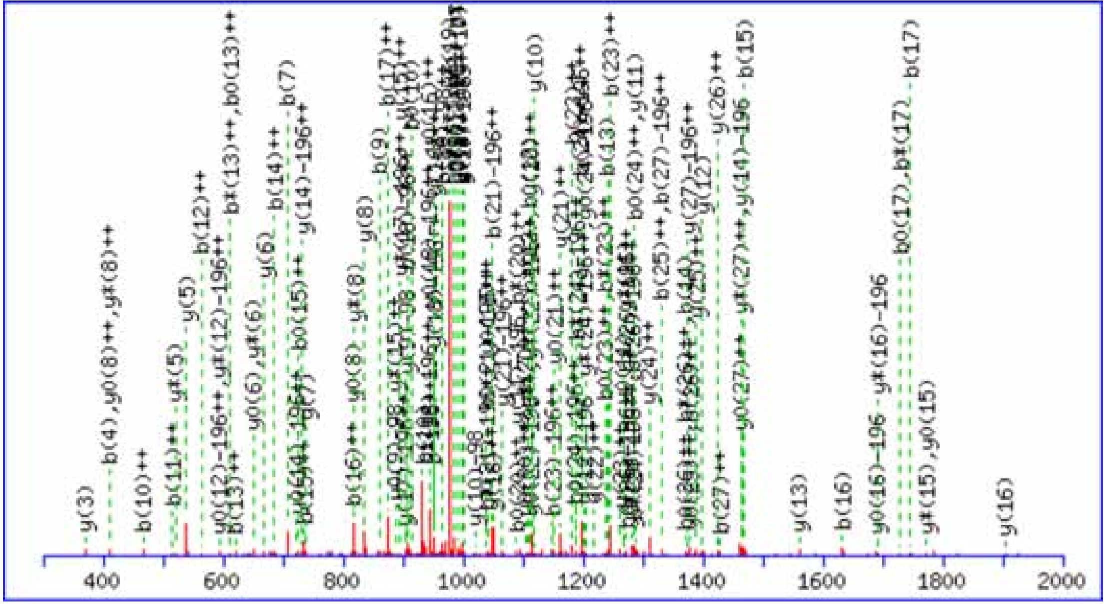
Matched b ions: b(4), b(6), b(7), b(9), b(10), b(11)++, b(13)++, b(13), b(14)++, b(15)++, b(15), b(16), b(16)++, b(17), b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)-98++, b(20)++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(24)-98++, b(25)++, b(25)-98++, b(26)-98++, b(27)++, b(27)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12)-98++, y(12)-98, y(12), y(13), y(13)-98, y(13)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(21)++, y(21)-98++, y(22)-98++, y(22)++, y(23)++, y(24)++, y(24)-98++, y(25)-98++, y(25)++, y(26)++, y(26)-98++, y(27)-98++, y(27)++
Precursor origin neutral loss: +

Peptide No.316

GPARPSLPGAPPDEVYLSDSPAEPAPVK
Confirmed sites: @S:18,@S:20
Ambiguous sites:

MS/MS Fragmentation of GPARPSLPGAPPDEVYLSDSPAEPAPVK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 6685: 3029.421684 from(1010.814504,3+)
Title: Elution from: 50.772 to 50.772 scan no 4625 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3029.4188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S20 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K28 : Dimethyl (K)
Ions Score: 84 Expect: 4.3e-007

Matched b ions: b(4), b(7), b(9), b(10), b(10)++, b(11)++, b(12)++, b(13)++, b(13), b(14)++, b(14), b(15)++, b(15), b(16)++, b(16), b(17)++, b(17), b(18)-98++, b(19)-98++, b(20)-98++, b(20)-196++, b(21)-196++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++, b(23)++, b(23)-196++, b(24)-196++, b(24)-98++, b(25)-98++, b(25)++, b(26)++, b(26)-196++, b(26)-98++, b(27)-98++, b(27)-196++, b(27)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9)-98, y(10)-98, y(10), y(11), y(11)-98, y(11)-196, y(12)-98++, y(12), y(12)-98, y(12)-196, y(13), y(13)-98++, y(13)-98, y(14)-196++, y(14)-98++, y(14)-196, y(15)-98, y(15)++, y(16), y(16)++, y(16)-98++, y(17)-98++, y(17)-196++, y(17)++, y(18)++, y(18)-196++, y(18)-98++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(21)-196++, y(22)-98++, y(22)++, y(23)++, y(24)++, y(24)-98++, y(25)++, y(25)-98++, y(26)-98++, y(26)++, y(27)-196++, y(27)-98++
Precursor origin neutral loss: +

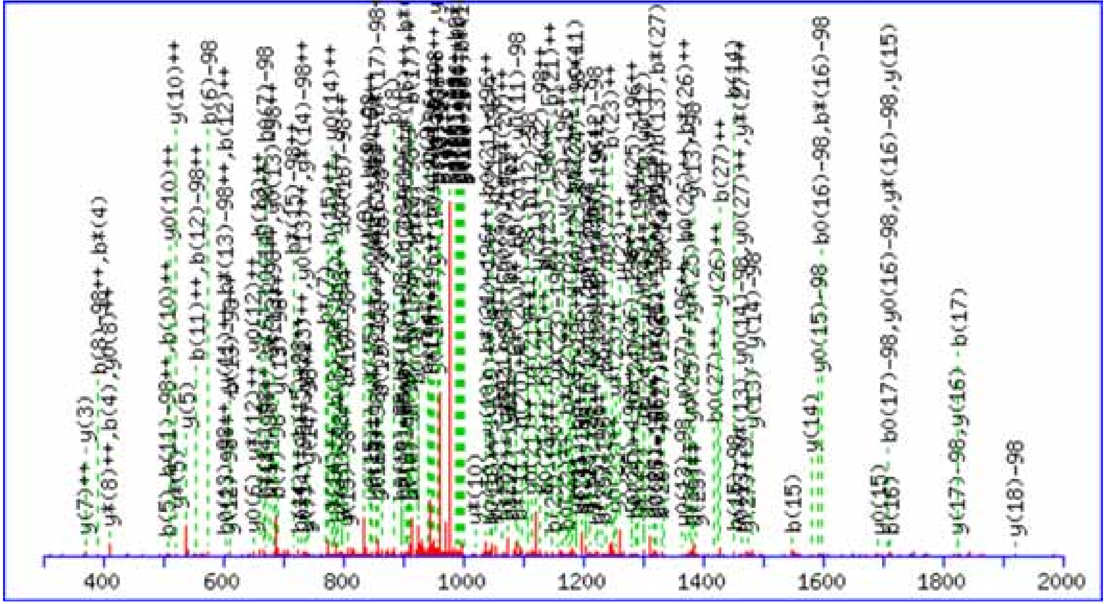
Peptide No.317

GPARPSLPGAPPDEVYLSDSPAEPAPVK
Confirmed sites: @S:6,@S:18
Ambiguous sites:

MS/MS Fragmentation of GPARPSLPGAPPDEVYLSDSPAEPAPVK

Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 7407: 3029.420025 from(1010.813951,3+)
Title: Elution from: 51.455 to 51.455 scan no 4896 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3029.4188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K28 : Dimethyl (K)
Ions Score: 56 **Expect:** 0.00029

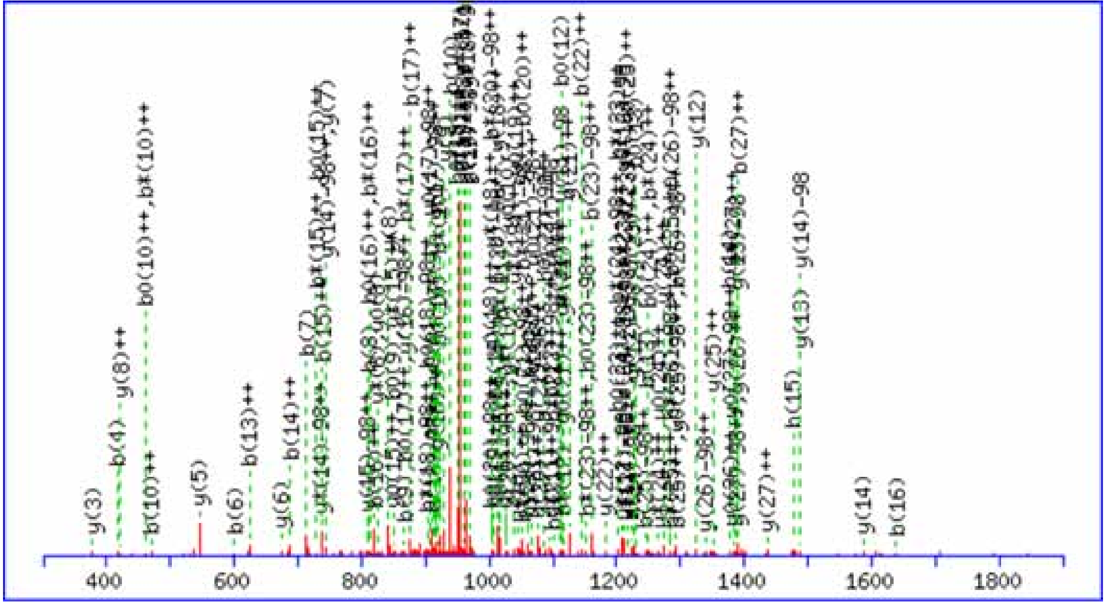
Matched b ions: b(4), b(5), b(6)-98, b(7)-98, b(7), b(8)-98++, b(8)-98, b(8), b(9)-98, b(9), b(10)++, b(10)-98, b(11)-98++, b(11)++, b(12)-98++, b(12), b(12)++, b(12)-98, b(13)++, b(13), b(13)-98, b(13)-98++, b(14)++, b(14), b(14)-98++, b(15)++, b(15), b(15)-98++, b(15)-98, b(16), b(16)++, b(16)-98++, b(17), b(17)-98++, b(17)++, b(18)-196++, b(18)-98++, b(18)++, b(19)++, b(19)-196++, b(20)-98++, b(20)++, b(20)-196++, b(21)-196++, b(21)-98++, b(21)++, b(22)++, b(23)-98++, b(23)++, b(23)-196++, b(24)-196++, b(24)-98++, b(25)-196++, b(25)-98++, b(25)++, b(26)++, b(26)-196++, b(26)-98++, b(27)++, b(27)-98++, b(27)-196++
Matched y ions: y(3), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(11)-98, y(12), y(12)-98, y(12)-98++, y(13), y(13)-98, y(13)-98++, y(14)-98, y(14), y(14)-98++, y(14)++, y(15), y(15)++, y(15)-98++, y(16)-98++, y(16), y(16)++, y(17)++, y(17)-98, y(17)-98++, y(18)-98, y(18)-98++, y(19)-98++, y(19)++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(23)++, y(23)-196++, y(23)-98++, y(24)-98++, y(24)++, y(24)-196++, y(25)-196++, y(25)++, y(26)++, y(27)++, y(27)-98++
Precursor origin neutral loss: +

Peptide No.318

GPARPSLPGAPPDEVYLSDSPAEPAPVK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of GPARPSLPGAPPDEVYLSDSPAEPAPVK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 6875: 2961.521526 from(988.181118,3+)
Title: Elution from: 49.011 to 49.011 scan no 4475 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2961.5161
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K28 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 82 Expect: 4.5e-007

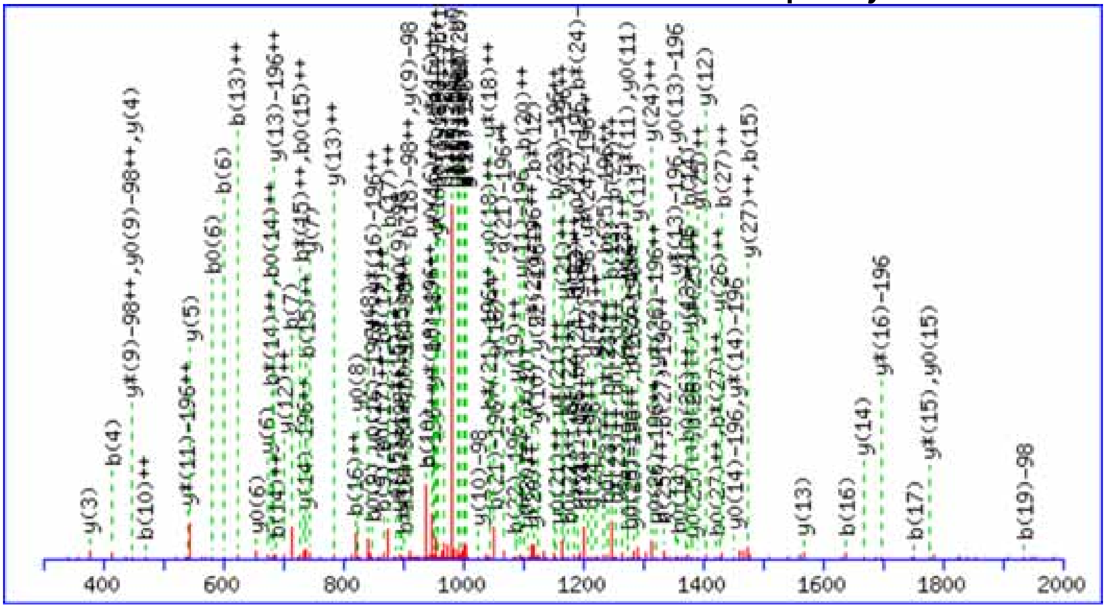
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(10), b(10)++, b(13)++, b(13), b(14)++, b(14), b(15)++, b(15), b(16)++, b(16), b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)-98++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(23)++, b(24)-98++, b(25)++, b(25)-98++, b(26)-98++, b(27)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(11), y(11)-98, y(12), y(12)-98, y(13)-98, y(13), y(14), y(14)-98, y(14)-98++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(23)++, y(24)++, y(24)-98++, y(25)++, y(26)-98++, y(26)++, y(27)++, y(27)-98++
Precursor origin neutral loss: +

Peptide No.319

GPARPSLPGAPPDEVYLSDSPAEPAPVK
Confirmed sites: @S:18,@S:20
Ambiguous sites:

MS/MS Fragmentation of GPARPSLPGAPPDEVYLSDSPAEPAPVK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 7587: 3041.485044 from(1014.835624,3+)
Title: Elution from: 50.777 to 50.777 scan no 4832 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3041.4824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S20 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K28 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 79 Expect: 1.2e-006

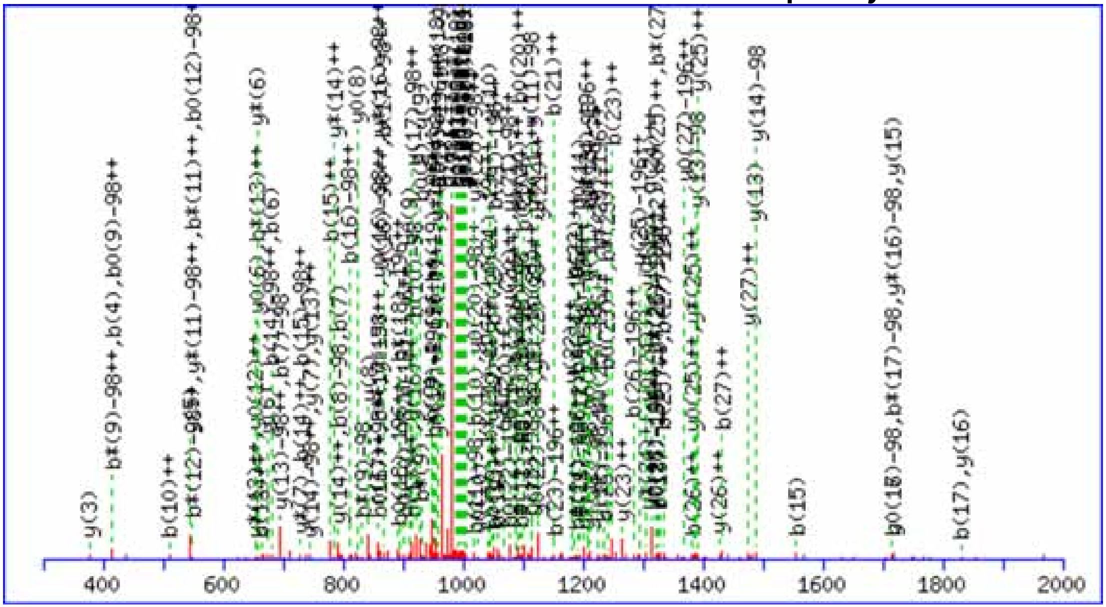
Matched b ions: b(4), b(6), b(7), b(9), b(10), b(10)++, b(13)++, b(13), b(14), b(14)++, b(15), b(15)++, b(16)++, b(16), b(17)++, b(17), b(18)-98++, b(18)++, b(19)-98, b(19)-98++, b(20)-98++, b(20)-196++, b(20)++, b(21)-196++, b(21)-98++, b(22)-98++, b(22)++, b(22)-196++, b(23)-98++, b(23)++, b(23)-196++, b(24)-196++, b(24)-98++, b(25)-98++, b(25)++, b(25)-196++, b(26)-196++, b(26)-98++, b(26)++, b(27)++, b(27)-196++, b(27)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(11)-196, y(12), y(12)-98++, y(12)-98, y(12)++, y(12)-196, y(13), y(13)-98++, y(13)-98, y(13)++, y(13)-196++, y(13)-196, y(14)-196++, y(14)-98, y(14)-98++, y(14), y(15)-98, y(15)-98++, y(15)++, y(16)++, y(17)-98++, y(17)-98, y(17)++, y(18)++, y(18)-196++, y(18)-98++, y(19)-196++, y(19)-98++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(21)-196++, y(22)-196++, y(22)++, y(23)-98++, y(23)++, y(23)-196++, y(24)++, y(24)-196++, y(24)-98++, y(25)++, y(25)-98++, y(26)++, y(27)++, y(27)-98++
Precursor origin neutral loss: +

Peptide No.320

GPARPSLPGAPPDEVYLSDSPAEPAPVK
Confirmed sites: @S:6,@S:18
Ambiguous sites:

MS/MS Fragmentation of GPARPSLPGAPPDEVYLSDSPAEPAPVK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 6693: 3041.486031 from(1014.835953,3+)
Title: Elution from: 51.337 to 51.337 scan no 4688 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3041.4824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K28 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 66 Expect: 2.4e-005

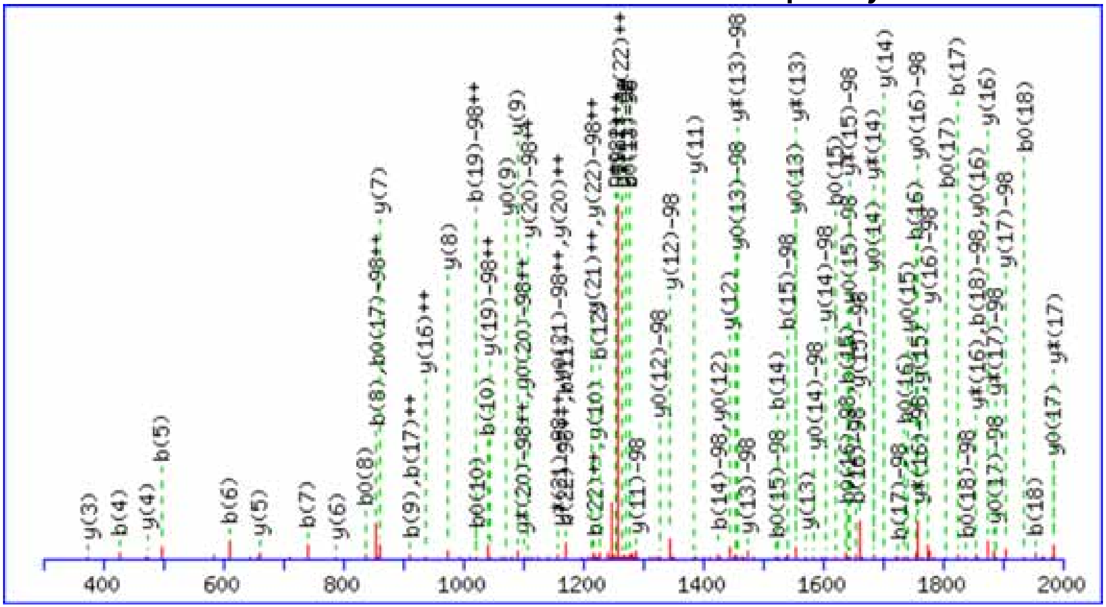
Matched b ions: b(4), b(6), b(7)-98, b(7), b(8)-98, b(9), b(10)++, b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(13)++, b(13), b(14)++, b(14)-98++, b(15), b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17), b(17)-98++, b(17)++, b(18)-196++, b(18)-98++, b(18)++, b(19)++, b(19)-196++, b(20)++, b(20)-98++, b(21)-98++, b(21)-196++, b(21)++, b(22)-196++, b(22)-98++, b(22)++, b(23)++, b(23)-98++, b(23)-196++, b(24)-98++, b(24)-196++, b(25)++, b(25)-98++, b(25)-196++, b(26)++, b(26)-98++, b(26)-196++, b(27)++, b(27)-196++, b(27)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12), y(12)-98, y(13)-98++, y(13), y(13)-98, y(13)++, y(14)++, y(14)-98++, y(14)-98, y(15), y(15)++, y(16), y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(19)-98++, y(19)++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(23)++, y(24)++, y(24)-98++, y(25)++, y(25)-196++, y(26)++, y(27)++
Precursor origin neutral loss: +

Peptide No.321

GPDEAIEDGEEGSEDDAEWVVTK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of GPDEAIEDGEEGSEDDAEWVVTK
Found in EHD2_MOUSE, EH domain-containing protein 2 OS=Mus musculus GN=Ehd2 PE=1 SV=1

Match to Query 6374: 2612.071204 from(1307.042878,2+)
Title: Elution from: 52.272 to 52.272 scan no 4861 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2612.0691
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K23 : Dimethyl (K)
Ions Score: 95 Expect: 1.7e-008

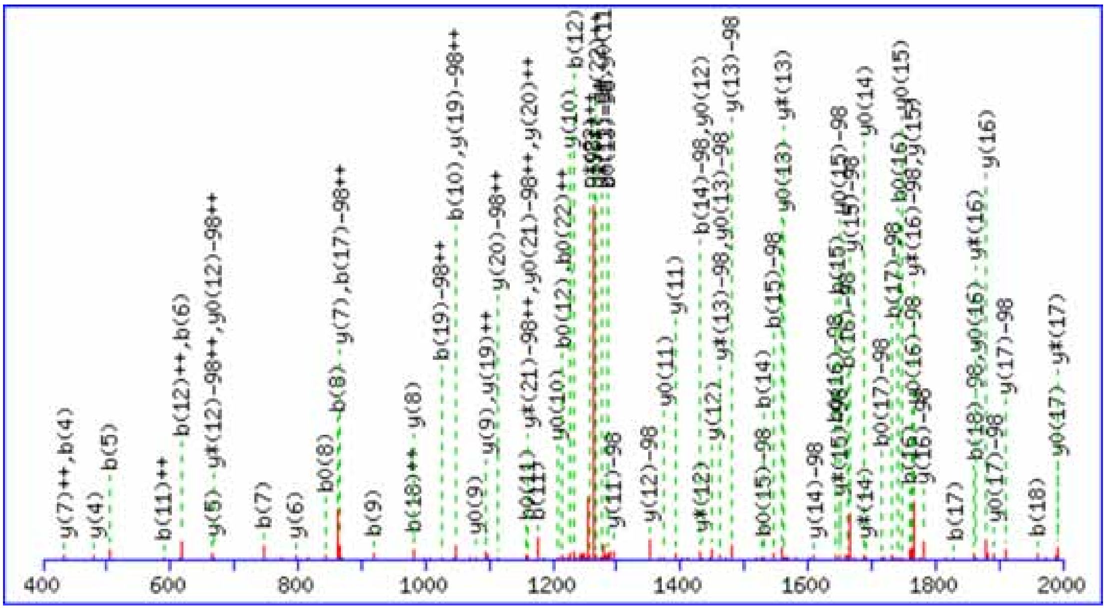
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(14)-98, b(14), b(15)-98, b(15), b(16)-98, b(16), b(17)++, b(17), b(17)-98, b(18), b(18)-98, b(19)-98++, b(22)-98++, b(22)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11), y(12)-98, y(12), y(13)-98, y(13), y(14)-98, y(14), y(15)-98, y(15), y(16), y(16)++, y(16)-98, y(17)-98, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(22)++, y(22)-98++
Precursor origin neutral loss: +

Peptide No.322

GPDEAIEDGEEGSEDDAEWVVTK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of GPDEAIEDGEEGSEDDAEWVVTK
Found in EHD2_MOUSE, EH domain-containing protein 2 OS=Mus musculus GN=Ehd2 PE=1 SV=1

Match to Query 6237: 2624.134192 from(1313.074372,2+)
Title: Elution from: 52.189 to 52.189 scan no 4774 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2624.1327
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K23 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 98 Expect: 1.2e-008

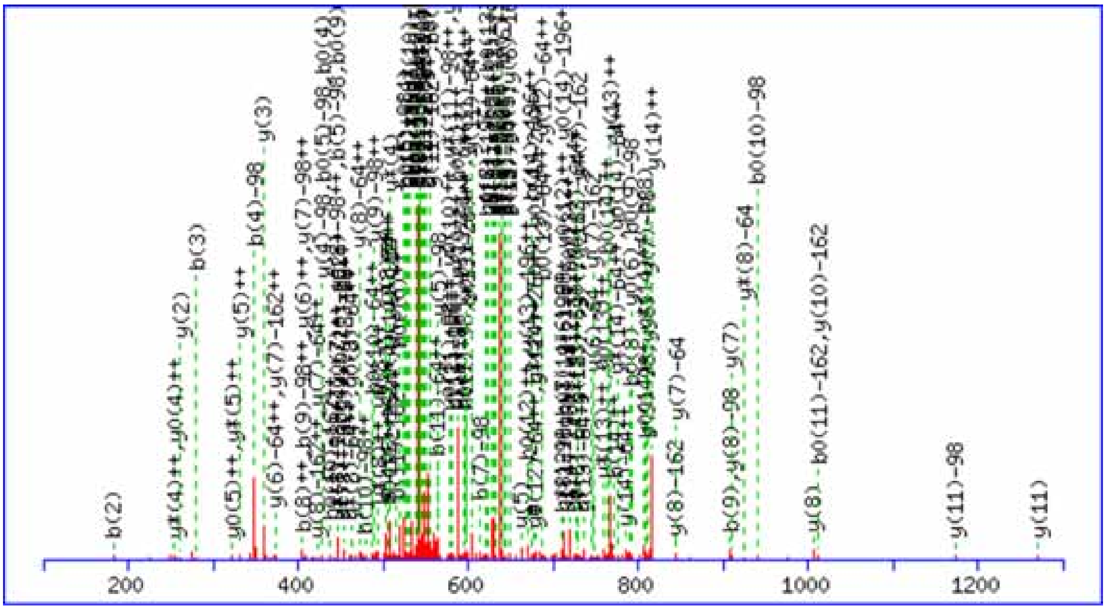
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(11)++, b(12)++, b(12), b(14)-98, b(14), b(15)-98, b(15), b(16)-98, b(16), b(17)-98++, b(17)-98, b(17), b(18)++, b(18), b(18)-98, b(19)-98++
Matched y ions: y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12)-98, y(12), y(13)-98, y(14)-98, y(15)-98, y(15), y(16), y(16)-98, y(17)-98, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(22)++
Precursor origin neutral loss: +

Peptide No.323

GPPSPPAPVMHSPSR
Confirmed sites: @S:4,@S:12
Ambiguous sites:

MS/MS Fragmentation of GPPSPPAPVMHSPSR
Found in SNW1_MOUSE, SNW domain-containing protein 1 OS=Mus musculus GN=Snw1 PE=1 SV=3

Match to Query 3836: 1716.709710 from(573.243846,3+)
Title: Elution from: 28.367 to 28.367 scan no 2080 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1716.7096
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00049

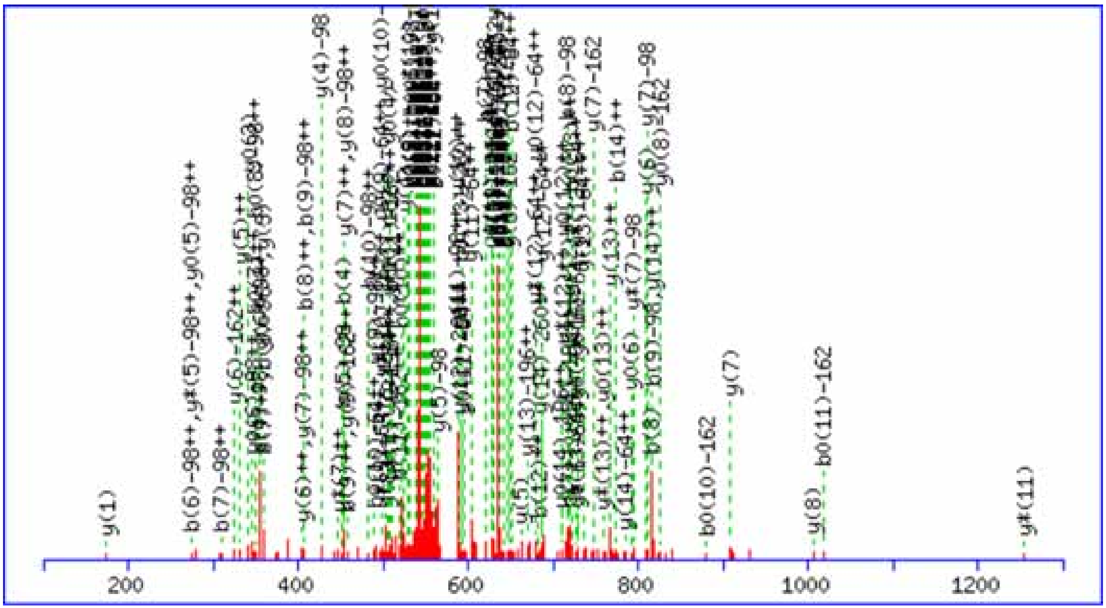
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8)++, b(8)-98, b(8), b(9), b(9)-98++, b(9)++, b(9)-98, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(12)-196++, b(13)-196++, b(13)-98++, b(13)++, b(14)-196++, b(14)++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)++, y(5), y(5)-98, y(6)++, y(6)-98, y(6), y(7)-98++, y(7), y(7)++, y(7)-98, y(8)-98, y(8), y(8)-98++, y(8)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98, y(11), y(11)-98++, y(12)++, y(12)-98++, y(12)-196++, y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++
Precursor origin neutral loss: +

Peptide No.324

GPPSPPAPVMHSPSR
Confirmed sites: @S:4,@S:12
Ambiguous sites:

MS/MS Fragmentation of GPPSPPAPVMHSPSR
Found in SNW1_MOUSE, SNW domain-containing protein 1 OS=Mus musculus GN=Snw1 PE=1 SV=3

Match to Query 2982: 1722.741873 from(575.254567,3+)
Title: Elution from: 28.241 to 28.241 scan no 1908 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1722.7414
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0078

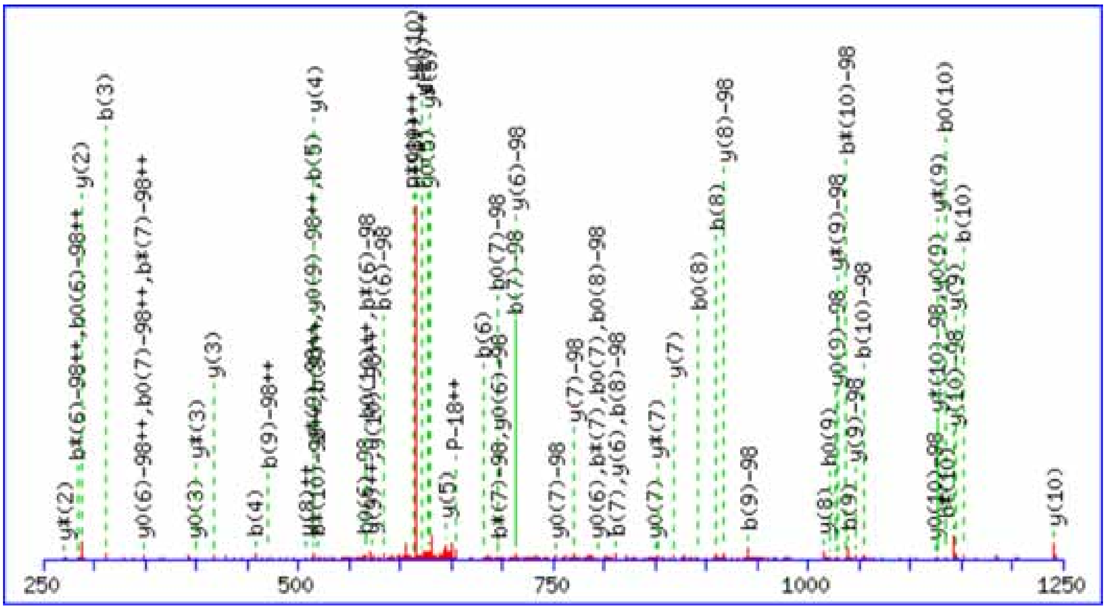
Matched b ions: b(4)-98, b(4), b(5), b(5)-98, b(6)-98++, b(6)-98, b(7)++, b(7), b(7)-98++, b(7)-98, b(8)-98++, b(8), b(8)++, b(8)-98, b(9)-98, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-196++, b(13)-98++, b(14)++
Matched y ions: y(1), y(3), y(4)-98, y(4), y(5)++, y(5)-98, y(5), y(6)++, y(6), y(6)-98++, y(7), y(7)-98++, y(7)-98, y(7)++, y(8), y(8)-98++, y(8)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(13)-196++, y(14)-196++, y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.325

GPQFGSEVELR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GPQFGSEVELR
Found in ACE_MOUSE, Angiotensin-converting enzyme OS=Mus musculus GN=Ace PE=1 SV=3

Match to Query 1330: 1325.602306 from(663.808429,2+)
Title: Elution from: 44.499 to 44.499 scan no 4039 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1325.6017
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 0.00023

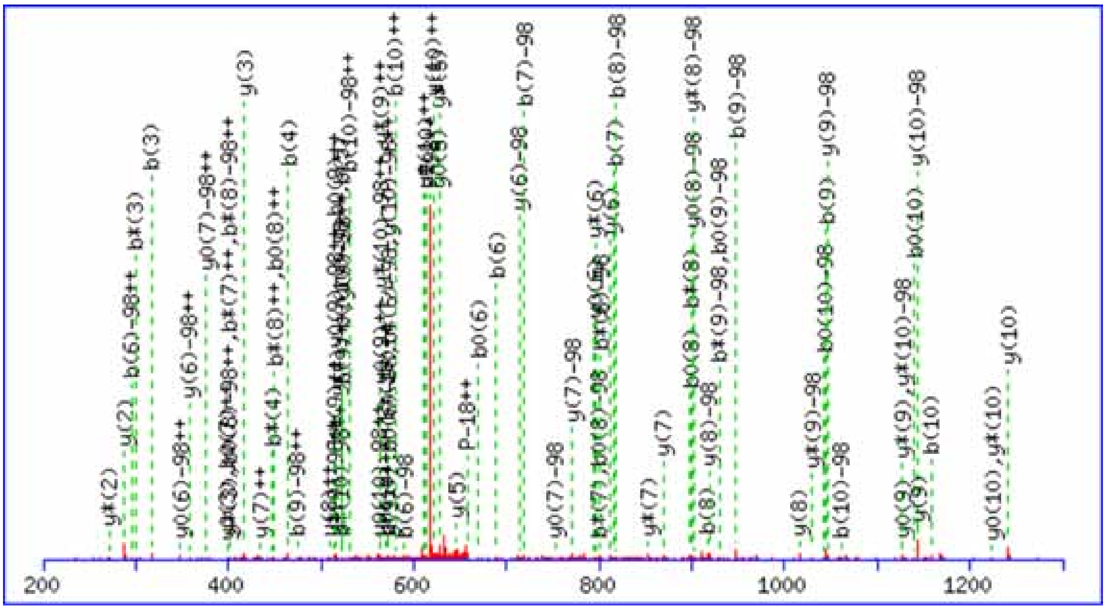
Matched b ions: b(3), b(4), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(9)-98++, b(9)++, b(10)-98, b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7)-98, y(7), y(8)-98, y(8), y(8)++, y(9), y(9)-98, y(9)++, y(10)-98, y(10), y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.326

GPQFGSEVELR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GPQFGSEVELR
Found in ACE_MOUSE, Angiotensin-converting enzyme OS=Mus musculus GN=Ace PE=1 SV=3

Match to Query 1502: 1331.634006 from(666.824279,2+)
Title: Elution from: 44.418 to 44.418 scan no 4050 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1331.6335
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 **Expect:** 0.00042

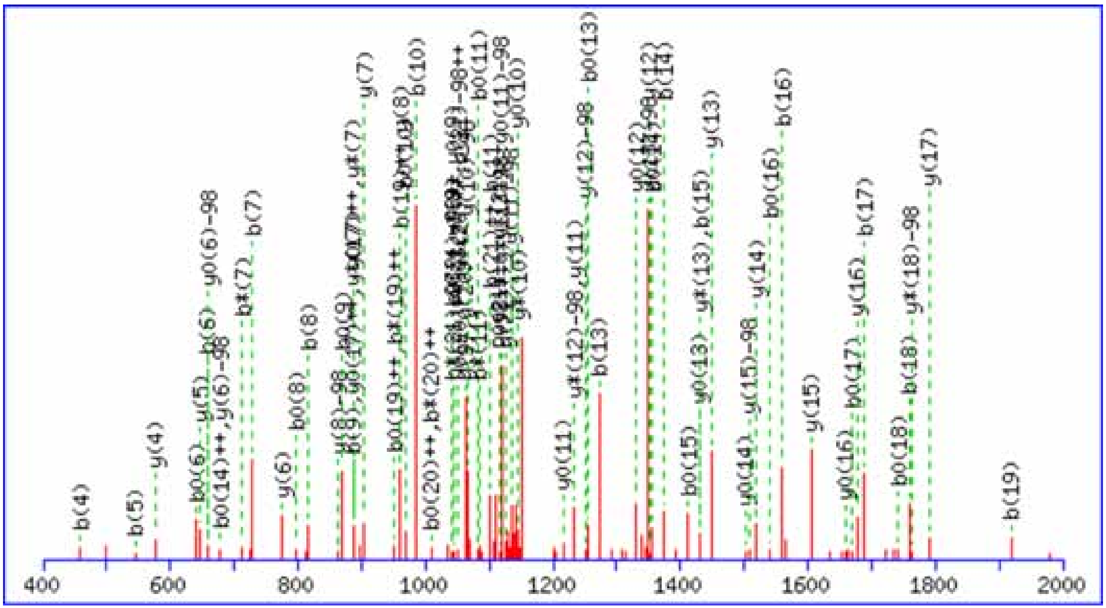
Matched b ions: b(3), b(4), b(5), b(6)-98++, b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(9)-98++, b(9)++, b(10), b(10)-98, b(10)-98++, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98++, y(6)-98, y(7)-98, y(7), y(7)++, y(8), y(8)-98, y(8)++, y(9)-98, y(9), y(9)-98++, y(9)++, y(10)-98, y(10), y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.327

GQEDSLASAVDATTGQEACDSD
Confirmed sites: @S:21
Ambiguous sites:

MS/MS Fragmentation of GQEDSLASAVDATTGQEACDSD
Found in CCD12_MOUSE, Coiled-coil domain-containing protein 12 OS=Mus musculus GN=Ccdc12 PE=1 SV=2

Match to Query 7140: 2333.885386 from(1167.949969,2+)
Title: Elution from: 53.723 to 53.723 scan no 5325 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2333.8843
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 118 Expect: 3.7e-011

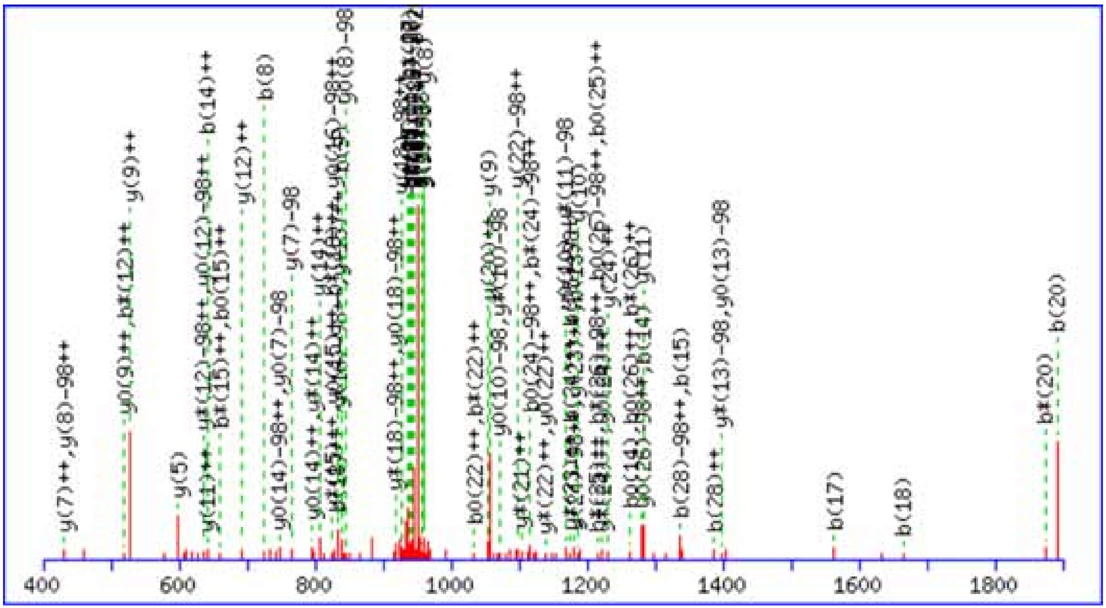
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(13), b(14), b(15), b(16), b(17), b(18), b(19), b(19)++, b(21)-98++, b(21)++
Matched y ions: y(4), y(5), y(6), y(6)-98, y(7), y(8), y(8)-98, y(9), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(14), y(15), y(15)-98, y(16), y(17), y(20)++, y(21)++
Precursor origin neutral loss: +

Peptide No.328

GQGSEPAAITGGQVGPETPEPPPSPPETR
Confirmed sites: @S:24
Ambiguous sites:

MS/MS Fragmentation of GQGSEPAAITGGQVGPETPEPPPSPPETR
Found in EH1L1_MOUSE, EH domain-binding protein 1-like protein 1 OS=Mus musculus GN=Ehbp1l1 PE=2 SV=1

Match to Query 8508: 2947.360755 from(983.460861,3+)
Title: Elution from: 42.898 to 42.898 scan no 4044 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2947.3601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S24 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.012

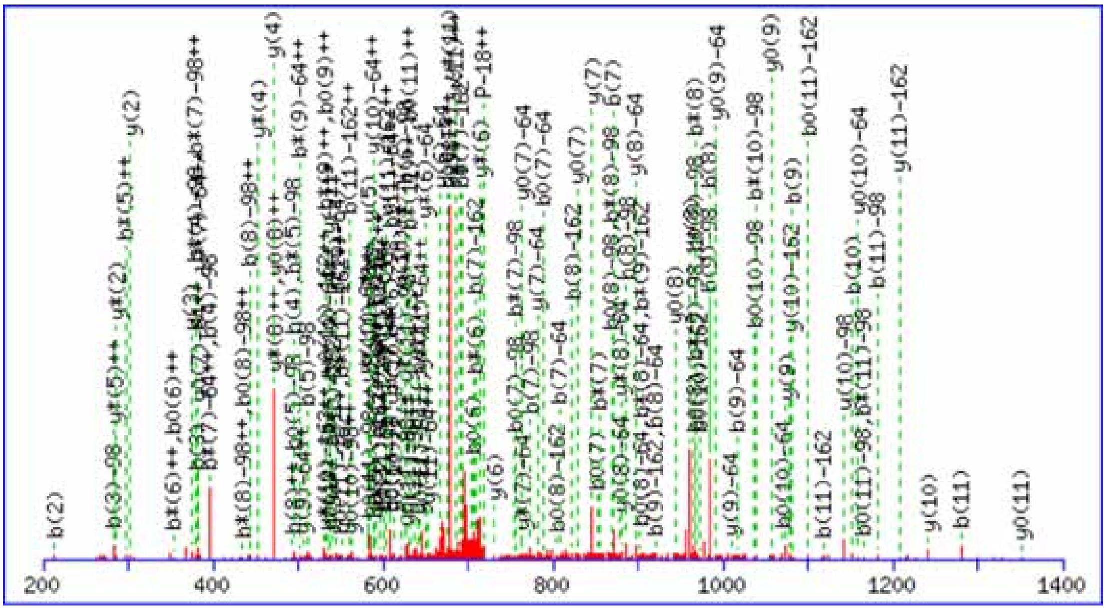
Matched b ions: b(8), b(9), b(10), b(13), b(14)++, b(14), b(15), b(17), b(18), b(18)++, b(20), b(20)++, b(24)++, b(25)-98++, b(28)-98++, b(28)++
Matched y ions: y(5), y(7)++, y(7)-98, y(8)-98++, y(8), y(9)++, y(9), y(9)-98, y(10), y(11), y(11)++, y(12)++, y(14)++, y(15)++, y(16)-98++, y(18)-98++, y(19)-98++, y(20)++, y(22)-98++, y(23)++, y(24)-98++, y(24)++
Precursor origin neutral loss: +

Peptide No.329

GQSIDDMIPAQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GQSIDDMIPAQK
Found in KCRM_MOUSE, Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1

Match to Query 1972: 1453.652730 from(727.833641,2+)
Title: Elution from: 33.611 to 33.611 scan no 2594 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1453.6524
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K12 : Dimethyl (K)
Ions Score: 55 Expect: 0.0001

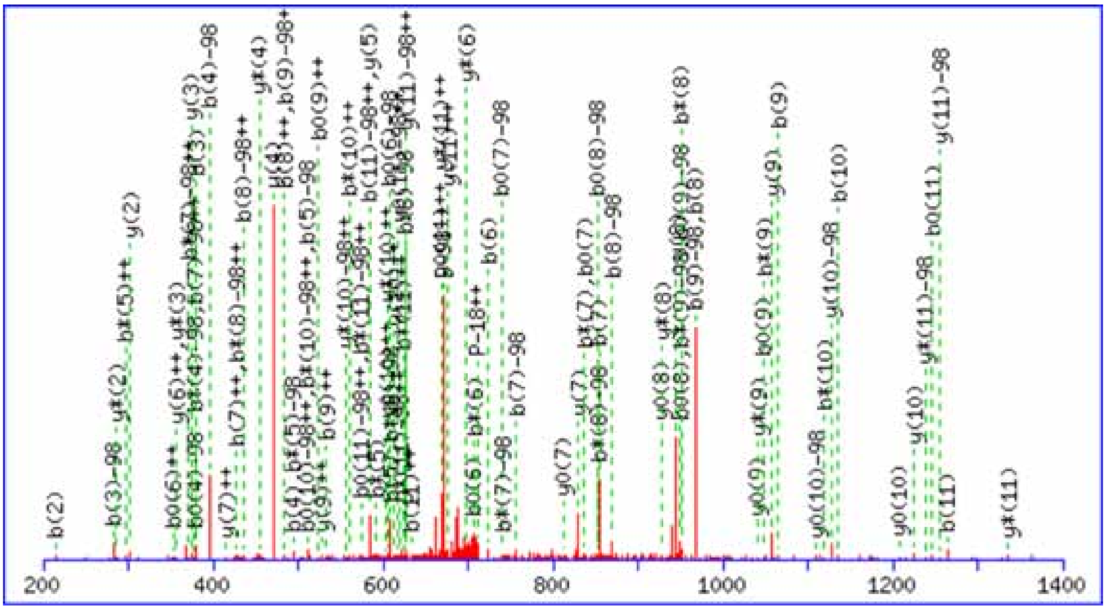
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(8)-98++, b(8)++, b(9)-98, b(9)++, b(9), b(10), b(11), b(11)-98, b(11)-98++, b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)-98, y(10), y(10)++, y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.330

GQSIDDMIPAQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GQSIDDMIPAQK
Found in KCRM_MOUSE, Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1

Match to Query 1458: 1437.658128 from(719.836340,2+)
Title: Elution from: 43.990 to 43.990 scan no 3870 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1437.6575
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K12 : Dimethyl (K)
Ions Score: 67 Expect: 6.5e-006

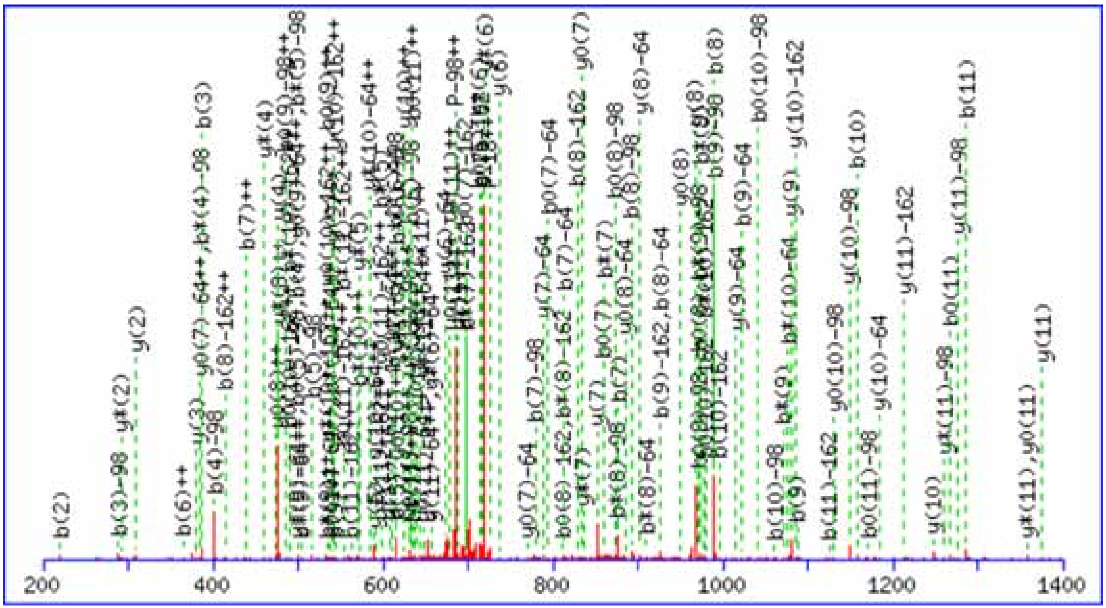
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(7)-98++, b(7)++, b(8), b(8)-98, b(8)-98++, b(8)++, b(9)-98, b(9), b(9)-98++, b(9)++, b(10), b(11)-98++, b(11), b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(7), y(7)++, y(8), y(9), y(9)++, y(10)-98, y(10), y(10)++, y(11)-98, y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.331

GQSIDDMIPAQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GQSIDDMIPAQK
Found in KCRM_MOUSE, Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1

Match to Query 2035: 1465.717232 from(733.865892,2+)
Title: Elution from: 34.033 to 34.033 scan no 2687 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1465.7160
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K12 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 53 Expect: 0.00024

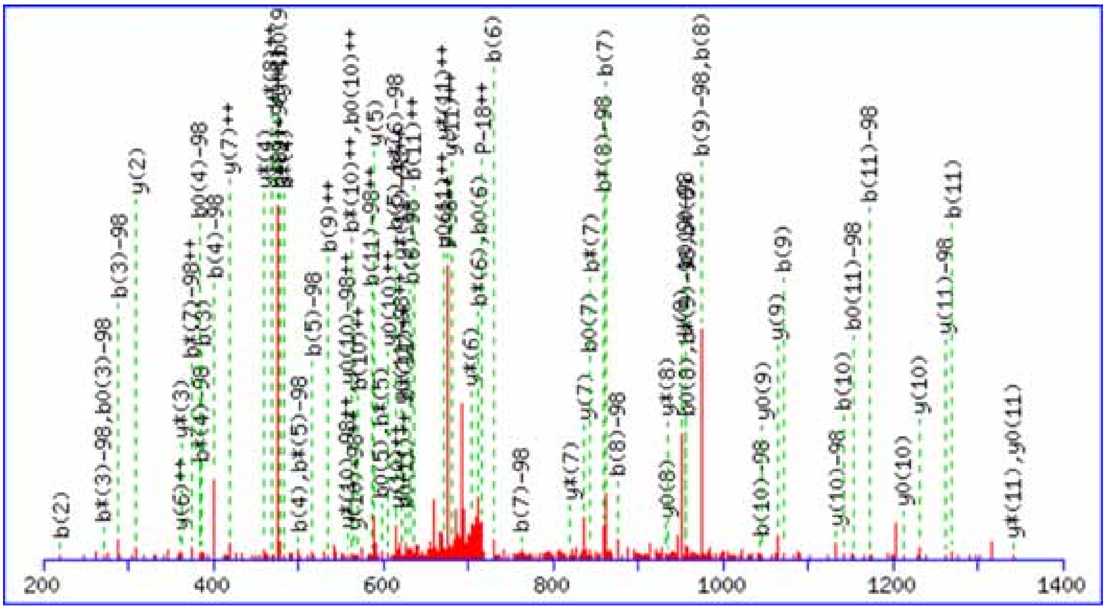
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)++, b(6)-98, b(7), b(7)-98, b(7)++, b(8), b(8)-98, b(9), b(9)-98, b(9)++, b(10), b(10)-98, b(11), b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)-98, y(10), y(10)++, y(11), y(11)-98, y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.332

GQSIDDMIPAQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GQSIDDMIPAQK
Found in KCRM_MOUSE, Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1

Match to Query 1965: 1449.720722 from(725.867637,2+)
Title: Elution from: 43.803 to 43.803 scan no 3970 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1449.7211
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 49 Expect: 0.0005

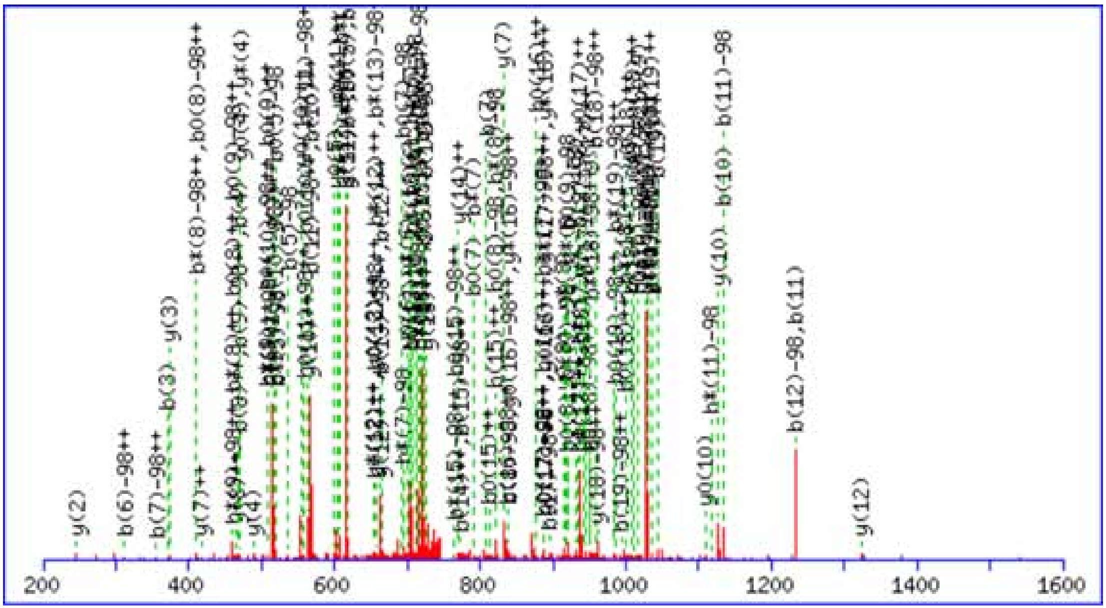
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(9)++, b(10), b(10)-98, b(10)++, b(11), b(11)-98++, b(11)++, b(11)-98
Matched y ions: y(2), y(4), y(5), y(6)++, y(7)++, y(7), y(8)++, y(8), y(9), y(10)-98, y(10), y(10)-98++, y(10)++, y(11)-98, y(11)++
Precursor origin neutral loss: +

Peptide No.333

GREPSSSQPVVPVDVEDQAK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of GREPSSSQPVVPVDVEDQAK
Found in PBIP1_MOUSE, Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Mus musculus GN=Pbxip1 PE=1 SV=2

Match to Query 7516: 2259.078516 from(754.033448,3+)
Title: Elution from: 38.170 to 38.170 scan no 3381 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2259.0784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
Ions Score: 36 **Expect:** 0.022

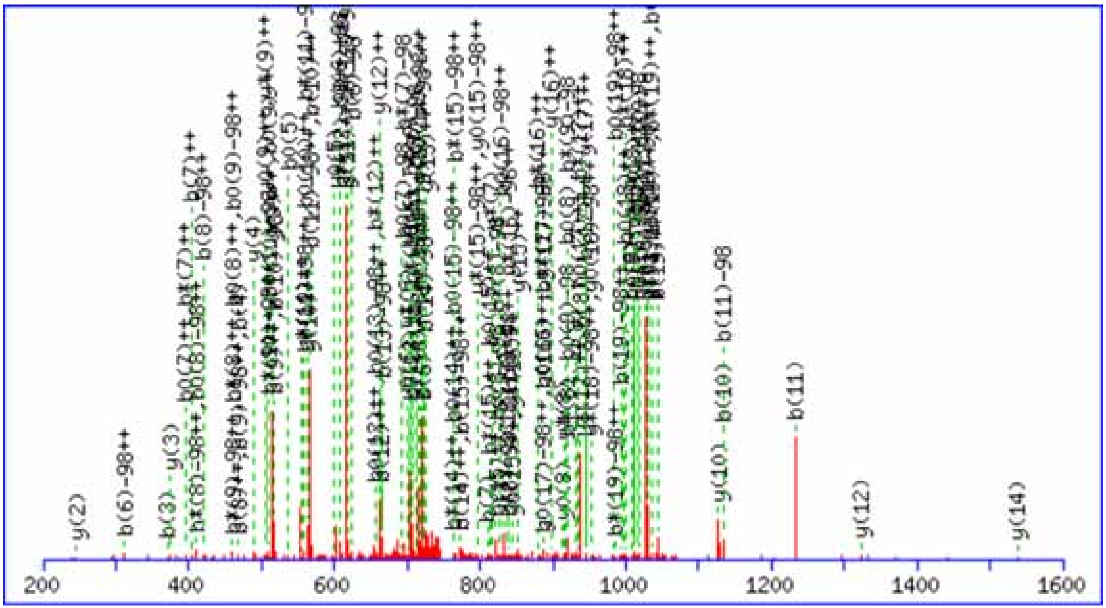
Matched b ions: b(3), b(4), b(5)-98, b(6)-98++, b(6), b(7)-98++, b(7)-98, b(7), b(8), b(8)++, b(8)-98, b(9)++, b(9)-98++, b(9)-98, b(9), b(10)-98++, b(10)++, b(10), b(10)-98, b(11)++, b(11), b(11)-98++, b(11)-98, b(12)-98++, b(12)-98, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(9), y(10), y(10)++, y(12), y(12)++, y(13)++, y(14)++, y(17)++, y(18)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.334

GREPSSSQPVVPVDVEDQAK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GREPSSSQPVVPVDVEDQAK
Found in PBIP1_MOUSE, Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Mus musculus GN=Pbxip1 PE=1 SV=2

Match to Query 5981: 2259.080808 from(754.034212,3+)
Title: Elution from: 38.053 to 38.053 scan no 3214 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2259.0784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl (K)
Ions Score: 54 **Expect:** 0.00033

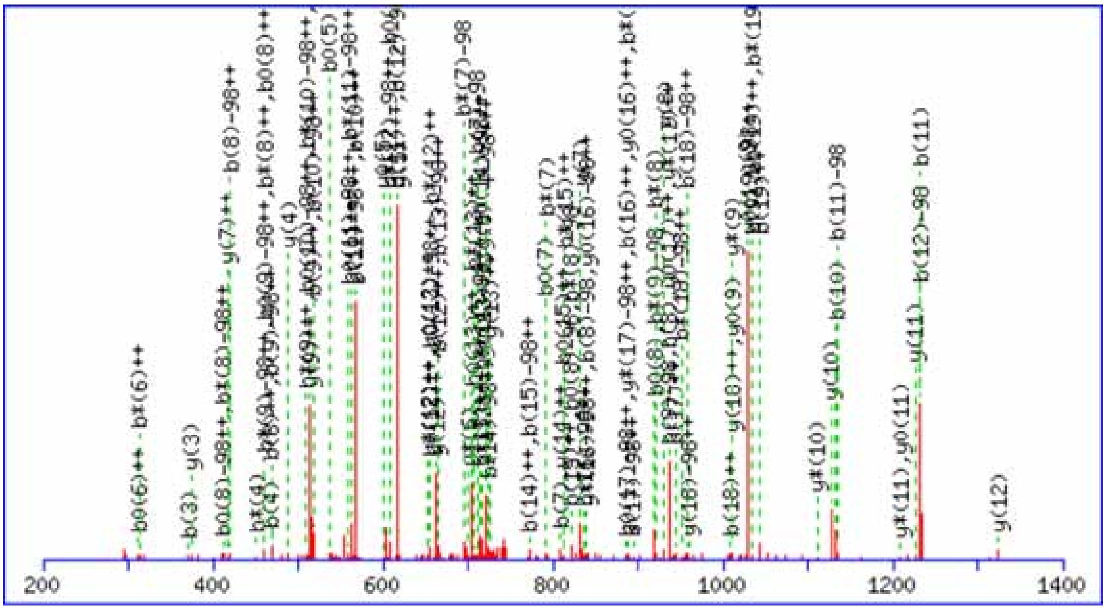
Matched b ions: b(3), b(4), b(6)-98++, b(6)-98, b(6), b(7)++, b(7)-98, b(7), b(8), b(8)-98++, b(8)++, b(8)-98, b(9)++, b(9), b(9)-98++, b(10)-98++, b(10)++, b(10), b(10)-98, b(11)++, b(11), b(11)-98++, b(11)-98, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(10)++, y(12), y(12)++, y(13)++, y(14), y(15)++, y(16)++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No.335

GREPSSSQPVVPVDVEDQAK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GREPSSSQPVVPVDVEDQAK
Found in PBIP1_MOUSE, Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Mus musculus GN=Pbxip1 PE=1 SV=2

Match to Query 6894: 2259.080886 from(754.034238,3+)
Title: Elution from: 38.197 to 38.197 scan no 3425 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2259.0784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
Ions Score: 66 Expect: 1.9e-005

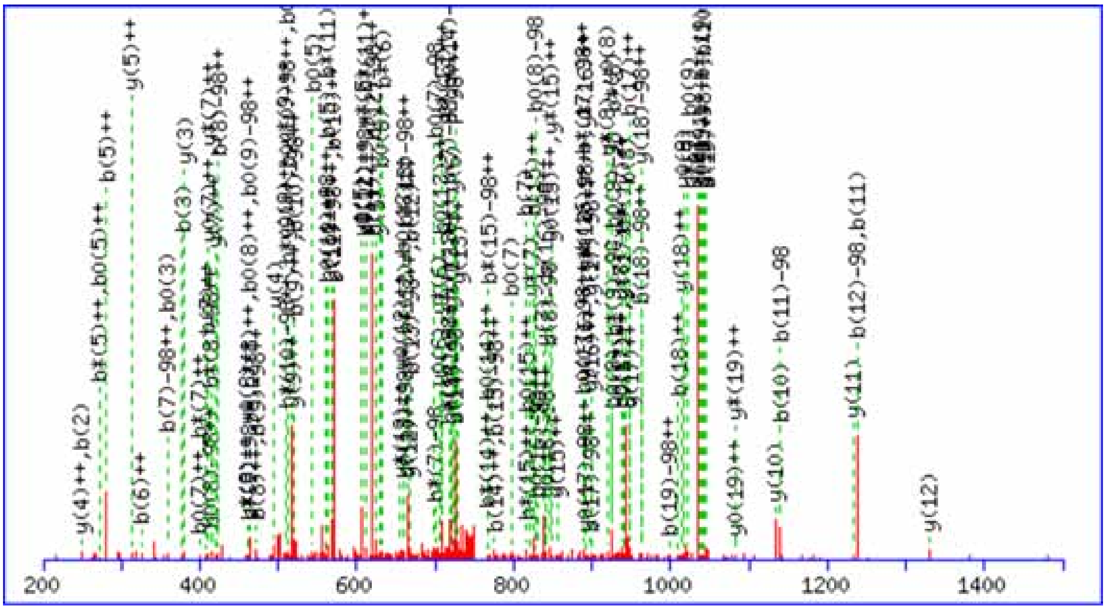
Matched b ions: b(3), b(4), b(7), b(7)-98, b(8)++, b(8), b(8)-98++, b(8)-98, b(9)-98++, b(9)-98, b(9)++, b(9), b(10)++, b(10), b(10)-98++, b(10)-98, b(11)-98++, b(11)++, b(11), b(11)-98, b(12)-98++, b(12)-98, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(12), y(12)++, y(13)++, y(14)++, y(18)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.336

GREPSSSQPVVPVDVEDQAK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GREPSSSQPVVPVDVEDQAK
Found in PBIP1_MOUSE, Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Mus musculus GN=Pbxip1 PE=1 SV=2

Match to Query 6289: 2271.142767 from(758.054865,3+)
Title: Elution from: 38.196 to 38.196 scan no 3262 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2271.1420
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 47 Expect: 0.0015

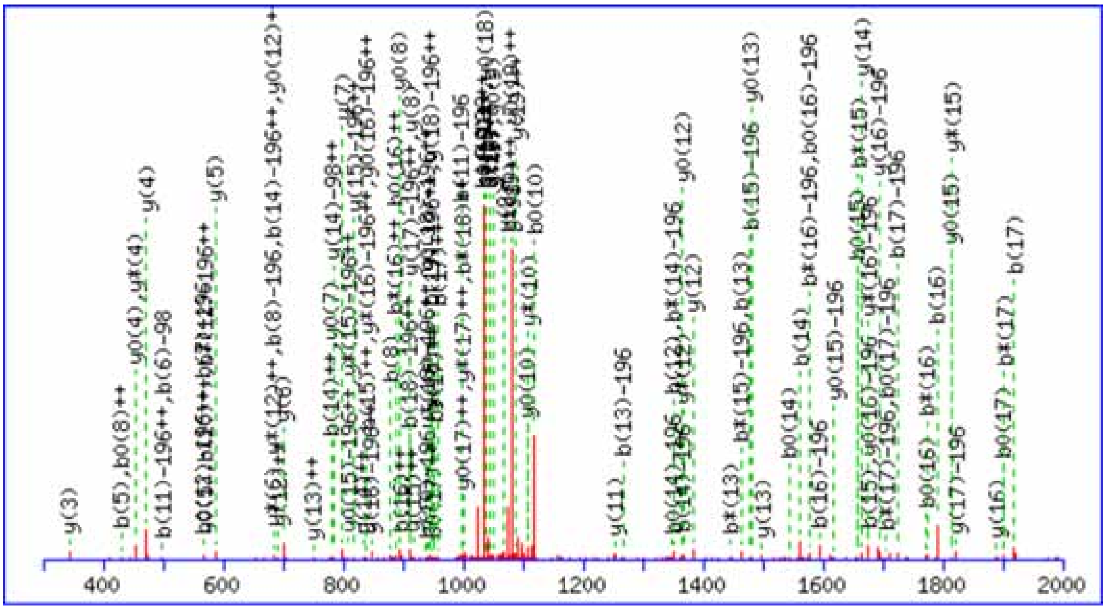
Matched b ions: b(2), b(3), b(5)++, b(5), b(6)++, b(7)-98, b(7)-98++, b(7)++, b(7), b(8), b(8)-98, b(8)++, b(8)-98++, b(9)-98++, b(9)++, b(9), b(10)++, b(10), b(10)-98++, b(10)-98, b(11)-98++, b(11)++, b(11), b(11)-98, b(12)-98++, b(12)-98, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(3), y(4), y(4)++, y(5)++, y(5), y(6), y(7), y(7)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(12), y(12)++, y(13)++, y(15)++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.337

GSAEGSSDEEGKLVIDEPAK
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of GSAEGSSDEEGKLVIDEPAK
Found in HDGF_MOUSE, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 5467: 2260.977532 from(1131.496042,2+)
Title: Elution from: 41.449 to 41.449 scan no 3553 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2260.9753
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl (K)
K20 : Dimethyl (K)
Ions Score: 50 Expect: 0.00057

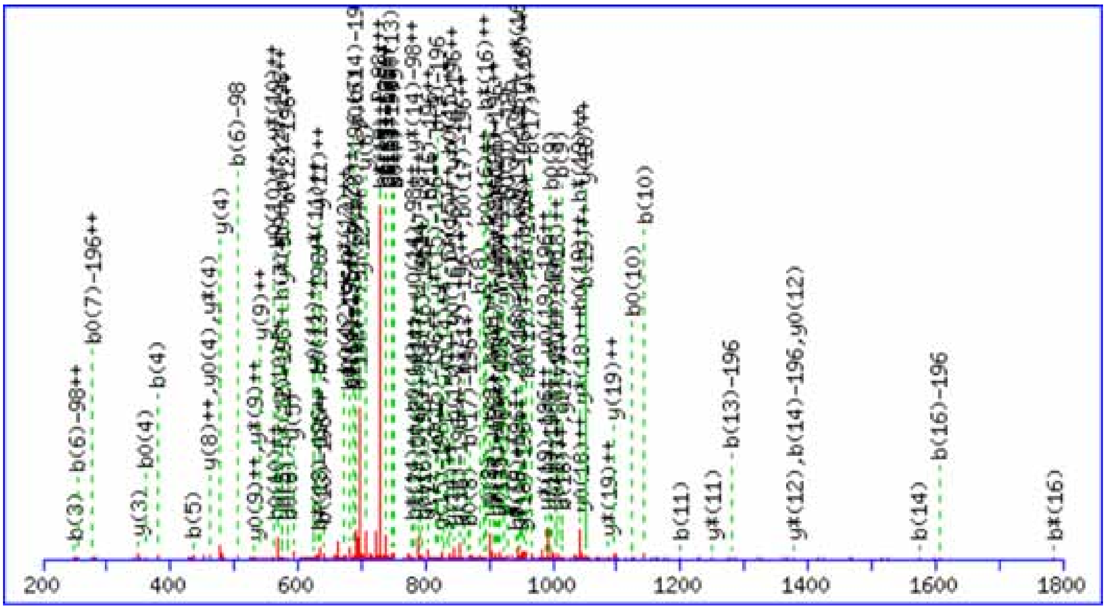
Matched b ions: b(5), b(6)-98, b(7)-196, b(8)-196, b(8)-98, b(8), b(9)-98++, b(9)-98, b(10)++, b(10)-196, b(10)-98, b(11)-196++, b(11)-196, b(11)-98, b(12)-98, b(12), b(13)-98++, b(13), b(13)-98, b(13)-196, b(14)-98, b(14), b(14)-196++, b(14)++, b(14)-196, b(15), b(15)-98, b(15)++, b(15)-196, b(16)++, b(16), b(16)-196, b(16)-98, b(17), b(17)-98, b(17)-196, b(17)++, b(18)-98, b(18)-196++, b(18)-98++, b(19)-98, b(19)-196++, b(19)-98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(12)++, y(13), y(13)++, y(14), y(14)-98++, y(14)++, y(15)-196++, y(15)-98++, y(15)++, y(16)-98++, y(16)-98, y(16)-196++, y(16)-196, y(16), y(16)++, y(17)-196++, y(17)-98, y(17)-196, y(18)-196++, y(18)-98++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.338

GSAEGSSDEEGKLVIDEPAK
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of GSAEGSSDEEGKLVIDEPAK
Found in HDGF_MOUSE, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 6075: 2279.072175 from(760.698001,3+)
Title: Elution from: 41.451 to 41.451 scan no 3671 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2279.0707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl:2H(4)13C(2) (K)
K20 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 38 Expect: 0.012

Matched b ions: b(3), b(4), b(5), b(6)-98, b(6)-98++, b(7)-196, b(7)-98, b(8)-98, b(8)-196, b(8), b(9)-196, b(9)-98, b(9), b(10), b(10)-98, b(10)-196, b(11), b(11)-98++, b(11)-196, b(11)-98, b(12)-98++, b(12)-196++, b(12)++, b(13)-98++, b(13)-196, b(13)-98, b(13)-196++, b(13)++, b(14)++, b(14)-196++, b(14)-196, b(14), b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-196, b(16)-98++, b(16)-196++, b(17)-98++, b(17)++, b(17)-196++, b(18)-196++, b(18)-98++, b(18)++, b(19)-196++, b(19)++, b(19)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(14)++, y(14)-98++, y(15)-196++, y(15)-98++, y(15)++, y(16)-98++, y(16)-196++, y(16)++, y(17)-196++, y(17)-98++, y(17)++, y(18)++, y(18)-196++, y(18)-98++, y(19)++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

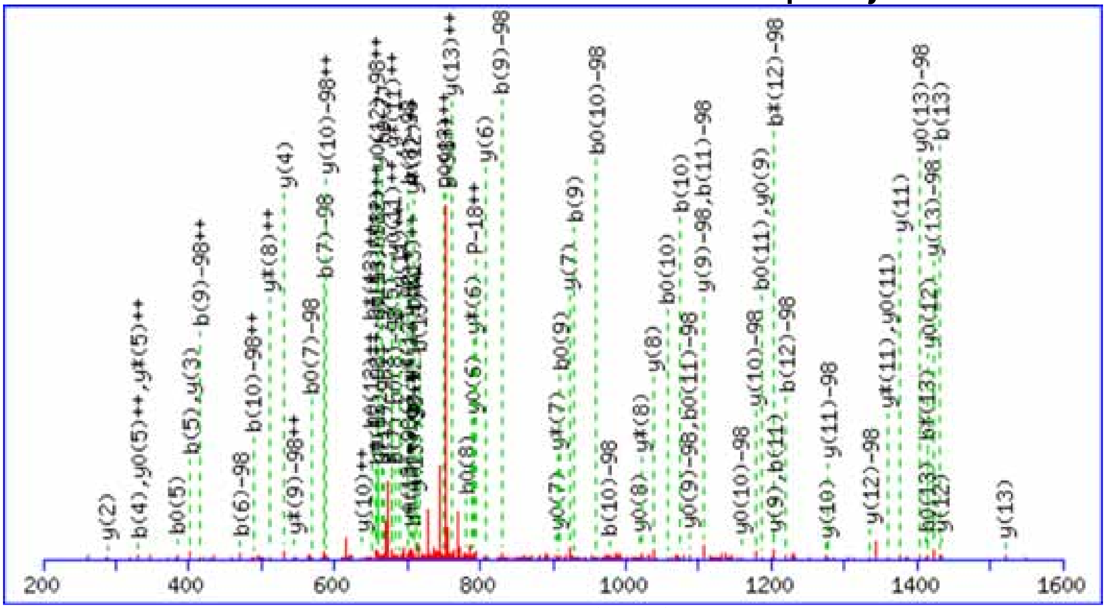
Peptide No.339

GSGTASDDEFENLR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GSGTASDDEFENLR
Found in HUWE1_MOUSE, E3 ubiquitin-protein ligase HUWE1 OS=Mus musculus GN=Huwe1 PE=1 SV=4

Match to Query 3129: 1604.637370 from(803.325961,2+)

Title: Elution from: 41.384 to 41.384 scan no 3848 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1604.6355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0034

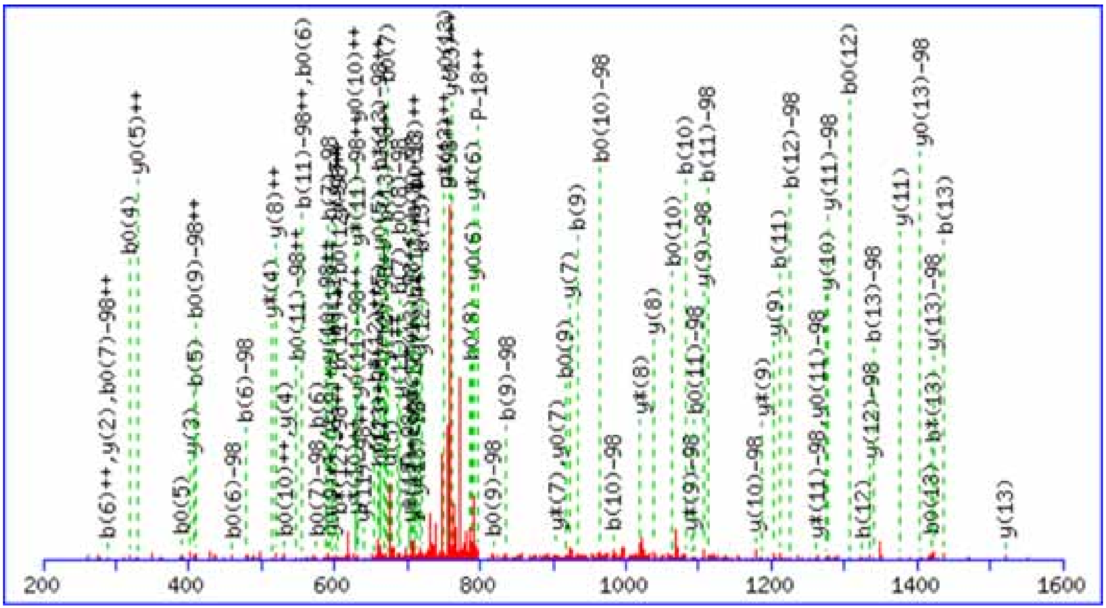
Matched b ions: b(4), b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(9)-98++, b(9)-98, b(9), b(10)-98, b(10)-98++, b(10), b(11)-98, b(11), b(12)-98, b(12)++, b(13), b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98, y(9), y(10)-98, y(10), y(10)-98++, y(10)++, y(11)-98, y(11), y(11)++, y(12)-98, y(12), y(12)-98++, y(13)-98, y(13), y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.340

GSGTASDDEFENLR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of GSGTASDDEFENLR
Found in HUWE1_MOUSE, E3 ubiquitin-protein ligase HUWE1 OS=Mus musculus GN=Huwe1 PE=1 SV=4

Match to Query 2107: 1610.667764 from(806.341158,2+)
Title: Elution from: 41.089 to 41.089 scan no 3506 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1610.6674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 **Expect:** 0.0082

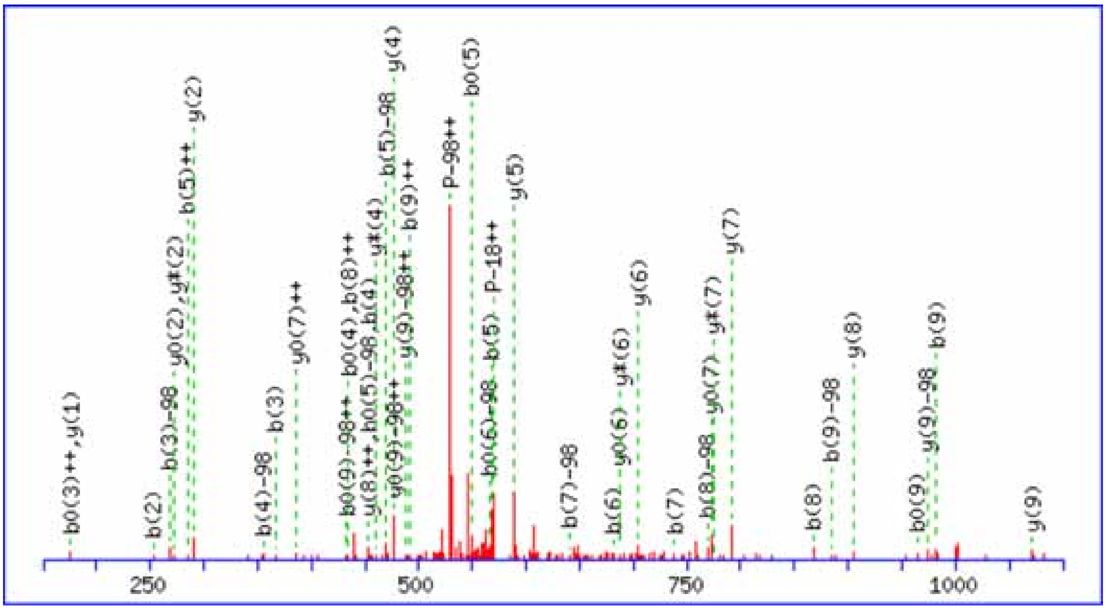
Matched b ions: b(5), b(6)-98, b(6)++, b(6), b(7)-98, b(7), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98++, b(11)-98, b(11)++, b(12)-98, b(12)++, b(12), b(13), b(13)-98++, b(13)++, b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8)++, y(8), y(9), y(9)-98, y(9)++, y(10)-98, y(10)-98++, y(10), y(11)-98, y(11), y(11)-98++, y(11)++, y(12)-98, y(12)-98++, y(12)++, y(13)-98, y(13), y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.341

GSLSDLGEDR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of GSLSDLGEDR
Found in CMYA5_MOUSE, Cardiomyopathy-associated protein 5 OS=Mus musculus GN=Cmya5 PE=1 SV=2

Match to Query 1033: 1155.481874 from(578.748213,2+)
Title: Elution from: 35.494 to 35.494 scan no 3056 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1155.4809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.0022

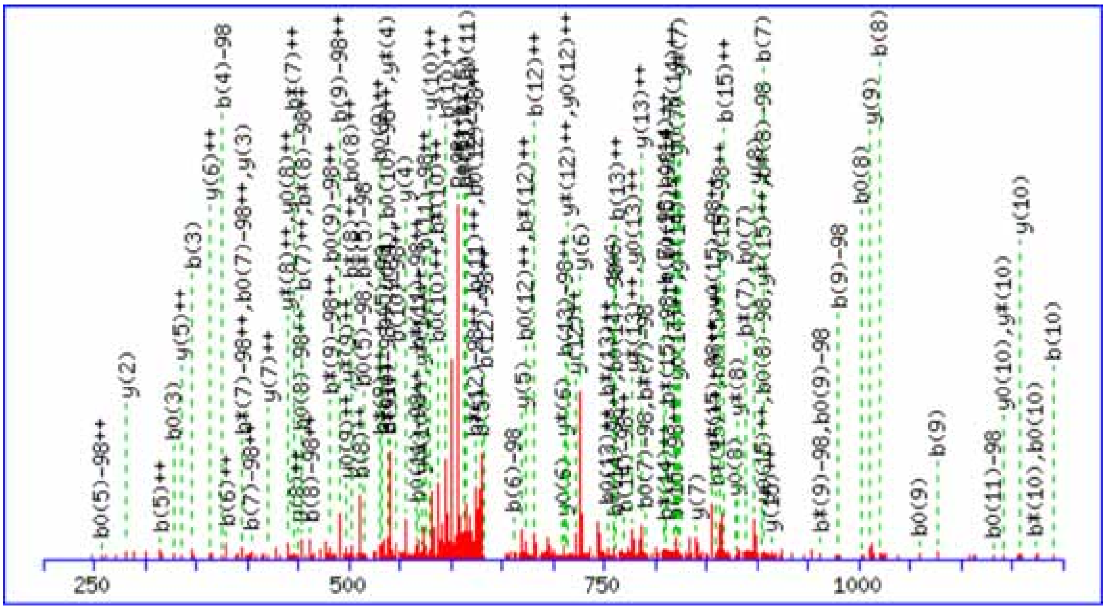
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(5)++, b(6), b(7)-98, b(7), b(8), b(8)-98, b(8)++, b(9)-98, b(9), b(9)++
Matched y ions: y(1), y(2), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)-98, y(9), y(9)-98++
Precursor origin neutral loss: +

Peptide No.342

GSSQREFNGLGDCLTK
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of GSSQREFNGLGDCLTK
Found in ADT1_MOUSE, ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4

Match to Query 3990: 1915.911951 from(639.644593,3+)
Title: Elution from: 42.066 to 42.066 scan no 3632 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1915.9135
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 32 Expect: 0.044

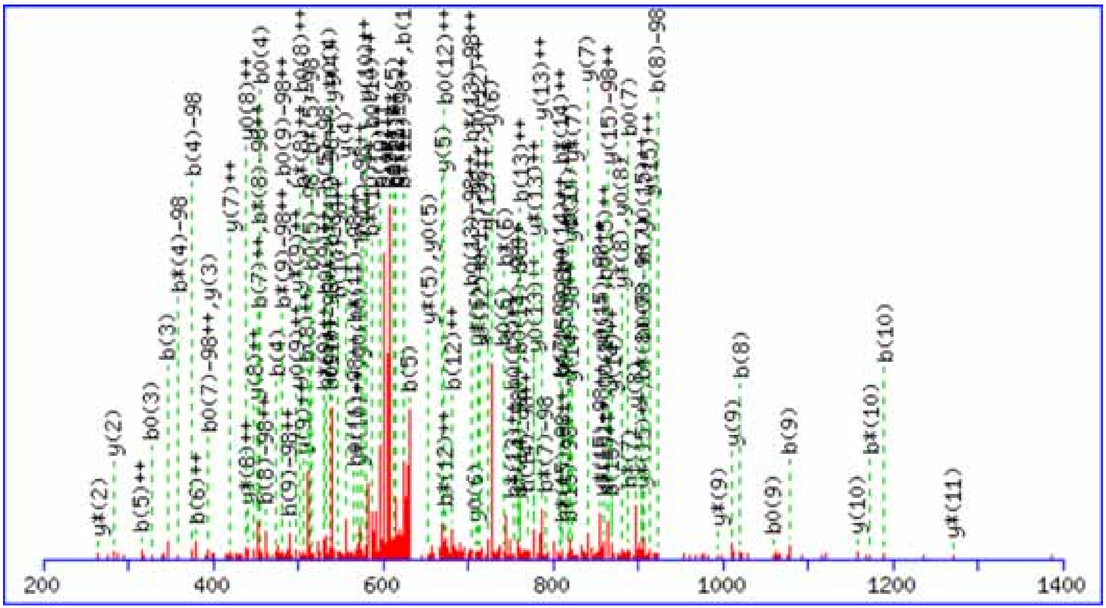
Matched b ions: b(3), b(4)-98, b(5)++, b(5)-98, b(5), b(6)++, b(6)-98, b(6), b(7)-98++, b(7)++, b(7)-98, b(7), b(8)++, b(8), b(8)-98++, b(9)++, b(9), b(9)-98++, b(9)-98, b(10), b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(10), y(10)++, y(12)++, y(13)++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.343

GSSQREFNGLGDCLTK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GSSQREFNGLGDCLTK
Found in ADT1_MOUSE, ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4

Match to Query 4334: 1915.917474 from(639.646434,3+)
Title: Elution from: 42.087 to 42.087 scan no 3723 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1915.9135
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 42 Expect: 0.004

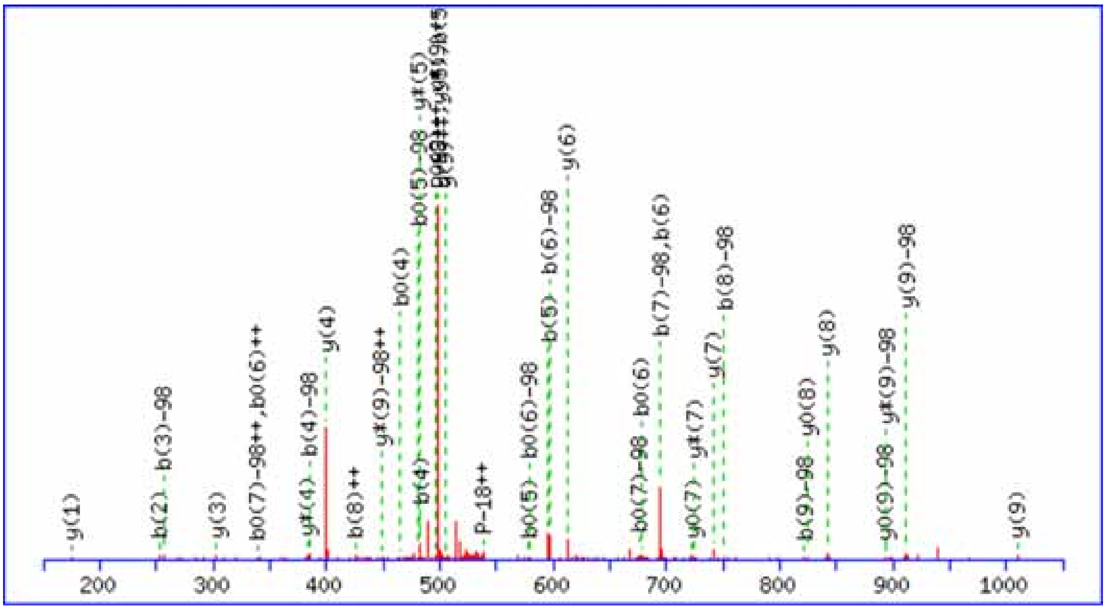
Matched b ions: b(3), b(4)-98, b(4), b(5)++, b(5), b(5)-98, b(6)++, b(6), b(7)++, b(7), b(7)-98, b(8)-98++, b(8)++, b(8), b(8)-98, b(9)++, b(9), b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(12)++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.344

GSTELVPGAR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of GSTELVPGAR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 743: 1093.517436 from(547.765994,2+)
Title: Elution from: 31.800 to 31.800 scan no 2552 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1093.5169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 1.8e-005

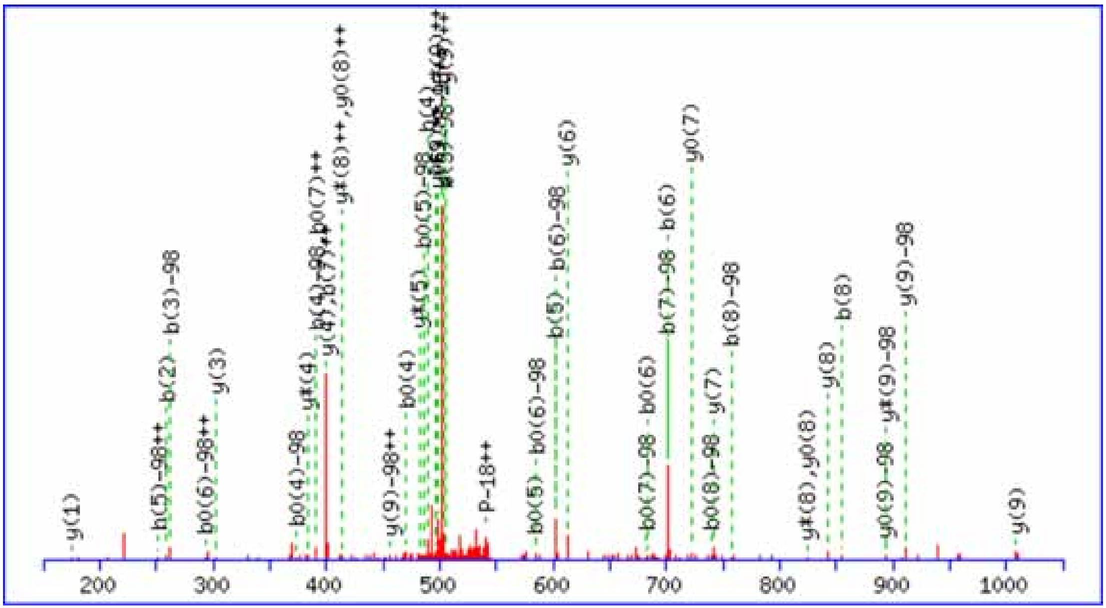
Matched b ions: b(2), b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(8)++, b(8)-98, b(9)-98
Matched y ions: y(1), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(9)++
Precursor origin neutral loss: +

Peptide No.345

GSTELVPGAR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of GSTELVPGAR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 627: 1099.548838 from(550.781695,2+)
Title: Elution from: 31.492 to 31.492 scan no 2312 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1099.5487
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.00098

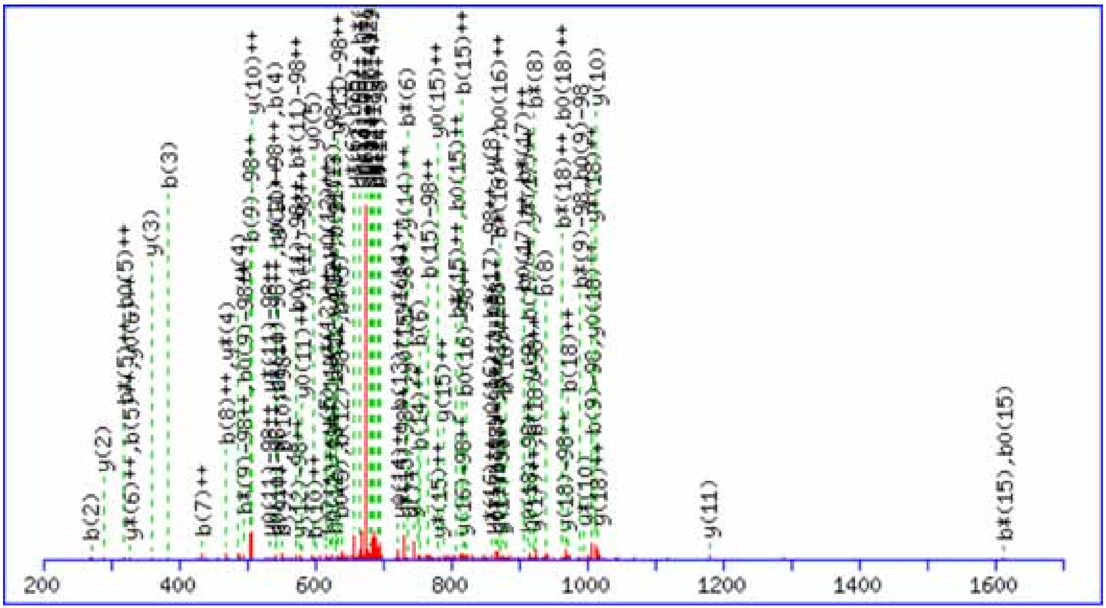
Matched b ions: b(2), b(3)-98, b(4)-98, b(4), b(5), b(5)-98++, b(5)-98, b(6), b(6)-98, b(7)++, b(7)-98, b(8), b(8)-98
Matched y ions: y(1), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.346

GWLRDPNASPGDAGEQAIR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of GWLRDPNASPGDAGEQAIR
Found in VINC_MOUSE, Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4

Match to Query 6222: 2116.972338 from(706.664722,3+)
Title: Elution from: 42.393 to 42.393 scan no 3978 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2116.9691
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 Expect: 3.3e-005

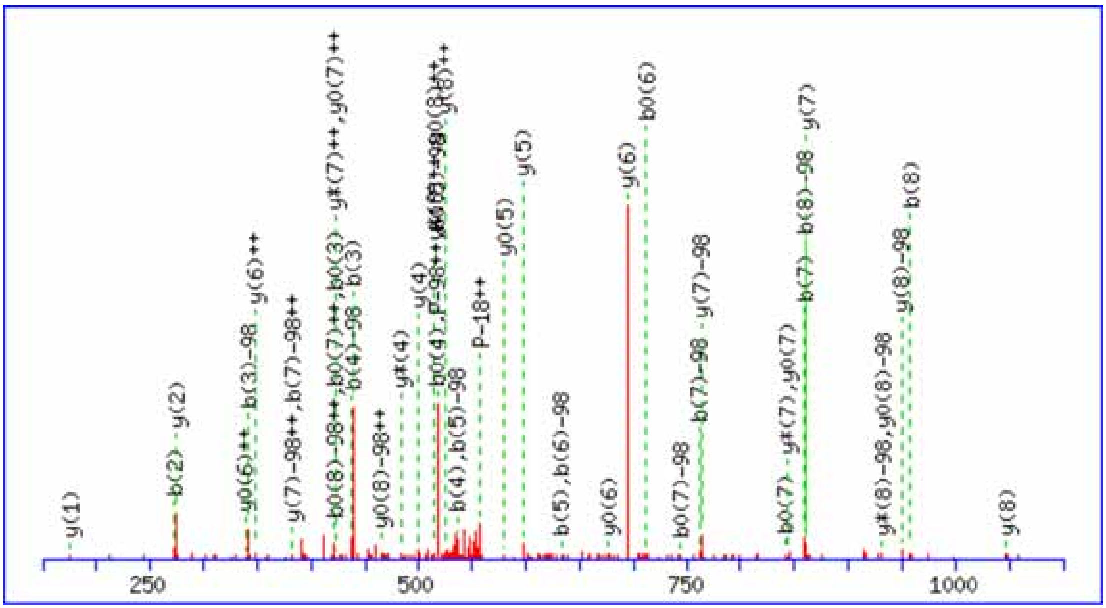
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6), b(7), b(7)++, b(8)++, b(8), b(9)-98, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.347

GWSPPPEVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GWSPPPEVR
Found in ACSA_MOUSE, Acetyl-coenzyme A synthetase, cytoplasmic OS=Mus musculus GN=Acss2 PE=1 SV=1

Match to Query 829: 1131.511600 from(566.763076,2+)
Title: Elution from: 42.005 to 42.005 scan no 3774 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1131.5114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.022

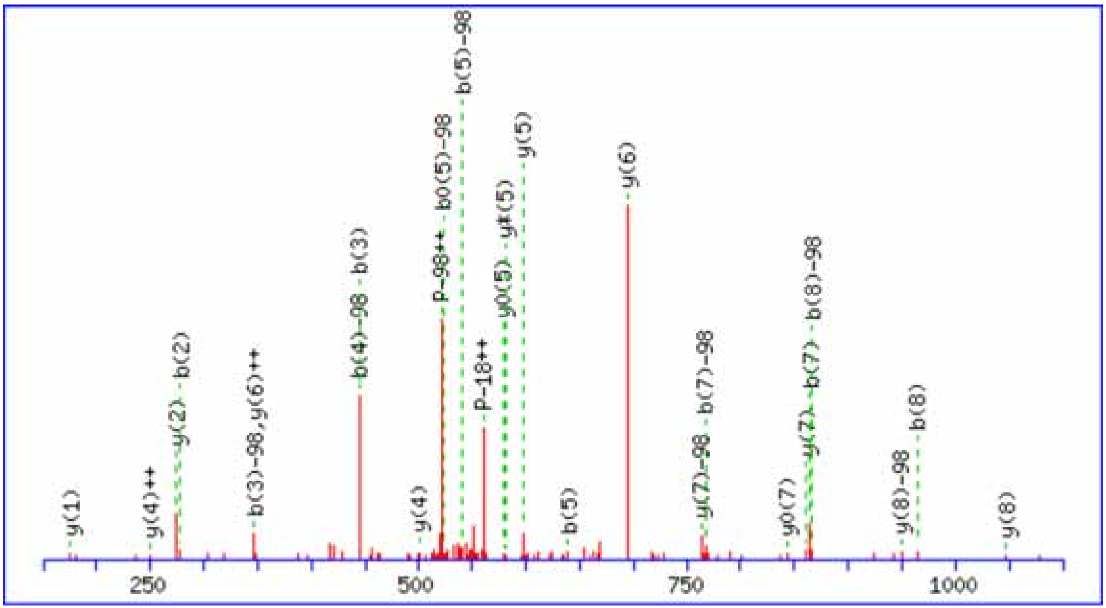
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(7), b(7)-98, b(7)-98++, b(8), b(8)-98
Matched y ions: y(1), y(2), y(4), y(5), y(6), y(6)++, y(7), y(7)-98, y(7)-98++, y(8), y(8)-98, y(8)++
Precursor origin neutral loss: +

Peptide No.348

GWSPPPEVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of GWSPPPEVR
Found in ACSA_MOUSE, Acetyl-coenzyme A synthetase, cytoplasmic OS=Mus musculus GN=Acss2 PE=1 SV=1

Match to Query 775: 1137.543390 from(569.778971,2+)
Title: Elution from: 41.905 to 41.905 scan no 3652 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1137.5432
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.0021

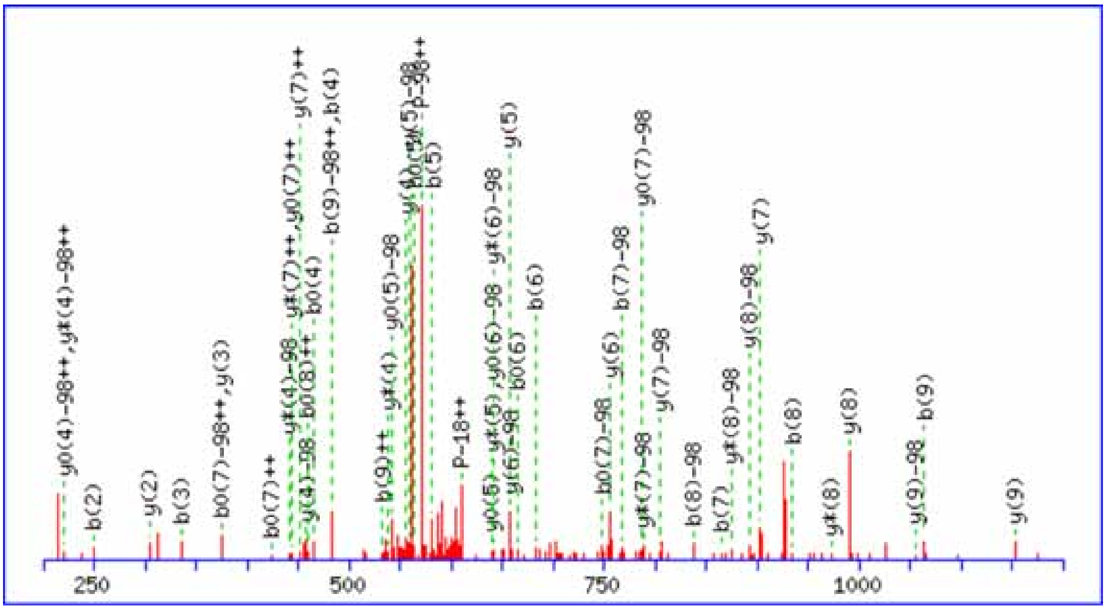
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5), b(5)-98, b(7), b(7)-98, b(8), b(8)-98
Matched y ions: y(1), y(2), y(4)++, y(4), y(5), y(6)++, y(6), y(7), y(7)-98, y(8), y(8)-98
Precursor origin neutral loss: +

Peptide No.349

GYSFVTTAER
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of GYSFVTTAER
Found in ACTS_MOUSE, Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1

Match to Query 1360: 1237.539128 from(619.776840,2+)
Title: Elution from: 39.998 to 39.998 scan no 3665 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1237.5380
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.00056

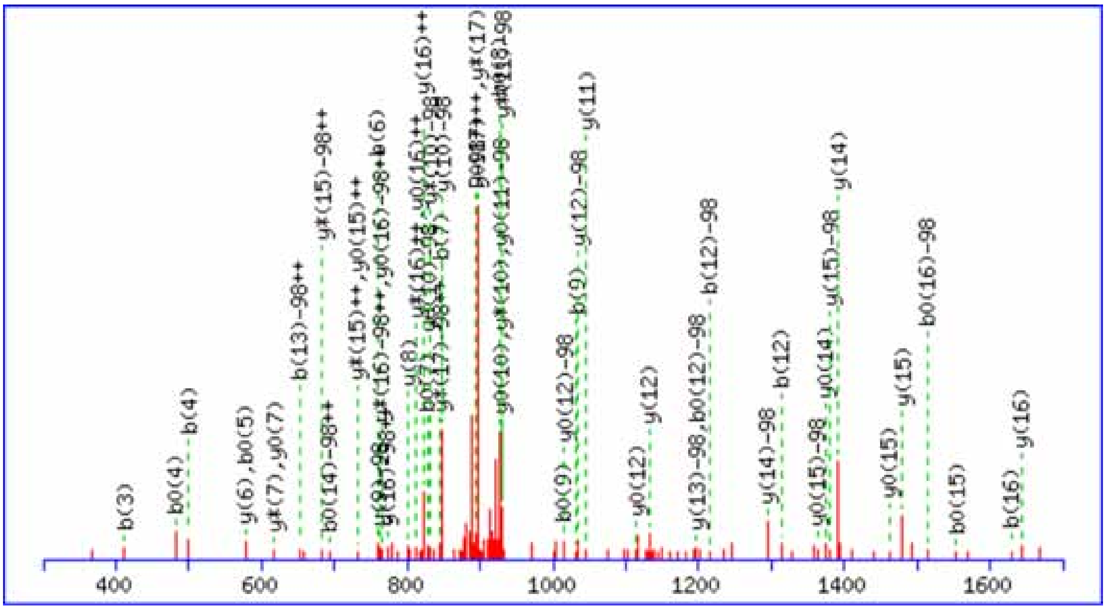
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98++, b(9), b(9)++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)++, y(7)-98, y(8), y(8)-98, y(9), y(9)-98
Precursor origin neutral loss: +

Peptide No.350

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4333: 1889.783610 from(945.899081,2+)
Title: Elution from: 39.266 to 39.266 scan no 3373 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1889.7833
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.022

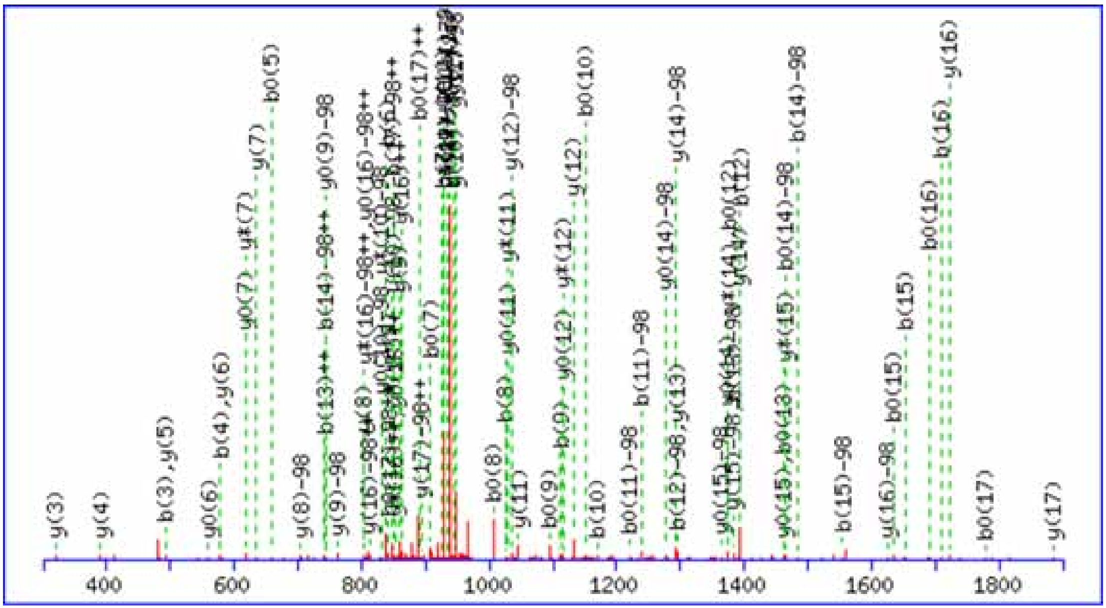
Matched b ions: b(3), b(4), b(6), b(7), b(9), b(12), b(12)-98, b(13)-98++, b(16)
Matched y ions: y(6), y(8), y(9)-98, y(10)-98, y(11), y(12)-98, y(12), y(13)-98, y(14)-98, y(14), y(15), y(15)-98, y(16), y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.351

GYYSPYSVSGSGSTAGSR
Confirmed sites: @Y:3,@S:11
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5472: 1969.750318 from(985.882435,2+)
Title: Elution from: 42.008 to 42.008 scan no 3931 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y3 : Phospho (Y)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 90 Expect: 2e-008

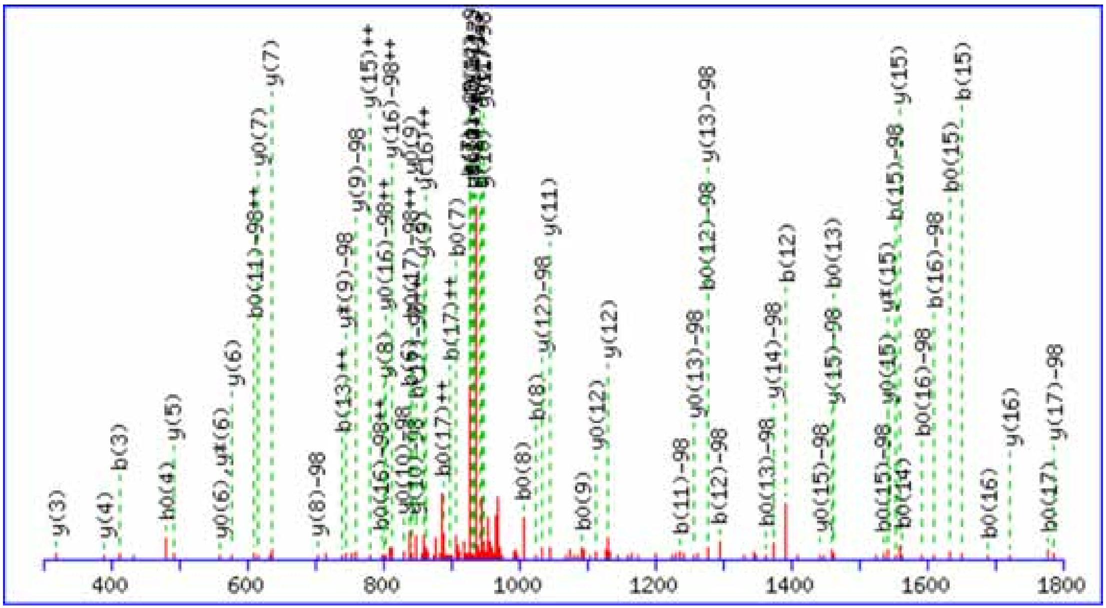
Matched b ions: b(3), b(4), b(6), b(7), b(8), b(9), b(10), b(11)-98, b(12)-98, b(12), b(13)-98, b(13)++, b(14)-98, b(14)-98++, b(15), b(15)-98, b(16), b(17)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(14)-98, y(14), y(15)-98, y(16), y(16)-98, y(16)-98++, y(16)++, y(17), y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.352

GYYSPYSVSGSGSTAGSR
Confirmed sites: @Y:6,@S:11
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 6363: 1969.750612 from(985.882582,2+)
Title: Elution from: 41.791 to 41.791 scan no 3889 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y6 : Phospho (Y)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 4.2e-006

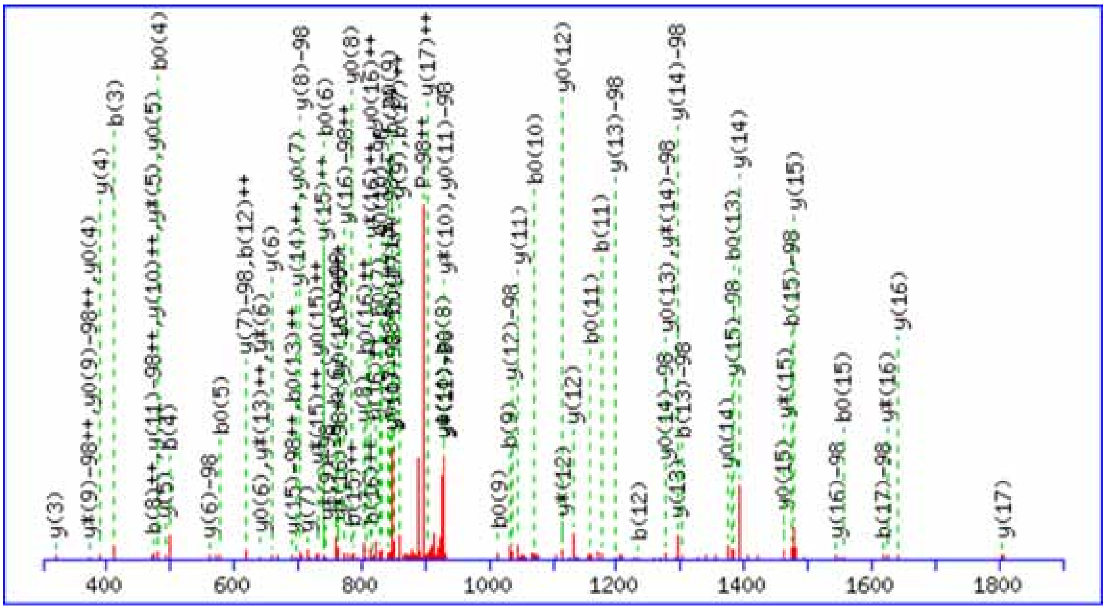
Matched b ions: b(3), b(6), b(7), b(8), b(11)-98, b(12)-98, b(12), b(13)++, b(15), b(15)-98, b(16)-98, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13)-98, y(14)-98, y(15)-98, y(15), y(15)++, y(16)-98++, y(16), y(16)++, y(17)-98, y(17)++
Precursor origin neutral loss: +

Peptide No.353

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4166: 1889.784782 from(945.899667,2+)
Title: Elution from: 39.319 to 39.319 scan no 3363 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1889.7833
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 91 Expect: 2.6e-008

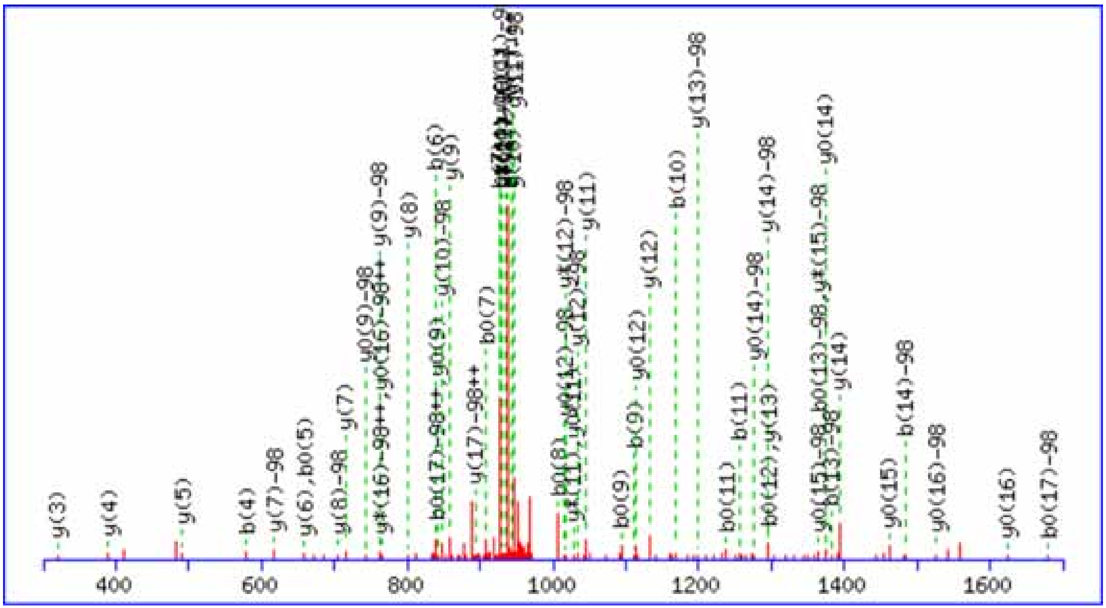
Matched b ions: b(3), b(4), b(6), b(7), b(8)++, b(9), b(11), b(12)++, b(12), b(13)-98, b(15)-98, b(15)++, b(16)++, b(17)-98, b(17)++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(7), y(8)-98, y(8), y(9)-98, y(9), y(10)-98, y(10)++, y(11), y(11)-98++, y(12), y(12)-98, y(13), y(13)-98, y(14)-98, y(14), y(14)++, y(15), y(15)-98, y(15)-98++, y(15)++, y(16), y(16)-98, y(16)++, y(16)-98++, y(17), y(17)++
Precursor origin neutral loss: +

Peptide No.354

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:13
Ambiguous sites: @Y:2orY:3orS:4

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4679: 1969.749864 from(985.882208,2+)
Title: Elution from: 41.959 to 41.959 scan no 3706 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y2 : Phospho (Y)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 **Expect:** 2e-006

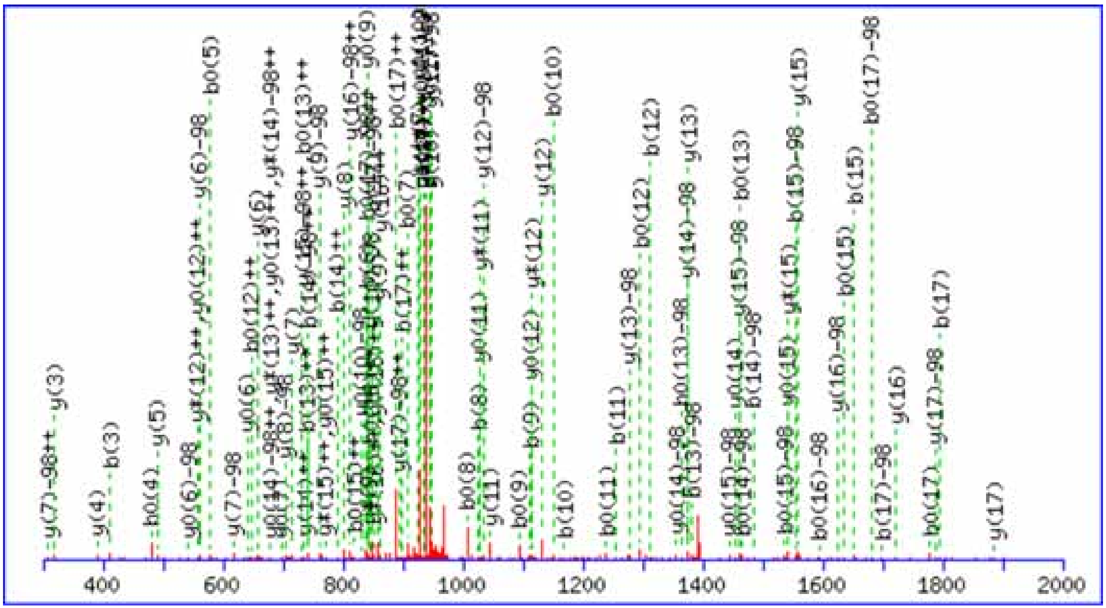
Matched b ions: b(4), b(6), b(7), b(9), b(10), b(11), b(13)-98, b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8)-98, y(8), y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(14)-98, y(14), y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.355

GYYSPYSVSGSGSTAGSR
Confirmed sites: @Y:6,@S:13
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4299: 1969.751248 from(985.882900,2+)
Title: Elution from: 41.819 to 41.819 scan no 3598 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y6 : Phospho (Y)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 90 Expect: 1.5e-008

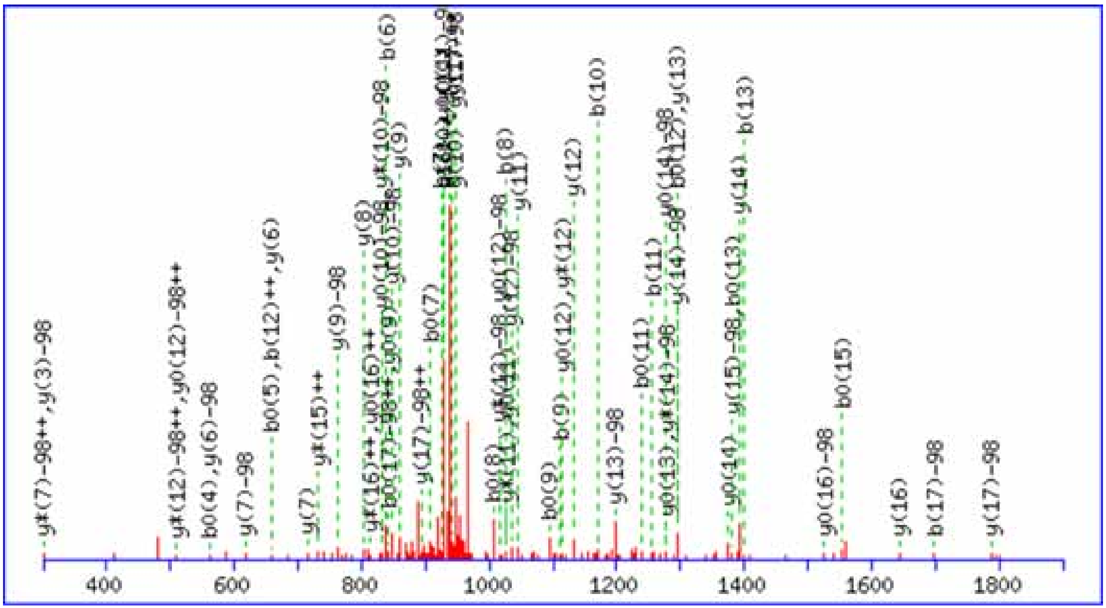
Matched b ions: b(3), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13)++, b(13)-98, b(14)-98, b(14)-98++, b(14)++, b(15), b(15)-98, b(17), b(17)-98, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(7)-98++, y(7), y(8), y(8)-98, y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(14)-98, y(14)++, y(15)-98, y(15), y(15)-98++, y(16), y(16)-98, y(16)-98++, y(16)++, y(17), y(17)-98, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.356

GYYSPYSVSGSGSTAGSR
Confirmed sites: @Y:2,@S:17
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4298: 1969.750974 from(985.882763,2+)
Title: Elution from: 42.166 to 42.166 scan no 3644 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y2 : Phospho (Y)
S17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 Expect: 0.00084

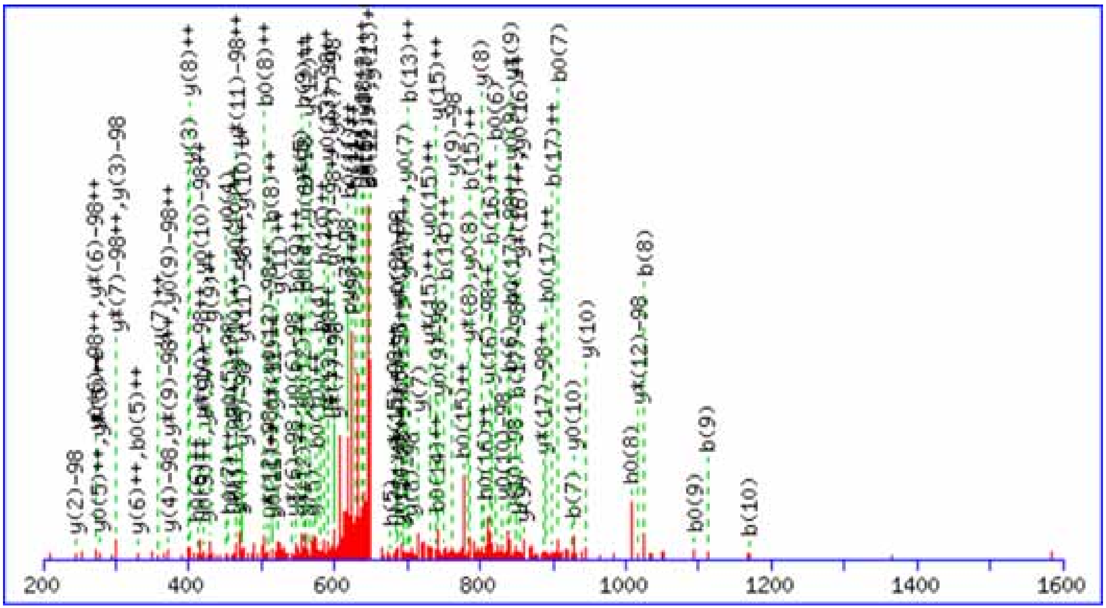
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(11), b(12)++, b(13), b(17)-98
Matched y ions: y(3)-98, y(6)-98, y(6), y(7)-98, y(7), y(8), y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(13)-98, y(13), y(14)-98, y(14), y(15)-98, y(16), y(17)-98, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.357

GYYSPYSVSGSGSTAGSR
Confirmed sites: @Y:3,@S:17
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4297: 1969.750608 from(657.590812,3+)
Title: Elution from: 42.110 to 42.110 scan no 3636 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y3 : Phospho (Y)
S17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.046

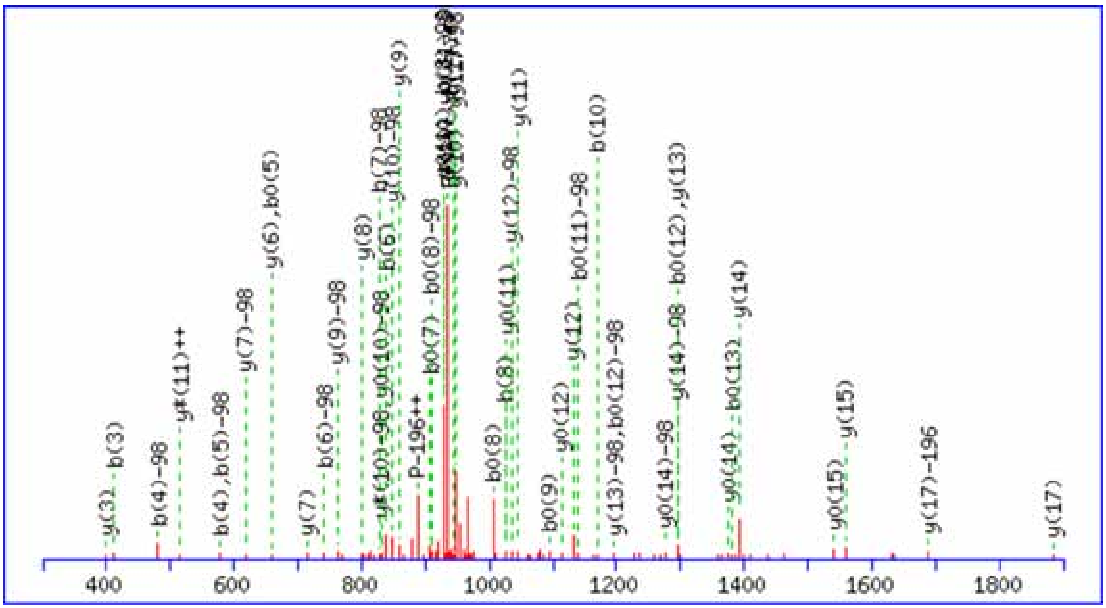
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(8)++, b(9), b(9)++, b(10), b(10)++, b(11)++, b(13)++, b(14)++, b(15)++, b(16)++, b(17)-98++, b(17)++
Matched y ions: y(2)-98, y(3)-98, y(3), y(4), y(4)-98, y(5), y(5)-98, y(6)-98, y(6)++, y(7), y(7)++, y(7)-98, y(8)++, y(8)-98, y(8), y(9), y(9)++, y(9)-98, y(10), y(10)++, y(10)-98, y(11)-98++, y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.358

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:4,@S:17
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4845: 1969.747976 from(985.881264,2+)
Title: Elution from: 41.979 to 41.979 scan no 3736 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 **Expect:** 2.1e-005

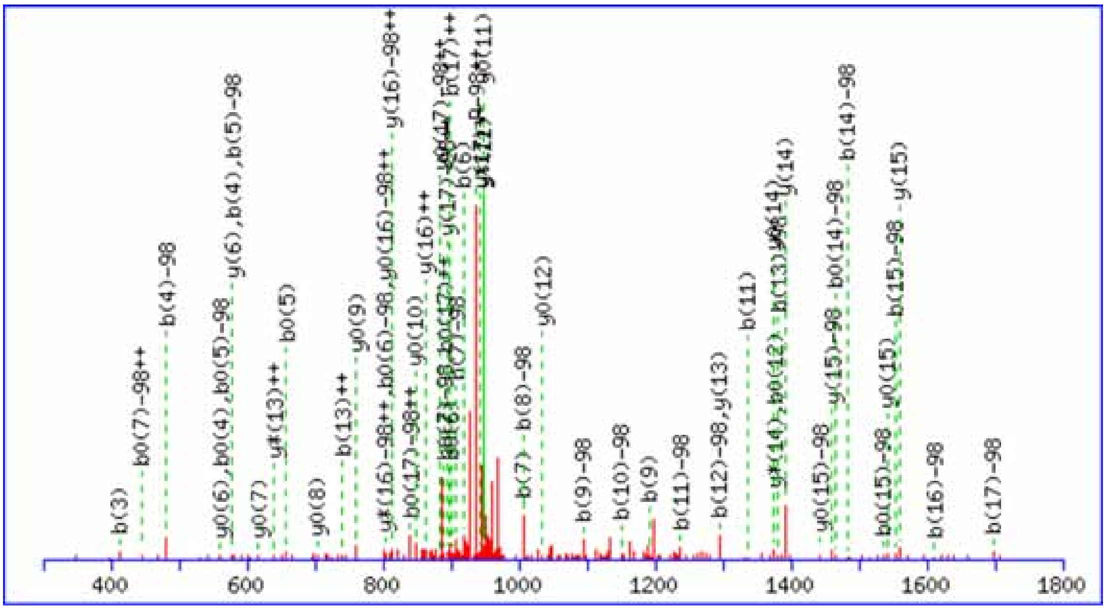
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6)-98, b(6), b(7)-98, b(8)-98, b(8), b(10)
Matched y ions: y(3), y(6), y(7)-98, y(7), y(8), y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(13)-98, y(13), y(14)-98, y(14), y(15)-98, y(15), y(16)-98++, y(17)-196, y(17), y(17)++
Precursor origin neutral loss: +

Peptide No.359

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:4,@Y:6
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 6361: 1969.750222 from(985.882387,2+)
Title: Elution from: 42.172 to 42.172 scan no 3942 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y6 : Phospho (Y)
Ions Score: 45 Expect: 0.00061

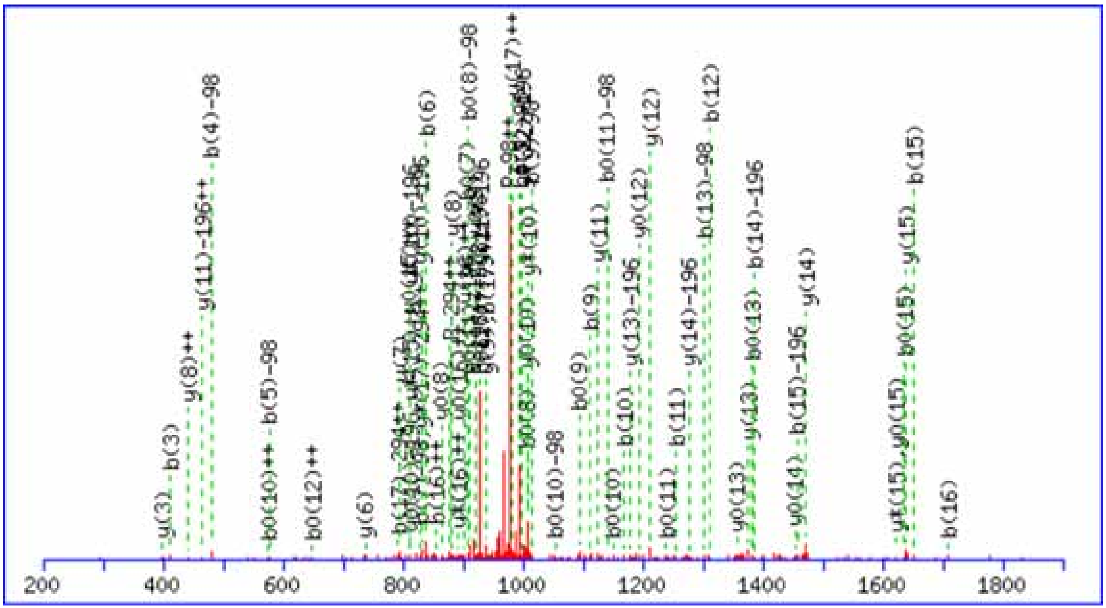
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6), b(7)-98, b(7), b(8)-98, b(9)-98, b(9), b(10)-98, b(11)-98, b(11), b(12)-98, b(13)-98, b(13)++, b(14)-98, b(15)-98, b(16)-98, b(17)-98, b(17)++
Matched y ions: y(6), y(13), y(14), y(15)-98, y(15), y(16)-98++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.360

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:4,@T:14,@S:17
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4599: 2049.718464 from(1025.866508,2+)
Title: Elution from: 46.258 to 46.258 scan no 4149 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2049.7159
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.046

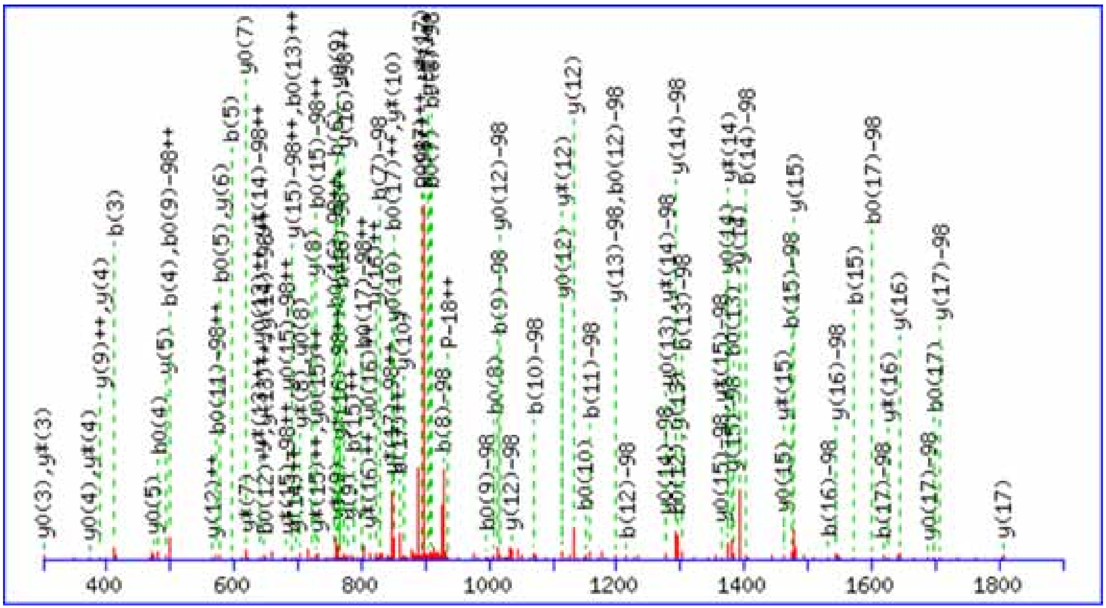
Matched b ions: b(3), b(4)-98, b(5)-98, b(6), b(7)-98, b(8)-98, b(9), b(9)-98, b(10), b(11), b(12), b(13)-98, b(14)-196, b(15), b(15)-98, b(15)-196, b(16), b(16)++, b(17)-98, b(17)-294++, b(17)-196++, b(17)-98++, b(17)++
Matched y ions: y(3), y(6)-98, y(6), y(7), y(7)-98, y(8)++, y(8)-98, y(8), y(9)-98, y(9), y(10)-196, y(10)-98, y(11), y(11)-196++, y(11)-196, y(12)-98, y(12), y(13), y(13)-196, y(13)-98, y(14), y(14)-98, y(14)-196, y(15)-98, y(15), y(15)-98++, y(16)-98++, y(16)-196++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.361

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4995: 1889.784820 from(945.899686,2+)
Title: Elution from: 39.411 to 39.411 scan no 3587 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1889.7833
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 86 Expect: 8.3e-008

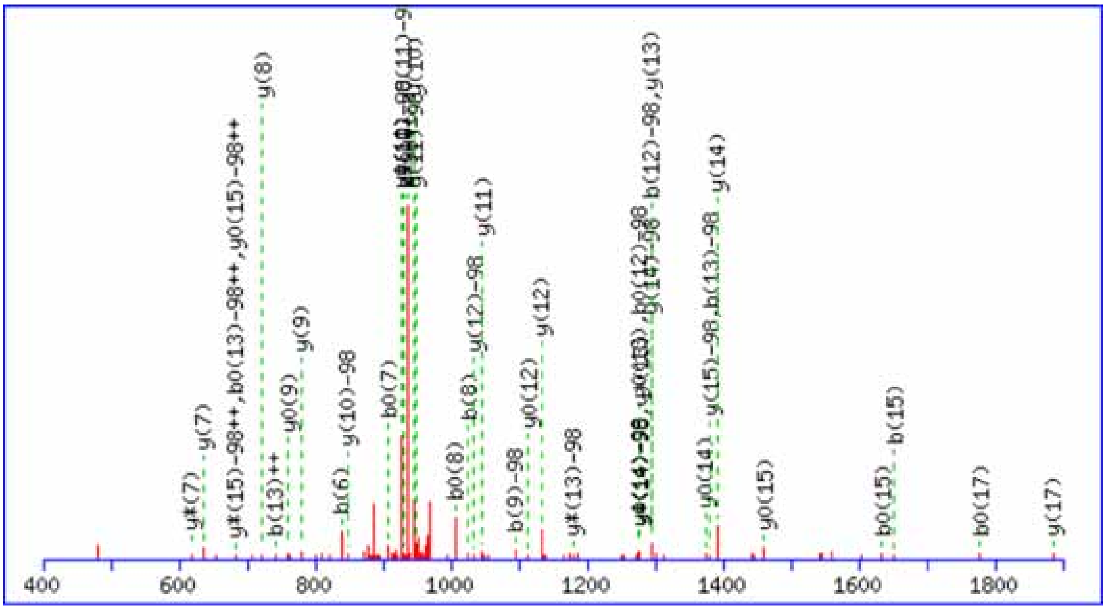
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(11)-98, b(12)-98, b(13)-98, b(14)-98, b(15)-98, b(15), b(15)++, b(16)-98, b(16)-98++, b(17)-98, b(17)++
Matched y ions: y(4), y(5), y(6), y(8), y(9)++, y(9), y(10), y(12), y(12)++, y(12)-98, y(13), y(13)++, y(13)-98, y(14)-98, y(14), y(14)-98++, y(14)++, y(15), y(15)-98, y(15)-98++, y(16)-98, y(16), y(16)-98++, y(16)++, y(17)-98, y(17), y(17)++
Precursor origin neutral loss: +

Peptide No.362

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:9
Ambiguous sites: @Y:2orY:3

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5055: 1969.750058 from(985.882305,2+)
Title: Elution from: 41.127 to 41.127 scan no 3656 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y3 : Phospho (Y)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.0034

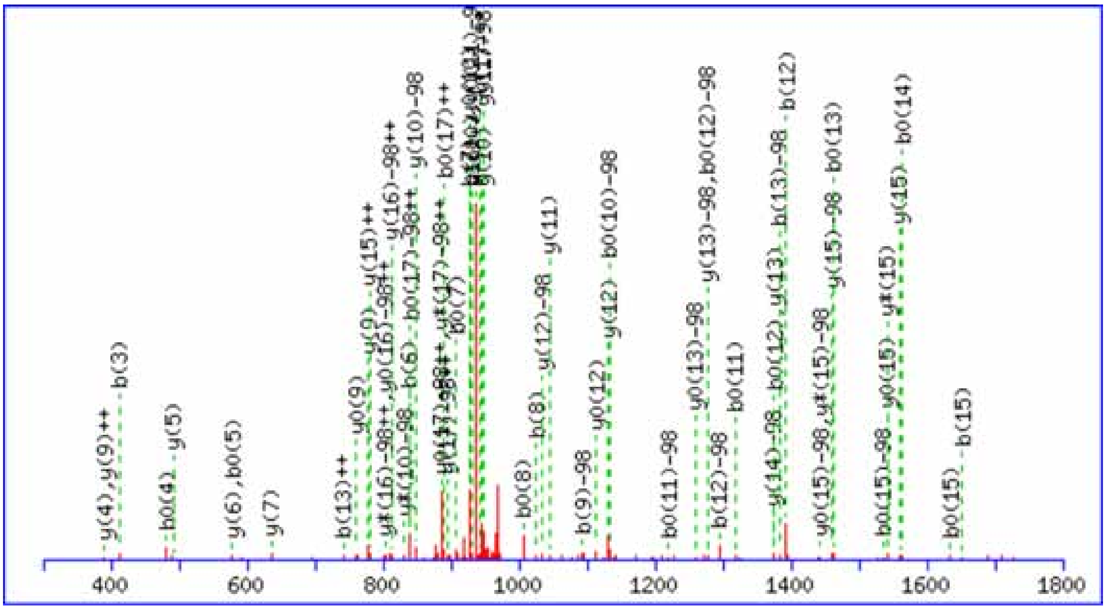
Matched b ions: b(6), b(8), b(9)-98, b(12)-98, b(13)++, b(13)-98, b(15)
Matched y ions: y(7), y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(14)-98, y(14), y(15)-98, y(17)
Precursor origin neutral loss: +

Peptide No.363

GYYSPYSVSGSGSTAGSR
Confirmed sites: @Y:6,@S:9
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4429: 1969.749156 from(985.881854,2+)
Title: Elution from: 41.032 to 41.032 scan no 3544 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y6 : Phospho (Y)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 6.3e-005

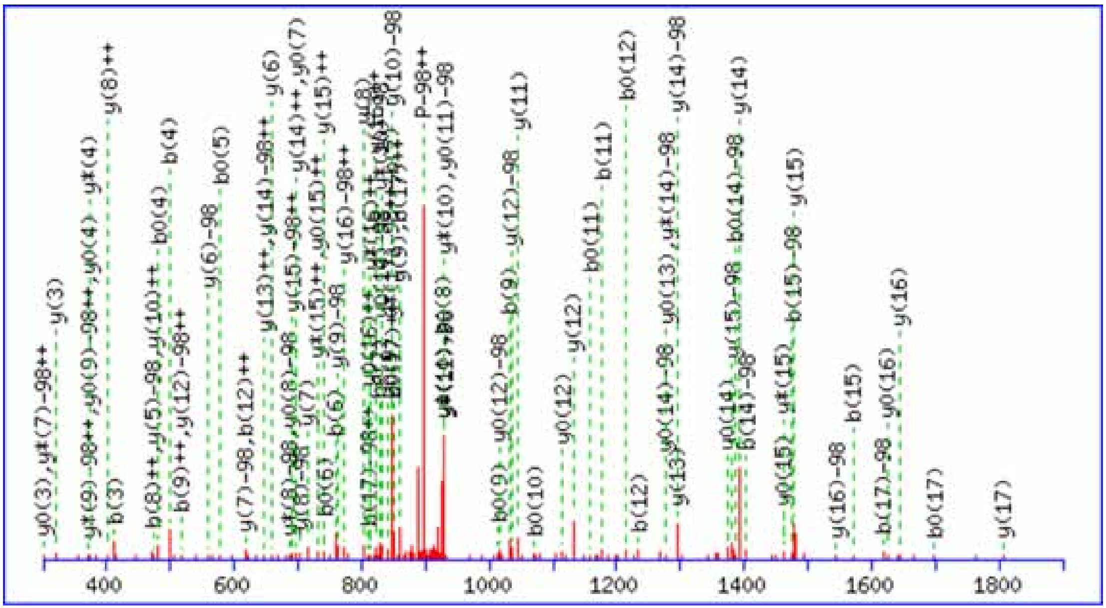
Matched b ions: b(3), b(6), b(7), b(8), b(9)-98, b(12)-98, b(12), b(13)++, b(13)-98, b(15)
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(9)++, y(10)-98, y(10), y(11)-98, y(11), y(12), y(12)-98, y(13)-98, y(13), y(14)-98, y(15)++, y(15)-98, y(15), y(16)-98++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.364

GYYSPYSVSGSGSTAGSR
Confirmed sites: @T:14
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 3827: 1889.784906 from(945.899729,2+)
Title: Elution from: 39.203 to 39.203 scan no 3254 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1889.7833
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 3.1e-005

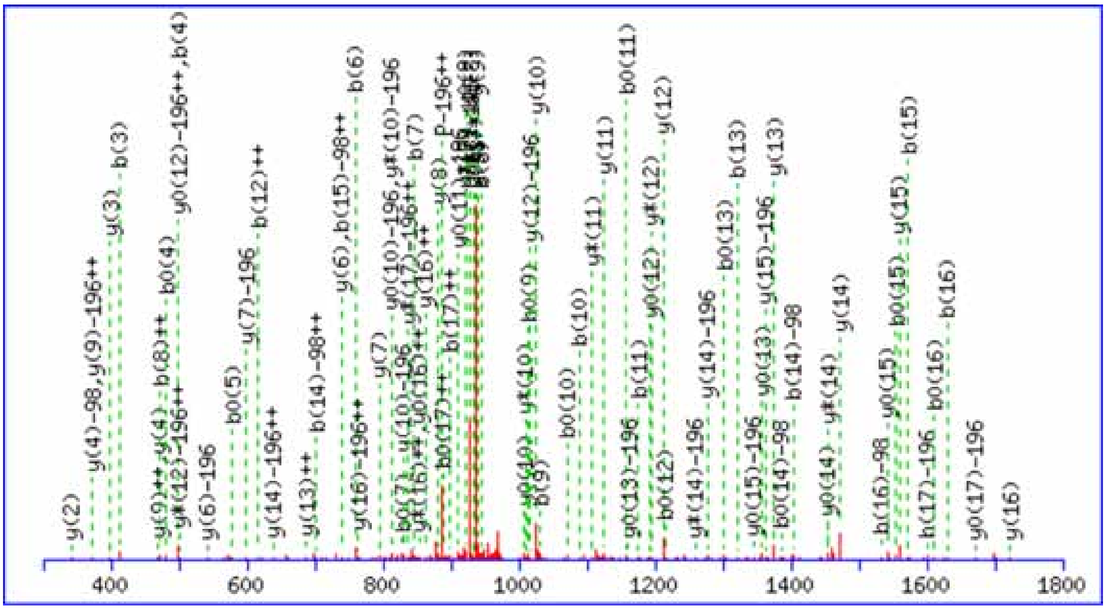
Matched b ions: b(3), b(4), b(6), b(7), b(8)++, b(9), b(9)++, b(11), b(12)++, b(12), b(14)-98, b(15), b(15)-98, b(17)-98, b(17)++, b(17)-98++
Matched y ions: y(3), y(5)-98, y(6)-98, y(6), y(7)-98, y(7), y(8)-98, y(8)++, y(8), y(9)-98, y(9), y(10)-98, y(10)++, y(11), y(12), y(12)-98, y(12)-98++, y(13), y(13)++, y(14), y(14)++, y(14)-98, y(14)-98++, y(15), y(15)-98++, y(15)-98, y(15)++, y(16)-98, y(16), y(16)-98++, y(16)++, y(17)
Precursor origin neutral loss: +

Peptide No.365

GYYSPYSVSGSGSTAGSR
Confirmed sites: @T:14,@S:17
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4681: 1969.751910 from(985.883231,2+)
Title: Elution from: 43.632 to 43.632 scan no 3915 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 6.3e-006

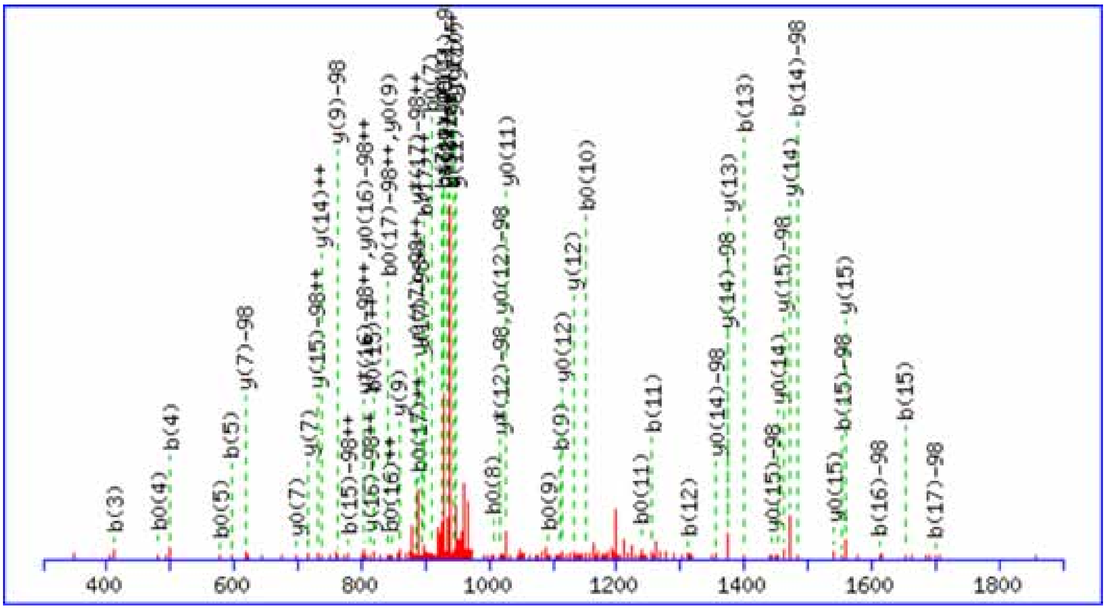
Matched b ions: b(3), b(4), b(6), b(7), b(8)++, b(8), b(9), b(10), b(11), b(12)++, b(13), b(14)-98, b(14)-98++, b(15)-98++, b(15), b(16), b(16)-98, b(17)-98, b(17)-196, b(17)-98++, b(17)++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(6), y(6)-196, y(6)-98, y(7)-98, y(7), y(7)-196, y(8)-98, y(8), y(9)-196++, y(9)-98, y(9)++, y(9), y(10), y(10)-98, y(10)-196, y(11), y(11)-98, y(11)-196, y(12)-98, y(12), y(12)-196, y(13)-98, y(13), y(13)-98++, y(13)++, y(14)-196, y(14)-98, y(14), y(14)-196++, y(14)-98++, y(15)-98++, y(15), y(15)-98, y(15)-196, y(16)-98++, y(16), y(16)-196++, y(16)++, y(16)-98
Precursor origin neutral loss: +

Peptide No.366

GYYSPYSVSGSGSTAGSR
Confirmed sites: @Y:6,@T:14
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5471: 1969.749654 from(985.882103,2+)
Title: Elution from: 43.224 to 43.224 scan no 4087 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1969.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y6 : Phospho (Y)
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.002

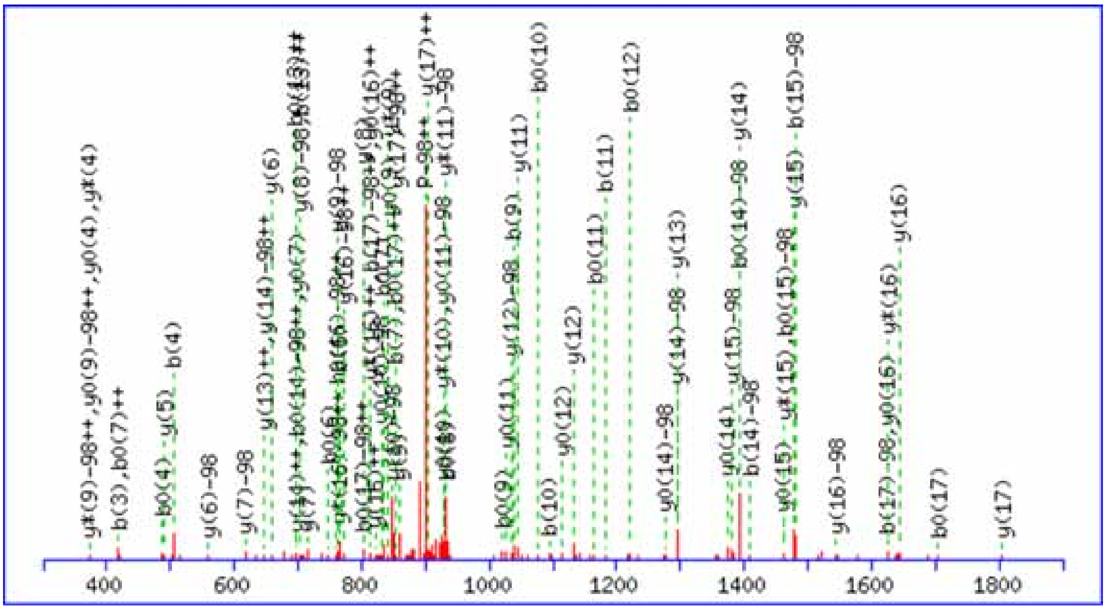
Matched b ions: b(3), b(4), b(5), b(7), b(9), b(11), b(12), b(13), b(14)-98, b(15), b(15)-98++, b(15)-98, b(16)-98, b(17)-98, b(17)++
Matched y ions: y(7)-98, y(7), y(9)-98, y(9), y(10), y(11)-98, y(12), y(13), y(14)-98, y(14), y(14)++, y(15)-98++, y(15), y(15)-98, y(16)-98++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.367

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4025: 1895.815552 from(948.915052,2+)
Title: Elution from: 39.306 to 39.306 scan no 3327 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1895.8151
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 Expect: 4.8e-005

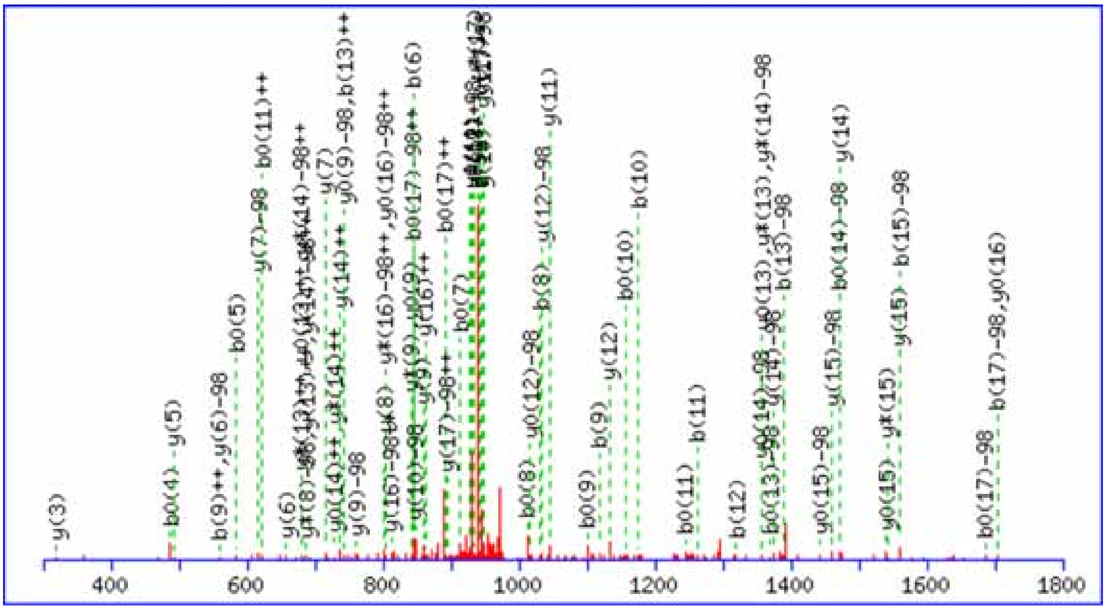
Matched b ions: b(3), b(4), b(6), b(7), b(9), b(10), b(11), b(13)++, b(14)-98, b(15)-98, b(17)-98, b(17)-98++
Matched y ions: y(5), y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-98, y(11), y(12), y(12)-98, y(13)++, y(13), y(14)-98, y(14), y(14)-98++, y(14)++, y(15), y(15)-98, y(16), y(16)-98, y(16)-98++, y(16)++, y(17), y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.368

GYYSPYSVSGSGSTAGSR
Confirmed sites: @Y:6,@S:13
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 6392: 1975.781750 from(988.898151,2+)
Title: Elution from: 42.035 to 42.035 scan no 3923 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1975.7814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y6 : Phospho (Y)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.002

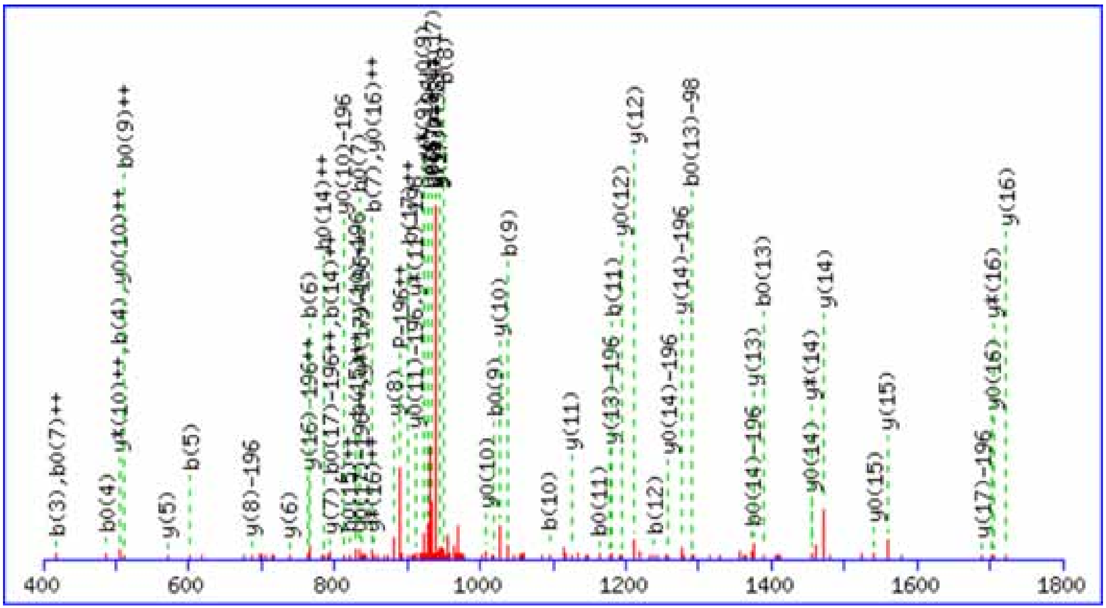
Matched b ions: b(6), b(8), b(9)++, b(9), b(10), b(11), b(12), b(13)-98, b(13)++, b(15)-98, b(17)-98
Matched y ions: y(3), y(5), y(6)-98, y(6), y(7)-98, y(7), y(8), y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(13)++, y(14), y(14)-98++, y(14)++, y(14)-98, y(15), y(15)-98, y(16)-98++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.369

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:13,@T:14
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4879: 1975.782452 from(988.898502,2+)
Title: Elution from: 43.757 to 43.757 scan no 3945 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1975.7814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 Expect: 1.2e-005

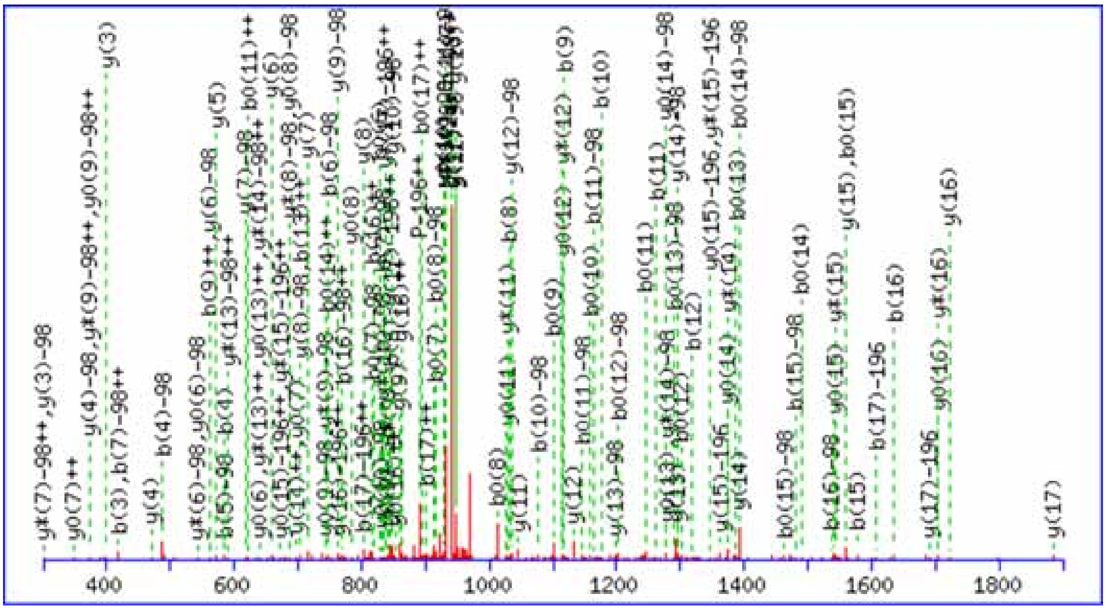
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(14)++, b(15)++, b(15)-98, b(17)-98++, b(17)-98, b(17)++
Matched y ions: y(5), y(6), y(7)-98, y(7), y(8), y(8)-196, y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(10)-196, y(11)-98, y(11), y(11)-196, y(12), y(12)-98, y(13), y(13)-196, y(14)-196, y(14)-98, y(14), y(15), y(15)-98, y(16), y(16)-196++, y(16)-98++, y(17)-196, y(17)++
Precursor origin neutral loss: +

Peptide No.370

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:4,@S:17
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4891: 1975.783878 from(988.899215,2+)
Title: Elution from: 42.065 to 42.065 scan no 3755 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1975.7814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 87 Expect: 4.1e-008

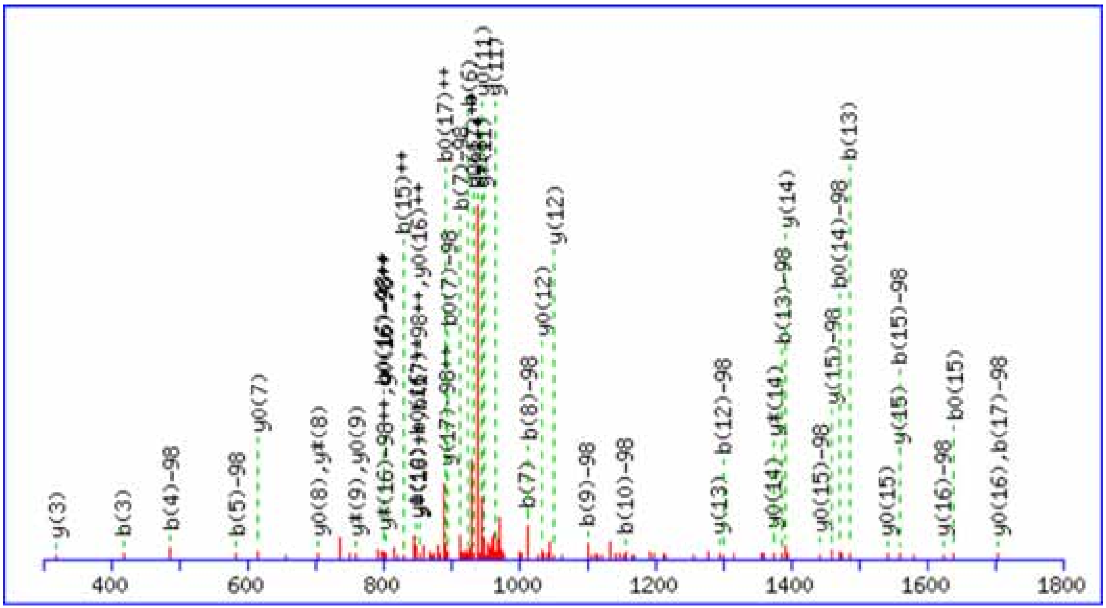
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6), b(6)-98, b(7)-98++, b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)++, b(10)-98, b(10), b(11), b(11)-98, b(12), b(13)++, b(15), b(15)-98, b(16), b(16)-98++, b(16)++, b(16)-98, b(17)-98, b(17)-196, b(17)-196++, b(17)-98++, b(17)++
Matched y ions: y(3)-98, y(3), y(4)-98, y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(14)-98, y(14), y(14)++, y(15)-98, y(15), y(15)-196, y(16), y(16)-196++, y(16)-98++, y(16)++, y(17), y(17)-196, y(17)-196++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.371

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:4,@Y:6
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4456: 1975.780580 from(988.897566,2+)
Title: Elution from: 41.936 to 41.936 scan no 3656 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1975.7814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y6 : Phospho (Y)
Ions Score: 49 **Expect:** 0.00031

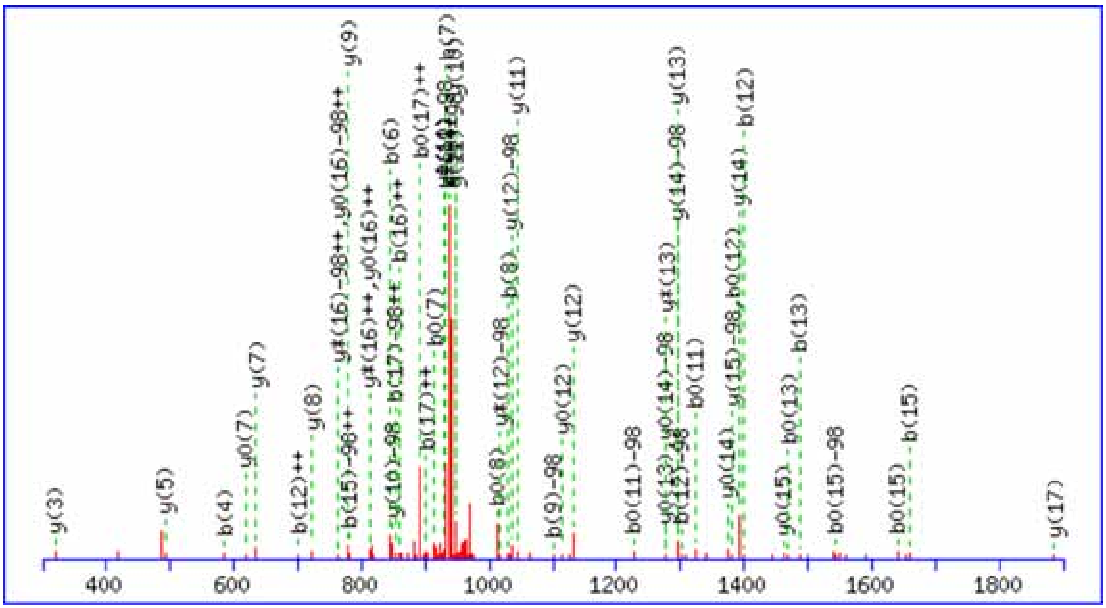
Matched b ions: b(3), b(4)-98, b(5)-98, b(6), b(7)-98, b(7), b(8)-98, b(9)-98, b(10)-98, b(12)-98, b(13)-98, b(13), b(15)-98, b(15)++, b(17)-98, b(17)-98++
Matched y ions: y(3), y(11), y(12), y(13), y(14), y(15)-98, y(15), y(16)-98, y(17)-98++
Precursor origin neutral loss: +

Peptide No.372

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:9
Ambiguous sites: @Y:2orY:3

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4702: 1975.783356 from(988.898954,2+)
Title: Elution from: 41.046 to 41.046 scan no 3590 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1975.7814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y2 : Phospho (Y)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 0.00018

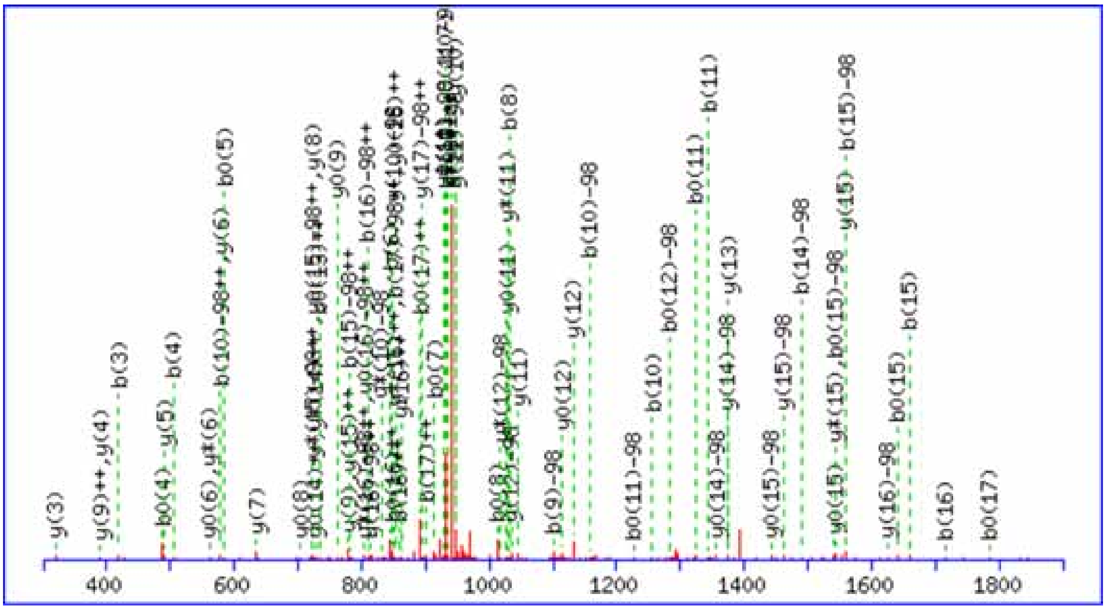
Matched b ions: b(4), b(6), b(7), b(8), b(9)-98, b(12)++, b(12), b(12)-98, b(13), b(15), b(15)-98++, b(16)++, b(17)++, b(17)-98++
Matched y ions: y(3), y(5), y(7), y(8), y(9), y(10)-98, y(10), y(11), y(11)-98, y(12)-98, y(12), y(13), y(14)-98, y(14), y(15)-98, y(17)
Precursor origin neutral loss: +

Peptide No.373

GYYSPYSVSGSGSTAGSR
Confirmed sites: @Y:6,@S:9
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 6391: 1975.781122 from(988.897837,2+)
Title: Elution from: 41.053 to 41.053 scan no 3787 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1975.7814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y6 : Phospho (Y)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 Expect: 3.8e-006

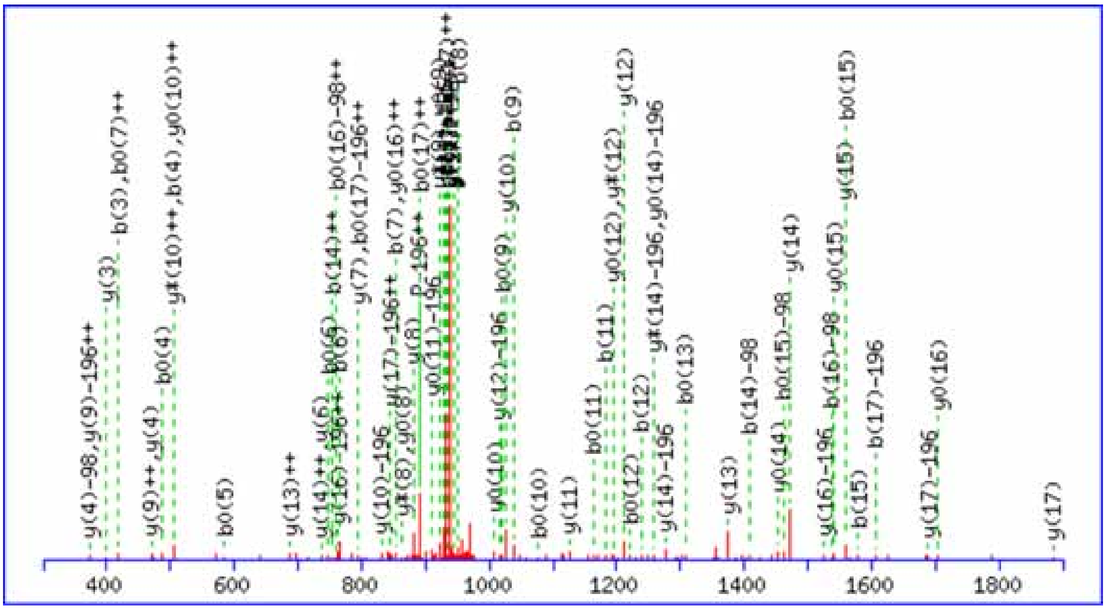
Matched b ions: b(3), b(4), b(6), b(7), b(8), b(9)-98, b(10)-98++, b(10), b(10)-98, b(11), b(14)-98, b(15), b(15)-98, b(15)-98++, b(16), b(16)-98++, b(16)++, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(14)-98, y(15)++, y(15)-98, y(15), y(16)-98++, y(16)-98, y(16)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.374

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:17
Ambiguous sites: @S:13orT:14

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4318: 1975.781818 from(988.898185,2+)
Title: Elution from: 43.618 to 43.618 scan no 3824 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1975.7814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 **Expect:** 3.3e-006

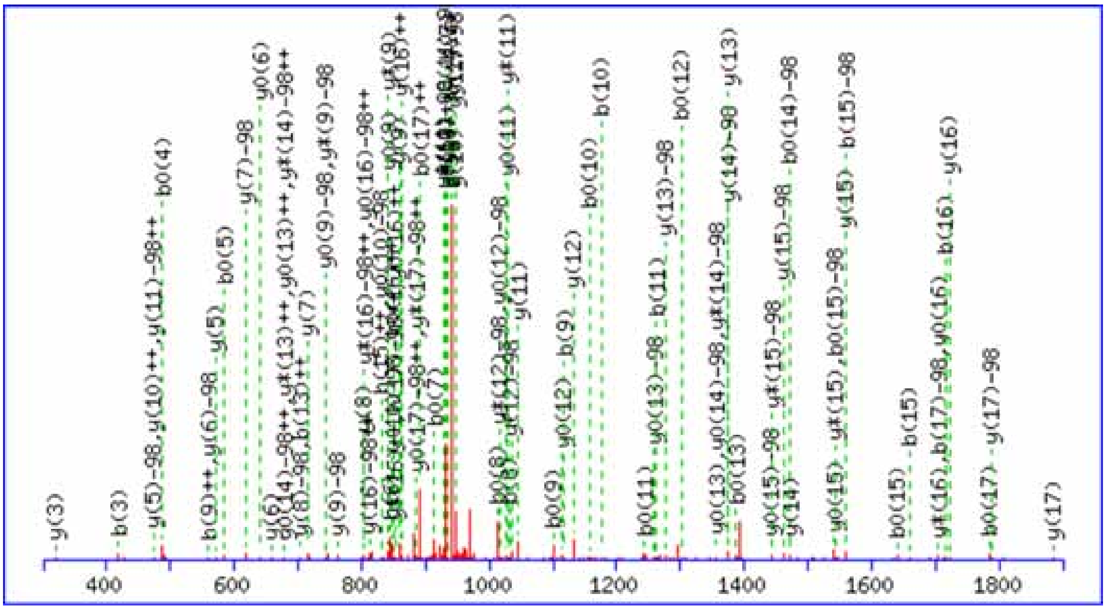
Matched b ions: b(3), b(4), b(6), b(7), b(8), b(9), b(11), b(12), b(14)-98, b(14)++, b(15), b(16)-98, b(17)-98, b(17)-98++, b(17)-196
Matched y ions: y(3), y(4), y(4)-98, y(6)-98, y(6), y(7)-98, y(7), y(8)-98, y(8), y(9)-98, y(9), y(9)++, y(9)-196++, y(10), y(10)-196, y(10)-98, y(11), y(11)-98, y(11)-196, y(12), y(12)-98, y(12)-196, y(13)++, y(13), y(14)-98, y(14), y(14)-196, y(14)-98++, y(14)++, y(15)-98, y(15), y(16)-98, y(16)-196++, y(16)-196, y(17)-98, y(17), y(17)-196, y(17)-196++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.375

GYYSPYSVSGSGSTAGSR
Confirmed sites: @Y:6,@T:14
Ambiguous sites:

MS/MS Fragmentation of GYYSPYSVSGSGSTAGSR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4317: 1975.781714 from(988.898133,2+)
Title: Elution from: 41.879 to 41.879 scan no 3606 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1975.7814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y6 : Phospho (Y)
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 86 **Expect:** 6.8e-008

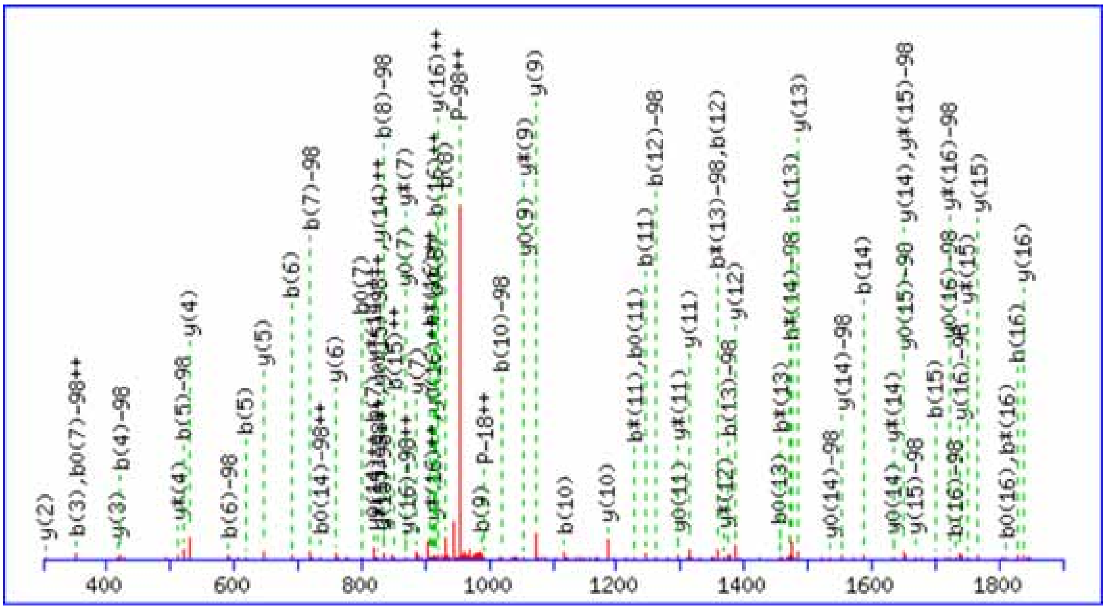
Matched b ions: b(3), b(6), b(7), b(8), b(9)++, b(9), b(10), b(11), b(13)++, b(15)-98, b(15), b(15)++, b(16), b(17)-98, b(17)-98++
Matched y ions: y(3), y(5), y(5)-98, y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)++, y(10)-98, y(11), y(11)-98++, y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(14)-98, y(14), y(15)-98, y(15), y(16)-98++, y(16), y(16)++, y(17), y(17)-98, y(17)++
Precursor origin neutral loss: +

Peptide No.376

HADSVAELGEQIDNLQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of HADSVAELGEQIDNLQR
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 4544: 2001.917954 from(1001.966253,2+)
Title: Elution from: 49.667 to 49.667 scan no 4509 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2001.9157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 94 Expect: 2.4e-008

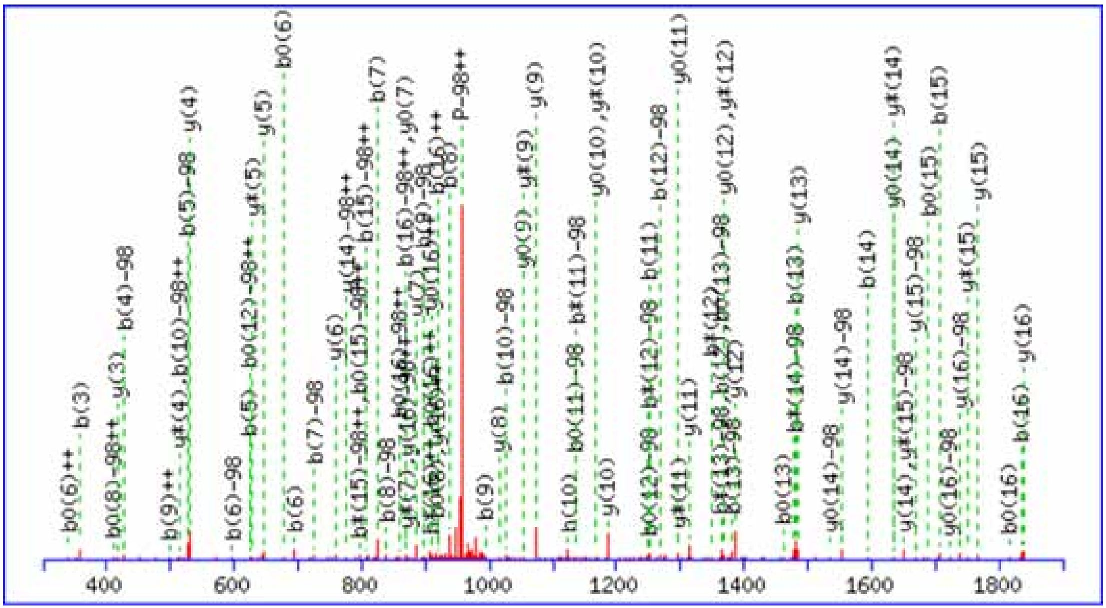
Matched b ions: b(3), b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9), b(10), b(10)-98, b(11), b(12)-98, b(12), b(13), b(13)-98, b(14), b(15), b(15)++, b(16), b(16)-98, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(14)-98, y(14), y(14)++, y(15), y(15)-98++, y(15)-98, y(16)-98, y(16), y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.377

HADSVAELGEQIDNLQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of HADSVAELGEQIDNLQR
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 4844: 2007.949348 from(1004.981950,2+)
Title: Elution from: 49.688 to 49.688 scan no 4637 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2007.9475
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 96 Expect: 1.7e-008

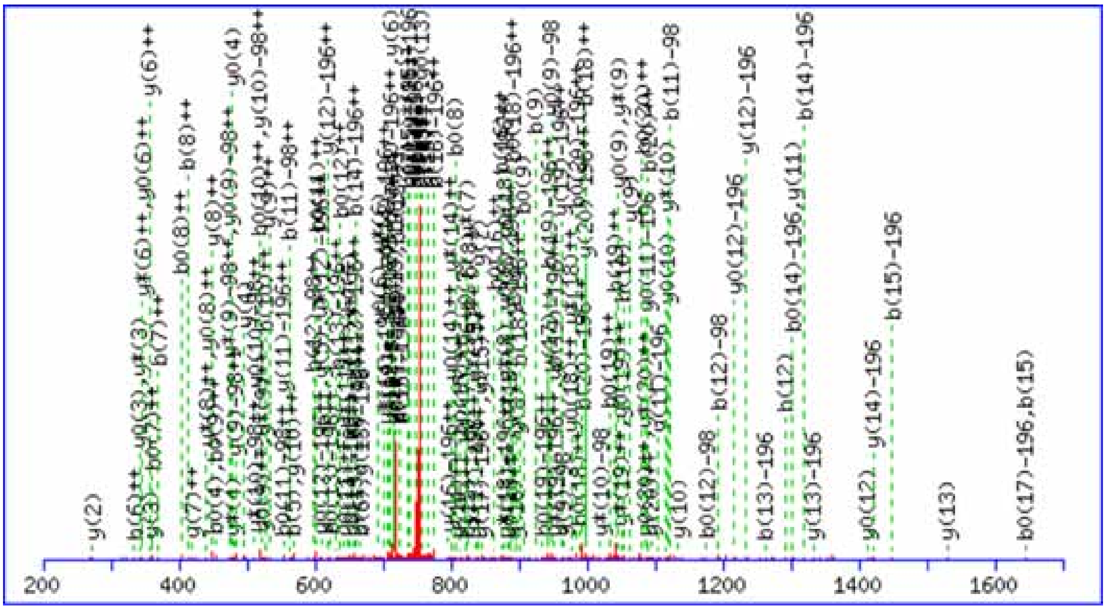
Matched b ions: b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(9)++, b(9)-98, b(9), b(10), b(10)-98++, b(10)-98, b(11), b(12), b(12)-98, b(13), b(13)-98, b(14), b(15), b(15)-98++, b(16), b(16)-98++, b(16)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)-98, y(14), y(14)-98++, y(15)-98, y(15), y(16), y(16)-98, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.378

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:11,@S:13
Ambiguous sites:

MS/MS Fragmentation of HAFSPVASVESASGETLHSPK
Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 5714: 2353.040166 from(785.353998,3+)
Title: Elution from: 41.679 to 41.679 scan no 3623 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2353.0392
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K21 : Dimethyl (K)
Ions Score: 56 Expect: 0.00017

Matched b ions: b(5), b(6), b(6)++, b(7)++, b(7), b(8)++, b(8), b(9), b(10)++, b(10), b(11)-98, b(11)-98++, b(12)-98, b(12), b(12)-98++, b(13)-98, b(13)-196, b(13)-196++, b(13)-98++, b(14)-98, b(14)-196++, b(14)-98++, b(14)++, b(14)-196, b(15)-98++, b(15)-196, b(15), b(15)++, b(15)-196++, b(16)-98++, b(16)++, b(16)-196++, b(17)-98++, b(18)-98++, b(18)++, b(18)-196++, b(19)-196++, b(19)++, b(19)-98++, b(20)-98++, b(20)-196++, b(20)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)-98++, y(9)++, y(9)-98, y(9), y(10)-98++, y(10)++, y(10), y(11)-98++, y(11)-98, y(11)++, y(11)-196++, y(11), y(11)-196, y(12)-196, y(12)-98++, y(12)-196++, y(12)++, y(12)-98, y(13), y(13)-196, y(13)-196++, y(13)-98++, y(13)++, y(14)-196, y(14)-196++, y(14)-98++, y(14)++, y(15)-196++, y(15)++, y(15)-98++, y(16)-98++, y(16)-196++, y(16)++, y(17)-196++, y(17)++, y(18)-196++, y(18)-98++, y(19)-196++, y(19)-98++, y(20)++, y(20)-98++, y(20)-196++
Precursor origin neutral loss: +

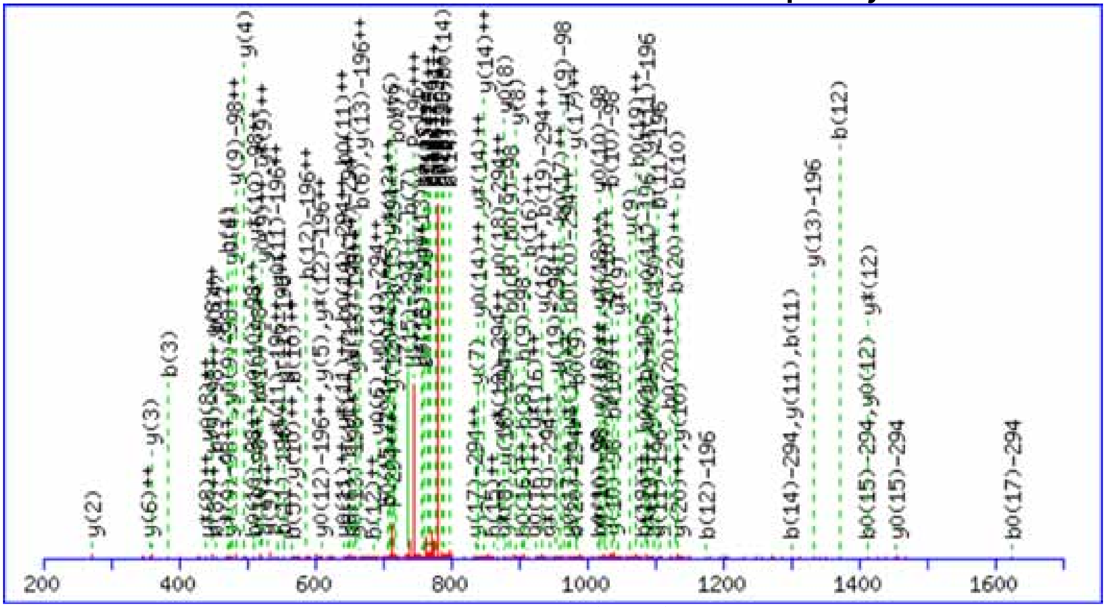
Peptide No.379

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:8,@S:11,@S:13
Ambiguous sites:

MS/MS Fragmentation of HAFSPVASVESASGETLHSPK
Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 6417: 2433.007314 from(812.009714,3+)

Title: Elution from: 44.003 to 44.003 scan no 3972 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2433.0056
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K21 : Dimethyl (K)
Ions Score: 35 Expect: 0.014

Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)++, b(8), b(9)-98++, b(9)-98, b(10), b(10)-98++, b(10)++, b(10)-98, b(11)++, b(11)-98, b(11)-98++, b(11), b(11)-196, b(11)-196++, b(12)-98, b(12)-196, b(12)-196++, b(12), b(12)++, b(13)-98, b(13)-196, b(13)-196++, b(13)-98++, b(13)++, b(14)-294++, b(14)-294, b(14)++, b(14)-196++, b(14)-98++, b(15)-98, b(15)-196++, b(15)-294++, b(15)++, b(16)-294++, b(16)-98++, b(16)++, b(18)++, b(18)-98++, b(18)-196++, b(19)-294++, b(19)-98++, b(19)++, b(19)-196++, b(20)-196++, b(20)-98++, b(20)-294++, b(20)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8)++, y(8), y(9)++, y(9)-98++, y(9), y(9)-98, y(10)-98++, y(10)-98, y(10)++, y(10), y(11)++, y(11)-98++, y(11), y(11)-196++, y(11)-196, y(12)-98++, y(12)-98, y(12)++, y(13)-196++, y(13)++, y(13)-196, y(13)-98++, y(14)-98++, y(14)-196++, y(14)++, y(15)-196++, y(15)-294++, y(15)-98++, y(16)++, y(16)-294++, y(16)-196++, y(17)-294++, y(17)-98++, y(17)++, y(18)++, y(18)-294++, y(18)-196++, y(18)-98++, y(19)-294++, y(19)++, y(19)-196++, y(19)-98++, y(20)-98++, y(20)-196++, y(20)++
Precursor origin neutral loss: +

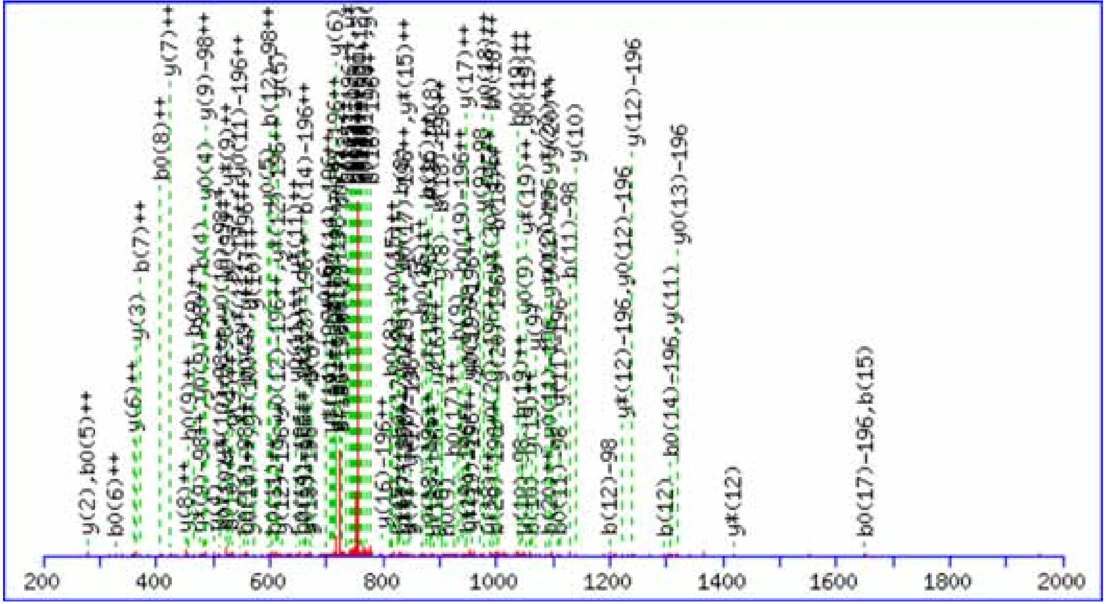
Peptide No.380

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:11,@S:13
Ambiguous sites:

MS/MS Fragmentation of HAFSPVASVESASGETLHSPK

Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 6271: 2365.103268 from(789.375032,3+)
Title: Elution from: 41.621 to 41.621 scan no 3694 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2365.1029
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 45 Expect: 0.0023

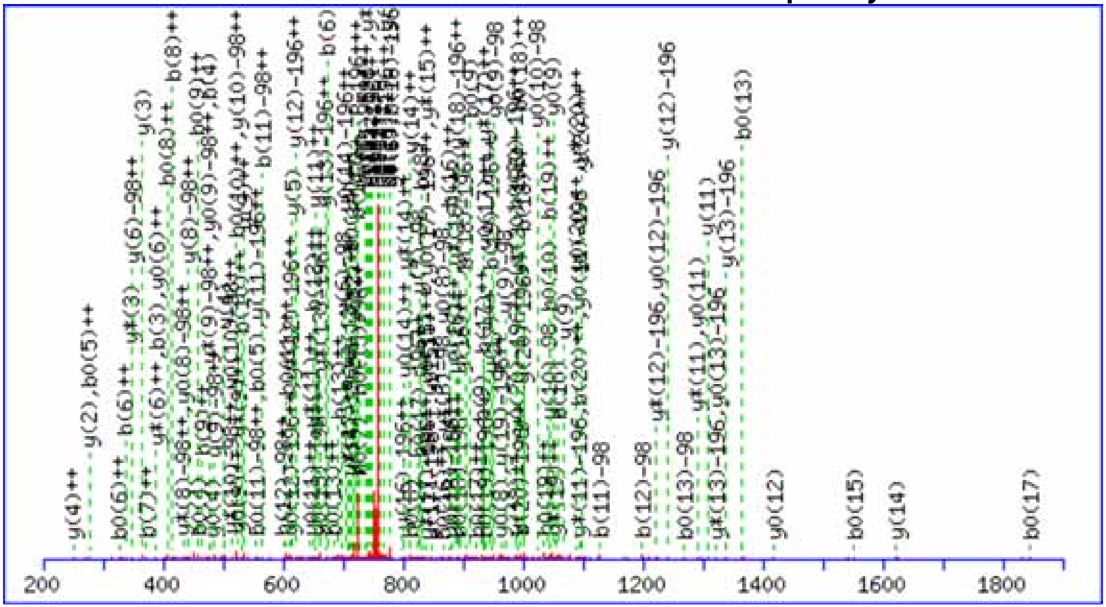
Matched b ions: b(4), b(6), b(7)++, b(7), b(8), b(9)++, b(9), b(10), b(10)++, b(11)-98, b(12)-98, b(12), b(12)-98++, b(13)-98, b(13)++, b(14)-196++, b(14)-98++, b(14)++, b(15)-98, b(15), b(15)-98++, b(15)-196++, b(15)++, b(16)++, b(16)-98++, b(16)-196++, b(17)-196++, b(17)-98++, b(18)-98++, b(18)-196++, b(18)++, b(19)-196++, b(19)-98++, b(19)++, b(20)++, b(20)-196++, b(20)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9)-98++, y(9)-98, y(9), y(10)-98++, y(10), y(10)++, y(10)-98, y(11)-98++, y(11), y(11)-98, y(11)++, y(11)-196++, y(11)-196, y(12)-98++, y(12)++, y(12)-196, y(12)-196++, y(13)-196++, y(13)++, y(13)-98++, y(14)-196++, y(14)-98++, y(15)-196++, y(15)-98++, y(16)-98++, y(16)-196++, y(16)++, y(17)-196++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(18)-196++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(20)-196++
Precursor origin neutral loss: +

Peptide No.381

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:11,@T:16
Ambiguous sites:

MS/MS Fragmentation of HAFSPVASVESASGETLHSPK
Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 6339: 2365.105029 from(789.375619,3+)
Title: Elution from: 41.639 to 41.639 scan no 3691 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2365.1029
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 36 Expect: 0.02

Matched b ions: b(3), b(4), b(6)++, b(6), b(7), b(7)++, b(8)++, b(8), b(9), b(9)++, b(10), b(10)++, b(11)-98, b(11)-98++, b(12)-98, b(12)-98++, b(12)++, b(13)++, b(14)++, b(15)-98++, b(16)-196++, b(16)-98++, b(16)++, b(17)++, b(18)-196++, b(18)++, b(18)-98++, b(19)-98++, b(19)-196++, b(19)++, b(20)-196++, b(20)-98++, b(20)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6)-98++, y(6)-98, y(7)-98, y(8)-98++, y(9)++, y(9)-98++, y(9), y(9)-98, y(10)-98++, y(10)-98, y(11)-98++, y(11), y(11)-98, y(11)-196++, y(11)++, y(12)++, y(12)-196, y(12)-196++, y(12)-98++, y(13)-196, y(13)++, y(13)-196++, y(13)-98++, y(14), y(14)-98++, y(14)-196++, y(14)++, y(15)-196++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)-196++, y(17)-98++, y(17)++, y(18)-196++, y(18)++, y(19)-196++, y(19)-98++, y(20)-196++, y(20)-98++, y(20)++
Precursor origin neutral loss: +

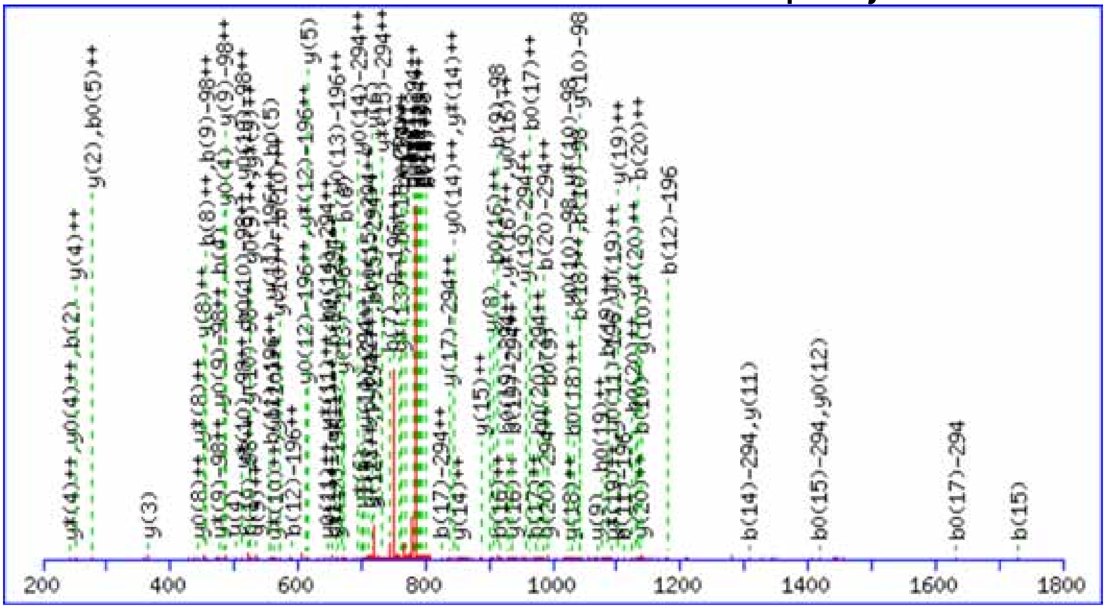
Peptide No.382

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:8,@S:11,@S:13
Ambiguous sites:

MS/MS Fragmentation of HAFSPVASVESASGETLHSPK
Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 6367: 2445.071271 from(816.031033,3+)

Title: Elution from: 43.870 to 43.870 scan no 3979 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2445.0692
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 36 Expect: 0.014

Matched b ions: b(2), b(4), b(6), b(7), b(8)++, b(9)-98, b(9)-98++, b(10)-98++, b(10), b(10)++, b(10)-98, b(11)-98++, b(11)-98, b(11)++, b(11)-196++, b(11)-196, b(12)-98, b(12)-196, b(12)-196++, b(12)-98++, b(13)-196, b(13)-98, b(13)-98++, b(13)-196++, b(14)-294++, b(14)-294, b(14)-196++, b(14)++, b(15)-294++, b(15)-98, b(15), b(15)-196++, b(16)-98++, b(16)++, b(17)-294++, b(17)++, b(18)-98++, b(18)++, b(18)-196++, b(19)-294++, b(19)++, b(19)-98++, b(19)-196++, b(20)-98++, b(20)-196++, b(20)-294++, b(20)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(8)++, y(8), y(9)++, y(9)-98++, y(9), y(10)-98++, y(10), y(10)++, y(10)-98, y(11)-98++, y(11)-98, y(11)++, y(11)-196++, y(11), y(12)++, y(12)-98++, y(13)-98++, y(13)-196++, y(13)++, y(14)++, y(14)-294++, y(14)-196++, y(14)-98++, y(15)++, y(15)-196++, y(15)-98++, y(16)++, y(16)-98++, y(16)-294++, y(16)-196++, y(17)-98++, y(17)-196++, y(17)-294++, y(18)-196++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(19)-294++, y(19)-196++, y(20)-196++, y(20)-98++, y(20)++, y(20)-294++
Precursor origin neutral loss: +

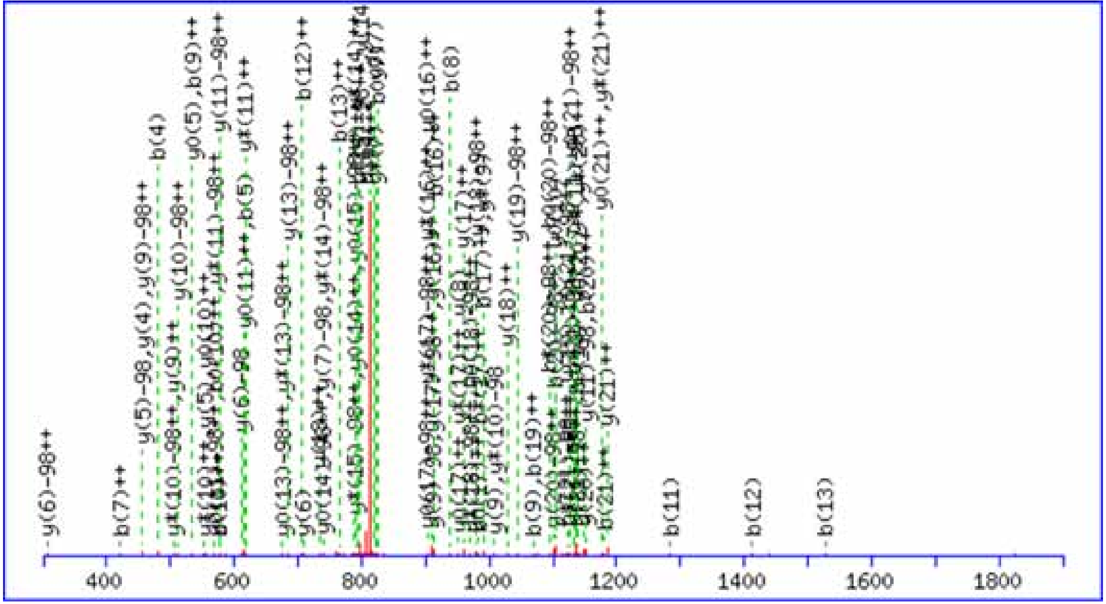
Peptide No.383

HALEHPEPESEQNGLERPGSGR
Confirmed sites: @S:20
Ambiguous sites:

MS/MS Fragmentation of HALEHPEPESEQNGLERPGSGR

Found in ANKR2_MOUSE, Ankyrin repeat domain-containing protein 2 OS=Mus musculus GN=Ankrd2 PE=2 SV=2

Match to Query 8140: 2533.135056 from(845.385628,3+)
Title: Elution from: 27.460 to 27.460 scan no 1868 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2533.1346
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S20 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 Expect: 3.7e-006

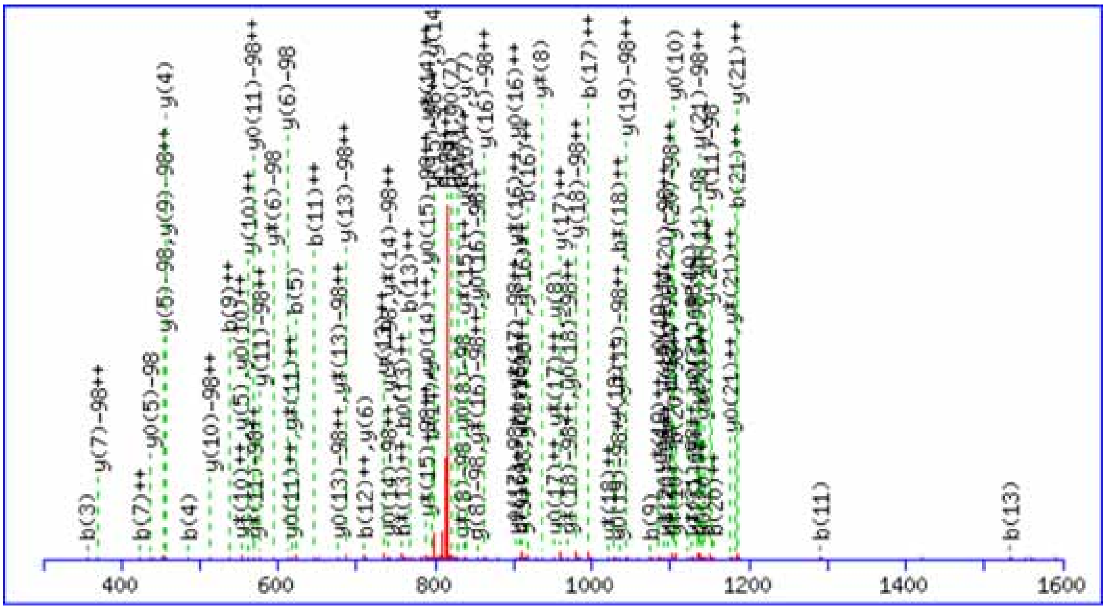
Matched b ions: b(4), b(5), b(7)++, b(8), b(9), b(9)++, b(10)++, b(11), b(12), b(12)++, b(13), b(13)++, b(14)++, b(16)++, b(17)++, b(19)++, b(20)-98++, b(20)++, b(21)-98++, b(21)++
Matched y ions: y(4), y(5)-98, y(5), y(6)-98++, y(6)-98, y(6), y(7)-98, y(8), y(9)-98++, y(9)-98, y(9)++, y(9), y(10)-98++, y(10), y(11)-98++, y(11)-98, y(13)-98++, y(13)++, y(14)++, y(15)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(20)-98++, y(20)++, y(21)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.384

HALEHPEPESEQNGLERPGSGR
Confirmed sites: @S:20
Ambiguous sites:

MS/MS Fragmentation of HALEHPEPESEQNGLERPGSGR
Found in ANKR2_MOUSE, Ankyrin repeat domain-containing protein 2 OS=Mus musculus GN=Ankrd2 PE=2 SV=2

Match to Query 6730: 2539.166070 from(847.395966,3+)
Title: Elution from: 27.557 to 27.557 scan no 1786 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2539.1665
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S20 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 0.00028

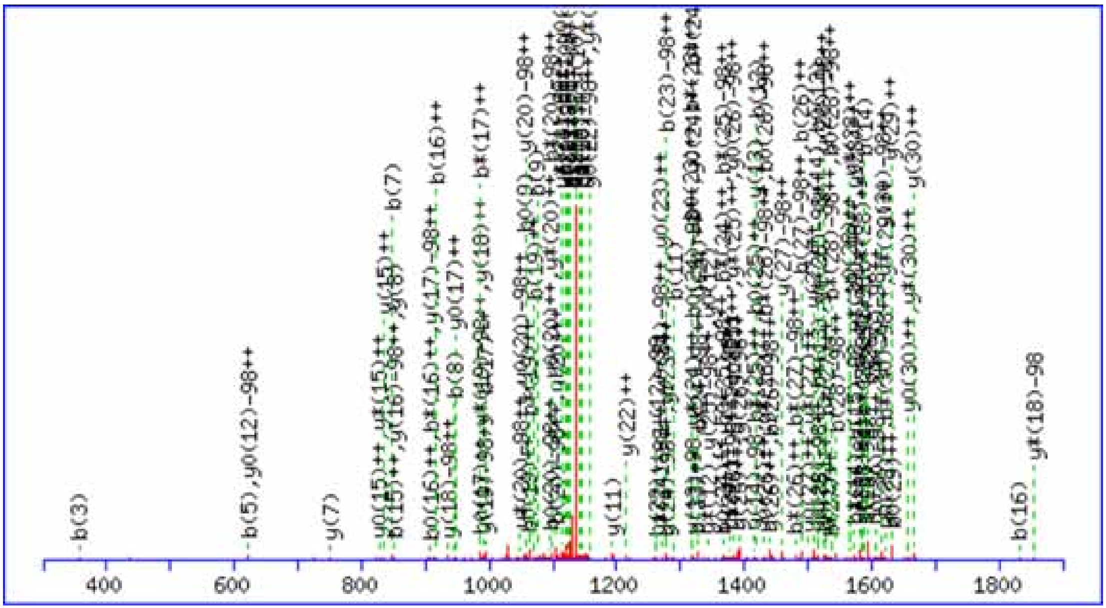
Matched b ions: b(3), b(4), b(5), b(7)++, b(9)++, b(9), b(11), b(11)++, b(12)++, b(13), b(13)++, b(14)++, b(16)++, b(17)++, b(20)-98++, b(20)++, b(21)++, b(21)-98++
Matched y ions: y(4), y(5)-98, y(5), y(6), y(6)-98, y(7)-98++, y(7)-98, y(7), y(8), y(8)-98, y(9)-98++, y(9)-98, y(10)-98++, y(10)++, y(10), y(11)-98++, y(11)-98, y(13)++, y(13)-98++, y(14)++, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.385

HALEHPEPESEQNGLERPGSGRETPQPIPAQ
Confirmed sites: @S:20
Ambiguous sites:

MS/MS Fragmentation of HALEHPEPESEQNGLERPGSGRETPQPIPAQ
Found in ANKR2_MOUSE, Ankyrin repeat domain-containing protein 2 OS=Mus musculus GN=Ankrd2 PE=2 SV=2

Match to Query 7543: 3500.652399 from(1167.891409,3+)
Title: Elution from: 34.723 to 34.723 scan no 2750 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3500.6534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S20 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 85 **Expect:** 4.1e-007

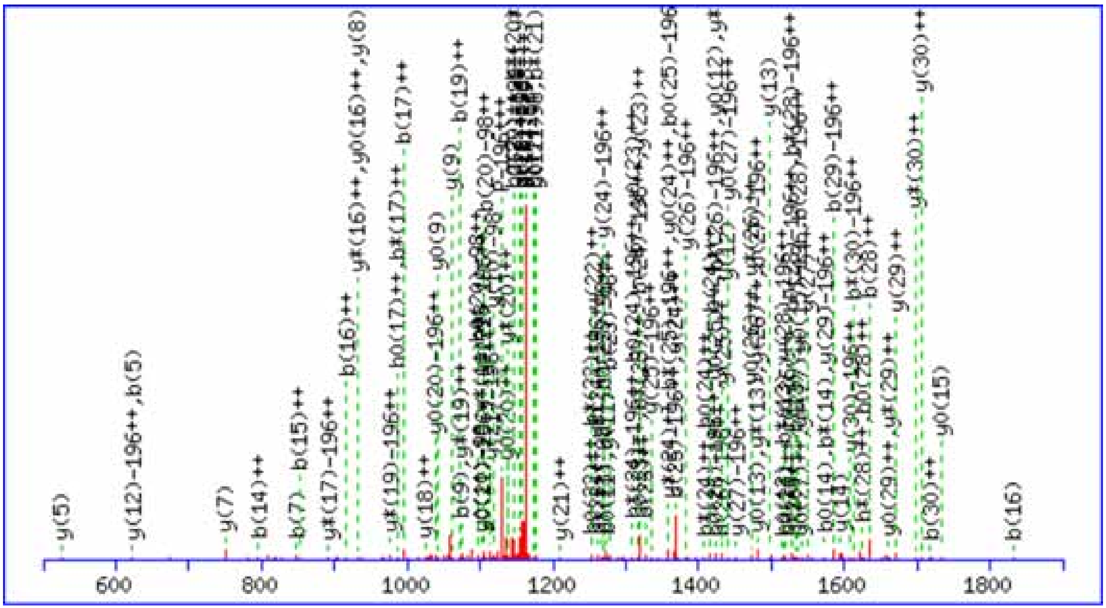
Matched b ions: b(3), b(5), b(7), b(8), b(9), b(11), b(12), b(14), b(15)++, b(16), b(16)++, b(17)++, b(19)++, b(20)-98++, b(21)-98++, b(22)++, b(23)++, b(23)-98++, b(24)-98++, b(24)++, b(25)-98++, b(26)-98++, b(26)++, b(27)-98++, b(27)++, b(28)++, b(28)-98++, b(29)-98++
Matched y ions: y(7), y(8), y(10), y(11), y(12)-98, y(13)-98, y(13), y(14), y(14)-98, y(15)++, y(15)-98, y(16)-98++, y(17)-98++, y(18)-98++, y(18)++, y(19)-98++, y(20)++, y(20)-98++, y(21)-98++, y(22)++, y(23)++, y(24)++, y(24)-98++, y(25)++, y(25)-98++, y(26)-98++, y(26)++, y(27)++, y(27)-98++, y(28)++, y(28)-98++, y(29)++, y(29)-98++, y(30)++, y(30)-98++
Precursor origin neutral loss: +

Peptide No.386

HALEHPEPESEQNGLERPGSGRETPQPIPAQ
Confirmed sites: @S:20,@T:24
Ambiguous sites:

MS/MS Fragmentation of HALEHPEPESEQNGLERPGSGRETPQPIPAQ
Found in ANKR2_MOUSE, Ankyrin repeat domain-containing protein 2 OS=Mus musculus GN=Ankrd2 PE=2 SV=2

Match to Query 7727: 3580.627077 from(1194.549635,3+)
Title: Elution from: 35.560 to 35.560 scan no 2899 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3580.6197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T24 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 4e-005

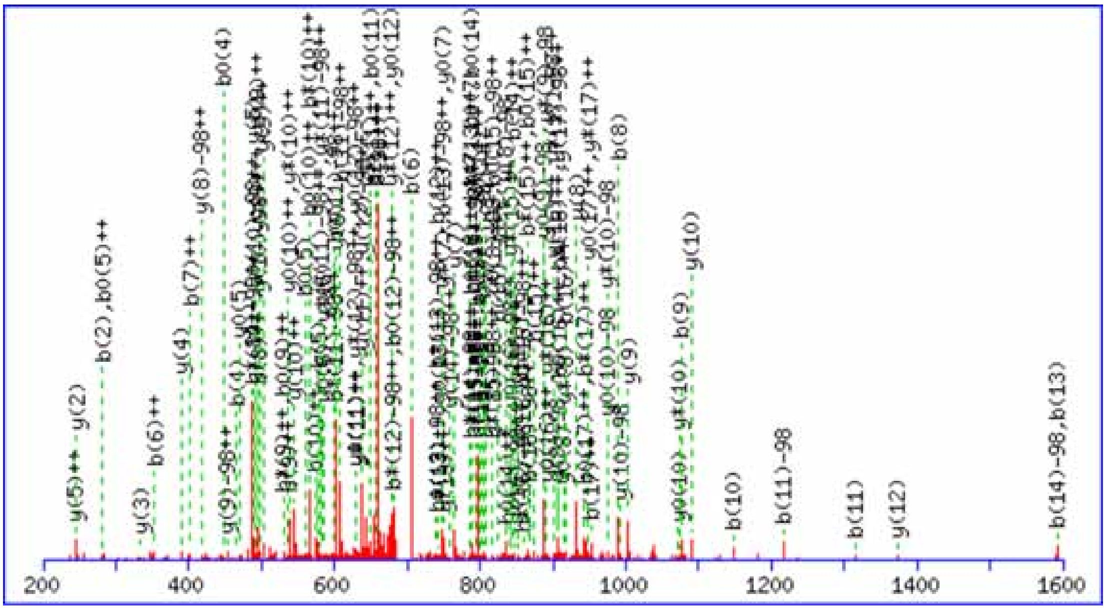
Matched b ions: b(5), b(7), b(9), b(10), b(13), b(14)++, b(15)++, b(16), b(16)++, b(17)++, b(19)++, b(20)-98++, b(20)++, b(22)++, b(23)-98++, b(23)++, b(24)-196++, b(24)-98++, b(24)++, b(25)-196++, b(25)-98++, b(26)-98++, b(26)-196++, b(26)++, b(27)-196++, b(27)-98++, b(28)-98++, b(28)++, b(28)-196++, b(29)-196++, b(29)-98++, b(30)++
Matched y ions: y(5), y(7), y(8), y(9), y(10)-98, y(11), y(11)-98, y(12)-196++, y(12), y(13), y(14), y(14)-98, y(15)-98++, y(15)-98, y(16)-98++, y(18)-98++, y(18)++, y(19)-98++, y(20)++, y(21)-98++, y(21)-196++, y(21)++, y(22)-196++, y(22)++, y(23)++, y(23)-98++, y(24)-98++, y(24)++, y(24)-196++, y(25)++, y(25)-98++, y(25)-196++, y(26)++, y(26)-98++, y(26)-196++, y(27)-98++, y(27)++, y(27)-196++, y(28)-196++, y(29)-98++, y(29)++, y(29)-196++, y(30)-98++, y(30)++, y(30)-196++
Precursor origin neutral loss: +

Peptide No.387

HDPSLQPWSASYDPGSAK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of HDPSLQPWSASYDPGSAK
Found in CAH3_MOUSE, Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3

Match to Query 5162: 2077.917204 from(693.646344,3+)
Title: Elution from: 44.989 to 44.989 scan no 4086 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2077.9146
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl (K)
Ions Score: 57 Expect: 0.00013

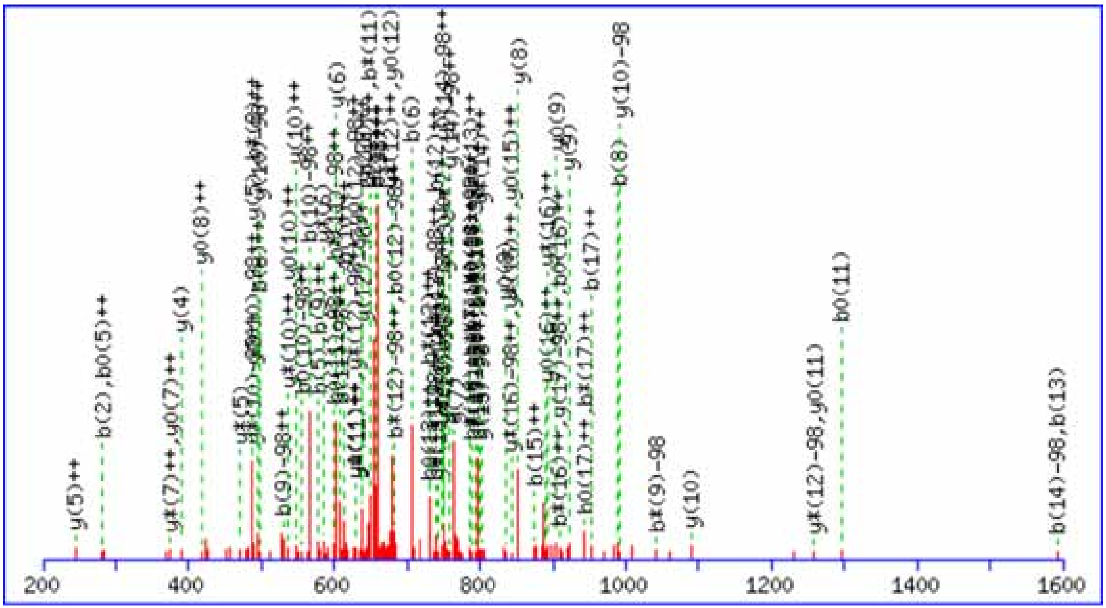
Matched b ions: b(2), b(4), b(5), b(6), b(6)++, b(7)++, b(7), b(8), b(8)++, b(9), b(9)++, b(10), b(10)++, b(11)-98, b(11), b(11)-98++, b(11)++, b(12)++, b(13)++, b(13), b(13)-98++, b(14)-98++, b(14)-98, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(8), y(8)-98++, y(8)-98, y(9), y(9)++, y(9)-98, y(9)-98++, y(10), y(10)++, y(10)-98++, y(10)-98, y(11)++, y(12), y(12)-98++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.388

HDPSLQPWSASYDPGSAK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of HDPSLQPWSASYDPGSAK
Found in CAH3_MOUSE, Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3

Match to Query 6031: 2077.916076 from(693.645968,3+)
Title: Elution from: 45.435 to 45.435 scan no 4356 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2077.9146
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl (K)
Ions Score: 32 Expect: 0.038

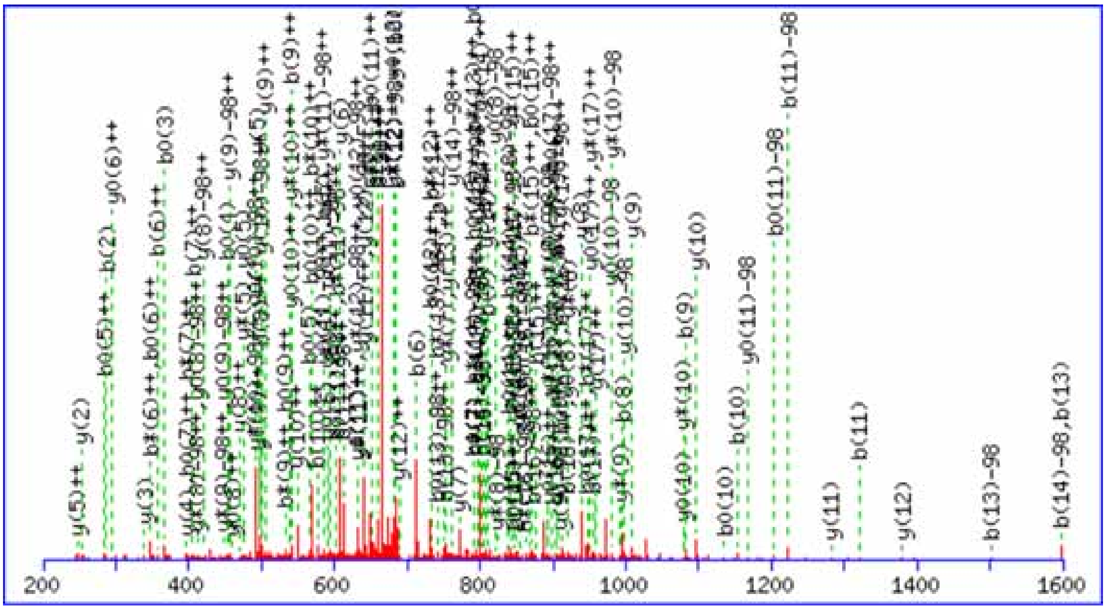
Matched b ions: b(2), b(5), b(6), b(8), b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(13), b(13)++, b(13)-98++, b(14)-98, b(14)-98++, b(15)++, b(17)++
Matched y ions: y(4), y(5)++, y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(10)-98++, y(10)++, y(11)++, y(12)-98++, y(13)++, y(14)-98++, y(15)-98++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.389

HDPSLQPWSASYDPGSAK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of HDPSLQPWSASYDPGSAK
Found in CAH3_MOUSE, Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3

Match to Query 4828: 2089.981320 from(697.667716,3+)
Title: Elution from: 44.998 to 44.998 scan no 3998 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2089.9782
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 53 Expect: 0.00034

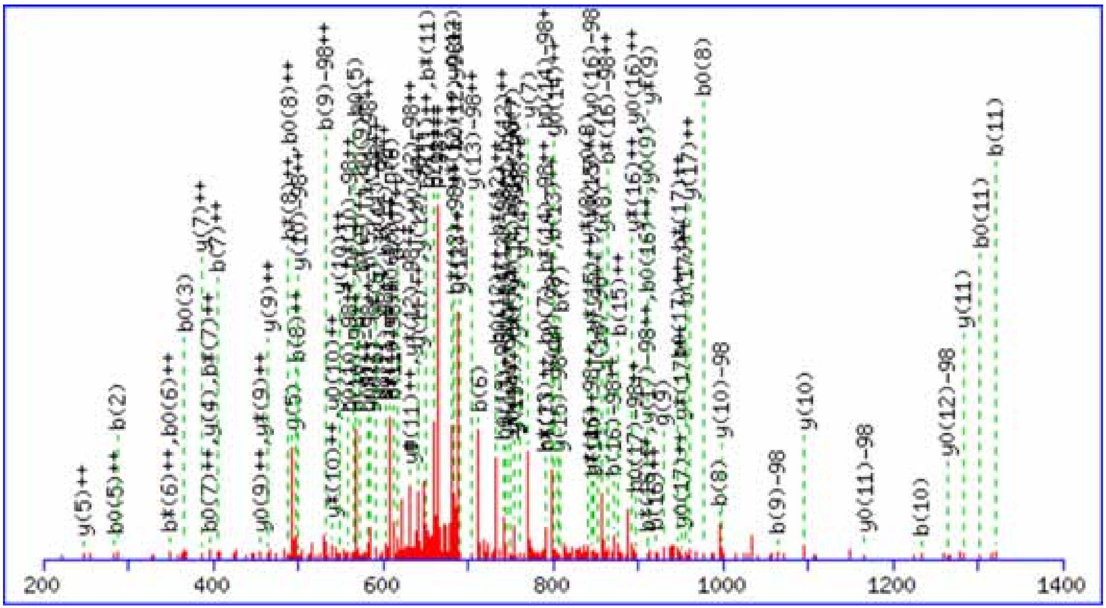
Matched b ions: b(2), b(5), b(6), b(6)++, b(7)++, b(7), b(8)++, b(8), b(9), b(9)++, b(10), b(10)++, b(11)-98, b(11), b(11)-98++, b(11)++, b(12)++, b(13)++, b(13)-98, b(13), b(13)-98++, b(14)-98++, b(14)-98, b(14)++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7), y(8), y(8)-98, y(8)-98++, y(8)++, y(9)-98, y(9), y(9)++, y(9)-98++, y(10), y(10)-98++, y(10)++, y(10)-98, y(11), y(11)++, y(11)-98++, y(12), y(12)-98++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.390

HDPSLQPWSASYDPGSAK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of HDPSLQPWSASYDPGSAK
Found in CAH3_MOUSE, Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3

Match to Query 5423: 2089.981269 from(697.667699,3+)
Title: Elution from: 45.369 to 45.369 scan no 4145 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2089.9782
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 35 Expect: 0.021

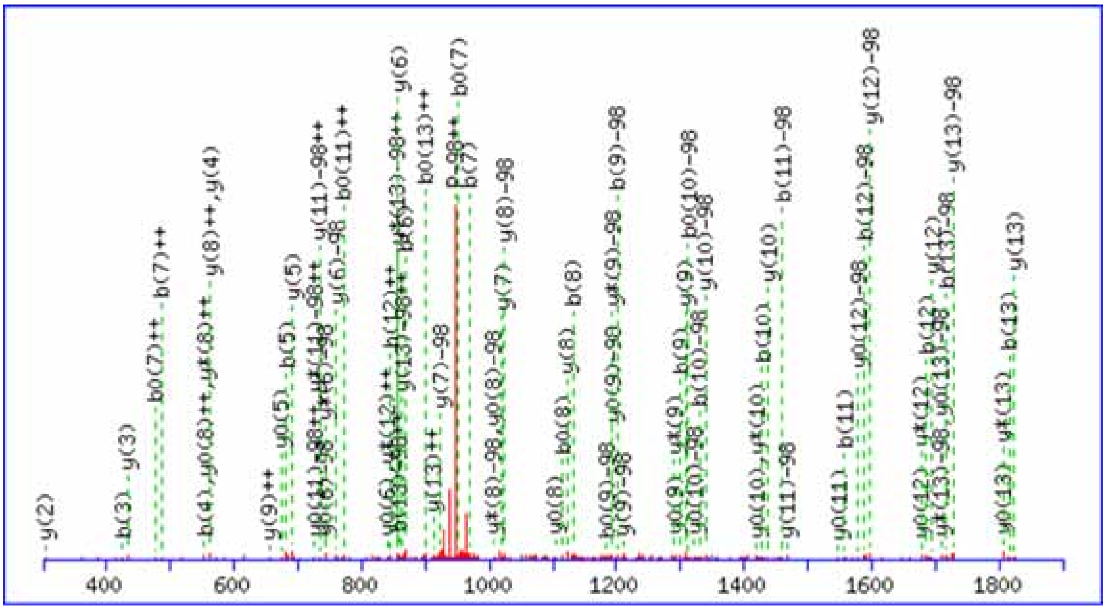
Matched b ions: b(2), b(5), b(6), b(7)++, b(7), b(8), b(8)++, b(9)-98, b(9)-98++, b(9)++, b(10)-98++, b(10), b(10)++, b(11), b(11)-98++, b(11)++, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(16)-98++, b(16)++, b(17)++
Matched y ions: y(4), y(5), y(5)++, y(6), y(7), y(7)++, y(8), y(9), y(9)++, y(10), y(10)-98, y(10)-98++, y(10)++, y(11), y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(15)-98++, y(16)-98++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.391

HEEEEWTYSEEEER
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of HEEEEWTYSEEEER
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 5542: 1988.731942 from(995.373247,2+)
Title: Elution from: 35.208 to 35.208 scan no 3018 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1988.7312
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 0.00011

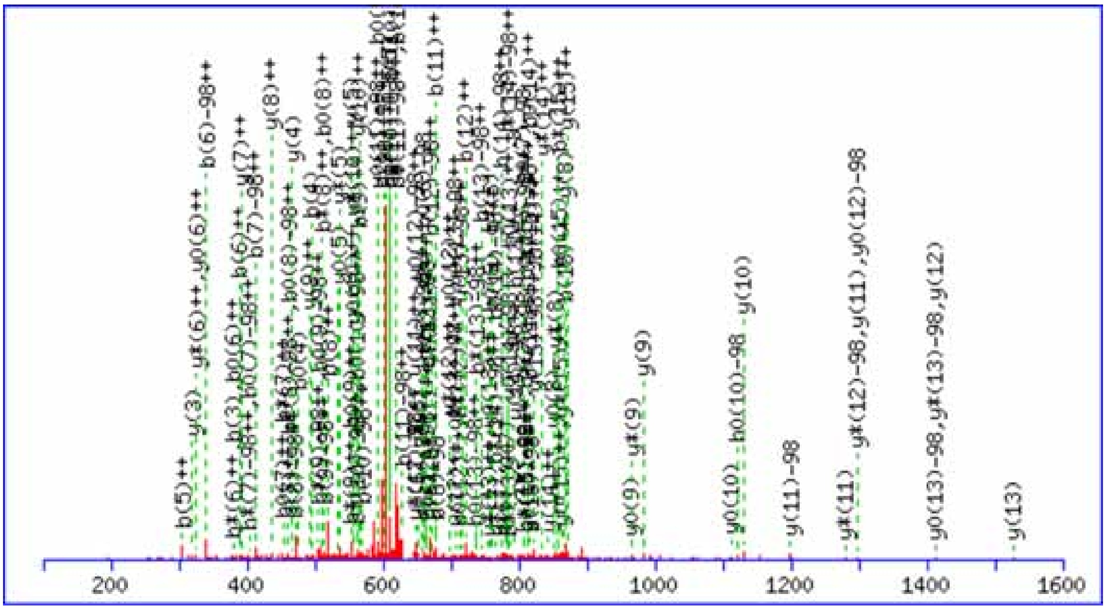
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(8), b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(12)++, b(13)-98, b(13), b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(7), y(8)++, y(8), y(8)-98, y(9), y(9)-98, y(9)++, y(10)-98, y(10), y(11)-98, y(11)-98++, y(12)-98, y(12), y(13)-98, y(13), y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.392

HGRDDSFDSLDSFGSR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of HGRDDSFDSLDSFGSR
Found in LIMC1_MOUSE, LIM and calponin homology domains-containing protein 1 OS=Mus musculus GN=Limch1 PE=1 SV=2

Match to Query 4535: 1904.769027 from(635.930285,3+)
Title: Elution from: 41.941 to 41.941 scan no 3738 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1904.7690
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.016

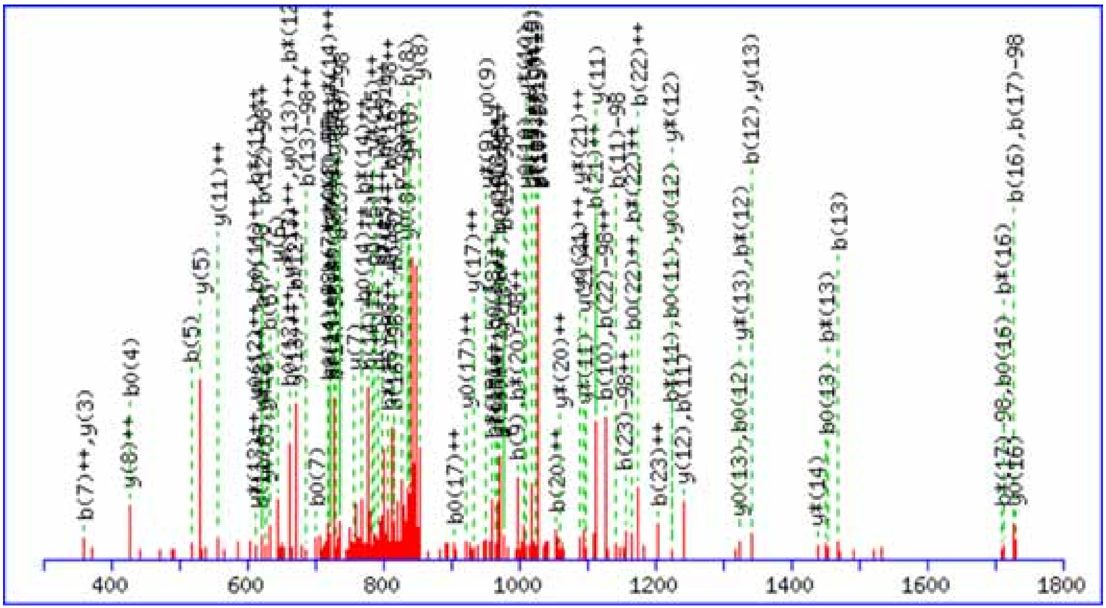
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)-98++, b(6)++, b(6), b(6)-98, b(7)-98++, b(7)++, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)-98, y(11), y(11)-98++, y(11)++, y(12), y(12)-98++, y(12)++, y(13), y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.393

HGSGADSDYENTQSGDPLLGLEGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of HGSGADSDYENTQSGDPLLGLEGK
Found in GIT1_MOUSE, ARF GTPase-activating protein GIT1 OS=Mus musculus GN=Git1 PE=1 SV=1

Match to Query 7821: 2582.120253 from(861.714027,3+)
Title: Elution from: 50.248 to 50.248 scan no 4947 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2582.1174
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K24 : Dimethyl (K)
Ions Score: 79 **Expect:** 7.8e-007

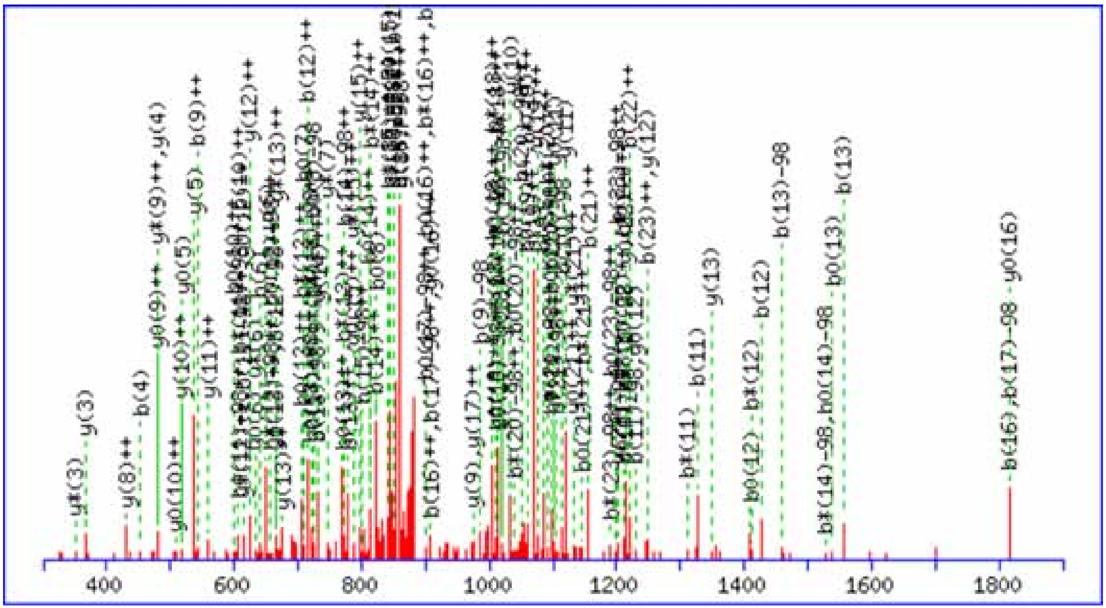
Matched b ions: b(5), b(6), b(7)++, b(7), b(7)-98, b(8)-98, b(8), b(9), b(10), b(10)-98, b(11), b(11)++, b(11)-98, b(12), b(12)++, b(12)-98++, b(13), b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(16), b(16)-98++, b(17)-98, b(18)++, b(19)++, b(19)-98++, b(20)++, b(21)++, b(22)-98++, b(22)++, b(23)++, b(23)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11)++, y(11), y(12), y(12)++, y(13), y(13)++, y(14)++, y(15)++, y(17)++, y(18)++, y(21)++
Precursor origin neutral loss:

Peptide No.394

HGSGADSDYENTQSGDPLLGLEGK
Confirmed sites: @S:3,@Y:9
Ambiguous sites:

MS/MS Fragmentation of **HGSGADSDYENTQSGDPLLGLEGK**
Found in **GIT1_MOUSE**, ARF GTPase-activating protein GIT1 OS=Mus musculus GN=Git1 PE=1 SV=1

Match to Query 8497: 2674.147077 from(892.389635,3+)
Title: Elution from: 55.069 to 55.069 scan no 5520 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2674.1473
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y9 : Phospho (Y)
K24 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 59 **Expect:** 7.9e-005

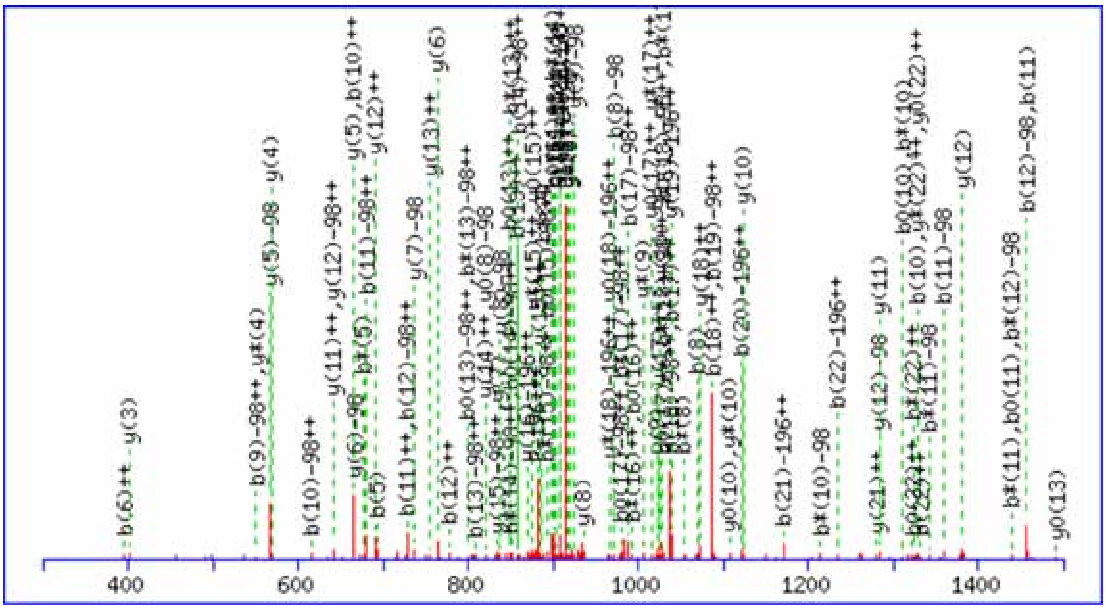
Matched b ions: b(4), b(6), b(8), b(9), b(9)-98, b(9)++, b(10), b(10)++, b(10)-98, b(11), b(11)-98++, b(11)-98, b(12)++, b(12), b(12)-98++, b(13), b(13)-98, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16), b(16)-98++, b(16)++, b(17)-98, b(17)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(23)++, b(23)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(8)++, y(8), y(9), y(10)++, y(10), y(11), y(11)++, y(12)++, y(12), y(13)++, y(13), y(14)++, y(15)++, y(17)++, y(18)++, y(19)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.395

HIKEEPLSEEEPCTSTAVPSPEK
Confirmed sites: @S:8,@S:20
Ambiguous sites:

MS/MS Fragmentation of HIKEEPLSEEEPCTSTAVPSPEK
Found in NOP58_MOUSE, Nucleolar protein 58 OS=Mus musculus GN=Nop58 PE=1 SV=1

Match to Query 8353: 2837.248806 from(946.756878,3+)
Title: Elution from: 38.930 to 38.930 scan no 3522 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2837.2483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K3 : Dimethyl (K)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S20 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K23 : Dimethyl (K)
Ions Score: 55 Expect: 0.0003

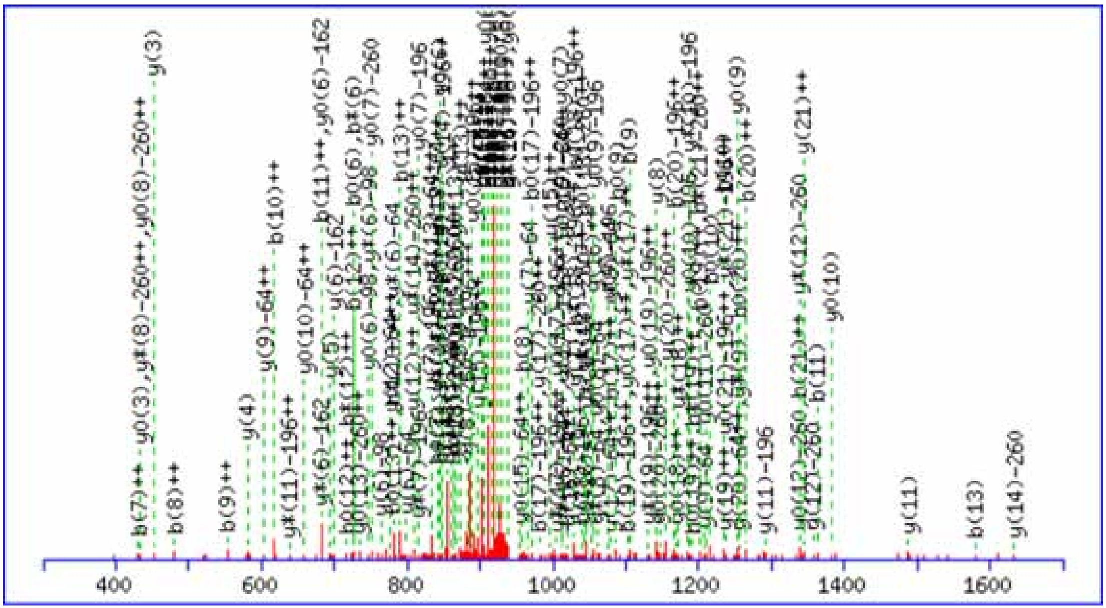
Matched b ions: b(5), b(6)++, b(7), b(8), b(8)-98, b(9)-98++, b(10)++, b(10), b(10)-98++, b(11)++, b(11), b(11)-98++, b(11)-98, b(12)-98++, b(12)-98, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(20)-98++, b(20)-196++, b(21)-196++, b(22)-98++, b(22)-196++, b(22)++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6), y(6)-98, y(7)-98, y(7), y(8)-98, y(8), y(9)-98, y(9), y(10), y(10)-98, y(11)++, y(11), y(12)-98, y(12), y(12)++, y(12)-98++, y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-196++, y(19)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.396

HIVNHDDVFEESEELSSDEEMK
Confirmed sites: @S:16,@S:17
Ambiguous sites:

MS/MS Fragmentation of HIVNHDDVFEESEELSSDEEMK
Found in LAP2_MOUSE, Protein LAP2 OS=Mus musculus GN=Erbb2ip PE=1 SV=2

Match to Query 6719: 2849.104671 from(950.708833,3+)
Title: Elution from: 43.829 to 43.829 scan no 3853 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2849.1027
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M21 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K22 : Dimethyl (K)
Ions Score: 48 Expect: 0.00068

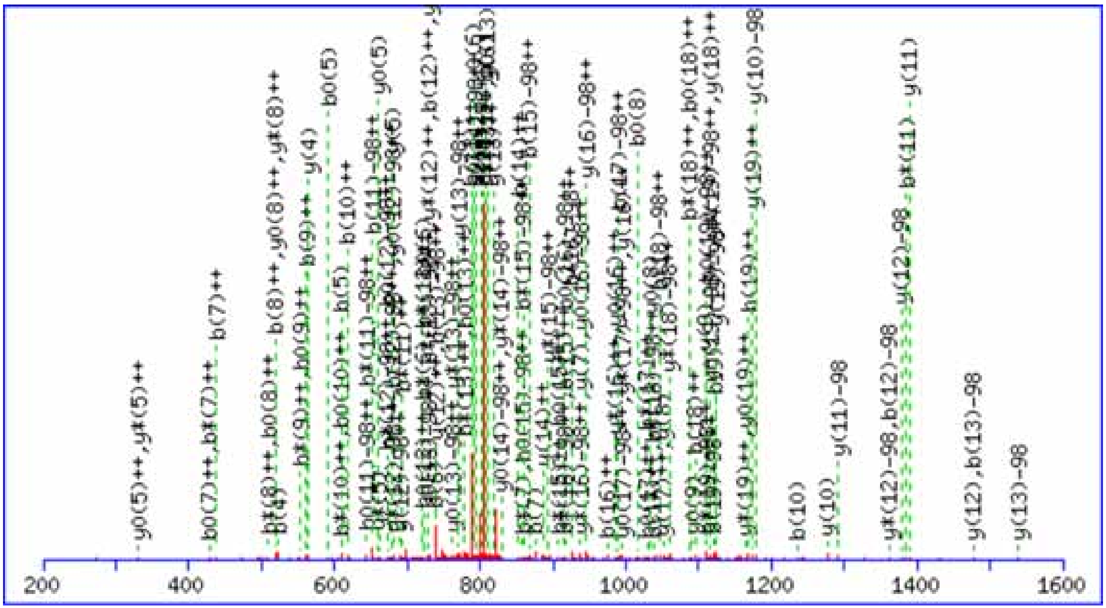
Matched b ions: b(7)++, b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(13)++, b(13), b(14)++, b(15)++, b(17)-98++, b(17)++, b(17)-196++, b(18)-98++, b(18)-196++, b(19)++, b(19)-98++, b(19)-196++, b(20)-98++, b(20)-196++, b(20)++, b(21)++, b(21)-98++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-196, y(7)-98, y(8)-98, y(8), y(8)-98++, y(9)-196, y(9)-98, y(11), y(11)-98++, y(11)-98, y(11)-196, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)-196++, y(15)-196++, y(15)++, y(16)-98++, y(16)++, y(17)-196++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.397

HNQDSQHCSLSGDEEDELFK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of HNQDSQHCSLSGDEEDELFK
Found in FKB15_MOUSE, FK506-binding protein 15 OS=Mus musculus GN=Fkbp15 PE=1 SV=2

Match to Query 7557: 2510.006985 from(837.676271,3+)
Title: Elution from: 41.105 to 41.105 scan no 3811 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2510.0057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
Ions Score: 42 Expect: 0.0025

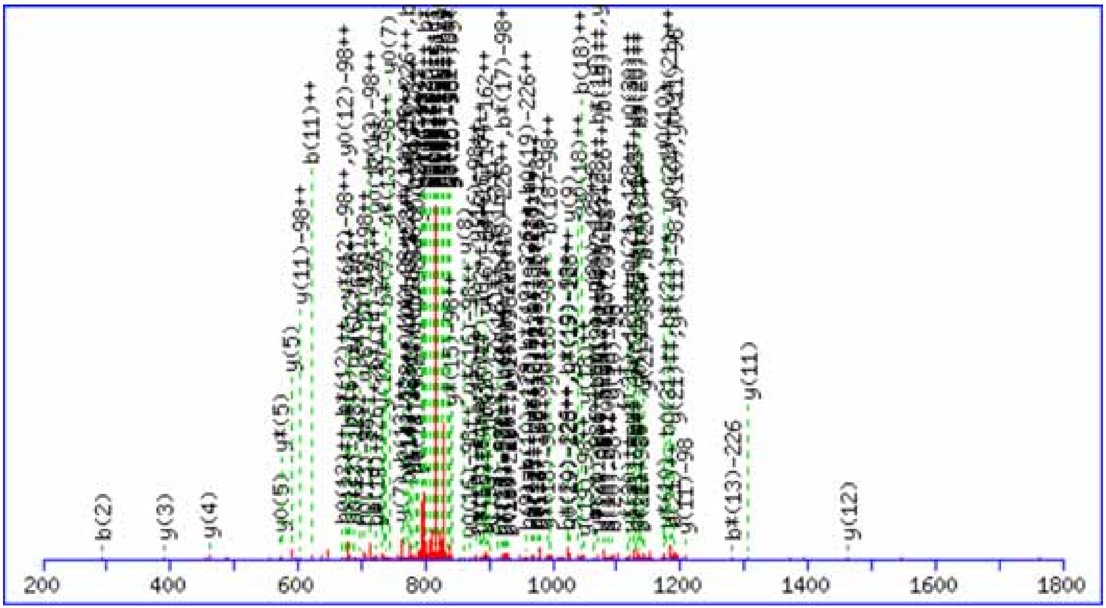
Matched b ions: b(4), b(5), b(6), b(7)++, b(7), b(8)++, b(9)++, b(9), b(10)++, b(10), b(11)-98++, b(12)-98, b(12)-98++, b(12)++, b(13)-98++, b(13)-98, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)-98, y(11), y(12)++, y(12), y(12)-98, y(12)-98++, y(13)-98, y(13)-98++, y(13)++, y(14)++, y(16)++, y(16)-98++, y(17)++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.398

HQGVMVGMGQKDSYVGDEAQSK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of HQGVMVGMGQKDSYVGDEAQSK
Found in ACTA_MOUSE, Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1

Match to Query 6184: 2546.121957 from(849.714595,3+)
Title: Elution from: 27.192 to 27.192 scan no 1682 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2546.1182
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K11 : Dimethyl (K)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K22 : Dimethyl (K)
Ions Score: 41 Expect: 0.0067

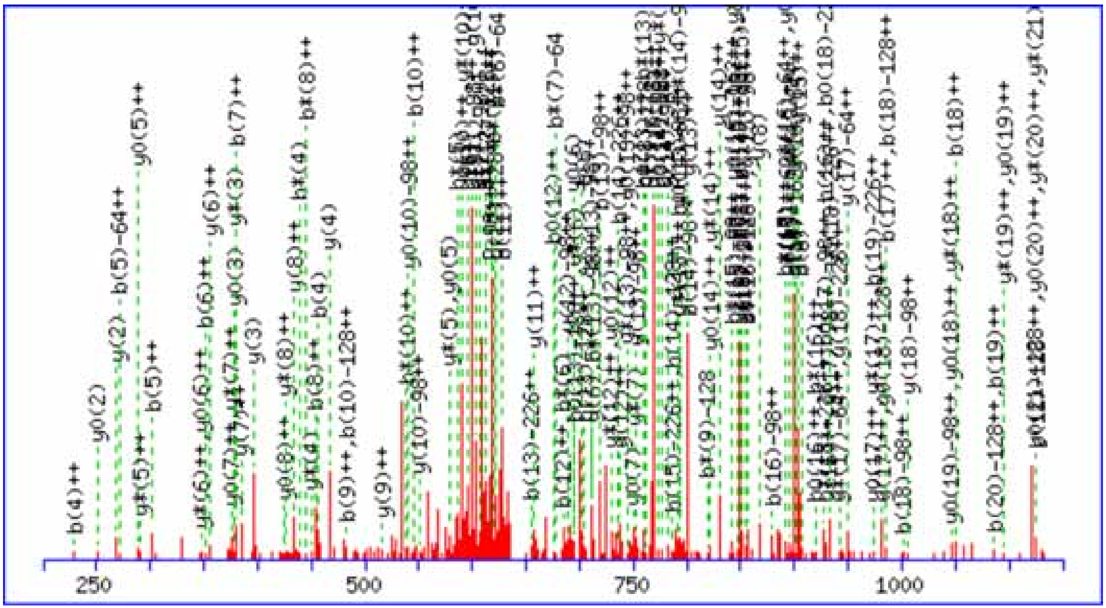
Matched b ions: b(2), b(6), b(8), b(9), b(10), b(11)++, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(15)++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(21)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(11), y(11)-98++, y(12), y(12)-98++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.399

HQGVMVGMGQKDSYVGDEAQSK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of HQGVMVGMGQKDSYVGDEAQSK
Found in ACTA_MOUSE, Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1

Match to Query 6239: 2564.215888 from(642.061248,4+)
Title: Elution from: 27.177 to 27.177 scan no 1680 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2564.2137
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K11 : Dimethyl:2H(4)13C(2) (K)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K22 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 66 Expect: 2.4e-005

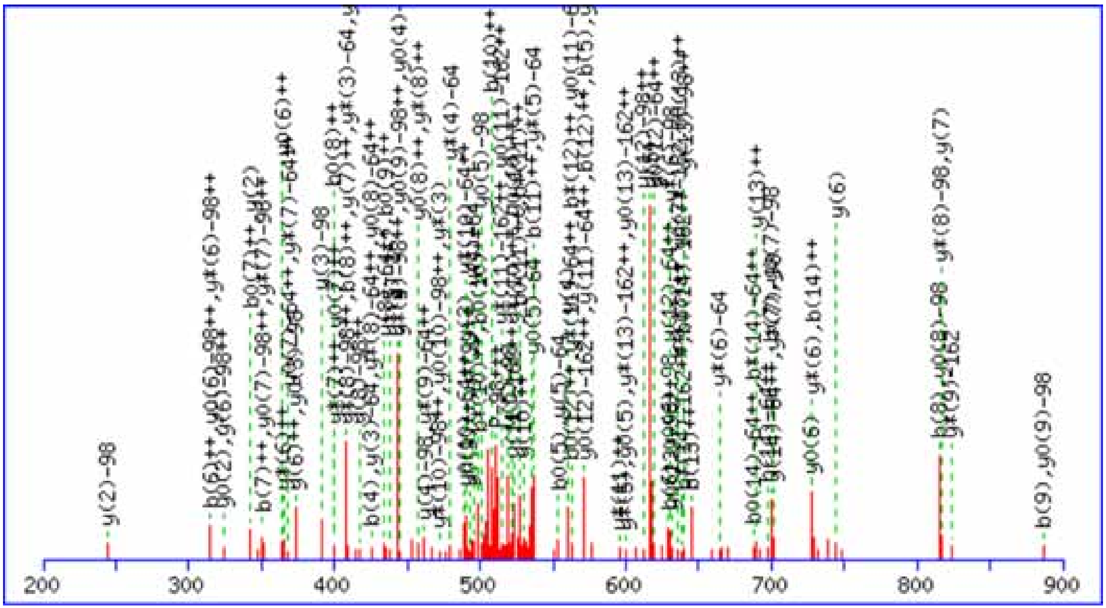
Matched b ions: b(4), b(4)++, b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(10)++, b(11)++, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(8), y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.400

HSGDFGADAQGAMSK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of HSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 2565: 1629.649599 from(544.223809,3+)
Title: Elution from: 23.660 to 23.660 scan no 1344 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1629.6494
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 66 Expect: 4.7e-006

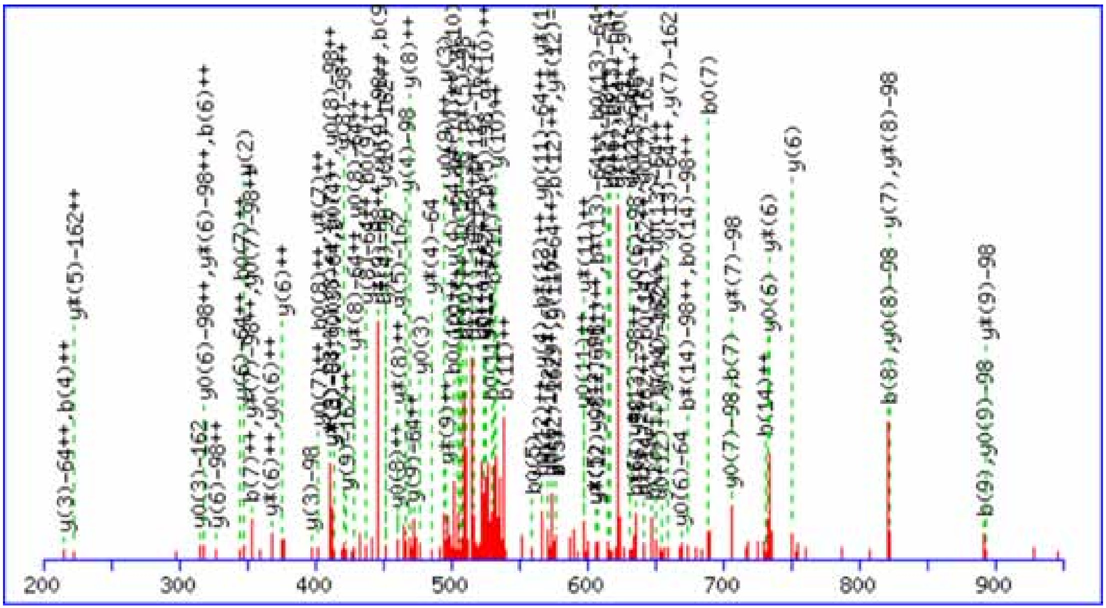
Matched b ions: b(4), b(5), b(6)++, b(6), b(7), b(7)++, b(8), b(8)++, b(9)++, b(9), b(10)++, b(11)++, b(12)++, b(13)++, b(14)++
Matched y ions: y(2), y(2)-98, y(3)-98, y(3), y(4), y(4)-98, y(5), y(5)-98, y(6)++, y(6), y(6)-98++, y(7)++, y(7), y(8)-98++, y(10)++, y(12)-98++, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.401

HSGDFGADAQGAMSK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of HSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 2505: 1641.713661 from(548.245163,3+)
Title: Elution from: 23.694 to 23.694 scan no 1330 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1641.7131
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 49 Expect: 0.00042

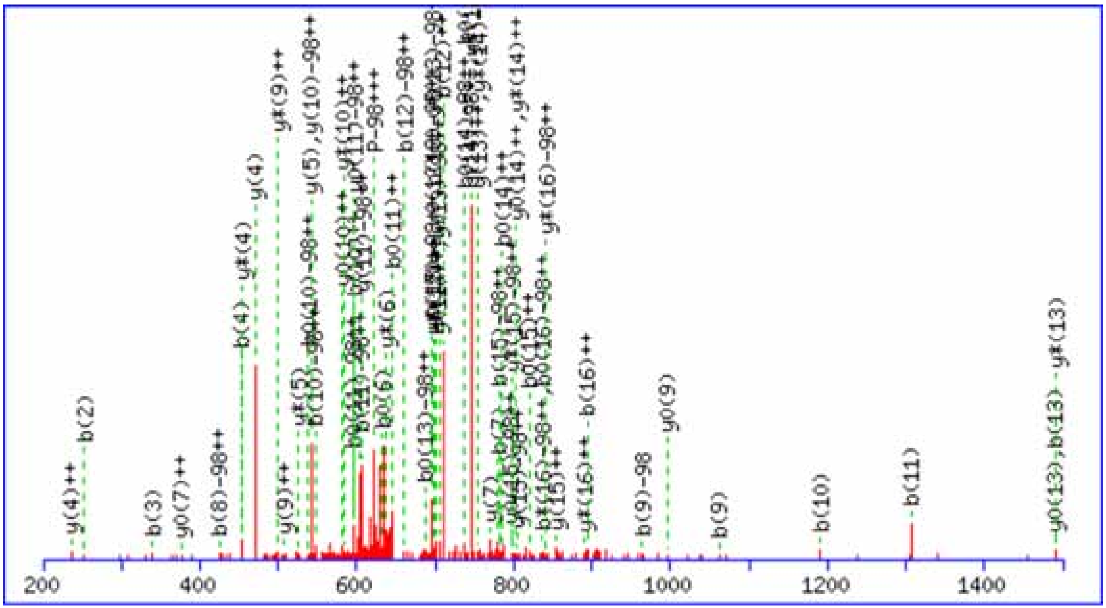
Matched b ions: b(4)++, b(5), b(6), b(6)++, b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(11)++, b(12)++, b(13)++, b(14)++
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(4), y(5), y(5)-98, y(6), y(6)++, y(6)-98++, y(7)++, y(7), y(8)-98++, y(8)++, y(9)++, y(10)++, y(11)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.402

HSSLPTESDEDIAPAQR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of HSSLPTESDEDIAPAQR
Found in AP3D1_MOUSE, AP-3 complex subunit delta-1 OS=Mus musculus GN=Ap3d1 PE=1 SV=1

Match to Query 4989: 1959.860118 from(654.293982,3+)
Title: Elution from: 34.856 to 34.856 scan no 2799 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1959.8575
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.053

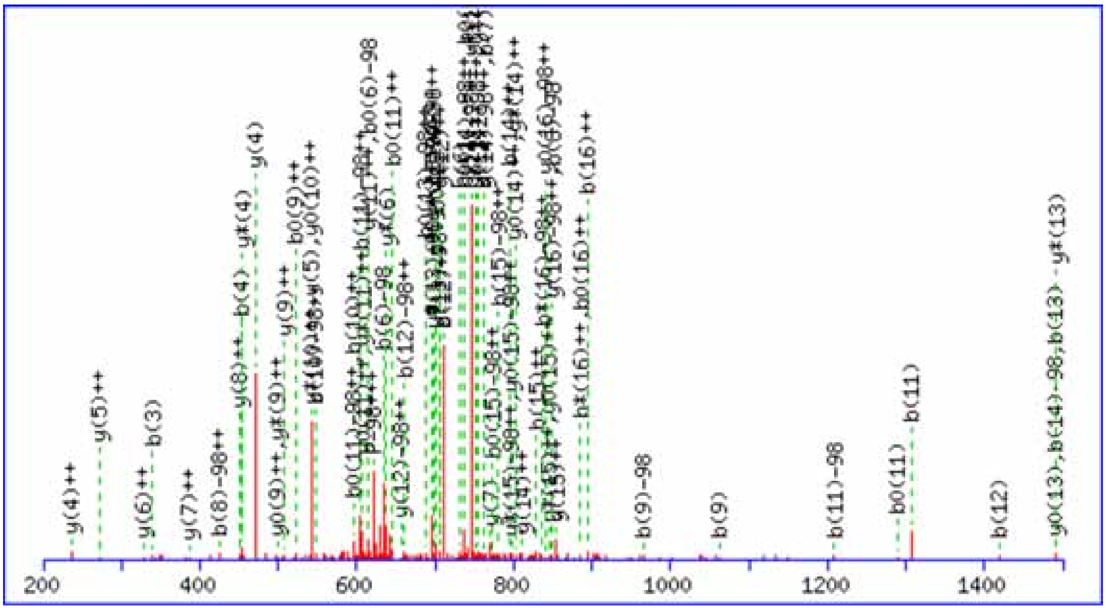
Matched b ions: b(2), b(3), b(4), b(7), b(8)-98++, b(9)-98, b(9), b(10), b(10)-98++, b(10)++, b(11), b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13), b(13)-98++, b(14)-98++, b(15)-98++, b(16)++
Matched y ions: y(4)++, y(4), y(5), y(7), y(9)++, y(10)-98++, y(11)-98++, y(12)++, y(13)-98++, y(13)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.403

HSSLPTESDEDIAPAQR
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of HSSLPTESDEDIAPAQR
Found in AP3D1_MOUSE, AP-3 complex subunit delta-1 OS=Mus musculus GN=Ap3d1 PE=1 SV=1

Match to Query 5425: 1959.858924 from(654.293584,3+)
Title: Elution from: 34.973 to 34.973 scan no 2985 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1959.8575
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.012

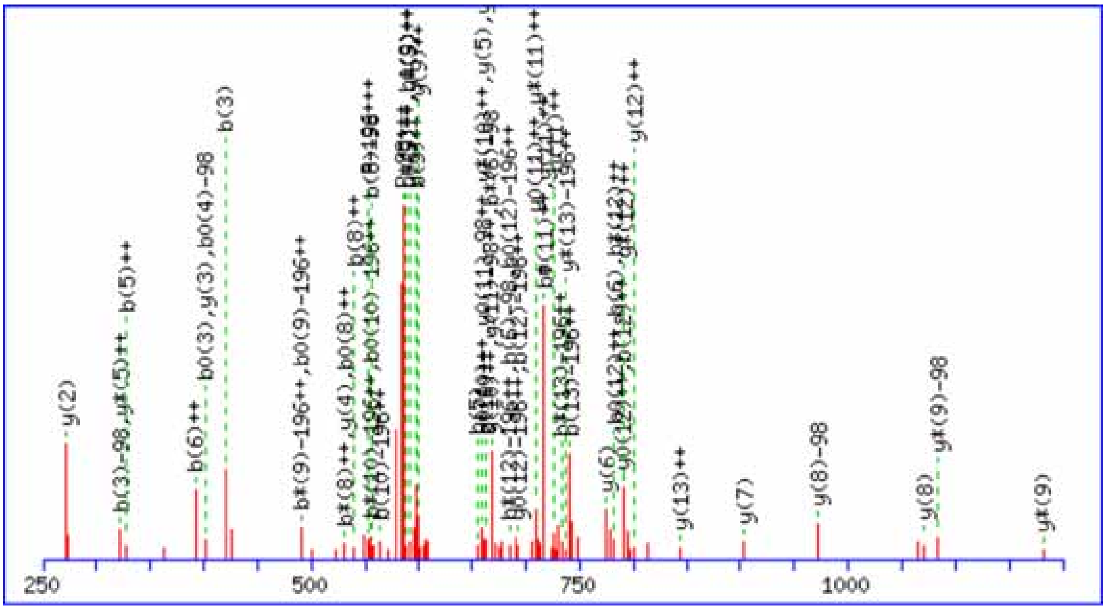
Matched b ions: b(3), b(4), b(6)-98, b(6), b(7)-98, b(8)-98++, b(8)-98, b(9)-98, b(9), b(10)++, b(10)-98++, b(11)-98, b(11), b(11)-98++, b(12)++, b(12), b(12)-98++, b(13)++, b(13), b(13)-98++, b(14)-98++, b(14)-98, b(14)++, b(15)++, b(15)-98++, b(16)++
Matched y ions: y(4)++, y(4), y(5), y(5)++, y(6)++, y(7), y(7)++, y(8)++, y(9)++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.404

HSSPHQSEDEEEPR
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of **HSSPHQSEDEEEPR**
Found in **GYS1_MOUSE**, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 4671: 1850.651610 from(617.891146,3+)
Title: Elution from: 19.241 to 19.241 scan no 899 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1850.6509
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.0016

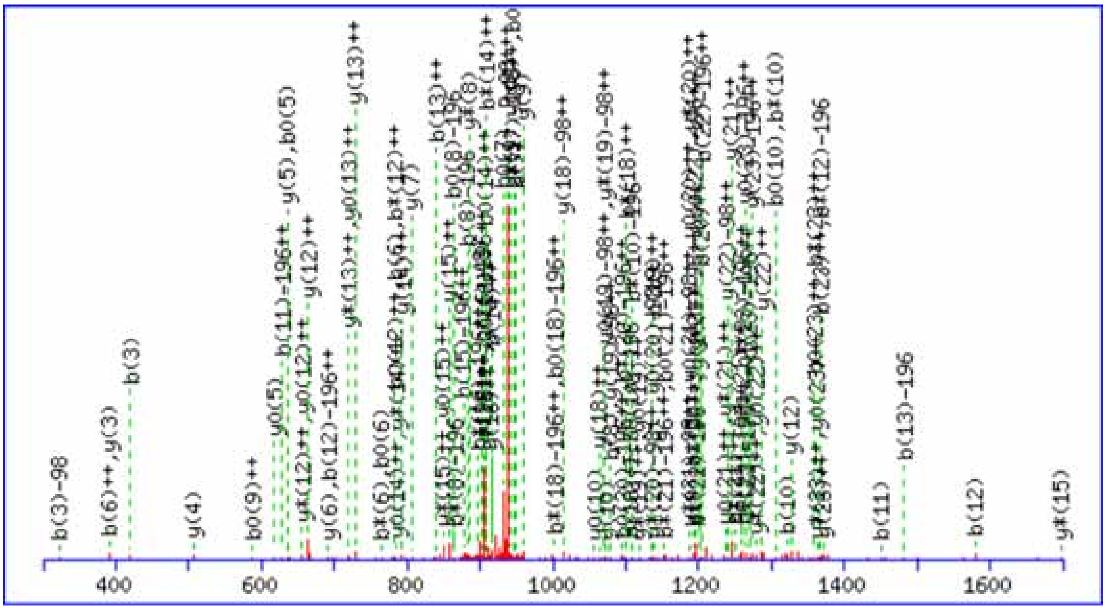
Matched b ions: b(3), b(3)-98, b(5)++, b(5)-98, b(5), b(6)++, b(6), b(6)-98, b(7)-98++, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)-196++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(12)-196++, b(13)-98++, b(13)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.405

HSSPHQSEDEEEPRDGPLGEDSER
Confirmed sites: @S:2,@S:7
Ambiguous sites:

MS/MS Fragmentation of **HSSPHQSEDEEEPRDGPLGEDSER**
Found in **GYS1_MOUSE**, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 6584: 2906.104287 from(969.708705,3+)
Title: Elution from: 28.031 to 28.031 scan no 1885 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2906.1029
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.0014

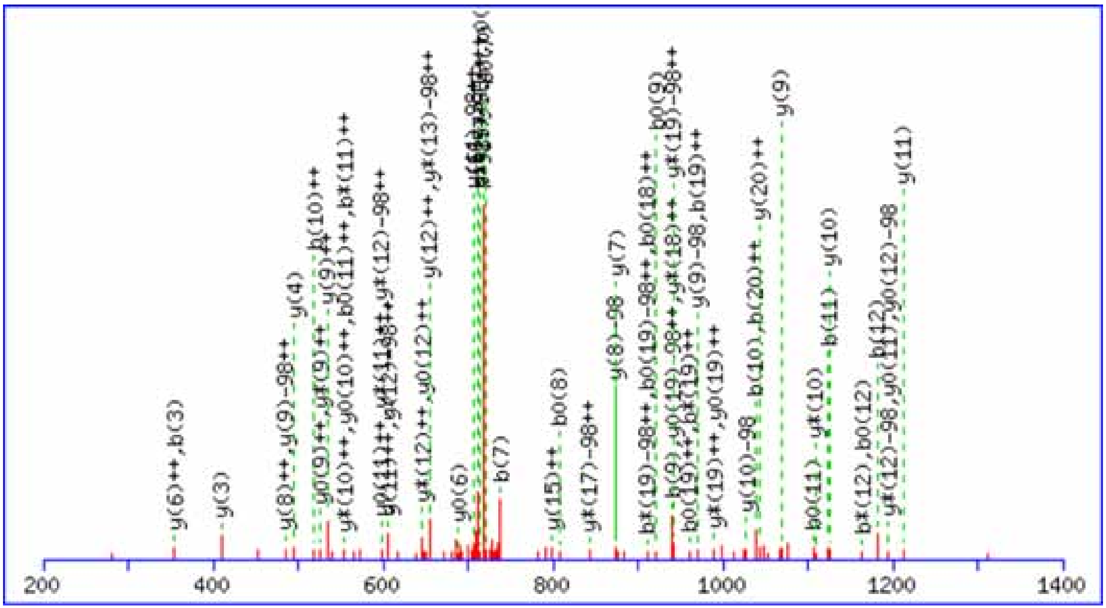
Matched b ions: b(3), b(3)-98, b(6)++, b(6), b(7)-98, b(7), b(8)-196, b(8), b(9)-98, b(9), b(10), b(11), b(11)-196++, b(11)-98, b(12)-98, b(12), b(12)-196++, b(13)-196, b(13)++, b(14)++, b(15)-98++, b(15)-196++, b(16)-196++, b(16)-98++, b(18)++, b(19)++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-196++, b(23)-98++, b(23)-196++, b(23)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12)++, y(12), y(13)++, y(14)++, y(15)++, y(16)++, y(18)++, y(18)-98++, y(19)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(23)++, y(23)-196++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.406

HSTPSNSSNPSGPPSPNSPHR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of HSTPSNSSNPSGPPSPNSPHR
Found in MRCKB_MOUSE, Serine/threonine-protein kinase MRCK beta OS=Mus musculus GN=Cdc42bpb PE=1 SV=1

Match to Query 6850: 2247.966849 from(750.329559,3+)
Title: Elution from: 20.567 to 20.567 scan no 1046 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2247.9658
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.0015

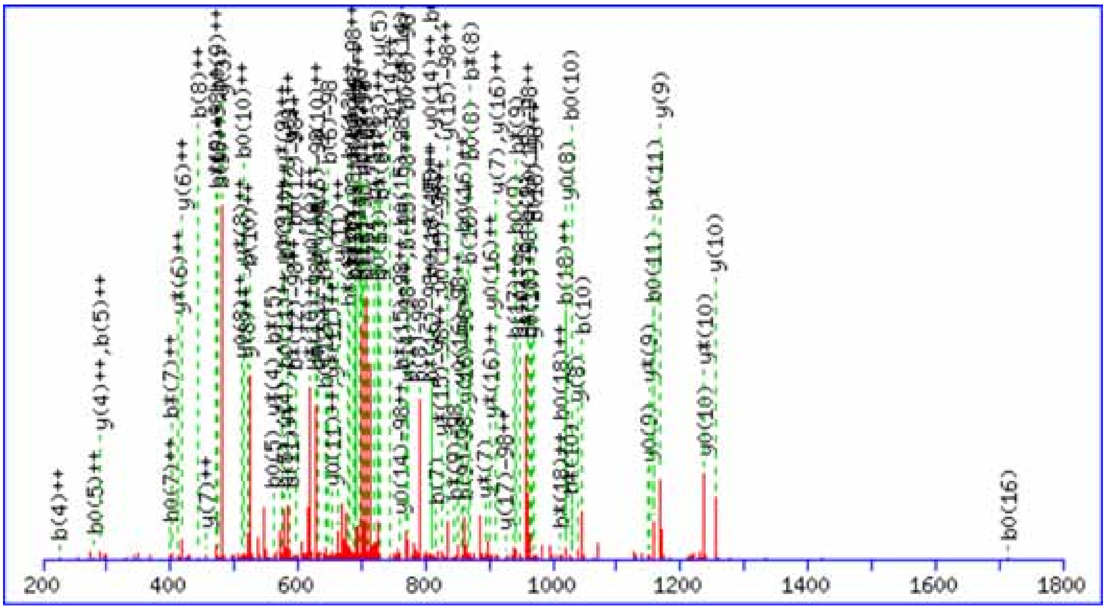
Matched b ions: b(3), b(7), b(9), b(10), b(10)++, b(11), b(12), b(19)++, b(20)++
Matched y ions: y(3), y(4), y(6)++, y(6), y(7), y(8)++, y(8)-98, y(9)++, y(9)-98++, y(9)-98, y(9), y(10), y(10)-98, y(11)++, y(11), y(12)++, y(12)-98++, y(13)++, y(14)-98++, y(15)++, y(20)++
Precursor origin neutral loss: +

Peptide No.407

HVEGQSAAAASEEALFPFCR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of HVEGQSAAAASEEALFPFCR
Found in CE170_MOUSE, Centrosomal protein of 170 kDa OS=Mus musculus GN=Cep170 PE=1 SV=2

Match to Query 6634: 2212.961583 from(738.661137,3+)
Title: Elution from: 39.922 to 39.922 scan no 3655 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2212.9612
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.02

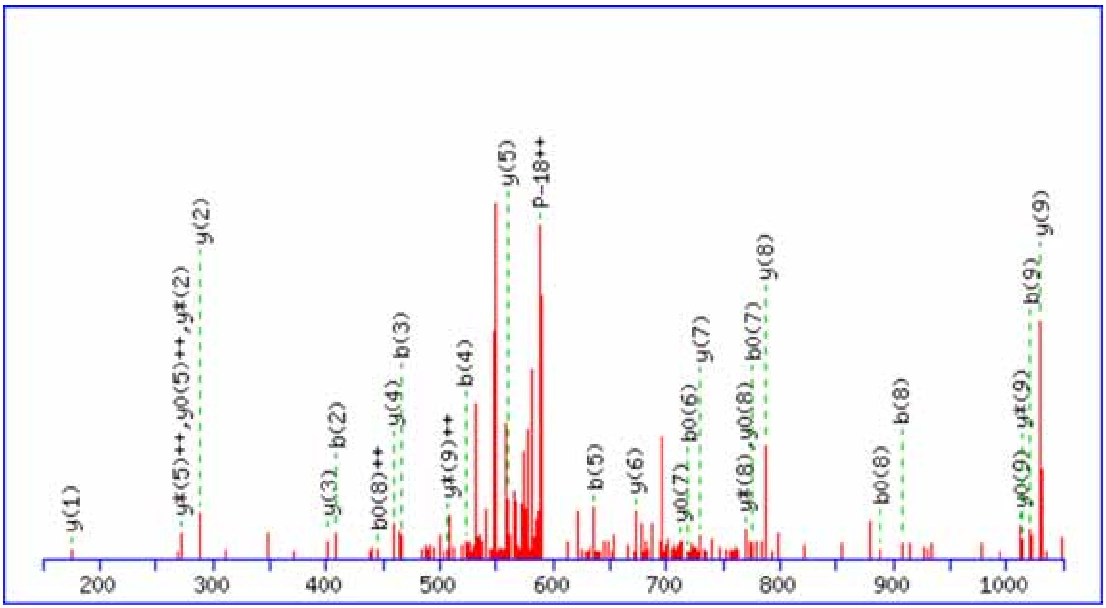
Matched b ions: b(4)++, b(5)++, b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(8)++, b(9)++, b(9)-98, b(9), b(10)++, b(10), b(10)-98++, b(10)-98, b(11)++, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(16)++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(3), y(4)++, y(4), y(5), y(6)++, y(7)++, y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(14)-98++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.408

HYGGLTGLNK
Confirmed sites: @Y:2
Ambiguous sites:

MS/MS Fragmentation of HYGGLTGLNK
Found in PGAM1_MOUSE, Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3

Match to Query 957: 1194.579576 from(598.297064,2+)
Title: Elution from: 27.700 to 27.700 scan no 1843 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1194.5798
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y2 : Phospho (Y)
K10 : Dimethyl (K)
Ions Score: 39 Expect: 0.0026

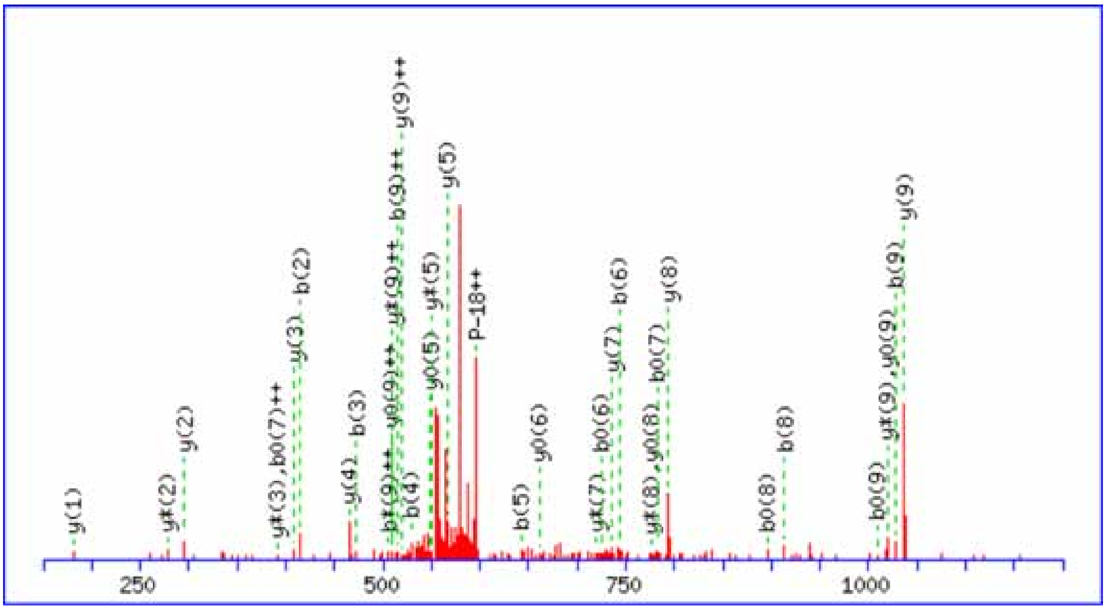
Matched b ions: b(2), b(3), b(4), b(5), b(8), b(9)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)
Precursor origin neutral loss: +

Peptide No.409

HYGGLTGLNK
Confirmed sites: @Y:2
Ambiguous sites:

MS/MS Fragmentation of HYGGLTGLNK
Found in PGAM1_MOUSE, Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3

Match to Query 852: 1206.644090 from(604.329321,2+)
Title: Elution from: 27.611 to 27.611 scan no 1796 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1206.6434
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y2 : Phospho (Y)
K10 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 39 Expect: 0.0048

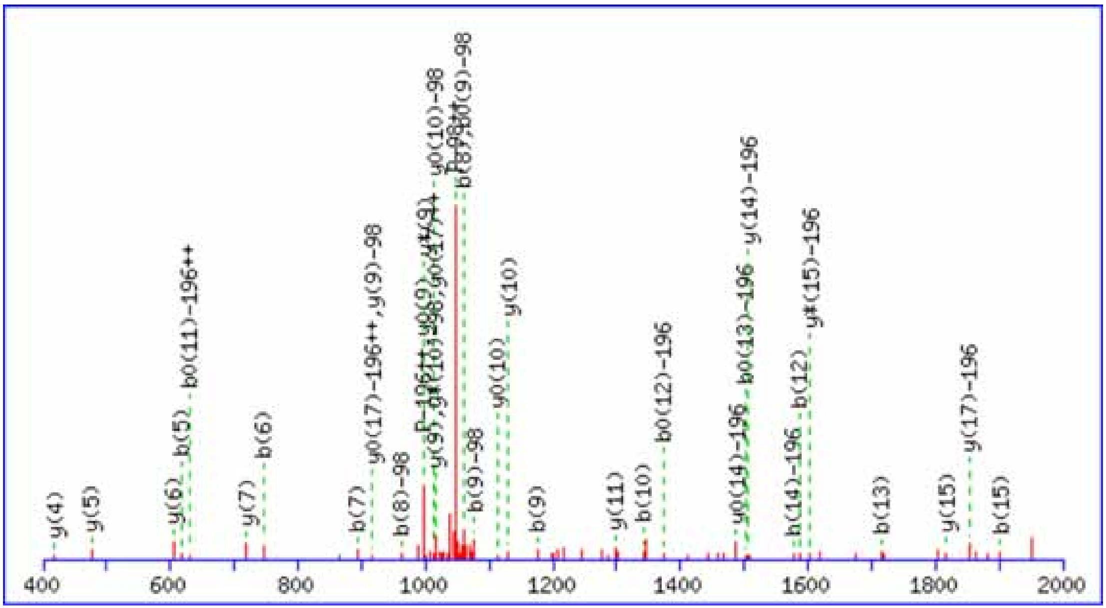
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(8), b(9), b(9)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(7), y(8), y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.410

IACDEEFSDSEDEGEGGR
Confirmed sites: @S:8,@S:10
Ambiguous sites:

MS/MS Fragmentation of IACDEEFSDSEDEGEGGR
Found in HDAC2_MOUSE, Histone deacetylase 2 OS=Mus musculus GN=Hdac2 PE=1 SV=1

Match to Query 6490: 2188.719490 from(1095.367021,2+)
Title: Elution from: 37.154 to 37.154 scan no 3283 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2188.7181
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0016

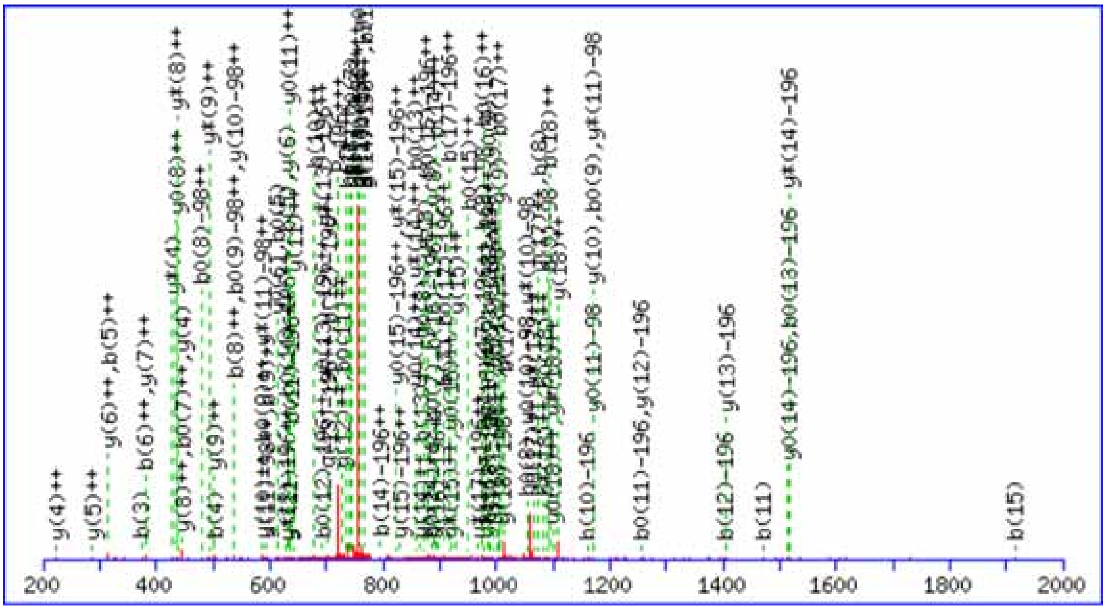
Matched b ions: b(5), b(6), b(7), b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11)-98, b(12)-98, b(12), b(13)-98, b(13), b(14)-196, b(14)-98, b(15)-98, b(15)
Matched y ions: y(4), y(5), y(6), y(7), y(9)-98, y(9), y(10), y(11), y(11)-98, y(12)-98, y(14)-98, y(14)-196, y(15), y(15)-98, y(17)-196, y(17)-98
Precursor origin neutral loss: +

Peptide No.411

IACEEEFSDSDEEGEGGRK
Confirmed sites: @S:8,@S:10
Ambiguous sites:

MS/MS Fragmentation of IACEEEFSDSDEEGEGGRK
Found in HDAC1_MOUSE, Histone deacetylase 1 OS=Mus musculus GN=Hdac1 PE=1 SV=1

Match to Query 6259: 2358.862518 from(787.294782,3+)
Title: Elution from: 33.185 to 33.185 scan no 2539 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2358.8600
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K19 : Dimethyl (K)
Ions Score: 45 **Expect:** 0.00065

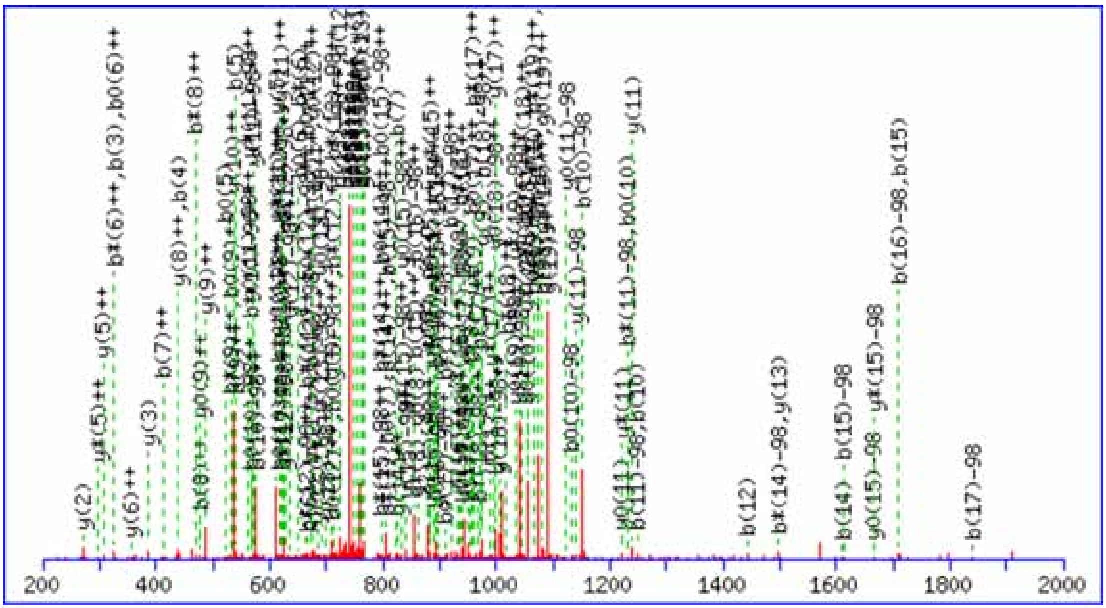
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7), b(8)++, b(8)-98, b(8), b(9)++, b(9)-98, b(10)-98, b(10)-196, b(10)++, b(10)-98++, b(11), b(11)-98, b(11)-196++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(12)-196, b(13)-196++, b(13)-98++, b(13)++, b(14)-98++, b(14)-196++, b(14)++, b(15), b(15)-98++, b(16)-196++, b(16)-98++, b(17)++, b(17)-196++, b(17)-98++, b(18)-98++, b(18)++
Matched y ions: y(4), y(4)++, y(5)++, y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)-98++, y(10), y(10)++, y(11)-98++, y(11)++, y(12)-98++, y(12)-196, y(12)-196++, y(12)++, y(13)-196++, y(13)-196, y(13)-98++, y(14)-196++, y(14)-98++, y(14)++, y(15)-98++, y(15)-196++, y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)-196++, y(17)-98++, y(17)++, y(18)-196++, y(18)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.412

IAIITQREESPPPAVPEIPK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of IAIITQREESPPPAVPEIPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 7695: 2320.245828 from(774.422552,3+)
Title: Elution from: 48.975 to 48.975 scan no 4830 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2320.2443
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
Ions Score: 53 Expect: 0.00028

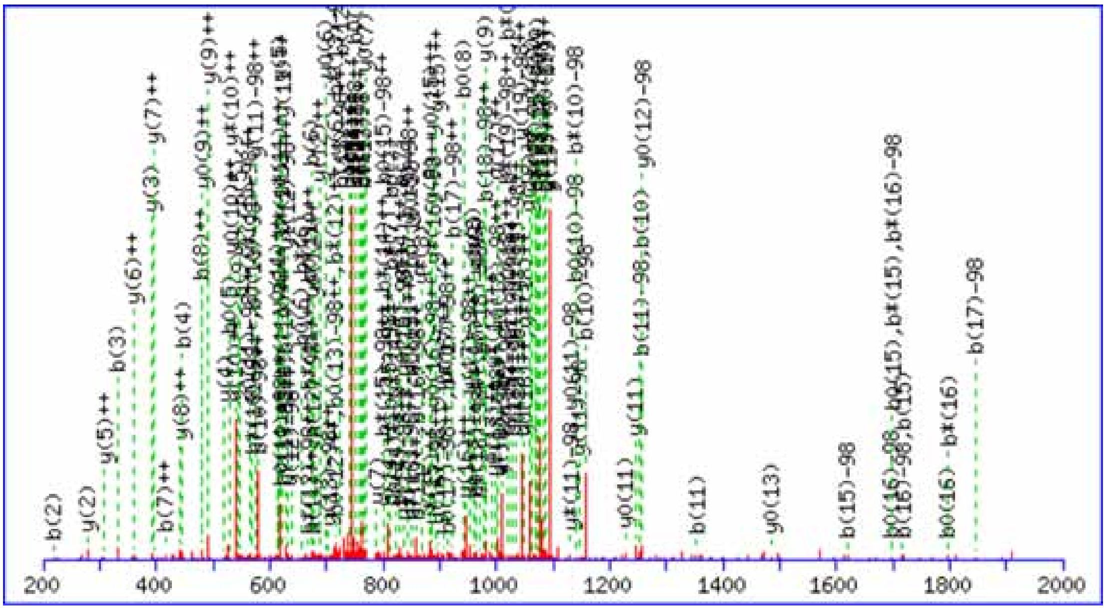
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)-98, b(10), b(10)-98++, b(10)++, b(11)-98, b(11)++, b(11)-98++, b(12), b(12)++, b(12)-98++, b(13)-98++, b(14), b(14)++, b(14)-98++, b(15)++, b(15), b(15)-98++, b(15)-98, b(16)-98++, b(16)-98, b(17)-98, b(17)-98++, b(17)++, b(18)-98++, b(19)++
Matched y ions: y(2), y(3), y(5), y(5)++, y(6), y(6)++, y(8), y(8)++, y(9)++, y(9), y(10)++, y(10), y(11), y(11)-98, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(13), y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.413

IAIITQREESPPPAVPEIPK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of IAIITQREESPPPAVPEIPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 6035: 2332.309488 from(778.443772,3+)
Title: Elution from: 49.134 to 49.134 scan no 4575 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2332.3079
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 44 **Expect:** 0.0014

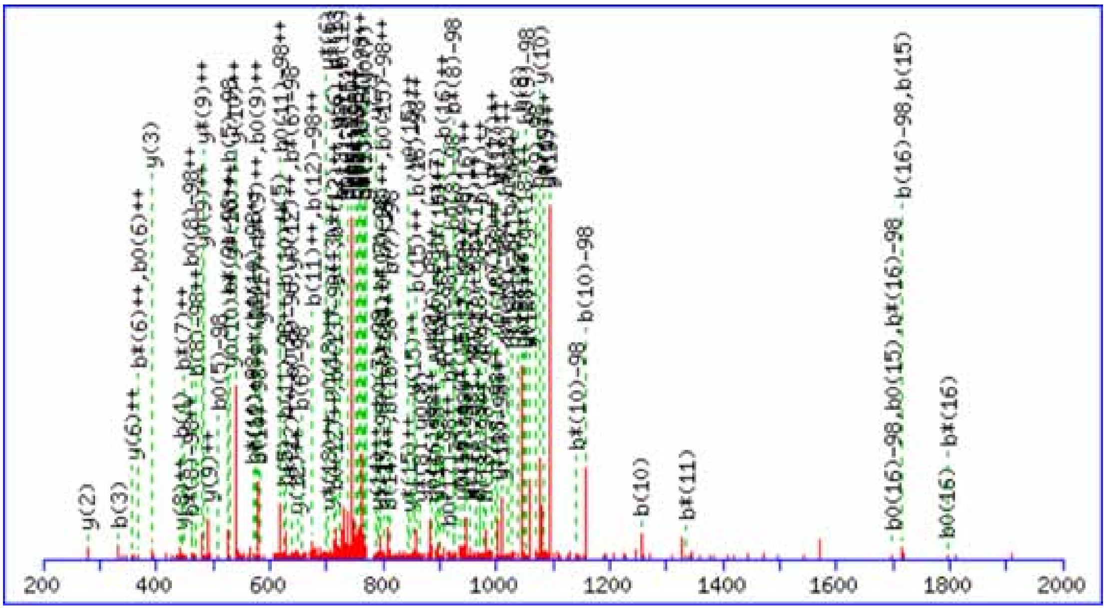
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)-98, b(10)-98++, b(10)++, b(10), b(11)-98++, b(11)-98, b(11), b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15), b(15)-98, b(15)-98++, b(16)-98++, b(16)-98, b(16)++, b(17)-98, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7)++, y(7), y(8), y(8)++, y(9)++, y(9), y(10)++, y(10), y(11), y(11)-98++, y(11)++, y(11)-98, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.414

IAIITQREESPPPAVPEIPK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of IAIITQREESPPPAVPEIPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 6259: 2332.310484 from(778.444104,3+)
Title: Elution from: 49.048 to 49.048 scan no 4569 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2332.3079
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 29 **Expect:** 0.042

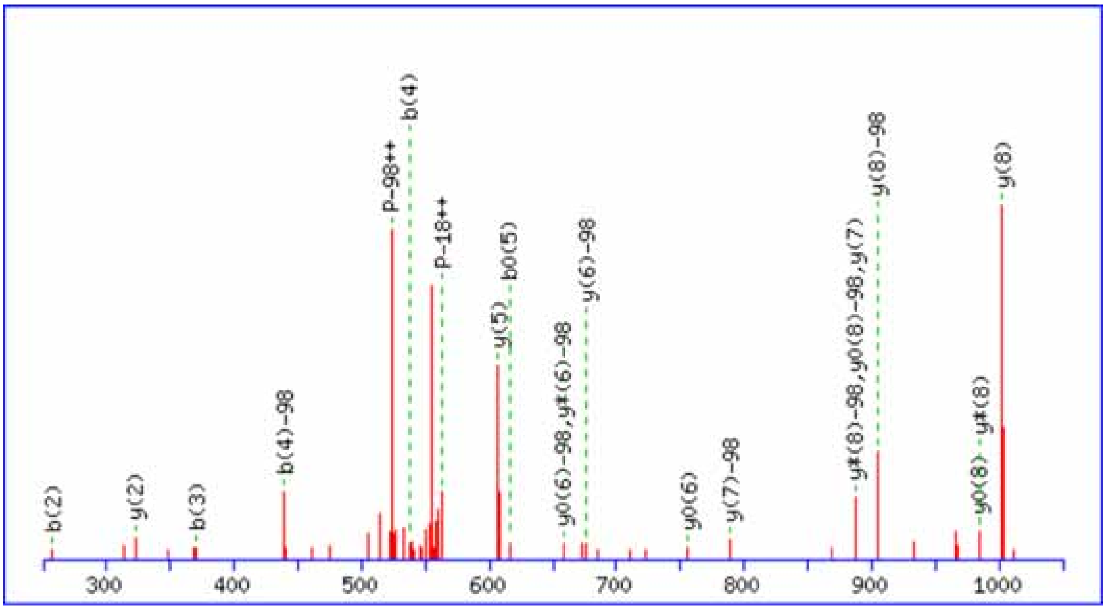
Matched b ions: b(3), b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(8)-98++, b(8), b(9)-98, b(10)-98++, b(10)++, b(10)-98, b(10), b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15), b(15)++, b(16)-98, b(16)-98++, b(16)++, b(17)++, b(18)-98++, b(18)++, b(19)-98++
Matched y ions: y(2), y(3), y(5), y(6)++, y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.415

IDISPSTFR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of IDISPSTFR
Found in TR150_MOUSE, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 977: 1142.538240 from(572.276396,2+)
Title: Elution from: 49.743 to 49.743 scan no 4887 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1142.5373
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 **Expect:** 0.0051

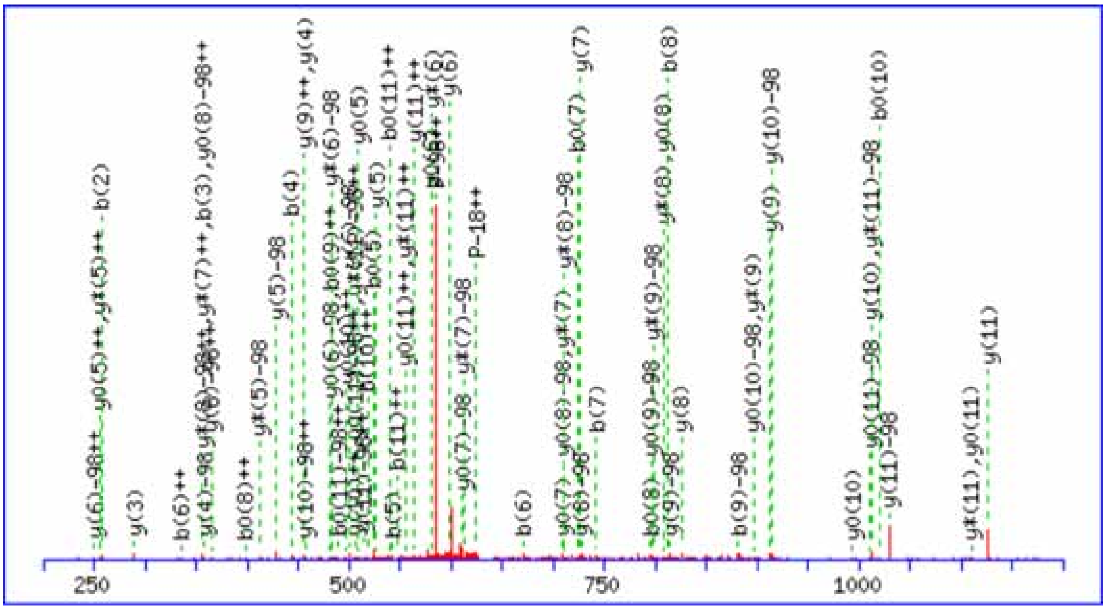
Matched b ions: b(2), b(3), b(4)-98, b(4)
Matched y ions: y(2), y(5), y(6)-98, y(7)-98, y(7), y(8)-98, y(8)
Precursor origin neutral loss: +

Peptide No.416

IDVSVEAASGGK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IDVSVEAASGGK
Found in DLDH_MOUSE, Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2

Match to Query 1321: 1267.607306 from(634.810929,2+)
Title: Elution from: 35.142 to 35.142 scan no 2839 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1267.6061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl (K)
Ions Score: 50 Expect: 0.00043

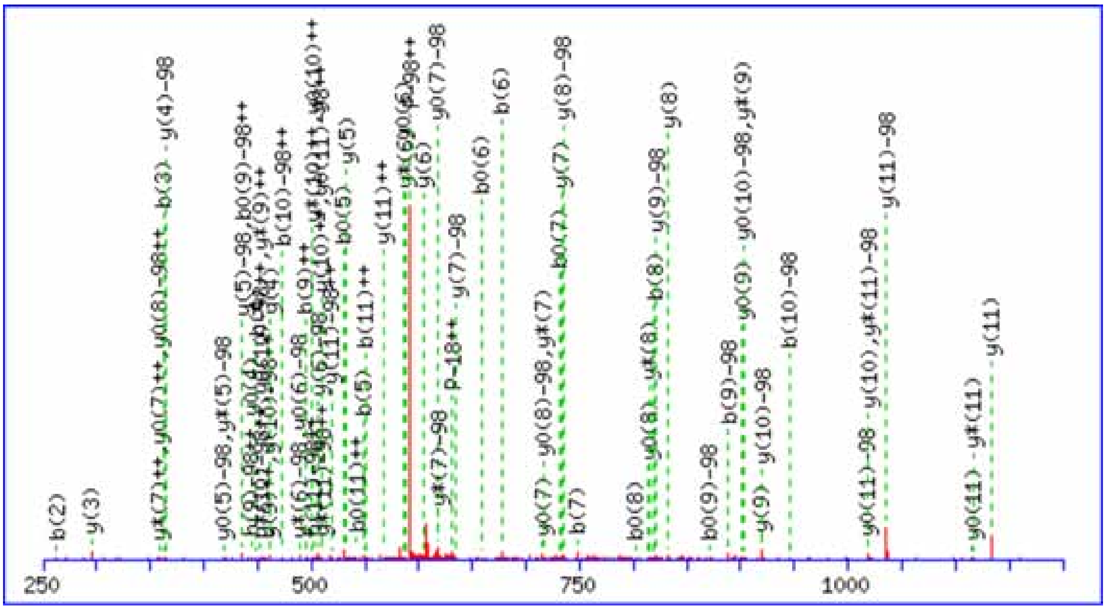
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(6)++, b(7), b(8), b(9)-98, b(10)++, b(11)++
Matched y ions: y(3), y(4)-98, y(4), y(5)-98, y(5), y(6)-98, y(6)-98++, y(6), y(7), y(8)-98, y(8), y(8)-98++, y(9)-98, y(9), y(9)++, y(10)-98, y(10), y(10)-98++, y(10)++, y(11)-98, y(11), y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.417

IDVSVEAASGGK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IDVSVEAASGGK
Found in DLDH_MOUSE, Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2

Match to Query 1208: 1279.669466 from(640.842009,2+)
Title: Elution from: 35.049 to 35.049 scan no 2782 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1279.6697
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 50 Expect: 0.00037

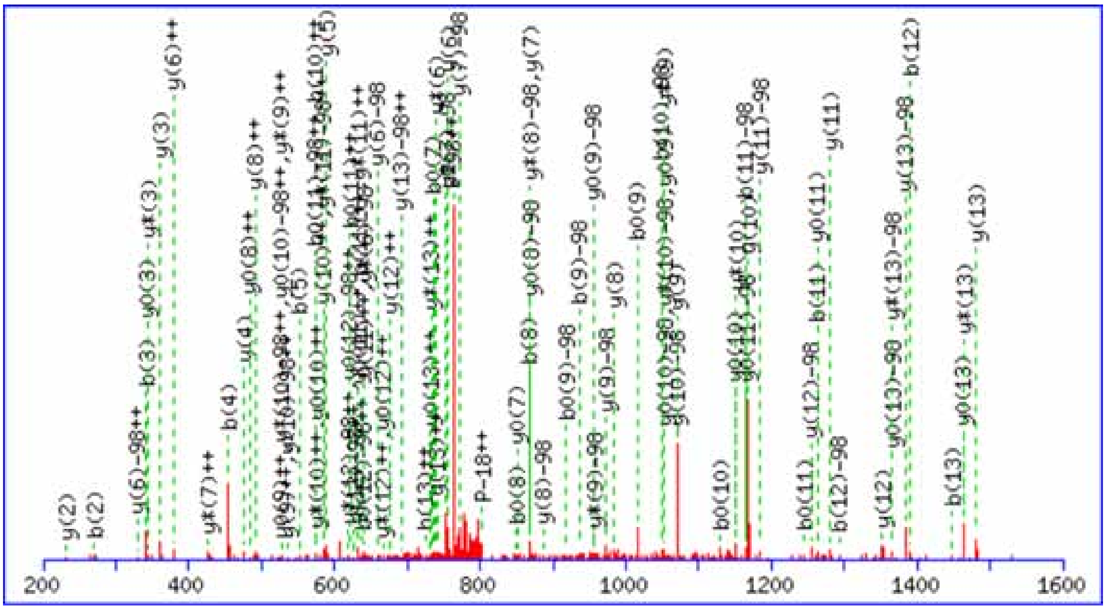
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(9)++, b(9)-98++, b(10)-98, b(10)-98++, b(11)-98++, b(11)++
Matched y ions: y(3), y(4), y(4)-98, y(5)-98, y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(9)-98, y(9), y(9)++, y(10)-98, y(10), y(10)-98++, y(10)++, y(11)-98, y(11), y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.418

IEALPSDISIDEGK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IEALPSDISIDEGK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2160: 1621.787422 from(811.900987,2+)
Title: Elution from: 50.071 to 50.071 scan no 4601 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1621.7851
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
Ions Score: 71 Expect: 4.1e-006

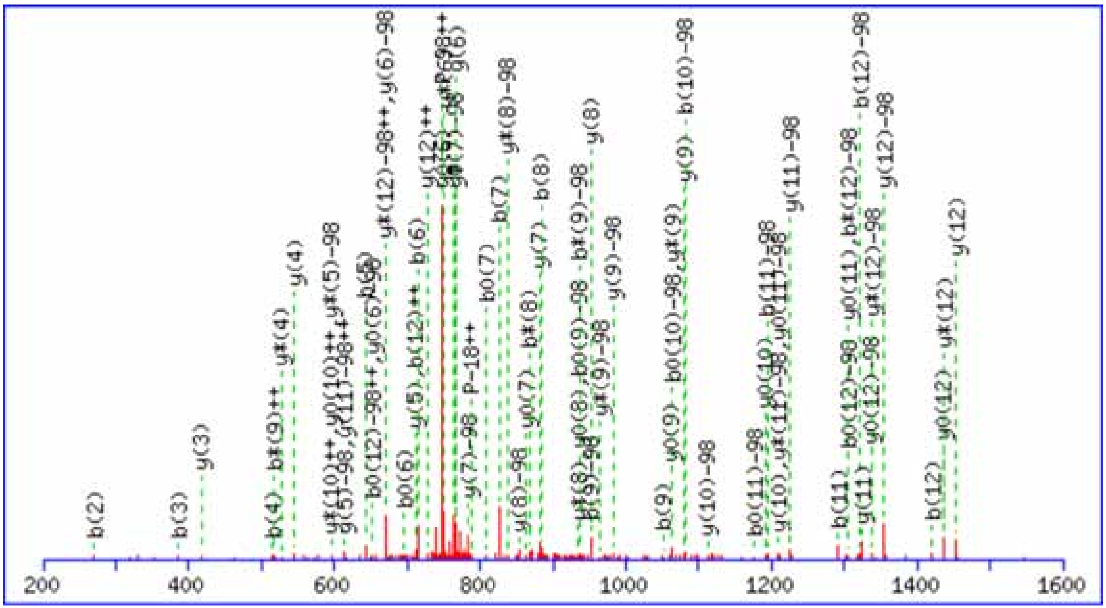
Matched b ions: b(2), b(3), b(4), b(5), b(7), b(8), b(9)-98, b(10)-98, b(10)++, b(11)++, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6)-98++, y(6), y(6)-98, y(7), y(7)-98, y(8)++, y(8), y(8)-98, y(9), y(9)-98, y(9)++, y(10)-98, y(10), y(10)++, y(10)-98++, y(11), y(11)++, y(11)-98, y(12)-98, y(12), y(12)-98++, y(12)++, y(13)-98, y(13), y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.419

IEDEQALGSQLQK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IEDEQALGSQLQK
Found in MYH7_MOUSE, Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1

Match to Query 2998: 1593.767504 from(797.891028,2+)
Title: Elution from: 39.536 to 39.536 scan no 3604 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1593.7651
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
Ions Score: 71 Expect: 4e-006

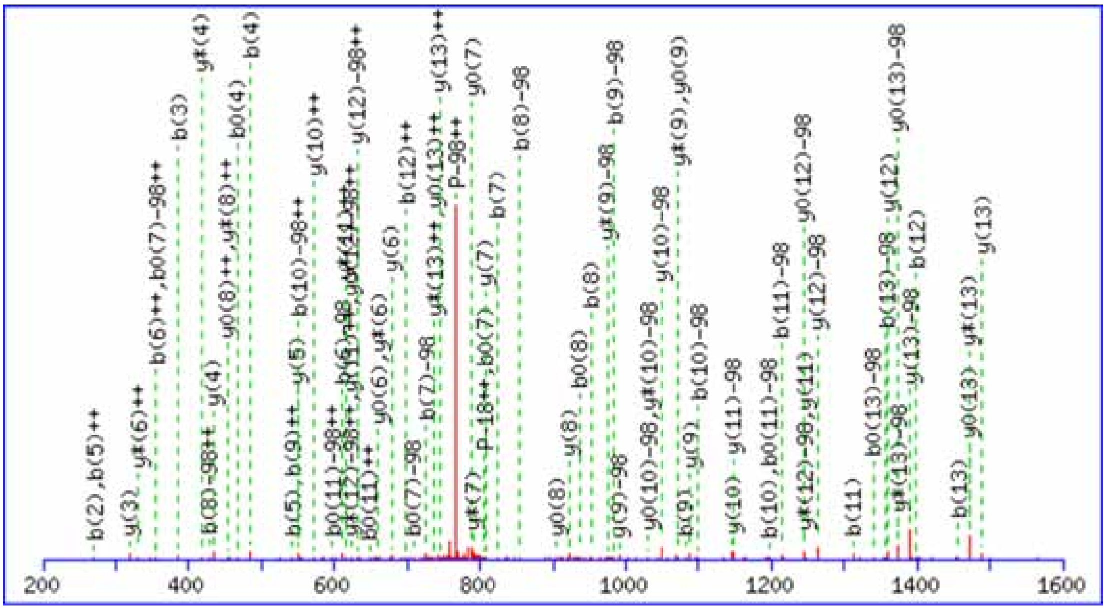
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(9), b(10)-98, b(11)-98, b(11), b(12), b(12)-98, b(12)++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11)-98, y(11), y(11)-98++, y(12)-98, y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.420

IEDVGSDEEDDSGK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of IEDVGSDEEDDSGK
Found in HS90B_MOUSE, Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=2

Match to Query 3314: 1629.630422 from(815.822487,2+)
Title: Elution from: 27.312 to 27.312 scan no 1936 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1629.6295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
Ions Score: 72 Expect: 1e-006

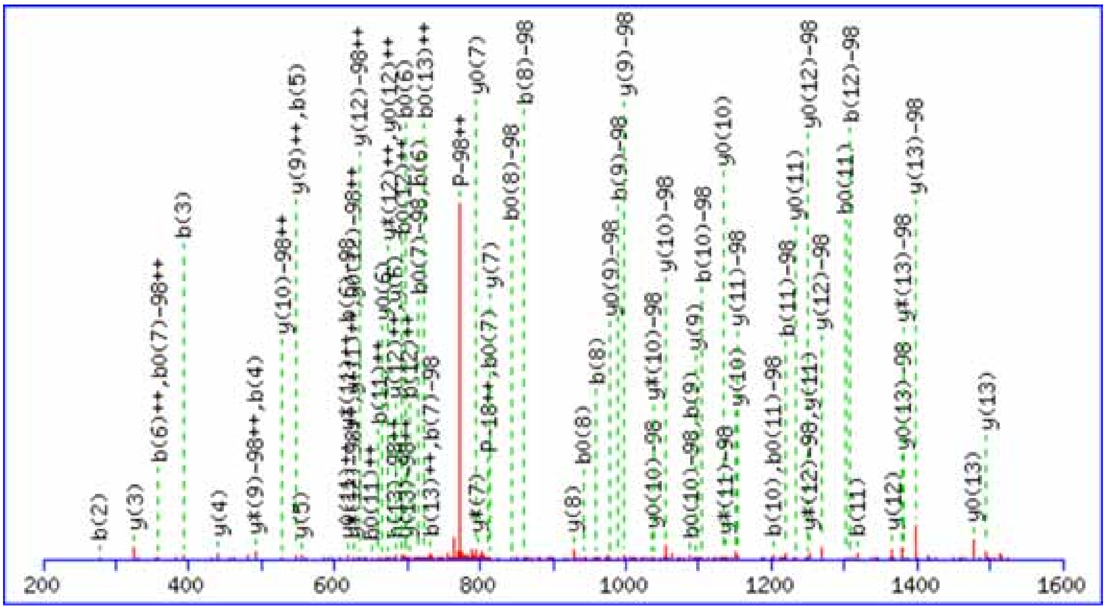
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6)-98, b(6)++, b(7)-98, b(7), b(8)-98++, b(8), b(8)-98, b(9)++, b(9), b(9)-98, b(10), b(10)-98++, b(10)-98, b(11), b(11)-98, b(12), b(12)++, b(13)-98, b(13)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98, y(9), y(10)-98, y(10), y(10)++, y(11)-98, y(11), y(11)++, y(12)-98, y(12), y(12)-98++, y(13)-98, y(13), y(13)++
Precursor origin neutral loss: +

Peptide No.421

IEDVGSDEEDDSGK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of IEDVGSDEEDDSGK
Found in HS90B_MOUSE, Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=2

Match to Query 2637: 1641.693848 from(821.854200,2+)
Title: Elution from: 27.219 to 27.219 scan no 1779 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1641.6931
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 53 Expect: 0.00017

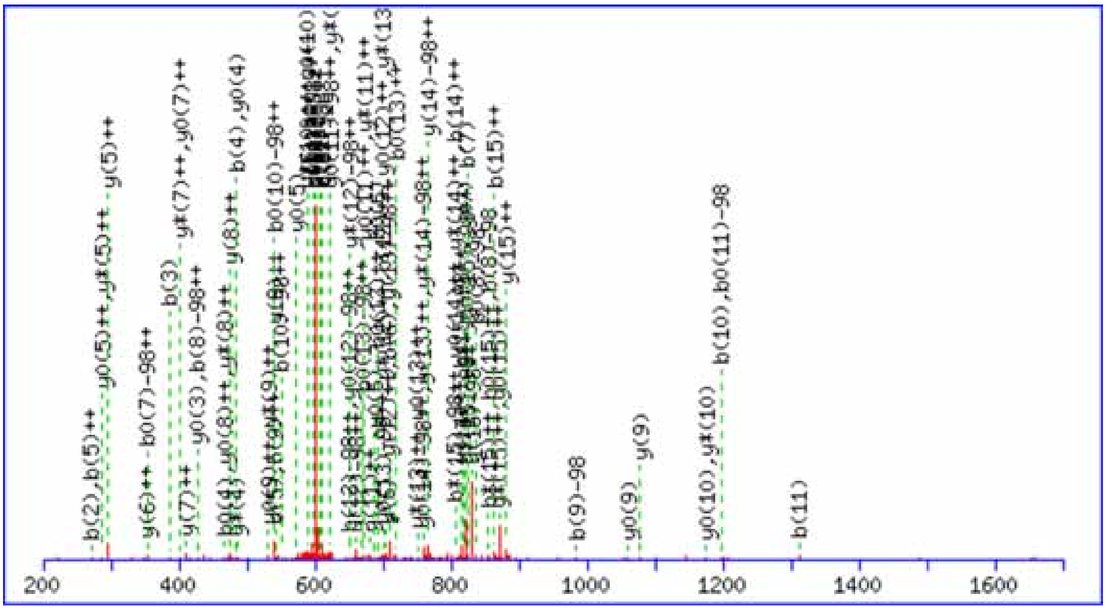
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(6)++, b(6), b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(11)++, b(12)++, b(12)-98, b(13)++, b(13)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9)-98, y(9), y(10)-98, y(10), y(10)-98++, y(11)-98, y(11), y(11)++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13)-98, y(13), y(13)-98++
Precursor origin neutral loss: +

Peptide No.422

IEDVGSDEEDDSGKDK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of IEDVGSDEEDDSGKDK
Found in HS90B_MOUSE, Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=2

Match to Query 5085: 1900.784307 from(634.602045,3+)
Title: Elution from: 25.238 to 25.238 scan no 1663 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1900.7827
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
K16 : Dimethyl (K)
Ions Score: 39 Expect: 0.0046

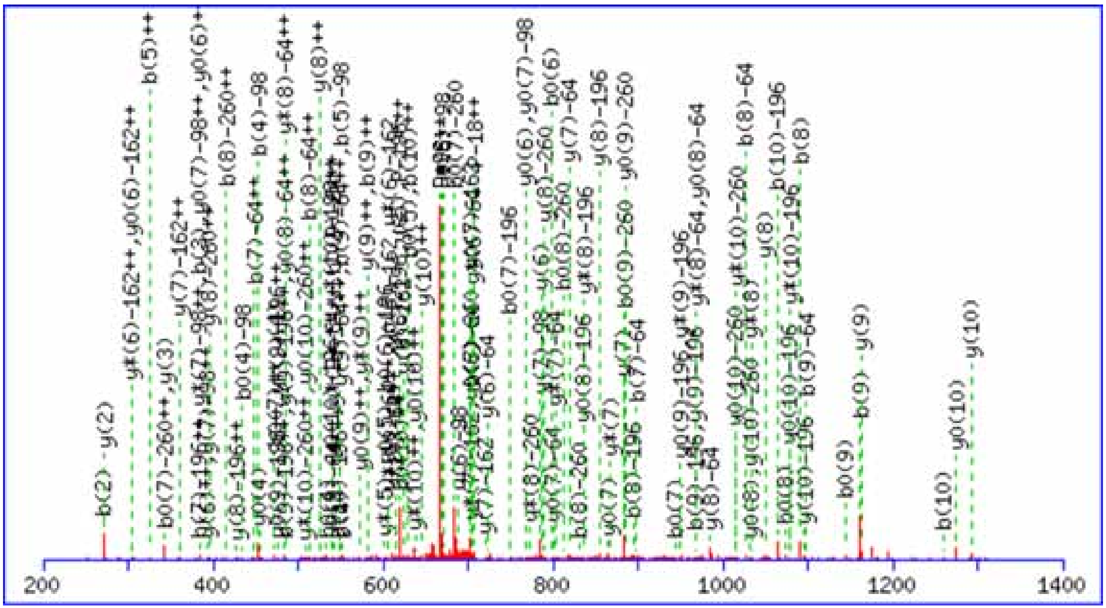
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6), b(6)-98, b(7), b(8)-98++, b(8)-98, b(9)-98, b(9)++, b(10), b(10)-98++, b(10)++, b(11), b(11)-98++, b(12)-98++, b(12)++, b(14)++, b(15)-98++, b(15)++
Matched y ions: y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(9), y(9)++, y(10)++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.423

IELSPSMEAPK
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of IELSPSMEAPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1692: 1432.597696 from(717.306124,2+)
Title: Elution from: 39.717 to 39.717 scan no 3435 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1432.5961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K11 : Dimethyl (K)
Ions Score: 45 Expect: 0.00057

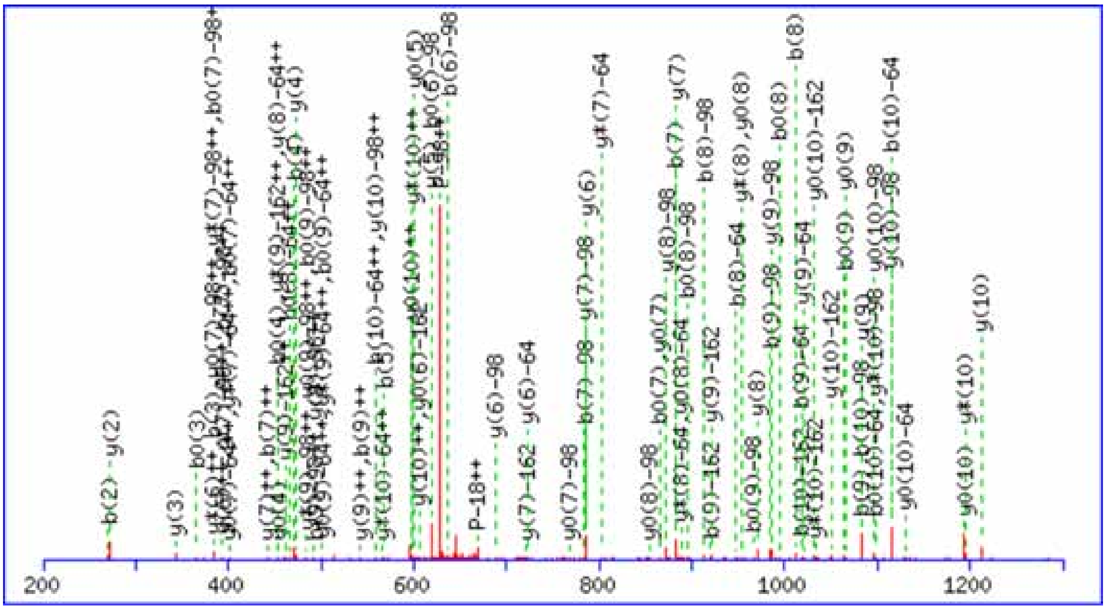
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)++, b(5)-98, b(6)-196, b(6)-98++, b(7)-196++, b(7)-98, b(8), b(8)-98, b(8)-196, b(9)-98++, b(9), b(9)-98, b(9)-196++, b(9)++, b(9)-196, b(10)-98, b(10)-196, b(10), b(10)-98++, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(6)-98, y(7)-98, y(7), y(7)-98++, y(8)-196++, y(8)-196, y(8), y(8)-98, y(8)-98++, y(8)++, y(9)-98++, y(9)-196++, y(9)-98, y(9), y(9)++, y(9)-196, y(10), y(10)-98, y(10)-196, y(10)-196++, y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.424

IELSPSMEAPK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of IELSPSMEAPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1282: 1352.631184 from(677.322868,2+)
Title: Elution from: 36.251 to 36.251 scan no 2942 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1352.6298
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K11 : Dimethyl (K)
Ions Score: 65 Expect: 9e-006

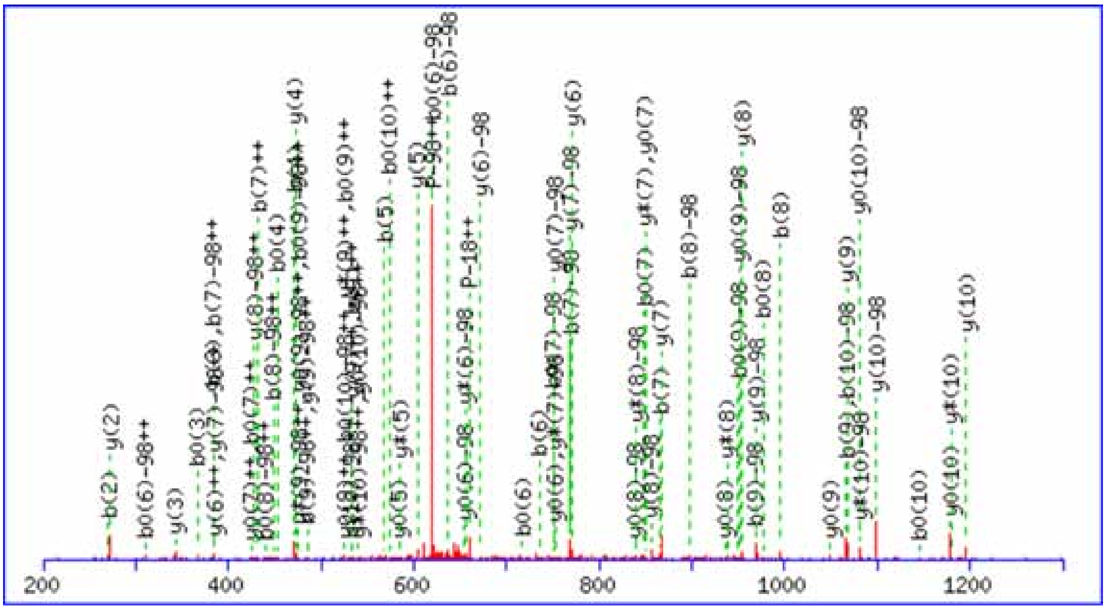
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(7)++, b(7)-98++, b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(9)++, b(9)-98++, b(10)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(6)++, y(7)-98, y(7), y(7)++, y(7)-98++, y(8)-98, y(8), y(9)-98, y(9), y(9)++, y(9)-98++, y(10)-98, y(10), y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.425

IELSPSMEAPK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of IELSPSMEAPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1122: 1336.636058 from(669.325305,2+)
Title: Elution from: 42.487 to 42.487 scan no 3687 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1336.6349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K11 : Dimethyl (K)
Ions Score: 63 Expect: 1.6e-005

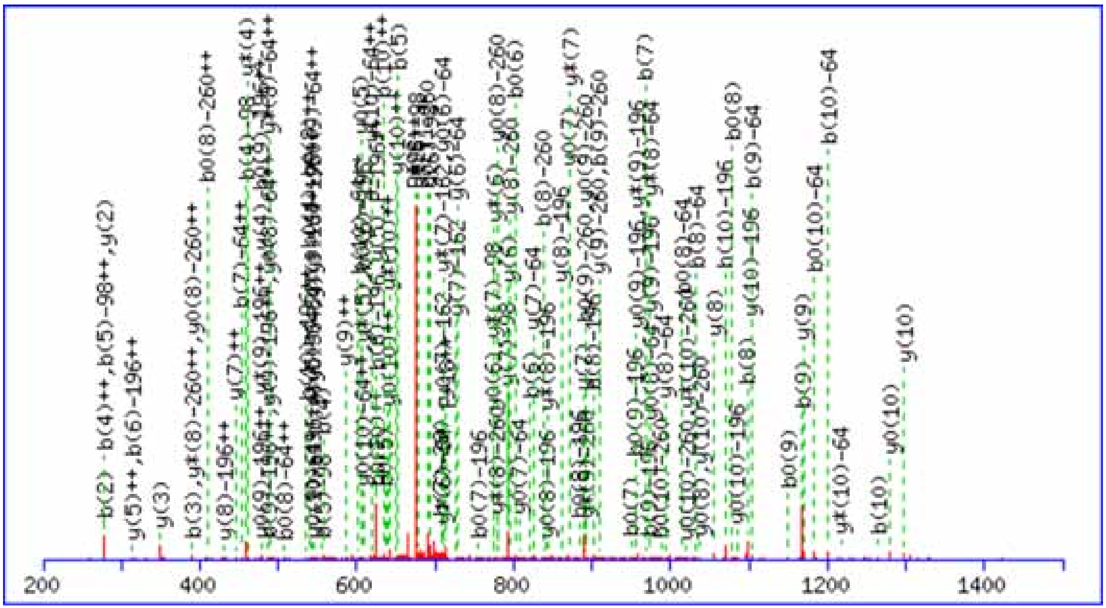
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(6), b(7)-98++, b(7)-98, b(7)++, b(7), b(8), b(8)-98, b(8)-98++, b(9), b(9)-98, b(9)-98++, b(9)++, b(10)-98, b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(6)-98, y(7)-98, y(7), y(7)-98++, y(8)-98, y(8), y(8)-98++, y(9)-98, y(9), y(9)-98++, y(9)++, y(10)-98, y(10)
Precursor origin neutral loss: +

Peptide No.426

IELSPSMEAPK
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of IELSPSMEAPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1956: 1444.661504 from(723.338028,2+)
Title: Elution from: 39.347 to 39.347 scan no 3388 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1444.6598
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K11 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 47 Expect: 0.00086

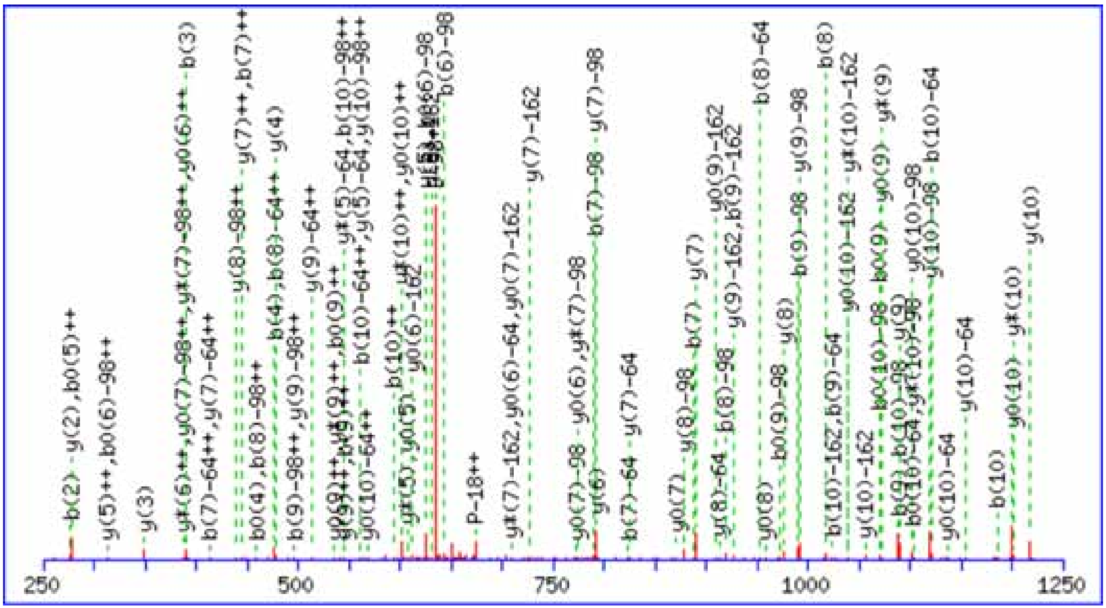
Matched b ions: b(2), b(3), b(4)++, b(4)-98, b(4), b(5)-98++, b(5)-98, b(5), b(6)-196, b(6)-196++, b(6), b(7)-98, b(7), b(8), b(8)-98, b(8)-196, b(9), b(9)-98, b(9)-98++, b(9)-196, b(9)-196++, b(10)-98, b(10)-196, b(10)++, b(10)-196++, b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6)-98, y(6), y(7)-98, y(7), y(7)++, y(8), y(8)-98, y(8)-196, y(8)-196++, y(9)-98, y(9), y(9)-98++, y(9)-196++, y(9)-196, y(9)++, y(10)-98, y(10), y(10)-196, y(10)++
Precursor origin neutral loss: +

Peptide No.427

IELSPSMEAPK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of IELSPSMEAPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1234: 1364.693554 from(683.354053,2+)
Title: Elution from: 36.364 to 36.364 scan no 2862 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1364.6935
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K11 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 67 Expect: 9.4e-006

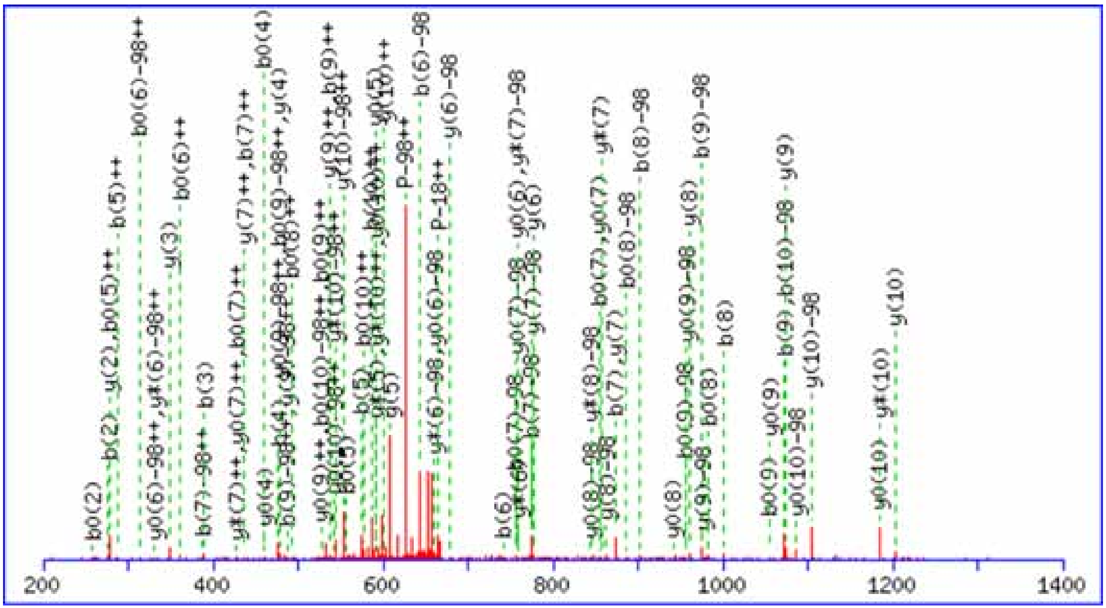
Matched b ions: b(2), b(3), b(4), b(6)-98, b(7)-98, b(7)++, b(7), b(8)-98++, b(8)-98, b(8), b(9)-98, b(9), b(9)-98++, b(9)++, b(10)-98, b(10), b(10)-98++, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7)-98, y(7), y(7)++, y(8)-98, y(8), y(8)-98++, y(9)-98, y(9), y(9)-98++, y(9)++, y(10)-98, y(10), y(10)-98++
Precursor origin neutral loss: +

Peptide No.428

IELSPSMEAPK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of IELSPSMEAPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1162: 1348.698490 from(675.356521,2+)
Title: Elution from: 42.459 to 42.459 scan no 3683 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1348.6985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K11 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 62 Expect: 3e-005

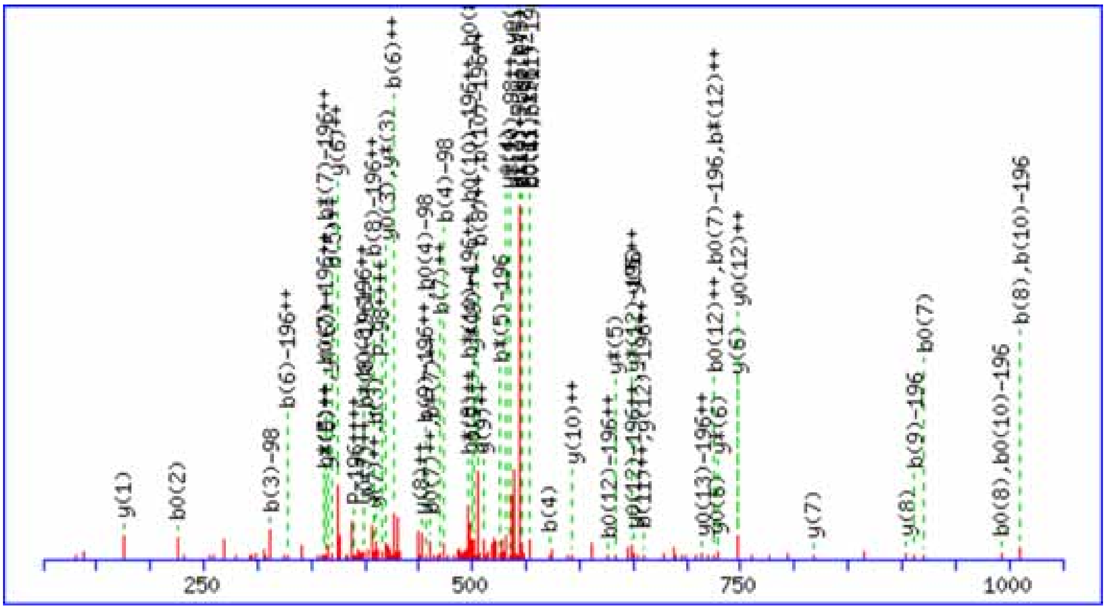
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6)-98, b(6), b(7), b(7)-98, b(7)-98++, b(7)++, b(8)-98, b(8), b(9)-98, b(9), b(9)-98++, b(9)++, b(10)-98, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7)-98, y(7), y(7)++, y(8)-98, y(8), y(9)-98, y(9), y(9)-98++, y(9)++, y(10)-98, y(10), y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.429

IESKSISAPVIFDR
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of IESKSISAPVIFDR
Found in SNX2_MOUSE, Sorting nexin-2 OS=Mus musculus GN=Snx2 PE=1 SV=2

Match to Query 3034: 1754.846856 from(439.718990,4+)
Title: Elution from: 23.401 to 23.401 scan no 1301 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1754.8469
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K4 : Dimethyl:2H(4)13C(2) (K)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.051

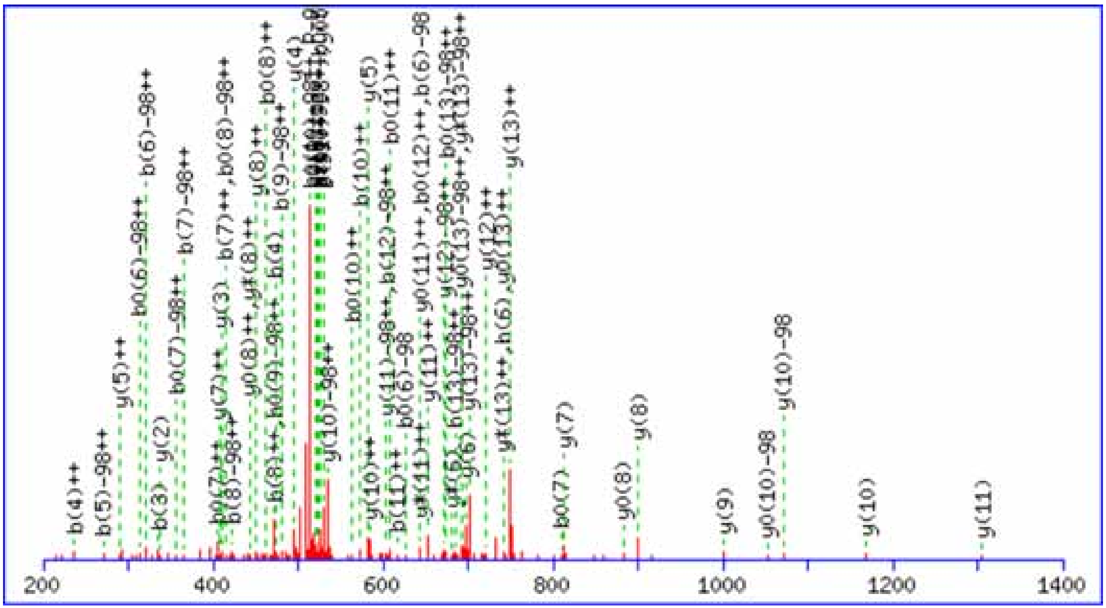
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-196, b(5)++, b(6)++, b(6)-196++, b(6)-98++, b(7)-98++, b(7)++, b(8)++, b(8), b(8)-196++, b(8)-98++, b(9)-98++, b(9)-98, b(9)-196, b(9)++, b(9)-196++, b(10)-196++, b(10)-196, b(10)-98++, b(11)-98++, b(11)++
Matched y ions: y(1), y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)-98++, y(10)++, y(12)-98++, y(12)-196++
Precursor origin neutral loss:

Peptide No.430

IGHHSTSDDSSAYR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of IGHHSTSDDSSAYR
Found in ODBA_MOUSE, 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1

Match to Query 3361: 1639.663590 from(547.561806,3+)
Title: Elution from: 20.427 to 20.427 scan no 1028 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1639.6628
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.0025

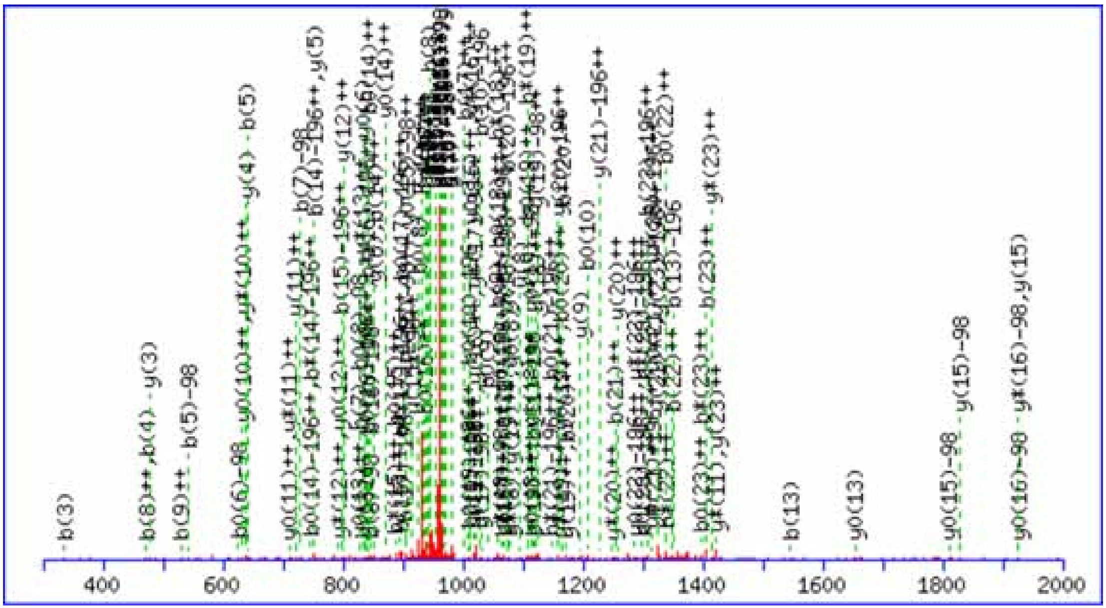
Matched b ions: b(3), b(4)++, b(4), b(5)-98++, b(6)-98++, b(6)-98, b(6), b(7)++, b(7)-98++, b(8)++, b(8)-98++, b(9)++, b(9)-98++, b(10)-98++, b(10)++, b(11)++, b(12)-98++, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(10)-98++, y(10)-98, y(10), y(10)++, y(11), y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.431

IGHHSTSDDSSAYRSVDEVNYWDK
Confirmed sites: @S:5,@S:10
Ambiguous sites:

MS/MS Fragmentation of IGHHSTSDDSSAYRSVDEVNYWDK
Found in ODBA_MOUSE, 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1

Match to Query 6907: 2983.207590 from(995.409806,3+)
Title: Elution from: 42.795 to 42.795 scan no 3731 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2983.2063
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K24 : Dimethyl (K)
Ions Score: 32 Expect: 0.035

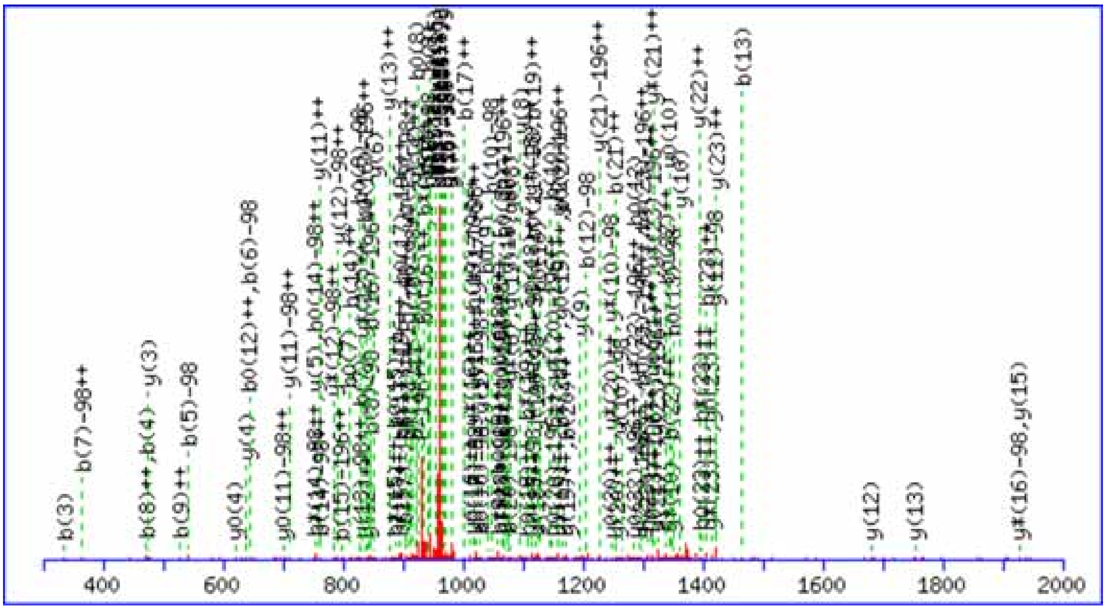
Matched b ions: b(3), b(4), b(5)-98, b(5), b(7)-98, b(7), b(8)++, b(8)-98, b(8), b(9), b(9)++, b(9)-98, b(10)-98, b(10)-196, b(11)-196, b(11)-98++, b(12)-98, b(13), b(13)-196, b(14)-196++, b(14)++, b(15)-196++, b(15)++, b(15)-98++, b(16)-98++, b(16)-196++, b(16)++, b(17)-196++, b(17)-98++, b(17)++, b(18)++, b(18)-196++, b(18)-98++, b(19)++, b(19)-98++, b(19)-196++, b(20)-98++, b(20)++, b(20)-196++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-196++, b(23)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11)++, y(12)++, y(13)++, y(15), y(15)-98++, y(15)++, y(15)-98, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-196++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(21)-196++, y(23)-196++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.432

IGHHSTSDDSSAYRSVDEVNYWDK
Confirmed sites: @S:5,@S:15
Ambiguous sites:

MS/MS Fragmentation of IGHHSTSDDSSAYRSVDEVNYWDK
Found in ODBA_MOUSE, 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1

Match to Query 6655: 2983.208151 from(995.409993,3+)
Title: Elution from: 42.824 to 42.824 scan no 3766 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2983.2063
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K24 : Dimethyl (K)
Ions Score: 37 **Expect:** 0.011

Matched b ions: b(3), b(4), b(5)-98, b(6)-98, b(7)-98++, b(7), b(8)++, b(8)-98, b(8), b(9), b(9)++, b(9)-98, b(10)-98, b(10), b(12)-98, b(13), b(14)++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)-98++, b(16)-196++, b(16)++, b(17)-98, b(17)-196++, b(17)-98++, b(17)++, b(18)++, b(18)-196++, b(18)-98++, b(19)++, b(19)-98++, b(19)-196++, b(20)-98++, b(20)++, b(20)-196++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(23)-196++, b(23)++, b(23)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)++, y(11)-98++, y(11)-98, y(12), y(12)-98++, y(12)++, y(13), y(13)-98++, y(13)++, y(14)++, y(15), y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)-196++, y(20)++, y(21)++, y(21)-196++, y(21)-98++, y(22)-196++, y(22)-98++, y(22)++, y(23)-196++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

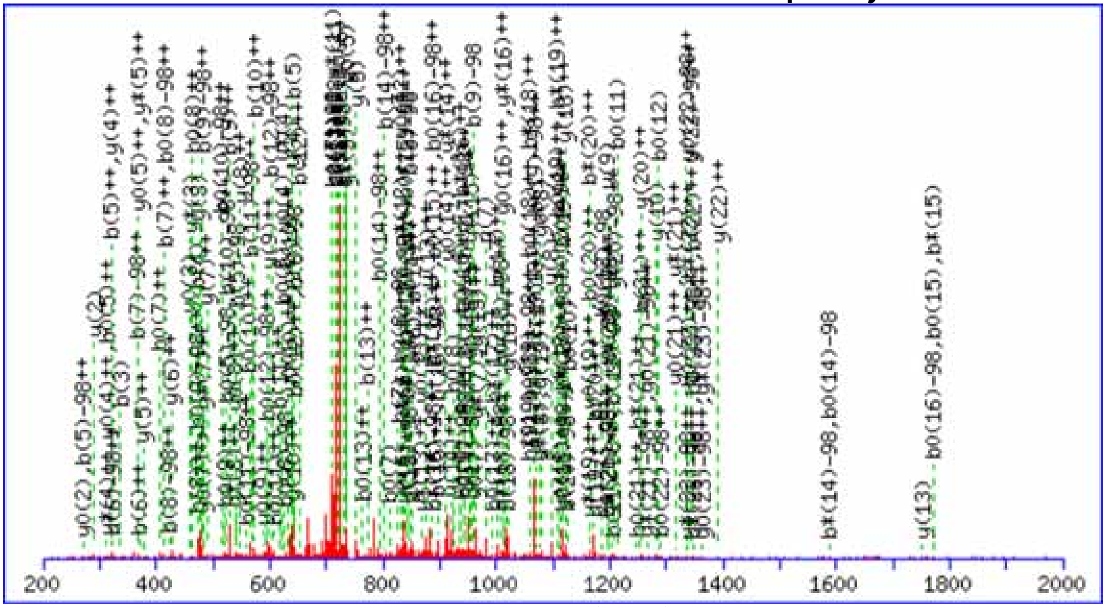
Peptide No.433

IGHHSTSDDSSAYRSVDEVNYWDK
Confirmed sites: @S:5,@Y:13
Ambiguous sites:

MS/MS Fragmentation of IGHHSTSDDSSAYRSVDEVNYWDK
Found in ODBA_MOUSE, 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1

Match to Query 7364: 2983.208508 from(746.809403,4+)

Title: Elution from: 42.833 to 42.833 scan no 3860 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2983.2063
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y13 : Phospho (Y)
K24 : Dimethyl (K)
Ions Score: 48 Expect: 0.001

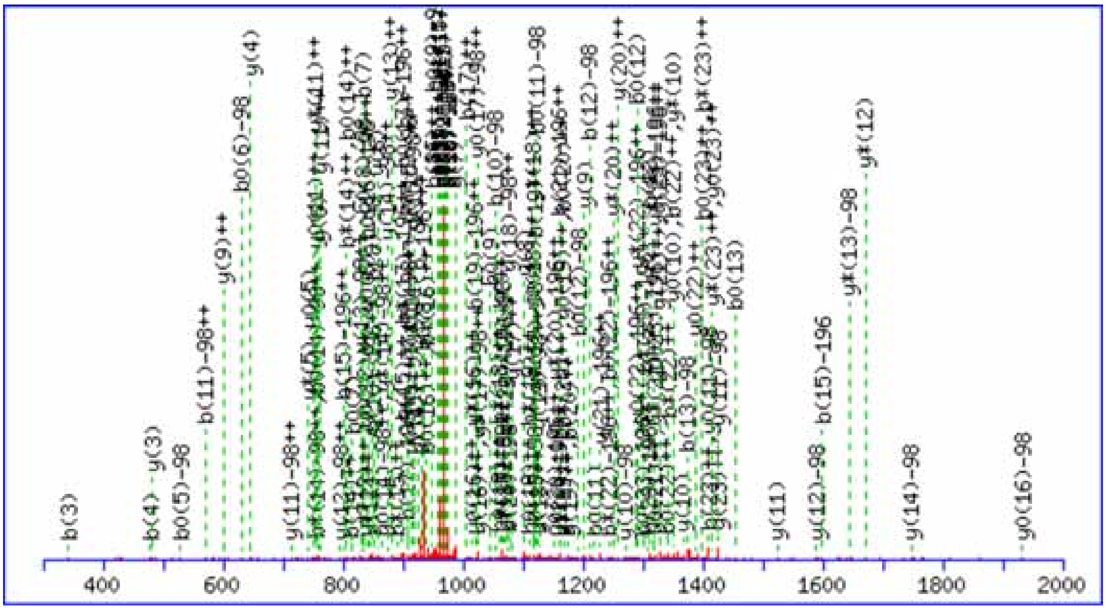
Matched b ions: b(3), b(4), b(5)++, b(5)-98++, b(5)-98, b(5), b(6)++, b(6)-98++, b(6)-98, b(7)-98++, b(7)++, b(7), b(7)-98, b(8)++, b(8)-98++, b(8)-98, b(8), b(9)++, b(9)-98++, b(9), b(9)-98, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(9), y(10), y(10)++, y(11)++, y(12)++, y(13), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(20)-98++, y(22)++, y(22)-98++
Precursor origin neutral loss: +

Peptide No.434

IGHHSTSDDSSAYRSVDEVNYWDK
Confirmed sites: @S:5,@S:15
Ambiguous sites:

MS/MS Fragmentation of IGHHSTSDDSSAYRSVDEVNYWDK
Found in ODBA_MOUSE, 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1

Match to Query 8844: 2995.270776 from(999.430868,3+)
Title: Elution from: 42.975 to 42.975 scan no 4046 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2995.2699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K24 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 40 Expect: 0.0071

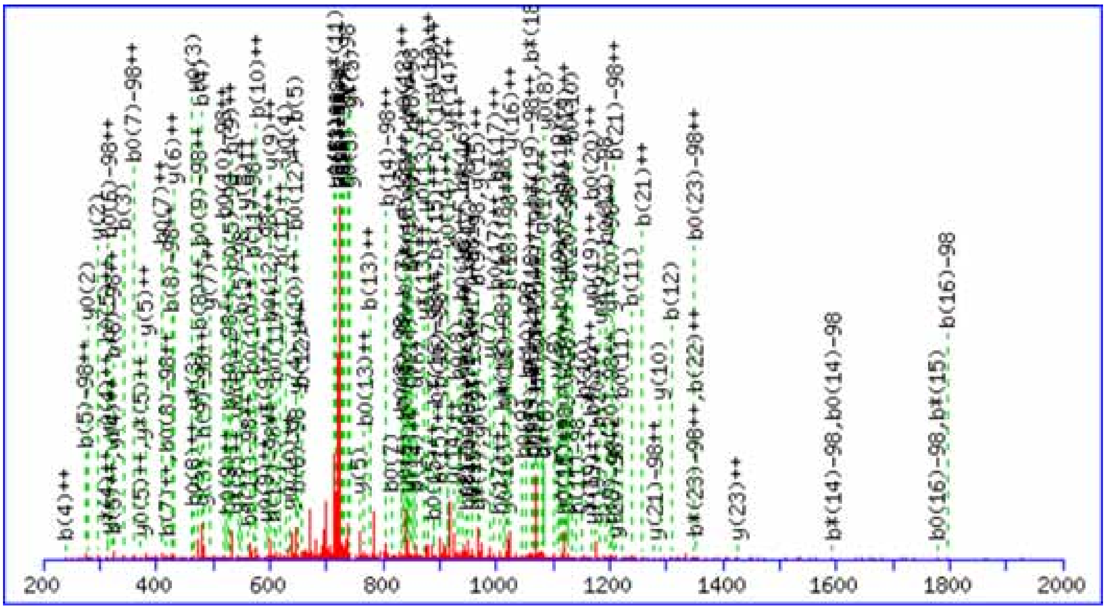
Matched b ions: b(3), b(4), b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(11)-98++, b(12)-98, b(12), b(13)-98, b(14)++, b(15)-98++, b(15)-196, b(15)++, b(15)-196++, b(16)-196++, b(16)-98++, b(16)++, b(17)-98++, b(17)-196++, b(17)++, b(18)++, b(18)-196++, b(18)-98++, b(19)-98++, b(19)++, b(19)-196++, b(20)-98++, b(20)++, b(20)-196++, b(21)-196++, b(22)++, b(22)-98++, b(23)++, b(23)-196++, b(23)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10)-98, y(10), y(11)-98++, y(11), y(11)++, y(11)-98, y(12)-98++, y(12)-98, y(12)++, y(13)-98++, y(13)++, y(14)-98, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-196++, y(20)-98++, y(20)++, y(21)-196++, y(21)++, y(21)-98++, y(23)-196++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.435

IGHHSTSDDSSAYRSVDEVNYWDK
Confirmed sites: @S:5,@Y:13
Ambiguous sites:

MS/MS Fragmentation of IGHHSTSDDSSAYRSVDEVNYWDK
Found in ODBA_MOUSE, 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1

Match to Query 6921: 2995.271828 from(749.825233,4+)
Title: Elution from: 42.761 to 42.761 scan no 3726 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2995.2699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y13 : Phospho (Y)
K24 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 50 Expect: 0.00078

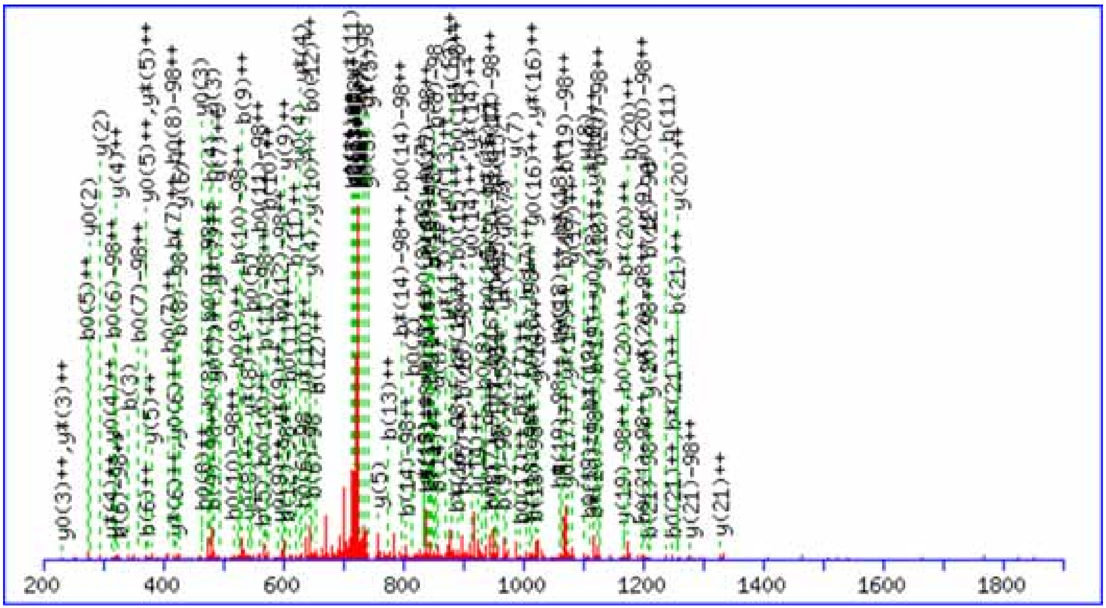
Matched b ions: b(3), b(4)++, b(4), b(5)-98++, b(5)++, b(5)-98, b(5), b(6)-98++, b(6)-98, b(7)++, b(7)-98, b(7), b(8)-98++, b(8)++, b(8)-98, b(8), b(9)-98, b(9)++, b(9)-98++, b(9), b(10)++, b(10)-98++, b(10)-98, b(10), b(11), b(11)++, b(11)-98++, b(11)-98, b(12)-98++, b(12)++, b(12), b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(9), y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)-98++, y(21)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.436

IGHHSTSDDSSAYRSVDEVNYWDK
Confirmed sites: @T:6,@Y:13
Ambiguous sites:

MS/MS Fragmentation of IGHHSTSDDSSAYRSVDEVNYWDK
Found in ODBA_MOUSE, 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1

Match to Query 6667: 2995.271564 from(749.825167,4+)
Title: Elution from: 42.740 to 42.740 scan no 3755 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2995.2699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y13 : Phospho (Y)
K24 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 59 Expect: 0.0001

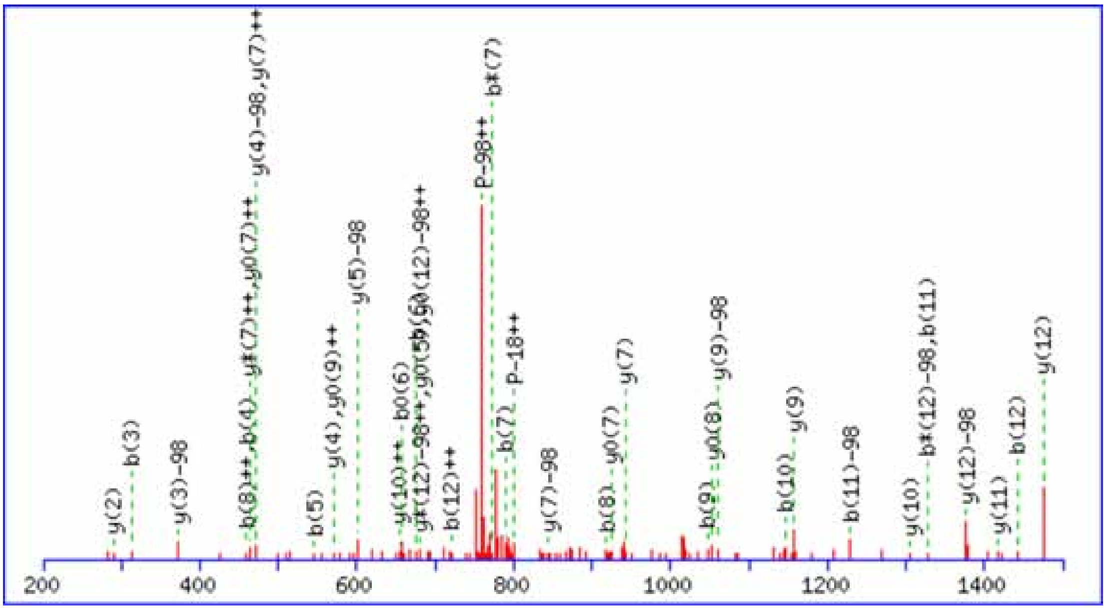
Matched b ions: b(3), b(4), b(5), b(6)-98++, b(6)++, b(6)-98, b(7)-98, b(7)++, b(7), b(8)-98++, b(8)++, b(8)-98, b(8), b(9)++, b(9)-98, b(9)-98++, b(9), b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(11), b(12)-98++, b(12)++, b(12)-98, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.437

IGIFSENEEVTDR
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of IGIFSENEEVTDR
Found in AT2A1_MOUSE, Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Mus musculus GN=Atp2a1 PE=2 SV=1

Match to Query 3197: 1615.715840 from(808.865196,2+)
Title: Elution from: 49.509 to 49.509 scan no 4857 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1615.7131
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.0039

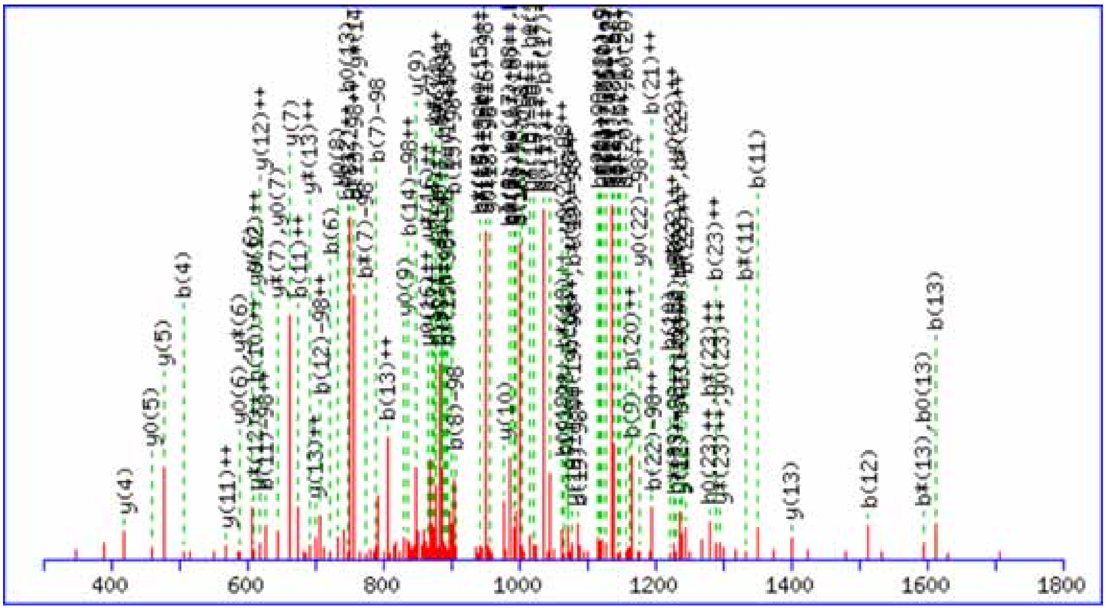
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)++, b(8), b(9), b(10), b(11)-98, b(11), b(12), b(12)++
Matched y ions: y(2), y(3)-98, y(4)-98, y(4), y(5)-98, y(7)++, y(7)-98, y(7), y(9), y(9)-98, y(10), y(10)++, y(11), y(12)-98, y(12)
Precursor origin neutral loss: +

Peptide No.438

IHNLSESDCGEYVCEVSGEGGTSK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of IHNLSESDCGEYVCEVSGEGGTSK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 8226: 2749.125546 from(917.382458,3+)
Title: Elution from: 42.999 to 42.999 scan no 4058 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2749.1248
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K24 : Dimethyl (K)
Ions Score: 77 Expect: 1e-006

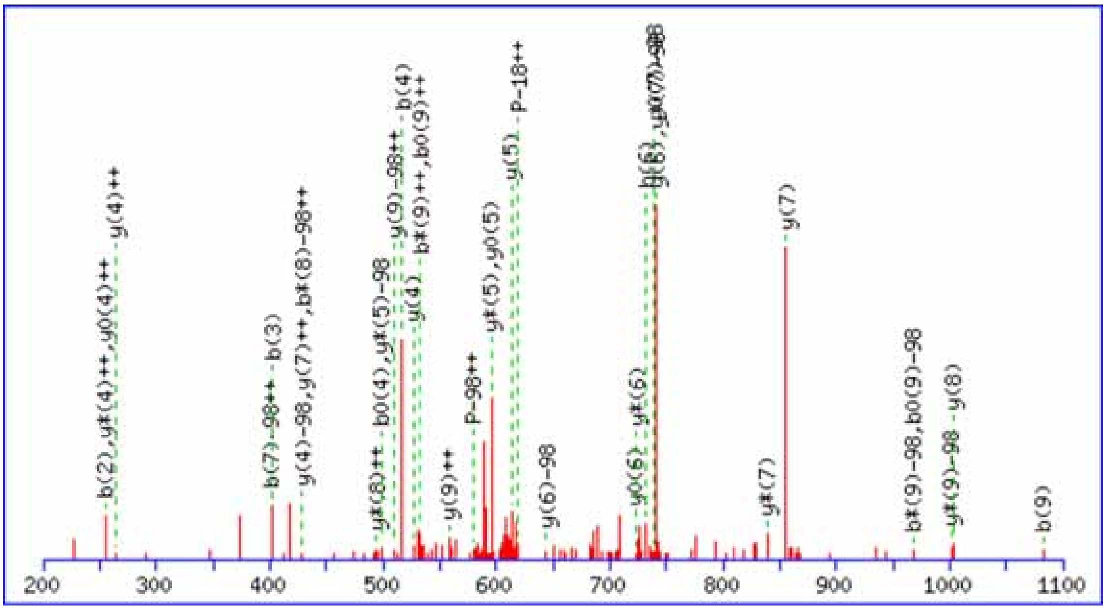
Matched b ions: b(4), b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10)++, b(10)-98, b(10), b(11), b(11)-98++, b(11)++, b(12), b(12)++, b(12)-98++, b(13), b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(16)++, y(18)++, y(19)++, y(20)-98++, y(20)++, y(22)++
Precursor origin neutral loss: +

Peptide No.439

ILFDQSSAIK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of ILFDQSSAIK
Found in DSE_MOUSE, Dermatan-sulfate epimerase OS=Mus musculus GN=Dse PE=2 SV=1

Match to Query 1218: 1256.638744 from(629.326648,2+)
Title: Elution from: 61.410 to 61.410 scan no 5842 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1256.6417
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K10 : Dimethyl (K)
Ions Score: 29 **Expect:** 0.045

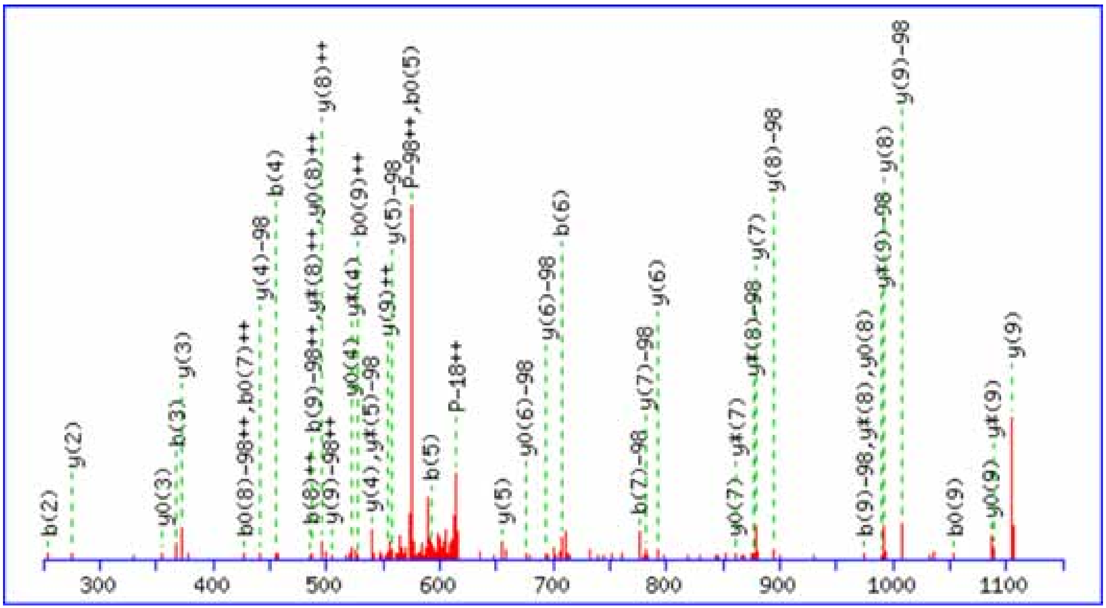
Matched b ions: b(2), b(3), b(4), b(6), b(7)-98++, b(9)
Matched y ions: y(4), y(4)++, y(4)-98, y(5), y(6), y(6)-98, y(7), y(7)++, y(8), y(9)-98++, y(9)++
Precursor origin neutral loss:

Peptide No.440

ILLSHDSPTR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **ILLSHDSPTR**
Found in **ABRA_MOUSE**, Actin-binding Rho-activating protein OS=Mus musculus GN=Abra PE=1 SV=1

Match to Query 1084: 1245.613036 from(623.813794,2+)
Title: Elution from: 27.406 to 27.406 scan no 1804 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1245.6118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 **Expect:** 9.3e-005

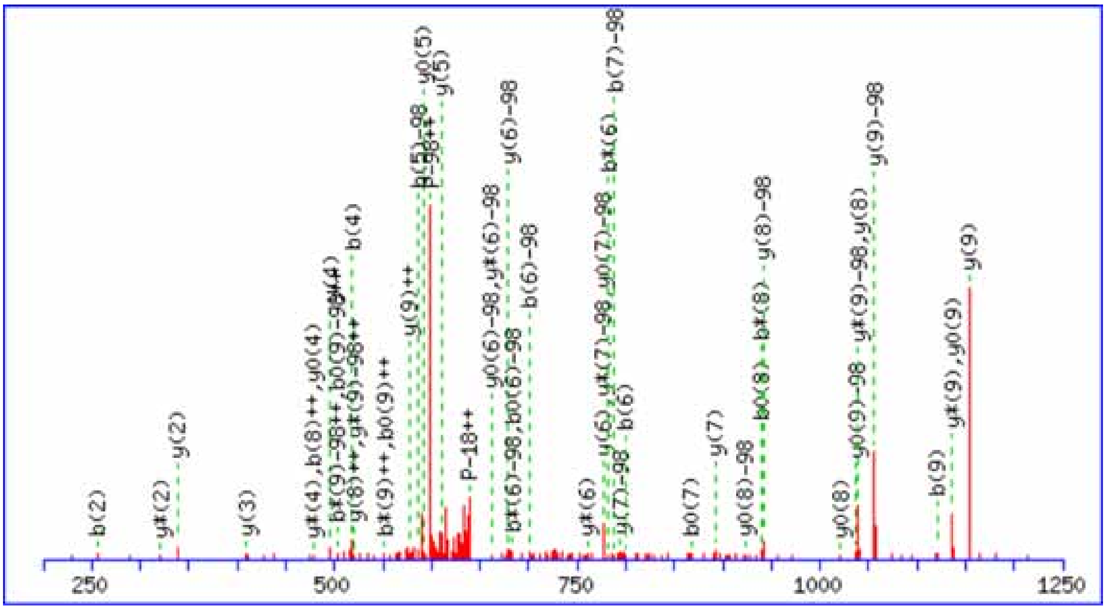
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)-98, b(8)++, b(9)-98, b(9)-98++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)++, y(8)-98, y(8), y(9)-98, y(9), y(9)++, y(9)-98++
Precursor origin neutral loss: +

Peptide No.441

INFDSNSAYR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of INFDSNSAYR
Found in SUCB1_MOUSE, Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Sucla2 PE=1 SV=2

Match to Query 1249: 1293.540118 from(647.777335,2+)
Title: Elution from: 40.422 to 40.422 scan no 3467 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1293.5390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0075

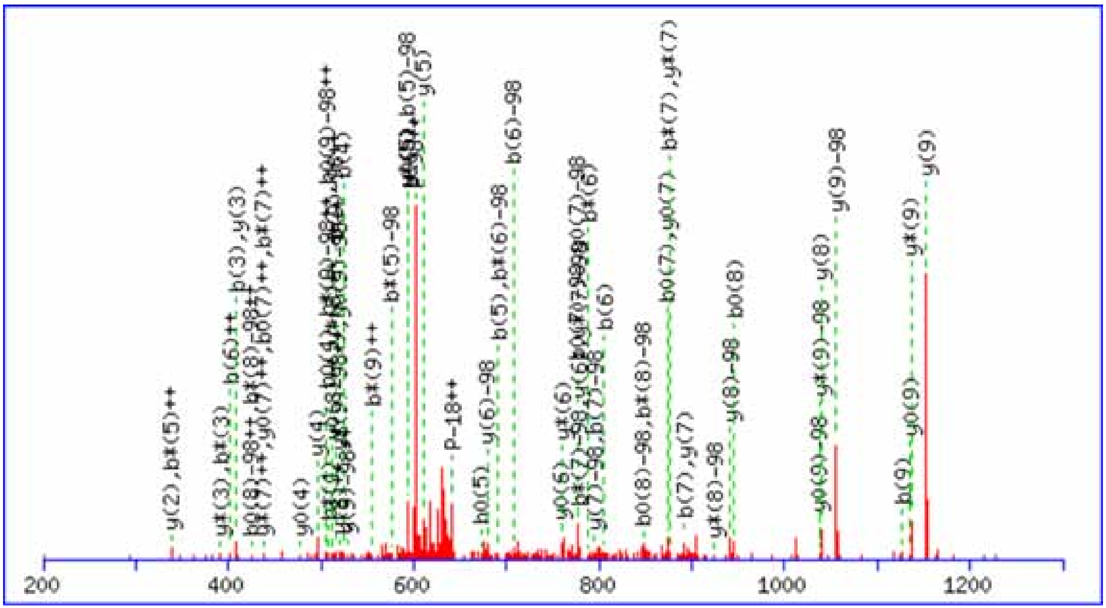
Matched b ions: b(2), b(4), b(5)-98, b(6)-98, b(6), b(7)-98, b(8)++, b(9)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7)-98, y(7), y(8)-98, y(8), y(8)++, y(9)-98, y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.442

INFDSNSAYR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of INFDSNSAYR
Found in SUCB1_MOUSE, Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Sucla2 PE=1 SV=2

Match to Query 1457: 1299.571674 from(650.793113,2+)
Title: Elution from: 40.467 to 40.467 scan no 3569 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1299.5709
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0052

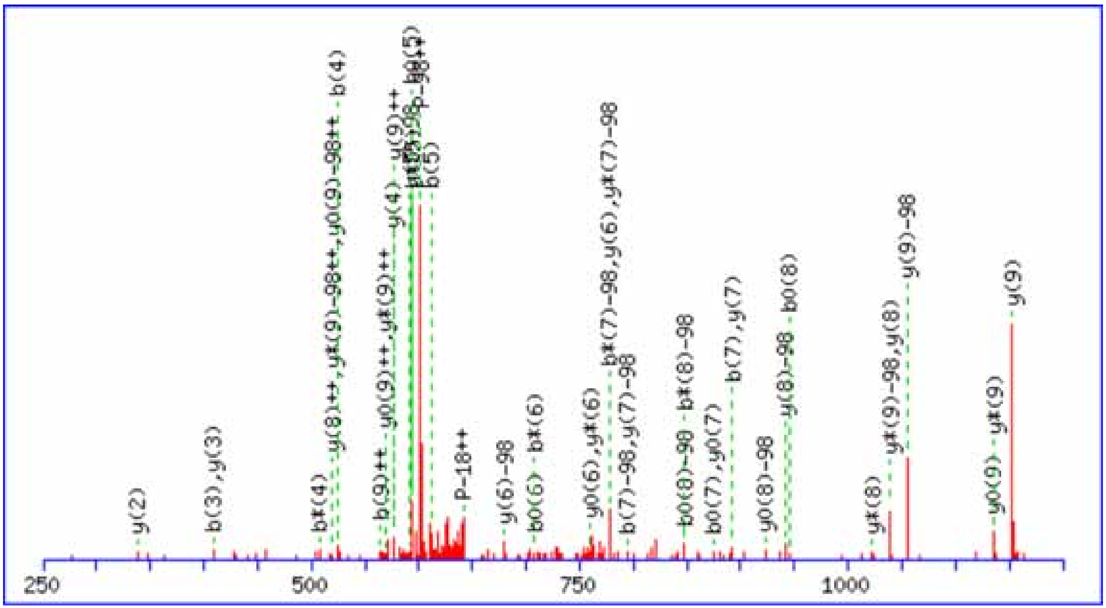
Matched b ions: b(3), b(4), b(5)-98, b(5), b(6)++, b(6)-98, b(6), b(7), b(7)-98, b(9), b(9)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8)-98, y(8), y(8)++, y(9)-98, y(9), y(9)-98++
Precursor origin neutral loss: +

Peptide No.443

INFDSNSAYR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of INFDSNSAYR
Found in SUCB1_MOUSE, Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Sucla2 PE=1 SV=2

Match to Query 1266: 1299.571728 from(650.793140,2+)
Title: Elution from: 40.429 to 40.429 scan no 3468 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1299.5709
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.019

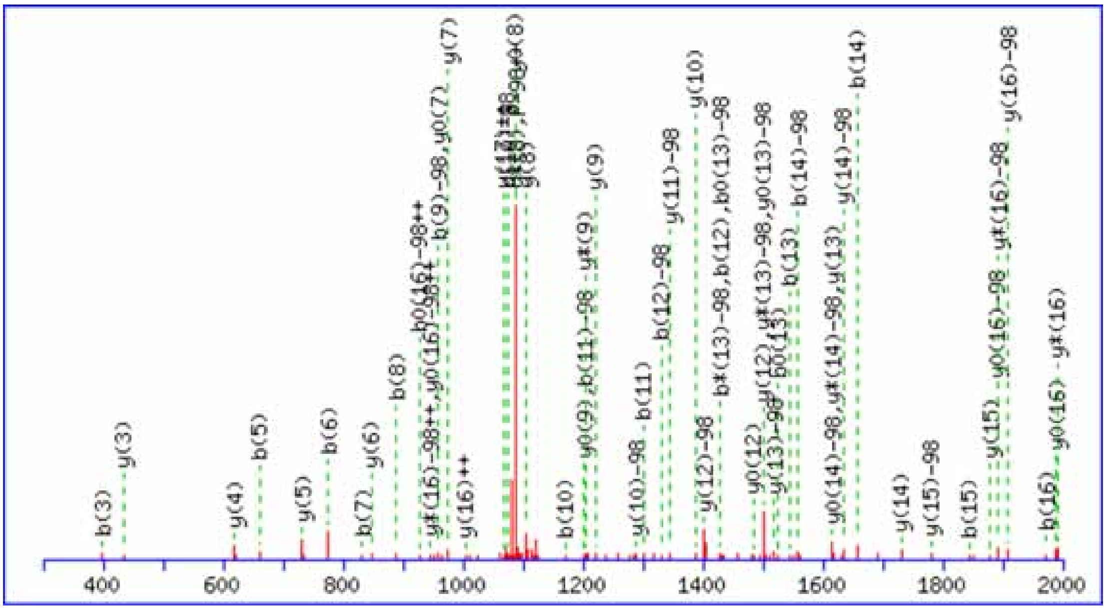
Matched b ions: b(3), b(4), b(5), b(7), b(7)-98, b(9)++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)-98, y(8), y(8)++, y(9)-98, y(9), y(9)++
Precursor origin neutral loss: +

Peptide No.444

IQQFDDGGSDEEDIWEEK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IQQFDDGGSDEEDIWEEK
Found in PP6R3_MOUSE, Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Mus musculus GN=Ppp6r3 PE=1 SV=1

Match to Query 6967: 2274.920706 from(1138.467629,2+)
Title: Elution from: 55.062 to 55.062 scan no 5464 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2274.9205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl (K)
Ions Score: 85 **Expect:** 1.1e-007

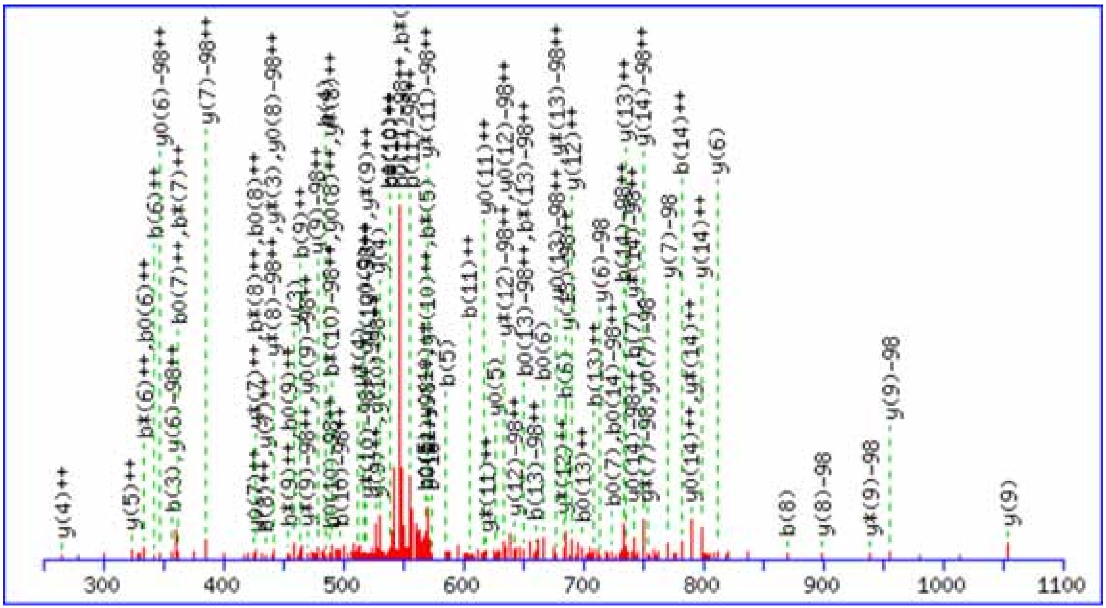
Matched b ions: b(3), b(5), b(6), b(7), b(8), b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(13), b(14), b(14)-98, b(15), b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(12)-98, y(12), y(13), y(13)-98, y(14), y(14)-98, y(15)-98, y(15), y(16)-98, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.445

IQSQTVGQGSDAHFR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of IQSQTVGQGSDAHFR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3389: 1737.784032 from(580.268620,3+)
Title: Elution from: 28.249 to 28.249 scan no 1913 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1737.7836
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.028

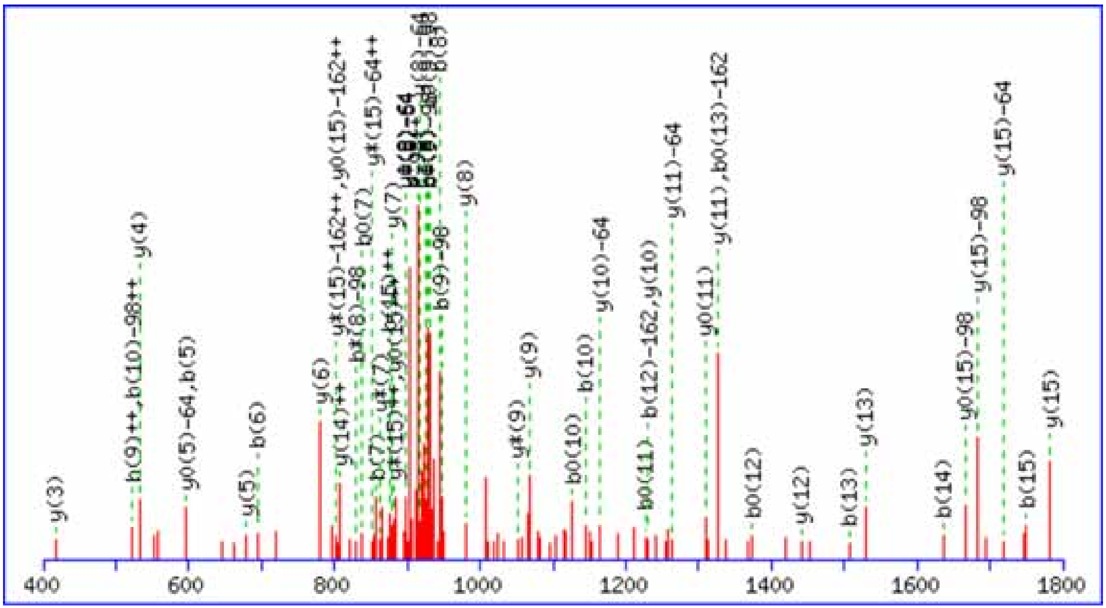
Matched b ions: b(3), b(4), b(5), b(6), b(6)++, b(7), b(8), b(8)++, b(9)++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(4)++, y(5)++, y(6)-98++, y(6), y(6)-98, y(7)-98++, y(7)-98, y(7)++, y(8)-98, y(9)-98, y(9), y(9)++, y(9)-98++, y(10)-98++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.446

ISSSNPYSTVTMDELR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of ISSSNPYSTVTMDELR
Found in ACTN2_MOUSE, Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1

Match to Query 5229: 1922.833696 from(962.424124,2+)
Title: Elution from: 47.162 to 47.162 scan no 4566 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1922.8333
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 57 Expect: 8e-005

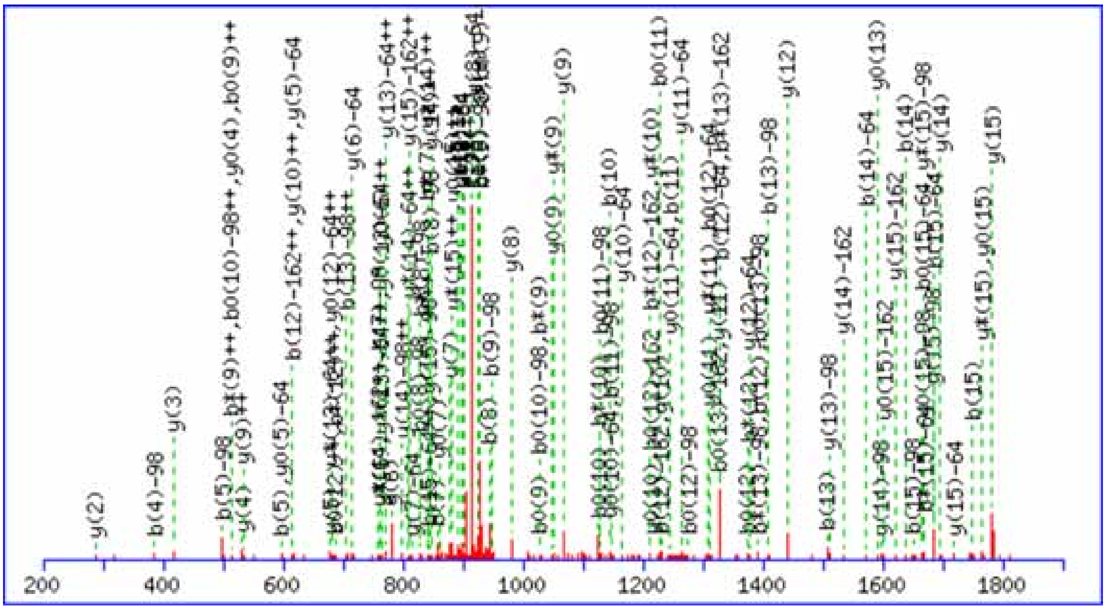
Matched b ions: b(5), b(6), b(7), b(8), b(9)++, b(9)-98, b(10)-98++, b(10), b(13), b(14), b(15), b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)++, y(15)-98, y(15)
Precursor origin neutral loss: +

Peptide No.447

ISSSNPYSTVTMDELR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ISSSNPYSTVTMDELR
Found in ACTN2_MOUSE, Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1

Match to Query 6070: 1922.834730 from(962.424641,2+)
Title: Elution from: 47.343 to 47.343 scan no 4617 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1922.8333
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 78 Expect: 6.4e-007

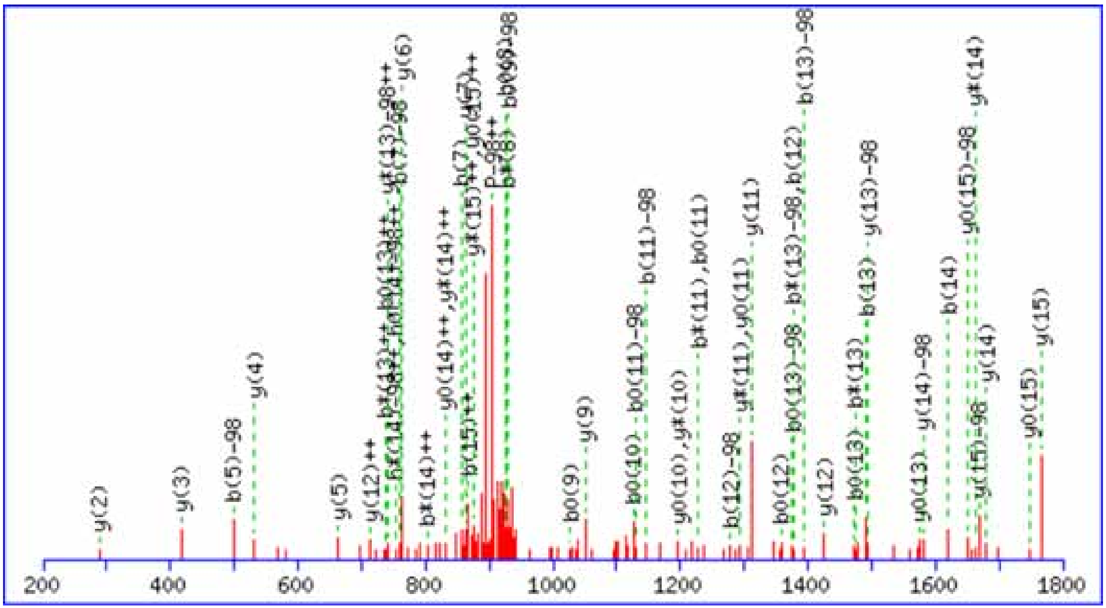
Matched b ions: b(4)-98, b(5)-98, b(5), b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(10), b(11), b(11)-98, b(12), b(13), b(13)-98, b(13)-98++, b(14), b(15), b(15)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(12), y(13)-98, y(14)-98, y(14), y(14)-98++, y(14)++, y(15)-98, y(15), y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.448

ISSSNPYSTVTMDELR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ISSSNPYSTVTMDELR
Found in ACTN2_MOUSE, Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1

Match to Query 4457: 1906.836210 from(954.425381,2+)
Title: Elution from: 52.460 to 52.460 scan no 4954 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1906.8383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 5.4e-006

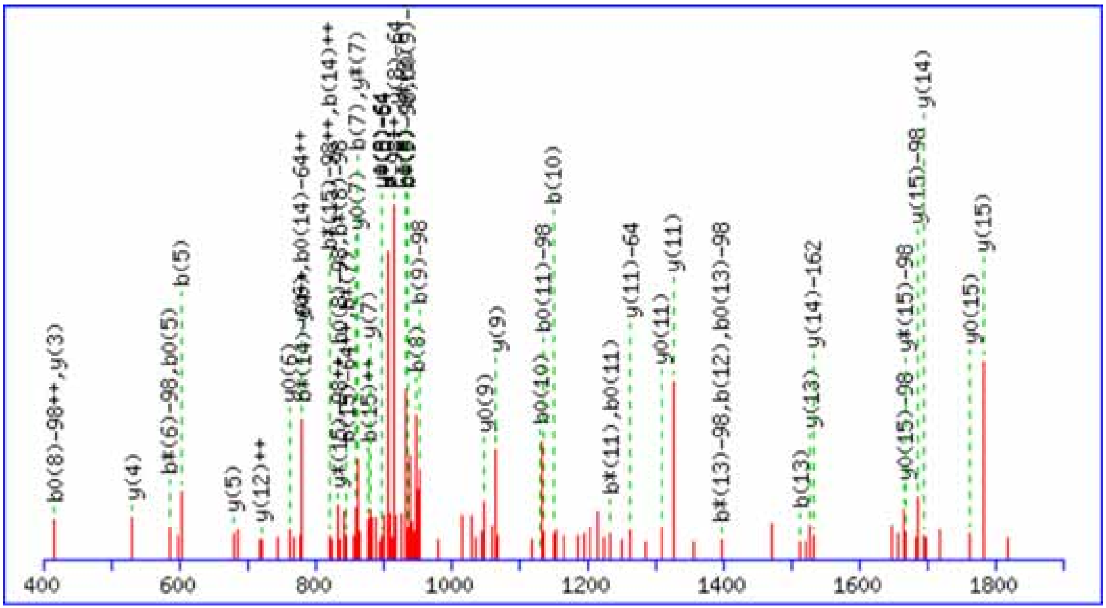
Matched b ions: b(5)-98, b(7)-98, b(7), b(11)-98, b(12)-98, b(12), b(13), b(13)-98, b(14), b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9), y(11), y(12), y(12)++, y(13)-98, y(14)-98, y(14), y(15)-98, y(15)
Precursor origin neutral loss: +

Peptide No.449

ISSSNPYSTVTMDELR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of ISSSNPYSTVTMDELR
Found in ACTN2_MOUSE, Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1

Match to Query 4215: 1928.866576 from(965.440564,2+)
Title: Elution from: 46.977 to 46.977 scan no 4224 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1928.8651
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 41 Expect: 0.004

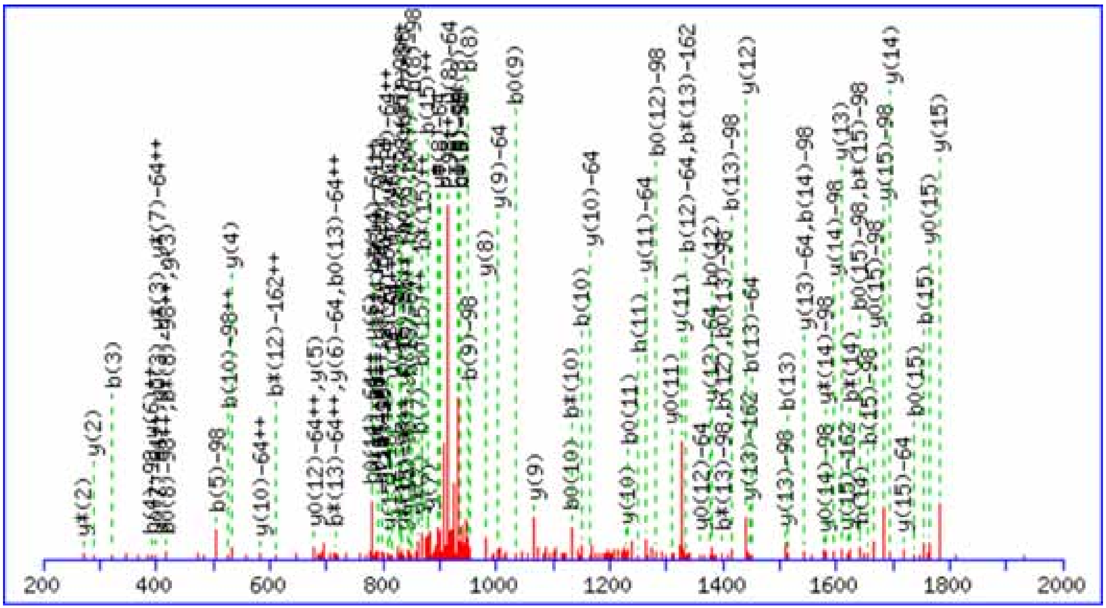
Matched b ions: b(5), b(7), b(8), b(9)-98, b(10), b(12), b(13), b(14)++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(11), y(12)++, y(13), y(14), y(15)-98, y(15)
Precursor origin neutral loss: +

Peptide No.450

ISSSNPYSTVTMDELR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ISSSNPYSTVTMDELR
Found in ACTN2_MOUSE, Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1

Match to Query 4082: 1928.867784 from(965.441168,2+)
Title: Elution from: 47.476 to 47.476 scan no 4294 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1928.8651
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 63 Expect: 2.6e-005

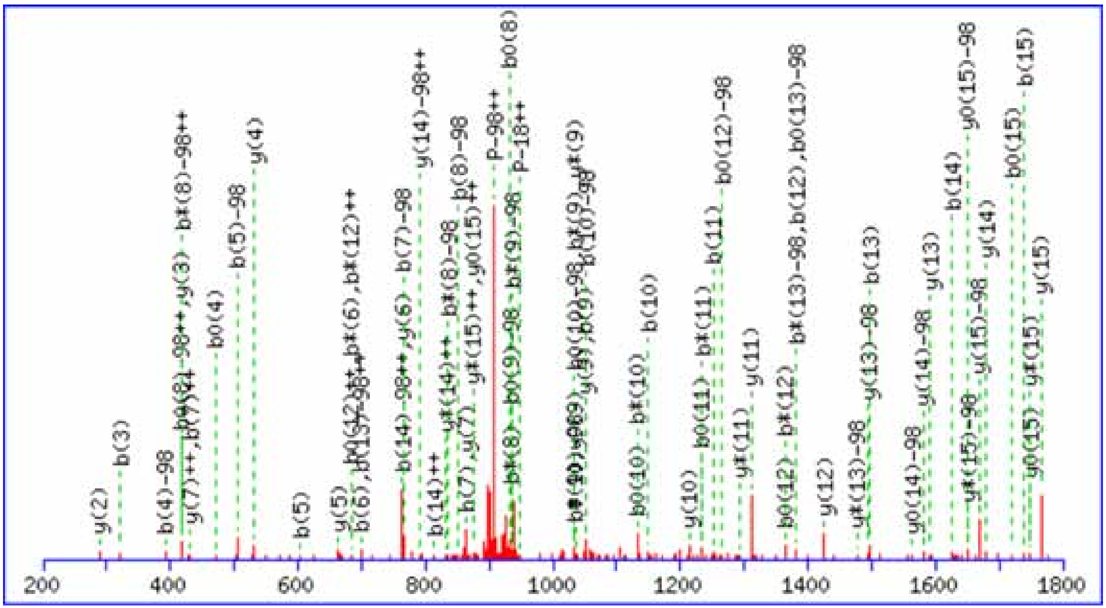
Matched b ions: b(3), b(4)-98, b(5)-98, b(7), b(8)-98, b(8), b(9)-98, b(10), b(10)-98++, b(11), b(12), b(13)-98, b(13), b(14)-98, b(14), b(15), b(15)-98++, b(15)++, b(15)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(11), y(12), y(13)-98, y(13), y(14), y(14)-98, y(14)-98++, y(15)-98, y(15), y(15)-98++
Precursor origin neutral loss: +

Peptide No.451

ISSSNPYSTVTMDELR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of ISSSNPYSTVTMDELR
Found in ACTN2_MOUSE, Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1

Match to Query 3972: 1912.872506 from(957.443529,2+)
Title: Elution from: 52.531 to 52.531 scan no 4882 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1912.8701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 83 **Expect:** 2.7e-007

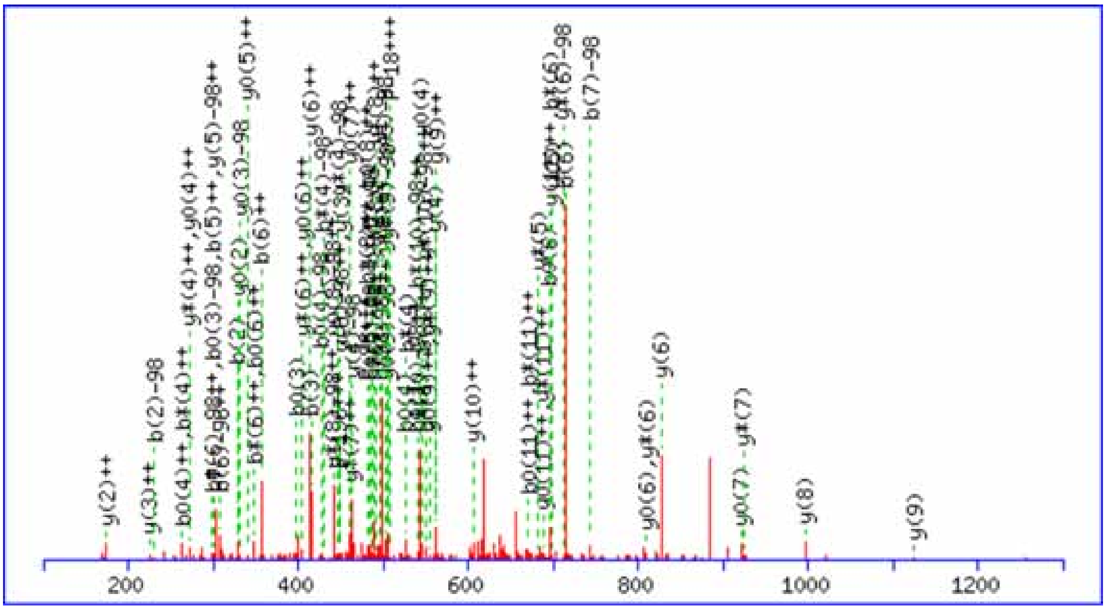
Matched b ions: b(3), b(4)-98, b(5)-98, b(5), b(6), b(7), b(7)-98, b(7)++, b(8)-98, b(9), b(10)-98, b(10), b(11), b(12), b(13), b(13)-98++, b(14)-98++, b(14), b(14)++, b(15)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(9), y(10), y(11), y(12), y(13)-98, y(13), y(14)-98, y(14), y(14)-98++, y(15)-98, y(15)
Precursor origin neutral loss: +

Peptide No.452

ITSKGLKHLTSK
Confirmed sites: @T:2,@S:11
Ambiguous sites:

MS/MS Fragmentation of ITSKGLKHLTSK
Found in CCD71_MOUSE, Coiled-coil domain-containing protein 71 OS=Mus musculus GN=Ccdc71 PE=2 SV=1

Match to Query 3507: 1539.850578 from(514.290802,3+)
Title: Elution from: 43.023 to 43.023 scan no 4053 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1539.8463
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K12 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 29 **Expect:** 0.047

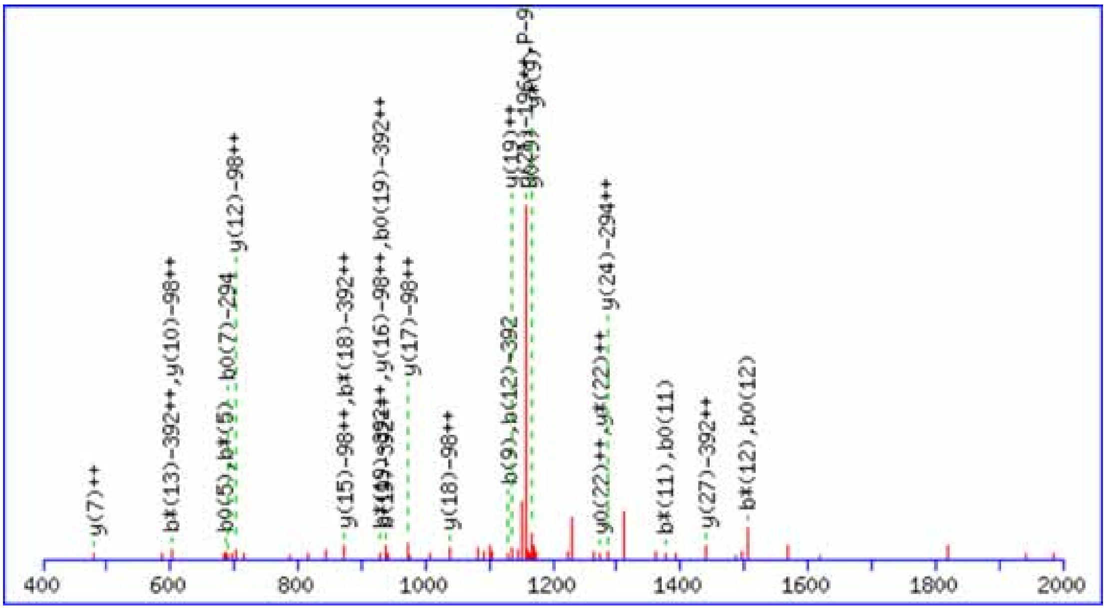
Matched b ions: b(2), b(2)-98, b(3), b(4), b(4)++, b(5)-98, b(5)++, b(6)++, b(6), b(6)-98++, b(7)-98, b(8)++, b(8)-98++, b(9)-98++, b(9)++, b(11)-98++
Matched y ions: y(2)++, y(3)++, y(3), y(4)-98, y(4), y(5)-98++, y(5), y(6)++, y(6), y(8)++, y(8), y(8)-98++, y(9), y(9)++, y(10)++, y(11)++, y(11)-98++
Precursor origin neutral loss:

Peptide No.453

ITTNNSMGASPESLMVLSNDSGHEEVKEK
Confirmed sites: @T:2,@T:3,@S:6,@S:10,@S:21
Ambiguous sites:

MS/MS Fragmentation of ITTNNSMGASPESLMVLSNDSGHEEVKEK
Found in OSMR_MOUSE, Oncostatin-M-specific receptor subunit beta OS=Mus musculus GN=Osmr PE=1 SV=1

Match to Query 7556: 3565.369365 from(1189.463731,3+)
Title: Elution from: 51.254 to 51.254 scan no 4875 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 3565.3698
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S21 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K27 : Dimethyl (K)
K29 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 40 Expect: 0.0041

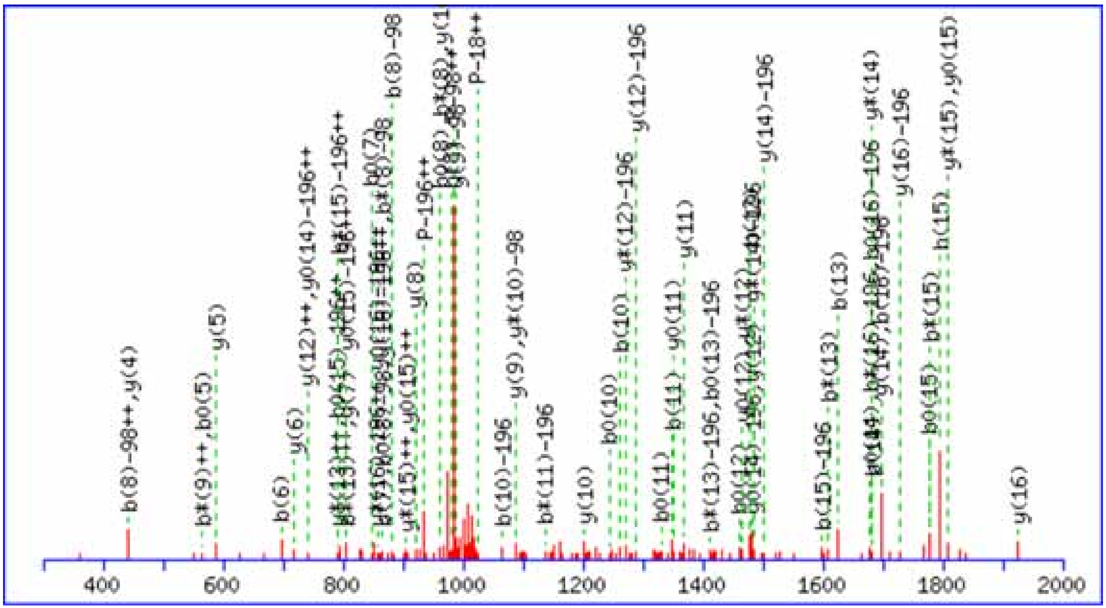
Matched b ions: b(8)-98++, b(9), b(10)-196, b(12)-392, b(19)-392++, b(20)-196++, b(22)-294++, b(23)-196++
Matched y ions: y(7)++, y(10)-98++, y(12)-98++, y(15)-98++, y(16)-98++, y(17)-98++, y(18)-98++, y(19)++, y(20)-98++, y(21)-196++, y(24)-294++, y(26)-98++, y(27)-392++
Precursor origin neutral loss: +

Peptide No.454

IVETINSDSDSEFGIPK
Confirmed sites: @S:7,@S:9
Ambiguous sites:

MS/MS Fragmentation of IVETINSDSDSEFGIPK
Found in TOP2B_MOUSE, DNA topoisomerase 2-beta OS=Mus musculus GN=Top2b PE=1 SV=2

Match to Query 5319: 2065.891198 from(1033.952875,2+)
Title: Elution from: 56.486 to 56.486 scan no 5337 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2065.8898
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 63 Expect: 2.5e-005

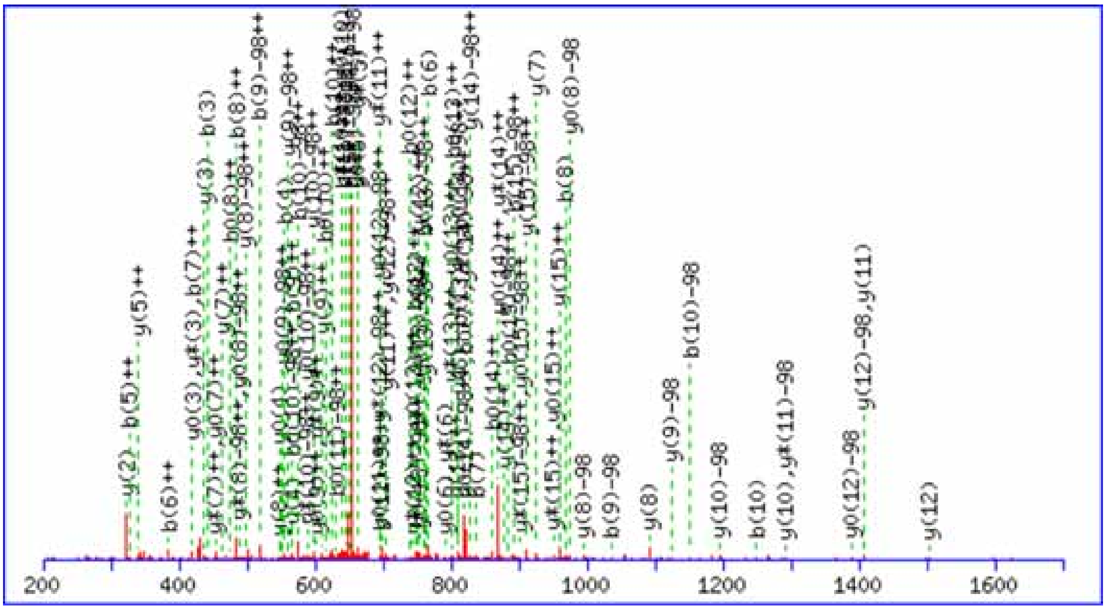
Matched b ions: b(6), b(7), b(8)-98++, b(8)-98, b(8), b(10), b(10)-196, b(11), b(12), b(13), b(13)-98, b(14), b(14)-98++, b(15)-98, b(15), b(15)-196, b(16)-196, b(16)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(11), y(11)-98, y(12), y(12)++, y(12)-98, y(12)-196, y(13)-98, y(14), y(14)-98, y(14)-196, y(15)-98++, y(15)-98, y(16), y(16)++, y(16)-196++, y(16)-98, y(16)-196
Precursor origin neutral loss: +

Peptide No.455

IYHLPDAESDEDEDFK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IYHLPDAESDEDEDFK
Found in SEPT2_MOUSE, Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2

Match to Query 4783: 2057.855466 from(686.959098,3+)
Title: Elution from: 46.238 to 46.238 scan no 4143 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2057.8507
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K16 : Dimethyl (K)
Ions Score: 36 Expect: 0.0091

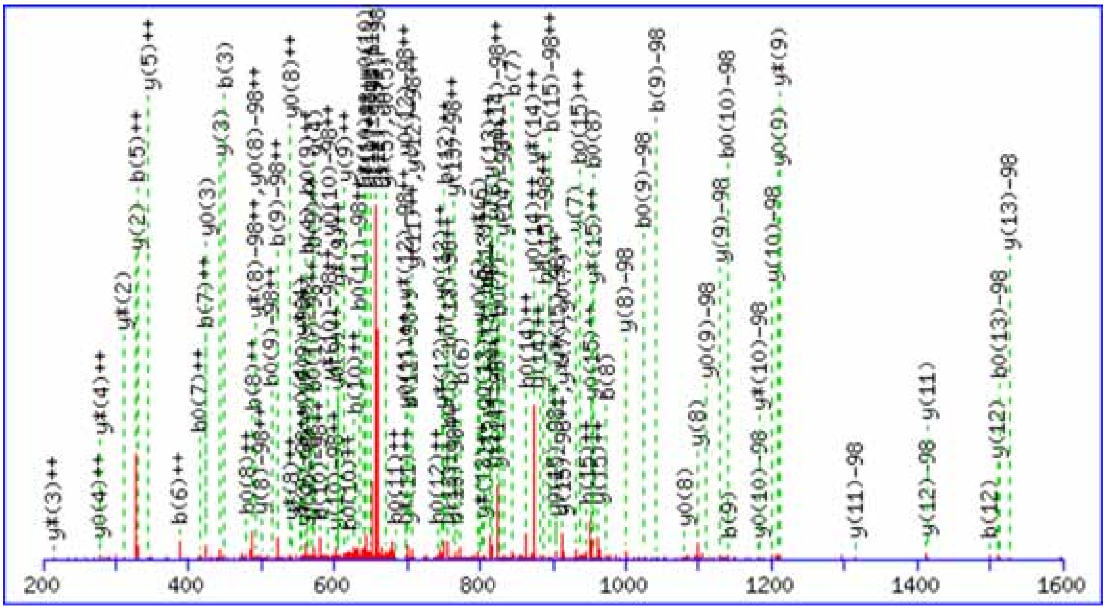
Matched b ions: b(3), b(4), b(5)++, b(5), b(6), b(6)++, b(7)++, b(7), b(8)++, b(8), b(9)-98++, b(9)++, b(9)-98, b(10)-98++, b(10), b(10)-98, b(10)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(6), y(7), y(7)++, y(8), y(8)-98, y(8)-98++, y(8)++, y(9)-98, y(9)-98++, y(9)++, y(10)-98, y(10), y(10)-98++, y(10)++, y(11)-98++, y(11), y(11)++, y(12)-98, y(12), y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.456

IYHLPDAESDEDEDFK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IYHLPDAESDEDEDFK
Found in SEPT2_MOUSE, Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2

Match to Query 6825: 2069.916129 from(690.979319,3+)
Title: Elution from: 46.230 to 46.230 scan no 4471 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2069.9143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 60 Expect: 4.8e-005

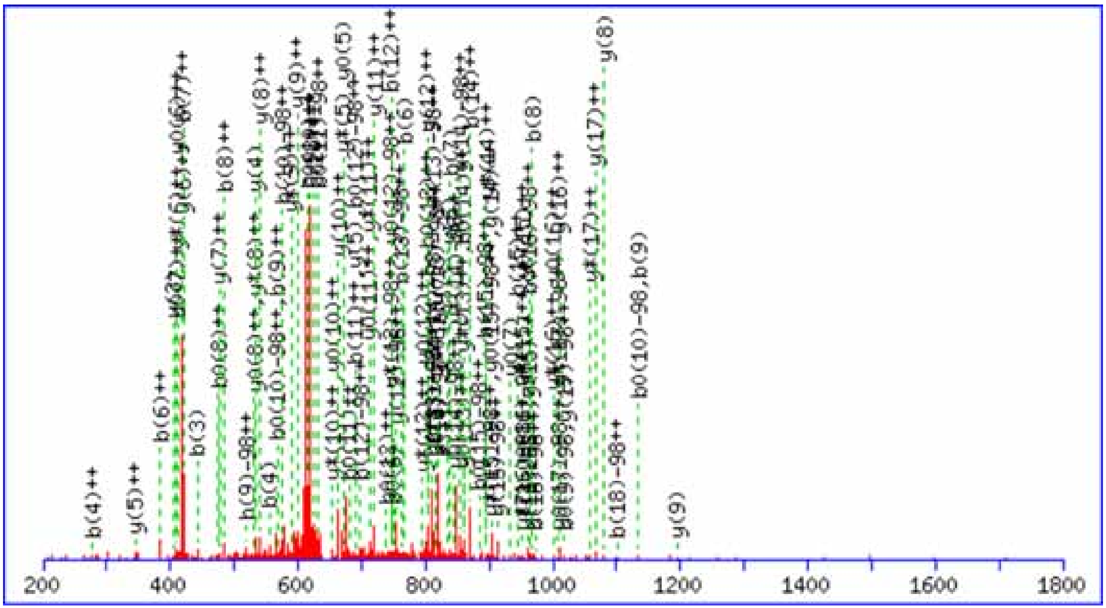
Matched b ions: b(2), b(3), b(4), b(5), b(5)++, b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)-98++, b(9), b(9)++, b(9)-98, b(10)-98++, b(10)++, b(11)-98++, b(12)++, b(12), b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(6), y(7), y(8), y(8)-98, y(8)-98++, y(9)-98, y(9)-98++, y(9)++, y(10)-98, y(10)-98++, y(10)++, y(11)-98++, y(11)-98, y(11), y(11)++, y(12)-98, y(12)++, y(12), y(12)-98++, y(13)-98, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.457

IYHLPDAESDEDEDFKEQTR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IYHLPDAESDEDEDFKEQTR
Found in SEPT2_MOUSE, Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2

Match to Query 6258: 2572.100976 from(644.032520,4+)
Title: Elution from: 42.952 to 42.952 scan no 3754 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2572.1006
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K16 : Dimethyl (K)
Ions Score: 37 Expect: 0.013

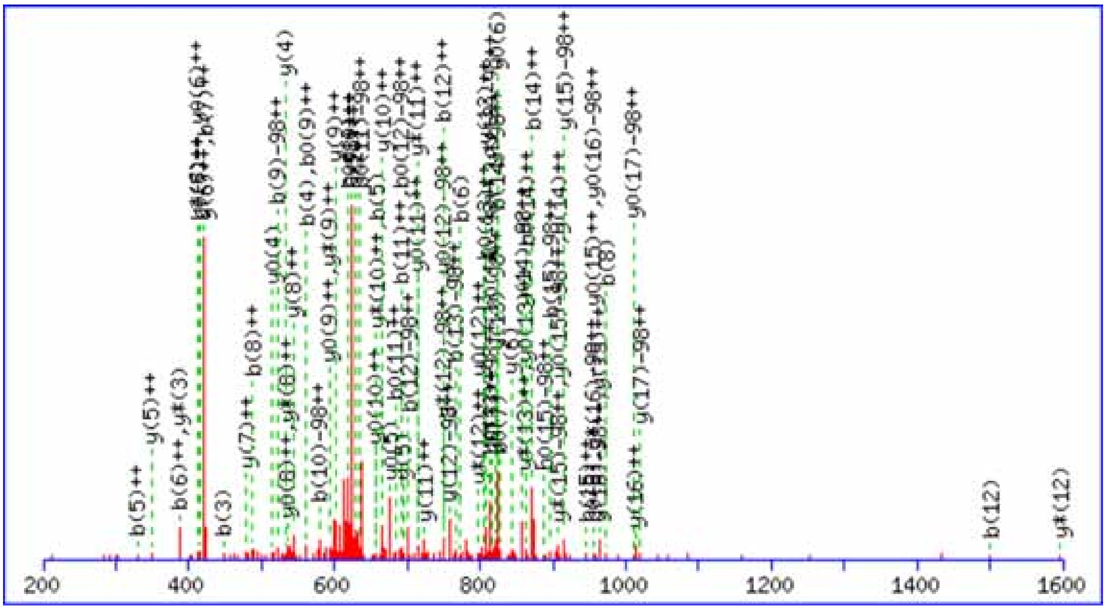
Matched b ions: b(3), b(4)++, b(4), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9), b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(18)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9)++, y(9), y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.458

IYHLPDAESDEDEDFKEQTR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IYHLPDAESDEDEDFKEQTR
Found in SEPT2_MOUSE, Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2

Match to Query 6147: 2584.164484 from(647.048397,4+)
Title: Elution from: 42.956 to 42.956 scan no 3783 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2584.1642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 39 Expect: 0.0091

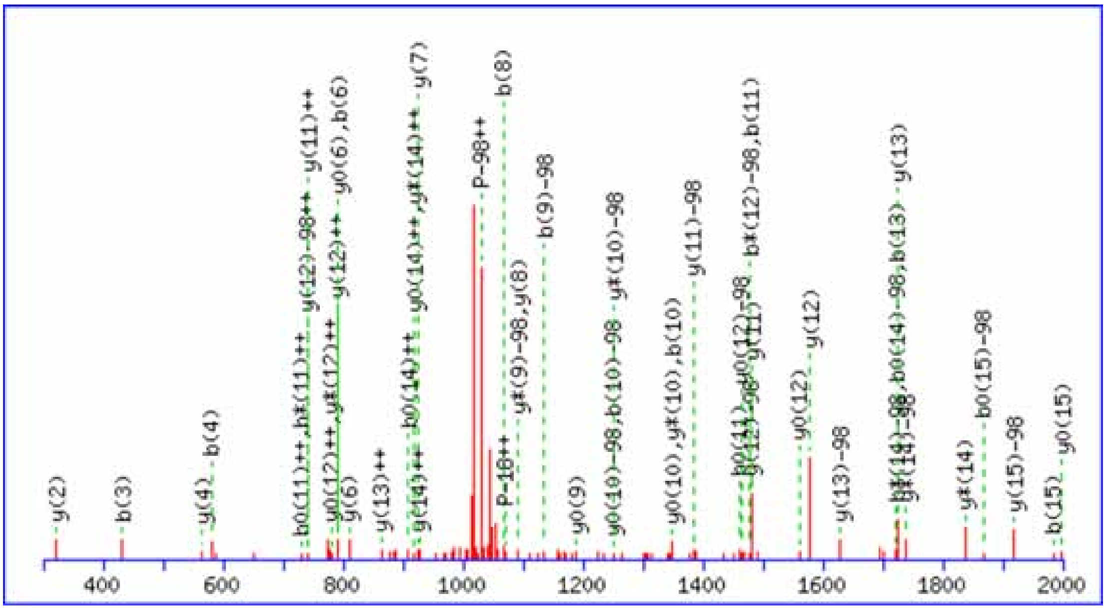
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7)++, b(8)++, b(8), b(9)-98++, b(10)-98++, b(10)++, b(11)++, b(12), b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++
Matched y ions: y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(8)++, y(9)++, y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.459

IYQFPDCDSDEDEDFK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of IYQFPDCDSDEDEDFK
Found in SEPT4_MOUSE, Septin-4 OS=Mus musculus GN=Sept4 PE=1 SV=1

Match to Query 6314: 2157.812506 from(1079.913529,2+)
Title: Elution from: 51.896 to 51.896 scan no 5131 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2157.8126
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl (K)
Ions Score: 28 **Expect:** 0.033

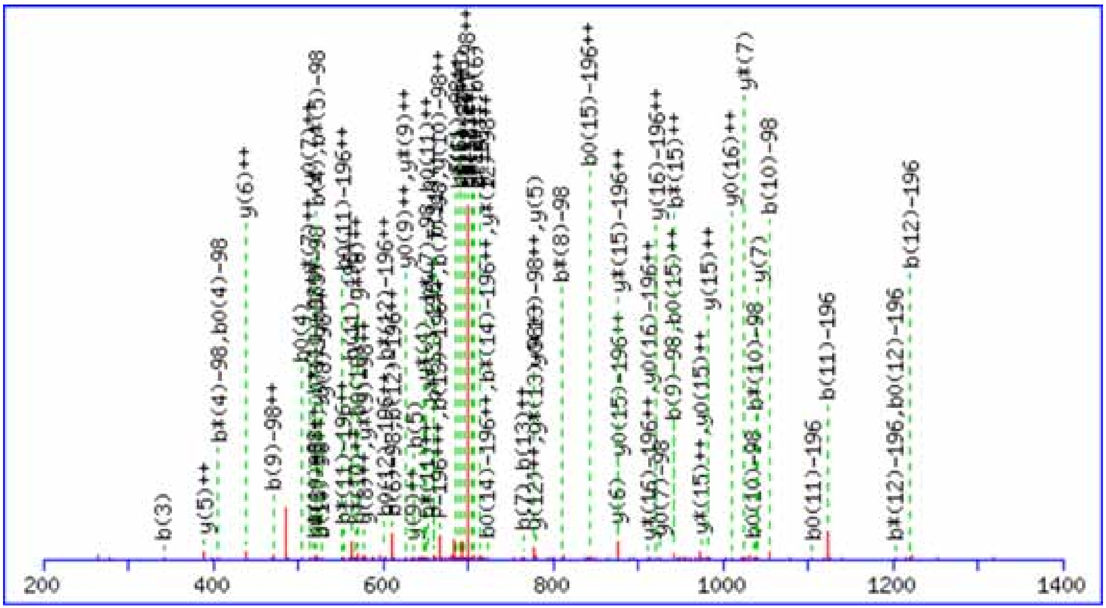
Matched b ions: b(3), b(4), b(6), b(8), b(9)-98, b(10), b(10)-98, b(11), b(13), b(14), b(14)-98, b(14)++, b(15)
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(11), y(11)-98, y(11)++, y(12)-98, y(12), y(12)++, y(12)-98++, y(13)-98, y(13), y(13)++, y(14)++, y(15)-98
Precursor origin neutral loss: +

Peptide No.460

KALTDAGCNLSPLQYIK
Confirmed sites: @T:4,@S:11,@Y:15
Ambiguous sites:

MS/MS Fragmentation of KALTDAGCNLSPLQYIK
Found in SCFD1_MOUSE, Sec1 family domain-containing protein 1 OS=Mus musculus GN=Scfd1 PE=2 SV=1

Match to Query 5155: 2192.984445 from(732.002091,3+)
Title: Elution from: 39.055 to 39.055 scan no 3235 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2192.9807
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl (K)
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y15 : Phospho (Y)
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 36 Expect: 0.015

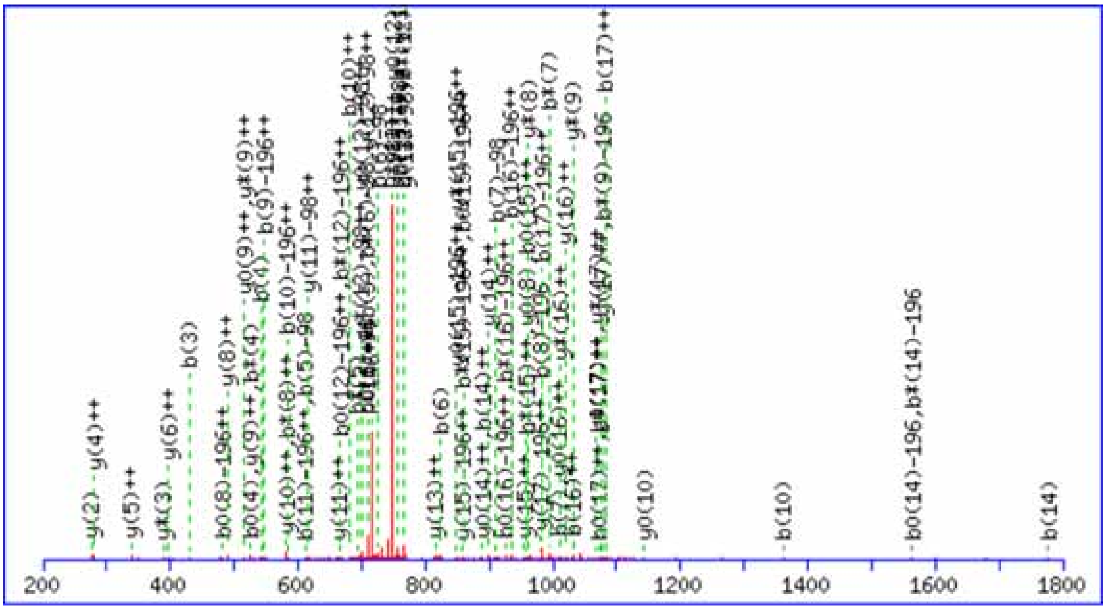
Matched b ions: b(3), b(4), b(5), b(6)-98, b(6), b(7)-98, b(7), b(9)-98, b(9)-98++, b(10)-98, b(10)-98++, b(11)-98++, b(11)-196, b(11)-98, b(11)-196++, b(11)++, b(12)-196++, b(12)-98, b(12)-196, b(12)-98++, b(12)++, b(13)-196++, b(13)-98++, b(13)++
Matched y ions: y(5)++, y(5), y(6), y(6)++, y(7)++, y(7), y(8)++, y(8)-98++, y(9)++, y(10)-98++, y(10)++, y(11)-98++, y(12)++, y(15)++, y(16)-196++
Precursor origin neutral loss: +

Peptide No.461

KDELSDWSLAGEDDRETR
Confirmed sites: @S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of KDELSDWSLAGEDDRETR
Found in FXR1_MOUSE, Fragile X mental retardation syndrome-related protein 1 OS=Mus musculus GN=Fxr1 PE=1 SV=2

Match to Query 7148: 2336.958474 from(779.993434,3+)
Title: Elution from: 46.578 to 46.578 scan no 4494 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2336.9563
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.013

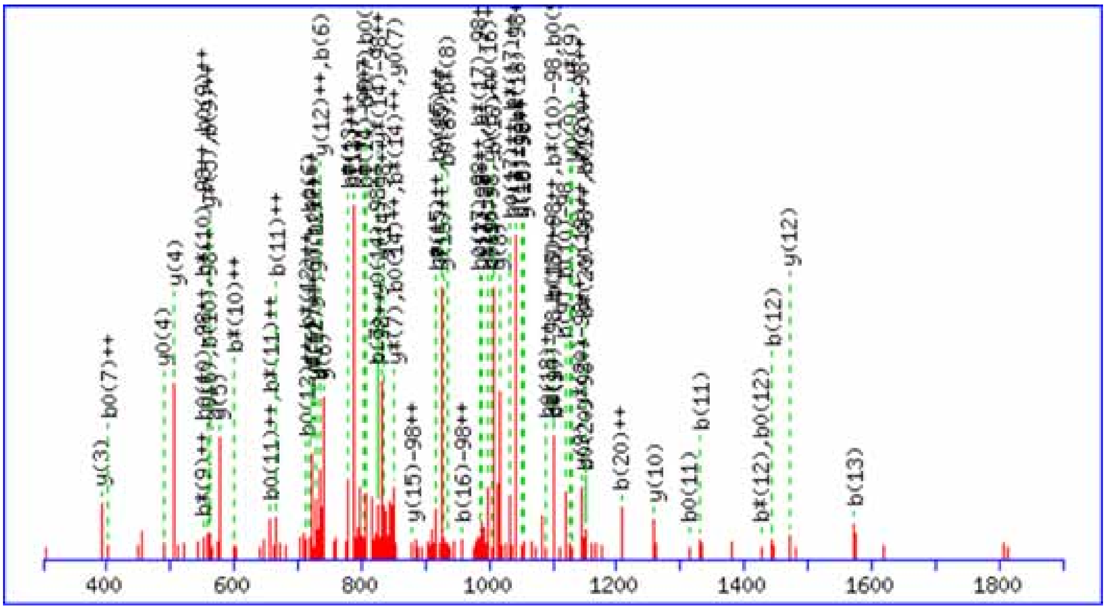
Matched b ions: b(3), b(4), b(5), b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(8)-196, b(9)-98, b(9)-196++, b(10), b(10)-196++, b(10)++, b(11)++, b(11)-196++, b(11)-98++, b(13)-98, b(14)-98, b(14), b(14)++, b(16)-98++, b(16)-196++, b(16)++, b(17)++, b(17)-196++
Matched y ions: y(2), y(4)++, y(5)++, y(6)++, y(8)++, y(9)++, y(10)++, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(17)++, y(17)-98++, y(17)-196++
Precursor origin neutral loss: +

Peptide No.462

KDSEGYSESPDLEFEYADTDK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of KDSEGYSESPDLEFEYADTDK
Found in FA40A_MOUSE, Protein FAM40A OS=Mus musculus GN=Fam40a PE=1 SV=2

Match to Query 7843: 2588.075727 from(863.699185,3+)
Title: Elution from: 48.778 to 48.778 scan no 4765 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2588.0731
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl (K)
Ions Score: 49 Expect: 0.00066

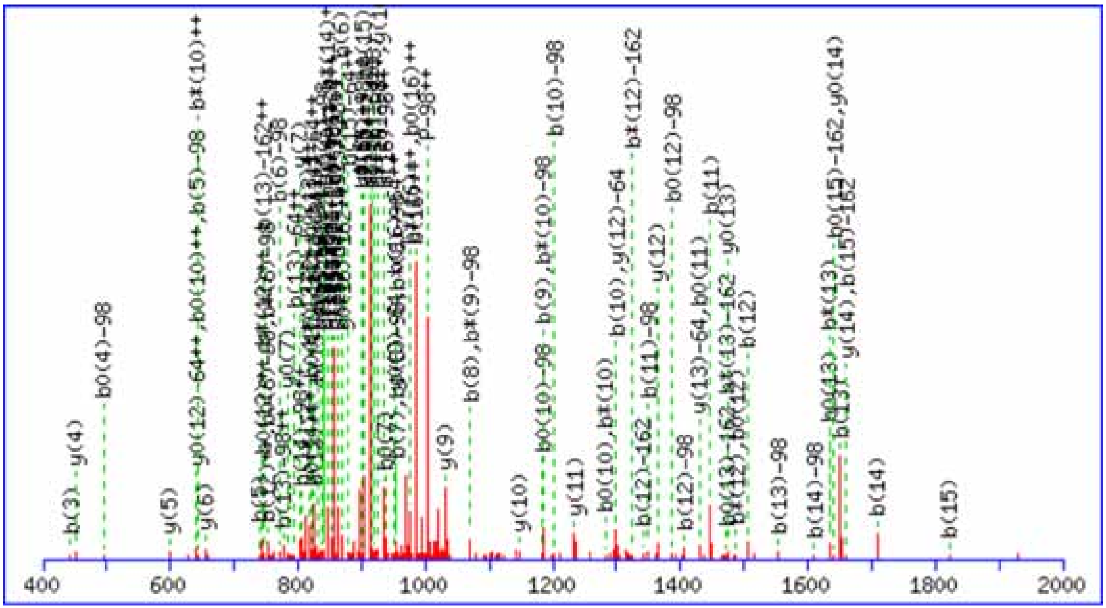
Matched b ions: b(6), b(7), b(9), b(9)++, b(10)-98, b(10)-98++, b(11)++, b(11), b(12), b(12)++, b(13)++, b(13), b(15)++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)++
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(12), y(12)++, y(14)-98++, y(15)++, y(15)-98++, y(17)-98++, y(18)++, y(18)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.463

KEESEEESDDDMGFGLFD
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KEESEEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5260: 2100.777298 from(1051.395925,2+)
Title: Elution from: 58.619 to 58.619 scan no 5532 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2100.7759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 78 **Expect:** 2.9e-007

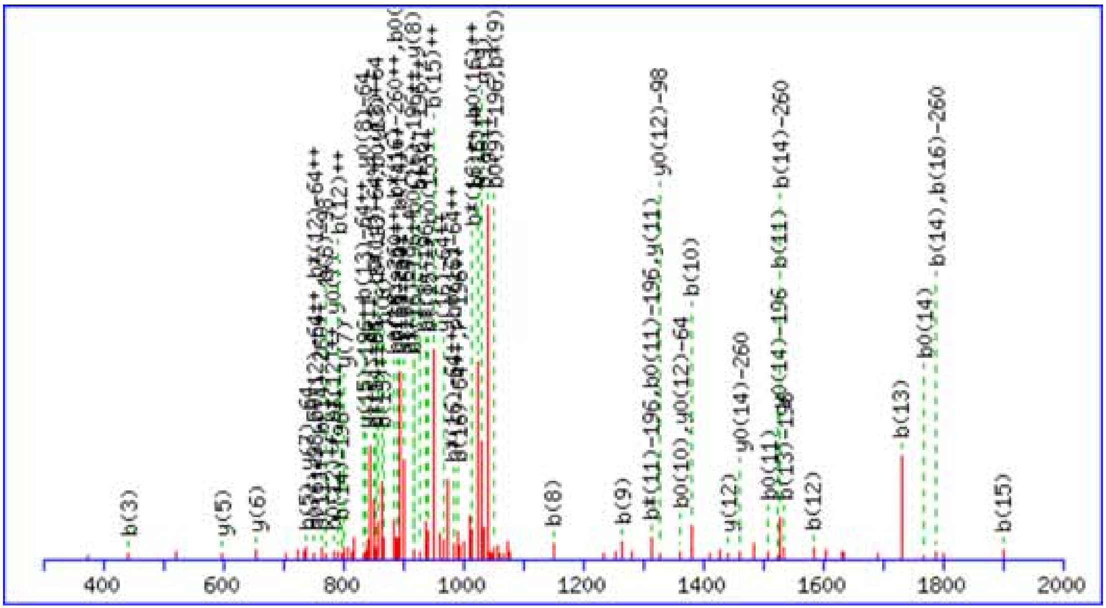
Matched b ions: b(3), b(5)-98, b(5), b(6), b(6)-98, b(7), b(8), b(9), b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(12)++, b(13)++, b(13), b(13)-98, b(13)-98++, b(14)++, b(14), b(14)-98++, b(14)-98, b(15)++, b(15), b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14), y(14)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.464

KEESEESDDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 6425: 2180.743048 from(1091.378800,2+)
Title: Elution from: 69.135 to 69.135 scan no 6690 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2180.7422
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 76 Expect: 2.4e-007

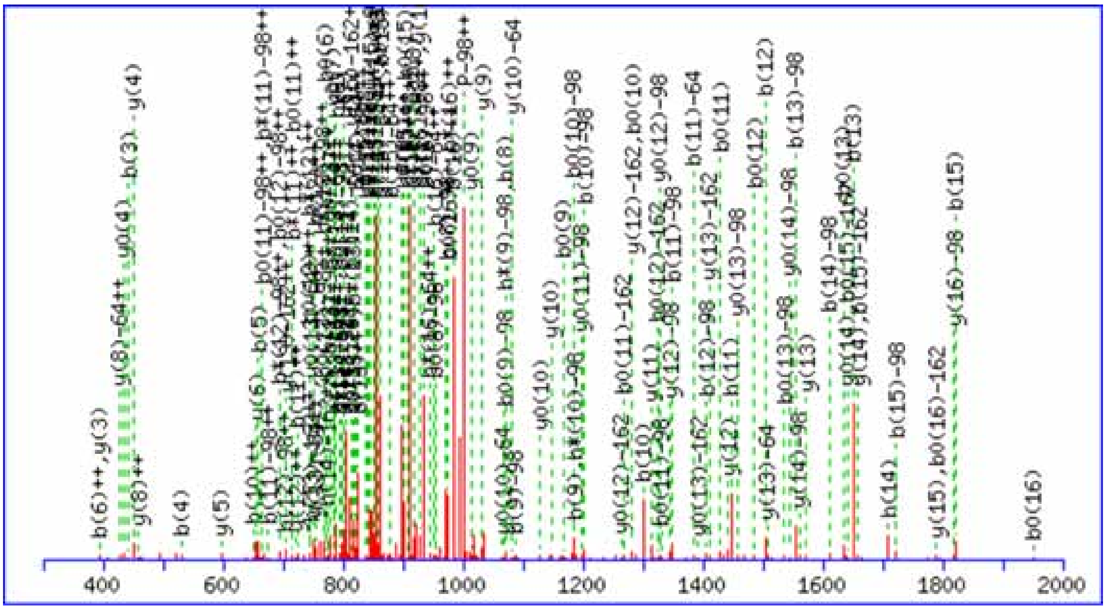
Matched b ions: b(3), b(5), b(6)-98, b(6), b(7)-98, b(8), b(8)-98, b(9), b(10), b(10)-98, b(11), b(11)++, b(11)-98, b(12), b(12)-98, b(12)++, b(13), b(13)++, b(13)-196, b(13)-98, b(13)-98++, b(14)-98++, b(14), b(14)++, b(14)-98, b(14)-196++, b(15)++, b(15), b(15)-98++, b(15)-98, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(15)-98++, y(15)-98, y(15)-196++
Precursor origin neutral loss: +

Peptide No.465

KEESEESDDDMGFGLFD
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 6156: 2100.776272 from(1051.395412,2+)
Title: Elution from: 58.434 to 58.434 scan no 5789 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2100.7759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 70 **Expect:** 1.7e-006

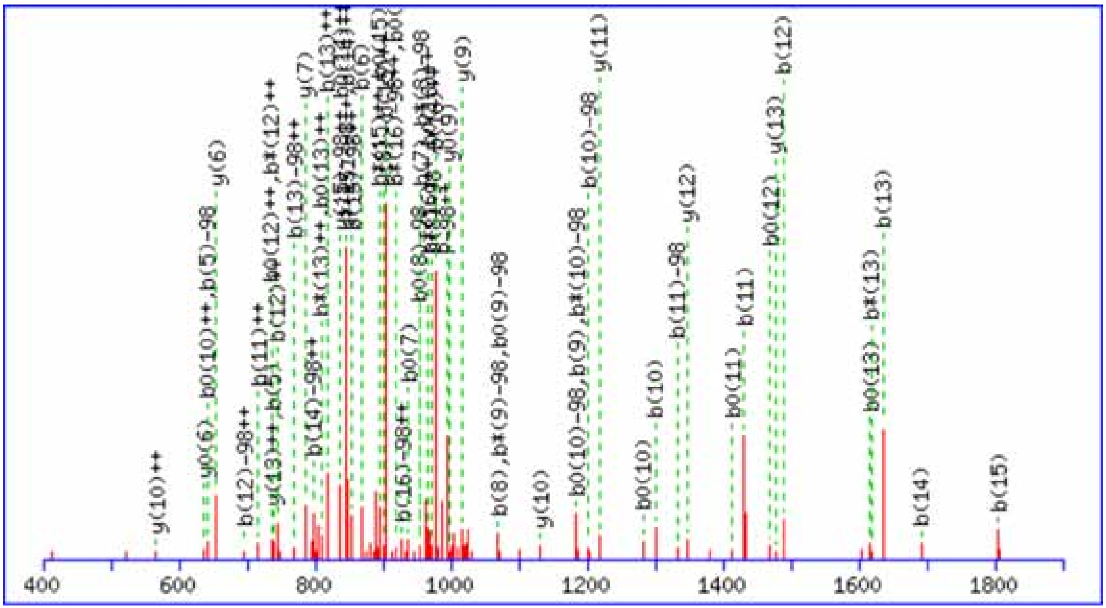
Matched b ions: b(3), b(4), b(5), b(6), b(6)++, b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(10)++, b(11), b(11)-98, b(11)-98++, b(11)++, b(12), b(12)++, b(12)-98, b(12)-98++, b(13)-98, b(13), b(13)-98++, b(13)++, b(14)++, b(14), b(14)-98++, b(14)-98, b(15)++, b(15), b(15)-98++, b(15)-98, b(16)++, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11), y(12), y(12)-98, y(12)++, y(13), y(14)-98, y(14), y(15), y(15)-98++, y(16)-98, y(16)-98++
Precursor origin neutral loss: +

Peptide No.466

KEESEESDDDMGFGLFD
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KEESEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 6087: 2084.784412 from(1043.399482,2+)
Title: Elution from: 66.413 to 66.413 scan no 6464 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2084.7809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 6.6e-005

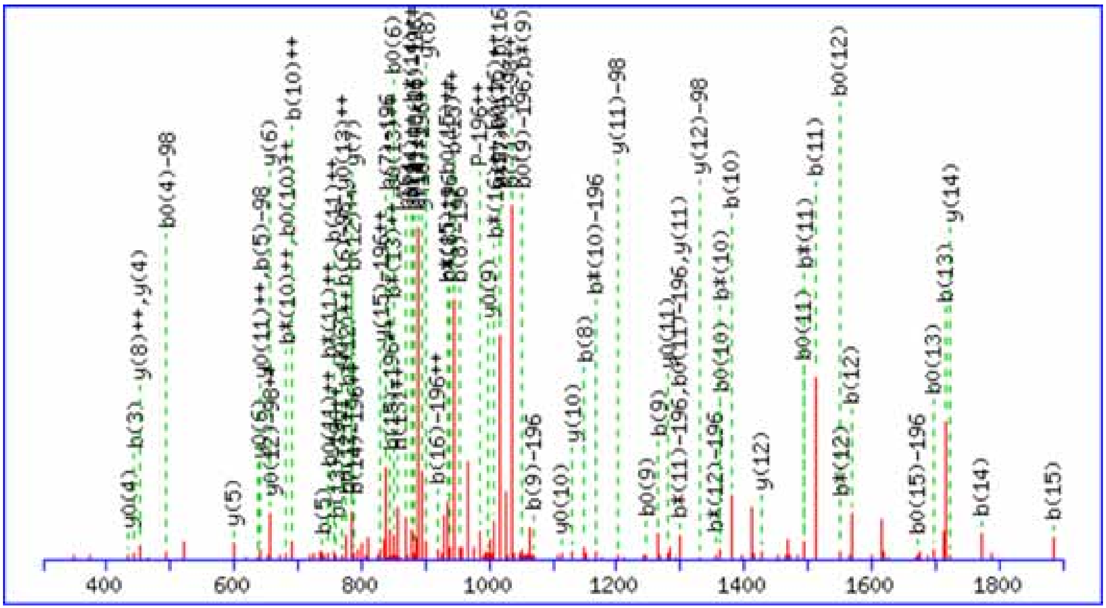
Matched b ions: b(5)-98, b(5), b(6), b(7), b(8), b(8)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(11)++, b(12)++, b(12), b(12)-98++, b(13), b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(14), b(15)++, b(15), b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(12), y(13), y(13)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.467

KEESEESDDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5002: 2164.749058 from(1083.381805,2+)
Title: Elution from: 74.726 to 74.726 scan no 6760 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2164.7473
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 Expect: 1.1e-006

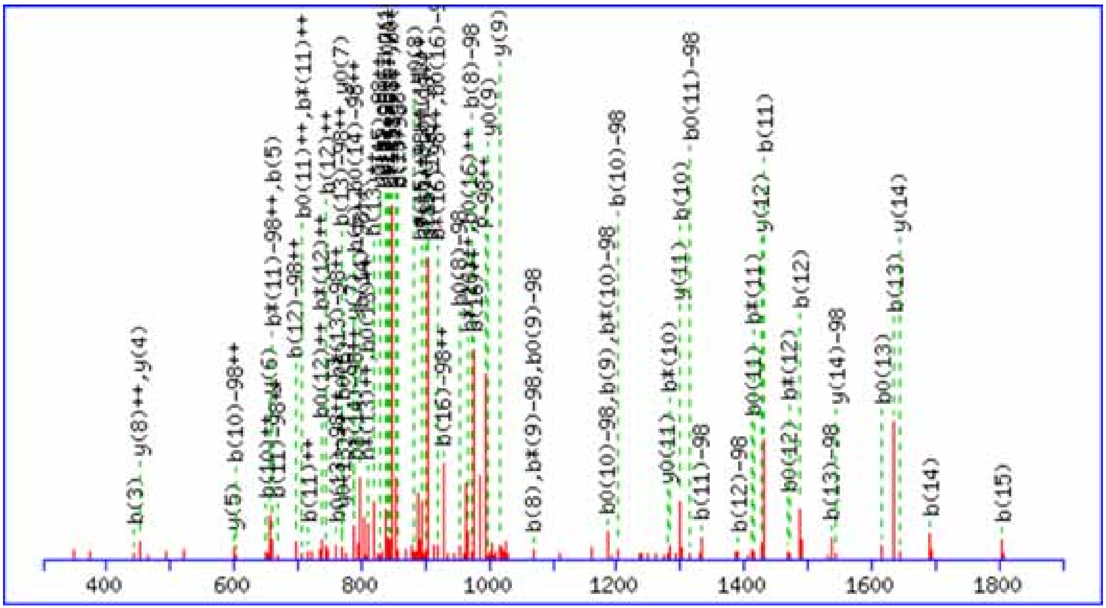
Matched b ions: b(3), b(5)-98, b(5), b(6), b(6)-98, b(7)-196, b(7)-98, b(7), b(8), b(8)-98, b(8)-196, b(9), b(9)-98, b(9)-196, b(10), b(10)-98++, b(10)++, b(10)-98, b(11), b(11)-98, b(11)++, b(12), b(12)++, b(12)-98++, b(12)-98, b(13), b(13)-98, b(13)++, b(13)-98++, b(13)-196++, b(14)-98++, b(14)++, b(14), b(14)-98, b(14)-196++, b(15), b(15)++, b(15)-98++, b(15)-98, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11), y(11)-98, y(12), y(12)-98, y(14), y(14)-98, y(15)-98++, y(15)-196++, y(16)-196++
Precursor origin neutral loss: +

Peptide No.468

KEESEESDDDMGFGLFD
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5397: 2084.783162 from(1043.398857,2+)
Title: Elution from: 65.698 to 65.698 scan no 6175 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2084.7809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 Expect: 2.2e-006

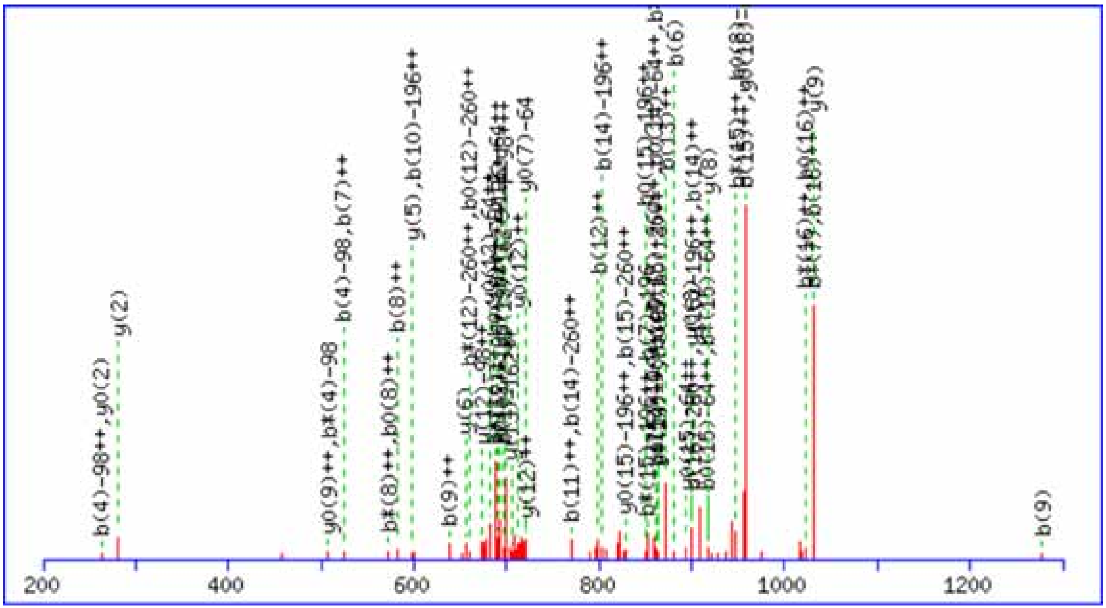
Matched b ions: b(3), b(5), b(6), b(7)-98, b(8), b(8)-98, b(9), b(10), b(10)-98++, b(10)-98, b(10)++, b(11), b(11)-98, b(11)++, b(11)-98++, b(12), b(12)-98++, b(12)++, b(12)-98, b(13), b(13)-98, b(13)++, b(13)-98++, b(14)++, b(14), b(14)-98++, b(15)++, b(15), b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(11), y(12), y(14), y(14)-98, y(15)-98++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.469

KEESEESDDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5915: 2192.809932 from(731.943920,3+)
Title: Elution from: 66.592 to 66.592 scan no 6248 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2192.8058
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 40 Expect: 0.0019

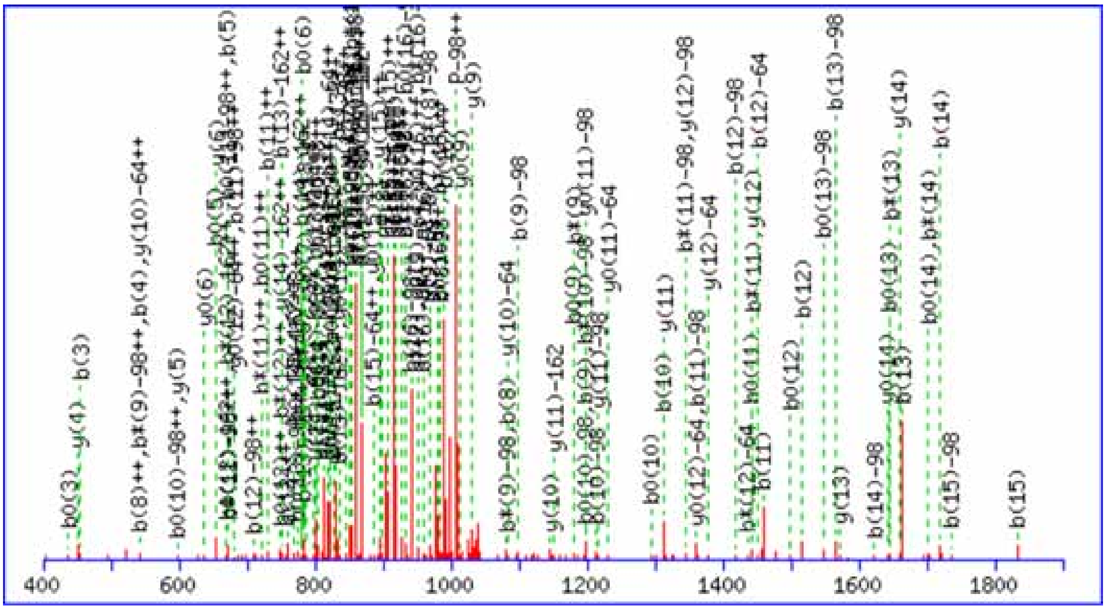
Matched b ions: b(4)-98++, b(4)-98, b(6), b(7)++, b(7)-196, b(8)++, b(9)++, b(9), b(10)-196++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(14)-196++, b(15)++, b(15)-98++, b(15)-196++, b(16)++
Matched y ions: y(2), y(5), y(6), y(8), y(9), y(12)++, y(12)-98++, y(16)-196++
Precursor origin neutral loss: +

Peptide No.470

KEESEESDDDMGFGLFD
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5492: 2112.840794 from(1057.427673,2+)
Title: Elution from: 58.103 to 58.103 scan no 5507 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2112.8395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 77 Expect: 5.6e-007

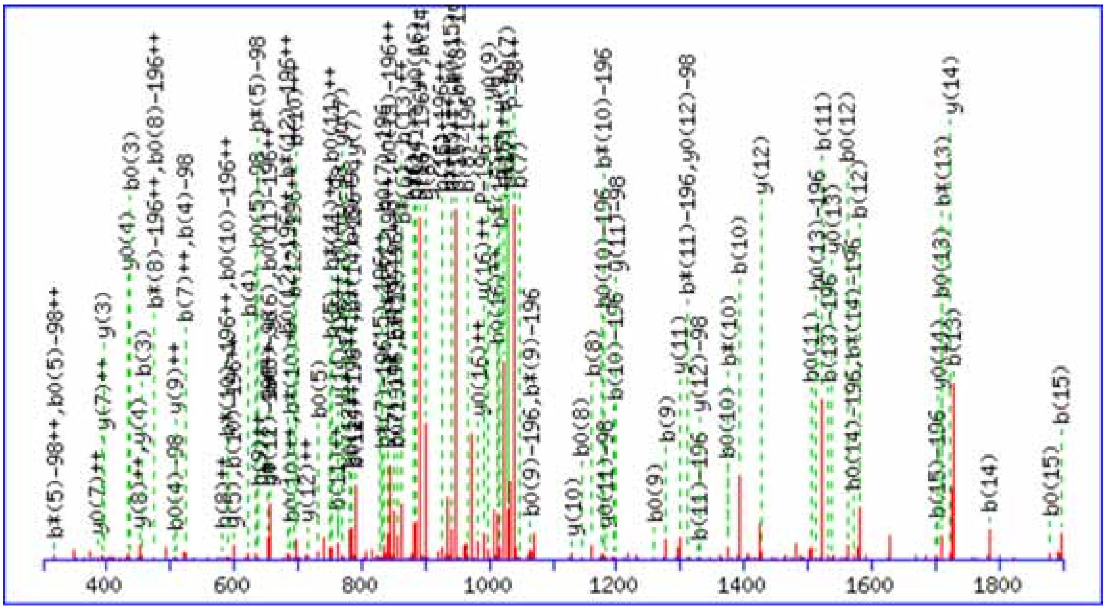
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(7), b(8)++, b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(11)++, b(11)-98++, b(12), b(12)++, b(12)-98, b(12)-98++, b(13), b(13)-98++, b(13)-98, b(13)++, b(14)++, b(14), b(14)-98++, b(14)-98, b(15)++, b(15), b(15)-98++, b(15)-98, b(16)++, b(16)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12)-98, y(12), y(13), y(13)++, y(14), y(15)-98++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.471

KEESEEESDDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 7112: 2176.811570 from(1089.413061,2+)
Title: Elution from: 74.184 to 74.184 scan no 7248 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2176.8109
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.00093

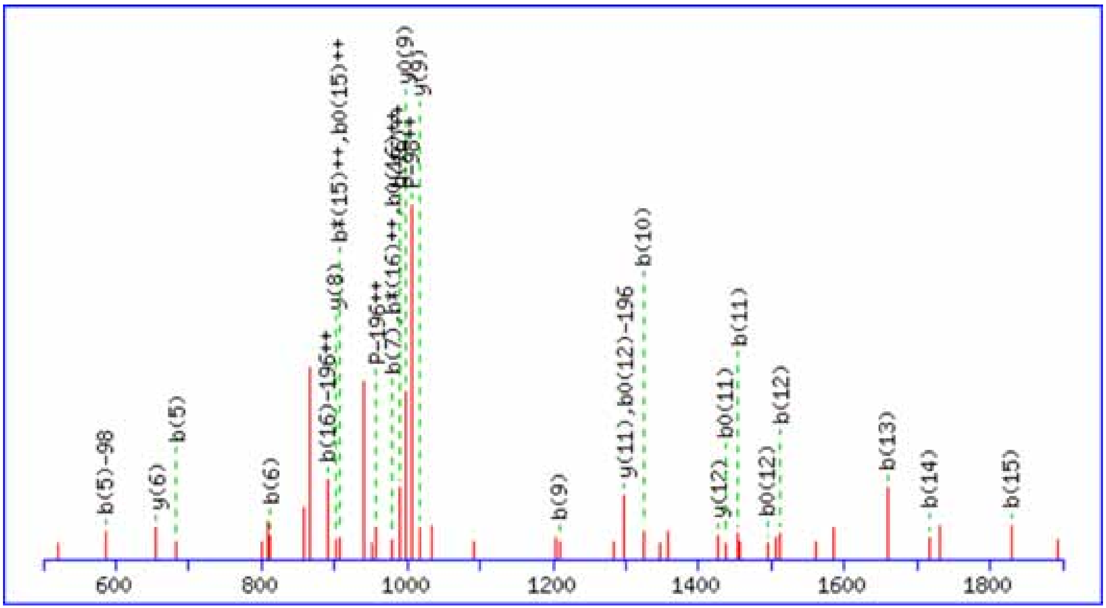
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7)++, b(7)-98++, b(7)-196, b(7), b(8), b(8)++, b(8)-98, b(8)-196, b(9), b(9)-98++, b(9)-98, b(9)++, b(10)-196++, b(10), b(10)++, b(10)-98, b(10)-196, b(11)-98, b(11), b(11)++, b(11)-196, b(12)++, b(12)-98, b(12), b(12)-98++, b(12)-196++, b(13)-98, b(13), b(13)++, b(13)-98++, b(13)-196, b(14)++, b(14)-98++, b(14), b(14)-98, b(15)++, b(15), b(15)-98++, b(15)-196, b(15)-98, b(15)-196++, b(16)-98++, b(16)++, b(16)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10), y(11), y(11)-98, y(12), y(12)++, y(12)-98, y(14), y(14)-196++, y(15)-196++, y(15)-98++, y(15)++, y(16)-196++, y(16)++
Precursor origin neutral loss: +

Peptide No.472

KEESEESDDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESDDDMGFGLFD
Found in RLA2_MOUSE, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5276: 2108.687154 from(1055.350853,2+)
Title: Elution from: 74.025 to 74.025 scan no 6783 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2108.6847
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.00011

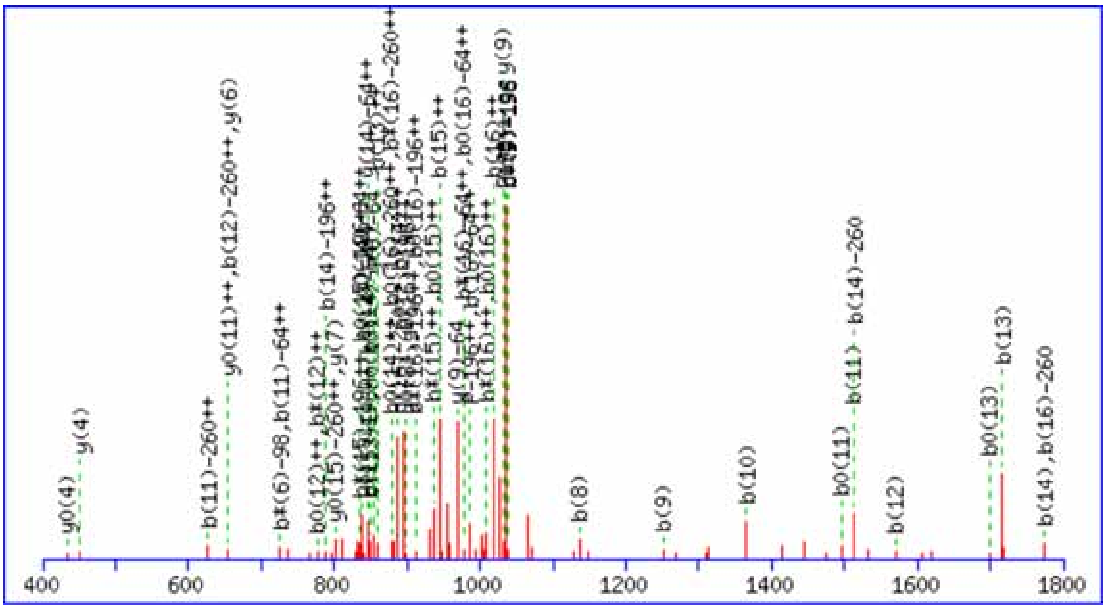
Matched b ions: b(5)-98, b(5), b(6), b(7), b(9), b(10), b(11)-98, b(11), b(12), b(13), b(13)-98, b(14)-98++, b(14), b(15)-98++, b(15)-98, b(15), b(16)-196++, b(16)-98++, b(16)++
Matched y ions: y(6), y(8), y(9), y(11), y(12)
Precursor origin neutral loss: +

Peptide No.473

KEESEEESEDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 6350: 2166.728508 from(1084.371530,2+)
Title: Elution from: 66.005 to 66.005 scan no 6426 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2166.7265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 37 Expect: 0.0017

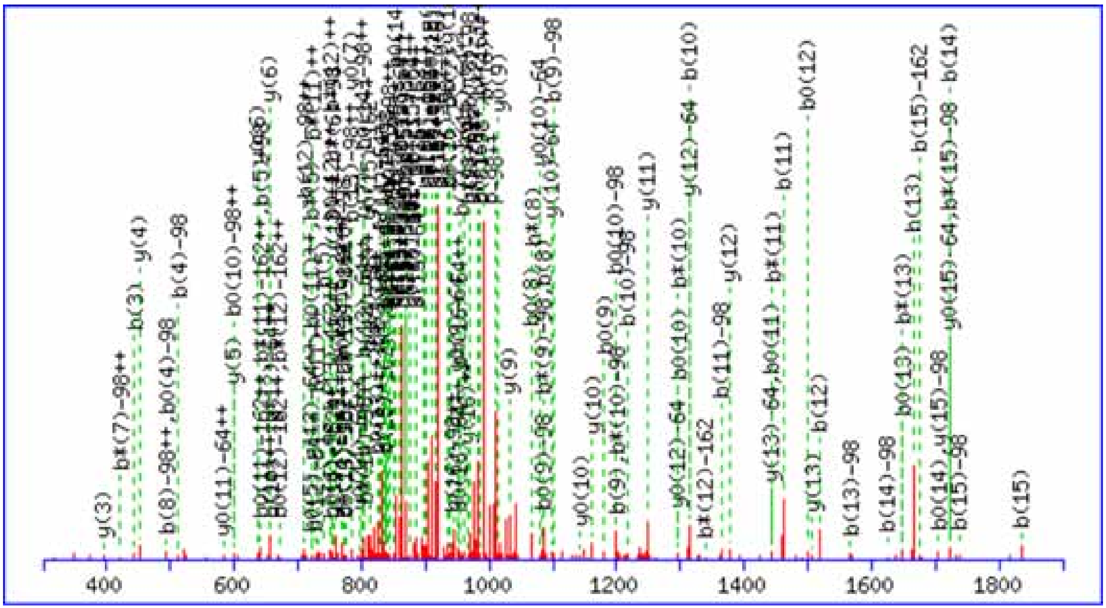
Matched b ions: b(8), b(8)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98++, b(13), b(13)-98++, b(13)-98, b(13)++, b(14), b(14)++, b(14)-98++, b(14)-196++, b(15)-98++, b(15)++, b(15)-196++, b(16)++, b(16)-98++
Matched y ions: y(4), y(6), y(7), y(9)
Precursor origin neutral loss: +

Peptide No.474

KEESEESEDDMGFGLFD
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KEESEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 6971: 2114.795108 from(1058.404830,2+)
Title: Elution from: 58.467 to 58.467 scan no 5856 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2114.7915
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 55 **Expect:** 6e-005

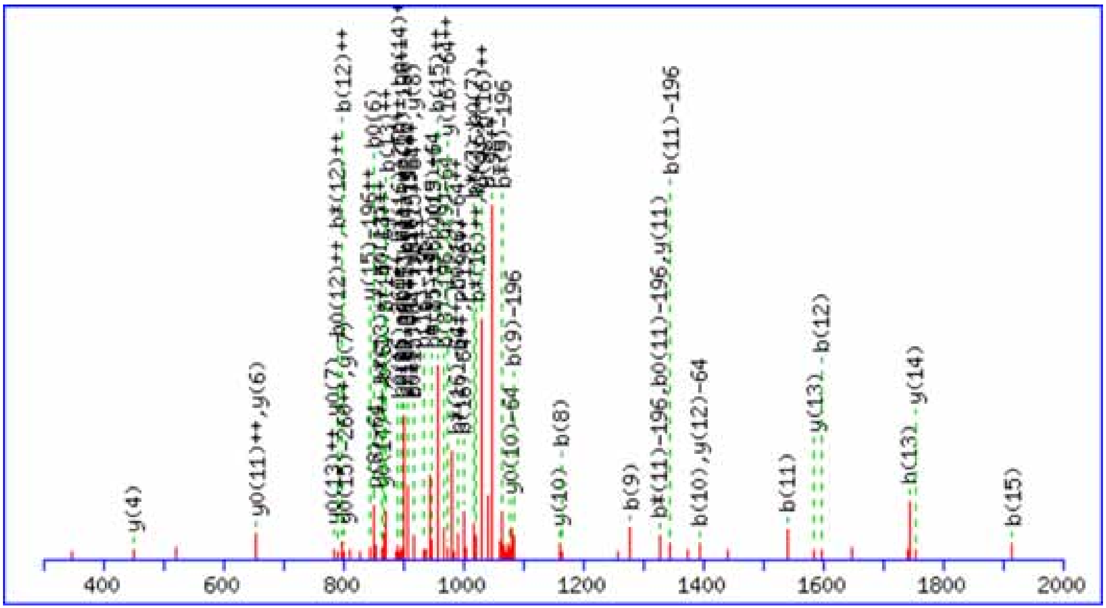
Matched b ions: b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7), b(8)-98++, b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)++, b(10)-98, b(11)-98, b(11), b(11)++, b(12), b(12)-98++, b(12)++, b(13), b(13)-98, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(14), b(14)-98, b(15)++, b(15), b(15)-98, b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)++, y(14)++, y(15)-98++, y(15)-98, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.475

KEESEESEDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 6542: 2194.759058 from(1098.386805,2+)
Title: Elution from: 71.008 to 71.008 scan no 6827 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2194.7578
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 59 Expect: 1.3e-005

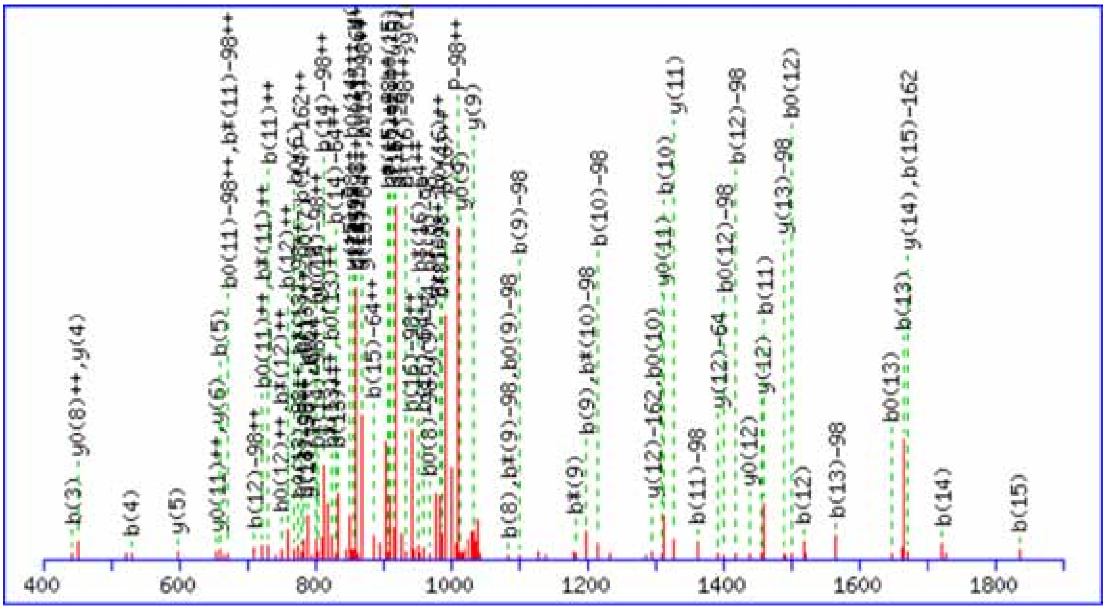
Matched b ions: b(6), b(7)-98, b(8), b(8)-98, b(8)-196, b(9), b(9)-196, b(10), b(11), b(11)-196, b(11)-98, b(12)++, b(12), b(13), b(13)-98, b(13)++, b(14)++, b(14)-98++, b(15), b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(16)-196++
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(13), y(14), y(15)-196++, y(15)-98++, y(16)-196++
Precursor origin neutral loss: +

Peptide No.476

KEESEESEDDMGFGLFD
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 6211: 2114.793296 from(1058.403924,2+)
Title: Elution from: 58.190 to 58.190 scan no 5767 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2114.7915
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 71 Expect: 1.6e-006

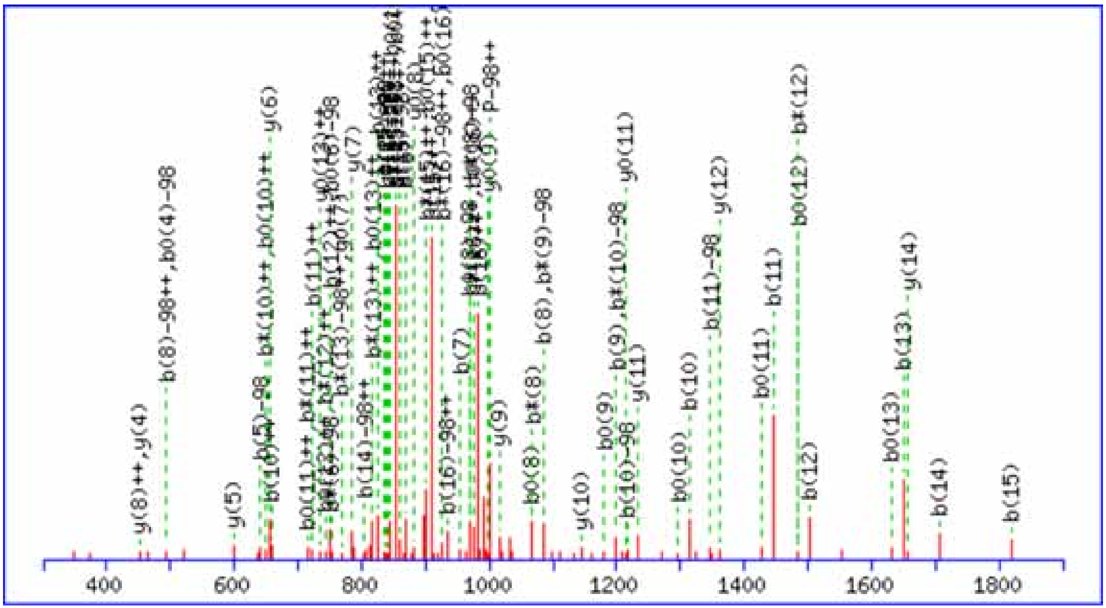
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11)++, b(11)-98, b(11), b(12), b(12)-98++, b(12)-98, b(12)++, b(13)-98, b(13), b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(14), b(15)++, b(15), b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(13)-98, y(14)-98++, y(14), y(15)-98++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.477

KEESEESEDDMGFGLFD
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KEESEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 6143: 2098.799224 from(1050.406888,2+)
Title: Elution from: 66.216 to 66.216 scan no 6447 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2098.7966
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 Expect: 2e-005

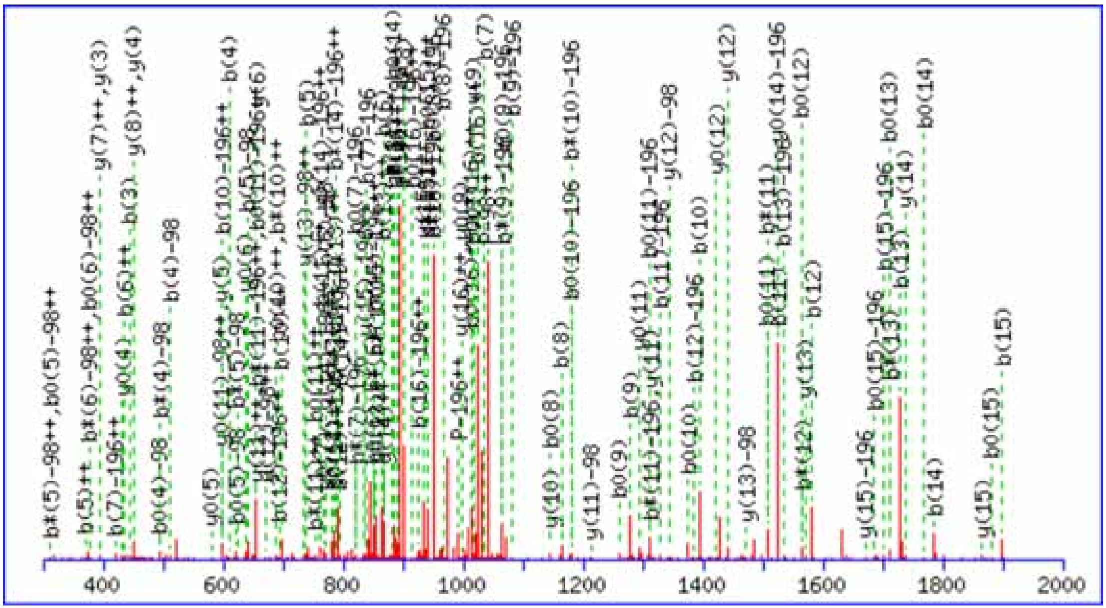
Matched b ions: b(5)-98, b(6), b(7), b(8), b(8)-98++, b(9), b(10), b(10)++, b(10)-98, b(11), b(11)-98, b(11)++, b(12), b(12)++, b(13)++, b(13), b(14)++, b(14), b(14)-98++, b(15), b(15)++, b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11), y(12), y(14), y(15)-98++
Precursor origin neutral loss: +

Peptide No.478

KEESEESEDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 6398: 2178.764374 from(1090.389463,2+)
Title: Elution from: 73.698 to 73.698 scan no 7006 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2178.7629
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 **Expect:** 5.2e-006

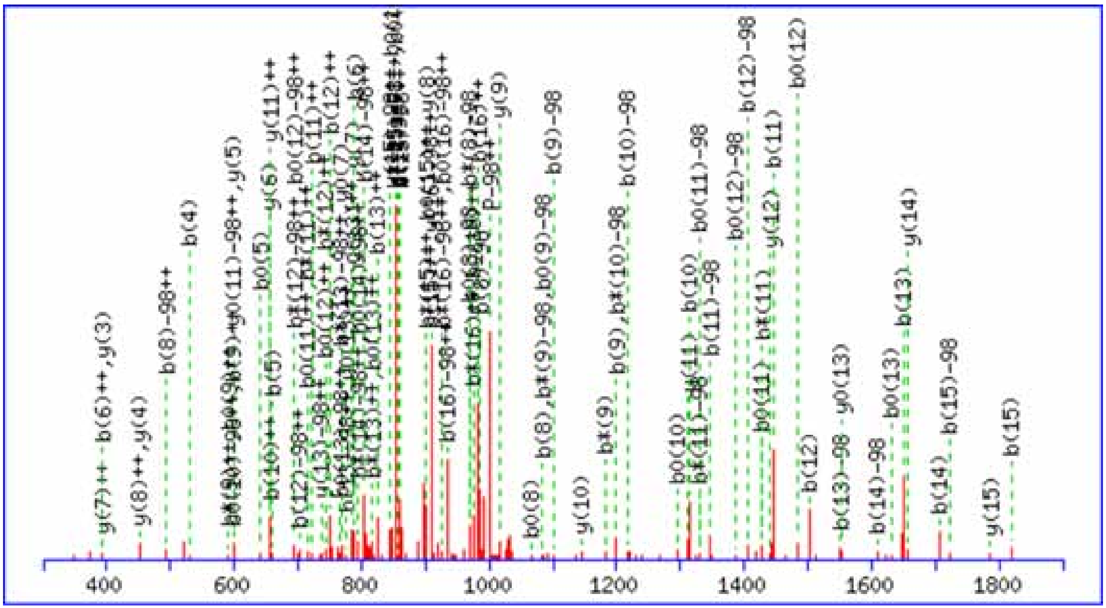
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5)++, b(5), b(6), b(6)++, b(6)-98, b(7)-196++, b(7)-98, b(7)-196, b(7), b(8), b(8)-98, b(8)-196, b(9), b(9)-98, b(9)-196, b(10), b(10)++, b(10)-98, b(10)-196++, b(10)-98++, b(11)-98, b(11), b(11)++, b(11)-196, b(11)-98++, b(12)++, b(12), b(12)-98, b(12)-98++, b(12)-196++, b(12)-196, b(13)-98, b(13), b(13)++, b(13)-196, b(13)-98++, b(14)++, b(14), b(14)-98++, b(14)-98, b(14)-196++, b(15)++, b(15), b(15)-98++, b(15)-98, b(15)-196++, b(15)-196, b(16)-98++, b(16)++, b(16)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9), y(10), y(11), y(11)-98, y(11)++, y(12), y(12)-98++, y(12)-98, y(13)++, y(13), y(13)-98++, y(13)-98, y(14)-98, y(14), y(14)-196++, y(14)++, y(15), y(15)-98++, y(15)-98, y(15)-196++, y(15)++, y(15)-196, y(16)++
Precursor origin neutral loss: +

Peptide No.479

KEESEESEDDMGFGLFD
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 6934: 2098.798506 from(1050.406529,2+)
Title: Elution from: 65.444 to 65.444 scan no 6500 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2098.7966
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 5.5e-005

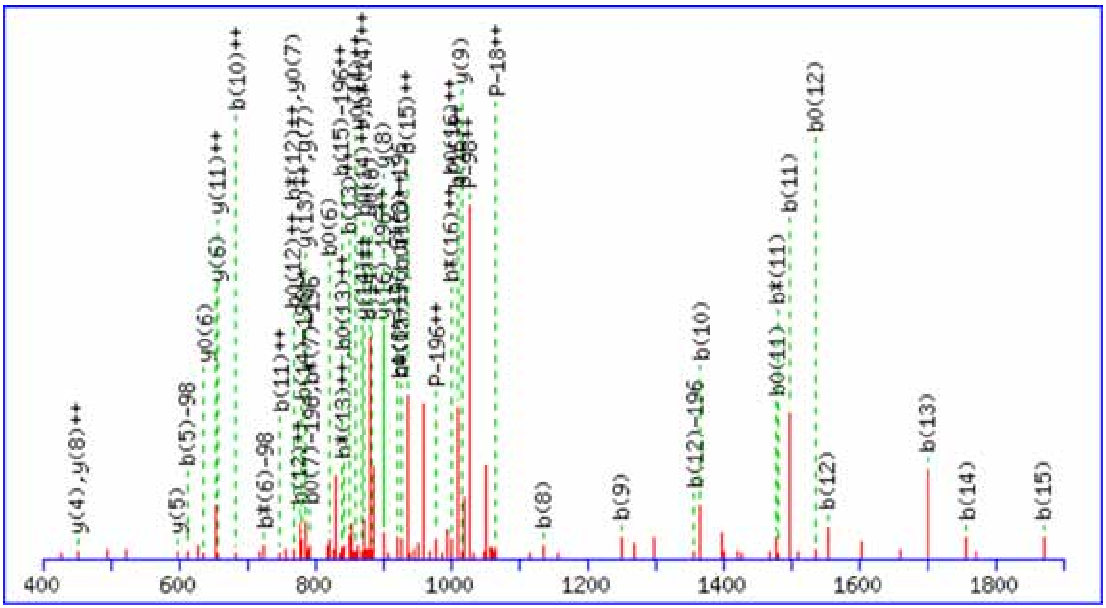
Matched b ions: b(4), b(5), b(6)++, b(6), b(7)-98, b(8)-98++, b(8), b(8)-98, b(9), b(9)++, b(9)-98, b(10), b(10)-98, b(10)++, b(11), b(11)-98, b(11)++, b(12), b(12)++, b(12)-98++, b(12)-98, b(13)-98, b(13), b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(14)-98, b(14), b(15), b(15)++, b(15)-98++, b(15)-98, b(16)++, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(10), y(11), y(11)++, y(12), y(13)++, y(13)-98++, y(14), y(15), y(15)-98++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.480

KEESEESEDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 5552: 2150.732580 from(1076.373566,2+)
Title: Elution from: 74.190 to 74.190 scan no 6840 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2150.7316
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 2.9e-005

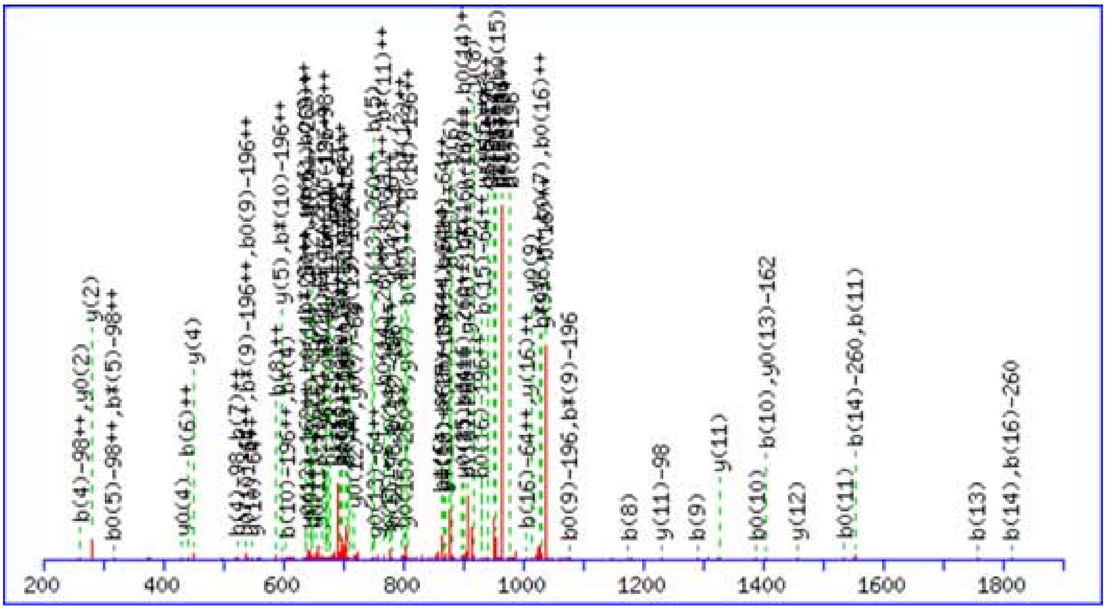
Matched b ions: b(5)-98, b(8), b(9), b(10), b(10)-98, b(10)++, b(11), b(11)-98, b(11)++, b(12), b(12)++, b(12)-196, b(13), b(13)-98, b(13)++, b(14)++, b(14), b(14)-98++, b(14)-98, b(14)-196++, b(15), b(15)-98++, b(15)++, b(15)-98, b(15)-196++, b(16)-98++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(11)++, y(13)++, y(14)-98++, y(14)++, y(16)-196++
Precursor origin neutral loss: +

Peptide No.481

KEESEESEDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 5755: 2206.822572 from(736.614800,3+)
Title: Elution from: 65.736 to 65.736 scan no 6191 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2206.8215
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 63 Expect: 9.3e-006

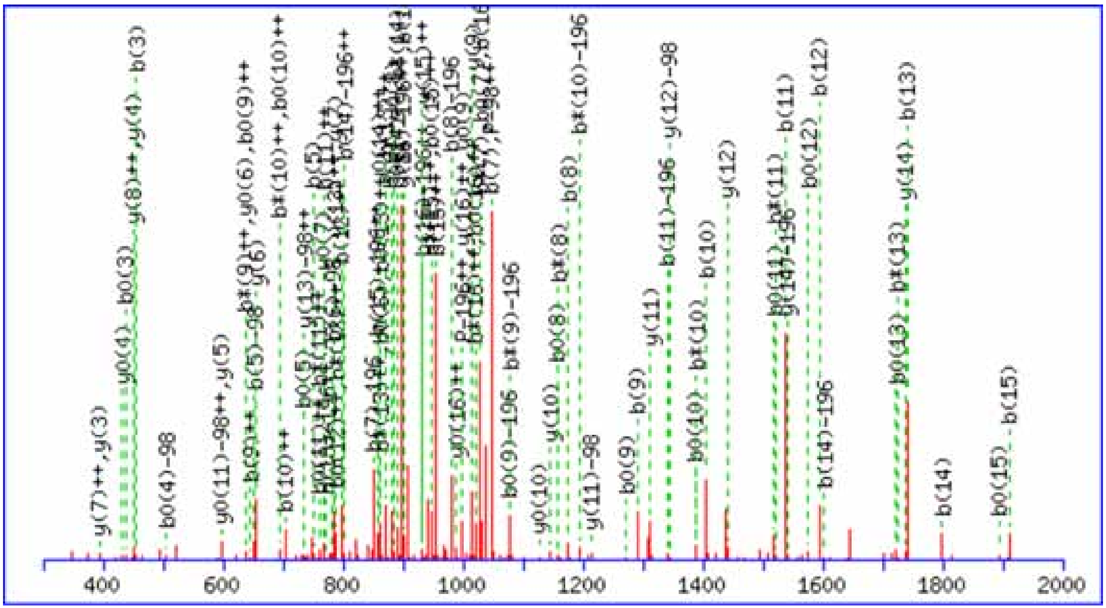
Matched b ions: b(4)-98++, b(4)-98, b(5), b(6)++, b(6)-98, b(6), b(7)++, b(7)-98, b(8)-98++, b(8), b(8)-98, b(8)++, b(8)-196, b(9)++, b(9), b(10), b(10)++, b(10)-98, b(10)-98++, b(10)-196++, b(11), b(11)++, b(11)-196++, b(12)++, b(12)-196++, b(12)-98++, b(13), b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14), b(14)-98++, b(14)-196++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(11)-98, y(11)++, y(12), y(14)-196++, y(15)++, y(16)-196++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.482

KEESEESEDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of KEESEESEDDMGFGLFD
Found in RLA1_MOUSE, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 5203: 2190.826578 from(1096.420565,2+)
Title: Elution from: 73.747 to 73.747 scan no 6425 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2190.8265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 Expect: 4.5e-007

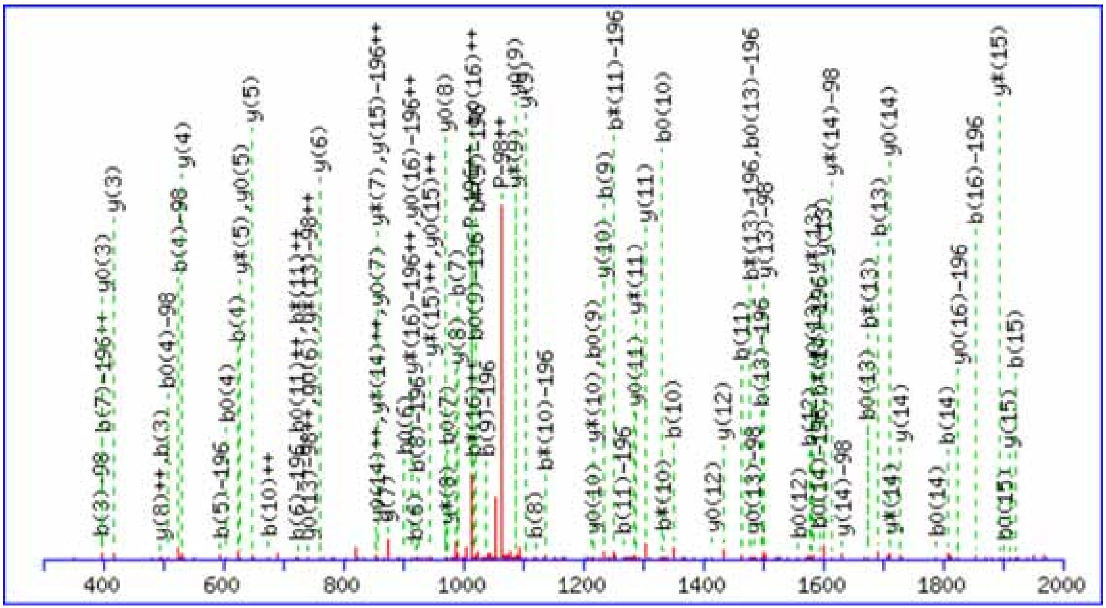
Matched b ions: b(3), b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-196, b(7)-98, b(8), b(8)-98, b(8)-196, b(9), b(9)-98, b(9)++, b(10)-98++, b(10), b(10)++, b(10)-98, b(11), b(11)-98, b(11)-196, b(11)++, b(11)-98++, b(12)++, b(12), b(12)-98++, b(12)-98, b(13), b(13)-98, b(13)-98++, b(13)++, b(13)-196++, b(14)++, b(14), b(14)-98++, b(14)-98, b(14)-196, b(14)-196++, b(15)++, b(15), b(15)-98++, b(15)-98, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9), y(10), y(11), y(11)-98, y(12), y(12)-98, y(13)++, y(13)-98++, y(14), y(14)-196, y(15)-98++, y(15)++, y(16)-196++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.483

KETESEAEDDNLDDLER
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of KETESEAEDDNLDDLER
Found in SRRM1_MOUSE, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=1

Match to Query 6075: 2222.851686 from(1112.433119,2+)
Title: Elution from: 41.469 to 41.469 scan no 3702 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2222.8504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 Expect: 5.9e-006

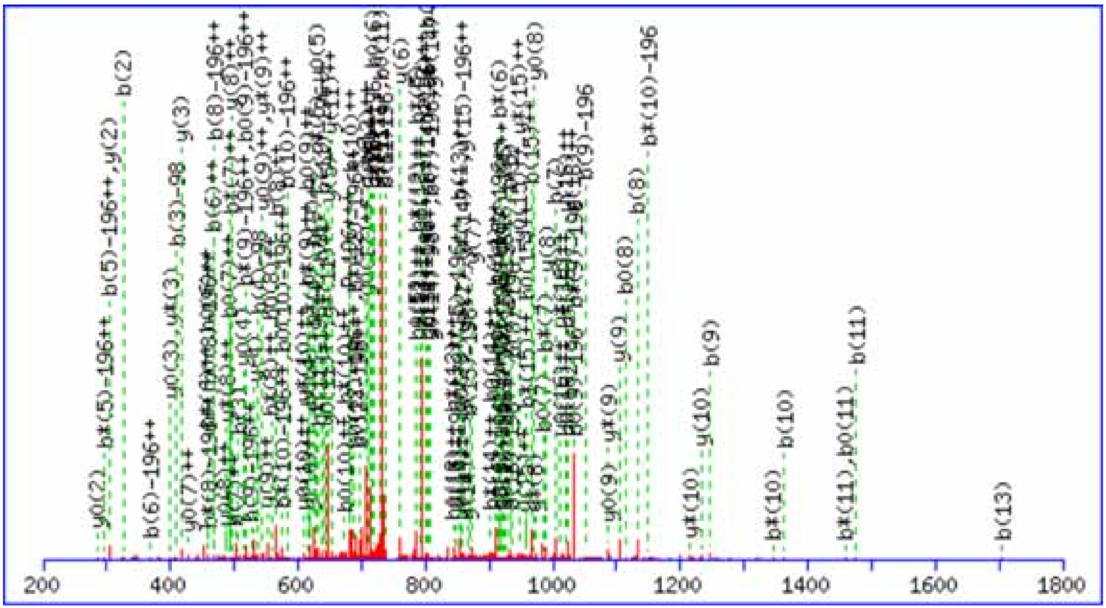
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5)-196, b(6)-98, b(6)-196, b(6), b(7)-196++, b(7)-98, b(7), b(8)-196, b(8)-98, b(8), b(9), b(9)-196, b(9)-98, b(10), b(10)++, b(10)-98, b(11), b(11)-98, b(11)-196, b(12), b(12)-98, b(13), b(13)-196, b(13)-98, b(14), b(14)-98, b(15), b(16)-98, b(16)-196
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(11), y(12), y(13)-98, y(13), y(14)-98, y(14), y(15)-98, y(15)-196++, y(15), y(16)-98, y(16)-98++
Precursor origin neutral loss: +

Peptide No.484

KETESEAEDDNLDDLER
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of KETESEAEDDNLDDLER
Found in SRRM1_MOUSE, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=1

Match to Query 5736: 2234.917638 from(745.979822,3+)
Title: Elution from: 41.382 to 41.382 scan no 3630 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2234.9141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 2.6e-005

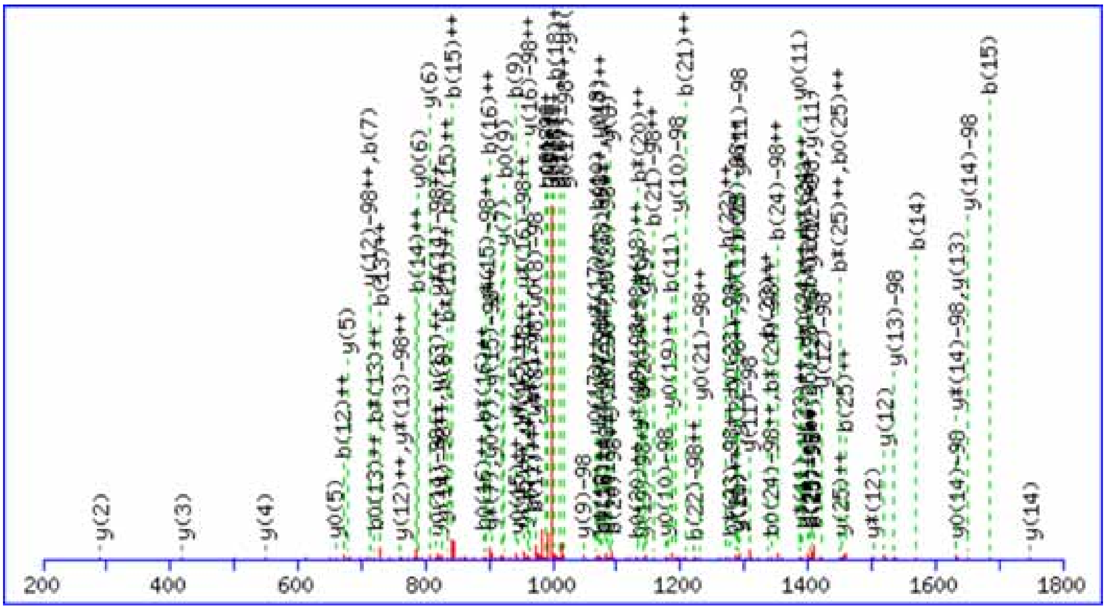
Matched b ions: b(2), b(3)-98, b(3), b(4), b(4)-98, b(5)-196++, b(5)-98, b(5), b(6)-98++, b(6)++, b(6)-98, b(6), b(6)-196++, b(6)-196, b(7)-98++, b(7), b(7)++, b(7)-98, b(7)-196, b(8)++, b(8), b(8)-98++, b(8)-196++, b(8)-98, b(8)-196, b(9), b(9)++, b(9)-98++, b(9)-196++, b(9)-196, b(9)-98, b(10), b(10)++, b(10)-98++, b(10)-196++, b(11), b(11)-98++, b(11)-196++, b(11)++, b(12)++, b(12)-196++, b(13), b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-98++, b(16)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)-98++, y(15)-196++, y(15)++, y(16)-196++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.485

KGATPAEDDDEDKDIDLFGSDEEEEDK
Confirmed sites: @S:19
Ambiguous sites:

MS/MS Fragmentation of KGATPAEDDDEDKDIDLFGSDEEEEDK
Found in EF1D_MOUSE, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 8615: 3088.318317 from(1030.446715,3+)
Title: Elution from: 44.979 to 44.979 scan no 4300 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3088.3173
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
K12 : Dimethyl (K)
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K26 : Dimethyl (K)
Ions Score: 82 Expect: 5.6e-007

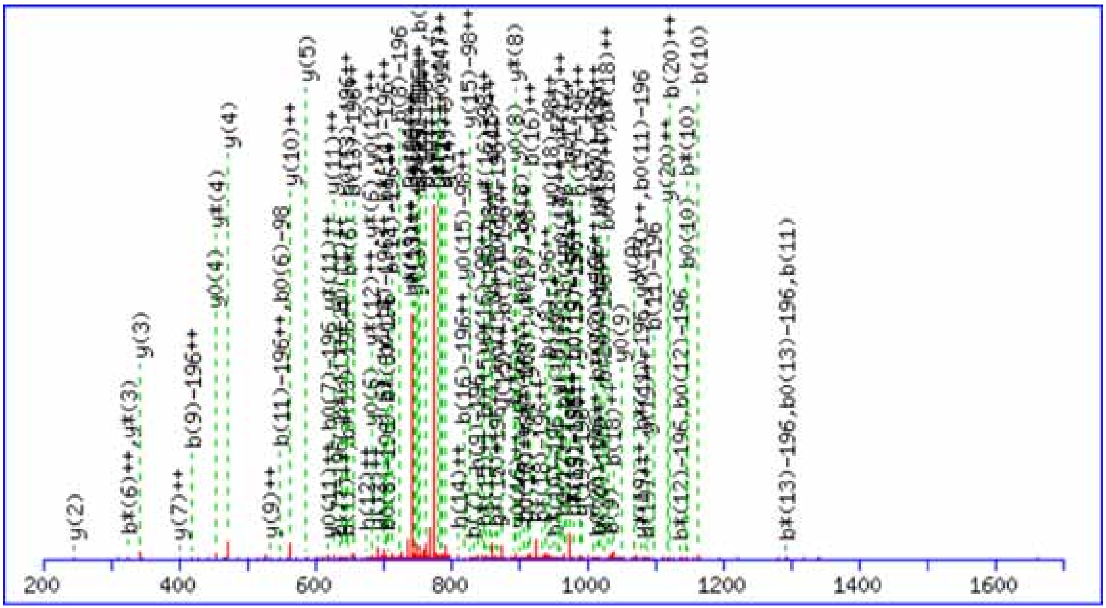
Matched b ions: b(7), b(8), b(9), b(10), b(11), b(12)++, b(13)++, b(14)++, b(14), b(15)++, b(15), b(16)++, b(17)++, b(18)++, b(19)++, b(20)-98++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(23)++, b(24)-98++, b(24)++, b(25)-98++, b(25)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98, y(10)-98, y(10), y(11)-98, y(11), y(12), y(12)-98++, y(12)-98, y(12)++, y(13), y(13)-98, y(13)++, y(14), y(14)-98, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(21)++, y(22)-98++, y(23)++, y(25)-98++, y(25)++
Precursor origin neutral loss: +

Peptide No.486

KGSAEGSSDEEGKLVIDEPAK
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of KGSAEGSSDEEGKLVIDEPAK
Found in HDGF_MOUSE, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 6163: 2417.103354 from(806.708394,3+)
Title: Elution from: 36.553 to 36.553 scan no 2981 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2417.1015
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
K21 : Dimethyl (K)
Ions Score: 33 Expect: 0.044

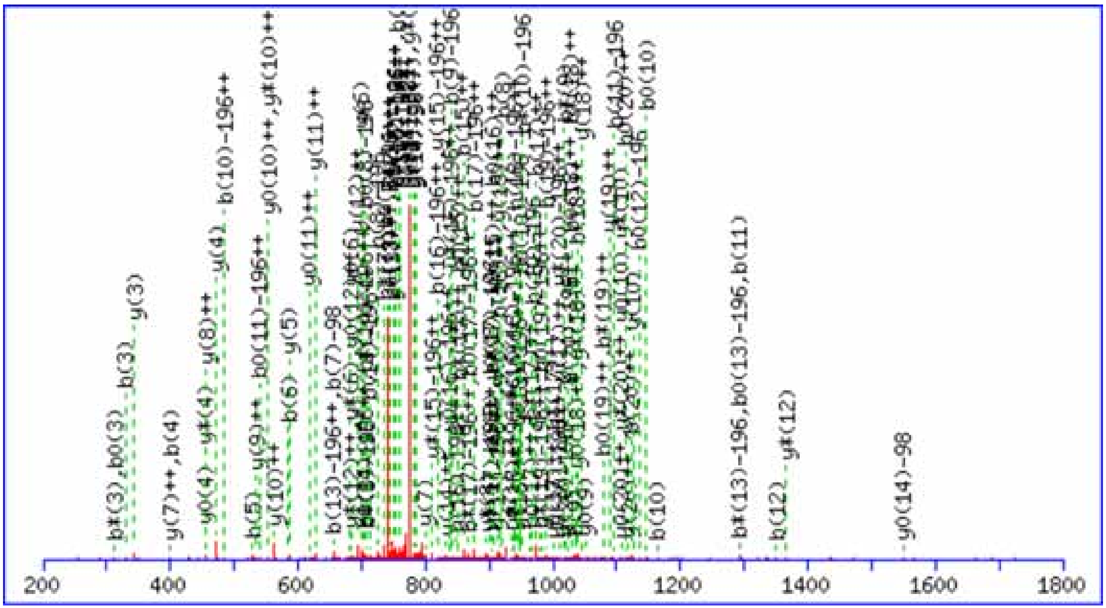
Matched b ions: b(7)-98, b(7)-196, b(7), b(8)-196, b(9), b(9)-196++, b(9)-196, b(9)-98, b(10), b(10)-98, b(10)-98++, b(10)-196, b(11), b(11)-98, b(11)-196, b(11)-196++, b(11)++, b(12)++, b(13)++, b(13)-196++, b(13)-98++, b(14)-98++, b(14)-196++, b(14)++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-196++, b(16)-98++, b(17)-98++, b(17)++, b(17)-196++, b(18)++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)-196++, b(19)++, b(20)-98++, b(20)++, b(20)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(8), y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(18)-98++, y(19)-98++, y(19)-196++, y(19)++, y(20)-98++, y(20)-196++, y(20)++
Precursor origin neutral loss: +

Peptide No.487

KGSAEGSSDEEGKLVIDEPAK
Confirmed sites: @S:7,@S:8
Ambiguous sites:

MS/MS Fragmentation of KGSAEGSSDEEGKLVIDEPAK
Found in HDGF_MOUSE, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 6409: 2417.103168 from(806.708332,3+)
Title: Elution from: 36.523 to 36.523 scan no 2996 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2417.1015
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
K21 : Dimethyl (K)
Ions Score: 36 Expect: 0.02

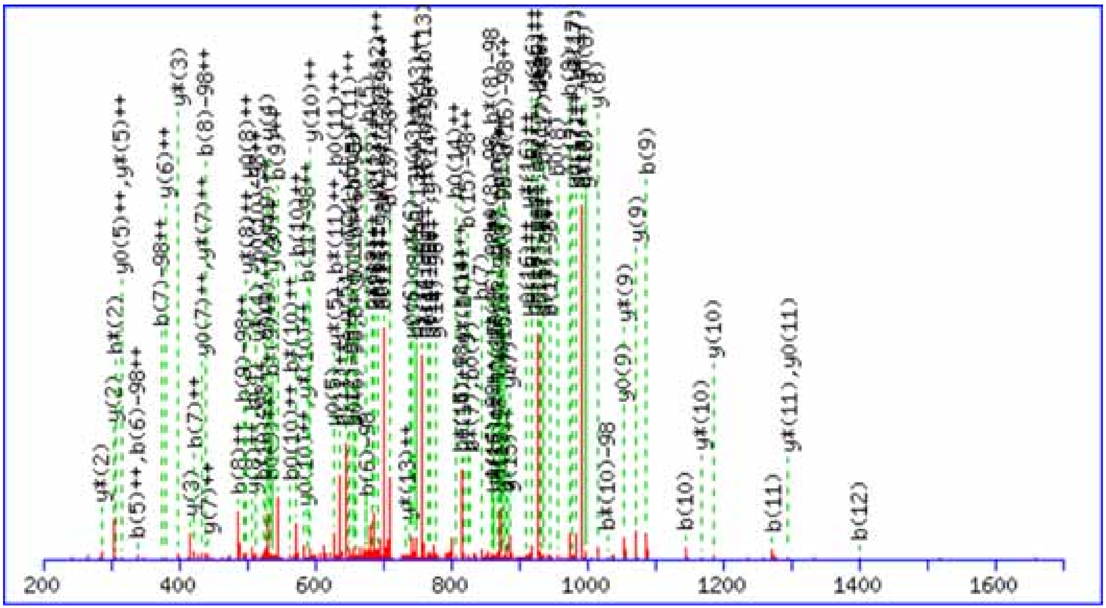
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(7)-98, b(8)-196, b(8), b(9), b(9)-196, b(9)-98, b(10), b(10)-98, b(10)-196++, b(10)-196, b(11)-98, b(11), b(11)-196, b(12), b(12)-98++, b(13)++, b(13)-196++, b(13)-98++, b(14)-98++, b(14)-196++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-98++, b(16)-196++, b(17)-98++, b(17)++, b(17)-196++, b(18)++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)-196++, b(20)++, b(20)-98++, b(20)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(8)++, y(9)++, y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(15)-196++, y(16)-98++, y(16)-196++, y(16)++, y(17)-196++, y(17)++, y(18)++, y(18)-196++, y(18)-98++, y(19)-98++, y(19)++, y(20)-196++, y(20)++
Precursor origin neutral loss: +

Peptide No.488

KHADSVAELGEQIDNLQR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of KHADSVAELGEQIDNLQR
Found in MYH7_MOUSE, Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1

Match to Query 6317: 2158.043337 from(720.355055,3+)
Title: Elution from: 45.075 to 45.075 scan no 4313 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2158.0419
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 99 **Expect:** 9.5e-009

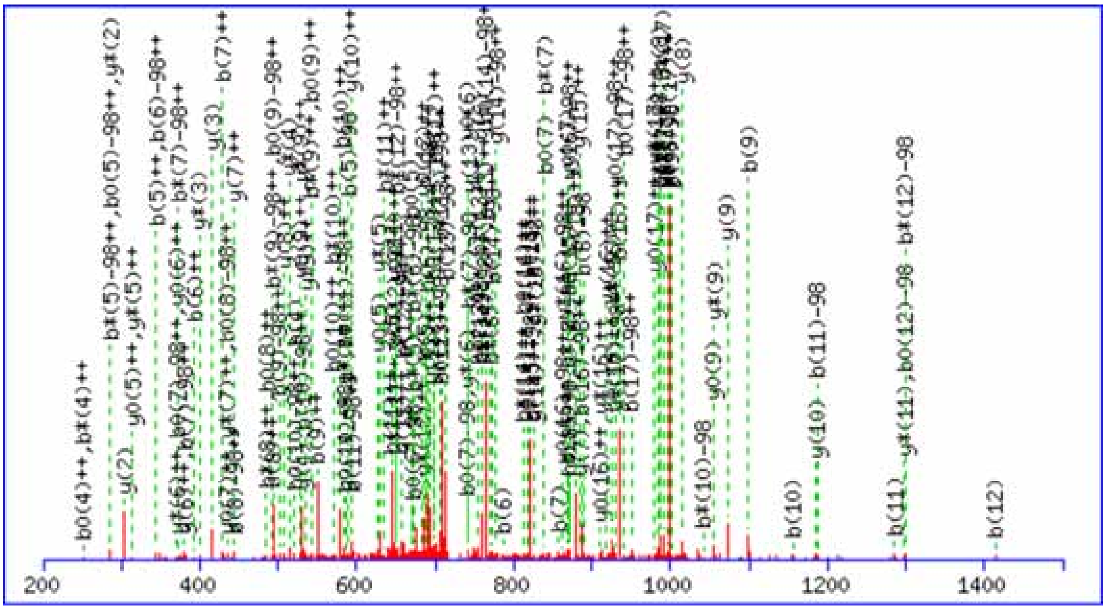
Matched b ions: b(4), b(5)++, b(5), b(6)-98++, b(6)-98, b(7)++, b(7), b(7)-98++, b(7)-98, b(8)++, b(8), b(8)-98++, b(8)-98, b(9)++, b(9), b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)++, b(11), b(11)-98++, b(12)++, b(12), b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)-98++, y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss:

Peptide No.489

KHADSVAELGEQIDNLQR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of KHADSVAELGEQIDNLQR
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 5027: 2170.109607 from(724.377145,3+)
Title: Elution from: 44.890 to 44.890 scan no 3983 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2170.1055
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 76 Expect: 1.6e-006

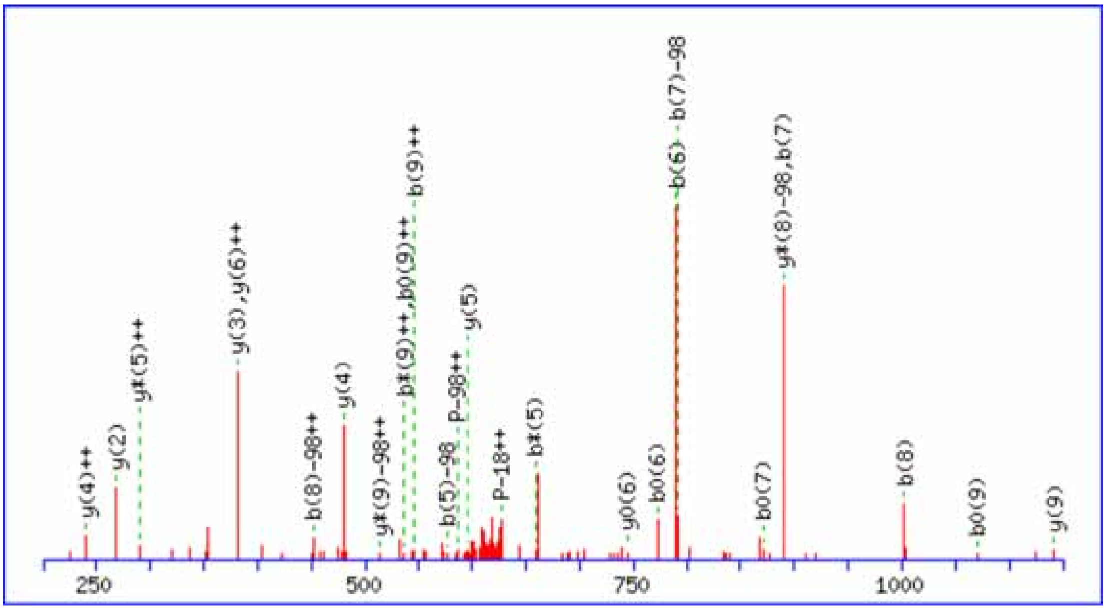
Matched b ions: b(4), b(5)++, b(5)-98, b(5), b(6)-98++, b(6)++, b(6)-98, b(6), b(7)-98++, b(7)-98, b(7)++, b(7), b(8)++, b(8), b(8)-98++, b(8)-98, b(9)++, b(9), b(9)-98++, b(9)-98, b(10)-98++, b(10)++, b(10), b(11), b(11)++, b(11)-98, b(11)-98++, b(12)++, b(12), b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(16)-98++, y(16)++, y(17)++
Precursor origin neutral loss:

Peptide No.490

KHLESDVLSK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of KHLESDVLSK
Found in AL2SB_MOUSE, Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 12 protein homolog OS=Mus musculus GN=Als2cr12 PE=2 SV=1

Match to Query 2103: 1268.661968 from(635.338260,2+)
Title: Elution from: 62.005 to 62.005 scan no 6207 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1268.6590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K10 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 32 Expect: 0.022

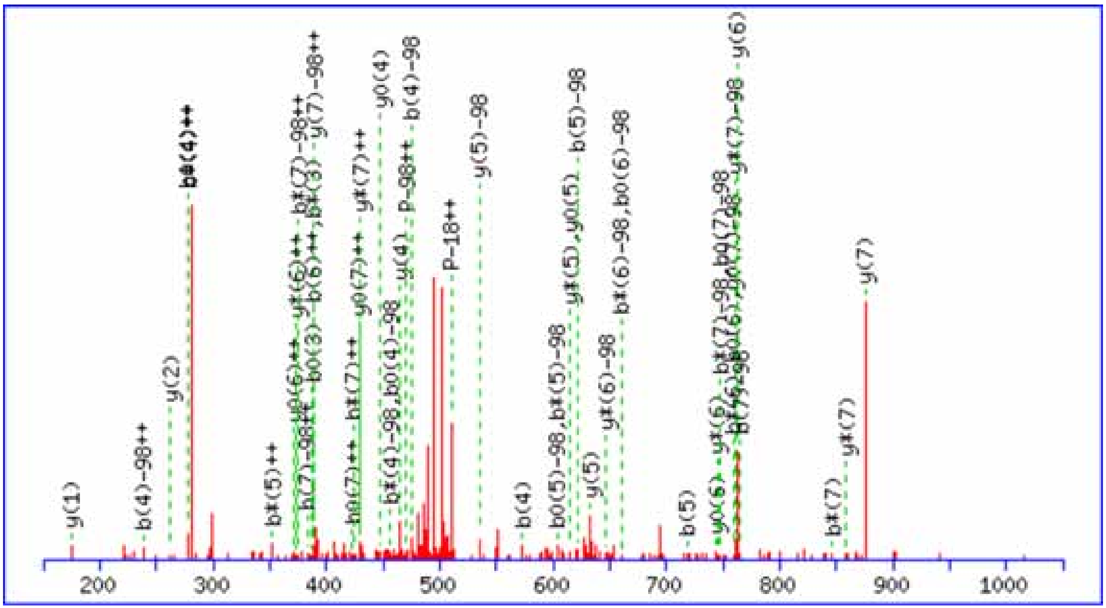
Matched b ions: b(5)-98, b(6), b(7), b(7)-98, b(8), b(8)-98++, b(9)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6)++, y(9)
Precursor origin neutral loss:

Peptide No.491

KIESFGSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KIESFGSK
Found in PPIF_MOUSE, Peptidyl-prolyl cis-trans isomerase F, mitochondrial OS=Mus musculus GN=Ppif PE=2 SV=1

Match to Query 553: 1036.543228 from(519.278890,2+)
Title: Elution from: 29.167 to 29.167 scan no 2030 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1036.5418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K8 : Dimethyl (K)
Ions Score: 29 **Expect:** 0.042

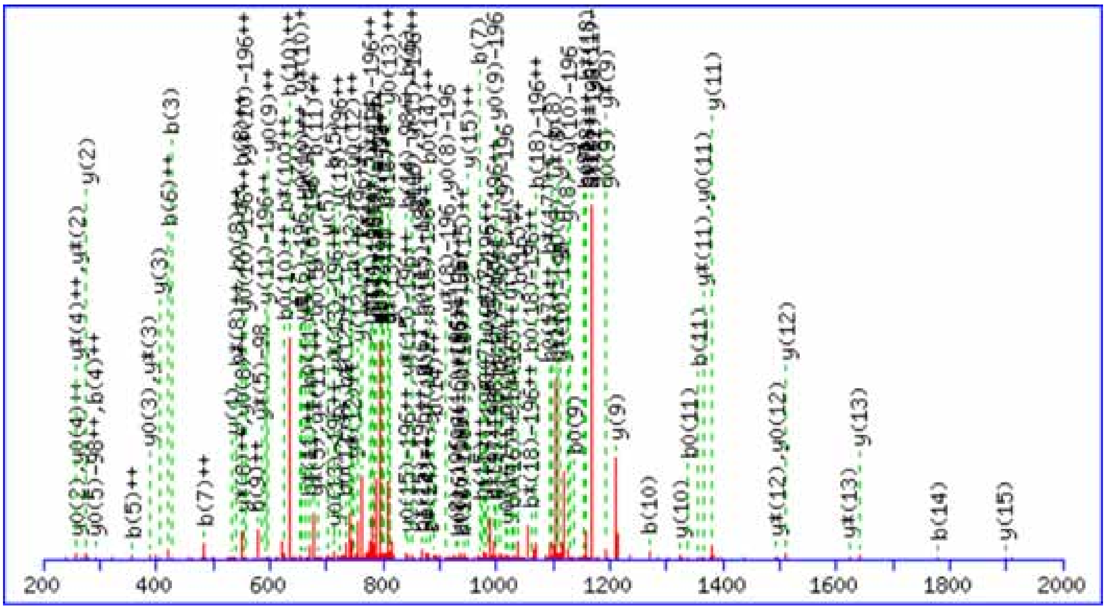
Matched b ions: b(4)-98++, b(4)-98, b(4), b(5)-98, b(5), b(6)++, b(7)-98++, b(7)-98
Matched y ions: y(1), y(2), y(4), y(5), y(5)-98, y(6), y(7), y(7)-98++
Precursor origin neutral loss:

Peptide No.492

KLEKEEEEGISQESSEEEQ
Confirmed sites: @S:14,@S:15
Ambiguous sites:

MS/MS Fragmentation of KLEKEEEEGISQESSEEEQ
Found in HMGA1_MOUSE, High mobility group protein HMG-I/HMG-Y OS=Mus musculus GN=Hmga1 PE=1 SV=4

Match to Query 6302: 2480.014845 from(827.678891,3+)
Title: Elution from: 30.194 to 30.194 scan no 2133 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2480.0131
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
K4 : Dimethyl (K)
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 Expect: 3e-007

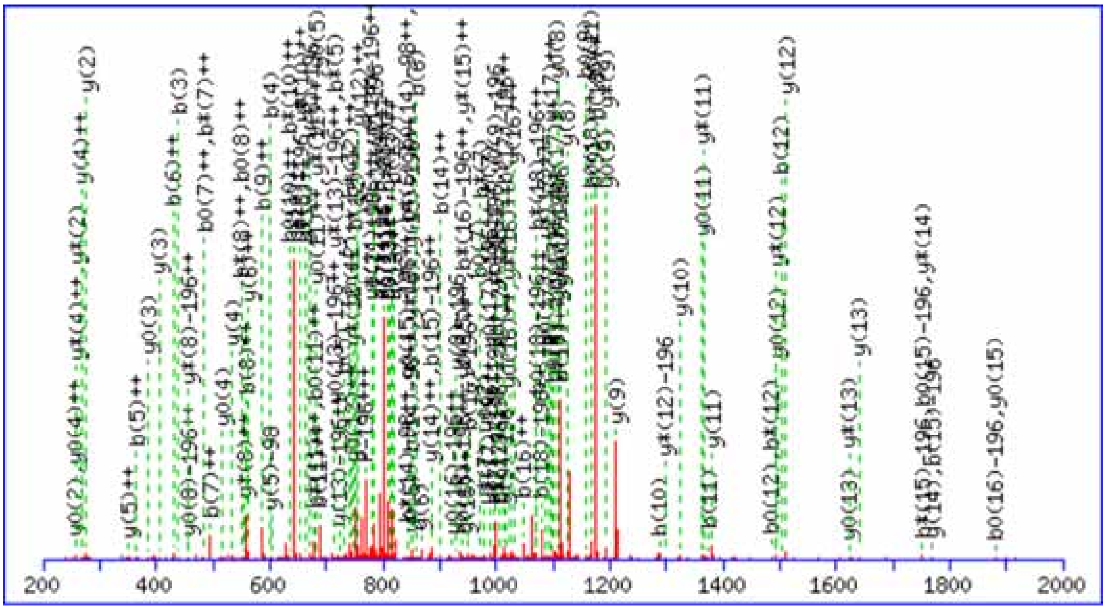
Matched b ions: b(3), b(4)++, b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(13)++, b(14), b(14)-98++, b(14)++, b(15)-196++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(16)-196++, b(17)++, b(17)-98++, b(17)-196++, b(18)++, b(18)-98++, b(18)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-196, y(6)-98, y(7), y(7)-98, y(7)-196, y(8), y(8)-196, y(8)-98, y(9), y(9)-98, y(9)-98++, y(9)-196, y(10), y(10)-98++, y(10)++, y(10)-196, y(11), y(11)-98, y(11)-196++, y(12), y(12)++, y(12)-98++, y(13), y(13)-196++, y(13)-98++, y(14)-196++, y(15), y(15)-196++, y(15)++, y(16)-98++, y(16)-196++, y(16)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.493

KLEKEEEEGISQESSEEEQ
Confirmed sites: @S:14,@S:15
Ambiguous sites:

MS/MS Fragmentation of KLEKEEEEGISQESSEEEQ
Found in HMGA1_MOUSE, High mobility group protein HMG-I/HMG-Y OS=Mus musculus GN=Hmga1 PE=1 SV=4

Match to Query 6587: 2498.109249 from(833.710359,3+)
Title: Elution from: 30.290 to 30.290 scan no 2144 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2498.1086
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
K4 : Dimethyl:2H(4)13C(2) (K)
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 Expect: 3.7e-005

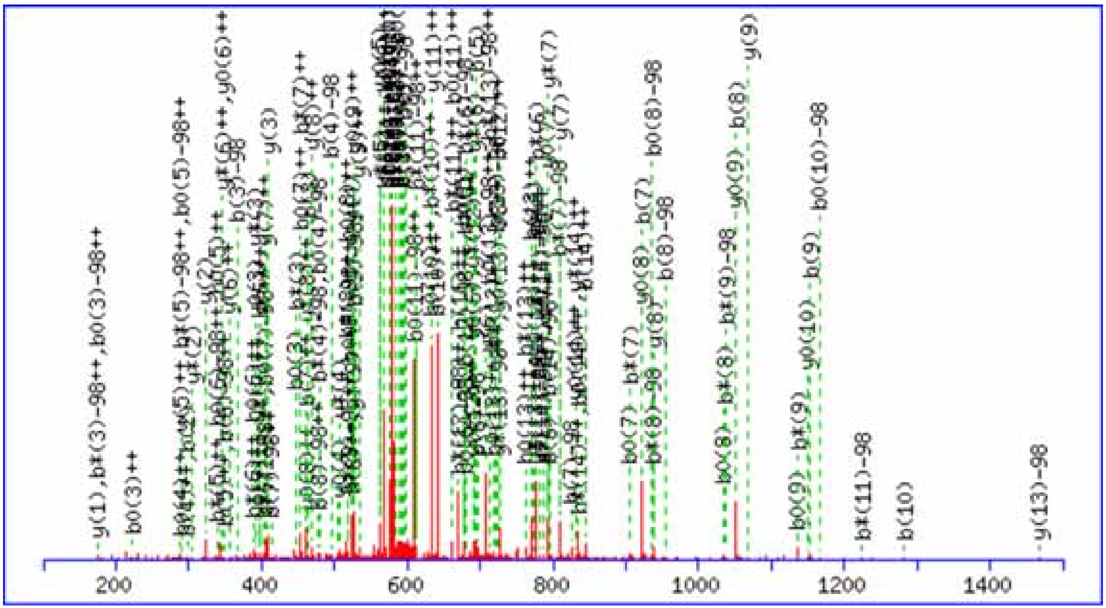
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(9)++, b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(12), b(13)++, b(14)-98++, b(14)++, b(15)-196++, b(15)-196, b(15)-98++, b(16)-98++, b(16)++, b(16)-196++, b(17)++, b(17)-196++, b(17)-98++, b(18)++, b(18)-98++, b(18)-196++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5)++, y(5)-98, y(6), y(6)-196, y(6)-98, y(7)-196, y(7), y(7)-98, y(8)-98, y(8)++, y(8)-196, y(8), y(9), y(9)-98, y(9)-196, y(9)-98++, y(10), y(10)-98++, y(10)++, y(11)-98, y(11), y(11)-98++, y(12), y(12)++, y(13), y(13)-196++, y(13)-98++, y(13)++, y(14)++, y(14), y(15)-196++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-196++, y(17)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.494

KLSETVEETEGNSFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KLSETVEETEGNSFK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4074: 1860.877416 from(621.299748,3+)
Title: Elution from: 37.240 to 37.240 scan no 3100 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1860.8757
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 49 **Expect:** 0.00078

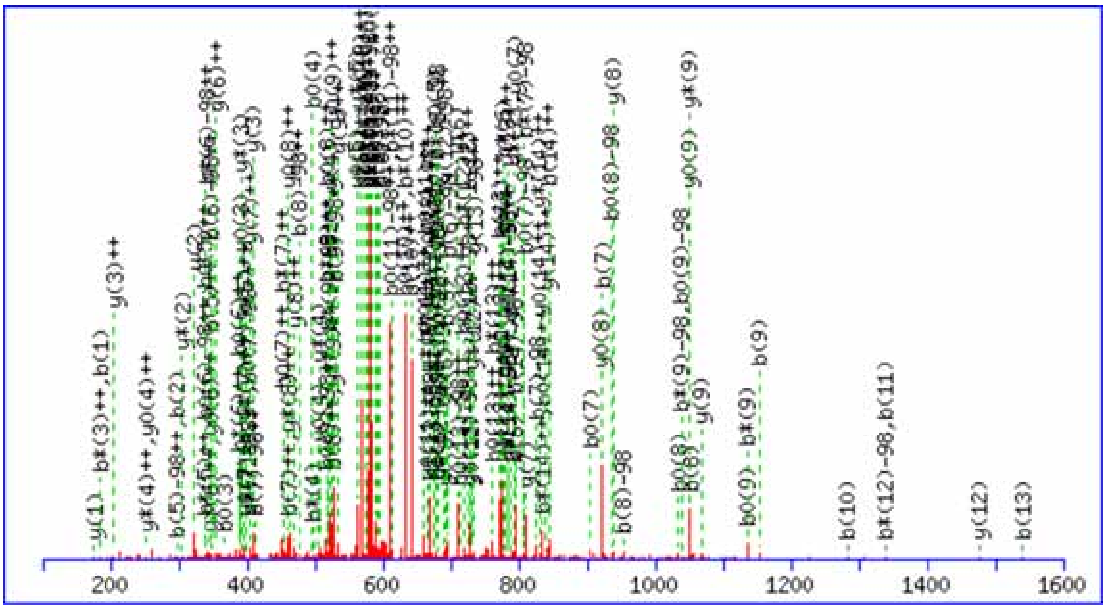
Matched b ions: b(2), b(3)-98, b(3), b(4)++, b(4)-98, b(4), b(5), b(5)++, b(5)-98, b(6), b(6)-98, b(6)-98++, b(6)++, b(7)++, b(7), b(7)-98, b(7)-98++, b(8), b(8)++, b(8)-98++, b(8)-98, b(9), b(9)++, b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(11)++, y(13)-98
Precursor origin neutral loss:

Peptide No.495

KLSETVEETEGNSFK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of KLSETVEETEGNSFK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3854: 1860.876735 from(621.299521,3+)
Title: Elution from: 37.347 to 37.347 scan no 3113 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1860.8757
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 53 Expect: 0.00029

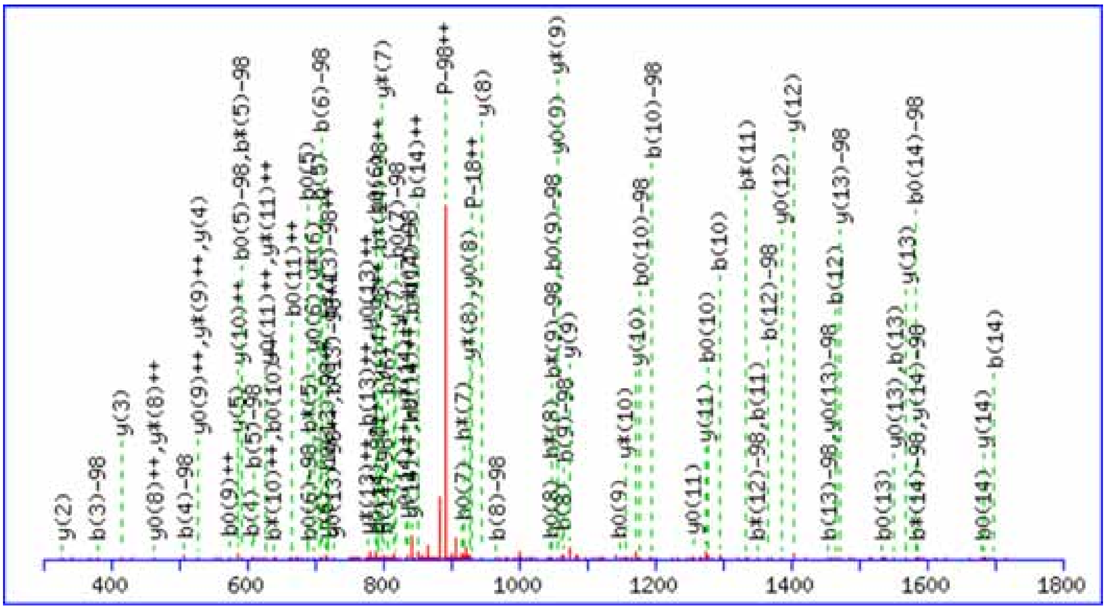
Matched b ions: b(1), b(2), b(5), b(5)-98++, b(5)++, b(5)-98, b(6), b(6)-98++, b(6)++, b(6)-98, b(7), b(7)++, b(7)-98, b(7)-98++, b(8), b(8)++, b(8)-98, b(8)-98++, b(9), b(9)++, b(9)-98++, b(10), b(10)++, b(10)-98++, b(11), b(11)++, b(12)++, b(12)-98++, b(13)++, b(13), b(14)++, b(14)-98++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(11)++, y(12), y(12)-98++, y(13)-98++, y(13)++, y(14)++
Precursor origin neutral loss:

Peptide No.496

KLSETVEETEGNSFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KLSETVEETEGNSFK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4252: 1878.971820 from(940.493186,2+)
Title: Elution from: 37.213 to 37.213 scan no 3096 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1878.9712
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 71 Expect: 4.9e-006

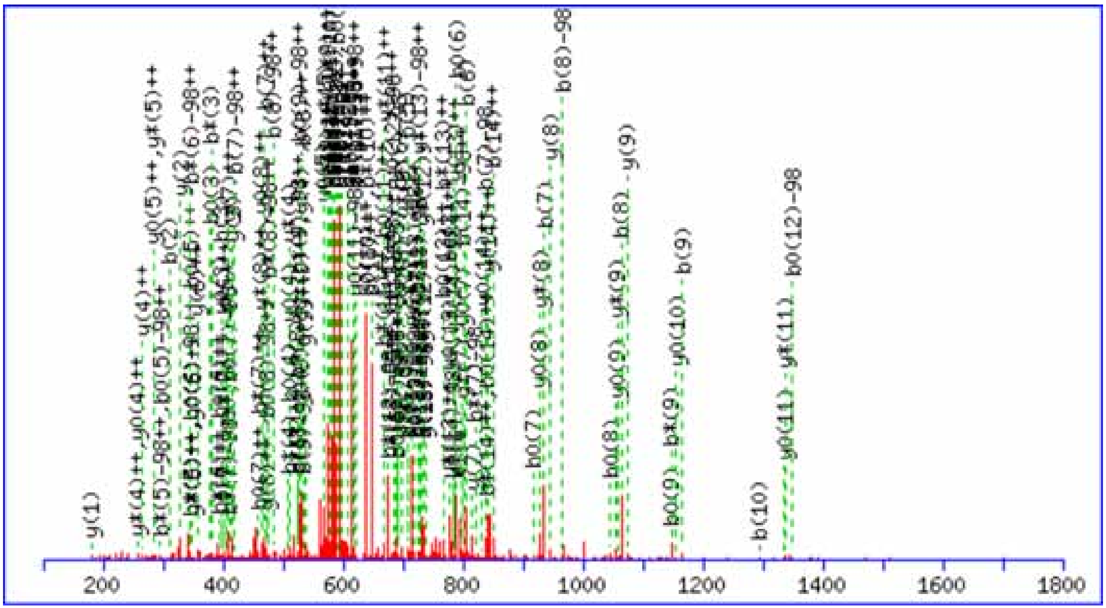
Matched b ions: b(3)-98, b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7)-98, b(8)-98, b(8), b(9)-98, b(10), b(10)-98, b(11), b(12), b(12)-98, b(13), b(13)-98, b(13)-98++, b(13)++, b(14)-98++, b(14), b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(12), y(13), y(13)-98, y(14)-98, y(14)++, y(14), y(14)-98++
Precursor origin neutral loss: +

Peptide No.497

KLSETVEETEGNSFK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of KLSETVEETEGNSFK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4049: 1878.971586 from(627.331138,3+)
Title: Elution from: 37.352 to 37.352 scan no 3114 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1878.9712
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 33 Expect: 0.033

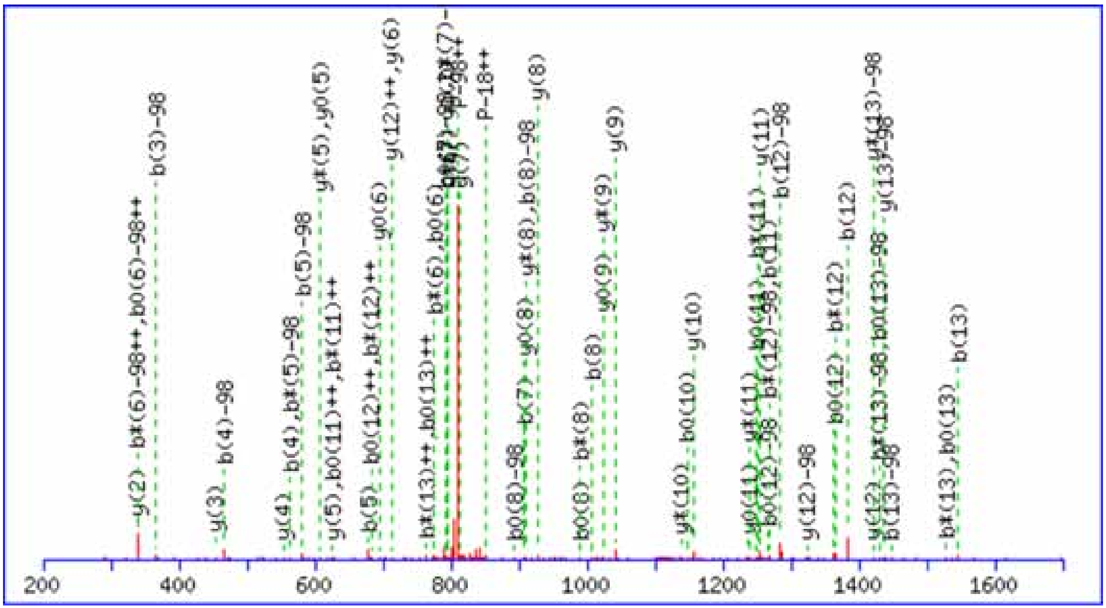
Matched b ions: b(2), b(3), b(4), b(5)-98, b(5), b(6), b(6)++, b(6)-98, b(7), b(7)++, b(7)-98, b(7)-98++, b(8), b(8)++, b(8)-98, b(8)-98++, b(9), b(9)++, b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5), y(6), y(6)++, y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.498

KLSVDNNTSATDYK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of KLSVDNNTSATDYK
Found in SVIL_MOUSE, Supervillin OS=Mus musculus GN=Svil PE=1 SV=1

Match to Query 3860: 1718.813558 from(860.414055,2+)
Title: Elution from: 30.489 to 30.489 scan no 2372 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1718.8128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
Ions Score: 39 **Expect:** 0.0068

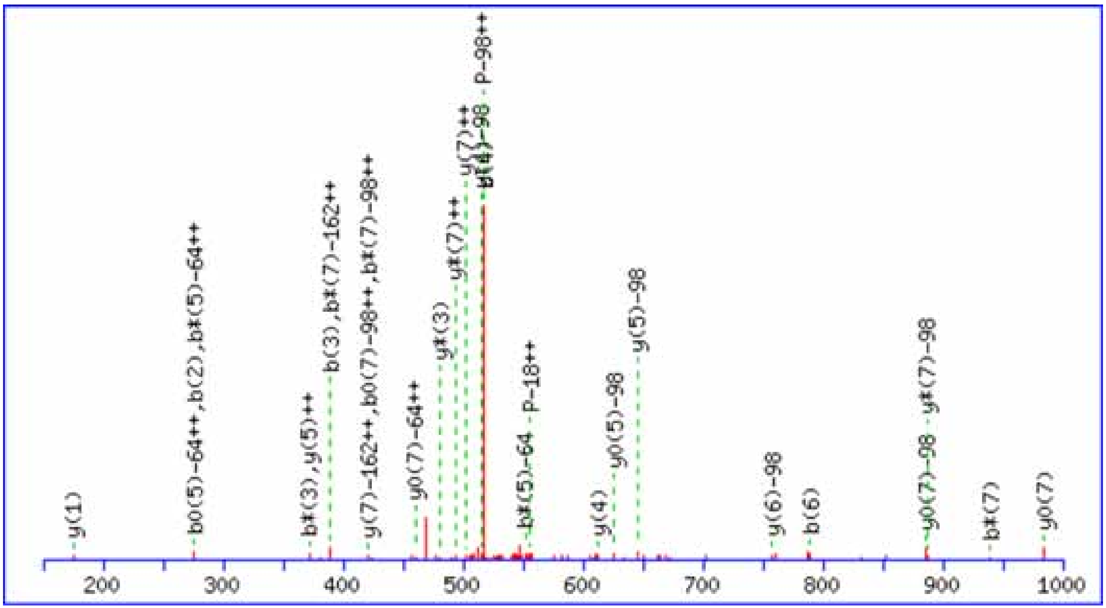
Matched b ions: b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6), b(7), b(8), b(8)-98, b(11), b(12)-98, b(12), b(13), b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(12)-98, y(13)-98
Precursor origin neutral loss: +

Peptide No.499

KMIEDRSR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of KMIEDRSR
Found in CSTF3_MOUSE, Cleavage stimulation factor subunit 3 OS=Mus musculus GN=Cstf3 PE=1 SV=1

Match to Query 735: 1129.497796 from(565.756174,2+)
Title: Elution from: 51.228 to 51.228 scan no 4674 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1129.4951
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.04

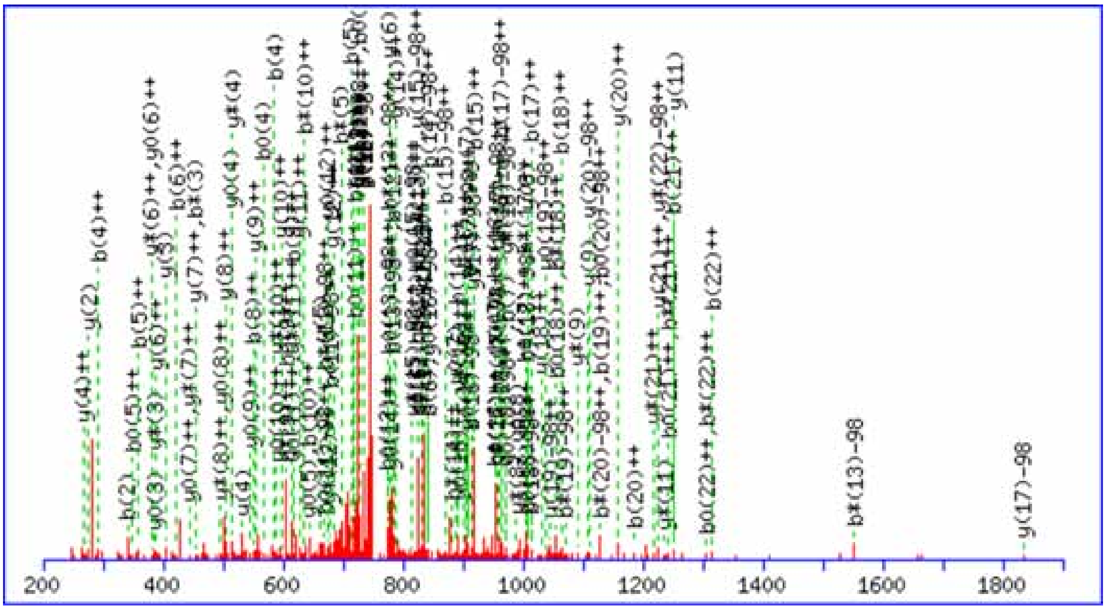
Matched b ions: b(2), b(3), b(4), b(6)
Matched y ions: y(1), y(4)-98, y(4), y(5)-98, y(5)++, y(6)-98, y(7)++
Precursor origin neutral loss: +

Peptide No.500

KREDEEEEEGSIVNGSTTEDEEQTR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of KREDEEEEEGSIVNGSTTEDEEQTR
Found in NEXN_MOUSE, Nexilin OS=Mus musculus GN=Nexn PE=1 SV=2

Match to Query 8599: 3031.281648 from(758.827688,4+)
Title: Elution from: 31.933 to 31.933 scan no 2570 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3031.2778
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.0036

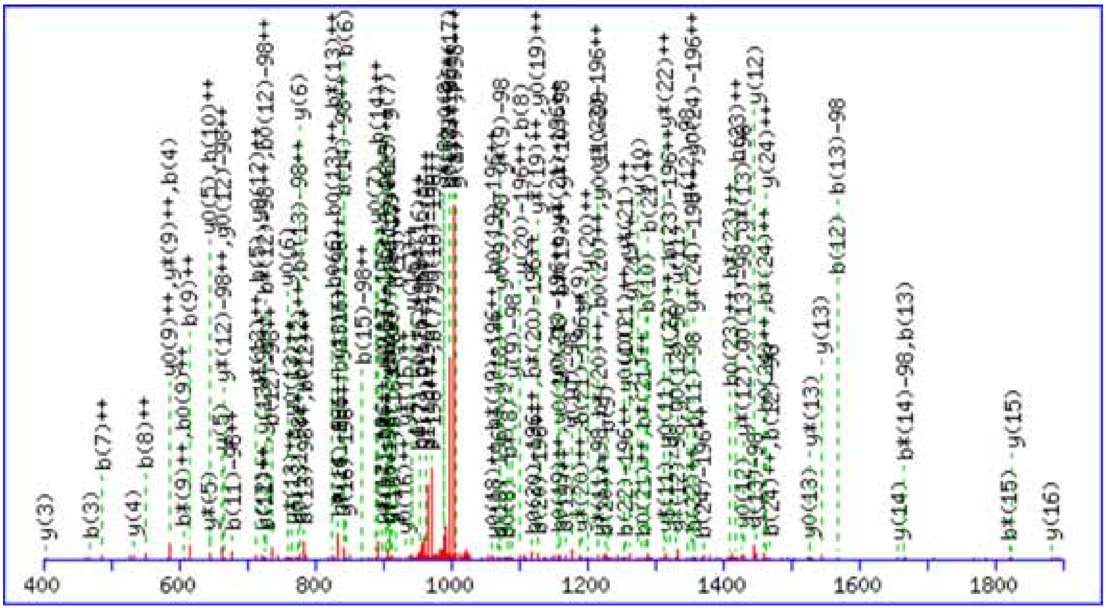
Matched b ions: b(2), b(4)++, b(4), b(5)++, b(5), b(6)++, b(6), b(7), b(8)++, b(9)++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(20)++, b(21)++, b(22)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(8), y(9), y(9)++, y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)-98++, y(16)++, y(17)-98, y(17)-98++, y(18)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.501

KREDEEEEEGSIVNGSTTEDEEQTR
Confirmed sites: @S:11,@T:17
Ambiguous sites:

MS/MS Fragmentation of KREDEEEEEGSIVNGSTTEDEEQTR
Found in NEXN_MOUSE, Nexilin OS=Mus musculus GN=Nexn PE=1 SV=2

Match to Query 8627: 3111.245820 from(1038.089216,3+)
Title: Elution from: 31.776 to 31.776 scan no 2549 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3111.2442
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 **Expect:** 2.1e-005

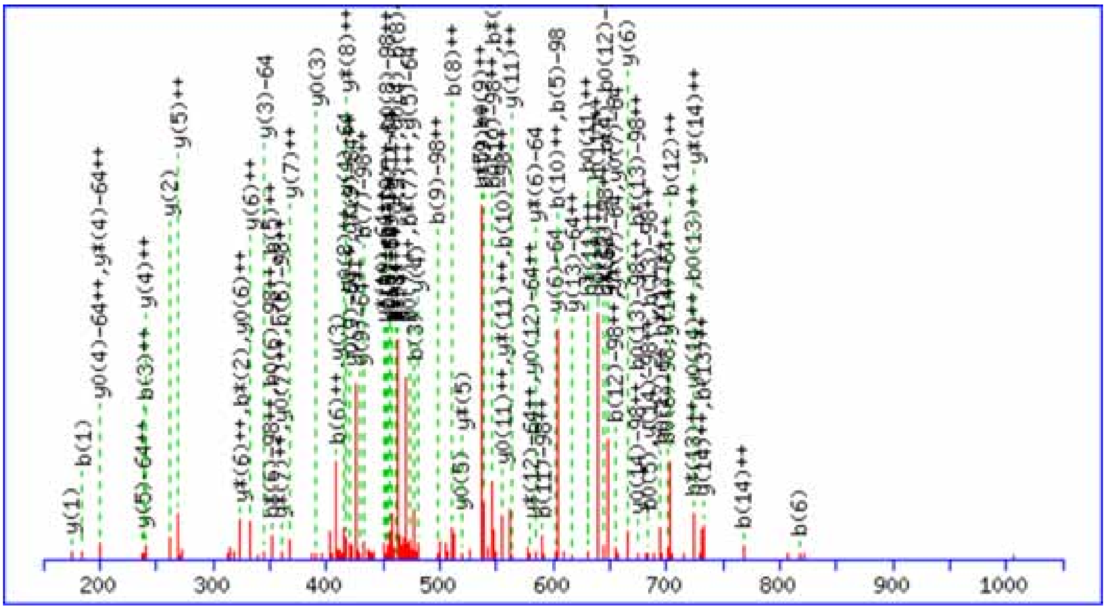
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)-98++, b(11)++, b(11)-98, b(12)++, b(12)-98++, b(12), b(12)-98, b(13)-98++, b(13)++, b(13), b(13)-98, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(17)-196++, b(17)-98++, b(18)-196++, b(18)-98++, b(19)-98++, b(19)++, b(19)-196++, b(20)-98++, b(20)-196++, b(20)++, b(21)++, b(21)-196++, b(22)-98++, b(22)-196++, b(22)++, b(23)-196++, b(23)++, b(23)-98++, b(24)-196++, b(24)-98++, b(24)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10)-98, y(10), y(11), y(12), y(12)-98, y(12)++, y(13), y(13)-98, y(13)-98++, y(14), y(15), y(15)++, y(16), y(16)-98, y(16)-196++, y(16)-98++, y(16)++, y(17)++, y(17)-196++, y(17)-98++, y(18)-196++, y(18)-98++, y(18)++, y(19)-98++, y(20)-98++, y(20)-196++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(24)-98++, y(24)++
Precursor origin neutral loss: +

Peptide No.502

KRHSGDFGADAQGAMSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KRHSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 4744: 1941.878044 from(486.476787,4+)
Title: Elution from: 20.610 to 20.610 scan no 997 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1941.8768
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K17 : Dimethyl (K)
Ions Score: 70 Expect: 4.9e-006

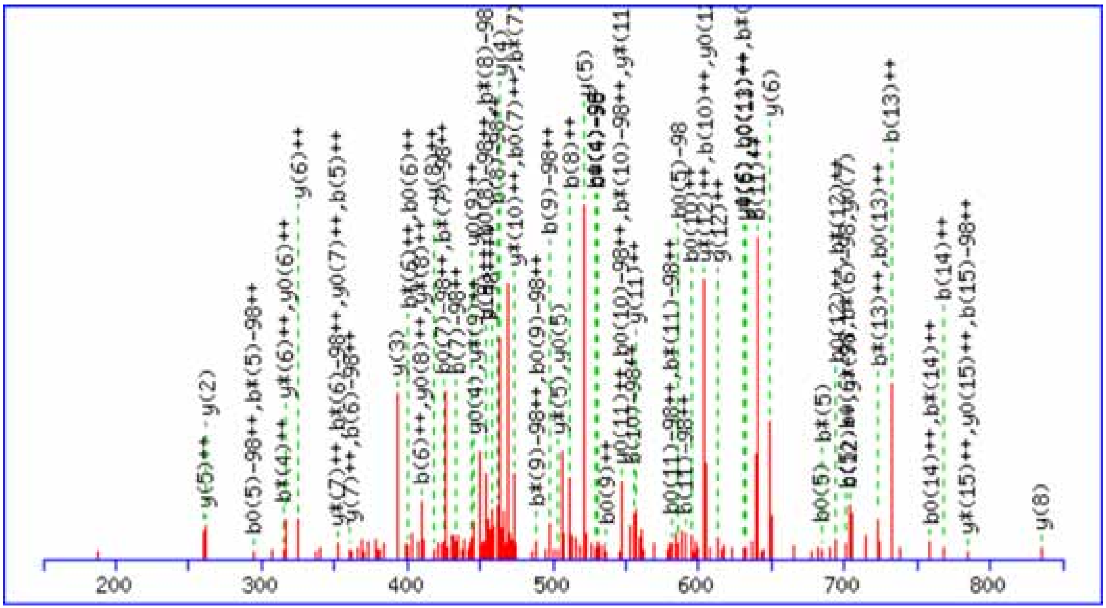
Matched b ions: b(1), b(3)++, b(3), b(4)-98, b(4), b(5)-98, b(5)++, b(6), b(6)++, b(6)-98++, b(7)-98++, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(9)++, y(11)++, y(14)++, y(14)-98++
Precursor origin neutral loss:

Peptide No.503

KRHSGDFGADAQGAMSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KRHSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 4653: 1925.882008 from(482.477778,4+)
Title: Elution from: 25.642 to 25.642 scan no 1548 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1925.8819
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 44 Expect: 0.0025

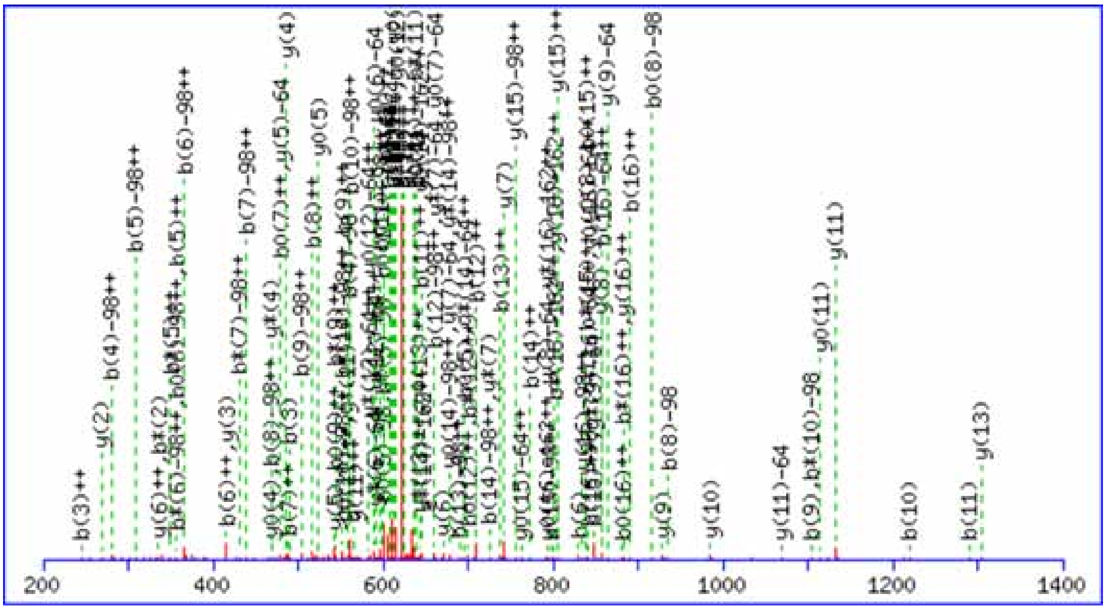
Matched b ions: b(4)-98, b(5)-98, b(5)++, b(5), b(6)++, b(6)-98++, b(7)-98++, b(8)++, b(8)-98++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(13)++, b(14)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6)++, y(6), y(7)++, y(8), y(8)++, y(9)++, y(11)++, y(12)++
Precursor origin neutral loss:

Peptide No.504

KRHSGDFGADAQGAMSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KRHSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 4789: 1959.974232 from(654.332020,3+)
Title: Elution from: 20.677 to 20.677 scan no 984 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1959.9722
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 67 Expect: 1.4e-005

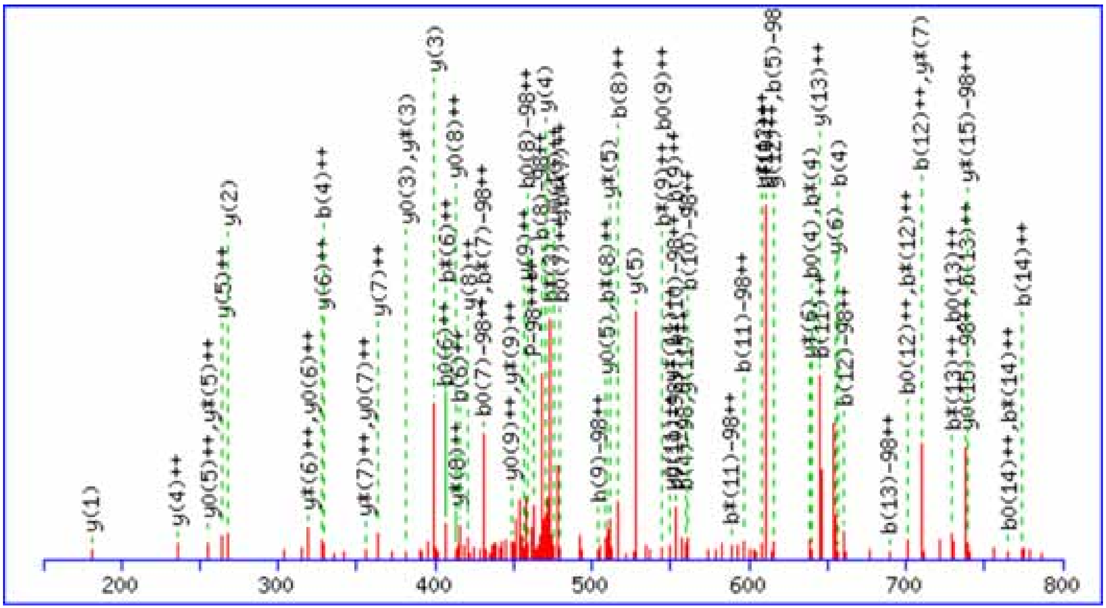
Matched b ions: b(3)++, b(3), b(4)-98++, b(4)-98, b(5)-98, b(5)-98++, b(5)++, b(6)++, b(6), b(6)-98++, b(7)++, b(7)-98++, b(8)++, b(8)-98, b(8)-98++, b(9)-98++, b(9), b(9)++, b(10), b(10)++, b(10)-98++, b(11), b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)++, y(13), y(15)++, y(15)-98++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.505

KRHSGDFGADAQGAMSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KRHSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 4530: 1943.977496 from(487.001650,4+)
Title: Elution from: 25.443 to 25.443 scan no 1535 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1943.9773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 41 Expect: 0.0052

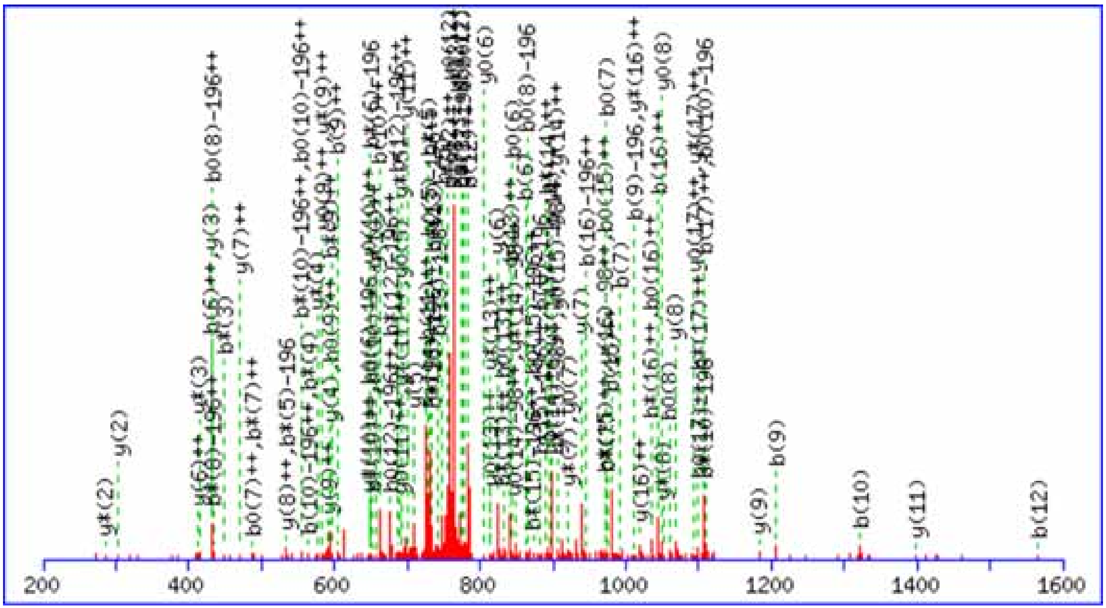
Matched b ions: b(4)++, b(4)-98, b(4), b(5)-98, b(6)++, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6)++, y(6), y(7)++, y(8)++, y(9)++, y(11)++, y(12)++, y(13)++
Precursor origin neutral loss:

Peptide No.506

KSLDSDESEDEDDDYQQK
Confirmed sites: @S:2,@S:5
Ambiguous sites:

MS/MS Fragmentation of KSLDSDESEDEDDDYQQK
Found in HAP28_MOUSE, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 5779: 2388.881145 from(797.300991,3+)
Title: Elution from: 30.980 to 30.980 scan no 2142 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2388.8771
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl (K)
Ions Score: 41 Expect: 0.0018

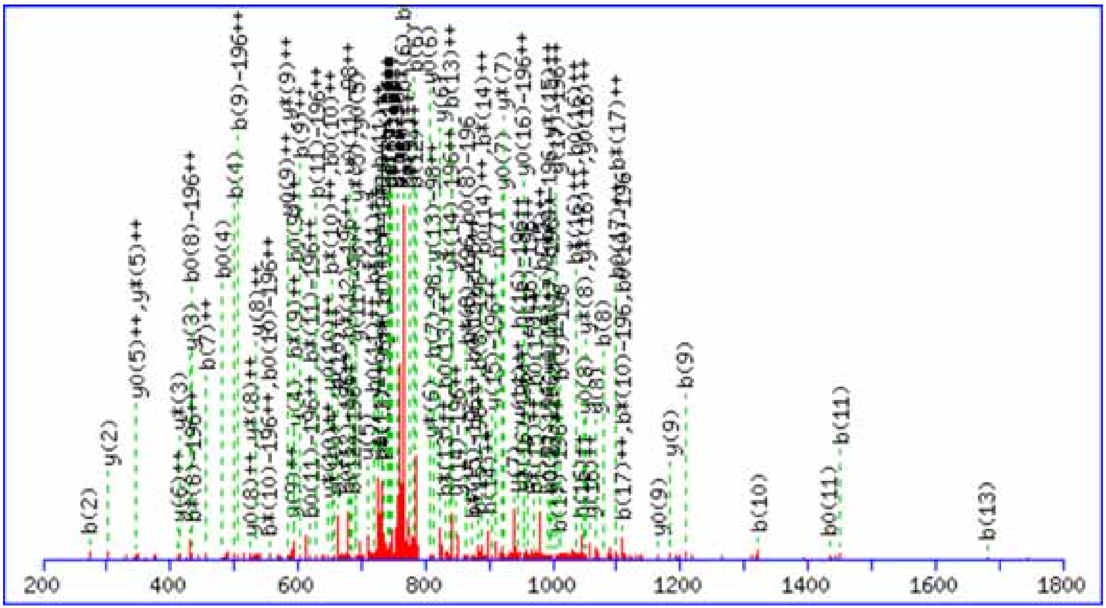
Matched b ions: b(5), b(5)-98, b(6)++, b(6)-98, b(6), b(7), b(8)-98, b(8)-98++, b(8)-196, b(9), b(9)-98++, b(9)-98, b(9)++, b(9)-196, b(10)++, b(10), b(10)-98++, b(10)-196++, b(10)-98, b(11)++, b(11)-98++, b(12)++, b(12), b(12)-196++, b(12)-98++, b(13)++, b(13)-196++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(8), y(9), y(9)++, y(10)++, y(11), y(11)++, y(12)++, y(14)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.507

KSLDSDESEDEDDDYQQK
Confirmed sites: @S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of KSLDSDESEDEDDDYQQK
Found in HAP28_MOUSE, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 6299: 2388.882930 from(797.301586,3+)
Title: Elution from: 31.160 to 31.160 scan no 2263 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2388.8771
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl (K)
Ions Score: 51 Expect: 0.00017

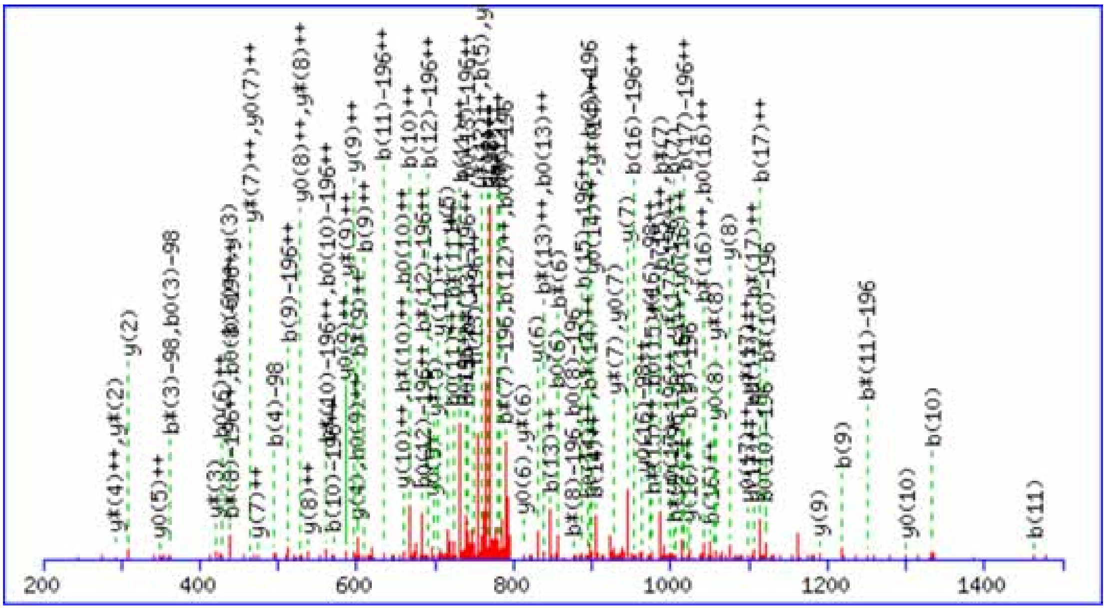
Matched b ions: b(2), b(4), b(6), b(7)++, b(7), b(7)-98, b(8)-98++, b(8)-98, b(8)-196, b(8), b(9)-98, b(9), b(9)-98++, b(9)++, b(9)-196++, b(9)-196, b(10)++, b(10), b(10)-98++, b(11), b(11)++, b(11)-98++, b(11)-196++, b(12)++, b(12)-196++, b(12)-98++, b(13), b(13)++, b(13)-196++, b(14)++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-196++, b(16)-98++, b(17)++, b(17)-98++, b(17)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8)++, y(8), y(9), y(9)++, y(10)++, y(11)-98++, y(11)++, y(12)-98++, y(13)-98++, y(14)-196++, y(14)++, y(15)-196++, y(15)-98++, y(16)++, y(16)-196++, y(17)-196++
Precursor origin neutral loss: +

Peptide No.508

KSLDSDESEDEDDDYQQK
Confirmed sites: @S:2,@S:5
Ambiguous sites:

MS/MS Fragmentation of KSLDSDESEDEDDDYQQK
Found in HAP28_MOUSE, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 6399: 2406.974121 from(803.331983,3+)
Title: Elution from: 31.267 to 31.267 scan no 2280 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2406.9725
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 41 Expect: 0.0034

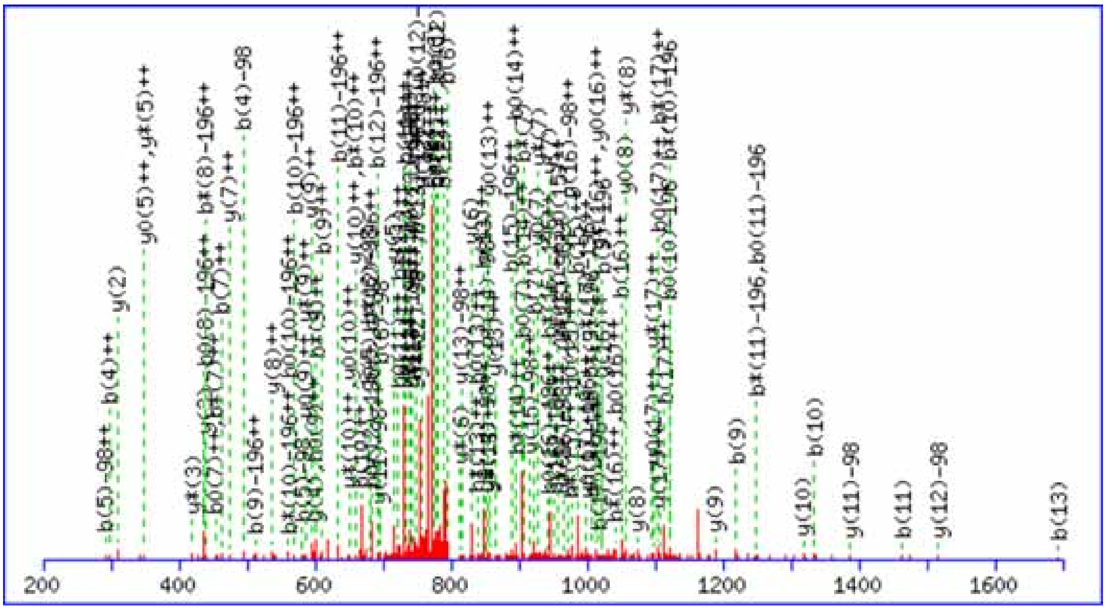
Matched b ions: b(4)-98, b(5), b(6)++, b(6)-98, b(7)-98, b(7), b(8)-98++, b(8)-98, b(8)-196, b(9)-196++, b(9), b(9)-98++, b(9)-98, b(9)-196, b(9)++, b(10), b(10)-98++, b(10)++, b(10)-98, b(10)-196++, b(11)++, b(11), b(11)-98++, b(11)-196++, b(12)++, b(12)-98++, b(12)-196++, b(13)++, b(13)-196++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-196++, b(16)-98++, b(17)++, b(17)-98++, b(17)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9), y(9)++, y(10)++, y(11)++, y(12)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.509

KSLDSDESEDEDDDYQQK
Confirmed sites: @S:2,@S:8
Ambiguous sites:

MS/MS Fragmentation of KSLDSDESEDEDDDYQQK
Found in HAP28_MOUSE, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 6315: 2406.975969 from(803.332599,3+)
Title: Elution from: 31.115 to 31.115 scan no 2257 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2406.9725
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 47 **Expect:** 0.00079

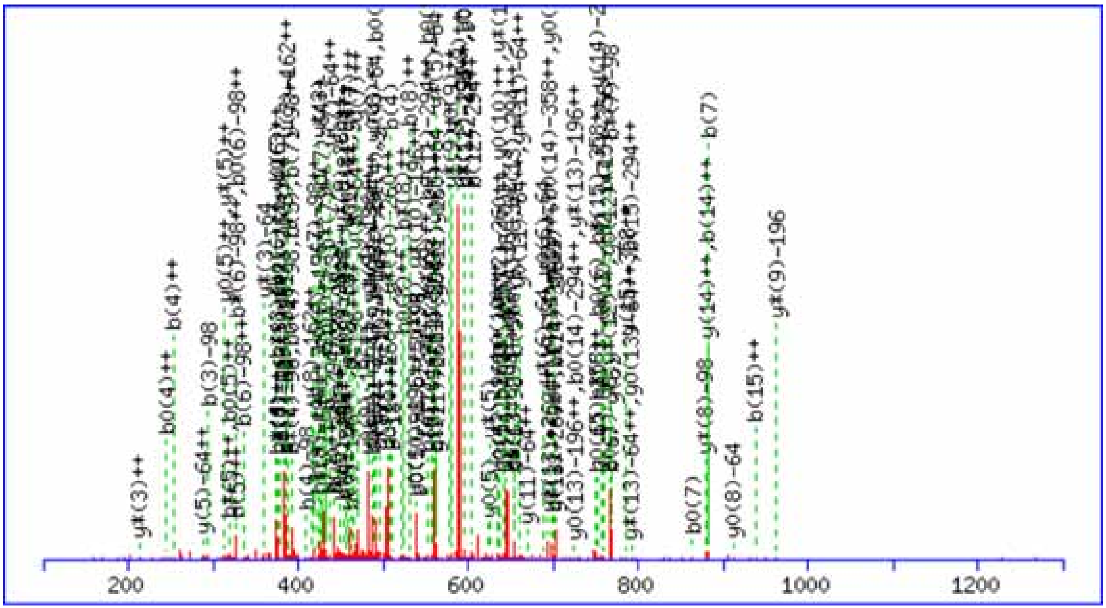
Matched b ions: b(4)++, b(4)-98, b(5)-98++, b(5)-98, b(5), b(6), b(6)-98, b(7)++, b(7), b(8)-98++, b(8)-98, b(9)-98++, b(9), b(9)-196++, b(9)-98, b(9)++, b(9)-196, b(10)++, b(10), b(10)-98, b(10)-98++, b(10)-196++, b(11), b(11)-98++, b(11)++, b(11)-196++, b(12)++, b(12)-98++, b(12)-196++, b(13), b(13)++, b(13)-196++, b(14)++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-196++, b(16)-98++, b(17)++, b(17)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)-98, y(11)-98++, y(11)++, y(12)-98, y(12)-98++, y(13)-98++, y(13)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.510

KSPDFNLTGSQSNMLK
Confirmed sites: @S:2,@T:8,@S:10
Ambiguous sites:

MS/MS Fragmentation of KSPDFNLTGSQSNMLK
Found in NMDE1_MOUSE, Glutamate [NMDA] receptor subunit epsilon-1 OS=Mus musculus GN=Grin2a PE=1 SV=2

Match to Query 5426: 2055.818844 from(514.961987,4+)
Title: Elution from: 35.040 to 35.040 scan no 2825 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2055.8239
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 30 **Expect:** 0.026

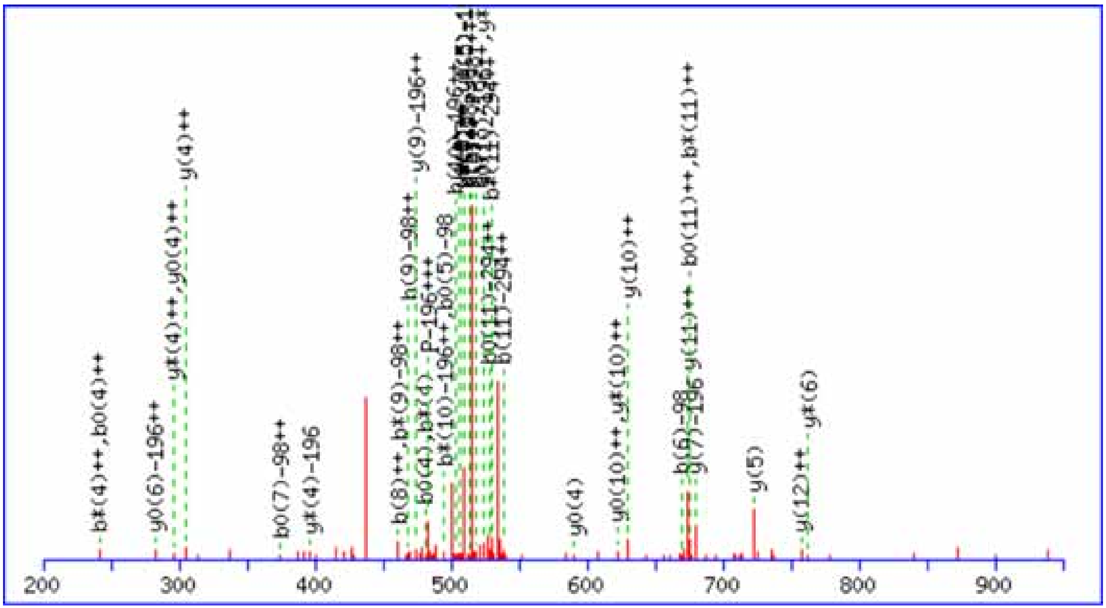
Matched b ions: b(3), b(3)-98, b(4)++, b(4)-98, b(4), b(5)++, b(5)-98, b(5), b(6)++, b(6), b(6)-98++, b(7)++, b(7), b(7)-98++, b(8)-98++, b(8)++, b(9)++, b(9)-196++, b(10)++, b(10)-294++, b(10)-98++, b(11)-294++, b(11)-98++, b(12)-98++, b(12)++, b(12)-196++, b(12)-294++, b(13)-98++, b(14)++, b(15)++, b(15)-294++
Matched y ions: y(3), y(5), y(6)++, y(6), y(7)++, y(7)-98++, y(8)-98++, y(8)++, y(9)++, y(9)-98++, y(9)-196++, y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)-98++, y(14)++
Precursor origin neutral loss:

Peptide No.511

KSSDIKPGLSSKK
Confirmed sites: @S:2,@S:10,@S:11
Ambiguous sites:

MS/MS Fragmentation of KSSDIKPGLSSKK
Found in NUFP2_MOUSE, Nuclear fragile X mental retardation-interacting protein 2 OS=Mus musculus GN=Nufip2 PE=1 SV=1

Match to Query 2941: 1641.721431 from(548.247753,3+)
Title: Elution from: 20.948 to 20.948 scan no 1033 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1641.7181
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K6 : Dimethyl (K)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.017

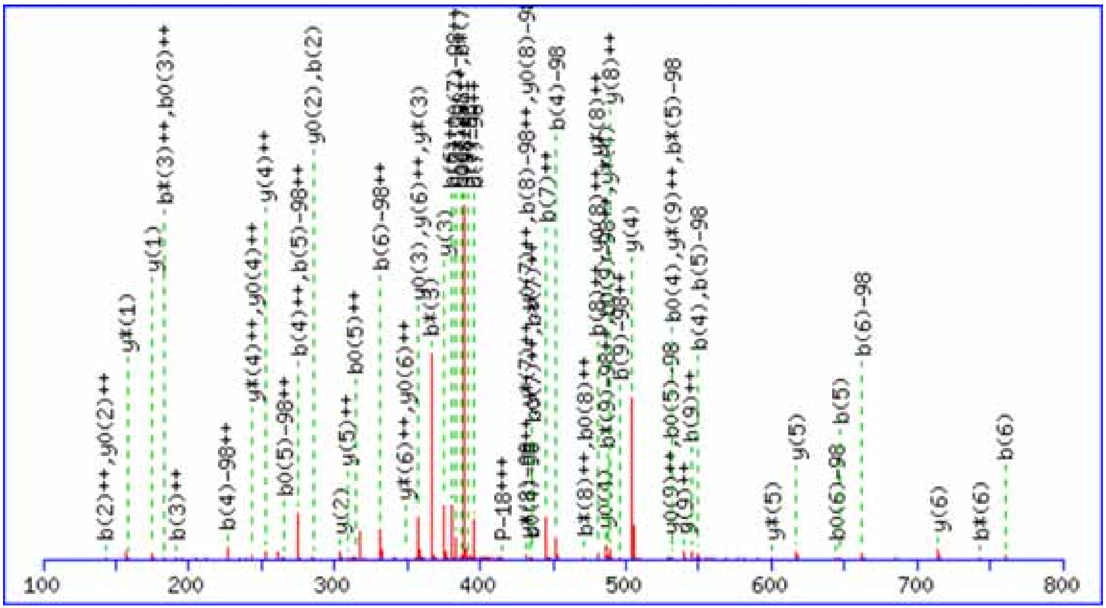
Matched b ions: b(2), b(5)-98, b(6)-98, b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(10)-196++, b(11)-294++
Matched y ions: y(4)++, y(4)-98, y(5), y(7)-196, y(7)-98, y(8)++, y(8)-98++, y(9)-98++, y(9)-196++, y(10)++, y(11)++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.512

KTPSPIEAER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KTPSPIEAER
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1477: 1262.627931 from(421.883253,3+)
Title: Elution from: 23.851 to 23.851 scan no 1478 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1262.6271
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0081

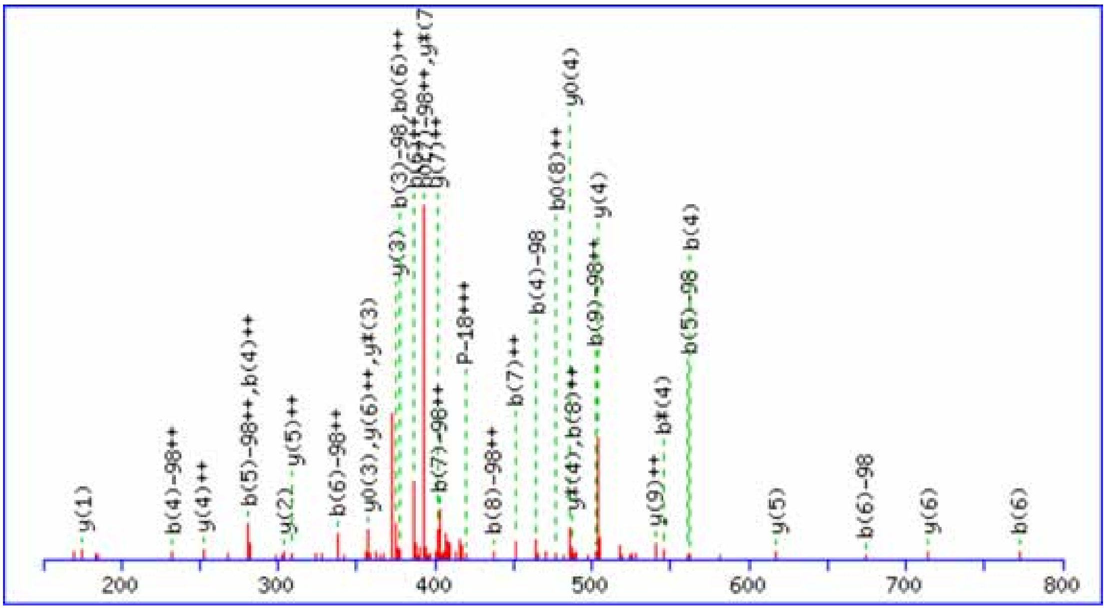
Matched b ions: b(2)++, b(2), b(3)++, b(3), b(4)-98++, b(4)++, b(4), b(4)-98, b(5)-98++, b(5)-98, b(5), b(6), b(6)-98++, b(6)-98, b(6)++, b(7)++, b(7)-98++, b(8)++, b(8)-98++, b(9)++, b(9)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5), y(5)++, y(6), y(6)++, y(7)-98++, y(8)++, y(9)++
Precursor origin neutral loss: +

Peptide No.513

KTPSPIEAER
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of KTPSPIEAER
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1354: 1274.690937 from(425.904255,3+)
Title: Elution from: 23.819 to 23.819 scan no 1352 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1274.6908
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0084

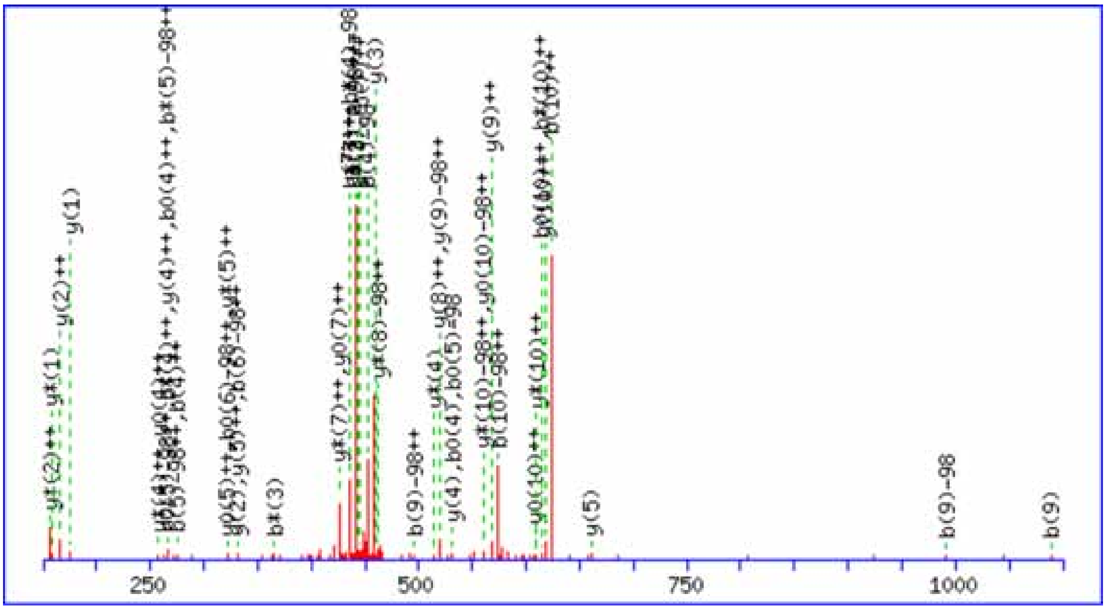
Matched b ions: b(3)-98, b(4)++, b(4)-98++, b(4)-98, b(4), b(5)-98++, b(5)-98, b(6), b(6)-98, b(6)-98++, b(6)++, b(7)-98++, b(7)++, b(8)++, b(8)-98++, b(9)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6), y(6)++, y(7)++, y(9)++
Precursor origin neutral loss: +

Peptide No.514

KTPSPIEAERK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of KTPSPIEAERK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2099: 1418.753610 from(473.925146,3+)
Title: Elution from: 21.730 to 21.730 scan no 1196 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1418.7534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K11 : Dimethyl (K)
Ions Score: 39 Expect: 0.0061

Matched b ions: b(4)++, b(4)-98, b(5)-98++, b(6)-98++, b(7)++, b(9)-98, b(9), b(9)-98++, b(10)++, b(10)-98++
Matched y ions: y(1), y(2)++, y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(7)++, y(8)++, y(9)-98++, y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.515

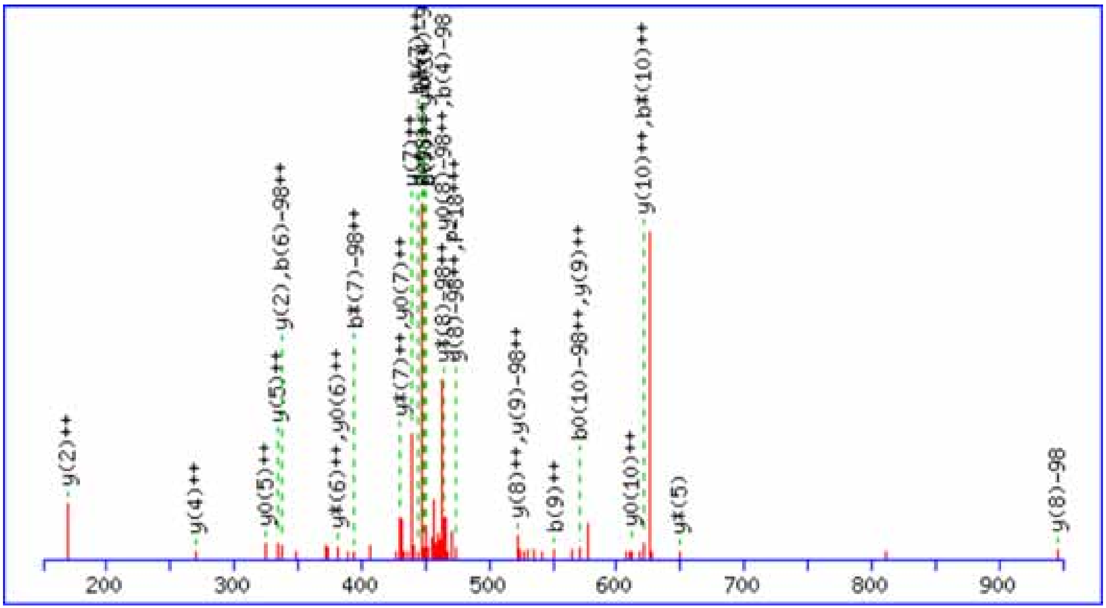
KTPSPIEAERK

Confirmed sites: @S:4

Ambiguous sites:

MS/MS Fragmentation of KTPSPIEAERK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1727: 1436.849877 from(479.957235,3+)
Title: Elution from: 21.731 to 21.731 scan no 1112 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1436.8488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K1 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K11 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 29 **Expect:** 0.03

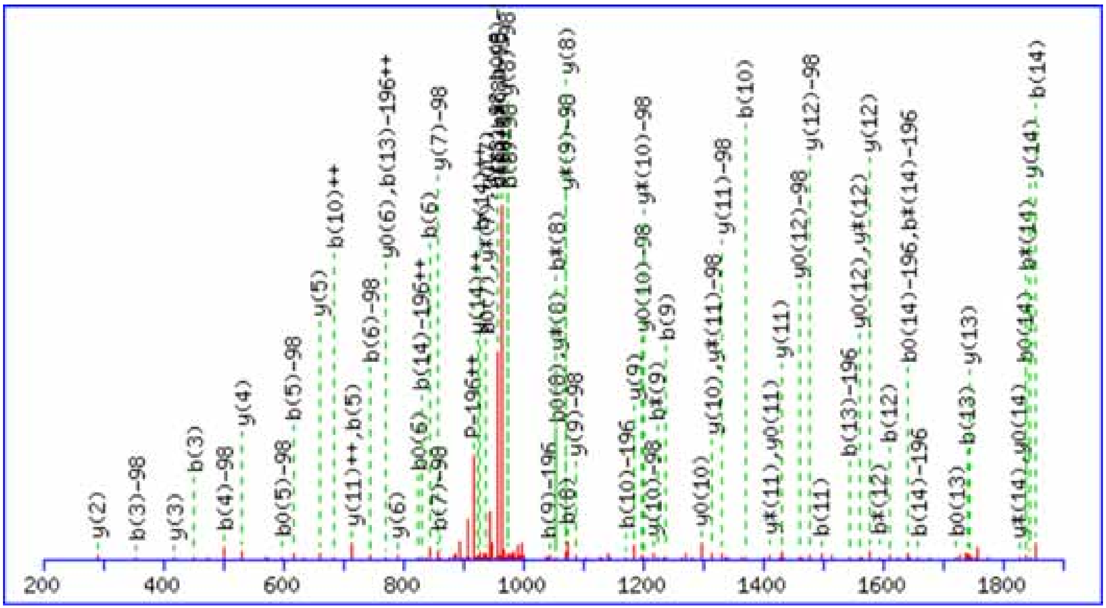
Matched b ions: b(4)-98, b(6)-98++, b(7)++, b(9)++
Matched y ions: y(2)++, y(2), y(4)++, y(5)++, y(7)++, y(8)-98, y(8)++, y(8)-98++, y(9)-98++, y(9)++, y(10)++
Precursor origin neutral loss: +

Peptide No.516

KTSFDENDSEELEDK
Confirmed sites: @S:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of KTSFDENDSEELEDK
Found in IF2P_MOUSE, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 5742: 2028.784856 from(1015.399704,2+)
Title: Elution from: 35.338 to 35.338 scan no 3036 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2028.7853
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 69 Expect: 2.8e-006

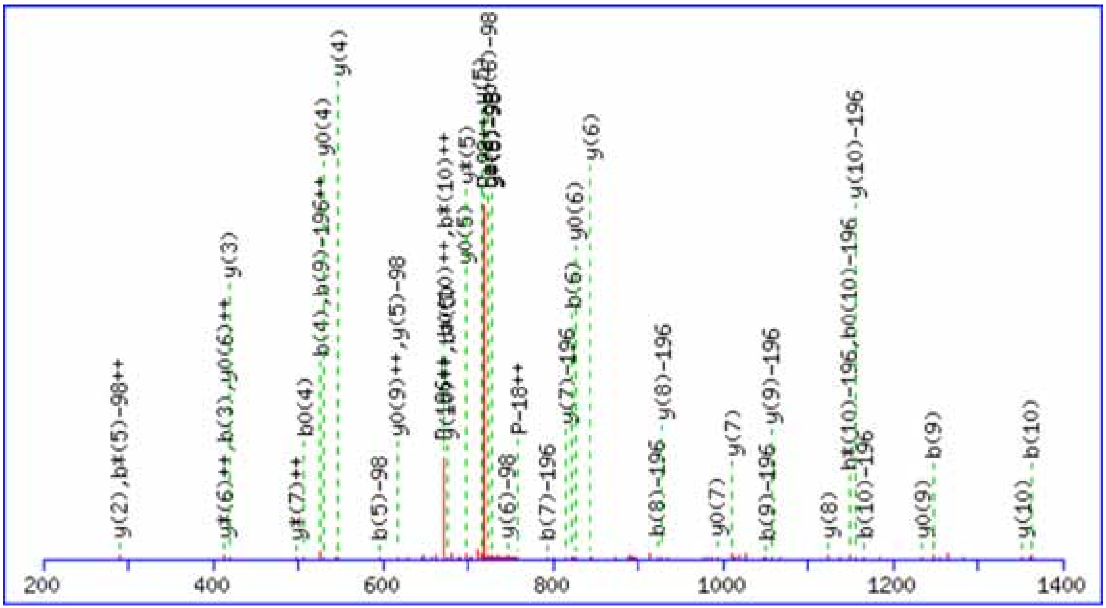
Matched b ions: b(3), b(3)-98, b(4)-98, b(5), b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(9)-98++, b(9), b(9)-196, b(10)-98, b(10)++, b(10)-98++, b(10)-196, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13)-196++, b(13), b(13)-196, b(14)-98, b(14), b(14)-196, b(14)-196++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-98, y(10), y(11)++, y(11), y(11)-98, y(12), y(12)-98, y(13)-98, y(13), y(14), y(14)-98, y(14)++
Precursor origin neutral loss: +

Peptide No.517

KVELSESEEDK
Confirmed sites: @S:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of KVELSESEEDK
Found in SRRM1_MOUSE, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=1

Match to Query 2743: 1535.642354 from(768.828453,2+)
Title: Elution from: 27.785 to 27.785 scan no 2000 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1535.6408
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K1 : Dimethyl (K)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K11 : Dimethyl (K)
Ions Score: 34 Expect: 0.009

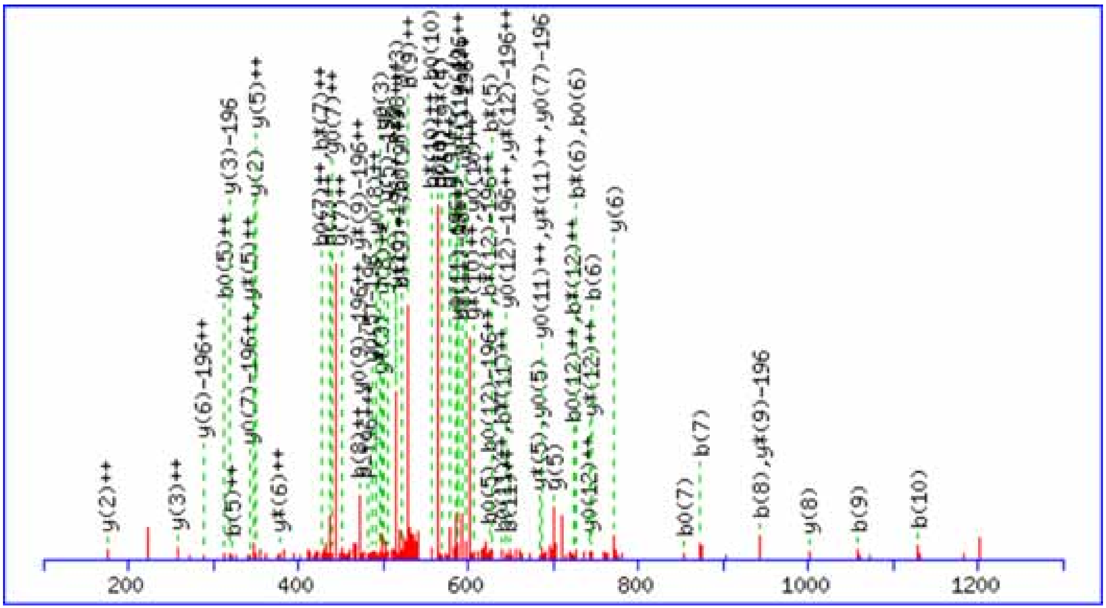
Matched b ions: b(3), b(4), b(5)-98, b(6), b(6)-98, b(7)-98, b(7)-196, b(8)-98, b(8)-196, b(9)-196++, b(9)-98, b(9), b(9)-196, b(10)-98, b(10), b(10)-196
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6)-98, y(6), y(7)-98, y(7)-196, y(7), y(8)-98, y(8), y(8)-196, y(9)-196, y(10), y(10)-98, y(10)-196, y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.518

LDCAKTKADASSK
Confirmed sites: @S:11,@S:12
Ambiguous sites:

MS/MS Fragmentation of LDCAKTKADASSK
Found in SMC2_MOUSE, Structural maintenance of chromosomes protein 2 OS=Mus musculus GN=Smc2 PE=1 SV=1

Match to Query 3400: 1643.743608 from(548.921812,3+)
Title: Elution from: 29.600 to 29.600 scan no 2250 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1643.7455
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K5 : Dimethyl (K)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 29 Expect: 0.051

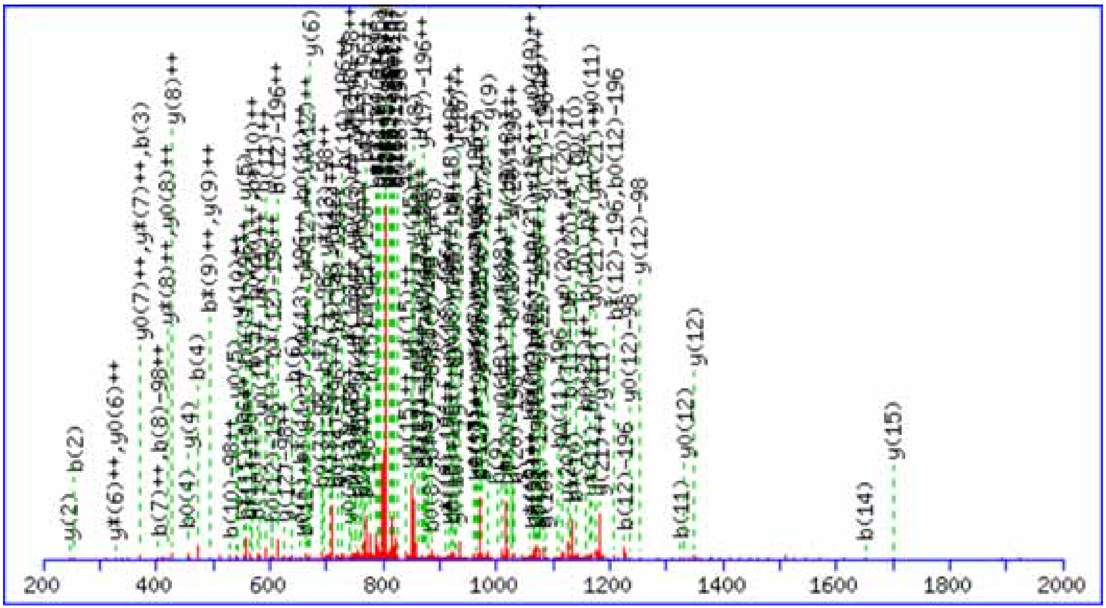
Matched b ions: b(5)++, b(6), b(7), b(7)++, b(8), b(8)++, b(9), b(9)++, b(10)++, b(10), b(11)++, b(12)-98++
Matched y ions: y(2), y(2)++, y(3)++, y(3), y(3)-196, y(4), y(5), y(5)++, y(5)-196, y(6), y(6)-196++, y(7)++, y(7)-98++, y(8), y(8)++, y(9)-98, y(9)-98++, y(9)++, y(10)-98++, y(10)-98, y(10)-196++, y(11)-196++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.519

LDNTPASPPRSPTEPSDTPIAK
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of LDNTPASPPRSPTEPSDTPIAK
Found in TACC2_MOUSE, Transforming acidic coiled-coil-containing protein 2 OS=Mus musculus GN=Tacc2 PE=1 SV=2

Match to Query 7545: 2506.141596 from(836.387808,3+)
Title: Elution from: 36.853 to 36.853 scan no 3242 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2506.1393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K22 : Dimethyl (K)
Ions Score: 47 Expect: 0.0016

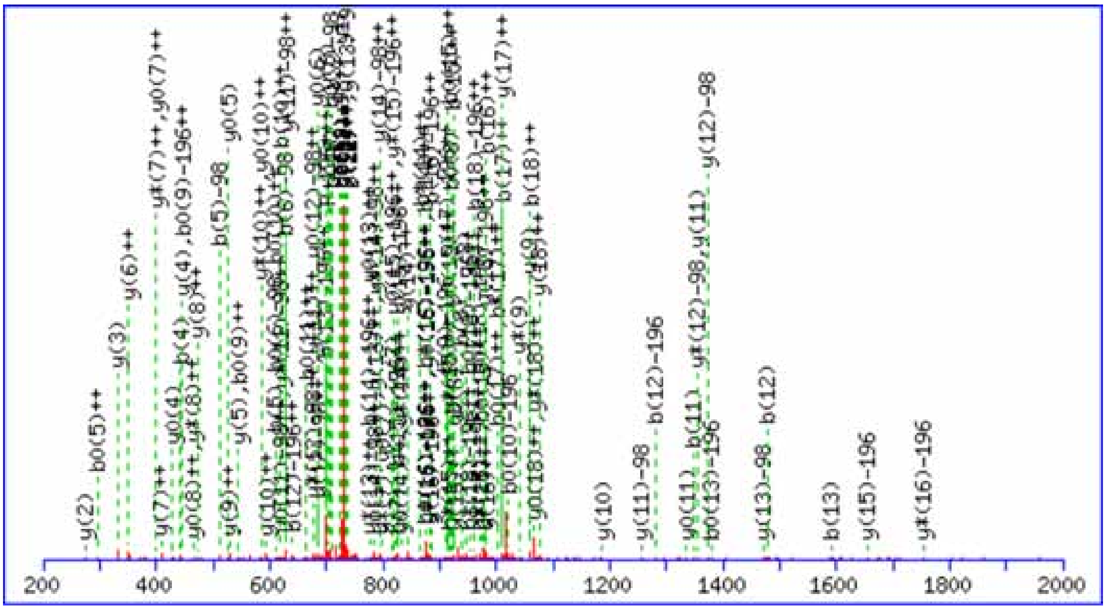
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)-98, b(7)++, b(7), b(8)-98++, b(8)-98, b(9), b(10)-98++, b(10)++, b(10)-98, b(10), b(11), b(11)-98++, b(11)-98, b(11)-196++, b(11)++, b(11)-196, b(12)-196++, b(12)-196, b(12)-98++, b(12)++, b(13)-196++, b(13)++, b(14), b(14)-196++, b(14)-98++, b(14)++, b(15)-196++, b(15)++, b(16)-196++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(17)-196++, b(18)-196++, b(18)++, b(19)-98++, b(19)++, b(20)-196++, b(20)-98++, b(20)++, b(21)-196++, b(21)++, b(21)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10)++, y(10), y(11), y(11)++, y(12), y(12)-98, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15), y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++, y(18)-98++, y(18)++, y(18)-196++, y(19)++, y(19)-98++, y(19)-196++, y(20)++, y(20)-98++, y(20)-196++, y(21)-98++, y(21)++, y(21)-196++
Precursor origin neutral loss: +

Peptide No.520

LEGDSDVDSELEDRVDGVK
Confirmed sites: @S:5,@S:9
Ambiguous sites:

MS/MS Fragmentation of LEGDSDVDSELEDRVDGVK
Found in MY18A_MOUSE, Myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2

Match to Query 7015: 2291.946918 from(764.989582,3+)
Title: Elution from: 53.395 to 53.395 scan no 5287 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2291.9447
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K19 : Dimethyl (K)
Ions Score: 43 Expect: 0.0022

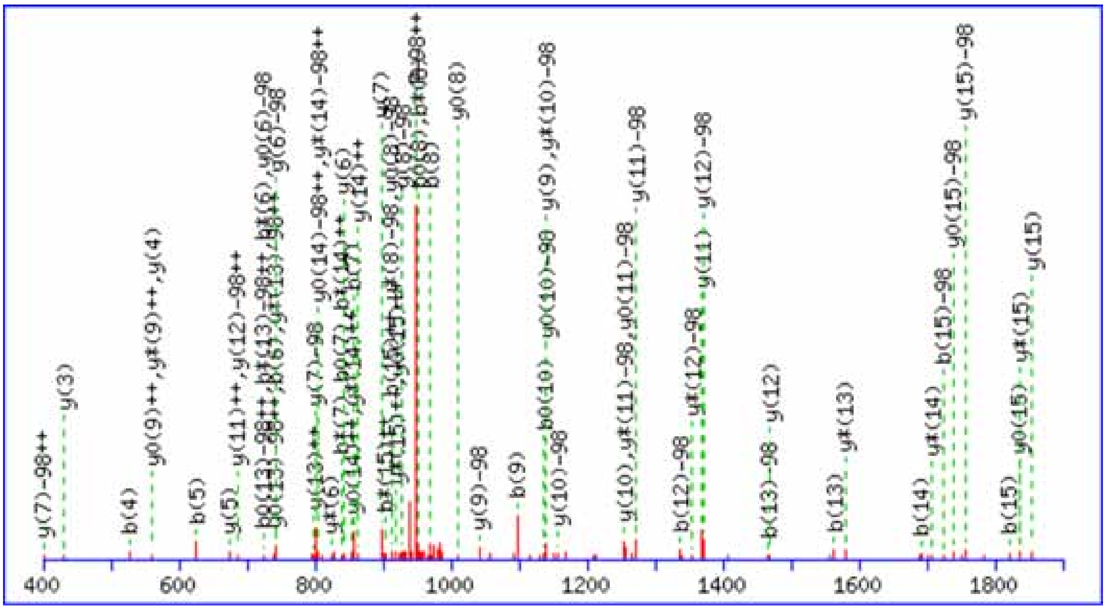
Matched b ions: b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8), b(9)-196, b(9)-98, b(10)-98, b(10)++, b(11), b(12)-98, b(12), b(12)-196++, b(12)-196, b(12)++, b(13), b(13)-98, b(13)-196++, b(13)-98++, b(14)-196++, b(14)-98++, b(14)++, b(15)-196++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(16)-196++, b(17)-98++, b(17)++, b(18)-98++, b(18)-196++, b(18)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)-98++, y(11)-98, y(11), y(11)++, y(12)-98, y(12)++, y(12)-98++, y(13)++, y(13)-98, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)-98, y(15)-196++, y(15)++, y(15)-196, y(16)-196++, y(16)-98++, y(16)++, y(17)++, y(17)-196++, y(17)-98++, y(18)++, y(18)-196++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.521

LEQQVDDLEGSLEQEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of LEQQVDDLEGSLEQEK
Found in MYH7_MOUSE, Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1

Match to Query 5562: 1994.912164 from(998.463358,2+)
Title: Elution from: 44.692 to 44.692 scan no 4267 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1994.9085
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K16 : Dimethyl (K)
Ions Score: 52 Expect: 0.00033

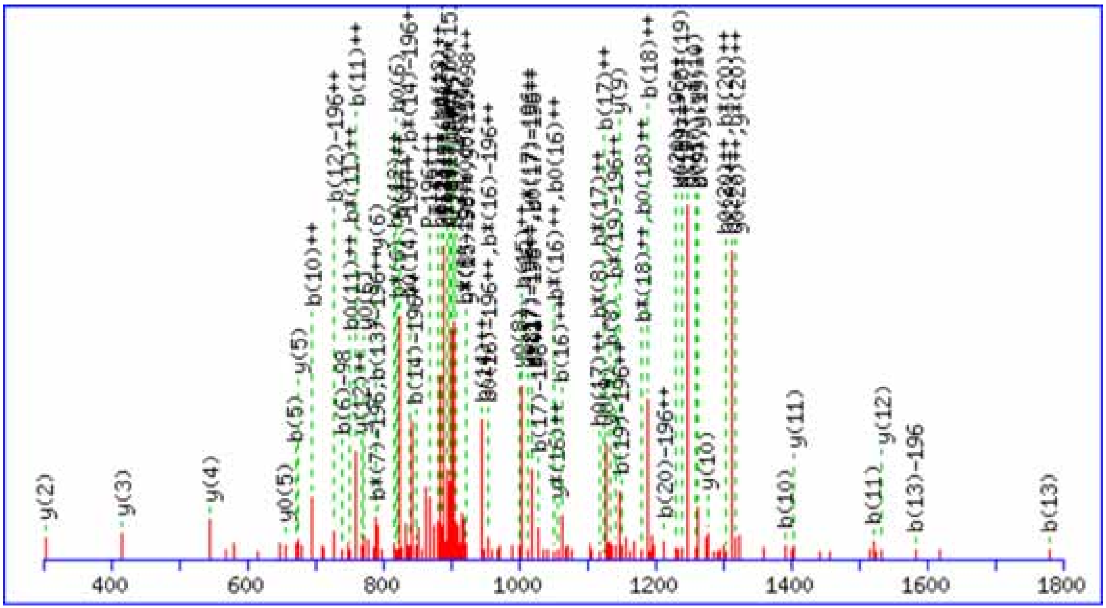
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(12)-98, b(13), b(13)-98, b(14), b(15), b(15)-98, b(15)++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7)-98++, y(7)-98, y(7), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11)-98, y(11), y(11)++, y(12)-98, y(12), y(12)-98++, y(13)++, y(14)++, y(15)-98, y(15)
Precursor origin neutral loss: +

Peptide No.522

LEREDSSEEEEEEEIDDEEIER
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of LEREDSSEEEEEEEIDDEEIER
Found in MFAP1_MOUSE, Microfibrillar-associated protein 1 OS=Mus musculus GN=Mfap1 PE=1 SV=1

Match to Query 7149: 2796.042597 from(933.021475,3+)
Title: Elution from: 42.350 to 42.350 scan no 3795 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2796.0423
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 86 **Expect:** 6.6e-008

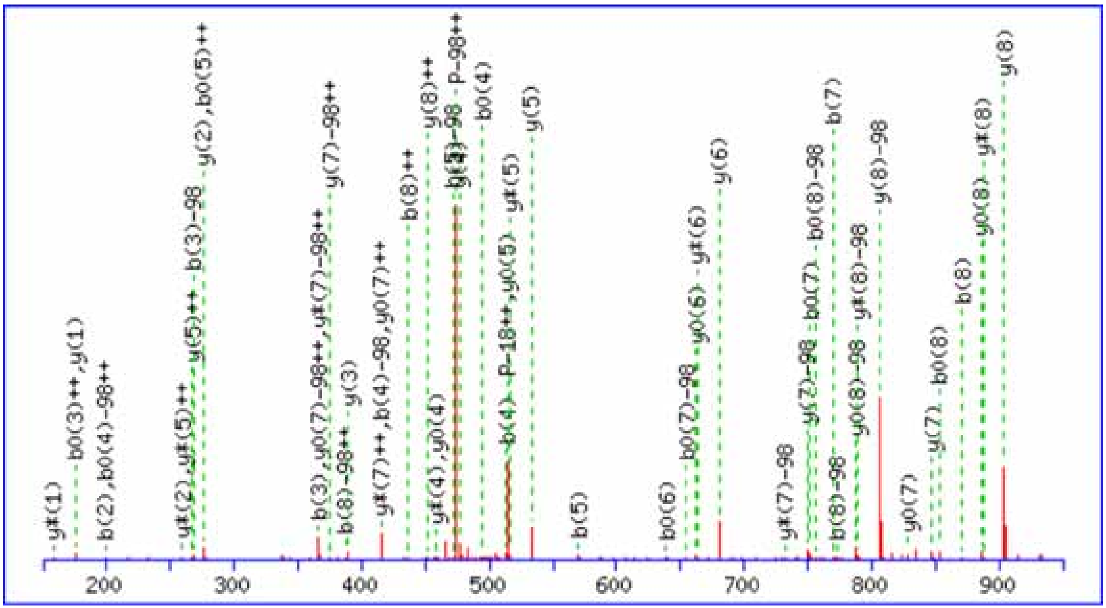
Matched b ions: b(5), b(6)-98, b(7)-98, b(8), b(8)-98, b(9), b(10)++, b(10)-98++, b(10), b(10)-98, b(11)++, b(11), b(11)-98++, b(12)++, b(12)-196++, b(12)-98++, b(13)++, b(13), b(13)-196++, b(13)-196, b(13)-98++, b(14)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(17)++, b(17)-196++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-196++, b(19)-98++, b(20)++, b(20)-98++, b(20)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(14)++, y(16)-98++, y(17)-98++, y(19)++, y(19)-98++, y(20)-196++
Precursor origin neutral loss: +

Peptide No.523

LGSFGSITR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LGSFGSITR
Found in FLNC_MOUSE, Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3

Match to Query 558: 1044.500662 from(523.257607,2+)
Title: Elution from: 45.079 to 45.079 scan no 4135 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1044.5005
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 0.00014

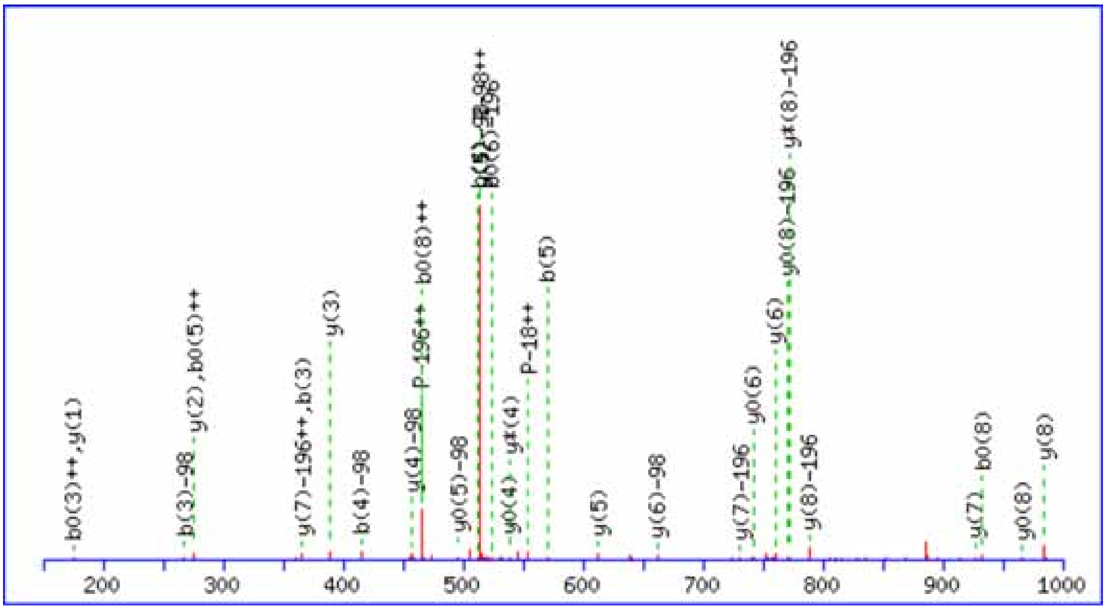
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(7), b(8)-98++, b(8), b(8)++, b(8)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6), y(7)-98, y(7), y(7)-98++, y(8)-98, y(8), y(8)++
Precursor origin neutral loss: +

Peptide No.524

LGSFGSITR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of LGSFGSITR
Found in FLNC_MOUSE, Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3

Match to Query 894: 1124.467290 from(563.240921,2+)
Title: Elution from: 51.751 to 51.751 scan no 5114 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1124.4668
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0058

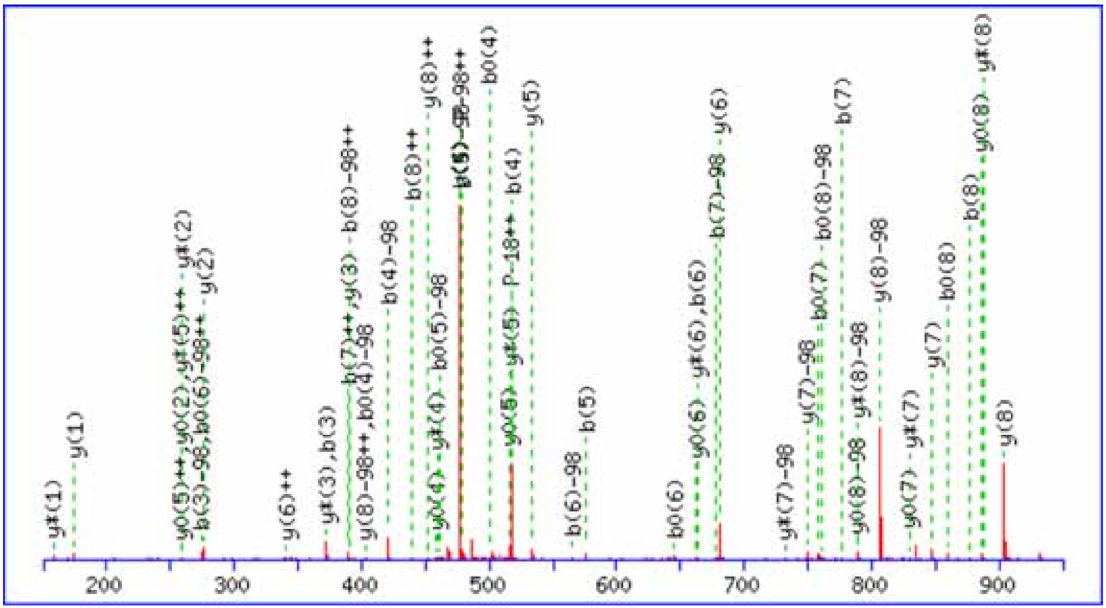
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5), b(6)-98, b(7)-98, b(8)-98
Matched y ions: y(1), y(2), y(3), y(4)-98, y(5), y(5)-98, y(6), y(6)-98, y(7)-196++, y(7)-98++, y(7)-196, y(7)-98, y(7), y(8)-196, y(8)-98, y(8)
Precursor origin neutral loss: +

Peptide No.525

LGSFGSITR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LGSFGSITR
Found in FLNC_MOUSE, Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3

Match to Query 585: 1050.532202 from(526.273377,2+)
Title: Elution from: 45.059 to 45.059 scan no 4132 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1050.5323
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.00047

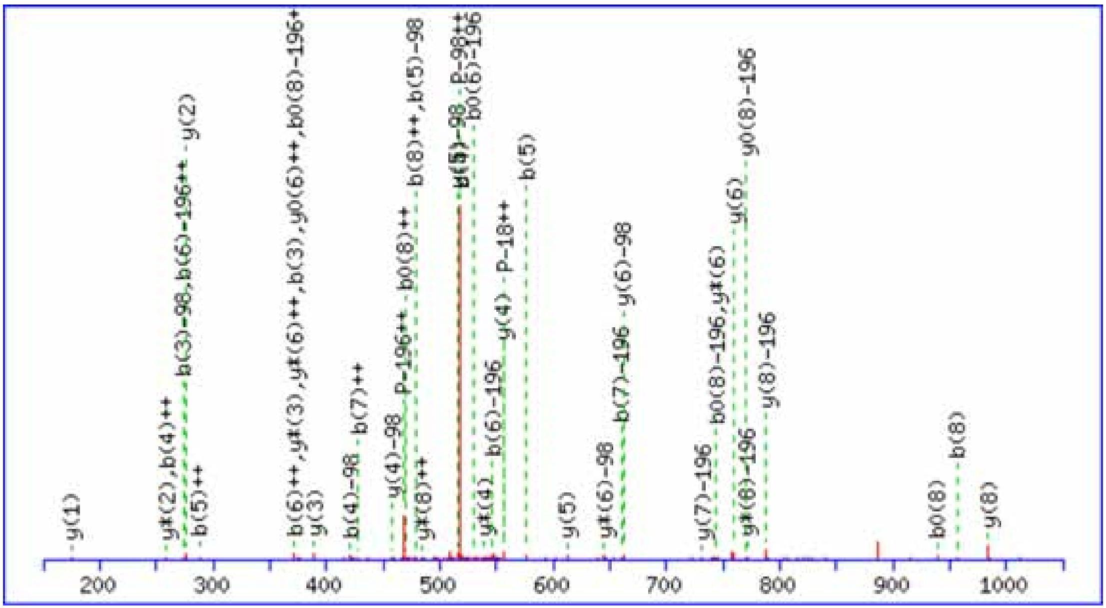
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(7)++, b(7)-98, b(7), b(8)-98++, b(8)++, b(8)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)-98, y(7), y(8)-98, y(8), y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.526

LGSFGSITR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of LGSFGSITR
Found in FLNC_MOUSE, Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3

Match to Query 648: 1130.499398 from(566.256975,2+)
Title: Elution from: 51.360 to 51.360 scan no 4824 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1130.4986
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0063

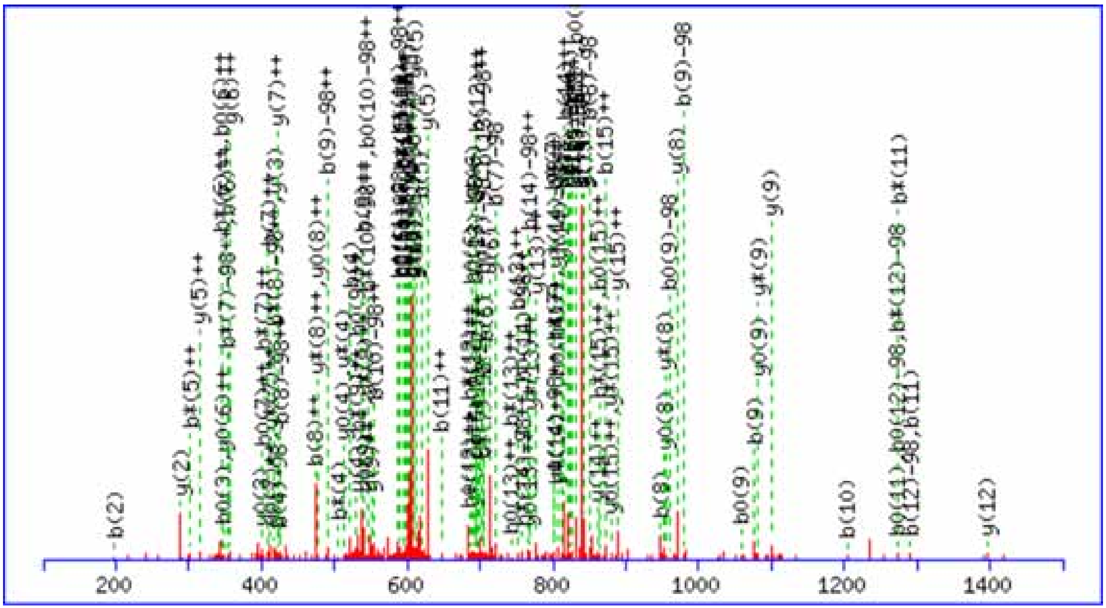
Matched b ions: b(3), b(3)-98, b(4)++, b(4)-98, b(4), b(5)++, b(5), b(5)-98, b(6)++, b(6)-98, b(6)-196++, b(6)-196, b(7)-98, b(7)-196, b(7)++, b(8), b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(4)-98, y(5), y(5)-98, y(6)-98, y(6), y(7)-196, y(7)-98, y(8)-196, y(8)-98, y(8)
Precursor origin neutral loss: +

Peptide No.527

LGSRPSIQEQSPLELR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LGSRPSIQEQSPLELR
Found in XIRP1_MOUSE, Xin actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 PE=1 SV=2

Match to Query 5164: 1916.973282 from(639.998370,3+)
Title: Elution from: 45.388 to 45.388 scan no 4350 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1916.9720
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.0058

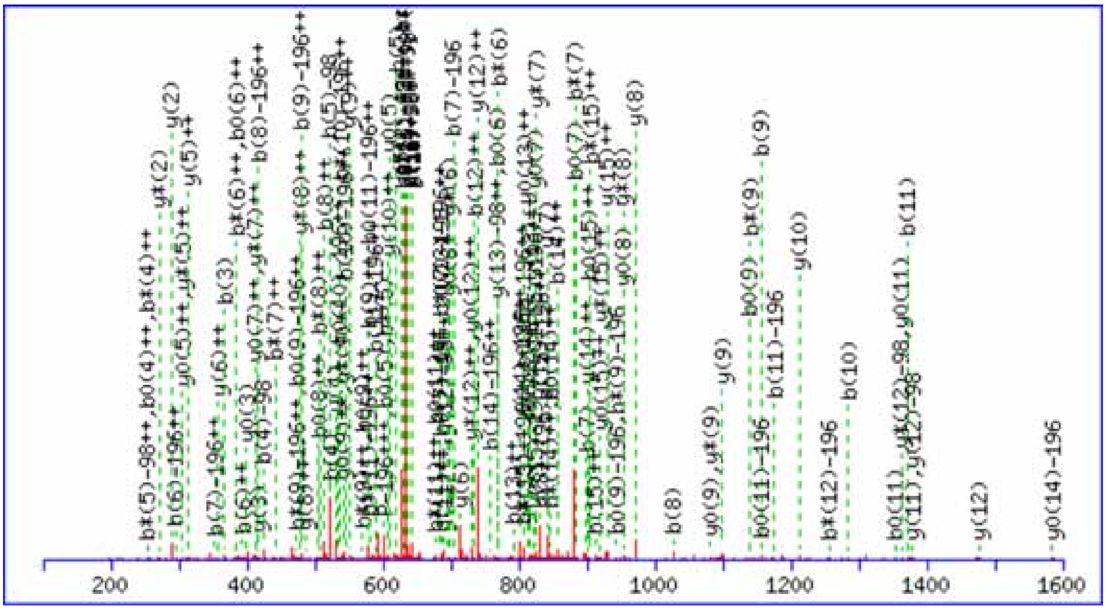
Matched b ions: b(2), b(4), b(4)-98, b(5), b(6)-98, b(6)++, b(6), b(7)-98, b(7), b(7)++, b(8)++, b(8), b(8)-98++, b(8)-98, b(9)++, b(9), b(9)-98++, b(9)-98, b(10)++, b(10), b(10)-98++, b(11), b(11)-98++, b(11)++, b(12)-98, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(9), y(9)++, y(10)++, y(12), y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.528

LGSRPSIQEQSPLELR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of LGSRPSIQEQSPLELR
Found in XIRP1_MOUSE, Xin actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 PE=1 SV=2

Match to Query 4965: 1996.938870 from(666.653566,3+)
Title: Elution from: 49.287 to 49.287 scan no 4601 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1996.9384
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 0.00022

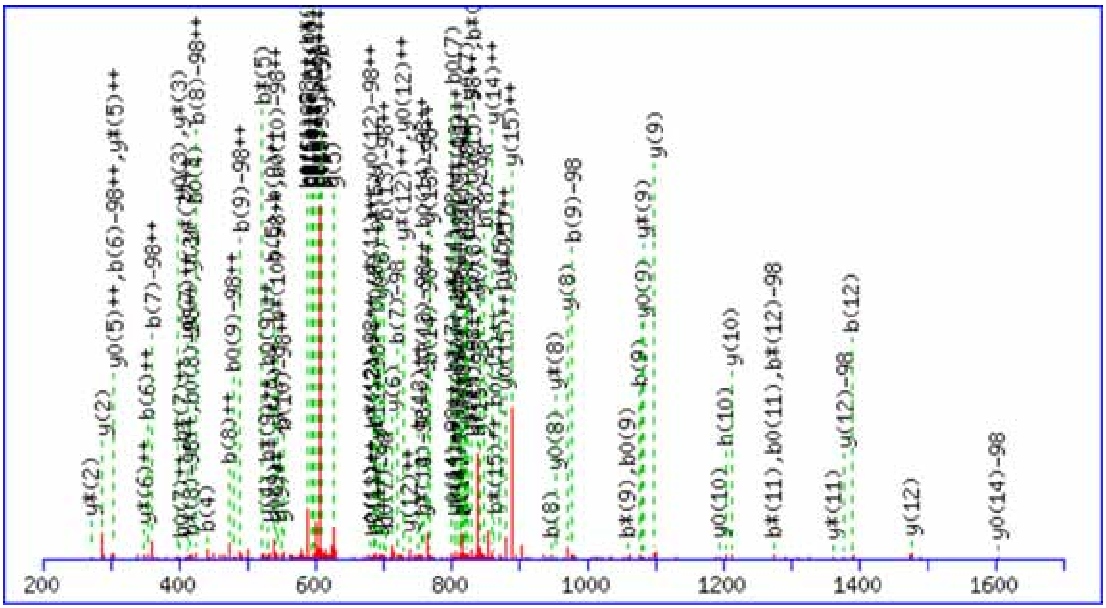
Matched b ions: b(3), b(4), b(4)-98, b(5)-98, b(5), b(6)-98++, b(6)-196++, b(6)++, b(6)-98, b(7)-98++, b(7)-98, b(7), b(7)-196++, b(7)-196, b(8)-98++, b(8), b(8)-196, b(8)-98, b(8)++, b(8)-196++, b(9)-98, b(9), b(9)-98++, b(9)-196++, b(9)++, b(10)-98++, b(10)-98, b(10), b(10)++, b(10)-196++, b(11)-98, b(11)-98++, b(11), b(11)-196++, b(11)++, b(11)-196, b(12)-196++, b(12)-98, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(14)-196++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(11)-98++, y(12)++, y(12), y(12)-98, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-196++, y(14)-98++, y(15)-98++, y(15)-196++, y(15)++
Precursor origin neutral loss: +

Peptide No.529

LGSRPSIQEQSPLELR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LGSRPSIQEQSPLELR
Found in XIRP1_MOUSE, Xin actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 PE=1 SV=2

Match to Query 5166: 1916.974566 from(639.998798,3+)
Title: Elution from: 43.757 to 43.757 scan no 4147 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1916.9720
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.0025

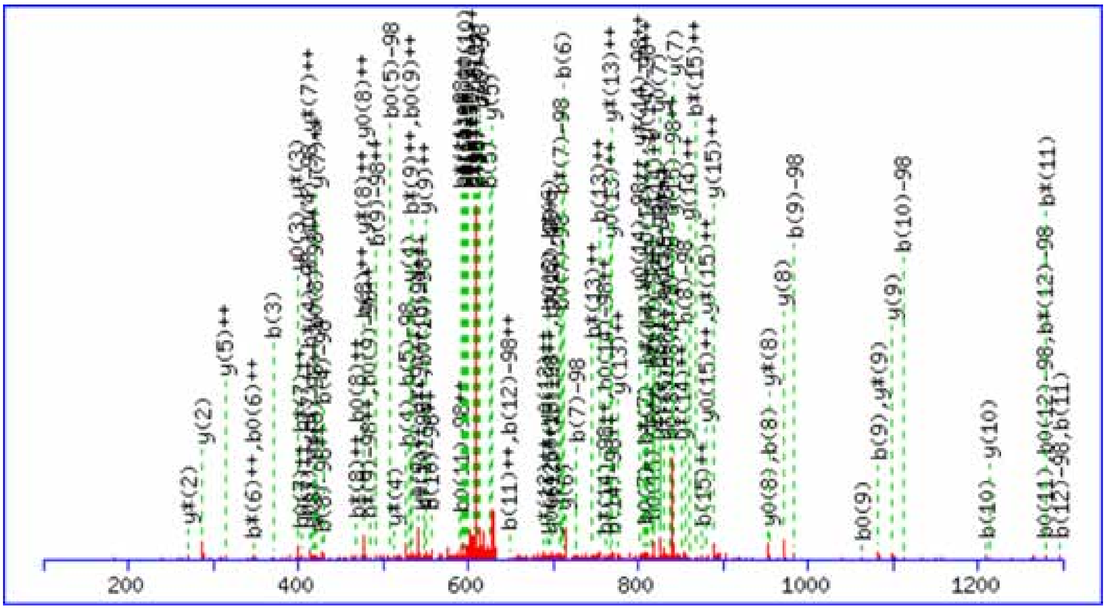
Matched b ions: b(4), b(5), b(6)-98, b(6)-98++, b(6)++, b(7)-98++, b(7)-98, b(7), b(8)-98++, b(8)++, b(8)-98, b(8), b(9)++, b(9), b(9)-98++, b(9)-98, b(10), b(10)-98++, b(10)++, b(11)-98++, b(12), b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11)++, y(12), y(12)-98, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.530

LGSRPSIQEQSPLELR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LGSRPSIQEQSPLELR
Found in XIRP1_MOUSE, Xin actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 PE=1 SV=2

Match to Query 4555: 1923.006741 from(642.009523,3+)
Title: Elution from: 45.795 to 45.795 scan no 4200 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1923.0039
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0099

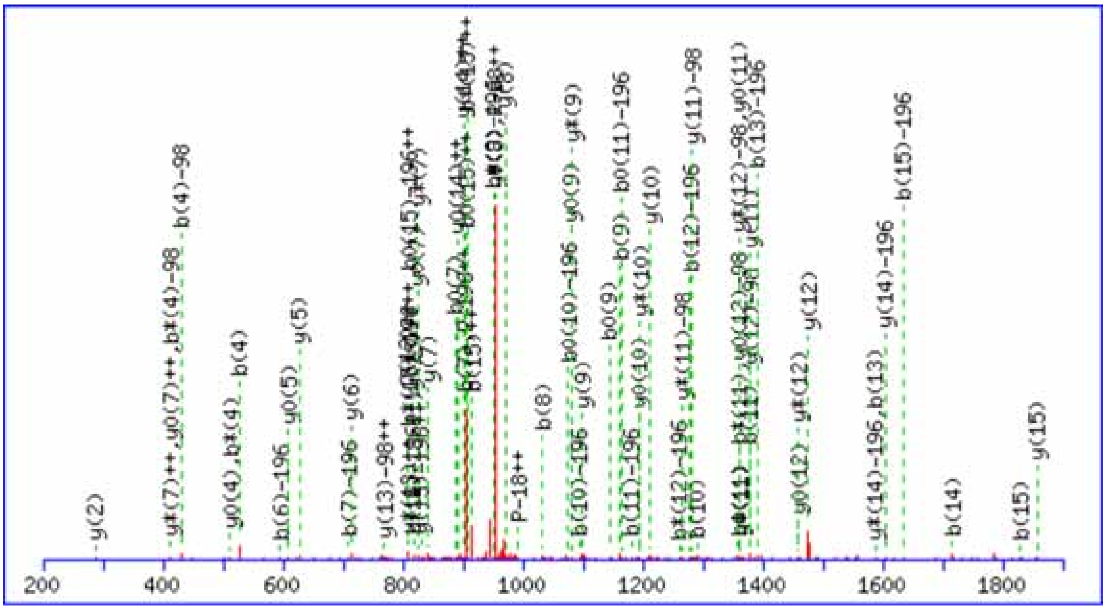
Matched b ions: b(3), b(4), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)++, b(7), b(7)-98, b(8)++, b(8), b(8)-98++, b(8)-98, b(9)++, b(9), b(9)-98, b(9)-98++, b(10), b(10)-98++, b(10)-98, b(10)++, b(11), b(11)-98++, b(11)++, b(12)-98, b(12)++, b(12)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7), y(7)++, y(8), y(9), y(9)++, y(10), y(10)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.531

LGSRPSIQEQSPLELR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of LGSRPSIQEQSPLELR
Found in XIRP1_MOUSE, Xin actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 PE=1 SV=2

Match to Query 6502: 2002.970128 from(1002.492340,2+)
Title: Elution from: 49.098 to 49.098 scan no 4847 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2002.9702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 0.00023

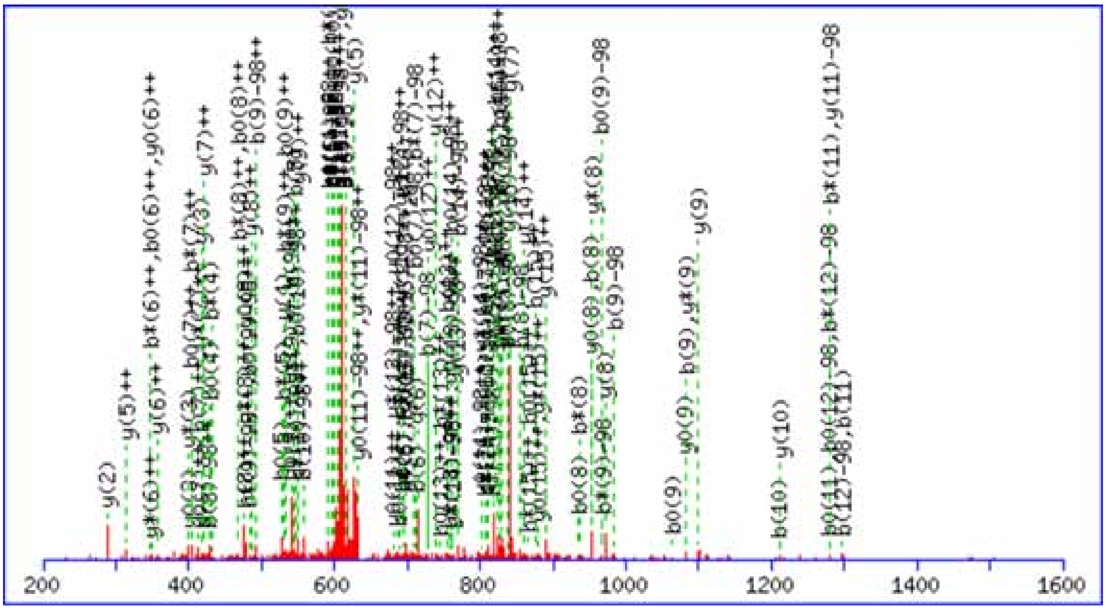
Matched b ions: b(4)-98, b(4), b(6)-196, b(6)-98, b(7)-98, b(7), b(7)-196, b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(10)-98++, b(10)-196, b(11), b(11)-98, b(11)-196, b(12)-196, b(12)-98, b(13), b(13)-98, b(13)-196, b(14)-98, b(14), b(15)-196++, b(15)-196, b(15), b(15)-98, b(15)-98++, b(15)++
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12)-98, y(12), y(13)++, y(13)-98++, y(14)-98++, y(14)-196, y(14)++, y(15), y(15)-98, y(15)-196++
Precursor origin neutral loss: +

Peptide No.532

LGSRPSIQEQSPLELR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LGSRPSIQEQSPLELR
Found in XIRP1_MOUSE, Xin actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 PE=1 SV=2

Match to Query 6079: 1923.005994 from(642.009274,3+)
Title: Elution from: 45.662 to 45.662 scan no 4394 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1923.0039
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.027

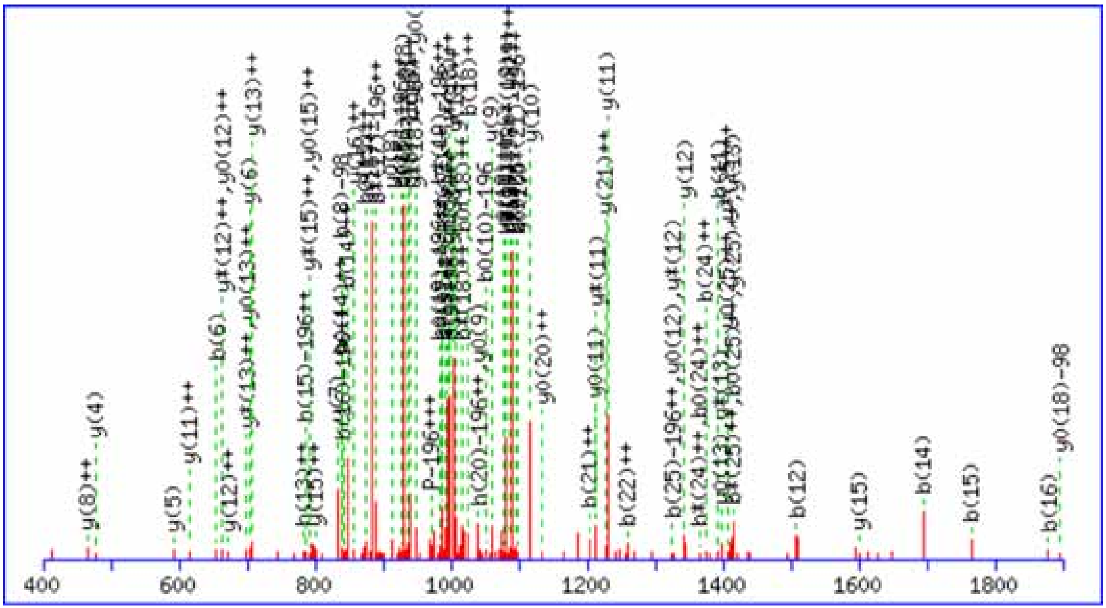
Matched b ions: b(5), b(6)-98, b(6), b(7), b(7)++, b(7)-98, b(8)-98++, b(8)++, b(8), b(8)-98, b(9), b(9)-98++, b(9)-98, b(9)++, b(10), b(10)++, b(10)-98++, b(11), b(11)-98++, b(12)-98, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)-98, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.533

LHGGFDSDCSEDGEALNGEPELDLTSK
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of LHGGFDSDCSEDGEALNGEPELDLTSK
Found in GTPB1_MOUSE, GTP-binding protein 1 OS=Mus musculus GN=Gtpbp1 PE=1 SV=2

Match to Query 8624: 3107.237943 from(1036.753257,3+)
Title: Elution from: 57.247 to 57.247 scan no 5682 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3107.2356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K27 : Dimethyl (K)
Ions Score: 62 **Expect:** 3.3e-005

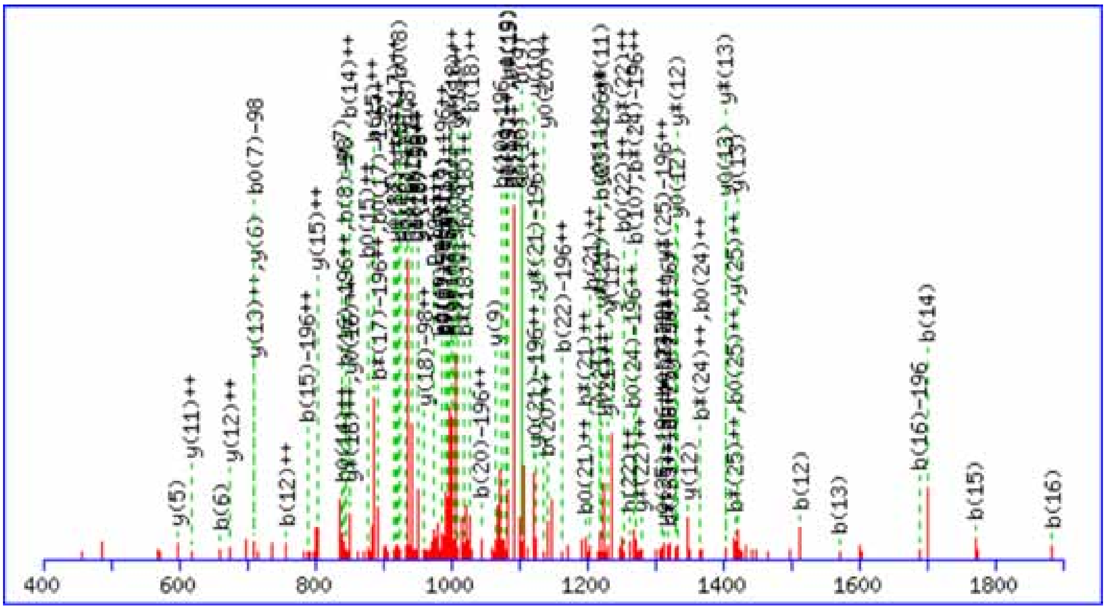
Matched b ions: b(6), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(11), b(11)-98, b(12)-98, b(12), b(13)++, b(14)-98, b(14), b(14)-98++, b(14)++, b(15)++, b(15), b(15)-98++, b(15)-196++, b(16), b(16)-98++, b(16)++, b(16)-196++, b(17)++, b(17)-98++, b(18)++, b(18)-196++, b(18)-98++, b(19)++, b(19)-98++, b(19)-196++, b(20)-98++, b(20)-196++, b(21)++, b(22)++, b(24)++, b(25)-196++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(13)++, y(13), y(15)++, y(15), y(16)++, y(18)++, y(19)++, y(21)++, y(25)++, y(26)-98++
Precursor origin neutral loss: +

Peptide No.534

LHGGFDSDCSEDGEALNGEPELDLTSK
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of LHGGFDSDCSEDGEALNGEPELDLTSK
Found in GTPB1_MOUSE, GTP-binding protein 1 OS=Mus musculus GN=Gtpbp1 PE=1 SV=2

Match to Query 8896: 3119.300298 from(1040.774042,3+)
Title: Elution from: 56.881 to 56.881 scan no 5694 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3119.2992
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K27 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 39 Expect: 0.0087

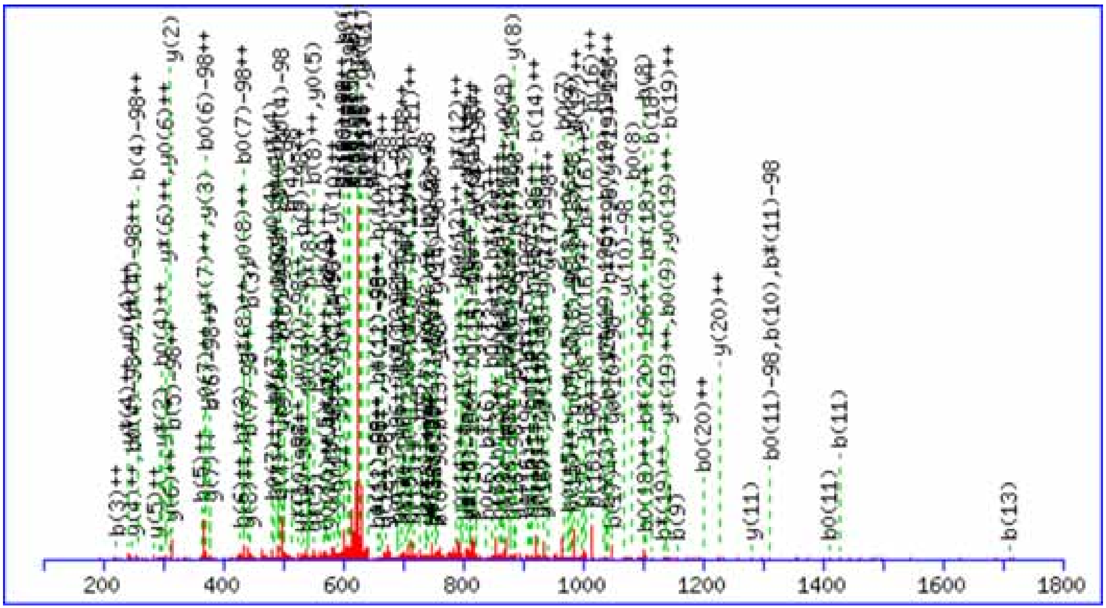
Matched b ions: b(6), b(8), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(10)-196, b(11)-98, b(12), b(12)-98, b(12)-98++, b(12)++, b(13), b(13)-98++, b(14)-98, b(14), b(14)++, b(14)-98++, b(15)-98++, b(15), b(15)++, b(15)-196++, b(16), b(16)++, b(16)-196, b(16)-98++, b(16)-196++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-196++, b(19)-98++, b(20)-98++, b(20)-196++, b(20)++, b(21)++, b(22)++, b(22)-196++, b(23)-98++, b(23)++, b(23)-196++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(15)++, y(18)-98++, y(18)++, y(21)++, y(23)-98++, y(25)++, y(25)-196++
Precursor origin neutral loss: +

Peptide No.535

LKFSDEEDGRDSDEEGAEGHK
Confirmed sites: @S:4,@S:12
Ambiguous sites:

MS/MS Fragmentation of LKFSDEEDGRDSDEEGAEGHK
Found in PRC2A_MOUSE, Protein PRRC2A OS=Mus musculus GN=Prrc2a PE=1 SV=1

Match to Query 7849: 2593.028756 from(649.264465,4+)
Title: Elution from: 31.927 to 31.927 scan no 2569 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2593.0258
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl (K)
Ions Score: 46 **Expect:** 0.0011

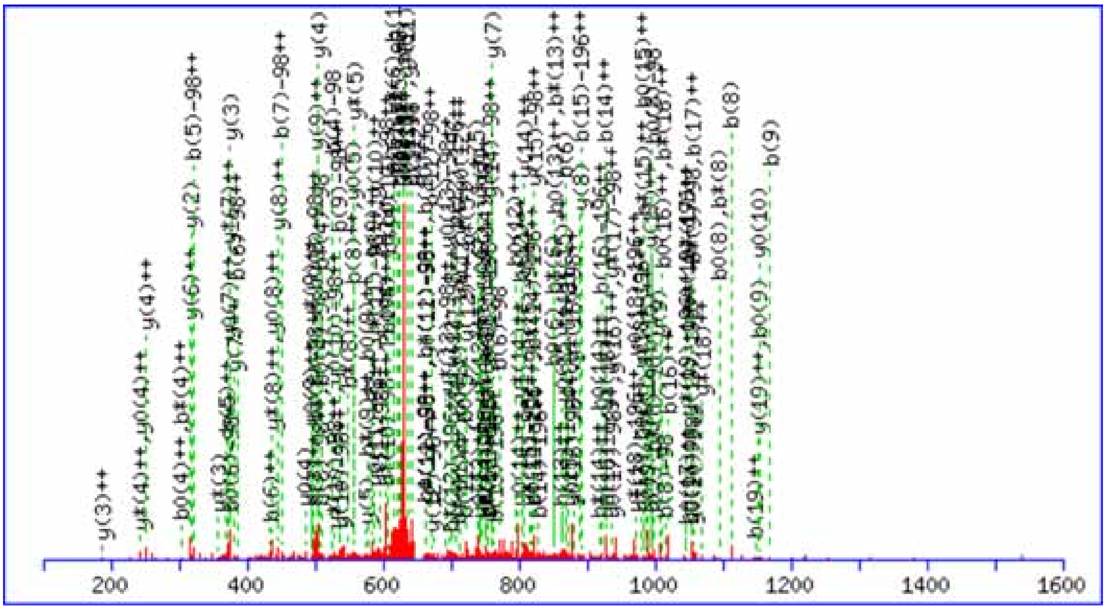
Matched b ions: b(3)++, b(3), b(4)-98++, b(4)-98, b(4), b(5)-98++, b(5)++, b(5)-98, b(5), b(6), b(6)++, b(6)-98++, b(6)-98, b(7)++, b(7), b(7)-98++, b(7)-98, b(8), b(8)++, b(8)-98, b(8)-98++, b(9)-98++, b(9)++, b(9), b(10), b(10)-98++, b(10)++, b(11), b(11)++, b(11)-98++, b(12)-196++, b(12)-98++, b(12)++, b(13)++, b(13), b(13)-98++, b(13)-196++, b(14)-98++, b(14)++, b(14)-196++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++, b(17)++, b(17)-98++, b(18)-196++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(9)++, y(10)++, y(10)-98++, y(10)-98, y(11), y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-196++, y(19)-98++, y(20)++
Precursor origin neutral loss: +

Peptide No.536

LKFSDEEDGRDSDEEGAEGHK
Confirmed sites: @S:4,@S:12
Ambiguous sites:

MS/MS Fragmentation of LKFSDEEDGRDSDEEGAEGHK
Found in PRC2A_MOUSE, Protein PRRC2A OS=Mus musculus GN=Prrc2a PE=1 SV=1

Match to Query 6857: 2611.122780 from(653.787971,4+)
Title: Elution from: 31.680 to 31.680 scan no 2330 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2611.1212
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K2 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 33 **Expect:** 0.035

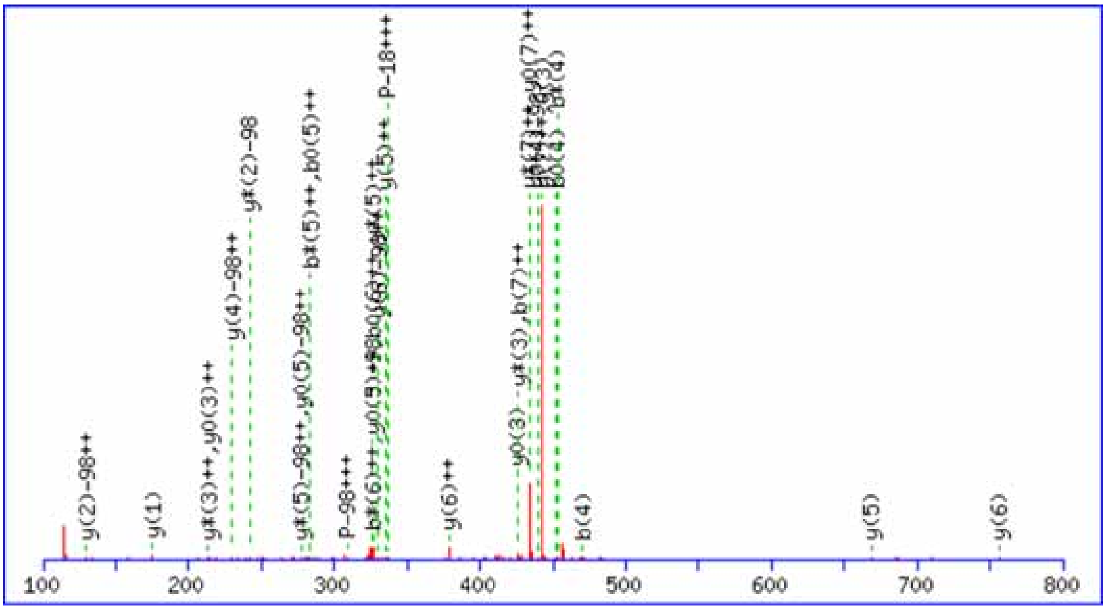
Matched b ions: b(4), b(4)-98, b(5), b(5)-98++, b(5)-98, b(5)++, b(6)-98, b(6)++, b(6)-98++, b(6), b(7)++, b(7)-98++, b(7), b(8), b(8)-98++, b(8)++, b(8)-98, b(9)++, b(9)-98++, b(9), b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)-196++, b(12)-98++, b(12)++, b(13)-98++, b(13)-196++, b(13)++, b(14)++, b(14)-98++, b(14)-196++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++, b(17)++, b(17)-98++, b(18)-98++, b(19)++
Matched y ions: y(2), y(3), y(3)++, y(4)++, y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(9)++, y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(17)++, y(18)-196++, y(19)++, y(19)-196++
Precursor origin neutral loss: +

Peptide No.537

LKSLLSTK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of LKSLLSTK
Found in BICD2_MOUSE, Protein bicaudal D homolog 2 OS=Mus musculus GN=Bicd2 PE=1 SV=1

Match to Query 543: 1024.592982 from(342.538270,3+)
Title: Elution from: 27.666 to 27.666 scan no 1984 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1024.5933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K8 : Dimethyl (K)
Ions Score: 27 **Expect:** 0.043

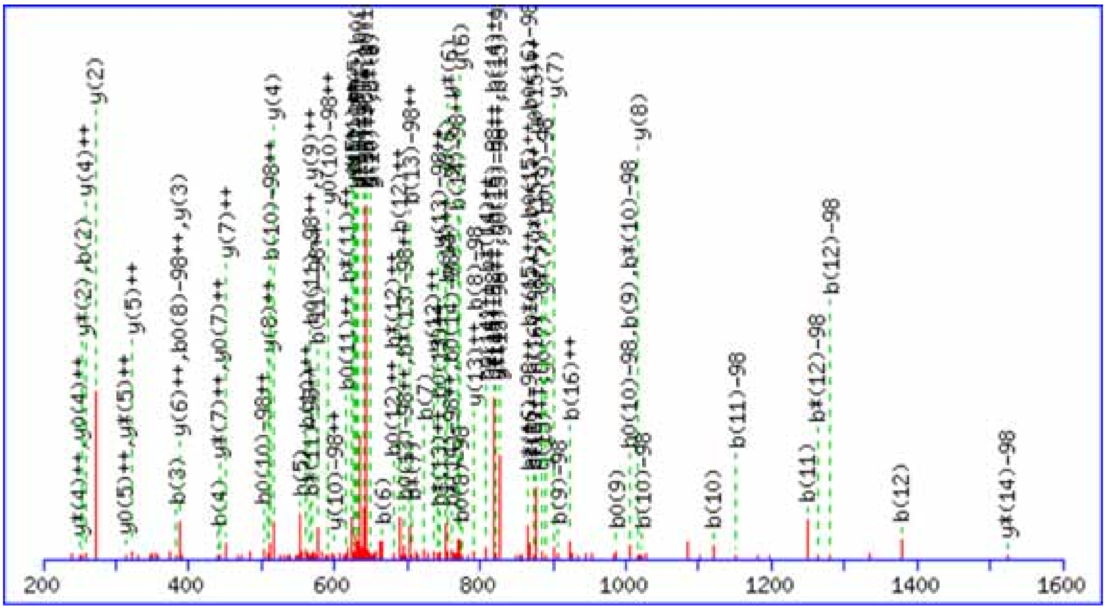
Matched b ions: b(4), b(7)++
Matched y ions: y(1), y(2)-98++, y(3), y(4)-98++, y(5), y(5)++, y(6)++, y(6), y(6)-98++, y(7)++
Precursor origin neutral loss:

Peptide No.538

LLQGLLGSDDEEQEDPK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of LLQGLLGSDDEEQEDPK
Found in SRPK3_MOUSE, Serine/threonine-protein kinase SRPK3 OS=Mus musculus GN=Srpk3 PE=2 SV=1

Match to Query 5715: 2020.924542 from(674.648790,3+)
Title: Elution from: 51.473 to 51.473 scan no 5084 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2020.9242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K17 : Dimethyl (K)
Ions Score: 46 Expect: 0.0019

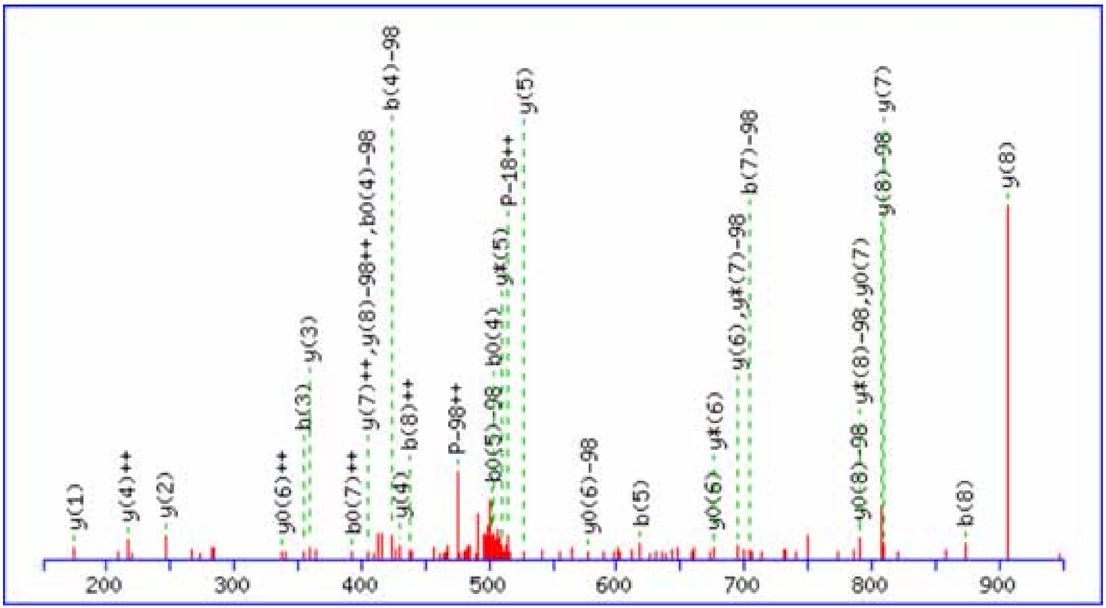
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)-98, b(9), b(9)-98, b(10), b(10)-98++, b(10)-98, b(10)++, b(11)-98, b(11), b(11)++, b(11)-98++, b(12), b(12)-98++, b(12)++, b(12)-98, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9)++, y(10)-98++, y(10)++, y(11)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.539

LPDSPALAK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of LPDSPALAK
Found in STIM1_MOUSE, Stromal interaction molecule 1 OS=Mus musculus GN=Stim1 PE=1 SV=1

Match to Query 598: 1046.541572 from(524.278062,2+)
Title: Elution from: 32.504 to 32.504 scan no 2647 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1046.5413
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K9 : Dimethyl (K)
Ions Score: 29 Expect: 0.037

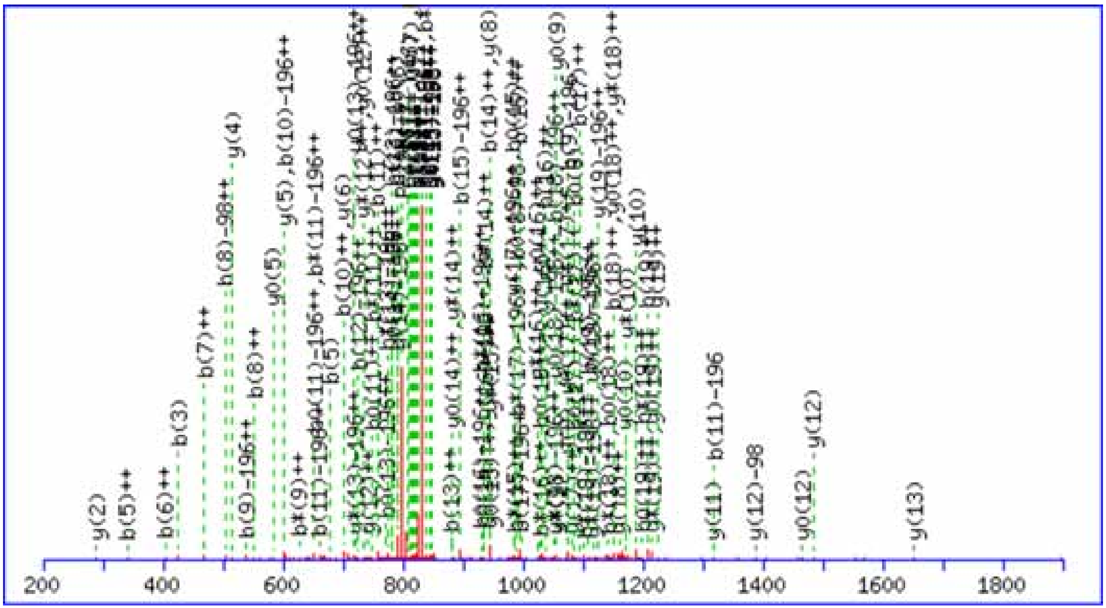
Matched b ions: b(3), b(4)-98, b(5), b(7)-98, b(8), b(8)++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(7)++, y(8)-98, y(8), y(8)-98++
Precursor origin neutral loss: +

Peptide No.540

LQRPKEESSEDENEVSNILR
Confirmed sites: @S:8,@S:9
Ambiguous sites:

MS/MS Fragmentation of LQRPKEESSEDENEVSNILR
Found in OTUD4_MOUSE, OTU domain-containing protein 4 OS=Mus musculus GN=Otud4 PE=1 SV=1

Match to Query 6865: 2587.158096 from(863.393308,3+)
Title: Elution from: 44.836 to 44.836 scan no 4078 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2587.1567
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K5 : Dimethyl (K)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 **Expect:** 0.00018

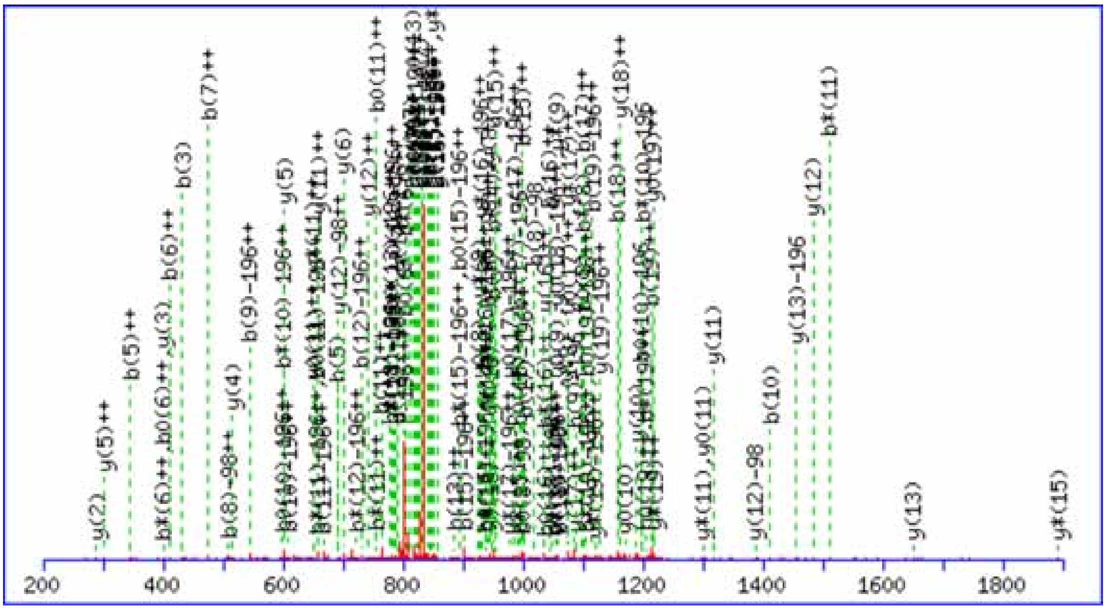
Matched b ions: b(3), b(5)++, b(5), b(6)++, b(6), b(7)++, b(8)-98++, b(8)++, b(9)-196++, b(9)-196, b(10)-196++, b(10)-98++, b(10)++, b(11)++, b(11)-196++, b(11)-98++, b(11)-196, b(12)-98++, b(12)++, b(12)-196++, b(13)-98++, b(13)-196++, b(13)++, b(14)++, b(14)-98++, b(14)-196++, b(15)-98++, b(15)++, b(15)-196++, b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(18)-196++, b(19)++, b(19)-98++, b(19)-196++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(12), y(12)++, y(13)-98, y(13), y(13)++, y(14)-196++, y(14)-98++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)-98++, y(17)-196++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)-196++, y(19)++
Precursor origin neutral loss: +

Peptide No.541

LQRPKEESSEDENEVSNILR
Confirmed sites: @S:8,@S:9
Ambiguous sites:

MS/MS Fragmentation of LQRPKEESSEDENEVSNILR
Found in OTUD4_MOUSE, OTU domain-containing protein 4 OS=Mus musculus GN=Otud4 PE=1 SV=1

Match to Query 6345: 2599.223319 from(867.415049,3+)
Title: Elution from: 44.667 to 44.667 scan no 3954 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2599.2204
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K5 : Dimethyl:2H(4)13C(2) (K)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0055

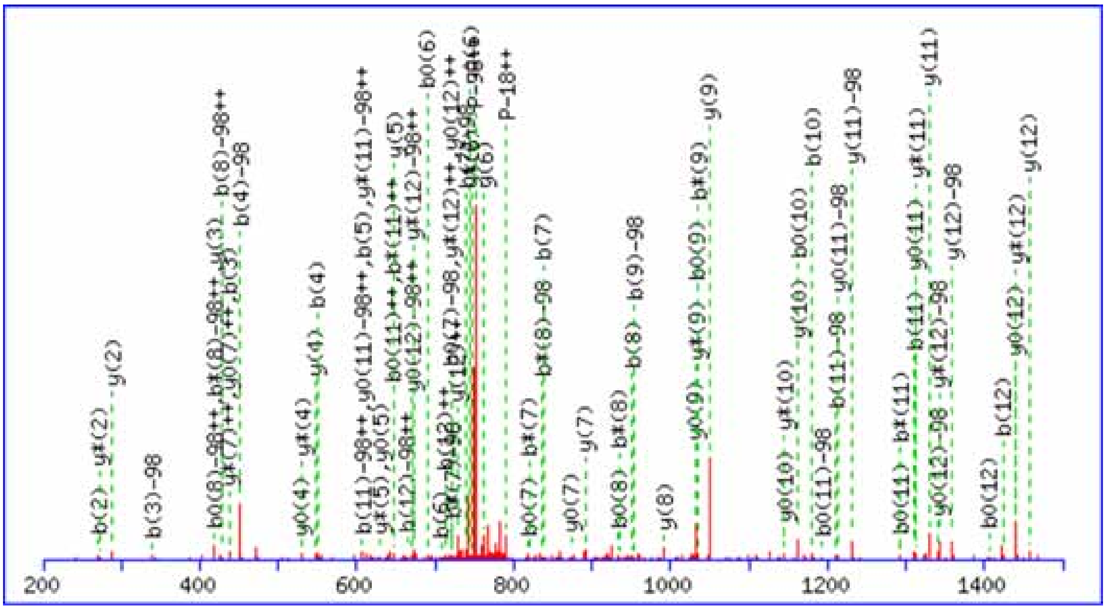
Matched b ions: b(3), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8)-98++, b(8)-98, b(9)-196++, b(9)-98++, b(9)-196, b(9)-98, b(10)-98++, b(10), b(10)-196++, b(11)++, b(11)-196++, b(11)-98++, b(11)-98, b(12)++, b(12)-196++, b(12)-98++, b(13)-196++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(14)-196++, b(15)-196++, b(15)++, b(15)-98++, b(16)-196++, b(16)-98++, b(16)++, b(17)-196++, b(17)++, b(18)++, b(18)-196++, b(18)-98++, b(19)++, b(19)-196++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13), y(13)-98, y(13)-196, y(13)++, y(14)-98++, y(14)-196++, y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(19)-98++, y(19)-196++
Precursor origin neutral loss: +

Peptide No.542

LQSIGTENTEENR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LQSIGTENTEENR
Found in ALDOA_MOUSE, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 3088: 1597.699006 from(799.856779,2+)
Title: Elution from: 29.877 to 29.877 scan no 2288 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1597.6985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 0.00017

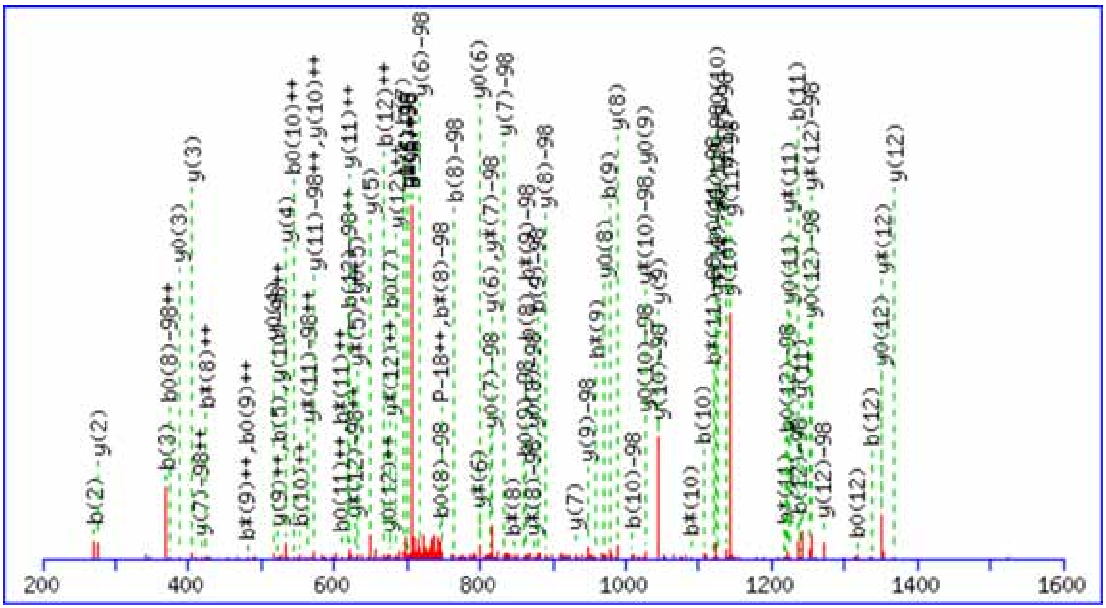
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(6), b(7)-98, b(7), b(8)-98++, b(8), b(9)-98, b(10), b(11)-98++, b(11), b(11)-98, b(12), b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12), y(12)-98, y(12)++
Precursor origin neutral loss: +

Peptide No.543

LQVPGGDSDEETK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of LQVPGGDSDEETK
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 2540: 1509.661052 from(755.837802,2+)
Title: Elution from: 34.386 to 34.386 scan no 2904 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1509.6600
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 57 Expect: 5.9e-005

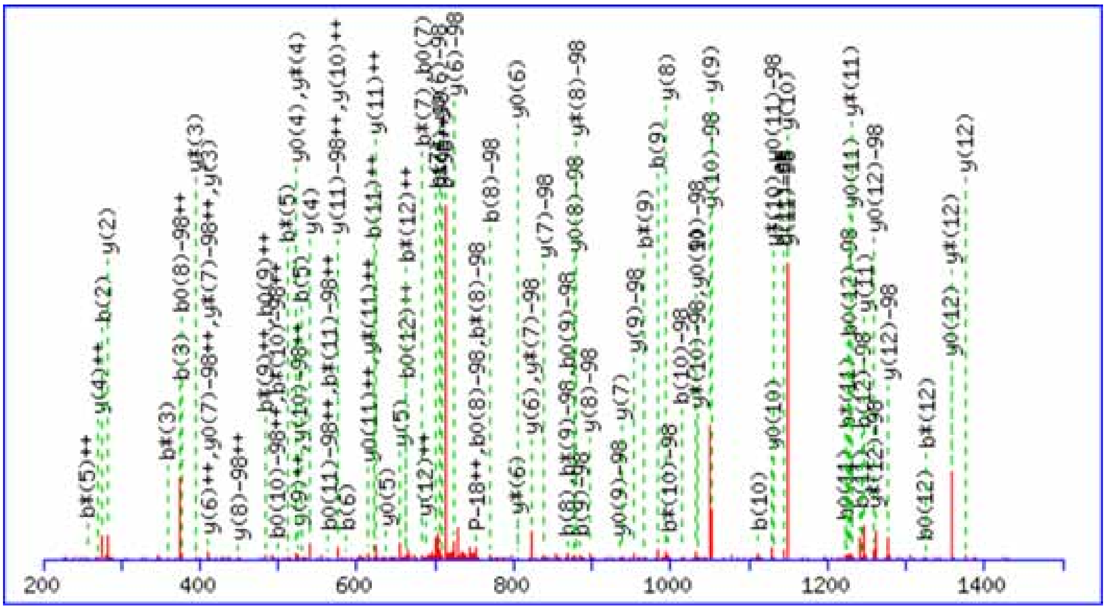
Matched b ions: b(2), b(3), b(5), b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)++, b(10), b(10)-98, b(11), b(11)-98, b(12)++, b(12), b(12)-98++, b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7)-98++, y(7), y(7)-98, y(8), y(8)-98, y(9)-98, y(9), y(9)++, y(10)-98, y(10), y(10)++, y(10)-98++, y(11), y(11)++, y(11)-98, y(11)-98++, y(12)-98, y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.544

LQVPGGDSDEETK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of LQVPGGDSDEETK
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 2052: 1521.723996 from(761.869274,2+)
Title: Elution from: 33.875 to 33.875 scan no 2624 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1521.7236
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 55 Expect: 0.00013

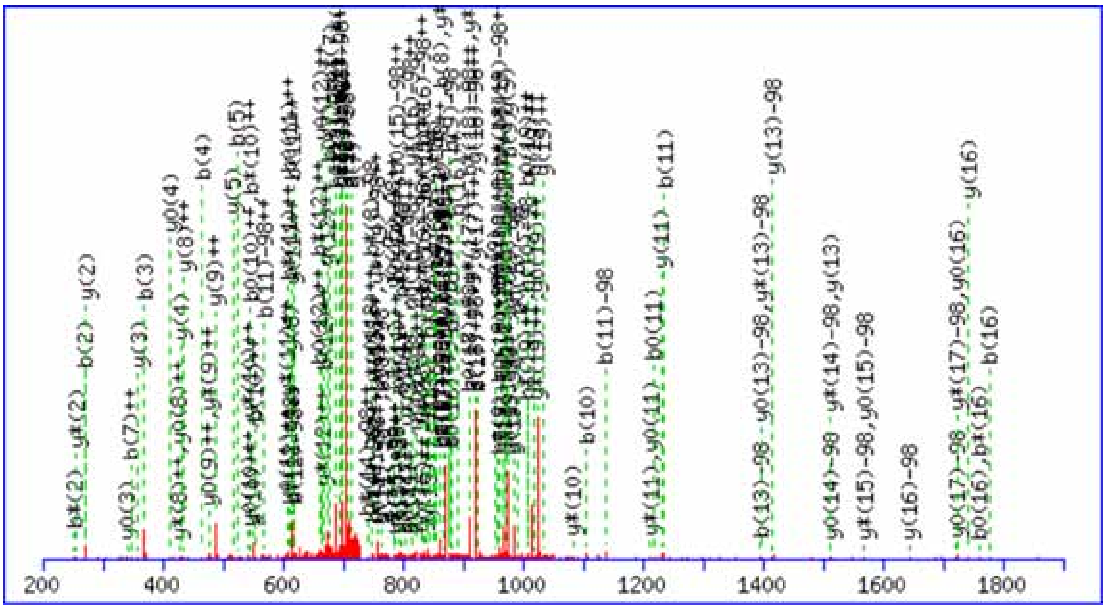
Matched b ions: b(2), b(3), b(5), b(6), b(7), b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(11)++, b(12)-98
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6)++, y(6), y(6)-98, y(7)-98, y(7), y(8)-98, y(8), y(8)-98++, y(9)++, y(9), y(9)-98, y(10)-98, y(10), y(10)-98++, y(10)++, y(11), y(11)++, y(11)-98, y(11)-98++, y(12)-98, y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.545

LQVPGGDSDEETKTPSASPR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of LQVPGGDSDEETKTPSASPR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 5592: 2206.016547 from(736.346125,3+)
Title: Elution from: 34.518 to 34.518 scan no 2705 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2206.0155
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
Ions Score: 53 Expect: 0.00033

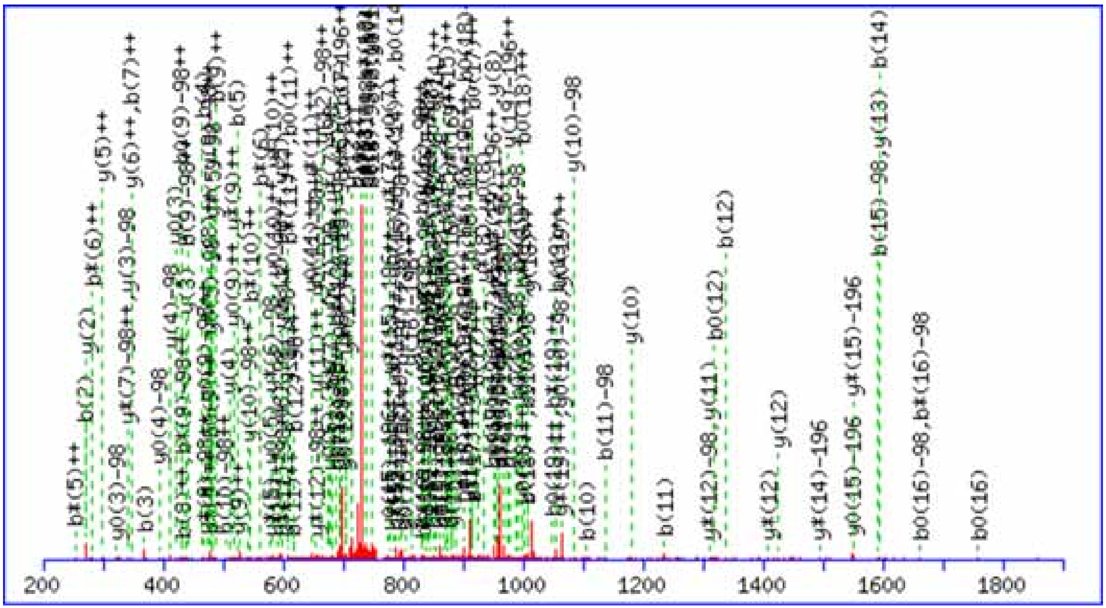
Matched b ions: b(2), b(3), b(4), b(5), b(7)++, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)++, b(10)-98, b(11)-98, b(11), b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)-98, b(14)++, b(14)-98++, b(15)-98++, b(16), b(16)++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)++, y(9), y(10)++, y(11)++, y(11), y(12)++, y(13)++, y(13)-98, y(13), y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98, y(16)-98++, y(16), y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.546

LQVPGGDSDEETKTPSASPR
Confirmed sites: @S:8,@S:18
Ambiguous sites:

MS/MS Fragmentation of LQVPGGDSDEETKTPSASPR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 5570: 2285.983779 from(763.001869,3+)
Title: Elution from: 36.685 to 36.685 scan no 2909 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2285.9818
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.027

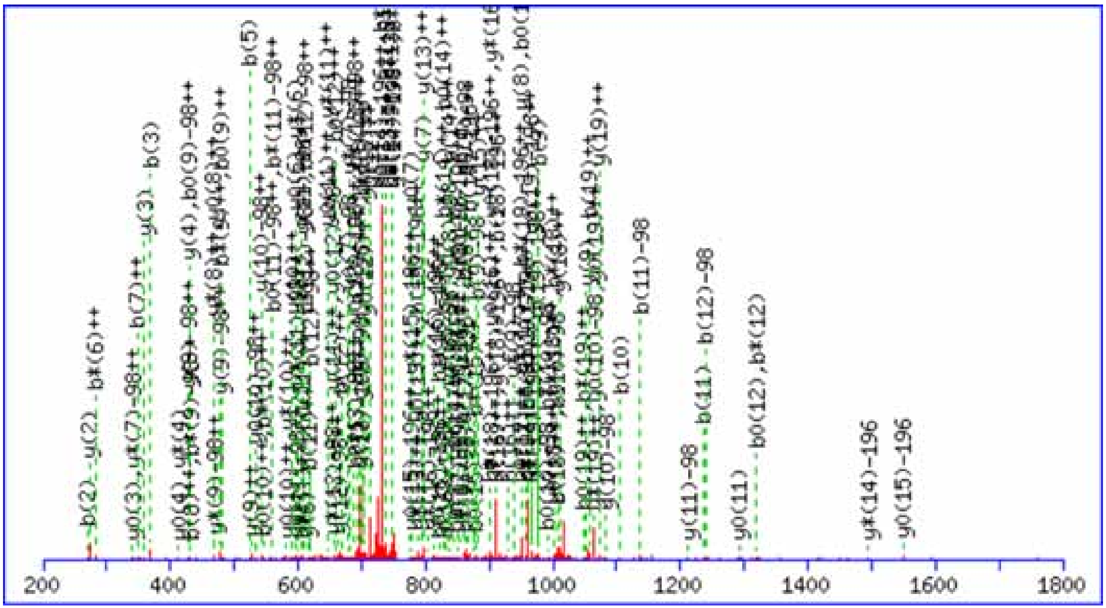
Matched b ions: b(2), b(3), b(4), b(5), b(7)++, b(7), b(8), b(8)++, b(9)++, b(9)-98++, b(9)-98, b(9), b(10), b(10)-98, b(10)-98++, b(11), b(11)++, b(11)-98, b(12), b(12)-98++, b(13)-98++, b(13)++, b(14), b(14)++, b(14)-98++, b(15)-98++, b(15)-98, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)-196++, b(18)-98++, b(18)++, b(19)-196++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(4), y(5), y(5)++, y(6)-98, y(6)++, y(6), y(7)-98, y(7), y(8), y(8)-98, y(8)++, y(9)-98++, y(9)++, y(9)-98, y(10)-98++, y(10)++, y(10)-98, y(10), y(11), y(11)-98++, y(11)++, y(12), y(12)++, y(12)-98++, y(13)-196++, y(13)++, y(13), y(13)-98, y(13)-98++, y(14)-98++, y(14)++, y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(16)-196++, y(17)-98++, y(17)++, y(17)-196++, y(18)-196++, y(18)-98++, y(18)++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.547

LQVPGGDSDEETKTPSASPR
Confirmed sites: @S:8,@T:14
Ambiguous sites:

MS/MS Fragmentation of LQVPGGDSDEETKTPSASPR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 5568: 2285.984916 from(763.002248,3+)
Title: Elution from: 36.661 to 36.661 scan no 2991 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2285.9818
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.0058

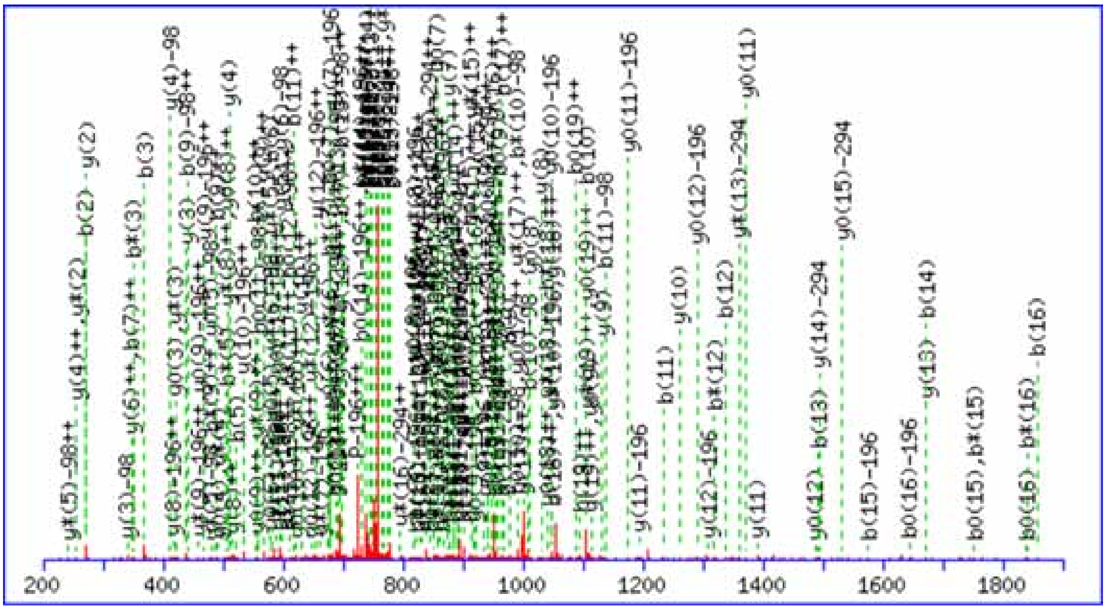
Matched b ions: b(2), b(3), b(5), b(7)++, b(7), b(8), b(8)++, b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(11)++, b(12)-98, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)-196++, b(14)++, b(15)-196++, b(15)-98++, b(16)-98, b(16)-196++, b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(18)-98++, b(18)-196++, b(18)++, b(19)-196++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(6), y(7)-98, y(7), y(8), y(8)-98++, y(8)-98, y(9)-98++, y(9)++, y(9), y(10)-98++, y(10)++, y(10)-98, y(11)-98++, y(11)++, y(11)-98, y(12)++, y(12)-98++, y(13)++, y(13)-98, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(16)-196++, y(17)++, y(17)-196++, y(17)-98++, y(18)-98++, y(18)-196++, y(18)++, y(19)++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.548

LQVPGGDSDEETKTPSASPR
Confirmed sites: @S:8,@T:14,@S:18
Ambiguous sites:

MS/MS Fragmentation of LQVPGGDSDEETKTPSASPR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 5738: 2365.950210 from(789.657346,3+)
Title: Elution from: 38.788 to 38.788 scan no 3261 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2365.9481
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.046

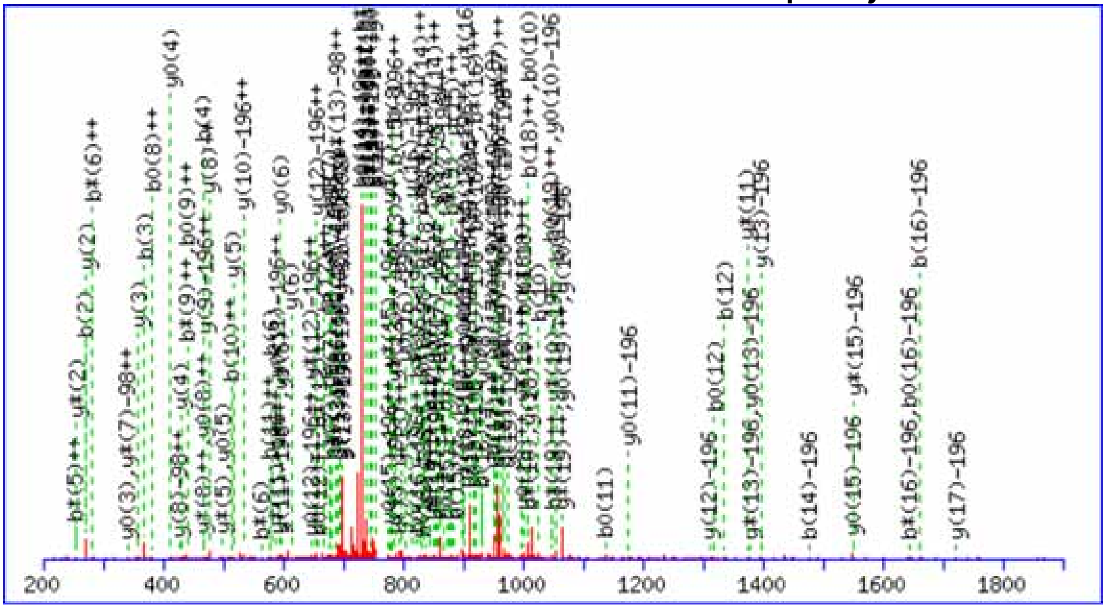
Matched b ions: b(2), b(3), b(5), b(6), b(7), b(7)++, b(8)-98, b(8), b(9)-98++, b(9)++, b(9)-98, b(9), b(10)++, b(10)-98, b(10), b(11)-98, b(11), b(11)++, b(12), b(13), b(13)-98++, b(13)++, b(14)-98, b(14)-196++, b(14)++, b(14), b(15)-196, b(15)-98, b(15)-98++, b(15)++, b(16), b(16)-196++, b(16)-98++, b(17)-196++, b(17)-98++, b(17)++, b(18)-98++, b(18)-196++, b(18)-294++, b(18)++, b(19)-196++, b(19)-294++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(3)-98, y(4)++, y(4)-98, y(4), y(5), y(6)-98, y(6), y(6)++, y(7), y(7)-196, y(7)-98, y(8)++, y(8)-196++, y(8)-98++, y(8)-98, y(8), y(9)-98++, y(9)++, y(9)-196++, y(9)-196, y(9)-98, y(9), y(10)-196++, y(10)-98++, y(10)++, y(10), y(11), y(11)++, y(11)-196++, y(11)-98++, y(11)-196, y(12)-98++, y(12)-196++, y(12)++, y(12)-196, y(13), y(13)++, y(13)-294++, y(13)-196++, y(14)++, y(14)-294, y(14)-294++, y(14)-196++, y(14)-98++, y(15)-196, y(15)-294++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(16)-196++, y(17)++, y(17)-98++, y(17)-196++, y(17)-294++, y(18)-98++, y(18)-196++, y(18)-294++, y(18)++, y(19)-294++, y(19)-196++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.549

LQVPGGDSDEETKTPSASPR
Confirmed sites: @T:12,@T:14
Ambiguous sites:

MS/MS Fragmentation of LQVPGGDSDEETKTPSASPR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 5921: 2285.983269 from(763.001699,3+)
Title: Elution from: 36.809 to 36.809 scan no 3019 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2285.9818
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.047

Matched b ions: b(2), b(3), b(4), b(6), b(7), b(8), b(9), b(10)++, b(10), b(11)++, b(12), b(12)++, b(13)-98++, b(13)++, b(14)-196, b(14)-196++, b(14)-98++, b(14)++, b(15)-196++, b(15)-98++, b(15)++, b(16)-196, b(16)-98, b(16)-98++, b(16)-196++, b(16)++, b(17)-98++, b(17)-196++, b(17)++, b(18)-196++, b(18)-98++, b(18)++, b(19)-196++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8), y(8)-98++, y(8)++, y(8)-98, y(9)-98++, y(9)-196++, y(9)-98, y(10)-196, y(10)-196++, y(10)-98++, y(11)-196++, y(11)++, y(11)-98++, y(12)-196, y(12)-196++, y(12)-98++, y(12)++, y(13)-98++, y(13)-196++, y(13)++, y(13)-196, y(14)++, y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(16)-98, y(16)-196++, y(17)-98++, y(17)++, y(17)-196++, y(17)-196, y(18)-196++, y(18)-98++, y(18)++, y(19)-98++, y(19)-196++
Precursor origin neutral loss: +

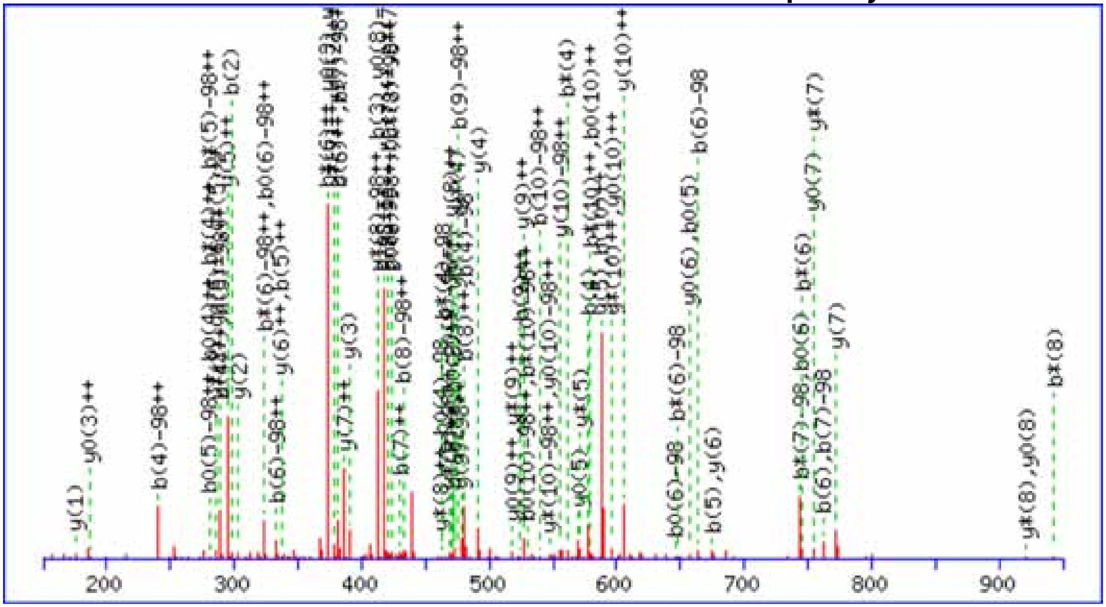
Peptide No.550

LRLSPSPTSQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of LRLSPSPTSQR
Found in LMNA_MOUSE, Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2

Match to Query 1823: 1348.686606 from(450.569478,3+)

Title: Elution from: 30.901 to 30.901 scan no 2429 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1348.6864
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.023

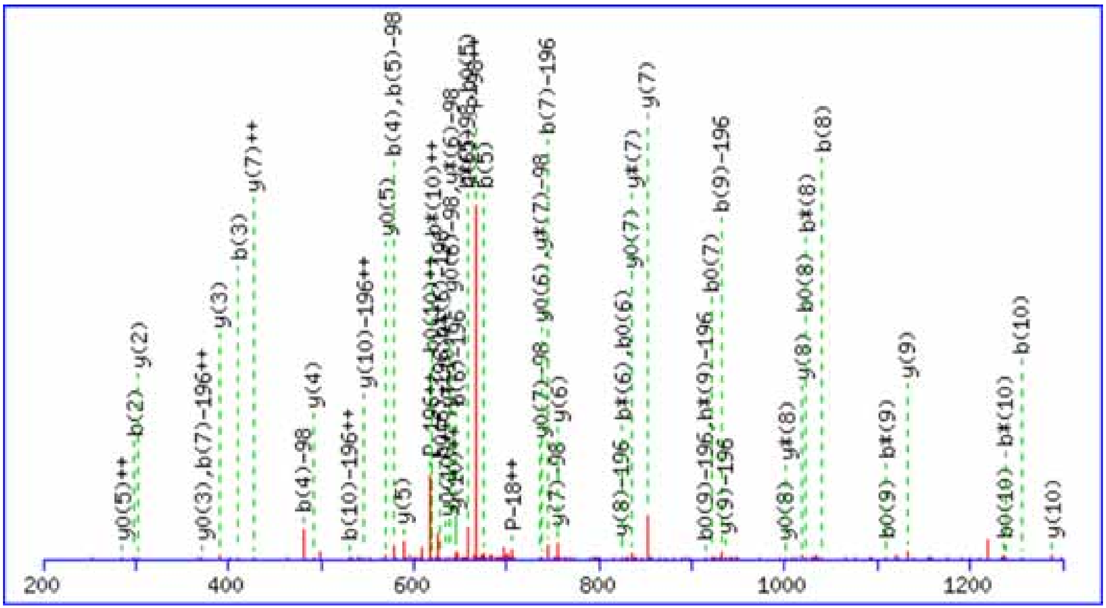
Matched b ions: b(2), b(3), b(4)-98++, b(4)-98, b(4)++, b(4), b(5)-98++, b(5), b(5)++, b(6), b(6)-98++, b(6)-98, b(6)++, b(7)-98, b(7)-98++, b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(9)++, b(10)++, b(10)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8)-98++, y(8)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.551

LRLSPSPTSQR
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of LRLSPSPTSQR
Found in LMNA_MOUSE, Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2

Match to Query 2159: 1428.653294 from(715.333923,2+)
Title: Elution from: 33.645 to 33.645 scan no 2802 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1428.6527
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0085

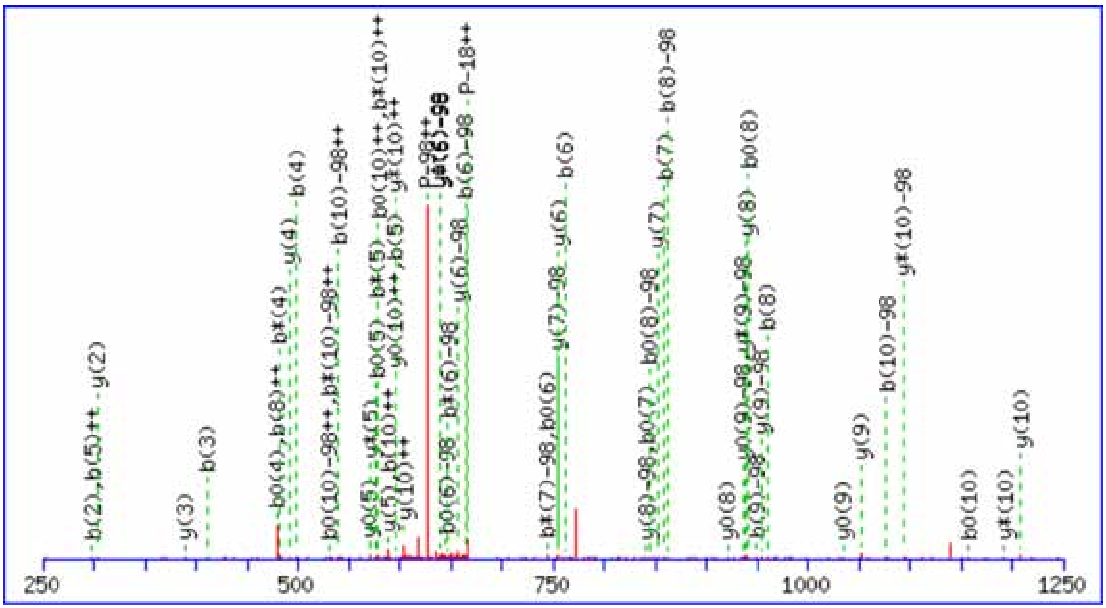
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98++, b(6)-98, b(6)-196, b(7)-196++, b(7)-196, b(8)-98, b(8), b(9)-196, b(9)-98, b(10), b(10)-98, b(10)-196++, b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(7)++, y(8), y(8)-98, y(8)-196, y(9), y(9)-98, y(9)-196, y(10), y(10)-98, y(10)++, y(10)-98++, y(10)-196++
Precursor origin neutral loss: +

Peptide No.552

LRLSPSPTSQR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LRLSPSPTSQR
Found in LMNA_MOUSE, Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2

Match to Query 1821: 1348.686320 from(675.350436,2+)
Title: Elution from: 30.835 to 30.835 scan no 2419 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1348.6864
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.022

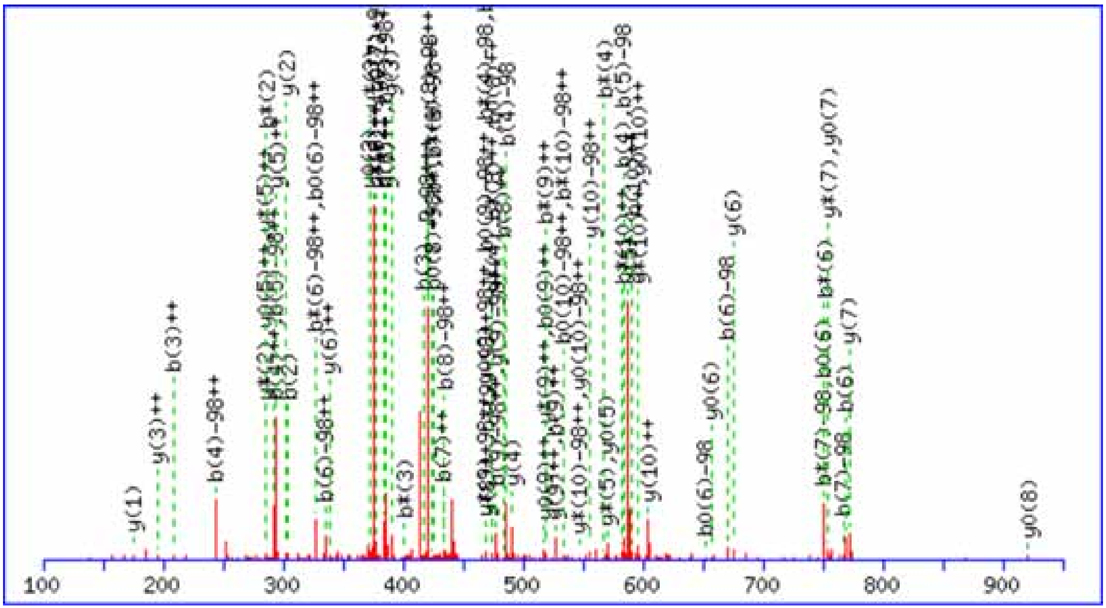
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6)-98, b(6), b(7), b(8)++, b(8)-98, b(8), b(9)-98, b(10)++, b(10)-98++, b(10)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.553

LRLSPSPTSQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of LRLSPSPTSQR
Found in LMNA_MOUSE, Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2

Match to Query 1405: 1354.718016 from(452.579948,3+)
Title: Elution from: 30.626 to 30.626 scan no 2190 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1354.7182
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.018

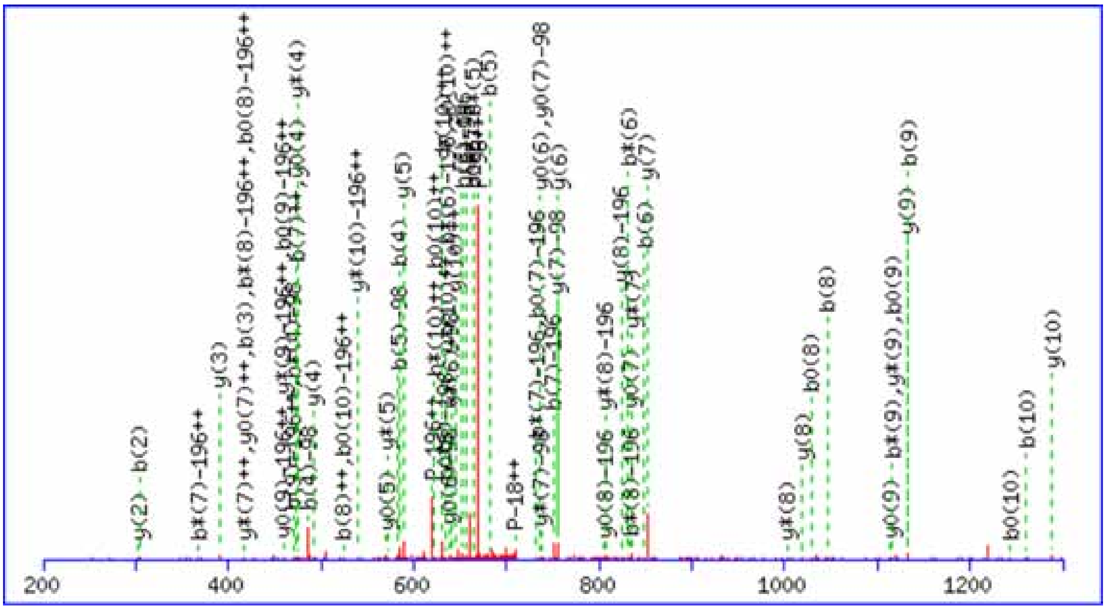
Matched b ions: b(2), b(3)++, b(3), b(4)-98++, b(4)-98, b(4)++, b(4), b(5)-98++, b(5)-98, b(6)-98, b(6), b(6)-98++, b(6)++, b(7)-98++, b(7)-98, b(7)++, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)++
Matched y ions: y(1), y(2), y(3)++, y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8)-98++, y(8)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.554

LRLSPSPTSQR
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of LRLSPSPTSQR
Found in LMNA_MOUSE, Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2

Match to Query 2937: 1434.685652 from(718.350102,2+)
Title: Elution from: 33.044 to 33.044 scan no 2645 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1434.6845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.019

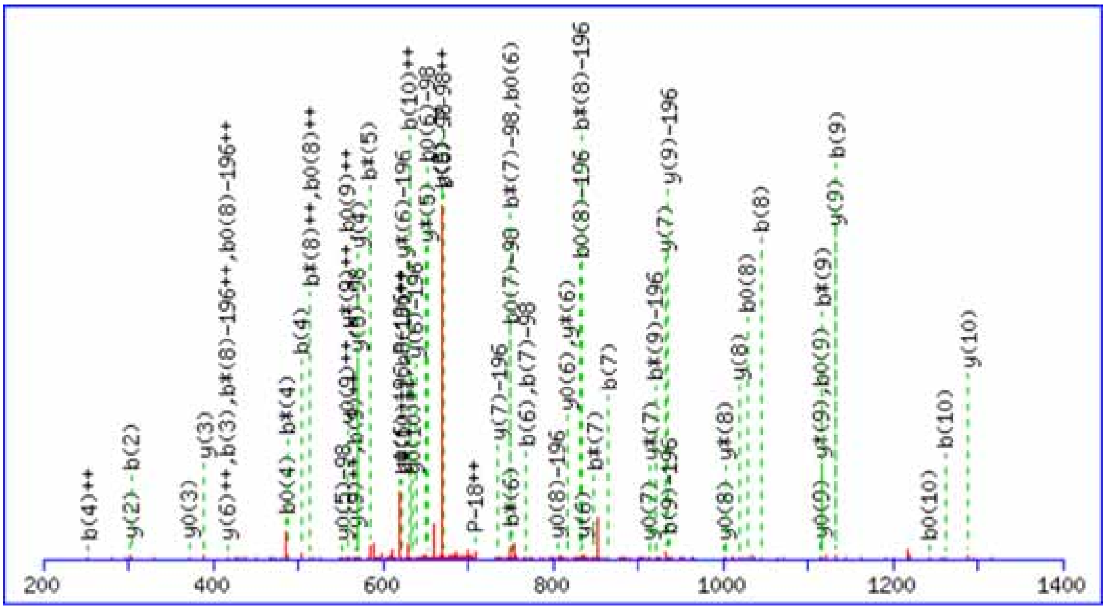
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6)-196, b(6), b(7)-196, b(7)++, b(7)-98, b(8)-98++, b(8)++, b(8)-98, b(8), b(9), b(9)-98, b(9)-196++, b(10), b(10)-98, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(8)-196, y(9)-98, y(9), y(10), y(10)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.555

LRLSPSPTSQR
Confirmed sites: @S:6,@T:8
Ambiguous sites:

MS/MS Fragmentation of LRLSPSPTSQR
Found in LMNA_MOUSE, Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2

Match to Query 1703: 1434.685198 from(718.349875,2+)
Title: Elution from: 33.480 to 33.480 scan no 2574 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1434.6845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0086

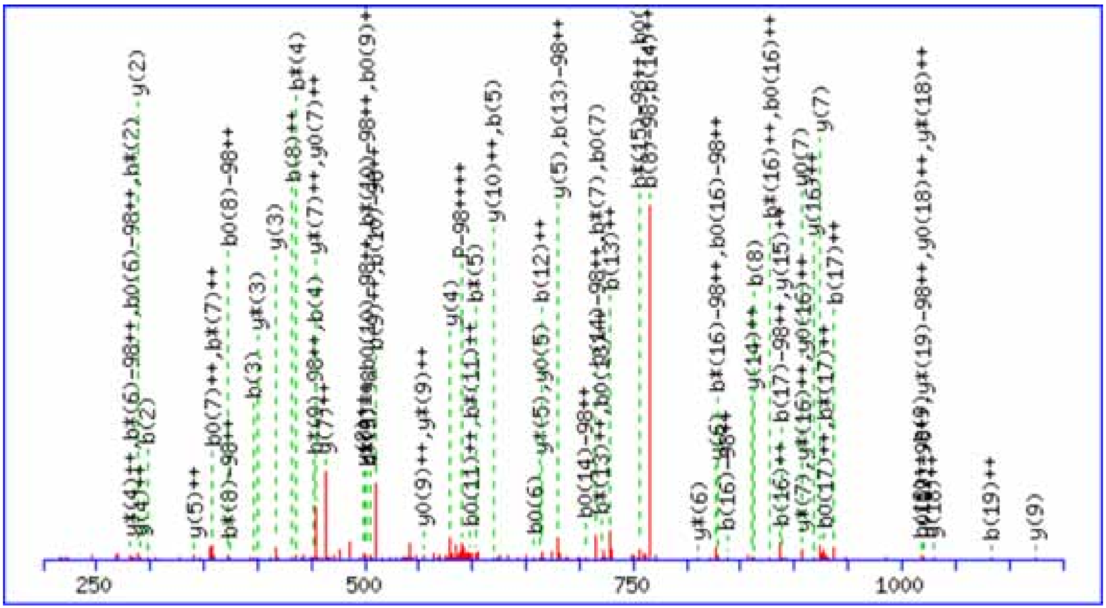
Matched b ions: b(2), b(3), b(4)++, b(4), b(6)-98, b(6), b(7), b(7)-98, b(8)-98++, b(8), b(8)-98, b(9)-98, b(9), b(9)-98++, b(9)-196, b(9)++, b(10), b(10)-98, b(10)-98++, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6)++, y(6), y(6)-196, y(6)-98, y(7), y(7)-98++, y(7)-98, y(7)-196, y(8), y(8)-98, y(9)-98, y(9), y(9)-98++, y(9)-196, y(9)++, y(10), y(10)-98, y(10)-98++
Precursor origin neutral loss: +

Peptide No.556

LRPGSGGEKPPDEAPFTYQLK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LRPGSGGEKPPDEAPFTYQLK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 5793: 2450.226248 from(613.563838,4+)
Title: Elution from: 44.244 to 44.244 scan no 3921 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2450.2246
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K9 : Dimethyl (K)
K21 : Dimethyl (K)
Ions Score: 43 Expect: 0.0042

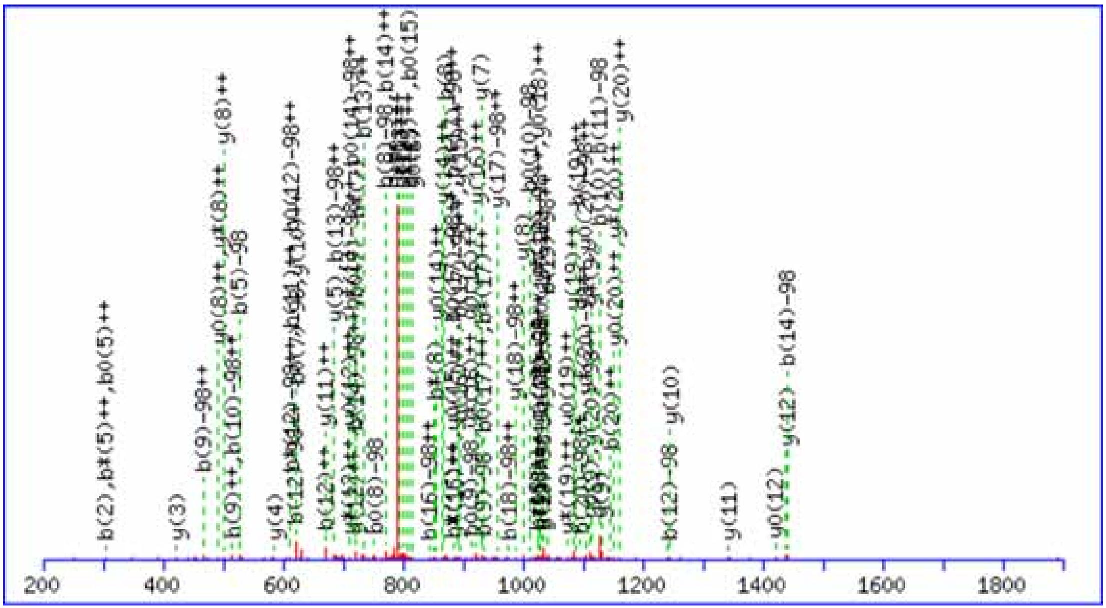
Matched b ions: b(2), b(3), b(4), b(5), b(8)-98, b(8)++, b(8), b(9), b(9)++, b(10)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(19)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(5)++, y(6), y(7)++, y(7), y(8)++, y(9), y(10)++, y(14)++, y(15)++, y(16)++, y(18)++
Precursor origin neutral loss:

Peptide No.557

LRPGSGGEKPPDEAPFTYQLK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of LRPGSGGEKPPDEAPFTYQLK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 7930: 2468.321484 from(823.781104,3+)
Title: Elution from: 44.214 to 44.214 scan no 4197 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2468.3201
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K9 : Dimethyl:2H(4)13C(2) (K)
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 48 Expect: 0.00084

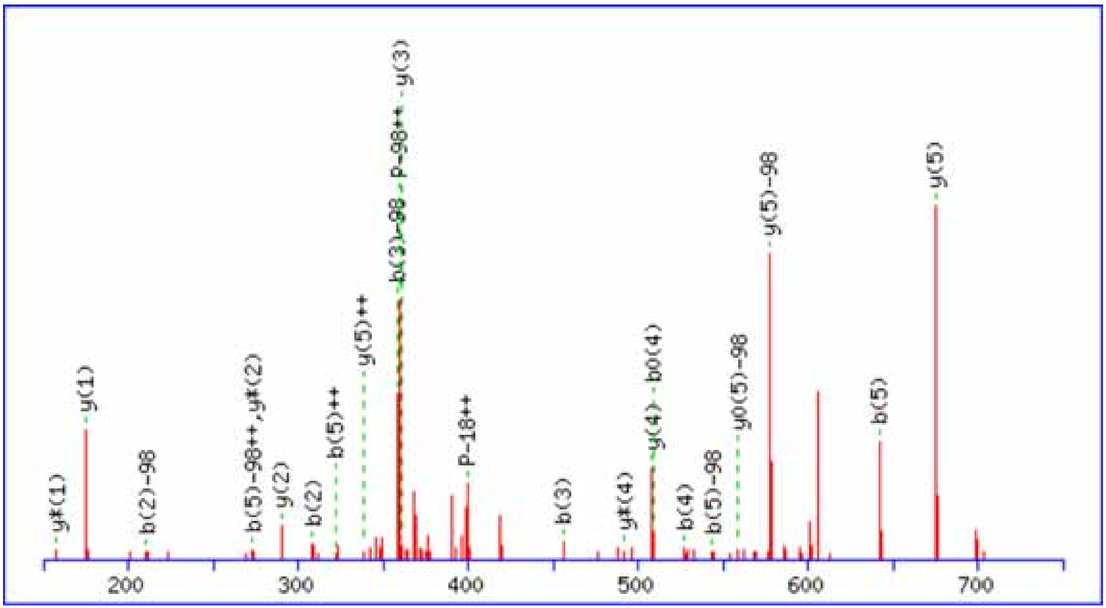
Matched b ions: b(2), b(5)-98, b(8)-98, b(8), b(9)++, b(9)-98++, b(9)-98, b(9), b(10)-98++, b(10), b(10)-98, b(11)-98, b(11)++, b(12)-98++, b(12)++, b(12)-98, b(13)-98++, b(13)++, b(14)-98++, b(14)-98, b(14)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-98++, b(20)++
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(8)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)++, y(20)-98++
Precursor origin neutral loss: +

Peptide No.558

LSFADR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of LSFADR
Found in KPCT_MOUSE, Protein kinase C theta type OS=Mus musculus GN=Prkcq PE=1 SV=1

Match to Query 178: 815.357910 from(408.686231,2+)
Title: Elution from: 37.609 to 37.609 scan no 3346 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 815.3578
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0051

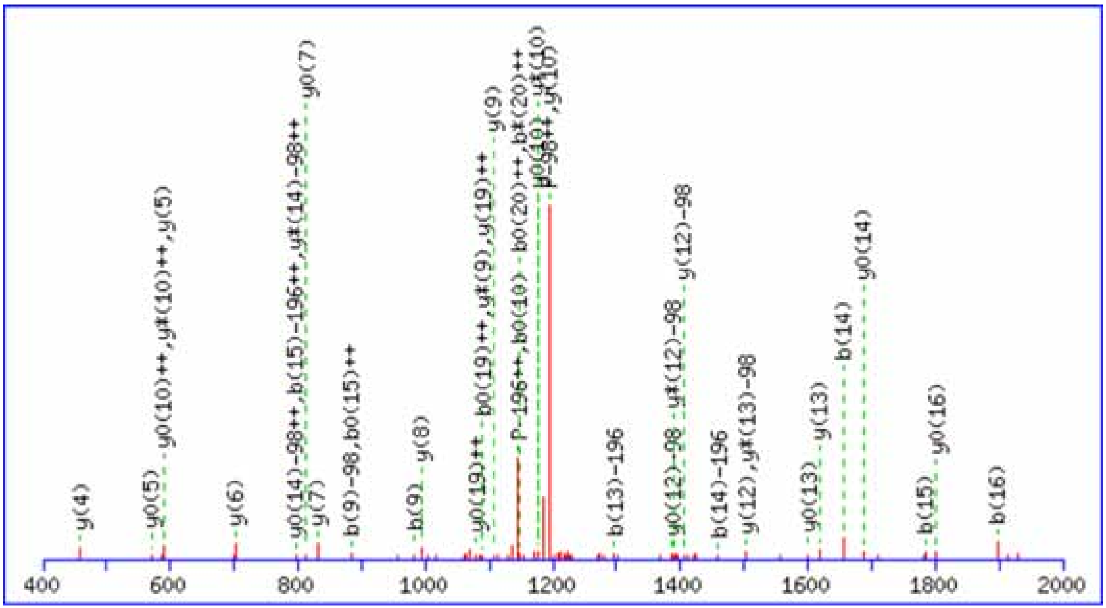
Matched b ions: b(2)-98, b(2), b(3)-98, b(3), b(4), b(5), b(5)-98++, b(5)-98, b(5)++
Matched y ions: y(1), y(2), y(3), y(4), y(5)-98, y(5), y(5)++
Precursor origin neutral loss: +

Peptide No.559

LSLDEGGSDTESLYEIEGLNK
Confirmed sites: @S:2,@T:10
Ambiguous sites:

MS/MS Fragmentation of LSLDEGGSDTESLYEIEGLNK
Found in CAC1S_MOUSE, Voltage-dependent L-type calcium channel subunit alpha-1S OS=Mus musculus GN=Cacna1s PE=1 SV=2

Match to Query 6691: 2484.063194 from(1243.038873,2+)
Title: Elution from: 66.247 to 66.247 scan no 6222 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2484.0597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl (K)
Ions Score: 53 Expect: 0.00028

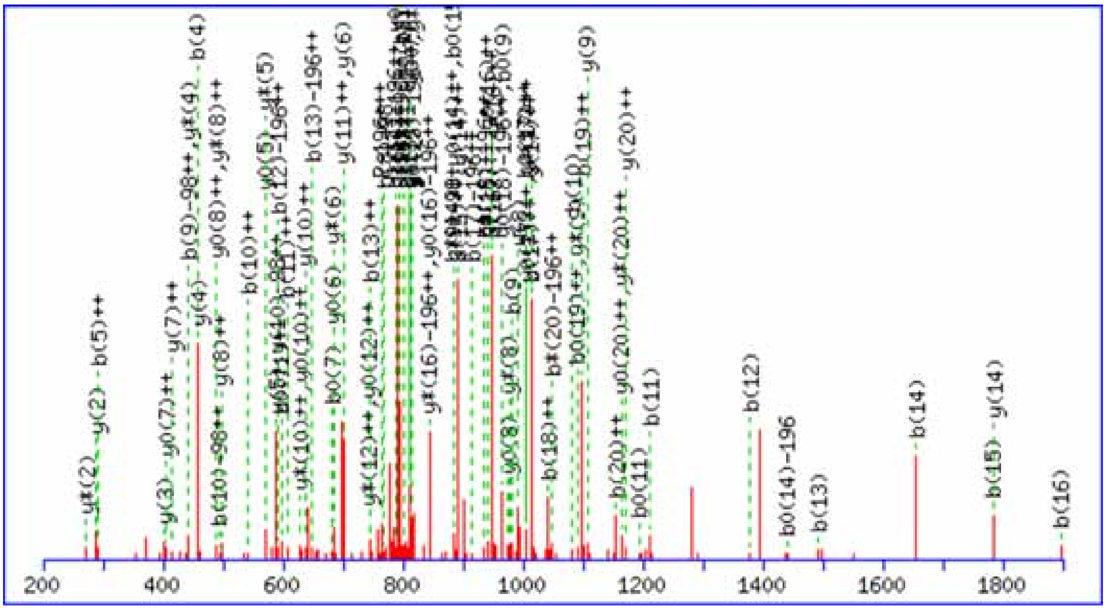
Matched b ions: b(9)-98, b(9), b(11)-98, b(12)-98, b(13)-98, b(13)-196, b(14), b(14)-196, b(14)-98, b(15), b(15)-98, b(15)-196++, b(16), b(16)-98, b(17)-98, b(18)-98++, b(20)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12), y(12)-98, y(13), y(19)++
Precursor origin neutral loss: +

Peptide No.560

LSLDEGGSDTESLYEIEGLNK
Confirmed sites: @S:8,@S:12
Ambiguous sites:

MS/MS Fragmentation of LSLDEGGSDTESLYEIEGLNK
Found in CAC1S_MOUSE, Voltage-dependent L-type calcium channel subunit alpha-1S OS=Mus musculus GN=Cacna1s PE=1 SV=2

Match to Query 6309: 2484.061959 from(829.027929,3+)
Title: Elution from: 66.062 to 66.062 scan no 6151 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2484.0597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl (K)
Ions Score: 50 **Expect:** 0.00061

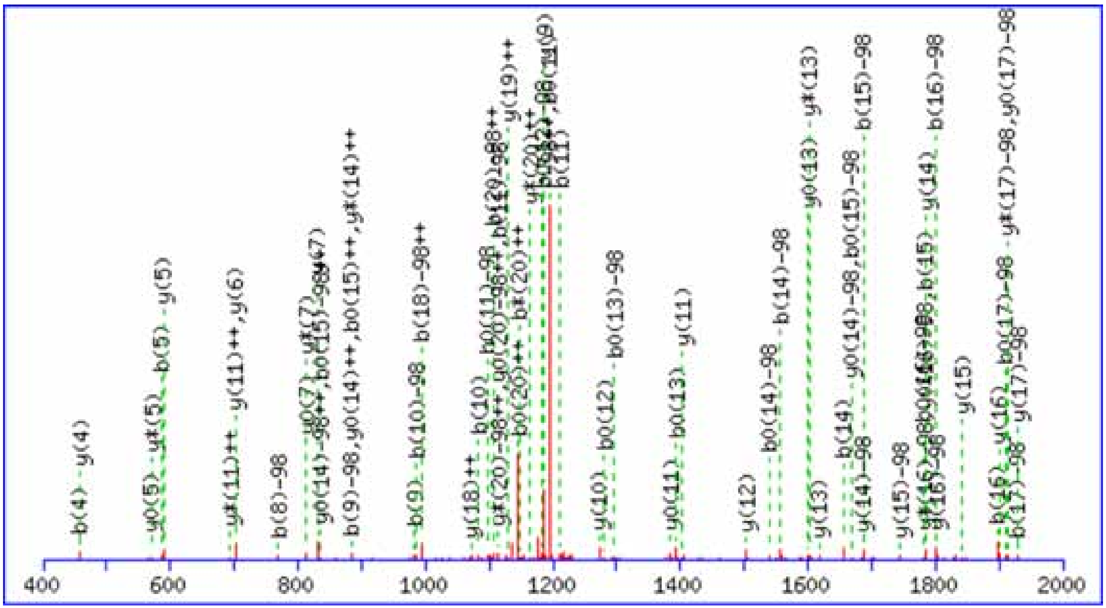
Matched b ions: b(4), b(5)++, b(8)-98, b(9)-98, b(9)-98++, b(9), b(10)-98++, b(10)++, b(10), b(11), b(11)++, b(12)-98, b(12)-98++, b(12), b(12)-196++, b(13)-98++, b(13)-98, b(13), b(13)-196++, b(13)++, b(14), b(14)-98++, b(15), b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16), b(16)-98++, b(17)++, b(17)-98++, b(17)-196++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(8)++, y(8), y(9), y(10)-98++, y(10)++, y(11)++, y(13)++, y(14)++, y(14), y(14)-98++, y(14)-196++, y(16)++, y(17)++, y(20)++
Precursor origin neutral loss: +

Peptide No.561

LSLDEGGSDTESLYEIEGLNK
Confirmed sites: @S:8,@Y:14
Ambiguous sites:

MS/MS Fragmentation of LSLDEGGSDTESLYEIEGLNK
Found in CAC1S_MOUSE, Voltage-dependent L-type calcium channel subunit alpha-1S OS=Mus musculus GN=Cacna1s PE=1 SV=2

Match to Query 5968: 2484.061820 from(1243.038186,2+)
Title: Elution from: 65.942 to 65.942 scan no 6074 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2484.0597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y14 : Phospho (Y)
K21 : Dimethyl (K)
Ions Score: 57 Expect: 0.00014

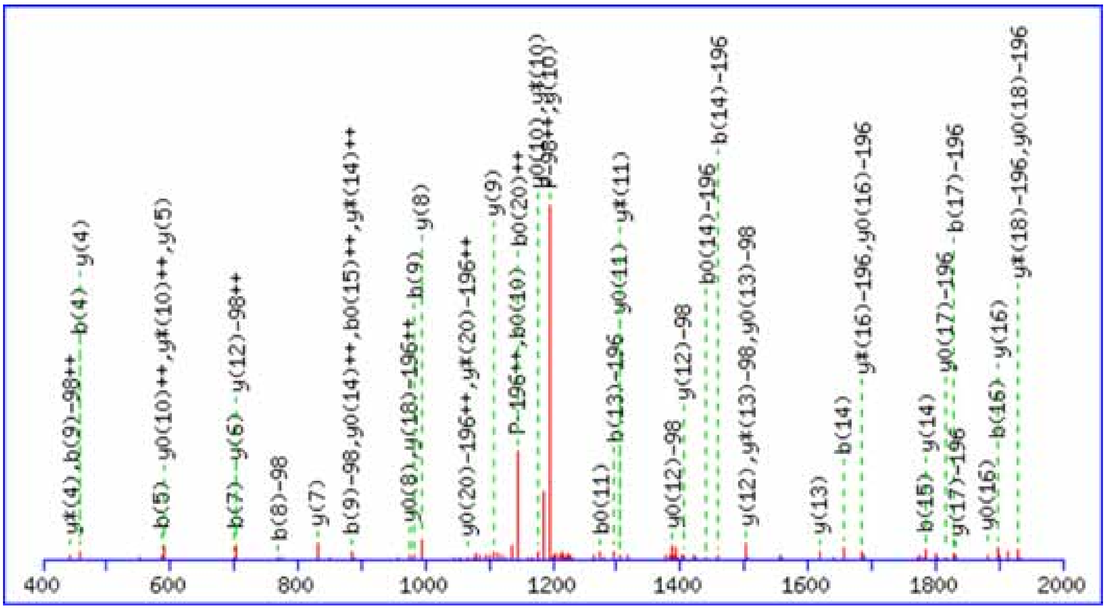
Matched b ions: b(4), b(5), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(14), b(14)-98, b(15)-98, b(15), b(16)-98, b(16), b(17)-98, b(18)-98++, b(20)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10), y(11)++, y(11), y(12), y(13), y(14)-98, y(14), y(15)-98, y(15), y(16)-98, y(16), y(17)-98, y(18)++, y(19)++
Precursor origin neutral loss: +

Peptide No.562

LSLDEGGSDTESLYEIEGLNK
Confirmed sites: @S:8,@T:10
Ambiguous sites:

MS/MS Fragmentation of LSLDEGGSDTESLYEIEGLNK
Found in CAC1S_MOUSE, Voltage-dependent L-type calcium channel subunit alpha-1S OS=Mus musculus GN=Cacna1s PE=1 SV=2

Match to Query 7994: 2484.061490 from(1243.038021,2+)
Title: Elution from: 65.977 to 65.977 scan no 6543 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2484.0597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl (K)
Ions Score: 68 **Expect:** 9.5e-006

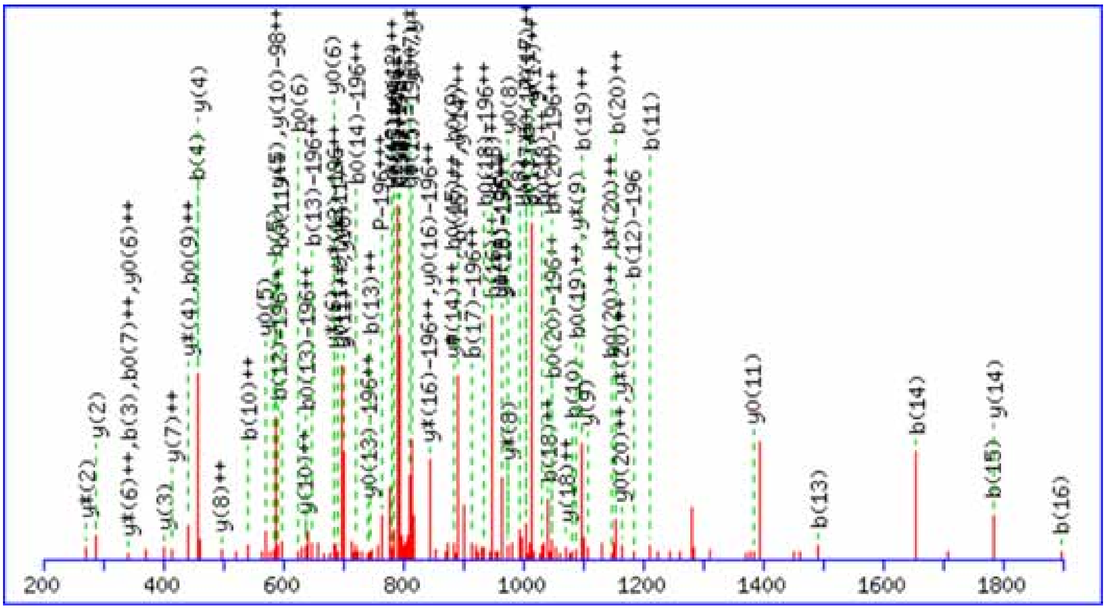
Matched b ions: b(4), b(5), b(7), b(8)-98, b(9)-98, b(9), b(9)-98++, b(10)-98, b(11)-98, b(12)-98, b(13)-196, b(13)-98, b(14), b(14)-98, b(14)-196, b(15), b(15)-98, b(16), b(16)-98, b(17)-98, b(17)-196, b(18)-98++, b(20)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12), y(12)-98++, y(12)-98, y(13), y(14)-98, y(14), y(16), y(16)-98, y(17)-196, y(17)-98, y(18)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.563

LSLDEGGSDTESLYEIEGLNK
Confirmed sites: @T:10,@S:12
Ambiguous sites:

MS/MS Fragmentation of LSLDEGGSDTESLYEIEGLNK
Found in CAC1S_MOUSE, Voltage-dependent L-type calcium channel subunit alpha-1S OS=Mus musculus GN=Cacna1s PE=1 SV=2

Match to Query 6480: 2484.061005 from(829.027611,3+)
Title: Elution from: 65.950 to 65.950 scan no 6209 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2484.0597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl (K)
Ions Score: 40 Expect: 0.0057

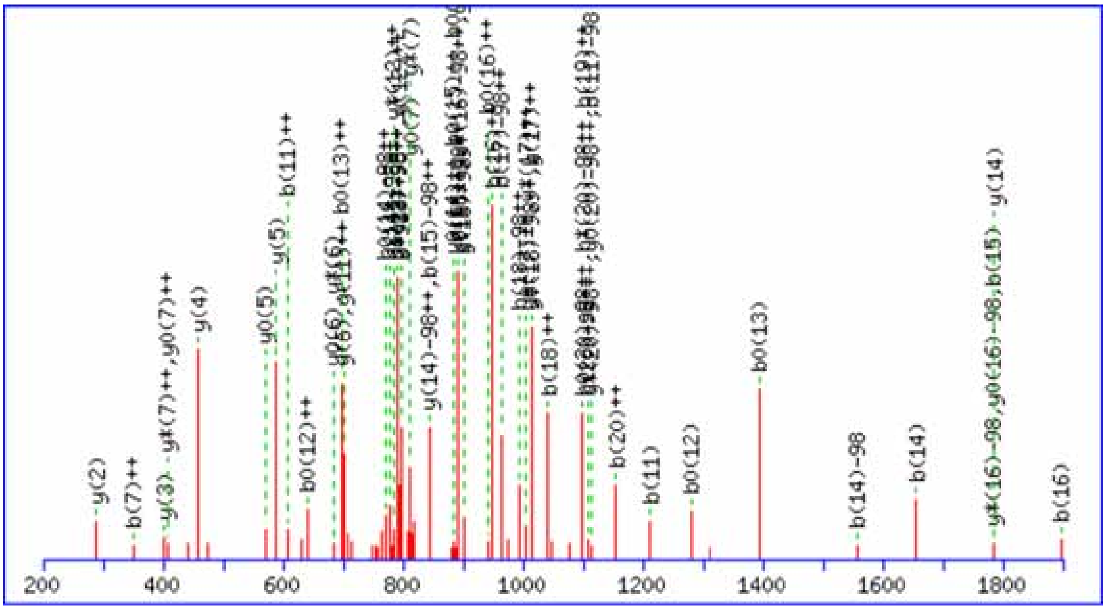
Matched b ions: b(3), b(4), b(5), b(10)++, b(10), b(11), b(12)-98, b(12)-98++, b(12)-196++, b(12)-196, b(13)-98++, b(13)-98, b(13), b(13)-196++, b(13)++, b(14), b(14)-98++, b(15), b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16), b(16)-98++, b(17)++, b(17)-98++, b(17)-196++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(8)++, y(8), y(9), y(10)-98++, y(10)++, y(11)++, y(12)++, y(13)-98++, y(14)++, y(14), y(14)-98++, y(15)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.564

LSLDEGGSDTESLYEIEGLNK
Confirmed sites: @T:10
Ambiguous sites: @S:12orY:14

MS/MS Fragmentation of LSLDEGGSDTESLYEIEGLNK
Found in CAC1S_MOUSE, Voltage-dependent L-type calcium channel subunit alpha-1S OS=Mus musculus GN=Cacna1s PE=1 SV=2

Match to Query 7495: 2484.063363 from(829.028397,3+)
Title: Elution from: 66.036 to 66.036 scan no 6430 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2484.0597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y14 : Phospho (Y)
K21 : Dimethyl (K)
Ions Score: 58 **Expect:** 8.9e-005

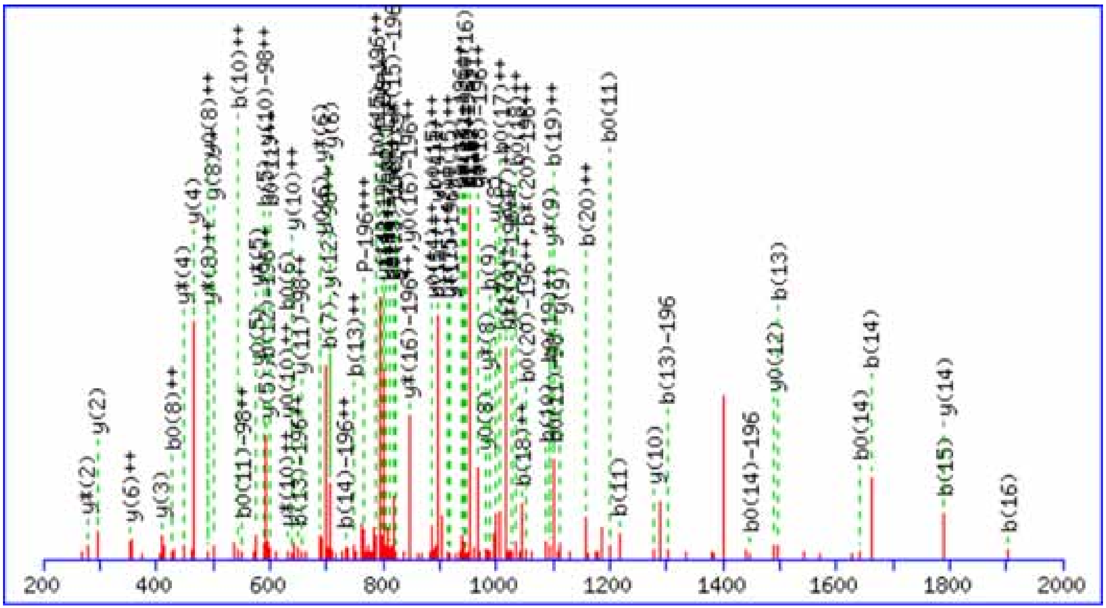
Matched b ions: b(7)++, b(11)++, b(11), b(11)-98, b(14)-98, b(14), b(14)-98++, b(15), b(15)++, b(15)-98++, b(16)++, b(16), b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(11)++, y(12)++, y(14)++, y(14), y(14)-98++, y(16)-98++, y(17)++
Precursor origin neutral loss:

Peptide No.565

LSLDEGGSDTESLYEIEGLNK
Confirmed sites: @S:8,@S:12
Ambiguous sites:

MS/MS Fragmentation of LSLDEGGSDTESLYEIEGLNK
Found in CAC1S_MOUSE, Voltage-dependent L-type calcium channel subunit alpha-1S OS=Mus musculus GN=Cacna1s PE=1 SV=2

Match to Query 6515: 2496.125715 from(833.049181,3+)
Title: Elution from: 65.974 to 65.974 scan no 6212 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2496.1234
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 36 **Expect:** 0.017

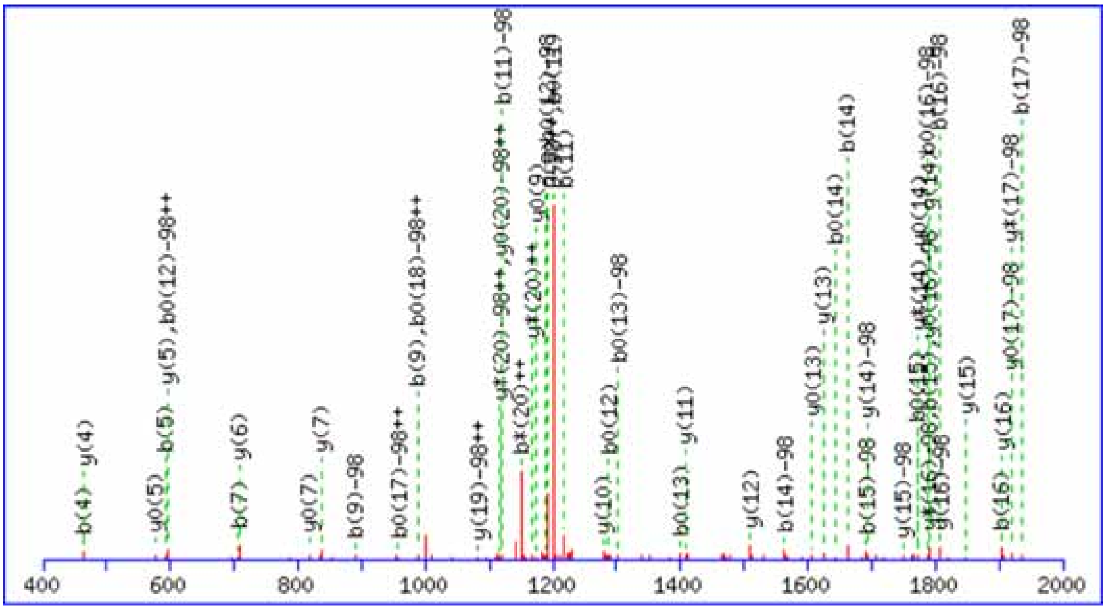
Matched b ions: b(5), b(7), b(9), b(10)++, b(10), b(11), b(12)-196++, b(12)-98, b(12)-98++, b(13)-98++, b(13)-98, b(13), b(13)-196, b(13)-196++, b(13)++, b(14), b(14)-98++, b(14)-196++, b(15), b(15)++, b(15)-98++, b(16)++, b(16), b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(18)-196++, b(19)++, b(19)-98++, b(20)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(8)++, y(8), y(9), y(10)-98++, y(10), y(10)++, y(11)-98++, y(12)-98++, y(13)++, y(14)++, y(14), y(14)-98++, y(14)-196++, y(16)++, y(17)++, y(17)-196++, y(17)-98++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.566

LSLDEGGSDTESLYEIEGLNK
Confirmed sites: @S:8,@Y:14
Ambiguous sites:

MS/MS Fragmentation of **LSLDEGGSDTESLYEIEGLNK**
Found in **CAC1S_MOUSE**, Voltage-dependent L-type calcium channel subunit alpha-1S OS=Mus musculus GN=Cacna1s PE=1 SV=2

Match to Query 6010: 2496.127264 from(1249.070908,2+)
Title: Elution from: 66.144 to 66.144 scan no 6088 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2496.1234
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y14 : Phospho (Y)
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 62 Expect: 4.6e-005

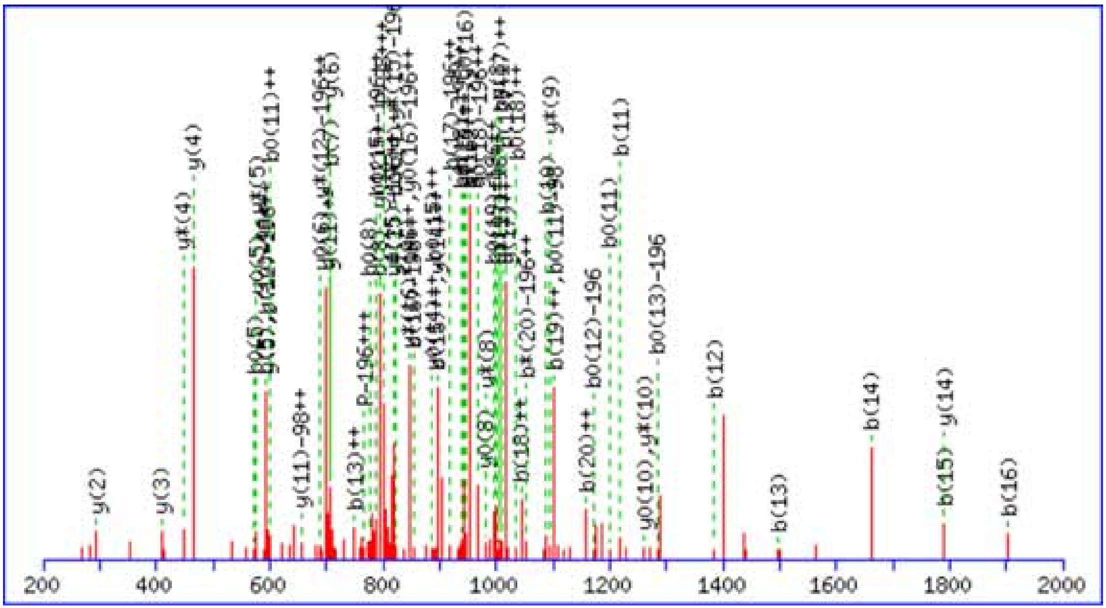
Matched b ions: b(4), b(5), b(7), b(9)-98, b(9), b(11), b(11)-98, b(14), b(14)-98, b(15)-98, b(15), b(16), b(16)-98, b(17)-98
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(14)-98, y(14), y(15)-98, y(15), y(16), y(16)-98, y(19)-98++
Precursor origin neutral loss: +

Peptide No.567

LSLDEGGSDTESLYEIEGLNK
Confirmed sites: @T:10,@S:12
Ambiguous sites:

MS/MS Fragmentation of LSLDEGGSDTESLYEIEGLNK
Found in CAC1S_MOUSE, Voltage-dependent L-type calcium channel subunit alpha-1S OS=Mus musculus GN=Cacna1s PE=1 SV=2

Match to Query 8039: 2496.124350 from(833.048726,3+)
Title: Elution from: 66.062 to 66.062 scan no 6552 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2496.1234
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 40 Expect: 0.0074

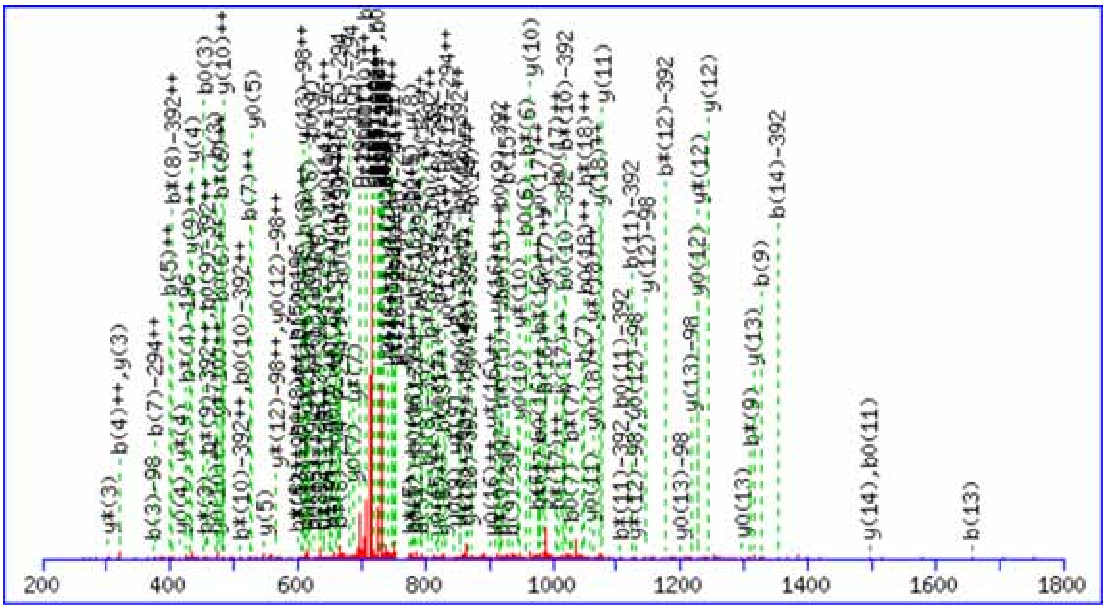
Matched b ions: b(5), b(7), b(8), b(10), b(11), b(12)-196++, b(12)-98, b(12)-98++, b(12), b(13)-98++, b(13)-98, b(13), b(13)++, b(14)-98, b(14), b(14)-98++, b(15), b(15)-98++, b(15)++, b(16)++, b(16), b(16)-98++, b(16)-196++, b(17)++, b(17)-98++, b(17)-196++, b(18)++, b(18)-98++, b(19)++, b(19)-196++, b(19)-98++, b(20)++, b(20)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(13)-98++, y(14)-98++, y(14)++, y(14), y(15)-98++, y(16)++, y(17)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.568

LSRSRTASLTSAASIDGSR
Confirmed sites: @S:2,@S:4,@T:6,@S:8
Ambiguous sites:

MS/MS Fragmentation of LSRSRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6339: 2288.943735 from(763.988521,3+)
Title: Elution from: 41.262 to 41.262 scan no 3674 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2288.9417
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 **Expect:** 0.00049

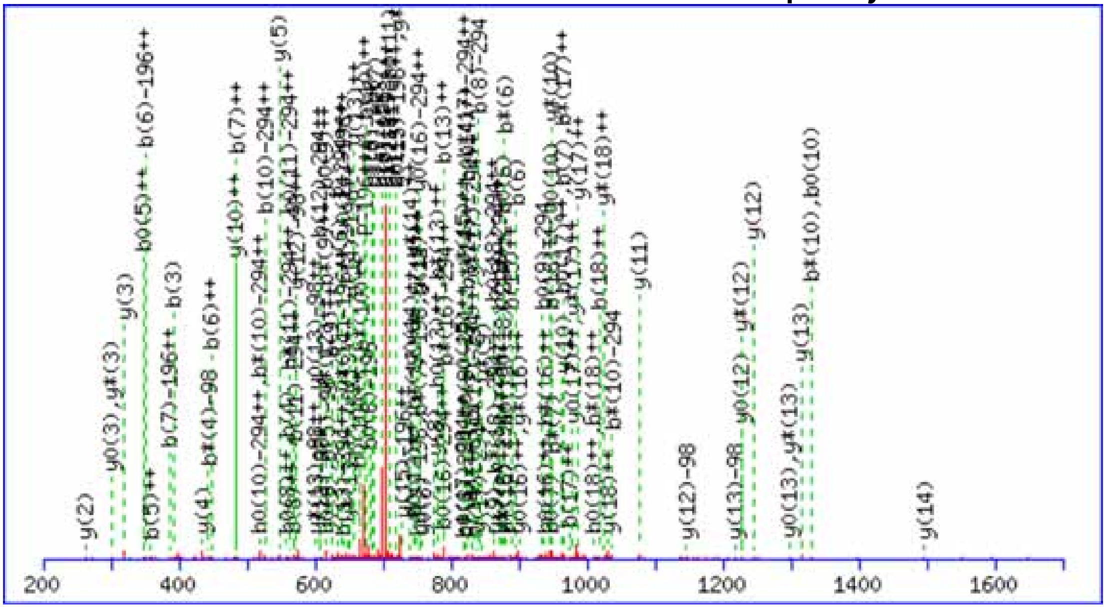
Matched b ions: b(3), b(3)-98, b(4)++, b(5)++, b(5), b(5)-196, b(5)-98, b(6)-196, b(6)-98++, b(6)-196++, b(6)-294, b(6)-98, b(6), b(7)-98++, b(7)-196++, b(7)-98, b(7)-294++, b(7)++, b(7)-294, b(7), b(8)-98++, b(8)-294, b(8)-196++, b(8)++, b(8)-392, b(8)-196, b(9)-98++, b(9)-196++, b(9)++, b(9)-392, b(9)-294, b(9)-98, b(9), b(10)++, b(10)-196++, b(10)-294++, b(10)-98++, b(11)-294++, b(11)-196++, b(11)-98++, b(11)-392, b(12)++, b(12)-294++, b(12)-196++, b(12)-98++, b(13), b(13)-196++, b(13)++, b(13)-98++, b(13)-392++, b(13)-294++, b(14)-294++, b(14)++, b(14)-392, b(14)-196++, b(14)-98++, b(15)-392++, b(15)-294++, b(15)-196++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(16)-392++, b(16)-294++, b(16)-196++, b(17)-196++, b(17)-98++, b(17)++, b(18)-392++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(12)-98, y(12), y(13), y(13)-98++, y(13)++, y(13)-98, y(14), y(14)-196++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(15)-196++, y(16)-98++, y(16)-196++, y(16)++, y(17)++, y(17)-196++, y(17)-98++, y(18)++, y(18)-98++, y(18)-294++, y(18)-196++
Precursor origin neutral loss: +

Peptide No.569

LSRSRTASLTSAASIDGSR
Confirmed sites: @S:4,@T:6,@S:8
Ambiguous sites:

MS/MS Fragmentation of LSRSRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 5774: 2208.976476 from(737.332768,3+)
Title: Elution from: 37.281 to 37.281 scan no 3106 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2208.9754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 0.00013

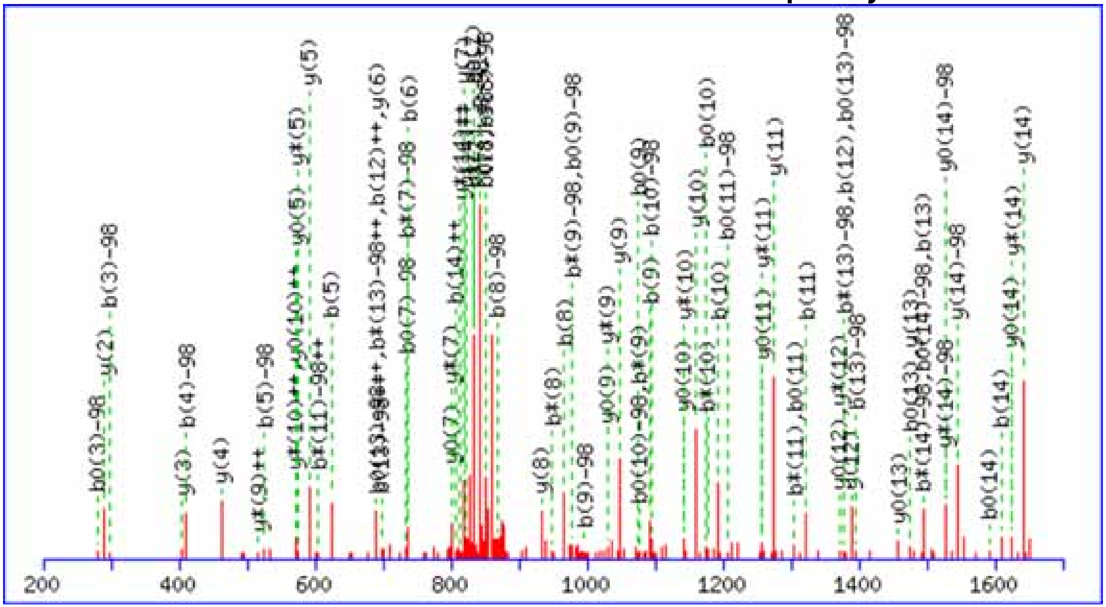
Matched b ions: b(3), b(4), b(5)-98, b(5)++, b(6)-196++, b(6)-196, b(6)-98++, b(6)++, b(6), b(6)-98, b(7)-98++, b(7)++, b(7), b(7)-196++, b(7)-98, b(8)-98++, b(8)-196++, b(8)++, b(8)-294, b(8)-196, b(9)-98++, b(9)-196++, b(9)++, b(10)-98, b(10)-98++, b(10)-294++, b(10)-196++, b(10)++, b(11)-294++, b(11)-98++, b(11)++, b(12)-98++, b(12)-294++, b(12)-196++, b(12)++, b(13)++, b(13)-294++, b(13)-196++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)-196++, b(15)++, b(16)-98++, b(16)++, b(16)-196++, b(17)-196++, b(17)-98++, b(17)++, b(18)-294++, b(18)-98++, b(18)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(12), y(12)-98, y(12)-98++, y(13), y(13)-98, y(13)++, y(13)-98++, y(14)-98, y(14), y(14)-98++, y(14)-196++, y(14)++, y(15)-196++, y(15)-98++, y(16)-196++, y(16)-98++, y(17)++, y(17)-98++, y(17)-294++, y(17)-196++, y(18)-98++, y(18)++, y(18)-196++
Precursor origin neutral loss: +

Peptide No.570

LSSIDLNDQVEGDDR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of LSSIDLNDQVEGDDR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 3259: 1782.768284 from(892.391418,2+)
Title: Elution from: 45.399 to 45.399 scan no 4149 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1782.7673
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 96 Expect: 9.9e-009

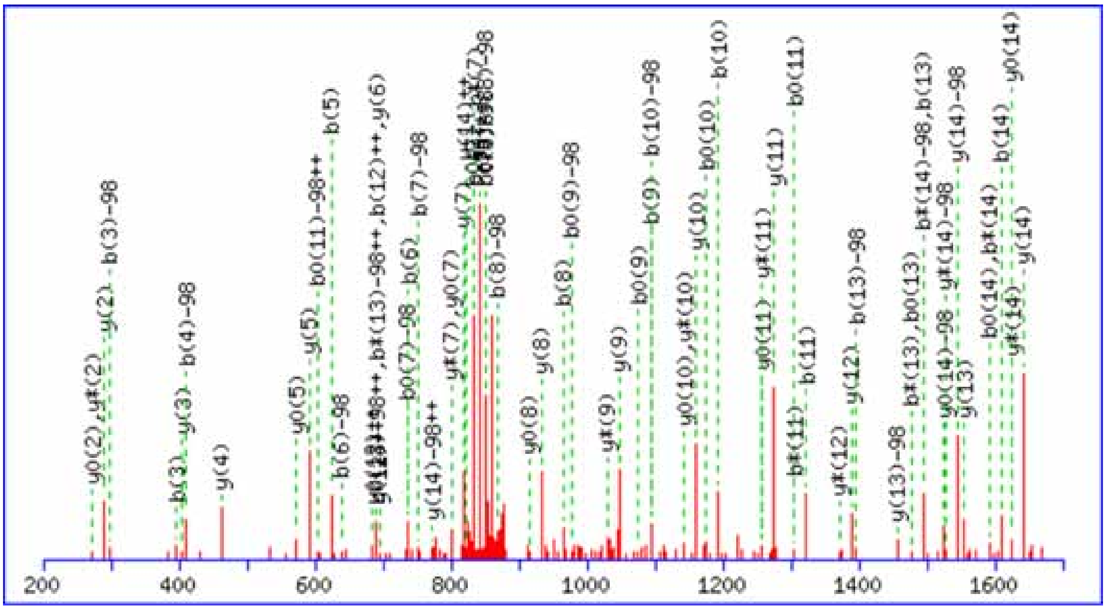
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(5), b(6), b(7), b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11), b(12)++, b(12), b(13), b(13)-98, b(13)-98++, b(14), b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)-98, y(14), y(14)++
Precursor origin neutral loss: +

Peptide No.571

LSSIDLNDQVEGDDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LSSIDLNDQVEGDDR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 3262: 1782.769466 from(892.392009,2+)
Title: Elution from: 45.346 to 45.346 scan no 4051 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1782.7673
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 93 Expect: 1.7e-008

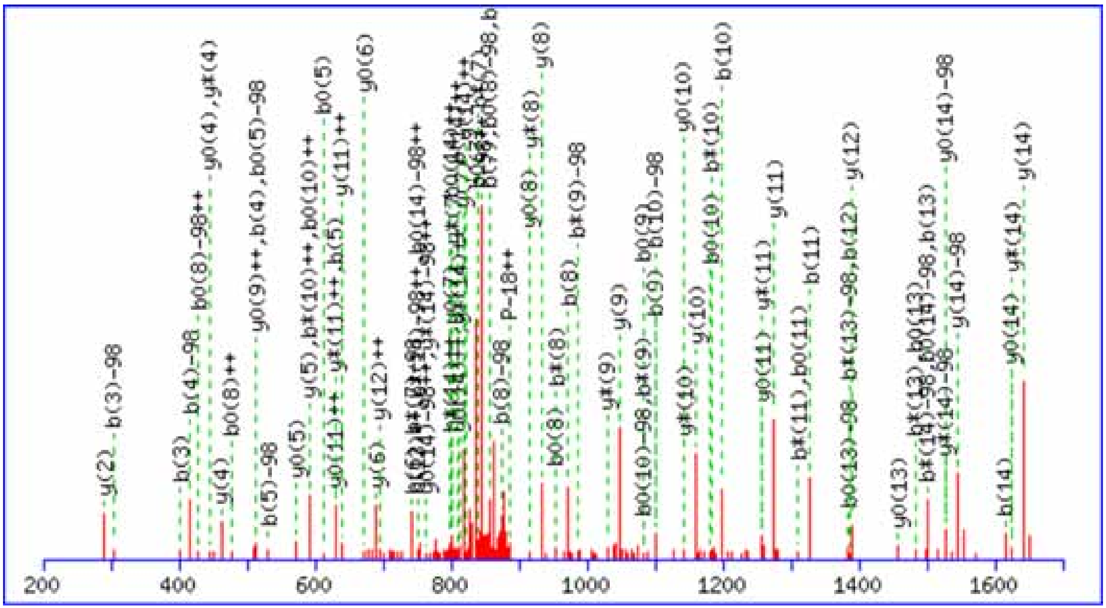
Matched b ions: b(3)-98, b(3), b(4)-98, b(5), b(6), b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9), b(10), b(10)-98, b(11), b(12)++, b(13), b(13)-98, b(14)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(13)-98, y(13), y(14)-98, y(14), y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.572

LSSIDLNQDQVEGDDR
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of LSSIDLNDQVEGDDR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 3540: 1788.802004 from(895.408278,2+)
Title: Elution from: 45.352 to 45.352 scan no 4168 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1788.7991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 84 Expect: 1.5e-007

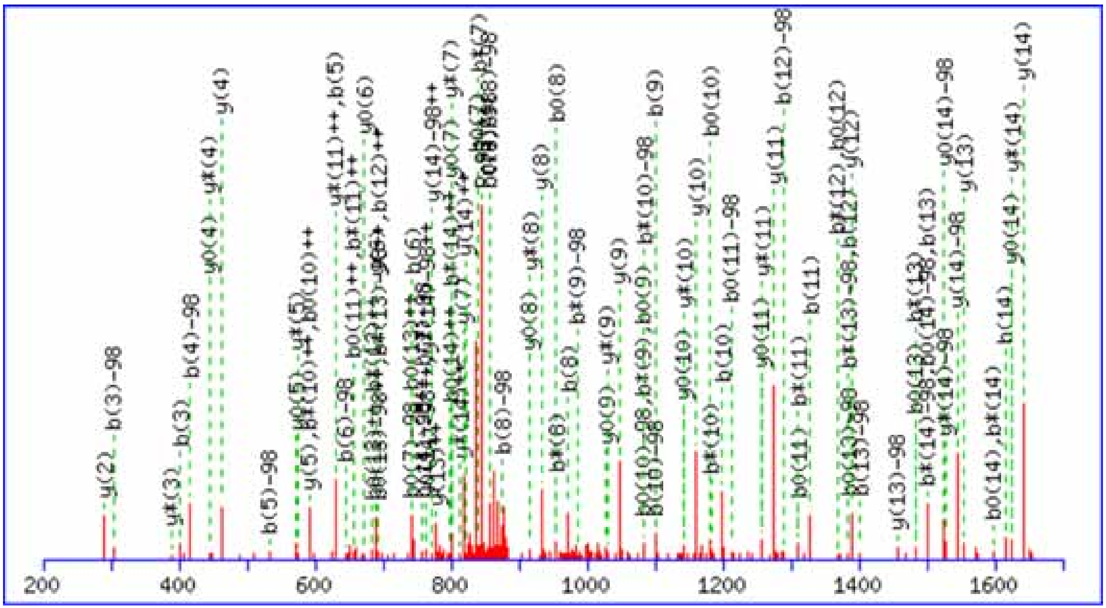
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(7), b(8), b(8)-98, b(9), b(10), b(10)-98, b(11), b(12), b(13), b(13)++, b(14), b(14)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(14)-98, y(14), y(14)++
Precursor origin neutral loss: +

Peptide No.573

LSSIDLNDQVEGDDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of LSSIDLNDQVEGDDR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 4873: 1788.800926 from(895.407739,2+)
Title: Elution from: 45.298 to 45.298 scan no 4345 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1788.7991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 100 Expect: 4.6e-009

Matched b ions: b(3)-98, b(3), b(4)-98, b(5), b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9), b(10), b(10)-98, b(11), b(12)-98, b(12)++, b(12), b(13), b(13)-98, b(14), b(14)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)-98, y(13), y(13)++, y(14)-98, y(14), y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.574

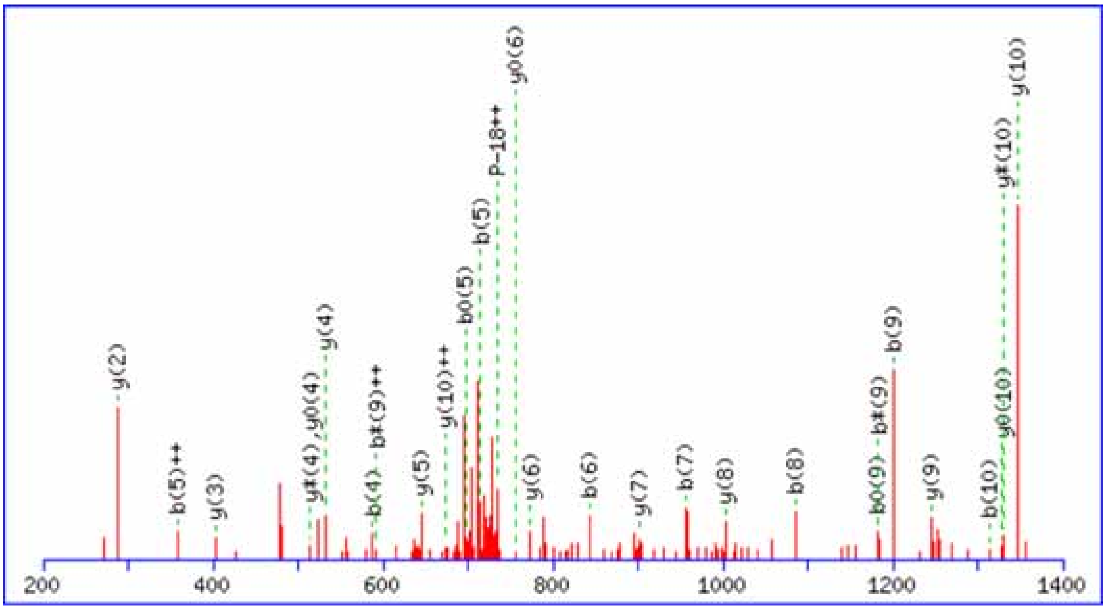
LTYTQQLEDLK

Confirmed sites: @Y:3

Ambiguous sites:

MS/MS Fragmentation of LTYTQQLEDLK
Found in MYH7_MOUSE, Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1

Match to Query 2348: 1486.733210 from(744.373881,2+)
Title: Elution from: 44.754 to 44.754 scan no 4275 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1486.7320
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y3 : Phospho (Y)
K11 : Dimethyl (K)
Ions Score: 43 Expect: 0.0022

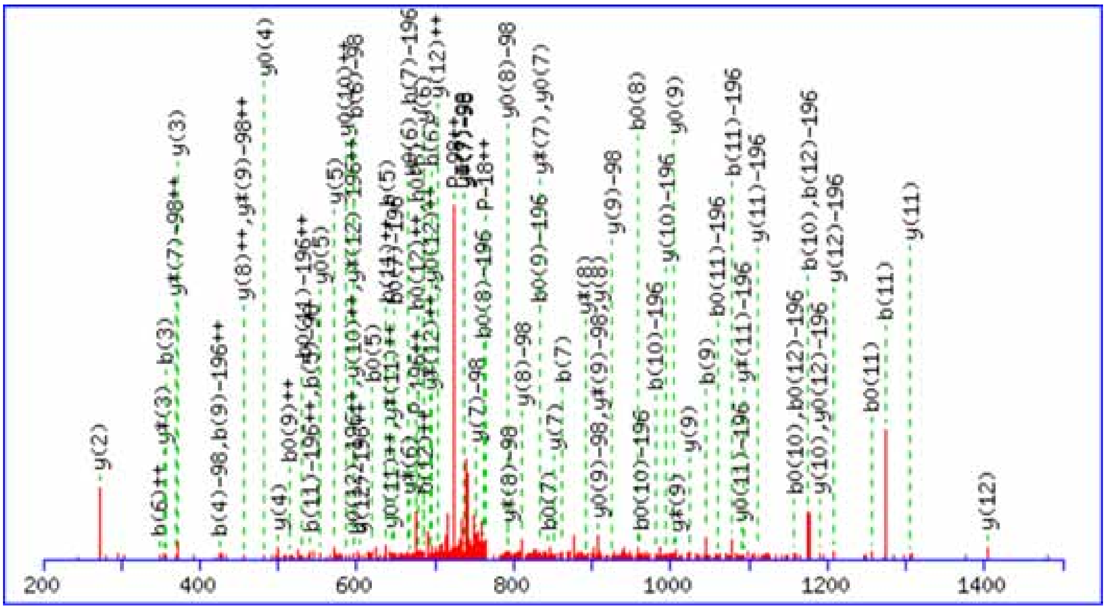
Matched b ions: b(4), b(5)++, b(5), b(6), b(7), b(8), b(9), b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.575

LVDSDGSLAEVPK
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of LVDSDGSLAEVPK
Found in STEA3_MOUSE, Metalloreductase STEAP3 OS=Mus musculus GN=Steap3 PE=1 SV=1

Match to Query 2171: 1544.678566 from(773.346559,2+)
Title: Elution from: 44.513 to 44.513 scan no 4041 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1544.6776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 30 **Expect:** 0.029

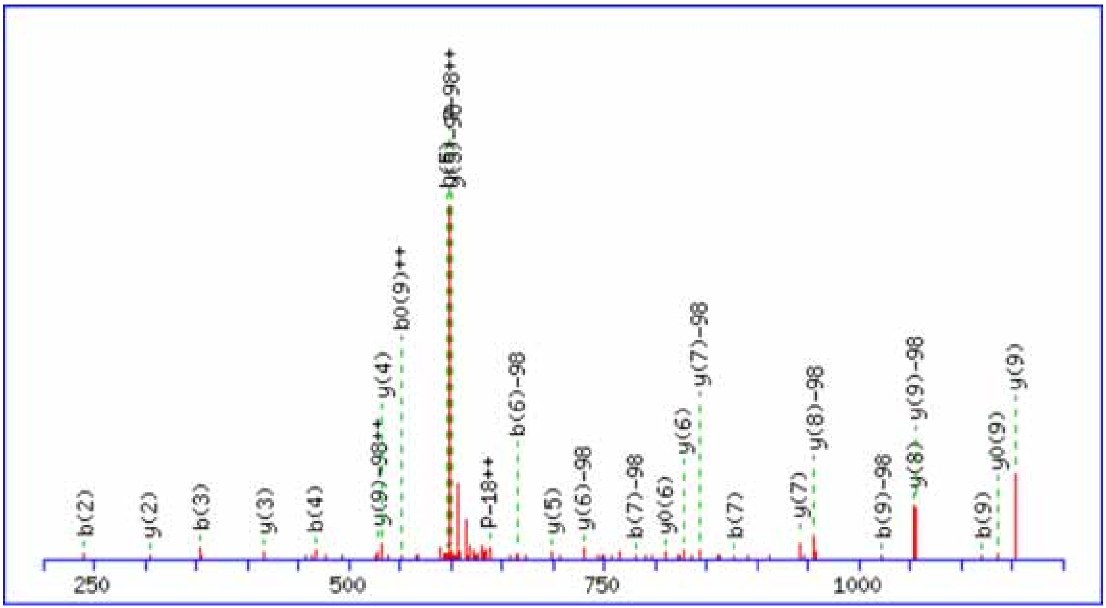
Matched b ions: b(3), b(4)-98, b(5), b(5)-98, b(6)++, b(6)-98, b(6), b(7)-98, b(7)-196, b(7), b(8)-98, b(9), b(9)-196++, b(9)-98, b(10), b(10)-98, b(10)-98++, b(10)-196, b(11)++, b(11), b(11)-98, b(11)-196++, b(11)-196, b(12)-196, b(12)-98, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8), y(8)-98, y(8)++, y(9), y(9)-98, y(10), y(10)++, y(10)-196, y(10)-98, y(11)-98, y(11), y(11)-98++, y(11)-196, y(12), y(12)-98, y(12)-196, y(12)-196++, y(12)++
Precursor origin neutral loss: +

Peptide No.576

LVIIESDLER
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LVIIESDLER
Found in TPM1_MOUSE, Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1

Match to Query 1252: 1293.659410 from(647.836981,2+)
Title: Elution from: 50.416 to 50.416 scan no 4589 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1293.6581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 9.4e-005

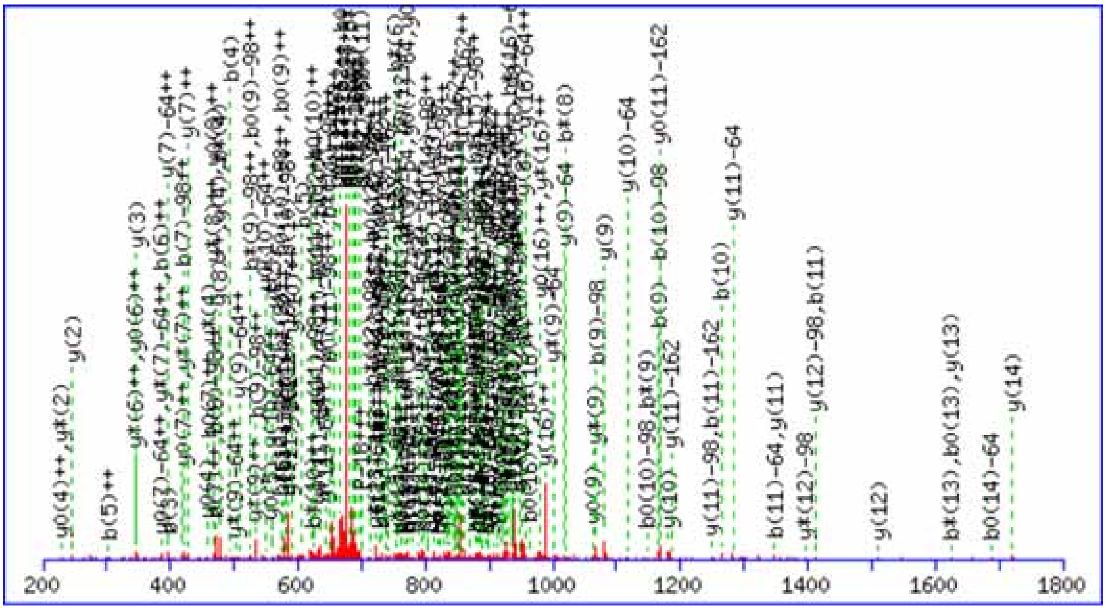
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(7), b(7)-98, b(9)-98, b(9)
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6)-98, y(6), y(7)-98, y(7), y(8)-98, y(8), y(9), y(9)-98, y(9)-98++
Precursor origin neutral loss: +

Peptide No.577

LVRPLYSVEVMETETAR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of LVRPLYSVEVMETETAR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 5293: 2116.028811 from(706.350213,3+)
Title: Elution from: 45.852 to 45.852 scan no 4189 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2116.0275
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 70 Expect: 7.1e-006

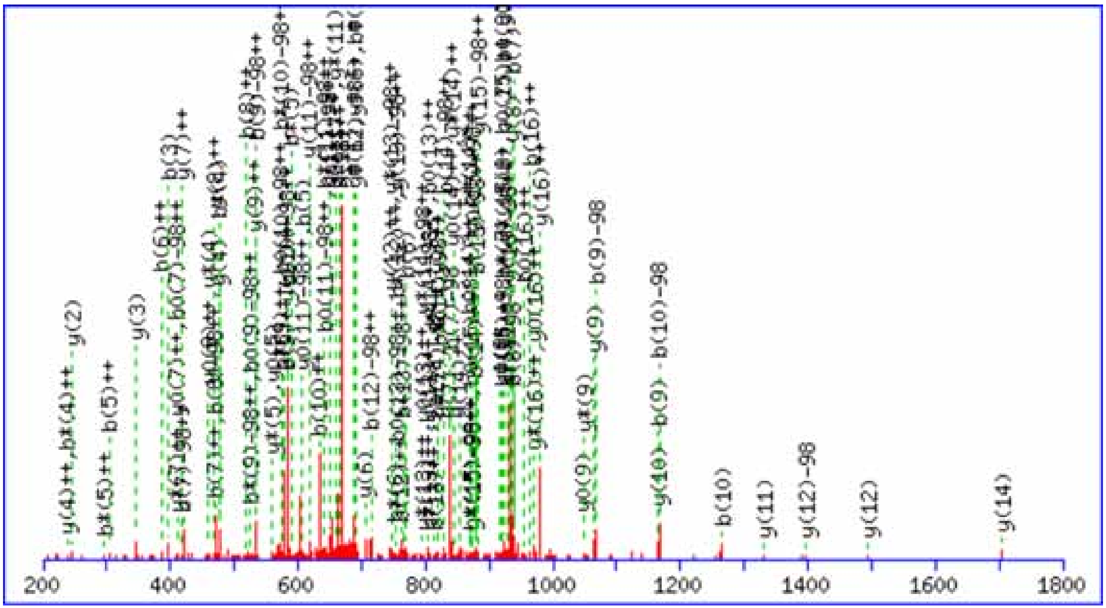
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7)-98++, b(7)-98, b(7), b(8)-98++, b(8)-98, b(9)++, b(9)-98, b(9)-98++, b(9), b(10)-98++, b(10)-98, b(10), b(10)++, b(11), b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(7)++, y(8)++, y(8), y(9), y(10), y(10)++, y(11)++, y(11), y(11)-98, y(11)-98++, y(12), y(12)-98, y(12)++, y(13), y(13)++, y(13)-98++, y(14), y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.578

LVRPLYSVEVMETETAR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of LVRPLYSVEVMETETAR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 6940: 2100.033930 from(701.018586,3+)
Title: Elution from: 51.985 to 51.985 scan no 5196 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2100.0326
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 5.6e-005

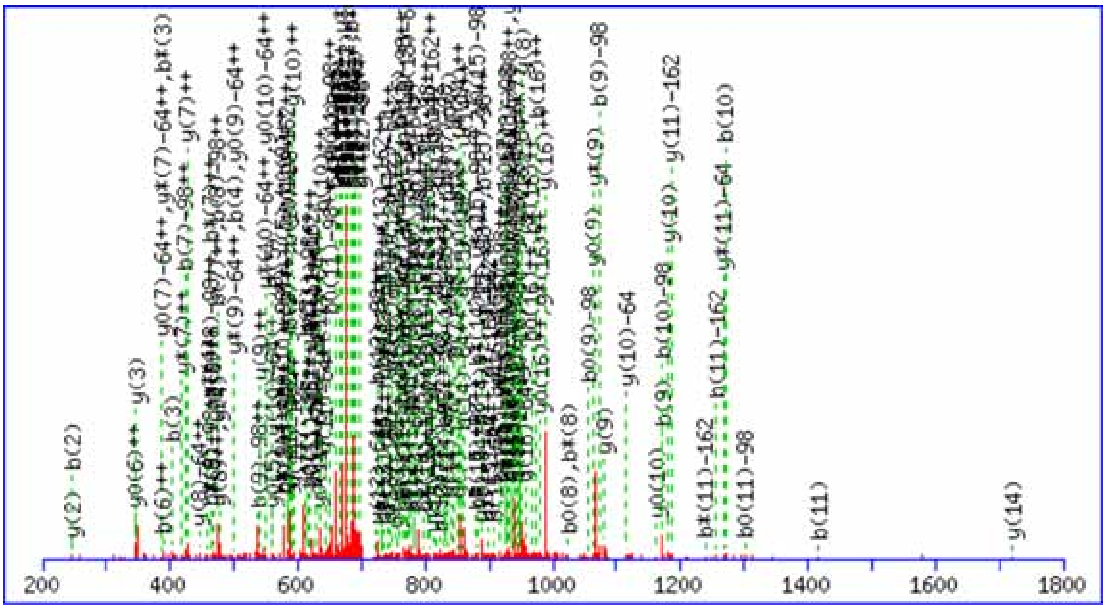
Matched b ions: b(3), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7)-98++, b(7)-98, b(7), b(8)-98++, b(8)-98, b(8)++, b(9)++, b(9)-98, b(9), b(9)-98++, b(10)-98++, b(10)-98, b(10), b(10)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(10), y(11), y(11)-98++, y(11)++, y(12), y(12)-98, y(12)++, y(13)++, y(13)-98++, y(14), y(14)++, y(14)-98++, y(15)-98++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.579

LVRPLYSVEVMETETAR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of LVRPLYSVEVMETETAR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4915: 2122.062894 from(708.361574,3+)
Title: Elution from: 46.215 to 46.215 scan no 4143 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2122.0593
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 39 Expect: 0.0084

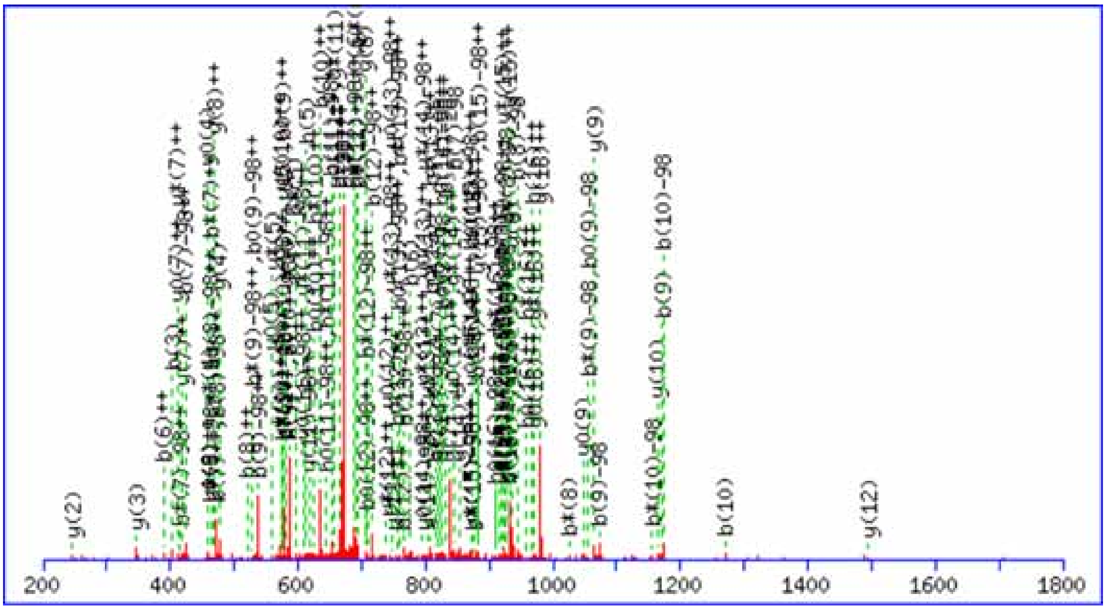
Matched b ions: b(2), b(3), b(4), b(5), b(6)++, b(6), b(7)++, b(7)-98++, b(7)-98, b(7), b(8)-98++, b(8)-98, b(9), b(9)-98++, b(9)++, b(9)-98, b(10), b(10)-98++, b(10)-98, b(10)++, b(11), b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14), y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.580

LVRPLYSVEVMETETAR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of LVRPLYSVEVMETETAR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4881: 2106.066156 from(703.029328,3+)
Title: Elution from: 52.303 to 52.303 scan no 4865 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2106.0644
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0046

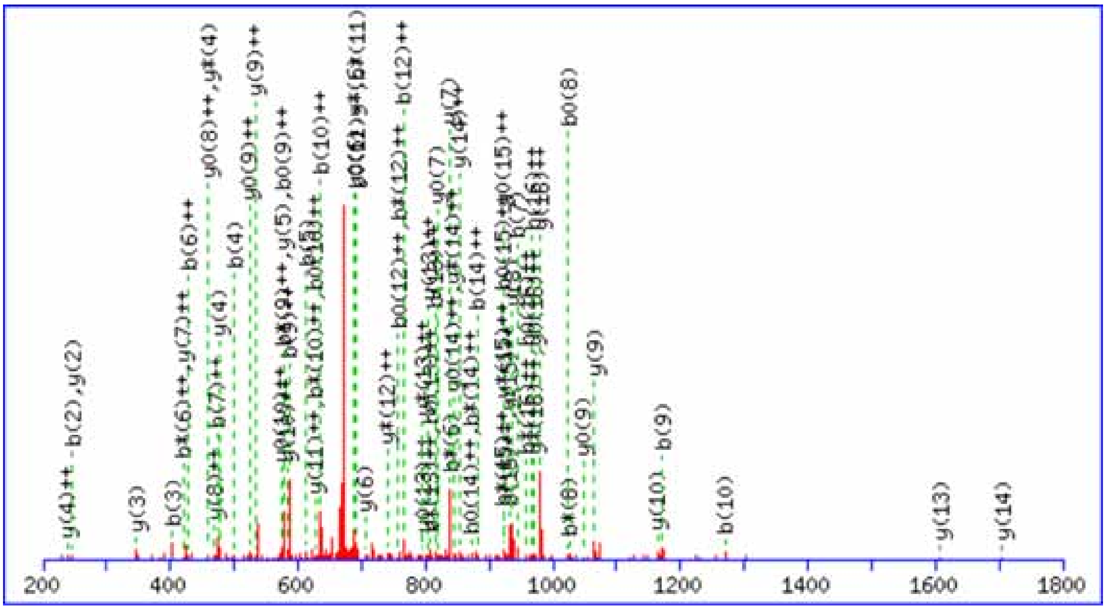
Matched b ions: b(3), b(5), b(6)++, b(6), b(7)-98++, b(7)++, b(7)-98, b(8)-98++, b(8)-98, b(8)++, b(9)-98++, b(9)++, b(9)-98, b(9), b(10)-98++, b(10)-98, b(10), b(10)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(10), y(10)++, y(11)-98++, y(11)++, y(12), y(12)++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.581

LVRPLYSVEVMETETAR
Confirmed sites: @Y:6
Ambiguous sites:

MS/MS Fragmentation of LVRPLYSVEVMETETAR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 5415: 2106.063483 from(703.028437,3+)
Title: Elution from: 52.036 to 52.036 scan no 4965 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2106.0644
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y6 : Phospho (Y)
Ions Score: 59 Expect: 8.6e-005

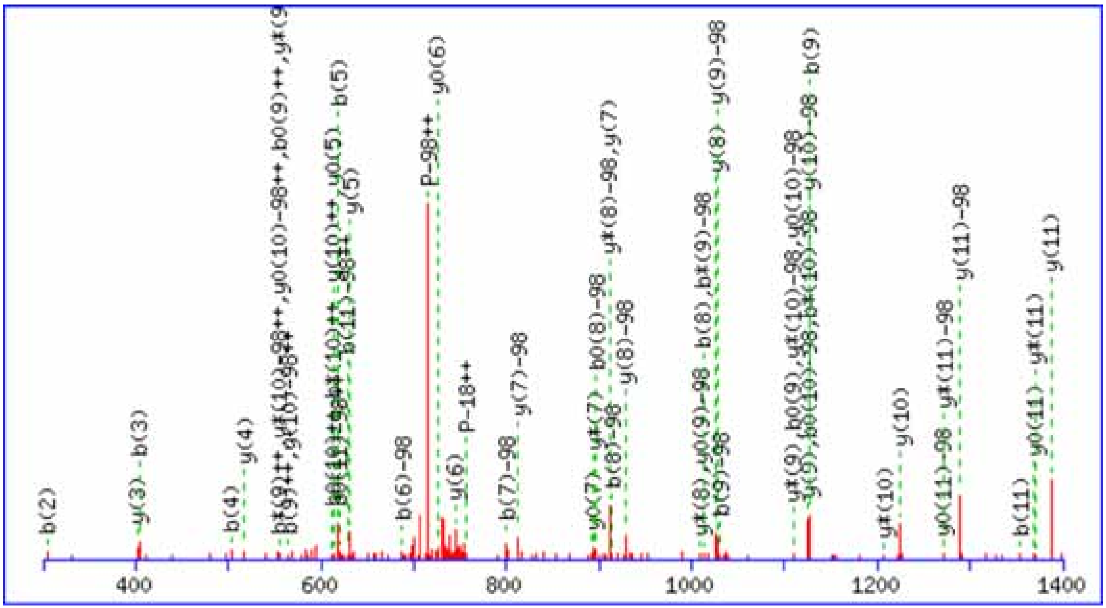
Matched b ions: b(2), b(3), b(4), b(5), b(6)++, b(7)++, b(7), b(9)++, b(9), b(10), b(10)++, b(12)++, b(13)++, b(14)++, b(15)++, b(16)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(13), y(13)++, y(14), y(14)++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.582

LYVVDSINDLNK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LYVVDSINDLNK
Found in CG053_MOUSE, Coiled-coil domain-containing transmembrane protein C7orf53 homolog OS=Mus musculus GN=Gm889 PE=2 SV=1

Match to Query 2704: 1527.759180 from(764.886866,2+)
Title: Elution from: 51.317 to 51.317 scan no 5068 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1527.7585
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl (K)
Ions Score: 48 **Expect:** 0.00073

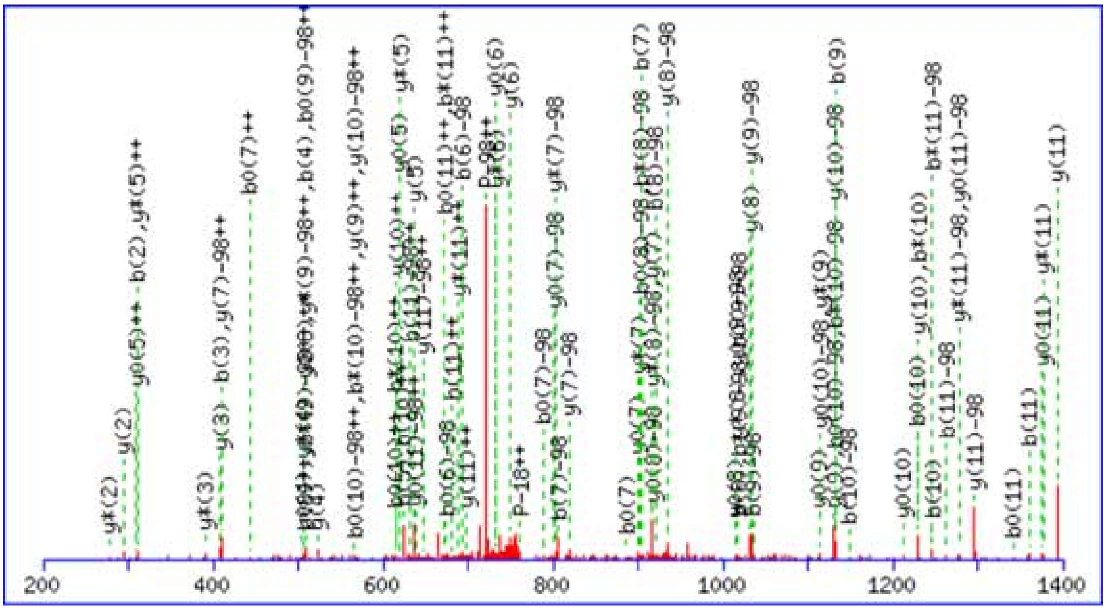
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(9)++, b(11), b(11)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8), y(8)-98, y(9)-98, y(9), y(10)-98, y(10), y(10)-98++, y(10)++, y(11)-98, y(11)
Precursor origin neutral loss: +

Peptide No.583

LYVVDSINDLNK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of LYVVDSINDLNK
Found in CG053_MOUSE, Coiled-coil domain-containing transmembrane protein C7orf53 homolog OS=Mus musculus GN=Gm889 PE=2 SV=1

Match to Query 1851: 1539.822626 from(770.918589,2+)
Title: Elution from: 51.272 to 51.272 scan no 4743 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1539.8222
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 81 Expect: 3.1e-007

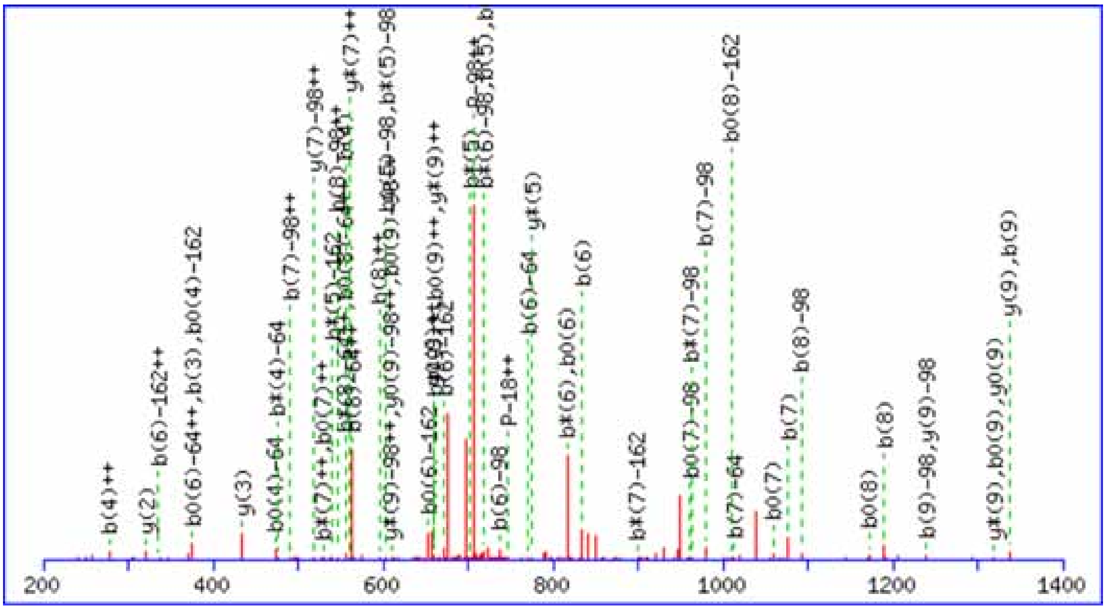
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(7)-98, b(7), b(8)++, b(8)-98, b(8), b(9), b(9)-98, b(10)++, b(10), b(10)-98, b(11), b(11)-98, b(11)-98++, b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98++, y(7), y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(9)++, y(10), y(10)-98, y(10)-98++, y(10)++, y(11)-98, y(11), y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.584

MAKTYDYLFK
Confirmed sites: @T:4,@Y:7
Ambiguous sites:

MS/MS Fragmentation of MAKTYDYLFK
Found in RAB8A_MOUSE, Ras-related protein Rab-8A OS=Mus musculus GN=Rab8a PE=1 SV=2

Match to Query 2551: 1510.618728 from(756.316640,2+)
Title: Elution from: 54.468 to 54.468 scan no 5403 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1510.6220
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y7 : Phospho (Y)
K10 : Dimethyl (K)
Ions Score: 27 Expect: 0.032

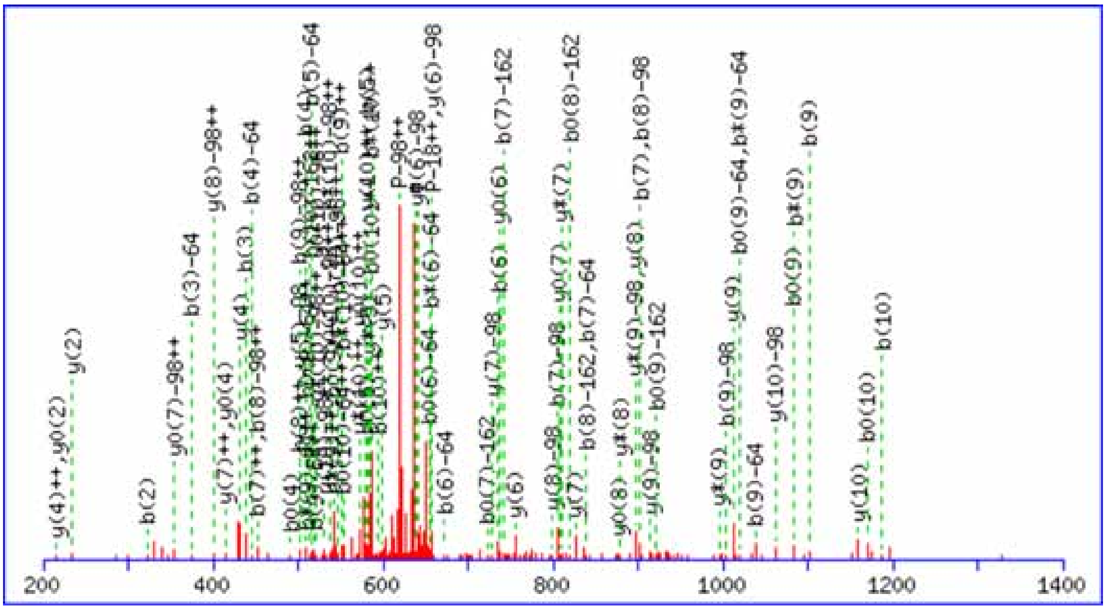
Matched b ions: b(3), b(4)++, b(4), b(5), b(6), b(6)-98, b(7), b(7)-98, b(7)-98++, b(8), b(8)-98, b(8)-98++, b(8)++, b(9), b(9)-98
Matched y ions: y(2), y(3), y(7)-98++, y(9), y(9)-98
Precursor origin neutral loss: +

Peptide No.585

MFDAAKSPTSQ
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of MFDAAKSPTSQ
Found in TNNI1_MOUSE, Troponin I, slow skeletal muscle OS=Mus musculus GN=Tnni1 PE=2 SV=3

Match to Query 1211: 1333.562994 from(667.788773,2+)
Title: Elution from: 26.466 to 26.466 scan no 1645 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1333.5625
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K6 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0043

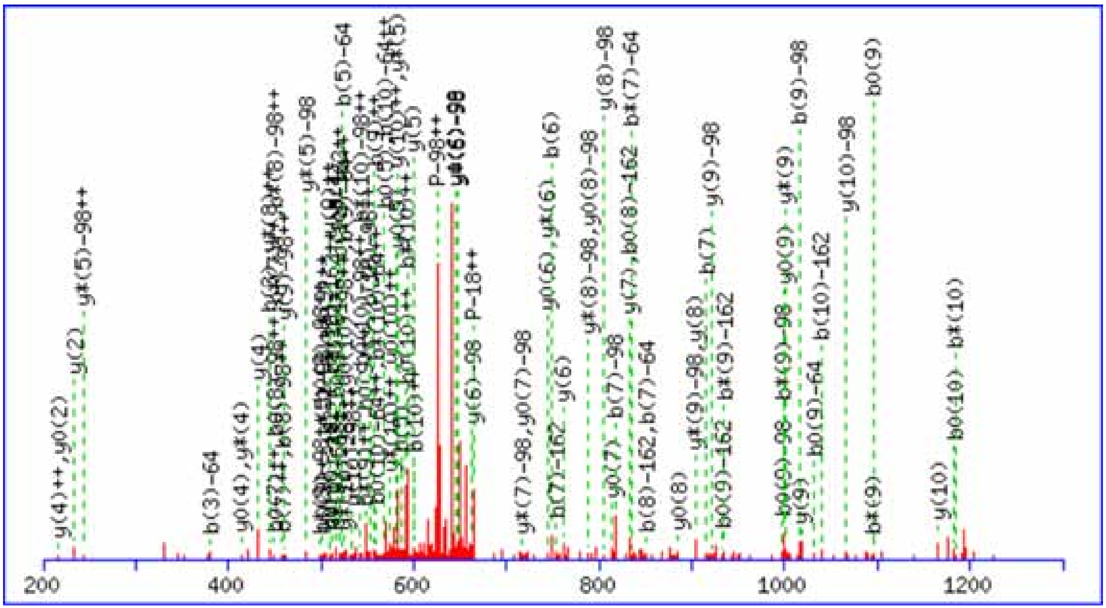
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)-98, b(7), b(7)++, b(8)-98, b(8)-98++, b(8)++, b(9), b(9)-98++, b(9)++, b(9)-98, b(10), b(10)-98++, b(10)++
Matched y ions: y(2), y(4), y(4)++, y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)++, y(7)-98, y(8), y(8)-98++, y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(10)++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.586

MFDAAKSPTSQ
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of MFDAAKSPTSQ
Found in TNNI1_MOUSE, Troponin I, slow skeletal muscle OS=Mus musculus GN=Tnni1 PE=2 SV=3

Match to Query 1139: 1345.626952 from(673.820752,2+)
Title: Elution from: 26.299 to 26.299 scan no 1573 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1345.6261
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K6 : Dimethyl:2H(4)13C(2) (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0058

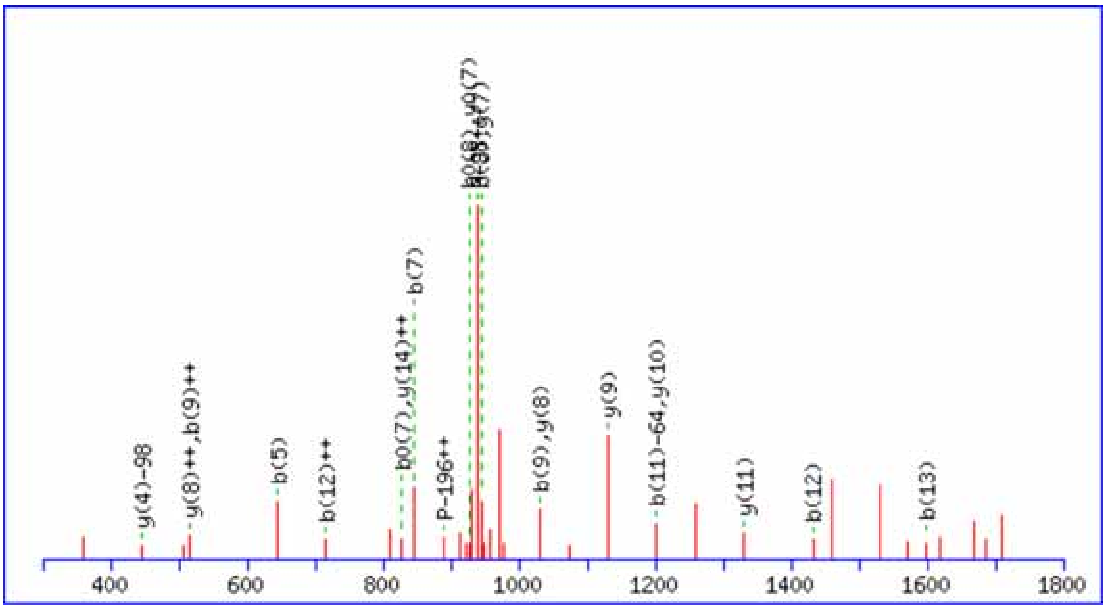
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(7)++, b(7), b(8)-98++, b(9)-98, b(9)++, b(10)-98++, b(10)++
Matched y ions: y(2), y(4), y(4)++, y(5)-98, y(5), y(6), y(6)-98, y(7), y(8), y(8)-98, y(9), y(9)-98++, y(9)++, y(9)-98, y(10)++, y(10), y(10)-98, y(10)-98++
Precursor origin neutral loss: +

Peptide No.587

MFVSGEAVSAYSSAMR
Confirmed sites: @S:4,@S:13
Ambiguous sites: @Y:11orS:12

MS/MS Fragmentation of MFVSGEAVSAYSSAMR
Found in DSEL_MOUSE, Dermatan-sulfate epimerase-like protein OS=Mus musculus GN=Dsel PE=2 SV=1

Match to Query 5496: 1975.693590 from(988.854071,2+)
Title: Elution from: 69.021 to 69.021 scan no 6678 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1975.6899
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.053

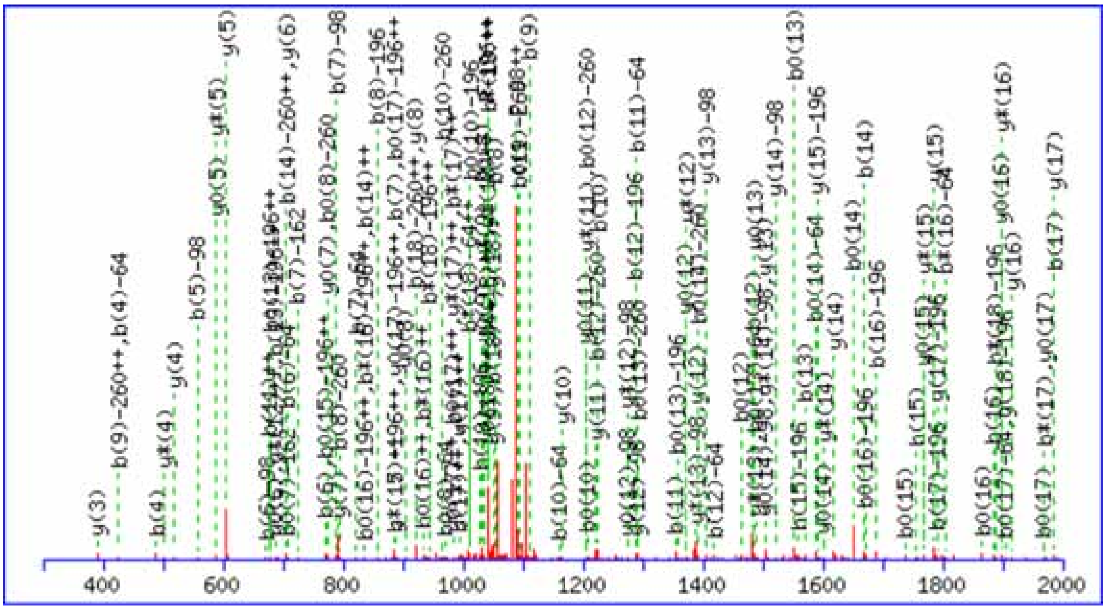
Matched b ions: b(5), b(7), b(8), b(9)++, b(9), b(12)++, b(12), b(13)
Matched y ions: y(4)-98, y(7), y(8)++, y(8), y(9)-98++, y(9), y(10), y(11), y(12)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.588

MLAESDDSGDEESVSQTDK
Confirmed sites: @S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of MLAESDDSGDEESVSQTDK
Found in OSBP1_MOUSE, Oxysterol-binding protein 1 OS=Mus musculus GN=Osbp PE=1 SV=2

Match to Query 6961: 2273.819012 from(1137.916782,2+)
Title: Elution from: 32.035 to 32.035 scan no 2584 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2273.8171
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl (K)
Ions Score: 70 Expect: 1.1e-006

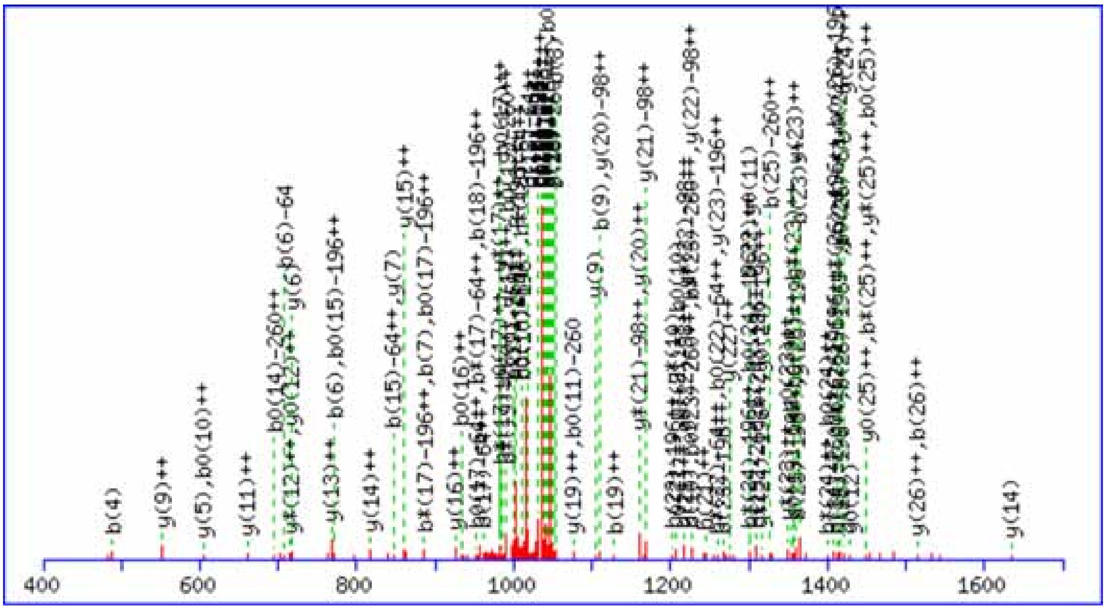
Matched b ions: b(4), b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(8)-196, b(8), b(9)-98, b(9), b(10), b(10)-196, b(11), b(11)-98, b(11)++, b(12), b(12)-98, b(12)-196, b(13)-196++, b(13), b(13)-98, b(14), b(14)-98, b(14)++, b(15)-196, b(15), b(16)-98, b(16)-196, b(16), b(17), b(17)-196, b(17)-98++, b(17)-98, b(17)++, b(18)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98, y(13), y(13)-98, y(14), y(14)-98, y(15), y(15)-98, y(15)-196, y(16)-98, y(16), y(17)-98, y(17), y(17)-196, y(17)-98++, y(17)++, y(18)++, y(18)-196
Precursor origin neutral loss: +

Peptide No.589

MLAESDDSGDEESVSQTDKTELQSTLR
Confirmed sites: @S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of MLAESDDSGDEESVSQTDKTELQSTLR
Found in OSBP1_MOUSE, Oxysterol-binding protein 1 OS=Mus musculus GN=Osbp PE=1 SV=2

Match to Query 6737: 3202.317720 from(1068.446516,3+)
Title: Elution from: 47.118 to 47.118 scan no 4233 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3202.3149
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K19 : Dimethyl (K)
Ions Score: 60 Expect: 7.9e-005

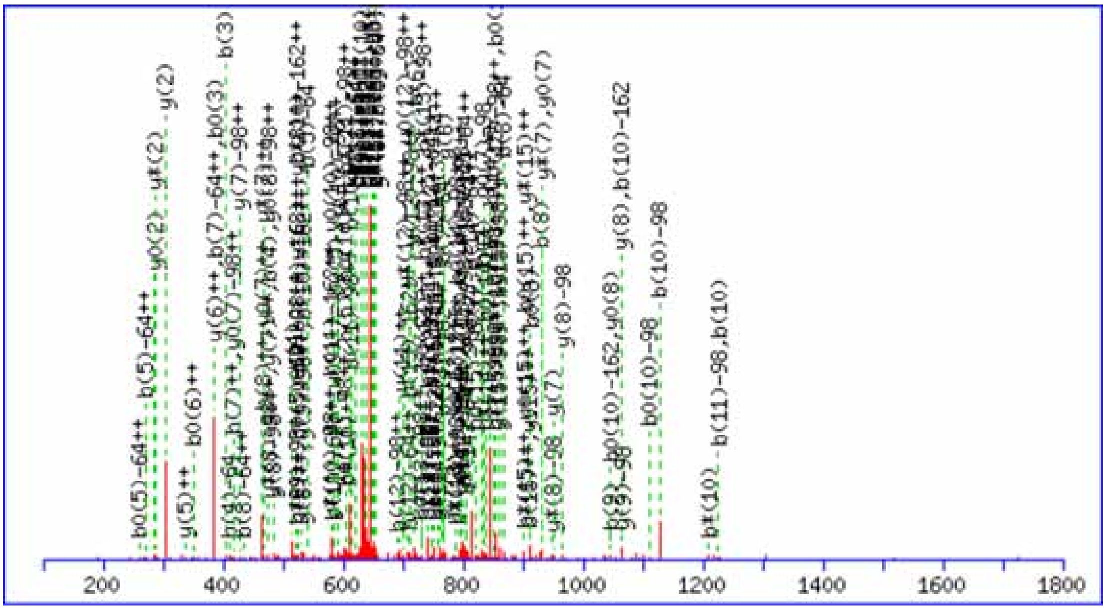
Matched b ions: b(4), b(6), b(7), b(8)-98, b(8), b(9), b(10), b(10)-196, b(10)-98, b(18)-196++, b(18)++, b(19)++, b(19)-196++, b(21)++, b(22)++, b(22)-196++, b(23)++, b(23)-196++, b(23)-98++, b(24)-196++, b(24)++, b(25)-98++, b(25)-196++, b(26)-196++, b(26)++, b(26)-98++
Matched y ions: y(5), y(6), y(7), y(9)++, y(9), y(11)++, y(13)++, y(14), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)-98++, y(22)++, y(23)-98++, y(23)-196++, y(23)++, y(24)++, y(24)-98++, y(25)-98++, y(25)-196++, y(26)-196++, y(26)++, y(26)-98++
Precursor origin neutral loss: +

Peptide No.590

MLDAEDIVNTPKPDER
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of MLDAEDIVNTPKPDER
Found in ACTN2_MOUSE, Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1

Match to Query 5556: 1993.908390 from(665.643406,3+)
Title: Elution from: 39.490 to 39.490 scan no 3598 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1993.9067
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K12 : Dimethyl (K)
Ions Score: 43 **Expect:** 0.0031

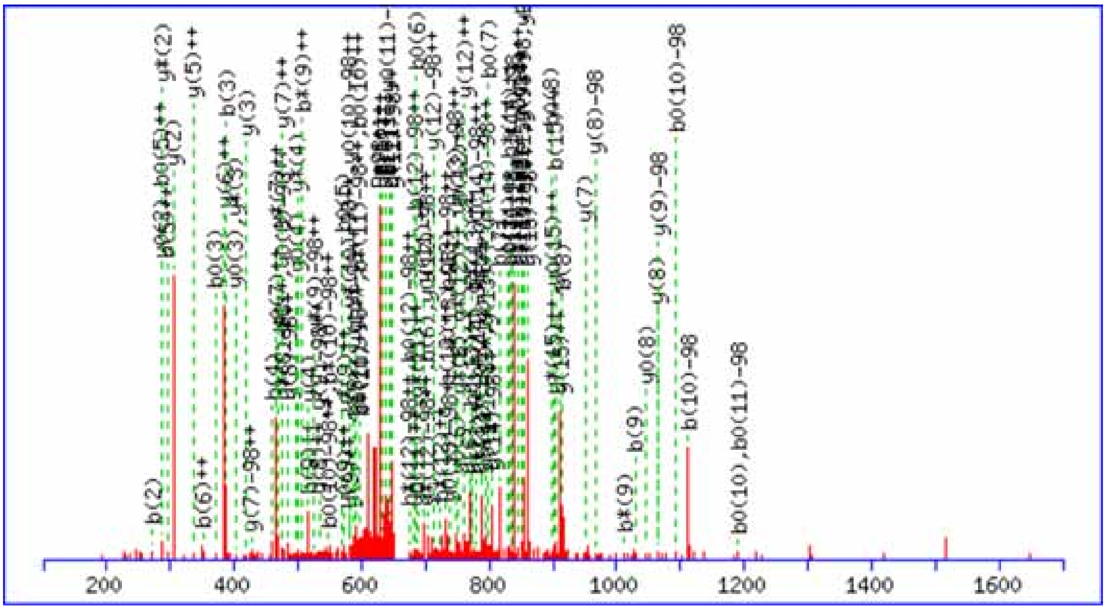
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(7)++, b(8)++, b(8), b(9), b(9)++, b(10)-98, b(10), b(10)++, b(11)-98, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(4), y(5)++, y(6)++, y(6), y(7)++, y(7), y(7)-98++, y(7)-98, y(8), y(8)-98++, y(8)++, y(8)-98, y(9)++, y(9)-98++, y(9)-98, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.591

MLDAEDIVNTPKPDER
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of MLDAEDIVNTPKPDER
Found in ACTN2_MOUSE, **Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1**

Match to Query 4328: 1977.914979 from(660.312269,3+)
Title: Elution from: 42.816 to 42.816 scan no 3734 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1977.9118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl (K)
Ions Score: 37 **Expect:** 0.013

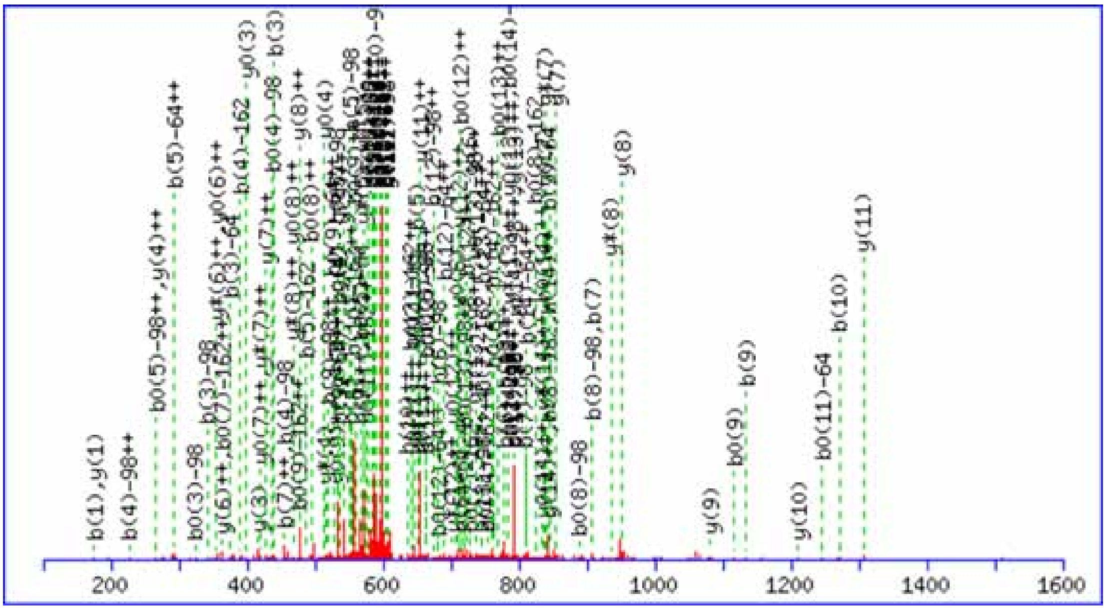
Matched b ions: b(2), b(3), b(4), b(5), b(5)++, b(6)++, b(6), b(7), b(8), b(9), b(9)++, b(10)-98, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(6), y(6)++, y(7)++, y(7)-98++, y(7)-98, y(7), y(8), y(8)-98++, y(8)++, y(8)-98, y(9)-98, y(9)++, y(9)-98++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.592

MPSIPEEPEHGDLER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of MPSIPEEPEHGDLER
Found in SPEG_MOUSE, Striated muscle-specific serine/threonine-protein kinase OS=Mus musculus GN=Speg PE=1 SV=2

Match to Query 3704: 1858.782315 from(620.601381,3+)
Title: Elution from: 36.027 to 36.027 scan no 2913 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1858.7808
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 0.00083

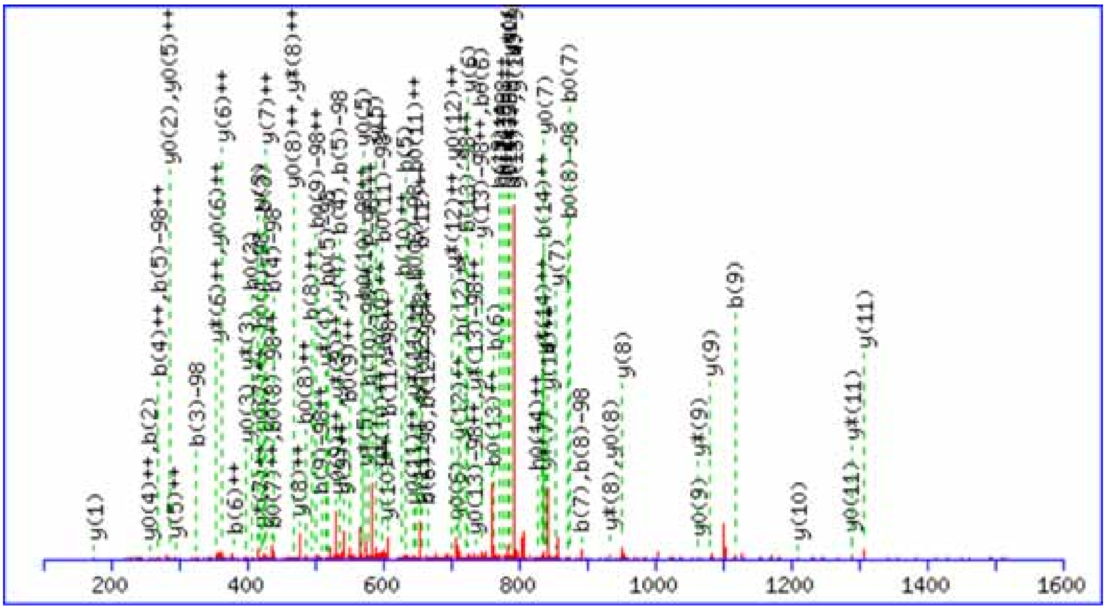
Matched b ions: b(1), b(3)-98, b(3), b(4)-98++, b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)++, b(7), b(7)-98, b(8)-98, b(9), b(9)-98++, b(9)++, b(10)-98++, b(10), b(10)++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(14)-98++, b(14)++
Matched y ions: y(1), y(3), y(4)++, y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.593

MPSIPEEPEHGDLER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of MPSIPEEPEHGDLER
Found in SPEG_MOUSE, Striated muscle-specific serine/threonine-protein kinase OS=Mus musculus GN=Speg PE=1 SV=2

Match to Query 3287: 1842.788442 from(615.270090,3+)
Title: Elution from: 42.492 to 42.492 scan no 3688 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1842.7859
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0081

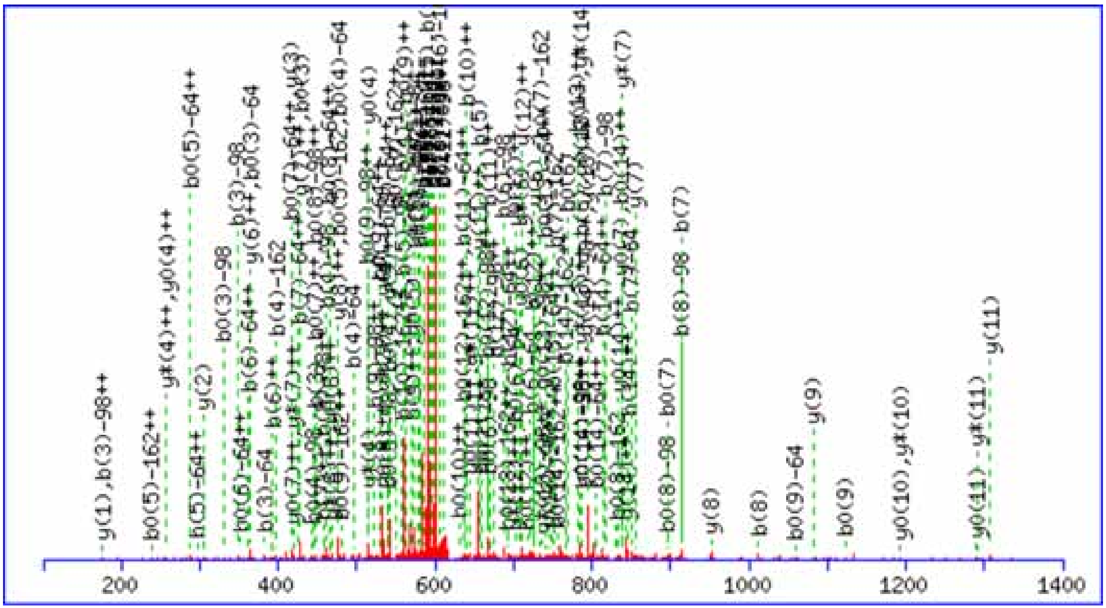
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4)++, b(4), b(5)-98++, b(5)-98, b(5), b(6), b(6)++, b(6)-98, b(7)-98, b(7), b(8)-98, b(8)++, b(9), b(9)-98++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++
Matched y ions: y(1), y(3), y(4), y(5), y(5)++, y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9)++, y(9), y(10)++, y(10), y(11), y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.594

MPSIPEEPEHGDLER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of MPSIPEEPEHGDLER
Found in SPEG_MOUSE, Striated muscle-specific serine/threonine-protein kinase OS=Mus musculus GN=Speg PE=1 SV=2

Match to Query 3768: 1864.815165 from(622.612331,3+)
Title: Elution from: 35.992 to 35.992 scan no 2908 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1864.8126
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.0039

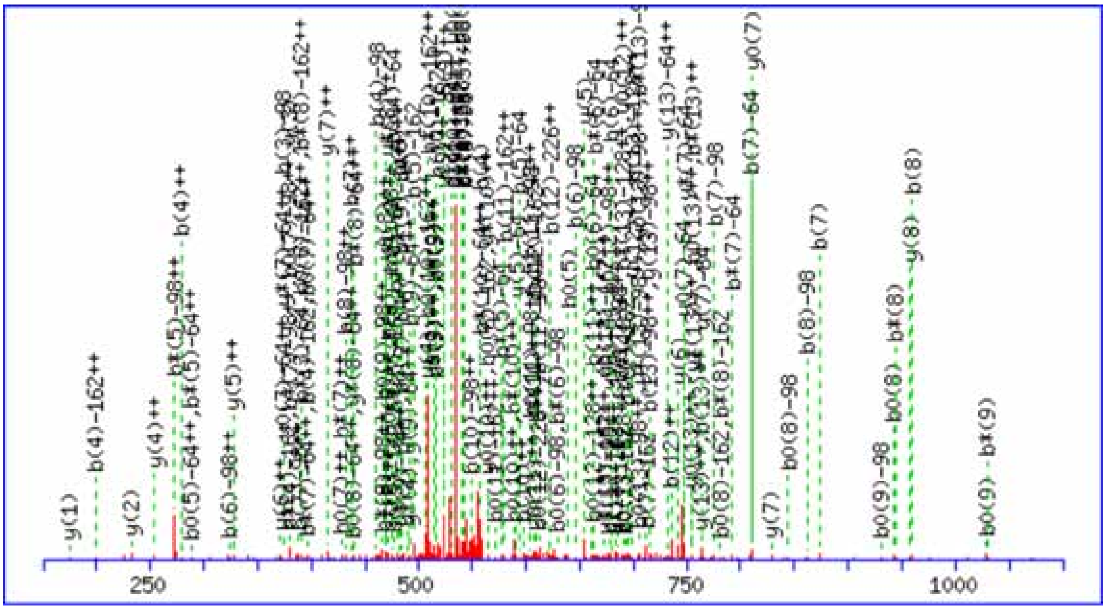
Matched b ions: b(3)-98, b(3)-98++, b(3), b(4), b(4)-98, b(5)-98, b(5), b(6), b(6)++, b(6)-98, b(7), b(7)++, b(7)-98, b(8), b(8)-98, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(14)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9)++, y(9), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.595

MQSSVSESSFQMGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 3716: 1699.658661 from(567.560163,3+)
Title: Elution from: 30.848 to 30.848 scan no 2421 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1699.6583
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 33 Expect: 0.01

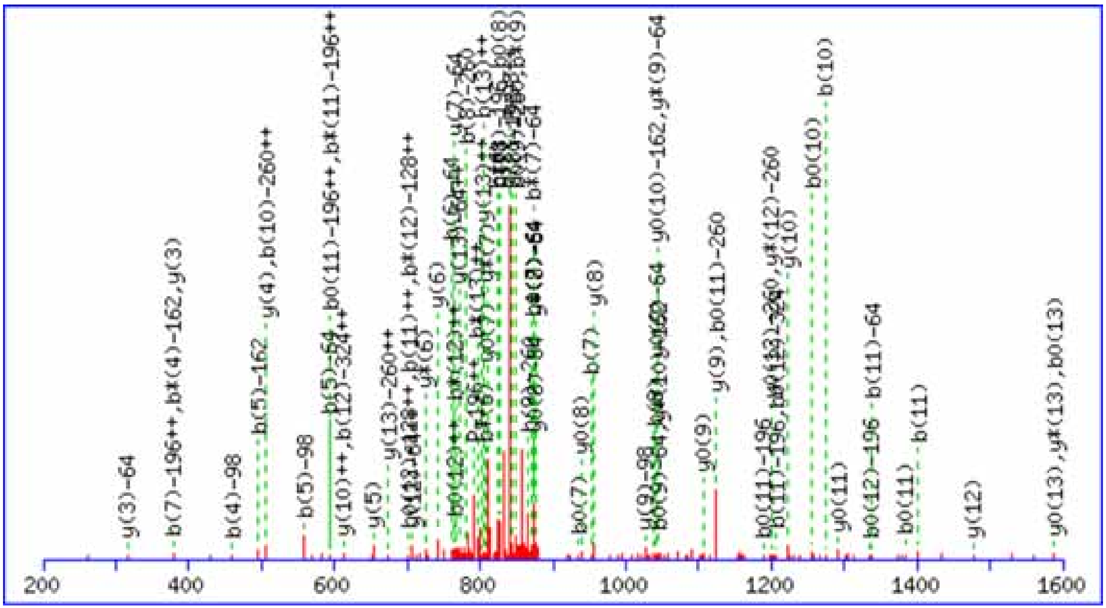
Matched b ions: b(3), b(3)-98, b(4)++, b(4), b(4)-98, b(6)-98++, b(6)-98, b(7), b(7)-98++, b(7)++, b(7)-98, b(8), b(8)-98++, b(8)-98, b(8)++, b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6)++, y(6), y(7)++, y(7), y(8), y(9)++, y(12)++, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.596

MQSSVSESSFQMGR
Confirmed sites: @S:6
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 4182: 1779.624562 from(890.819557,2+)
Title: Elution from: 32.863 to 32.863 scan no 2696 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1779.6246
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 Expect: 0.02

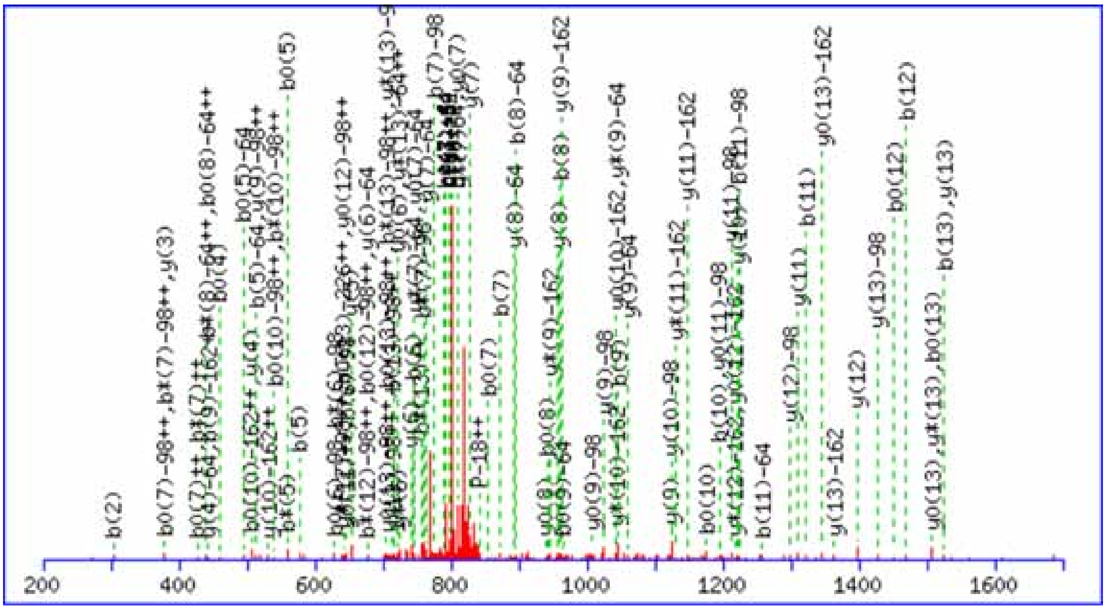
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(6), b(7)-196++, b(7)-98++, b(7)-98, b(7), b(8), b(8)-196, b(9)-98, b(10), b(11), b(11)-98, b(11)++, b(11)-196, b(12)-98++, b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98, y(9), y(10), y(10)++, y(12), y(12)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.597

MQSSVSESSFQMGR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 2855: 1699.659700 from(850.837126,2+)
Title: Elution from: 30.713 to 30.713 scan no 2202 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1699.6583
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 44 Expect: 0.00066

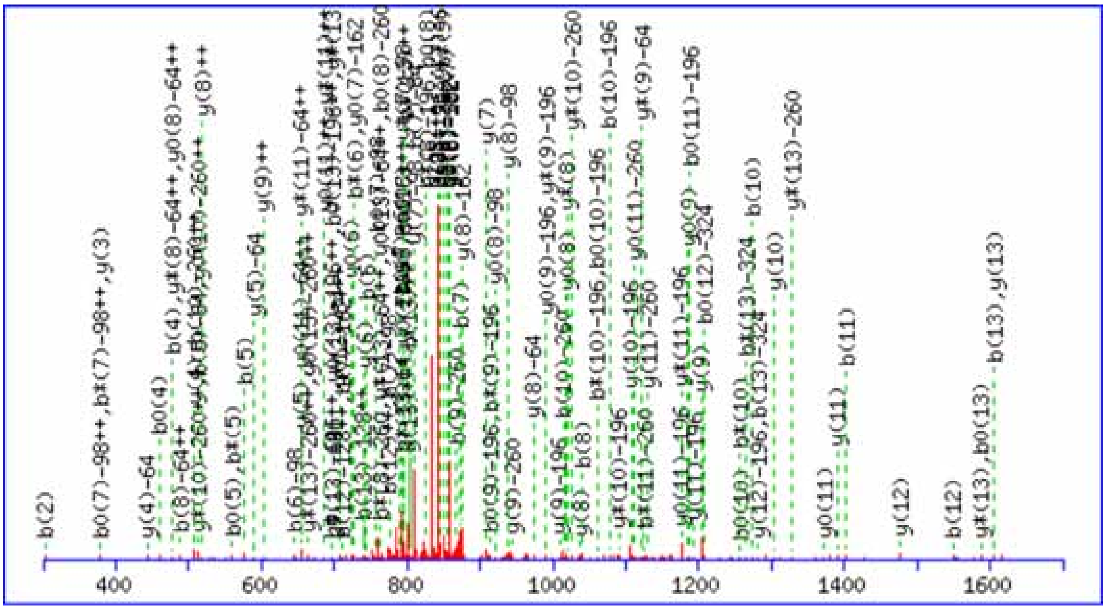
Matched b ions: b(2), b(5), b(6)-98, b(6), b(7), b(7)-98, b(8), b(9), b(10), b(11), b(11)-98, b(12), b(13), b(13)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(9)-98++, y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(13)-98++
Precursor origin neutral loss: +

Peptide No.598

MQSSVSESSFQMGR
Confirmed sites: @S:6,@S:8
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 3484: 1779.624888 from(890.819720,2+)
Title: Elution from: 31.152 to 31.152 scan no 2262 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1779.6246
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 42 Expect: 0.00059

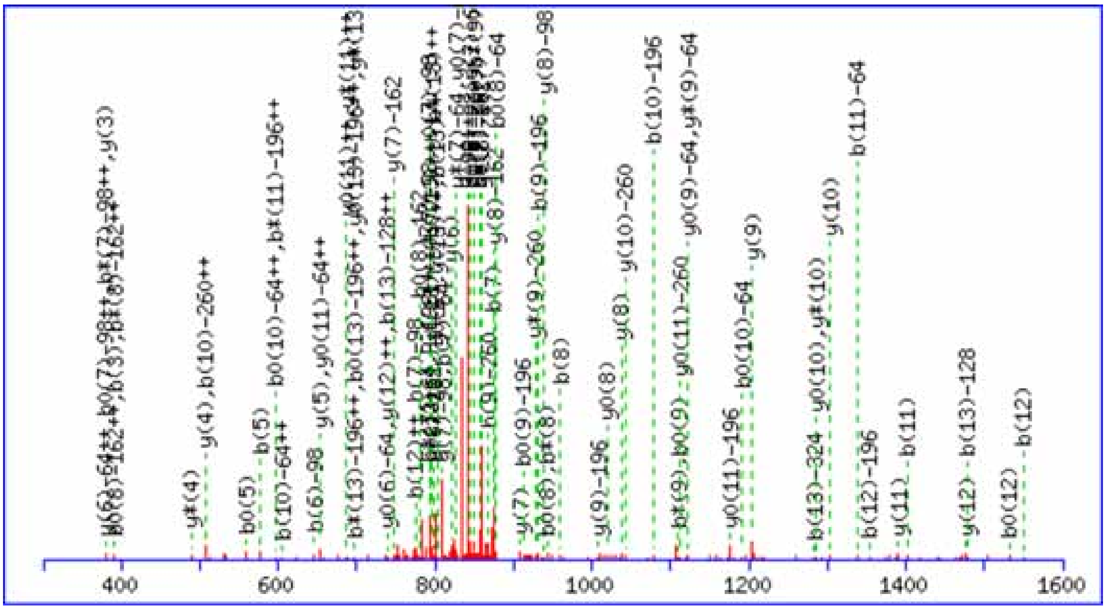
Matched b ions: b(2), b(4), b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(8)-196, b(10)-98, b(10)-196, b(10), b(11), b(11)-98, b(12), b(12)++, b(13), b(13)-98++, b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8)-98, y(8), y(8)++, y(9), y(9)-98, y(9)++, y(9)-196, y(10)-196, y(10), y(10)-98, y(10)-98++, y(11), y(11)-98, y(11)-98++, y(11)-196, y(12), y(12)-98, y(12)-196, y(13), y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.599

MQSSVSESSFQMGR
Confirmed sites: @S:6,@S:9
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 3169: 1779.625794 from(890.820173,2+)
Title: Elution from: 31.254 to 31.254 scan no 2274 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1779.6246
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 49 Expect: 0.00011

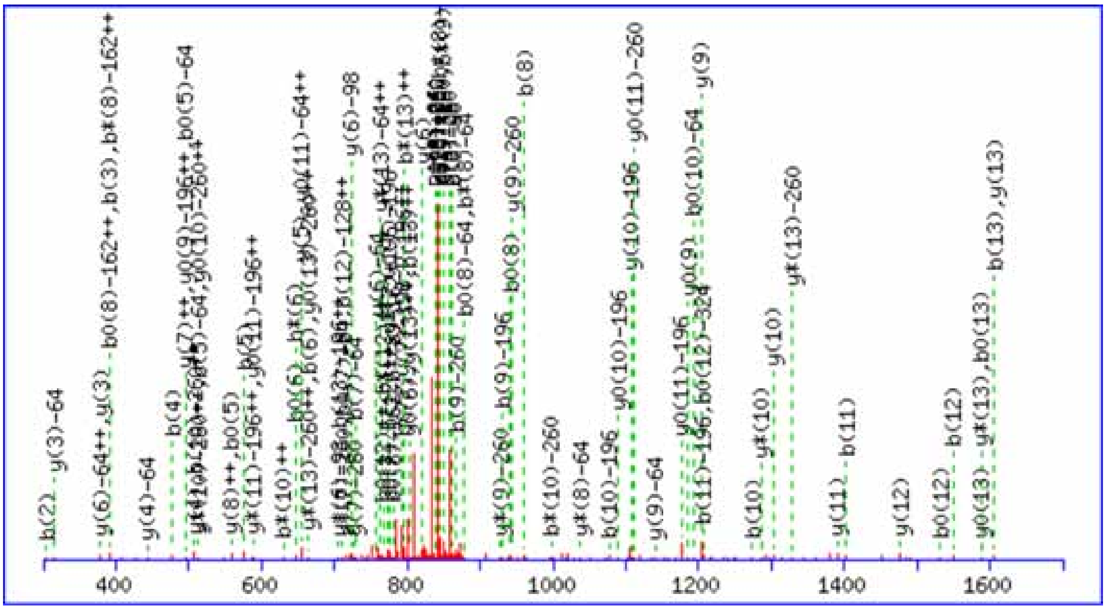
Matched b ions: b(3), b(5), b(6)-98, b(7)-98, b(7), b(8), b(9)-196, b(9)-98, b(10)-98, b(10)-196, b(11), b(12)++, b(12), b(12)-196, b(13)-98++, b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9)-98, y(9), y(9)-196, y(10), y(10)-98, y(11), y(11)-98++, y(11)-98, y(12), y(12)-98, y(12)++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.600

MQSSVSESSFQMGR
Confirmed sites: @S:8,@S:9
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 3583: 1779.624724 from(890.819638,2+)
Title: Elution from: 31.305 to 31.305 scan no 2317 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1779.6246
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 59 Expect: 1.2e-005

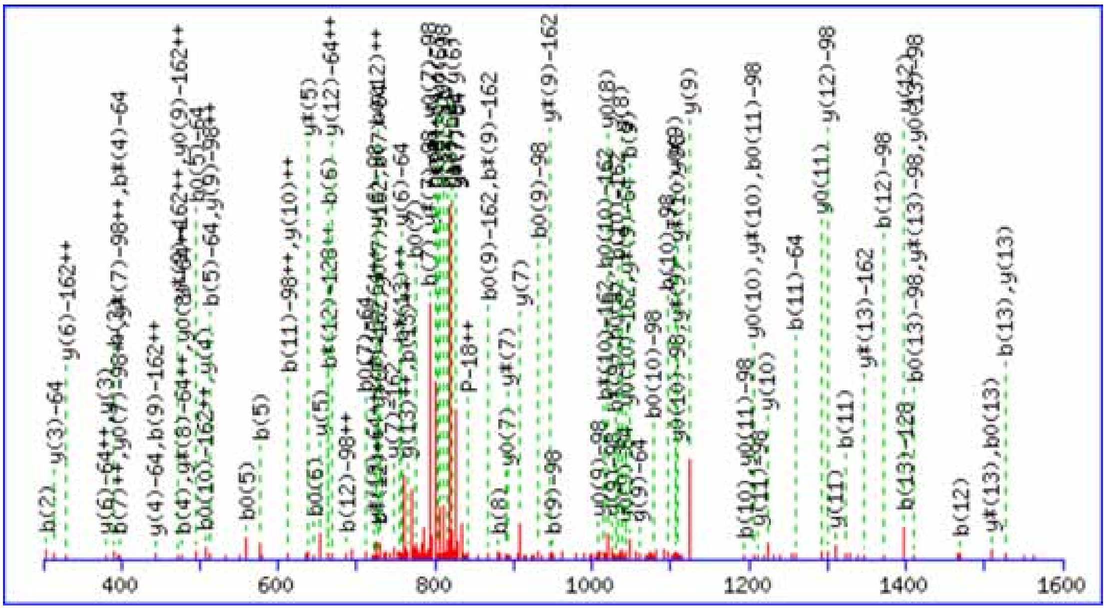
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(8)-98, b(9)-196, b(9)-98, b(10)-98, b(10)-196, b(10)-98++, b(10), b(11), b(11)-196, b(11)-98, b(12), b(12)-98, b(12)++, b(13), b(13)-196++, b(13)++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7)++, y(7)-196, y(8)-98, y(8)++, y(9), y(9)-98, y(10)-98, y(10), y(10)-196, y(11), y(11)-98++, y(11)-98, y(12), y(12)-98, y(13), y(13)++
Precursor origin neutral loss: +

Peptide No.601

MQSSVSESSFQMGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 3718: 1699.658804 from(850.836678,2+)
Title: Elution from: 28.590 to 28.590 scan no 2110 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1699.6583
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 49 Expect: 0.00021

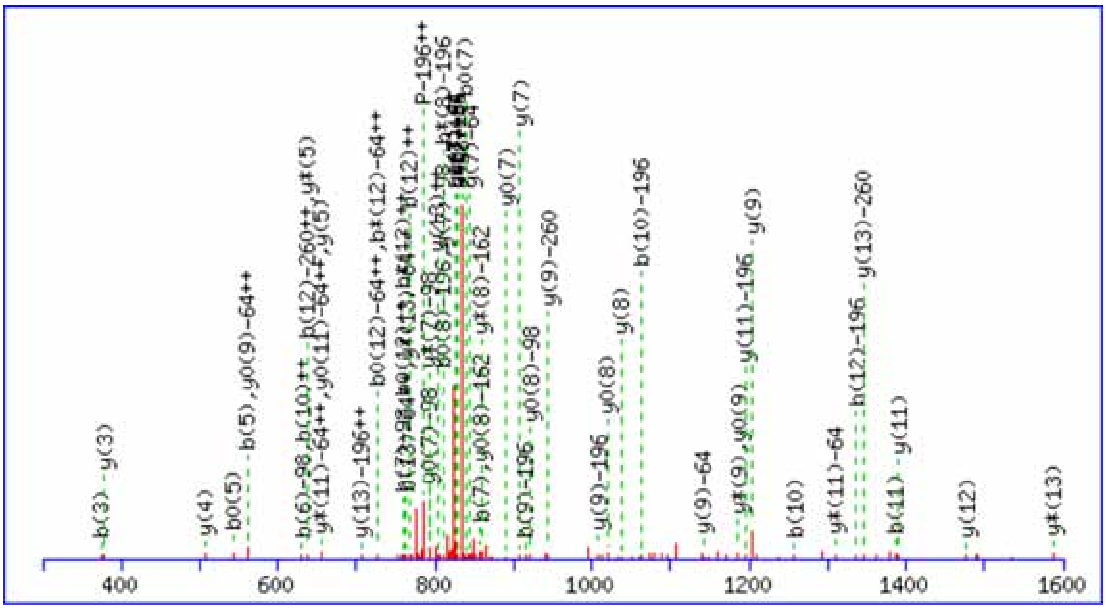
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(7)++, b(8), b(9)-98, b(9), b(10), b(10)-98, b(11)-98++, b(11), b(12), b(12)-98++, b(12)-98, b(13), b(13)++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(9), y(9)-98, y(9)-98++, y(10), y(10)++, y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)++
Precursor origin neutral loss: +

Peptide No.602

MQSSVSESSFQMGR
Confirmed sites: @S:6,@S:8
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 4087: 1763.629254 from(882.821903,2+)
Title: Elution from: 36.036 to 36.036 scan no 3130 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1763.6297
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 Expect: 0.017

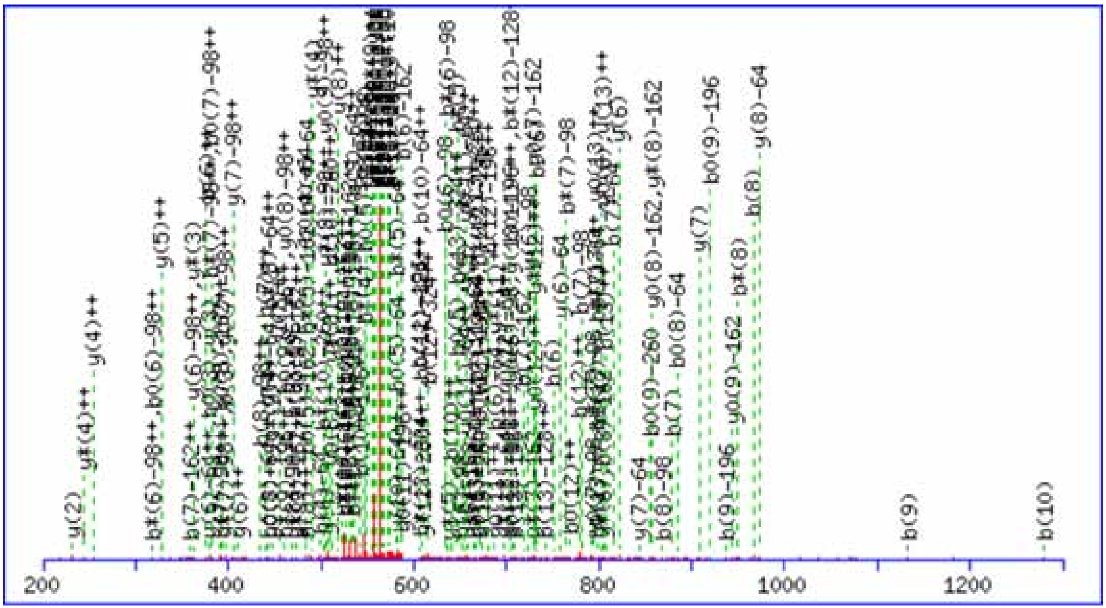
Matched b ions: b(3), b(5), b(6)-98, b(7)-98, b(7), b(8)-196, b(9)-98++, b(9)-196, b(9)-98, b(10)++, b(10)-98, b(10), b(10)-196, b(11), b(12)-196, b(12)++, b(13)-98
Matched y ions: y(3), y(4), y(5), y(7), y(7)-98, y(8), y(9)-98, y(9), y(9)-196, y(11)-98, y(11), y(11)-196, y(12)-98, y(12), y(13)-196++, y(13)++
Precursor origin neutral loss: +

Peptide No.603

MQSSVSESSFQMGR
Confirmed sites: @S:4,@S:9
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 3280: 1785.657279 from(596.226369,3+)
Title: Elution from: 31.386 to 31.386 scan no 2296 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1785.6564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 Expect: 0.032

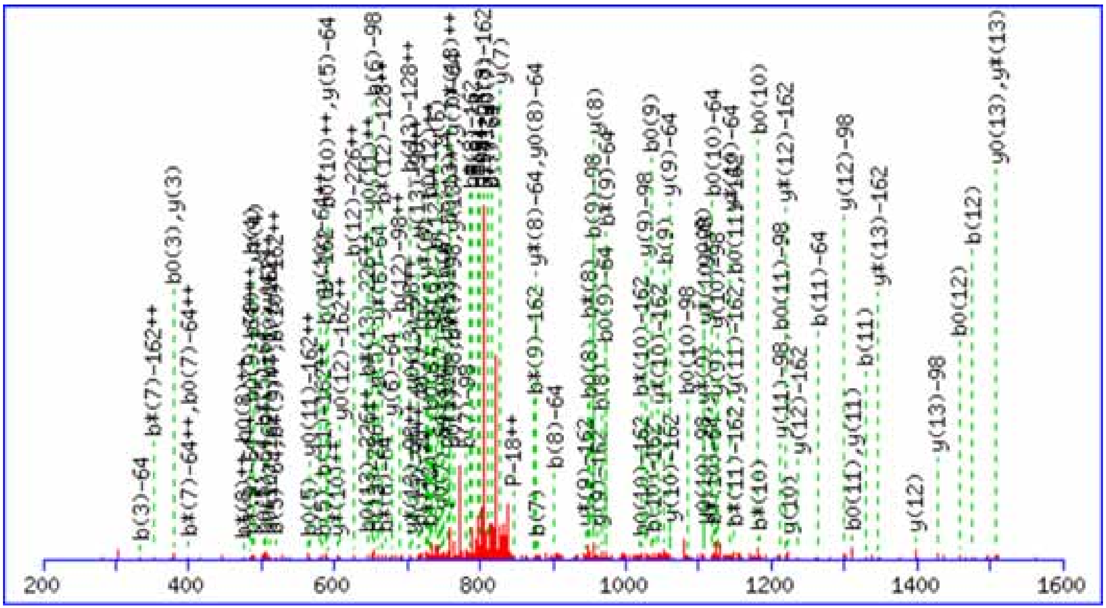
Matched b ions: b(3), b(4), b(5)-98, b(6), b(6)++, b(6)-98, b(7)-98++, b(7), b(7)-98, b(7)++, b(8), b(8)++, b(8)-98++, b(8)-98, b(9)-98, b(9), b(9)-196, b(9)-196++, b(9)++, b(10)-98, b(10), b(10)-196++, b(10)++, b(11)-98++, b(11)-196++, b(11)++, b(12)++, b(12)-98++, b(12)-196++, b(13)-196++, b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(5)++, y(6), y(6)-98++, y(6)++, y(6)-98, y(7)++, y(7)-98++, y(7), y(8)-98++, y(8)++, y(10)-98++, y(11)-98++, y(12)-98++, y(13)-196++, y(13)++
Precursor origin neutral loss: +

Peptide No.604

MQSSVSESSFQMGR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 2759: 1705.690934 from(853.852743,2+)
Title: Elution from: 30.706 to 30.706 scan no 2200 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1705.6901
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 43 Expect: 0.001

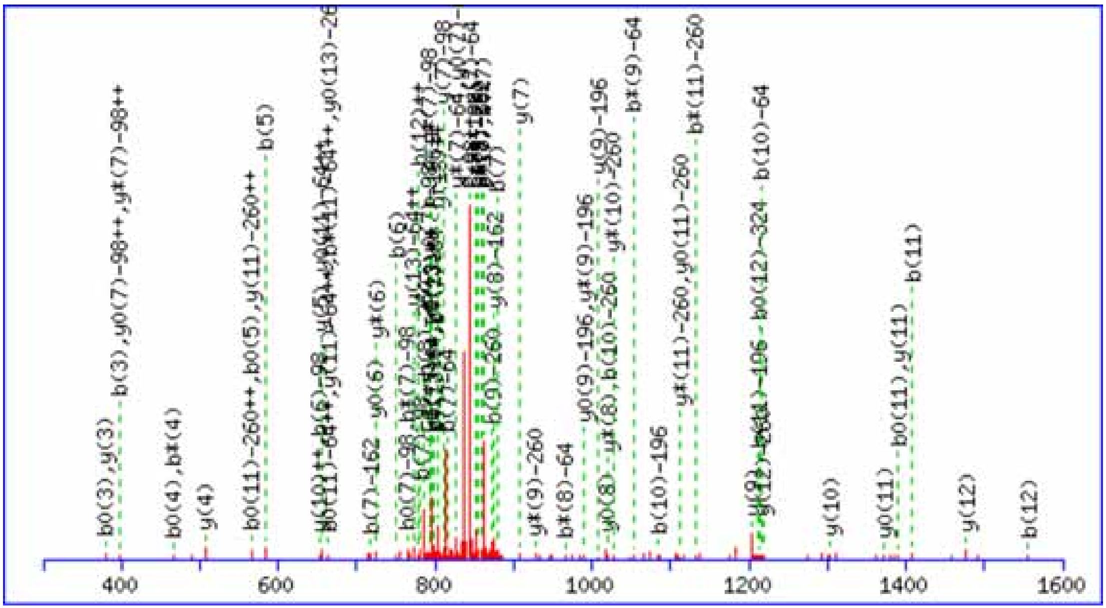
Matched b ions: b(4), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8), b(8)++, b(9), b(9)-98, b(11), b(12), b(12)-98++, b(12)++, b(13)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13)-98, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.605

MQSSVSESSFQMGR
Confirmed sites: @S:6,@S:8
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 3284: 1785.657024 from(893.835788,2+)
Title: Elution from: 31.232 to 31.232 scan no 2278 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1785.6564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 31 Expect: 0.0096

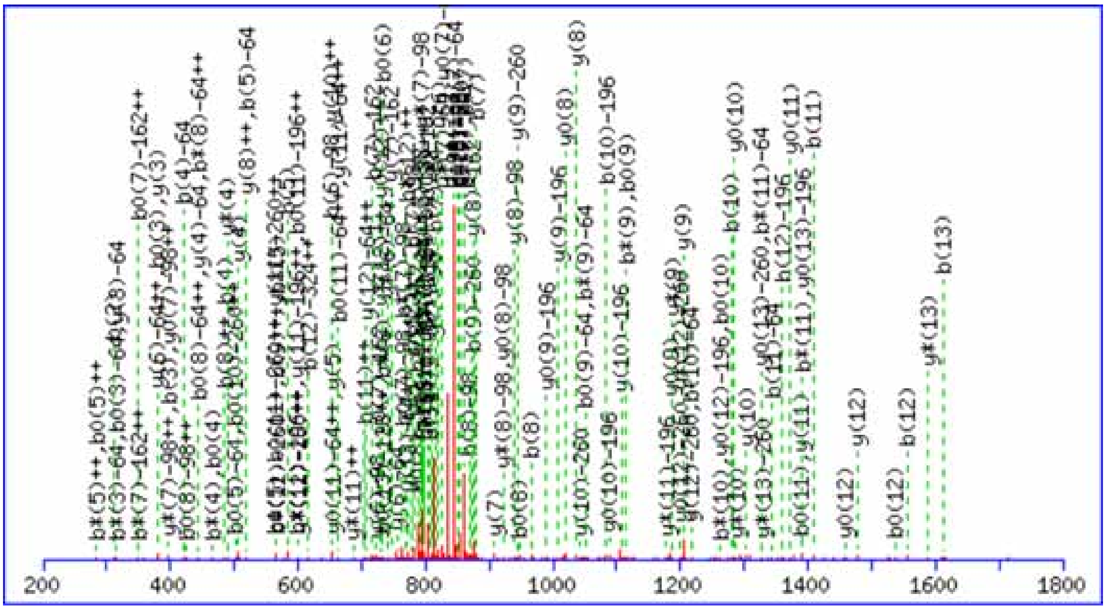
Matched b ions: b(3), b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8)-196, b(10)-98, b(10)-196, b(11)-98, b(11), b(11)-196, b(12), b(12)-98, b(12)++
Matched y ions: y(3), y(4), y(5), y(7), y(7)-98, y(9)-98, y(9), y(9)-196, y(10)++, y(10)-98, y(10), y(11)-98, y(11), y(12), y(12)-98, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.606

MQSSVSESSFQMGR
Confirmed sites: @S:6,@S:9
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 4845: 1785.656322 from(893.835437,2+)
Title: Elution from: 31.205 to 31.205 scan no 2389 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1785.6564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 66 Expect: 3e-006

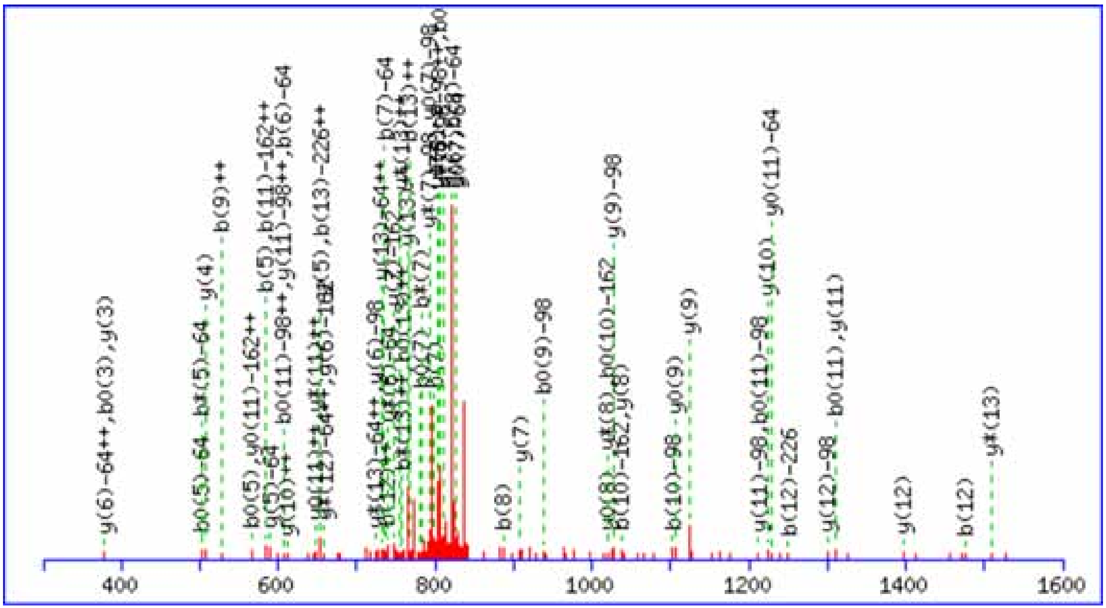
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(7)-98, b(7), b(8), b(8)++, b(8)-98, b(9)-98, b(9)++, b(10)-98, b(10)-196, b(10), b(11), b(11)-98, b(11)++, b(12), b(12)-98, b(12)++, b(12)-196, b(13), b(13)++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)++, y(8)-98, y(9)-98, y(9), y(9)-196, y(10)++, y(10)-98, y(10), y(10)-196, y(11), y(11)-98, y(11)-196++, y(12)-98, y(12), y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.607

MQSSVSESSFQMGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of MQSSVSESSFQMGR
Found in SYNP2_MOUSE, Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2

Match to Query 3214: 1705.691610 from(853.853081,2+)
Title: Elution from: 28.538 to 28.538 scan no 1950 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1705.6901
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 62 Expect: 1.4e-005

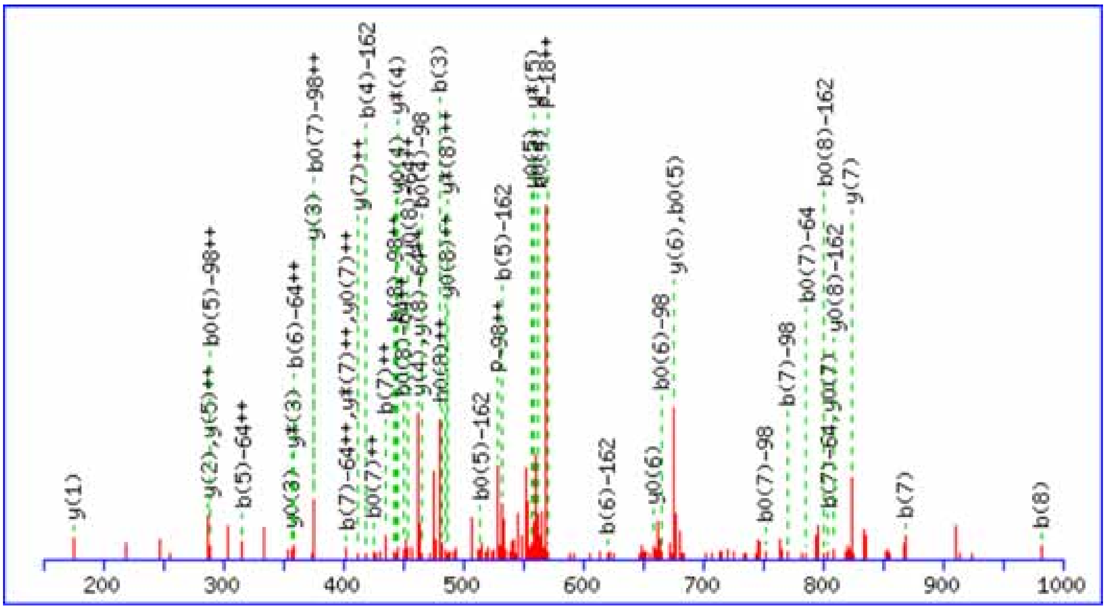
Matched b ions: b(5), b(7), b(8), b(9)++, b(10)-98, b(12), b(12)++, b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(9)-98, y(9), y(10), y(10)++, y(11), y(11)-98, y(11)-98++, y(12), y(12)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.608

MSMTLSSLK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of MSMTLSSLK
Found in PA24A_MOUSE, Cytosolic phospholipase A2 OS=Mus musculus GN=Pla2g4a PE=1 SV=1

Match to Query 922: 1154.554958 from(578.284755,2+)
Title: Elution from: 42.546 to 42.546 scan no 3848 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1154.5540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K9 : Dimethyl (K)
Ions Score: 31 Expect: 0.025

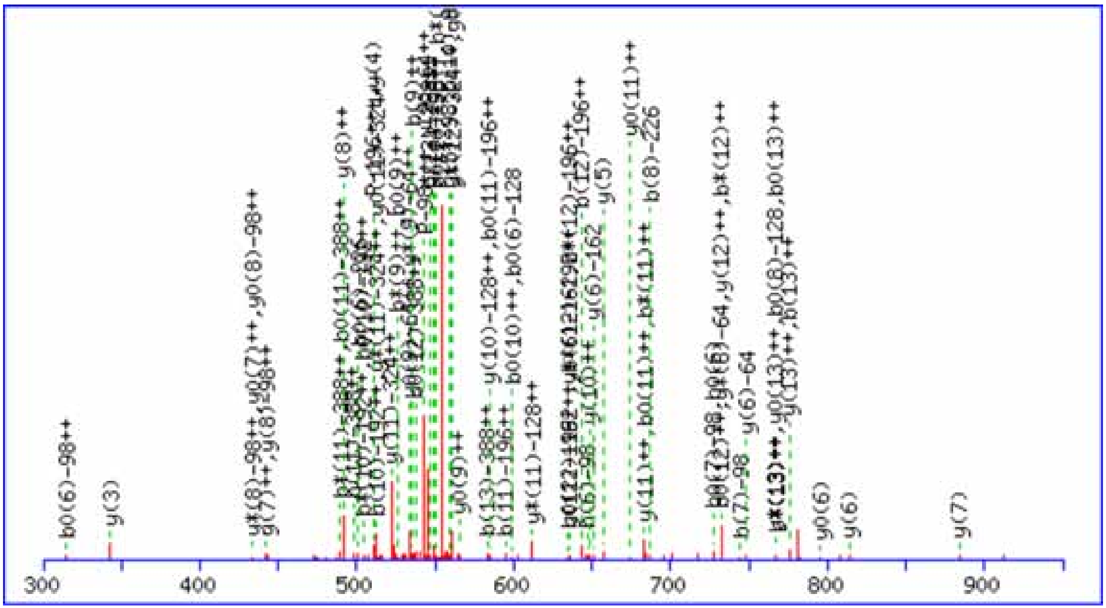
Matched b ions: b(3), b(7)++, b(7), b(7)-98, b(8), b(8)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5)++, y(6), y(7), y(7)++
Precursor origin neutral loss: +

Peptide No.609

MSPAMSPARMSPAR
Confirmed sites: @S:6,@S:11
Ambiguous sites:

MS/MS Fragmentation of MSPAMSPARMSPAR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3208: 1724.649993 from(575.890607,3+)
Title: Elution from: 20.067 to 20.067 scan no 953 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1724.6486
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.036

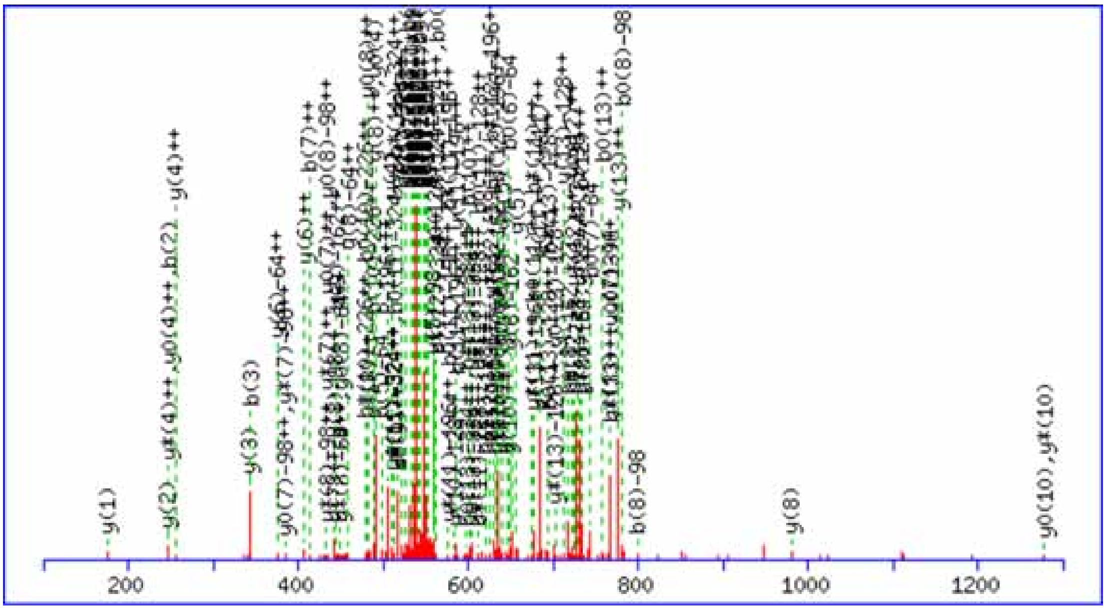
Matched b ions: b(6)-98, b(7)-98, b(9)++, b(10)-98++, b(11)-98++, b(11)-196++, b(12)-196++, b(13)++, b(13)-98++
Matched y ions: y(3), y(4), y(5), y(5)-98, y(6), y(7), y(7)++, y(8)++, y(8)-98++, y(9)-98++, y(10)++, y(10)-196++, y(10)-98++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(12)-196++, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.610

MSPAMSPARMSPAR
Confirmed sites: @S:6,@S:11
Ambiguous sites:

MS/MS Fragmentation of MSPAMSPARMSPAR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3770: 1708.655472 from(570.559100,3+)
Title: Elution from: 22.774 to 22.774 scan no 1334 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1708.6537
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.017

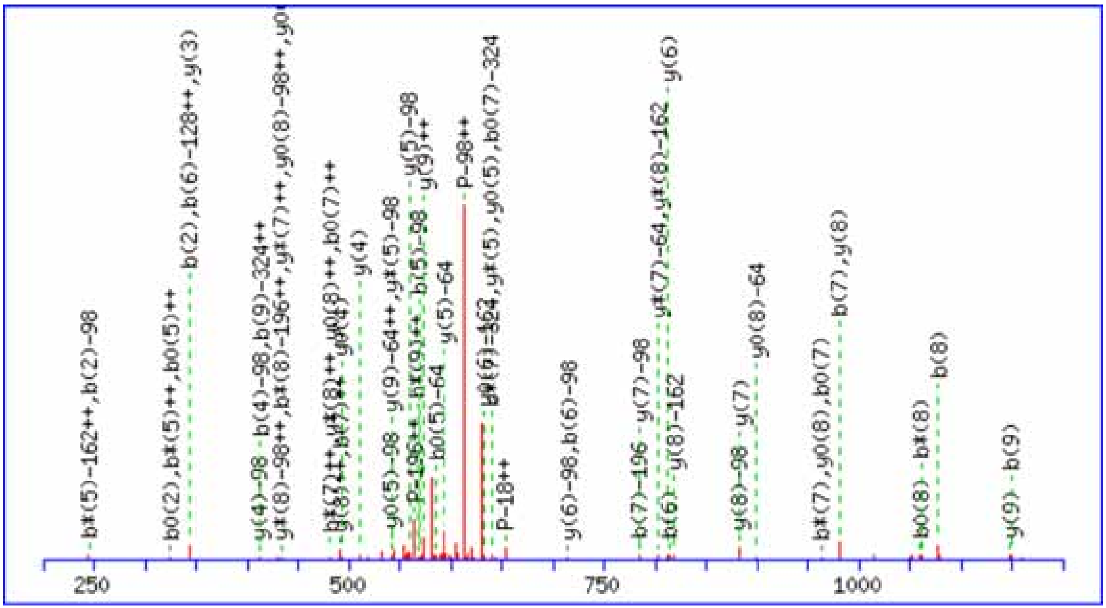
Matched b ions: b(2), b(3), b(5), b(6)-98, b(6), b(7)++, b(7)-98, b(8)-98, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(11)-196++, b(12)-196++, b(12)-98++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(5)-98, y(6)++, y(7)++, y(8)-98++, y(8), y(8)++, y(9)-98++, y(10)++, y(10)-196++, y(10)-98++, y(11)-98++, y(11)++, y(11)-196++, y(12)-98++, y(12)++, y(12)-196++, y(13)-98++, y(13)++, y(13)-196++
Precursor origin neutral loss: +

Peptide No.611

MSPARMSPAR
Confirmed sites: @S:2,@S:7
Ambiguous sites:

MS/MS Fragmentation of MSPARMSPAR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1719: 1322.491790 from(662.253171,2+)
Title: Elution from: 17.093 to 17.093 scan no 769 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1322.4913
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.011

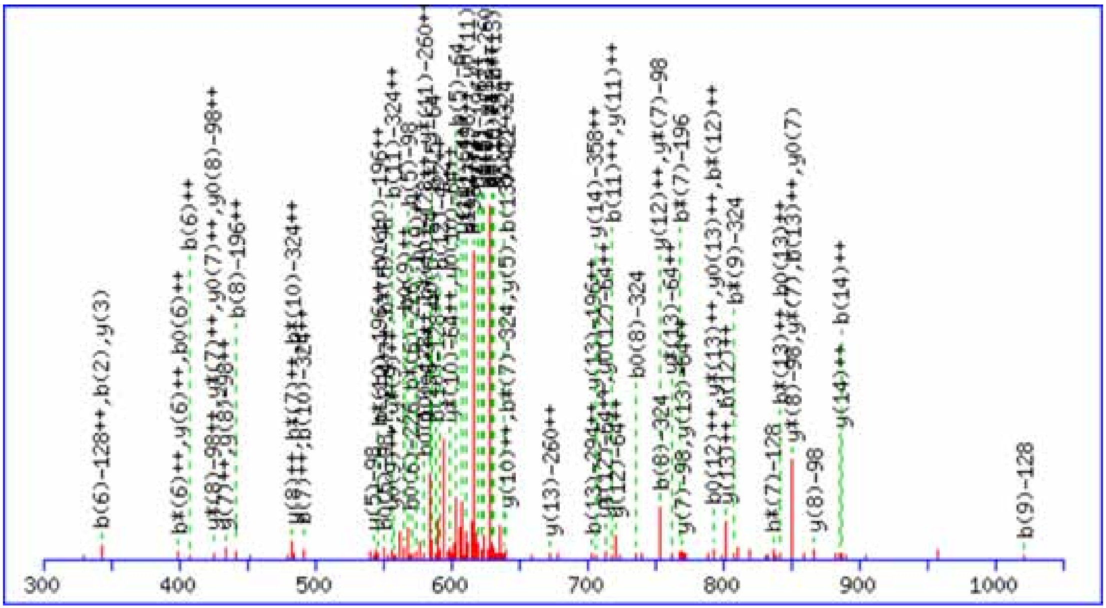
Matched b ions: b(2), b(2)-98, b(4)-98, b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(7)++, b(7)-196, b(8), b(8)-98++, b(8)-98, b(9), b(9)-98
Matched y ions: y(3), y(4)-98, y(4), y(5)-98, y(6)-98, y(6), y(7), y(7)-98, y(8)-98, y(8), y(8)++, y(9), y(9)-98, y(9)++
Precursor origin neutral loss: +

Peptide No.612

MSPARMSPARMSPAR
Confirmed sites: @S:2,@S:7,@S:12
Ambiguous sites:

MS/MS Fragmentation of MSPARMSPARMSPAR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 6232: 1944.720768 from(649.247532,3+)
Title: Elution from: 22.680 to 22.680 scan no 1246 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1944.7211
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.044

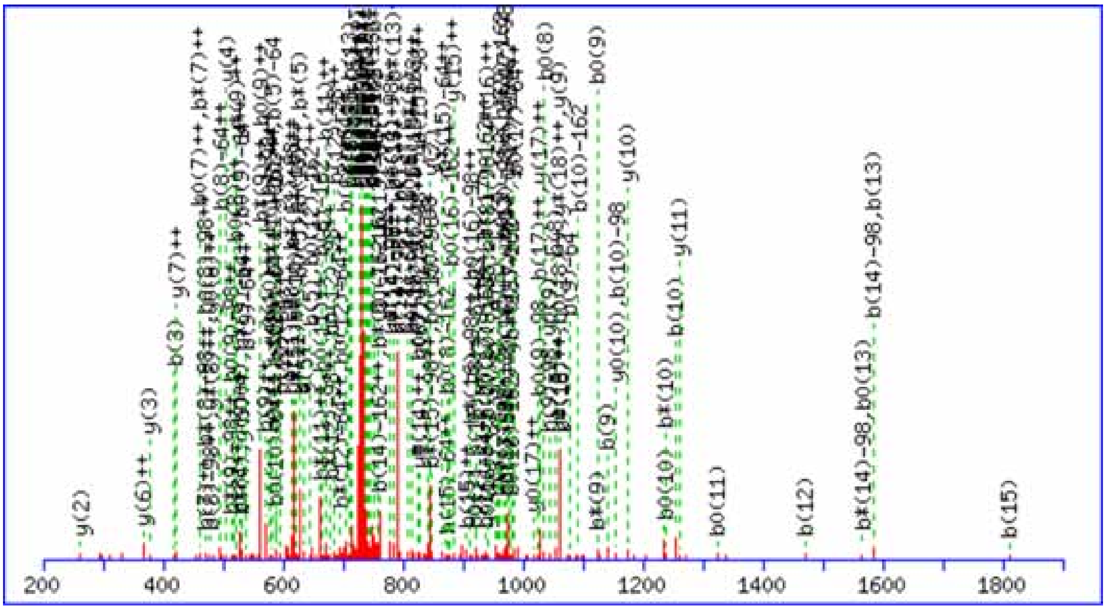
Matched b ions: b(2), b(5)-98, b(6)++, b(7)++, b(7)-98++, b(7)-98, b(8)-98++, b(8)-196++, b(9)++, b(10)-98++, b(11)-196++, b(11)++, b(12)-98++, b(12)++, b(12)-196++, b(13)-196++, b(13)++, b(13)-98++, b(13)-294++, b(14)-98++, b(14)++, b(14)-196++
Matched y ions: y(3), y(5), y(5)-98, y(6)++, y(7)++, y(7)-98, y(8)++, y(8)-98++, y(8)-98, y(10)++, y(10)-98++, y(11)-196++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++
Precursor origin neutral loss: +

Peptide No.613

MSREPTLDSISELPEEDSR
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of MSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 7085: 2314.006470 from(772.342766,3+)
Title: Elution from: 48.578 to 48.578 scan no 4741 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2314.0035
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00056

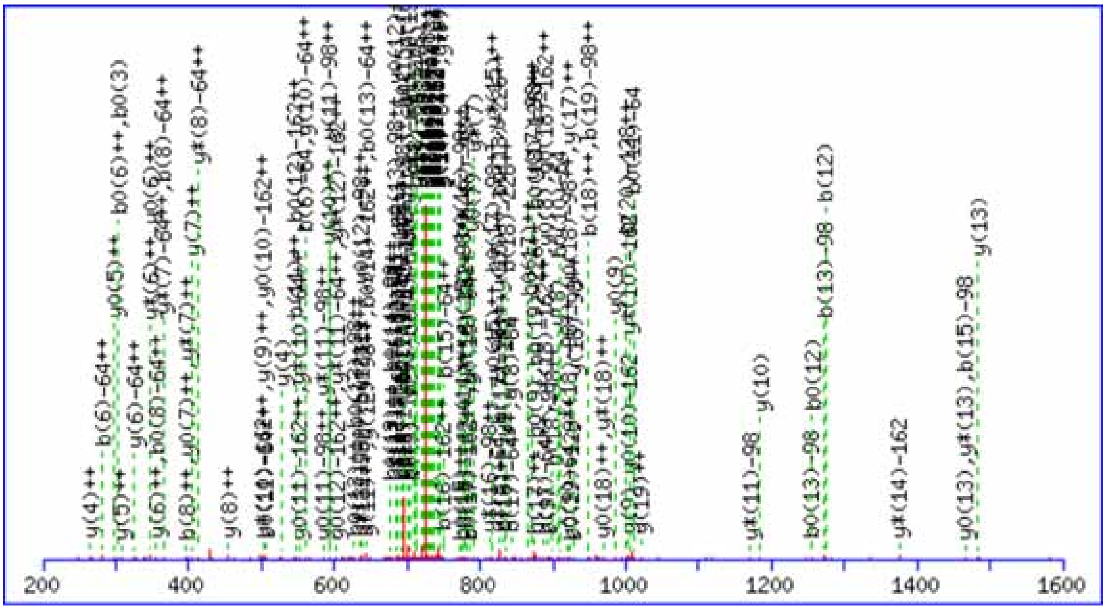
Matched b ions: b(3), b(5), b(6)-98, b(6), b(7)++, b(7), b(7)-98, b(8)++, b(8)-98, b(8), b(8)-98++, b(9), b(9)++, b(9)-98, b(10), b(10)++, b(10)-98, b(10)-98++, b(11)++, b(12), b(12)++, b(12)-98++, b(13)++, b(13), b(13)-98++, b(14)-98++, b(14)-98, b(15), b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(13)++, y(15)++, y(17)++, y(17)-98++
Precursor origin neutral loss:

Peptide No.614

MSSDTSPAVVTTPPPPSMPHK
Confirmed sites: @T:12
Ambiguous sites:

MS/MS Fragmentation of MSSDTSPAVVTTPPPPSMPHK
Found in ADDG_MOUSE, Gamma-adducin OS=Mus musculus GN=Add3 PE=1 SV=1

Match to Query 6140: 2274.987312 from(759.336380,3+)
Title: Elution from: 48.224 to 48.224 scan no 4485 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2274.9902
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M18 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 34 Expect: 0.021

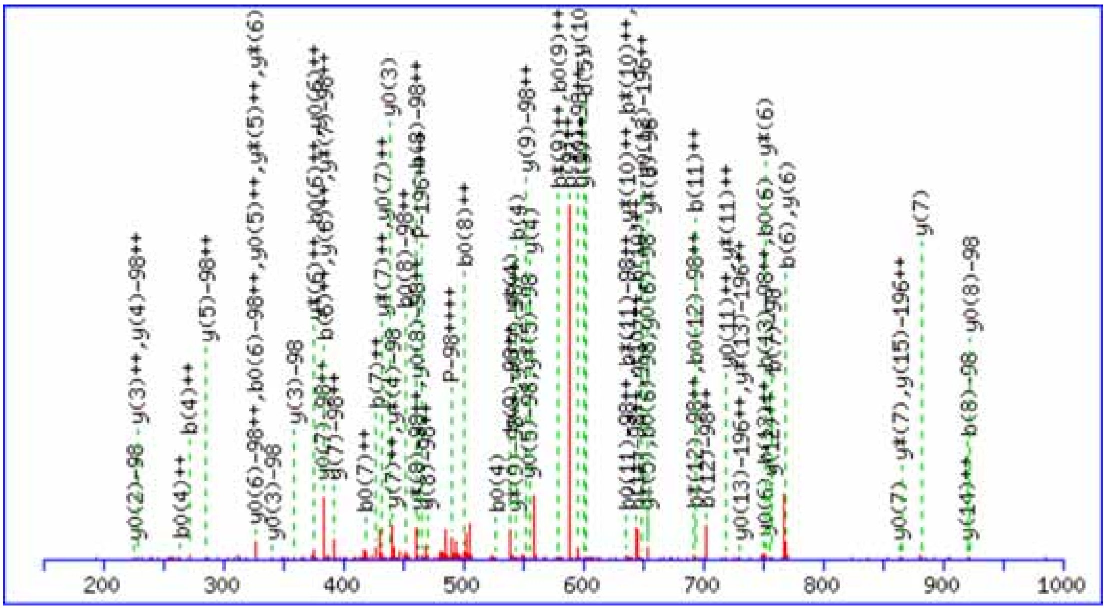
Matched b ions: b(7), b(8)++, b(9), b(11)++, b(12)++, b(12), b(13)-98, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)-98, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-98++
Matched y ions: y(4)++, y(4), y(5)++, y(6)++, y(6), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13), y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(17)++, y(17)-98++, y(18)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.615

MSYYGSSYRIVNVDSK
Confirmed sites: @S:6,@S:15
Ambiguous sites:

MS/MS Fragmentation of MSYYGSSYRIVNVDSK
Found in IRK16_MOUSE, Inward rectifier potassium channel 16 OS=Mus musculus GN=Kcnj16 PE=2 SV=1

Match to Query 4664: 2055.836048 from(514.966288,4+)
Title: Elution from: 33.705 to 33.705 scan no 2499 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2055.8414
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl (K)
Ions Score: 30 Expect: 0.03

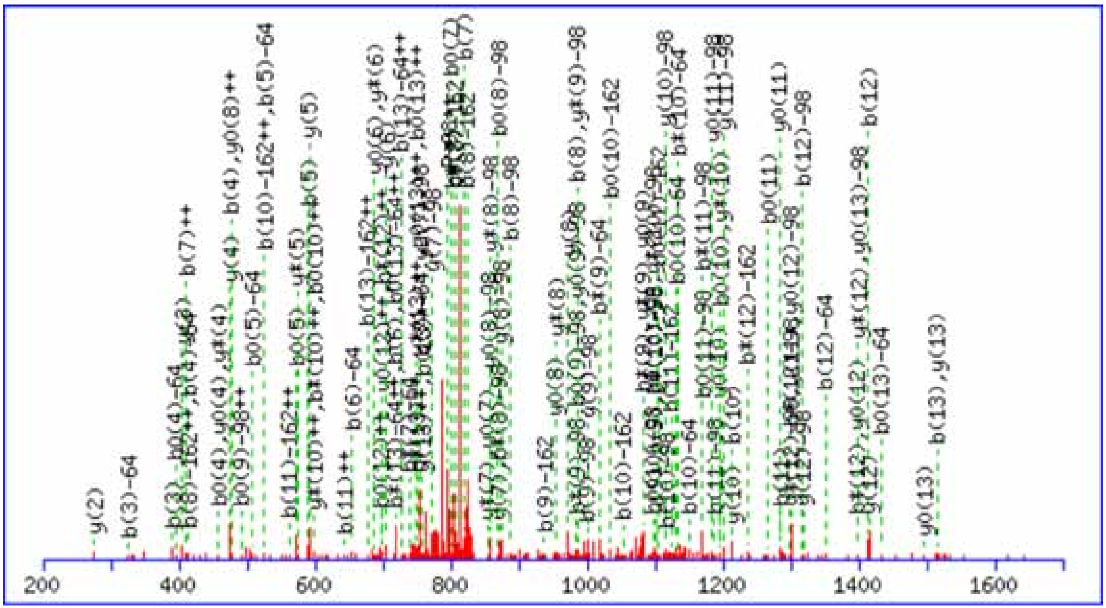
Matched b ions: b(4)++, b(4), b(5), b(6)++, b(6), b(7)++, b(7)-98, b(8)-98++, b(8)-98, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(15)-98++
Matched y ions: y(3)++, y(3)-98, y(4)-98++, y(4), y(5)-98++, y(6)++, y(6), y(7)++, y(7)-98++, y(7), y(8)-98++, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(12)++, y(14)++, y(15)-196++
Precursor origin neutral loss:

Peptide No.616

MVDSLQTSLDAETR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of MVDSLQTSLDAETR
Found in MYH7_MOUSE, Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1

Match to Query 3617: 1688.732834 from(845.373693,2+)
Title: Elution from: 39.379 to 39.379 scan no 3583 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1688.7328
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 0.00024

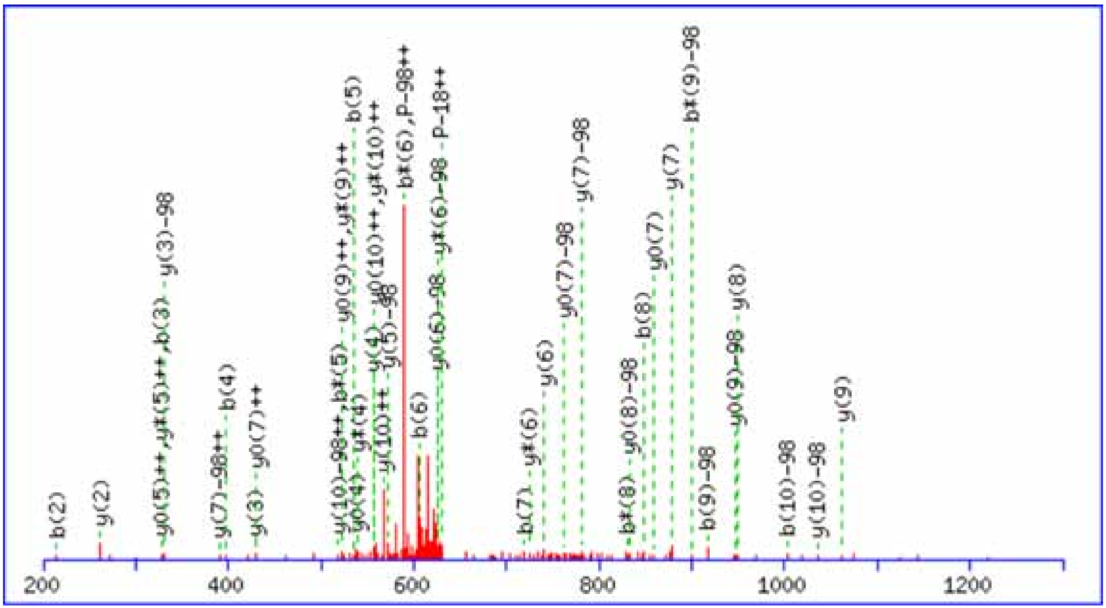
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(8), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(11)++, b(12), b(12)-98, b(13), b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)++
Precursor origin neutral loss: +

Peptide No.617

NALAHALQSSR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of NALAHALQSSR
Found in MYH6_MOUSE, Myosin-6 OS=Mus musculus GN=Myh6 PE=1 SV=2

Match to Query 1525: 1274.613666 from(638.314109,2+)
Title: Elution from: 30.138 to 30.138 scan no 2323 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1274.6132
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.015

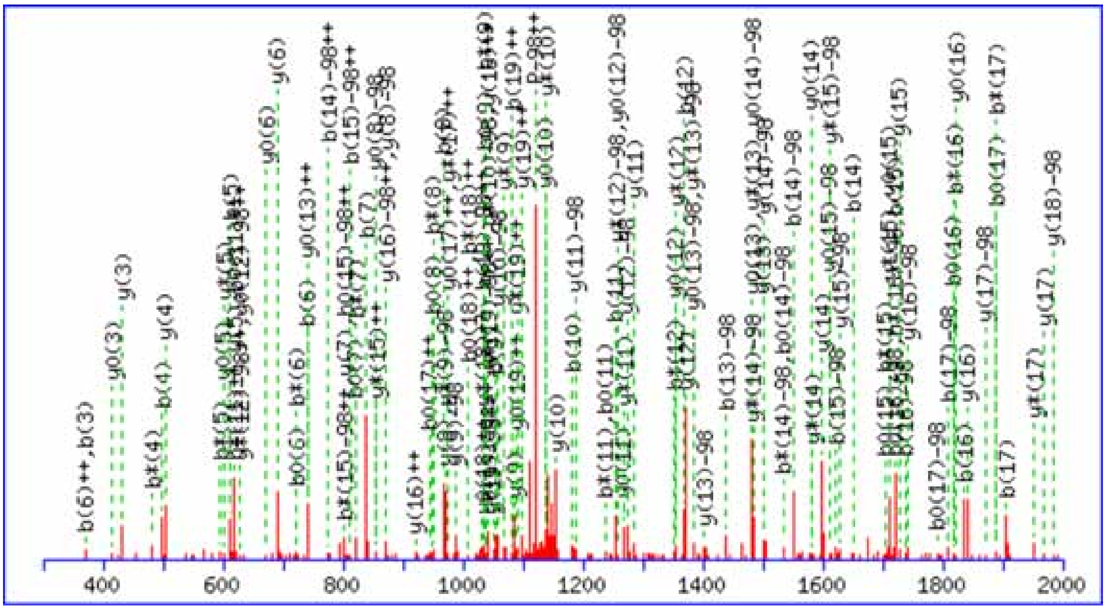
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10)-98
Matched y ions: y(2), y(3)-98, y(3), y(4), y(5)-98, y(6), y(7), y(7)-98++, y(7)-98, y(8), y(9), y(10)++, y(10)-98, y(10)-98++
Precursor origin neutral loss: +

Peptide No.618

NDLQLQVQSEADSLADAEER
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of NDLQLQVQSEADSLADAEER
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 6204: 2338.035336 from(1170.024944,2+)
Title: Elution from: 57.008 to 57.008 scan no 5431 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2338.0325
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 97 **Expect:** 1.4e-008

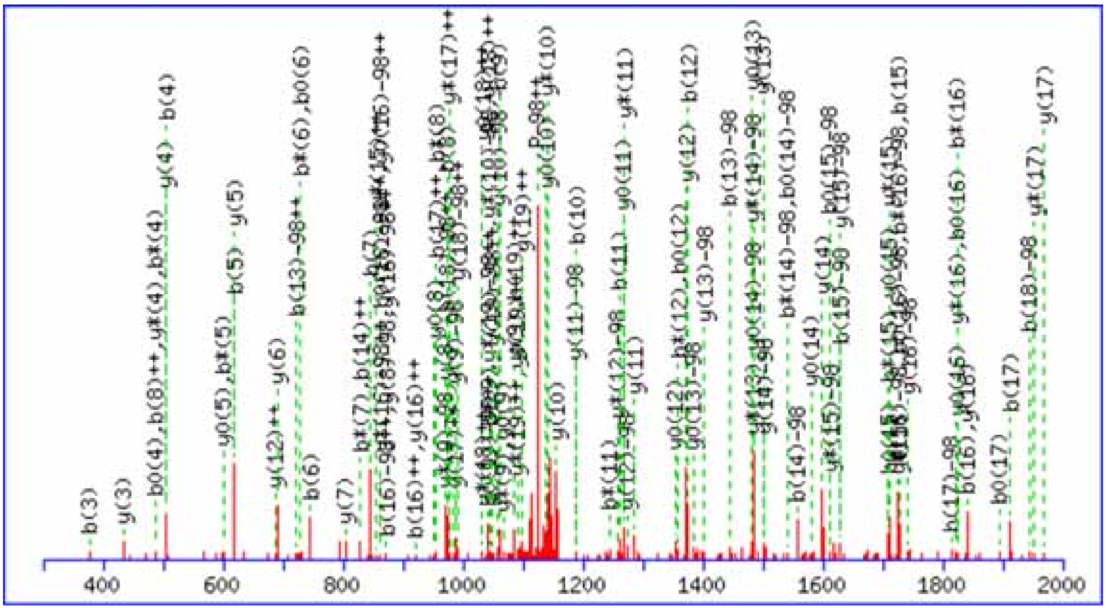
Matched b ions: b(3), b(4), b(5), b(6)++, b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13)-98, b(14)-98, b(14)-98++, b(14), b(15), b(15)-98, b(15)-98++, b(16), b(16)-98, b(17), b(17)-98, b(19)-98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(13)-98, y(13), y(14), y(14)-98, y(15)-98, y(15), y(16), y(16)-98++, y(16)++, y(16)-98, y(17), y(17)-98, y(18)++, y(18)-98, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.619

NDLQLQVQSEADSLADAEER
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of NDLQLQVQSEADSLADAEER
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 7737: 2344.065370 from(1173.039961,2+)
Title: Elution from: 57.036 to 57.036 scan no 5714 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2344.0643
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 Expect: 8.7e-009

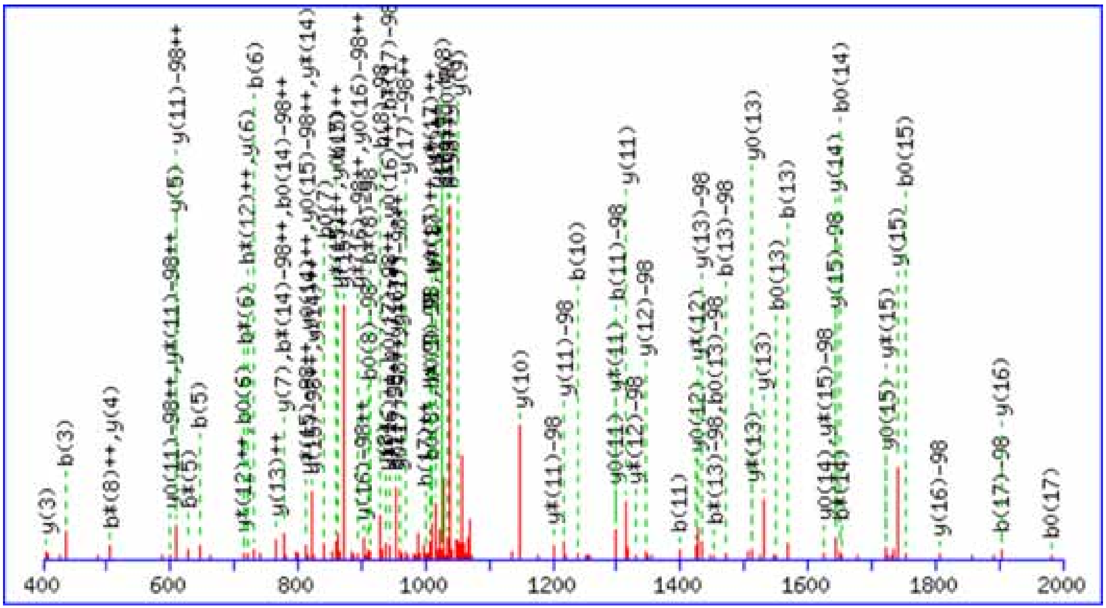
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(8)++, b(9), b(10), b(11), b(12), b(13)-98, b(13)-98++, b(14)-98, b(14)++, b(15), b(15)-98, b(16), b(16)-98++, b(16)++, b(17), b(17)-98, b(17)++, b(18)-98, b(18)-98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(12)++, y(13)-98, y(13), y(14), y(14)-98, y(15)-98, y(15), y(16), y(16)-98++, y(16)-98, y(16)++, y(17), y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.620

NEYPLSQSPNCGITTTEK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of NEYPLSQSPNCGITTTEK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 6388: 2173.960790 from(1087.987671,2+)
Title: Elution from: 41.508 to 41.508 scan no 3864 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2173.9602
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl (K)
Ions Score: 62 Expect: 3.5e-005

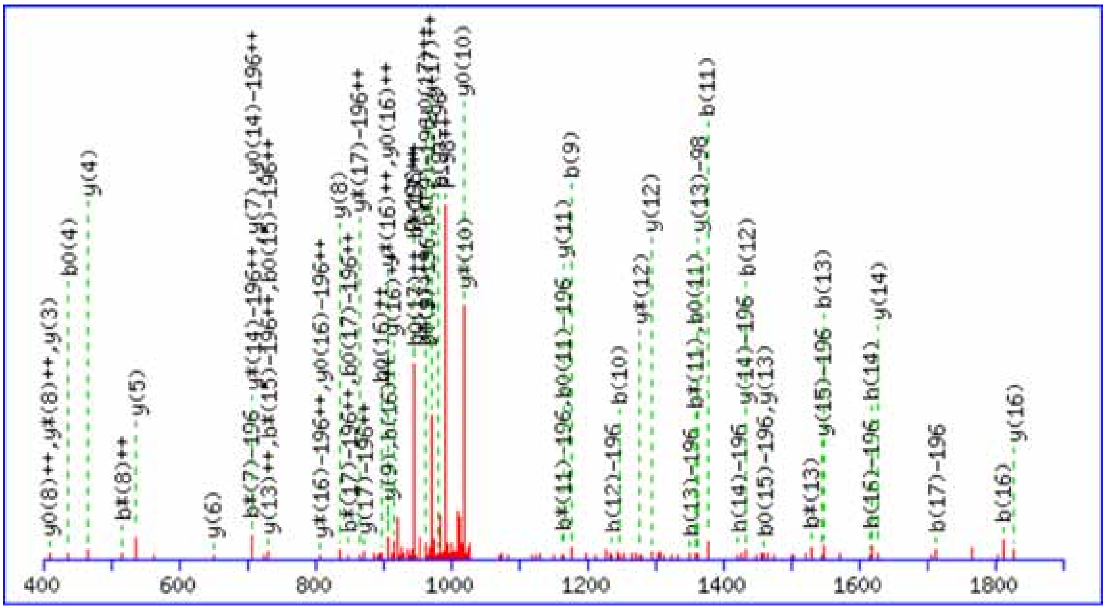
Matched b ions: b(3), b(5), b(6), b(7), b(8)-98, b(8), b(9)-98, b(10), b(11), b(11)-98, b(13), b(13)-98, b(17)-98++, b(17)-98, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(11)-98++, y(12)-98, y(13), y(13)++, y(13)-98, y(14)++, y(14), y(15)++, y(15)-98, y(15), y(15)-98++, y(16)++, y(16), y(16)-98, y(16)-98++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.621

NISLSSEEEEAEGLAGHPR
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of NISLSSEEEEAEGLAGHPR
Found in PARF_MOUSE, Putative GTP-binding protein Parf OS=Mus musculus GN=Parf PE=1 SV=2

Match to Query 4801: 2082.868414 from(1042.441483,2+)
Title: Elution from: 47.333 to 47.333 scan no 4275 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2082.8660
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 Expect: 4e-005

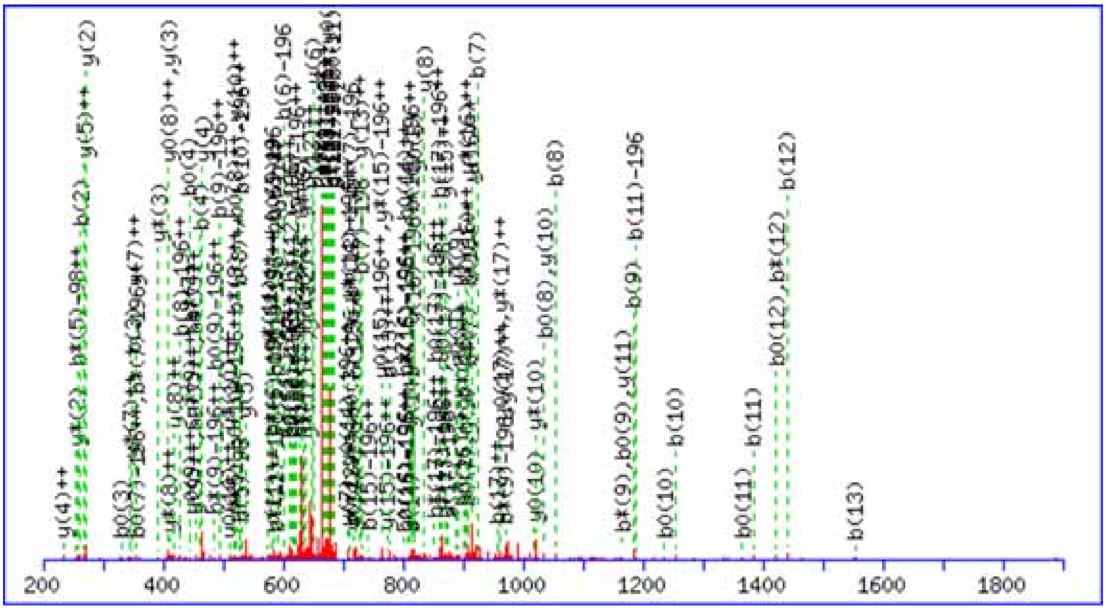
Matched b ions: b(8)-98, b(9), b(9)-196, b(10), b(11), b(11)-98, b(12), b(12)-196, b(13), b(13)-196, b(13)-98, b(14), b(14)-98, b(14)-196, b(16)++, b(16), b(16)-98, b(16)-196, b(17)-98, b(17)-196, b(17)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(13)++, y(13)-98, y(13), y(14)-196, y(14)-98, y(14), y(15)-196, y(16), y(16)-98++, y(16)++, y(17)-196++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.622

NISLSSEEEAEGLAGHPR
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of NISLSSEEEAEGLAGHPR
Found in PARF_MOUSE, Putative GTP-binding protein Parf OS=Mus musculus GN=Parf PE=1 SV=2

Match to Query 5367: 2088.898692 from(697.306840,3+)
Title: Elution from: 47.176 to 47.176 scan no 4388 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2088.8978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00054

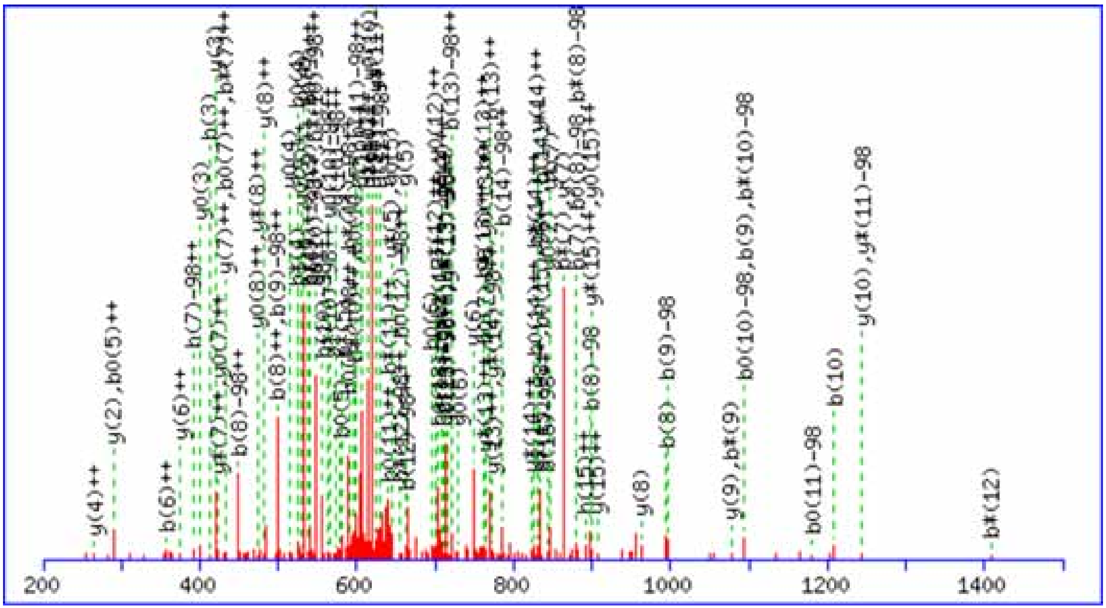
Matched b ions: b(2), b(3), b(4), b(5)-98, b(6)-98++, b(6)-196, b(7)-98++, b(7)-98, b(7)-196, b(7), b(8), b(8)-98++, b(8)-196++, b(8)++, b(8)-98, b(9), b(9)-98, b(9)-196++, b(9)-98++, b(9)++, b(10), b(10)++, b(10)-98, b(10)-196++, b(10)-98++, b(11), b(11)-98, b(11)-196, b(11)-98++, b(12), b(12)-98, b(12)-98++, b(12)-196++, b(12)++, b(13), b(13)++, b(13)-196++, b(13)-98++, b(14)++, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++, b(17)-98++, b(17)-196++, b(17)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5)++, y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(14)-196++, y(15)-98++, y(15)-196++, y(15)++, y(16)++, y(16)-98++, y(16)-196++, y(17)-98++, y(17)++, y(17)-196++
Precursor origin neutral loss: +

Peptide No.623

NKLEGDSDVDSELEDR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NKLEGDSDVDSELEDR
Found in MY18A_MOUSE, Myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2

Match to Query 5403: 1955.836491 from(652.952773,3+)
Title: Elution from: 38.090 to 38.090 scan no 3411 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1955.8361
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0027

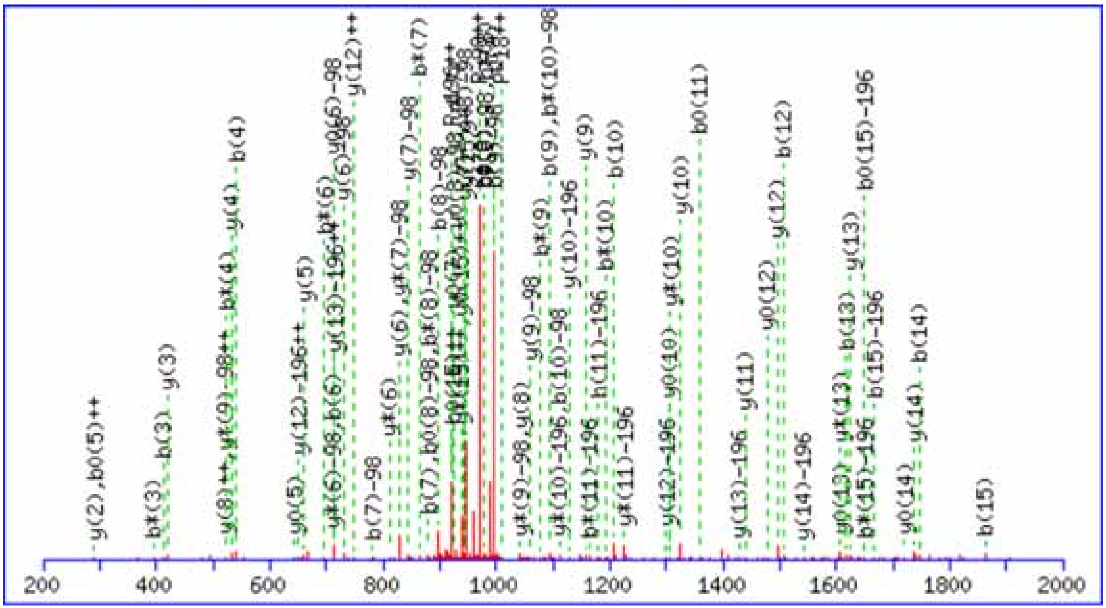
Matched b ions: b(3), b(4), b(6), b(6)++, b(7), b(7)-98++, b(8)-98++, b(8), b(8)++, b(8)-98, b(9), b(9)++, b(9)-98++, b(9)-98, b(10), b(10)++, b(10)-98++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)-98++, y(10)++, y(11)-98++, y(12)++, y(13)++, y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.624

NKLEGDSDVDSELEDR
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of NKLEGDSDVDSELEDR
Found in MY18A_MOUSE, Myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2

Match to Query 5757: 2035.803536 from(1018.909044,2+)
Title: Elution from: 39.915 to 39.915 scan no 3654 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2035.8024
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 **Expect:** 1.3e-005

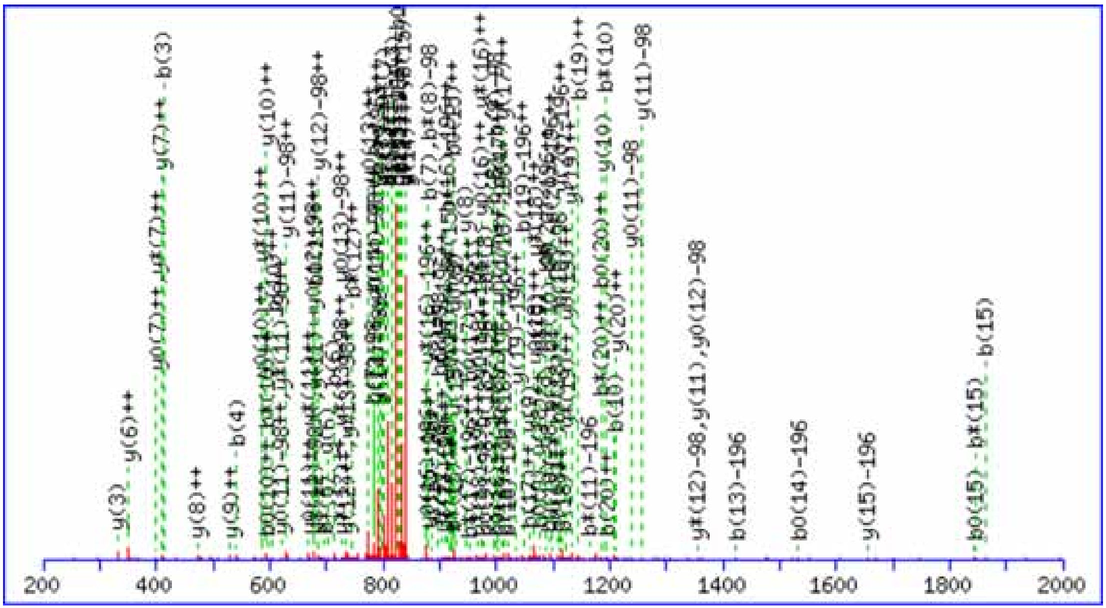
Matched b ions: b(3), b(4), b(6), b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11)-98, b(11)-196, b(12)-98, b(12), b(13), b(14), b(14)-98, b(15), b(15)-98, b(15)-196
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)++, y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(10)-196, y(11)-98, y(11), y(12)-98, y(12), y(12)-196, y(12)-196++, y(12)++, y(13)-196++, y(13), y(13)-196, y(13)-98, y(14), y(14)-98, y(14)-196, y(14)-98++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.625

NKLEGDSDVDSELEDRVDGVK
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of NKLEGDSDVDSELEDRVDGVK
Found in MY18A_MOUSE, Myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2

Match to Query 7773: 2562.115260 from(855.045696,3+)
Title: Elution from: 48.453 to 48.453 scan no 4725 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2562.1139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl (K)
Ions Score: 34 Expect: 0.027

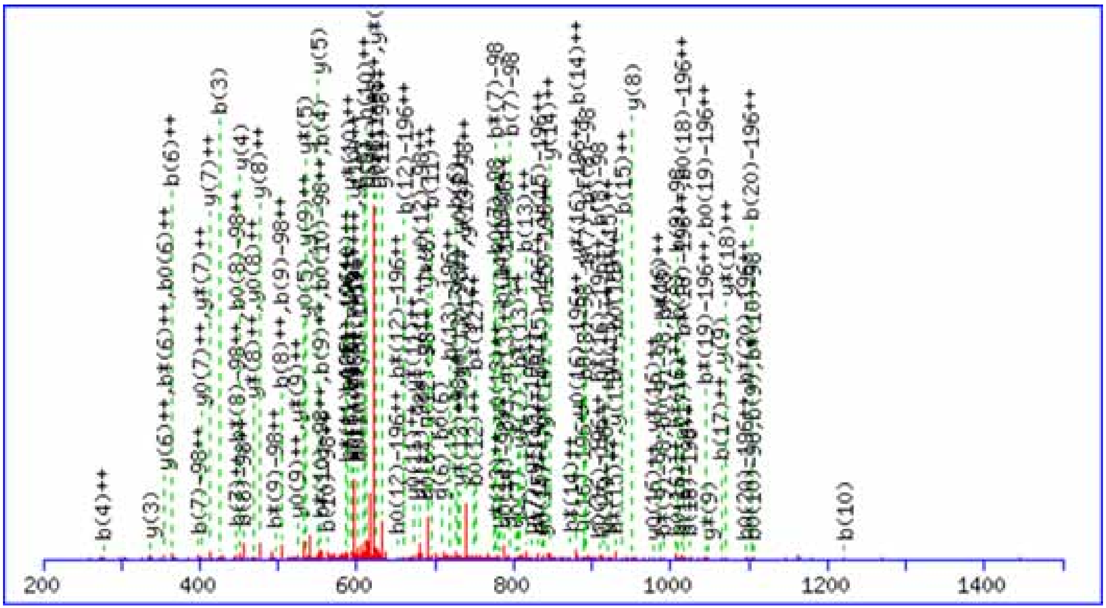
Matched b ions: b(3), b(4), b(6), b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)++, b(10)-98, b(11)-98, b(13)-196, b(13)-98, b(13)++, b(14)-98++, b(15), b(15)-196++, b(16)-196++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)-196++, b(18)++, b(19)++, b(19)-196++, b(19)-98++, b(20)-98++, b(20)++, b(20)-196++
Matched y ions: y(3), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)-98++, y(11)++, y(11)-98, y(11), y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(15)-196, y(15)-196++, y(16)-196++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(18)-98++, y(18)-196++, y(19)++, y(19)-196++, y(19)-98++, y(20)++, y(20)-196++
Precursor origin neutral loss: +

Peptide No.626

NKLEGDSDVDSELEDRVDGVK
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of NKLEGDSDVDSELEDRVDGVK
Found in MY18A_MOUSE, Myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2

Match to Query 8314: 2580.212664 from(646.060442,4+)
Title: Elution from: 48.333 to 48.333 scan no 4746 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2580.2094
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K2 : Dimethyl:2H(4)13C(2) (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 55 Expect: 0.00029

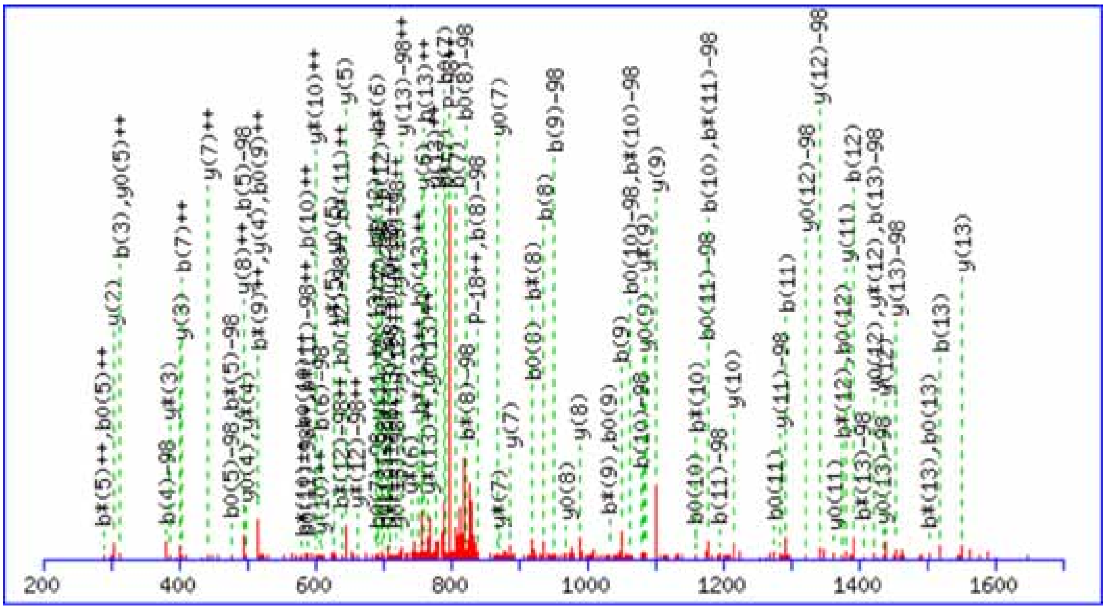
Matched b ions: b(3), b(4), b(4)++, b(5), b(6)++, b(6), b(7)-98++, b(7)++, b(7)-98, b(7), b(8)-98++, b(8), b(8)++, b(8)-98, b(9)-98++, b(9), b(9)++, b(9)-98, b(10), b(10)++, b(10)-98++, b(11)-196++, b(11)++, b(12)-98++, b(12)-196++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-98++, b(14)-196++, b(15)-196++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-196++, b(19)-98++, b(20)-196++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(15)-98++, y(15)++, y(15)-196++, y(16)++, y(16)-196++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++
Precursor origin neutral loss: +

Peptide No.627

NLGSINTELQDVQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of NLGSINTELQDVQR
Found in SC22B_MOUSE, Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=3

Match to Query 3145: 1693.804362 from(847.909457,2+)
Title: Elution from: 52.136 to 52.136 scan no 4991 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1693.8036
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 2.1e-006

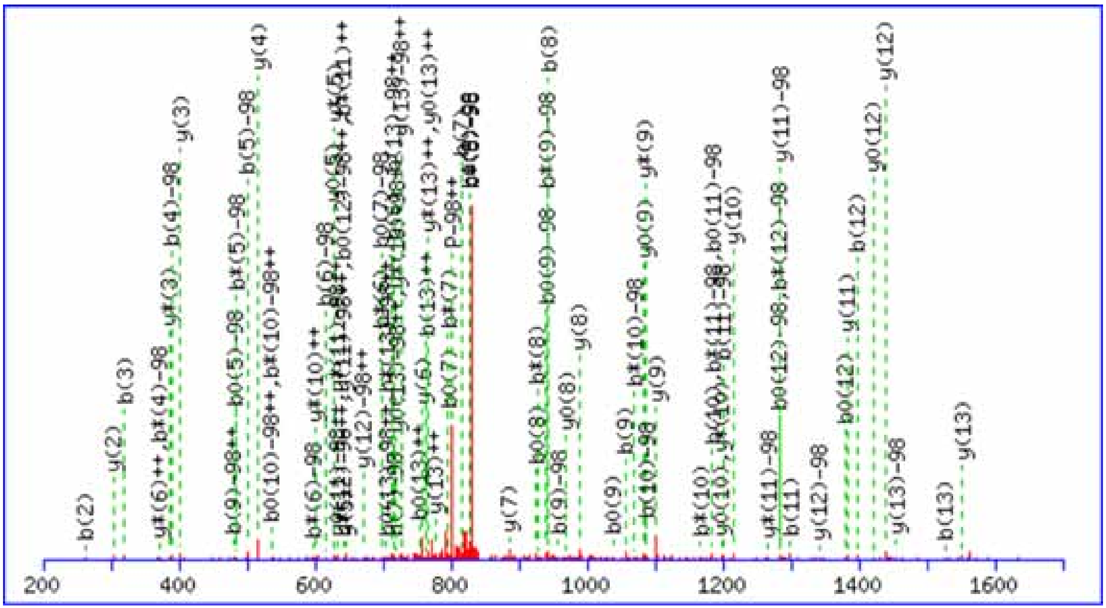
Matched b ions: b(3), b(4)-98, b(5)-98, b(6), b(6)-98, b(7)++, b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)++, b(10)-98, b(11), b(11)-98, b(12), b(12)++, b(13), b(13)-98, b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(10), y(10)++, y(11)-98, y(11), y(11)++, y(12)-98, y(12), y(12)++, y(13), y(13)-98, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.628

NLGSINTELQDVQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of NLGSINTELQDVQR
Found in SC22B_MOUSE, Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=3

Match to Query 2745: 1699.837510 from(850.926031,2+)
Title: Elution from: 52.115 to 52.115 scan no 4913 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1699.8354
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 88 **Expect:** 9e-008

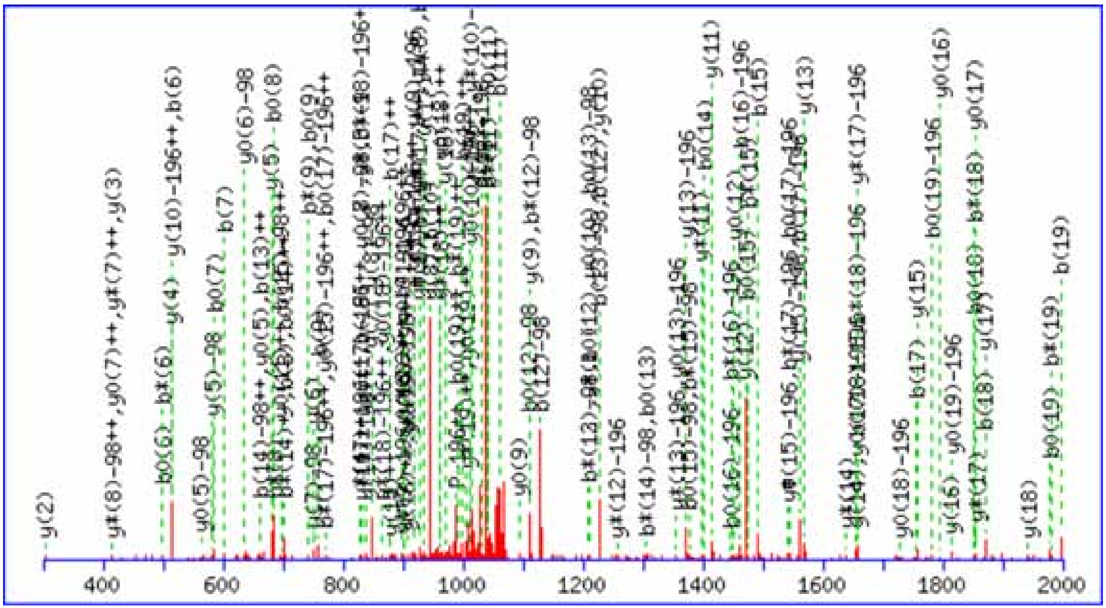
Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8), b(9), b(9)-98++, b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12), b(13), b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11), y(11)-98++, y(12), y(12)-98, y(12)-98++, y(13), y(13)-98++, y(13)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.629

NSAGGTSVGWDSPPASPLQR
Confirmed sites: @S:12,@S:16
Ambiguous sites:

MS/MS Fragmentation of NSAGGTSVGWDSPPASPLQR
Found in SNTA1_MOUSE, Alpha-1-syntrophin OS=Mus musculus GN=Snta1 PE=1 SV=1

Match to Query 5031: 2170.910288 from(1086.462420,2+)
Title: Elution from: 47.282 to 47.282 scan no 4268 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2170.9086
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 93 Expect: 2.3e-008

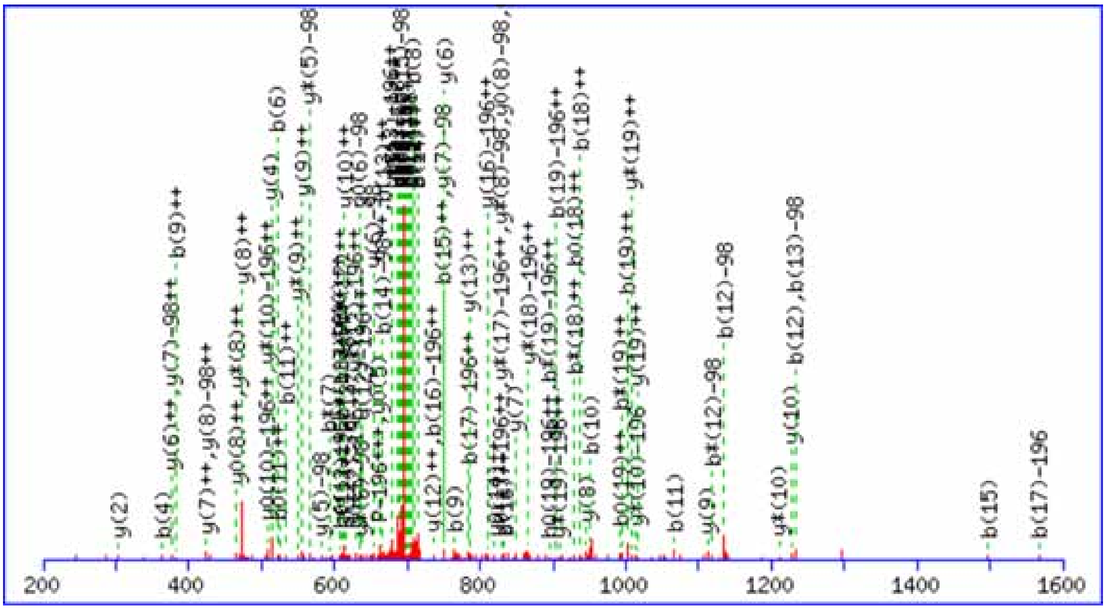
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(11), b(12)-98, b(12), b(13)-98, b(13)++, b(14)-98++, b(15), b(15)-98++, b(16)-98, b(16)-196, b(16)++, b(17)-196, b(17)-98, b(17), b(17)-98++, b(17)++, b(18)-98, b(18), b(18)-98++, b(19), b(19)-98, b(19)-196++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6), y(7), y(7)-98, y(8)-98, y(8), y(9), y(9)-98, y(9)-196, y(10)-98, y(10), y(10)-196++, y(10)-196, y(11), y(11)-98, y(11)-98++, y(12)-98, y(12), y(13)-196, y(13)-98, y(13), y(14), y(14)-98++, y(14)-98, y(14)++, y(15)-196, y(15), y(15)-98++, y(15)++, y(16), y(16)-98++, y(16)++, y(17), y(17)-98++, y(17)-196++, y(17)++, y(17)-98, y(18), y(18)-98++, y(18)++, y(19)++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.630

NSAGGTSVGWDSPPASPLQR
Confirmed sites: @S:12,@S:16
Ambiguous sites:

MS/MS Fragmentation of NSAGGTSVGWDSPPASPLQR
Found in SNTA1_MOUSE, Alpha-1-syntrophin OS=Mus musculus GN=Snta1 PE=1 SV=1

Match to Query 5119: 2176.942002 from(726.654610,3+)
Title: Elution from: 47.205 to 47.205 scan no 4242 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2176.9404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 0.00092

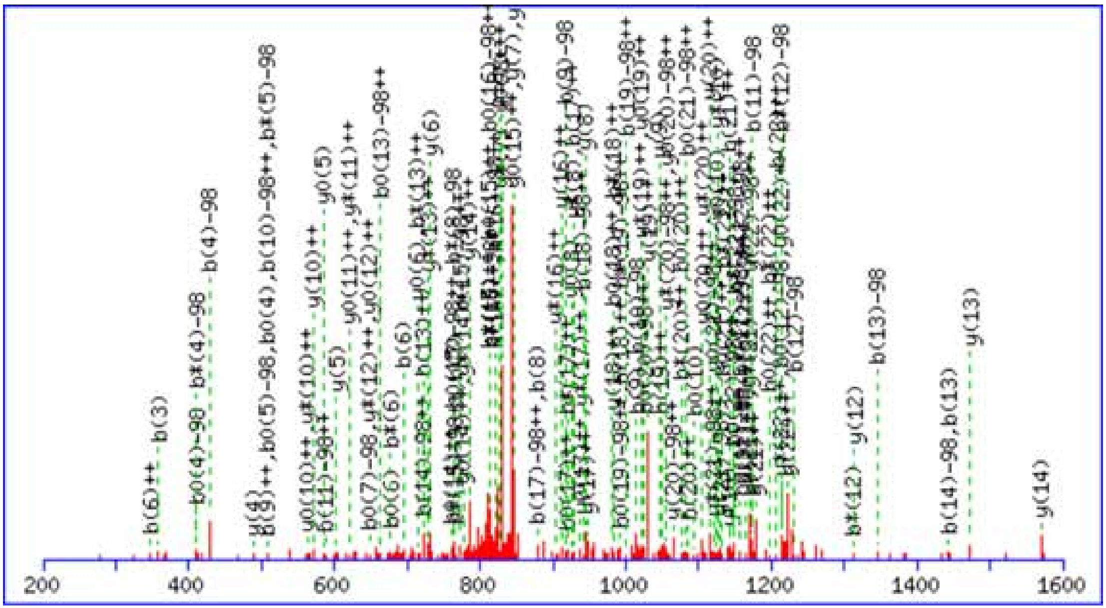
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(9)++, b(10), b(11), b(11)++, b(12)-98, b(12), b(12)++, b(13)-98, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15), b(15)++, b(15)-98++, b(16)-98, b(16)-98++, b(16)++, b(16)-196++, b(17)-196, b(17)-196++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(19)-196++
Matched y ions: y(2), y(4), y(5), y(5)-98, y(6)++, y(6)-98, y(6), y(7)++, y(7)-98, y(7)-98++, y(7), y(8)-98++, y(8)++, y(8), y(9)++, y(9)-98++, y(9), y(9)-98, y(10)++, y(10), y(10)-98++, y(10)-98, y(11)-196++, y(11)++, y(12)-196++, y(12)-98++, y(12)++, y(13)++, y(13)-196++, y(15)-98++, y(16)-196++, y(18)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.631

NSESPAAIHPCGNPTVIEDALEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of NSESPAAIHPCGNPTVIEDALEK
Found in LMOD2_MOUSE, Leiomodin-2 OS=Mus musculus GN=Lmod2 PE=1 SV=1

Match to Query 7829: 2584.189110 from(862.403646,3+)
Title: Elution from: 51.843 to 51.843 scan no 5126 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2584.1880
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K23 : Dimethyl (K)
Ions Score: 42 Expect: 0.0054

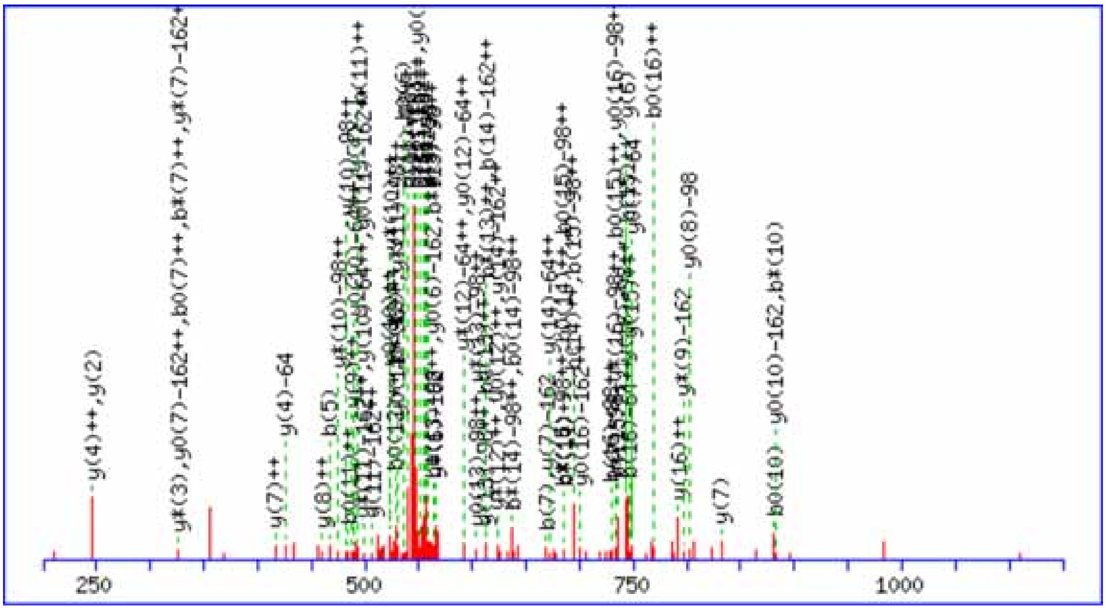
Matched b ions: b(3), b(4)-98, b(6)++, b(6), b(7), b(8), b(9), b(9)++, b(9)-98, b(10)-98, b(10)-98++, b(11)-98, b(11)-98++, b(12)-98, b(13)-98, b(13)++, b(13), b(14)-98, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(21)++, b(22)-98++, b(22)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(12), y(13), y(14), y(14)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(22)-98++
Precursor origin neutral loss: +

Peptide No.632

NSSSGSNSGSSSSMPAR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of NSSSGSNSGSSSSMPAR
Found in MKL2_MOUSE, MKL/myocardin-like protein 2 OS=Mus musculus GN=Mkl2 PE=1 SV=1

Match to Query 3217: 1728.678594 from(577.233474,3+)
Title: Elution from: 23.104 to 23.104 scan no 1247 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1728.6834
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 Expect: 0.034

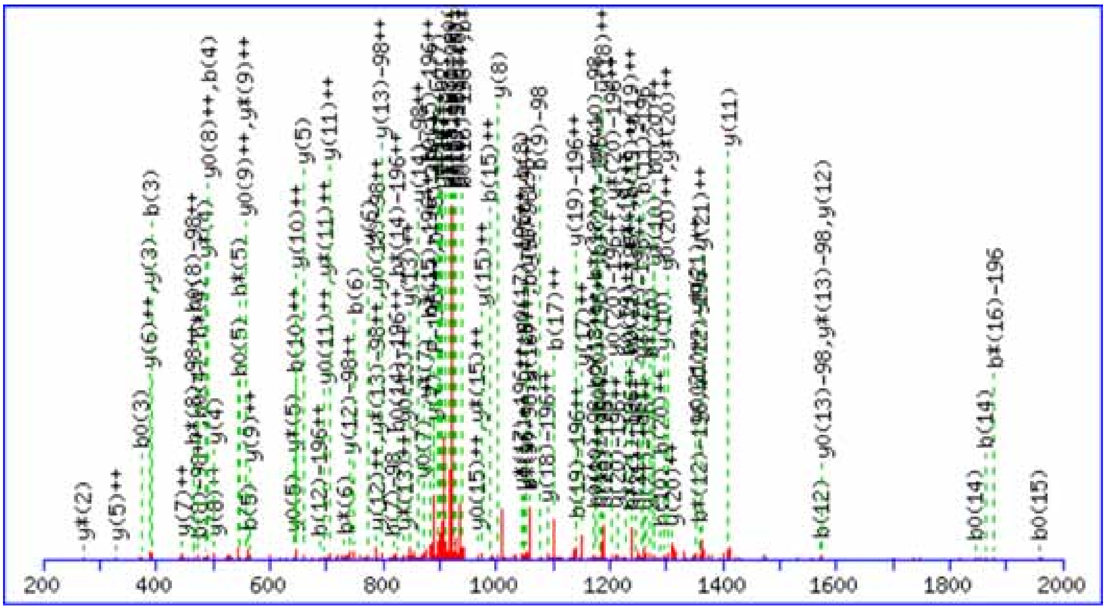
Matched b ions: b(5), b(6), b(7), b(11)++, b(14)++, b(15)-98++, b(15)++, b(16)-98++
Matched y ions: y(2), y(4)++, y(4), y(5)-98, y(6), y(7), y(7)++, y(7)-98, y(8)++, y(9)++, y(10)-98++, y(11)-98++, y(13)-98++, y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.633

NTFTAWSEEDSDYEIDDRDVNK
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of NTFTAWSEEDSDYEIDDRDVNK
Found in LARP1_MOUSE, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 7219: 2864.112351 from(955.711393,3+)
Title: Elution from: 54.230 to 54.230 scan no 5185 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2864.1103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K22 : Dimethyl (K)
Ions Score: 80 **Expect:** 3.9e-007

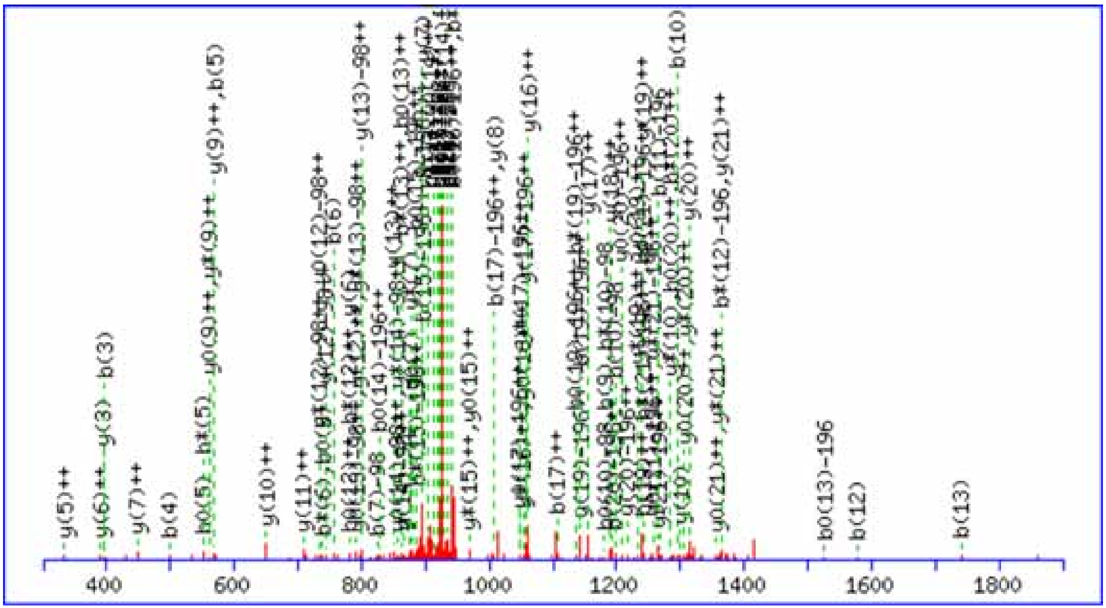
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(8), b(8)-98++, b(9)-98, b(10)++, b(10), b(11)-196, b(11)-98, b(12)-98, b(12), b(12)-196++, b(13)-98++, b(14), b(14)-98++, b(15)-98, b(15)-196++, b(15)-98++, b(15)++, b(17)++, b(17)-98++, b(18)++, b(19)-196++, b(19)-98++, b(19)++, b(20)-196++, b(20)-98++, b(20)++, b(21)-196++, b(21)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(10), y(11), y(11)++, y(12)++, y(12), y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(17)-196++, y(18)-98++, y(18)++, y(18)-196++, y(19)-98++, y(19)++, y(19)-196++, y(20)++, y(20)-98++, y(20)-196++, y(21)++, y(21)-98++, y(21)-196++
Precursor origin neutral loss: +

Peptide No.634

NTFTAWSEEDSDYEIDDRDVNK
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of NTFTAWSEEDSDYEIDDRDVNK
Found in LARP1_MOUSE, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 7398: 2876.172651 from(959.731493,3+)
Title: Elution from: 54.275 to 54.275 scan no 5205 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2876.1739
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K22 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 80 **Expect:** 5.3e-007

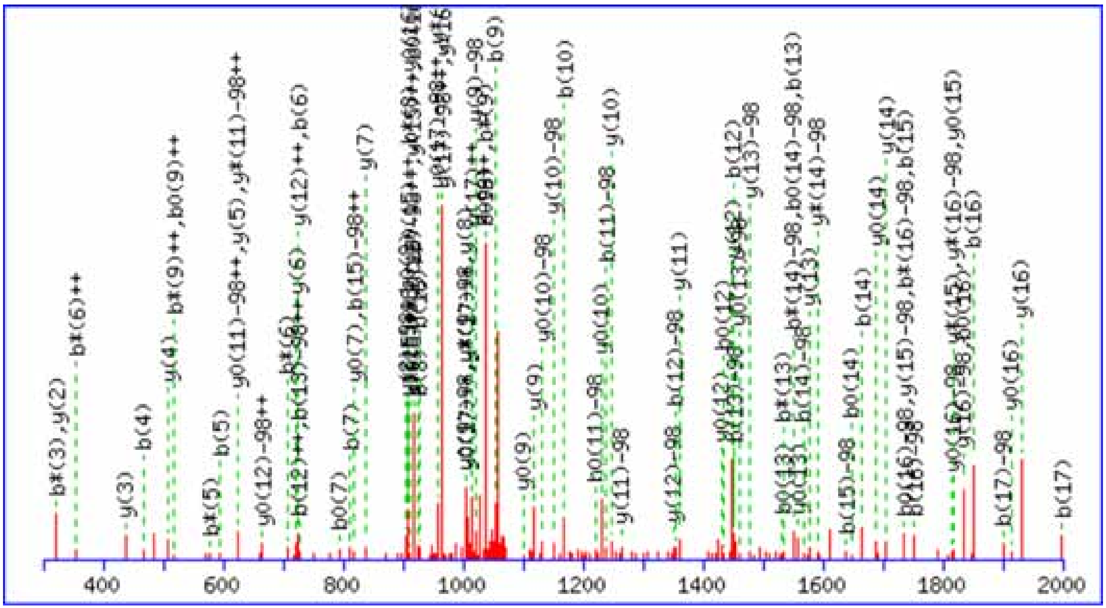
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(7), b(9), b(10)-98, b(10), b(11)-98, b(11)-196, b(12), b(13), b(13)-98++, b(14)++, b(14)-98++, b(15)-196++, b(15)-98++, b(17)-98++, b(17)++, b(17)-196++, b(18)-98++, b(19)++, b(19)-98++, b(19)-196++, b(20)-196++, b(20)-98++, b(21)-98++
Matched y ions: y(3), y(5)++, y(6)++, y(6), y(7)++, y(7), y(8), y(9)++, y(10)++, y(10), y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(19)-196++, y(20)++, y(20)-98++, y(20)-196++, y(21)++, y(21)-98++, y(21)-196++
Precursor origin neutral loss: +

Peptide No.635

NVPQEESLEDSDVDADFK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of NVPQEESLEDSDVDADFK
Found in IMA3_MOUSE, Importin subunit alpha-3 OS=Mus musculus GN=Kpna3 PE=1 SV=1

Match to Query 5622: 2171.915212 from(1086.964882,2+)
Title: Elution from: 48.843 to 48.843 scan no 4552 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2171.9147
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl (K)
Ions Score: 94 Expect: 1.8e-008

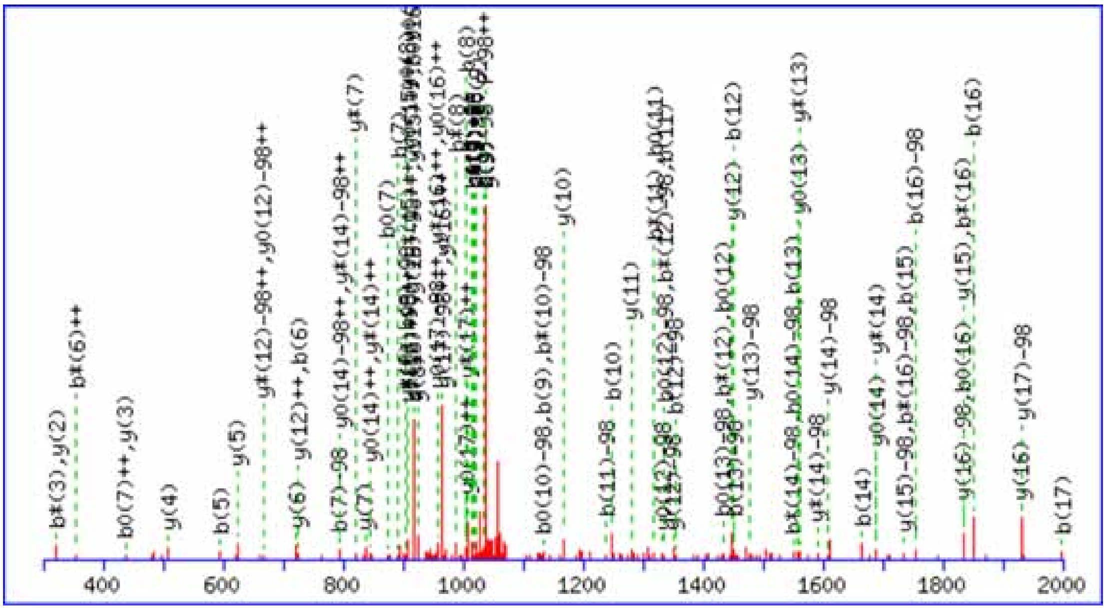
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11)-98, b(12), b(12)-98, b(12)++, b(13), b(13)-98++, b(13)-98, b(14), b(14)-98, b(15), b(15)-98, b(15)-98++, b(16), b(16)-98, b(16)++, b(17), b(17)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12)++, y(12), y(12)-98, y(13), y(13)-98, y(14), y(15)++, y(15)-98, y(16)-98++, y(16)++, y(16), y(16)-98, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.636

NVPQEESLEDSDVDADFK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NVPQEESLEDSDVDADFK
Found in IMA3_MOUSE, Importin subunit alpha-3 OS=Mus musculus GN=Kpna3 PE=1 SV=1

Match to Query 5415: 2171.915450 from(1086.965001,2+)
Title: Elution from: 49.343 to 49.343 scan no 4597 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2171.9147
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl (K)
Ions Score: 88 Expect: 7.1e-008

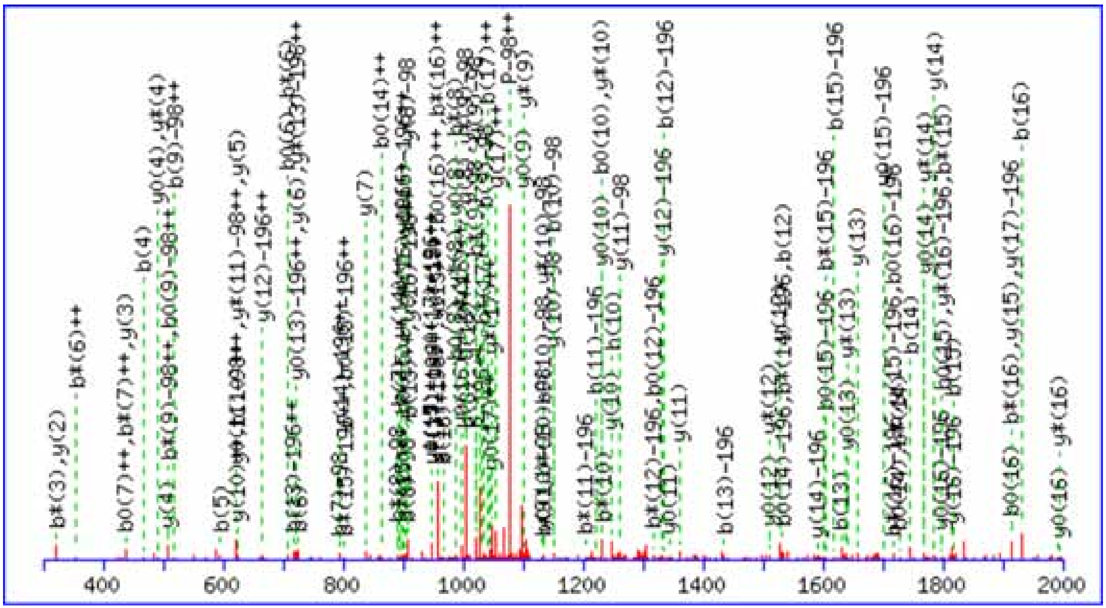
Matched b ions: b(5), b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(14), b(15), b(16)-98, b(16), b(17)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(12), y(12)++, y(13)-98, y(14)-98, y(15)++, y(15)-98, y(15), y(16)-98++, y(16)++, y(16), y(16)-98, y(17)-98++, y(17)-98, y(17)++
Precursor origin neutral loss: +

Peptide No.637

NVPQEESLEDSDVDADFK
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of NVPQEESLEDSDVDADFK
Found in IMA3_MOUSE, Importin subunit alpha-3 OS=Mus musculus GN=Kpna3 PE=1 SV=1

Match to Query 7504: 2251.882466 from(1126.948509,2+)
Title: Elution from: 51.668 to 51.668 scan no 5158 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2251.8811
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl (K)
Ions Score: 65 Expect: 1.1e-005

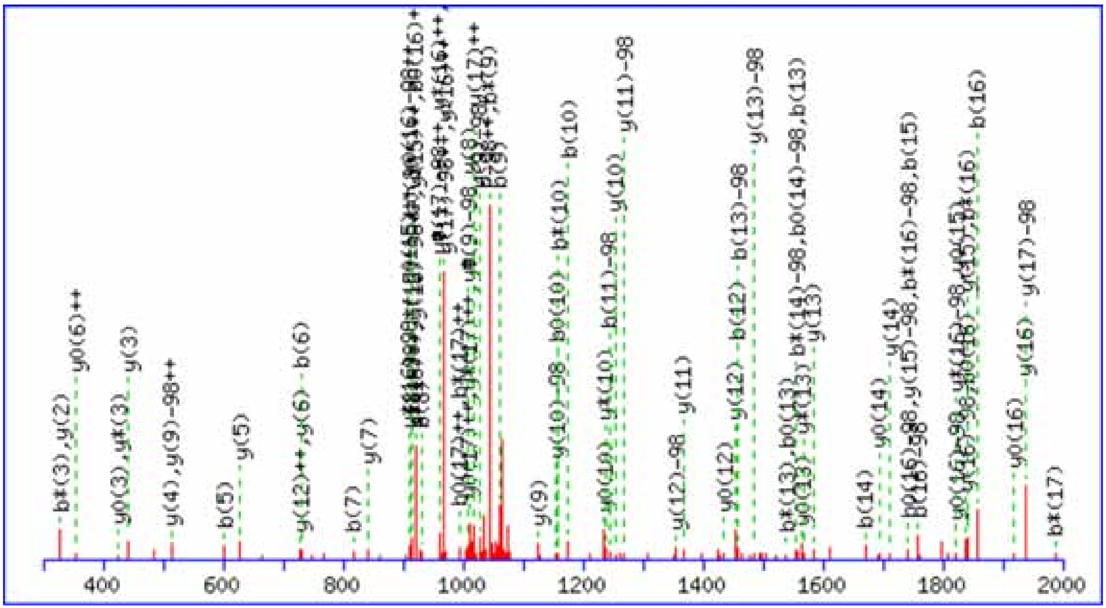
Matched b ions: b(4), b(5), b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98++, b(9)-98, b(10), b(10)-98, b(10)++, b(11)-196, b(11)-98, b(12)-98, b(12), b(12)-98++, b(12)-196, b(13), b(13)-98, b(13)-196++, b(13)-196, b(14), b(14)-98, b(15)++, b(15)-98, b(15), b(15)-196, b(16), b(16)-98, b(16)++, b(17)-98, b(17)-98++, b(17)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9)-98, y(10)-98, y(10)++, y(10), y(11), y(11)-98, y(12)-98, y(12), y(12)-196++, y(12)-196, y(13), y(13)-98, y(14)-196++, y(14)-98++, y(14), y(14)++, y(14)-196, y(14)-98, y(15)-98++, y(15)++, y(15), y(15)-196, y(15)-98, y(16)++, y(16)-98, y(16)-196++, y(16)-98++, y(16)-196, y(17)-98++, y(17)-196++, y(17)-196, y(17)++
Precursor origin neutral loss: +

Peptide No.638

NVPQEESLEDSDVDADFK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of NVPQEESLEDSDVDADFK
Found in IMA3_MOUSE, Importin subunit alpha-3 OS=Mus musculus GN=Kpna3 PE=1 SV=1

Match to Query 5181: 2183.978792 from(1092.996672,2+)
Title: Elution from: 48.777 to 48.777 scan no 4418 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2183.9784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 94 Expect: 2.5e-008

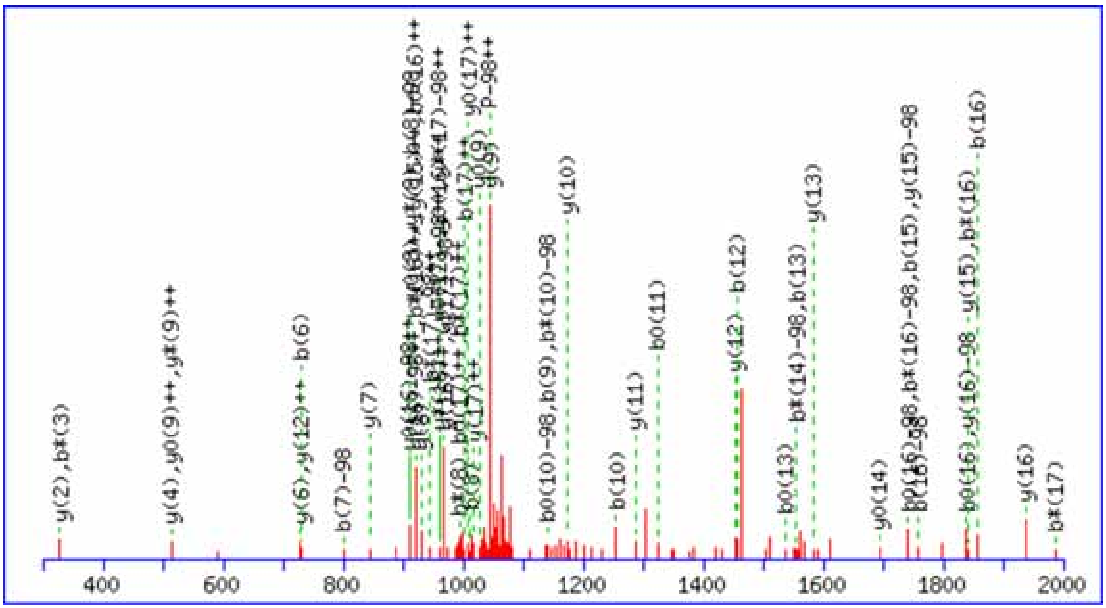
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(11)-98, b(12), b(13), b(13)-98, b(14), b(15), b(16)-98, b(16)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98++, y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)-98, y(12)-98, y(12), y(12)++, y(13), y(13)-98, y(14), y(15)++, y(15), y(15)-98, y(16)-98++, y(16)++, y(16), y(16)-98, y(17)-98++, y(17)-98, y(17)++
Precursor origin neutral loss: +

Peptide No.639

NVPQEESLEDSDVDADFK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of NVPQEESLEDSDVDADFK
Found in IMA3_MOUSE, Importin subunit alpha-3 OS=Mus musculus GN=Kpna3 PE=1 SV=1

Match to Query 5182: 2183.979986 from(1092.997269,2+)
Title: Elution from: 49.320 to 49.320 scan no 4474 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2183.9784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 48 **Expect:** 0.001

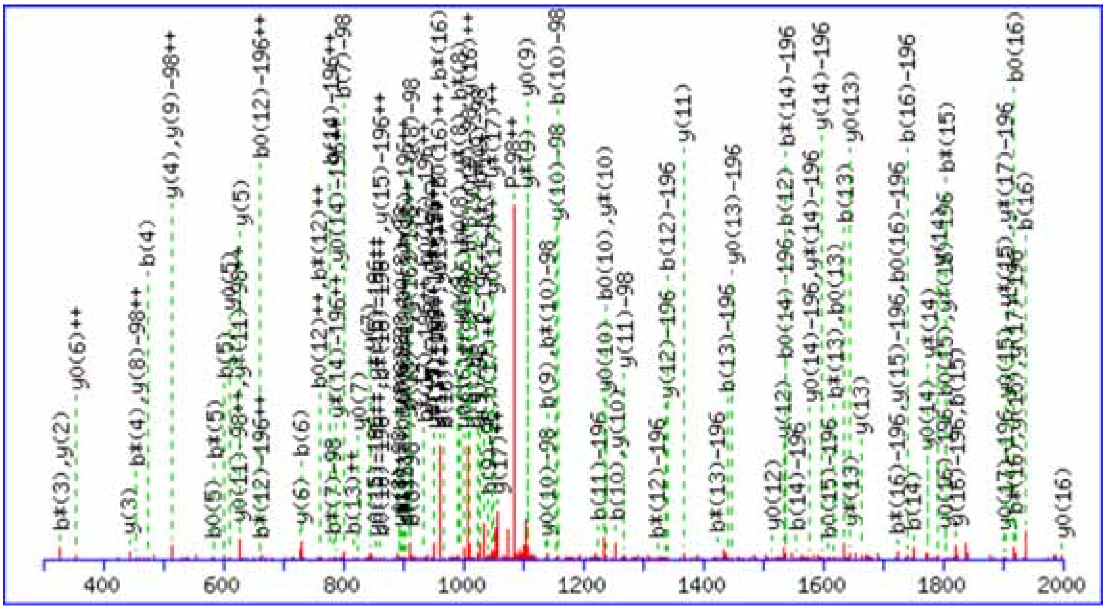
Matched b ions: b(6), b(7)-98, b(8)-98, b(8), b(9), b(10), b(12), b(13), b(15), b(16), b(16)-98, b(17)++
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13), y(15)++, y(15)-98, y(15), y(16)-98++, y(16)++, y(16)-98, y(16), y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.640

NVPQEESLEDSDVDADFK
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of NVPQEESLEDSDVDADFK
Found in IMA3_MOUSE, Importin subunit alpha-3 OS=Mus musculus GN=Kpna3 PE=1 SV=1

Match to Query 5499: 2263.946658 from(1132.980605,2+)
Title: Elution from: 51.908 to 51.908 scan no 4821 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2263.9447
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 61 Expect: 3.2e-005

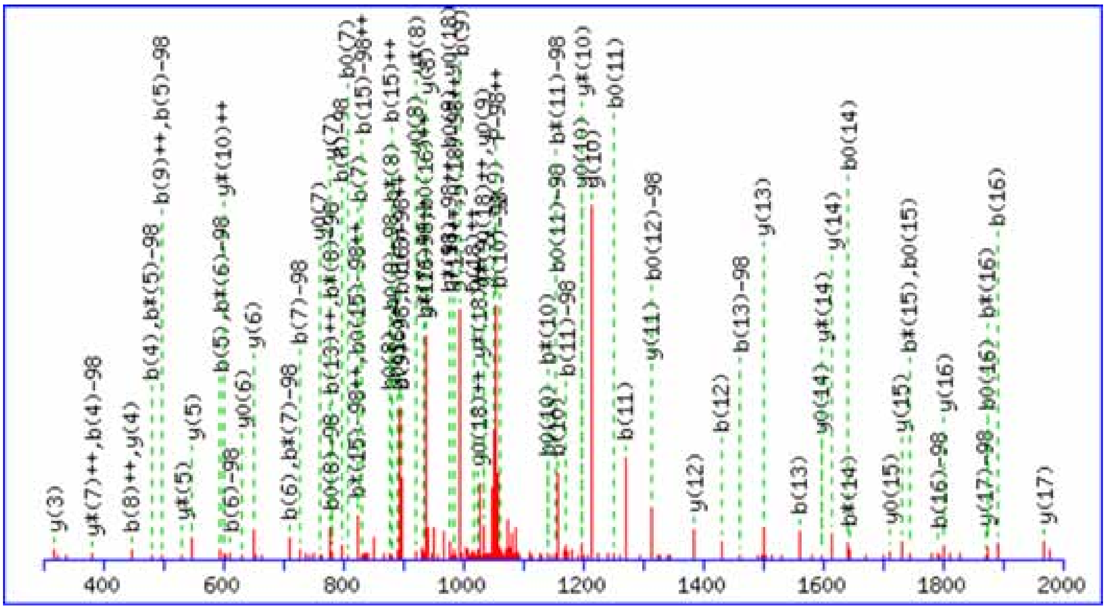
Matched b ions: b(4), b(5), b(6), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11)-98++, b(11)-196, b(11)-98, b(12)-98, b(12), b(12)-196, b(13), b(13)-98, b(13)++, b(13)-196, b(14), b(14)-98, b(14)-196++, b(14)-196, b(15), b(15)++, b(15)-98, b(15)-98++, b(16)-98, b(16), b(16)-196, b(16)-98++, b(16)++, b(17)-98, b(17)-98++, b(17)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(8)-98++, y(9)-98++, y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(12)-98, y(12), y(12)-196, y(13), y(13)-98, y(13)-98++, y(14)-98++, y(14)++, y(14)-98, y(14), y(14)-196, y(15)++, y(15)-98, y(15)-98++, y(15)-196, y(15), y(15)-196++, y(16)-98++, y(16)-196, y(16)-196++, y(16)++, y(16)-98, y(17)-196++, y(17)-98++, y(17)++, y(17)-196
Precursor origin neutral loss: +

Peptide No.641

NVSADDDAVYICETTEGSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NVSADDDAVYICETTEGSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6015: 2208.890180 from(1105.452366,2+)
Title: Elution from: 48.014 to 48.014 scan no 4513 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2208.8882
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 148 Expect: 6.3e-014

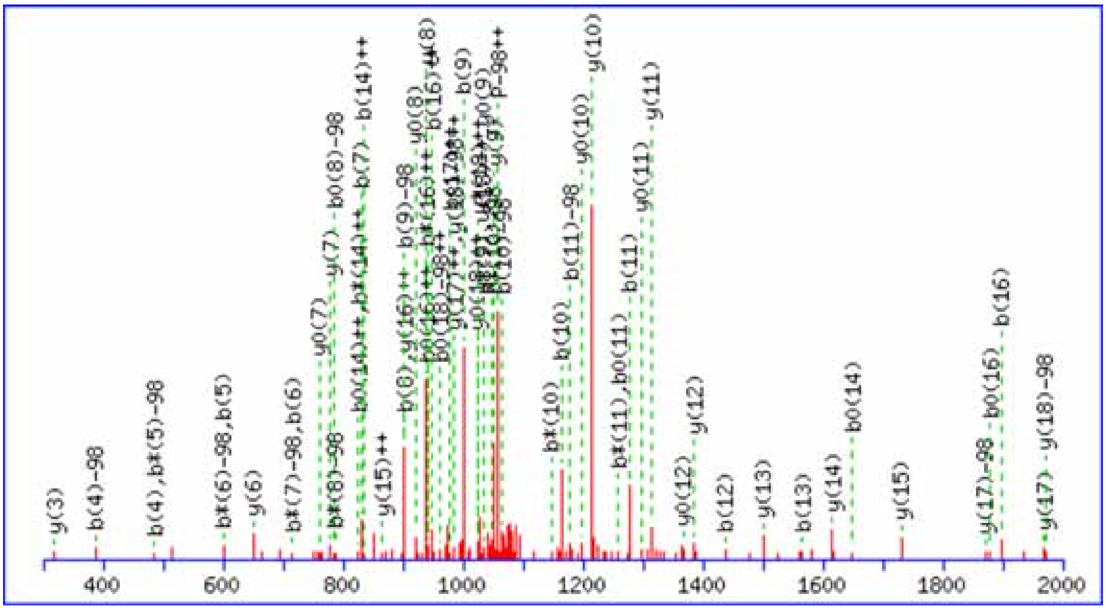
Matched b ions: b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8)++, b(8), b(8)-98, b(9), b(9)-98, b(9)++, b(10), b(10)-98, b(11), b(11)-98, b(12), b(13), b(13)++, b(13)-98, b(15)-98++, b(15)++, b(16), b(16)-98++, b(16)-98, b(18)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(17)-98, y(17)-98++, y(17)++, y(18)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.642

NVSADDDAVYICETTEGSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of NVSADDDAVYICETTEGSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 5314: 2214.920332 from(1108.467442,2+)
Title: Elution from: 47.943 to 47.943 scan no 4318 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2214.9200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 80 Expect: 4.6e-007

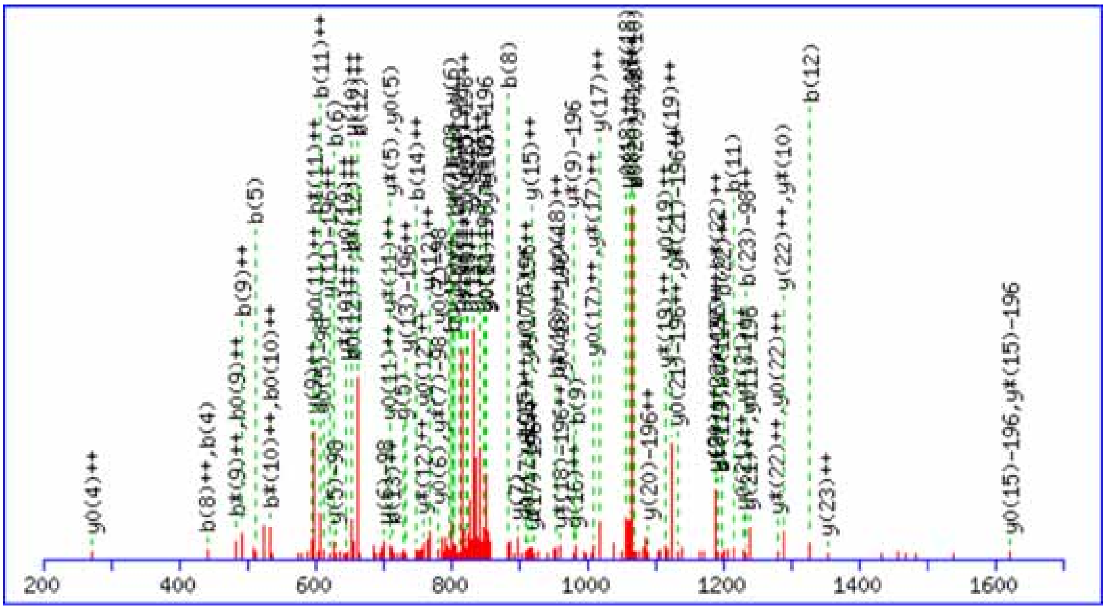
Matched b ions: b(4)-98, b(4), b(5), b(6), b(7), b(8), b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12), b(13), b(14)++, b(16), b(16)++, b(17)++
Matched y ions: y(3), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(15)++, y(16)++, y(17), y(17)-98, y(17)++, y(18)-98, y(18)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.643

QADVADQQTTELPAENGETENQSPASEEEK
Confirmed sites: @S:23,@S:26
Ambiguous sites:

MS/MS Fragmentation of QADVADQQTTELPAENGETENQSPASEEEK
Found in HMGN1_MOUSE, Non-histone chromosomal protein HMG-14 OS=Mus musculus GN=Hmgn1 PE=1 SV=2

Match to Query 8781: 3460.408528 from(866.109408,4+)
Title: Elution from: 40.463 to 40.463 scan no 3728 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3460.4079
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S23 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S26 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K30 : Dimethyl (K)
Ions Score: 64 **Expect:** 2.7e-005

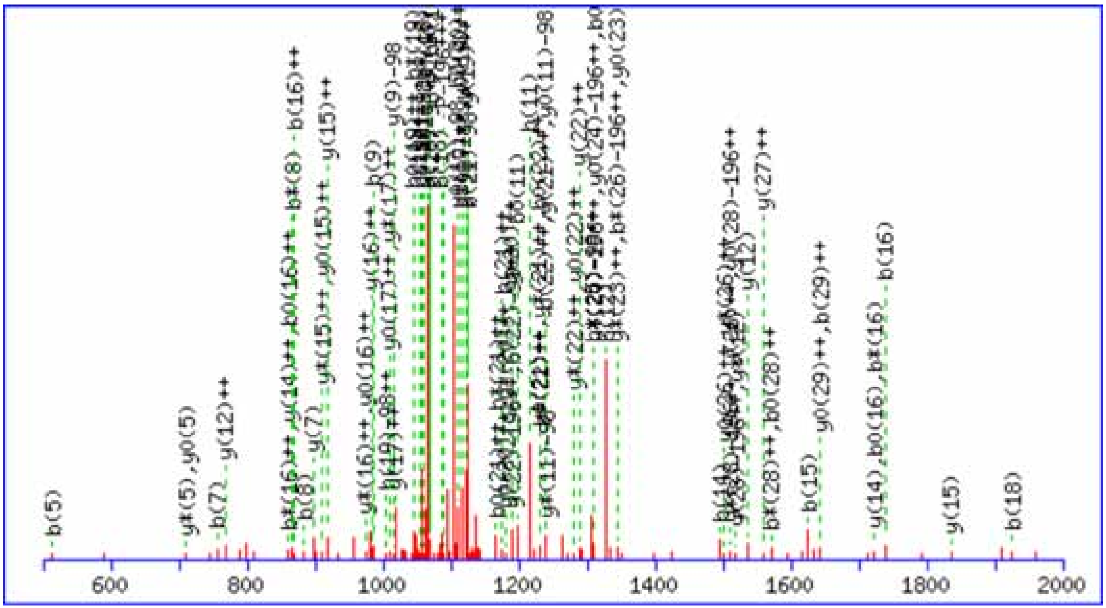
Matched b ions: b(4), b(5), b(6), b(8)++, b(8), b(9)++, b(9), b(11)++, b(11), b(12)++, b(12), b(13)++, b(14)++, b(15)++, b(22)++, b(23)-98++
Matched y ions: y(5), y(5)-98, y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98++, y(9)++, y(9), y(10)++, y(10)-98++, y(11)-196, y(11)-196++, y(12)++, y(13)++, y(13)-196++, y(14)-98++, y(15)++, y(15)-196++, y(16)++, y(17)++, y(17)-196++, y(18)++, y(18)-98++, y(19)++, y(20)++, y(20)-98++, y(20)-196++, y(21)++, y(21)-98++, y(22)++, y(22)-196++, y(22)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.644

QADVADQQTTELPAENGETENQSPASEEEK
Confirmed sites: @T:19,@S:26
Ambiguous sites:

MS/MS Fragmentation of QADVADQQTTELPAENGETENQSPASEEEK
Found in HMGN1_MOUSE, Non-histone chromosomal protein HMG-14 OS=Mus musculus GN=Hmgn1 PE=1 SV=2

Match to Query 8782: 3460.409067 from(1154.476965,3+)
Title: Elution from: 40.278 to 40.278 scan no 3703 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3460.4079
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S26 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K30 : Dimethyl (K)
Ions Score: 55 **Expect:** 0.00023

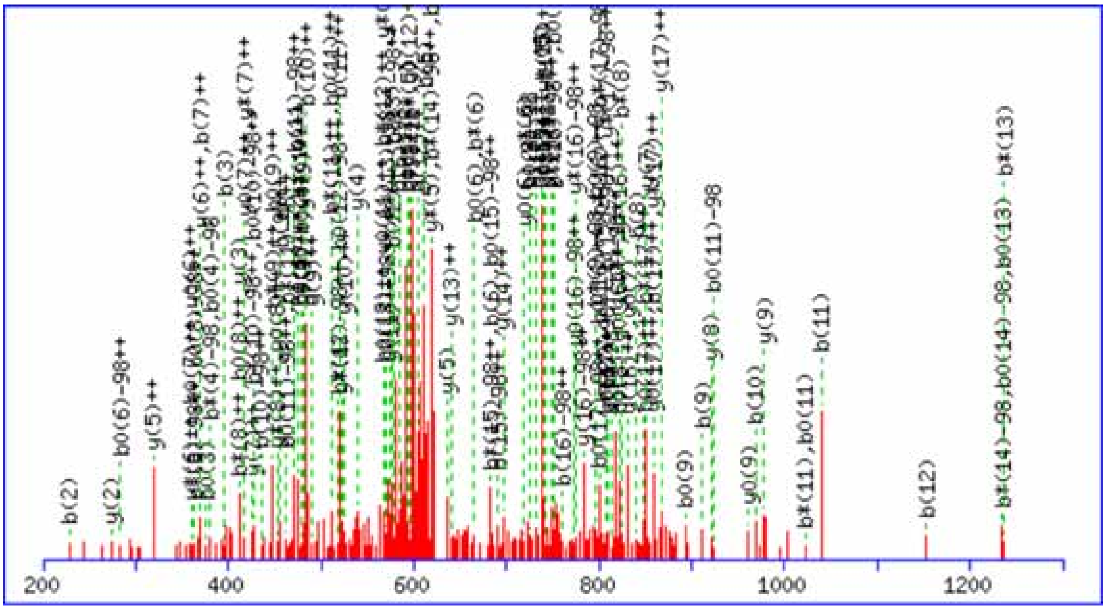
Matched b ions: b(5), b(7), b(8), b(9), b(10), b(11), b(12), b(14), b(15), b(16), b(16)++, b(18), b(19)-98++, b(19)++, b(20)-98++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(29)++, b(29)-98++
Matched y ions: y(7), y(9)-98, y(12), y(12)++, y(14), y(14)++, y(15)-98, y(15), y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(22)-98++, y(22)++, y(22)-196++, y(26)++, y(27)-98++, y(27)++, y(28)-196++
Precursor origin neutral loss: +

Peptide No.645

QASTDAGTAGALTPQHVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QASTDAGTAGALTPQHVR
Found in YAP1_MOUSE, Yorkie homolog OS=Mus musculus GN=Yap1 PE=1 SV=2

Match to Query 3807: 1887.884565 from(630.302131,3+)
Title: Elution from: 30.137 to 30.137 scan no 2028 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1887.8840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.0058

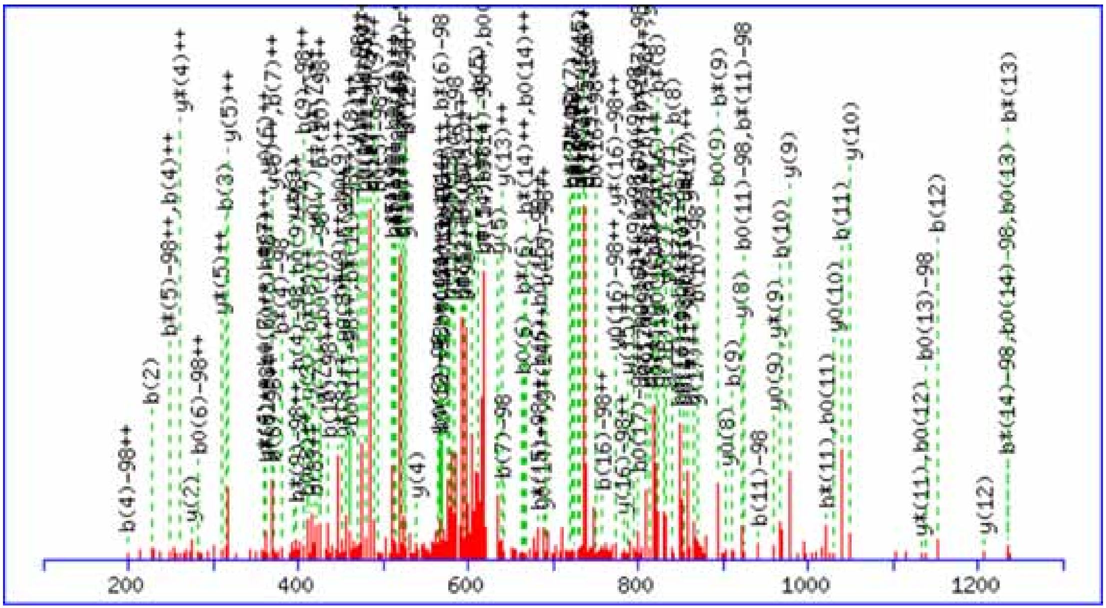
Matched b ions: b(2), b(3), b(5), b(6), b(6)-98, b(7)++, b(7), b(8)-98, b(8), b(9), b(9)++, b(9)-98, b(10)++, b(10), b(10)-98++, b(11), b(11)++, b(11)-98++, b(12), b(12)++, b(13)-98++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(9), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.646

QASTDAGTAGALTPQHVR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of QASTDAGTAGALTPQHVR
Found in YAP1_MOUSE, Yorkie homolog OS=Mus musculus GN=Yap1 PE=1 SV=2

Match to Query 4987: 1887.884190 from(630.302006,3+)
Title: Elution from: 30.334 to 30.334 scan no 2350 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1887.8840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 0.00083

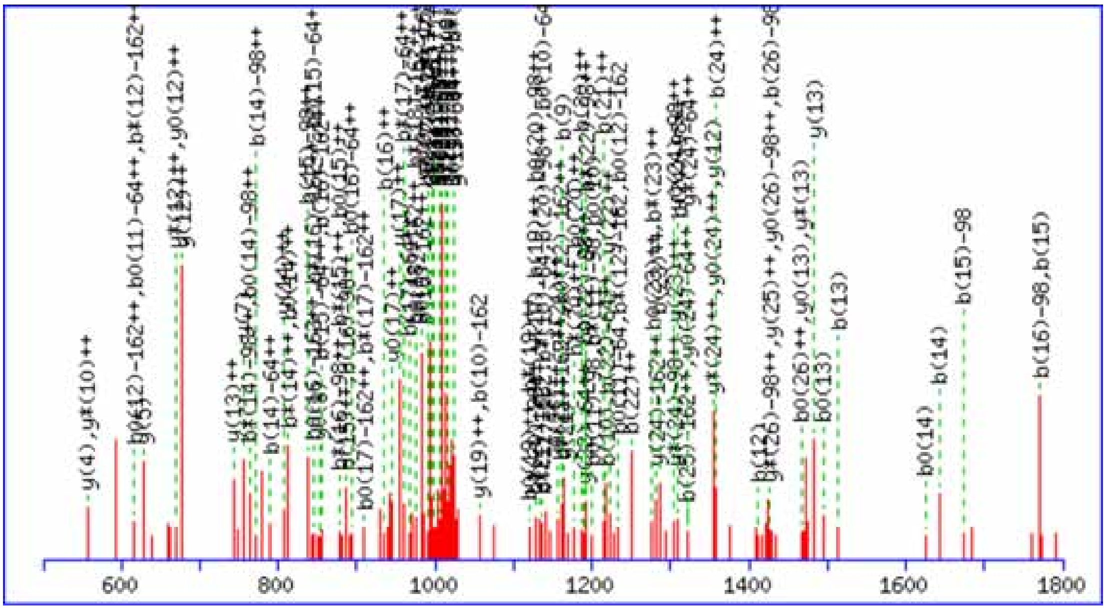
Matched b ions: b(2), b(3), b(4)-98, b(4)++, b(4)-98++, b(5), b(5)-98, b(6)-98, b(6), b(7)++, b(7), b(7)-98, b(8)++, b(8)-98++, b(8), b(9)++, b(9), b(9)-98++, b(9)-98, b(10)++, b(10), b(10)-98++, b(10)-98, b(11)++, b(11), b(11)-98, b(11)-98++, b(12), b(12)++, b(12)-98++, b(13)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(12), y(12)++, y(13)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.647

QDEDSDSEMGPPTEEPEEEDGAAFSFK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of QDEDSDSEMGPPTEEPEEEDGAAFSFK
Found in MXRA7_MOUSE, Matrix-remodeling-associated protein 7 OS=Mus musculus GN=Mxra7 PE=1 SV=2

Match to Query 8637: 3124.193745 from(1042.405191,3+)
Title: Elution from: 52.514 to 52.514 scan no 5202 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3124.1904
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K27 : Dimethyl (K)
Ions Score: 31 Expect: 0.037

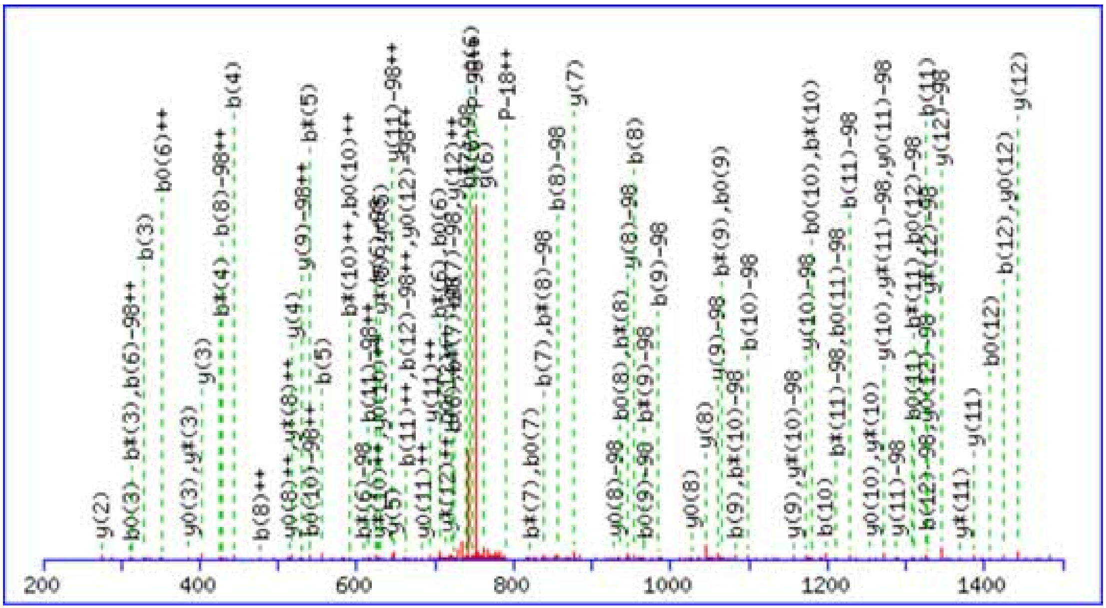
Matched b ions: b(8), b(9), b(10), b(12), b(13), b(14), b(14)-98++, b(15), b(15)-98++, b(15)++, b(15)-98, b(16)-98, b(16)-98++, b(16)++, b(17)++, b(18)-98++, b(19)++, b(20)-98++, b(20)++, b(21)++, b(22)++, b(23)++, b(24)++, b(24)-98++, b(26)-98++
Matched y ions: y(4), y(5), y(7), y(9), y(10), y(12)++, y(12), y(13), y(13)++, y(14)++, y(17)++, y(18)++, y(19)++, y(21)++, y(22)++, y(23)++, y(25)++
Precursor origin neutral loss: +

Peptide No.648

QGDNISDDEDEVR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of QGDNISDDEDEVR
Found in STX4_MOUSE, Syntaxin-4 OS=Mus musculus GN=Stx4 PE=1 SV=1

Match to Query 3092: 1598.610406 from(800.312479,2+)
Title: Elution from: 31.658 to 31.658 scan no 2533 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1598.6097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 Expect: 9.2e-007

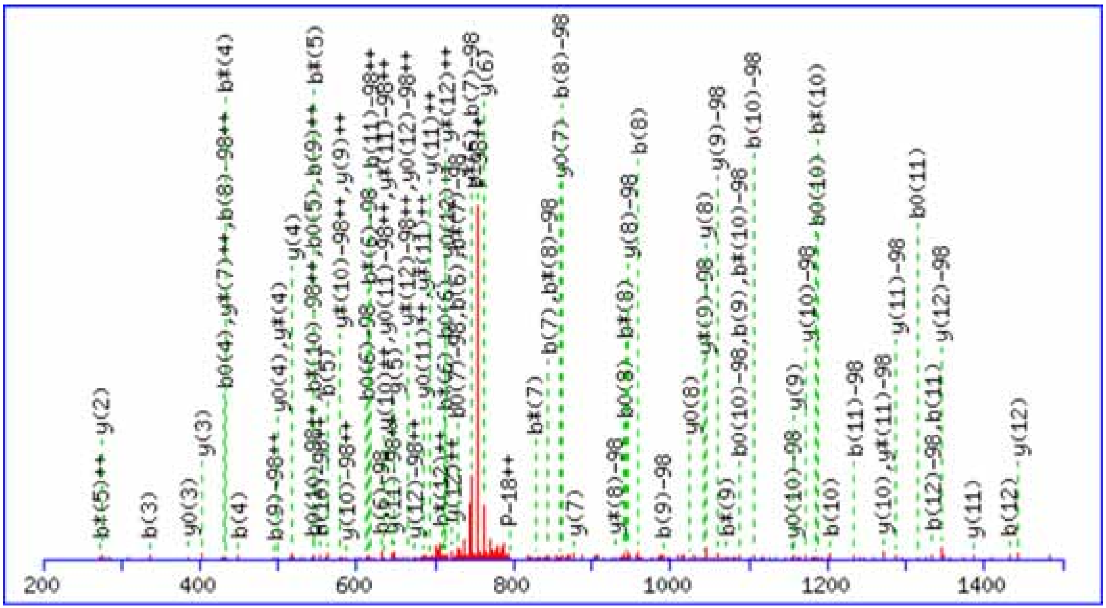
Matched b ions: b(3), b(4), b(5), b(6)-98, b(6)-98++, b(6), b(7), b(7)-98, b(8), b(8)-98++, b(8)-98, b(8)++, b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(11)-98++, b(11)++, b(12)-98, b(12), b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(9)-98++, y(10)-98, y(10), y(11), y(11)-98++, y(11)-98, y(11)++, y(12)-98, y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.649

QGDNISDDEDEVR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of QGDNISDDEDEVR
Found in STX4_MOUSE, Syntaxin-4 OS=Mus musculus GN=Stx4 PE=1 SV=1

Match to Query 2688: 1604.641296 from(803.327924,2+)
Title: Elution from: 31.568 to 31.568 scan no 2353 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1604.6415
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 Expect: 2.1e-007

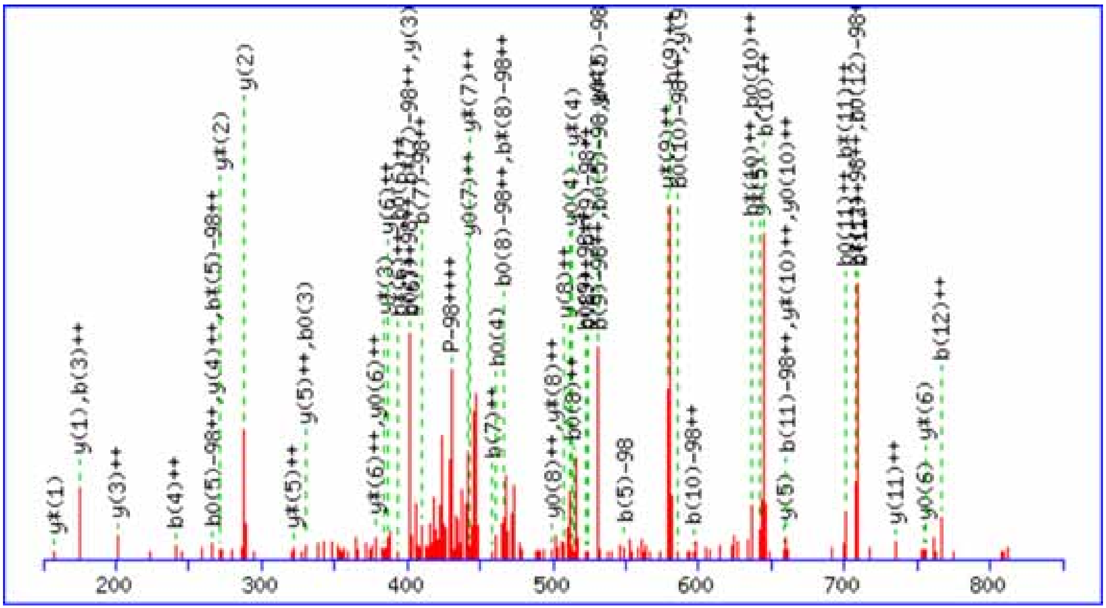
Matched b ions: b(3), b(4), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8), b(8)-98++, b(8)-98, b(9), b(9)++, b(9)-98++, b(9)-98, b(10), b(10)-98, b(10)-98++, b(11)-98, b(11), b(11)-98++, b(12)-98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9)-98, y(9), y(9)++, y(10)-98, y(10), y(10)-98++, y(10)++, y(11), y(11)-98, y(11)-98++, y(11)++, y(12)-98, y(12), y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.650

QGEMSRNENQELIR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of QGEMSRNENQELIR
Found in LYST_MOUSE, Lysosomal-trafficking regulator OS=Mus musculus GN=Lyst PE=1 SV=1

Match to Query 5104: 1816.834088 from(455.215798,4+)
Title: Elution from: 30.296 to 30.296 scan no 2259 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1816.8351
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.0066

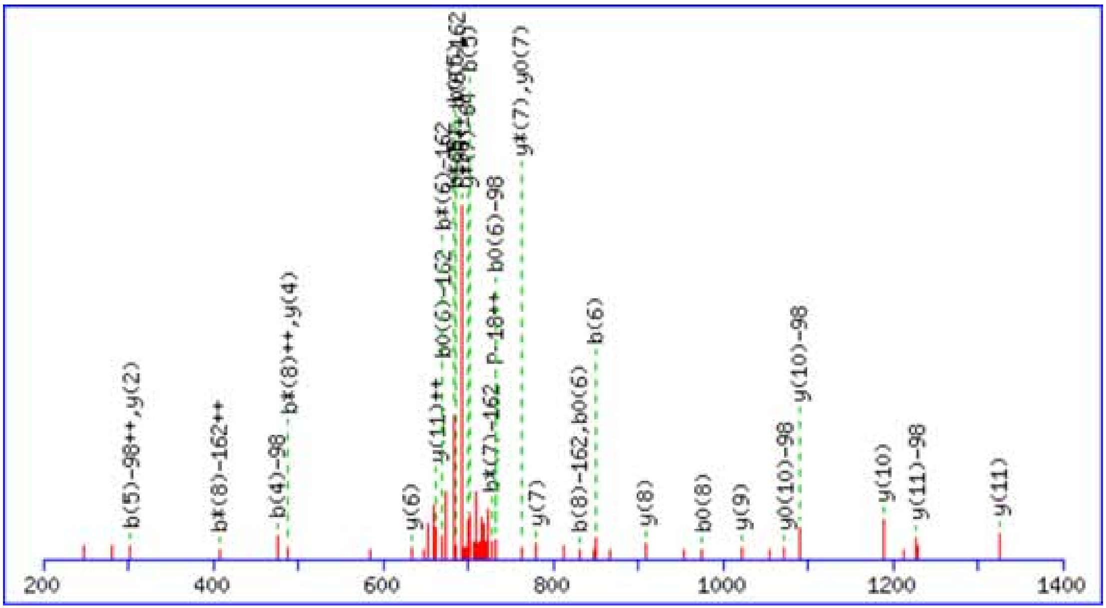
Matched b ions: b(3)++, b(4)++, b(5)-98, b(6)++, b(7)-98++, b(7)++, b(8)++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(4)++, y(5)++, y(5), y(6)++, y(8)++, y(9)++, y(11)++
Precursor origin neutral loss: +

Peptide No.651

QHSLQMGSSVQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QHSLQMGSSVQR
Found in MYOM3_MOUSE, Myomesin-3 OS=Mus musculus GN=Myom3 PE=2 SV=1

Match to Query 2338: 1480.649334 from(741.331943,2+)
Title: Elution from: 20.627 to 20.627 scan no 1054 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1480.6494
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 **Expect:** 0.0093

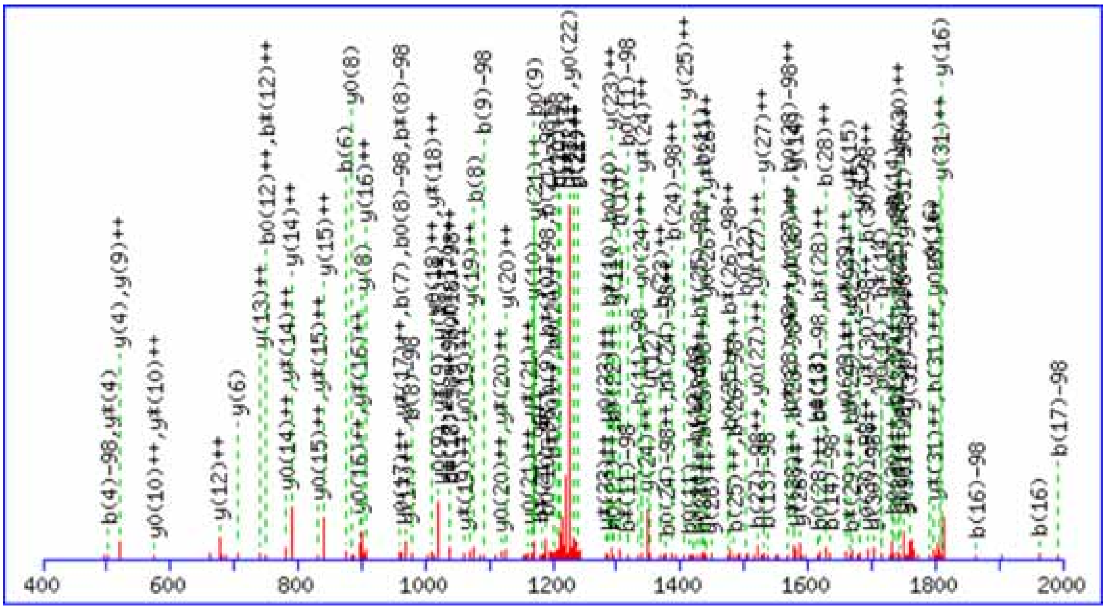
Matched b ions: b(4)-98, b(5)-98++, b(5), b(6)
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11), y(11)-98, y(11)++
Precursor origin neutral loss: +

Peptide No.652

QISYNCSDLDQSNVTEETPEGEEHPVADTENK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QISYNCSDLDQSNVTEETPEGEEHPVADTENK
Found in PAIRB_MOUSE, Plasminogen activator inhibitor 1 RNA-binding protein OS=Mus musculus GN=Serbp1 PE=1 SV=2

Match to Query 8887: 3770.580453 from(1257.867427,3+)
Title: Elution from: 44.497 to 44.497 scan no 4242 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3770.5778
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K32 : Dimethyl (K)
Ions Score: 134 Expect: 3.4e-012

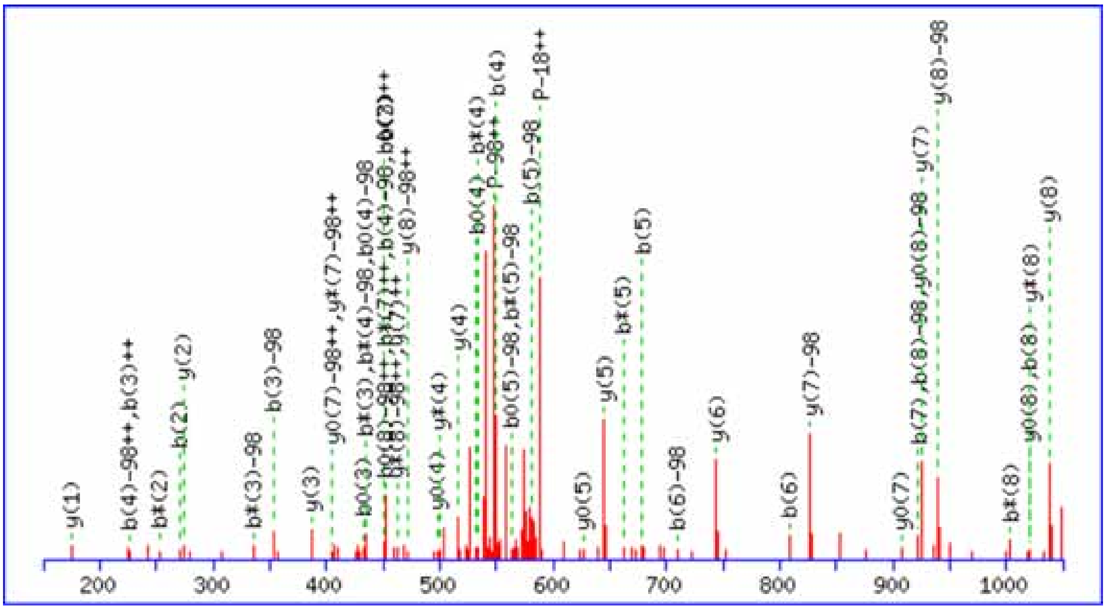
Matched b ions: b(4)-98, b(6), b(7), b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12)-98, b(13)-98, b(14), b(14)-98, b(15)-98, b(16), b(16)-98, b(17)-98, b(20)++, b(21)-98++, b(21)++, b(23)++, b(24)++, b(24)-98++, b(25)-98++, b(25)++, b(26)-98++, b(27)-98++, b(27)++, b(28)++, b(28)-98++, b(30)-98++, b(30)++, b(31)++, b(31)-98++
Matched y ions: y(4), y(6), y(8), y(9)++, y(9), y(10), y(11), y(12)++, y(12), y(13)++, y(14)++, y(14), y(15)++, y(15), y(16)++, y(16), y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)++, y(23)++, y(24)++, y(25)++, y(26)++, y(27)++, y(28)++, y(29)++, y(30)++, y(30)-98++, y(31)-98++, y(31)++
Precursor origin neutral loss: +

Peptide No.653

QITVEELVR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of QITVEELVR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 955: 1193.605788 from(597.810170,2+)
Title: Elution from: 48.472 to 48.472 scan no 4383 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1193.6057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 0.00013

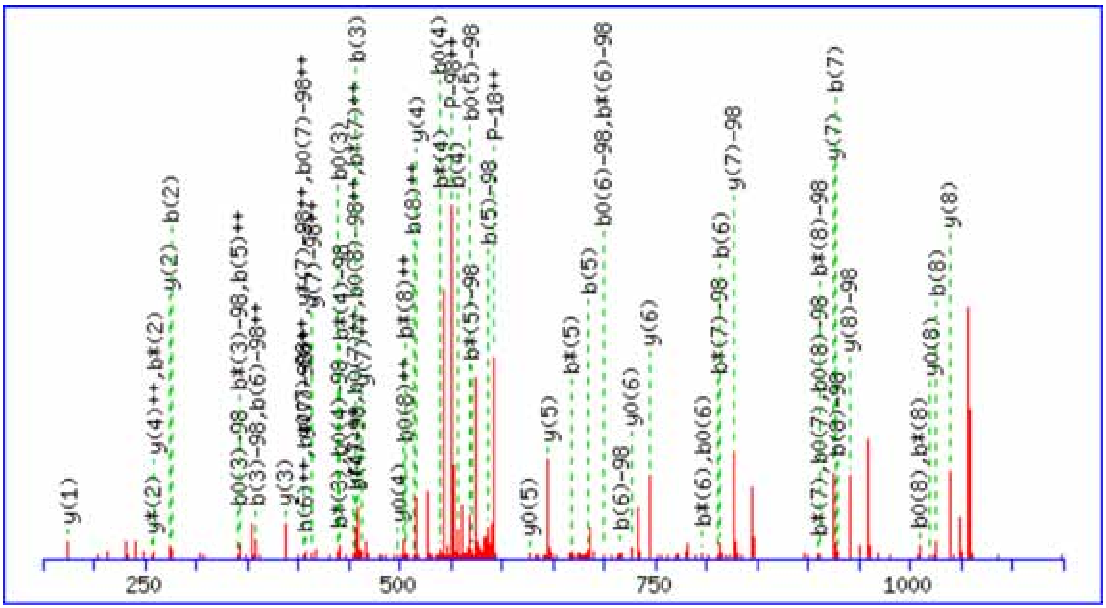
Matched b ions: b(2), b(3)-98, b(3), b(3)++, b(4)-98, b(4)-98++, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7), b(8)-98, b(8)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(7)++, y(8), y(8)-98, y(8)-98++
Precursor origin neutral loss: +

Peptide No.654

QITVEELVR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of QITVEELVR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 758: 1199.638696 from(600.826624,2+)
Title: Elution from: 48.655 to 48.655 scan no 4434 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1199.6375
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.0023

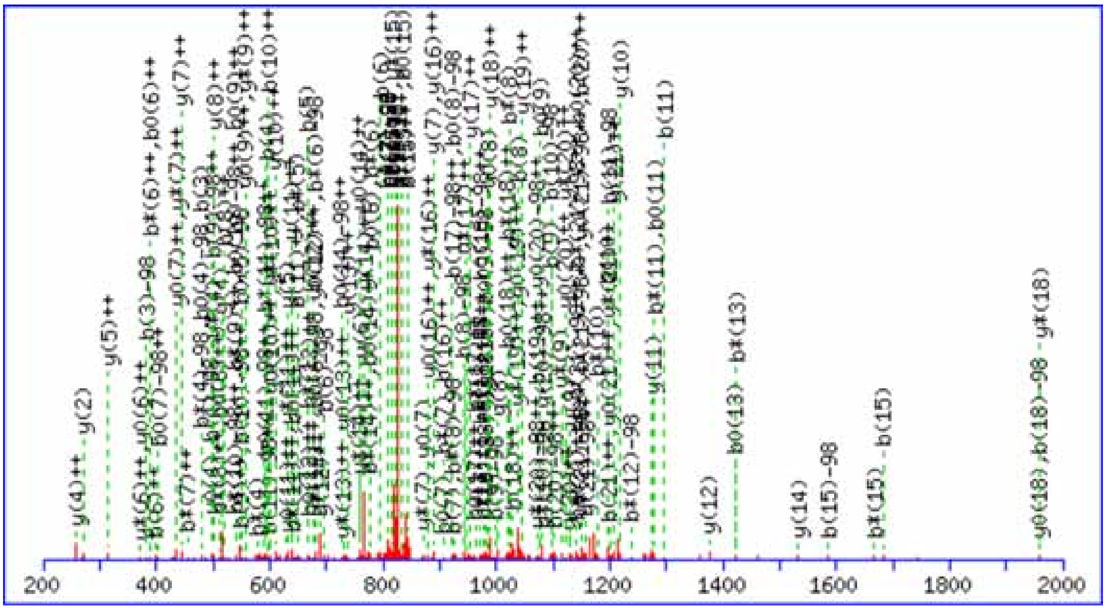
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)++, b(5), b(5)-98, b(6)-98++, b(6), b(6)++, b(6)-98, b(7), b(8), b(8)-98, b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5), y(6), y(7)-98, y(7), y(7)-98++, y(7)++, y(8)-98, y(8)
Precursor origin neutral loss: +

Peptide No.655

QKSDAEEDGVTGSQDEEDSKPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QKSDAEEDGVTGSQDEEDSKPK
Found in CALX_MOUSE, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 7804: 2570.127705 from(857.716511,3+)
Title: Elution from: 22.878 to 22.878 scan no 1348 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2570.1272
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
K22 : Dimethyl (K)
Ions Score: 80 Expect: 6.8e-007

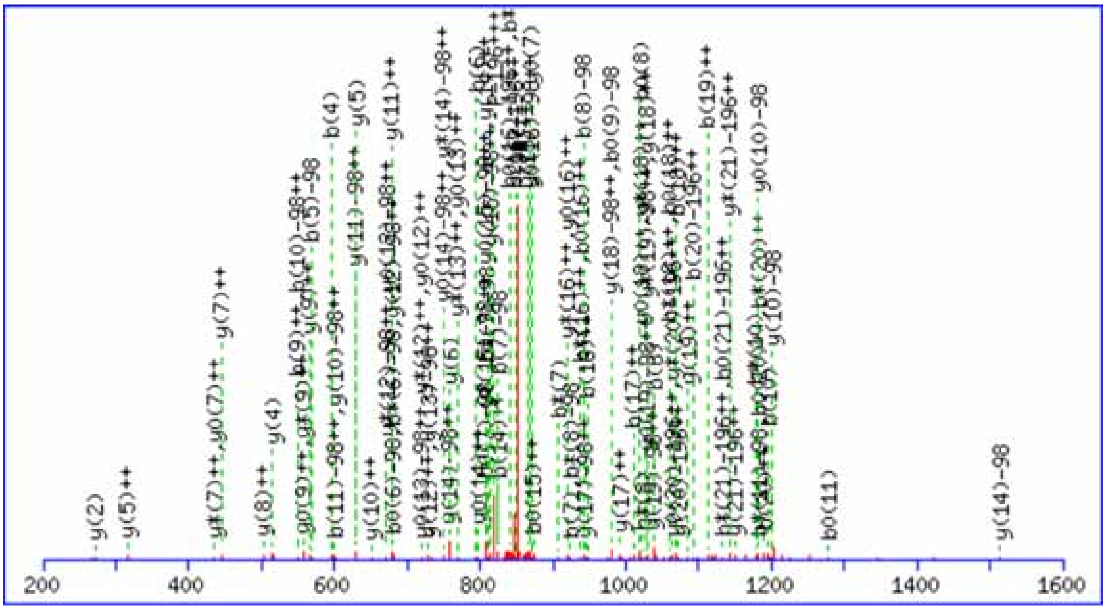
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5), b(6)++, b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(8)++, b(9)++, b(9)-98++, b(9)-98, b(9), b(10)-98++, b(10), b(10)-98, b(10)++, b(11), b(11)-98++, b(11)++, b(11)-98, b(12)++, b(15)-98, b(15), b(15)++, b(16)++, b(17)-98++, b(17)++, b(18)-98, b(18)++, b(18)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(21)++
Matched y ions: y(2), y(4)++, y(4), y(5), y(5)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13)++, y(14), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.656

QKSDAEEDGVTGSQDEEDSKPK
Confirmed sites: @S:3,@S:13
Ambiguous sites:

MS/MS Fragmentation of QKSDAEEDGVTGSQDEEDSKPK
Found in CALX_MOUSE, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 7121: 2650.095585 from(884.372471,3+)
Title: Elution from: 23.663 to 23.663 scan no 1332 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2650.0936
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
K22 : Dimethyl (K)
Ions Score: 52 Expect: 0.00032

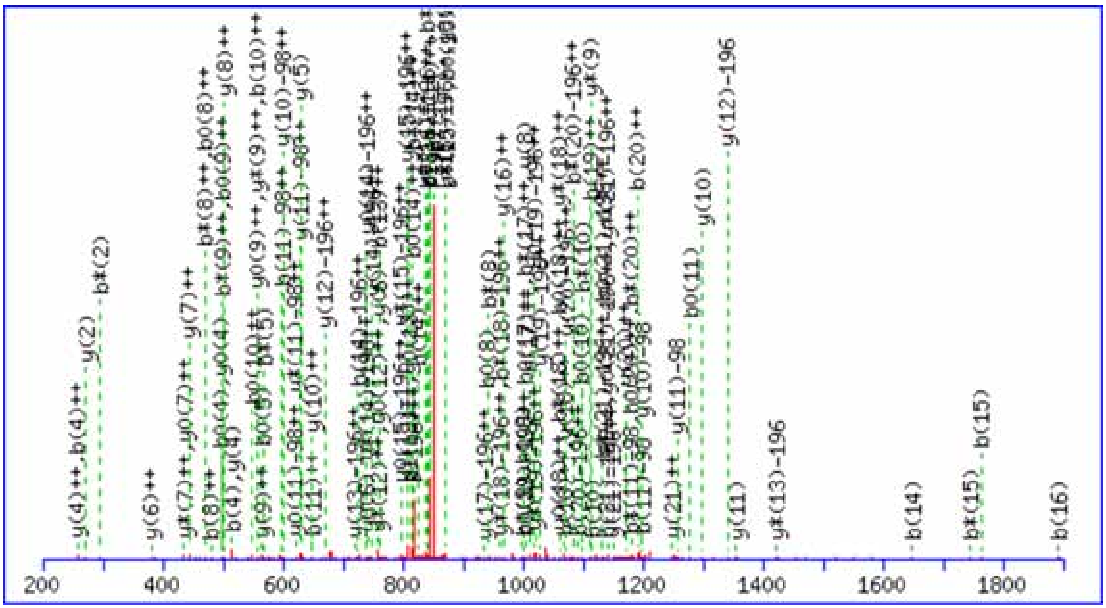
Matched b ions: b(4), b(5)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(9)++, b(10), b(10)-98++, b(11)-98++, b(13)-98, b(14)++, b(15)-98++, b(16)-196++, b(16)++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)-98++, b(20)++, b(20)-196++, b(21)-98++
Matched y ions: y(2), y(4), y(5)++, y(5), y(6), y(7)++, y(8)++, y(9)++, y(10)-98++, y(10)++, y(10)-98, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(14)-98++, y(14)-98, y(14)++, y(15)-98++, y(15)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)-196++, y(20)-98++, y(21)-196++
Precursor origin neutral loss: +

Peptide No.657

QKSDAEEDGVTGSQDEEDSKPK
Confirmed sites: @T:11,@S:13
Ambiguous sites:

MS/MS Fragmentation of QKSDAEEDGVTGSQDEEDSKPK
Found in CALX_MOUSE, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 8022: 2650.094718 from(884.372182,3+)
Title: Elution from: 23.651 to 23.651 scan no 1451 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2650.0936
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
K22 : Dimethyl (K)
Ions Score: 33 Expect: 0.026

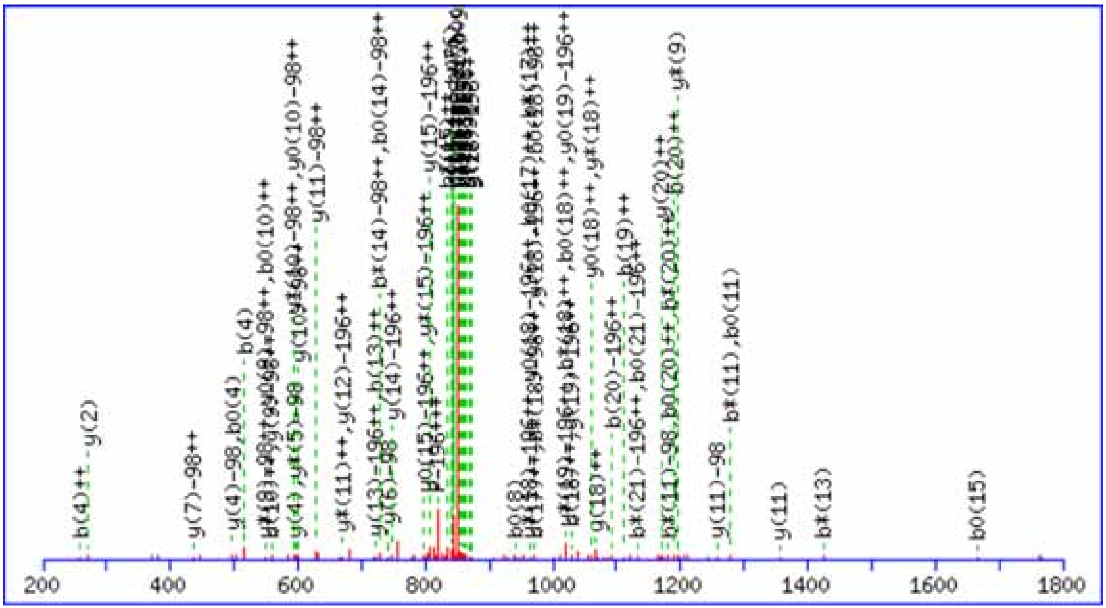
Matched b ions: b(4)++, b(4), b(7), b(8)++, b(10)++, b(10), b(11)-98++, b(11)++, b(11)-98, b(13)-98, b(13)++, b(14), b(14)++, b(14)-196++, b(15), b(15)-98++, b(16), b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(20)-98++, b(20)++, b(20)-196++, b(21)-196++, b(21)-98++
Matched y ions: y(2), y(4)++, y(4), y(5), y(6)++, y(6), y(7)++, y(8), y(8)++, y(9)++, y(10), y(10)-98++, y(10)++, y(10)-98, y(11)-98++, y(11), y(11)-98, y(12)-196++, y(12)-196, y(12)-98++, y(13)-196++, y(14)++, y(14)-196++, y(14)-98++, y(15)-196++, y(15)-98++, y(16)-98++, y(16)-196++, y(16)++, y(17)-196++, y(17)-98++, y(18)++, y(18)-98++, y(19)-196++, y(19)-98++, y(20)-98++, y(20)-196++, y(20)++, y(21)-196++, y(21)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.658

QKSDAEEDGVTGSQDEEDSKPK
Confirmed sites: @T:11,@S:19
Ambiguous sites:

MS/MS Fragmentation of QKSDAEEDGVTGSQDEEDSKPK
Found in CALX_MOUSE, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 6286: 2650.096065 from(884.372631,3+)
Title: Elution from: 23.604 to 23.604 scan no 1337 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2650.0936
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl (K)
K22 : Dimethyl (K)
Ions Score: 38 **Expect:** 0.0081

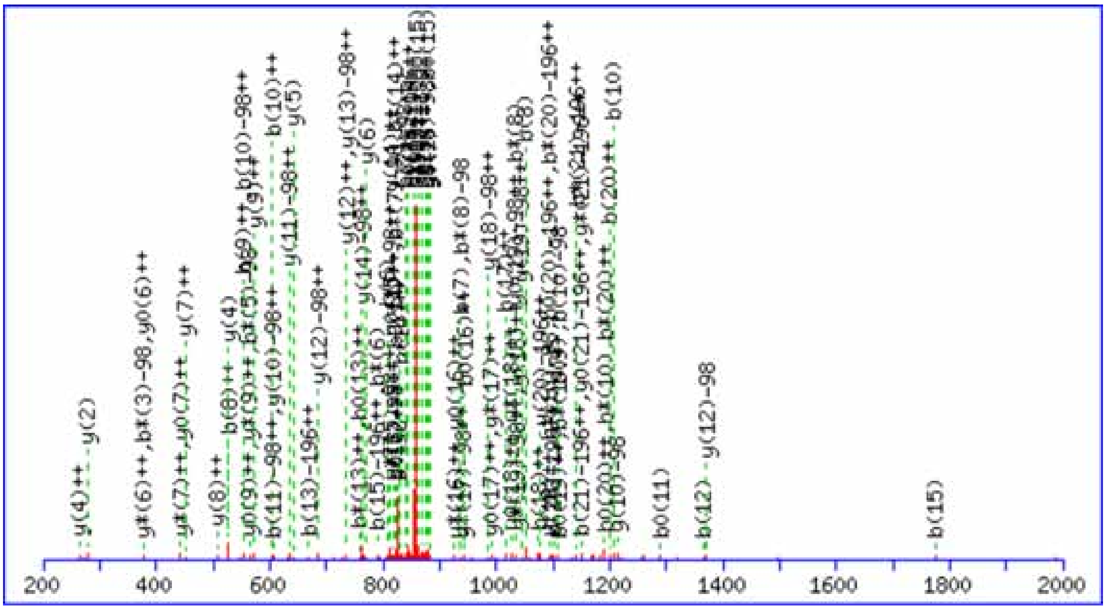
Matched b ions: b(4), b(4)++, b(7), b(10)++, b(13)++, b(15)++, b(16)-98++, b(17)++, b(18)++, b(19)++, b(20)-196++, b(20)++, b(21)-98++
Matched y ions: y(2), y(4)-98, y(4), y(6), y(6)-98, y(7)-98++, y(7)-98, y(9)-98++, y(10)-98++, y(11)-98++, y(11), y(11)-98, y(12)-196++, y(13)-196++, y(14)++, y(14)-196++, y(14)-98++, y(15)-196++, y(15)-98++, y(16)-196++, y(18)-98++, y(18)++, y(18)-196++, y(19)-196++, y(20)-98++, y(20)++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.659

QKSDAEEDGVTGSQDEEDSKPK
Confirmed sites: @S:3,@S:13
Ambiguous sites:

MS/MS Fragmentation of QKSDAEEDGVTGSQDEEDSKPK
Found in CALX_MOUSE, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 6337: 2674.222161 from(892.414663,3+)
Title: Elution from: 23.531 to 23.531 scan no 1328 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2674.2208
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K2 : Dimethyl:2H(4)13C(2) (K)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K20 : Dimethyl:2H(4)13C(2) (K)
K22 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 51 Expect: 0.00079

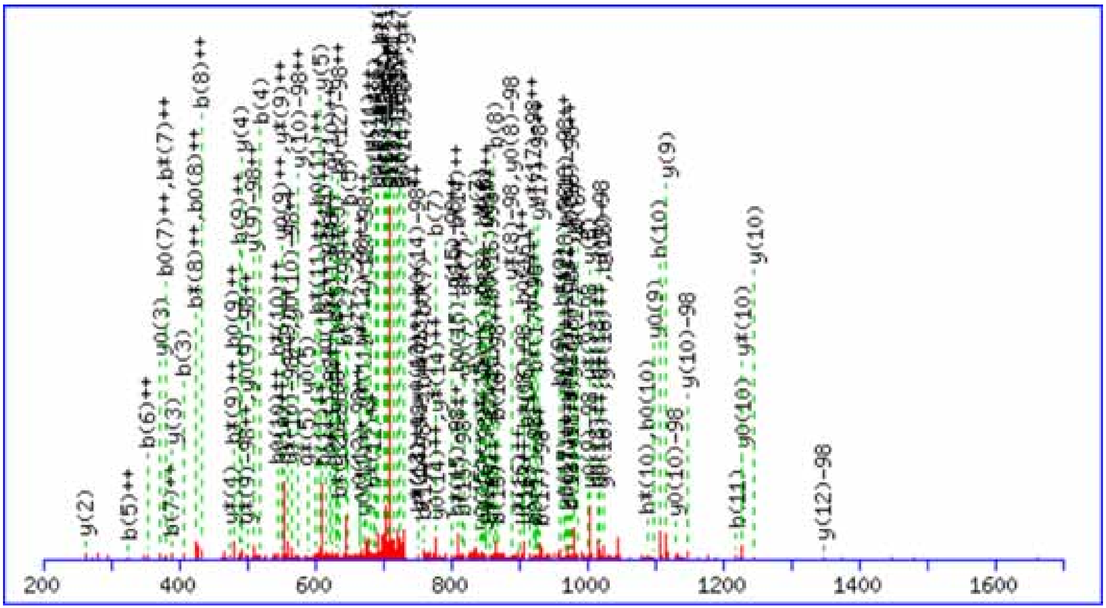
Matched b ions: b(6), b(7)-98, b(7), b(8), b(8)++, b(9)++, b(9), b(10)-98++, b(10), b(10)++, b(10)-98, b(11)-98++, b(12), b(13)-196++, b(14)++, b(15), b(15)-196++, b(15)-98++, b(16)-196++, b(17)++, b(18)++, b(18)-98++, b(20)-98++, b(20)-196++, b(20)++, b(21)-196++, b(21)-98++
Matched y ions: y(2), y(4), y(4)++, y(5), y(6), y(7)++, y(8)++, y(9)++, y(10)-98, y(10)-98++, y(11)-98++, y(12)-98, y(12)-98++, y(12)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-196++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.660

QLHIEGASLELSDDDTESK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of QLHIEGASLELSDDDTESK
Found in MYH10_MOUSE, Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2

Match to Query 5676: 2222.002143 from(741.674657,3+)
Title: Elution from: 48.639 to 48.639 scan no 4520 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2221.9991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl (K)
Ions Score: 48 Expect: 0.0011

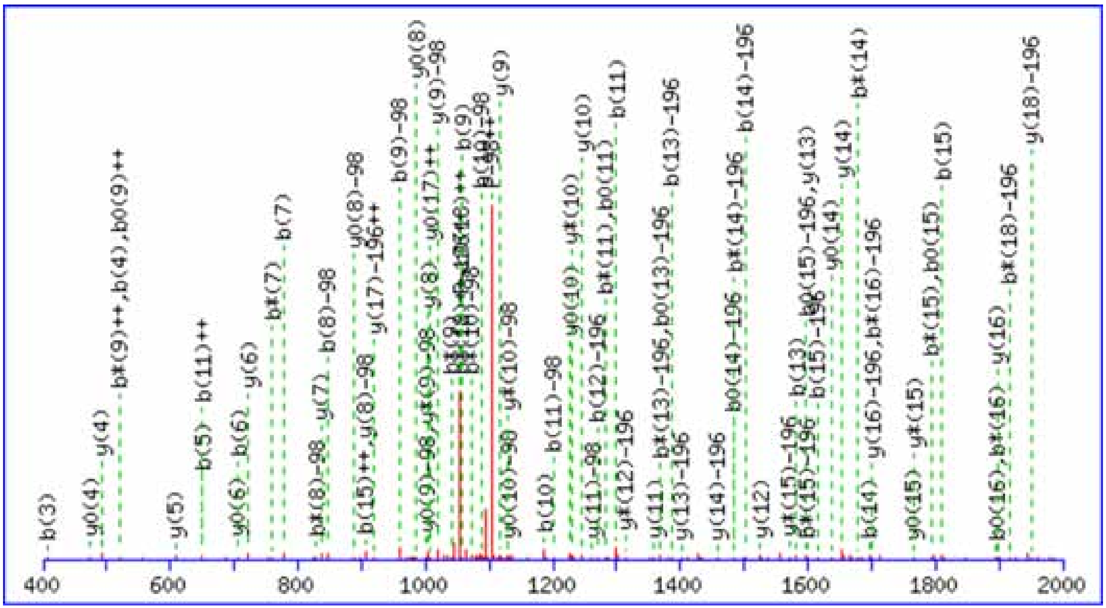
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7), b(7)++, b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(11), b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9), y(9)++, y(9)-98++, y(9)-98, y(10)-98, y(10)++, y(10), y(10)-98++, y(11)-98++, y(11)++, y(12)-98, y(12)++, y(12)-98++, y(13)-98++, y(15)-98++, y(15)++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.661

QLHIEGASLELSDDDTESK
Confirmed sites: @S:8,@S:12
Ambiguous sites:

MS/MS Fragmentation of QLHIEGASLELSDDDTESK
Found in MYH10_MOUSE, Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2

Match to Query 7046: 2301.968130 from(1151.991341,2+)
Title: Elution from: 51.465 to 51.465 scan no 5083 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2301.9654
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl (K)
Ions Score: 52 Expect: 0.00032

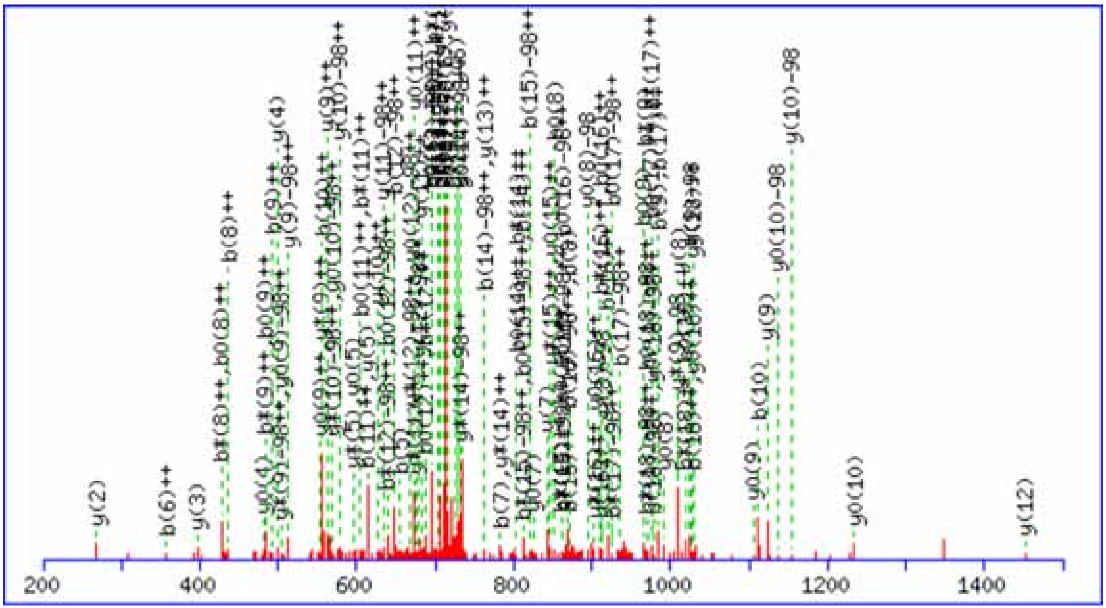
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)++, b(11)-98, b(12)-98, b(12)-196, b(13), b(13)-98, b(13)-196, b(14), b(14)-98, b(14)-196, b(15)++, b(15)-98, b(15), b(15)-196, b(16)-98++, b(17)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98, y(10), y(11), y(11)-98, y(12)-98, y(12), y(13)-98, y(13), y(13)-196, y(14)-98, y(14), y(14)-196, y(14)-98++, y(15)-98, y(16)-98, y(16), y(16)-196, y(17)-98++, y(17)-196++, y(18)-196
Precursor origin neutral loss: +

Peptide No.662

QLHIEGASLELSDDDTESK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of QLHIEGASLELSDDDTESK
Found in MYH10_MOUSE, Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2

Match to Query 5732: 2234.065980 from(745.695936,3+)
Title: Elution from: 48.661 to 48.661 scan no 4523 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2234.0627
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 58 Expect: 0.00011

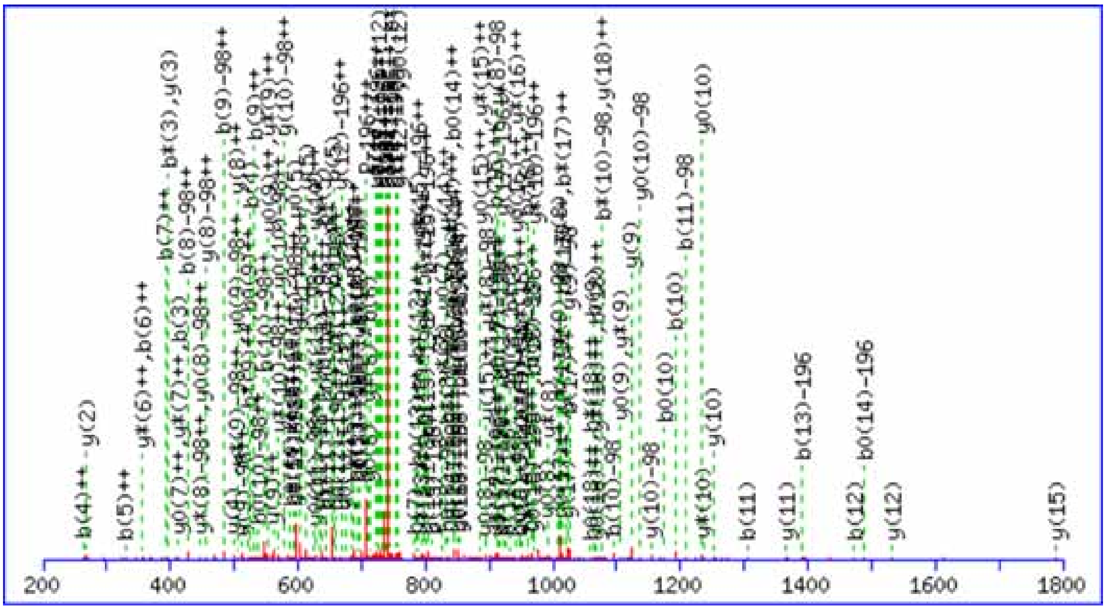
Matched b ions: b(5), b(6), b(6)++, b(7), b(8)++, b(8), b(9), b(9)++, b(10)++, b(10), b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)-98++, b(18)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(9)++, y(9)-98++, y(10)-98, y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(12), y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.663

QLHIEGASLELSDDDTESK
Confirmed sites: @S:8,@S:12
Ambiguous sites:

MS/MS Fragmentation of QLHIEGASLELSDDDTESK
Found in MYH10_MOUSE, Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2

Match to Query 6395: 2314.030218 from(772.350682,3+)
Title: Elution from: 51.302 to 51.302 scan no 4895 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2314.0291
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 54 **Expect:** 0.00029

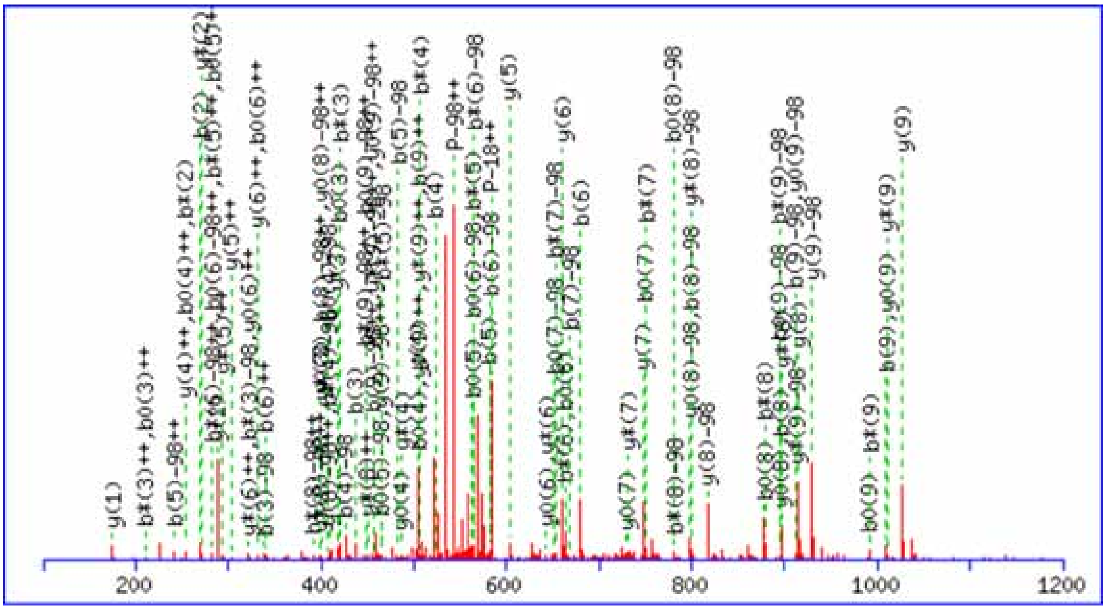
Matched b ions: b(3), b(4)++, b(4), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8)-98++, b(8)-98, b(9)-98++, b(9)-98, b(9)++, b(9), b(10)-98++, b(10)++, b(10), b(10)-98, b(11), b(11)++, b(11)-98++, b(11)-98, b(12), b(12)-98++, b(12)-196++, b(12)++, b(13)++, b(13)-196, b(13)-196++, b(13)-98++, b(14)++, b(14)-98++, b(14)-196++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(17)-196++, b(18)++, b(18)-196++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(8)-98++, y(8)++, y(9), y(9)++, y(9)-98, y(9)-98++, y(10)-98, y(10), y(10)++, y(10)-98++, y(11), y(11)-98++, y(11)++, y(12), y(12)-98, y(12)-196++, y(12)-98++, y(13)-98++, y(13)++, y(14)-98++, y(14)-196++, y(14)++, y(15), y(15)++, y(15)-196++, y(15)-98++, y(16)++, y(16)-196++, y(16)-98++, y(17)-196++, y(17)-98++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No.664

QLSSGVSEIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QLSSGVSEIR
Found in HSPB1_MOUSE, Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3

Match to Query 1153: 1182.564692 from(592.289622,2+)
Title: Elution from: 34.335 to 34.335 scan no 2897 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1182.5645
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.0003

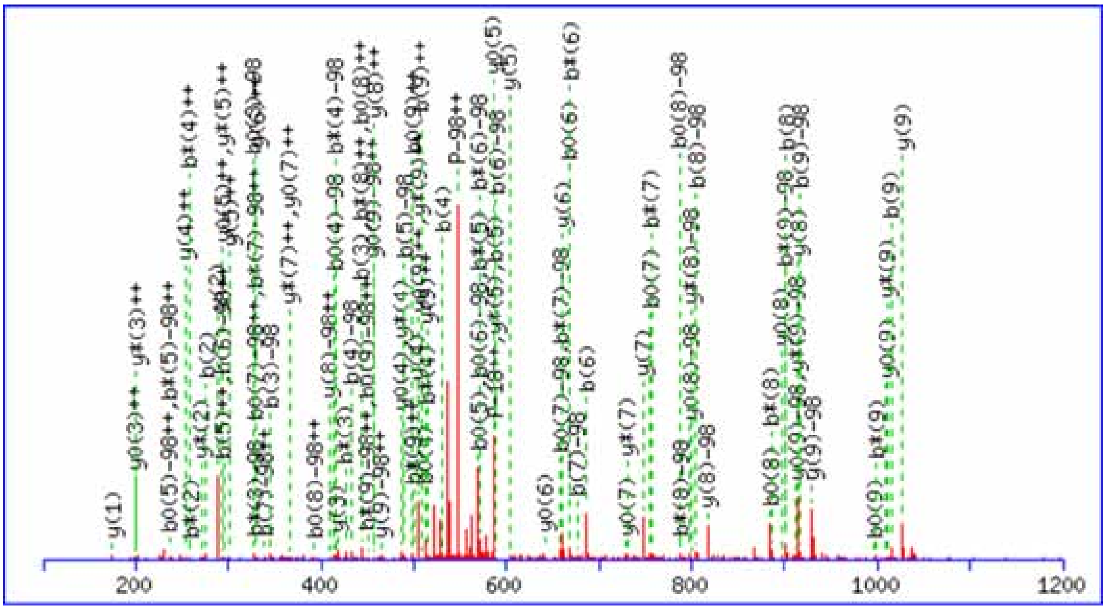
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98++, b(5), b(5)-98, b(6), b(6)++, b(6)-98, b(7)-98, b(8)-98, b(8), b(8)-98++, b(9), b(9)-98, b(9)-98++, b(9)++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(8)-98, y(8), y(8)-98++, y(9)-98, y(9), y(9)-98++
Precursor origin neutral loss: +

Peptide No.665

QLSSGVSEIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QLSSGVSEIR
Found in HSPB1_MOUSE, Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3

Match to Query 1027: 1188.596590 from(595.305571,2+)
Title: Elution from: 34.232 to 34.232 scan no 2715 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1188.5964
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 0.00041

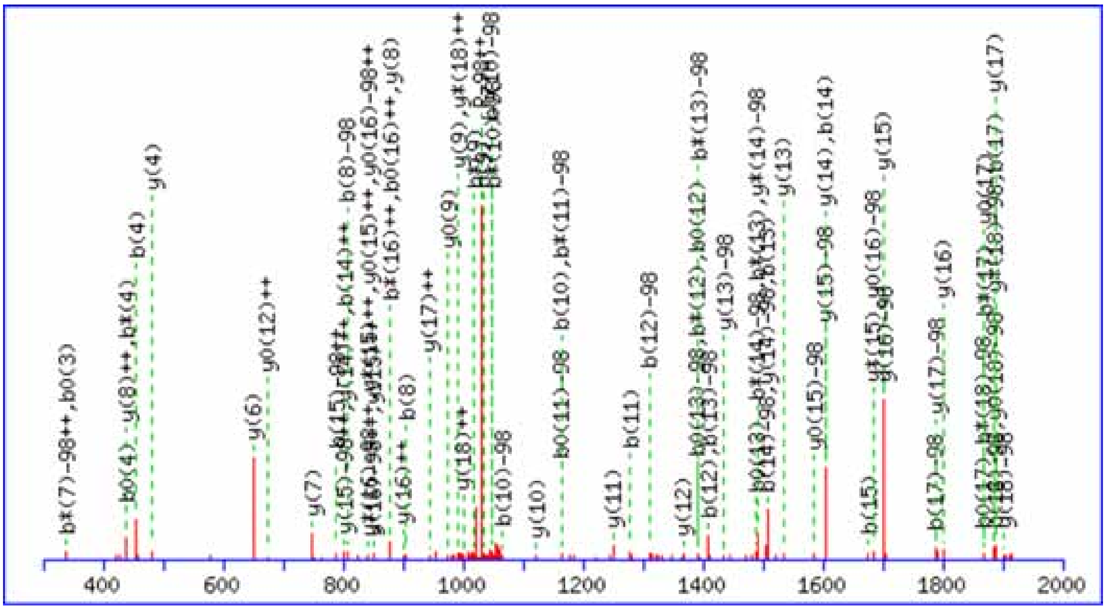
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(5), b(5)++, b(5)-98, b(6), b(6)-98++, b(6)-98, b(7)-98++, b(7)-98, b(8)-98, b(8), b(9), b(9)++, b(9)-98
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5)++, y(5), y(6), y(6)++, y(7), y(8)-98, y(8), y(8)-98++, y(8)++, y(9), y(9)-98, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.666

QLSVPASDEEDEVPAPIPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of QLSVPASDEEDEVPAPIPR
Found in ABCF1_MOUSE, ATP-binding cassette sub-family F member 1 OS=Mus musculus GN=Abcf1 PE=1 SV=1

Match to Query 6310: 2156.005366 from(1079.009959,2+)
Title: Elution from: 50.216 to 50.216 scan no 4943 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2156.0038
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 Expect: 3.1e-005

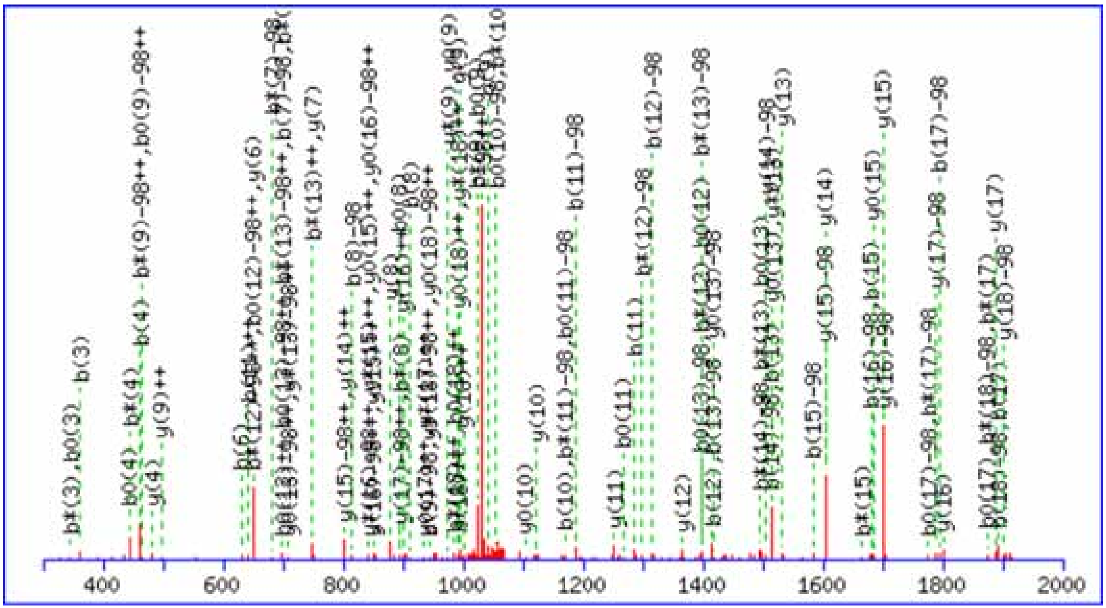
Matched b ions: b(4), b(8)-98, b(8), b(9), b(10), b(10)-98, b(11), b(12), b(12)-98, b(13)-98, b(13), b(14)-98, b(14)++, b(14), b(15)-98++, b(15), b(17), b(17)-98, b(18)-98
Matched y ions: y(4), y(6), y(7), y(8), y(8)++, y(9), y(10), y(11), y(12), y(13), y(13)-98, y(14)-98, y(14)++, y(14), y(15)-98, y(15), y(15)-98++, y(15)++, y(16)-98, y(16), y(16)-98++, y(16)++, y(17)-98, y(17), y(17)++, y(18)++, y(18)-98
Precursor origin neutral loss: +

Peptide No.667

QLSVPASDEEDEVPAPIPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of QLSVPASDEEDEVPAPIPR
Found in ABCF1_MOUSE, ATP-binding cassette sub-family F member 1 OS=Mus musculus GN=Abcf1 PE=1 SV=1

Match to Query 5577: 2162.034694 from(1082.024623,2+)
Title: Elution from: 50.322 to 50.322 scan no 4722 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2162.0356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 **Expect:** 4.9e-007

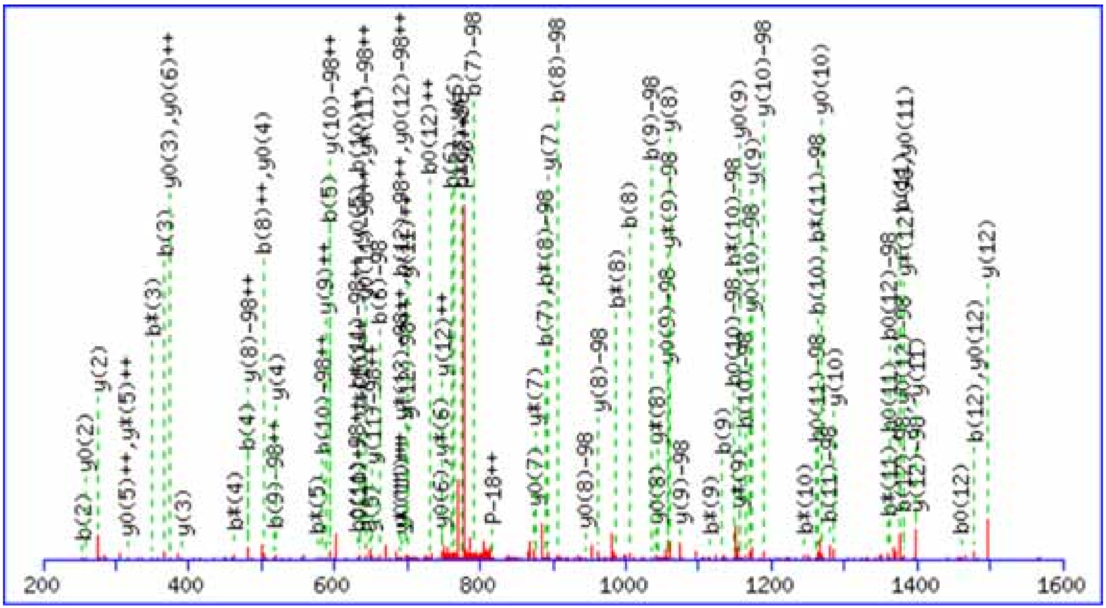
Matched b ions: b(3), b(4), b(6), b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(10), b(11)-98, b(11), b(11)++, b(12), b(12)-98, b(13)-98, b(13), b(14)-98, b(15), b(15)-98, b(16)-98, b(17), b(17)-98, b(18)-98, b(18)++
Matched y ions: y(4), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11), y(12), y(13), y(14)++, y(14), y(14)-98, y(15)-98++, y(15)-98, y(15), y(15)++, y(16), y(16)-98, y(16)-98++, y(16)++, y(17)-98, y(17), y(17)-98++, y(18)-98, y(18)++
Precursor origin neutral loss: +

Peptide No.668

QPLLLSEDEEDTK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of QPLLLSEDEEDTK
Found in EIF3C_MOUSE, Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Eif3c PE=1 SV=1

Match to Query 3431: 1651.757164 from(826.885858,2+)
Title: Elution from: 42.947 to 42.947 scan no 4051 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1651.7593
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 37 Expect: 0.0067

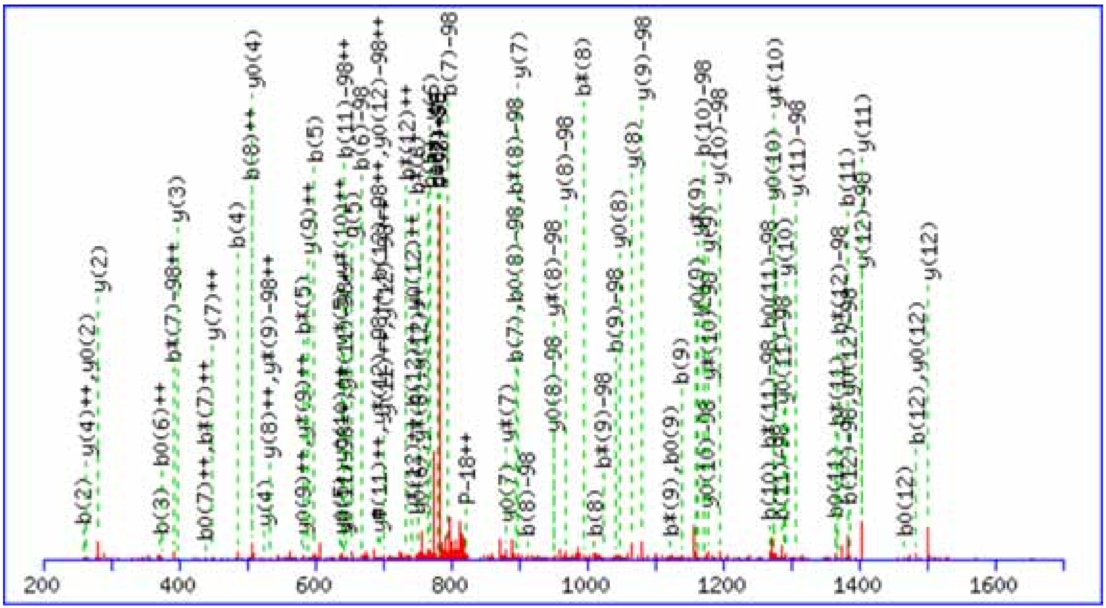
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8), b(8)++, b(8)-98, b(9)-98++, b(9)-98, b(9), b(10), b(10)-98, b(10)++, b(10)-98++, b(11)-98, b(11), b(12), b(12)-98, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(8)-98++, y(9), y(9)-98, y(9)++, y(10)-98, y(10), y(10)-98++, y(11), y(11)-98++, y(11)++, y(12)-98, y(12), y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.669

QPLLLSEDEEDTK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of QPLLLSEDEEDTK
Found in EIF3C_MOUSE, Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Eif3c PE=1 SV=1

Match to Query 2693: 1663.821568 from(832.918060,2+)
Title: Elution from: 42.981 to 42.981 scan no 3871 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1663.8230
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 34 Expect: 0.02

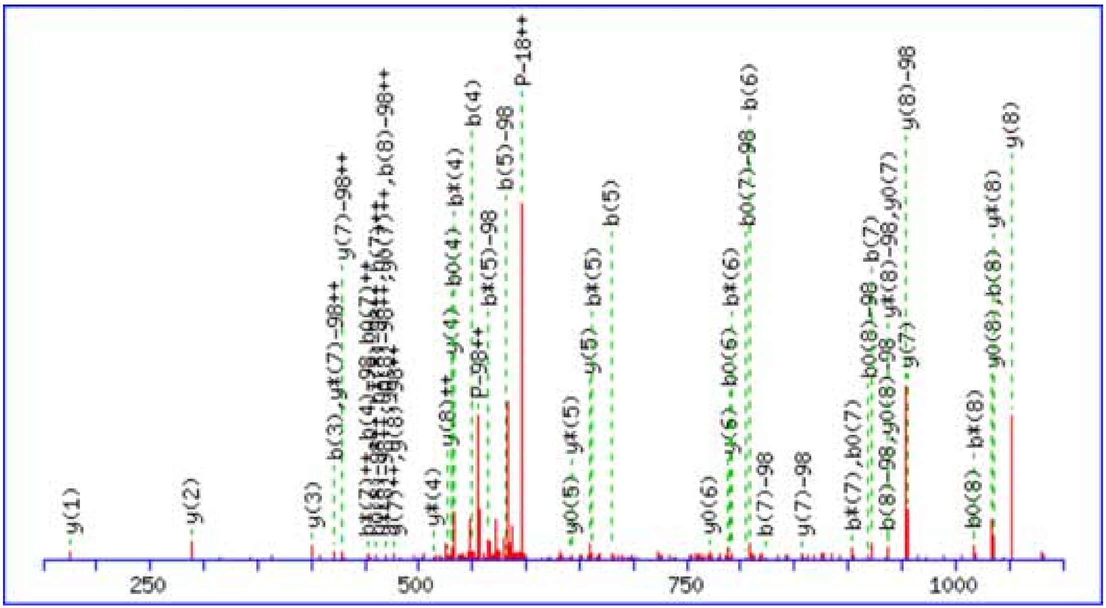
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)++, b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11)-98, b(11), b(11)-98++, b(12), b(12)-98, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(7)++, y(8)-98, y(8), y(8)++, y(9)-98, y(9), y(9)++, y(10)-98, y(10), y(11), y(11)++, y(11)-98, y(12)-98, y(12), y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.670

QPSEEEIIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QPSEEEIIK
Found in PEA15_MOUSE, Astrocytic phosphoprotein PEA-15 OS=Mus musculus GN=Pea15 PE=1 SV=1

Match to Query 1218: 1207.574476 from(604.794514,2+)
Title: Elution from: 33.185 to 33.185 scan no 2739 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1207.5737
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K9 : Dimethyl (K)
Ions Score: 38 Expect: 0.0052

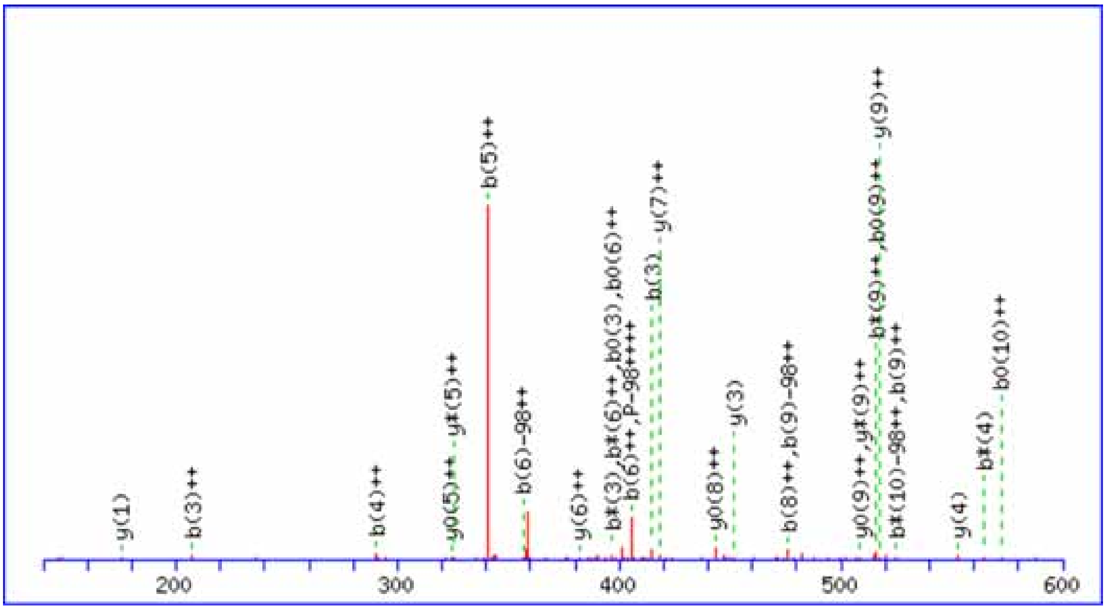
Matched b ions: b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(7), b(7)++, b(7)-98, b(8), b(8)-98, b(8)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98, y(7)-98++, y(7)++, y(8)-98, y(8), y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.671

QQESTKAAPLTYIK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of QQESTKAAPLTYIK
Found in NCOR1_MOUSE, Nuclear receptor corepressor 1 OS=Mus musculus GN=Ncor1 PE=1 SV=1

Match to Query 3260: 1712.879960 from(429.227266,4+)
Title: Elution from: 29.189 to 29.189 scan no 2033 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1712.8750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl (K)
Ions Score: 34 Expect: 0.023

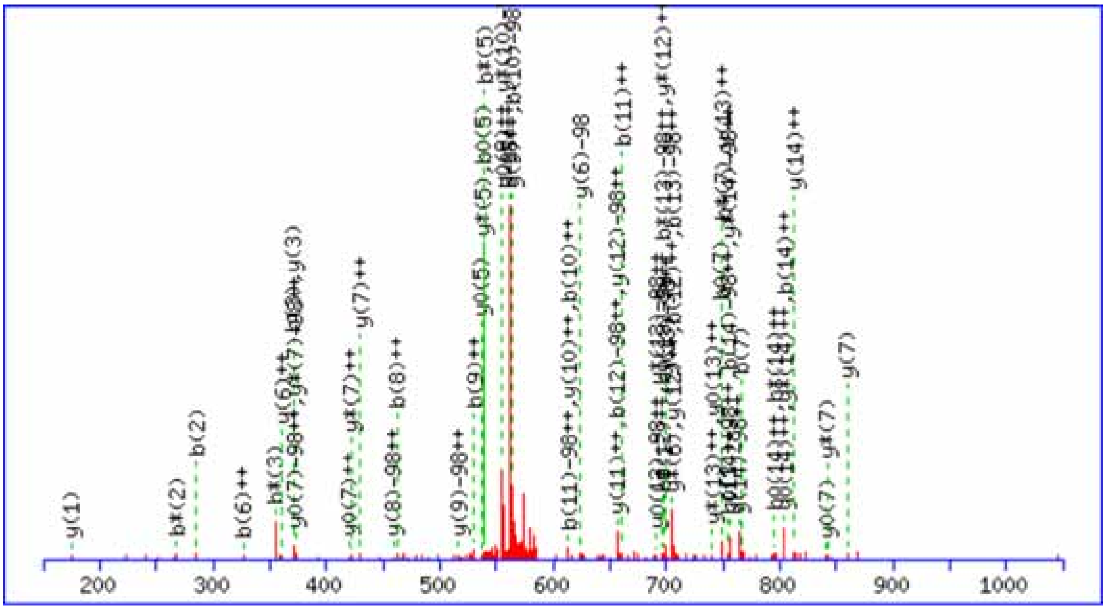
Matched b ions: b(3)++, b(3), b(4)++, b(5)++, b(6)++, b(6)-98++, b(8)++, b(9)-98++, b(9)++
Matched y ions: y(1), y(3), y(4), y(6)++, y(7)++, y(9)++
Precursor origin neutral loss: +

Peptide No.672

QQSPSPIRHSPSPVR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of QQSPSPIRHSPSPVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4190: 1779.878817 from(594.300215,3+)
Title: Elution from: 22.509 to 22.509 scan no 1299 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1779.8781
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.0084

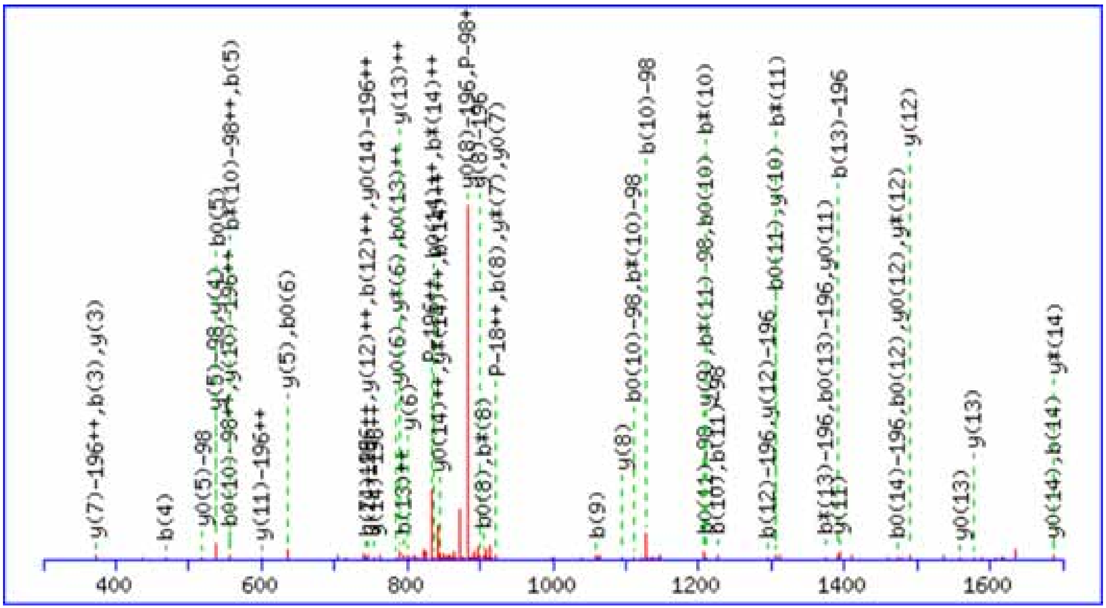
Matched b ions: b(2), b(3), b(5), b(6)++, b(7), b(8)++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++
Matched y ions: y(1), y(3), y(5), y(6)++, y(6)-98, y(7)++, y(7), y(8)-98++, y(9)++, y(9)-98++, y(10)-98++, y(10)++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.673

QQSPSPIRHSPSPVR
Confirmed sites: @S:10,@S:12
Ambiguous sites:

MS/MS Fragmentation of QQSPSPIRHSPSPVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4744: 1859.844742 from(930.929647,2+)
Title: Elution from: 23.381 to 23.381 scan no 1415 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1859.8444
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.009

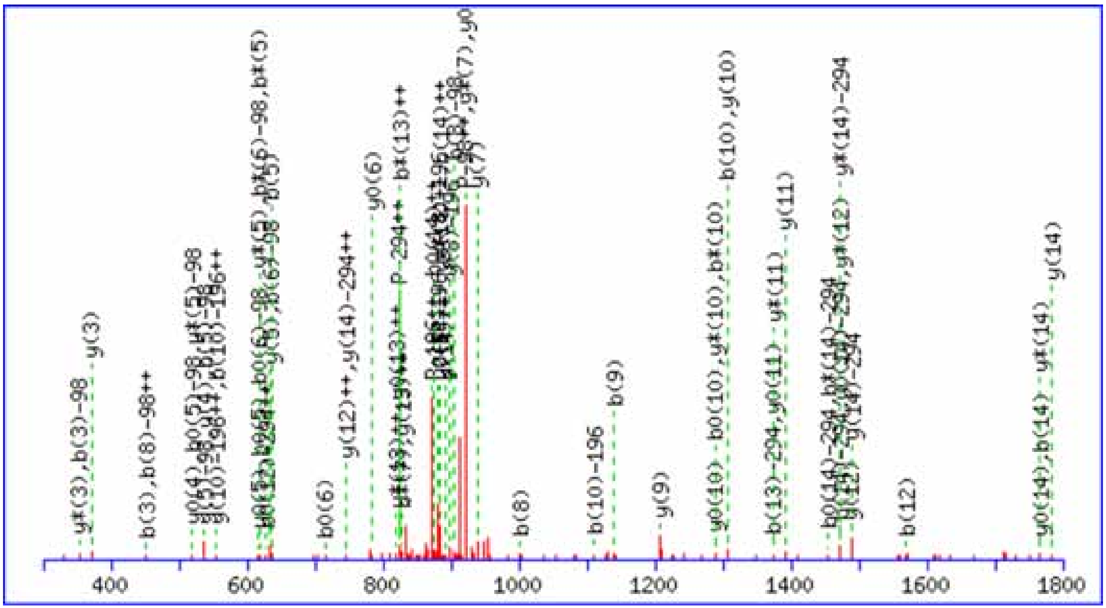
Matched b ions: b(3), b(4), b(5), b(8), b(9), b(10)-98, b(10), b(11)-98, b(12)-98, b(12)++, b(12)-196, b(13)-98, b(13)-196, b(13)-98++, b(13)++, b(14)-98, b(14), b(14)-196++, b(14)++, b(14)-98++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6)-98, y(6), y(7)-196++, y(7)-98, y(7)-196, y(8)-98, y(8)-196, y(8), y(9), y(9)-98++, y(9)-98, y(10), y(10)-196++, y(10)-98, y(11), y(11)-196++, y(11)-98, y(12), y(12)-98, y(12)++, y(12)-196, y(13)-98++, y(13)++, y(13), y(14)-196++, y(14)-98, y(14)-98++
Precursor origin neutral loss: +

Peptide No.674

QQSPSPIRHSPSPVR
Confirmed sites: @S:3,@S:10,@S:12
Ambiguous sites:

MS/MS Fragmentation of QQSPSPIRHSPSPVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4505: 1939.813308 from(970.913930,2+)
Title: Elution from: 25.127 to 25.127 scan no 1494 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1939.8108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00039

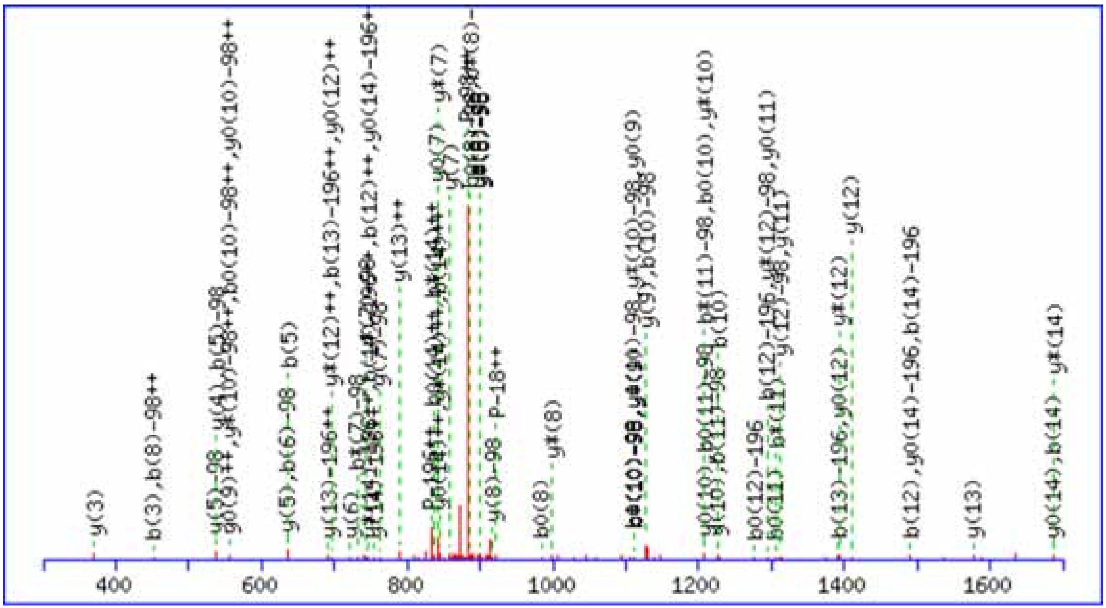
Matched b ions: b(3)-98, b(3), b(5)-98, b(5), b(6)-98, b(8)-98++, b(8), b(8)-98, b(9), b(10)-98, b(10), b(10)-196++, b(10)-196, b(11)-98, b(12)-98, b(12)-196, b(12), b(13)-294, b(14)-196, b(14), b(14)-294, b(14)-98, b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6)-98++, y(7), y(7)-98, y(8)-196, y(9), y(9)-98++, y(9)-98, y(10), y(10)-196++, y(11), y(12), y(12)-98, y(12)++, y(13)-98++, y(13)++, y(13)-98, y(14), y(14)-294, y(14)-294++, y(14)++
Precursor origin neutral loss: +

Peptide No.675

QQSPSPIRHSPSPVR
Confirmed sites: @S:3,@S:12
Ambiguous sites:

MS/MS Fragmentation of QQSPSPIRHSPSPVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3846: 1859.845856 from(930.930204,2+)
Title: Elution from: 23.473 to 23.473 scan no 1281 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1859.8444
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.0026

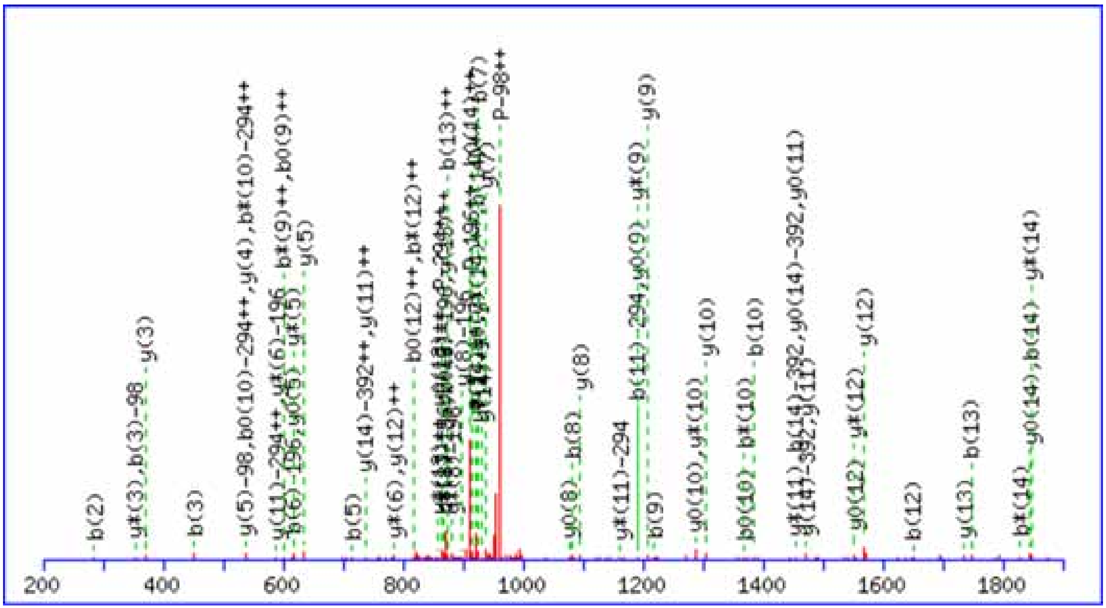
Matched b ions: b(3), b(5), b(5)-98, b(6)-98, b(8)-98++, b(10)-98, b(10), b(11)-98, b(12)-98, b(12), b(12)-196, b(12)++, b(12)-98++, b(13)-98, b(13)-196, b(13)-196++, b(14)-196, b(14), b(14)-196++, b(14)++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6), y(7), y(7)-98, y(8)-98, y(9), y(10), y(11), y(12)-98, y(12), y(13)-98++, y(13)-196++, y(13), y(13)++, y(14)-196++
Precursor origin neutral loss: +

Peptide No.676

QQSPSPIRHSPSPVR
Confirmed sites: @S:3,@S:5,@S:10,@S:12
Ambiguous sites:

MS/MS Fragmentation of QQSPSPIRHSPSPVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4632: 2019.778530 from(1010.896541,2+)
Title: Elution from: 25.972 to 25.972 scan no 1621 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2019.7771
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 0.00018

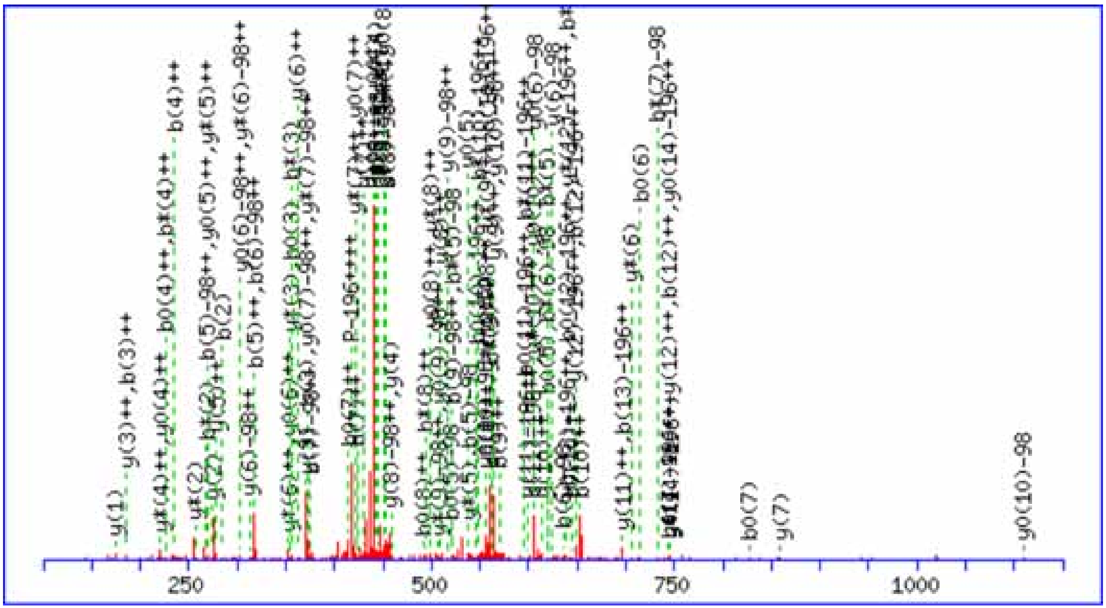
Matched b ions: b(2), b(3), b(3)-98, b(5)-98, b(5), b(6)-98, b(6)-196, b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10)-196, b(10), b(11)-196, b(11)-294, b(11)-98, b(12), b(12)-196, b(12)-98, b(13)-98, b(13)-196, b(13), b(13)++, b(14), b(14)-196, b(14)-98, b(14)-392, b(14)-294, b(14)-98++, b(14)++, b(14)-196++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(8)-196, y(9), y(10)-98, y(10), y(11), y(11)-294++, y(11)++, y(11)-98, y(12), y(12)-98, y(12)++, y(12)-98++, y(13)-98, y(13), y(13)-98++, y(13)-196++, y(13)++, y(13)-196, y(14)-392, y(14)-294, y(14)-294++, y(14)-392++, y(14)-196++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.677

QQSPSPIRHSPSPVR
Confirmed sites: @S:5,@S:10
Ambiguous sites:

MS/MS Fragmentation of QQSPSPIRHSPSPVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4740: 1859.843544 from(465.968162,4+)
Title: Elution from: 23.456 to 23.456 scan no 1425 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1859.8444
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.024

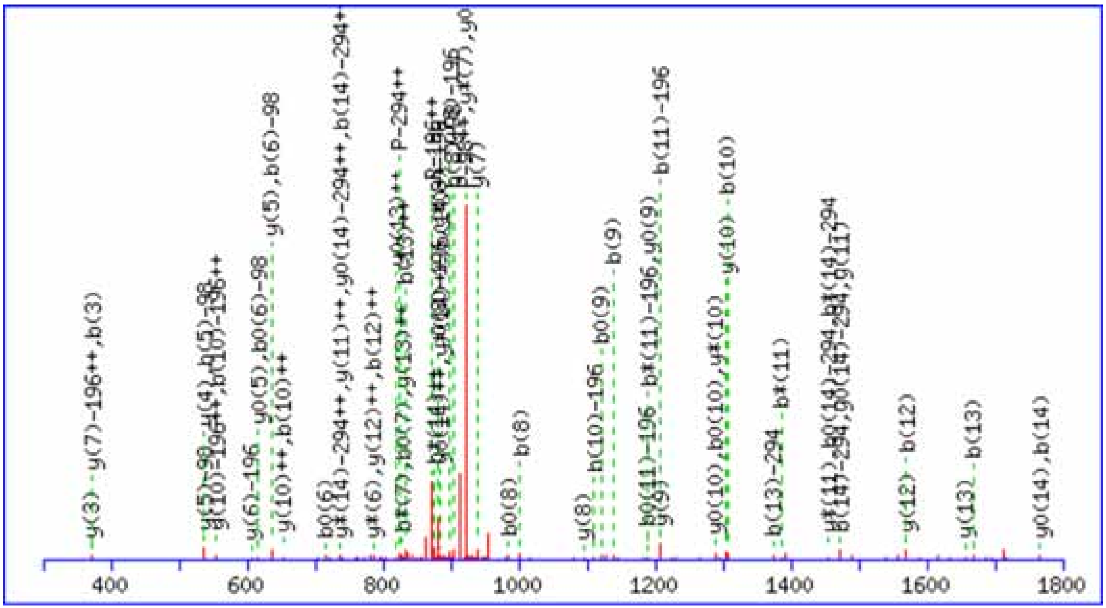
Matched b ions: b(2), b(3)++, b(3), b(4)++, b(5)++, b(5)-98++, b(5)-98, b(6)-98++, b(6)-98, b(7)-98++, b(7)++, b(8)-98++, b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(10)-196++, b(11)-98++, b(11)-196++, b(12)++, b(12)-196++, b(12)-98++, b(13)-98++, b(13)-196++, b(14)-196++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(5)++, y(5), y(6)-98++, y(6)++, y(6)-98, y(7), y(7)++, y(8)-98++, y(8)++, y(9)++, y(9)-98++, y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(11)-196++, y(12)++, y(12)-196++, y(12)-98++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.678

QQSPSPIRHSPSPVR
Confirmed sites: @S:5,@S:10,@S:12
Ambiguous sites:

MS/MS Fragmentation of QQSPSPIRHSPSPVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 5331: 1939.811784 from(970.913168,2+)
Title: Elution from: 24.872 to 24.872 scan no 1614 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1939.8108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 **Expect:** 0.00034

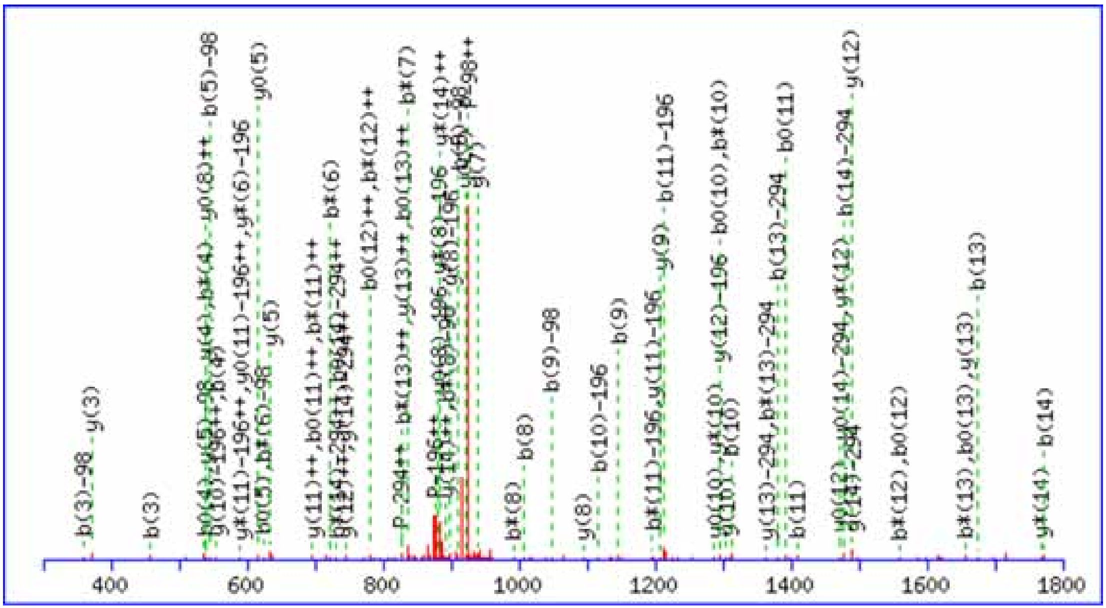
Matched b ions: b(3), b(5)-98, b(6)-98, b(8), b(8)-98, b(9), b(10)-98, b(10)-196++, b(10), b(10)++, b(10)-196, b(11)-98, b(11)-196, b(11)-98++, b(12)-98++, b(12)-196, b(12)-98, b(12), b(12)++, b(13)-196++, b(13)-98, b(13), b(13)-294, b(13)-196, b(13)-98++, b(13)++, b(14)-294++, b(14)-98, b(14)-294, b(14), b(14)-98++, b(14)-196, b(14)-196++, b(14)++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6)-196, y(6)-98, y(7)-196++, y(7)-98, y(7), y(8), y(8)-196, y(9), y(9)-98++, y(9)-98, y(10), y(10)-98, y(10)-196++, y(10)++, y(11)++, y(11)-98, y(11), y(12)-98++, y(12), y(12)-196, y(12)-98, y(12)++, y(13), y(13)-98, y(13)++, y(13)-98++, y(14)-98, y(14)-196, y(14)-196++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.679

QQSPSPIRHSPSPVR
Confirmed sites: @S:3,@S:10,@S:12
Ambiguous sites:

MS/MS Fragmentation of QQSPSPIRHSPSPVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4931: 1945.842174 from(973.928363,2+)
Title: Elution from: 25.154 to 25.154 scan no 1512 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1945.8426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.02

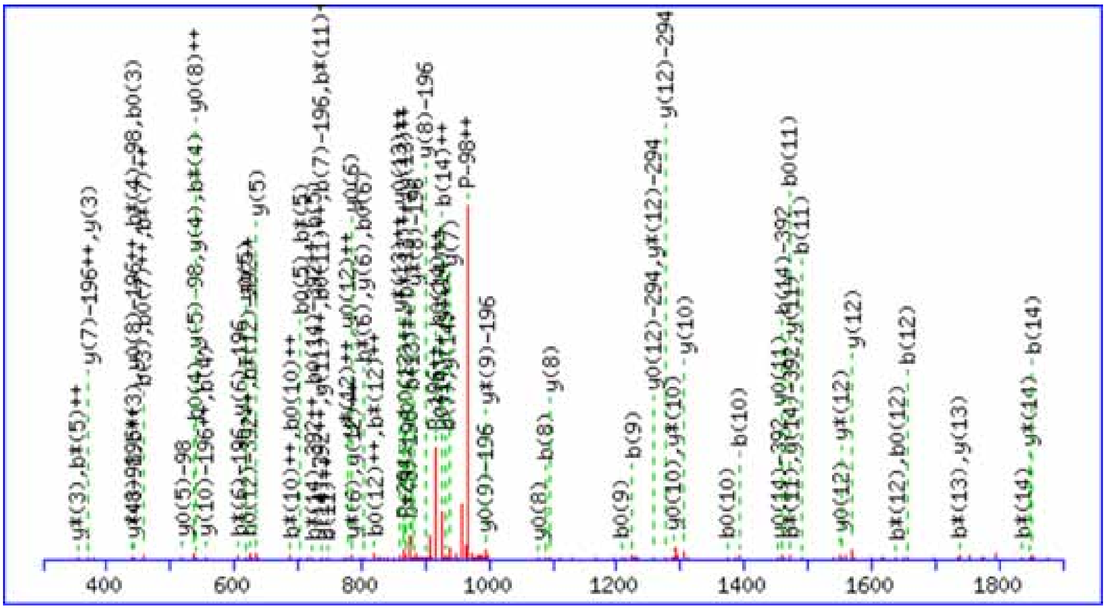
Matched b ions: b(3), b(3)-98, b(4), b(5)-98, b(8), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(10)-196, b(11)-98, b(11), b(11)-196, b(12)-98, b(12)-196, b(13)-196, b(13), b(13)-294, b(14), b(14)-294, b(14)-98
Matched y ions: y(3), y(4), y(5)-98, y(5), y(7), y(8), y(8)-196, y(9)-98++, y(9), y(10)-196++, y(10), y(11)++, y(11)-98, y(11)-196, y(12)++, y(12)-98, y(12), y(12)-98++, y(12)-196, y(13), y(13)++, y(13)-196++, y(13)-98, y(13)-98++, y(13)-294, y(14)-294++, y(14)-294, y(14)-196, y(14)-196++, y(14)++
Precursor origin neutral loss: +

Peptide No.680

QQSPSPIRHSPSPVR
Confirmed sites: @S:3,@S:5,@S:10,@S:12
Ambiguous sites:

MS/MS Fragmentation of QQSPSPIRHSPSPVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4918: 2025.810410 from(1013.912481,2+)
Title: Elution from: 26.012 to 26.012 scan no 1591 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2025.8089
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00047

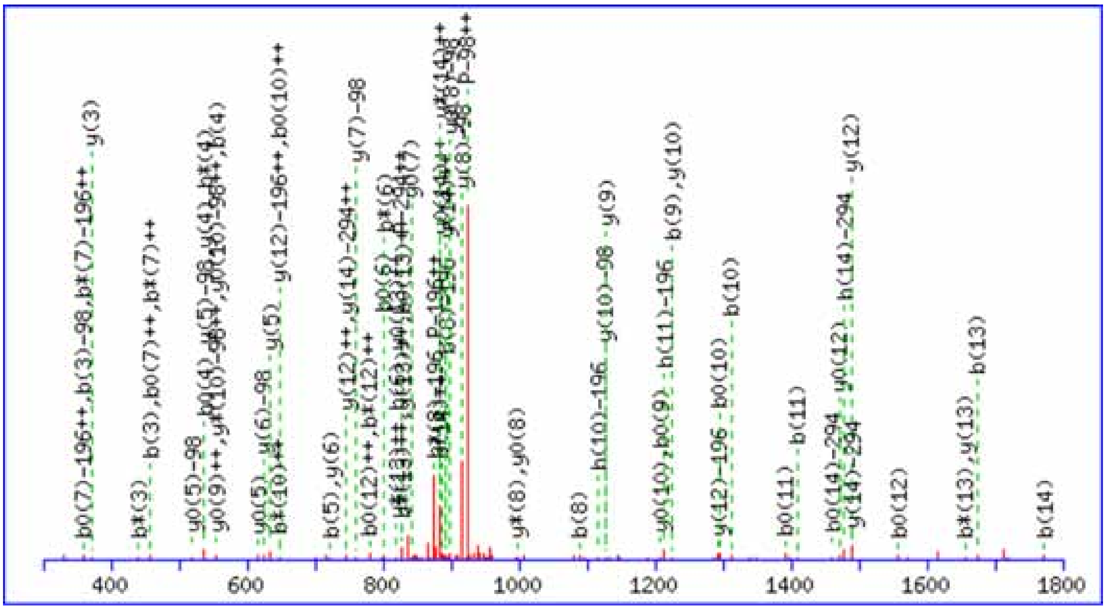
Matched b ions: b(3), b(4), b(5)-98, b(5), b(7)-196, b(7)-98, b(7), b(8), b(8)-98, b(9), b(10)-98, b(10), b(10)-196, b(11)-196, b(11)-98, b(11), b(11)++, b(12)-196, b(12)-98, b(12), b(13)-196, b(13)-98, b(13)++, b(14), b(14)-392, b(14)-294, b(14)-98, b(14)-196, b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(4)-98, y(5)-98, y(5), y(6)-98, y(6)-196, y(6), y(7)-196++, y(7), y(7)-98, y(8), y(8)-98, y(8)-196, y(9)-98++, y(10)-98, y(10), y(10)-196++, y(11)-98++, y(11), y(11)++, y(11)-98, y(11)-196, y(12)-196++, y(12)-98, y(12), y(12)++, y(12)-98++, y(12)-196, y(12)-294, y(13)-98++, y(13), y(13)-196++, y(13)-294++, y(13)-98, y(13)++, y(14)-294++, y(14)-392, y(14)-294, y(14)-392++, y(14)-196++, y(14)++
Precursor origin neutral loss: +

Peptide No.681

QQSPSPIRHSPSPVR
Confirmed sites: @S:3,@S:5,@S:12
Ambiguous sites:

MS/MS Fragmentation of QQSPSPIRHSPSPVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4720: 1945.844048 from(973.929300,2+)
Title: Elution from: 25.195 to 25.195 scan no 1493 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1945.8426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0066

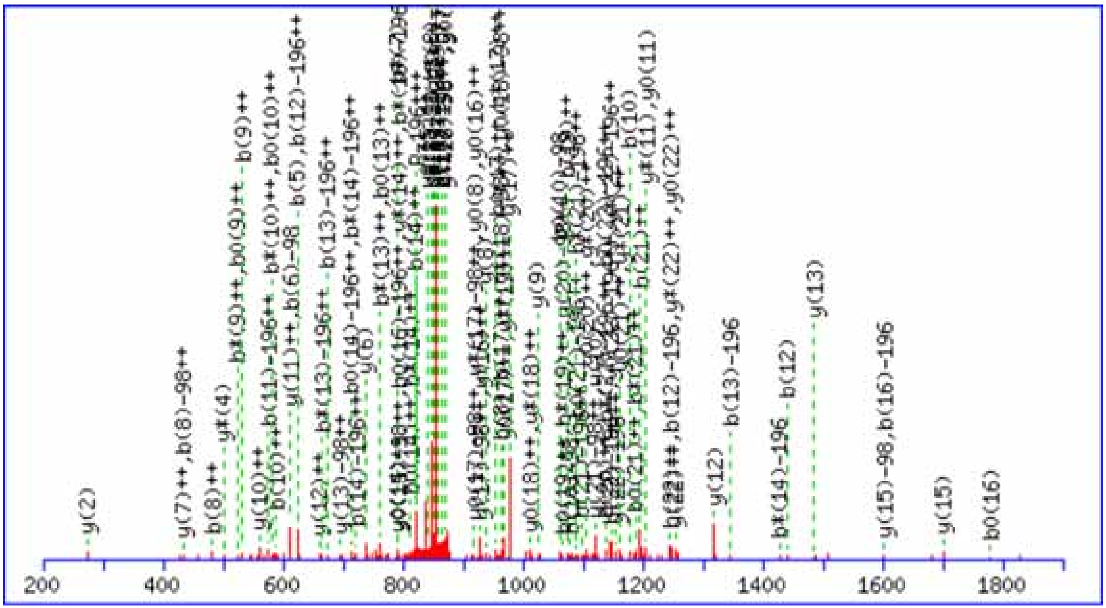
Matched b ions: b(3), b(3)-98, b(4), b(5)-98, b(5), b(6), b(8), b(8)-196, b(9)-98, b(9), b(10)-98, b(10), b(10)-196, b(11)-196, b(11)-98, b(11), b(12)-98, b(13)-196, b(13), b(14), b(14)-294, b(14)-98, b(14)++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6)-98, y(6), y(7)-98, y(8)-98, y(9), y(10)-98, y(10), y(11)-98, y(11)-98++, y(12)-98, y(12), y(12)-196, y(12)-196++, y(12)++, y(13)-98++, y(13)-98, y(13)++, y(13), y(13)-196, y(14)-294++, y(14)-294, y(14)++
Precursor origin neutral loss: +

Peptide No.682

QSLGESPRTLSPTPSAEGYQDVR
Confirmed sites: @S:2,@S:11
Ambiguous sites:

MS/MS Fragmentation of QSLGESPRTLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 7023: 2662.170387 from(888.397405,3+)
Title: Elution from: 42.562 to 42.562 scan no 3814 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2662.1677
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 0.0017

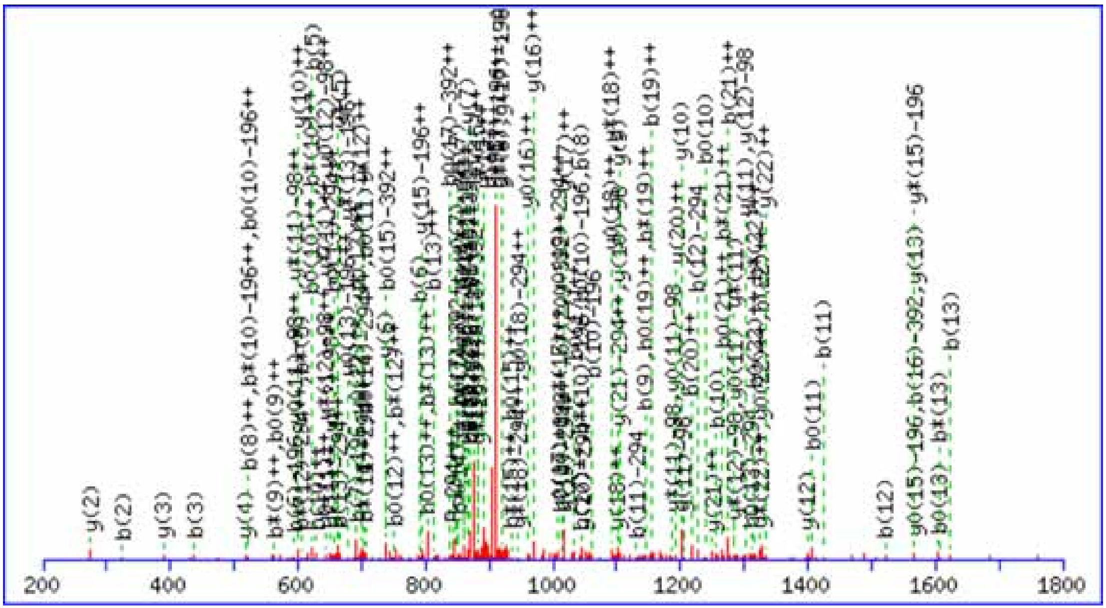
Matched b ions: b(5), b(6)-98, b(8)-98++, b(8)++, b(8), b(8)-98, b(9)++, b(10)++, b(10), b(10)-98, b(11)-98++, b(11)-196++, b(11)-98, b(12), b(12)-196++, b(12)-196, b(13)-196, b(13)-98++, b(13)-196++, b(14)-196++, b(14)++, b(15)++, b(16)-196, b(16)-98, b(16)-98++, b(17)++, b(17)-196++, b(17)-98++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(21)-196++, b(22)-98++, b(22)-196++, b(22)++
Matched y ions: y(2), y(6), y(7)++, y(7), y(8), y(9), y(10)++, y(10), y(11)++, y(12), y(12)++, y(13), y(13)-98++, y(15)-98, y(15), y(15)++, y(16)++, y(17)++, y(17)-98++, y(20)-98++, y(21)-98++, y(22)-98++, y(22)++, y(22)-196++
Precursor origin neutral loss: +

Peptide No.683

QSLGESPRTLSPTPSAEGYQDVR
Confirmed sites: @S:2,@S:6,@S:11,@S:15
Ambiguous sites:

MS/MS Fragmentation of QSLGESPRTLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 7209: 2822.101704 from(941.707844,3+)
Title: Elution from: 48.276 to 48.276 scan no 4492 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2822.1003
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.0011

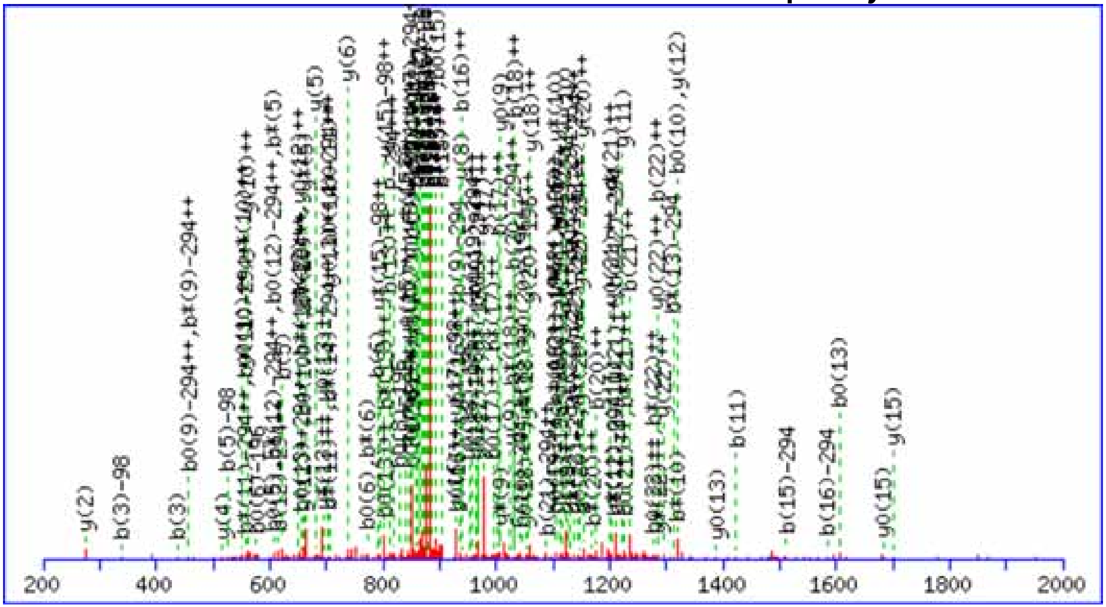
Matched b ions: b(2), b(3), b(5), b(6)-98, b(6)-196, b(6), b(7)-196, b(7)-98, b(8), b(8)-98++, b(8)++, b(8)-98, b(9)-98, b(9), b(10)++, b(10)-98, b(10), b(10)-196, b(11)-98++, b(11)-98, b(11)-196, b(11), b(11)-196++, b(11)-294, b(12)-196++, b(12)-196, b(12), b(12)-294, b(13), b(13)-294++, b(13)-196++, b(13)-98++, b(13)++, b(14)-196++, b(14)++, b(15)-98++, b(15)-294++, b(15)-196++, b(16)-392, b(16)-294++, b(16)-196++, b(16)-98++, b(17)++, b(17)-294++, b(17)-98++, b(17)-392++, b(17)-196++, b(18)-392++, b(18)-294++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(21)-196++, b(22)-98++, b(22)-196++, b(22)++, b(22)-294++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(9), y(10)-98, y(10), y(10)++, y(11), y(11)++, y(11)-98, y(12), y(12)++, y(12)-98, y(12)-98++, y(13), y(13)-98, y(15)-196++, y(15)-98++, y(15)++, y(16)-196++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(18)-98++, y(18)-196++, y(19)-294++, y(20)-294++, y(20)-196++, y(20)-98++, y(20)++, y(21)-294++, y(21)-98++, y(21)++, y(21)-196++, y(22)-294++, y(22)-196++, y(22)-98++, y(22)++
Precursor origin neutral loss: +

Peptide No.684

QSLGESPRTLSPTPSAEGYQDVR
Confirmed sites: @S:2,@S:6,@T:9
Ambiguous sites:

MS/MS Fragmentation of QSLGESPRTLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 7095: 2742.136080 from(915.052636,3+)
Title: Elution from: 45.655 to 45.655 scan no 4207 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2742.1340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.021

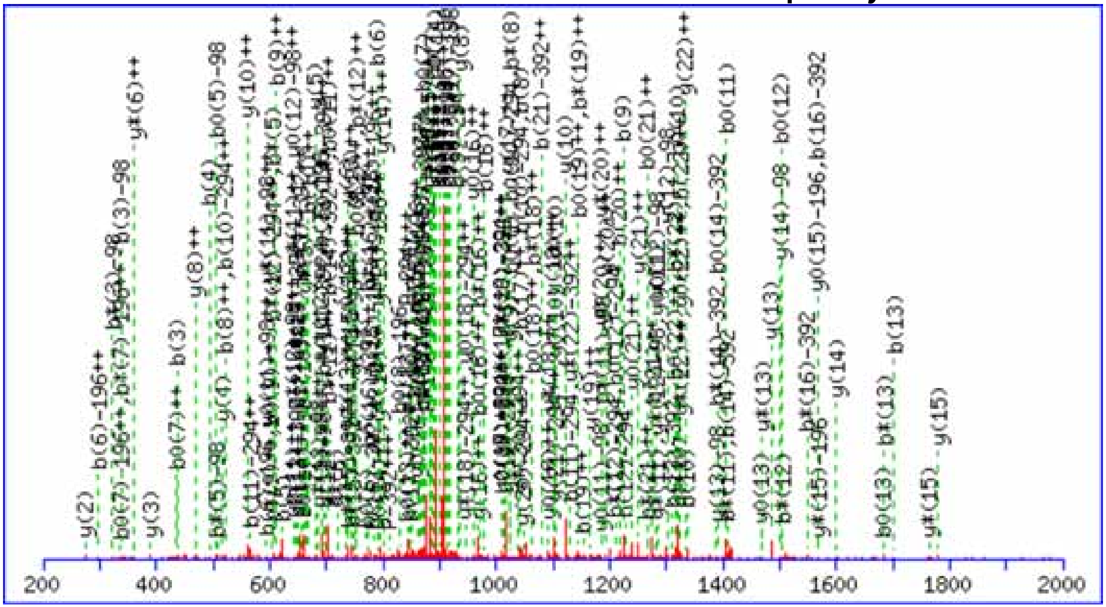
Matched b ions: b(3)-98, b(3), b(5), b(5)-98, b(6)-98, b(6), b(7), b(8), b(8)-196, b(8)-98, b(9)-98++, b(9)-294, b(9)-98, b(10)-196++, b(10)-98++, b(10)-294, b(10)-98, b(11)-98++, b(11)-98, b(11)-196++, b(11), b(11)-196, b(12)-196++, b(12)-196, b(12)-294++, b(12)-98, b(13)-98++, b(13)++, b(14)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-196++, b(15)-98++, b(15)-294, b(16)-196, b(16)-98, b(16)-294, b(16)-98++, b(16)-196++, b(16)++, b(17)++, b(17)-294++, b(18)-294++, b(18)++, b(19)++, b(19)-294++, b(19)-98++, b(20)++, b(20)-294++, b(20)-98++, b(21)++, b(21)-98++, b(21)-294++, b(21)-196++, b(22)-98++, b(22)-196++, b(22)++, b(22)-294++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(12), y(12)++, y(13)++, y(15), y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(18)-196++, y(19)++, y(20)++, y(20)-98++, y(20)-196++, y(21)++, y(21)-98++, y(21)-196++, y(22)-196++, y(22)++, y(22)-98++, y(22)-294++
Precursor origin neutral loss: +

Peptide No.685

QSLGESPRTLSPTPSAEGYQDVR
Confirmed sites: @S:2,@S:6,@T:9,@T:13
Ambiguous sites:

MS/MS Fragmentation of QSLGESPRTLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 8669: 2822.102814 from(941.708214,3+)
Title: Elution from: 47.876 to 47.876 scan no 4687 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2822.1003
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.0014

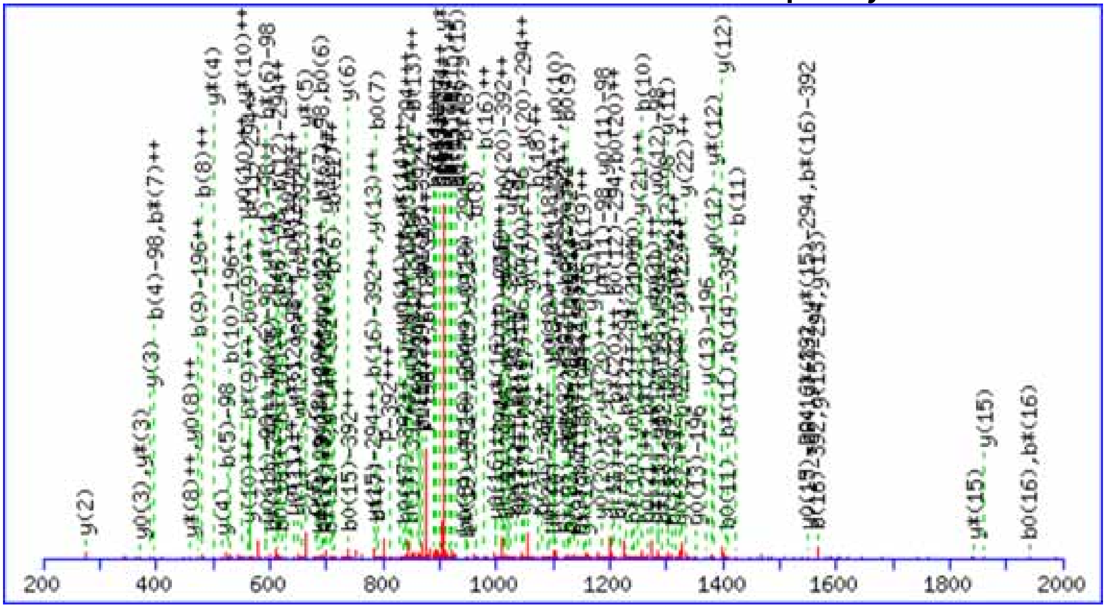
Matched b ions: b(3), b(3)-98, b(4), b(5), b(6)-196++, b(6)-98, b(6)-196, b(6), b(7)-196, b(7)-98, b(7), b(8), b(8)-98++, b(8)++, b(8)-98, b(9)-98++, b(9)-98, b(9)-196++, b(9)++, b(9)-294, b(9)-196, b(9), b(10)-98++, b(10)-98, b(10)-196++, b(10)-294, b(10), b(10)-294++, b(10)++, b(11)-294++, b(11)-98++, b(11)-294, b(11)-98, b(12)-196++, b(12)-294, b(12)-196, b(13)-98, b(13), b(13)-294++, b(13)-392++, b(13)-196++, b(13)-98++, b(13)-392, b(13)-294, b(13)-196, b(14)-392++, b(14)-196, b(14)-392, b(14)-98, b(14)-294++, b(14)-196++, b(14)++, b(15)-98++, b(15)-392++, b(15)-294++, b(15)-196++, b(16)-98, b(16)-294, b(16)-392++, b(16)-294++, b(16)-196++, b(16)-98++, b(16)++, b(16)-392, b(17)++, b(17)-98++, b(17)-392++, b(17)-294++, b(17)-196++, b(18)-392++, b(18)-294++, b(18)-196++, b(18)-98++, b(19)-98++, b(19)-196++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(21)-392++, b(21)-294++, b(21)-196++, b(22)-196++, b(22)-98++, b(22)++, b(22)-294++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10)++, y(10), y(11)++, y(12)-98++, y(12)-98, y(12)++, y(13), y(13)++, y(13)-98++, y(13)-98, y(14), y(14)-98++, y(14)++, y(14)-98, y(15), y(15)-98, y(15)-196++, y(15)-98++, y(15)++, y(16)-196++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(18)-98++, y(18)-196++, y(19)-294++, y(19)++, y(20)-98++, y(20)++, y(20)-294++, y(20)-196++, y(21)++, y(21)-294++, y(21)-98++, y(21)-196++, y(22)-294++, y(22)-196++, y(22)-98++, y(22)++
Precursor origin neutral loss: +

Peptide No.686

QSLGESPRTLSPTPSAEGYQDVR
Confirmed sites: @S:2,@T:9,@S:11,@T:13
Ambiguous sites:

MS/MS Fragmentation of QSLGESPRTLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 7361: 2822.101743 from(941.707857,3+)
Title: Elution from: 47.423 to 47.423 scan no 4446 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2822.1003
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.056

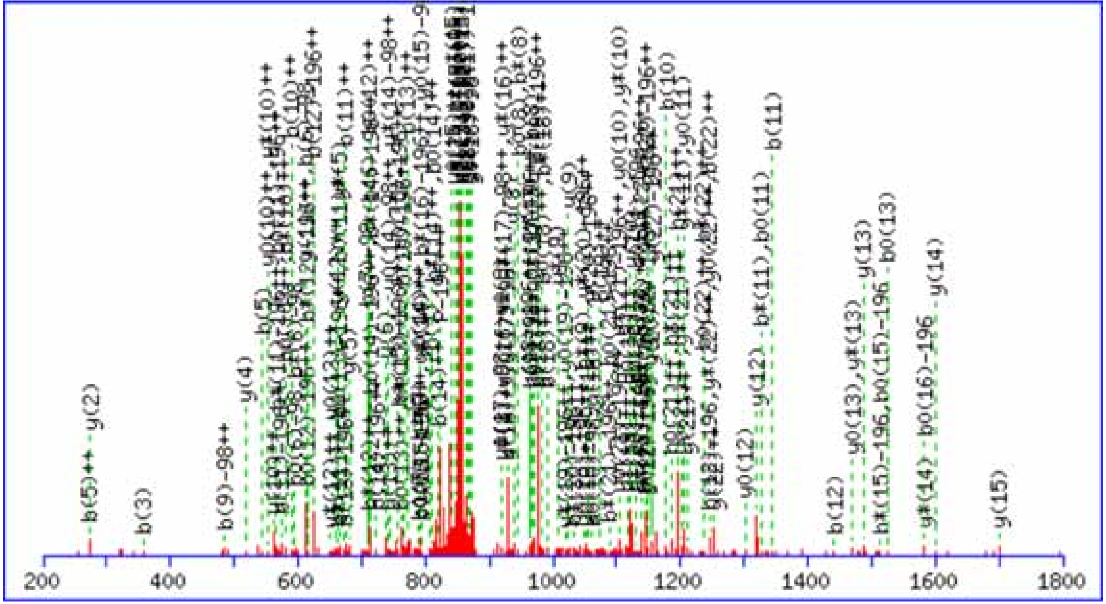
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(8)++, b(8), b(9)-98++, b(9)-98, b(9)-196++, b(9), b(10)-196++, b(10)-98++, b(10)-98, b(10), b(10)++, b(11)-98++, b(11)-98, b(11)-196++, b(11)-294++, b(11)-196, b(11), b(11)++, b(12)-196++, b(12)-196, b(12)-294++, b(12)-294, b(12)-98, b(12)-98++, b(13)-98++, b(13)-196++, b(13)-196, b(13)-98, b(13)-294++, b(13)-392++, b(13)-392, b(13)++, b(14)-196++, b(14)-196, b(14)-294++, b(14)-294, b(14)-392++, b(14)-392, b(14)-98++, b(14)++, b(15)-98++, b(15)-196++, b(16)-392, b(16)-196, b(16)-392++, b(16)-196++, b(16)-98, b(16)-98++, b(16)++, b(17)-98, b(17)-98++, b(17)++, b(17)-294++, b(17)-392++, b(17)-196++, b(18)-392++, b(18)-294++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-392++, b(20)-196++, b(20)-98++, b(20)++, b(21)++, b(21)-98++, b(21)-196++, b(21)-392++, b(21)-294++, b(22)-98++, b(22)-196++, b(22)++, b(22)-294++, b(22)-392++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9), y(10)++, y(11)++, y(11), y(11)-98, y(12), y(12)++, y(12)-98++, y(12)-98, y(13), y(13)-98, y(13)++, y(13)-98++, y(13)-196++, y(13)-196, y(14)-98, y(14)++, y(14)-98++, y(15)-294, y(15), y(15)-98, y(15)-294++, y(15)-98++, y(15)-196++, y(15)++, y(16)++, y(16)-294++, y(16)-196++, y(16)-98++, y(17)++, y(17)-98++, y(17)-294++, y(17)-196++, y(18)-196++, y(18)-98++, y(18)++, y(19)-294++, y(19)++, y(20)-294++, y(20)-98++, y(21)-98++, y(21)-294++, y(21)-196++, y(21)++, y(22)-98++, y(22)++, y(22)-196++, y(22)-392++, y(22)-294++
Precursor origin neutral loss: +

Peptide No.687

QSLGESPRTLSPTPSAEGYQDVR
Confirmed sites: @S:6,@S:11
Ambiguous sites:

MS/MS Fragmentation of QSLGESPRTLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 6783: 2662.170864 from(888.397564,3+)
Title: Elution from: 42.761 to 42.761 scan no 3811 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2662.1677
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.0023

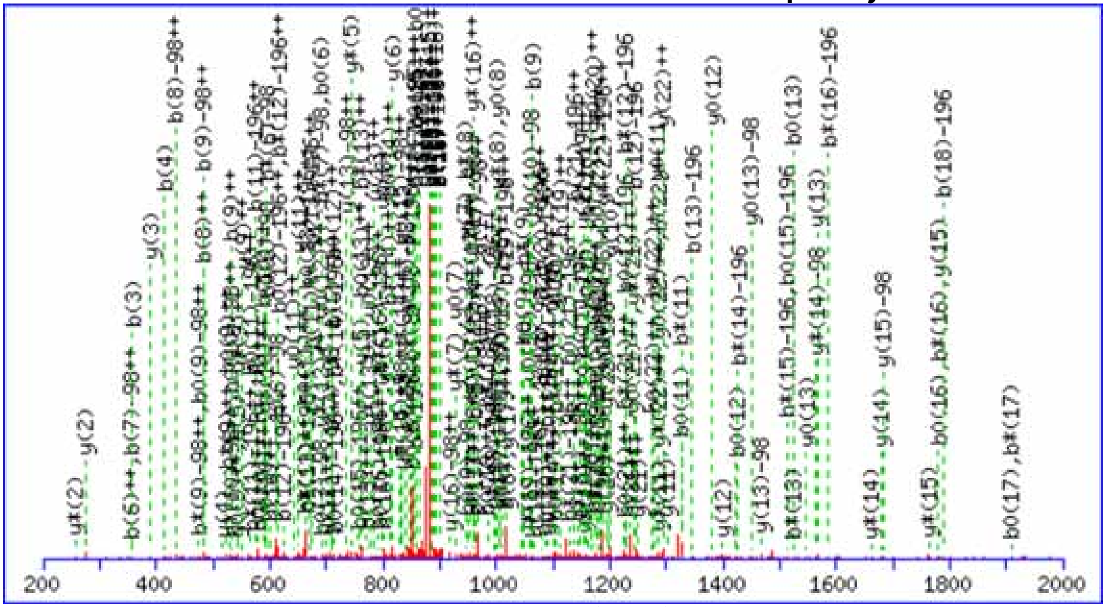
Matched b ions: b(3), b(5)++, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8), b(8)-98, b(9)-98++, b(9)-98, b(10), b(10)++, b(11)-98++, b(11)-196++, b(11)-98, b(11), b(11)-196, b(11)++, b(12)-196++, b(12), b(12)-98, b(12)-196, b(13)-196++, b(13)-98++, b(13)++, b(14)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-196++, b(15)-98++, b(16)-98++, b(17)++, b(17)-196++, b(17)-98++, b(18)++, b(19)-196++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)-98++, b(22)-196++, b(22)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11)++, y(12), y(12)++, y(13), y(13)++, y(14), y(15)++, y(15), y(16)++, y(17)++, y(17)-98++, y(18)-196++, y(18)++, y(19)-98++, y(20)++, y(20)-98++, y(20)-196++, y(21)-98++, y(21)++, y(22)++, y(22)-98++, y(22)-196++
Precursor origin neutral loss: +

Peptide No.688

QSLGESPRTLSPTPSAEGYQDVR
Confirmed sites: @S:6,@S:11,@Y:19
Ambiguous sites:

MS/MS Fragmentation of QSLGESPRTLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 7145: 2742.135117 from(915.052315,3+)
Title: Elution from: 45.015 to 45.015 scan no 4103 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2742.1340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y19 : Phospho (Y)
Ions Score: 39 Expect: 0.0076

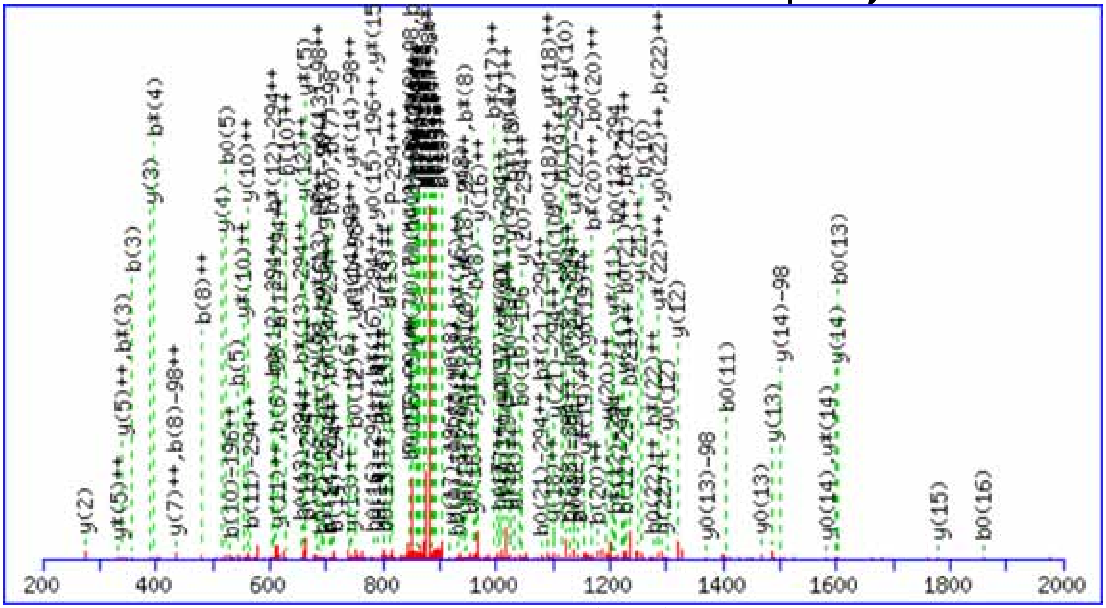
Matched b ions: b(3), b(4), b(5), b(6)-98, b(6)++, b(6), b(7)-98++, b(7)-98, b(8)-98++, b(8)++, b(8), b(8)-98, b(9)-98++, b(9)++, b(9), b(10), b(10)++, b(10)-98, b(11)-98++, b(11)-98, b(11)-196++, b(11)++, b(11)-196, b(12)-196++, b(12)-196, b(12)-98++, b(13)-196++, b(13)-98++, b(13)++, b(13)-196, b(14)-98++, b(15)-98++, b(16)-98++, b(16)-196++, b(16)++, b(17)-196++, b(17)++, b(18)-196, b(18)-196++, b(18)-98++, b(19)++, b(19)-196++, b(19)-98++, b(20)-98++, b(20)++, b(20)-196++, b(21)-98++, b(21)-196++, b(21)++, b(22)-196++, b(22)-98++, b(22)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(11), y(12), y(12)++, y(13), y(13)-98, y(13)-98++, y(13)++, y(14), y(15)-98, y(15), y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(18)-196++, y(19)-196++, y(19)-98++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(21)-196++, y(22)++, y(22)-98++, y(22)-196++
Precursor origin neutral loss: +

Peptide No.689

QSLGESPRTLSPTPSAEGYQDVR
Confirmed sites: @S:6,@T:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of QSLGESPRTLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 6443: 2742.135915 from(915.052581,3+)
Title: Elution from: 44.958 to 44.958 scan no 4009 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2742.1340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 0.00017

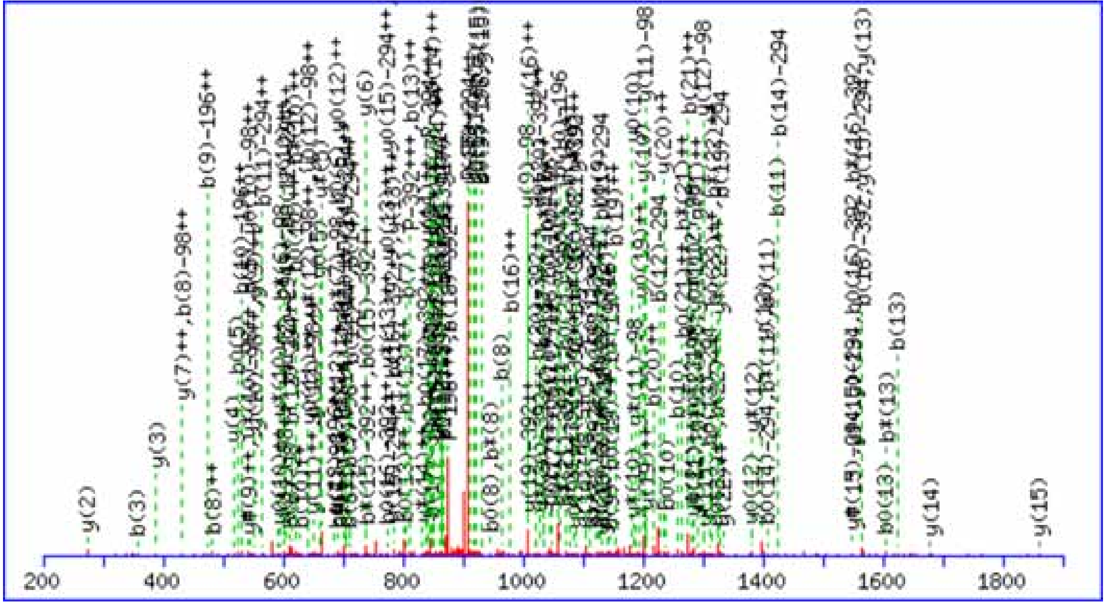
Matched b ions: b(3), b(5), b(6)-98, b(6), b(7)-98, b(8)-98++, b(8)++, b(8)-98, b(8), b(9)-98++, b(9), b(9)-98, b(10)-98++, b(10)-98, b(10)-196++, b(10), b(10)++, b(11)-98++, b(11)-98, b(11)-196++, b(11)-294++, b(11)-196, b(12)-196++, b(12)-196, b(12)-294++, b(12)-294, b(13)-196++, b(13)-98++, b(13)-98, b(13)-294++, b(13)++, b(14)-294++, b(14)-196, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)-98, b(16)-196, b(16)-98++, b(16)-196++, b(17)++, b(17)-294++, b(17)-98++, b(18)-294++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-196++, b(20)-98++, b(21)++, b(21)-196++, b(21)-98++, b(22)-98++, b(22)-294++, b(22)-196++, b(22)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(8), y(9), y(10)++, y(10), y(11)++, y(11), y(12), y(12)++, y(13), y(13)++, y(13)-98++, y(14), y(14)-98, y(14)-98++, y(14)++, y(15), y(15)-98, y(15)++, y(15)-98++, y(16)-196++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++, y(18)-98++, y(18)++, y(18)-196++, y(19)-294++, y(19)-196++, y(20)++, y(20)-294++, y(20)-196++, y(20)-98++, y(21)-98++, y(21)-196++, y(21)++, y(21)-294++, y(22)++, y(22)-98++, y(22)-196++
Precursor origin neutral loss: +

Peptide No.690

QSLGESPRTLSPTPSAEGYQDVR
Confirmed sites: @S:6,@T:9,@S:11,@S:15
Ambiguous sites:

MS/MS Fragmentation of QSLGESPRTLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 7180: 2822.102679 from(941.708169,3+)
Title: Elution from: 47.257 to 47.257 scan no 4399 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2822.1003
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.012

Matched b ions: b(3), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98++, b(8)++, b(8)-98, b(8), b(9)-98++, b(9), b(9)-196++, b(9)-98, b(10)-98++, b(10)-98, b(10)-196++, b(10), b(10)++, b(10)-196, b(11)-98++, b(11)-98, b(11)-196++, b(11), b(11)-294++, b(11)++, b(11)-294, b(11)-196, b(12)-196++, b(12)-196, b(12)-294++, b(12)-98++, b(12)-294, b(13), b(13)++, b(13)-98, b(13)-98++, b(13)-196++, b(13)-294, b(14)-98++, b(14)-196++, b(14)-294++, b(14)++, b(14)-294, b(15)-196++, b(15)-98++, b(15)-294++, b(16)-392, b(16)-392++, b(16)-294++, b(16)-196++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(17)-294++, b(17)-392++, b(17)-196++, b(18)-392++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(19)-294++, b(19)-196++, b(20)-98++, b(20)++, b(20)-392++, b(20)-294++, b(20)-196++, b(21)-98++, b(21)++, b(21)-196++, b(21)-392++, b(21)-294++, b(22)-196++, b(22)-98++, b(22)-294++, b(22)++, b(22)-392++
Matched y ions: y(2), y(3), y(4), y(6), y(7)++, y(7), y(9)++, y(9), y(9)-98, y(10)-98, y(10), y(10)++, y(10)-98++, y(11)++, y(11), y(11)-98++, y(11)-98, y(12), y(12)++, y(12)-98++, y(12)-98, y(13), y(13)++,

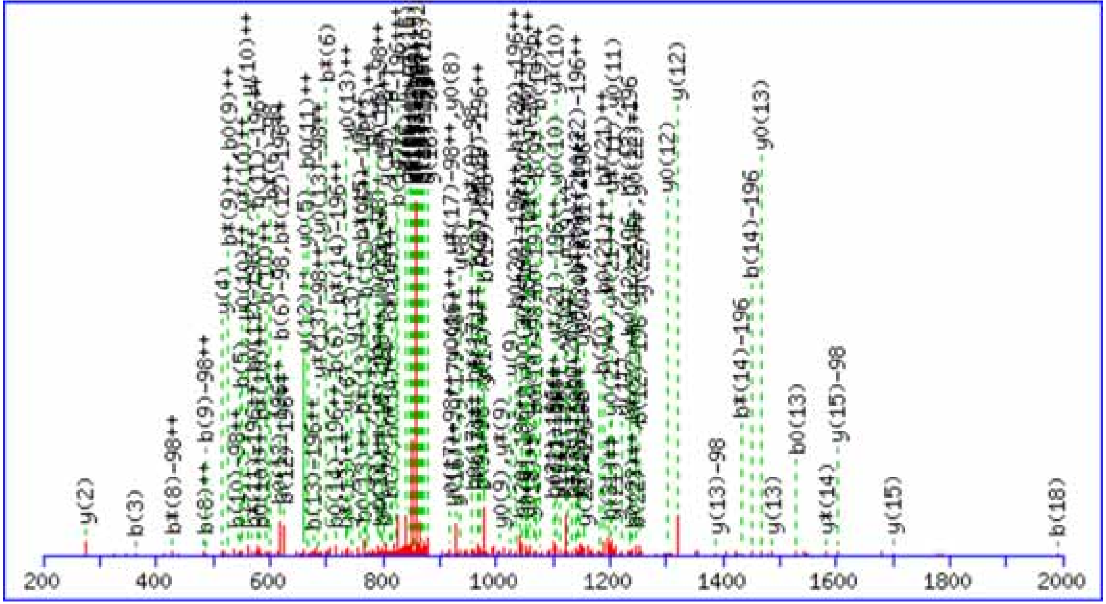
y(13)-98, y(13)-98++, y(13)-196++, y(14), y(14)++, y(14)-98++, y(15)-294, y(15), y(15)-294++, y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(16)-196++, y(16)-98++, y(16)-294++, y(17)++, y(17)-98++, y(17)-294++, y(17)-196++, y(18)-196++, y(18)-98++, y(18)++, y(19)-392++, y(19)++, y(20)-294++, y(20)-196++, y(20)-98++, y(20)++, y(21)-196++, y(21)-98++, y(21)-294++, y(21)++, y(22)-98++, y(22)-196++, y(22)-294++, y(22)++
Precursor origin neutral loss: +

Peptide No.691

QSLGESPRTLSPTPSAEGYQDVR
Confirmed sites: @S:6,@S:11
Ambiguous sites:

MS/MS Fragmentation of QSLGESPRTLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 7161: 2668.200828 from(890.407552,3+)
Title: Elution from: 42.732 to 42.732 scan no 3873 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2668.1995
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.025

Matched b ions: b(3), b(5), b(6)-98, b(6), b(7), b(8)++, b(8), b(8)-98, b(9)-98++, b(9)-98, b(9), b(10)++, b(10)-98++, b(10), b(11)-98++, b(11)-196++, b(11)-98, b(11)-196, b(12)-196++, b(12)-196, b(13)-98, b(13)-196++, b(13)-98++, b(13)++, b(14)-196, b(14)-98++, b(14)++, b(15)++, b(15)-196++, b(16)-98++, b(17)-196++, b(17)-98++, b(17)++, b(18), b(18)-98++, b(19)-196++, b(19)++, b(20)-196++, b(20)++, b(21)++, b(21)-98++, b(21)-196++, b(22)-98++, b(22)-196++, b(22)++
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(12), y(12)++, y(13), y(13)-98,

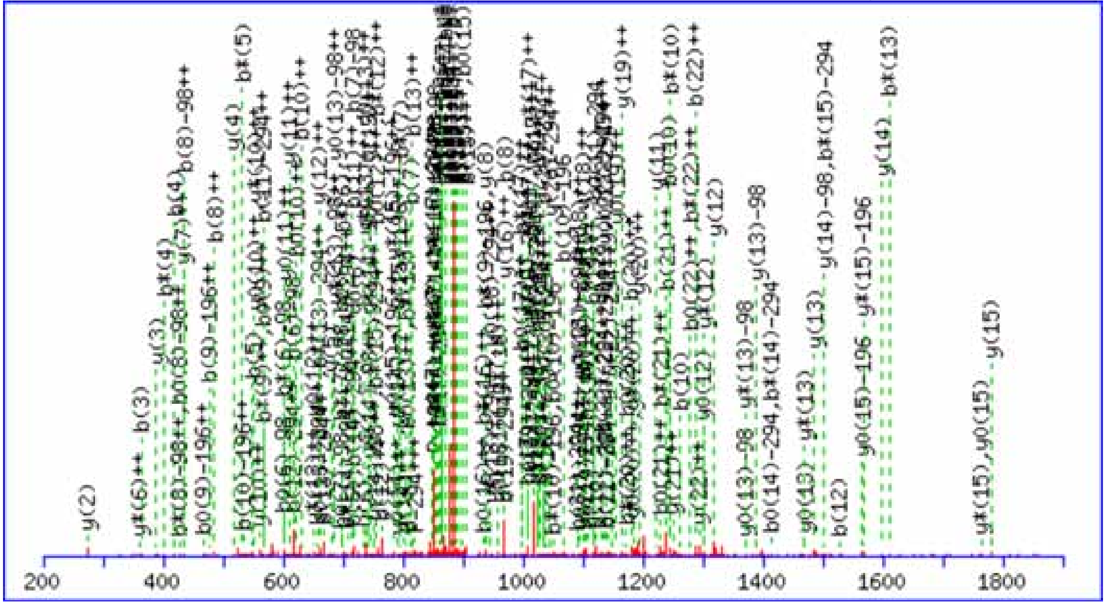
y(13)++, y(14)++, y(15)-98, y(15), y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(20)-196++, y(21)-98++, y(21)++, y(21)-196++, y(22)-98++, y(22)++, y(22)-196++
Precursor origin neutral loss: +

Peptide No.692

QSLGESPRTLSPTPSAEGYQDVR
Confirmed sites: @S:6,@T:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of QSLGESPRTLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 7292: 2748.169068 from(917.063632,3+)
Title: Elution from: 45.127 to 45.127 scan no 4158 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2748.1658
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.028

Matched b ions: b(3), b(4), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98++, b(8), b(8)++, b(8)-98, b(9)-98++, b(9)-98, b(9)-196++, b(10)-98++, b(10)-196, b(10)-98, b(10)-196++, b(10)++, b(10), b(11)-196++, b(11)-98++, b(11)-98, b(11)-294++, b(11)++, b(11)-294, b(11)-196, b(12)-196++, b(12)-196, b(12)++, b(12)-294++, b(12)-98++, b(12), b(13)-98++, b(13)-196++, b(13)-98, b(13)-294++, b(13)++, b(14)-196++, b(14)-294++, b(14)-196, b(14)-98, b(14)-98++, b(14)++, b(15)-98++, b(15)-196++, b(15)++, b(16)-196++, b(16)-98++, b(17)++, b(17)-294++, b(17)-98++, b(18)-294++, b(18)-196++, b(18)-98++, b(18)++, b(19)-196++, b(19)-98++, b(19)++, b(19)-294++, b(20)++, b(20)-294++, b(20)-98++,

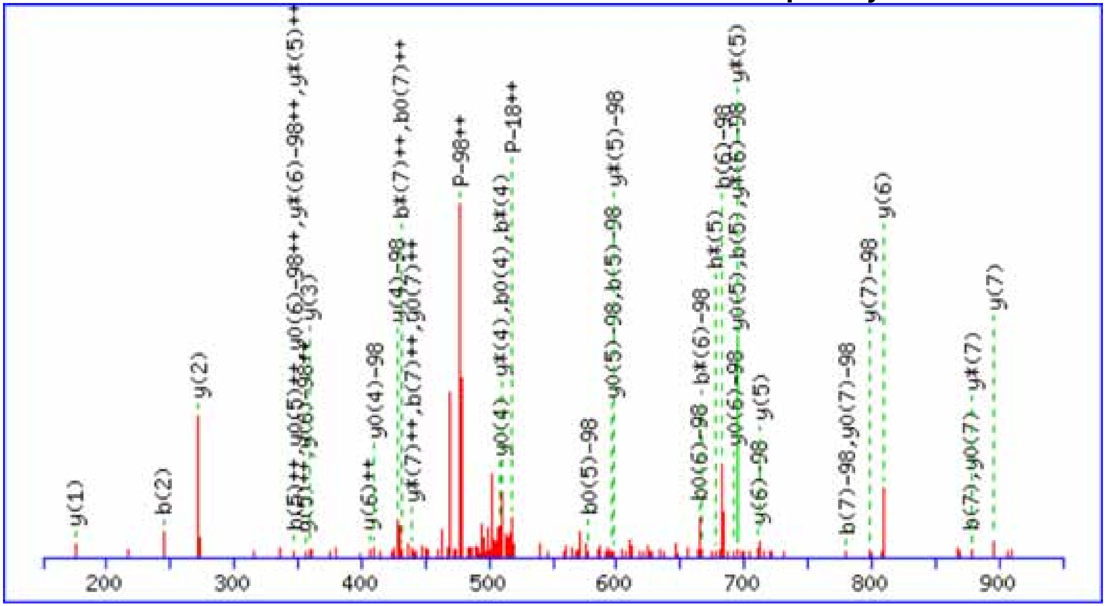
b(21)++, b(21)-98++, b(21)-196++, b(21)-294++, b(22)-98++, b(22)-196++, b(22)-294++, b(22)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(10)++, y(11)++, y(11), y(12), y(12)++, y(13), y(13)++, y(13)-98, y(14), y(14)-98++, y(14)++, y(14)-98, y(15), y(15)-98, y(15)++, y(15)-196++, y(15)-98++, y(16)++, y(16)-196++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(18)-196++, y(19)-294++, y(19)-196++, y(19)++, y(19)-98++, y(20)-98++, y(20)-294++, y(20)-196++, y(20)++, y(21)-294++, y(21)-98++, y(21)-196++, y(21)++, y(22)++, y(22)-98++, y(22)-294++, y(22)-196++
Precursor origin neutral loss: +

Peptide No.693

QSPWSSPK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of QSPWSSPK
Found in LMOD2_MOUSE, Leiomodin-2 OS=Mus musculus GN=Lmod2 PE=1 SV=1

Match to Query 539: 1051.475982 from(526.745267,2+)
Title: Elution from: 30.511 to 30.511 scan no 2173 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1051.4739
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K8 : Dimethyl (K)
Ions Score: 25 **Expect:** 0.051

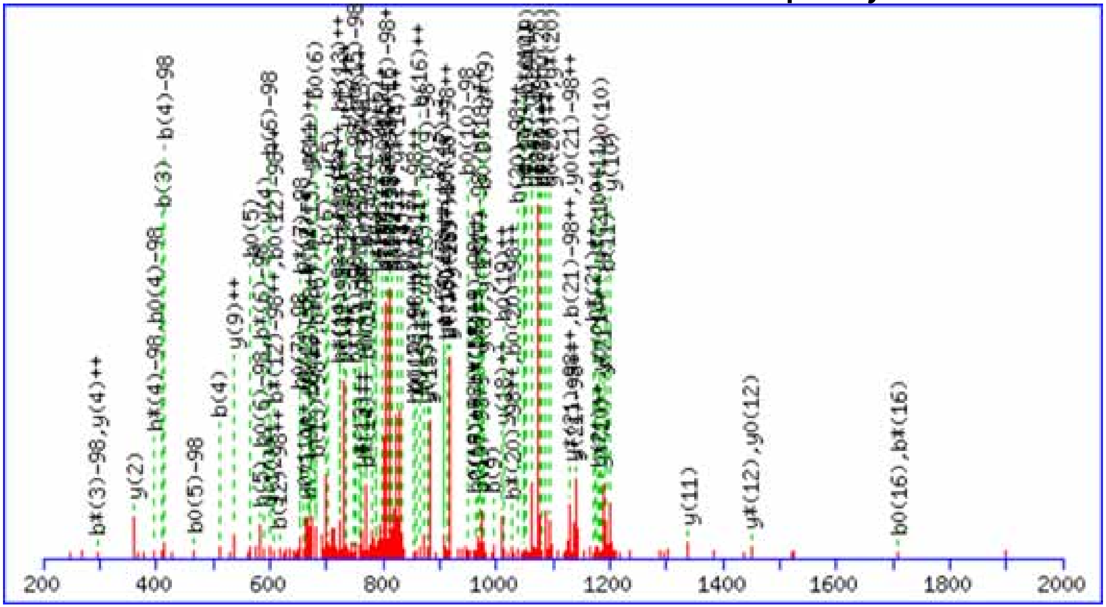
Matched b ions: b(2), b(5)++, b(5), b(5)-98, b(6)-98, b(7), b(7)-98, b(7)++
Matched y ions: y(1), y(2), y(3), y(4)-98, y(5), y(5)++, y(6), y(6)-98, y(6)-98++, y(6)++, y(7), y(7)-98
Precursor origin neutral loss: +

Peptide No.694

QSSTADAPEAQHEPGITITEWK
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of QSSTADAPEAQHEPGITITEWK
Found in KPBB_MOUSE, Phosphorylase b kinase regulatory subunit beta OS=Mus musculus GN=Phkb PE=1 SV=1

Match to Query 6004: 2531.159946 from(844.727258,3+)
Title: Elution from: 47.758 to 47.758 scan no 4296 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2531.1581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K22 : Dimethyl (K)
Ions Score: 41 Expect: 0.0073

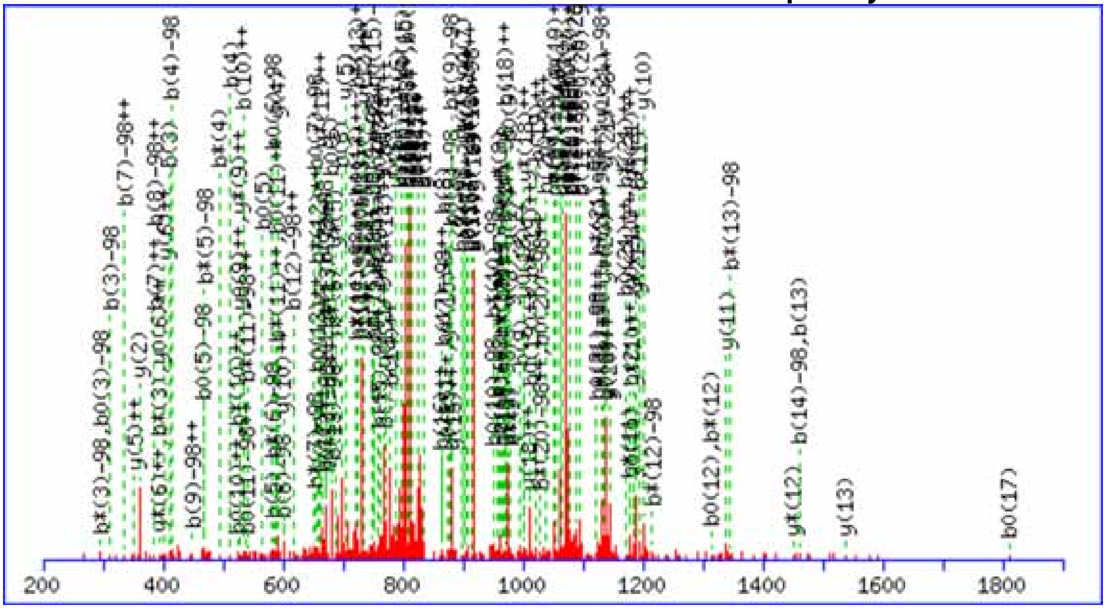
Matched b ions: b(3), b(4)-98, b(4), b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(9), b(10)-98, b(11), b(11)-98, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(18)++, b(19)-98++, b(20)++, b(20)-98++, b(21)-98++, b(21)++
Matched y ions: y(2), y(4)++, y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(21)++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.695

QSSTADAPEAQHEPGITITEWK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QSSTADAPEAQHEPGITITEWK
Found in KPBB_MOUSE, Phosphorylase b kinase regulatory subunit beta OS=Mus musculus GN=Phkb PE=1 SV=1

Match to Query 6612: 2531.162280 from(844.728036,3+)
Title: Elution from: 47.810 to 47.810 scan no 4466 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2531.1581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K22 : Dimethyl (K)
Ions Score: 61 Expect: 7.3e-005

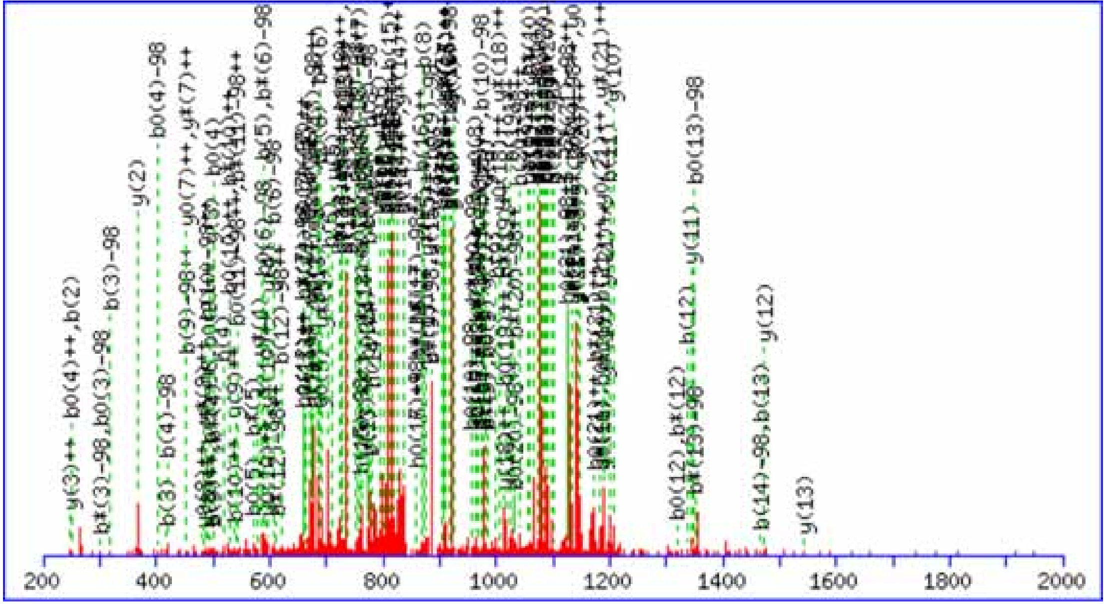
Matched b ions: b(3), b(3)-98, b(4)-98, b(4), b(5), b(6), b(6)-98, b(7), b(7)-98++, b(7)++, b(7)-98, b(8)-98++, b(8), b(9), b(9)-98++, b(9)-98, b(10)++, b(10)-98, b(10), b(11), b(11)-98, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(13), b(14)-98++, b(14)-98, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++
Matched y ions: y(2), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(13), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.696

QSSTADAPEAQHEPGITITEWK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of QSSTADAPEAQHEPGITITEWK
Found in KPBB_MOUSE, Phosphorylase b kinase regulatory subunit beta OS=Mus musculus GN=Phkb PE=1 SV=1

Match to Query 6181: 2543.224410 from(848.748746,3+)
Title: Elution from: 47.964 to 47.964 scan no 4351 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2543.2217
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K22 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 43 Expect: 0.005

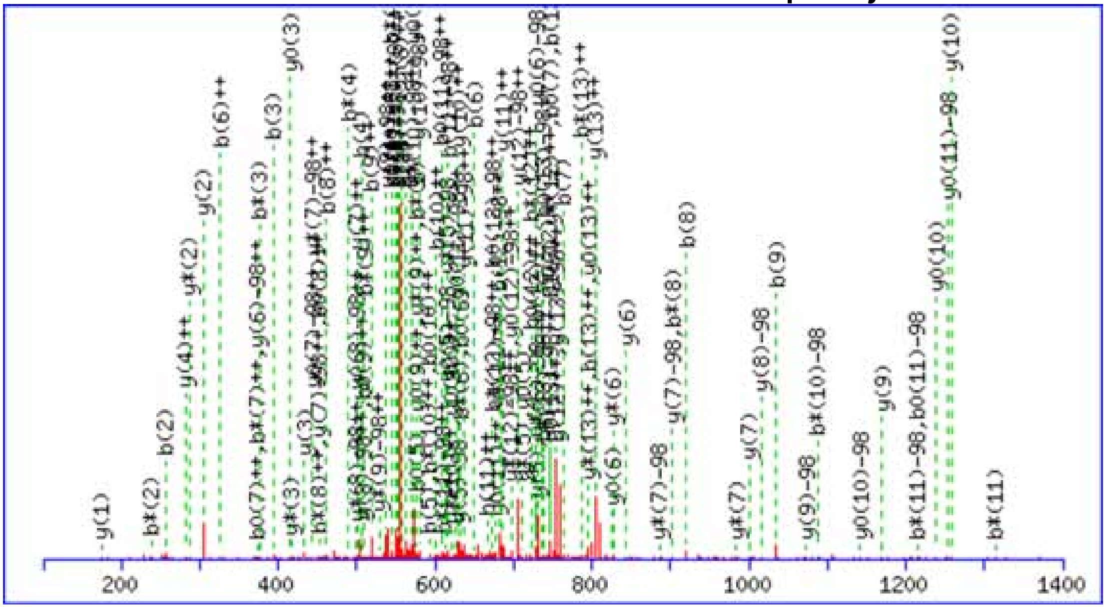
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(9)++, b(9), b(9)-98++, b(9)-98, b(10)++, b(10)-98++, b(10)-98, b(10), b(11), b(11)-98, b(12)++, b(12), b(12)-98++, b(13)++, b(13)-98++, b(13), b(14)-98++, b(14)-98, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(19)++, b(19)-98++, b(20)-98++, b(20)++, b(21)++, b(21)-98++
Matched y ions: y(2), y(3)++, y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.697

QVHISGIRDSEEER
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of QVHISGIRDSEEER
Found in MYOM1_MOUSE, Myomesin-1 OS=Mus musculus GN=Myom1 PE=1 SV=2

Match to Query 4078: 1761.804885 from(588.275571,3+)
Title: Elution from: 28.878 to 28.878 scan no 2149 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1761.8047
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.0058

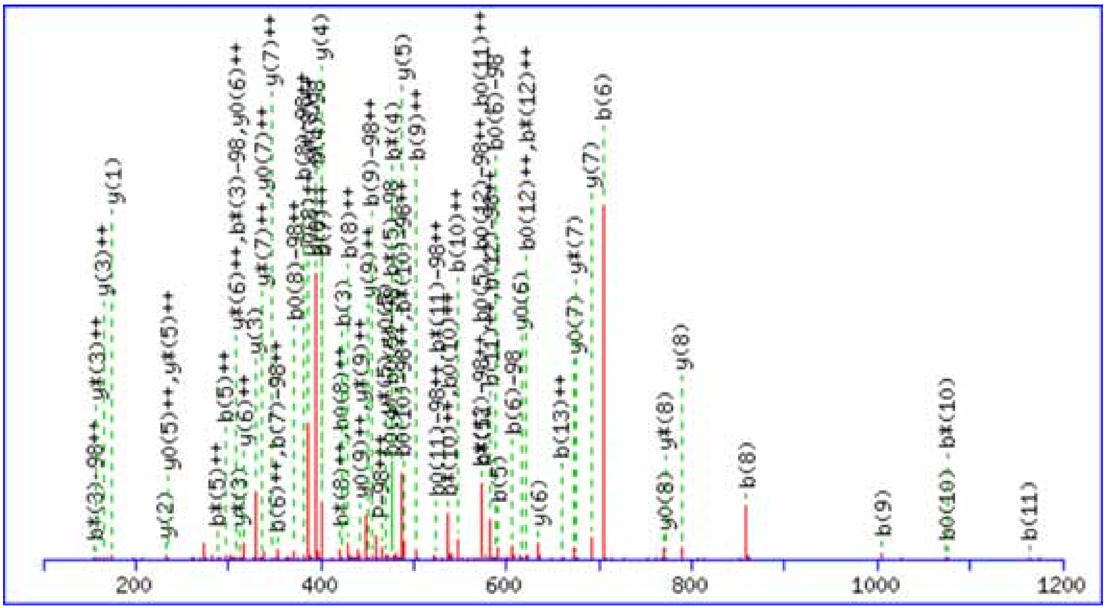
Matched b ions: b(2), b(3), b(4), b(5), b(6)++, b(6), b(7), b(8), b(8)++, b(9), b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5)-98, y(5), y(6)-98++, y(6)-98, y(6), y(7), y(7)-98++, y(7)++, y(7)-98, y(8)-98++, y(8)++, y(8)-98, y(9)-98, y(9)-98++, y(9), y(10)++, y(10), y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.698

RASAPLPGFSAPGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RASAPLPGFSAPGR
Found in HSPB6_MOUSE, Heat shock protein beta-6 OS=Mus musculus GN=Hspb6 PE=1 SV=1

Match to Query 1543: 1490.740614 from(497.920814,3+)
Title: Elution from: 39.490 to 39.490 scan no 3290 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1490.7395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 Expect: 4.2e-005

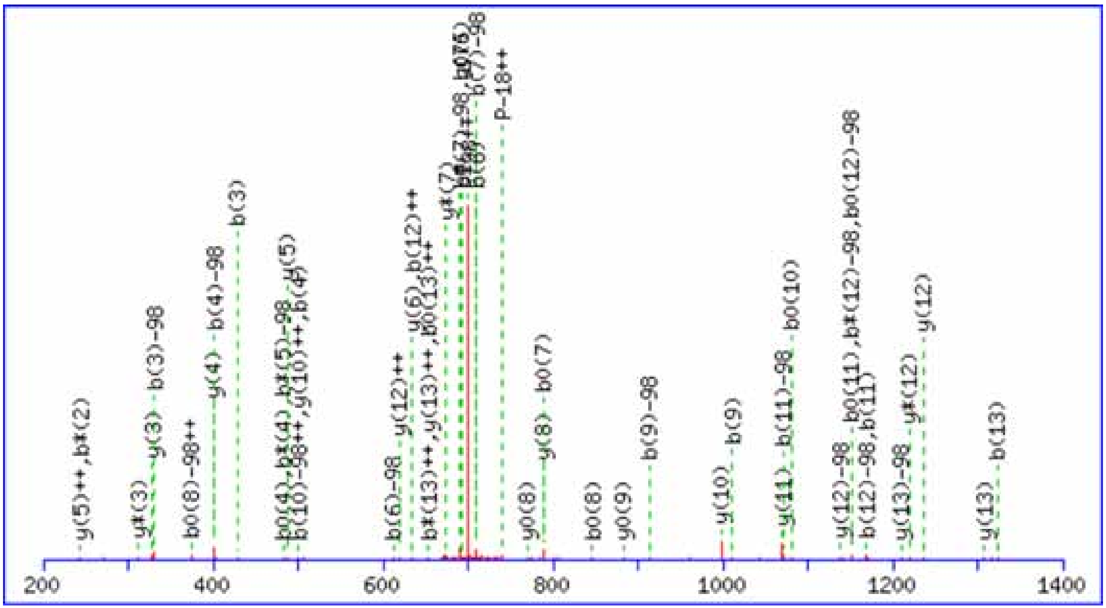
Matched b ions: b(3), b(4)-98, b(5), b(5)++, b(6), b(6)++, b(6)-98, b(7)-98++, b(7)++, b(8), b(8)++, b(8)-98++, b(9), b(9)++, b(9)-98++, b(10)++, b(11), b(11)++, b(12)-98++, b(13)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(8), y(9)++
Precursor origin neutral loss:

Peptide No.699

RASAPLPGFSAPGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RASAPLPGFSAPGR
Found in HSPB6_MOUSE, Heat shock protein beta-6 OS=Mus musculus GN=Hspb6 PE=1 SV=1

Match to Query 1875: 1496.771792 from(749.393172,2+)
Title: Elution from: 39.361 to 39.361 scan no 3335 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1496.7713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 5.6e-006

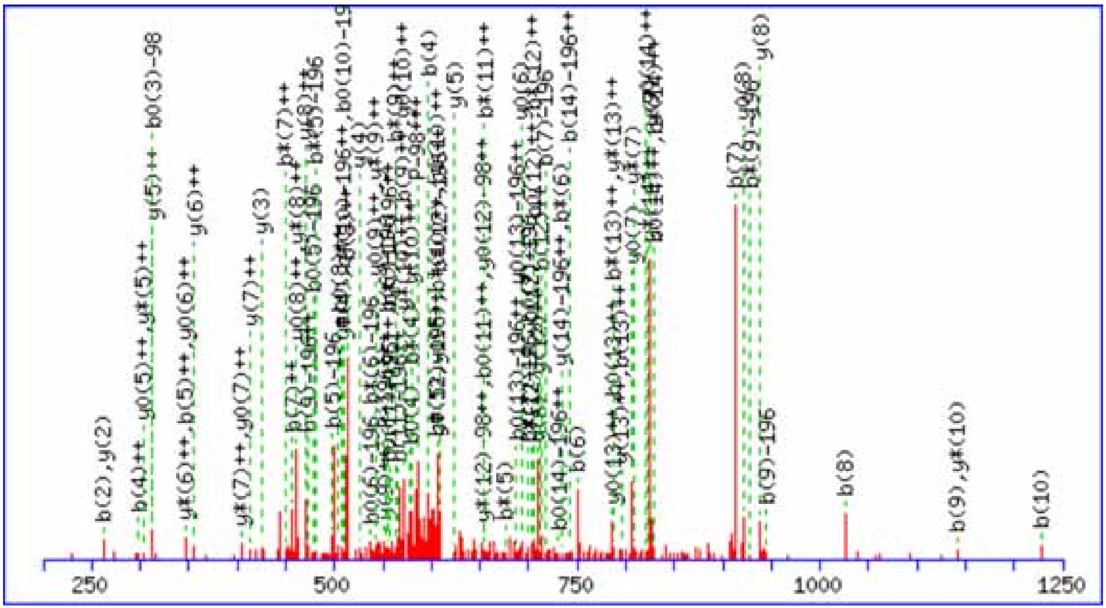
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(6)-98, b(6), b(7)-98, b(9)-98, b(9), b(10)-98++, b(11), b(11)-98, b(12)-98, b(12)++, b(13)
Matched y ions: y(3), y(4), y(5), y(5)++, y(6), y(7), y(8), y(10), y(10)++, y(11), y(12)++, y(12)-98, y(12), y(13), y(13)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.700

RASSPGYIDSPTYSR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of RASSPGYIDSPTYSR
Found in ABLM3_MOUSE, Actin-binding LIM protein 3 OS=Mus musculus GN=Ablim3 PE=1 SV=2

Match to Query 3746: 1849.787337 from(617.603055,3+)
Title: Elution from: 35.069 to 35.069 scan no 2796 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1849.7861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.042

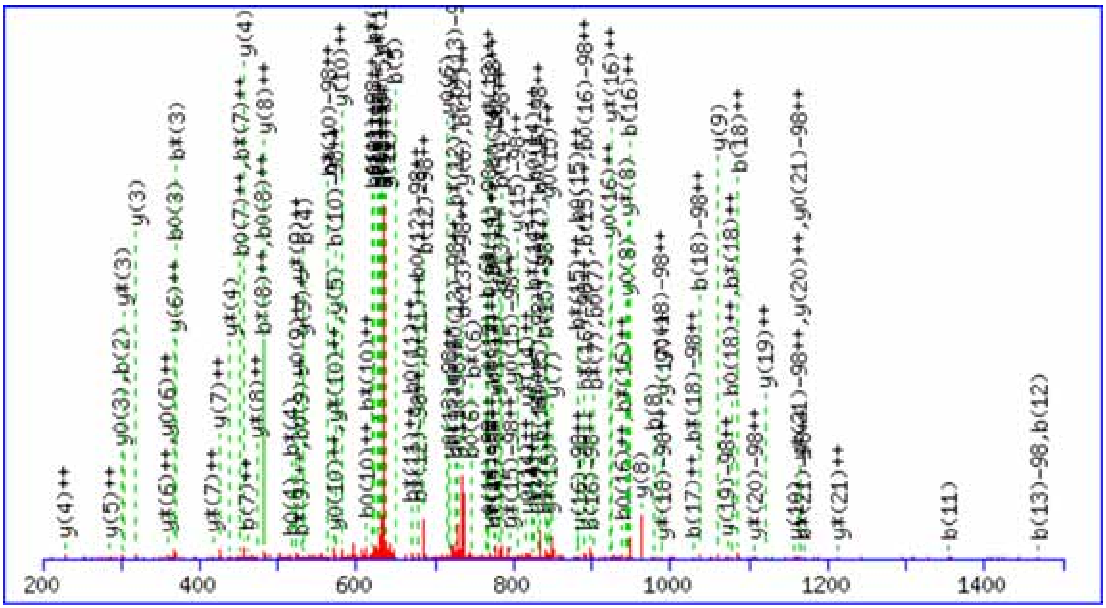
Matched b ions: b(2), b(4), b(4)++, b(4)-98, b(5)++, b(5)-98++, b(5)-196, b(5)-98, b(6), b(6)-196, b(6)-98, b(7), b(7)++, b(7)-196, b(7)-98, b(8)++, b(8), b(8)-98, b(9), b(9)++, b(9)-196, b(9)-196++, b(9)-98++, b(10), b(10)-98++, b(11)-98, b(11)-196++, b(12)++, b(12)-98++, b(13)++, b(14)-196++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(12)++, y(13)++, y(14)-196++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.701

RDSFDDRGPSLNPVLDYDHGSR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of RDSFDDRGPSLNPVLDYDHGSR
Found in MATR3_MOUSE, Matrin-3 OS=Mus musculus GN=Matr3 PE=1 SV=1

Match to Query 6705: 2625.161324 from(657.297607,4+)
Title: Elution from: 44.725 to 44.725 scan no 4050 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2625.1609
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.0073

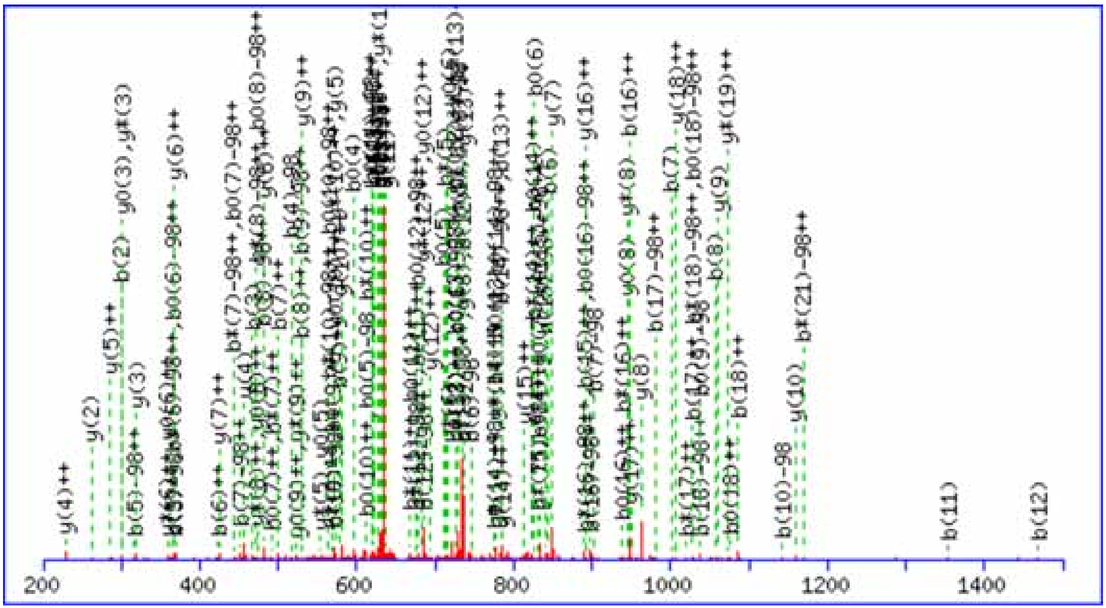
Matched b ions: b(2), b(4), b(5), b(6), b(7)++, b(8), b(10)-98++, b(10)++, b(11), b(11)-98++, b(11)++, b(12)++, b(12), b(12)-98++, b(13)-98++, b(13)-98, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(3), y(4)++, y(4), y(5), y(5)++, y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(16)-98++, y(17)++, y(19)-98++, y(19)++, y(20)++
Precursor origin neutral loss: +

Peptide No.702

RDSFDDRGPSLNPVLDYDHGSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RDSFDDRGPSLNPVLDYDHGSR
Found in MATR3_MOUSE, Matrin-3 OS=Mus musculus GN=Matr3 PE=1 SV=1

Match to Query 7953: 2625.161196 from(657.297575,4+)
Title: Elution from: 45.031 to 45.031 scan no 4307 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2625.1609
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 0.00018

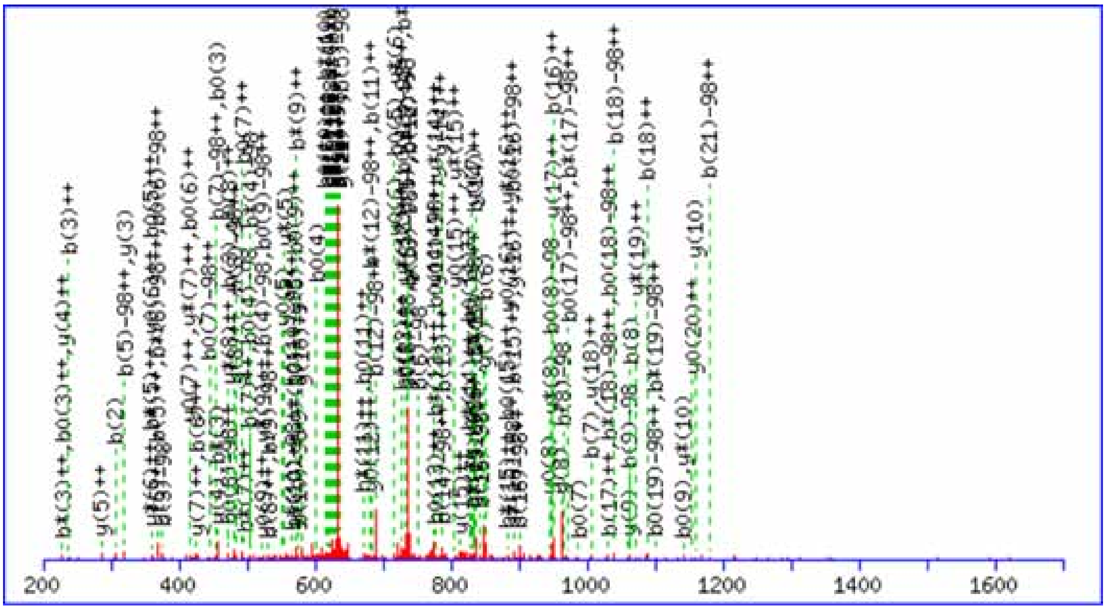
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5), b(5)-98, b(5)++, b(5)-98++, b(6), b(6)++, b(6)-98, b(7)++, b(7)-98++, b(7)-98, b(7), b(8)-98++, b(8)++, b(8), b(9)-98++, b(9)++, b(10)-98, b(10)++, b(10)-98++, b(11)-98++, b(11), b(11)++, b(12)++, b(12), b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6), y(6)++, y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No.703

RDSFDDRGPSLNPVLDYDHGSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RDSFDDRGPSLNPVLDYDHGSR
Found in MATR3_MOUSE, Matrin-3 OS=Mus musculus GN=Matr3 PE=1 SV=1

Match to Query 6247: 2631.193108 from(658.805553,4+)
Title: Elution from: 44.657 to 44.657 scan no 3972 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2631.1927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.0076

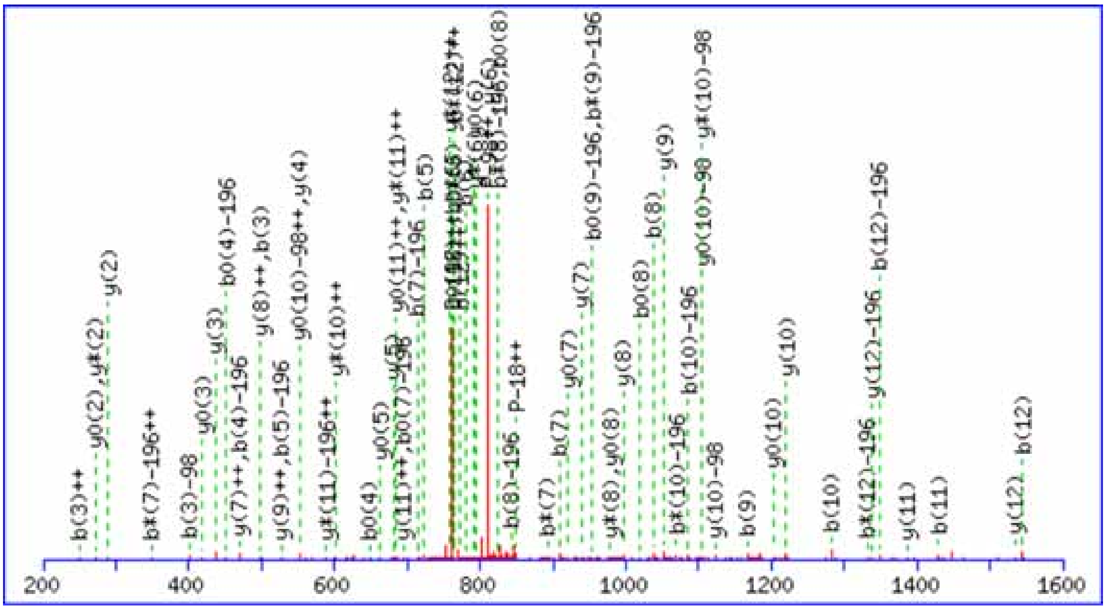
Matched b ions: b(2), b(3)-98, b(3), b(3)++, b(4)-98, b(4), b(5)-98++, b(5)++, b(5), b(5)-98, b(6)++, b(6), b(6)-98, b(7)-98++, b(7)++, b(7), b(8), b(8)-98++, b(8)++, b(8)-98, b(9)-98, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(18)-98++, b(21)-98++
Matched y ions: y(3), y(4), y(4)++, y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(10), y(10)++, y(11)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No.704

RFSSGGEEEDFDR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of RFSSGGEEEDFDR
Found in ABLM3_MOUSE, Actin-binding LIM protein 3 OS=Mus musculus GN=Ablim3 PE=1 SV=2

Match to Query 2962: 1717.603500 from(859.809026,2+)
Title: Elution from: 36.785 to 36.785 scan no 3033 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1717.6022
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 3.4e-008

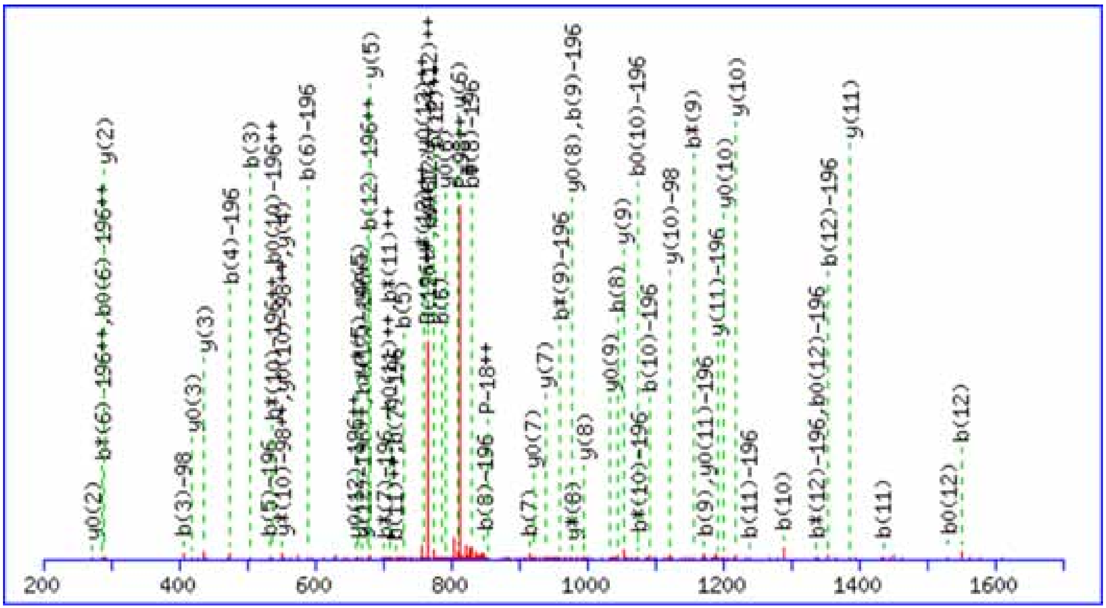
Matched b ions: b(3)++, b(3)-98, b(3), b(4)-196, b(4)-98, b(5), b(5)-98, b(5)-196, b(6)-98, b(6), b(7)-98, b(7), b(7)-196, b(8)-98++, b(8), b(8)-98, b(8)-196, b(9), b(9)-98, b(10), b(10)-196, b(10)-98, b(11), b(11)-98, b(12)-98++, b(12)-98, b(12), b(12)-196, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)-98, y(11)-98, y(11), y(11)++, y(12), y(12)-98, y(12)-196
Precursor origin neutral loss: +

Peptide No.705

RFSSGGEEEDFDR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of RFSSGGEEEDFDR
Found in ABLM3_MOUSE, Actin-binding LIM protein 3 OS=Mus musculus GN=Ablim3 PE=1 SV=2

Match to Query 2991: 1723.635044 from(862.824798,2+)
Title: Elution from: 36.765 to 36.765 scan no 3030 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1723.6340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0052

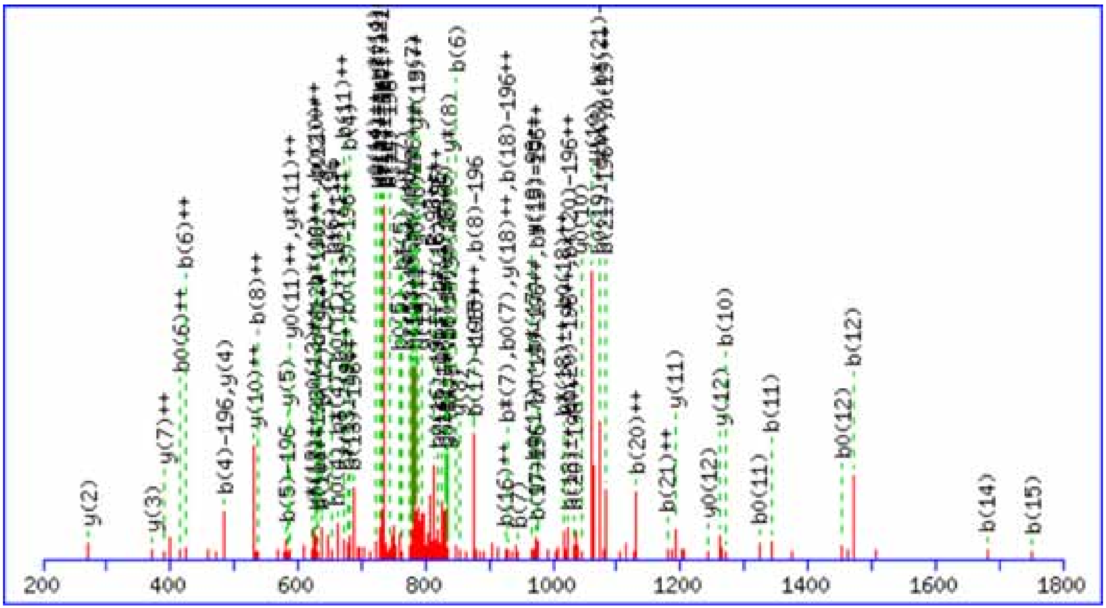
Matched b ions: b(3)-98, b(3), b(4)-98, b(4)-196, b(4)-98++, b(5)-98, b(5)-196, b(5), b(6)-196, b(6), b(7), b(7)-196, b(7)-98, b(8), b(8)-98, b(8)-196, b(9), b(9)-98, b(9)-98++, b(9)-196, b(10), b(10)-196, b(10)-98, b(11), b(11)++, b(11)-98, b(11)-196, b(11)-98++, b(12)-98, b(12), b(12)-196, b(12)-98++, b(12)-196++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)-98, y(11), y(11)-196, y(12)-98, y(12)-98++, y(12)-196++, y(12)++
Precursor origin neutral loss: +

Peptide No.706

RFSTPAPQPTAEPLAPTVLVPR
Confirmed sites: @S:3,@T:4
Ambiguous sites:

MS/MS Fragmentation of RFSTPAPQPTAEPLAPTVLVPR
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 6439: 2532.255840 from(845.092556,3+)
Title: Elution from: 56.718 to 56.718 scan no 5345 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2532.2543
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 Expect: 0.00068

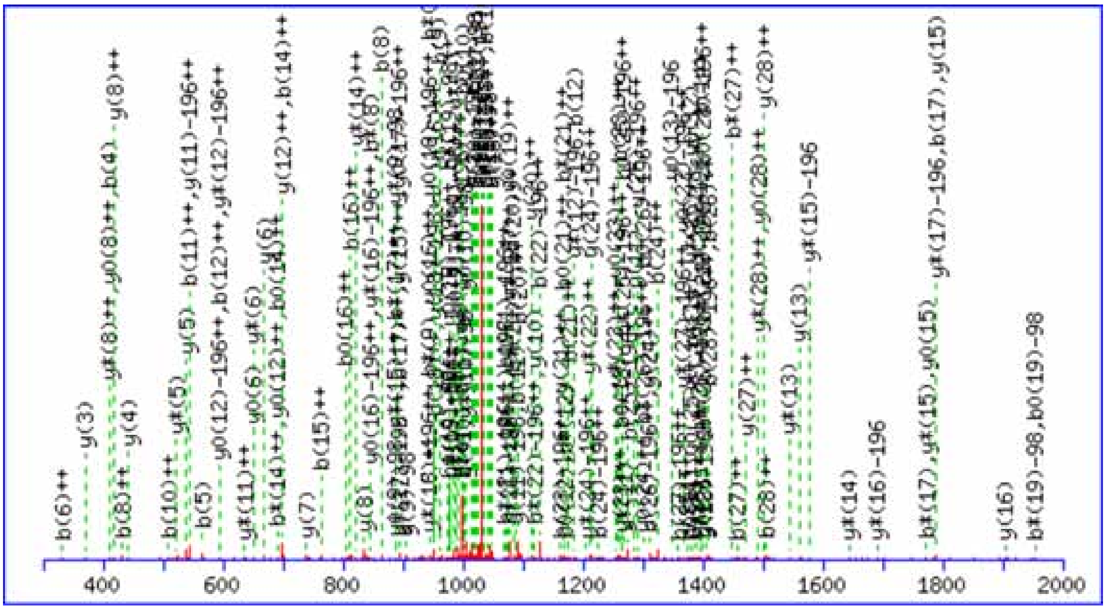
Matched b ions: b(4)-196, b(4)-98, b(4), b(5)-196, b(5)-98, b(6)++, b(6)-98, b(6)-196, b(6), b(7)-98++, b(7), b(8)-196, b(8), b(8)++, b(8)-98, b(9)-98, b(9)-98++, b(9)-196, b(10)++, b(10)-98++, b(10), b(11), b(11)++, b(11)-98, b(11)-98++, b(12)++, b(12), b(12)-196++, b(12)-98++, b(12)-98, b(13)-98++, b(13)-98, b(13)-196++, b(13)++, b(14), b(14)-196++, b(14)-98++, b(15)++, b(15), b(15)-98++, b(15)-196++, b(16)-98++, b(16)-98, b(16)-196++, b(16)++, b(17)-196++, b(17)++, b(18)++, b(18)-196++, b(18)-98++, b(19)++, b(19)-98++, b(20)-98++, b(20)++, b(20)-196++, b(21)-196++, b(21)-98++, b(21)++
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(7)++, y(8), y(10)++, y(10), y(11), y(12), y(12)++, y(14)++, y(15)++, y(18)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.707

RGPARPSLPGAPPDEVYLSDSPAEPAPVK
Confirmed sites: @S:19,@S:21
Ambiguous sites:

MS/MS Fragmentation of RGPARPSLPGAPPDEVYLSDSPAEPAPVK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 8673: 3185.520879 from(1062.847569,3+)
Title: Elution from: 47.904 to 47.904 scan no 4655 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3185.5199
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S21 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K29 : Dimethyl (K)
Ions Score: 88 **Expect:** 1.7e-007

Matched b ions: b(4), b(5), b(6)++, b(8)++, b(8), b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(12), b(14)++, b(14), b(15)++, b(16)++, b(17), b(17)++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(21)-196++, b(21)++, b(22)-196++, b(22)-98++, b(23)-98++, b(23)-196++, b(23)++, b(24)-98++, b(24)++, b(24)-196++, b(25)-196++, b(25)-98++, b(25)++, b(26)++, b(26)-98++, b(26)-196++, b(27)-98++, b(27)++, b(27)-196++, b(28)-196++, b(28)++, b(28)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)-98, y(10)-98, y(10), y(11)-196++, y(11)-98++, y(11)-98, y(11)-196, y(11), y(12)++, y(12), y(12)-98++, y(12)-98, y(13), y(13)-98, y(15), y(15)++, y(15)-98, y(15)-98++, y(16), y(16)-98++, y(16)++, y(17)-98, y(17)-98++, y(17)++, y(18)++, y(18)-196++, y(18)-98++, y(19)-196++, y(19)-98++, y(20)-196++, y(20)++, y(21)++, y(21)-98++, y(22)-98++, y(23)-98++, y(23)++, y(24)-196++, y(24)++, y(24)-98++, y(25)-98++, y(25)-196++, y(25)++, y(26)-98++, y(27)++, y(28)-196++, y(28)++
Precursor origin neutral loss: +

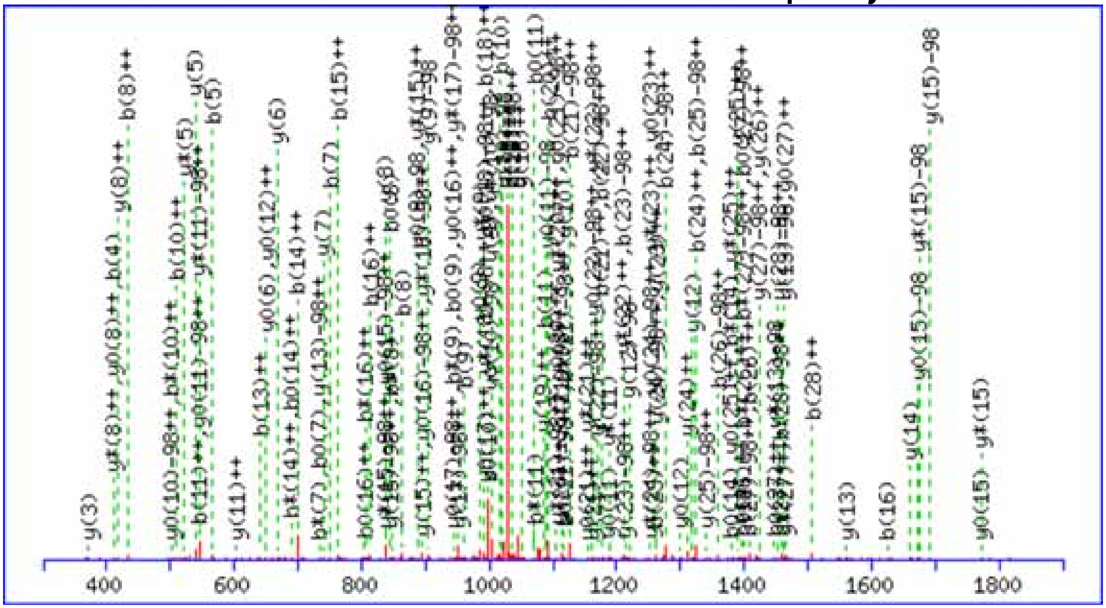
Peptide No.708

RGPARPSLPGAPPDEVYLSDSPAEPAPVK
Confirmed sites: @Y:17,@S:21
Ambiguous sites:

MS/MS Fragmentation of RGPARPSLPGAPPDEVYLSDSPAEPAPVK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 8674: 3185.521257 from(1062.847695,3+)

Title: Elution from: 47.572 to 47.572 scan no 4613 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3185.5199
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y17 : Phospho (Y)
S21 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K29 : Dimethyl (K)
Ions Score: 95 Expect: 3.4e-008

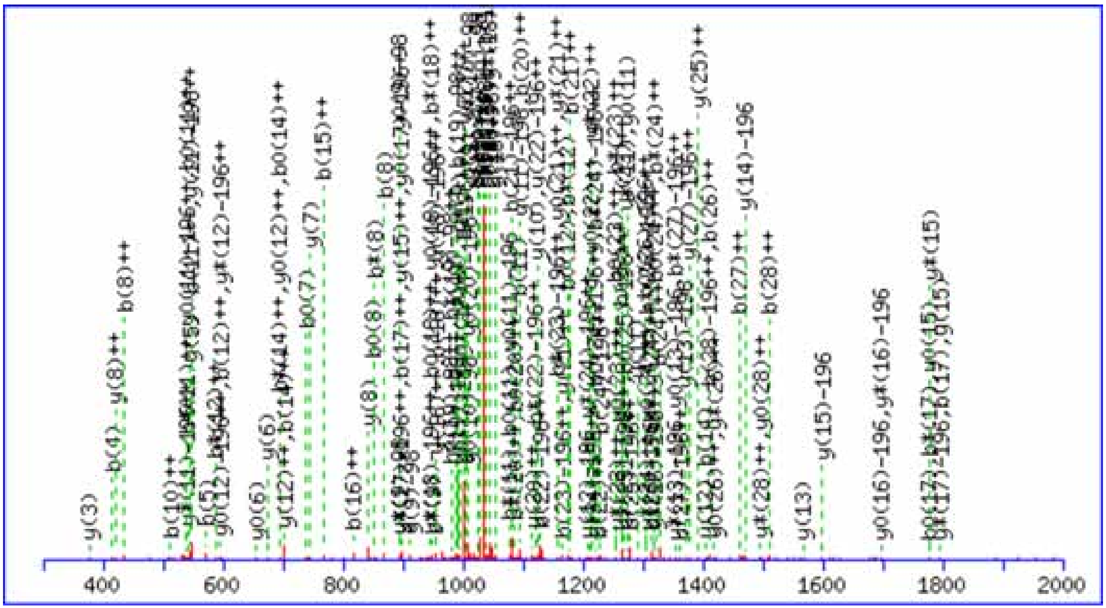
Matched b ions: b(4), b(5), b(7), b(8)++, b(8), b(9), b(10)++, b(10), b(11)++, b(11), b(13)++, b(14)++, b(14), b(15)++, b(16), b(16)++, b(18)++, b(19)++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(23)-98++, b(23)++, b(24)-98++, b(24)++, b(25)-98++, b(26)++, b(26)-98++, b(27)++, b(27)-98++, b(28)-98++, b(28)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(8)++, y(9)-98, y(9), y(10), y(10)-98, y(11)++, y(12)-98, y(12), y(13), y(13)-98++, y(13)-98, y(14), y(15)++, y(15)-98, y(15)-98++, y(17)-98++, y(18)++, y(19)-98++, y(19)++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(23)++, y(23)-98++, y(24)-98++, y(24)++, y(25)-98++, y(25)++, y(26)++, y(27)-98++, y(28)-98++
Precursor origin neutral loss: +

Peptide No.709

RGPARPSLPGAPPDEVYLSDSPAEPAPVK
Confirmed sites: @S:19,@S:21
Ambiguous sites:

MS/MS Fragmentation of RGPARPSLPGAPPDEVYLSDSPAEPAPVK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 7484: 3197.585061 from(1066.868963,3+)
Title: Elution from: 47.614 to 47.614 scan no 4407 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3197.5835
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S21 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K29 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 98 Expect: 1.6e-008

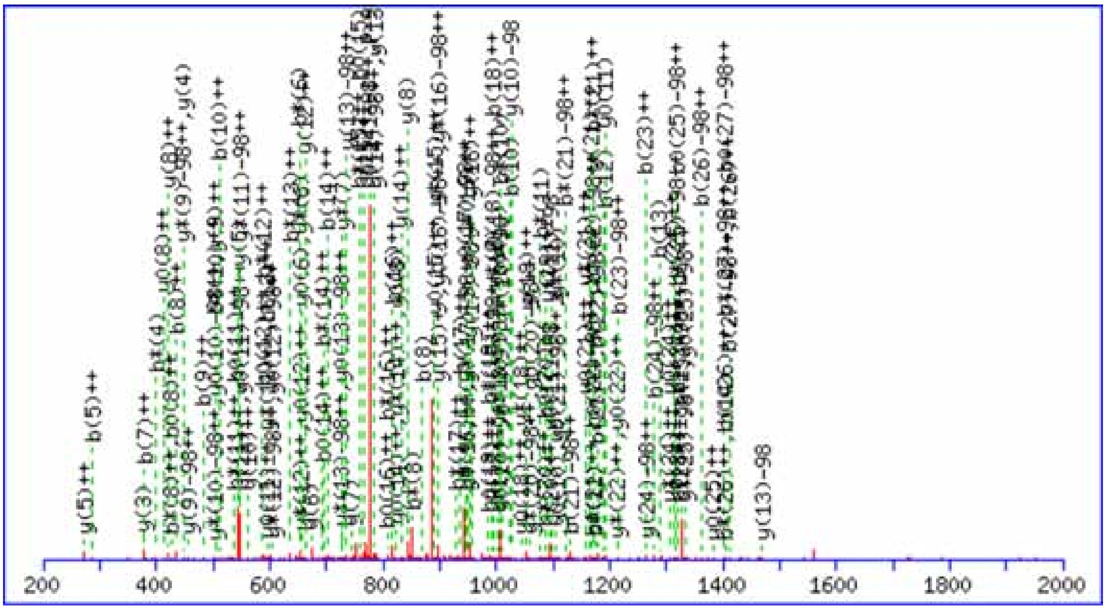
Matched b ions: b(4), b(5), b(8)++, b(8), b(10)++, b(10), b(11)++, b(11), b(12)++, b(14)++, b(14), b(15)++, b(16)++, b(17)++, b(17), b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-196++, b(21)-98++, b(21)++, b(22)-196++, b(22)-98++, b(22)++, b(23)++, b(23)-98++, b(23)-196++, b(24)++, b(24)-196++, b(24)-98++, b(25)-98++, b(25)-196++, b(26)-196++, b(26)++, b(26)-98++, b(27)-98++, b(27)++, b(27)-196++, b(28)++, b(28)-98++, b(28)-196++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(8)++, y(9)-98, y(9), y(10)-98, y(10), y(11)-196++, y(11)-196, y(11)-98, y(11), y(12)++, y(12), y(12)-98, y(12)-196, y(13)-98, y(13), y(13)-196, y(14)-98, y(14)-196, y(15)++, y(15)-196, y(15)-98, y(15), y(16)++, y(17)-98++, y(17)++, y(18)-196++, y(18)-98++, y(18)++, y(19)-196++, y(19)-98++, y(20)++, y(21)++, y(21)-98++, y(22)-196++, y(23)++, y(24)-98++, y(24)++, y(24)-196++, y(25)++, y(25)-98++, y(26)-98++, y(27)-196++
Precursor origin neutral loss: +

Peptide No.710

RGPARPSLPGAPPDEVYLSDSPAEPAPVK
Confirmed sites: @Y:17,@S:21
Ambiguous sites:

MS/MS Fragmentation of RGPARPSLPGAPPDEVYLSDSPAEPAPVK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 8924: 3197.586440 from(800.403886,4+)
Title: Elution from: 47.519 to 47.519 scan no 4641 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3197.5835
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y17 : Phospho (Y)
S21 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K29 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 82 **Expect:** 5.6e-007

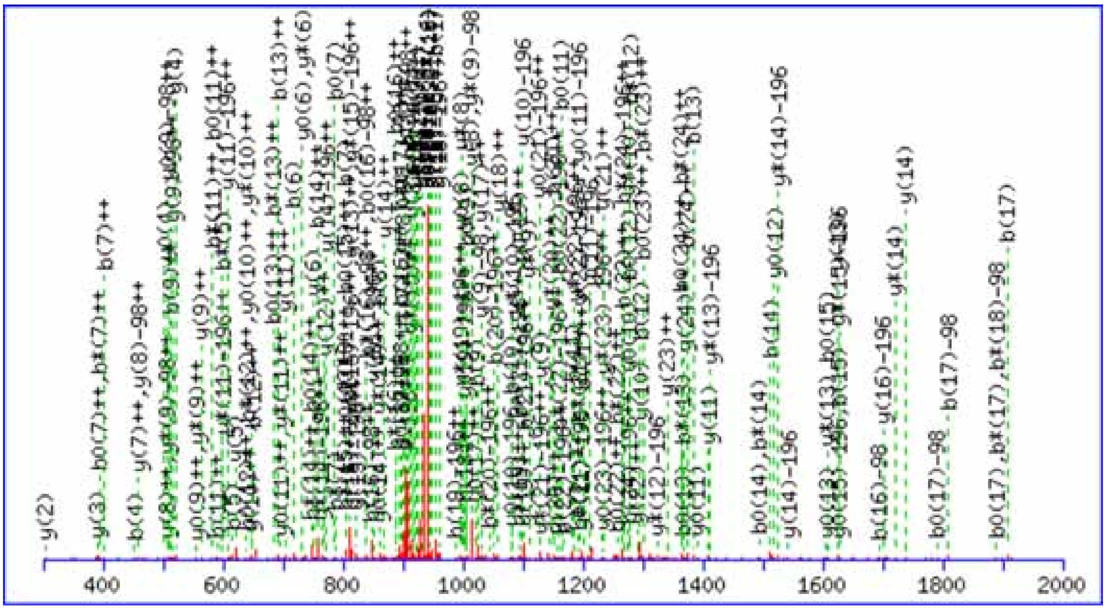
Matched b ions: b(5)++, b(7)++, b(8)++, b(8), b(9)++, b(10)++, b(10), b(11)++, b(12)++, b(12), b(13), b(14), b(14)++, b(15)++, b(16)++, b(17)++, b(18)++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(23)++, b(23)-98++, b(24)++, b(24)-98++, b(25)-98++, b(26)++, b(26)-98++, b(27)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(9)-98++, y(10)++, y(10)-98, y(12)++, y(13)++, y(13)-98, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(21)++, y(24)-98++, y(24)++
Precursor origin neutral loss: +

Peptide No.711

RGPNYTSGYGTNSELSNPSETESER
Confirmed sites: @S:16,@S:19
Ambiguous sites:

MS/MS Fragmentation of RGPNYTSGYGTNSELSNPSETESER
Found in FXR1_MOUSE, Fragile X mental retardation syndrome-related protein 1 OS=Mus musculus GN=Fxr1 PE=1 SV=2

Match to Query 8466: 2919.160677 from(974.060835,3+)
Title: Elution from: 37.431 to 37.431 scan no 3322 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2919.1597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 **Expect:** 9.5e-005

Matched b ions: b(4), b(5), b(6), b(7)++, b(7), b(8), b(9), b(9)++, b(10), b(11), b(11)++, b(12), b(12)++, b(13)++, b(13), b(14)++, b(14), b(15)++, b(15), b(16)-98++, b(16)++, b(16)-98, b(17)-98, b(17), b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-196++, b(19)-98++, b(20)-98++, b(20)++, b(20)-196++, b(21)-196++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(22)-196++, b(24)++, b(24)-98++, b(24)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(8)++, y(8)-98++, y(8)-98, y(9)-98++, y(9), y(9)++, y(9)-98, y(10), y(10)-98, y(10)-98++, y(10)++, y(10)-196, y(11)-98, y(11), y(11)-98++, y(11)++, y(11)-196++, y(11)-196, y(12)-98, y(12)-98++, y(12)++, y(13)++, y(13), y(13)-98, y(13)-98++, y(14), y(14)-196, y(14)-98++, y(14)-196++, y(14)++, y(15)-196++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(16)-196++, y(16)-196, y(17)++, y(17)-196++, y(18)-196++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(19)-196++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(22)-196++, y(22)++, y(23)-98++, y(23)++, y(24)++, y(24)-98++
Precursor origin neutral loss: +

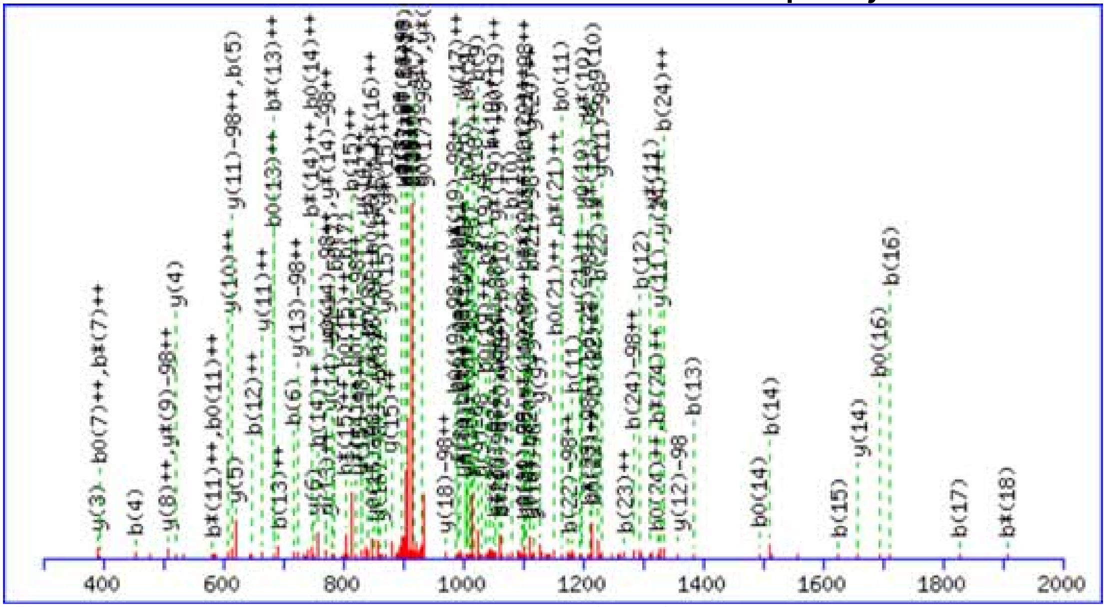
Peptide No.712

RGPNYTSGYGTNSELSNPSETESER
Confirmed sites: @S:19
Ambiguous sites:

MS/MS Fragmentation of RGPNYTSGYGTNSELSNPSETESER
Found in FXR1_MOUSE, Fragile X mental retardation syndrome-related protein 1 OS=Mus musculus GN=Fxr1 PE=1 SV=2

Match to Query 8356: 2839.190961 from(947.404263,3+)

Title: Elution from: 35.682 to 35.682 scan no 3082 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2839.1933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 Expect: 5.5e-007

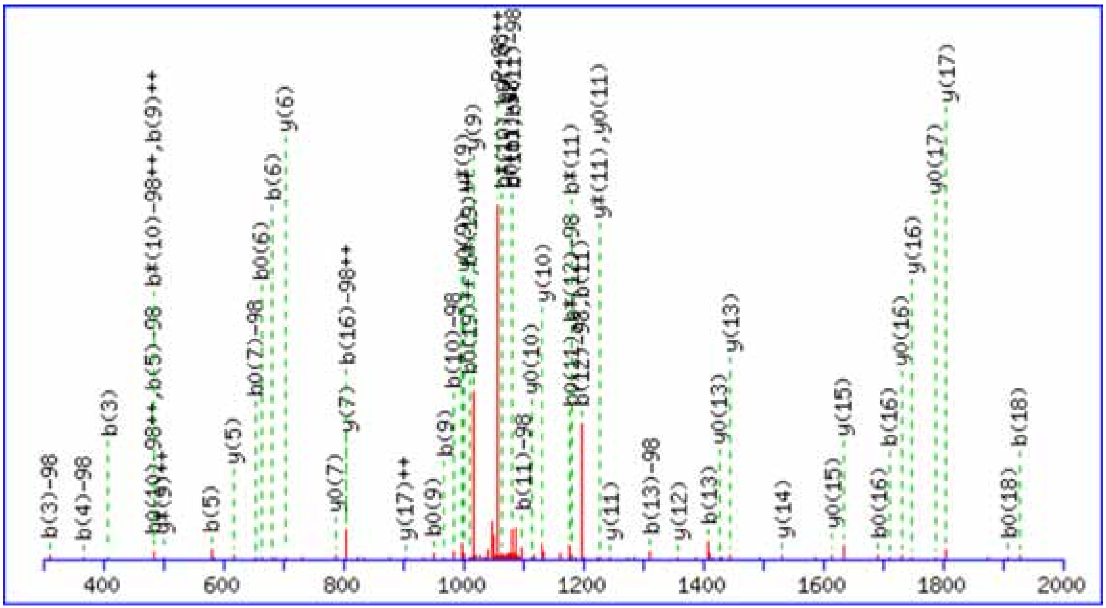
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(12)++, b(13)++, b(13), b(14)++, b(14), b(15)++, b(15), b(16), b(16)++, b(17), b(17)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(24)++, b(24)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)++, y(10)-98, y(11), y(11)-98++, y(11)++, y(11)-98, y(12)-98, y(13)++, y(13)-98++, y(14), y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(24)++
Precursor origin neutral loss: +

Peptide No.713

RGSGDTSSLIDPDTSLSELR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RGSGDTSSLIDPDTSLSELR
Found in LRRF2_MOUSE, Leucine-rich repeat flightless-interacting protein 2 OS=Mus musculus GN=Lrrfip2 PE=1 SV=1

Match to Query 6636: 2213.023824 from(1107.519188,2+)
Title: Elution from: 52.498 to 52.498 scan no 5200 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2213.0213
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 9.6e-006

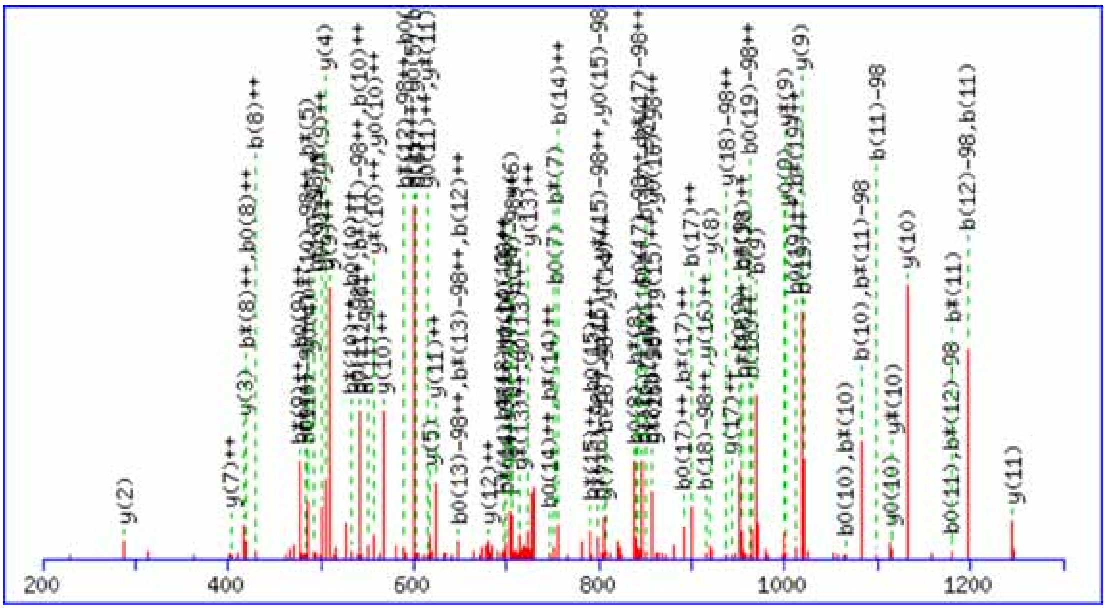
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6), b(9)++, b(9), b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(13), b(13)-98, b(16)-98++, b(16), b(18)
Matched y ions: y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17)++, y(17)
Precursor origin neutral loss: +

Peptide No.714

RGSGDTSSLIDPDTSLSELR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of RGSGDTSSLIDPDTSLSELR
Found in LRRF2_MOUSE, Leucine-rich repeat flightless-interacting protein 2 OS=Mus musculus GN=Lrrfip2 PE=1 SV=1

Match to Query 6635: 2213.022876 from(738.681568,3+)
Title: Elution from: 52.474 to 52.474 scan no 5197 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2213.0213
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 2.2e-005

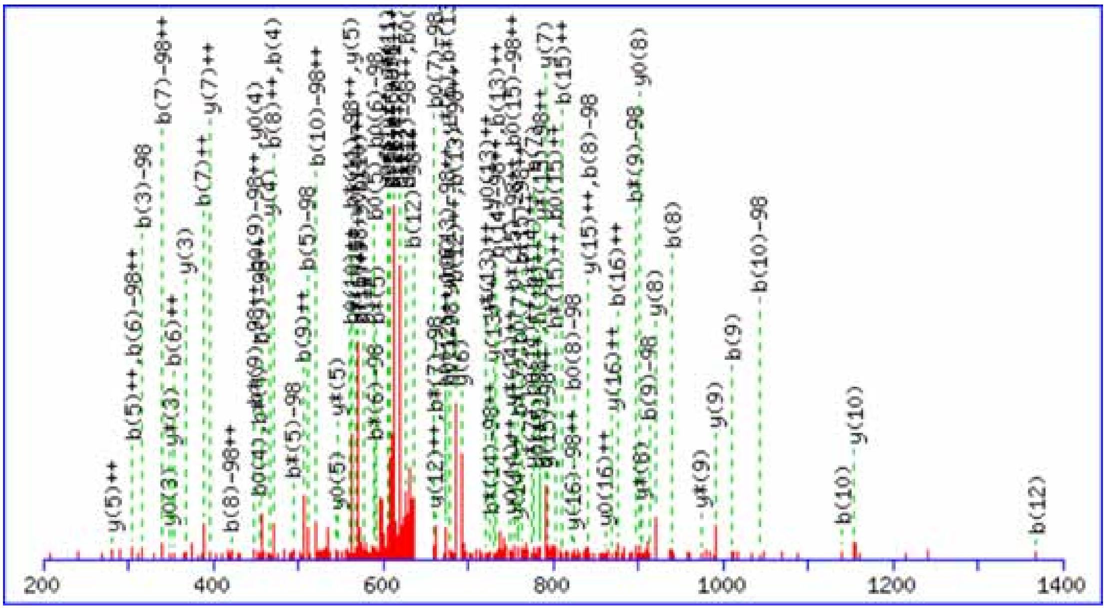
Matched b ions: b(6), b(8), b(8)++, b(9), b(9)++, b(10), b(10)++, b(10)-98++, b(11)++, b(11), b(11)-98, b(11)-98++, b(12)-98++, b(12)-98, b(12)++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)-98++
Precursor origin neutral loss:

Peptide No.715

RGSGHPAYAEVEPVGEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RGSGHPAYAEVEPVGEK
Found in PXDC2_MOUSE, Plexin domain-containing protein 2 OS=Mus musculus GN=Plxdc2 PE=1 SV=1

Match to Query 4819: 1929.963051 from(644.328293,3+)
Title: Elution from: 28.780 to 28.780 scan no 1983 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1929.9622
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 38 Expect: 0.01

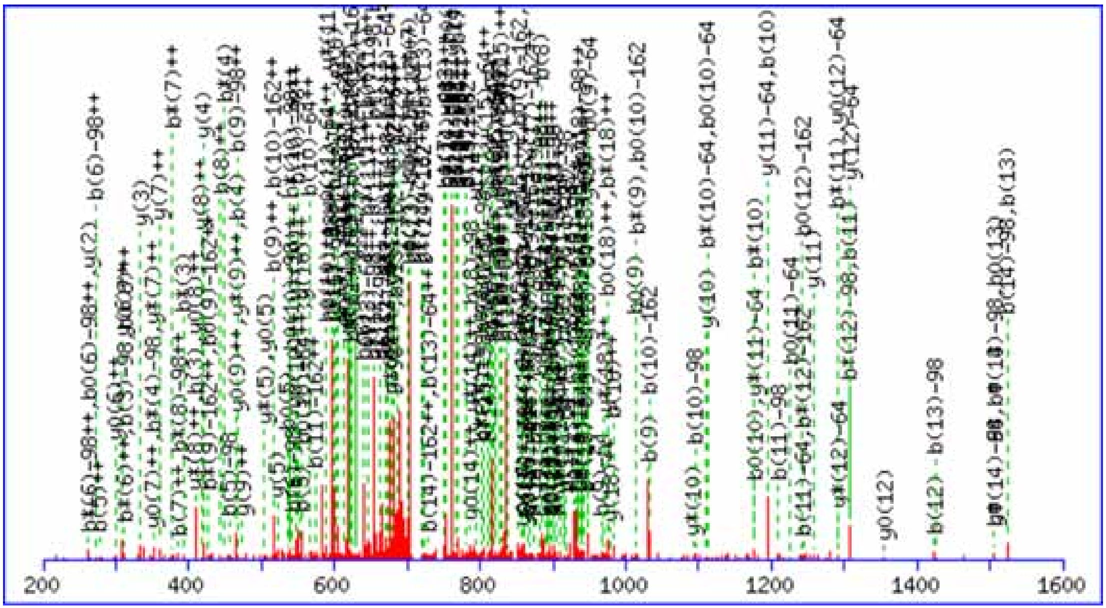
Matched b ions: b(3)-98, b(4), b(5)++, b(5), b(5)-98, b(6)-98++, b(6)-98, b(6)++, b(7)++, b(7)-98++, b(7)-98, b(7), b(8)++, b(8)-98, b(8)-98++, b(8), b(9)++, b(9)-98++, b(9), b(9)-98, b(10)++, b(10), b(10)-98++, b(10)-98, b(11)-98++, b(11)++, b(12), b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6), y(7), y(7)++, y(8), y(9), y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.716

RGSGSSEDMYLDTPTSASR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RGSGSSEDMYLDTPTSASR
Found in PPR3A_MOUSE, Protein phosphatase 1 regulatory subunit 3A OS=Mus musculus GN=Ppp1r3a PE=1 SV=1

Match to Query 6996: 2139.878685 from(714.300171,3+)
Title: Elution from: 32.453 to 32.453 scan no 2563 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2139.8780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 59 **Expect:** 5.1e-005

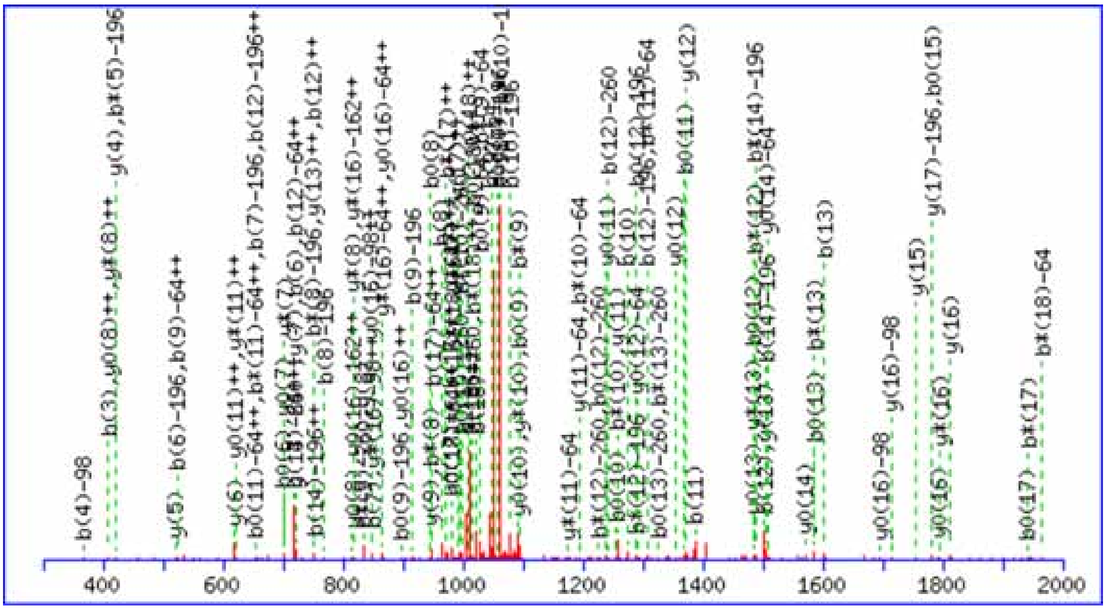
Matched b ions: b(3), b(3)-98, b(4), b(5)++, b(5)-98, b(5), b(6)-98++, b(6), b(6)-98, b(7), b(7)++, b(7)-98, b(8), b(8)-98, b(8)++, b(9)++, b(9), b(9)-98, b(9)-98++, b(10)++, b(10), b(10)-98, b(10)-98++, b(11), b(11)++, b(11)-98++, b(11)-98, b(12), b(12)-98++, b(13)++, b(13), b(13)-98, b(14)-98++, b(14)-98, b(14)++, b(15)++, b(15)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(10), y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(18)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.717

RGSGSSEDMYLDTPTSASR
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of RGSGSSEDMYLDTPTSASR
Found in PPR3A_MOUSE, Protein phosphatase 1 regulatory subunit 3A OS=Mus musculus GN=Ppp1r3a PE=1 SV=1

Match to Query 5807: 2219.845112 from(1110.929832,2+)
Title: Elution from: 36.211 to 36.211 scan no 2955 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2219.8443
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 39 Expect: 0.0027

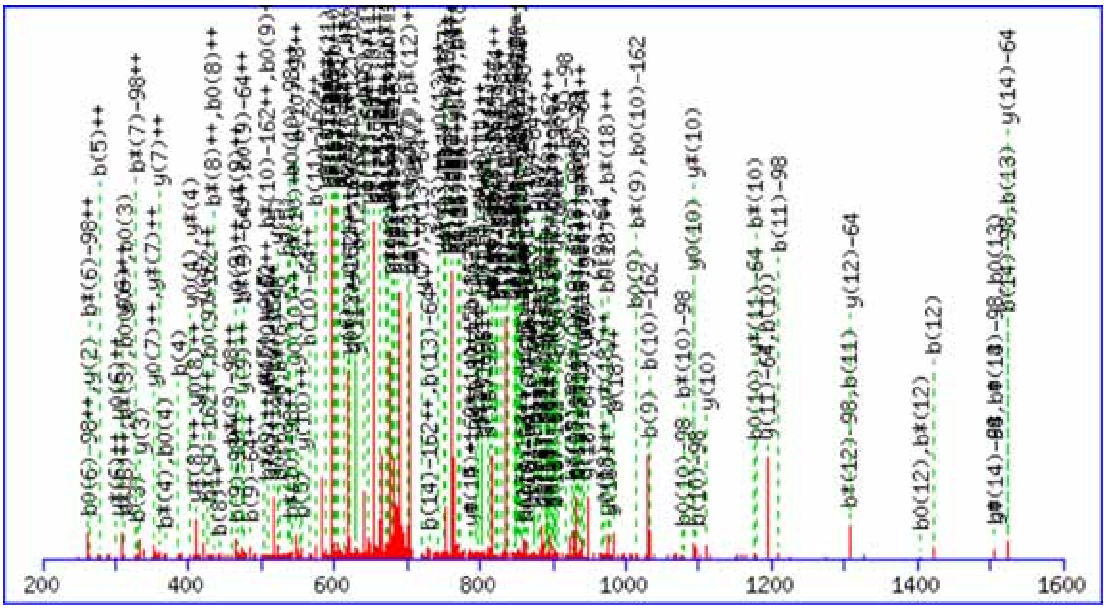
Matched b ions: b(3), b(4)-98, b(5)-98, b(6), b(6)-196, b(7)-98, b(7), b(7)-196, b(8), b(8)-98, b(8)-196, b(9)-98, b(9)-196, b(10)-196, b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(12)++, b(12)-196, b(12)-196++, b(12)-98++, b(13), b(13)-98++, b(13)-98, b(14)-98, b(14)-196++, b(14)-196, b(16)-98, b(17)-98, b(17)++, b(18)-98, b(18)-98++, b(18)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(13), y(13)++, y(15), y(16), y(16)-98, y(17)-196, y(17)-98, y(17)++
Precursor origin neutral loss: +

Peptide No.718

RGSGSSEDMYLDTPTSASR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of RGSGSSEDMYLDTPTSASR
Found in PPR3A_MOUSE, Protein phosphatase 1 regulatory subunit 3A OS=Mus musculus GN=Ppp1r3a PE=1 SV=1

Match to Query 5707: 2139.879378 from(714.300402,3+)
Title: Elution from: 32.547 to 32.547 scan no 2483 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2139.8780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M9 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 58 **Expect:** 6.2e-005

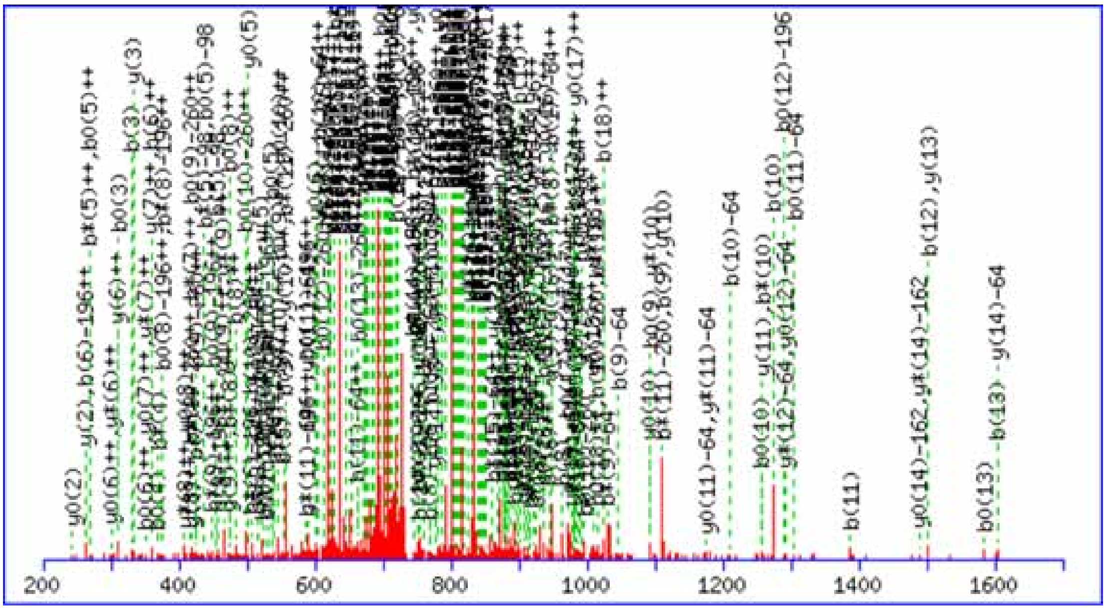
Matched b ions: b(3), b(4), b(5)++, b(5), b(6), b(7), b(7)-98, b(8), b(8)++, b(8)-98, b(9)++, b(9), b(9)-98++, b(9)-98, b(10)++, b(10), b(10)-98++, b(10)-98, b(11)++, b(11), b(11)-98, b(11)-98++, b(12), b(12)-98++, b(13)++, b(13), b(14)-98++, b(14)-98, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(18)-98++, y(18)++
Precursor origin neutral loss:

Peptide No.719

RGSGSSEDMYLDTPTSASR
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of RGSGSSEDMYLDTPTSASR
Found in PPR3A_MOUSE, Protein phosphatase 1 regulatory subunit 3A OS=Mus musculus GN=Ppp1r3a PE=1 SV=1

Match to Query 5661: 2219.845992 from(740.955940,3+)
Title: Elution from: 36.205 to 36.205 scan no 2936 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2219.8443
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 54 Expect: 0.0001

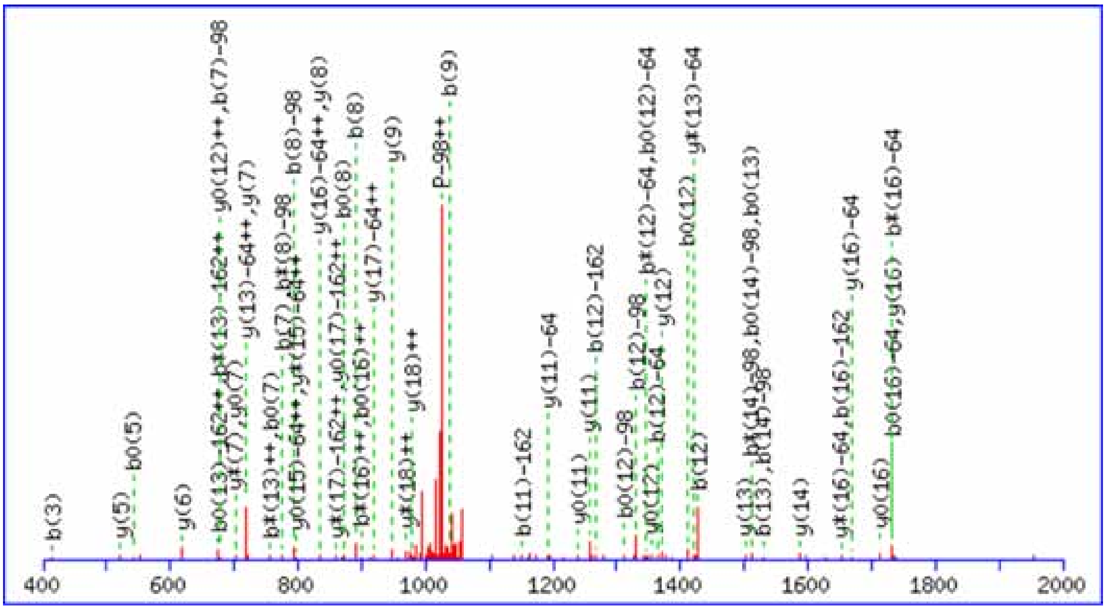
Matched b ions: b(3), b(5)-98, b(5), b(6)-196++, b(6)++, b(6)-98++, b(6), b(6)-196, b(6)-98, b(7)++, b(7)-98, b(7)-98++, b(7)-196, b(7), b(8)++, b(8), b(8)-98++, b(8)-196, b(8)-98, b(9), b(9)++, b(9)-98++, b(9)-196++, b(9)-196, b(9)-98, b(10)++, b(10)-98, b(10), b(10)-98++, b(10)-196++, b(11), b(11)++, b(11)-98++, b(12), b(12)-98++, b(12)++, b(12)-196++, b(13)++, b(13), b(13)-98++, b(13)-196++, b(14)-98++, b(14)-98, b(14)-196++, b(14)++, b(15)-196++, b(15)++, b(16)-196++, b(16)-98++, b(16)++, b(17)-98++, b(17)-196++, b(17)++, b(18)-98++, b(18)++, b(18)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(13), y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)-196++, y(17)++, y(18)-196++
Precursor origin neutral loss: +

Peptide No.720

RGSGSSEDMYLDTPTSASR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RGSGSSEDMYLDTPTSASR
Found in PPR3A_MOUSE, Protein phosphatase 1 regulatory subunit 3A OS=Mus musculus GN=Ppp1r3a PE=1 SV=1

Match to Query 5340: 2145.909788 from(1073.962170,2+)
Title: Elution from: 32.513 to 32.513 scan no 2440 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2145.9098
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 38 Expect: 0.0066

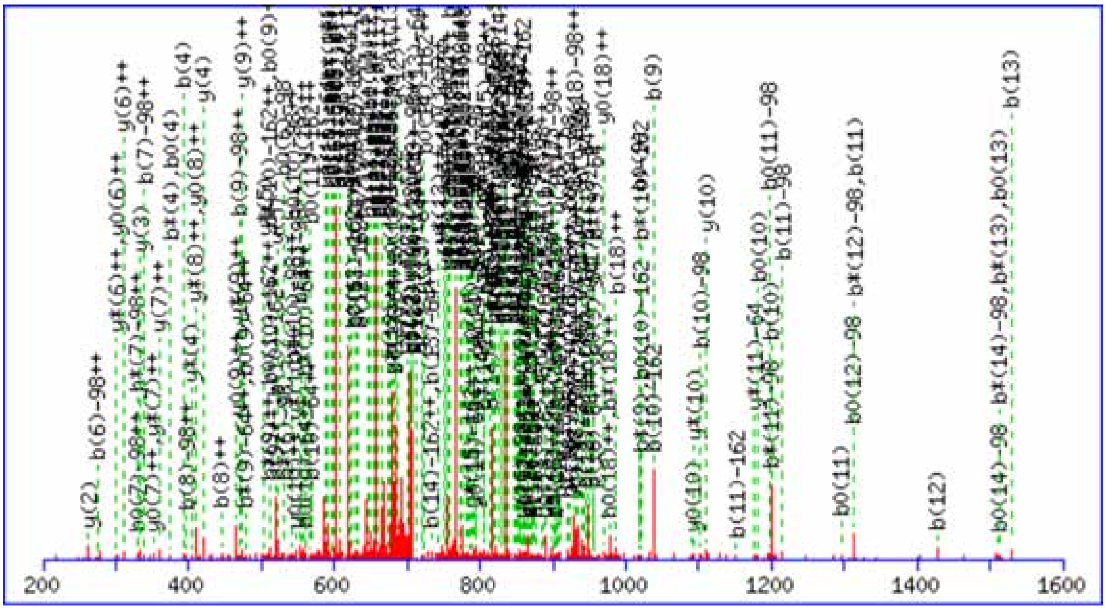
Matched b ions: b(3), b(7), b(7)-98, b(8), b(8)-98, b(9), b(12)-98, b(12), b(13), b(14)-98
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(13), y(14), y(16), y(18)++
Precursor origin neutral loss: +

Peptide No.721

RGSGSSEDMYLDTPTSASR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of RGSGSSEDMYLDTPTSASR
Found in PPR3A_MOUSE, Protein phosphatase 1 regulatory subunit 3A OS=Mus musculus GN=Ppp1r3a PE=1 SV=1

Match to Query 4955: 2145.910692 from(716.310840,3+)
Title: Elution from: 32.378 to 32.378 scan no 2325 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2145.9098
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 47 Expect: 0.00084

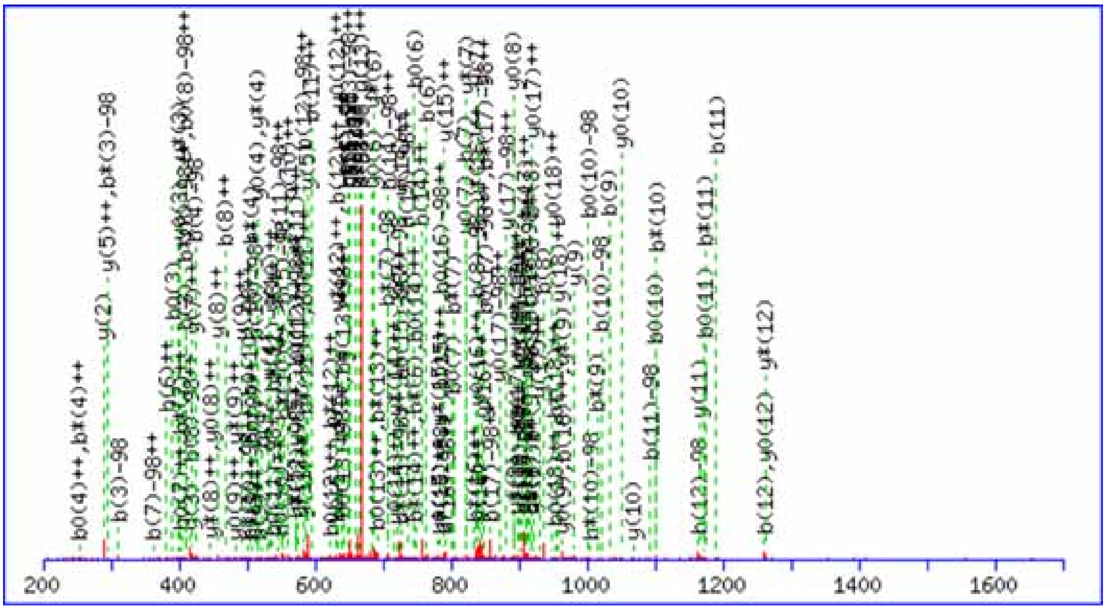
Matched b ions: b(4), b(6)-98++, b(6), b(7)-98, b(7), b(7)-98++, b(8), b(8)++, b(8)-98++, b(8)-98, b(9), b(9)++, b(9)-98, b(9)-98++, b(10)++, b(10), b(10)-98, b(10)-98++, b(11)++, b(11), b(11)-98, b(11)-98++, b(12), b(12)-98++, b(13)++, b(13), b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)++, b(18)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.722

RGSLELGNPSAAHLGDELK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RGSLELGNPSAAHLGDELK
Found in SVIL_MOUSE, Supervillin OS=Mus musculus GN=Svil PE=1 SV=1

Match to Query 5471: 2099.042646 from(700.688158,3+)
Title: Elution from: 44.412 to 44.412 scan no 4027 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2099.0412
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K19 : Dimethyl (K)
Ions Score: 57 Expect: 0.00015

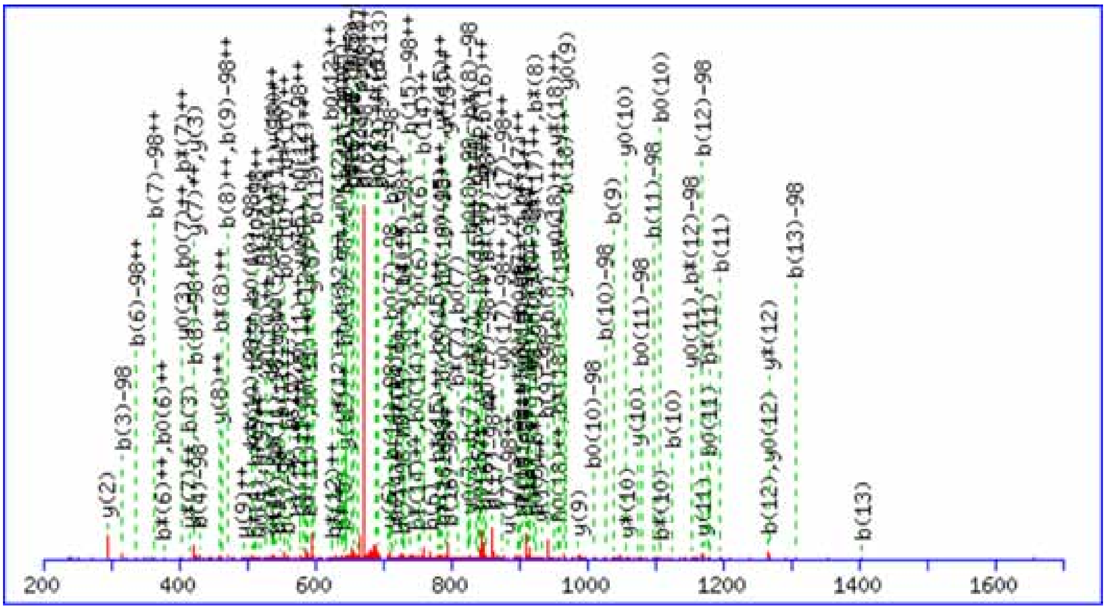
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)++, b(6), b(6)-98, b(7)-98++, b(7)-98, b(7), b(8), b(8)-98++, b(8)-98, b(8)++, b(9), b(9)++, b(10)-98, b(10)++, b(10)-98++, b(11)-98, b(11), b(11)-98++, b(11)++, b(12)-98, b(12), b(12)-98++, b(12)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(7)++, y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11)++, y(11), y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.723

RGSLELGNPSAAHLGDELK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RGSLELGNPSAAHLGDELK
Found in SVIL_MOUSE, Supervillin OS=Mus musculus GN=Svil PE=1 SV=1

Match to Query 5281: 2111.105607 from(704.709145,3+)
Title: Elution from: 44.407 to 44.407 scan no 4011 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2111.1048
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K19 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 54 Expect: 0.00028

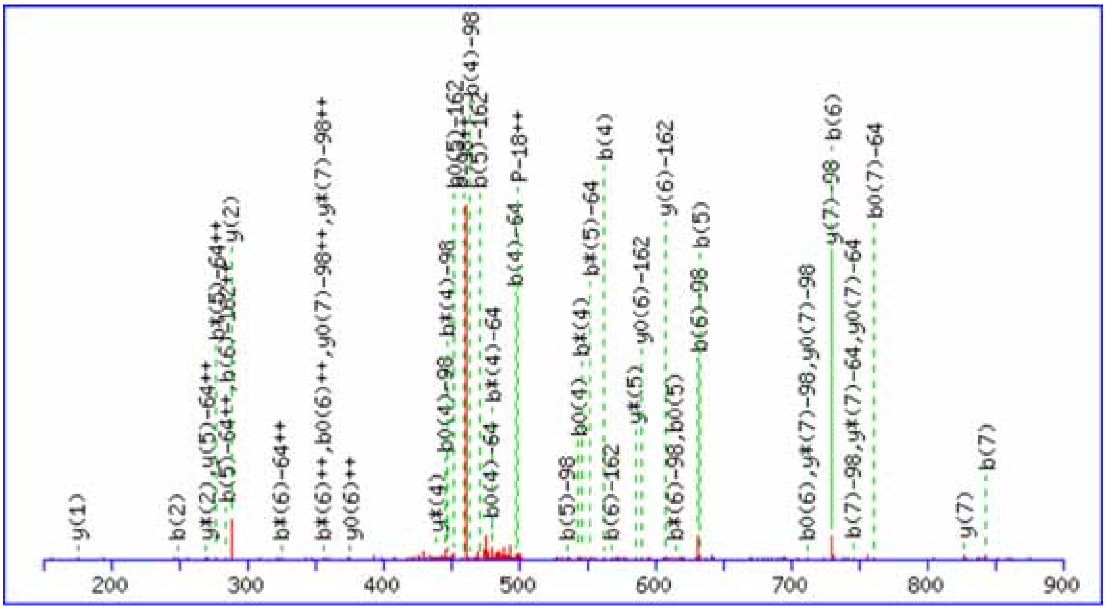
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(6)-98++, b(7), b(7)-98++, b(7)-98, b(8), b(8)++, b(8)-98++, b(8)-98, b(9)-98, b(9)-98++, b(9)++, b(9), b(10)-98, b(10)-98++, b(10)++, b(10), b(11)-98, b(11), b(11)-98++, b(11)++, b(12)-98, b(12), b(12)-98++, b(12)++, b(13), b(13)-98, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(11), y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.724

RGSMAPLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RGSMAPLR
Found in CILP1_MOUSE, Cartilage intermediate layer protein 1 OS=Mus musculus GN=Cilp PE=2 SV=1

Match to Query 494: 1016.502094 from(509.258323,2+)
Title: Elution from: 29.734 to 29.734 scan no 2108 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1016.5050
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 26 Expect: 0.052

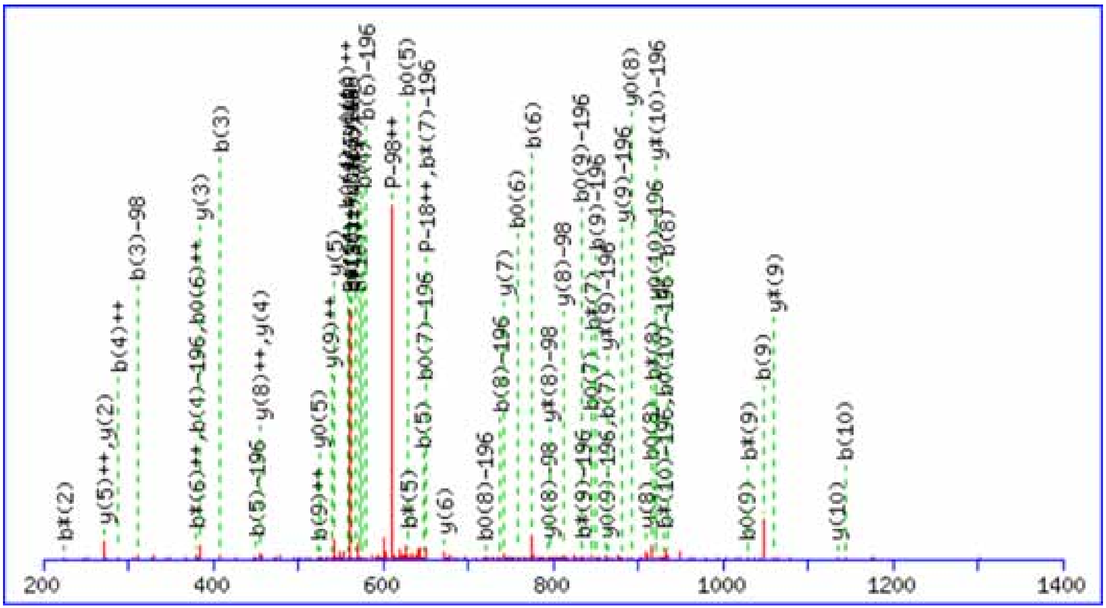
Matched b ions: b(2), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(7), b(7)-98
Matched y ions: y(1), y(2), y(7), y(7)-98
Precursor origin neutral loss: +

Peptide No.725

RGSSAESALPR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of RGSSAESALPR
Found in SPEG_MOUSE, Striated muscle-specific serine/threonine-protein kinase OS=Mus musculus GN=Speg PE=1 SV=2

Match to Query 1702: 1317.548330 from(659.781441,2+)
Title: Elution from: 28.703 to 28.703 scan no 2125 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1317.5479
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.011

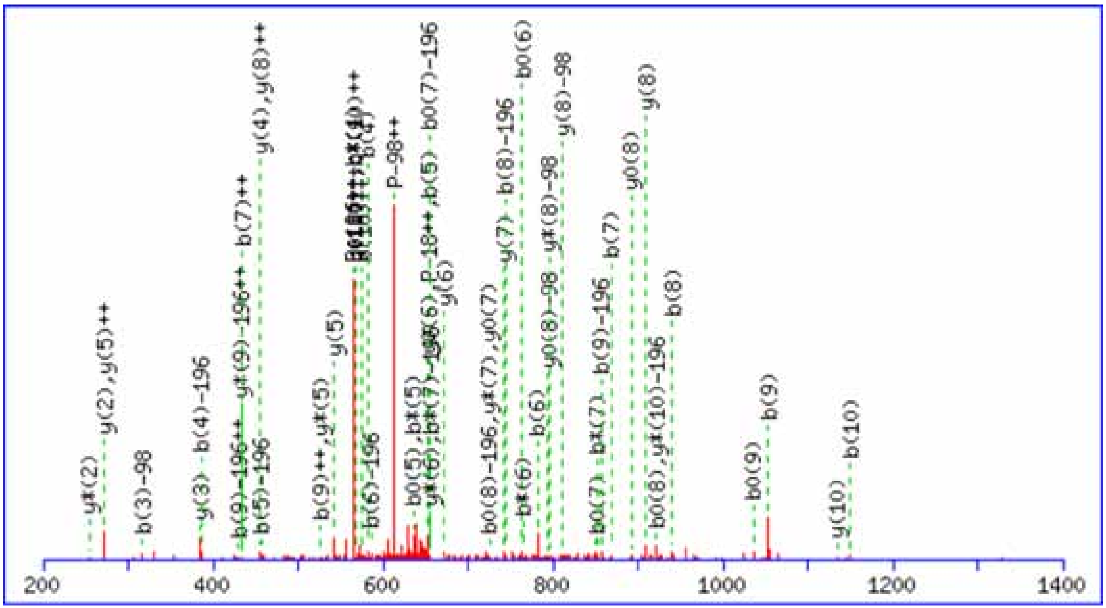
Matched b ions: b(3)-98, b(3), b(4)-196, b(4)-98, b(4)++, b(4), b(5)-98, b(5)-196, b(5), b(6), b(6)-98, b(6)-196, b(7), b(7)-98++, b(7)-98, b(8), b(8)-98, b(8)-196, b(9), b(9)-98, b(9)-196, b(9)++, b(10), b(10)-98++, b(10)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(8)++, y(8), y(8)-98, y(9)-98, y(9)++, y(9)-196, y(10), y(10)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.726

RGSSAESALPR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of RGSSAESALPR
Found in SPEG_MOUSE, Striated muscle-specific serine/threonine-protein kinase OS=Mus musculus GN=Speg PE=1 SV=2

Match to Query 1342: 1323.580584 from(662.797568,2+)
Title: Elution from: 28.585 to 28.585 scan no 1952 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1323.5797
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00016

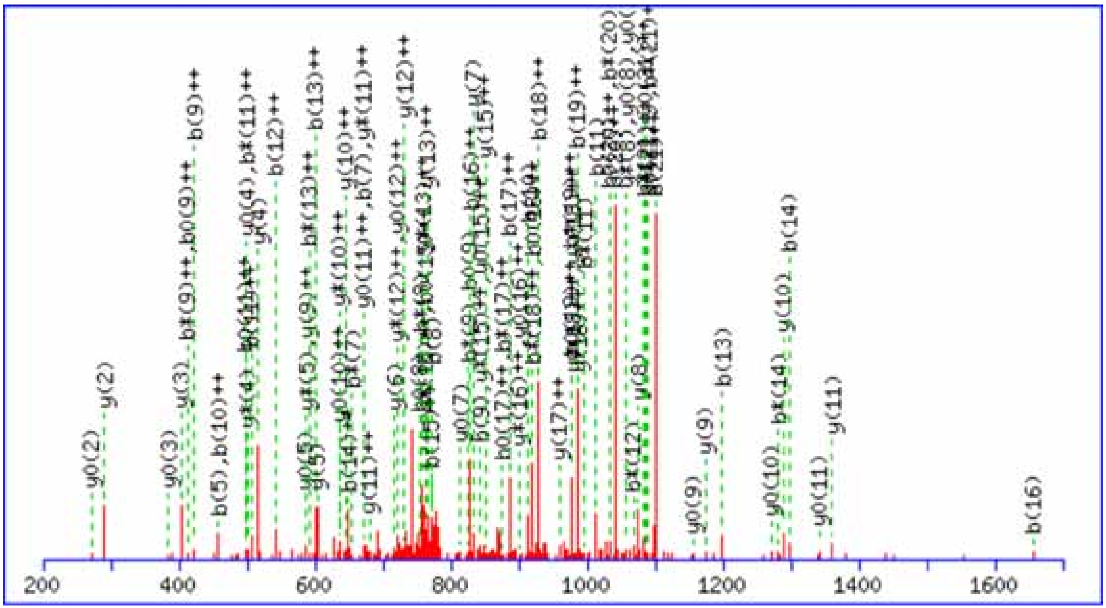
Matched b ions: b(3)-98, b(4)-196, b(4)-98, b(4), b(5)-196, b(5), b(5)-98, b(6), b(6)-98, b(6)-196, b(7)-98++, b(7), b(7)++, b(7)-98, b(8), b(8)-98, b(8)-196, b(9), b(9)-98, b(9)-196, b(9)-196++, b(9)++, b(10), b(10)-98++, b(10)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(8), y(8)++, y(8)-98, y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.727

RGTGGVDTAAVADVYDISNIDR
Confirmed sites: @Y:15
Ambiguous sites:

MS/MS Fragmentation of RGTGGVDTAAVADVYDISNIDR
Found in KCRS_MOUSE, Creatine kinase S-type, mitochondrial OS=Mus musculus GN=Ckmt2 PE=1 SV=1

Match to Query 6352: 2372.101902 from(791.707910,3+)
Title: Elution from: 52.606 to 52.606 scan no 4971 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2372.1009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y15 : Phospho (Y)
Ions Score: 91 Expect: 6.7e-008

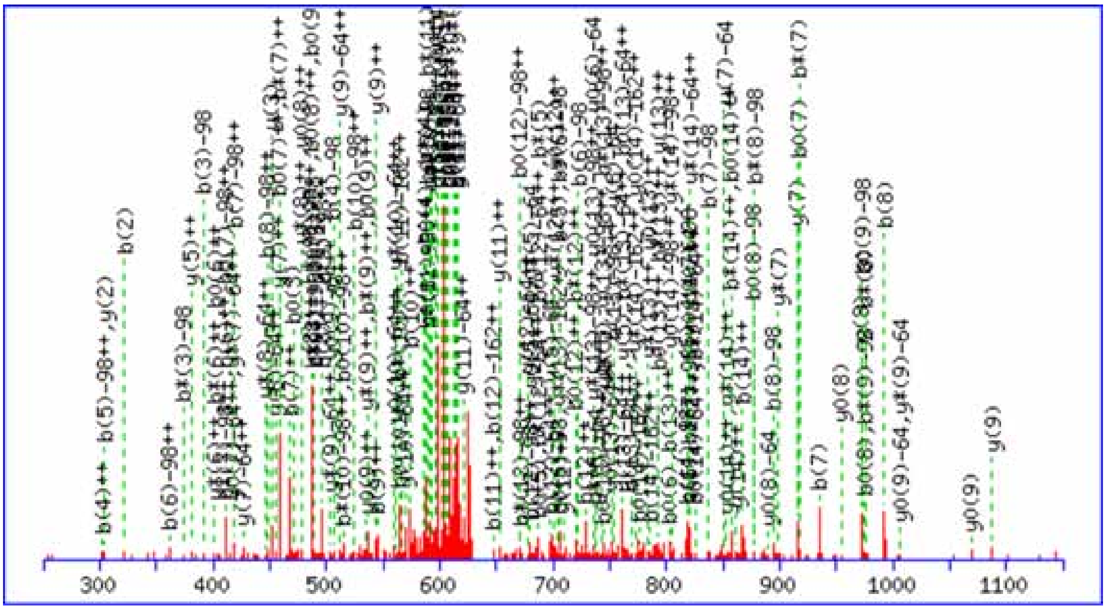
Matched b ions: b(5), b(7), b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(12), b(13)++, b(13), b(14)++, b(14), b(15)++, b(16)++, b(16), b(17)++, b(18)++, b(19)++, b(20)++, b(21)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(15)++, y(17)++, y(18)++
Precursor origin neutral loss:

Peptide No.728

RHSDTDDGPGMYFEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RHSDTDDGPGMYFEK
Found in CMYA5_MOUSE, Cardiomyopathy-associated protein 5 OS=Mus musculus GN=Cmya5 PE=1 SV=2

Match to Query 4686: 1905.762840 from(636.261556,3+)
Title: Elution from: 34.280 to 34.280 scan no 2722 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1905.7604
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K15 : Dimethyl (K)
Ions Score: 61 **Expect:** 2.2e-005

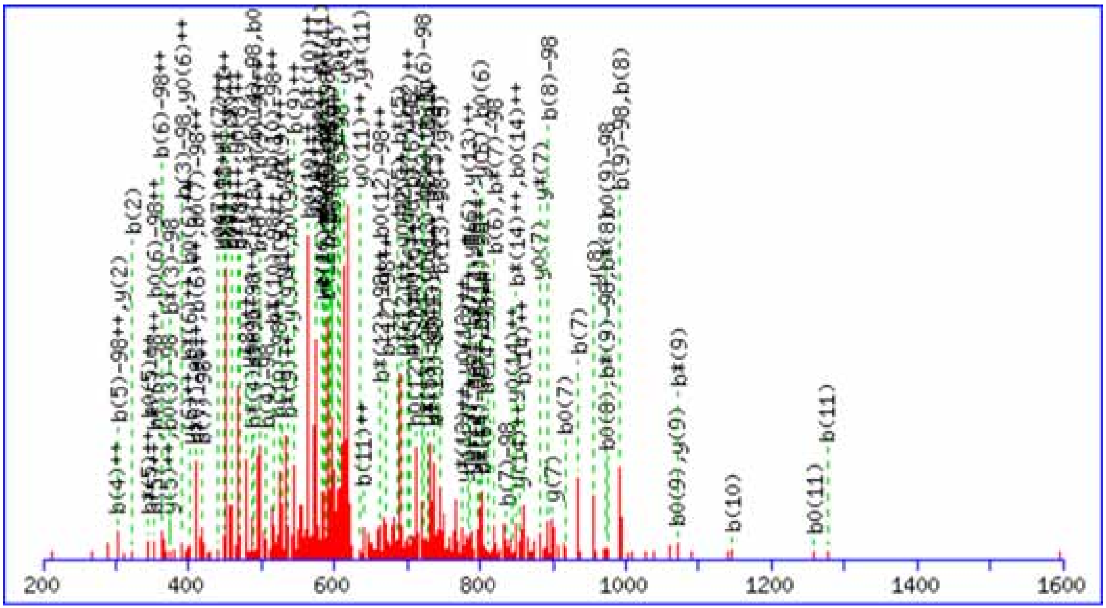
Matched b ions: b(2), b(3)-98, b(3), b(4), b(4)++, b(4)-98, b(5)-98++, b(5), b(5)-98, b(6)++, b(6), b(6)-98++, b(6)-98, b(7), b(7)-98++, b(7)++, b(7)-98, b(8), b(8)++, b(8)-98++, b(8)-98, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.729

RHSDTDDGPGMYFEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RHSDTDDGPGMYFEK
Found in CMYA5_MOUSE, Cardiomyopathy-associated protein 5 OS=Mus musculus GN=Cmya5 PE=1 SV=2

Match to Query 4994: 1889.765682 from(630.929170,3+)
Title: Elution from: 37.330 to 37.330 scan no 3308 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1889.7655
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 39 Expect: 0.0039

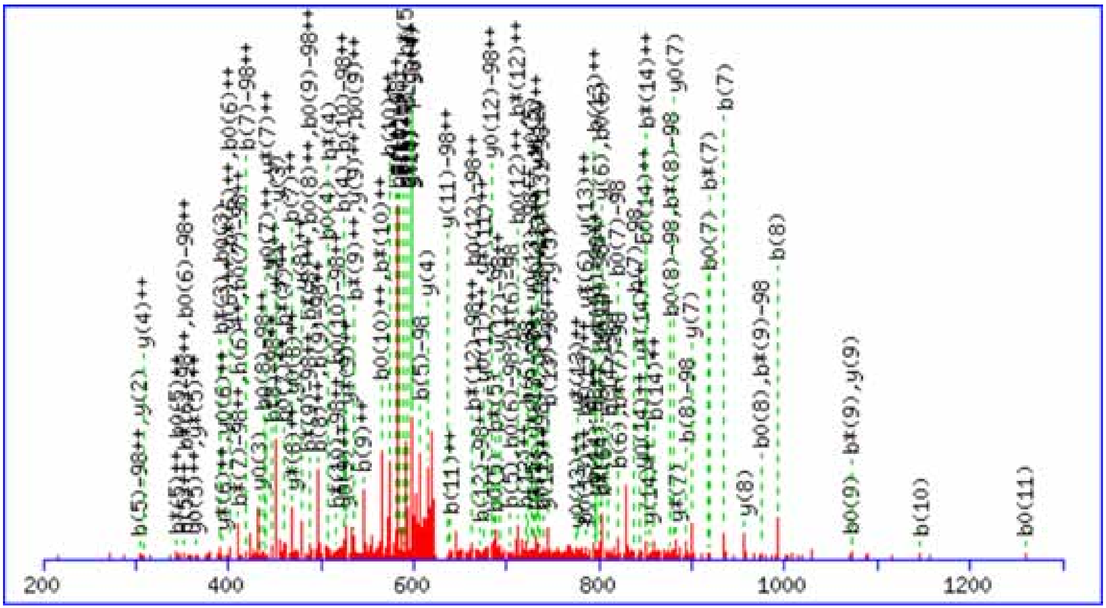
Matched b ions: b(2), b(3)-98, b(3), b(4)++, b(4)-98, b(4), b(5)-98++, b(5)++, b(5)-98, b(5), b(6)++, b(6)-98++, b(6), b(6)-98, b(7)++, b(7), b(7)-98++, b(7)-98, b(8), b(8)++, b(8)-98, b(8)-98++, b(9)-98, b(9)-98++, b(9)++, b(10), b(10)++, b(10)-98++, b(11), b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(14)++, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(12)++, y(13)-98++, y(13)++, y(14)++
Precursor origin neutral loss:

Peptide No.730

RHSDTDDGPGMYFEK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of RHSDTDDGPGMYFEK
Found in CMYA5_MOUSE, Cardiomyopathy-associated protein 5 OS=Mus musculus GN=Cmya5 PE=1 SV=2

Match to Query 3826: 1889.765481 from(630.929103,3+)
Title: Elution from: 36.849 to 36.849 scan no 2930 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1889.7655
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 39 Expect: 0.004

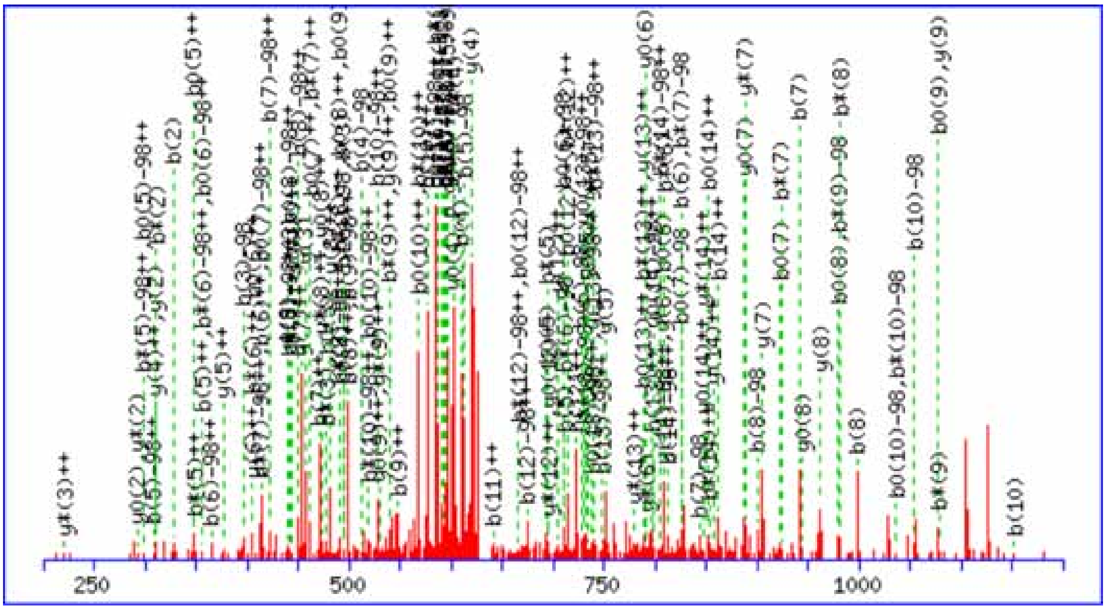
Matched b ions: b(4), b(5)-98++, b(5)++, b(5)-98, b(5), b(6)++, b(6), b(6)-98, b(7)++, b(7), b(7)-98++, b(7)-98, b(8), b(8)++, b(8)-98, b(8)-98++, b(9)-98++, b(9)++, b(10), b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(11)-98++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.731

RHSDTDDGPGMYFEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RHSDTDDGPGMYFEK
Found in CMYA5_MOUSE, Cardiomyopathy-associated protein 5 OS=Mus musculus GN=Cmya5 PE=1 SV=2

Match to Query 3911: 1901.828301 from(634.950043,3+)
Title: Elution from: 36.997 to 36.997 scan no 2951 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1901.8291
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 33 Expect: 0.022

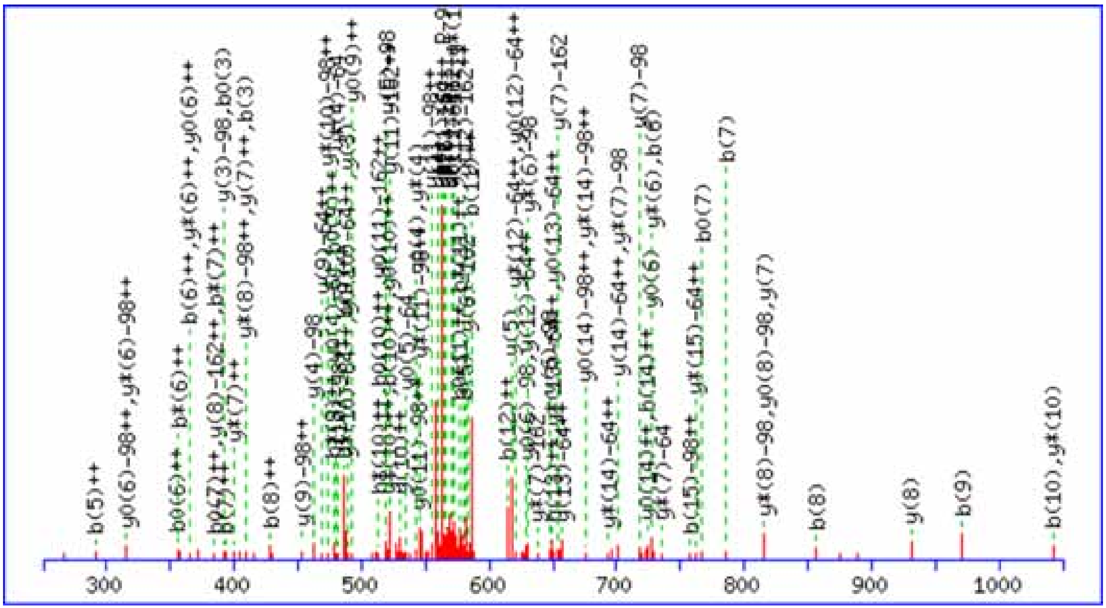
Matched b ions: b(2), b(3)-98, b(3), b(4), b(4)-98, b(5)-98++, b(5)-98, b(5)++, b(5), b(6)-98++, b(6)++, b(6), b(6)-98, b(7), b(7)++, b(7)-98++, b(7)-98, b(8)++, b(8), b(8)-98++, b(8)-98, b(9)-98++, b(9)++, b(10)++, b(10)-98, b(10), b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(5)++, y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.732

RHSGDFGADAQGAMSK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of RHSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 3624: 1785.750912 from(596.257580,3+)
Title: Elution from: 21.804 to 21.804 scan no 1111 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1785.7505
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl (K)
Ions Score: 58 Expect: 5.1e-005

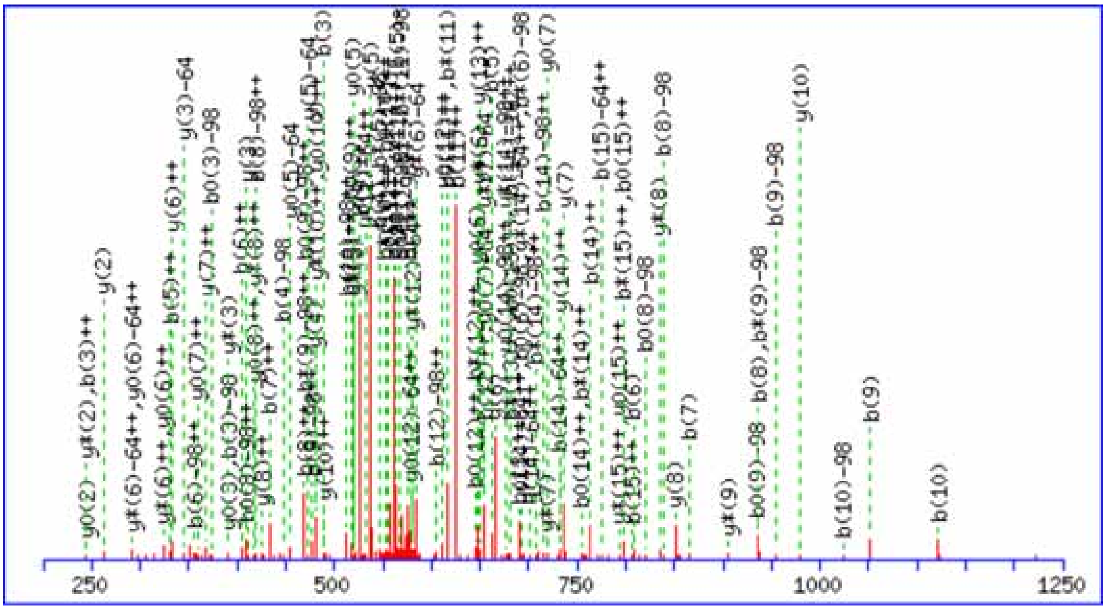
Matched b ions: b(3), b(5)++, b(5), b(6), b(6)++, b(7), b(7)++, b(8)++, b(8), b(9), b(9)++, b(10), b(10)++, b(11)++, b(12)++, b(13)++, b(14)++, b(15)-98++
Matched y ions: y(3)-98, y(3), y(4)-98, y(4), y(5), y(5)-98, y(6)-98, y(7), y(7)++, y(7)-98, y(8), y(9)-98++, y(10)-98++, y(10)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.733

RHSGDFGADAQGAMSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RHSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 3282: 1785.751713 from(596.257847,3+)
Title: Elution from: 22.160 to 22.160 scan no 1124 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1785.7505
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K16 : Dimethyl (K)
Ions Score: 83 **Expect:** 1.7e-007

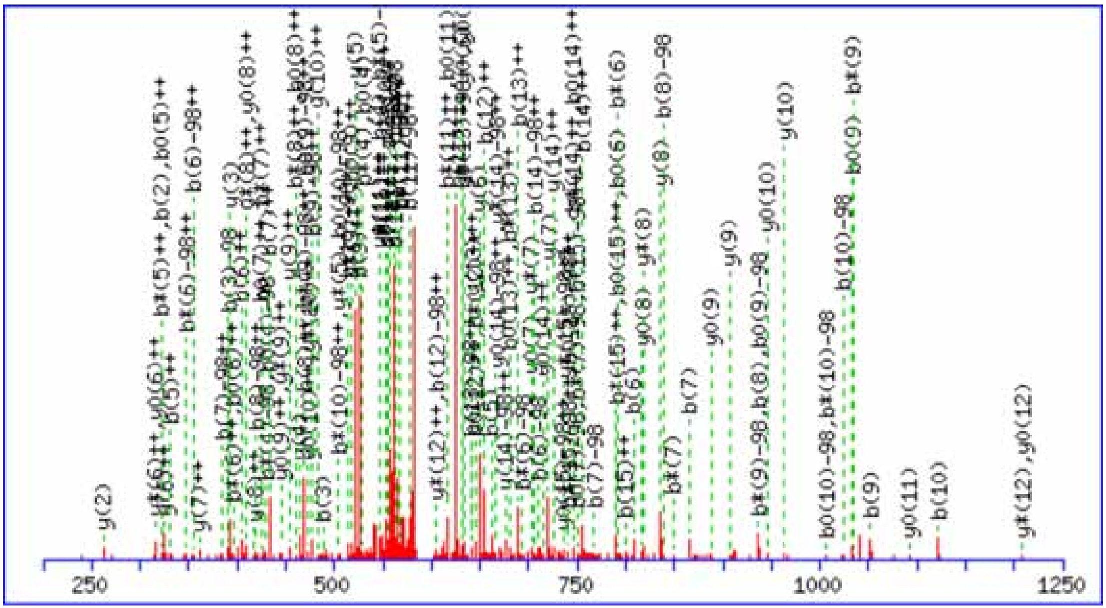
Matched b ions: b(3)-98, b(3)++, b(3), b(4)-98, b(4), b(5)-98, b(5)++, b(5), b(6)++, b(6), b(6)-98++, b(7)++, b(7), b(8), b(8)++, b(8)-98, b(8)-98++, b(9), b(9)++, b(9)-98, b(9)-98++, b(10)-98, b(10)++, b(10), b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(10), y(10)++, y(11)++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.734

RHSGDFGADAQGAMSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RHSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 3211: 1769.756820 from(590.926216,3+)
Title: Elution from: 28.117 to 28.117 scan no 1894 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1769.7556
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl (K)
Ions Score: 82 Expect: 2.1e-007

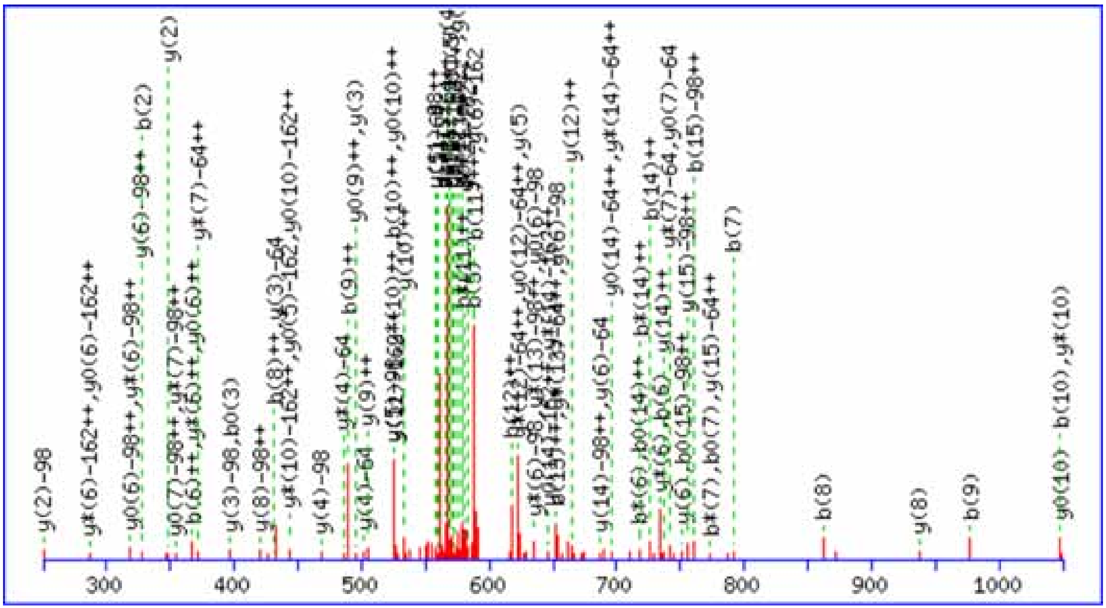
Matched b ions: b(2), b(3)-98, b(3), b(4), b(5)++, b(5), b(5)-98, b(6)++, b(6), b(6)-98++, b(6)-98, b(7)++, b(7), b(7)-98++, b(7)-98, b(8), b(8)++, b(8)-98++, b(8)-98, b(9)++, b(9), b(9)-98++, b(10), b(10)++, b(10)-98, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(9), y(10), y(10)++, y(11)++, y(13)++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.735

RHSGDFGADAQGAMSK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of RHSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 3273: 1797.814962 from(600.278930,3+)
Title: Elution from: 21.703 to 21.703 scan no 1098 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1797.8142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 62 Expect: 3.4e-005

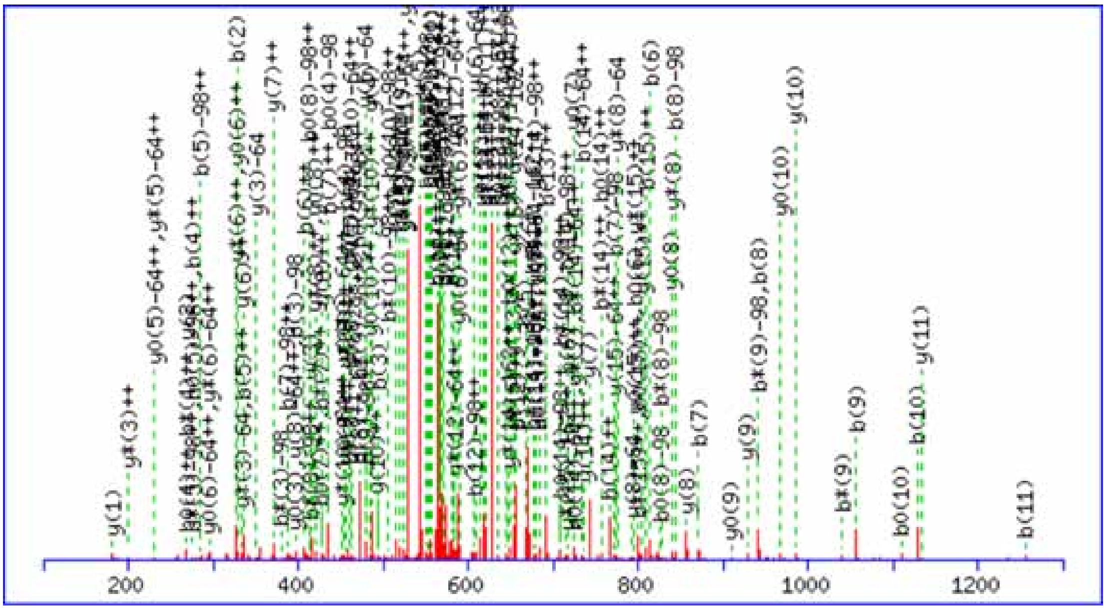
Matched b ions: b(2), b(5), b(6), b(6)++, b(7), b(8)++, b(8), b(9), b(9)++, b(10)++, b(10), b(11)++, b(12)++, b(13)++, b(14)++, b(15)-98++
Matched y ions: y(2)-98, y(2), y(3)-98, y(3), y(4)-98, y(4), y(5)-98, y(5), y(6)-98, y(6)-98++, y(6), y(8)-98++, y(8), y(9)++, y(10)++, y(11)-98++, y(12)++, y(14)-98++, y(14)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.736

RHSGDFGADAQGAMSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RHSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 3354: 1797.815178 from(600.279002,3+)
Title: Elution from: 22.128 to 22.128 scan no 1120 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1797.8142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 74 **Expect:** 2.3e-006

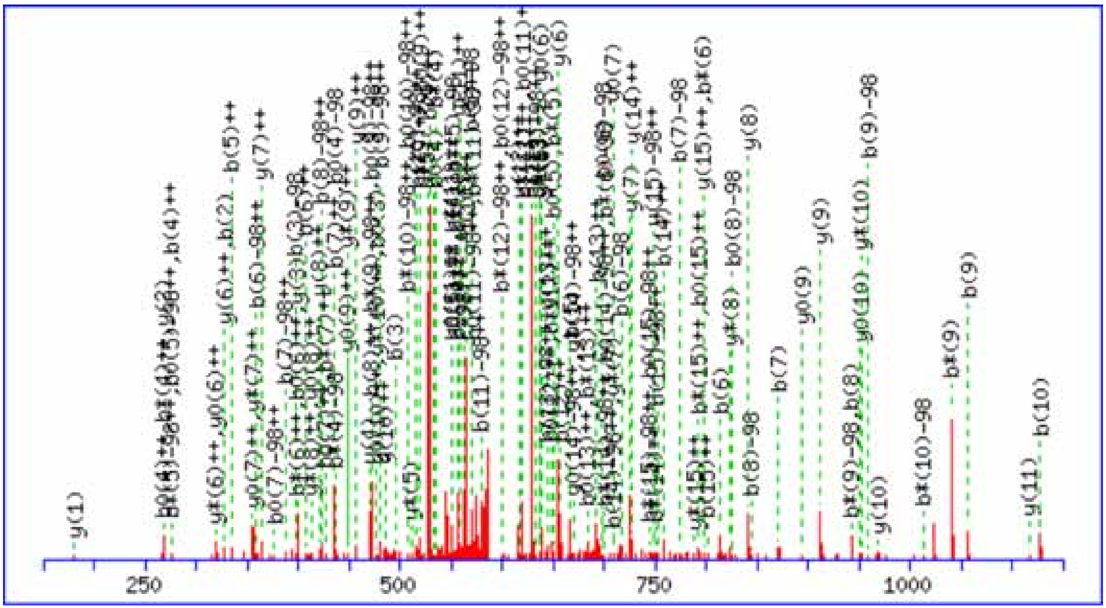
Matched b ions: b(2), b(3)-98, b(3), b(4)++, b(4)-98, b(4), b(5)-98, b(5)++, b(5), b(5)-98++, b(6), b(6)++, b(6)-98, b(7)++, b(7), b(7)-98++, b(7)-98, b(8)++, b(8), b(8)-98, b(9), b(9)++, b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)++, b(11), b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(10), y(10)++, y(11), y(11)++, y(13)++, y(14)++, y(15)++
Precursor origin neutral loss:

Peptide No.737

RHSGDFGADAQGAMSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RHSGDFGADAQGAMSK
Found in MYG_MOUSE, Myoglobin OS=Mus musculus GN=Mb PE=1 SV=3

Match to Query 3260: 1781.820306 from(594.947378,3+)
Title: Elution from: 28.039 to 28.039 scan no 1886 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1781.8192
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 91 **Expect:** 4.9e-008

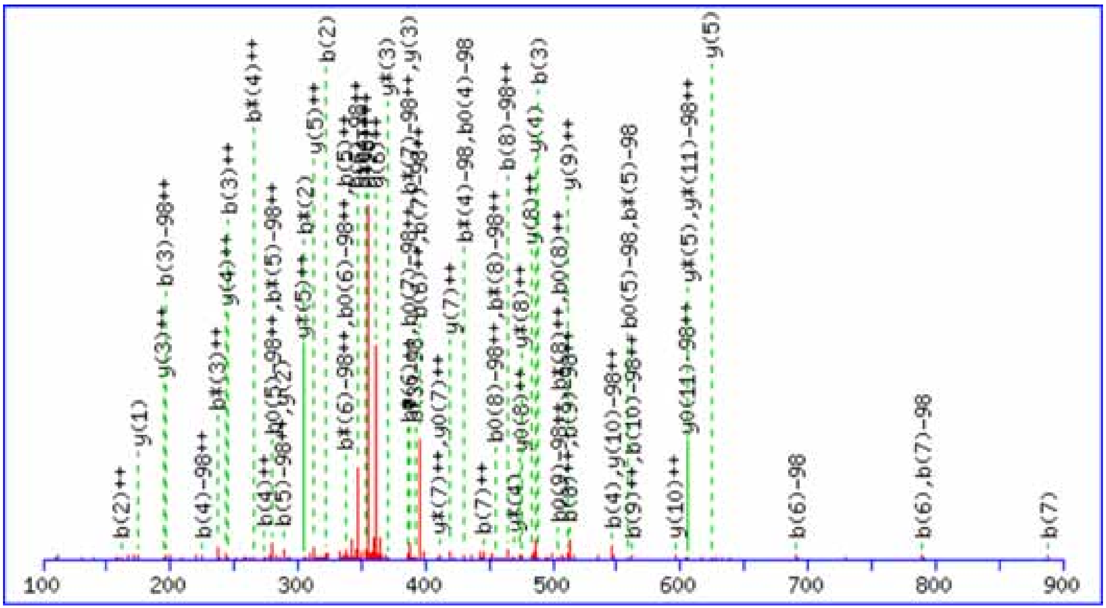
Matched b ions: b(2), b(3)-98, b(3), b(4)++, b(4), b(5)++, b(5), b(5)-98, b(6), b(6)-98, b(6)-98++, b(6)++, b(7)++, b(7), b(7)-98++, b(7)-98, b(8)++, b(8), b(8)-98++, b(8)-98, b(9)++, b(9), b(9)-98++, b(9)-98, b(10), b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)-98++, y(15)++
Precursor origin neutral loss:

Peptide No.738

RHSGQDVHVVLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RHSGQDVHVVLK
Found in NSF1C_MOUSE, NSFL1 cofactor p47 OS=Mus musculus GN=Nsfl1c PE=1 SV=1

Match to Query 3226: 1509.781696 from(378.452700,4+)
Title: Elution from: 23.180 to 23.180 scan no 1309 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1509.7817
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl (K)
Ions Score: 42 Expect: 0.0033

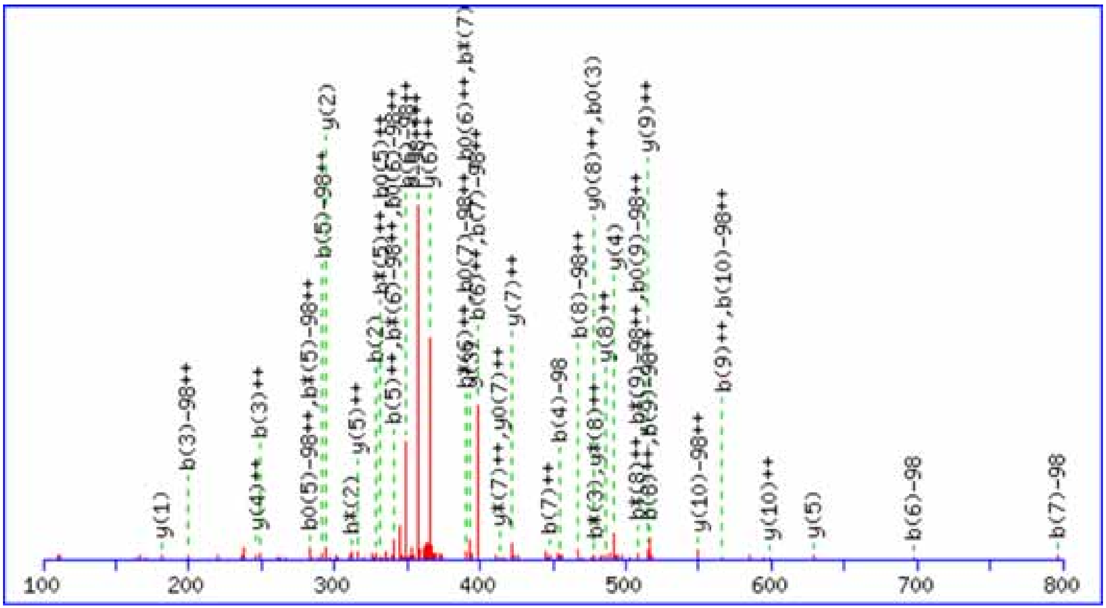
Matched b ions: b(2)++, b(2), b(3)-98++, b(3)++, b(3)-98, b(3), b(4), b(4)-98++, b(4)++, b(5)-98++, b(5)++, b(6)-98, b(6), b(6)++, b(6)-98++, b(7)-98, b(7), b(7)-98++, b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(4)++, y(5), y(5)++, y(6)++, y(7)++, y(8)++, y(9)++, y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.739

RHSGQDVHVVLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RHSGQDVHVVLK
Found in NSF1C_MOUSE, NSFL1 cofactor p47 OS=Mus musculus GN=Nsfl1c PE=1 SV=1

Match to Query 2037: 1521.846104 from(381.468802,4+)
Title: Elution from: 23.256 to 23.256 scan no 1253 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1521.8453
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 45 Expect: 0.0012

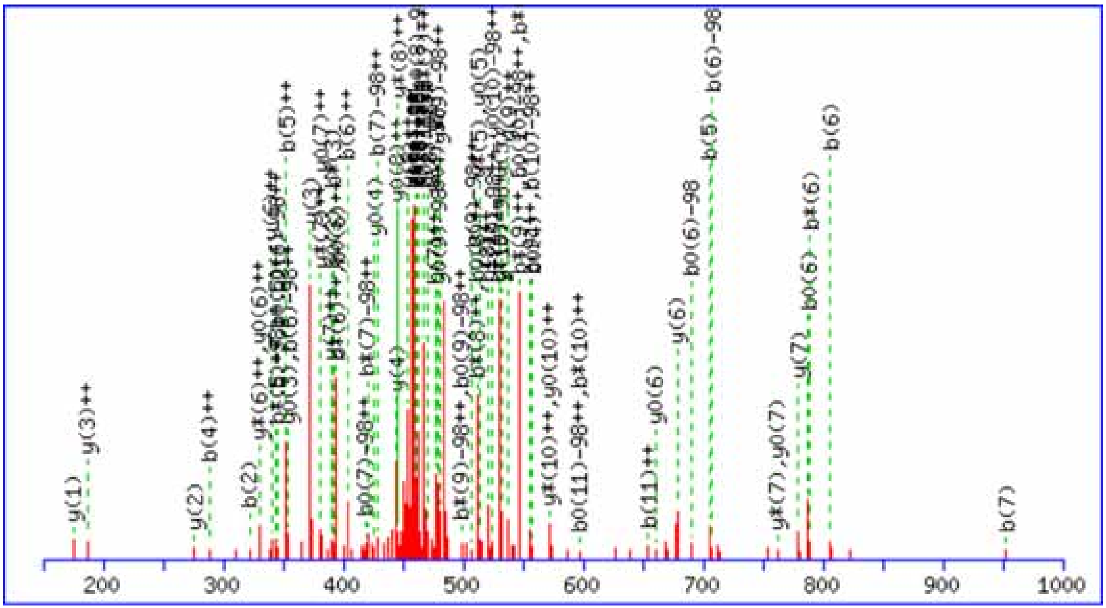
Matched b ions: b(2), b(3)-98++, b(3)++, b(4)-98, b(5)-98++, b(5)++, b(6)-98, b(6)++, b(6)-98++, b(7)-98, b(7)-98++, b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5), y(5)++, y(6)++, y(7)++, y(8)++, y(9)++, y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.740

RHSSETFSAPTR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RHSSETFSAPTR
Found in IRS1_MOUSE, Insulin receptor substrate 1 OS=Mus musculus GN=Irs1 PE=1 SV=1

Match to Query 2342: 1482.661932 from(495.227920,3+)
Title: Elution from: 22.524 to 22.524 scan no 1301 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1482.6616
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.014

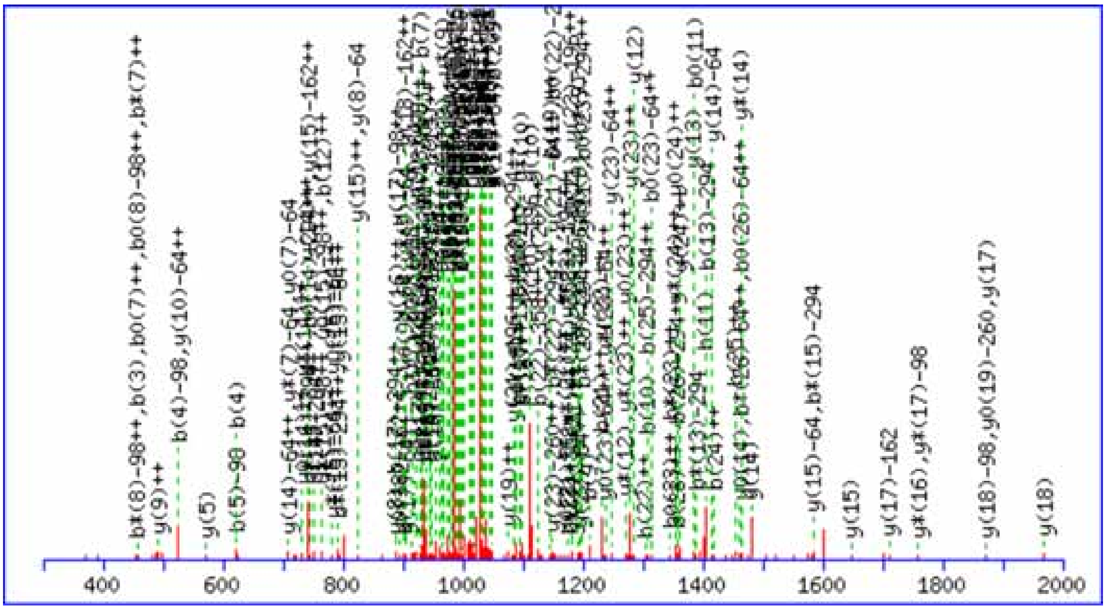
Matched b ions: b(2), b(4)++, b(4)-98, b(5)++, b(5), b(6), b(6)-98++, b(6)-98, b(6)++, b(7), b(7)++, b(7)-98++, b(8)++, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++, b(11)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(9)++, y(10)-98++
Precursor origin neutral loss:

Peptide No.741

RKDSPPLVTPPQSPPSSQPPAMTQAPR
Confirmed sites: @S:4,@T:9,@S:13
Ambiguous sites:

MS/MS Fragmentation of RKDSPPLVTPPQSPPSSQPPAMTQAPR
Found in SMTL2_MOUSE, Smoothelin-like protein 2 OS=Mus musculus GN=Smtnl2 PE=1 SV=1

Match to Query 8669: 3178.437129 from(1060.486319,3+)
Title: Elution from: 37.593 to 37.593 scan no 3344 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3178.4324
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 53 Expect: 0.00052

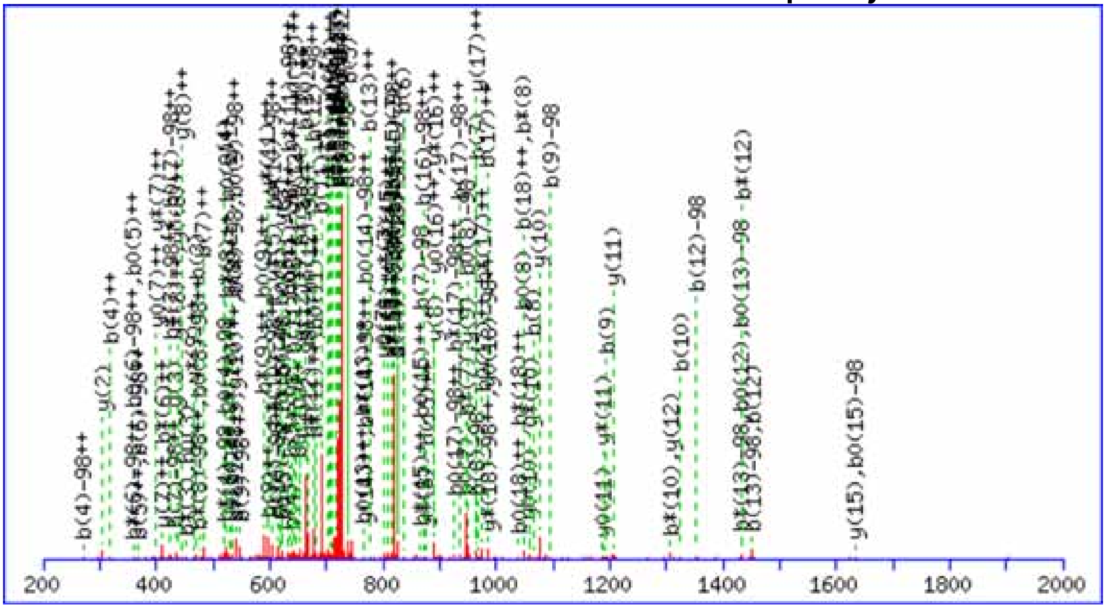
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(7), b(8), b(8)-98, b(9)-98, b(9), b(9)-196, b(10)-196, b(10)-98, b(10), b(11), b(11)-98, b(12)++, b(12)-98++, b(13)-98++, b(13)-98, b(13)-196, b(13)-196++, b(13)-294, b(14)-196++, b(14)-196, b(14)-294++, b(15)++, b(17)-196++, b(17)-196, b(17)-98, b(17)-98++, b(17)-294++, b(18)++, b(18)-196++, b(19)-98++, b(19)-294++, b(19)-196++, b(19)++, b(20)-294++, b(20)-98++, b(21)++, b(21)-98++, b(21)-294++, b(22)++, b(23)++, b(23)-98++, b(24)++, b(25)++, b(25)-196++, b(25)-98++, b(25)-294++, b(26)-98++, b(26)-294++, b(26)-196++
Matched y ions: y(5), y(8), y(9)++, y(9), y(10), y(11), y(12), y(13), y(14)++, y(14), y(15)++, y(15), y(16)++, y(17), y(17)++, y(17)-98++, y(18)-98++, y(18)-98, y(18), y(18)++, y(19)++, y(19)-196++, y(20)-196++, y(20)++, y(20)-98++, y(21)++, y(21)-196++, y(22)++, y(22)-98++, y(23)-98++, y(23)++, y(23)-196++, y(24)++, y(24)-98++
Precursor origin neutral loss: +

Peptide No.742

RKESTPETEEGAPTTSEEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RKESTPETEEGAPTTSEEK
Found in SMPX_MOUSE, Small muscular protein OS=Mus musculus GN=Smpx PE=2 SV=2

Match to Query 5522: 2269.037994 from(757.353274,3+)
Title: Elution from: 21.748 to 21.748 scan no 1114 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2269.0362
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl (K)
Ions Score: 60 Expect: 7.9e-005

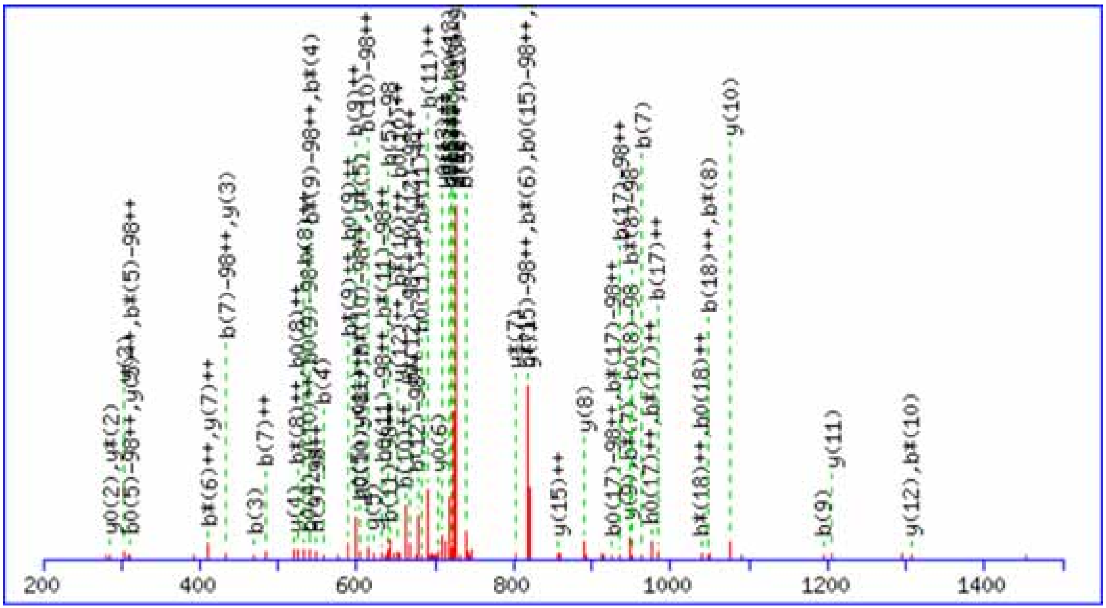
Matched b ions: b(3), b(4)-98, b(4)++, b(4)-98++, b(4), b(5)++, b(5)-98, b(5), b(6)-98++, b(6)-98, b(6), b(7)-98++, b(7)++, b(7), b(7)-98, b(8)++, b(8)-98, b(8), b(9)-98++, b(9)++, b(9), b(9)-98, b(10)++, b(10), b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12), b(12)-98++, b(12)-98, b(13)-98++, b(13)-98, b(13)++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(10)++, y(10), y(11), y(12), y(12)++, y(13)++, y(14)++, y(15), y(15)++, y(17)++
Precursor origin neutral loss: +

Peptide No.743

RKESTPETEEGAPTTSEEK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of RKESTPETEEGAPTTSEEK
Found in SMPX_MOUSE, Small muscular protein OS=Mus musculus GN=Smpx PE=2 SV=2

Match to Query 6125: 2269.038915 from(757.353581,3+)
Title: Elution from: 21.885 to 21.885 scan no 1096 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2269.0362
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl (K)
Ions Score: 62 Expect: 4.3e-005

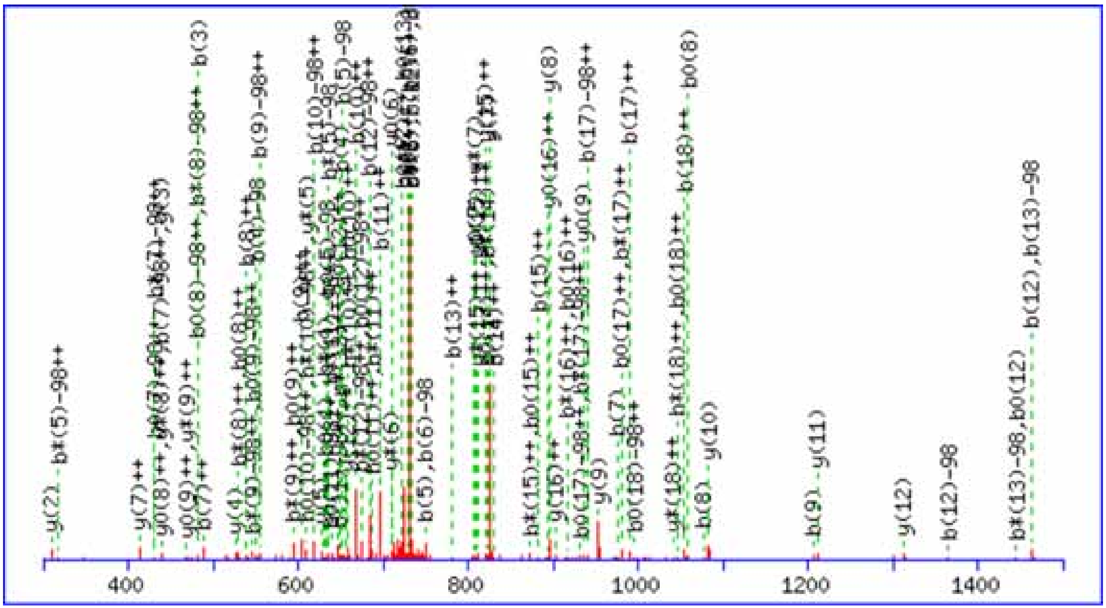
Matched b ions: b(3), b(4), b(5), b(5)-98, b(7)-98++, b(7)++, b(7), b(8)++, b(9)++, b(9), b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(17)++, b(17)-98++, b(18)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13)++, y(15)++
Precursor origin neutral loss: +

Peptide No.744

RKESTPETEEGAPTTSEEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RKESTPETEEGAPTTSEEK
Found in SMPX_MOUSE, Small muscular protein OS=Mus musculus GN=Smpx PE=2 SV=2

Match to Query 5923: 2287.132788 from(763.384872,3+)
Title: Elution from: 21.720 to 21.720 scan no 1100 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2287.1317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K2 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K19 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 45 Expect: 0.0026

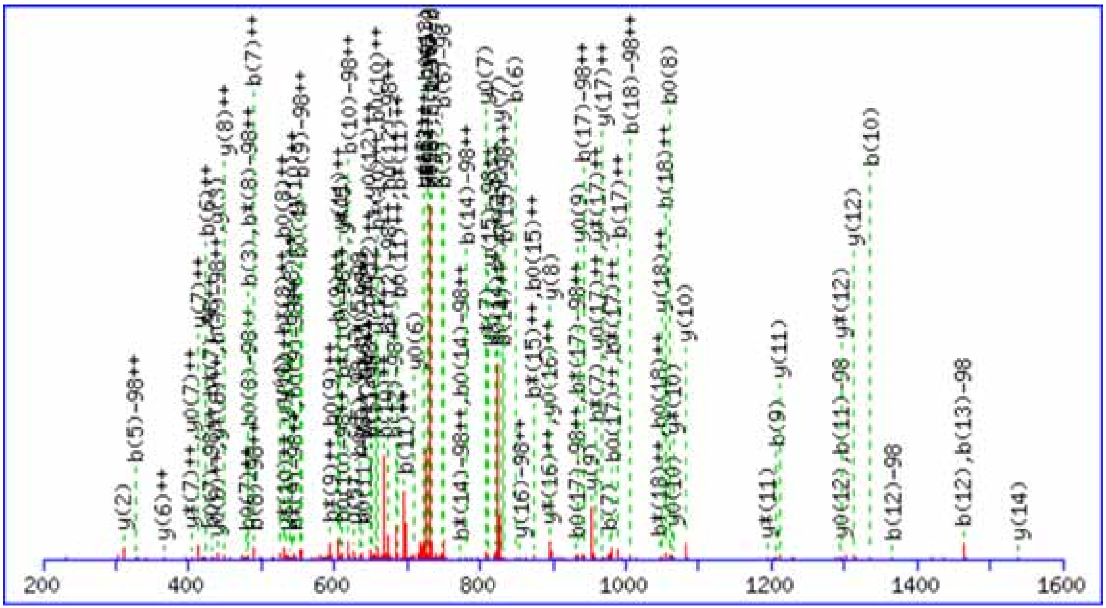
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(7)++, b(7)-98++, b(7), b(8)++, b(8), b(9), b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12), b(12)-98++, b(12)-98, b(13)-98++, b(13)-98, b(13)++, b(14)++, b(15)++, b(17)++, b(17)-98++, b(18)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.745

RKESTPETEEGAPTTSEEK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of RKESTPETEEGAPTTSEEK
Found in SMPX_MOUSE, Small muscular protein OS=Mus musculus GN=Smpx PE=2 SV=2

Match to Query 5574: 2287.133082 from(763.384970,3+)
Title: Elution from: 21.698 to 21.698 scan no 1108 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2287.1317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K2 : Dimethyl:2H(4)13C(2) (K)
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K19 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 54 **Expect:** 0.0003

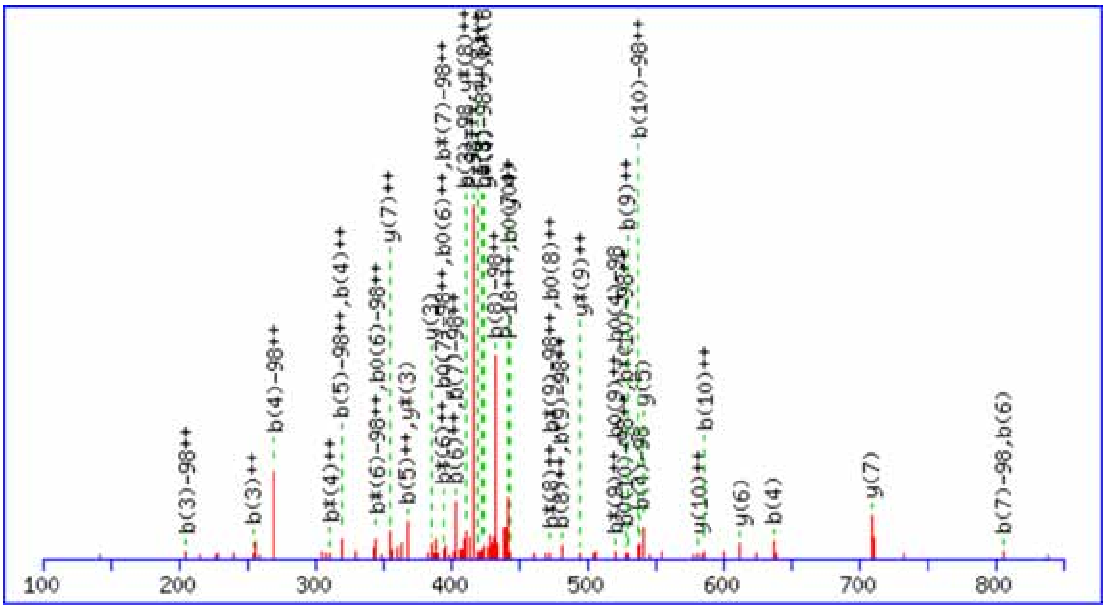
Matched b ions: b(3), b(5)-98++, b(5), b(5)-98, b(6)++, b(6), b(6)-98, b(7)++, b(7)-98++, b(7), b(8)-98++, b(8)++, b(9)++, b(9), b(9)-98++, b(10)-98++, b(10), b(10)++, b(11)-98, b(11)++, b(11)-98++, b(12)++, b(12), b(12)-98, b(12)-98++, b(13)-98++, b(13)-98, b(14)-98++, b(14)++, b(15)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13)++, y(14), y(15)-98++, y(16)-98++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No.746

RKSEPAVGPLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RKSEPAVGPLR
Found in SRBS2_MOUSE, Sorbin and SH3 domain-containing protein 2 OS=Mus musculus GN=Sorbs2 PE=1 SV=2

Match to Query 1523: 1344.728604 from(449.250144,3+)
Title: Elution from: 24.049 to 24.049 scan no 1358 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1344.7278
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.0019

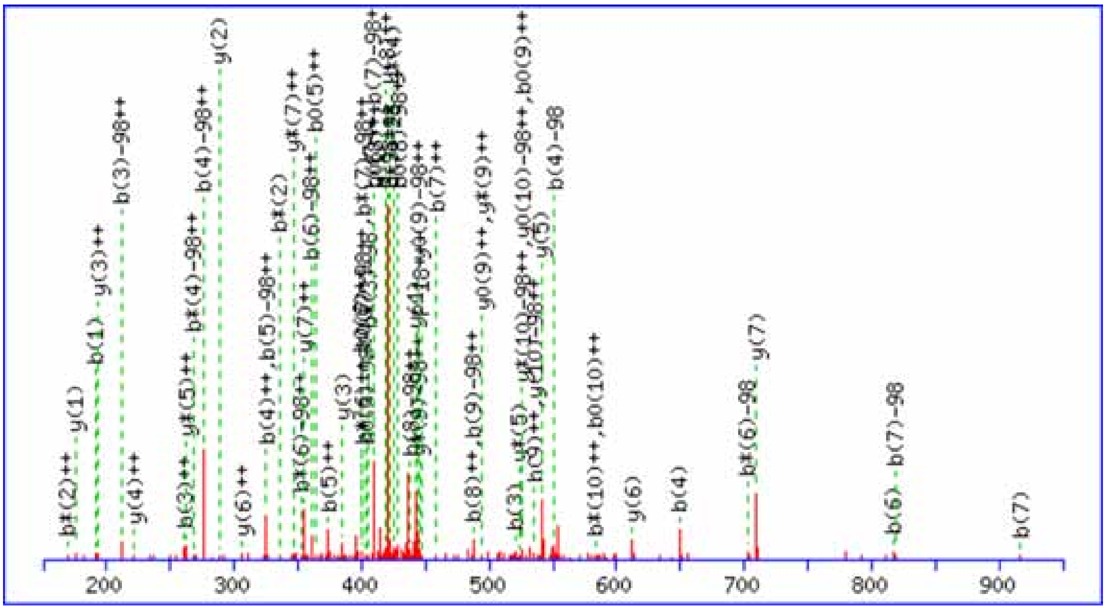
Matched b ions: b(3)-98++, b(3)++, b(3)-98, b(4)-98++, b(4)++, b(4)-98, b(4), b(5)-98++, b(5)++, b(6), b(6)++, b(7)-98, b(7)-98++, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(10)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(10)++
Precursor origin neutral loss: +

Peptide No.747

RKSEPAVGPLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RKSEPAVGPLR
Found in SRBS2_MOUSE, Sorbin and SH3 domain-containing protein 2 OS=Mus musculus GN=Sorbs2 PE=1 SV=2

Match to Query 1456: 1356.791193 from(453.271007,3+)
Title: Elution from: 23.860 to 23.860 scan no 1367 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1356.7915
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K2 : Dimethyl:2H(4)13C(2) (K)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.022

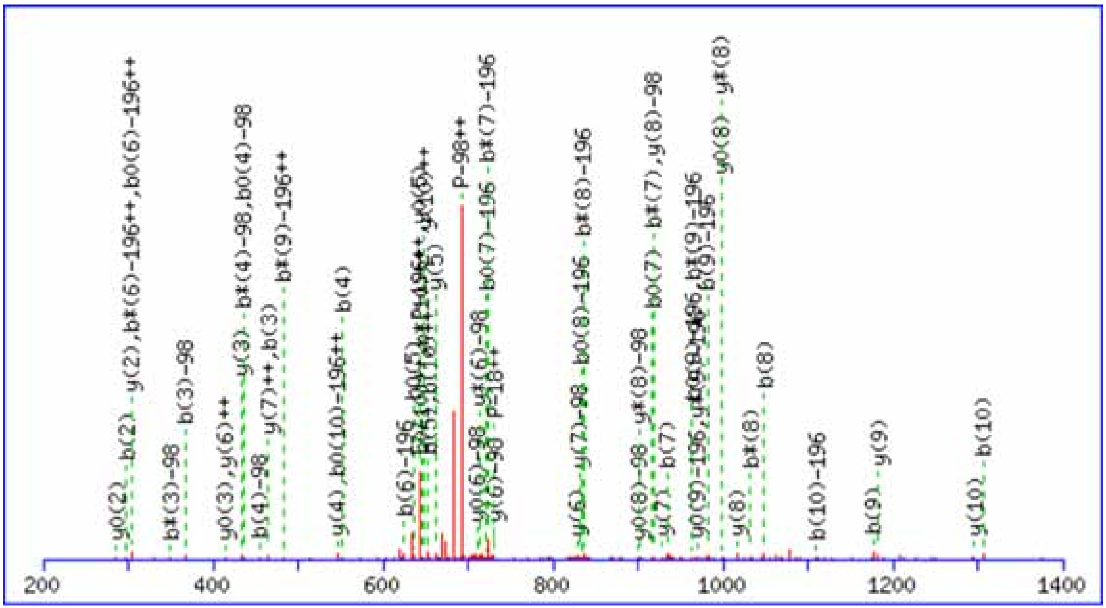
Matched b ions: b(1), b(3)-98++, b(3)++, b(3)-98, b(3), b(4)-98++, b(4), b(4)++, b(4)-98, b(5)-98++, b(5)++, b(6)++, b(6), b(6)-98++, b(7), b(7)-98++, b(7)-98, b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(9)++
Matched y ions: y(1), y(2), y(3)++, y(3), y(4), y(4)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.748

RLSSTSDIEEK
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of RLSSTSDIEEK
Found in MYPT2_MOUSE, Protein phosphatase 1 regulatory subunit 12B OS=Mus musculus GN=Ppp1r12b PE=1 SV=2

Match to Query 2334: 1479.626122 from(740.820337,2+)
Title: Elution from: 29.620 to 29.620 scan no 2253 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1479.6259
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K11 : Dimethyl (K)
Ions Score: 39 Expect: 0.0029

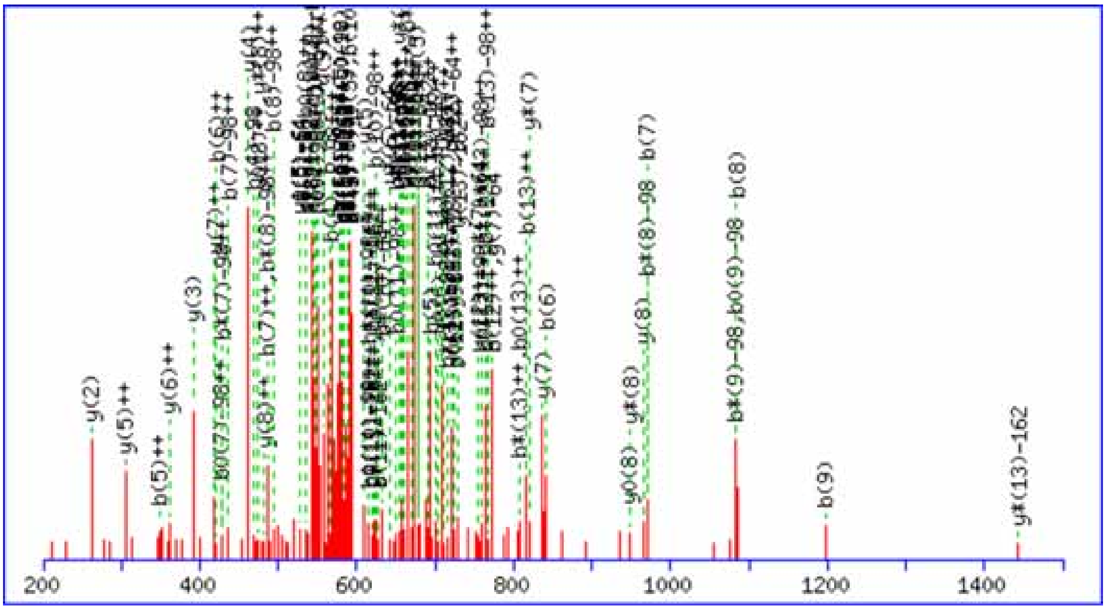
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(6)-98, b(6)-196, b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(9), b(9)-196, b(10)-98, b(10), b(10)-196, b(10)-98++, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(6)-98, y(7)++, y(7)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)++
Precursor origin neutral loss: +

Peptide No.749

RLSTQFENLMAESR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of RLSTQFENLMAESR
Found in SYNCI_MOUSE, Syncoilin OS=Mus musculus GN=Sync PE=1 SV=1

Match to Query 4360: 1804.818690 from(602.613506,3+)
Title: Elution from: 41.870 to 41.870 scan no 3913 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1804.8179
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 45 Expect: 0.0018

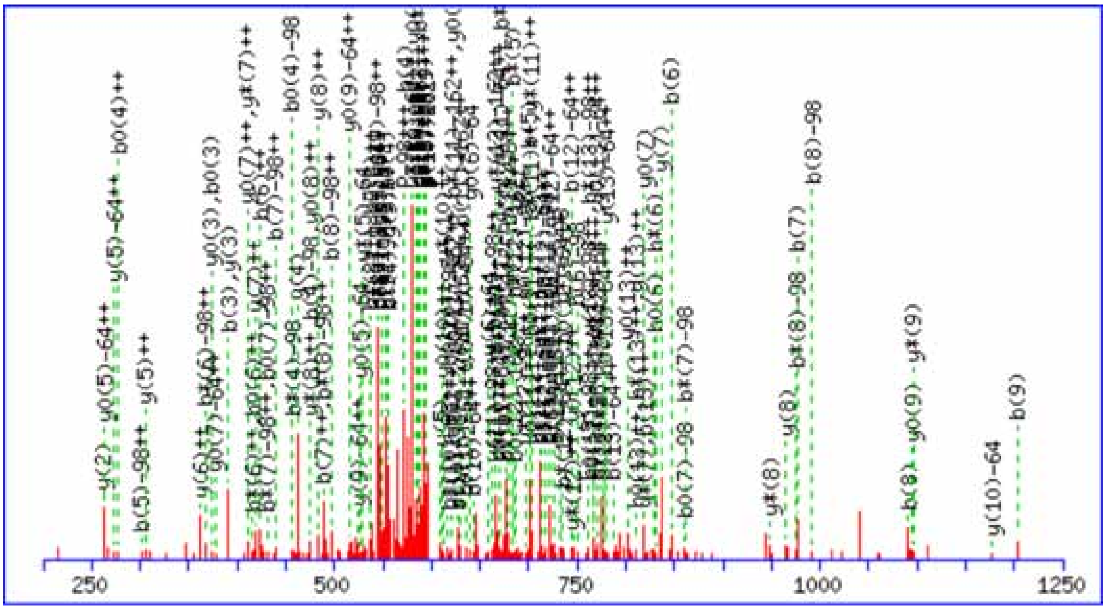
Matched b ions: b(4)-98, b(4), b(5), b(5)++, b(6), b(6)++, b(7), b(7)++, b(7)-98++, b(8)++, b(8), b(8)-98++, b(9), b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.750

RLSTQFENLMAESR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of RLSTQFENLMAESR
Found in SYNCI_MOUSE, Syncoilin OS=Mus musculus GN=Sync PE=1 SV=1

Match to Query 3828: 1810.850778 from(604.624202,3+)
Title: Elution from: 41.512 to 41.512 scan no 3708 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1810.8497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 48 Expect: 0.001

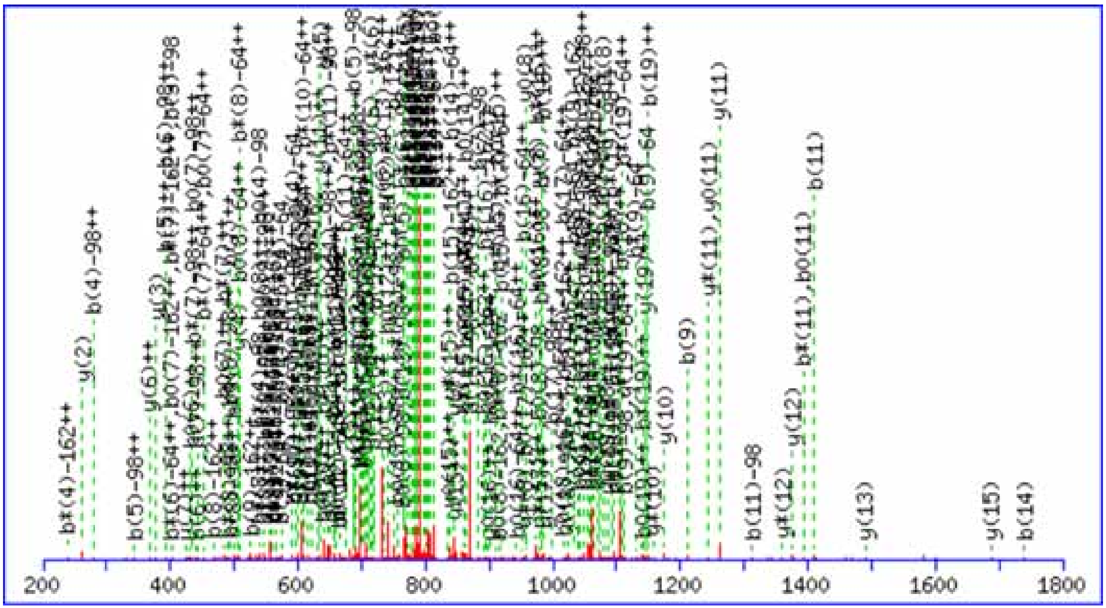
Matched b ions: b(3), b(4), b(4)-98, b(5), b(5)-98++, b(6)++, b(6), b(6)-98, b(7), b(7)++, b(7)-98++, b(8)++, b(8), b(8)-98++, b(8)-98, b(9), b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(11)++, y(11)-98++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.751

RMSREPTLDSISELPEEDSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 7461: 2470.106235 from(824.376021,3+)
Title: Elution from: 44.188 to 44.188 scan no 4203 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2470.1046
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 4.9e-006

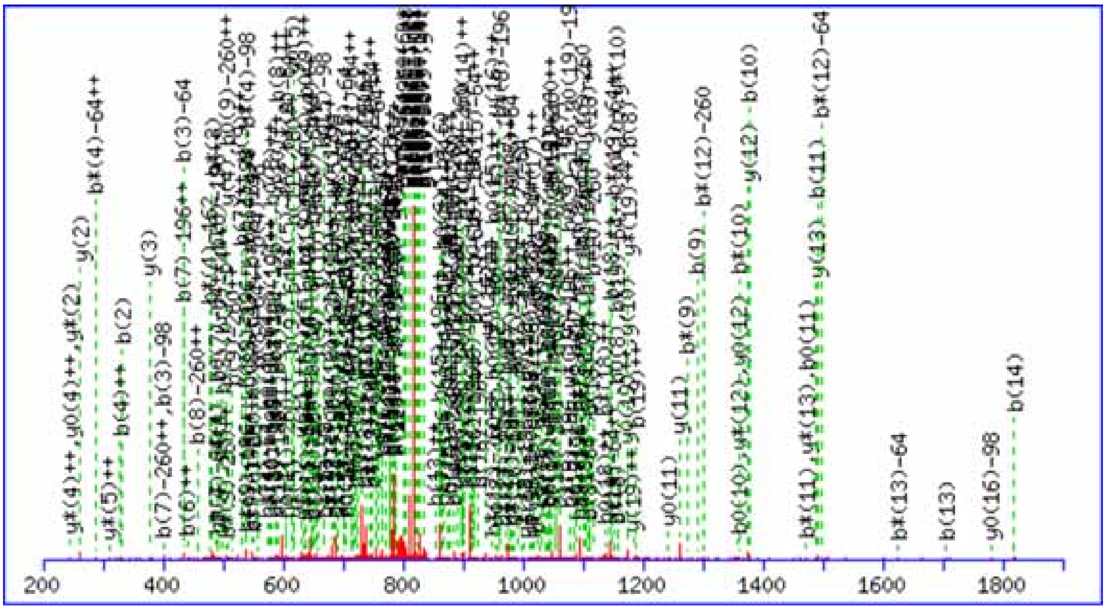
Matched b ions: b(3)-98, b(3), b(4)-98++, b(4)-98, b(4), b(5)-98++, b(5)++, b(5), b(5)-98, b(6)-98++, b(6)++, b(6)-98, b(7)-98++, b(7)++, b(7)-98, b(7), b(8)++, b(8)-98++, b(8), b(9)++, b(9)-98++, b(9), b(9)-98, b(10)-98++, b(10)++, b(11), b(11)++, b(11)-98, b(11)-98++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14), b(15)-98++, b(15)++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(13), y(14)++, y(15), y(15)++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.752

RMSREPTLDSISELPEEDSR
Confirmed sites: @S:3,@T:7
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6688: 2550.072513 from(851.031447,3+)
Title: Elution from: 46.507 to 46.507 scan no 4310 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2550.0710
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.0014

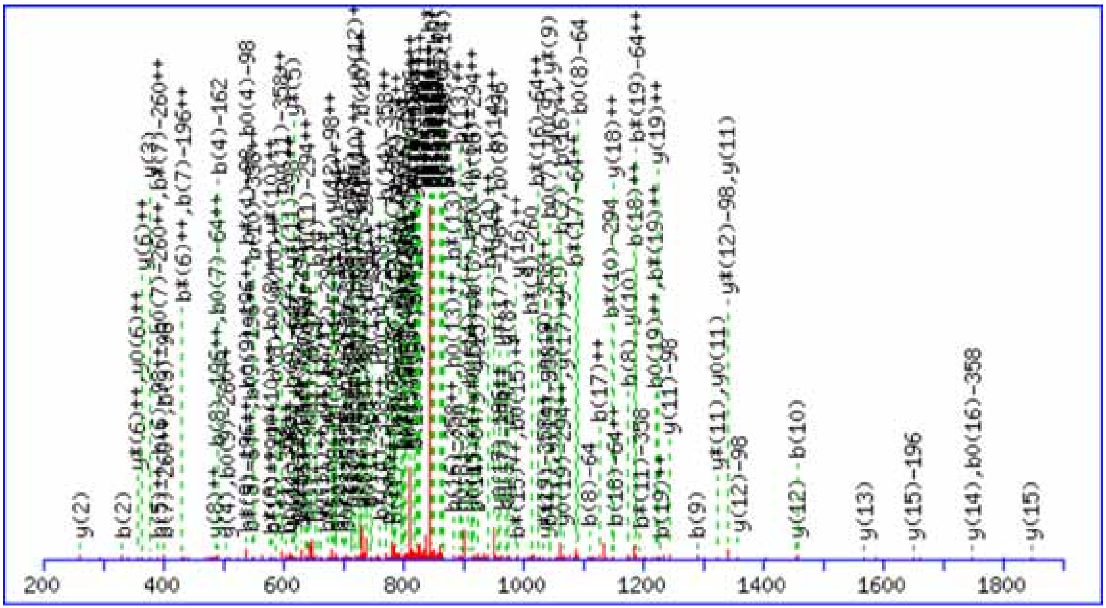
Matched b ions: b(2), b(3)-98, b(3), b(4)++, b(4)-98, b(4), b(5), b(5)-98, b(6)++, b(6)-98, b(7)-196++, b(7)-98++, b(7), b(7)-98, b(7)++, b(7)-196, b(8)-98++, b(8), b(8)-196++, b(8)++, b(8)-196, b(8)-98, b(9)-98++, b(9)-196++, b(9), b(9)++, b(9)-196, b(9)-98, b(10), b(10)-98++, b(10)-196++, b(10)++, b(10)-98, b(11), b(11)-196++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(12)++, b(13), b(13)++, b(13)-196++, b(13)-98++, b(14)++, b(14)-98++, b(14), b(14)-196++, b(15)-98++, b(15)-196++, b(15)++, b(16)-98++, b(16)++, b(16)-196++, b(17)++, b(17)-98++, b(17)-196++, b(18)++, b(18)-98++, b(18)-196++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(18)-98++, y(18)-196++, y(18)++, y(19)-196++, y(19)++
Precursor origin neutral loss: +

Peptide No.753

RMSREPTLDSISELPEEDSR
Confirmed sites: @S:3,@T:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6892: 2630.040498 from(877.687442,3+)
Title: Elution from: 49.005 to 49.005 scan no 4614 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2630.0373
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 Expect: 7.4e-007

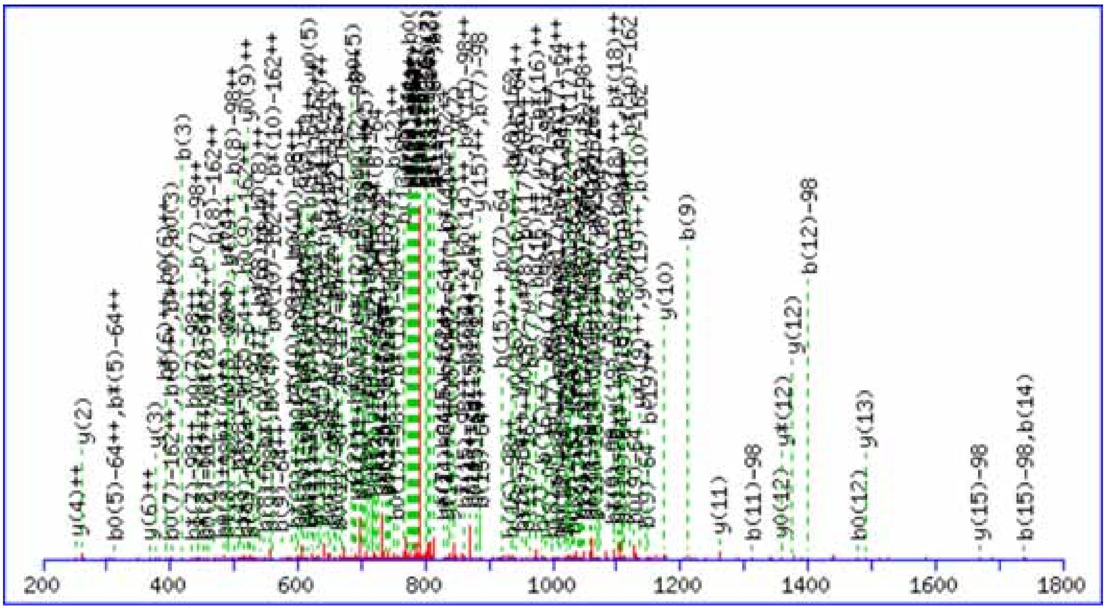
Matched b ions: b(2), b(3)-98, b(4), b(5)++, b(5), b(5)-98, b(6)-98++, b(6)-98, b(7), b(7)-196++, b(7)-98, b(7)-196, b(7)-98++, b(8)-98++, b(8)-196++, b(8), b(8)++, b(9)++, b(9), b(9)-98++, b(9)-196++, b(10), b(10)-98++, b(10)-196++, b(10)-98, b(10)-294++, b(10)++, b(11)-98++, b(11)-196++, b(11)-294++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)-294++, b(13)-196++, b(13)++, b(14)++, b(14)-98++, b(14)-98, b(14)-196++, b(14)-294++, b(15)-98++, b(15)-196++, b(15)-294++, b(16)-98++, b(16)-294++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(18)-196++, b(19)++
Matched y ions: y(2), y(3), y(4), y(6), y(6)++, y(7), y(8), y(8)++, y(9), y(10), y(10)++, y(11), y(11)-98, y(11)-98++, y(12), y(12)-98++, y(12)-98, y(12)++, y(13), y(13)-98++, y(13)++, y(14), y(14)-98++, y(15), y(15)-98, y(15)-196, y(15)++, y(15)-196++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.754

RMSREPTLDSISELPEEDSR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6444: 2470.107438 from(824.376422,3+)
Title: Elution from: 44.085 to 44.085 scan no 4004 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2470.1046
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 **Expect:** 0.00082

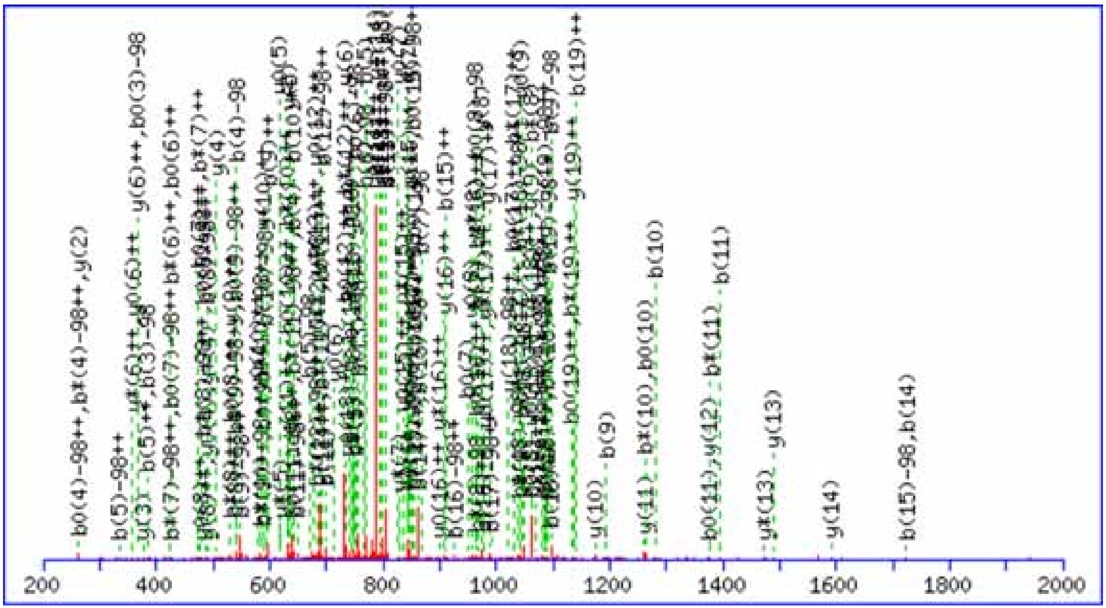
Matched b ions: b(3), b(5), b(6)++, b(6), b(7)-98++, b(7)++, b(7)-98, b(7), b(8)++, b(8)-98++, b(8)-98, b(8), b(9), b(9)++, b(9)-98++, b(9)-98, b(10)++, b(10)-98++, b(11)-98, b(11)++, b(11)-98++, b(12)-98, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14), b(15)-98++, b(15)-98, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(9)++, y(10), y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14)-98++, y(14)++, y(15)-98, y(15)++, y(17)++, y(18)-98++, y(18)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.755

RMSREPTLDSISELPEEDSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6215: 2454.111171 from(819.044333,3+)
Title: Elution from: 46.575 to 46.575 scan no 4278 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2454.1097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 4.7e-005

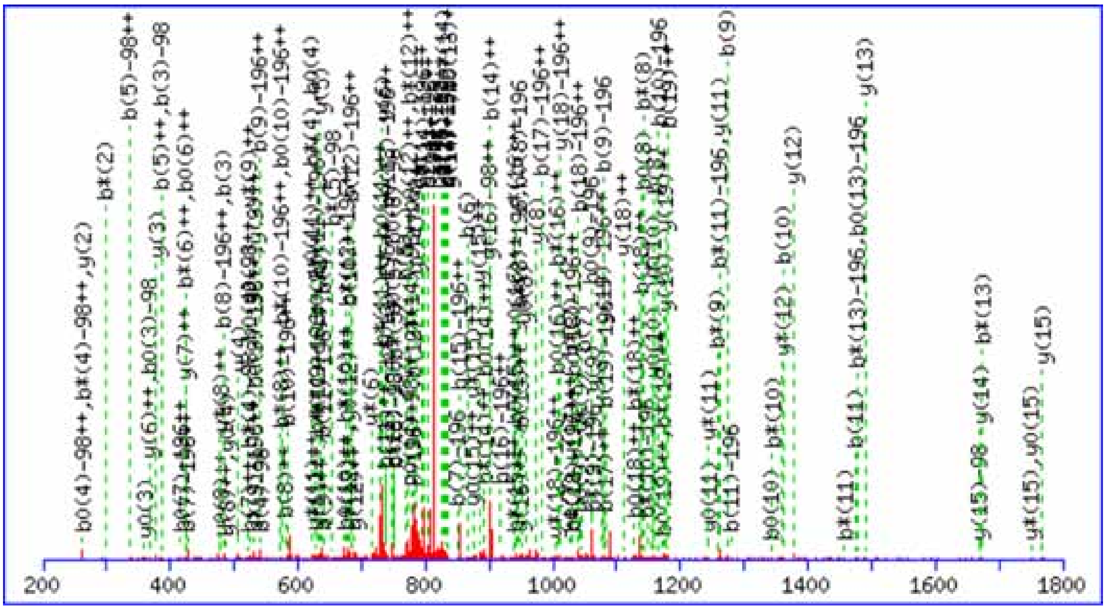
Matched b ions: b(3)-98, b(4), b(4)-98, b(5)++, b(5)-98++, b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(8)++, b(8), b(8)-98++, b(9)-98++, b(9)++, b(9), b(9)-98, b(10)++, b(10)-98++, b(10), b(11), b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14), b(15)-98++, b(15)-98, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(12), y(13), y(13)++, y(14), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.756

RMSREPTLDSISELPEEDSR
Confirmed sites: @S:3,@T:7
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6631: 2534.079663 from(845.700497,3+)
Title: Elution from: 48.971 to 48.971 scan no 4609 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2534.0761
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00071

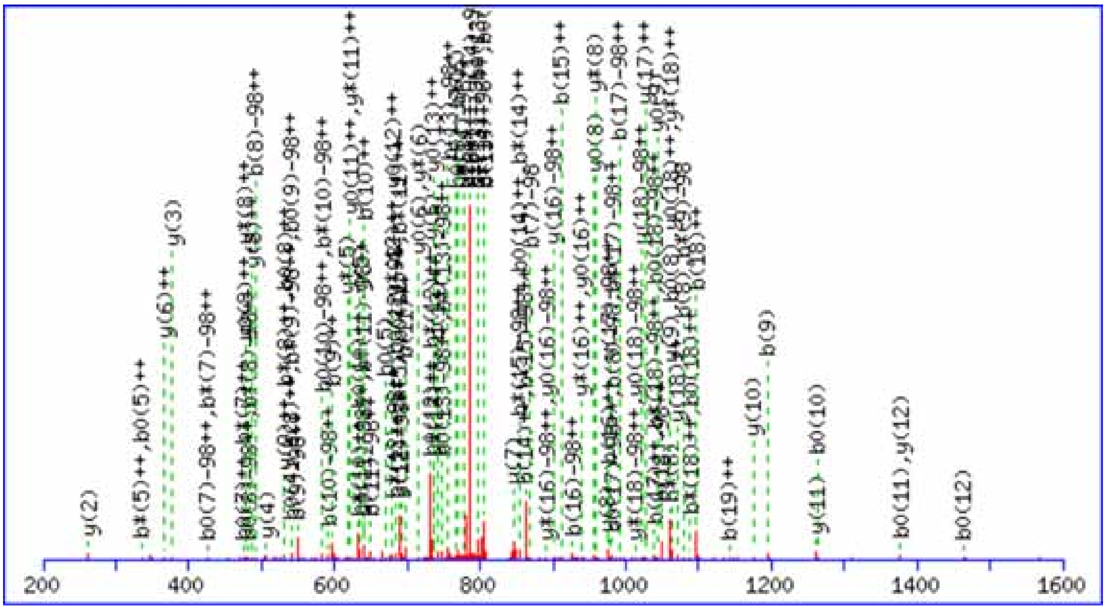
Matched b ions: b(3), b(3)-98, b(4)-98, b(4), b(5)-98++, b(5)++, b(5), b(6), b(7)-196++, b(7)-98++, b(7)++, b(7)-196, b(7)-98, b(7), b(8)-98, b(8)-98++, b(8)-196++, b(8)++, b(8), b(9)-196++, b(9)-98++, b(9)++, b(9), b(9)-98, b(9)-196, b(10)-98++, b(10)-196++, b(10)++, b(10)-196, b(10), b(11)-98, b(11)-196, b(11)-196++, b(11)-98++, b(11)++, b(11), b(12)-98++, b(12)++, b(12)-196++, b(13)-196++, b(13)-98++, b(14)++, b(14)-98++, b(14)-196++, b(15)-98++, b(15)++, b(15)-196++, b(16)-196++, b(16)-98++, b(17)++, b(17)-196++, b(17)-98++, b(18)-98++, b(18)-196++, b(18)++, b(19)++, b(19)-196++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(11), y(11)++, y(12), y(12)++, y(13), y(14), y(14)-98++, y(14)++, y(15)-98, y(15), y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(18)-98++, y(18)-196++, y(18)++, y(19)++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.757

RMSREPTLDSISELPEEDSR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 7399: 2454.109824 from(819.043884,3+)
Title: Elution from: 46.654 to 46.654 scan no 4502 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2454.1097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 0.00039

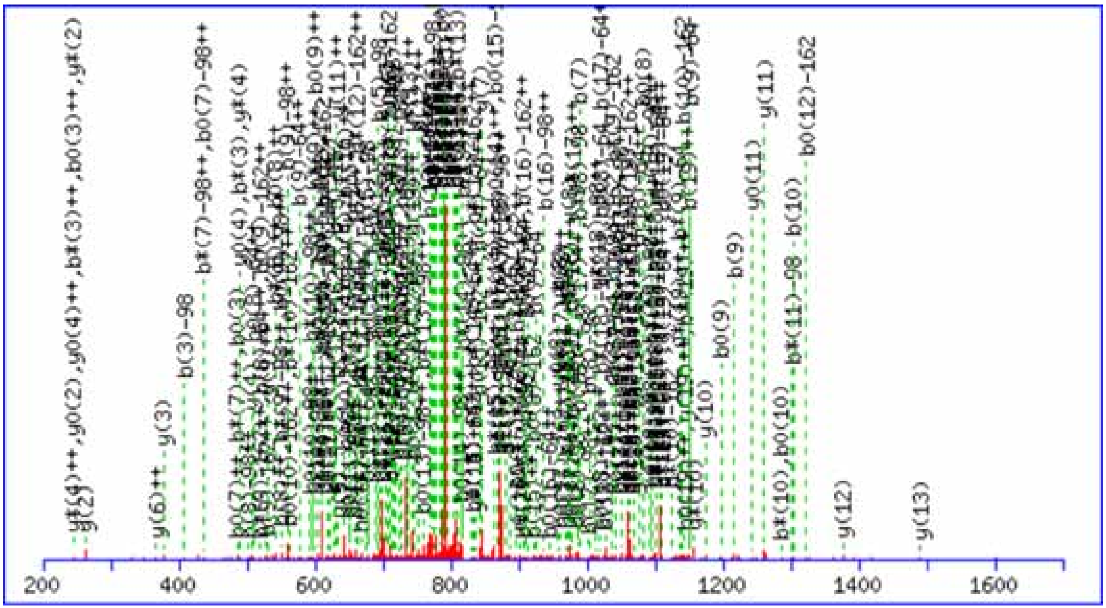
Matched b ions: b(5), b(6), b(7)-98, b(8)++, b(8)-98++, b(8), b(8)-98, b(9)-98++, b(9)++, b(9), b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(11), y(12), y(12)++, y(14)-98++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.758

RMSREPTLDSISELPEEDSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6664: 2476.138914 from(826.386914,3+)
Title: Elution from: 44.123 to 44.123 scan no 4032 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2476.1365
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0057

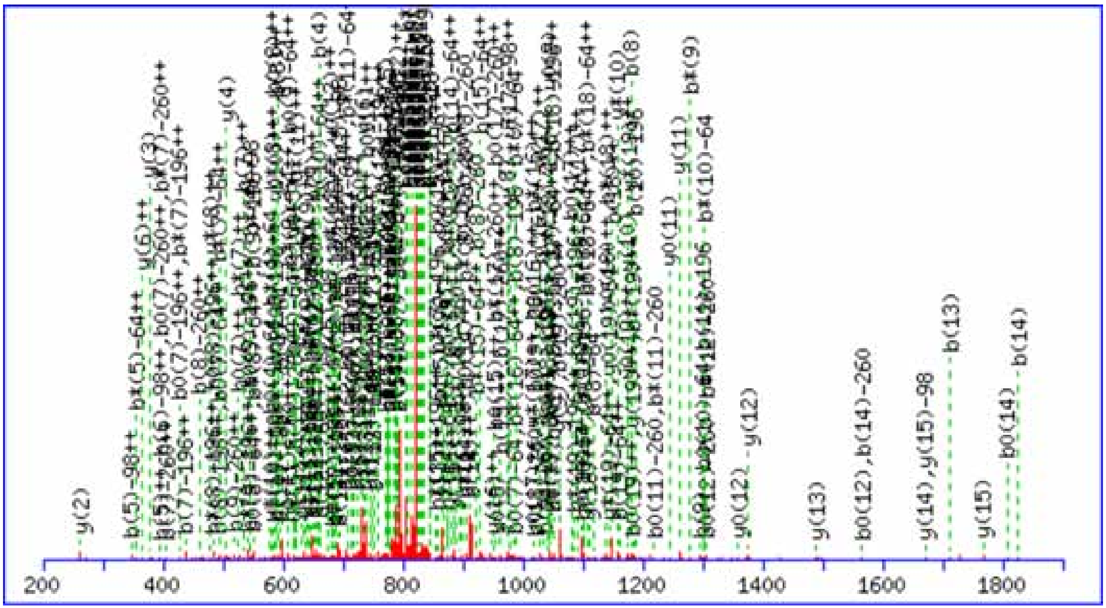
Matched b ions: b(3)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7), b(8)++, b(8)-98++, b(8)-98, b(8), b(9)++, b(9), b(9)-98++, b(10)-98++, b(10), b(10)++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(9)++, y(10), y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14)++, y(16)++, y(17)++, y(18)++, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.759

RMSREPTLDSISELPEEDSR
Confirmed sites: @S:3,@T:7
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6085: 2556.107496 from(853.043108,3+)
Title: Elution from: 46.410 to 46.410 scan no 4163 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2556.1028
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 0.00028

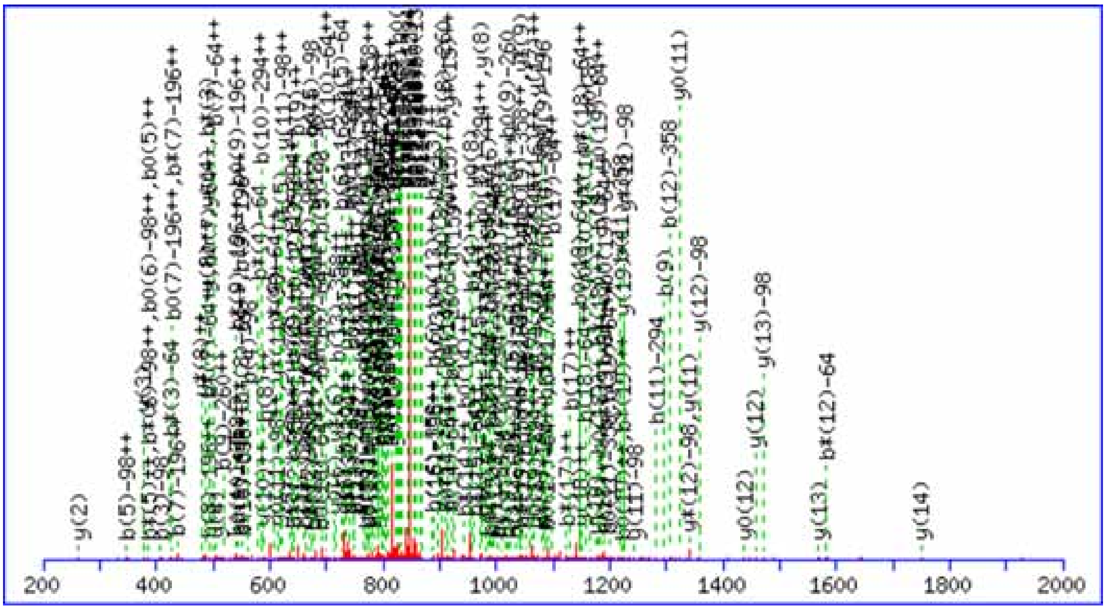
Matched b ions: b(4), b(5)-98++, b(5)++, b(5)-98, b(5), b(6)-98++, b(6)-98, b(7)-196++, b(7)-98++, b(7)++, b(7)-98, b(8)-98++, b(8), b(8)-196++, b(8)++, b(8)-196, b(9)++, b(9)-196++, b(9)-98++, b(9), b(9)-196, b(9)-98, b(10)-196, b(10)-196++, b(10)-98++, b(10)++, b(11)-196, b(11)-196++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(12)++, b(13), b(13)-196++, b(13)-98++, b(13)++, b(14)++, b(14)-98, b(14), b(14)-98++, b(14)-196++, b(15)-98++, b(15)-196++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(18)-196++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14), y(14)-98++, y(14)++, y(15)-98, y(15), y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.760

RMSREPTLDSISELPEEDSR
Confirmed sites: @S:3,@T:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 7089: 2636.070168 from(879.697332,3+)
Title: Elution from: 48.984 to 48.984 scan no 4632 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2636.0691
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.016

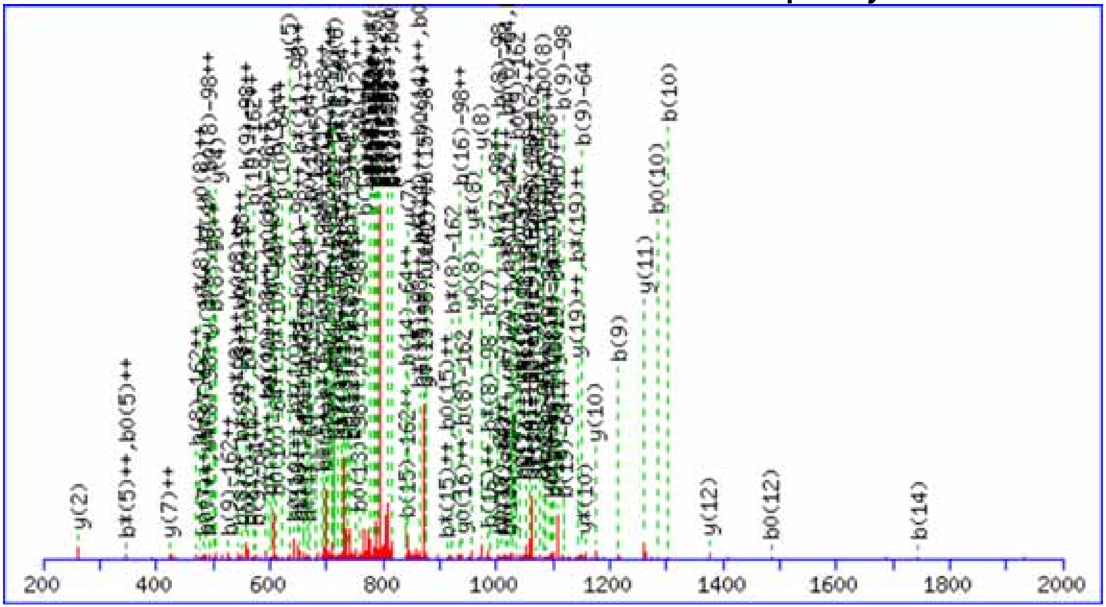
Matched b ions: b(3)-98, b(4), b(4)-98, b(5)-98++, b(5), b(5)-98, b(6)-98, b(6), b(7)-196++, b(7)-98++, b(7)-98, b(7), b(8)-98++, b(8)++, b(8)-196++, b(8)-196, b(8)-98, b(8), b(9)-98++, b(9)-196++, b(9)++, b(9)-98, b(9), b(10)++, b(10)-196++, b(10)-196, b(10)-98++, b(10)-294++, b(11)-98++, b(11)-196++, b(11)-294, b(11)-294++, b(12)-196++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(13)-294++, b(13)-196++, b(14)-98++, b(14)++, b(14)-196++, b(14)-294++, b(15)-196++, b(15)-98++, b(15)-294++, b(16)++, b(16)-98++, b(17)-98++, b(17)-294++, b(17)++, b(18)-98++, b(18)++, b(18)-196++, b(18)-294++, b(19)-294++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(10)++, y(11), y(11)-98++, y(11)++, y(11)-98, y(12), y(12)-98++, y(12)-98, y(13), y(13)-98, y(13)-98++, y(13)++, y(14), y(14)-98++, y(15)-98, y(15)++, y(15)-196++, y(16)++, y(16)-98++, y(16)-196++, y(17)-98++, y(17)++, y(18)-294++, y(18)++, y(19)-98++, y(19)-196++, y(19)++
Precursor origin neutral loss: +

Peptide No.761

RMSREPTLDSISELPEEDSR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 5857: 2476.138203 from(826.386677,3+)
Title: Elution from: 43.947 to 43.947 scan no 3883 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2476.1365
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.016

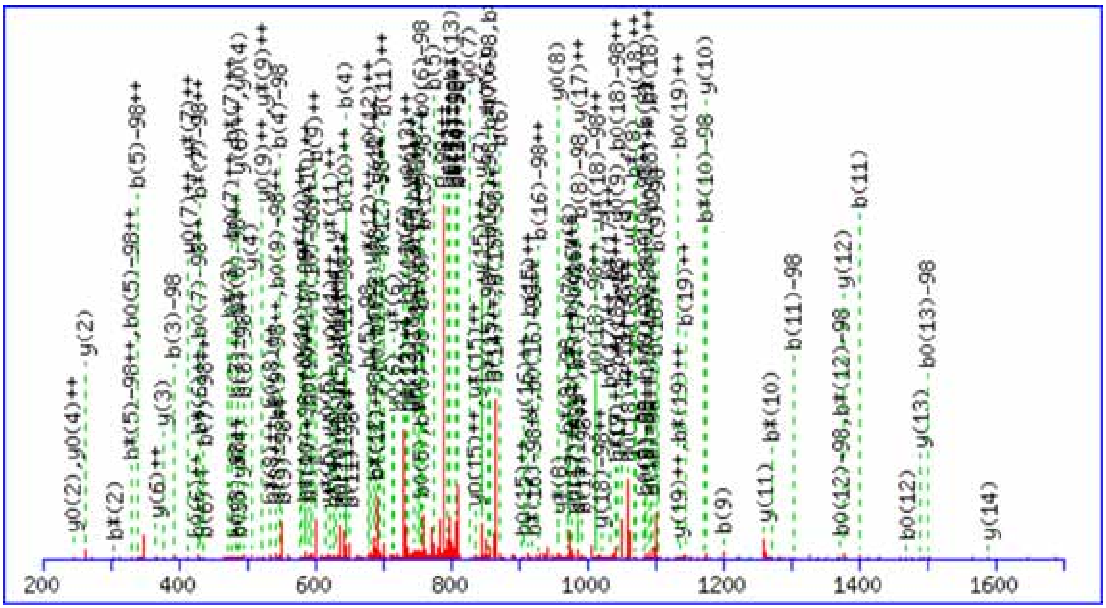
Matched b ions: b(5), b(6), b(7)++, b(7), b(8)++, b(8)-98++, b(8)-98, b(9)-98++, b(9)++, b(9), b(9)-98, b(10)++, b(10), b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14), b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(10), y(11), y(12), y(14)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.762

RMSREPTLDSISELPEEDSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6615: 2460.143556 from(821.055128,3+)
Title: Elution from: 46.659 to 46.659 scan no 4351 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2460.1415
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.0018

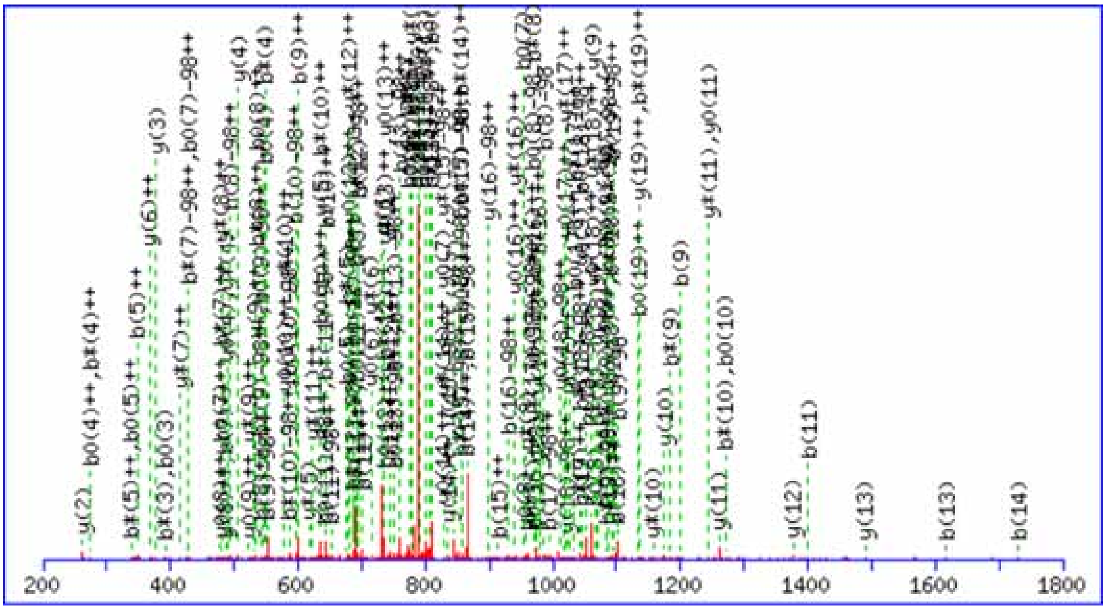
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98++, b(5)-98, b(5), b(6)++, b(6), b(7)-98++, b(7)++, b(7), b(8)++, b(8)-98++, b(8)-98, b(8), b(9)++, b(9), b(9)-98++, b(9)-98, b(10)-98++, b(10)++, b(11), b(11)-98, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14), y(14)++, y(15)++, y(16)++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.763

RMSREPTLDSISELPEEDSR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of RMSREPTLDSISELPEEDSR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6402: 2460.143274 from(821.055034,3+)
Title: Elution from: 46.600 to 46.600 scan no 4323 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2460.1415
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.0071

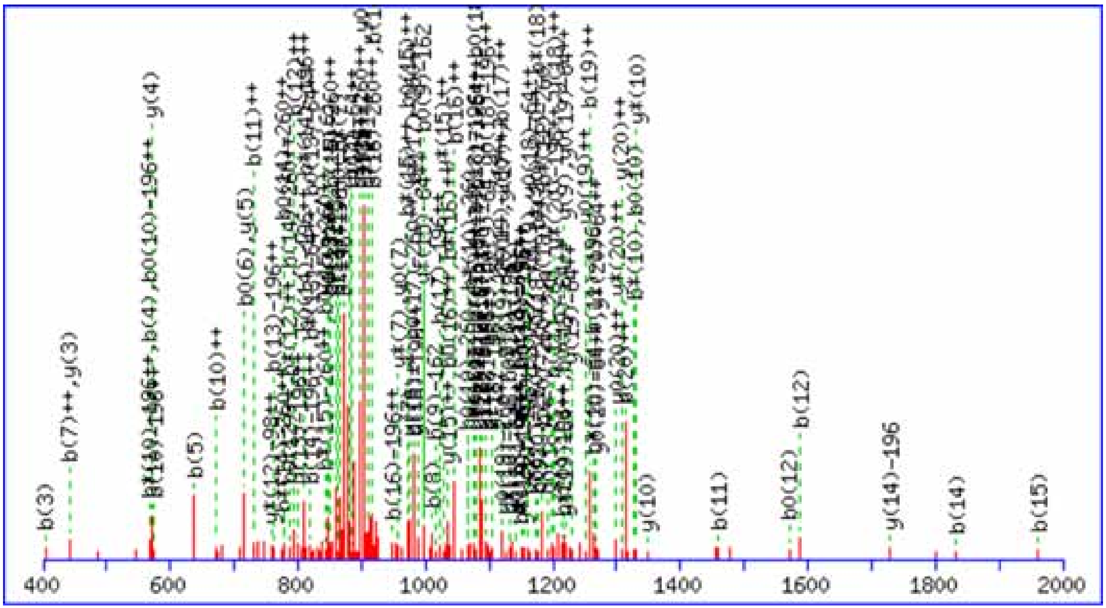
Matched b ions: b(5)++, b(5), b(6), b(7)++, b(7), b(8)-98++, b(8)-98, b(8), b(8)++, b(9)-98++, b(9)++, b(9), b(9)-98, b(10)++, b(10)-98++, b(11), b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(13), b(14)++, b(14), b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(11), y(12), y(12)++, y(13), y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.764

RPDYAPMESSDEEDEEFQFIK
Confirmed sites: @S:9,@S:10
Ambiguous sites:

MS/MS Fragmentation of RPDYAPMESSDEEDEEFQFIK
Found in MFAP1_MOUSE, Microfibrillar-associated protein 1 OS=Mus musculus GN=Mfap1 PE=1 SV=1

Match to Query 8641: 2805.145902 from(936.055910,3+)
Title: Elution from: 57.051 to 57.051 scan no 5716 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2805.1442
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 64 Expect: 2.3e-005

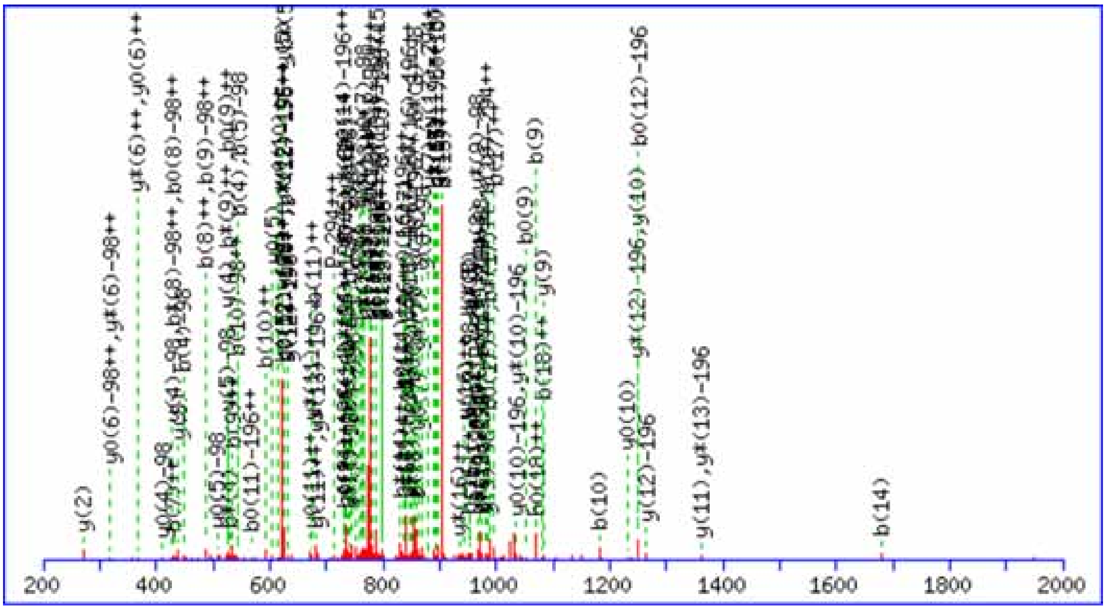
Matched b ions: b(3), b(4), b(5), b(7)++, b(7), b(8), b(9)-98, b(9), b(10)-196++, b(10)++, b(11)-98++, b(11), b(11)++, b(11)-196, b(12), b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14), b(14)++, b(14)-196++, b(14)-98++, b(15), b(15)++, b(16)++, b(16)-98++, b(16)-196++, b(17)++, b(17)-98++, b(17)-196++, b(18)-196++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(19)-196++, b(20)++, b(20)-98++, b(20)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(13)-196++, y(13)-98++, y(14)-196, y(14)-196++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)++, y(18)++, y(18)-98++, y(18)-196++, y(20)++
Precursor origin neutral loss: +

Peptide No.765

RPPSPDVIVLSDSEQPSSPR
Confirmed sites: @S:4,@S:11,@S:18
Ambiguous sites:

MS/MS Fragmentation of RPPSPDVIVLSDSEQPSSPR
Found in P66A_MOUSE, Transcriptional repressor p66 alpha OS=Mus musculus GN=Gatad2a PE=1 SV=2

Match to Query 7335: 2430.028980 from(811.016936,3+)
Title: Elution from: 47.968 to 47.968 scan no 4663 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2430.0270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.0015

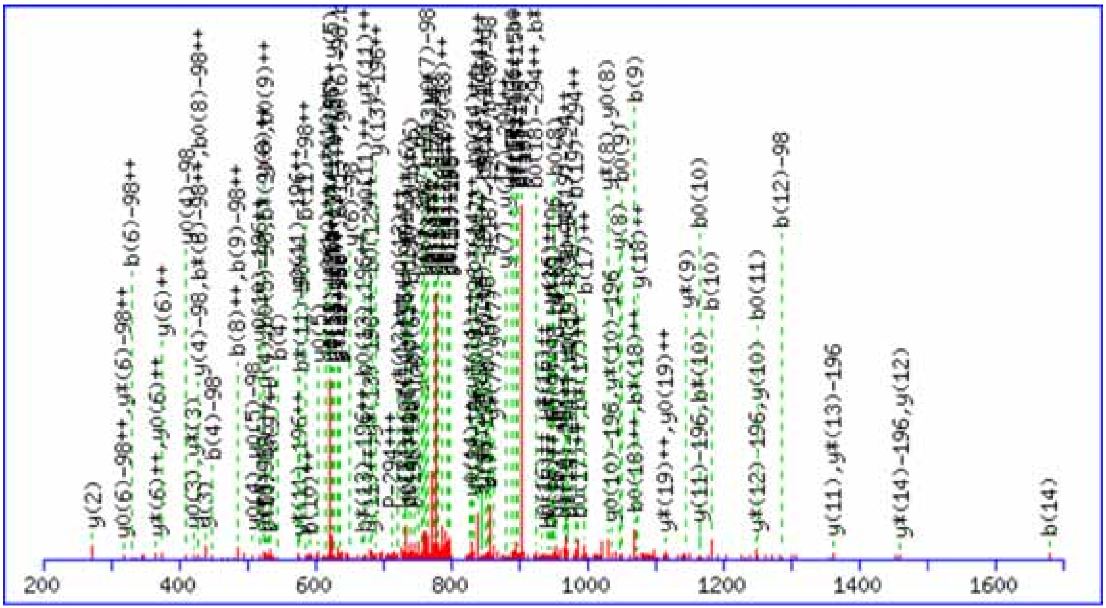
Matched b ions: b(4)-98, b(4), b(5)-98, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9)-98++, b(9), b(9)-98, b(10), b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14), b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)-196++, b(16)++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(18)-196++, b(19)-196++, b(19)-98++, b(19)-294++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5), y(5)-98, y(6), y(7)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(10)-98++, y(10)++, y(11), y(11)++, y(11)-98, y(11)-98++, y(12)-98, y(12)-98++, y(12)-196++, y(12)-196, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)-196++, y(14)++, y(15)-196++, y(15)++, y(16)-98++, y(16)++, y(17)-294++
Precursor origin neutral loss: +

Peptide No.766

RPPSPDVIVLSDSEQPSSPR
Confirmed sites: @S:4,@S:13,@S:18
Ambiguous sites:

MS/MS Fragmentation of RPPSPDVIVLSDSEQPSSPR
Found in P66A_MOUSE, Transcriptional repressor p66 alpha OS=Mus musculus GN=Gatad2a PE=1 SV=2

Match to Query 6335: 2430.028221 from(811.016683,3+)
Title: Elution from: 47.962 to 47.962 scan no 4486 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2430.0270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.006

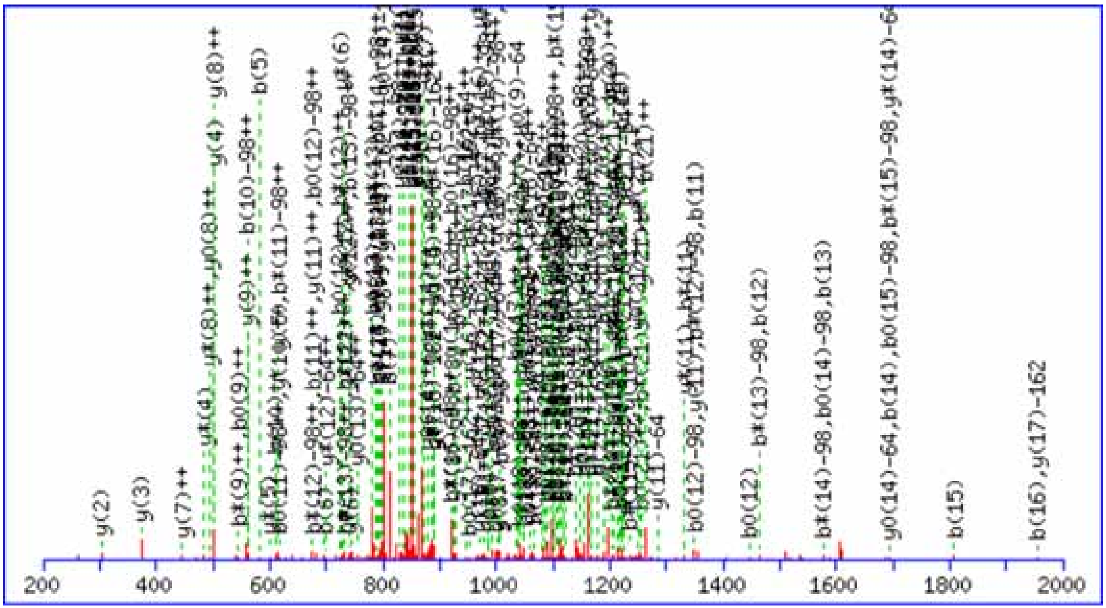
Matched b ions: b(4)-98, b(4), b(6)-98++, b(6), b(7)-98, b(7), b(8)++, b(8), b(9)-98++, b(9), b(9)++, b(9)-98, b(10), b(10)++, b(11)-98++, b(11)++, b(12)-98, b(13)-98, b(13)-98++, b(13)++, b(14), b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)-196++, b(16)++, b(17)++, b(17)-196++, b(18)-98++, b(18)-196++, b(19)-196++, b(19)-294++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5), y(5)-98, y(6)++, y(6), y(6)-98, y(7)-98, y(7), y(8)++, y(8)-196, y(8)-98, y(8), y(9)-98, y(10), y(10)-196++, y(10)-98++, y(10)++, y(10)-98, y(11), y(11)-98++, y(11)-98, y(11)++, y(11)-196, y(12), y(12)-196++, y(12)-98++, y(12)++, y(13)++, y(13)-196++, y(13)-98++, y(14)-98++, y(14)-196++, y(15)++, y(15)-196++, y(15)-98++, y(16)-196++, y(16)-98++, y(16)++, y(17)-294++, y(17)-196++, y(18)++
Precursor origin neutral loss: +

Peptide No.767

RPSPDDDLTDEDNDDMQLQAQR
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of RPSPDDDLTDEDNDDMQLQAQR
Found in NEDD4_MOUSE, E3 ubiquitin-protein ligase NEDD4 OS=Mus musculus GN=Nedd4 PE=1 SV=3

Match to Query 8131: 2697.086730 from(900.036186,3+)
Title: Elution from: 35.035 to 35.035 scan no 2994 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2697.0861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 46 Expect: 0.0012

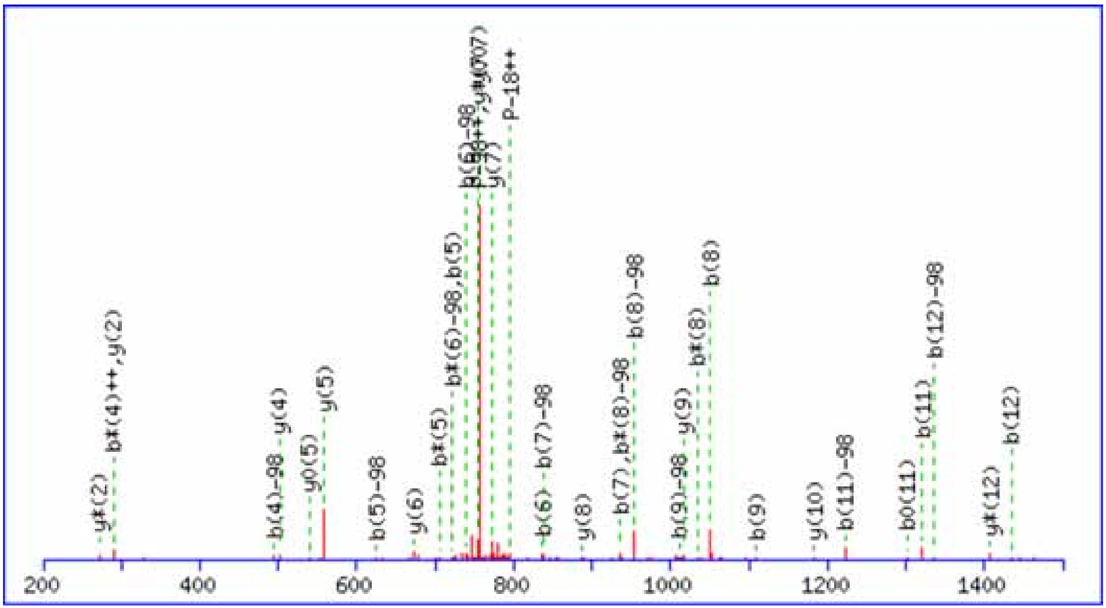
Matched b ions: b(5), b(6), b(7), b(8), b(9)-98, b(9), b(10)++, b(10), b(10)-98++, b(10)-98, b(11)++, b(11), b(12)++, b(12), b(13), b(13)-98++, b(13)++, b(14), b(14)-98++, b(14)++, b(15), b(15)-98++, b(16), b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(14)++, y(14)-98++, y(16)++, y(16)-98++, y(18)-98++, y(18)++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.768

RQISEDVDGPDNR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RQISEDVDGPDNR
Found in NEDD4_MOUSE, E3 ubiquitin-protein ligase NEDD4 OS=Mus musculus GN=Nedd4 PE=1 SV=3

Match to Query 3161: 1607.694484 from(804.854518,2+)
Title: Elution from: 25.324 to 25.324 scan no 1675 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1607.6941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.0024

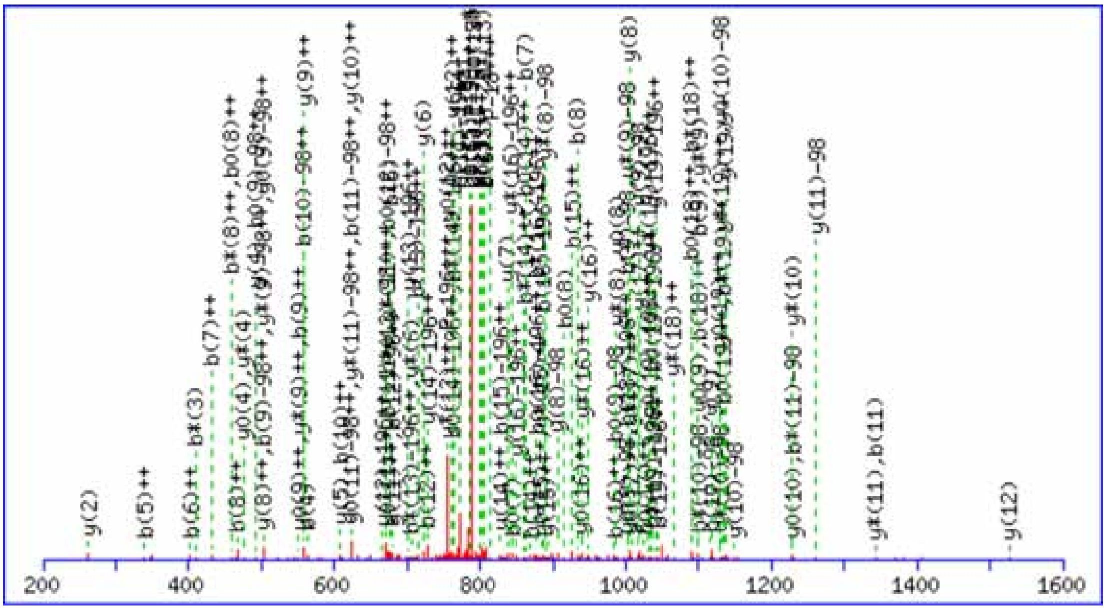
Matched b ions: b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(11)-98, b(11), b(12)-98, b(12)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10)
Precursor origin neutral loss: +

Peptide No.769

RQLHIEGASLELSDDDTESK
Confirmed sites: @S:9,@S:13
Ambiguous sites:

MS/MS Fragmentation of RQLHIEGASLELSDDDTESK
Found in MYH10_MOUSE, Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2

Match to Query 7407: 2458.067979 from(820.363269,3+)
Title: Elution from: 45.831 to 45.831 scan no 4403 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2458.0665
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl (K)
Ions Score: 48 **Expect:** 0.0011

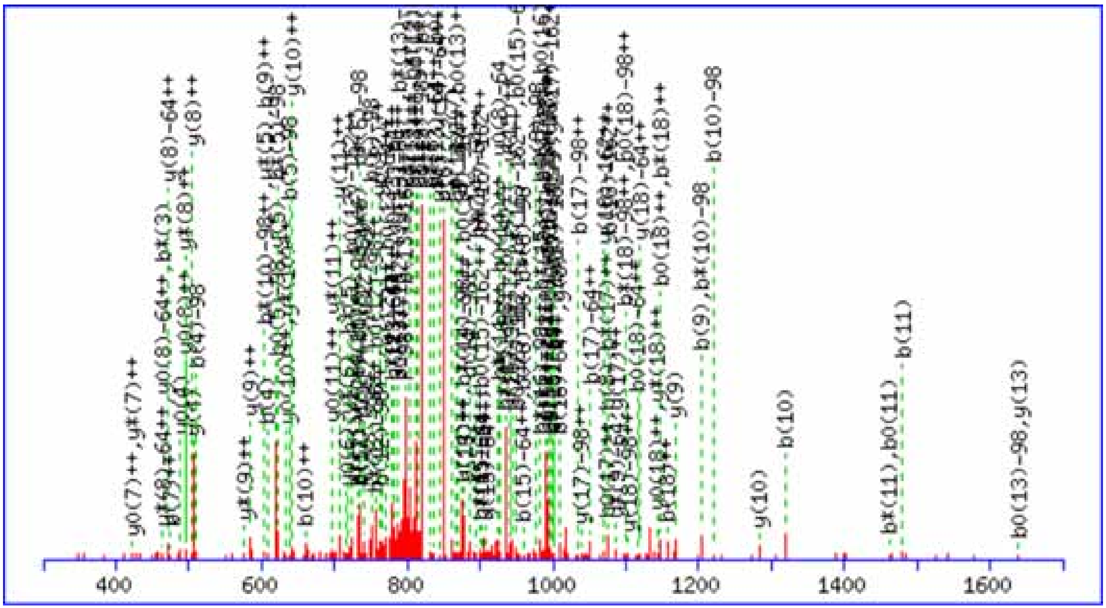
Matched b ions: b(4), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)-98++, b(9), b(9)++, b(9)-98, b(10)-98++, b(10)++, b(10)-98, b(11)-98++, b(11), b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)-196++, b(14)-196++, b(14)++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++, b(17)-98++, b(18)-98++, b(18)++, b(18)-196++, b(19)-196++, b(19)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)++, y(8)-98, y(8), y(9), y(9)-98, y(9)++, y(10)++, y(10)-98, y(11)-98, y(11)++, y(12), y(12)-196++, y(12)-98++, y(12)++, y(13)-196++, y(13)++, y(14)-196++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)-196++, y(16)++, y(17)++, y(18)-98++, y(19)++, y(19)-196++
Precursor origin neutral loss: +

Peptide No.770

RQSQQLPEEDCMQLNPSFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RQSQQLPEEDCMQLNPSFK
Found in PPAC3_MOUSE, Probable lipid phosphate phosphatase PPAPDC3 OS=Mus musculus GN=Ppapdc3 PE=1 SV=1

Match to Query 7499: 2486.099229 from(829.707019,3+)
Title: Elution from: 40.785 to 40.785 scan no 3771 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2486.0971
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K19 : Dimethyl (K)
Ions Score: 38 **Expect:** 0.012

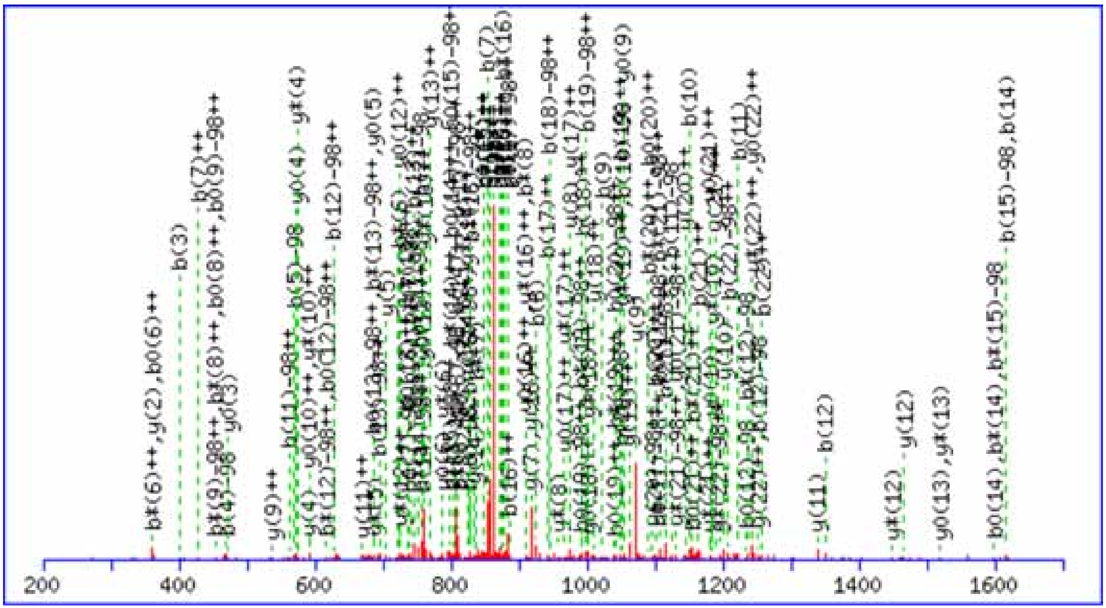
Matched b ions: b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7)++, b(8), b(8)-98, b(9), b(9)++, b(10), b(10)++, b(10)-98, b(11), b(11)++, b(12)-98++, b(12)++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(17)-98++, b(18)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(13), y(14)++, y(15)++, y(17)++, y(17)-98++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.771

RQSSTADAPEAQHEPGITITEWK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RQSSTADAPEAQHEPGITITEWK
Found in KPBB_MOUSE, Phosphorylase b kinase regulatory subunit beta OS=Mus musculus GN=Phkb PE=1 SV=1

Match to Query 8124: 2687.259183 from(896.760337,3+)
Title: Elution from: 43.460 to 43.460 scan no 4112 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2687.2592
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K23 : Dimethyl (K)
Ions Score: 34 **Expect:** 0.035

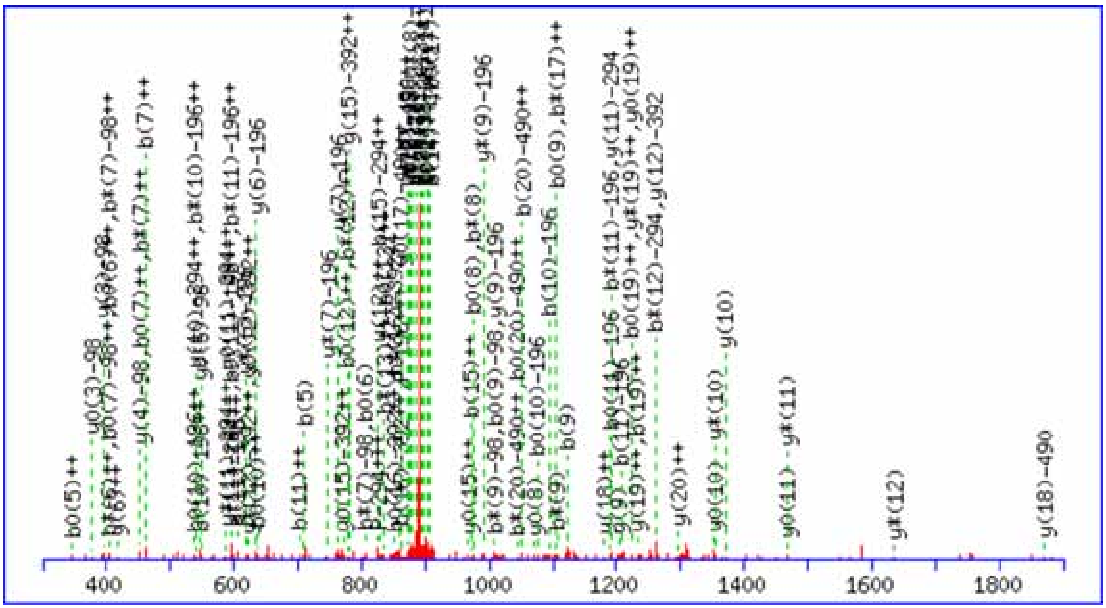
Matched b ions: b(3), b(4)-98, b(5)-98, b(6), b(7)-98, b(7), b(7)++, b(8), b(8)-98, b(9), b(10), b(10)-98, b(11)-98++, b(11), b(11)-98, b(12), b(12)-98++, b(12)-98, b(13)++, b(13)-98++, b(14)-98++, b(14), b(14)++, b(15)-98, b(15)-98++, b(15)++, b(16)++, b(17)++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(22)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(11), y(11)++, y(12), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(22)++
Precursor origin neutral loss: +

Peptide No.772

RQTESNPAMSNSDEESNGTMK
Confirmed sites: @S:5,@S:10,@S:12,@S:16,@T:19
Ambiguous sites:

MS/MS Fragmentation of RQTESNPAMSNSDEESNGTMK
Found in ATRX_MOUSE, Transcriptional regulator ATRX OS=Mus musculus GN=Atrx PE=1 SV=2

Match to Query 7128: 2773.896882 from(925.639570,3+)
Title: Elution from: 28.102 to 28.102 scan no 1860 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2773.8905
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 21 Expect: 0.046

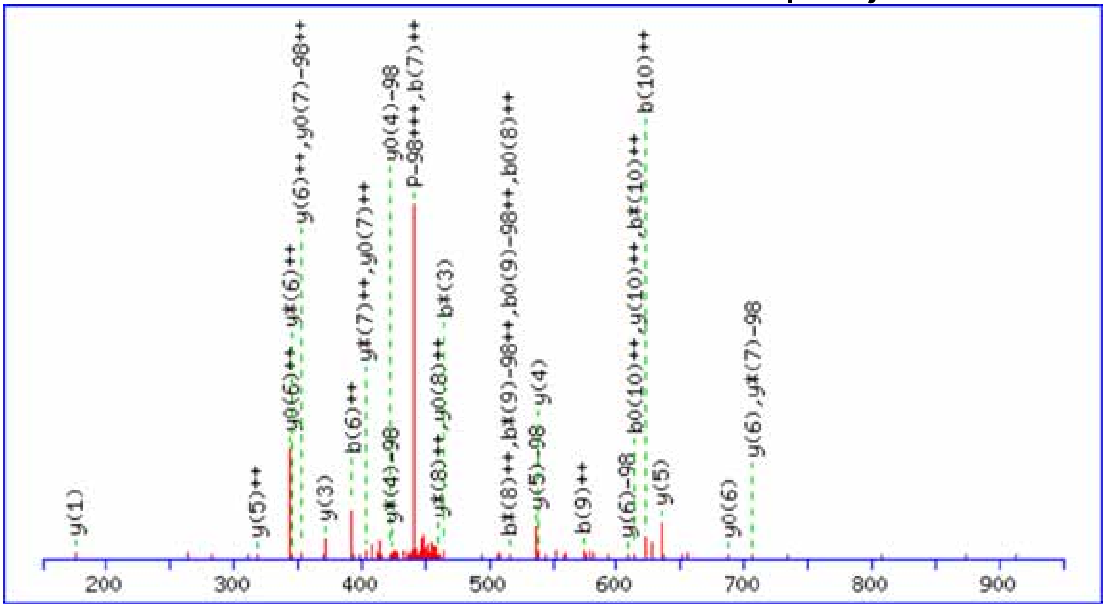
Matched b ions: b(5), b(7)++, b(8)-98, b(9), b(10)-98++, b(10)-196++, b(10)-98, b(10)-196, b(11)-98++, b(11)-196, b(11)-196++, b(11)++, b(11)-98, b(13)-196++, b(14)-98++, b(14)++, b(15)-294++, b(15)-196++, b(15)++, b(16)-98++, b(16)-392++, b(16)-294++, b(17)-294++, b(18)-196++, b(18)-98++, b(19)-196++, b(19)++, b(20)-490++, b(20)-392++, b(20)-294++, b(20)-98++
Matched y ions: y(3)-98, y(4)-98, y(6)-196, y(6)++, y(7)-196, y(7)-98, y(8)-196, y(8)-98, y(9)-196, y(9)-98, y(9), y(10), y(10)-294++, y(11)-294++, y(11)-294, y(11)-196++, y(12)++, y(12)-392, y(12)-98++, y(13)++, y(13)-294++, y(13)-98++, y(14)-98, y(14)-294++, y(15)-196, y(15)-196++, y(15)-392++, y(16)-294++, y(17)-196++, y(17)-490++, y(18)-490, y(18)++, y(19)-196++, y(19)++, y(20)-98++, y(20)++
Precursor origin neutral loss: +

Peptide No.773

RQYDDAPSVPR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of RQYDDAPSVPR
Found in K1462_MOUSE, Uncharacterized protein KIAA1462 OS=Mus musculus GN=Kiaa1462 PE=1 SV=2

Match to Query 2853: 1416.660930 from(473.227586,3+)
Title: Elution from: 22.387 to 22.387 scan no 1212 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1416.6611
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.026

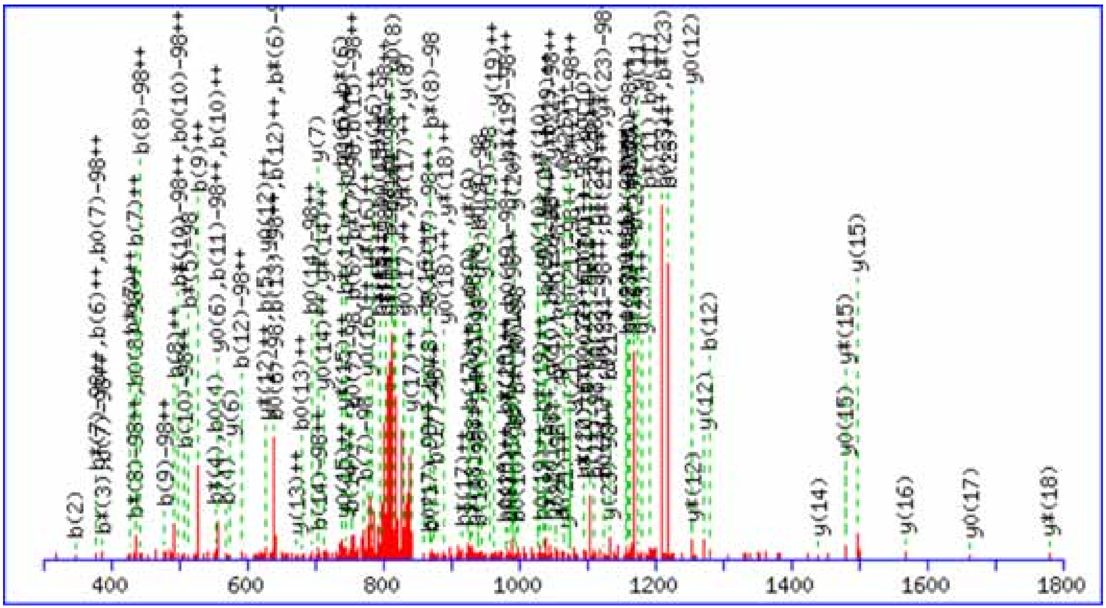
Matched b ions: b(6)++, b(7)++, b(9)++, b(10)++
Matched y ions: y(1), y(3), y(4), y(5)-98, y(5), y(5)++, y(6), y(6)++, y(6)-98, y(10)++
Precursor origin neutral loss: +

Peptide No.774

RRGSGQDLAGPAPETLEQTEGATP
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RRGSGQDLAGPAPETLEQTEGATP
Found in PDE7B_MOUSE, cAMP-specific 3',5'-cyclic phosphodiesterase 7B OS=Mus musculus GN=Pde7b PE=2 SV=1

Match to Query 6694: 2551.215723 from(851.412517,3+)
Title: Elution from: 40.707 to 40.707 scan no 3573 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2551.2128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 73 Expect: 4.4e-006

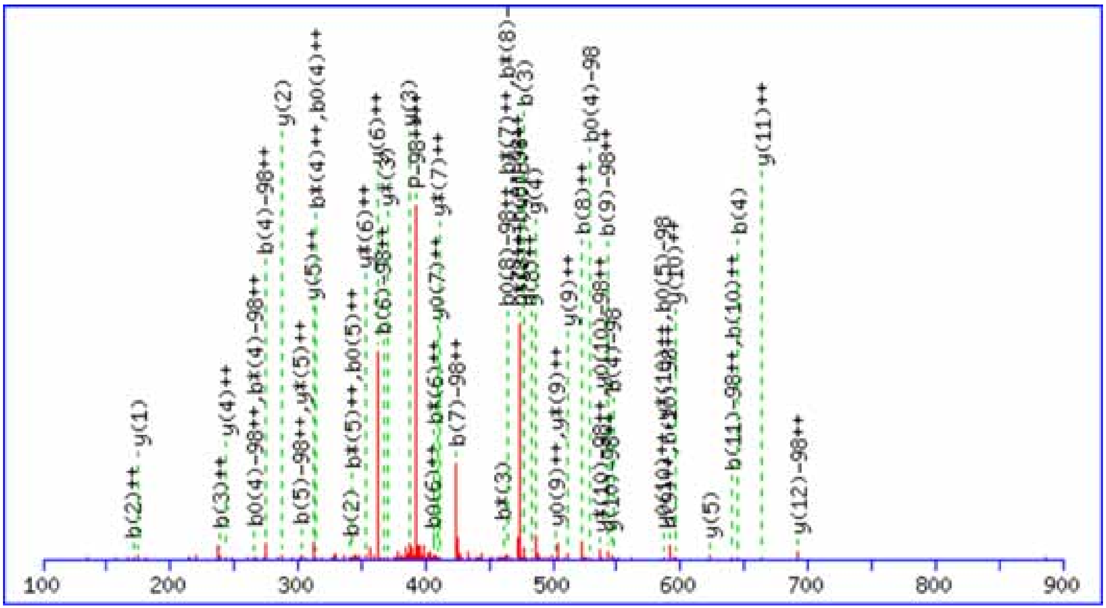
Matched b ions: b(2), b(4), b(5), b(6)++, b(6), b(7)-98++, b(7)++, b(7)-98, b(7), b(8)++, b(8), b(8)-98++, b(9)++, b(9)-98++, b(9), b(9)-98, b(10)++, b(10)-98++, b(11), b(11)-98++, b(11)-98, b(12)++, b(12), b(12)-98++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(22)++, b(23)++, b(23)-98++
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)++, y(14), y(15), y(16), y(16)++, y(17)++, y(19)++, y(20)++, y(21)++, y(22)-98++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.775

RRHSGQDVHVVLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RRHSGQDVHVVLK
Found in NSF1C_MOUSE, NSFL1 cofactor p47 OS=Mus musculus GN=Nsfl1c PE=1 SV=1

Match to Query 2609: 1665.883324 from(417.478107,4+)
Title: Elution from: 22.661 to 22.661 scan no 1207 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1665.8828
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
Ions Score: 49 **Expect:** 0.00061

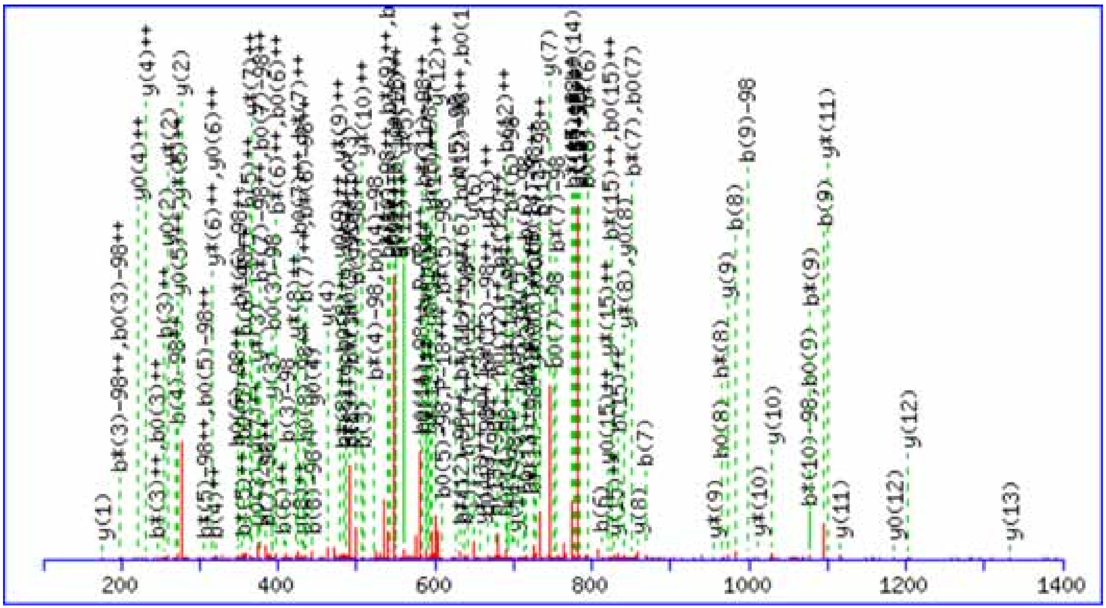
Matched b ions: b(2)++, b(2), b(3)++, b(3), b(4)-98++, b(4), b(4)-98, b(5)-98++, b(6)-98++, b(7)++, b(7)-98++, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)-98++, b(10)++, b(11)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5)++, y(5), y(6)++, y(8)++, y(9)++, y(10)-98++, y(10)++, y(11)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.776

RRSESSGNLPSVADTR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RRSESSGNLPSVADTR
Found in AKAP1_MOUSE, A-kinase anchor protein 1, mitochondrial OS=Mus musculus GN=Akap1 PE=1 SV=3

Match to Query 4591: 1838.864043 from(613.961957,3+)
Title: Elution from: 26.972 to 26.972 scan no 1890 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1838.8636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.0015

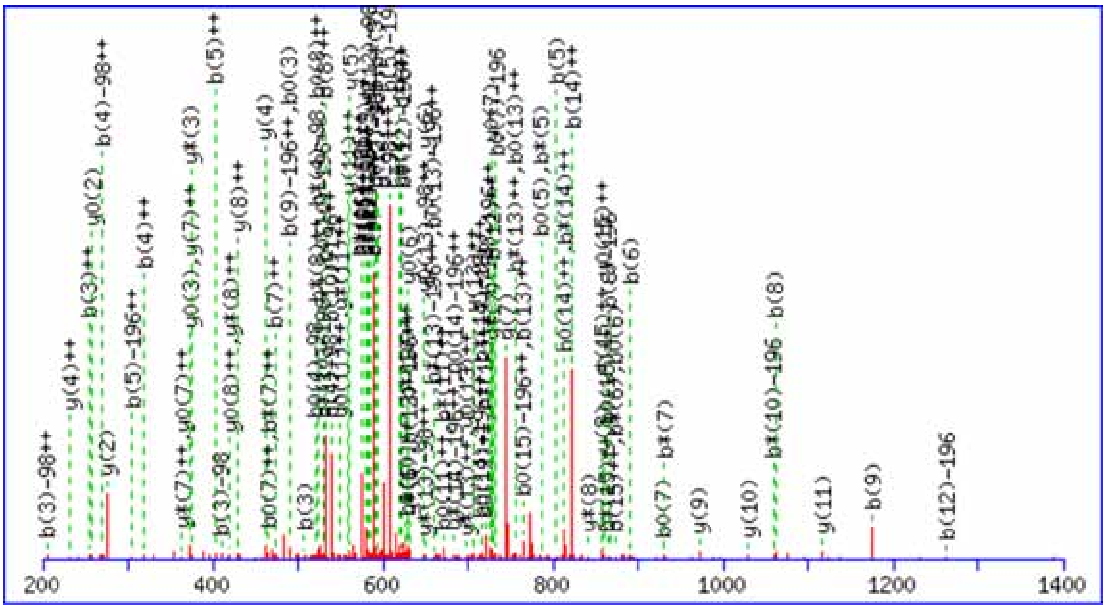
Matched b ions: b(3)++, b(3)-98, b(3), b(4)-98, b(4)++, b(4)-98++, b(4), b(5)++, b(5)-98, b(5), b(6)-98++, b(6)++, b(6)-98, b(6), b(7)-98++, b(7), b(7)++, b(8), b(8)++, b(8)-98++, b(9)++, b(9), b(9)-98++, b(9)-98, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(11), y(11)++, y(12)++, y(12), y(13), y(13)++, y(14)-98++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.777

RRSESSGNLPSVADTR
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of RRSESSGNLPSVADTR
Found in AKAP1_MOUSE, A-kinase anchor protein 1, mitochondrial OS=Mus musculus GN=Akap1 PE=1 SV=3

Match to Query 5183: 1918.830471 from(640.617433,3+)
Title: Elution from: 29.869 to 29.869 scan no 2287 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1918.8299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.016

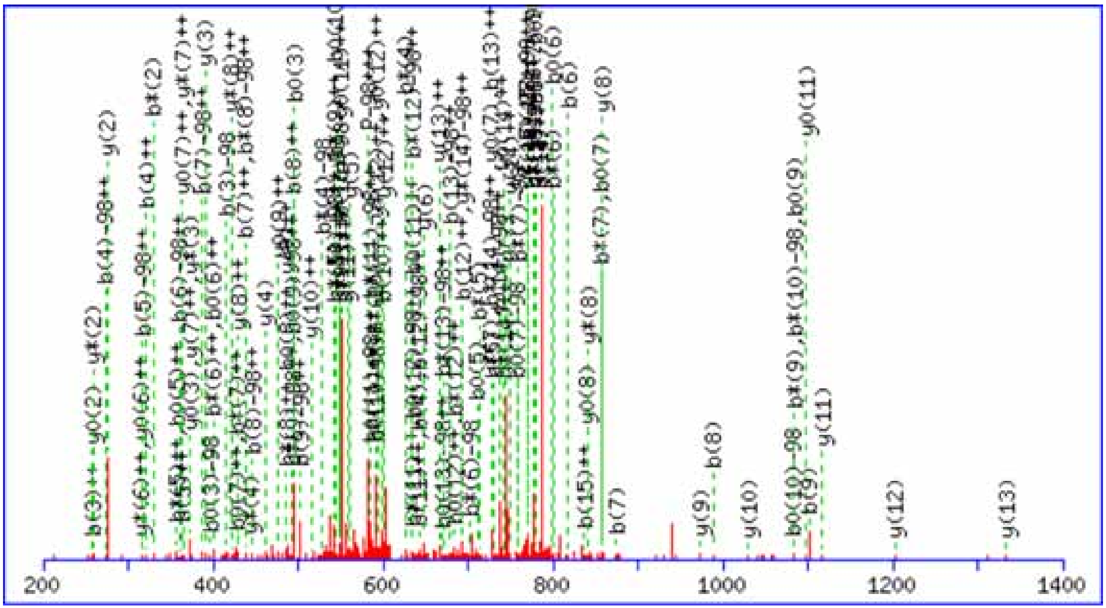
Matched b ions: b(3)-98++, b(3)-98, b(3)++, b(3), b(4)-98, b(4)-98++, b(4)++, b(5)-196, b(5)-98++, b(5)++, b(5)-196++, b(5)-98, b(5), b(6)-98++, b(6), b(6)-98, b(7)++, b(8)-98++, b(8), b(8)++, b(8)-98, b(8)-196, b(9)++, b(9), b(9)-98, b(9)-196++, b(9)-98++, b(10)-98++, b(10)-196++, b(11)-98++, b(11)-196++, b(12)-196, b(12)-196++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(14)-196++, b(15)-98++, b(15)++
Matched y ions: y(2), y(4), y(4)++, y(5), y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(10), y(11), y(11)++, y(12)-98++, y(13)++, y(14)-98++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.778

RRSESSGNLPSVADTR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RRSESSGNLPSVADTR
Found in AKAP1_MOUSE, A-kinase anchor protein 1, mitochondrial OS=Mus musculus GN=Akap1 PE=1 SV=3

Match to Query 3298: 1844.897061 from(615.972963,3+)
Title: Elution from: 26.730 to 26.730 scan no 1626 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1844.8954
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.0016

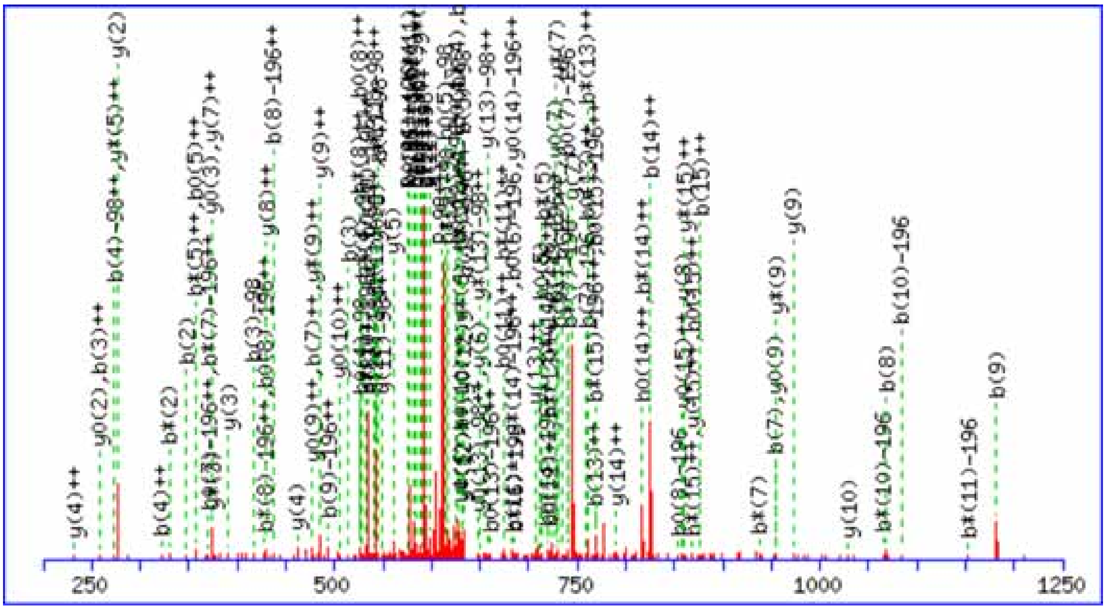
Matched b ions: b(3)++, b(3)-98, b(4)-98++, b(4), b(4)++, b(4)-98, b(5)-98++, b(5)++, b(5), b(6)-98++, b(6), b(7)-98, b(7)-98++, b(7), b(7)++, b(8)++, b(8), b(8)-98++, b(9)++, b(9), b(9)-98++, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.779

RRSESSGNLPSVADTR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of RRSESSGNLPSVADTR
Found in AKAP1_MOUSE, A-kinase anchor protein 1, mitochondrial OS=Mus musculus GN=Akap1 PE=1 SV=3

Match to Query 4782: 1924.861767 from(642.627865,3+)
Title: Elution from: 29.832 to 29.832 scan no 2121 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1924.8617
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.031

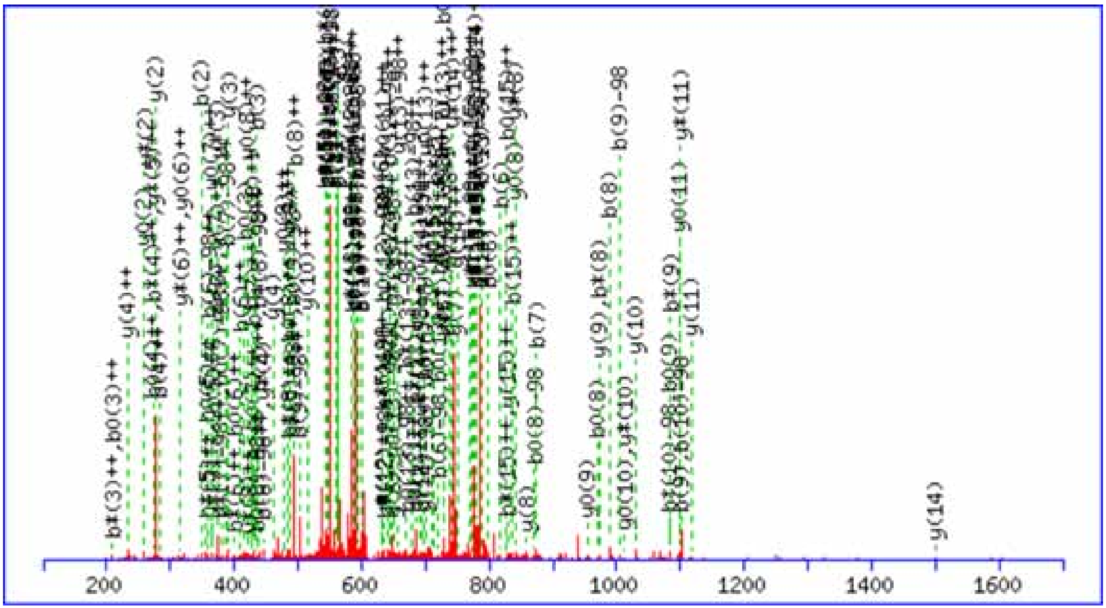
Matched b ions: b(2), b(3)++, b(3)-98, b(3), b(4)-98++, b(4)++, b(4)-98, b(5), b(5)-98, b(6)-98++, b(6)-98, b(7), b(7)++, b(7)-98++, b(7)-196, b(8)-98++, b(8), b(8)++, b(8)-196++, b(9)++, b(9), b(9)-196++, b(9)-98, b(9)-98++, b(10)-98++, b(10)-98, b(10)-196, b(10)-196++, b(11)++, b(11)-98++, b(11)-196++, b(12)-98++, b(12)-196++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(14)-196++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(11)-98++, y(11)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.780

RRSESSGNLPSVADTR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of RRSESSGNLPSVADTR
Found in AKAP1_MOUSE, A-kinase anchor protein 1, mitochondrial OS=Mus musculus GN=Akap1 PE=1 SV=3

Match to Query 4044: 1844.895594 from(615.972474,3+)
Title: Elution from: 26.958 to 26.958 scan no 1740 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1844.8954
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 0.00014

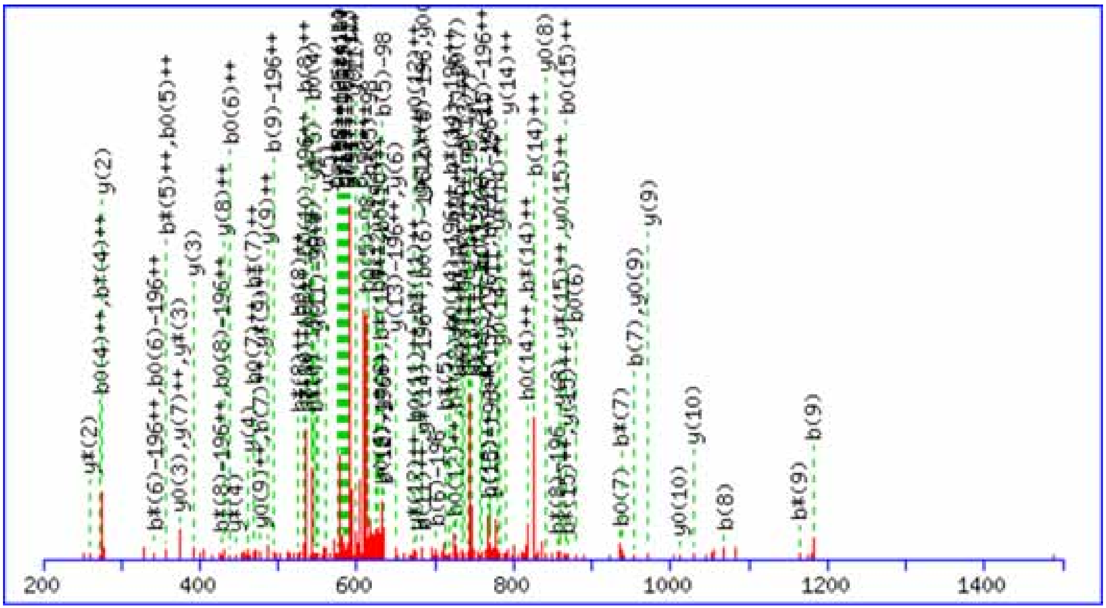
Matched b ions: b(2), b(3), b(4)++, b(4), b(5)++, b(5)-98, b(5), b(6), b(6)-98++, b(6)++, b(6)-98, b(7), b(7)-98, b(7)-98++, b(7)++, b(8)++, b(8), b(8)-98++, b(9)++, b(9), b(9)-98, b(9)-98++, b(10)-98++, b(10)-98, b(10)++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(14), y(14)-98++, y(14)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.781

RRSESSGNLPSVADTR
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of RRSESSGNLPSVADTR
Found in AKAP1_MOUSE, A-kinase anchor protein 1, mitochondrial OS=Mus musculus GN=Akap1 PE=1 SV=3

Match to Query 4403: 1924.863618 from(642.628482,3+)
Title: Elution from: 29.654 to 29.654 scan no 2063 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1924.8617
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.028

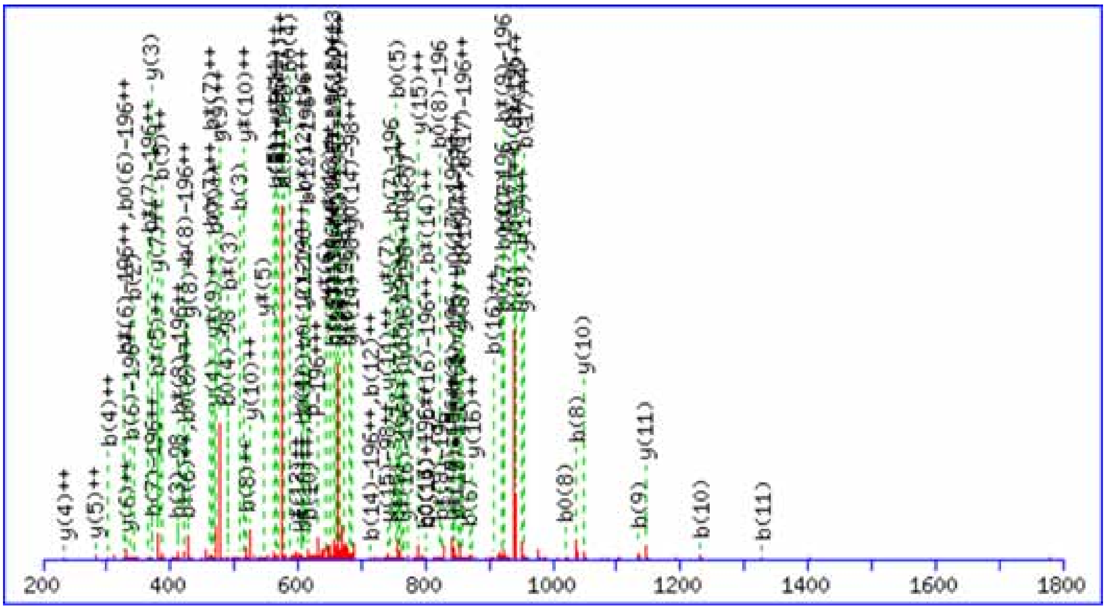
Matched b ions: b(5)-98, b(6)-98++, b(6)-196, b(6)-98, b(7), b(7)-98, b(7)-98++, b(7)++, b(7)-196, b(8)++, b(8), b(8)-98++, b(9)++, b(9), b(9)-98++, b(9)-98, b(9)-196++, b(10)-98++, b(10)-196++, b(10)-98, b(11)++, b(11)-196++, b(11)-98++, b(12)-98++, b(12)-196++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(14)-196++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(11)-98++, y(11)++, y(12)-196++, y(12)-98++, y(12)++, y(13)++, y(13)-196++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-196++
Precursor origin neutral loss: +

Peptide No.782

RRSPSPAPPPPPPPPPPR
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of RRSPSPAPPPPPPPPPPR
Found in SRRM1_MOUSE, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=1

Match to Query 6083: 2084.013492 from(695.678440,3+)
Title: Elution from: 28.033 to 28.033 scan no 2034 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2084.0122
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 **Expect:** 6.9e-006

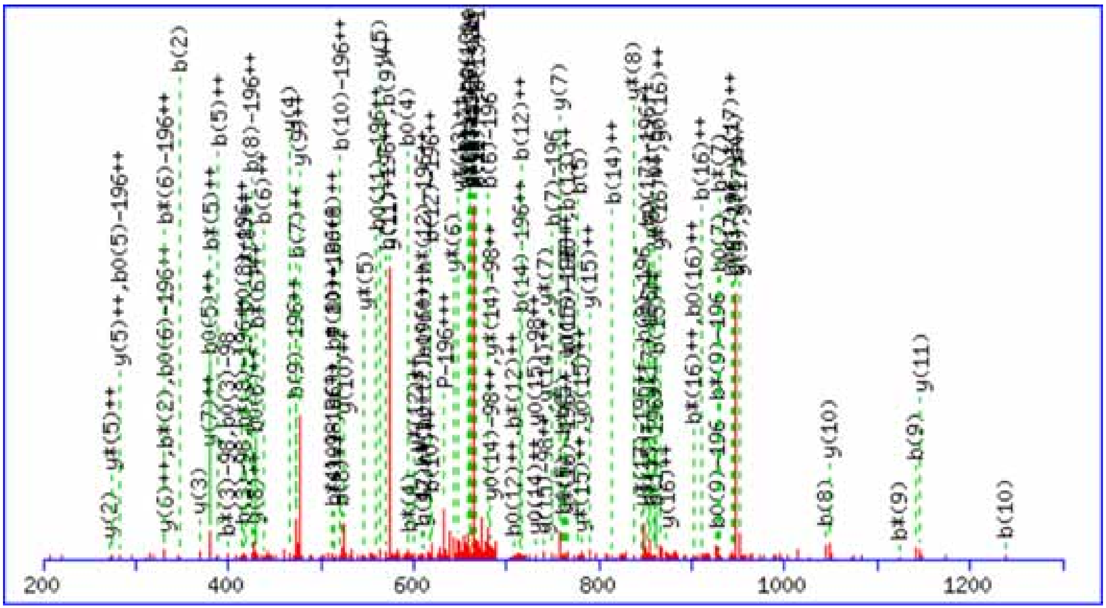
Matched b ions: b(2), b(3)-98, b(3), b(4)++, b(4), b(5)++, b(5)-98, b(5), b(5)-98++, b(5)-196, b(6)-98++, b(6)-98, b(6)-196++, b(6)-196, b(6), b(7)-98, b(7), b(7)++, b(7)-98++, b(7)-196++, b(7)-196, b(8), b(8)-98++, b(8)-196++, b(8)++, b(8)-98, b(8)-196, b(9), b(9)-98++, b(9)-196, b(9)++, b(10)++, b(10), b(10)-98++, b(11), b(11)-98++, b(11)-196++, b(11)++, b(12)-98, b(12)-196++, b(12)-98++, b(12)++, b(13)-196++, b(13)-98++, b(13)++, b(14)-196++, b(14)-98++, b(15)-196++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-196++, b(17)-98++
Matched y ions: y(3), y(4)++, y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(11), y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.783

RRSPSPAPPPPPPPPPPR
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of RRSPSPAPPPPPPPPPPR
Found in SRRM1_MOUSE, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=1

Match to Query 5617: 2090.045427 from(697.689085,3+)
Title: Elution from: 27.865 to 27.865 scan no 1862 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2090.0440
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 **Expect:** 0.00011

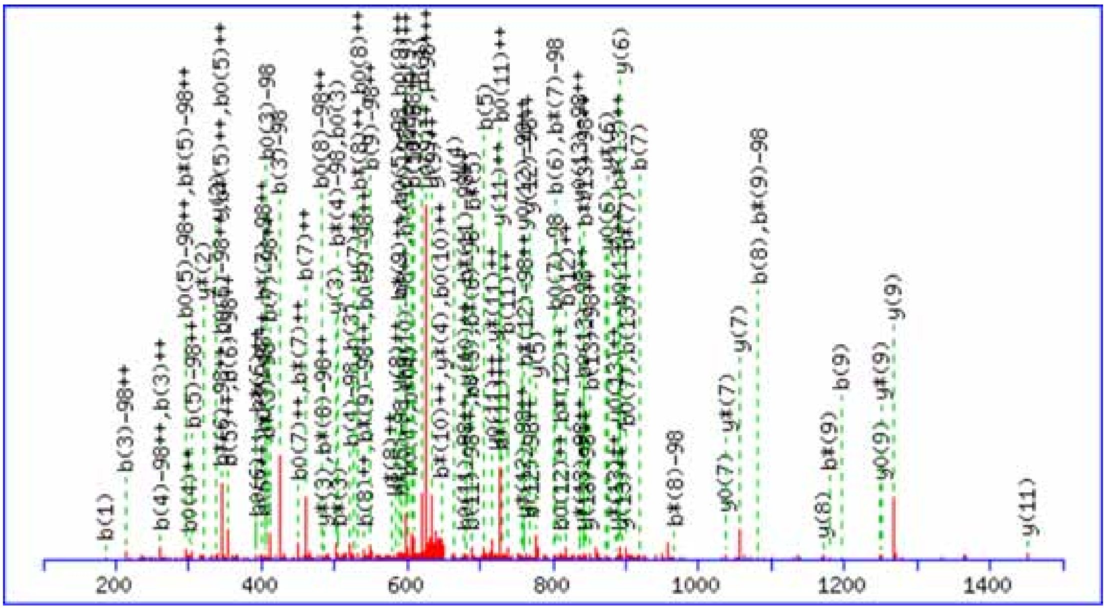
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5)++, b(5), b(6)-196, b(6)-98++, b(6)++, b(6)-98, b(7)-98, b(7), b(7)++, b(7)-98++, b(7)-196, b(8)-98++, b(8), b(8)++, b(8)-196++, b(8)-196, b(8)-98, b(9), b(9)-98++, b(9)-196++, b(9)++, b(9)-196, b(10), b(10)-196++, b(10)-98++, b(10)++, b(11)-196++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(12)++, b(13)-98++, b(13)-196++, b(13)++, b(14)-196++, b(14)-98++, b(14)++, b(15)-196++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)-196++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9)++, y(9), y(10), y(10)++, y(11)++, y(11), y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-196++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.784

RRTPSPDYDLYYYR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of RRTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4687: 1971.889203 from(658.303677,3+)
Title: Elution from: 40.317 to 40.317 scan no 3497 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1971.8880
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.026

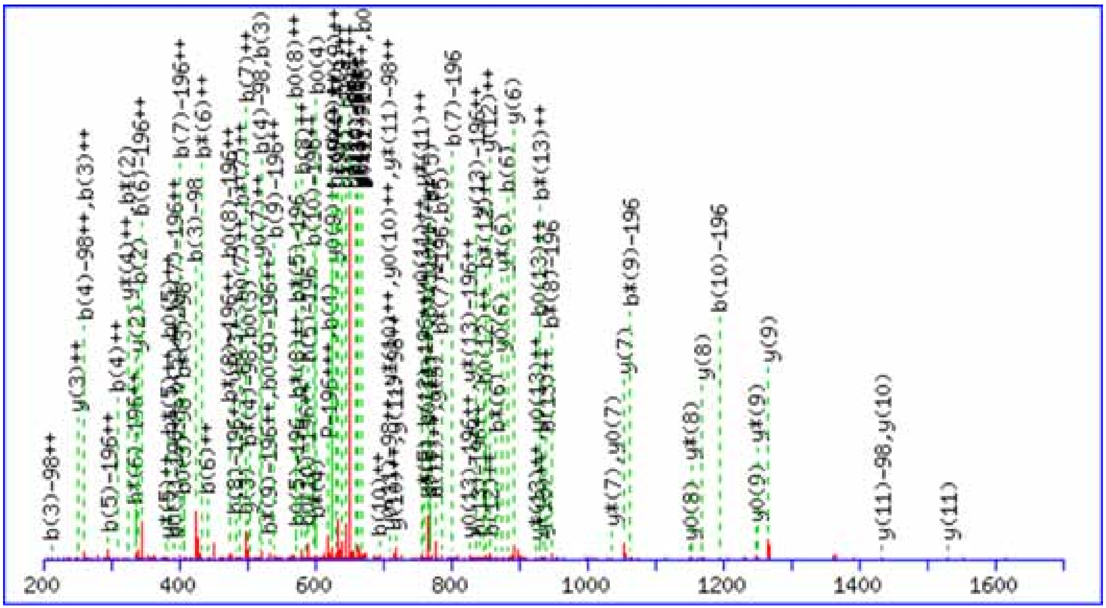
Matched b ions: b(1), b(3)++, b(3)-98, b(3), b(3)-98++, b(4)-98++, b(4)-98, b(4), b(5)++, b(5)-98++, b(5), b(5)-98, b(6)-98++, b(6)++, b(6), b(7)++, b(7)-98++, b(7), b(8)++, b(8), b(9)-98++, b(9)++, b(9), b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(11)++, y(11), y(12)-98++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.785

RRTPSPDYDLYYYR
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of RRTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 5376: 2051.855277 from(684.959035,3+)
Title: Elution from: 44.048 to 44.048 scan no 4022 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2051.8543
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 Expect: 0.0046

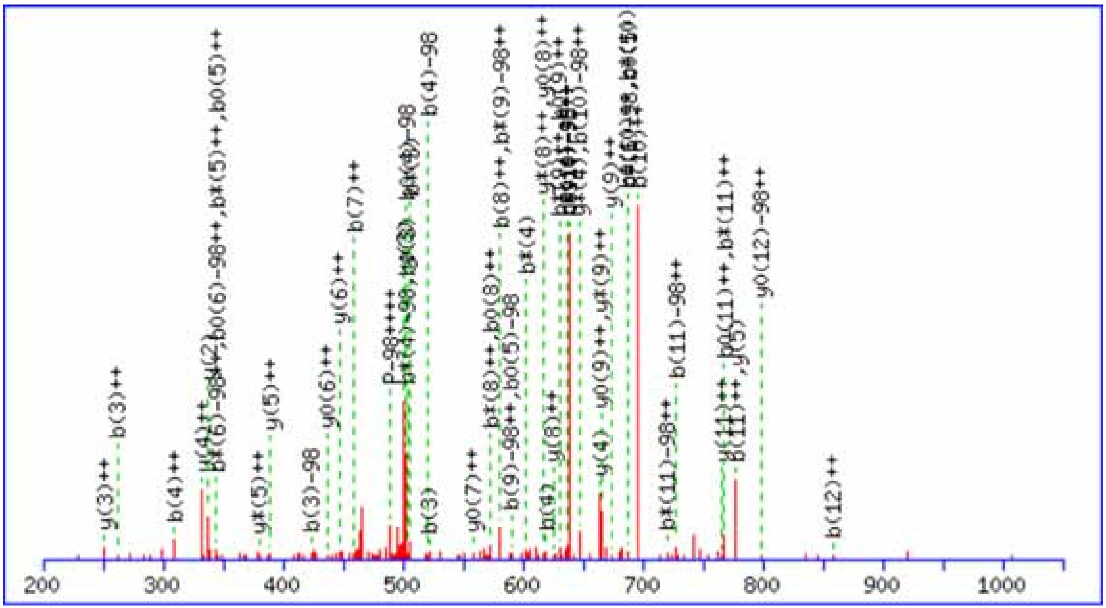
Matched b ions: b(2), b(3)-98, b(3)++, b(3)-98++, b(3), b(4)-98++, b(4)-98, b(4), b(4)++, b(5)-196++, b(5)-98++, b(5)-196, b(5)++, b(5)-98, b(5), b(6)-196++, b(6)-98++, b(6)++, b(6)-98, b(6), b(7)++, b(7)-98, b(7)-98++, b(7)-196++, b(7)-196, b(8)++, b(8)-98++, b(8)-98, b(8)-196++, b(9)-98++, b(9)++, b(9)-196++, b(10)-98++, b(10)-196, b(10)-196++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(12)-196++, b(13)++, b(13)-98++, b(13)-196++
Matched y ions: y(2), y(3), y(3)++, y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(10)-98++, y(11)++, y(11)-98, y(11), y(11)-98++, y(12)-98, y(12)++, y(13)++, y(13)-196++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.786

RRTPSPDYDLYYYR
Confirmed sites: @T:3,@Y:8
Ambiguous sites:

MS/MS Fragmentation of RRTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4978: 2051.855968 from(513.971268,4+)
Title: Elution from: 43.675 to 43.675 scan no 3921 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2051.8543
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y8 : Phospho (Y)
Ions Score: 29 Expect: 0.052

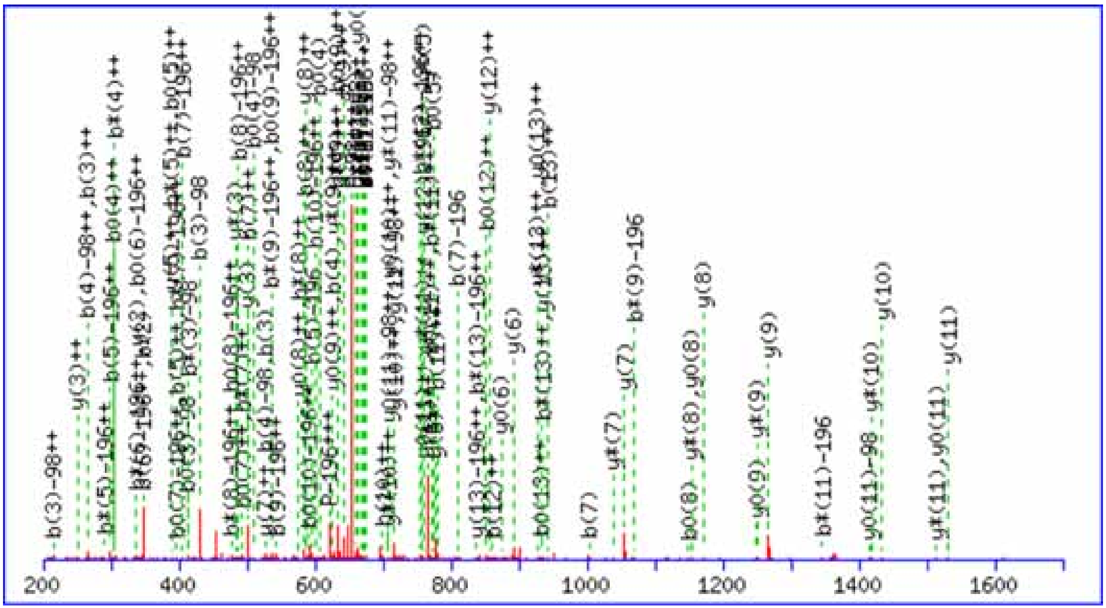
Matched b ions: b(3)++, b(3)-98, b(3), b(4)++, b(4), b(4)-98, b(7)++, b(8)++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++
Matched y ions: y(2), y(3), y(3)++, y(4)++, y(4), y(5), y(5)++, y(6)++, y(8)++, y(9)++, y(11)++
Precursor origin neutral loss:

Peptide No.787

RRTPSPDYDLYYYR
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of RRTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 5239: 2057.887440 from(686.969756,3+)
Title: Elution from: 43.692 to 43.692 scan no 3957 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2057.8861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.014

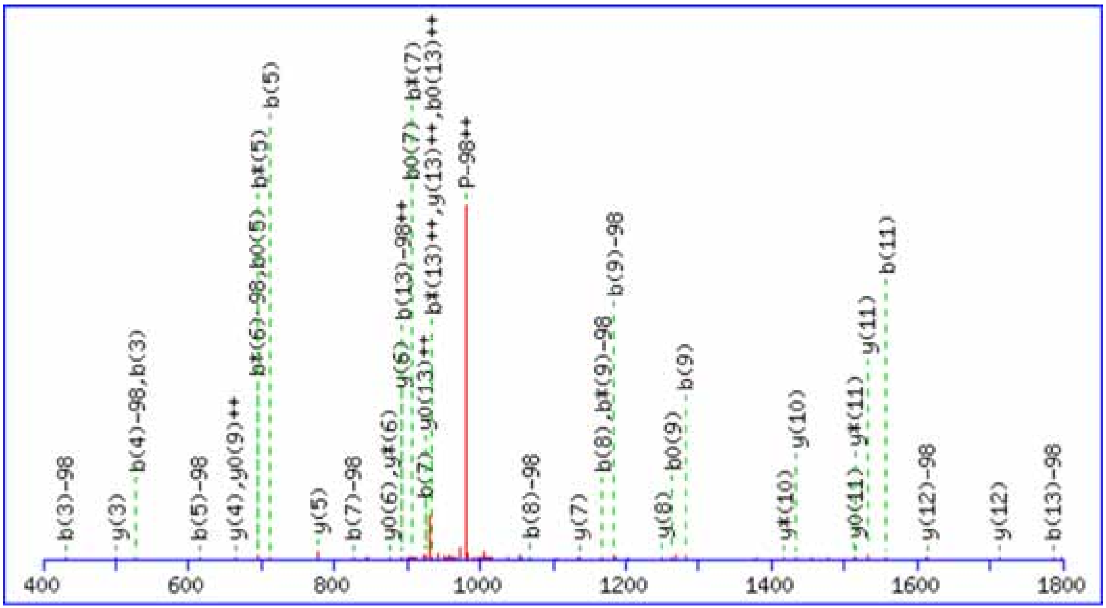
Matched b ions: b(2), b(3)-98, b(3)++, b(3), b(3)-98++, b(4)-98++, b(4)-98, b(4), b(5)-196++, b(5)-98++, b(5)-196, b(5)++, b(5)-98, b(6)-196++, b(6)-98++, b(7)++, b(7)-98++, b(7), b(7)-196++, b(7)-196, b(8)++, b(8)-98++, b(8)-98, b(8)-196++, b(9)-98++, b(9)-196++, b(9)++, b(10)-98++, b(10)-196++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(3)++, y(4), y(5), y(5)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(10)-98++, y(11)++, y(11), y(11)-98++, y(12)-98, y(12)-196++, y(12)-98++, y(12)++, y(13)++, y(13)-196++
Precursor origin neutral loss: +

Peptide No.788

RRTPSPDYDLYYYR
Confirmed sites: @T:3,@Y:8
Ambiguous sites:

MS/MS Fragmentation of RRTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 5454: 2057.886952 from(1029.950752,2+)
Title: Elution from: 43.419 to 43.419 scan no 3954 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2057.8861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y8 : Phospho (Y)
Ions Score: 33 Expect: 0.024

Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(11), b(13)-98, b(13)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(12), y(12)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.789

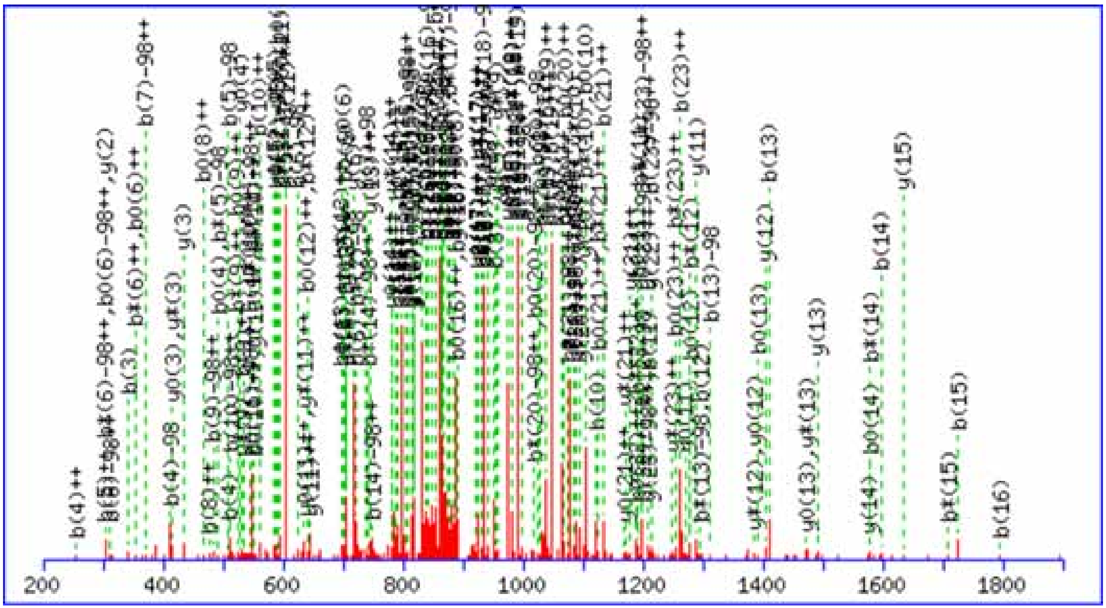
RSASPDDDLGSSNWEAADLGNEER

Confirmed sites: @S:4

Ambiguous sites:

MS/MS Fragmentation of RSASPDDDLGSSNWEAADLGNEER
Found in SMAP_MOUSE, Small acidic protein OS=Mus musculus GN=Smap PE=1 SV=1

Match to Query 8134: 2698.117233 from(900.379687,3+)
Title: Elution from: 47.270 to 47.270 scan no 4578 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2698.1144
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 97 Expect: 1.3e-008

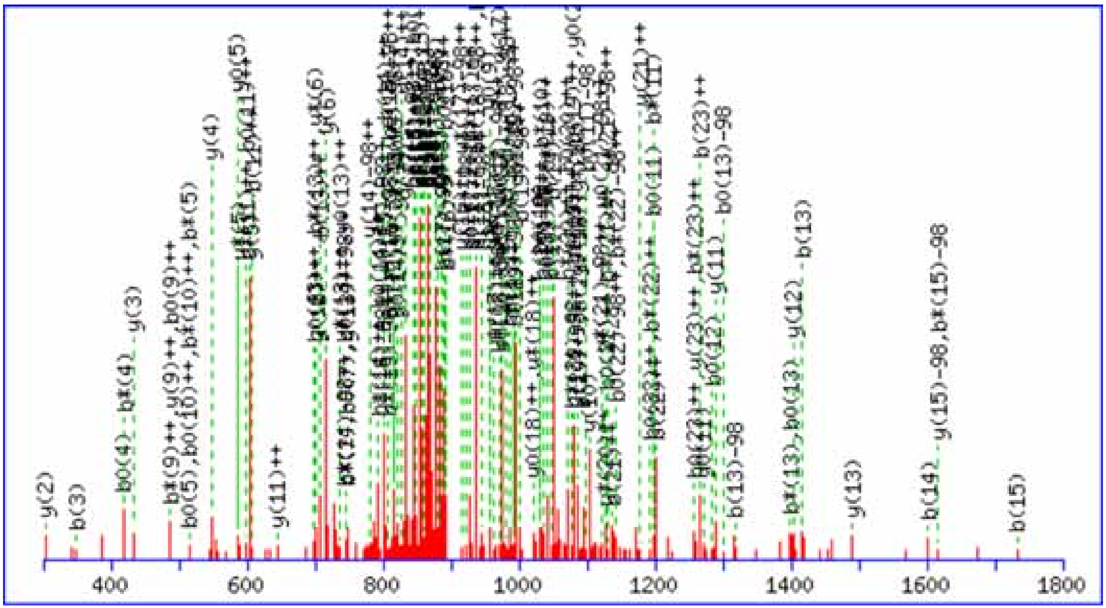
Matched b ions: b(3), b(4)-98, b(4), b(4)++, b(5)++, b(5)-98, b(6), b(6)-98++, b(6)-98, b(7)-98++, b(7), b(7)-98, b(8)-98, b(8), b(8)++, b(9), b(9)-98++, b(9)++, b(10)++, b(10), b(10)-98++, b(10)-98, b(11)++, b(11), b(12)-98, b(12), b(13), b(13)++, b(13)-98, b(14)++, b(14), b(14)-98++, b(15)++, b(15), b(15)-98++, b(16), b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(23)++, b(23)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(10)++, y(11)++, y(11), y(12), y(12)++, y(13)++, y(13), y(14), y(14)++, y(15)++, y(15), y(16)++, y(17)++, y(20)++, y(21)++, y(22)++, y(23)-98++
Precursor origin neutral loss:

Peptide No.790

RSASPDDDLGSSNWEAADLGNEER
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of RSASPDDDLGSSNWEAADLGNEER
Found in SMAP_MOUSE, Small acidic protein OS=Mus musculus GN=Smap PE=1 SV=1

Match to Query 7094: 2704.147917 from(902.389915,3+)
Title: Elution from: 47.199 to 47.199 scan no 4363 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2704.1462
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 Expect: 5.4e-006

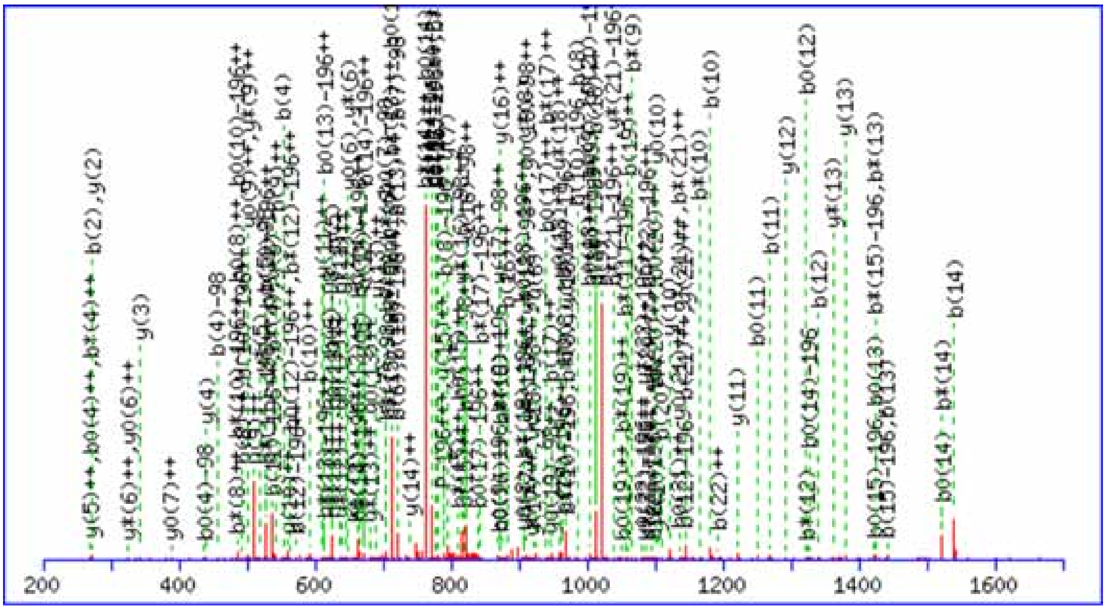
Matched b ions: b(3), b(8), b(10), b(11)++, b(13), b(13)++, b(13)-98, b(14), b(14)++, b(15)++, b(15), b(15)-98++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(23)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9)++, y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14)-98++, y(14)++, y(15)-98, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(21)-98++, y(21)++, y(23)++
Precursor origin neutral loss: +

Peptide No.791

RSDSAPPSPVSATVPEEEPPAPR
Confirmed sites: @S:4,@S:8
Ambiguous sites:

MS/MS Fragmentation of RSDSAPPSPVSATVPEEEPPAPR
Found in JPH2_MOUSE, Junctophilin-2 OS=Mus musculus GN=Jph2 PE=1 SV=2

Match to Query 8253: 2560.126374 from(854.382734,3+)
Title: Elution from: 39.111 to 39.111 scan no 3513 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2560.1247
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 **Expect:** 0.00023

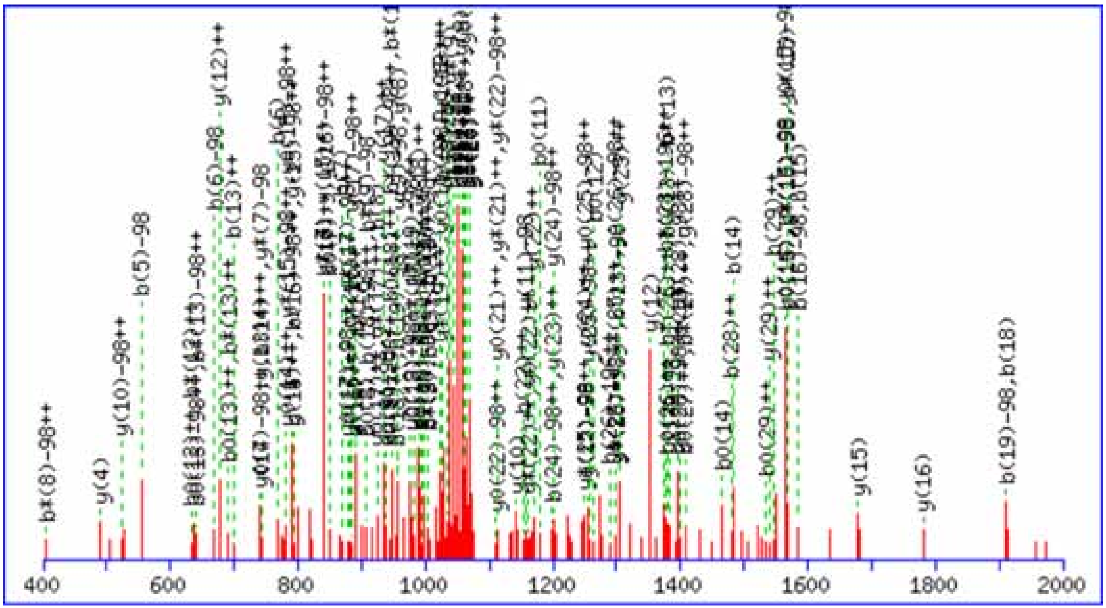
Matched b ions: b(2), b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(8)++, b(8)-196, b(8), b(9)++, b(9)-98++, b(9)-98, b(10), b(10)++, b(10)-98++, b(10)-196++, b(10)-196, b(10)-98, b(11), b(11)-196++, b(11)++, b(12), b(12)-98, b(12)++, b(12)-196++, b(12)-98++, b(12)-196, b(13)++, b(13), b(13)-98++, b(14)++, b(14), b(14)-98, b(14)-98++, b(14)-196++, b(15)-98++, b(15)-98, b(15)-196++, b(15)-196, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)-98++, b(19)-196++, b(19)++, b(20)++, b(20)-196++, b(20)-98++, b(21)++, b(21)-98++, b(22)-98++, b(22)-196++, b(22)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7), y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12)++, y(12), y(13), y(13)++, y(14)++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++
Precursor origin neutral loss:

Peptide No.792

RSNSVDTGPSSSLSTPTEPLSPTSSLGEER
Confirmed sites: @S:2,@S:25
Ambiguous sites:

MS/MS Fragmentation of RSNSVDTGPSSSLSTPTEPLSPTSSLGEER
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 8707: 3262.430268 from(1088.484032,3+)
Title: Elution from: 47.510 to 47.510 scan no 4607 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3262.4279
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S25 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.0059

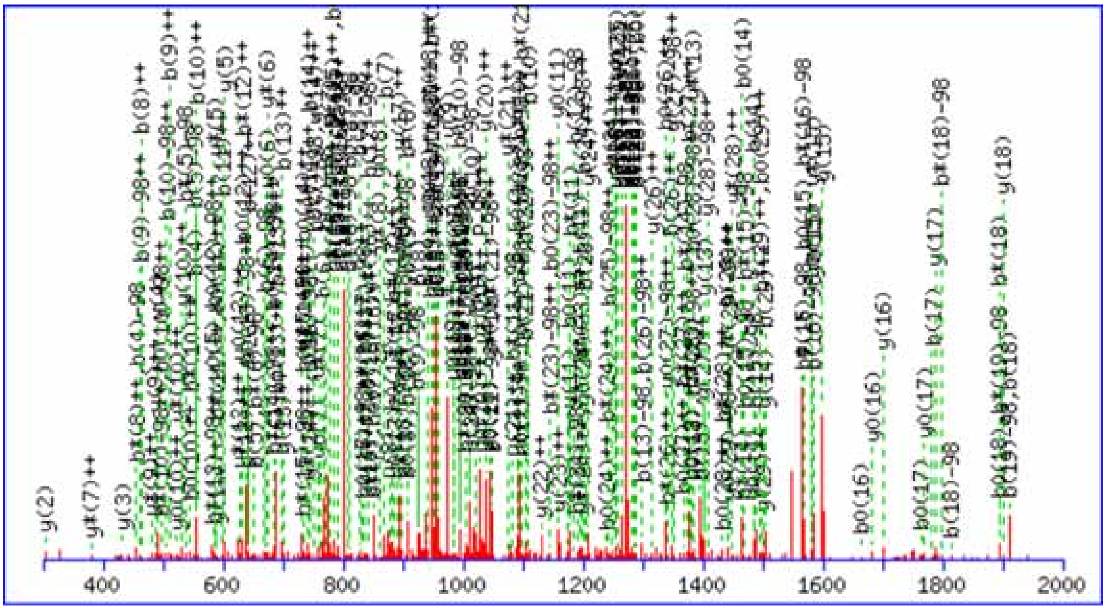
Matched b ions: b(5)-98, b(6)-98, b(6), b(7), b(8), b(9), b(13), b(13)++, b(13)-98, b(14), b(14)++, b(15), b(15)++, b(16)-98++, b(16)-98, b(16)++, b(17)++, b(18), b(18)++, b(18)-98++, b(19)-98, b(19)-98++, b(19)++, b(20)++, b(21)-98++, b(22)++, b(24)-98++, b(26)-196++, b(28)++, b(29)-98++, b(29)++
Matched y ions: y(4), y(8), y(9), y(9)-98, y(10), y(10)-98++, y(10)-98, y(11)-98, y(12)++, y(12), y(12)-98, y(13)++, y(13)-98, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(15), y(16), y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(19)++, y(22)++, y(23)++, y(24)-98++, y(24)++, y(25)++, y(25)-98++, y(28)-98++, y(29)++
Precursor origin neutral loss: +

Peptide No.793

RSNSVDTGPSSSLSTPTEPLSPTSSLGEER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RSNSVDTGPSSSLSTPTEPLSPTSSLGEER
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 7475: 3182.462004 from(1061.827944,3+)
Title: Elution from: 45.474 to 45.474 scan no 4159 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3182.4616
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 85 **Expect:** 3.2e-007

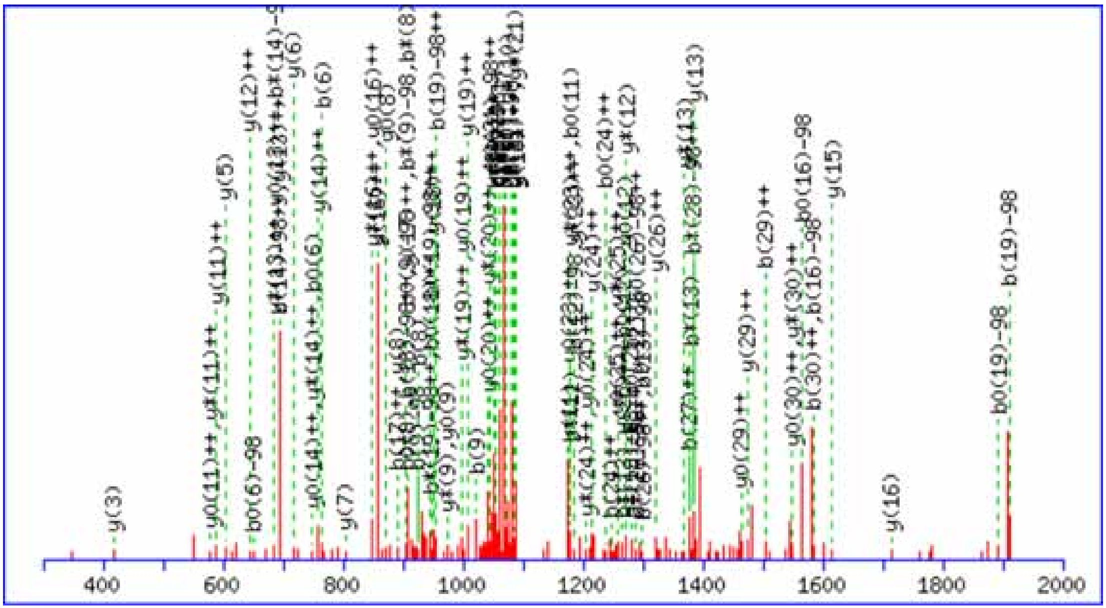
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8)++, b(8)-98, b(8), b(9)-98++, b(9), b(9)++, b(9)-98, b(10)-98++, b(10)++, b(10)-98, b(10), b(11), b(11)++, b(11)-98, b(12)++, b(12)-98, b(12), b(13), b(13)++, b(13)-98, b(14), b(14)++, b(15)-98, b(15), b(15)-98++, b(15)++, b(16)-98, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(17), b(18)++, b(18), b(18)-98, b(18)-98++, b(19)-98++, b(19)-98, b(19)++, b(20)-98++, b(21)++, b(22)-98++, b(23)++, b(24)-98++, b(24)++, b(25)-98++, b(26)++, b(26)-98++, b(27)++, b(28)++, b(29)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)++, y(11)++, y(11), y(12), y(12)++, y(13), y(13)++, y(14)++, y(14), y(15)++, y(15), y(16), y(16)++, y(17)++, y(17), y(18), y(18)++, y(19)++, y(20)++, y(21)++, y(22)++, y(23)++, y(24)++, y(25)++, y(26)++, y(27)-98++, y(27)++, y(28)-98++, y(29)++
Precursor origin neutral loss: +

Peptide No.794

RSNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of RSNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 7518: 3296.495151 from(1099.838993,3+)
Title: Elution from: 47.790 to 47.790 scan no 4431 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 3296.5045
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.021

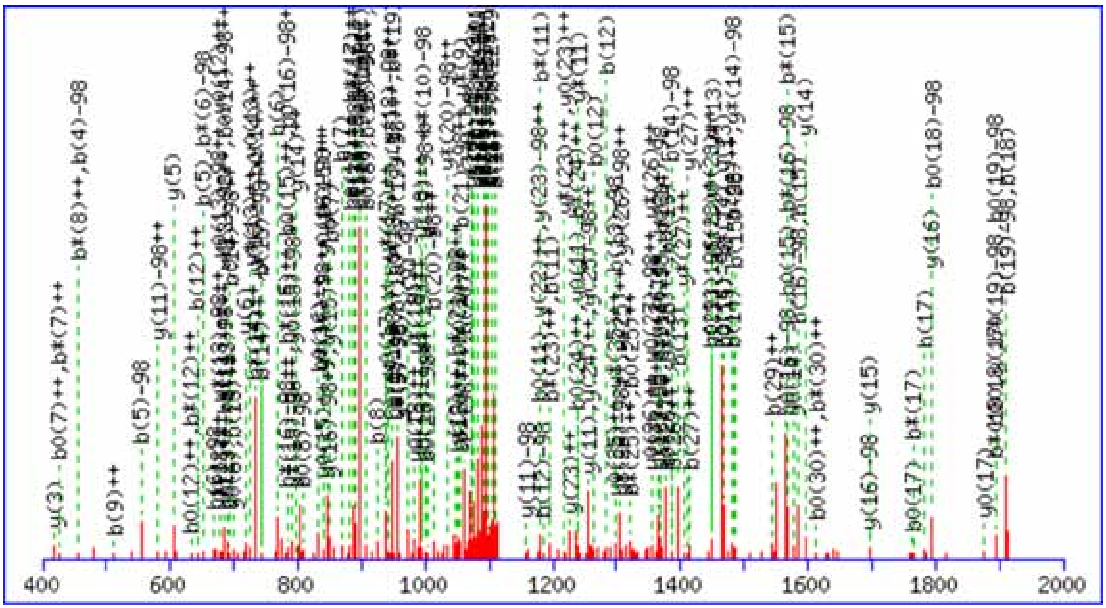
Matched b ions: b(6), b(8), b(9), b(9)-98, b(12)-98, b(13)-98, b(14)-98++, b(16)-98, b(17)++, b(18)-98++, b(19)-98, b(19)-98++, b(20)++, b(21)-98++, b(24)++, b(26)-98++, b(27)++, b(29)++, b(30)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(10), y(11), y(11)++, y(12)++, y(12), y(13)++, y(13), y(14)++, y(15), y(16)++, y(16), y(17)++, y(18)++, y(19)++, y(20)++, y(23)++, y(24)++, y(25)++, y(26)++, y(29)++
Precursor origin neutral loss: +

Peptide No.795

RSNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Confirmed sites:
Ambiguous sites: @S:2orS:4, @T:23orS:24orS:25

MS/MS Fragmentation of RSNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 8764: 3376.472094 from(1126.497974,3+)
Title: Elution from: 47.123 to 47.123 scan no 4561 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3376.4709
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S25 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 **Expect:** 2e-005

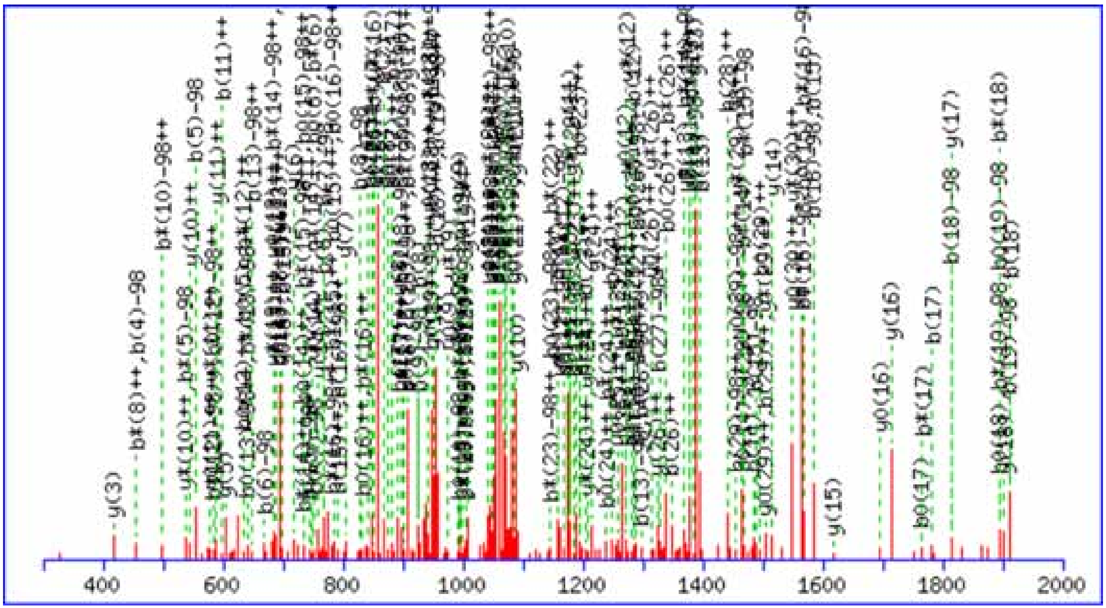
Matched b ions: b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7), b(8), b(9)++, b(10), b(11), b(11)-98, b(12)-98, b(12)++, b(12), b(13), b(13)++, b(13)-98, b(14), b(14)-98++, b(14)++, b(14)-98, b(15), b(15)-98, b(15)-98++, b(16)-98, b(17), b(17)++, b(18)++, b(18), b(18)-98++, b(19)-98++, b(19)-98, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)-98++, b(26)++, b(27)++, b(28)++, b(29)++, b(29)-196++
Matched y ions: y(3), y(5), y(6), y(9)-98, y(9), y(10)-98, y(11), y(11)-98++, y(11)-98, y(12)++, y(12), y(13)-98++, y(13)++, y(13), y(13)-98, y(14), y(14)++, y(15), y(15)++, y(16)++, y(16), y(16)-98++, y(16)-98, y(17)++, y(17), y(17)-98++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)++, y(22)++, y(23)-98++, y(23)++, y(24)++, y(25)-98++, y(25)++, y(26)++, y(27)-98++, y(27)++, y(30)-98++
Precursor origin neutral loss: +

Peptide No.796

RSNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RSNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 8733: 3296.503641 from(1099.841823,3+)
Title: Elution from: 44.770 to 44.770 scan no 4277 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3296.5045
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 96 Expect: 2.8e-008

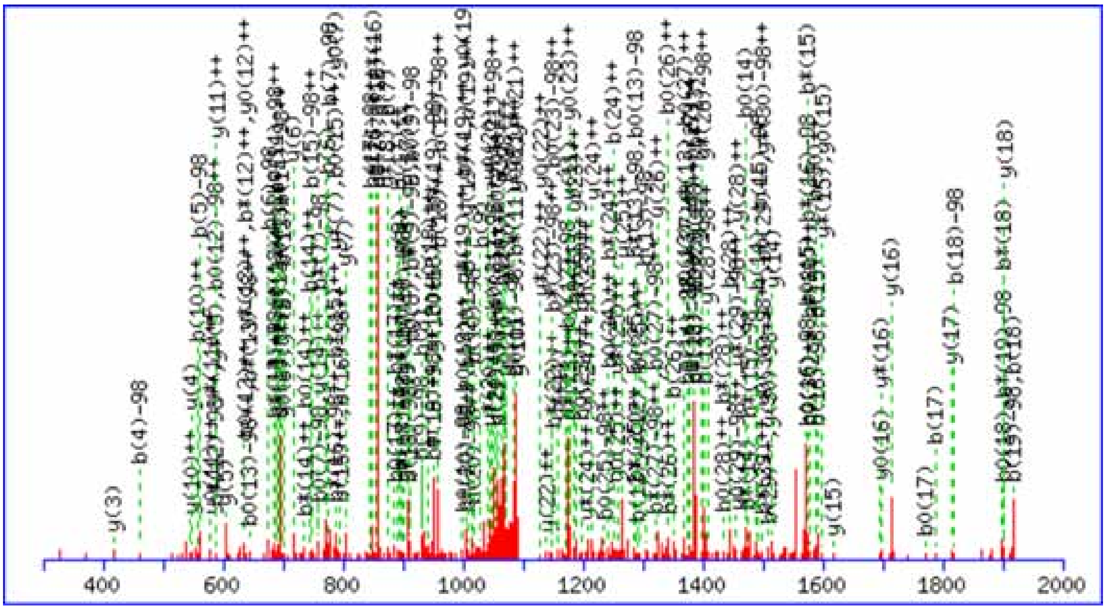
Matched b ions: b(4)-98, b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(11), b(11)++, b(12)-98, b(12), b(13), b(13)-98++, b(13)++, b(13)-98, b(14)-98++, b(14), b(14)-98, b(15), b(15)-98, b(15)-98++, b(15)++, b(16)-98, b(16)-98++, b(16)++, b(17), b(17)++, b(18)++, b(18)-98, b(18), b(18)-98++, b(19)-98++, b(19)-98, b(19)++, b(20)++, b(21)-98++, b(23)++, b(24)++, b(26)++, b(26)-98++, b(27)-98++, b(27)++, b(28)++, b(29)++, b(29)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(13)++, y(13), y(14)++, y(14), y(15), y(16)++, y(16), y(17)++, y(17), y(18)++, y(18), y(19)++, y(20)++, y(23)++, y(24)++, y(25)++, y(26)++, y(29)-98++
Precursor origin neutral loss:

Peptide No.797

RSNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RSNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 7503: 3302.538246 from(1101.853358,3+)
Title: Elution from: 44.691 to 44.691 scan no 4083 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3302.5363
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 Expect: 0.00068

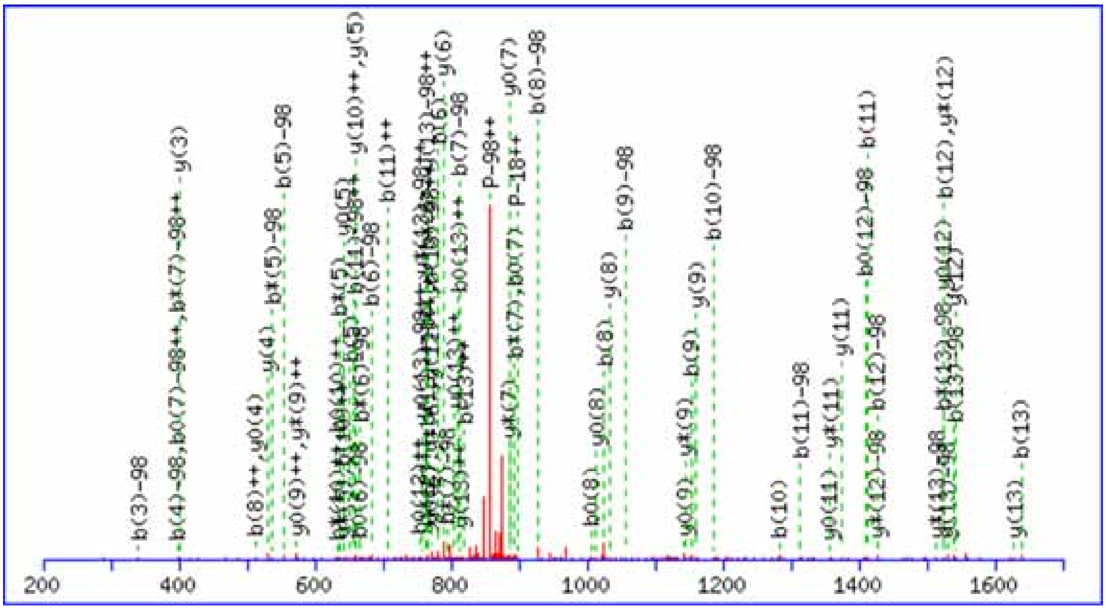
Matched b ions: b(4)-98, b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8), b(9)-98, b(9), b(10)++, b(10)-98, b(12), b(13), b(13)++, b(13)-98, b(14), b(14)-98++, b(14)++, b(15), b(15)-98++, b(15)++, b(15)-98, b(16)-98, b(16)-98++, b(17), b(17)-98++, b(17)++, b(18), b(18)++, b(18)-98, b(18)-98++, b(19)-98, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(23)++, b(24)++, b(25)++, b(26)++, b(27)++, b(28)++, b(29)++, b(30)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(10)++, y(11), y(11)++, y(12), y(13)++, y(13), y(14), y(14)++, y(15), y(16)++, y(16), y(17), y(17)++, y(18)++, y(18), y(19)++, y(20)++, y(22)++, y(23)++, y(24)++, y(25)++, y(26)++, y(27)++, y(28)++, y(28)-98++, y(30)-98++
Precursor origin neutral loss: +

Peptide No.798

RSSGREEDEEELLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RSSGREEDEEELLR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 3461: 1811.804838 from(906.909695,2+)
Title: Elution from: 30.364 to 30.364 scan no 2173 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1811.8050
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.0028

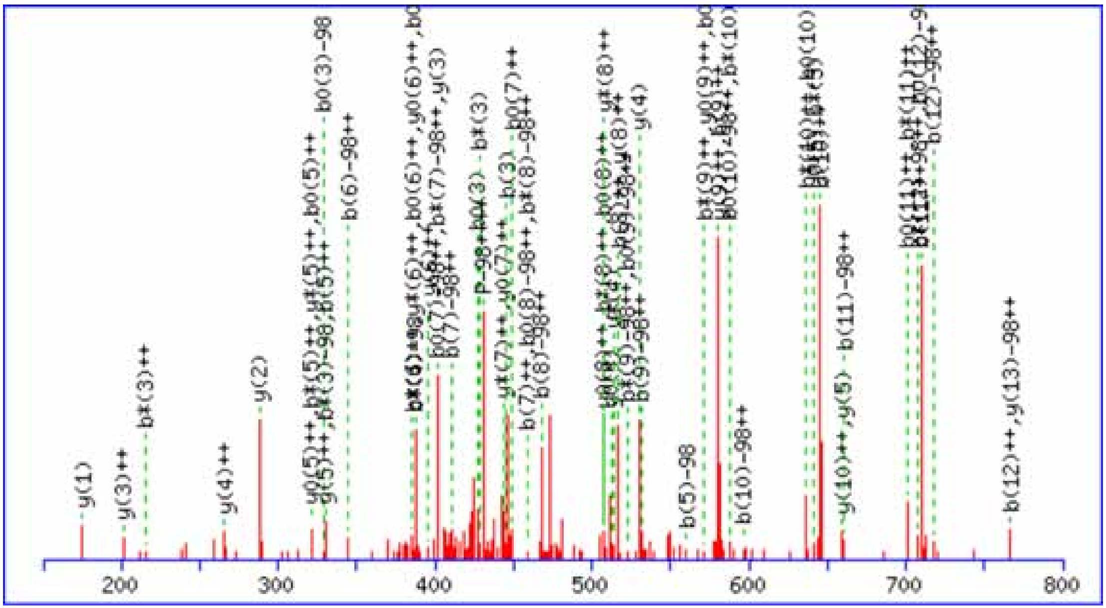
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(8), b(8)-98, b(8)++, b(9), b(9)-98, b(10), b(10)-98, b(10)++, b(11), b(11)-98, b(11)-98++, b(11)++, b(12)-98, b(12), b(12)++, b(13), b(13)-98++, b(13)-98, b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(10)++, y(11), y(12)++, y(12), y(13), y(13)-98, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.799

RSSGREEDEEELLR
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of RSSGREEDEEELLR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 3529: 1817.836560 from(455.466416,4+)
Title: Elution from: 30.585 to 30.585 scan no 2184 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1817.8368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 **Expect:** 0.0013

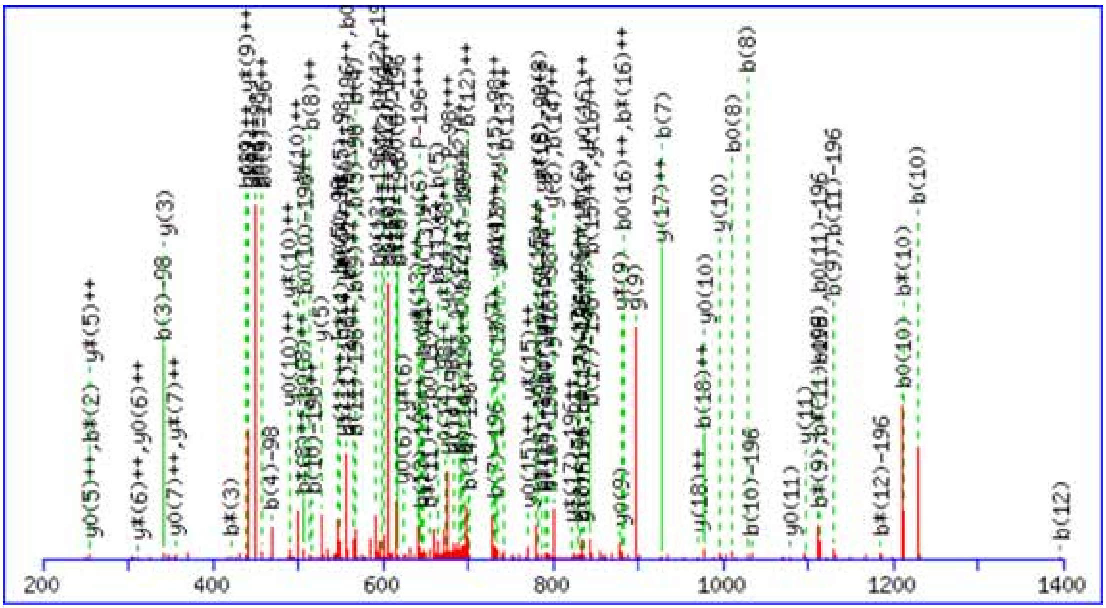
Matched b ions: b(3), b(5)++, b(5)-98, b(6)-98++, b(7)-98++, b(7)++, b(8)++, b(8)-98++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(4)++, y(5)++, y(5), y(6)++, y(8)++, y(9)++, y(10)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.800

RSSQPSPTTVPASDSPPAK
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of RSSQPSPTTVPASDSPPAK
Found in MA7D1_MOUSE, MAP7 domain-containing protein 1 OS=Mus musculus GN=Map7d1 PE=1 SV=1

Match to Query 6235: 2124.950529 from(709.324119,3+)
Title: Elution from: 27.725 to 27.725 scan no 1992 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2124.9494
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl (K)
Ions Score: 34 Expect: 0.021

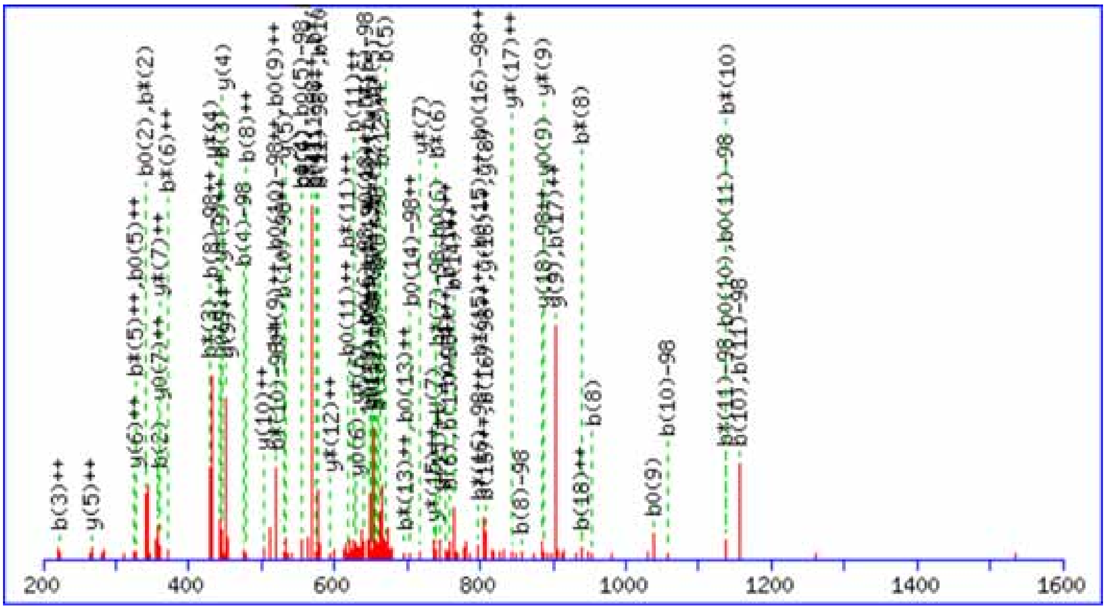
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(7)-196, b(7)-98, b(7), b(8), b(8)-98++, b(8)++, b(8)-196, b(9)-98, b(9)++, b(9)-98++, b(9), b(10), b(10)-98, b(10)++, b(10)-196, b(10)-98++, b(10)-196++, b(11)-98++, b(11)-98, b(11)++, b(11)-196++, b(11)-196, b(12), b(12)++, b(12)-196++, b(12)-98++, b(13)-196++, b(13)-98++, b(13)++, b(14)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)-196++, b(17)-196++, b(18)++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(11), y(11)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++, y(17)-196++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No.801

RSSQPSPTTVPASDSPPAK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of RSSQPSPTTVPASDSPPAK
Found in MA7D1_MOUSE, MAP7 domain-containing protein 1 OS=Mus musculus GN=Map7d1 PE=1 SV=1

Match to Query 5444: 2057.047617 from(686.689815,3+)
Title: Elution from: 26.375 to 26.375 scan no 1662 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2057.0467
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 32 **Expect:** 0.043

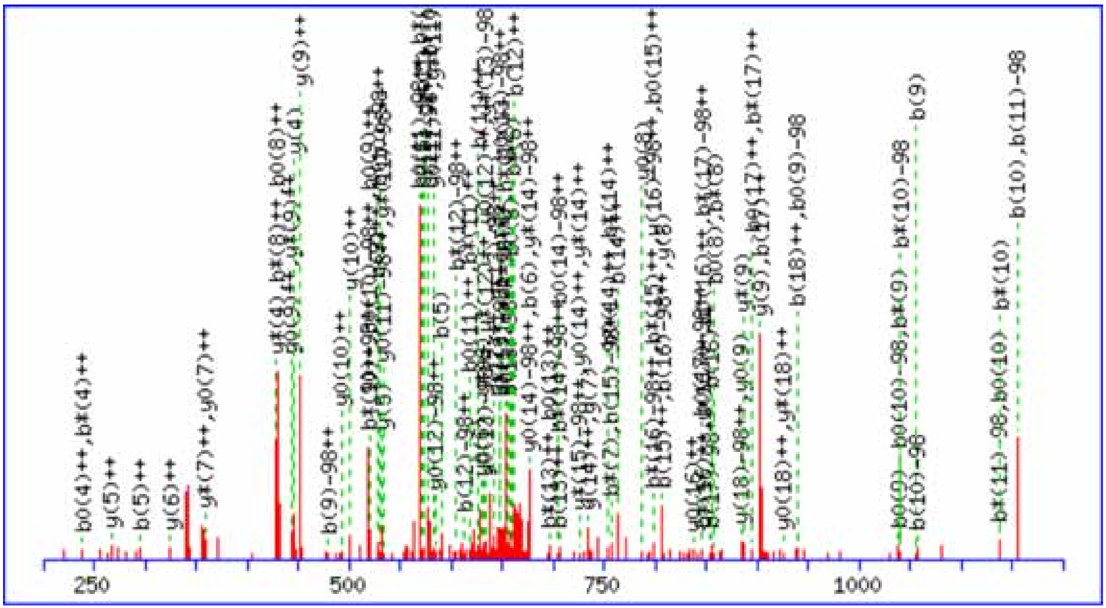
Matched b ions: b(2), b(3)++, b(3), b(4)-98, b(4), b(5), b(6), b(6)-98, b(8)-98++, b(8), b(8)-98, b(8)++, b(10), b(10)++, b(10)-98, b(10)-98++, b(11)-98, b(11)-98++, b(11)++, b(12)++, b(13)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(17)++, b(18)++
Matched y ions: y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(8), y(9), y(9)++, y(10)++, y(13)++, y(15)++, y(16)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.802

RSSQPSPTTVPASDSPPAK
Confirmed sites:
Ambiguous sites: @T:8orT:9

MS/MS Fragmentation of RSSQPSPTTVPASDSPPAK
Found in MA7D1_MOUSE, MAP7 domain-containing protein 1 OS=Mus musculus GN=Map7d1 PE=1 SV=1

Match to Query 5252: 2057.049135 from(686.690321,3+)
Title: Elution from: 26.339 to 26.339 scan no 1630 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2057.0467
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 34 Expect: 0.025

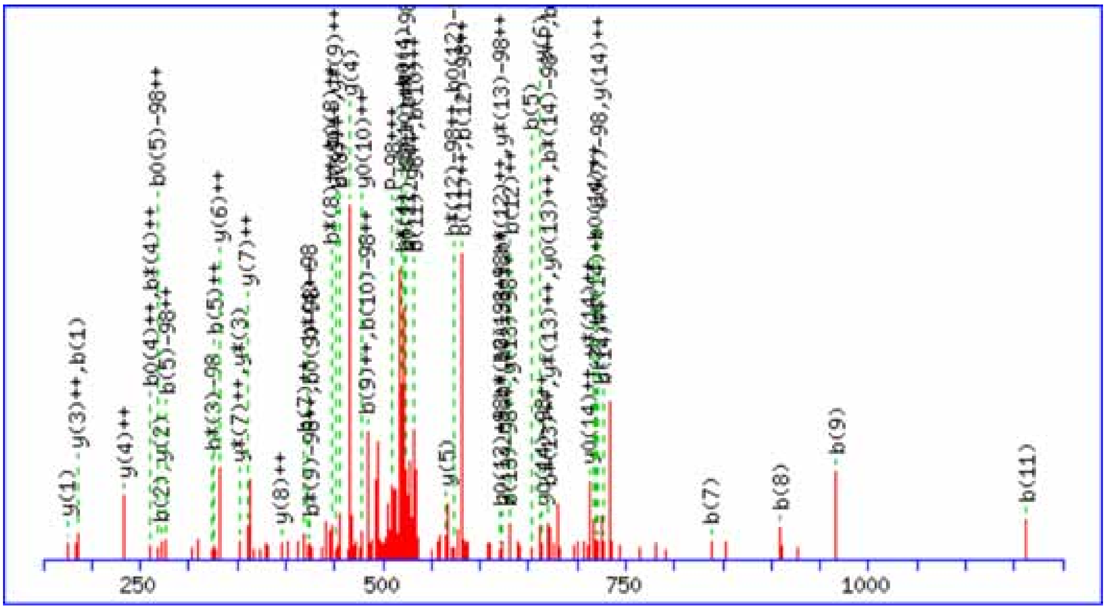
Matched b ions: b(5)++, b(5), b(6), b(9)++, b(9), b(9)-98++, b(10), b(10)++, b(10)-98, b(10)-98++, b(11)-98, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++
Matched y ions: y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(8), y(9), y(9)++, y(10)++, y(12)++, y(13)-98++, y(14)++, y(16)-98++, y(16)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.803

RSSVNGEAGPVPPPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RSSVNGEAGPVPPPR
Found in EH1L1_MOUSE, EH domain-binding protein 1-like protein 1 OS=Mus musculus GN=Ehbp1l1 PE=2 SV=1

Match to Query 2417: 1626.788652 from(543.270160,3+)
Title: Elution from: 25.233 to 25.233 scan no 1508 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1626.7879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.0071

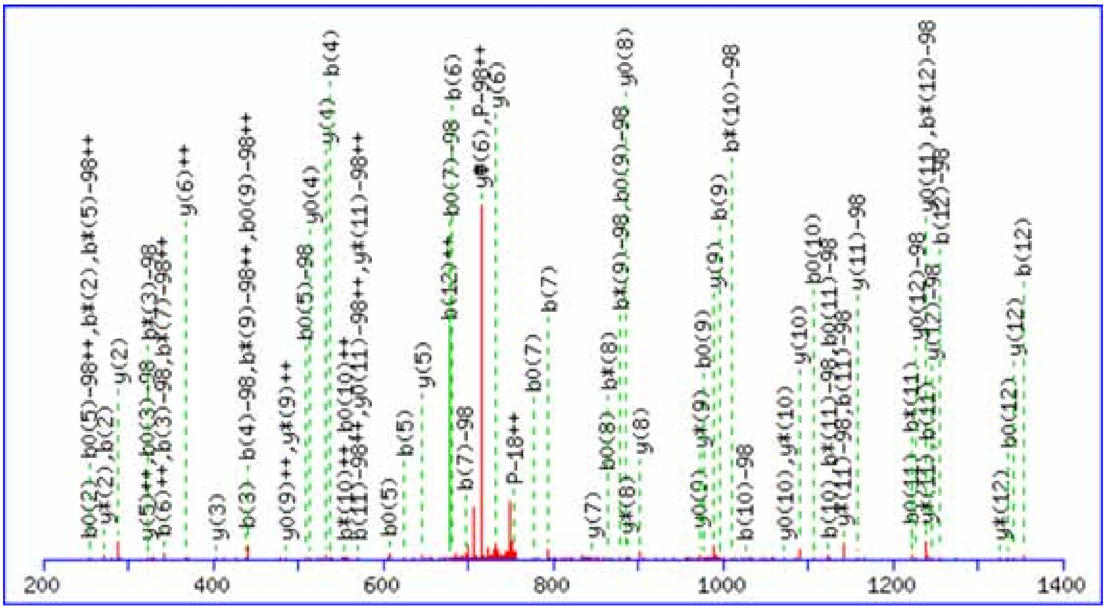
Matched b ions: b(1), b(2), b(5)-98++, b(5)++, b(5), b(7), b(7)++, b(8)++, b(8), b(9), b(9)++, b(10)++, b(10)-98++, b(11)++, b(11), b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(14)++
Matched y ions: y(1), y(2), y(3)++, y(4)++, y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(13)-98++, y(14)++
Precursor origin neutral loss:

Peptide No.804

RSSVSGISLEDNR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RSSVSGISLEDNR
Found in PDLI4_MOUSE, PDZ and LIM domain protein 4 OS=Mus musculus GN=Pdlim4 PE=1 SV=2

Match to Query 2693: 1526.709668 from(764.362110,2+)
Title: Elution from: 32.692 to 32.692 scan no 2673 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1526.7090
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 1.5e-005

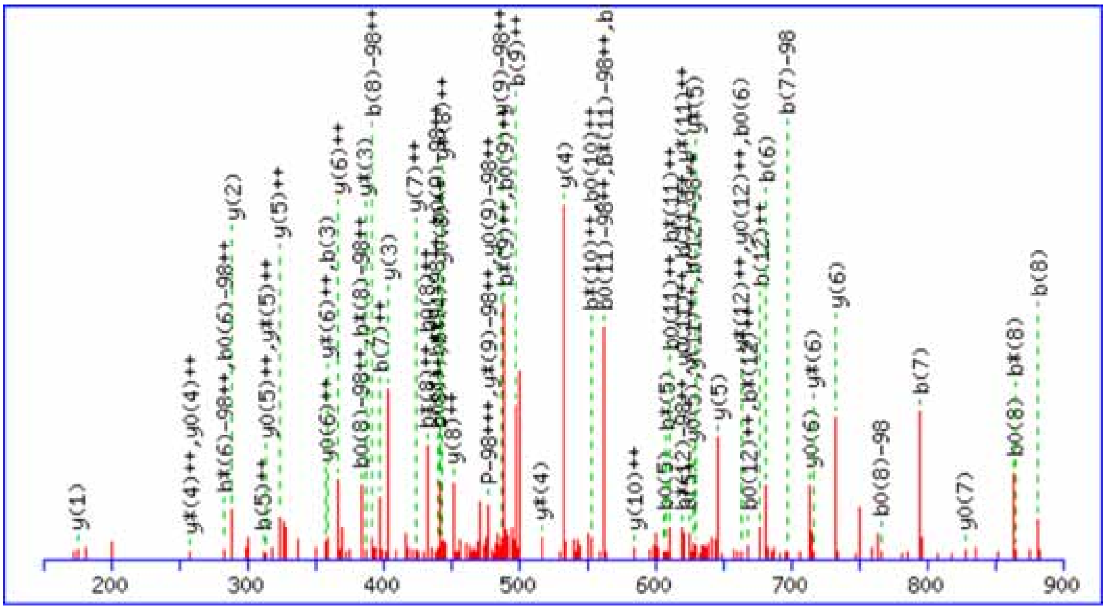
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(6)++, b(6), b(7), b(7)-98, b(9), b(10), b(10)-98, b(11)-98, b(11), b(11)-98++, b(12), b(12)-98, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(8), y(9), y(10), y(11)-98, y(12), y(12)-98
Precursor origin neutral loss: +

Peptide No.805

RSSVSGISLEDNR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of RSSVSGISLEDNR
Found in PDLI4_MOUSE, PDZ and LIM domain protein 4 OS=Mus musculus GN=Pdlim4 PE=1 SV=2

Match to Query 2692: 1526.709495 from(509.910441,3+)
Title: Elution from: 32.706 to 32.706 scan no 2675 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1526.7090
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.0019

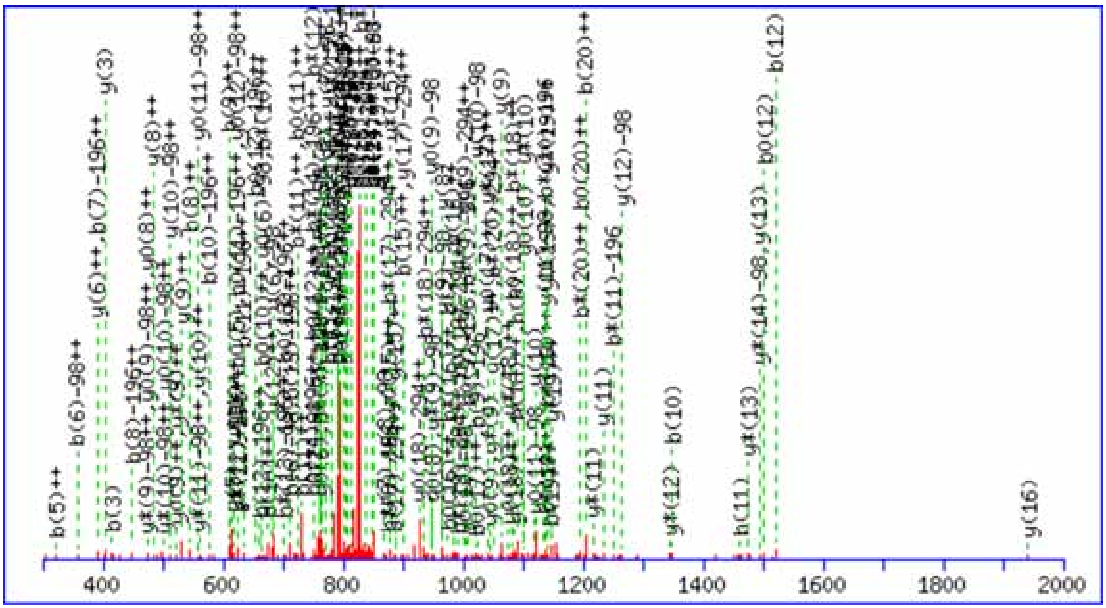
Matched b ions: b(3), b(5), b(5)++, b(6), b(7), b(7)++, b(7)-98, b(8), b(8)++, b(8)-98++, b(9)++, b(10)++, b(11)++, b(12)++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6)++, y(6), y(7)++, y(8)++, y(9)-98++, y(10)++, y(11)++
Precursor origin neutral loss:

Peptide No.806

RTEARSSDEENGPPSSPDLDR
Confirmed sites: @S:6,@S:7,@S:16
Ambiguous sites:

MS/MS Fragmentation of RTEARSSDEENGPPSSPDLDR
Found in AKTS1_MOUSE, Proline-rich AKT1 substrate 1 OS=Mus musculus GN=Akt1s1 PE=1 SV=1

Match to Query 7818: 2581.974612 from(861.665480,3+)
Title: Elution from: 29.658 to 29.658 scan no 2258 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2581.9724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.0013

Matched b ions: b(3), b(5)++, b(6)-98++, b(6), b(6)-98, b(7)-196++, b(7)-196, b(7)-98, b(7), b(8)-98++, b(8), b(8)-196++, b(8)++, b(9)-98++, b(9)++, b(9)-196, b(9)-98, b(10), b(10)++, b(10)-98++, b(10)-196++, b(11)-98++, b(11)++, b(11), b(11)-196++, b(12), b(12)++, b(12)-98, b(12)-98++, b(12)-196++, b(13)-98++, b(13)++, b(13)-196++, b(14)-98++, b(15)-196++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(16)-294++, b(16)-196++, b(17)-196++, b(17)-98++, b(17)-294++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(19)-196++, b(20)++, b(20)-98++, b(20)-196++
Matched y ions: y(3), y(5), y(6)++, y(6)-98, y(6), y(7)-98, y(7), y(8), y(8)++, y(8)-98, y(9)++, y(9), y(9)-98, y(10), y(10)++, y(10)-98++, y(10)-98, y(11), y(11)++, y(11)-98, y(12)++, y(12)-98, y(13), y(14)++, y(15)-196++, y(15)-98++, y(15)++, y(16), y(17)-294++, y(17)-196++, y(17)++, y(18)++, y(18)-196++, y(19)-294++, y(19)++, y(20)-196++
Precursor origin neutral loss: +

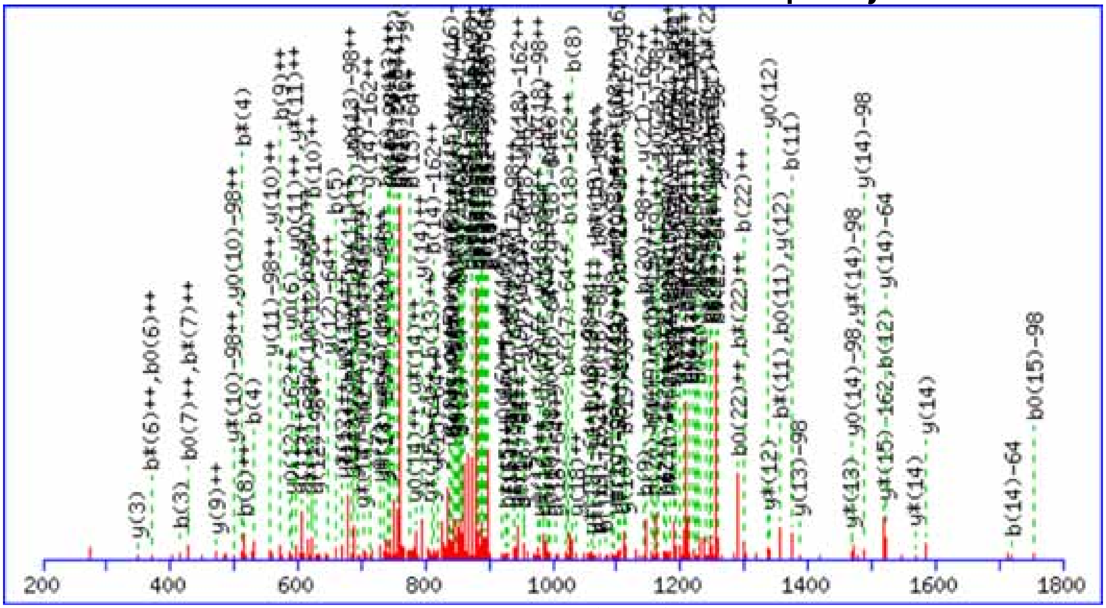
Peptide No.807

RTEDQVNCLTQMPSSIHSDGESN
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of RTEDQVNCLTQMPSSIHSDGESN
Found in LRC39_MOUSE, Leucine-rich repeat-containing protein 39 OS=Mus musculus GN=Lrrc39 PE=2 SV=1

Match to Query 8194: 2728.111482 from(910.377770,3+)

Title: Elution from: 34.903 to 34.903 scan no 2975 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2728.1106
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 Expect: 1e-005

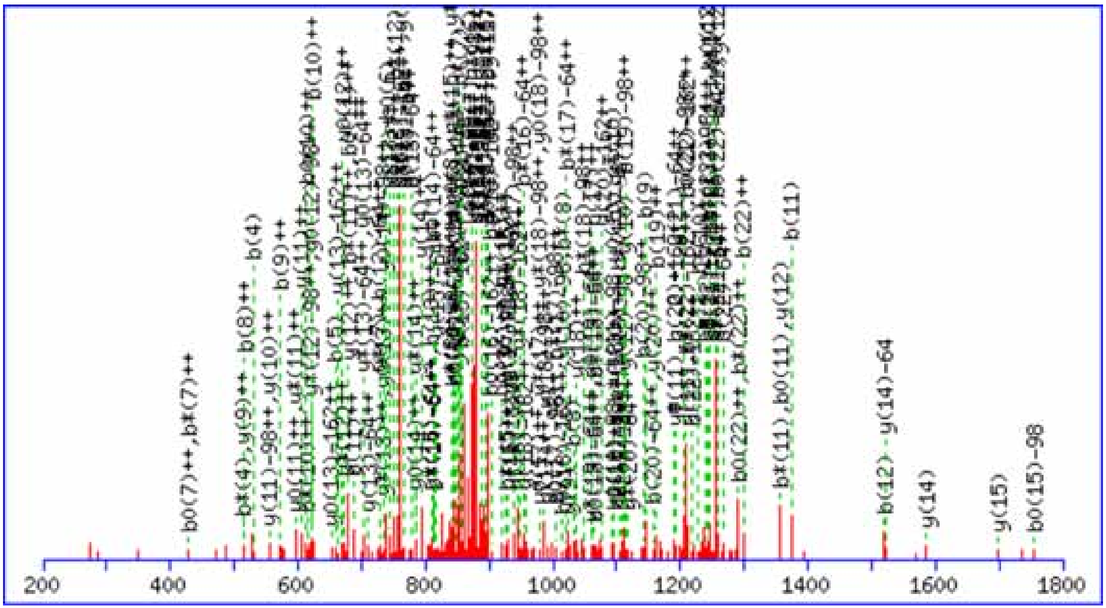
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)++, b(8), b(9), b(9)++, b(10)++, b(10), b(11), b(11)++, b(12)++, b(12), b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(16)-98++, b(16)++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++
Matched y ions: y(3), y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(11)-98++, y(11)-98, y(12)++, y(12), y(12)-98, y(12)-98++, y(13)-98, y(13)++, y(13)-98++, y(14), y(14)-98, y(14)++, y(14)-98++, y(15)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++, y(20)++, y(21)-98++, y(21)++, y(22)-98++
Precursor origin neutral loss: +

Peptide No.808

RTEDQVNCLTQMPSSIHSDGESN
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of RTEDQVNCLTQMPSSIHSDGESN
Found in LRC39_MOUSE, Leucine-rich repeat-containing protein 39 OS=Mus musculus GN=Lrrc39 PE=2 SV=1

Match to Query 6425: 2728.113153 from(910.378327,3+)
Title: Elution from: 34.648 to 34.648 scan no 2728 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2728.1106
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0033

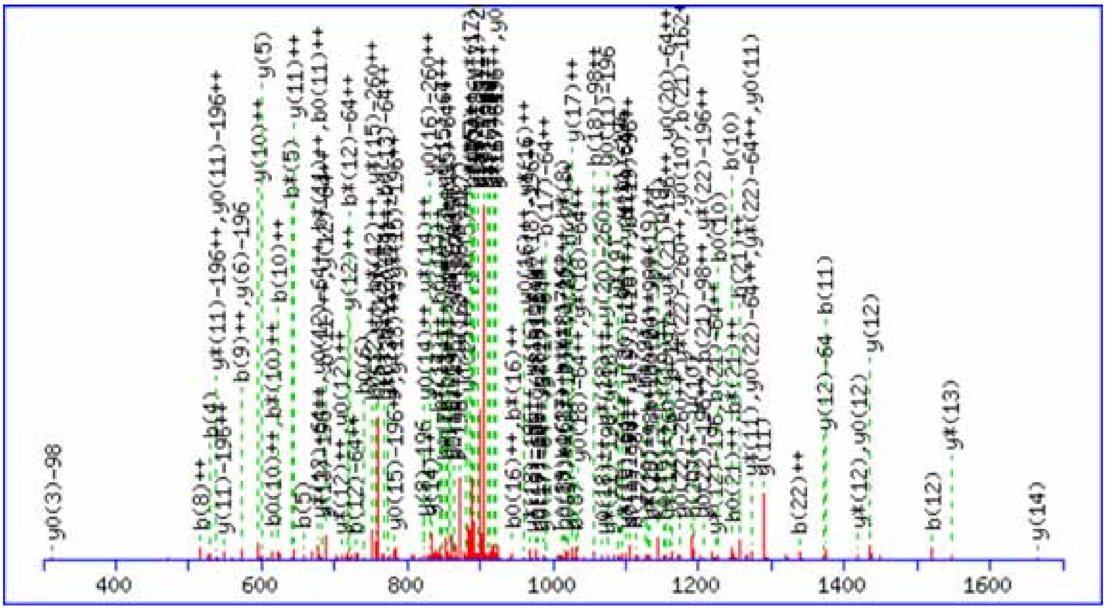
Matched b ions: b(4), b(5), b(6), b(7), b(8)++, b(8), b(9), b(9)++, b(10)++, b(10), b(11), b(11)++, b(12)++, b(12), b(13)++, b(14)++, b(15)-98++, b(16)-98++, b(17)++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++
Matched y ions: y(8), y(9), y(9)++, y(9)-98, y(10)++, y(10), y(10)-98, y(11)-98++, y(11)++, y(11)-98, y(11), y(12)++, y(12), y(12)-98, y(13)++, y(14), y(14)++, y(15), y(15)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(20)-98++, y(20)++
Precursor origin neutral loss: +

Peptide No.809

RTEDQVNCLTQMPSSIHSDGESN
Confirmed sites: @S:18,@S:22
Ambiguous sites:

MS/MS Fragmentation of RTEDQVNCLTQMPSSIHSDGESN
Found in LRC39_MOUSE, Leucine-rich repeat-containing protein 39 OS=Mus musculus GN=Lrrc39 PE=2 SV=1

Match to Query 8301: 2808.077166 from(937.032998,3+)
Title: Elution from: 37.827 to 37.827 scan no 3376 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2808.0769
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S22 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 **Expect:** 3.2e-006

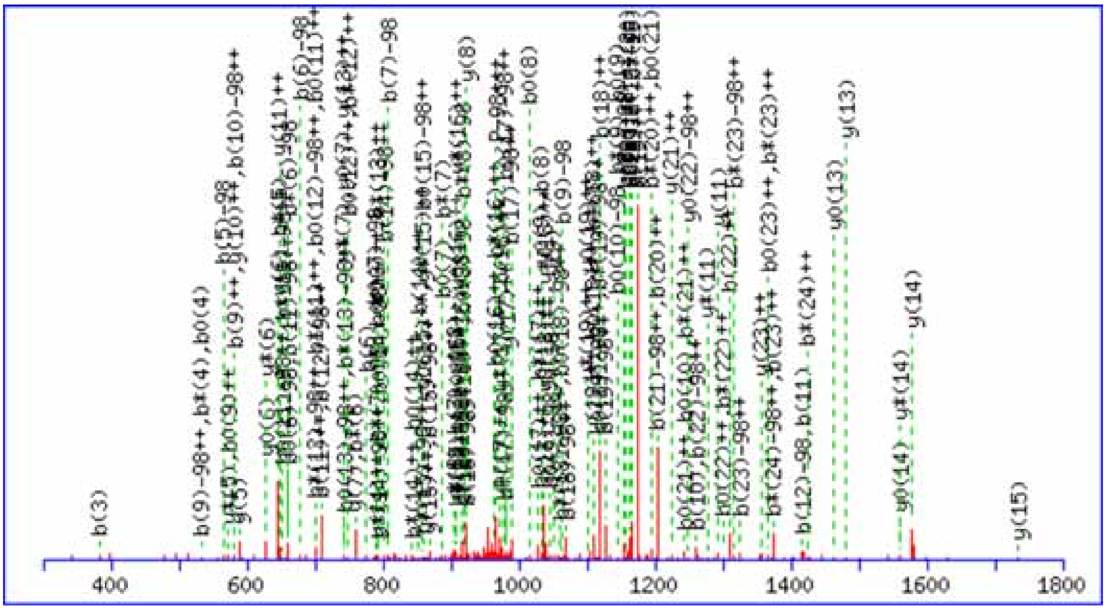
Matched b ions: b(4), b(5), b(6), b(7), b(8)++, b(8), b(9), b(9)++, b(10)++, b(10), b(11)++, b(11), b(12)++, b(12), b(14)++, b(15)++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++
Matched y ions: y(5), y(6)-196, y(6)-98, y(6), y(7), y(7)-98, y(8)-98, y(8), y(8)-196, y(9), y(9)-196, y(9)-98, y(10)++, y(10), y(10)-98++, y(10)-98, y(11)-98++, y(11)-98, y(11), y(11)++, y(11)-196++, y(11)-196, y(12), y(12)-98, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(13)-196++, y(14), y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)-196++, y(18)++, y(20)-196++, y(22)-98++
Precursor origin neutral loss: +

Peptide No.810

RTPSLLEQEVKPSTELEYLGPDEND
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RTPSLLEQEVKPSTELEYLGPDEND
Found in GTR4_MOUSE, Solute carrier family 2, facilitated glucose transporter member 4 OS=Mus musculus GN=Slc2a4 PE=1 SV=2

Match to Query 7221: 2994.412614 from(999.144814,3+)
Title: Elution from: 56.811 to 56.811 scan no 5357 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2994.4110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K11 : Dimethyl (K)
Ions Score: 78 Expect: 1.6e-006

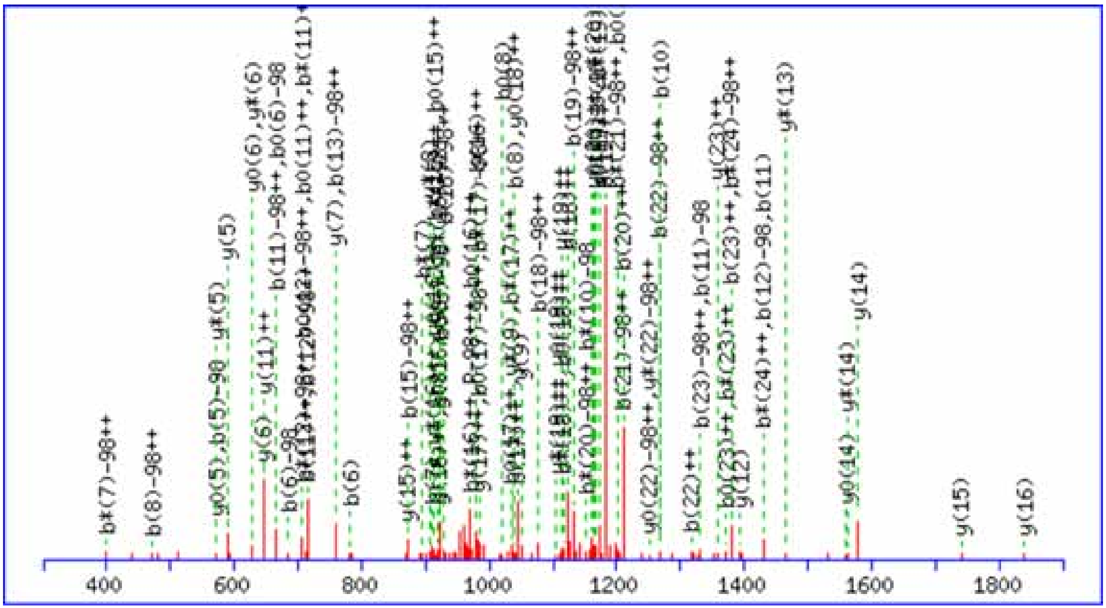
Matched b ions: b(3), b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(8), b(9)-98++, b(9), b(9)++, b(9)-98, b(10), b(10)-98++, b(10)-98, b(11)++, b(11), b(11)-98++, b(12)-98++, b(12)-98, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(11)++, y(13), y(13)++, y(14), y(14)++, y(15), y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(23)++
Precursor origin neutral loss: +

Peptide No.811

RTPSLLEQEVKPSTELEYLGPDEND
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RTPSLLEQEVKPSTELEYLGPDEND
Found in GTR4_MOUSE, Solute carrier family 2, facilitated glucose transporter member 4 OS=Mus musculus GN=Slc2a4 PE=1 SV=2

Match to Query 6677: 3006.474426 from(1003.165418,3+)
Title: Elution from: 56.627 to 56.627 scan no 5158 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3006.4747
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K11 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 74 **Expect:** 3.9e-006

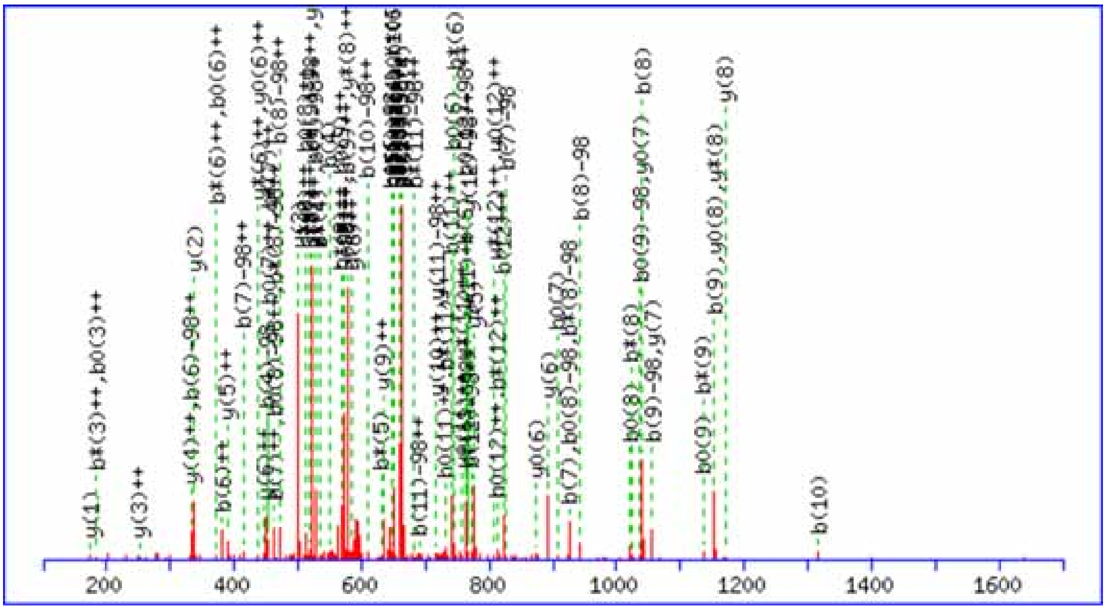
Matched b ions: b(5)-98, b(6)-98, b(6), b(7), b(8)-98++, b(8), b(9), b(10), b(11)++, b(11), b(11)-98++, b(11)-98, b(12)-98++, b(12)-98, b(13)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(12), y(14), y(15), y(15)++, y(16), y(16)++, y(17)++, y(19)++, y(23)++
Precursor origin neutral loss: +

Peptide No.812

RTPSPDYDLYYYR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4446: 1815.787146 from(606.269658,3+)
Title: Elution from: 45.548 to 45.548 scan no 4368 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1815.7869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.0008

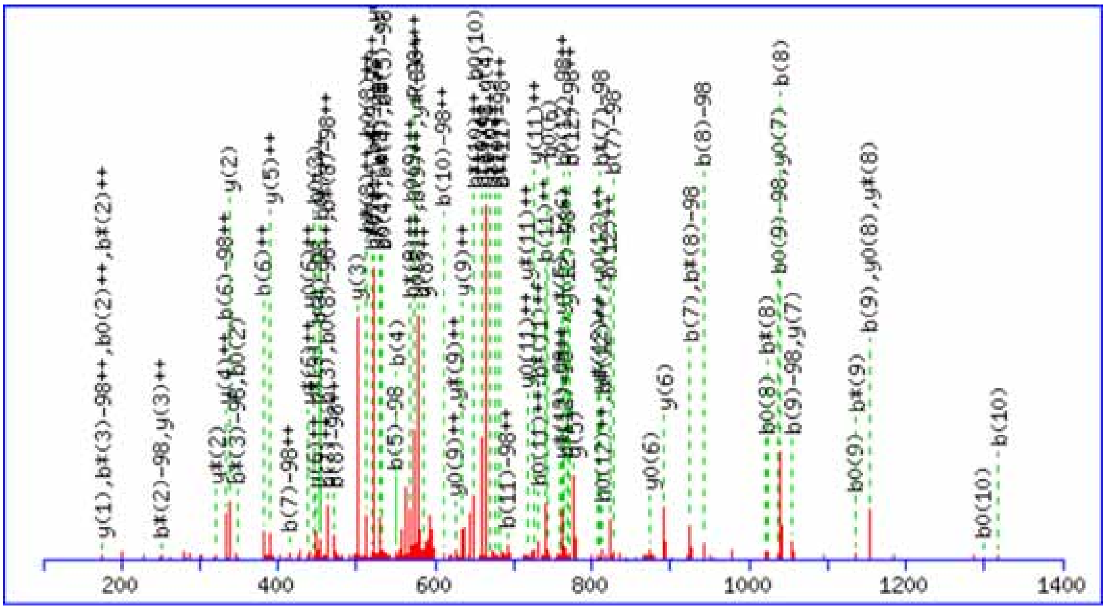
Matched b ions: b(4)-98, b(4), b(5), b(6)-98, b(6)-98++, b(6), b(6)++, b(7)++, b(7), b(7)-98, b(7)-98++, b(8)++, b(8), b(8)-98++, b(8)-98, b(9), b(9)++, b(9)-98, b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(4)++, y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.813

RTPSPDYDLYYYR
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of RTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3512: 1815.788370 from(606.270066,3+)
Title: Elution from: 45.458 to 45.458 scan no 4157 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1815.7869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00096

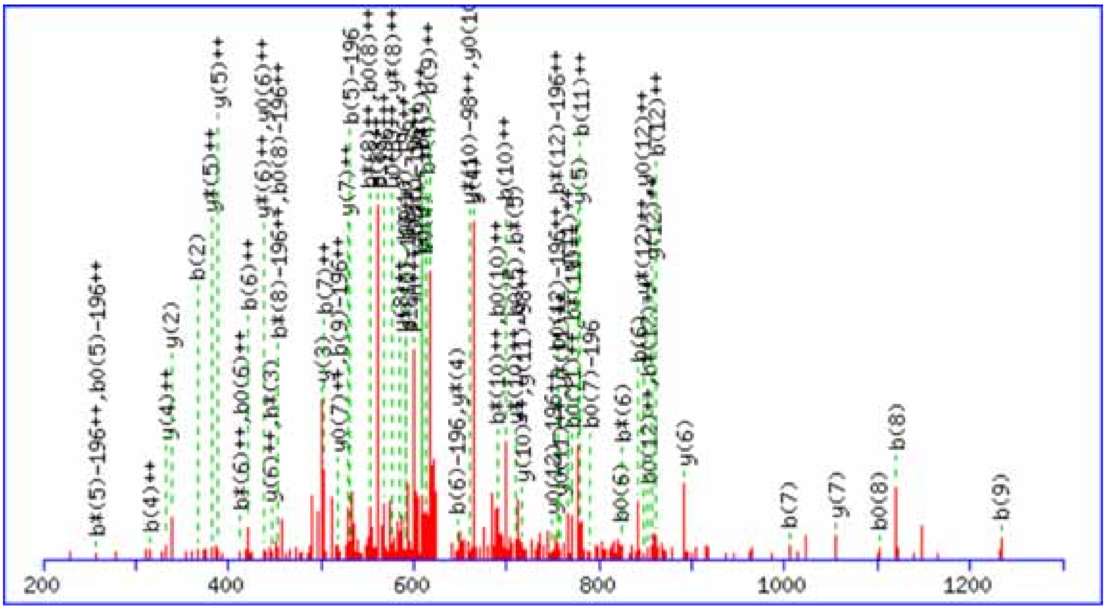
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6)-98, b(6)-98++, b(6)++, b(6), b(7)++, b(7), b(7)-98, b(7)-98++, b(8)++, b(8), b(8)-98, b(8)-98++, b(9), b(9)++, b(9)-98, b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(4)++, y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8)++, y(9)++, y(10)++, y(11)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.814

RTPSPDYDLYYYR
Confirmed sites: @T:2,@S:4
Ambiguous sites:

MS/MS Fragmentation of RTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 5899: 1895.755347 from(632.925725,3+)
Title: Elution from: 49.641 to 49.641 scan no 4913 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1895.7532
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.0011

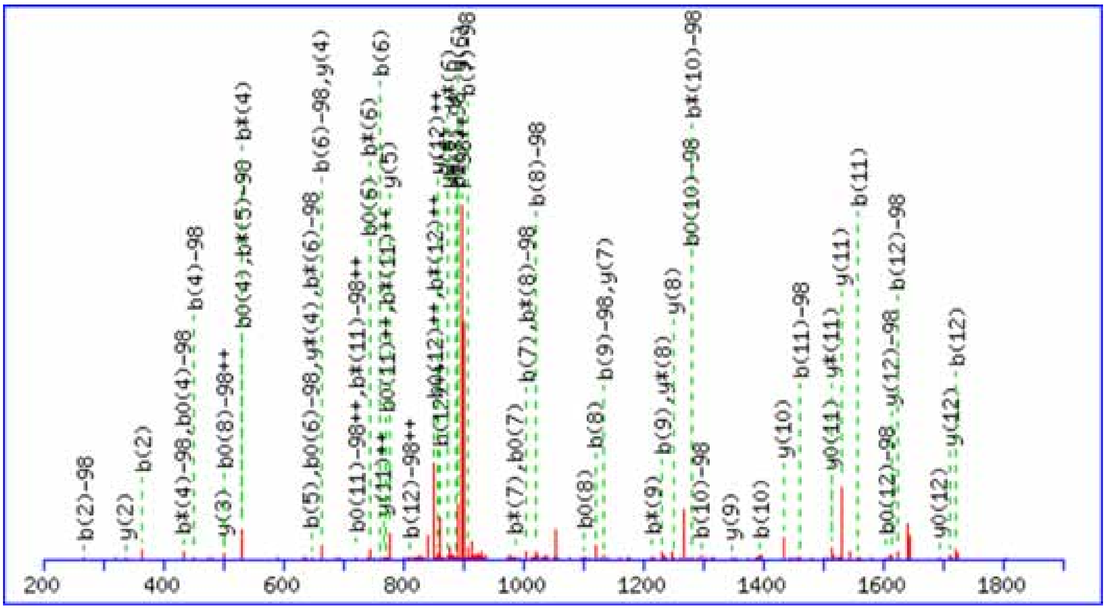
Matched b ions: b(2), b(4)++, b(4)-98, b(5)-196, b(6)++, b(6), b(6)-98, b(6)-98++, b(6)-196, b(7)++, b(7), b(7)-98++, b(8)++, b(8)-98, b(8), b(8)-98++, b(9), b(9)++, b(9)-196++, b(9)-98++, b(10)++, b(10)-196++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8)++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.815

RTPSPDYDLYYYR
Confirmed sites: @T:2,@Y:7
Ambiguous sites:

MS/MS Fragmentation of RTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3853: 1895.756362 from(948.885457,2+)
Title: Elution from: 49.392 to 49.392 scan no 4518 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1895.7532
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y7 : Phospho (Y)
Ions Score: 37 Expect: 0.0061

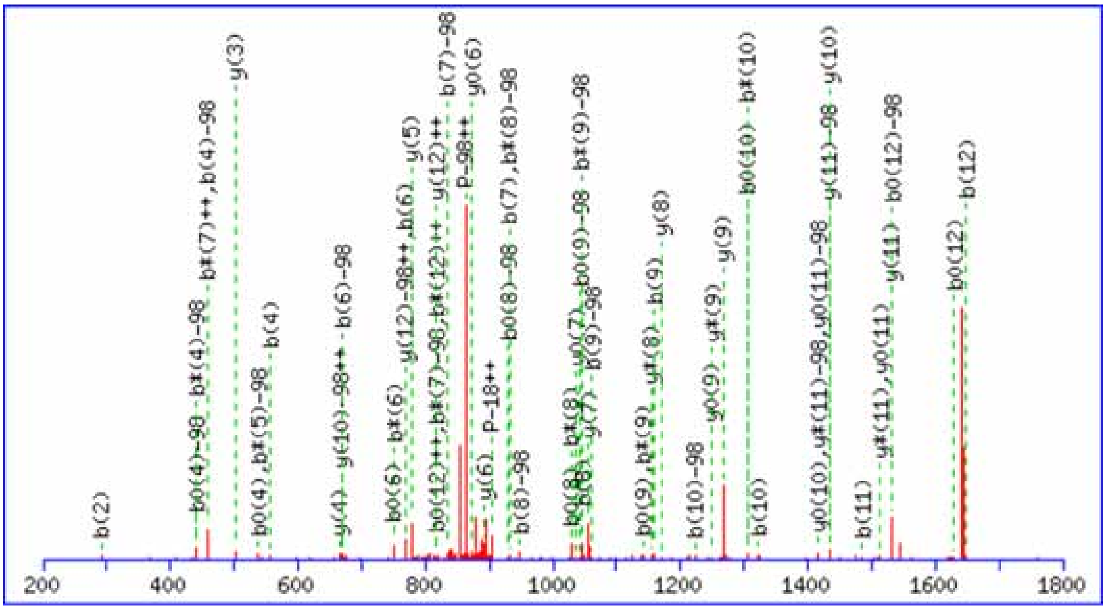
Matched b ions: b(2), b(2)-98, b(4)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)-98, y(12)++
Precursor origin neutral loss: +

Peptide No.816

RTPSPDYDLYYYR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3156: 1821.820192 from(911.917372,2+)
Title: Elution from: 45.378 to 45.378 scan no 4046 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1821.8187
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.00073

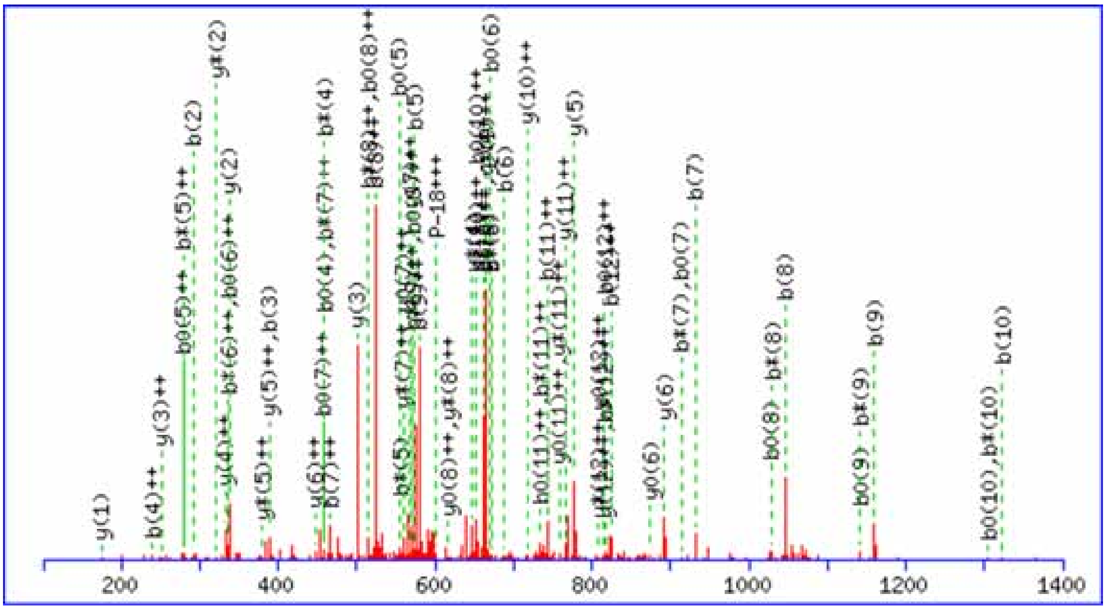
Matched b ions: b(2), b(4)-98, b(4), b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11), b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98++, y(11), y(11)-98, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.817

RTPSPDYDLYYYR
Confirmed sites: @Y:7
Ambiguous sites:

MS/MS Fragmentation of RTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 5142: 1821.819798 from(608.280542,3+)
Title: Elution from: 45.476 to 45.476 scan no 4367 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1821.8187
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y7 : Phospho (Y)
Ions Score: 31 Expect: 0.043

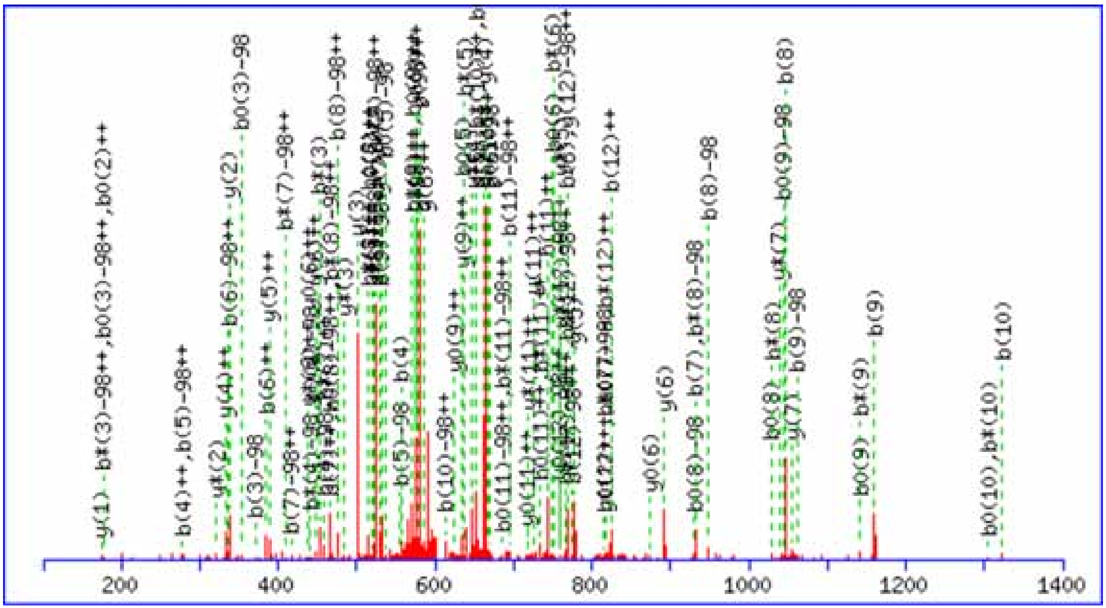
Matched b ions: b(2), b(3), b(4)++, b(5), b(6), b(7)++, b(7), b(8)++, b(8), b(9), b(9)++, b(10)++, b(10), b(11)++, b(12)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(4)++, y(5), y(5)++, y(6), y(6)++, y(7)++, y(10)++, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.818

RTPSPDYDLYYYR
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of RTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3555: 1821.820158 from(608.280662,3+)
Title: Elution from: 45.488 to 45.488 scan no 4161 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1821.8187
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.002

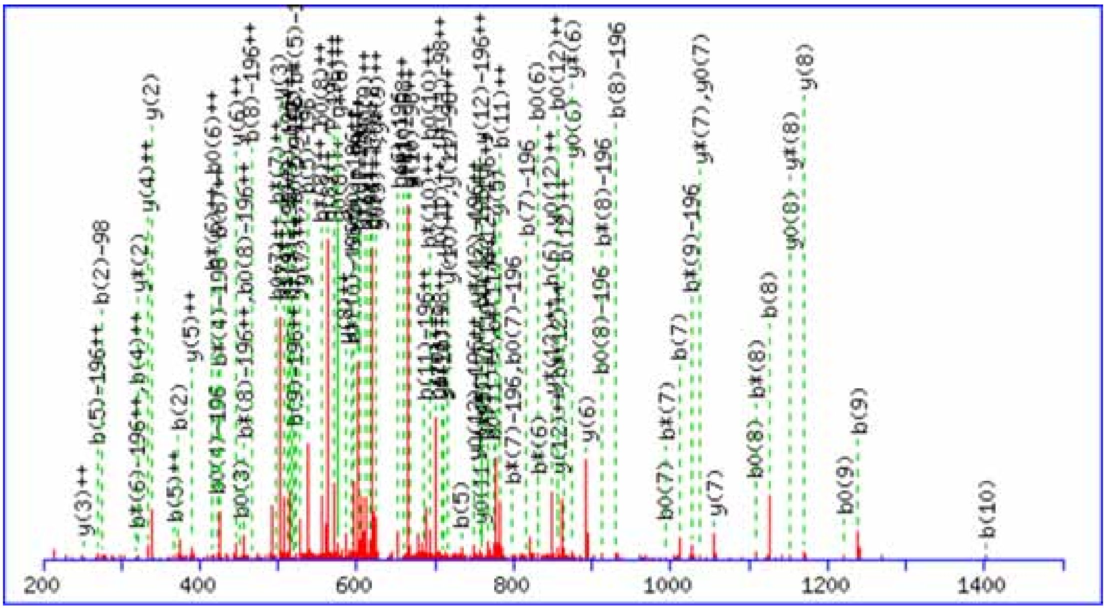
Matched b ions: b(3)-98, b(4)++, b(4)-98, b(4), b(5)-98++, b(5), b(5)-98, b(6), b(6)-98++, b(6)++, b(6)-98, b(7)++, b(7), b(7)-98++, b(8)++, b(8), b(8)-98++, b(8)-98, b(9), b(9)++, b(9)-98++, b(9)-98, b(10), b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8)++, y(9)++, y(11)++, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.819

RTPSPDYDLYYYR
Confirmed sites: @T:2,@S:4
Ambiguous sites:

MS/MS Fragmentation of RTPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4507: 1901.786868 from(634.936232,3+)
Title: Elution from: 49.422 to 49.422 scan no 4662 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1901.7850
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00066

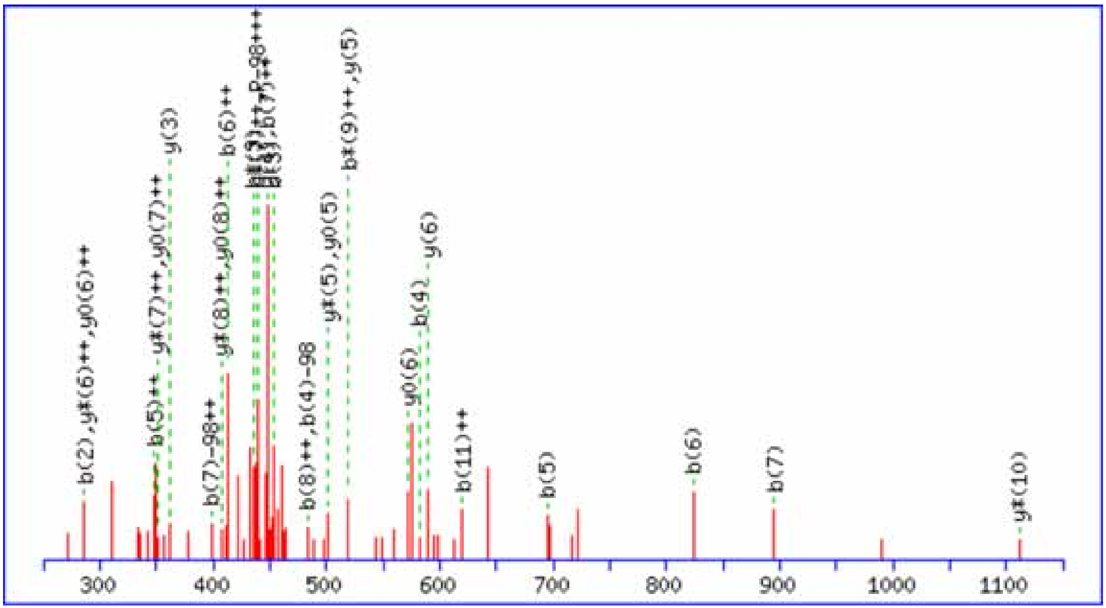
Matched b ions: b(2)-98, b(2), b(4)-98++, b(4)-98, b(4)++, b(5)-196++, b(5)++, b(5)-98++, b(5)-196, b(5), b(6)-98++, b(6), b(6)++, b(6)-98, b(6)-196, b(7), b(7)++, b(7)-98, b(7)-98++, b(7)-196, b(8)++, b(8), b(8)-98, b(8)-98++, b(8)-196++, b(8)-196, b(9), b(9)++, b(9)-98++, b(9)-98, b(9)-196++, b(10), b(10)++, b(10)-98++, b(10)-196++, b(11)++, b(11)-98++, b(11)-196++, b(12)-196++, b(12)++, b(12)-98++
Matched y ions: y(2), y(3), y(3)++, y(4), y(4)++, y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-196++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.820

RTSELEAASSVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RTSELEAASSVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2072: 1412.665599 from(471.895809,3+)
Title: Elution from: 28.071 to 28.071 scan no 2039 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1412.6660
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.019

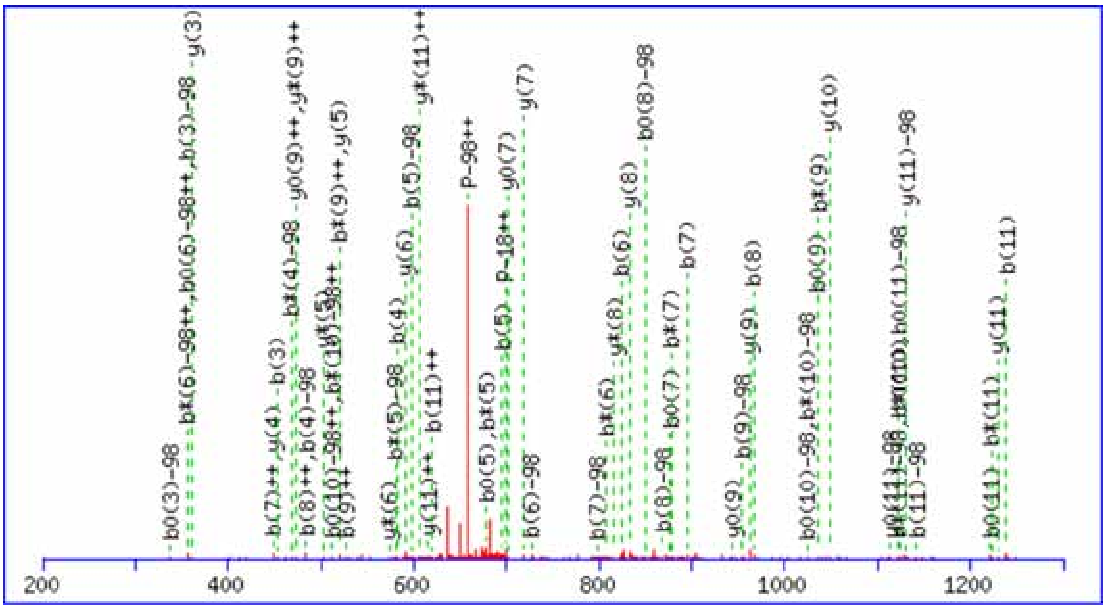
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5), b(5)++, b(6), b(6)++, b(7)++, b(7), b(7)-98++, b(8)++, b(11)++
Matched y ions: y(3), y(4), y(5), y(6)
Precursor origin neutral loss: +

Peptide No.821

RTSELEAASSVR
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of RTSELEAASSVR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2073: 1412.666082 from(707.340317,2+)
Title: Elution from: 28.064 to 28.064 scan no 2038 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1412.6660
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.0022

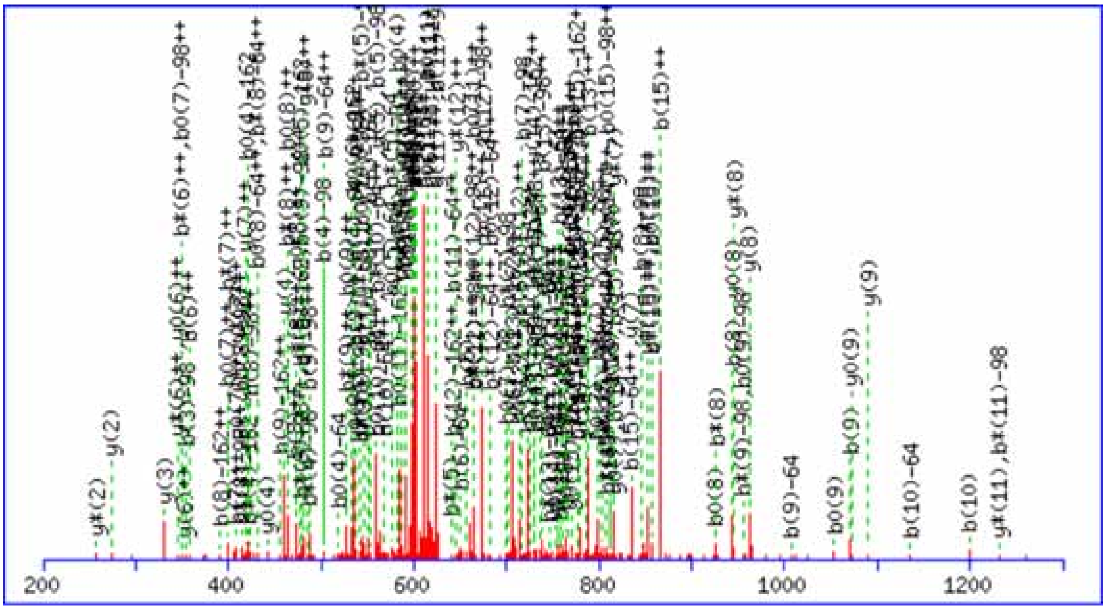
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)++, b(7), b(7)-98, b(8)++, b(8), b(8)-98, b(9)++, b(9)-98, b(11), b(11)-98, b(11)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(11)++
Precursor origin neutral loss: +

Peptide No.822

RTSMGGTQQQFVEGVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RTSMGGTQQQFVEGVR**
Found in **CTNB1_MOUSE**, Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1

Match to Query 5093: 1903.862547 from(635.628125,3+)
Title: Elution from: 31.768 to 31.768 scan no 2548 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1903.8612
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 57 Expect: 0.00011

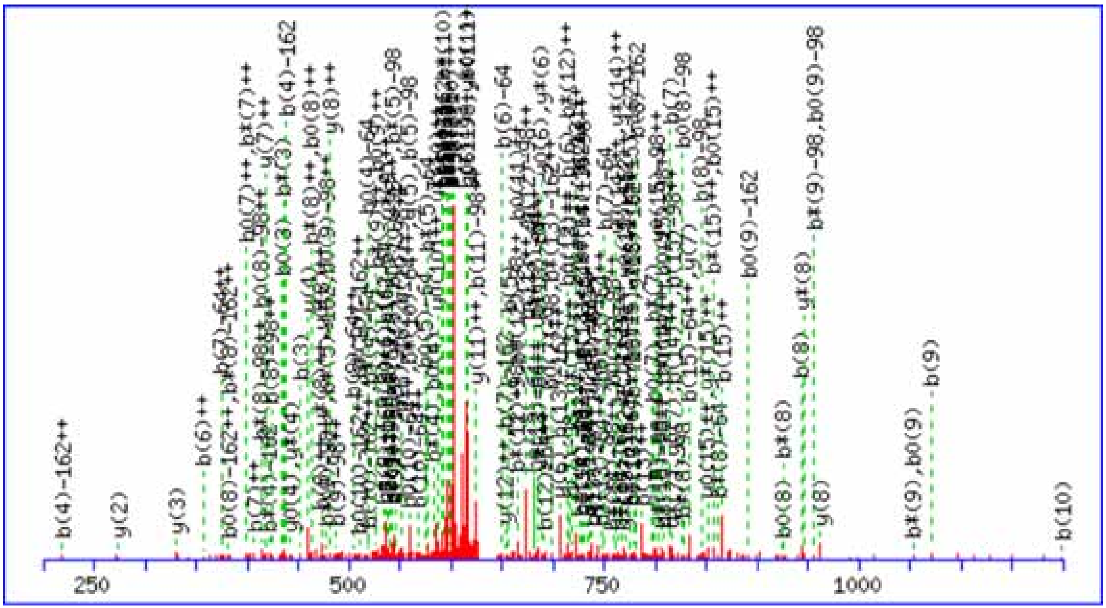
Matched b ions: b(3)-98, b(4), b(4)-98, b(5)-98, b(5), b(6), b(6)++, b(6)-98, b(7)++, b(7), b(7)-98, b(8), b(8)-98++, b(8)++, b(8)-98, b(9)++, b(9), b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(11)++, y(14)-98++, y(14)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.823

RTSMGGTQQQFVEGVR
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of RTSMGGTQQQFVEGVR
Found in CTNB1_MOUSE, Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1

Match to Query 4089: 1903.862919 from(635.628249,3+)
Title: Elution from: 31.706 to 31.706 scan no 2338 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1903.8612
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 37 Expect: 0.011

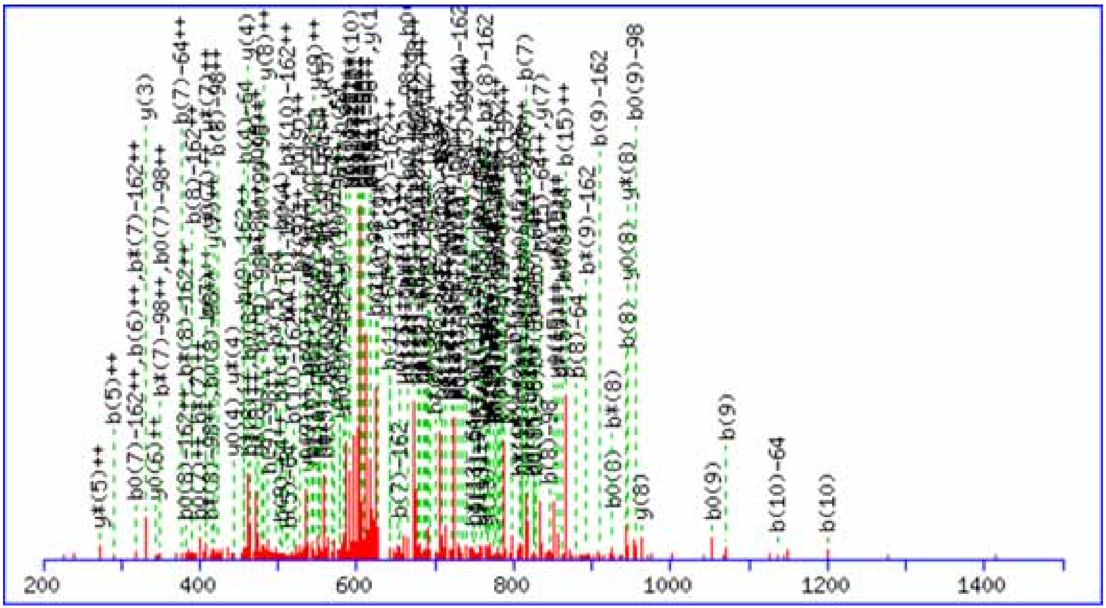
Matched b ions: b(3), b(4), b(5)-98, b(5), b(6)-98, b(6), b(6)++, b(7)++, b(7), b(7)-98, b(8)++, b(8), b(8)-98++, b(8)-98, b(9), b(9)-98++, b(9)++, b(10), b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.824

RTSMGGTQQQFVEGVR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of RTSMGGTQQQFVEGVR
Found in CTNB1_MOUSE, Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1

Match to Query 3925: 1903.861149 from(635.627659,3+)
Title: Elution from: 31.508 to 31.508 scan no 2206 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1903.8612
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 Expect: 6.9e-005

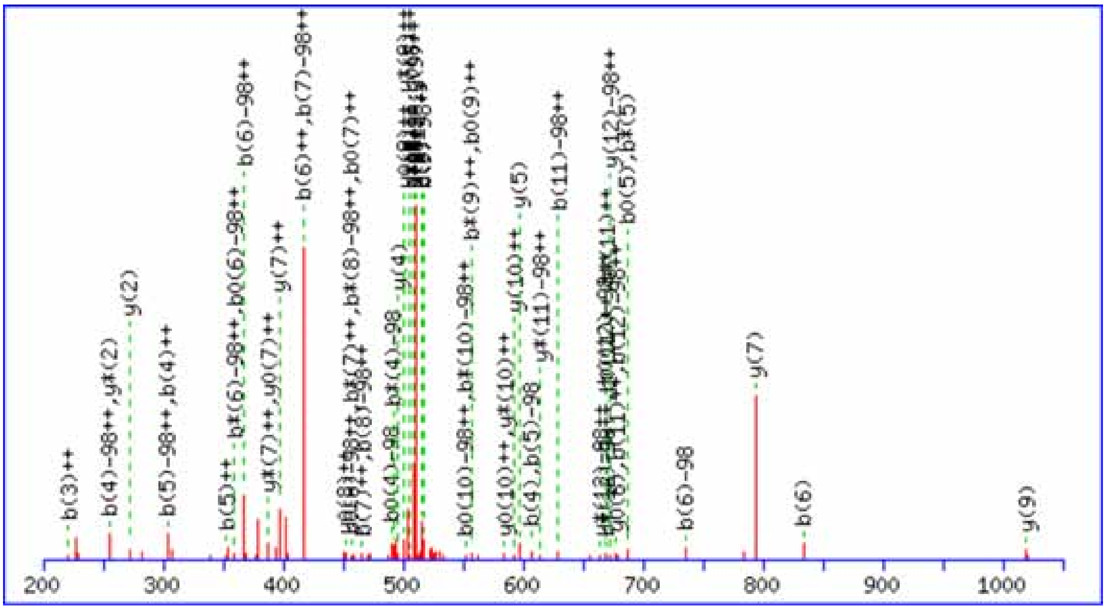
Matched b ions: b(5)++, b(5), b(6)++, b(7)++, b(7), b(8), b(8)++, b(8)-98++, b(8)-98, b(9), b(9)-98++, b(9)++, b(10), b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.825

RVKSPEPVTSHPK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RVKSPEPVTSHPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3267: 1624.871049 from(542.630959,3+)
Title: Elution from: 18.976 to 18.976 scan no 876 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1624.8702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K3 : Dimethyl (K)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
Ions Score: 40 Expect: 0.0049

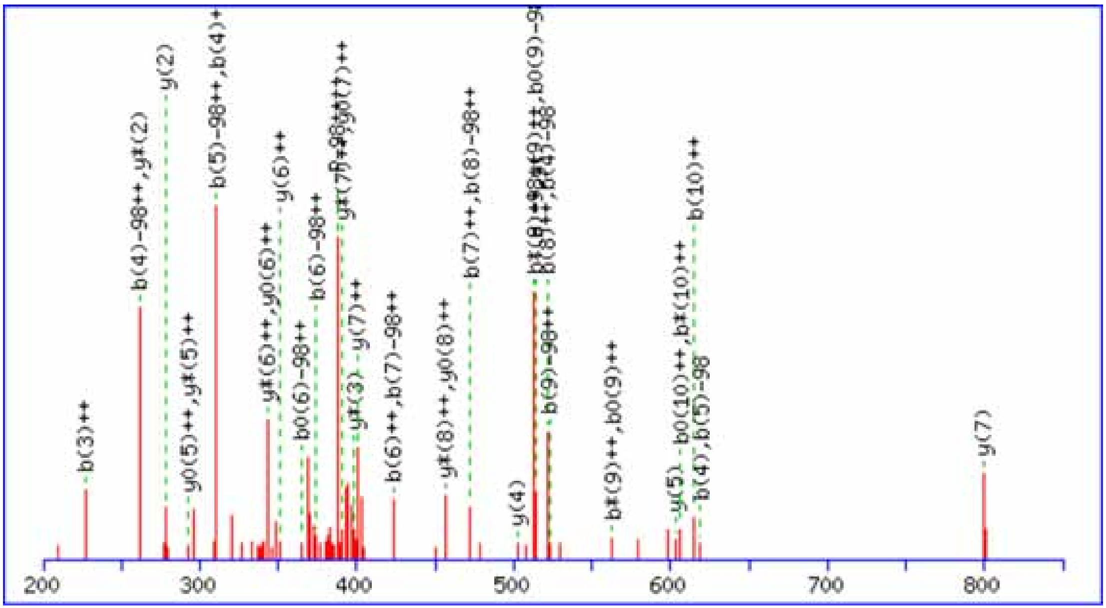
Matched b ions: b(3)++, b(4)++, b(4)-98++, b(4)-98, b(4), b(5)-98++, b(5)-98, b(5)++, b(6)++, b(6), b(6)-98++, b(6)-98, b(7)-98++, b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(11)-98++, b(11)++, b(12)-98++
Matched y ions: y(2), y(4), y(5), y(7), y(7)++, y(9)++, y(9), y(10)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.826

RVKSPEPVTSHPK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of RVKSPEPVTSHPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2648: 1642.965052 from(411.748539,4+)
Title: Elution from: 18.869 to 18.869 scan no 856 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1642.9656
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K3 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 40 Expect: 0.0025

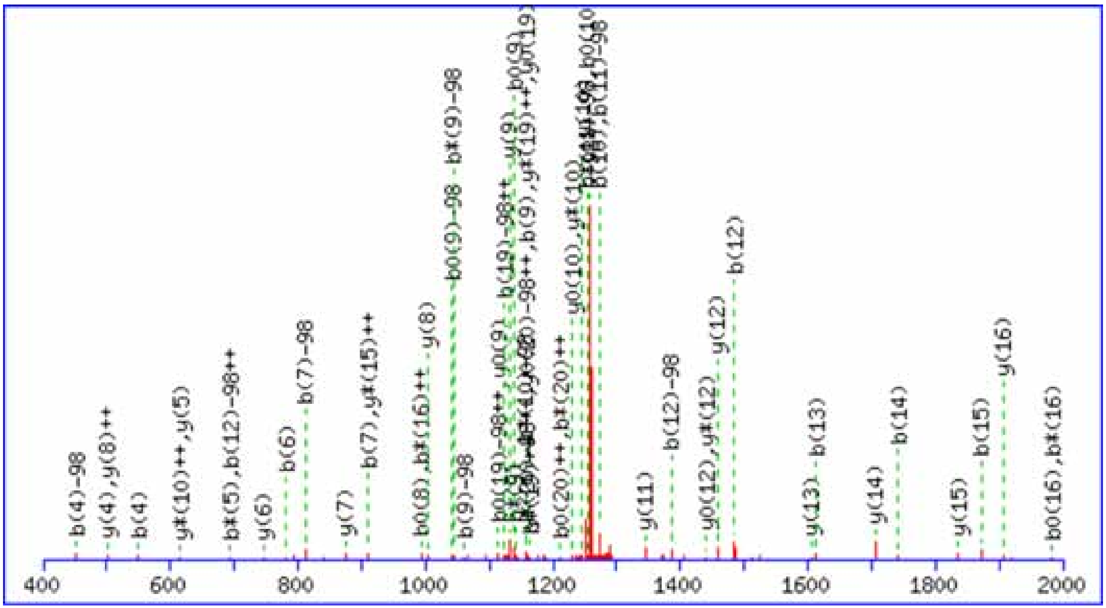
Matched b ions: b(3)++, b(4)-98++, b(4)++, b(4)-98, b(4), b(5)-98++, b(5)-98, b(6)++, b(6)-98++, b(7)-98++, b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(10)++
Matched y ions: y(2), y(4), y(5), y(6)++, y(7), y(7)++, y(9)++
Precursor origin neutral loss: +

Peptide No.827

RVSVCAETFNPDEEEEDNDPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RVSVCAETFNPDEEEEDNDPR
Found in KAP2_MOUSE, cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Mus musculus GN=Prkar2a PE=1 SV=2

Match to Query 7041: 2615.048994 from(1308.531773,2+)
Title: Elution from: 41.946 to 41.946 scan no 3766 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2615.0483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 Expect: 1.6e-006

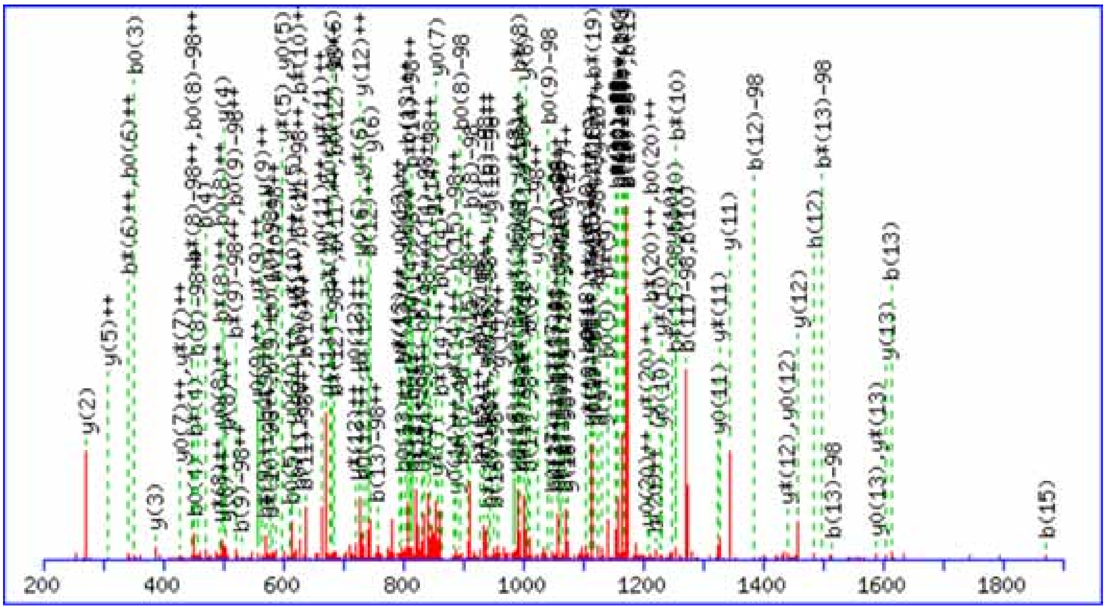
Matched b ions: b(4)-98, b(4), b(6), b(7)-98, b(7), b(9), b(9)-98, b(10), b(11)-98, b(12)-98, b(12), b(12)-98++, b(13), b(14), b(15), b(19)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16)
Precursor origin neutral loss: +

Peptide No.828

RVSVCAETFNPDEEEEDNDPR
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of RVSVCAETFNPDEEEEDNDPR
Found in KAP2_MOUSE, cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Mus musculus GN=Prkar2a PE=1 SV=2

Match to Query 6868: 2615.049630 from(872.690486,3+)
Title: Elution from: 41.693 to 41.693 scan no 3704 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2615.0483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.0015

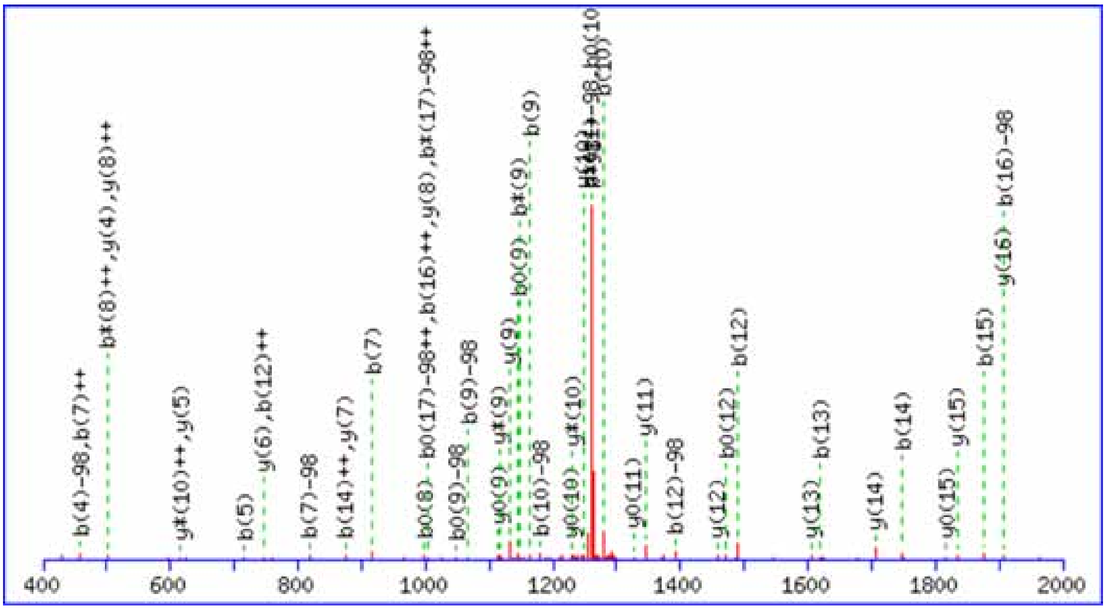
Matched b ions: b(4), b(7), b(8)++, b(8), b(8)-98++, b(8)-98, b(9), b(9)++, b(9)-98++, b(9)-98, b(10)++, b(10), b(10)-98++, b(10)-98, b(11)-98++, b(11)-98, b(11)++, b(12), b(12)++, b(12)-98, b(13), b(13)++, b(13)-98, b(13)-98++, b(14)-98++, b(15), b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)-98++, b(20)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(8), y(8)++, y(9)++, y(9), y(10), y(11)++, y(11), y(12), y(12)++, y(13), y(13)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)-98++
Precursor origin neutral loss:

Peptide No.829

RVSVCAETFNPDEEEEDNDPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RVSVCAETFNPDEEEEDNDPR
Found in KAP2_MOUSE, cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Mus musculus GN=Prkar2a PE=1 SV=2

Match to Query 8395: 2621.081026 from(1311.547789,2+)
Title: Elution from: 41.858 to 41.858 scan no 3898 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2621.0801
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 5.6e-006

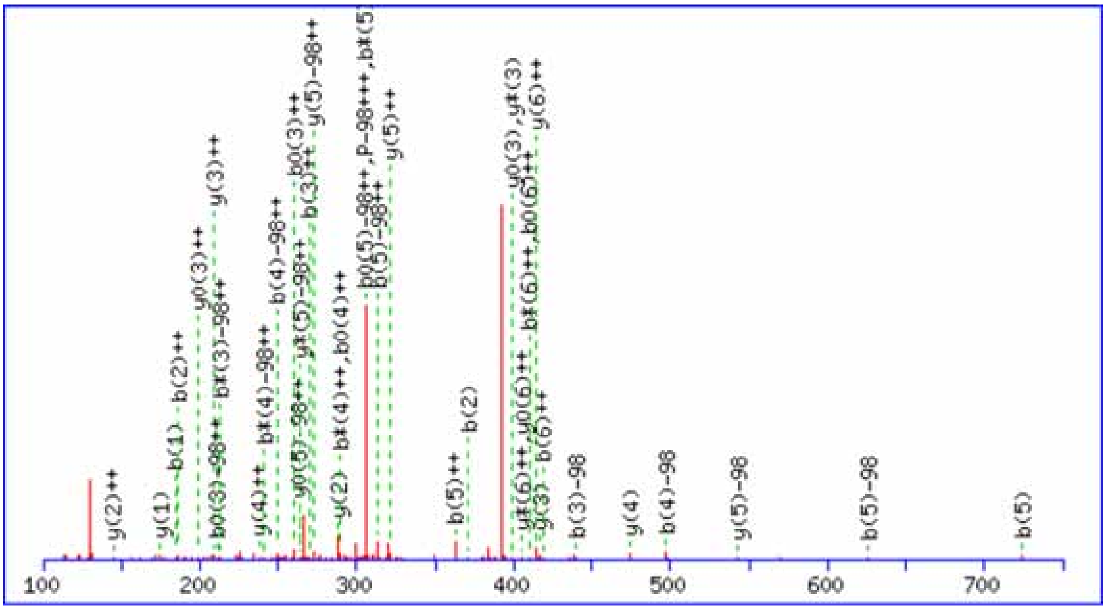
Matched b ions: b(4)-98, b(5), b(7)++, b(7)-98, b(7), b(9)-98, b(9), b(10), b(10)-98, b(12), b(12)++, b(12)-98, b(13), b(14), b(14)++, b(15), b(16)++, b(16)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16)
Precursor origin neutral loss: +

Peptide No.830

RWSGELR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RWSGELR
Found in PLIN5_MOUSE, Perilipin-5 OS=Mus musculus GN=Plin5 PE=1 SV=1

Match to Query 474: 1010.470068 from(337.830632,3+)
Title: Elution from: 29.810 to 29.810 scan no 2118 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1010.4698
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.042

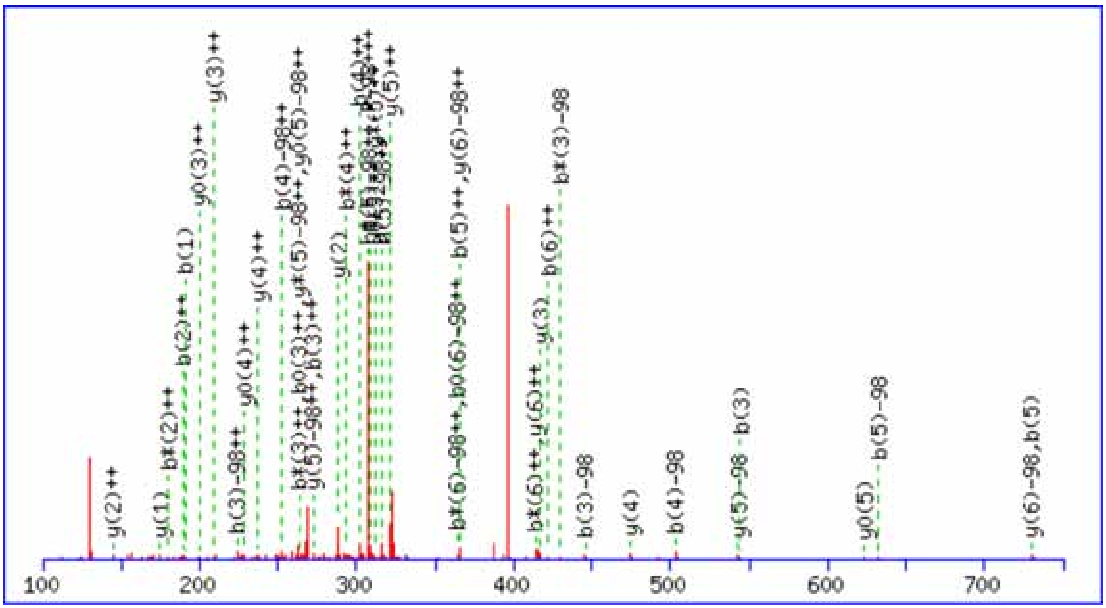
Matched b ions: b(1), b(2)++, b(2), b(3)-98, b(3)++, b(4)-98, b(4)-98++, b(5)-98, b(5), b(5)-98++, b(5)++, b(6)++
Matched y ions: y(1), y(2), y(2)++, y(3), y(3)++, y(4), y(4)++, y(5)-98, y(5)-98++, y(5)++, y(6)++
Precursor origin neutral loss: +

Peptide No.831

RWSGELR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of RWSGELR
Found in PLIN5_MOUSE, Perilipin-5 OS=Mus musculus GN=Plin5 PE=1 SV=1

Match to Query 428: 1016.502492 from(339.841440,3+)
Title: Elution from: 29.751 to 29.751 scan no 2072 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1016.5017
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.02

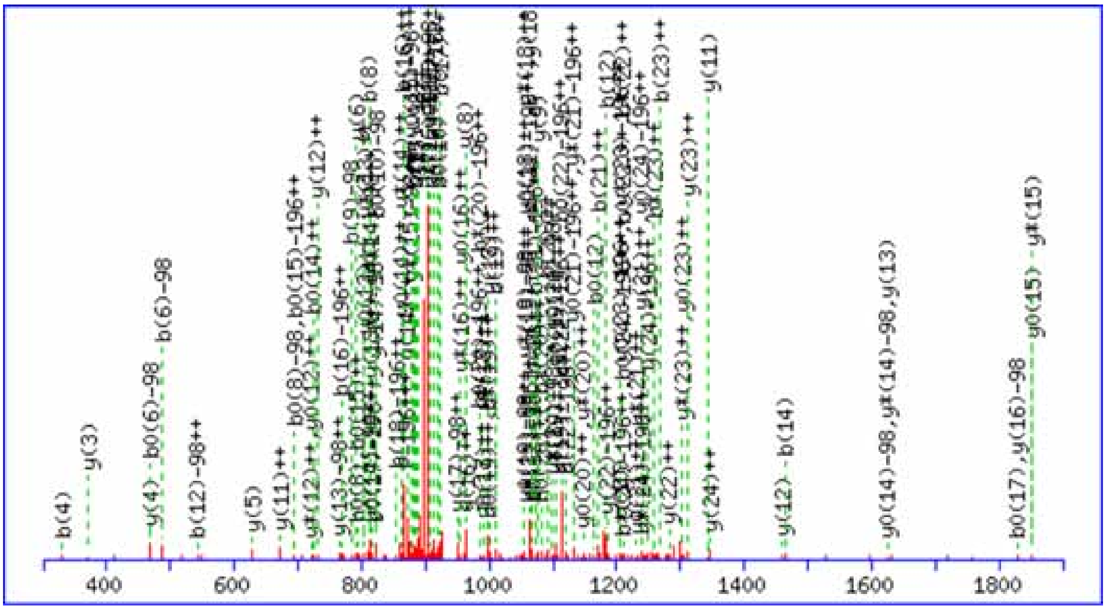
Matched b ions: b(1), b(2)++, b(3), b(3)-98, b(3)-98++, b(3)++, b(4)-98, b(4)++, b(4)-98++, b(5)-98, b(5), b(5)-98++, b(5)++, b(6)++
Matched y ions: y(1), y(2), y(2)++, y(3), y(3)++, y(4), y(4)++, y(5)-98, y(5)++, y(5)-98++, y(6)++, y(6)-98, y(6)-98++
Precursor origin neutral loss: +

Peptide No.832

SAGSSSPEAGEDSDHEDGNYCPPVK
Confirmed sites: @S:13
Ambiguous sites: @S:5orS:6

MS/MS Fragmentation of SAGSSSPEAGEDSDHEDGNYCPPVK
Found in RANB3_MOUSE, Ran-binding protein 3 OS=Mus musculus GN=Ranbp3 PE=1 SV=2

Match to Query 8299: 2807.034132 from(936.685320,3+)
Title: Elution from: 32.969 to 32.969 scan no 2710 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2807.0307
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K25 : Dimethyl (K)
Ions Score: 56 **Expect:** 5.4e-005

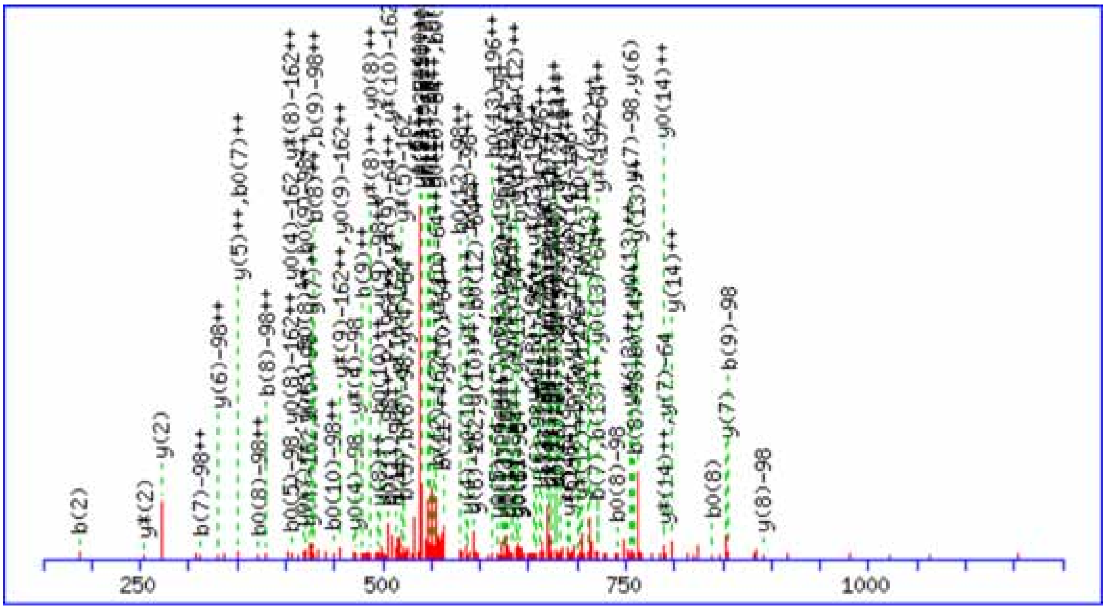
Matched b ions: b(4), b(6)-98, b(8), b(9)-98, b(9), b(11), b(12)-98++, b(12), b(14), b(16)++, b(16)-196++, b(16)-98++, b(17)++, b(17)-98++, b(18)-196++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(21)-196++, b(22)-98++, b(22)-196++, b(23)++, b(24)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(11), y(12)++, y(12), y(13)++, y(13), y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(16)++, y(16)-98, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(19)++, y(19)-98++, y(21)++, y(21)-98++, y(22)-196++, y(22)-98++, y(22)++, y(23)++, y(23)-98++, y(24)-98++, y(24)++, y(24)-196++
Precursor origin neutral loss: +

Peptide No.833

SAPASPTHPGLMSPR
Confirmed sites: @S:5,@S:13
Ambiguous sites:

MS/MS Fragmentation of SAPASPTHPGLMSPR
Found in FOXK1_MOUSE, Forkhead box protein K1 OS=Mus musculus GN=Foxk1 PE=1 SV=2

Match to Query 3780: 1708.706844 from(570.576224,3+)
Title: Elution from: 28.983 to 28.983 scan no 2164 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1708.7045
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.041

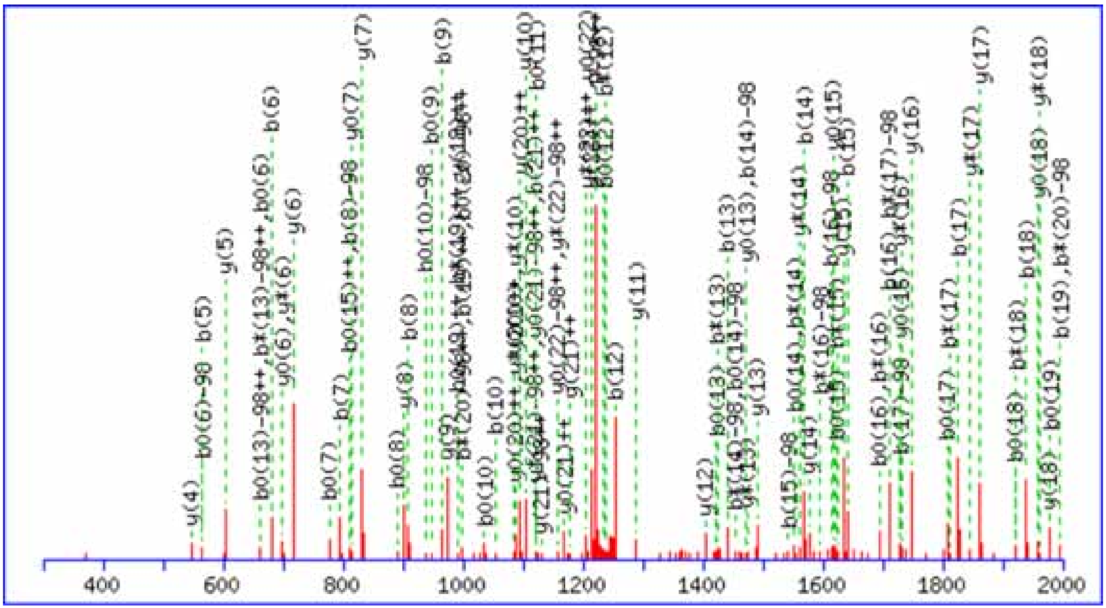
Matched b ions: b(2), b(5)-98, b(5), b(6)-98, b(7)-98++, b(7)-98, b(7), b(8)-98++, b(8)++, b(8)-98, b(9)-98, b(9)-98++, b(9)++, b(10)++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)-196++, b(13)++, b(14)-196++, b(14)-98++
Matched y ions: y(2), y(4), y(5)++, y(5), y(6)-98++, y(6), y(6)-98, y(7), y(7)++, y(7)-98, y(8)-98, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)++, y(14)-98++, y(14)-196++
Precursor origin neutral loss: +

Peptide No.834

SASPDDDLGSSNWEAADLGNEER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SASPDDDLGSSNWEAADLGNEER
Found in SMAP_MOUSE, Small acidic protein OS=Mus musculus GN=Smap PE=1 SV=1

Match to Query 7703: 2542.014850 from(1272.014701,2+)
Title: Elution from: 52.490 to 52.490 scan no 5199 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2542.0133
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 124 Expect: 1.9e-011

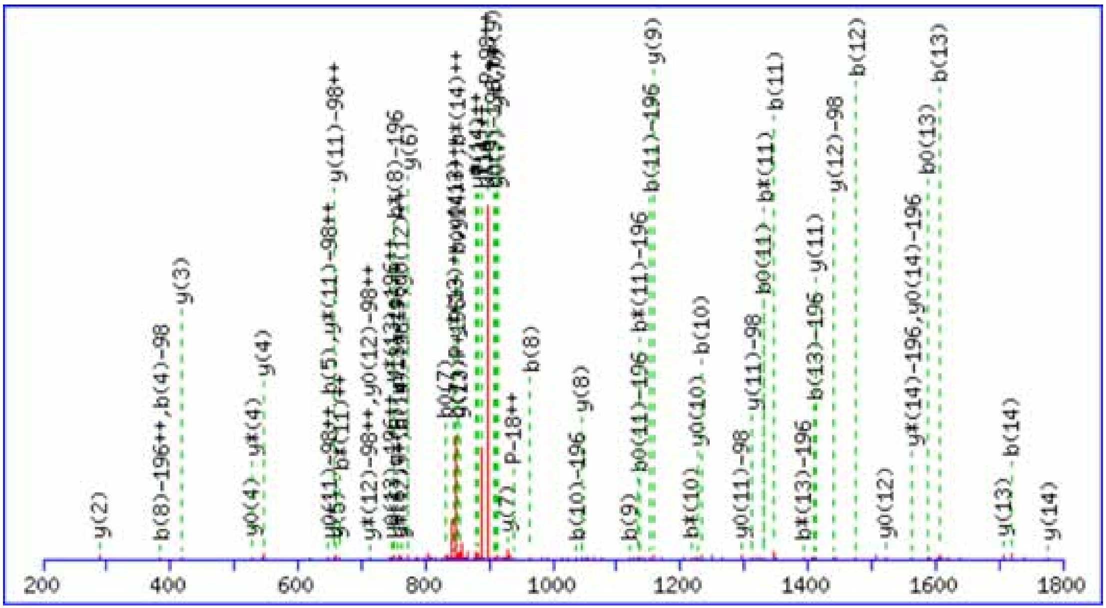
Matched b ions: b(5), b(6), b(7), b(8), b(8)-98, b(9), b(10), b(12), b(13), b(14), b(14)-98, b(15), b(15)-98, b(16), b(16)-98, b(17), b(17)-98, b(18), b(19), b(19)++, b(21)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(18)++, y(20)++, y(21)-98++, y(21)++, y(22)++
Precursor origin neutral loss: +

Peptide No.835

SASQSSLDKLDQELK
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SASQSSLDKLDQELK
Found in JIP4_MOUSE, C-Jun-amino-terminal kinase-interacting protein 4 OS=Mus musculus GN=Spag9 PE=1 SV=2

Match to Query 4343: 1891.858506 from(946.936529,2+)
Title: Elution from: 47.620 to 47.620 scan no 4408 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1891.8580
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K9 : Dimethyl (K)
K15 : Dimethyl (K)
Ions Score: 58 Expect: 9.8e-005

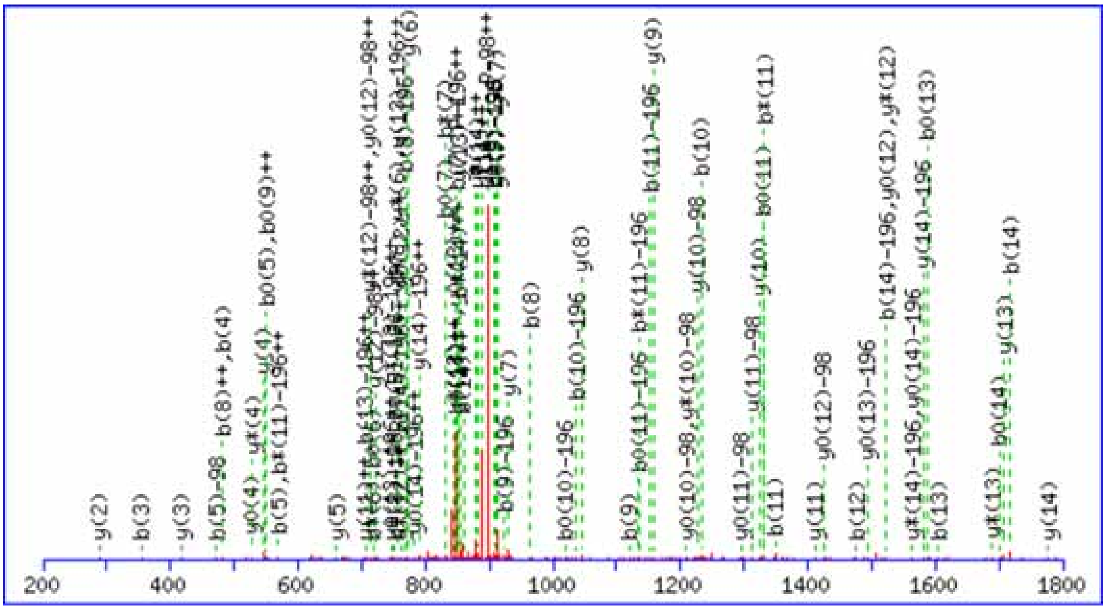
Matched b ions: b(4)-98, b(5), b(7), b(7)-98, b(8)-196++, b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(10)-196, b(11)-98, b(11), b(11)-196, b(12), b(13)-98, b(13), b(13)-196, b(14)-196++, b(14), b(14)-98, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(11)-98++, y(11)-98, y(12)-98, y(13), y(13)-196++, y(13)++, y(13)-98, y(13)-98++, y(14)-98++, y(14)++, y(14)
Precursor origin neutral loss: +

Peptide No.836

SASQSSLDKLDQELK
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of SASQSSLDKLDQELK
Found in JIP4_MOUSE, C-Jun-amino-terminal kinase-interacting protein 4 OS=Mus musculus GN=Spag9 PE=1 SV=2

Match to Query 3841: 1891.859512 from(946.937032,2+)
Title: Elution from: 47.561 to 47.561 scan no 4304 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1891.8580
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K9 : Dimethyl (K)
K15 : Dimethyl (K)
Ions Score: 64 Expect: 2.3e-005

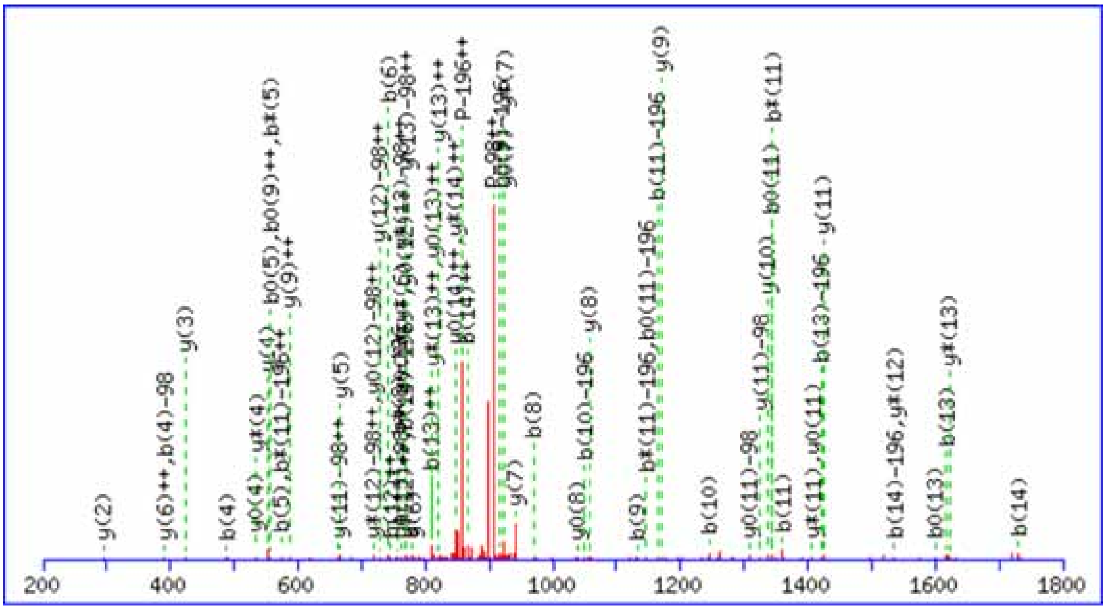
Matched b ions: b(3), b(4), b(5)-98, b(5), b(6)-98, b(7), b(7)-98, b(8)++, b(8)-98, b(8)-196, b(8), b(9)-98, b(9), b(9)-196, b(10), b(10)-98++, b(10)-196, b(10)-98, b(11)-196, b(11)-98, b(11), b(12), b(12)-98, b(13)-98, b(13), b(13)-196++, b(14), b(14)-196++, b(14)-196, b(14)-98, b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(11)++, y(12)-98++, y(13), y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(14), y(14)-98, y(14)-196, y(14)-196++
Precursor origin neutral loss: +

Peptide No.837

SASQSSLDKLDQELK
Confirmed sites: @S:1,@S:6
Ambiguous sites:

MS/MS Fragmentation of SASQSSLDKLDQELK
Found in JIP4_MOUSE, C-Jun-amino-terminal kinase-interacting protein 4 OS=Mus musculus GN=Spag9 PE=1 SV=2

Match to Query 6012: 1909.953740 from(955.984146,2+)
Title: Elution from: 47.411 to 47.411 scan no 4626 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1909.9535
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K9 : Dimethyl:2H(4)13C(2) (K)
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 35 Expect: 0.024

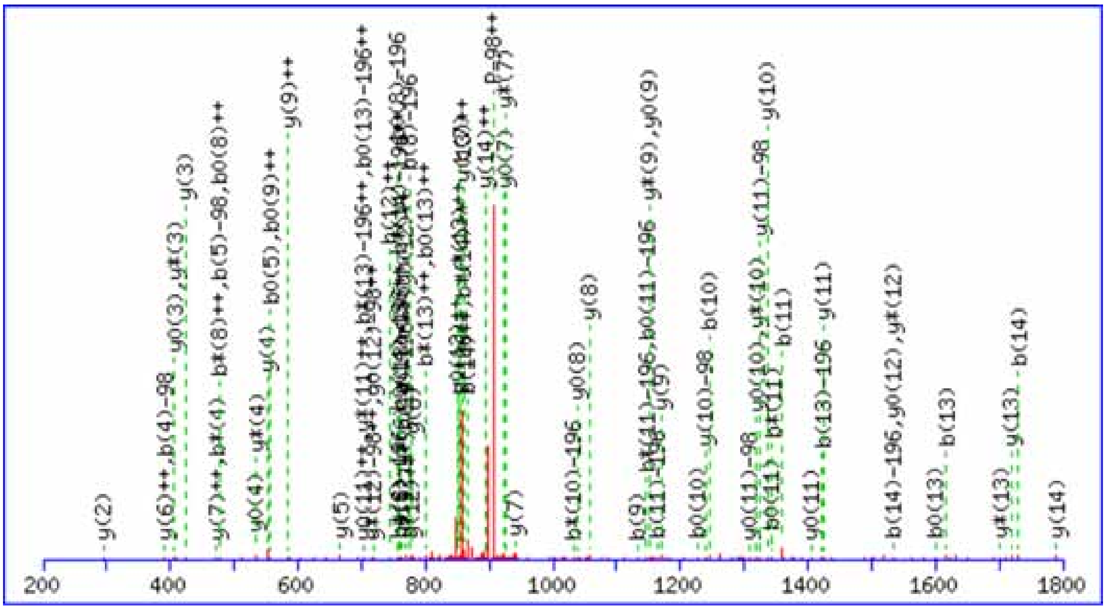
Matched b ions: b(4), b(4)-98, b(5), b(6), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10)-196, b(10), b(10)-98, b(10)-98++, b(11)-98, b(11), b(11)-196, b(12)-98, b(12)++, b(13), b(13)-98, b(13)-196, b(13)++, b(14)-196++, b(14), b(14)-98, b(14)-196, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(9)++, y(10), y(11), y(11)-98++, y(11)-98, y(12)-98++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.838

SASQSSLDKLDQELK
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of SASQSSLDKLDQELK
Found in JIP4_MOUSE, C-Jun-amino-terminal kinase-interacting protein 4 OS=Mus musculus GN=Spag9 PE=1 SV=2

Match to Query 4299: 1909.954108 from(955.984330,2+)
Title: Elution from: 47.550 to 47.550 scan no 4386 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1909.9535
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K9 : Dimethyl:2H(4)13C(2) (K)
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 56 Expect: 0.00018

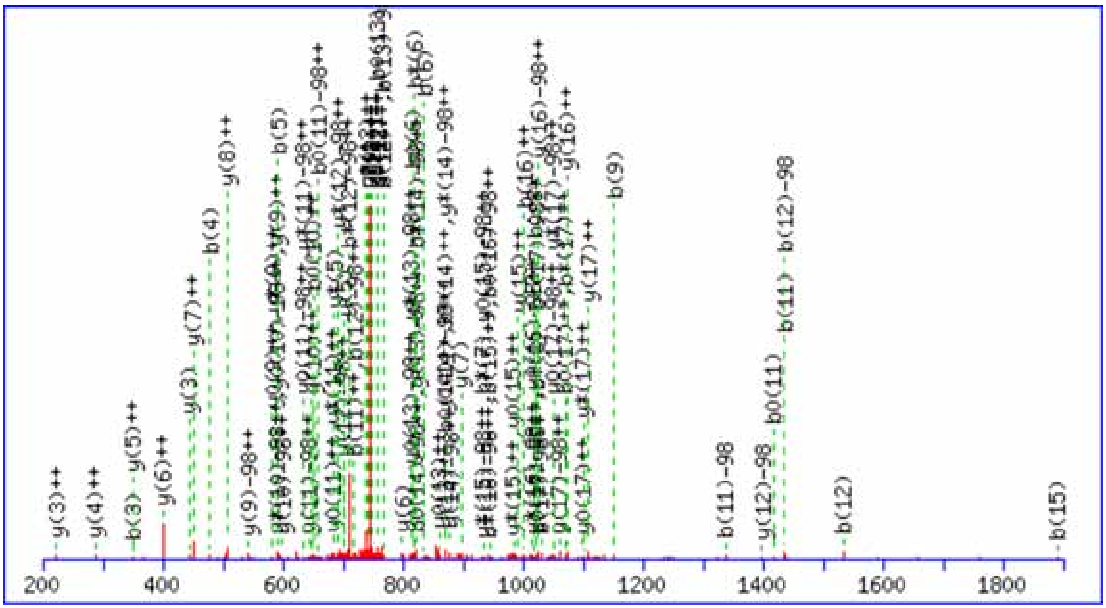
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(7)-98, b(7), b(8)-98, b(8)-196, b(9), b(9)-98, b(10), b(10)-98, b(11)-98, b(11), b(11)-196, b(12)++, b(12)-98, b(13)-98, b(13), b(13)-196, b(14)-196++, b(14)-98, b(14), b(14)-196, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(9), y(9)++, y(10)-98, y(10), y(11), y(11)-98, y(12)++, y(13), y(13)-98, y(13)-196++, y(13)++, y(13)-98++, y(14), y(14)-98, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.839

SAYQDYDSDSDVPEELKR
Confirmed sites: @Y:6,@S:10
Ambiguous sites:

MS/MS Fragmentation of SAYQDYDSDSDVPEELKR
Found in CC132_MOUSE, Coiled-coil domain-containing protein 132 OS=Mus musculus GN=Ccdc132 PE=1 SV=2

Match to Query 7134: 2331.919971 from(778.313933,3+)
Title: Elution from: 45.272 to 45.272 scan no 4335 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2331.9185
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y6 : Phospho (Y)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K17 : Dimethyl (K)
Ions Score: 35 Expect: 0.011

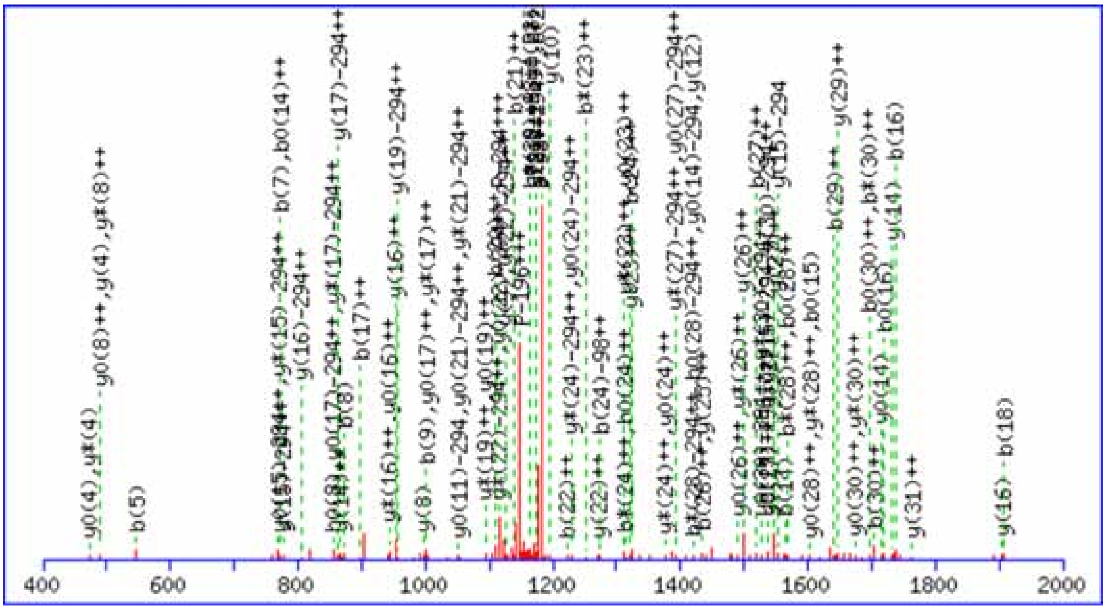
Matched b ions: b(3), b(4), b(5), b(6), b(9), b(11)-98, b(11), b(11)++, b(12)-98, b(12), b(12)-98++, b(12)++, b(13)-98++, b(15), b(15)++, b(16)++, b(17)-98++
Matched y ions: y(3)++, y(3), y(4)++, y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(9)++, y(9)-98++, y(10)-98++, y(10)++, y(11)-98++, y(12)-98, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.840

SCAAEPEVEPEAHEGDGDKKGSAEGSSDEEGK
Confirmed sites: @S:22,@S:26,@S:27
Ambiguous sites:

MS/MS Fragmentation of SCAAEPEVEPEAHEGDGDKKGSAEGSSDEEGK
Found in HDGF_MOUSE, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 8837: 3639.390354 from(1214.137394,3+)
Title: Elution from: 28.772 to 28.772 scan no 2135 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3639.3885
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K19 : Dimethyl (K)
K20 : Dimethyl (K)
S22 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S26 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S27 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K32 : Dimethyl (K)
Ions Score: 34 Expect: 0.017

Matched b ions: b(5), b(7), b(8), b(9), b(14), b(16), b(17)++, b(18), b(20)++, b(21)++, b(22)-98++, b(22)++, b(24)++, b(24)-98++, b(26)-98++, b(26)++, b(27)-196++, b(27)++, b(28)-196++, b(28)-98++, b(29)++, b(29)-98++, b(30)++, b(30)-98++, b(31)-98++
Matched y ions: y(4), y(8), y(8)-98, y(9), y(10), y(11)-196, y(12)-98, y(12), y(13)-98, y(14)-196++, y(14)-98, y(14)-98++, y(14)++, y(14), y(14)-196, y(15)-294++, y(15)-294, y(16)-196++, y(16)-98++, y(16)++, y(16), y(16)-294++, y(17)-294++, y(18)-98++, y(18)-196++, y(19)-98++, y(19)-294++, y(20)-98++, y(20)++, y(21)-196++, y(22)-196++, y(22)-98++, y(22)++, y(22)-294++, y(23)++, y(23)-294++, y(23)-196++, y(23)-98++, y(24)-98++, y(25)-98++, y(25)++, y(25)-196++, y(26)-98++, y(26)++, y(27)-196++, y(27)-98++, y(27)++, y(28)-98++, y(29)++, y(30)-98++, y(30)-294++, y(31)-196++, y(31)-98++, y(31)++
Precursor origin neutral loss: +

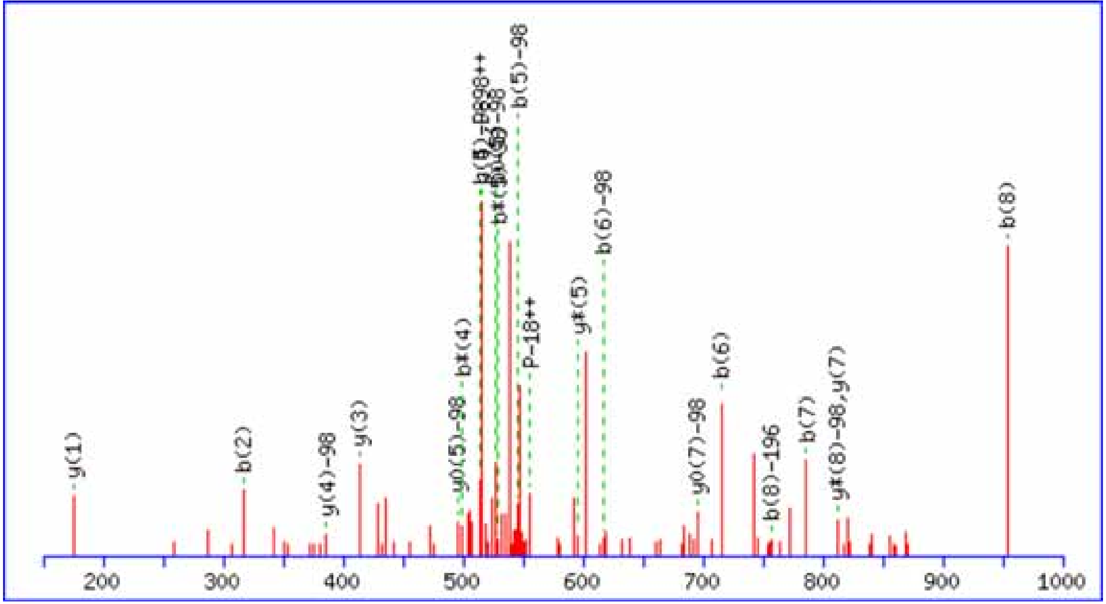
Peptide No.841

SDAKKAASK
Confirmed sites: @S:1,@S:8
Ambiguous sites:

MS/MS Fragmentation of SDAKKAASK
Found in CHID1_MOUSE, Chitinase domain-containing protein 1 OS=Mus musculus GN=Chid1 PE=2

SV=1

Match to Query 698: 1126.524608 from(564.269580,2+)
Title: Elution from: 64.023 to 64.023 scan no 6022 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1126.5248
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K9 : Dimethyl (K)
Ions Score: 42 Expect: 0.0017

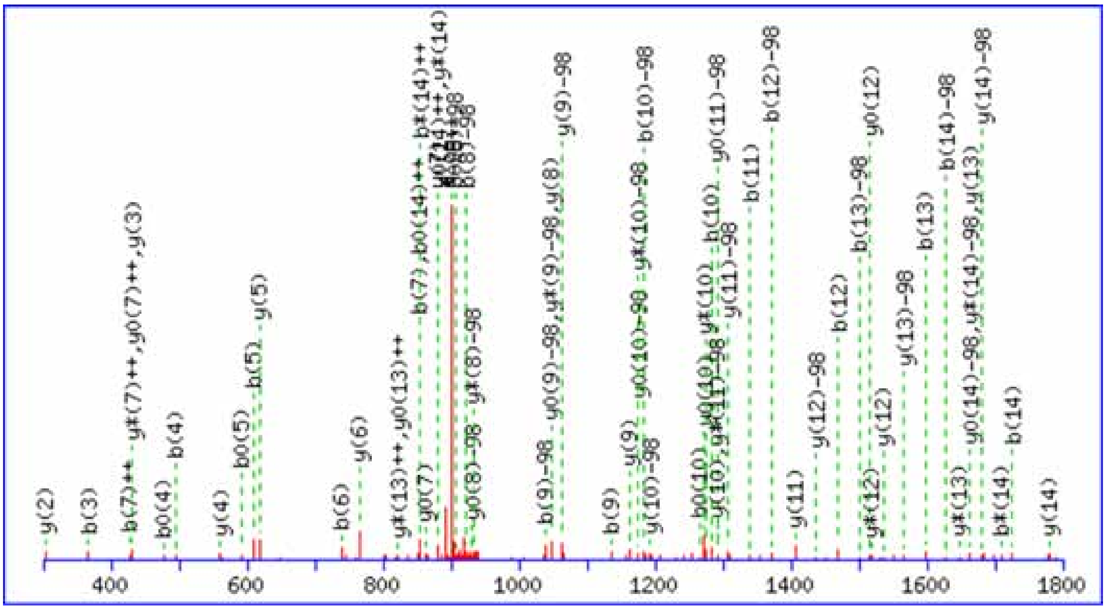
Matched b ions: b(2), b(4), b(5)-98, b(6), b(6)-98, b(7), b(8), b(8)-196
Matched y ions: y(1), y(3), y(4)-98, y(5)-98, y(7)
Precursor origin neutral loss: +

Peptide No.842

SDEEDEDSDFGEEQR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SDEEDEDSDFGEEQR
Found in GPAT1_MOUSE, Glycerol-3-phosphate acyltransferase 1, mitochondrial OS=Mus musculus GN=Gpam PE=1 SV=1

Match to Query 4062: 1899.674820 from(950.844686,2+)
Title: Elution from: 30.947 to 30.947 scan no 2244 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1899.6743
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 Expect: 2.1e-007

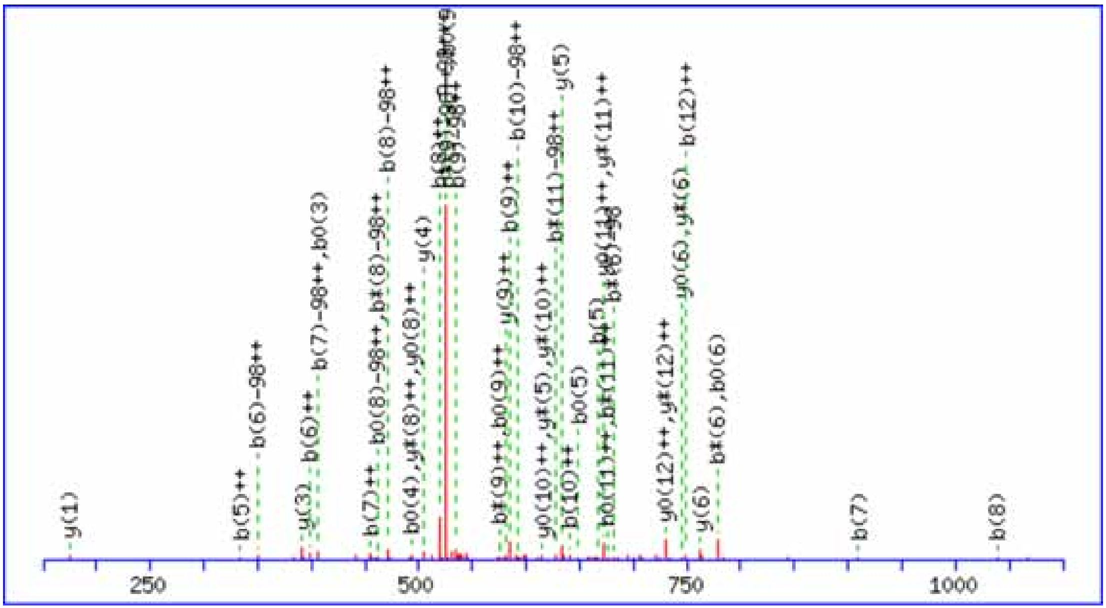
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11), b(12)-98, b(12), b(13), b(13)-98, b(14), b(14)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10)-98, y(10), y(11)-98, y(11), y(12)-98, y(12), y(13), y(13)-98, y(14), y(14)-98
Precursor origin neutral loss: +

Peptide No.843

SDLSRELEEISER
Confirmed sites:
Ambiguous sites: @S:1orS:4

MS/MS Fragmentation of SDLSRELEEISER
Found in MYH7_MOUSE, Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1

Match to Query 3545: 1669.757577 from(557.593135,3+)
Title: Elution from: 55.404 to 55.404 scan no 5497 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1669.7560
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.04

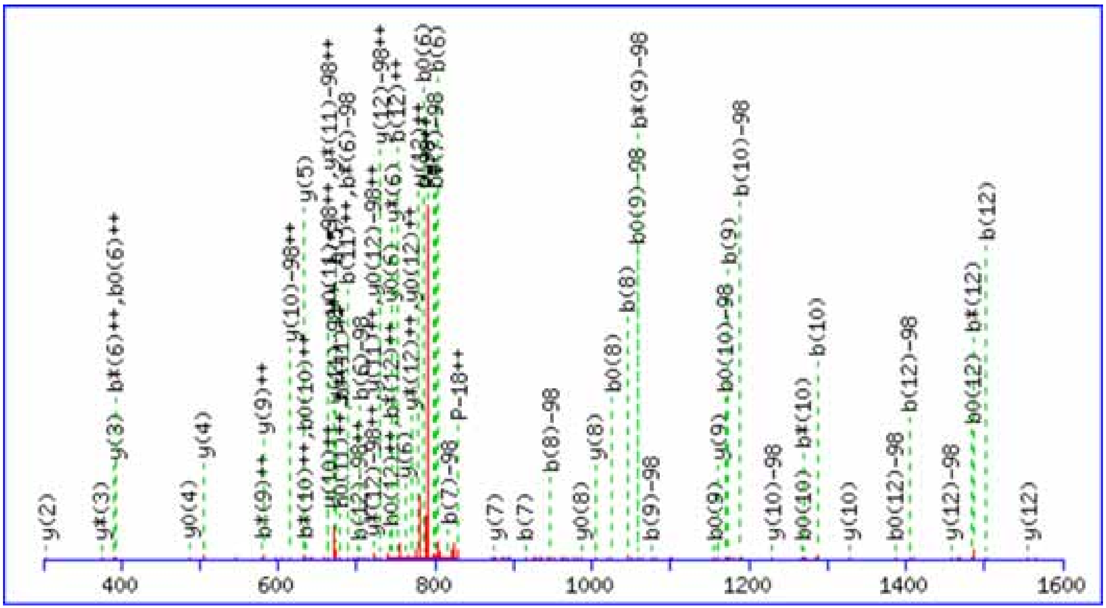
Matched b ions: b(5)++, b(5), b(6)-98++, b(6)++, b(7), b(7)-98++, b(7)++, b(8), b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(12)++
Matched y ions: y(1), y(3), y(4), y(5), y(6), y(9)++
Precursor origin neutral loss: +

Peptide No.844

SDLSRELEEISER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SDLSRELEEISER
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 3095: 1675.788832 from(838.901692,2+)
Title: Elution from: 55.235 to 55.235 scan no 5287 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1675.7878
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.048

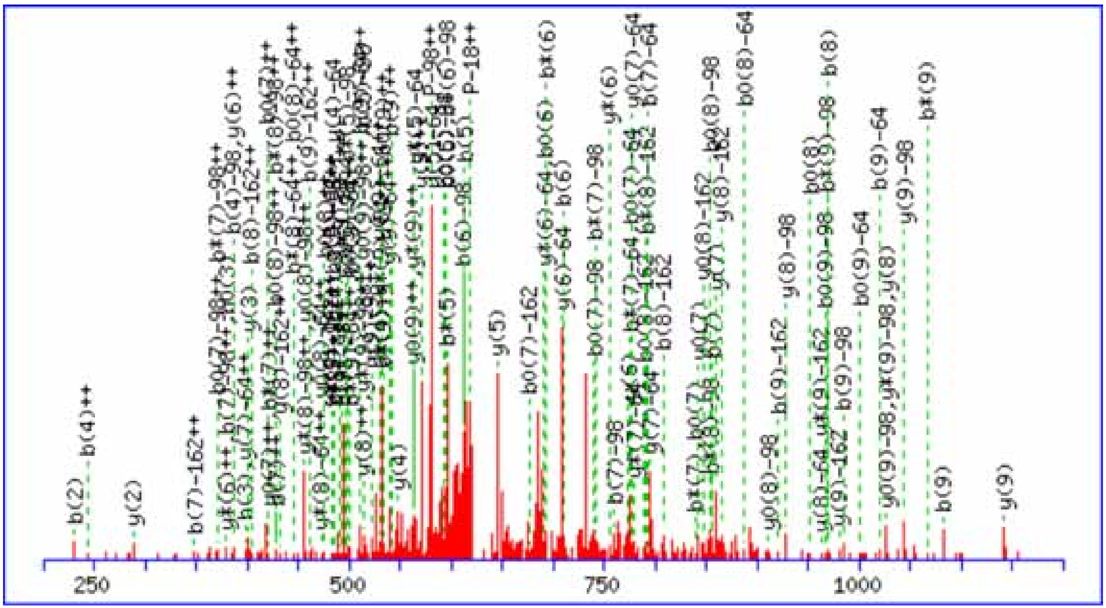
Matched b ions: b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11)++, b(12)-98, b(12), b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)-98, y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(12), y(12)-98, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.845

SDSSQPMLLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SDSSQPMLLR
Found in DMD_MOUSE, Dystrophin OS=Mus musculus GN=Dmd PE=1 SV=2

Match to Query 1079: 1256.547170 from(629.280861,2+)
Title: Elution from: 34.032 to 34.032 scan no 2650 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1256.5472
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 33 Expect: 0.0095

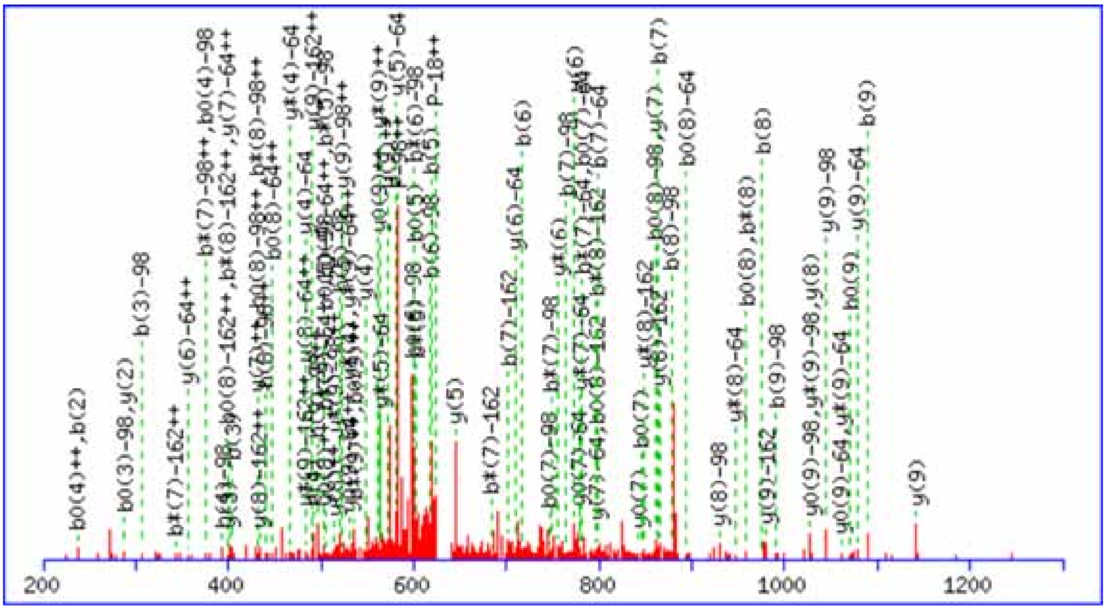
Matched b ions: b(2), b(3), b(4)-98, b(4)++, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98++, b(7), b(7)-98, b(7)++, b(8), b(8)++, b(9)-98, b(9), b(9)-98++, b(9)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(8)-98, y(8)++, y(9)-98, y(9), y(9)++, y(9)-98++
Precursor origin neutral loss: +

Peptide No.846

SDSSQPMLLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SDSSQPMLLR
Found in DMD_MOUSE, Dystrophin OS=Mus musculus GN=Dmd PE=1 SV=2

Match to Query 1300: 1262.578936 from(632.296744,2+)
Title: Elution from: 34.146 to 34.146 scan no 2703 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1262.5790
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 29 Expect: 0.035

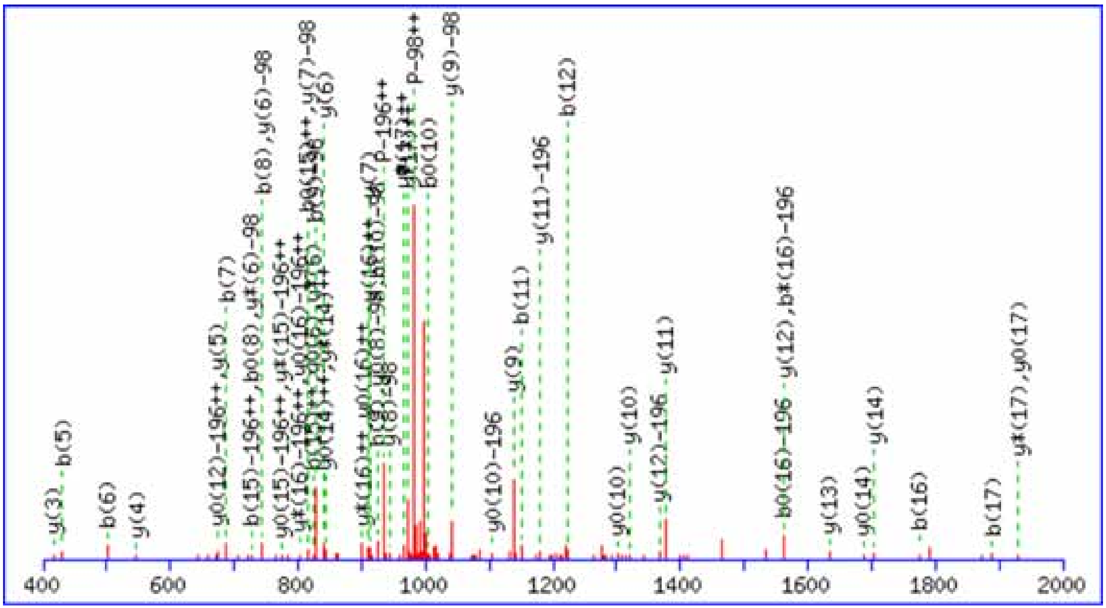
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98++, b(8)-98, b(9)-98++, b(9), b(9)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)-98, y(8), y(8)++, y(9)-98, y(9), y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.847

SEGGAAWGTPEASQEELR
Confirmed sites: @T:9,@S:13
Ambiguous sites:

MS/MS Fragmentation of SEGGAAWGTPEASQEELR
Found in SPEG_MOUSE, Striated muscle-specific serine/threonine-protein kinase OS=Mus musculus GN=Speg PE=1 SV=2

Match to Query 5940: 2061.808208 from(1031.911380,2+)
Title: Elution from: 45.654 to 45.654 scan no 4380 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2061.8082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 Expect: 2.5e-005

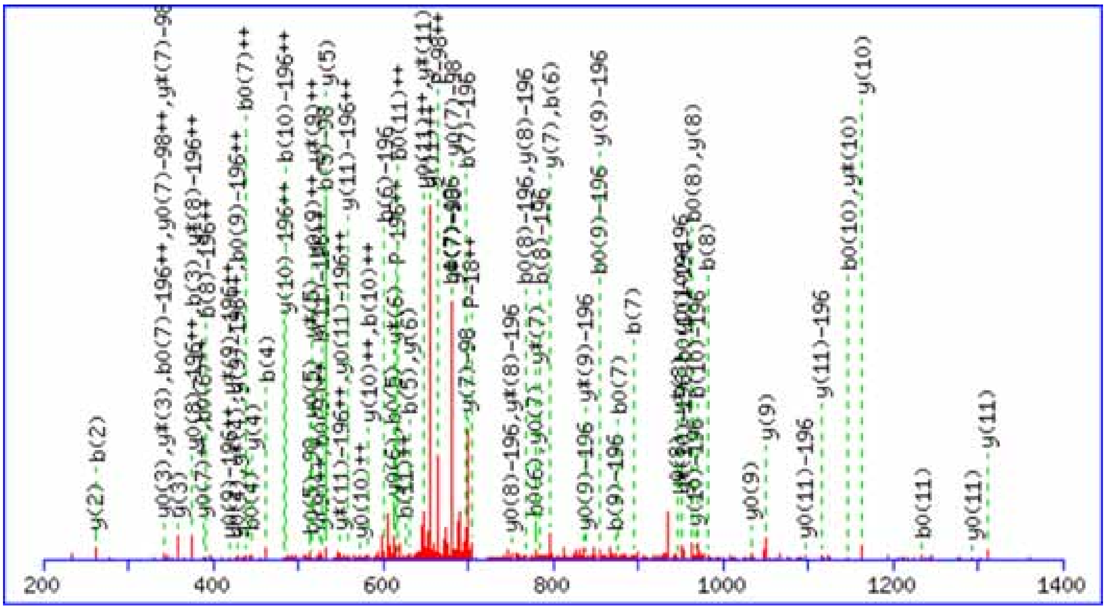
Matched b ions: b(5), b(6), b(7), b(8), b(9)-98, b(9), b(10)-98, b(11), b(12), b(13)-98, b(15)-98++, b(15)-196++, b(15)++, b(16), b(17)-98, b(17)
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(7), y(8)-98, y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)-98, y(11)-196, y(12)-98, y(12), y(12)-196, y(13), y(13)-98, y(14), y(16)++, y(16)-98++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.848

SFISSSPSSPSR
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of SFISSSPSSPSR
Found in SRBS2_MOUSE, Sorbin and SH3 domain-containing protein 2 OS=Mus musculus GN=Sorbs2 PE=1 SV=2

Match to Query 1871: 1425.559834 from(713.787193,2+)
Title: Elution from: 36.175 to 36.175 scan no 2950 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1425.5578
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.0073

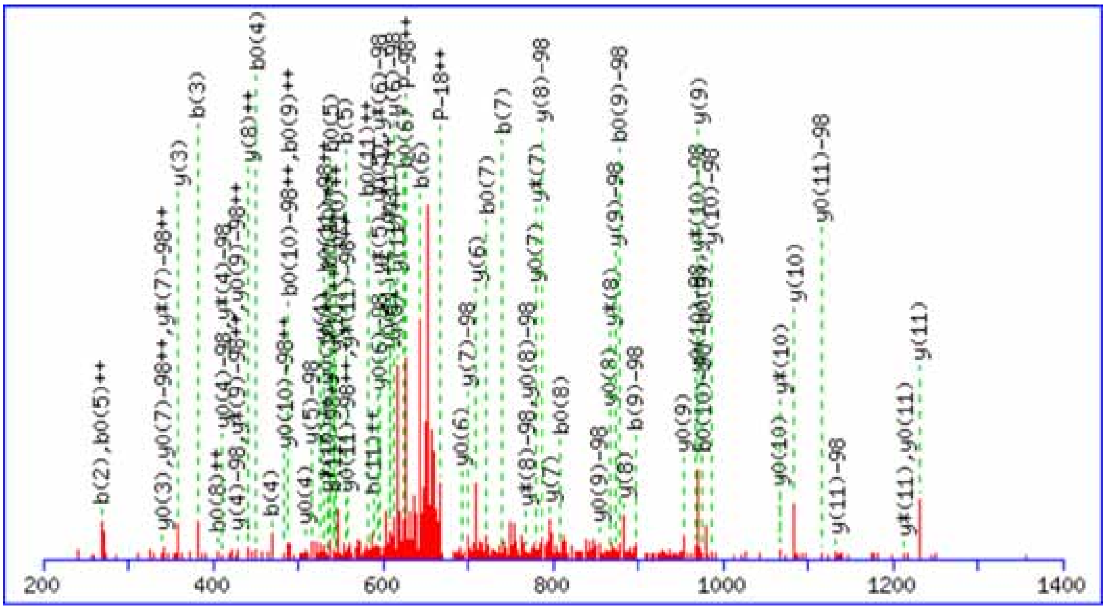
Matched b ions: b(2), b(3), b(4), b(5)-98, b(5), b(6), b(6)-98, b(6)-196, b(7)-98++, b(7)-196, b(7), b(8)-196++, b(8)-196, b(8)-98, b(8), b(9)-98, b(9)-98++, b(9)-196, b(10)-196, b(10)-98, b(10)-196++, b(10)-98++, b(10)++, b(11)-196++, b(11)-98++, b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8)-98, y(8), y(8)-98++, y(8)-196, y(9), y(9)++, y(9)-196++, y(9)-98, y(9)-196, y(10), y(10)-98, y(10)-196++, y(10)-98++, y(10)++, y(10)-196, y(11)-98++, y(11)++, y(11), y(11)-98, y(11)-196, y(11)-196++
Precursor origin neutral loss: +

Peptide No.849

SFISSSPSSPSR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SFISSSPSSPSR
Found in SRBS2_MOUSE, Sorbin and SH3 domain-containing protein 2 OS=Mus musculus GN=Sorbs2 PE=1 SV=2

Match to Query 2513: 1351.624532 from(676.819542,2+)
Title: Elution from: 31.795 to 31.795 scan no 2470 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1351.6233
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.024

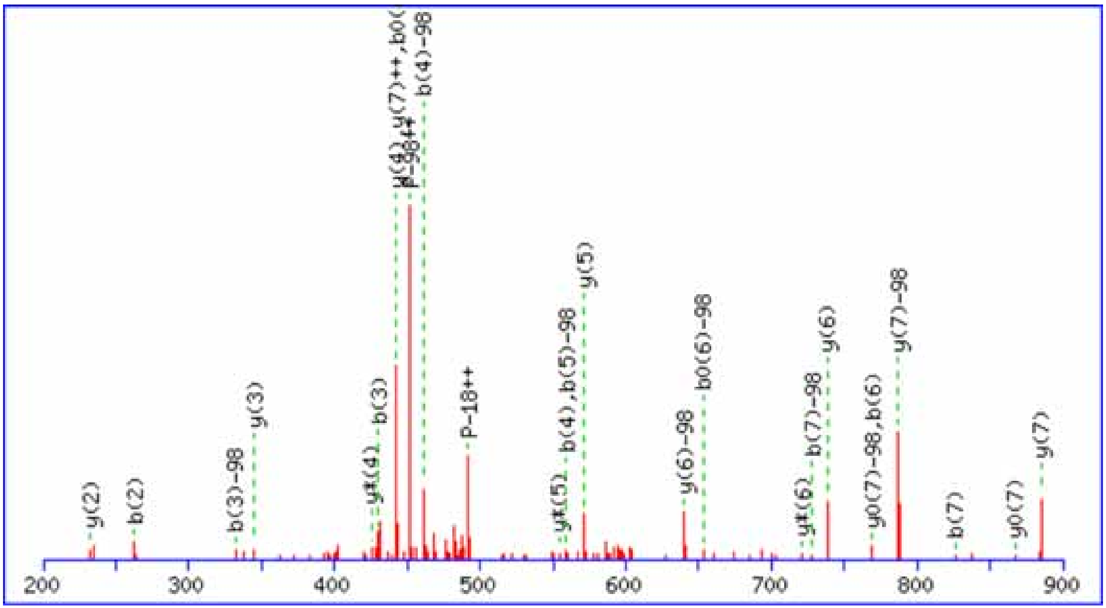
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(9)-98, b(10)++, b(11)-98++, b(11)++
Matched y ions: y(3), y(4)-98, y(4), y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(8)++, y(9), y(9)-98, y(10), y(10)-98, y(10)++, y(11), y(11)-98, y(11)++
Precursor origin neutral loss: +

Peptide No.850

SFSEPLGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SFSEPLGR
Found in MLF1_MOUSE, Myeloid leukemia factor 1 OS=Mus musculus GN=Mlf1 PE=1 SV=1

Match to Query 458: 999.442634 from(500.728593,2+)
Title: Elution from: 40.415 to 40.415 scan no 3721 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 999.4426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.0055

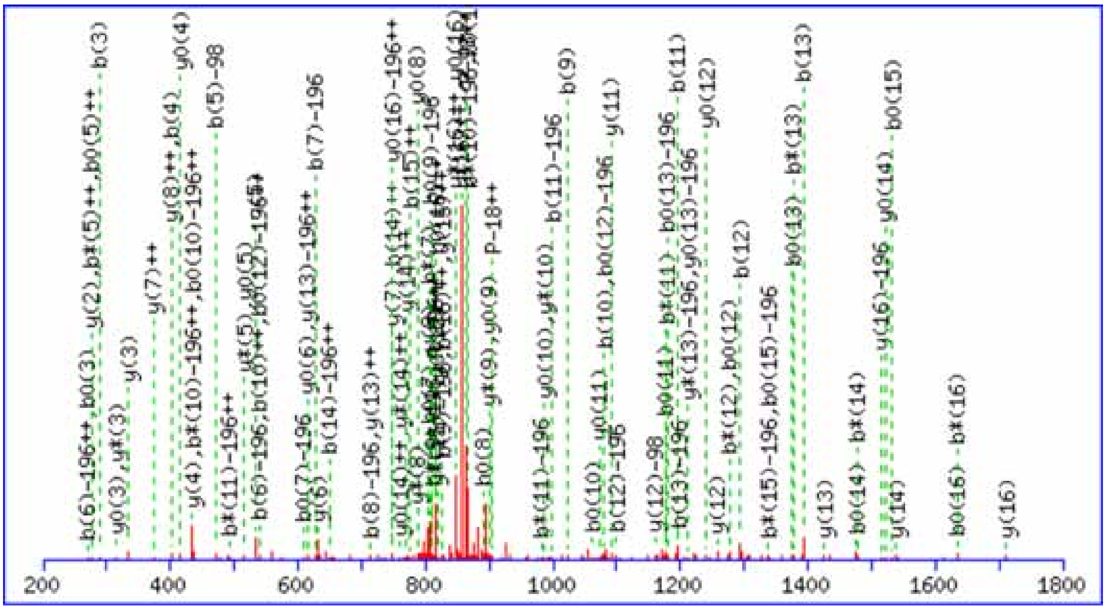
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(6), b(7), b(7)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(7), y(7)++
Precursor origin neutral loss: +

Peptide No.851

SGDNSSSSLGDVVTGTR
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of SGDNSSSSLGDVVTGTR
Found in CACB1_MOUSE, Voltage-dependent L-type calcium channel subunit beta-1 OS=Mus musculus GN=Cacnb1 PE=1 SV=1

Match to Query 5196: 1825.713812 from(913.864182,2+)
Title: Elution from: 42.484 to 42.484 scan no 3985 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1825.7132
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 **Expect:** 2.2e-006

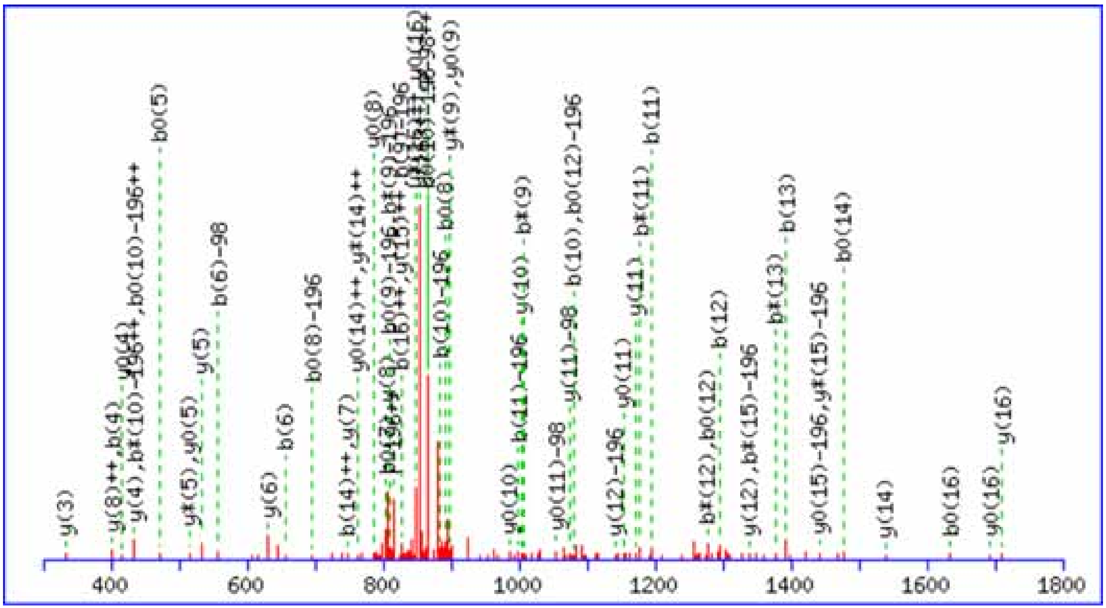
Matched b ions: b(3), b(4), b(5)-98, b(6)-196, b(6)-196++, b(7)-98, b(7)-196, b(8)-196, b(8)-98, b(9), b(9)-98, b(9)-196, b(10), b(10)++, b(10)-98, b(11), b(11)-196, b(11)-98, b(12), b(12)-98, b(12)-196, b(13), b(13)-98, b(13)-196, b(14)++, b(14)-196++, b(15)++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(11), y(12), y(12)-98, y(13)++, y(13)-196++, y(13), y(13)-98, y(14), y(14)++, y(15)++, y(16)++, y(16), y(16)-98, y(16)-98++, y(16)-196
Precursor origin neutral loss: +

Peptide No.852

SGDNSSSSLGDVVTGTR
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of SGDNSSSSLGDVVTGTR
Found in CACB1_MOUSE, Voltage-dependent L-type calcium channel subunit beta-1 OS=Mus musculus GN=Cacnb1 PE=1 SV=1

Match to Query 3827: 1825.713966 from(913.864259,2+)
Title: Elution from: 42.450 to 42.450 scan no 3809 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1825.7132
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00022

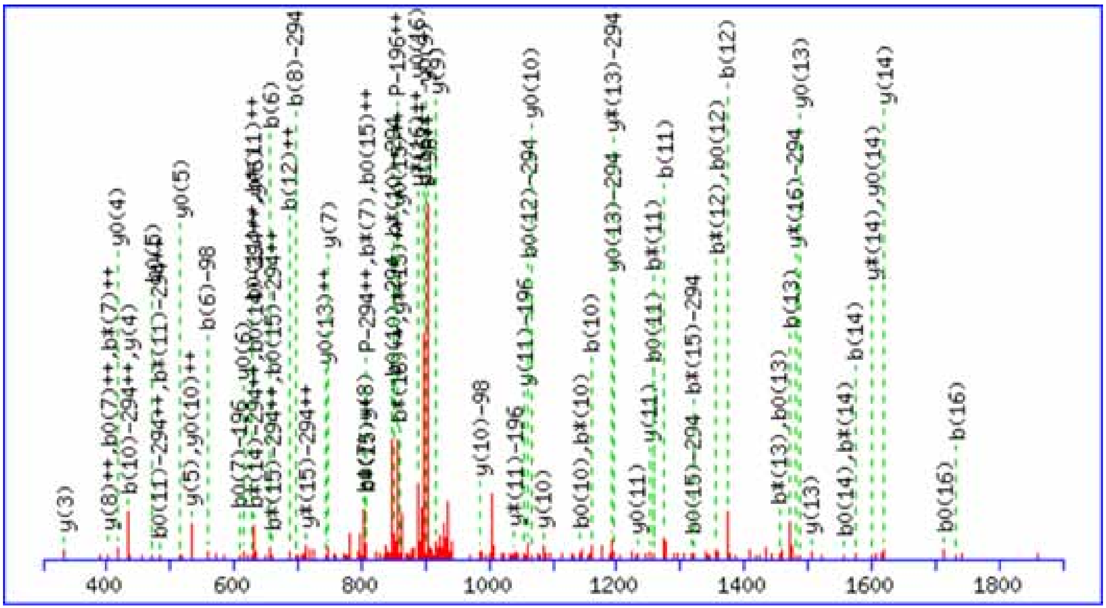
Matched b ions: b(4), b(6)-98, b(6), b(7)-98, b(8)-98, b(9)-196, b(9)-98, b(10)-196, b(10), b(11), b(11)-98, b(11)-196, b(12), b(12)-98, b(13), b(13)-98, b(14)++, b(16)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(10), y(11), y(11)-98, y(12), y(12)-196, y(12)-98, y(13)-98, y(14), y(14)-98, y(15)++, y(16)-98++, y(16)++, y(16)
Precursor origin neutral loss: +

Peptide No.853

SGDNSSSSLGDVVTGTR
Confirmed sites: @S:6,@S:7,@S:8
Ambiguous sites:

MS/MS Fragmentation of SGDNSSSSLGDVVTGTR
Found in CACB1_MOUSE, Voltage-dependent L-type calcium channel subunit beta-1 OS=Mus musculus GN=Cacnb1 PE=1 SV=1

Match to Query 3933: 1905.678622 from(953.846587,2+)
Title: Elution from: 46.825 to 46.825 scan no 4224 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1905.6796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.00053

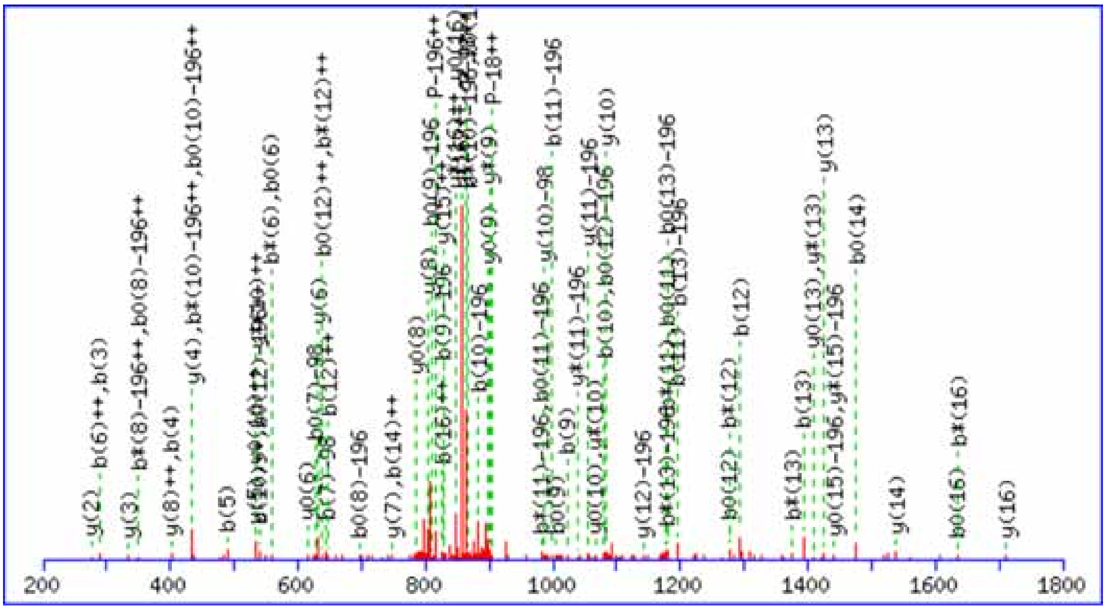
Matched b ions: b(6), b(6)-98, b(7)-98, b(8)-294, b(8)-196, b(8)-98, b(9)-98, b(9)-196, b(10)-294++, b(10)-98, b(10), b(10)-196++, b(11), b(11)-98, b(11)-196, b(12), b(12)-98, b(12)++, b(12)-196, b(13), b(13)-98, b(14), b(15)-196, b(15)-196++, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(10)-98, y(11), y(11)-196, y(11)-98, y(12)-196, y(12)-98++, y(12)-98, y(13)-98, y(13), y(14)-196++, y(14), y(14)-98++, y(14)-98, y(16)-196++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.854

SGDNSSSSLGDVVTGTR
Confirmed sites: @S:7,@S:8
Ambiguous sites:

MS/MS Fragmentation of SGDNSSSSLGDVVTGTR
Found in CACB1_MOUSE, Voltage-dependent L-type calcium channel subunit beta-1 OS=Mus musculus GN=Cacnb1 PE=1 SV=1

Match to Query 3191: 1825.717376 from(913.865964,2+)
Title: Elution from: 42.364 to 42.364 scan no 3670 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1825.7132
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 7.7e-006

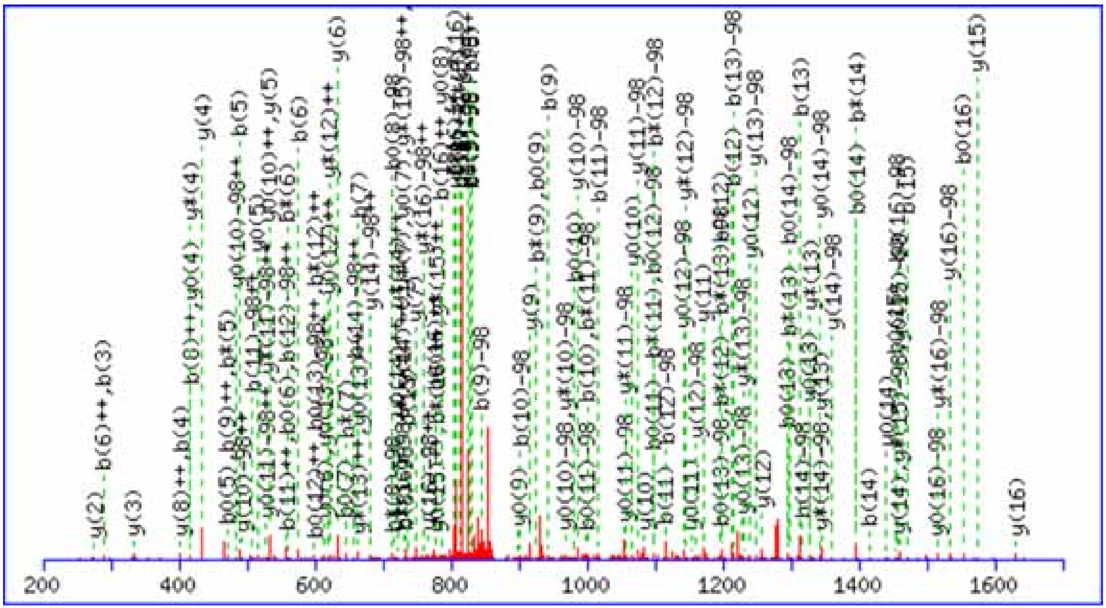
Matched b ions: b(3), b(4), b(5), b(6)++, b(7)-98, b(8)-98, b(9)-98, b(9)-196, b(9), b(10)-98, b(10)++, b(10), b(10)-196, b(11), b(11)-196, b(11)-98, b(12), b(12)-98, b(12)++, b(13), b(13)-98, b(13)-98++, b(13)-196, b(14)++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(10), y(10)-98, y(11)-196, y(12)-196, y(13), y(13)-98, y(14), y(14)-98, y(15)++, y(16)++, y(16), y(16)-98++
Precursor origin neutral loss: +

Peptide No.855

SGDNSSSSLGDVVTGTR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SGDNSSSSLGDVVTGTR
Found in CACB1_MOUSE, Voltage-dependent L-type calcium channel subunit beta-1 OS=Mus musculus GN=Cacnb1 PE=1 SV=1

Match to Query 2992: 1745.747884 from(873.881218,2+)
Title: Elution from: 38.298 to 38.298 scan no 3222 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1745.7469
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 91 **Expect:** 2.8e-008

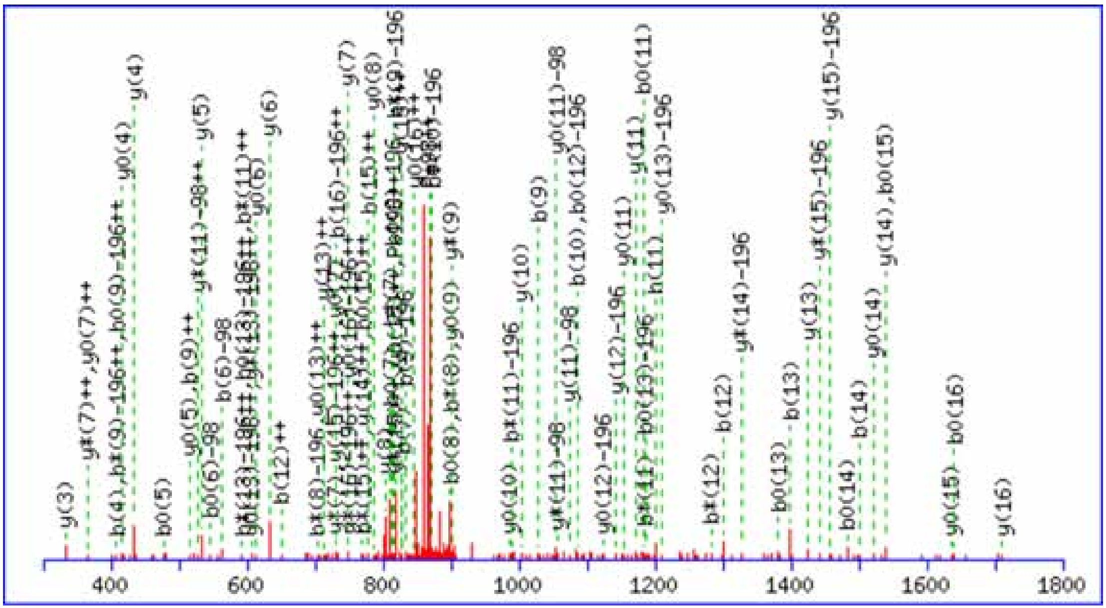
Matched b ions: b(3), b(4), b(5), b(6)++, b(6), b(7), b(8)-98, b(8)++, b(8), b(9)++, b(9)-98, b(9), b(10), b(10)-98, b(11)++, b(11), b(11)-98, b(11)-98++, b(12)-98++, b(12), b(12)-98, b(13), b(13)-98, b(14), b(14)-98++, b(14)-98, b(15), b(15)++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10)-98, y(10), y(10)-98++, y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(14), y(14)-98++, y(14)++, y(14)-98, y(15), y(16)++, y(16), y(16)-98, y(16)-98++
Precursor origin neutral loss: +

Peptide No.856

SGDNSSSSLGDVVTGTR
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of SGDNSSSSLGDVVTGTR
Found in CACB1_MOUSE, Voltage-dependent L-type calcium channel subunit beta-1 OS=Mus musculus GN=Cacnb1 PE=1 SV=1

Match to Query 3629: 1831.745782 from(916.880167,2+)
Title: Elution from: 42.681 to 42.681 scan no 3830 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1831.7451
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.008

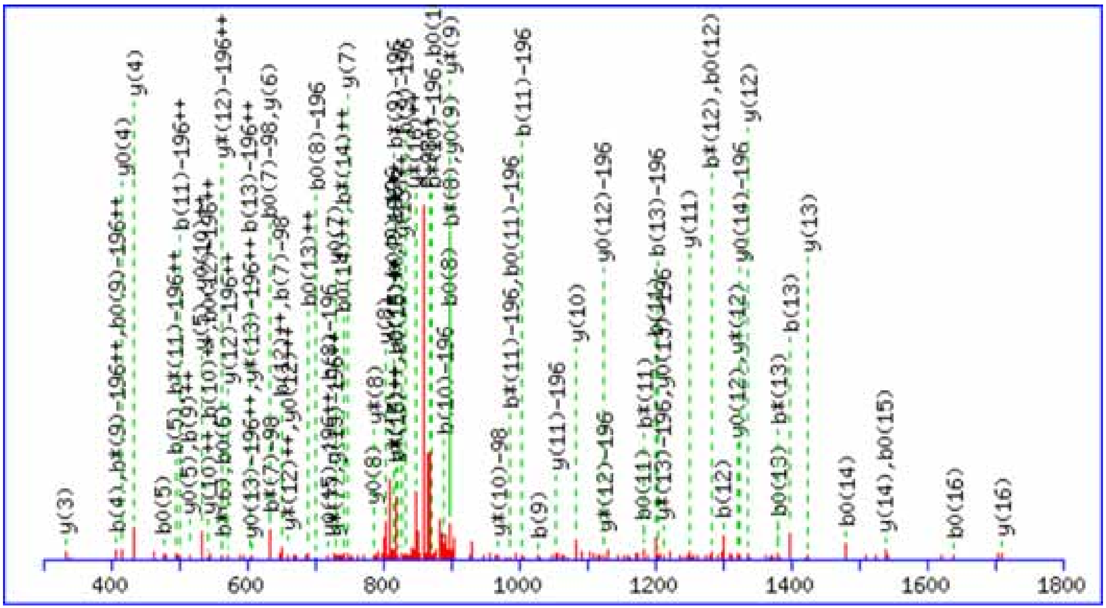
Matched b ions: b(4), b(6)-98, b(7)-98, b(7)-98++, b(7), b(8)-98, b(9)++, b(9), b(9)-98, b(9)-196, b(10)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(12)++, b(13), b(13)-98, b(13)-98++, b(14), b(14)-98, b(15)-98, b(15)-98++, b(15)++, b(16)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(11)-98, y(12)-196, y(12)-98, y(13), y(13)-98, y(13)++, y(14), y(14)-98, y(14)++, y(15)-196, y(15)-196++, y(15)-98++, y(15)++, y(16)-98, y(16), y(16)-98++
Precursor origin neutral loss: +

Peptide No.857

SGDNSSSSLGDVVTGTR
Confirmed sites: @S:7,@S:8
Ambiguous sites:

MS/MS Fragmentation of SGDNSSSSLGDVVTGTR
Found in CACB1_MOUSE, Voltage-dependent L-type calcium channel subunit beta-1 OS=Mus musculus GN=Cacnb1 PE=1 SV=1

Match to Query 3981: 1831.745818 from(916.880185,2+)
Title: Elution from: 42.460 to 42.460 scan no 3836 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1831.7451
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 Expect: 3.7e-005

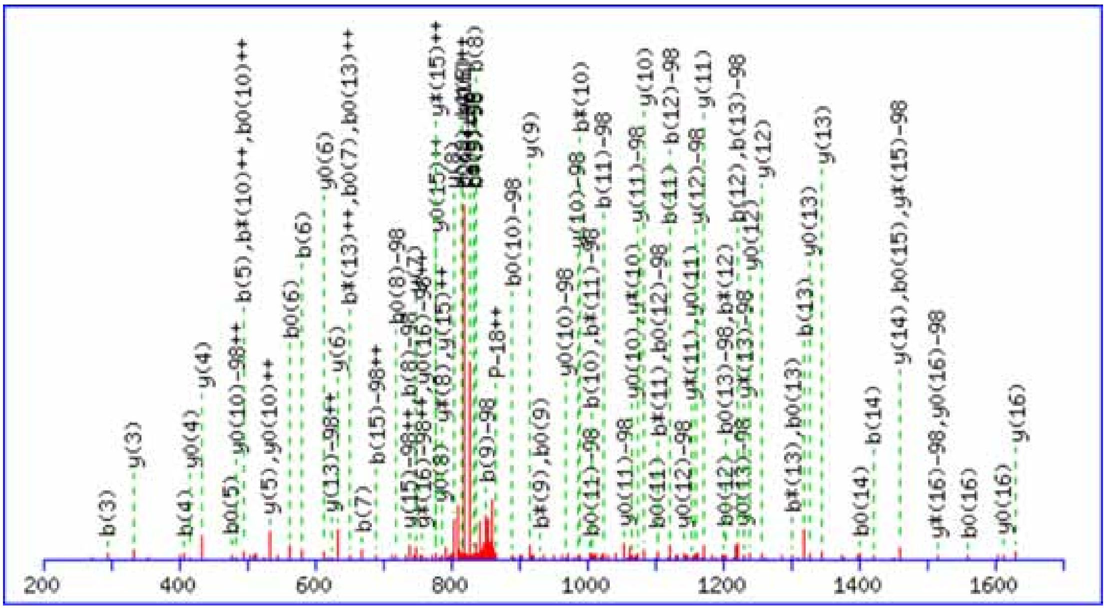
Matched b ions: b(4), b(5), b(7)-98, b(8)-98, b(8)-196, b(9), b(9)++, b(9)-196, b(9)-98, b(10)-98++, b(10)-98, b(10)++, b(10)-196, b(11), b(11)-196, b(11)-98, b(11)-196++, b(12)++, b(12), b(12)-98, b(13)-98++, b(13), b(13)-98, b(13)-196++, b(13)-196, b(14)-98++, b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(10)++, y(11), y(11)-196, y(11)-98, y(12), y(12)-196++, y(13), y(14), y(15)-196++, y(15)++, y(16), y(16)-98++
Precursor origin neutral loss: +

Peptide No.858

SGDNSSSSLGDVVTGTR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of SGDNSSSSLGDVVTGTR
Found in CACB1_MOUSE, Voltage-dependent L-type calcium channel subunit beta-1 OS=Mus musculus GN=Cacnb1 PE=1 SV=1

Match to Query 3130: 1751.779474 from(876.897013,2+)
Title: Elution from: 38.112 to 38.112 scan no 3179 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1751.7787
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 91 Expect: 3.5e-008

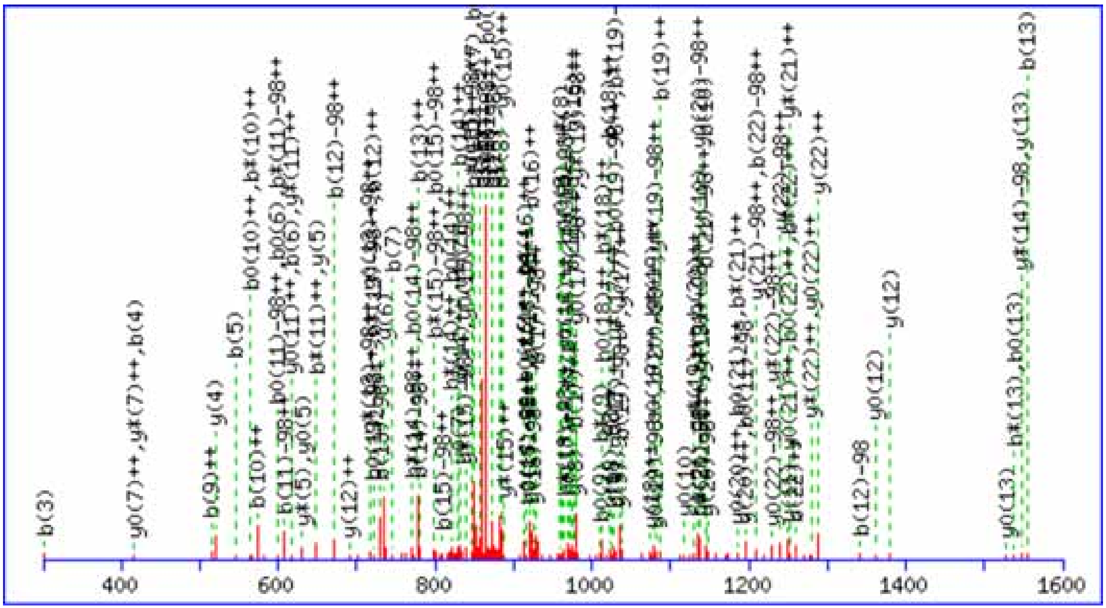
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)-98, b(8), b(9)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13), b(14), b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98++, y(14), y(15)-98++, y(15)++, y(16), y(16)++
Precursor origin neutral loss: +

Peptide No.859

SGENEAQKEDSEDTGELSESQEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of SGENEAQKEDSEDTGELSESQEK
Found in SH3BG_MOUSE, SH3 domain-binding glutamic acid-rich protein OS=Mus musculus GN=Sh3bgr PE=2 SV=1

Match to Query 6372: 2689.115241 from(897.379023,3+)
Title: Elution from: 28.349 to 28.349 scan no 1922 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2689.1127
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K8 : Dimethyl (K)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K23 : Dimethyl (K)
Ions Score: 76 Expect: 1.3e-006

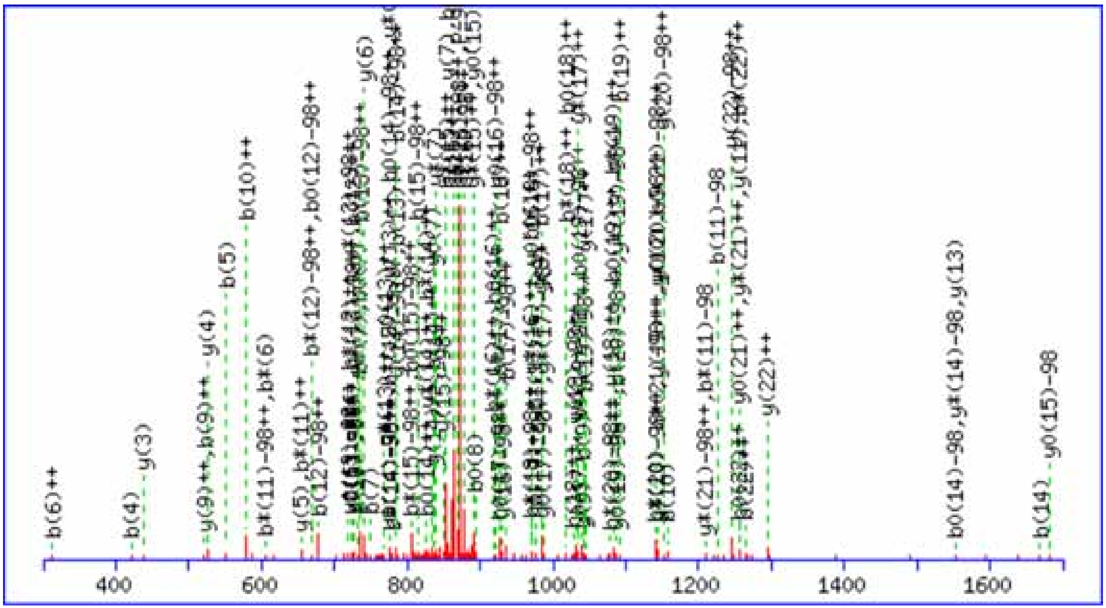
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9)++, b(9), b(10)++, b(10), b(11)-98++, b(12)-98, b(12)-98++, b(12)++, b(13)++, b(13), b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(22)++, b(22)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(13), y(14)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(20)++, y(20)-98++, y(21)-98++, y(22)++, y(22)-98++
Precursor origin neutral loss: +

Peptide No.860

SGENEAQKEDSEDTGELSESQEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of SGENEAQKEDSEDTGELSESQEK
Found in SH3BG_MOUSE, SH3 domain-binding glutamic acid-rich protein OS=Mus musculus GN=Sh3bgr PE=2 SV=1

Match to Query 6875: 2707.209180 from(903.410336,3+)
Title: Elution from: 28.384 to 28.384 scan no 1896 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2707.2081
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K8 : Dimethyl:2H(4)13C(2) (K)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K23 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 52 Expect: 0.00058

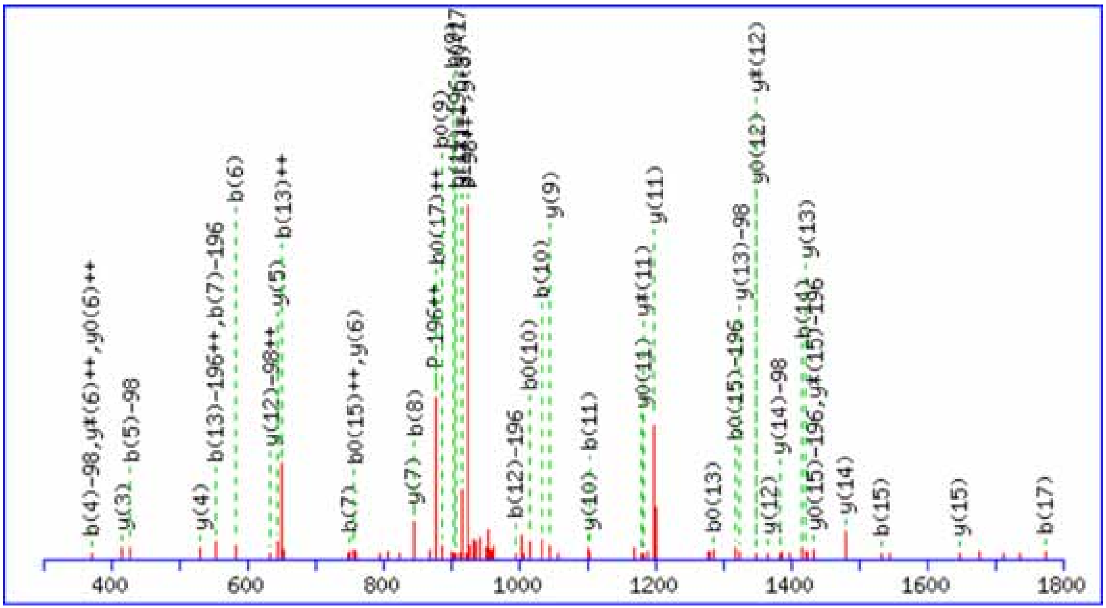
Matched b ions: b(4), b(5), b(6)++, b(7), b(9)++, b(9), b(10)++, b(10), b(11)-98, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14), b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-98++, b(22)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(11), y(13), y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(16)-98++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(20)-98++, y(22)-98++, y(22)++
Precursor origin neutral loss: +

Peptide No.861

SGESGGSPGEASILDELK
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of SGESGGSPGEASILDELK
Found in SMTL1_MOUSE, Smoothelin-like protein 1 OS=Mus musculus GN=Smtnl1 PE=1 SV=1

Match to Query 5365: 1947.813412 from(974.913982,2+)
Title: Elution from: 63.796 to 63.796 scan no 6247 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1947.8115
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl (K)
Ions Score: 68 Expect: 5.6e-006

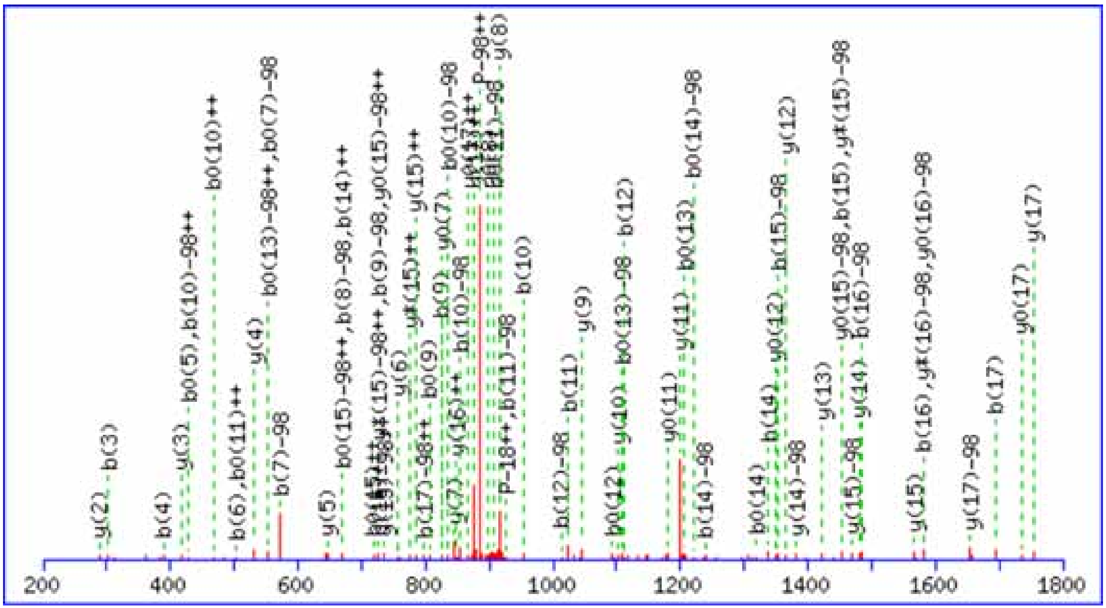
Matched b ions: b(4)-98, b(5)-98, b(6), b(7)-196, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10), b(10)-98, b(11)-98, b(11), b(11)-196, b(12)-196, b(13)-196++, b(13)++, b(14)-98, b(14), b(15)-98, b(15), b(17)-98, b(17)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98++, y(12), y(13)-98, y(13), y(14), y(14)-98, y(15), y(17)-98++, y(17)-98, y(17)++
Precursor origin neutral loss: +

Peptide No.862

SGESGGSPGEASILDELK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SGESGGSPGEASILDELK
Found in SMTL1_MOUSE, Smoothelin-like protein 1 OS=Mus musculus GN=Smtnl1 PE=1 SV=1

Match to Query 3830: 1867.846388 from(934.930470,2+)
Title: Elution from: 56.218 to 56.218 scan no 5120 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1867.8452
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl (K)
Ions Score: 93 Expect: 2.7e-008

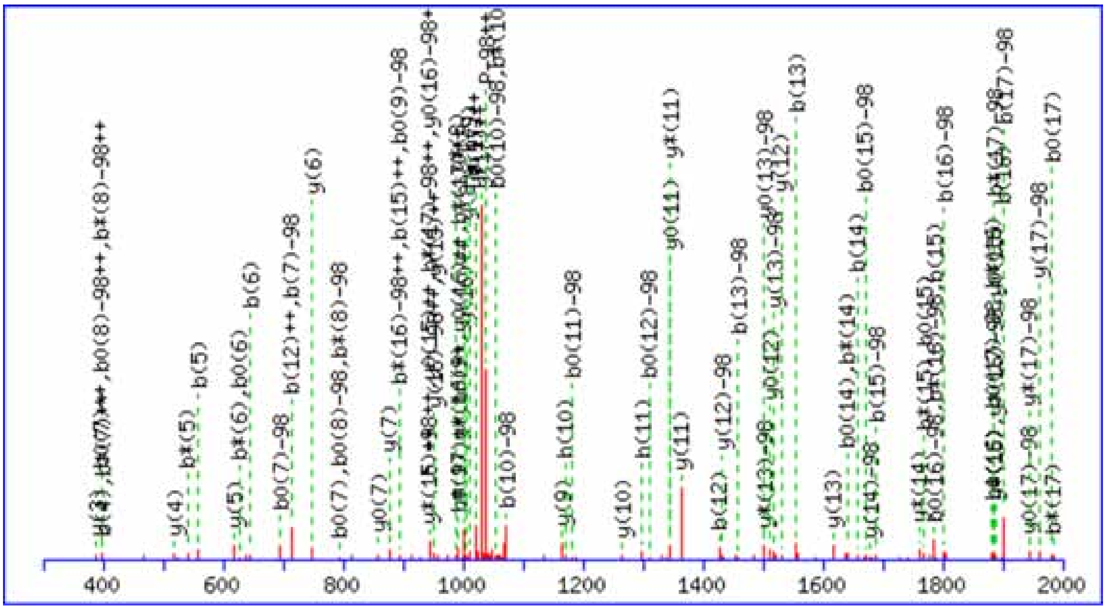
Matched b ions: b(3), b(4), b(6), b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98++, b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(12), b(14), b(14)++, b(14)-98, b(15), b(15)++, b(15)-98, b(16), b(16)-98, b(17), b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)-98, y(14), y(15)-98++, y(15), y(15)++, y(15)-98, y(16)++, y(17)-98, y(17)++, y(17)
Precursor origin neutral loss: +

Peptide No.863

SGPQCSSPTCQEETEDVR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SGPQCSSPTCQEETEDVR
Found in PALMD_MOUSE, Palmdelphin OS=Mus musculus GN=Palmd PE=1 SV=1

Match to Query 6387: 2173.831394 from(1087.922973,2+)
Title: Elution from: 28.452 to 28.452 scan no 2091 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2173.8293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 9.8e-007

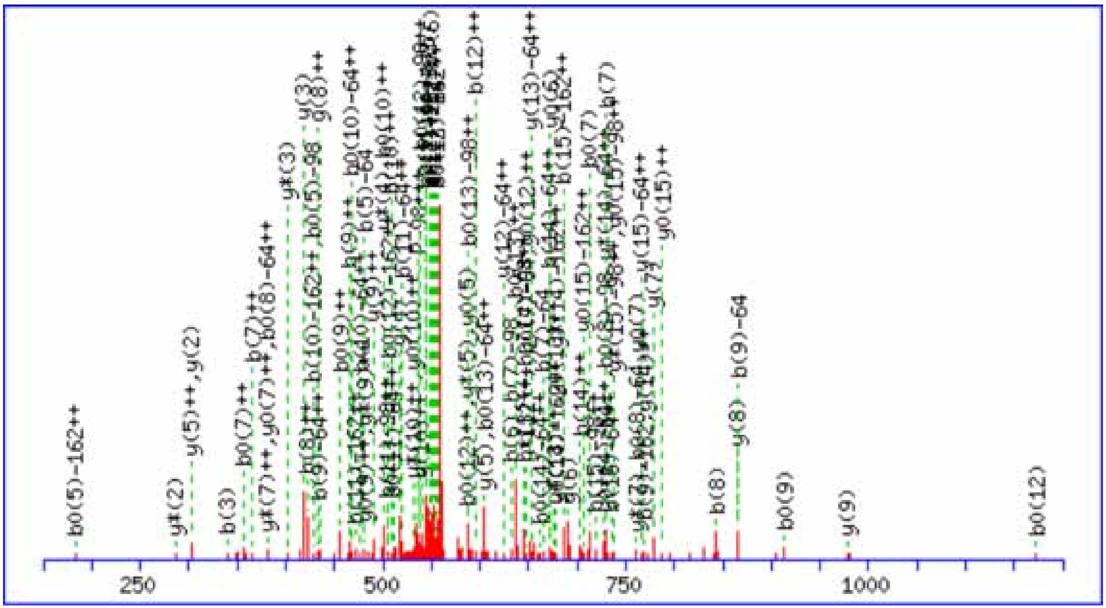
Matched b ions: b(4), b(5), b(6), b(7)-98, b(9), b(10), b(10)-98, b(11), b(12)++, b(12), b(13), b(13)-98, b(14), b(15), b(15)++, b(15)-98, b(16), b(16)-98, b(17)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(12), y(13), y(13)-98, y(14)-98, y(15)++, y(16)-98++, y(16)++, y(17)++, y(17)-98
Precursor origin neutral loss: +

Peptide No.864

SGSGMSVISSSSVDQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SGSGMSVISSSSVDQR
Found in ITSN1_MOUSE, Intersectin-1 OS=Mus musculus GN=Itsn1 PE=1 SV=1

Match to Query 3749: 1706.721822 from(569.914550,3+)
Title: Elution from: 31.830 to 31.830 scan no 2556 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1706.7182
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 42 Expect: 0.0017

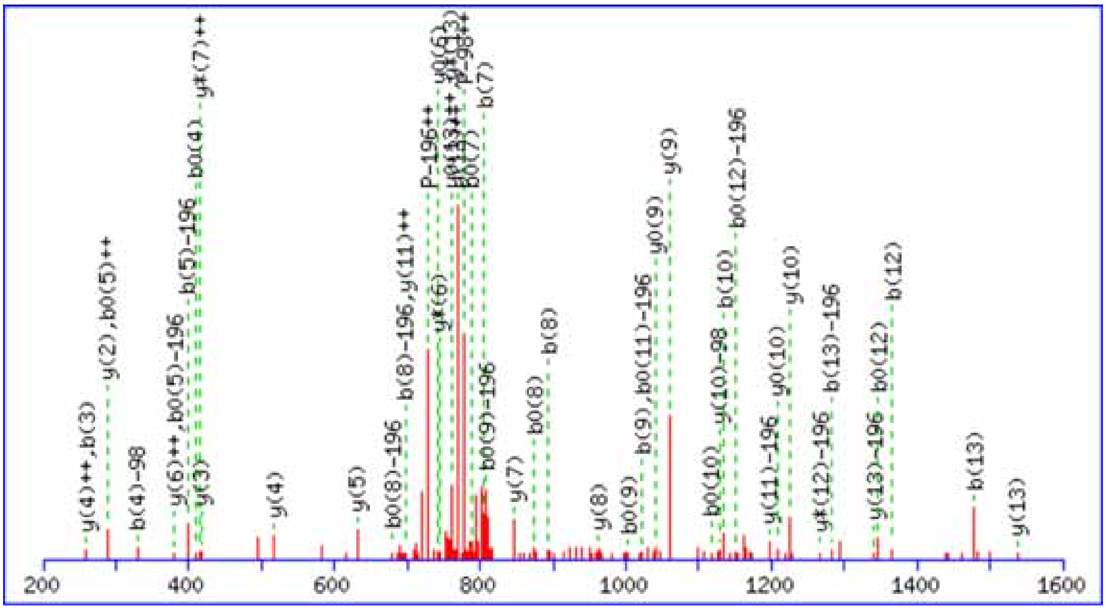
Matched b ions: b(3), b(5), b(6), b(7), b(7)++, b(7)-98, b(8)++, b(8), b(9)++, b(10)++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)++, b(14)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(14)++
Precursor origin neutral loss:

Peptide No.865

SGSSSPDSEITELK
Confirmed sites: @S:4,@S:5
Ambiguous sites:

MS/MS Fragmentation of SGSSSPDSEITELK
Found in PYRG1_MOUSE, CTP synthase 1 OS=Mus musculus GN=Ctps PE=1 SV=2

Match to Query 3428: 1651.664366 from(826.839459,2+)
Title: Elution from: 46.305 to 46.305 scan no 4462 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1651.6631
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
Ions Score: 49 Expect: 0.00027

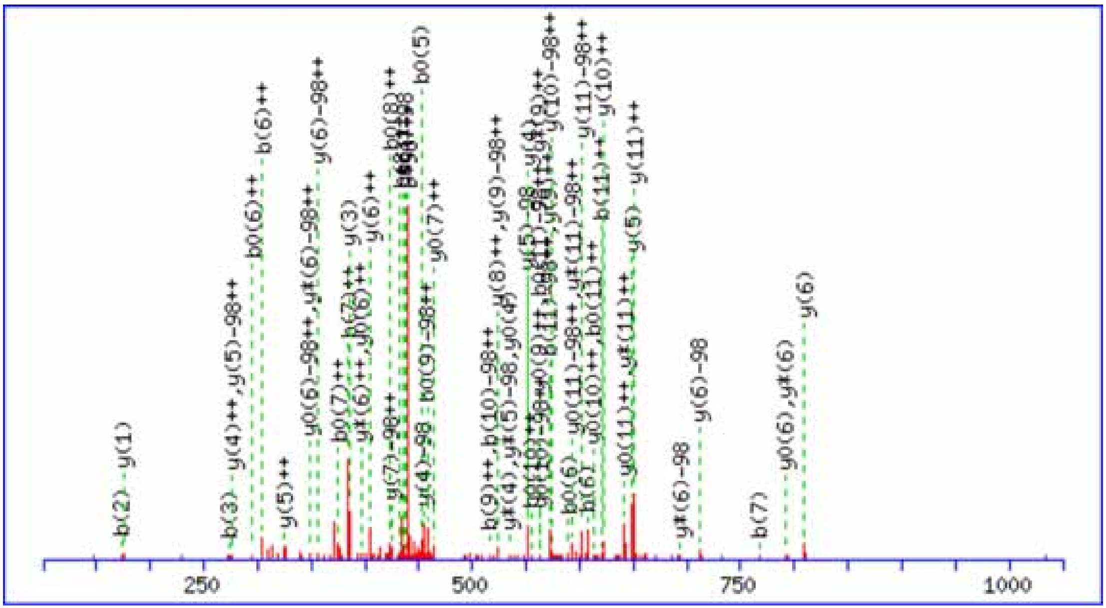
Matched b ions: b(3), b(4)-98, b(5)-196, b(5)-98, b(7), b(7)-98, b(8)-98++, b(8), b(8)-196, b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(12), b(12)-98, b(13), b(13)-196, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(11)-196, y(11)++, y(13)++, y(13)-98++, y(13)-98, y(13), y(13)-196
Precursor origin neutral loss: +

Peptide No.866

SGTPVHCPSPIR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SGTPVHCPSPIR
Found in BAG3_MOUSE, BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=1

Match to Query 2082: 1414.640979 from(472.554269,3+)
Title: Elution from: 27.067 to 27.067 scan no 1903 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1414.6428
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.045

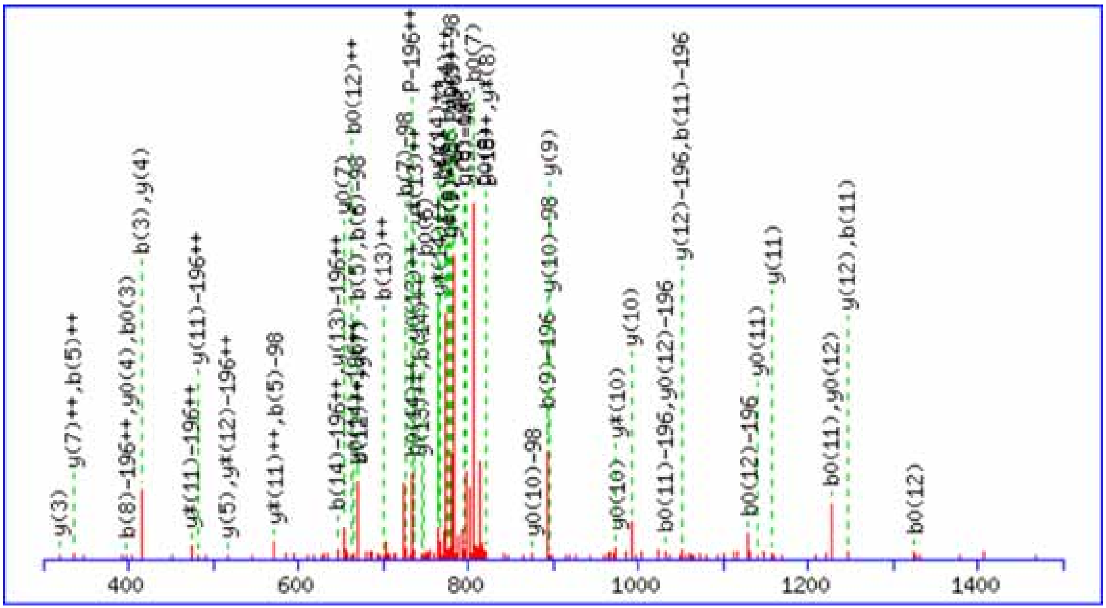
Matched b ions: b(2), b(3), b(6)++, b(6), b(7)++, b(7), b(8)++, b(9)++, b(10)-98++, b(11)-98++, b(11)++
Matched y ions: y(1), y(3), y(4), y(4)-98, y(4)++, y(5)-98, y(5), y(5)++, y(5)-98++, y(6), y(6)-98, y(6)++, y(6)-98++, y(7)-98++, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.867

SGYSSPGSPGTPGSR
Confirmed sites: @Y:3,@S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of SGYSSPGSPGTPGSR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 3482: 1660.556810 from(831.285681,2+)
Title: Elution from: 28.960 to 28.960 scan no 2161 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1660.5573
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y3 : Phospho (Y)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 Expect: 0.05

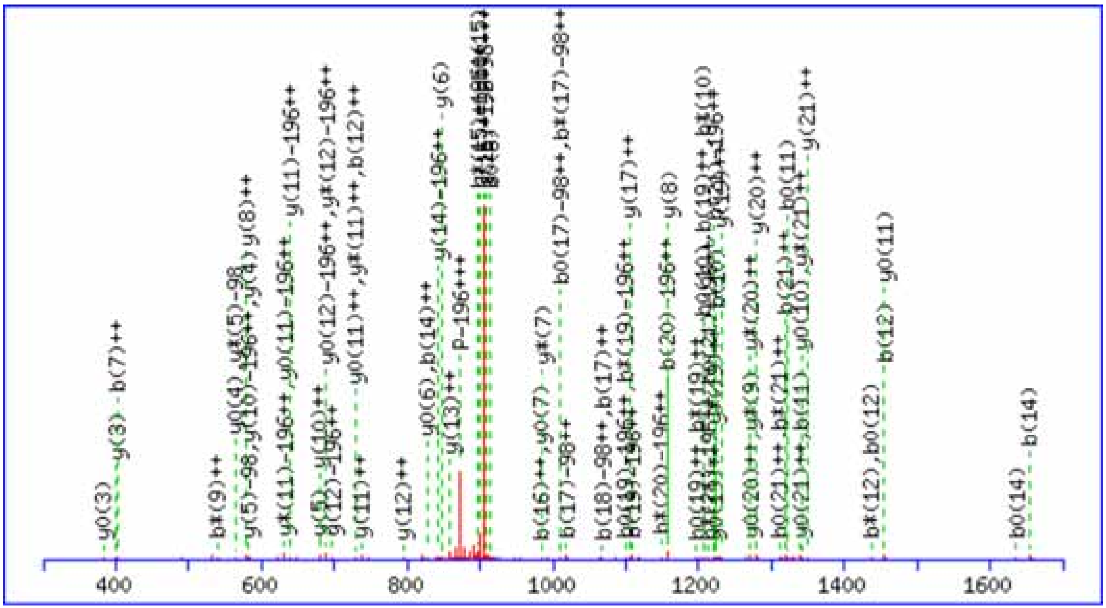
Matched b ions: b(3), b(5)-98, b(5)++, b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(8)-196++, b(8)-196, b(9)-196, b(11)-196, b(11), b(11)-98, b(12)++, b(12)-98, b(13)++, b(14)-196++, b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5), y(7), y(7)++, y(9), y(9)-98, y(10), y(10)-98, y(11)-196++, y(11), y(11)-98, y(12)-196, y(12), y(12)-98, y(13)-196++, y(13)-98++, y(13)++, y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.868

SHPRPAEEYEDDAERRSPTPER
Confirmed sites: @S:17,@T:19
Ambiguous sites:

MS/MS Fragmentation of SHPRPAEEYEDDAERRSPTPER
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 8312: 2811.165873 from(938.062567,3+)
Title: Elution from: 25.817 to 25.817 scan no 1742 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2811.1650
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.034

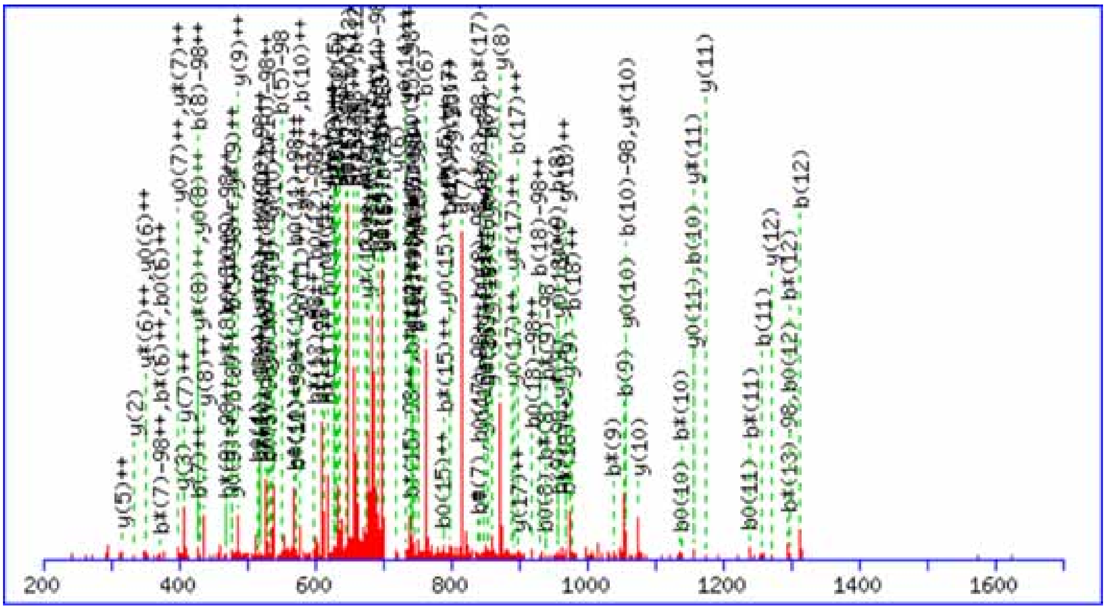
Matched b ions: b(7)++, b(10), b(11), b(12), b(12)++, b(14), b(14)++, b(15)++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(19)-98++, b(19)-196++, b(19)++, b(20)-196++, b(20)-98++, b(21)-98++, b(21)++, b(21)-196++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6), y(8)-98++, y(8)++, y(8), y(10)-98++, y(10)++, y(10)-196++, y(11)-98++, y(11)++, y(11)-196++, y(12)-196++, y(12)++, y(13)++, y(14)-98++, y(14)-196++, y(15)-196++, y(17)++, y(18)-98++, y(19)++, y(20)++, y(20)-98++, y(21)++
Precursor origin neutral loss: +

Peptide No.869

SHSLDNPPVTTGPSPEACK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SHSLDNPPVTTGPSPEACK
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 5315: 2128.952856 from(710.658228,3+)
Title: Elution from: 31.912 to 31.912 scan no 2355 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2128.9500
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl (K)
Ions Score: 49 Expect: 0.00067

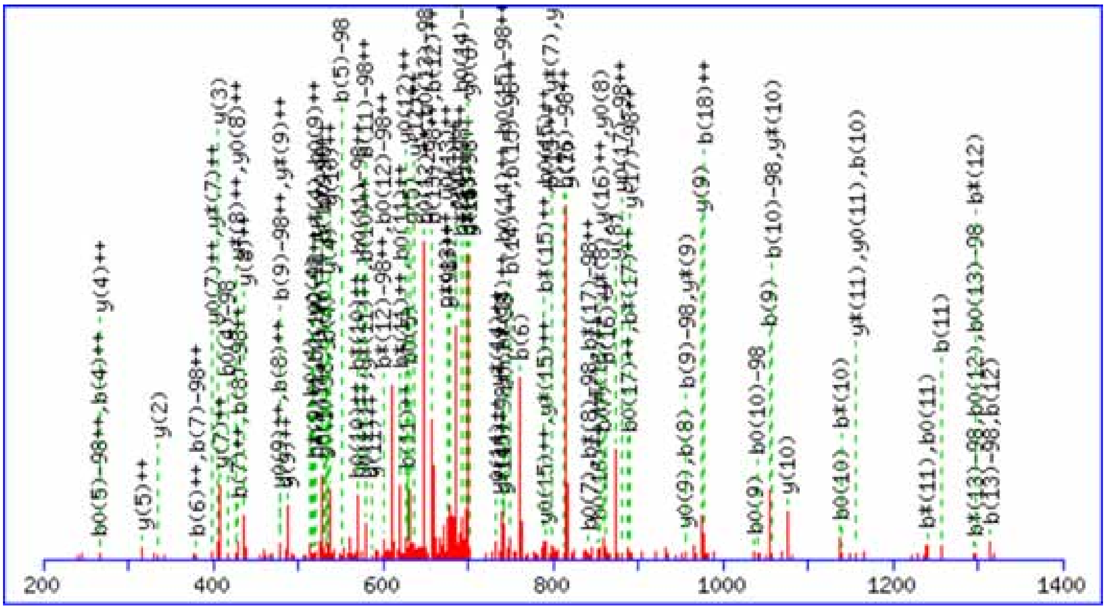
Matched b ions: b(4), b(5), b(5)-98, b(6), b(6)-98, b(7), b(7)++, b(8)++, b(8), b(8)-98++, b(9)++, b(9), b(9)-98++, b(9)-98, b(10), b(10)-98++, b(10)++, b(10)-98, b(11), b(11)++, b(12), b(12)++, b(12)-98++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(10), y(11), y(12)++, y(12), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++
Precursor origin neutral loss:

Peptide No.870

SHSLDNPPVTTGPSPEACK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SHSLDNPPVTTGPSPEACK
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 6249: 2128.951428 from(710.657752,3+)
Title: Elution from: 31.911 to 31.911 scan no 2567 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2128.9500
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl (K)
Ions Score: 58 Expect: 9.8e-005

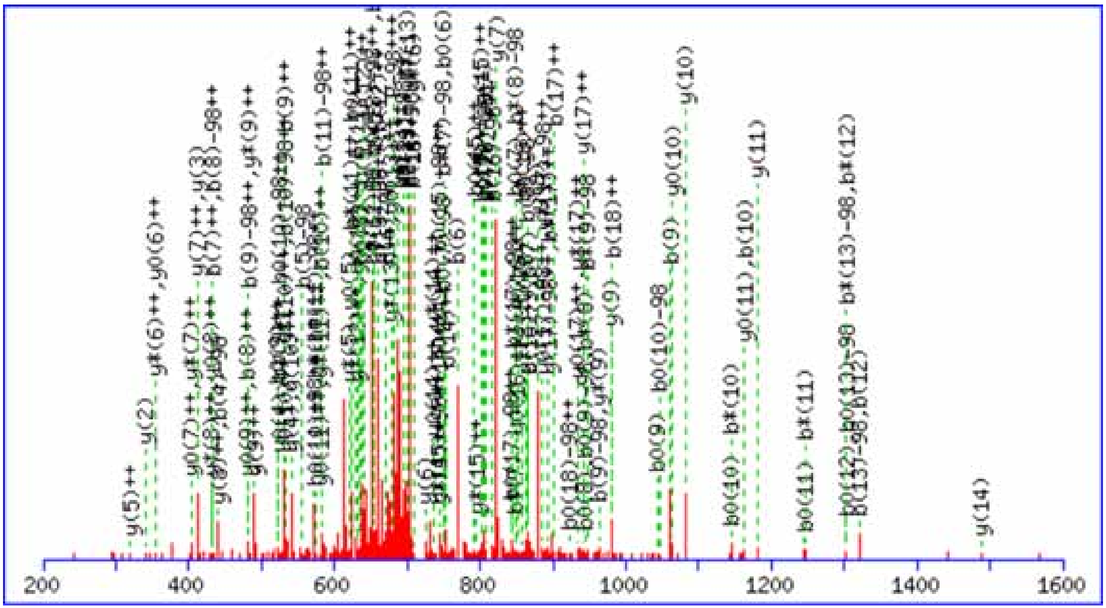
Matched b ions: b(4)++, b(4), b(5), b(5)-98, b(6), b(6)++, b(7)++, b(7), b(7)-98++, b(8)-98++, b(8)++, b(8), b(9)++, b(9), b(9)-98, b(9)-98++, b(10)++, b(10), b(10)-98, b(10)-98++, b(11), b(11)-98++, b(11)++, b(12), b(12)++, b(13)-98, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(18)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5)++, y(5), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++
Precursor origin neutral loss:

Peptide No.871

SHSLDNPPVTTGPSPEACK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SHSLDNPPVTTGPSPEACK
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 5709: 2141.016417 from(714.679415,3+)
Title: Elution from: 31.832 to 31.832 scan no 2386 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2141.0137
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 71 Expect: 5.3e-006

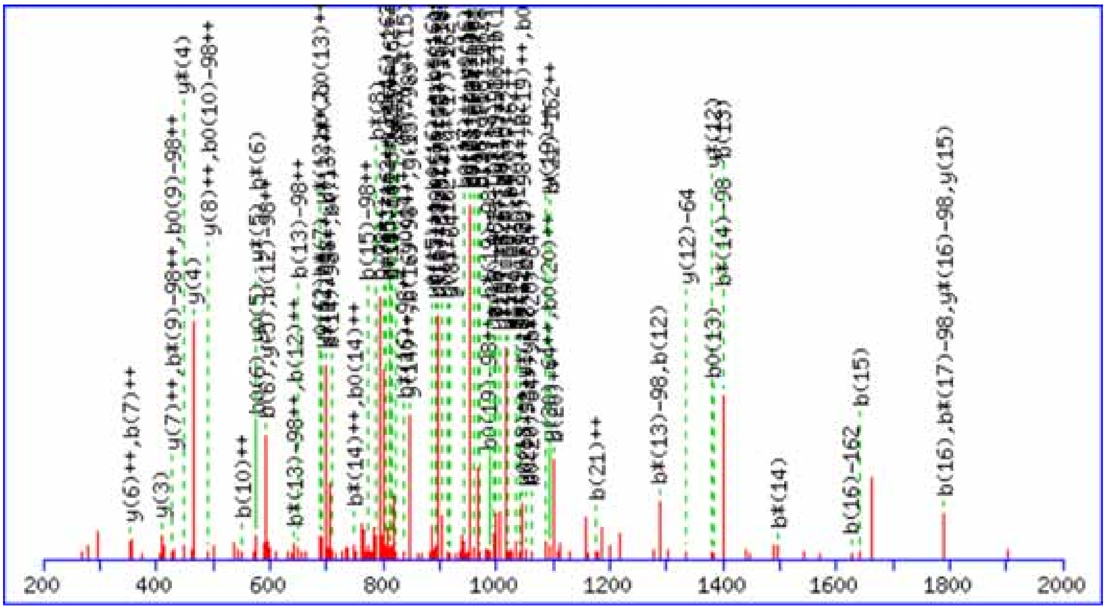
Matched b ions: b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)++, b(8)++, b(8)-98, b(8)-98++, b(9)++, b(9), b(9)-98++, b(9)-98, b(10), b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12), b(12)++, b(13)-98, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(18)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(10), y(11), y(12)++, y(13)++, y(14), y(14)++, y(15)++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.872

SKAATTNPSQGEDLKMDEGNFK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SKAATTNPSQGEDLKMDEGNFK
Found in NCAM1_MOUSE, Neural cell adhesion molecule 1 OS=Mus musculus GN=Ncam1 PE=1 SV=3

Match to Query 6518: 2497.128066 from(833.383298,3+)
Title: Elution from: 65.974 to 65.974 scan no 6212 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2497.1256
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Dimethyl:2H(4)13C(2) (K)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 38 Expect: 0.011

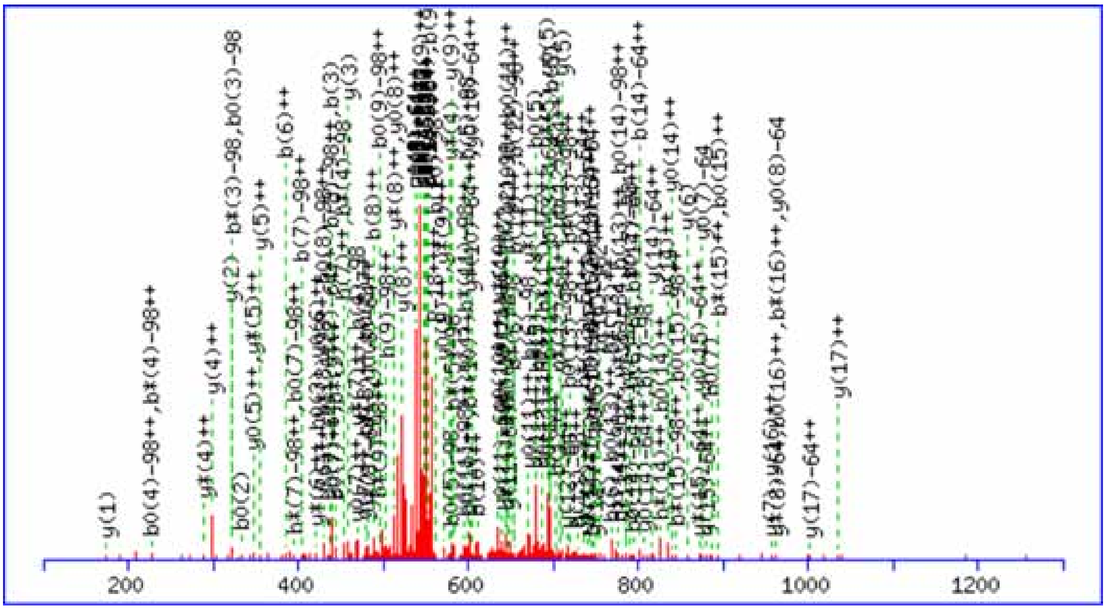
Matched b ions: b(6), b(7)++, b(7), b(8), b(9), b(10)++, b(12)-98++, b(12), b(12)++, b(13)++, b(13), b(13)-98++, b(14)-98++, b(15), b(15)-98++, b(15)++, b(16), b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++
Matched y ions: y(3), y(4), y(5), y(6)++, y(7)++, y(8)++, y(14)++, y(15), y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++, y(18)++, y(19)++
Precursor origin neutral loss: +

Peptide No.873

SKSEEAHAEDSVMDHHFR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SKSEEAHAEDSVMDHHFR
Found in PAIRB_MOUSE, Plasminogen activator inhibitor 1 RNA-binding protein OS=Mus musculus GN=Serbp1 PE=1 SV=2

Match to Query 5853: 2262.939920 from(566.742256,4+)
Title: Elution from: 27.491 to 27.491 scan no 1780 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2262.9365
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K2 : Dimethyl (K)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 40 Expect: 0.004

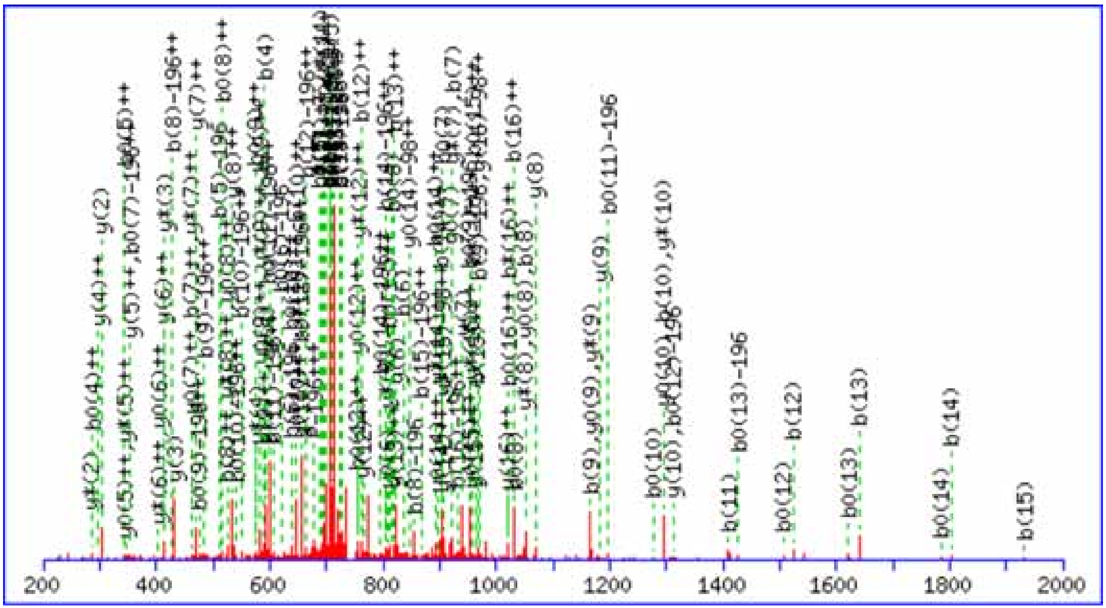
Matched b ions: b(3), b(4)-98, b(5), b(5)-98, b(6)-98, b(6), b(6)++, b(7)++, b(7)-98++, b(7)-98, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.874

SLDSDESEDEDDDYQQK
Confirmed sites: @S:1,@S:4
Ambiguous sites:

MS/MS Fragmentation of SLDSDESEDEDDDYQQK
Found in HAP28_MOUSE, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 5361: 2232.753582 from(745.258470,3+)
Title: Elution from: 34.228 to 34.228 scan no 2571 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2232.7508
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 56 **Expect:** 1.6e-005

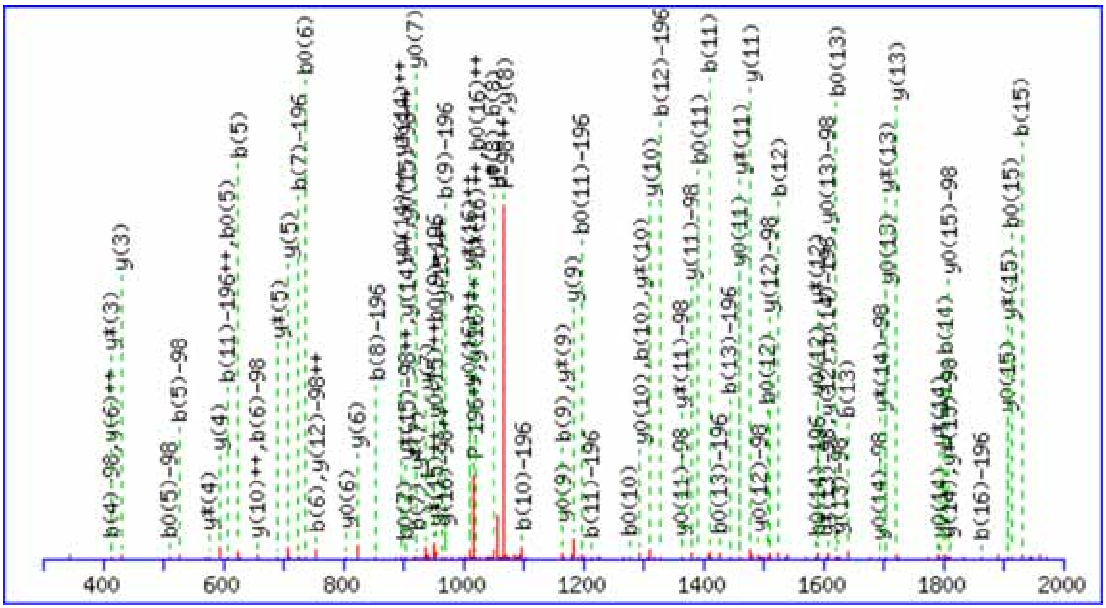
Matched b ions: b(4), b(5), b(5)-98, b(5)-196, b(6)-196, b(6), b(7)-98++, b(7)-98, b(7), b(7)++, b(7)-196, b(8)-98, b(8), b(8)++, b(8)-98++, b(8)-196++, b(8)-196, b(9), b(9)-98++, b(9)-98, b(9)++, b(9)-196++, b(9)-196, b(10)-98++, b(10), b(10)-98, b(10)++, b(10)-196++, b(11), b(11)-98++, b(11)-98, b(11)-196++, b(11)++, b(12), b(12)-98, b(12)-98++, b(12)++, b(12)-196++, b(13), b(13)-98++, b(13)-98, b(13)-196++, b(13)++, b(14)++, b(14), b(14)-98++, b(14)-196++, b(15), b(15)-98++, b(15)++, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(5)++, y(6)++, y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.875

SLDSDESEDEDDDYQQK
Confirmed sites: @S:1,@S:7
Ambiguous sites:

MS/MS Fragmentation of SLDSDESEDEDDDYQQK
Found in HAP28_MOUSE, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 7426: 2232.750698 from(1117.382625,2+)
Title: Elution from: 34.445 to 34.445 scan no 2845 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2232.7508
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 84 **Expect:** 3.1e-008

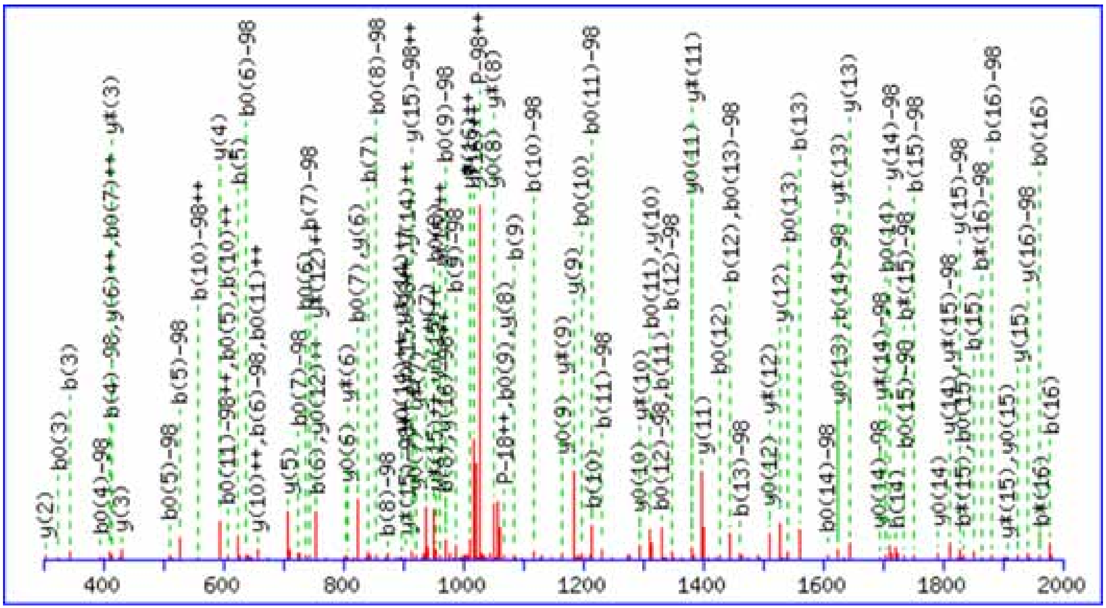
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7)-98++, b(7)-196, b(7), b(8)-98, b(8)-196, b(8), b(9)-98, b(9), b(9)-196, b(10), b(10)-98, b(10)-196, b(11)-98, b(11), b(11)-98++, b(11)-196++, b(11)-196, b(12), b(12)-98, b(12)-196, b(13), b(13)-98, b(13)-196, b(14), b(14)-196, b(14)-98, b(15), b(15)-98, b(15)-98++, b(16)-98, b(16)-196, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)-98, y(12)-98++, y(12), y(12)-98, y(13), y(13)-98, y(14)++, y(14), y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.876

SLDSDESEDEDDDYQQK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SLDSDESEDEDDDYQQK
Found in HAP28_MOUSE, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 6296: 2152.786234 from(1077.400393,2+)
Title: Elution from: 32.761 to 32.761 scan no 2683 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2152.7845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K17 : Dimethyl (K)
Ions Score: 108 Expect: 2.1e-010

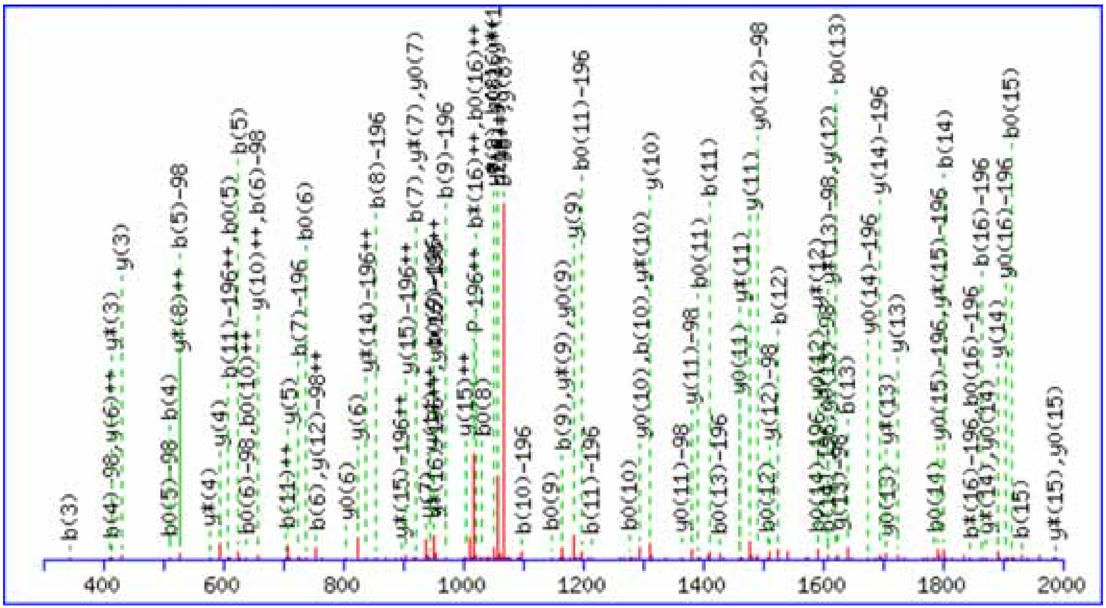
Matched b ions: b(3), b(4)-98, b(5), b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(10)++, b(10)-98++, b(11)-98, b(11), b(12), b(12)-98, b(13), b(13)-98, b(14), b(14)-98, b(15), b(15)-98, b(16), b(16)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10)++, y(10), y(11), y(12), y(13), y(14)-98, y(14), y(14)++, y(15)-98, y(15), y(15)-98++, y(15)++, y(16)-98, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.877

SLDSDESEDEDDDYQQK
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of SLDSDESEDEDDDYQQK
Found in HAP28_MOUSE, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 6116: 2232.750854 from(1117.382703,2+)
Title: Elution from: 34.638 to 34.638 scan no 2771 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2232.7508
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 91 **Expect:** 5.4e-009

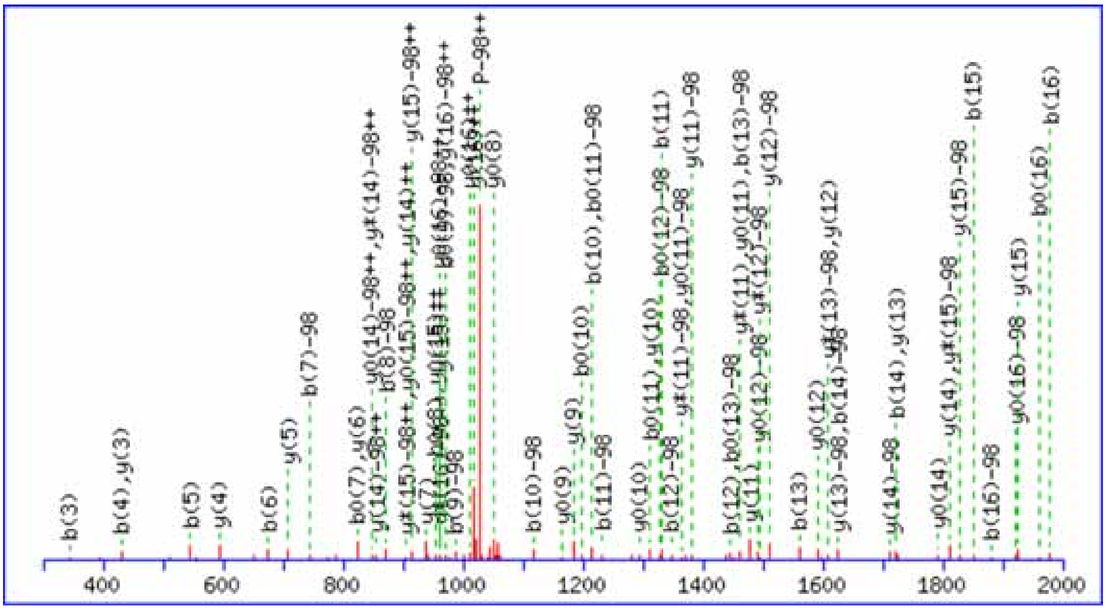
Matched b ions: b(3), b(4), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7)-98++, b(7)-196, b(7), b(8)-98, b(8)-196, b(8), b(9)-98, b(9), b(9)-196, b(10), b(10)-98, b(10)-196, b(11)-98, b(11)-98++, b(11), b(11)-196++, b(11)++, b(11)-196, b(12), b(12)-98, b(13), b(13)-98, b(14)-98, b(14), b(14)-196, b(15), b(15)-98, b(16)-98, b(16)-196
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(10)++, y(11)-98, y(11), y(12)-98++, y(12), y(12)-98, y(13), y(13)-98, y(14)-98, y(14), y(14)-196, y(14)-98++, y(14)++, y(15)-196++, y(15)-98++, y(15)-98, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.878

SLDSDESEDEDDDYQQK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SLDSDESEDEDDDYQQK
Found in HAP28_MOUSE, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 6294: 2152.785664 from(1077.400108,2+)
Title: Elution from: 31.859 to 31.859 scan no 2560 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2152.7845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K17 : Dimethyl (K)
Ions Score: 88 **Expect:** 2.2e-008

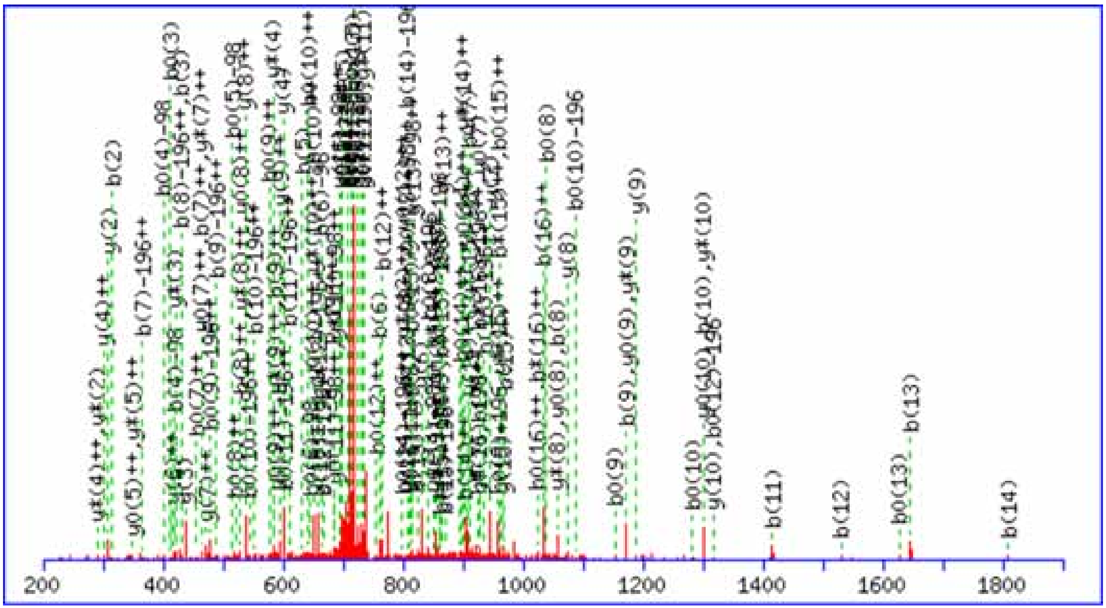
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(8)-98, b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12)-98, b(12), b(13), b(13)-98, b(14), b(14)-98, b(15), b(16), b(16)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(11)-98, y(12)-98, y(12), y(13), y(13)-98, y(14)-98, y(14), y(14)-98++, y(14)++, y(15), y(15)-98++, y(15)-98, y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.879

SLDSDESEDEDDDYQQK
Confirmed sites: @S:1,@S:7
Ambiguous sites:

MS/MS Fragmentation of SLDSDESEDEDDDYQQK
Found in HAP28_MOUSE, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 5417: 2244.815433 from(749.279087,3+)
Title: Elution from: 34.175 to 34.175 scan no 2564 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2244.8145
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 34 Expect: 0.0058

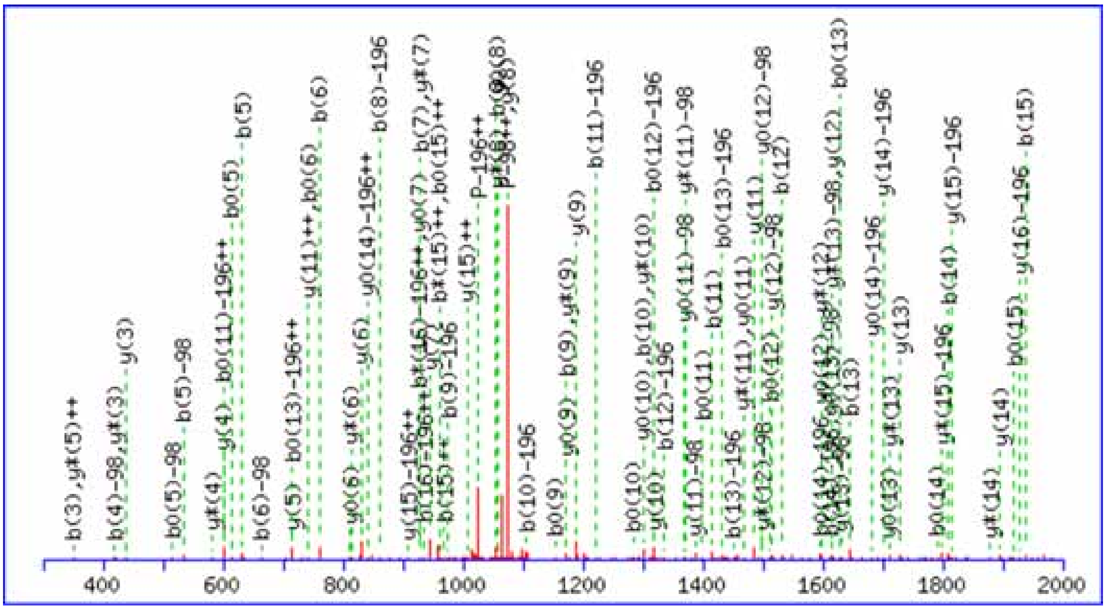
Matched b ions: b(2), b(3), b(4)-98, b(5), b(6), b(6)-98, b(7)-98, b(7)++, b(7), b(7)-196, b(7)-196++, b(7)-98++, b(8)-98++, b(8)-98, b(8), b(8)++, b(8)-196++, b(8)-196, b(9), b(9)-98++, b(9)-98, b(9)++, b(9)-196++, b(10)-98++, b(10), b(10)-98, b(10)++, b(10)-196++, b(11), b(11)-98++, b(11)-98, b(11)-196++, b(11)++, b(12)-98++, b(12), b(12)++, b(12)-196++, b(13), b(13)-98++, b(13)-98, b(13)-196++, b(13)++, b(14), b(14)++, b(14)-98++, b(14)-196++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(8), y(9), y(9)++, y(10)++, y(10), y(11)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.880

SLDSDESEDEDDDYQQK
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of SLDSDESEDEDDDYQQK
Found in HAP28_MOUSE, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 5931: 2244.815554 from(1123.415053,2+)
Title: Elution from: 34.299 to 34.299 scan no 2690 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2244.8145
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 79 **Expect:** 1.9e-007

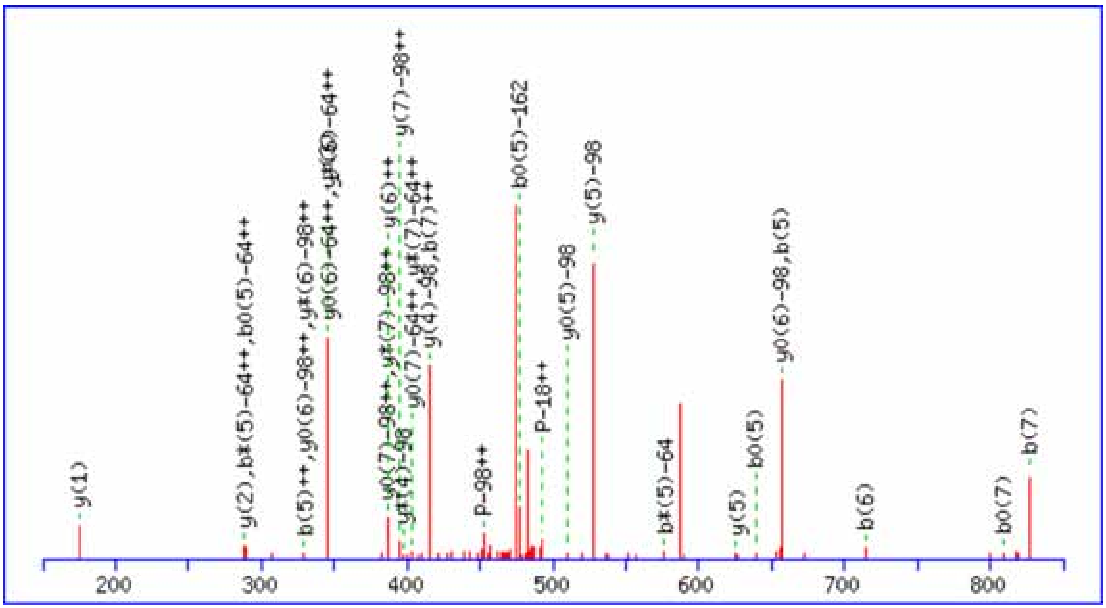
Matched b ions: b(3), b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(8)-196, b(8), b(9)-98, b(9), b(9)-196, b(10)-98, b(10), b(10)-98++, b(10)-196, b(11)-98, b(11), b(11)-196, b(12), b(12)-98, b(12)-196, b(13), b(13)-98, b(13)-196, b(14)-98, b(14), b(14)-196, b(15), b(15)-98, b(15)++, b(16)-98, b(16)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(11)++, y(12), y(12)-98, y(13), y(13)-98, y(14)-98, y(14), y(14)-196, y(15)-196++, y(15)-196, y(15)-98, y(15)++, y(15)-98++, y(16)-196, y(16)-98++
Precursor origin neutral loss: +

Peptide No.881

SLMNSGIK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SLMNSGIK
Found in FAT3_MOUSE, Protocadherin Fat 3 OS=Mus musculus GN=Fat3 PE=1 SV=2

Match to Query 775: 1000.465058 from(501.239805,2+)
Title: Elution from: 50.494 to 50.494 scan no 5016 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1000.4664
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K8 : Dimethyl (K)
Ions Score: 30 **Expect:** 0.021

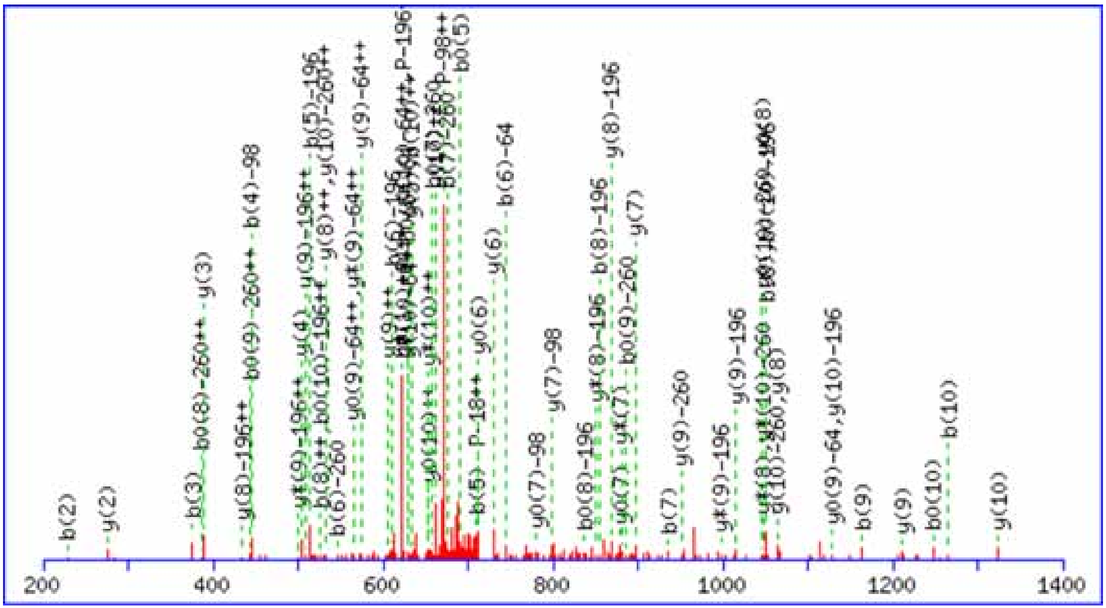
Matched b ions: b(5), b(5)++, b(6), b(7), b(7)++
Matched y ions: y(1), y(2), y(3), y(4)-98, y(5)-98, y(5), y(6)++, y(7)-98++
Precursor origin neutral loss:

Peptide No.882

SLMSSPEDLTK
Confirmed sites: @S:4,@S:5
Ambiguous sites:

MS/MS Fragmentation of SLMSSPEDLTK
Found in MAP1B_MOUSE, Microtubule-associated protein 1B OS=Mus musculus GN=Map1b PE=1 SV=1

Match to Query 2199: 1438.571940 from(720.293246,2+)
Title: Elution from: 40.629 to 40.629 scan no 3750 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1438.5703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K11 : Dimethyl (K)
Ions Score: 39 Expect: 0.0021

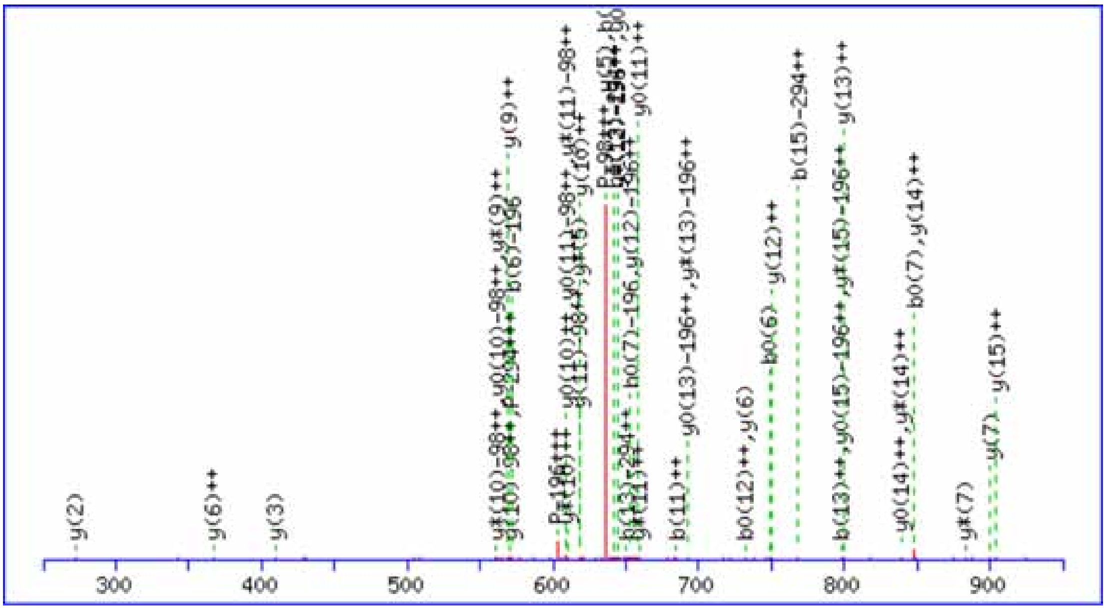
Matched b ions: b(2), b(3), b(4)-98, b(5)-196, b(5)-98, b(5), b(6)-196, b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(8)++, b(8)-196, b(9), b(9)-98, b(9)-98++, b(10), b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8)-98, y(8)-196, y(8), y(8)-196++, y(8)++, y(9)-196, y(9)-98, y(9), y(9)-196++, y(9)-98++, y(9)++, y(10)-98++, y(10), y(10)-98, y(10)++, y(10)-196
Precursor origin neutral loss: +

Peptide No.883

SLPPSPVTHSPLLHPR
Confirmed sites: @S:1,@S:5,@S:10
Ambiguous sites:

MS/MS Fragmentation of SLPPSPVTHSPLLHPR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 4540: 2001.889806 from(668.303878,3+)
Title: Elution from: 42.778 to 42.778 scan no 3760 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2001.8880
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.014

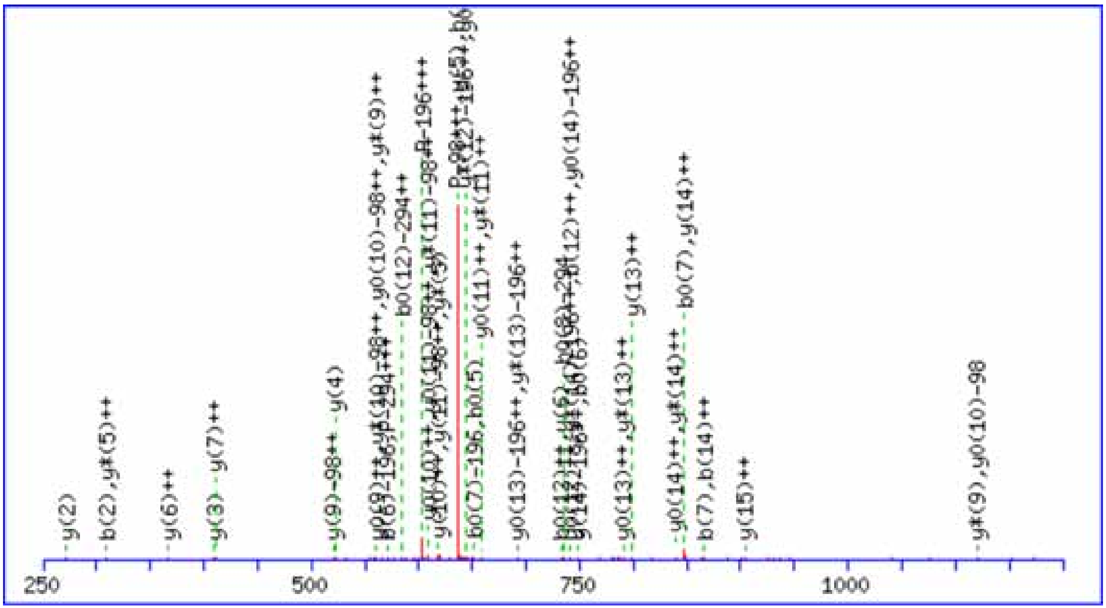
Matched b ions: b(5)-98, b(6)-196, b(7)-98, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(11)-196++, b(12)-98++, b(12)-196++, b(13)-98++, b(13)++, b(13)-294++, b(14)-98++, b(14)-196++, b(15)-196++, b(15)-294++
Matched y ions: y(2), y(3), y(5), y(6)++, y(6), y(7), y(9)++, y(10)-98++, y(10)++, y(11)-98++, y(12)++, y(12)-196++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.884

SLPPSPVTHSPLLHPR
Confirmed sites: @S:1,@S:5,@T:8
Ambiguous sites:

MS/MS Fragmentation of SLPPSPVTHSPLLHPR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 5594: 2001.888660 from(668.303496,3+)
Title: Elution from: 42.935 to 42.935 scan no 4049 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2001.8880
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 **Expect:** 0.028

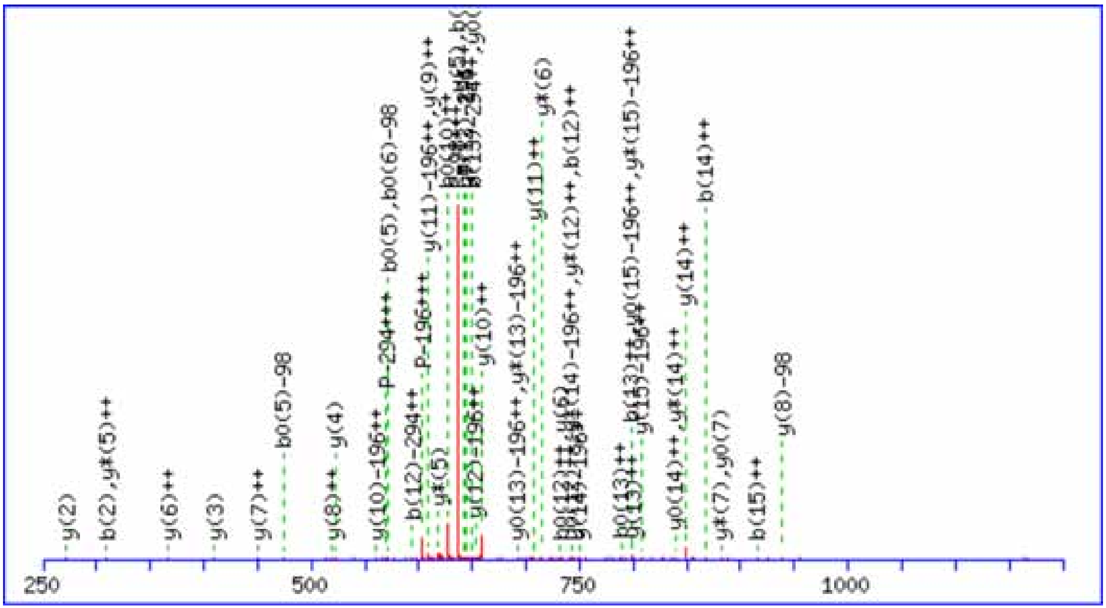
Matched b ions: b(2), b(6)-196, b(7)-98, b(7), b(10)++, b(10)-98, b(10)-196, b(10)-98++, b(11)-98++, b(11)-196, b(12)-98++, b(12)++, b(12)-196++, b(13)-98++, b(14)-98++, b(14)-196++, b(14)++, b(15)-196++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(9)-98++, y(10)++, y(11)-98++, y(13)++, y(14)++, y(14)-196++, y(14)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.885

SLPPSPVTHSPLLHPR
Confirmed sites: @S:1,@T:8,@S:10
Ambiguous sites:

MS/MS Fragmentation of SLPPSPVTHSPLLHPR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 4423: 2001.891495 from(668.304441,3+)
Title: Elution from: 43.553 to 43.553 scan no 3815 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2001.8880
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.0034

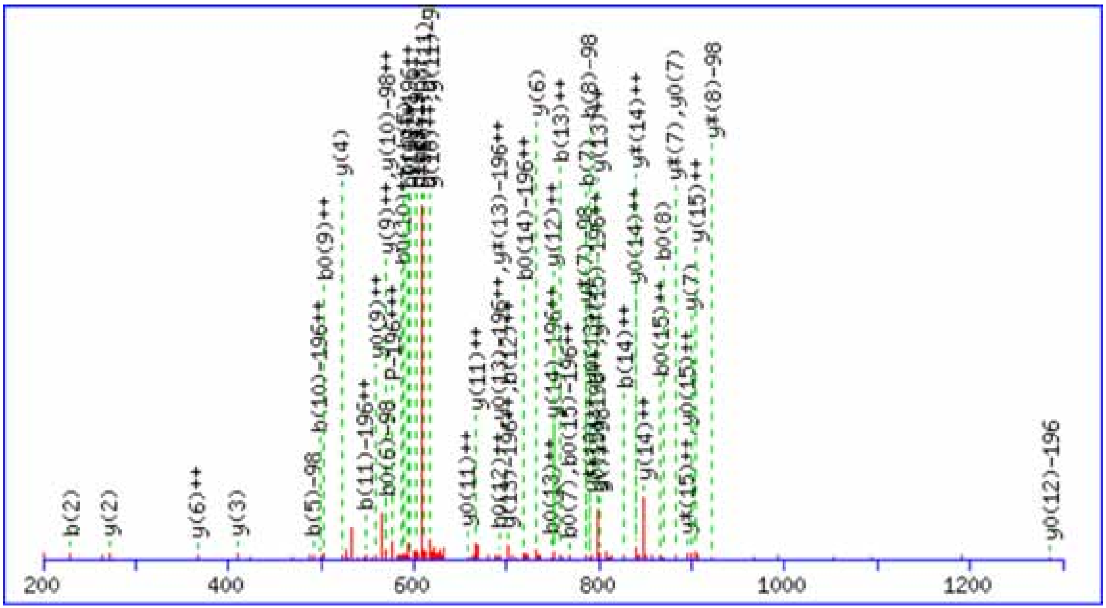
Matched b ions: b(2), b(10)++, b(10)-98++, b(11)-98++, b(12)++, b(12)-294++, b(12)-196++, b(12)-98++, b(13)++, b(13)-98++, b(13)-294++, b(13)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-196++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(8)-98, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(10)-196++, y(11)++, y(11)-196++, y(11)-98++, y(12)-196++, y(13)++, y(14)++, y(14)-98++, y(14)-196++, y(15)-98++, y(15)-196++
Precursor origin neutral loss: +

Peptide No.886

SLPPSPVTHSPLLHPR
Confirmed sites: @S:5,@S:10
Ambiguous sites:

MS/MS Fragmentation of SLPPSPVTHSPLLHPR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 5221: 1921.922703 from(641.648177,3+)
Title: Elution from: 43.078 to 43.078 scan no 4068 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1921.9216
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.028

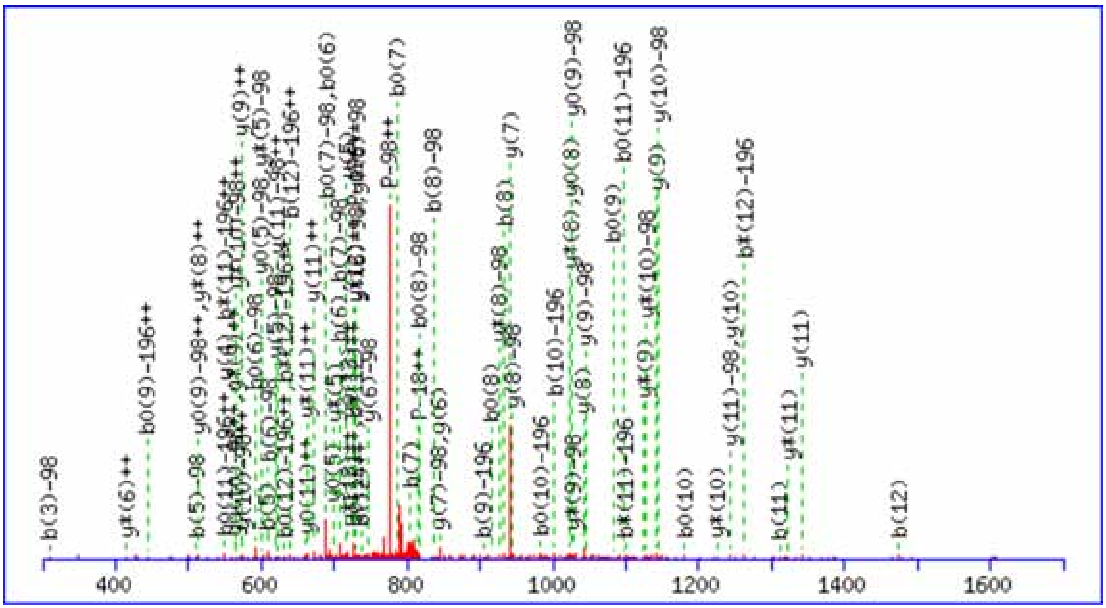
Matched b ions: b(2), b(5)-98, b(5), b(7), b(8)-98, b(10)-98, b(10)-196++, b(10)-98++, b(10)++, b(11)-98, b(11)-196++, b(11)-98++, b(12)++, b(12)-196++, b(13)++, b(14)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(6)++, y(6), y(7)-98, y(7), y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(13)-196++, y(13)-98++, y(14)-98++, y(14)++, y(14)-196++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.887

SLPTTVPESPNYR
Confirmed sites: @S:1,@S:9
Ambiguous sites:

MS/MS Fragmentation of SLPTTVPESPNYR
Found in LARP1_MOUSE, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 2621: 1647.694788 from(824.854670,2+)
Title: Elution from: 45.480 to 45.480 scan no 4160 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1647.6946
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 **Expect:** 0.03

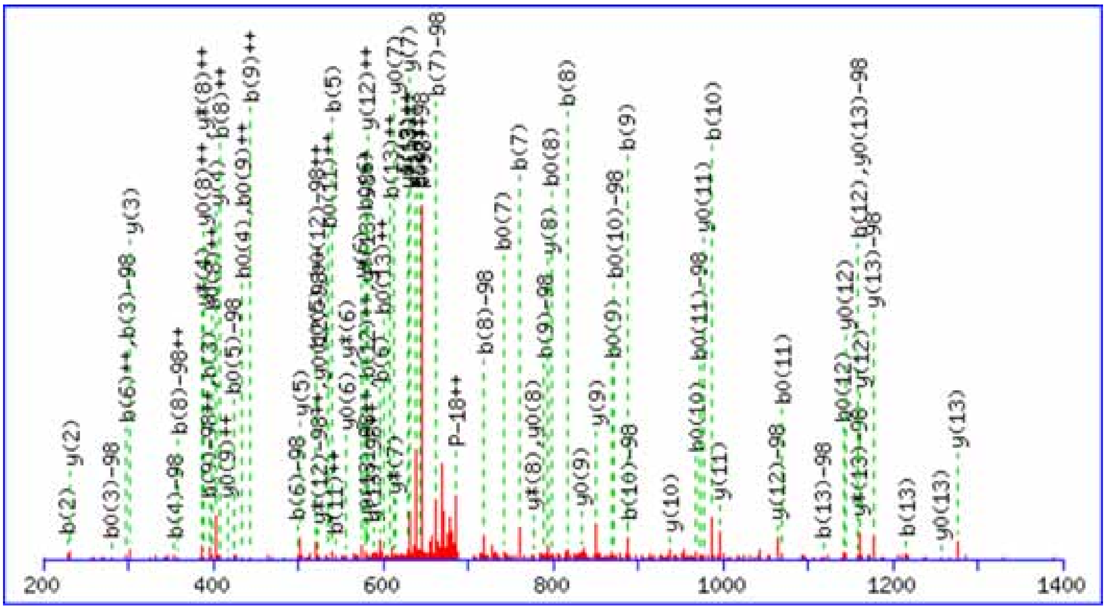
Matched b ions: b(3)-98, b(5), b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(9)-196, b(10)-98++, b(10)-196, b(10)-98, b(11), b(11)-98++, b(12)-98++, b(12), b(12)-98, b(12)-196++, b(12)++
Matched y ions: y(4), y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)++, y(9)-98, y(10), y(10)-98++, y(10)-98, y(11)-98, y(11), y(11)++, y(11)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.888

SLSGSGYGAVTAGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSGSGYGAVTAGK
Found in SMTL2_MOUSE, Smoothelin-like protein 2 OS=Mus musculus GN=Smtnl2 PE=1 SV=1

Match to Query 1531: 1389.655032 from(695.834792,2+)
Title: Elution from: 37.286 to 37.286 scan no 3104 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1389.6541
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
Ions Score: 77 Expect: 7.6e-007

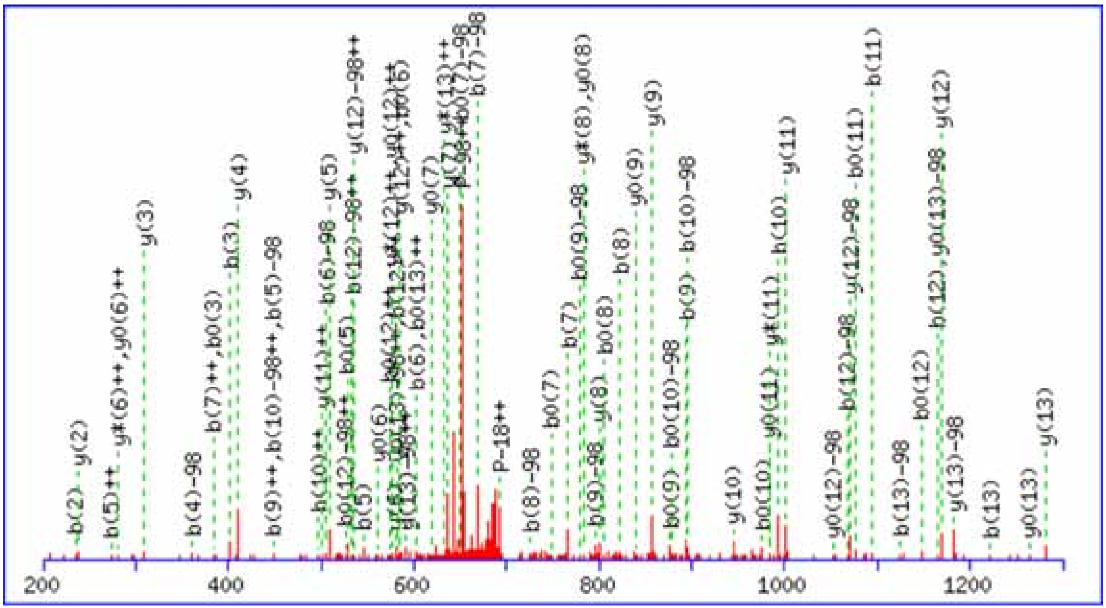
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(5), b(6)-98, b(6), b(6)++, b(7), b(7)-98, b(8)++, b(8)-98, b(8), b(8)-98++, b(9)-98++, b(9), b(9)++, b(9)-98, b(10), b(10)-98, b(11)++, b(12), b(12)++, b(13), b(13)++, b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(12), y(12)++, y(13), y(13)++, y(13)-98, y(13)-98++
Precursor origin neutral loss: +

Peptide No.889

SLSGSGYGAVTAGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSGSGYGAVTAGK
Found in SMTL2_MOUSE, Smoothelin-like protein 2 OS=Mus musculus GN=Smtnl2 PE=1 SV=1

Match to Query 1596: 1401.718638 from(701.866595,2+)
Title: Elution from: 37.106 to 37.106 scan no 3049 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1401.7177
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K14 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 83 Expect: 2.4e-007

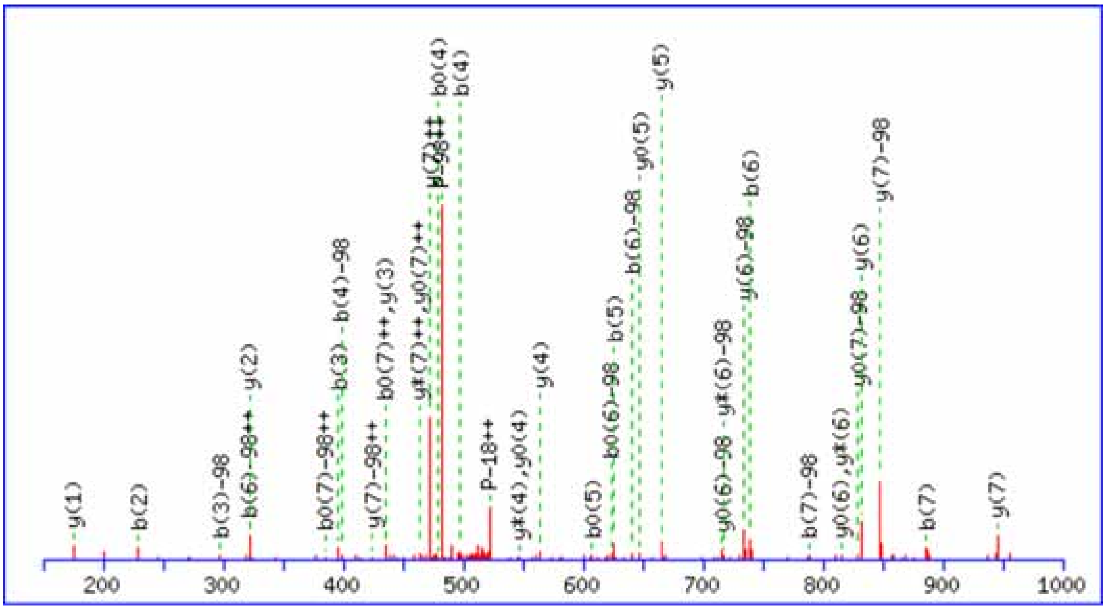
Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(5), b(5)++, b(6)-98, b(6), b(7), b(7)-98, b(7)++, b(8), b(8)-98, b(9)++, b(9), b(9)-98, b(10), b(10)-98++, b(10)-98, b(10)++, b(11), b(12)-98, b(12), b(12)-98++, b(12)++, b(13), b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)-98, y(12), y(12)++, y(12)-98++, y(13)-98, y(13), y(13)-98++
Precursor origin neutral loss: +

Peptide No.890

SLSTELFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SLSTELFK
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 622: 1059.525500 from(530.770026,2+)
Title: Elution from: 51.381 to 51.381 scan no 4886 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1059.5253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K8 : Dimethyl (K)
Ions Score: 49 **Expect:** 0.00028

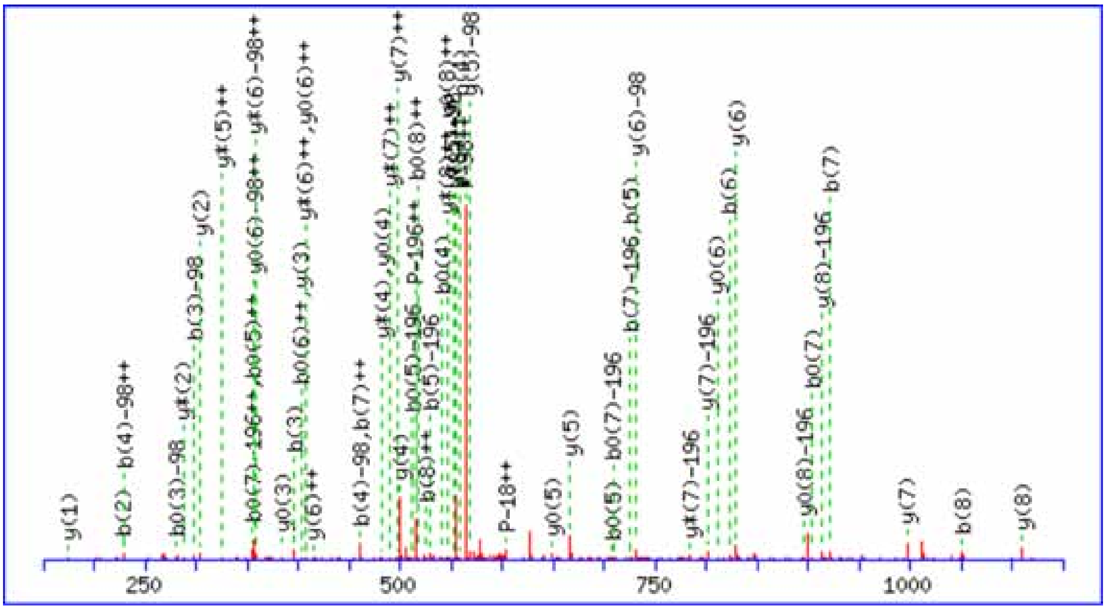
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(6)-98++, b(6), b(6)-98, b(7), b(7)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7)++, y(7)-98, y(7), y(7)-98++
Precursor origin neutral loss: +

Peptide No.891

SLSYSPVER
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SLSYSPVER
Found in SRRM2_MOUSE, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=2

Match to Query 1296: 1224.483814 from(613.249183,2+)
Title: Elution from: 39.105 to 39.105 scan no 3546 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1224.4828
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.022

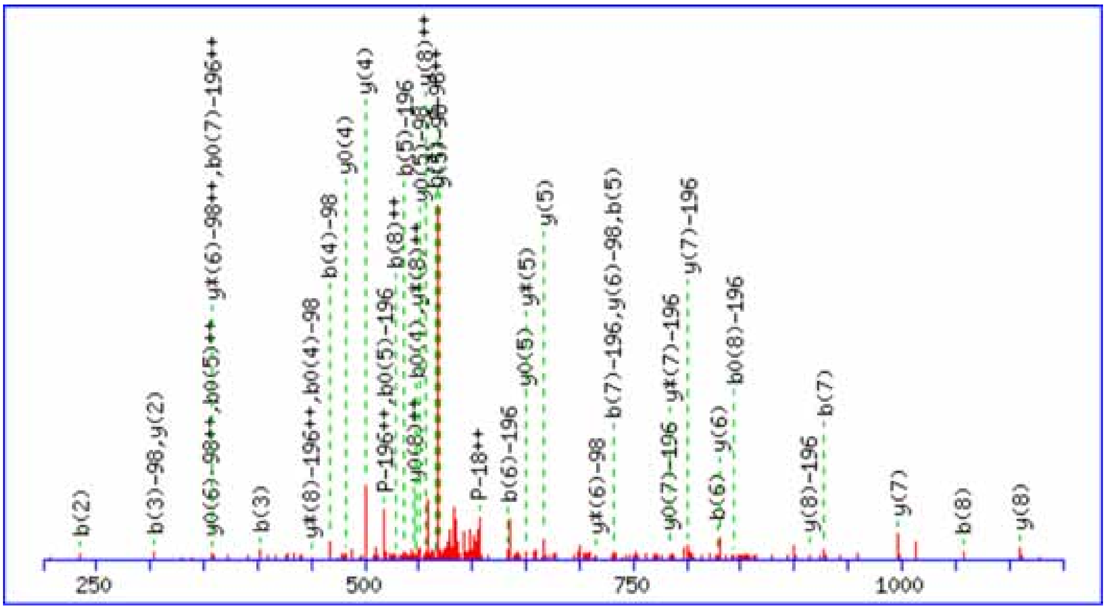
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4)-98++, b(4), b(5)-98, b(5), b(5)-196, b(6)-98, b(6), b(7)++, b(7), b(7)-98, b(7)-196, b(8), b(8)-98, b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)-98, y(6)-98, y(6), y(6)++, y(7)-98, y(7)-196, y(7), y(7)++, y(8)-98, y(8), y(8)++, y(8)-196, y(8)-98++
Precursor origin neutral loss: +

Peptide No.892

SLSYSPVER
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SLSYSPVER
Found in SRRM2_MOUSE, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=2

Match to Query 1052: 1230.515064 from(616.264808,2+)
Title: Elution from: 38.931 to 38.931 scan no 3280 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1230.5147
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.01

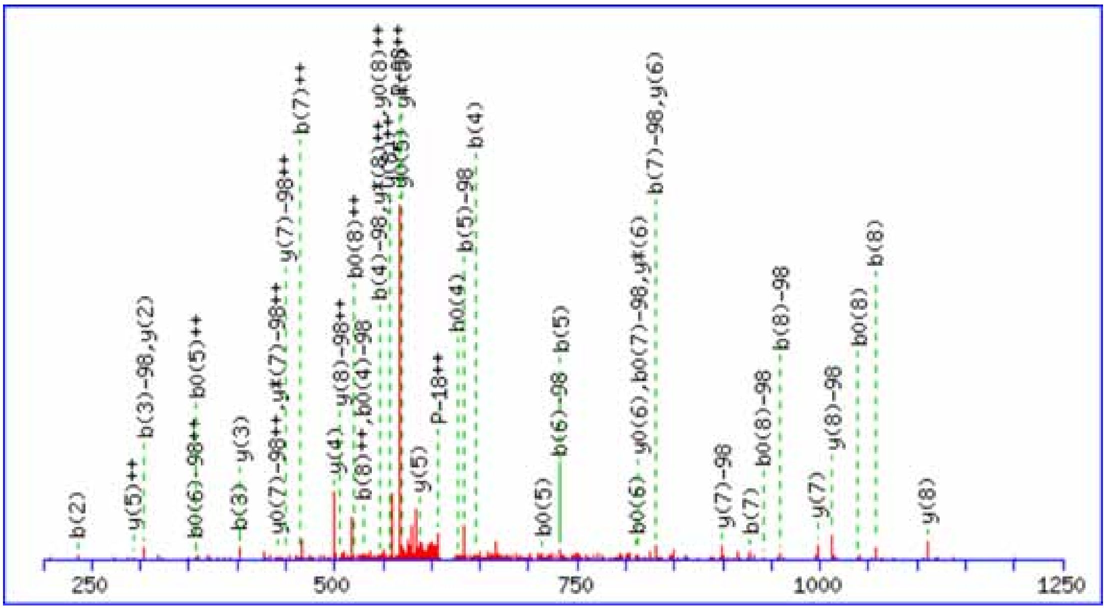
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(5)-196, b(6)-196, b(6)-98, b(6), b(7)-98, b(7), b(7)-196, b(8), b(8)-98, b(8)-98++, b(8)++
Matched y ions: y(2), y(4), y(5), y(5)-98, y(6), y(6)-98, y(7)-196, y(7), y(7)-98, y(7)-98++, y(8)-98, y(8), y(8)-196, y(8)++
Precursor origin neutral loss: +

Peptide No.893

SLSYSPVER
Confirmed sites: @S:3,@Y:4
Ambiguous sites:

MS/MS Fragmentation of SLSYSPVER
Found in SRRM2_MOUSE, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=2

Match to Query 1015: 1230.514966 from(616.264759,2+)
Title: Elution from: 38.916 to 38.916 scan no 3324 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1230.5147
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y4 : Phospho (Y)
Ions Score: 33 Expect: 0.0074

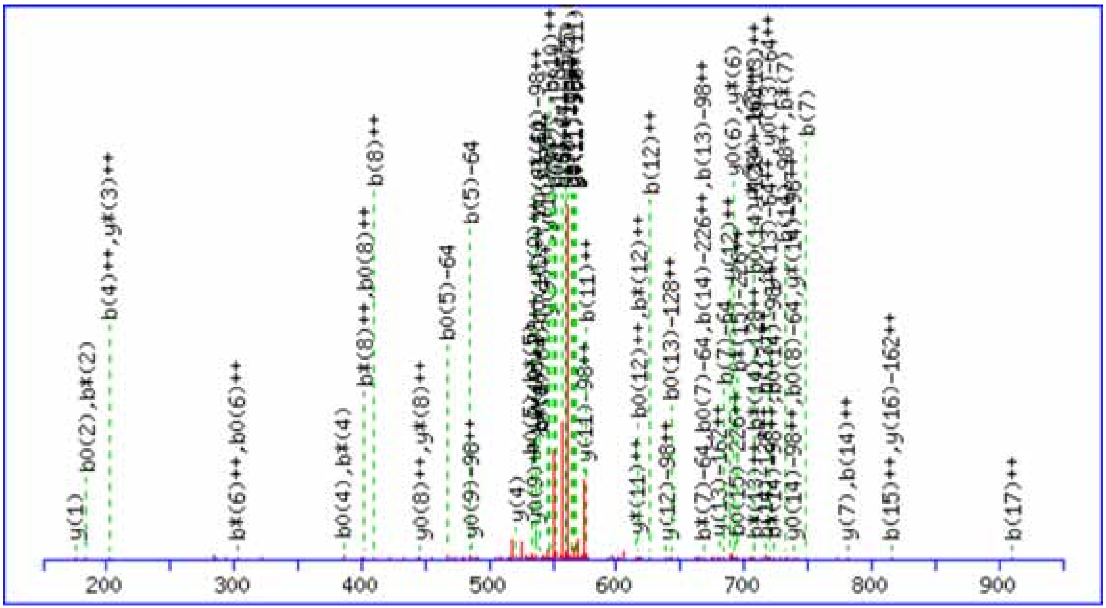
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(7)++, b(8), b(8)-98, b(8)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(7)-98, y(7)-98++, y(8)-98, y(8), y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.894

SNNSMAQAMKGVTKAMGTMNR
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of SNNSMAQAMKGVTKAMGTMNR
Found in CHM2A_MOUSE, Charged multivesicular body protein 2a OS=Mus musculus GN=Chmp2a PE=1 SV=1

Match to Query 5683: 2338.984896 from(585.753500,4+)
Title: Elution from: 24.974 to 24.974 scan no 1429 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2338.9891
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.002

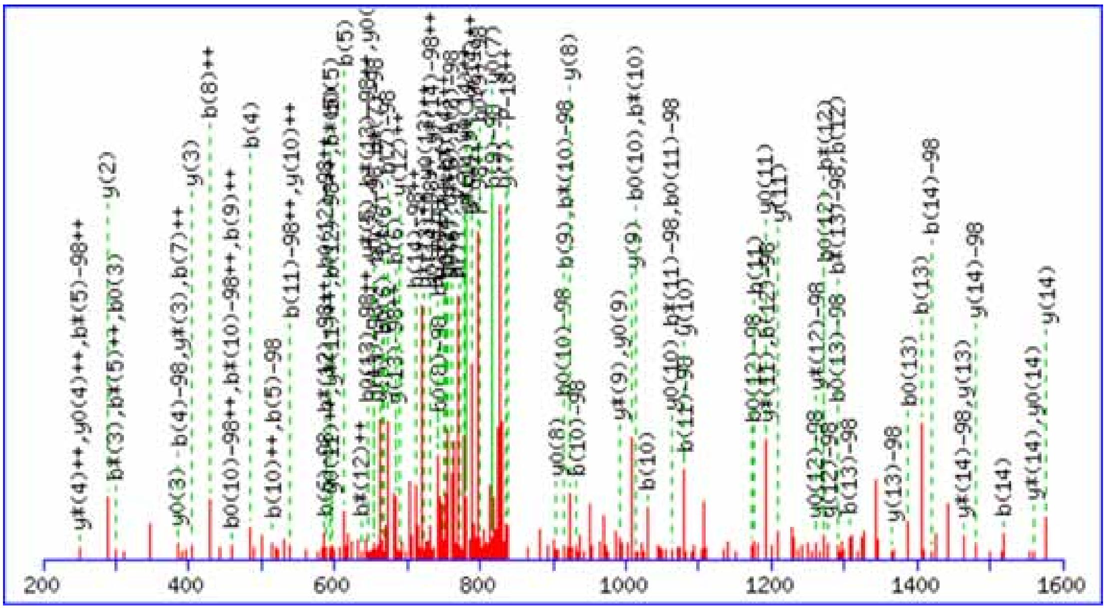
Matched b ions: b(2), b(4)++, b(5), b(7), b(8)++, b(10)++, b(11)++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(17)++
Matched y ions: y(1), y(4), y(7), y(9)++, y(10)-98++, y(11)-98++, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.895

SNSSEASSGDFLDLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SNSSEASSGDFLDLK
Found in HN1_MOUSE, Hematological and neurological expressed 1 protein OS=Mus musculus GN=Hn1 PE=1 SV=3

Match to Query 3630: 1691.729966 from(846.872259,2+)
Title: Elution from: 52.066 to 52.066 scan no 5153 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1691.7291
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 34 Expect: 0.013

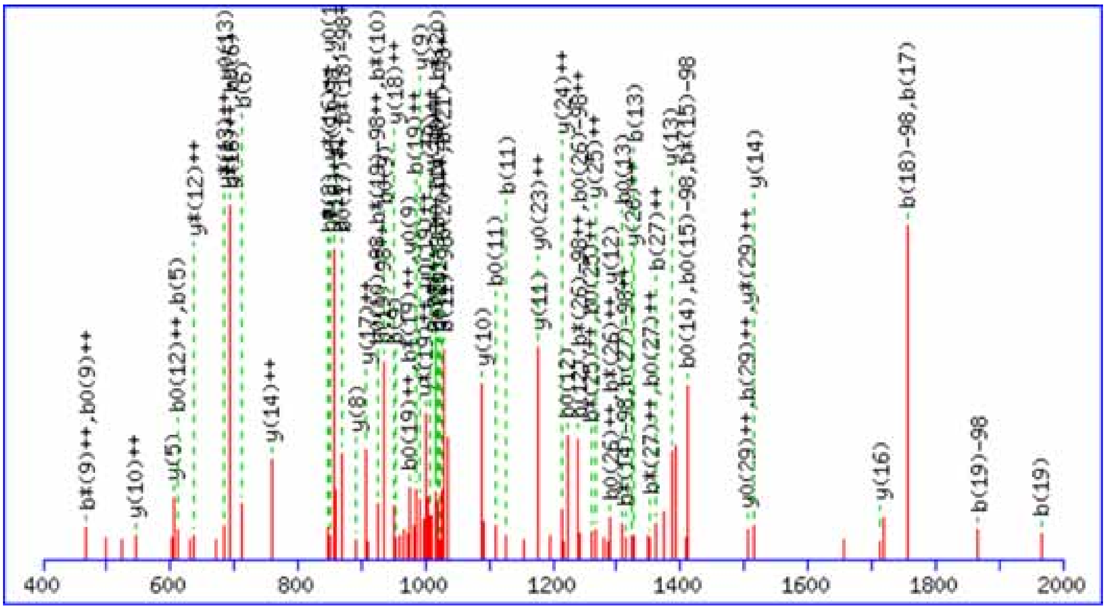
Matched b ions: b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(7)++, b(7)-98, b(7), b(8)++, b(8)-98, b(9)++, b(9), b(9)-98, b(10), b(10)++, b(10)-98, b(11)-98++, b(11)-98, b(11), b(12)-98, b(12)-98++, b(12)++, b(12), b(13), b(13)-98, b(13)-98++, b(14), b(14)-98++, b(14)-98
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(12)++, y(12)-98, y(13), y(13)-98++, y(13)-98, y(14), y(14)-98, y(14)++
Precursor origin neutral loss: +

Peptide No.896

SNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 6983: 3140.405130 from(1047.808986,3+)
Title: Elution from: 49.700 to 49.700 scan no 4558 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3140.4034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.004

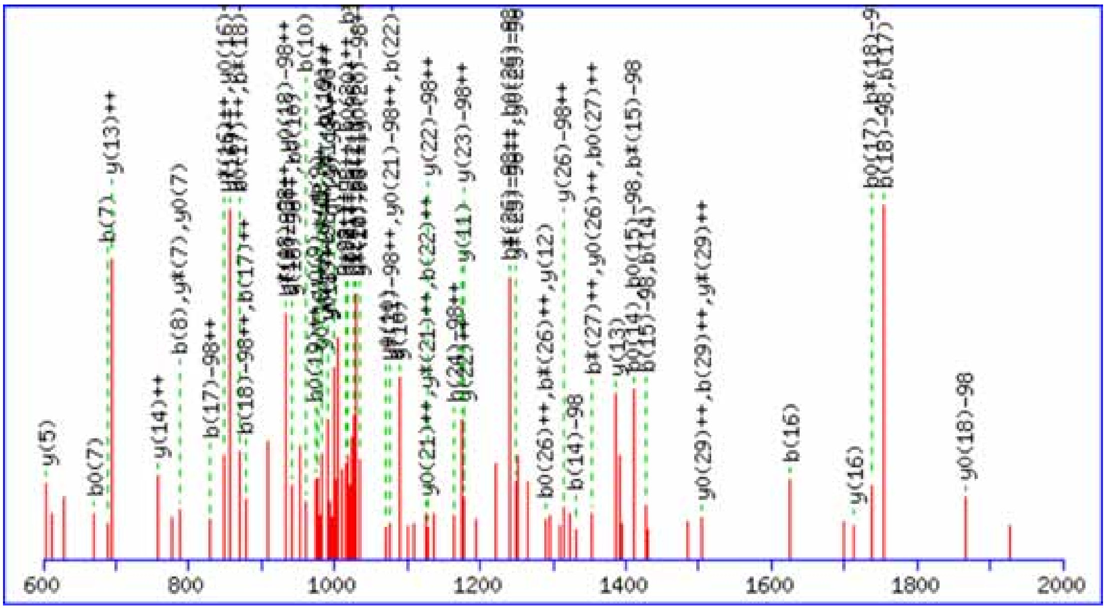
Matched b ions: b(5), b(6), b(9)-98, b(9), b(11)-98, b(11), b(12), b(13), b(17), b(18)-98, b(19), b(19)-98, b(19)++, b(19)-98++, b(20)++, b(21)-98++, b(27)++, b(27)-98++, b(29)++
Matched y ions: y(5), y(8), y(9), y(10), y(10)++, y(11), y(12), y(13)++, y(13), y(14), y(14)++, y(16)++, y(16), y(17)++, y(18)++, y(19)++, y(24)++, y(25)++, y(26)++
Precursor origin neutral loss:

Peptide No.897

SNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Confirmed sites: @T:14
Ambiguous sites:

MS/MS Fragmentation of SNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 7463: 3140.405643 from(1047.809157,3+)
Title: Elution from: 49.619 to 49.619 scan no 4640 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3140.4034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 **Expect:** 0.033

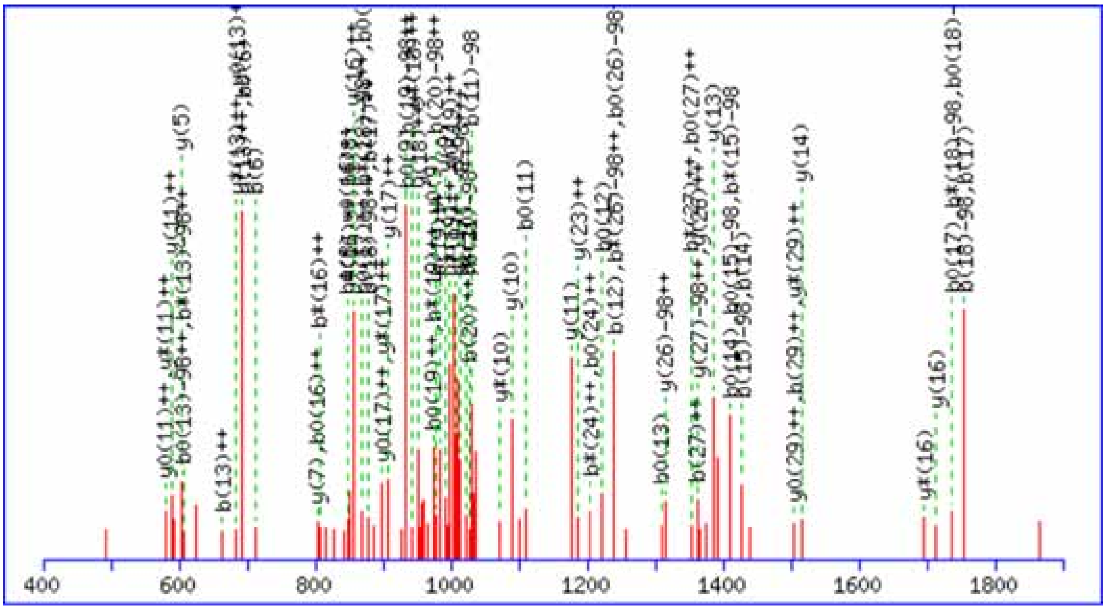
Matched b ions: b(7), b(8), b(10), b(13), b(14), b(14)-98, b(15)-98, b(16), b(17), b(17)++, b(17)-98++, b(18)-98, b(18)-98++, b(19)-98++, b(19)++, b(20)++, b(21)-98++, b(22)++, b(22)-98++, b(24)-98++, b(29)++
Matched y ions: y(5), y(10), y(11), y(12), y(13)++, y(13), y(14)++, y(16)++, y(16), y(18)-98++, y(18)++, y(19)-98++, y(22)++, y(22)-98++, y(23)-98++, y(26)-98++
Precursor origin neutral loss:

Peptide No.898

SNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of SNSVDTGPSSSLSTPTEPLSPTSSLGEERN
Found in **GYS1_MOUSE**, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 7611: 3140.405883 from(1047.809237,3+)
Title: Elution from: 49.535 to 49.535 scan no 4695 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3140.4034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 0.00031

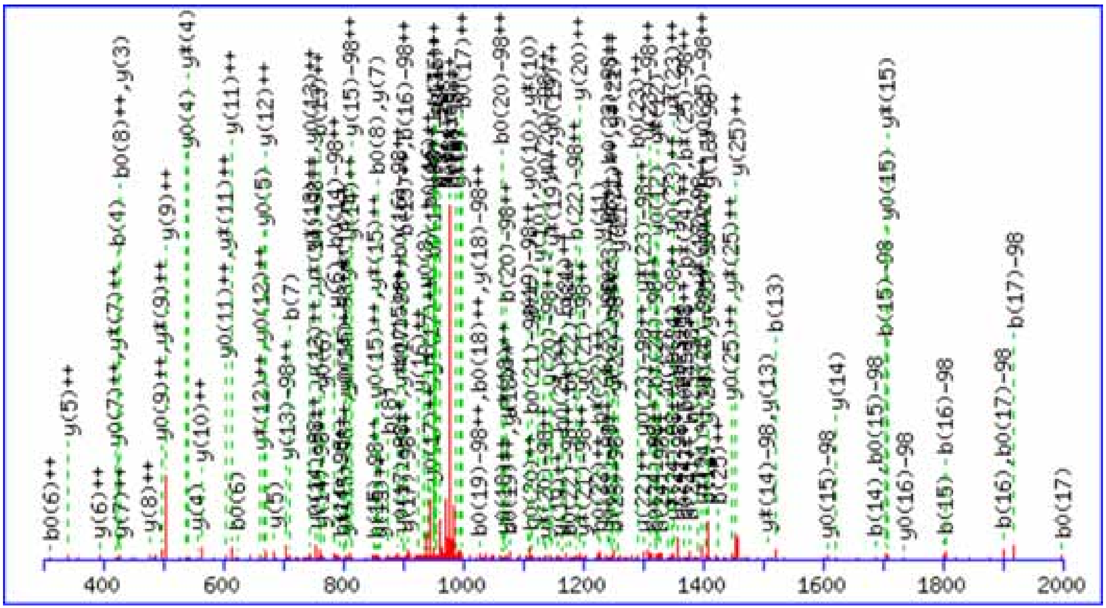
Matched b ions: b(6), b(11)-98, b(12), b(13)++, b(14), b(15)-98, b(17), b(17)++, b(18)-98, b(18)-98++, b(19)++, b(19)-98++, b(20)-98++, b(20)++, b(21)-98++, b(27)++, b(29)++
Matched y ions: y(5), y(7), y(9), y(10), y(11)++, y(11), y(13)++, y(13), y(14), y(16)++, y(16), y(17)++, y(18)++, y(19)++, y(23)++, y(26)-98++, y(26)++, y(27)-98++
Precursor origin neutral loss:

Peptide No.899

SPPDSEAYYGETDSDVDGPATQEKPR
Confirmed sites: @Y:9,@S:14
Ambiguous sites:

MS/MS Fragmentation of SPPDSEAYYGETDSDVDGPATQEKPR
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 7402: 3026.210766 from(1009.744198,3+)
Title: Elution from: 39.060 to 39.060 scan no 3349 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3026.2107
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y9 : Phospho (Y)
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K24 : Dimethyl (K)
Ions Score: 82 **Expect:** 3.4e-007

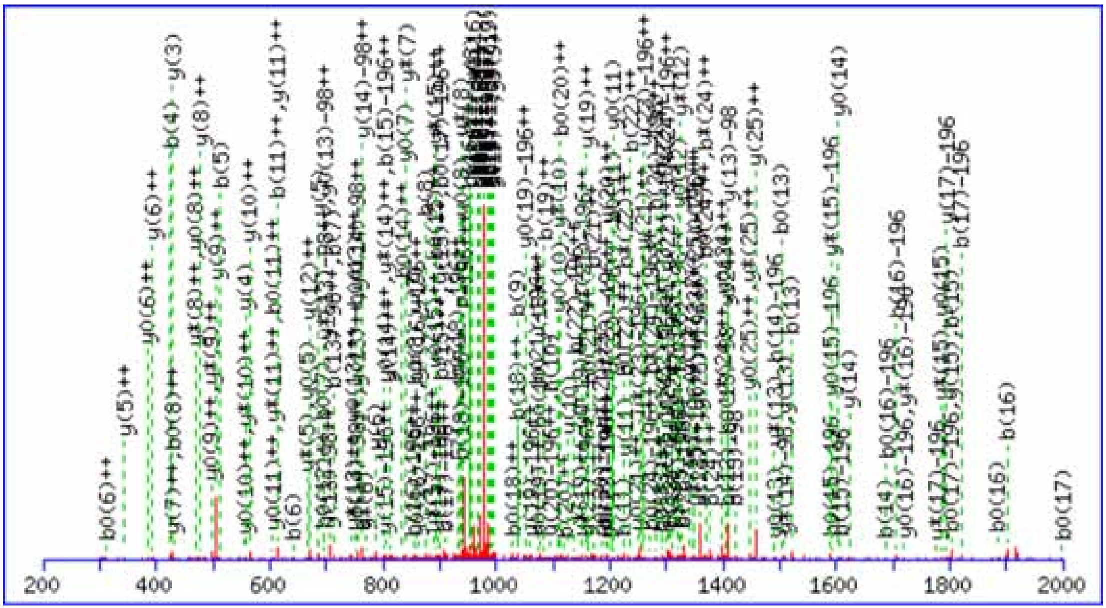
Matched b ions: b(4), b(7), b(8), b(12), b(13), b(13)++, b(14), b(14)-98++, b(15), b(15)-98, b(15)-98++, b(15)++, b(16)-98, b(16), b(16)-98++, b(16)++, b(17)-98, b(17)-98++, b(18)-98++, b(20)-98++, b(21)++, b(22)-98++, b(23)-98++, b(24)++, b(24)-98++, b(25)-98++, b(25)++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13)-98++, y(13)++, y(13), y(13)-98, y(14)-98++, y(14)++, y(14), y(15)-98++, y(15)++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(22)-98++, y(22)++, y(23)++, y(23)-98++, y(24)++, y(24)-98++, y(25)-98++, y(25)++
Precursor origin neutral loss: +

Peptide No.900

SPPDSEAYYGETDSDVDGPATQEKPR
Confirmed sites: @T:12,@S:14
Ambiguous sites:

MS/MS Fragmentation of SPPDSEAYYGETDSDVDGPATQEKPR
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 6937: 3026.210922 from(1009.744250,3+)
Title: Elution from: 38.881 to 38.881 scan no 3211 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3026.2107
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K24 : Dimethyl (K)
Ions Score: 78 **Expect:** 7.9e-007

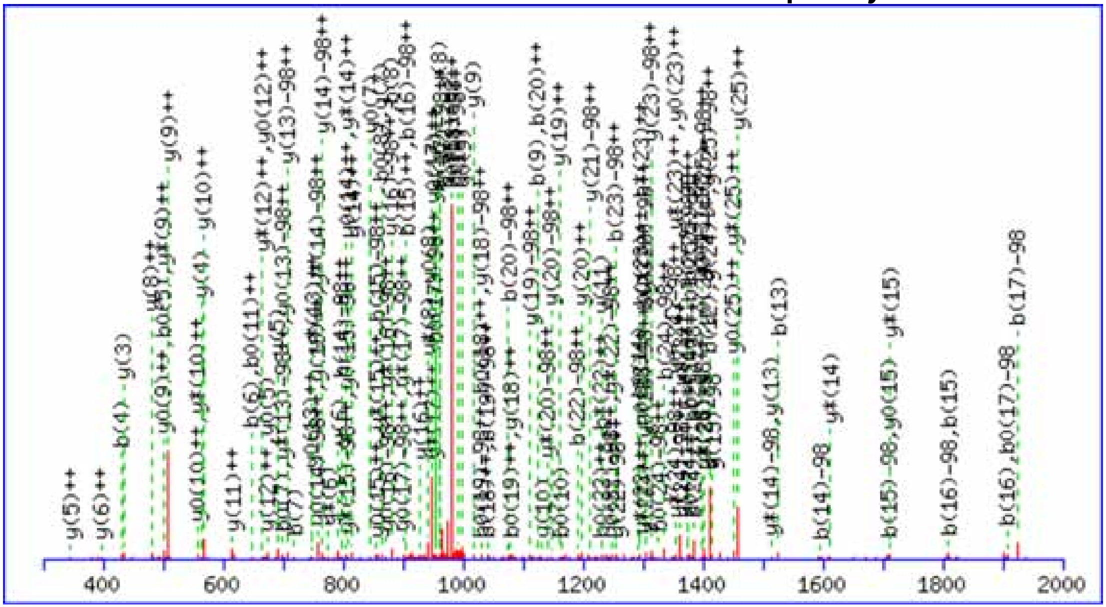
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11)++, b(11), b(12)-98, b(12), b(13), b(13)-98, b(13)-98++, b(14)-98, b(14), b(14)-196, b(15), b(15)-98, b(15)-98++, b(15)-196++, b(15)-196, b(15)++, b(16)-98, b(16), b(16)-196++, b(16)-196, b(16)++, b(16)-98++, b(17)-98, b(17)-196, b(17)-98++, b(17)-196++, b(18)-196++, b(18)-98++, b(18)++, b(18)-98, b(19)-196++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(21)++, b(21)-196++, b(21)-98++, b(22)-196++, b(22)-98++, b(22)++, b(23)++, b(24)-98++, b(24)++, b(24)-196++, b(25)-98++, b(25)-196++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13)-98++, y(13), y(13)++, y(13)-98, y(14)-98++, y(14)++, y(14), y(15), y(15)-98++, y(15)-196++, y(15)-98, y(15)++, y(16)++, y(17)-196, y(17)-196++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(18)-196++, y(19)++, y(19)-196++, y(19)-98++, y(20)++, y(20)-196++, y(20)-98++, y(21)-196++, y(21)++, y(22)-98++, y(22)++, y(22)-196++, y(23)++, y(23)-196++, y(23)-98++, y(24)-98++, y(24)++, y(24)-196++, y(25)-196++, y(25)-98++, y(25)++
Precursor origin neutral loss: +

Peptide No.901

SPPDSEAYYGETDSDVDGPATQEKPR
Confirmed sites: @Y:9,@S:14
Ambiguous sites:

MS/MS Fragmentation of SPPDSEAYYGETDSDVDGPATQEKPR
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 7583: 3038.277090 from(1013.766306,3+)
Title: Elution from: 39.010 to 39.010 scan no 3372 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3038.2744
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y9 : Phospho (Y)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K24 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 91 Expect: 6e-008

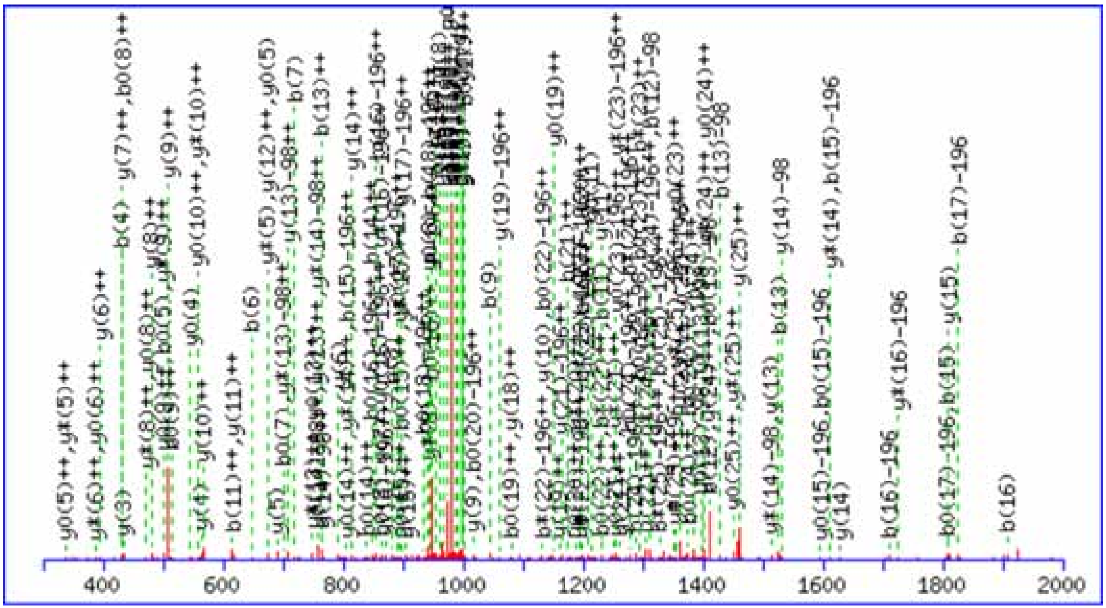
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(12), b(13), b(14)-98, b(14)-98++, b(15)-98, b(15), b(15)-98++, b(15)++, b(16)-98, b(16), b(16)-98++, b(16)++, b(17)-98, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(20)++, b(20)-98++, b(22)-98++, b(23)-98++, b(23)++, b(24)-98++, b(24)++, b(25)-98++
Matched y ions: y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(13)++, y(13)-98++, y(13), y(13)-98, y(14)++, y(14)-98++, y(16)-98++, y(16)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)++, y(20)-98++, y(21)-98++, y(22)++, y(22)-98++, y(23)-98++, y(23)++, y(24)++, y(24)-98++, y(25)-98++, y(25)++
Precursor origin neutral loss: +

Peptide No.902

SPPDSEAYYGETDSDVDGPATQEKPR
Confirmed sites: @T:12,@S:14
Ambiguous sites:

MS/MS Fragmentation of SPPDSEAYYGETDSDVDGPATQEKPR
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 7253: 3038.275611 from(1013.765813,3+)
Title: Elution from: 39.000 to 39.000 scan no 3318 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3038.2744
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K24 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 88 Expect: 1.3e-007

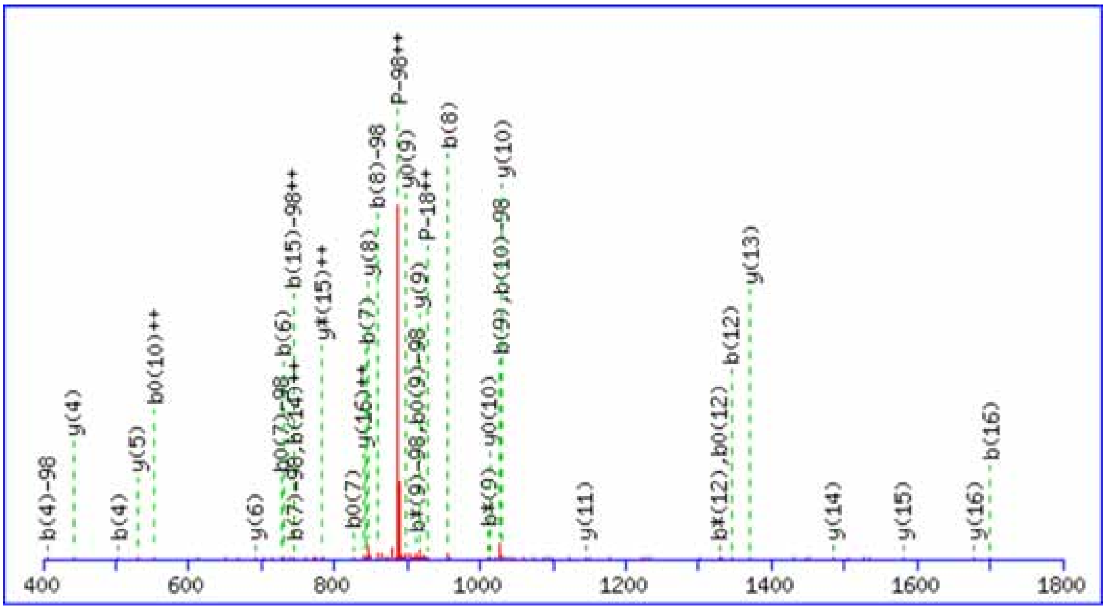
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(11)++, b(11), b(12)-98, b(12), b(13), b(13)++, b(13)-98, b(14)-98, b(14)++, b(15)-98++, b(15)-196, b(15)-98, b(15), b(15)-196++, b(16)-196++, b(16)-196, b(16)-98, b(16), b(16)-98++, b(16)++, b(17)-196, b(17)-98, b(17)-98++, b(18)-98, b(18)-196++, b(18)-98++, b(19)-196++, b(21)++, b(23)-98++, b(24)-98++, b(24)-196++, b(24)++, b(25)-98++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(13)-98++, y(13)++, y(13), y(14)-98++, y(14), y(14)++, y(14)-98, y(15)-98++, y(15)-98, y(15), y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(17)-196++, y(18)-196++, y(18)++, y(19)-98++, y(19)-196++, y(19)++, y(20)++, y(20)-98++, y(21)-196++, y(21)++, y(22)++, y(22)-196++, y(22)-98++, y(23)-98++, y(23)++, y(24)-196++, y(24)++, y(24)-98++, y(25)-98++, y(25)++, y(25)-196++
Precursor origin neutral loss: +

Peptide No.903

SPPNPENIAPGYSGPLK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPPNPENIAPGYSGPLK
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 4323: 1872.903416 from(937.458984,2+)
Title: Elution from: 48.923 to 48.923 scan no 4624 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1872.9022
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K17 : Dimethyl (K)
Ions Score: 52 Expect: 0.00041

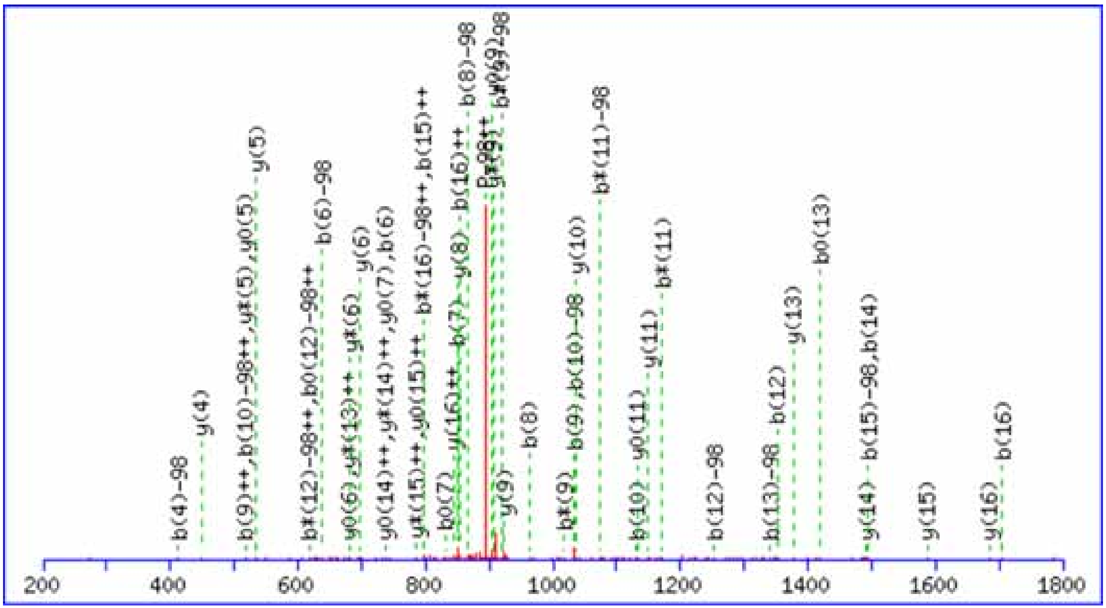
Matched b ions: b(4), b(4)-98, b(6), b(7)-98, b(7), b(8), b(8)-98, b(9), b(10)-98, b(12), b(14)++, b(15)-98++, b(16)
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(13), y(14), y(15), y(16), y(16)++
Precursor origin neutral loss: +

Peptide No.904

SPPNPENIAPGYSGPLK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SPPNPENIAPGYSGPLK
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 4506: 1884.967834 from(943.491193,2+)
Title: Elution from: 48.609 to 48.609 scan no 4585 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1884.9659
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 43 Expect: 0.0028

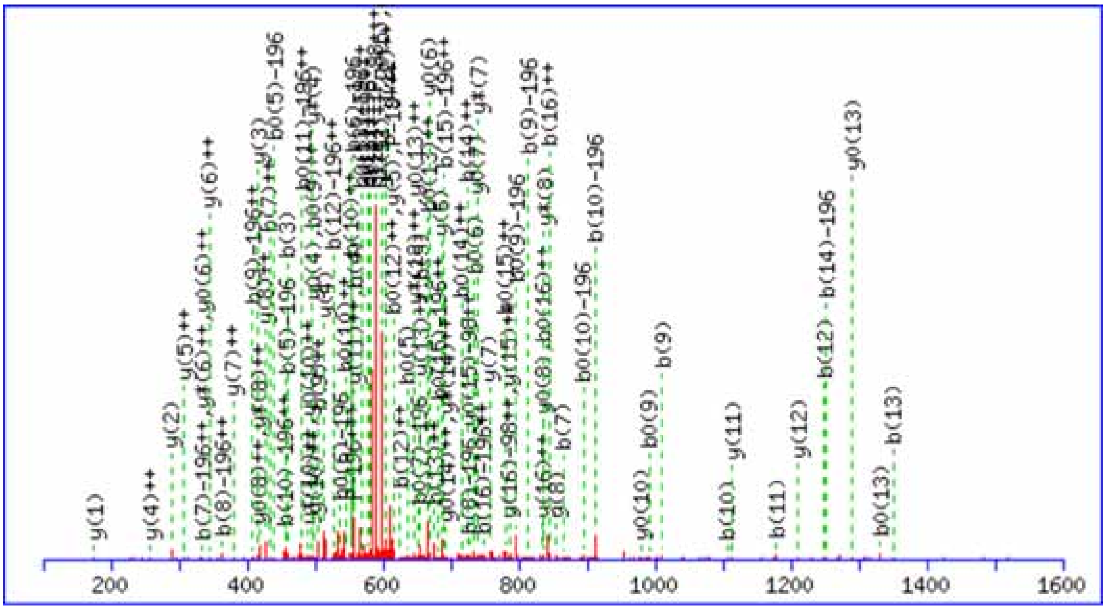
Matched b ions: b(4)-98, b(6)-98, b(6), b(7), b(8)-98, b(8), b(9), b(9)++, b(10)-98, b(10)-98++, b(10), b(12), b(12)-98, b(13)-98, b(14), b(15)-98, b(15)++, b(16), b(16)++
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(13), y(14), y(15), y(16), y(16)++
Precursor origin neutral loss: +

Peptide No.905

SPSPPPDGSPAATPEIR
Confirmed sites: @S:1,@S:3
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 4788: 1862.786640 from(621.936156,3+)
Title: Elution from: 36.628 to 36.628 scan no 3210 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1862.7852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.024

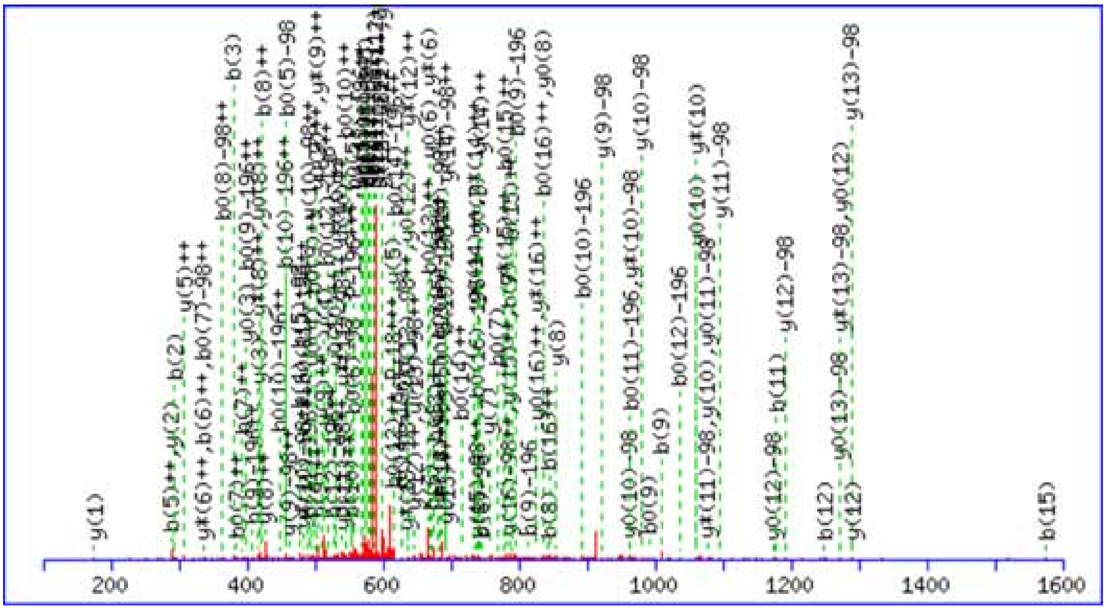
Matched b ions: b(3), b(4), b(4)-98, b(5)-98, b(5)-196, b(5), b(6)-196, b(6)-98, b(7)-196++, b(7)++, b(7), b(8)-196++, b(8)-196, b(9)-98, b(9), b(9)-98++, b(9)++, b(9)-196++, b(9)-196, b(10)-196, b(10)-196++, b(10)-98, b(10), b(10)-98++, b(10)++, b(11)++, b(11), b(11)-98, b(11)-98++, b(12), b(12)-196++, b(12)-98++, b(12)++, b(13)++, b(13), b(13)-98, b(13)-196++, b(13)-98++, b(14)-98++, b(14)-98, b(14)-196, b(14)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-196++, b(16)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(8), y(10)++, y(11)++, y(11), y(12), y(12)++, y(13)++, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.906

SPSPPPDGSPAATPEIR
Confirmed sites: @S:1,@S:9
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 4095: 1862.787438 from(621.936422,3+)
Title: Elution from: 36.393 to 36.393 scan no 2978 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1862.7852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.0013

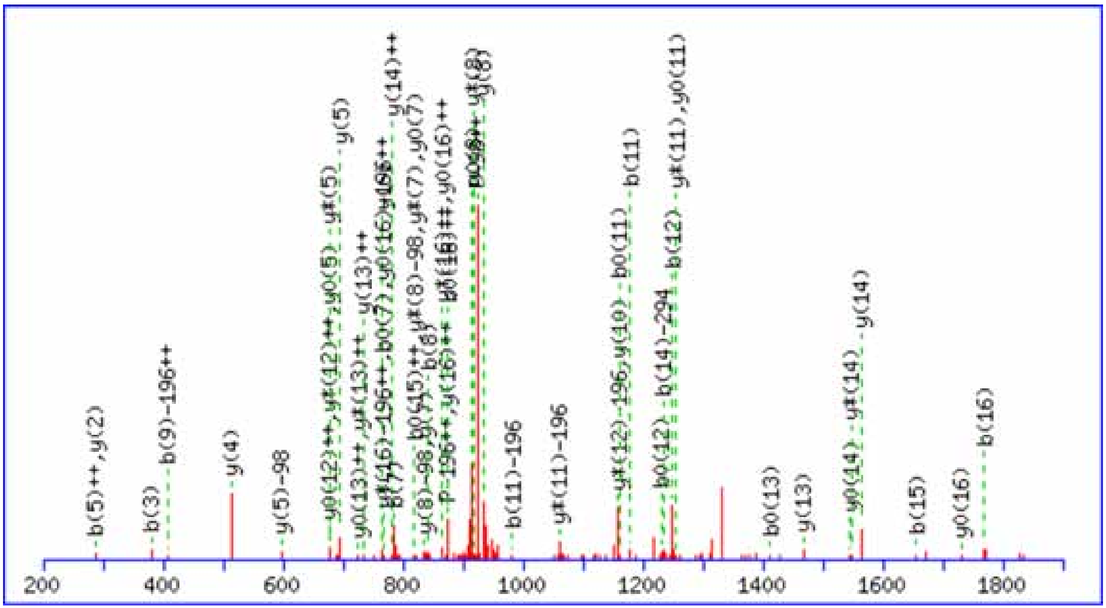
Matched b ions: b(2), b(3), b(4), b(5)++, b(5)-98, b(5), b(6)-98, b(6)++, b(6), b(7), b(7)++, b(8), b(8)++, b(8)-98, b(9)-98, b(9), b(9)-98++, b(9)++, b(9)-196++, b(9)-196, b(10)-98, b(10)-196++, b(10)-98++, b(10)++, b(11)++, b(11), b(11)-98++, b(11)-196++, b(12), b(12)-98++, b(12)-196++, b(13)++, b(13)-196++, b(13)-98++, b(14)-98++, b(14)-196++, b(15), b(15)-98++, b(15)-196++, b(15)++, b(16)++, b(16)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(8)++, y(8), y(9)-98++, y(9)++, y(9)-98, y(10), y(10)-98, y(10)-98++, y(10)++, y(11)-98, y(11)++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13)-98, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.907

SPSPPPDGSPAATPEIR
Confirmed sites: @S:1,@S:9,@T:13
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 5343: 1942.751358 from(972.382955,2+)
Title: Elution from: 37.778 to 37.778 scan no 3369 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1942.7516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0042

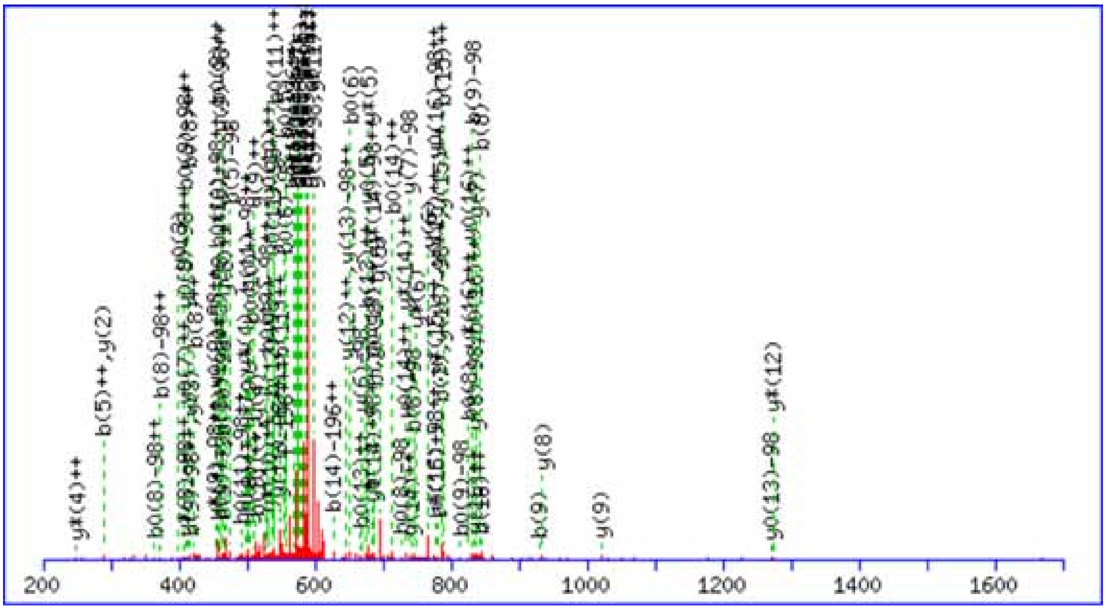
Matched b ions: b(3), b(5)++, b(7), b(8), b(9)-196++, b(9)-98, b(11), b(11)-196, b(12), b(12)-98, b(13)-98, b(13)-196, b(14)-196, b(14)-294, b(15), b(16)-98, b(16), b(16)-196++, b(16)-98++
Matched y ions: y(2), y(4), y(5)-98, y(5), y(6), y(7), y(8), y(8)-98, y(10)-98, y(10), y(13), y(13)++, y(14)-98, y(14), y(14)++, y(14)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.908

SPSPPPDGSPAATPEIR
Confirmed sites: @S:1,@T:13
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 4774: 1862.784933 from(621.935587,3+)
Title: Elution from: 33.860 to 33.860 scan no 2831 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1862.7852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 **Expect:** 0.039

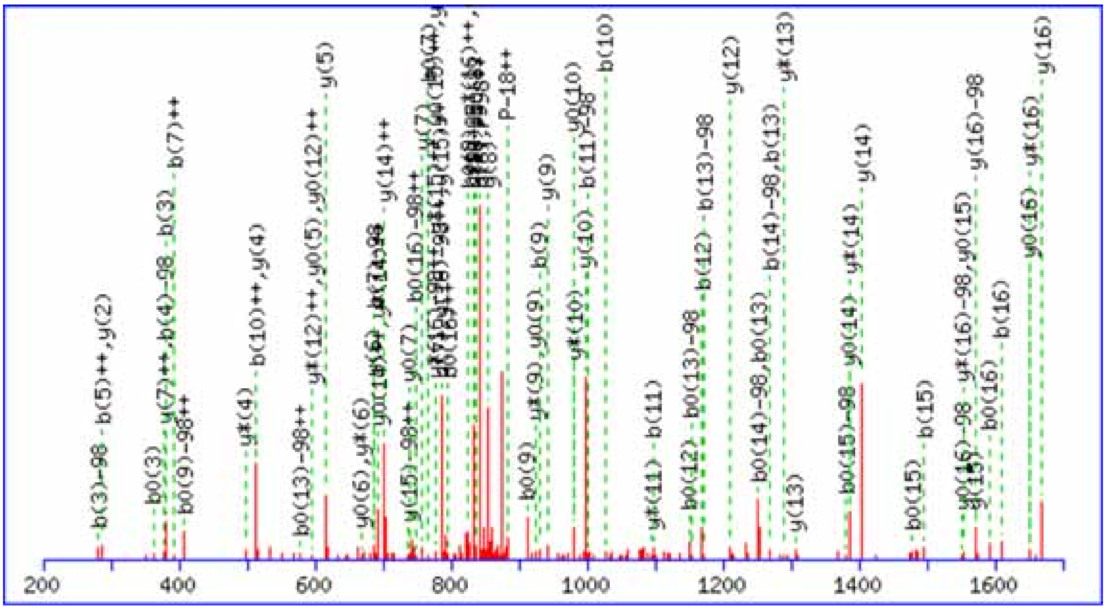
Matched b ions: b(5)++, b(5)-98, b(5), b(6)-98, b(7), b(7)-98, b(8)++, b(8)-98, b(8), b(8)-98++, b(9)-98++, b(9), b(9)-98, b(9)++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-196++, b(13)-98++, b(13)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)++, y(8)-98, y(9), y(9)-98++, y(9)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)-98++, y(14)++, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.909

SPSPPPDGSPAATPEIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 4229: 1782.820550 from(892.417551,2+)
Title: Elution from: 35.617 to 35.617 scan no 3073 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1782.8189
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 Expect: 1.1e-006

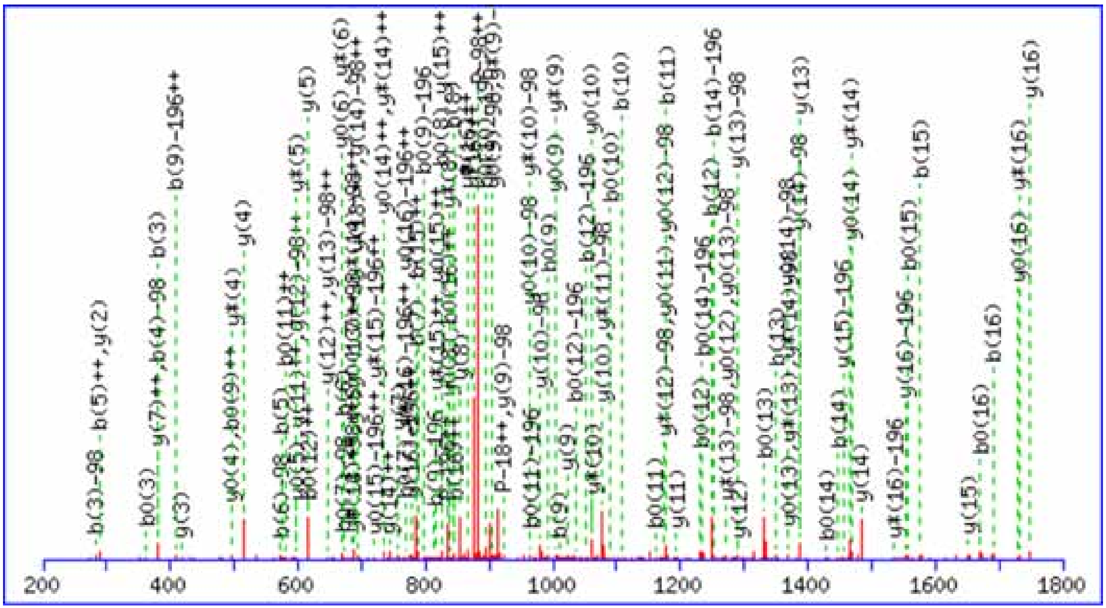
Matched b ions: b(3), b(3)-98, b(4)-98, b(5)++, b(7)++, b(7), b(7)-98, b(8), b(9), b(9)-98, b(10)++, b(10), b(11), b(11)-98, b(12), b(13), b(13)-98, b(14)-98, b(15), b(16)
Matched y ions: y(2), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(12), y(13), y(14)++, y(14), y(15), y(15)++, y(15)-98++, y(16)-98, y(16), y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.910

SPSPPPDGSPAATPEIR
Confirmed sites: @S:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 3468: 1862.786812 from(932.400682,2+)
Title: Elution from: 37.573 to 37.573 scan no 3032 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1862.7852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 84 **Expect:** 1.2e-007

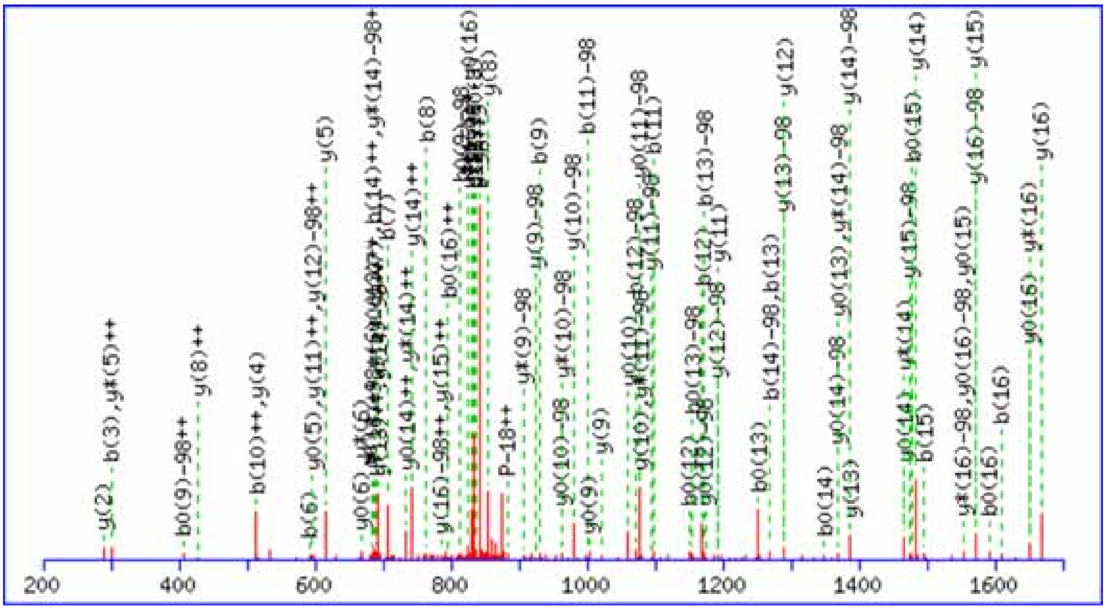
Matched b ions: b(3), b(3)-98, b(4)-98, b(5)++, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8), b(9)-196++, b(9)-98, b(9)-196, b(9), b(10)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(12)-196, b(13), b(13)-98, b(14)-98, b(14)-196, b(14), b(15), b(15)-98, b(15)++, b(16), b(16)-98, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11)++, y(11), y(12), y(12)-98++, y(12)++, y(13)++, y(13), y(13)-98++, y(13)-98, y(14), y(14)++, y(14)-98, y(14)-98++, y(15), y(15)-98, y(15)-196, y(15)++, y(15)-98++, y(16), y(16)++, y(16)-196, y(16)-98, y(16)-98++, y(16)-196++
Precursor origin neutral loss: +

Peptide No.911

SPSPPPDGSPAATPEIR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 3606: 1782.819892 from(892.417222,2+)
Title: Elution from: 33.747 to 33.747 scan no 2648 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1782.8189
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 90 Expect: 5.2e-008

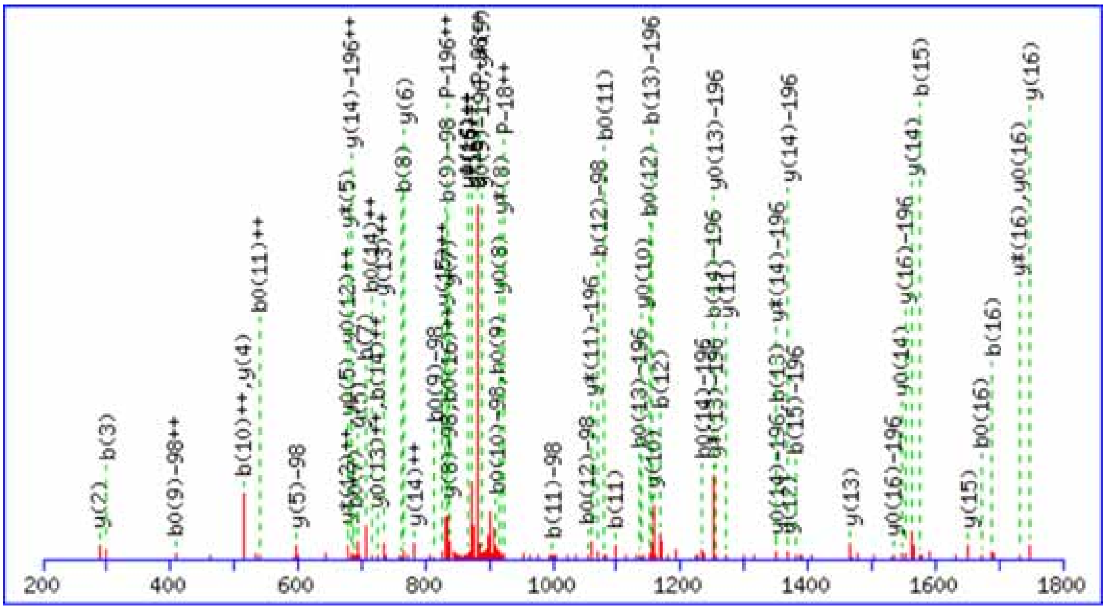
Matched b ions: b(3), b(6), b(7), b(8), b(9), b(9)-98, b(10)++, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(14)-98, b(14)++, b(15), b(16)
Matched y ions: y(2), y(4), y(5), y(6), y(8)++, y(8), y(9), y(9)-98, y(10)-98, y(10), y(11)++, y(11), y(11)-98, y(12)-98, y(12), y(12)-98++, y(13)++, y(13), y(13)-98, y(14)++, y(14)-98, y(14), y(14)-98++, y(15), y(15)-98, y(15)++, y(16)-98, y(16), y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.912

SPSPPPDGSPAATPEIR
Confirmed sites: @S:9,@T:13
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 4779: 1862.785764 from(932.400158,2+)
Title: Elution from: 33.679 to 33.679 scan no 2807 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1862.7852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 0.00019

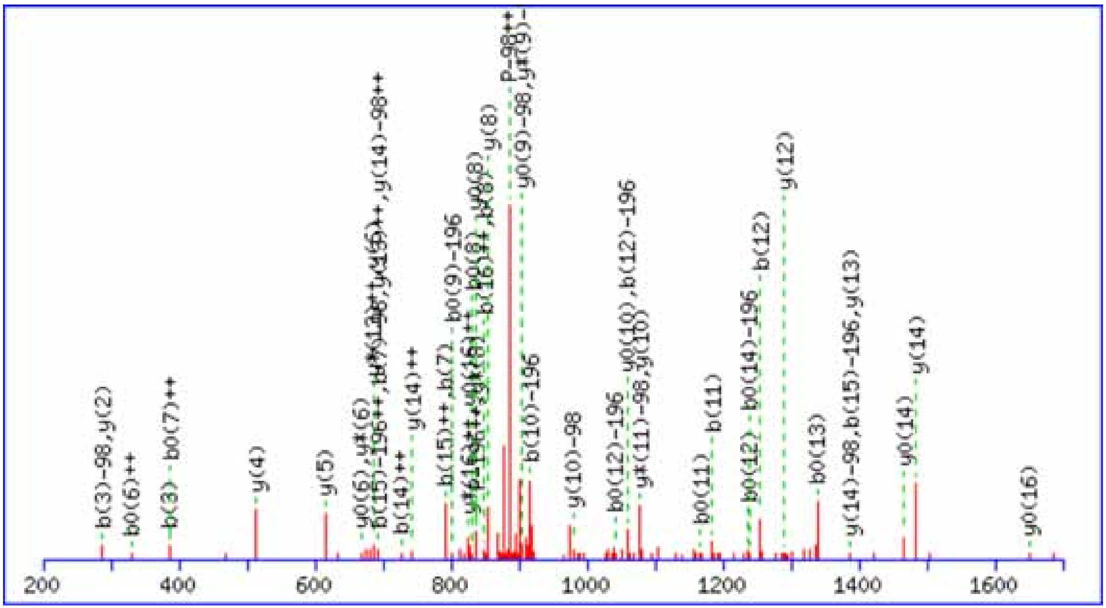
Matched b ions: b(3), b(7), b(8), b(9)-98, b(10)++, b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13), b(13)-196, b(14)-196, b(14)-98, b(14)++, b(15)-98, b(15), b(15)-196, b(16), b(16)-98
Matched y ions: y(2), y(4), y(5)-98, y(5), y(6), y(7), y(8)-98, y(9)-98, y(10)-98, y(10), y(11), y(12), y(12)-98, y(13)-98, y(13), y(13)-98++, y(13)++, y(14)-98, y(14), y(14)++, y(14)-196++, y(14)-98++, y(14)-196, y(15), y(15)-98, y(15)++, y(16)-98, y(16), y(16)++, y(16)-196, y(16)-98++
Precursor origin neutral loss: +

Peptide No.913

SPSPPPDGSPAATPEIR
Confirmed sites: @S:9
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 3847: 1868.818860 from(935.416706,2+)
Title: Elution from: 35.834 to 35.834 scan no 2886 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1868.8171
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0096

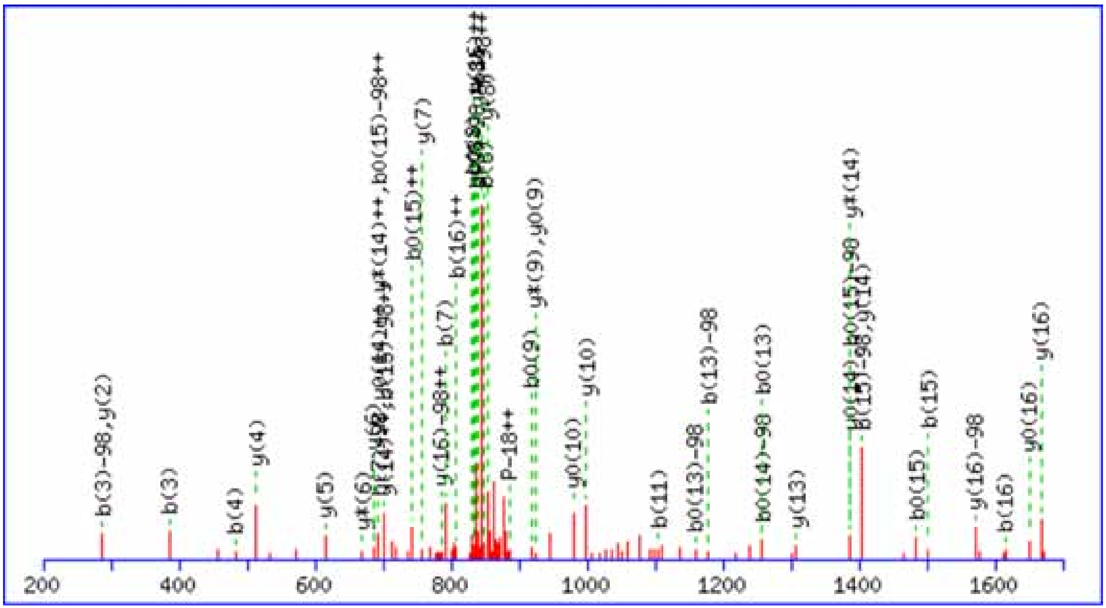
Matched b ions: b(3), b(3)-98, b(7)-98, b(7), b(8), b(9)-98, b(10)-196, b(11), b(12), b(12)-196, b(12)-98, b(13)-98, b(14)++, b(15)-196++, b(15)-98, b(15)-98++, b(15)++, b(15)-196, b(16)++
Matched y ions: y(2), y(4), y(5), y(6), y(8), y(10), y(10)-98, y(12), y(13)++, y(13), y(14)-98++, y(14), y(14)++, y(14)-98
Precursor origin neutral loss: +

Peptide No.914

SPSPPPDGSPAATPEIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 4874: 1788.850580 from(895.432566,2+)
Title: Elution from: 34.784 to 34.784 scan no 2894 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1788.8507
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 **Expect:** 0.00083

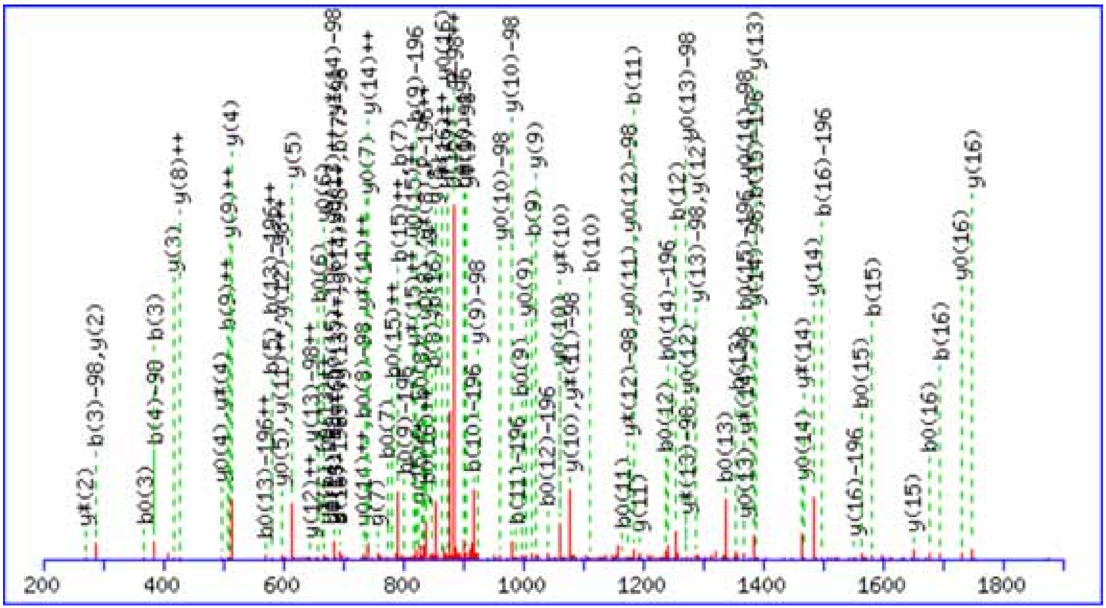
Matched b ions: b(3), b(3)-98, b(4), b(7)-98, b(7), b(8), b(9)-98, b(11), b(13)-98, b(15)-98++, b(15)-98, b(15), b(16), b(16)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(10), y(13), y(14)++, y(14), y(16)-98, y(16), y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.915

SPSPPPDGSPAATPEIR
Confirmed sites: @S:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 3818: 1868.818500 from(935.416526,2+)
Title: Elution from: 37.203 to 37.203 scan no 3075 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1868.8171
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 96 **Expect:** 1.2e-008

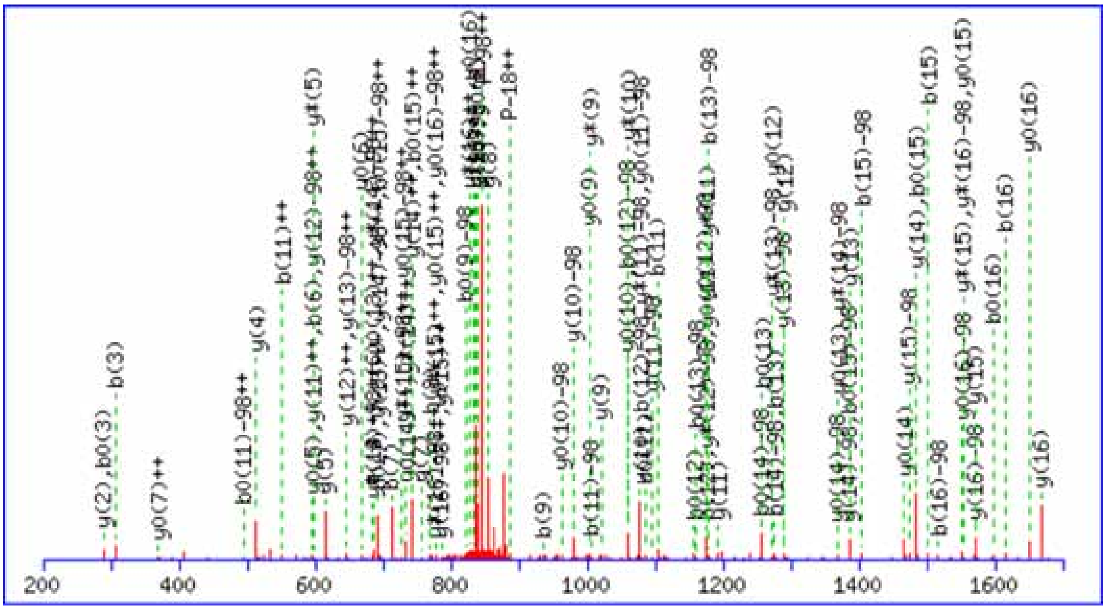
Matched b ions: b(3)-98, b(3), b(4)-98, b(5), b(7), b(7)-98, b(8), b(9), b(9)++, b(9)-98, b(9)-196, b(10)-196, b(10)-98, b(10)-98++, b(10), b(11)-98, b(11), b(11)-196, b(12), b(12)-98, b(13), b(13)-98, b(13)-196++, b(15)++, b(15)-98, b(15)-98++, b(15)-196, b(15), b(15)-196++, b(16), b(16)-98, b(16)++, b(16)-98++, b(16)-196
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(9)++, y(9)-98, y(10), y(10)-98, y(11)++, y(11), y(12)-98++, y(12), y(12)++, y(13)++, y(13), y(13)-98, y(13)-98++, y(14), y(14)++, y(14)-98, y(14)-98++, y(15)-98, y(15), y(15)++, y(16)-98, y(16), y(16)-196, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.916

SPSPPPDGSPAATPEIR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 3541: 1788.850514 from(895.432533,2+)
Title: Elution from: 33.530 to 33.530 scan no 2583 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1788.8507
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 89 Expect: 6.6e-008

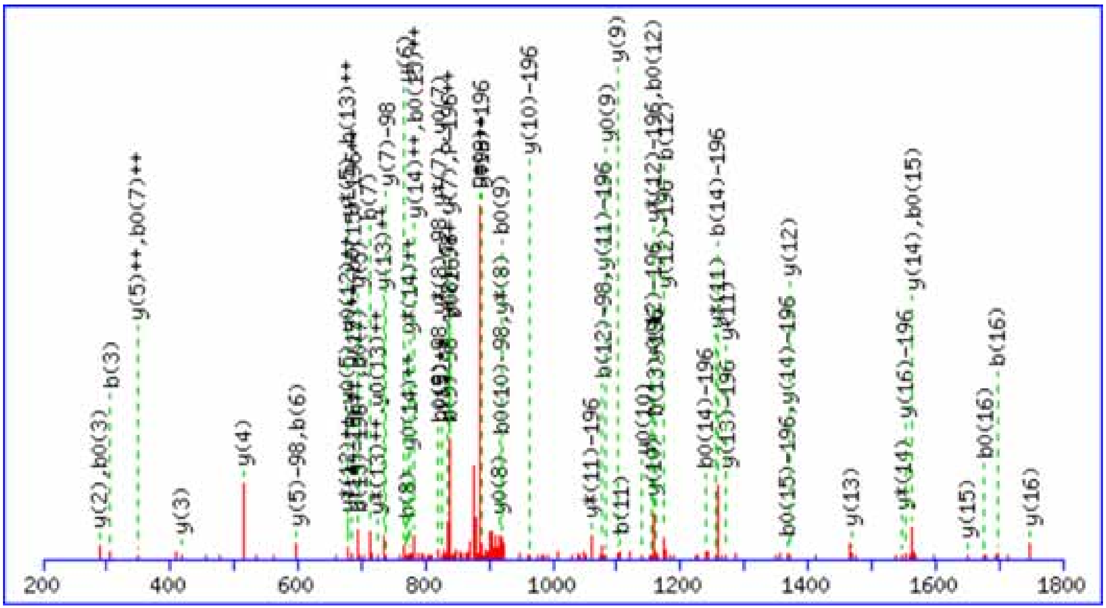
Matched b ions: b(3), b(6), b(7), b(8), b(9), b(9)-98, b(11), b(11)++, b(11)-98, b(12)-98, b(12), b(13)-98, b(13), b(14)-98, b(15)-98, b(15), b(16), b(16)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11), y(11)++, y(11)-98, y(12)++, y(12), y(12)-98++, y(13), y(13)-98++, y(13)++, y(13)-98, y(14)++, y(14)-98, y(14), y(14)-98++, y(15), y(15)-98, y(15)++, y(16)-98, y(16), y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.917

SPSPPPDGSPAATPEIR
Confirmed sites: @S:9,@T:13
Ambiguous sites:

MS/MS Fragmentation of SPSPPPDGSPAATPEIR
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 3817: 1868.818338 from(935.416445,2+)
Title: Elution from: 34.262 to 34.262 scan no 2669 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1868.8171
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 7.4e-005

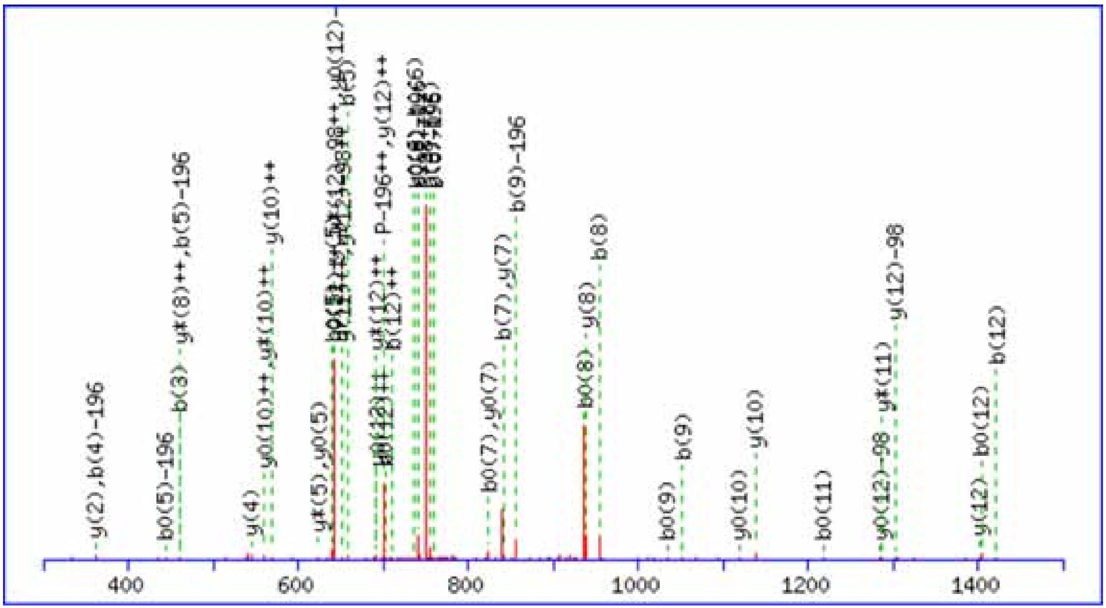
Matched b ions: b(3), b(6), b(7), b(8), b(9)-98, b(11), b(12), b(12)-98, b(13)-98, b(13)++, b(13)-196, b(14)-196, b(14)-98, b(14)-98++, b(15)-196++, b(16)-98, b(16)
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(5)++, y(6), y(7), y(7)-98, y(8)-98, y(9), y(10)-98, y(10), y(10)-196, y(11)-98, y(11)-196, y(11), y(12)++, y(12)-196, y(12), y(12)-98, y(13)-98, y(13), y(13)-98++, y(13)++, y(13)-196, y(14)-98, y(14), y(14)-196++, y(14)-98++, y(14)-196, y(14)++, y(15), y(15)++, y(16), y(16)-196, y(16)-98, y(16)-98++
Precursor origin neutral loss: +

Peptide No.918

SPSPTPSLPPSWK
Confirmed sites: @S:1,@S:3
Ambiguous sites:

MS/MS Fragmentation of SPSPTPSLPPSWK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 3043: 1595.704352 from(798.859452,2+)
Title: Elution from: 51.627 to 51.627 scan no 5098 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1595.7038
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 50 Expect: 0.00038

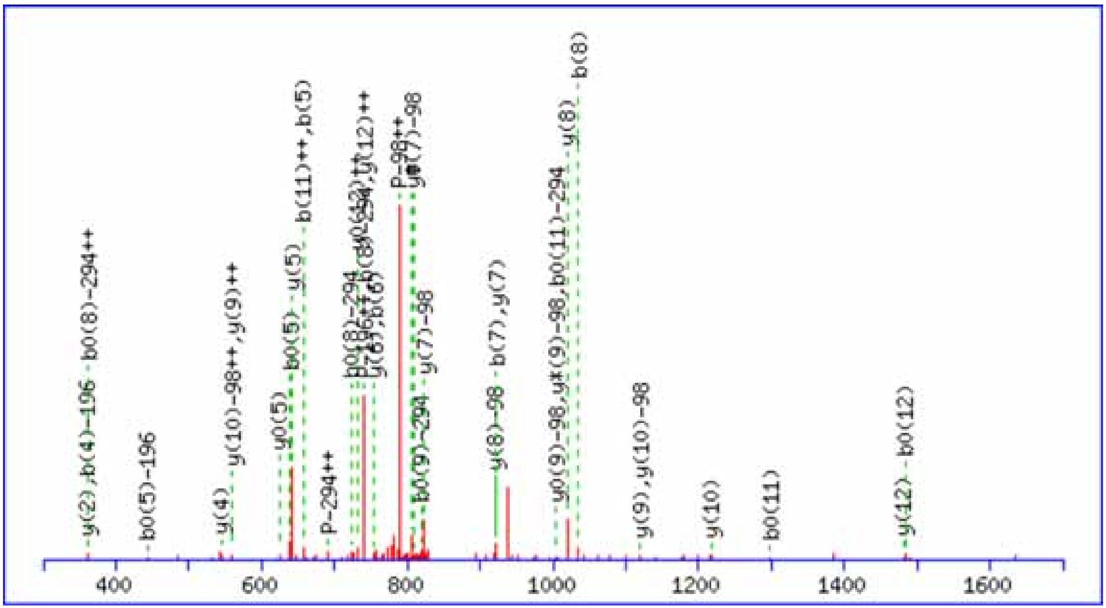
Matched b ions: b(3)-98, b(3), b(4)-196, b(5)-196, b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(8)-196, b(9), b(9)-196, b(9)-98, b(10)-98, b(11)-98++, b(12)-98, b(12), b(12)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(10), y(10)++, y(11)++, y(12)++, y(12), y(12)-98, y(12)-98++
Precursor origin neutral loss: +

Peptide No.919

SPSPTPSLPPSWK
Confirmed sites: @S:1,@S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of SPSPTPSLPPSWK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 3580: 1675.672512 from(838.843532,2+)
Title: Elution from: 55.345 to 55.345 scan no 5493 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1675.6701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 30 **Expect:** 0.019

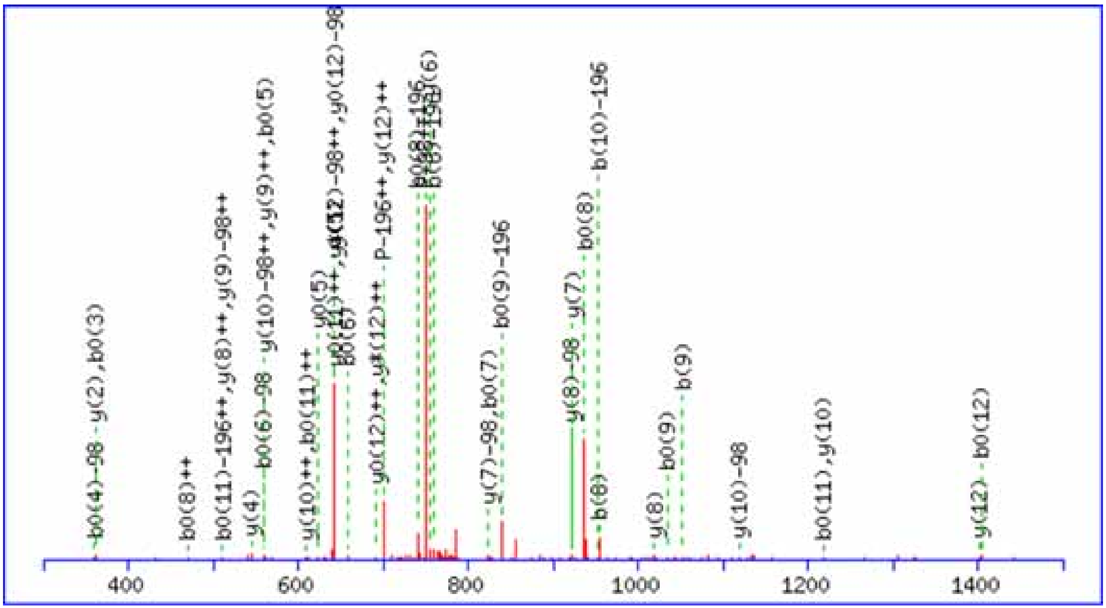
Matched b ions: b(3)-98, b(4)-196, b(5)-98, b(5), b(6), b(7)-196, b(7), b(7)-98, b(8)-294, b(8)-98, b(8), b(9)-196, b(9)-98, b(11)-196, b(11)-98, b(11)-196++, b(11)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)++, y(10)-98, y(10), y(10)-98++, y(12)++, y(12), y(12)-98++
Precursor origin neutral loss: +

Peptide No.920

SPSPTPSLPPSWK
Confirmed sites: @S:1,@S:7
Ambiguous sites:

MS/MS Fragmentation of SPSPTPSLPPSWK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 3053: 1595.704702 from(798.859627,2+)
Title: Elution from: 56.860 to 56.860 scan no 5639 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1595.7038
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 32 Expect: 0.02

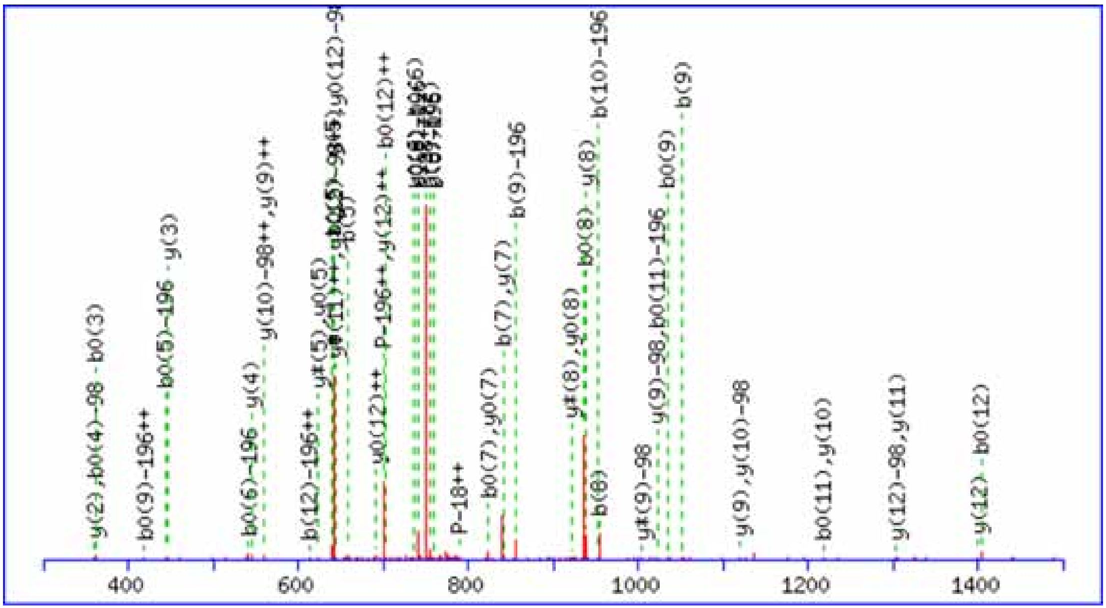
Matched b ions: b(7)-98, b(8), b(8)-98, b(8)-196, b(9)-98, b(9), b(10)-98, b(10)-196, b(11)-98++, b(12)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7)-98, y(7), y(8), y(8)++, y(8)-98, y(9)++, y(9)-98++, y(10), y(10)-98++, y(10)-98, y(10)++, y(12)++, y(12)
Precursor origin neutral loss: +

Peptide No.921

SPSPTPSLPPSWK
Confirmed sites: @S:1,@T:5
Ambiguous sites:

MS/MS Fragmentation of SPSPTPSLPPSWK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 3041: 1595.704288 from(798.859420,2+)
Title: Elution from: 53.715 to 53.715 scan no 5324 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1595.7038
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 60 **Expect:** 3.5e-005

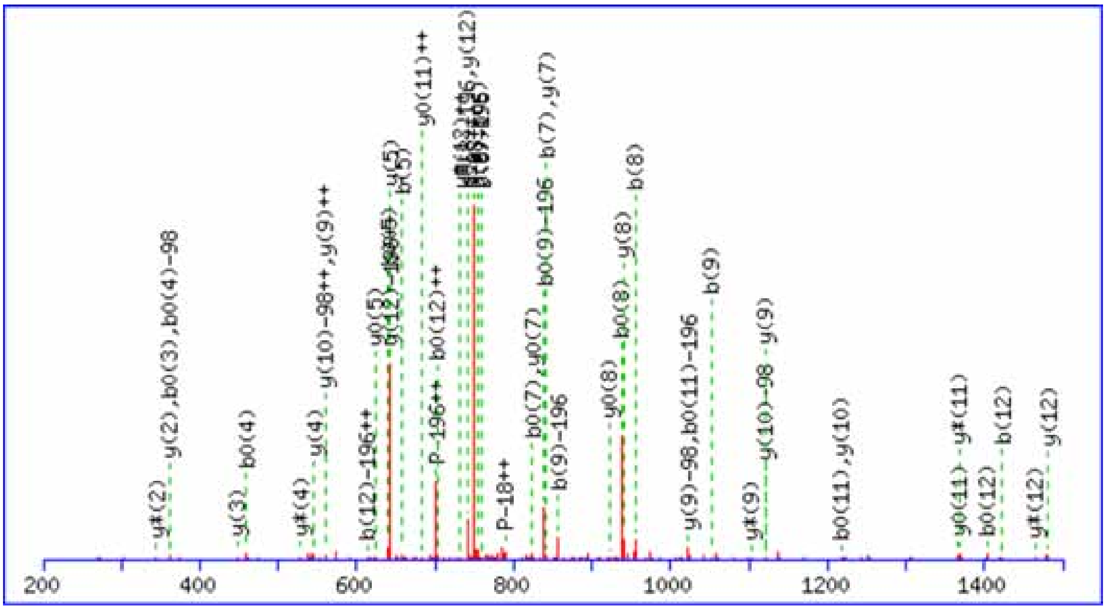
Matched b ions: b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(8)-196, b(9), b(9)-196, b(9)-98, b(10)-98, b(10)-196, b(12)-98, b(12)-196++, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(9)-98, y(10), y(10)-98++, y(10)-98, y(11), y(12)++, y(12), y(12)-98
Precursor origin neutral loss: +

Peptide No.922

SPSPTPSLPPSWK
Confirmed sites: @S:3,@T:5
Ambiguous sites:

MS/MS Fragmentation of SPSPTPSLPPSWK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 3061: 1595.705258 from(798.859905,2+)
Title: Elution from: 54.763 to 54.763 scan no 5435 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1595.7038
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl (K)
Ions Score: 37 Expect: 0.0064

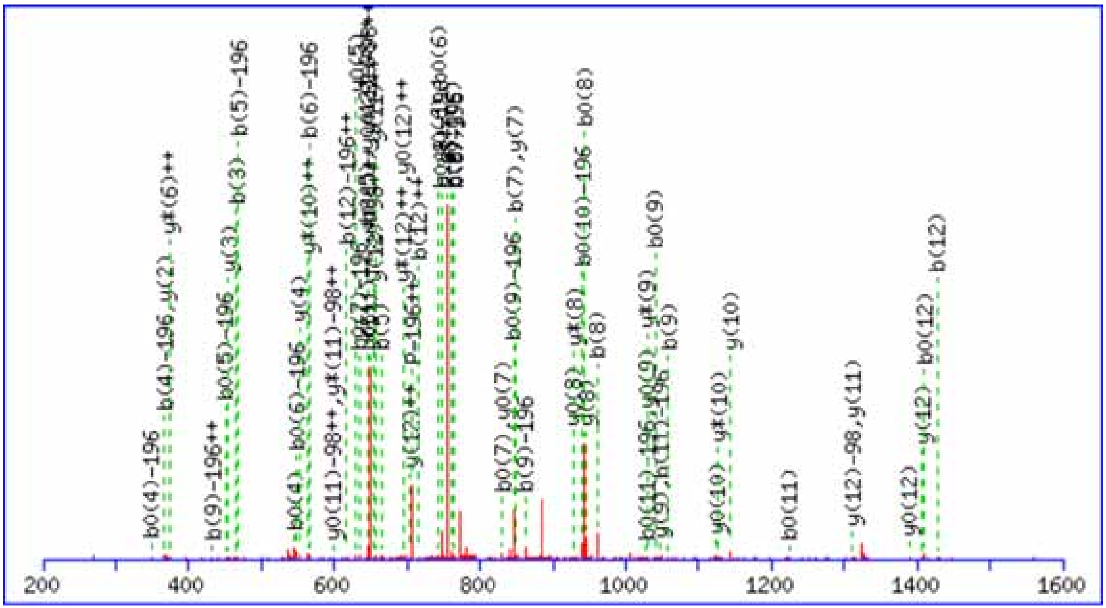
Matched b ions: b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(8)-196, b(9)-196, b(9)-98, b(9), b(10)-98, b(11)-98, b(12), b(12)-196++, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98, y(9)++, y(9), y(10)-98++, y(10), y(10)-98, y(11)-98++, y(12), y(12)++, y(12)-98++, y(12)-196++
Precursor origin neutral loss: +

Peptide No.923

SPSPTPSLPPSWK
Confirmed sites: @S:1,@S:3
Ambiguous sites:

MS/MS Fragmentation of SPSPTPSLPPSWK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 2395: 1607.767948 from(804.891250,2+)
Title: Elution from: 51.571 to 51.571 scan no 4861 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1607.7674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 45 Expect: 0.0017

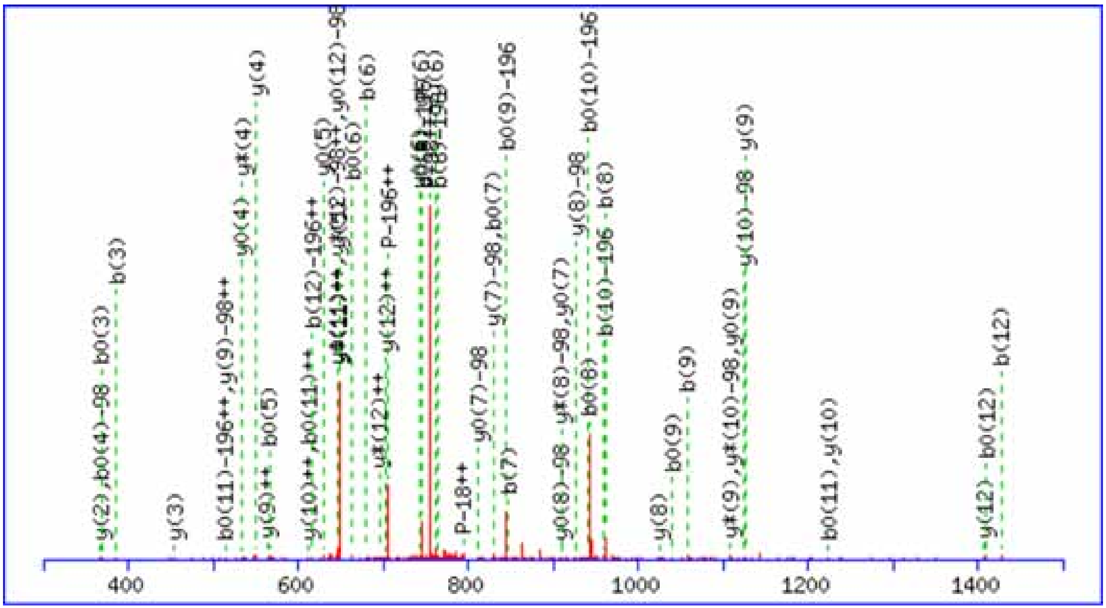
Matched b ions: b(3)-98, b(3), b(4)-196, b(5), b(5)-98, b(5)-196, b(6)-98, b(6), b(6)-196, b(7)-98, b(7), b(8)-98++, b(8), b(8)-98, b(8)-196, b(9)-196++, b(9)-98, b(9), b(9)-196, b(10)-98, b(11)-196, b(12), b(12)-98, b(12)-196++, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)-98, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.924

SPSPTPSLPPSWK
Confirmed sites: @S:1,@S:7
Ambiguous sites:

MS/MS Fragmentation of SPSPTPSLPPSWK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 2719: 1607.767910 from(804.891231,2+)
Title: Elution from: 51.281 to 51.281 scan no 4892 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1607.7674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 30 Expect: 0.047

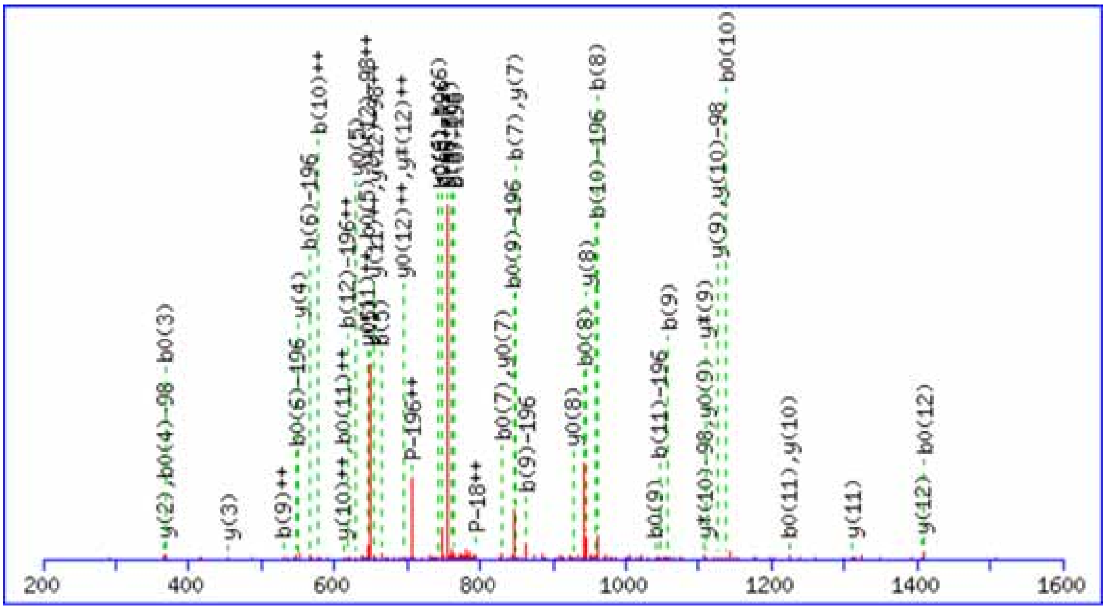
Matched b ions: b(3), b(6), b(7)-98, b(7), b(8)-98, b(8), b(8)-196, b(9)-98, b(9), b(10)-98, b(10)-196, b(12)-98, b(12), b(12)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98, y(8), y(8)-98, y(9)++, y(9)-98++, y(9), y(10), y(10)++, y(10)-98, y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.925

SPSPTPSLPPSWK
Confirmed sites: @S:1,@T:5
Ambiguous sites:

MS/MS Fragmentation of SPSPTPSLPPSWK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 2443: 1607.767976 from(804.891264,2+)
Title: Elution from: 51.243 to 51.243 scan no 4676 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1607.7674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 39 Expect: 0.0065

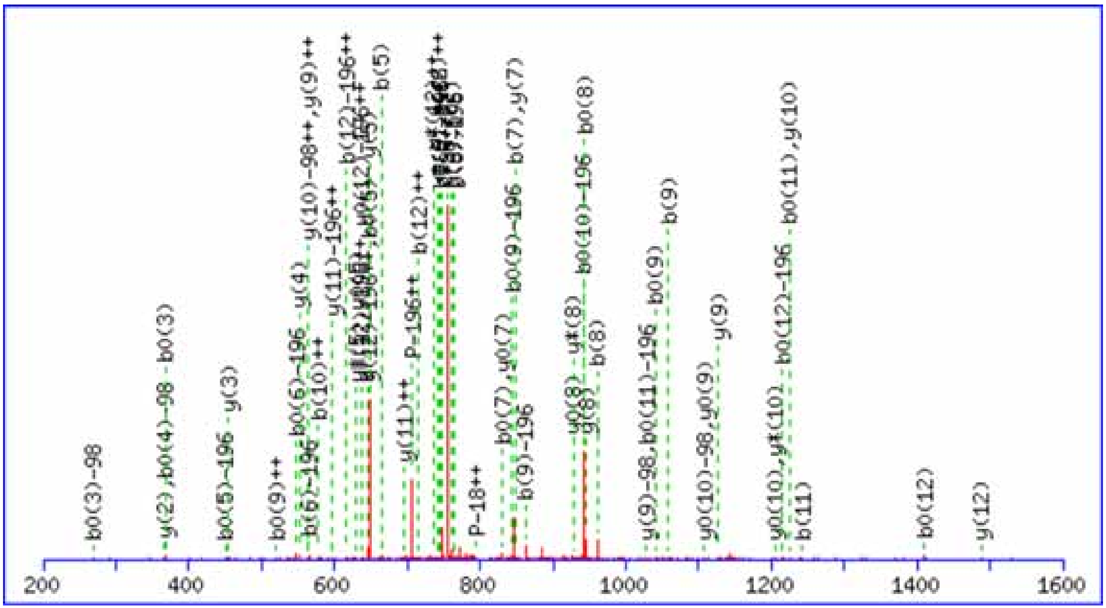
Matched b ions: b(5)-98, b(5), b(6), b(6)-196, b(7)-98, b(7), b(8)-98, b(8), b(8)-196, b(9)-196, b(9)-98, b(9), b(9)++, b(10)-98, b(10)-98++, b(10)-196, b(10)++, b(11)-196, b(12)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(10)++, y(11), y(11)++, y(12), y(12)-98++
Precursor origin neutral loss: +

Peptide No.926

SPSPTPSLPPSWK
Confirmed sites: @S:3,@T:5
Ambiguous sites:

MS/MS Fragmentation of SPSPTPSLPPSWK
Found in SYP2L_MOUSE, Synaptopodin 2-like protein OS=Mus musculus GN=Synpo2l PE=2 SV=1

Match to Query 2403: 1607.768760 from(804.891656,2+)
Title: Elution from: 51.933 to 51.933 scan no 4906 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1607.7674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K13 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 34 Expect: 0.019

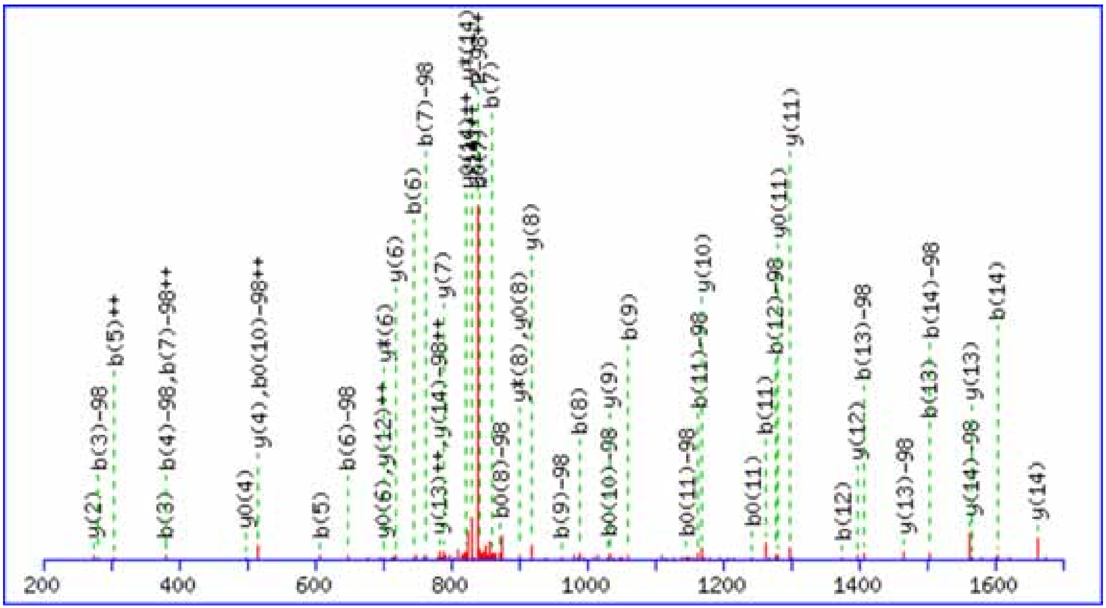
Matched b ions: b(5)-98, b(5), b(6), b(6)-98, b(6)-196, b(7)-98, b(7), b(8)-98, b(8), b(8)-196, b(9)-98, b(9)-196, b(9), b(10)-98, b(10)++, b(11)-98, b(11), b(12)-98, b(12)-98++, b(12)-196++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(9)-98, y(10), y(10)-98++, y(11)-98++, y(11)-196++, y(11)++, y(12), y(12)-196++, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.927

SPSVEHDEASDLEVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SPSVEHDEASDLEVR
Found in SMTL2_MOUSE, Smoothelin-like protein 2 OS=Mus musculus GN=Smtnl2 PE=1 SV=1

Match to Query 4171: 1776.756300 from(889.385426,2+)
Title: Elution from: 34.765 to 34.765 scan no 2956 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1776.7567
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 Expect: 7.4e-007

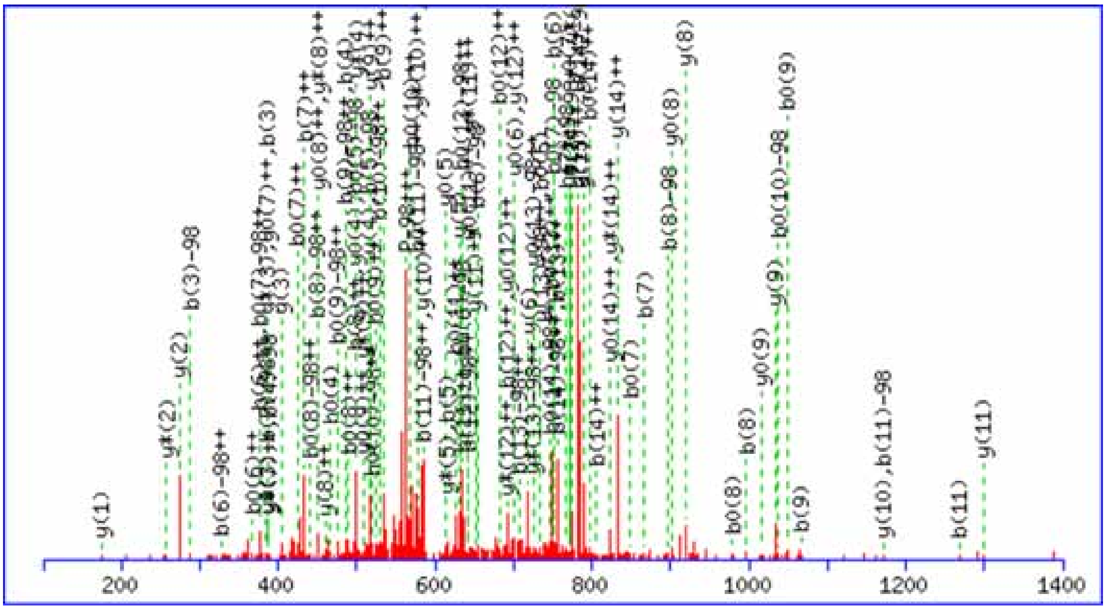
Matched b ions: b(3), b(3)-98, b(4)-98, b(5), b(5)++, b(6)-98, b(6), b(7)-98++, b(7)-98, b(7), b(8), b(9), b(9)-98, b(11), b(11)-98, b(12)-98, b(12), b(13)-98, b(13), b(14), b(14)-98
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(13)-98, y(13), y(13)++, y(14)-98, y(14), y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.928

SPSVEHDEASDLEVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SPSVEHDEASDLEVR
Found in SMTL2_MOUSE, Smoothelin-like protein 2 OS=Mus musculus GN=Smtnl2 PE=1 SV=1

Match to Query 3260: 1782.790872 from(595.270900,3+)
Title: Elution from: 34.747 to 34.747 scan no 2749 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1782.7885
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.00082

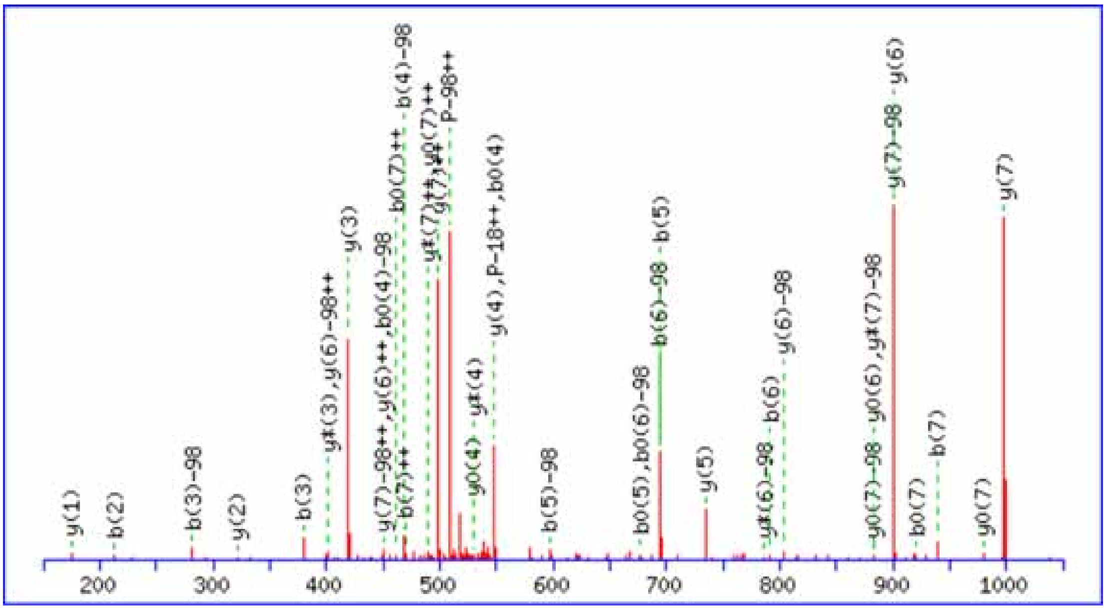
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)++, b(6)-98++, b(6)-98, b(6), b(7)++, b(7)-98++, b(7)-98, b(7), b(8)-98++, b(8)++, b(8), b(8)-98, b(9)++, b(9)-98++, b(9), b(10)++, b(10)-98++, b(11)-98++, b(11), b(11)-98, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(10), y(11), y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.929

SPSWEPFR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SPSWEPFR
Found in HSPB1_MOUSE, Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3

Match to Query 651: 1112.469378 from(557.241965,2+)
Title: Elution from: 50.157 to 50.157 scan no 4700 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1112.4692
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 **Expect:** 8.7e-005

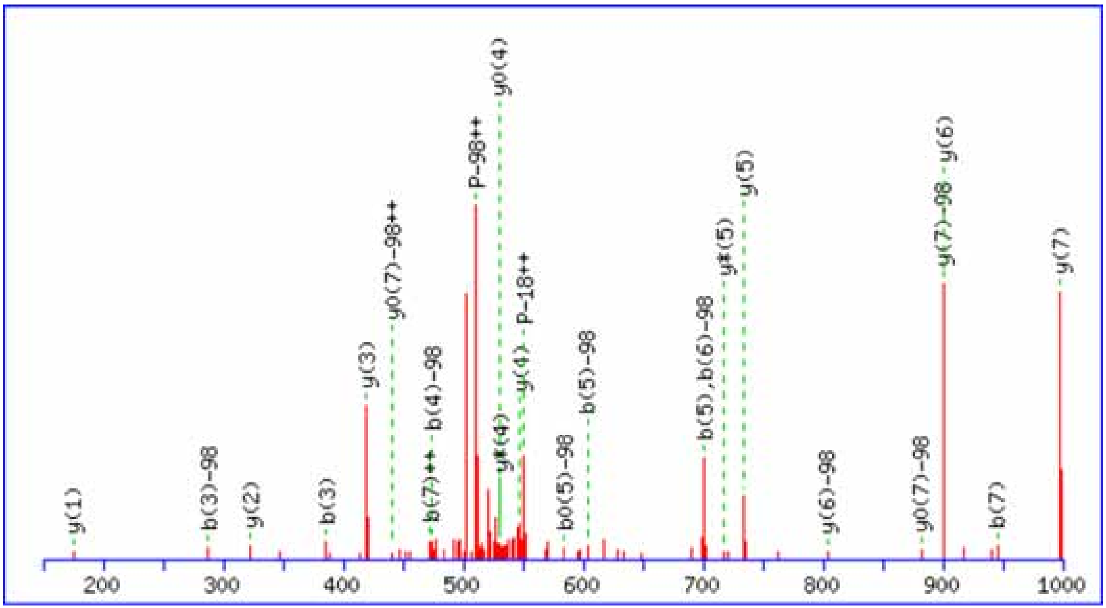
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5), b(5)-98, b(6), b(6)-98, b(7), b(7)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)-98, y(6), y(6)++, y(6)-98++, y(7)-98, y(7), y(7)++, y(7)-98++
Precursor origin neutral loss: +

Peptide No.930

SPSWEPFR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SPSWEPFR**
Found in **HSPB1_MOUSE**, Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3

Match to Query 772: 1118.500710 from(560.257631,2+)
Title: Elution from: 49.435 to 49.435 scan no 4684 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1118.5010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.00068

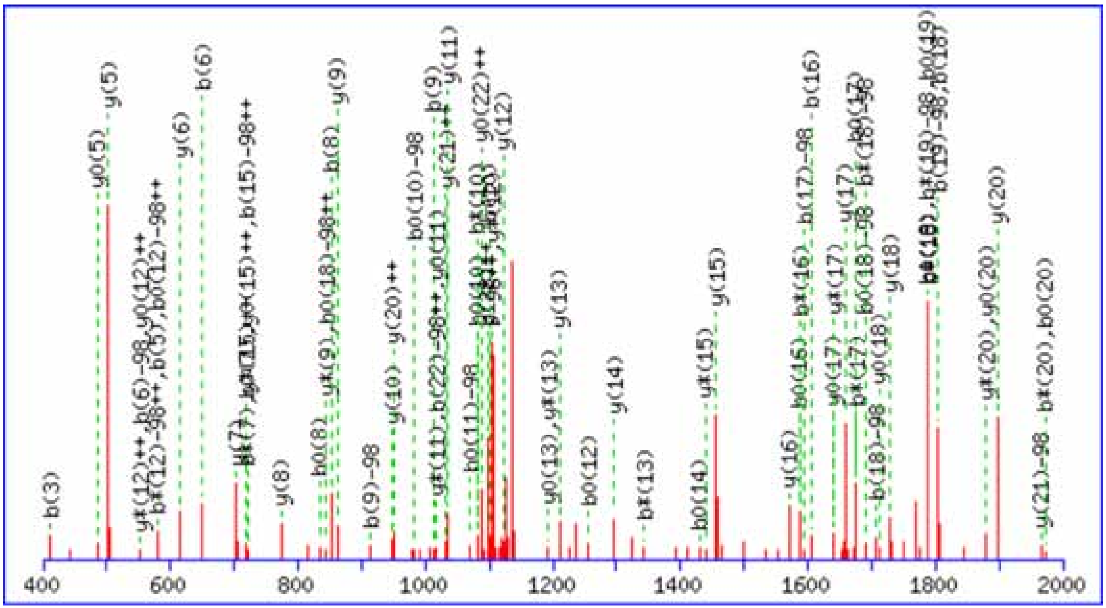
Matched b ions: b(3)-98, b(3), b(4)-98, b(5), b(5)-98, b(6)-98, b(7), b(7)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(7)
Precursor origin neutral loss: +

Peptide No.931

SQSPAASDCSSSSSSASLPSSGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SQSPAASDCSSSSSSASLPSSGR
Found in BAG3_MOUSE, BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=1

Match to Query 5972: 2306.933636 from(1154.474094,2+)
Title: Elution from: 27.573 to 27.573 scan no 1791 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2306.9322
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 **Expect:** 6.9e-008

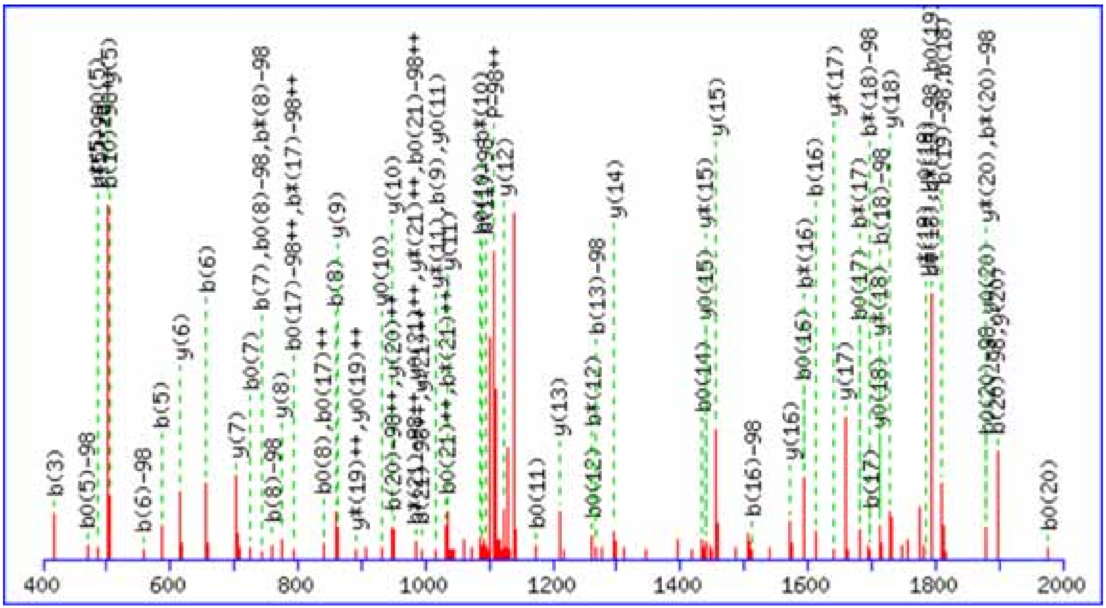
Matched b ions: b(3), b(5), b(6)-98, b(6), b(8), b(9)-98, b(9), b(10), b(15)-98++, b(16), b(17)-98, b(18), b(18)-98, b(19)-98, b(22)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(20)++, y(20), y(21)-98, y(21)++, y(22)++
Precursor origin neutral loss: +

Peptide No.932

SQSPAASDCSSSSSSASLPSSGR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SQSPAASDCSSSSSSASLPSSGR
Found in BAG3_MOUSE, BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=1

Match to Query 5632: 2312.964968 from(1157.489760,2+)
Title: Elution from: 27.579 to 27.579 scan no 1827 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2312.9640
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 92 Expect: 2.8e-008

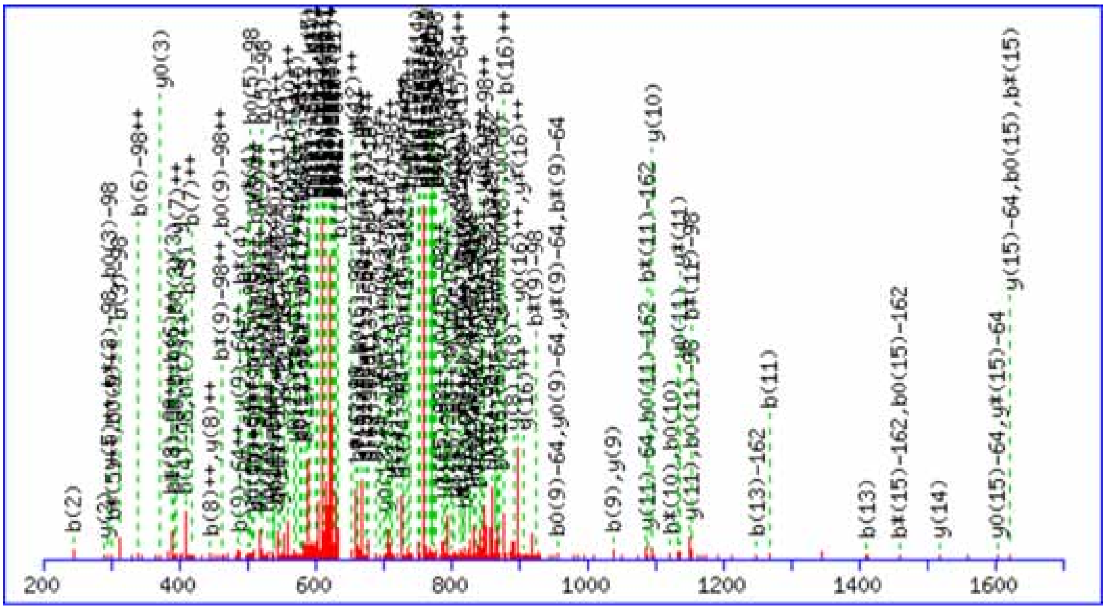
Matched b ions: b(3), b(5), b(5)-98, b(6), b(6)-98, b(7), b(8), b(8)-98, b(9), b(10)-98++, b(11)-98, b(13)-98, b(16), b(16)-98, b(17), b(18), b(18)-98, b(19)-98, b(20)-98, b(20)-98++, b(21)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(20), y(20)++, y(21)++
Precursor origin neutral loss: +

Peptide No.933

SQSPLRGGMTEAAQTDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SQSPLRGGMTEAAQTDK
Found in BAG3_MOUSE, BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=1

Match to Query 5263: 1927.871721 from(643.631183,3+)
Title: Elution from: 24.263 to 24.263 scan no 1534 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1927.8710
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K17 : Dimethyl (K)
Ions Score: 43 Expect: 0.0026

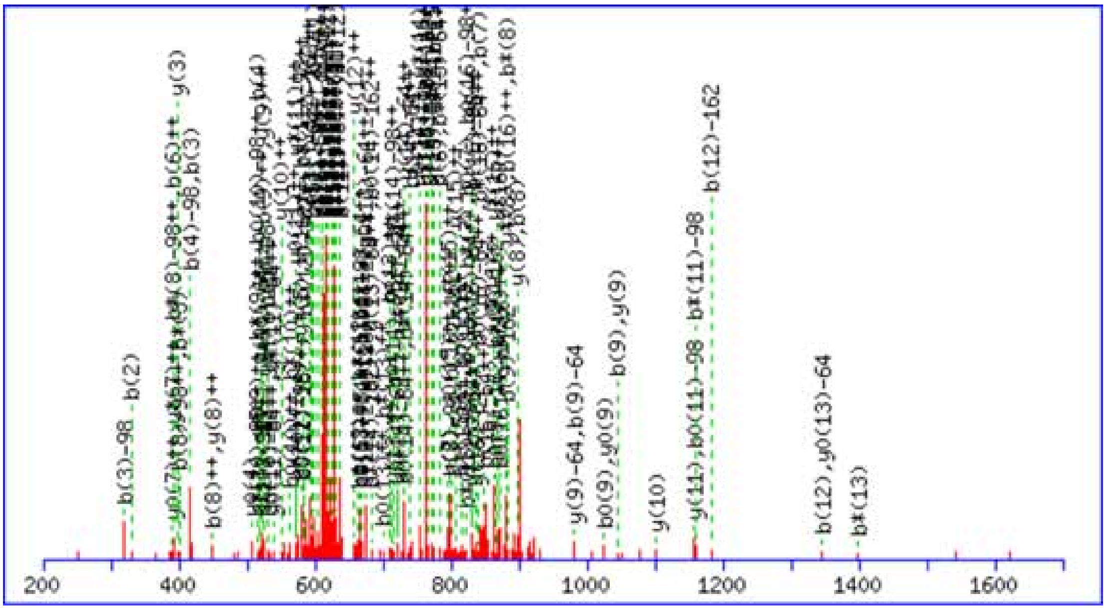
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6)++, b(6)-98++, b(6)-98, b(6), b(7), b(7)-98, b(7)++, b(8)++, b(8)-98, b(8), b(9)++, b(9), b(10)++, b(11), b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13), b(13)++, b(14)-98++, b(14)++, b(15)++, b(16)++, b(16)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(14), y(15)-98++, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.934

SQSPLRGGMTEAAQTDK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SQSPLRGGMTEAAQTDK
Found in BAG3_MOUSE, BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=1

Match to Query 4506: 1939.935102 from(647.652310,3+)
Title: Elution from: 24.214 to 24.214 scan no 1397 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1939.9347
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 49 **Expect:** 0.00095

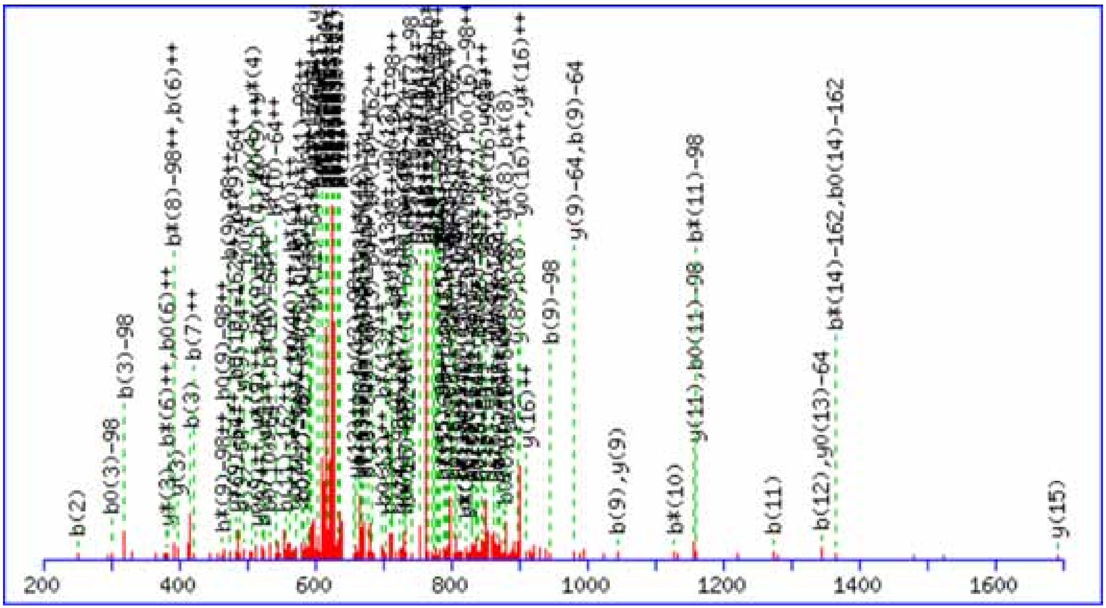
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)++, b(6), b(7), b(8)++, b(8)-98++, b(8), b(8)-98, b(9)++, b(9), b(10)-98++, b(10)++, b(11)++, b(12)++, b(12), b(12)-98++, b(13)++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.935

SQSPLRGGMTEAAQTDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SQSPLRGGMTEAAQTDK
Found in BAG3_MOUSE, BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=1

Match to Query 4893: 1939.936350 from(647.652726,3+)
Title: Elution from: 24.111 to 24.111 scan no 1389 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1939.9347
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 39 Expect: 0.0094

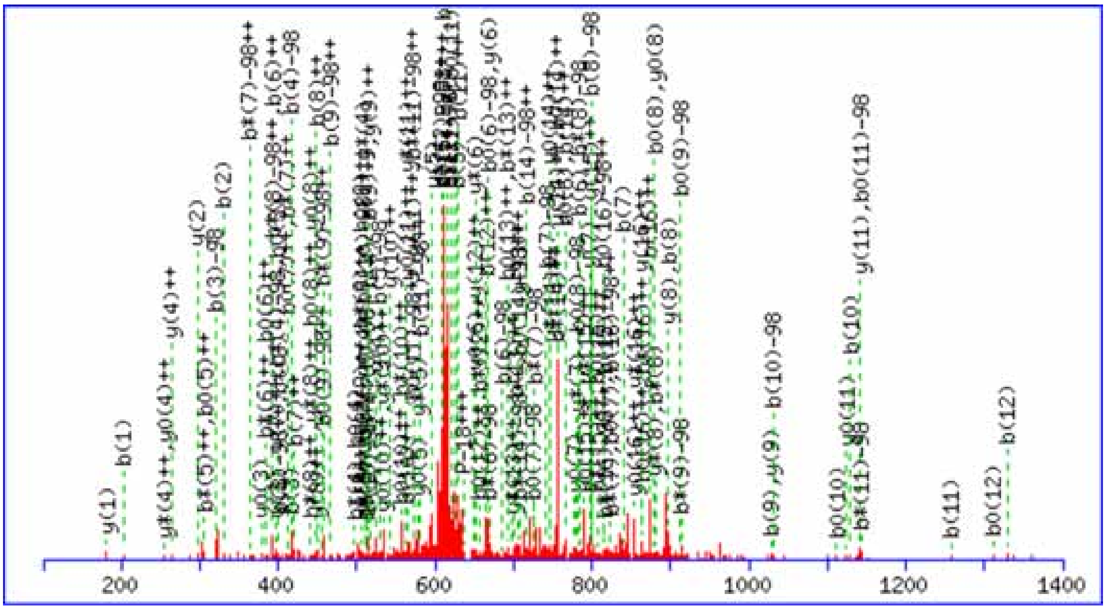
Matched b ions: b(2), b(3)-98, b(3), b(4), b(5), b(6)++, b(6), b(7)++, b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)++, b(9)-98++, b(9)-98, b(10)-98++, b(10)++, b(11), b(11)-98++, b(11)++, b(12), b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15), y(15)-98++, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.936

SQSPLRGGMTEAAQTDK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SQSPLRGGMTEAAQTDK
Found in BAG3_MOUSE, BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=1

Match to Query 6087: 1923.940770 from(642.320866,3+)
Title: Elution from: 31.634 to 31.634 scan no 2448 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1923.9397
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 41 Expect: 0.006

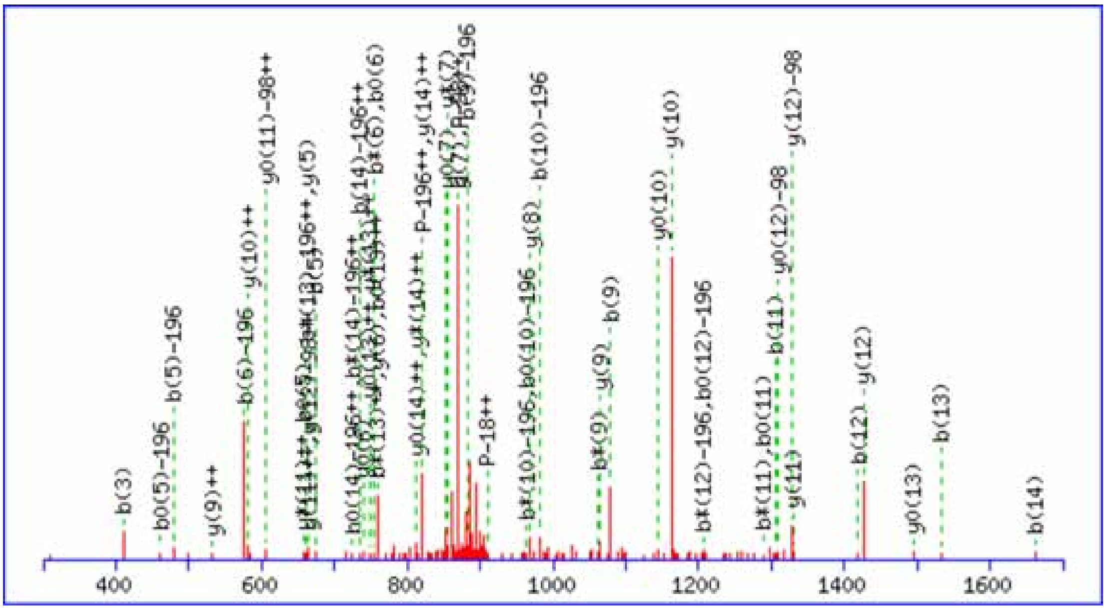
Matched b ions: b(1), b(2), b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6)++, b(6)-98, b(6), b(7)++, b(7)-98, b(7), b(8), b(8)++, b(8)-98++, b(8)-98, b(9), b(9)++, b(9)-98++, b(10), b(10)-98, b(10)++, b(10)-98++, b(11), b(11)++, b(11)-98++, b(12), b(12)-98++, b(12)++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++
Precursor origin neutral loss: +

Peptide No.937

SQSPSPPPLPEDLEK
Confirmed sites: @S:1,@S:5
Ambiguous sites:

MS/MS Fragmentation of SQSPSPPPLPEDLEK
Found in ACINU_MOUSE, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=2

Match to Query 3877: 1835.801240 from(918.907896,2+)
Title: Elution from: 50.001 to 50.001 scan no 4728 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1835.7995
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 36 **Expect:** 0.0096

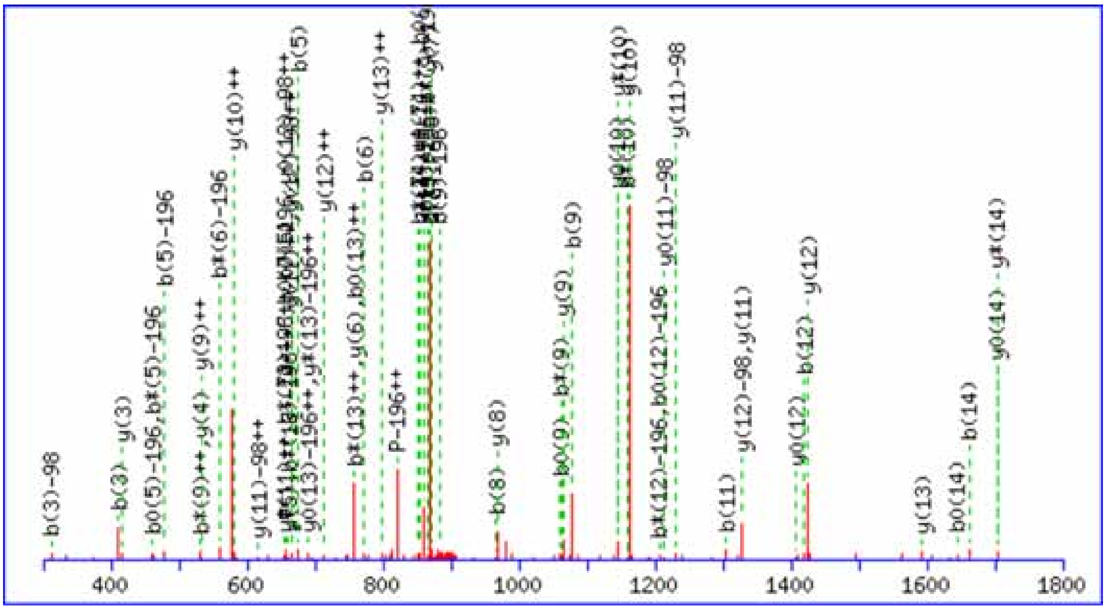
Matched b ions: b(3), b(5)-98, b(5)-196, b(5), b(6)-196, b(6)-98, b(7), b(7)-98, b(9)-98, b(9), b(9)-196, b(10)-196, b(10)-98, b(11)-98, b(11), b(12), b(12)-98++, b(13), b(14), b(14)-196++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11)++, y(11), y(12)-98++, y(12)-98, y(12), y(14)++
Precursor origin neutral loss: +

Peptide No.938

SQSPSPPPLPEDLEK
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SQSPSPPPLPEDLEK
Found in ACINU_MOUSE, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=2

Match to Query 4578: 1835.800552 from(918.907552,2+)
Title: Elution from: 50.310 to 50.310 scan no 4955 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1835.7995
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 58 Expect: 5.6e-005

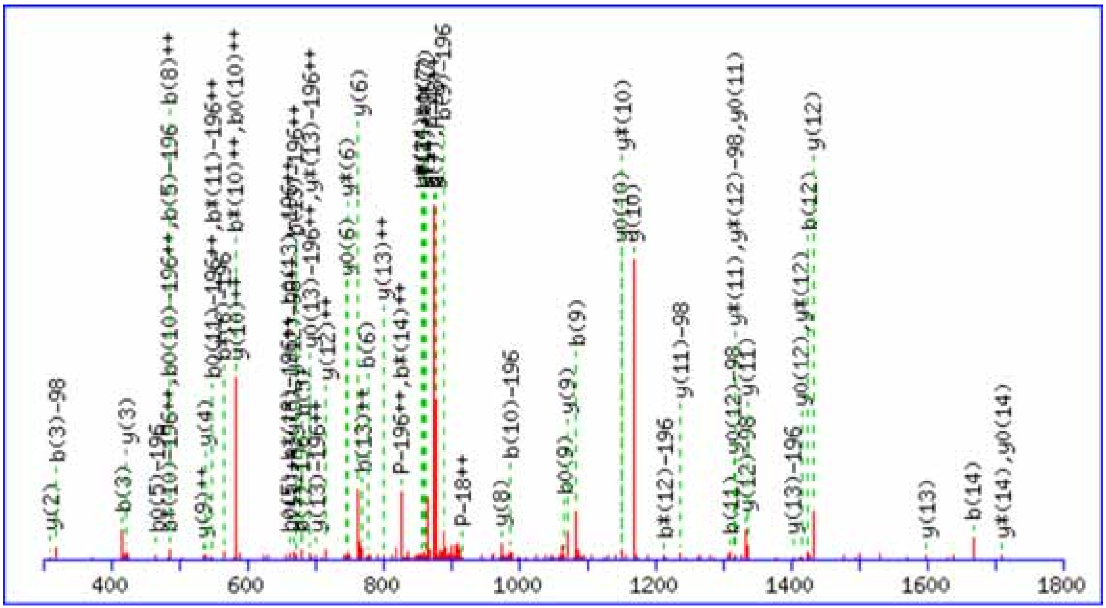
Matched b ions: b(3), b(3)-98, b(5)-196, b(5)-98, b(5), b(6)-98, b(6), b(7), b(8), b(8)-98, b(9), b(9)-98, b(9)-196, b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(12)-98++, b(14), b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)-98, y(11)++, y(11)-98++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13), y(13)++, y(13)-98, y(13)-98++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.939

SQSPSPPPLPEDLEK
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SQSPSPPPLPEDLEK
Found in ACINU_MOUSE, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=2

Match to Query 5341: 1847.865020 from(924.939786,2+)
Title: Elution from: 50.077 to 50.077 scan no 4967 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1847.8631
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 55 Expect: 0.00017

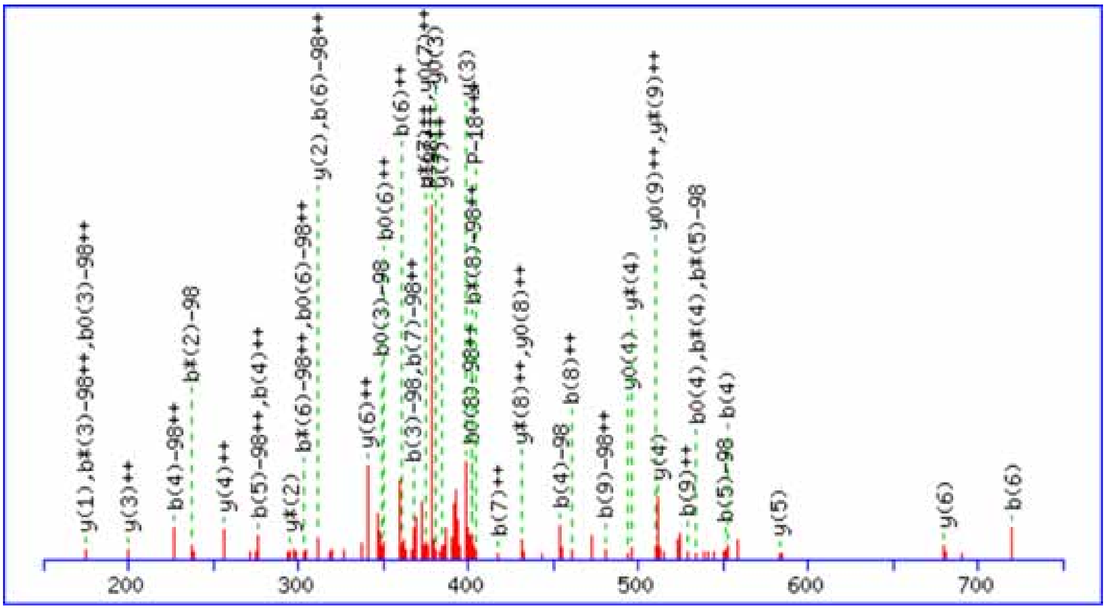
Matched b ions: b(3)-98, b(3), b(5)-98, b(5), b(5)-196, b(6)-98, b(6), b(7), b(7)-196, b(7)-98, b(8)++, b(9), b(9)-98, b(9)-196, b(10)-98, b(10)-196, b(11)-98, b(11), b(12), b(12)-98, b(13)++, b(13)-196++, b(14)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11)-98, y(11)++, y(11), y(12)-98, y(12), y(12)-98++, y(12)++, y(13), y(13)-98, y(13)-196, y(13)-98++, y(13)-196++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.940

SRLSPALSHR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SRLSPALSHR
Found in MYPN_MOUSE, Myopalladin OS=Mus musculus GN=Mypn PE=2 SV=2

Match to Query 1017: 1230.624225 from(411.215351,3+)
Title: Elution from: 23.263 to 23.263 scan no 1254 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1230.6234
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.046

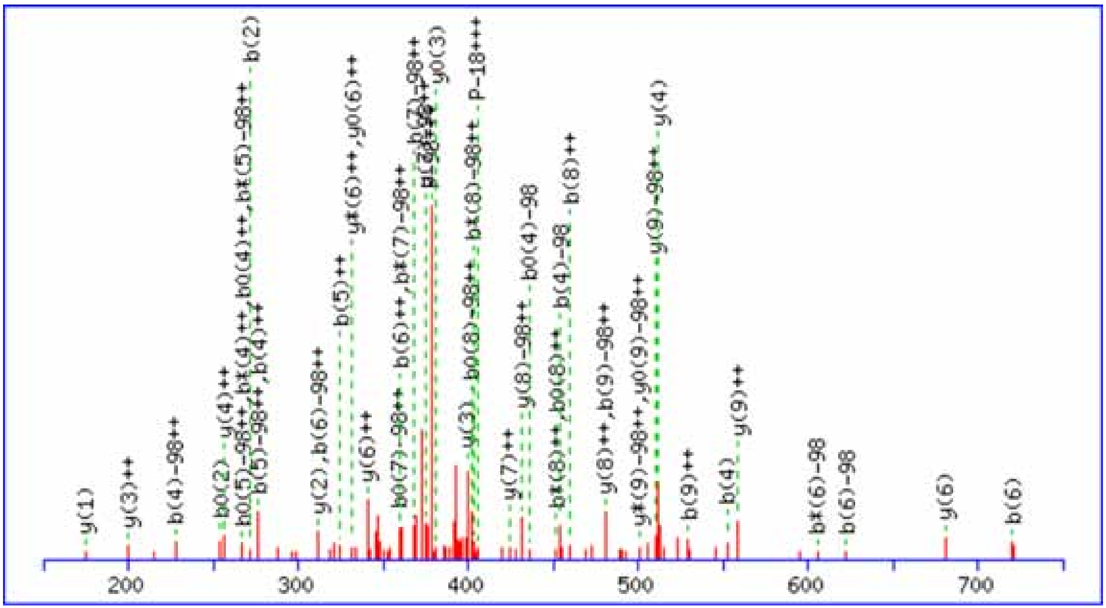
Matched b ions: b(3)-98, b(4)-98++, b(4), b(4)-98, b(4)++, b(5)-98++, b(5)-98, b(6), b(6)++, b(6)-98++, b(7)-98++, b(7)++, b(8)++, b(9)-98++, b(9)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(4)++, y(5), y(6)++, y(6), y(7)++
Precursor origin neutral loss: +

Peptide No.941

SRLSPALSHR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SRLSPALSHR
Found in MYPN_MOUSE, Myopalladin OS=Mus musculus GN=Mypn PE=2 SV=2

Match to Query 1174: 1230.623715 from(411.215181,3+)
Title: Elution from: 23.322 to 23.322 scan no 1291 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1230.6234
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.0089

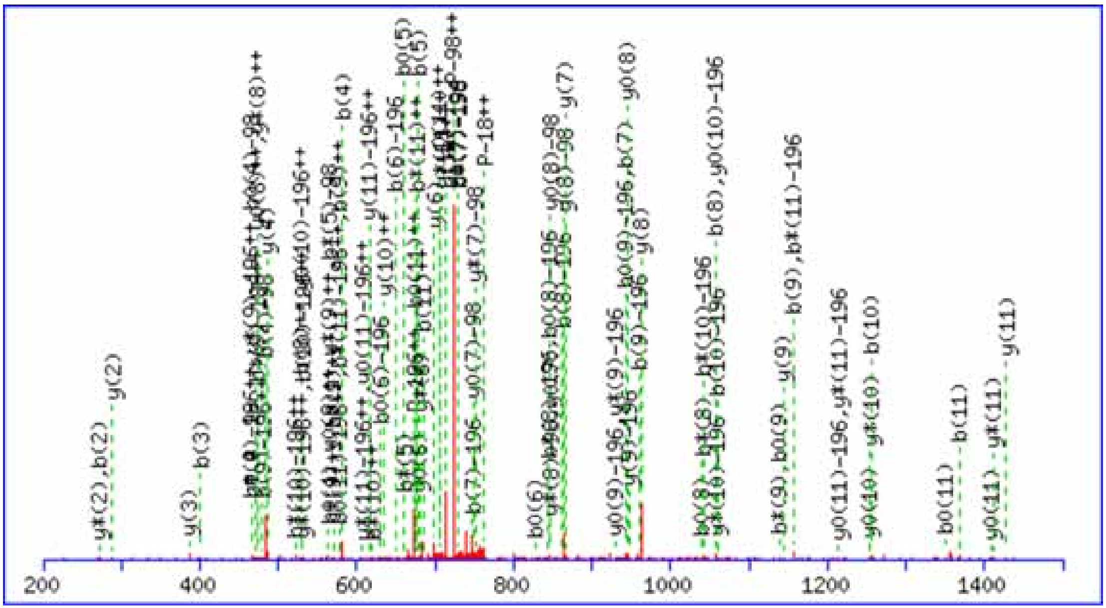
Matched b ions: b(2), b(4)-98++, b(4)++, b(4)-98, b(4), b(5)-98++, b(5)++, b(6)-98, b(6), b(6)++, b(6)-98++, b(7)-98++, b(8)++, b(9)-98++, b(9)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4)++, y(4), y(6), y(6)++, y(7)-98++, y(7)++, y(8)++, y(8)-98++, y(9)++, y(9)-98++
Precursor origin neutral loss: +

Peptide No.942

SRQTPSPDVVLR
Confirmed sites: @T:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of SRQTPSPDVVLR
Found in LIMC1_MOUSE, LIM and calponin homology domains-containing protein 1 OS=Mus musculus GN=Limch1 PE=1 SV=2

Match to Query 3516: 1541.700748 from(771.857650,2+)
Title: Elution from: 35.084 to 35.084 scan no 2936 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1541.7004
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.012

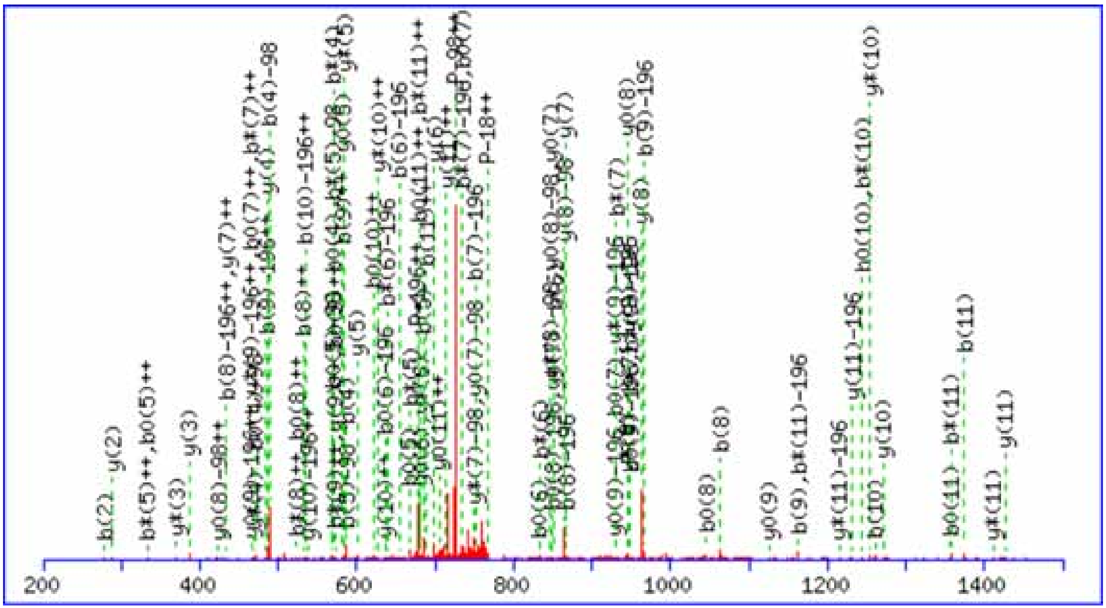
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5), b(6)-98, b(6)-196, b(7)-196, b(7), b(7)-98, b(8), b(8)-98, b(8)-98++, b(8)++, b(8)-196, b(9), b(9)-98, b(9)-196++, b(9)-98++, b(9)++, b(9)-196, b(10), b(10)-98, b(10)-196++, b(10)-196, b(11)-98, b(11), b(11)-98++, b(11)++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98++, y(9)-196, y(9)-98, y(10)++, y(11)++, y(11), y(11)-196++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.943

SRQTPSPDVVLR
Confirmed sites: @T:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of SRQTPSPDVVLR
Found in LIMC1_MOUSE, LIM and calponin homology domains-containing protein 1 OS=Mus musculus GN=Limch1 PE=1 SV=2

Match to Query 3553: 1547.732934 from(774.873743,2+)
Title: Elution from: 35.122 to 35.122 scan no 2941 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1547.7322
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.035

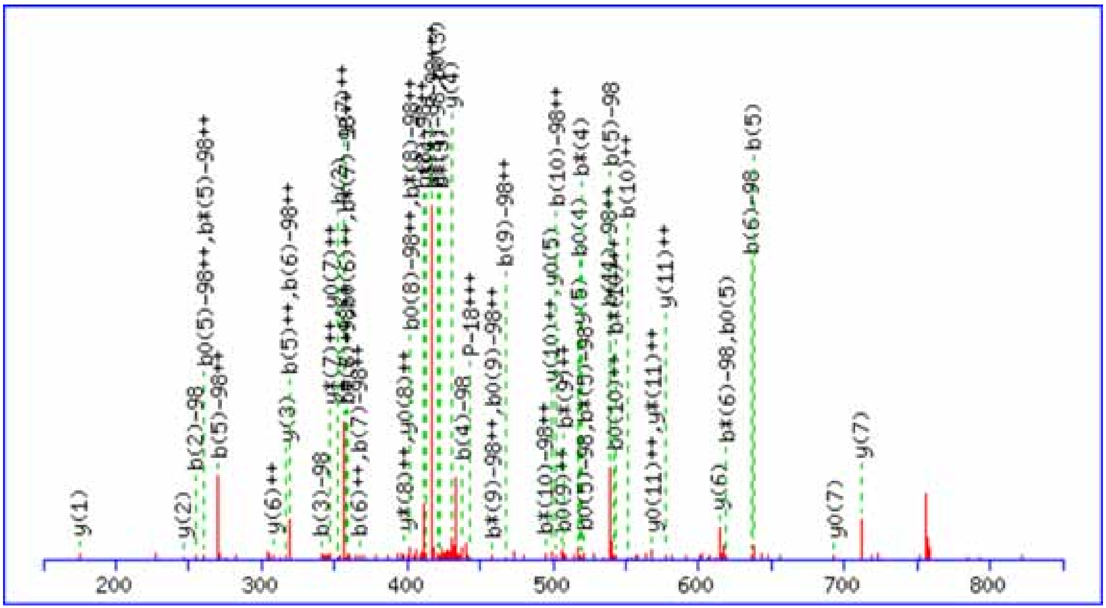
Matched b ions: b(2), b(4)-98, b(4), b(5)-98, b(5), b(6)-196, b(6)-98, b(6), b(7), b(7)-196, b(8), b(8)-98, b(8)-196++, b(8)-196, b(8)++, b(9), b(9)-98, b(9)-196++, b(9)-98++, b(9)++, b(9)-196, b(10), b(10)-98, b(10)-196++, b(10)-98++, b(11), b(11)-98, b(11)-98++, b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)-98, y(8), y(9)-98, y(9)-98++, y(9)-196, y(9)++, y(10)-98++, y(10)-196++, y(10)++, y(10)-98, y(10), y(11), y(11)++, y(11)-196
Precursor origin neutral loss: +

Peptide No.944

SRSPTPPSIAAK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SRSPTPPSIAAK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2489: 1346.695209 from(449.905679,3+)
Title: Elution from: 26.852 to 26.852 scan no 1785 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1346.6959
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl (K)
Ions Score: 37 Expect: 0.0075

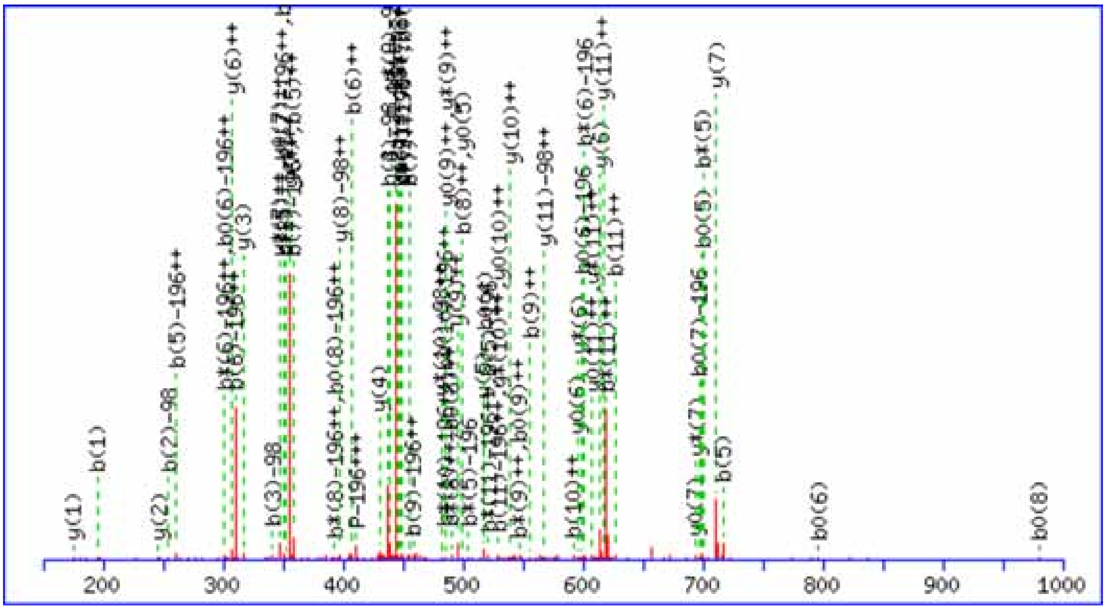
Matched b ions: b(2)-98, b(2), b(3)-98, b(4)-98, b(5)-98++, b(5)-98, b(5)++, b(5), b(6)-98++, b(6)++, b(6)-98, b(7)-98++, b(8)-98++, b(9)-98++, b(10)-98++, b(10)++, b(11)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.945

SRSPTPPSIAAK
Confirmed sites: @S:1,@T:5
Ambiguous sites:

MS/MS Fragmentation of SRSPTPPSIAAK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2135: 1426.662843 from(476.561557,3+)
Title: Elution from: 27.951 to 27.951 scan no 2023 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1426.6622
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl (K)
Ions Score: 36 Expect: 0.0084

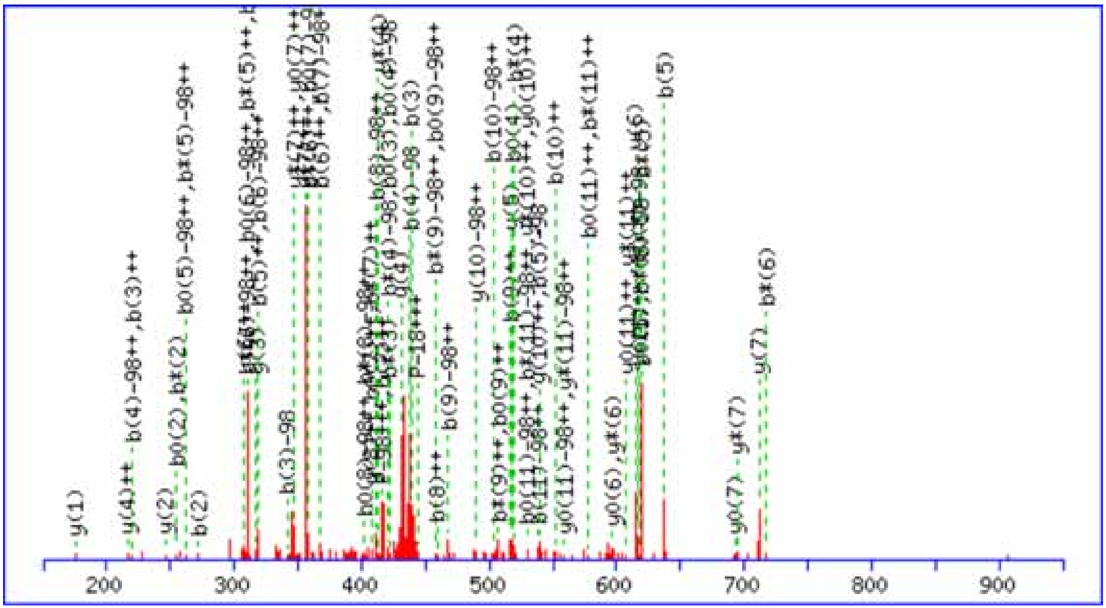
Matched b ions: b(1), b(2)-98, b(2), b(3), b(3)-98, b(4)-98, b(5)-196++, b(5)-98, b(5)-98++, b(5)++, b(5), b(5)-196, b(6)-196++, b(6)-98++, b(6)-98, b(6)++, b(7)-196++, b(7)++, b(7)-98++, b(8)-98++, b(8)++, b(9)++, b(9)-196++, b(9)-98++, b(10)-98++, b(10)++, b(11)-196++, b(11)++, b(11)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8)-98++, y(8)++, y(9)++, y(9)-98++, y(10)++, y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.946

SRSPTPPSIAAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SRSPTPPSIAAK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1397: 1346.696004 from(449.905944,3+)
Title: Elution from: 25.105 to 25.105 scan no 1517 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1346.6959
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K12 : Dimethyl (K)
Ions Score: 37 Expect: 0.0083

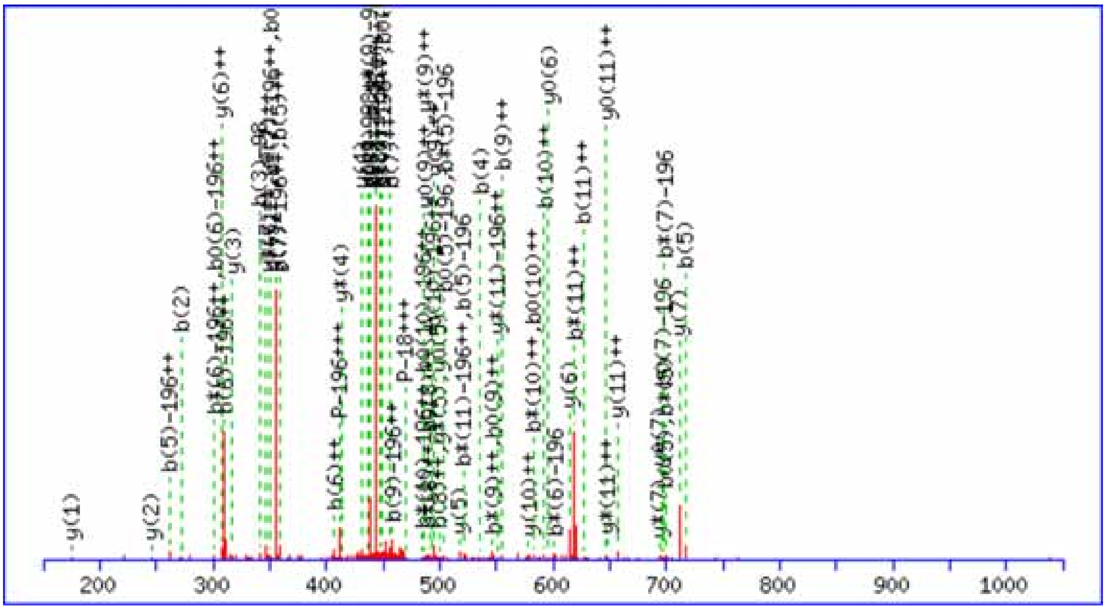
Matched b ions: b(2), b(3)++, b(3), b(3)-98, b(4)-98, b(4)-98++, b(5), b(5)-98, b(5)++, b(6)-98++, b(6)++, b(7)++, b(7)-98++, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)-98++, b(10)++, b(11)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5), y(6), y(6)++, y(7)++, y(7), y(8)++, y(10)++, y(10)-98++, y(11)++
Precursor origin neutral loss:

Peptide No.947

SRSPTPPSIAAK
Confirmed sites: @S:3,@T:5
Ambiguous sites:

MS/MS Fragmentation of SRSPTPPSIAAK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1880: 1426.662438 from(476.561422,3+)
Title: Elution from: 27.795 to 27.795 scan no 1823 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1426.6622
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl (K)
Ions Score: 34 Expect: 0.015

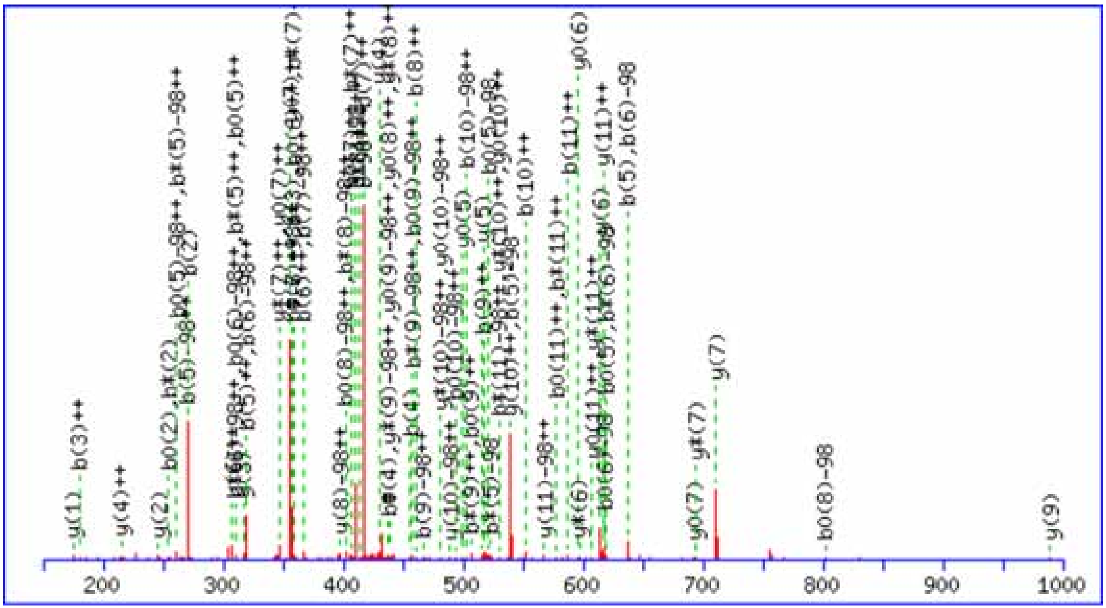
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-196++, b(5)-98, b(5)-98++, b(5), b(5)++, b(5)-196, b(6)-196++, b(6)-98++, b(6)++, b(7)-196++, b(7)++, b(7)-98++, b(8)-98++, b(8)++, b(9)-196++, b(9)++, b(9)-98++, b(10)-196++, b(10)-98++, b(10)++, b(11)-98++, b(11)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8)++, y(9)++, y(9)-98++, y(10)-98++, y(10)++, y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.948

SRSPTPPSIAAK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of SRSPTPPSIAAK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1806: 1346.695575 from(449.905801,3+)
Title: Elution from: 26.932 to 26.932 scan no 1885 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1346.6959
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl (K)
Ions Score: 38 **Expect:** 0.0067

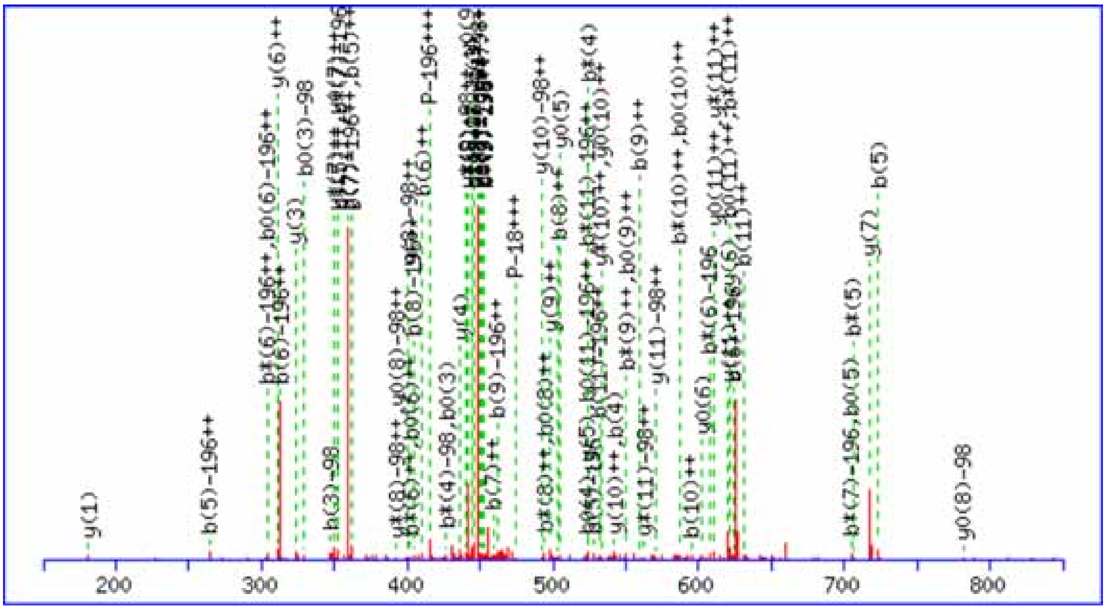
Matched b ions: b(2), b(3)++, b(3), b(4), b(5)-98++, b(5)-98, b(5), b(5)++, b(6)-98, b(6)-98++, b(6)++, b(7)++, b(7)-98++, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5), y(6), y(6)++, y(7)++, y(7), y(8)-98++, y(9), y(10)++, y(10)-98++, y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.949

SRSPTPPSIAAK
Confirmed sites: @S:1,@T:5
Ambiguous sites:

MS/MS Fragmentation of SRSPTPPSIAAK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1737: 1438.725519 from(480.582449,3+)
Title: Elution from: 27.685 to 27.685 scan no 1841 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1438.7258
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K12 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 35 Expect: 0.015

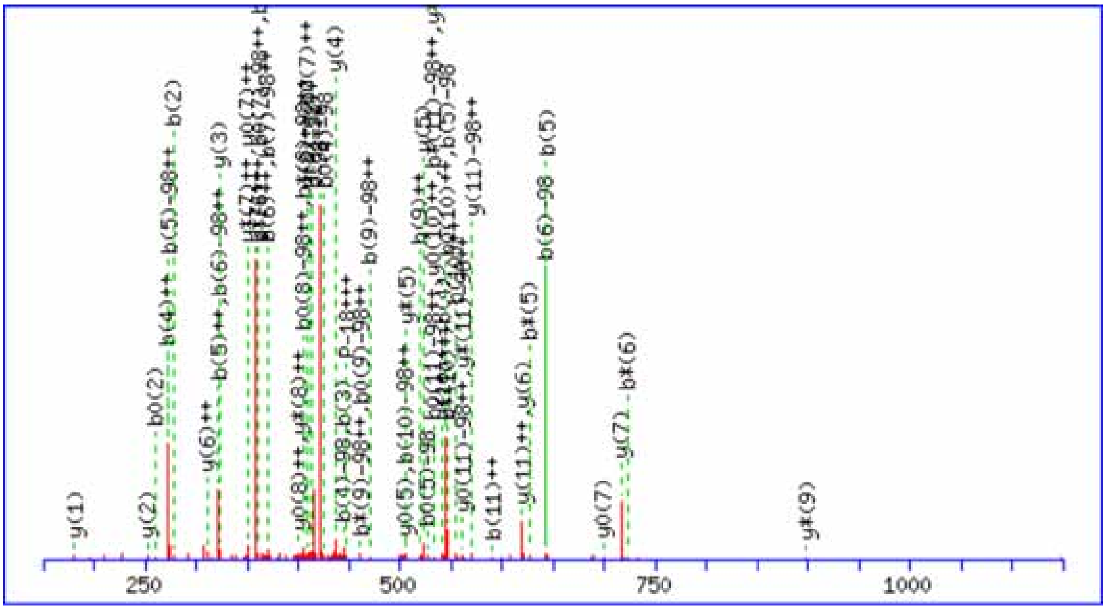
Matched b ions: b(3), b(3)-98, b(4), b(4)-98, b(5)-196++, b(5)-98, b(5)-98++, b(5)++, b(5), b(5)-196, b(6)-196++, b(6)-98++, b(6)++, b(6)-196, b(7)-196++, b(7)-98++, b(7)++, b(8)-196++, b(8)-98++, b(8)++, b(9)-196++, b(9)++, b(10)++, b(10)-98++, b(11)-196++, b(11)++
Matched y ions: y(1), y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8)++, y(8)-98++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.950

SRSPTPPSIAAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SRSPTPPSIAAK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1312: 1358.758896 from(453.926908,3+)
Title: Elution from: 26.981 to 26.981 scan no 1713 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1358.7595
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 41 Expect: 0.0033

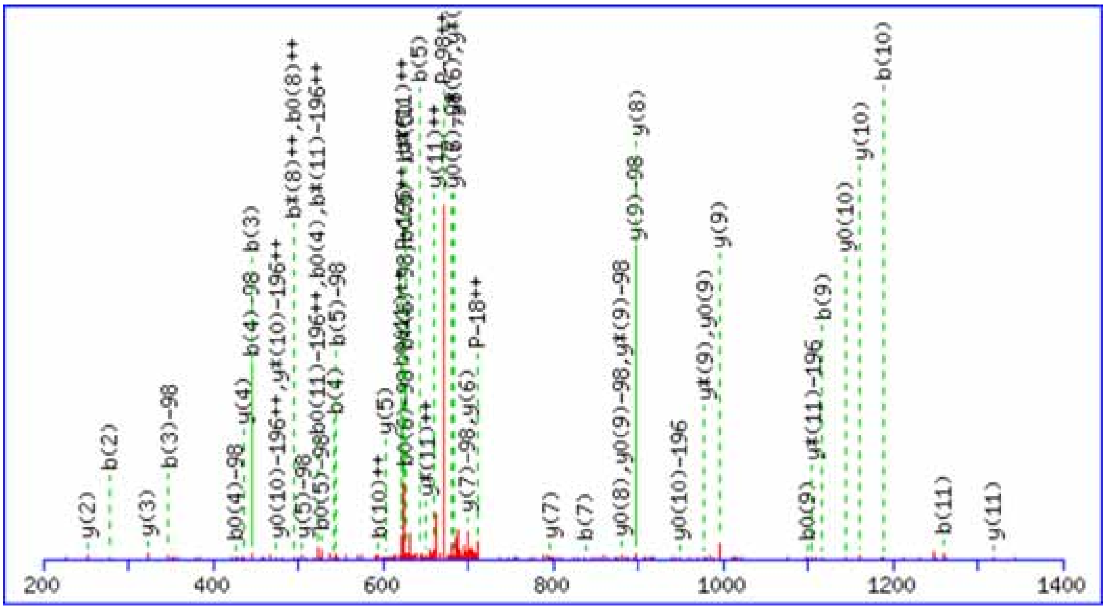
Matched b ions: b(2), b(3), b(4)++, b(4)-98, b(4), b(5)-98++, b(5)-98, b(5)++, b(5), b(6)-98++, b(6)-98, b(6)++, b(7)-98++, b(8)-98++, b(9)++, b(9)-98++, b(10)-98++, b(10)++, b(11)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8)++, y(10)++, y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.951

SRSPTPPSIAAK
Confirmed sites: @S:3,@S:8
Ambiguous sites:

MS/MS Fragmentation of SRSPTPPSIAAK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1943: 1438.727296 from(720.370924,2+)
Title: Elution from: 27.772 to 27.772 scan no 1820 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1438.7258
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K12 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 35 Expect: 0.014

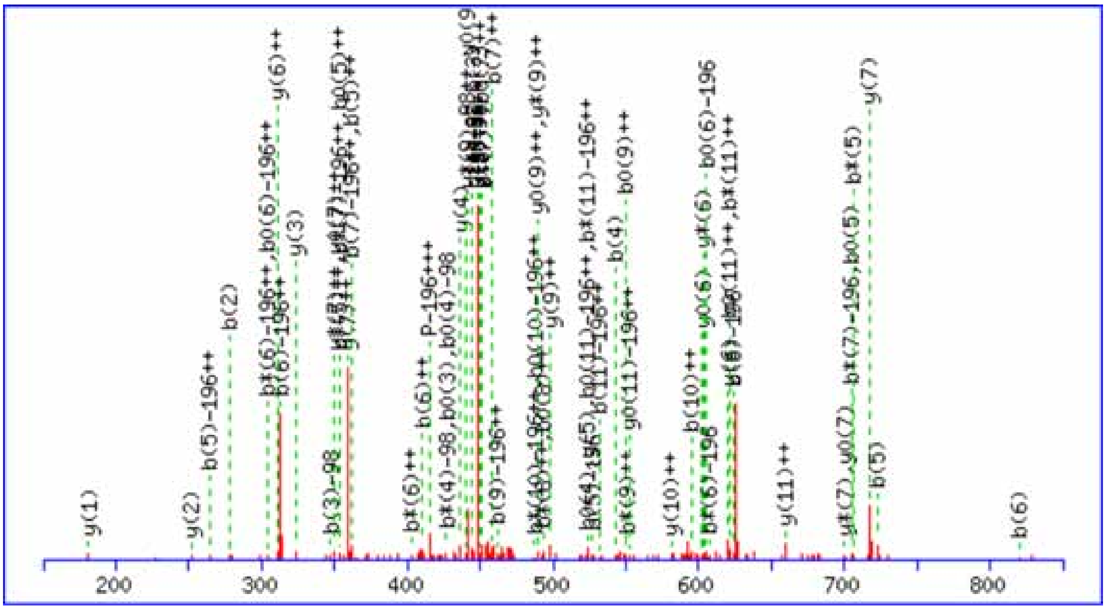
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(7), b(8)-98, b(9), b(9)-98++, b(10), b(10)-98++, b(10)++, b(11)-98, b(11)
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6), y(7)-98, y(7), y(8), y(9)-98, y(9), y(10), y(11), y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.952

SRSPTPPSIAAK
Confirmed sites: @S:3,@T:5
Ambiguous sites:

MS/MS Fragmentation of SRSPTPPSIAAK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1980: 1438.725060 from(480.582296,3+)
Title: Elution from: 27.668 to 27.668 scan no 1835 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1438.7258
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K12 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 32 Expect: 0.025

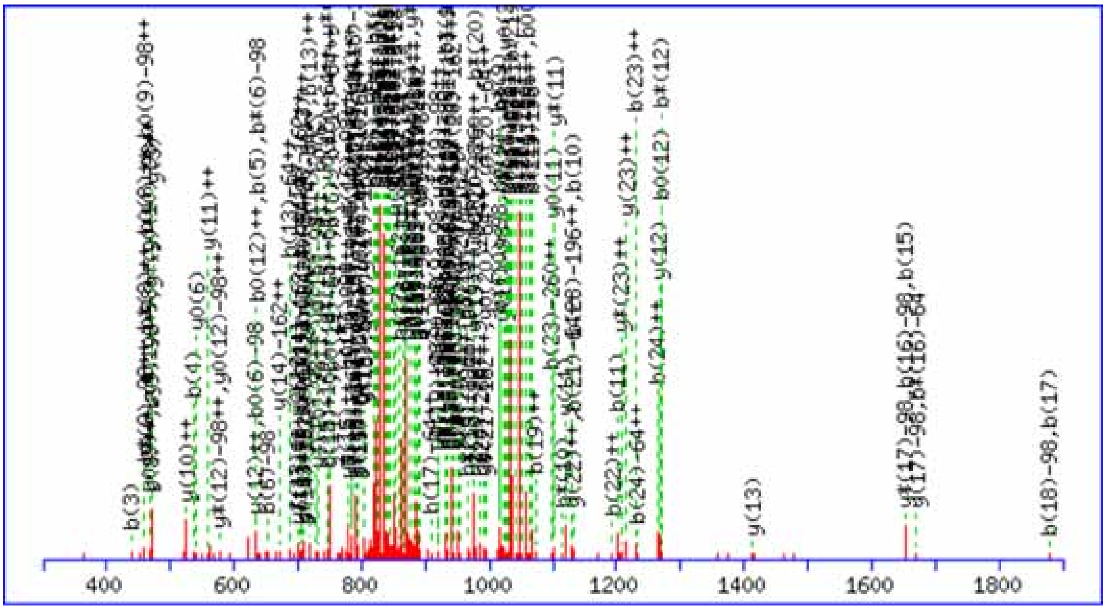
Matched b ions: b(2), b(3)-98, b(3), b(4), b(4)-98, b(5)-98, b(5)-196++, b(5)-98++, b(5), b(5)++, b(5)-196, b(6)-196++, b(6), b(6)-98, b(6)-98++, b(6)++, b(6)-196, b(7)-196++, b(7)-98++, b(7)++, b(8)-98++, b(9)-196++, b(10)-98++, b(10)++, b(11)-196++, b(11)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8)++, y(9)++, y(9)-98++, y(10)-98++, y(10)++, y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.953

SRSPVDSPVPASMFAPEPSSPGAAR
Confirmed sites: @S:3,@S:19
Ambiguous sites:

MS/MS Fragmentation of SRSPVDSPVPASMFAPEPSSPGAAR
Found in GTPB1_MOUSE, GTP-binding protein 1 OS=Mus musculus GN=Gtpbp1 PE=1 SV=2

Match to Query 6388: 2700.167982 from(901.063270,3+)
Title: Elution from: 43.796 to 43.796 scan no 3867 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2700.1656
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 Expect: 1.4e-005

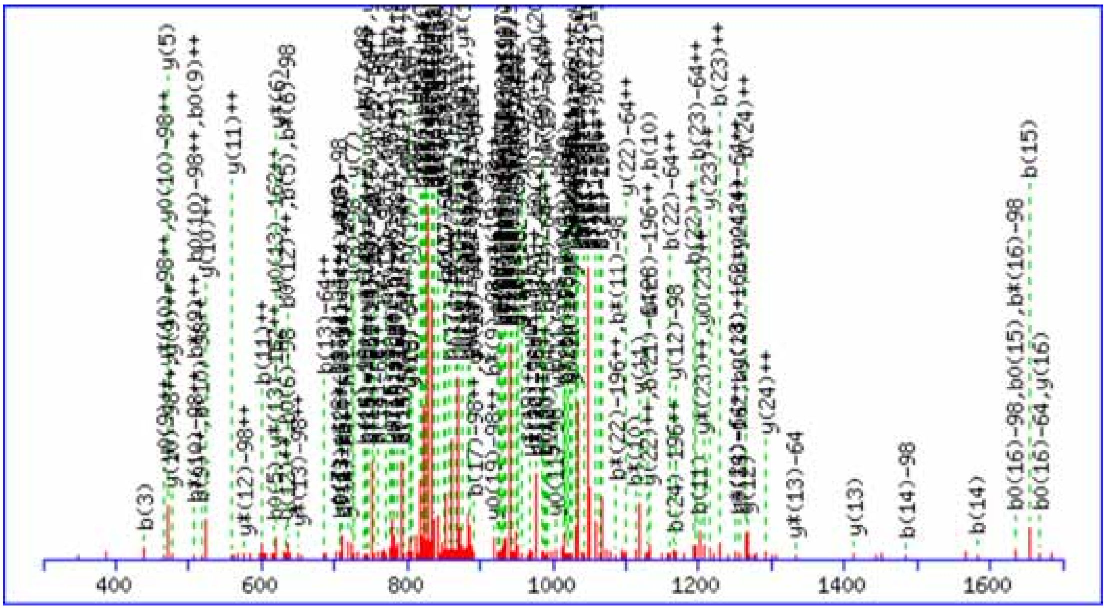
Matched b ions: b(3), b(4), b(5), b(6), b(6)-98, b(7), b(8)++, b(8)-98, b(8), b(9), b(9)-98++, b(9)-98, b(10), b(11), b(13)++, b(14)++, b(15)++, b(15), b(15)-98++, b(16)-98++, b(16)-98, b(16)++, b(17), b(17)++, b(17)-98++, b(18)-98, b(18)-98++, b(19)++, b(19)-98++, b(20)-98++, b(21)-196++, b(22)++, b(23)++, b(23)-196++, b(24)++, b(24)-98++
Matched y ions: y(5), y(8), y(9), y(9)-98, y(10), y(10)++, y(10)-98, y(11), y(11)++, y(11)-98, y(12), y(12)++, y(13), y(13)++, y(14)++, y(14)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-98, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(20)++, y(21)-98++, y(22)++, y(23)++
Precursor origin neutral loss: +

Peptide No.954

SRSPVDSPVPASMFAPEPSSPGAAR
Confirmed sites: @S:3,@S:20
Ambiguous sites:

MS/MS Fragmentation of SRSPVDSPVPASMFAPEPSSPGAAR
Found in GTPB1_MOUSE, GTP-binding protein 1 OS=Mus musculus GN=Gtpbp1 PE=1 SV=2

Match to Query 7087: 2700.169734 from(901.063854,3+)
Title: Elution from: 44.019 to 44.019 scan no 3974 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2700.1656
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 86 **Expect:** 2.1e-007

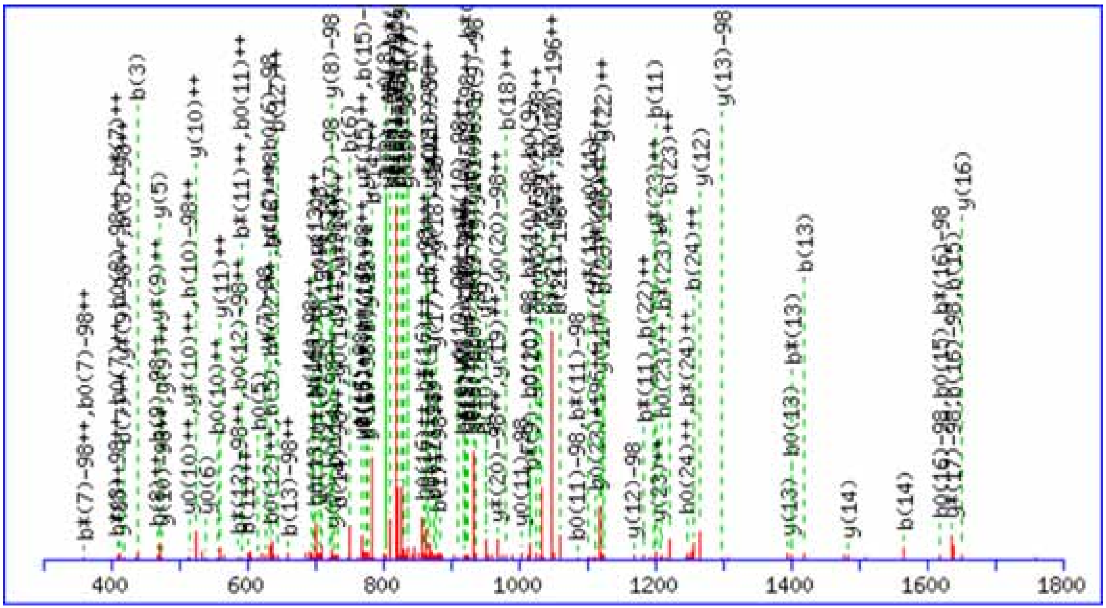
Matched b ions: b(3), b(5), b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)++, b(9)-98, b(10)-98, b(10)-98++, b(10), b(11), b(11)++, b(13)++, b(14)-98, b(14), b(14)++, b(14)-98++, b(15)++, b(15), b(15)-98++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)-98++, b(20)-196++, b(21)-196++, b(22)++, b(23)++, b(23)-196++, b(23)-98++, b(24)++, b(24)-98++, b(24)-196++
Matched y ions: y(5), y(7), y(8)-98, y(8), y(9)++, y(9), y(10), y(10)++, y(10)-98++, y(10)-98, y(11), y(11)++, y(11)-98, y(12), y(12)-98, y(12)++, y(13), y(13)++, y(14)++, y(15)++, y(16)++, y(16), y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(21)-98++, y(22)++, y(23)++, y(23)-98++, y(24)++
Precursor origin neutral loss: +

Peptide No.955

SRSPVDSPVPASMFAPEPSSPGAAR
Confirmed sites: @S:3,@S:19
Ambiguous sites:

MS/MS Fragmentation of SRSPVDSPVPASMFAPEPSSPGAAR
Found in GTPB1_MOUSE, GTP-binding protein 1 OS=Mus musculus GN=Gtpbp1 PE=1 SV=2

Match to Query 8117: 2684.173020 from(895.731616,3+)
Title: Elution from: 52.058 to 52.058 scan no 5152 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2684.1707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 **Expect:** 9.4e-006

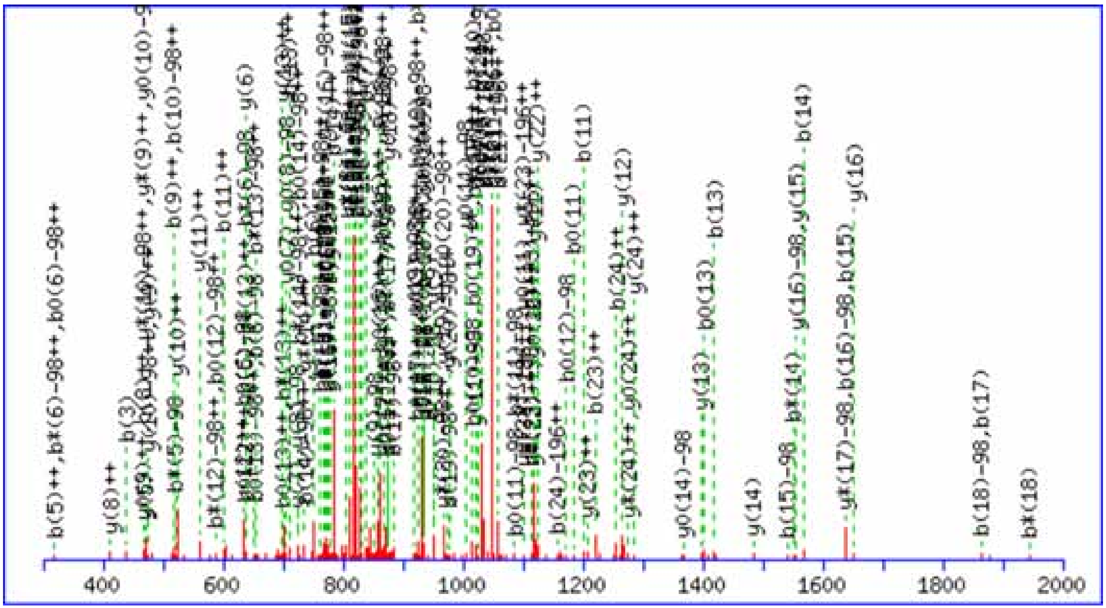
Matched b ions: b(3), b(5), b(6), b(7)++, b(7), b(8), b(8)-98++, b(8)++, b(9), b(9)-98++, b(9)-98, b(10)-98++, b(11), b(11)++, b(12)++, b(13), b(13)++, b(13)-98++, b(14)++, b(14), b(14)-98++, b(15)++, b(15), b(15)-98++, b(16)-98++, b(16)-98, b(16)++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(20)-98++, b(21)-196++, b(22)++, b(23)++, b(23)-196++, b(24)++, b(24)-98++
Matched y ions: y(5), y(7)-98, y(7), y(8)++, y(8), y(8)-98, y(9), y(9)++, y(10)++, y(10), y(10)-98, y(10)-98++, y(11), y(11)++, y(12), y(12)++, y(12)-98, y(13), y(13)-98, y(13)++, y(14), y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16), y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(21)-98++, y(22)++, y(23)++
Precursor origin neutral loss:

Peptide No.956

SRSPVDSPVPASMFAPEPSSPGAAR
Confirmed sites: @S:3,@S:20
Ambiguous sites:

MS/MS Fragmentation of SRSPVDSPVPASMFAPEPSSPGAAR
Found in GTPB1_MOUSE, GTP-binding protein 1 OS=Mus musculus GN=Gtpbp1 PE=1 SV=2

Match to Query 7071: 2684.173269 from(895.731699,3+)
Title: Elution from: 51.947 to 51.947 scan no 4908 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2684.1707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 79 Expect: 1e-006

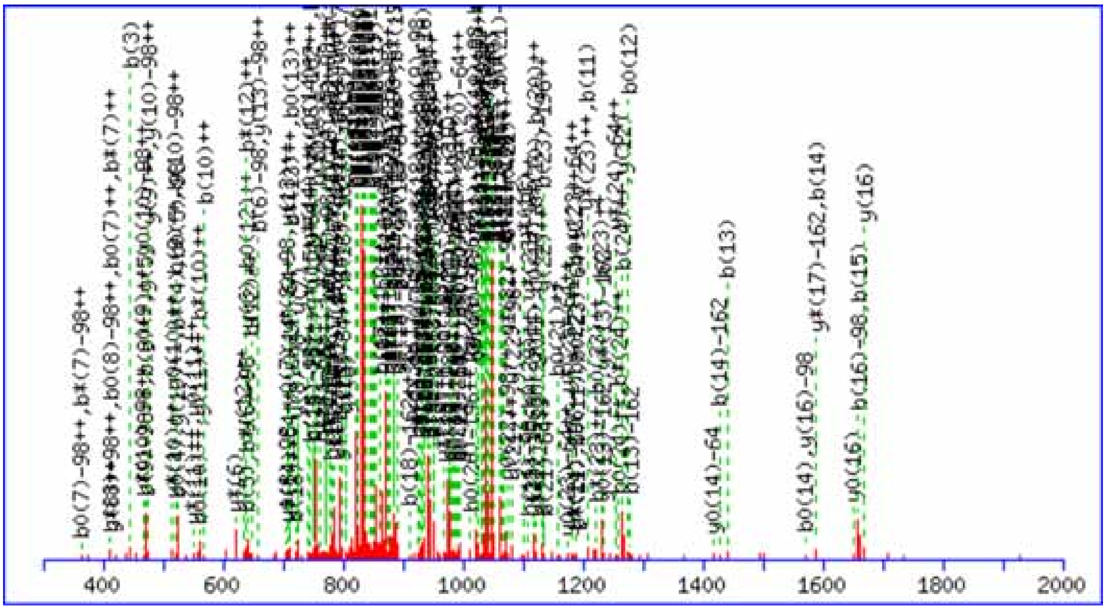
Matched b ions: b(3), b(5), b(5)++, b(6), b(6)-98, b(7), b(8)++, b(8), b(9)++, b(9), b(10)-98++, b(10)-98, b(11)++, b(11), b(13), b(13)++, b(14)++, b(14), b(14)-98++, b(15)++, b(15), b(15)-98, b(15)-98++, b(16)-98++, b(16)-98, b(16)++, b(17)++, b(17), b(17)-98++, b(18)-98++, b(18)-98, b(19)-98++, b(20)-98++, b(21)-196++, b(23)++, b(23)-98++, b(24)++, b(24)-98++, b(24)-196++
Matched y ions: y(5), y(6), y(7), y(8)++, y(8), y(8)-98, y(9)++, y(9), y(9)-98, y(10)++, y(10), y(10)-98, y(10)-98++, y(11), y(11)++, y(11)-98, y(12), y(12)++, y(13), y(13)++, y(14), y(15), y(15)++, y(16), y(16)++, y(16)-98, y(16)-98++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)-98++, y(22)++, y(23)++, y(23)-98++, y(24)++
Precursor origin neutral loss: +

Peptide No.957

SRSPVDSPVPASMFAPEPSSPGAAR
Confirmed sites: @S:3,@S:20
Ambiguous sites:

MS/MS Fragmentation of SRSPVDSPVPASMFAPEPSSPGAAR
Found in GTPB1_MOUSE, GTP-binding protein 1 OS=Mus musculus GN=Gtpbp1 PE=1 SV=2

Match to Query 7235: 2706.200805 from(903.074211,3+)
Title: Elution from: 43.924 to 43.924 scan no 4006 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2706.1974
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 **Expect:** 2e-005

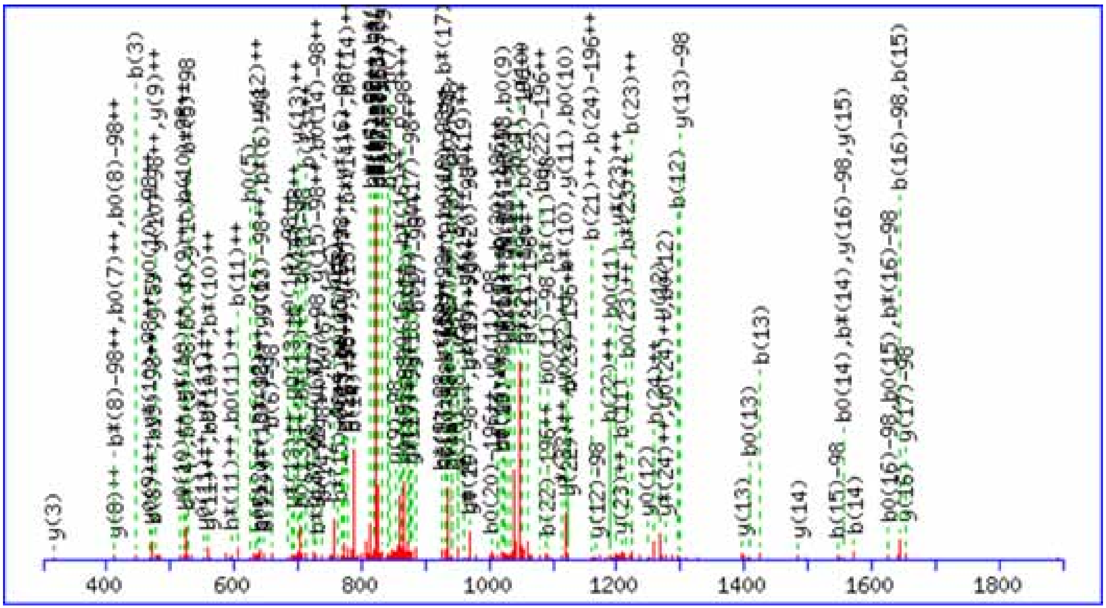
Matched b ions: b(3), b(5), b(6), b(6)-98, b(7)-98, b(7), b(8)++, b(8), b(9)-98++, b(9), b(9)++, b(9)-98, b(10)-98++, b(10)++, b(10)-98, b(11), b(11)-98, b(12)++, b(13), b(13)++, b(14), b(14)++, b(14)-98++, b(15)++, b(15), b(15)-98++, b(16)-98++, b(16)-98, b(16)++, b(17)++, b(18)-98++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(20)-196++, b(21)-98++, b(21)-196++, b(22)-98++, b(23)++, b(23)-98++, b(23)-196++, b(24)++, b(24)-98++
Matched y ions: y(5), y(6), y(7), y(8)-98, y(8)++, y(8), y(9)++, y(9)-98, y(9), y(10), y(10)++, y(10)-98++, y(10)-98, y(11), y(11)++, y(11)-98, y(12), y(12)++, y(13)++, y(13)-98++, y(14)++, y(15)++, y(16), y(16)++, y(16)-98, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(23)-196++, y(24)-98++
Precursor origin neutral loss: +

Peptide No.958

SRSPVDSPVPASMFAPEPSSPGAAR
Confirmed sites: @S:3,@S:20
Ambiguous sites:

MS/MS Fragmentation of SRSPVDSPVPASMFAPEPSSPGAAR
Found in GTPB1_MOUSE, GTP-binding protein 1 OS=Mus musculus GN=Gtpbp1 PE=1 SV=2

Match to Query 7035: 2690.204850 from(897.742226,3+)
Title: Elution from: 51.920 to 51.920 scan no 4952 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2690.2025
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 5.6e-006

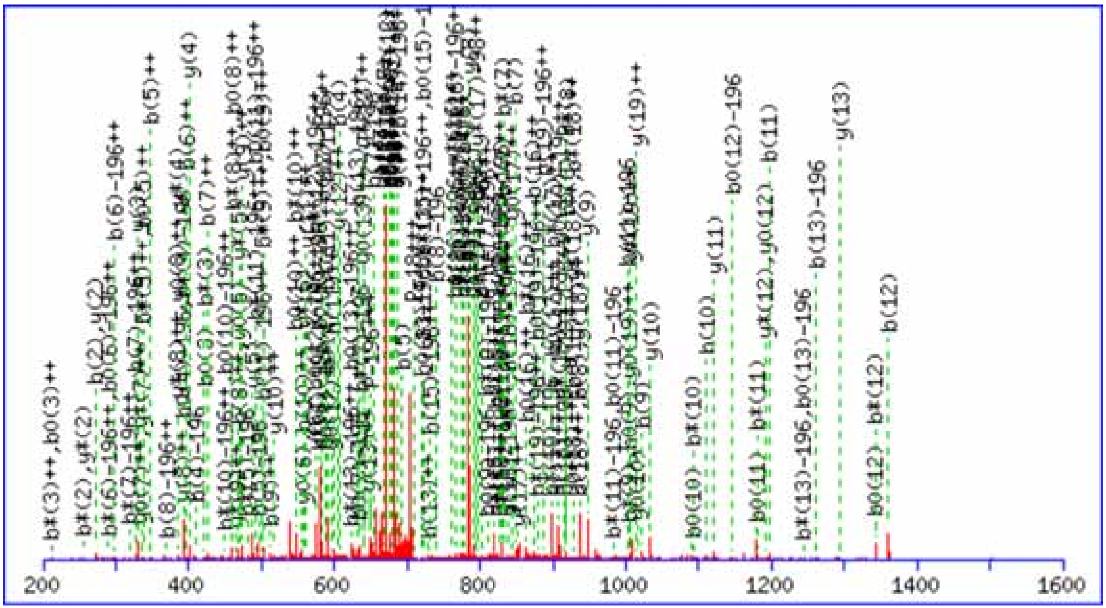
Matched b ions: b(3), b(5), b(6), b(6)-98, b(7), b(8)++, b(8)-98, b(8), b(9)-98++, b(9), b(9)++, b(9)-98, b(10)-98++, b(11), b(11)++, b(12)++, b(12), b(13), b(13)++, b(14)++, b(14), b(14)-98++, b(15)++, b(15), b(15)-98, b(15)-98++, b(16)-98++, b(16)-98, b(16)++, b(17)++, b(17)-98++, b(18)-98++, b(20)-98++, b(20)-196++, b(21)-196++, b(21)++, b(22)-196++, b(22)++, b(23)++, b(23)-196++, b(23)-98++, b(24)++, b(24)-98++, b(24)-196++
Matched y ions: y(3), y(5), y(6), y(7), y(8)++, y(8), y(8)-98, y(9)++, y(9), y(9)-98, y(10)++, y(10), y(10)-98++, y(10)-98, y(11), y(11)++, y(11)-98, y(12), y(12)++, y(12)-98, y(13), y(13)++, y(13)-98, y(14), y(14)-98++, y(15), y(15)++, y(15)-98++, y(16)++, y(16), y(16)-98, y(16)-98++, y(17)-98++, y(17)-98, y(17)++, y(18)++, y(18)-98++, y(19)++, y(20)++, y(21)-98++, y(22)++, y(23)++
Precursor origin neutral loss: +

Peptide No.959

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 7011: 2142.900369 from(715.307399,3+)
Title: Elution from: 34.820 to 34.820 scan no 2899 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2142.8984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 **Expect:** 0.00044

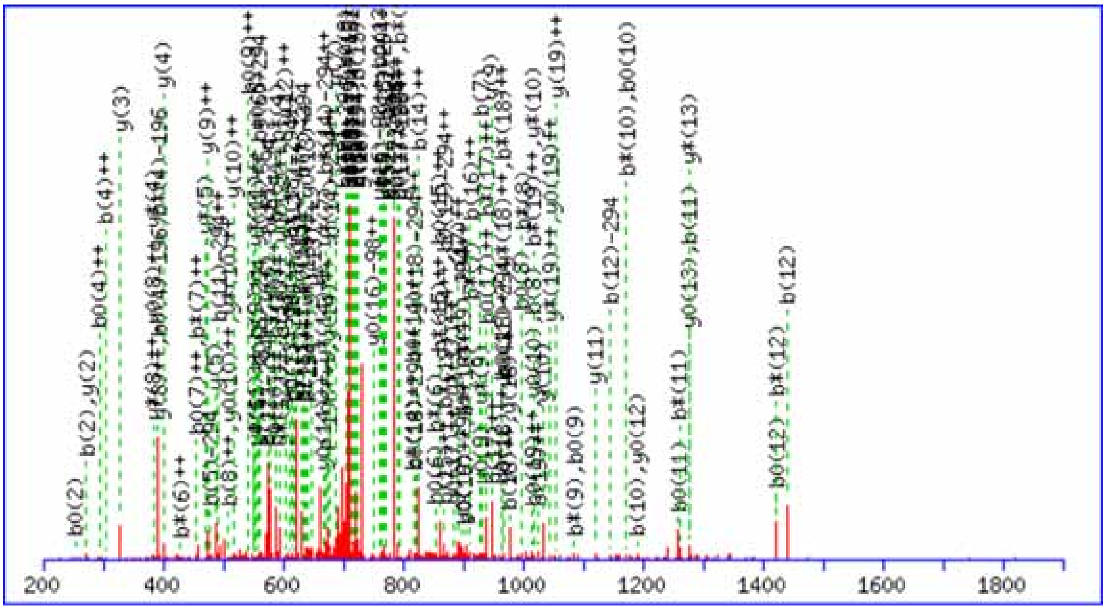
Matched b ions: b(2), b(4)-98++, b(4)-196, b(4), b(5)-98++, b(5)++, b(5)-196, b(5)-98, b(5), b(6), b(6)-196++, b(6)-98++, b(6)++, b(6)-98, b(7)++, b(7), b(7)-196++, b(7)-196, b(7)-98, b(8), b(8)++, b(8)-196++, b(8)-196, b(8)-98, b(9), b(9)++, b(9)-98++, b(9)-196, b(9)-98, b(10), b(10)++, b(10)-196, b(11), b(11)++, b(11)-196++, b(11)-98++, b(11)-196, b(11)-98, b(12), b(12)-98, b(12)++, b(12)-196++, b(12)-98++, b(13)-98, b(13)-196, b(13)-98++, b(13)++, b(13)-196++, b(14)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)-196++, b(16)++, b(16)-98++, b(17)++, b(17)-196++, b(17)-98++, b(18)++, b(18)-196++, b(18)-98++, b(19)-98++, b(19)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(13), y(13)++, y(14)++, y(17)++, y(18)++, y(18)-196++, y(18)-98++, y(19)-196++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.960

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:3,@S:4,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 6690: 2222.866704 from(741.962844,3+)
Title: Elution from: 38.641 to 38.641 scan no 3484 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2222.8647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 0.00016

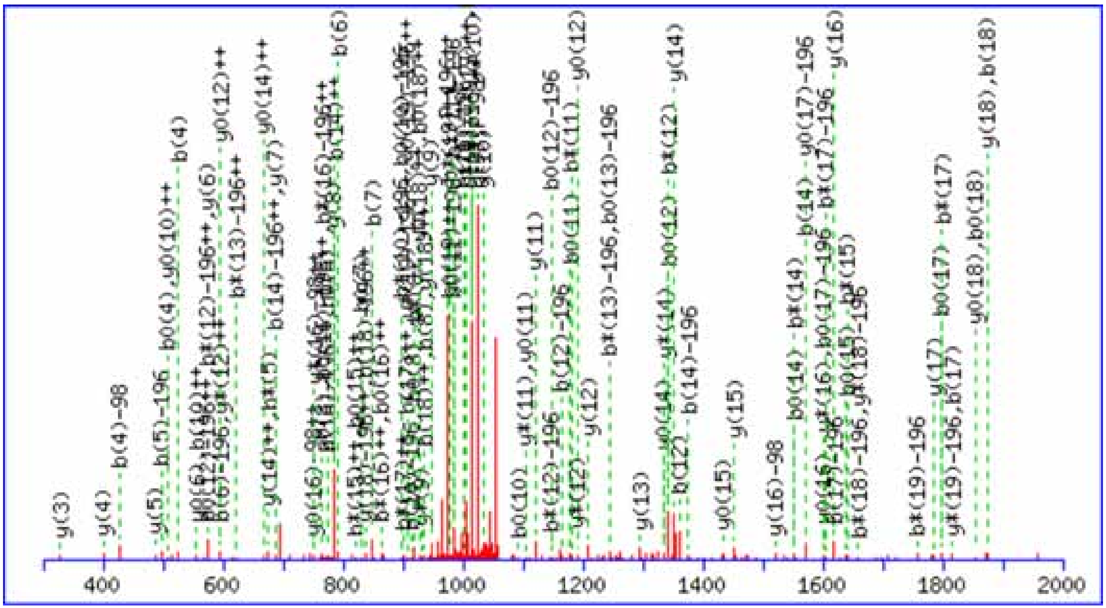
Matched b ions: b(2), b(4)++, b(4)-98, b(5)-196, b(5)-294, b(5)-98, b(5), b(6)-294, b(6)-98++, b(6)-196, b(6)-98, b(7)-294, b(7)-196, b(7)-98, b(7), b(8)-98++, b(8), b(8)++, b(8)-294, b(8)-196, b(8)-98, b(9)-98++, b(9)++, b(9)-196, b(9)-98, b(10), b(10)++, b(10)-98, b(10)-98++, b(10)-196, b(11), b(11)-98, b(11)-294++, b(11)-98++, b(11)++, b(12), b(12)-294++, b(12)-294, b(12)-98, b(12)++, b(12)-196++, b(12)-98++, b(13)-98, b(13)++, b(13)-196, b(13)-98++, b(13)-294++, b(13)-196++, b(14)++, b(14)-294++, b(14)-196++, b(14)-98++, b(15)++, b(15)-294++, b(15)-98++, b(16)-294++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(17)-196++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(19)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(18)-98++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.961

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:4,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5333: 2142.899252 from(1072.456902,2+)
Title: Elution from: 34.924 to 34.924 scan no 2761 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2142.8984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 84 Expect: 1.7e-007

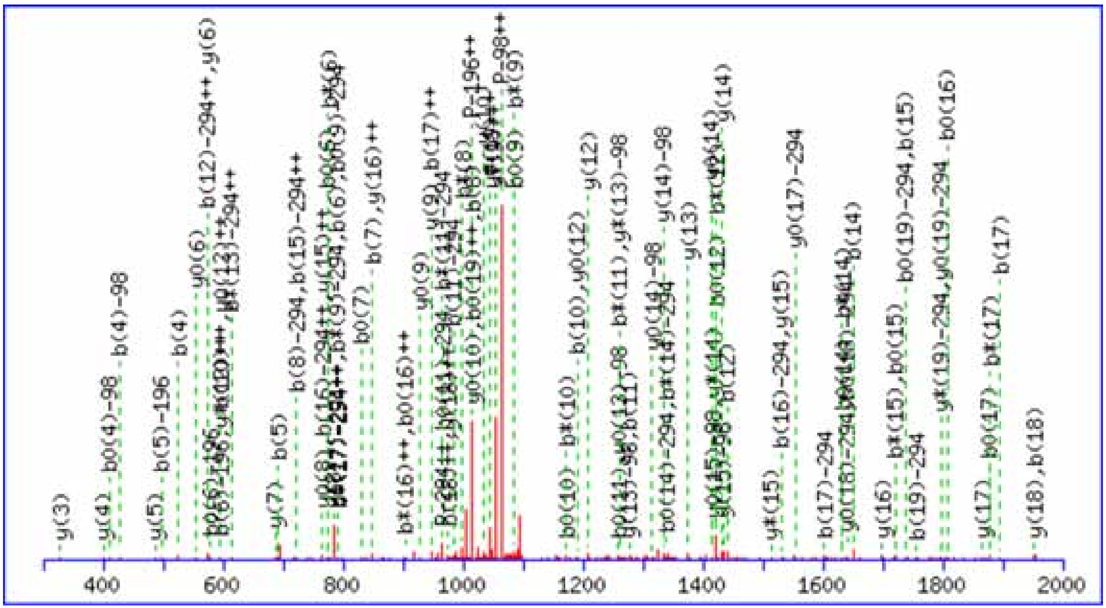
Matched b ions: b(4)-98, b(4), b(5)-196, b(5)-98, b(6)-98, b(6)-196, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9), b(10)++, b(10)-196, b(11)-196, b(12), b(12)-98, b(12)-196, b(13)-98, b(14)++, b(14), b(14)-196++, b(14)-98, b(14)-196, b(15)-98++, b(16)-196++, b(17), b(17)-196, b(17)++, b(18), b(18)-196++, b(18)++, b(19)-98, b(19)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(16), y(16)-98, y(17), y(17)-98, y(18), y(18)-196++, y(18)++, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.962

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:4,@S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5682: 2222.864666 from(1112.439609,2+)
Title: Elution from: 38.459 to 38.459 scan no 3244 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2222.8647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 **Expect:** 2.6e-005

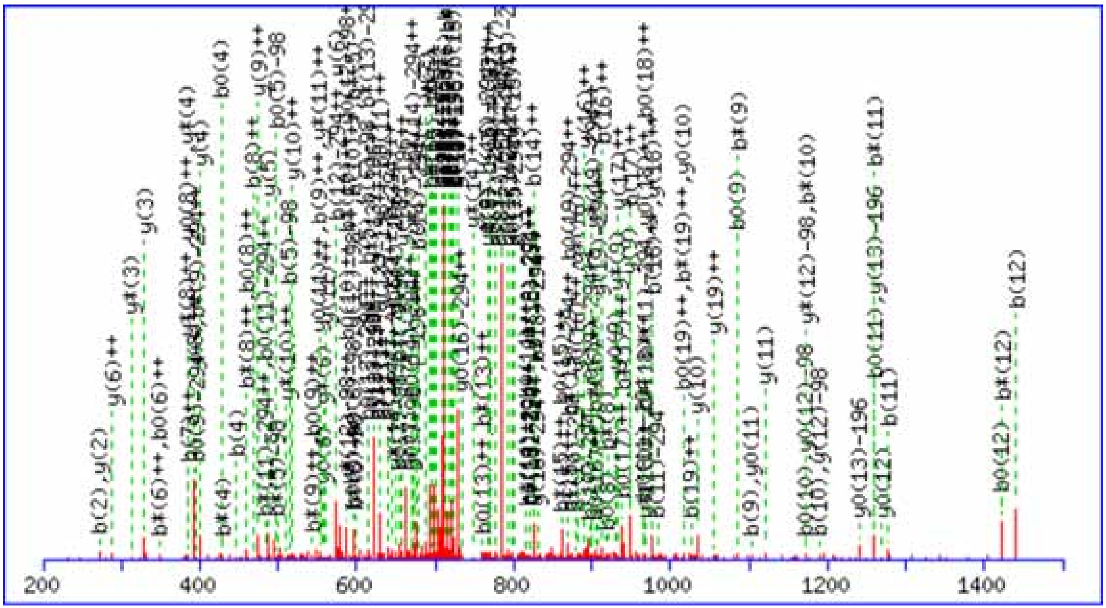
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(5)-196, b(6)-98, b(6)-196, b(6), b(7), b(8)-98, b(8)-196++, b(8)-294, b(8), b(9)-98, b(10)++, b(10)-196++, b(10)-98, b(10), b(11), b(11)-294, b(11)-196, b(11)-98, b(12)-294++, b(12)-98, b(12), b(12)-196, b(13)-98, b(13)-98++, b(14)-98, b(14), b(14)-196, b(15)-294++, b(15)-98, b(15), b(16)-294++, b(16)-294, b(16)-98++, b(17)-196, b(17)-294, b(17), b(17)-98, b(17)++, b(18), b(18)-98, b(18)++, b(18)-196, b(19)-98, b(19)-294, b(19)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12), y(13)-98, y(13), y(14), y(14)-98, y(15)++, y(15)-98, y(15), y(16)++, y(16)-98, y(16), y(17), y(18), y(18)-98, y(18)++, y(18)-196, y(19)-98++, y(19)++, y(19)-196++
Precursor origin neutral loss: +

Peptide No.963

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:5,@S:8,@S:9
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5929: 2222.866533 from(741.962787,3+)
Title: Elution from: 38.364 to 38.364 scan no 3253 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2222.8647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 Expect: 2e-005

Matched b ions: b(2), b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)++, b(7), b(7)-98, b(8)++, b(9)-98++, b(9), b(9)-98, b(9)++, b(9)-196, b(10), b(10)++, b(10)-196++, b(10)-98++, b(10)-294, b(10)-196, b(11), b(11)-98++, b(11)++, b(11)-294, b(12), b(12)-294++, b(12)-98, b(12)++, b(12)-196++, b(12)-98++, b(13)-98, b(13)-98++, b(13)++, b(13)-294++, b(13)-196++, b(14)++, b(14)-98++, b(14)-294++, b(14)-196++, b(15)++, b(15)-294++, b(15)-98++, b(16)++, b(16)-294++, b(16)-98++, b(17)++, b(17)-294++, b(17)-196++, b(17)-98++, b(18)++, b(18)-98++, b(18)-294++, b(18)-196++, b(19)-98++, b(19)-196++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12)-98, y(12)-98++, y(12)++, y(13)-196, y(13)-196++, y(13)-98++, y(13)++, y(14)-196++, y(14)-98++, y(15)-196++, y(16)-196++, y(16)++, y(16)-98++, y(17)-294++, y(17)-196++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(18)-294++, y(18)-196++, y(19)-98++, y(19)++, y(19)-294++
Precursor origin neutral loss: +

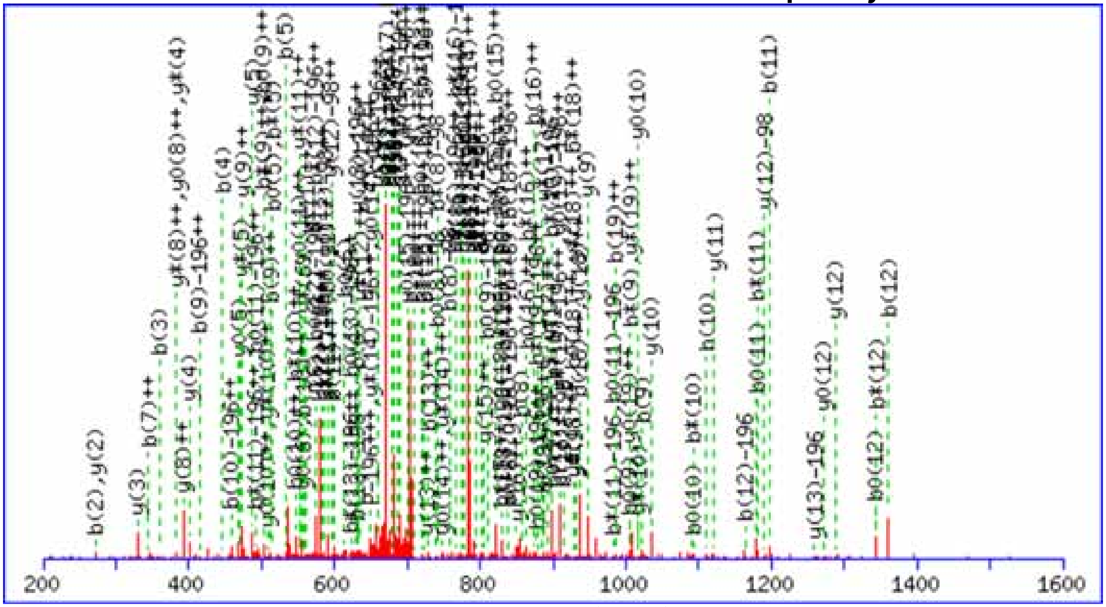
Peptide No.964

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:8,@S:9
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5719: 2142.899952 from(715.307260,3+)

Title: Elution from: 34.932 to 34.932 scan no 2810 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2142.8984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00046

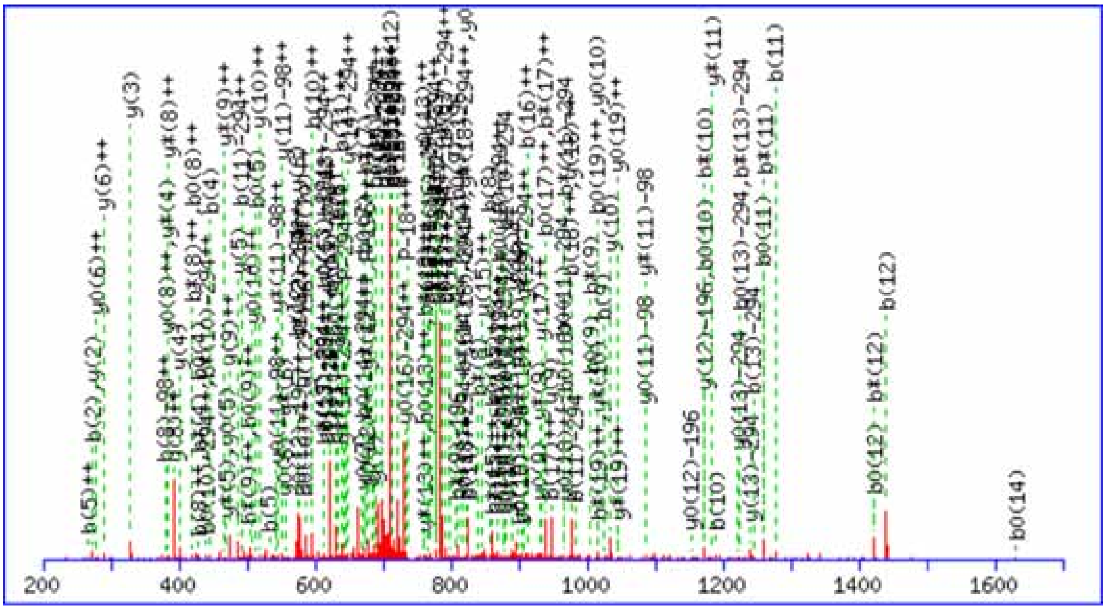
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)++, b(7), b(8)-98, b(8), b(9), b(9)++, b(9)-196++, b(10)++, b(10), b(10)-196++, b(10)-196, b(10)-98, b(11), b(11)++, b(11)-98++, b(12), b(12)++, b(12)-98, b(12)-196++, b(12)-98++, b(12)-196, b(13)-98, b(13)-98++, b(13)++, b(13)-196++, b(14)++, b(14)-196++, b(15)++, b(15)-98++, b(16)-196++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-196++, b(18)-98++, b(19)-98++, b(19)-196++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(11), y(11)++, y(12), y(12)-98++, y(12)-98, y(13)-196++, y(13)-98++, y(13)++, y(13)-196, y(14)-196++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(17)-196++, y(17)-98++, y(17)++, y(18)++, y(18)-196++, y(18)-98++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.965

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:8,@S:9,@S:10
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 7378: 2222.865534 from(741.962454,3+)
Title: Elution from: 38.336 to 38.336 scan no 3402 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2222.8647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 0.00011

Matched b ions: b(2), b(4), b(5)++, b(5), b(6), b(7), b(8)++, b(8)-98++, b(8), b(9)-98, b(9), b(10), b(10)++, b(10)-98, b(10)-196++, b(10)-98++, b(11), b(11)-98, b(11)-294++, b(11)-98++, b(11)++, b(11)-294, b(12), b(12)-294++, b(12)-98, b(12)++, b(12)-196, b(12)-196++, b(12)-98++, b(13)-98, b(13)-196, b(13)-98++, b(13)++, b(13)-294, b(13)-294++, b(13)-196++, b(14)++, b(14)-98++, b(14)-196++, b(15)++, b(15)-294++, b(15)-98++, b(16)-294++, b(16)-196++, b(16)-98++, b(16)++, b(17)++, b(17)-196++, b(17)-98++, b(18)++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)-196++, b(19)-294++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)-98++, y(12)-196, y(12)-196++, y(12)-98++, y(12)++, y(12)-98, y(13)-294++, y(13)-294, y(13)-98++, y(14)-294++, y(14)-196++, y(14)-98++, y(14)++, y(15)++, y(15)-294++, y(15)-196++, y(15)-98++, y(16)++, y(16)-196++, y(17)-294++, y(17)++, y(17)-196++, y(17)-98++, y(18)++, y(18)-98++, y(18)-196++, y(19)-294++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

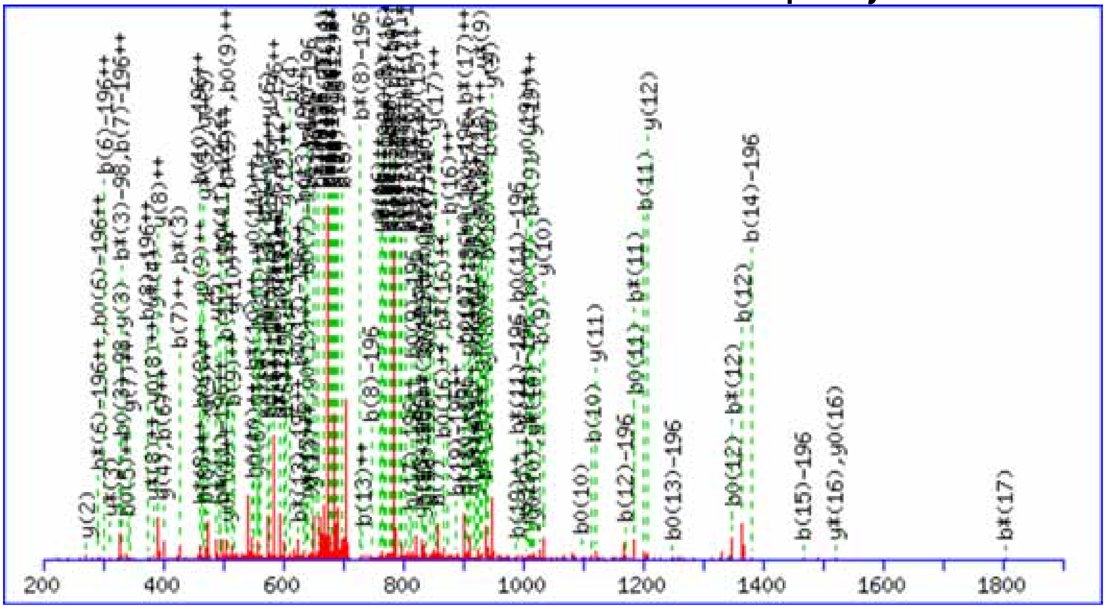
Peptide No.966

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4963: 2148.932199 from(717.318009,3+)

Title: Elution from: 34.753 to 34.753 scan no 2646 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2148.9302
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 0.00026

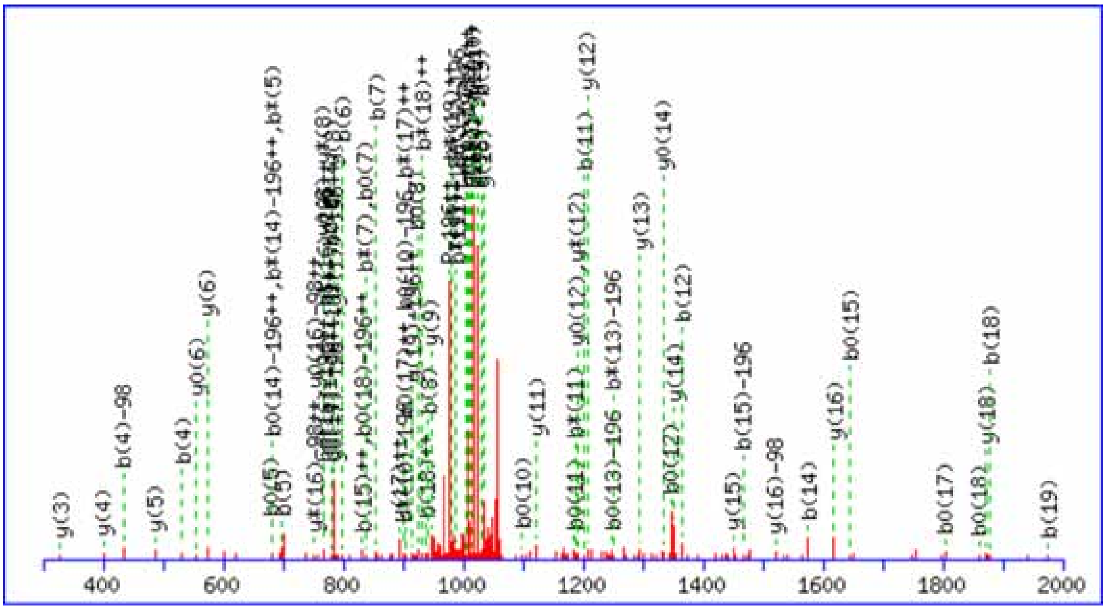
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6)++, b(6), b(6)-196, b(6)-196++, b(6)-98, b(7)++, b(7)-196++, b(7)-98++, b(7)-196, b(7)-98, b(7), b(8), b(8)++, b(8)-196++, b(8)-196, b(8)-98, b(9), b(9)++, b(9)-98++, b(9)-196, b(9)-98, b(10), b(10)++, b(10)-196++, b(10)-98++, b(10)-196, b(10)-98, b(11), b(11)++, b(11)-196, b(11)-196++, b(11)-98, b(12)-98, b(12), b(12)++, b(12)-196, b(12)-196++, b(12)-98++, b(13)-98, b(13)-98++, b(13)-196++, b(13)++, b(14)++, b(14)-196, b(14)-196++, b(14)-98++, b(15)-196, b(15)++, b(16)-196++, b(16)-98++, b(16)++, b(17)++, b(17)-196++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)-196++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13)++, y(14)++, y(16)++, y(17)++, y(17)-98++, y(18)-196++, y(18)-98++, y(18)++, y(19)-196++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.967

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:4,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 7025: 2148.930630 from(1075.472591,2+)
Title: Elution from: 34.953 to 34.953 scan no 2917 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2148.9302
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 Expect: 1.1e-006

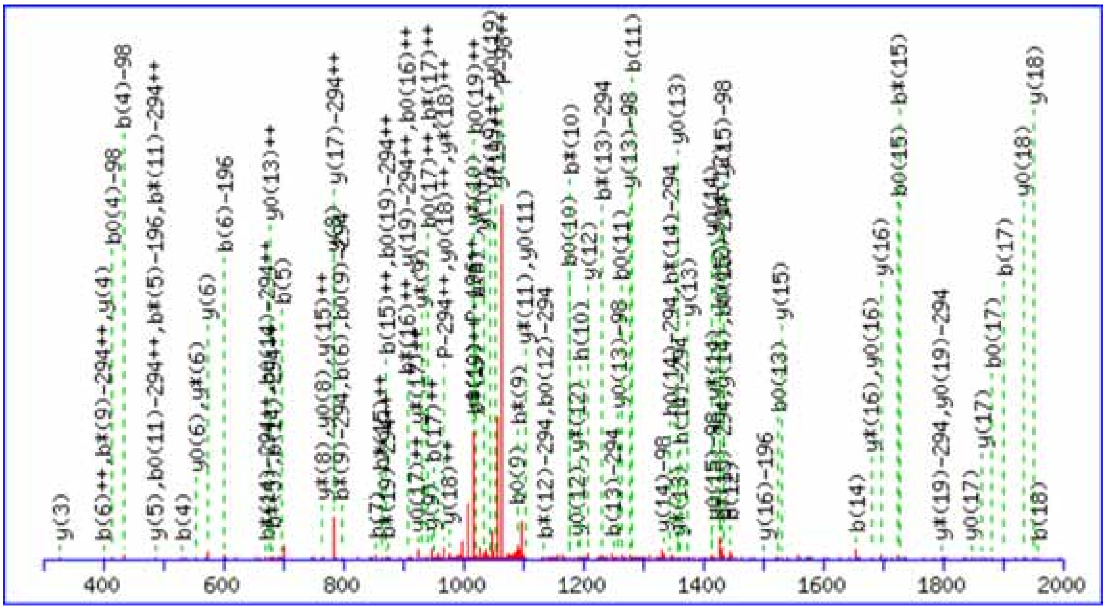
Matched b ions: b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(8), b(9)-98, b(9), b(10)-98, b(11)-196, b(11)-98, b(11), b(12)-98, b(12), b(13)-98, b(14), b(14)-98, b(14)-98++, b(15)++, b(15)-196, b(16)-98, b(18), b(18)++, b(19), b(19)-98, b(19)-98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(16)-98, y(17)++, y(18), y(19)-196++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.968

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:4,@S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5708: 2228.898312 from(1115.456432,2+)
Title: Elution from: 38.520 to 38.520 scan no 3252 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2228.8965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 0.00014

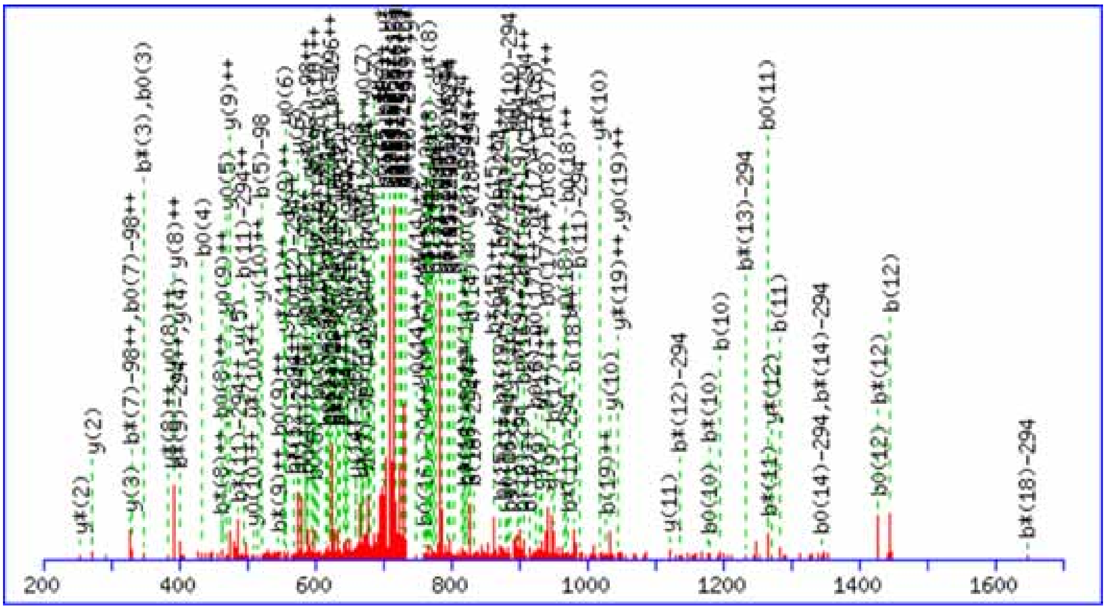
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6)++, b(6)-98, b(6)-196, b(6), b(7), b(8)-98, b(8)-196, b(8), b(9)-196, b(9)-98, b(10)-98, b(10)-196, b(10), b(11)-196, b(11), b(12), b(12)-98, b(12)-196, b(13)-98, b(13)-196, b(13)-294, b(14)-98, b(14), b(14)-294++, b(14)-294, b(15)++, b(16)-98, b(17)-98, b(17), b(17)++, b(17)-196, b(18), b(18)-98++, b(19)-98
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(12), y(13)-98, y(13), y(14), y(14)-98, y(15), y(15)++, y(15)-98, y(16), y(16)-98, y(16)-196, y(17)-98, y(17), y(17)-294++, y(18), y(18)++, y(18)-98, y(19)-294++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.969

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:5,@S:8,@S:9
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5709: 2228.898366 from(743.973398,3+)
Title: Elution from: 38.735 to 38.735 scan no 3281 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2228.8965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00038

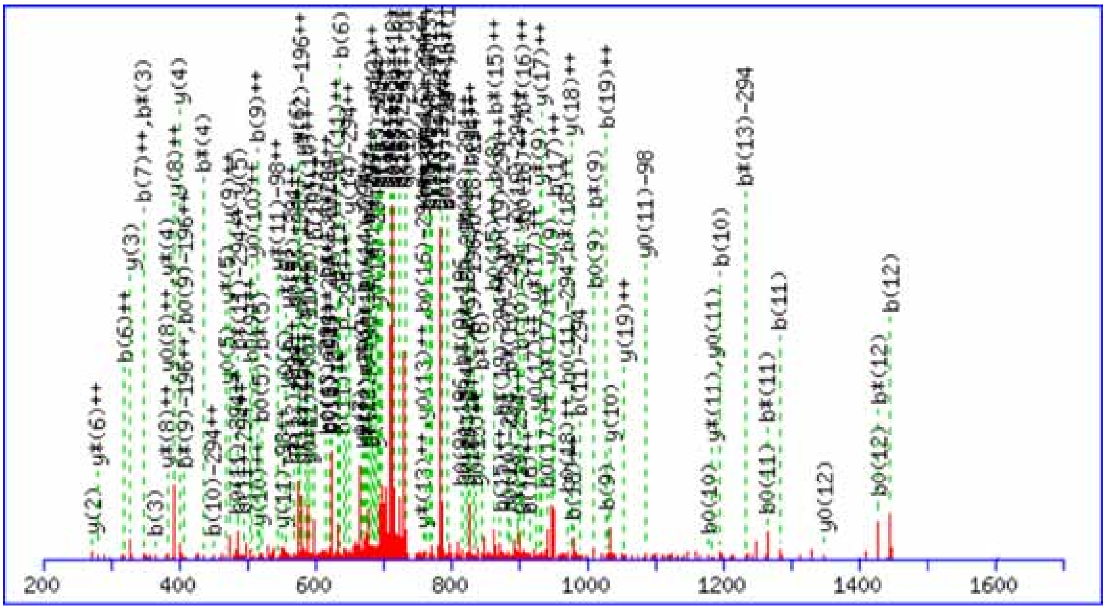
Matched b ions: b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8), b(8)-98, b(9)-196++, b(9)-98++, b(9)++, b(9)-294, b(10), b(10)-294, b(10)++, b(10)-196++, b(10)-98++, b(11), b(11)-294++, b(11)-196++, b(11)-98++, b(11)++, b(11)-294, b(12), b(12)-98, b(12)++, b(12)-294++, b(12)-196++, b(12)-98++, b(13)-98, b(13)-98++, b(13)-294++, b(13)-196++, b(13)++, b(14)++, b(14)-196++, b(14)-98++, b(14)-294++, b(15)-294++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(17)-196++, b(18)++, b(18)-294++, b(18)-98++, b(19)-98++, b(19)-294++, b(19)-196++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(12)-98++, y(12)++, y(13)-196++, y(13)-98++, y(13)++, y(14)-196++, y(14)-98++, y(15)-196++, y(15)++, y(16)-196++, y(16)-98++, y(17)-294++, y(17)-196++, y(17)-98++, y(17)++, y(18)-294++, y(18)-98++, y(19)-294++, y(19)-196++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.970

SRSSSVGSSSSYPISSAGPR
Confirmed sites: @S:8,@S:9,@S:10
Ambiguous sites:

MS/MS Fragmentation of SRSSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5707: 2228.897307 from(743.973045,3+)
Title: Elution from: 38.407 to 38.407 scan no 3237 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2228.8965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0084

Matched b ions: b(3), b(6)++, b(6), b(7)++, b(7), b(8), b(8)-98, b(9), b(9)++, b(9)-196, b(9)-98, b(10)-294, b(10), b(10)++, b(10)-98, b(10)-294++, b(10)-98++, b(11), b(11)-294++, b(11)-196++, b(11)-98++, b(11)++, b(11)-294, b(12), b(12)-98, b(12)++, b(12)-294++, b(12)-196++, b(12)-98++, b(13)-98, b(13)-196, b(13)-98++, b(13)-294++, b(13)-196++, b(13)++, b(14)++, b(14)-294++, b(14)-196++, b(14)-98++, b(15)++, b(15)-294++, b(15)-98++, b(16)-294++, b(16)-196++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(17)-196++, b(18)++, b(18)-294++, b(18)-196++, b(18)-98++, b(19)-98++, b(19)-196++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11)-98++, y(12)-196++, y(12)++, y(13)-294++, y(13)-196++, y(13)-98++, y(13)++, y(14)-196++, y(14)-294++, y(15)-294++, y(15)-98++, y(16)-196++, y(16)-98++, y(17)-294++, y(17)-196++, y(17)-98++, y(17)++, y(18)-294++, y(18)-98++, y(18)++, y(19)-196++, y(19)++
Precursor origin neutral loss: +

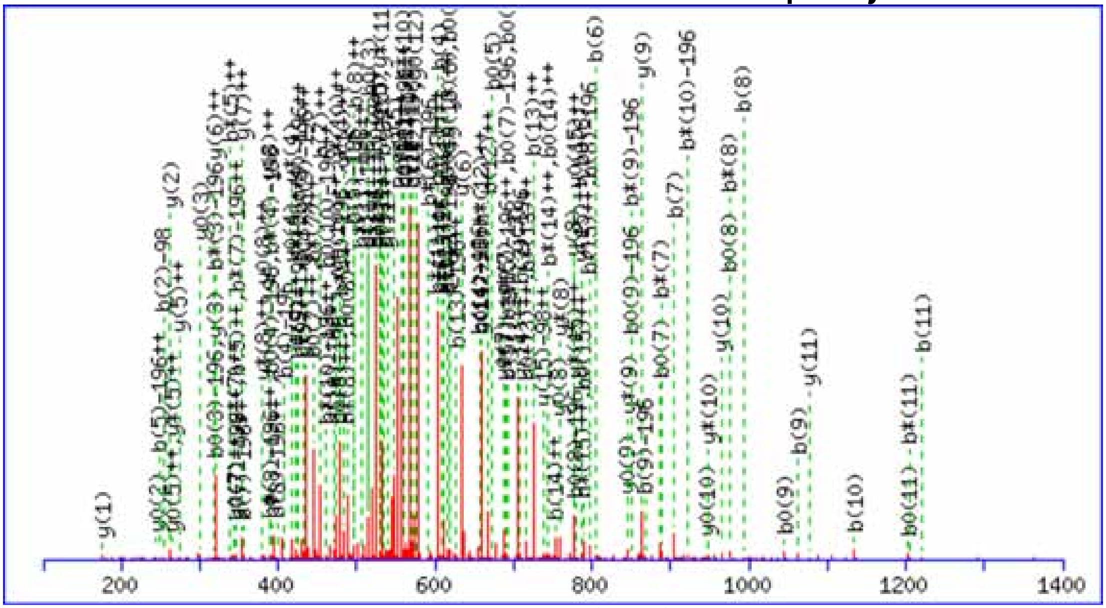
Peptide No.971

SRTASLTSAASIDGSR
Confirmed sites: @S:1,@T:3
Ambiguous sites:

MS/MS Fragmentation of SRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3099: 1766.761332 from(589.927720,3+)

Title: Elution from: 36.127 to 36.127 scan no 2927 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1766.7601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 Expect: 9.2e-006

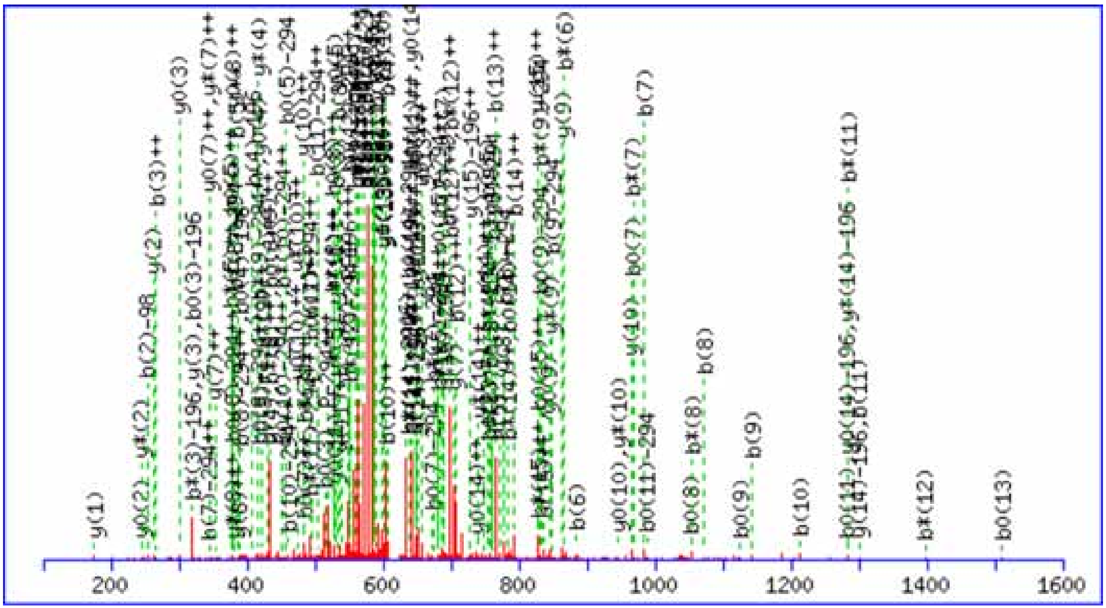
Matched b ions: b(2)-98, b(3)-98, b(3), b(4)-98++, b(4)-196, b(4), b(5)-196++, b(5)-98++, b(5)++, b(5)-196, b(5)-98, b(5), b(6)-98++, b(6)-98, b(6), b(6)-196, b(7), b(7)++, b(7)-196++, b(7)-98++, b(7)-196, b(7)-98, b(8)-196, b(8), b(8)-196++, b(8)-98++, b(8)++, b(8)-98, b(9)-196++, b(9), b(9)++, b(9)-98++, b(9)-196, b(9)-98, b(10)++, b(10), b(10)-98, b(10)-98++, b(10)-196++, b(11), b(11)-98, b(11)++, b(11)-196++, b(11)-98++, b(12)++, b(12)-196++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14)-98++, b(14)++, b(14)-196++, b(15)++, b(15)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.972

SRTASLTSAASIDGSR
Confirmed sites: @S:1,@T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 5326: 1846.727190 from(616.583006,3+)
Title: Elution from: 39.959 to 39.959 scan no 3633 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1846.7264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00021

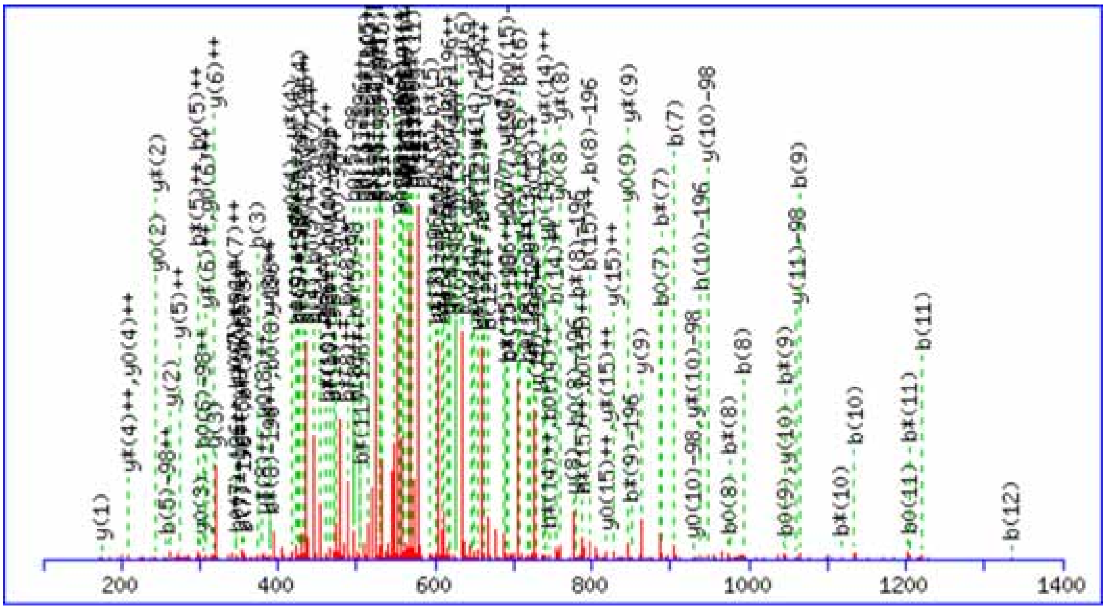
Matched b ions: b(2)-98, b(3)-98, b(3)++, b(3), b(4)-98++, b(4), b(4)-196, b(4)-98, b(5)-196++, b(5)++, b(5)-196, b(5)-98, b(5), b(6), b(6)-98, b(6)-196++, b(6)-98++, b(6)-294, b(6)-196, b(7), b(7)-98, b(7)-98++, b(7)++, b(7)-294++, b(7)-196++, b(7)-196, b(8), b(8)-294++, b(8)-98++, b(8)++, b(8)-294, b(8)-196, b(8)-98, b(9), b(9)++, b(9)-98++, b(9)-196++, b(9)-294, b(9)-196, b(9)-98, b(10)-98, b(10), b(10)-98++, b(10)-294++, b(10)-196++, b(10)++, b(11), b(11)++, b(11)-196, b(11)-294++, b(11)-98++, b(12)++, b(12)-294++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-294++, b(14)-196++, b(14)-98++, b(15)++, b(15)-294++, b(15)-196++, b(15)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(9), y(10), y(10)++, y(11)++, y(12)-98++, y(13)++, y(14)-98, y(14)-196, y(14)-196++, y(14)-98++, y(14)++, y(15)-196++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.973

SRTASLTSAASIDGSR
Confirmed sites: @S:5,@T:7
Ambiguous sites:

MS/MS Fragmentation of SRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 4744: 1766.760699 from(589.927509,3+)
Title: Elution from: 36.024 to 36.024 scan no 3071 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1766.7601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 Expect: 7e-006

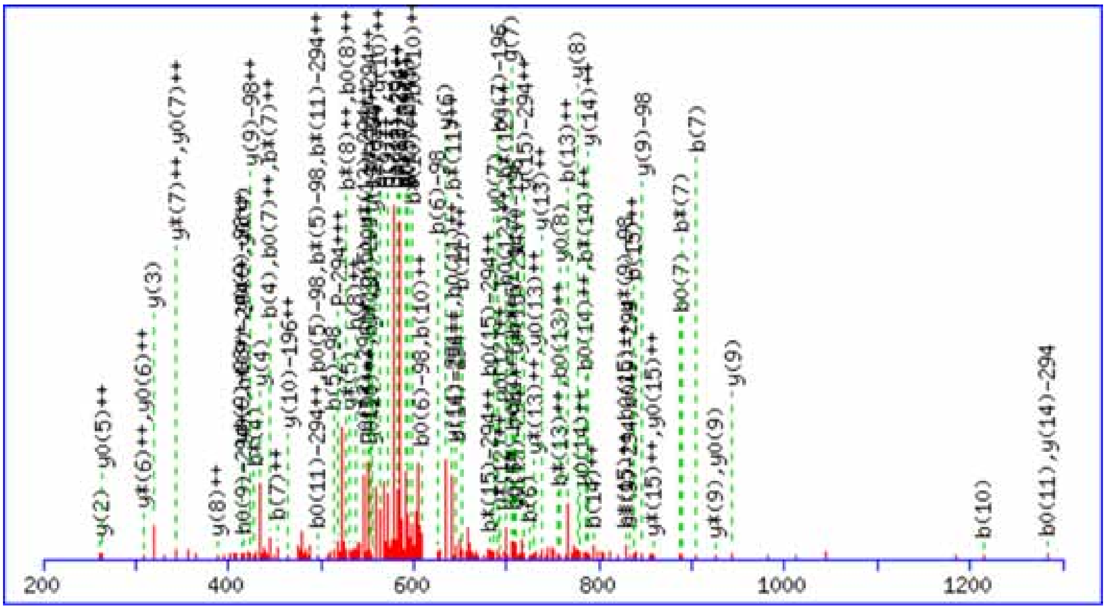
Matched b ions: b(3), b(4), b(5), b(5)-98++, b(5)-98, b(6)-98, b(7), b(7)++, b(7)-196++, b(7)-98++, b(7)-98, b(8)-196, b(8), b(8)-98++, b(8)++, b(8)-98, b(9)-196++, b(9), b(9)-98, b(9)++, b(9)-98++, b(10), b(10)++, b(10)-98, b(10)-196, b(10)-196++, b(10)-98++, b(11), b(11)++, b(11)-196++, b(11)-98++, b(12), b(12)++, b(12)-196++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14)-98++, b(14)++, b(15)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(10), y(10)-98, y(10)-98++, y(11)-98++, y(11)++, y(11)-98, y(12)-196++, y(12)-98++, y(12)++, y(13)-196++, y(13)-98++, y(14)-196++, y(14)-98++, y(15)-98++, y(15)-196++, y(15)++
Precursor origin neutral loss:

Peptide No.974

SRTASLTSAASIDGSR
Confirmed sites: @S:5,@T:7,@S:8
Ambiguous sites:

MS/MS Fragmentation of SRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 4649: 1846.727079 from(616.582969,3+)
Title: Elution from: 38.106 to 38.106 scan no 3413 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1846.7264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.014

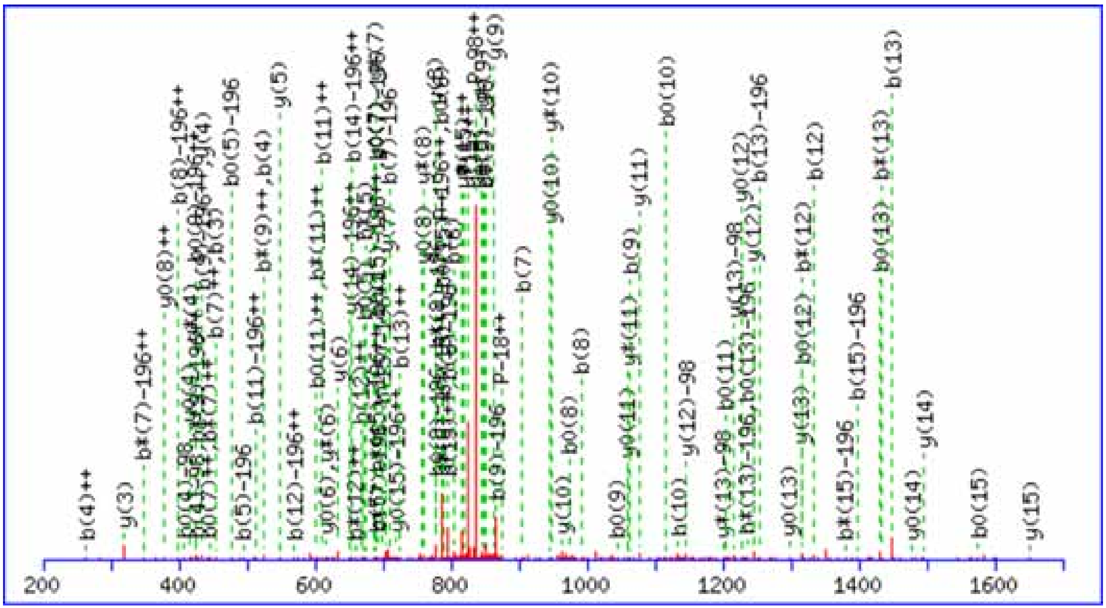
Matched b ions: b(4), b(5)-98, b(6)-98, b(6), b(7)++, b(7), b(7)-196, b(8)-196++, b(8)-98++, b(8)++, b(9)-98++, b(9)-98, b(9)++, b(9)-196++, b(10), b(10)-98++, b(10)-196++, b(10)++, b(11)-196++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-98++, b(14)-294++, b(14)-196++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(9)-98++, y(9)-98, y(10)++, y(10)-196++, y(10)-98++, y(11)-98++, y(12)-196++, y(12)-294++, y(13)-294++, y(13)-196++, y(13)++, y(14)-294, y(14)-294++, y(14)-196++, y(14)++, y(15)-294++
Precursor origin neutral loss: +

Peptide No.975

SRTASLTSAASIDGSR
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3190: 1766.760832 from(884.387692,2+)
Title: Elution from: 35.889 to 35.889 scan no 2893 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1766.7601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 97 Expect: 8.5e-009

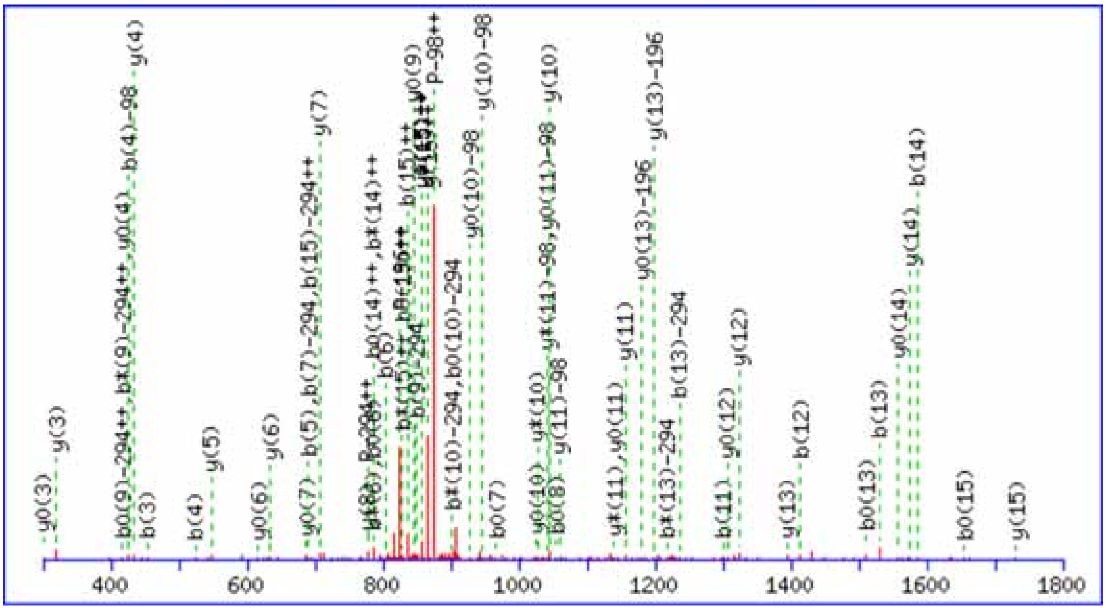
Matched b ions: b(3), b(4)-98, b(4), b(4)++, b(5)-98, b(5)-196, b(5), b(6)-98, b(6), b(7)++, b(7)-196, b(7), b(8)-196++, b(8)-196, b(8)-98, b(8), b(9)-196++, b(9)-196, b(9)-98, b(9), b(10), b(10)-98, b(11)-196++, b(11)++, b(11)-98, b(12)-98, b(12), b(12)-196++, b(12)++, b(13)-98, b(13), b(13)++, b(13)-196, b(14)-98++, b(14)-196++, b(15)-196, b(15)-196++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98, y(13)-98, y(13), y(14), y(14)-196++, y(14)-98, y(15)++, y(15), y(15)-98++
Precursor origin neutral loss: +

Peptide No.976

SRTASLTSAASIDGSR
Confirmed sites: @T:3,@S:5,@T:7
Ambiguous sites:

MS/MS Fragmentation of SRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3601: 1846.727500 from(924.371026,2+)
Title: Elution from: 36.587 to 36.587 scan no 2986 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1846.7264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.00078

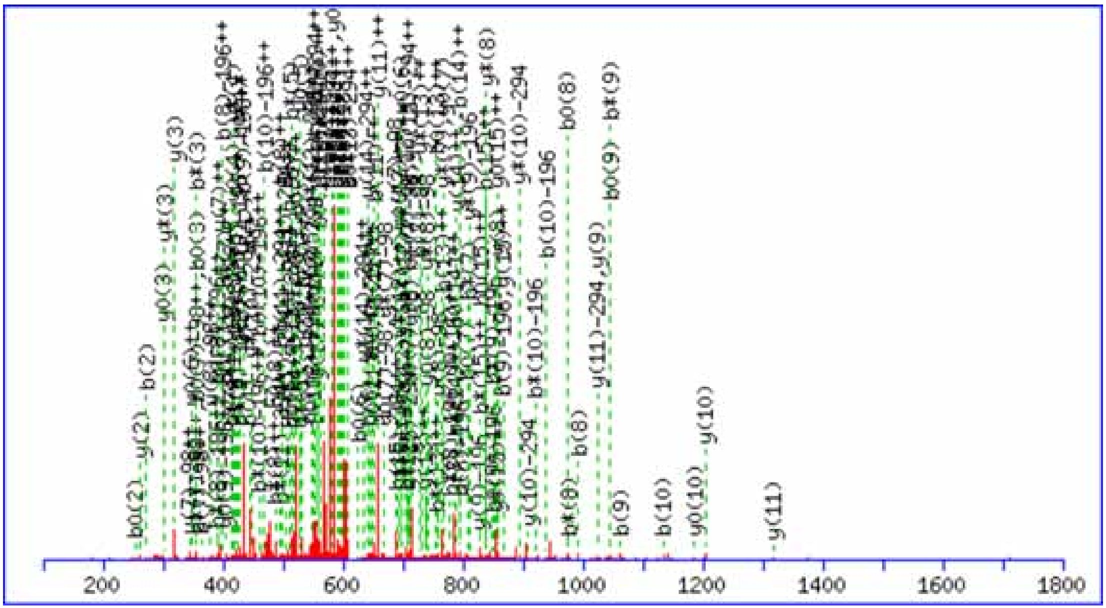
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-294, b(7)-98++, b(7)-98, b(8)-98, b(8)-196, b(9)-98, b(9)-294, b(10)-98, b(11)-98, b(11), b(11)-196, b(12)-98, b(12)-196, b(12), b(13)-98, b(13), b(13)-294, b(13)-196, b(14)-196++, b(14), b(14)-98++, b(15)-294++, b(15)-98, b(15)-196, b(15)-196++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13)-98, y(13), y(13)-196, y(14)-196++, y(14), y(14)-98, y(14)-98++, y(15), y(15)++, y(15)-98++, y(15)-98, y(15)-196++
Precursor origin neutral loss: +

Peptide No.977

SRTASLTSAASIDGSR
Confirmed sites: @T:7,@S:8,@S:11
Ambiguous sites:

MS/MS Fragmentation of SRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3944: 1846.727532 from(616.583120,3+)
Title: Elution from: 36.339 to 36.339 scan no 2970 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1846.7264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00057

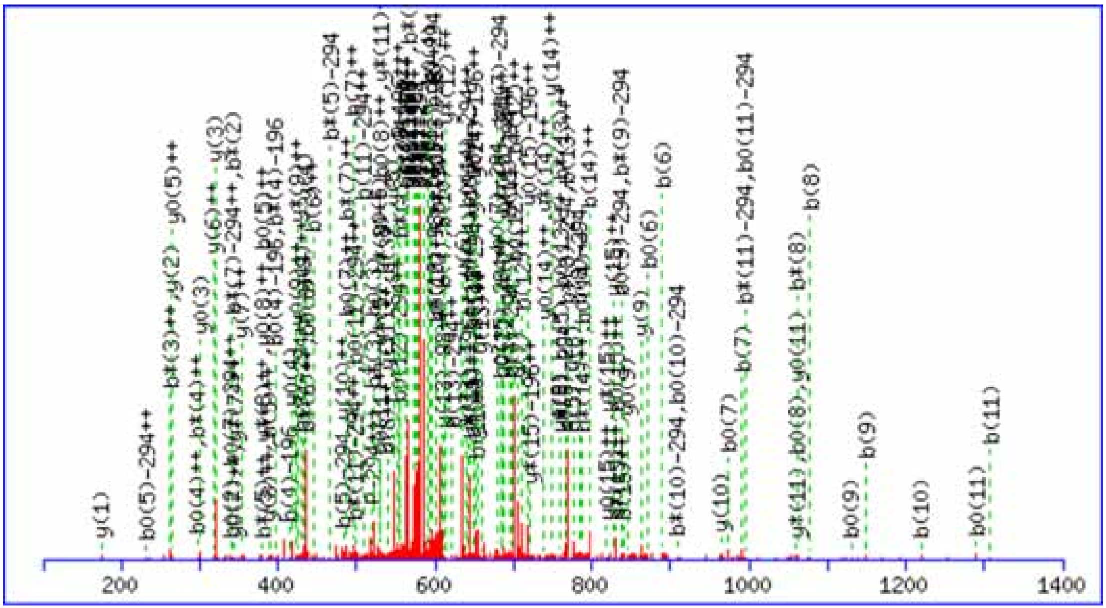
Matched b ions: b(2), b(4), b(5), b(6), b(7)-98++, b(7)++, b(7)-98, b(8), b(8)-196++, b(8)-98++, b(8)++, b(8)-196, b(8)-98, b(9)-196++, b(9), b(9)++, b(9)-98++, b(9)-196, b(9)-98, b(10)++, b(10), b(10)-98++, b(10)-196++, b(10)-196, b(11)-98, b(11)-98++, b(11)-196++, b(11)-294++, b(11)++, b(12)-98, b(12)-98++, b(12)-294++, b(12)++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-294++, b(14)-196++, b(14)-98++, b(15)-98++, b(15)-294++, b(15)-196++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98++, y(7)-98, y(7)++, y(8), y(8)++, y(8)-98++, y(8)-98, y(9)-98, y(9)-196++, y(9)++, y(9)-196, y(9), y(10), y(10)++, y(10)-98++, y(10)-98, y(10)-196++, y(10)-294, y(11), y(11)++, y(11)-294++, y(11)-196++, y(11)-294, y(12)-196++, y(12)-294++, y(12)-98++, y(12)++, y(13)-294++, y(13)-196++, y(13)-98++, y(13)++, y(14)++, y(14)-294++, y(14)-196++, y(14)-98++, y(15)-196++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.978

SRTASLTSAASIDGSR
Confirmed sites: @S:1,@T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3782: 1852.758735 from(618.593521,3+)
Title: Elution from: 39.953 to 39.953 scan no 3467 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1852.7582
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 9.8e-005

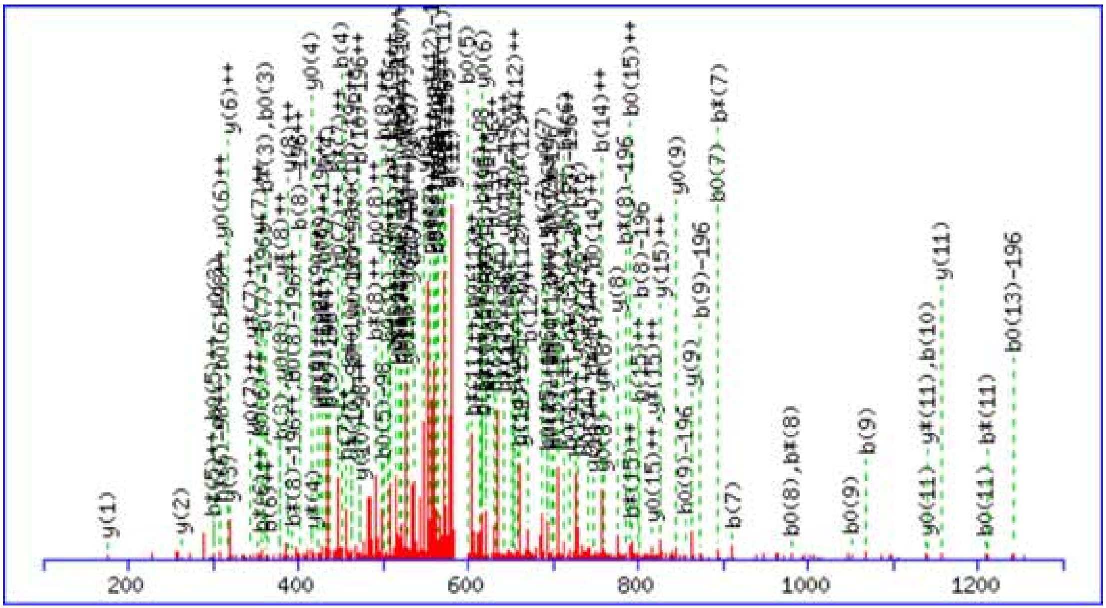
Matched b ions: b(3), b(4)-196, b(4)-98, b(4), b(5), b(5)-98++, b(5)++, b(5)-294, b(5)-196, b(5)-98, b(6), b(6)-98, b(6)-294, b(6)-196++, b(6)-98++, b(6)++, b(6)-196, b(7), b(7)-98, b(7)-98++, b(7)-196++, b(7)++, b(7)-294, b(7)-196, b(8), b(8)-98++, b(8)++, b(8)-294, b(8)-98, b(9), b(9)++, b(9)-98, b(9)-294++, b(9)-196++, b(9)-98++, b(10), b(10)-98++, b(10)-98, b(10)-196++, b(10)++, b(11), b(11)-98++, b(11)-294++, b(11)-196++, b(11)++, b(12)++, b(12)-294++, b(12)-98++, b(13)++, b(13)-98++, b(13)-294++, b(13)-196++, b(14)++, b(14)-294++, b(14)-196++, b(14)-98++, b(15)-294++, b(15)-196++, b(15)-98++, b(15)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)-98++, y(13)-98++, y(13)++, y(14)-98++, y(14)-196++, y(14)++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.979

SRTASLTSAASIDGSR
Confirmed sites: @S:5,@T:7
Ambiguous sites:

MS/MS Fragmentation of SRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 4784: 1772.792898 from(591.938242,3+)
Title: Elution from: 36.366 to 36.366 scan no 3120 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1772.7919
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 **Expect:** 0.00061

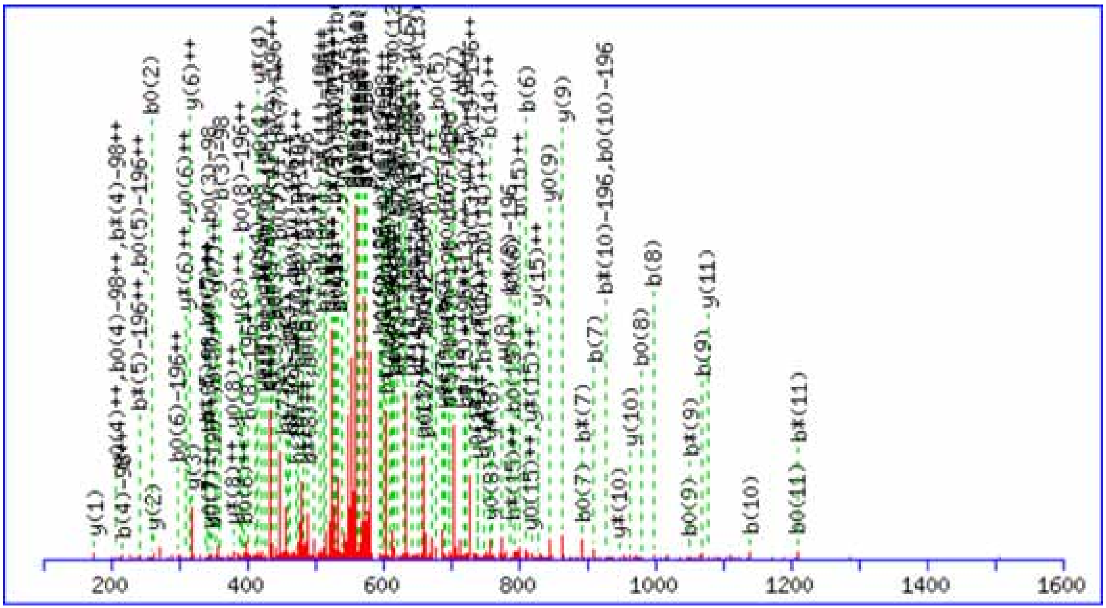
Matched b ions: b(3), b(4), b(5)-98, b(5), b(6)++, b(6)-98, b(6), b(7), b(7)++, b(7)-196++, b(7)-98++, b(7)-98, b(8)-98++, b(8)-196++, b(8)++, b(8)-196, b(9), b(9)++, b(9)-98, b(9)-196++, b(9)-98++, b(9)-196, b(10)++, b(10), b(10)-196++, b(10)-98++, b(11)-196++, b(11)-98++, b(11)++, b(12)-98++, b(12)-196++, b(12)++, b(13)++, b(13)-196++, b(13)-98++, b(14)++, b(14)-196++, b(14)-98++, b(15)-196++, b(15)-98++, b(15)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)-98++, y(10)++, y(11)++, y(11), y(11)-98++, y(12)-196++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)-196++, y(14)++, y(15)-196++, y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.980

SRTASLTSAASIDGSR
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3131: 1772.791926 from(591.937918,3+)
Title: Elution from: 36.049 to 36.049 scan no 2916 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1772.7919
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 1.5e-006

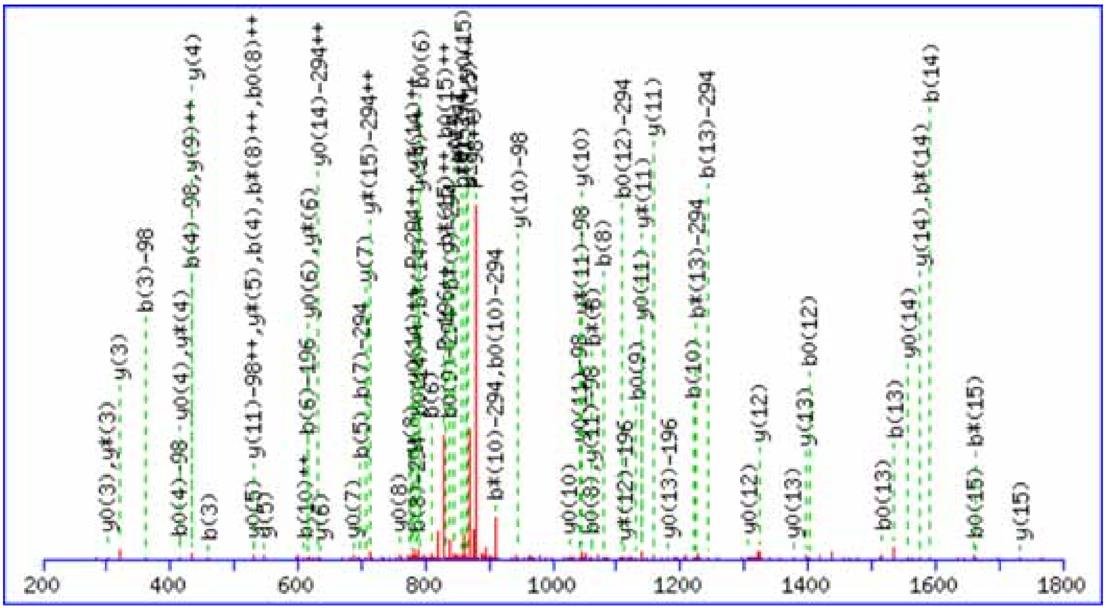
Matched b ions: b(3)-98, b(3), b(4)-98, b(4)-98++, b(4), b(5)-98++, b(5)++, b(5)-98, b(5), b(6)-98++, b(6), b(6)-196, b(6)-98, b(7), b(7)++, b(7)-98++, b(7)-98, b(8), b(8)-196++, b(8)-98++, b(8)++, b(9), b(9)-98, b(9)++, b(9)-196++, b(9)-98++, b(10), b(10)++, b(10)-196++, b(10)-98++, b(11)++, b(11)-196++, b(11)-98++, b(12)++, b(12)-196++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)-98++, y(13)-98++, y(13)++, y(14)-196++, y(14)++, y(15)-196++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.981

SRTASLTSAASIDGSR
Confirmed sites: @T:3,@S:5,@T:7
Ambiguous sites:

MS/MS Fragmentation of SRTASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3382: 1852.759088 from(927.386820,2+)
Title: Elution from: 36.425 to 36.425 scan no 2871 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1852.7582
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.0017

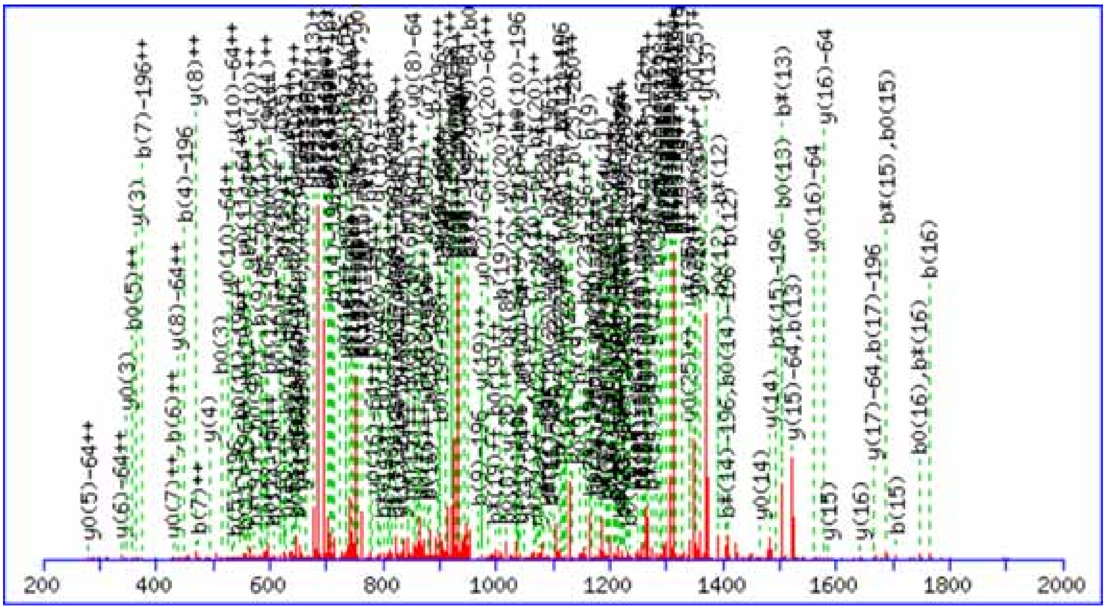
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6)-196, b(6), b(7)-98, b(7)-294, b(7)-196, b(8), b(8)-294, b(8)-196, b(8)-98, b(9)-98, b(9)-294, b(9)-196, b(10)-98, b(10), b(10)++, b(11)-98, b(11)-196, b(12)-98, b(12)-196, b(13)-98, b(13), b(13)-196, b(13)-294, b(14), b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(10)-98, y(11)-98++, y(11), y(11)-98, y(12)-98, y(12), y(13), y(13)-98, y(14)-98, y(14), y(14)++, y(15), y(15)-98, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.982

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:1,@T:3
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6787: 2892.173463 from(965.065097,3+)
Title: Elution from: 38.279 to 38.279 scan no 3128 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2892.1708
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 69 **Expect:** 7.6e-006

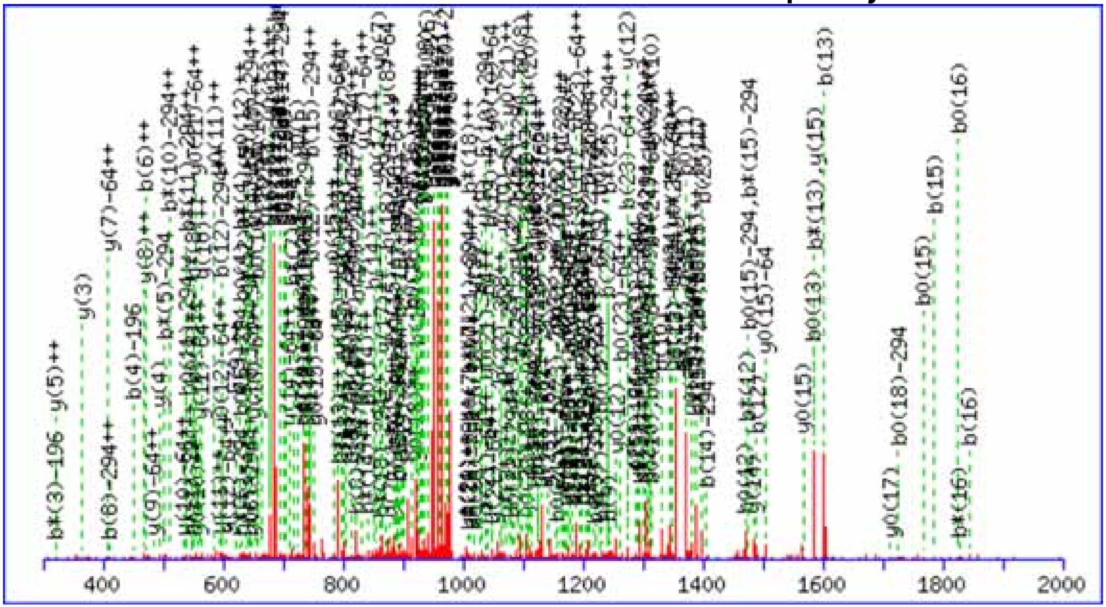
Matched b ions: b(4), b(4)-196, b(5)-196, b(5)-98, b(5), b(6)++, b(6), b(6)-196, b(6)-98, b(7)-196, b(7)++, b(7)-196++, b(7)-98++, b(7)-98, b(7), b(8)-98++, b(8)-98, b(8), b(9), b(9)-98, b(9)-98++, b(9)++, b(9)-196, b(10)-98, b(10)++, b(10), b(11)++, b(11)-196++, b(11)-196, b(11)-98, b(11), b(12), b(12)++, b(12)-196++, b(12)-98++, b(12)-196, b(12)-98, b(13), b(13)-98, b(13)++, b(13)-98++, b(13)-196++, b(13)-196, b(14)-98, b(14)-98++, b(14)-196++, b(14)++, b(15)-98, b(15), b(15)++, b(15)-196++, b(15)-98++, b(16), b(16)++, b(16)-98, b(16)-98++, b(17)-98++, b(17)-196, b(17)-196++, b(17)++, b(18)-196++, b(18)-98++, b(19)++, b(19)-196++, b(20)++, b(20)-98++, b(21)-98++, b(22)++, b(22)-196++, b(22)-98++, b(23)++, b(23)-98++, b(23)-196++, b(24)-98++, b(24)++, b(24)-196++, b(25)++, b(25)-196++, b(25)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10)++, y(10), y(11), y(11)++, y(12), y(12)++, y(13)++, y(13), y(14)++, y(14), y(15), y(15)++, y(16)++, y(16), y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)++, y(24)-98++, y(25)++, y(25)-98++
Precursor origin neutral loss: +

Peptide No.983

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:1,@T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 8815: 2972.139255 from(991.720361,3+)
Title: Elution from: 40.578 to 40.578 scan no 3720 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2972.1371
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 48 Expect: 0.00055

Matched b ions: b(3)-98, b(4)-196, b(4)-98, b(4), b(5)-196++, b(5), b(6)-196++, b(6)++, b(6)-294, b(6)-196, b(6)-98, b(6), b(7)-294, b(7)-196, b(7)-98, b(7), b(8)-294, b(8)-98, b(8)-294++, b(9)-98, b(9)-196, b(9)-98++, b(9), b(9)++, b(9)-294, b(10), b(10)-196++, b(10)++, b(10)-294, b(10)-196, b(10)-98, b(11)-294, b(11), b(11)++, b(11)-98++, b(11)-294++, b(11)-196++, b(11)-98, b(12)-294++, b(12)-294, b(12), b(12)-196++, b(12)++, b(12)-98, b(13), b(13)-98, b(13)++, b(13)-98++, b(13)-196++, b(13)-294, b(13)-196, b(14)-98, b(14)-196, b(14)-98++, b(14)-196++, b(14)-294++, b(14)++, b(14)-294, b(15)-98, b(15), b(15)++, b(15)-294++, b(15)-98++, b(16), b(16)-98++, b(16)++, b(17)-294++, b(17)-196++, b(17)-98++, b(17)++, b(18)-294++, b(18)-196++, b(18)-98++, b(18)++, b(19)++, b(19)-294++, b(19)-196++, b(19)-98++, b(20)-294++, b(20)-196++, b(20)-98++, b(20)++, b(21)-196++, b(21)-98++, b(22)-294++, b(22)-196++, b(22)-98++, b(22)++, b(23)++, b(23)-98++, b(23)-294++, b(24)-98++, b(24)++, b(24)-196++, b(25)++, b(25)-196++, b(25)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13)++, y(13), y(14)++, y(14), y(15)++, y(15), y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(22)++, y(23)-98++, y(23)++, y(24)-98++, y(24)++, y(25)++, y(25)-196++, y(25)-98++
Precursor origin neutral loss: +

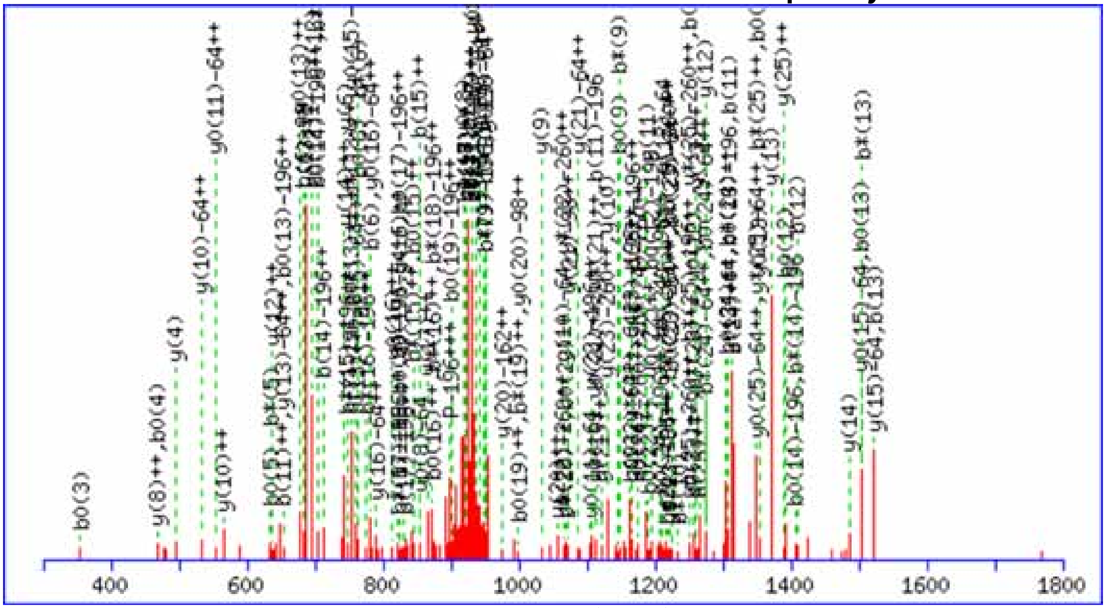
Peptide No.984

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5,@S:7

Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6569: 2892.173262 from(965.065030,3+)
Title: Elution from: 37.622 to 37.622 scan no 3116 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2892.1708
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 Expect: 0.018

Matched b ions: b(6), b(6)-98, b(7)-196, b(7), b(8)-98++, b(8)-98, b(9)-98++, b(9), b(9)-98, b(10), b(11)-196, b(11)++, b(11), b(11)-98, b(12), b(13), b(13)++, b(13)-98, b(13)-98++, b(14)-98, b(14)-98++, b(14)-196++, b(15)++, b(17)-196++, b(17)++, b(18)-98++, b(23)-98++, b(23)++, b(23)-196++, b(24)++, b(24)-98++, b(24)-196++, b(25)-98++
Matched y ions: y(4), y(6), y(8)++, y(8), y(9), y(10), y(10)++, y(11), y(12), y(12)++, y(13)++, y(13), y(14)++, y(14), y(16)++, y(17)++, y(18)++, y(20)++, y(21)-98++, y(21)++, y(22)-196++, y(22)-98++, y(23)-196++, y(23)-98++, y(23)++, y(24)-98++, y(25)-98++, y(25)++
Precursor origin neutral loss: +

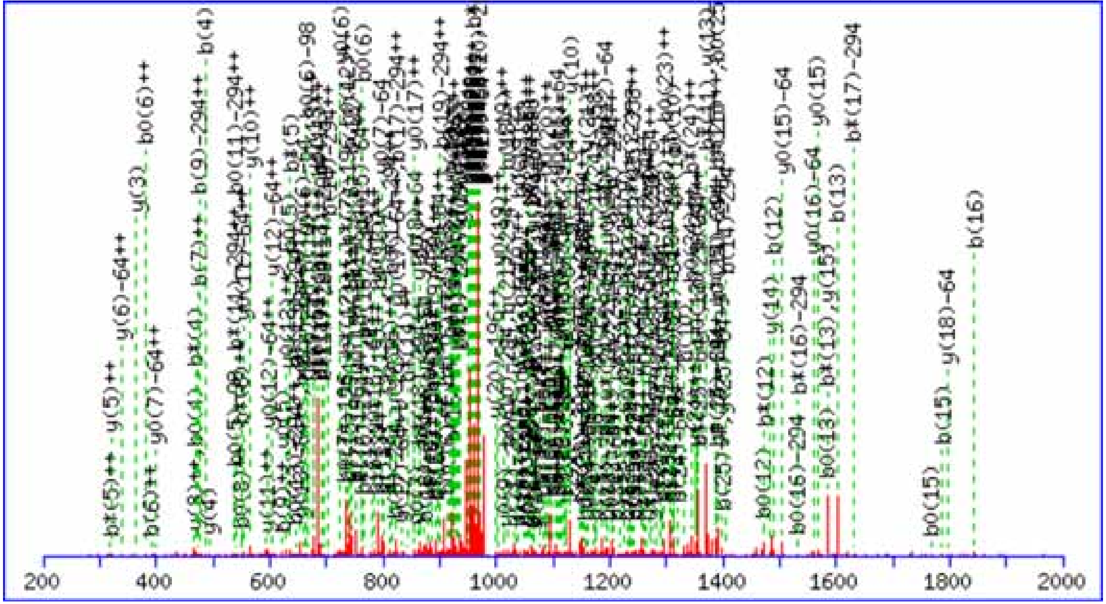
Peptide No.985

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5,@S:7,@S:8
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC

Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7174: 2972.137377 from(991.719735,3+)
Title: Elution from: 40.732 to 40.732 scan no 3550 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2972.1371
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 Expect: 0.011

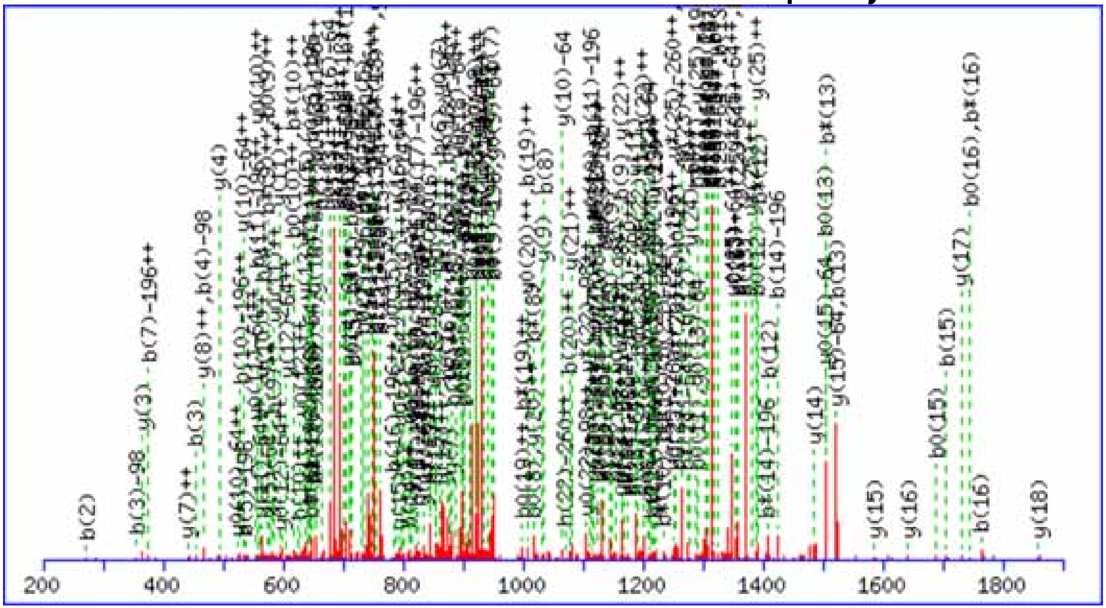
Matched b ions: b(4), b(6)++, b(6), b(7)++, b(7)-196, b(7)-98++, b(7), b(8)-294, b(8)-196, b(8)-98, b(9)-98, b(9)-196, b(9)-294++, b(9)++, b(9)-294, b(9), b(10)++, b(10)-196, b(10)-98, b(10), b(11)-294, b(11), b(11)-196++, b(11)-196, b(11)-98++, b(11)++, b(11)-98, b(12), b(12)-294, b(12)-98++, b(12)++, b(12)-196, b(13)-294++, b(13)-98, b(13), b(13)-98++, b(13)++, b(13)-196++, b(13)-294, b(13)-196, b(14)-196, b(14)-98, b(14)-196++, b(14)-98++, b(14)-294++, b(14)-294, b(15), b(15)-98, b(15)-196++, b(15)-98++, b(15)++, b(16), b(16)-98++, b(16)-196++, b(16)++, b(17)-196++, b(17)-294++, b(17)-98++, b(17)++, b(18)++, b(18)-196++, b(18)-294++, b(18)-98++, b(19)++, b(19)-294++, b(19)-196++, b(19)-98++, b(20)-98++, b(20)-294++, b(20)++, b(21)-294++, b(21)-98++, b(22)-196++, b(22)-98++, b(22)++, b(23)-98++, b(23)++, b(23)-294++, b(24)++, b(24)-98++, b(24)-196++, b(25)++, b(25)-98++
Matched y ions: y(3), y(4), y(5)++, y(6), y(7), y(8)++, y(8), y(9), y(10)++, y(10), y(11), y(11)++, y(12), y(13)++, y(13), y(14)++, y(14), y(15)++, y(15), y(16)++, y(17)++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)-196++, y(20)++, y(21)-196++, y(21)-98++, y(21)++, y(22)-196++, y(22)-98++, y(22)-294++, y(22)++, y(23)-294++, y(23)-196++, y(23)-98++, y(24)-294++, y(24)-98++, y(24)++, y(25)-98++, y(25)-294++, y(25)-196++
Precursor origin neutral loss: +

Peptide No.986

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 8416: 2892.172458 from(965.064762,3+)
Title: Elution from: 38.527 to 38.527 scan no 3469 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2892.1708
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 69 Expect: 6.9e-006

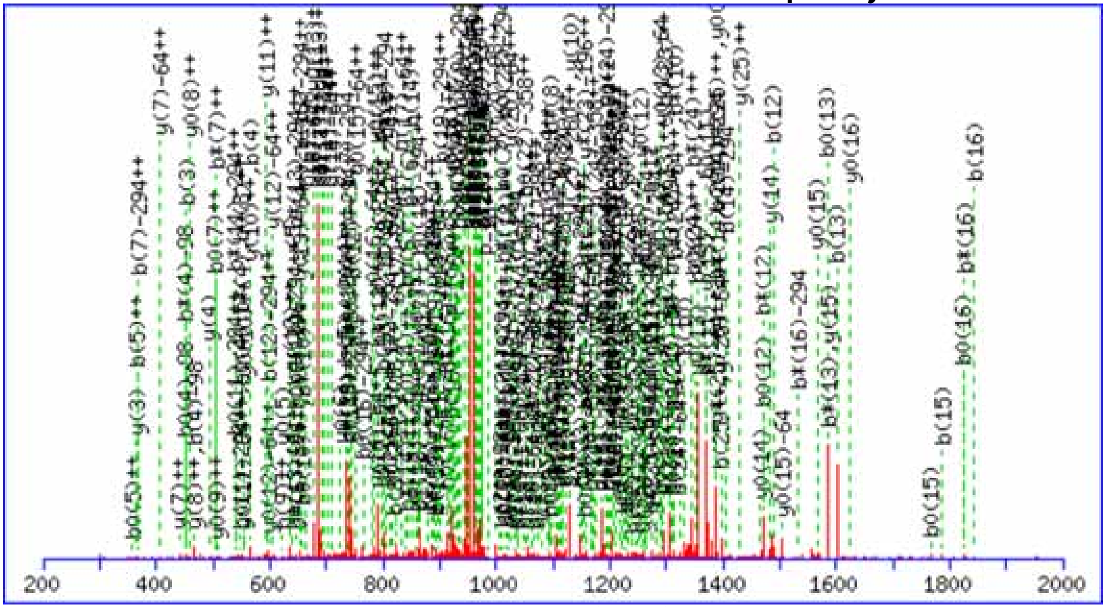
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5)-196, b(5), b(6), b(6)-98, b(7)-196, b(7)-196++, b(7)-98, b(7), b(8)-98++, b(8), b(8)-98, b(9), b(9)-98++, b(9)-98, b(9)++, b(10)-196++, b(10), b(10)-98++, b(10)++, b(11)++, b(11)-196++, b(11)-98++, b(11)-196, b(11)-98, b(11), b(12), b(12)-98++, b(12)++, b(12)-196, b(13), b(13)-98, b(13)++, b(13)-98++, b(13)-196++, b(13)-196, b(14)-98, b(14)-196, b(14)-98++, b(14)-196++, b(14)++, b(15)++, b(15), b(15)-196++, b(16), b(16)-98++, b(16)-196++, b(16)++, b(17)-196++, b(17)-98++, b(17)++, b(18)-98, b(18)-196++, b(18)-98++, b(19)++, b(19)-196++, b(20)++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(24)-98++, b(24)++, b(24)-196++, b(25)++, b(25)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(10)++, y(10), y(11), y(11)++, y(12)++, y(12), y(13)++, y(13), y(14)++, y(14), y(15), y(15)++, y(16), y(16)++, y(17)++, y(17), y(18), y(18)++, y(20)++, y(21)++, y(22)++, y(22)-98++, y(23)++, y(24)-196++, y(24)-98++, y(25)-98++, y(25)++, y(25)-196++
Precursor origin neutral loss: +

Peptide No.987

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @T:3,@S:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7177: 2972.139240 from(991.720356,3+)
Title: Elution from: 40.297 to 40.297 scan no 3494 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2972.1371
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 68 Expect: 5.6e-006

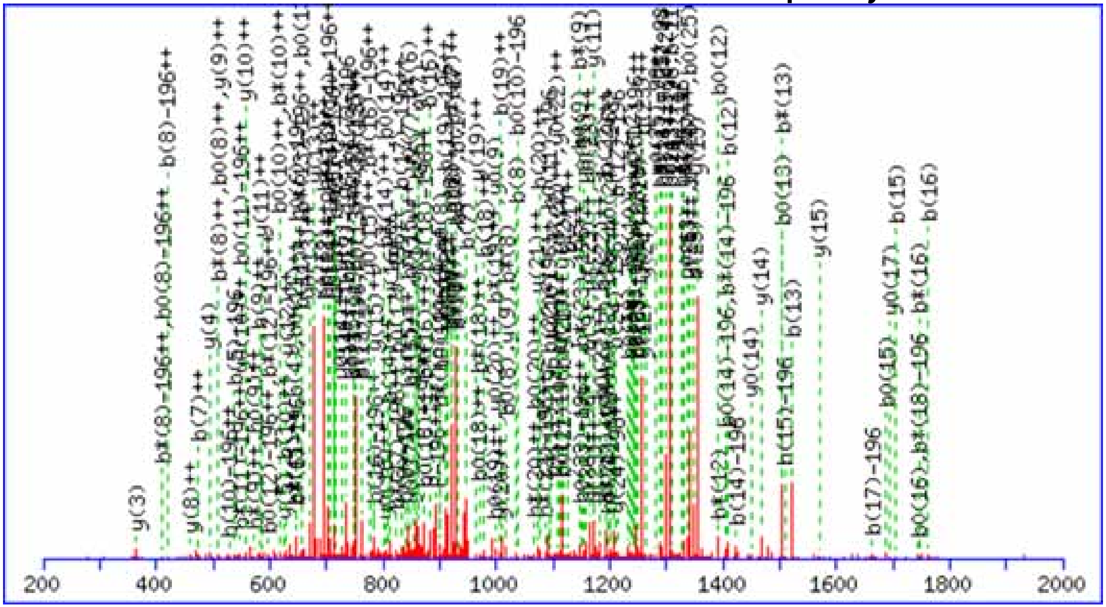
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5)++, b(5), b(6)-98, b(6), b(6)-196, b(7)-294++, b(7)-294, b(7)-196, b(7)-98, b(8)-294, b(8)-98, b(8)-196++, b(8)-196, b(8), b(9)-98, b(9), b(9)-98++, b(9)++, b(9)-294, b(9)-196, b(10)-98, b(10), b(10)-294, b(11)-196++, b(11)-294, b(11), b(11)-294++, b(11)-98++, b(11)-196, b(11)-98, b(12), b(12)-294++, b(12)-98++, b(12)++, b(12)-196++, b(12)-294, b(12)-98, b(13), b(13)++, b(13)-98, b(13)-294++, b(13)-98++, b(13)-196++, b(13)-294, b(13)-196, b(14)-98, b(14)-98++, b(14)-196, b(14)-196++, b(14)-294++, b(14)++, b(14)-294, b(15), b(15)++, b(15)-98++, b(16), b(16)-98++, b(16)++, b(17)-98, b(17)++, b(17)-196++, b(17)-294++, b(17)-98++, b(18)-196++, b(18)-98++, b(18)++, b(19)-294++, b(19)-196++, b(19)-98++, b(19)++, b(20)-98++, b(20)-294++, b(20)-196++, b(20)++, b(21)-294++, b(21)-98++, b(22)-294++, b(22)++, b(22)-196++, b(22)-98++, b(23)++, b(23)-294++, b(23)-196++, b(23)-98++, b(24)++, b(24)-98++, b(24)-294++, b(24)-196++, b(25)++, b(25)-294++, b(25)-196++, b(25)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(10)++, y(10), y(11), y(11)++, y(12), y(12)++, y(13)++, y(13), y(14)++, y(14), y(15), y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(22)++, y(22)-196++, y(22)-98++, y(23)++, y(23)-98++, y(24)-294++, y(24)-98++, y(25)-98++, y(25)-196++, y(25)-294++, y(25)++
Precursor origin neutral loss: +

Peptide No.988

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:1,@T:3
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6757: 2876.177658 from(959.733162,3+)
Title: Elution from: 43.149 to 43.149 scan no 3779 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2876.1759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 2.1e-006

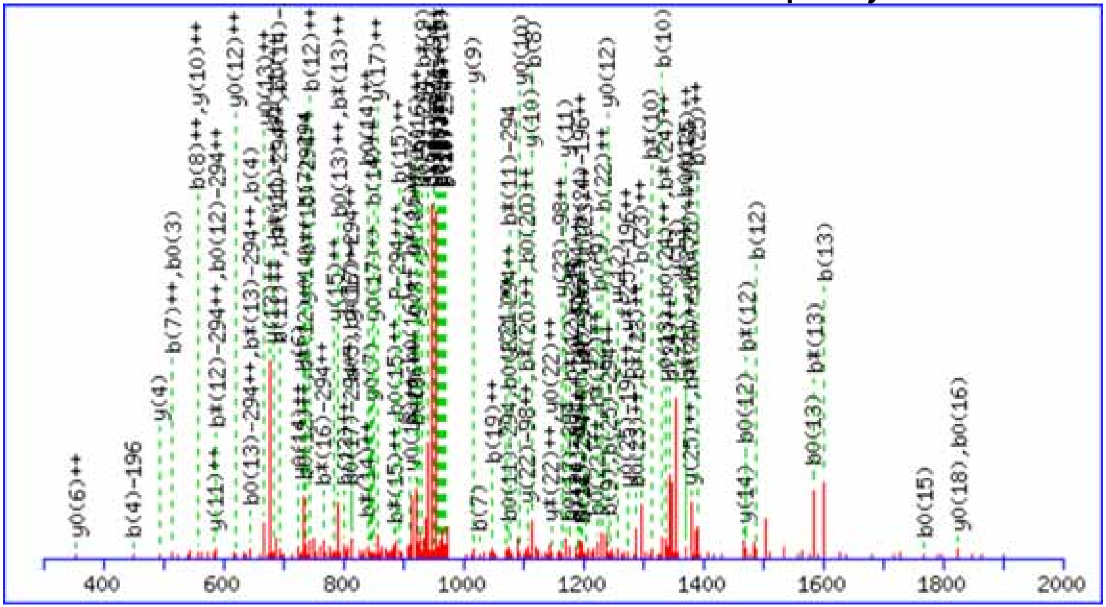
Matched b ions: b(4), b(4)-98, b(5)-98, b(5)-196, b(6), b(6)-98, b(7)++, b(7)-196, b(7), b(7)-98, b(8)-196++, b(8)-196, b(8)-98, b(8), b(9), b(9)++, b(9)-98, b(10), b(10)-196++, b(10)++, b(10)-98, b(11)++, b(11)-196, b(11)-98, b(11), b(12), b(12)-98++, b(12)++, b(12)-196, b(12)-98, b(13), b(13)-98, b(13)++, b(13)-98++, b(13)-196, b(14)-98, b(14)-196, b(14)-98++, b(14)-196++, b(14)++, b(15)-98++, b(15)++, b(15)-196, b(15), b(16), b(16)-98, b(16)++, b(16)-196++, b(16)-98++, b(17)-196, b(17)-98, b(17)-98++, b(17)-196++, b(17)++, b(18)++, b(18)-98++, b(19)-196++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)++, b(22)-196++, b(22)-98++, b(23)++, b(23)-98++, b(23)-196++, b(24)-98++, b(24)++, b(24)-196++, b(25)++, b(25)-196++, b(25)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13)++, y(13), y(14), y(14)++, y(15)++, y(15), y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)++, y(23)++, y(24)-98++, y(24)++, y(25)++, y(25)-98++
Precursor origin neutral loss: +

Peptide No.989

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:1,@T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6863: 2956.143444 from(986.388424,3+)
Title: Elution from: 46.789 to 46.789 scan no 4219 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2956.1422
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0071

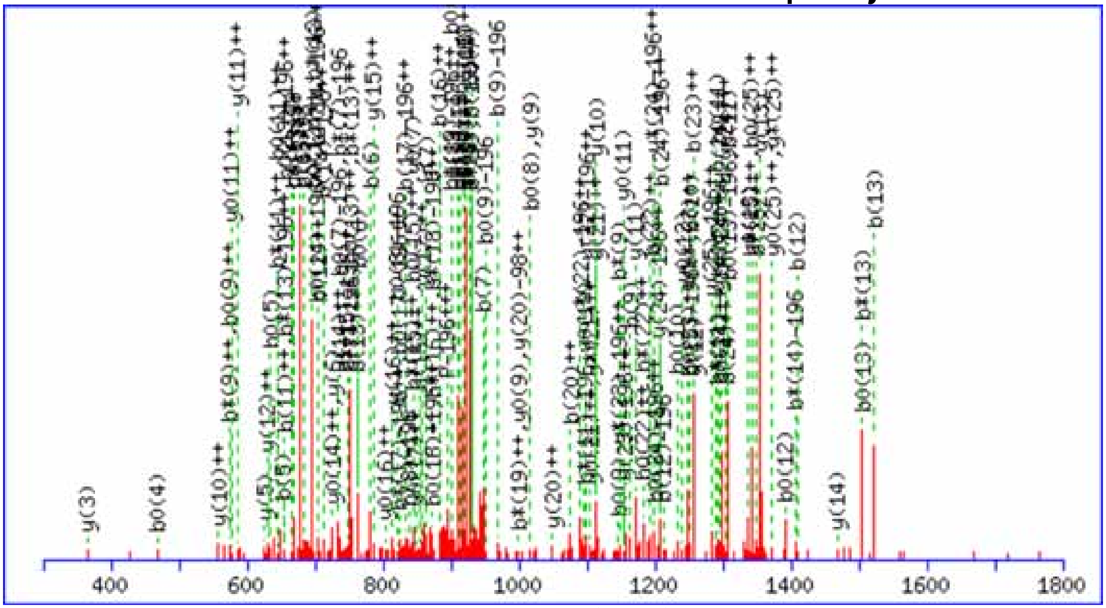
Matched b ions: b(4)-196, b(4), b(5), b(5)-196, b(6), b(6)-196, b(6)-98, b(7)++, b(7)-294, b(7)-98, b(7), b(8), b(8)++, b(8)-98, b(9)-196++, b(9)-98, b(9)-196, b(9)-294, b(9), b(10)-98, b(10)-98++, b(10), b(11)-98++, b(11)++, b(12)-294, b(12), b(12)++, b(13)-98, b(13), b(13)++, b(13)-98++, b(14)-98, b(14)-98++, b(14)-196++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(17)-196++, b(18)-196++, b(18)-98++, b(19)-196++, b(19)++, b(20)-294++, b(22)++, b(23)++, b(23)-98++, b(24)++, b(24)-98++, b(24)-196++, b(24)-294++, b(25)++, b(25)-98++, b(25)-294++
Matched y ions: y(4), y(6), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(13)++, y(13), y(14), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(21)++, y(22)-98++, y(23)-98++, y(25)++, y(25)-98++
Precursor origin neutral loss: +

Peptide No.990

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7046: 2876.179116 from(959.733648,3+)
Title: Elution from: 42.921 to 42.921 scan no 3833 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2876.1759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0041

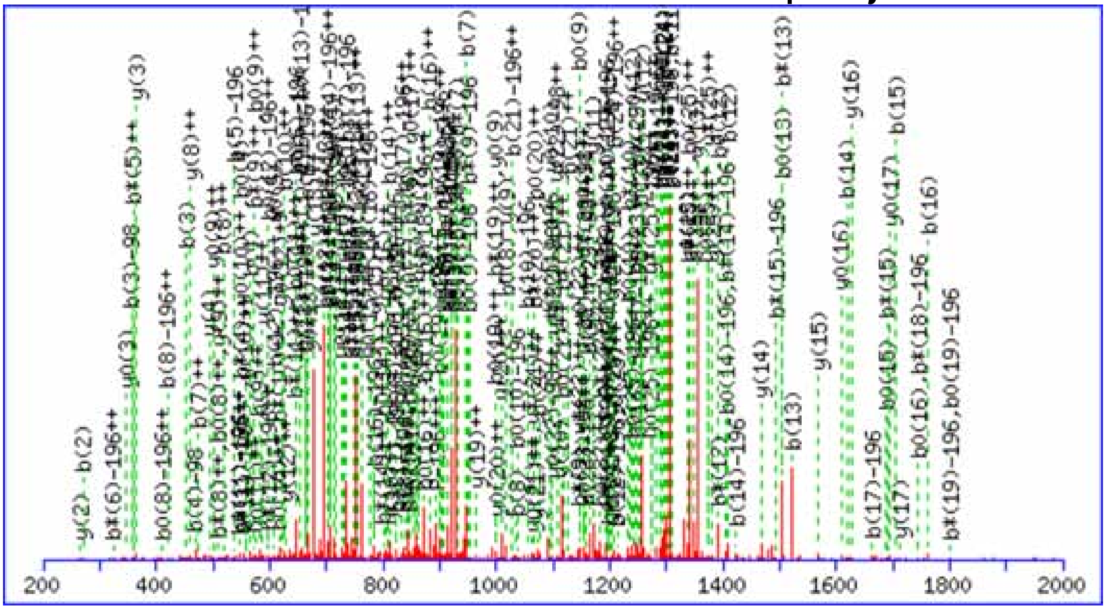
Matched b ions: b(5), b(6), b(6)-98, b(7)-196, b(7), b(7)-98, b(8)-98++, b(8)-196, b(8)-98, b(9)-196, b(9), b(9)-98, b(10)-98++, b(10)-98, b(10), b(11)++, b(11), b(12), b(12)++, b(12)-196, b(13), b(13)++, b(13)-98, b(13)-98++, b(14)-98, b(14)-98++, b(14)-196++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)++, b(18)-98++, b(19)-196++, b(20)++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(24)-98++, b(24)++, b(24)-196++, b(25)++, b(25)-196++, b(25)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(11)++, y(12)++, y(12), y(13)++, y(13), y(14)++, y(14), y(15)++, y(16)++, y(17)++, y(18)++, y(20)++, y(20)-98++, y(21)++, y(22)-196++, y(22)-98++, y(23)-196++, y(23)-98++, y(24)-196++, y(24)++, y(25)-196++, y(25)-98++
Precursor origin neutral loss: +

Peptide No.991

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7045: 2876.177280 from(959.733036,3+)
Title: Elution from: 43.272 to 43.272 scan no 3876 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2876.1759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 Expect: 1.5e-005

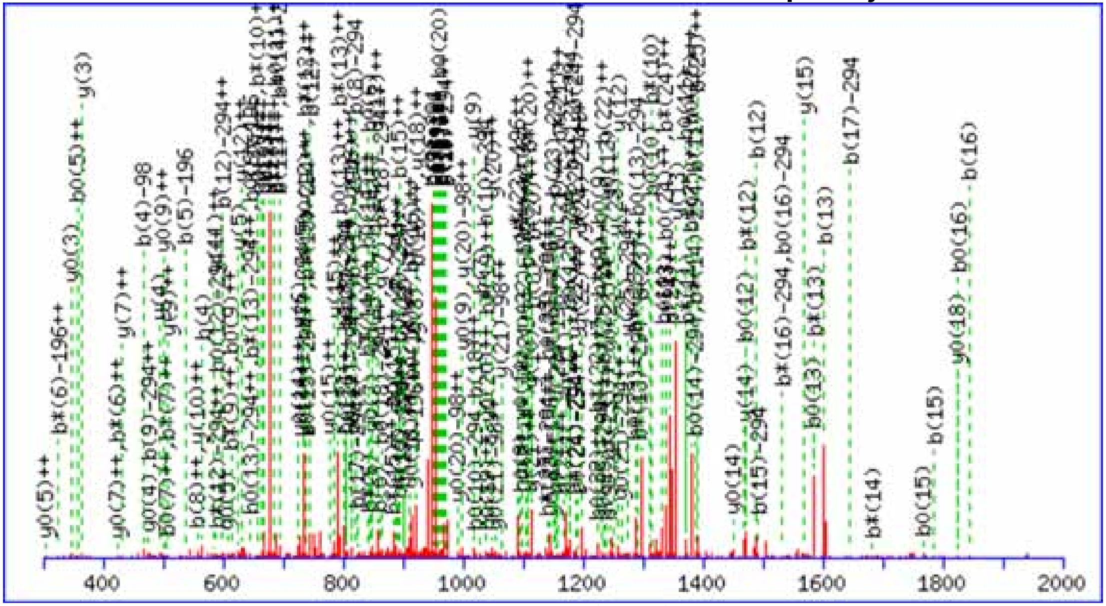
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5)-196, b(5), b(6), b(6)-196, b(6)-98, b(7)-98++, b(7)-196, b(7), b(7)++, b(7)-98, b(8)-98++, b(8), b(8)-196++, b(8)++, b(8)-196, b(8)-98, b(9), b(9)++, b(9)-98++, b(9)-98, b(10)++, b(10)-196, b(10), b(10)-98++, b(10)-98, b(11)++, b(11)-196++, b(11)-98, b(11), b(12), b(12)-98++, b(12)++, b(12)-196++, b(12)-196, b(12)-98, b(13), b(13)++, b(13)-98, b(13)-98++, b(13)-196++, b(14)-98, b(14)-98++, b(14)-196, b(14)-196++, b(14), b(14)++, b(15)-98, b(15), b(15)++, b(15)-98++, b(15)-196++, b(16), b(16)++, b(16)-98, b(16)-196++, b(16)-98++, b(17)-98, b(17)-196, b(17)-98++, b(17)-196++, b(17)++, b(18)-98++, b(19)-196++, b(20)-98++, b(20)++, b(21)-196++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)++, b(23)-196++, b(23)-98++, b(24)-98++, b(24)++, b(24)-196++, b(25)++, b(25)-196++, b(25)-98++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13)++, y(13), y(14)++, y(14), y(15), y(15)++, y(16)++, y(16), y(17)++, y(17), y(18)++, y(19)++, y(20)++, y(21)++, y(22)++, y(22)-98++, y(23)-98++, y(23)++, y(24)-196++, y(24)-98++, y(24)++, y(25)-98++, y(25)-196++, y(25)++
Precursor origin neutral loss: +

Peptide No.992

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @T:3,@S:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7496: 2956.144785 from(986.388871,3+)
Title: Elution from: 46.350 to 46.350 scan no 4311 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2956.1422
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00078

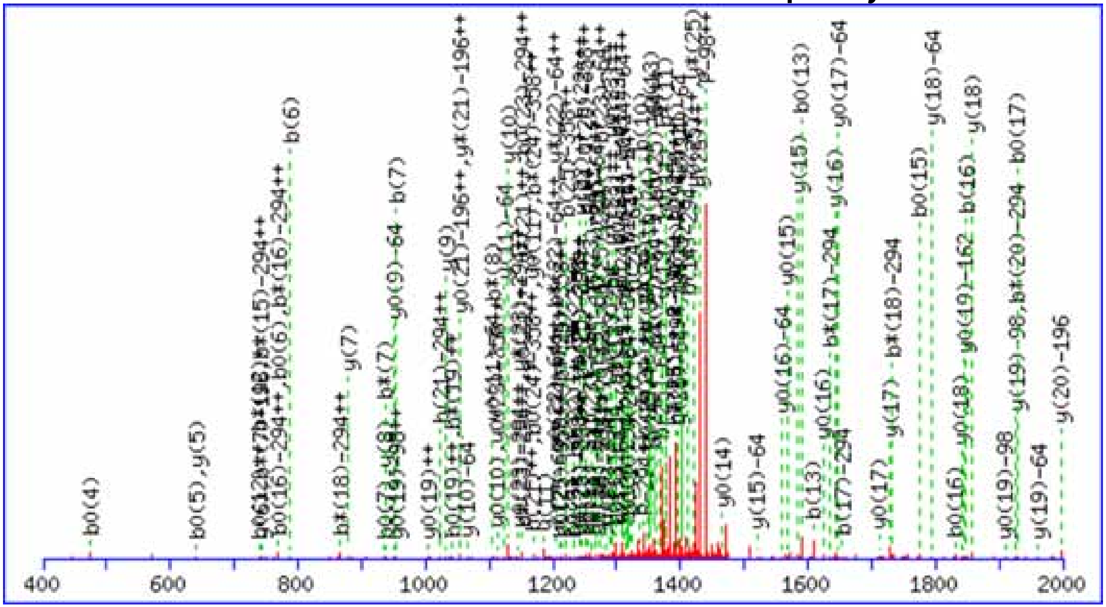
Matched b ions: b(4)-98, b(4), b(5)-98, b(5)-196, b(5), b(6)-98, b(6), b(7)-294, b(7)-196, b(7)-98, b(7), b(8)-98, b(8)++, b(8), b(8)-98++, b(8)-294, b(9)-196, b(9)-98, b(9)-294++, b(9)-98++, b(9), b(9)-294, b(10), b(10)++, b(10)-98++, b(10)-294, b(10)-98, b(11)++, b(11)-98++, b(11)-98, b(11), b(12), b(12)-294++, b(12)-196++, b(12)++, b(13), b(13)-98, b(13)++, b(13)-98++, b(13)-196, b(13)-196++, b(14)-98, b(14)++, b(14)-98++, b(14)-196++, b(15), b(15)++, b(15)-196++, b(15)-98++, b(15)-294, b(16), b(16)++, b(16)-98++, b(16)-98, b(16)-196++, b(17)-294, b(17)-196, b(17)-98++, b(17)-196++, b(17)-294++, b(17)++, b(18)-98, b(18)-196++, b(18)-98++, b(18)++, b(19)-294++, b(19)-196++, b(19)-98++, b(20)-196++, b(20)-294++, b(20)++, b(21)++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(23)-294++, b(24)-98++, b(24)++, b(24)-196++, b(25)++, b(25)-196++, b(25)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(12), y(13)++, y(13), y(14), y(14)++, y(15)++, y(15), y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(22)-196++, y(22)-98++, y(23)-196++, y(23)-98++, y(23)++, y(24)-294++, y(24)-196++, y(25)-196++, y(25)-98++, y(25)-294++
Precursor origin neutral loss: +

Peptide No.993

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5,@S:7,@S:8
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6895: 2978.168984 from(1490.091768,2+)
Title: Elution from: 40.466 to 40.466 scan no 3422 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2978.1690
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 46 Expect: 0.0011

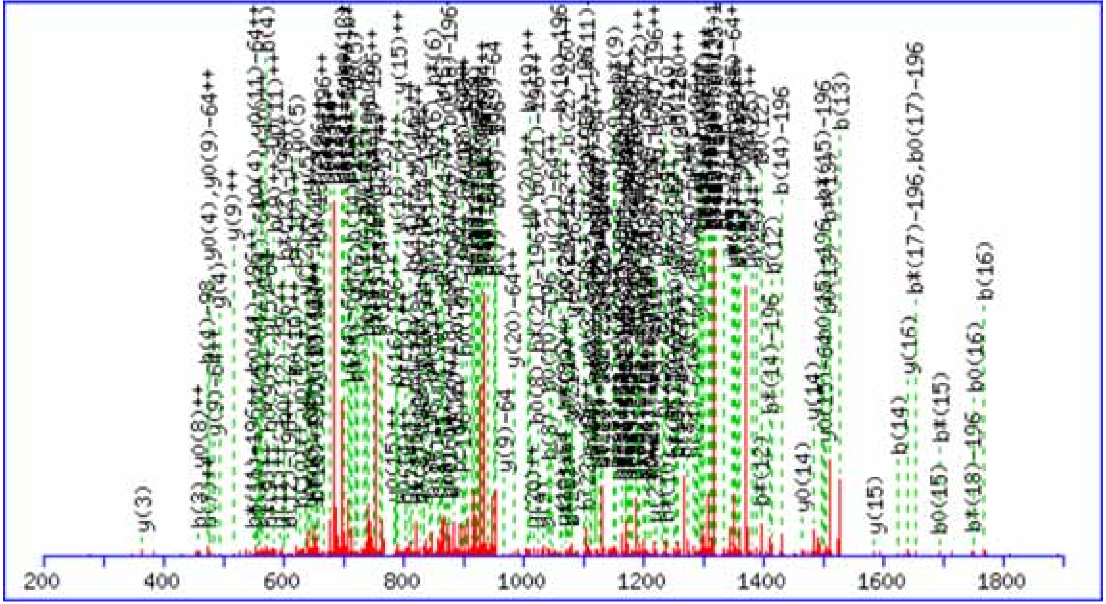
Matched b ions: b(6), b(7), b(8)-98, b(9)-196, b(9)-98, b(9), b(10), b(10)-196, b(10)-98, b(11)-98, b(11), b(12)-196, b(12)-98, b(13), b(13)-98, b(13)-294, b(13)-196, b(14)-98, b(14)-196, b(14)-294, b(16), b(16)-196, b(16)-98, b(17)-98, b(17)-294, b(17)-196, b(21)-294++, b(21)++, b(21)-196++, b(22)-98++, b(22)-196++, b(22)++, b(23)++, b(23)-196++, b(23)-98++, b(24)-98++, b(24)-294++, b(24)-196++, b(24)++, b(25)-98++, b(25)++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(15), y(16), y(17), y(18), y(19)-98, y(20)-196, y(21)-98++, y(22)++, y(23)-196++, y(24)-98++, y(24)++, y(25)-294++, y(25)-196++, y(25)-98++, y(25)++
Precursor origin neutral loss: +

Peptide No.994

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6577: 2898.205035 from(967.075621,3+)
Title: Elution from: 37.932 to 37.932 scan no 3155 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2898.2026
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 69 Expect: 7.8e-006

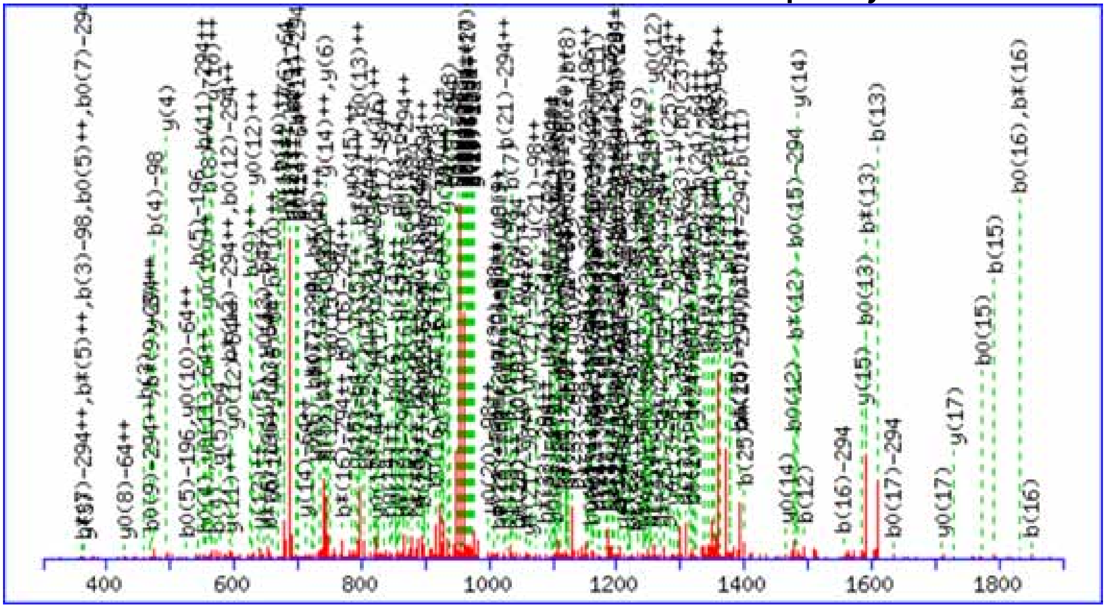
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98++, b(6)-98, b(7), b(7)-98, b(7)++, b(8), b(8)-196, b(8)-98, b(9), b(9)-98++, b(9)++, b(9)-98, b(10)++, b(10)-196, b(10)-98, b(10), b(11)++, b(11)-98, b(11), b(12)-98, b(12), b(12)-196, b(12)-196++, b(12)-98++, b(12)++, b(13)-98, b(13), b(13)++, b(13)-98++, b(13)-196++, b(13)-196, b(14)-196, b(14)-98, b(14), b(14)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16), b(16)++, b(16)-196++, b(16)-98++, b(17)++, b(17)-98, b(17)-98++, b(17)-196++, b(18)-98++, b(18)-196++, b(19)++, b(19)-196++, b(20)-98++, b(20)++, b(21)++, b(21)-98++, b(22)-196++, b(22)++, b(22)-98++, b(23)++, b(23)-196++, b(23)-98++, b(24)-98++, b(24)++, b(24)-196++, b(25)-98++, b(25)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13)++, y(13), y(14)++, y(14), y(15), y(15)++, y(16), y(16)++, y(17)++, y(18)++, y(20)++, y(21)++, y(22)++, y(22)-98++, y(23)-98++, y(23)++, y(24)++, y(25)++, y(25)-196++
Precursor origin neutral loss: +

Peptide No.995

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @T:3,@S:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6639: 2978.169153 from(993.730327,3+)
Title: Elution from: 40.189 to 40.189 scan no 3440 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2978.1690
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 57 Expect: 7.5e-005

Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(5)-196, b(6), b(6)-98++, b(6)-98, b(7)-196++, b(7), b(7)-98, b(7)-98++, b(7)-196, b(8), b(8)-98++, b(8)++, b(8)-196, b(8)-98, b(9)-98, b(9)-98++, b(9), b(9)++, b(9)-294, b(10)++, b(10)-294, b(10)-98, b(10), b(11)-294++, b(11)-196++, b(11)++, b(11)-294, b(11)-98, b(11), b(12)-196, b(12), b(12)++, b(12)-294, b(13), b(13)-98, b(13)++, b(13)-196++, b(13)-98++, b(13)-294, b(13)-196, b(14)-98, b(14)-98++, b(14)-196, b(14)-196++, b(14)++, b(15), b(15)++, b(15)-98++, b(16), b(16)-98++, b(16)++, b(16)-294, b(17)++, b(17)-294++, b(17)-196++, b(17)-98++, b(18)-98++, b(19)-294++, b(19)-196++, b(19)-98++, b(20)++, b(20)-294++, b(20)-98++, b(21)-98++, b(21)-294++, b(21)-196++, b(21)++, b(22)-294++, b(22)-196++, b(22)-98++, b(22)++, b(23)++, b(23)-98++, b(23)-294++, b(23)-196++, b(24)-98++, b(24)++, b(24)-196++, b(24)-294++, b(25)++, b(25)-196++, b(25)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12),

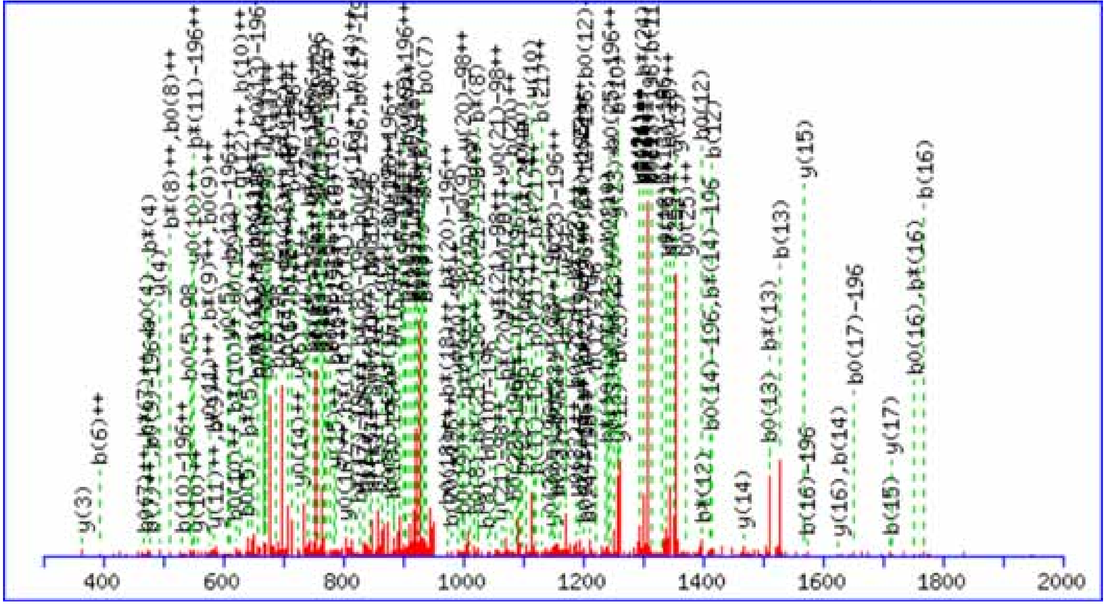
y(12)++, y(13)++, y(13), y(14)++, y(14), y(15), y(15)++, y(16)++, y(17)++, y(17), y(18)++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)-196++, y(22)++, y(22)-98++, y(23)-196++, y(23)++, y(24)-294++, y(24)-98++, y(24)++, y(25)-294++, y(25)-98++
Precursor origin neutral loss: +

Peptide No.996

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 8725: 2882.208315 from(961.743381,3+)
Title: Elution from: 43.045 to 43.045 scan no 4056 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2882.2077
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 Expect: 0.00075

Matched b ions: b(5), b(6)++, b(6)-98, b(6), b(7)-98, b(7)++, b(7)-196, b(8)-98, b(8), b(8)-196, b(9)-98, b(9), b(9)++, b(10)-98, b(10)-98++, b(10)-196++, b(10)++, b(10), b(11)++, b(11)-196, b(11), b(12)-98++, b(12), b(12)-196++, b(12)++, b(12)-196, b(13), b(13)-98, b(13)++, b(13)-98++, b(13)-196++, b(13)-196, b(14)-98, b(14)-98++, b(14)++, b(14), b(14)-196++, b(15)++, b(15), b(15)-196++, b(15)-98++, b(16), b(16)-196, b(16)-98++, b(16)-196++, b(16)++, b(17)-98, b(17)-196++, b(17)-98++, b(17)++, b(18)-196++, b(18)-98++, b(19)-196++, b(19)++, b(20)-196++, b(20)-98++, b(20)++, b(21)++, b(22)++, b(22)-196++, b(22)-98++, b(23)++, b(23)-98++, b(23)-196++, b(24)-98++, b(24)++, b(24)-196++, b(25)++, b(25)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13),

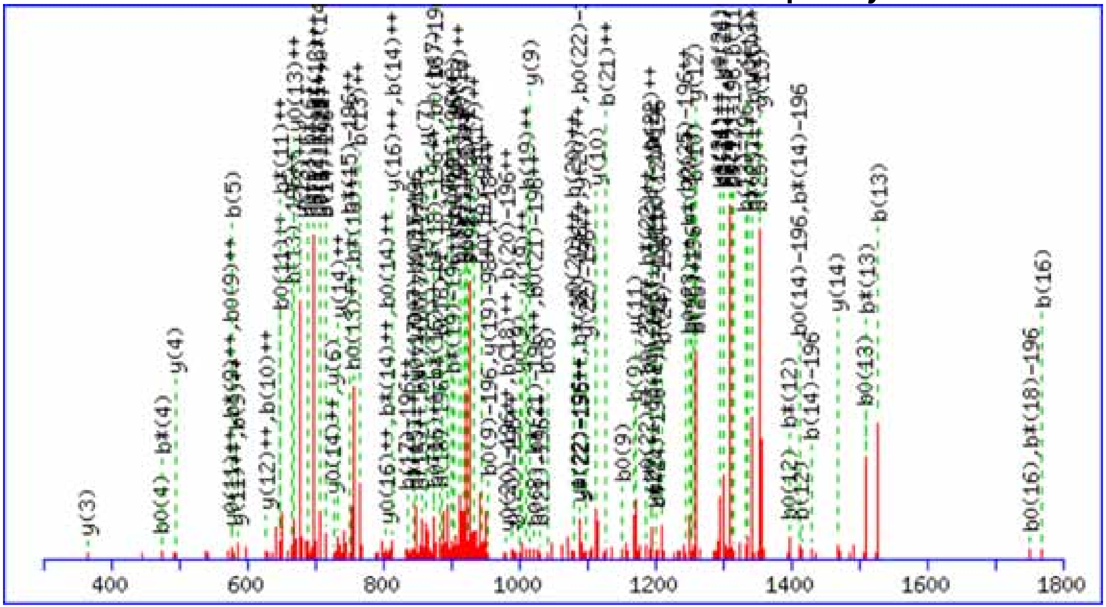
y(13)++, y(14), y(14)++, y(15), y(15)++, y(16)++, y(16), y(17)++, y(17), y(18)++, y(20)-98++, y(21)-98++, y(22)-98++, y(22)++, y(23)-196++, y(23)-98++, y(23)++, y(24)++, y(25)-98++
Precursor origin neutral loss: +

Peptide No.997

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:7,@S:8
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6551: 2882.210367 from(961.744065,3+)
Title: Elution from: 43.049 to 43.049 scan no 3793 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2882.2077
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.0017

Matched b ions: b(5), b(6), b(7), b(8)-98, b(8)-196, b(8), b(9)++, b(9)-98, b(9), b(10)++, b(10)-98++, b(10)-98, b(10), b(11), b(12), b(12)++, b(12)-98++, b(13), b(13)++, b(13)-98, b(13)-98++, b(13)-196++, b(13)-196, b(14)-98, b(14)-98++, b(14)-196, b(14)++, b(14)-196++, b(15)++, b(15)-98++, b(16), b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)++, b(18)-196++, b(18)-98++, b(18)++, b(19)-196++, b(19)++, b(20)-196++, b(20)++, b(21)-196++, b(21)-98++, b(21)++, b(22)++, b(23)++, b(23)-98++, b(24)-98++, b(24)++, b(24)-196++, b(25)++, b(25)-196++, b(25)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(13)++, y(13), y(14), y(14)++, y(16)++, y(17)++, y(18)++, y(19)++, y(19)-98++, y(20)-196++, y(20)++, y(22)-196++, y(22)++, y(23)-98++, y(24)-98++, y(25)-98++

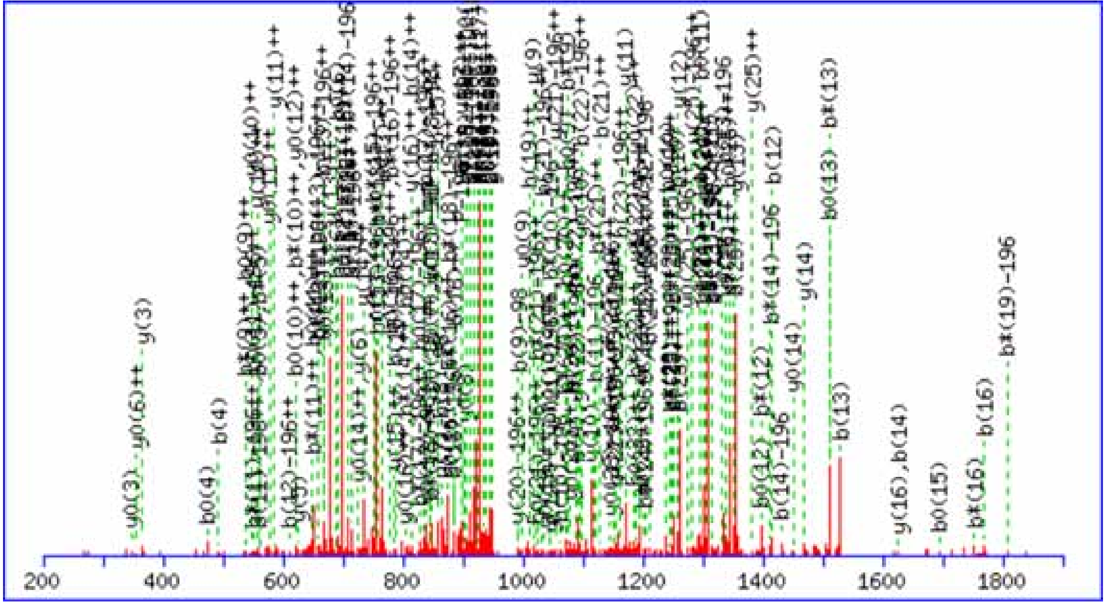
Precursor origin neutral loss: +

Peptide No.998

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:8,@S:10
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7069: 2882.211429 from(961.744419,3+)
Title: Elution from: 43.109 to 43.109 scan no 3857 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2882.2077
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.024

Matched b ions: b(4), b(6), b(8)-98, b(9), b(9)-98, b(10)-196, b(10)-98, b(10), b(11)-196++, b(11)++, b(11)-196, b(11), b(12), b(12)-98++, b(12)-196++, b(12)++, b(13), b(13)-98, b(13)++, b(13)-196++, b(13)-98++, b(13)-196, b(14)-98, b(14), b(14)-196, b(14)-98++, b(14)-196++, b(14)++, b(15)++, b(15)-196++, b(15)-98++, b(16), b(16)-196++, b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)++, b(18)-196++, b(18)-98++, b(19)-196++, b(19)++, b(20)-98++, b(20)++, b(21)-196++, b(21)-98++, b(21)++, b(22)++, b(22)-196++, b(22)-98++, b(23)++, b(23)-196++, b(23)-98++, b(24)-98++, b(24)++, b(24)-196++, b(25)++, b(25)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(13), y(13)++, y(14), y(14)++, y(15)++, y(16), y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(19)-196++, y(19)++, y(20)-196++, y(21)-196++, y(21)++, y(22)-98++, y(22)++, y(23)-98++, y(24)++, y(25)-196++, y(25)-98++, y(25)++

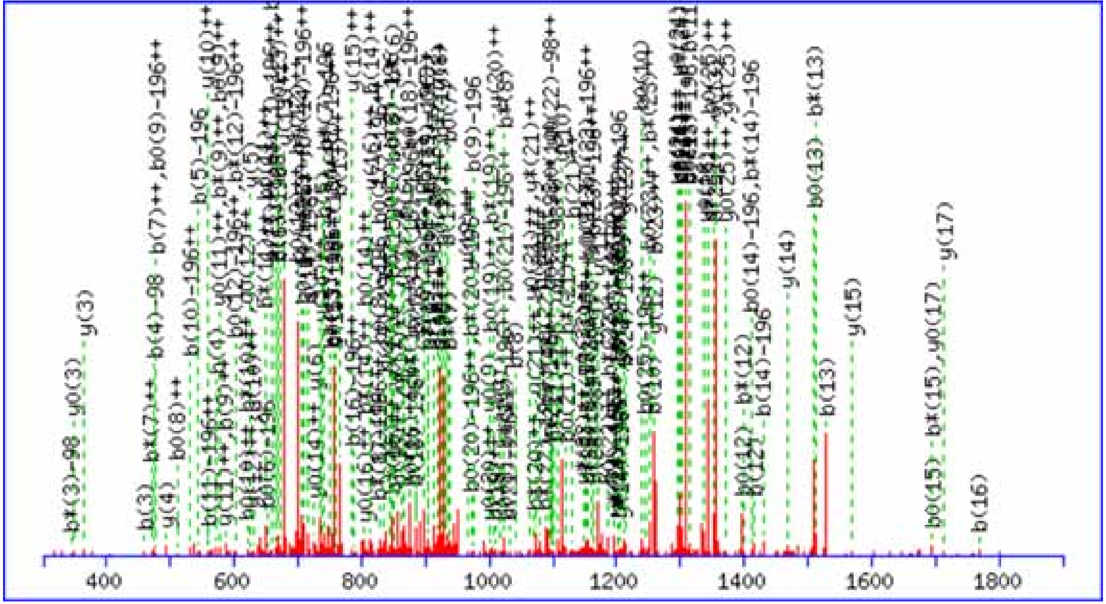
Precursor origin neutral loss: +

Peptide No.999

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7411: 2882.207754 from(961.743194,3+)
Title: Elution from: 43.161 to 43.161 scan no 3927 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2882.2077
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 Expect: 0.00012

Matched b ions: b(3), b(4)-98, b(4), b(5)-196, b(5)-98, b(5), b(6), b(6)-196, b(6)-98, b(7)-98, b(7)++, b(8)-98, b(8)-196, b(8), b(9)-98++, b(9)++, b(9), b(9)-98, b(9)-196, b(10)-196++, b(10)++, b(10)-98, b(10), b(11)-196++, b(11)++, b(11), b(12)++, b(12)-98++, b(12)-98, b(12), b(13), b(13)++, b(13)-98, b(13)-98++, b(13)-196++, b(14)-98, b(14)-98++, b(14)-196, b(14)-196++, b(14)++, b(15)++, b(15)-196++, b(15)-98++, b(16), b(16)-98, b(16)++, b(16)-196++, b(16)-98++, b(17)-98++, b(17)-196++, b(17)++, b(18)-196++, b(18)-98++, b(19)-196++, b(19)++, b(20)++, b(21)-196++, b(21)-98++, b(21)++, b(22)++, b(22)-196++, b(22)-98++, b(23)++, b(23)-98++, b(23)-196++, b(24)++, b(24)-98++, b(24)-196++, b(25)++, b(25)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13)++, y(13), y(14)++, y(14), y(15), y(15)++, y(16)++, y(17)++, y(17), y(18)++, y(19)++, y(20)++, y(21)++, y(22)++, y(22)-98++, y(23)++, y(23)-98++, y(24)++, y(24)-196++

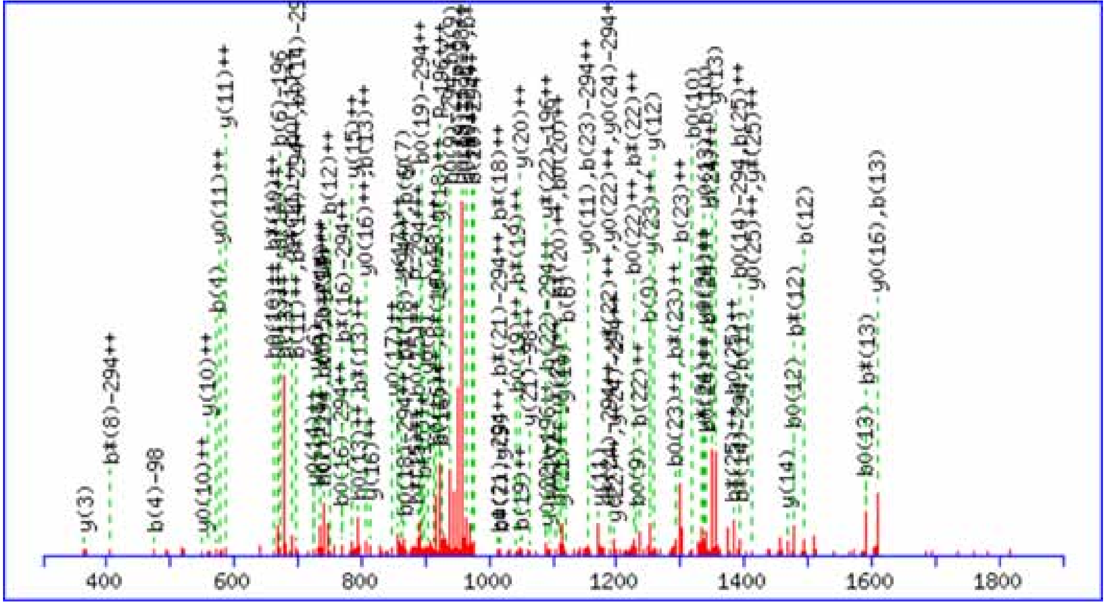
Precursor origin neutral loss: +

Peptide No.1000

SRTLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5,@S:7
Ambiguous sites: @S:1orT:3

MS/MS Fragmentation of SRTLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7508: 2962.176756 from(988.399528,3+)
Title: Elution from: 46.834 to 46.834 scan no 4374 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2962.1740
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.001

Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6)-196, b(6), b(7)-294, b(7)-196, b(7)-98, b(8)-196, b(8), b(9)-294, b(9), b(9)-98, b(9)-98++, b(10)-196++, b(10)++, b(10)-196, b(10), b(11), b(11)++, b(11)-196, b(12)-196, b(12)-98++, b(12)++, b(12), b(13), b(13)-98, b(13)++, b(13)-98++, b(13)-196, b(14)-98, b(14)-196, b(14)-98++, b(14)-196++, b(15)-196++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-196++, b(17)-98++, b(18)-98++, b(18)-196++, b(19)-196++, b(19)++, b(20)-294++, b(21)-196++, b(21)-98++, b(22)++, b(22)-294++, b(23)-98++, b(23)++, b(23)-294++, b(24)-196++, b(24)++, b(24)-98++, b(25)++, b(25)-98++
Matched y ions: y(3), y(6), y(7), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(13)++, y(13), y(14), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(23)++, y(23)-98++, y(24)-294++

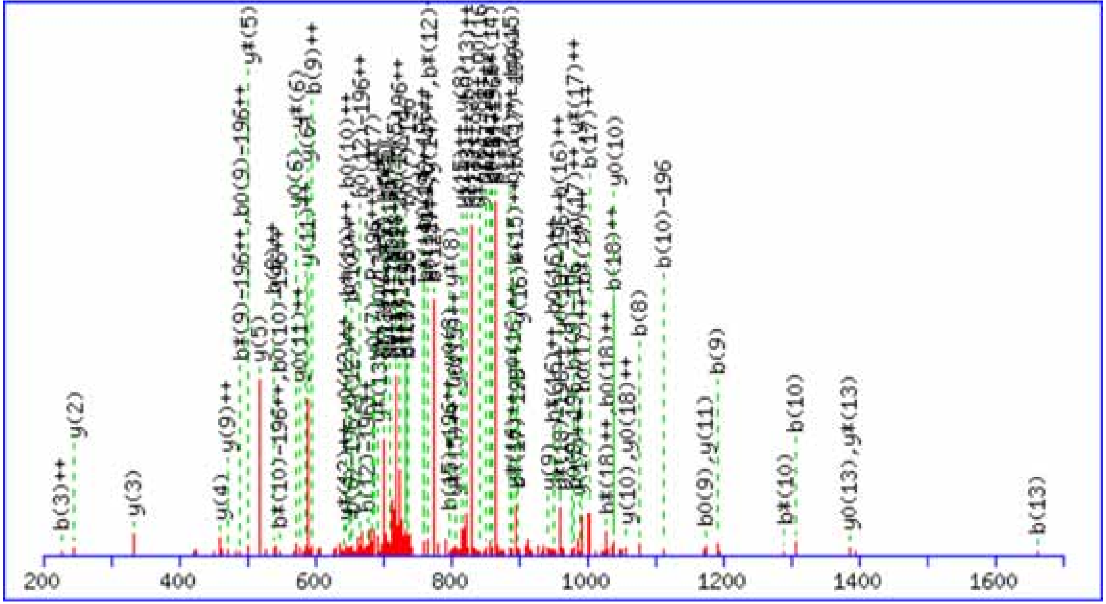
Precursor origin neutral loss: +

Peptide No.1001

SRTSVQTEDDQLIAGQSAR
Confirmed sites: @T:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of SRTSVQTEDDQLIAGQSAR
Found in CTNA1_MOUSE, Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1

Match to Query 6861: 2248.973490 from(750.665106,3+)
Title: Elution from: 36.904 to 36.904 scan no 3249 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2248.9726
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 2.3e-005

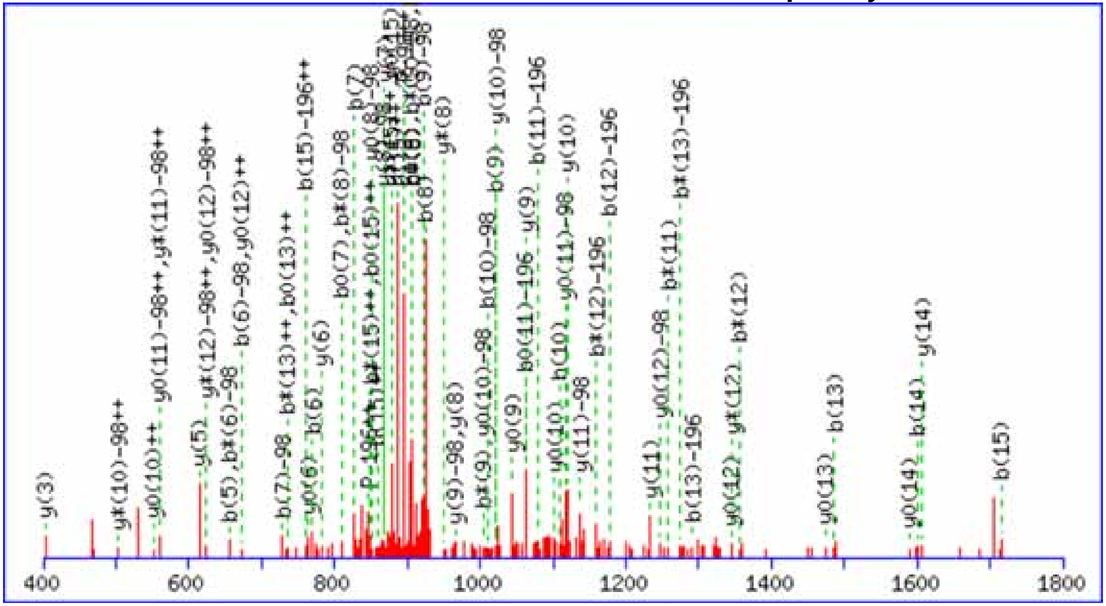
Matched b ions: b(3)++, b(5), b(6)-196, b(7)-98++, b(7)-98, b(8), b(8)++, b(8)-98++, b(8)-98, b(9), b(9)++, b(9)-98++, b(10), b(10)-196, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(12)-196++, b(13), b(13)++, b(13)-196++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)-98++, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.1002

SSDEENGPPSSPDLDR
Confirmed sites: @S:2,@S:11
Ambiguous sites:

MS/MS Fragmentation of SSDEENGPPSSPDLDR
Found in AKTS1_MOUSE, Proline-rich AKT1 substrate 1 OS=Mus musculus GN=Akt1s1 PE=1 SV=1

Match to Query 4989: 1888.676878 from(945.345715,2+)
Title: Elution from: 33.614 to 33.614 scan no 2798 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1888.6765
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.016

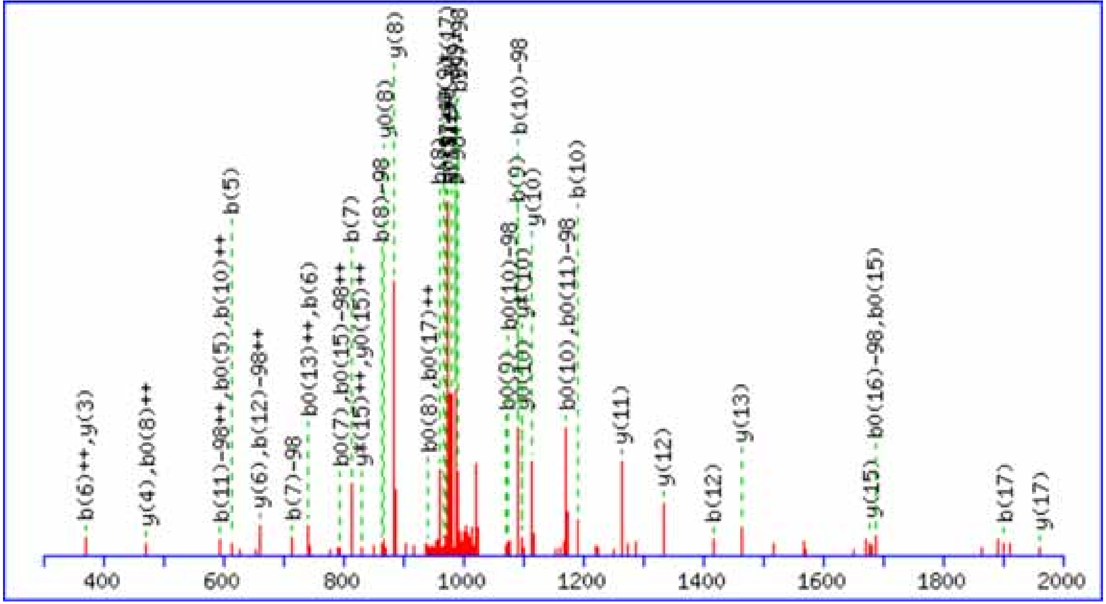
Matched b ions: b(5), b(6), b(6)-98, b(7)-98, b(7), b(8), b(9)-98, b(9), b(10)-98, b(10), b(11)-196, b(11)-98, b(12)-98, b(12)-196, b(13), b(13)-196, b(14), b(15), b(15)-196++, b(15)-98++, b(15)++
Matched y ions: y(3), y(5), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(14), y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.1003

SSDSEEAFETPESTTPVK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of SSDSEEAFETPESTTPVK
Found in TACC2_MOUSE, Transforming acidic coiled-coil-containing protein 2 OS=Mus musculus GN=Tacc2 PE=1 SV=2

Match to Query 6010: 2075.881228 from(1038.947890,2+)
Title: Elution from: 40.931 to 40.931 scan no 3790 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2075.8824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K18 : Dimethyl (K)
Ions Score: 67 Expect: 9.3e-006

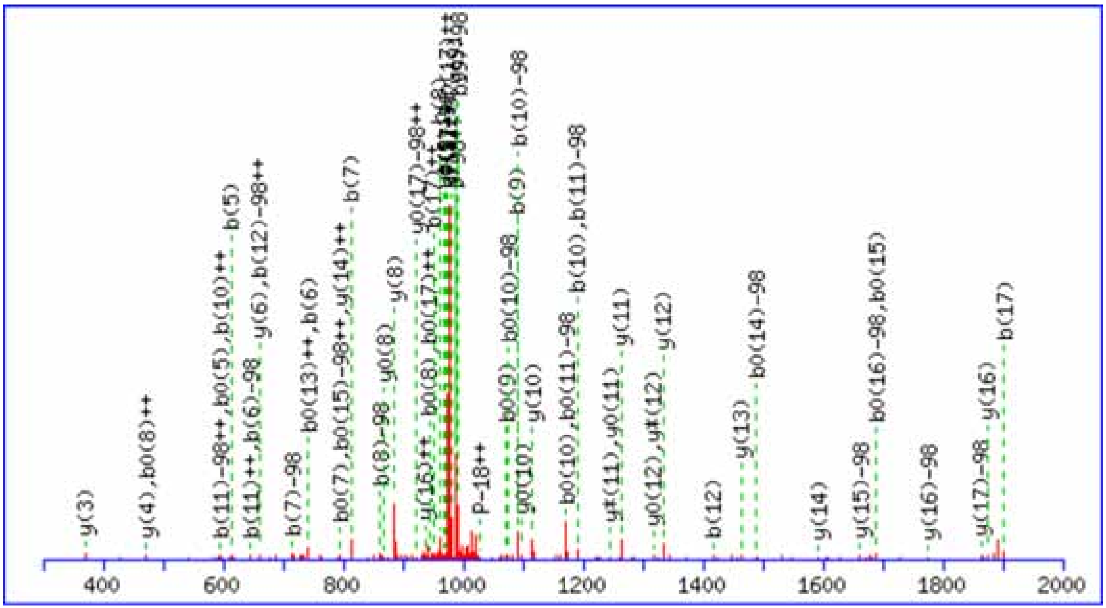
Matched b ions: b(5), b(6)++, b(6), b(7), b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10)++, b(10)-98, b(10), b(11)-98++, b(12)-98++, b(12), b(17)
Matched y ions: y(3), y(4), y(6), y(8), y(9), y(10), y(11), y(12), y(13), y(15), y(17)++, y(17)
Precursor origin neutral loss: +

Peptide No.1004

SSDSEEAFETPESTTPVK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SSDSEEAFETPESTTPVK
Found in TACC2_MOUSE, Transforming acidic coiled-coil-containing protein 2 OS=Mus musculus GN=Tacc2 PE=1 SV=2

Match to Query 5556: 2075.881484 from(1038.948018,2+)
Title: Elution from: 40.760 to 40.760 scan no 3609 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2075.8824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl (K)
Ions Score: 68 Expect: 6.2e-006

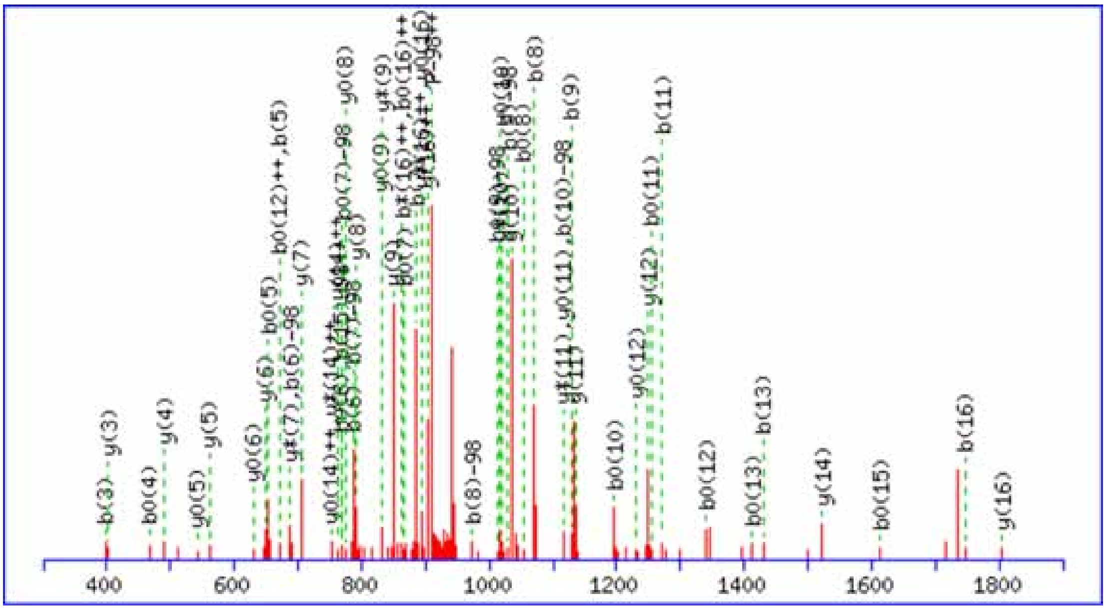
Matched b ions: b(5), b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10)++, b(10), b(10)-98, b(11)-98++, b(11)++, b(11)-98, b(12)-98++, b(12), b(17), b(17)++
Matched y ions: y(3), y(4), y(6), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15)-98, y(16)-98, y(16), y(16)++, y(17)-98, y(17)++
Precursor origin neutral loss: +

Peptide No.1005

SSDSWDVWGSGSASNNK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of SSDSWDVWGSGSASNNK
Found in ARFG1_MOUSE, ADP-ribosylation factor GTPase-activating protein 1 OS=Mus musculus GN=Arfgap1 PE=1 SV=2

Match to Query 5181: 1918.776868 from(960.395710,2+)
Title: Elution from: 52.042 to 52.042 scan no 5150 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1918.7734
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 83 Expect: 1.6e-007

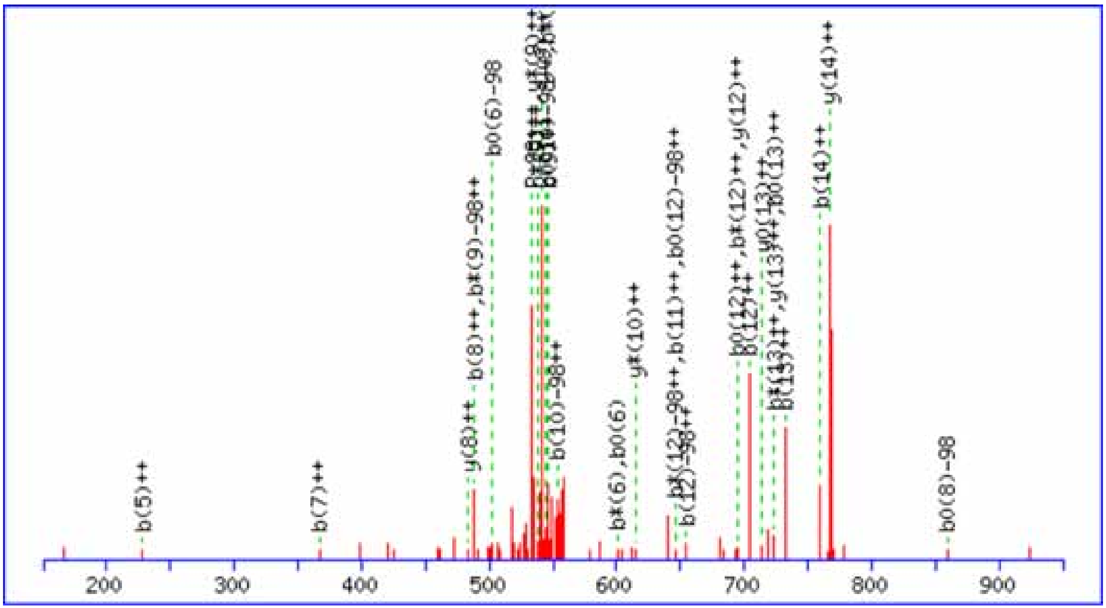
Matched b ions: b(3), b(5), b(6), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(11), b(13), b(15)-98++, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(14), y(14)++, y(16), y(16)++
Precursor origin neutral loss: +

Peptide No.1006

SSGGSKDYNLSDGGK
Confirmed sites: @S:1,@Y:8
Ambiguous sites:

MS/MS Fragmentation of SSGGSKDYNLSDGGK
Found in SMGC_MOUSE, Submandibular gland protein C OS=Mus musculus GN=Muc19 PE=1 SV=1

Match to Query 2842: 1698.718254 from(567.246694,3+)
Title: Elution from: 21.489 to 21.489 scan no 1057 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1698.7175
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K6 : Dimethyl:2H(4)13C(2) (K)
Y8 : Phospho (Y)
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 30 Expect: 0.033

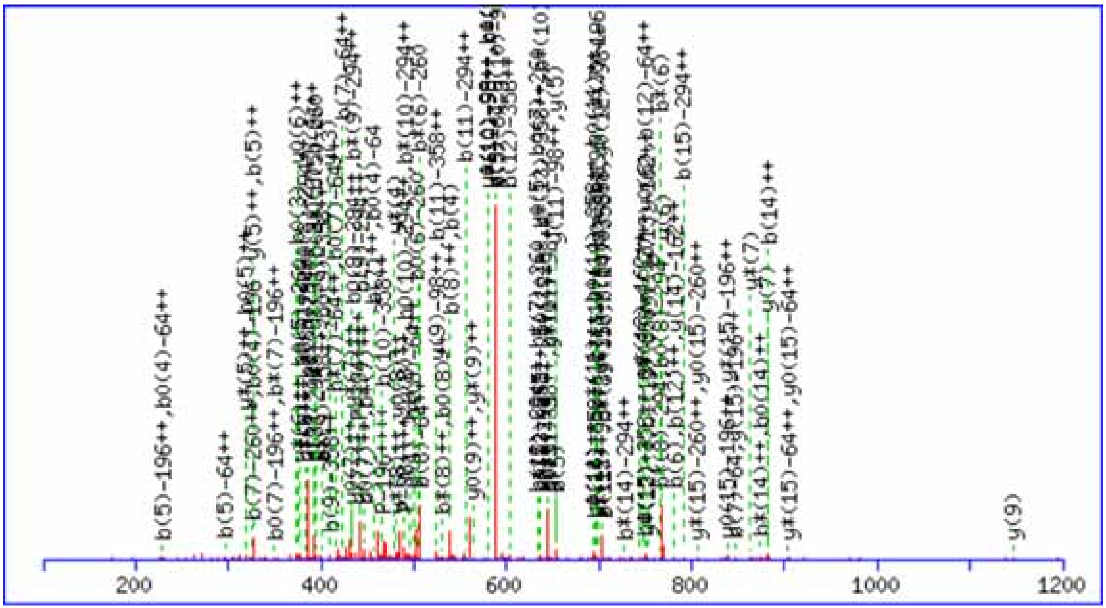
Matched b ions: b(5)++, b(7)++, b(8)++, b(9)++, b(10)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(14)++
Matched y ions: y(8)++, y(9)++, y(12)++, y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.1007

SSGMDKESVLDKSDLK
Confirmed sites: @S:1,@S:2,@S:8
Ambiguous sites:

MS/MS Fragmentation of SSGMDKESVLDKSDLK
Found in ZN148_MOUSE, Zinc finger protein 148 OS=Mus musculus GN=Znf148 PE=1 SV=2

Match to Query 6745: 2055.836032 from(514.966284,4+)
Title: Elution from: 33.850 to 33.850 scan no 2759 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2055.8338
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K12 : Dimethyl (K)
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 29 **Expect:** 0.037

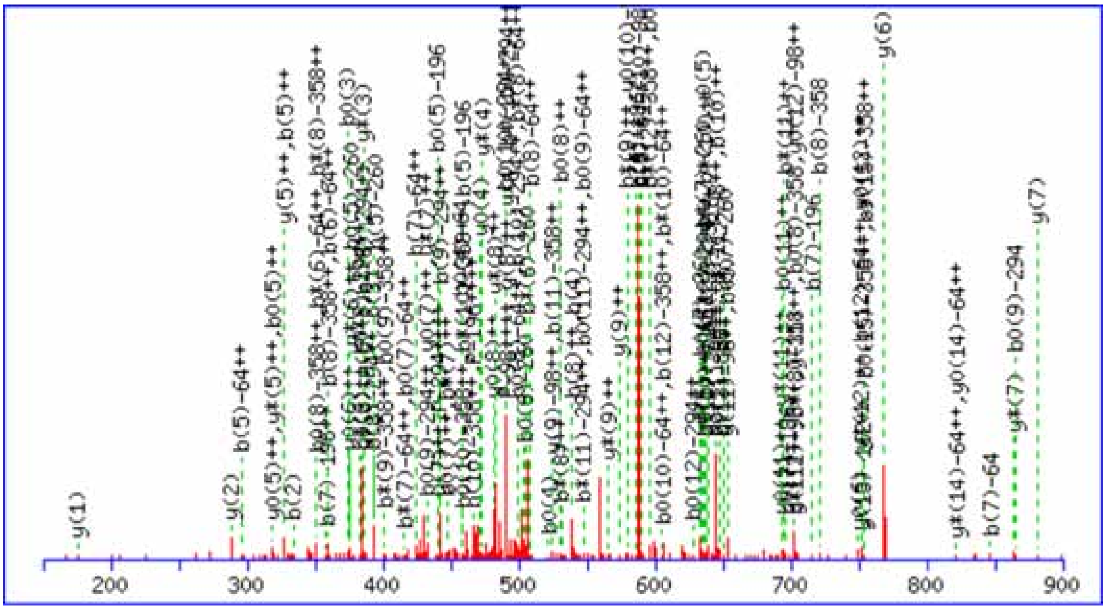
Matched b ions: b(3), b(4)-98, b(4), b(5)++, b(5)-196++, b(5), b(5)-98, b(6), b(6)++, b(7)++, b(8)-196++, b(8)-196, b(8)-294++, b(8)++, b(8)-98++, b(9)++, b(9)-196, b(9)-98++, b(9)-196++, b(9)-294++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(11)-294++, b(12)++, b(12)-294++, b(12)-98++, b(13)-196++, b(14)++, b(14)-98++, b(15)-294++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(9), y(9)-98++, y(10)-98++, y(11)++, y(11)-98++, y(15)-196++
Precursor origin neutral loss:

Peptide No.1008

SSGMDKESVLDKSDLK
Confirmed sites: @S:1,@S:2,@S:8
Ambiguous sites:

MS/MS Fragmentation of SSGMDKESVLDKSDLK
Found in ZN148_MOUSE, Zinc finger protein 148 OS=Mus musculus GN=Znf148 PE=1 SV=2

Match to Query 5241: 2055.836396 from(514.966375,4+)
Title: Elution from: 33.065 to 33.065 scan no 2516 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2055.8338
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K12 : Dimethyl:2H(4)13C(2) (K)
K16 : Dimethyl (K)
Ions Score: 35 Expect: 0.011

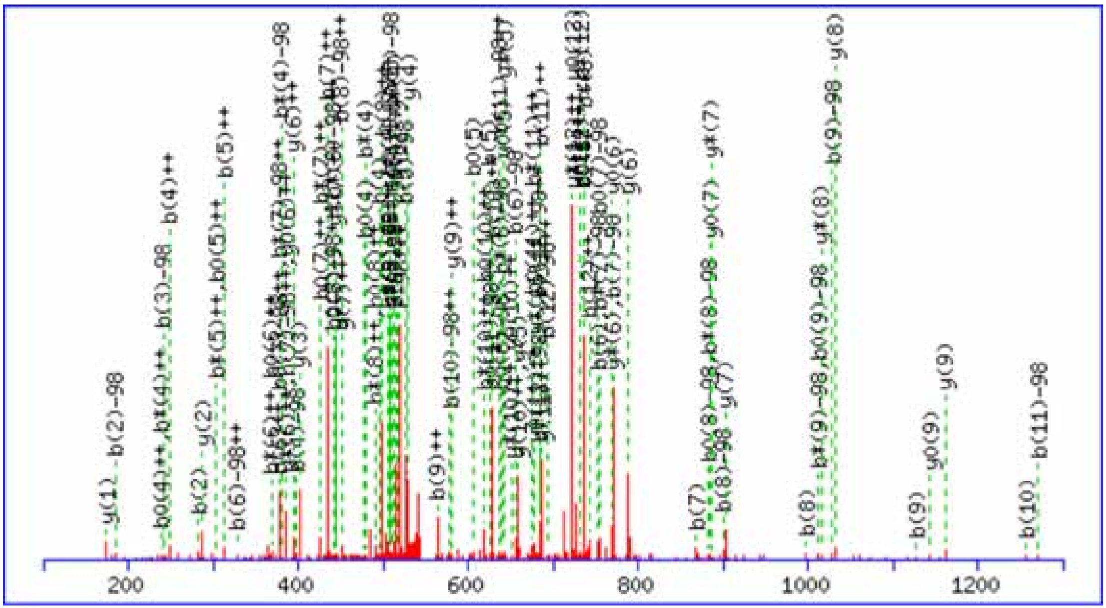
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)++, b(5), b(5)-196, b(6)-196, b(6)-98, b(7)-196++, b(7)-196, b(8)-98++, b(8)-196++, b(8)-294++, b(8)++, b(9)-196++, b(9)++, b(9)-98++, b(9)-294++, b(10)++, b(10)-98++, b(10)-294++, b(10)-196++, b(11)++, b(11)-196++, b(11)-98++, b(12)-294++, b(12)-196++, b(14)-98++
Matched y ions: y(1), y(2), y(4), y(5)++, y(6)++, y(6), y(7), y(7)++, y(8)++, y(9)-98++, y(9)++, y(10)-98++, y(10)++, y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.1009

SSGREEDEEELLR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SSGREEDEEELLR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 3004: 1655.703942 from(552.908590,3+)
Title: Elution from: 35.106 to 35.106 scan no 2834 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1655.7039
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 Expect: 1.6e-005

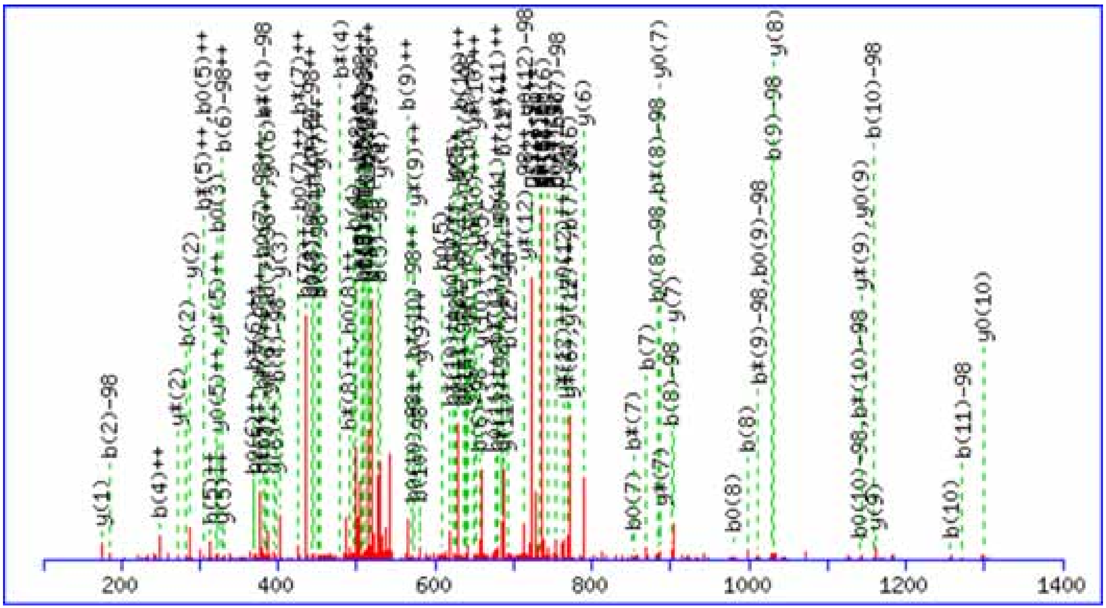
Matched b ions: b(2)-98, b(2), b(3)-98, b(4)++, b(4)-98, b(4), b(5)++, b(5)-98, b(5), b(6)++, b(6)-98, b(6), b(6)-98++, b(7)++, b(7)-98, b(7), b(7)-98++, b(8)++, b(8)-98, b(8), b(8)-98++, b(9)-98, b(9)-98++, b(9), b(9)++, b(10)++, b(10), b(10)-98++, b(11)-98, b(11)-98++, b(11)++, b(12)-98++, b(12)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1010

SSGREEDEEELLR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of SSGREEDEEELLR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 3463: 1655.703513 from(552.908447,3+)
Title: Elution from: 35.195 to 35.195 scan no 3016 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1655.7039
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 0.00026

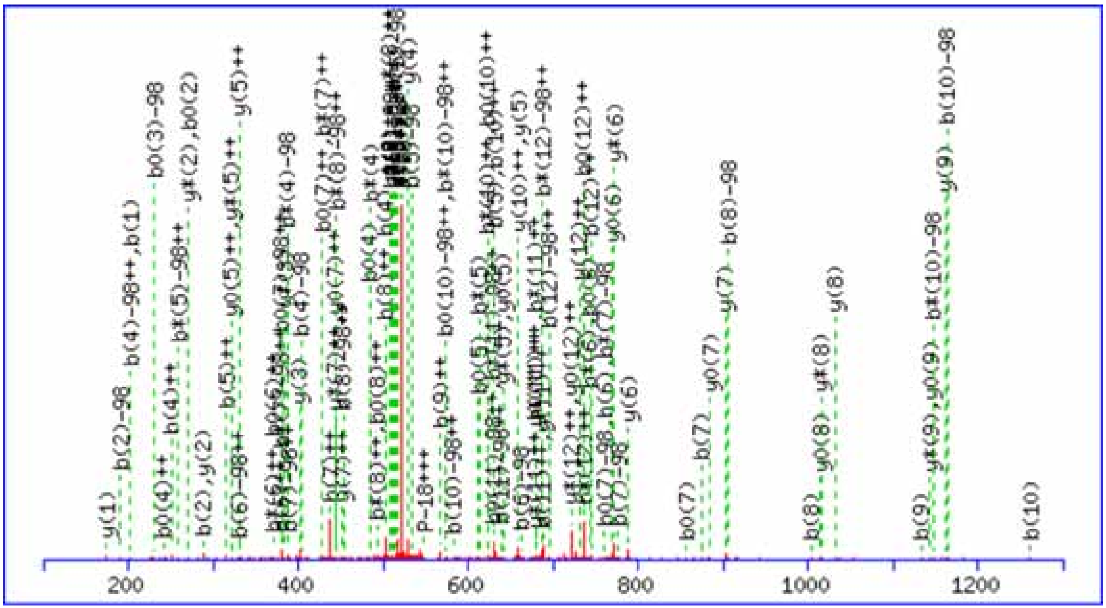
Matched b ions: b(2)-98, b(2), b(4)++, b(4)-98, b(4), b(5)++, b(5)-98, b(5), b(6)++, b(6)-98, b(6)-98++, b(6), b(7)++, b(7)-98, b(7), b(7)-98++, b(8), b(8)++, b(8)-98, b(8)-98++, b(9)-98++, b(9)-98, b(9)++, b(10)++, b(10), b(10)-98++, b(10)-98, b(11)-98, b(11)++, b(11)-98++, b(12)-98++, b(12)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(11)++, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1011

SSGREEDEEELLR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SSGREEDEEELLR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 3025: 1661.735580 from(554.919136,3+)
Title: Elution from: 35.259 to 35.259 scan no 2856 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1661.7357
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 2.2e-005

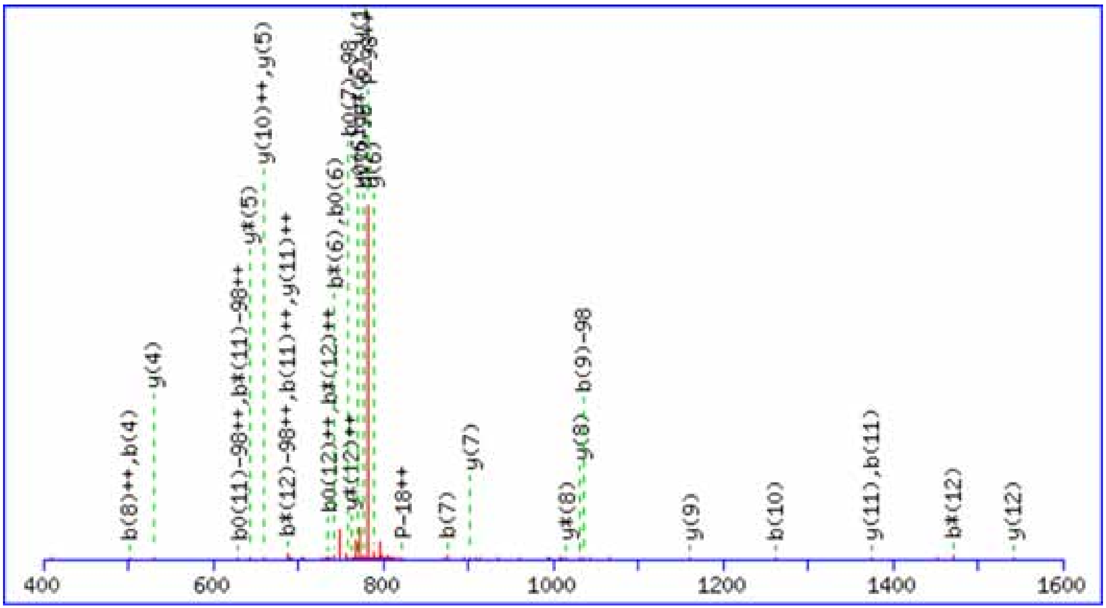
Matched b ions: b(1), b(2), b(2)-98, b(4)++, b(4), b(4)-98++, b(4)-98, b(5), b(5)++, b(5)-98, b(6)++, b(6)-98++, b(6)-98, b(6), b(7)++, b(7)-98, b(7)-98++, b(7), b(8)++, b(8), b(8)-98, b(8)-98++, b(9), b(9)++, b(9)-98++, b(10)++, b(10), b(10)-98, b(10)-98++, b(11)++, b(11)-98++, b(12)-98++, b(12)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(10)++, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1012

SSGREEDEEELLR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of SSGREEDEEELLR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 4188: 1661.737034 from(831.875793,2+)
Title: Elution from: 35.071 to 35.071 scan no 2934 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1661.7357
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.027

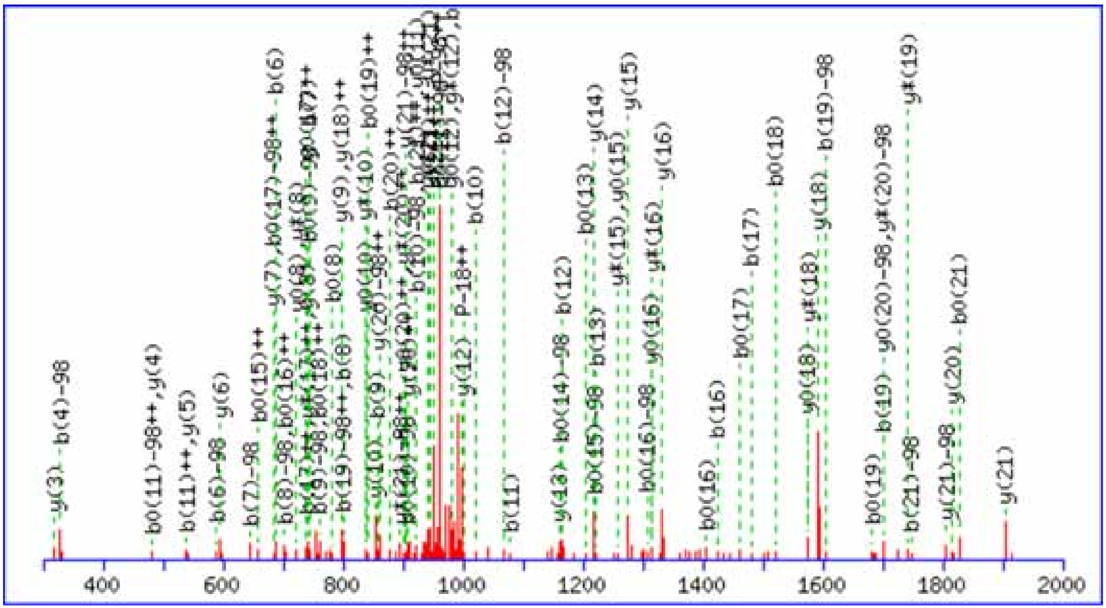
Matched b ions: b(4), b(7), b(7)-98, b(8)++, b(9)-98, b(10), b(11)++, b(11)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(11)++, y(11), y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.1013

SSGSPYGGGYGSGGGSGGYGSR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SSGSPYGGGYGSGGGSGGYGSR
Found in ROA3_MOUSE, Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnrnpa3 PE=1 SV=1

Match to Query 4509: 2017.781850 from(1009.898201,2+)
Title: Elution from: 30.956 to 30.956 scan no 2139 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2017.7804
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 92 Expect: 1.5e-008

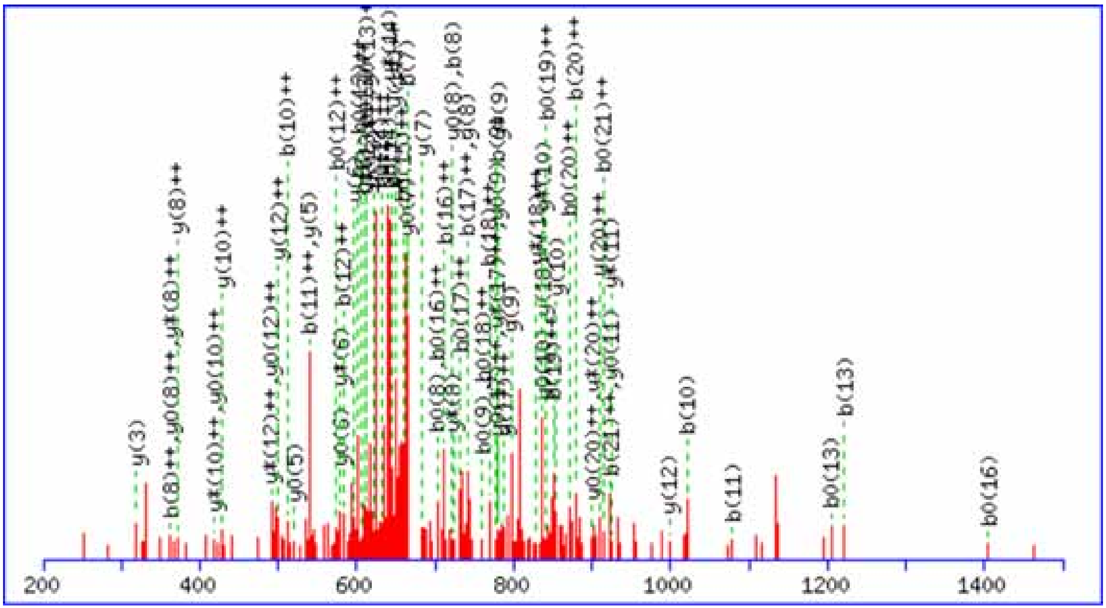
Matched b ions: b(4)-98, b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10), b(10)-98, b(11)++, b(11), b(11)-98, b(12), b(12)-98, b(13), b(16), b(17)++, b(17), b(19)-98++, b(19), b(19)-98, b(20)++, b(21)-98, b(21)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(18)++, y(18), y(20)-98++, y(20)++, y(20), y(21)-98, y(21), y(21)++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.1014

SSGSPYGGGYGSGGGSGGYGSR
Confirmed sites: @Y:10
Ambiguous sites:

MS/MS Fragmentation of SSGSPYGGGYGSGGGSGGYGSR
Found in ROA3_MOUSE, Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnrnpa3 PE=1 SV=1

Match to Query 5686: 2017.781394 from(673.601074,3+)
Title: Elution from: 31.463 to 31.463 scan no 2507 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2017.7804
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y10 : Phospho (Y)
Ions Score: 33 **Expect:** 0.013

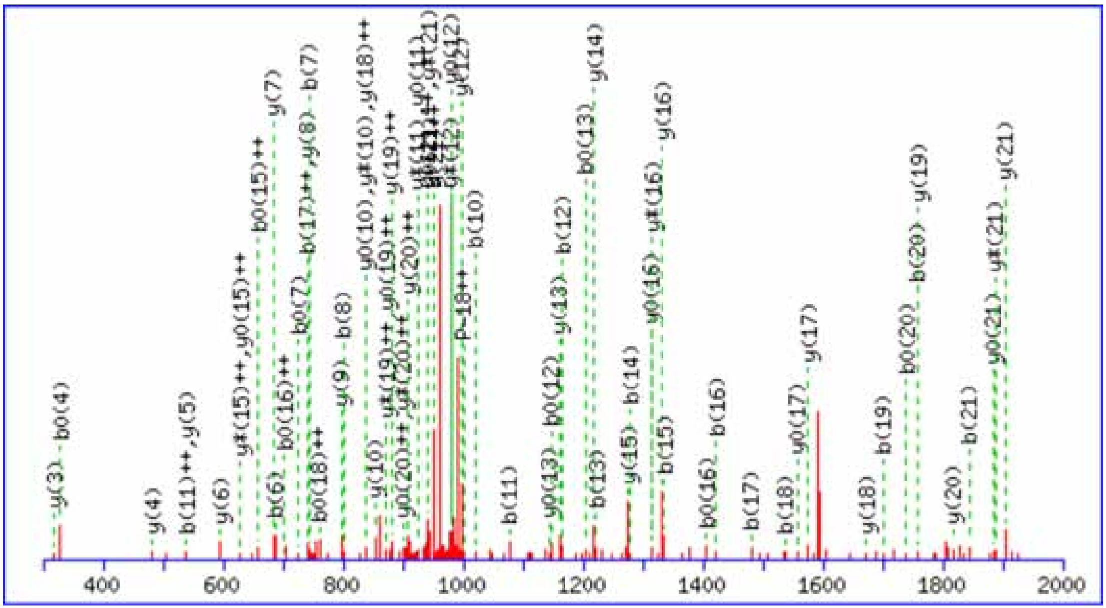
Matched b ions: b(6), b(7), b(8)++, b(8), b(9), b(10), b(10)++, b(11)++, b(11), b(12)++, b(13), b(13)++, b(14)++, b(16)++, b(17)++, b(18)++, b(19)++, b(20)++, b(21)++
Matched y ions: y(3), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10)++, y(10), y(12)++, y(12), y(13)++, y(14)++, y(17)++, y(18)++, y(20)++
Precursor origin neutral loss: +

Peptide No.1015

SSGSPYGGGYGSGGGSGGYGSR
Confirmed sites: @Y:6
Ambiguous sites:

MS/MS Fragmentation of SSGSPYGGGYGSGGGSGGYGSR
Found in ROA3_MOUSE, Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnrnpa3 PE=1 SV=1

Match to Query 4878: 2017.779886 from(1009.897219,2+)
Title: Elution from: 31.203 to 31.203 scan no 2267 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2017.7804
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y6 : Phospho (Y)
Ions Score: 116 Expect: 6.9e-011

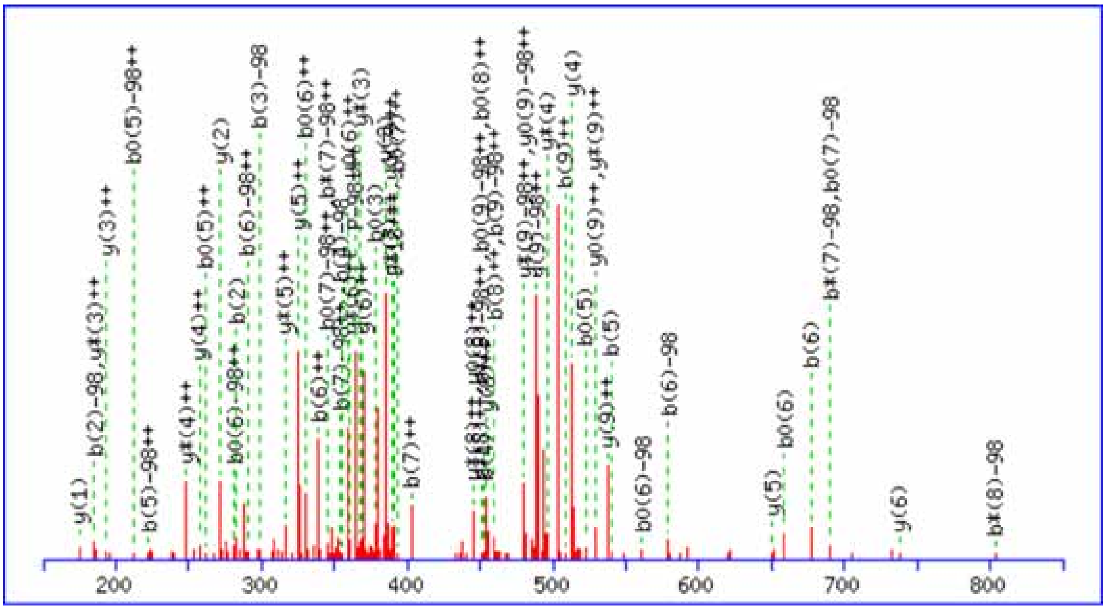
Matched b ions: b(6), b(7), b(8), b(10), b(11), b(11)++, b(12), b(13), b(14), b(15), b(16), b(17), b(17)++, b(18), b(19), b(20), b(21)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(18)++, y(19)++, y(19), y(20)++, y(20), y(21), y(21)++
Precursor origin neutral loss: +

Peptide No.1016

SSLGSHQLPR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of SSLGSHQLPR
Found in BAG3_MOUSE, BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=1

Match to Query 1169: 1188.565104 from(397.195644,3+)
Title: Elution from: 27.240 to 27.240 scan no 1926 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1188.5652
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.051

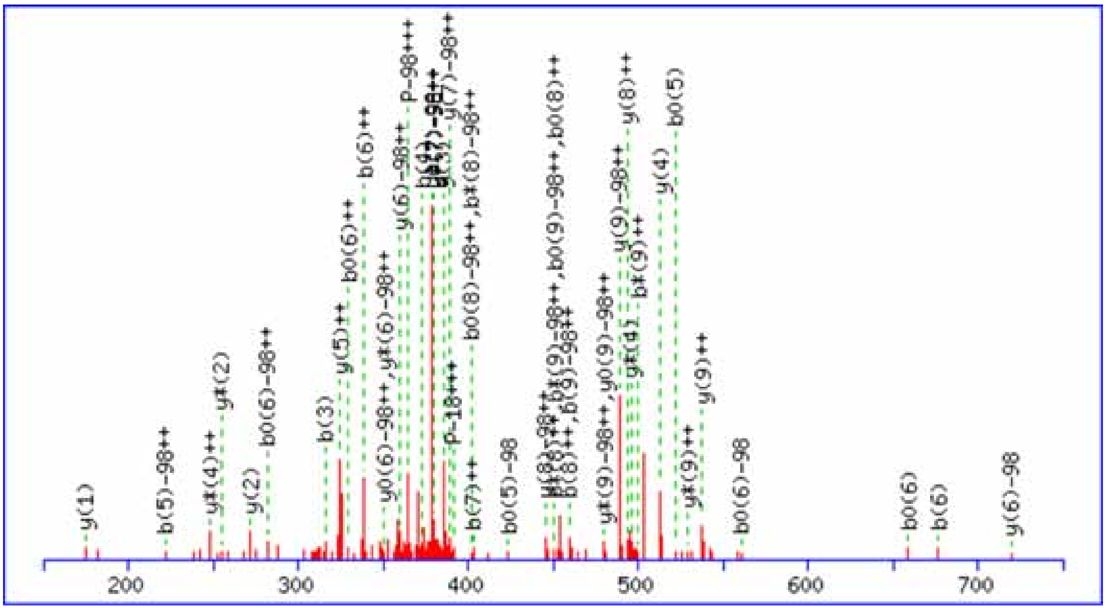
Matched b ions: b(2)-98, b(2), b(3)-98, b(4)-98, b(4), b(5)-98++, b(5), b(6), b(6)-98, b(6)++, b(6)-98++, b(7)++, b(7)-98++, b(8)++, b(9)-98++, b(9)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(4)++, y(5)++, y(5), y(6), y(6)++, y(8)++, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1017

SSLGSHQLPR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **SSLGSHQLPR**
Found in **BAG3_MOUSE**, BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=1

Match to Query 937: 1188.565209 from(397.195679,3+)
Title: Elution from: 27.198 to 27.198 scan no 1776 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1188.5652
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.0095

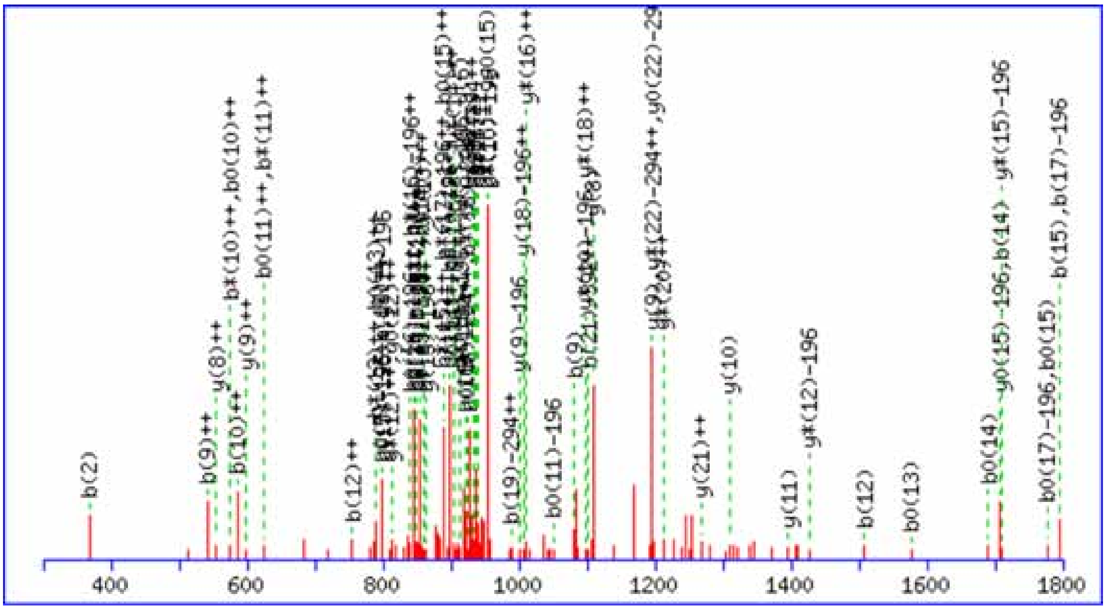
Matched b ions: b(3), b(4), b(5)-98++, b(6), b(6)++, b(7)++, b(8)++, b(9)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5)++, y(6)-98, y(6)-98++, y(7)-98++, y(8)++, y(8)-98++, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1018

SSPDDGNDVSPYSLSPVSNKSQK
Confirmed sites: @S:1,@S:2,@Y:12,@S:18,@S:21
Ambiguous sites:

MS/MS Fragmentation of SSPDDGNDVSPYSLSPVSNKSQK
Found in FZR_MOUSE, Fizzy-related protein homolog OS=Mus musculus GN=Fzr1 PE=1 SV=1

Match to Query 8445: 2903.099187 from(968.707005,3+)
Title: Elution from: 45.205 to 45.205 scan no 4326 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2903.1031
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y12 : Phospho (Y)
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K20 : Dimethyl (K)
S21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K23 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 27 Expect: 0.057

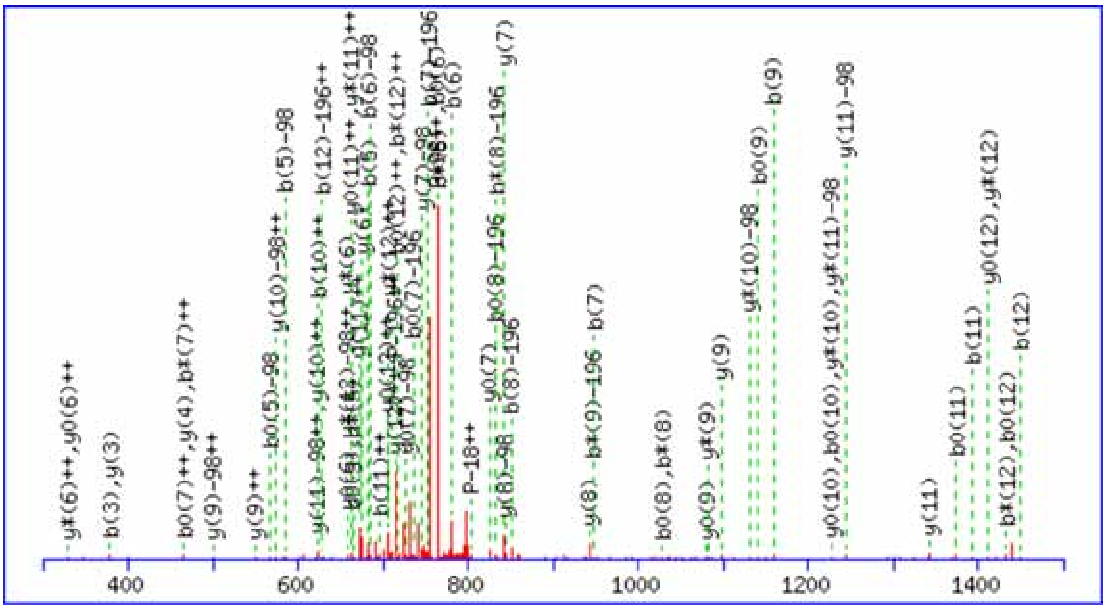
Matched b ions: b(2), b(5)-98, b(8)-98, b(9)++, b(9), b(10)++, b(12)++, b(12), b(13)++, b(14), b(14)++, b(15), b(15)++, b(15)-98++, b(15)-196++, b(16)-98, b(16)-98++, b(16)-196++, b(17)-196, b(17)-196++, b(17)-98++, b(18)-294++, b(19)-294++, b(21)-392++, b(21)-98++
Matched y ions: y(6), y(7)-98, y(8), y(8)++, y(8)-98, y(8)-196, y(9), y(9)++, y(9)-196, y(10), y(10)-98, y(11), y(14)-98++, y(15)-196++, y(15)-98++, y(16)-196++, y(18)-196++, y(21)++
Precursor origin neutral loss: +

Peptide No.1019

SSPFKVSPLSFGR
Confirmed sites: @S:1,@S:7
Ambiguous sites:

MS/MS Fragmentation of SSPFKVSPLSFGR
Found in SDPR_MOUSE, Serum deprivation-response protein OS=Mus musculus GN=Sdpr PE=1 SV=3

Match to Query 2403: 1623.746754 from(812.880653,2+)
Title: Elution from: 56.827 to 56.827 scan no 5359 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1623.7463
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K5 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00094

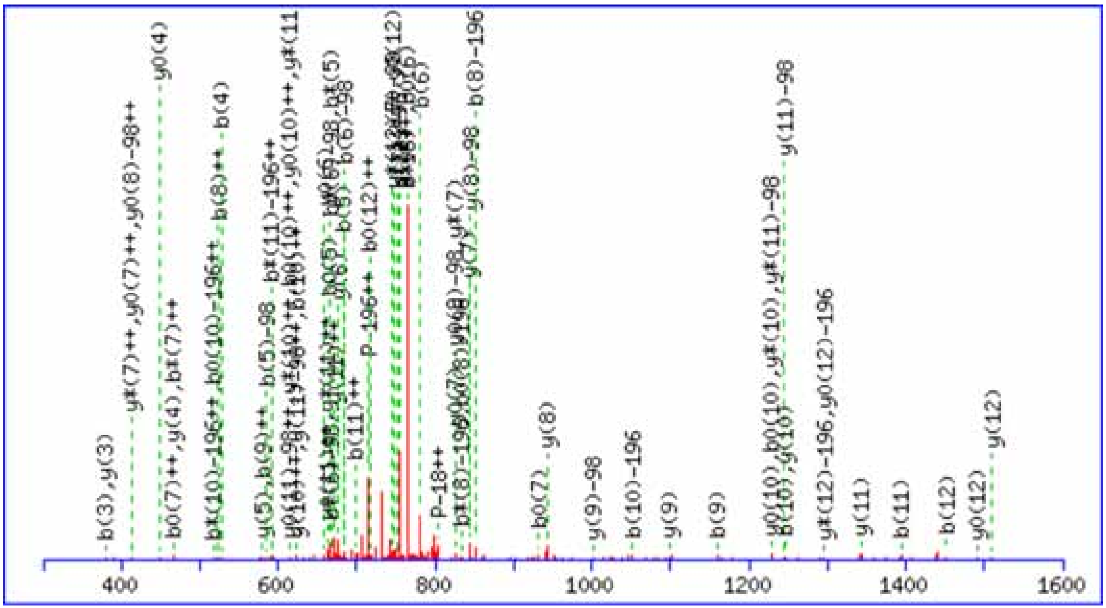
Matched b ions: b(3), b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7), b(7)-196, b(8)-98, b(8)-196, b(9), b(10)-98++, b(10)++, b(11), b(11)++, b(12), b(12)-98++, b(12)-196++
Matched y ions: y(3), y(4), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(11)-98, y(11), y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1020

SSPFKVSPLSFGR
Confirmed sites: @S:2,@S:7
Ambiguous sites:

MS/MS Fragmentation of SSPFKVSPLSFGR
Found in SDPR_MOUSE, Serum deprivation-response protein OS=Mus musculus GN=Sdpr PE=1 SV=3

Match to Query 2819: 1623.747496 from(812.881024,2+)
Title: Elution from: 56.702 to 56.702 scan no 5429 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1623.7463
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K5 : Dimethyl (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 0.00058

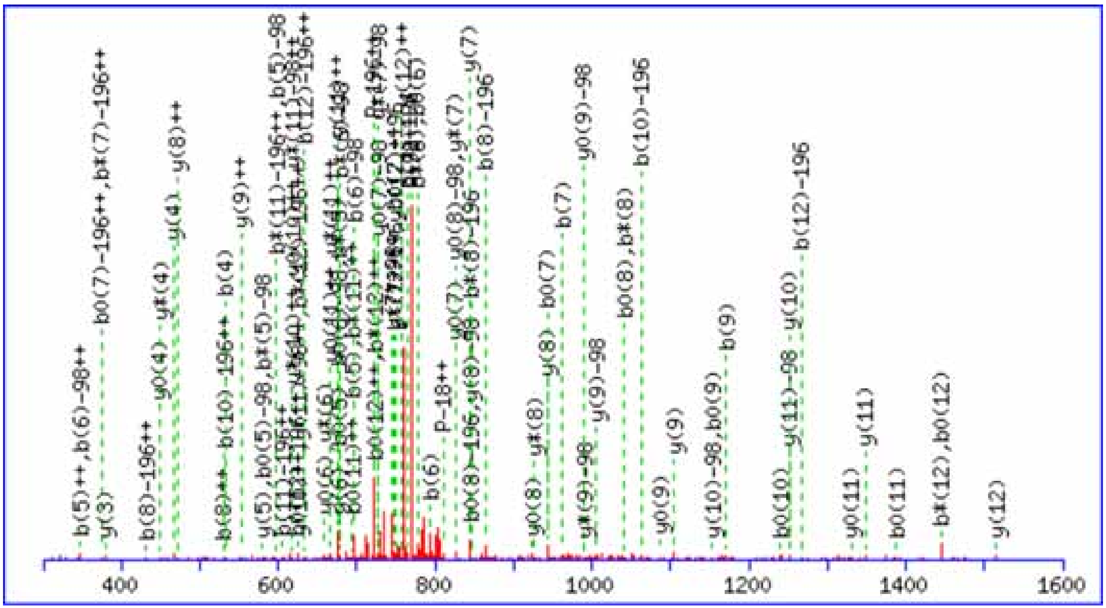
Matched b ions: b(3), b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7)-196, b(8)++, b(8)-196, b(9), b(9)++, b(10)-98++, b(10)-196, b(10), b(10)++, b(11), b(11)++, b(12)-98++, b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)++, y(11)++, y(11), y(11)-98, y(11)-98++, y(12), y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.1021

SSPFKVSPLSFGR
Confirmed sites: @S:2,@S:7
Ambiguous sites:

MS/MS Fragmentation of SSPFKVSPLSFGR
Found in SDPR_MOUSE, Serum deprivation-response protein OS=Mus musculus GN=Sdpr PE=1 SV=3

Match to Query 2569: 1635.810736 from(818.912644,2+)
Title: Elution from: 56.760 to 56.760 scan no 5367 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1635.8099
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K5 : Dimethyl:2H(4)13C(2) (K)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.0062

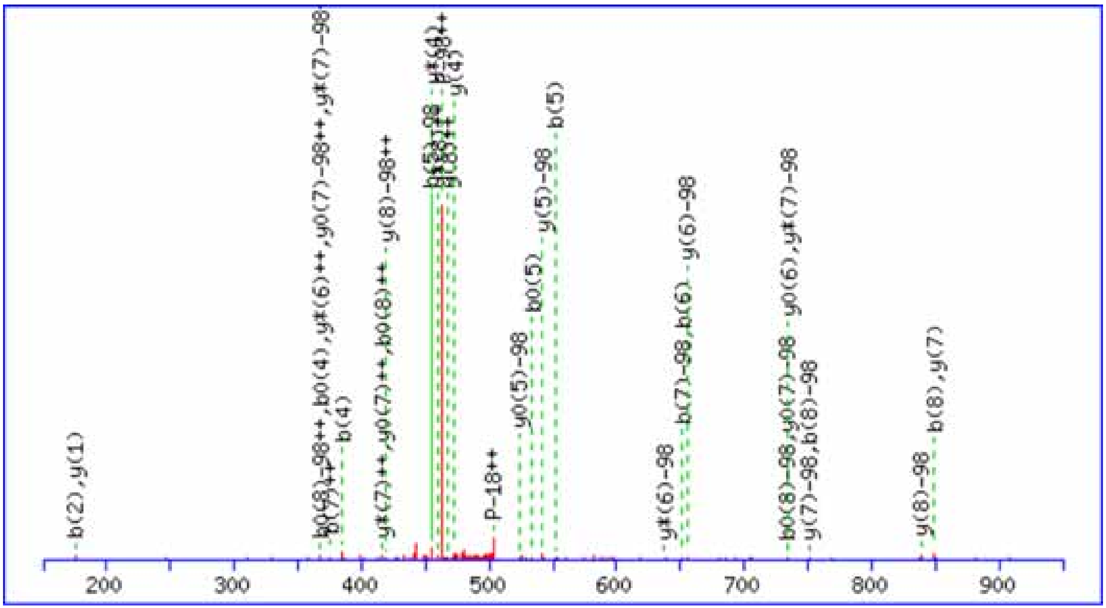
Matched b ions: b(4), b(5)++, b(5), b(5)-98, b(6)-98++, b(6)-98, b(6), b(7)-98, b(7), b(7)-196, b(8)-196, b(8)-196++, b(8)++, b(8)-98, b(9), b(9)-98, b(10)-196, b(10)-98, b(10)-196++, b(11)-98, b(11)-196++, b(12)-196++, b(12)-196
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(8)++, y(9), y(9)++, y(9)-98, y(10), y(10)-98, y(10)++, y(11)++, y(11), y(11)-98, y(11)-98++, y(12), y(12)-98, y(12)-98++, y(12)++
Precursor origin neutral loss: +

Peptide No.1022

SSPLSVVVR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of SSPLSVVVR
Found in SN_MOUSE, Sialoadhesin OS=Mus musculus GN=Siglec1 PE=1 SV=1

Match to Query 538: 1022.518302 from(512.266427,2+)
Title: Elution from: 22.615 to 22.615 scan no 1313 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1022.5162
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.054

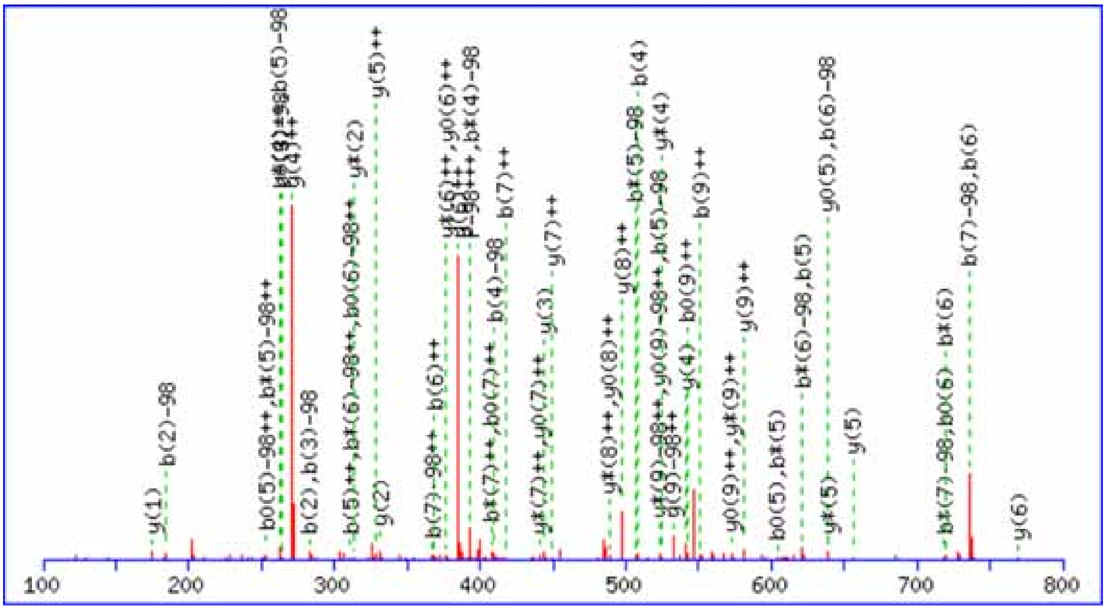
Matched b ions: b(2), b(4), b(5)-98, b(5), b(6), b(7)-98, b(7)++, b(8), b(8)-98
Matched y ions: y(1), y(4), y(5)-98, y(6)-98, y(7), y(7)-98, y(8)-98, y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.1023

SSPQLDPLRK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of SSPQLDPLRK
Found in LS14A_MOUSE, Protein LSM14 homolog A OS=Mus musculus GN=Lsm14a PE=1 SV=1

Match to Query 1530: 1275.658305 from(426.226711,3+)
Title: Elution from: 34.363 to 34.363 scan no 2901 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1275.6588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K10 : Dimethyl (K)
Ions Score: 30 Expect: 0.028

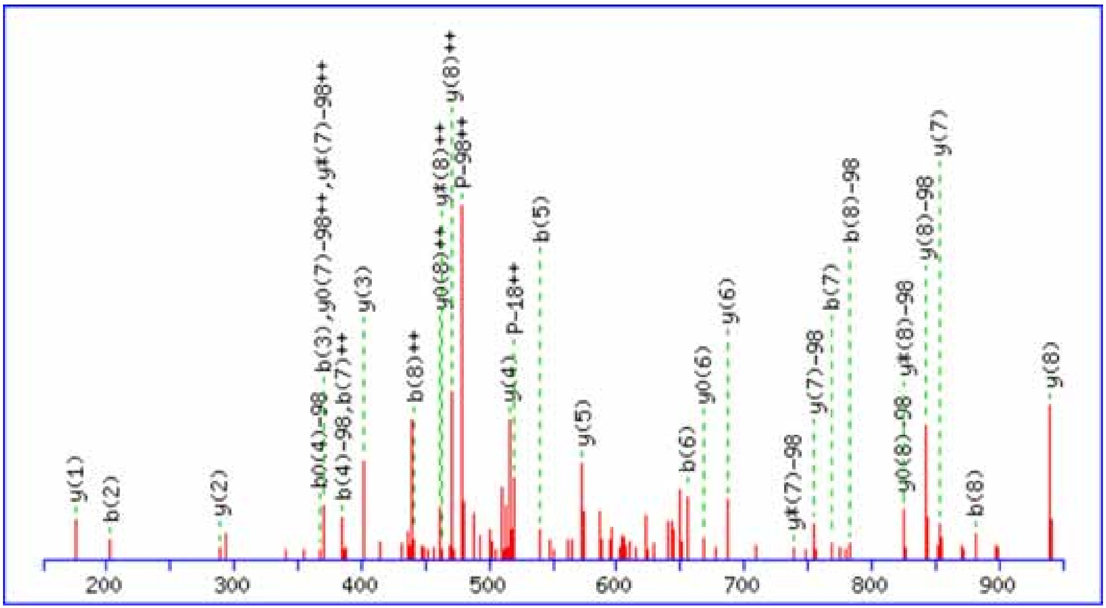
Matched b ions: b(2)-98, b(2), b(3)-98, b(4), b(4)-98, b(5)-98++, b(5), b(5)-98, b(5)++, b(6)-98, b(6), b(6)++, b(7)-98, b(7)-98++, b(7)++, b(9)++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6)++, y(6), y(7)++, y(8)++, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1024

SSSLGDLLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SSSLGDLLR
Found in PKHO2_MOUSE, Pleckstrin homology domain-containing family O member 2 OS=Mus musculus GN=Plekho2 PE=1 SV=1

Match to Query 636: 1054.506484 from(528.260518,2+)
Title: Elution from: 50.769 to 50.769 scan no 5003 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1054.5060
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 8.3e-005

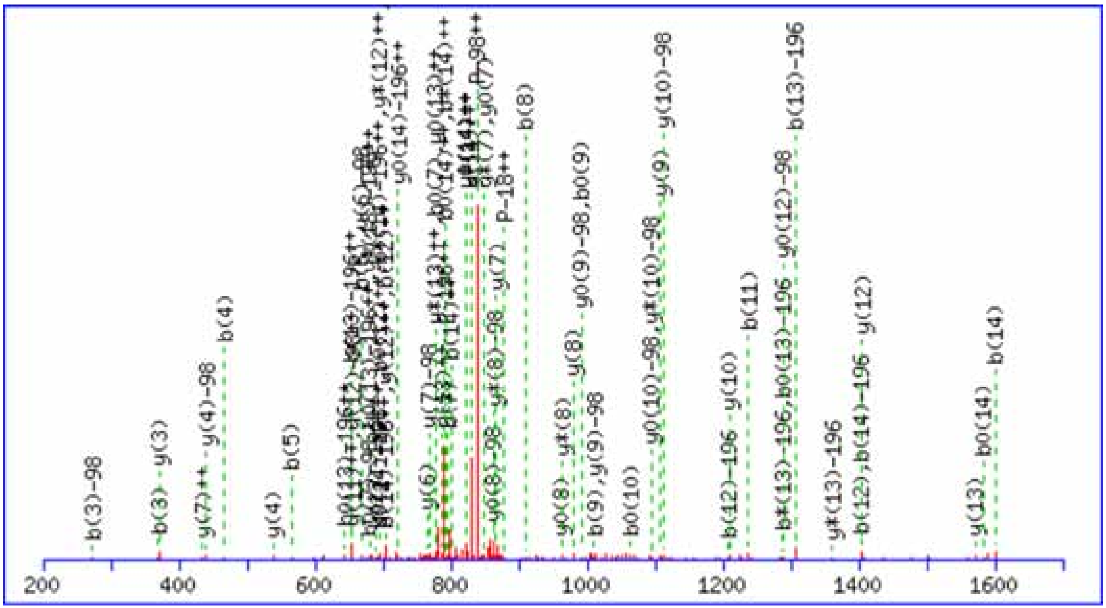
Matched b ions: b(2), b(3), b(4)-98, b(5), b(6), b(7), b(7)++, b(8), b(8)-98, b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8)++, y(8)-98, y(8)
Precursor origin neutral loss: +

Peptide No.1025

SSSPVTELTARSPVK
Confirmed sites: @S:3,@S:12
Ambiguous sites:

MS/MS Fragmentation of SSSPVTELTARSPVK
Found in SRRM2_MOUSE, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=2

Match to Query 4153: 1773.832224 from(887.923388,2+)
Title: Elution from: 38.051 to 38.051 scan no 3406 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1773.8315
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 38 **Expect:** 0.0099

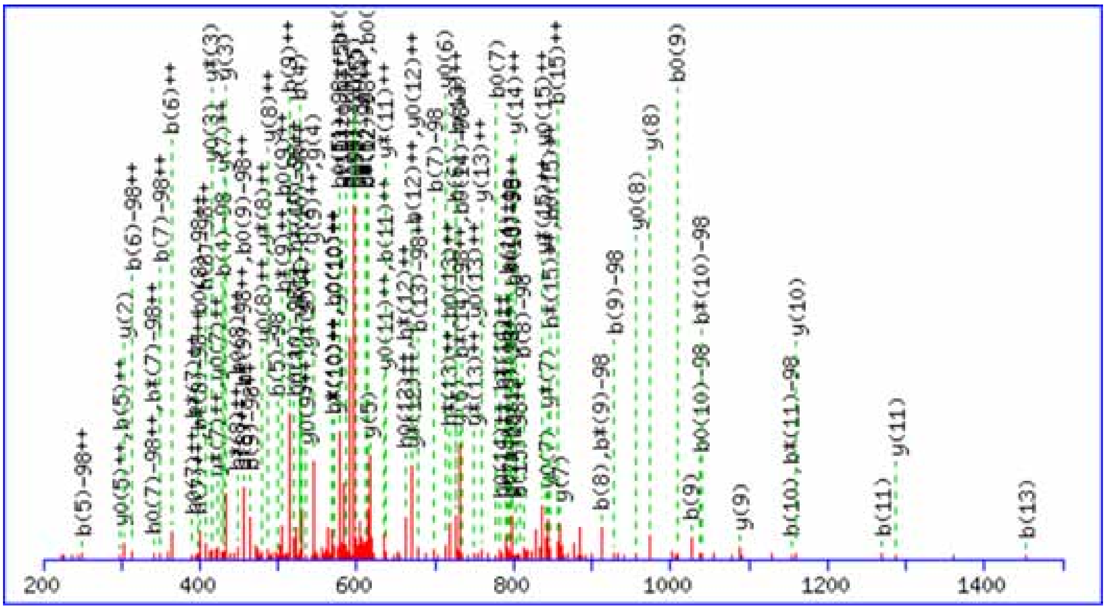
Matched b ions: b(3), b(3)-98, b(4), b(5), b(6), b(7), b(8), b(9), b(11), b(12)++, b(12)-98, b(12), b(12)-98++, b(12)-196, b(13)-196, b(13)-98, b(13)-196++, b(14)-196++, b(14), b(14)-196, b(14)-98, b(14)++
Matched y ions: y(3), y(4)-98, y(4), y(5), y(6), y(6)-98, y(7)++, y(7)-98, y(7), y(8), y(9), y(9)-98, y(10)-98, y(10), y(11)++, y(12)-98++, y(12)++, y(12), y(13), y(13)-196++, y(13)-98++, y(13)++, y(14)++, y(14)-98, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1026

SSSRAEANDQDAIQEK
Confirmed sites:
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of SSSRAEANDQDAIQEK
Found in MYOTI_MOUSE, Myotilin OS=Mus musculus GN=Myot PE=2 SV=1

Match to Query 4967: 1883.827023 from(628.949617,3+)
Title: Elution from: 23.225 to 23.225 scan no 1394 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1883.8262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl (K)
Ions Score: 62 Expect: 3e-005

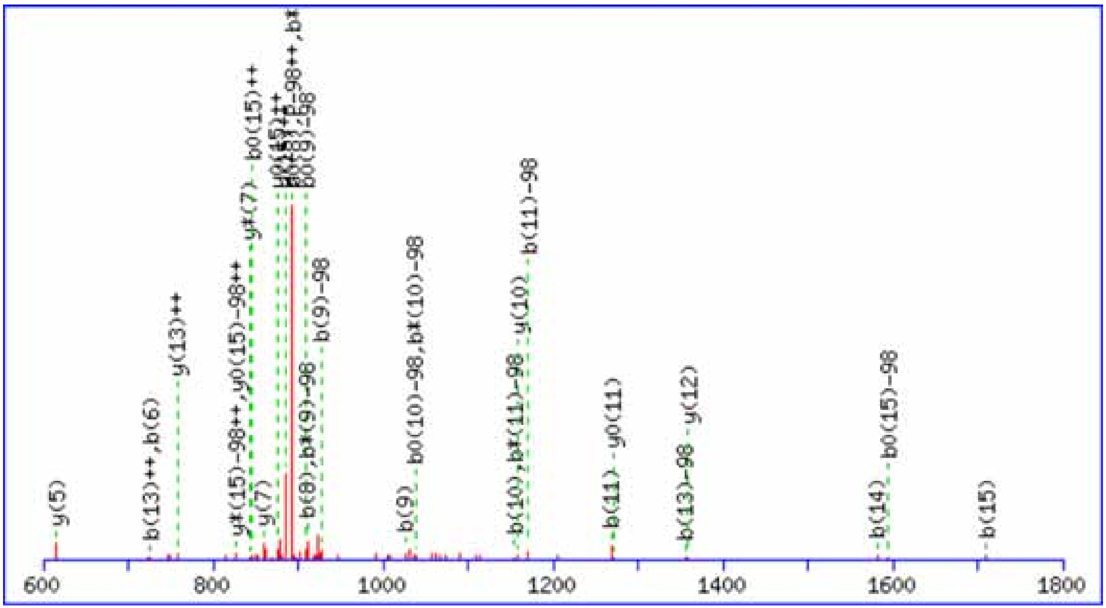
Matched b ions: b(4)-98, b(4), b(5)-98++, b(5)++, b(5), b(5)-98, b(6)++, b(6)-98++, b(6), b(7)++, b(7), b(7)-98, b(7)-98++, b(8)++, b(8)-98++, b(8), b(8)-98, b(9)++, b(9), b(9)-98++, b(9)-98, b(10)++, b(10), b(10)-98++, b(11), b(11)++, b(11)-98++, b(12)++, b(13), b(13)++, b(13)-98++, b(14)++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(13)++, y(14)++
Precursor origin neutral loss: +

Peptide No.1027

SSSRAEANDQDAIQEK
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of SSSRAEANDQDAIQEK
Found in MYOTI_MOUSE, Myotilin OS=Mus musculus GN=Myot PE=2 SV=1

Match to Query 4968: 1883.827302 from(942.920927,2+)
Title: Elution from: 23.257 to 23.257 scan no 1398 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1883.8262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl (K)
Ions Score: 30 Expect: 0.042

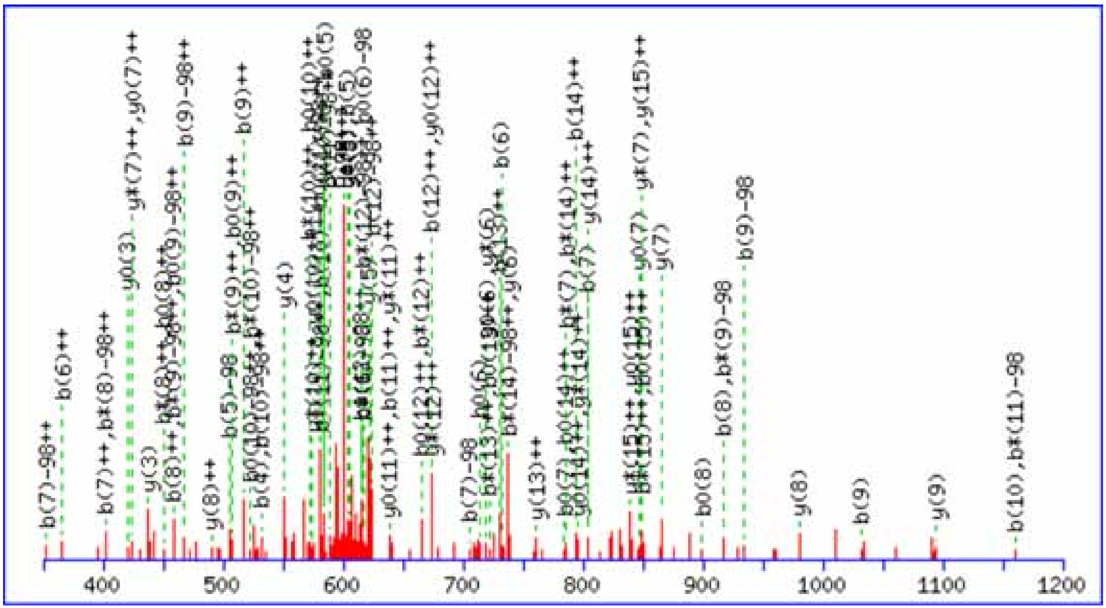
Matched b ions: b(6), b(8), b(9)-98, b(9), b(10), b(11)-98, b(11), b(13)-98, b(13)++, b(14), b(15)
Matched y ions: y(5), y(7), y(10), y(12), y(13)++, y(15)++
Precursor origin neutral loss: +

Peptide No.1028

SSSRAEANDQDAIQEK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SSSRAEANDQDAIQEK
Found in MYOTI_MOUSE, Myotilin OS=Mus musculus GN=Myot PE=2 SV=1

Match to Query 4195: 1895.892285 from(632.971371,3+)
Title: Elution from: 23.203 to 23.203 scan no 1276 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1895.8898
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 35 **Expect:** 0.018

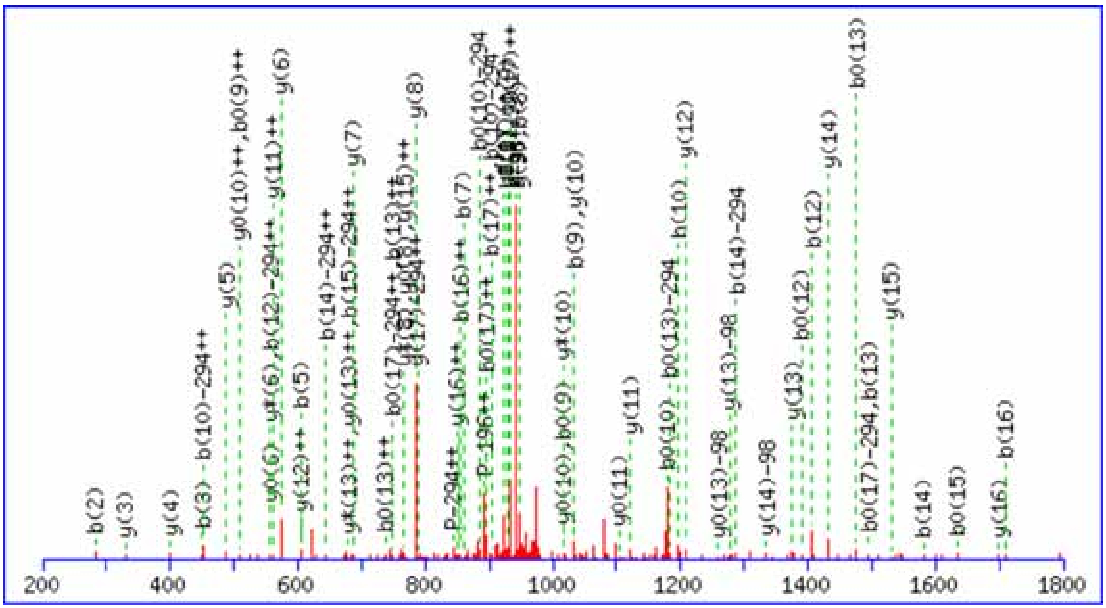
Matched b ions: b(4), b(5)-98, b(5), b(6)++, b(6), b(7)++, b(7)-98++, b(7), b(7)-98, b(8), b(8)++, b(9)++, b(9)-98, b(9), b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10)++, y(13)++, y(14)++, y(15)++
Precursor origin neutral loss: +

Peptide No.1029

SSSVGSSSSYPISSAGPR
Confirmed sites: @S:2,@S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of SSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4910: 1979.733692 from(990.874122,2+)
Title: Elution from: 44.617 to 44.617 scan no 4073 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1979.7316
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 **Expect:** 4.9e-006

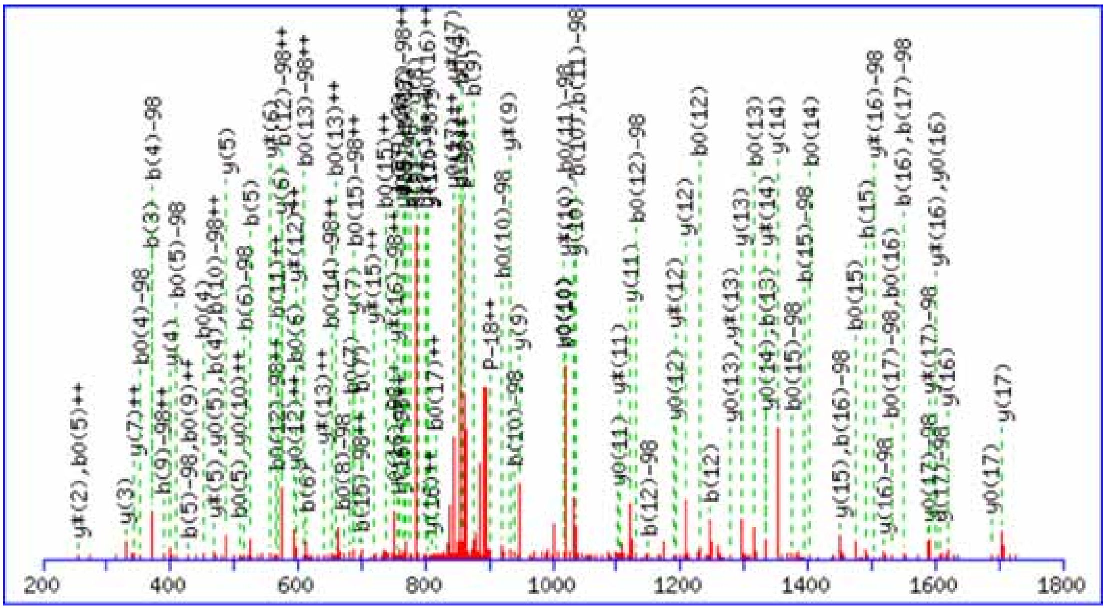
Matched b ions: b(2), b(3), b(4)-98, b(5), b(5)-98, b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9), b(10), b(10)-98, b(10)-294++, b(10)-294, b(11)-98, b(11)-196, b(12)-98, b(12), b(12)-196++, b(12)-294++, b(13), b(13)++, b(14), b(14)-294, b(14)-294++, b(15)-294++, b(16), b(16)-98, b(16)++, b(17)-98, b(17)-196, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(13), y(13)-98, y(14), y(14)-98, y(15)++, y(15), y(16), y(16)-98++, y(16)++, y(17)++, y(17)-196++, y(17)-294++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1030

SSSVGSSSSYPISSAGPR
Confirmed sites: **@S:3**
Ambiguous sites:

MS/MS Fragmentation of SSSVGSSSSYPISSAGPR
Found in **PLEC_MOUSE**, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 3779: 1819.800928 from(910.907740,2+)
Title: Elution from: 35.603 to 35.603 scan no 2869 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1819.7989
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 88 Expect: 8.1e-008

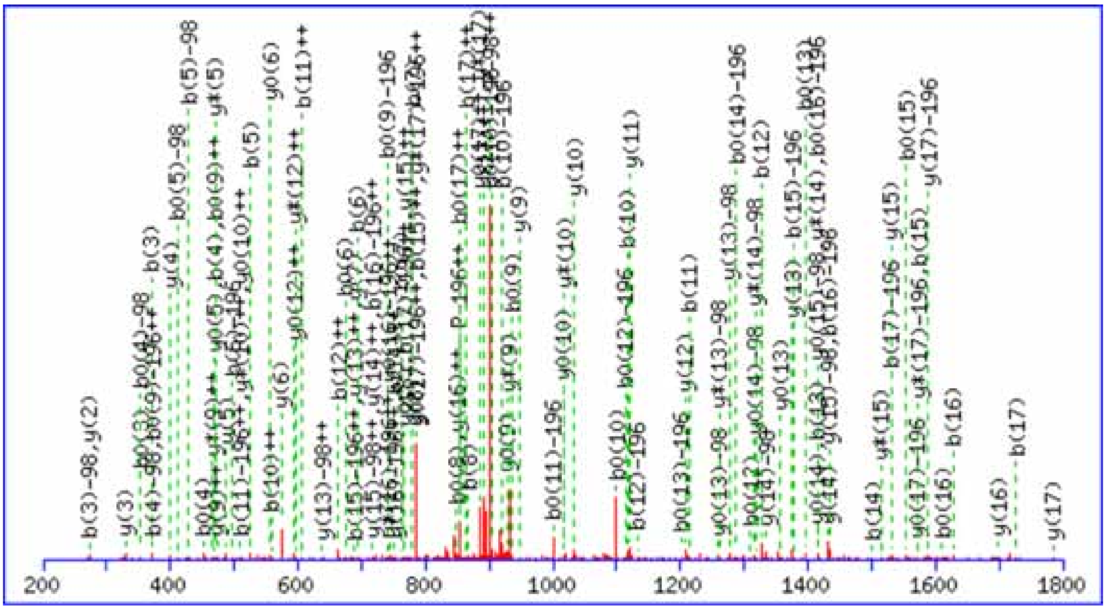
Matched b ions: b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7), b(8), b(9)-98++, b(9), b(9)-98, b(10)-98++, b(10), b(10)-98, b(11)-98, b(11)++, b(12), b(12)-98++, b(12)-98, b(13), b(15), b(15)-98++, b(15)-98, b(16)-98, b(16), b(17)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16)-98, y(16), y(16)-98++, y(16)++, y(17)++, y(17), y(17)-98, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1031

SSSVGSSSSYPISSAGPR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of SSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5941: 1899.766500 from(950.890526,2+)
Title: Elution from: 39.839 to 39.839 scan no 3616 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1899.7652
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 98 **Expect:** 5.1e-009

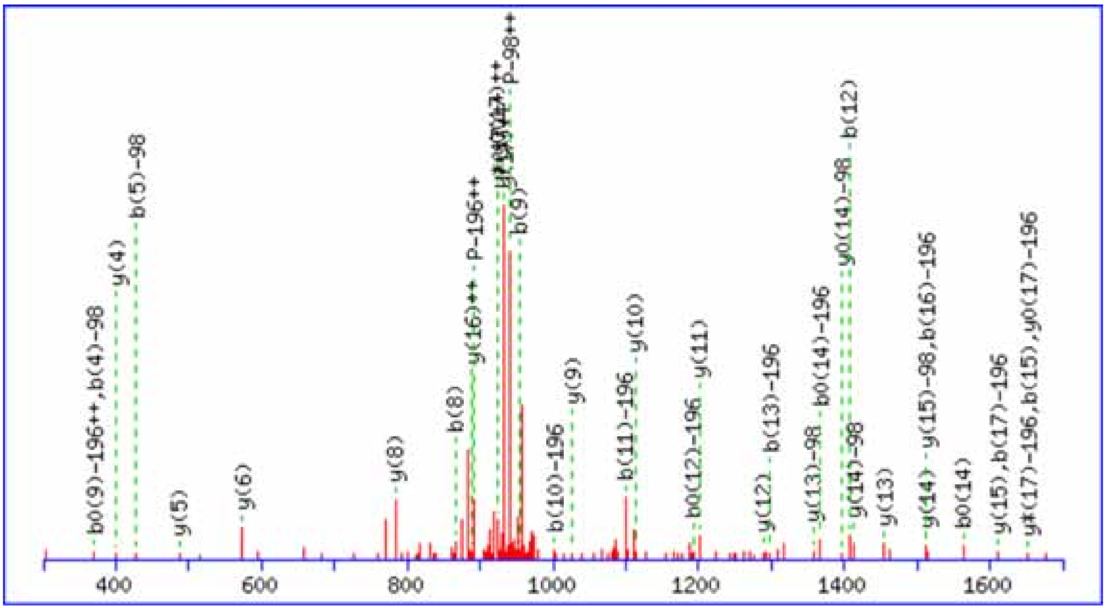
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6)-196, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98++, b(9)-98, b(10)-98, b(10), b(10)++, b(10)-196, b(11)-98, b(11), b(11)-98++, b(11)-196++, b(11)++, b(12), b(12)++, b(12)-98, b(12)-196, b(13), b(13)-98, b(14), b(14)++, b(15)-98, b(15), b(15)-196, b(15)-196++, b(15)-98++, b(15)++, b(16)-196, b(16), b(16)-98, b(16)-98++, b(16)-196++, b(17)-196, b(17)-98, b(17)-196++, b(17)++, b(17)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11), y(12), y(13), y(13)-98, y(13)-98++, y(13)++, y(14), y(14)-98, y(14)++, y(15)-98, y(15), y(15)++, y(15)-98++, y(16), y(16)++, y(16)-196++, y(16)-98++, y(16)-98, y(17)-196, y(17), y(17)++, y(17)-98, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1032

SSSVGSSSSYPISSAGPR
Confirmed sites: @S:3,@S:6,@Y:10
Ambiguous sites:

MS/MS Fragmentation of SSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 5110: 1979.732652 from(990.873602,2+)
Title: Elution from: 42.859 to 42.859 scan no 3890 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1979.7316
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y10 : Phospho (Y)
Ions Score: 37 Expect: 0.0031

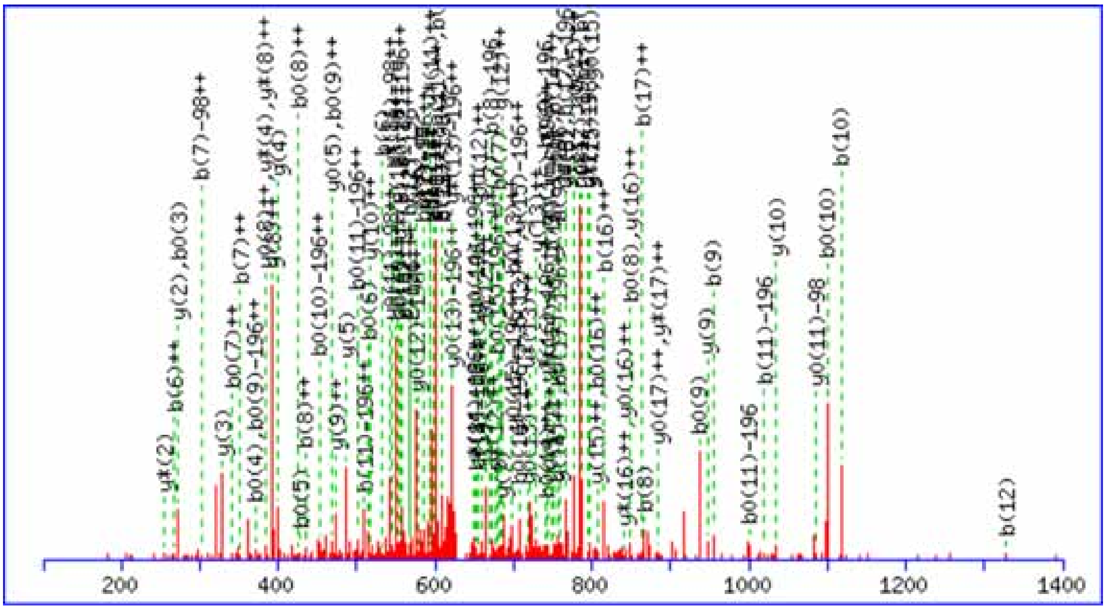
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(7)-98, b(8)-98, b(8), b(9)-98++, b(9), b(10)-98, b(10)-196, b(11)-196, b(12), b(12)-98, b(13)-196, b(13)-98, b(15), b(16)-98, b(16)-196, b(17)-196
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(12), y(13), y(13)-98, y(14)-98, y(14), y(15), y(15)-98, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.1033

SSSVGSSSSYPISSAGPR
Confirmed sites: @S:7,@S:8
Ambiguous sites:

MS/MS Fragmentation of SSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 3899: 1899.767826 from(634.263218,3+)
Title: Elution from: 39.968 to 39.968 scan no 3355 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1899.7652
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.0014

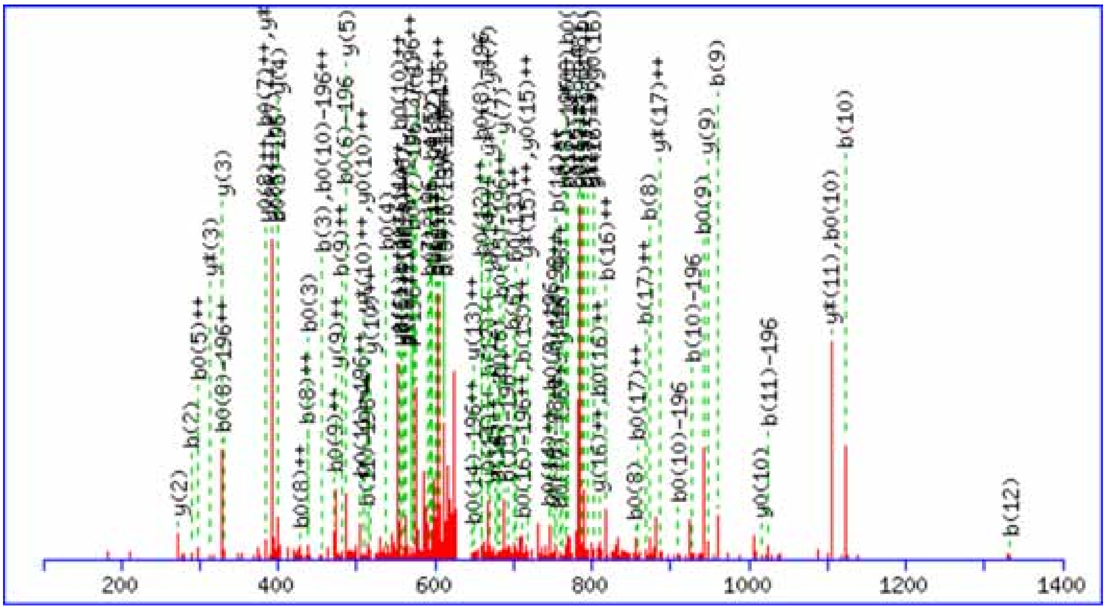
Matched b ions: b(6)++, b(6), b(7)-98, b(7)-98++, b(7)++, b(8), b(8)-98, b(8)-98++, b(8)++, b(8)-196, b(9), b(9)-98++, b(9)-196, b(10), b(10)++, b(10)-98++, b(10)-98, b(11)-98, b(11)-98++, b(11)-196++, b(11)-196, b(11)++, b(12), b(12)++, b(12)-98++, b(12)-196++, b(13)-196++, b(13)++, b(13)-98++, b(14)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(11)-98++, y(12)-196++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(14)-196++, y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(16)-196++, y(16)-98++, y(17)-196++
Precursor origin neutral loss: +

Peptide No.1034

SSSVGSSSSYPISSAGPR
Confirmed sites: @S:2,@S:3
Ambiguous sites:

MS/MS Fragmentation of SSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4274: 1905.798405 from(636.273411,3+)
Title: Elution from: 40.238 to 40.238 scan no 3488 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1905.7971
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0024

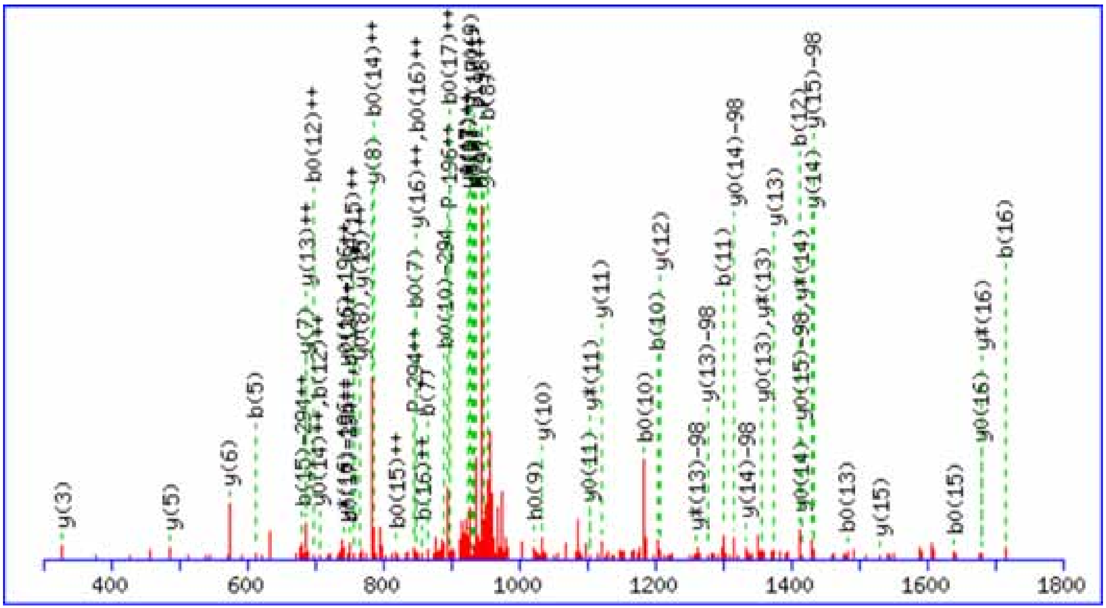
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(6), b(7)++, b(7)-98, b(7)-196, b(7), b(8), b(8)++, b(8)-98, b(9), b(9)++, b(10)-98, b(10), b(10)++, b(10)-196, b(10)-98++, b(11)-196, b(11)-98, b(11)++, b(11)-98++, b(11)-196++, b(12), b(12)++, b(12)-196++, b(12)-98++, b(13)-196++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)-196++, b(17)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(16)++, y(16)-98++, y(17)-196++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1035

SSSVGSSSSYPISSAGPR
Confirmed sites: @S:2,@S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of SSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4919: 1985.765628 from(993.890090,2+)
Title: Elution from: 44.658 to 44.658 scan no 4058 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1985.7634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 Expect: 0.0047

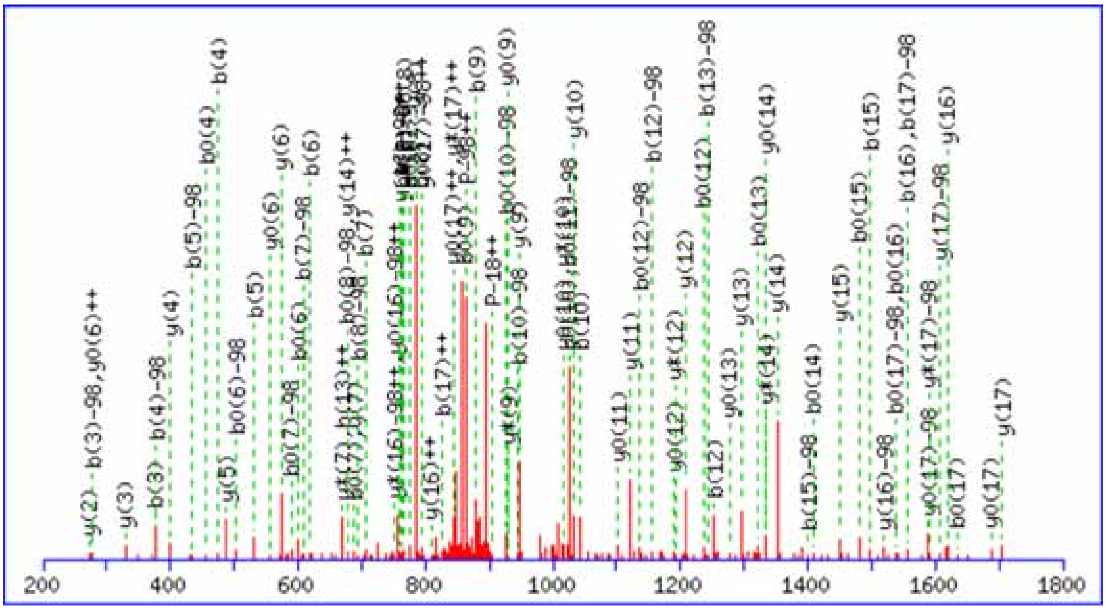
Matched b ions: b(4)-98, b(5), b(5)-98, b(6)-98, b(7)-98, b(7), b(8)-196, b(8), b(9)-196, b(9)-98, b(10), b(10)-98, b(11), b(11)-196, b(12), b(12)-98, b(12)++, b(12)-196, b(13)++, b(13)-196, b(14)-196, b(15)-196, b(15)-294++, b(16), b(16)++, b(17)-98, b(17)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)++, y(13)-98, y(14), y(14)-98, y(15)-98, y(15), y(15)++, y(16)++, y(17)-196++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.1036

SSSVGSSSSYPISSAGPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 3953: 1825.831772 from(913.923162,2+)
Title: Elution from: 35.721 to 35.721 scan no 2921 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1825.8307
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 131 Expect: 4.3e-012

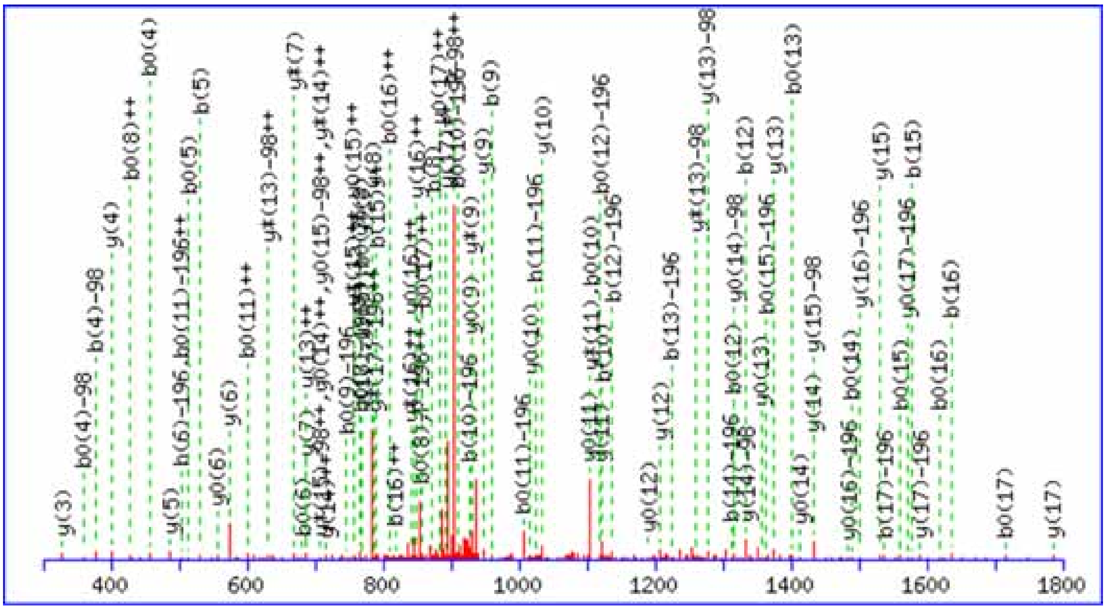
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9), b(10), b(10)-98, b(12), b(12)-98, b(13)++, b(13)-98, b(15), b(15)-98, b(16), b(17)-98, b(17)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(16)-98, y(16), y(16)-98++, y(16)++, y(17), y(17)-98
Precursor origin neutral loss: +

Peptide No.1037

SSSVGSSSSYPISSAGPR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of SSSVGSSSSYPISSAGPR
Found in PLEC_MOUSE, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4448: 1905.798608 from(953.906580,2+)
Title: Elution from: 39.893 to 39.893 scan no 3459 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1905.7971
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 95 Expect: 1.2e-008

Matched b ions: b(4)-98, b(5), b(6)-98, b(6)-196, b(7)-98, b(8)-98, b(8), b(9)-98++, b(9)-98, b(9), b(10), b(10)-98++, b(10)-196, b(10)-98, b(11)-98, b(11)-196, b(12), b(12)-196, b(12)-98, b(13)-196, b(13)-98, b(14)-98++, b(14)-196, b(15), b(15)++, b(16), b(16)-98, b(16)++, b(17)-98, b(17)-196, b(17)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)++, y(13)-98, y(13), y(14), y(14)-98, y(14)++, y(15)++, y(15), y(15)-98, y(16)-196, y(16)-98, y(16)-98++, y(16)++, y(17), y(17)-98, y(17)-196, y(17)-98++, y(17)++
Precursor origin neutral loss: +

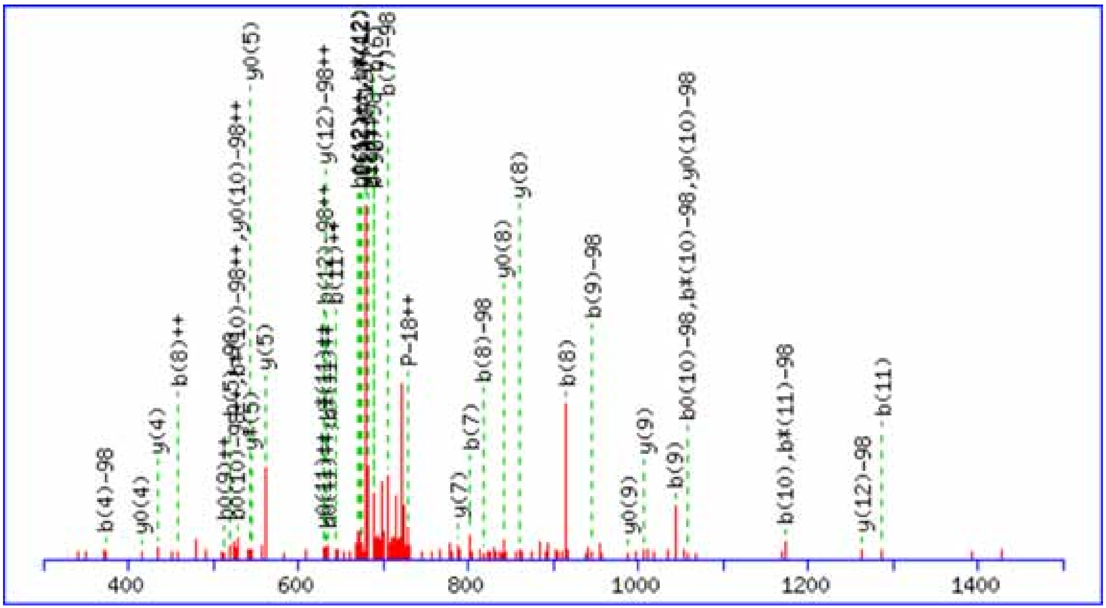
Peptide No.1038

SSTSFANIQENAT

Confirmed sites:
Ambiguous sites: @S:2orT:3orS:4

MS/MS Fragmentation of SSTSFANIQENAT
Found in OSTM1_MOUSE, Osteopetrosis-associated transmembrane protein 1 OS=Mus musculus GN=Ostm1 PE=1 SV=1

Match to Query 2328: 1476.614904 from(739.314728,2+)
Title: Elution from: 43.570 to 43.570 scan no 4127 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1476.6133
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.014

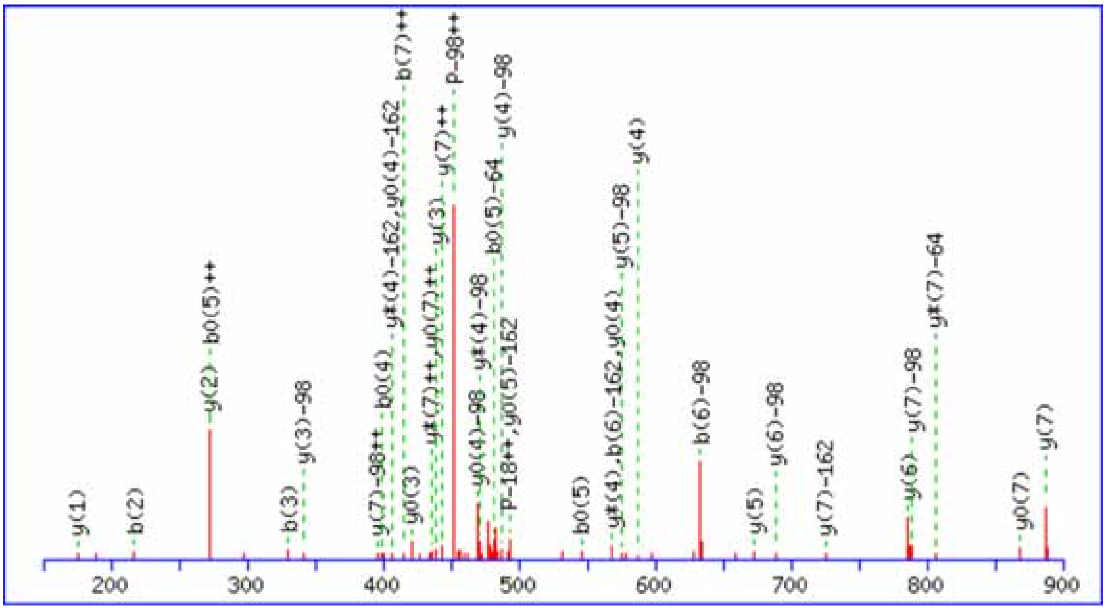
Matched b ions: b(4)-98, b(5)-98, b(6), b(7), b(7)-98, b(8), b(8)++, b(8)-98, b(9), b(9)-98, b(10), b(11), b(11)++, b(12)++, b(12)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(12)-98, y(12)++, y(12)-98++
Precursor origin neutral loss: +

Peptide No.1039

STLSMSPR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of STLSMSPR
Found in PPR1A_MOUSE, Protein phosphatase 1 regulatory subunit 1A OS=Mus musculus GN=Ppp1r1a PE=2 SV=1

Match to Query 447: 1001.425324 from(501.719938,2+)
Title: Elution from: 20.916 to 20.916 scan no 1029 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1001.4253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0049

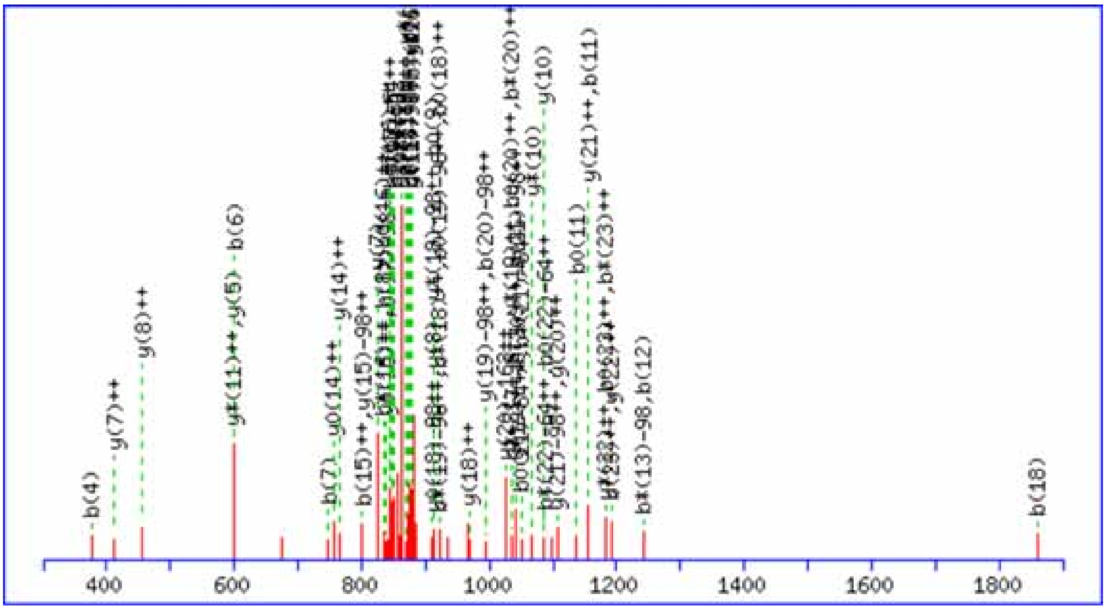
Matched b ions: b(2), b(3), b(6)-98, b(7)++
Matched y ions: y(1), y(2), y(3)-98, y(3), y(4), y(4)-98, y(5), y(5)-98, y(6)-98, y(6), y(7), y(7)-98, y(7)++, y(7)-98++
Precursor origin neutral loss: +

Peptide No.1040

STSAPQMSPGSSDNQSSSPQPAQQK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of STSAPQMSPGSSDNQSSSPQPAQQK
Found in UBP2L_MOUSE, Ubiquitin-associated protein 2-like OS=Mus musculus GN=Ubap2l PE=1 SV=1

Match to Query 8112: 2683.147017 from(895.389615,3+)
Title: Elution from: 22.750 to 22.750 scan no 1331 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2683.1433
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K25 : Dimethyl (K)
Ions Score: 52 Expect: 0.00049

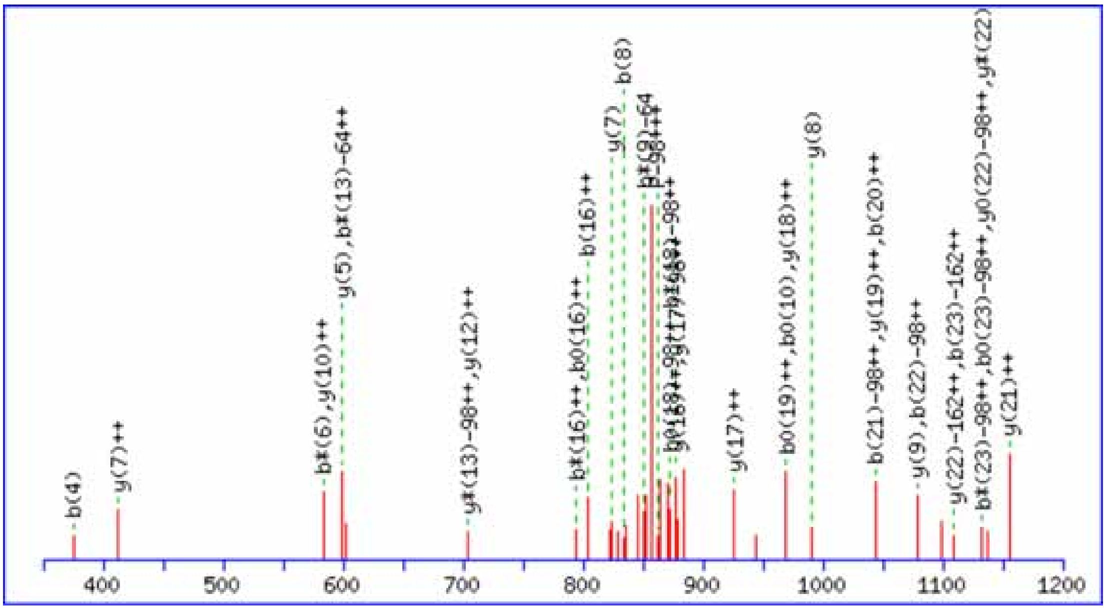
Matched b ions: b(4), b(6), b(7), b(8), b(11), b(12), b(15)++, b(16)++, b(17)-98++, b(18), b(20)++, b(20)-98++, b(21)-98++, b(23)++
Matched y ions: y(5), y(7), y(7)++, y(8)++, y(8), y(10), y(14)++, y(15)-98++, y(16)++, y(17)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++
Precursor origin neutral loss: +

Peptide No.1041

STSAPQMSPGSSDNQSSSPQPAQQK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of STSAPQMSPGSSDNQSSSPQPAQQK
Found in UBP2L_MOUSE, Ubiquitin-associated protein 2-like OS=Mus musculus GN=Ubap2l PE=1 SV=1

Match to Query 7024: 2683.141671 from(895.387833,3+)
Title: Elution from: 22.124 to 22.124 scan no 1136 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2683.1433
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K25 : Dimethyl (K)
Ions Score: 41 **Expect:** 0.0053

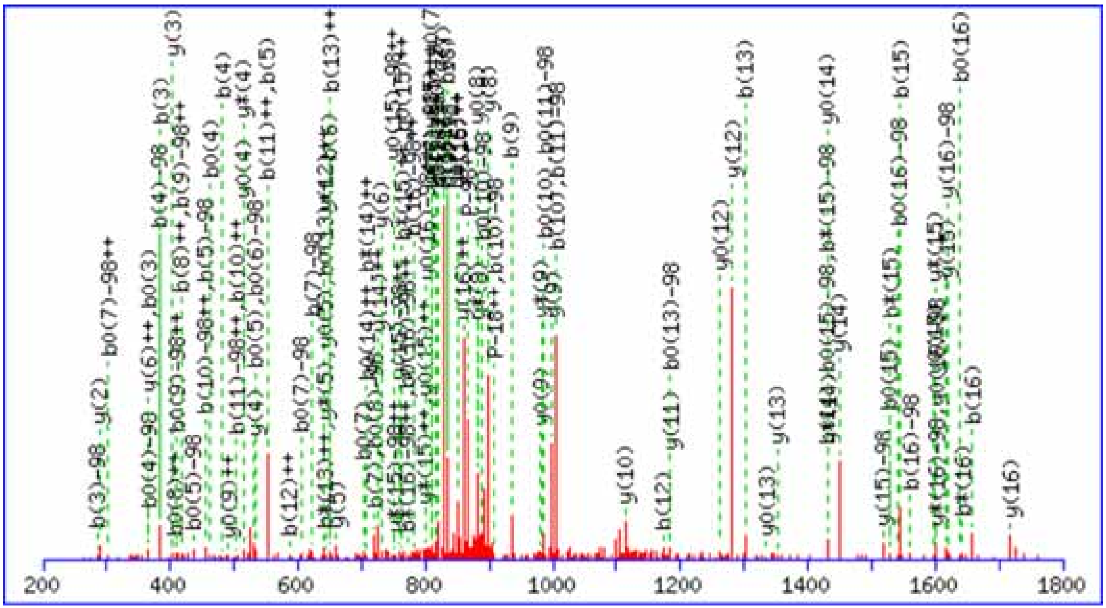
Matched b ions: b(4), b(8), b(16)++, b(20)++, b(21)-98++, b(22)-98++
Matched y ions: y(5), y(7)++, y(7), y(8), y(9), y(10)++, y(12)++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(19)++, y(21)++
Precursor origin neutral loss:

Peptide No.1042

STSPAPADVAPAQEDLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of STSPAPADVAPAQEDLR
Found in G3BP1_MOUSE, Ras GTPase-activating protein-binding protein 1 OS=Mus musculus GN=G3bp1 PE=1 SV=1

Match to Query 3982: 1831.835836 from(916.925194,2+)
Title: Elution from: 37.171 to 37.171 scan no 3121 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1831.8353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 95 Expect: 1.6e-008

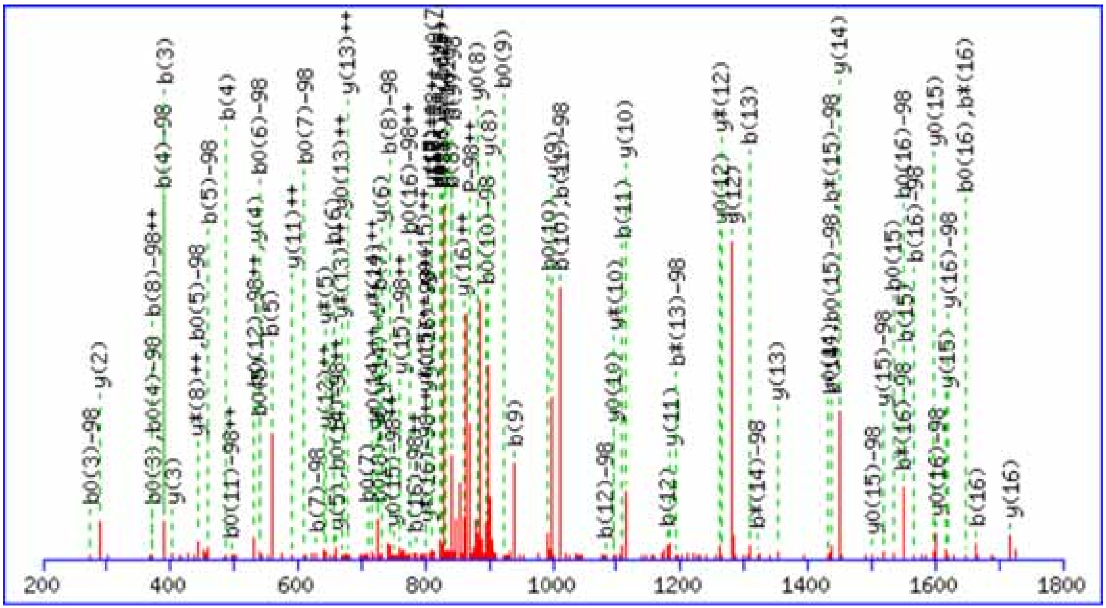
Matched b ions: b(3), b(3)-98, b(4)-98, b(4), b(5), b(5)-98, b(6), b(7), b(7)-98, b(8), b(8)++, b(9), b(9)-98++, b(9)-98, b(10), b(10)-98++, b(10)++, b(10)-98, b(11)++, b(11)-98, b(11)-98++, b(12), b(12)++, b(13), b(13)++, b(14), b(15), b(16), b(16)-98, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(13), y(14)++, y(14), y(15)-98, y(15), y(15)-98++, y(15)++, y(16), y(16)++, y(16)-98, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1043

STSPAPADVAPAQEDLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of STSPAPADVAPAQEDLR
Found in G3BP1_MOUSE, Ras GTPase-activating protein-binding protein 1 OS=Mus musculus GN=G3bp1 PE=1 SV=1

Match to Query 4004: 1837.867476 from(919.941014,2+)
Title: Elution from: 37.164 to 37.164 scan no 3120 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1837.8671
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 98 Expect: 1e-008

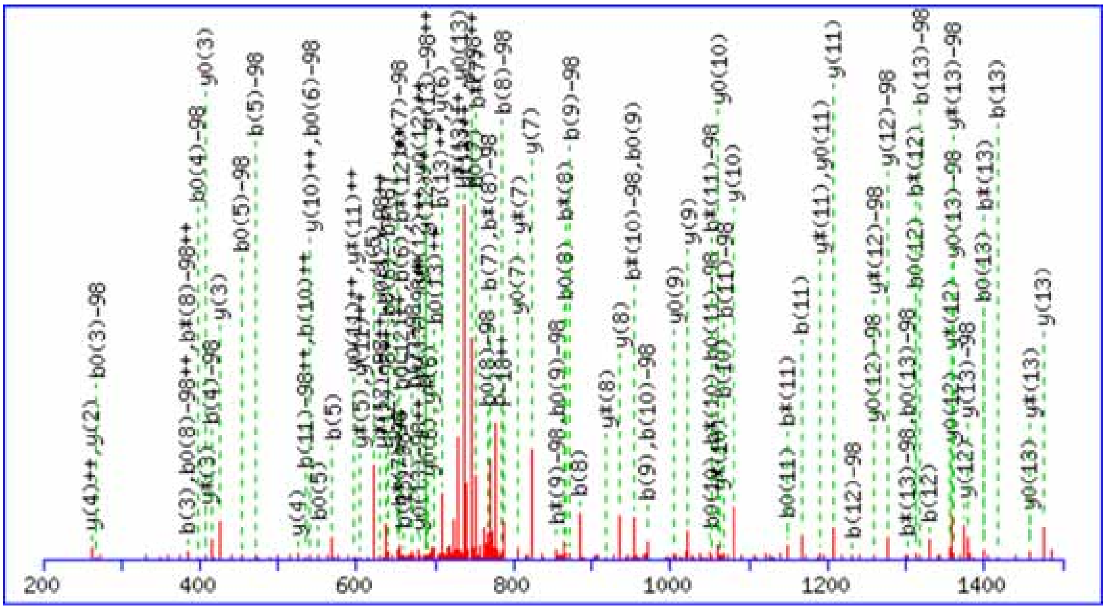
Matched b ions: b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(8)-98++, b(9), b(9)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(13), b(14), b(15), b(16), b(16)-98, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14), y(14)++, y(15)-98, y(15), y(15)-98++, y(15)++, y(16), y(16)-98, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1044

STSQGSINSPVYSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of STSQGSINSPVYSR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 2979: 1589.708964 from(795.861758,2+)
Title: Elution from: 32.754 to 32.754 scan no 2682 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1589.7086
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 96 Expect: 9.1e-009

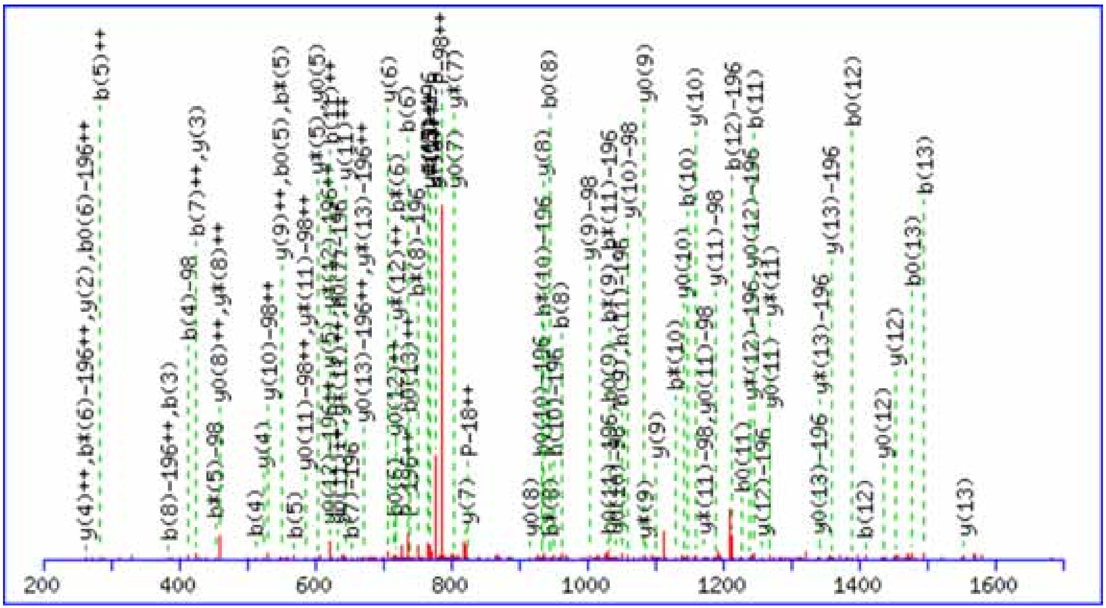
Matched b ions: b(3), b(4)-98, b(5), b(5)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10)++, b(10), b(11), b(11)-98, b(11)-98++, b(12), b(12)-98, b(13)++, b(13)-98, b(13)-98++, b(13)
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)-98++, y(12)-98, y(12)++, y(13)++, y(13), y(13)-98, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1045

STSQGSINSPVYSR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of STSQGSINSPVYSR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 3069: 1669.676270 from(835.845411,2+)
Title: Elution from: 35.458 to 35.458 scan no 2885 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1669.6750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.011

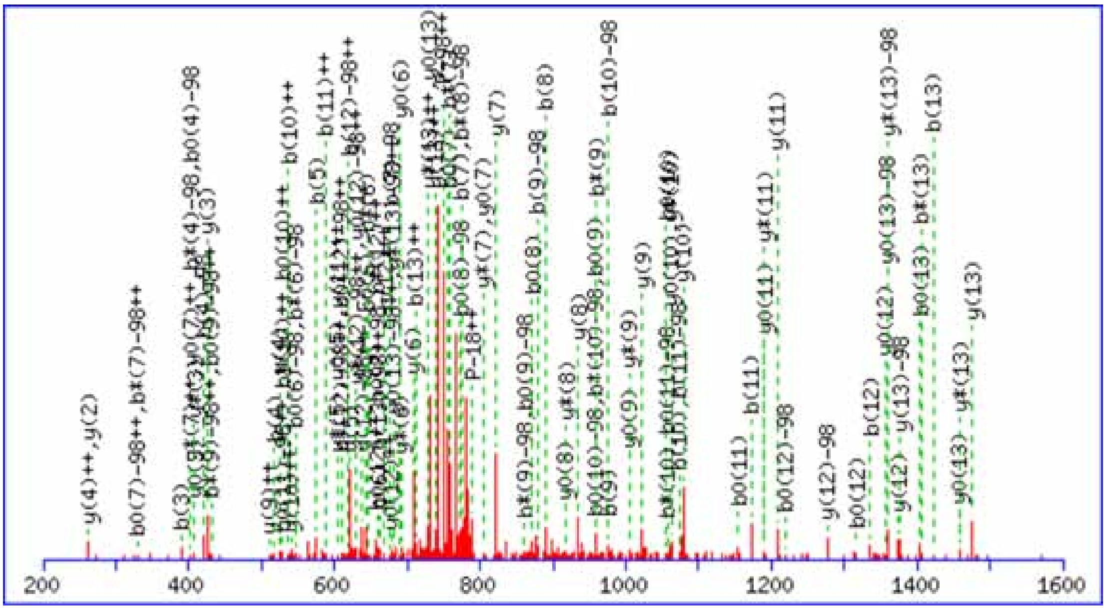
Matched b ions: b(3), b(4)-98, b(4), b(5), b(5)++, b(6)-98, b(6), b(7)++, b(7)-98, b(7)-196, b(8)-98, b(8), b(8)-196++, b(8)-196, b(9)-98, b(9), b(10)-196, b(10)-98, b(10), b(11)-196, b(11), b(11)-98, b(11)++, b(12), b(12)-98, b(12)-196, b(13), b(13)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(7), y(8), y(9)-98, y(9)++, y(9), y(10)-98++, y(10), y(10)-98, y(11)++, y(11)-98, y(12), y(12)-98, y(12)-196, y(12)-98++, y(13)-98++, y(13)++, y(13), y(13)-98, y(13)-196
Precursor origin neutral loss: +

Peptide No.1046

STSQGSINSPVYSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of STSQGSINSPVYSR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 2383: 1595.740580 from(798.877566,2+)
Title: Elution from: 32.519 to 32.519 scan no 2446 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1595.7405
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 Expect: 1.5e-006

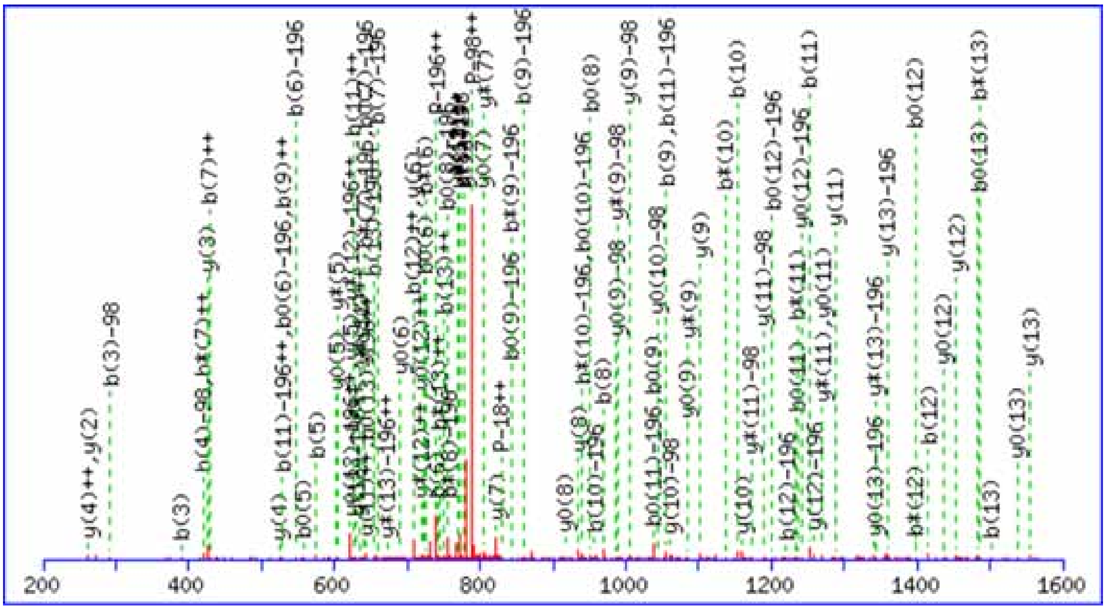
Matched b ions: b(3), b(4)-98, b(4), b(5), b(6), b(7), b(7)-98, b(8), b(9), b(9)-98, b(10)++, b(10), b(10)-98, b(11), b(11)-98, b(11)++, b(12), b(12)-98++, b(12)++, b(13), b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)++, y(10), y(11), y(11)++, y(12), y(12)-98, y(12)-98++, y(13), y(13)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.1047

STSQGSINSPVYSR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of STSQGSINSPVYSR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 4248: 1675.707852 from(838.861202,2+)
Title: Elution from: 35.493 to 35.493 scan no 2993 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1675.7068
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 **Expect:** 6.8e-006

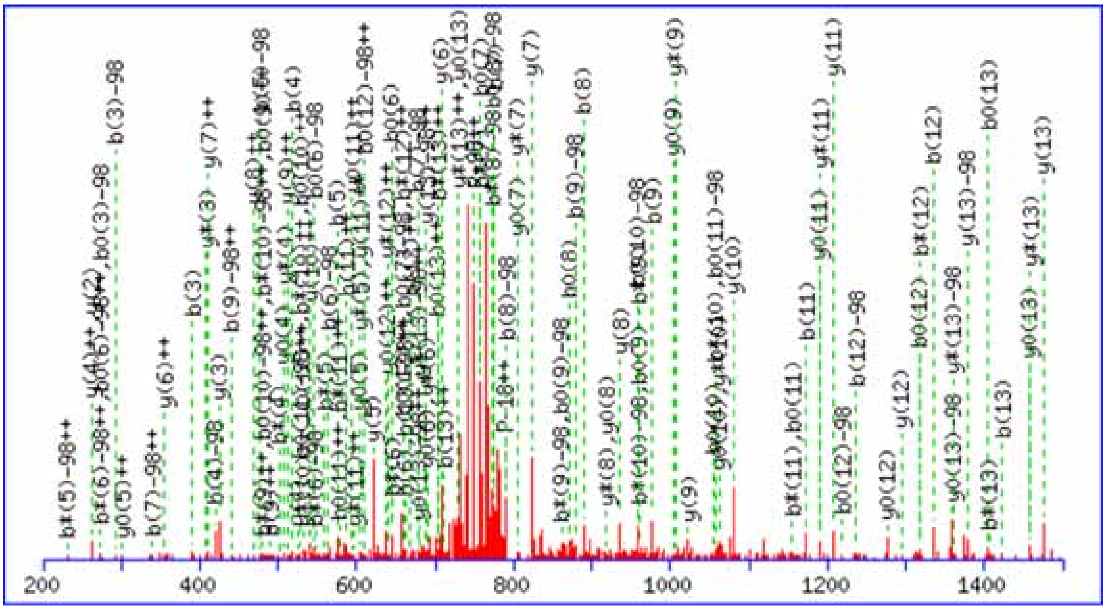
Matched b ions: b(3)-98, b(3), b(4)-98, b(5), b(6)-98, b(6)-196, b(6), b(7)-98, b(7)++, b(7)-196, b(8)-98, b(8), b(8)-196, b(9)++, b(9), b(9)-98, b(9)-196, b(10)-98++, b(10)-98, b(10)-196, b(10), b(11)-196++, b(11), b(11)-98, b(11)-196, b(11)++, b(12), b(12)++, b(12)-98, b(12)-196, b(12)-98++, b(13), b(13)-196++, b(13)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11)++, y(11)-98, y(11), y(12)-98, y(12)-196, y(12), y(12)-196++, y(13), y(13)-196, y(13)-98, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1048

STSQGSINSPVYSR
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of STSQGSINSPVYSR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 2604: 1595.741252 from(798.877902,2+)
Title: Elution from: 32.577 to 32.577 scan no 2457 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1595.7405
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 Expect: 0.0002

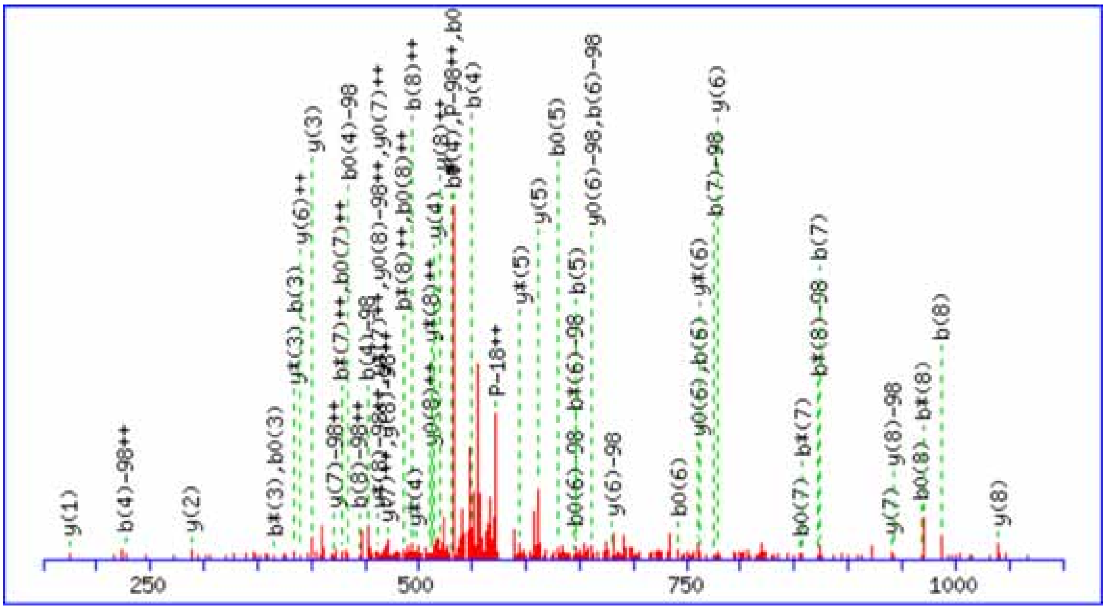
Matched b ions: b(3)-98, b(3), b(4), b(4)-98, b(5), b(5)-98, b(6)-98, b(6), b(7)-98++, b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)-98++, b(9)-98, b(9)++, b(11), b(11)++, b(12), b(12)-98, b(12)++, b(13), b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12), y(13), y(13)-98, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1049

SVKSPLLIR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of SVKSPLLIR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1548: 1159.736922 from(580.875737,2+)
Title: Elution from: 35.478 to 35.478 scan no 2991 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1159.7366
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K3 : Dimethyl:2H(4)13C(2) (K)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 Expect: 0.053

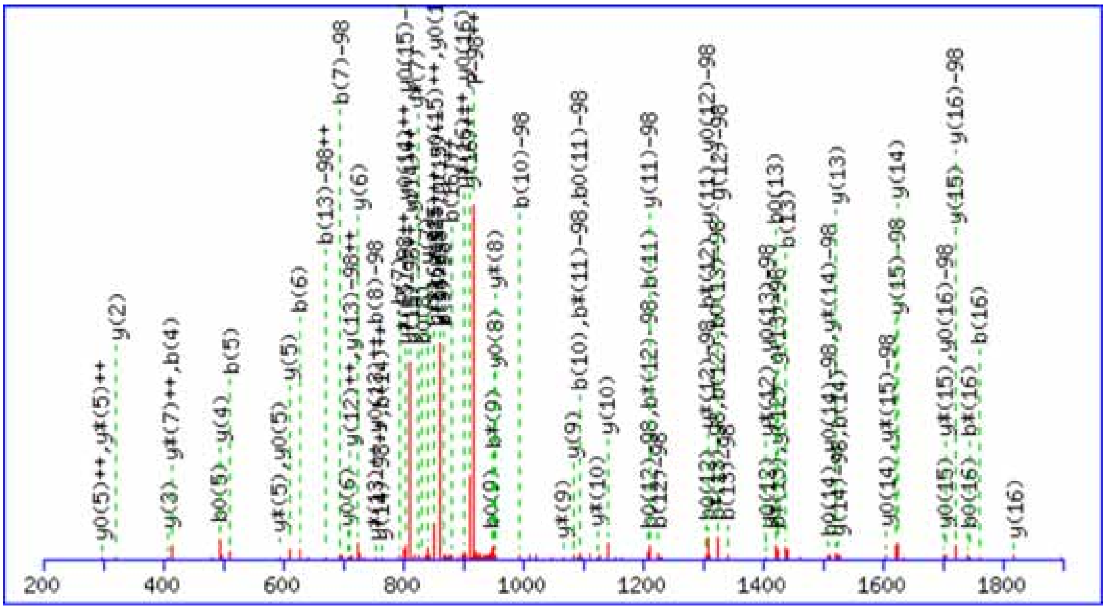
Matched b ions: b(3), b(4)-98, b(4)-98++, b(4), b(5), b(6), b(6)-98, b(7), b(7)-98, b(8), b(8)-98++, b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(6)-98, y(7), y(7)++, y(7)-98++, y(8), y(8)-98++, y(8)++, y(8)-98
Precursor origin neutral loss: +

Peptide No.1050

SVPTVDSGNEDDDSSFK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SVPTVDSGNEDDDSSFK
Found in IF2P_MOUSE, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 5289: 1933.782588 from(967.898570,2+)
Title: Elution from: 39.193 to 39.193 scan no 3558 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1933.7830
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K17 : Dimethyl (K)
Ions Score: 98 Expect: 5.1e-009

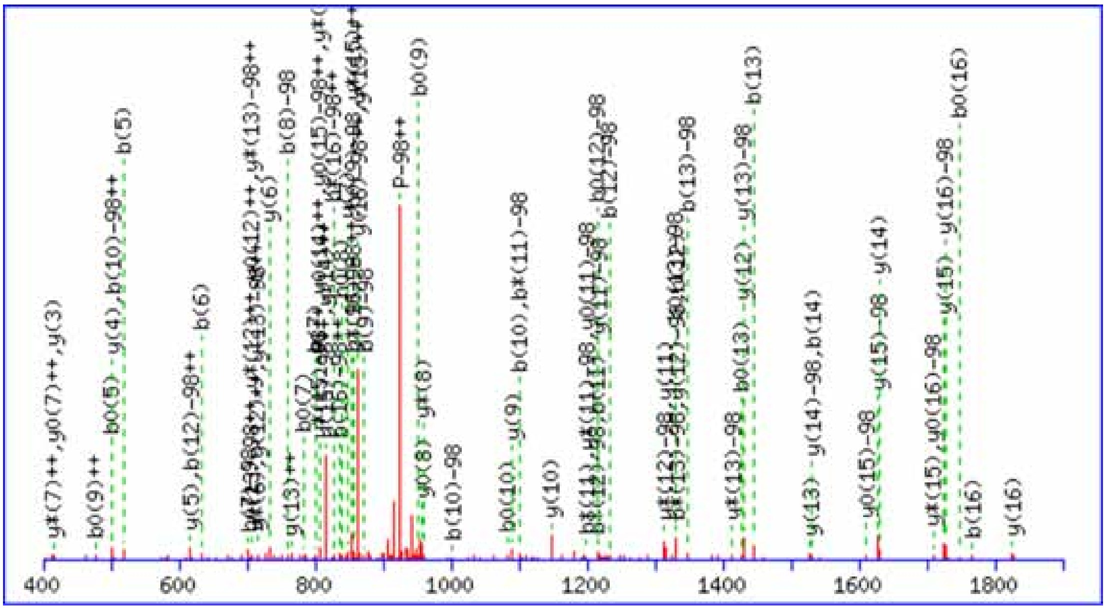
Matched b ions: b(4), b(5), b(6), b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(10), b(10)-98, b(11), b(12)-98, b(12), b(13), b(13)-98, b(13)-98++, b(14), b(14)++, b(16), b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11)-98, y(11), y(12)-98, y(12), y(12)++, y(13), y(13)-98, y(13)-98++, y(14), y(14)++, y(14)-98, y(14)-98++, y(15)++, y(15)-98++, y(15)-98, y(15), y(16)-98++, y(16)-98, y(16), y(16)++
Precursor origin neutral loss: +

Peptide No.1051

SVPTVDSGNEDDDSSFK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of SVPTVDSGNEDDDSSFK
Found in IF2P_MOUSE, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 4306: 1945.846922 from(973.930737,2+)
Title: Elution from: 39.070 to 39.070 scan no 3299 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1945.8466
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 82 Expect: 3.2e-007

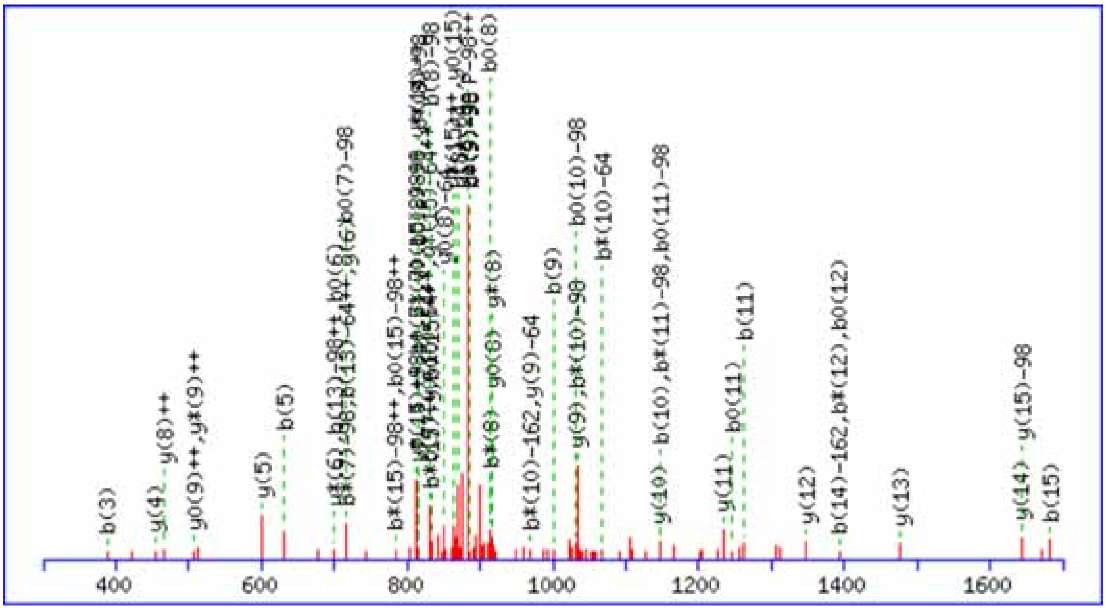
Matched b ions: b(5), b(6), b(7)-98, b(7), b(8)-98, b(9)-98, b(10)-98++, b(10), b(10)-98, b(11), b(12)-98++, b(12), b(12)-98, b(13), b(13)-98, b(14), b(16), b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11)-98, y(11), y(12)-98, y(12), y(12)++, y(13), y(13)++, y(13)-98, y(13)-98++, y(14)++, y(14), y(14)-98, y(15)++, y(15)-98, y(15), y(15)-98++, y(16)-98++, y(16), y(16)-98
Precursor origin neutral loss: +

Peptide No.1052

SVSENSLVAMDFSGEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of SVSENSLVAMDFSGEK
Found in GRB14_MOUSE, Growth factor receptor-bound protein 14 OS=Mus musculus GN=Grb14 PE=1 SV=1

Match to Query 3781: 1862.866420 from(932.440486,2+)
Title: Elution from: 48.409 to 48.409 scan no 4375 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1862.8645
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K16 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 47 **Expect:** 0.0011

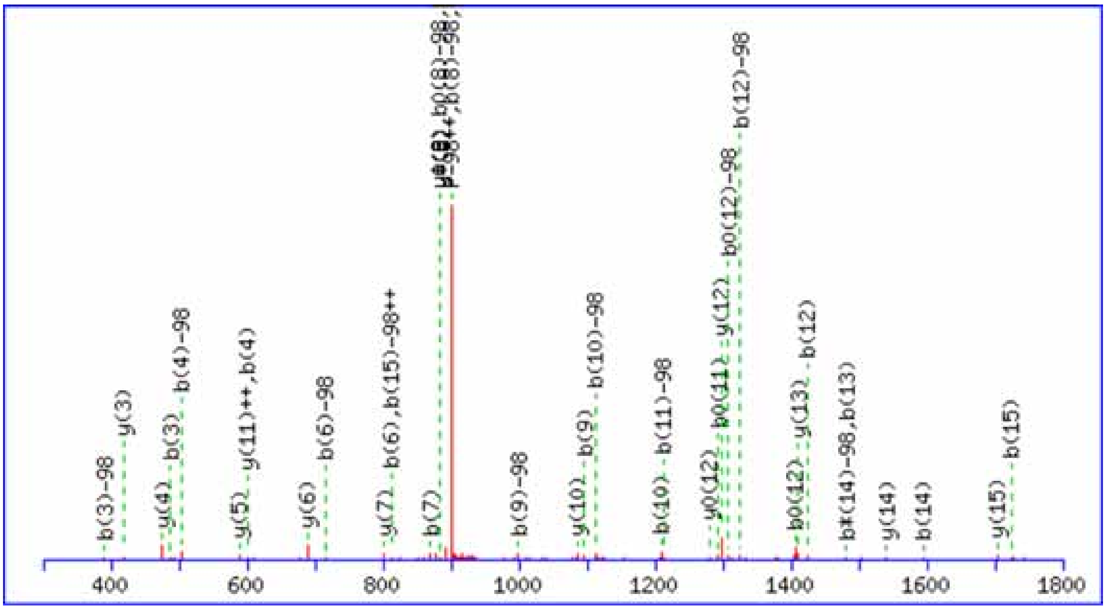
Matched b ions: b(3), b(5), b(7), b(8)-98, b(9), b(10), b(11), b(13)-98++, b(15)
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(9), y(10), y(11), y(12), y(13), y(14), y(15)-98
Precursor origin neutral loss: +

Peptide No.1053

SYELPDGQVITIGNER
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SYELPDGQVITIGNER
Found in ACTA_MOUSE, Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1

Match to Query 4384: 1897.882490 from(949.948521,2+)
Title: Elution from: 61.127 to 61.127 scan no 5803 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1897.8822
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 95 **Expect:** 2e-008

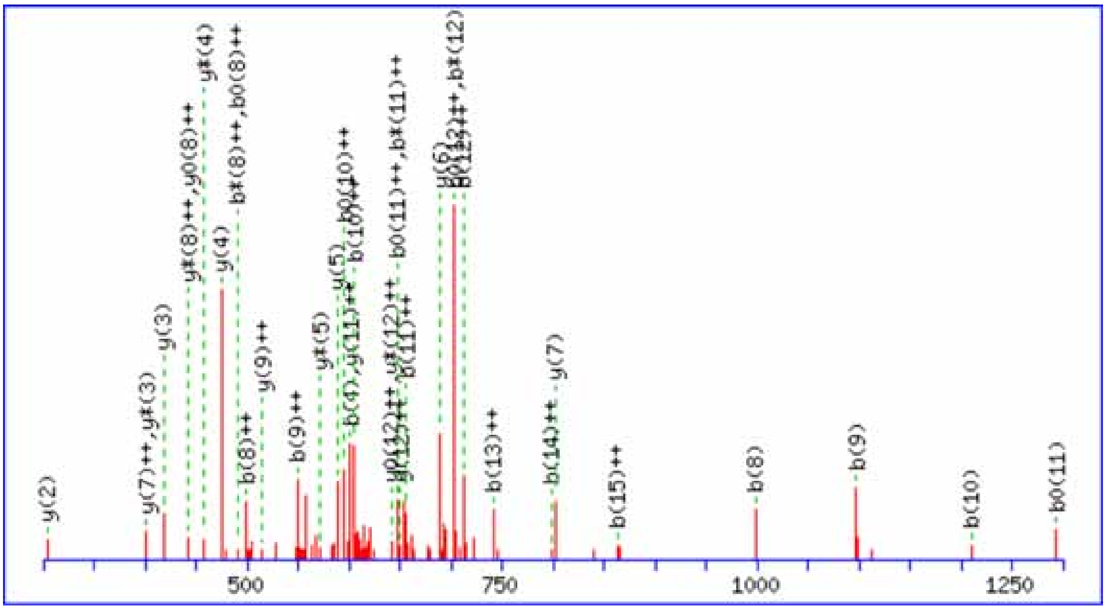
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(6)-98, b(6), b(7), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(12)-98, b(12), b(13), b(14), b(15), b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11)++, y(12), y(13), y(14), y(15)
Precursor origin neutral loss: +

Peptide No.1054

SYELPDGQVITIGNER
Confirmed sites:
Ambiguous sites: @S:1orY:2

MS/MS Fragmentation of **SYELPDGQVITIGNER**
Found in **ACTS_MOUSE**, Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1

Match to Query 4622: 1897.882113 from(633.634647,3+)
Title: Elution from: 61.063 to 61.063 scan no 5826 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1897.8822
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y2 : Phospho (Y)
Ions Score: 50 **Expect:** 0.00055

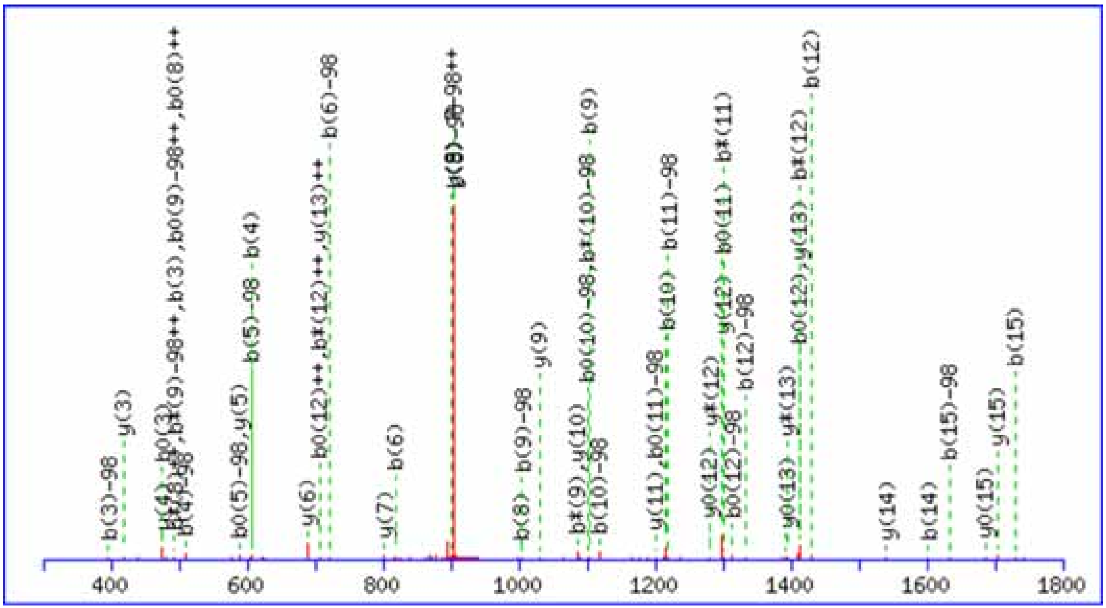
Matched b ions: b(4), b(8), b(8)++, b(9), b(9)++, b(10), b(10)++, b(11)++, b(12)++, b(13)++, b(14)++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(9)++, y(11)++, y(12)++
Precursor origin neutral loss: +

Peptide No.1055

SYELPDGQVITIGNER
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of SYELPDGQVITIGNER
Found in ACTA_MOUSE, Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1

Match to Query 3927: 1903.915538 from(952.965045,2+)
Title: Elution from: 61.151 to 61.151 scan no 5668 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1903.9141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 89 Expect: 8.1e-008

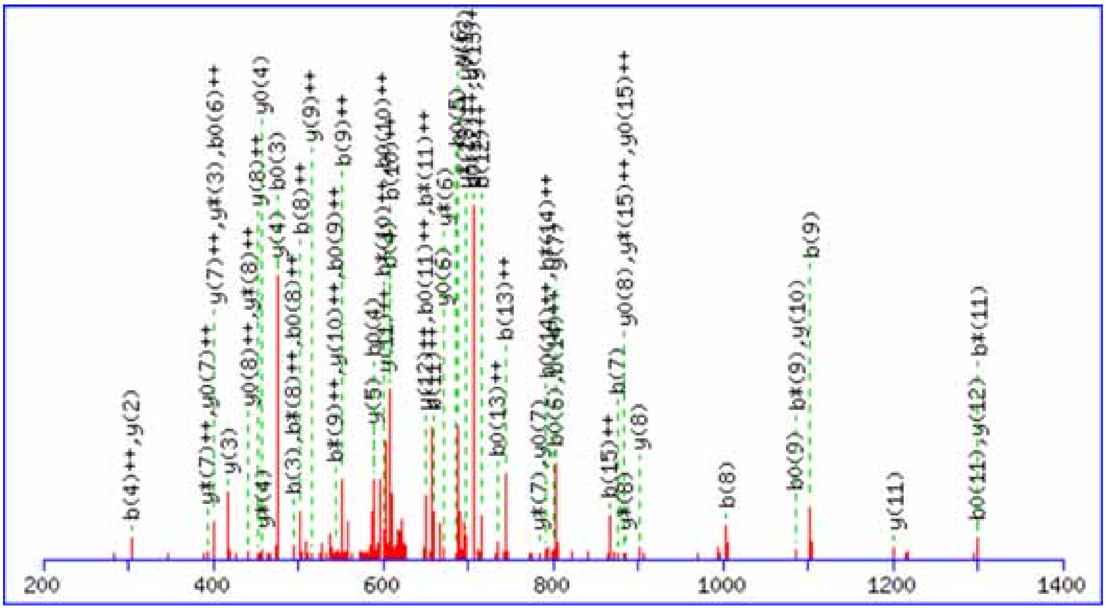
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(6)-98, b(6), b(8), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(12), b(12)-98, b(14), b(15)-98, b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)++, y(14), y(15)
Precursor origin neutral loss: +

Peptide No.1056

SYELPDGQVITIGNER
Confirmed sites:
Ambiguous sites: @S:1orY:2

MS/MS Fragmentation of **SYELPDGQVITIGNER**
Found in **ACTA_MOUSE**, Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1

Match to Query 4531: 1903.915716 from(635.645848,3+)
Title: Elution from: 61.041 to 61.041 scan no 5807 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1903.9141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y2 : Phospho (Y)
Ions Score: 61 Expect: 4.8e-005

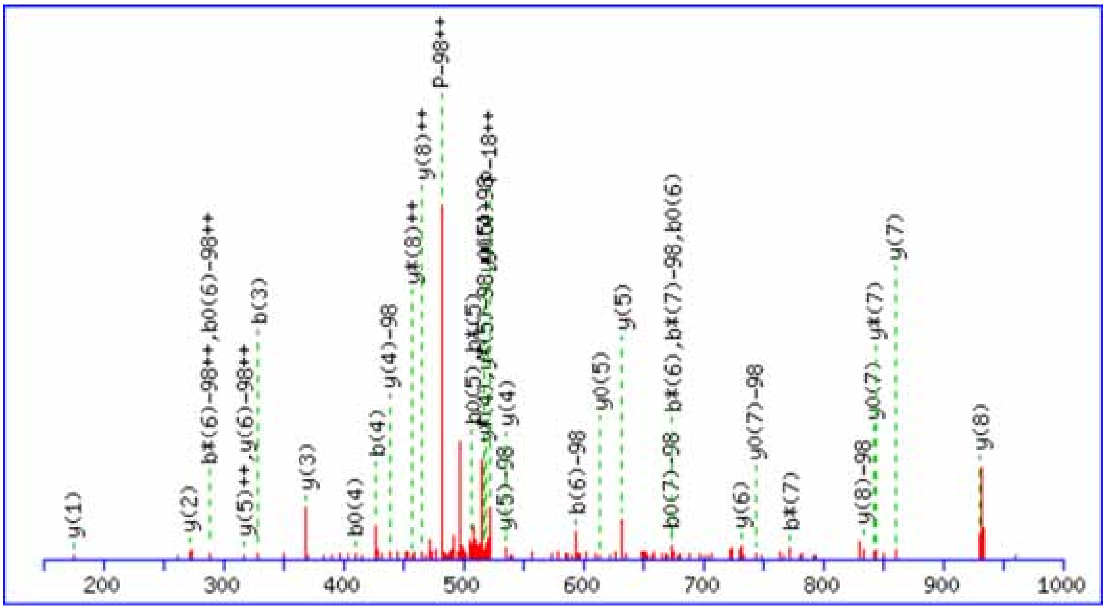
Matched b ions: b(3), b(4)++, b(4), b(7), b(8), b(8)++, b(9)++, b(9), b(10)++, b(11)++, b(12)++, b(13)++, b(14)++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.1057

TAQVPSPPR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of TAQVPSPPR
Found in ACINU_MOUSE, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=2

Match to Query 649: 1059.511204 from(530.762878,2+)
Title: Elution from: 29.972 to 29.972 scan no 2301 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1059.5114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 **Expect:** 0.0024

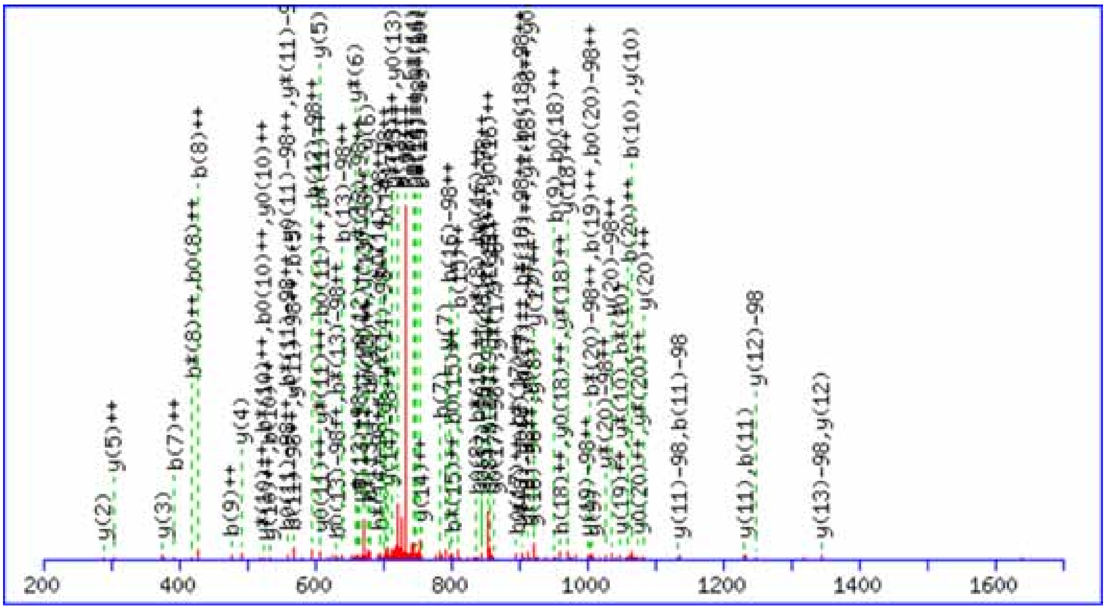
Matched b ions: b(3), b(4), b(6)-98
Matched y ions: y(1), y(2), y(3), y(4)-98, y(4), y(5), y(5)++, y(5)-98, y(6), y(6)-98++, y(7), y(8), y(8)-98, y(8)++
Precursor origin neutral loss: +

Peptide No.1058

TARPNSEAPLSGSEDADDSNK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of TARPNSEAPLSGSEDADDSNK
Found in IF2P_MOUSE, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 5951: 2295.987234 from(766.336354,3+)
Title: Elution from: 26.404 to 26.404 scan no 1637 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2295.9856
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K21 : Dimethyl (K)
Ions Score: 93 Expect: 2.9e-008

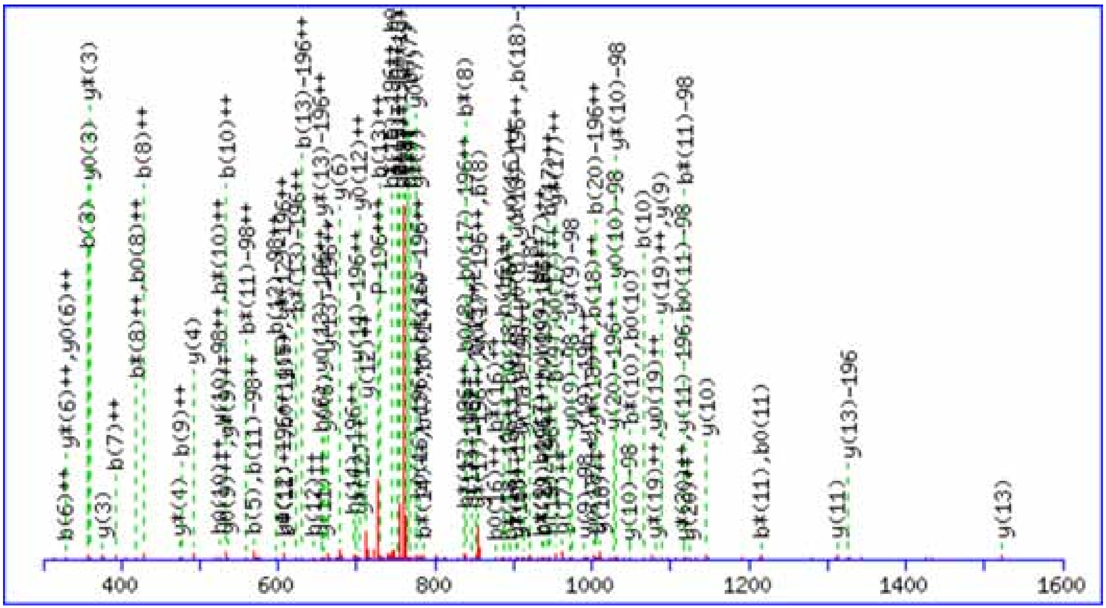
Matched b ions: b(5), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10), b(10)++, b(11)-98++, b(11), b(11)-98, b(12)-98++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(20)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11)-98++, y(11), y(11)-98, y(12)++, y(12), y(12)-98, y(13)-98++, y(13)-98, y(13)++, y(14)-98++, y(14)++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)++
Precursor origin neutral loss: +

Peptide No.1059

TARPNSEAPLSGSEDADDSNK
Confirmed sites: @S:11,@S:13
Ambiguous sites:

MS/MS Fragmentation of TARPNSEAPLSGSEDADDSNK
Found in IF2P_MOUSE, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 7246: 2375.953269 from(792.991699,3+)
Title: Elution from: 27.442 to 27.442 scan no 1953 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2375.9519
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K21 : Dimethyl (K)
Ions Score: 59 **Expect:** 5.2e-005

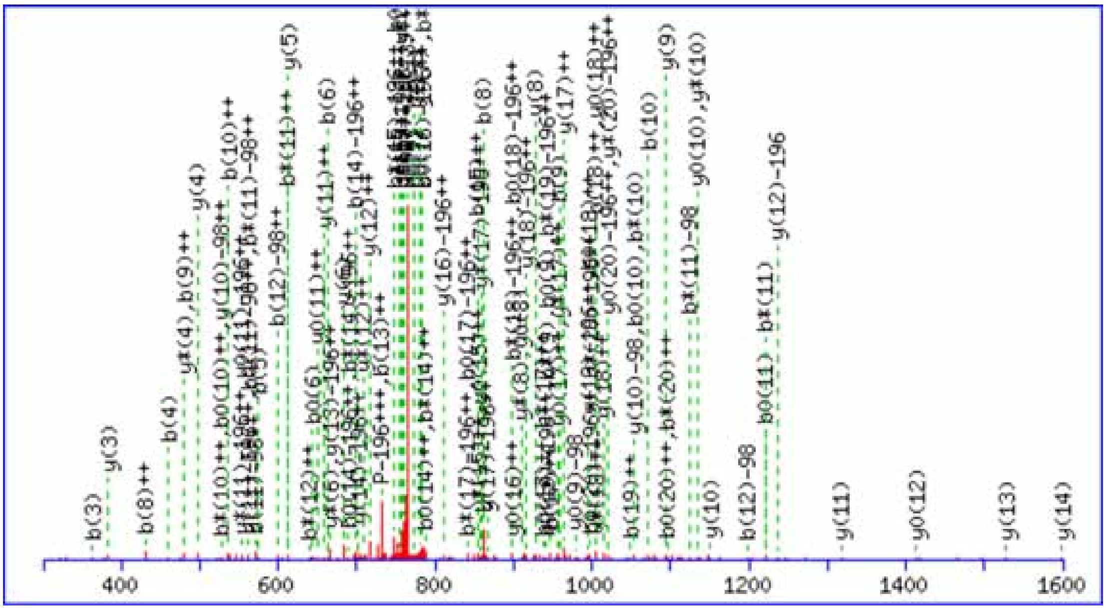
Matched b ions: b(3), b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)-196++, b(13)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(17)-196++, b(18)-98++, b(18)++, b(18)-196++, b(19)-196++, b(20)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9)-98, y(9), y(10), y(10)-98, y(10)-98++, y(11), y(11)-98, y(11)-196, y(11)-98++, y(11)++, y(12)++, y(12)-98, y(12)-98++, y(13)-98++, y(13)-98, y(13), y(13)-196, y(13)-196++, y(13)++, y(14)-196++, y(14)-98++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(18)-196++, y(19)-98++, y(19)-196++, y(19)++, y(20)-98++, y(20)++, y(20)-196++
Precursor origin neutral loss: +

Peptide No.1060

TARPNSEAPLSGSEDADDSNK
Confirmed sites: @S:11,@S:13
Ambiguous sites:

MS/MS Fragmentation of TARPNSEAPLSGSEDADDSNK
Found in IF2P_MOUSE, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 5747: 2388.017823 from(797.013217,3+)
Title: Elution from: 27.382 to 27.382 scan no 1801 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2388.0155
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K21 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 38 **Expect:** 0.011

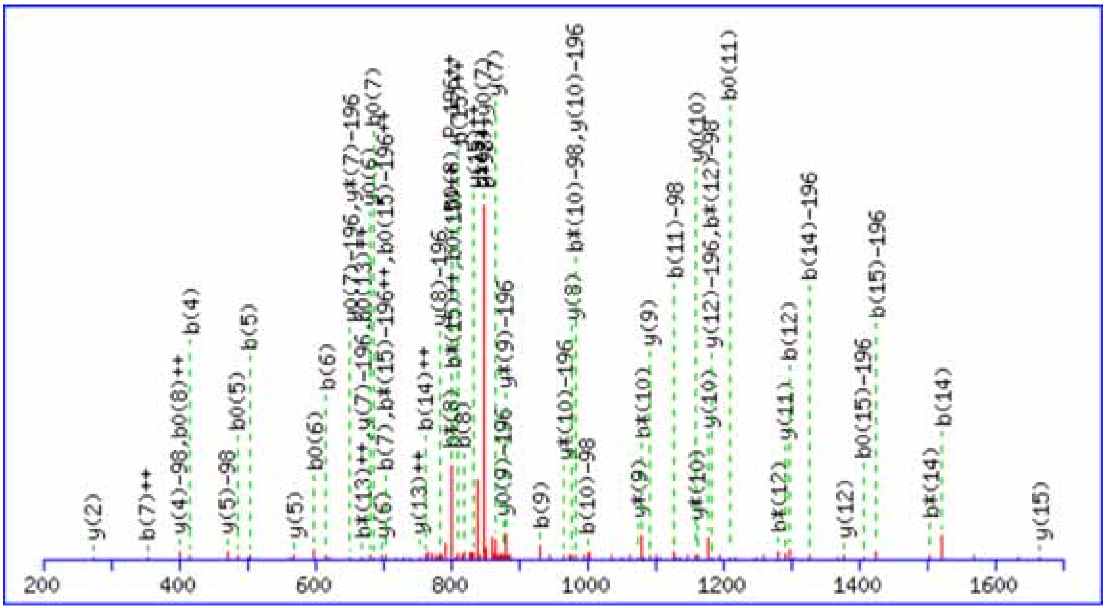
Matched b ions: b(3), b(4), b(5), b(6), b(8)++, b(8), b(9)++, b(9), b(10), b(10)++, b(11)-98++, b(12)-98, b(12)-98++, b(13)-98++, b(13)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(19)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(10)-98, y(10), y(10)-98++, y(11)-98, y(11)-196++, y(11), y(11)++, y(12)++, y(12)-98++, y(12)-196, y(13)-98++, y(13)++, y(13), y(13)-196++, y(14), y(14)-98++, y(14)-196++, y(16)-98++, y(16)-196++, y(17)++, y(17)-98++, y(17)-196++, y(18)-98++, y(18)++, y(18)-196++, y(19)-196++, y(19)-98++, y(20)-98++
Precursor origin neutral loss: +

Peptide No.1061

TASESISNLSEAGSVK
Confirmed sites: @S:10,@S:14
Ambiguous sites:

MS/MS Fragmentation of TASESISNLSEAGSVK
Found in CLIP1_MOUSE, CAP-Gly domain-containing linker protein 1 OS=Mus musculus GN=Clip1 PE=1 SV=1

Match to Query 4273: 1794.769182 from(898.391867,2+)
Title: Elution from: 39.815 to 39.815 scan no 3641 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1794.7689
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K16 : Dimethyl (K)
Ions Score: 50 Expect: 0.0004

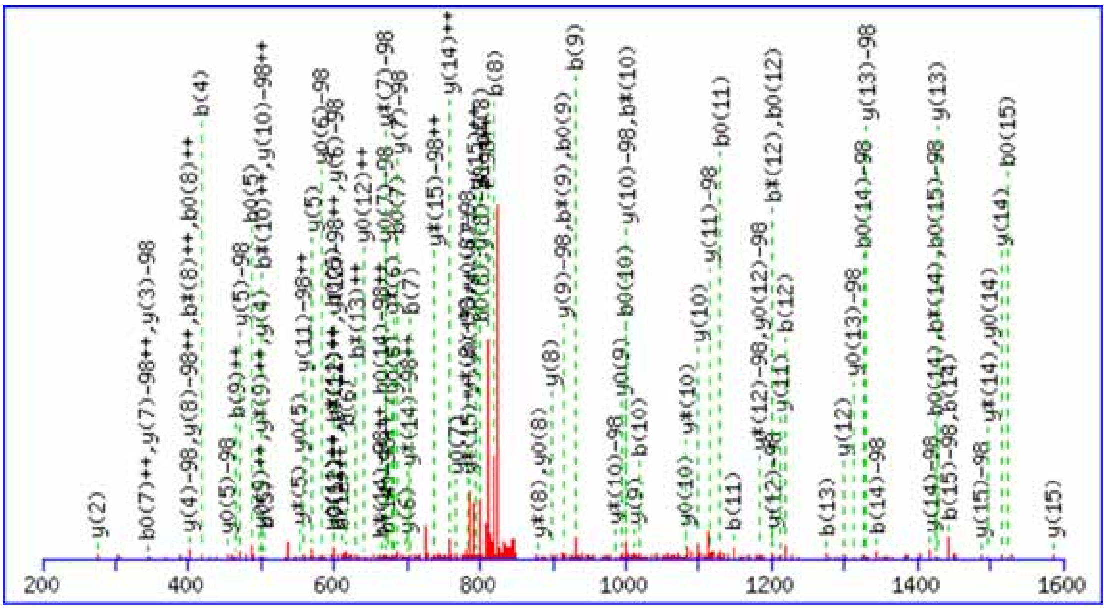
Matched b ions: b(4), b(5), b(6), b(7)++, b(7), b(8), b(9), b(10)-98, b(11)-98, b(12), b(14)-98, b(14), b(14)-196, b(14)++, b(15)-98, b(15)-196, b(15)-98++, b(15)++
Matched y ions: y(2), y(4)-98, y(5)-98, y(5), y(6), y(7)-98, y(7)-196, y(7), y(8)-98, y(8), y(8)-196, y(9), y(9)-98, y(10)-98, y(10), y(10)-196, y(11)-98, y(11), y(12)-98, y(12), y(12)-196, y(13)++, y(15), y(15)-98, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1062

TASESISNLSEAGSVK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of TASESISNLSEAGSVK
Found in CLIP1_MOUSE, CAP-Gly domain-containing linker protein 1 OS=Mus musculus GN=Clip1 PE=1 SV=1

Match to Query 3818: 1714.803526 from(858.409039,2+)
Title: Elution from: 38.340 to 38.340 scan no 3444 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1714.8026
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K16 : Dimethyl (K)
Ions Score: 71 Expect: 3.8e-006

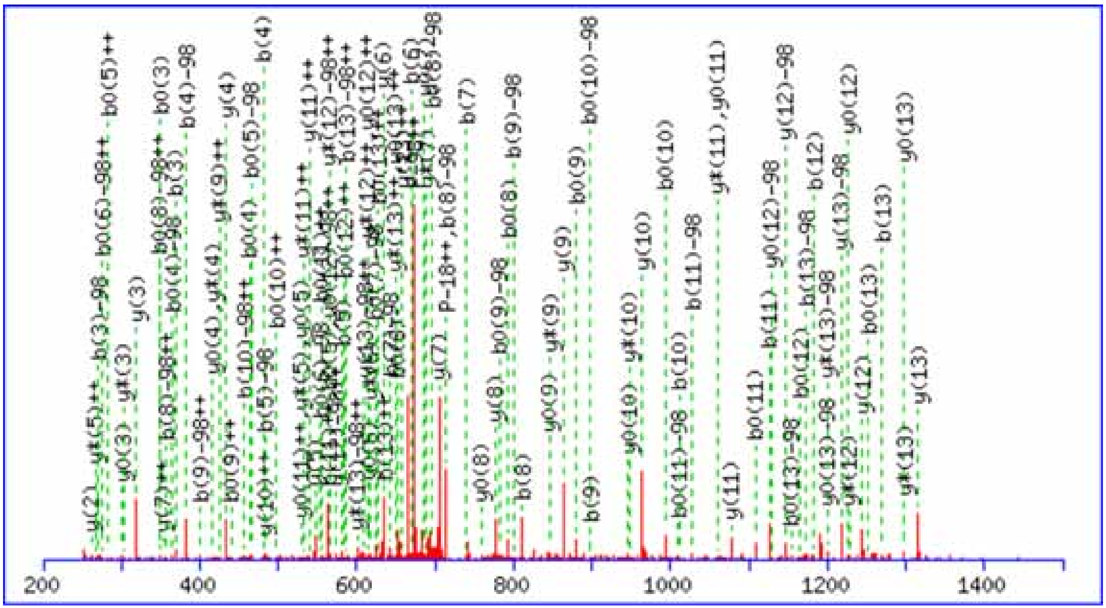
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(9)++, b(10), b(11), b(12), b(12)++, b(13), b(14)-98, b(14), b(14)-98++, b(15)-98
Matched y ions: y(2), y(3)-98, y(4)-98, y(4), y(5)-98, y(5), y(6)-98, y(6), y(7)-98, y(7)-98++, y(7), y(8)-98++, y(8)-98, y(8), y(9)-98, y(9), y(10)-98, y(10), y(10)-98++, y(11), y(11)-98++, y(11)-98, y(12), y(12)-98++, y(12)-98, y(13)-98, y(13), y(14), y(14)-98, y(14)++, y(15), y(15)-98, y(15)++
Precursor origin neutral loss: +

Peptide No.1063

TASLTSAASIDGSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2972: 1443.661080 from(722.837816,2+)
Title: Elution from: 37.215 to 37.215 scan no 3245 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1443.6606
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 80 Expect: 2.9e-007

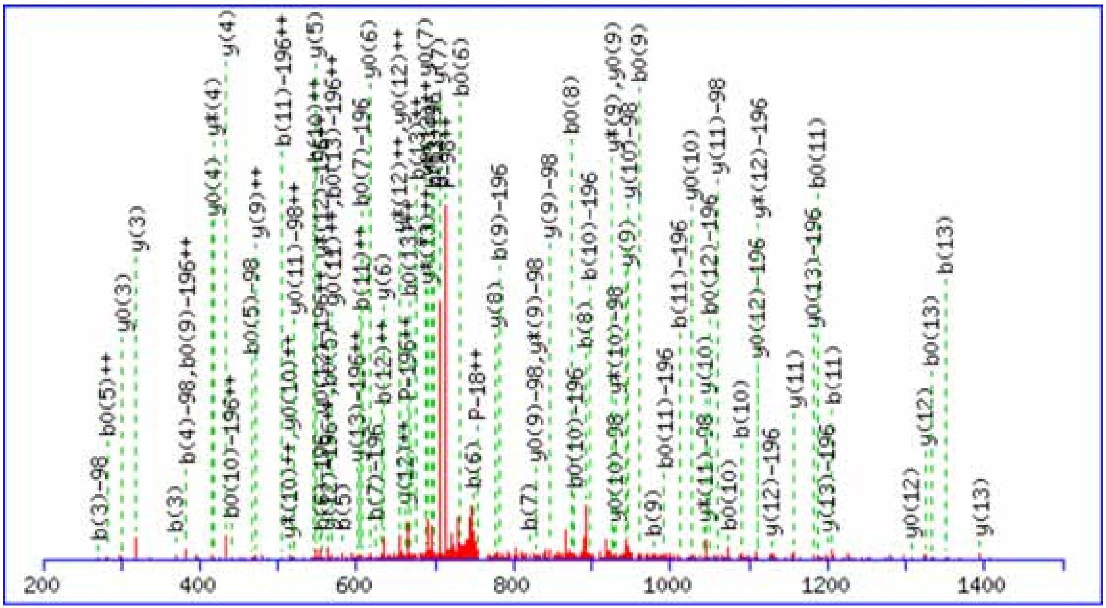
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(7)-98, b(7), b(8), b(8)-98, b(8)-98++, b(9)-98++, b(9)-98, b(9), b(10)-98++, b(10), b(11), b(11)++, b(11)-98, b(12), b(13)-98, b(13), b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)-98, y(12)-98++, y(13)-98, y(13), y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1064

TASLTSAASIDGSR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3368: 1523.627988 from(762.821270,2+)
Title: Elution from: 40.458 to 40.458 scan no 3703 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1523.6270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 Expect: 8e-006

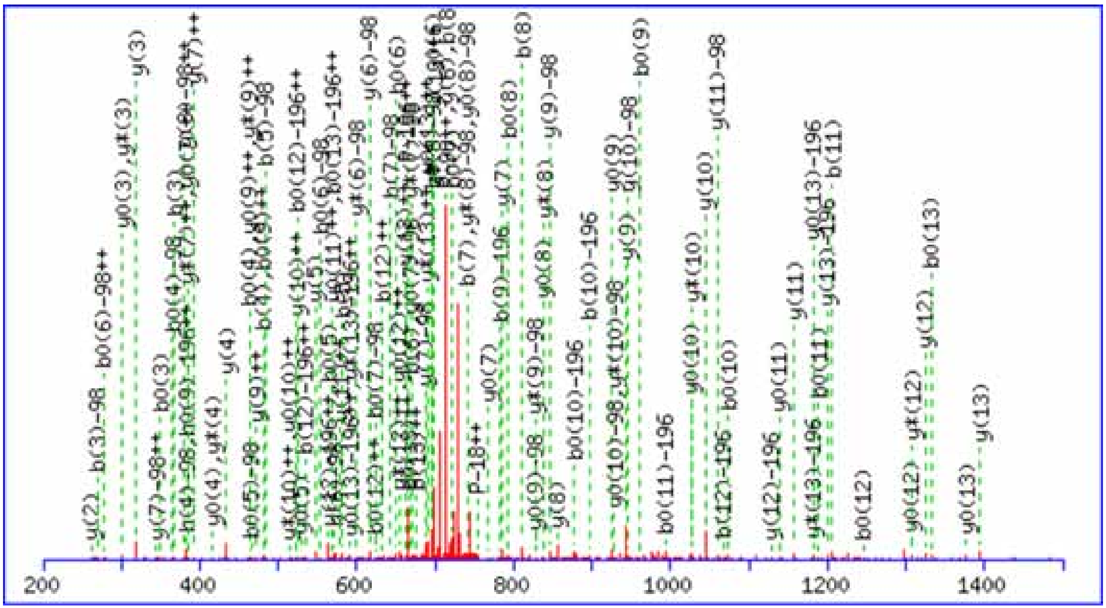
Matched b ions: b(3), b(3)-98, b(4)-98, b(5), b(6)-196, b(6), b(6)-98, b(7)-196, b(7)-98, b(7), b(8), b(8)-98, b(8)-98++, b(8)-196, b(9), b(9)-98++, b(9)-196, b(9)-98, b(10)-98, b(10), b(10)++, b(10)-196, b(11), b(11)-98, b(11)-196++, b(11)-98++, b(11)++, b(11)-196, b(12)++, b(12)-98, b(13), b(13)-98++, b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(9)++, y(10), y(10)-98, y(11), y(11)-98, y(12)-196++, y(12), y(12)-98, y(12)-196, y(12)-98++, y(12)++, y(13), y(13)-98, y(13)-196, y(13)-196++, y(13)++
Precursor origin neutral loss: +

Peptide No.1065

TASLTSAASIDGSR
Confirmed sites: @S:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 1966: 1523.628504 from(762.821528,2+)
Title: Elution from: 37.940 to 37.940 scan no 3178 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1523.6270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 95 Expect: 6.8e-009

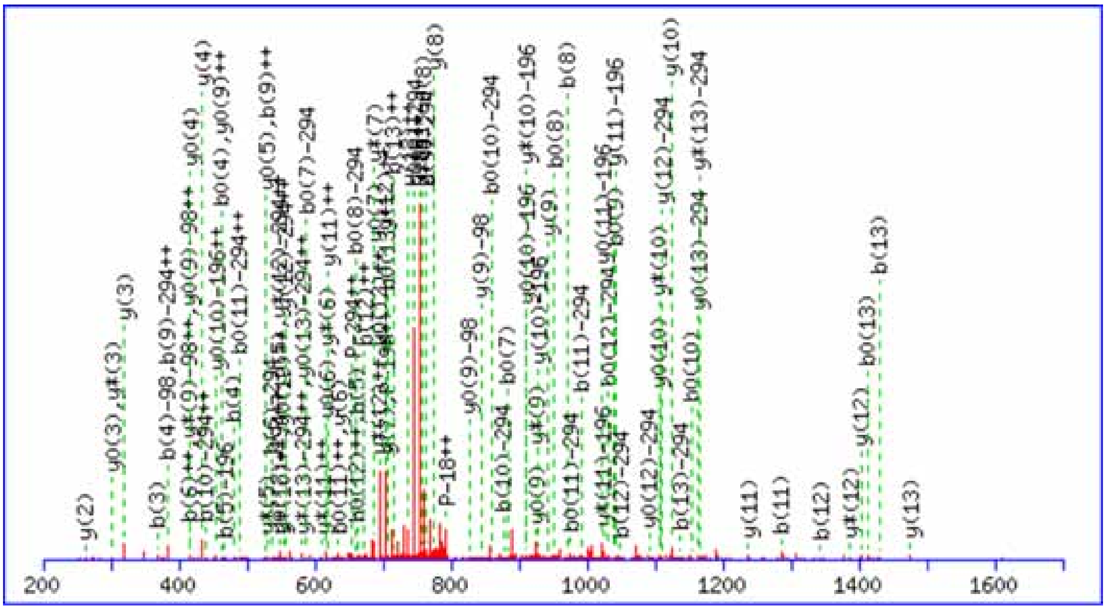
Matched b ions: b(3), b(3)-98, b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9)-196, b(10)-98, b(10)-196, b(11), b(11)-98, b(12)-196, b(12)-196++, b(12)++, b(13)-98++, b(13)++, b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)++, y(7)-98++, y(7)-98, y(8), y(8)-98++, y(9), y(9)-98, y(9)++, y(10), y(10)++, y(10)-98, y(11), y(11)++, y(11)-98, y(12)-196++, y(12)-98, y(12), y(12)-196, y(12)-98++, y(12)++, y(13)-98, y(13), y(13)-196, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1066

TASLTSAASIDGSR
Confirmed sites: @S:3,@T:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2056: 1603.594446 from(802.804499,2+)
Title: Elution from: 40.665 to 40.665 scan no 3451 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1603.5933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.0042

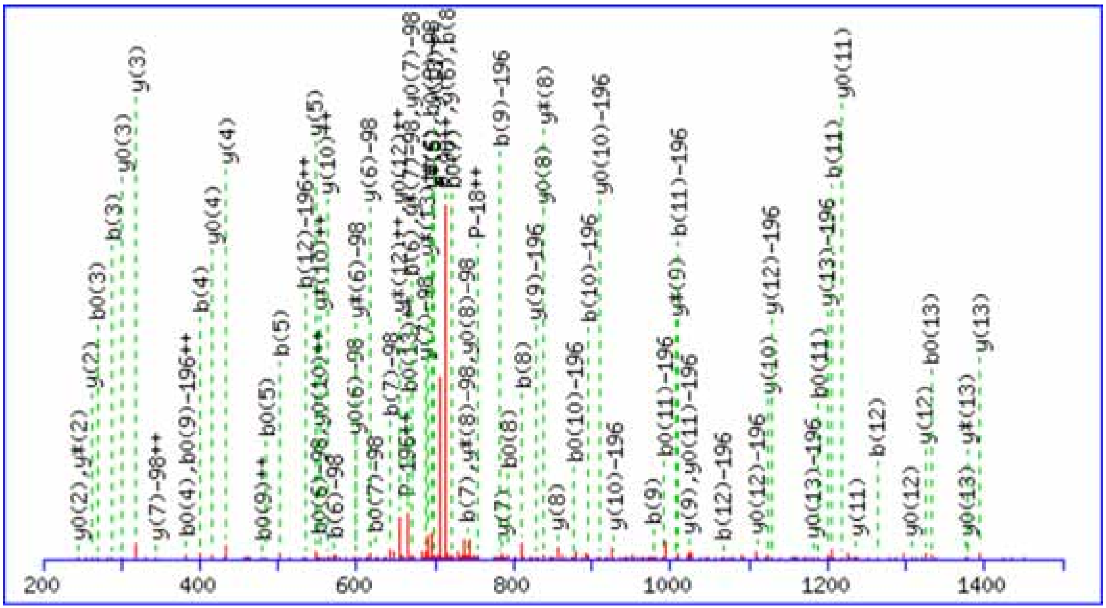
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5)-196, b(5), b(6)-196, b(6)-98, b(6)++, b(6)-294, b(7)-196, b(8)-98, b(8)-196, b(8), b(9)-294++, b(9)++, b(9)-98, b(9)-98++, b(9)-294, b(10)-98, b(10)-294++, b(10)-196, b(10)-196++, b(10)-294, b(11)-98, b(11), b(11)-196, b(11)-196++, b(11)-294, b(12), b(12)++, b(12)-294, b(13)-98, b(13), b(13)-98++, b(13)++, b(13)-294
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98, y(9), y(10), y(10)-196, y(10)-98, y(11), y(11)++, y(11)-196, y(11)-98, y(12), y(12)-98, y(12)-294++, y(12)-98++, y(12)++, y(12)-294, y(13), y(13)-98, y(13)-196, y(13)-196++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1067

TASLTSAASIDGSR
Confirmed sites: @S:6,@S:9
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2642: 1523.627214 from(762.820883,2+)
Title: Elution from: 40.013 to 40.013 scan no 3667 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1523.6270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 **Expect:** 9.5e-008

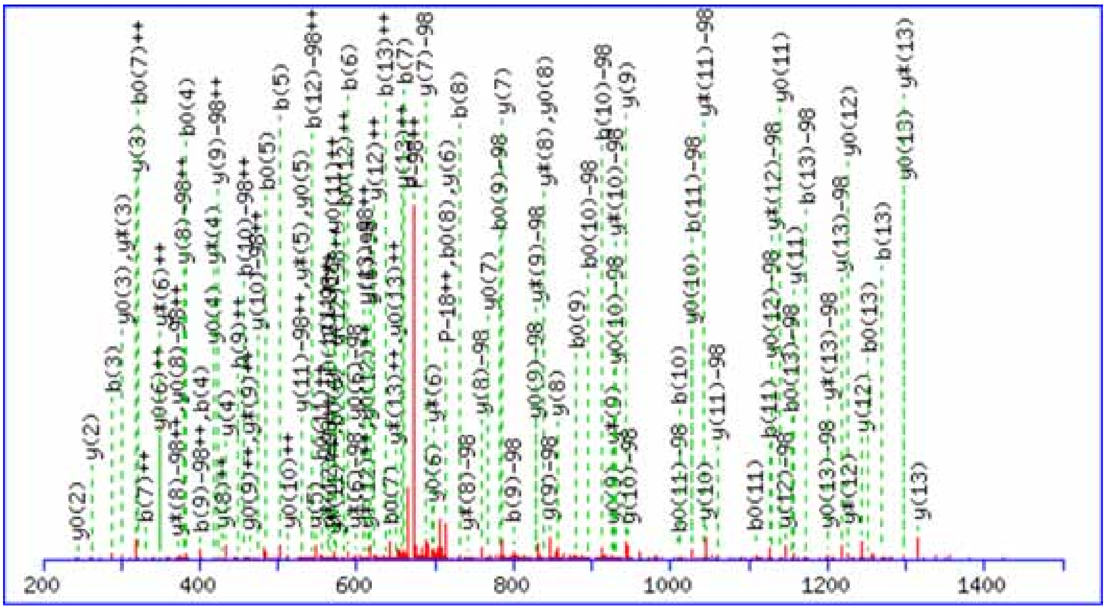
Matched b ions: b(3), b(4), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9)-196, b(9), b(10)-98, b(10)-196, b(11)-98, b(11), b(11)-196, b(12), b(12)-196++, b(12)-196, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)-98++, y(7)-98, y(8), y(9)-98, y(9), y(9)-98++, y(9)-196, y(10), y(10)-98, y(10)-98++, y(10)-196, y(10)++, y(11), y(11)-98++, y(11)-98, y(12)-98, y(12), y(12)-196, y(12)-98++, y(13)-98, y(13), y(13)-196, y(13)++
Precursor origin neutral loss: +

Peptide No.1068

TASLTSAASIDGSR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2973: 1443.661278 from(722.837915,2+)
Title: Elution from: 35.312 to 35.312 scan no 2967 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1443.6606
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 86 Expect: 7.7e-008

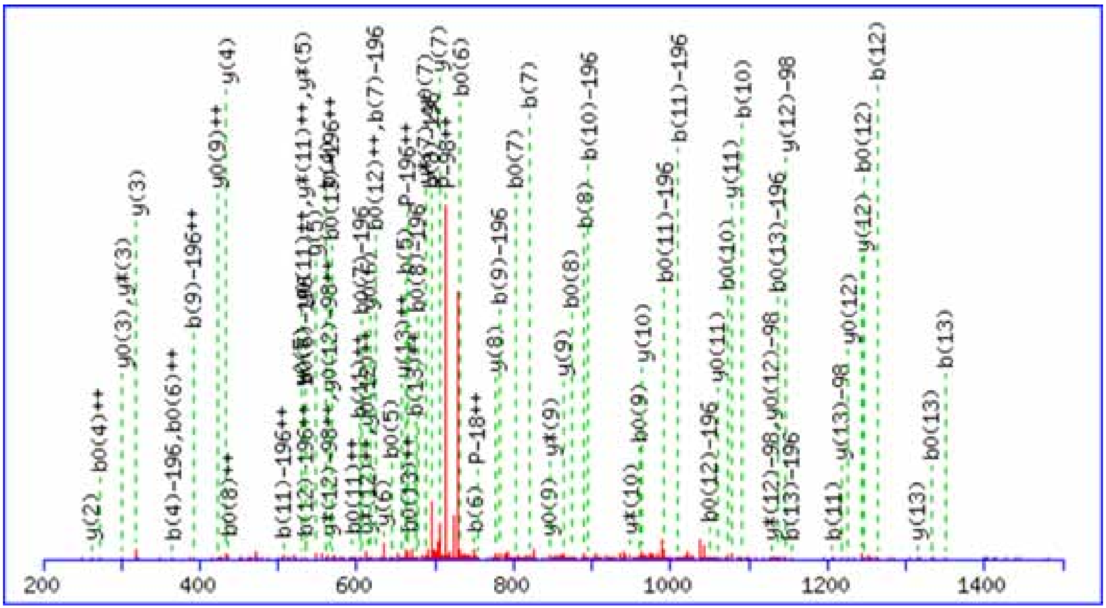
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(8), b(9)-98++, b(9)-98, b(9)++, b(10)-98, b(10)-98++, b(10), b(11), b(11)-98, b(11)++, b(12)-98++, b(13)++, b(13)-98, b(13)
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(8)++, y(8)-98++, y(9)-98, y(9), y(9)-98++, y(10), y(10)-98, y(10)-98++, y(11)-98, y(11), y(11)-98++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13), y(13)-98, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1069

TASLTSAASIDGSR
Confirmed sites: @T:1,@S:3
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3365: 1523.627438 from(762.820995,2+)
Title: Elution from: 41.329 to 41.329 scan no 3825 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1523.6270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.009

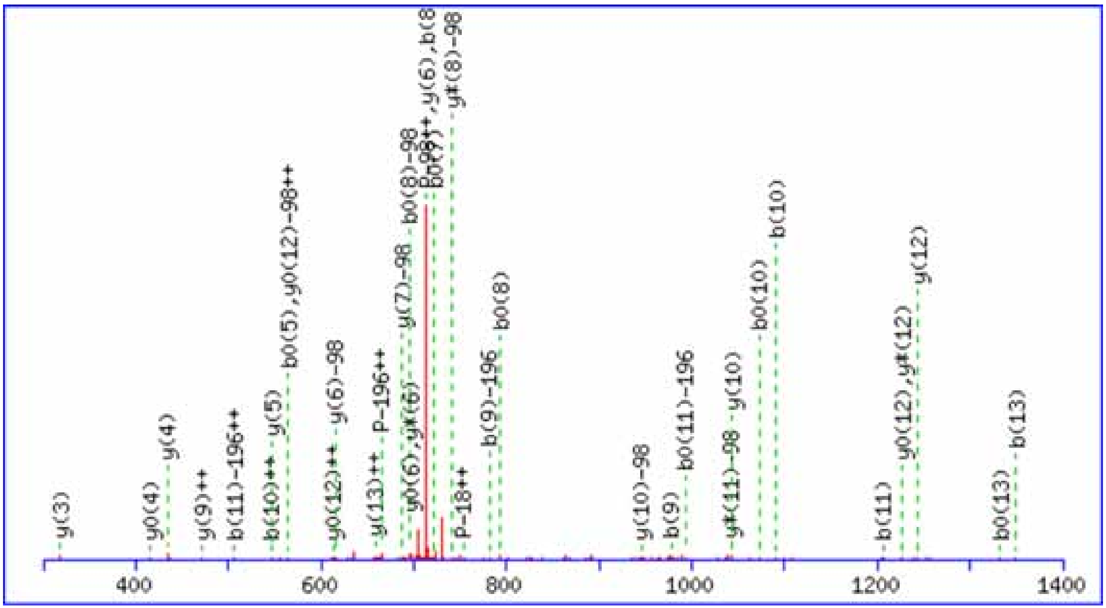
Matched b ions: b(3)-98, b(4)-196, b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)-196, b(7)-98, b(7), b(8)-98, b(8), b(8)-196, b(9)-196++, b(9)-196, b(9)-98, b(10)-196, b(10)-98, b(10), b(11), b(11)-98++, b(11)-196++, b(11)++, b(11)-196, b(11)-98, b(12), b(12)-196++, b(12)-98++, b(13)-98, b(13), b(13)-196, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98, y(13)-98, y(13)++, y(13)
Precursor origin neutral loss: +

Peptide No.1070

TASLTSAASIDGSR
Confirmed sites: @T:1,@S:9
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2646: 1523.627756 from(762.821154,2+)
Title: Elution from: 41.578 to 41.578 scan no 3874 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1523.6270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.011

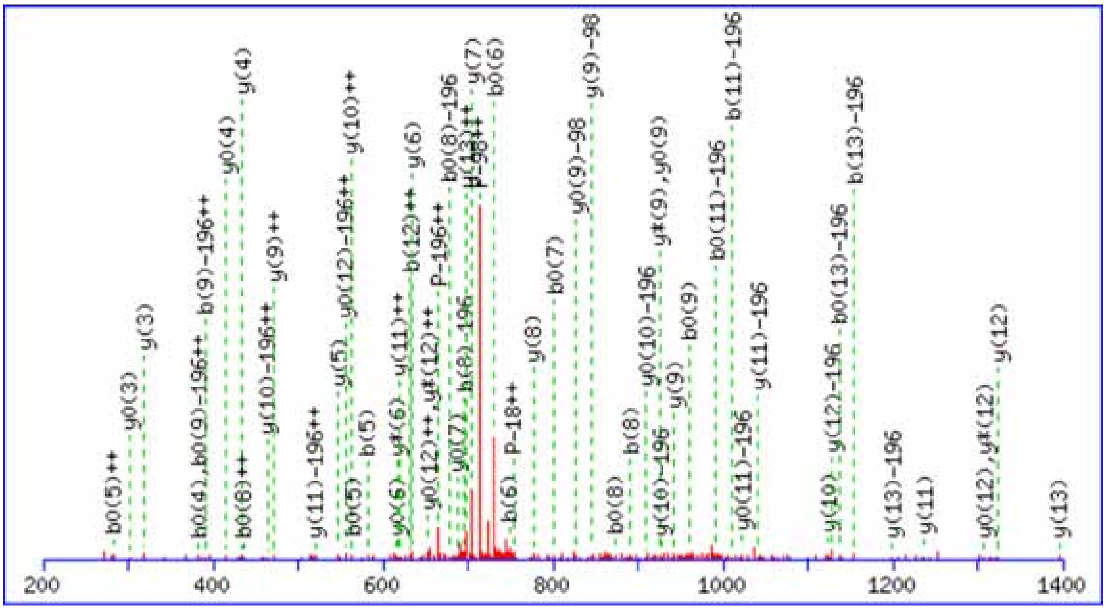
Matched b ions: b(8)-98, b(9)-196, b(9), b(10)-98, b(10), b(10)++, b(11), b(11)-98, b(11)-196++, b(11)-98++, b(13), b(13)-98
Matched y ions: y(3), y(4), y(5), y(6), y(6)-98, y(7)-98, y(9)++, y(10), y(10)-98, y(12), y(13)++
Precursor origin neutral loss: +

Peptide No.1071

TASLTSAASIDGSR
Confirmed sites: @T:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2645: 1523.627698 from(762.821125,2+)
Title: Elution from: 41.263 to 41.263 scan no 3832 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1523.6270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.012

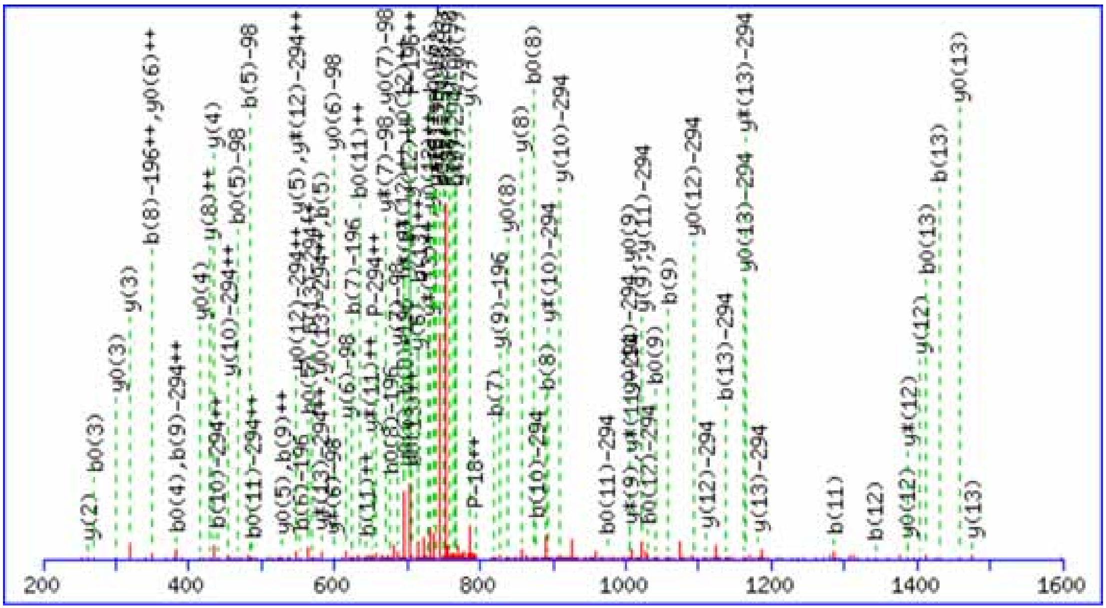
Matched b ions: b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(8)-196, b(8), b(9)-98, b(9)-196++, b(10)-98, b(11)-98++, b(11)-98, b(11)-196, b(12)++, b(13)-98, b(13)-196, b(13)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(9)-98, y(10)-98++, y(10), y(10)-196++, y(10)++, y(10)-196, y(11)-196++, y(11), y(11)++, y(11)-196, y(12)-196, y(12), y(12)-98, y(12)-98++, y(13), y(13)-196, y(13)++
Precursor origin neutral loss: +

Peptide No.1072

TASLTSAASIDGSR
Confirmed sites: @T:5,@S:6,@S:9
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2681: 1603.593660 from(802.804106,2+)
Title: Elution from: 40.828 to 40.828 scan no 3616 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1603.5933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0025

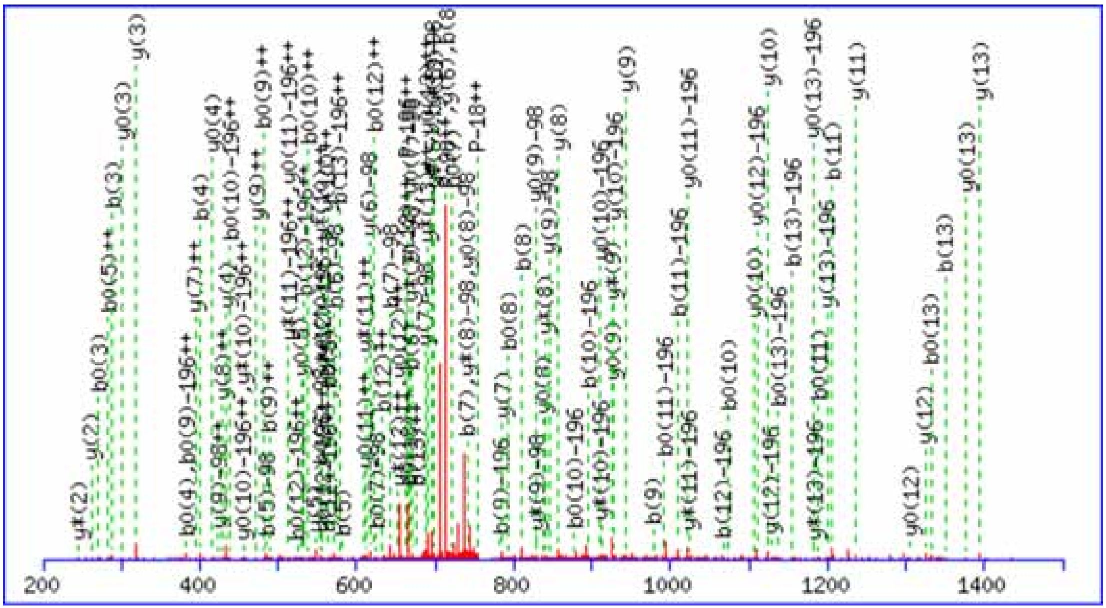
Matched b ions: b(5), b(5)-98, b(6)-98, b(6)-196, b(6), b(7)-98, b(7)-196, b(7), b(8), b(8)-196++, b(8)-196, b(8)-98, b(9)-294++, b(9)-98++, b(9)-98, b(9)-196, b(9)++, b(9)-294, b(9), b(10)-98, b(10)-294++, b(10)-196++, b(10)-196, b(10)-98++, b(10)-294, b(11)-98, b(11), b(11)-196, b(11)-196++, b(11)++, b(12)-98, b(12), b(12)-98++, b(12)-196, b(13), b(13)-294++, b(13)++, b(13)-294, b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)++, y(8)-98, y(9), y(9)-98, y(9)-196, y(10)-294++, y(10)-196, y(10)-294, y(10)-98, y(10)-98++, y(11)-294, y(11)-196, y(12)-98, y(12), y(12)-196, y(12)-98++, y(12)++, y(12)-294, y(13), y(13)-98, y(13)-196, y(13)-196++, y(13)-98++, y(13)++, y(13)-294
Precursor origin neutral loss: +

Peptide No.1073

TASLTSAASIDGSR
Confirmed sites: @T:5,@S:9
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 1965: 1523.628340 from(762.821446,2+)
Title: Elution from: 39.753 to 39.753 scan no 3421 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1523.6270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 73 Expect: 1.1e-006

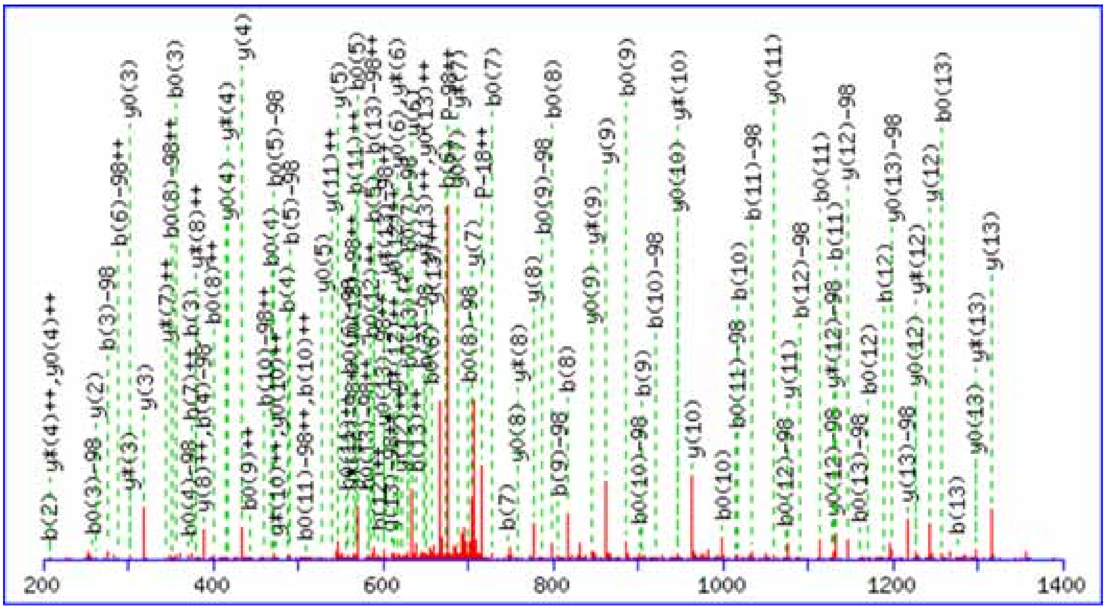
Matched b ions: b(3), b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9)++, b(9)-196, b(9), b(10)-98, b(10)-196, b(11)-98, b(11), b(11)-98++, b(11)-196, b(12)-196++, b(12)++, b(12)-196, b(12)-98, b(13), b(13)-196, b(13)-98, b(13)-196++, b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)++, y(7)-98, y(8), y(8)++, y(9)++, y(9), y(9)-98++, y(9)-98, y(10), y(10)-98, y(10)++, y(10)-196, y(11), y(11)-98, y(12)-98, y(12), y(12)-196, y(12)-196++, y(12)-98++, y(12)++, y(13)-98, y(13), y(13)-98++, y(13)++, y(13)-196
Precursor origin neutral loss: +

Peptide No.1074

TASLTSAASIDGSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2993: 1449.692724 from(725.853638,2+)
Title: Elution from: 37.210 to 37.210 scan no 3244 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1449.6924
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 **Expect:** 4.8e-007

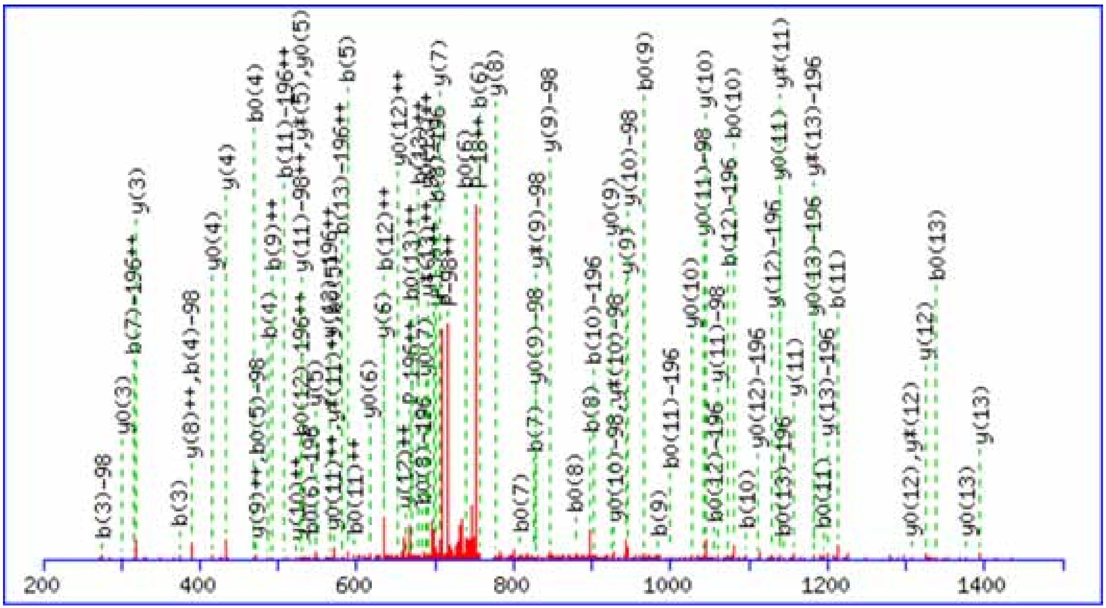
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98++, b(6), b(7)++, b(7)-98, b(7), b(8), b(9)-98, b(9), b(10), b(10)-98++, b(10)++, b(10)-98, b(11), b(11)-98, b(11)++, b(12), b(12)++, b(12)-98, b(13)-98++, b(13)++, b(13)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(11), y(11)++, y(12)-98, y(12), y(12)++, y(13)-98, y(13), y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1075

TASLTSAASIDGSR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2321: 1529.658974 from(765.836763,2+)
Title: Elution from: 40.410 to 40.410 scan no 3531 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1529.6588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.0011

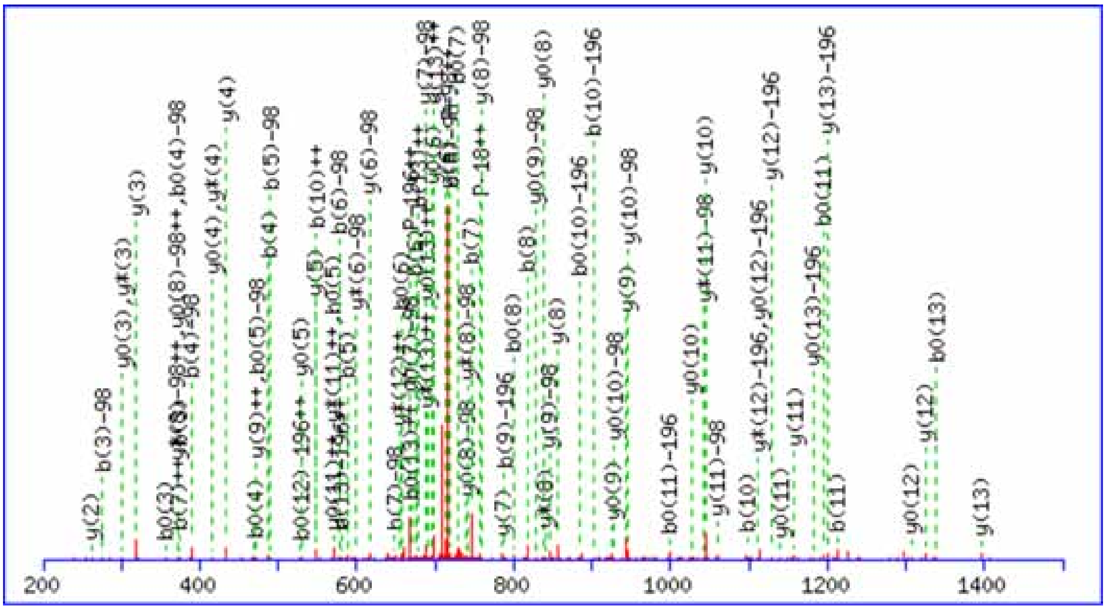
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5), b(6)-98, b(6), b(7)-196++, b(7)-98, b(7), b(8)-98, b(8), b(8)-196, b(9)++, b(9)-98, b(9), b(10), b(10)-196, b(10)-98, b(11), b(11)-98, b(11)-196++, b(12)-196, b(12)++, b(12)-98, b(13)-98++, b(13)-196++, b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)-98, y(9), y(9)++, y(10), y(10)-98, y(10)++, y(11), y(11)-98++, y(11)-98, y(12), y(12)-98, y(12)-196, y(12)-196++, y(12)-98++, y(12)++, y(13), y(13)-196, y(13)-98, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1076

TASLTSAASIDGSR
Confirmed sites: @S:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 1803: 1529.660082 from(765.837317,2+)
Title: Elution from: 37.906 to 37.906 scan no 3077 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1529.6588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 76 Expect: 7.2e-007

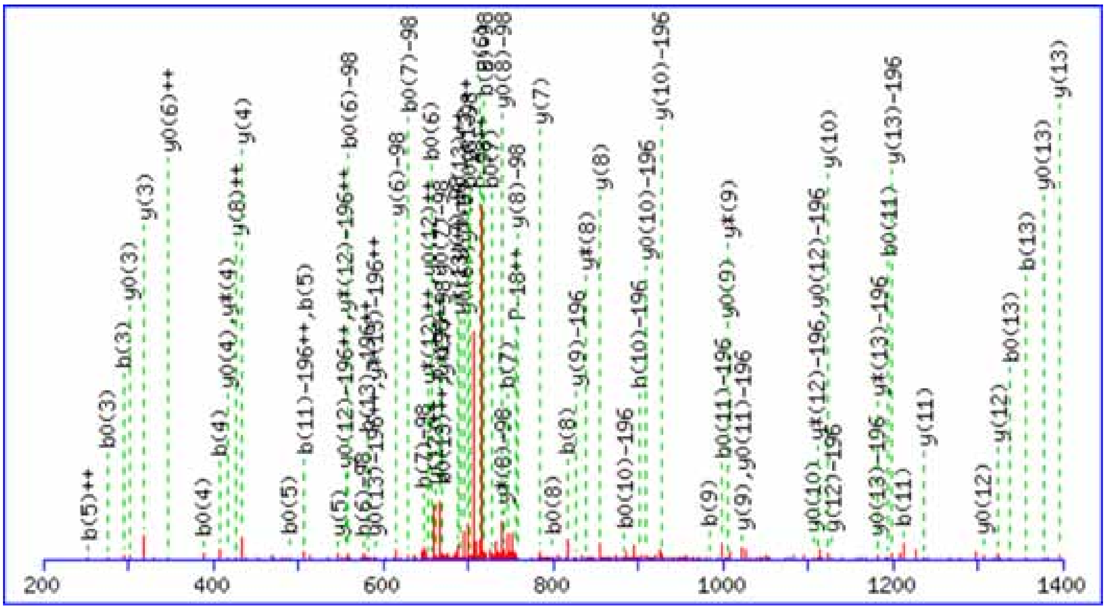
Matched b ions: b(3)-98, b(3), b(4), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)++, b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(9)-196, b(10)-98, b(10)-196, b(10)++, b(10), b(11), b(11)-98, b(13)-196++, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(9)++, y(10), y(10)-98, y(11)-98, y(11), y(12)-98, y(12), y(12)-98++, y(12)-196, y(13)-98, y(13), y(13)-196, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1077

TASLTSAASIDGSR
Confirmed sites: @S:6,@S:9
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2115: 1529.659342 from(765.836947,2+)
Title: Elution from: 39.619 to 39.619 scan no 3367 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1529.6588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 Expect: 3.4e-005

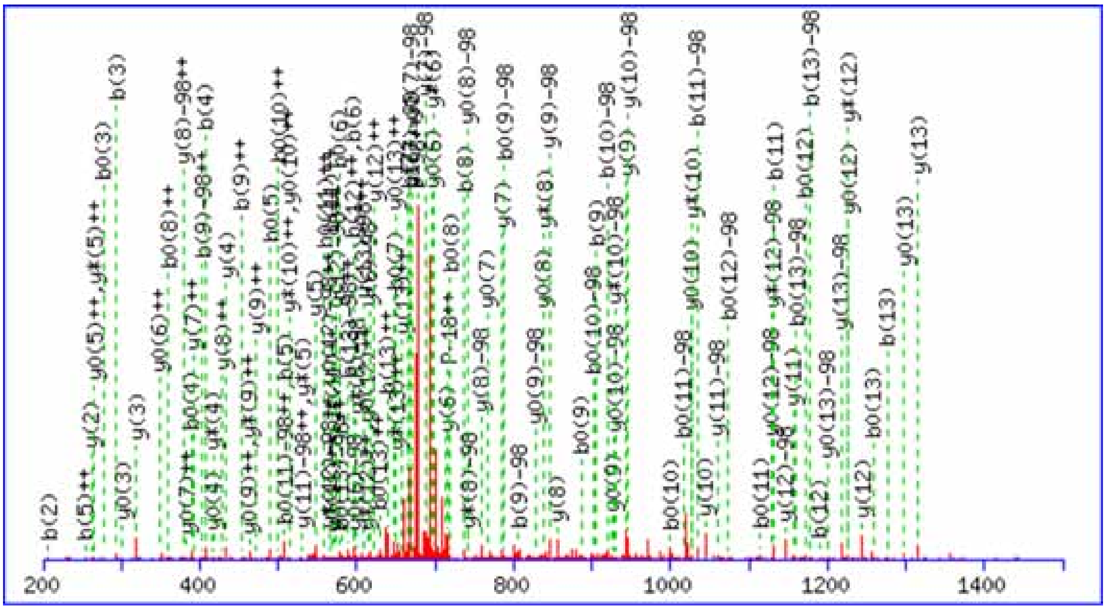
Matched b ions: b(3), b(4), b(5), b(5)++, b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(9), b(10)-98, b(10)-196, b(11)-196++, b(11)-98, b(11), b(13), b(13)-98++, b(13)-196++
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)++, y(8)-98, y(9), y(9)-98, y(9)-196, y(10), y(10)-98, y(10)-196, y(11)-98, y(11), y(12)-98, y(12), y(12)-196, y(12)-98++, y(12)++, y(13)-98, y(13), y(13)-98++, y(13)-196, y(13)++
Precursor origin neutral loss: +

Peptide No.1078

TASLTSAASIDGSR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2994: 1449.692872 from(725.853712,2+)
Title: Elution from: 35.318 to 35.318 scan no 2968 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1449.6924
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 Expect: 3.6e-006

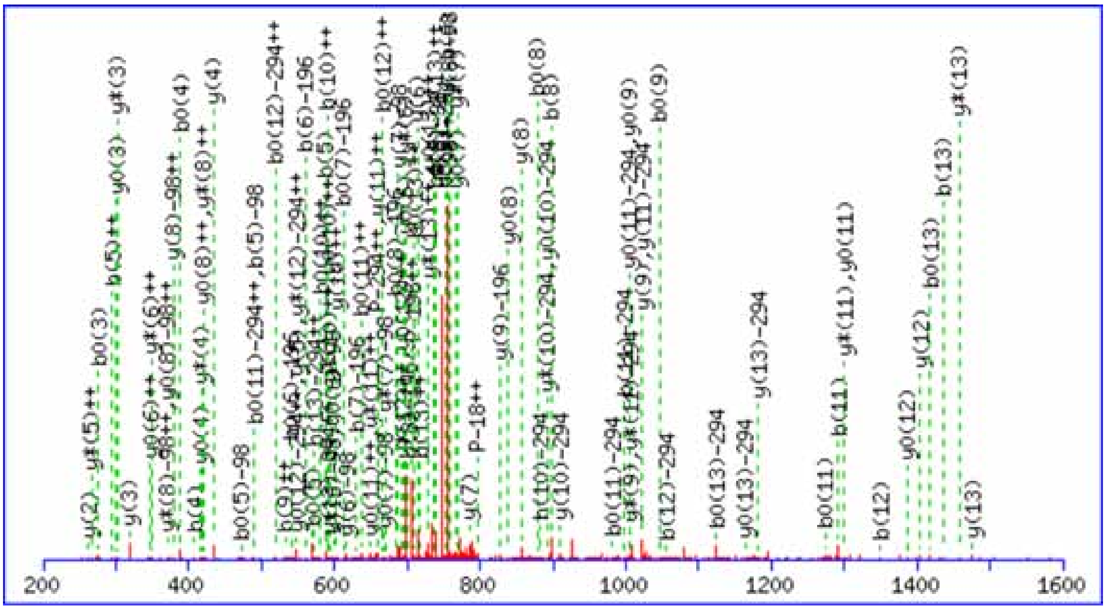
Matched b ions: b(2), b(3), b(4), b(5), b(5)++, b(6), b(7), b(8), b(9)-98, b(9)-98++, b(9)++, b(9), b(10)-98, b(11), b(11)-98, b(11)++, b(12)++, b(12), b(13)-98++, b(13), b(13)++, b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)++, y(7)-98, y(8), y(8)-98, y(8)-98++, y(8)++, y(9)-98, y(9), y(9)++, y(10)-98, y(10), y(11), y(11)-98, y(11)-98++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13), y(13)-98, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1079

TASLTSAASIDGSR
Confirmed sites: @T:5,@S:6,@S:9
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2674: 1609.626394 from(805.820473,2+)
Title: Elution from: 40.640 to 40.640 scan no 3563 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1609.6251
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.0011

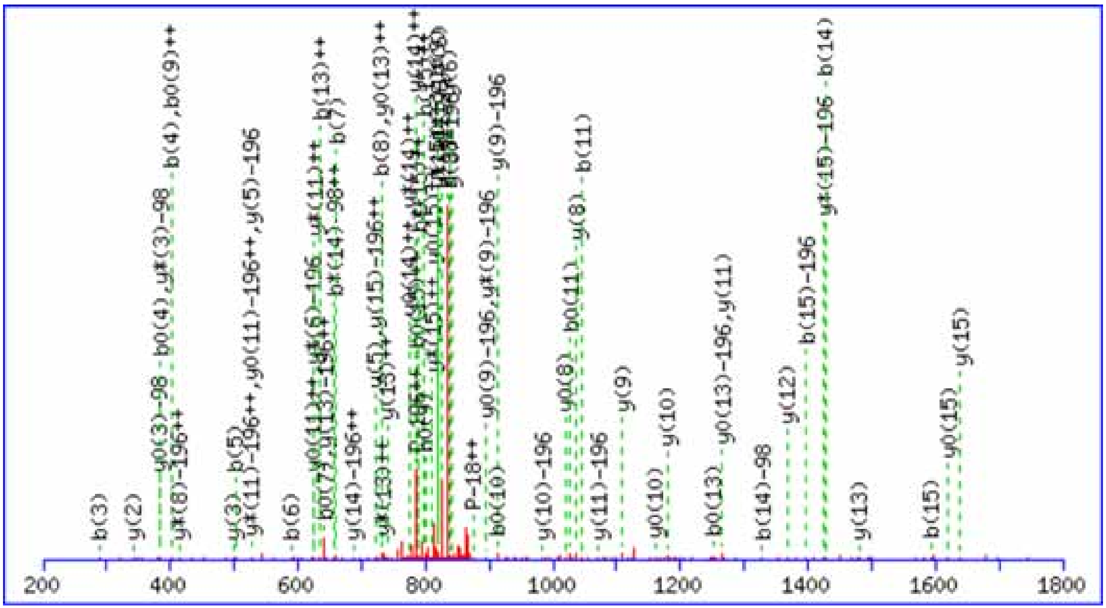
Matched b ions: b(4), b(5), b(5)++, b(5)-98, b(6), b(6)-196, b(6)-98, b(7)-98, b(7)-196, b(8), b(8)-196, b(9)-196++, b(9)-98, b(9)-196, b(9)++, b(10)-98, b(10)-98++, b(10)++, b(10)-294, b(10)-196, b(11)-98, b(11), b(11)-196, b(11)-98++, b(11)-294, b(12), b(12)-196++, b(12)-98++, b(12)-294, b(13), b(13)-294++, b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98++, y(8)-98, y(9), y(9)-98, y(9)-196, y(10)-196, y(10)-294, y(10)-98, y(10)++, y(11)-294, y(11)++, y(11)-196, y(11)-98, y(12)-98, y(12), y(12)-196++, y(12)-196, y(12)-98++, y(13), y(13)-98, y(13)-196, y(13)++, y(13)-294, y(13)-98++, y(13)-294++, y(13)-196++
Precursor origin neutral loss: +

Peptide No.1080

TASLTSAASIDGSRSR
Confirmed sites: @S:13,@S:15
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSRSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 4111: 1766.760326 from(884.387439,2+)
Title: Elution from: 34.466 to 34.466 scan no 2915 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1766.7601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.045

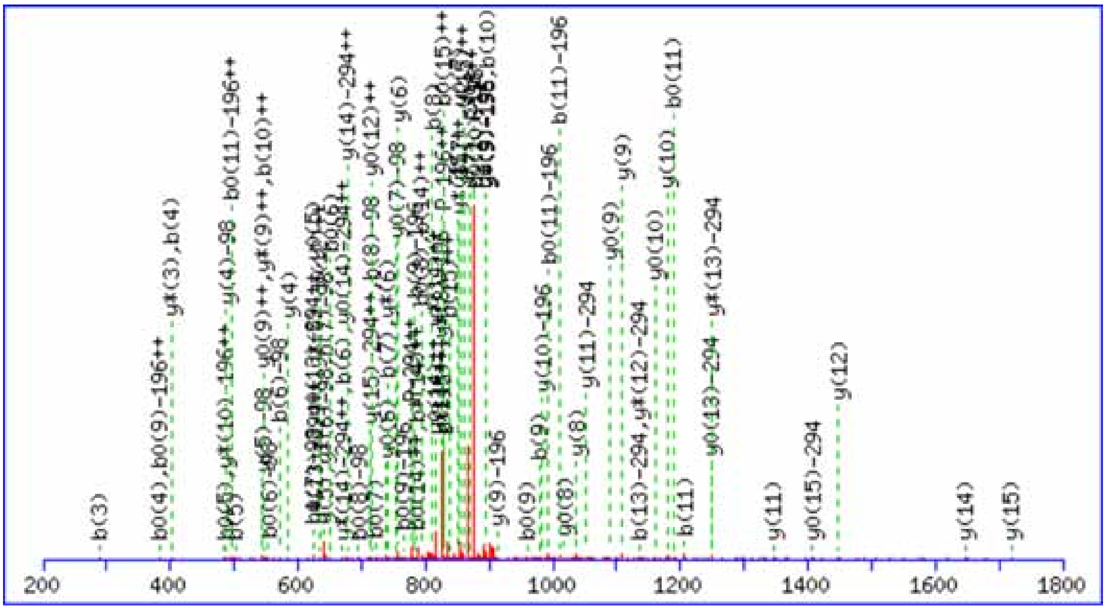
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(11), b(13)++, b(14), b(14)-98, b(15)-98, b(15)-196, b(15), b(15)++
Matched y ions: y(2), y(3), y(5)-98, y(5)-196, y(5), y(6)-98, y(6), y(7)-98, y(8), y(8)-98, y(8)-196, y(9), y(9)-98, y(9)-196, y(10), y(10)-98, y(10)-196, y(11), y(11)-98, y(11)-196, y(12), y(12)-98, y(12)-98++, y(13)-196++, y(13)-98, y(13), y(13)++, y(14)-196++, y(14)-98++, y(14)-98, y(14)++, y(15), y(15)-196++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1081

TASLTSAASIDGSRSR
Confirmed sites: @S:6,@S:9,@S:13
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSRSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3604: 1846.728664 from(924.371608,2+)
Title: Elution from: 38.490 to 38.490 scan no 3248 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1846.7264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.011

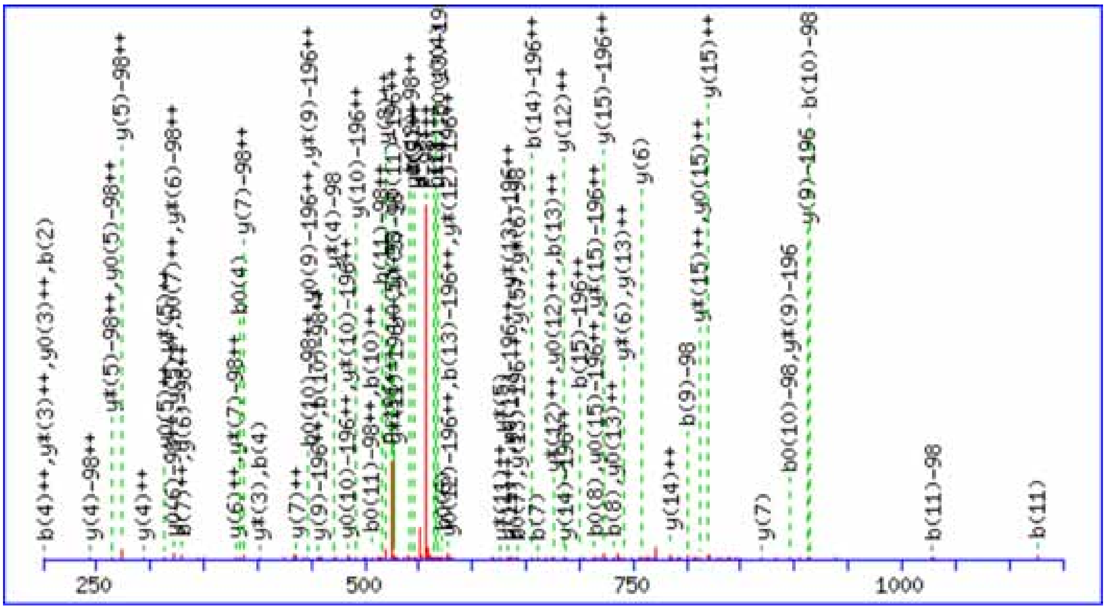
Matched b ions: b(3), b(4), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-196, b(9)-98, b(9), b(10)-98, b(10)++, b(10)-196, b(11)-98, b(11), b(11)-196, b(12)-98, b(12)++, b(13)-98, b(13)-294, b(14)-98, b(14)-196++, b(14)-98++, b(14)++, b(15)-98, b(15)-196++, b(15)++
Matched y ions: y(4)-98, y(4), y(5)-98, y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(9)-196, y(10), y(10)-196, y(10)-98, y(11), y(11)-98++, y(11)-98, y(11)-294, y(11)-196, y(12), y(12)-98, y(13)-196++, y(13)-98++, y(13)-196, y(14), y(14)-98++, y(14)-294++, y(14)-196++, y(14)++, y(15), y(15)-98, y(15)-294++, y(15)-196++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1082

TASLTSAASIDGSRSR
Confirmed sites: @S:9,@S:13
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSRSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 4115: 1766.761065 from(589.927631,3+)
Title: Elution from: 34.461 to 34.461 scan no 2914 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1766.7601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.031

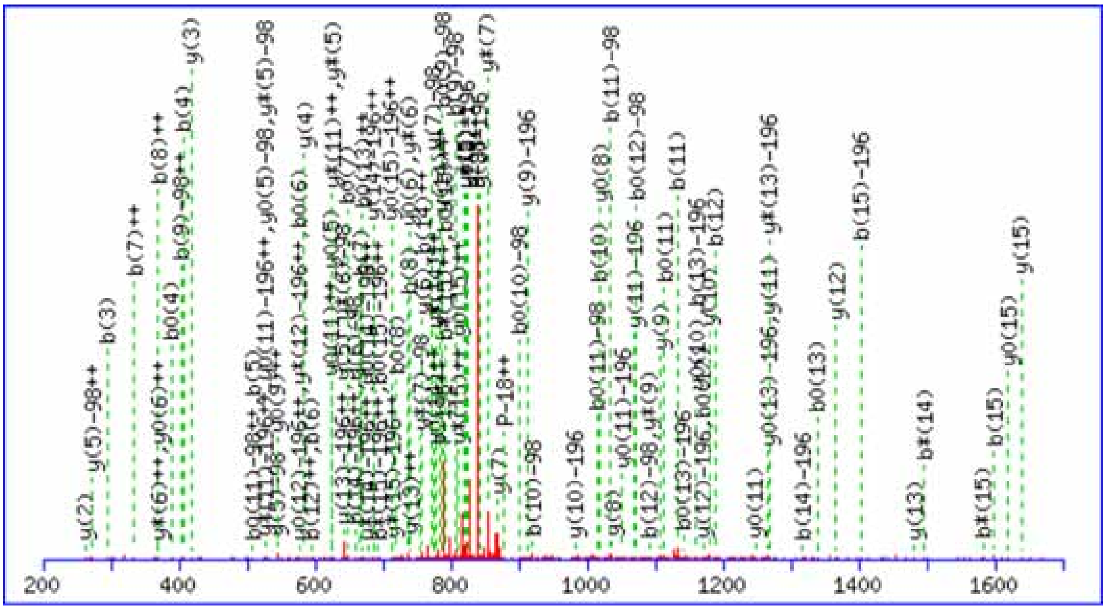
Matched b ions: b(2), b(4)++, b(4), b(7)++, b(7), b(8), b(9)-98, b(10)-98, b(10)-98++, b(10)++, b(11)-98, b(11), b(11)-98++, b(11)++, b(12)-98++, b(13)-196++, b(13)++, b(14)-196++, b(14)-98++, b(15)-98++, b(15)-196++
Matched y ions: y(4)-98++, y(4)++, y(5)-98++, y(5)++, y(5), y(6)-98++, y(6)++, y(6), y(7)++, y(7)-98++, y(7), y(8)-98, y(8)++, y(8)-98++, y(9)-196, y(9)-196++, y(9)-98++, y(10)-196++, y(10)-98++, y(11)++, y(12)++, y(12)-98++, y(13)-196++, y(13)++, y(14)-196++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(15)-196++
Precursor origin neutral loss: +

Peptide No.1083

TASLTSAASIDGSRSR
Confirmed sites: @S:9,@S:13
Ambiguous sites:

MS/MS Fragmentation of TASLTSAASIDGSRSR
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3452: 1772.793564 from(887.404058,2+)
Title: Elution from: 34.349 to 34.349 scan no 2697 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1772.7919
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 Expect: 2e-005

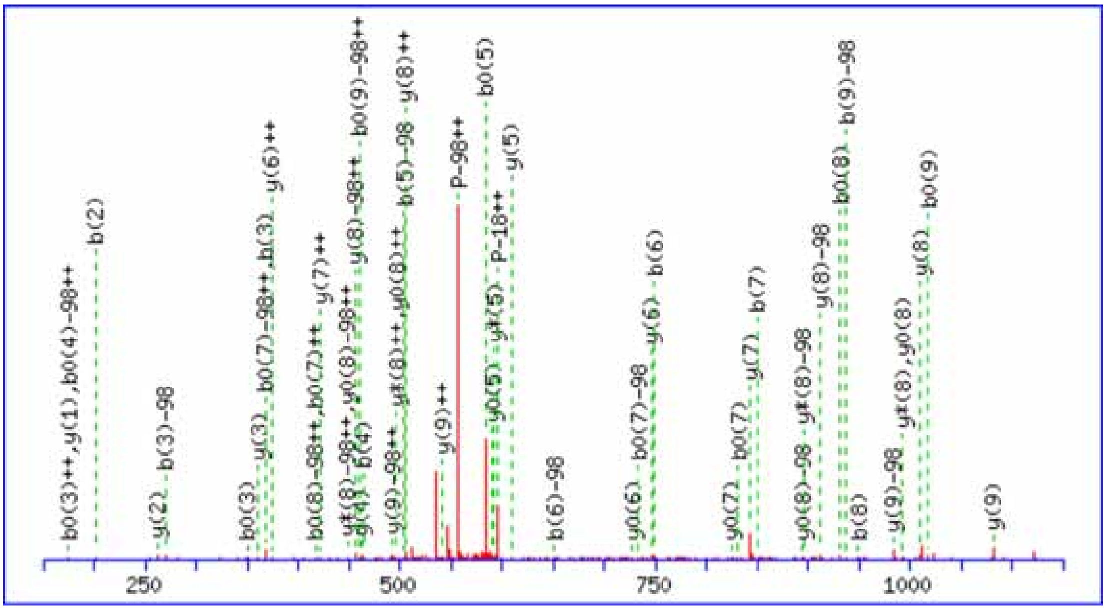
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(8), b(8)++, b(9)-98++, b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12)++, b(12), b(12)-98, b(13)-196, b(13)-98, b(14)++, b(14)-98, b(14)-196++, b(14)-196, b(15)-98, b(15), b(15)-196, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(5)-98++, y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(8)-196, y(9), y(9)-98, y(9)-196, y(10), y(10)-196, y(10)-98, y(11), y(11)-98++, y(11)-98, y(11)-196, y(12), y(12)-98, y(12)-196, y(13)-196++, y(13), y(13)-98++, y(13)++, y(14)-98++, y(14)-196++, y(14)++, y(15), y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.1084

TASPHFTVSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TASPHFTVSK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 879: 1209.580046 from(605.797299,2+)
Title: Elution from: 28.754 to 28.754 scan no 1945 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1209.5795
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K10 : Dimethyl (K)
Ions Score: 45 Expect: 0.00085

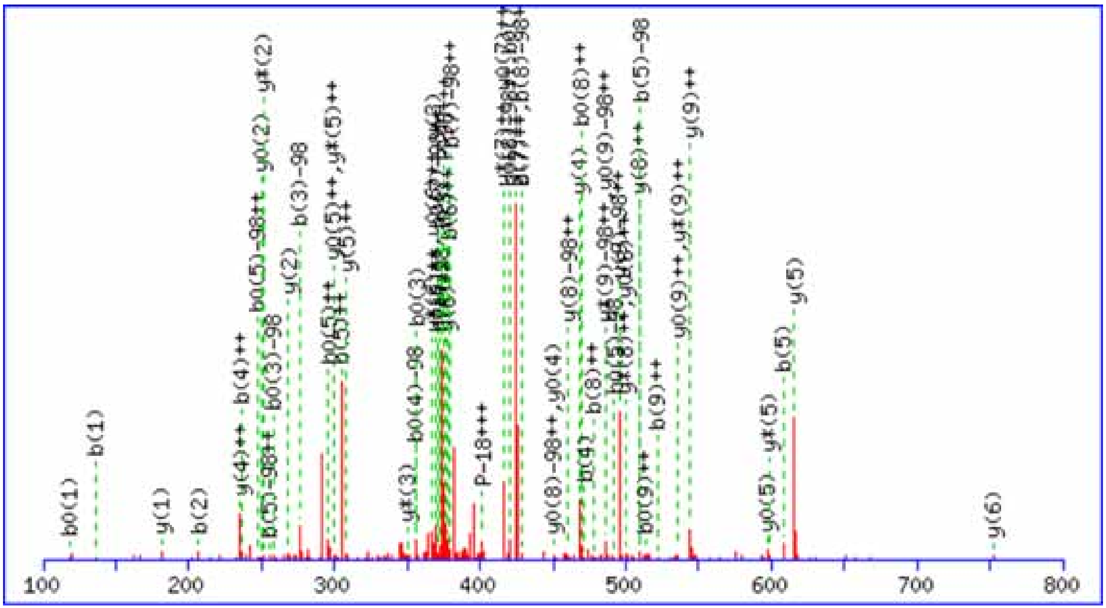
Matched b ions: b(2), b(3)-98, b(3), b(4), b(5)-98, b(6), b(6)-98, b(7), b(8), b(9)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8)-98++, y(8)-98, y(8), y(8)++, y(9), y(9)-98, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1085

TASPHFTVSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TASPHFTVSK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 902: 1221.643386 from(408.221738,3+)
Title: Elution from: 28.718 to 28.718 scan no 1940 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1221.6431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K10 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 29 Expect: 0.046

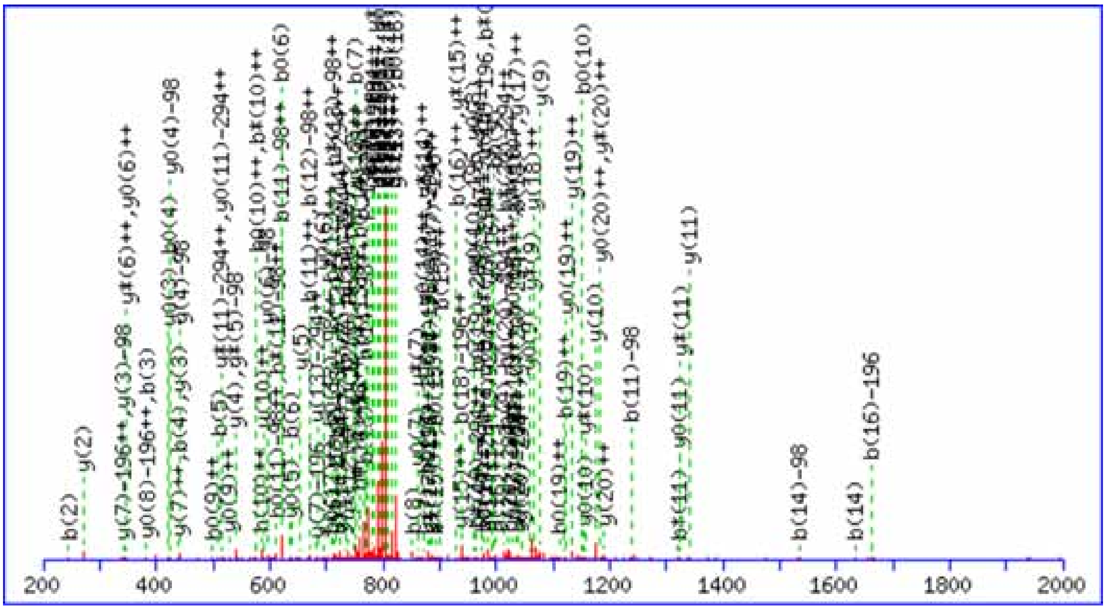
Matched b ions: b(1), b(2), b(3), b(3)-98, b(4)++, b(4)-98, b(4), b(5)++, b(5), b(5)-98++, b(5)-98, b(6)++, b(7)-98++, b(7)++, b(8)-98++, b(8)++, b(9)++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6), y(6)++, y(7)++, y(8)++, y(8)-98++, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1086

TDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @S:11,@S:15,@S:19
Ambiguous sites:

MS/MS Fragmentation of TDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 6740: 2510.056116 from(837.692648,3+)
Title: Elution from: 37.604 to 37.604 scan no 3182 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2510.0533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K10 : Dimethyl (K)
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 0.00064

Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10)++, b(11)-98++, b(11)++, b(11)-98, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14), b(14)-98, b(14)++, b(14)-98++, b(15)-98++, b(15)-196++, b(15)++, b(16)-196, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(17)-196++, b(18)-196++, b(18)++, b(18)-98++, b(19)-196++, b(19)-98++, b(19)-294++, b(19)++, b(20)-294++, b(20)-196++
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(4), y(5), y(6), y(7)++, y(7), y(7)-196++, y(7)-196, y(7)-98, y(8)-98, y(8), y(8)-196, y(9)-196, y(9)-98, y(9), y(10), y(10)-98, y(10)-196, y(10)++, y(11), y(11)-98, y(11)-196++, y(11)-196, y(12)-98++, y(12)++, y(13)-294++, y(13)-196++, y(13)-98++, y(14)-98, y(14)++, y(14)-294++, y(14)-196++, y(15)++, y(15)-294++, y(15)-98++, y(16)-98++, y(16)++, y(17)-196++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)-294++, y(19)++, y(19)-98++, y(19)-196++, y(20)++, y(20)-98++, y(20)-294++, y(20)-196++
Precursor origin neutral loss: +

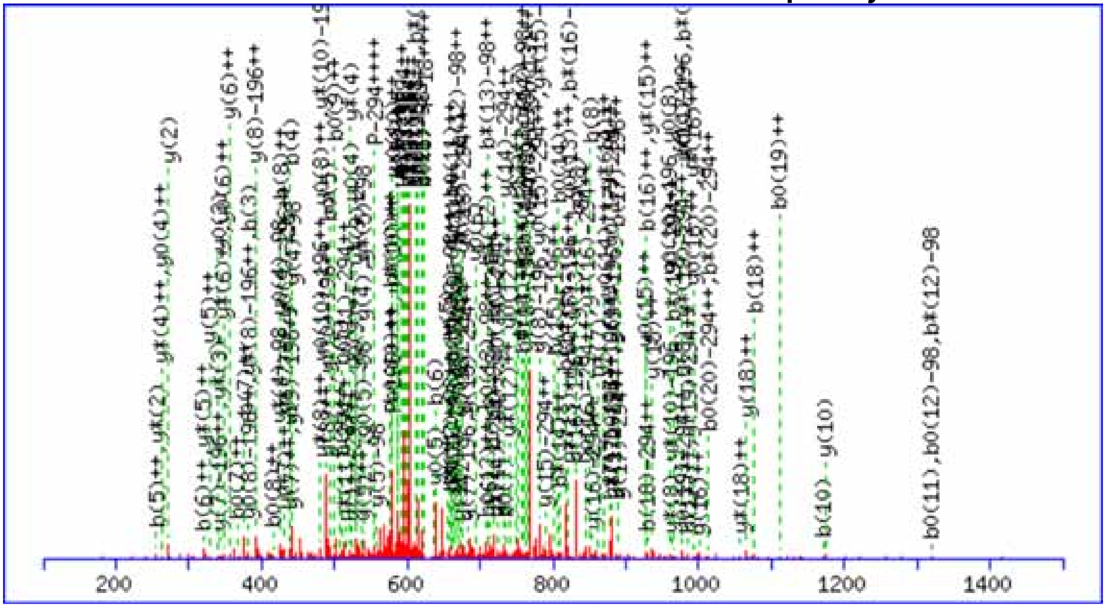
Peptide No.1087

TDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @S:11,@S:15,@T:18
Ambiguous sites:

MS/MS Fragmentation of TDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 5931: 2510.054176 from(628.520820,4+)

Title: Elution from: 37.584 to 37.584 scan no 3111 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2510.0533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K10 : Dimethyl (K)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 Expect: 0.0059

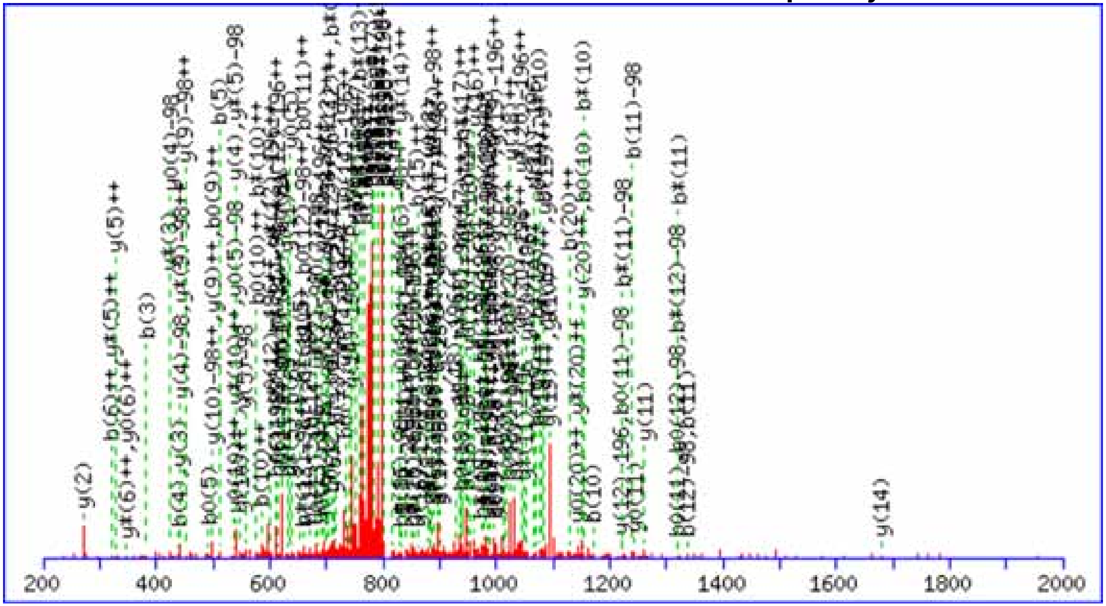
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(10), b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-196++, b(15)-98++, b(16)-196++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(17)-196++, b(18)-196++, b(18)++, b(18)-294++
Matched y ions: y(2), y(4)-98, y(4), y(5)++, y(5)-98, y(5), y(6)++, y(6), y(6)-98, y(7)++, y(7)-98++, y(7)-98, y(7), y(7)-196++, y(7)-196, y(8)-98++, y(8)-196++, y(8)++, y(8)-98, y(8)-196, y(8), y(9)-196++, y(9)-98++, y(9)-196, y(9)++, y(9)-98, y(10), y(10)-196++, y(10)-196, y(10)-98, y(10)++, y(10)-98++, y(11)-294++, y(11)-196++, y(11)++, y(12)-294++, y(12)-196++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(13)-196++, y(13)-294++, y(14)-98++, y(14)++, y(14)-196++, y(14)-294++, y(15)++, y(15)-294++, y(15)-196++, y(15)-98++, y(16)++, y(16)-294++, y(16)-196++, y(16)-98++, y(17)-294++, y(17)-196++, y(18)++, y(18)-196++, y(19)-294++
Precursor origin neutral loss: +

Peptide No.1088

TDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @S:11,@S:19
Ambiguous sites:

MS/MS Fragmentation of TDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 6167: 2430.087669 from(811.036499,3+)
Title: Elution from: 35.778 to 35.778 scan no 2878 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2430.0869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K10 : Dimethyl (K)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.0063

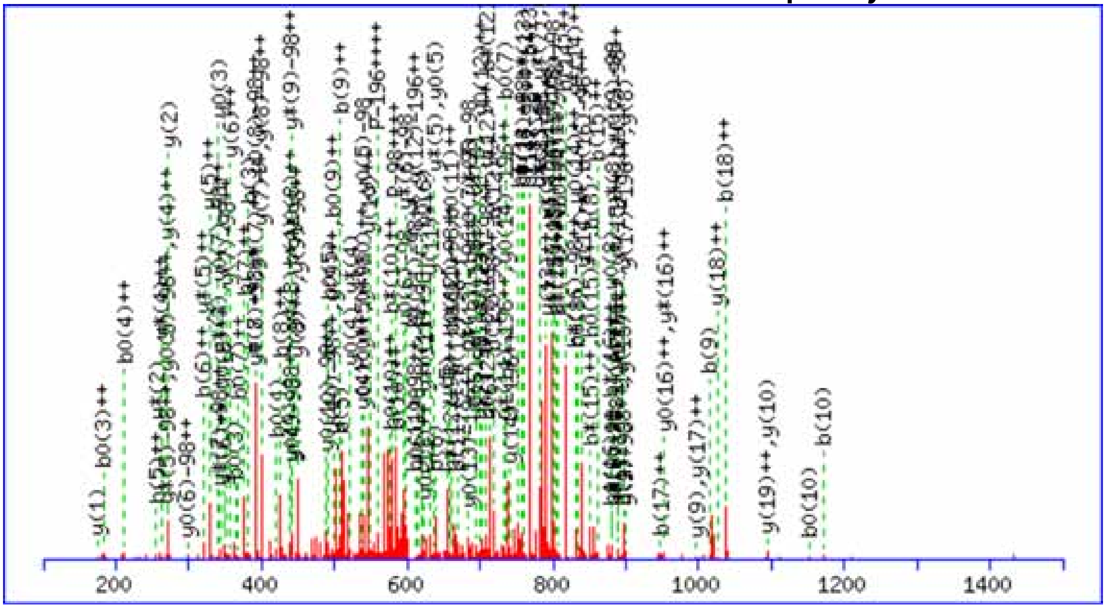
Matched b ions: b(3), b(4), b(5), b(6)++, b(6), b(7), b(8), b(9), b(10)++, b(10), b(11)-98++, b(11)-98, b(11), b(11)++, b(12)-98, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)-98++, b(19)-196++, b(19)++, b(20)-196++, b(20)-98++, b(20)++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)++, y(5)-98, y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(9)++, y(9)-98++, y(9)-98, y(9), y(10)-98++, y(10), y(10)-98, y(10)++, y(11), y(11)-98, y(11)-98++, y(11)++, y(11)-196, y(12)-196++, y(12)++, y(12)-98++, y(12)-196, y(12)-98, y(13)++, y(13)-196++, y(13)-98++, y(14), y(14)-196++, y(14)-98++, y(14)++, y(15)++, y(15)-196++, y(15)-98++, y(16)++, y(16)-196++, y(16)-98++, y(17)-196++, y(17)++, y(17)-98++, y(18)++, y(18)-196++, y(18)-98++, y(19)++, y(19)-98++, y(19)-196++, y(20)++, y(20)-98++, y(20)-196++
Precursor origin neutral loss: +

Peptide No.1089

TDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @S:11,@T:18
Ambiguous sites:

MS/MS Fragmentation of TDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 7337: 2430.088244 from(608.529337,4+)
Title: Elution from: 35.876 to 35.876 scan no 3108 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2430.0869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K10 : Dimethyl (K)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.0059

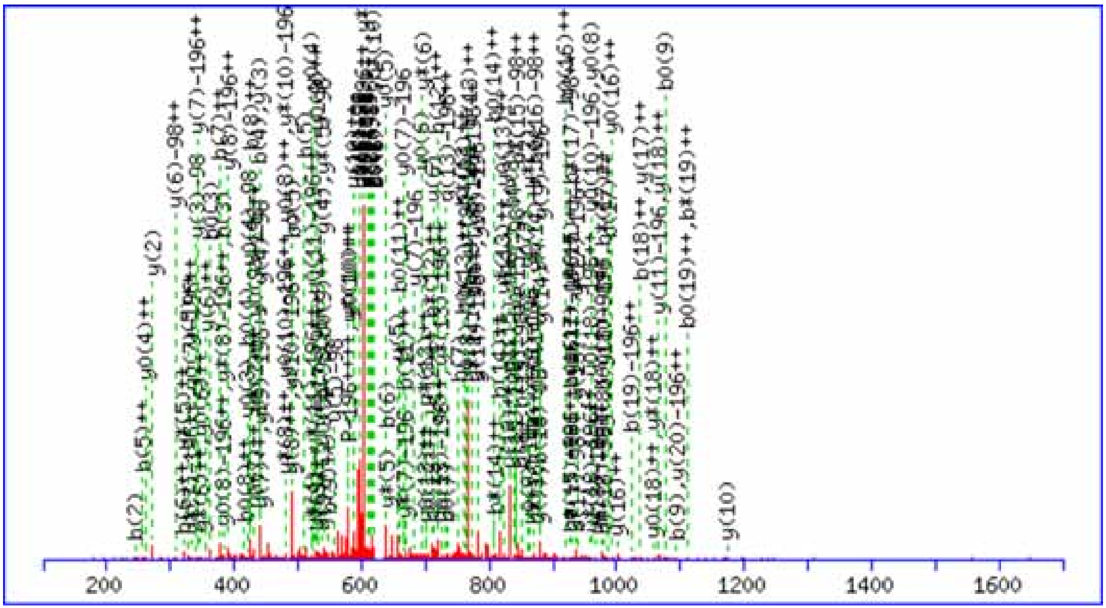
Matched b ions: b(3), b(4), b(5), b(5)++, b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9), b(9)++, b(10), b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++
Matched y ions: y(1), y(2), y(4)++, y(4), y(4)-98, y(5), y(5)++, y(6), y(6)++, y(6)-98, y(7), y(7)++, y(7)-98++, y(7)-98, y(8), y(8)-98++, y(8)++, y(8)-98, y(9)-98++, y(9)-98, y(9)++, y(9), y(10), y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(12)++, y(12)-196++, y(12)-98++, y(13)++, y(13)-196++, y(13)-98++, y(14)-98++, y(14)++, y(14)-196++, y(15)-196++, y(15)++, y(17)-196++, y(17)++, y(18)-98++, y(18)++, y(19)++
Precursor origin neutral loss: +

Peptide No.1090

TDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @Y:9,@S:15,@S:19
Ambiguous sites:

MS/MS Fragmentation of TDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 6739: 2510.054720 from(628.520956,4+)
Title: Elution from: 37.685 to 37.685 scan no 3193 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2510.0533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y9 : Phospho (Y)
K10 : Dimethyl (K)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.0051

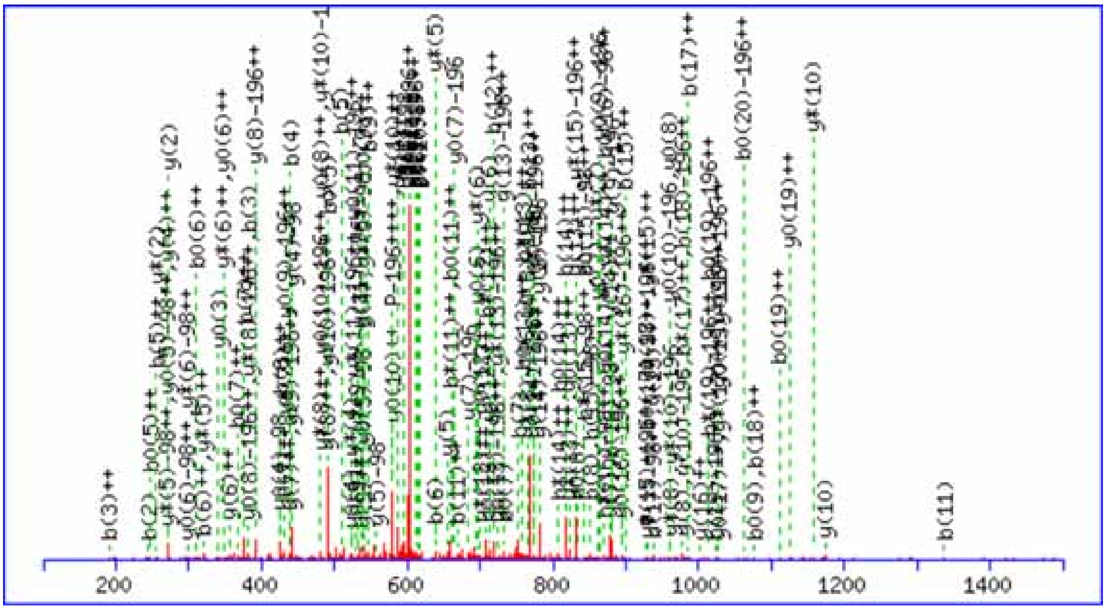
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9), b(9)++, b(11)++, b(12)++, b(13)++, b(14)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(19)-196++
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(4), y(5)++, y(5)-98, y(5), y(6), y(6)-98++, y(6)++, y(6)-98, y(7)++, y(7)-98, y(7)-98++, y(7), y(7)-196++, y(7)-196, y(8)-98++, y(8)++, y(8), y(8)-196, y(8)-196++, y(8)-98, y(9)-196++, y(9)-98++, y(9)++, y(9)-196, y(9)-98, y(10)-196++, y(10)-196, y(10), y(10)++, y(10)-98, y(10)-98++, y(11)-196, y(11)-196++, y(11)-98++, y(12)++, y(12)-196++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)-196++, y(14)++, y(15)++, y(15)-98++, y(15)-196++, y(16)++, y(16)-98++, y(17)-196++, y(17)++, y(18)++, y(18)-196++, y(20)-196++
Precursor origin neutral loss: +

Peptide No.1091

TDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @Y:9,@S:15,@T:18
Ambiguous sites:

MS/MS Fragmentation of TDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 7561: 2510.054064 from(628.520792,4+)
Title: Elution from: 37.733 to 37.733 scan no 3363 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2510.0533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y9 : Phospho (Y)
K10 : Dimethyl (K)
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 5.4e-005

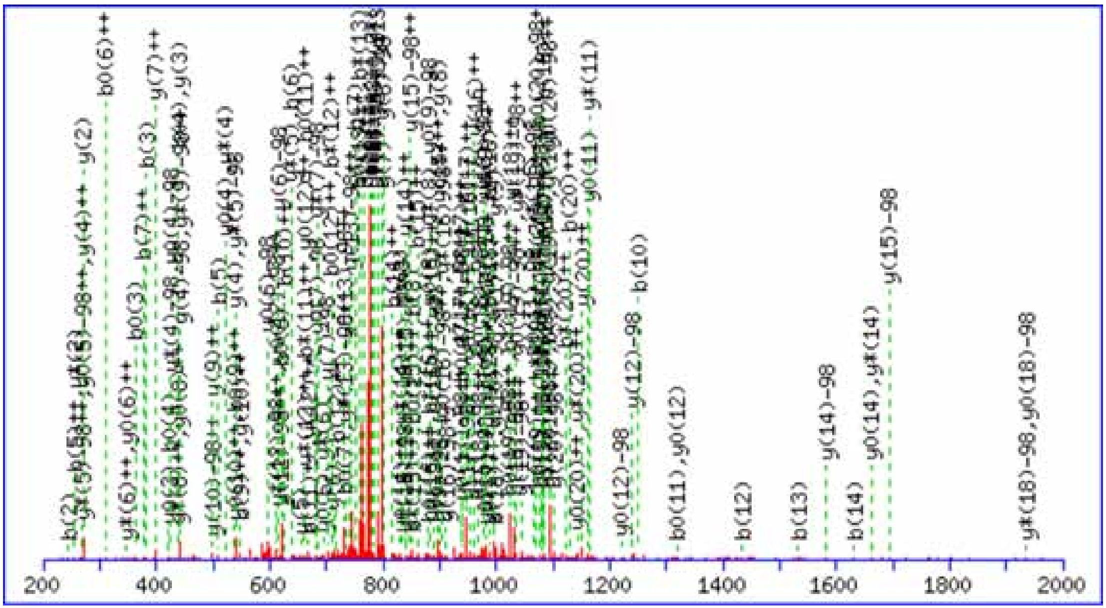
Matched b ions: b(2), b(3)++, b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(11), b(11)++, b(12)++, b(13)++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-196++, b(18)++, b(18)-98++, b(19)-196++
Matched y ions: y(2), y(4), y(4)-98, y(4)++, y(5)-98, y(5), y(6)++, y(6)-98, y(6), y(7)-98++, y(7)++, y(7)-98, y(7), y(7)-196, y(8)++, y(8), y(8)-196++, y(8)-98++, y(8)-196, y(8)-98, y(9)-98++, y(9)-196++, y(9)-196, y(9)-98, y(9)++, y(10)-196++, y(10)-196, y(10)++, y(10), y(10)-98, y(10)-98++, y(11)-196++, y(12)++, y(12)-196++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)-196++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1092

TDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @Y:9,@S:19
Ambiguous sites:

MS/MS Fragmentation of TDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 7338: 2430.088815 from(811.036881,3+)
Title: Elution from: 36.066 to 36.066 scan no 3134 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2430.0869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y9 : Phospho (Y)
K10 : Dimethyl (K)
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.011

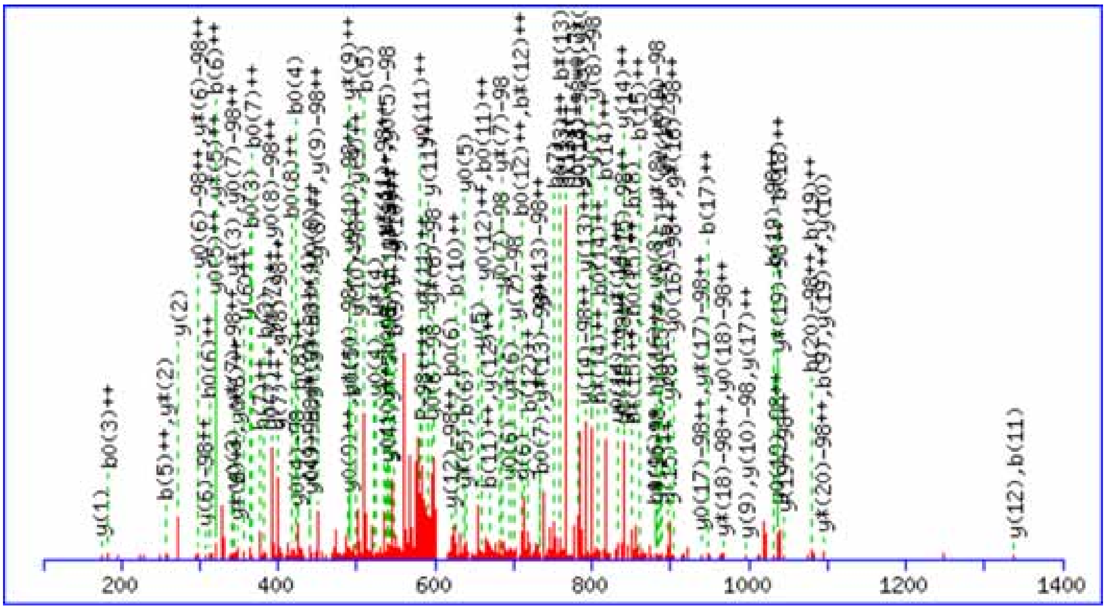
Matched b ions: b(2), b(3), b(4), b(5), b(5)++, b(6), b(7)++, b(7), b(8), b(9), b(9)++, b(10), b(10)++, b(11)++, b(12), b(12)++, b(13), b(13)++, b(14), b(14)++, b(15)++, b(16)++, b(17)++, b(18)++, b(19)-98++, b(19)++, b(20)-98++, b(20)++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(4)++, y(5), y(6), y(6)-98, y(7)++, y(7)-98, y(7), y(8), y(8)-98, y(9)-98, y(9)++, y(9), y(10), y(10)-98++, y(10)-98, y(10)++, y(11)-98, y(12)-98++, y(12)-98, y(12)++, y(13)++, y(13)-98++, y(14)-98, y(14)-98++, y(14)++, y(15)++, y(15)-98, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++
Precursor origin neutral loss: +

Peptide No.1093

TDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @Y:9,@T:18
Ambiguous sites:

MS/MS Fragmentation of TDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 6336: 2430.088912 from(608.529504,4+)
Title: Elution from: 35.799 to 35.799 scan no 2897 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2430.0869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y9 : Phospho (Y)
K10 : Dimethyl (K)
T18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.003

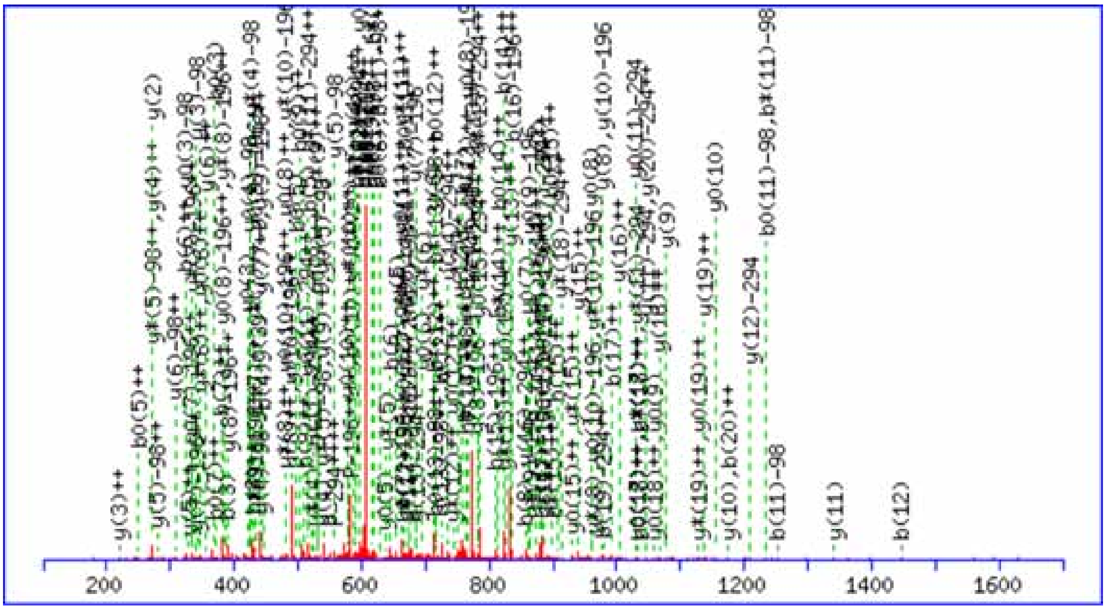
Matched b ions: b(3), b(4), b(5), b(5)++, b(6)++, b(6), b(7), b(7)++, b(8)++, b(8), b(9), b(9)++, b(10)++, b(11), b(11)++, b(12)++, b(13)++, b(14)++, b(15)++, b(16)++, b(17)++, b(18)++, b(19)++, b(19)-98++, b(20)-98++
Matched y ions: y(1), y(2), y(4)-98, y(4), y(5), y(6), y(6)++, y(6)-98++, y(7)++, y(7), y(7)-98, y(8), y(8)-98++, y(8)++, y(8)-98, y(9)-98++, y(9)++, y(9), y(10), y(10)-98++, y(10)++, y(10)-98, y(11)-98++, y(11)++, y(12), y(12)-98++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(17)++, y(19)++, y(19)-98++
Precursor origin neutral loss:

Peptide No.1094

TDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @S:11,@S:15,@S:19
Ambiguous sites:

MS/MS Fragmentation of TDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 6675: 2522.118324 from(631.536857,4+)
Title: Elution from: 37.604 to 37.604 scan no 3150 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2522.1169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K10 : Dimethyl:2H(4)13C(2) (K)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 0.00022

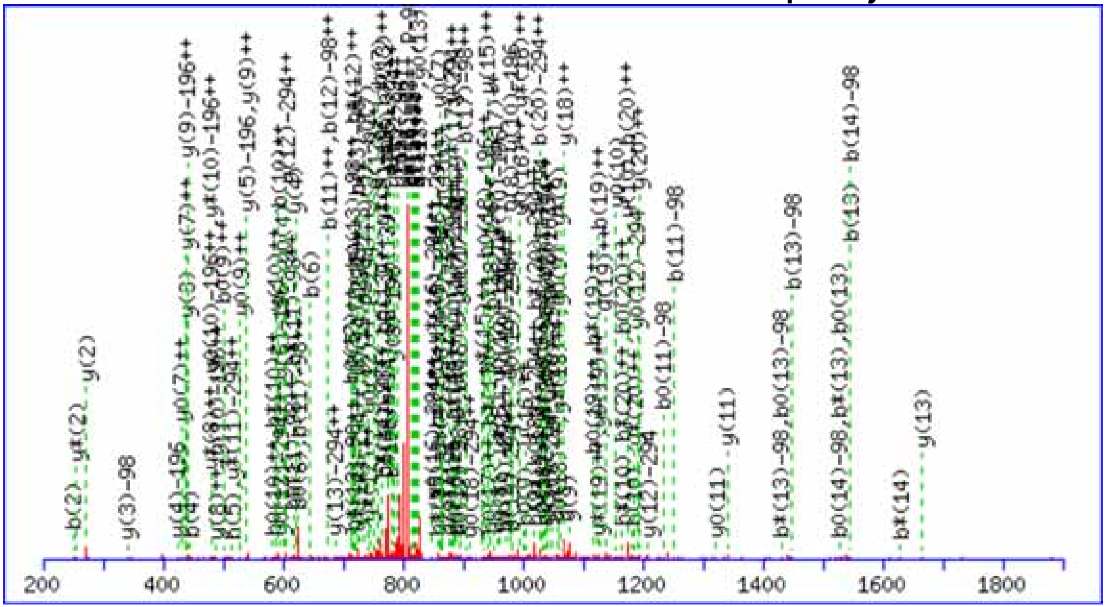
Matched b ions: b(3), b(4), b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(10)++, b(11)-98, b(11)++, b(11)-98++, b(12), b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)-196++, b(15)++, b(16)-196++, b(16)-98++, b(17)++, b(17)-98++, b(19)-196++, b(19)-294++, b(19)-98++, b(20)++, b(20)-196++
Matched y ions: y(2), y(3), y(3)++, y(3)-98, y(4), y(4)++, y(4)-98, y(5)-98++, y(5)++, y(5)-98, y(5), y(6), y(6)-98++, y(6)++, y(6)-98, y(7)++, y(7)-98++, y(7), y(7)-98, y(7)-196++, y(7)-196, y(8)-98++, y(8)++, y(8)-196++, y(8), y(8)-98, y(8)-196, y(9)-196++, y(9)-98++, y(9)++, y(9)-98, y(9), y(10)-196++, y(10)-98++, y(10)-196, y(10), y(10)++, y(11), y(11)-98, y(11)-294++, y(11)-196++, y(11)-98++, y(11)++, y(11)-294, y(12)-294, y(12)++, y(12)-294++, y(12)-98++, y(13)++, y(13)-98++, y(13)-294++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++, y(14)-294++, y(15)++, y(15)-98++, y(16)-294++, y(16)-196++, y(16)-98++, y(16)++, y(18)++, y(19)-98++, y(19)++, y(20)-294++
Precursor origin neutral loss: +

Peptide No.1095

TDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @S:11,@T:18,@S:19
Ambiguous sites:

MS/MS Fragmentation of TDHGAEIVYKSPVVSGDTSPR
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 6676: 2522.119272 from(841.713700,3+)
Title: Elution from: 37.514 to 37.514 scan no 3137 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2522.1169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K10 : Dimethyl:2H(4)13C(2) (K)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.023

Matched b ions: b(2), b(4), b(5), b(6), b(7), b(8), b(9), b(10)++, b(10), b(11)-98++, b(11)-98, b(11)++, b(12)-98++, b(12)++, b(13)-98, b(13), b(13)-98++, b(13)++, b(14)-98, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(17)-98++, b(17)++, b(18)-196++, b(18)-98++, b(18)++, b(19)-196++, b(19)-98++, b(19)++, b(19)-294++, b(20)++, b(20)-294++, b(20)-196++, b(20)-98++
Matched y ions: y(2), y(3)-98, y(3), y(4)-196, y(4), y(5)-196, y(5), y(5)-98, y(6)-98++, y(6), y(6)-196, y(6)-98, y(7), y(7)++, y(7)-98, y(8)-98, y(8), y(8)-98++, y(8)++, y(8)-196, y(9), y(9)++, y(9)-196++, y(9)-196, y(9)-98, y(10), y(10)-98, y(10)-196, y(10)-98++, y(10)++, y(10)-196++, y(11), y(11)-98, y(11)-196, y(11)-98++, y(11)-294, y(12)-98, y(12)-294++, y(12)-98++, y(12)++, y(12)-294, y(13), y(13)-196++, y(13)-294++, y(13)-98++, y(14)-196++, y(14)++, y(15)++, y(15)-294++, y(15)-98++, y(16)-294++, y(16)-196++, y(16)++, y(17)++, y(17)-294++, y(17)-196++, y(18)-98++, y(18)++, y(18)-196++, y(19)-98++, y(19)++, y(19)-196++, y(20)++, y(20)-98++, y(20)-294++
Precursor origin neutral loss: +

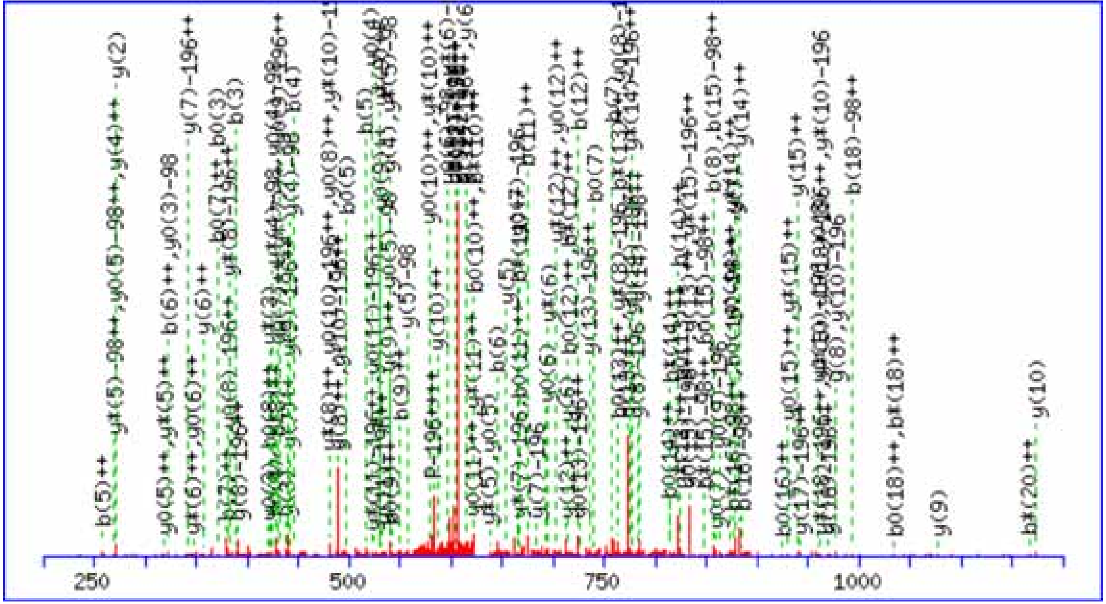
Peptide No.1096

TDHGAEIVYKSPVVSGDTSPR
Confirmed sites: @Y:9,@S:15,@S:19
Ambiguous sites:

MS/MS Fragmentation of TDHGAEIVYKSPVVSGDTSPR

Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 6800: 2522.116800 from(631.536476,4+)
Title: Elution from: 37.567 to 37.567 scan no 3177 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2522.1169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y9 : Phospho (Y)
K10 : Dimethyl:2H(4)13C(2) (K)
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.016

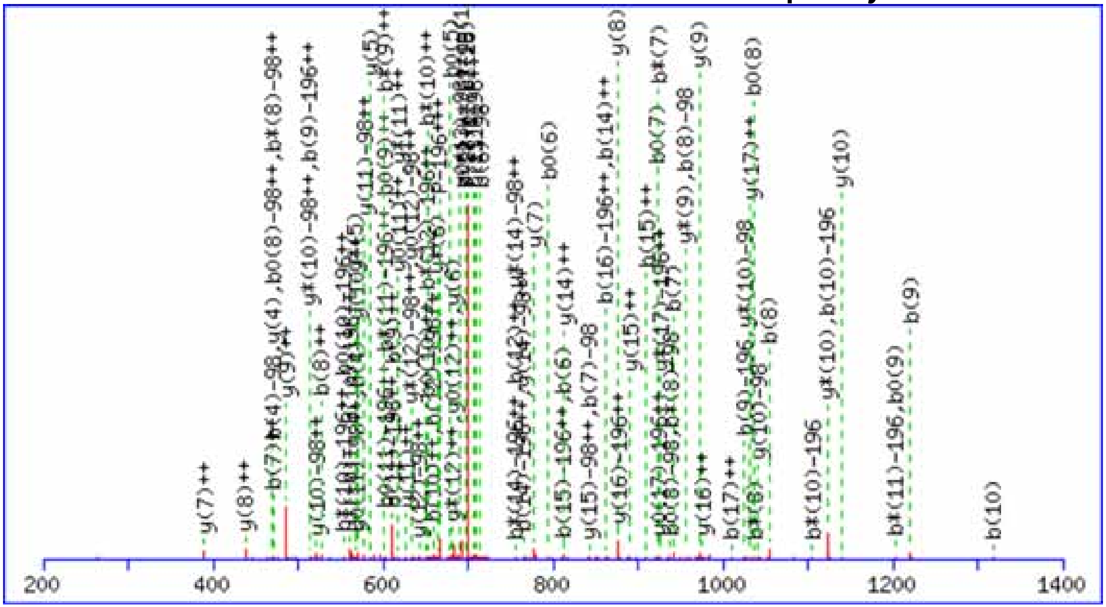
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(11)++, b(12)++, b(13)++, b(14)++, b(15)-98++, b(16)-98++, b(18)-98++, b(19)-98++
Matched y ions: y(2), y(3), y(4)++, y(4)-98, y(4), y(5)-98, y(5), y(6), y(6)++, y(6)-98, y(7), y(7)-98++, y(7)++, y(7)-196++, y(7)-196, y(7)-98, y(8)++, y(8)-98++, y(8), y(8)-196++, y(8)-196, y(8)-98, y(9)-98++, y(9)-196++, y(9), y(9)++, y(10)-196++, y(10), y(10)-196, y(10)-98++, y(10)++, y(11)-98++, y(11)-196++, y(12)++, y(12)-196++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)++, y(14)-98++, y(14)-196++, y(15)++, y(15)-98++, y(17)-196++, y(18)-196++
Precursor origin neutral loss: +

Peptide No.1097

TDSREDEISPPPPNPVVK
Confirmed sites: @S:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of TDSREDEISPPPPNPVVK
Found in KAP0_MOUSE, cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3

Match to Query 5760: 2191.982559 from(731.668129,3+)
Title: Elution from: 38.960 to 38.960 scan no 3330 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2191.9803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl (K)
Ions Score: 62 Expect: 3.8e-005

Matched b ions: b(4)-98, b(4), b(5), b(6), b(6)-98, b(7), b(7)++, b(7)-98, b(8), b(8)++, b(8)-98, b(9)++, b(9)-98, b(9), b(9)-98++, b(9)-196++, b(9)-196, b(10)-98++, b(10)-196, b(10)-98, b(10), b(10)-196++, b(10)++, b(11)-196++, b(11)-98, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(12)++, b(13)-196++, b(13)-98++, b(14)-98++, b(14)-196++, b(14)++, b(15)-196++, b(15)++, b(15)-98++, b(16)-196++, b(17)-98++, b(17)++
Matched y ions: y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10)++, y(10)-98++, y(10), y(10)-98, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

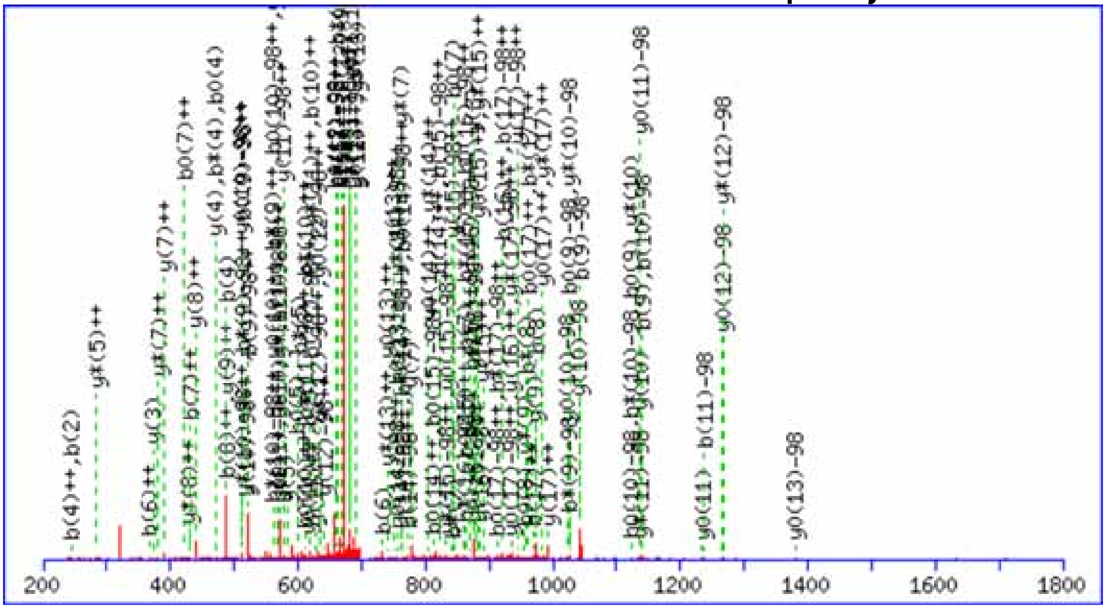
Peptide No.1098

TDSREDEISPPPPNPVVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of TDSREDEISPPPPNPVVK
Found in KAP0_MOUSE, cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3

Match to Query 4900: 2112.015801 from(705.012543,3+)

Title: Elution from: 36.063 to 36.063 scan no 2821 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2112.0140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl (K)
Ions Score: 34 Expect: 0.029

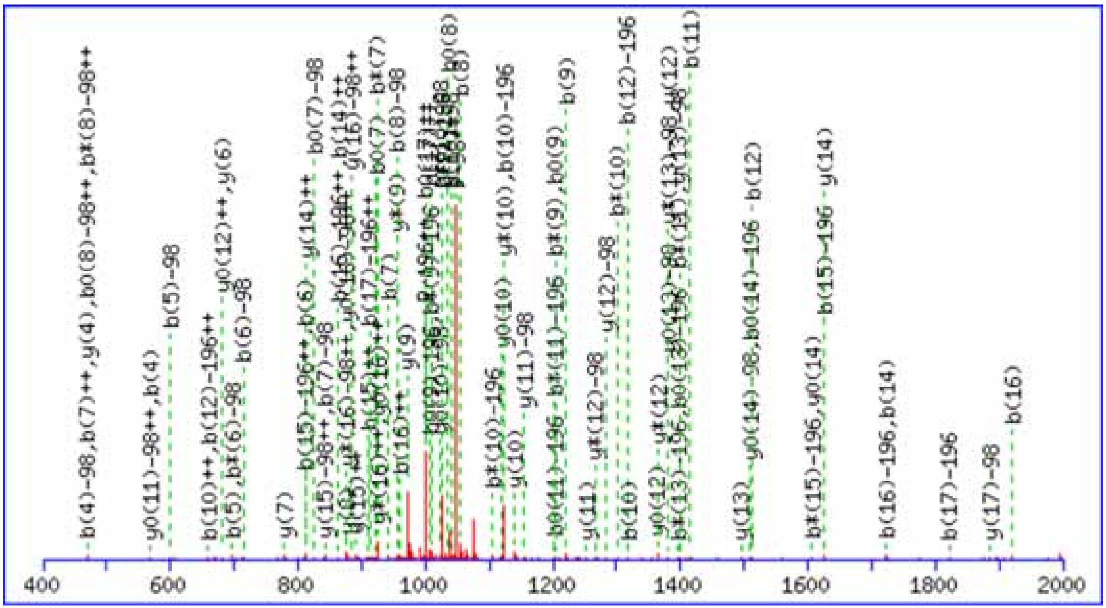
Matched b ions: b(2), b(4)++, b(4), b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9)-98, b(9), b(9)-98++, b(10)-98++, b(10)-98, b(10)++, b(11)-98++, b(11)++, b(11)-98, b(12)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10)++, y(10)-98++, y(10), y(10)-98, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1099

TDSREDEISPPPPNPVVK
Confirmed sites: @T:1,@S:9
Ambiguous sites:

MS/MS Fragmentation of TDSREDEISPPPPNPVVK
Found in KAP0_MOUSE, cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3

Match to Query 6505: 2191.980176 from(1096.997364,2+)
Title: Elution from: 39.315 to 39.315 scan no 3574 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2191.9803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl (K)
Ions Score: 46 Expect: 0.0015

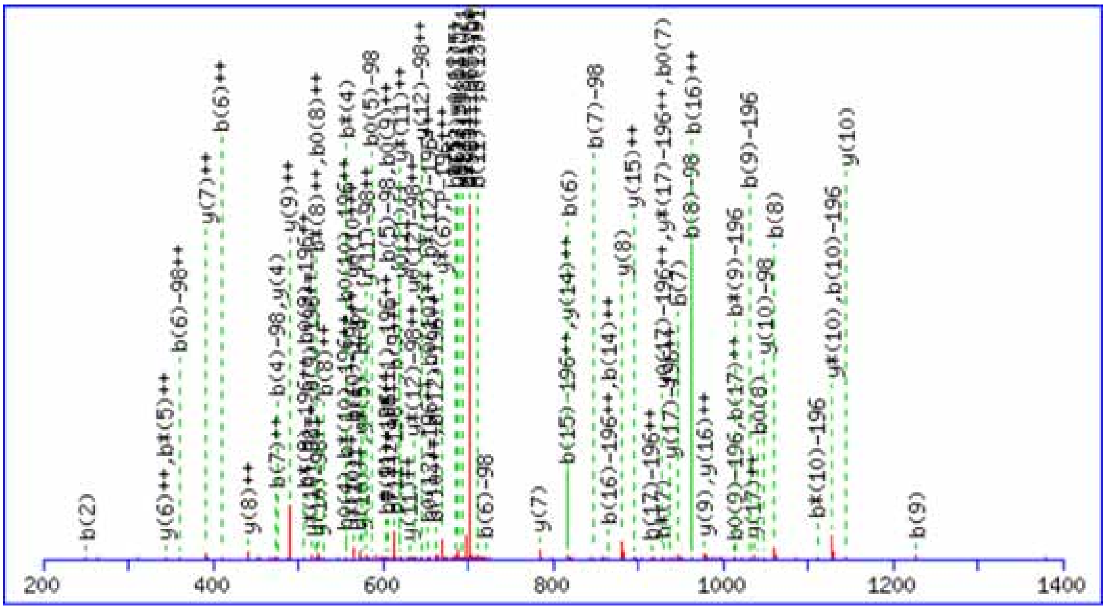
Matched b ions: b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7)++, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(9)-196, b(10)-196, b(10)-98, b(10)++, b(10), b(11), b(11)-98++, b(11)-98, b(12)-98, b(12)-196++, b(12)-196, b(12), b(14)-98, b(14), b(14)-98++, b(14)++, b(15)-196++, b(15)-98, b(15)-196, b(15)++, b(16)-196, b(16)-98, b(16), b(16)++, b(16)-196++, b(16)-98++, b(17)-196, b(17)-98, b(17)-98++, b(17)-196++, b(17)++
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(12)-98, y(12), y(13), y(13)-98, y(14), y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(17)-98
Precursor origin neutral loss: +

Peptide No.1100

TDSREDEISPPPPNPVVK
Confirmed sites: @S:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of TDSREDEISPPPPNPVVK
Found in KAP0_MOUSE, cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3

Match to Query 7268: 2204.045121 from(735.688983,3+)
Title: Elution from: 38.936 to 38.936 scan no 3487 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2204.0439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 54 Expect: 0.00034

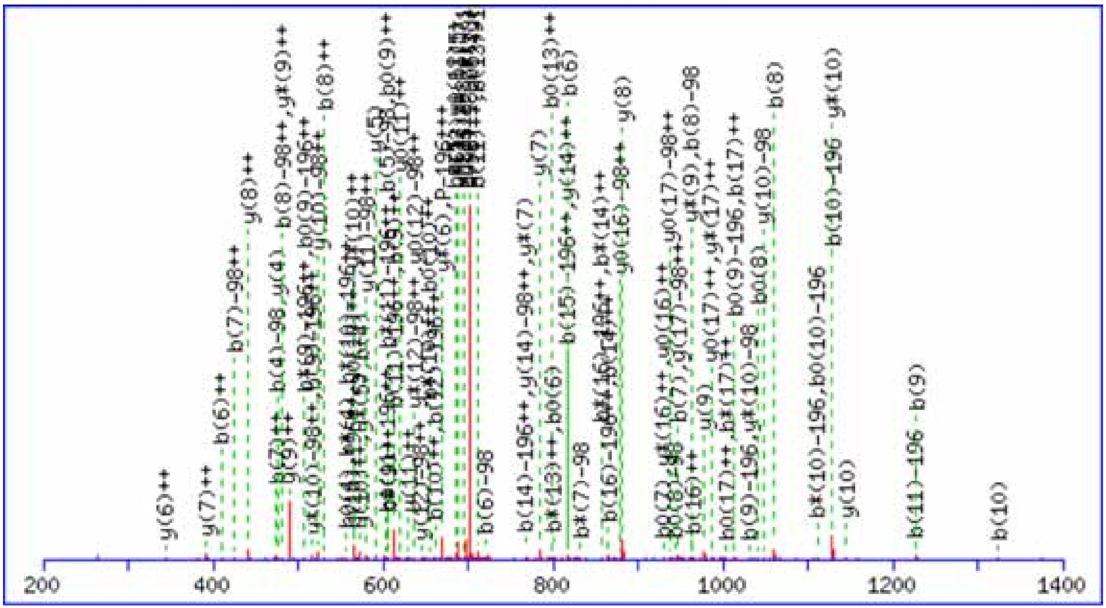
Matched b ions: b(2), b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98++, b(6)++, b(6)-98, b(7), b(7)++, b(7)-98, b(8), b(8)++, b(8)-98, b(9)++, b(9)-98, b(9), b(9)-98++, b(9)-196++, b(9)-196, b(10)-98++, b(10)-196, b(10)-98, b(10)-196++, b(10)++, b(11)-196++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(13)-196++, b(14)-98++, b(14)++, b(15)-196++, b(15)-98++, b(16)-196++, b(16)++, b(17)++, b(17)-196++, b(17)-98++
Matched y ions: y(4), y(6)++, y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10)-98++, y(10)++, y(10), y(10)-98, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-196++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1101

TDSREDEISPPPPNPVVK
Confirmed sites: @T:1,@S:9
Ambiguous sites:

MS/MS Fragmentation of TDSREDEISPPPPNPVVK
Found in KAP0_MOUSE, cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3

Match to Query 5576: 2204.046480 from(735.689436,3+)
Title: Elution from: 39.289 to 39.289 scan no 3359 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2204.0439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 61 Expect: 5.4e-005

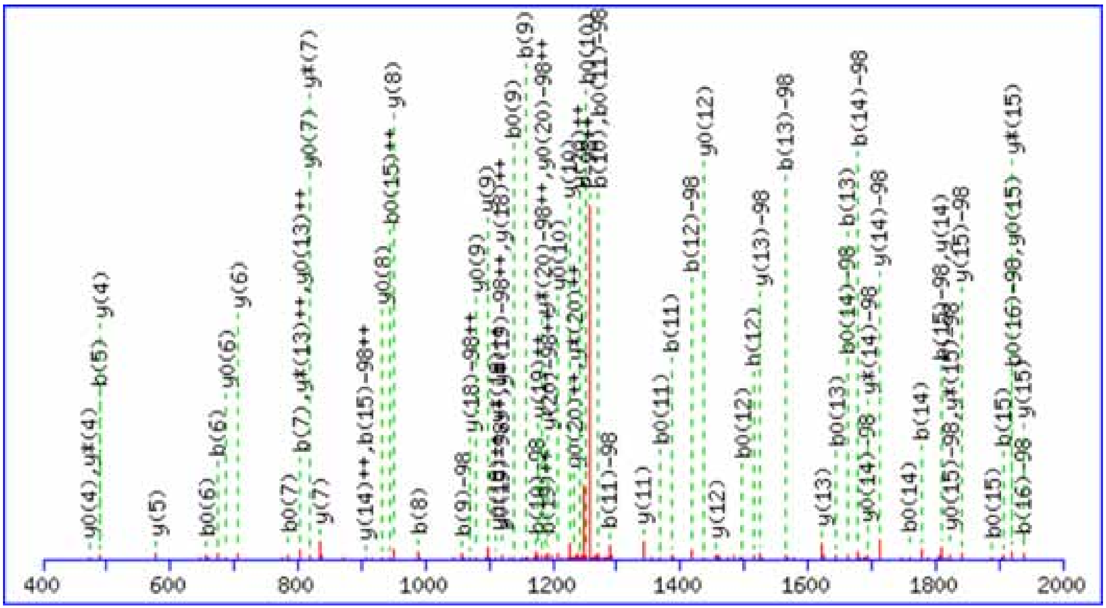
Matched b ions: b(4), b(4)-98, b(5), b(5)-98, b(6), b(6)++, b(6)-98, b(7), b(7)++, b(7)-98++, b(8), b(8)-98, b(8)++, b(8)-98++, b(9)++, b(9)-98, b(9), b(9)-98++, b(9)-196++, b(9)-196, b(10)-98++, b(10), b(10)-98, b(10)-196, b(10)-196++, b(10)++, b(11)-196++, b(11)-98, b(11)-196, b(11)++, b(11)-98++, b(12)-98++, b(12)-196++, b(13)-196++, b(14)-98++, b(14)++, b(14)-196++, b(15)-196++, b(15)-98++, b(16)-196++, b(16)++, b(17)-98++, b(17)++
Matched y ions: y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10)-98++, y(10)++, y(10), y(10)-98, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(14)++, y(14)-98++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1102

TEDGGWEWSDDEFDEESEEGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of TEDGGWEWSDDEFDEESEEGR
Found in OXSR1_MOUSE, Serine/threonine-protein kinase OSR1 OS=Mus musculus GN=Oxsr1 PE=1 SV=1

Match to Query 6667: 2610.920318 from(1306.467435,2+)
Title: Elution from: 59.375 to 59.375 scan no 5600 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2610.9184
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 94 Expect: 5.6e-009

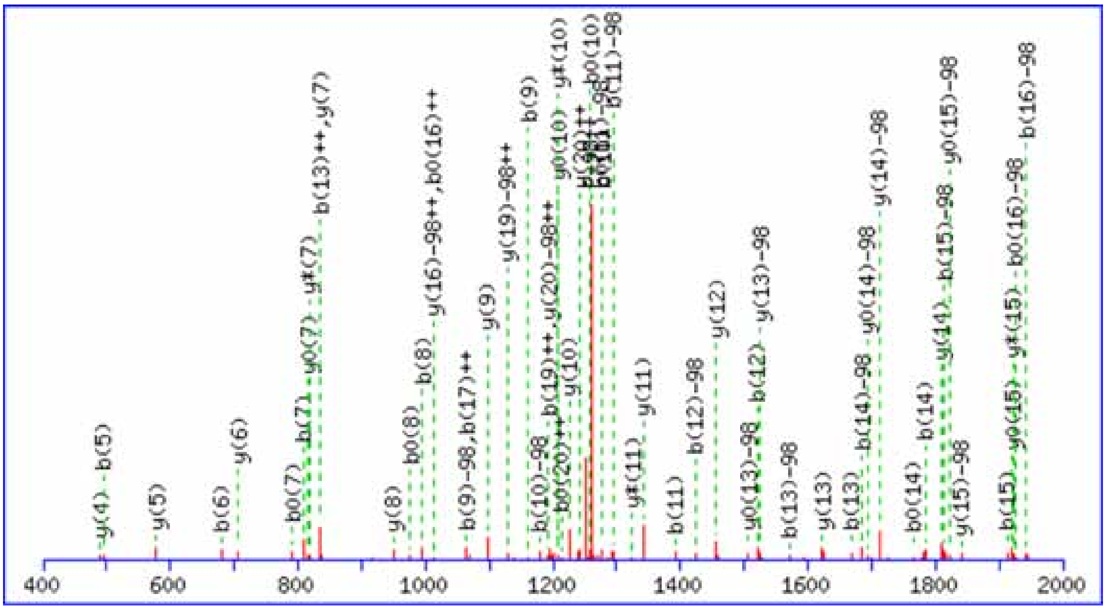
Matched b ions: b(5), b(6), b(7), b(8), b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(12), b(13)-98, b(13), b(14)-98, b(14), b(15)-98, b(15), b(15)-98++, b(16)-98, b(19)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)-98, y(13), y(14)-98, y(14), y(14)++, y(15)-98, y(15), y(18)++, y(18)-98++, y(19)++, y(20)-98++, y(20)++
Precursor origin neutral loss: +

Peptide No.1103

TEDGGWEWSDDEFDEESEEGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of TEDGGWEWSDDEFDEESEEGR
Found in OXSR1_MOUSE, Serine/threonine-protein kinase OSR1 OS=Mus musculus GN=Oxsr1 PE=1 SV=1

Match to Query 6221: 2616.950658 from(1309.482605,2+)
Title: Elution from: 59.368 to 59.368 scan no 5400 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2616.9502
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 84 **Expect:** 7.2e-008

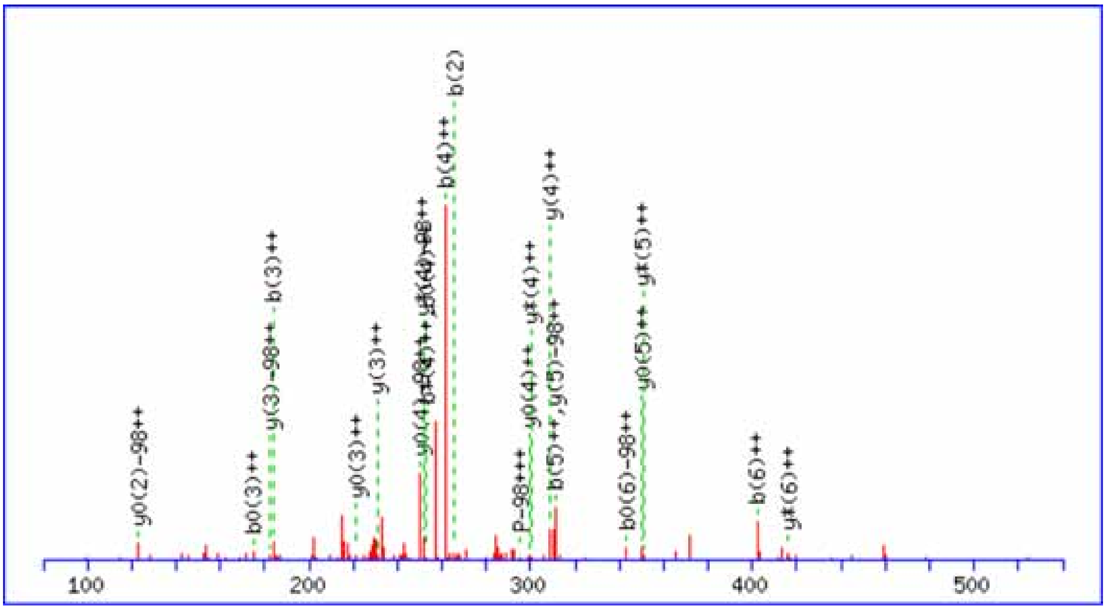
Matched b ions: b(5), b(6), b(7), b(8), b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(13)++, b(13)-98, b(13), b(14)-98, b(14), b(15)-98, b(15), b(16)-98, b(17)++, b(19)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)-98, y(13), y(14)-98, y(14), y(15)-98, y(16)-98++, y(19)-98++, y(20)++, y(20)-98++
Precursor origin neutral loss: +

Peptide No.1104

TETKVTK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of TETKVTK
Found in ARVC_MOUSE, Armadillo repeat protein deleted in velo-cardio-facial syndrome homolog OS=Mus musculus GN=Arvcf PE=1 SV=2

Match to Query 426: 981.577290 from(328.199706,3+)
Title: Elution from: 37.497 to 37.497 scan no 3167 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 981.5784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K4 : Dimethyl (K)
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K7 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 32 **Expect:** 0.0051

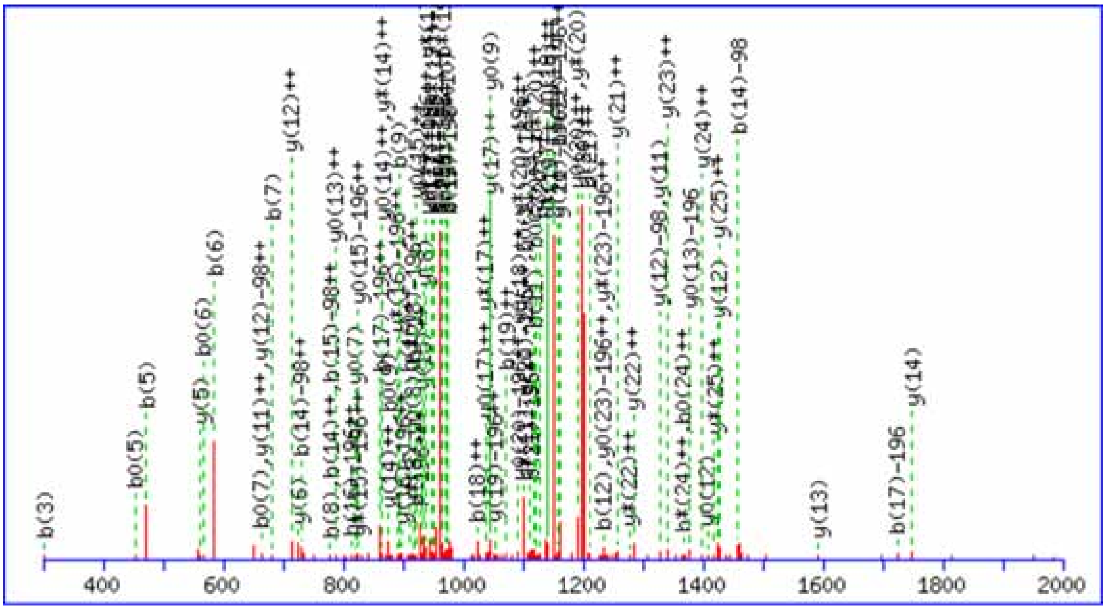
Matched b ions: b(2), b(3)++, b(4)++, b(5)++, b(6)++
Matched y ions: y(3)-98++, y(3)++, y(4)++, y(5)-98++
Precursor origin neutral loss:

Peptide No.1105

TGDLGIPPNPEDRSPSPEPIYNSEGK
Confirmed sites: @S:14,@S:16
Ambiguous sites:

MS/MS Fragmentation of TGDLGIPPNPEDRSPSPEPIYNSEGK
Found in SF01_MOUSE, Splicing factor 1 OS=Mus musculus GN=Sf1 PE=1 SV=5

Match to Query 8552: 2981.311665 from(994.777831,3+)
Title: Elution from: 48.975 to 48.975 scan no 4790 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2981.3096
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K26 : Dimethyl (K)
Ions Score: 68 **Expect:** 1.5e-005

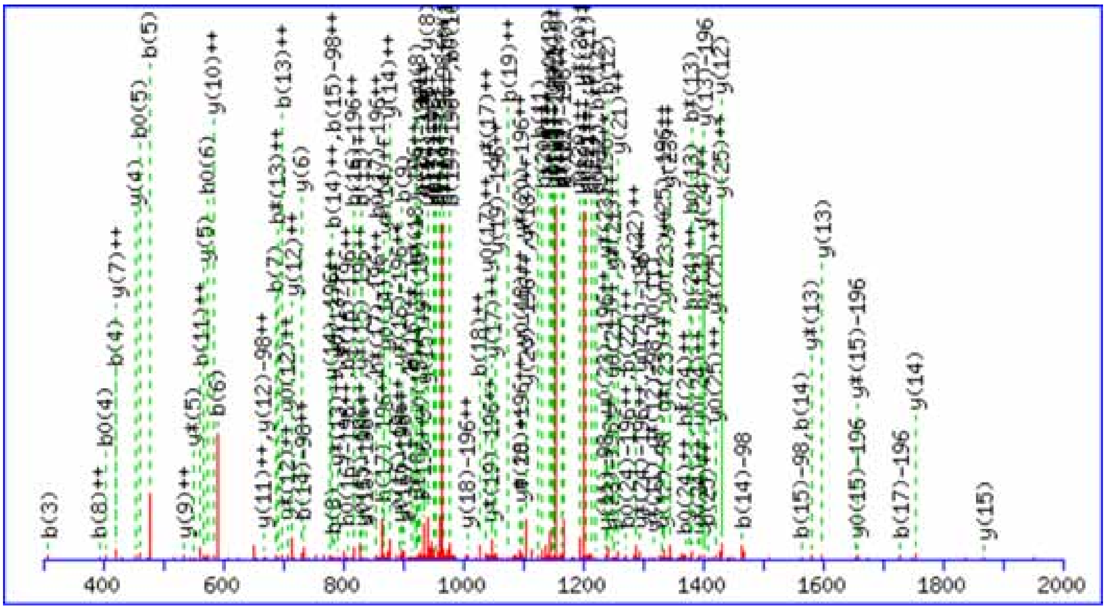
Matched b ions: b(3), b(5), b(6), b(7), b(8), b(9), b(11), b(12), b(14)-98++, b(14)-98, b(14)++, b(15)-98++, b(16)-98++, b(16)-98, b(16)-196++, b(16)++, b(17)-196++, b(17)-196, b(17)-98++, b(18)-98, b(18)++, b(18)-98++, b(19)-98++, b(19)-196++, b(19)++, b(20)++, b(21)-98++, b(21)++, b(21)-196++, b(24)-98++
Matched y ions: y(5), y(6), y(8), y(10), y(11)++, y(11), y(12)++, y(12)-98++, y(12), y(12)-98, y(13), y(14), y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(17)++, y(17)-196++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(19)-196++, y(20)-196++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(21)-196++, y(22)++, y(22)-98++, y(23)++, y(24)++, y(25)-98++, y(25)++
Precursor origin neutral loss: +

Peptide No.1106

TGDLGIPPNPEDRSPSPEPIYNSEGK
Confirmed sites: @S:14,@S:16
Ambiguous sites:

MS/MS Fragmentation of TGDLGIPPNPEDRSPSPEPIYNSEGK
Found in SF01_MOUSE, Splicing factor 1 OS=Mus musculus GN=Sf1 PE=1 SV=5

Match to Query 7403: 2993.375436 from(998.799088,3+)
Title: Elution from: 48.031 to 48.031 scan no 4460 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2993.3733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K26 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 86 **Expect:** 2.6e-007

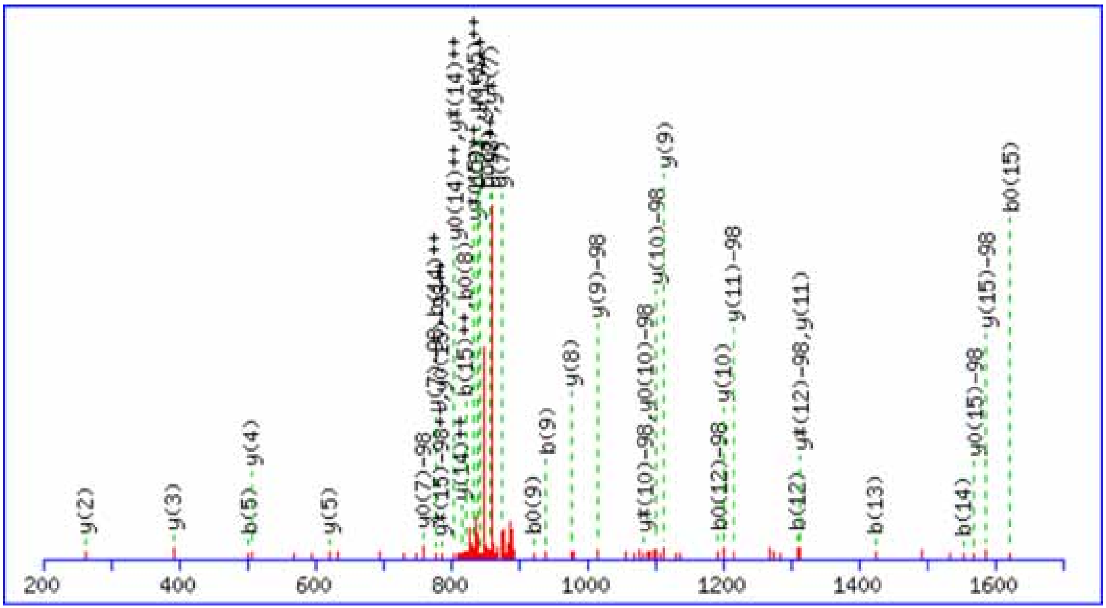
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)++, b(8), b(9), b(11)++, b(11), b(12), b(13)++, b(13), b(14)-98++, b(14)-98, b(14), b(14)++, b(15)-98, b(15)-98++, b(15)++, b(16)-98++, b(16)-98, b(16)-196++, b(16)++, b(17)-196++, b(17)-196, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)-196++, b(19)++, b(20)-98++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(24)-98++, b(24)++, b(25)-98++, b(25)++
Matched y ions: y(4), y(5), y(6), y(7)++, y(8), y(9)++, y(10), y(10)++, y(11)++, y(11)-98, y(12)++, y(12), y(12)-98, y(12)-98++, y(13), y(13)-196, y(14)-98, y(14), y(14)++, y(14)-98++, y(14)-196++, y(15), y(15)-196++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(17)++, y(17)-196++, y(18)++, y(18)-98++, y(18)-196++, y(19)-98++, y(19)++, y(19)-196++, y(20)-196++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(23)++, y(23)-98++, y(23)-196++, y(24)++, y(25)-98++, y(25)++, y(25)-196++
Precursor origin neutral loss: +

Peptide No.1107

TGEADLSHTSSDDESR
Confirmed sites:
Ambiguous sites: @S:10orS:11

MS/MS Fragmentation of TGEADLSHTSSDDESR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 3486: 1813.701834 from(907.858193,2+)
Title: Elution from: 24.275 to 24.275 scan no 1379 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1813.7003
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.0005

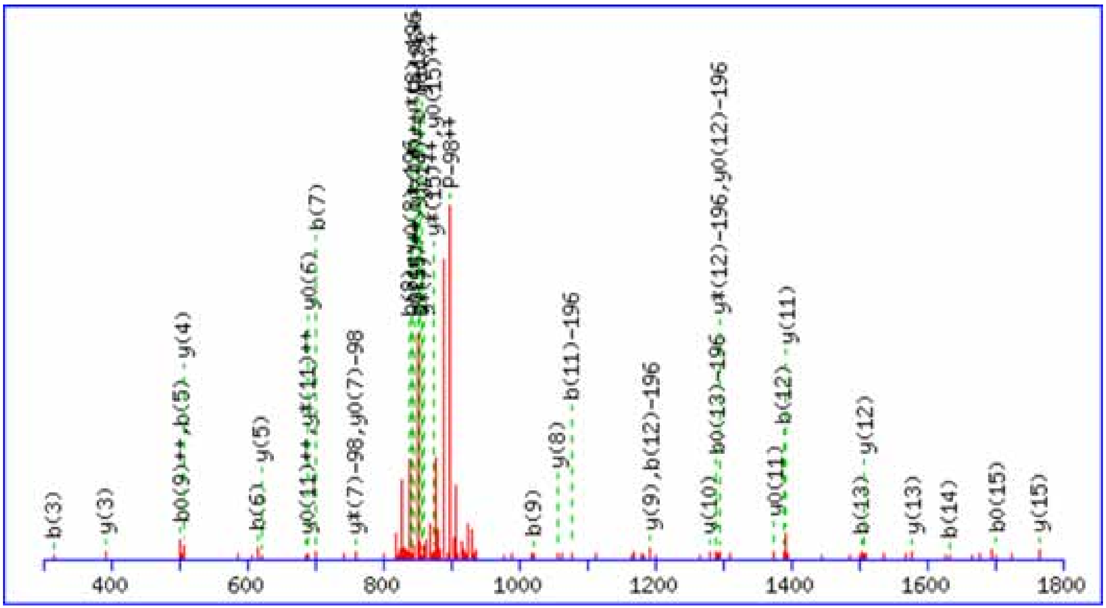
Matched b ions: b(5), b(8), b(9), b(12), b(13), b(14), b(14)++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(7)-98, y(8), y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(14)++, y(15)-98, y(15)++
Precursor origin neutral loss: +

Peptide No.1108

TGEADLSHTSSDDESR
Confirmed sites: @T:9
Ambiguous sites: @S:10orS:11

MS/MS Fragmentation of TGEADLSHTSSDDESR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 4350: 1893.667506 from(947.841029,2+)
Title: Elution from: 25.520 to 25.520 scan no 1535 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1893.6667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.00029

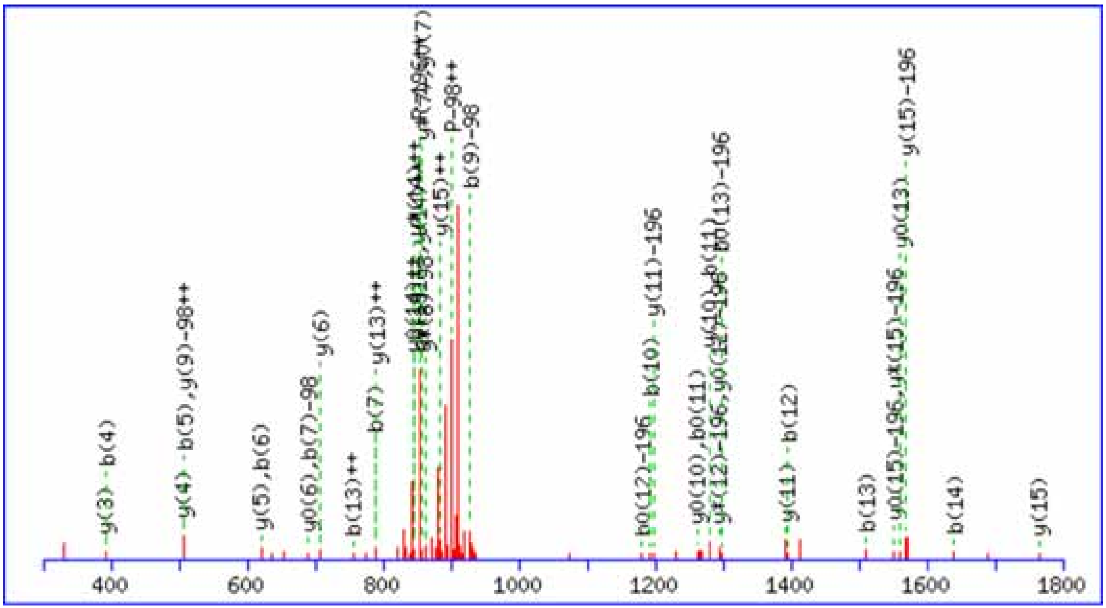
Matched b ions: b(3), b(5), b(6), b(7), b(8), b(9), b(11)-196, b(12)-196, b(12)-98, b(12), b(13), b(14)-98, b(14)
Matched y ions: y(3), y(4), y(5), y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(13), y(13)-98++, y(14)++, y(15), y(15)-98
Precursor origin neutral loss: +

Peptide No.1109

TGEADLSHTSSDDESR
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of TGEADLSHTSSDDESR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 3896: 1899.698468 from(950.856510,2+)
Title: Elution from: 25.322 to 25.322 scan no 1467 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1899.6985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.00089

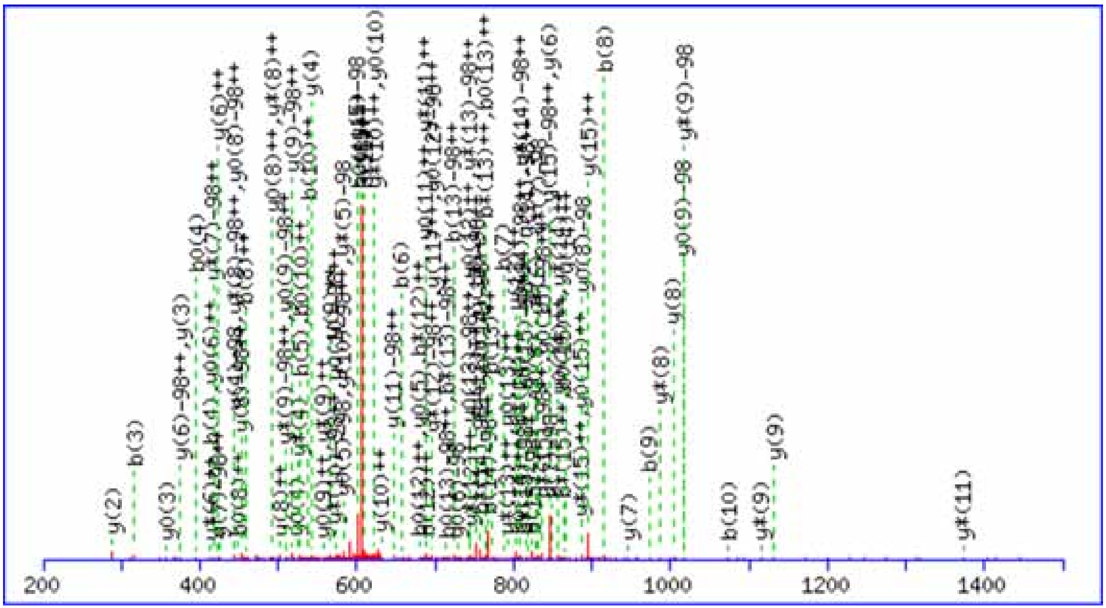
Matched b ions: b(4), b(5), b(6), b(7), b(7)-98, b(9)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(13)++, b(14)
Matched y ions: y(3), y(4), y(5), y(6), y(9)-98++, y(10), y(10)-98, y(11), y(11)-98, y(11)-196, y(13)++, y(14)++, y(15)-196, y(15), y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1110

TGEPDEEEGTFRSSIR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of TGEPDEEEGTFRSSIR
Found in PLM_MOUSE, Phospholemman OS=Mus musculus GN=Fxyd1 PE=1 SV=1

Match to Query 3994: 1916.816277 from(639.946035,3+)
Title: Elution from: 33.658 to 33.658 scan no 2492 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1916.8153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.014

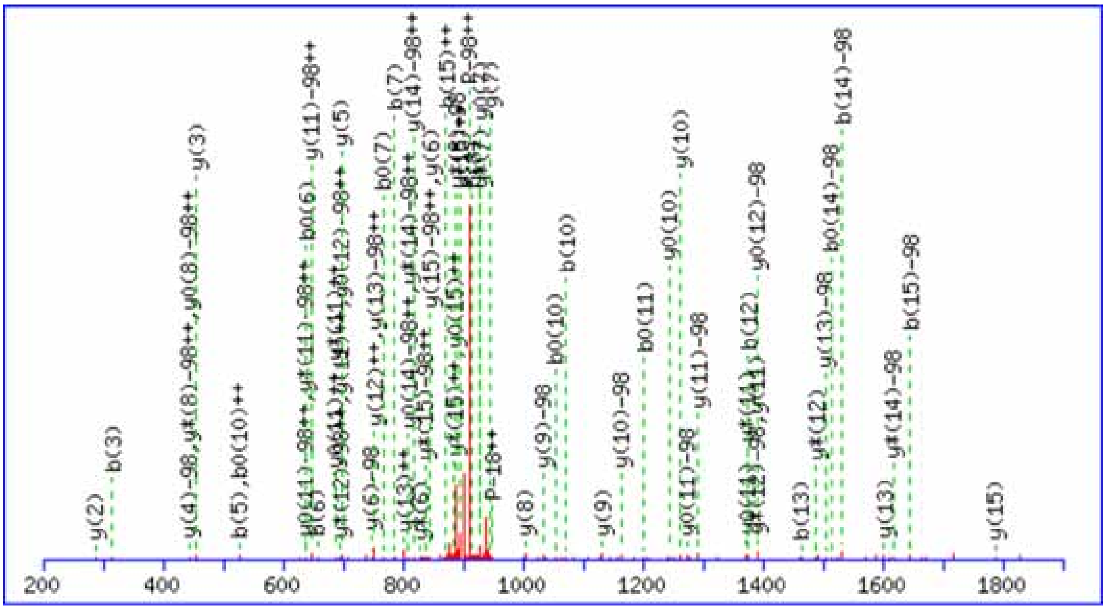
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(8)++, b(9), b(10), b(10)++, b(11)++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15)-98++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(6), y(6)-98++, y(6)++, y(7)-98++, y(7)-98, y(7), y(8)-98++, y(8), y(8)++, y(9)-98++, y(9), y(9)++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1111

TGEPDEEEGTFRSSIR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of TGEPDEEEGTFRSSIR
Found in PLM_MOUSE, Phospholemman OS=Mus musculus GN=Fxyd1 PE=1 SV=1

Match to Query 5154: 1916.814870 from(959.414711,2+)
Title: Elution from: 33.969 to 33.969 scan no 2846 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1916.8153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.0018

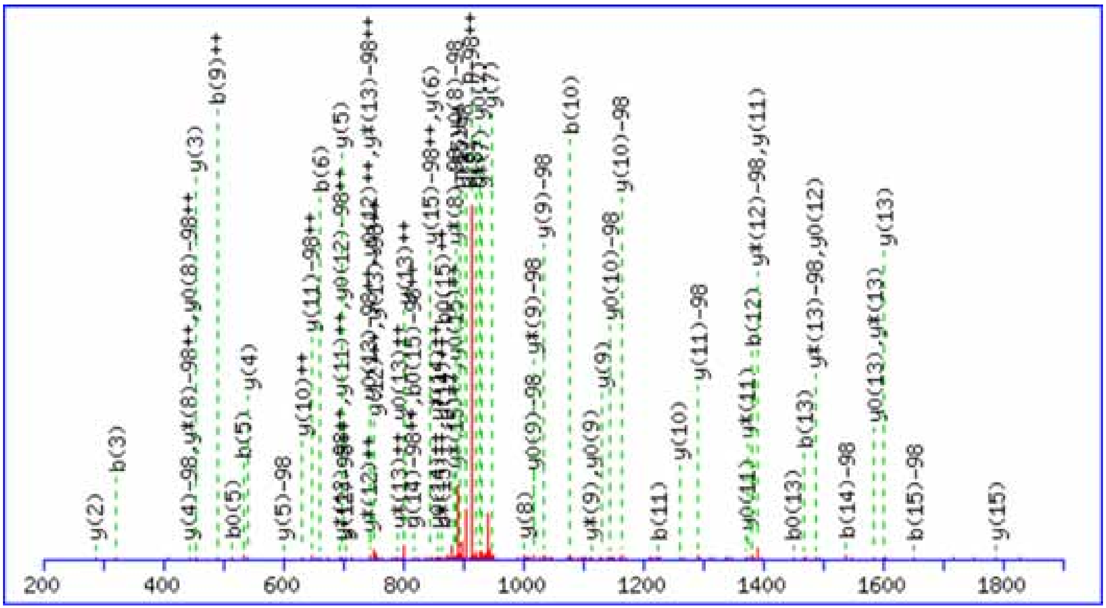
Matched b ions: b(3), b(5), b(6), b(7), b(8), b(10), b(12), b(13), b(14)-98, b(15)-98, b(15)++
Matched y ions: y(2), y(3), y(4)-98, y(5), y(6)-98, y(6), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11)-98++, y(11)-98, y(11), y(11)++, y(12)++, y(13)-98++, y(13), y(13)++, y(13)-98, y(14)-98++, y(15), y(15)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.1112

TGEPDEEEGTFRSSIR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of TGEPDEEEGTFRSSIR
Found in PLM_MOUSE, Phospholemman OS=Mus musculus GN=Fxyd1 PE=1 SV=1

Match to Query 4033: 1922.848032 from(962.431292,2+)
Title: Elution from: 33.353 to 33.353 scan no 2453 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1922.8471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 Expect: 0.0085

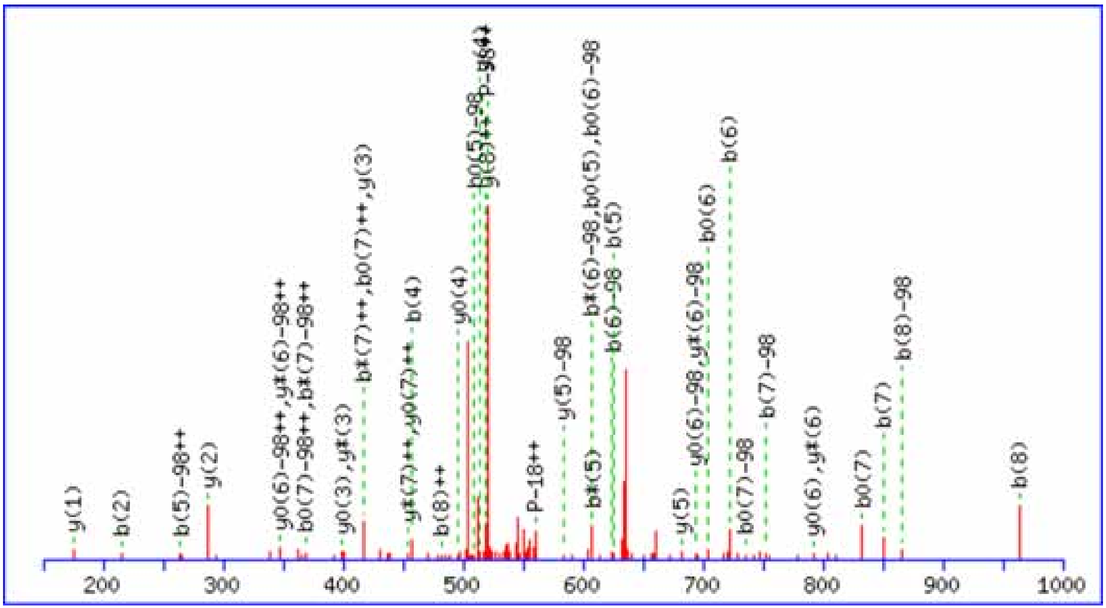
Matched b ions: b(3), b(5), b(6), b(8), b(9)++, b(10), b(11), b(12), b(13), b(14)-98, b(15)-98
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10)-98, y(10), y(10)++, y(11)-98++, y(11)-98, y(11), y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(13), y(14)-98++, y(14)++, y(15), y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1113

TLDQSPELR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of TLDQSPELR
Found in MTOR_MOUSE, Serine/threonine-protein kinase mTOR OS=Mus musculus GN=Mtor PE=1 SV=2

Match to Query 774: 1137.506950 from(569.760751,2+)
Title: Elution from: 47.591 to 47.591 scan no 4280 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1137.5067
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.025

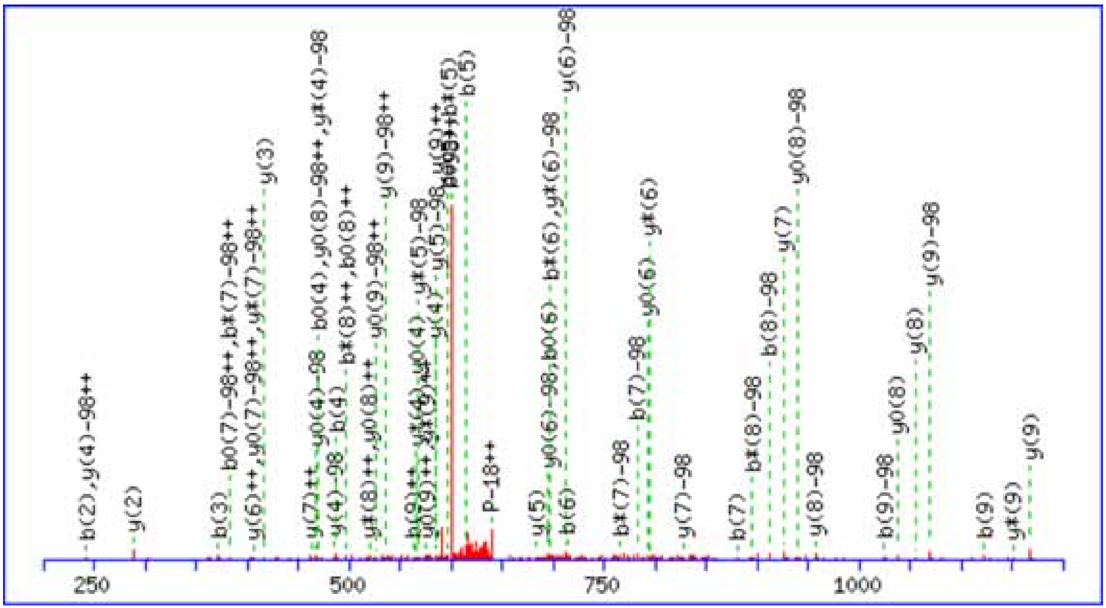
Matched b ions: b(2), b(4), b(5)-98++, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)-98, y(8)++
Precursor origin neutral loss: +

Peptide No.1114

TLEDQVSELK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of TLEDQVSELK
Found in MYH1_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Match to Query 1104: 1296.621778 from(649.318165,2+)
Title: Elution from: 39.854 to 39.854 scan no 3435 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1296.6214
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K10 : Dimethyl (K)
Ions Score: 30 Expect: 0.038

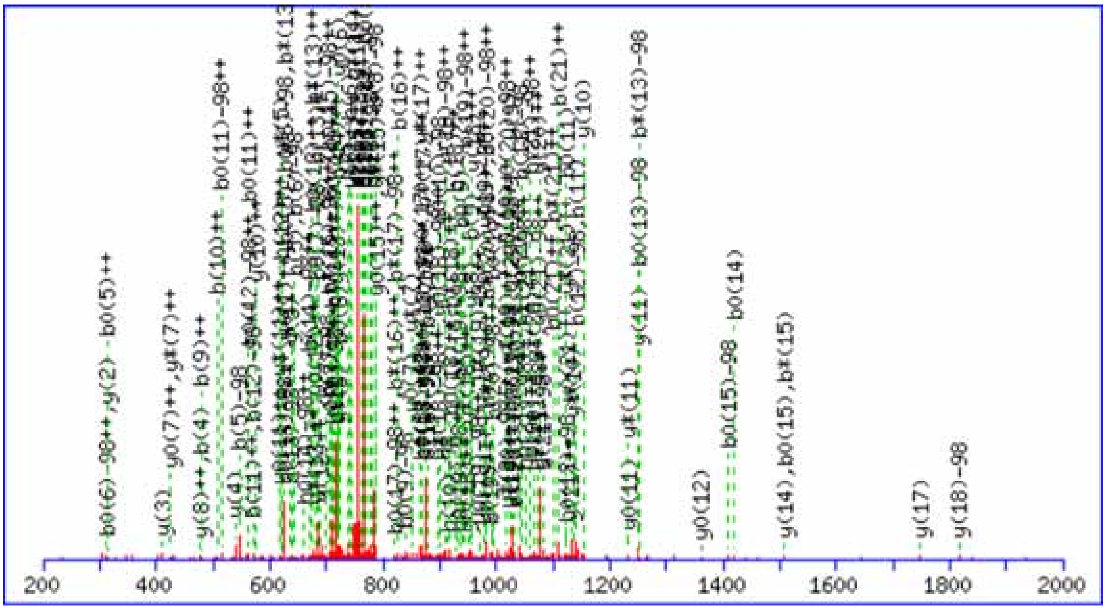
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)-98, b(7), b(8)-98, b(9), b(9)-98, b(9)++
Matched y ions: y(2), y(3), y(4)-98++, y(4)-98, y(4), y(5)-98, y(5), y(6)-98, y(6)++, y(7), y(7)++, y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1115

TLPHSPGSAGEPQASQTVQVHR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of TLPHSPGSAGEPQASQTVQVHR
Found in MYOM3_MOUSE, Myomesin-3 OS=Mus musculus GN=Myom3 PE=2 SV=1

Match to Query 7269: 2391.133866 from(798.051898,3+)
Title: Elution from: 32.481 to 32.481 scan no 2644 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2391.1332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 0.00041

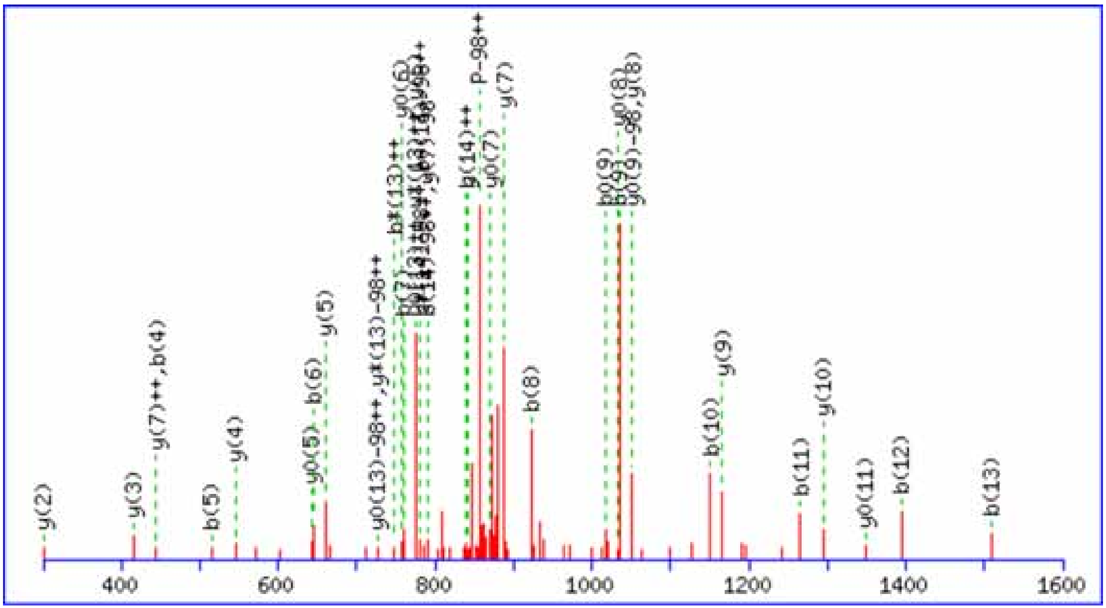
Matched b ions: b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(9)++, b(9), b(10)++, b(10)-98, b(11), b(11)++, b(11)-98, b(12)-98, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(10)++, y(11)++, y(11), y(12)++, y(13)++, y(14), y(14)++, y(17)++, y(17), y(18)-98, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.1116

TLSNAEDYLDDEDSD
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of TLSNAEDYLDDEDSD
Found in OSTF1_MOUSE, Osteoclast-stimulating factor 1 OS=Mus musculus GN=Ostf1 PE=1 SV=2

Match to Query 4396: 1808.651428 from(905.332990,2+)
Title: Elution from: 51.388 to 51.388 scan no 5075 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1808.6513
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 95 Expect: 3.8e-009

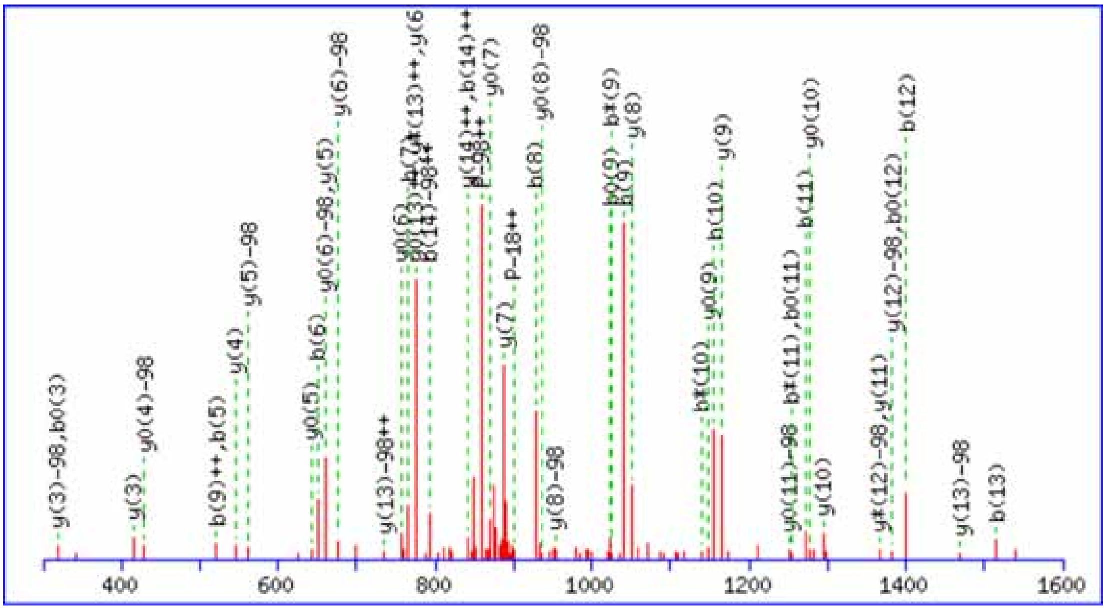
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13), b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(7)-98, y(8), y(9), y(10), y(14)++
Precursor origin neutral loss: +

Peptide No.1117

TLSNAEDYLDDEDSD
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of TLSNAEDYLDDEDSD
Found in OSTF1_MOUSE, Osteoclast-stimulating factor 1 OS=Mus musculus GN=Ostf1 PE=1 SV=2

Match to Query 3496: 1814.686002 from(908.350277,2+)
Title: Elution from: 50.986 to 50.986 scan no 4793 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1814.6831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 79 **Expect:** 1.9e-007

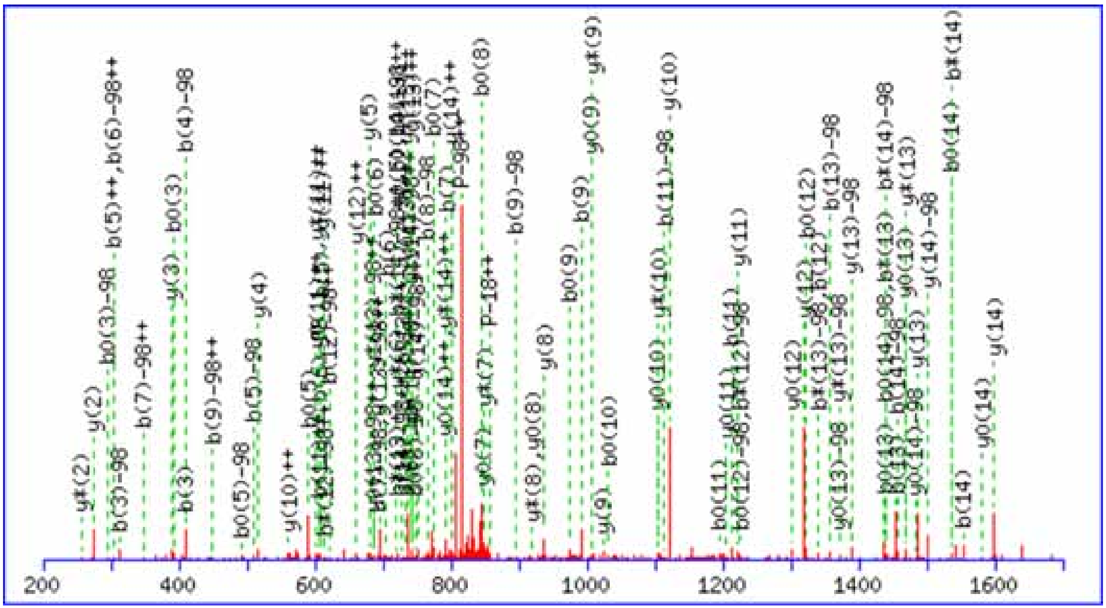
Matched b ions: b(5), b(6), b(7), b(8), b(9)++, b(9), b(10), b(11), b(12), b(13), b(14)-98++, b(14)++
Matched y ions: y(3), y(3)-98, y(4), y(5), y(5)-98, y(6), y(6)-98, y(7), y(8), y(8)-98, y(9), y(10), y(11), y(12)-98, y(13)-98, y(13)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1118

TLSPTPSAEGYQDVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 3009: 1727.777658 from(864.896105,2+)
Title: Elution from: 38.091 to 38.091 scan no 3217 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1727.7767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 Expect: 2.6e-006

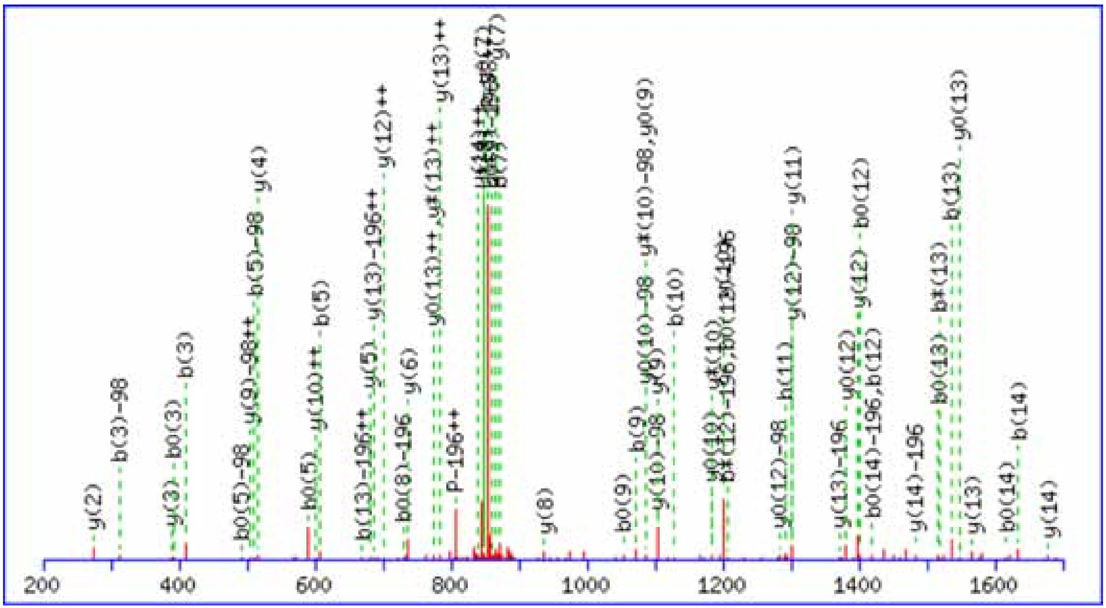
Matched b ions: b(3), b(3)-98, b(4)-98, b(5)-98, b(5), b(5)++, b(6)-98++, b(6)-98, b(6), b(7)-98, b(7)-98++, b(7), b(8)-98, b(9), b(9)-98++, b(9)-98, b(11), b(11)++, b(11)-98, b(12), b(12)-98++, b(13), b(13)-98, b(13)++, b(14), b(14)-98, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13), y(13)-98++, y(13)-98, y(13)++, y(14), y(14)-98, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1119

TLSPTPSAEGYQDVR
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of TLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 4384: 1807.743862 from(904.879207,2+)
Title: Elution from: 41.037 to 41.037 scan no 3802 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1807.7431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 1e-005

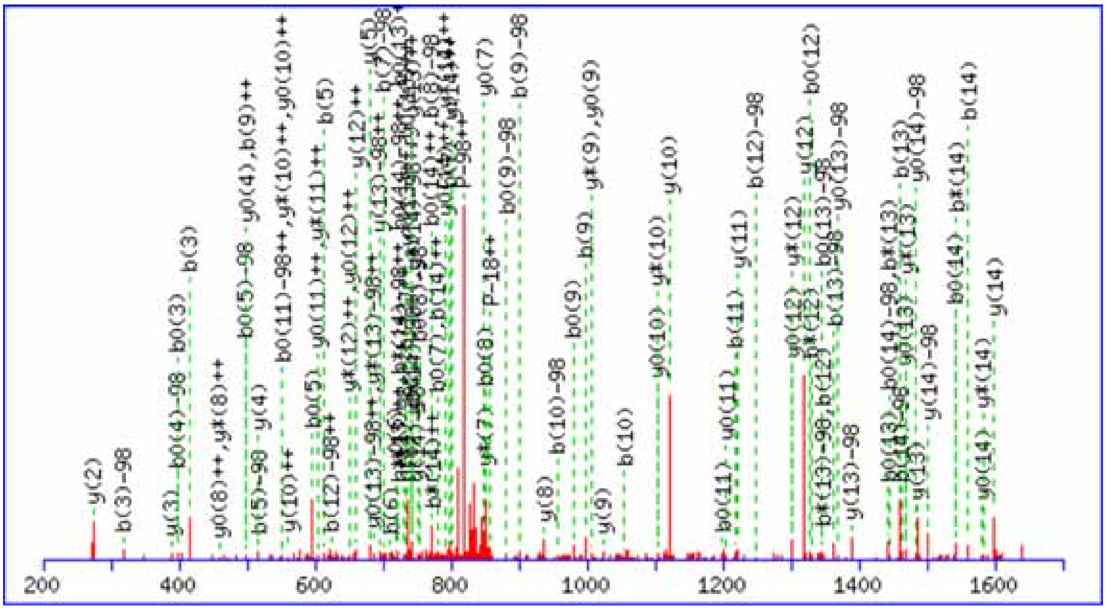
Matched b ions: b(3), b(3)-98, b(5)-98, b(5), b(7)-98, b(7), b(8)-98, b(9), b(9)-98, b(10), b(11), b(11)-98, b(12), b(13), b(13)-196++, b(13)-98, b(14), b(14)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98++, y(10)-98, y(10), y(10)++, y(11), y(12)-98, y(12), y(12)++, y(13)-98++, y(13), y(13)-98, y(13)-196, y(13)-196++, y(13)++, y(14), y(14)-98, y(14)-196, y(14)++
Precursor origin neutral loss: +

Peptide No.1120

TLSPTPSAEGYQDVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 3030: 1733.809666 from(867.912109,2+)
Title: Elution from: 38.068 to 38.068 scan no 3173 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1733.8085
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 85 Expect: 1.6e-007

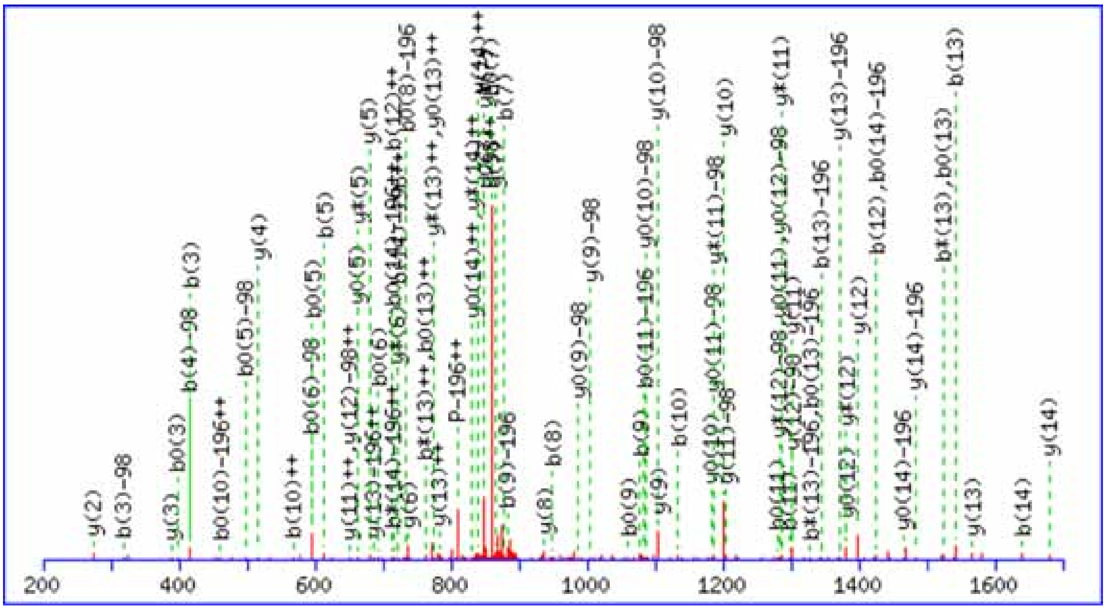
Matched b ions: b(3), b(3)-98, b(5)-98, b(5), b(6), b(7)-98, b(7), b(8)-98, b(9), b(9)-98, b(9)++, b(10)-98, b(10), b(11), b(12)-98, b(12)-98++, b(12), b(13), b(13)-98, b(13)++, b(14), b(14)-98, b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(10)++, y(11), y(12), y(12)++, y(13), y(13)-98, y(13)++, y(13)-98++, y(14), y(14)-98, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1121

TLSPTPSAEGYQDVR
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of TLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 3093: 1813.776092 from(907.895322,2+)
Title: Elution from: 40.857 to 40.857 scan no 3473 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1813.7749
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 **Expect:** 8.8e-006

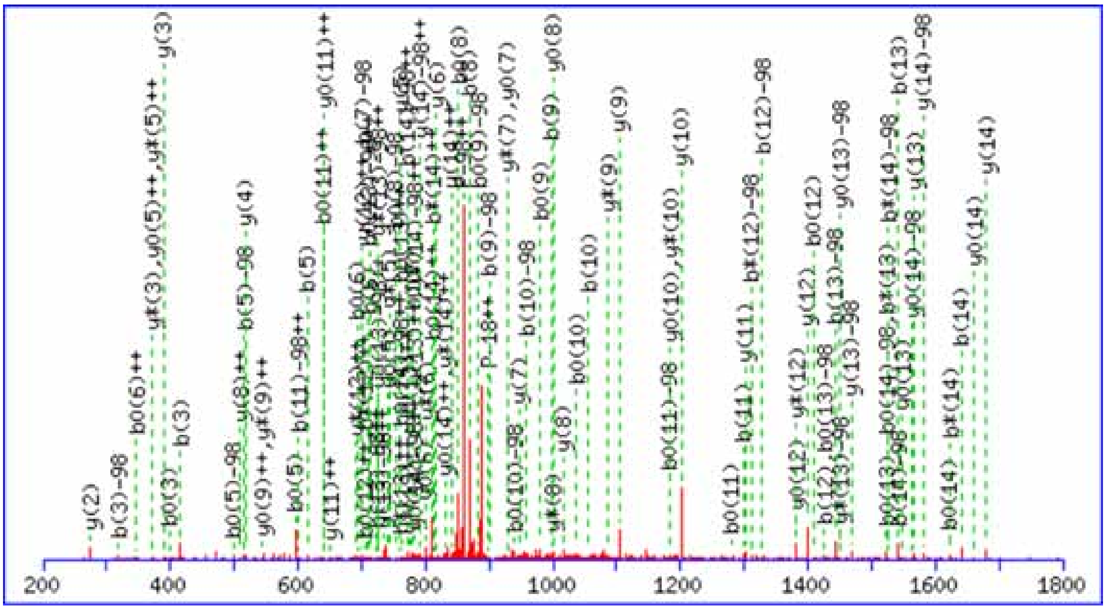
Matched b ions: b(3), b(3)-98, b(4)-98, b(5), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(9)-196, b(10)-98, b(10)++, b(10), b(11)-98, b(11), b(12), b(12)-98, b(12)++, b(13), b(13)-98, b(13)-196, b(14)-98++, b(14), b(14)-98, b(14)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10)-98, y(10), y(11), y(11)-98, y(11)++, y(12)-98, y(12), y(12)-98++, y(13), y(13)-98, y(13)-196, y(13)-196++, y(13)-98++, y(13)++, y(14), y(14)-98, y(14)-196, y(14)++
Precursor origin neutral loss: +

Peptide No.1122

TLSPTPSAEGYQDVR
Confirmed sites: @S:3,@Y:11
Ambiguous sites:

MS/MS Fragmentation of TLSPTPSAEGYQDVR
Found in ABLM1_MOUSE, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 3094: 1813.776232 from(907.895392,2+)
Title: Elution from: 40.518 to 40.518 scan no 3429 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1813.7749
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y11 : Phospho (Y)
Ions Score: 36 **Expect:** 0.0091

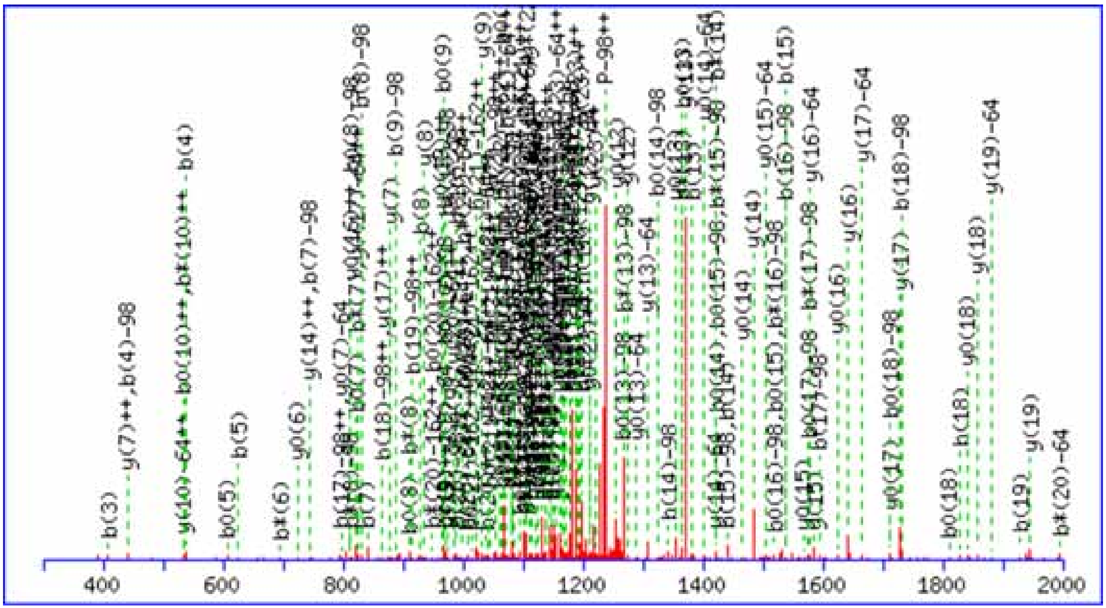
Matched b ions: b(3), b(3)-98, b(5)-98, b(5), b(6), b(7)-98, b(8), b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98++, b(12), b(12)-98, b(13), b(13)-98, b(13)-98++, b(14), b(14)-98, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10), y(11), y(11)++, y(12), y(12)++, y(13)-98++, y(13)-98, y(13), y(13)++, y(14), y(14)-98, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1123

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6751: 2569.072518 from(1285.543535,2+)
Title: Elution from: 39.176 to 39.176 scan no 3366 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2569.0714
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 46 **Expect:** 0.0014

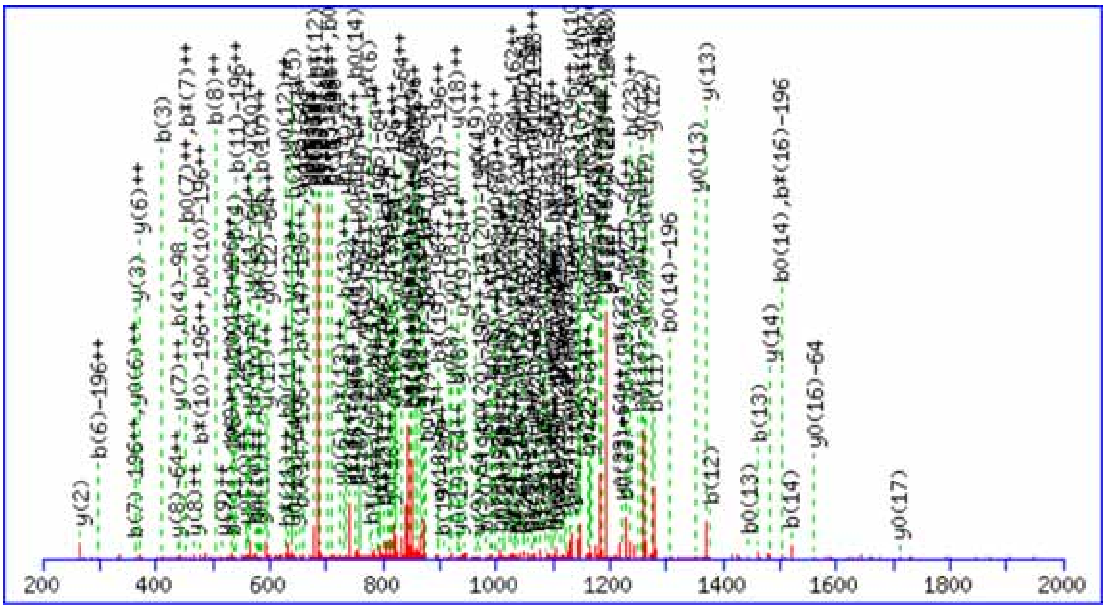
Matched b ions: b(3), b(4)-98, b(4), b(5), b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(13), b(14), b(14)-98, b(15)-98, b(15), b(16)-98, b(17)-98, b(17)-98++, b(18)-98, b(18), b(18)-98++, b(19), b(19)-98++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)-98++, b(23)++
Matched y ions: y(7)++, y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(16), y(17), y(17)++, y(18), y(19), y(19)++, y(21)++, y(22)-98++, y(22)++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.1124

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:3
Ambiguous sites: @S:5orS:6

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6754: 2649.039264 from(884.020364,3+)
Title: Elution from: 42.276 to 42.276 scan no 3744 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2649.0377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 44 **Expect:** 0.0018

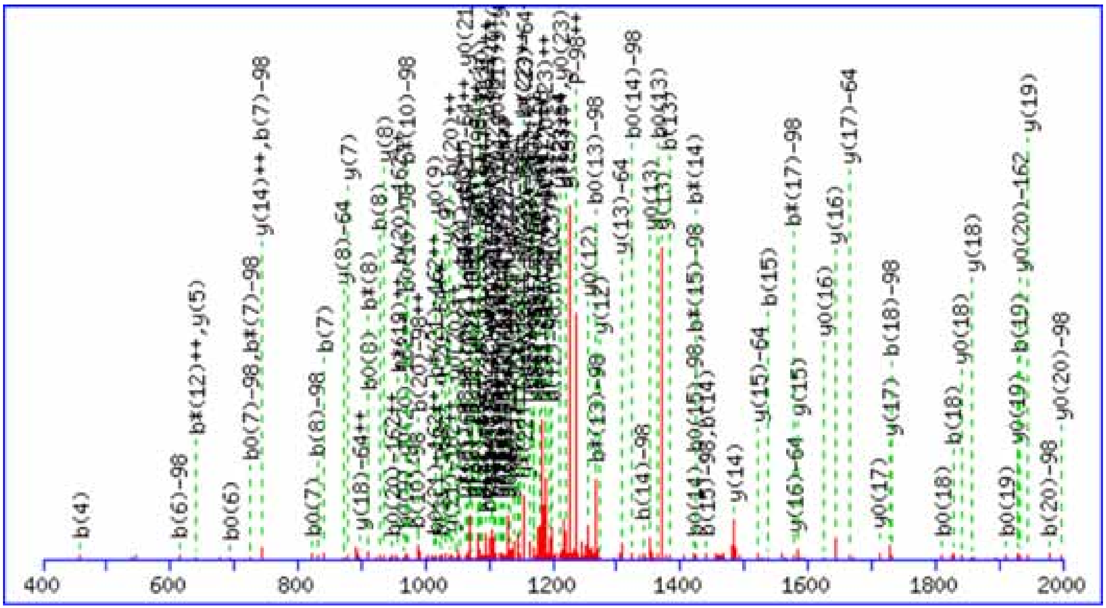
Matched b ions: b(3), b(4)-98, b(4), b(6)-196++, b(6)-98, b(7), b(7)-98++, b(7)-196++, b(7)-98, b(8), b(8)-196, b(8)++, b(9), b(9)-196, b(9)++, b(10)-98++, b(10)++, b(10), b(11), b(11)++, b(11)-98++, b(11)-196++, b(11)-98, b(12)-98, b(12)-98++, b(12)++, b(12), b(12)-196, b(13), b(13)-98, b(13)++, b(14), b(14)++, b(14)-98++, b(15)-98, b(15)-98++, b(15)-196++, b(15)++, b(16)-196++, b(16)-98++, b(16)++, b(17)-98++, b(18)-196++, b(19)++, b(19)-196++, b(20)++, b(20)-196++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(22)-196++, b(23)++, b(23)-98++
Matched y ions: y(2), y(3), y(5), y(6)++, y(6), y(7)++, y(8)++, y(8), y(9), y(9)++, y(10)++, y(10), y(11)++, y(11), y(12), y(12)++, y(13)++, y(13), y(14)++, y(14), y(15)++, y(16)++, y(17)++, y(18)++, y(20)-98++, y(20)++, y(21)++, y(22)-196++, y(23)++, y(23)-196++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1125

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6554: 2569.071532 from(1285.543042,2+)
Title: Elution from: 39.014 to 39.014 scan no 3320 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2569.0714
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 60 Expect: 6e-005

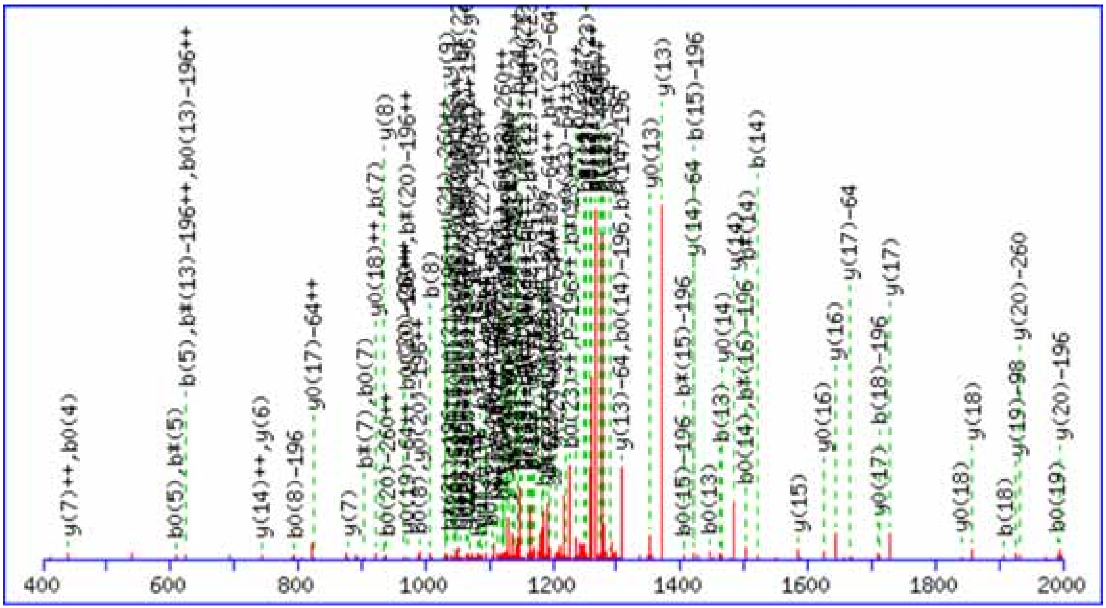
Matched b ions: b(4), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(13), b(14), b(14)-98, b(15)-98, b(15), b(18), b(18)-98, b(19), b(20)-98++, b(20)-98, b(20)++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++, b(23)++
Matched y ions: y(5), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)++, y(14), y(15), y(16), y(17), y(18), y(19), y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.1126

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7111: 2649.038408 from(1325.526480,2+)
Title: Elution from: 42.287 to 42.287 scan no 3812 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2649.0377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 69 **Expect:** 4.7e-006

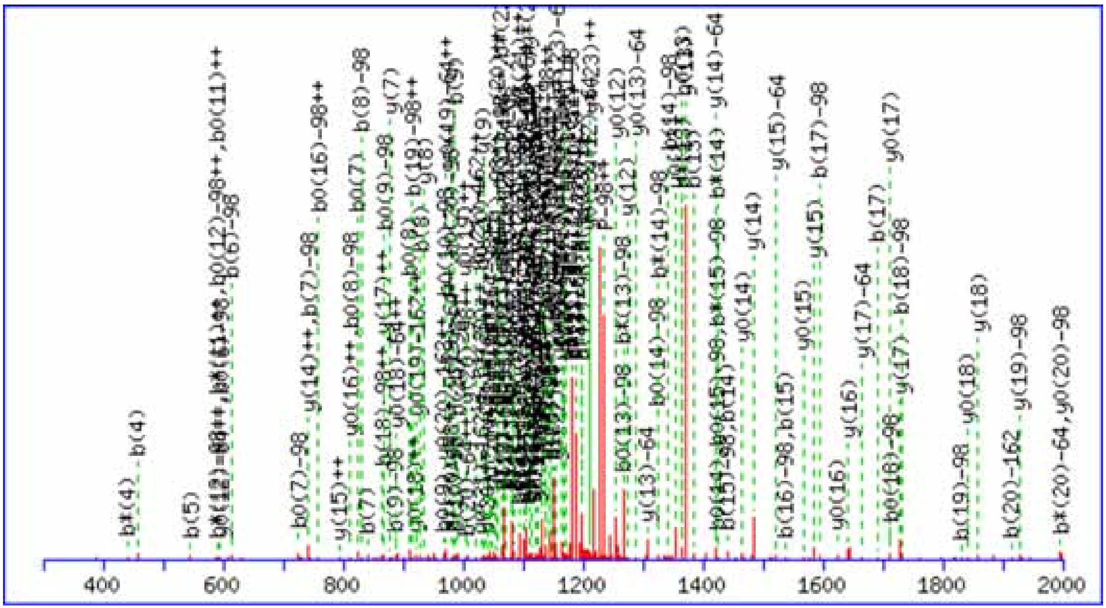
Matched b ions: b(5), b(6)-98, b(7)-98, b(7), b(8), b(9), b(9)-98, b(10)-98, b(10), b(11)-196, b(11), b(11)-98, b(12)-98, b(12)-196, b(13)-196, b(13), b(14), b(14)-98, b(15)-98, b(15)-196, b(18), b(18)-196, b(21)-98++, b(21)-196++, b(21)++, b(22)++, b(22)-196++, b(22)-98++, b(23)-98++, b(23)-196++, b(23)++
Matched y ions: y(6), y(7)++, y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(16), y(17), y(18), y(19)-98, y(20)-196, y(20)-98++, y(21)-196++, y(21)-98++, y(21)++, y(22)-196++, y(22)-98++, y(22)++, y(23)-196++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1127

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7796: 2569.072358 from(1285.543455,2+)
Title: Elution from: 39.003 to 39.003 scan no 3532 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2569.0714
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 70 Expect: 5.3e-006

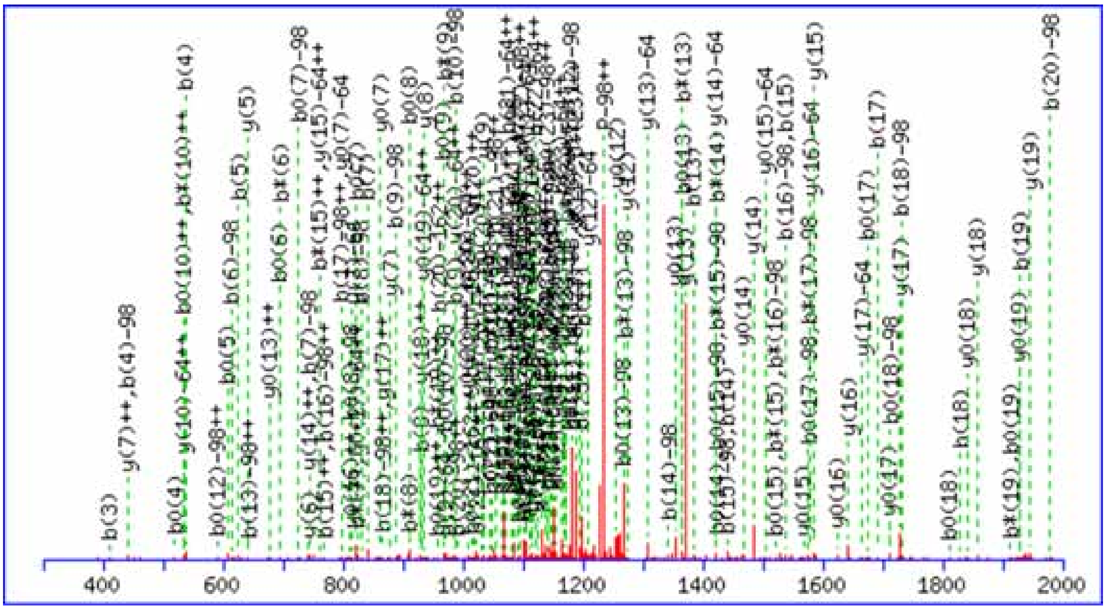
Matched b ions: b(4), b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(12)-98, b(13), b(14), b(14)-98, b(15)-98, b(15), b(16)-98, b(17)-98, b(17), b(18)-98, b(18)-98++, b(19)-98, b(19)-98++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)-98++, b(23)++
Matched y ions: y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)++, y(14), y(15), y(15)++, y(16), y(17), y(17)++, y(18), y(19)-98, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1128

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6823: 2569.072094 from(1285.543323,2+)
Title: Elution from: 39.244 to 39.244 scan no 3370 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2569.0714
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 66 **Expect:** 1.5e-005

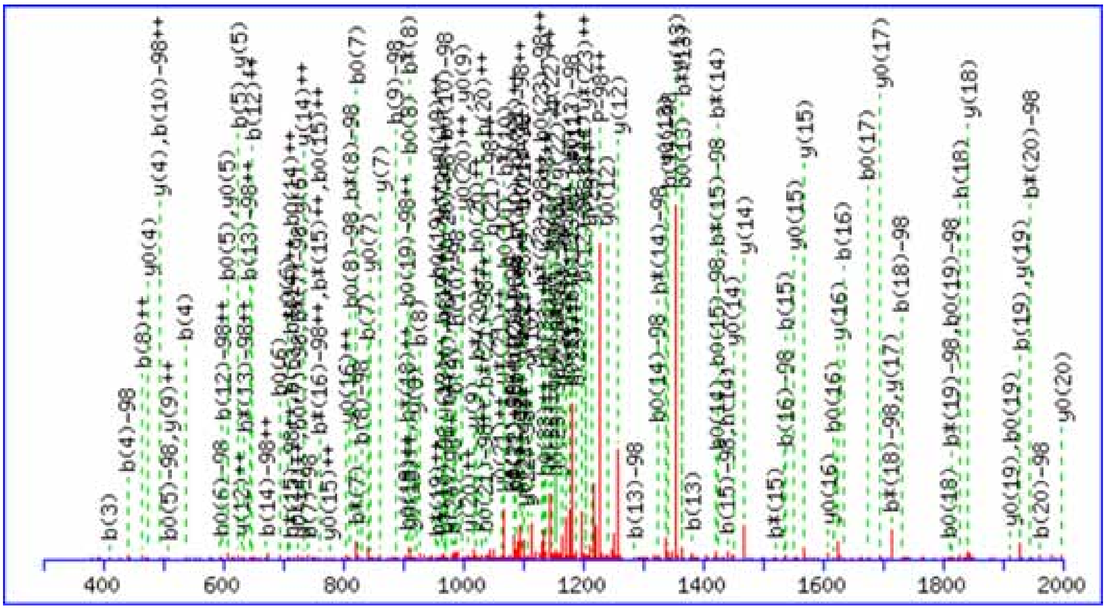
Matched b ions: b(3), b(4)-98, b(4), b(5), b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(13)-98++, b(13), b(14), b(14)-98, b(15)-98, b(15)++, b(15), b(16)-98++, b(16)-98, b(17), b(17)-98++, b(18)-98, b(18), b(18)-98++, b(19), b(20)-98++, b(20)-98, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++, b(23)++
Matched y ions: y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)++, y(14), y(15), y(16), y(17), y(17)++, y(18), y(18)++, y(19), y(20)++, y(21)++, y(23)++
Precursor origin neutral loss: +

Peptide No.1129

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6203: 2553.077606 from(1277.546079,2+)
Title: Elution from: 44.462 to 44.462 scan no 3928 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2553.0764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 3.2e-007

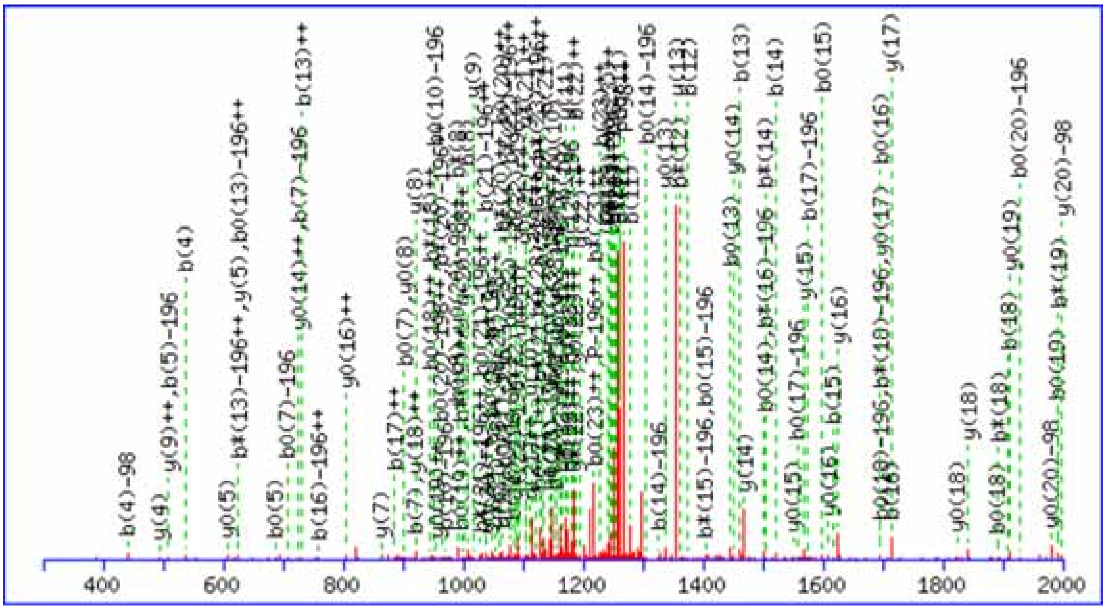
Matched b ions: b(3), b(4)-98, b(4), b(5), b(6), b(7)-98, b(7), b(8)++, b(8), b(8)-98, b(9), b(9)-98, b(10)-98++, b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(12)-98++, b(12)++, b(13), b(13)-98++, b(13)-98, b(14), b(14)-98, b(14)-98++, b(15)-98, b(15), b(16)-98, b(16), b(18), b(18)-98, b(19), b(19)++, b(20)-98, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)++, b(23)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11), y(12)++, y(12), y(13), y(14), y(14)++, y(15), y(16), y(17), y(18), y(19), y(19)++, y(20)++, y(22)-98++, y(22)++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.1130

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 8407: 2633.043474 from(1317.529013,2+)
Title: Elution from: 48.064 to 48.064 scan no 4713 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2633.0428
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 Expect: 6.7e-005

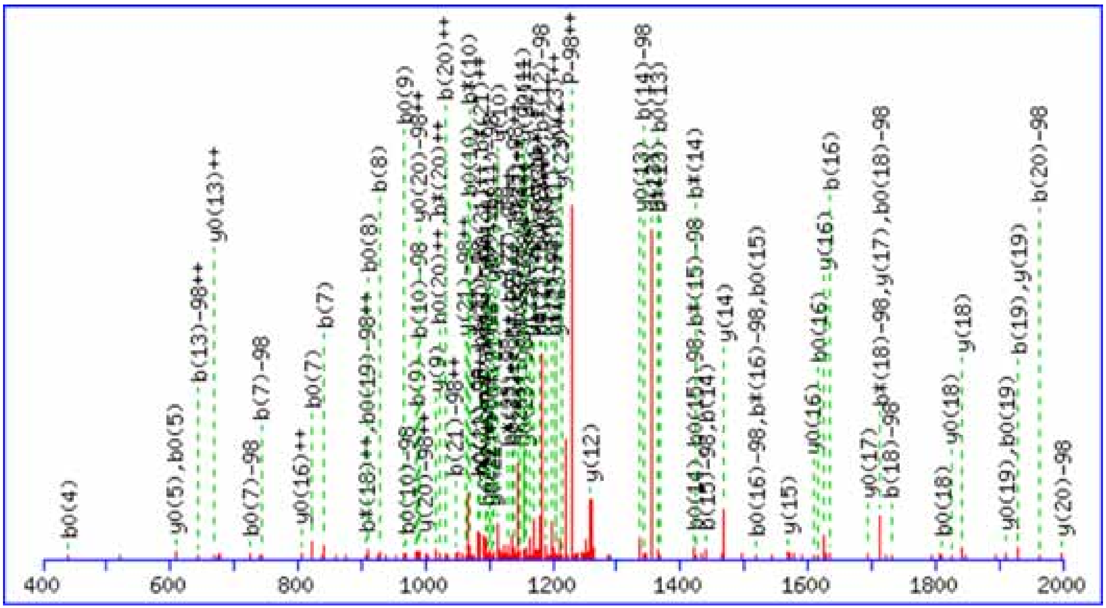
Matched b ions: b(4)-98, b(4), b(5)-98, b(5)-196, b(6)-98, b(7)-98, b(7), b(7)-196, b(8), b(8)-98, b(9), b(9)-98, b(10)-196, b(10), b(11), b(11)-196, b(11)-98, b(12)-98, b(12)-196, b(12), b(13), b(13)++, b(14), b(14)-98, b(14)-196, b(15)-98, b(15), b(16), b(16)-196++, b(16)-98, b(17)-196, b(17)++, b(18), b(18)-98++, b(19)-98, b(19)-98++, b(21)-98++, b(21)++, b(21)-196++, b(22)++, b(22)-196++, b(22)-98++, b(23)-196++, b(23)-98++, b(23)++
Matched y ions: y(4), y(5), y(7), y(8), y(9)++, y(9), y(10), y(11), y(13), y(14), y(15), y(16), y(17), y(18)++, y(18), y(20)-98, y(20)-98++, y(21)++, y(22)-98++, y(22)++, y(23)-196++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.1131

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6880: 2553.077972 from(1277.546262,2+)
Title: Elution from: 44.544 to 44.544 scan no 4088 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2553.0764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 Expect: 7.3e-006

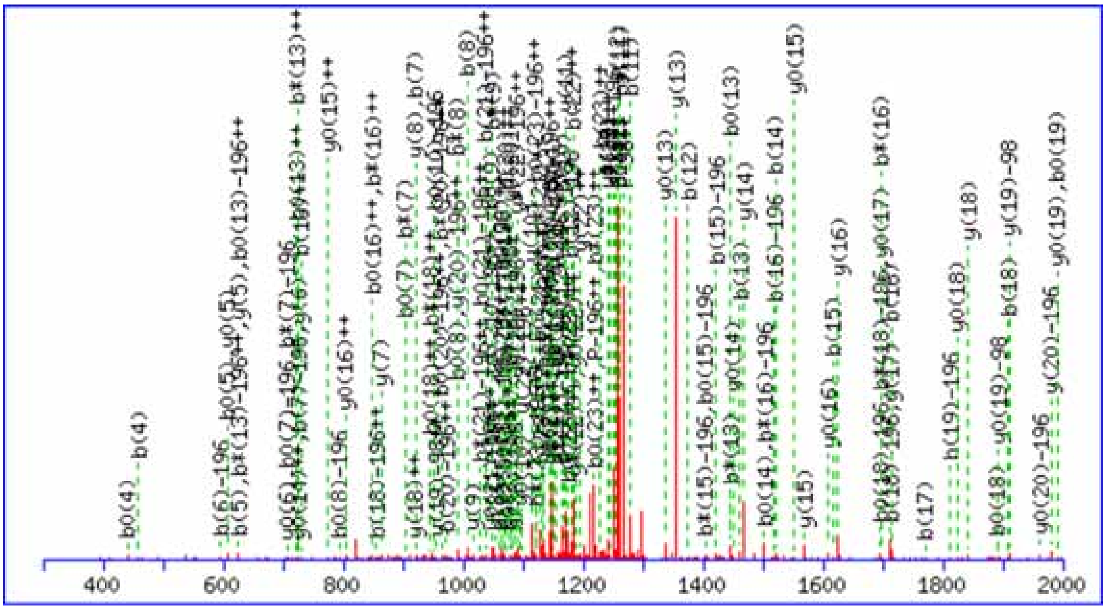
Matched b ions: b(7), b(7)-98, b(8), b(9), b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(13)-98++, b(14), b(14)-98, b(15)-98, b(16), b(18)-98, b(19), b(20)-98, b(20)++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++, b(23)++
Matched y ions: y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(19), y(20)-98, y(20)-98++, y(21)-98++, y(22)-98++, y(22)++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.1132

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6418: 2633.041318 from(1317.527935,2+)
Title: Elution from: 48.221 to 48.221 scan no 4385 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2633.0428
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 **Expect:** 6e-006

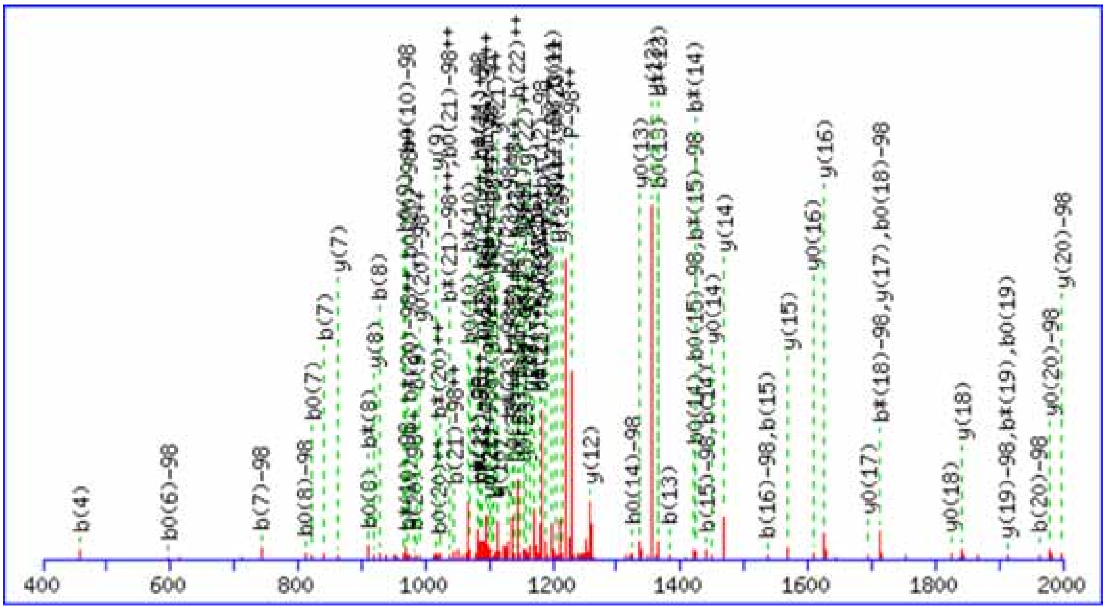
Matched b ions: b(4), b(5), b(6)-196, b(7)-98, b(7)-196, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(12), b(12)-196, b(13), b(13)++, b(13)-98, b(14), b(14)-98, b(15)-98, b(15)-196, b(15), b(16), b(16)-196, b(17), b(18)-196, b(18)-98, b(18)-196++, b(18)-98++, b(18), b(19)-98, b(19)-196, b(19)-98++, b(20)-196++, b(20)++, b(21)-98++, b(21)++, b(21)-196++, b(22)++, b(22)-196++, b(22)-98++, b(23)-196++, b(23)-98++, b(23)++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(18)++, y(19)-98, y(19)-98++, y(20)-196++, y(20)-196, y(20)-98++, y(21)-196++, y(21)-98++, y(21)++, y(22)-98++, y(22)-196++, y(22)++, y(23)-196++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.1133

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7740: 2553.078654 from(1277.546603,2+)
Title: Elution from: 44.235 to 44.235 scan no 4209 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2553.0764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 75 Expect: 2.1e-006

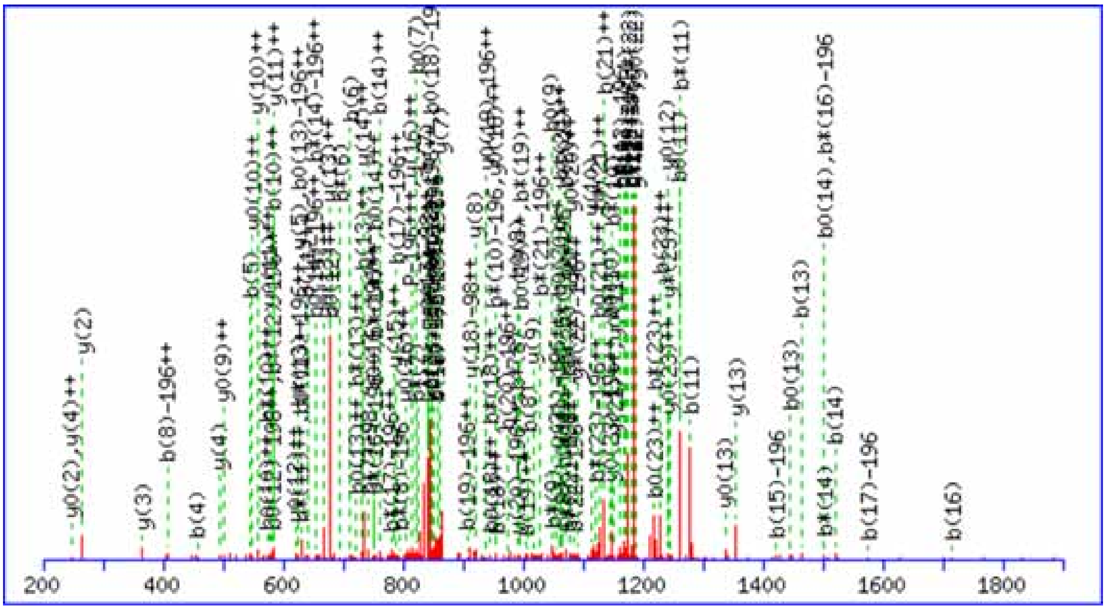
Matched b ions: b(4), b(7)-98, b(7), b(8), b(9), b(10), b(11), b(11)-98, b(12)-98, b(13), b(14), b(15)-98, b(15), b(16)-98, b(20)-98, b(20)-98++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)-98++, b(23)++
Matched y ions: y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(19)-98, y(20)-98, y(21)++, y(22)-98++, y(22)++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.1134

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:6,@S:8
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6724: 2633.044155 from(878.688661,3+)
Title: Elution from: 48.194 to 48.194 scan no 4469 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2633.0428
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 Expect: 0.0021

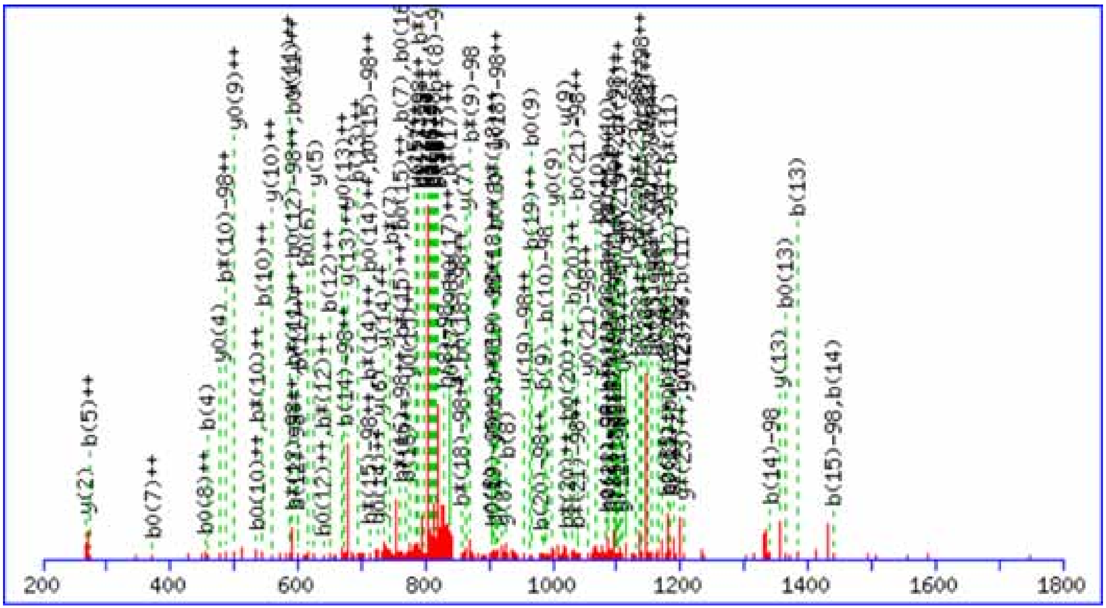
Matched b ions: b(4), b(5), b(6), b(7)-98, b(7), b(8)-196++, b(8)-98++, b(8), b(9), b(10)++, b(10), b(11), b(11)++, b(11)-98, b(12)-98, b(12)-98++, b(12)-196, b(13), b(13)++, b(13)-98++, b(14), b(14)-98, b(14)-98++, b(14)++, b(15)-98, b(15)-196, b(15)-98++, b(16), b(16)++, b(17)-196, b(17)-196++, b(18)++, b(18)-196++, b(19)++, b(19)-196++, b(20)++, b(20)-196++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(22)-196++, b(23)++, b(23)-98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(7), y(8), y(9), y(10)++, y(10), y(11)++, y(11), y(13)++, y(13), y(14)++, y(15)++, y(16)++, y(17)-98++, y(18)-98++, y(19)-98++, y(20)-196++, y(21)-196++, y(21)++, y(22)-98++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1135

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6204: 2553.077799 from(852.033209,3+)
Title: Elution from: 44.165 to 44.165 scan no 3887 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2553.0764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 Expect: 0.025

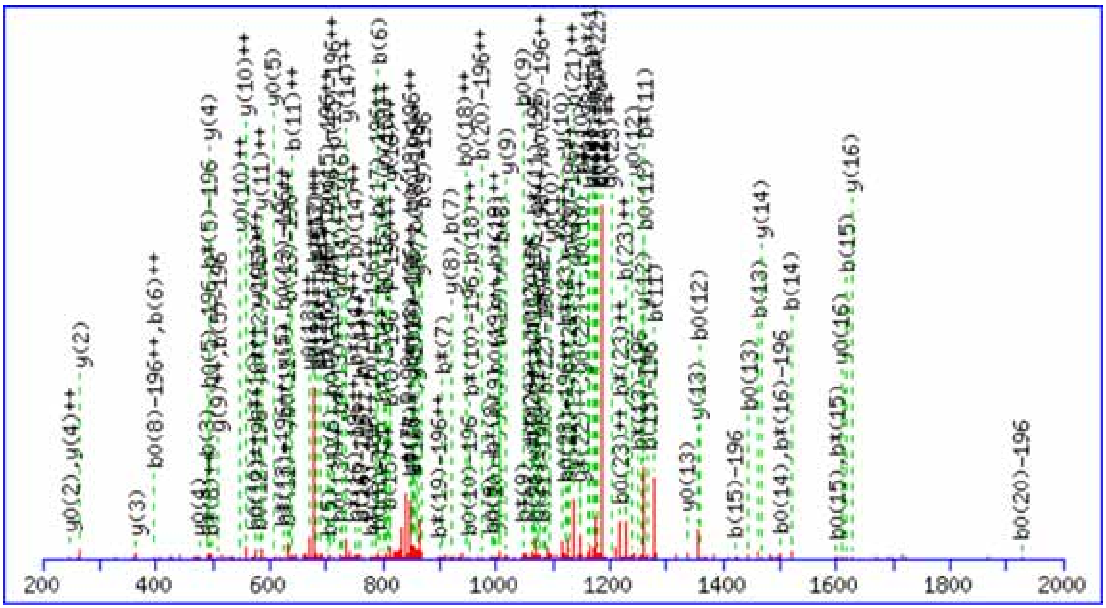
Matched b ions: b(4), b(5)++, b(7), b(8), b(8)-98, b(9), b(10)++, b(10), b(10)-98, b(11), b(11)++, b(11)-98, b(12)-98, b(12)++, b(12)-98++, b(13), b(13)++, b(14)-98, b(14), b(14)-98++, b(15)-98, b(15)++, b(16)++, b(17)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(22)++, b(22)-98++, b(23)++, b(23)-98++
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(11)++, y(13)++, y(13), y(14)++, y(15)++, y(16)++, y(18)-98++, y(19)-98++, y(21)++, y(22)-98++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1136

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @T:1,@S:3
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6955: 2633.044500 from(878.688776,3+)
Title: Elution from: 48.093 to 48.093 scan no 4468 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2633.0428
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0026

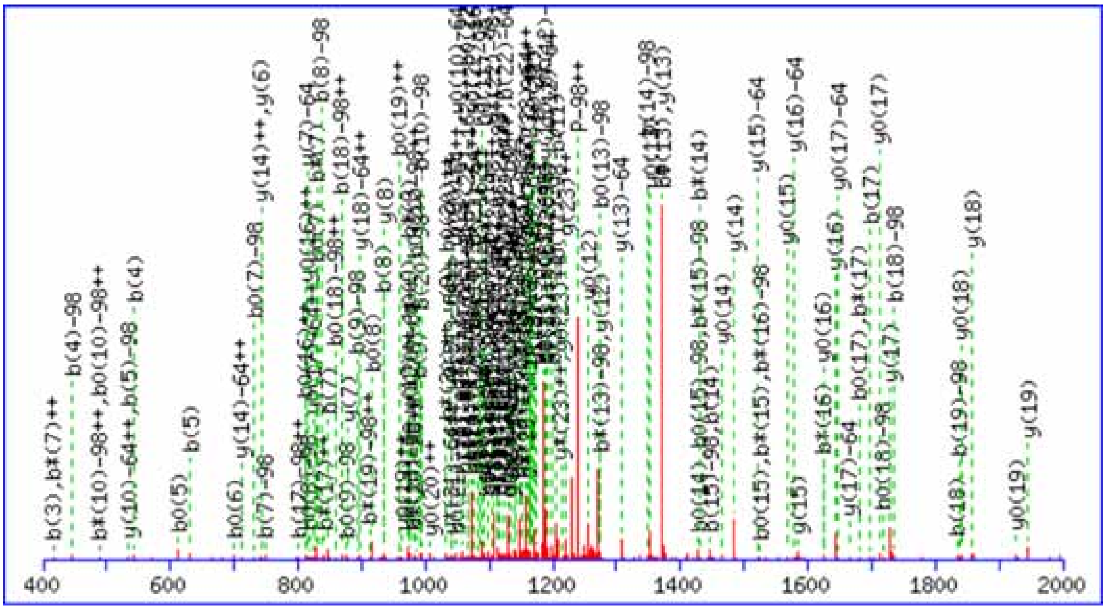
Matched b ions: b(3), b(4)-98++, b(5)-196, b(5)-98, b(5), b(6)-98, b(6)++, b(6), b(7)-98, b(7), b(8), b(8)-196, b(9)-196, b(9), b(10), b(10)-98++, b(11), b(11)++, b(11)-196, b(11)-98, b(12)-98, b(12)-98++, b(12)++, b(12)-196, b(13), b(13)-196, b(13)-196++, b(13)-98++, b(14), b(14)-98, b(14)-98++, b(14)++, b(15)-98, b(15), b(15)-196, b(15)-196++, b(15)-98++, b(15)++, b(16)-98, b(16)++, b(16)-196++, b(16)-98++, b(17)-196++, b(17)-98++, b(18)-196++, b(18)-98++, b(18)++, b(19)++, b(20)++, b(20)-98++, b(20)-196++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(22)-196++, b(23)++, b(23)-196++, b(23)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)++, y(10), y(11)++, y(11), y(12), y(13)++, y(13), y(14)++, y(14), y(16), y(16)++, y(17)++, y(21)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1137

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6572: 2575.103776 from(1288.559164,2+)
Title: Elution from: 39.208 to 39.208 scan no 3348 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2575.1032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 61 **Expect:** 5.1e-005

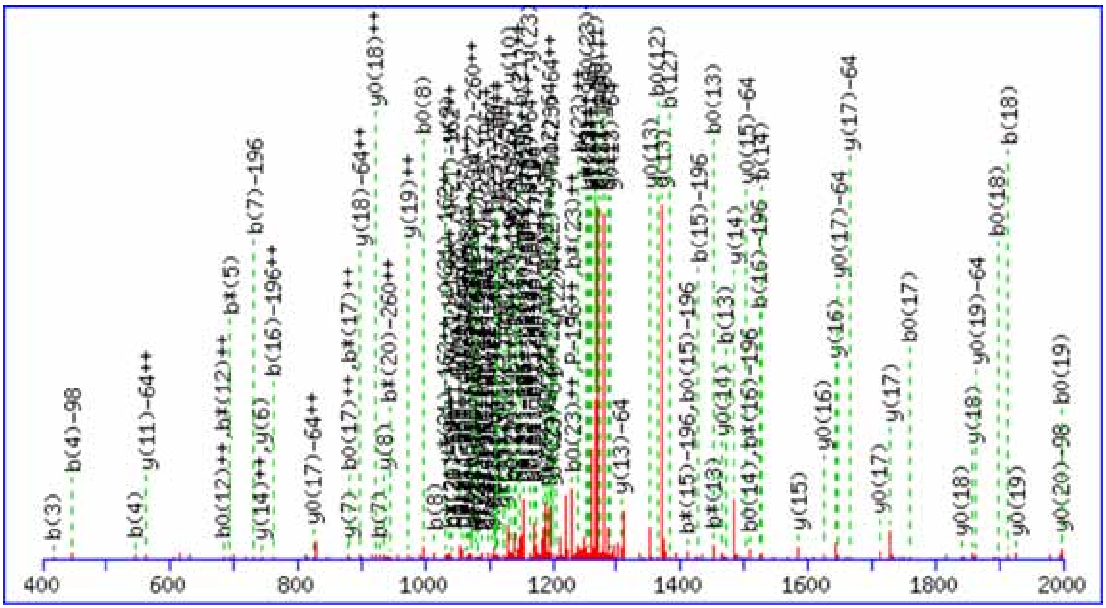
Matched b ions: b(3), b(4)-98, b(4), b(5), b(5)-98, b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(14), b(14)-98, b(15)-98, b(17)-98++, b(17), b(18)-98, b(18), b(18)-98++, b(19)-98, b(20)-98++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(23)++
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(16), y(17), y(18), y(19), y(19)++, y(21)++, y(22)-98++, y(22)++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1138

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6773: 2655.070412 from(1328.542482,2+)
Title: Elution from: 41.944 to 41.944 scan no 3704 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2655.0695
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 47 **Expect:** 0.001

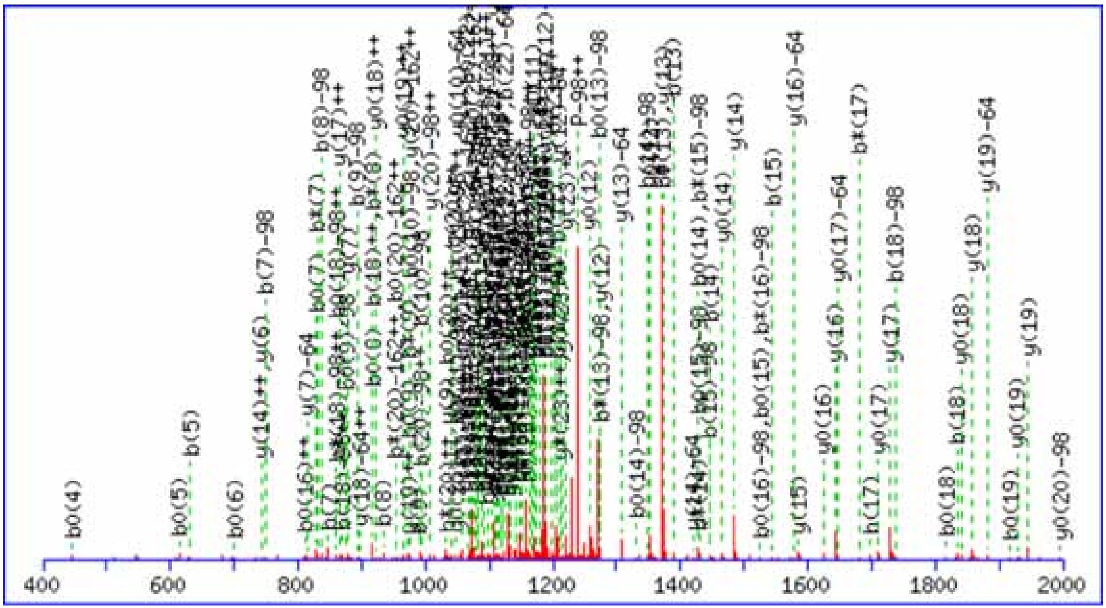
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6)-98, b(7)-98, b(7)-196, b(7), b(8), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(11)-196, b(12)-196, b(12)-98, b(12), b(13)-98, b(13)-196, b(13), b(14), b(14)-98, b(15)-98, b(15)-196, b(16)-98++, b(16)-196++, b(16)-196, b(18), b(18)-98, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)++, b(22)-196++, b(22)-98++, b(23)-196++, b(23)-98++, b(23)++
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(16), y(17), y(18), y(19)++, y(20)++, y(21)-98++, y(22)-196++, y(22)-98++, y(22)++, y(23)++, y(23)-98++, y(23)-196++
Precursor origin neutral loss: +

Peptide No.1139

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6770: 2575.103904 from(1288.559228,2+)
Title: Elution from: 39.183 to 39.183 scan no 3367 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2575.1032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 73 Expect: 3.2e-006

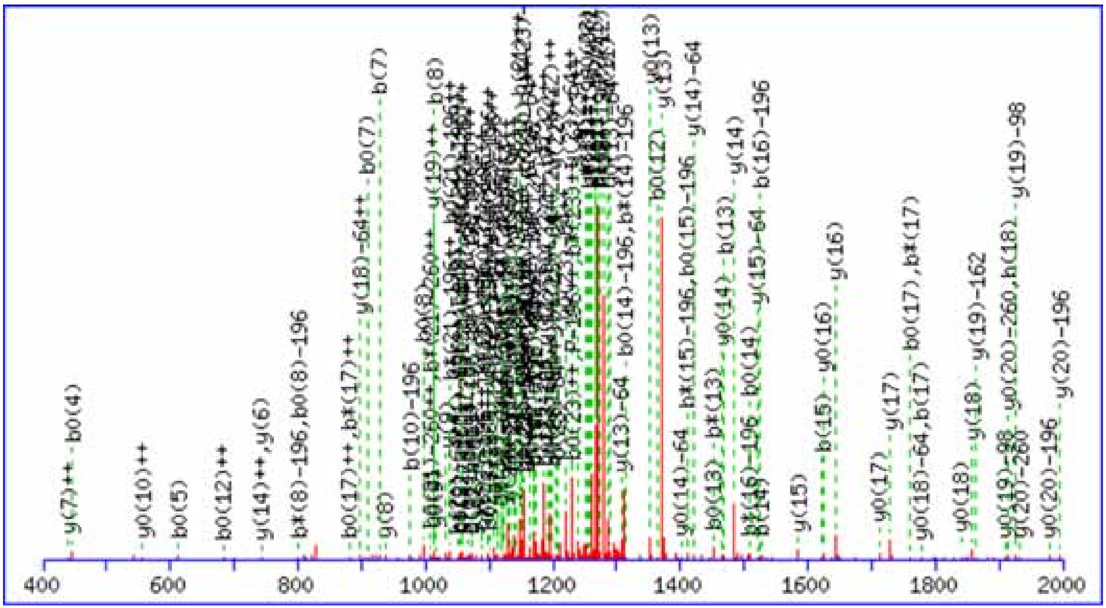
Matched b ions: b(5), b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(13), b(14), b(14)-98, b(15)-98, b(15), b(17), b(18), b(18)-98++, b(18)-98, b(18)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(23)++
Matched y ions: y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(16), y(17), y(17)++, y(18), y(19), y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.1140

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6481: 2655.070050 from(1328.542301,2+)
Title: Elution from: 41.917 to 41.917 scan no 3611 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2655.0695
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 58 Expect: 8.5e-005

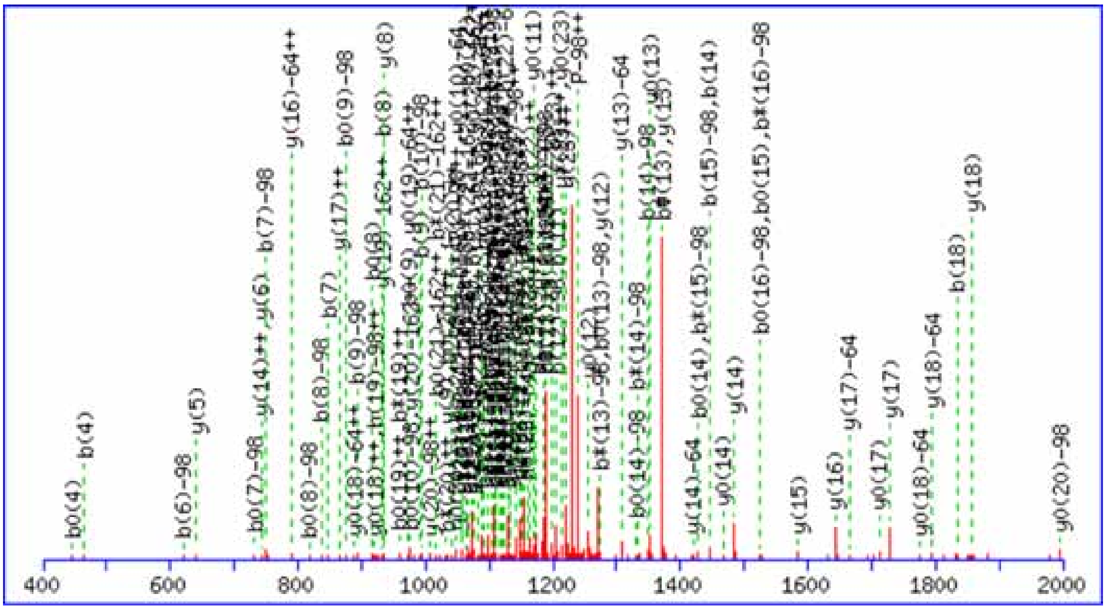
Matched b ions: b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9), b(10)-196, b(10)-98, b(10), b(11)-98, b(11), b(11)-196, b(12)-196, b(12)-98, b(13)-98, b(13), b(13)-196, b(14), b(15), b(15)-98, b(16)-98++, b(16)-98, b(16)-196, b(17), b(18), b(18)-98++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(22)-196++, b(23)++, b(23)-196++, b(23)-98++
Matched y ions: y(6), y(7)++, y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(16), y(17), y(18), y(19)-98, y(19)++, y(20)-196, y(20)++, y(21)-98++, y(22)-196++, y(22)-98++, y(22)++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1141

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites:
Ambiguous sites: @S:5orS:6

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6573: 2575.104478 from(1288.559515,2+)
Title: Elution from: 38.873 to 38.873 scan no 3300 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2575.1032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M20 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 70 Expect: 6.4e-006

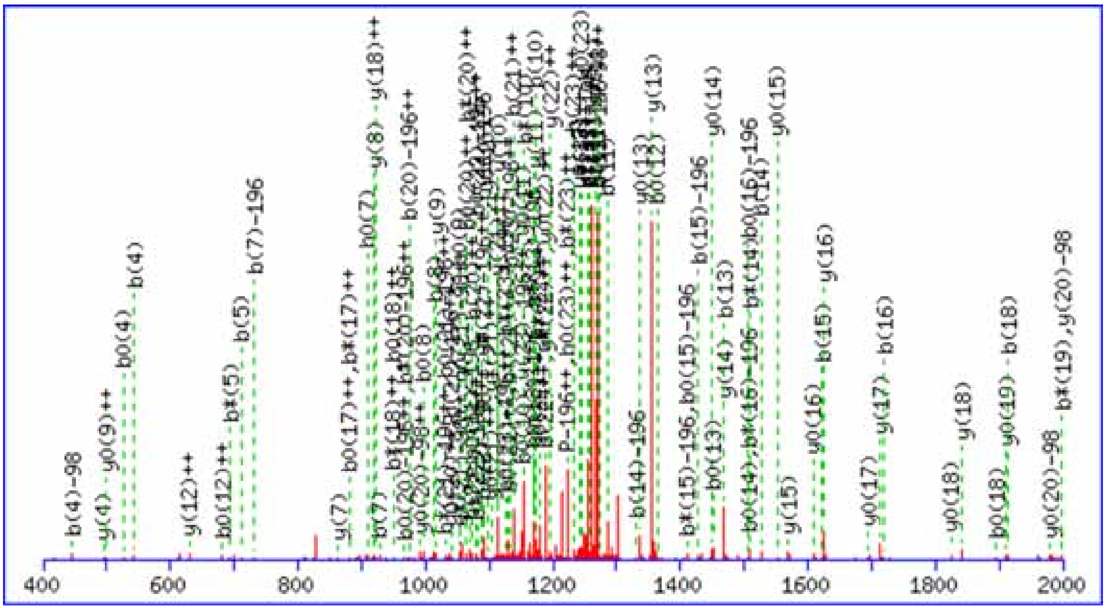
Matched b ions: b(4), b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(14), b(14)-98, b(15)-98, b(18), b(19)-98++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(23)++
Matched y ions: y(5), y(6), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(16), y(17), y(17)++, y(18), y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1142

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6967: 2639.074148 from(1320.544350,2+)
Title: Elution from: 47.821 to 47.821 scan no 4435 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2639.0746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 **Expect:** 0.00038

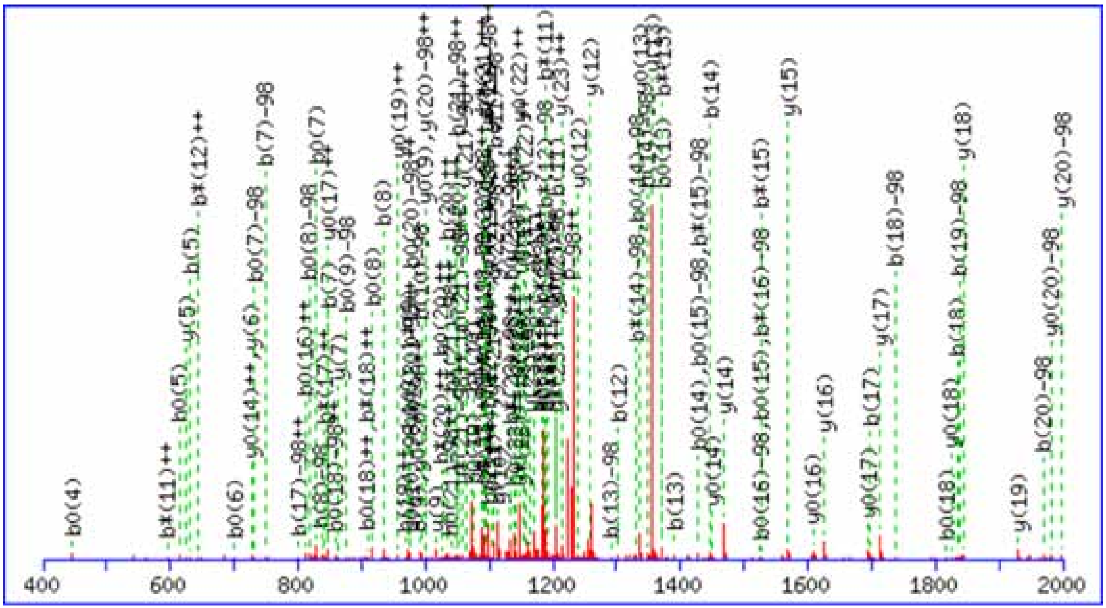
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(7)-98, b(7)-196, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(11)-98, b(11)-196, b(11), b(12)-98, b(13)-196, b(13)-98, b(13), b(14), b(14)-196, b(14)-98, b(15)-98, b(15), b(15)-196, b(16)-98++, b(16), b(16)-98, b(18)-98++, b(18), b(20)++, b(20)-196++, b(21)-98++, b(21)++, b(21)-196++, b(22)++, b(22)-196++, b(22)-98++, b(23)-196++, b(23)-98++, b(23)++
Matched y ions: y(4), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(18)++, y(20)-98, y(21)++, y(22)-98++, y(22)++, y(23)-196++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1143

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6796: 2559.109892 from(1280.562222,2+)
Title: Elution from: 44.349 to 44.349 scan no 4018 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2559.1083
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 **Expect:** 1.6e-005

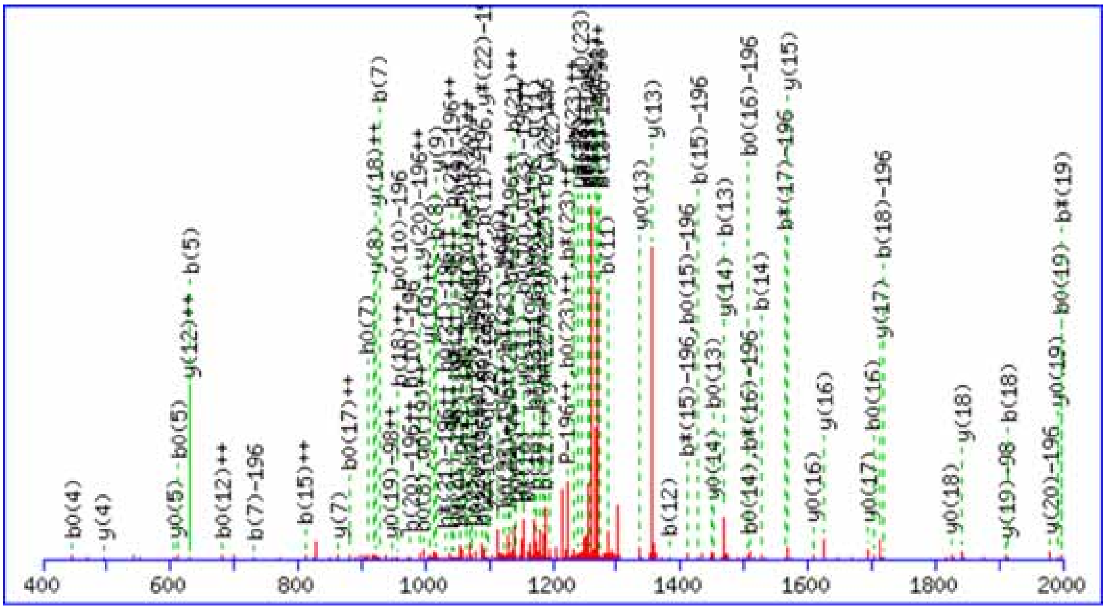
Matched b ions: b(5), b(7), b(7)-98, b(8), b(8)-98, b(9), b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(12), b(13)-98, b(13), b(14), b(14)-98, b(17), b(17)-98++, b(18), b(18)-98, b(19)-98, b(19)++, b(20)-98, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(23)++
Matched y ions: y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(19), y(20)-98, y(20)-98++, y(20)++, y(21)-98++, y(22)-98++, y(22)++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.1144

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 7095: 2639.075034 from(1320.544793,2+)
Title: Elution from: 48.173 to 48.173 scan no 4532 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2639.0746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 4.7e-005

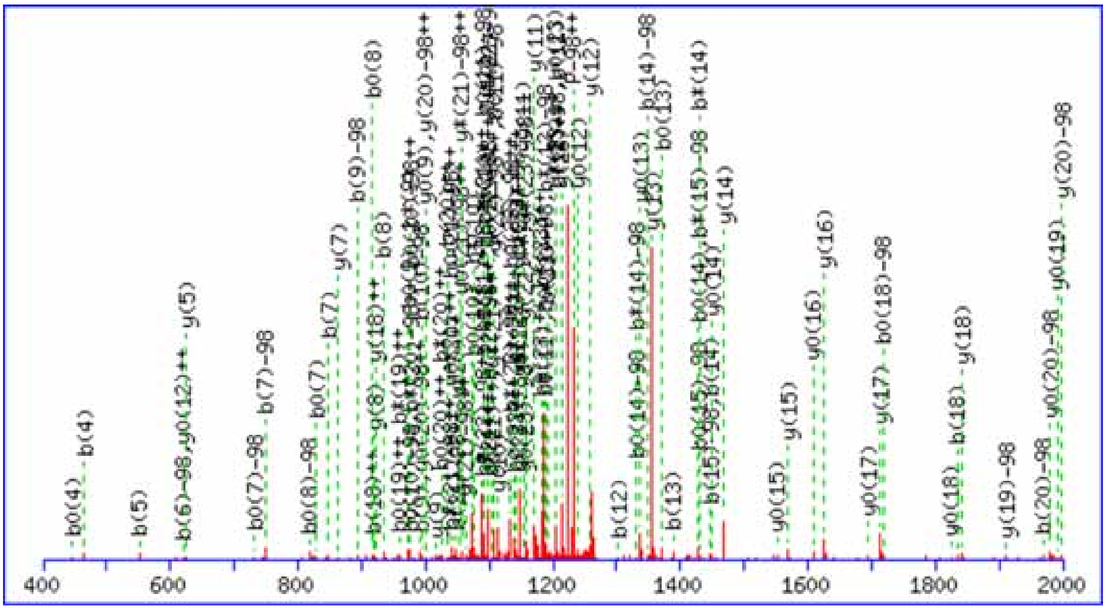
Matched b ions: b(5), b(6)-98, b(7)-98, b(7)-196, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10)-196, b(10)-98, b(10), b(11)-98, b(11)-196, b(11), b(12)-196, b(12)-98, b(12), b(13), b(13)-196, b(14)-98, b(14), b(15)++, b(15)-196, b(16)-98++, b(18), b(18)-98, b(18)-196, b(18)-98++, b(18)++, b(20)-196++, b(20)++, b(21)++, b(21)-98++, b(21)-196++, b(22)-98++, b(22)++, b(22)-196++, b(23)-196++, b(23)-98++, b(23)++
Matched y ions: y(4), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(18)++, y(19)-98, y(19)++, y(20)-196, y(20)-196++, y(20)++, y(20)-98++, y(21)-196++, y(21)-98++, y(22)-196++, y(22)-98++, y(22)++, y(23)-196++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1145

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6215: 2559.107016 from(1280.560784,2+)
Title: Elution from: 44.195 to 44.195 scan no 3891 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2559.1083
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 Expect: 4.9e-005

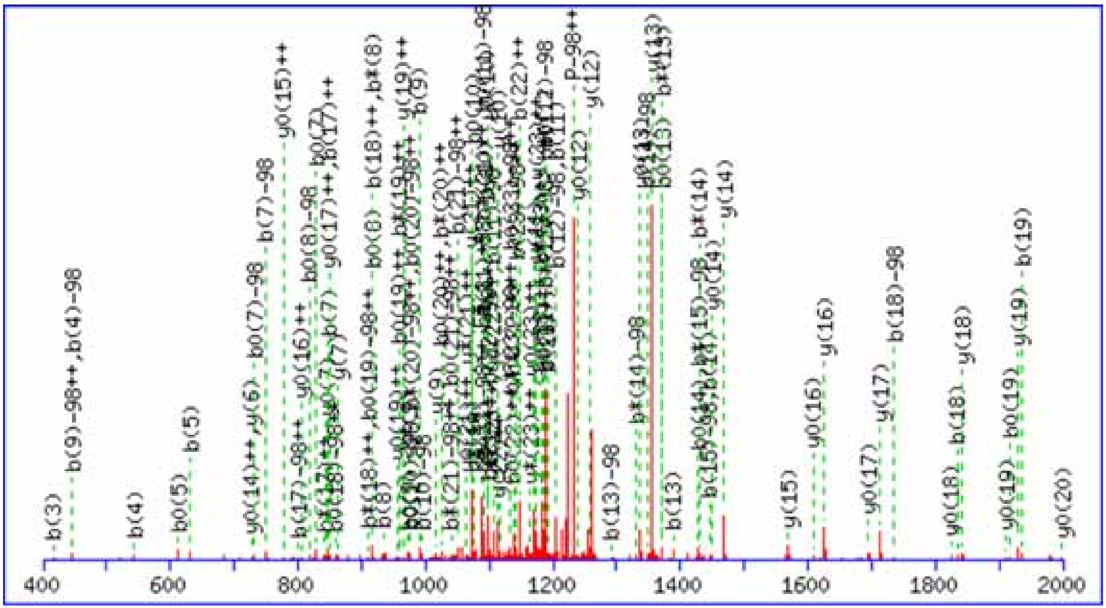
Matched b ions: b(4), b(5), b(6)-98, b(7)-98, b(7), b(8), b(9), b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(12), b(13), b(14), b(14)-98, b(15)-98, b(18), b(18)++, b(20)-98, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(23)++
Matched y ions: y(5), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(18)++, y(19)-98, y(20)-98, y(20)-98++, y(20)++, y(21)-98++, y(22)-98++, y(22)++, y(23)++
Precursor origin neutral loss: +

Peptide No.1146

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6713: 2559.109840 from(1280.562196,2+)
Title: Elution from: 44.299 to 44.299 scan no 4034 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2559.1083
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 Expect: 5.5e-005

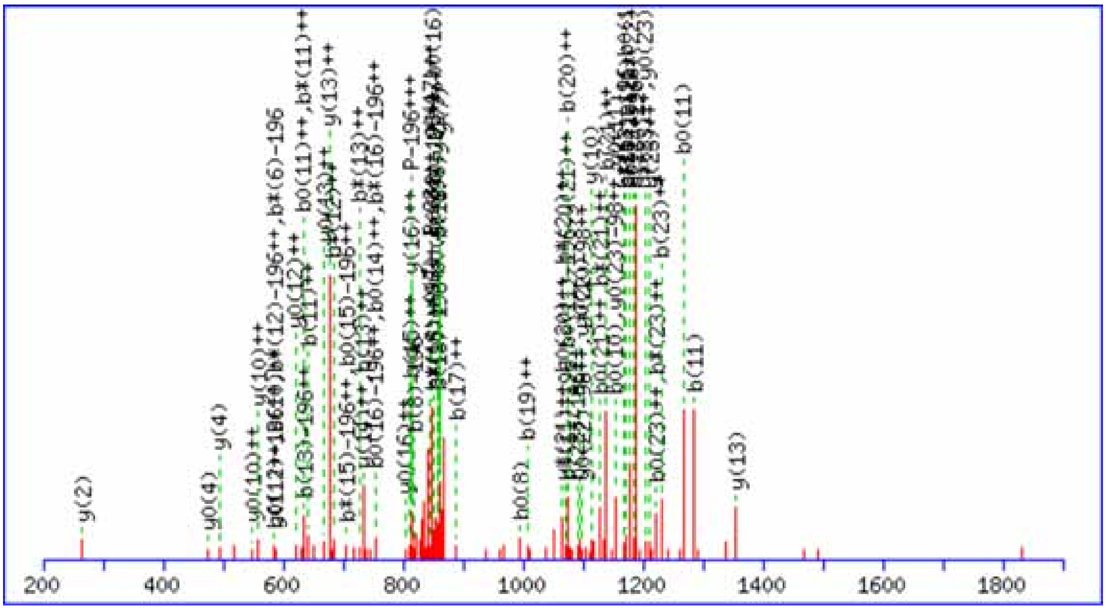
Matched b ions: b(3), b(4)-98, b(4), b(5), b(7)-98, b(7), b(8), b(9)-98++, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(13), b(13)-98, b(14), b(14)-98, b(15)-98, b(17)-98++, b(17)++, b(18)-98, b(18), b(18)++, b(19), b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++, b(23)++
Matched y ions: y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(19), y(19)++, y(21)++, y(22)++, y(23)++
Precursor origin neutral loss: +

Peptide No.1147

TLSQSSESGTLPSGPPGHTMEVSC
Confirmed sites: @T:1,@S:3
Ambiguous sites:

MS/MS Fragmentation of TLSQSSESGTLPSGPPGHTMEVSC
Found in NDRG2_MOUSE, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 6261: 2639.077188 from(880.699672,3+)
Title: Elution from: 47.750 to 47.750 scan no 4295 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2639.0746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.016

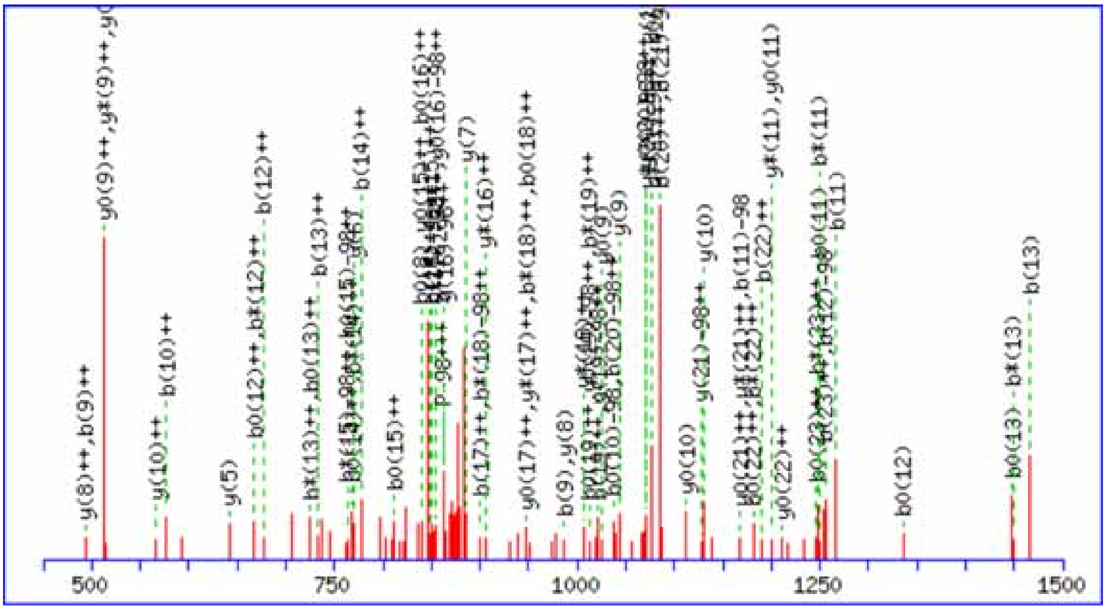
Matched b ions: b(7)-98, b(8)-196, b(10)-98, b(10)++, b(10), b(11)-98, b(11), b(11)++, b(12)-98++, b(12)-98, b(12)-196, b(13)++, b(13)-196++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(18)-196++, b(19)++, b(20)++, b(21)++, b(22)-98++, b(22)++, b(22)-196++, b(23)++
Matched y ions: y(2), y(4), y(7), y(10)++, y(10), y(11)++, y(11), y(13)++, y(13), y(14)++, y(16)++, y(17)++, y(21)++, y(23)++
Precursor origin neutral loss: +

Peptide No.1148

TNSPDLDSQSLSLSSGTDQEPLQR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of TNSPDLDSQSLSLSSGTDQEPLQR
Found in ABLM2_MOUSE, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 7022: 2682.204609 from(895.075479,3+)
Title: Elution from: 49.153 to 49.153 scan no 4634 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2682.2021
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 0.0011

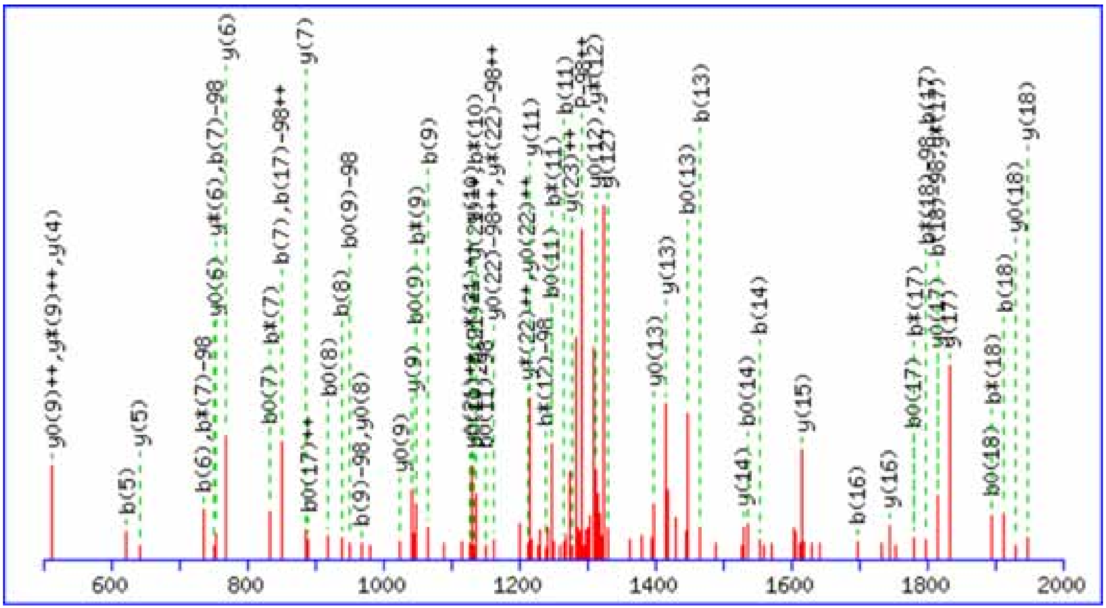
Matched b ions: b(9)++, b(9), b(10)++, b(11), b(11)-98, b(12)-98, b(12)++, b(13), b(13)++, b(14)++, b(16)++, b(17)++, b(17)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(22)++, b(23)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(10)++, y(15)++, y(16)-98++, y(19)-98++, y(19)++, y(21)-98++
Precursor origin neutral loss: +

Peptide No.1149

TNSPDLDSQSLSLSSGTDQEPLQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TNSPDLDSQSLSLSSGTDQEPLQR
Found in ABLM2_MOUSE, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 8108: 2682.202874 from(1342.108713,2+)
Title: Elution from: 49.288 to 49.288 scan no 4829 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2682.2021
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 86 Expect: 2e-007

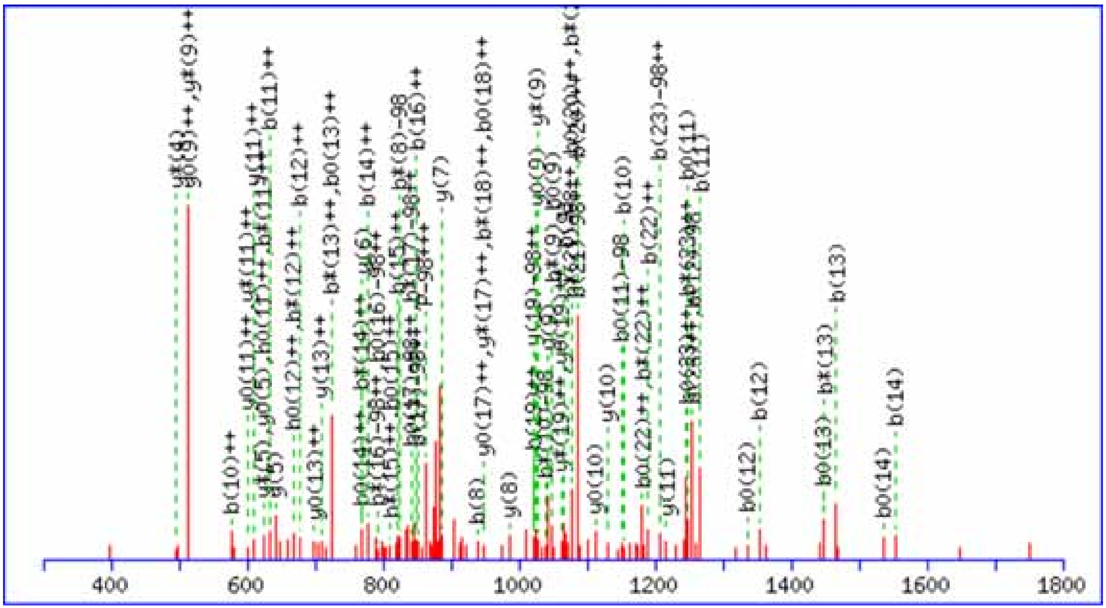
Matched b ions: b(5), b(6), b(7), b(7)-98, b(8), b(9)-98, b(9), b(11), b(13), b(14), b(16), b(17)-98++, b(17), b(18), b(18)-98, b(21)++
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(21)++, y(23)++
Precursor origin neutral loss: +

Peptide No.1150

TNSPDLDSQSLSLSSGTDQEPLQR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of TNSPDLDSQSLSLSSGTDQEPLQR
Found in ABLM2_MOUSE, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 7067: 2682.203382 from(895.075070,3+)
Title: Elution from: 49.292 to 49.292 scan no 4602 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2682.2021
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.0063

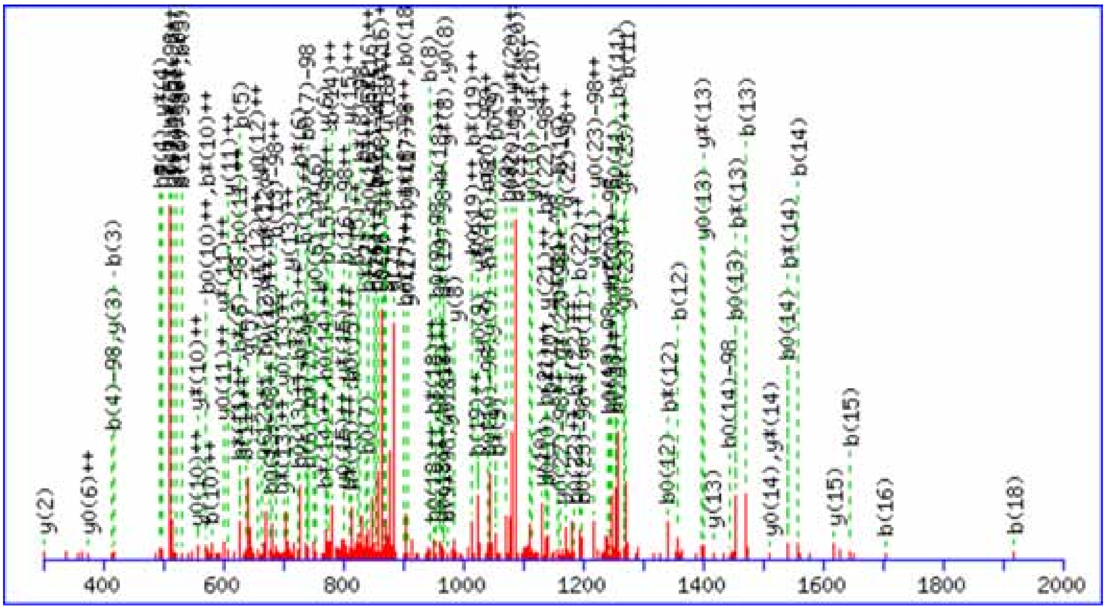
Matched b ions: b(8), b(9), b(10)++, b(10), b(11)++, b(11), b(12)-98, b(12), b(12)++, b(13), b(14), b(14)++, b(15)++, b(16)++, b(17)-98++, b(19)++, b(20)++, b(21)-98++, b(22)++, b(23)++, b(23)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(11), y(13)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.1151

TNSPDLDSQSLSLSSGTDQEPLQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TNSPDLDSQSLSLSSGTDQEPLQR
Found in ABLM2_MOUSE, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 8524: 2688.236064 from(897.085964,3+)
Title: Elution from: 49.201 to 49.201 scan no 4861 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2688.2340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 Expect: 1.9e-006

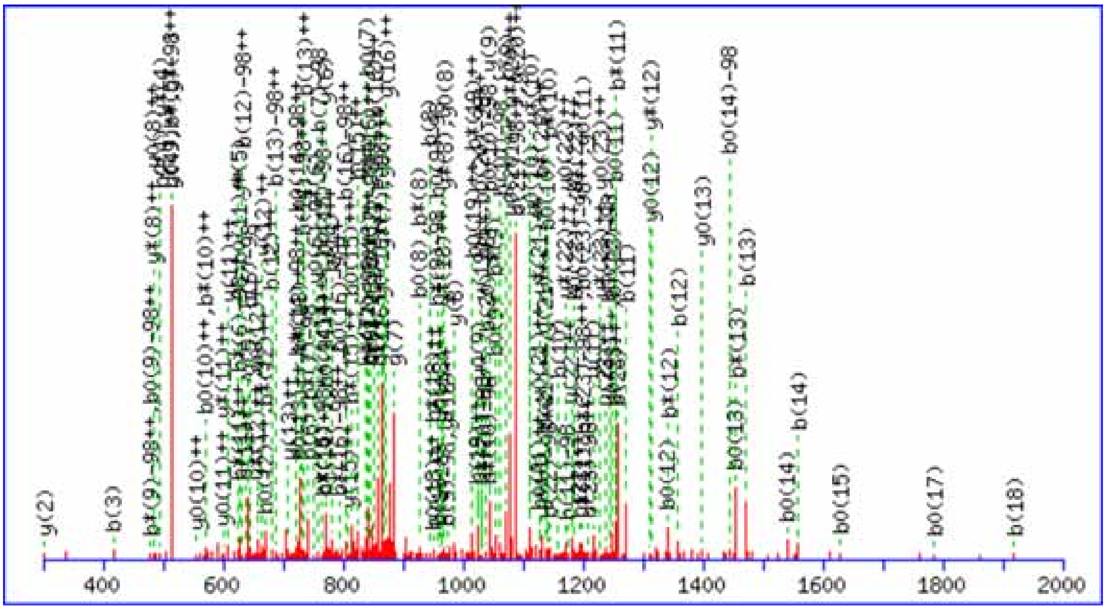
Matched b ions: b(3), b(4), b(4)-98, b(5)-98, b(5), b(6), b(7), b(8), b(9)-98, b(9), b(10)++, b(10)-98++, b(10), b(11), b(11)++, b(12), b(12)++, b(13), b(13)-98++, b(13)++, b(14)++, b(14), b(15), b(15)-98++, b(15)++, b(16), b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18), b(18)++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)++, b(23)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(11), y(11)++, y(12)++, y(13), y(13)++, y(15), y(15)++, y(16)++, y(18)++, y(20)++, y(21)++, y(22)-98++
Precursor origin neutral loss: +

Peptide No.1152

TNSPDLDSQSLSLSSGTDQEPLQR
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of TNSPDLDSQSLSLSSGTDQEPLQR
Found in ABLM2_MOUSE, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 7211: 2688.236019 from(897.085949,3+)
Title: Elution from: 49.238 to 49.238 scan no 4660 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2688.2340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 5.9e-005

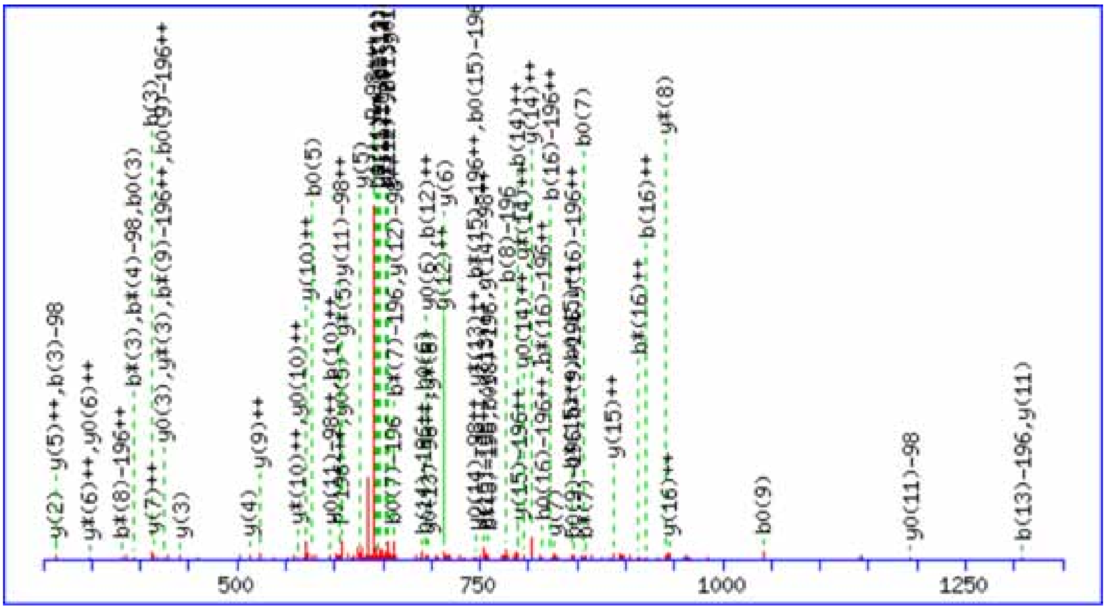
Matched b ions: b(3), b(4), b(6), b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(11), b(11)++, b(11)-98, b(12), b(12)++, b(12)-98++, b(13), b(13)-98++, b(13)++, b(14), b(14)++, b(14)-98++, b(15)++, b(16)-98++, b(16)++, b(18), b(18)++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)++, b(23)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)++, y(23)++
Precursor origin neutral loss: +

Peptide No.1153

TNSPSISPSMLSNAEHK
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of TNSPSISPSMLSNAEHK
Found in ATX2_MOUSE, Ataxin-2 OS=Mus musculus GN=Atxn2 PE=1 SV=1

Match to Query 5678: 2014.848906 from(672.623578,3+)
Title: Elution from: 45.484 to 45.484 scan no 4360 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2014.8472
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 43 Expect: 0.0022

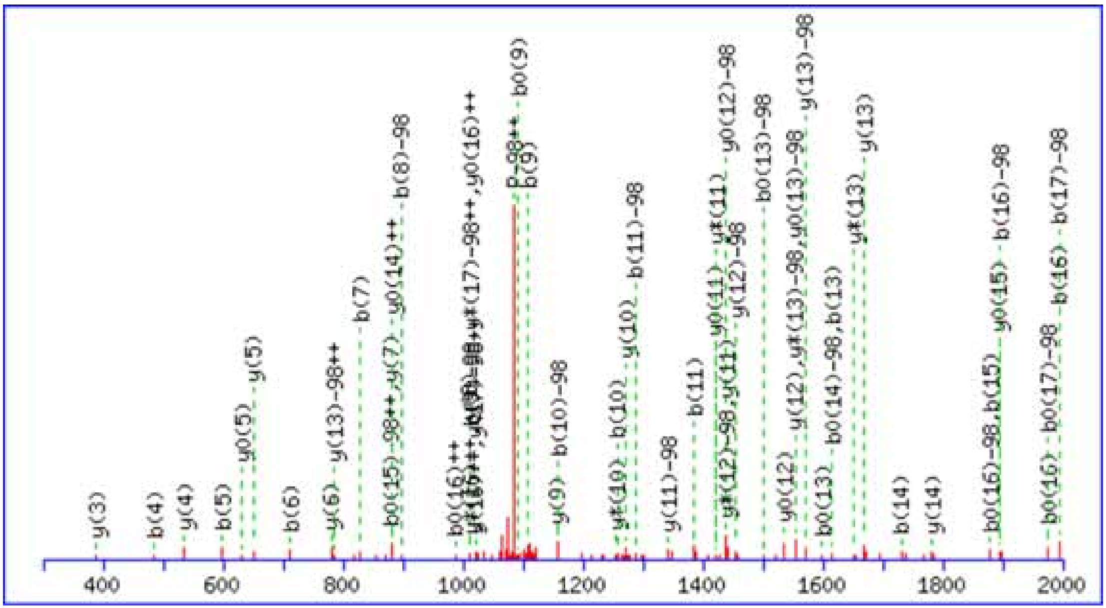
Matched b ions: b(3), b(3)-98, b(7)-98, b(8)-196, b(9)-98, b(10)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-196, b(13)-196++, b(14)-196++, b(14)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-196++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(9)++, y(10)++, y(11), y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-196++, y(16)-98++, y(16)++, y(16)-196++
Precursor origin neutral loss: +

Peptide No.1154

TPEELDDSDFETEDFDVR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of TPEELDDSDFETEDFDVR
Found in CTNA1_MOUSE, Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1

Match to Query 6274: 2265.883916 from(1133.949234,2+)
Title: Elution from: 57.154 to 57.154 scan no 5472 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2265.8839
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 90 Expect: 3.4e-008

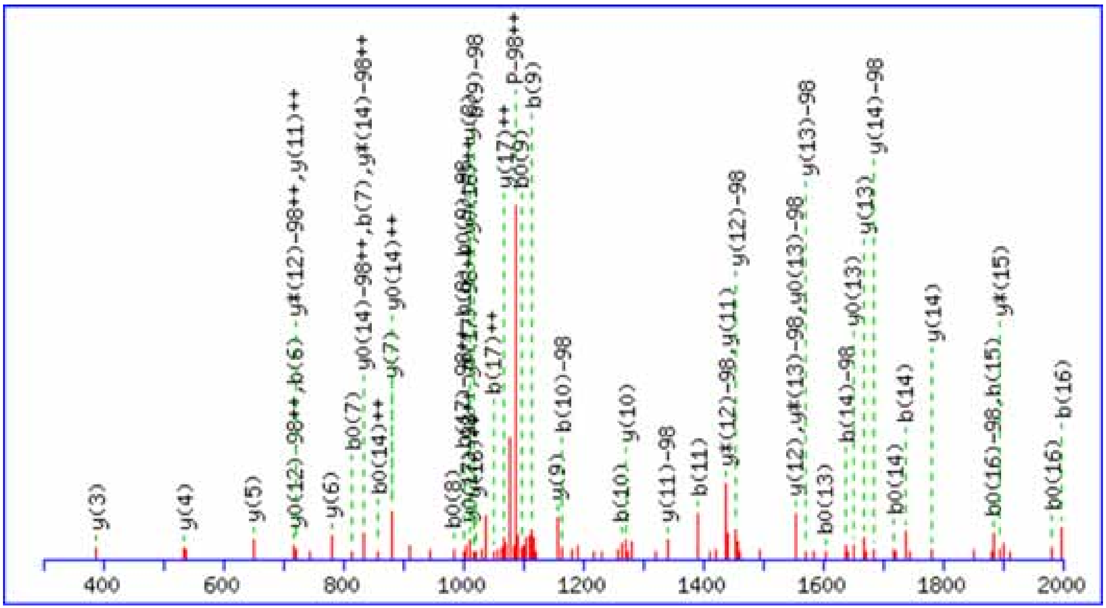
Matched b ions: b(4), b(5), b(6), b(7), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(13), b(14), b(15), b(16), b(16)-98, b(17)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98++, y(13)-98, y(14), y(16)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1155

TPEELDDSDFETEDFDVR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of TPEELDDSDFETEDFDVR
Found in CTNA1_MOUSE, Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1

Match to Query 5529: 2271.917570 from(1136.966061,2+)
Title: Elution from: 57.198 to 57.198 scan no 5213 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2271.9157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 75 Expect: 1.3e-006

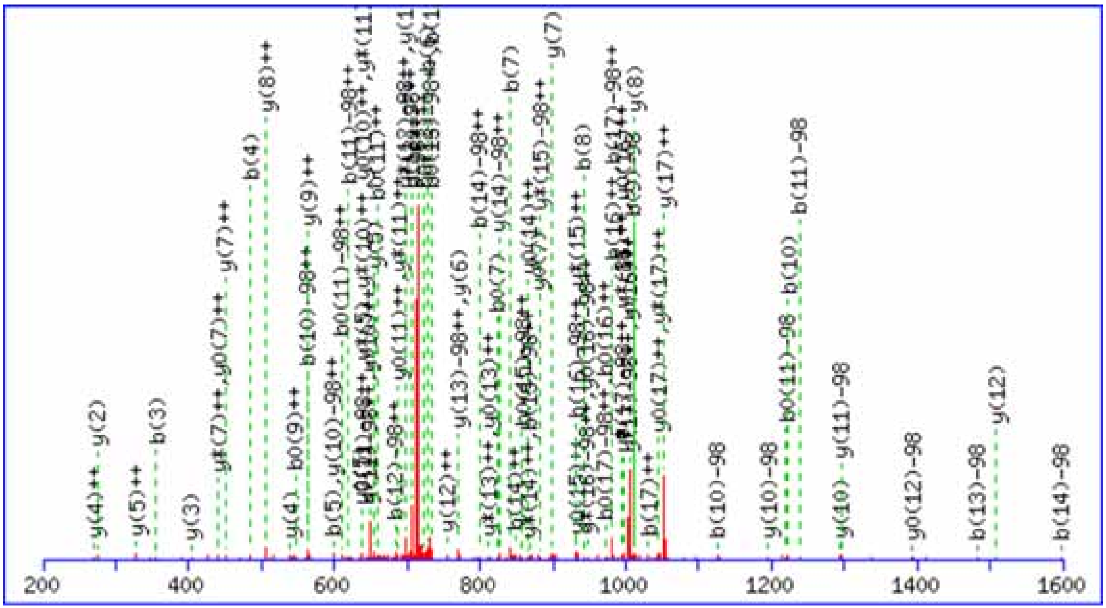
Matched b ions: b(6), b(7), b(8), b(9), b(9)-98, b(10), b(10)-98, b(11), b(14), b(14)-98, b(15), b(16), b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11), y(11)++, y(12), y(12)-98, y(13), y(13)-98, y(14), y(14)-98, y(16)++, y(17)++
Precursor origin neutral loss: +

Peptide No.1156

TPEELEDVSDLEDDHEVR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of TPEELEDVSDLEDDHEVR
Found in CTNA3_MOUSE, Catenin alpha-3 OS=Mus musculus GN=Ctnna3 PE=1 SV=2

Match to Query 6734: 2233.929402 from(745.650410,3+)
Title: Elution from: 47.433 to 47.433 scan no 4599 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2233.9264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 Expect: 0.00045

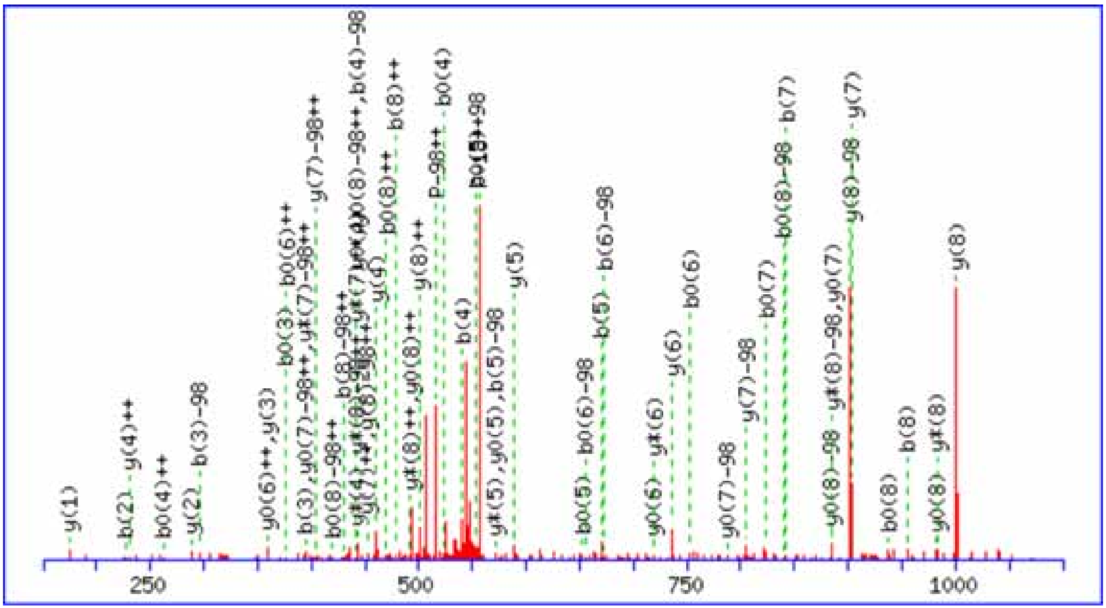
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10)-98, b(10), b(10)-98++, b(11)-98, b(11)-98++, b(12)-98++, b(12)++, b(13)-98, b(14)-98, b(14)++, b(14)-98++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(10), y(10)-98++, y(10)-98, y(11)-98++, y(11)-98, y(11)++, y(12), y(12)-98++, y(12)++, y(13)-98++, y(14)-98++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.1157

TPSFETALR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TPSFETALR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 813: 1128.521846 from(565.268199,2+)
Title: Elution from: 42.380 to 42.380 scan no 3825 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1128.5216
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 2.1e-005

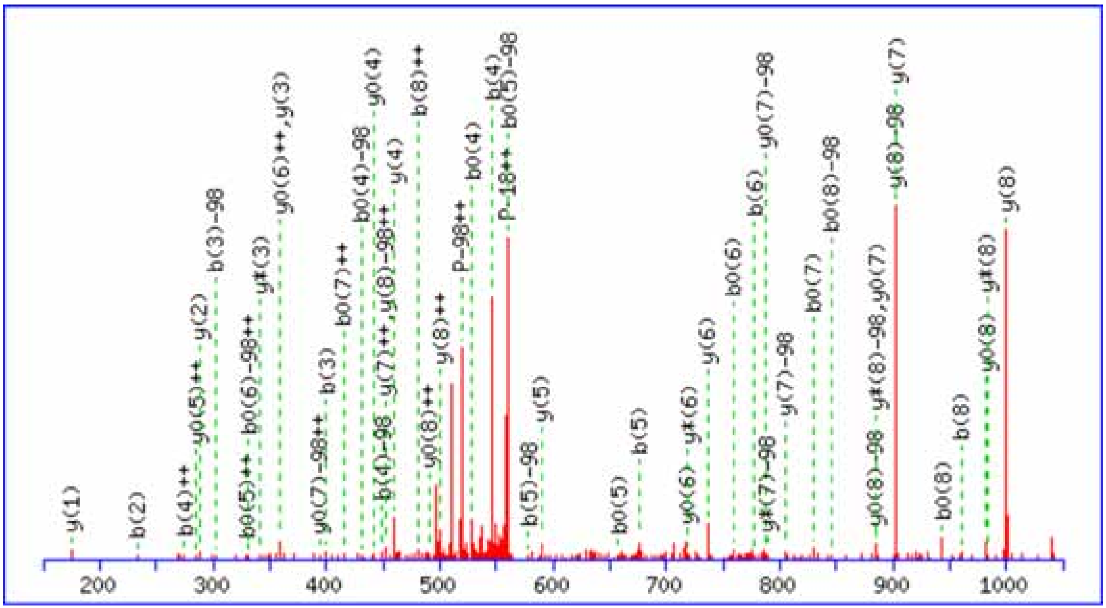
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(7), b(8), b(8)-98++, b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5), y(6), y(7)-98, y(7), y(7)++, y(7)-98++, y(8)-98, y(8), y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.1158

TPSFETALR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TPSFETALR
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 660: 1134.553100 from(568.283826,2+)
Title: Elution from: 42.339 to 42.339 scan no 3753 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1134.5534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 7.4e-005

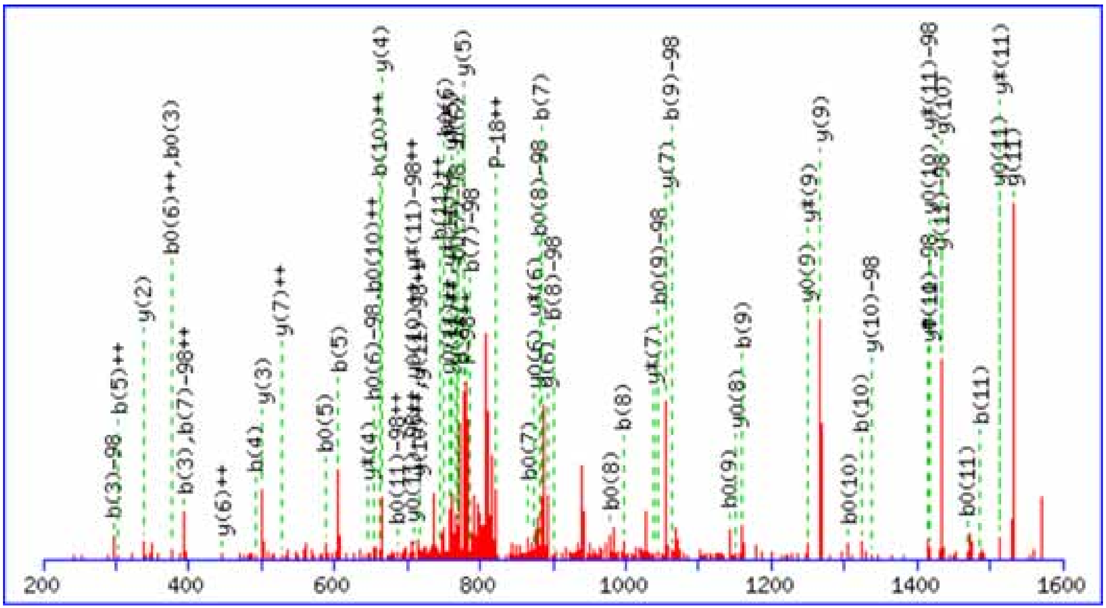
Matched b ions: b(2), b(3), b(3)-98, b(4)++, b(4)-98, b(4), b(5), b(5)-98, b(6), b(8), b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(7)-98, y(8)-98, y(8), y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.1159

TPSPDYDLYYYR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2335: 1659.689122 from(830.851837,2+)
Title: Elution from: 50.334 to 50.334 scan no 4634 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1659.6858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.00095

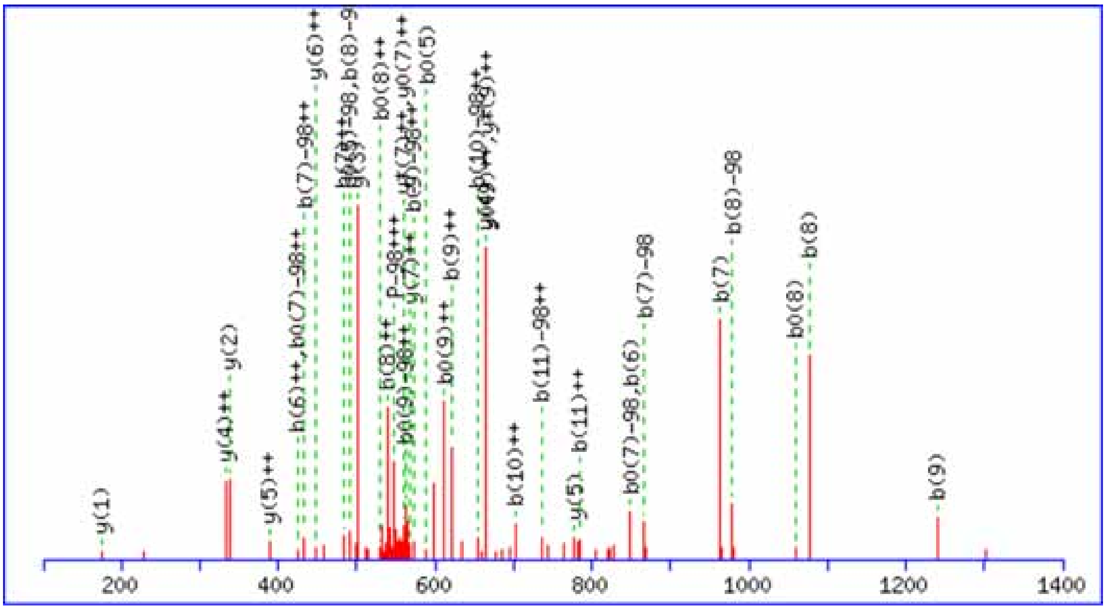
Matched b ions: b(3)-98, b(3), b(4), b(5), b(5)++, b(6), b(7)-98++, b(7), b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)++, b(11)++, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(9), y(10), y(10)++, y(10)-98, y(11)-98, y(11), y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.1160

TPSPDYDLYYYR
Confirmed sites: @Y:6
Ambiguous sites: @T:1orS:3

MS/MS Fragmentation of TPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3982: 1739.651199 from(580.891009,3+)
Title: Elution from: 56.230 to 56.230 scan no 5575 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1739.6521
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y6 : Phospho (Y)
Ions Score: 32 Expect: 0.0095

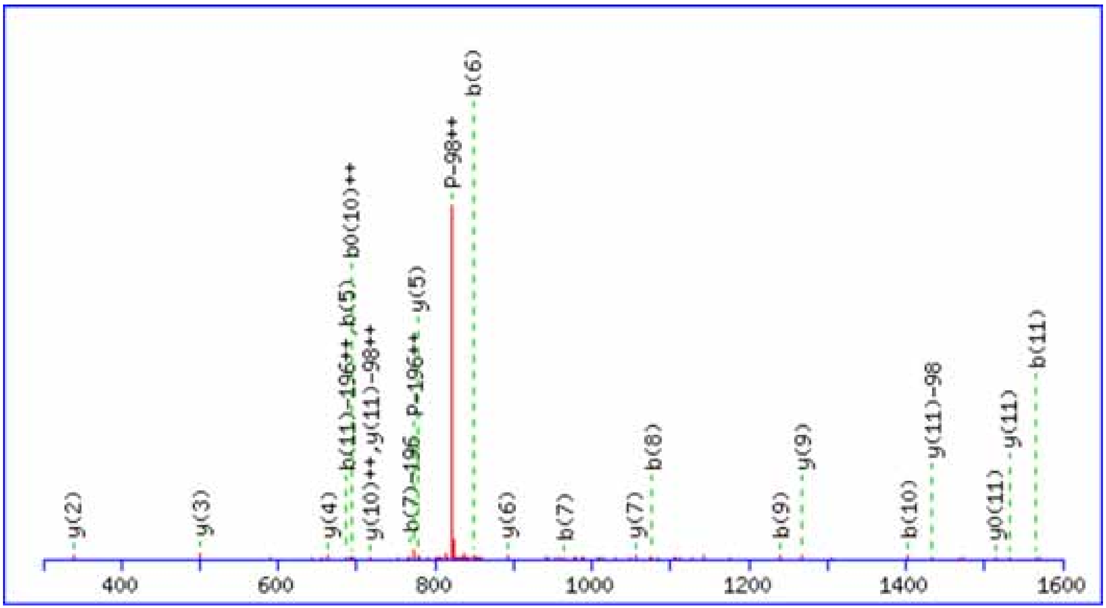
Matched b ions: b(6), b(6)++, b(7)-98++, b(7), b(7)-98, b(7)++, b(8)-98, b(8), b(8)++, b(8)-98++, b(9), b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++, b(11)++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5)++, y(5), y(6)++, y(7)++
Precursor origin neutral loss: +

Peptide No.1161

TPSPDYDLYYYR
Confirmed sites: @T:1,@S:3
Ambiguous sites:

MS/MS Fragmentation of TPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 3057: 1739.653504 from(870.834028,2+)
Title: Elution from: 55.920 to 55.920 scan no 5282 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1739.6521
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.024

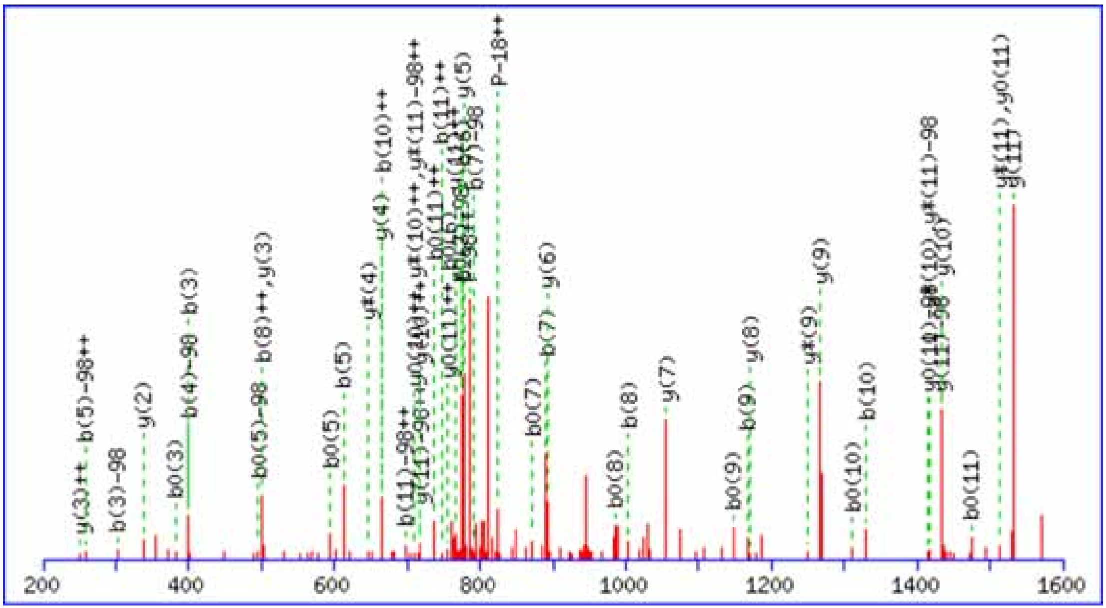
Matched b ions: b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-196, b(8), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11)-98, b(11), b(11)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9), y(10)++, y(11)-98, y(11)-98++, y(11)
Precursor origin neutral loss: +

Peptide No.1162

TPSPDYDLYYYR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2741: 1665.719594 from(833.867073,2+)
Title: Elution from: 50.331 to 50.331 scan no 4580 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1665.7176
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.00064

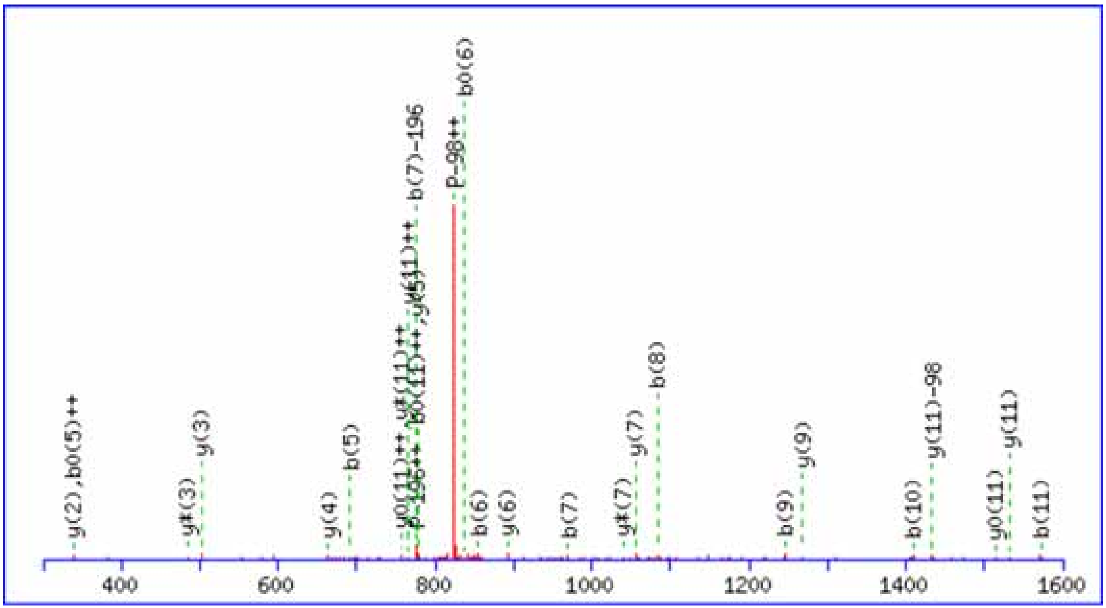
Matched b ions: b(3), b(3)-98, b(4)-98, b(5), b(5)-98++, b(6), b(7), b(7)-98, b(8)++, b(8), b(9), b(10), b(10)++, b(11)-98++, b(11)++
Matched y ions: y(2), y(3), y(3)++, y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11)-98, y(11), y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.1163

TPSPDYDLYYYR
Confirmed sites: @T:1,@S:3
Ambiguous sites:

MS/MS Fragmentation of TPSPDYDLYYYR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2687: 1745.684712 from(873.849632,2+)
Title: Elution from: 56.077 to 56.077 scan no 5214 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1745.6839
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 **Expect:** 0.0024

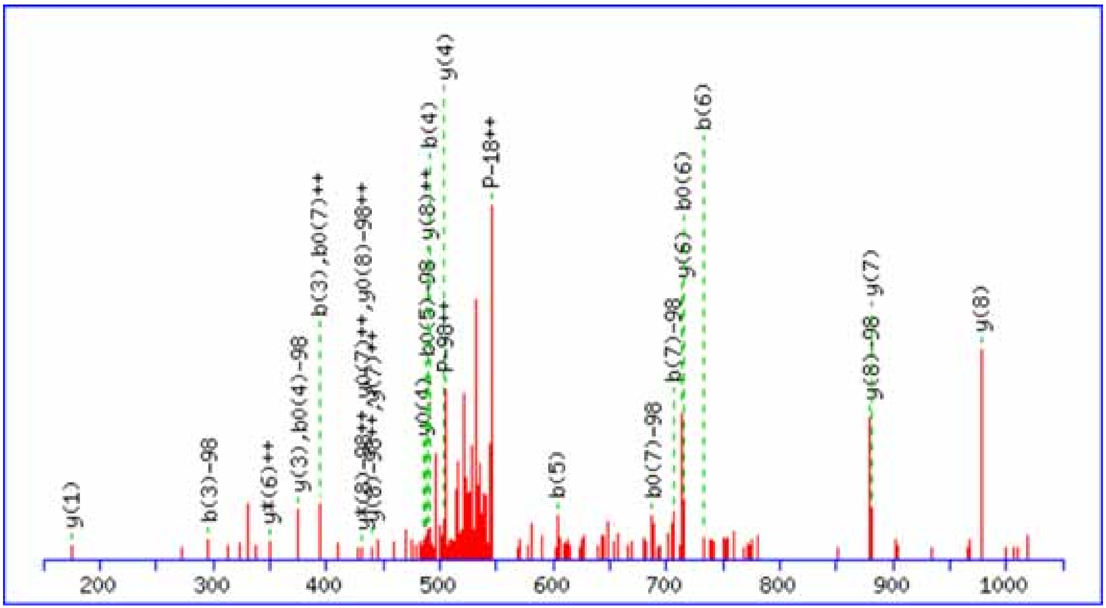
Matched b ions: b(3)-98, b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-196, b(8), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11)-98, b(11)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9), y(11)-98, y(11), y(11)++
Precursor origin neutral loss: +

Peptide No.1164

TPSPIEAER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TPSPIEAER
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 727: 1106.501264 from(554.257908,2+)
Title: Elution from: 25.269 to 25.269 scan no 1527 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1106.5009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.034

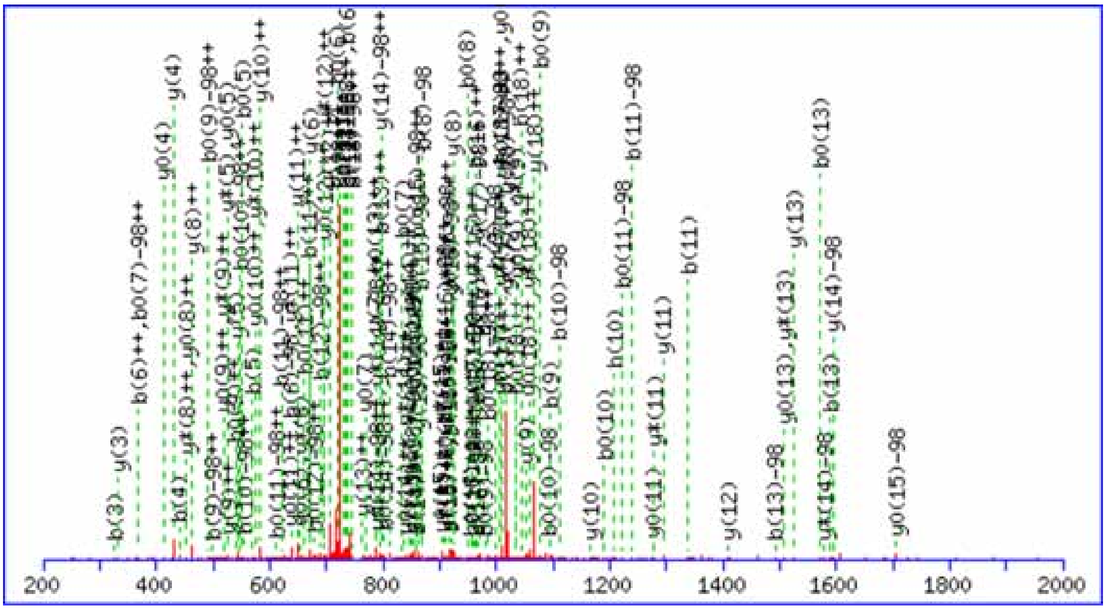
Matched b ions: b(3), b(3)-98, b(4), b(5), b(6), b(7)-98
Matched y ions: y(1), y(3), y(4), y(6), y(7), y(7)++, y(8)-98, y(8), y(8)-98++, y(8)++
Precursor origin neutral loss: +

Peptide No.1165

TPVDESDDEIEHDEIPTGK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of TPVDESDDEIEHDEIPTGK
Found in MYPN_MOUSE, Myopalladin OS=Mus musculus GN=Mypn PE=2 SV=2

Match to Query 6080: 2260.964535 from(754.662121,3+)
Title: Elution from: 39.798 to 39.798 scan no 3446 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2260.9624
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K19 : Dimethyl (K)
Ions Score: 53 Expect: 0.0003

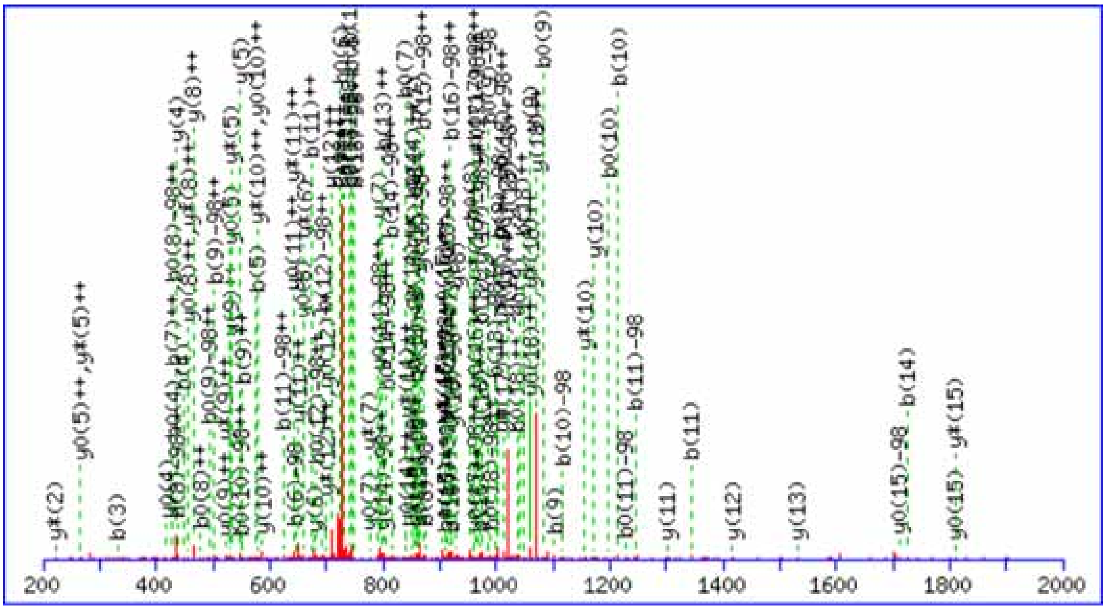
Matched b ions: b(3), b(4), b(5), b(6)-98, b(6)++, b(6), b(7), b(8), b(8)-98, b(9)-98++, b(9), b(9)-98, b(10), b(10)-98++, b(10)-98, b(11)-98, b(11), b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98, b(13), b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(11), y(12), y(12)++, y(13), y(13)++, y(14)-98, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.1166

TPVDESDDEIEHDEIPTGK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of TPVDESDDEIEHDEIPTGK
Found in MYPN_MOUSE, Myopalladin OS=Mus musculus GN=Mypn PE=2 SV=2

Match to Query 5529: 2273.027634 from(758.683154,3+)
Title: Elution from: 39.753 to 39.753 scan no 3324 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2273.0260
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K19 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 37 **Expect:** 0.013

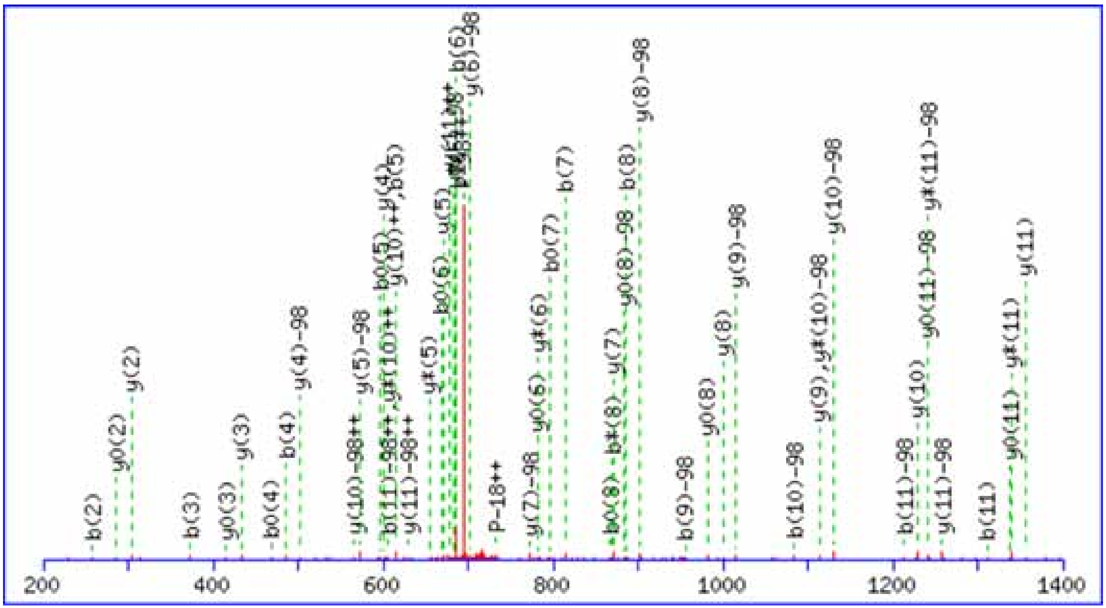
Matched b ions: b(3), b(4), b(5), b(6), b(6)-98, b(7)++, b(7), b(8)-98++, b(8), b(8)-98, b(9)-98++, b(9), b(9)++, b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14), b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(18)-98++, b(18)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13), y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++
Precursor origin neutral loss: +

Peptide No.1167

TQDIEAEASEER
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **TQDIEAEASEER**
Found in **SRCA_MOUSE**, Sarcalumenin OS=Mus musculus GN=Srl PE=1 SV=1

Match to Query 2344: 1484.603392 from(743.308972,2+)
Title: Elution from: 29.419 to 29.419 scan no 2225 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1484.6031
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 87 Expect: 3.5e-008

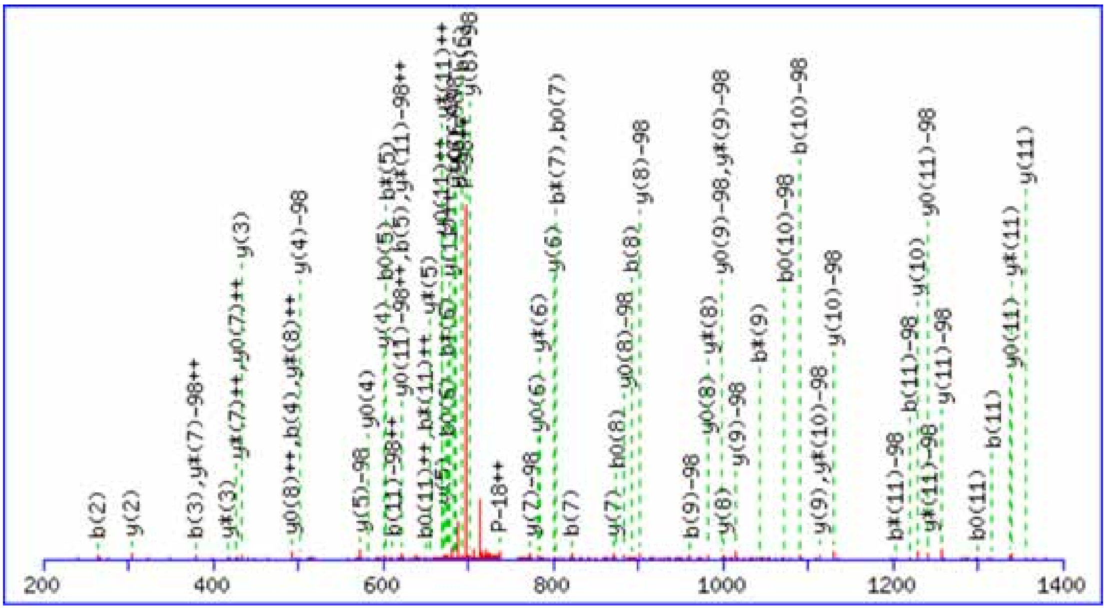
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10)-98, b(11)-98, b(11), b(11)-98++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5), y(6)-98, y(7), y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(10)-98, y(10)++, y(10), y(10)-98++, y(11)-98, y(11), y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.1168

TQDIEAEASEER
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of TQDIEAEASEER
Found in SRCA_MOUSE, Sarcalumenin OS=Mus musculus GN=Srl PE=1 SV=1

Match to Query 1843: 1490.635748 from(746.325150,2+)
Title: Elution from: 29.309 to 29.309 scan no 2049 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1490.6350
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 Expect: 8.4e-006

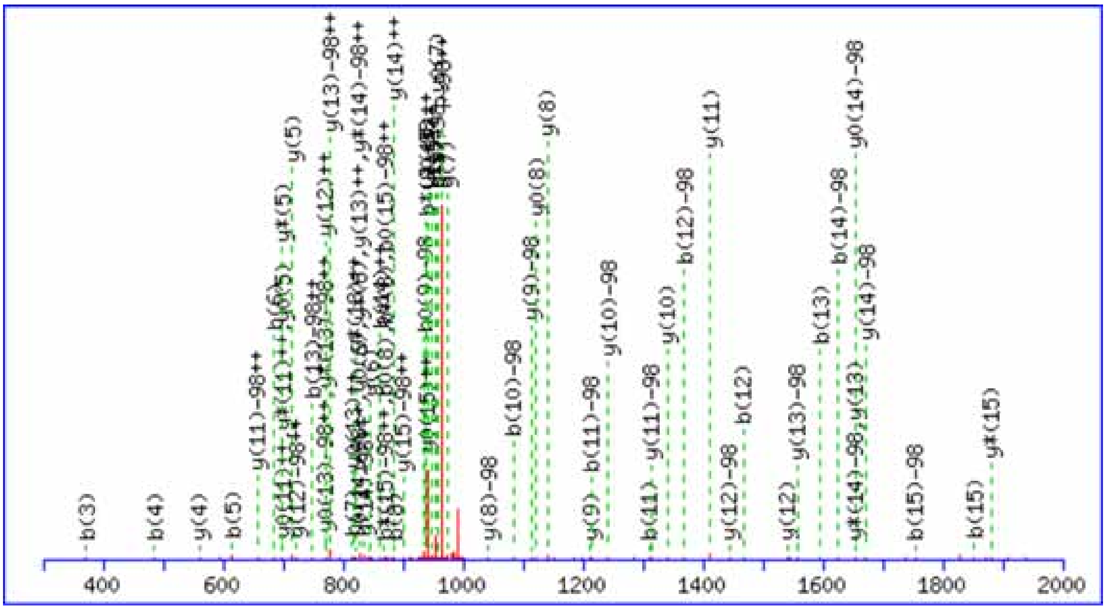
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10)-98, b(11)-98, b(11), b(11)-98++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5)-98, y(5), y(6)-98, y(6), y(7)-98, y(7), y(8)-98, y(8), y(9)-98, y(9), y(10)-98, y(10), y(11)-98, y(11), y(11)++
Precursor origin neutral loss: +

Peptide No.1169

TQDIEAEASEERQQER
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of TQDIEAEASEERQQER
Found in SRCA_MOUSE, Sarcalumenin OS=Mus musculus GN=Srl PE=1 SV=1

Match to Query 4659: 2025.865020 from(1013.939786,2+)
Title: Elution from: 30.434 to 30.434 scan no 2180 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2025.8640
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 Expect: 2e-006

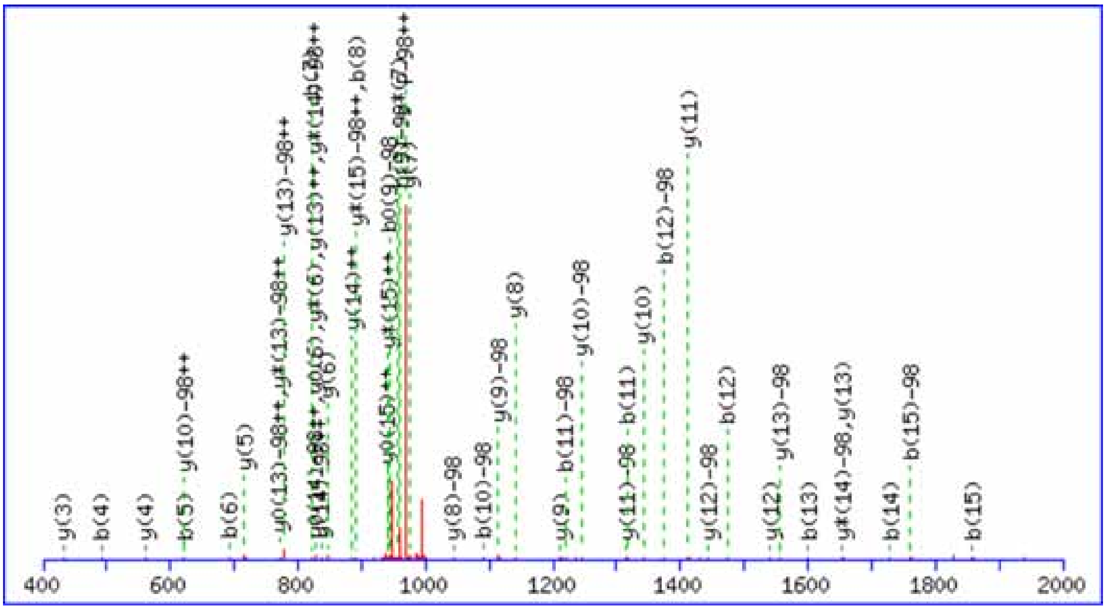
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10)-98, b(11)-98, b(11), b(12), b(12)-98, b(13), b(13)-98++, b(14)-98, b(14)++, b(15)-98, b(15)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-98, y(10), y(11)-98, y(11), y(11)-98++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13)-98++, y(13)-98, y(13), y(13)++, y(14)-98++, y(14)-98, y(14)++, y(15)-98++, y(15)++
Precursor origin neutral loss: +

Peptide No.1170

TQDIEAEASEERQQER
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of TQDIEAEASEERQQER
Found in SRCA_MOUSE, Sarcalumenin OS=Mus musculus GN=Srl PE=1 SV=1

Match to Query 4563: 2031.896132 from(1016.955342,2+)
Title: Elution from: 30.218 to 30.218 scan no 2039 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2031.8958
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 0.00019

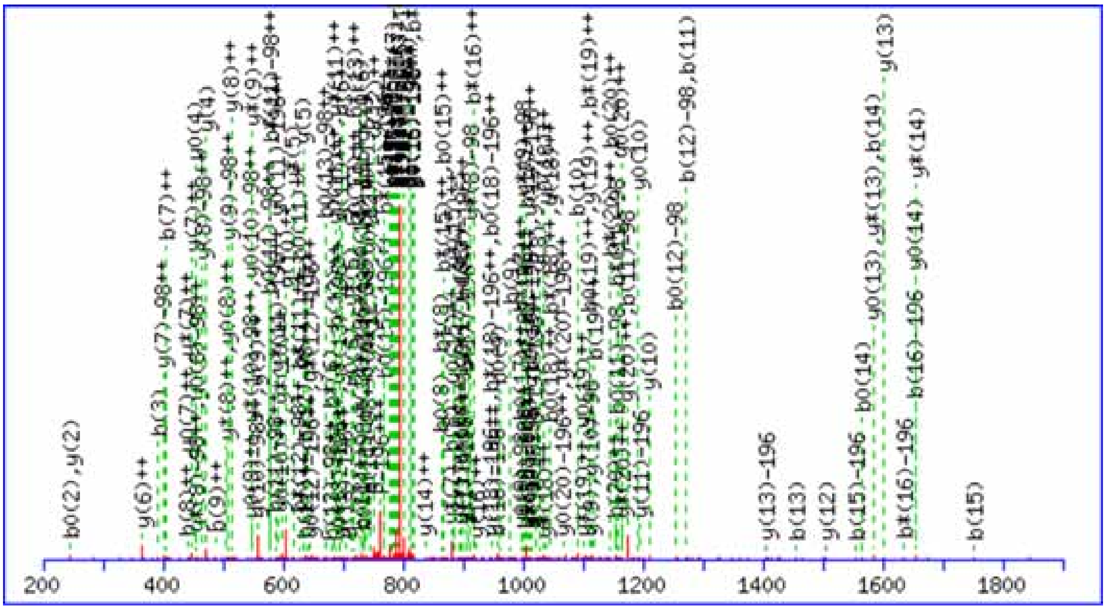
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(13), b(14), b(15), b(15)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10)-98++, y(10), y(10)-98, y(11)-98, y(11), y(12), y(12)-98, y(13)-98++, y(13), y(13)++, y(13)-98, y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1171

TQESCGIAPLTPSQSPKPEAR
Confirmed sites: @T:11,@S:15
Ambiguous sites:

MS/MS Fragmentation of TQESCGIAPLTPSQSPKPEAR
Found in HS12B_MOUSE, Heat shock 70 kDa protein 12B OS=Mus musculus GN=Hspa12b PE=1 SV=1

Match to Query 7986: 2481.166668 from(828.062832,3+)
Title: Elution from: 36.029 to 36.029 scan no 3072 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2481.1648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K17 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 33 **Expect:** 0.042

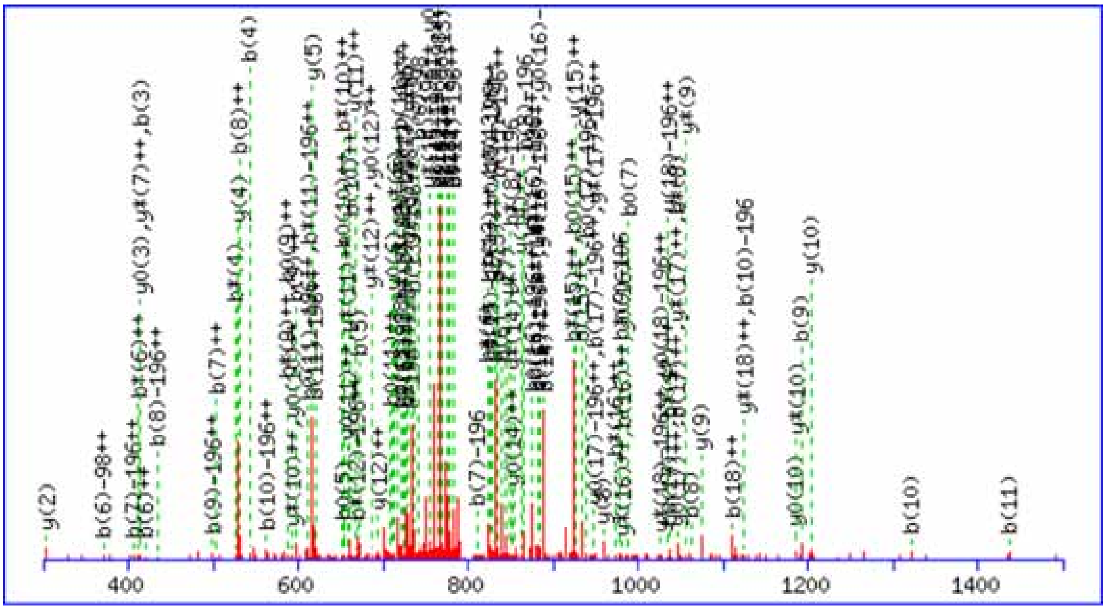
Matched b ions: b(3), b(5), b(6), b(7), b(7)++, b(8), b(8)++, b(9)++, b(9), b(10), b(11)-98, b(11), b(11)-98++, b(11)++, b(12)-98, b(12)-98++, b(12)++, b(13), b(13)-98++, b(13)++, b(14), b(14)-98++, b(14)++, b(15)-98, b(15)-196, b(15), b(15)-196++, b(16)-196, b(17)++, b(17)-98++, b(17)-196++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)++, b(19)-196++, b(20)++, b(20)-98++
Matched y ions: y(2), y(4), y(5), y(6)++, y(6), y(7)-98++, y(7)++, y(7), y(7)-98, y(8)++, y(8)-98++, y(8), y(9)++, y(9), y(9)-98++, y(9)-98, y(10)++, y(10)-98++, y(10), y(10)-98, y(11)-98, y(11)-98++, y(11)++, y(11)-196, y(12), y(12)++, y(12)-98++, y(13)-196, y(13)++, y(13), y(13)-98++, y(13)-196++, y(14)-196++, y(14)-98++, y(14)++, y(15)-196++, y(16)++, y(16)-98++, y(17)-196++, y(18)-98++, y(18)-196++, y(18)++, y(19)-196++, y(19)-98++, y(19)++, y(20)++, y(20)-98++
Precursor origin neutral loss: +

Peptide No.1172

TREQESSGEEDNDLSPEER
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of TREQESSGEEDNDLSPEER
Found in IPP2_MOUSE, Protein phosphatase inhibitor 2 OS=Mus musculus GN=Ppp1r2 PE=1 SV=3

Match to Query 7828: 2393.890872 from(798.970900,3+)
Title: Elution from: 28.841 to 28.841 scan no 2057 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2393.8897
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.00091

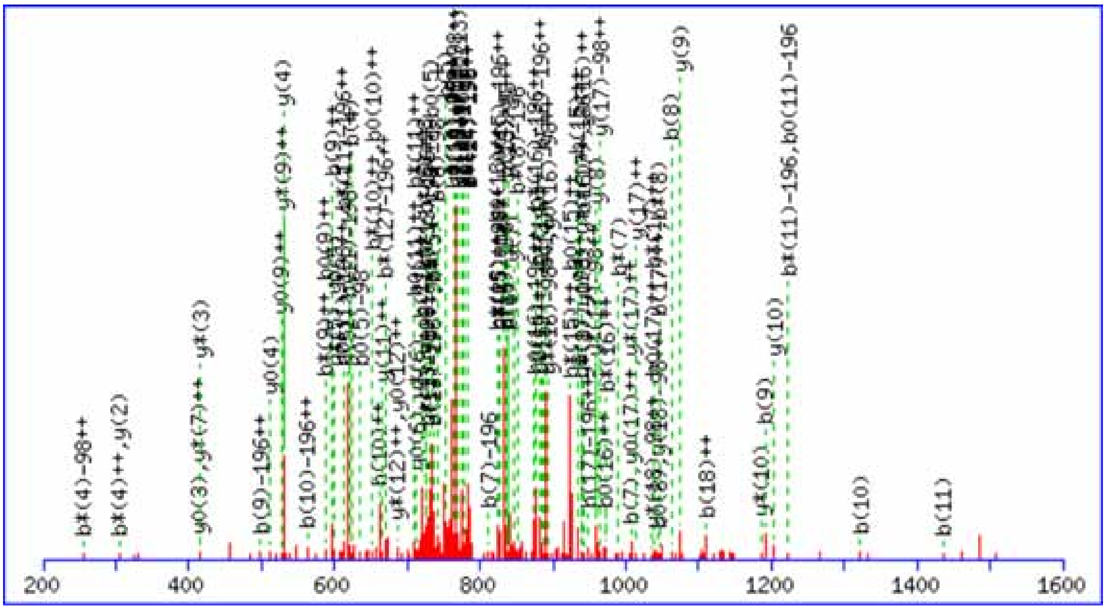
Matched b ions: b(3), b(4), b(5), b(6)-98++, b(6)++, b(6)-98, b(6), b(7)-196++, b(7)++, b(7)-98, b(7)-196, b(8)-98++, b(8)++, b(8)-196, b(8)-196++, b(8)-98, b(8), b(9)-196++, b(9), b(9)++, b(9)-98++, b(10), b(10)-196++, b(10)++, b(10)-98++, b(10)-196, b(11), b(11)-98, b(11)-98++, b(11)-196++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)-98++, b(16)-196++, b(16)++, b(17)++, b(17)-196++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)-196++, y(14)-98++, y(14)++, y(15)++, y(18)-196++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1173

TREQESSGEEDNDLSPEER
Confirmed sites: @T:1,@S:7
Ambiguous sites:

MS/MS Fragmentation of TREQESSGEEDNDLSPEER
Found in IPP2_MOUSE, Protein phosphatase inhibitor 2 OS=Mus musculus GN=Ppp1r2 PE=1 SV=3

Match to Query 6379: 2393.894106 from(798.971978,3+)
Title: Elution from: 28.812 to 28.812 scan no 1951 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2393.8897
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.0042

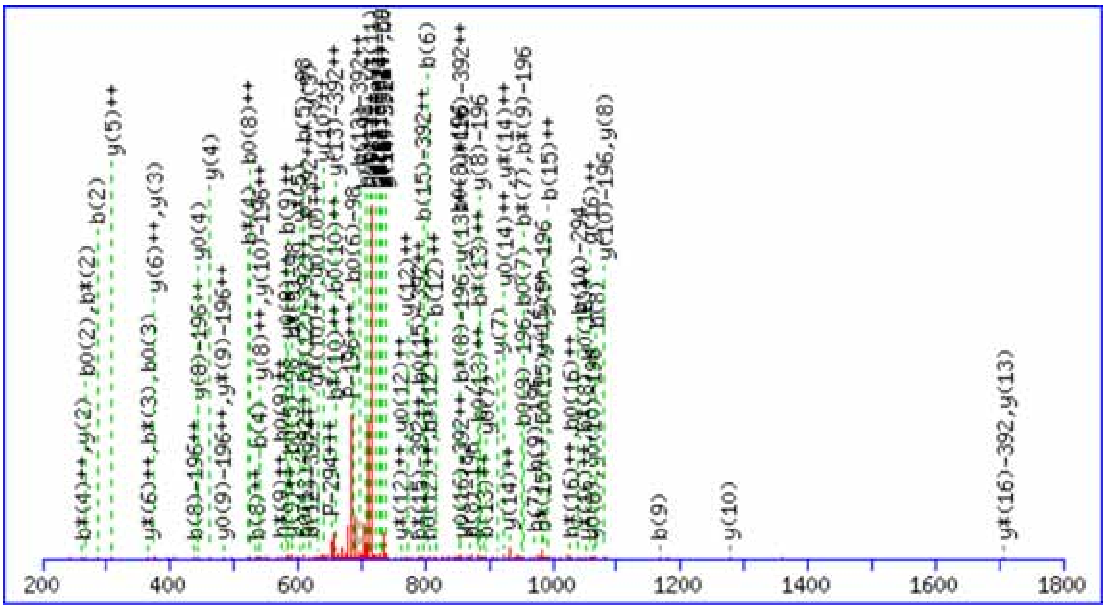
Matched b ions: b(4), b(5), b(6)-98, b(6), b(7)-196, b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)++, b(9)-98++, b(9)-196++, b(10), b(10)-98++, b(10)-98, b(10)++, b(10)-196++, b(11), b(11)++, b(11)-196++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(15)-196++, b(16)-98++, b(16)-196++, b(17)-196++, b(17)++, b(18)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(13)-98++, y(13)++, y(14)-98++, y(15)-98++, y(15)++, y(17)-98++, y(17)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1174

TRPRSPSPVSSERSLSR
Confirmed sites: @S:5,@S:7,@S:10,@S:11
Ambiguous sites:

MS/MS Fragmentation of TRPRSPSPVSSERSLSR
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 7478: 2245.905150 from(749.642326,3+)
Title: Elution from: 26.064 to 26.064 scan no 1679 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2245.9048
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.013

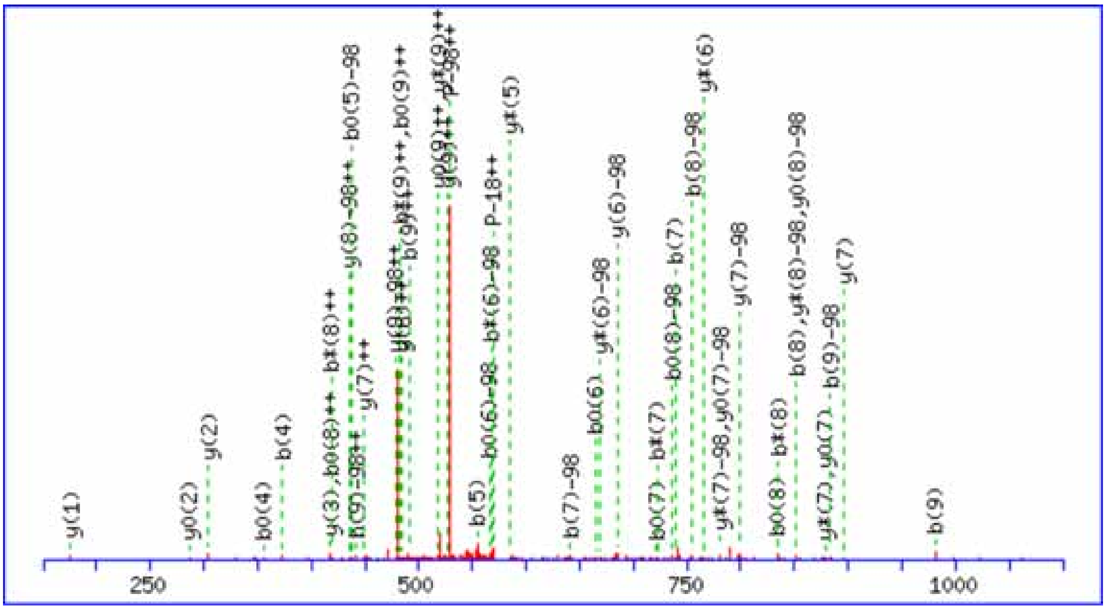
Matched b ions: b(2), b(4), b(5)-98, b(6)-98, b(6), b(7)-98++, b(7)-98, b(7), b(8)-196++, b(8)++, b(8), b(8)-196, b(9)-98++, b(9), b(9)++, b(9)-98, b(9)-196, b(10)-98++, b(10)-196++, b(10)-294, b(11)-98++, b(11)-196++, b(12)-196++, b(12)++, b(12)-392++, b(13)++, b(13)-392++, b(13)-98++, b(14)-98++, b(14)-196++, b(15)-98++, b(15)-392++, b(15)++, b(16)-196++, b(16)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(7), y(8), y(8)-196++, y(8)++, y(8)-98, y(8)-196, y(9)++, y(9)-98, y(9)-98++, y(9)-196, y(10)-98++, y(10)-196, y(10)-98, y(10), y(10)++, y(10)-196++, y(11)-196++, y(11)-98++, y(11)++, y(12)++, y(12)-196++, y(12)-98++, y(13), y(13)-98++, y(13)++, y(13)-392++, y(13)-294++, y(14)++, y(14)-196++, y(14)-98++, y(14)-392++, y(15)-98++, y(15)++, y(15)-294++, y(15)-196++, y(16)++, y(16)-294++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1175

TSALTQGLER
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of TSALTQGLER
Found in CG059_MOUSE, UPF0539 protein C7orf59 homolog OS=Mus musculus PE=2 SV=2

Match to Query 735: 1154.530622 from(578.272587,2+)
Title: Elution from: 29.946 to 29.946 scan no 2101 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1154.5332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.042

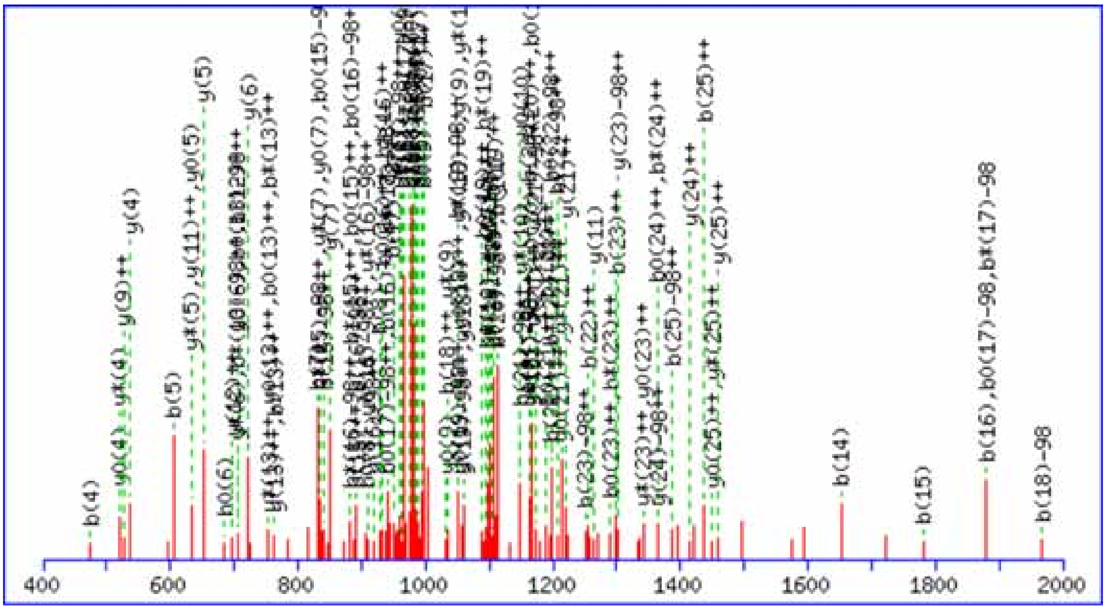
Matched b ions: b(4), b(5), b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(9)-98++, b(9)++
Matched y ions: y(1), y(2), y(3), y(6)-98, y(7)-98, y(7), y(7)++, y(8)-98++, y(8)++, y(9)-98++, y(9)++
Precursor origin neutral loss: +

Peptide No.1176

TSEEEPEPSVSENEEVDAEEANSFQK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of TSEEEPEPSVSENEEVDAEEANSFQK
Found in TXLNB_MOUSE, Beta-taxilin OS=Mus musculus GN=Txlnb PE=2 SV=2

Match to Query 8603: 3045.250971 from(1016.090933,3+)
Title: Elution from: 47.099 to 47.099 scan no 4558 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3045.2499
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K26 : Dimethyl (K)
Ions Score: 74 **Expect:** 2.6e-006

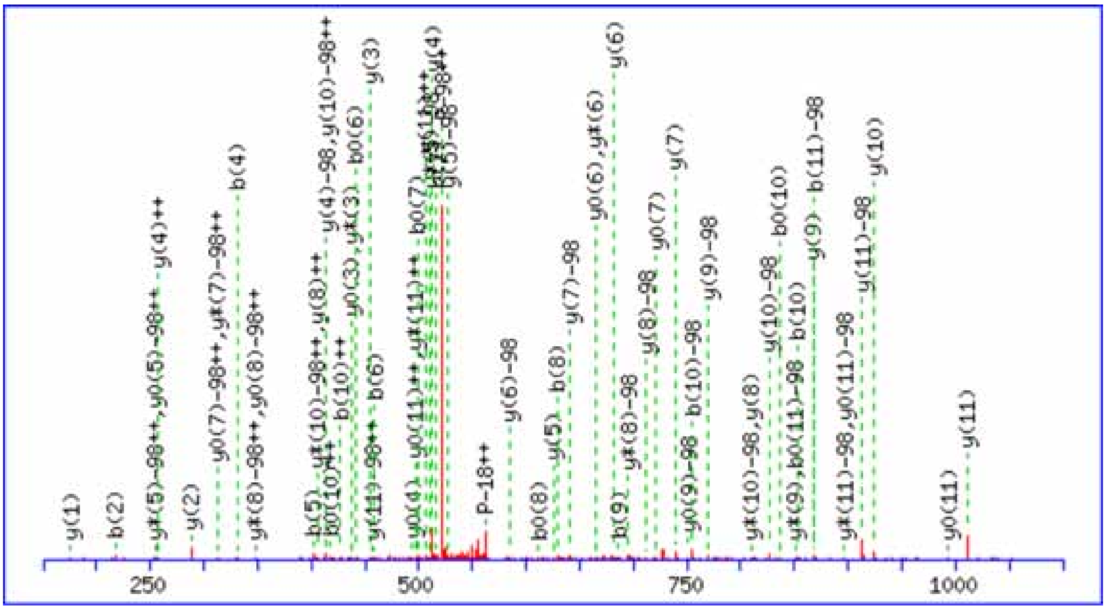
Matched b ions: b(4), b(5), b(7), b(8), b(10), b(12)++, b(13)++, b(14), b(15), b(15)++, b(15)-98++, b(16), b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)-98, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(25)++, b(25)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11)++, y(11), y(12)++, y(13)++, y(16)++, y(16)-98++, y(17)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(21)++, y(21)-98++, y(23)-98++, y(24)-98++, y(24)++, y(25)++
Precursor origin neutral loss: +

Peptide No.1177

TSGGAGGLGSLR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of TSGGAGGLGSLR
Found in DESM_MOUSE, Desmin OS=Mus musculus GN=Des PE=1 SV=3

Match to Query 967: 1139.533618 from(570.774085,2+)
Title: Elution from: 32.398 to 32.398 scan no 2633 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1139.5336
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 Expect: 0.00018

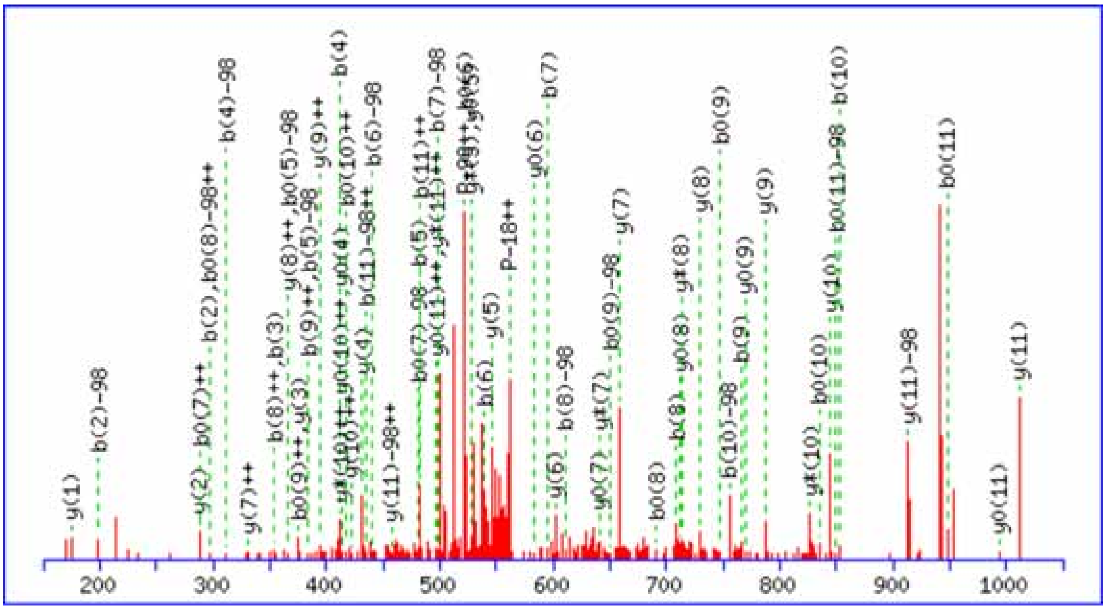
Matched b ions: b(2), b(4), b(5), b(6), b(7), b(8), b(9), b(10)-98, b(10)++, b(10), b(11)-98
Matched y ions: y(1), y(2), y(3), y(4)-98, y(4), y(4)++, y(5)-98, y(5), y(6)-98, y(6), y(7)-98, y(7), y(8), y(8)-98, y(8)++, y(9), y(9)-98, y(10)-98, y(10)-98++, y(10), y(11)-98, y(11), y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.1178

TSGGAGGLGSLR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of TSGGAGGLGSLR
Found in DESM_MOUSE, Desmin OS=Mus musculus GN=Des PE=1 SV=3

Match to Query 675: 1139.533598 from(570.774075,2+)
Title: Elution from: 34.327 to 34.327 scan no 2678 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1139.5336
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 82 Expect: 1.2e-007

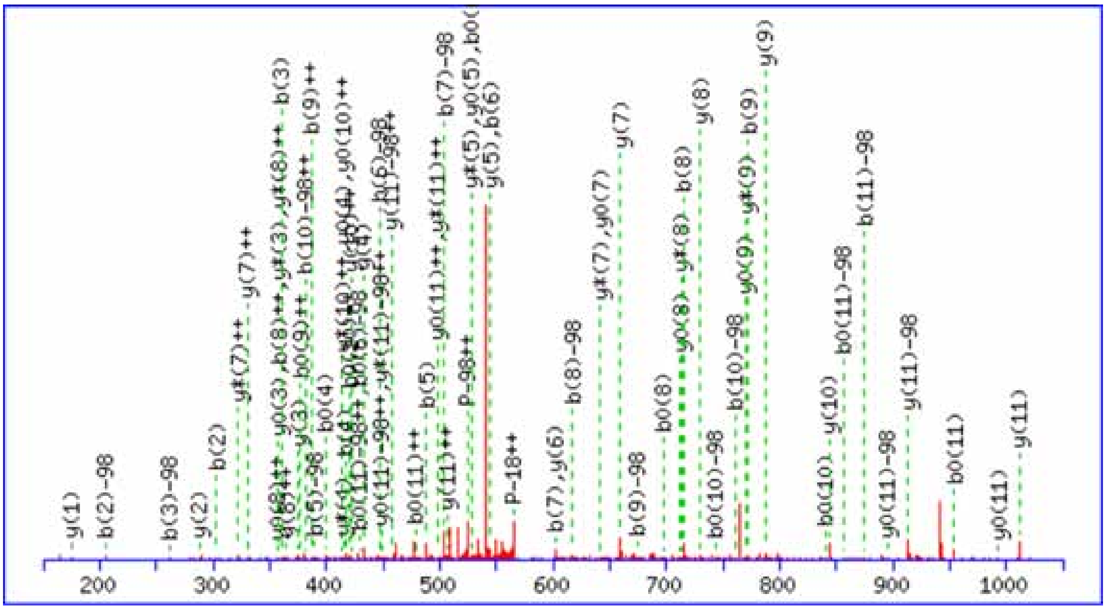
Matched b ions: b(2)-98, b(2), b(3), b(4), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)++, b(8), b(8)-98, b(9), b(9)++, b(10)-98, b(10), b(11)-98++, b(11)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)-98, y(11)-98++
Precursor origin neutral loss: +

Peptide No.1179

TSGGAGGLGSLR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of TSGGAGGLGSLR
Found in DESM_MOUSE, Desmin OS=Mus musculus GN=Des PE=1 SV=3

Match to Query 689: 1145.565990 from(573.790271,2+)
Title: Elution from: 34.467 to 34.467 scan no 2698 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1145.5654
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 0.00037

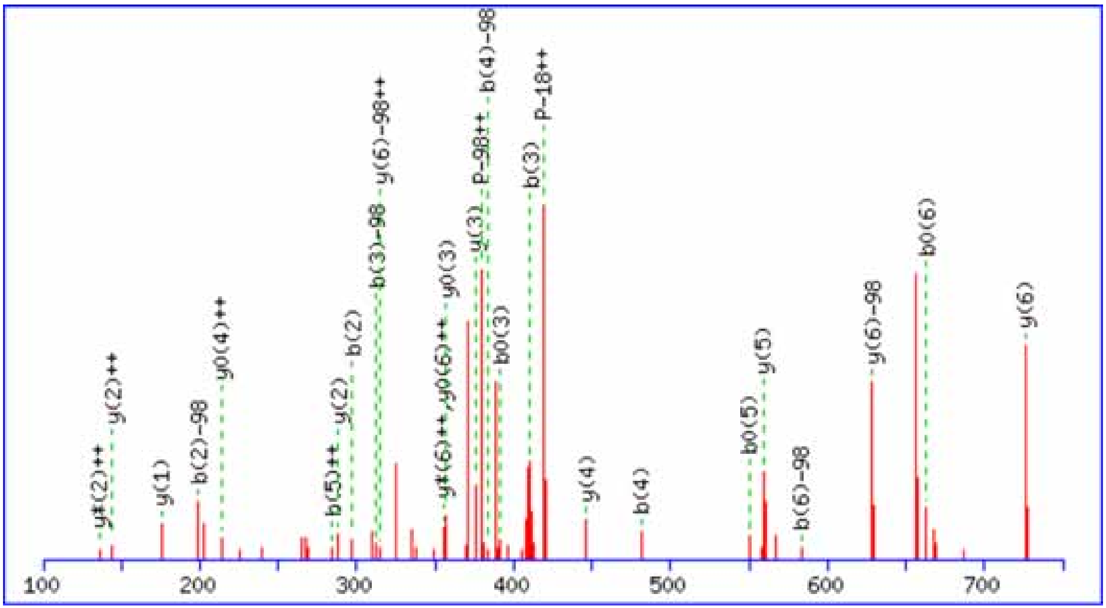
Matched b ions: b(2)-98, b(2), b(3), b(3)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(8)++, b(9), b(9)++, b(9)-98, b(10)-98++, b(10)-98, b(11)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(10), y(10)++, y(11), y(11)-98, y(11)-98++, y(11)++
Precursor origin neutral loss: +

Peptide No.1180

TSLASLR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of TSLASLR
Found in JPH1_MOUSE, Junctophilin-1 OS=Mus musculus GN=Jph1 PE=1 SV=1

Match to Query 238: 854.426086 from(428.220319,2+)
Title: Elution from: 37.400 to 37.400 scan no 3086 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 854.4263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.023

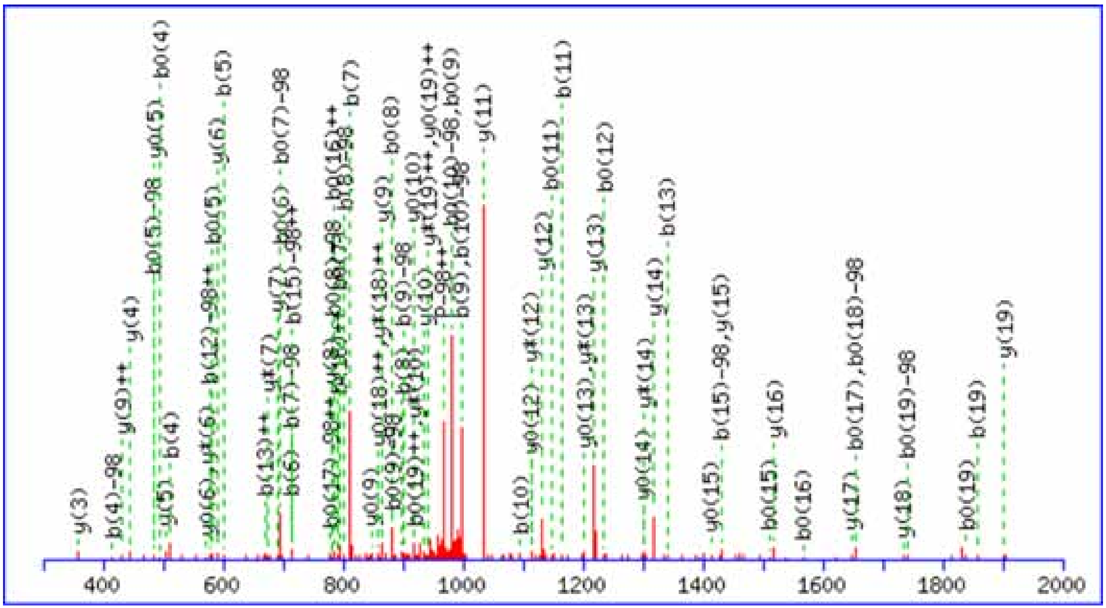
Matched b ions: b(2)-98, b(2), b(3), b(3)-98, b(4), b(4)-98, b(5)++, b(6)-98
Matched y ions: y(1), y(2), y(2)++, y(3), y(4), y(5), y(6)-98, y(6), y(6)-98++
Precursor origin neutral loss: +

Peptide No.1181

TSSESIVSVPASSTSGSPSR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **TSSESIVSVPASSTSGSPSR**
Found in **ABLM2_MOUSE**, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 5128: 2029.920428 from(1015.967490,2+)
Title: Elution from: 38.408 to 38.408 scan no 3259 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2029.9205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 94 Expect: 2.6e-008

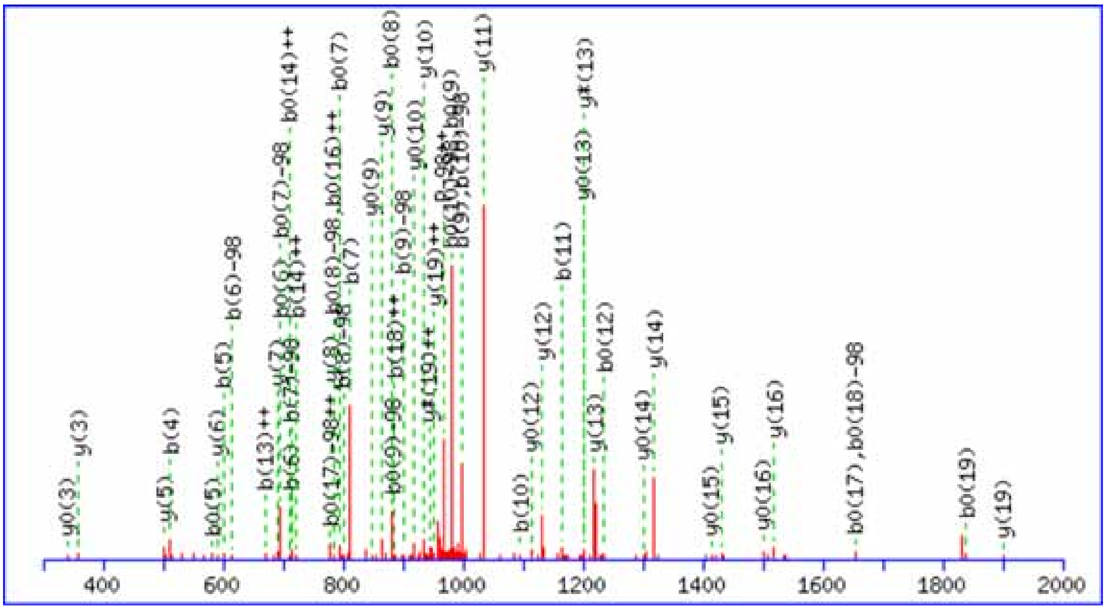
Matched b ions: b(4), b(4)-98, b(5), b(6), b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10)-98, b(10), b(11), b(12)-98++, b(13)++, b(13), b(15)-98, b(15)-98++, b(16)++, b(19)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(17), y(18), y(19)
Precursor origin neutral loss: +

Peptide No.1182

TSSESIVSVPASSTSGSPSR
Confirmed sites:
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of TSSESIVSVPASSTSGSPSR
Found in ABLM2_MOUSE, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 5321: 2029.922266 from(1015.968409,2+)
Title: Elution from: 38.477 to 38.477 scan no 3300 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2029.9205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 Expect: 3.5e-007

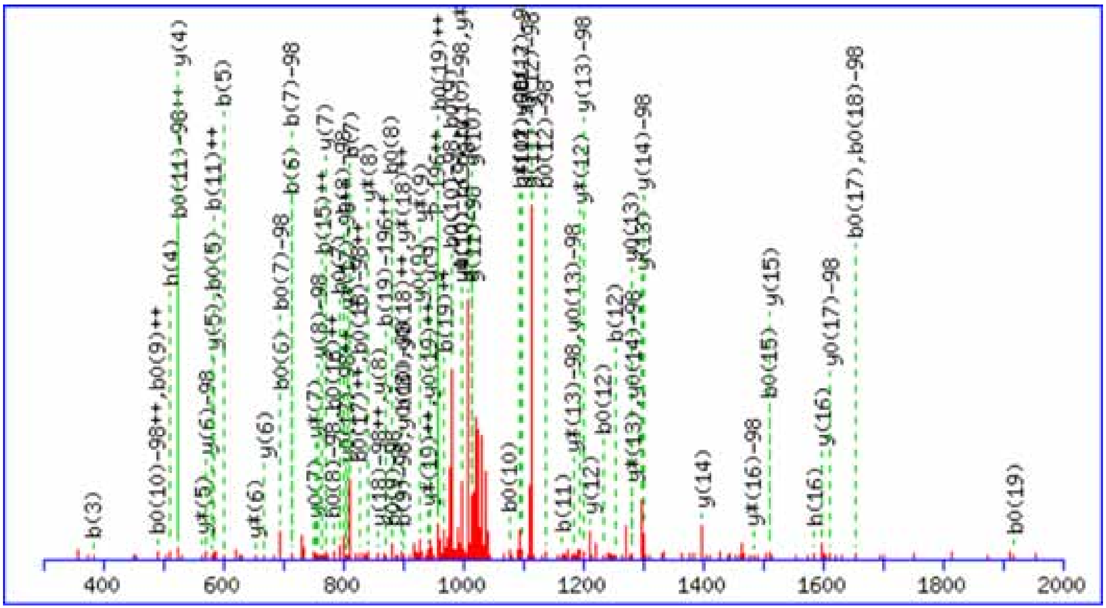
Matched b ions: b(4), b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(11), b(13)++, b(14)++, b(18)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(19), y(19)++
Precursor origin neutral loss: +

Peptide No.1183

TSSESIVSVPASSTSGSPSR
Confirmed sites:
Ambiguous sites: @T:1orS:2, @S:17orS:19

MS/MS Fragmentation of TSSESIVSVPASSTSGSPSR
Found in ABLM2_MOUSE, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 6959: 2109.883504 from(1055.949028,2+)
Title: Elution from: 41.696 to 41.696 scan no 3876 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2109.8868
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.031

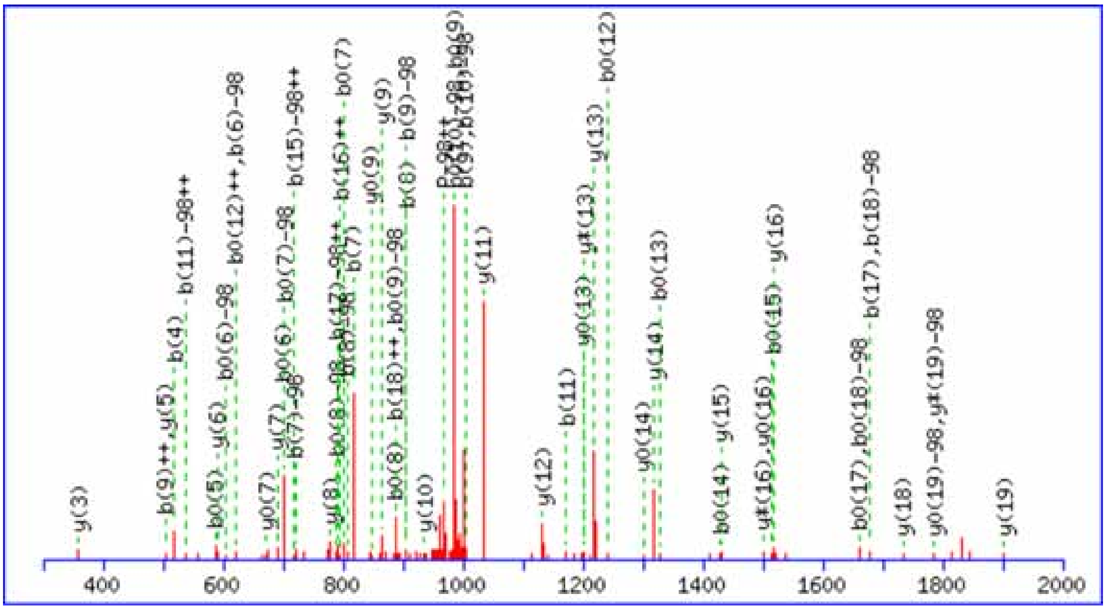
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11)++, b(11), b(12), b(15)++, b(16), b(19)-98++, b(19)-196++, b(19)++
Matched y ions: y(4), y(5), y(6)-98, y(6), y(7), y(8)-98, y(8), y(9), y(10), y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(14), y(14)-98, y(15), y(16), y(18)-98++
Precursor origin neutral loss: +

Peptide No.1184

TSSESIVSVPASSTSGSPSR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of TSSESIVSVPASSTSGSPSR
Found in ABLM2_MOUSE, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 5143: 2035.956144 from(1018.985348,2+)
Title: Elution from: 38.416 to 38.416 scan no 3260 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2035.9523
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 99 Expect: 9.2e-009

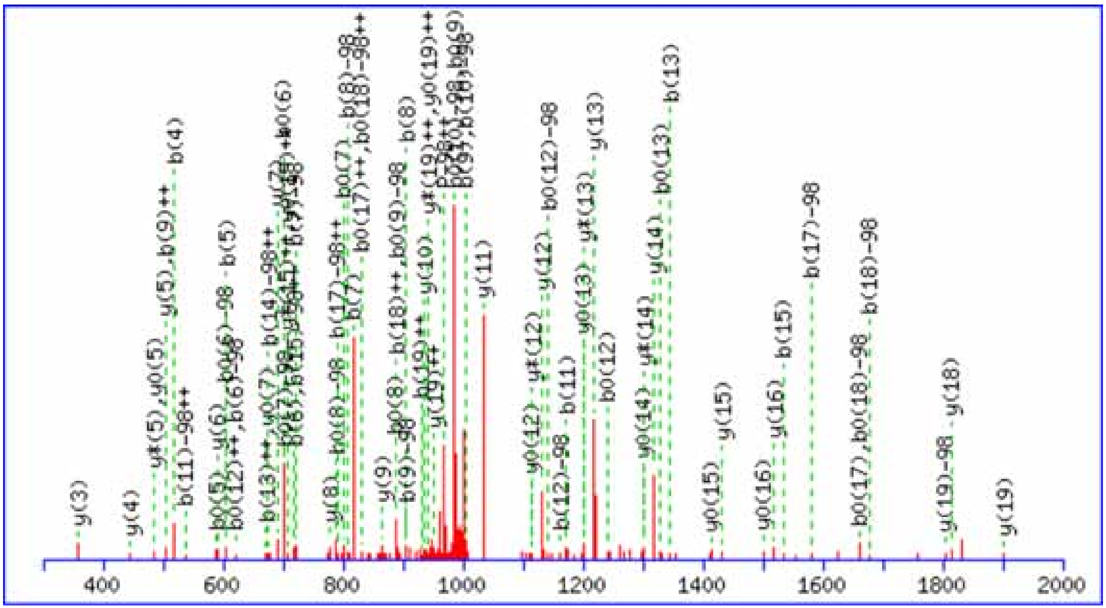
Matched b ions: b(4), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(9)++, b(9)-98, b(9), b(10)-98, b(11)-98++, b(11), b(15)-98++, b(16)++, b(17), b(17)-98++, b(18)++, b(18)-98
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(18), y(19)
Precursor origin neutral loss: +

Peptide No.1185

TSSESIVSVPASSTSGSPSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TSSESIVSVPASSTSGSPSR
Found in ABLM2_MOUSE, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 5336: 2035.953180 from(1018.983866,2+)
Title: Elution from: 38.552 to 38.552 scan no 3310 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2035.9523
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 87 Expect: 1.4e-007

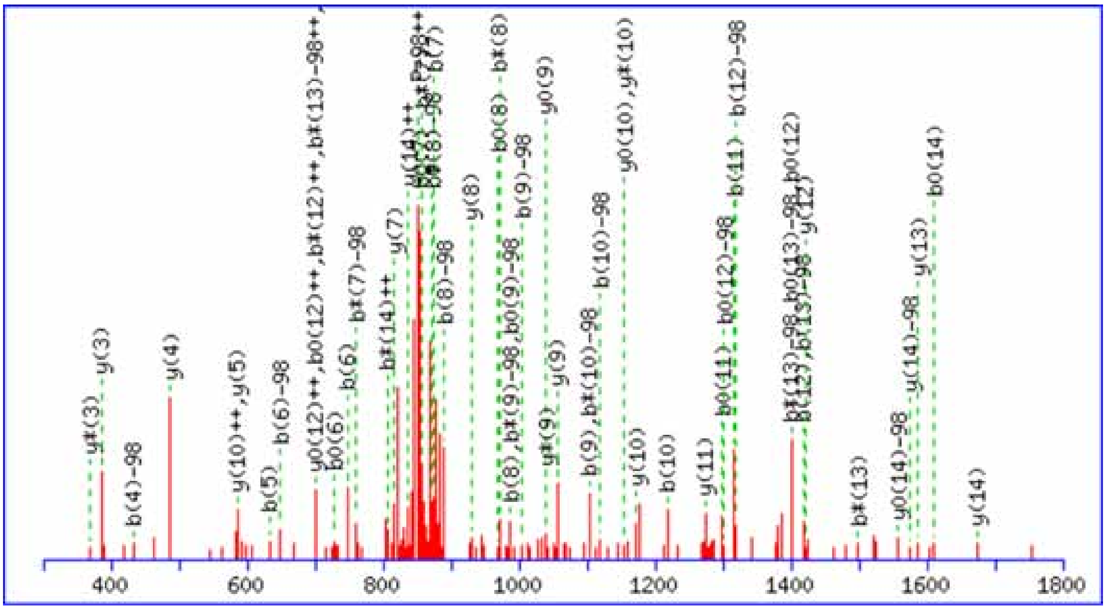
Matched b ions: b(4), b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9)++, b(9)-98, b(9), b(10)-98, b(11)-98++, b(11), b(12)-98, b(13)++, b(13), b(14)-98++, b(15), b(15)-98++, b(17)-98, b(17)-98++, b(18)++, b(18)-98, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(18), y(19), y(19)-98, y(19)++
Precursor origin neutral loss: +

Peptide No.1186

TSSFTDQLDDVTPNR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TSSFTDQLDDVTPNR
Found in GOGA4_MOUSE, Golgin subfamily A member 4 OS=Mus musculus GN=Golga4 PE=1 SV=2

Match to Query 4344: 1802.774780 from(902.394666,2+)
Title: Elution from: 47.107 to 47.107 scan no 4559 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1802.7724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0019

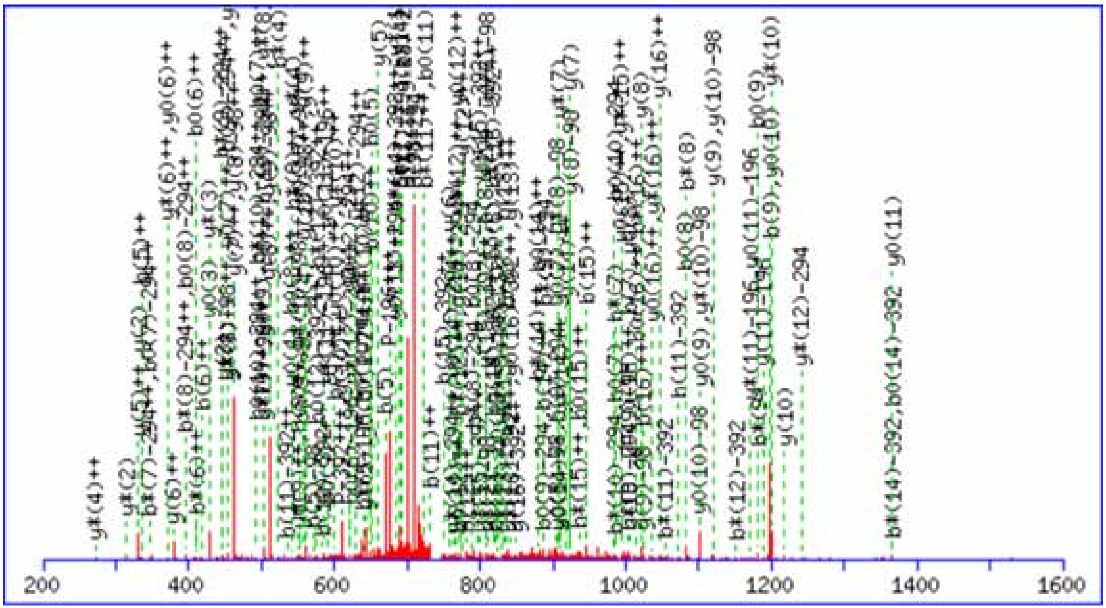
Matched b ions: b(4)-98, b(5), b(6), b(6)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(11), b(12), b(12)-98, b(13)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(12), y(13), y(14), y(14)-98, y(14)++
Precursor origin neutral loss: +

Peptide No.1187

TSSKESSPVPSPTLDRK
Confirmed sites: @S:3,@S:6,@S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of TSSKESSPVPSPTLDRK
Found in SPTB2_MOUSE, Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2

Match to Query 5656: 2218.897647 from(740.639825,3+)
Title: Elution from: 33.308 to 33.308 scan no 2545 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2218.8966
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K4 : Dimethyl (K)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 29 Expect: 0.045

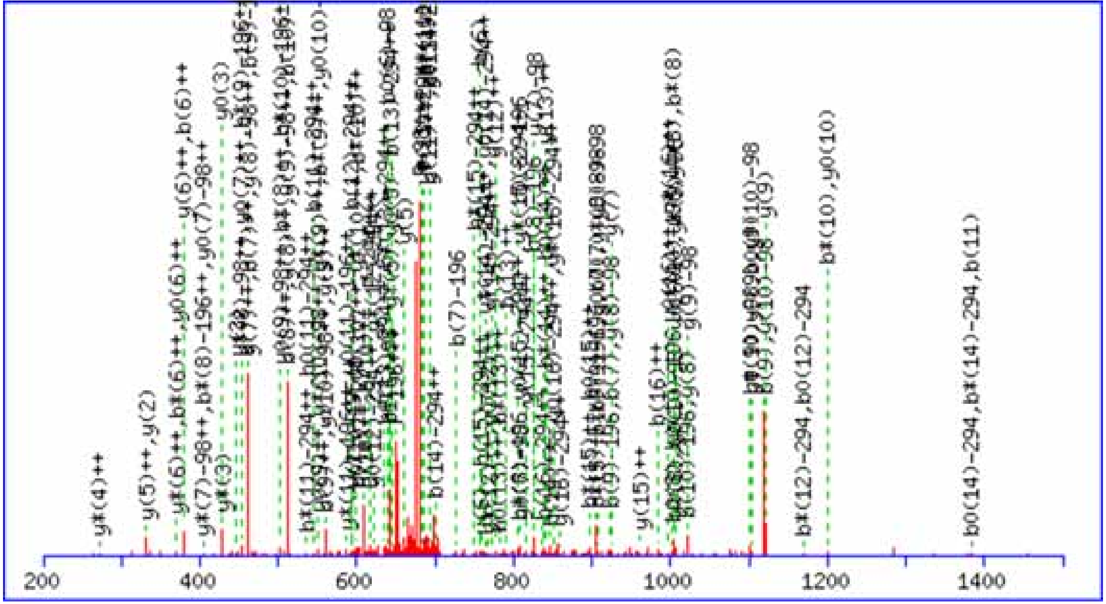
Matched b ions: b(5), b(5)++, b(5)-98, b(6)-98++, b(6), b(6)++, b(6)-196, b(7), b(7)-98++, b(7)++, b(7)-98, b(7)-294, b(7)-196, b(8)-98, b(8)-196++, b(8)-98++, b(8)-196, b(8)++, b(8)-294, b(9)-98, b(9), b(9)-196, b(9)-294++, b(9)-196++, b(9)-294, b(9)-98++, b(9)++, b(10)-196, b(10)-98, b(10)-294, b(10)-294++, b(10)-196++, b(10)++, b(10)-98++, b(11)-98, b(11)-196, b(11)-196++, b(11)-392++, b(11)-98++, b(11)++, b(11)-392, b(12)-196, b(12)++, b(12)-294++, b(12)-392++, b(12)-196++, b(12)-98++, b(13)-294++, b(13)-196++, b(13)-98++, b(13)++, b(14)-392++, b(14)++, b(14)-98++, b(14)-196++, b(15)++, b(15)-98++, b(15)-392++, b(15)-294++, b(15)-196++, b(16)-98++, b(16)-294++, b(16)-196++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)-98++, y(8)++, y(8), y(8)-98, y(9)-98++, y(9)++, y(9), y(9)-98, y(10)++, y(10)-98++, y(10)-98, y(10), y(11)++, y(11)-98++, y(11)-196, y(12)-294++, y(12)-196++, y(12)-98++, y(12)++, y(13)-98++, y(13)-294++, y(13)++, y(14)-98++, y(14)-294++, y(14)-196++, y(14)++, y(15)++, y(15)-196++, y(15)-392++, y(15)-294++, y(15)-98++, y(16)-98++, y(16)++, y(16)-392++, y(16)-294++, y(16)-196++
Precursor origin neutral loss: +

Peptide No.1188

TSSKESSPVPSPTLDRK
Confirmed sites: @S:6,@S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of TSSKESSPVPSPTLDRK
Found in SPTB2_MOUSE, Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2

Match to Query 5036: 2138.931195 from(713.984341,3+)
Title: Elution from: 30.179 to 30.179 scan no 2149 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2138.9303
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K4 : Dimethyl (K)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K17 : Dimethyl (K)
Ions Score: 30 Expect: 0.048

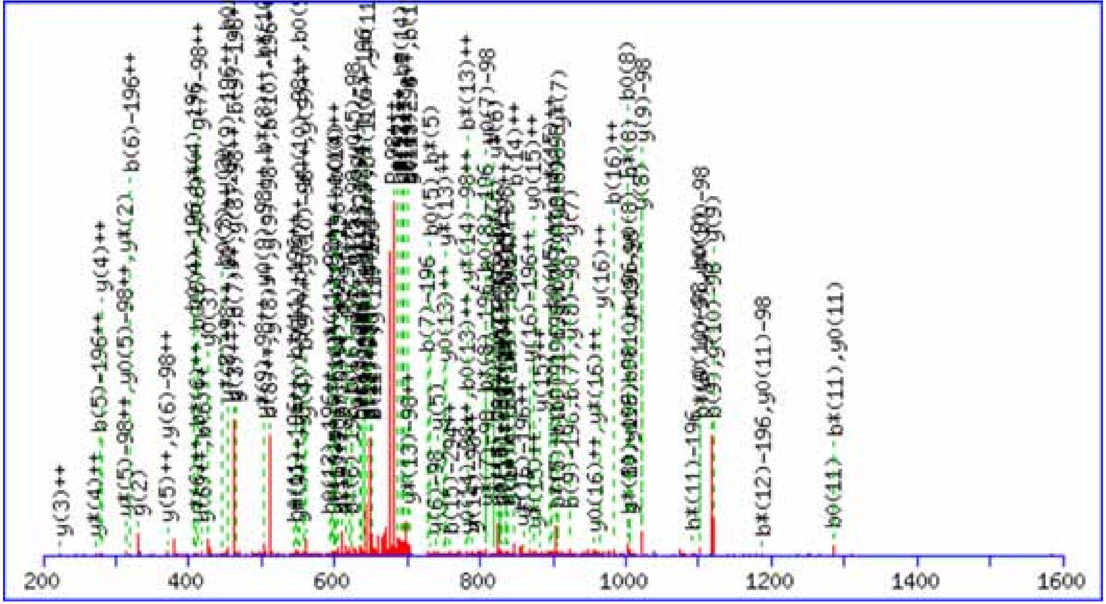
Matched b ions: b(6)++, b(6), b(7)++, b(7)-98, b(7), b(7)-196, b(8)-98++, b(8)++, b(8)-196, b(8)-98, b(9)-196++, b(9)-98++, b(9)-98, b(9), b(9)++, b(9)-196, b(10)-196++, b(10)-196, b(10)-98, b(10)-98++, b(10)++, b(11)-98, b(11), b(11)-98++, b(11)-294++, b(11)-196++, b(11)++, b(12)-196, b(12)-98, b(12)-196++, b(12)-294++, b(12)-98++, b(13)-294++, b(13)-196++, b(13)++, b(14)++, b(14)-294++, b(14)-196++, b(14)-98++, b(15)++, b(15)-98++, b(15)-196++, b(15)-294++, b(16)++, b(16)-294++
Matched y ions: y(2), y(3), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7)-98, y(7), y(8)-98++, y(8)++, y(8), y(8)-98, y(9)-98++, y(9)++, y(9), y(9)-98, y(10)-98, y(10)-98++, y(10)++, y(11)-196++, y(11)-98++, y(11)++, y(12)-196++, y(12)-98++, y(12)++, y(13)-294++, y(13)-98++, y(13)++, y(14)-294++, y(15)-294++, y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(16)-196++, y(16)-294++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1189

TSSKESSPVPSPTLDRK
Confirmed sites: @T:1,@S:2,@T:13
Ambiguous sites:

MS/MS Fragmentation of TSSKESSPVPSPTLDRK
Found in SPTB2_MOUSE, Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2

Match to Query 6995: 2138.931111 from(713.984313,3+)
Title: Elution from: 30.073 to 30.073 scan no 2227 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2138.9303
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K4 : Dimethyl (K)
T13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K17 : Dimethyl (K)
Ions Score: 39 Expect: 0.0069

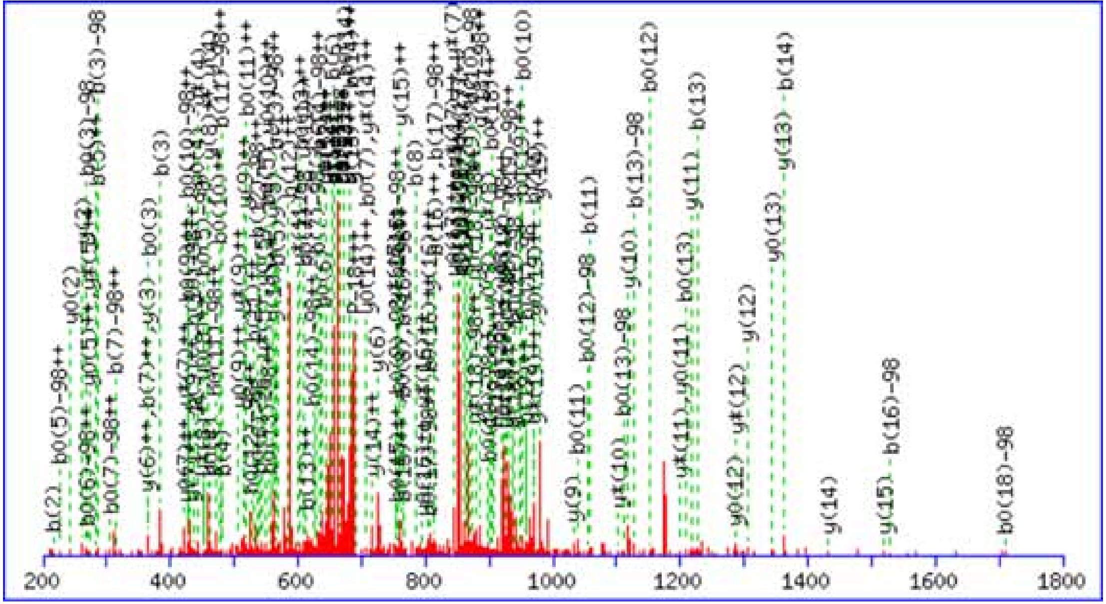
Matched b ions: b(3), b(5)-196++, b(5)-98, b(6)++, b(6)-196++, b(6)-98++, b(6)-196, b(6)-98, b(6), b(7)++, b(7)-98, b(7)-98++, b(7), b(7)-196, b(8)-98++, b(8)++, b(8)-98, b(9)-196++, b(9)-98, b(9), b(9)-98++, b(9)++, b(9)-196, b(10)++, b(10)-98, b(10)-196++, b(10)-98++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(12)++, b(13)-294++, b(13)-196++, b(14)++, b(14)-294++, b(14)-98++, b(15)-196++, b(15)++, b(15)-98++, b(15)-294++, b(16)++, b(16)-196++, b(16)-294++
Matched y ions: y(2), y(3)++, y(3), y(4)++, y(4), y(5)-98, y(5)++, y(5), y(6)++, y(6)-98++, y(6)-98, y(6), y(7)++, y(7)-98, y(7)-98++, y(7), y(8)-98++, y(8), y(8)++, y(8)-98, y(9)-98++, y(9), y(9)++, y(9)-98, y(10)++, y(10)-98, y(10)-98++, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1190

TSSPSSAGSVSLGHYTPTSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TSSPSSAGSVSLGHYTPTSR
Found in ABLM2_MOUSE, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 6882: 2085.935973 from(696.319267,3+)
Title: Elution from: 36.360 to 36.360 scan no 3119 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2085.9368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 0.00013

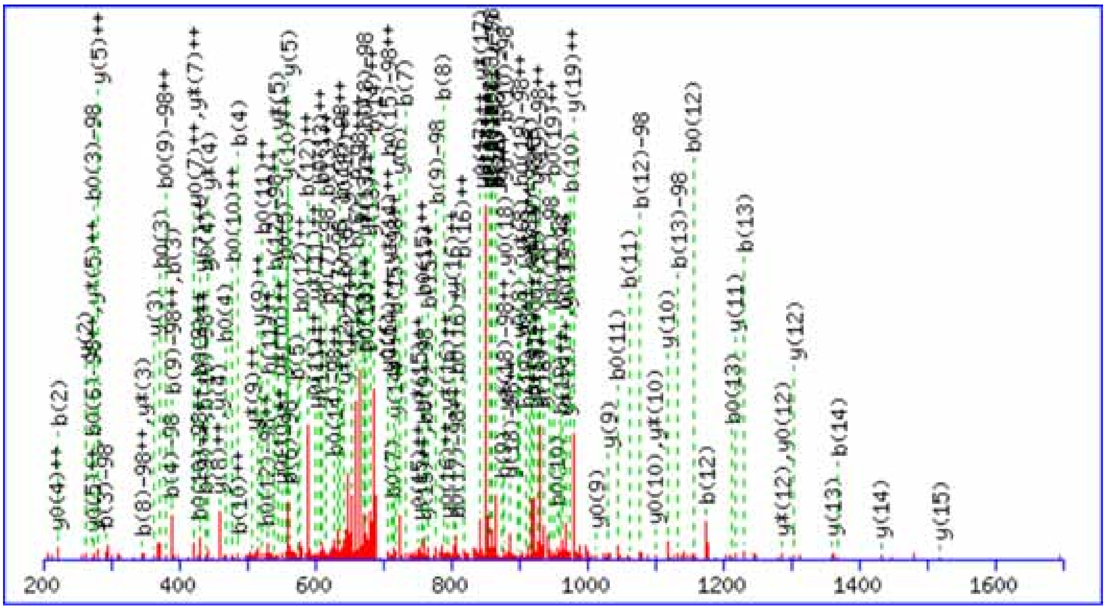
Matched b ions: b(2), b(3), b(3)-98, b(4), b(5)++, b(5), b(6), b(7)-98++, b(7)++, b(7)-98, b(8), b(9)++, b(9), b(10)-98++, b(10)-98, b(10), b(11), b(11)-98++, b(11)++, b(11)-98, b(12)-98++, b(12)++, b(13)-98, b(13), b(13)-98++, b(13)++, b(14), b(14)++, b(14)-98++, b(15)++, b(16)-98, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14), y(14)++, y(15)++, y(15), y(16)++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++
Precursor origin neutral loss: +

Peptide No.1191

TSSPSSAGSVSLGHYTPTSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of TSSPSSAGSVSLGHYTPTSR
Found in ABLM2_MOUSE, Actin-binding LIM protein 2 OS=Mus musculus GN=Ablim2 PE=1 SV=1

Match to Query 4969: 2091.969381 from(698.330403,3+)
Title: Elution from: 36.259 to 36.259 scan no 2937 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2091.9686
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 Expect: 1.8e-006

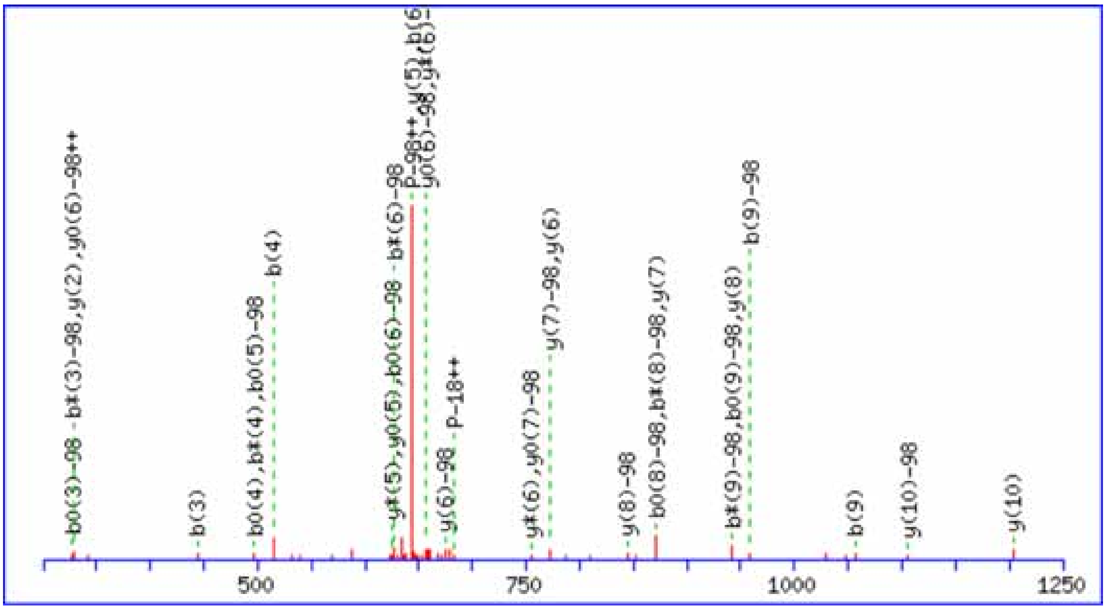
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98++, b(8), b(9)-98++, b(9)-98, b(9)++, b(9), b(10)++, b(10)-98++, b(10)-98, b(10), b(11)++, b(11)-98, b(11), b(12)++, b(12), b(12)-98, b(12)-98++, b(13), b(13)-98, b(13)++, b(14), b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14), y(14)++, y(15), y(15)++, y(16)++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++
Precursor origin neutral loss: +

Peptide No.1192

TVKAVEDEATK
Confirmed sites: @T:1,@T:10
Ambiguous sites:

MS/MS Fragmentation of TVKAVEDEATK
Found in TLN1_MOUSE, Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=1

Match to Query 1532: 1383.617610 from(692.816081,2+)
Title: Elution from: 61.740 to 61.740 scan no 5586 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1383.6148
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K3 : Dimethyl:2H(4)13C(2) (K)
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 Expect: 0.00068

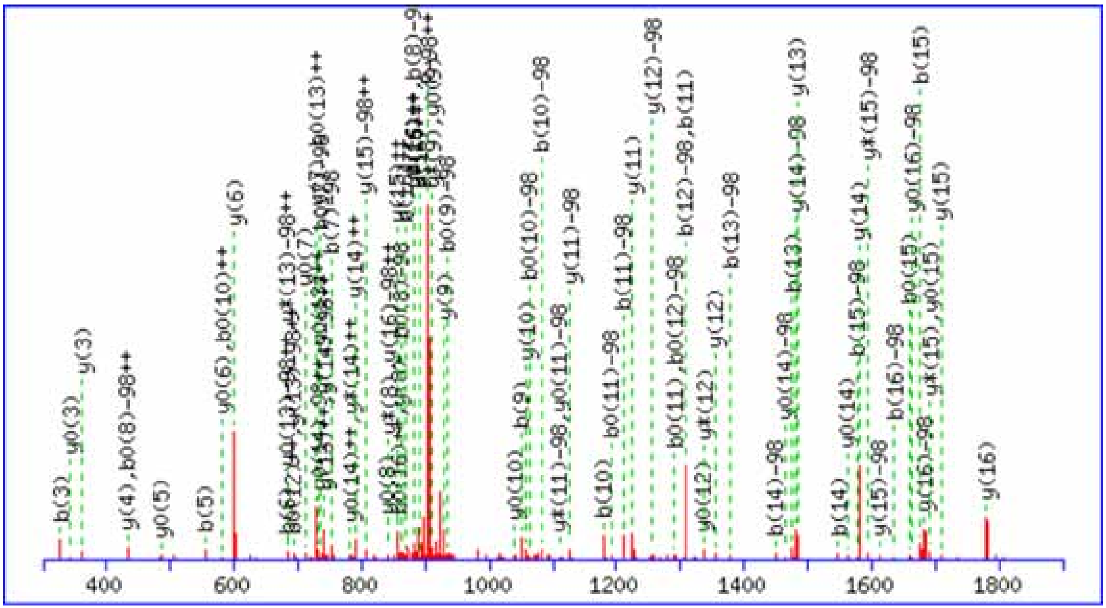
Matched b ions: b(3), b(4), b(6)-98, b(9)-98, b(9)
Matched y ions: y(2), y(5), y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)-98, y(10), y(10)-98
Precursor origin neutral loss: +

Peptide No.1193

VAEPEESEAEEPAAEGR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of VAEPEESEAEEPAAEGR
Found in MXRA7_MOUSE, Matrix-remodeling-associated protein 7 OS=Mus musculus GN=Mxra7 PE=1 SV=2

Match to Query 5107: 1906.785174 from(954.399863,2+)
Title: Elution from: 31.283 to 31.283 scan no 2482 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1906.7833
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 76 Expect: 9e-007

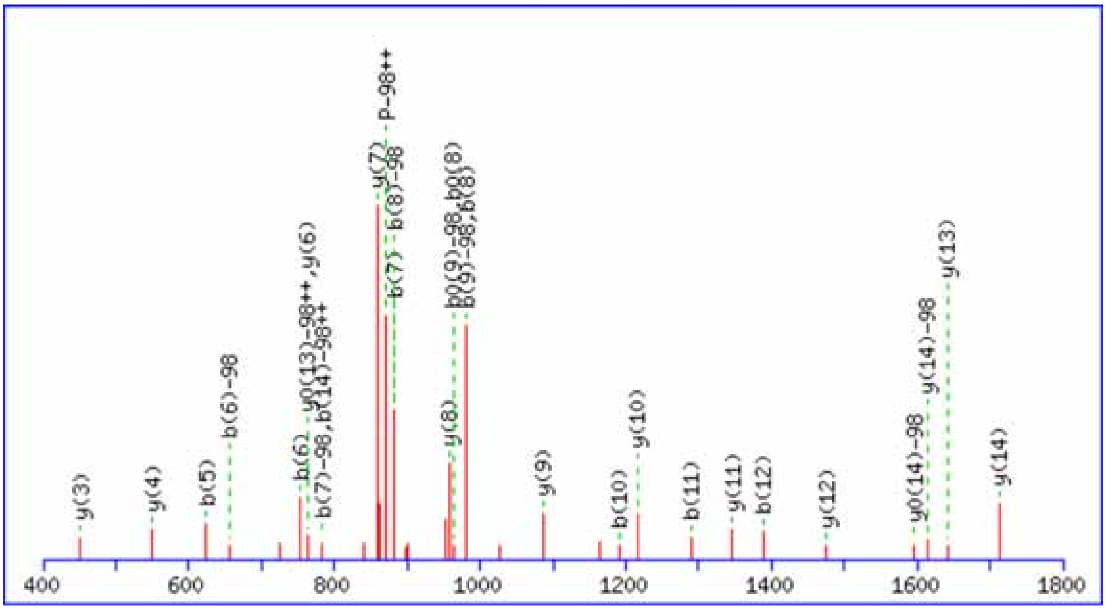
Matched b ions: b(3), b(5), b(6), b(7)-98, b(8)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(12)-98, b(13), b(13)-98, b(14), b(14)-98, b(15), b(15)-98, b(16)-98, b(16)++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12)-98, y(12), y(13)-98++, y(13)++, y(13), y(14)-98, y(14), y(14)-98++, y(14)++, y(15)-98++, y(15)-98, y(15), y(15)++, y(16)-98, y(16), y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1194

VASEEEEVPLVVYLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VASEEEEVPLVVYLK
Found in SYNPO_MOUSE, Synaptopodin OS=Mus musculus GN=Synpo PE=1 SV=2

Match to Query 3660: 1838.933838 from(920.474195,2+)
Title: Elution from: 65.212 to 65.212 scan no 6125 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1838.9318
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 95 Expect: 1.8e-008

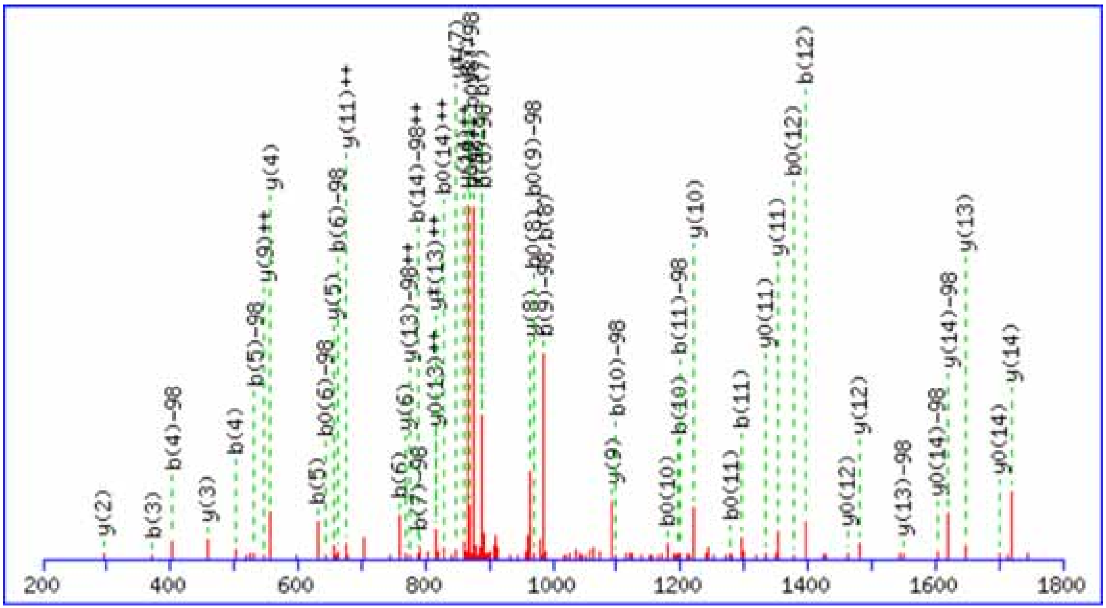
Matched b ions: b(5), b(6), b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(10), b(11), b(12), b(14)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)-98, y(14)
Precursor origin neutral loss: +

Peptide No.1195

VASEEEEVPLVVYLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VASEEEEVPLVVYLK
Found in SYNPO_MOUSE, Synaptopodin OS=Mus musculus GN=Synpo PE=1 SV=2

Match to Query 3366: 1850.997470 from(926.506011,2+)
Title: Elution from: 65.329 to 65.329 scan no 6018 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1850.9954
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K15 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 94 **Expect:** 2e-008

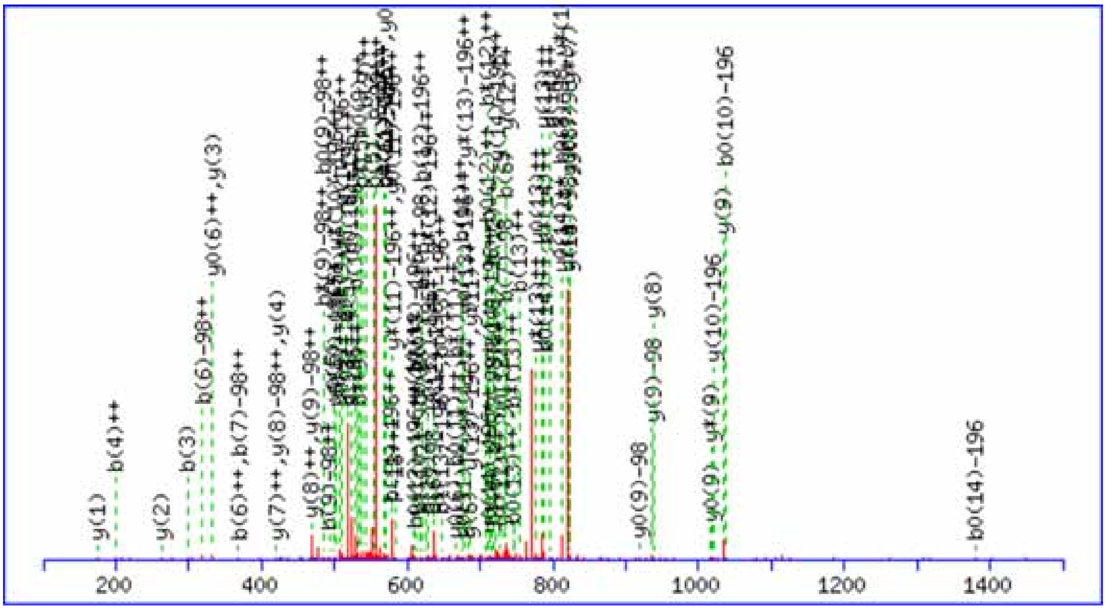
Matched b ions: b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12), b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(11), y(11)++, y(12), y(13)-98, y(13), y(13)-98++, y(14)-98, y(14), y(14)++
Precursor origin neutral loss: +

Peptide No.1196

VAVVRTPPKSPSASK
Confirmed sites: @T:6,@S:10
Ambiguous sites:

MS/MS Fragmentation of VAVVRTPPKSPSASK
Found in TAU_MOUSE, Microtubule-associated protein tau OS=Mus musculus GN=Mapt PE=1 SV=3

Match to Query 4121: 1766.910324 from(589.977384,3+)
Title: Elution from: 26.221 to 26.221 scan no 1789 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1766.9097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K9 : Dimethyl (K)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 35 Expect: 0.019

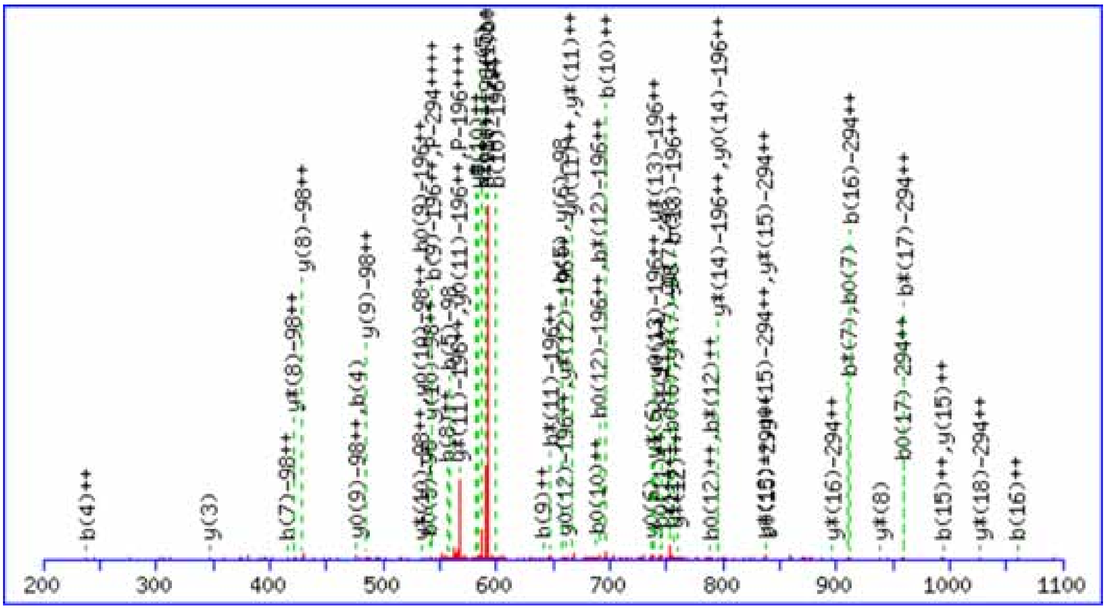
Matched b ions: b(2), b(3), b(4)++, b(5), b(6)-98++, b(6)++, b(6)-98, b(6), b(7)-98++, b(7)-98, b(9)-98++, b(9)++, b(10)-98++, b(10)-196++, b(10)++, b(11)-196++, b(11)-98++, b(11)++, b(12)-98++, b(12)-196++, b(12)++, b(13)++, b(14)-98++, b(14)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7)++, y(8)++, y(8)-98++, y(8), y(9)-98++, y(9)-98, y(9), y(9)++, y(10)-196, y(10)++, y(10)-196++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-196++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++
Precursor origin neutral loss: +

Peptide No.1197

VCTDTDRWSLISLSNKNGR
Confirmed sites: @T:5,@S:9,@S:14
Ambiguous sites:

MS/MS Fragmentation of VCTDTDRWSLISLSNKNGR
Found in FA46C_MOUSE, Protein FAM46C OS=Mus musculus GN=Fam46c PE=2 SV=1

Match to Query 6404: 2460.992232 from(616.255334,4+)
Title: Elution from: 26.342 to 26.342 scan no 1633 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2460.9899
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 **Expect:** 0.044

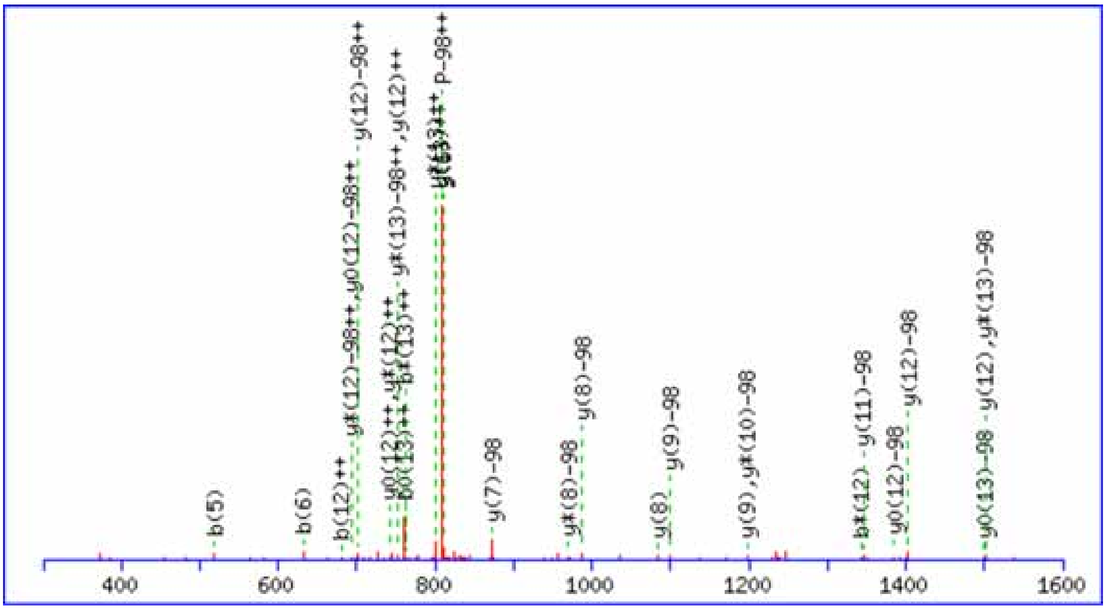
Matched b ions: b(4)++, b(4), b(5)-98, b(5), b(7)-98++, b(8)++, b(9)-98++, b(9)-196++, b(9)++, b(10)++, b(10)-98++, b(10)-196++, b(11)++, b(11)-98++, b(13)-196++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-294++
Matched y ions: y(3), y(5), y(6)-98, y(8)-98++, y(9)-98++, y(10)++, y(10)-98++, y(13)-98++, y(15)++, y(15)-196++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.1198

VDGMDILCVREATK
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of VDGMDILCVREATK
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 4471: 1713.785034 from(857.899793,2+)
Title: Elution from: 61.206 to 61.206 scan no 6136 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1713.7831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
Ions Score: 32 **Expect:** 0.029

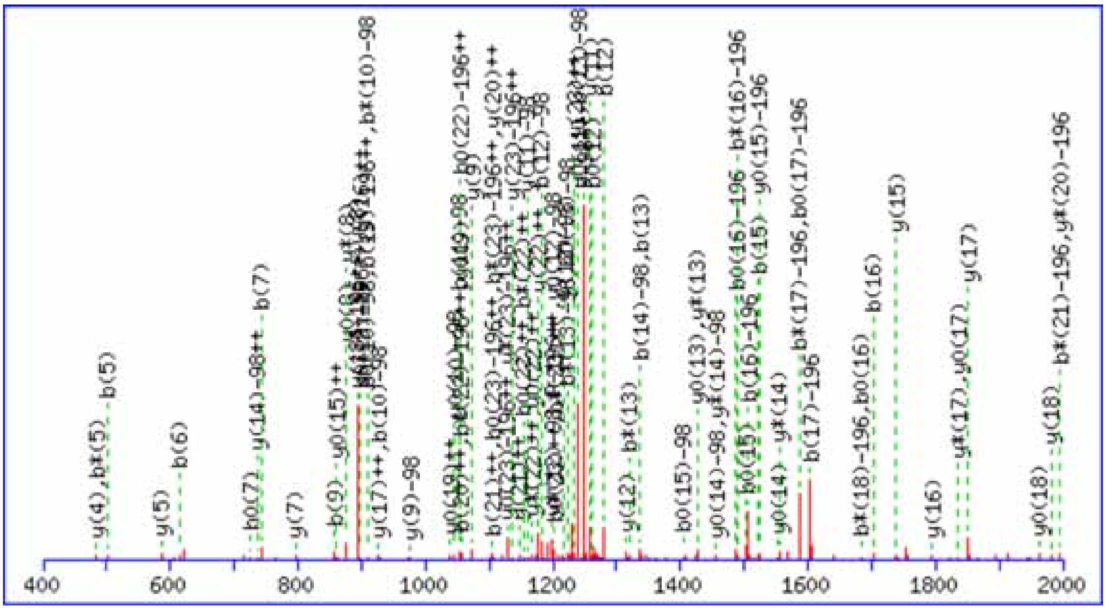
Matched b ions: b(5), b(6), b(12)++
Matched y ions: y(6), y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(11)-98, y(12)-98, y(12), y(12)-98++, y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.1199

VDGSNLEGGSQQGPSTPPNTPDPR
Confirmed sites: @S:10,@T:16
Ambiguous sites:

MS/MS Fragmentation of VDGSNLEGGSQQGPSTPPNTPDPR
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 6318: 2594.068850 from(1298.041701,2+)
Title: Elution from: 37.317 to 37.317 scan no 2999 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2594.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 **Expect:** 8.5e-006

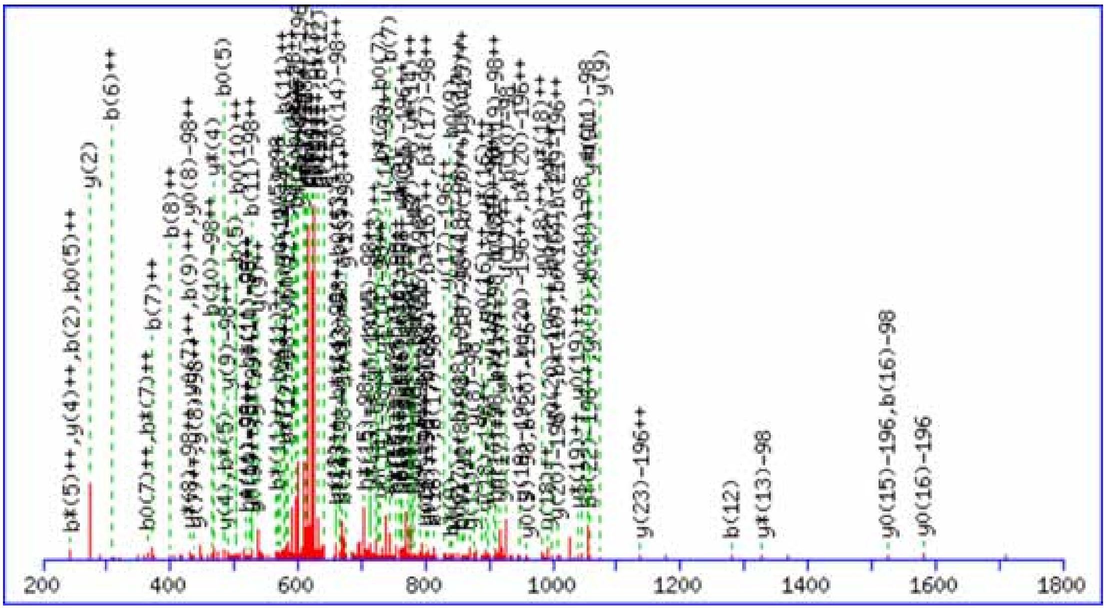
Matched b ions: b(5), b(6), b(7), b(9), b(10)-98, b(11)-98, b(12)-98, b(12), b(13), b(13)-98, b(14)-98, b(15), b(16)-196, b(16)-98, b(16), b(17)-196, b(17)-98, b(19)-98, b(19)-196++, b(20)++, b(21)-98++, b(21)++
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(9)-98, y(11), y(11)-98, y(12), y(12)-98, y(14)-98++, y(15), y(15)-98, y(16), y(16)++, y(17)-98, y(17), y(17)++, y(18)-196++, y(18), y(19)-98, y(20)-98++, y(20)++, y(21)++, y(22)++, y(22)-98++, y(23)-196++, y(23)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.1200

VDGSNLEGGSQQGPSTPPNTPDPR
Confirmed sites: @S:10,@T:20
Ambiguous sites:

MS/MS Fragmentation of VDGSNLEGGSQQGPSTPPNTPDPR
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 7860: 2594.070148 from(649.524813,4+)
Title: Elution from: 37.550 to 37.550 scan no 3338 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2594.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T20 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 **Expect:** 0.011

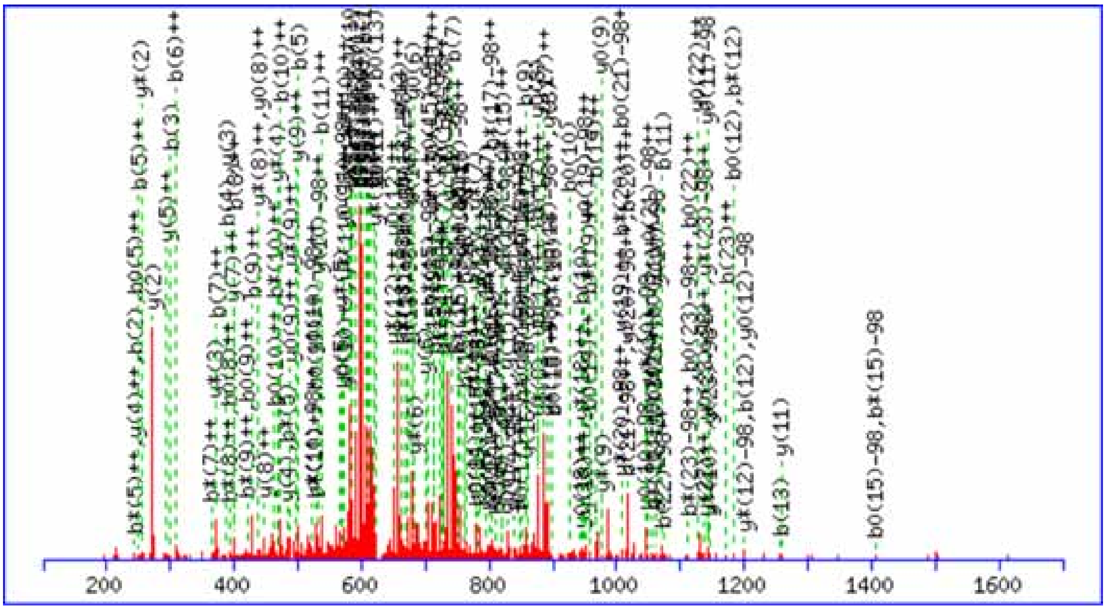
Matched b ions: b(2), b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)-98, b(10)-98++, b(11)-98, b(11)-98++, b(11)++, b(12), b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(20)++, b(20)-98++, b(20)-196++, b(21)-98++, b(21)-196++
Matched y ions: y(2), y(4)++, y(4), y(5)-98, y(5), y(6), y(7)++, y(7)-98, y(8)-98++, y(8)-98, y(9)++, y(9), y(9)-98++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(15)++, y(15)-196++, y(16)++, y(16)-196++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++, y(18)++, y(18)-196++, y(19)-196++, y(20)-98++, y(20)-196++, y(23)-196++
Precursor origin neutral loss: +

Peptide No.1201

VDGSNLEGGSQQGPSTPPNTPDPR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of VDGSNLEGGSQQGPSTPPNTPDPR
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 6385: 2514.104236 from(629.533335,4+)
Title: Elution from: 35.219 to 35.219 scan no 2803 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2514.1024
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 Expect: 0.00029

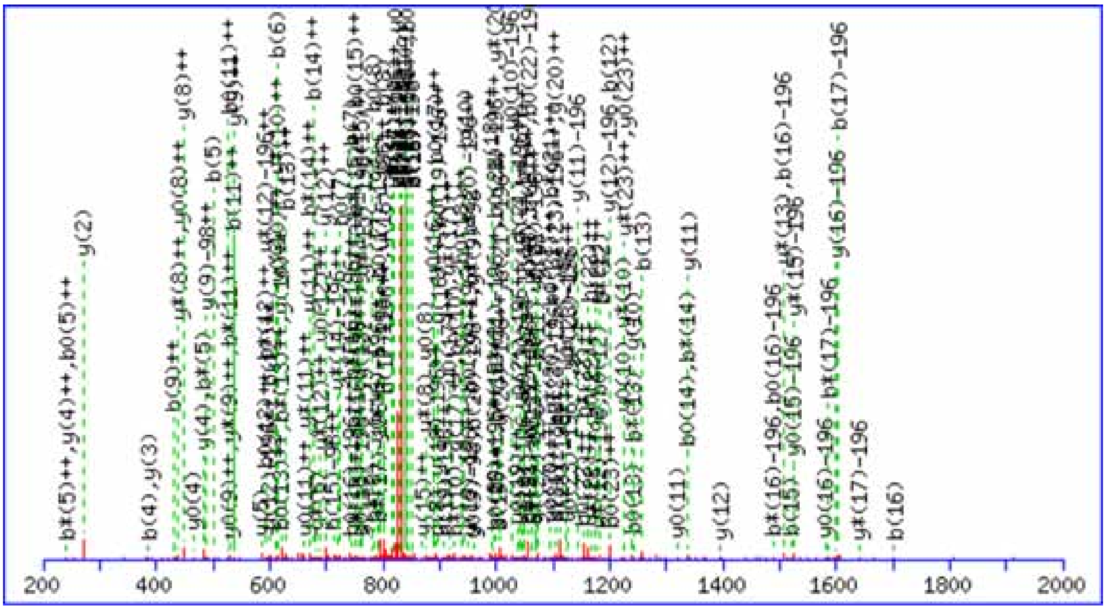
Matched b ions: b(2), b(3), b(4), b(5), b(5)++, b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11), b(11)++, b(12), b(12)++, b(13), b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(19)++, b(20)++, b(21)-98++, b(22)-98++, b(23)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9)++, y(10)++, y(10)-98++, y(10)-98, y(11)-98++, y(11), y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(19)++, y(20)-98++, y(22)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1202

VDGSNLEGGSQQGPSTPPNTPDPR
Confirmed sites: @S:15,@T:16
Ambiguous sites:

MS/MS Fragmentation of VDGSNLEGGSQQGPSTPPNTPDPR
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 7863: 2594.070321 from(865.697383,3+)
Title: Elution from: 37.985 to 37.985 scan no 3397 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2594.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0032

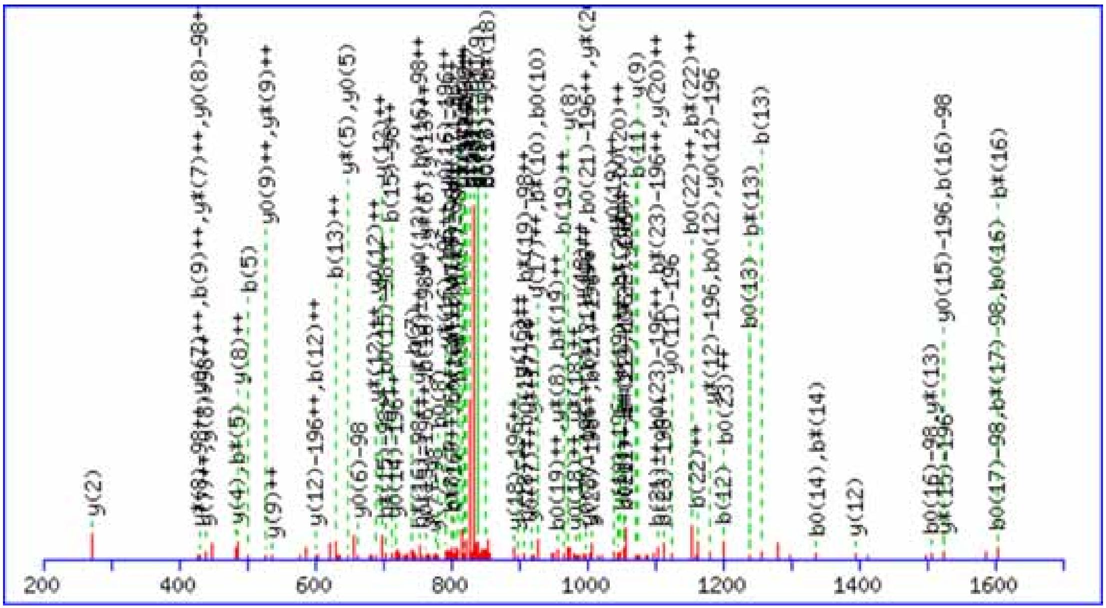
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)++, b(10), b(11), b(11)++, b(12), b(12)++, b(13), b(13)++, b(14)++, b(15), b(15)-98++, b(15)++, b(16)-98, b(16)-196, b(16), b(16)-196++, b(16)-98++, b(16)++, b(17)-196, b(17)-98, b(17)-196++, b(17)-98++, b(18)-196++, b(19)-98, b(19)-98++, b(19)++, b(19)-196++, b(20)-98++, b(20)++, b(20)-196++, b(21)-196++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(22)-196++, b(23)-196++, b(23)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(8)++, y(8), y(9), y(9)-98++, y(9)++, y(10)++, y(10)-196, y(10), y(11)-98++, y(11)++, y(11), y(11)-98, y(11)-196, y(12)++, y(12)-196, y(12), y(12)-98++, y(12)-196++, y(12)-98, y(13)-98++, y(13)++, y(14)-98++, y(15)-98++, y(15)++, y(15)-98, y(16)-196++, y(16)-98++, y(16)-196, y(16)++, y(17)++, y(17)-98++, y(17)-196++, y(18)-196++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(19)-196++, y(20)-196++, y(20)-98++, y(20)++, y(22)-98++, y(22)++
Precursor origin neutral loss: +

Peptide No.1203

VDGSNLEGGSQQGPSTPPNTPDPR
Confirmed sites: @S:15,@T:20
Ambiguous sites:

MS/MS Fragmentation of VDGSNLEGGSQQGPSTPPNTPDPR
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 7861: 2594.070219 from(865.697349,3+)
Title: Elution from: 36.468 to 36.468 scan no 3189 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2594.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 **Expect:** 0.00036

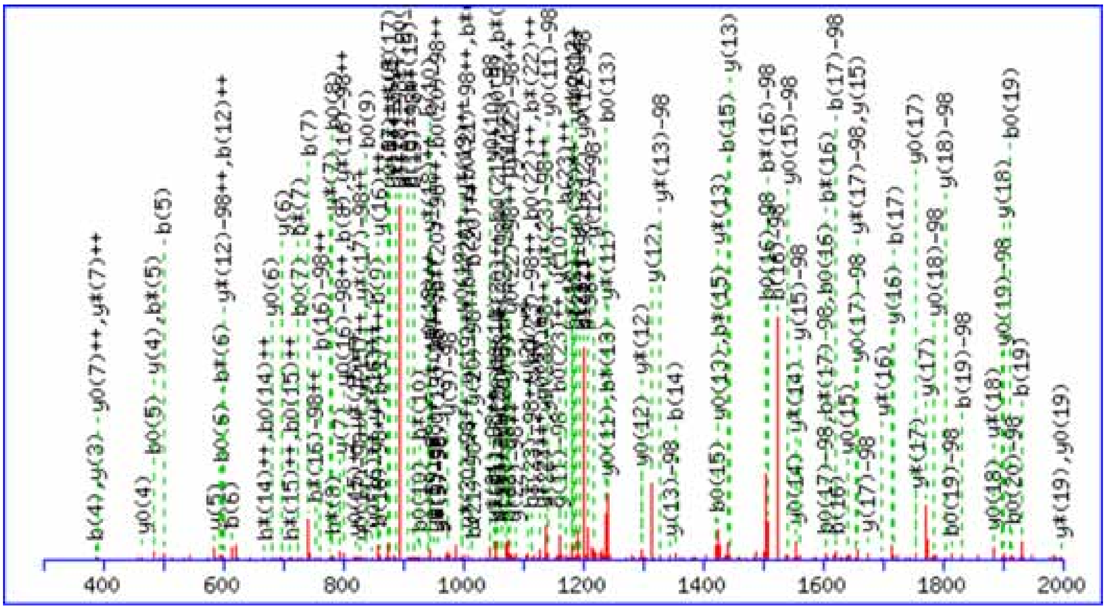
Matched b ions: b(5), b(7), b(8), b(9)++, b(11), b(12), b(12)++, b(13)++, b(13), b(15)-98++, b(16)-98, b(16)-98++, b(16)++, b(17)-98++, b(18)++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(21)-196++, b(21)++, b(22)++, b(22)-98++, b(23)-98++, b(23)-196++
Matched y ions: y(2), y(4), y(7)++, y(7)-98, y(8)++, y(8)-98++, y(8), y(9)++, y(9), y(10)-196, y(11)-98, y(12)++, y(12), y(12)-98, y(12)-196++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(16)-196++, y(16)-98++, y(16)++, y(17)++, y(17)-196++, y(18)-196++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)-196++, y(20)++
Precursor origin neutral loss: +

Peptide No.1204

VDGSNLEGGSQQGPSTPPNTPDPR
Confirmed sites: @T:16
Ambiguous sites:

MS/MS Fragmentation of VDGSNLEGGSQQGPSTPPNTPDPR
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 6622: 2514.103842 from(1258.059197,2+)
Title: Elution from: 35.121 to 35.121 scan no 2803 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2514.1024
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 83 Expect: 3.6e-007

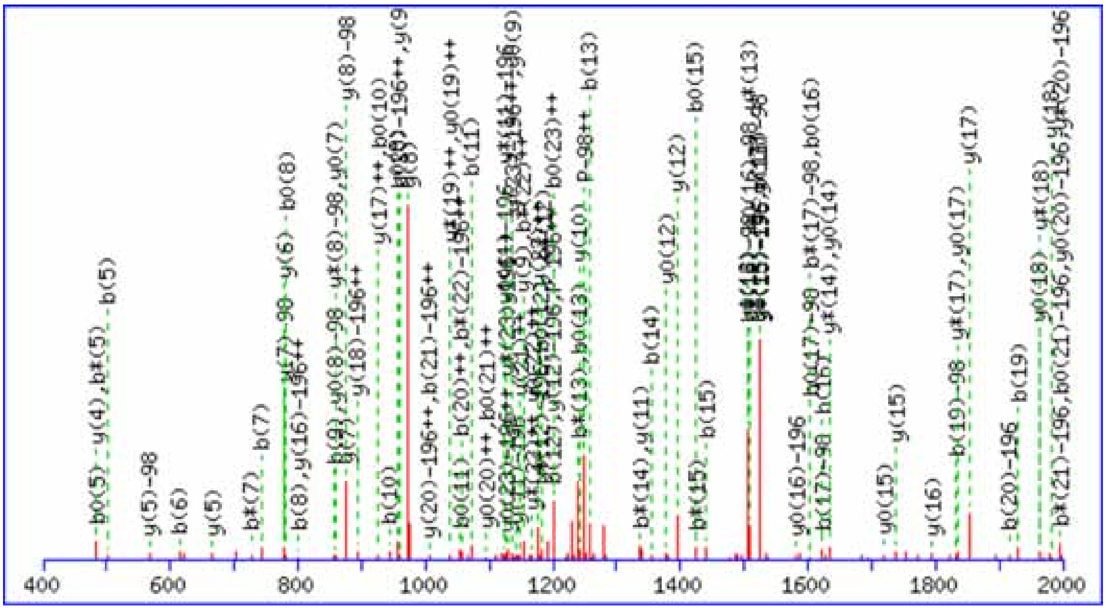
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(12)++, b(14), b(15), b(16)-98, b(16), b(16)-98++, b(17)++, b(17)-98, b(17), b(18)-98++, b(18)++, b(19), b(19)-98, b(19)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(23)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(11)-98, y(12), y(12)-98, y(13)-98, y(13), y(15), y(15)++, y(15)-98, y(16), y(16)++, y(17), y(17)-98, y(17)++, y(18), y(18)-98, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(22)++, y(22)-98++, y(23)++
Precursor origin neutral loss:

Peptide No.1205

VDGSNLEGGSQQGPSTPPNTPDPR
Confirmed sites: @T:16,@T:20
Ambiguous sites:

MS/MS Fragmentation of VDGSNLEGGSQQGPSTPPNTPDPR
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 7859: 2594.069940 from(1298.042246,2+)
Title: Elution from: 35.116 to 35.116 scan no 3005 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2594.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
T16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T20 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 91 **Expect:** 4.3e-008

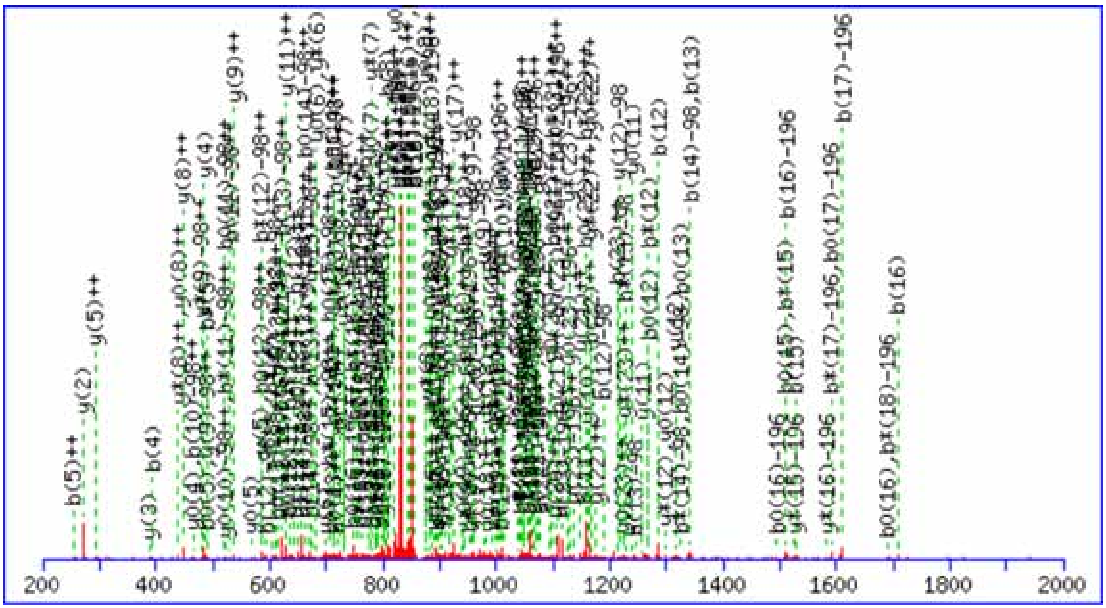
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13), b(14), b(15), b(16)-98, b(16), b(17)-98, b(19), b(19)-98, b(20)++, b(20)-196++, b(20)-196, b(21)-98++, b(21)-196++
Matched y ions: y(4), y(5)-98, y(5), y(6), y(7), y(7)-98, y(8)-98, y(8), y(9), y(9)-98, y(9)-196, y(10)-98, y(10), y(11), y(11)-98, y(11)-196, y(12), y(12)-196, y(13), y(15), y(16), y(16)-196++, y(17), y(17)-98, y(17)++, y(18)-196++, y(18), y(19)-98, y(20)-98++, y(20)-196++, y(21)++, y(22)++, y(22)-98++, y(23)-196++
Precursor origin neutral loss: +

Peptide No.1206

VDGSNLEGGSQQGPSTPPNTPDPR
Confirmed sites: @S:10,@T:16
Ambiguous sites:

MS/MS Fragmentation of VDGSNLEGGSQQGPSTPPNTPDPR
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 6889: 2600.102994 from(867.708274,3+)
Title: Elution from: 37.582 to 37.582 scan no 3147 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2600.1005
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.0098

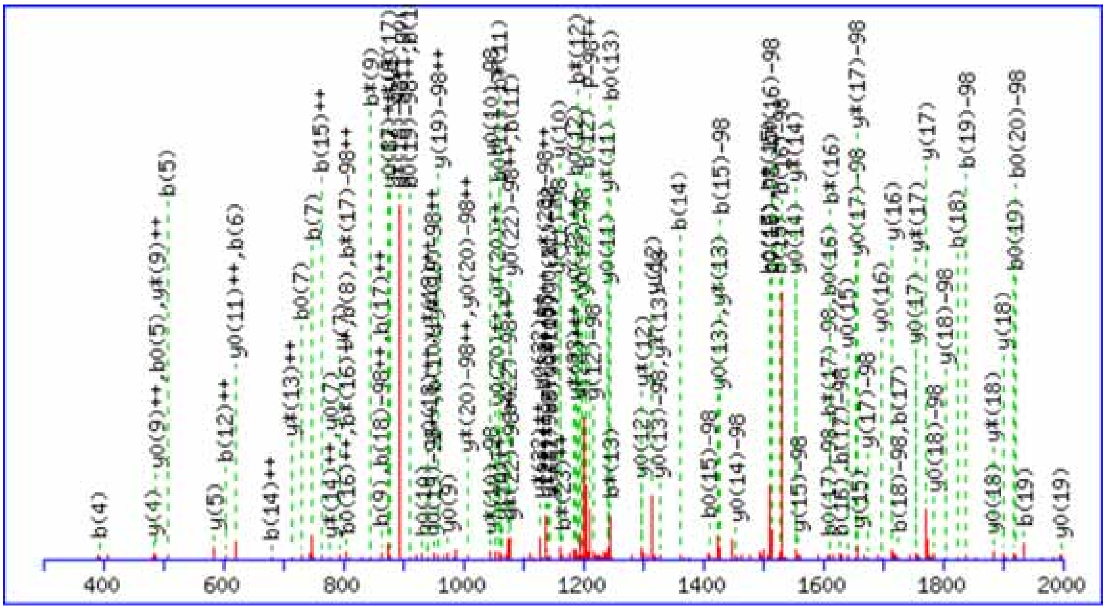
Matched b ions: b(4), b(5)++, b(6), b(7), b(8), b(10)-98++, b(11)-98, b(11)-98++, b(11), b(12), b(12)-98++, b(12)++, b(12)-98, b(13), b(13)++, b(13)-98++, b(13)-98, b(14)-98, b(14)-98++, b(14)++, b(15), b(15)-98++, b(15)++, b(16)-196, b(16)-98, b(16), b(16)++, b(16)-196++, b(16)-98++, b(17)-196, b(17)-98, b(17)-196++, b(17)-98++, b(17)++, b(18)-196++, b(18)-98++, b(19)++, b(19)-196++, b(19)-98++, b(20)-98++, b(20)++, b(20)-196++, b(21)-196++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(22)-196++, b(23)-98++, b(23)-196++, b(23)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7), y(8)++, y(8), y(9)++, y(9)-98++, y(9)-98, y(9), y(10)-98, y(10), y(11)++, y(11), y(12)++, y(12), y(12)-98++, y(12)-98, y(13)++, y(13)-98++, y(14)++, y(15)-196++, y(15)-98++, y(16)-196++, y(16)-98++, y(16)++, y(17)++, y(17)-196++, y(17)-98++, y(18)-196++, y(18)-98++, y(18)++, y(19)++, y(20)-98++, y(20)-196++, y(20)++, y(21)++, y(21)-196++, y(21)-98++, y(22)++, y(22)-196++, y(22)-98++, y(23)-196++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1207

VDGSNLEGGSQQGPSTPPNTPDPR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of VDGSNLEGGSQQGPSTPPNTPDPR
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 6588: 2520.134240 from(1261.074396,2+)
Title: Elution from: 35.281 to 35.281 scan no 2828 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2520.1342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 Expect: 8.3e-006

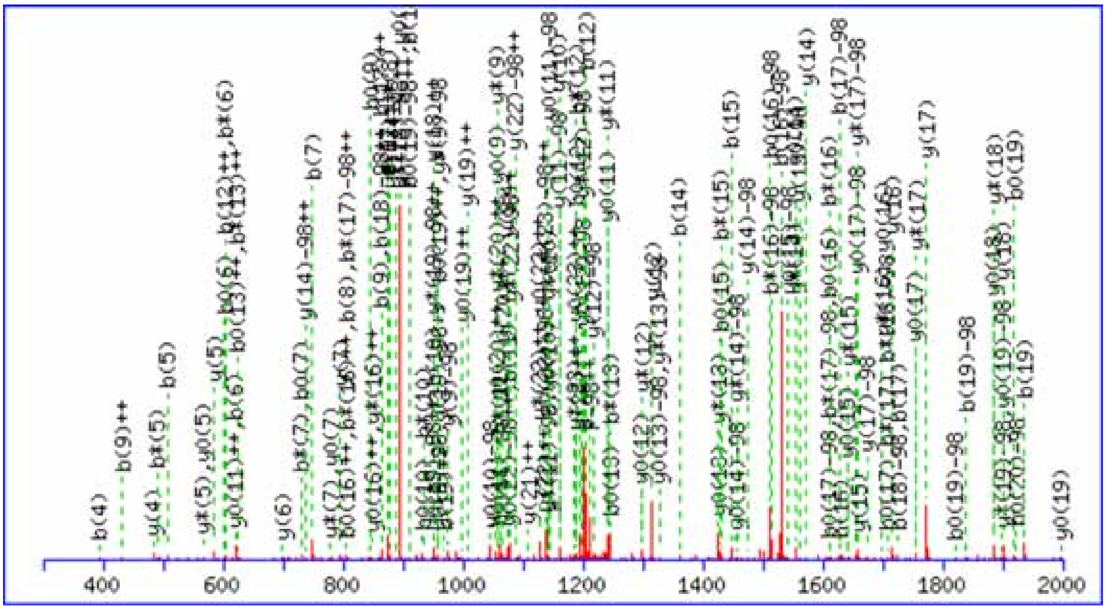
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(12)++, b(14)++, b(14), b(15)++, b(15)-98, b(15), b(16)-98, b(16), b(17)-98, b(17)++, b(17), b(18)-98++, b(18), b(18)++, b(18)-98, b(19), b(19)-98, b(22)-98++
Matched y ions: y(4), y(5), y(7), y(8), y(10), y(11)-98, y(12), y(12)-98, y(15), y(15)-98, y(16), y(17), y(17)-98, y(18), y(18)-98, y(19)-98++, y(20)++, y(22)++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1208

VDGSNLEGGSQQGPSTPPNTPDPR
Confirmed sites: @T:16
Ambiguous sites:

MS/MS Fragmentation of VDGSNLEGGSQQGPSTPPNTPDPR
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 6649: 2520.133988 from(1261.074270,2+)
Title: Elution from: 35.334 to 35.334 scan no 2834 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2520.1342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 89 Expect: 9.9e-008

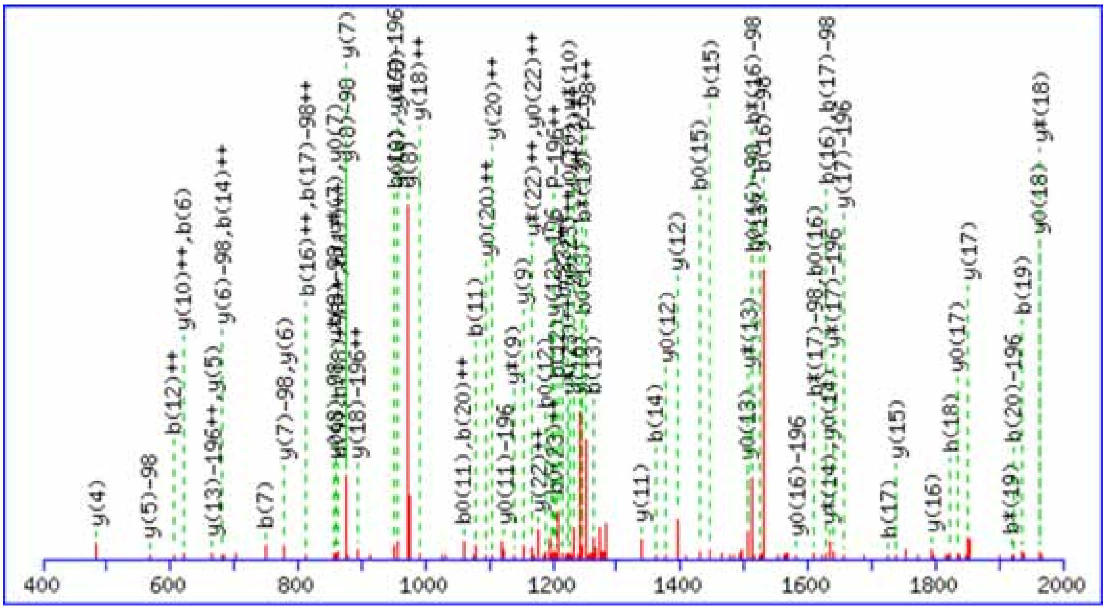
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(9)++, b(10), b(11), b(12), b(12)++, b(14), b(15), b(16)-98, b(16), b(17)++, b(17)-98, b(17), b(18)-98++, b(18)-98, b(18)++, b(19), b(19)-98, b(19)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(11)-98, y(12), y(12)-98, y(14)-98++, y(14)-98, y(14), y(15), y(15)-98, y(16), y(17), y(17)-98, y(17)++, y(18), y(18)++, y(19)-98++, y(19)++, y(20)++, y(21)++, y(22)++, y(22)-98++, y(23)++
Precursor origin neutral loss: +

Peptide No.1209

VDGSNLEGGSQQGPSTPPNTPDPR
Confirmed sites: @T:16,@T:20
Ambiguous sites:

MS/MS Fragmentation of VDGSNLEGGSQQGPSTPPNTPDPR
Found in MYOZ2_MOUSE, Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1

Match to Query 8362: 2600.098546 from(1301.056549,2+)
Title: Elution from: 34.910 to 34.910 scan no 2911 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2600.1005
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 76 **Expect:** 1.5e-006

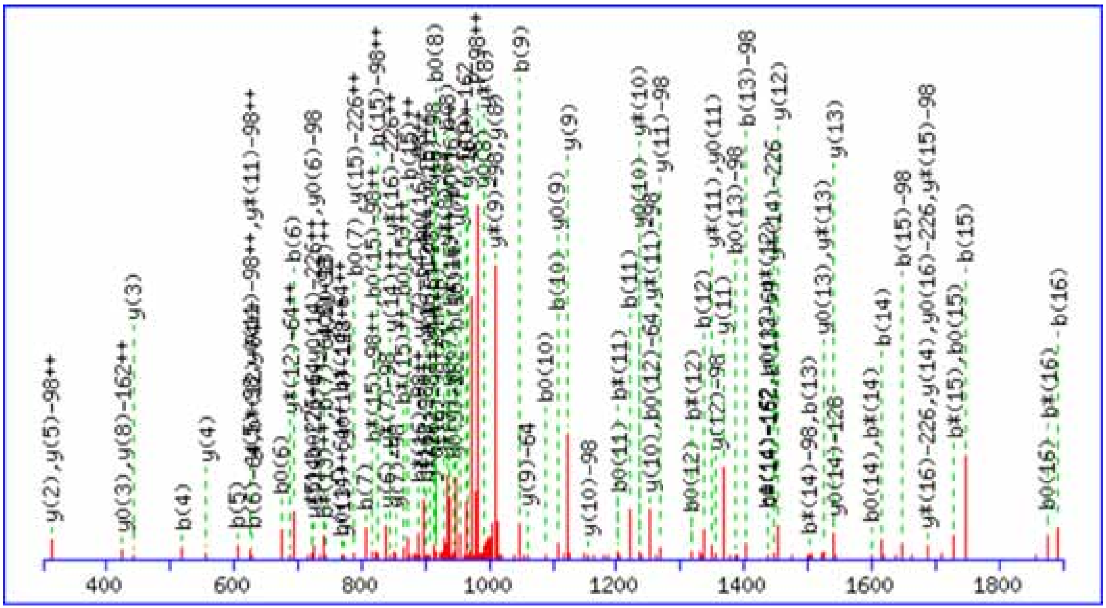
Matched b ions: b(6), b(7), b(9), b(10), b(11), b(12), b(12)++, b(13), b(14)++, b(14), b(15), b(16)-98, b(16), b(16)++, b(17), b(17)++, b(17)-98, b(17)-98++, b(18)-98++, b(18), b(19), b(20)++, b(20)-196, b(23)++
Matched y ions: y(4), y(5)-98, y(5), y(6), y(6)-98, y(7)-98, y(7), y(8)-98, y(8), y(9), y(10)++, y(10), y(11)-98++, y(11), y(11)-98, y(12), y(12)-196, y(13)-196++, y(13), y(14)-98, y(15)-98, y(15), y(16), y(17)-98, y(17), y(17)-98++, y(17)-196, y(18)++, y(18)-196++, y(19)-196++, y(20)++, y(22)++, y(23)++, y(23)-98++
Precursor origin neutral loss: +

Peptide No.1210

VENMSSNQDGNDSDEFM
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of VENMSSNQDGNDSDEFM
Found in CCD25_MOUSE, Coiled-coil domain-containing protein 25 OS=Mus musculus GN=Ccdc25 PE=1 SV=1

Match to Query 4680: 2057.687500 from(1029.851026,2+)
Title: Elution from: 31.200 to 31.200 scan no 2171 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2057.6867
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 95 Expect: 2.9e-009

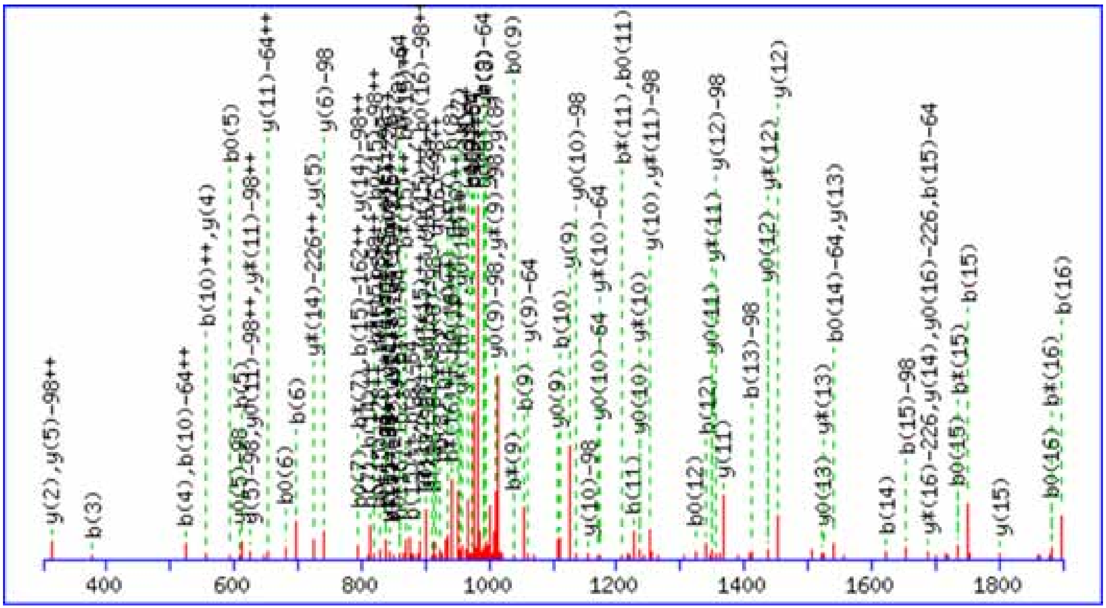
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13)-98, b(13), b(14), b(15), b(15)-98, b(15)++, b(15)-98++, b(16)-98++, b(16), b(16)++
Matched y ions: y(2), y(3), y(4), y(5)-98++, y(5)-98, y(5), y(6)-98, y(6), y(7)-98, y(7), y(8), y(8)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)++, y(14), y(14)++, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1211

VENMSSNQDGNDSDEFM
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of VENMSSNQDGNDSDEFM
Found in CCD25_MOUSE, Coiled-coil domain-containing protein 25 OS=Mus musculus GN=Ccdc25 PE=1 SV=1

Match to Query 5310: 2063.721260 from(1032.867906,2+)
Title: Elution from: 31.444 to 31.444 scan no 2304 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2063.7186
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 98 Expect: 1.8e-009

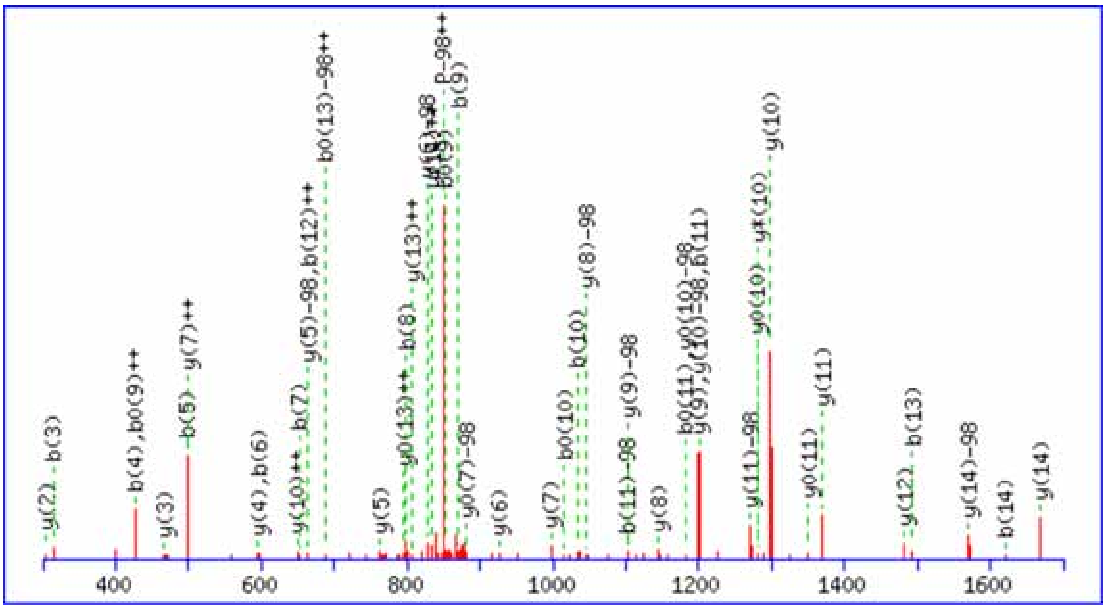
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10)++, b(10), b(11), b(12), b(13)-98, b(14)++, b(14), b(15)-98, b(15), b(15)++, b(15)-98++, b(16)-98++, b(16), b(16)++
Matched y ions: y(2), y(4), y(5)-98++, y(5)-98, y(5), y(6)-98, y(6), y(7), y(8)-98, y(8), y(9), y(10), y(10)-98, y(11), y(12), y(12)-98, y(13), y(14), y(14)-98++, y(14)++, y(15)++, y(15), y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1212

VGEIAPGFAYSEYEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of VGEIAPGFAYSEYEK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4275: 1794.812356 from(898.413454,2+)
Title: Elution from: 53.516 to 53.516 scan no 5299 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1794.8117
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K15 : Dimethyl (K)
Ions Score: 61 Expect: 4.1e-005

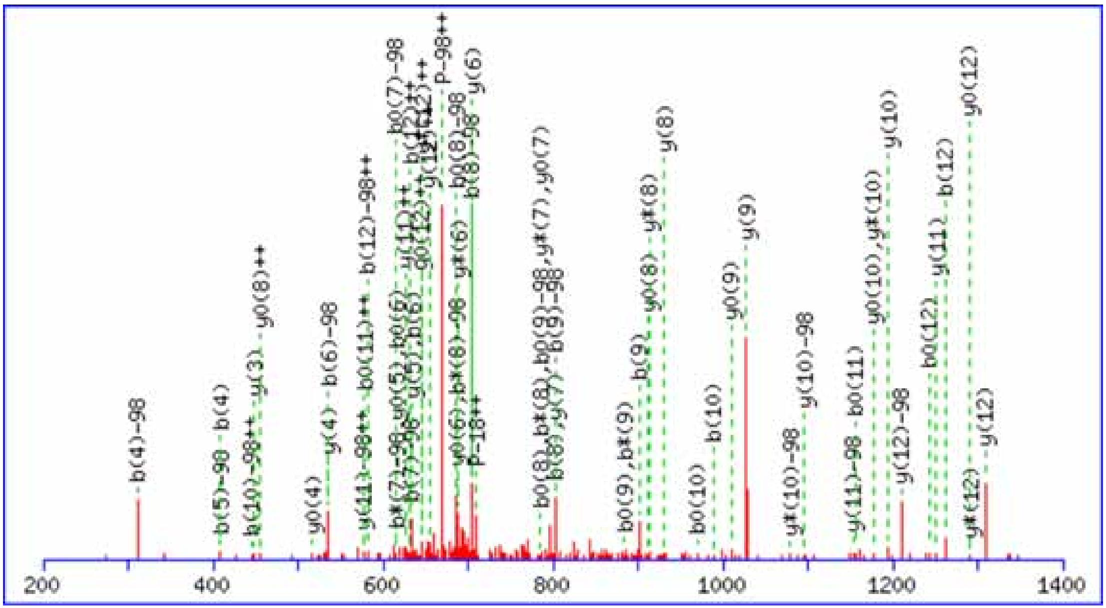
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11)-98, b(11), b(12)++, b(13), b(14)
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)++, y(8), y(8)-98, y(9), y(9)-98, y(10)++, y(10)-98, y(10), y(11), y(11)-98, y(12), y(13)++, y(14)-98, y(14), y(14)++
Precursor origin neutral loss: +

Peptide No.1213

VGGSPQPAVSWSK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of VGGSPQPAVSWSK
Found in OBSCN_MOUSE, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 2183: 1434.691842 from(718.353197,2+)
Title: Elution from: 38.021 to 38.021 scan no 3402 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1434.6908
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K13 : Dimethyl (K)
Ions Score: 40 **Expect:** 0.0037

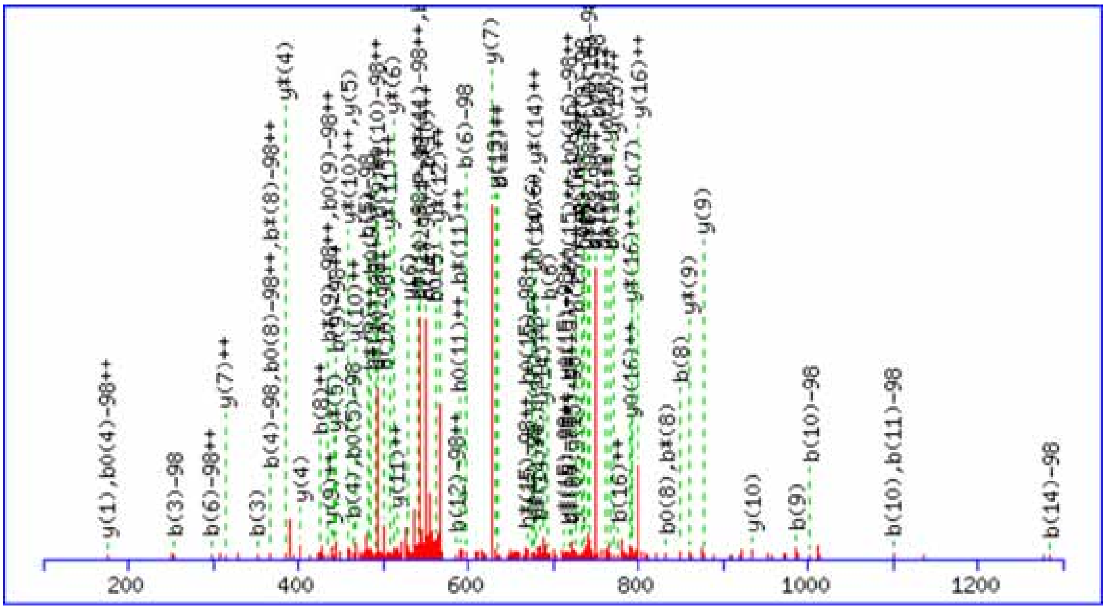
Matched b ions: b(4)-98, b(4), b(5)-98, b(6)-98, b(6), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10)-98++, b(10), b(12), b(12)-98++, b(12)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(11), y(11)-98++, y(11)++, y(12)-98, y(12), y(12)++
Precursor origin neutral loss: +

Peptide No.1214

VGSLDNVGHLPAGGAVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VGSLDNVGHLPAGGAVK
Found in MAP4_MOUSE, Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3

Match to Query 4556: 1725.883416 from(576.301748,3+)
Title: Elution from: 40.232 to 40.232 scan no 3671 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1725.8815
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K17 : Dimethyl (K)
Ions Score: 40 Expect: 0.0057

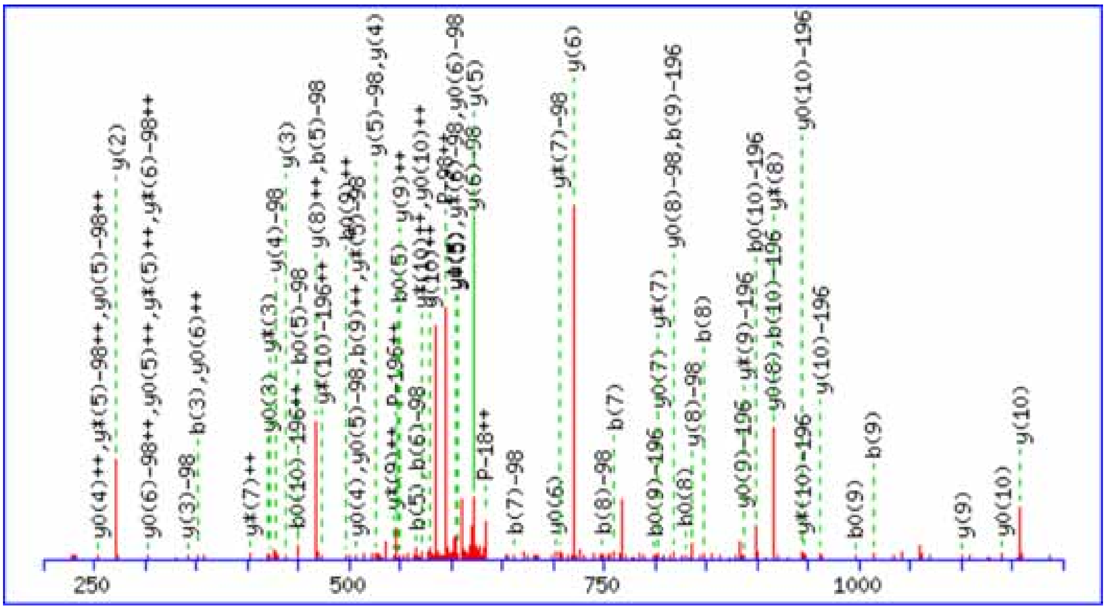
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(6)-98++, b(6)-98, b(6), b(7), b(8)-98, b(8), b(8)++, b(9)-98++, b(9), b(9)++, b(10), b(10)++, b(10)-98, b(10)-98++, b(11)-98, b(11)-98++, b(12)-98++, b(12)++, b(14)-98, b(15)-98++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(1), y(4), y(5), y(6), y(7), y(7)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1215

VGSLTPPSSPK
Confirmed sites: @S:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of VGSLTPPSSPK
Found in AAK1_MOUSE, AP2-associated protein kinase 1 OS=Mus musculus GN=Aak1 PE=1 SV=2

Match to Query 1567: 1284.577358 from(643.295955,2+)
Title: Elution from: 34.493 to 34.493 scan no 2919 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1284.5768
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K11 : Dimethyl (K)
Ions Score: 29 Expect: 0.033

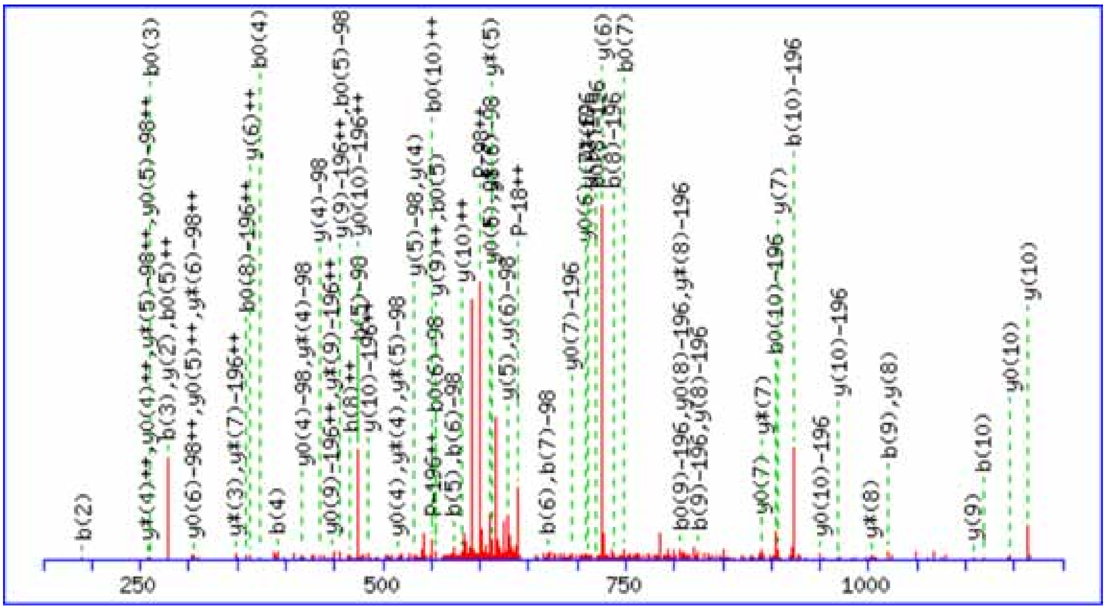
Matched b ions: b(3)-98, b(3), b(5)-98, b(5), b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(9)-196, b(9), b(9)++, b(10)-196, b(10)-98, b(10)-98++
Matched y ions: y(2), y(3)-98, y(3), y(4)-98, y(4), y(5)-98, y(5), y(6), y(6)-98, y(8)++, y(8)-98, y(9), y(9)++, y(10)-98, y(10), y(10)-196, y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.1216

VGSLTPPSSPK
Confirmed sites: @T:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of VGSLTPPSSPK
Found in AAK1_MOUSE, AP2-associated protein kinase 1 OS=Mus musculus GN=Aak1 PE=1 SV=2

Match to Query 1251: 1296.640614 from(649.327583,2+)
Title: Elution from: 34.469 to 34.469 scan no 2710 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1296.6404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K11 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 35 Expect: 0.011

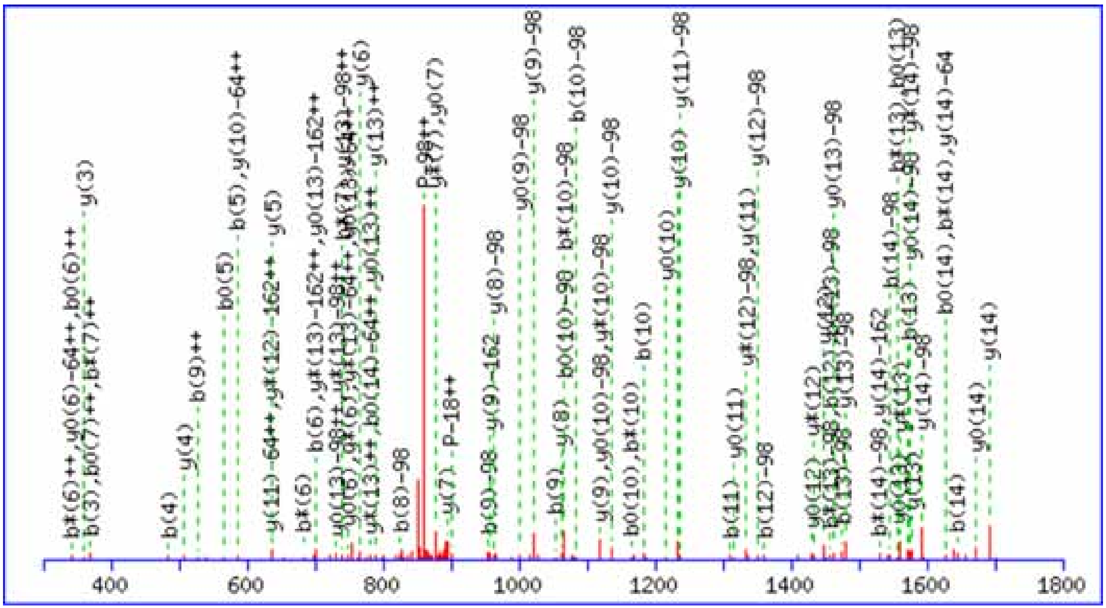
Matched b ions: b(2), b(3), b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(8)-196, b(8)++, b(8)-98, b(9)-98, b(9), b(9)-196, b(10)-196, b(10)-98, b(10)
Matched y ions: y(2), y(4)-98, y(4), y(5), y(5)-98, y(6), y(6)++, y(6)-98, y(7), y(7)-98, y(7)-196, y(8)-98, y(8), y(8)-196, y(9)-196++, y(9), y(9)++, y(9)-98++, y(10), y(10)-98, y(10)-196++, y(10)++, y(10)-98++, y(10)-196
Precursor origin neutral loss: +

Peptide No.1217

VIENTDGSEEEMDAR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of VIENTDGSEEEMDAR
Found in MYH11_MOUSE, Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1

Match to Query 3496: 1817.702638 from(909.858595,2+)
Title: Elution from: 26.338 to 26.338 scan no 1664 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1817.7026
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 70 Expect: 1.5e-006

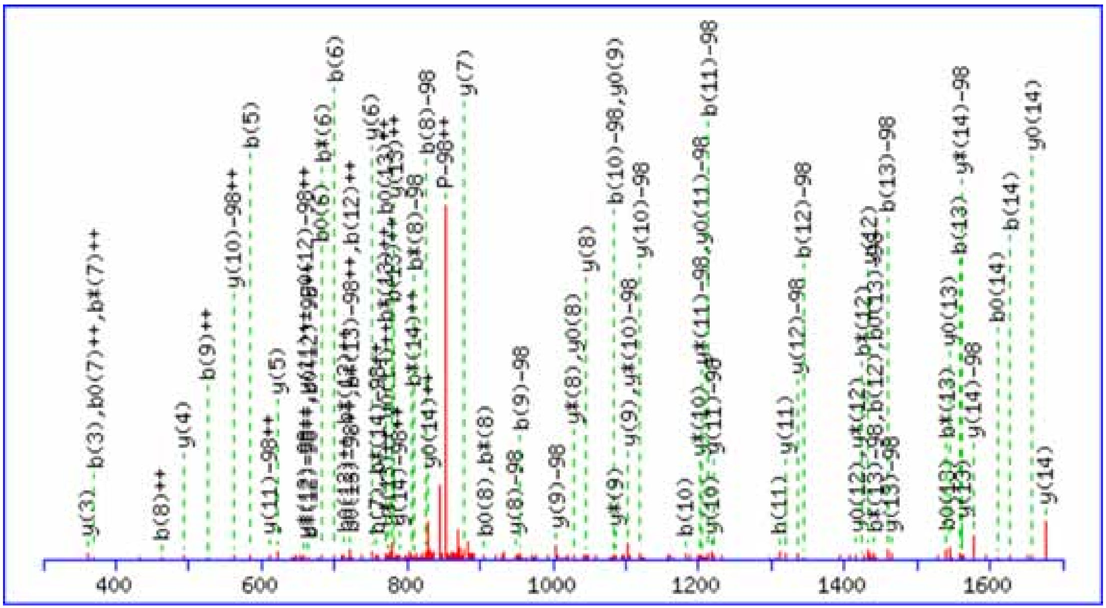
Matched b ions: b(3), b(4), b(5), b(6), b(8)-98, b(9)-98, b(9)++, b(9), b(10), b(10)-98, b(11), b(12)-98, b(12), b(13)-98, b(13), b(14), b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12)-98, y(12), y(13)-98, y(13)-98++, y(13), y(13)++, y(14)-98, y(14)
Precursor origin neutral loss: +

Peptide No.1218

VIENTDGSEEEMDAR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of VIENTDGSEEEMDAR
Found in MYH11_MOUSE, Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1

Match to Query 3411: 1801.706986 from(901.860769,2+)
Title: Elution from: 31.049 to 31.049 scan no 2250 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1801.7077
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 **Expect:** 1.5e-005

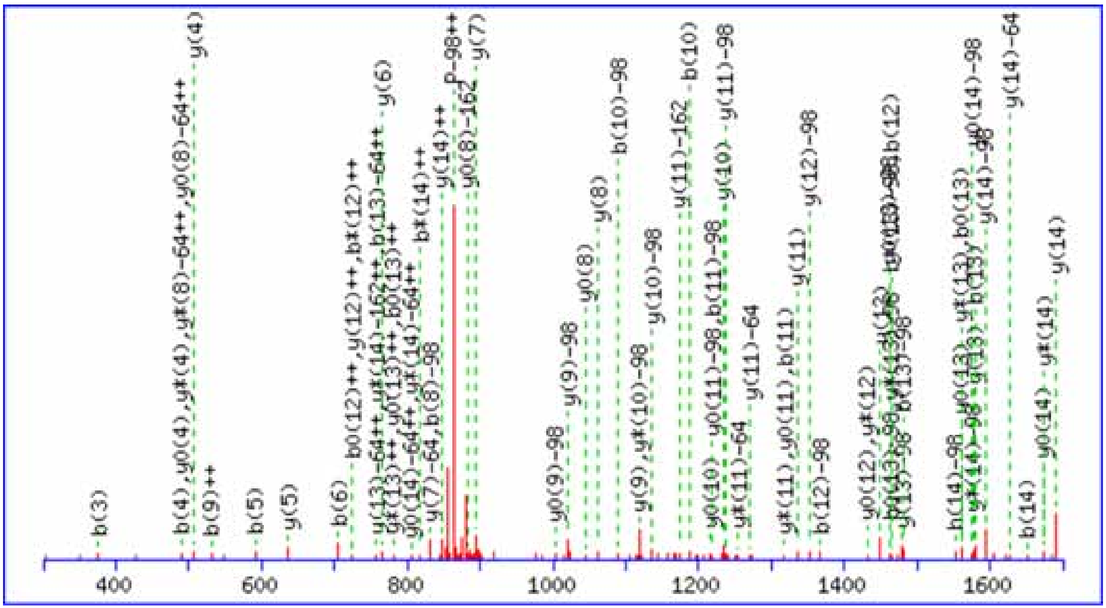
Matched b ions: b(3), b(5), b(6), b(7), b(8)++, b(8)-98, b(9)++, b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12)++, b(12), b(12)-98, b(13)-98, b(13), b(13)++, b(14)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(10)-98++, y(11), y(11)-98++, y(11)-98, y(11)++, y(12), y(12)-98, y(13), y(13)-98, y(13)++, y(14)-98, y(14), y(14)-98++
Precursor origin neutral loss: +

Peptide No.1219

VIENTDGSEEEMDAR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of VIENTDGSEEEMDAR
Found in MYH11_MOUSE, Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1

Match to Query 3917: 1823.735010 from(912.874781,2+)
Title: Elution from: 26.305 to 26.305 scan no 1653 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1823.7344
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 67 Expect: 4.4e-006

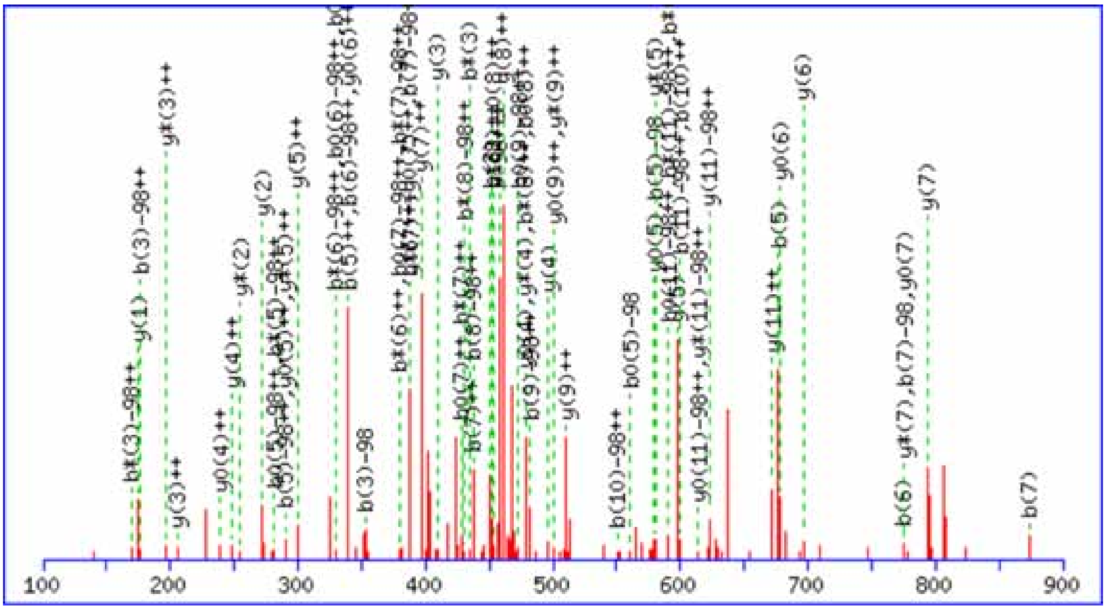
Matched b ions: b(3), b(4), b(5), b(6), b(8)-98, b(9)++, b(10), b(10)-98, b(11), b(11)-98, b(12)-98, b(12), b(13), b(13)-98, b(14), b(14)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12), y(12)-98, y(12)++, y(13)-98, y(13), y(14)-98, y(14), y(14)++
Precursor origin neutral loss: +

Peptide No.1220

VKSPEPVTSHPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VKSPEPVTSHPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 2296: 1468.769553 from(490.597127,3+)
Title: Elution from: 19.931 to 19.931 scan no 966 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1468.7691
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
K2 : Dimethyl (K)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K12 : Dimethyl (K)
Ions Score: 41 Expect: 0.0033

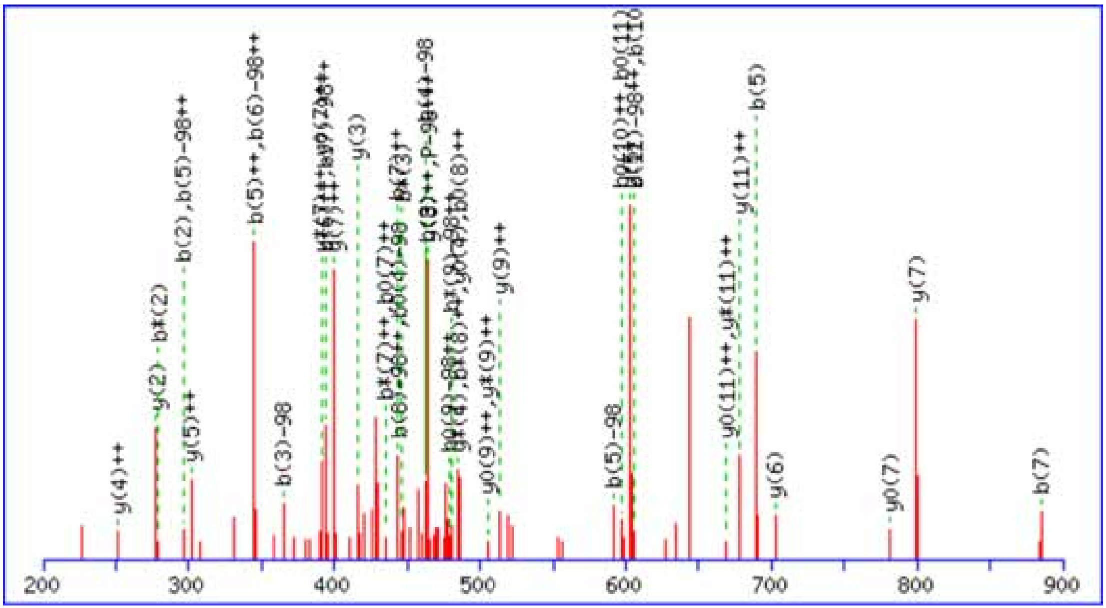
Matched b ions: b(3), b(3)-98++, b(3)-98, b(5)++, b(5), b(5)-98++, b(5)-98, b(6)-98++, b(6)++, b(6), b(7), b(7)-98++, b(7)++, b(7)-98, b(8)-98++, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++
Matched y ions: y(1), y(2), y(3)++, y(3), y(4)++, y(4), y(5), y(5)++, y(6), y(7)++, y(7), y(8)++, y(9)++, y(11)++, y(11)-98++
Precursor origin neutral loss: +

Peptide No.1221

VKSPEPVTSHPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VKSPEPVTSHPK
Found in TITIN_MOUSE, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 1832: 1486.864518 from(496.628782,3+)
Title: Elution from: 19.839 to 19.839 scan no 920 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1486.8645
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K2 : Dimethyl:2H(4)13C(2) (K)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
K12 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 50 Expect: 0.00029

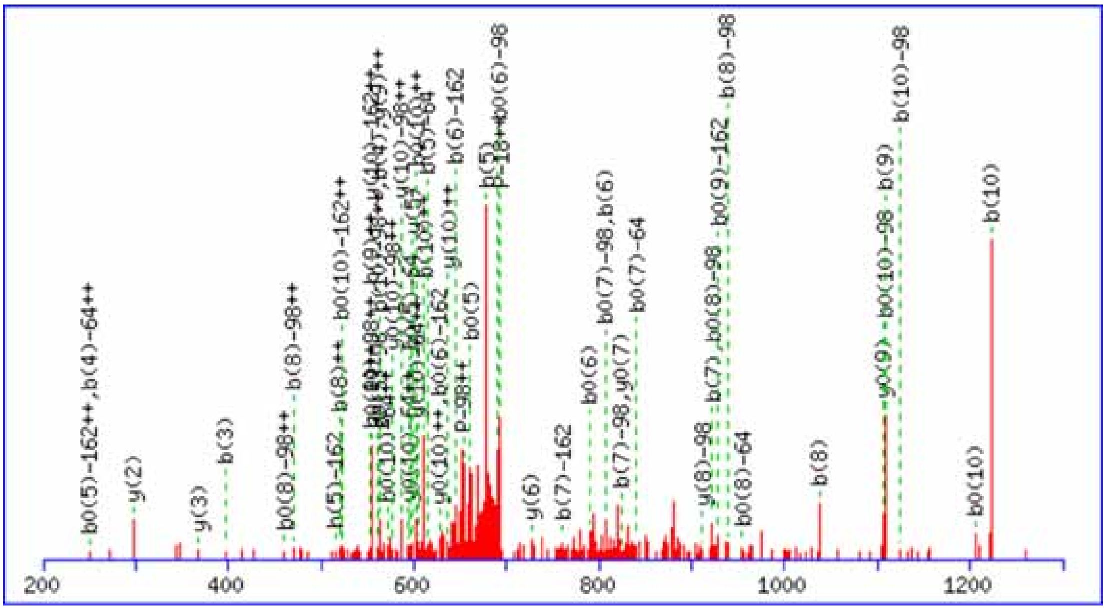
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(5)++, b(5), b(5)-98, b(5)-98++, b(6)-98++, b(6)++, b(7), b(7)-98++, b(7)++, b(8)-98++, b(10)++, b(11)-98++
Matched y ions: y(2), y(3), y(4)++, y(5), y(5)++, y(6), y(7), y(7)++, y(8)++, y(9)++, y(10)++, y(11)++
Precursor origin neutral loss: +

Peptide No.1222

VMDSDEDDADY
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of VMDSDEDDADY
Found in PDCD5_MOUSE, Programmed cell death protein 5 OS=Mus musculus GN=Pdcd5 PE=1 SV=3

Match to Query 1342: 1403.454348 from(702.734450,2+)
Title: Elution from: 31.079 to 31.079 scan no 2155 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1403.4536
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 0.021

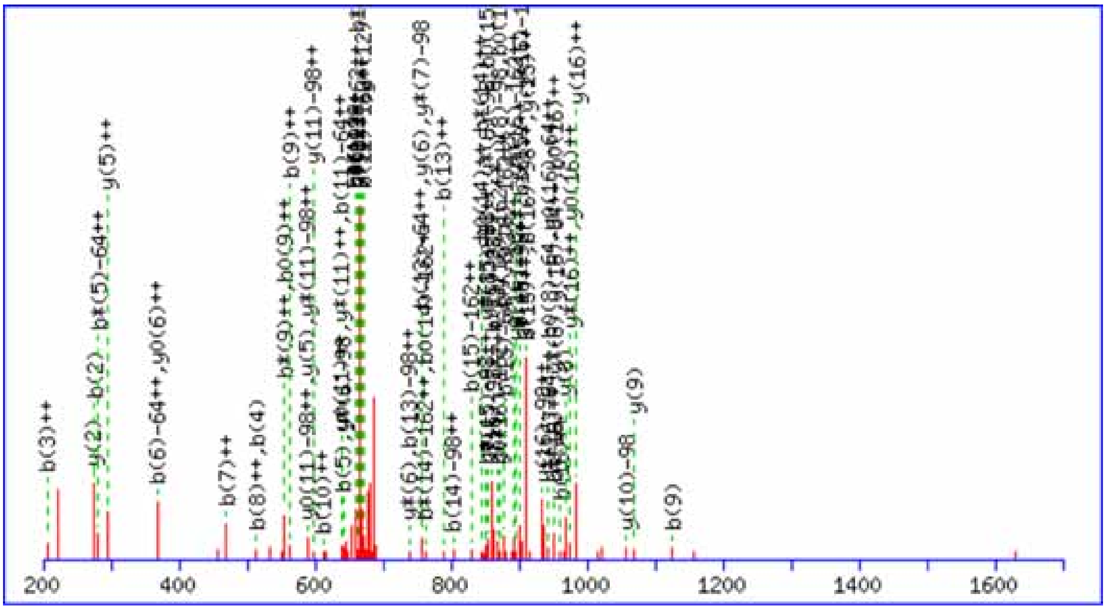
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(7)-98, b(8), b(8)-98++, b(8)++, b(8)-98, b(9), b(9)++, b(10)++, b(10), b(10)-98++, b(10)-98
Matched y ions: y(2), y(3), y(5), y(6), y(8)-98, y(9)++, y(10)-98++, y(10)++
Precursor origin neutral loss: +

Peptide No.1223

VMHTQCHSTPDSAEDVR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of VMHTQCHSTPDSAEDVR
Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 4855: 2092.835748 from(698.619192,3+)
Title: Elution from: 20.924 to 20.924 scan no 1031 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2092.8344
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 Expect: 0.00015

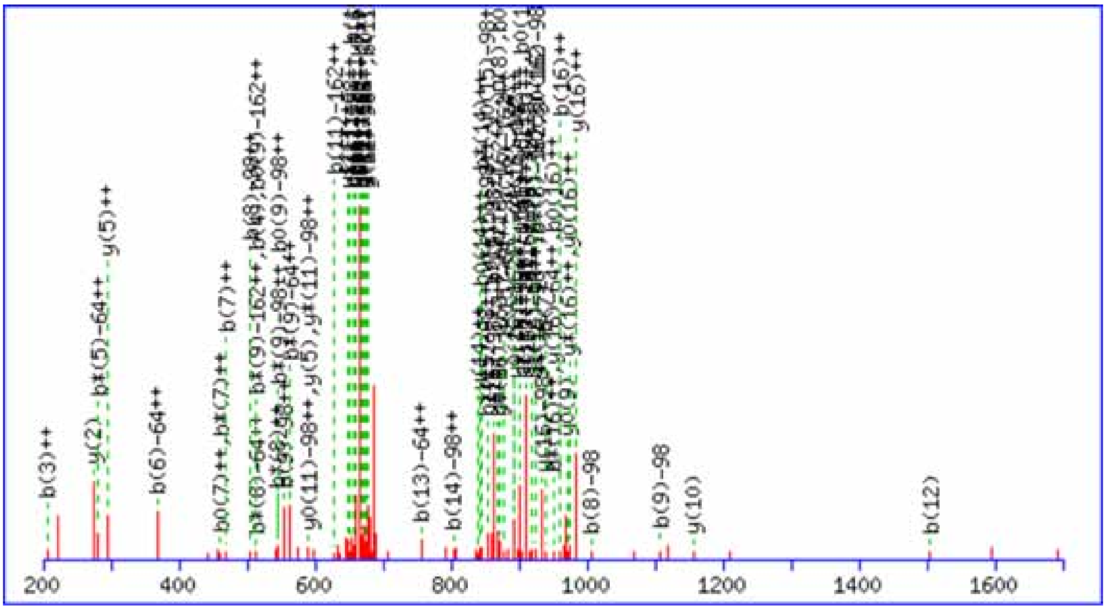
Matched b ions: b(2), b(3)++, b(4), b(5), b(7)++, b(8)++, b(9), b(9)++, b(10)++, b(11)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(2), y(5), y(5)++, y(6), y(6)-98, y(7), y(8), y(8)-98, y(9), y(10)-98, y(11)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1224

VMHTQCHSTPDSAEDVR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of VMHTQCHSTPDSAEDVR
Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 5235: 2092.835049 from(698.618959,3+)
Title: Elution from: 21.101 to 21.101 scan no 1047 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 2092.8344
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.013

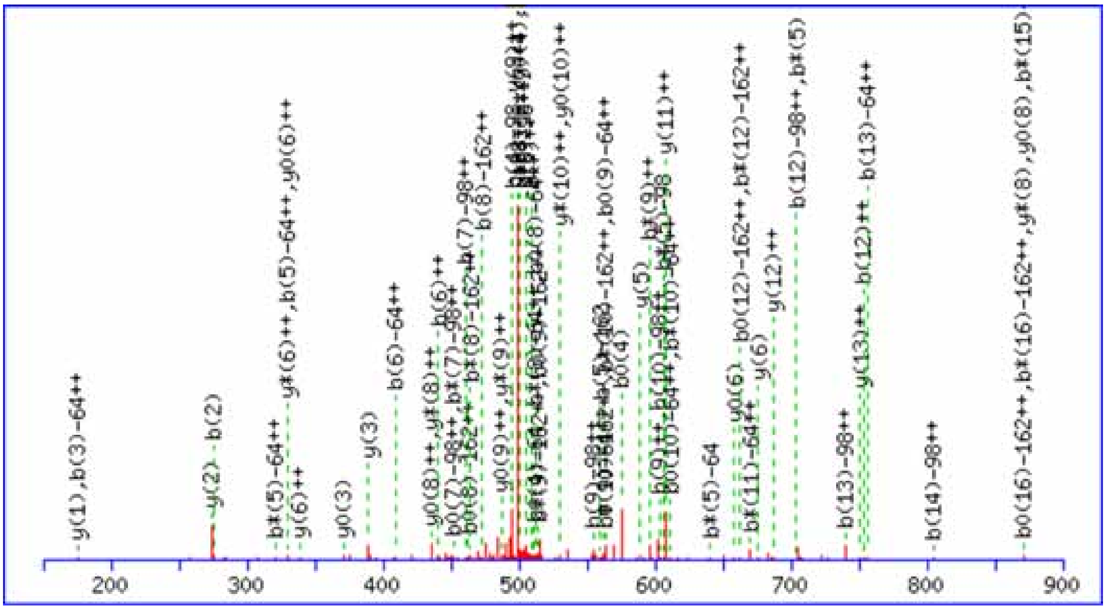
Matched b ions: b(3)++, b(4), b(7)++, b(7), b(8)-98, b(8)-98++, b(9)-98++, b(9)-98, b(10)++, b(11)-98++, b(12), b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(2), y(5)++, y(5), y(6), y(10), y(11)++, y(12)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1225

VMHTQCHSTPDSAEDVR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of VMHTQCHSTPDSAEDVR
Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 6124: 2092.836120 from(524.216306,4+)
Title: Elution from: 21.095 to 21.095 scan no 1114 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2092.8344
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.028

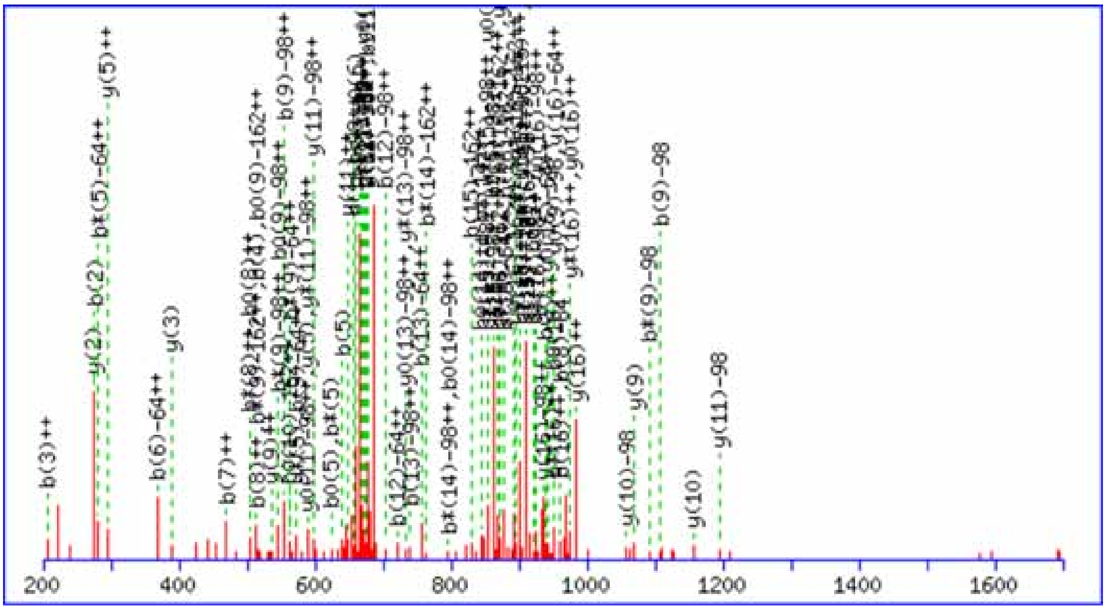
Matched b ions: b(2), b(4)-98, b(6)++, b(7)-98++, b(7)++, b(8)-98++, b(9)++, b(9)-98++, b(10)-98++, b(12)-98++, b(12)++, b(13)-98++, b(14)-98++
Matched y ions: y(1), y(2), y(3), y(5), y(6)++, y(6), y(9)++, y(11)++, y(12)++, y(13)++
Precursor origin neutral loss: +

Peptide No.1226

VMHTQCHSTPDSAEDVR
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of VMHTQCHSTPDSAEDVR
Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 6123: 2092.836111 from(698.619313,3+)
Title: Elution from: 21.055 to 21.055 scan no 1109 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2092.8344
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.0019

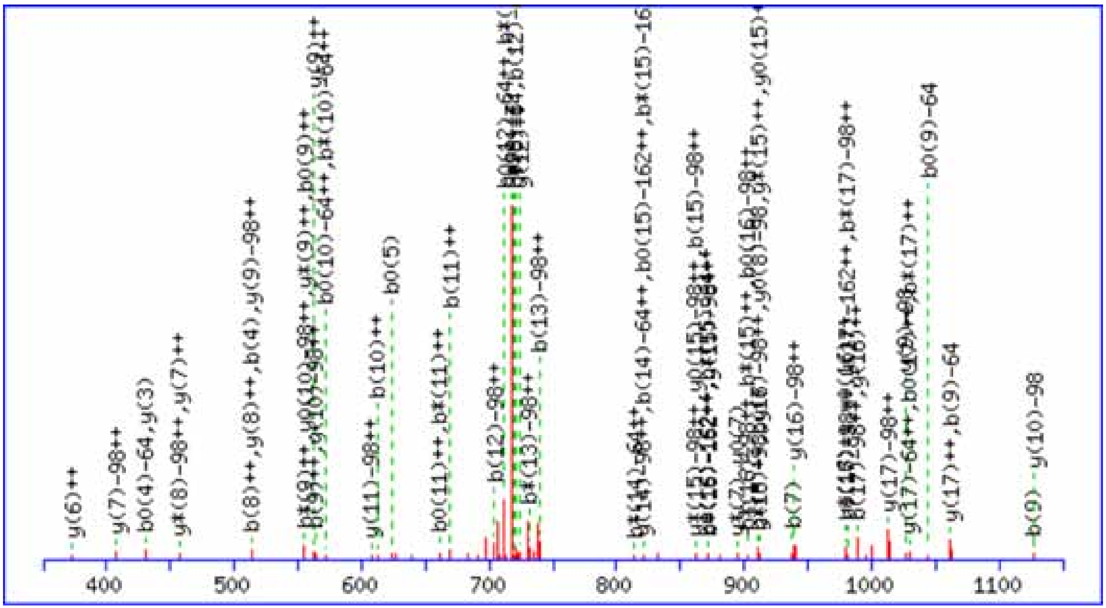
Matched b ions: b(2), b(3)++, b(4), b(5), b(7)++, b(7), b(8)++, b(9)-98++, b(9)-98, b(11)-98++, b(12)-98++, b(13)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(5)++, y(5), y(6), y(9), y(9)++, y(10), y(10)-98, y(11)-98, y(11)-98++, y(11)++, y(12)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1227

VMHTQCHSTPDSAEDVRK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of VMHTQCHSTPDSAEDVRK
Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 5434: 2248.962870 from(750.661566,3+)
Title: Elution from: 20.006 to 20.006 scan no 962 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2248.9606
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl (K)
Ions Score: 66 **Expect:** 1.3e-005

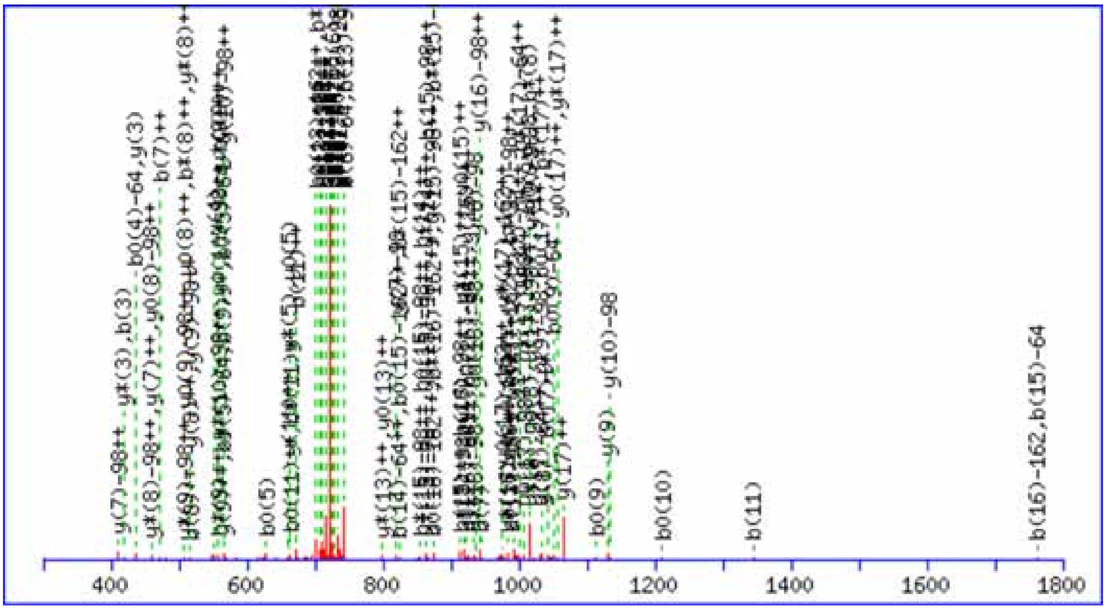
Matched b ions: b(4), b(7), b(8)++, b(9), b(9)++, b(10)++, b(11)++, b(12)-98++, b(13)-98++, b(15)-98++, b(15)++, b(16)-98++, b(17)-98++
Matched y ions: y(3), y(6)++, y(7)-98++, y(7)++, y(7), y(8)++, y(9)-98++, y(9)++, y(9)-98, y(10)-98, y(10)-98++, y(11)-98++, y(12)++, y(14)-98++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++
Precursor origin neutral loss: +

Peptide No.1228

VMHTQCHSTPDSAEDVRK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of VMHTQCHSTPDSAEDVRK
Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 5489: 2261.026059 from(754.682629,3+)
Title: Elution from: 20.143 to 20.143 scan no 950 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2261.0242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 42 Expect: 0.0055

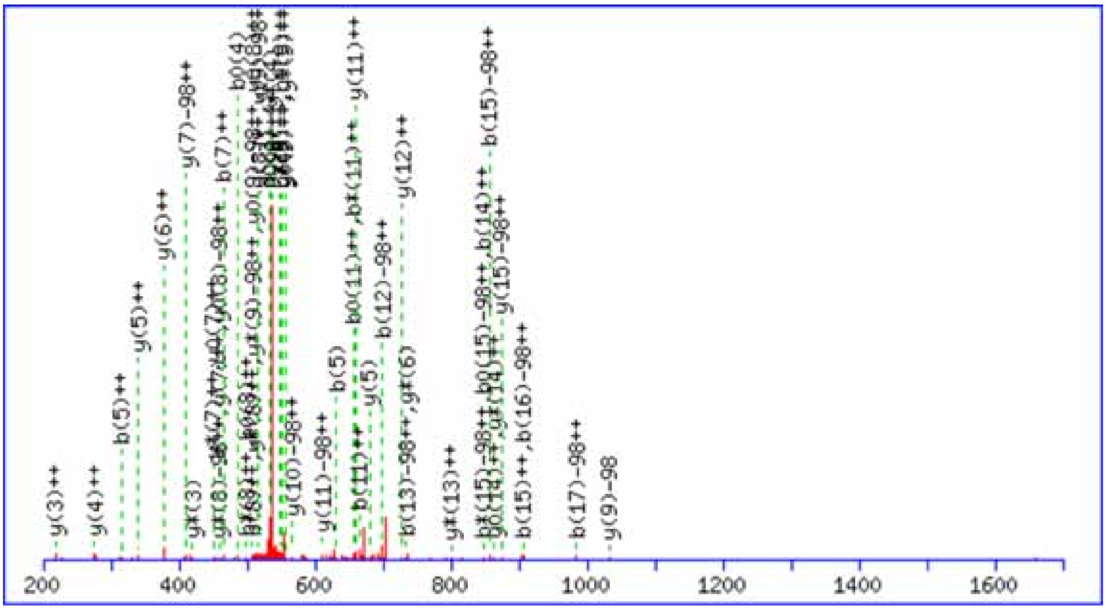
Matched b ions: b(3), b(7)++, b(7), b(8)++, b(9)++, b(11), b(11)++, b(12)-98++, b(13)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(7)-98++, y(7), y(7)++, y(7)-98, y(8), y(8)++, y(8)-98, y(9)++, y(9), y(9)-98, y(9)-98++, y(10)-98++, y(10)-98, y(11)++, y(12)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++
Precursor origin neutral loss: +

Peptide No.1229

VMHTQCHSTPDSAEDVRK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of VMHTQCHSTPDSAEDVRK
Found in FETUA_MOUSE, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 5438: 2245.031280 from(562.265096,4+)
Title: Elution from: 21.417 to 21.417 scan no 1077 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2245.0293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K18 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 34 Expect: 0.031

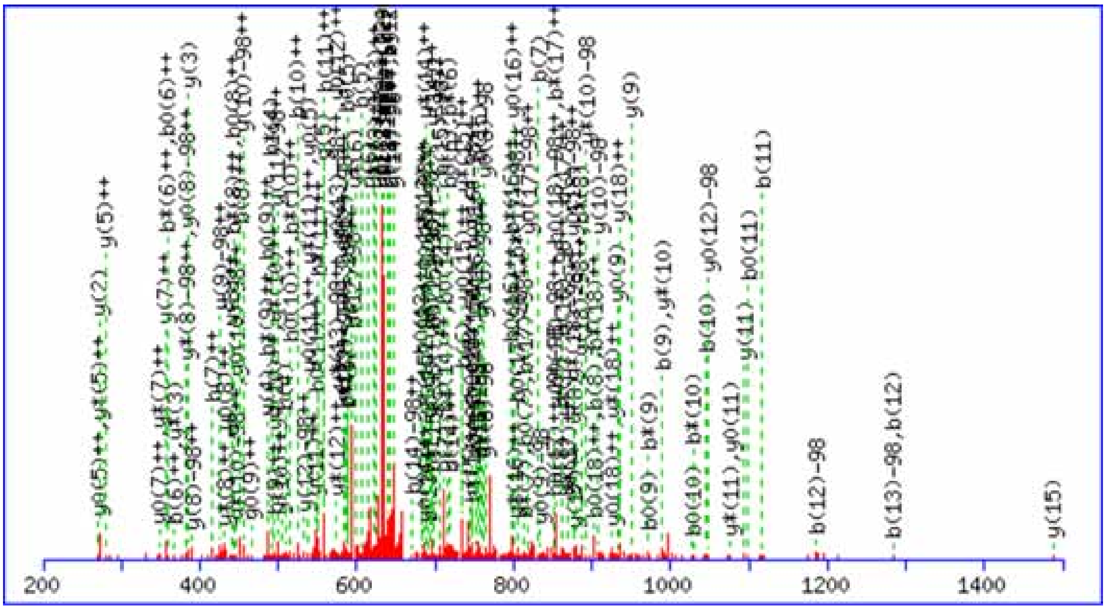
Matched b ions: b(5)++, b(5), b(7)++, b(8)++, b(11)++, b(12)-98++, b(13)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(17)-98++
Matched y ions: y(3)++, y(4)++, y(4), y(5)++, y(5), y(6)++, y(7)-98++, y(7)++, y(8)++, y(9)-98, y(9)-98++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(15)-98++
Precursor origin neutral loss: +

Peptide No.1230

VNHEPEPASGASPGATIPK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of VNHEPEPASGASPGATIPK
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 5157: 1993.953114 from(665.658314,3+)
Title: Elution from: 30.323 to 30.323 scan no 2183 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1993.9510
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K19 : Dimethyl (K)
Ions Score: 53 Expect: 0.00034

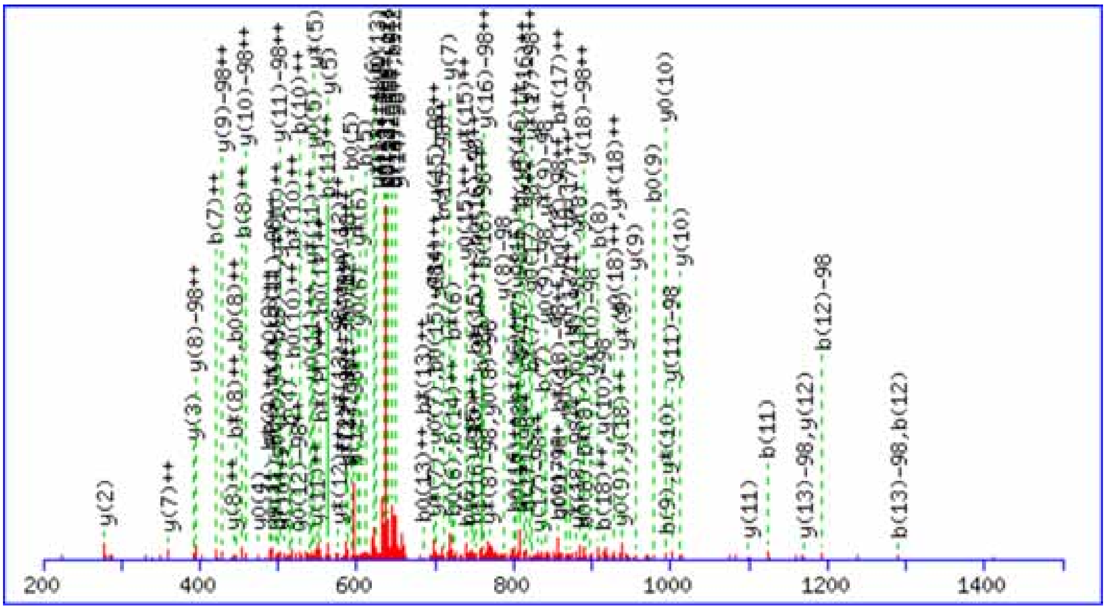
Matched b ions: b(4), b(5), b(6), b(6)++, b(7)++, b(7), b(8)++, b(8), b(9), b(9)++, b(10), b(10)++, b(11)++, b(11), b(12)-98, b(12), b(12)-98++, b(12)++, b(13)-98, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(17)++, b(17)-98++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(8), y(8)-98++, y(8)++, y(9)-98++, y(9)-98, y(9), y(10)-98++, y(10)++, y(10)-98, y(11), y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15), y(15)-98++, y(15)++, y(16)-98++, y(17)++, y(18)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1231

VNHEPEPASGASPGATIPK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of VNHEPEPASGASPGATIPK
Found in BIN1_MOUSE, Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1

Match to Query 4571: 2006.017380 from(669.679736,3+)
Title: Elution from: 30.279 to 30.279 scan no 2162 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2006.0146
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K19 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 50 **Expect:** 0.00069

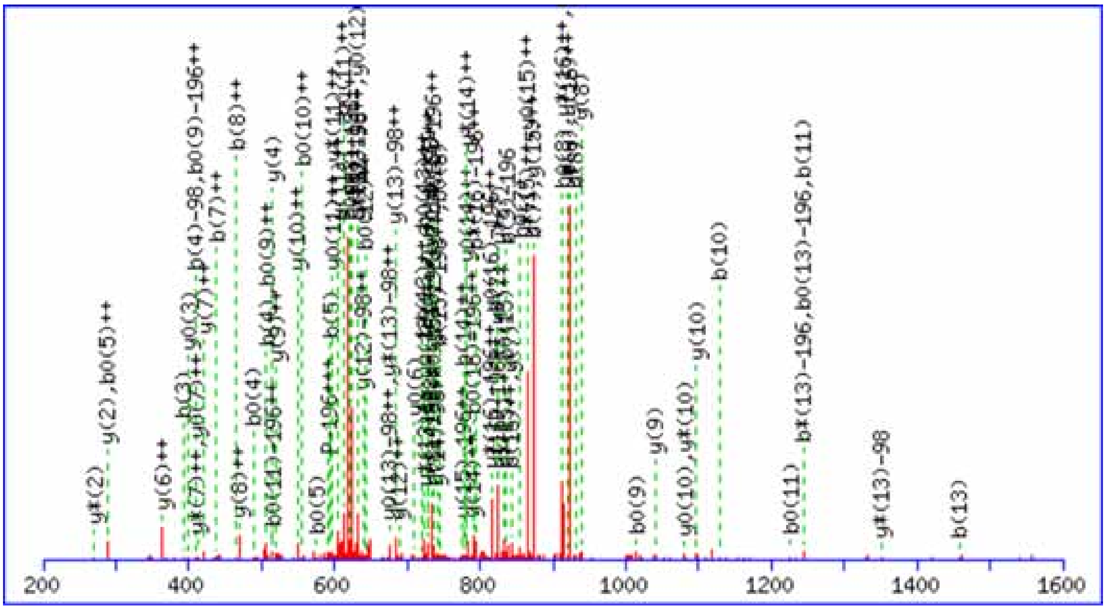
Matched b ions: b(4), b(5), b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(11), b(11)++, b(12)-98++, b(12)-98, b(12), b(12)++, b(13)-98, b(13)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(18)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)-98++, y(8), y(8)++, y(8)-98, y(9)-98++, y(9)-98, y(9), y(10)++, y(10)-98, y(10)-98++, y(10), y(11)-98, y(11), y(11)-98++, y(11)++, y(12)++, y(12), y(13)-98++, y(13)++, y(13)-98, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(18)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1232

VPSDSSLGTPDGRPELR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of VPSDSSLGTPDGRPELR
Found in CIP4_MOUSE, Cdc42-interacting protein 4 OS=Mus musculus GN=Trip10 PE=1 SV=2

Match to Query 5475: 1969.856460 from(657.626096,3+)
Title: Elution from: 38.000 to 38.000 scan no 3399 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1969.8547
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.0098

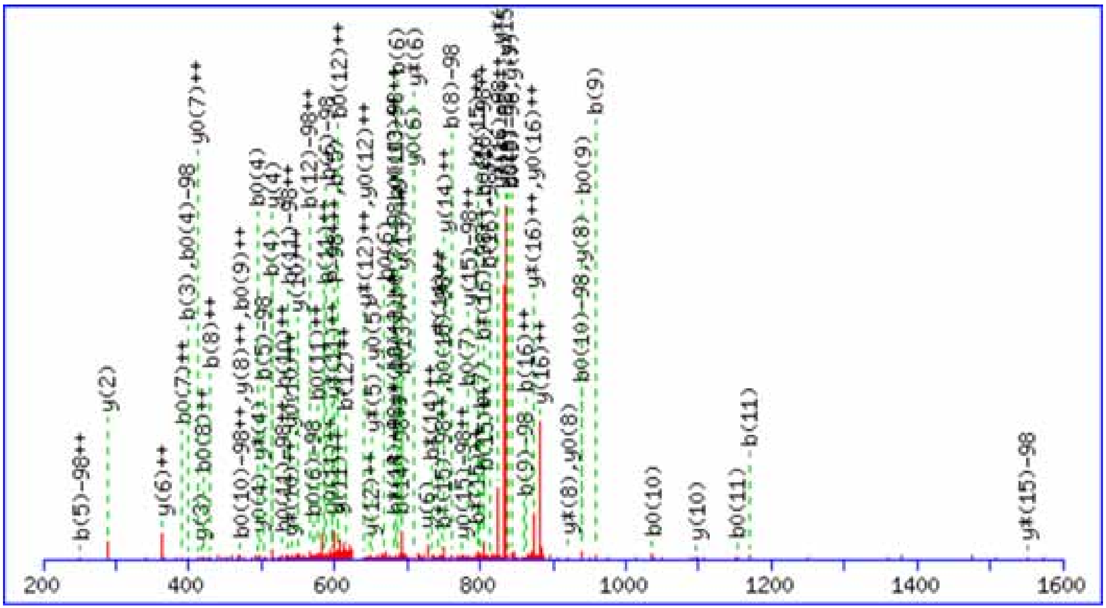
Matched b ions: b(3), b(4), b(4)-98, b(5), b(7), b(7)++, b(7)-98, b(8)++, b(8)-98, b(8)-196, b(8), b(9)-196, b(10), b(10)-98++, b(11), b(12)-98++, b(13), b(13)++, b(13)-196++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(15)-196++, b(16)-98++
Matched y ions: y(2), y(4), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(15)-196++, y(16)++, y(16)-196++, y(16)-98++
Precursor origin neutral loss: +

Peptide No.1233

VPSDSSLGTPDGRPELR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of VPSDSSLGTPDGRPELR
Found in CIP4_MOUSE, Cdc42-interacting protein 4 OS=Mus musculus GN=Trip10 PE=1 SV=2

Match to Query 4605: 1895.921718 from(632.981182,3+)
Title: Elution from: 36.418 to 36.418 scan no 3015 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1895.9202
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.055

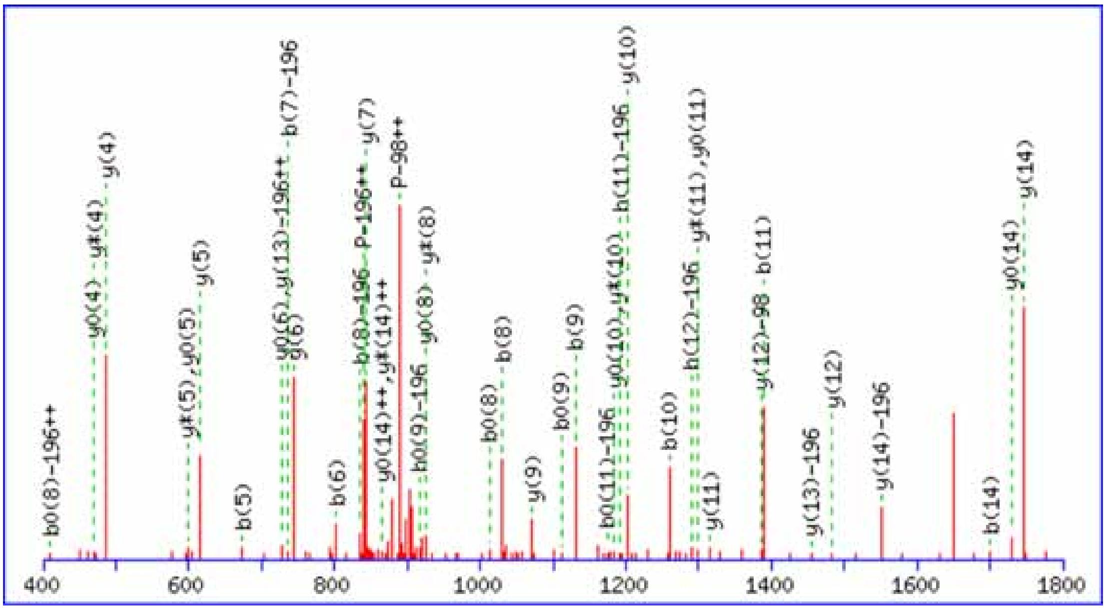
Matched b ions: b(3), b(4), b(5), b(5)-98++, b(5)-98, b(6)-98, b(6), b(7), b(8)++, b(8)-98, b(9), b(9)-98, b(10)++, b(11), b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(14)-98++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(6)++, y(6), y(7), y(8)++, y(8), y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++
Precursor origin neutral loss: +

Peptide No.1234

VPSSDEEVVEEPQSR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of VPSSDEEVVEEPQSR
Found in TB182_MOUSE, 182 kDa tankyrase-1-binding protein OS=Mus musculus GN=Tnks1bp1 PE=1 SV=2

Match to Query 4882: 1873.737866 from(937.876209,2+)
Title: Elution from: 37.087 to 37.087 scan no 3274 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1873.7384
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 **Expect:** 8.8e-006

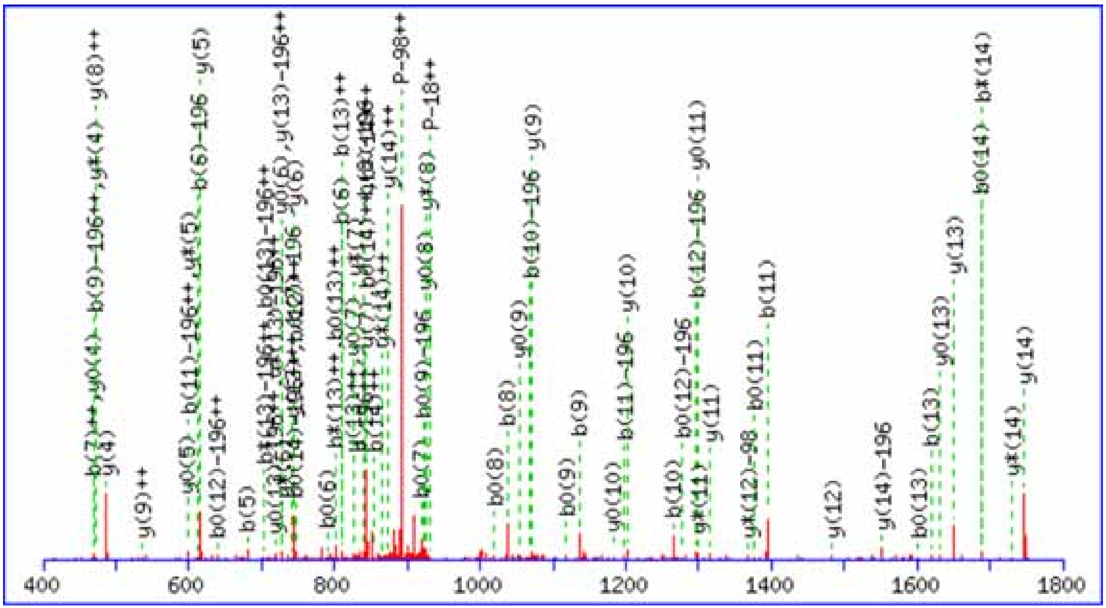
Matched b ions: b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7)-196, b(7)-98, b(8), b(8)-98, b(8)-196, b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(11)-196, b(12)-98, b(12)-196, b(13)-98, b(14)
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(12)-98, y(13)-196, y(13)-196++, y(14)-196, y(14)-98, y(14)
Precursor origin neutral loss: +

Peptide No.1235

VPSSDEEVVEEPQSR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of VPSSDEEVVEEPQSR
Found in TB182_MOUSE, 182 kDa tankyrase-1-binding protein OS=Mus musculus GN=Tnks1bp1 PE=1 SV=2

Match to Query 4254: 1879.772630 from(940.893591,2+)
Title: Elution from: 36.854 to 36.854 scan no 3044 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1879.7702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 0.00043

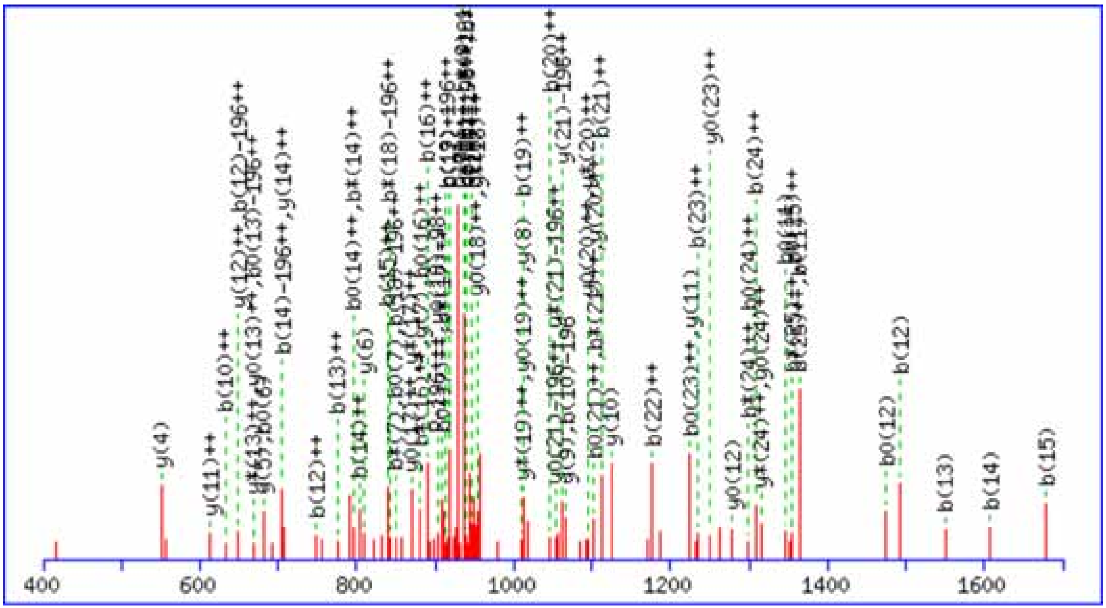
Matched b ions: b(4)-98, b(5), b(5)-98, b(6), b(6)-196, b(6)-98, b(7)++, b(7)-196, b(7)-98, b(8), b(8)-98++, b(8)-196, b(9), b(9)-196++, b(9)-98, b(10), b(10)-98, b(10)-196, b(11), b(11)-196++, b(11)-98, b(11)-196, b(12)-98, b(12)-196, b(12)++, b(13), b(13)-98, b(13)-98++, b(13)++, b(14)-98++, b(14)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(9), y(9)++, y(10), y(11), y(12), y(12)++, y(13)-98, y(13), y(13)-196++, y(13)++, y(14)-196, y(14)-98, y(14), y(14)++
Precursor origin neutral loss: +

Peptide No.1236

VQEAQDSDSDTEGGATGGEAEMDFLR
Confirmed sites: @S:7,@S:9
Ambiguous sites:

MS/MS Fragmentation of VQEAQDSDSDTEGGATGGEAEMDFLR
Found in SIRT2_MOUSE, NAD-dependent deacetylase sirtuin-2 OS=Mus musculus GN=Sirt2 PE=1 SV=2

Match to Query 6807: 2902.089858 from(968.370562,3+)
Title: Elution from: 60.834 to 60.834 scan no 5642 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2902.0889
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 95 **Expect:** 8e-009

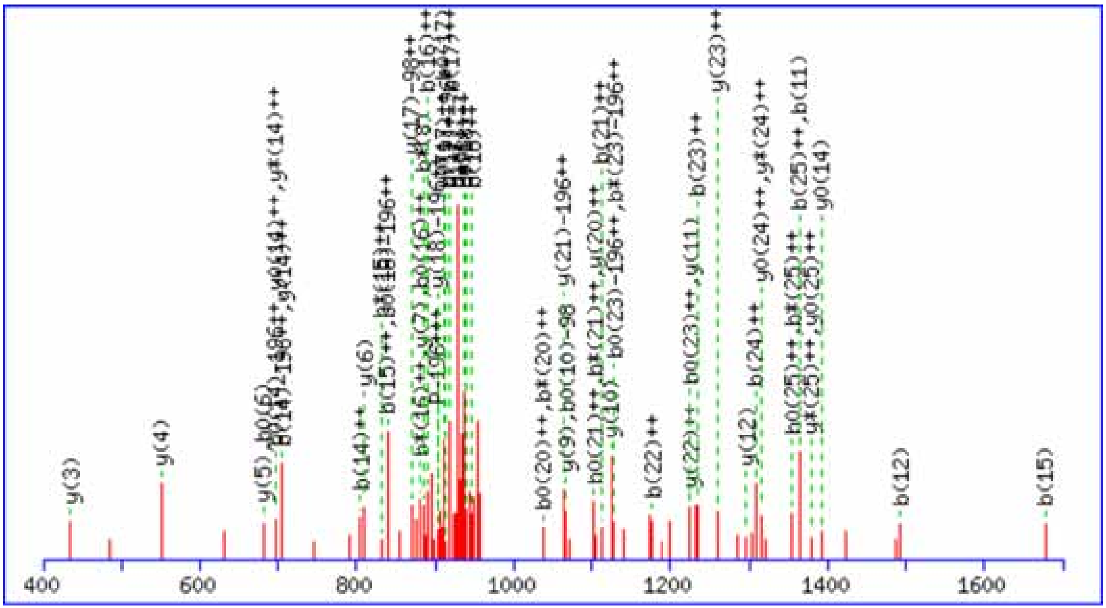
Matched b ions: b(10)-196, b(10)++, b(11), b(11)-98++, b(12), b(12)-196++, b(12)++, b(13), b(13)++, b(14)-196++, b(14), b(14)++, b(14)-98++, b(15)-98++, b(15), b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(18)-196++, b(19)++, b(19)-196++, b(20)++, b(21)++, b(21)-98++, b(22)++, b(23)-98++, b(23)++, b(24)++, b(25)++, b(25)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)++, y(14)++, y(20)++, y(20)-98++, y(21)-98++, y(21)-196++
Precursor origin neutral loss: +

Peptide No.1237

VQEAQDSDSDTEGGATGGEAEMDFLR
Confirmed sites: @S:9,@T:11
Ambiguous sites:

MS/MS Fragmentation of VQEAQDSDSDTEGGATGGEAEMDFLR
Found in SIRT2_MOUSE, NAD-dependent deacetylase sirtuin-2 OS=Mus musculus GN=Sirt2 PE=1 SV=2

Match to Query 7297: 2902.090938 from(968.370922,3+)
Title: Elution from: 60.744 to 60.744 scan no 5760 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2902.0889
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 Expect: 0.00047

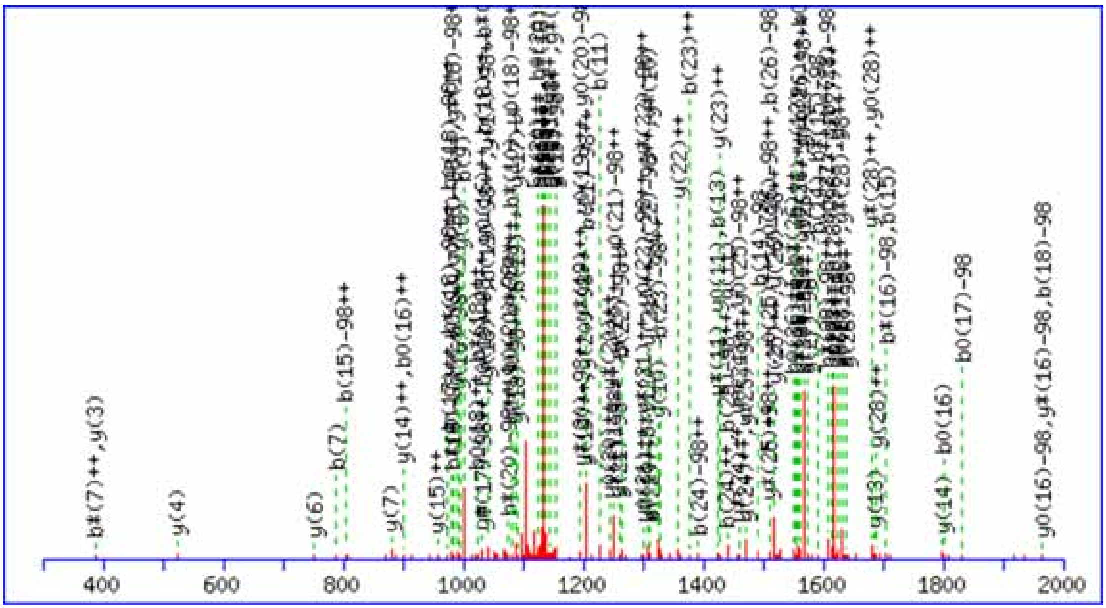
Matched b ions: b(11), b(12), b(14)-196++, b(14)++, b(15), b(15)-98++, b(15)++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(19)-196++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(23)++, b(24)++, b(24)-98++, b(25)++, b(25)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(14)++, y(17)++, y(17)-98++, y(18)-196++, y(20)++, y(21)-196++, y(21)-98++, y(22)++, y(23)++
Precursor origin neutral loss: +

Peptide No.1238

VQIPVSHPDPEPVSDNEDDSYDEEVHDPR
Confirmed sites: @S:14,@Y:21
Ambiguous sites:

MS/MS Fragmentation of VQIPVSHPDPEPVSDNEDDSYDEEVHDPR
Found in ZO1_MOUSE, Tight junction protein ZO-1 OS=Mus musculus GN=Tjp1 PE=1 SV=1

Match to Query 7715: 3503.411166 from(1168.810998,3+)
Title: Elution from: 44.599 to 44.599 scan no 4095 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3503.4079
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y21 : Phospho (Y)
Ions Score: 71 **Expect:** 5.8e-006

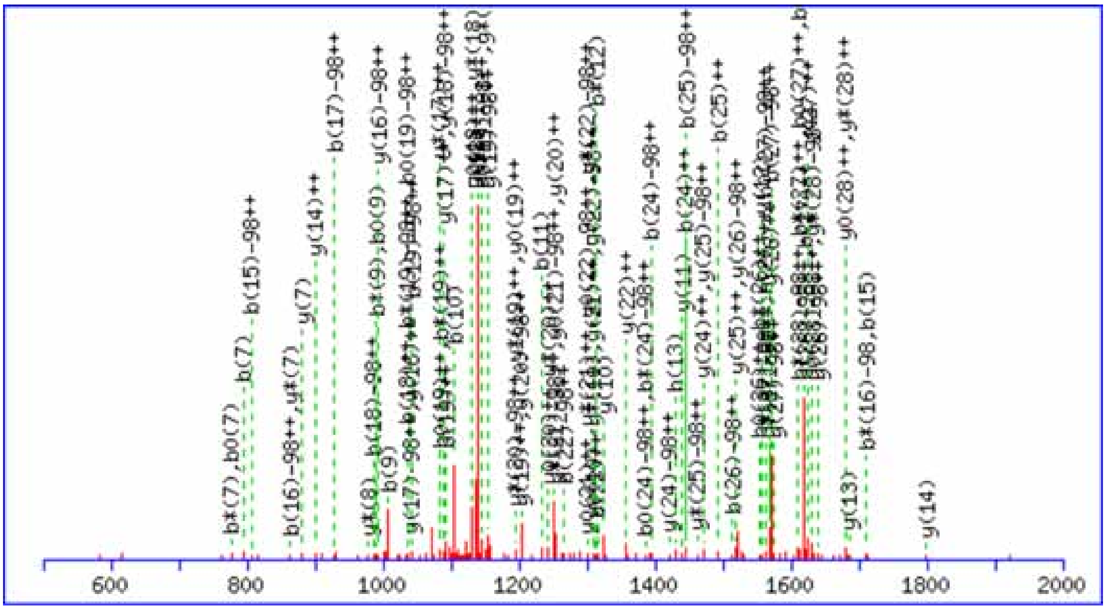
Matched b ions: b(7), b(9), b(11), b(13), b(14)-98, b(14), b(15), b(15)-98++, b(15)-98, b(17)++, b(18)-98++, b(18)-98, b(18)++, b(19)-98++, b(19)++, b(20)++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++, b(23)++, b(24)++, b(24)-98++, b(25)-98++, b(26)++, b(26)-98++, b(27)-98++, b(27)++, b(28)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)-98++, y(22)++, y(23)++, y(24)++, y(25)-98++, y(25)++, y(26)++, y(26)-98++, y(27)++, y(27)-98++, y(28)++, y(28)-98++
Precursor origin neutral loss: +

Peptide No.1239

VQIPVSHPDPEPVSDNEDDSYDEEVHDPR
Confirmed sites: @S:14
Ambiguous sites: @S:20orY:21

MS/MS Fragmentation of VQIPVSHPDPEPVSDNEDDSYDEEVHDPR
Found in ZO1_MOUSE, Tight junction protein ZO-1 OS=Mus musculus GN=Tjp1 PE=1 SV=1

Match to Query 6795: 3509.440902 from(1170.820910,3+)
Title: Elution from: 44.439 to 44.439 scan no 3946 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 3509.4398
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y21 : Phospho (Y)
Ions Score: 48 Expect: 0.0014

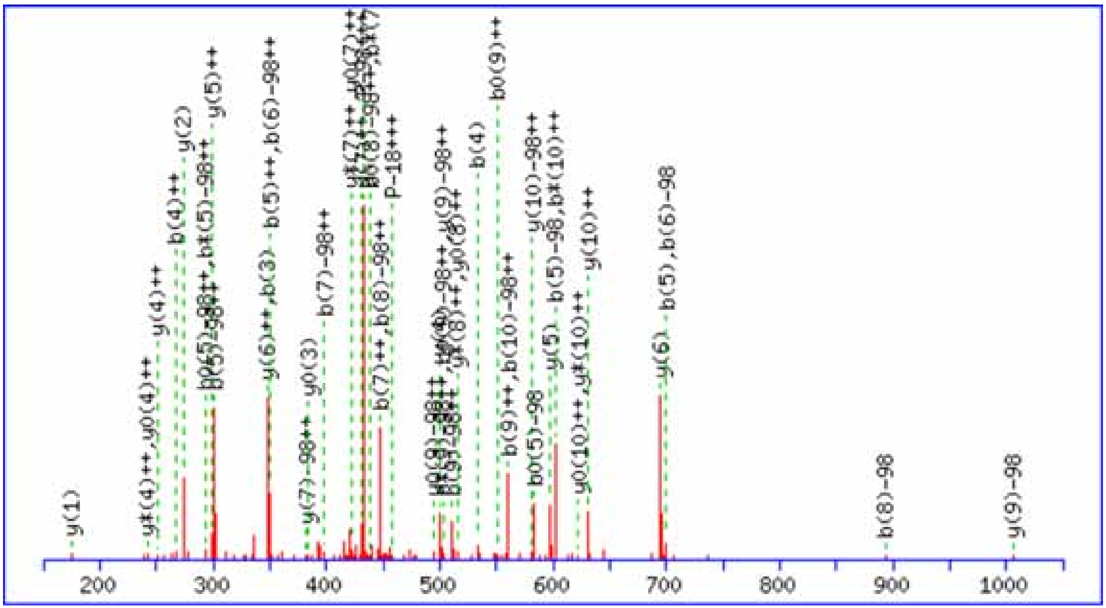
Matched b ions: b(7), b(9), b(10), b(11), b(13), b(15), b(15)-98++, b(16)-98++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(22)++, b(22)-98++, b(24)++, b(24)-98++, b(25)-98++, b(25)++, b(26)++, b(26)-98++, b(27)-98++, b(27)++, b(28)-98++
Matched y ions: y(7), y(10), y(11), y(12), y(13), y(14), y(14)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(22)++, y(22)-98++, y(24)++, y(24)-98++, y(25)-98++, y(25)++, y(26)++, y(26)-98++, y(27)++, y(27)-98++, y(28)-98++
Precursor origin neutral loss: +

Peptide No.1240

VRGWSPPPEVR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of VRGWSPPPEVR
Found in ACSA_MOUSE, Acetyl-coenzyme A synthetase, cytoplasmic OS=Mus musculus GN=Acss2 PE=1 SV=1

Match to Query 1807: 1392.711897 from(465.244575,3+)
Title: Elution from: 38.679 to 38.679 scan no 3327 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1392.7127
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 0.00013

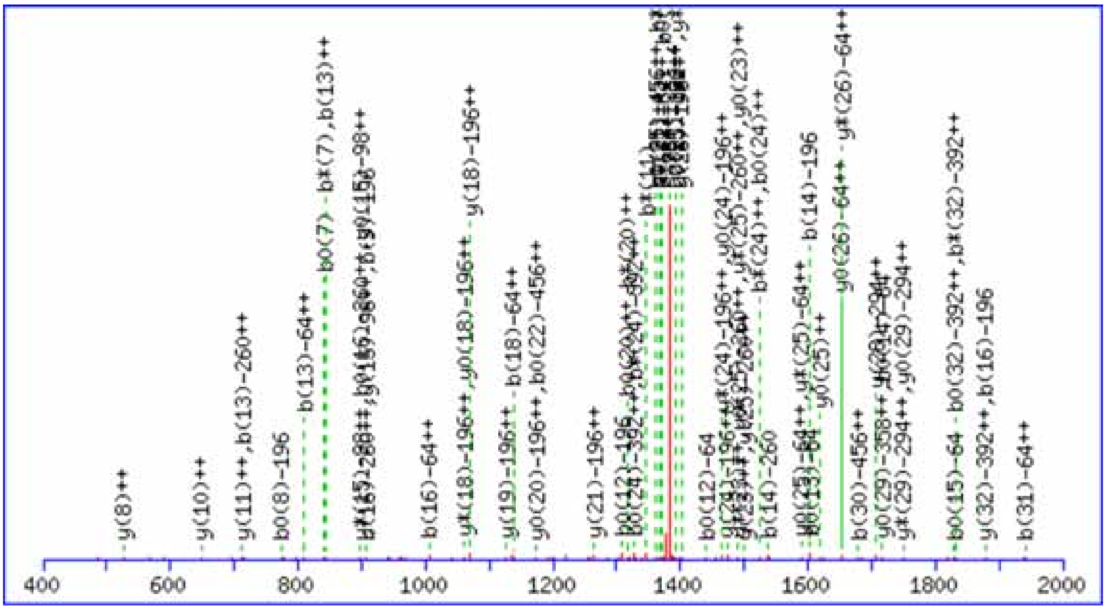
Matched b ions: b(3), b(4)++, b(4), b(5)-98, b(5)-98++, b(5)++, b(5), b(6)-98++, b(6)-98, b(7)++, b(7)-98++, b(8)-98, b(8)-98++, b(9)++, b(9)-98++, b(10)-98++
Matched y ions: y(1), y(2), y(4), y(4)++, y(5), y(5)++, y(6)++, y(6), y(7)++, y(7)-98++, y(9)-98, y(9)-98++, y(10)++, y(10)-98++
Precursor origin neutral loss: +

Peptide No.1241

VSGNVSKELMLCYLIKPSTMTAEDMETPECMKR
Confirmed sites: @S:2,@S:6,@S:18
Ambiguous sites: @T:19orT:21

MS/MS Fragmentation of VSGNVSKELMLCYLIKPSTMTAEDMETPECMKR
Found in SEN2_MOUSE, tRNA-splicing endonuclease subunit Sen2 OS=Mus musculus GN=Tsen2 PE=1 SV=1

Match to Query 7924: 4245.756366 from(1416.259398,3+)
Title: Elution from: 51.694 to 51.694 scan no 4939 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 4245.7543
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K7 : Dimethyl (K)
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K16 : Dimethyl:2H(4)13C(2) (K)
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.048

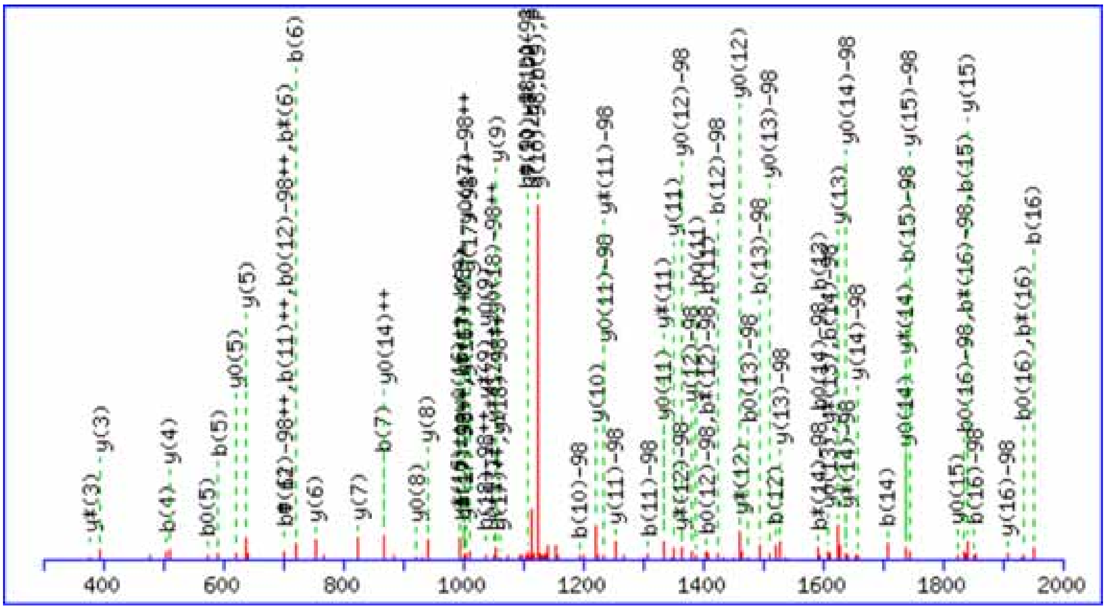
Matched b ions: b(9)-196, b(11)-98, b(11), b(12)-98++, b(13)++, b(14)-196, b(15)-98++, b(16)-196, b(18)-196++, b(22)-294++, b(22)-98++, b(23)-294++, b(23)-196++, b(24)-294++, b(29)-294++, b(32)-196++
Matched y ions: y(8)++, y(10)++, y(11)++, y(15)-98++, y(18)-196++, y(19)-196++, y(21)-196++, y(21)++, y(22)-98++, y(23)++, y(23)-196++, y(24)-196++, y(24)-98++, y(28)-294++, y(32)-392++
Precursor origin neutral loss: +

Peptide No.1242

VVDYSQFQESDDADEDYGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of VVDYSQFQESDDADEDYGR
Found in NUCKS_MOUSE, Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Mus musculus GN=Nucks1 PE=1 SV=1

Match to Query 7180: 2344.902846 from(1173.458699,2+)
Title: Elution from: 45.725 to 45.725 scan no 4389 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2344.9009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 86 **Expect:** 6.8e-008

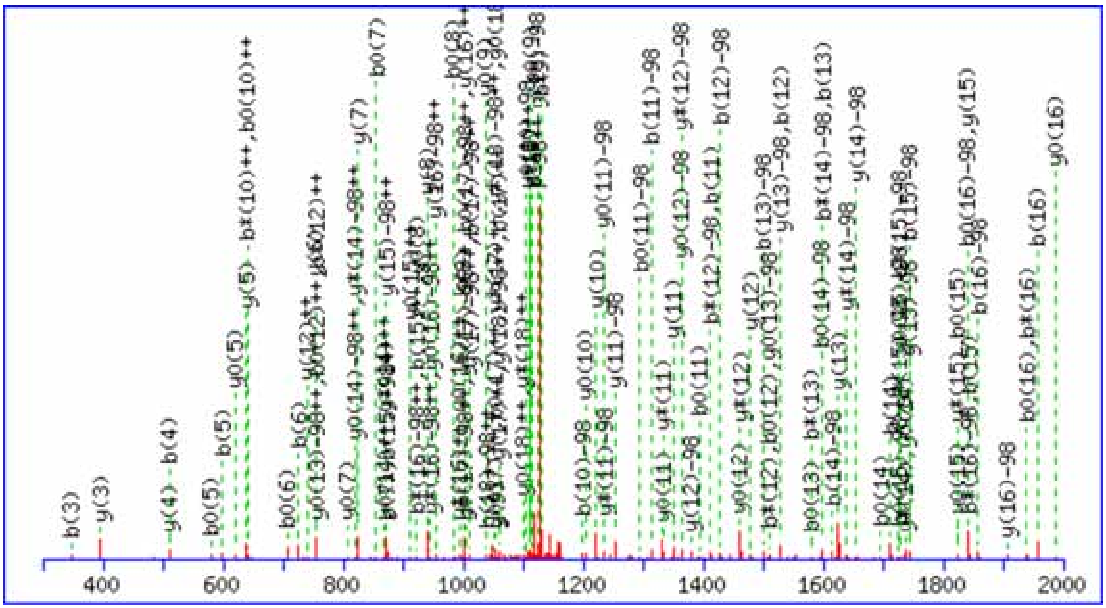
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10)-98, b(11), b(11)++, b(11)-98, b(12), b(12)-98, b(13)-98, b(13), b(14), b(14)-98, b(15), b(15)-98, b(16), b(16)-98, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)-98, y(11), y(12)-98, y(13)-98, y(13), y(14)-98, y(15), y(15)-98, y(16)-98, y(16)++, y(17)-98++, y(17)++, y(18)-98++
Precursor origin neutral loss: +

Peptide No.1243

VVDYSQFQESDDADEDYGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of VVDYSQFQESDDADEDYGR
Found in NUCKS_MOUSE, Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Mus musculus GN=Nucks1 PE=1 SV=1

Match to Query 6305: 2350.934368 from(1176.474460,2+)
Title: Elution from: 45.653 to 45.653 scan no 4181 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2350.9327
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 86 **Expect:** 8.8e-008

Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10)-98, b(11)-98, b(11), b(12), b(12)-98, b(13), b(13)-98, b(14), b(14)-98, b(15)-98++, b(15), b(15)-98, b(15)++, b(16)-98, b(16), b(17)-98++, b(17)++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11), y(11)-98, y(12)++, y(12)-98, y(12), y(13), y(13)-98, y(14)-98, y(15), y(15)-98, y(15)-98++, y(16)++, y(16)-98, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++
Precursor origin neutral loss: +

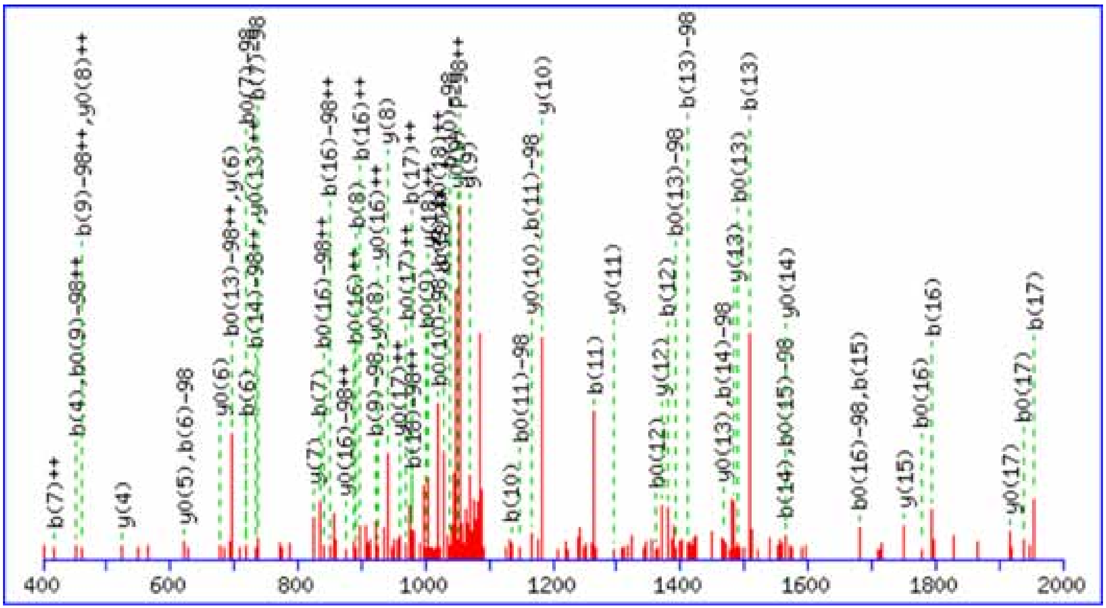
Peptide No.1244

YAALSVDGEDEDEGDDCTE

Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of YAALSVDGEDEDEGDDCTE
Found in IF4B_MOUSE, Eukaryotic translation initiation factor 4B OS=Mus musculus GN=Eif4b PE=1 SV=1

Match to Query 5812: 2202.791034 from(1102.402793,2+)
Title: Elution from: 45.325 to 45.325 scan no 4139 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2202.7884
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 Expect: 5.3e-005

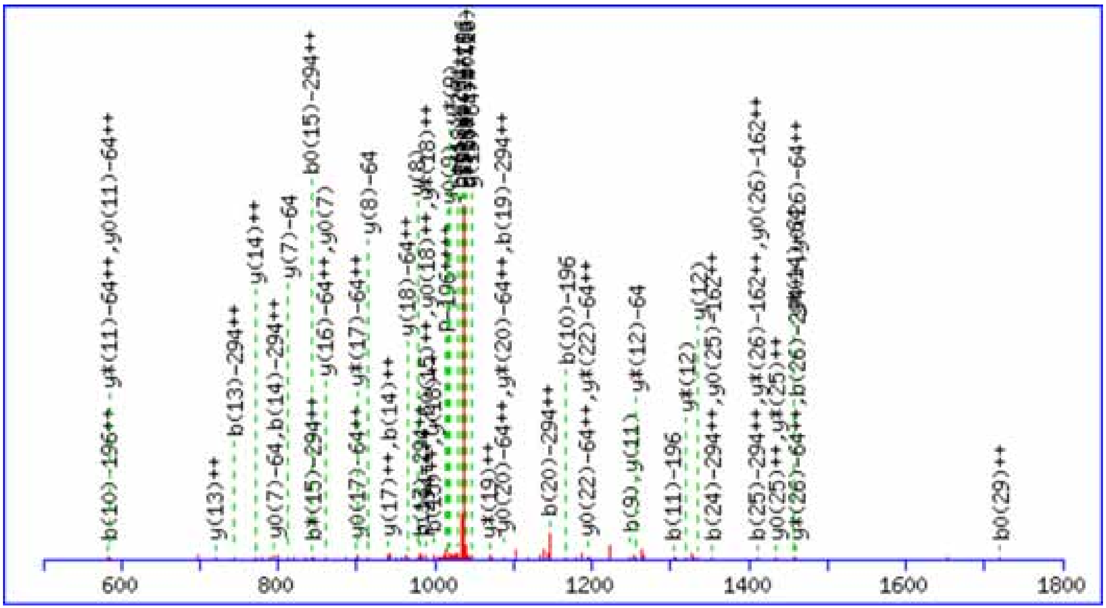
Matched b ions: b(4), b(6)-98, b(6), b(7)-98, b(7), b(7)++, b(8), b(9)-98, b(9), b(9)-98++, b(10), b(10)-98, b(11), b(11)-98, b(12), b(13), b(13)-98, b(14), b(14)-98++, b(14)-98, b(15), b(16), b(16)++, b(16)-98++, b(17), b(17)++, b(18)++, b(18)-98++
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10), y(12), y(13), y(15), y(18)++
Precursor origin neutral loss: +

Peptide No.1245

YATENDISSLHNSTLTCLVNQTTSLTGTSPEIMEK
Confirmed sites: @S:13
Ambiguous sites: @Y:1orT:3orS:8orS:9, @Y:1orT:3orS:8orS:9, @Y:1orT:3orS:8orS:9

MS/MS Fragmentation of YATENDISSLHNSTLTCLVNQTTSLTGTSPEIMEK
Found in SO1B2_MOUSE, Solute carrier organic anion transporter family member 1B2 OS=Mus musculus GN=Slco1b2 PE=1 SV=1

Match to Query 7377: 4246.754160 from(1062.695816,4+)
Title: Elution from: 60.483 to 60.483 scan no 5617 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 4246.7418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y1 : Phospho (Y)
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M33 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
K35 : Dimethyl (K)
Ions Score: 33 **Expect:** 0.046

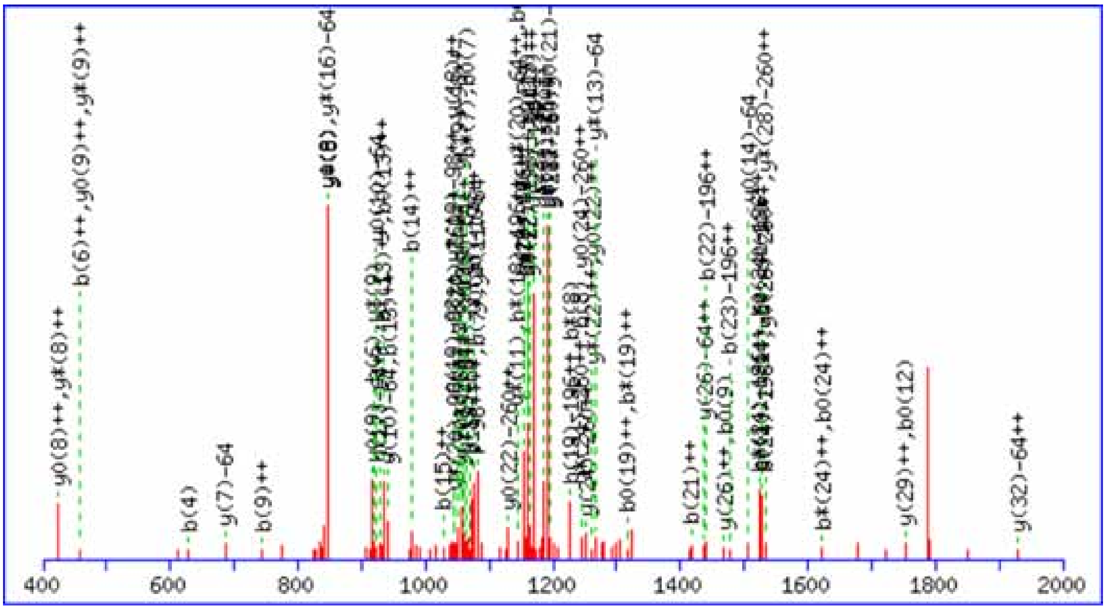
Matched b ions: b(9), b(10)-196++, b(10)-98, b(10)-196, b(11)-196, b(13)-294++, b(13)-98++, b(14)-294++, b(14)-196++, b(14)++, b(15)-196++, b(15)-98++, b(15)++, b(17)-294++, b(17)-196++, b(18)-294++, b(18)-196++, b(19)-294++, b(20)-294++, b(22)-196++, b(24)-294++, b(25)-294++, b(26)-294++
Matched y ions: y(8), y(9), y(11), y(12), y(13)++, y(14)++, y(17)++, y(18)++
Precursor origin neutral loss: +

Peptide No.1246

YDWEQKYYYGNLIAVSNSFLAYAIRAANNGSAMVR
Confirmed sites: @Y:9,@S:16,@S:18,@Y:22
Ambiguous sites:

MS/MS Fragmentation of YDWEQKYYYGNLIAVSNSFLAYAIRAANNGSAMVR
Found in EDC4_MOUSE, Enhancer of mRNA-decapping protein 4 OS=Mus musculus GN=Edc4 PE=1 SV=2

Match to Query 7010: 4421.932208 from(1106.490328,4+)
Title: Elution from: 55.069 to 55.069 scan no 5028 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 4421.9336
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
K6 : Dimethyl:2H(4)13C(2) (K)
Y9 : Phospho (Y)
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y22 : Phospho (Y)
M33 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 37 Expect: 0.024

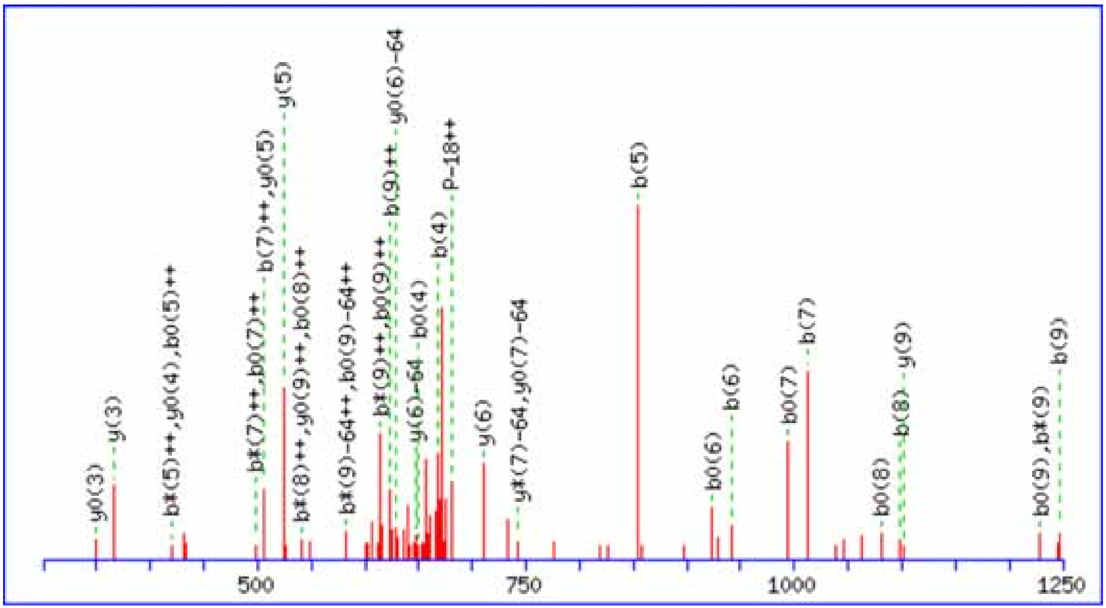
Matched b ions: b(4), b(6)++, b(6), b(7), b(8), b(9)++, b(13)++, b(14)++, b(15)++, b(17)++, b(18)-196++, b(19)-196++, b(21)++, b(22)-196++, b(23)-98++, b(23)-196++, b(24)-196++, b(28)-98++
Matched y ions: y(11), y(18)++, y(19)-98++, y(22)-196++, y(23)-98++, y(26)++, y(28)-98++, y(29)++
Precursor origin neutral loss: +

Peptide No.1247

YFENWSASMI
Confirmed sites: @Y:1
Ambiguous sites:

MS/MS Fragmentation of YFENWSASMI
Found in COX2_MOUSE, Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 PE=1 SV=1

Match to Query 1734: 1376.557024 from(689.285788,2+)
Title: Elution from: 60.527 to 60.527 scan no 5780 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1376.5572
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y1 : Phospho (Y)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 36 Expect: 0.0034

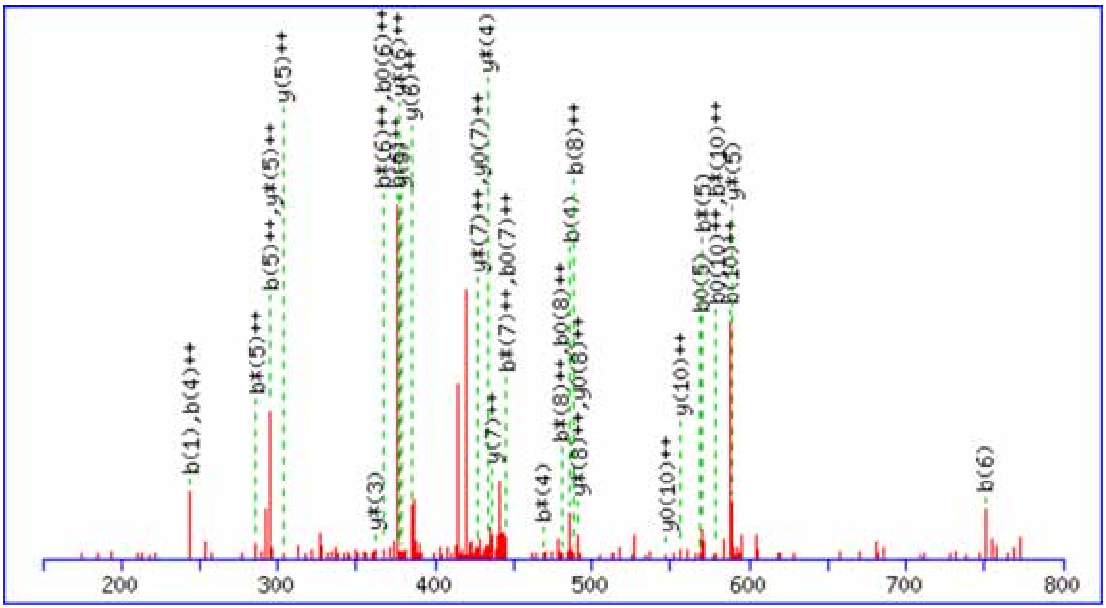
Matched b ions: b(4), b(5), b(6), b(7), b(7)++, b(8), b(9)++, b(9)
Matched y ions: y(3), y(5), y(6), y(9)
Precursor origin neutral loss:

Peptide No.1248

YGGKTYRAVVK
Confirmed sites: @Y:1
Ambiguous sites:

MS/MS Fragmentation of YGGKTYRAVVK
Found in SMBT2_MOUSE, Scm-like with four MBT domains protein 2 OS=Mus musculus GN=Sfmbt2 PE=2 SV=2

Match to Query 1190: 1354.719414 from(452.580414,3+)
Title: Elution from: 30.442 to 30.442 scan no 2070 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1354.7222
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y1 : Phospho (Y)
K11 : Dimethyl:2H(4)13C(2) (K)
Ions Score: 34 Expect: 0.014

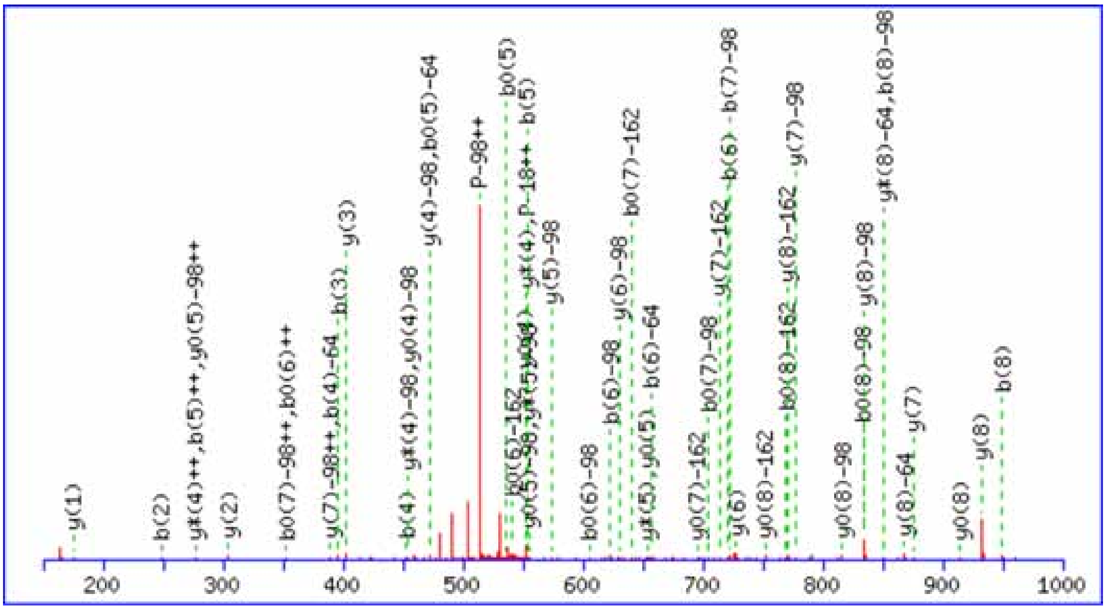
Matched b ions: b(1), b(4)++, b(4), b(5)++, b(6)++, b(6), b(8)++, b(10)++
Matched y ions: y(3), y(5)++, y(6)++, y(7)++, y(10)++
Precursor origin neutral loss: +

Peptide No.1249

YGMGTSVER
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of YGMGTSVER
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 883: 1122.441714 from(562.228133,2+)
Title: Elution from: 22.832 to 22.832 scan no 1342 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1122.4417
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.017

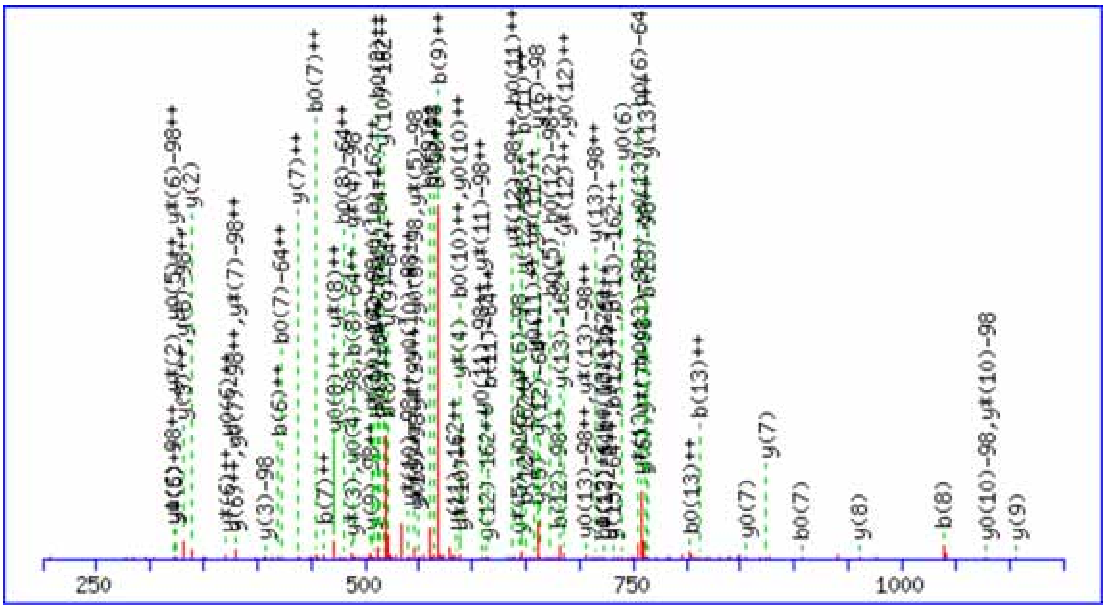
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6)-98, b(6), b(7)-98, b(8), b(8)-98
Matched y ions: y(1), y(2), y(3), y(4)-98, y(5)-98, y(6), y(6)-98, y(7)-98++, y(7), y(7)-98, y(8)-98, y(8)
Precursor origin neutral loss: +

Peptide No.1250

YHGHSMSDPGVSYR
Confirmed sites: @Y:1,@S:12
Ambiguous sites:

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3326: 1795.643397 from(599.555075,3+)
Title: Elution from: 24.902 to 24.902 scan no 1454 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1795.6426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y1 : Phospho (Y)
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.032

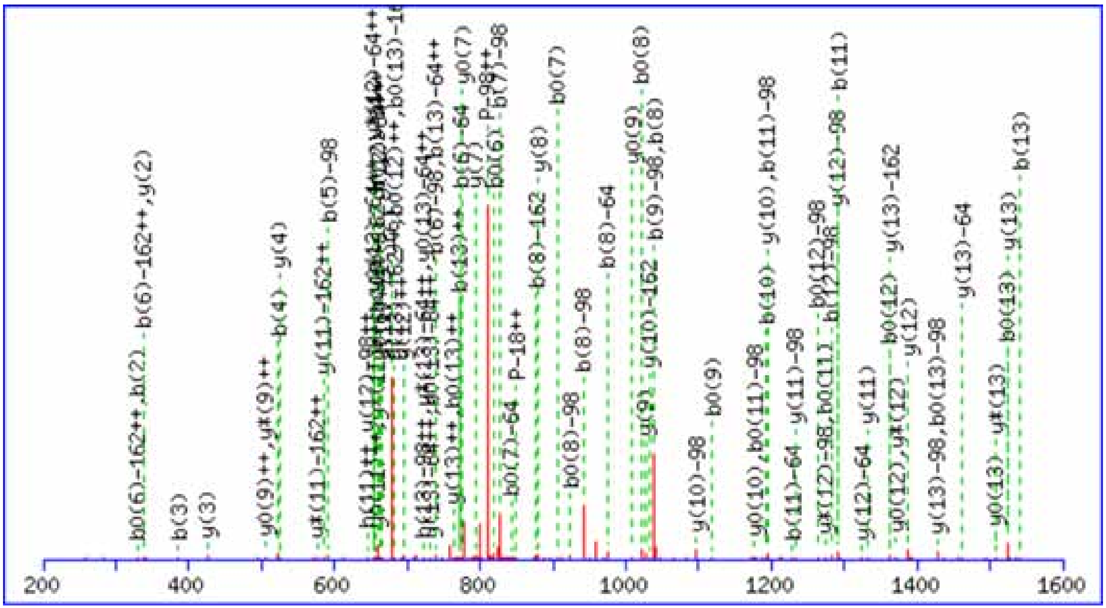
Matched b ions: b(6)++, b(7)++, b(8), b(8)++, b(9)++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(5)++, y(5), y(5)-98, y(6)-98++, y(6)-98, y(6), y(6)++, y(7), y(7)++, y(8), y(9), y(9)-98++, y(10)-98++, y(12)-98++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1251

YHGHSMSDPGVSYR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3823: 1715.676414 from(858.845483,2+)
Title: Elution from: 22.970 to 22.970 scan no 1360 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1715.6763
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 54 Expect: 8.1e-005

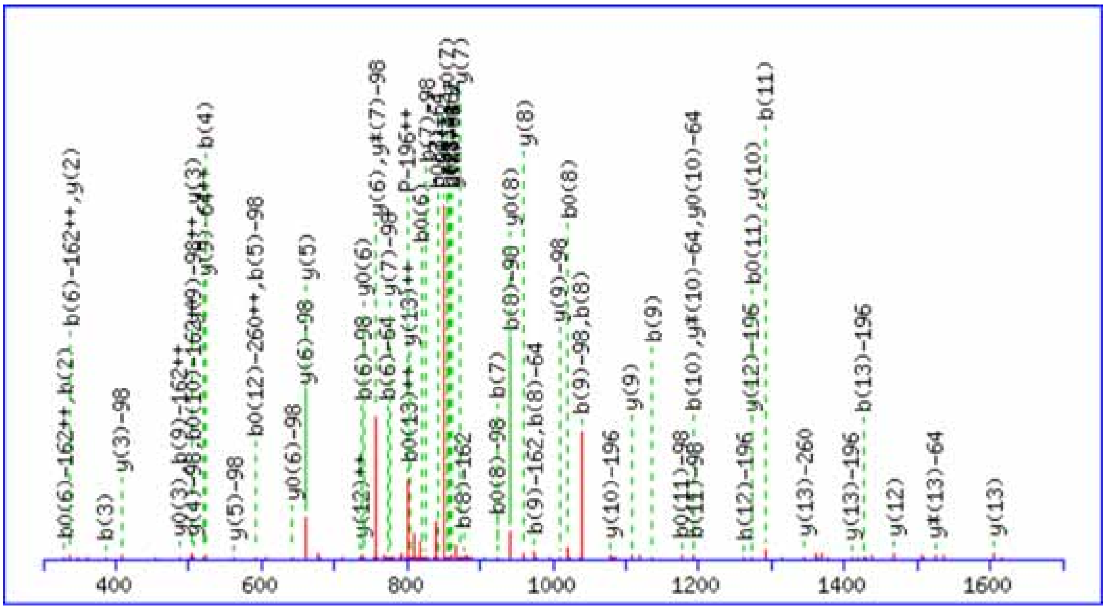
Matched b ions: b(2), b(3), b(4), b(5)-98, b(6)-98, b(7)-98, b(8)-98, b(8), b(9)-98, b(10), b(11)-98, b(11)++, b(11), b(12)-98, b(13), b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11), y(11)-98, y(11)++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13), y(13)-98, y(13)++
Precursor origin neutral loss: +

Peptide No.1252

YHGHSMSDPGVSYR
Confirmed sites: @S:5,@S:12
Ambiguous sites:

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 4277: 1795.643350 from(898.828951,2+)
Title: Elution from: 24.854 to 24.854 scan no 1611 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1795.6426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 Expect: 0.0015

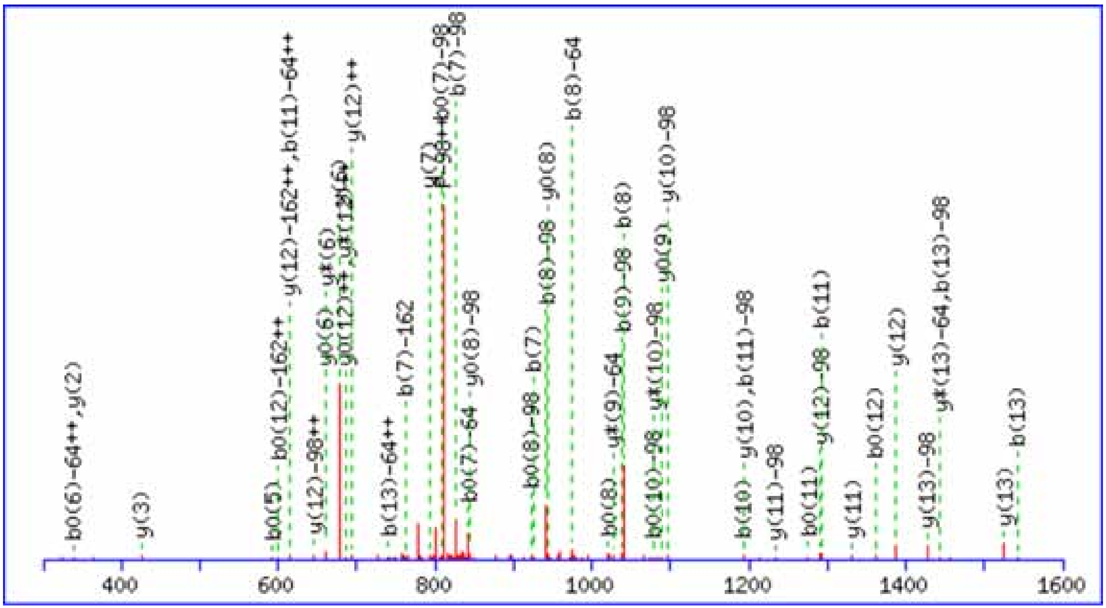
Matched b ions: b(2), b(3), b(4), b(5)-98, b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10), b(11), b(11)-98, b(12)-98, b(12)-196, b(13)-98, b(13)-196
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(5)-98, y(5), y(6)-98, y(6), y(7)-98, y(7), y(8), y(8)-98, y(9)-98++, y(9), y(9)-98, y(10)-98, y(10), y(10)-196, y(11)-98, y(12), y(12)-98, y(12)-196, y(12)++, y(13), y(13)-98, y(13)-196, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1253

YHGHSMSDPGVSYR
Confirmed sites:
Ambiguous sites: @S:5orS:7

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3278: 1715.677648 from(858.846100,2+)
Title: Elution from: 23.029 to 23.029 scan no 1255 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1715.6763
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.0038

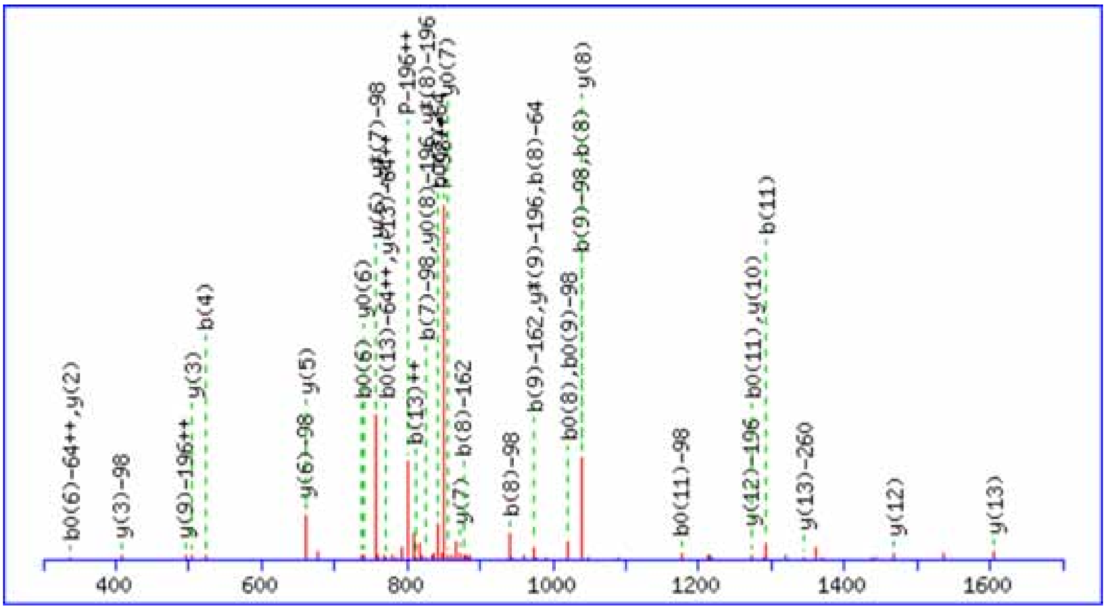
Matched b ions: b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(10), b(11)-98, b(11), b(13), b(13)-98
Matched y ions: y(2), y(3), y(6), y(7), y(10), y(10)-98, y(11)-98, y(11), y(12), y(12)-98, y(12)-98++, y(12)++, y(13)-98, y(13)
Precursor origin neutral loss: +

Peptide No.1254

YHGHSMSDPGVSYR
Confirmed sites: @S:7,@S:12
Ambiguous sites:

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3324: 1795.643472 from(898.829012,2+)
Title: Elution from: 24.825 to 24.825 scan no 1481 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1795.6426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 Expect: 0.0084

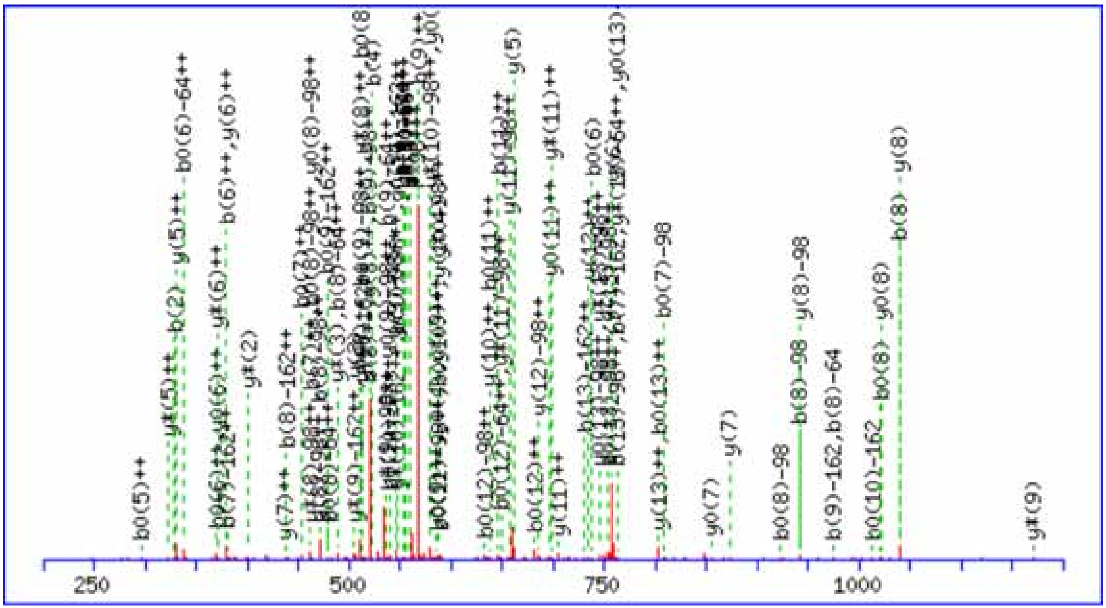
Matched b ions: b(4), b(7)-98, b(8)-98, b(8), b(9)-98, b(11), b(12)-98, b(13)++
Matched y ions: y(2), y(3)-98, y(3), y(5), y(6)-98, y(6), y(7), y(8), y(8)-98, y(9)-196++, y(9)-98, y(10)-98, y(10), y(12), y(12)-196, y(12)-98, y(13)
Precursor origin neutral loss: +

Peptide No.1255

YHGHSMSDPGVSYR
Confirmed sites: @S:7
Ambiguous sites: @S:12orY:13

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3562: 1795.642938 from(599.554922,3+)
Title: Elution from: 24.841 to 24.841 scan no 1447 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1795.6426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y13 : Phospho (Y)
Ions Score: 23 Expect: 0.06

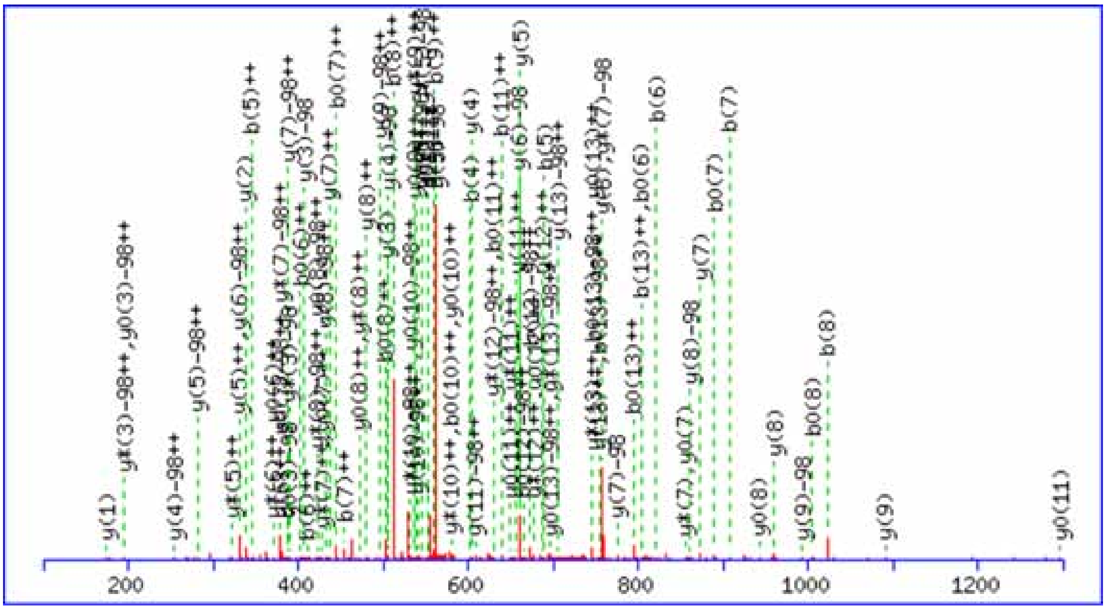
Matched b ions: b(2), b(4), b(6)++, b(7)++, b(8)++, b(8)-98, b(8), b(8)-98++, b(9)-98++, b(9)++, b(10)-98++, b(11)++, b(13)-98++
Matched y ions: y(3), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(8), y(8)-98, y(8)-98++, y(9)-98++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1256

YHGHSMSDPGVSYR
Confirmed sites: @Y:1,@S:12
Ambiguous sites:

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 4186: 1779.648303 from(594.223377,3+)
Title: Elution from: 29.681 to 29.681 scan no 2261 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1779.6477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y1 : Phospho (Y)
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.047

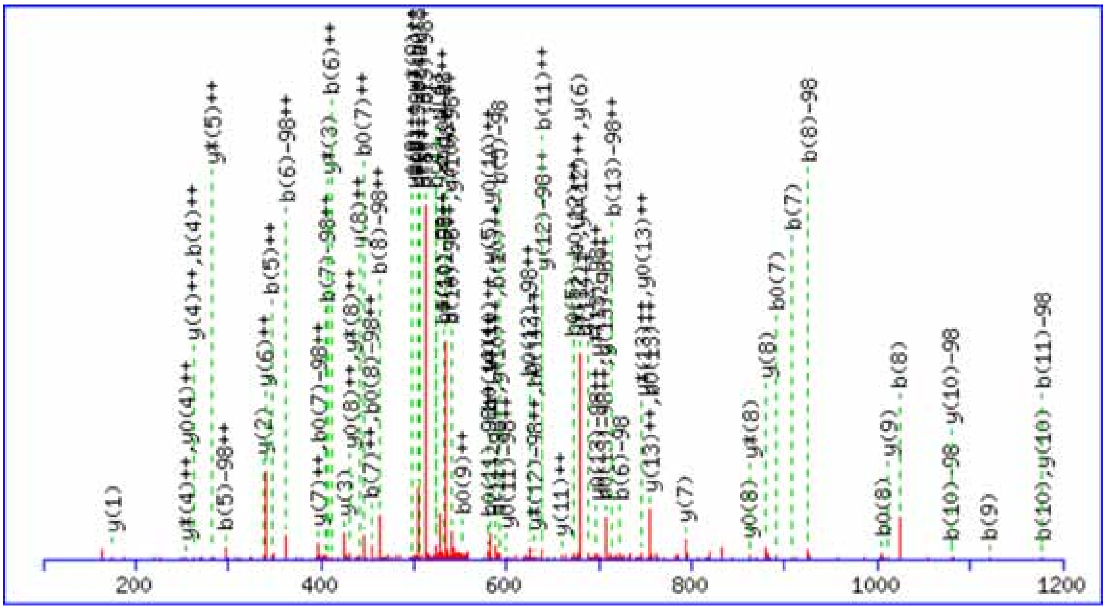
Matched b ions: b(4), b(5)++, b(5), b(6)++, b(6), b(7)++, b(7), b(8), b(8)++, b(9)++, b(11)++, b(12)-98++, b(13)-98++, b(13)++
Matched y ions: y(1), y(2), y(3)-98, y(3), y(4)-98++, y(4)-98, y(4), y(5)++, y(5), y(5)-98, y(5)-98++, y(6)-98++, y(6)++, y(6)-98, y(6), y(7), y(7)-98, y(7)++, y(7)-98++, y(8), y(8)-98, y(8)-98++, y(8)++, y(9), y(9)-98, y(9)-98++, y(9)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(13)-98++, y(13)++
Precursor origin neutral loss: +

Peptide No.1257

YHGHSMSDPGVSYR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3719: 1699.681347 from(567.567725,3+)
Title: Elution from: 27.344 to 27.344 scan no 1940 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1699.6814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 Expect: 6.8e-005

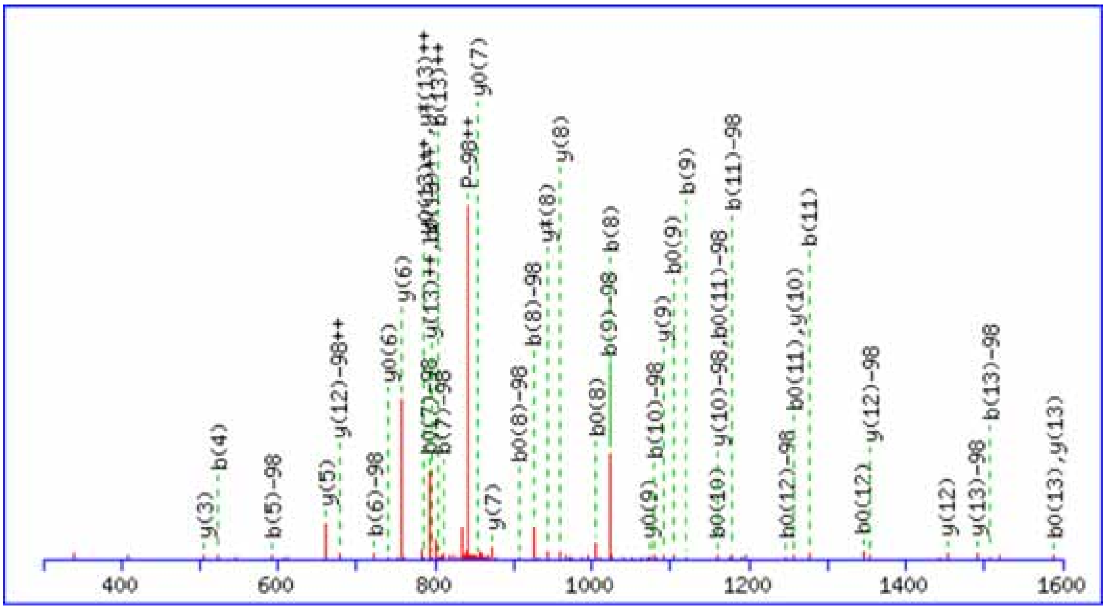
Matched b ions: b(4)++, b(4), b(5)-98++, b(5)++, b(5)-98, b(6)-98++, b(6)++, b(6)-98, b(7)++, b(7)-98++, b(7), b(8)-98++, b(8)++, b(8), b(8)-98, b(9)-98++, b(9), b(10), b(10)++, b(10)-98, b(10)-98++, b(11)-98++, b(11)-98, b(11)++, b(13)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)-98, y(10), y(10)++, y(10)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1258

YHGHSMSDPGVSYR
Confirmed sites: @S:5
Ambiguous sites: @S:12orY:13

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 4185: 1779.647728 from(890.831140,2+)
Title: Elution from: 29.846 to 29.846 scan no 2284 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1779.6477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y13 : Phospho (Y)
Ions Score: 55 Expect: 4.4e-005

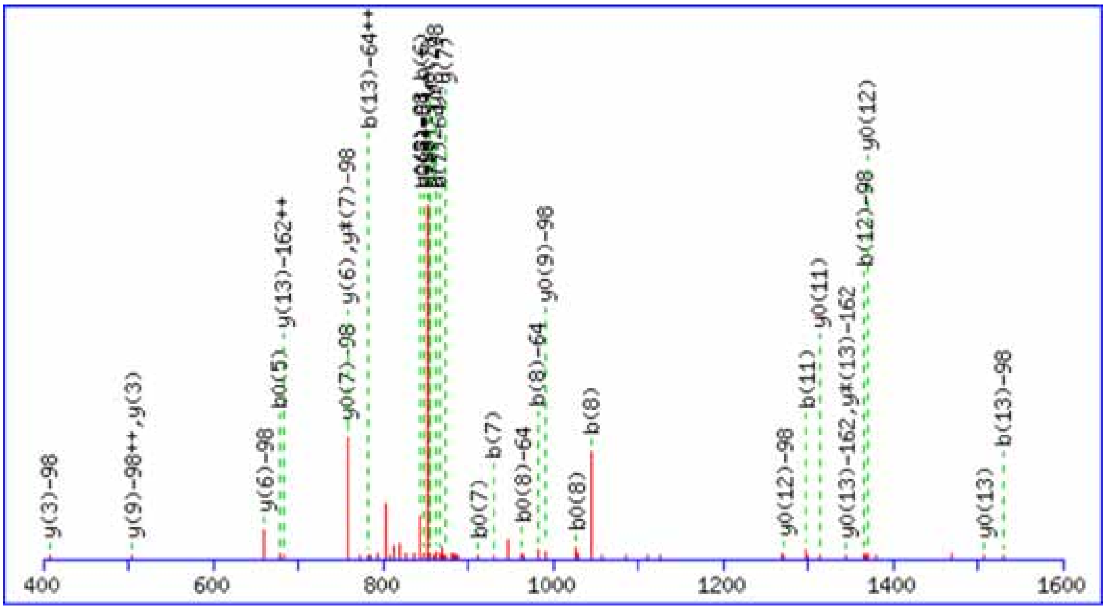
Matched b ions: b(4), b(5)-98, b(6)-98, b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(10)-98, b(11), b(11)-98, b(13)-98, b(13)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(12)-98++, y(12)-98, y(12), y(13)-98, y(13), y(13)++
Precursor origin neutral loss: +

Peptide No.1259

YHGHSMSDPGVSYR
Confirmed sites: @S:12
Ambiguous sites: @Y:1orS:5

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3015: 1801.675642 from(901.845097,2+)
Title: Elution from: 24.681 to 24.681 scan no 1398 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1801.6745
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
Y1 : Phospho (Y)
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.032

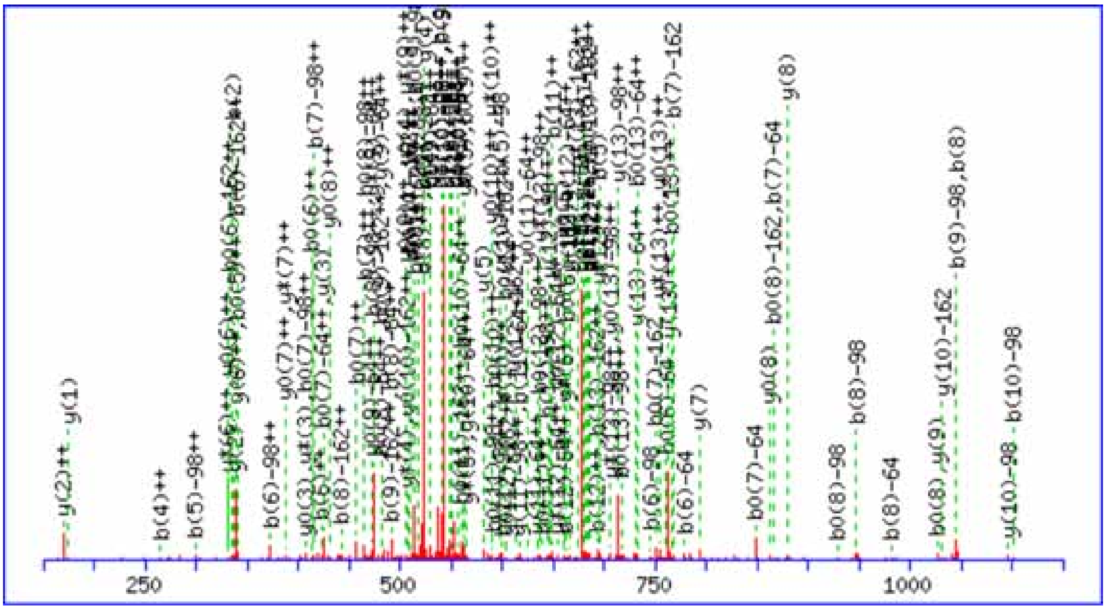
Matched b ions: b(6), b(7), b(8), b(11), b(12)-98, b(13)-98
Matched y ions: y(3), y(3)-98, y(6)-98, y(6), y(7), y(8)-98, y(9)-98++
Precursor origin neutral loss: +

Peptide No.1260

YHGHSMSDPGVSYR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 2858: 1721.709732 from(574.910520,3+)
Title: Elution from: 22.930 to 22.930 scan no 1241 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1721.7081
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 57 Expect: 4.8e-005

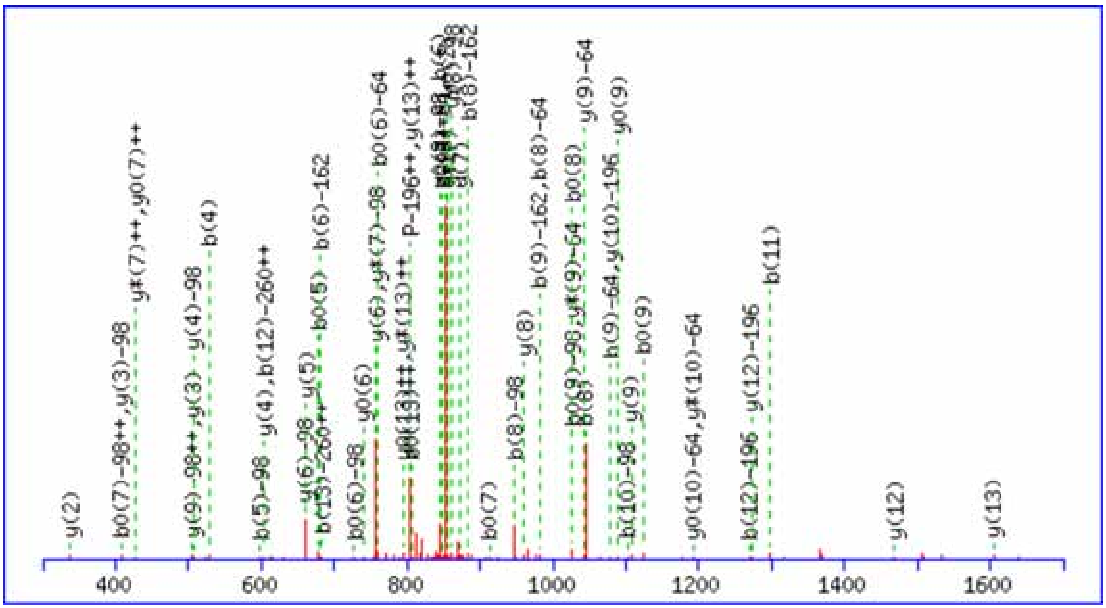
Matched b ions: b(2), b(4)++, b(4), b(5)-98, b(5)-98++, b(5), b(6)-98++, b(6)++, b(6)-98, b(7)-98++, b(7)++, b(8)-98, b(8), b(8)++, b(8)-98++, b(9)-98, b(9)-98++, b(10)-98, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)-98++, b(12)++
Matched y ions: y(1), y(2)++, y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(9)++, y(10)-98, y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1261

YHGHSMSDPGVSYR
Confirmed sites: @S:5,@S:12
Ambiguous sites:

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3407: 1801.674786 from(901.844669,2+)
Title: Elution from: 24.855 to 24.855 scan no 1448 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1801.6745
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 Expect: 0.00055

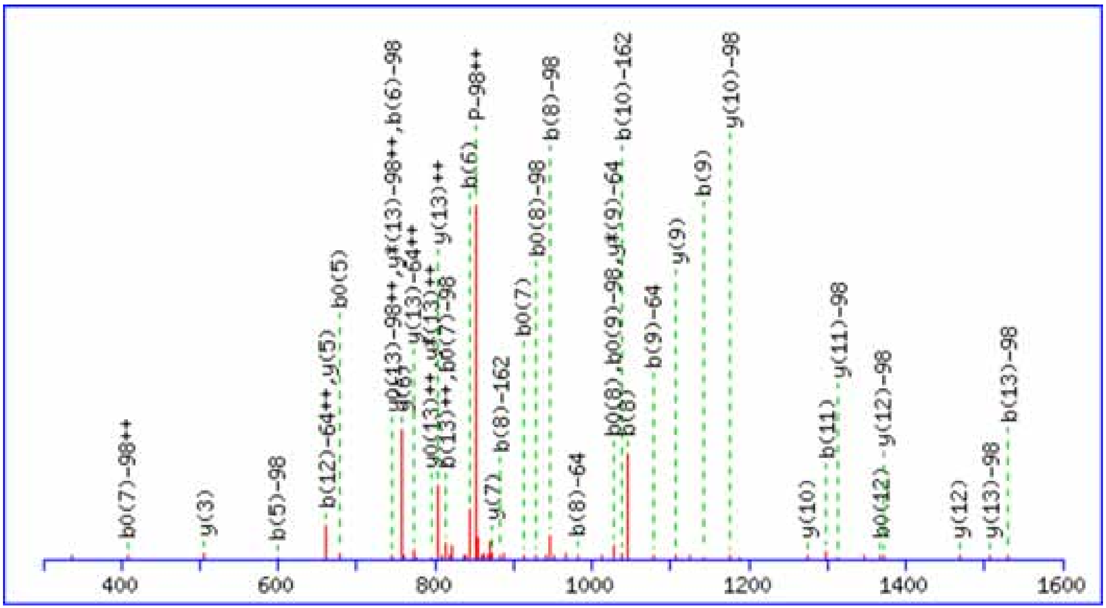
Matched b ions: b(4), b(5)-98, b(6), b(8)-98, b(8), b(10)-98, b(11), b(12)-98, b(12)-196, b(12)-98++
Matched y ions: y(2), y(3), y(3)-98, y(4), y(4)-98, y(5), y(6)-98, y(6), y(7), y(8), y(8)-98, y(9)-98++, y(9), y(10)-98, y(10)-196, y(12)-98, y(12)-196, y(12), y(13)-98, y(13), y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1262

YHGHSMSDPGVSYR
Confirmed sites: @S:5
Ambiguous sites: @S:12orY:13

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3631: 1801.675254 from(901.844903,2+)
Title: Elution from: 24.769 to 24.769 scan no 1438 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1801.6745
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y13 : Phospho (Y)
Ions Score: 40 **Expect:** 0.0015

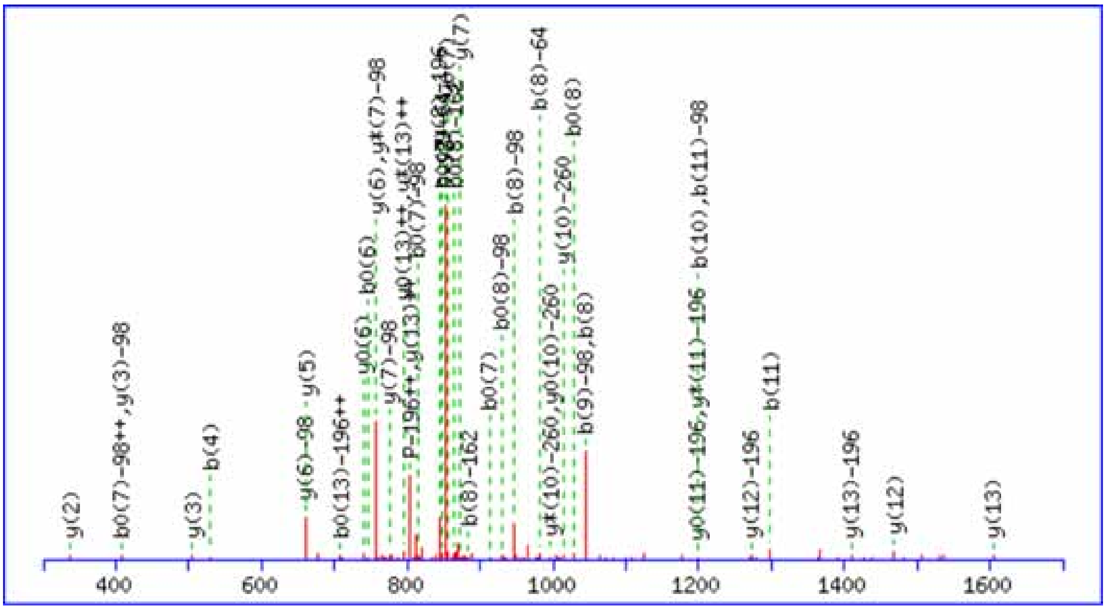
Matched b ions: b(5)-98, b(6), b(6)-98, b(8)-98, b(8), b(9), b(11), b(13)-98, b(13)++
Matched y ions: y(3), y(5), y(6), y(7), y(9), y(10)-98, y(10), y(11)-98, y(12)-98, y(12), y(13)++, y(13)-98
Precursor origin neutral loss: +

Peptide No.1263

YHGHSMSDPGVSYR
Confirmed sites: @S:7,@S:12
Ambiguous sites:

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3747: 1801.675896 from(901.845224,2+)
Title: Elution from: 24.849 to 24.849 scan no 1474 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1801.6745
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.0053

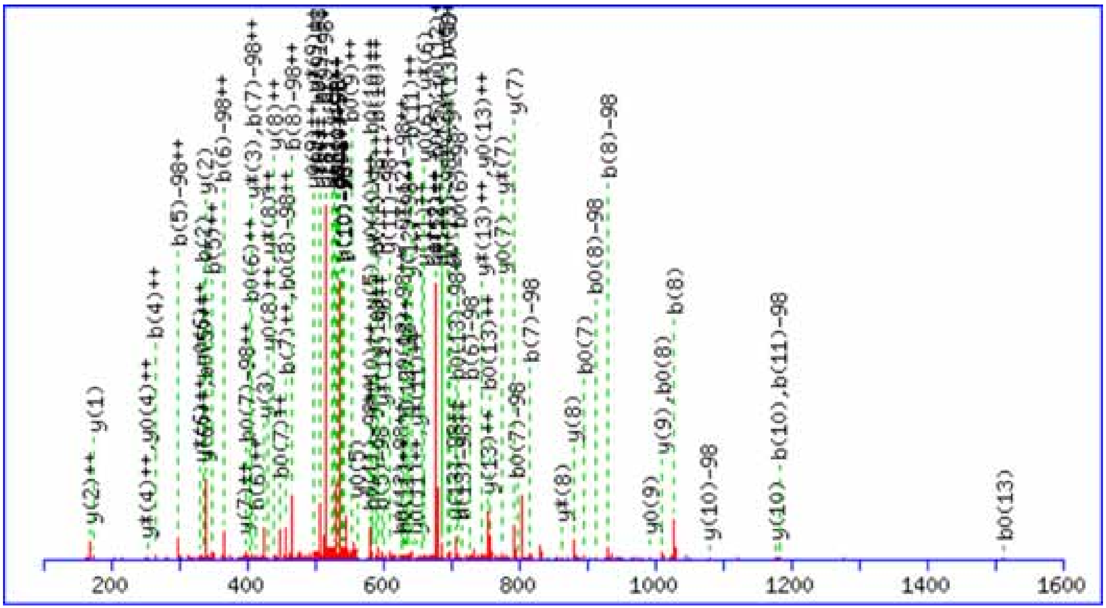
Matched b ions: b(4), b(8)-98, b(8), b(9)-98, b(10), b(11), b(11)-98, b(12)-98, b(13)-98, b(13)-98++
Matched y ions: y(2), y(3)-98, y(3), y(5), y(6)-98, y(6), y(7)-98, y(7), y(8)-196, y(10)-98, y(12), y(12)-196, y(13), y(13)++, y(13)-196, y(13)-98
Precursor origin neutral loss: +

Peptide No.1264

YHGHSMSDPGVSYR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of YHGHSMSDPGVSYR
Found in ODPA_MOUSE, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 4413: 1705.713660 from(569.578496,3+)
Title: Elution from: 27.202 to 27.202 scan no 1833 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1705.7132
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 Expect: 0.0018

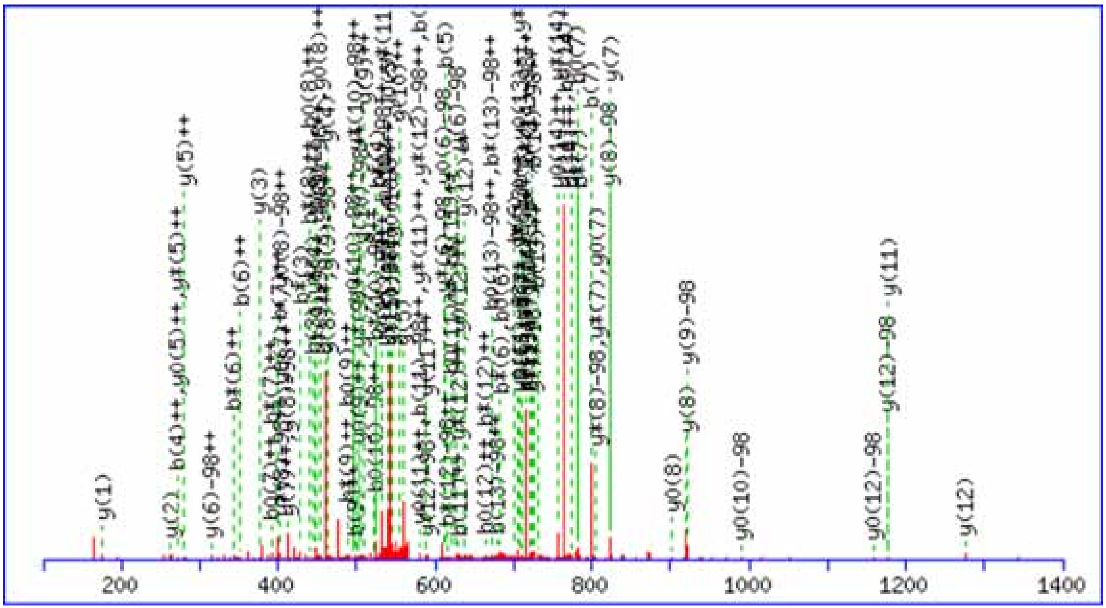
Matched b ions: b(2), b(4)++, b(4), b(5)-98++, b(5)++, b(5)-98, b(5), b(6)-98++, b(6)++, b(6)-98, b(7)++, b(7)-98++, b(7)-98, b(8)++, b(8), b(8)-98, b(8)-98++, b(9)-98++, b(10)++, b(10), b(10)-98++, b(11)-98++, b(11)++, b(11)-98, b(12)-98++, b(12)++, b(13)-98++
Matched y ions: y(1), y(2)++, y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)-98, y(10), y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++
Precursor origin neutral loss: +

Peptide No.1265

YPRPASVPPSPSLSR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 2965: 1717.856367 from(573.626065,3+)
Title: Elution from: 34.009 to 34.009 scan no 2647 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1717.8552
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.022

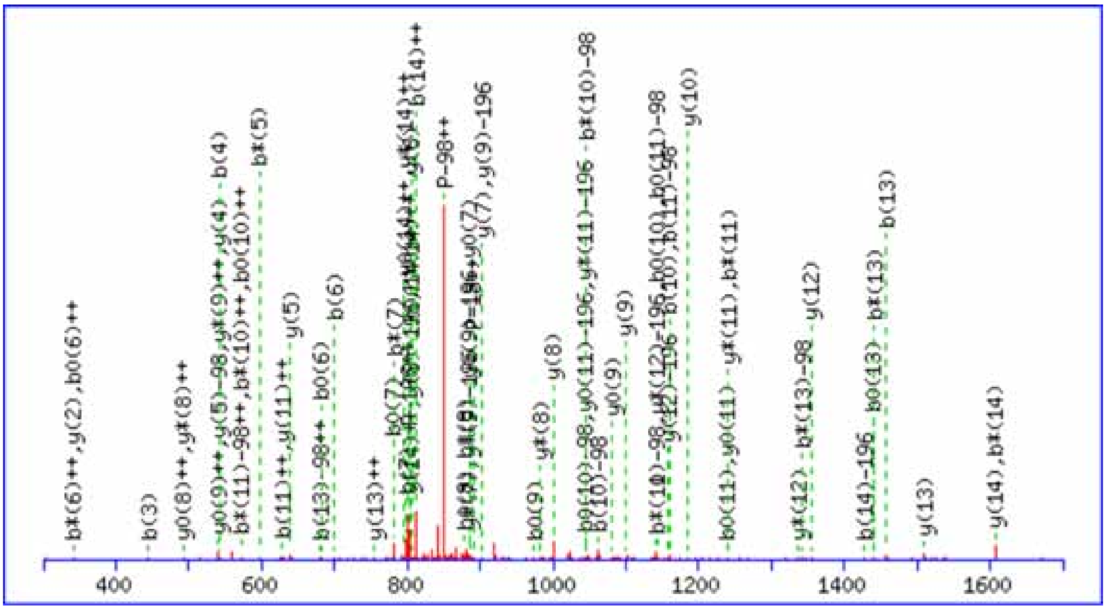
Matched b ions: b(3), b(4)++, b(4), b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6)-98++, y(6)-98, y(7)++, y(7)-98, y(7), y(8)++, y(8), y(8)-98++, y(8)-98, y(9)-98++, y(9)-98, y(9)++, y(10)-98++, y(10)++, y(11), y(11)-98++, y(11)++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13)++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1266

YPRPASVPPSPSLSR
Confirmed sites: @S:10,@S:14
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 3298: 1797.823246 from(899.918899,2+)
Title: Elution from: 36.565 to 36.565 scan no 2983 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1797.8216
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.043

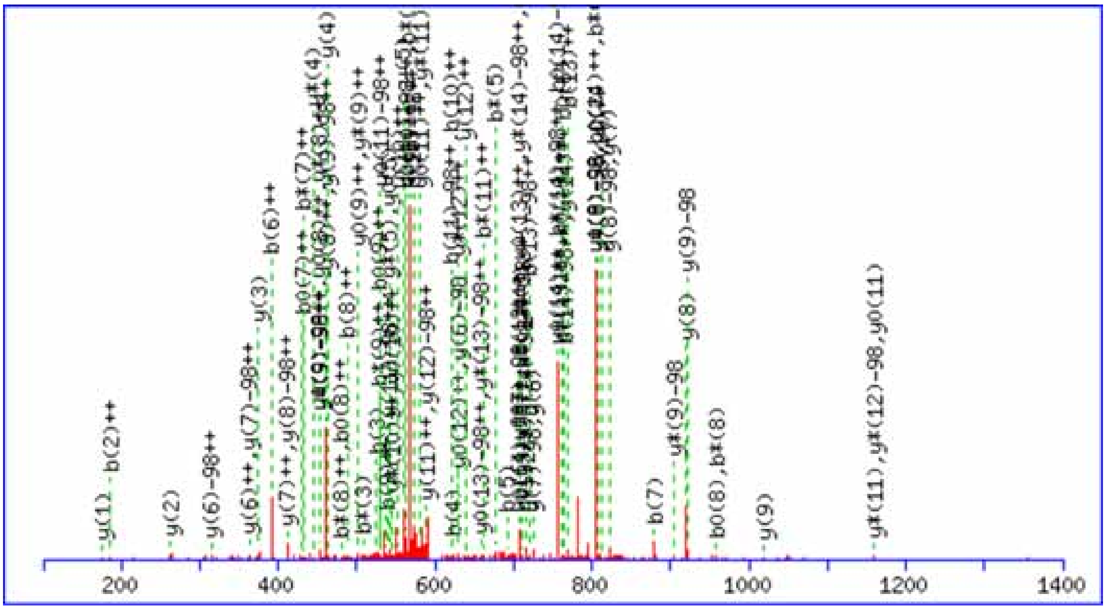
Matched b ions: b(3), b(4), b(6), b(7), b(10)-98, b(10), b(11)-98, b(11)++, b(13), b(13)-98++, b(14)-196, b(14)-98, b(14)++
Matched y ions: y(2), y(4), y(5)-98, y(5), y(6)-98, y(6), y(7)-98, y(7), y(8), y(8)-196, y(8)-98, y(9)-98, y(9)-196, y(9), y(10)-98, y(10), y(11)-98, y(11)++, y(12), y(12)-98++, y(12)-98, y(12)-196, y(13), y(13)++, y(14)-98, y(14), y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1267

YPRPASVPPSPSLSR
Confirmed sites: @Y:1,@S:10
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 2971: 1797.822402 from(600.281410,3+)
Title: Elution from: 41.309 to 41.309 scan no 3533 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1797.8216
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
Y1 : Phospho (Y)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 Expect: 0.01

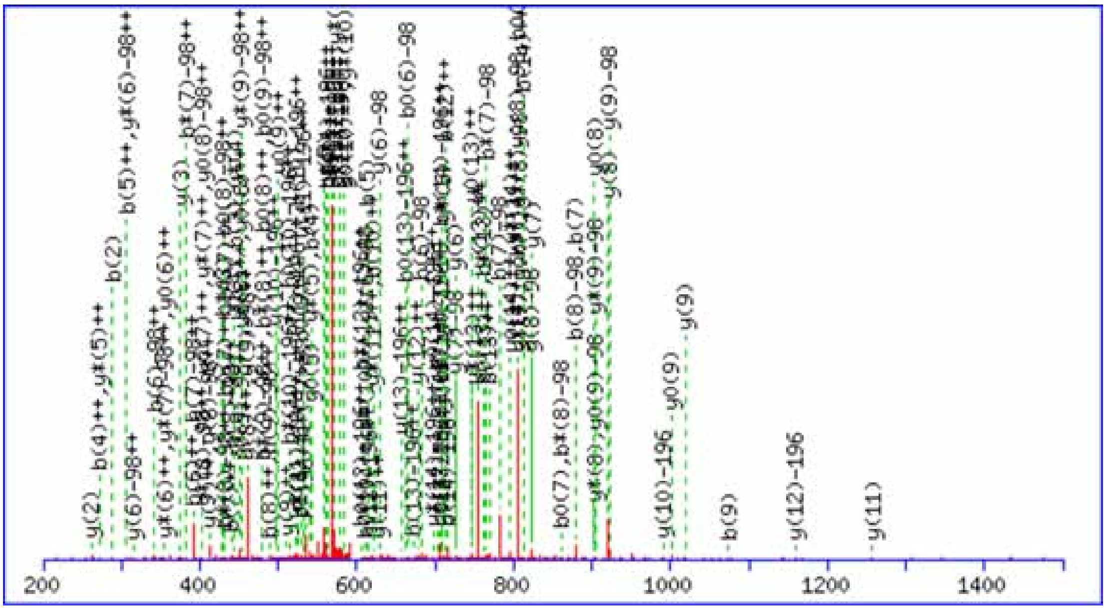
Matched b ions: b(2)++, b(3), b(4), b(5), b(6)++, b(7), b(8)++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)-98++, y(6)++, y(6), y(6)-98, y(7)++, y(7)-98++, y(7)-98, y(7), y(8)++, y(8), y(8)-98++, y(8)-98, y(9)-98++, y(9), y(9)-98, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(14)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1268

YPRPASVPPSPSLSR
Confirmed sites: @S:6,@S:10
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 3373: 1797.823014 from(600.281614,3+)
Title: Elution from: 34.633 to 34.633 scan no 2733 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1797.8216
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.0011

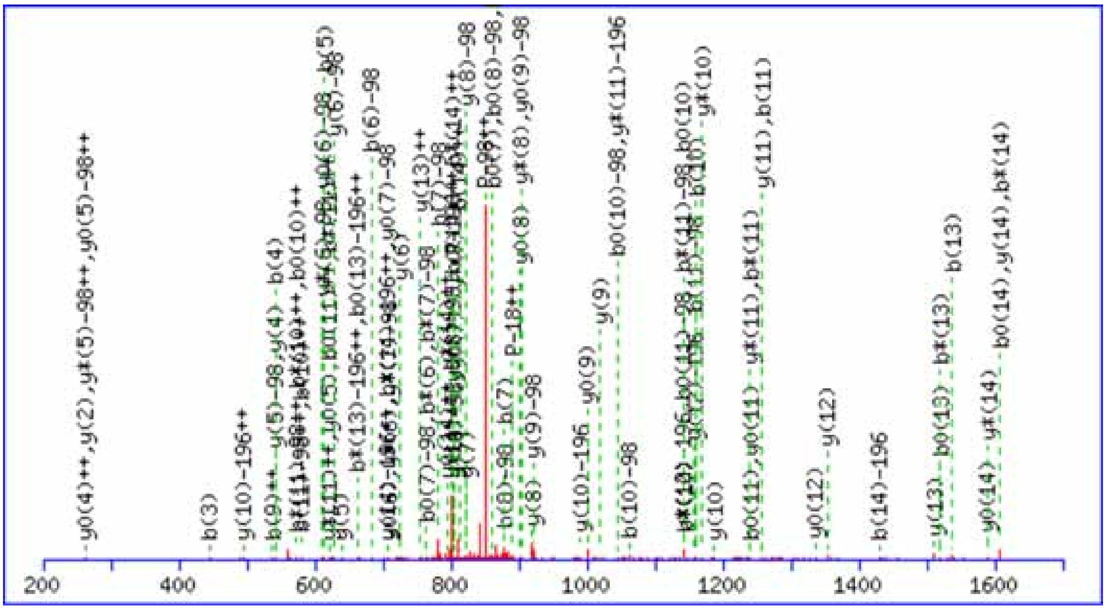
Matched b ions: b(2), b(3), b(4)++, b(4), b(5)++, b(5), b(6)++, b(6)-98, b(6)-98++, b(7)-98++, b(7), b(7)-98, b(7)++, b(8)-98, b(8)-98++, b(8)++, b(9)-98++, b(9), b(10)-98++, b(10)-98, b(10)-196++, b(10)++, b(11)-196++, b(12)-196++, b(12)-98++, b(12)++, b(13)++, b(13)-196++, b(13)-98++, b(14)-196++, b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(5), y(6)-98++, y(6)-98, y(6), y(7)++, y(7), y(7)-98, y(8)++, y(8), y(8)-98++, y(8)-98, y(9)-98++, y(9), y(9)-98, y(9)++, y(10)-196++, y(10)-98++, y(10)-196, y(11)-98, y(11), y(11)-98++, y(11)-196++, y(11)++, y(12)-196, y(12)-98, y(12)-98++, y(12)-196++, y(12)++, y(13)-98++, y(13)++, y(13)-196++, y(14)-196++, y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1269

YPRPASVPPSPSLSR
Confirmed sites: @S:6,@S:12
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 4924: 1797.821720 from(899.918136,2+)
Title: Elution from: 34.258 to 34.258 scan no 2818 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1797.8216
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 Expect: 2.5e-005

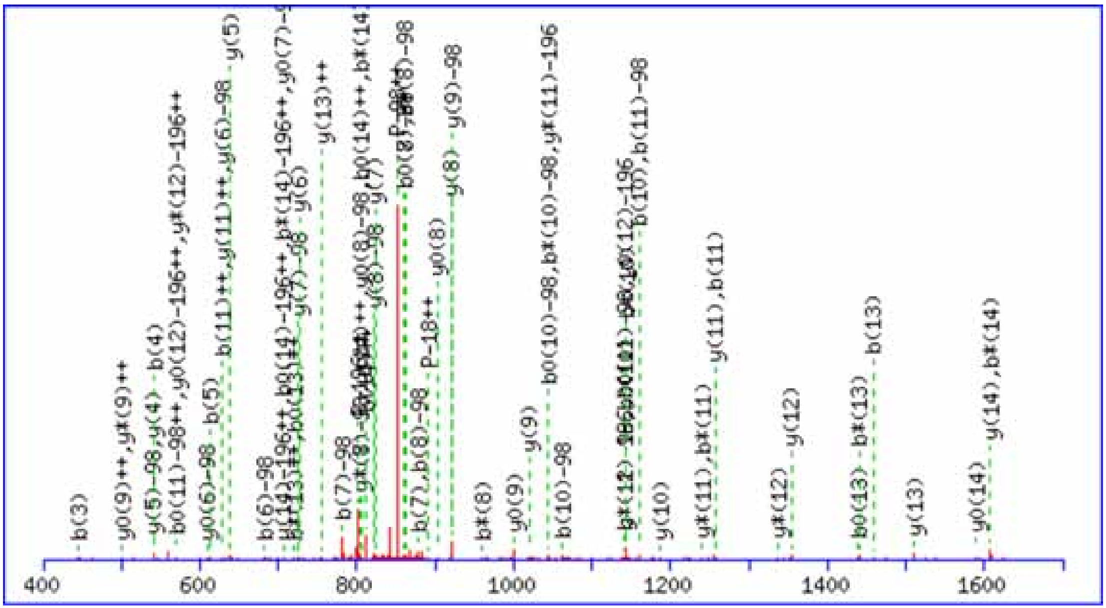
Matched b ions: b(3), b(4), b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(9)++, b(10)-98, b(10)++, b(10), b(11), b(11)-98++, b(11)-98, b(12)-98, b(13)-98, b(13), b(13)-98++, b(14)-196, b(14)-98++, b(14)++
Matched y ions: y(2), y(4), y(5)-98, y(5), y(6)-98, y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-196, y(10)-196++, y(10)-98, y(11), y(11)-98++, y(11)-98, y(12), y(12)-98++, y(12)-98, y(12)-196, y(13)++, y(13), y(13)-98++, y(14)-98, y(14), y(14)-98++, y(14)-196++, y(14)++
Precursor origin neutral loss: +

Peptide No.1270

YPRPASVPPSPSLSR
Confirmed sites: @S:6,@S:14
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 2977: 1797.822690 from(899.918621,2+)
Title: Elution from: 37.051 to 37.051 scan no 2959 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1797.8216
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.002

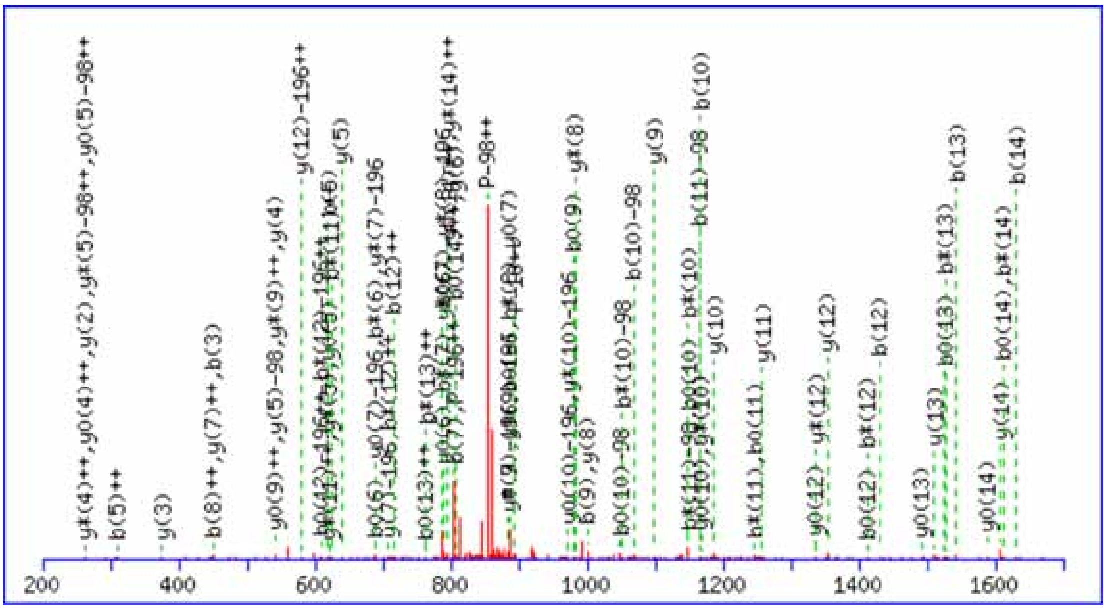
Matched b ions: b(3), b(4), b(5), b(6)-98, b(7), b(7)-98, b(8)-98, b(10), b(10)-98, b(11)-98, b(11), b(11)++, b(13), b(14)++
Matched y ions: y(4), y(5)-98, y(5), y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(11), y(11)++, y(12)-98, y(12), y(12)-98++, y(13), y(13)-98++, y(13)++, y(14)-98, y(14), y(14)-196++, y(14)++
Precursor origin neutral loss: +

Peptide No.1271

YPRPASVPPSPSLSR
Confirmed sites: @S:10,@S:12
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 3653: 1803.854710 from(902.934631,2+)
Title: Elution from: 34.265 to 34.265 scan no 2685 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1803.8534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.032

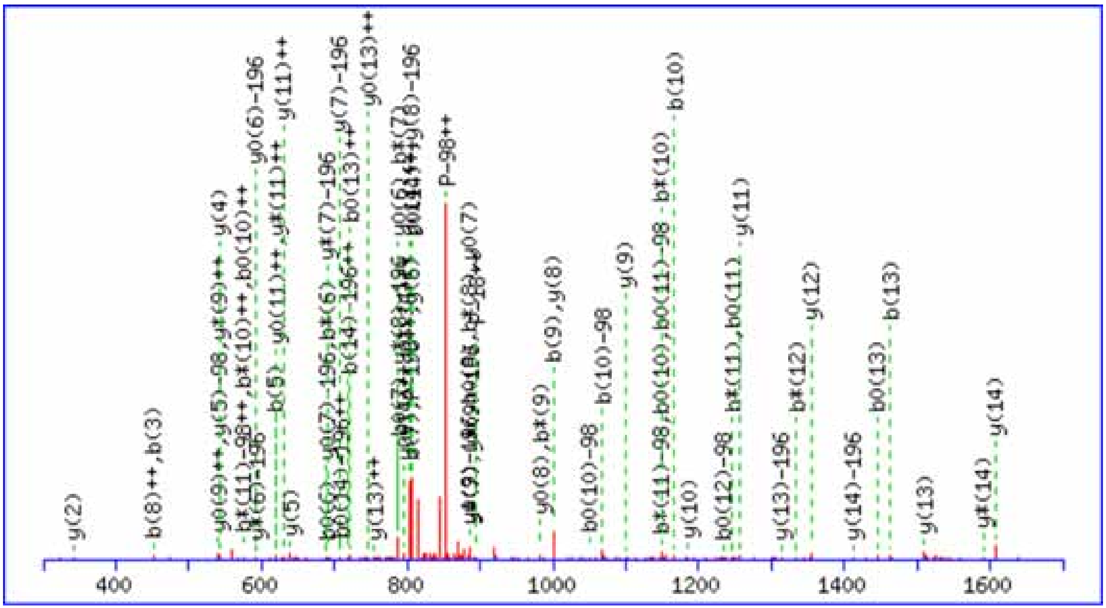
Matched b ions: b(3), b(5)++, b(5), b(7), b(8)++, b(9), b(10)-98, b(10), b(11)-98, b(12), b(12)++, b(13), b(13)-98, b(14), b(14)-98
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6)-98, y(6), y(7)++, y(7)-98, y(7)-196, y(8)-98++, y(8), y(9)-98, y(9), y(10), y(10)-98, y(11)-98++, y(11), y(12), y(12)-98, y(12)-196++, y(13)-98, y(13), y(14), y(14)-98
Precursor origin neutral loss: +

Peptide No.1272

YPRPASVPPSPSLSR
Confirmed sites: @S:10,@S:14
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 4997: 1803.854890 from(902.934721,2+)
Title: Elution from: 36.464 to 36.464 scan no 3134 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1803.8534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.0018

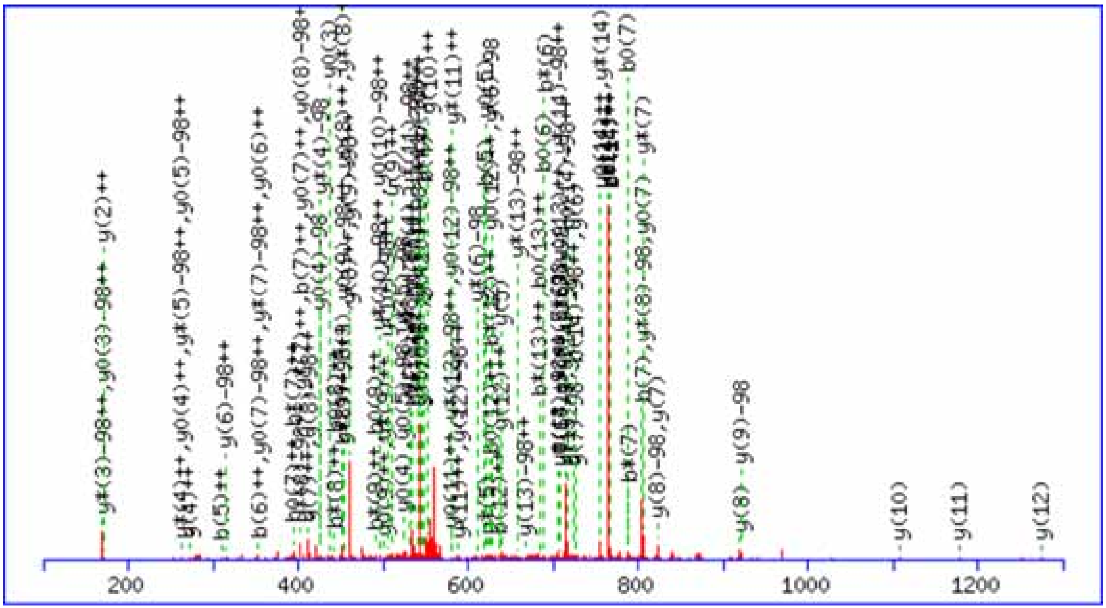
Matched b ions: b(3), b(5), b(7), b(8)++, b(9), b(10)-98, b(10), b(13), b(14)-98, b(14)-196++
Matched y ions: y(2), y(4), y(5), y(5)-98, y(6), y(6)-98, y(7)-98, y(7)-196, y(8)-98++, y(8), y(8)-196, y(9)-98, y(9), y(10), y(11), y(11)++, y(12)-98, y(12), y(12)-98++, y(13), y(13)-98++, y(13)-98, y(13)++, y(13)-196, y(14)-98, y(14), y(14)++, y(14)-196, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1273

YPRPASVPPSPSLSR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 3325: 1723.888455 from(575.636761,3+)
Title: Elution from: 34.124 to 34.124 scan no 2700 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1723.8871
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.012

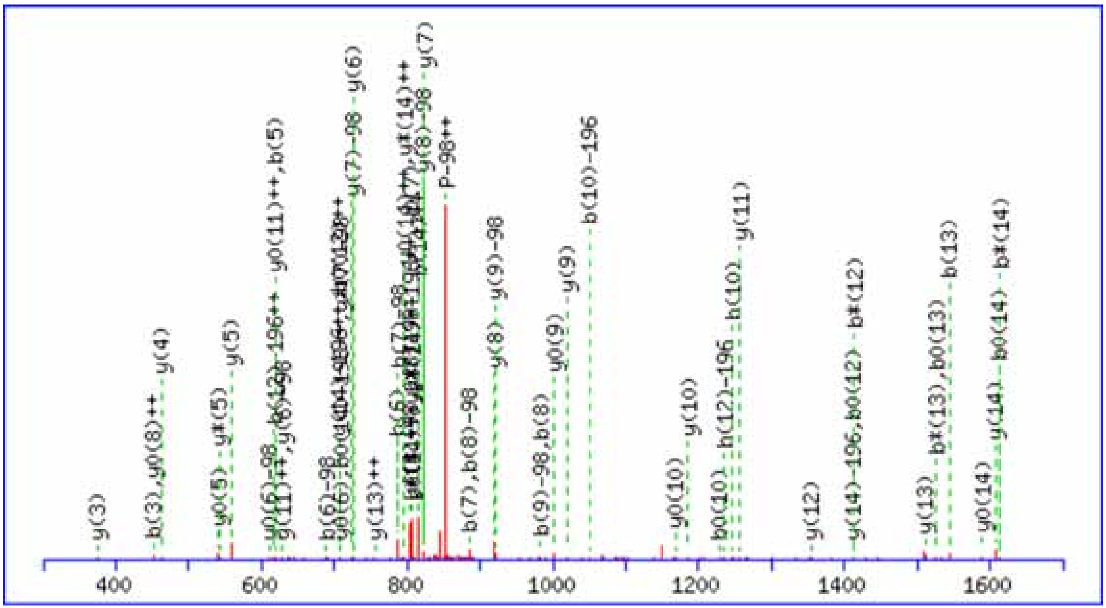
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7), b(7)++, b(8)++, b(10)++, b(12)++, b(14)-98++
Matched y ions: y(2)++, y(4), y(4)++, y(5), y(5)-98, y(6)-98++, y(6)-98, y(6), y(7)++, y(7), y(7)-98, y(8)++, y(8)-98++, y(8), y(8)-98, y(9)-98++, y(9)-98, y(9)++, y(10), y(10)++, y(10)-98++, y(11), y(11)-98++, y(11)++, y(12), y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1274

YPRPASVPPSPSLSR
Confirmed sites: @S:6,@S:10
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 3409: 1803.855744 from(902.935148,2+)
Title: Elution from: 35.479 to 35.479 scan no 2840 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1803.8534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 Expect: 0.00013

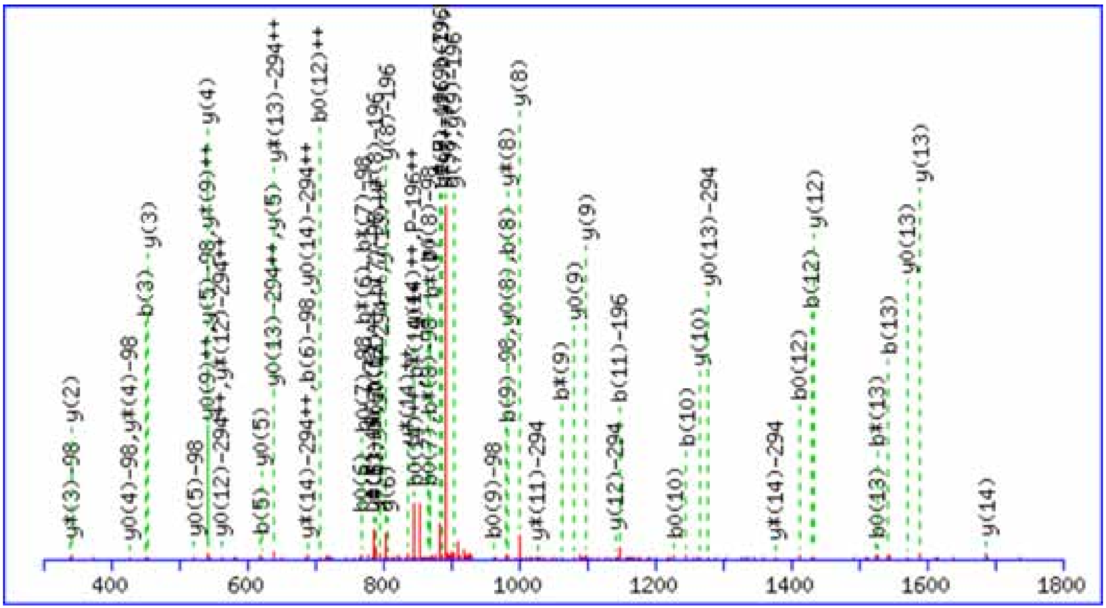
Matched b ions: b(3), b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(10)-98, b(10), b(10)-196, b(11)-98, b(12)-98, b(12)-196++, b(12)-196, b(13), b(13)-98, b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(11)++, y(11), y(12), y(12)-98++, y(12)-98, y(13)-98, y(13)++, y(13), y(13)-98++, y(14)-98, y(14), y(14)-196, y(14)-98++, y(14)++, y(14)-196++
Precursor origin neutral loss: +

Peptide No.1275

YPRPASVPPSPSLSR
Confirmed sites: @S:6,@S:10,@S:14
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 4009: 1883.819750 from(942.917151,2+)
Title: Elution from: 37.731 to 37.731 scan no 3149 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1883.8197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.011

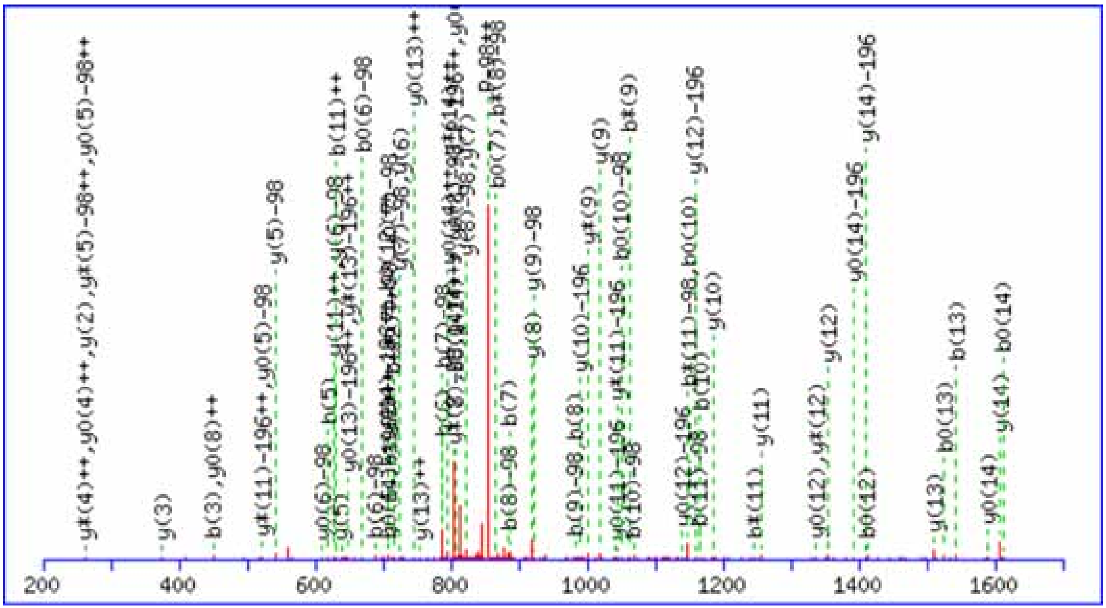
Matched b ions: b(3), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(10)-98, b(10), b(11)-196, b(12), b(13), b(13)-98++, b(14)-196, b(14)-98, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6), y(7)-98, y(7), y(8), y(8)-98++, y(8)-196, y(8)-98, y(9), y(9)-98, y(9)-196, y(10), y(10)-98, y(11)-98++, y(11)-196, y(12)-98, y(12)-196++, y(12), y(12)-294, y(13), y(13)++, y(13)-98++, y(14)-98, y(14), y(14)++, y(14)-98++, y(14)-196, y(14)-196++
Precursor origin neutral loss: +

Peptide No.1276

YPRPASVPPSPSLSR
Confirmed sites: @S:6,@S:12
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 3335: 1803.854272 from(902.934412,2+)
Title: Elution from: 35.661 to 35.661 scan no 2862 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1803.8534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 Expect: 0.0036

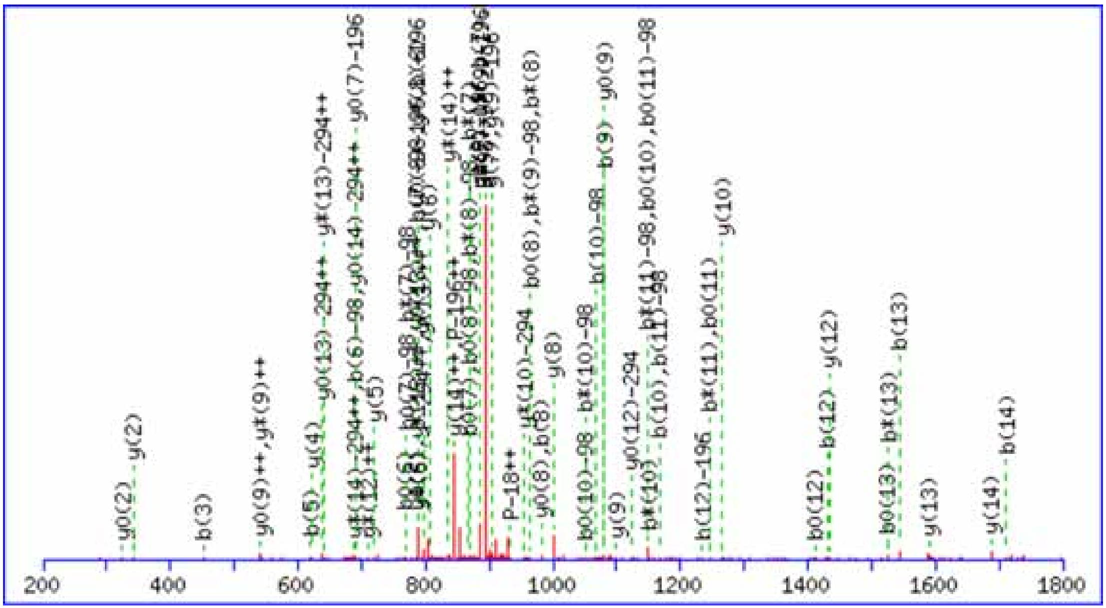
Matched b ions: b(3), b(5), b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(10)-98, b(10), b(11)++, b(11)-98, b(12)-98, b(12)++, b(13)-98, b(13), b(14)-98
Matched y ions: y(2), y(3), y(5), y(5)-98, y(6), y(6)-98, y(7)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-196, y(10)-98, y(10), y(11)-98, y(11)++, y(11), y(12)-98, y(12), y(12)-196, y(12)-98++, y(13)-98++, y(13)-98, y(13), y(13)++, y(14)-196++, y(14)-98, y(14), y(14)++, y(14)-196, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1277

YPRPASVPPSPSLSR
Confirmed sites: @S:6,@S:12,@S:14
Ambiguous sites:

MS/MS Fragmentation of YPRPASVPPSPSLSR
Found in GYS1_MOUSE, Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2

Match to Query 4487: 1883.821056 from(942.917804,2+)
Title: Elution from: 37.774 to 37.774 scan no 3205 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1883.8197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.032

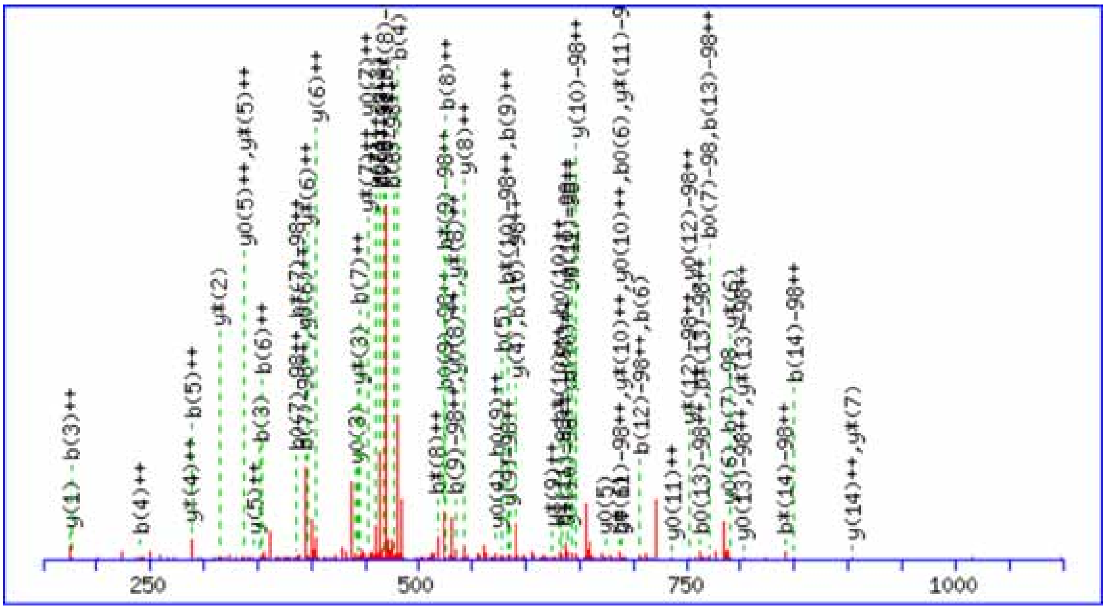
Matched b ions: b(3), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(10), b(10)-98, b(11)-98, b(12)-196, b(12), b(13)-98, b(13), b(14)-98, b(14), b(14)-98++
Matched y ions: y(2), y(4), y(5)-98, y(5), y(6), y(7)-98, y(7), y(8)-98++, y(8), y(8)-98, y(9)-98, y(9)-196, y(9), y(10)-196, y(10)-98, y(10), y(11)-98++, y(12)-98, y(12), y(12)-196++, y(13), y(13)-98, y(13)++, y(14)++, y(14), y(14)-98, y(14)-98++
Precursor origin neutral loss: +

Peptide No.1278

YSTEPKTYIDTMEKK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of YSTEPKTYIDTMEKK
Found in ZN654_MOUSE, Zinc finger protein 654 OS=Mus musculus GN=Znf654 PE=1 SV=2

Match to Query 4678: 1968.910184 from(493.234822,4+)
Title: Elution from: 27.227 to 27.227 scan no 1745 cid35.00 polarity:+:MA10



Monoisotopic mass of neutral peptide Mr(calc): 1968.9155
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
K14 : Dimethyl (K)
K15 : Dimethyl (K)
Ions Score: 34 Expect: 0.025

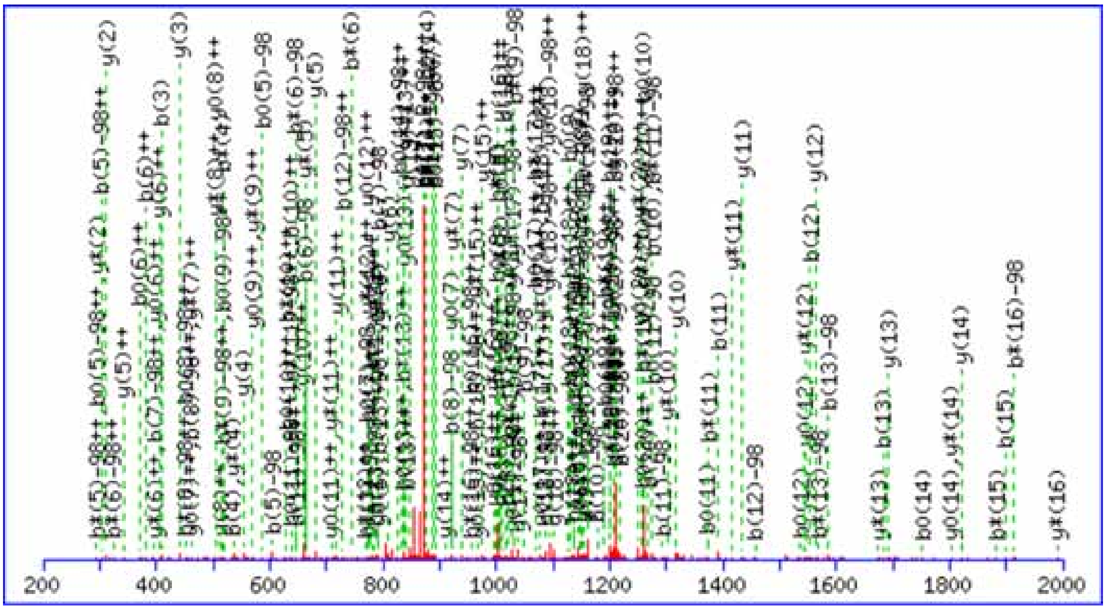
Matched b ions: b(3)++, b(3), b(4), b(4)++, b(5)++, b(5), b(6)++, b(6), b(7)-98++, b(7)-98, b(7)++, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(12)-98++, b(13)-98++, b(14)-98++
Matched y ions: y(1), y(3), y(4), y(5)++, y(6)++, y(7)++, y(8)++, y(9)-98++, y(9)++, y(10)-98++, y(14)++
Precursor origin neutral loss: +

Peptide No.1279

YTDQSGEEEEDYESEEQLQHR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of YTDQSGEEEEDYESEEQLQHR
Found in COQ9_MOUSE, Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Mus musculus GN=Coq9 PE=1 SV=1

Match to Query 7238: 2708.039709 from(903.687179,3+)
Title: Elution from: 36.331 to 36.331 scan no 3003 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2708.0399
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 Expect: 2.4e-007

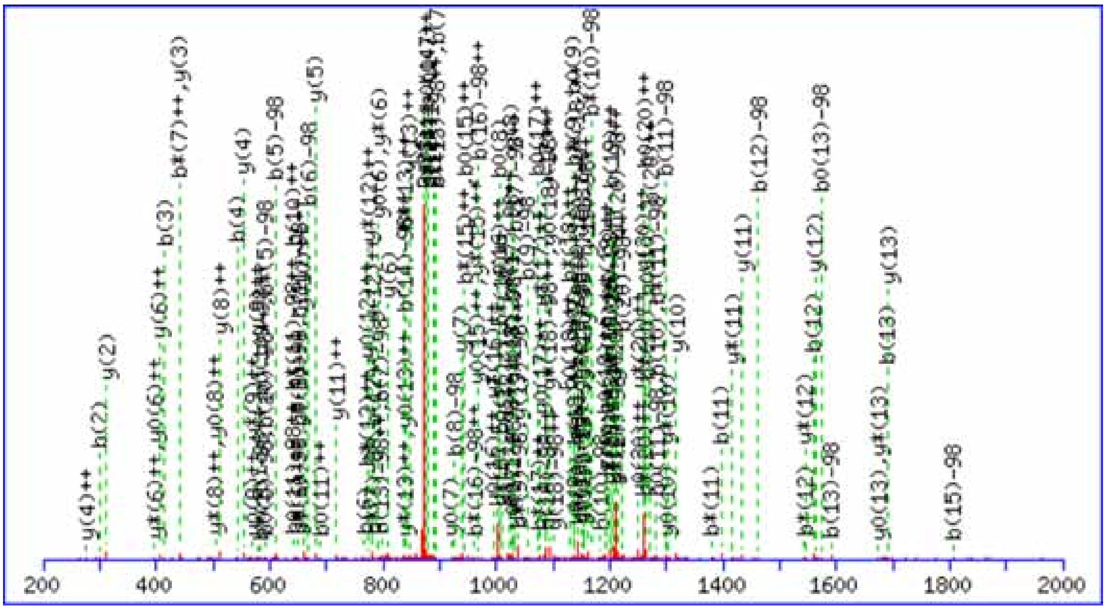
Matched b ions: b(3), b(4), b(5)-98++, b(5)-98, b(6)-98, b(6)++, b(7)-98++, b(7)-98, b(7), b(8)-98, b(8)-98++, b(8), b(9)-98, b(9), b(10)++, b(10)-98, b(10), b(11), b(11)-98++, b(11)-98, b(12)-98, b(12), b(12)-98++, b(12)++, b(13)-98, b(13), b(13)-98++, b(13)++, b(14)++, b(15), b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-98++, b(20)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6)++, y(6), y(7), y(8)++, y(8), y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13), y(13)++, y(14), y(14)++, y(15)++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)-98++, y(20)++
Precursor origin neutral loss: +

Peptide No.1280

YTDQSGEEEEDYESEEQLQHR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of YTDQSGEEEEDYESEEQLQHR
Found in COQ9_MOUSE, Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Mus musculus GN=Coq9 PE=1 SV=1

Match to Query 8556: 2714.072940 from(905.698256,3+)
Title: Elution from: 36.271 to 36.271 scan no 3106 cid35.00 polarity:+:MA10:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2714.0717
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Dimethyl:2H(4)13C(2) (N-term)
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 **Expect:** 9.9e-006

Matched b ions: b(2), b(3), b(4), b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98++, b(10)++, b(10)-98, b(11), b(11)-98, b(11)-98++, b(12), b(12)-98, b(12)++, b(13)-98, b(13), b(13)-98++, b(14)-98++, b(14)++, b(15)-98, b(16)-98++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6)++, y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13), y(13)++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++
Precursor origin neutral loss: +
