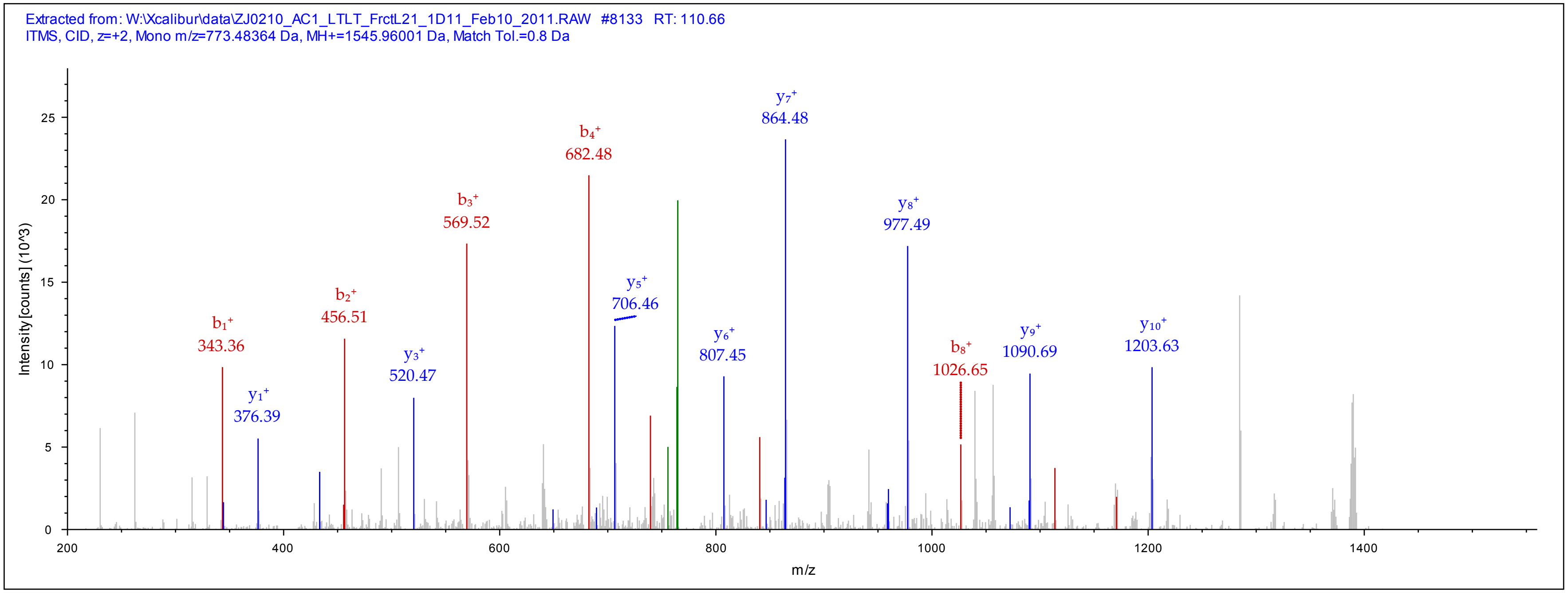
Annotated spectra for proteins identified on the basis of one unique peptide spectrum

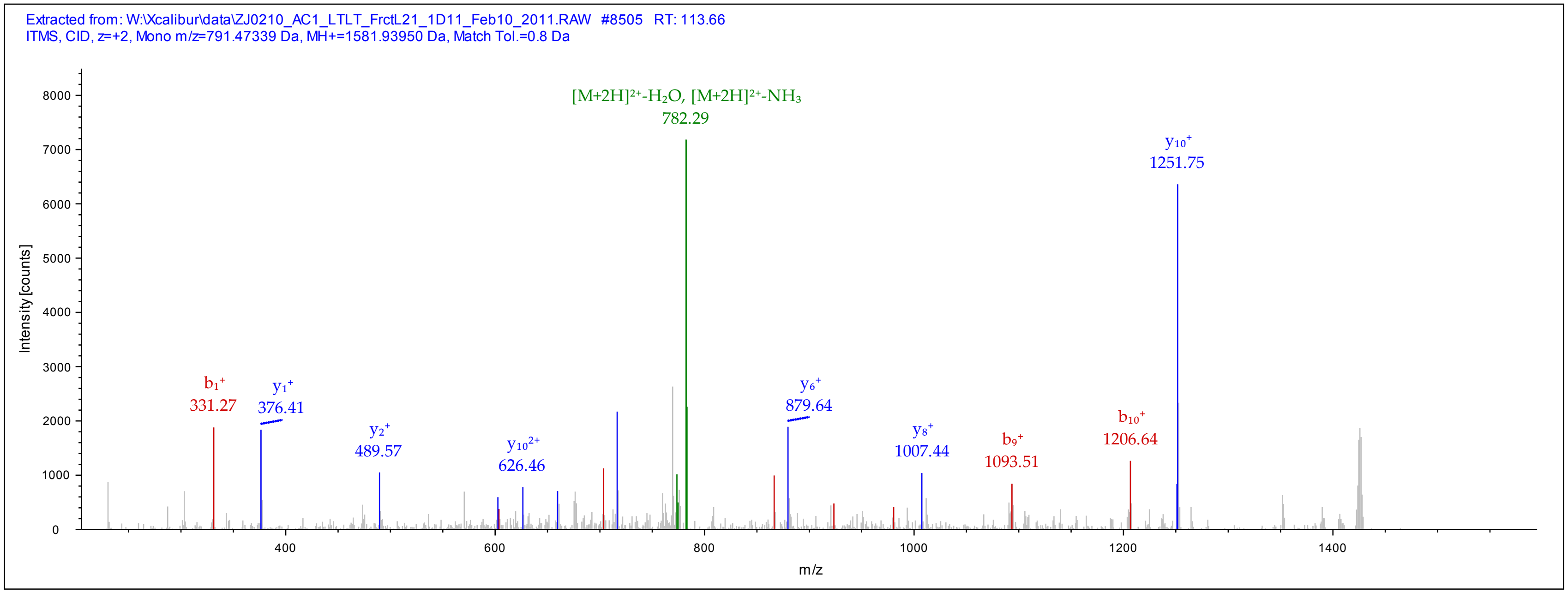
IPI:IPI00000695.1
Sequence: LLLLGTGESGK
L1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)
Charge: +2,   Monoisotopic m/z: 773.48364 Da (-0.83 mmu/-1.08 ppm),   MH+: 1545.96001 Da,   RT: 110.66 min,
Identified with: Mascot (v1.16); IonScore:46, Exp Value:1.4E-003, Matched Ions: 8/86
Fragment Match Tolerance: 0.8 Da

Protein References (3):
- Guanine nucleotide-binding protein subunit alpha-14
- Guanine nucleotide-binding protein subunit alpha-11
- Guanine nucleotide-binding protein G(q) subunit alpha



IPI:IPI00001539.8
Sequence: TPFGAYGGLLK, T1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)
Charge: +2,   Monoisotopic m/z: 791.47339 Da (-0.52 mmu/-0.65 ppm),   MH+: 1581.93950 Da,   RT: 113.66 min,
Identified with: Mascot (v1.16); IonScore:35, Exp Value:2.4E-002, Ions matched by search engine: 9/80
Fragment match tolerance used for search: 0.8 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- 3-ketoacyl-CoA thiolase, mitochondrial
- Putative uncharacterized protein ACAA2 (Fragment) lng=397



IPI:IPI00001593.1

Sequence: NALDPMSVLLAR, N1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 764.94006 Da (+0.45 mmu/+0.59 ppm), MH+: 1528.87285 Da, RT: 124.84 min,

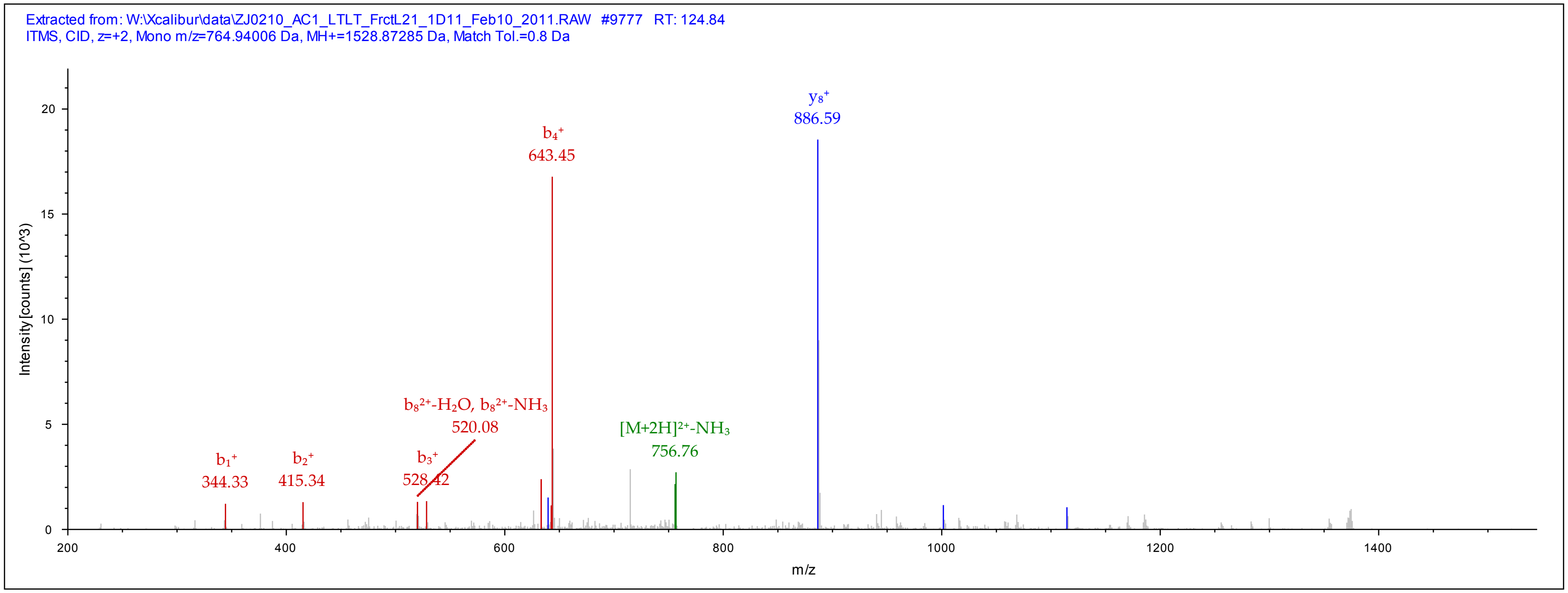
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.8E-002, Ions matched by search engine: 9/116

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Lysosomal Pro-X carboxypeptidase
- lysosomal Pro-X carboxypeptidase isoform 2 preproprotein



IPI:IPI00930609.1

Sequence: ALELNMLSLK, A1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 795.48840 Da (-0.3 mmu/-0.38 ppm),   MH+: 1589.96953 Da,   RT: 123.47 min,

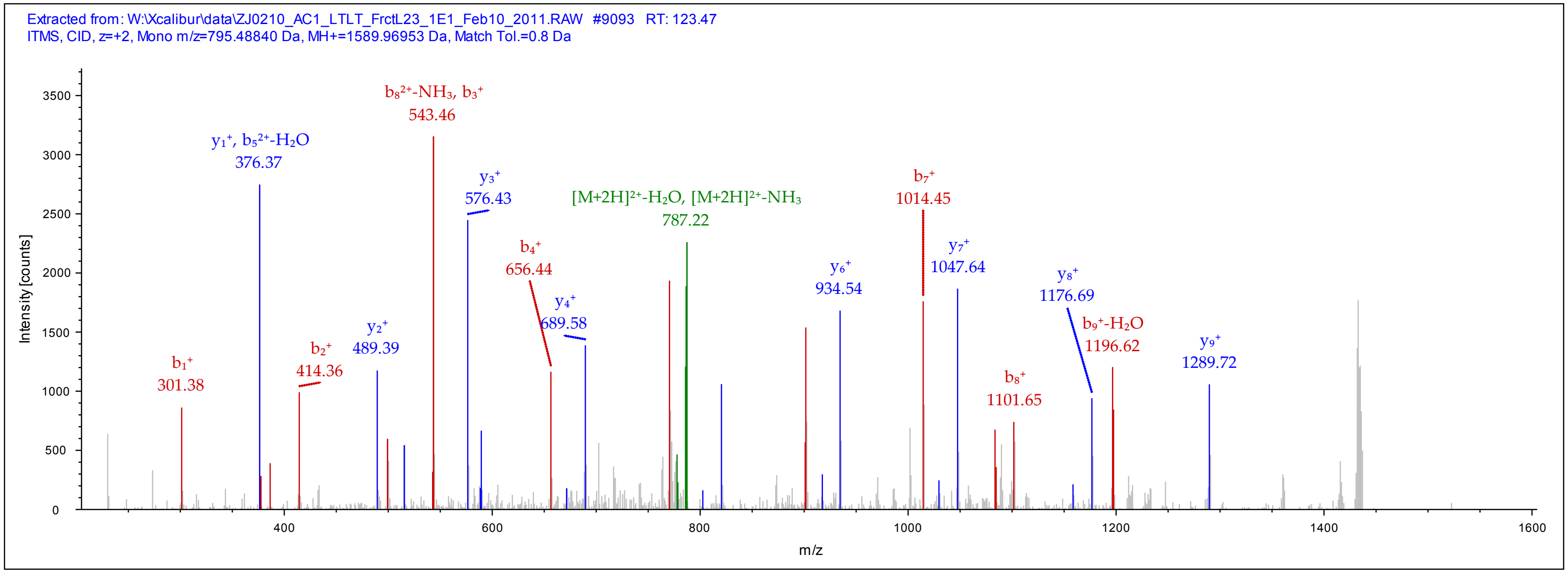
Identified with: Mascot (v1.16); IonScore:63, Exp Value:3.2E-005, Ions matched by search engine: 16/92

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3.

Protein references (2):

- Isoform 1 of Phosphoserine aminotransferase
- Phosphoserine aminotransferase



IPI:IPI00002280.1

Sequence: VLAQLLR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 521.35315 Da (+0.4 mmu/+0.77 ppm), MH+: 1041.69902 Da, RT: 108.61 min,

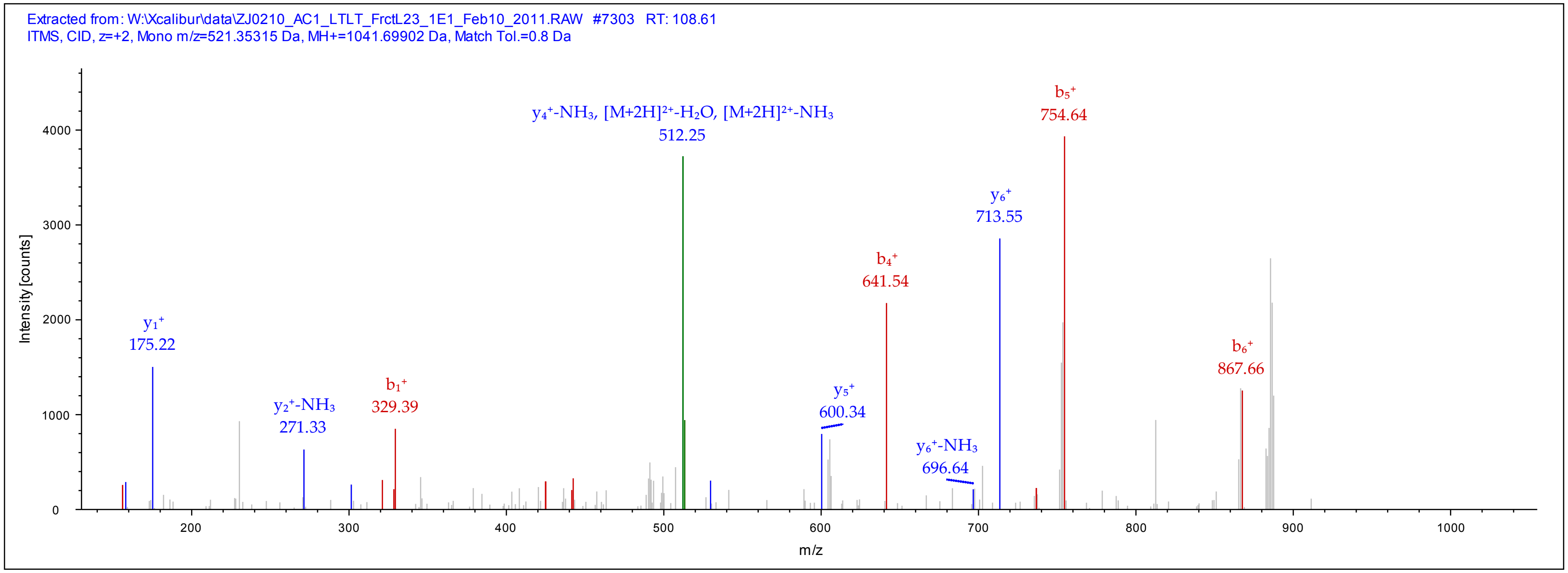
Identified with: Mascot (v1.16); IonScore:34, Exp Value:4.4E-003, Ions matched by search engine: 5/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- ProSAAS
- Complement component C1q receptor
- cDNA FLJ60144, highly similar to Complement component C1q receptor



IPI:IPI00003833.3

Sequence: EEGILGFFAGLVPR, E1-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 578.66565 Da (+1.18 mmu/+2.04 ppm), MH+: 1733.98239 Da, RT: 209.39 min,

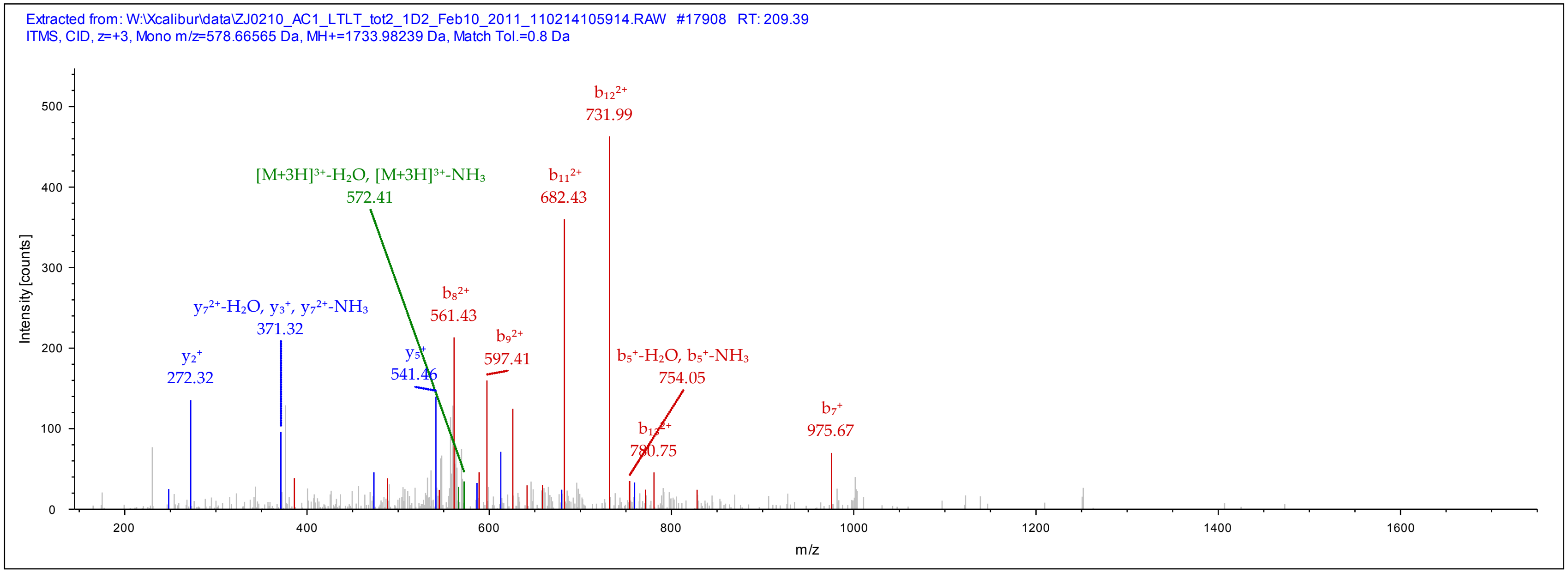
Identified with: Mascot (v1.16); IonScore:31, Exp Value:8.0E-002, Ions matched by search engine: 14/106

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Mitochondrial carrier homolog 2



IPI:IPI00004839.1

Sequence: IFDPQNPDENE, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 773.86664 Da (+1.83 mmu/+2.36 ppm), MH+: 1546.72600 Da, RT: 94.83 min,

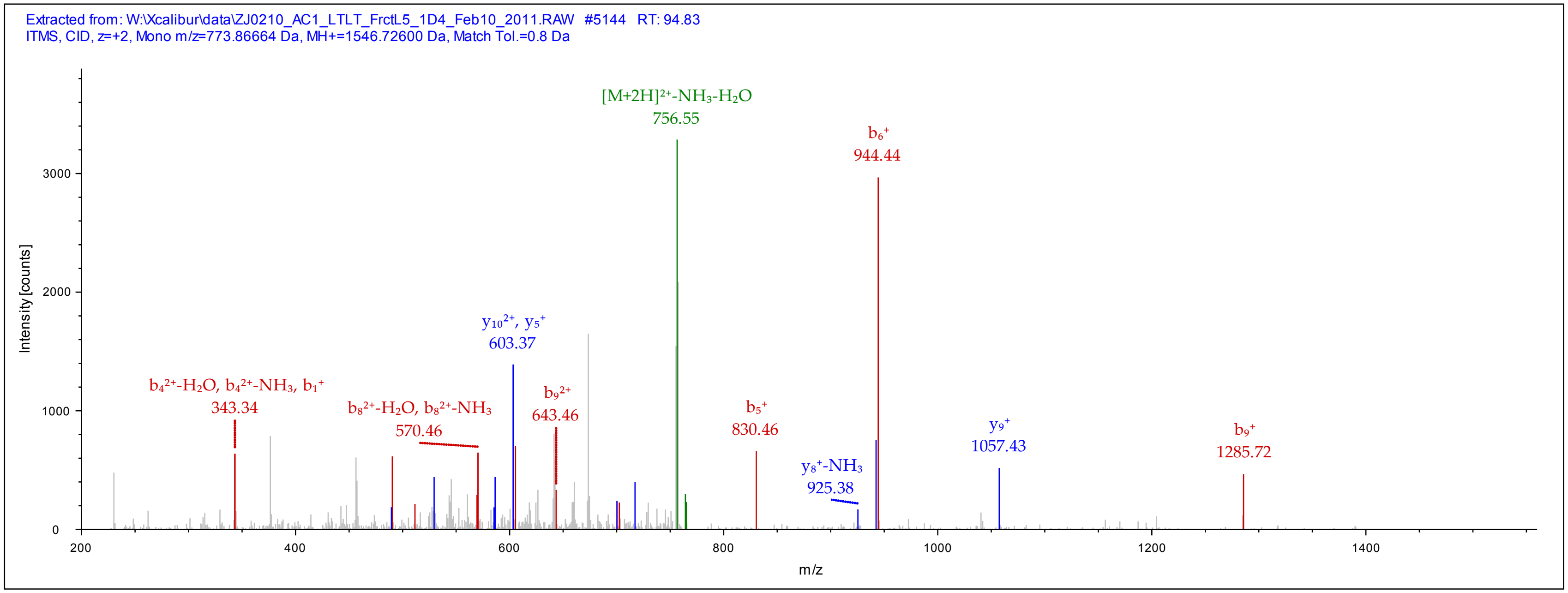
Identified with: Mascot (v1.16); IonScore:44, Exp Value:2.9E-003, Ions matched by search engine: 8/106

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Crk-like protein



IPI:IPI00005740.1

Sequence: ISASLLDSR, I1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 595.85034 Da (-0.43 mmu/-0.72 ppm),   MH+: 1190.69341 Da,   RT: 91.13 min,

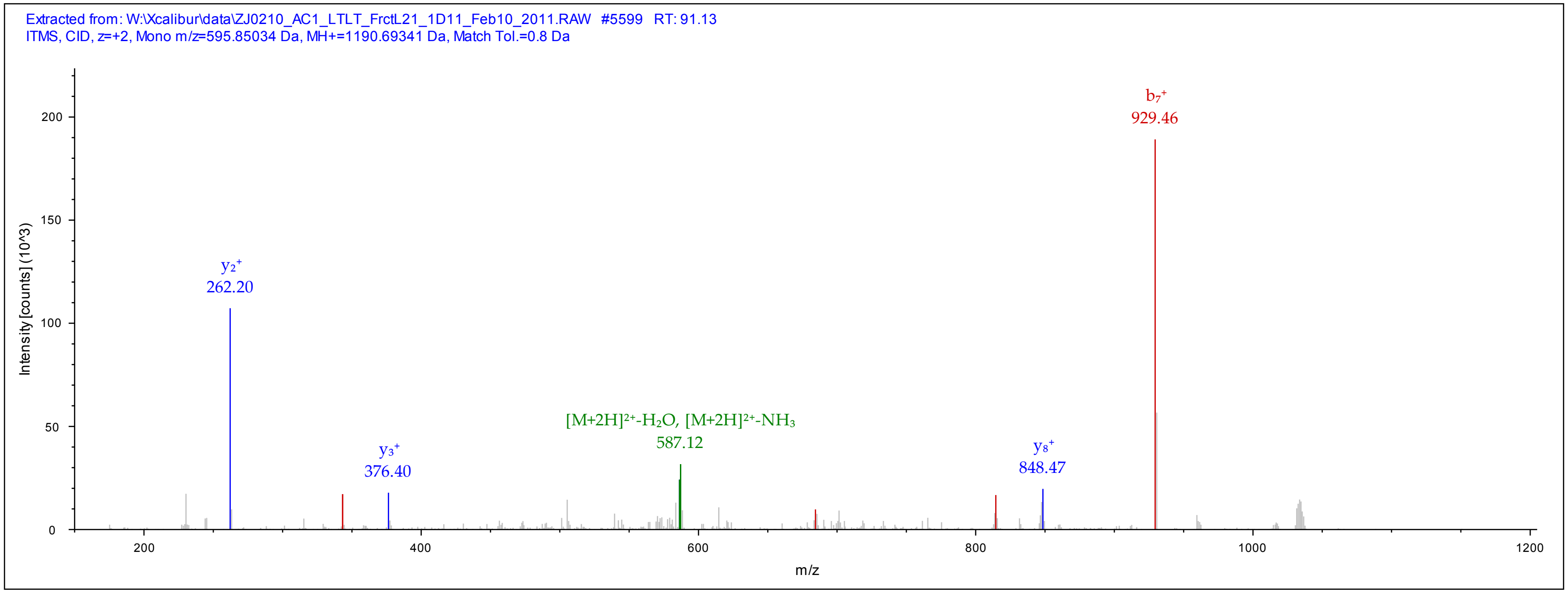
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.2E-002, Ions matched by search engine: 8/76

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Neighbor of COX4



IPI00006034.1

Sequence: TVYFAEK, T1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 658.38617 Da (-0.59 mmu/-0.89 ppm),   MH+: 1315.76506 Da,   RT: 88.52 min,

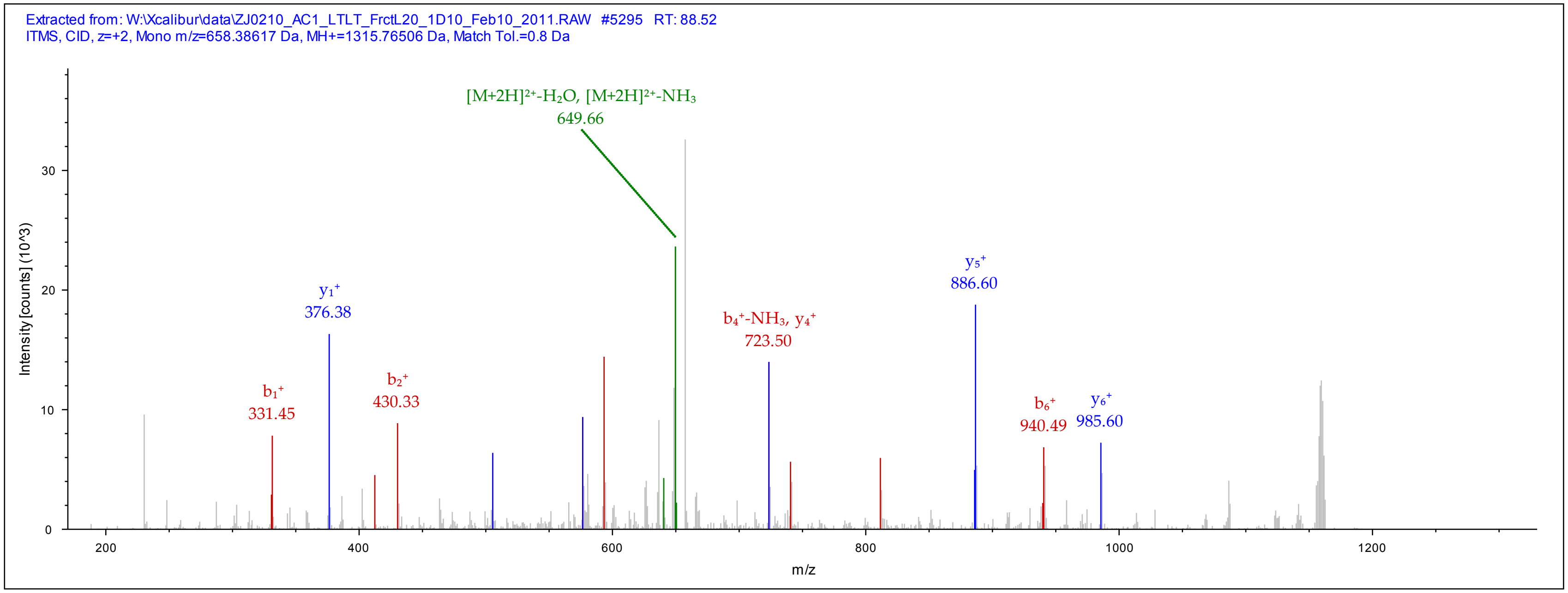
Identified with: Mascot (v1.16); IonScore:34, Exp Value:4.0E-002, Ions matched by search engine: 6/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Cysteine-rich protein 2 lng=208



IPI:IPI00007730.1

Sequence: YLEVEPVSR, Y1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 660.87195 Da (+0.25 mmu/+0.38 ppm), MH+: 1320.73662 Da, RT: 89.48 min,

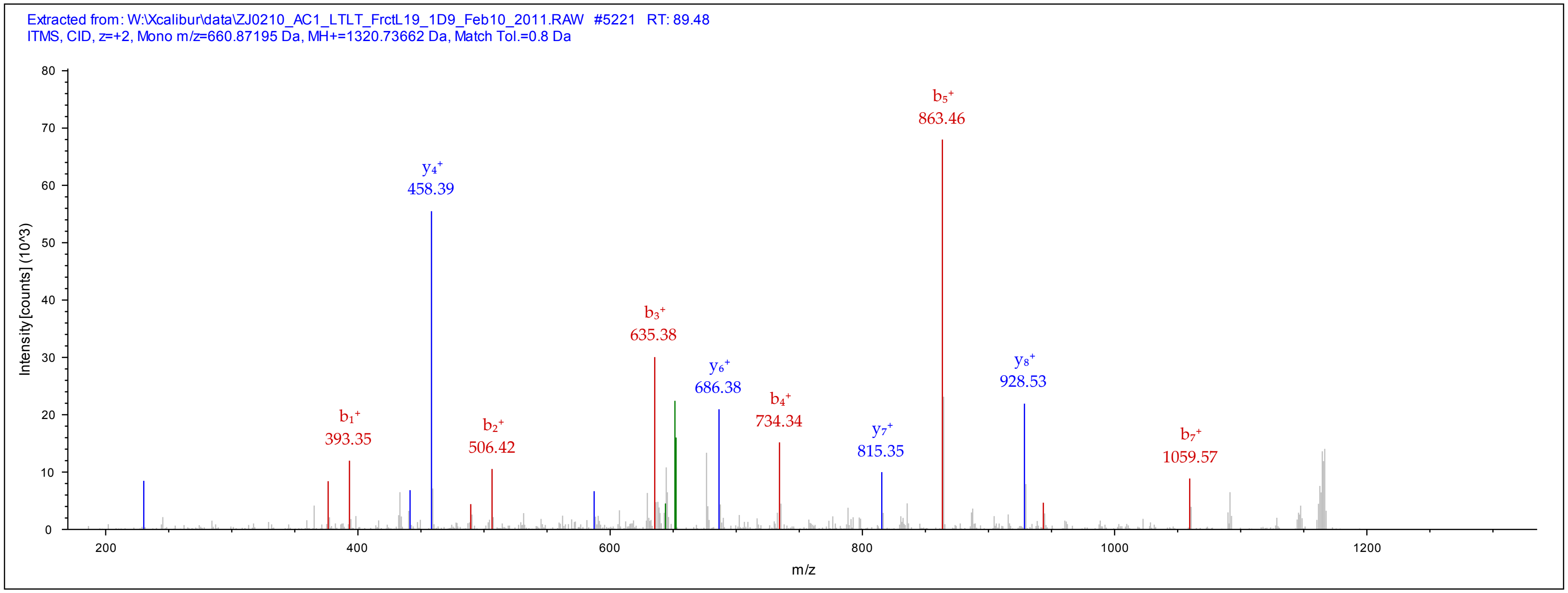
Identified with: Mascot (v1.16); IonScore:30, Exp Value:8.7E-002, Ions matched by search engine: 6/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Probable ergosterol biosynthetic protein 28



IPI:IPI00008728.1

Sequence: TLVQILTEPR, T1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 699.92999 Da (+0.44 mmu/+0.63 ppm),   MH+: 1398.85271 Da,   RT: 113.04 min,

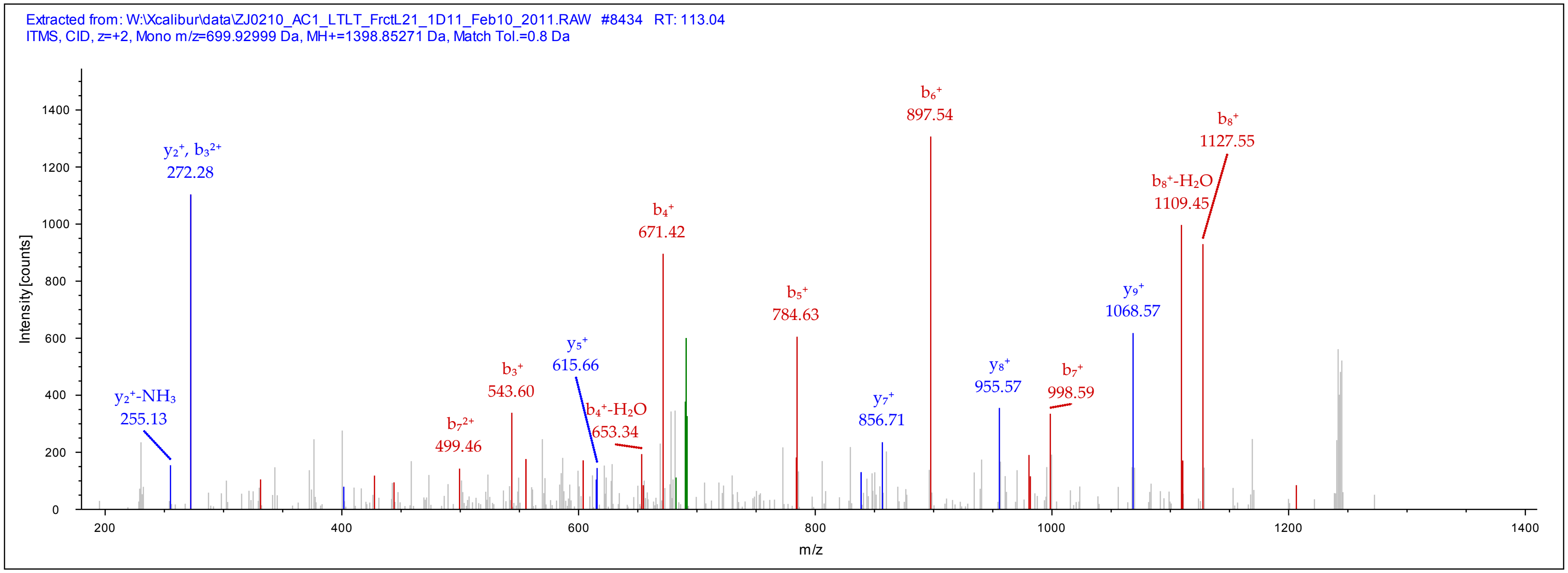
Identified with: Mascot (v1.16); IonScore:33, Exp Value:4.4E-002, Ions matched by search engine: 10/98

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial


Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL21_1D11_Feb10_2011.RAW   #8434   RT: 113.04
ITMS, CID, z=+2, Mono m/z=699.92999 Da, MH+=1398.85271 Da, Match Tol.=0.8 Da

IPI:IPI00008991.1

Sequence: LENLGIPEEELLR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 877.49829 Da (-0.25 mmu/-0.29 ppm), MH+: 1753.98931 Da, RT: 120.04 min,

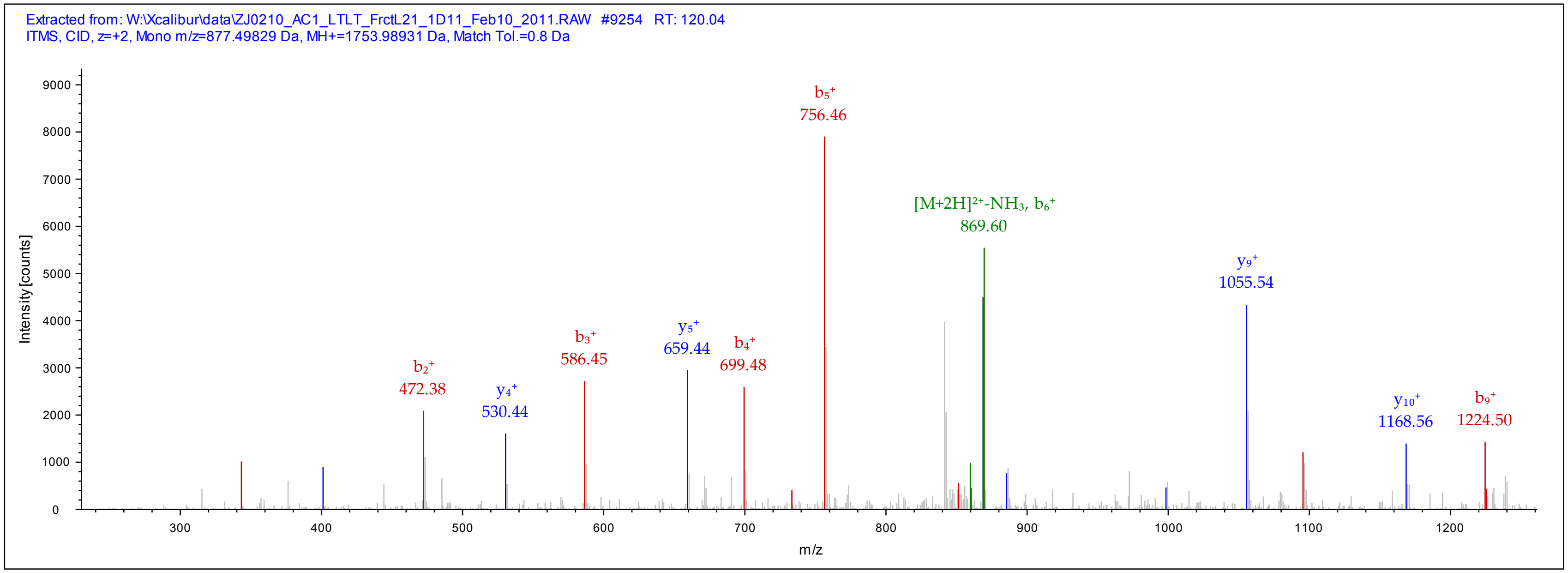
Identified with: Mascot (v1.16); IonScore:58, Exp Value:1.8E-004, Ions matched by search engine: 12/132

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Protein Dr1



IPI:IPI00009471.1

Sequence: ILILQGLK, I1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 678.47284 Da (-0.34 mmu/-0.5 ppm), MH+: 1355.93840 Da, RT: 126.53 min,

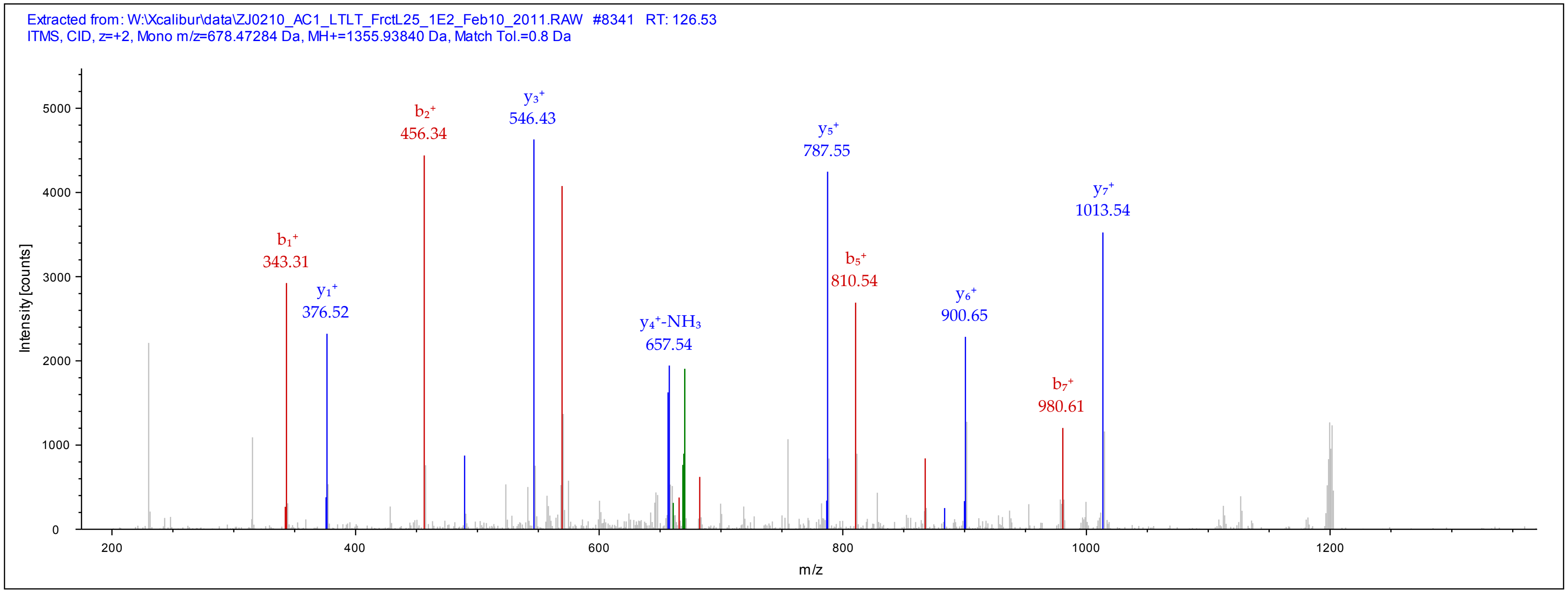
Identified with: Mascot (v1.16); IonScore:31, Exp Value:4.5E-003, Ions matched by search engine: 6/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- WD repeat-containing protein 3



IPI:IPI00009922.3

Sequence: GLGWVQFSSEEGLR, G1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 897.47321 Da (+0.35 mmu/+0.39 ppm), MH+: 1793.93913 Da, RT: 112.83 min,

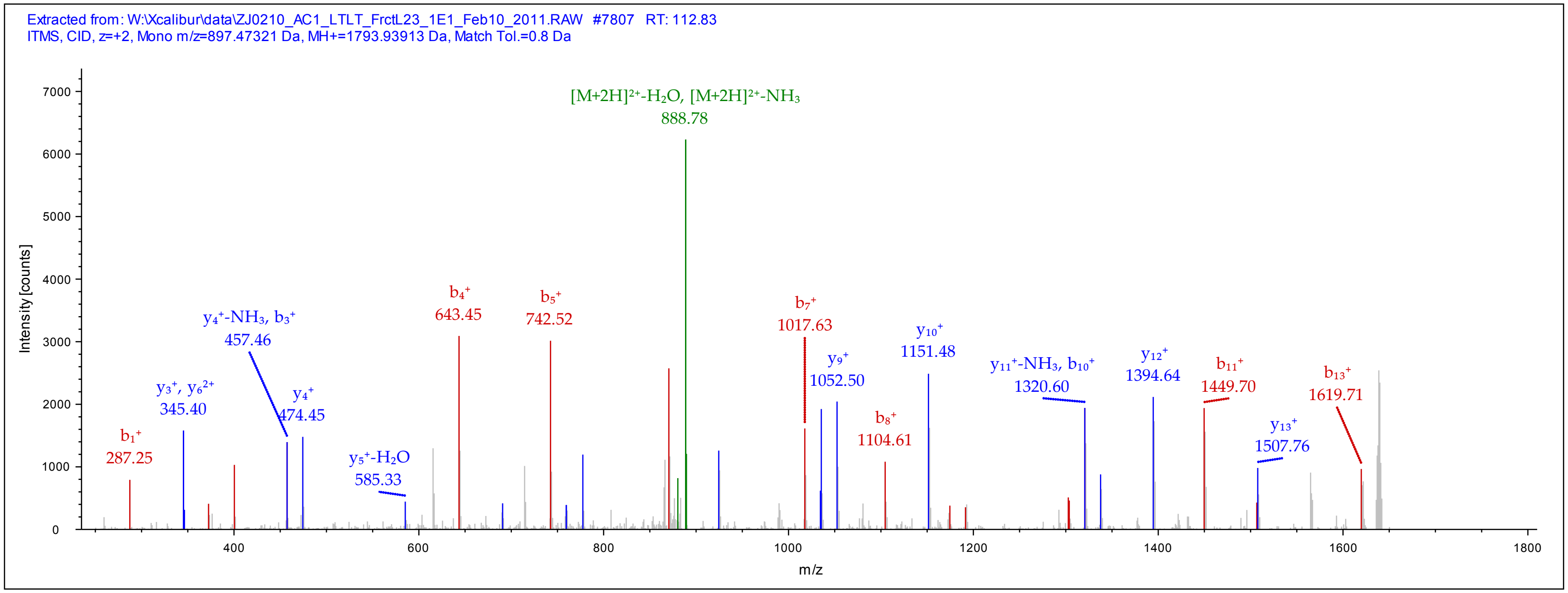
Identified with: Mascot (v1.16); IonScore:68, Exp Value:1.8E-005, Ions matched by search engine: 10/126

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- SRA stem-loop-interacting RNA-binding protein, mitochondrial



IPI:IPI00010182.4

Sequence: WDAWNELK, W1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 760.41846 Da (-0.67 mmu/-0.89 ppm),   MH+: 1519.82964 Da,   RT: 113.15 min,

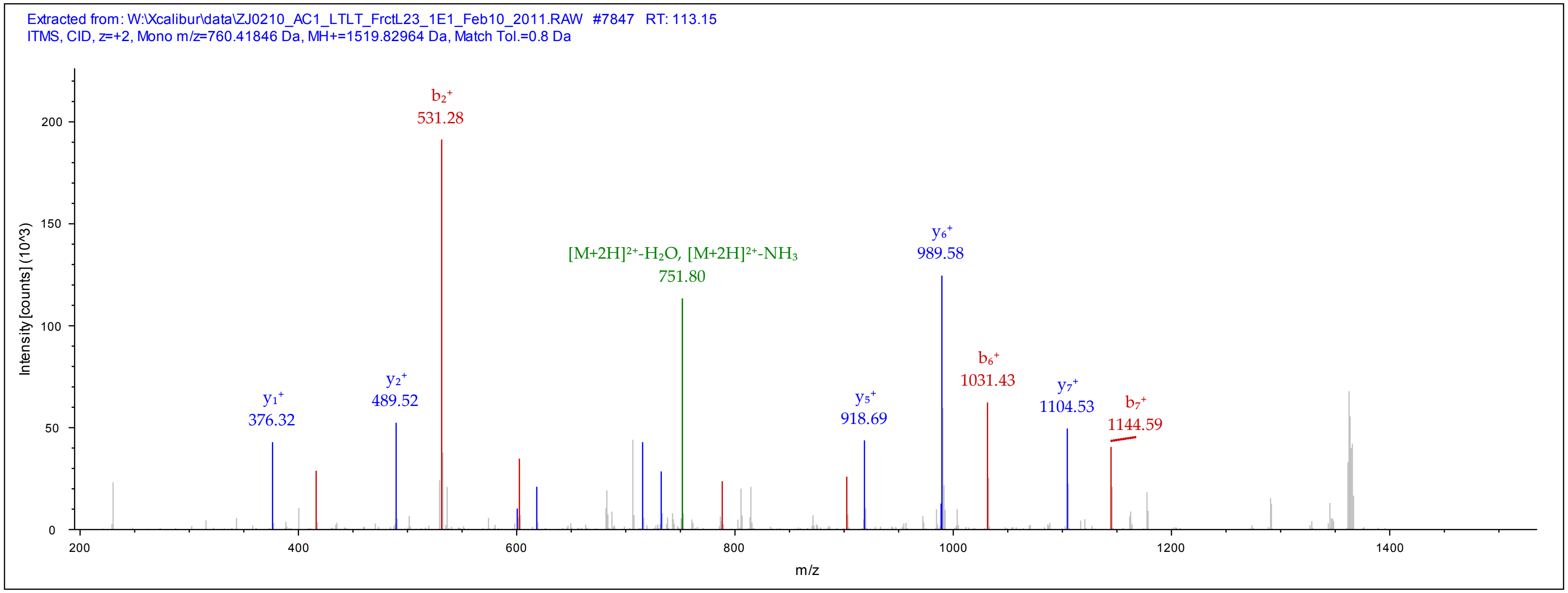
Identified with: Mascot (v1.16); IonScore:32, Exp Value:6.1E-002, Ions matched by search engine: 11/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Isoform 1 of Acyl-CoA-binding protein
- Isoform 2 of Acyl-CoA-binding protein
- Isoform 3 of Acyl-CoA-binding protein
- Diazepam binding inhibitor, splice form 1D
- Diazepam binding inhibitor, splice form 1G lng=148
- acyl-CoA-binding protein isoform 5
- Diazepam binding inhibitor, splice form 1A lng=97



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ITMS, CID, z=+2, Mono m/z=760.41846 Da, MH+=1519.82964 Da, Match Tol.=0.8 Da

IPI:IPI00010865.1

Sequence: GIAQMLEK, G1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 674.40723 Da (+0.05 mmu/+0.07 ppm),   MH+: 1347.80718 Da,   RT: 99.62 min,

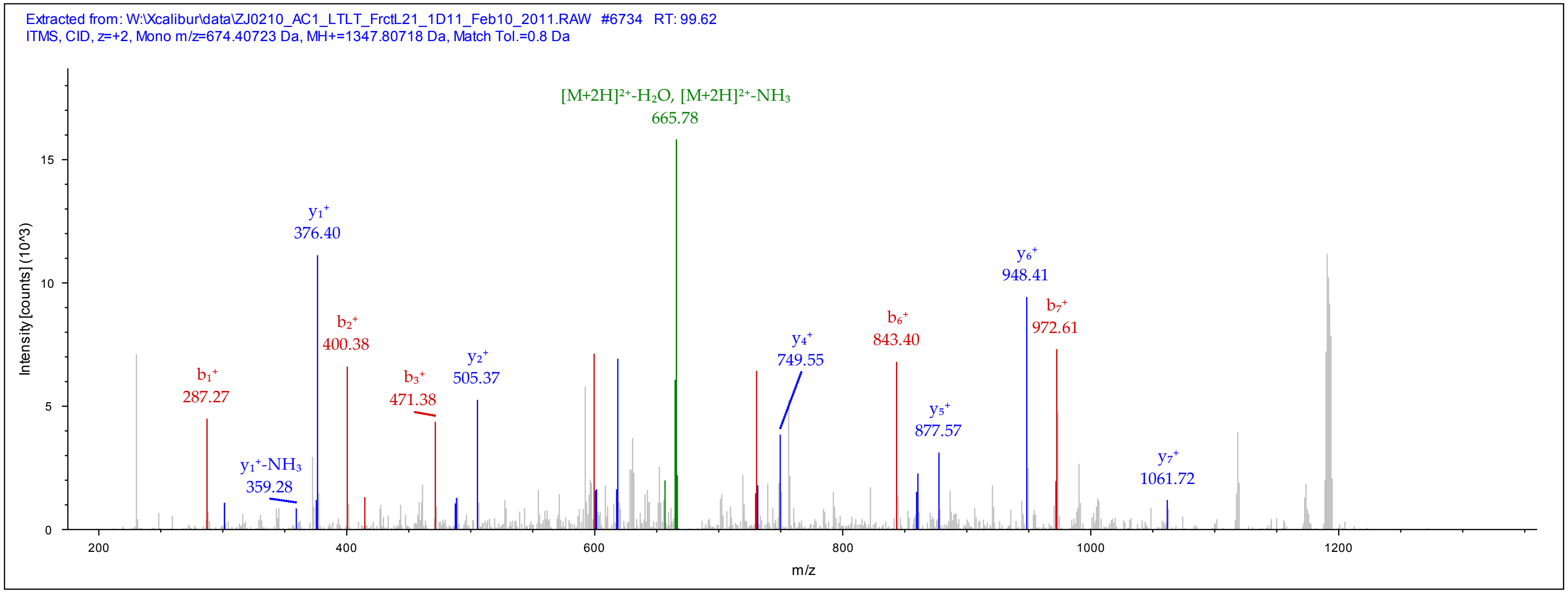
Identified with: Mascot (v1.16); IonScore:40, Exp Value:8.1E-003, Ions matched by search engine: 7/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Casein kinase II subunit beta
- Casein kinase 2, beta polypeptide lng=228
- Casein kinase 2, beta polypeptide, isoform CRA_d lng=234



IPI:IPI00011564.1

Sequence: ETEVIDPQDLLEGR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 921.99030 Da (+4.3 mmu/+4.66 ppm), MH+: 1842.97331 Da, RT: 114.18 min,

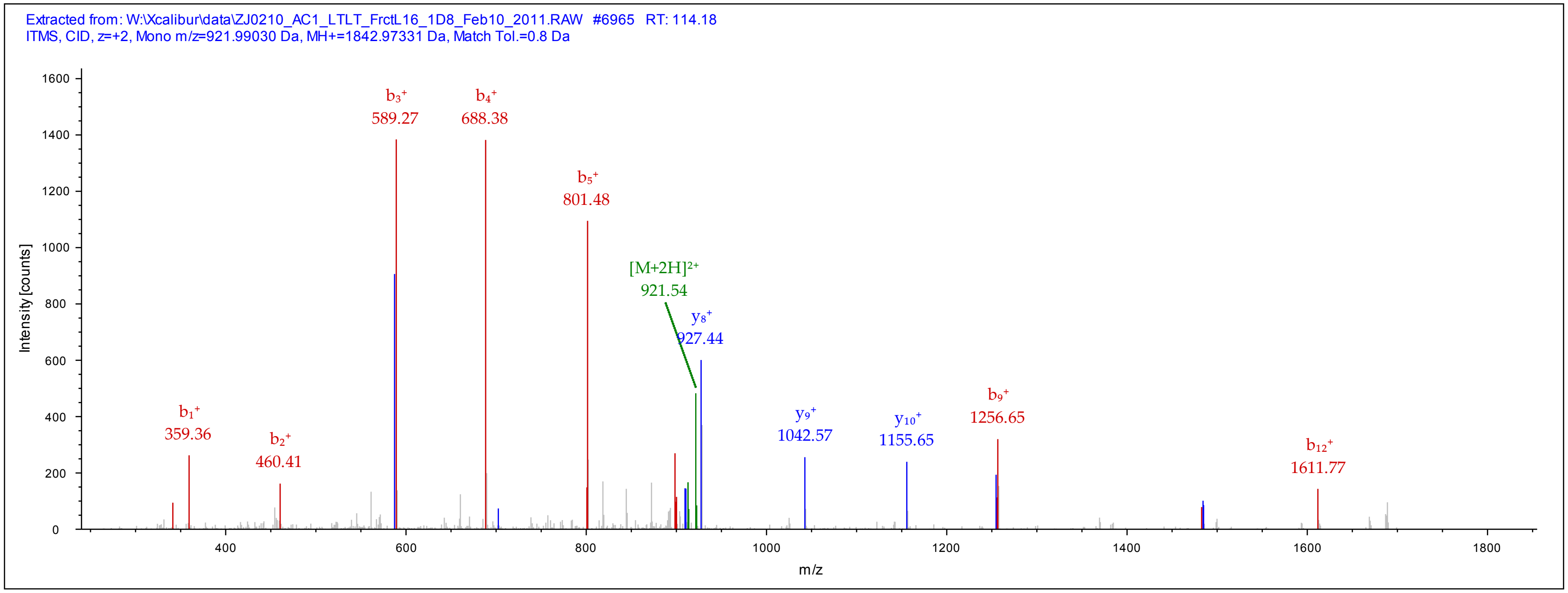
Identified with: Mascot (v1.16); IonScore:64, Exp Value:4.8E-005, Ions matched by search engine: 8/138

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Syndecan-4



IPI:IPI00011619.4

Sequence: AWTVLTEYYK, A1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 866.49231 Da (+2.57 mmu/+2.97 ppm),   MH+: 1731.97734 Da,   RT: 124.44 min,

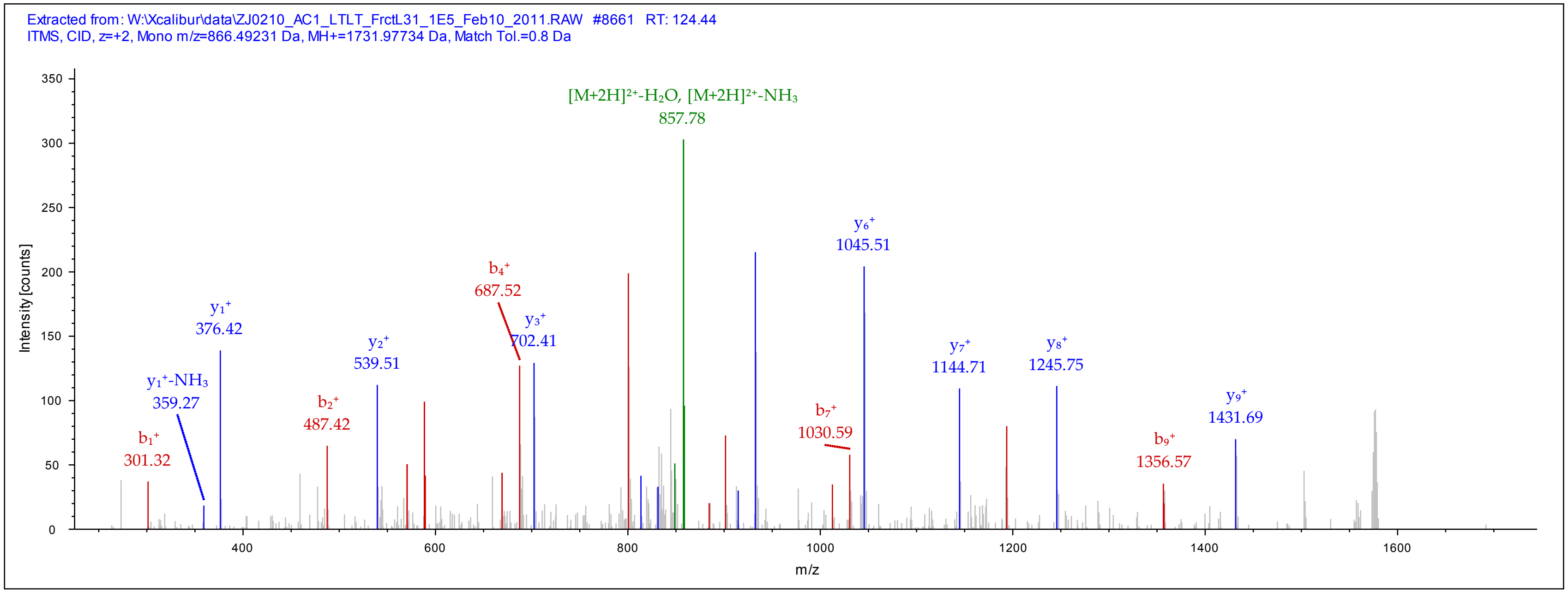
Identified with: Mascot (v1.16); IonScore:59, Exp Value:1.2E-004, Ions matched by search engine: 8/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1



IPI:IPI00011770.1

Sequence: LALFNPDVCWDR, L1-TMT6plex (229.16293 Da), C9-Carbamidomethyl (57.02146 Da)

Charge: +2, Monoisotopic m/z: 867.94531 Da (-0.11 mmu/-0.13 ppm), MH+: 1734.88335 Da, RT: 123.54 min,

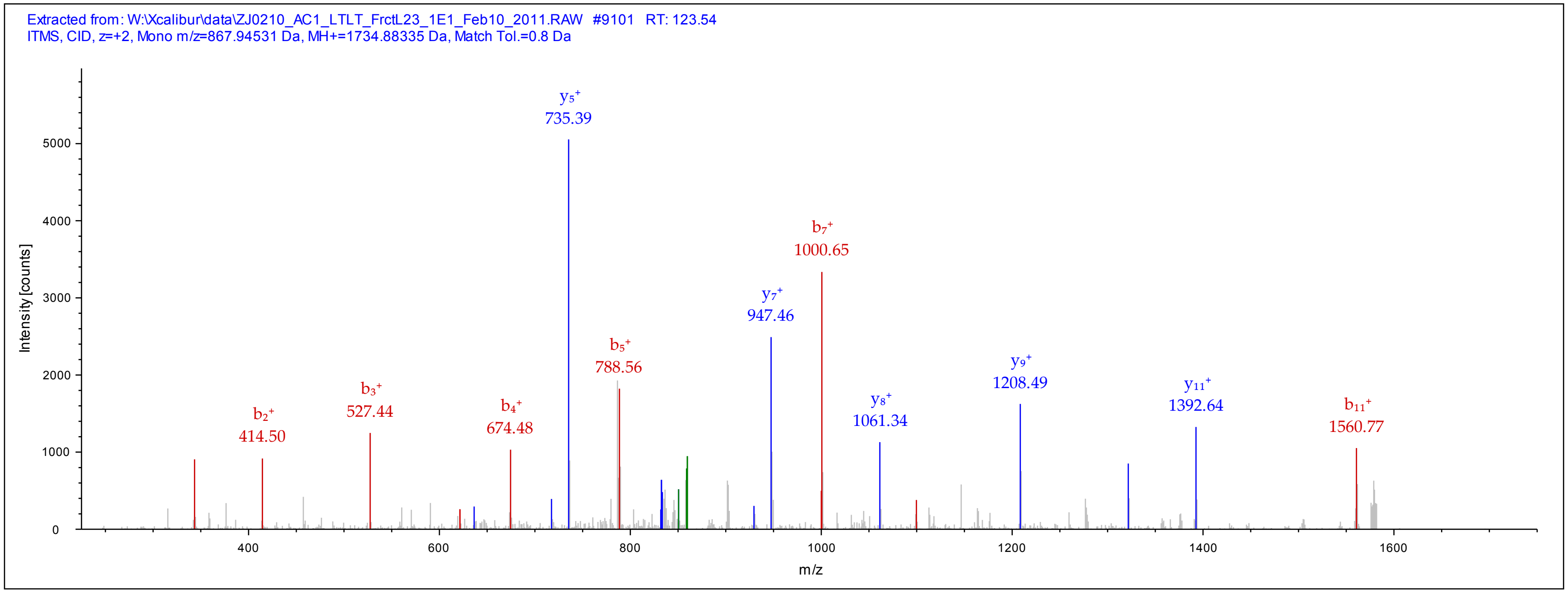
Identified with: Mascot (v1.16); IonScore:39, Exp Value:1.5E-002, Ions matched by search engine: 14/110

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4



IPI:IPI00013212.1

Sequence: LLYPPETGLFLVR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 874.02362 Da (+2.17 mmu/+2.48 ppm),   MH+: 1747.03996 Da,   RT: 134.96 min,

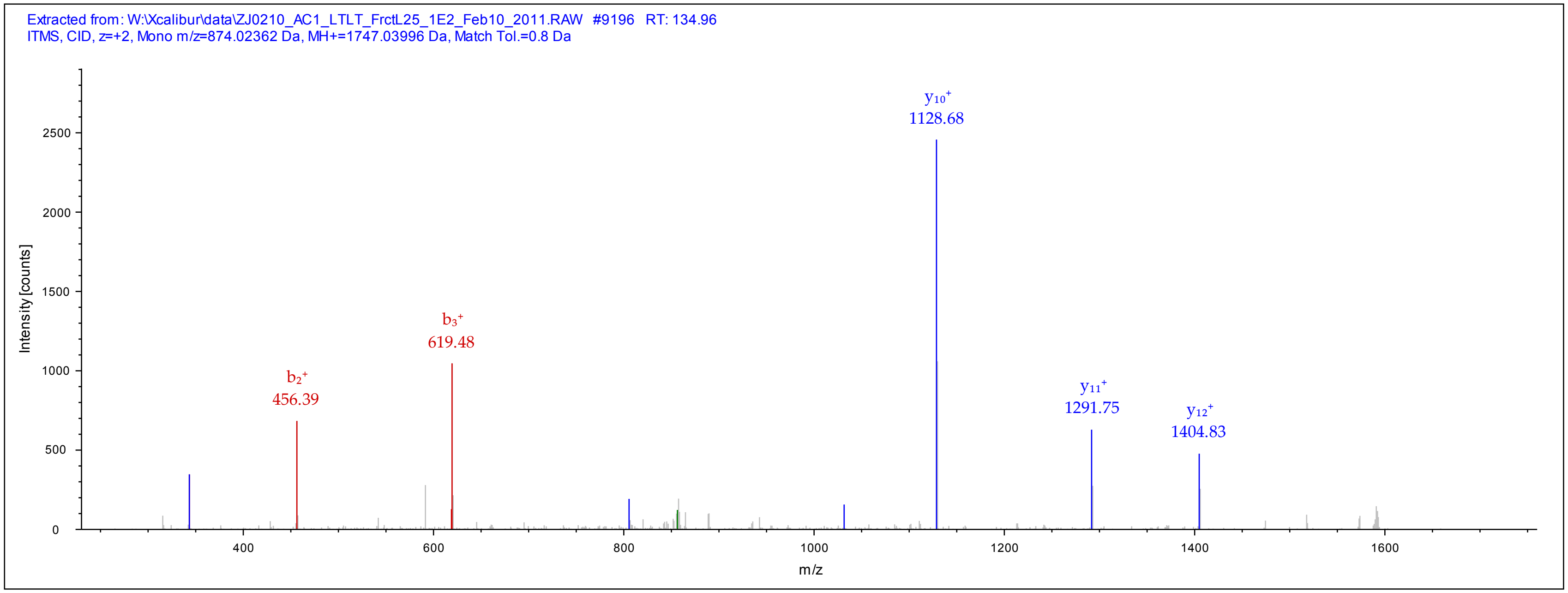
Identified with: Mascot (v1.16); IonScore:34, Exp Value:3.7E-002, Ions matched by search engine: 9/98

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Tyrosine-protein kinase CSK



IPI:IPI00014253.4

Sequence: VEEAIVAR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 558.33551 Da (+0.75 mmu/+1.35 ppm), MH+: 1115.66374 Da, RT: 81.79 min,

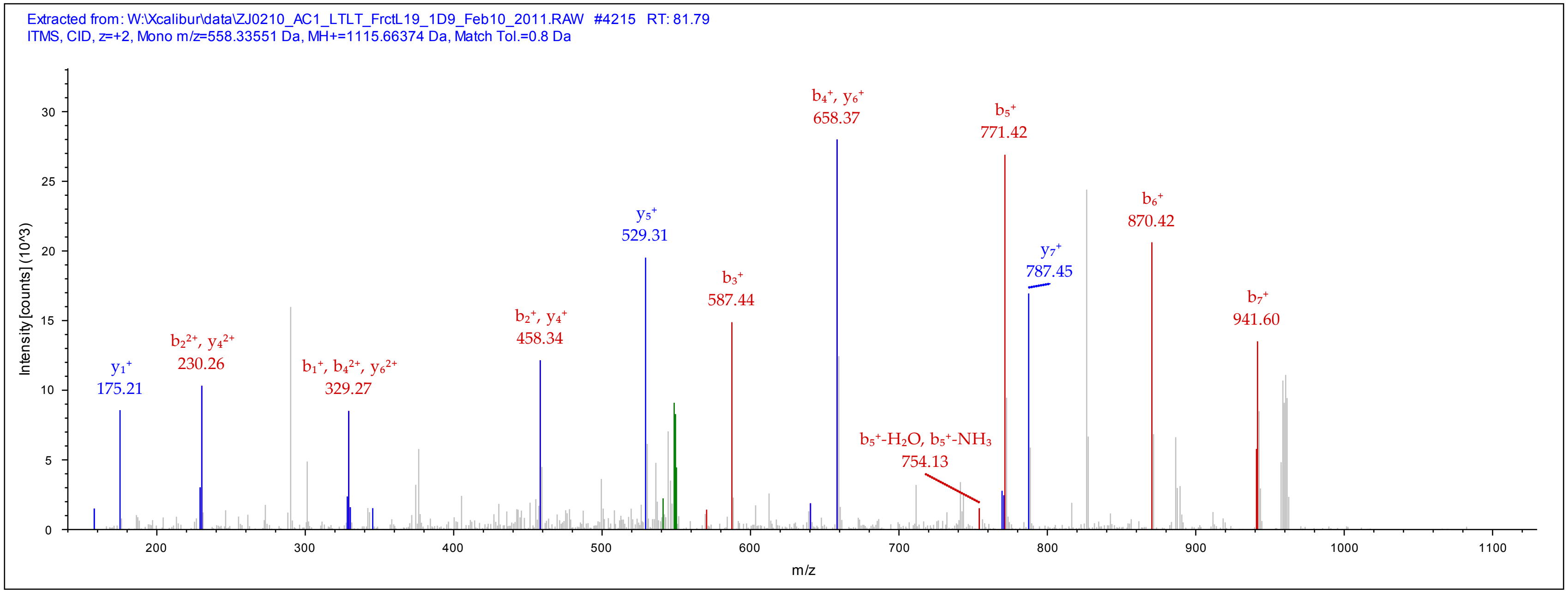
Identified with: Mascot (v1.16); IonScore:43, Exp Value:3.2E-003, Ions matched by search engine: 7/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

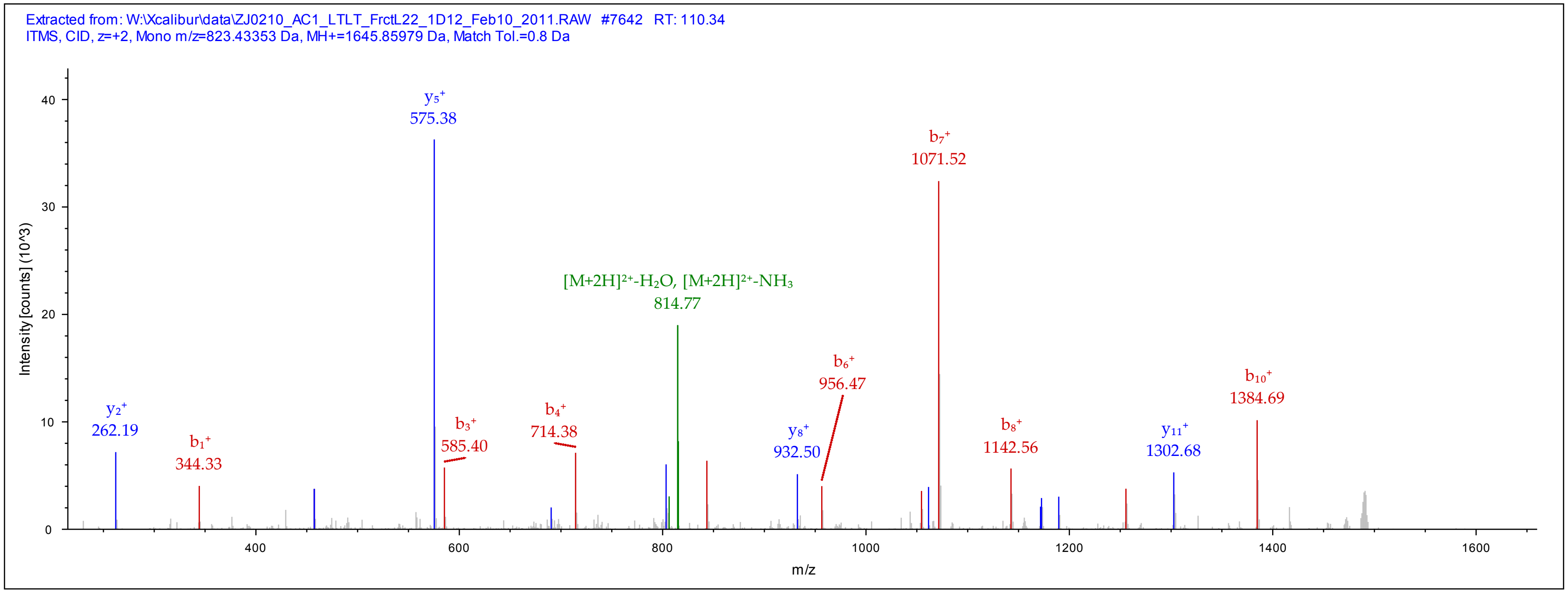
- Ribosome biogenesis regulatory protein homolog



IPI:IPI00015891.1

Sequence: NLQEEIDALESR, N1-TMT6plex (229.16293 Da)
Charge: +2,   Monoisotopic m/z: 823.43353 Da (+0.14 mmu/+0.17 ppm),   MH+: 1645.85979 Da,   RT: 110.34 min,
Identified with: Mascot (v1.16); IonScore:56, Exp Value:2.7E-004, Ions matched by search engine: 10/124
Fragment match tolerance used for search: 0.8 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Prefoldin subunit 4



IPI00016372.1

Sequence: EPESFPFVILGNK, E1-TMT6plex (229.16293 Da), K13-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 968.05640 Da (+3.14 mmu/+3.24 ppm),   MH+: 1935.10552 Da,   RT: 131.01 min,

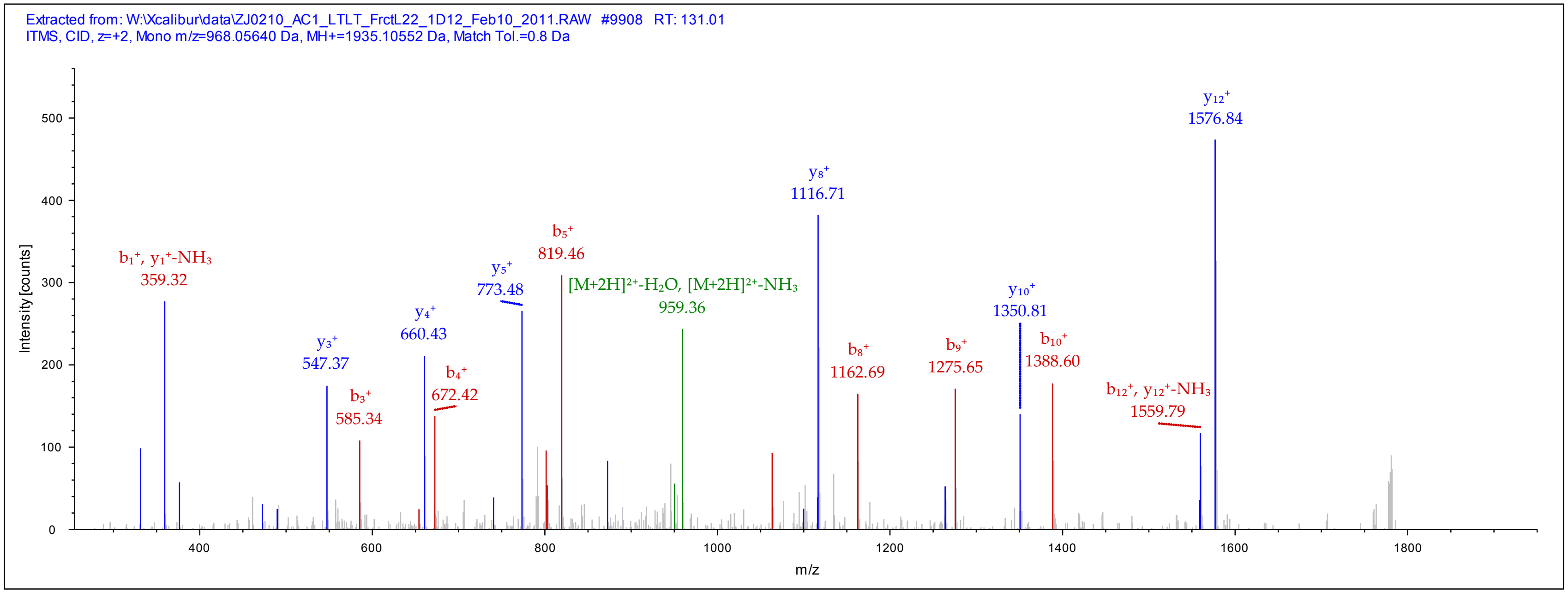
Identified with: Mascot (v1.16); IonScore:47, Exp Value:2.3E-003, Ions matched by search engine: 10/104

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Ras-related protein Rab-9A lng=201



IPI:IPI00018342.5

Sequence: GQLVPLETVLDMLR, G1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 907.02863 Da (+2.21 mmu/+2.43 ppm),   MH+: 1813.04997 Da,   RT: 211.33 min,

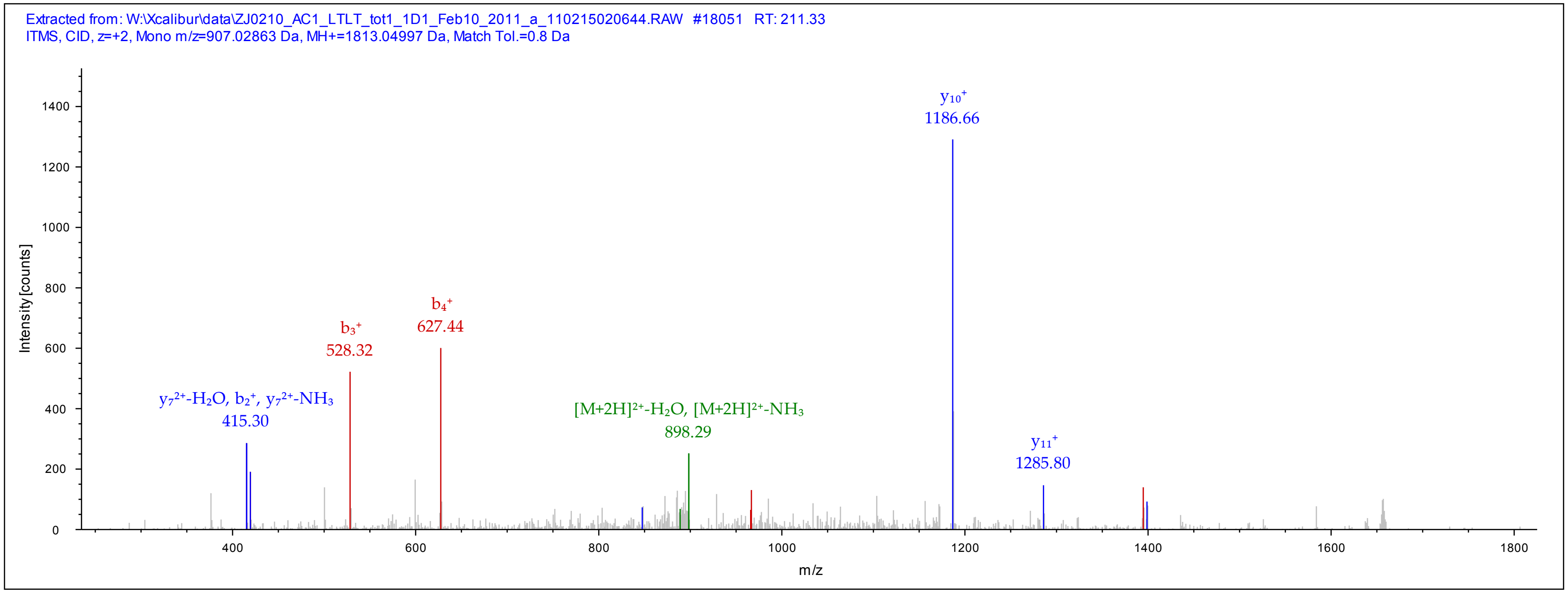
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.6E-002, Ions matched by search engine: 8/136

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Adenylate kinase isoenzyme 1
- Adenylate kinase 1 lng=210



IPI:IPI00019812.1

Sequence: LSTLVETTLK, L1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 781.99200 Da (-0.12 mmu/-0.16 ppm),   MH+: 1562.97673 Da,   RT: 116.44 min,

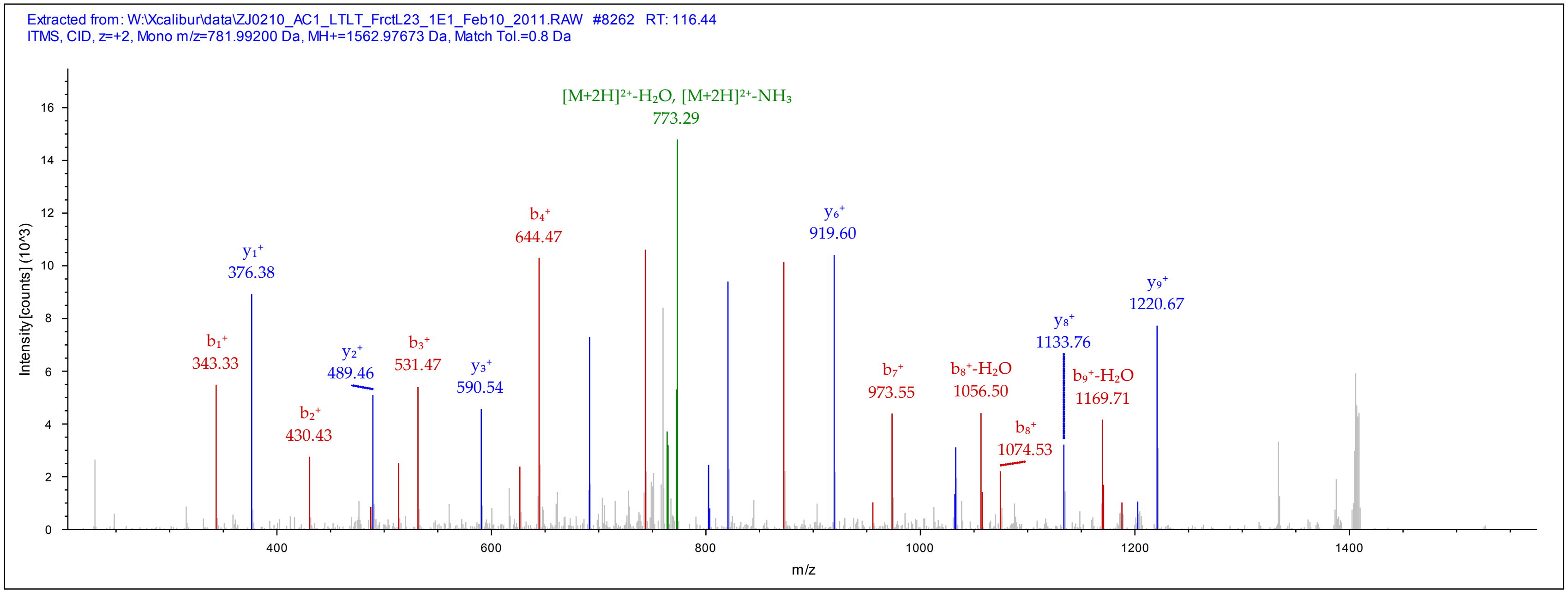
Identified with: Mascot (v1.16); IonScore:65, Exp Value:1.9E-005, Ions matched by search engine: 9/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Serine/threonine-protein phosphatase 5



IPI:IPI00019927.2

Sequence: DTTVGTLSQR, D1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 653.86353 Da (+1.66 mmu/+2.54 ppm), MH+: 1306.71977 Da, RT: 74.10 min,

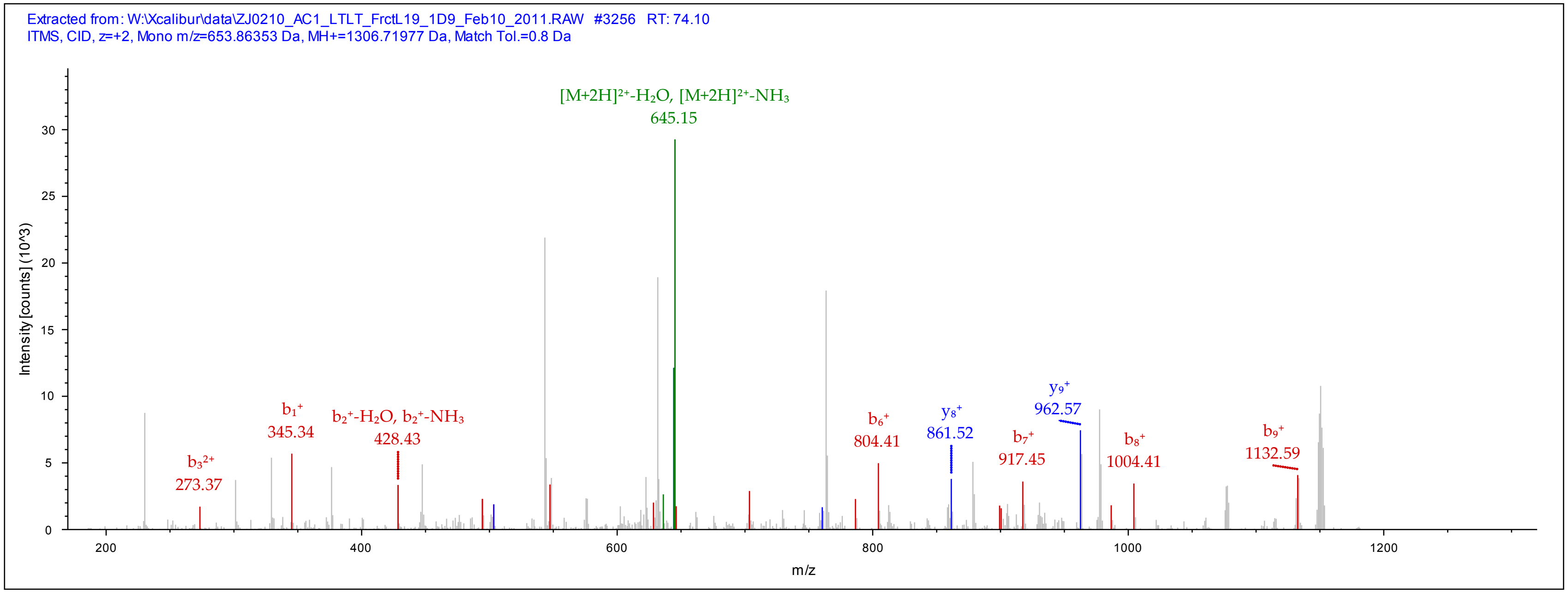
Identified with: Mascot (v1.16); IonScore:29, Exp Value:8.8E-002, Ions matched by search engine: 9/88

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 26S proteasome non-ATPase regulatory subunit 7



IPI:IPI00020164.1

Sequence: APVLVALALIEGGMK, A1-TMT6plex (229.16293 Da), K15-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 647.40637 Da (+0.87 mmu/+1.34 ppm), MH+: 1940.20456 Da, RT: 230.96 min,

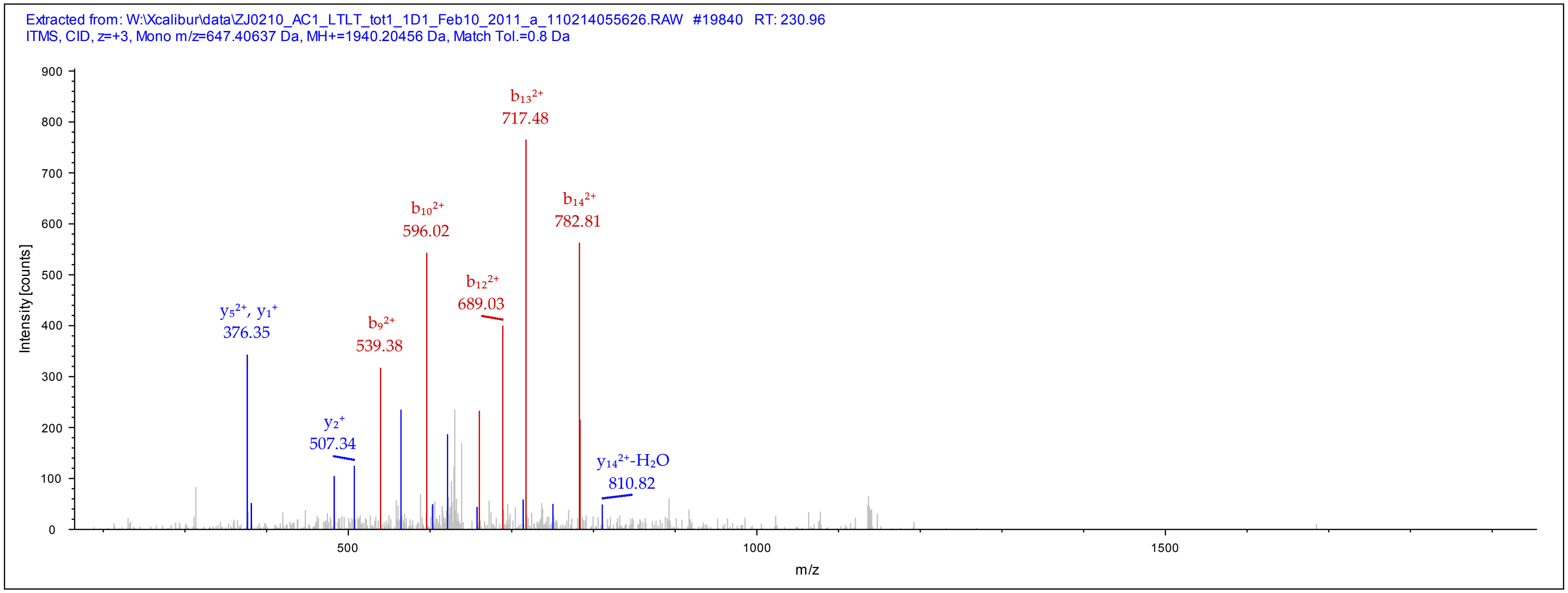
Identified with: Mascot (v1.16); IonScore:31, Exp Value:2.8E-002, Ions matched by search engine: 8/112

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Protein tyrosine phosphatase type IVA 1



IPI:IPI00020258.3

Sequence: DPTLTFRLLGSPR, D1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 851.51257 Da (+16.45 mmu/+19.32 ppm), MH+: 1702.01787 Da, RT: 106.91 min,

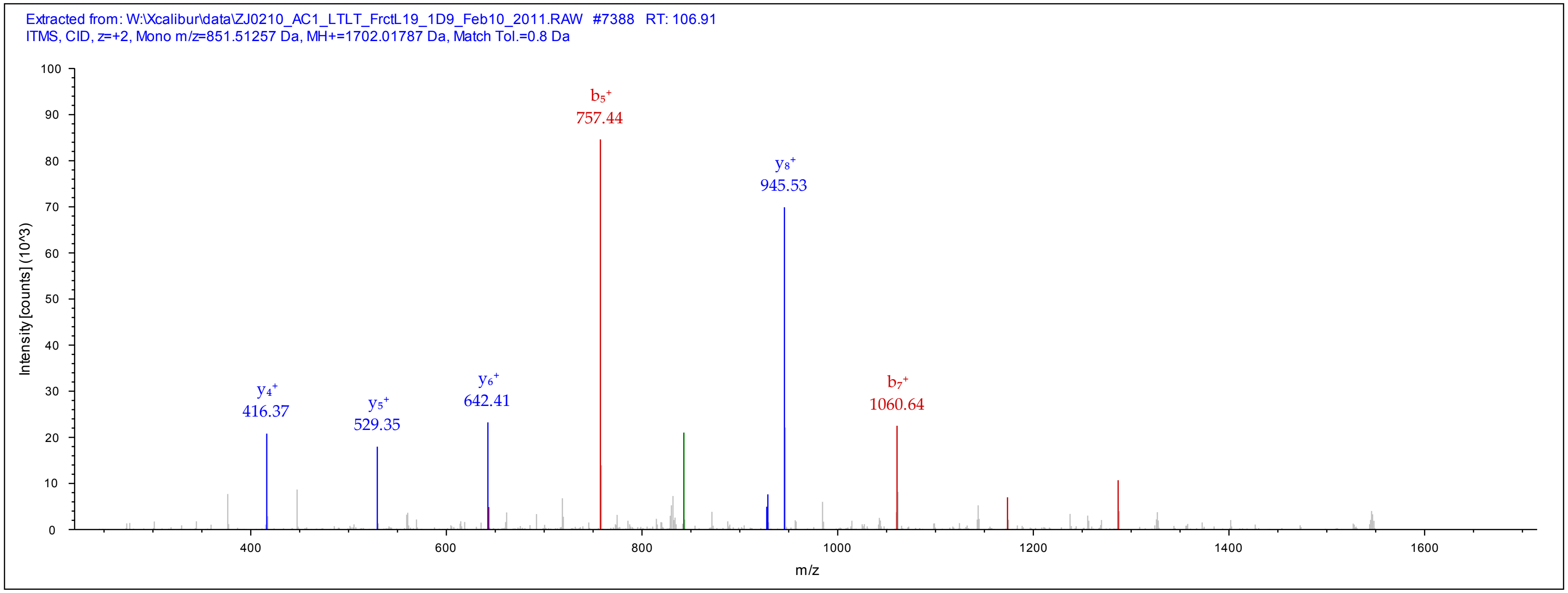
Identified with: Mascot (v1.16); IonScore:31, Exp Value:6.5E-002, Ions matched by search engine: 5/128

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Mitogen-activated protein kinase kinase kinase kinase 1



IPI:IPI00020719.2

Sequence: VSASTVPTDGSSR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 746.89679 Da (+2.89 mmu/+3.87 ppm), MH+: 1492.78630 Da, RT: 73.53 min,

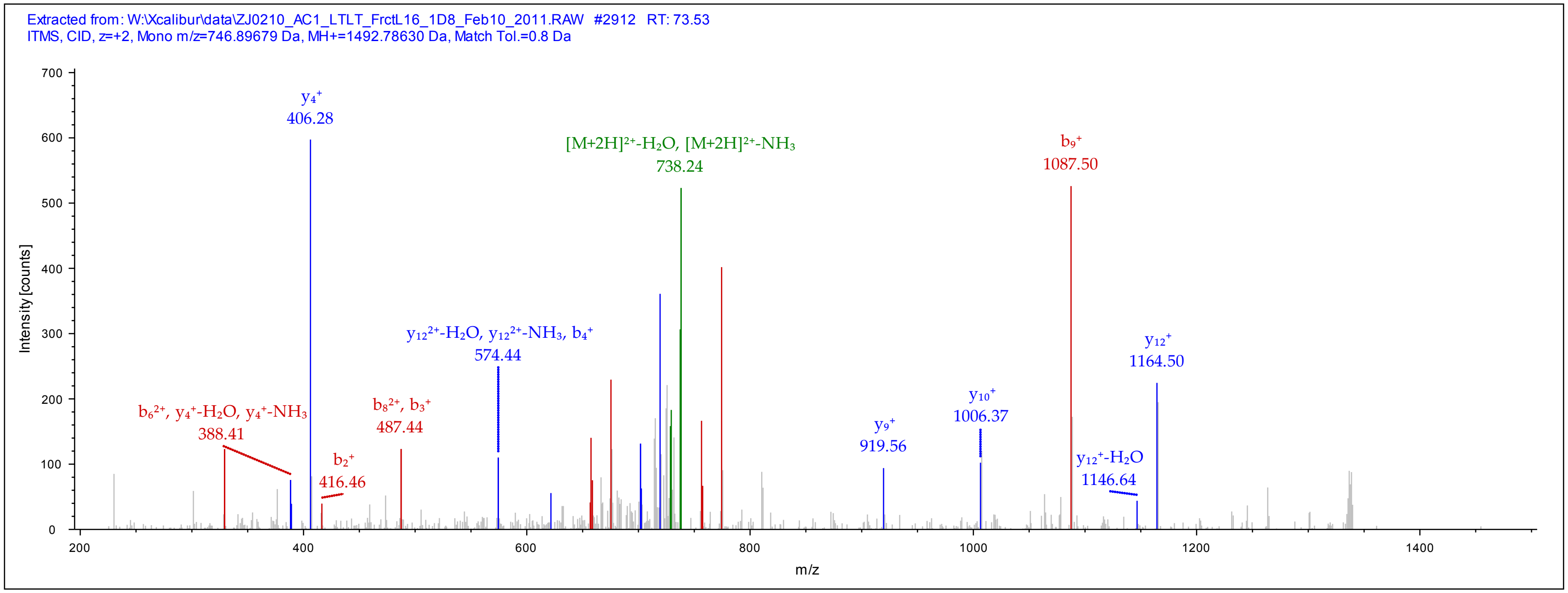
Identified with: Mascot (v1.16); IonScore:35, Exp Value:2.9E-002, Ions matched by search engine: 12/116

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Isoform 1 of Mitochondrial antiviral-signaling protein



IPI:IPI00021320.2

Sequence: AAPPDVGEER, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 635.33661 Da (+1.11 mmu/+1.75 ppm), MH+: 1269.66594 Da, RT: 71.11 min,

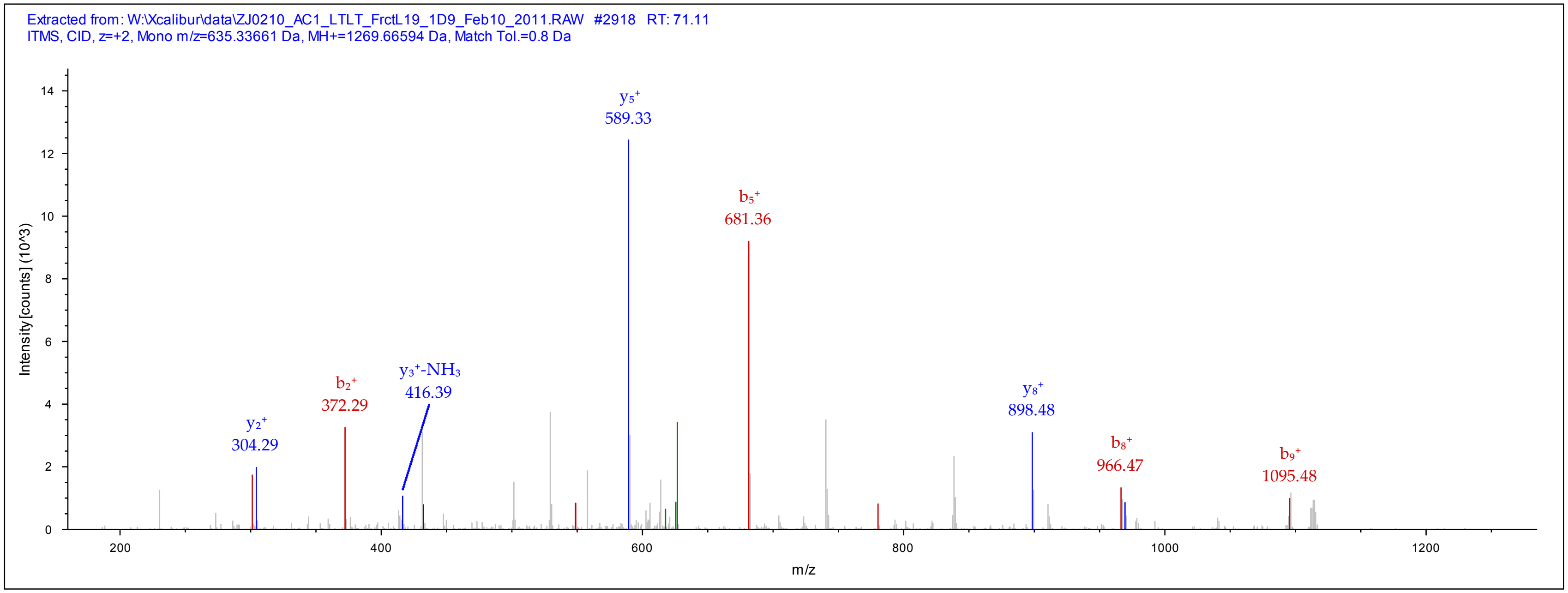
Identified with: Mascot (v1.16); IonScore:33, Exp Value:2.9E-002, Ions matched by search engine: 7/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 7SK snRNA methylphosphate capping enzyme



IPI:IPI00021785.2

Sequence: LVPQQLAH, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 567.84564 Da (+0.36 mmu/+0.63 ppm),   MH+: 1134.68401 Da,   RT: 87.80 min,

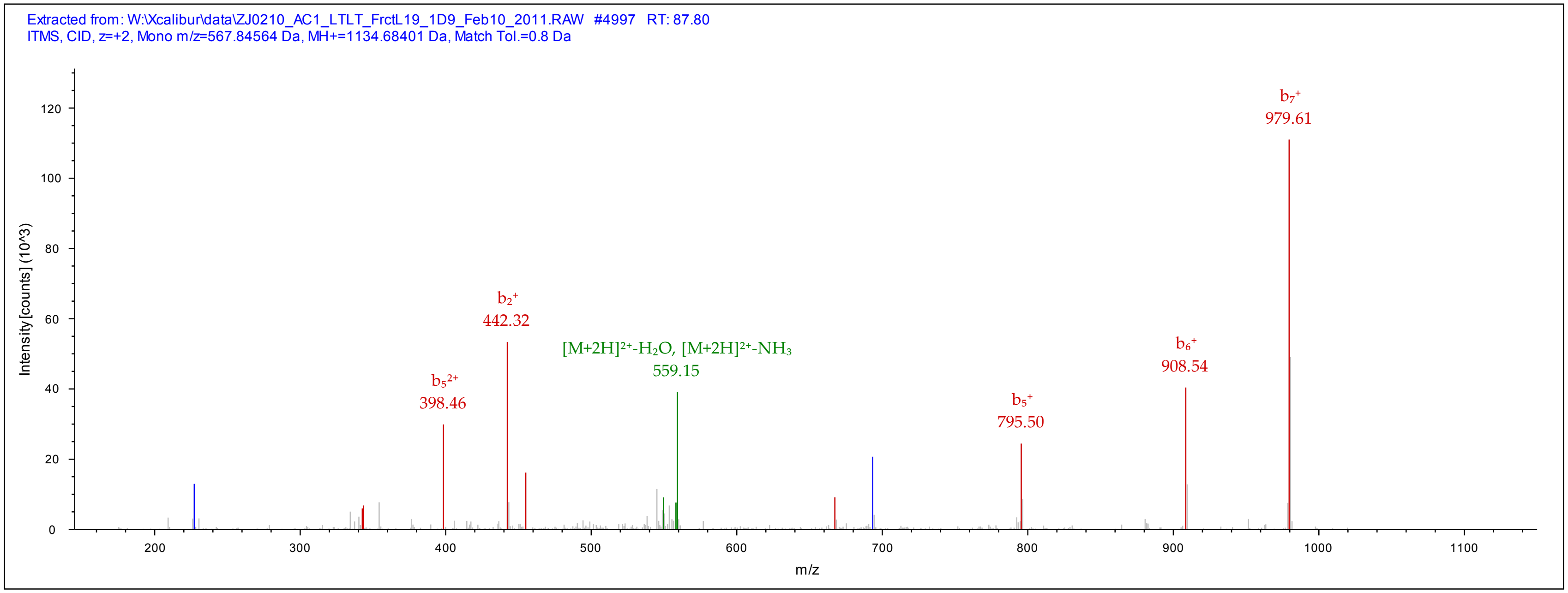
Identified with: Mascot (v1.16); IonScore:32, Exp Value:4.3E-002, Ions matched by search engine: 6/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Cytochrome c oxidase subunit 5B, mitochondrial



IPI:IPI00022215.1

Sequence: TLCPLCFSILK, T1-TMT6plex (229.16293 Da), C3-Carbamidomethyl (57.02146 Da), C6-Carbamidomethyl (57.02146 Da), K11-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 905.52264 Da (+0.42 mmu/+0.47 ppm),   MH+: 1810.03801 Da,   RT: 129.87 min,

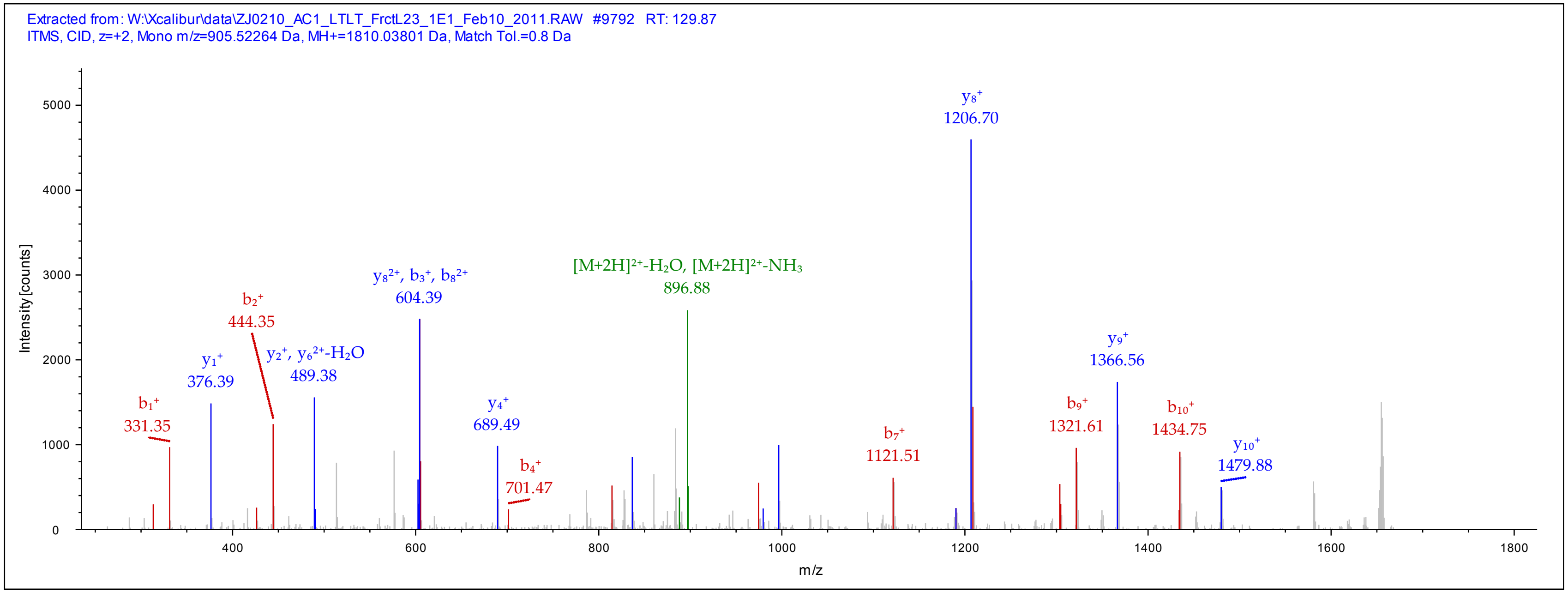
Identified with: Mascot (v1.16); IonScore:63, Exp Value:5.7E-005, Ions matched by search engine: 8/94

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Activity-dependent neuroprotector homeobox protein



IPI00022597.1

Sequence: LVICPDEGFYK, L1-TMT6plex (229.16293 Da), C4-Carbamidomethyl (57.02146 Da), K11-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 899.99426 Da (-0.09 mmu/-0.09 ppm),   MH+: 1798.98125 Da,   RT: 112.57 min,

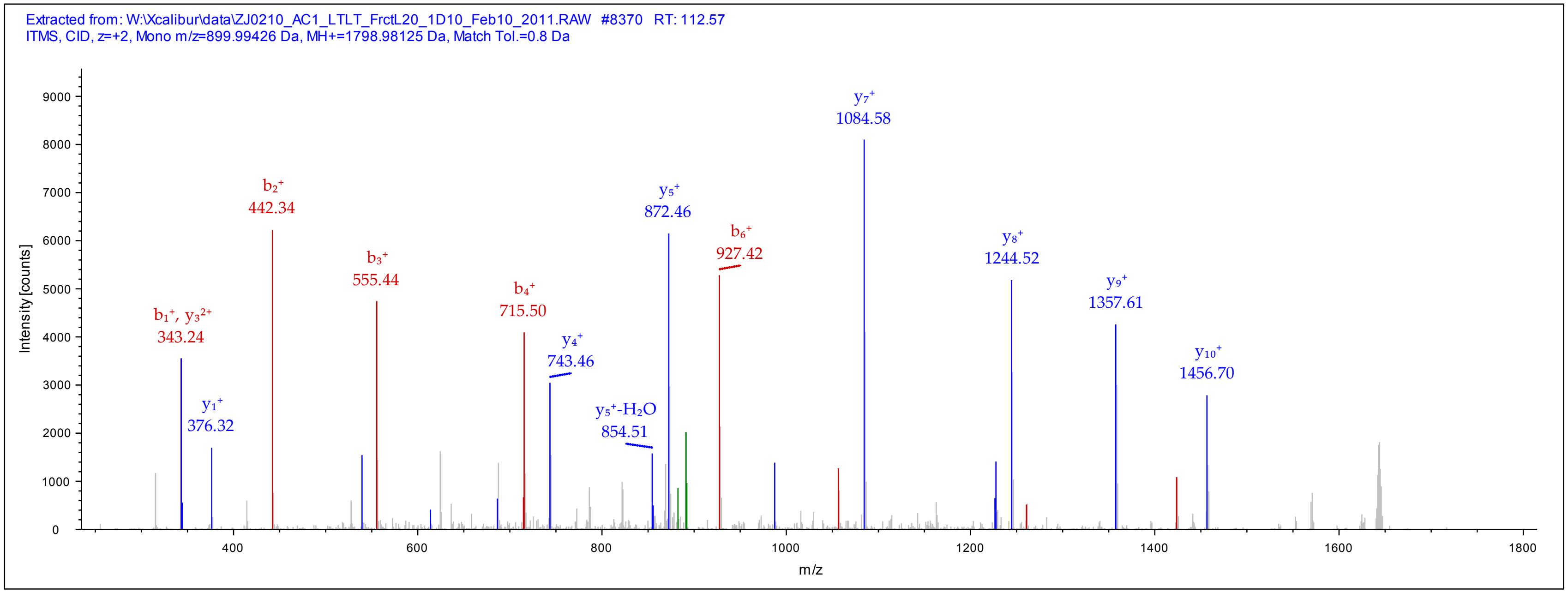
Identified with: Mascot (v1.16); IonScore:52, Exp Value:7.6E-004, Ions matched by search engine: 7/82

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- NEDD8-conjugating enzyme Ubc12 lng=183



IPI:IPI00023504.1

Sequence: ILIIGNSSVGK, I1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 779.99994 Da (-0.35 mmu/-0.45 ppm), MH+: 1558.99260 Da, RT: 109.68 min,

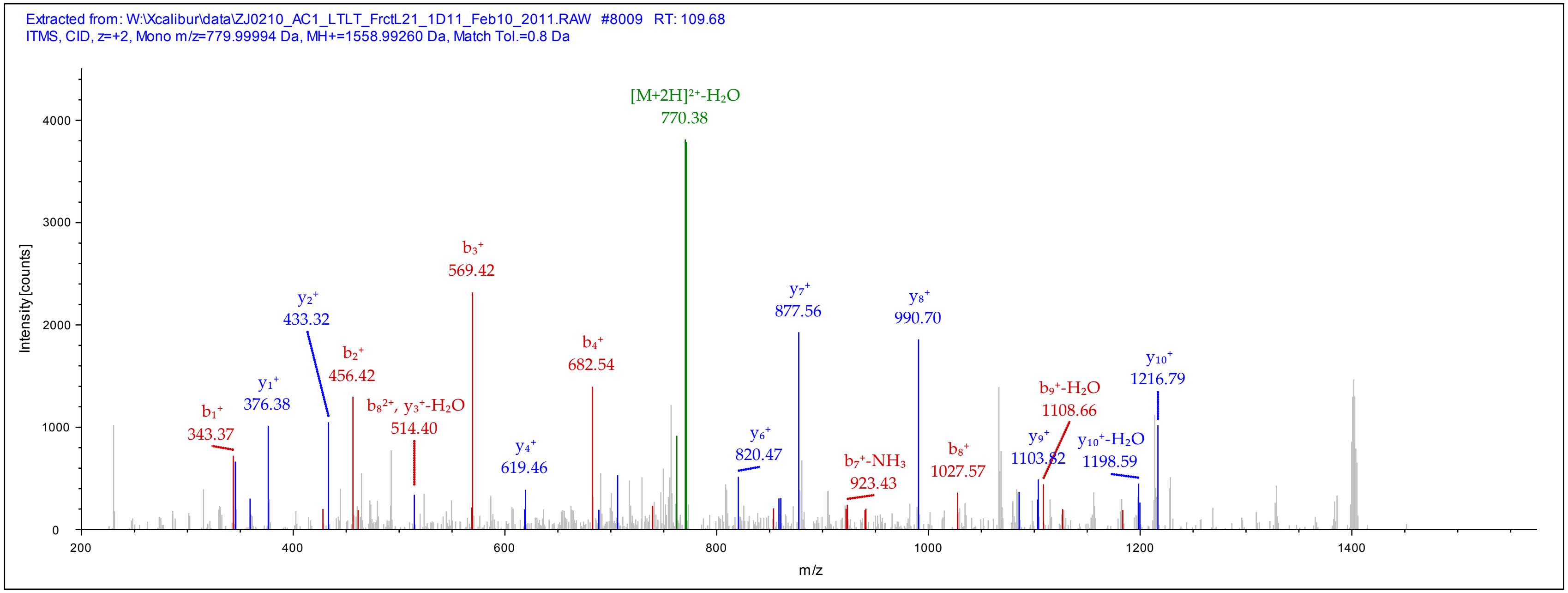
Identified with: Mascot (v1.16); IonScore:29, Exp Value:4.0E-002, Ions matched by search engine: 9/92

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Ras-related protein Rab-3A
- cDNA FLJ59582, highly similar to Ras-related protein Rab-3A lng=292



IPI:IPI00024920.1

Sequence: AQAELVGTADEATR, A1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 830.94012 Da (+1.28 mmu/+1.53 ppm),   MH+: 1660.87297 Da,   RT: 85.78 min,

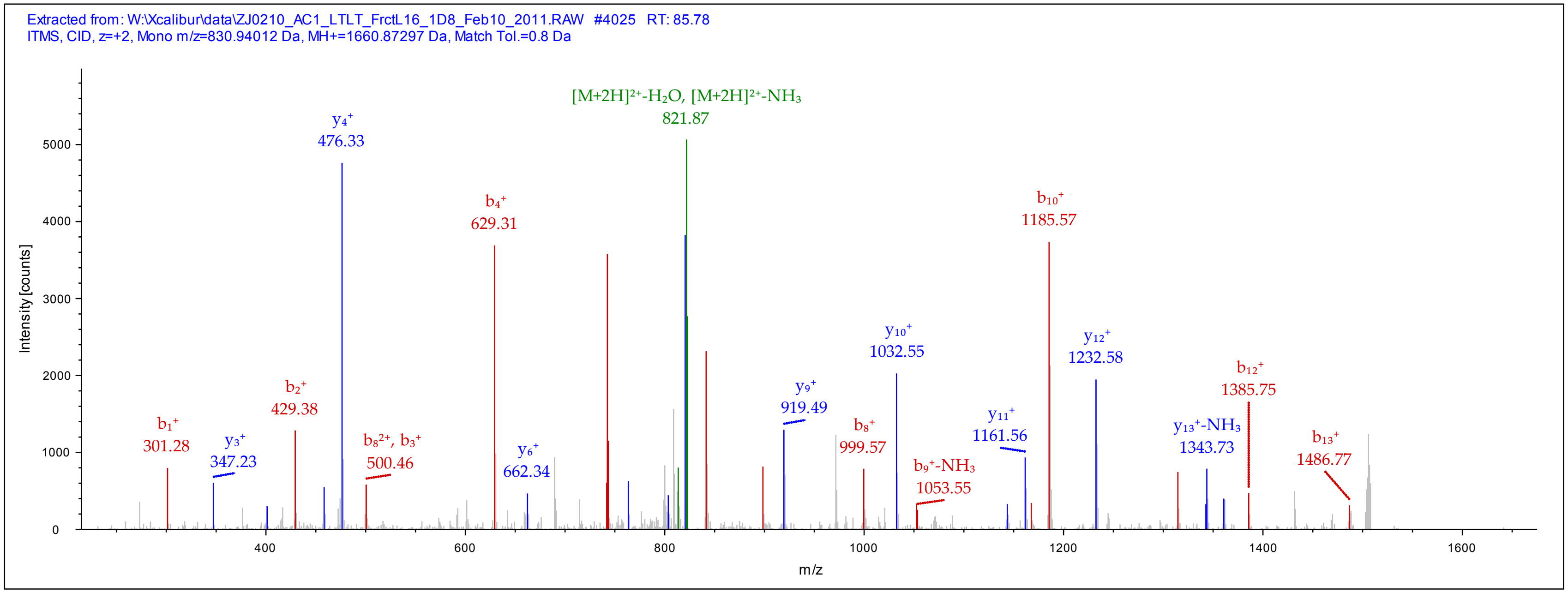
Identified with: Mascot (v1.16); IonScore:64, Exp Value:4.9E-005, Ions matched by search engine: 13/146

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- ATP synthase subunit delta, mitochondrial



IPI:IPI00024990.6

Sequence: AFPAWADTSVLSR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 825.44562 Da (-0.49 mmu/-0.6 ppm), MH+: 1649.88396 Da, RT: 112.99 min,

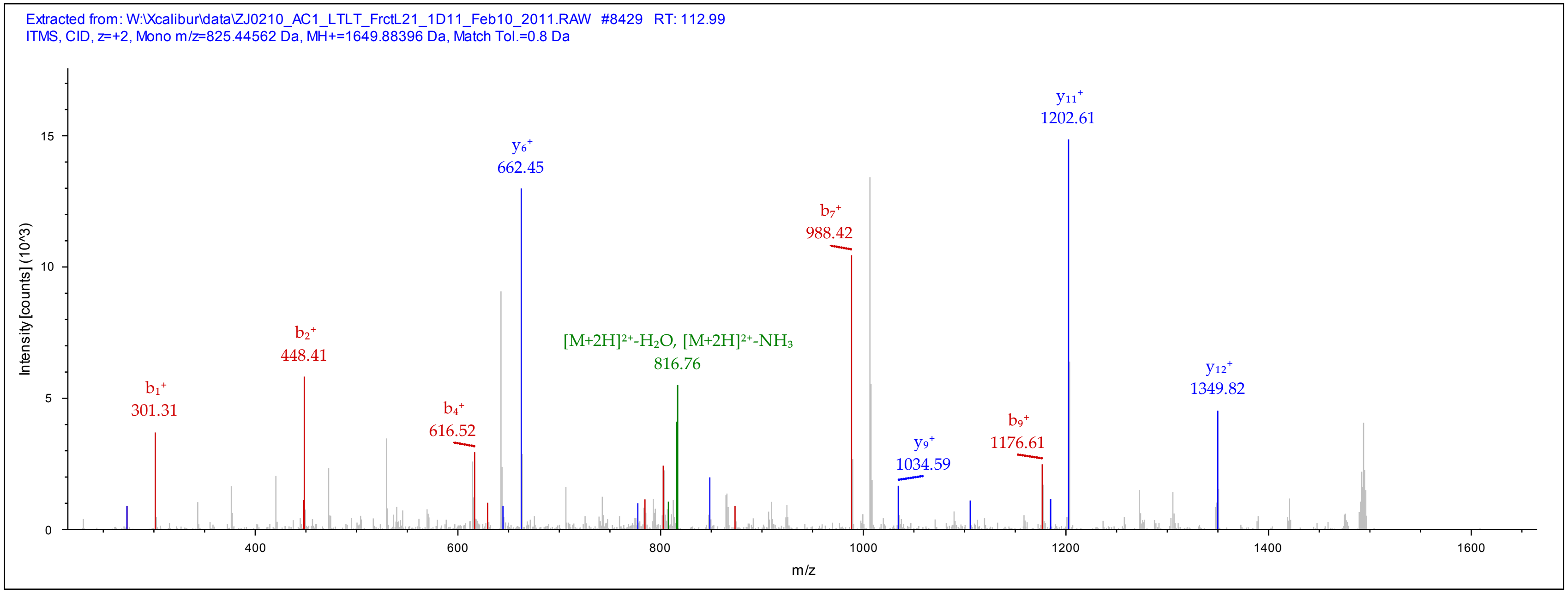
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.6E-002, Ions matched by search engine: 12/106

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial



IPI:IPI00025049.1

Sequence: TCDLVGEK, T1-TMT6plex (229.16293 Da), C2-Carbamidomethyl (57.02146 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 690.38409 Da (+0.2 mmu/+0.28 ppm), MH+: 1379.76091 Da, RT: 79.12 min,

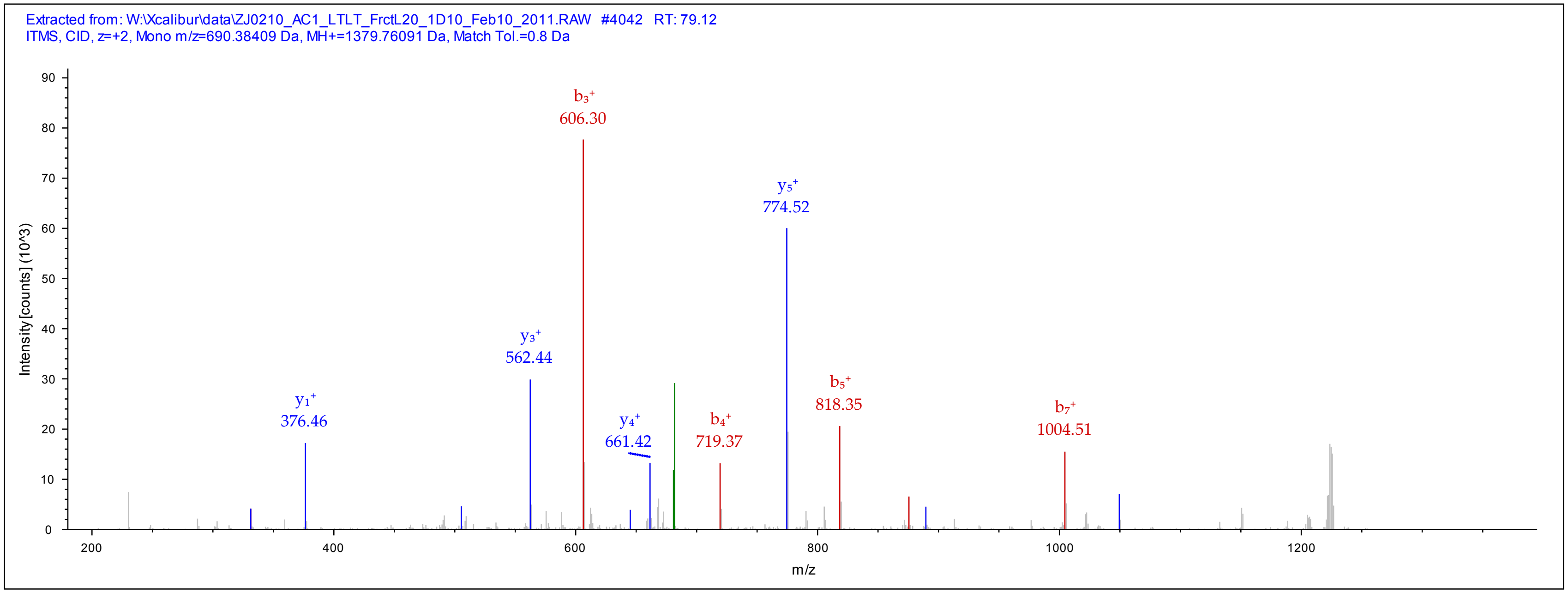
Identified with: Mascot (v1.16); IonScore:34, Exp Value:3.4E-002, Ions matched by search engine: 7/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Cation-dependent mannose-6-phosphate receptor



IPI:IPI00025318.1

Sequence: GDYDAFFEAR, G1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 710.34100 Da (+0.23 mmu/+0.33 ppm),   MH+: 1419.67473 Da,   RT: 97.59 min,

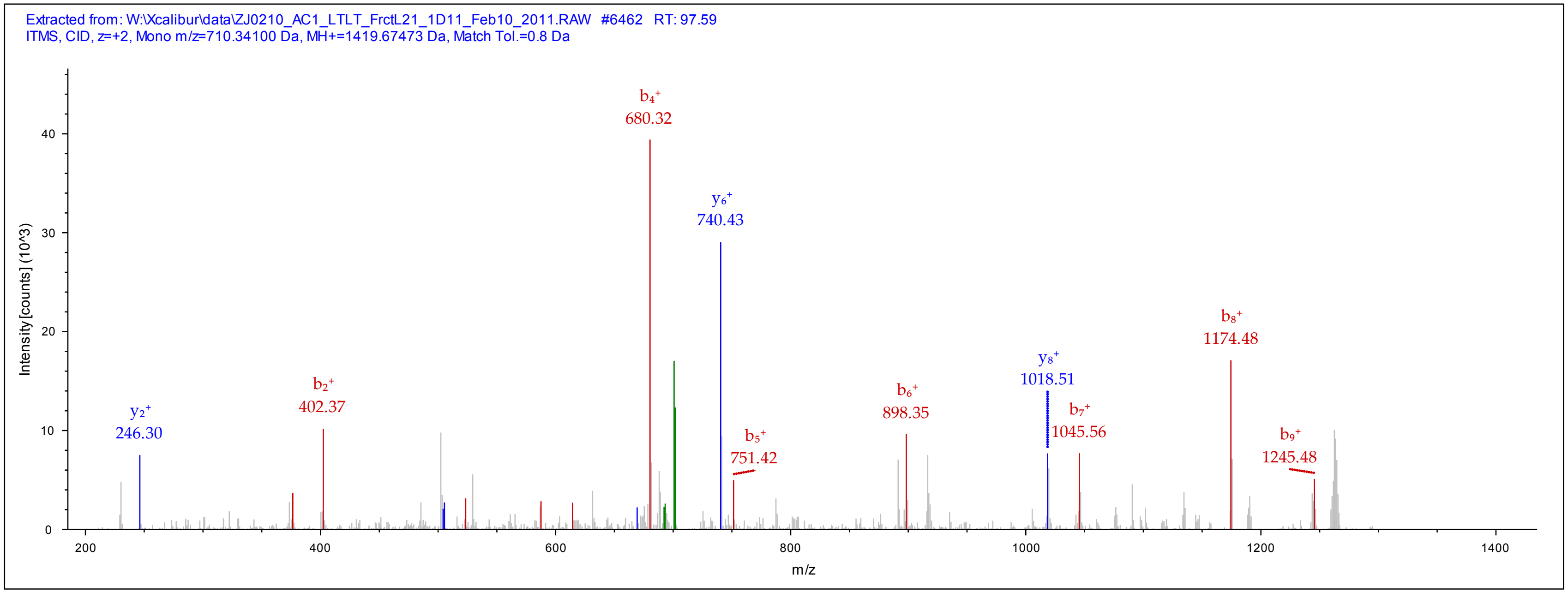
Identified with: Mascot (v1.16); IonScore:30, Exp Value:6.0E-002, Ions matched by search engine: 5/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

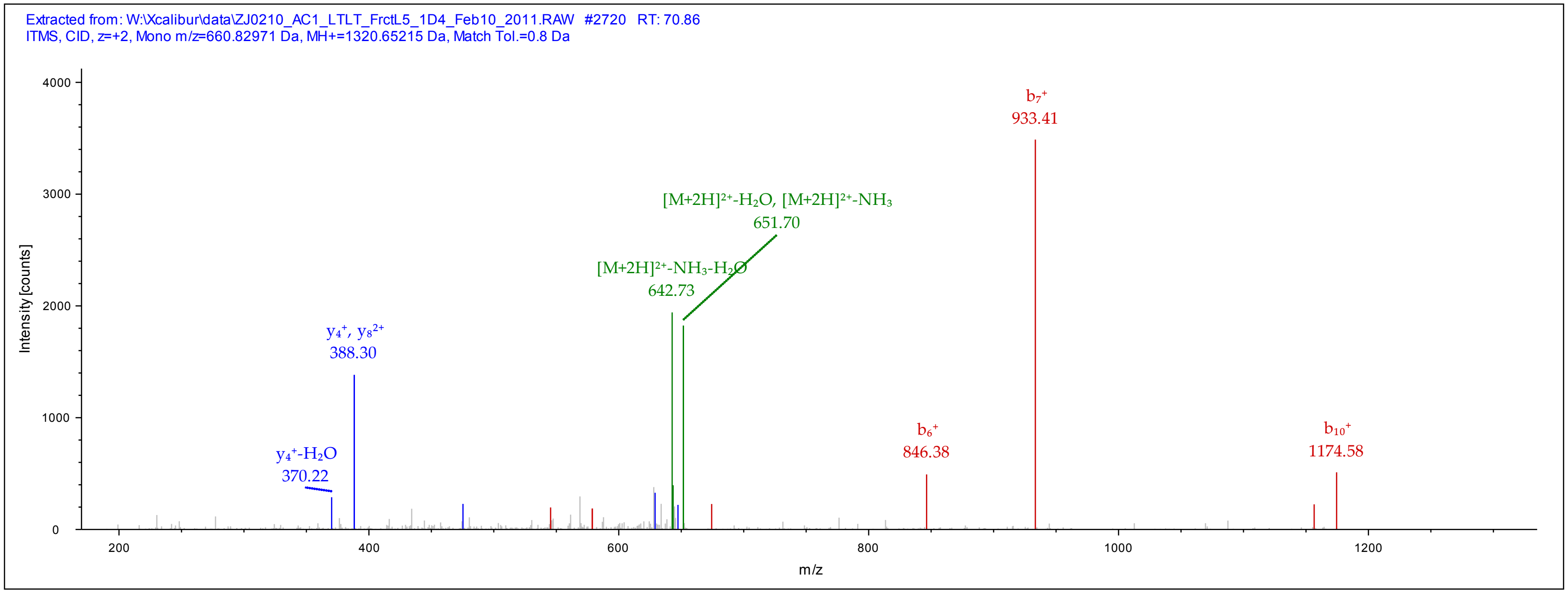
- SH3 domain-binding glutamic acid-rich-like protein



IPI:IPI00027144.8

Sequence: TLTEGDSPGSQ, T1-TMT6plex (229.16293 Da)
Charge: +2,   Monoisotopic m/z: 660.82971 Da (+2.02 mmu/+3.06 ppm),   MH+: 1320.65215 Da,   RT: 70.86 min,
Identified with: Mascot (v1.16); IonScore:34, Exp Value:2.6E-002, Ions matched by search engine: 6/98
Fragment match tolerance used for search: 0.8 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Cytochrome b561
- cDNA FLJ55917, highly similar to Cytochrome b561 domain-containing protein 1



IPI:IPI00029631.1

Sequence: ADTQTYQPYNK, A1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 893.97394 Da (+1.5 mmu/+1.68 ppm), MH+: 1786.94060 Da, RT: 78.45 min,

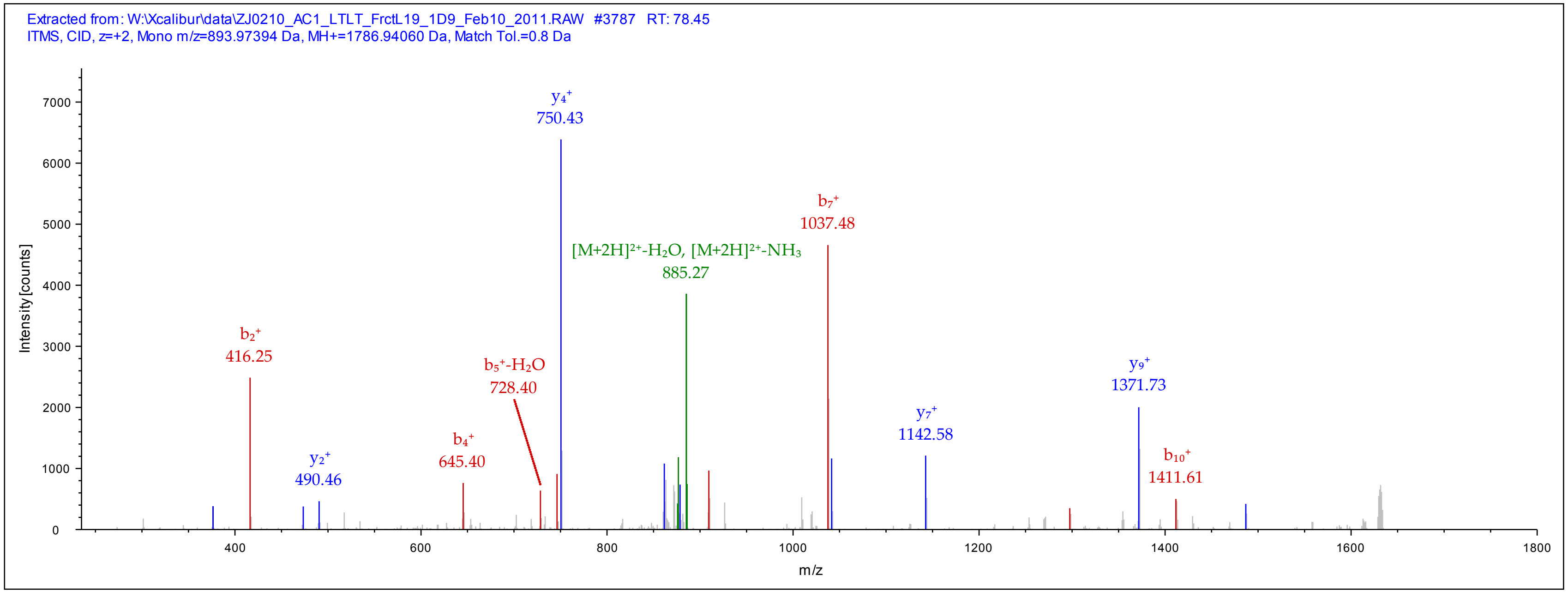
Identified with: Mascot (v1.16); IonScore:52, Exp Value:8.7E-004, Ions matched by search engine: 9/100

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Enhancer of rudimentary homolog



IPI:IPI00029665.8

Sequence: LSDYLFTLAR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 714.40924 Da (+0.79 mmu/+1.11 ppm),   MH+: 1427.81120 Da,   RT: 164.82 min,

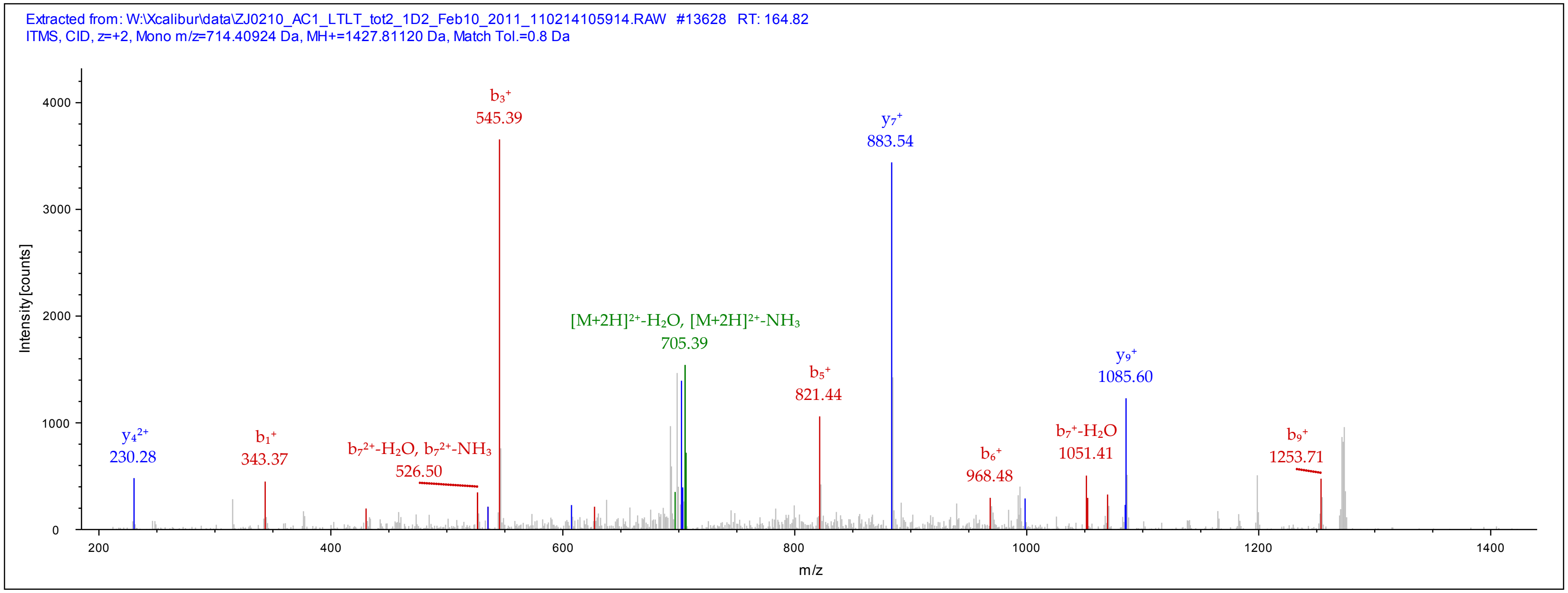
Identified with: Mascot (v1.16); IonScore:33, Exp Value:4.3E-002, Ions matched by search engine: 8/82

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial



IPI:IPI00029997.1

Sequence: VTLTLPVLNAAR, V1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 748.97235 Da (+0.59 mmu/+0.79 ppm),   MH+: 1496.93743 Da,   RT: 120.51 min,

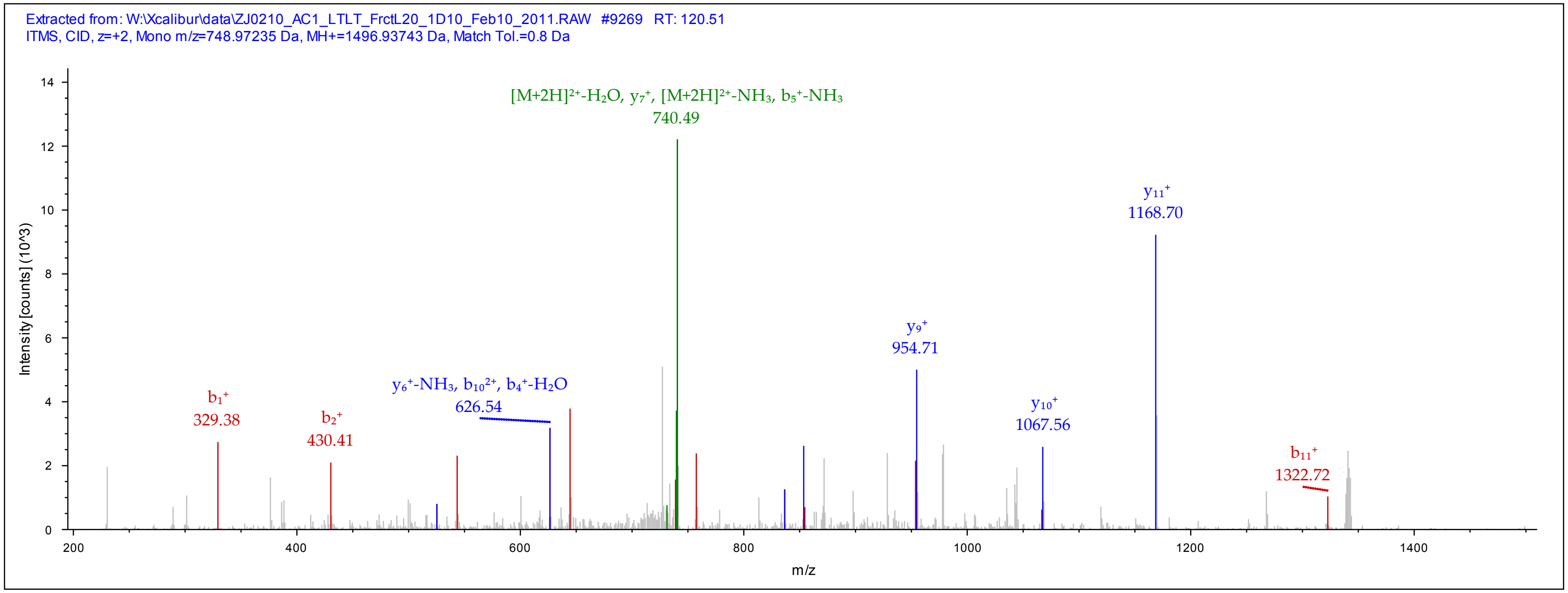
Identified with: Mascot (v1.16); IonScore:47, Exp Value:5.5E-004, Ions matched by search engine: 11/98

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 6-phosphogluconolactonase



IPI:IPI00032903.3

Sequence: TQIAPGSQTVLGIGPGPADLIDK, T1-TMT6plex (229.16293 Da), K23-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 902.85559 Da (+2.63 mmu/+2.92 ppm),   MH+: 2706.55222 Da,   RT: 122.09 min,

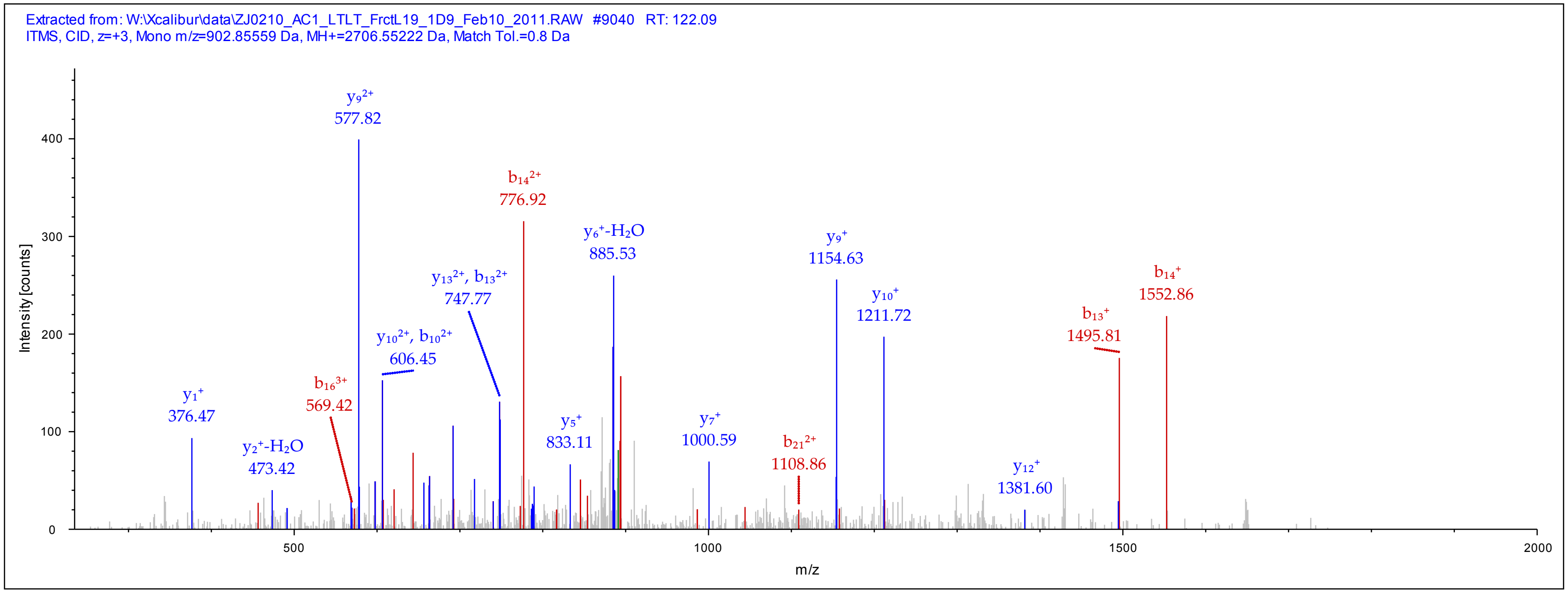
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.1E-002, Ions matched by search engine: 20/260

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Peptidyl-tRNA hydrolase 2, mitochondrial
- cDNA FLJ32471 fis, clone SKNMC2000322, highly similar to Peptidyl-tRNA hydrolase 2, mitochondrial lng=180



IPI:IPI00034159.1

Sequence: AYLESFYK, A1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 739.91870 Da (+0.29 mmu/+0.39 ppm), MH+: 1478.83013 Da, RT: 106.23 min,

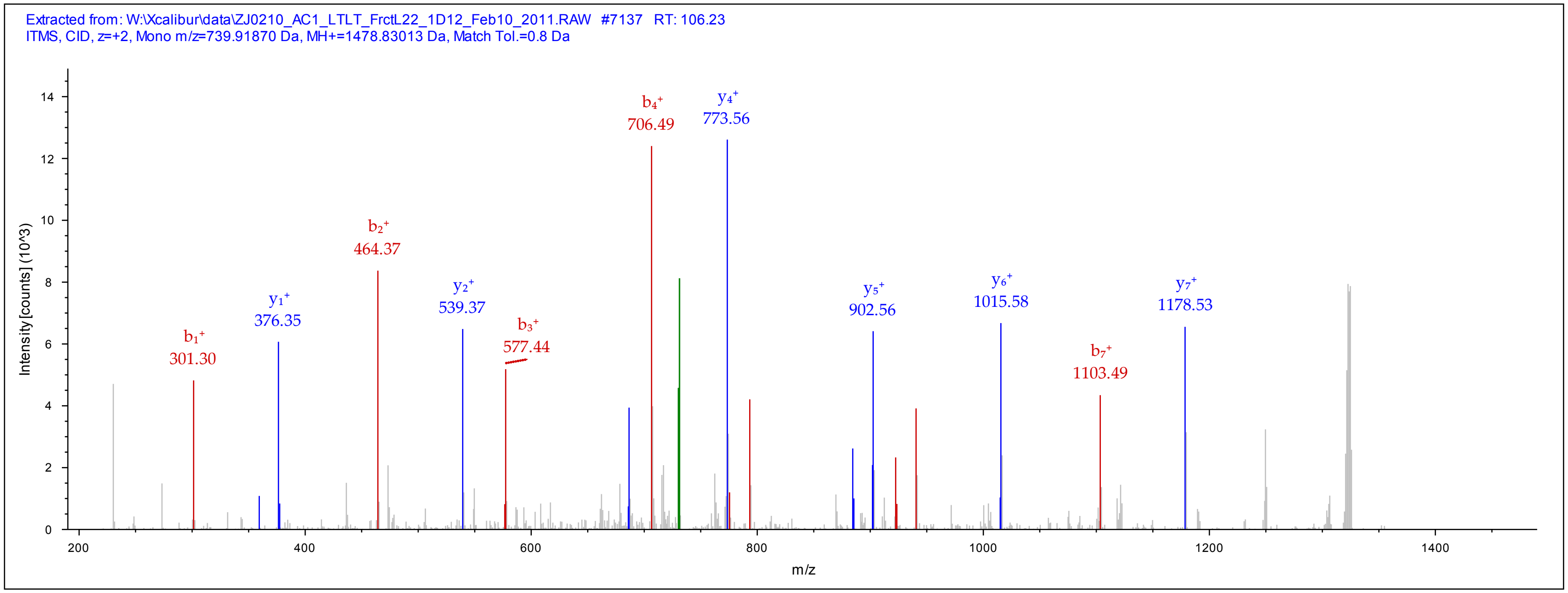
Identified with: Mascot (v1.16); IonScore:51, Exp Value:8.0E-004, Ions matched by search engine: 6/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; $b-H_2O$; $b-NH_3$; y; $y-H_2O$; $y-NH_3$

Protein references (2):

- V-type proton ATPase subunit d 1
- cDNA FLJ54755, highly similar to Vacuolar ATP synthase subunit d



IPI:IPI00103599.1

Sequence: TVNTFSQSVSSLFGEDNVR, T1-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 772.72681 Da (-0.38 mmu/-0.49 ppm),   MH+: 2316.16587 Da,   RT: 123.14 min,

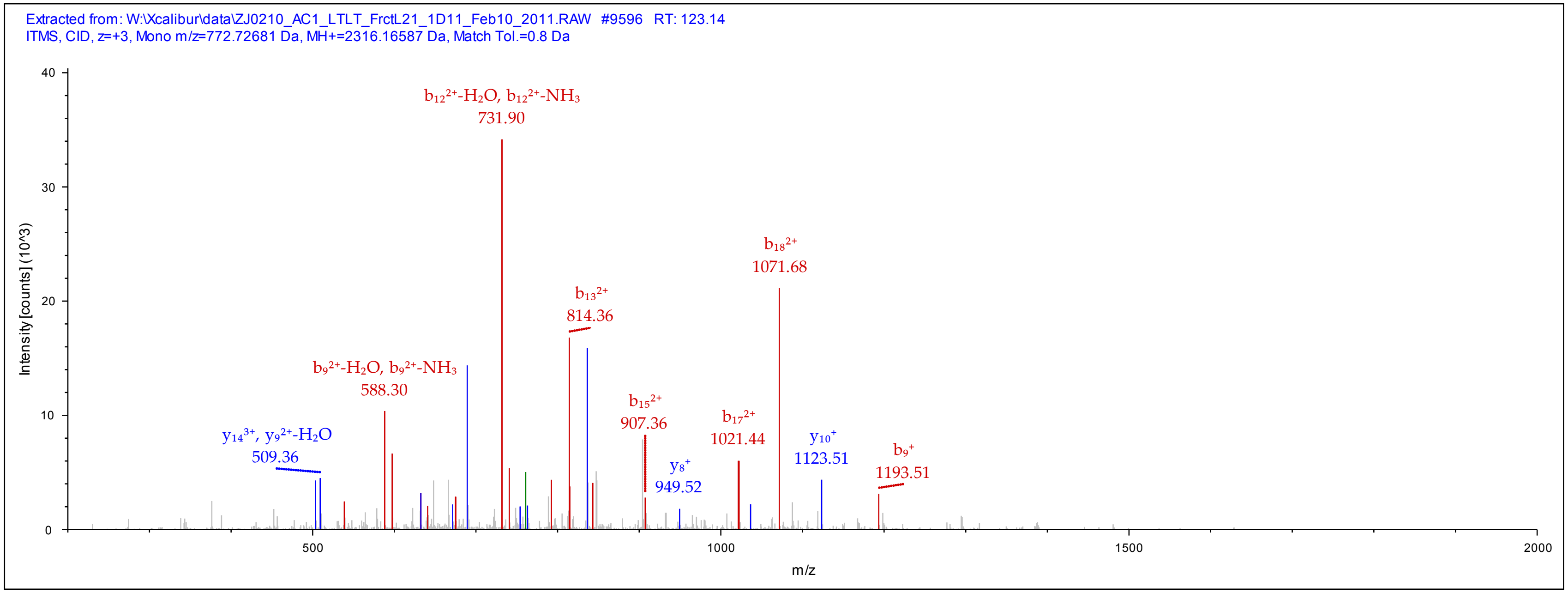
Identified with: Mascot (v1.16); IonScore:41, Exp Value:1.4E-002, Ions matched by search engine: 21/206

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- BRI3-binding protein



IPI:IPI00104050.3

Sequence: ASAVSELSPR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 623.35382 Da (+0.14 mmu/+0.23 ppm), MH+: 1245.70036 Da, RT: 77.42 min,

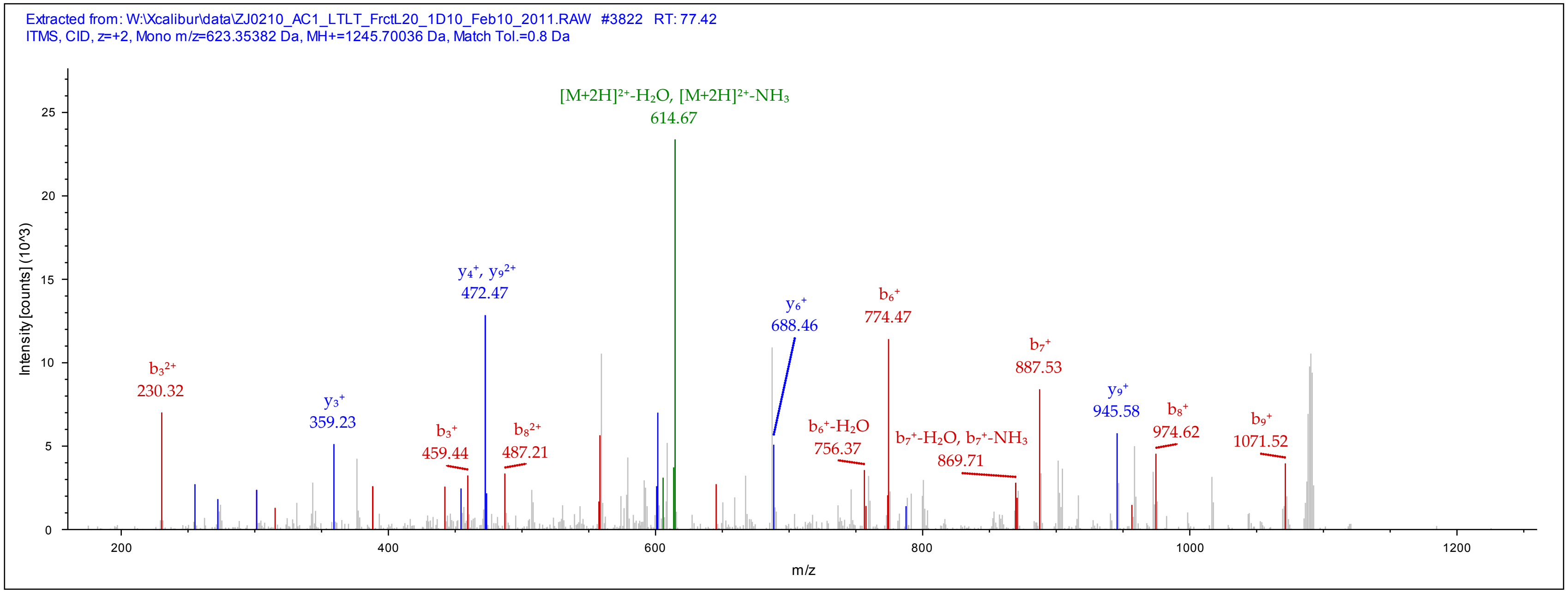
Identified with: Mascot (v1.16); IonScore:43, Exp Value:4.5E-003, Ions matched by search engine: 8/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Thyroid hormone receptor-associated protein 3



IPI:IPI00106491.3

Sequence: GEVGLLFTNR, G1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 667.88519 Da (+0.04 mmu/+0.06 ppm), MH+: 1334.76311 Da, RT: 98.90 min,

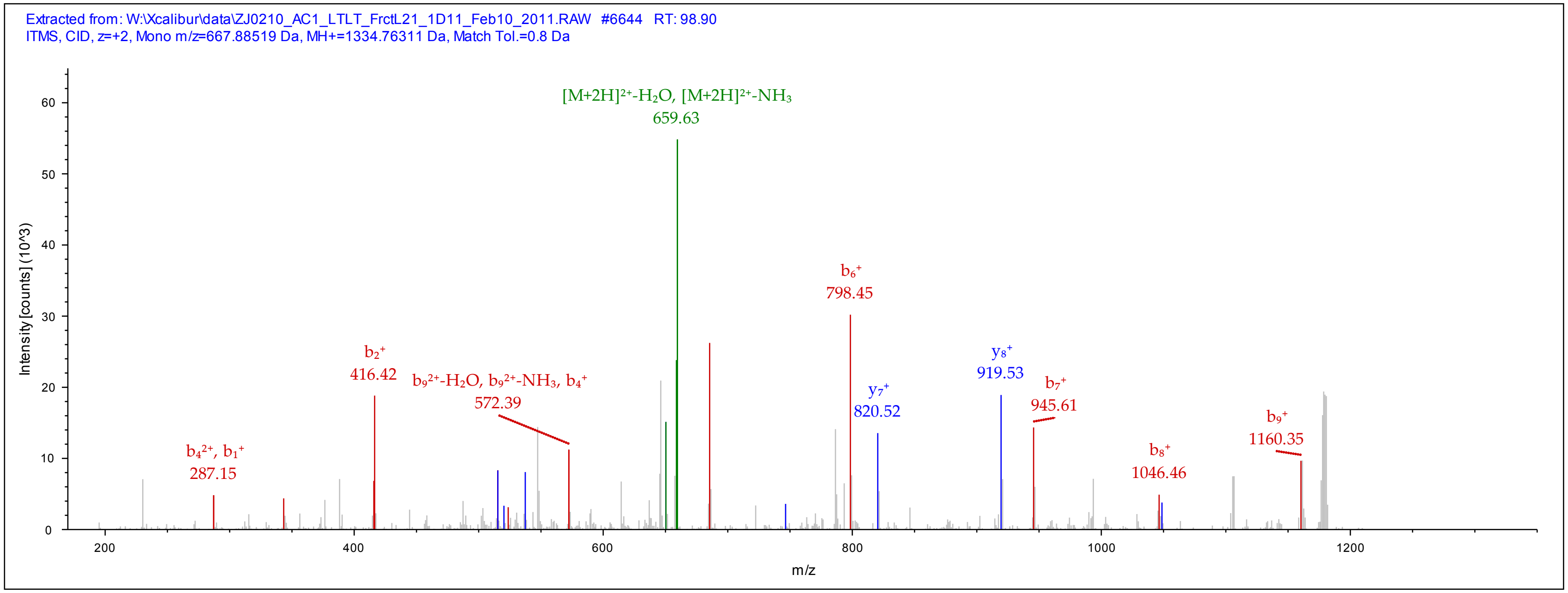
Identified with: Mascot (v1.16); IonScore:43, Exp Value:5.0E-003, Ions matched by search engine: 7/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- mRNA turnover protein 4 homolog



IPI:IPI00106495.1

Sequence: LNLAQFLNEDLS, L1-TMT6plex (229.16293 Da)

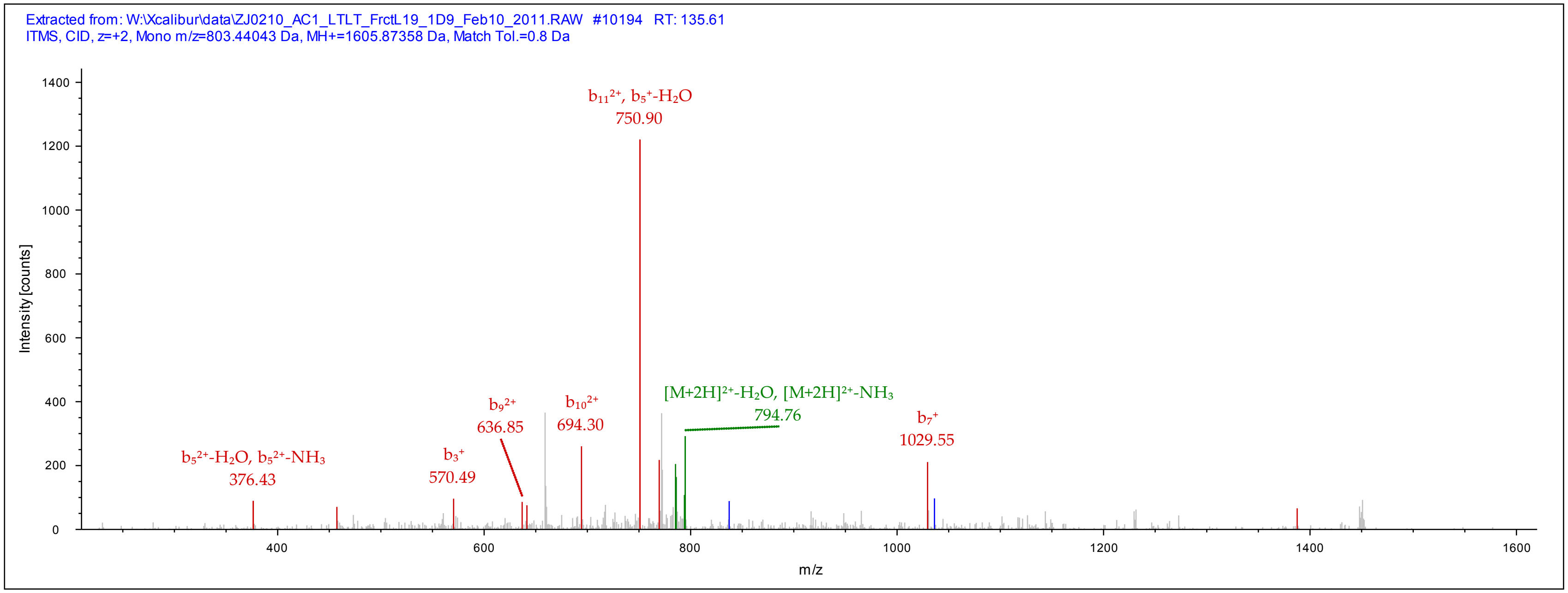
Charge: +2,   Monoisotopic m/z: 803.44043 Da (+2.49 mmu/+3.09 ppm),   MH+: 1605.87358 Da,   RT: 135.61 min,

Identified with: Mascot (v1.16); IonScore:34, Exp Value:4.7E-002, Ions matched by search engine: 9/106

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):



IPI:IPI00152240.3

Sequence: SLAPSLLDR, S1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 600.86169 Da (+0.55 mmu/+0.92 ppm),   MH+: 1200.71611 Da,   RT: 92.50 min,

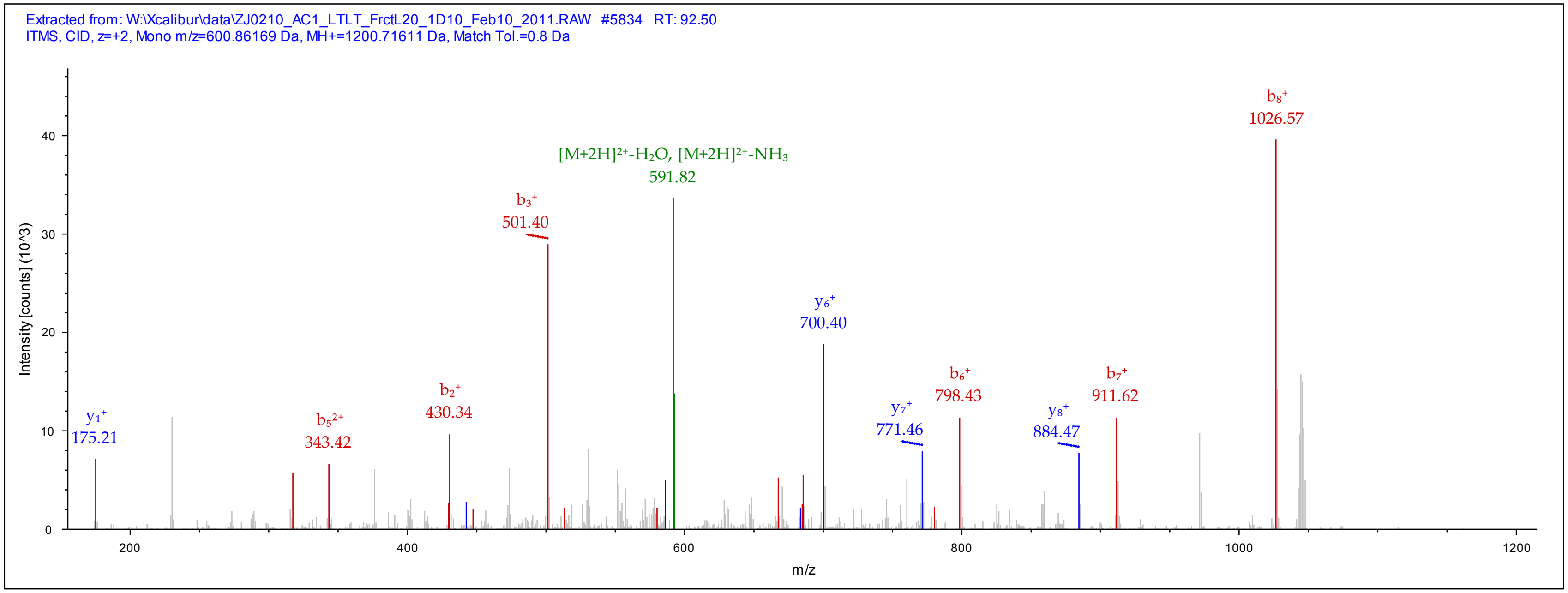
Identified with: Mascot (v1.16); IonScore:37, Exp Value:2.1E-002, Ions matched by search engine: 7/78

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Protein kish-A
- similar to transmembrane protein 167A



IPI:IPI00155729.6

Sequence: DLLLVAR, D1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 514.83710 Da (+0.16 mmu/+0.32 ppm), MH+: 1028.66692 Da, RT: 107.30 min,

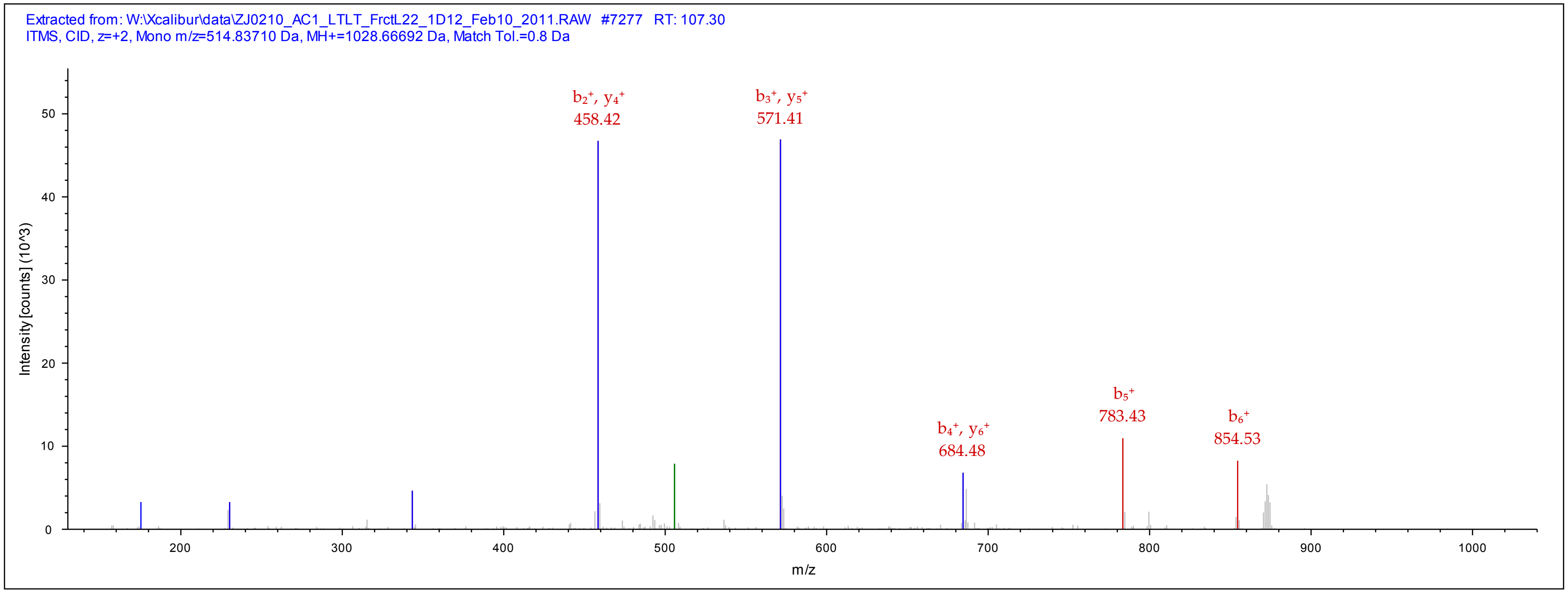
Identified with: Mascot (v1.16); IonScore:38, Exp Value:6.4E-003, Ions matched by search engine: 6/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Plexin-B3
- plexin B3 isoform 2 lng=1932



IPI:IPI00156689.3

Sequence: GVDIVMDPLGGSDTAK, G1-TMT6plex (229.16293 Da), K16-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 1017.05414 Da (+0.99 mmu/+0.98 ppm), MH+: 2033.10100 Da, RT: 113.43 min,

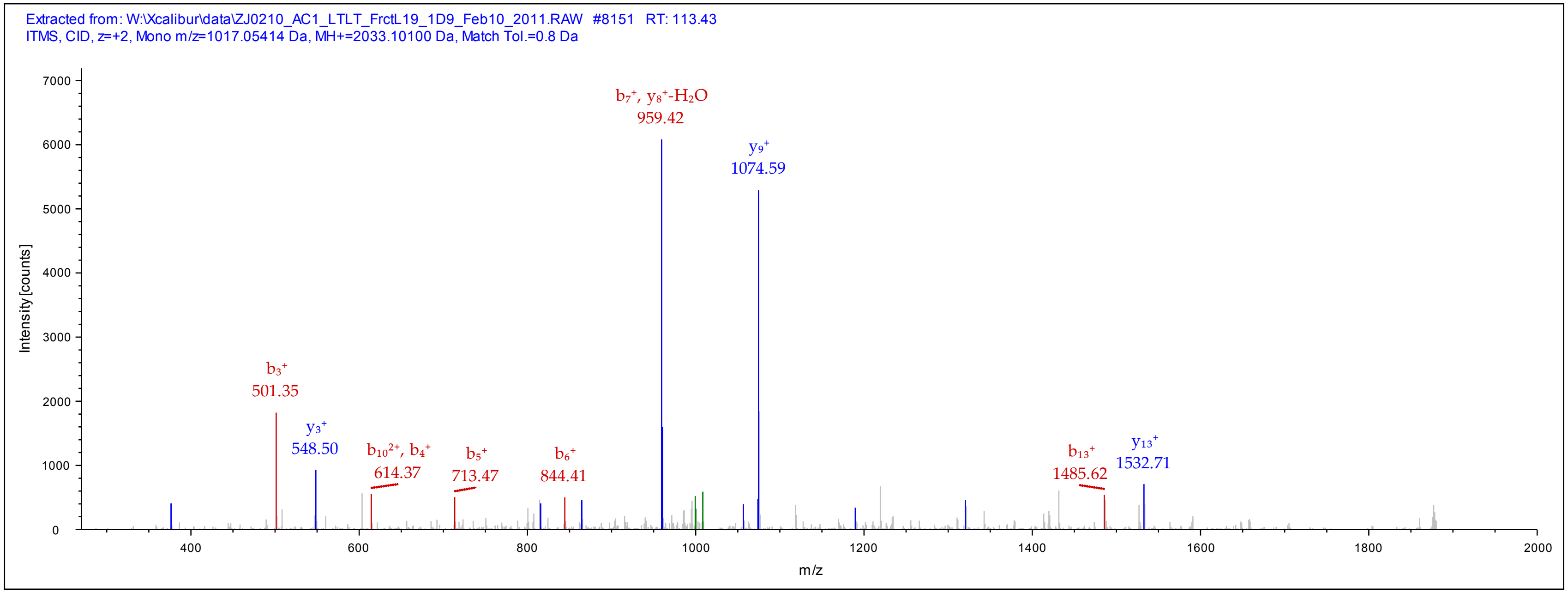
Identified with: Mascot (v1.16); IonScore:42, Exp Value:9.1E-003, Ions matched by search engine: 16/142

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Synaptic vesicle membrane protein VAT-1 homolog



IPI:IPI00167572.4

Sequence: SLCNLEESITSAGR, S1-TMT6plex (229.16293 Da), C3-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 883.45020 Da (-1.07 mmu/-1.21 ppm),   MH+: 1765.89311 Da,   RT: 106.02 min,

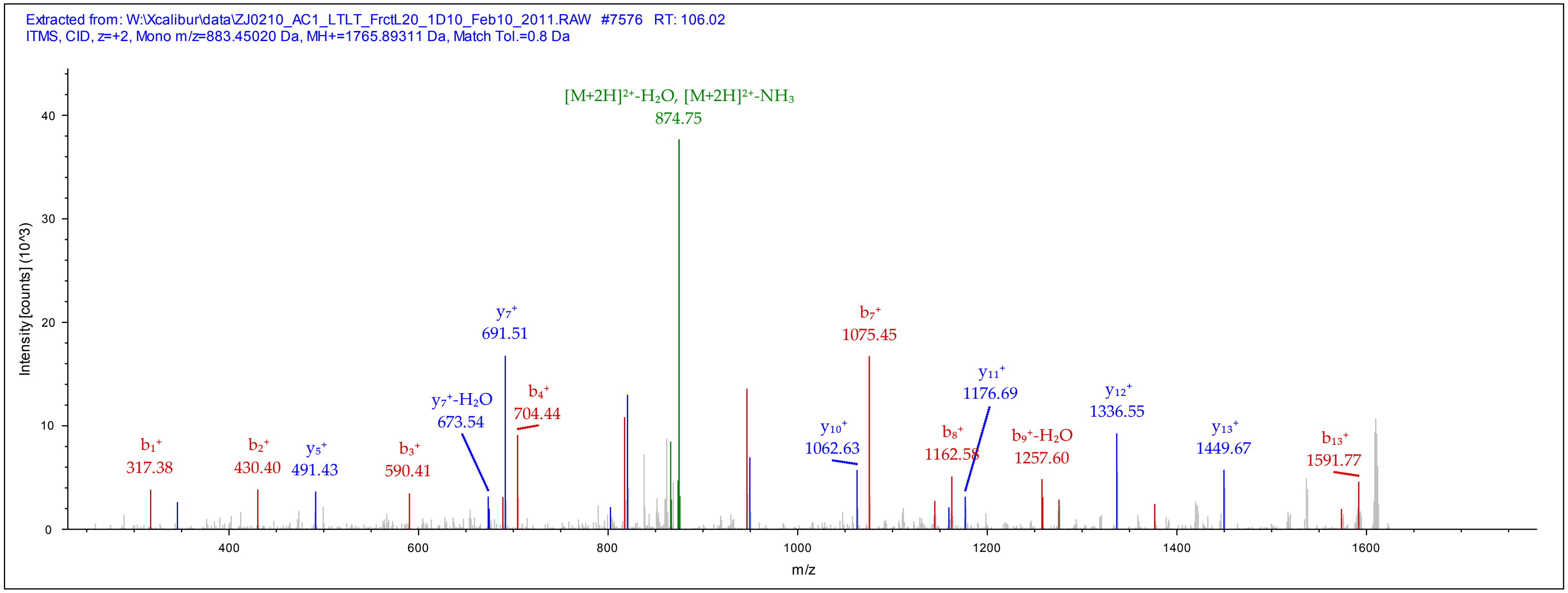
Identified with: Mascot (v1.16); IonScore:65, Exp Value:3.3E-005, Ions matched by search engine: 17/144

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Protein FAM98B
- family with sequence similarity 98, member B isoform 1



IPI:IPI00167925.5

Sequence: IARELR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 493.81369 Da (-5.39 mmu/-10.92 ppm), MH+: 986.62010 Da, RT: 95.63 min,

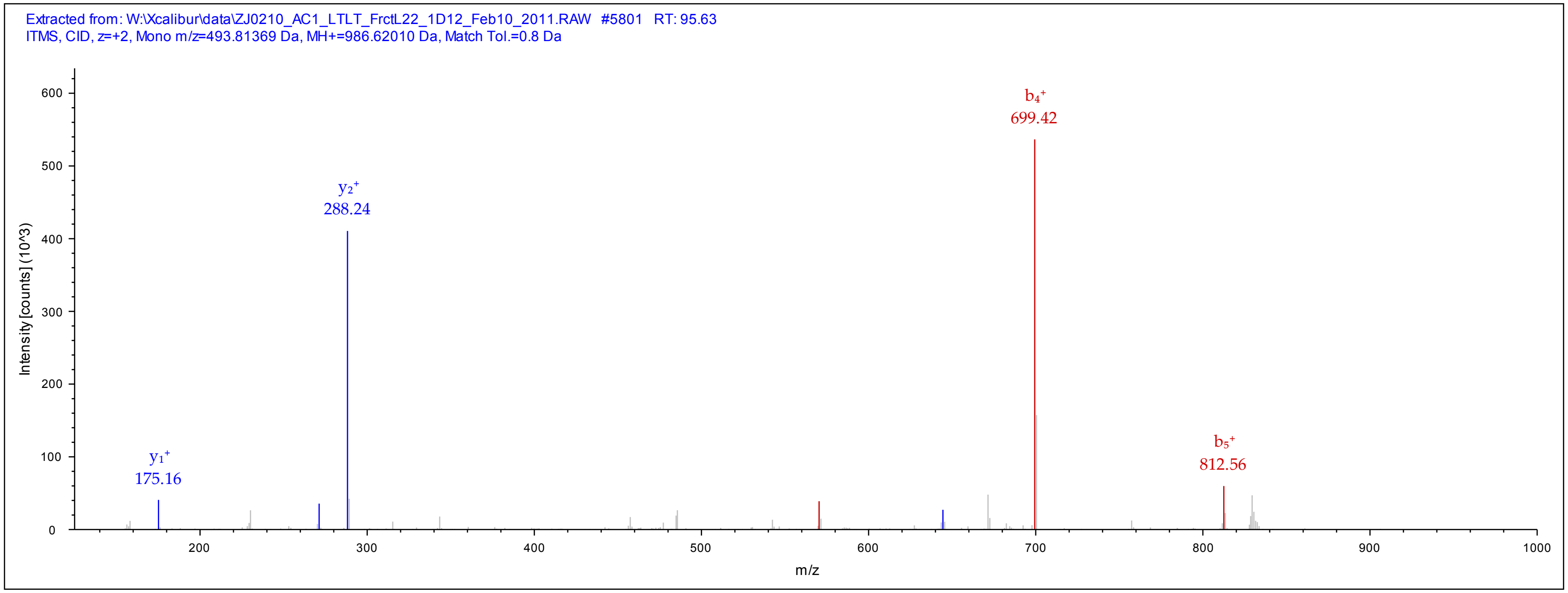
Identified with: Mascot (v1.16); IonScore:31, Exp Value:4.3E-002, Ions matched by search engine: 4/46

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- DDB1- and CUL4-associated factor 4-like protein 2



IPI:IPI00168631.1

Sequence: LLDFLNVK, L1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 710.45459 Da (+2.15 mmu/+3.03 ppm), MH+: 1419.90190 Da, RT: 136.04 min,

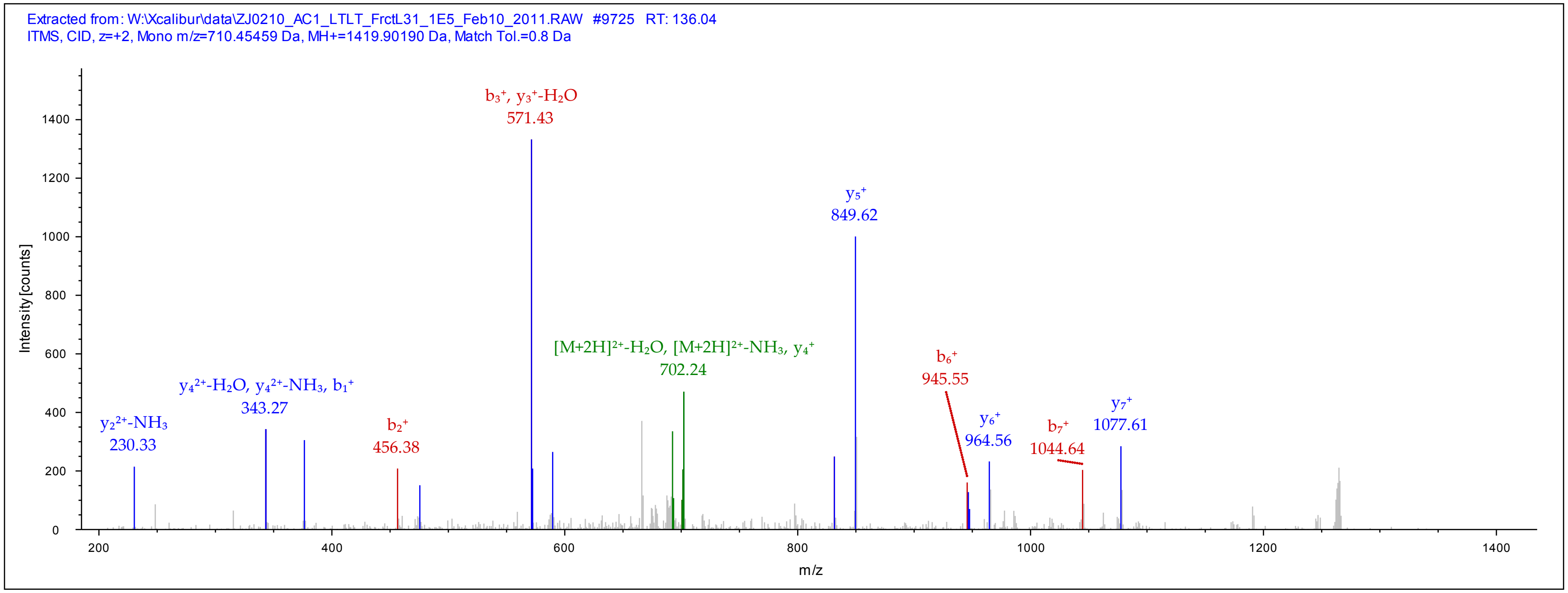
Identified with: Mascot (v1.16); IonScore:45, Exp Value:1.8E-003, Ions matched by search engine: 7/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- UPF0672 protein C3orf58



IPI:IPI00170972.2

Sequence: VAELLLAK, V1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 657.94214 Da (+0.43 mmu/+0.65 ppm),   MH+: 1314.87700 Da,   RT: 119.76 min,

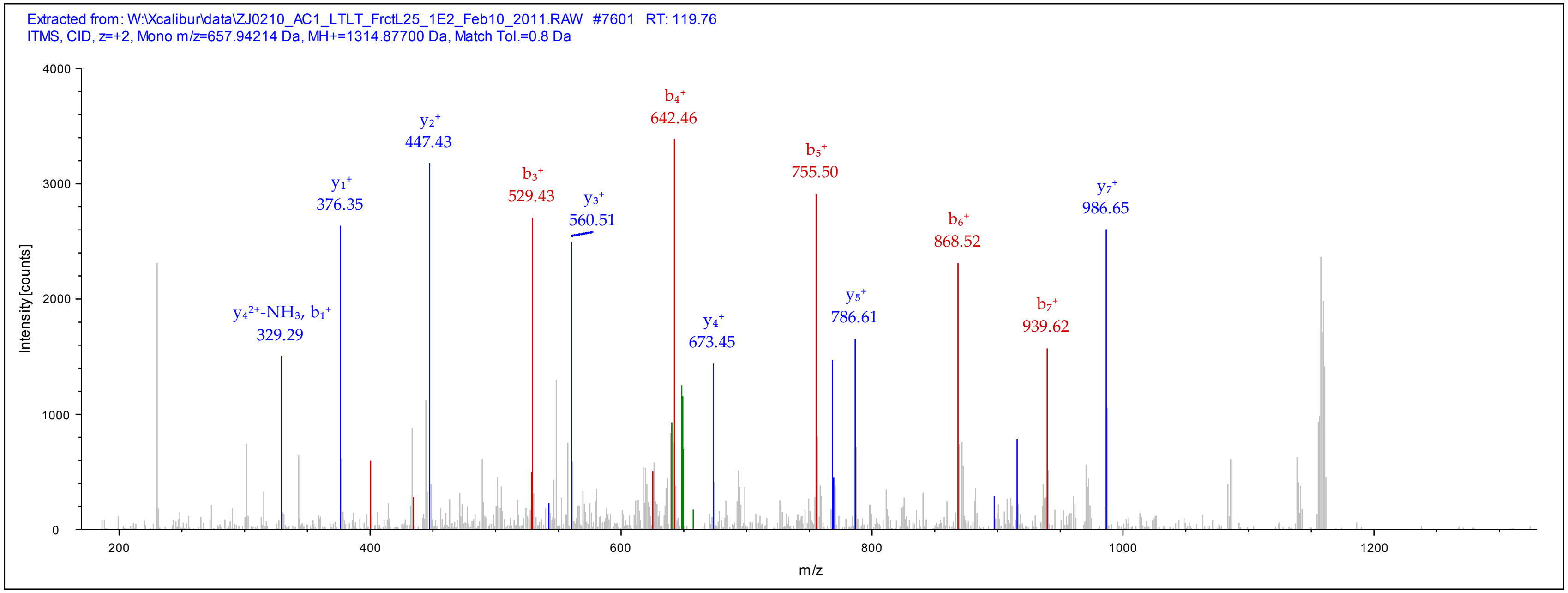
Identified with: Mascot (v1.16); IonScore:42, Exp Value:1.5E-003, Ions matched by search engine: 7/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- UPF0553 protein C9orf64



IPI:IPI00172591.5

Sequence: NLLTGLVR, N1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 557.86133 Da (+0.39 mmu/+0.7 ppm),   MH+: 1114.71538 Da,   RT: 103.32 min,

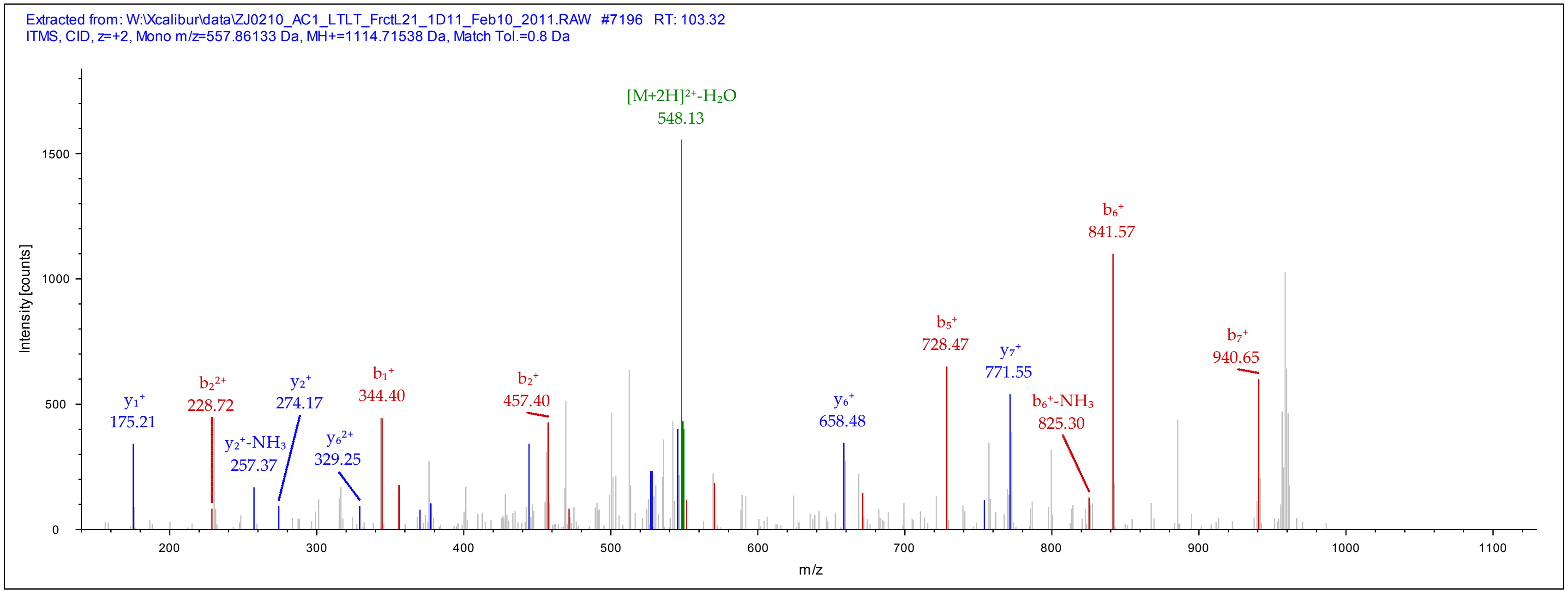
Identified with: Mascot (v1.16); IonScore:31, Exp Value:2.9E-002, Ions matched by search engine: 9/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 39S ribosomal protein L17, mitochondrial



IPI00172656.6

Sequence: NTLCAPEVISLINTR, N1-TMT6plex (229.16293 Da), C4-Carbamidomethyl (57.02146 Da)

Charge: +2, Monoisotopic m/z: 965.53522 Da (+0.09 mmu/+0.09 ppm), MH+: 1930.06316 Da, RT: 118.80 min,

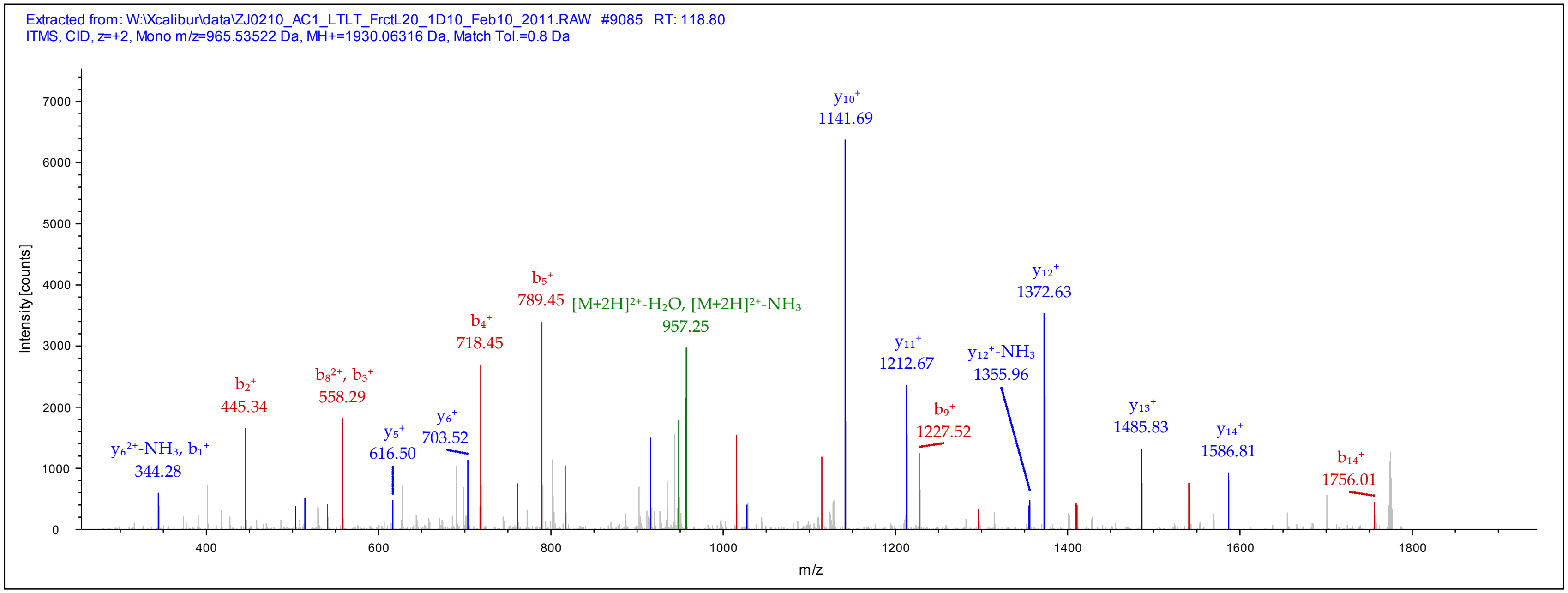
Identified with: Mascot (v1.16); IonScore:64, Exp Value:4.7E-005, Ions matched by search engine: 23/164

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- FAS-associated factor 2 lng=445



IPI:IPI00177008.1

Sequence: AQALLADVDTLLFDCDGVLWR, A1-TMT6plex (229.16293 Da), C15-Carbamidomethyl (57.02146 Da)

Charge: +3,   Monoisotopic m/z: 874.12799 Da (+1.69 mmu/+1.93 ppm),   MH+: 2620.36942 Da,   RT: 231.24 min,

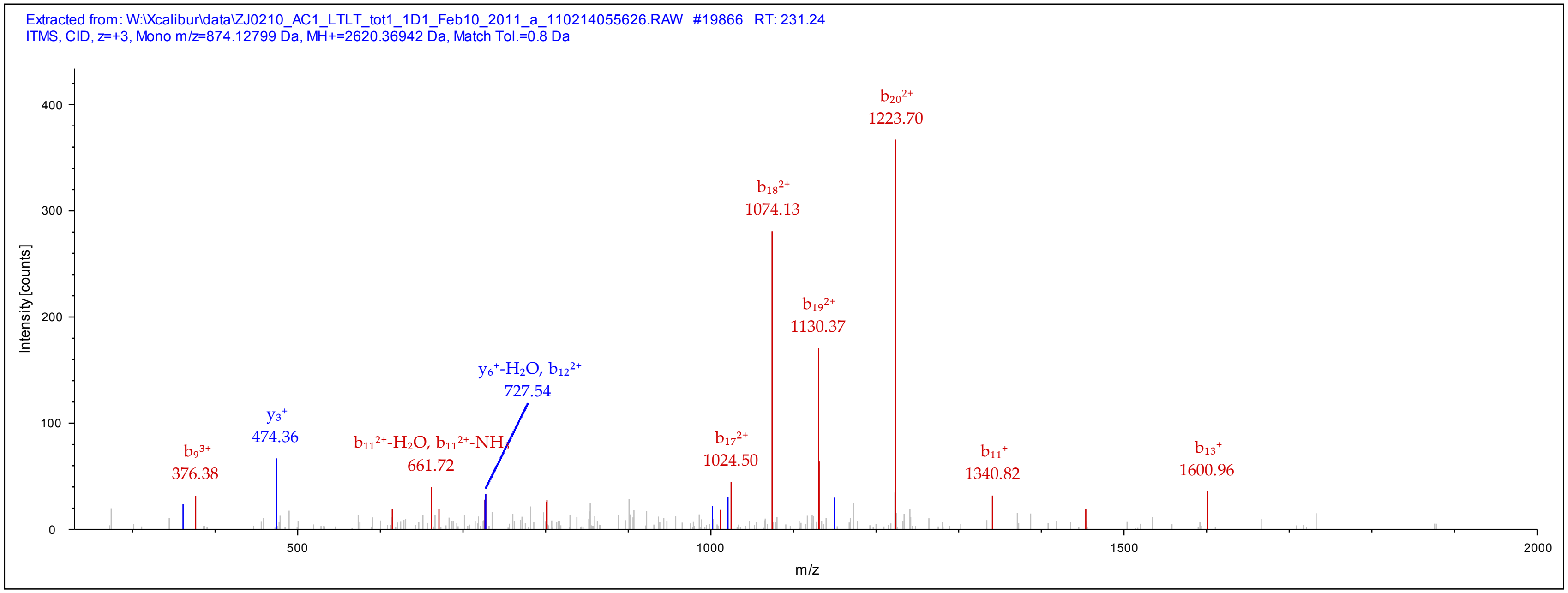
Identified with: Mascot (v1.16); IonScore:42, Exp Value:1.2E-002, Ions matched by search engine: 16/216

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Phosphoglycolate phosphatase



IPI:IPI00178188.5

Sequence: DIDPQNDLTFLR, D1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 838.44867 Da (+2.37 mmu/+2.82 ppm), MH+: 1675.89006 Da, RT: 111.45 min,

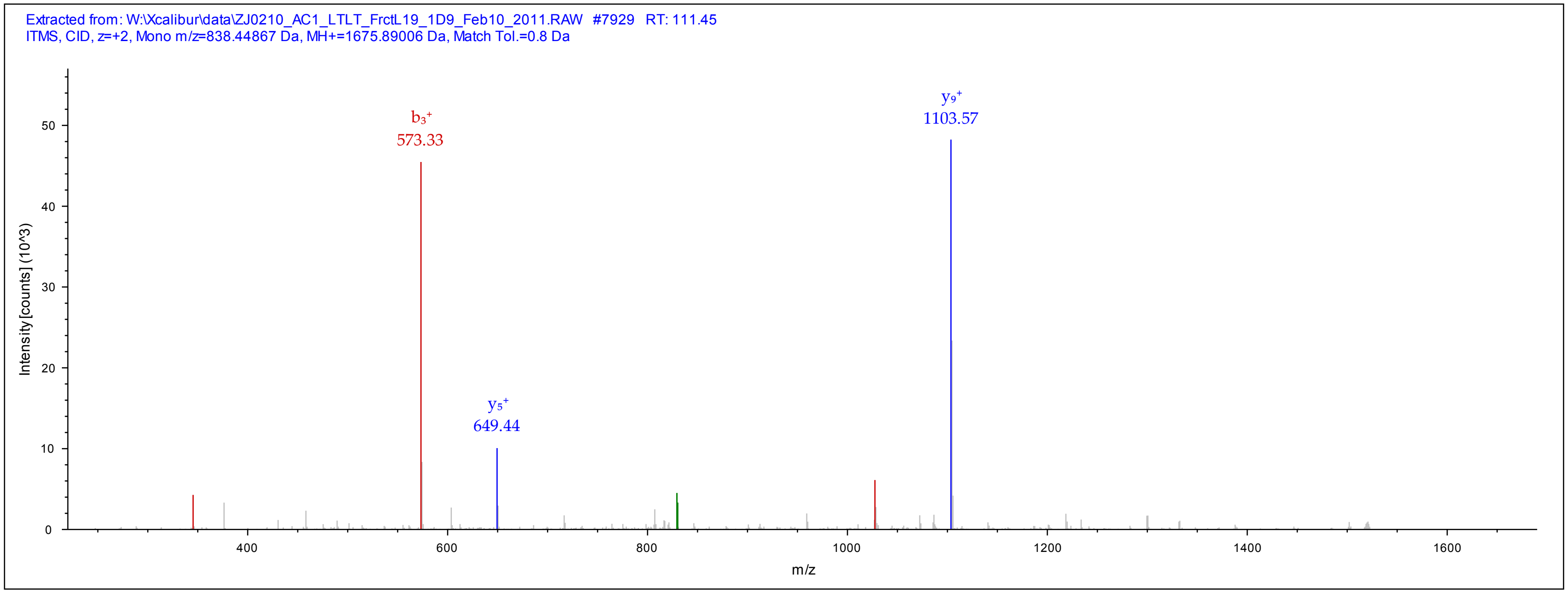
Identified with: Mascot (v1.16); IonScore:31, Exp Value:8.4E-002, Ions matched by search engine: 7/118

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Dynein light chain roadblock-type 2
- Isoform 1 of Dynein light chain roadblock-type 1
- Dynein, light chain, roadblock-type 1 lng=148
- cDNA FLJ59194, moderately similar to Dynein light chain 2A, cytoplasmic lng=121



IPI:IPI00847986.1

Sequence: TTPDVIFVFGFR, T1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 814.45648 Da (+0.54 mmu/+0.66 ppm),   MH+: 1627.90569 Da,   RT: 177.25 min,

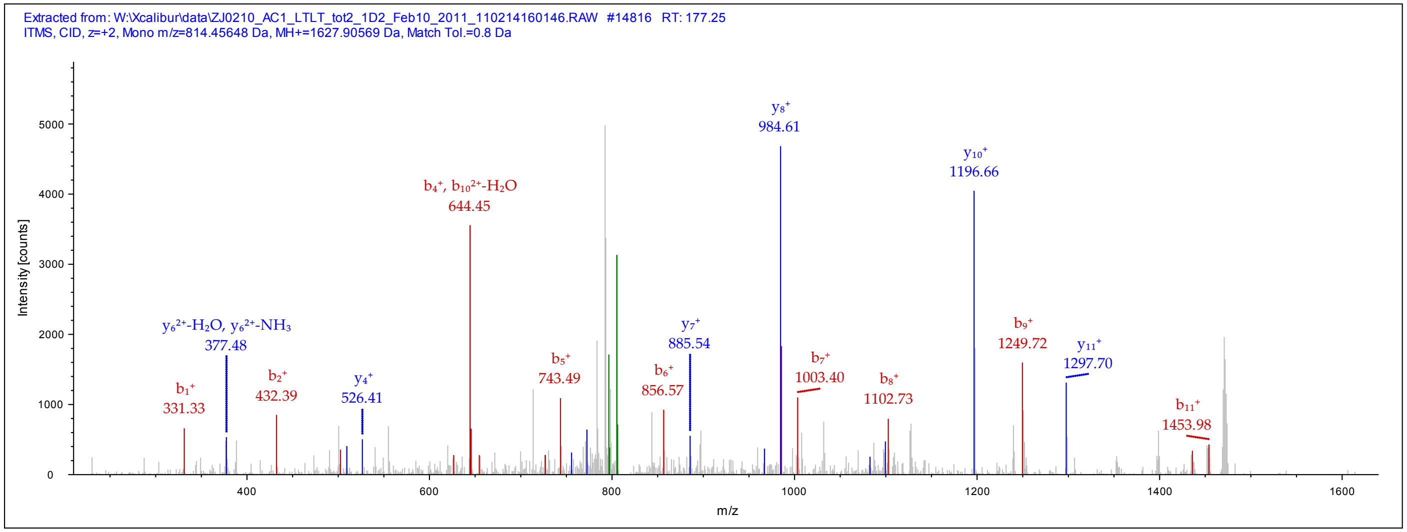
Identified with: Mascot (v1.16); IonScore:35, Exp Value:3.2E-002, Ions matched by search engine: 6/94

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform 1 of 40S ribosomal protein S24
- Isoform 2 of 40S ribosomal protein S24
- 15 kDa protein lng=132
- ribosomal protein S24 isoform d lng=289
- ribosomal protein S24 isoform e lng=132
- 16 kDa protein lng=137



IPI:IPI00293227.3

Sequence: QTFMAMLLK, Q1-TMT6plex (229.16293 Da), Q1-Gln->pyro-Glu (-17.02655 Da), M6-Oxidation (15.99492 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 655.86377 Da (-114661.91 mmu/-174825.8 ppm), MH+: 1310.72026 Da, RT: 121.72 min,

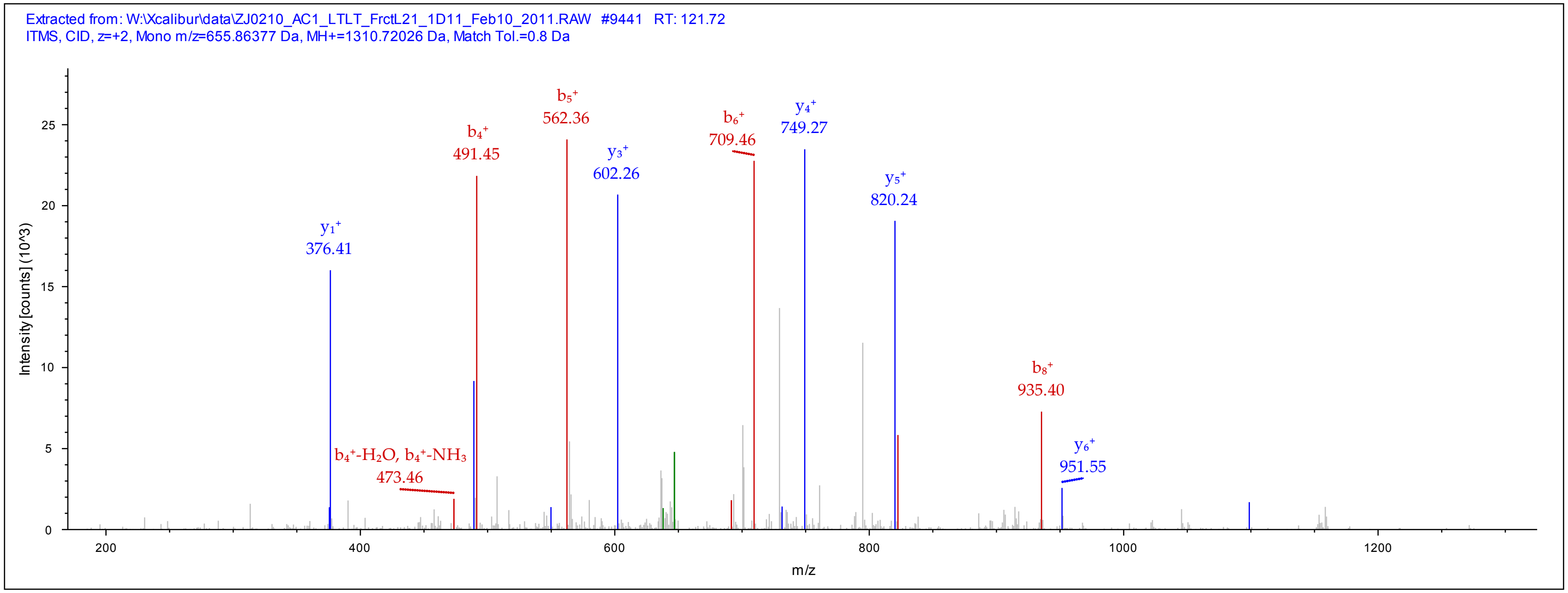
Identified with: Mascot (v1.16); IonScore:35, Exp Value:3.0E-002, Ions matched by search engine: 5/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Isoform 1 of NLR family CARD domain-containing protein 4



IPI:IPI00293303.1

Sequence: IVSLLAASEAEVEQLLSER, I1-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 762.76666 Da (+3.31 mmu/+4.34 ppm),   MH+: 2286.28543 Da,   RT: 239.14 min,

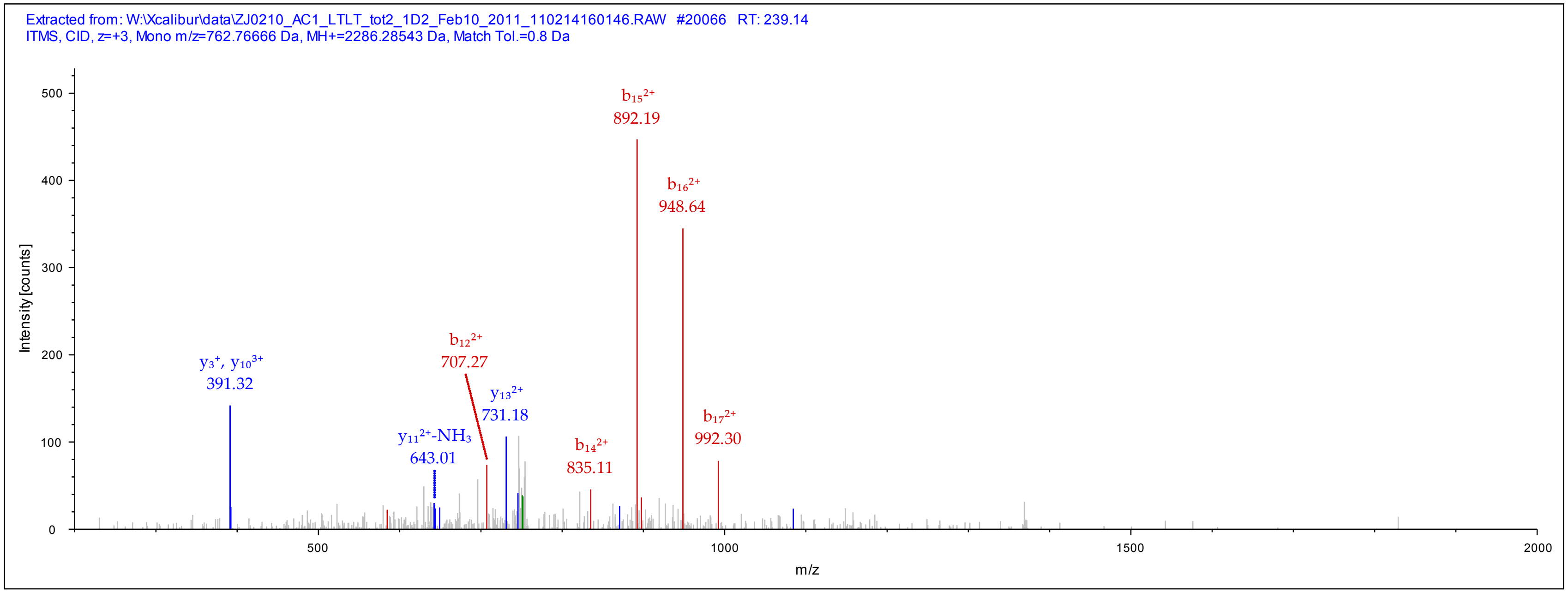
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.7E-002, Ions matched by search engine: 18/184

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Legumain



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_tot2_1D2_Feb10_2011_110214160146.RAW #20066 RT: 239.14

ITMS, CID, z=+3, Mono m/z=762.76666 Da, MH+=2286.28543 Da, Match Tol.=0.8 Da

IPI:IPI00293320.1

Sequence: AVMLR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 409.75775 Da (-1.89 mmu/-4.61 ppm), MH+: 818.50823 Da, RT: 83.88 min,

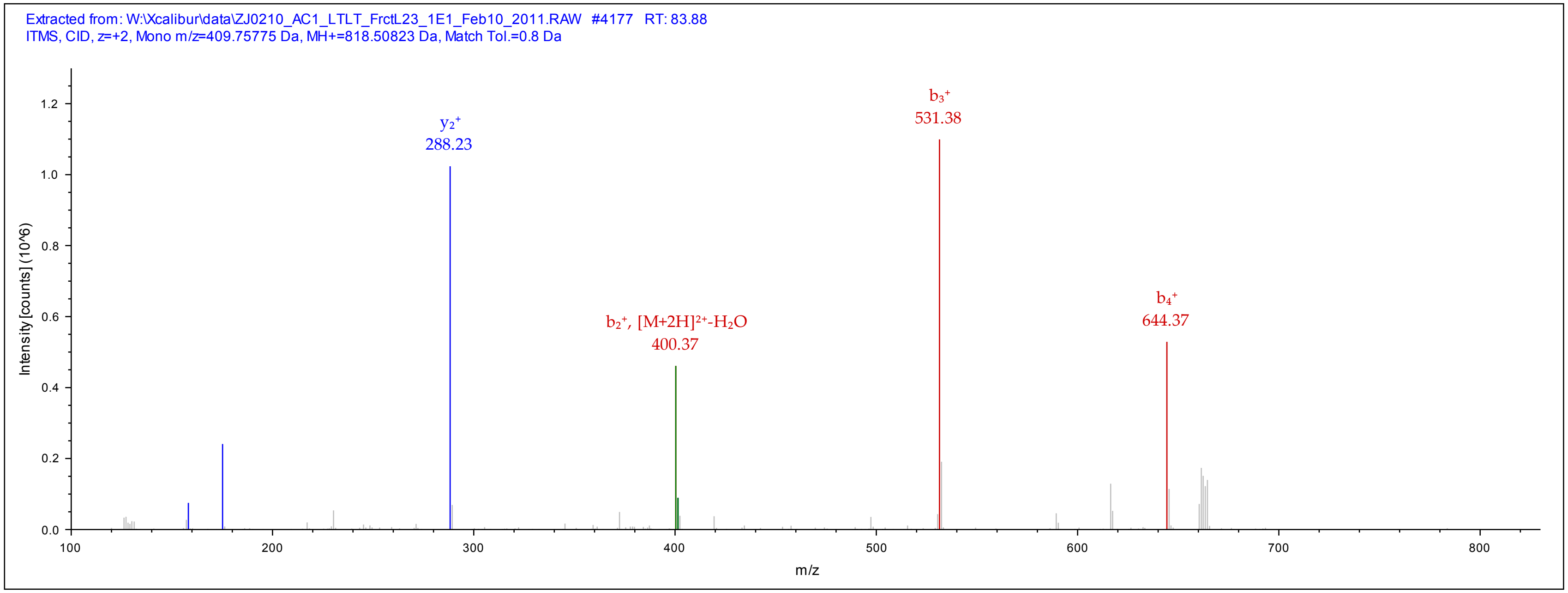
Identified with: Mascot (v1.16); IonScore:31, Exp Value:2.6E-002, Ions matched by search engine: 6/34

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Protein FAM43A



IPI:IPI00792295.2

Sequence: LSLLVLR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 521.86407 Da (+1.13 mmu/+2.16 ppm),   MH+: 1042.72087 Da,   RT: 123.40 min,

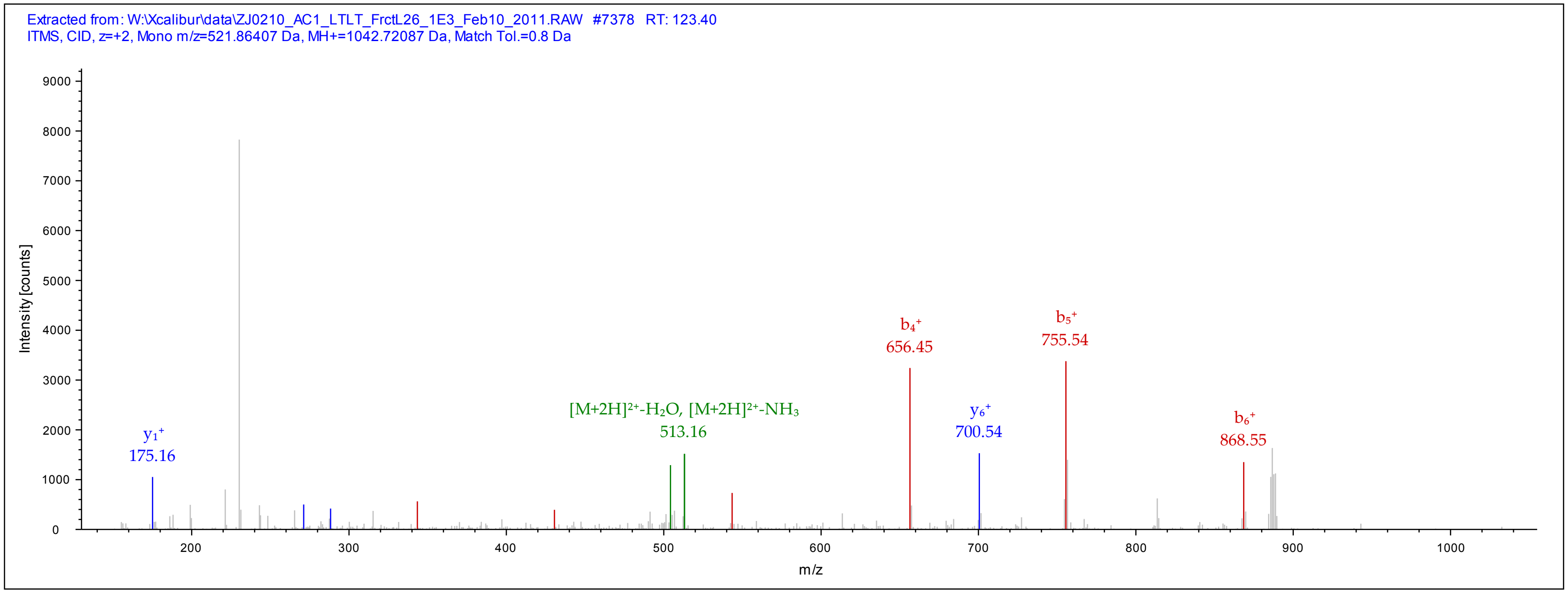
Identified with: Mascot (v1.16); IonScore:31, Exp Value:1.8E-002, Ions matched by search engine: 6/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Tight junction protein ZO-3
- tight junction protein ZO-3



IPI:IPI00294158.1

Sequence: GSLLFTAGPLEEER, G1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 874.47522 Da (+0.15 mmu/+0.17 ppm),   MH+: 1747.94316 Da,   RT: 111.98 min,

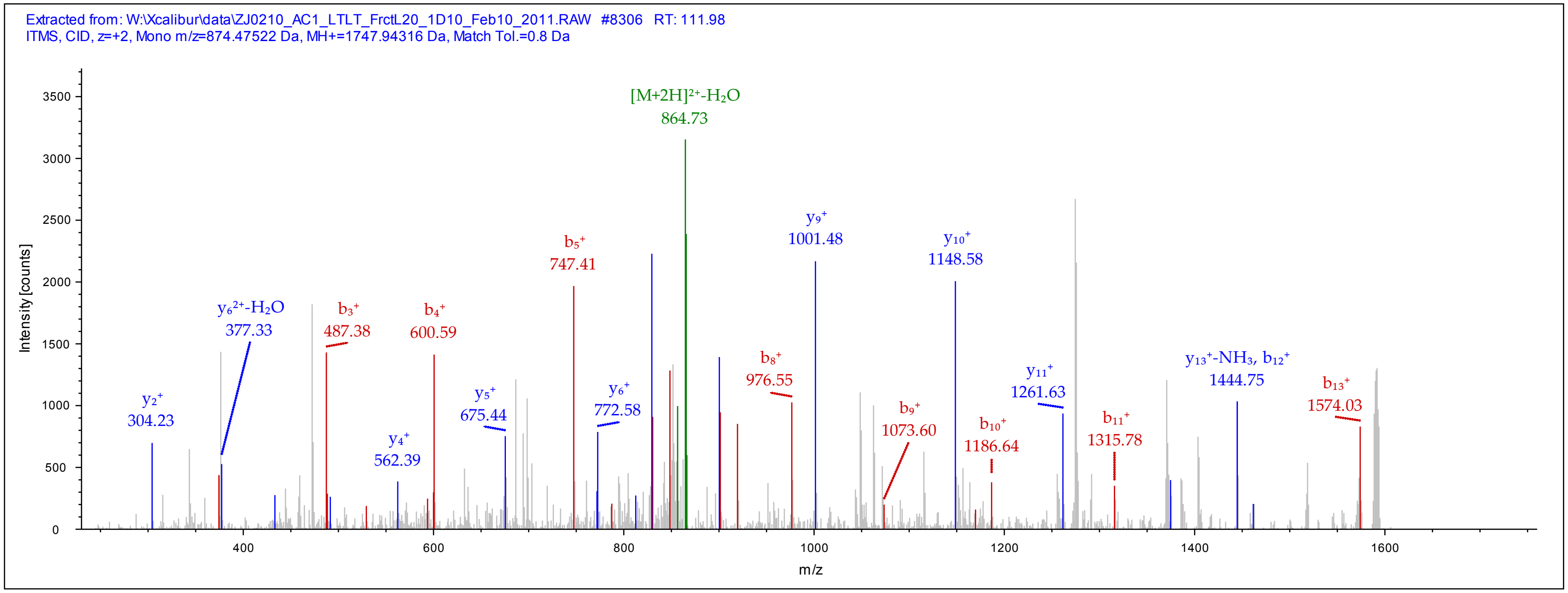
Identified with: Mascot (v1.16); IonScore:44, Exp Value:5.0E-003, Ions matched by search engine: 11/126

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Biliverdin reductase A



IPI:IPI00294242.2

Sequence: EAPETDTSPSLWDVEFAK, E1-TMT6plex (229.16293 Da), K18-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 827.42542 Da (+0.63 mmu/+0.76 ppm),   MH+: 2480.26169 Da,   RT: 120.29 min,

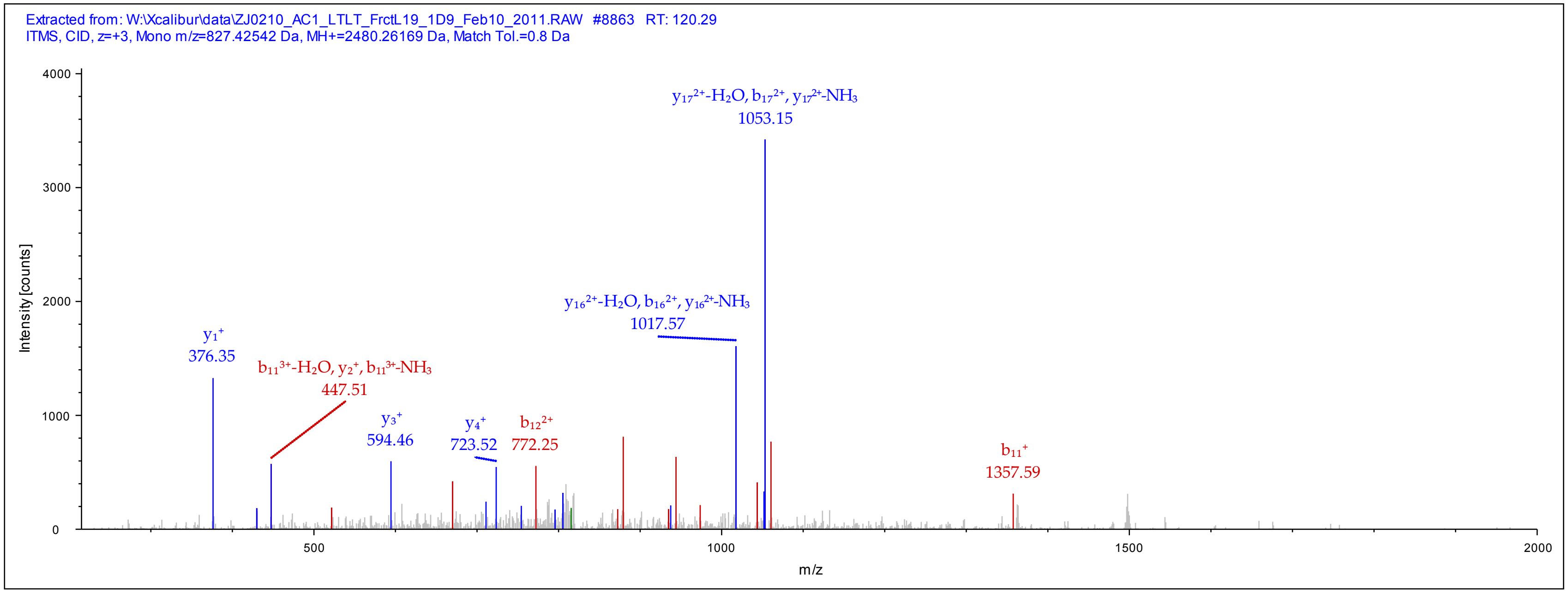
Identified with: Mascot (v1.16); IonScore:42, Exp Value:9.8E-003, Ions matched by search engine: 10/164

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 28S ribosomal protein S31, mitochondrial



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL19_1D9_Feb10_2011.RAW #8863 RT: 120.29

ITMS, CID, z=+3, Mono m/z=827.42542 Da, MH+=2480.26169 Da, Match Tol.=0.8 Da

IPI:IPI00941907.1

Sequence: LWQTVVGK, L1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 694.93658 Da (-0.37 mmu/-0.53 ppm), MH+: 1388.86589 Da, RT: 107.05 min,

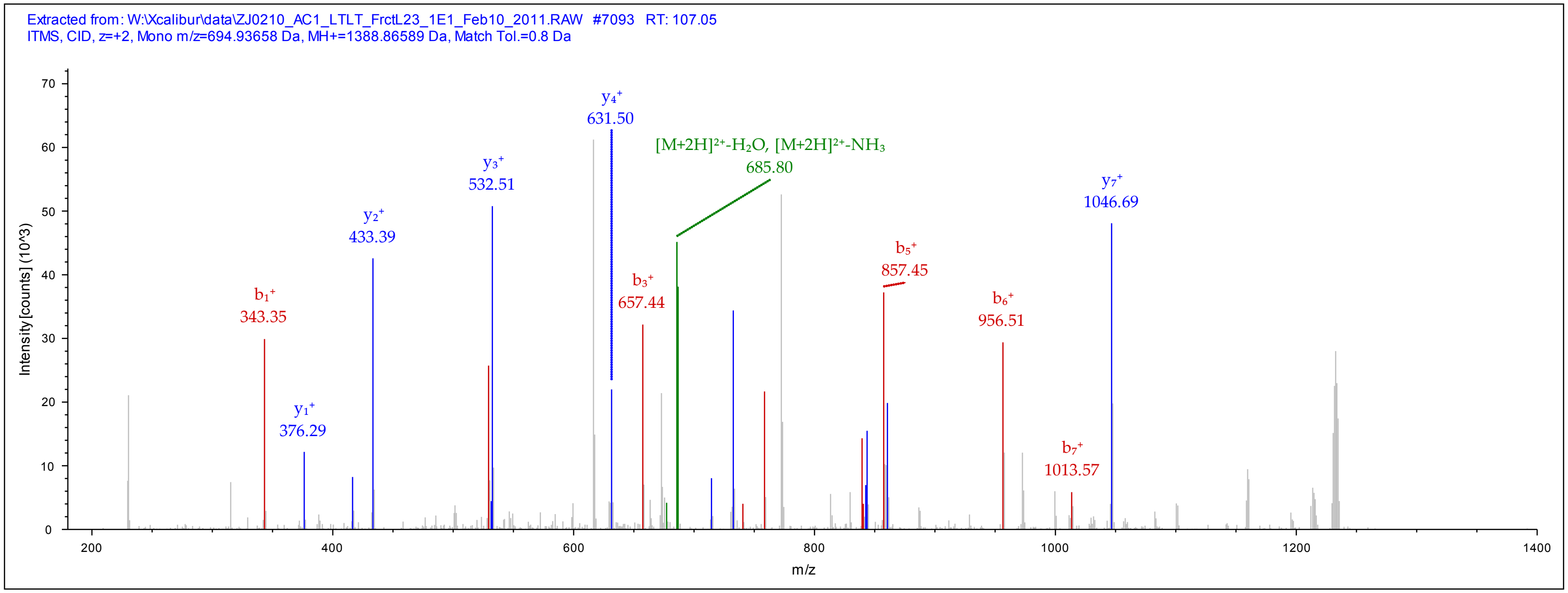
Identified with: Mascot (v1.16); IonScore:31, Exp Value:3.8E-002, Ions matched by search engine: 6/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Serine-threonine kinase receptor-associated protein
- cDNA FLJ51909, highly similar to Serine-threonine kinase receptor-associatedprotein lng=363



IPI:IPI00294578.1

Sequence: DCLTESNLIK, D1-TMT6plex (229.16293 Da), C2-Carbamidomethyl (57.02146 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 825.96124 Da (+0.74 mmu/+0.9 ppm), MH+: 1650.91521 Da, RT: 94.92 min,

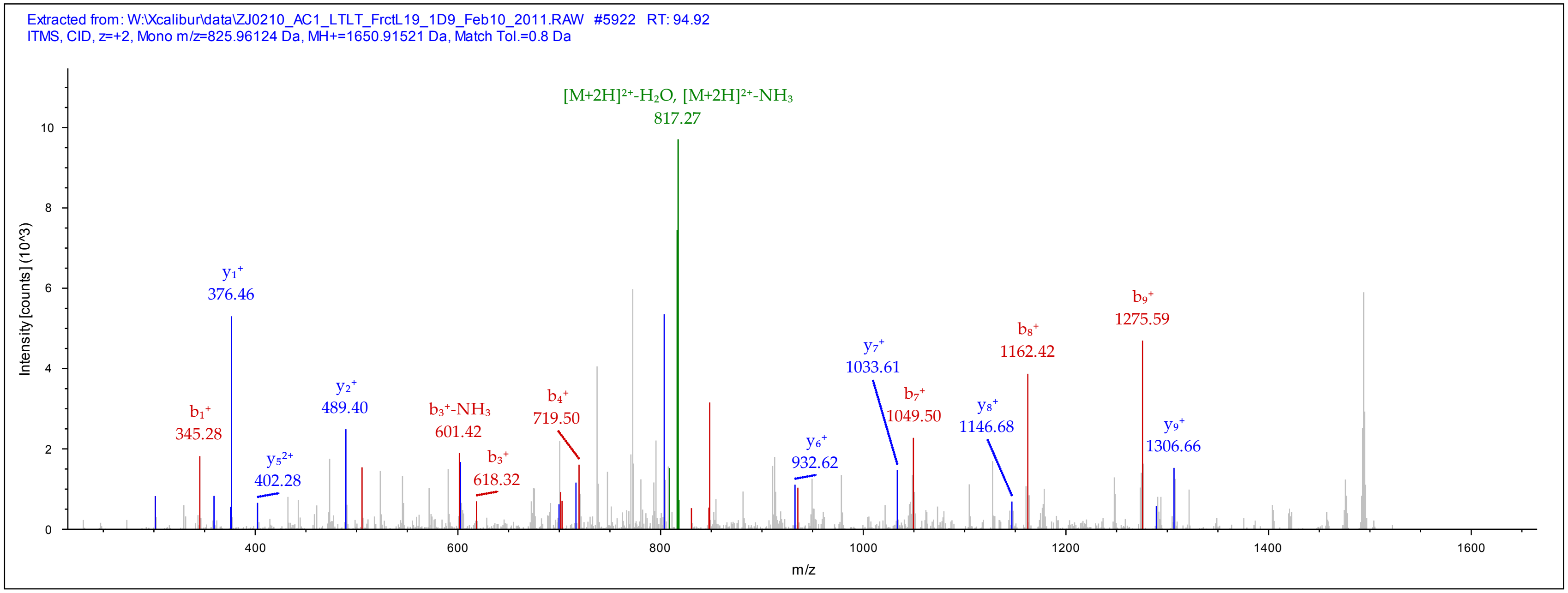
Identified with: Mascot (v1.16); IonScore:35, Exp Value:3.6E-002, Ions matched by search engine: 14/88

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

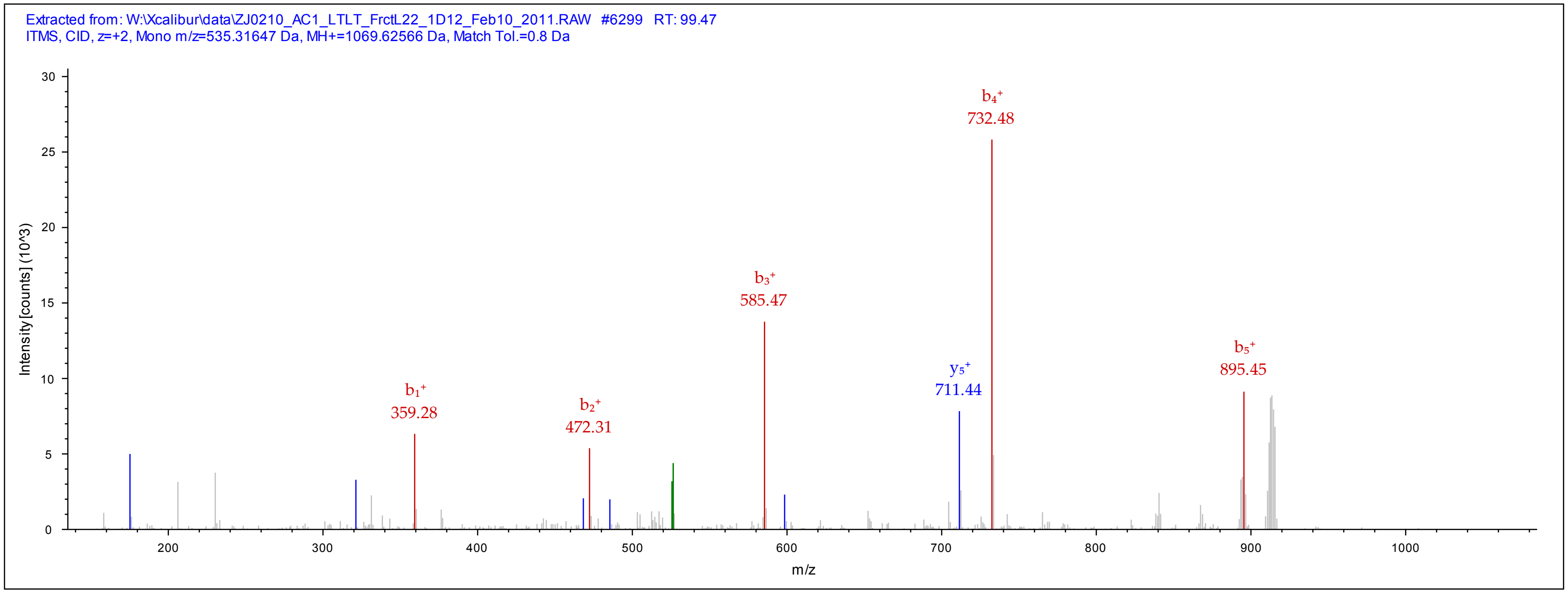
- Isoform 1 of Protein-glutamine gamma-glutamyltransferase 2



IPI:IPI00297211.1

Sequence: EILFYR, E1-TMT6plex (229.16293 Da)
Charge: +2, Monoisotopic m/z: 535.31647 Da (+0.64 mmu/+1.2 ppm), MH+: 1069.62566 Da, RT: 99.47 min,
Identified with: Mascot (v1.16); IonScore:32, Exp Value:4.6E-002, Ions matched by search engine: 5/40
Fragment match tolerance used for search: 0.8 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5



IPI:IPI00939720.1

Sequence: IQALLK, I1-TMT6plex (229.16293 Da), K6-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 572.39746 Da (+0.53 mmu/+0.93 ppm),   MH+: 1143.78765 Da,   RT: 94.67 min,

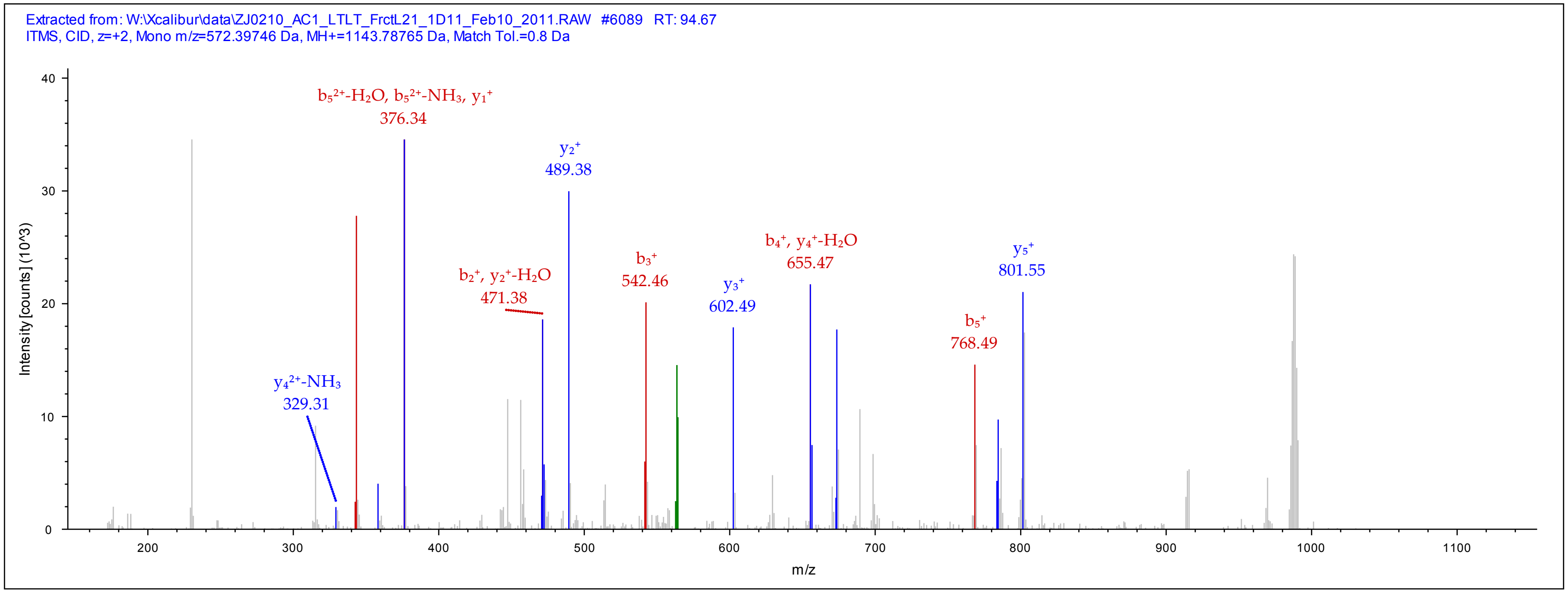
Identified with: Mascot (v1.16); IonScore:30, Exp Value:2.9E-002, Ions matched by search engine: 10/50

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Baculoviral IAP repeat-containing protein 6



IPI:IPI00301323.1

Sequence: VPLSEFDFSWSK, V1-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 950.51782 Da (+1.32 mmu/+1.39 ppm), MH+: 1900.02837 Da, RT: 169.32 min,

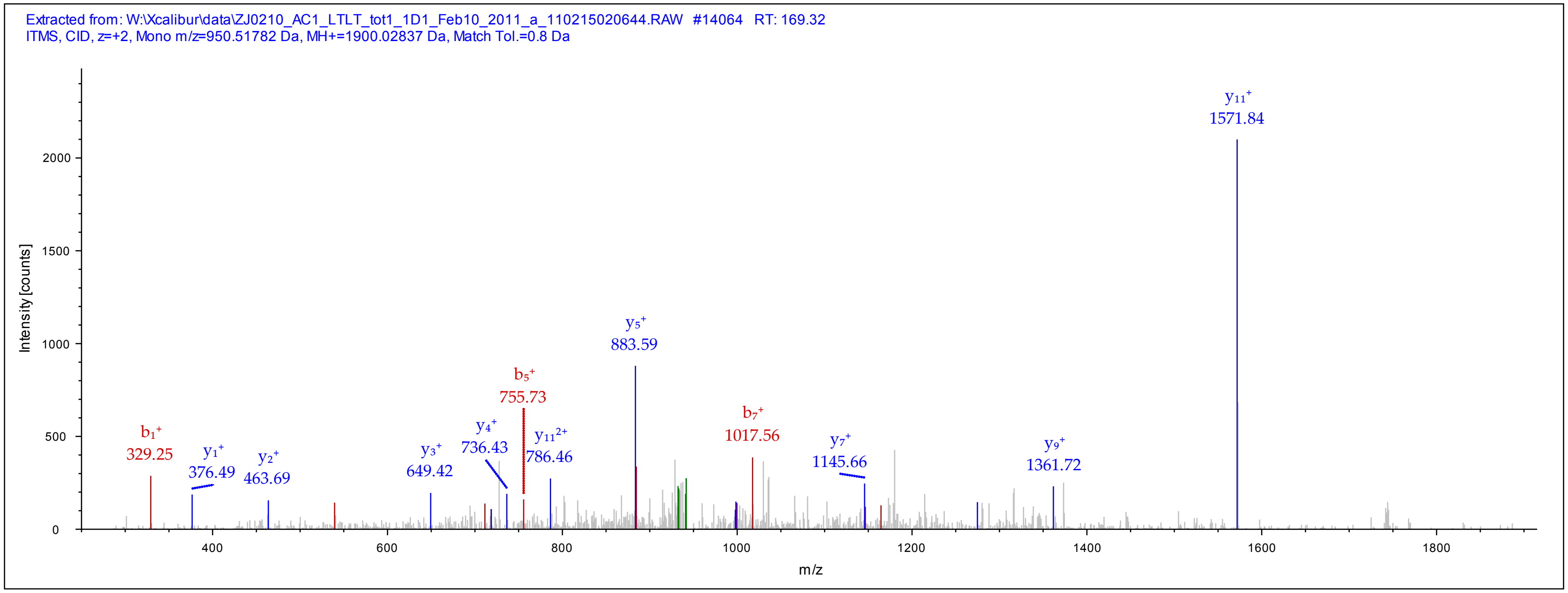
Identified with: Mascot (v1.16); IonScore:32, Exp Value:8.1E-002, Ions matched by search engine: 8/102

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- ATP-dependent RNA helicase DDX18

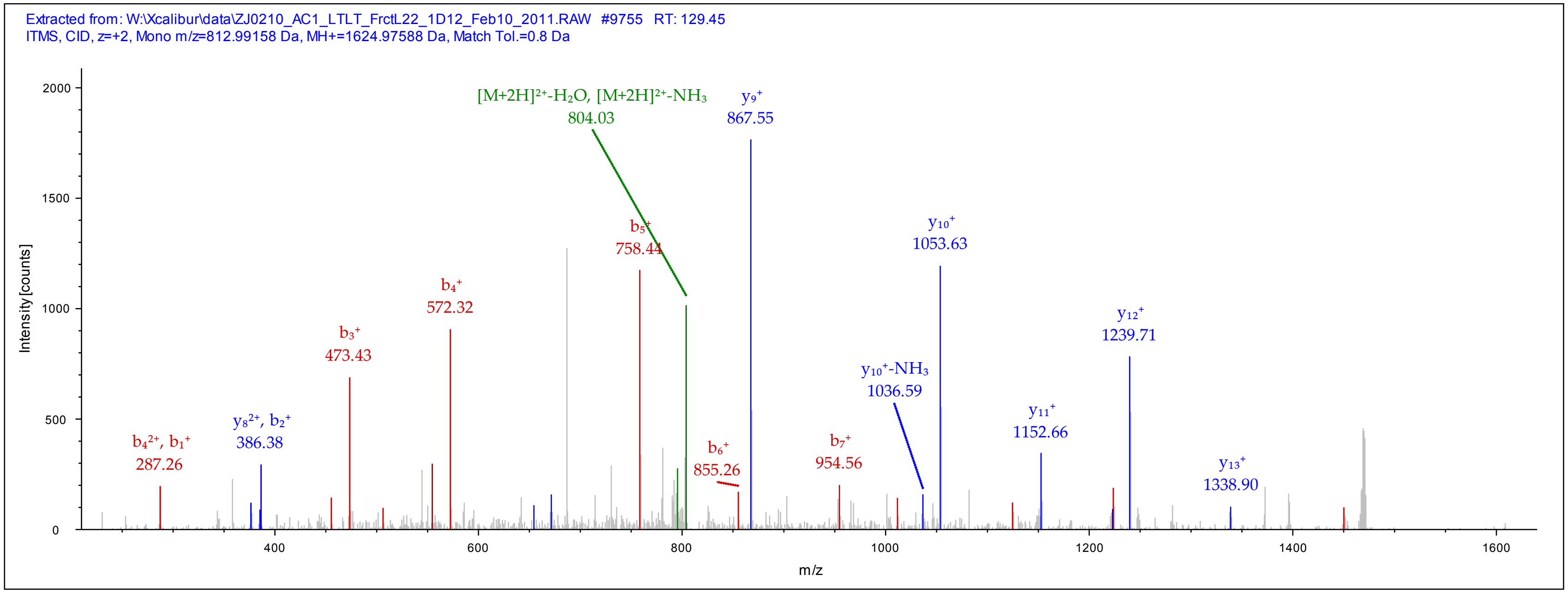


Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_tot1_1D1_Feb10_2011_a_110215020644.RAW #14064 RT: 169.32
ITMS, CID, z=+2, Mono m/z=950.51782 Da, MH+=1900.02837 Da, Match Tol.=0.8 Da

IPI:IPI00304331.2

Sequence: GVSVWPVGLVGGLR, G1-TMT6plex (229.16293 Da)
Charge: +2, Monoisotopic m/z: 812.99158 Da (+1.08 mmu/+1.33 ppm), MH+: 1624.97588 Da, RT: 129.45 min,
Identified with: Mascot (v1.16); IonScore:52, Exp Value:4.3E-004, Ions matched by search engine: 13/104
Fragment match tolerance used for search: 0.8 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3
- B3GAT3 protein (Fragment)



IPI:IPI00004454.3

equence: ELQSQIQEAR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 715.89423 Da (+0.53 mmu/+0.74 ppm),   MH+: 1430.78118 Da,   RT: 77.85 min,

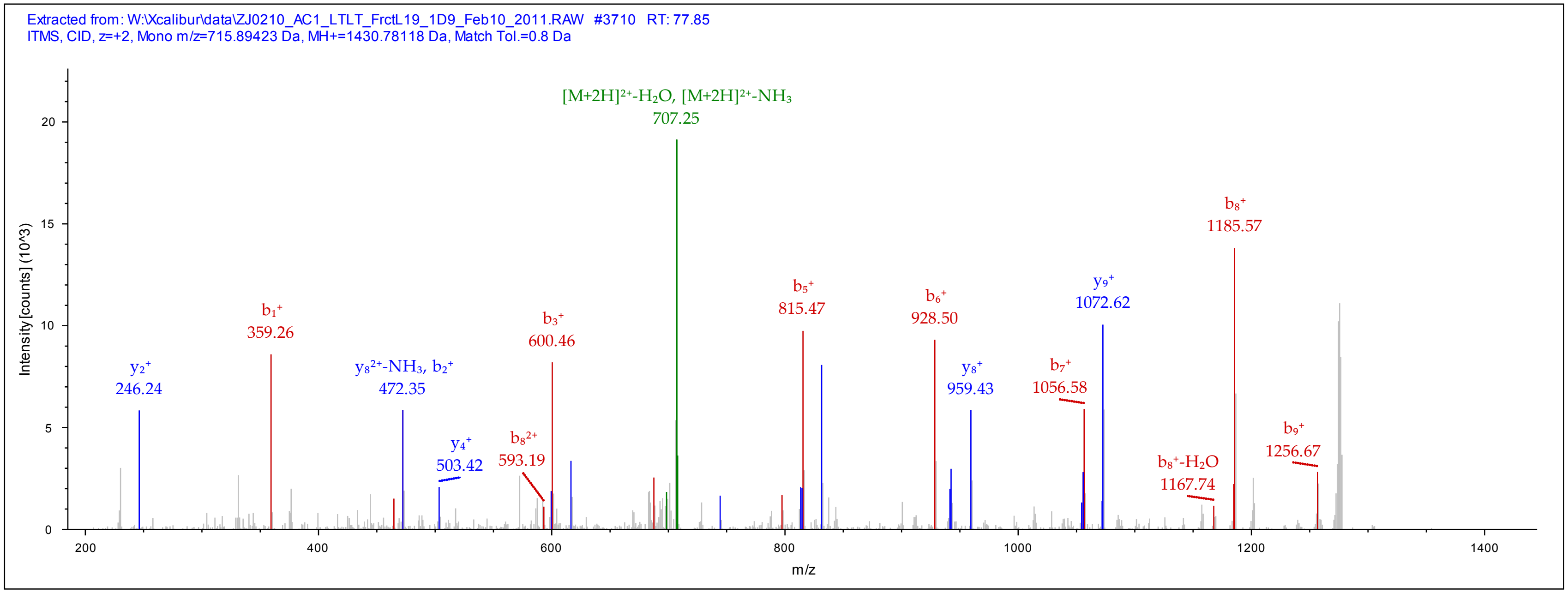
Identified with: Mascot (v1.16); IonScore:46, Exp Value:2.2E-003, Ions matched by search engine: 8/100

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Dolichol-phosphate mannosyltransferase subunit 3
- cDNA FLJ60436, highly similar to Homo sapiens dolichyl-phosphate mannosyltransferase polypeptide 3, transcript variant 1, mRNA



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL19_1D9_Feb10_2011.RAW #3710 RT: 77.85
ITMS, CID, z=+2, Mono m/z=715.89423 Da, MH+=1430.78118 Da, Match Tol.=0.8 Da

IPI:IPI00333619.4

Sequence: ILSLLEGQK, I1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 729.96997 Da (+1.52 mmu/+2.08 ppm),   MH+: 1458.93266 Da,   RT: 128.84 min,

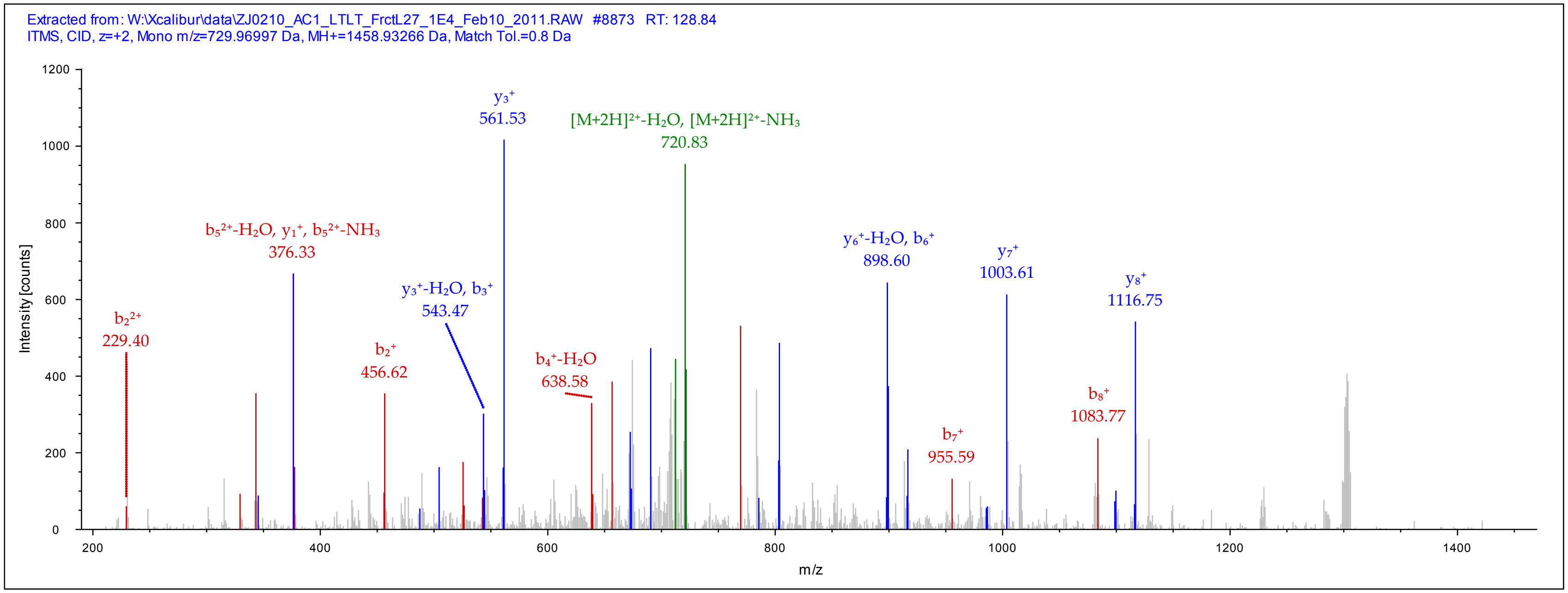
Identified with: Mascot (v1.16); IonScore:37, Exp Value:8.4E-003, Ions matched by search engine: 8/72

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Fatty aldehyde dehydrogenase
- Isoform 2 of Fatty aldehyde dehydrogenase



IPI:IPI00333634.4

Sequence: RQGLPR, R1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 478.31055 Da (+6.96 mmu/+14.56 ppm), MH+: 955.61382 Da, RT: 82.59 min,

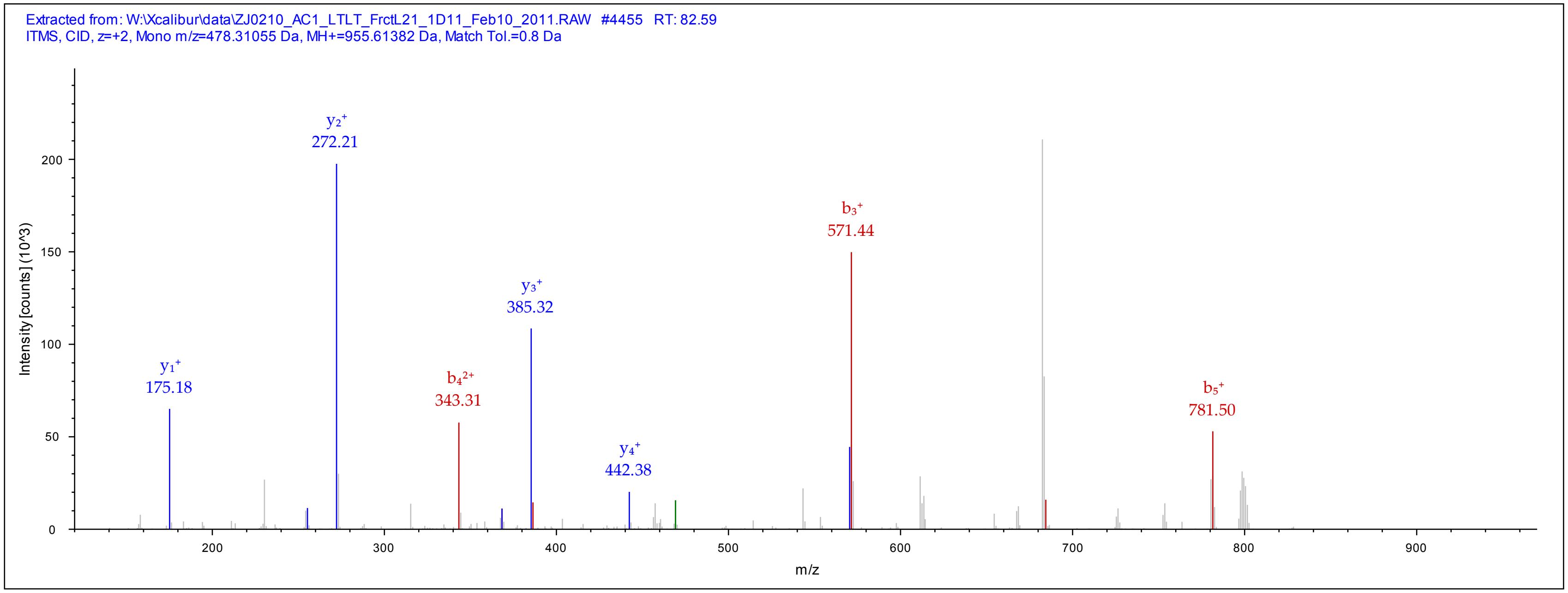
Identified with: Mascot (v1.16); IonScore:29, Exp Value:3.2E-002, Ions matched by search engine: 4/52

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Uncharacterized protein C20orf194



IPI:IPI00333763.7

Sequence: GTPEQPQCGFSNAVVQILR, G1-TMT6plex (229.16293 Da), C8-Carbamidomethyl (57.02146 Da)

Charge: +3,   Monoisotopic m/z: 777.41034 Da (+1.31 mmu/+1.69 ppm),   MH+: 2330.21646 Da,   RT: 119.09 min,

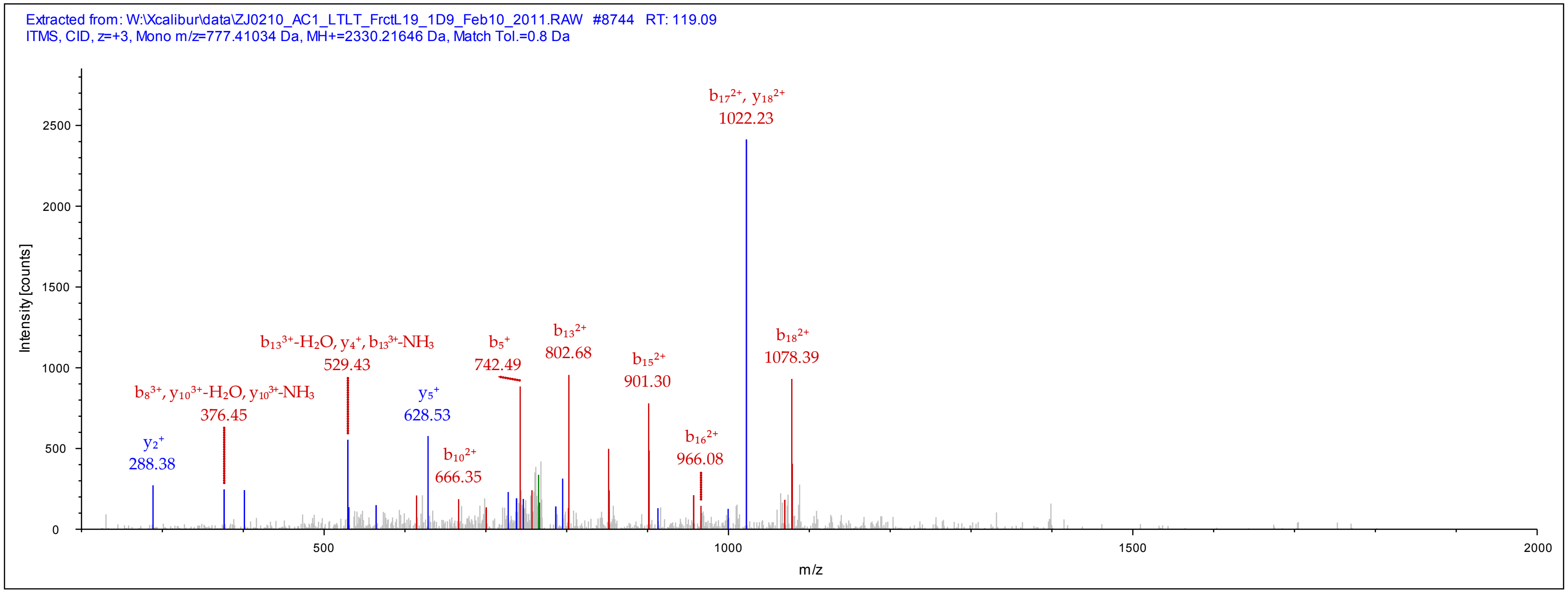
Identified with: Mascot (v1.16); IonScore:50, Exp Value:1.7E-003, Ions matched by search engine: 14/190

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Glutaredoxin-related protein 5, mitochondrial



IPI:IPI00383046.3

Sequence: NLIEWLNK, N1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 744.45465 Da (+1.68 mmu/+2.26 ppm), MH+: 1487.90203 Da, RT: 126.14 min,

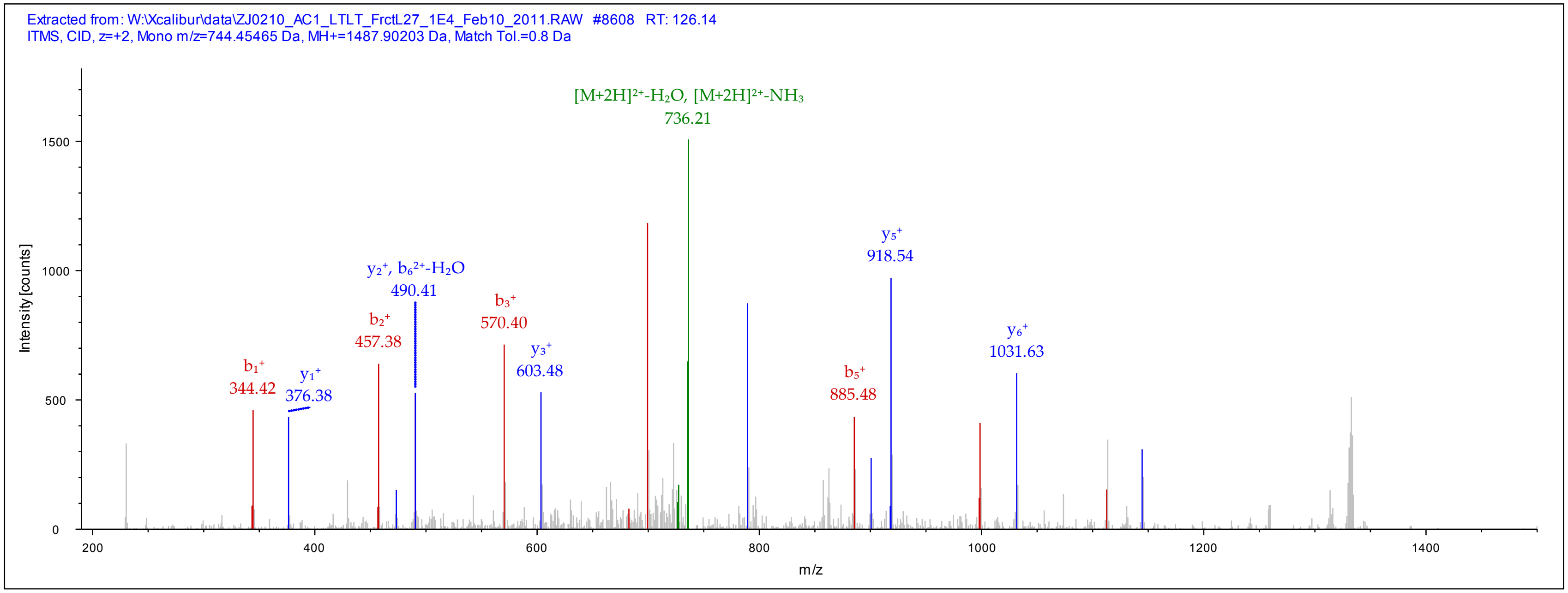
Identified with: Mascot (v1.16); IonScore:41, Exp Value:6.9E-003, Ions matched by search engine: 7/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

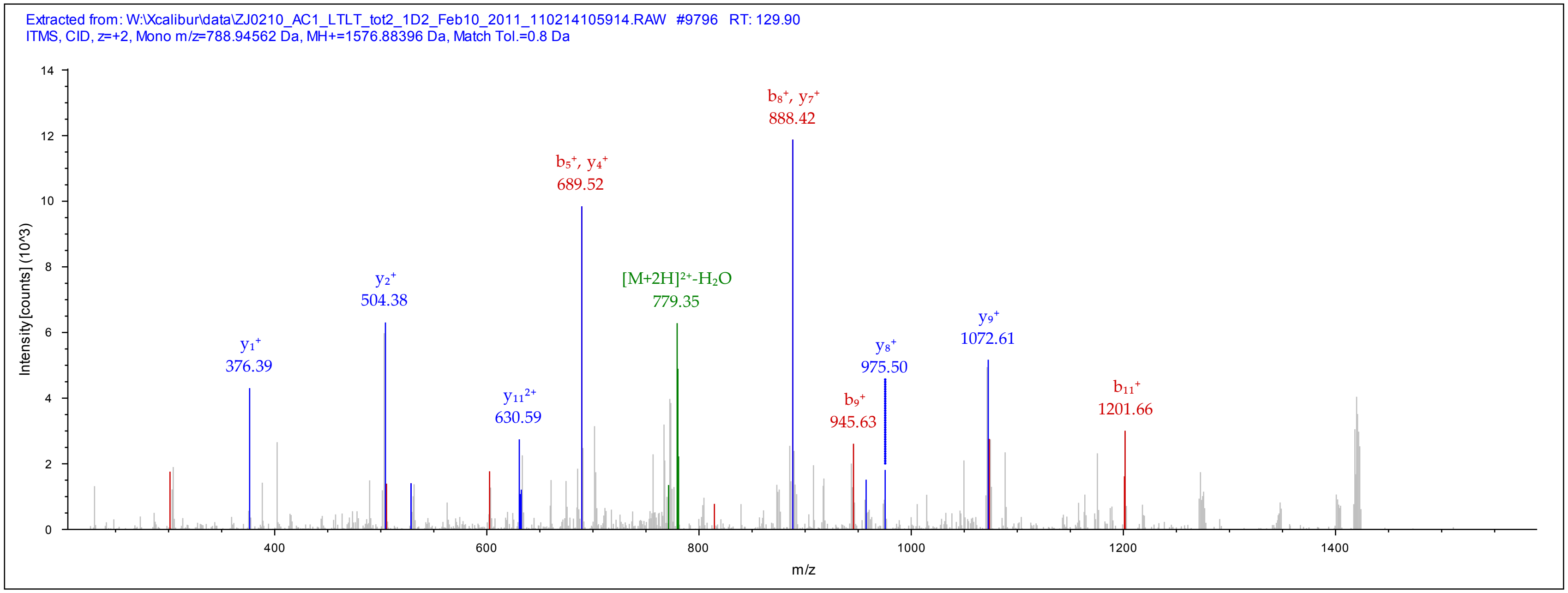
- Carboxymethylenebutenolidase homolog



IPI:IPI00396098.1

Sequence: STSPSAAGGQQK, S1-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)
Charge: +2,   Monoisotopic m/z: 788.94562 Da (+7.21 mmu/+9.13 ppm),   MH+: 1576.88396 Da,   RT: 129.90 min,
Identified with: Mascot (v1.16); IonScore:35, Exp Value:3.9E-002, Ions matched by search engine: 10/100
Fragment match tolerance used for search: 0.8 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- Zinc finger protein 800


Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_tot2_1D2_Feb10_2011_110214105914.RAW #9796 RT: 129.90
ITMS, CID, z=+2, Mono m/z=788.94562 Da, MH+=1576.88396 Da, Match Tol.=0.8 Da

IPI:IPI00064212.2

Sequence: AFLLESLLK, A1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 746.48236 Da (+1.16 mmu/+1.55 ppm),   MH+: 1491.95745 Da,   RT: 186.35 min,

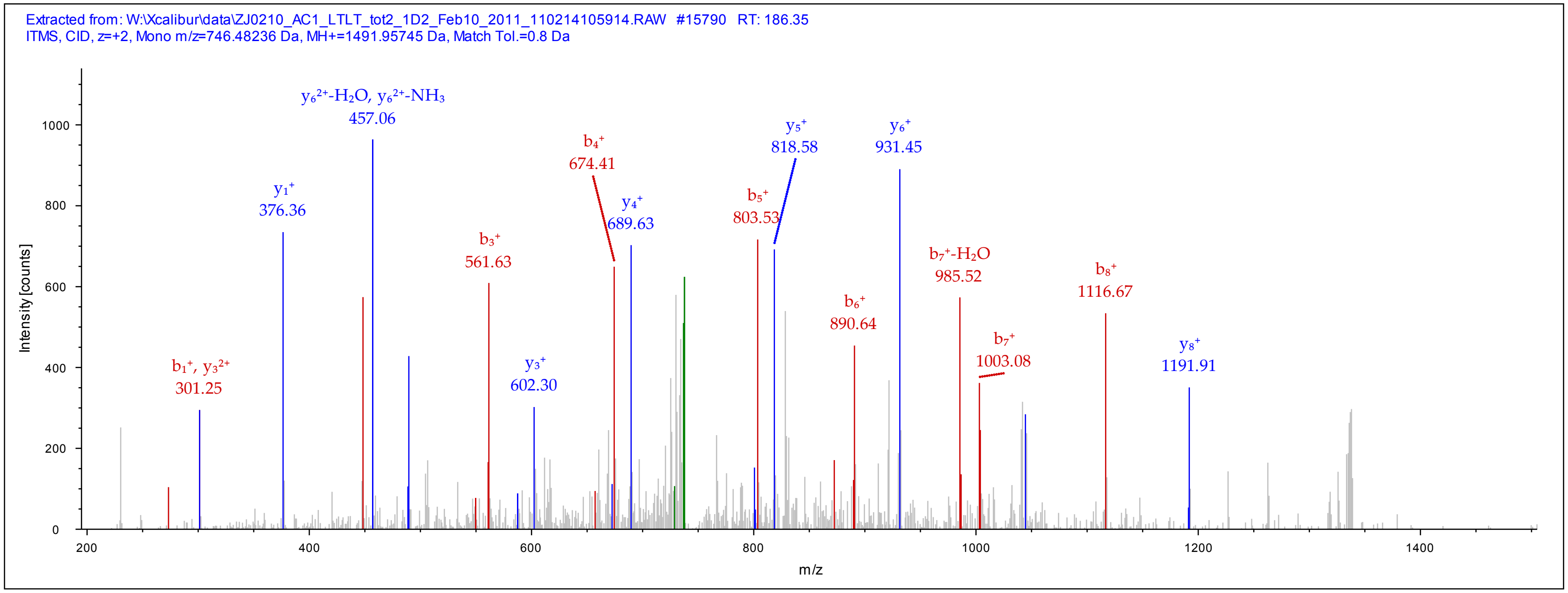
Identified with: Mascot (v1.16); IonScore:42, Exp Value:3.1E-003, Ions matched by search engine: 8/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Zinc finger protein 828



IPI:IPI00443799.2

Sequence: ETVENLPPLPLDPVLR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 1016.09094 Da (+2.88 mmu/+2.83 ppm),   MH+: 2031.17461 Da,   RT: 126.88 min,

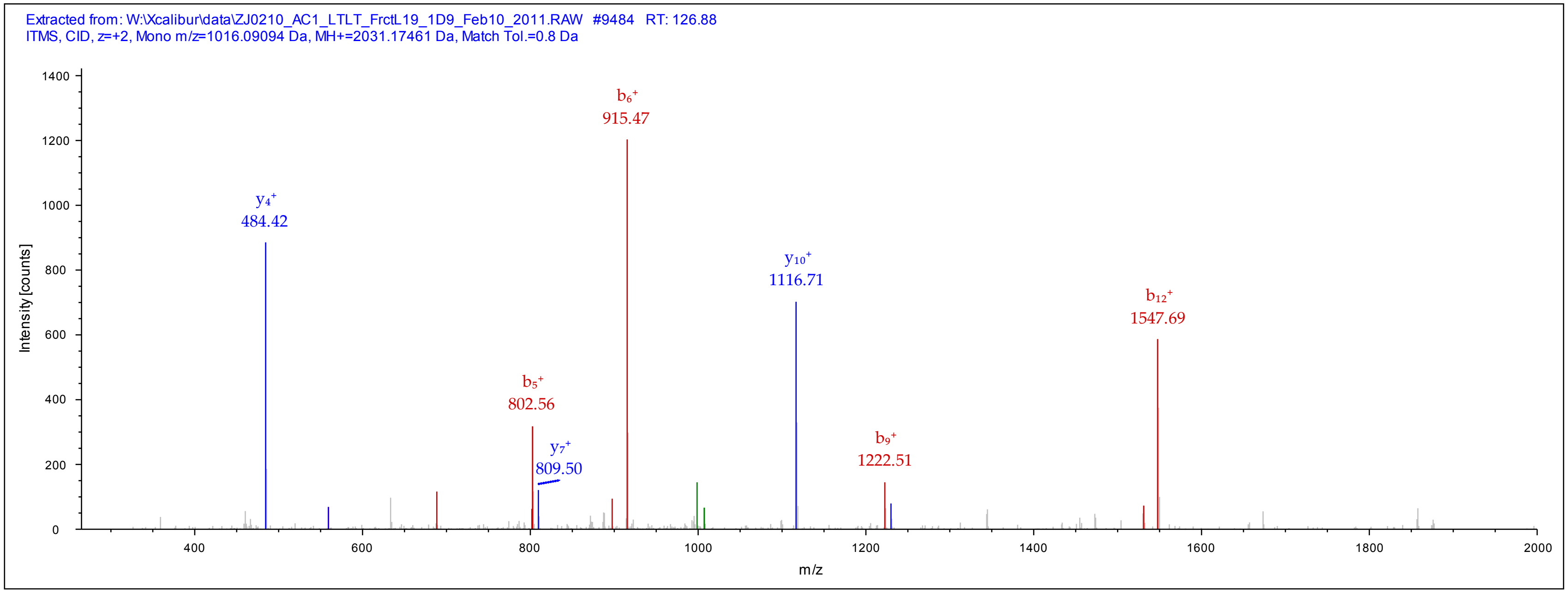
Identified with: Mascot (v1.16); IonScore:52, Exp Value:6.1E-004, Ions matched by search engine: 7/164

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Isoform 1 of Putative sodium-coupled neutral amino acid transporter 10



IPI:IPI00456940.5

Sequence: KIPLVPENLLK, K1-TMT6plex (229.16293 Da), K1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 651.10413 Da (+1.83 mmu/+2.81 ppm), MH+: 1951.29782 Da, RT: 122.32 min,

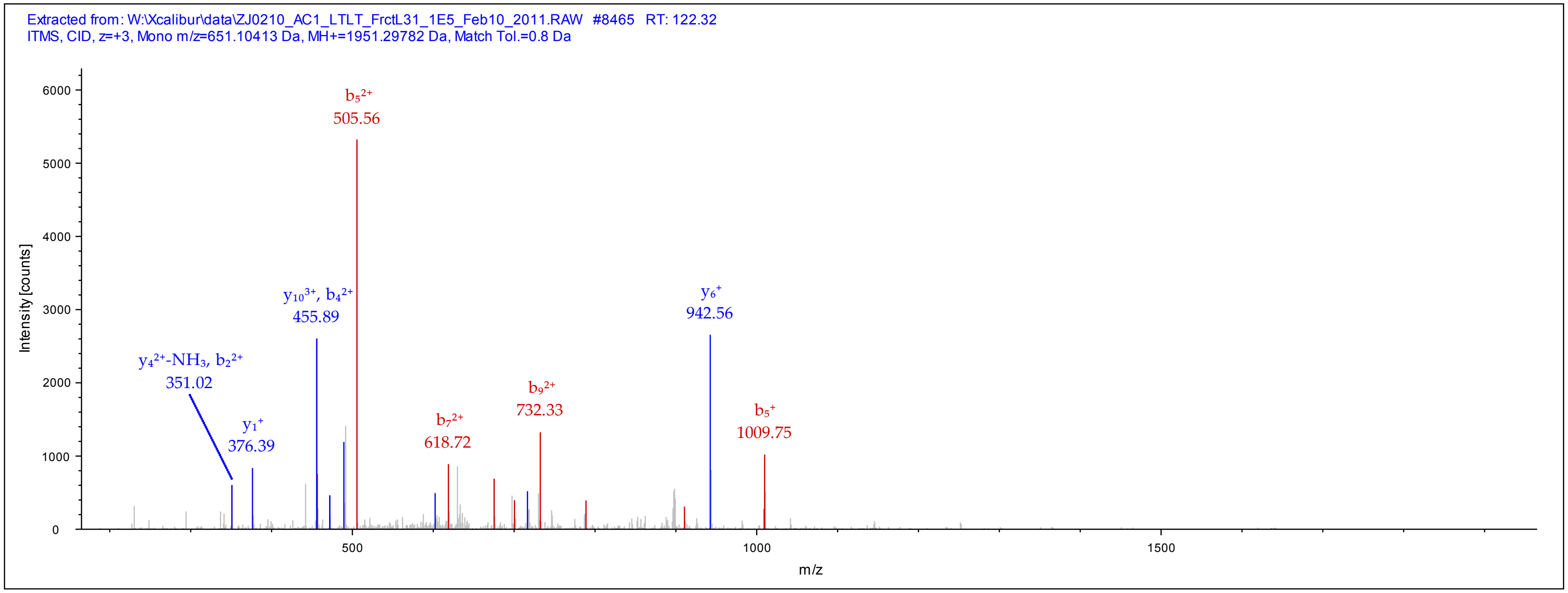
Identified with: Mascot (v1.16); IonScore:31, Exp Value:3.6E-003, Ions matched by search engine: 8/100

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60S ribosomal protein L7-like 1



IPI:IPI00853240.1

Sequence: ELALPLFSPATASR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 851.49335 Da (+2.83 mmu/+3.32 ppm),   MH+: 1701.97942 Da,   RT: 125.93 min,

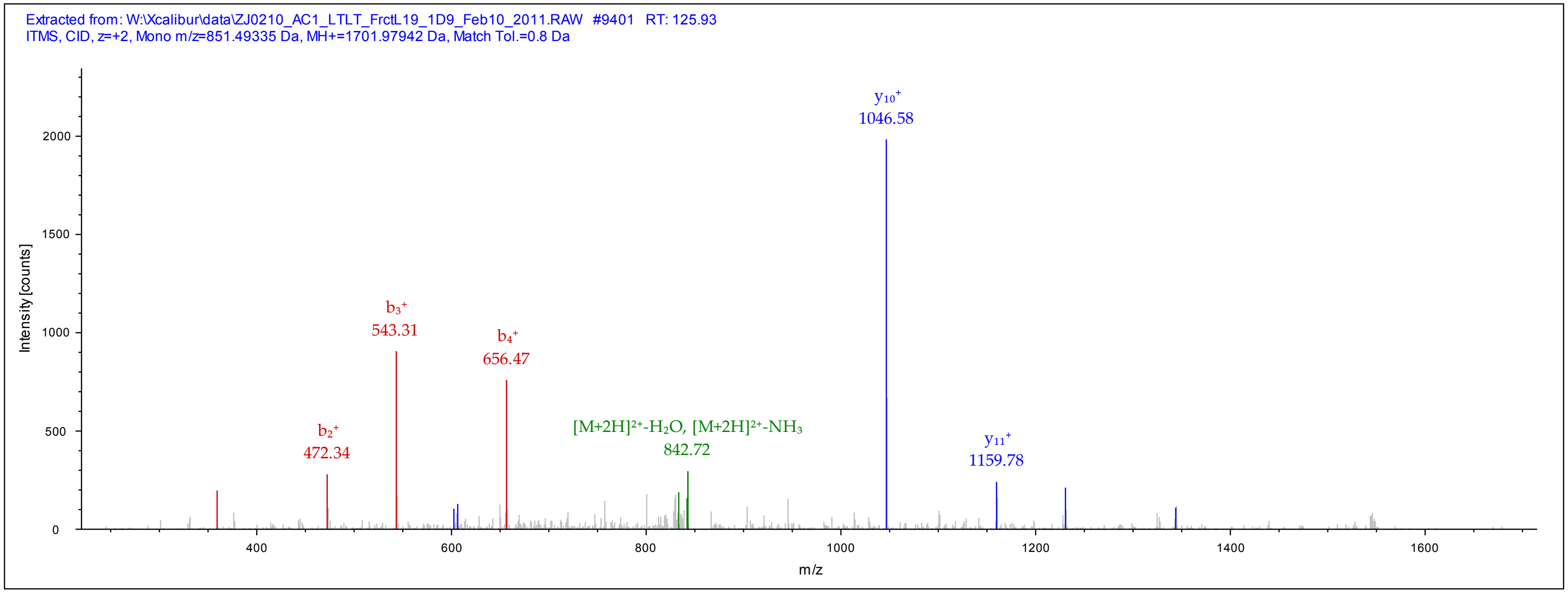
Identified with: Mascot (v1.16); IonScore:39, Exp Value:1.1E-002, Ions matched by search engine: 9/128

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Transcription initiation factor TFIID subunit 3



IPI:IPI00374563.3

Sequence: SIESTLDDLFR, S1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 762.91101 Da (+1.99 mmu/+2.61 ppm), MH+: 1524.81474 Da, RT: 133.01 min,

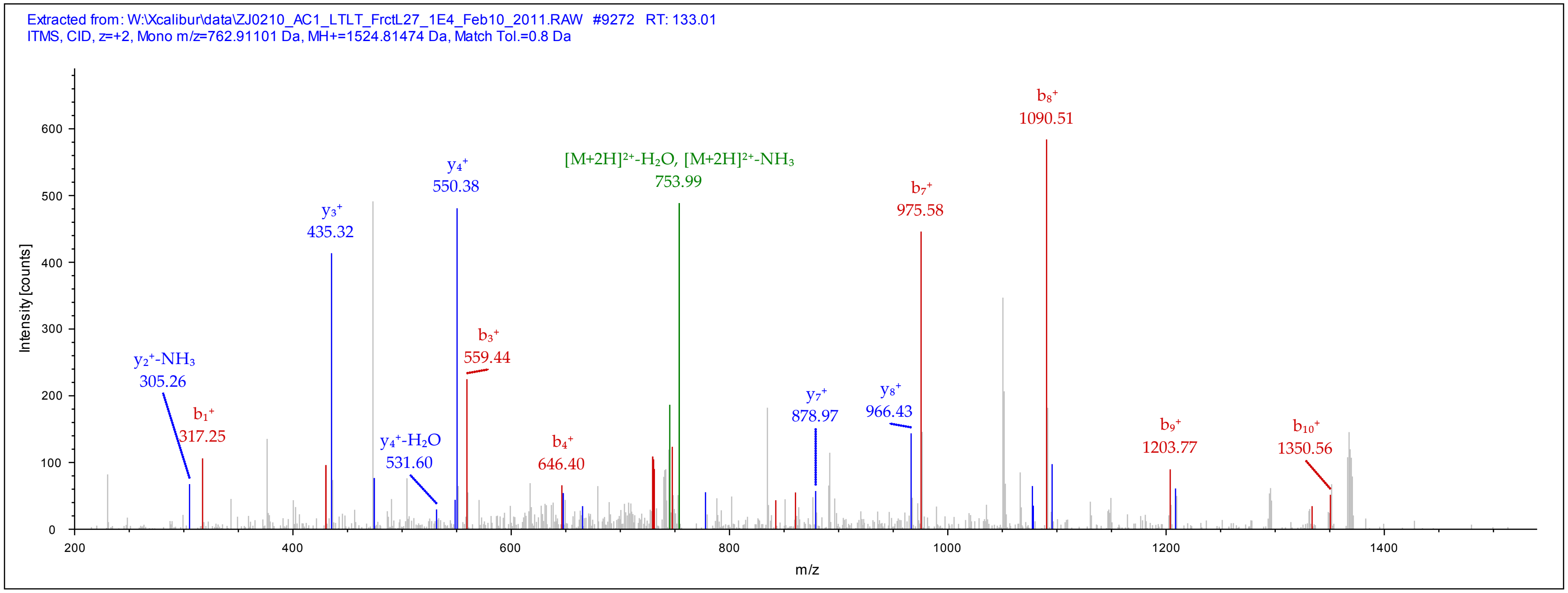
Identified with: Mascot (v1.16); IonScore:35, Exp Value:2.8E-002, Ions matched by search engine: 8/94

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Agrin



IPI00549640.3

Sequence: DVGSLDFEDLPLYK, D1-TMT6plex (229.16293 Da), K14-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 1035.06482 Da (+0.8 mmu/+0.77 ppm),   MH+: 2069.12236 Da,   RT: 127.22 min,

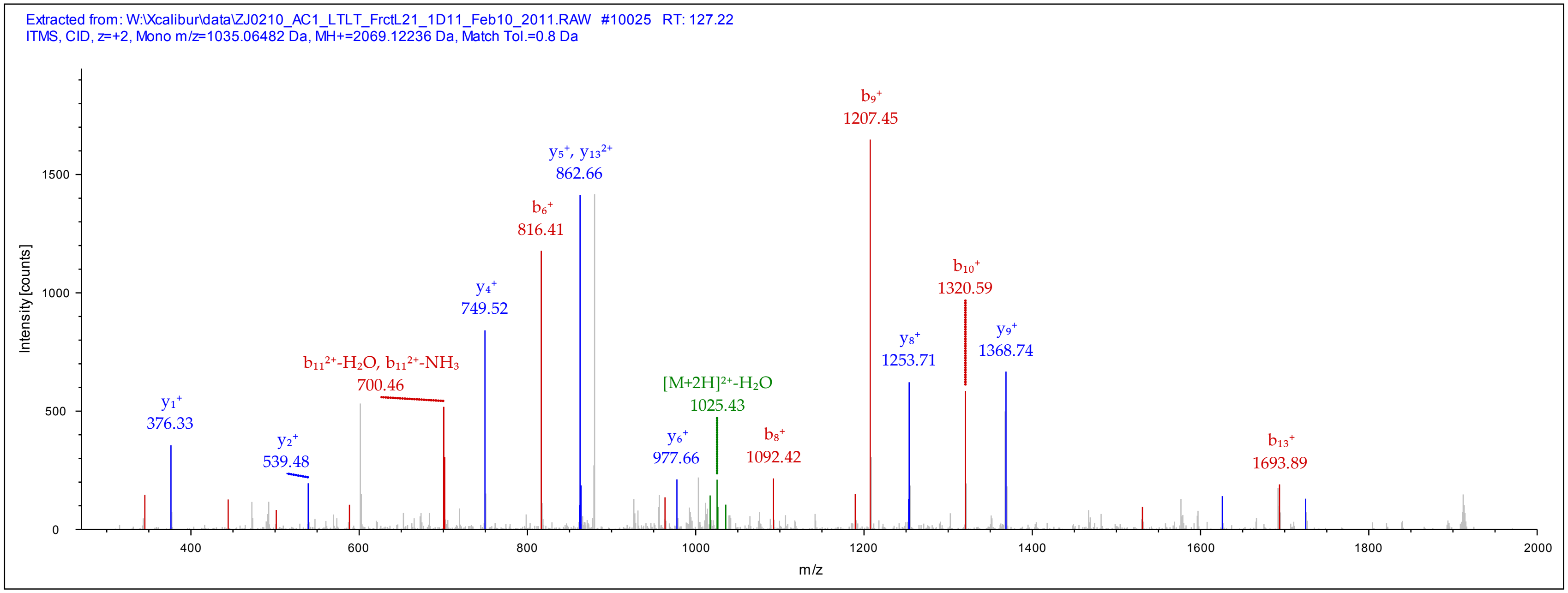
Identified with: Mascot (v1.16); IonScore:59, Exp Value:1.9E-004, Ions matched by search engine: 12/120

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 2 of Glycerophosphodiester phosphodiesterase domain-containing protein 3 lng=256
- Isoform 1 of Glycerophosphodiester phosphodiesterase domain-containing protein 3



IPI:IPI00550308.1

Sequence: FLSPQDTFEALK, F1-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 927.52478 Da (+0.45 mmu/+0.48 ppm),   MH+: 1854.04228 Da,   RT: 125.31 min,

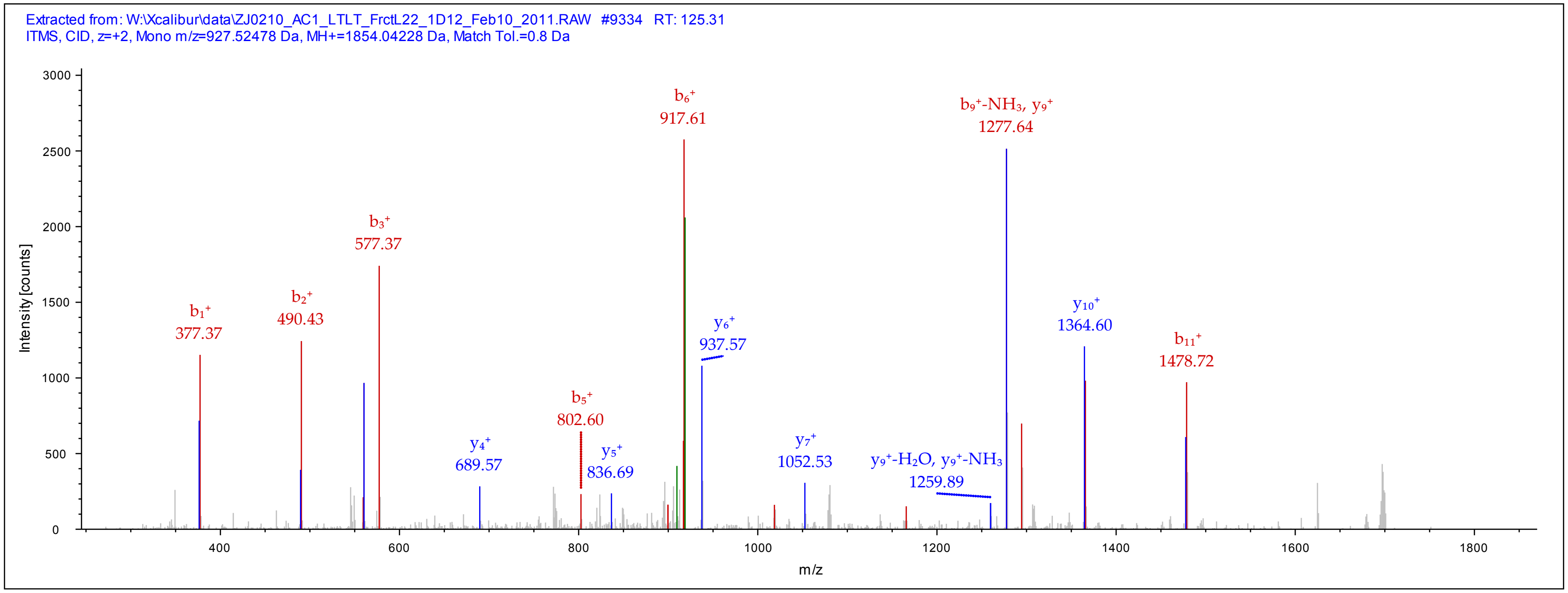
Identified with: Mascot (v1.16); IonScore:60, Exp Value:1.2E-004, Ions matched by search engine: 10/114

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- RNA-binding protein 12



IPI:IPI00030320.4

Sequence: TSDVTSTK, T1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 648.87640 Da (+2.19 mmu/+3.38 ppm),   MH+: 1296.74553 Da,   RT: 69.21 min,

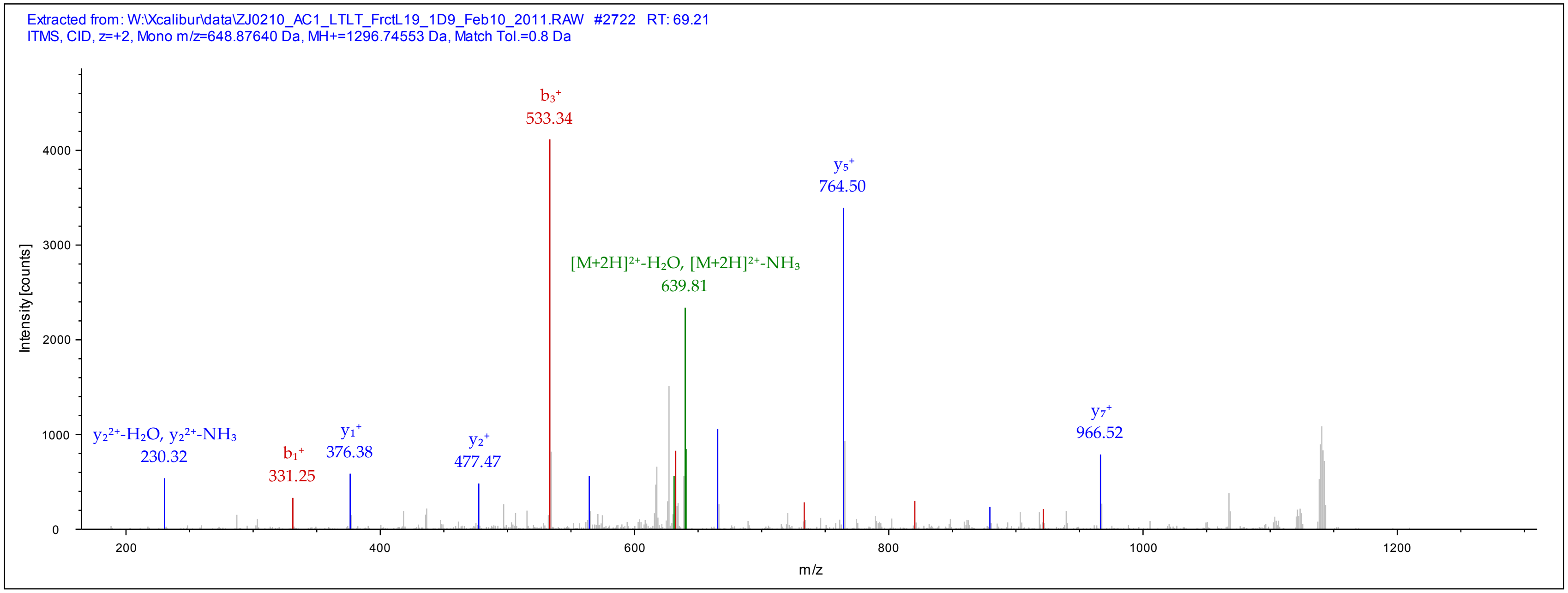
Identified with: Mascot (v1.16); IonScore:35, Exp Value:2.3E-002, Ions matched by search engine: 7/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Probable ATP-dependent RNA helicase DDX6



IPI:IPI00641435.1

Sequence: QVEVELLSR, Q1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 651.38580 Da (+0.82 mmu/+1.26 ppm), MH+: 1301.76433 Da, RT: 93.23 min,

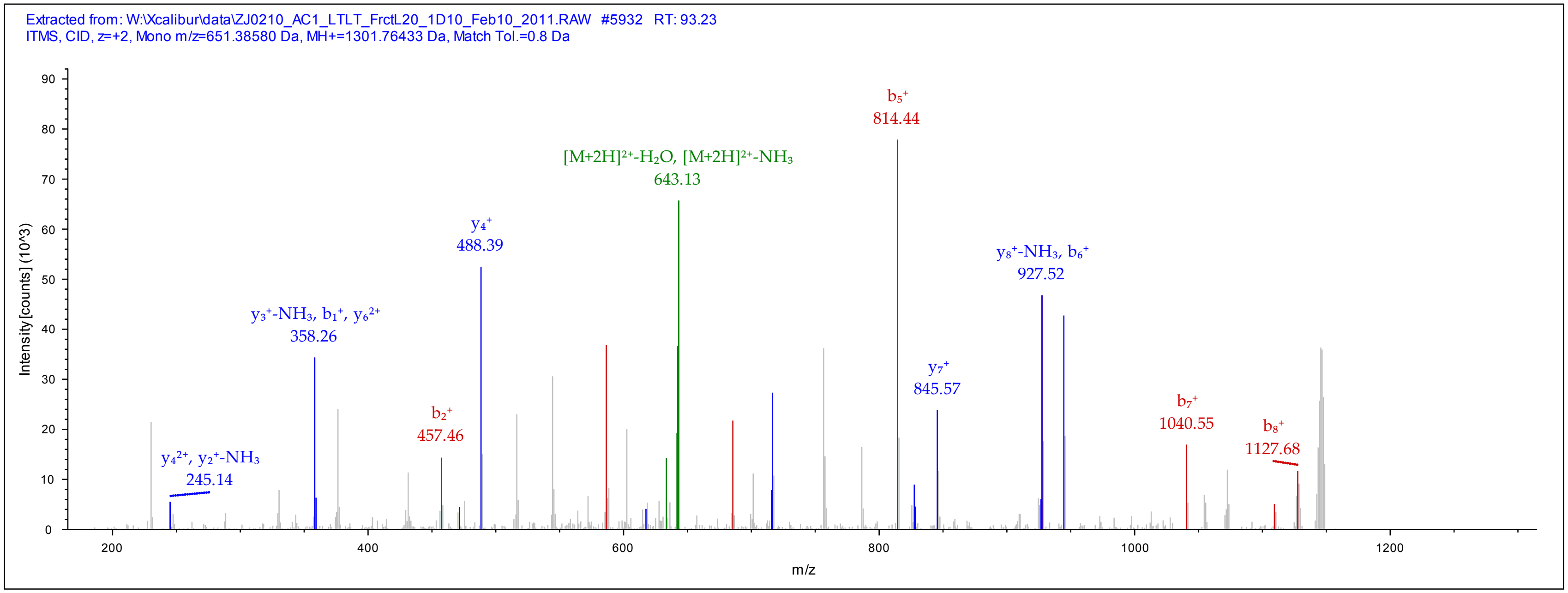
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.0E-002, Ions matched by search engine: 7/90

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- LAG1 longevity assurance homolog 2
- LAG1 homolog, ceramide synthase 2
- LAG1 homolog, ceramide synthase 2
- LAG1 homolog, ceramide synthase 2
- LAG1 homolog, ceramide synthase 2 lng=324



IPI:IPI00641582.1

Sequence: ELLALDSVDPEGR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 821.94641 Da (+0.27 mmu/+0.32 ppm),   MH+: 1642.88555 Da,   RT: 108.01 min,

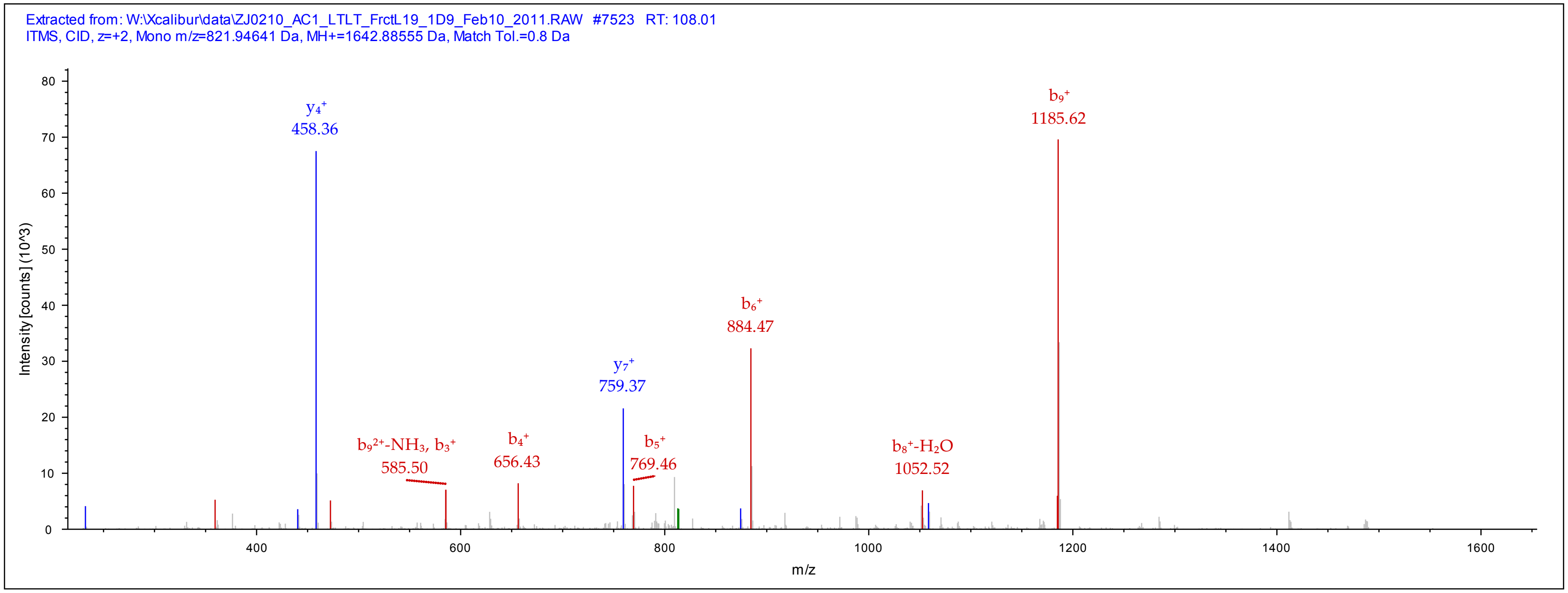
Identified with: Mascot (v1.16); IonScore:64, Exp Value:4.5E-005, Ions matched by search engine: 11/116

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- BAG family molecular chaperone regulator 3



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL19_1D9_Feb10_2011.RAW #7523 RT: 108.01
ITMS, CID, z=+2, Mono m/z=821.94641 Da, MH+=1642.88555 Da, Match Tol.=0.8 Da

IPI:IPI00647217.2

Sequence: SNVKPNSGELDPLYVVEVLLR, S1-TMT6plex (229.16293 Da), K4-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 933.87616 Da (+3.93 mmu/+4.2 ppm),   MH+: 2799.61393 Da,   RT: 213.83 min,

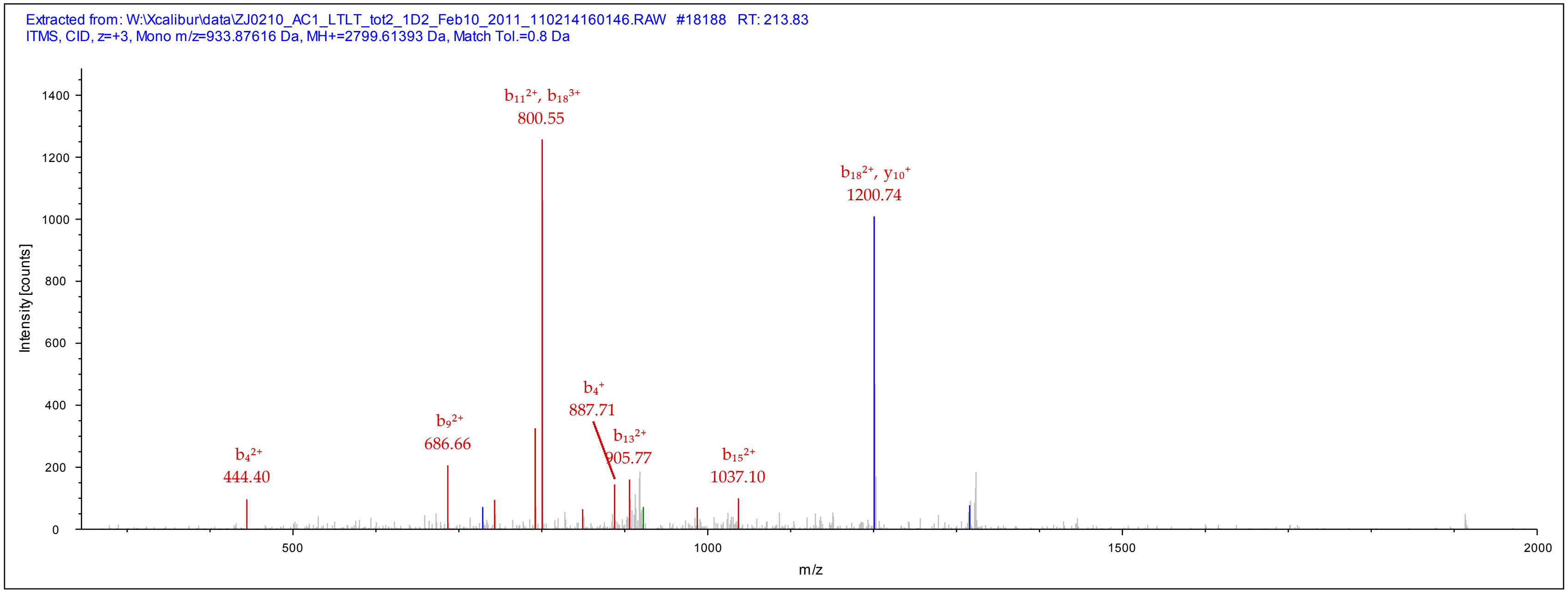
Identified with: Mascot (v1.16); IonScore:54, Exp Value:3.1E-004, Ions matched by search engine: 11/230

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Superkiller viralicidic activity 2-like 2



IPI:IPI00941359.1

Sequence: GEPPLPEEDLSK, G1-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 884.99243 Da (+2.11 mmu/+2.38 ppm), MH+: 1768.97759 Da, RT: 96.28 min,

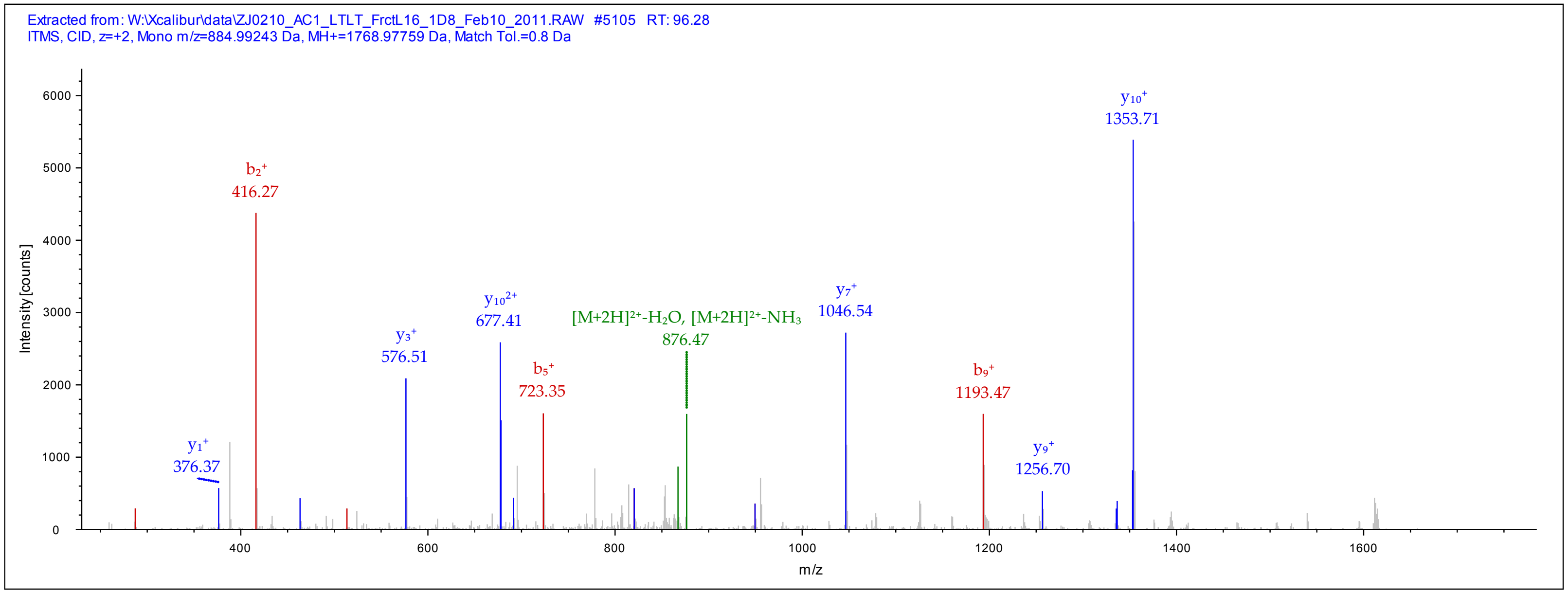
Identified with: Mascot (v1.16); IonScore:49, Exp Value:1.7E-003, Ions matched by search engine: 10/106

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Eukaryotic translation initiation factor 3 subunit H
- Eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa, isoform CRA_b lng=366



IPI:IPI00647720.1

Sequence: VNLEVIKPWITK, V1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 709.78857 Da (+0.08 mmu/+0.11 ppm), MH+: 2127.35117 Da, RT: 163.26 min,

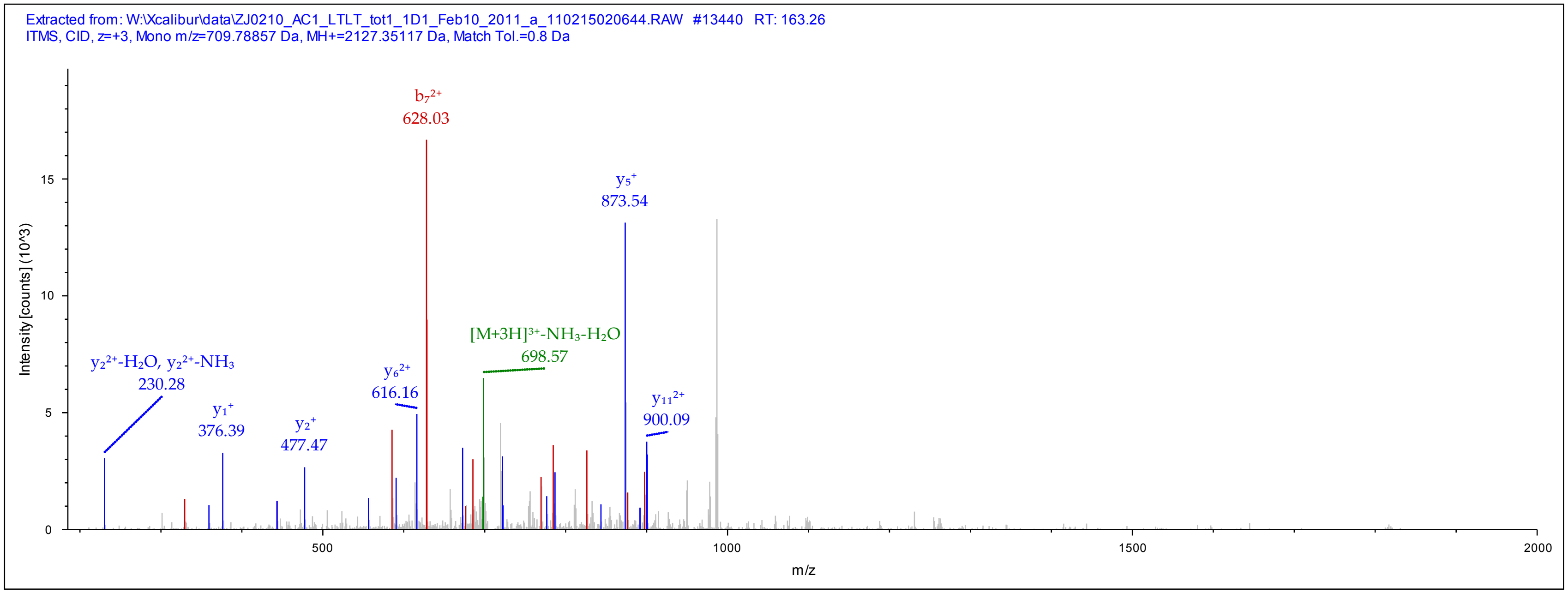
Identified with: Mascot (v1.16); IonScore:30, Exp Value:2.0E-002, Ions matched by search engine: 8/122

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Serine/arginine repetitive matrix protein 1
- cDNA FLJ61739, highly similar to Serine/arginine repetitive matrix protein 1



IPI:IPI00651738.1

Sequence: LGVLYWK, L1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 668.92517 Da (+1.86 mmu/+2.78 ppm),   MH+: 1336.84307 Da,   RT: 123.68 min,

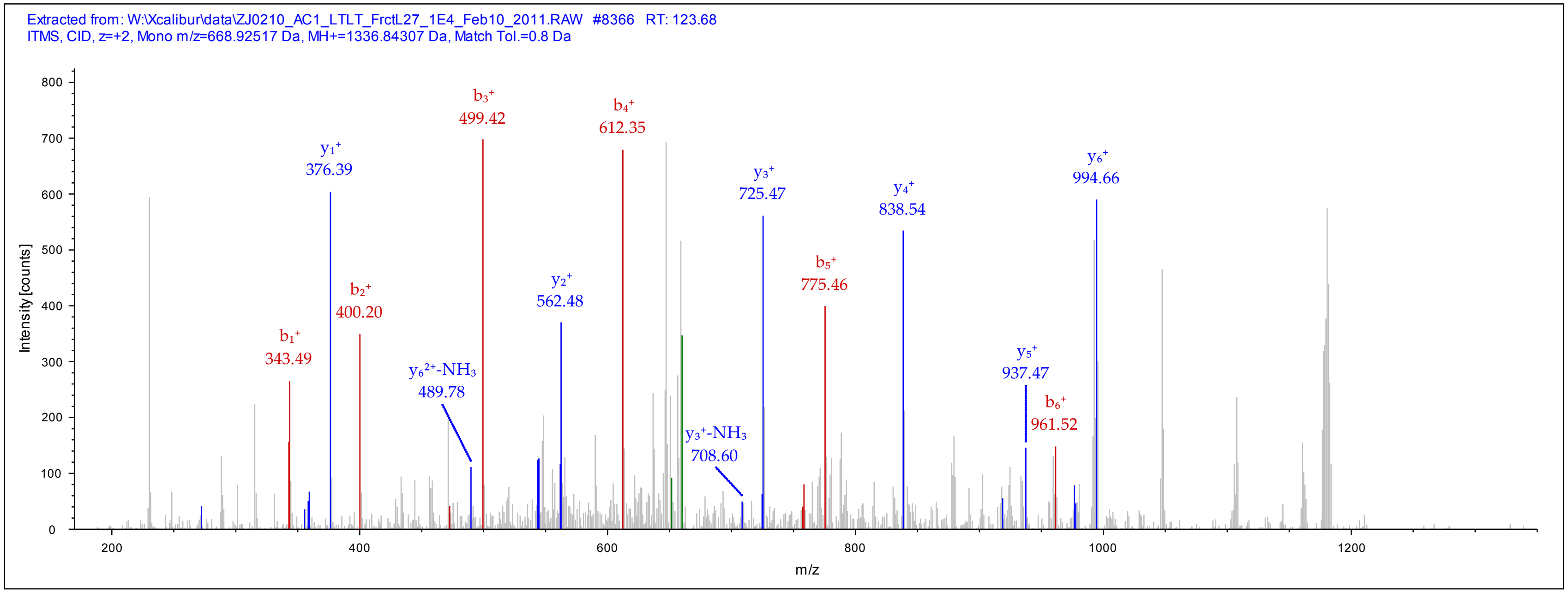
Identified with: Mascot (v1.16); IonScore:30, Exp Value:4.6E-002, Ions matched by search engine: 12/50

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Isoform 1 of 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase



IPI:IPI00745553.1

Sequence: ALLEVLGR, A1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 550.35583 Da (+0.34 mmu/+0.62 ppm),   MH+: 1099.70439 Da,   RT: 109.13 min,

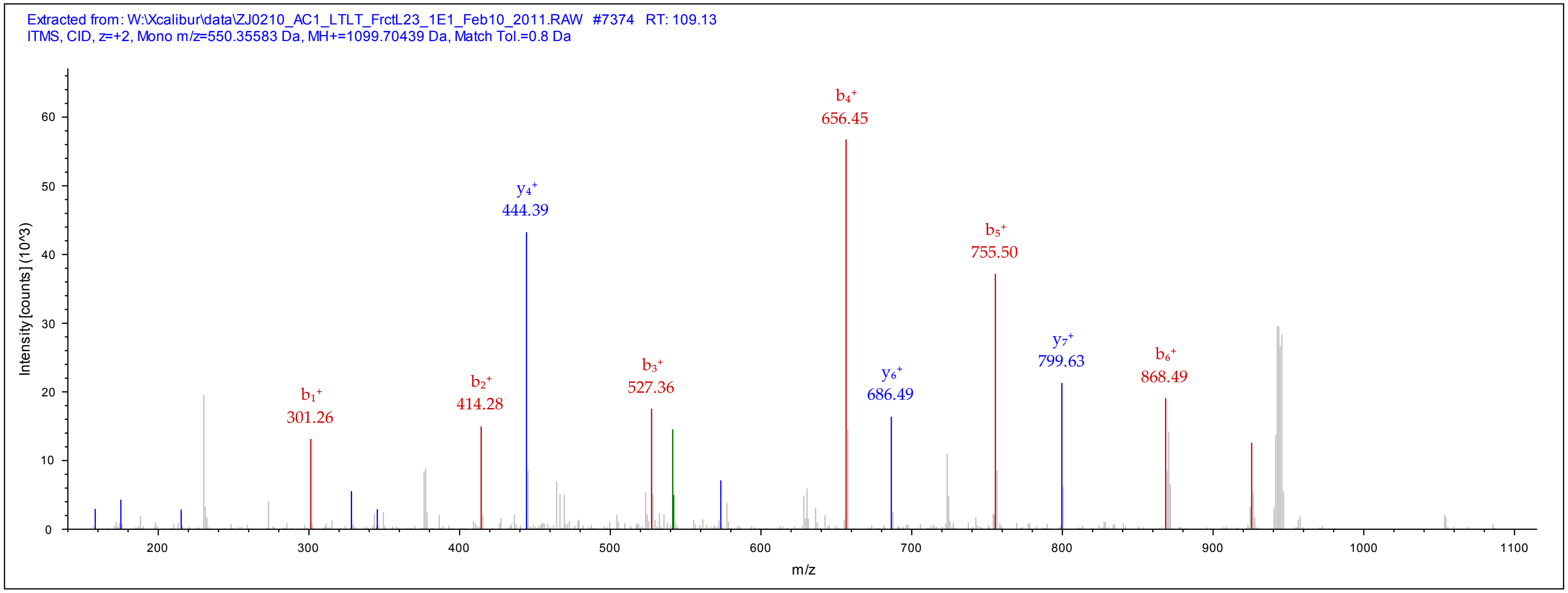
Identified with: Mascot (v1.16); IonScore:31, Exp Value:2.2E-002, Ions matched by search engine: 10/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 2 of Hydroxyacylglutathione hydrolase, mitochondrial
- Isoform 1 of Hydroxyacylglutathione hydrolase, mitochondrial



IPI:IPI00218606.7

Sequence: VANVSLLALYK, V1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 825.02460 Da (+0.84 mmu/+1.01 ppm),   MH+: 1649.04192 Da,   RT: 123.98 min,

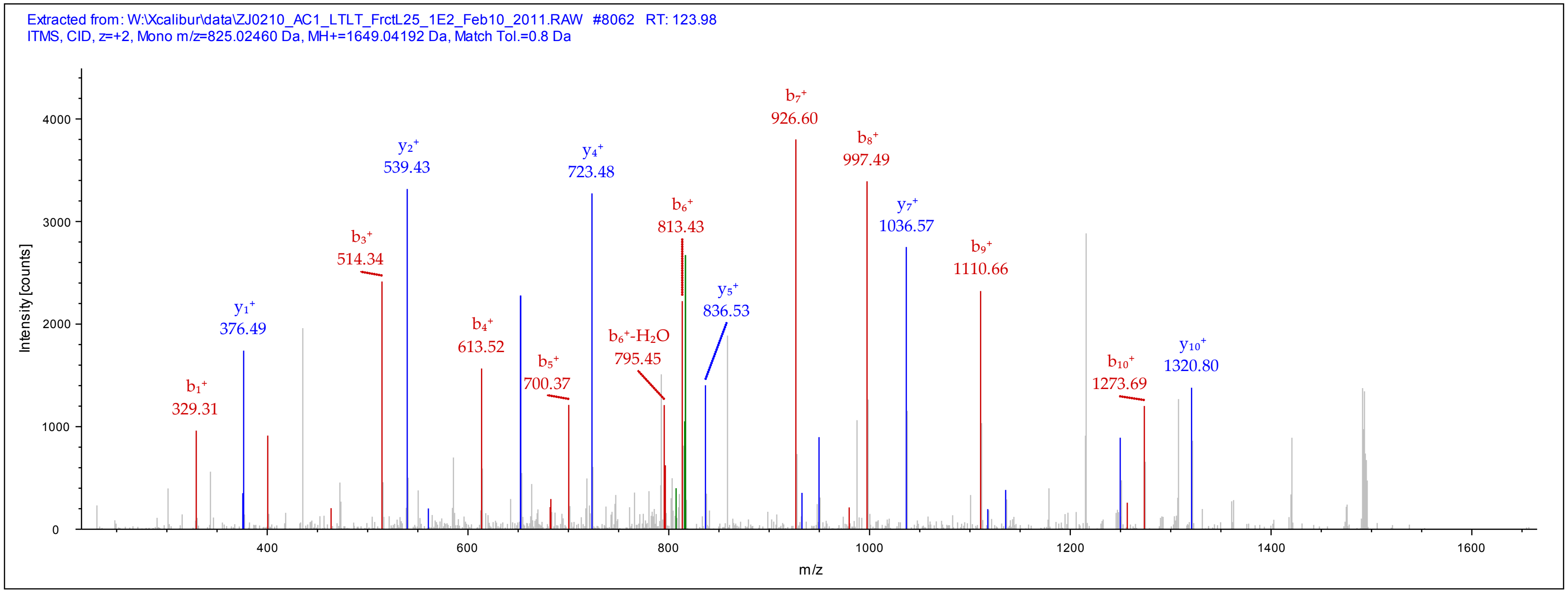
Identified with: Mascot (v1.16); IonScore:54, Exp Value:1.7E-004, Ions matched by search engine: 10/96

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 40S ribosomal protein S23



IPI:IPI00878215.1

Sequence: FVGIKDEDQLEAFLK, F1-TMT6plex (229.16293 Da), K5-TMT6plex (229.16293 Da), K15-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 813.80835 Da (+0.06 mmu/+0.07 ppm), MH+: 2439.41050 Da, RT: 167.13 min,

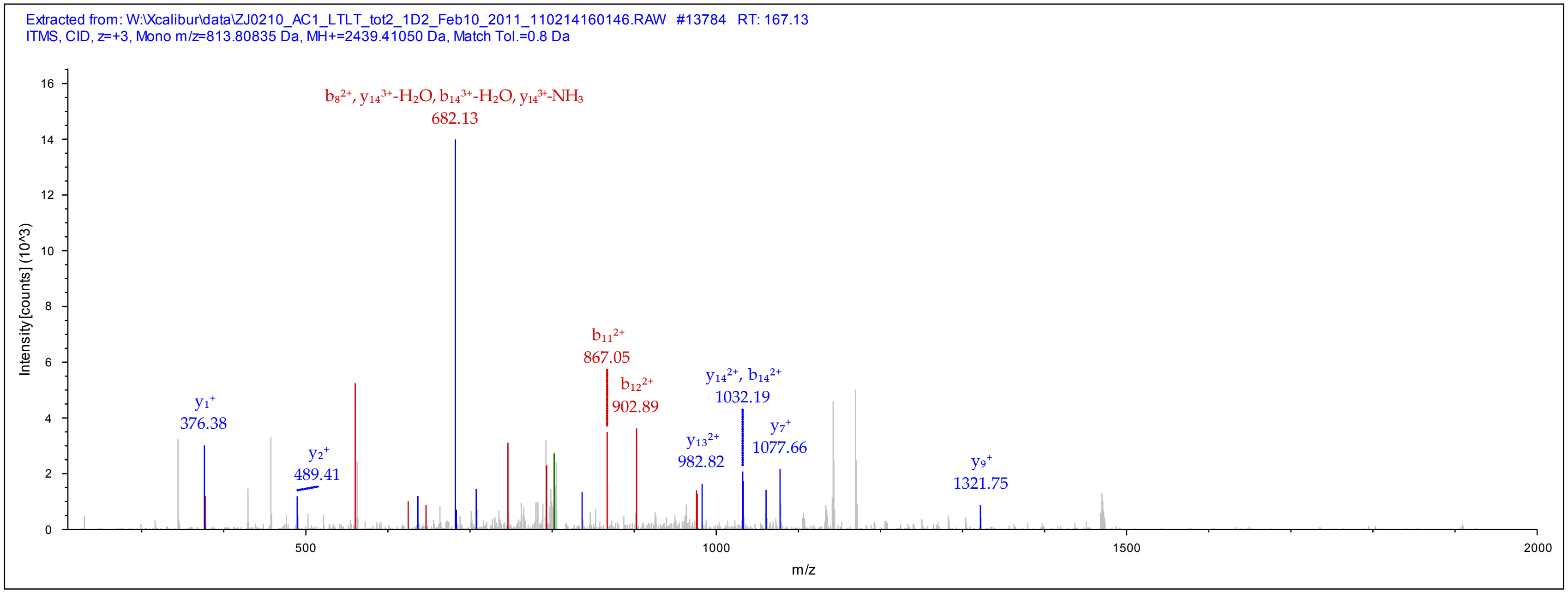
Identified with: Mascot (v1.16); IonScore:32, Exp Value:5.2E-002, Ions matched by search engine: 9/142

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Thioredoxin, mitochondrial
- cDNA FLJ55158, highly similar to Thioredoxin, mitochondrial lng=197



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_tot2_1D2_Feb10_2011_110214160146.RAW #13784 RT: 167.13
ITMS, CID, z=+3, Mono m/z=813.80835 Da, MH+=2439.41050 Da, Match Tol.=0.8 Da

IPI:IPI00007084.3

Sequence: IAPLEEGTLPFNLAEAQR, I1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 1099.60632 Da (+1.71 mmu/+1.55 ppm),   MH+: 2198.20537 Da,   RT: 125.94 min,

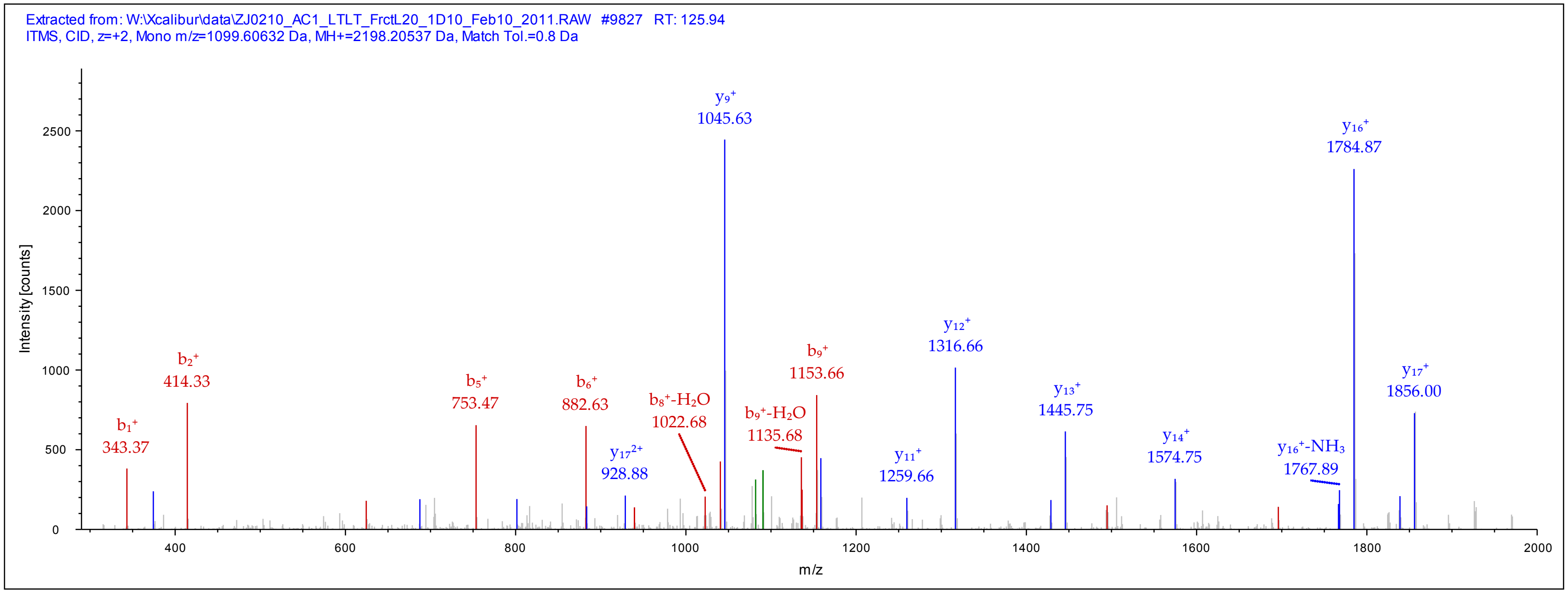
Identified with: Mascot (v1.16); IonScore:92, Exp Value:7.7E-008, Ions matched by search engine: 14/168

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Calcium-binding mitochondrial carrier protein Aralar2
- solute carrier family 25, member 13 isoform 1 lng=676



IPI:IPI00550234.4

Sequence: ALAAGGVGSIVR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 650.38831 Da (-12.68 mmu/-19.49 ppm), MH+: 1299.76933 Da, RT: 112.73 min,

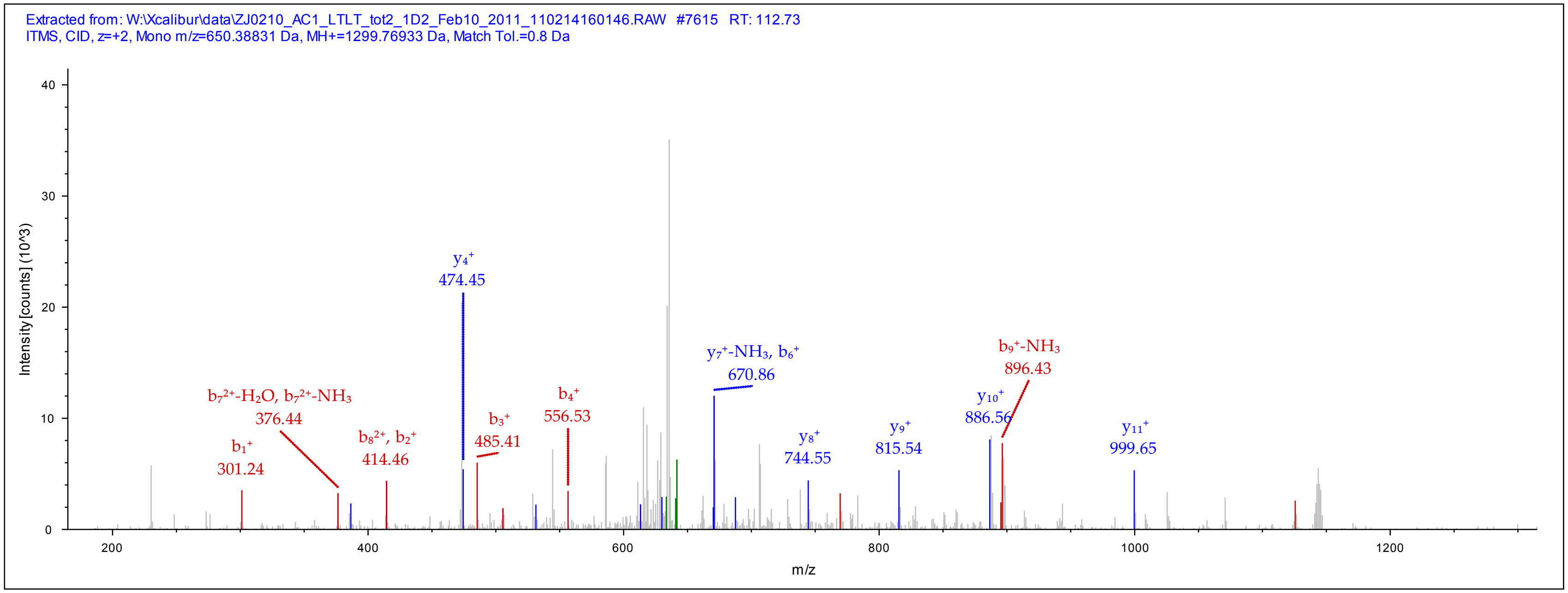
Identified with: Mascot (v1.16); IonScore:34, Exp Value:2.1E-002, Ions matched by search engine: 10/88

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Actin-related protein 2/3 complex subunit 5
- Isoform 2 of Actin-related protein 2/3 complex subunit 5 lng=154



IPI:IPI00956233.1

Sequence: VIDILR, V1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 479.31848 Da (+0.11 mmu/+0.22 ppm),   MH+: 957.62969 Da,   RT: 107.36 min,

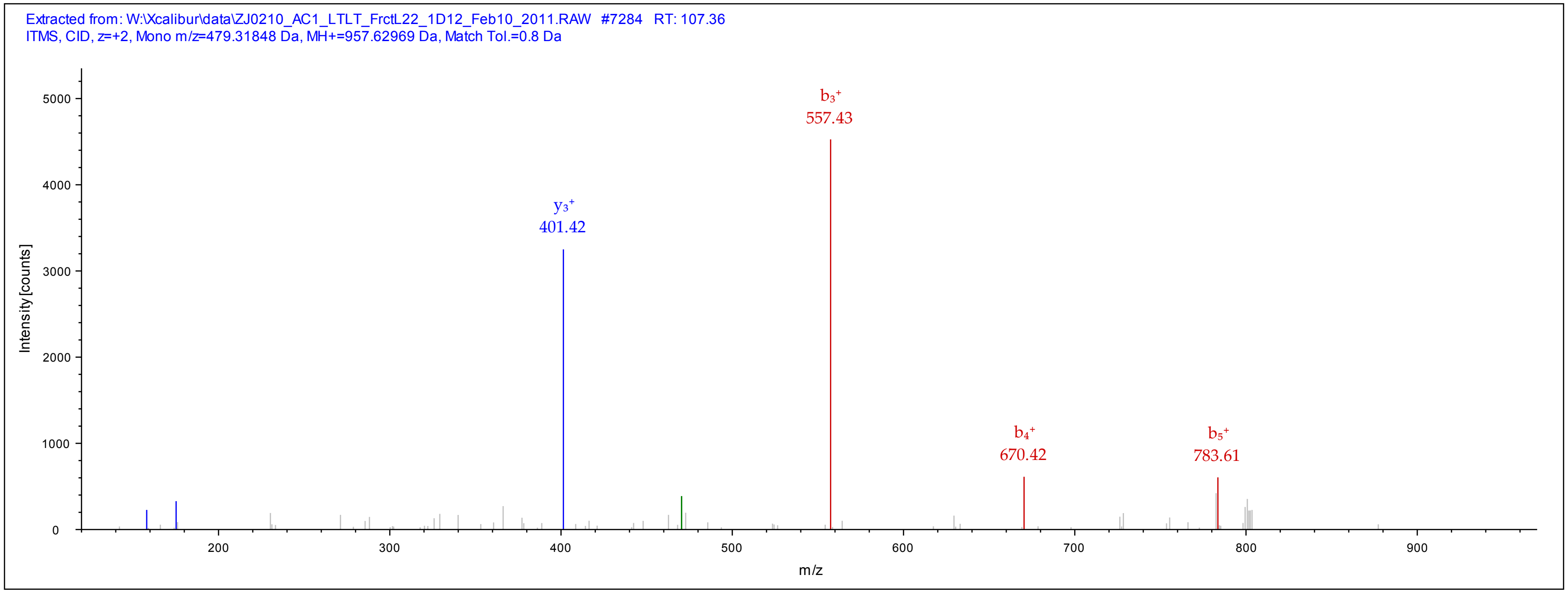
Identified with: Mascot (v1.16); IonScore:31, Exp Value:1.9E-002, Ions matched by search engine: 4/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- 47 kDa protein
- B-cell lymphoma 3-encoded protein lng=539
- B-cell lymphoma 3 protein



IPI00855846.1

Sequence: FGVLFR, F1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 484.29980 Da (-0.18 mmu/-0.37 ppm), MH+: 967.59233 Da, RT: 107.63 min,

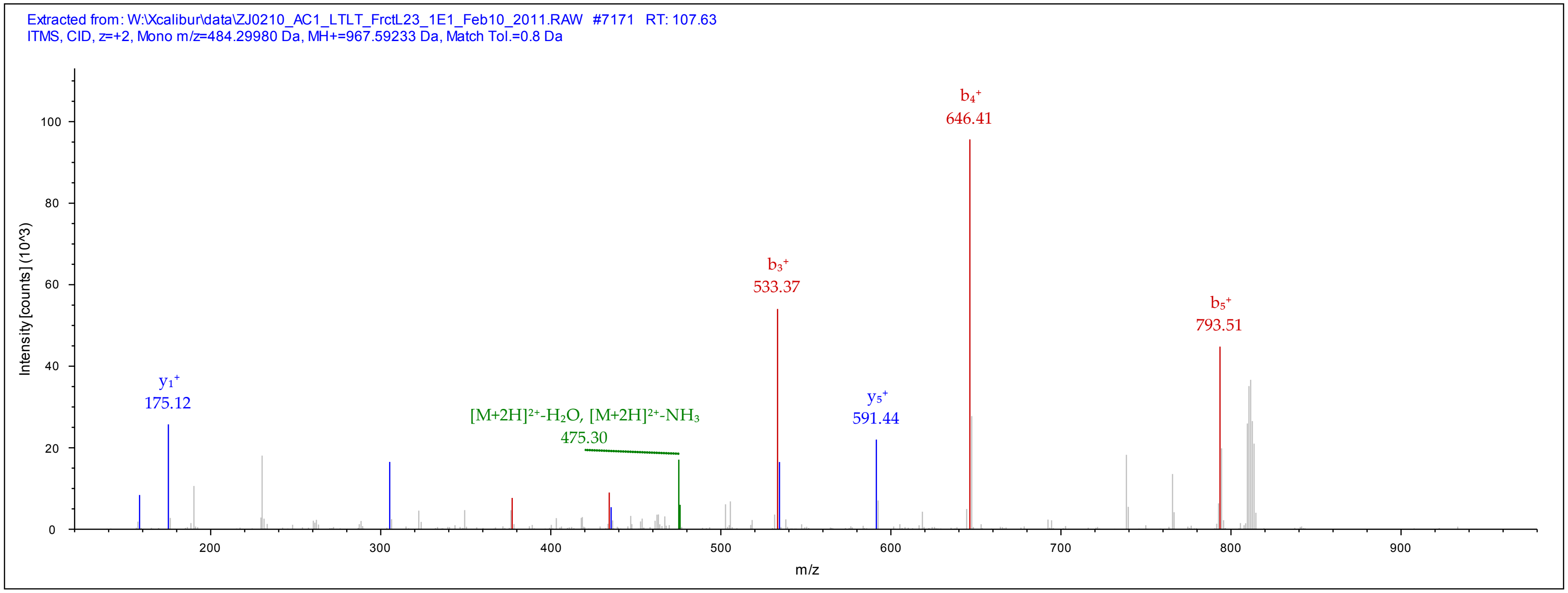
Identified with: Mascot (v1.16); IonScore:33, Exp Value:2.1E-002, Ions matched by search engine: 5/42

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- UPF0727 protein C6orf115 lng=81



IPI:IPI00306749.8

Sequence: ILDTLGLLR, I1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 621.90497 Da (+2.16 mmu/+3.47 ppm),   MH+: 1242.80266 Da,   RT: 132.55 min,

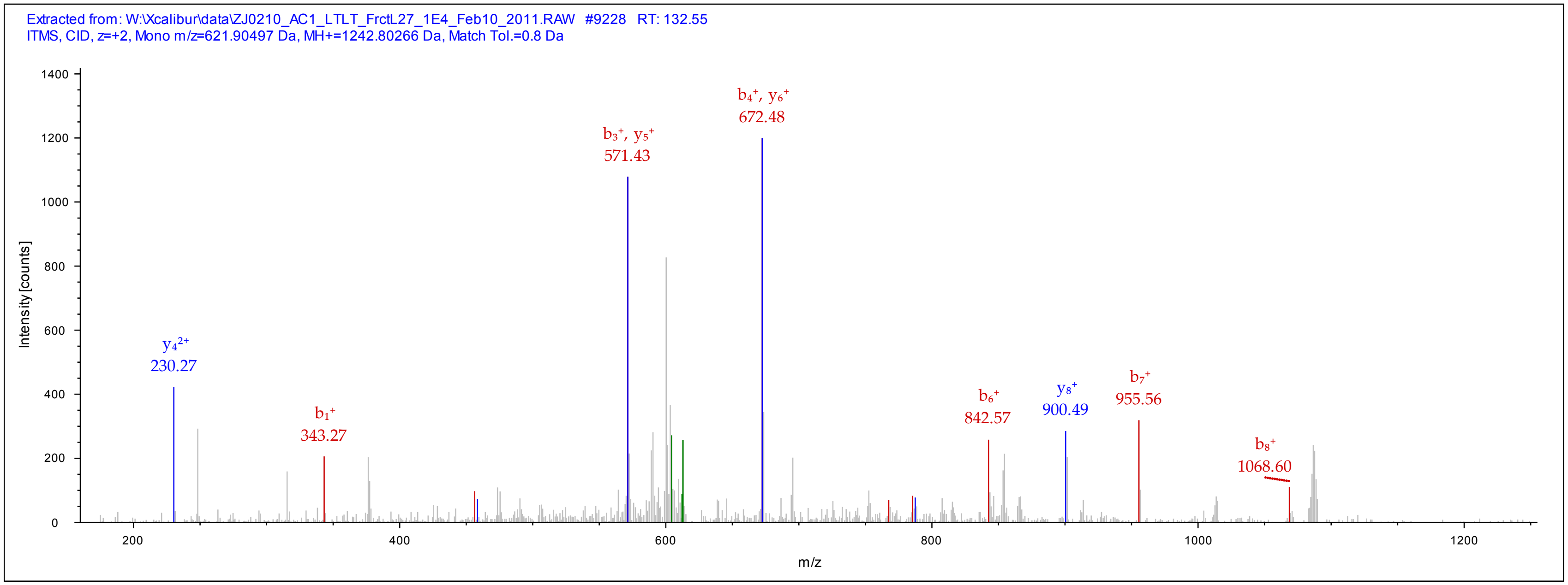
Identified with: Mascot (v1.16); IonScore:37, Exp Value:1.9E-002, Ions matched by search engine: 6/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Kanadaptin



IPI:IPI00788194.2

Sequence: MIQQEEIR, M1-TMT6plex (229.16293 Da), M1-Oxidation (15.99492 Da)

Charge: +2, Monoisotopic m/z: 646.34186 Da (-5.69 mmu/-8.8 ppm), MH+: 1291.67644 Da, RT: 90.43 min,

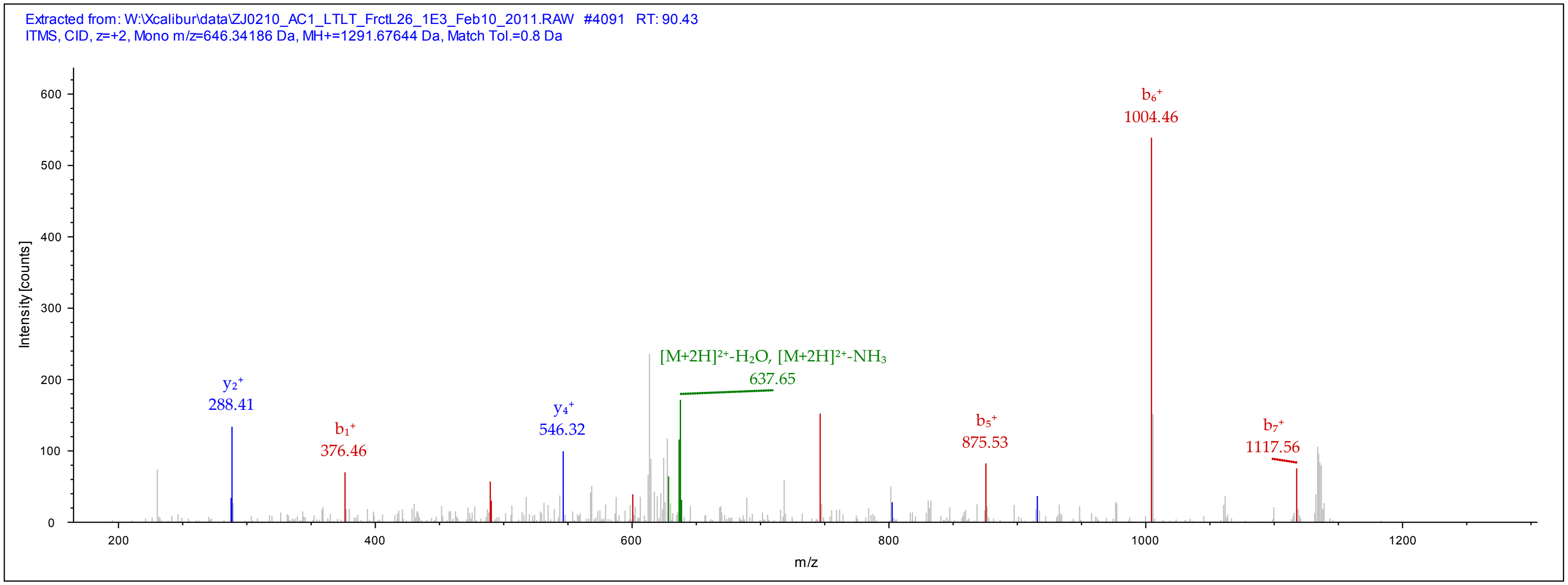
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.2E-002, Ions matched by search engine: 5/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (8):

- Putative uncharacterized protein C20orf69
- Septin-14
- cDNA FLJ60027, moderately similar to F-box only protein 25
- 26 kDa protein
- hypothetical protein XP_002342648
- hypothetical protein XP_002342211
- 19 kDa protein



IPI:IPI00009009.4

Sequence: QTTQDAPEEVR, Q1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 751.88898 Da (+2.9 mmu/+3.86 ppm),   MH+: 1502.77068 Da,   RT: 66.43 min,

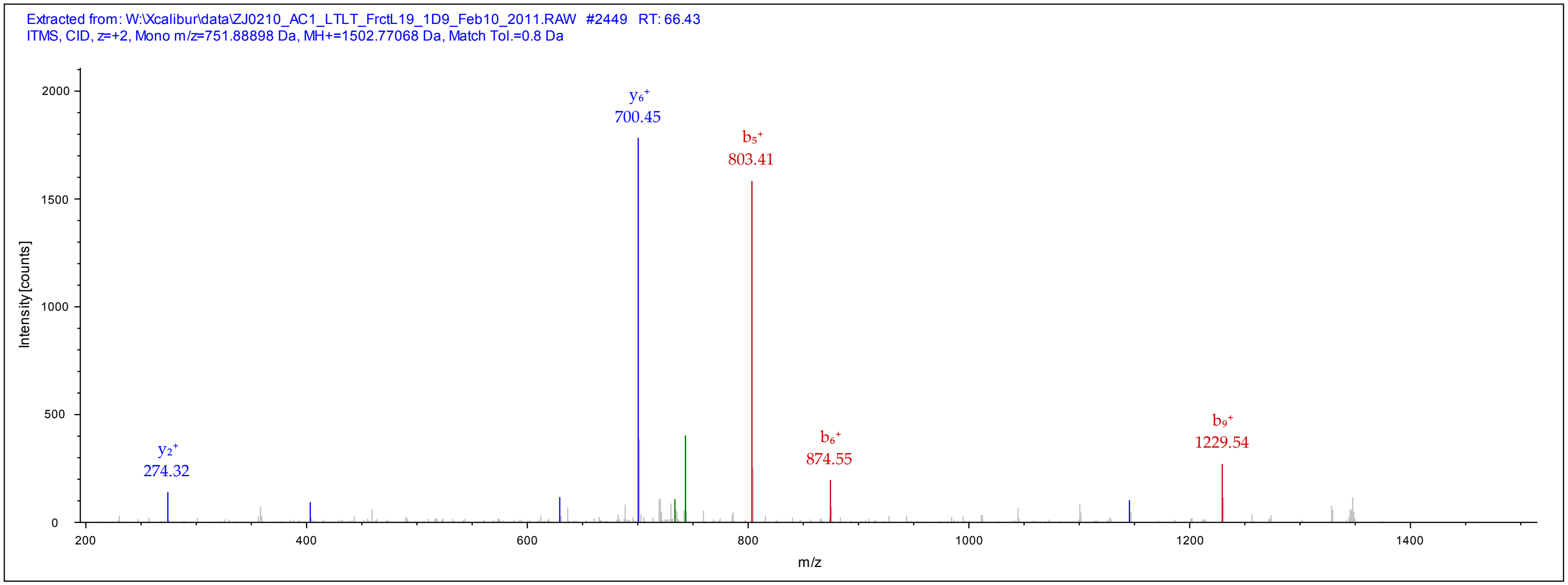
Identified with: Mascot (v1.16); IonScore:43, Exp Value:4.2E-003, Ions matched by search engine: 15/114

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Protein CWC15 homolog



IPI:IPI00152731.6

Sequence: LFENLK, L1-TMT6plex (229.16293 Da), K6-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 611.38501 Da (+0.99 mmu/+1.62 ppm), MH+: 1221.76274 Da, RT: 125.54 min,

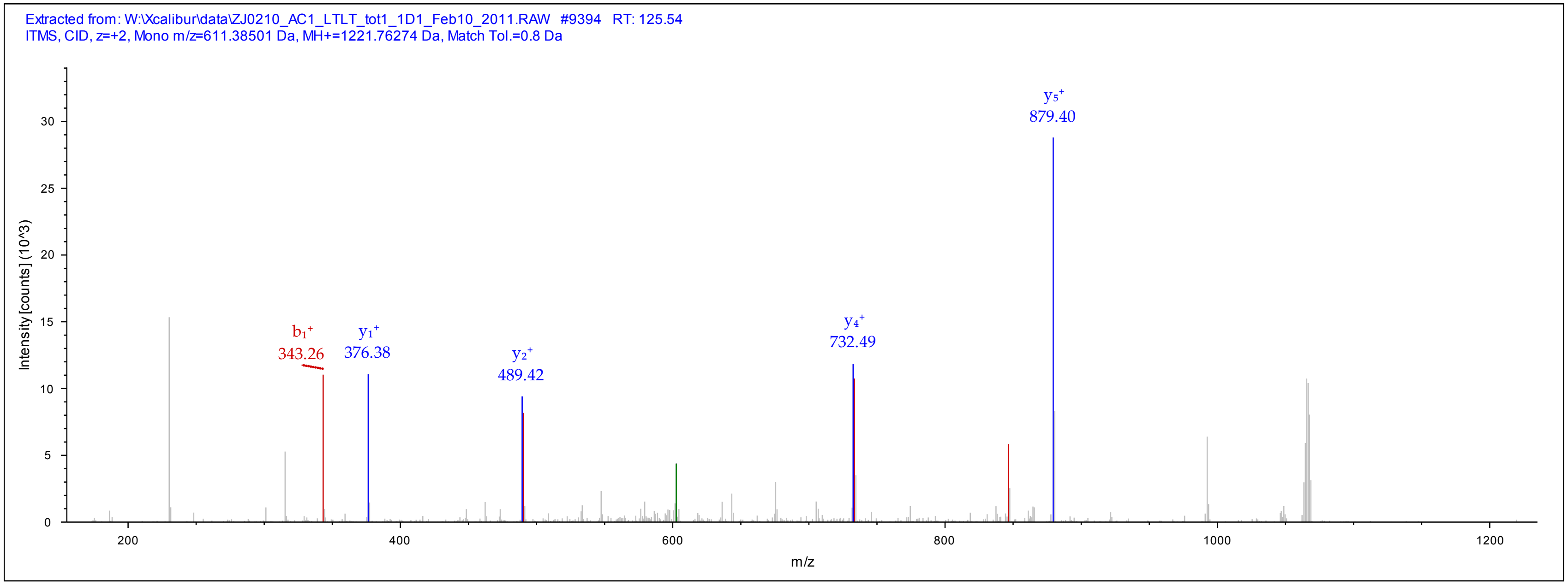
Identified with: Mascot (v1.16); IonScore:32, Exp Value:2.9E-002, Ions matched by search engine: 5/44

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Macrophage-expressed gene 1 protein



IPI:IPI00641181.5

Sequence: GDVTAEEAAGASPAK, G1-TMT6plex (229.16293 Da), K15-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 611.33209 Da (+0.49 mmu/+0.8 ppm),   MH+: 1831.98172 Da,   RT: 79.80 min,

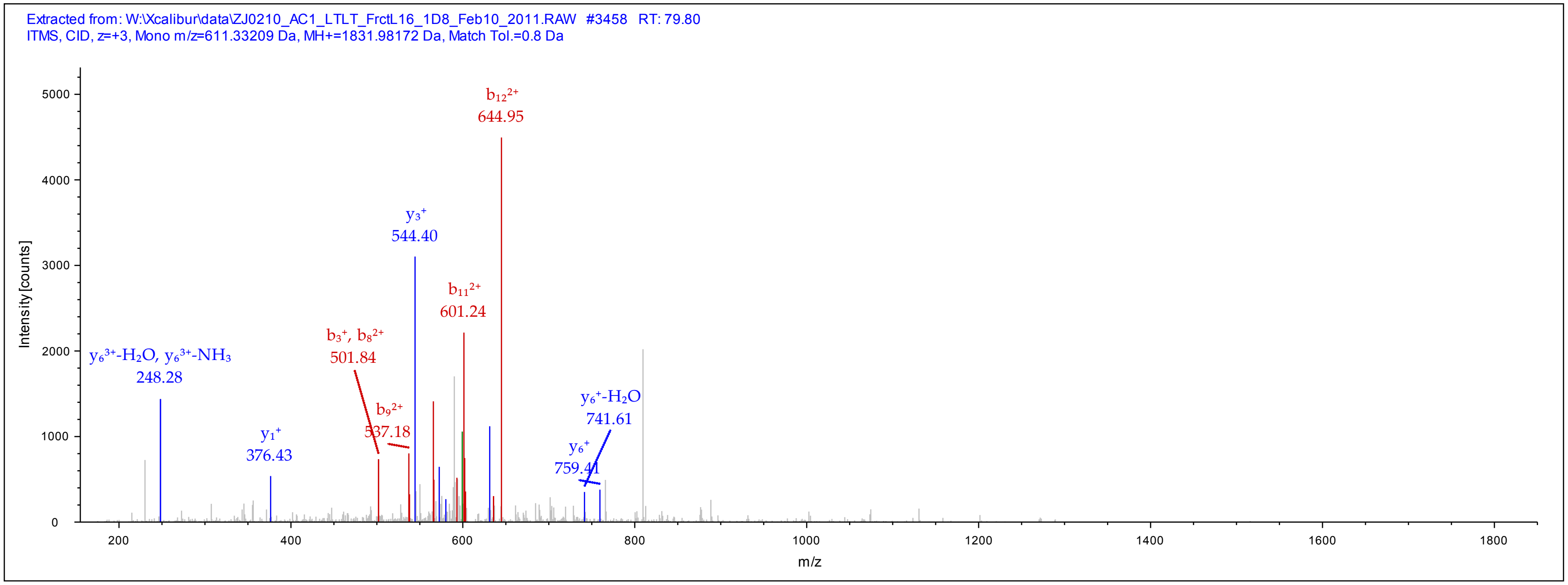
Identified with: Mascot (v1.16); IonScore:44, Exp Value:5.8E-003, Ions matched by search engine: 10/132

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- MARCKS-related protein



IPI:IPI00026496.3

Sequence: DECNVVEVVAR, D1-TMT6plex (229.16293 Da), C3-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 759.89459 Da (+1.74 mmu/+2.29 ppm),   MH+: 1518.78191 Da,   RT: 90.99 min,

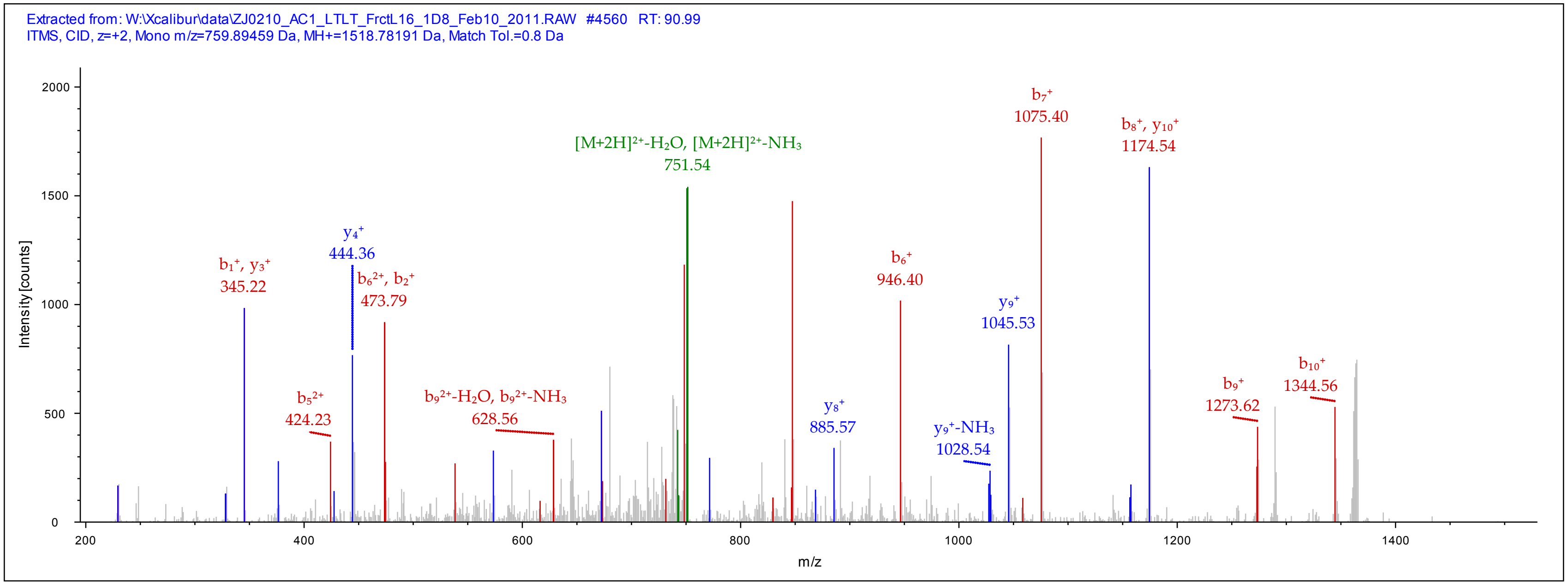
Identified with: Mascot (v1.16); IonScore:48, Exp Value:2.0E-003, Ions matched by search engine: 9/106

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Nucleoplasmin-3



IPI:IPI00023640.3

Sequence: VSEQGLIEILK, V1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 844.02393 Da (-0.04 mmu/-0.05 ppm),   MH+: 1687.04057 Da,   RT: 122.34 min,

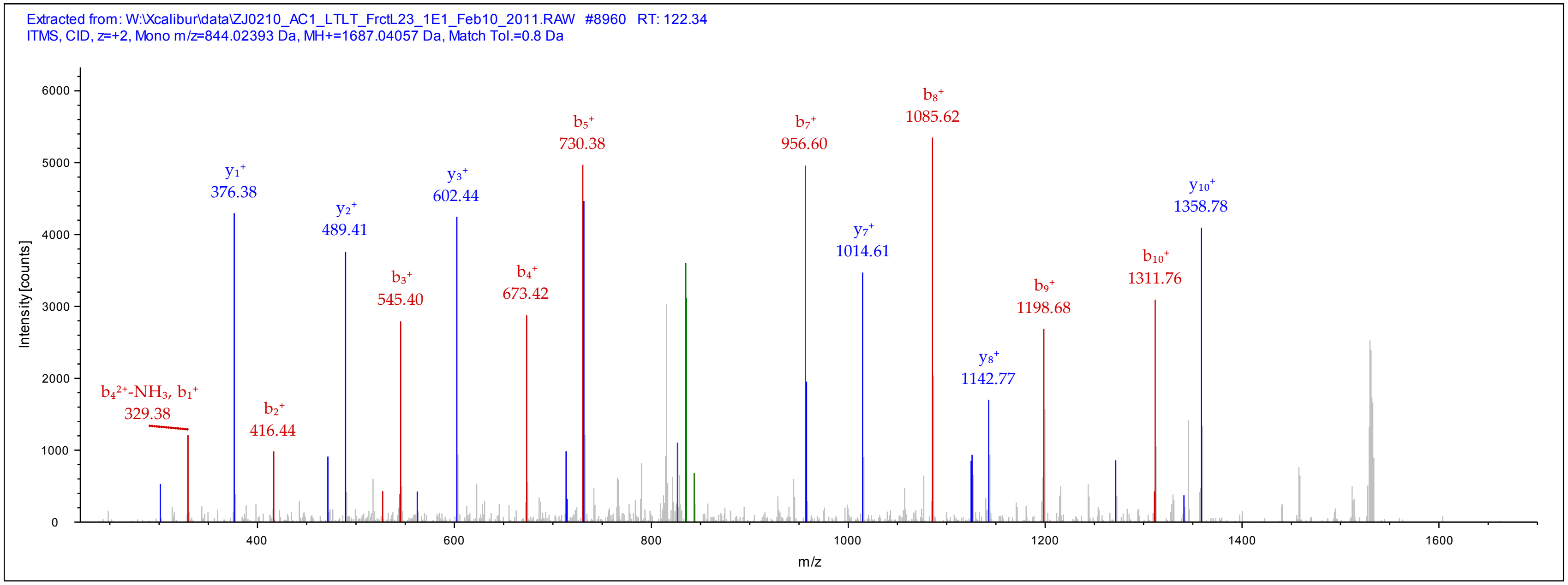
Identified with: Mascot (v1.16); IonScore:47, Exp Value:1.1E-003, Ions matched by search engine: 15/106

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Programmed cell death protein 5



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL23_1E1_Feb10_2011.RAW #8960 RT: 122.34
ITMS, CID, z=+2, Mono m/z=844.02393 Da, MH+=1687.04057 Da, Match Tol.=0.8 Da

IPI:IPI00218568.7

Sequence: AVGWNELEGR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 680.36462 Da (+0.04 mmu/+0.06 ppm), MH+: 1359.72197 Da, RT: 93.90 min,

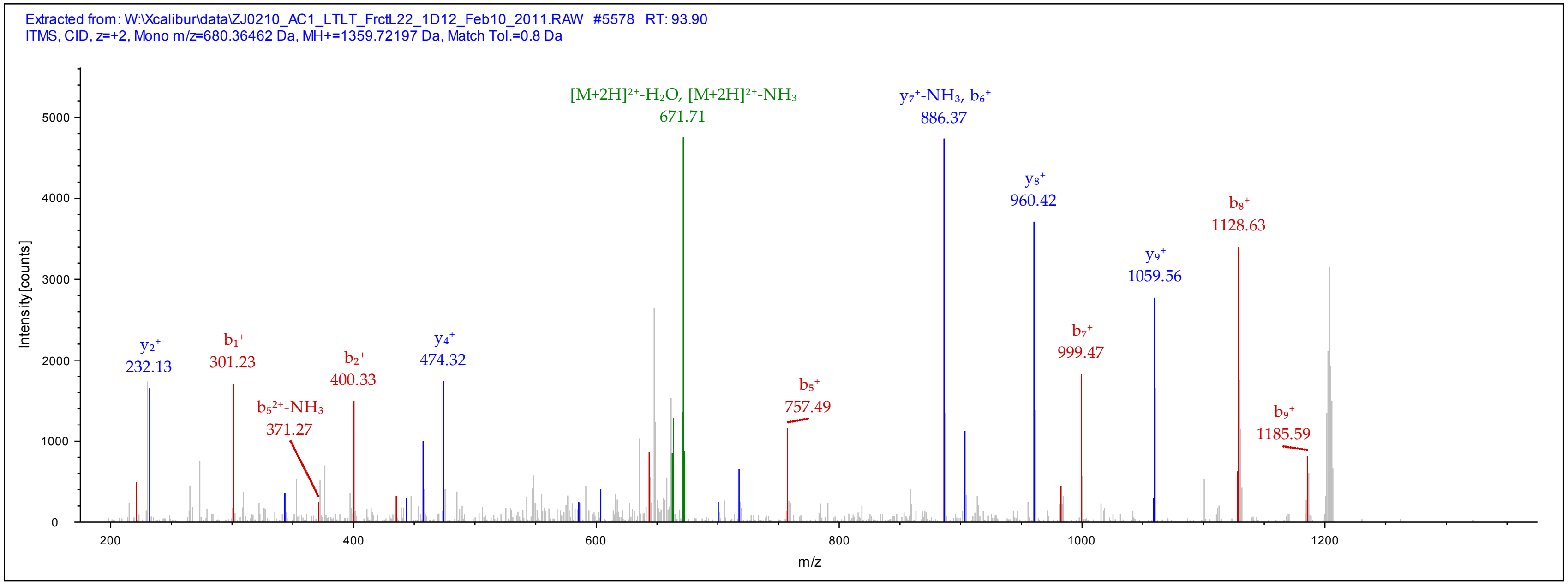
Identified with: Mascot (v1.16); IonScore:32, Exp Value:5.6E-002, Ions matched by search engine: 8/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Pterin-4-alpha-carbinolamine dehydratase



IPI:IPI00166137.5

Sequence: VFIGNLNTAIVK, V1-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 874.04846 Da (+0.69 mmu/+0.79 ppm),   MH+: 1747.08965 Da,   RT: 120.22 min,

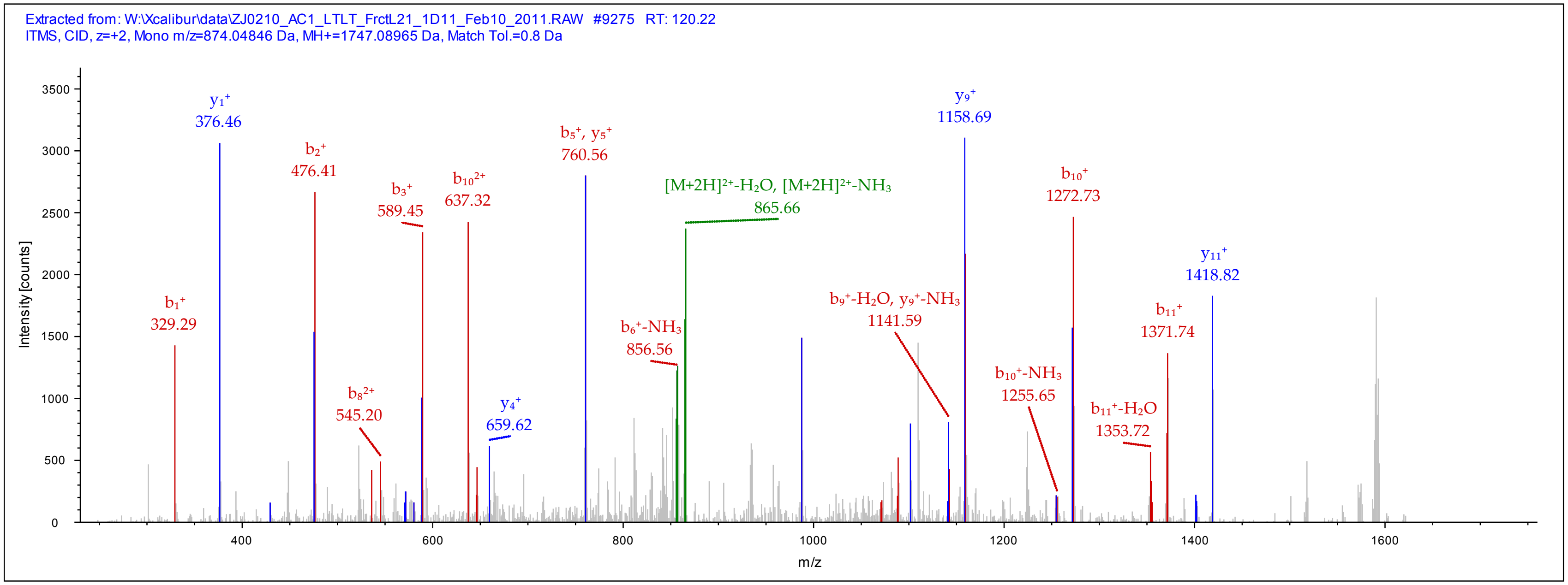
Identified with: Mascot (v1.16); IonScore:54, Exp Value:1.9E-004, Ions matched by search engine: 10/102

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of RNA-binding Raly-like protein
- RALY RNA binding protein-like isoform 1 lng=304



IPI:IPI00014235.3

Sequence: KAENPQCLLGDFVTEFFK, K1-TMT6plex (229.16293 Da), K1-TMT6plex (229.16293 Da), C7-Carbamidomethyl (57.02146 Da), K18-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 944.18951 Da (+4.08 mmu/+4.32 ppm), MH+: 2830.55399 Da, RT: 212.08 min,

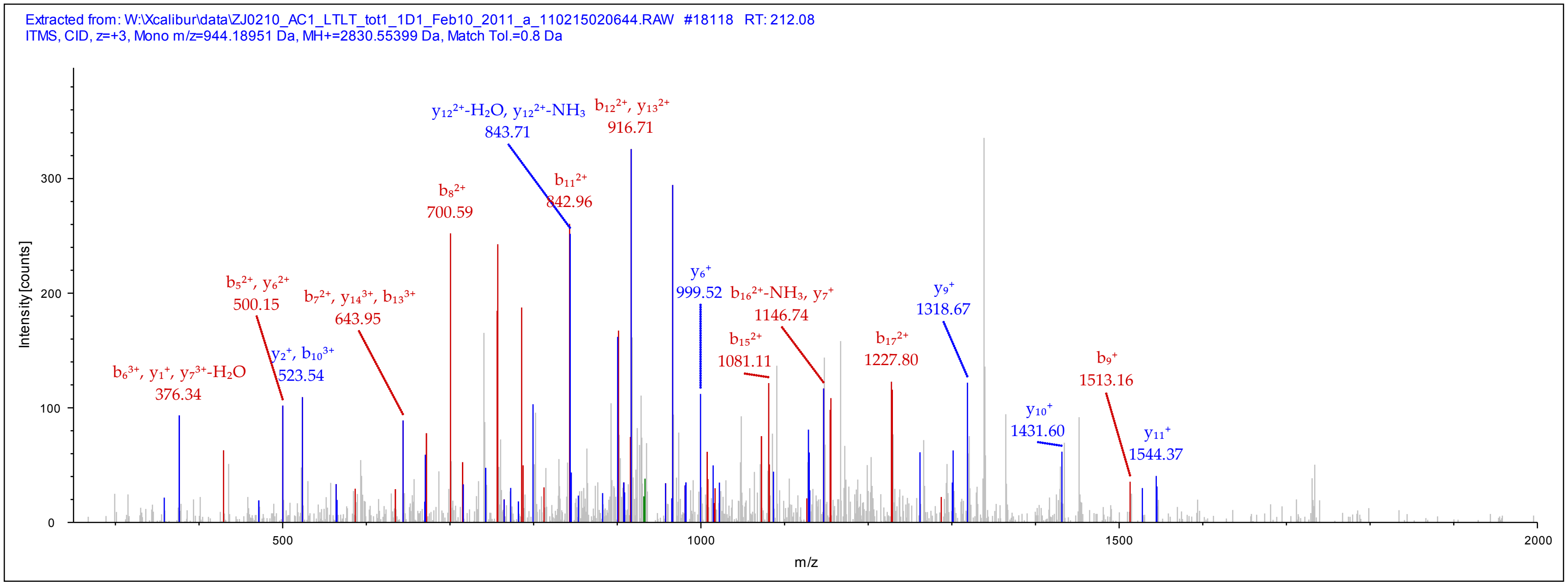
Identified with: Mascot (v1.16); IonScore:39, Exp Value:1.6E-002, Ions matched by search engine: 13/194

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Rab3 GTPase-activating protein catalytic subunit
- Putative uncharacterized protein RAB3GAP1 lng=988



IPI:IPI00000494.6

Sequence: QFSQYIK, Q1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 686.40466 Da (-0.81 mmu/-1.19 ppm),   MH+: 1371.80205 Da,   RT: 89.57 min,

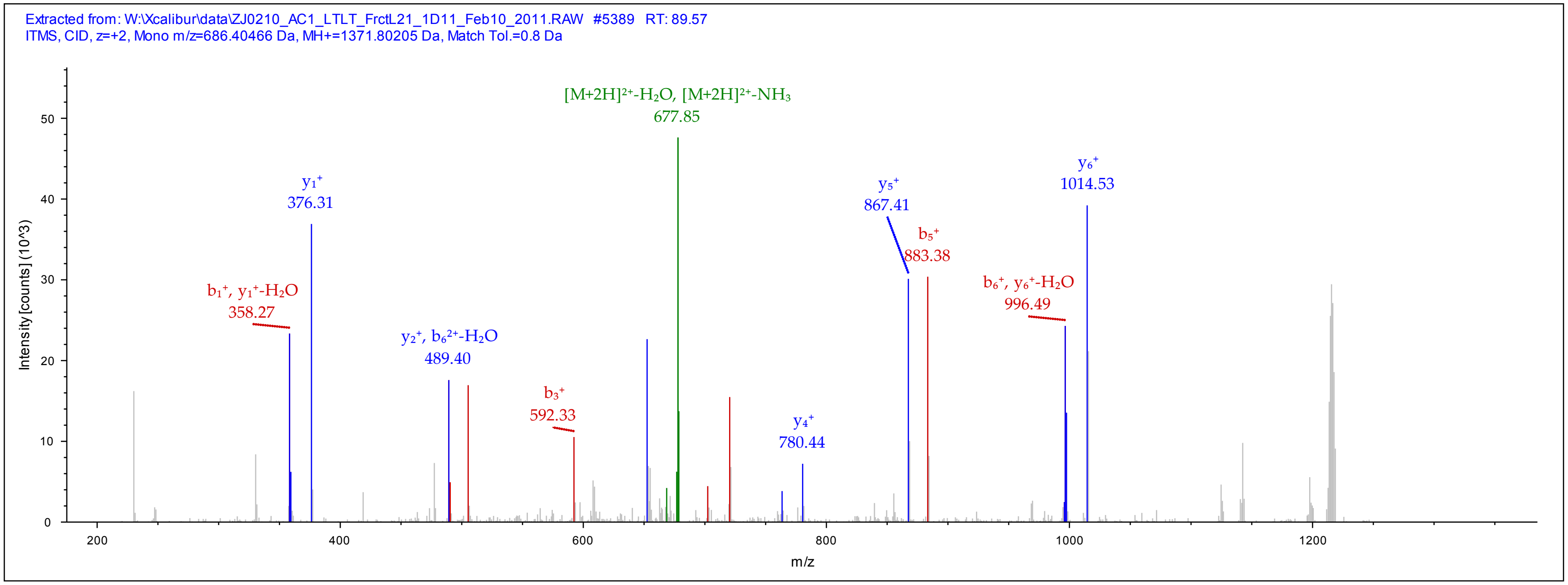
Identified with: Mascot (v1.16); IonScore:38, Exp Value:2.1E-002, Ions matched by search engine: 12/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 60S ribosomal protein L5



IPI:IPI00736155.3

Sequence: FLQEQNK, F1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 455.60303 Da (+0.22 mmu/+0.49 ppm),   MH+: 1364.79453 Da,   RT: 81.73 min,

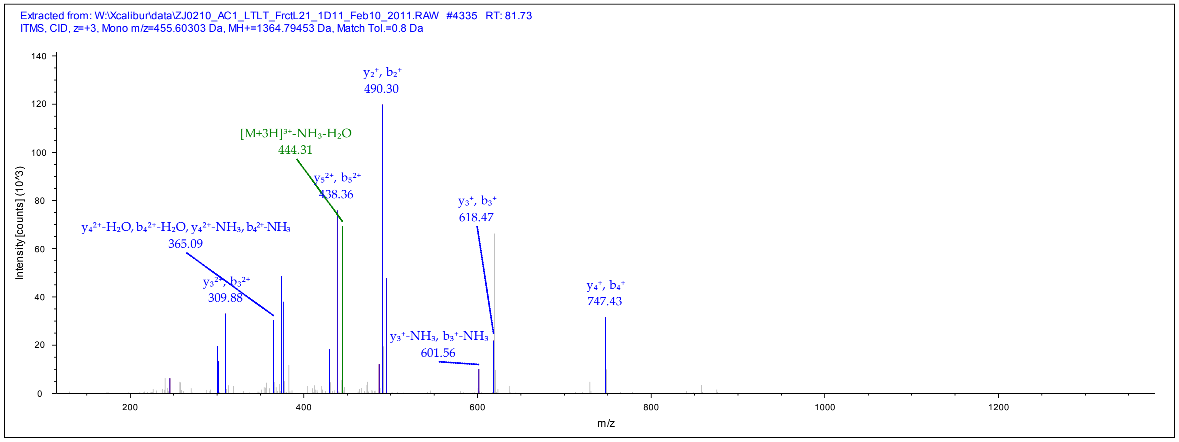
Identified with: Mascot (v1.16); IonScore:31, Exp Value:5.9E-002, Ions matched by search engine: 5/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (19):

- Putative ubiquitin carboxyl-terminal hydrolase 17-like protein 1 lng=530
- Ubiquitin carboxyl-terminal hydrolase 17-like protein 5 lng=530
- Ubiquitin carboxyl-terminal hydrolase 17-like protein 3
- Ubiquitin carboxyl-terminal hydrolase 17
- ubiquitin carboxyl-terminal hydrolase 17
- similar to deubiquitinating enzyme DUB1 lng=530
- Putative uncharacterized protein ENSP00000389443 lng=530
- Putative uncharacterized protein ENSP00000403760 lng=530
- hypothetical protein XP_002342480 lng=530
- hypothetical protein XP_002342479 lng=530
- hypothetical protein XP_002342478 lng=530



IPI:IPI00011631.6

Sequence: LVLEVLQK, L1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 700.46832 Da (+0.23 mmu/+0.33 ppm), MH+: 1399.92937 Da, RT: 125.08 min,

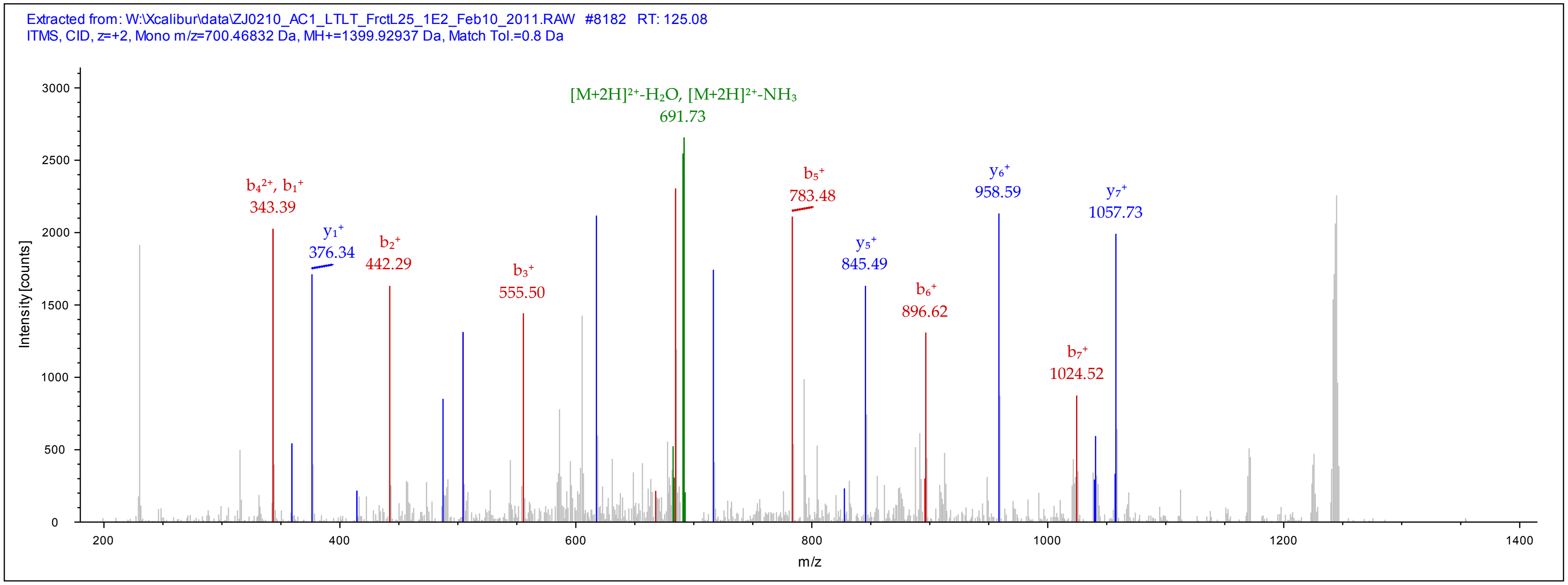
Identified with: Mascot (v1.16); IonScore:37, Exp Value:2.8E-003, Ions matched by search engine: 12/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Centromere/kinetochore protein zw10 homolog



IPI00003579.2

Sequence: LDEYKRLMSLGK, L1-TMT6plex (229.16293 Da), Y4-Phospho (79.96633 Da), K5-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 740.76367 Da (+11.13 mmu/+15.02 ppm),   MH+: 2220.27646 Da,   RT: 210.06 min,

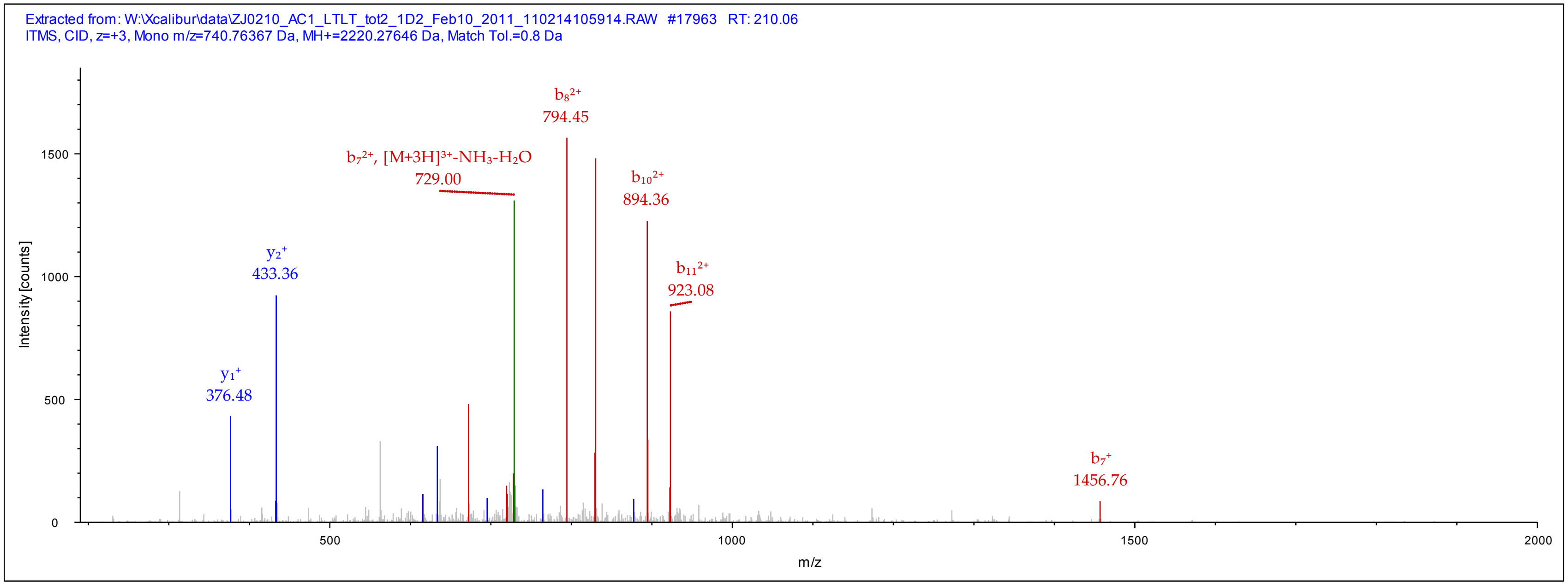
Identified with: Mascot (v1.16); IonScore:32, Exp Value:5.7E-002, Ions matched by search engine: 7/116

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Sarcosine dehydrogenase, mitochondrial
- Sarcosine dehydrogenase lng=283
- Sarcosine dehydrogenase, isoform CRA_d lng=396
- Sarcosine dehydrogenase lng=609



IPI00003799.2

Sequence: NQEQLLTLASILR, N1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 864.51733 Da (+2.82 mmu/+3.26 ppm), MH+: 1728.02739 Da, RT: 131.18 min,

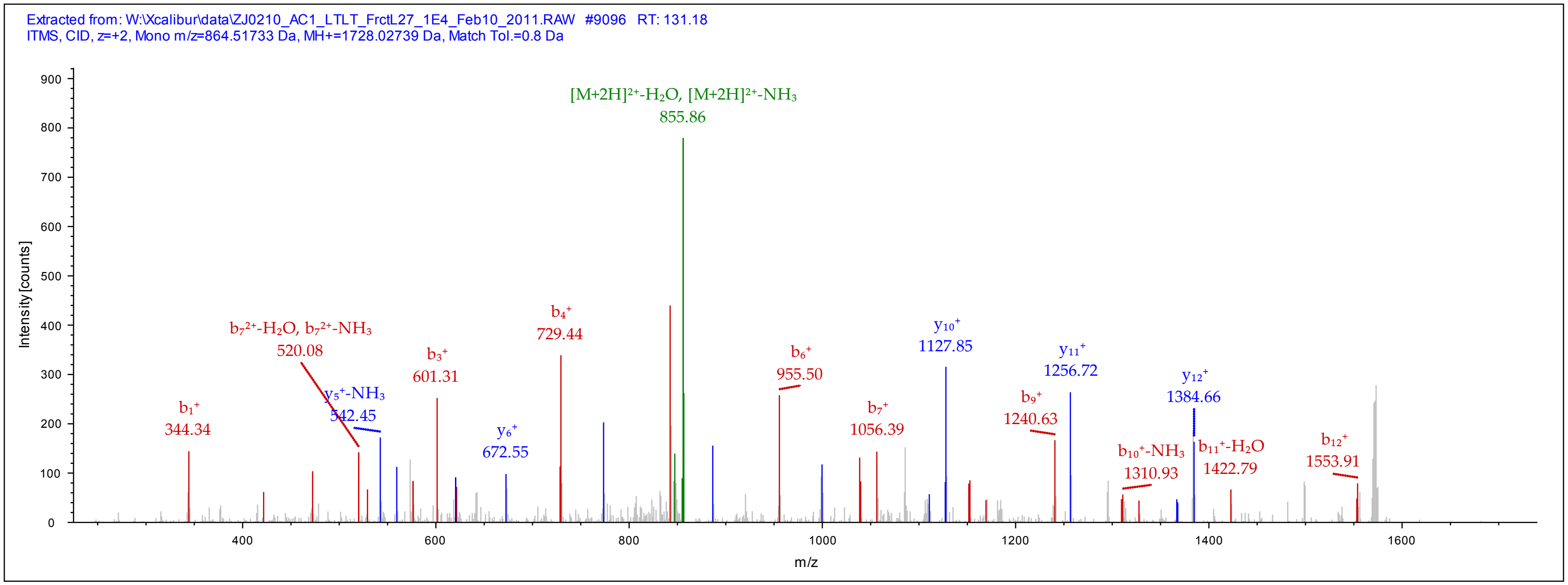
Identified with: Mascot (v1.16); IonScore:53, Exp Value:4.0E-004, Ions matched by search engine: 11/134

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 2 of Heme-binding protein 2 lng=184
- HEBP2 protein (Fragment)



IPI:IPI00008044.1

Sequence: SLLVLSLFR, S1-TMT6plex (229.16293 Da), S6-Phospho (79.96633 Da)

Charge: +3, Monoisotopic m/z: 452.94202 Da (+8.71 mmu/+19.23 ppm), MH+: 1356.81150 Da, RT: 91.49 min,

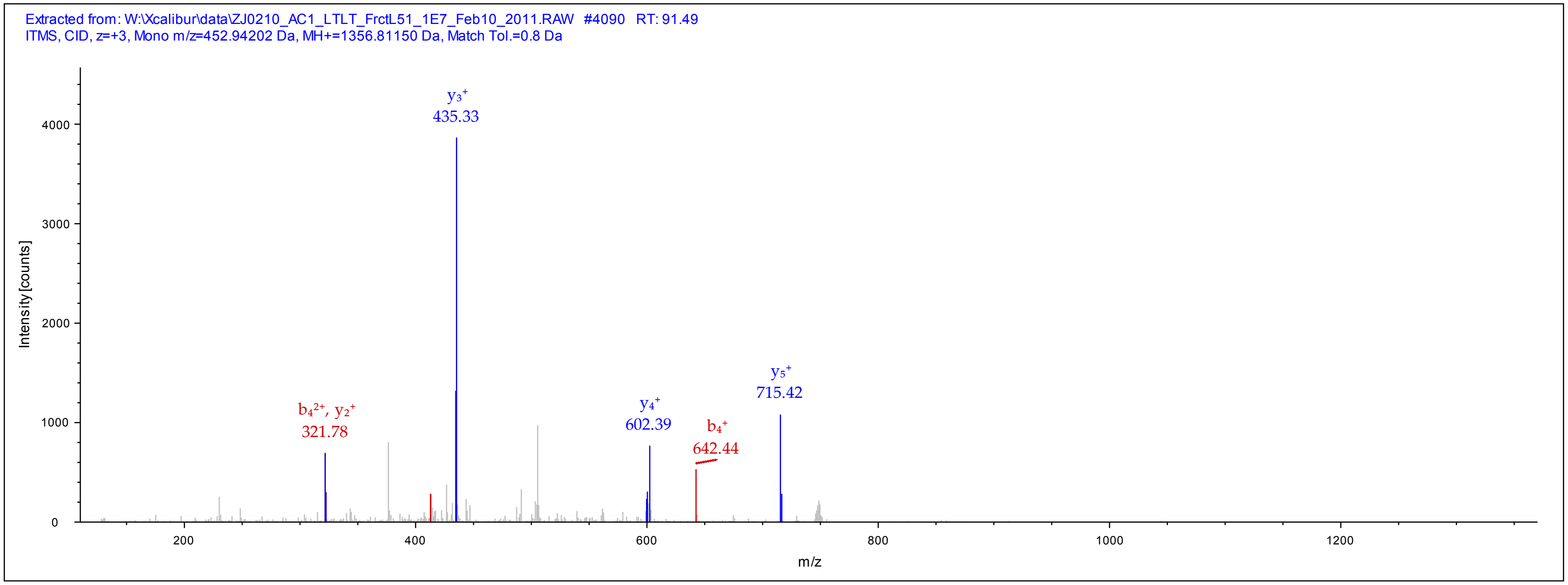
Identified with: Mascot (v1.16); IonScore:30, Exp Value:9.1E-002, Ions matched by search engine: 5/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- PRO3077



IPI:IPI00011643.1

Sequence: AWAGIDLK, A1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 666.40790 Da (-0.14 mmu/-0.21 ppm),   MH+: 1331.80852 Da,   RT: 104.36 min,

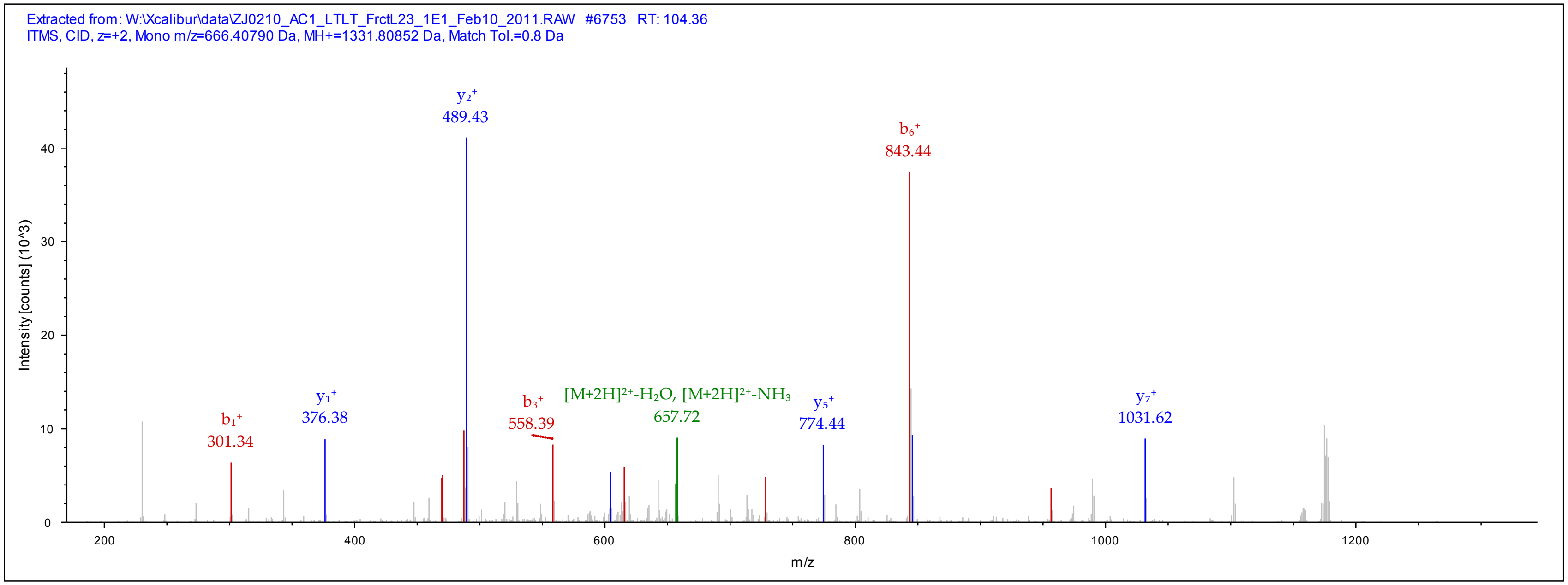
Identified with: Mascot (v1.16); IonScore:33, Exp Value:3.6E-002, Ions matched by search engine: 7/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Kunitz-type protease inhibitor 1
- Isoform 2 of Kunitz-type protease inhibitor 1



IPI:IPI00022830.3

Sequence: FYAGGSER, F1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 558.28784 Da (+0.04 mmu/+0.08 ppm), MH+: 1115.56841 Da, RT: 73.91 min,

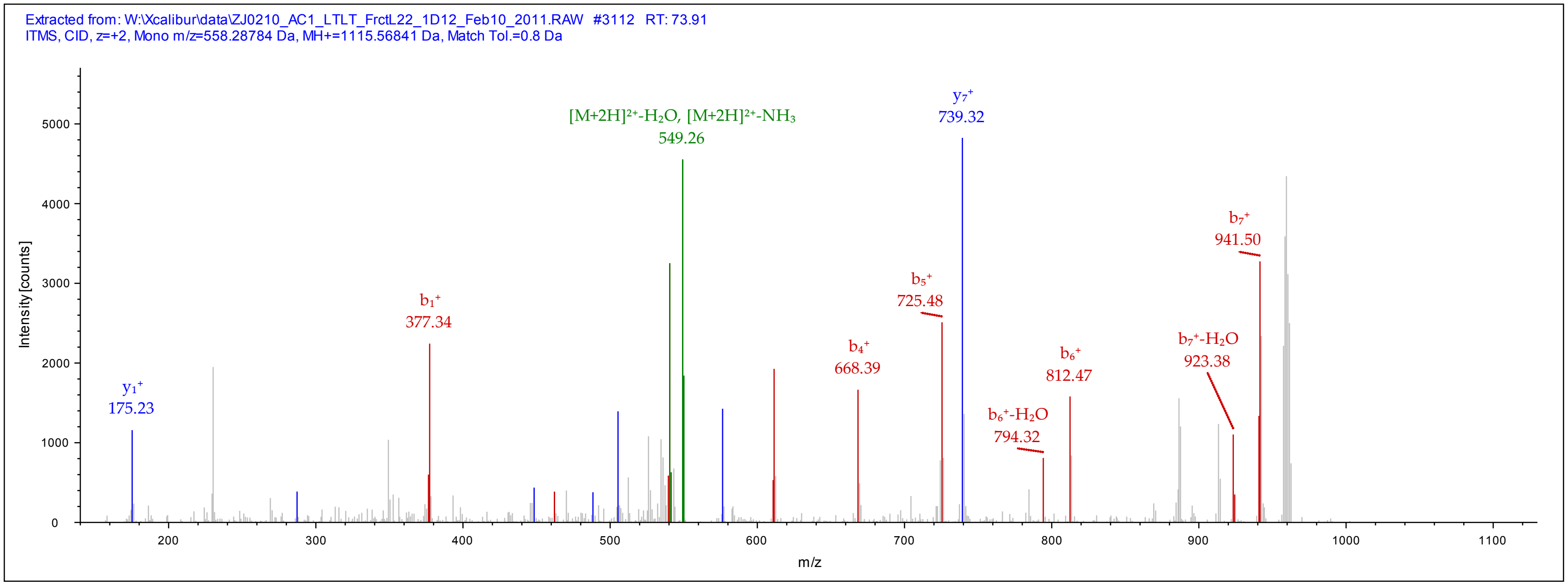
Identified with: Mascot (v1.16); IonScore:43, Exp Value:2.8E-003, Ions matched by search engine: 7/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of NSFL1 cofactor p47
- Isoform 2 of NSFL1 cofactor p47
- Isoform 3 of NSFL1 cofactor p47 lng=372



IPI00023780.3

Sequence: EINNAHAILTDATK, E1-TMT6plex (229.16293 Da), K14-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 657.04291 Da (+0.75 mmu/+1.14 ppm), MH+: 1969.11417 Da, RT: 96.13 min,

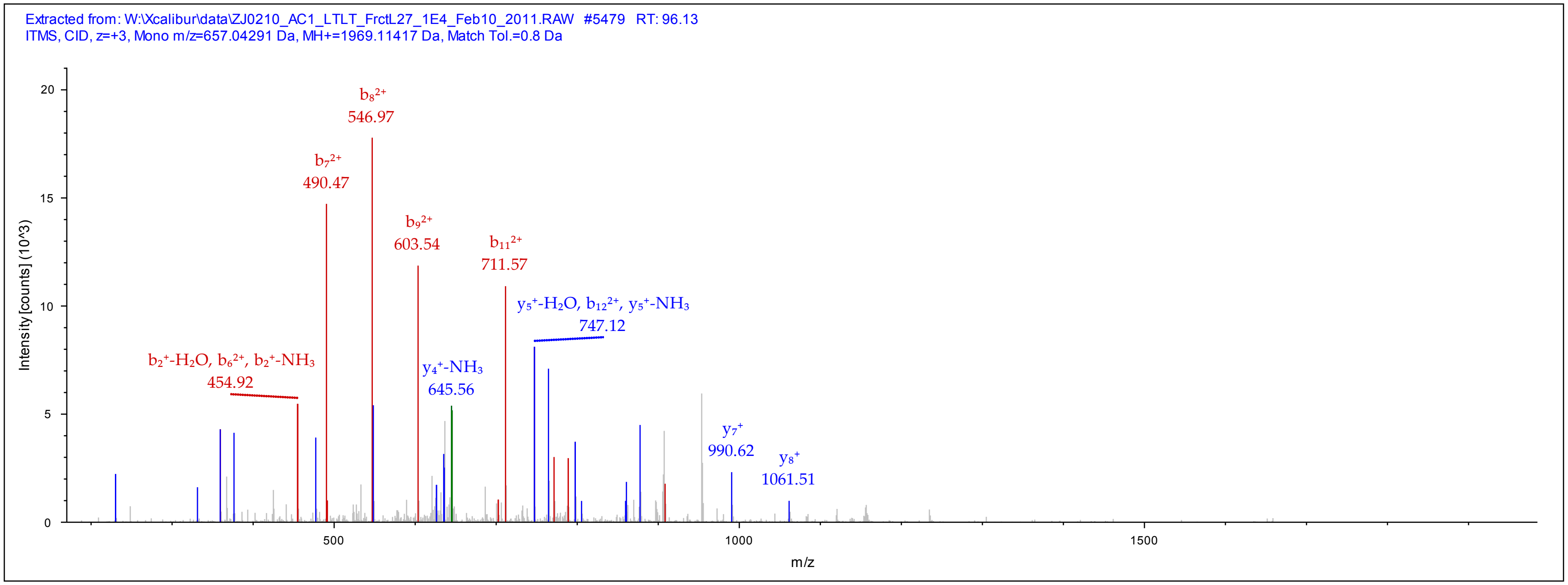
Identified with: Mascot (v1.16); IonScore:32, Exp Value:7.3E-002, Ions matched by search engine: 7/150

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of DnaJ homolog subfamily C member 5 lng=198
- Isoform 2 of DnaJ homolog subfamily C member 5 lng=167



IPI:IPI00735679.2

Sequence: YVFLDPLAGAVTK, Y1-TMT6plex (229.16293 Da), K13-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 926.55322 Da (+0.33 mmu/+0.36 ppm),   MH+: 1852.09917 Da,   RT: 131.17 min,

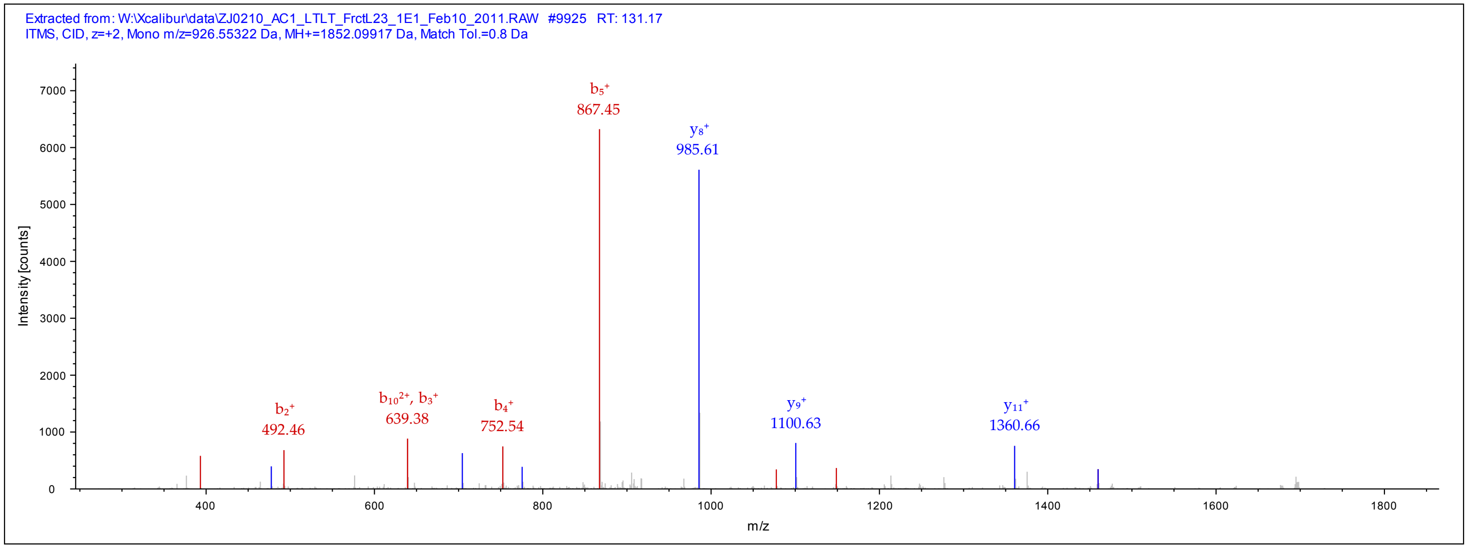
Identified with: Mascot (v1.16); IonScore:61, Exp Value:5.3E-005, Ions matched by search engine: 18/110

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (14):

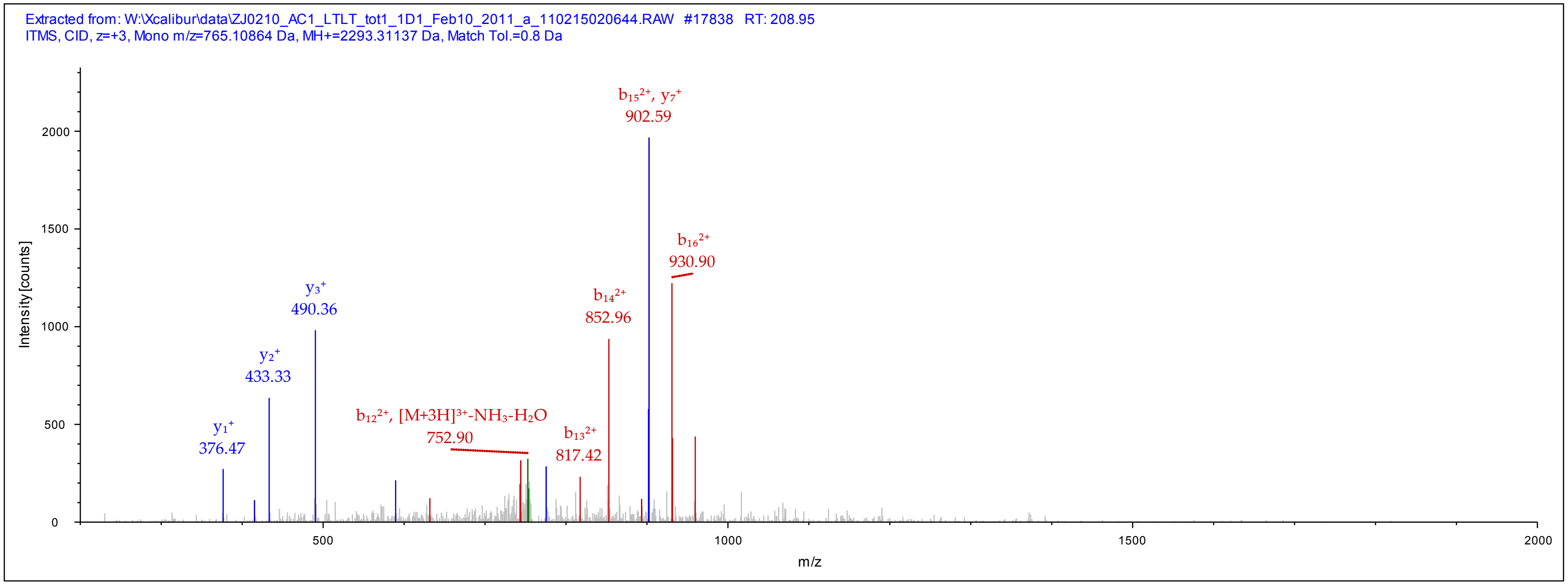
- Putative WAS protein family homolog 4
- Protein FAM39A
- FLJ00075 protein (Fragment)
- 39 kDa protein
- Actin nucleation promoting factor
- Uncharacterized protein
- WAS protein family homolog 6



IPI:IPI00031107.1
Sequence: LLGTIYTAAEEIEAVGGK
L1-TMT6plex (229.16293 Da), K18-TMT6plex (229.16293 Da)
Charge: +3,   Monoisotopic m/z: 765.10864 Da (+1.92 mmu/+2.51 ppm),   MH+: 2293.31137 Da,   RT: 208.95 min,

Identified with: Mascot (v1.16); IonScore:30, Exp Value:9.8E-002, Matched Ions: 18/154
Fragment Match Tolerance: 0.8 Da

Protein References (2):
- Isoform 1 of Hydroxysteroid dehydrogenase-like protein 2
- Isoform 2 of Hydroxysteroid dehydrogenase-like protein 2



IPI00056315.3

Sequence: LGELLK, L1-TMT6plex (229.16293 Da), K6-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 565.88177 Da (+0.66 mmu/+1.17 ppm), MH+: 1130.75627 Da, RT: 98.65 min,

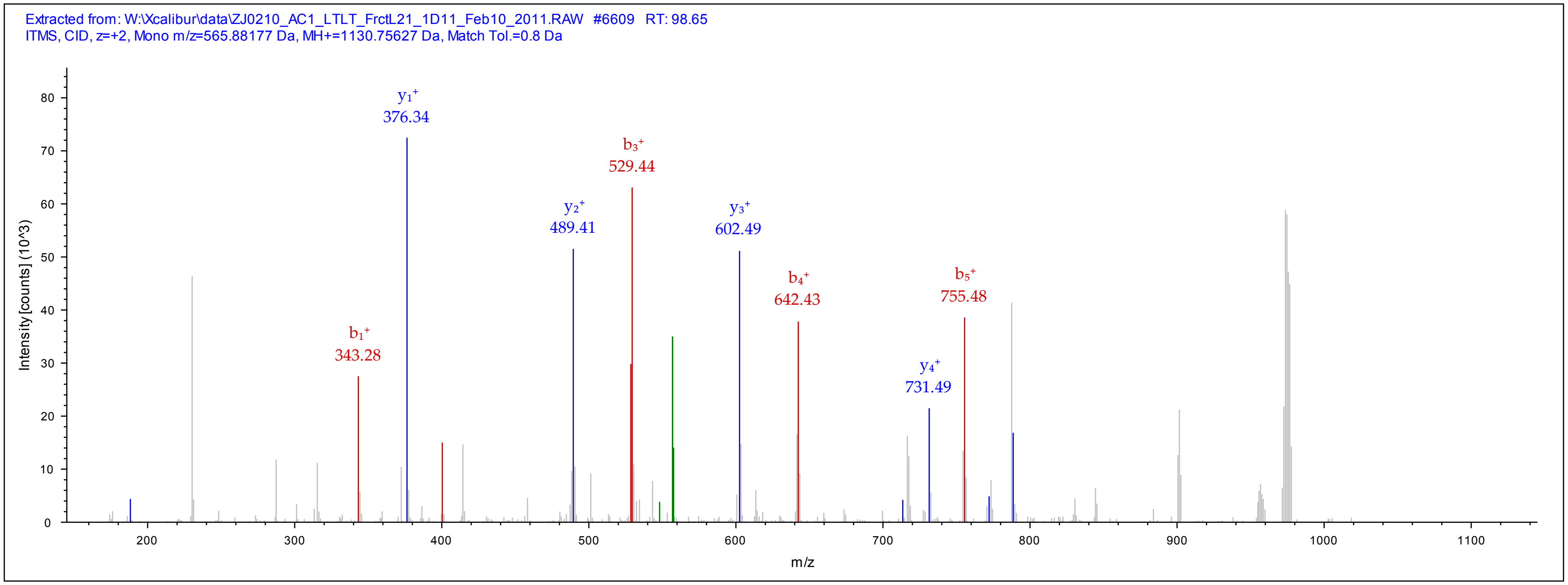
Identified with: Mascot (v1.16); IonScore:30, Exp Value:5.2E-002, Ions matched by search engine: 10/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Protein FAM195A
- Isoform 2 of Protein FAM195A lng=75



IPI:IPI00100559.1

Sequence: ELMQVVLAR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 644.38660 Da (+0.12 mmu/+0.19 ppm),   MH+: 1287.76592 Da,   RT: 107.08 min,

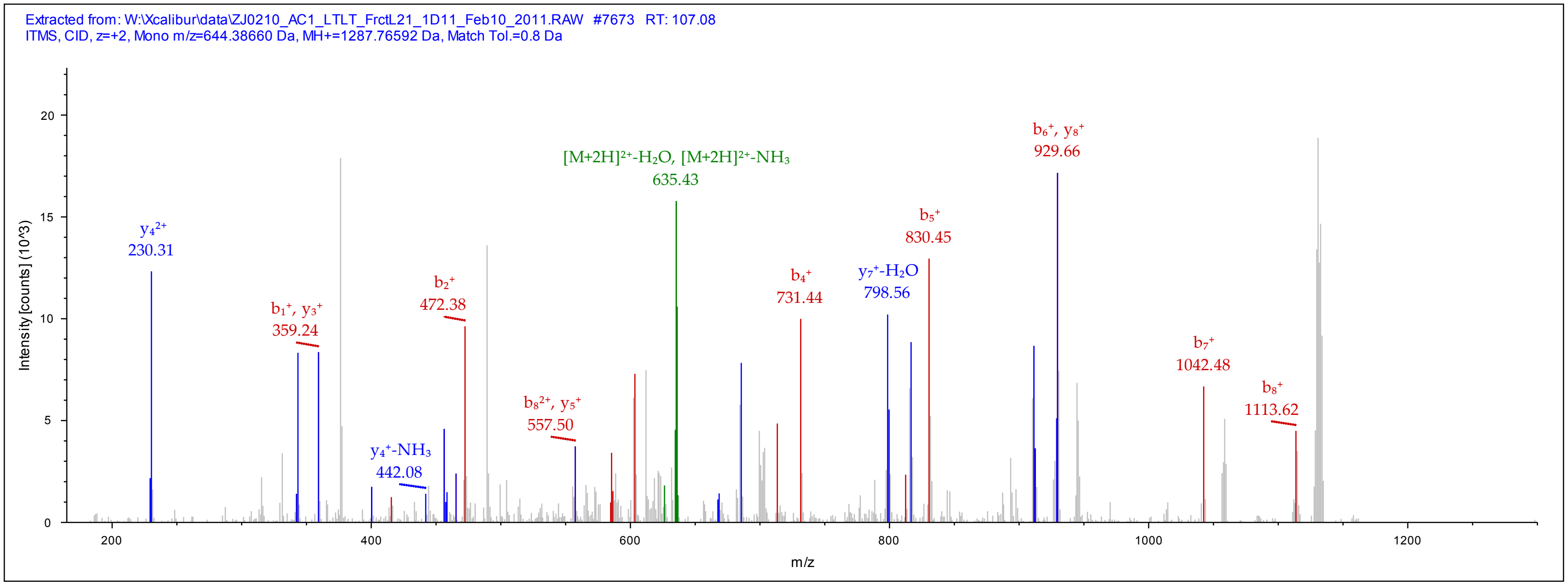
Identified with: Mascot (v1.16); IonScore:33, Exp Value:3.7E-002, Ions matched by search engine: 6/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of AP-1 complex subunit sigma-1A lng=158
- Isoform 2 of AP-1 complex subunit sigma-1A
- Putative uncharacterized protein AP1S1 lng=191



IPI:IPI00150057.6

Sequence: EVVESEGER, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 631.83014 Da (+5.19 mmu/+8.21 ppm),   MH+: 1262.65300 Da,   RT: 65.87 min,

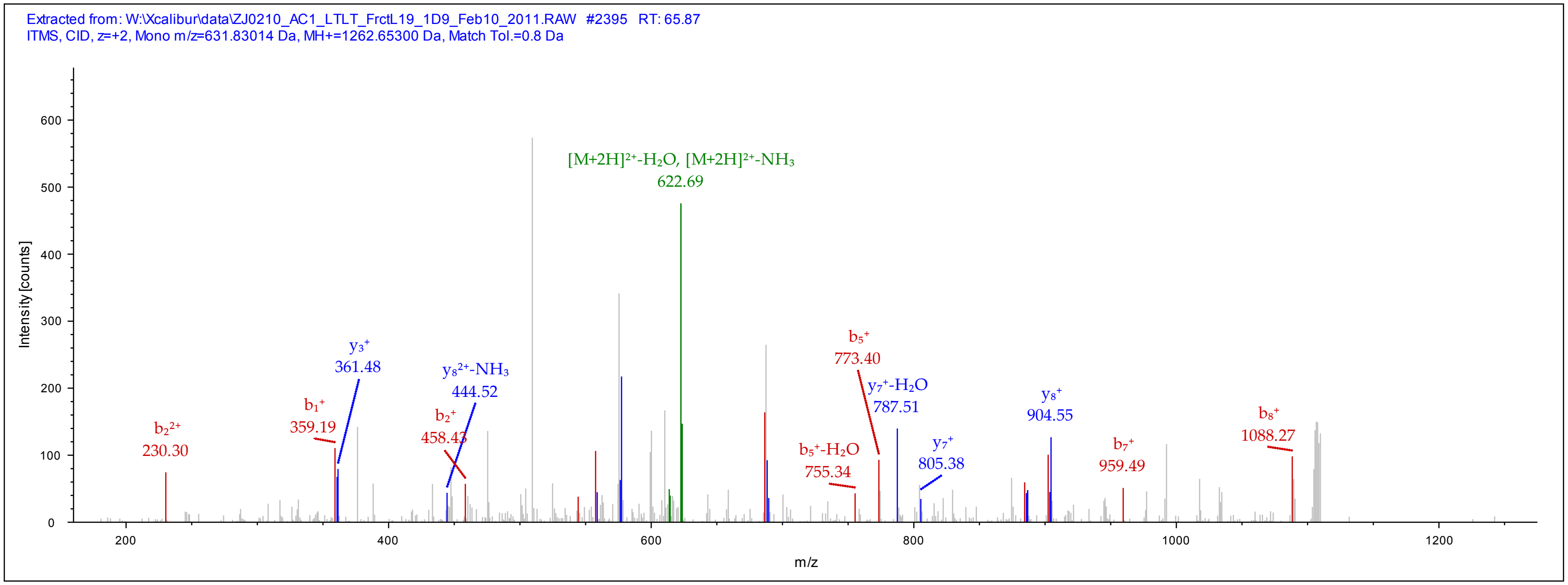
Identified with: Mascot (v1.16); IonScore:33, Exp Value:4.0E-002, Ions matched by search engine: 8/78

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of SWI/SNF complex subunit SMARCC2
- Isoform 2 of SWI/SNF complex subunit SMARCC2



IPI:IPI00939491.1

Sequence: VPEILQLSDALR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 791.97260 Da (+0.64 mmu/+0.8 ppm), MH+: 1582.93791 Da, RT: 129.10 min,

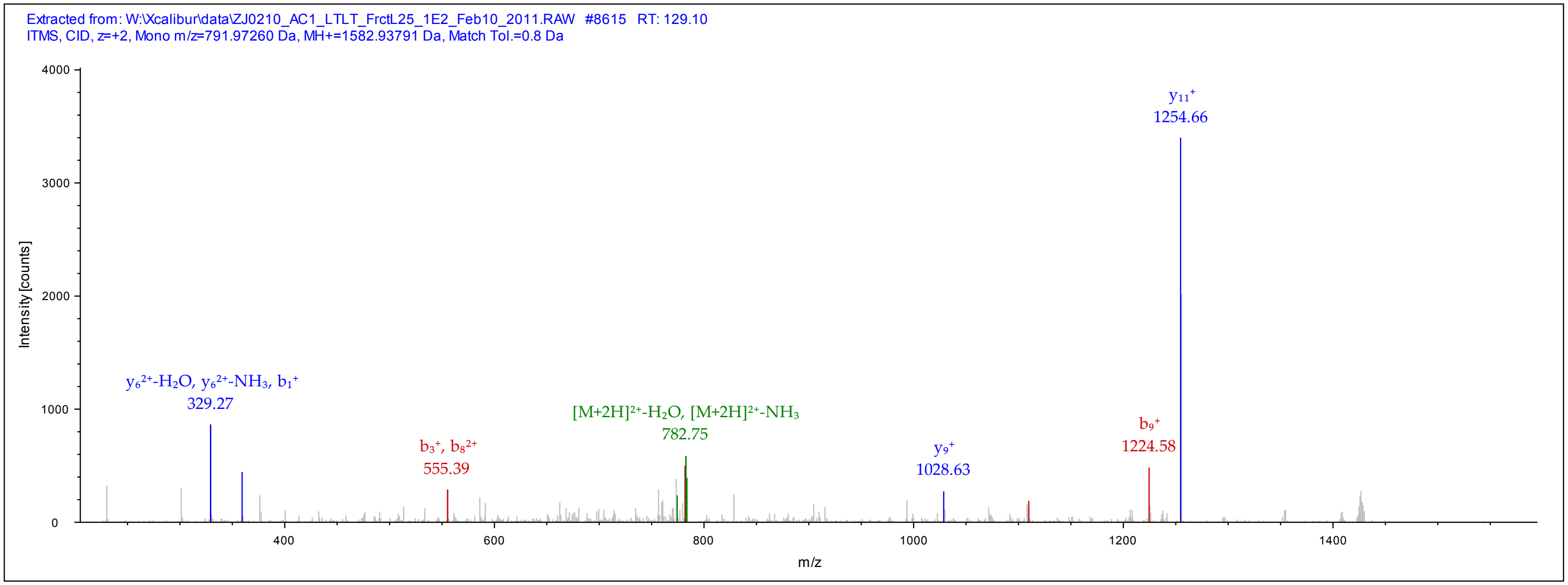
Identified with: Mascot (v1.16); IonScore:32, Exp Value:4.8E-002, Ions matched by search engine: 9/112

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of Cysteinyl-tRNA synthetase, cytoplasmic
- cysteinyl-tRNA synthetase, cytoplasmic isoform c
- Isoform 2 of Cysteinyl-tRNA synthetase, cytoplasmic
- cDNA FLJ38994 fis, clone NT2RI2009259, highly similar to Cysteinyl-tRNA synthetase
- cDNA FLJ59563, highly similar to Cysteinyl-tRNA synthetase lng=739



IPI:IPI00167490.1

Sequence: GPVYIGELPQDFLR, G1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 917.00916 Da (+0.08 mmu/+0.09 ppm), MH+: 1833.01103 Da, RT: 125.51 min,

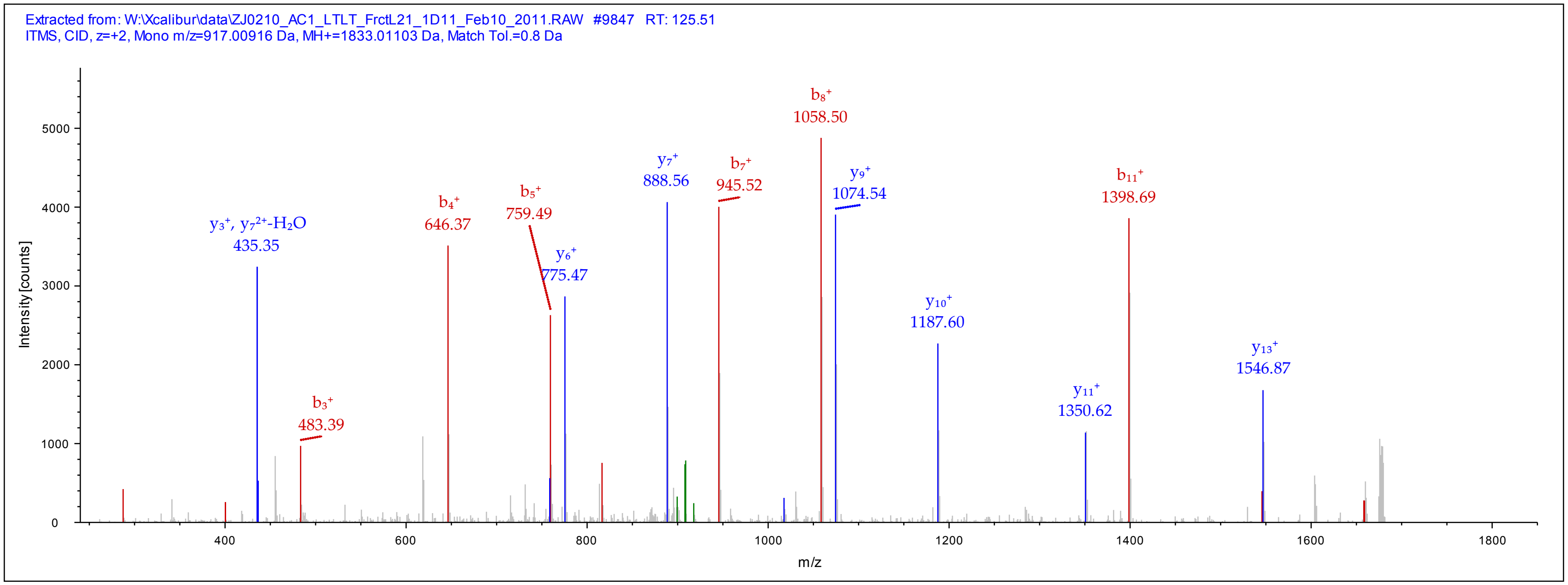
Identified with: Mascot (v1.16); IonScore:52, Exp Value:7.8E-004, Ions matched by search engine: 11/120

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Toll-interacting protein
- cDNA FLJ39374 fis, clone PEBLM2008576, highly similar to Homo sapiens TOLLIP protein
- Toll interacting protein variant (Fragment)



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL21_1D11_Feb10_2011.RAW #9847 RT: 125.51
ITMS, CID, z=+2, Mono m/z=917.00916 Da, MH+=1833.01103 Da, Match Tol.=0.8 Da

IPI:IPI00169168.1

Sequence: STFVLSNLAEVVER, S1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 897.00824 Da (+4.25 mmu/+4.74 ppm),   MH+: 1793.00920 Da,   RT: 129.68 min,

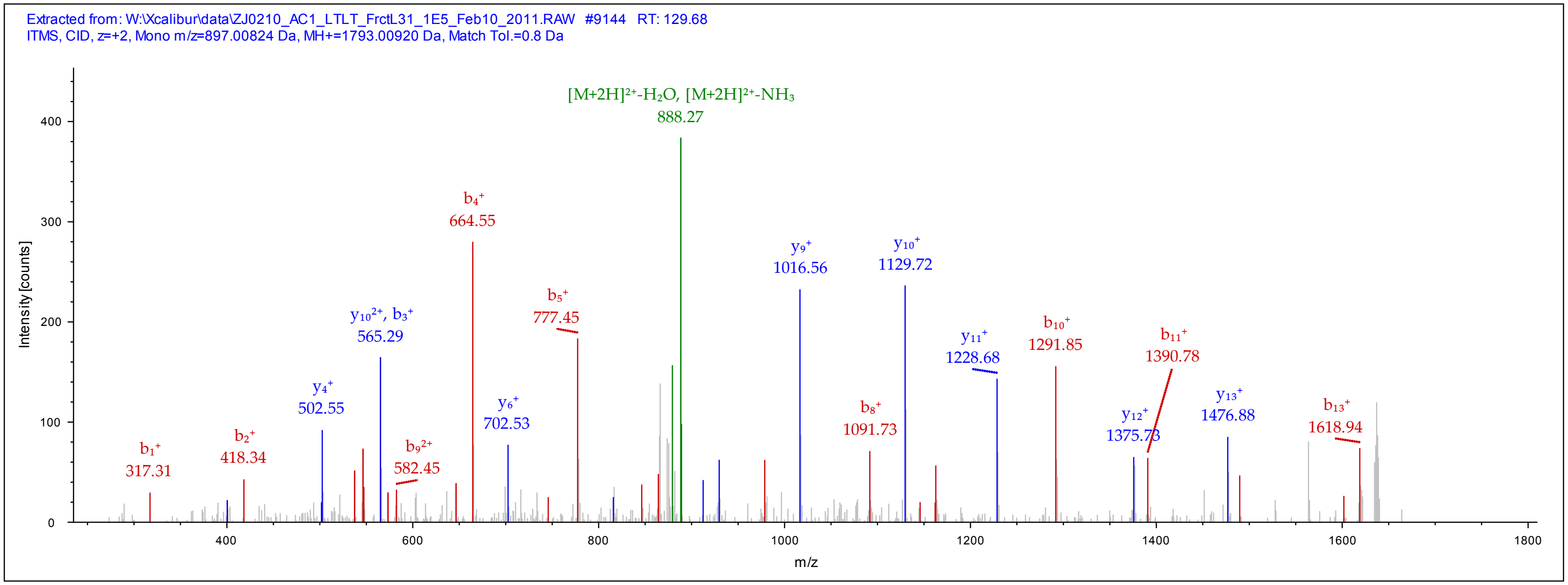
Identified with: Mascot (v1.16); IonScore:70, Exp Value:1.1E-005, Ions matched by search engine: 13/142

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of F-box only protein 22
- Isoform 3 of F-box only protein 22



IPI00903237.1

Sequence: SLSTAPVVQPLSIQDLVR, S1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 1076.63306 Da (+2.43 mmu/+2.26 ppm), MH+: 2152.25884 Da, RT: 125.79 min,

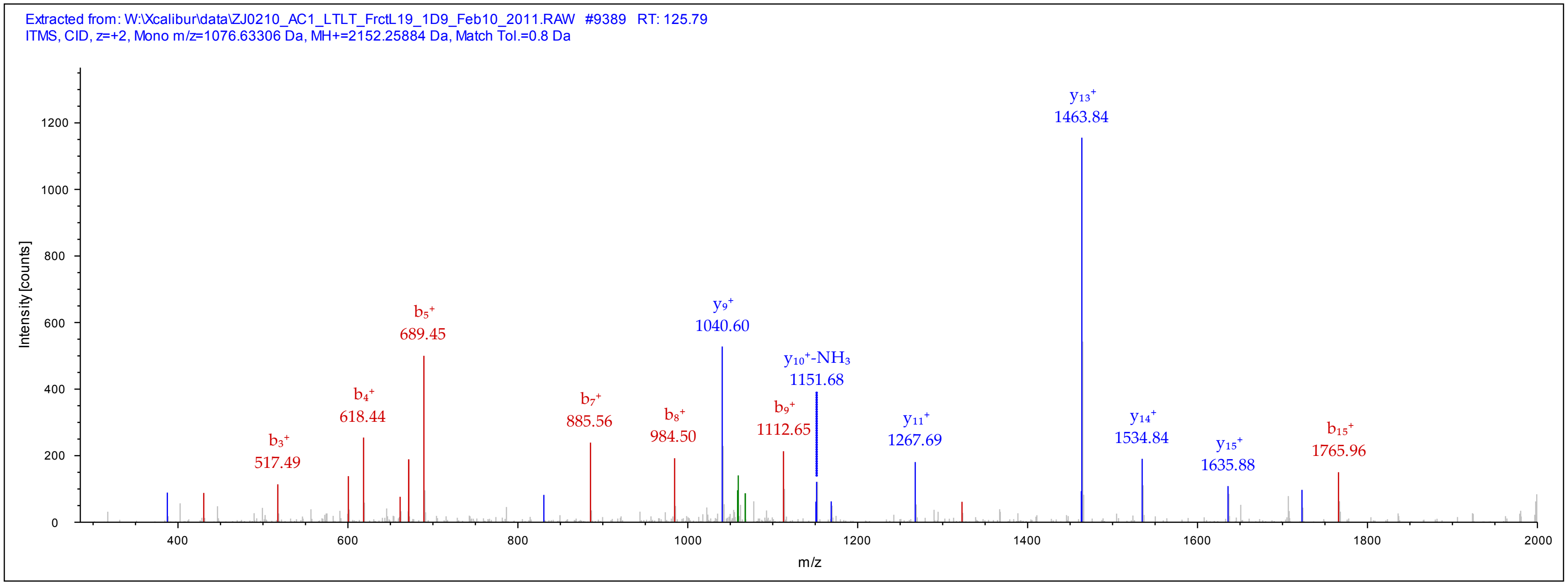
Identified with: Mascot (v1.16); IonScore:85, Exp Value:2.3E-007, Ions matched by search engine: 22/182

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Brefeldin A-inhibited guanine nucleotide-exchange protein 3
- Putative uncharacterized protein KIAA1244 lng=2106



IPI00181006.4

Sequence: LNPLVLLLDAALTGELEVVQQAVK, L1-TMT6plex (229.16293 Da), K24-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 1002.27698 Da (+3.34 mmu/+3.33 ppm), MH+: 3004.81638 Da, RT: 275.19 min,

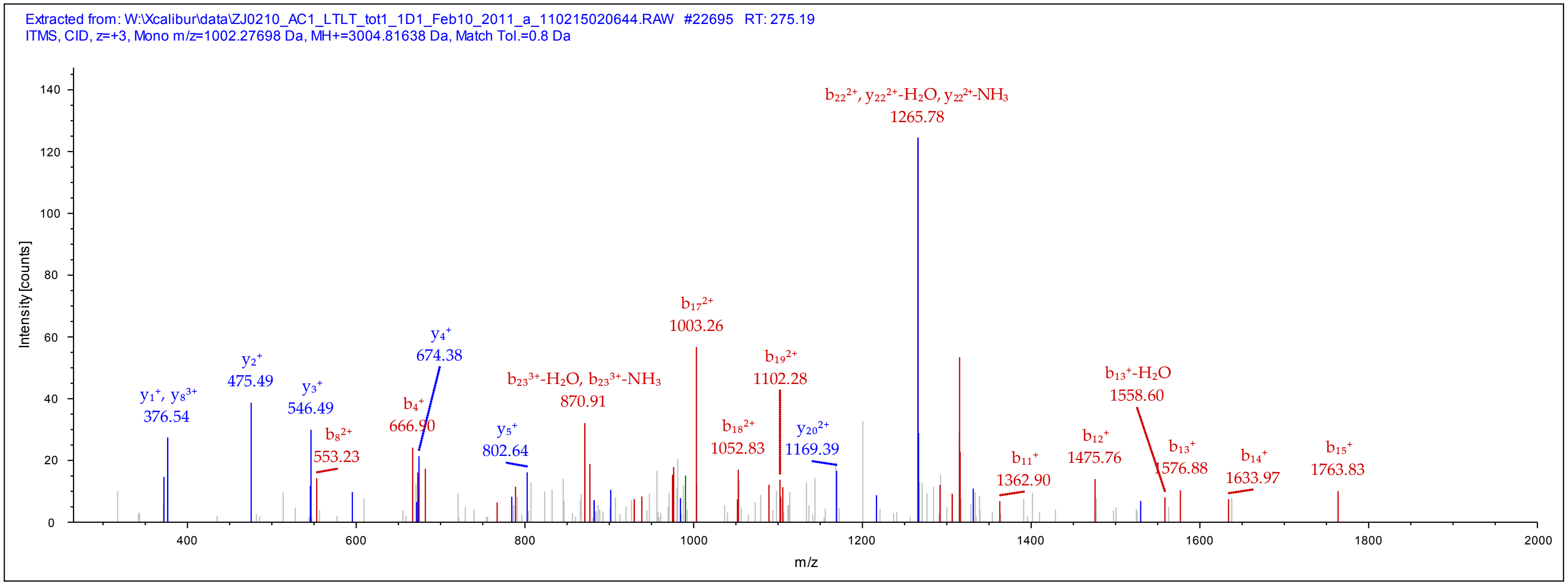
Identified with: Mascot (v1.16); IonScore:33, Exp Value:9.5E-003, Ions matched by search engine: 17/244

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of RelA-associated inhibitor
- Protein phosphatase 1, regulatory (Inhibitor) subunit 13 like, isoform CRA_b lng=407



IPI:IPI00215980.1

Sequence: VQVLPEVR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 584.86694 Da (+0.72 mmu/+1.23 ppm), MH+: 1168.72661 Da, RT: 89.41 min,

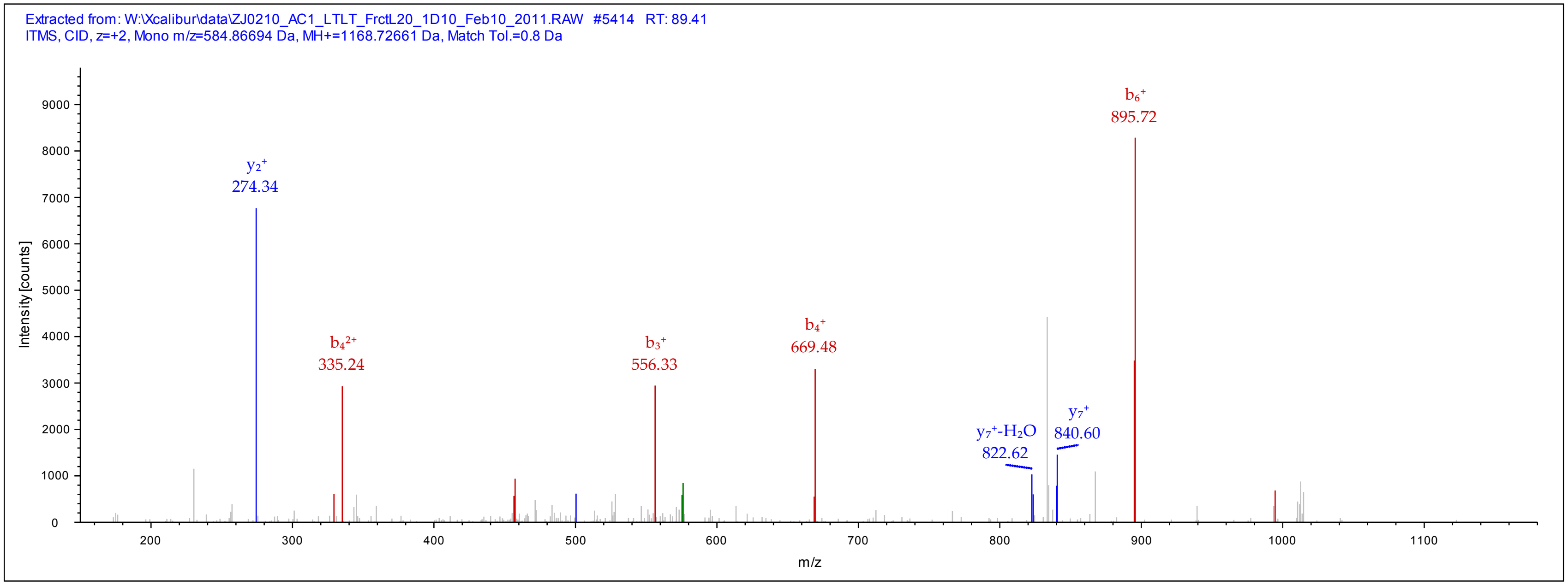
Identified with: Mascot (v1.16); IonScore:45, Exp Value:1.8E-003, Ions matched by search engine: 7/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform Delta of Poliovirus receptor-related protein 2
- Isoform Alpha of Poliovirus receptor-related protein 2



IPI:IPI00215995.1

Sequence: SETVLTCATGR, S1-TMT6plex (229.16293 Da), C7-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 712.37445 Da (+0.16 mmu/+0.23 ppm),   MH+: 1423.74162 Da,   RT: 79.88 min,

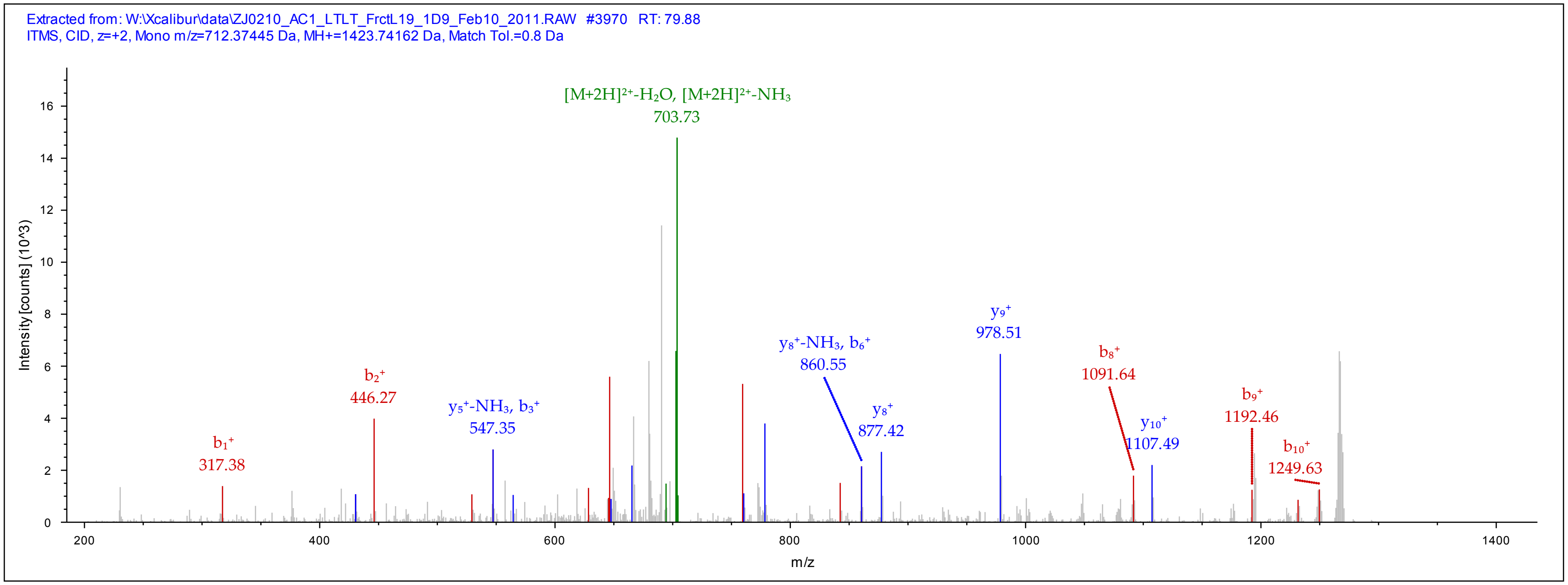
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.3E-002, Ions matched by search engine: 10/96

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform Alpha-3A of Integrin alpha-3
- Isoform Alpha-3B of Integrin alpha-3



IPI:IPI00216695.1

Sequence: FSDFLLDPYK, F1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 851.97876 Da (+2.29 mmu/+2.68 ppm),   MH+: 1702.95024 Da,   RT: 131.11 min,

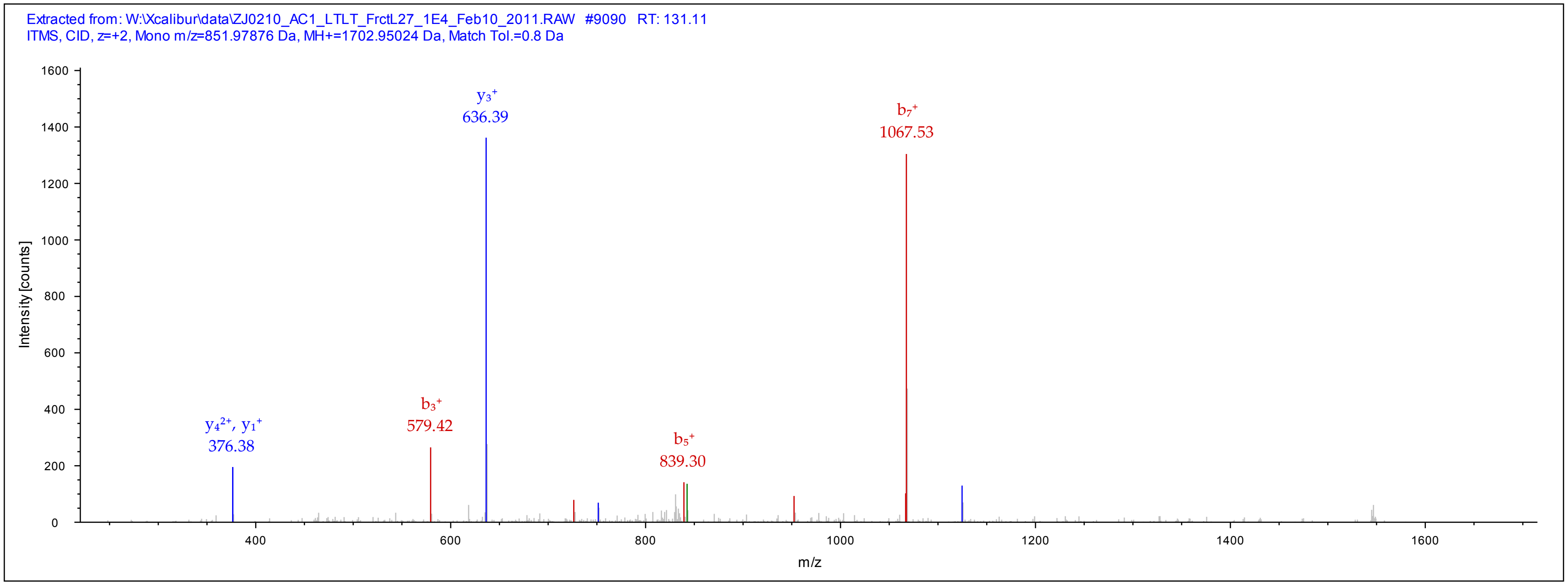
Identified with: Mascot (v1.16); IonScore:32, Exp Value:7.0E-002, Ions matched by search engine: 8/82

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Tyrosine-protein kinase BAZ1B
- Isoform 2 of Tyrosine-protein kinase BAZ1B



IPI:IPI00218435.1

Sequence: ALGEPITLFGEGPAER, A1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 943.51727 Da (+2.54 mmu/+2.69 ppm),   MH+: 1886.02727 Da,   RT: 118.96 min,

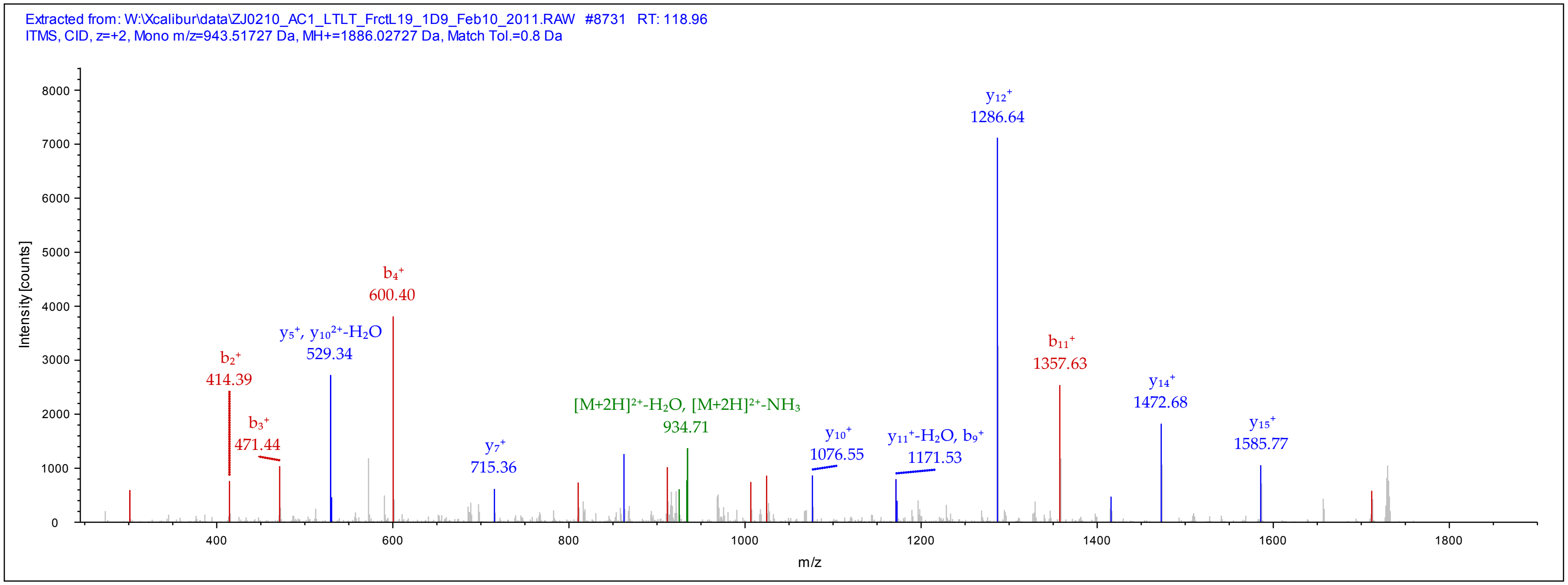
Identified with: Mascot (v1.16); IonScore:83, Exp Value:6.4E-007, Ions matched by search engine: 14/142

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of U4/U6 small nuclear ribonucleoprotein Prp4
- Isoform 2 of U4/U6 small nuclear ribonucleoprotein Prp4



IPI00220844.1

Sequence: DLPPILLVR, D1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 632.91400 Da (+0.82 mmu/+1.3 ppm), MH+: 1264.82073 Da, RT: 119.40 min,

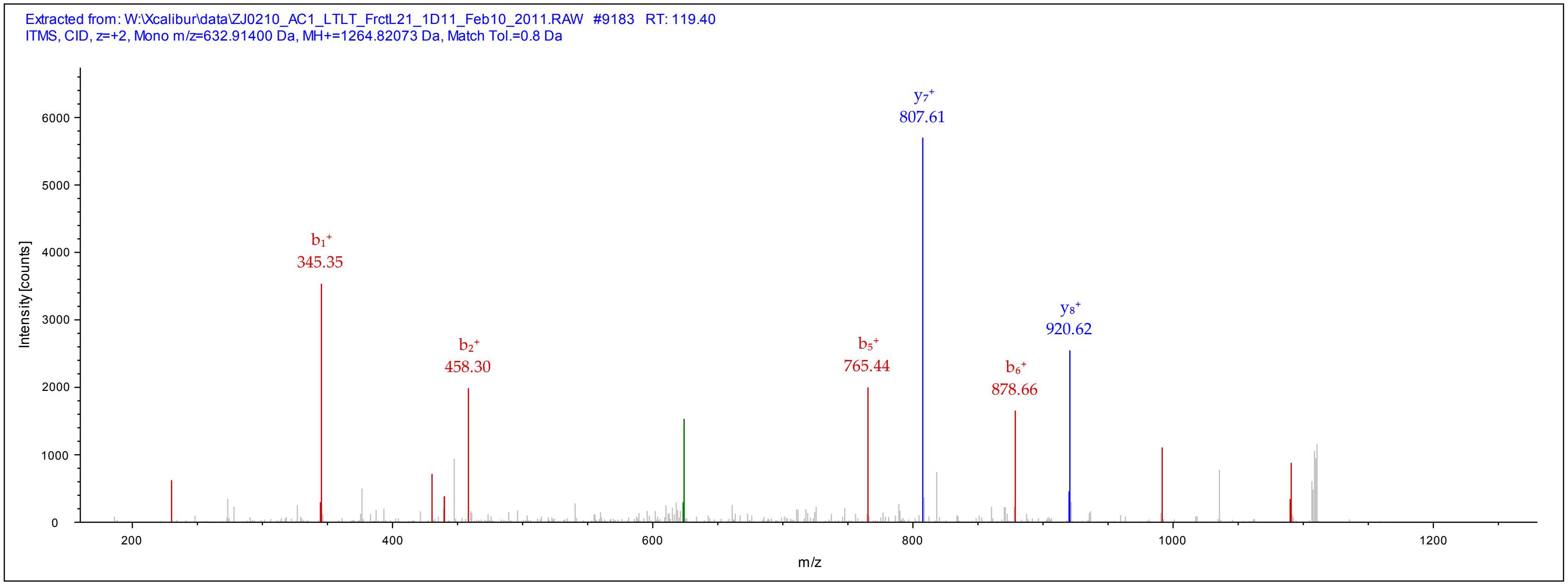
Identified with: Mascot (v1.16); IonScore:34, Exp Value:1.0E-002, Ions matched by search engine: 11/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Solute carrier family 12 member 2
- Isoform 2 of Solute carrier family 12 member 2 lng=1196



IPI:IPI00220887.1

Sequence: NALDLLLPK, N1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 727.97095 Da (-0.05 mmu/-0.07 ppm),   MH+: 1454.93462 Da,   RT: 123.93 min,

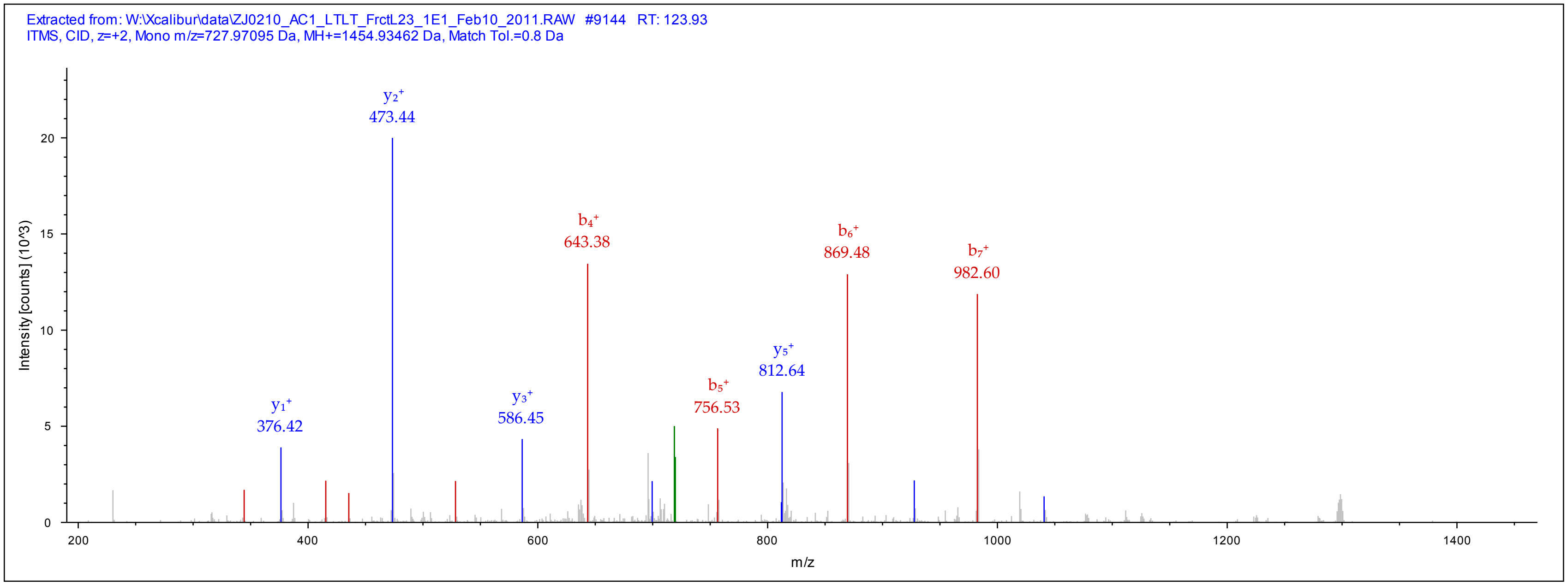
Identified with: Mascot (v1.16); IonScore:35, Exp Value:7.8E-003, Ions matched by search engine: 12/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Adenylosuccinate lyase
- Isoform 2 of Adenylosuccinate lyase
- Trinucleotide repeat containing 6B lng=745



IPI00297991.2

Sequence: LLDDLFR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 560.83344 Da (+1.59 mmu/+2.83 ppm),   MH+: 1120.65959 Da,   RT: 128.29 min,

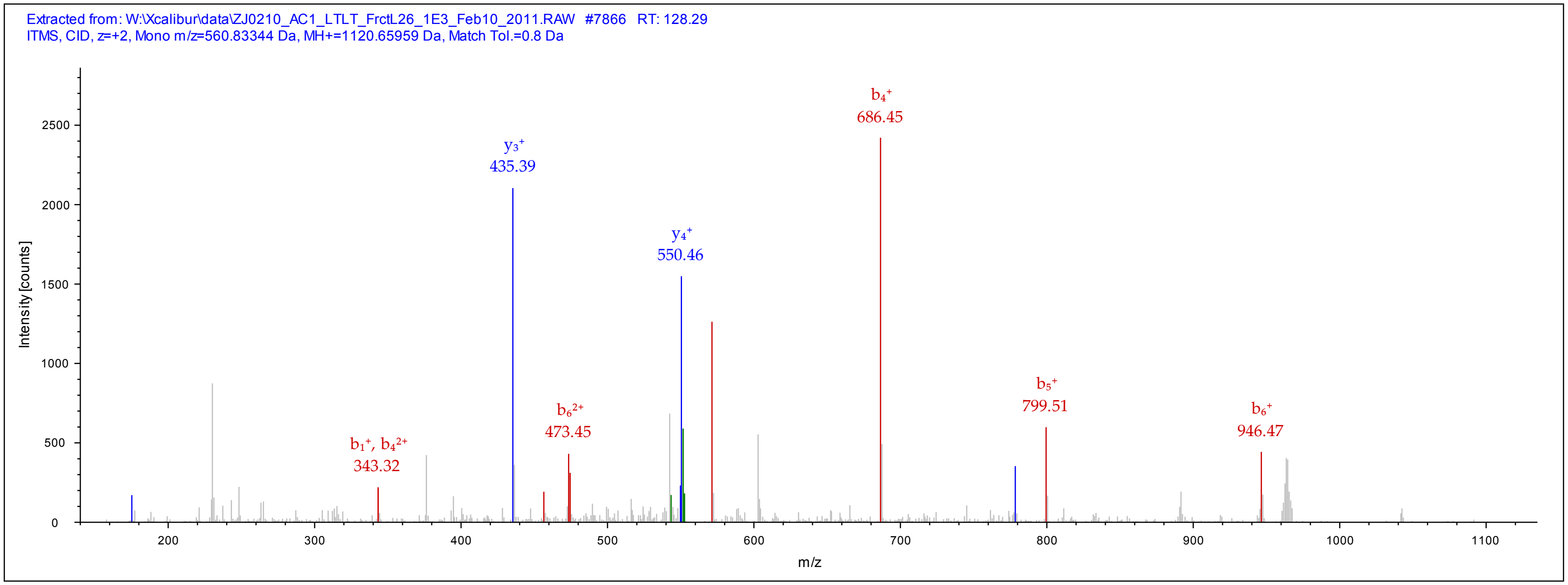
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.3E-002, Ions matched by search engine: 5/50

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 2 of Apoptotic chromatin condensation inducer in the nucleus lng=614
- Isoform 3 of Apoptotic chromatin condensation inducer in the nucleus lng=583
- apoptotic chromatin condensation inducer 1 isoform 3 lng=1301
- apoptotic chromatin condensation inducer 1 isoform 2 lng=1328
- Isoform 1 of Apoptotic chromatin condensation inducer in the nucleus



IPI:IPI00301252.2

Sequence: AVPLAVPLGQTEVFQALQR, A1-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 756.10925 Da (+0.34 mmu/+0.46 ppm),   MH+: 2266.31321 Da,   RT: 131.79 min,

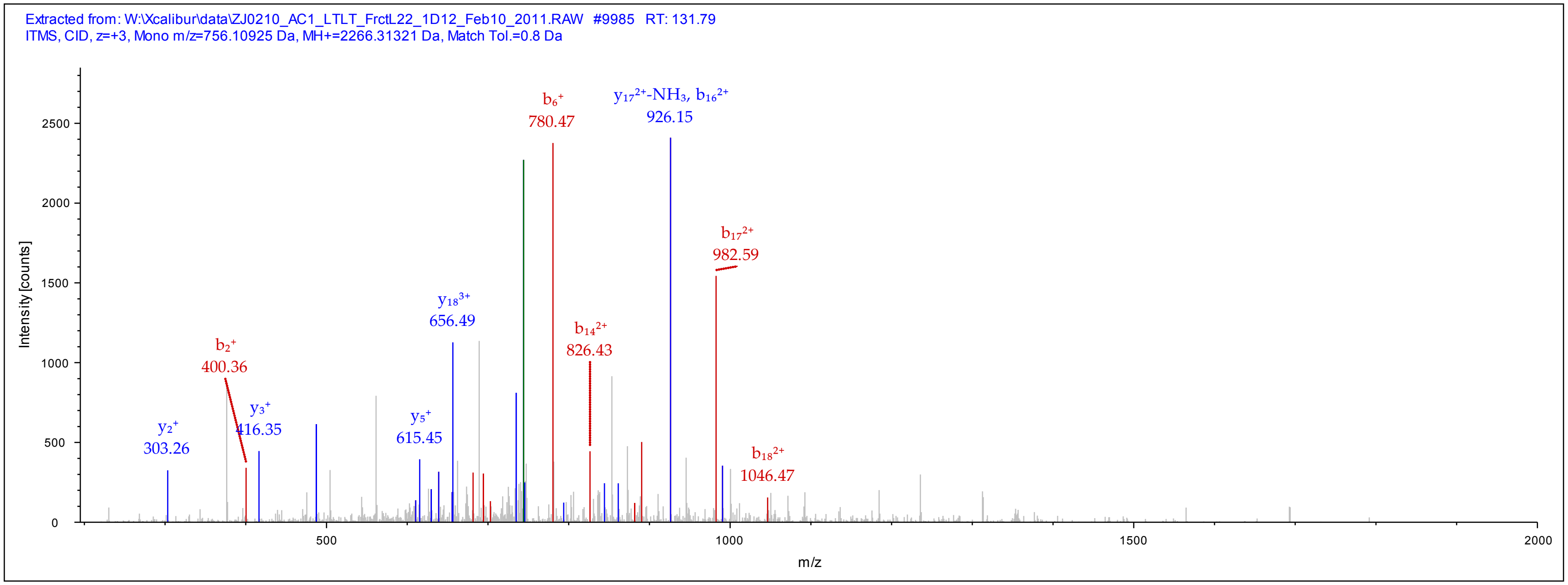
Identified with: Mascot (v1.16); IonScore:33, Exp Value:3.9E-002, Ions matched by search engine: 22/164

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of THO complex subunit 6 homolog
- Isoform 3 of THO complex subunit 6 homolog



IPI:IPI00303753.6

Sequence: LVDYLEGIR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 653.88220 Da (+0.13 mmu/+0.2 ppm), MH+: 1306.75713 Da, RT: 119.18 min,

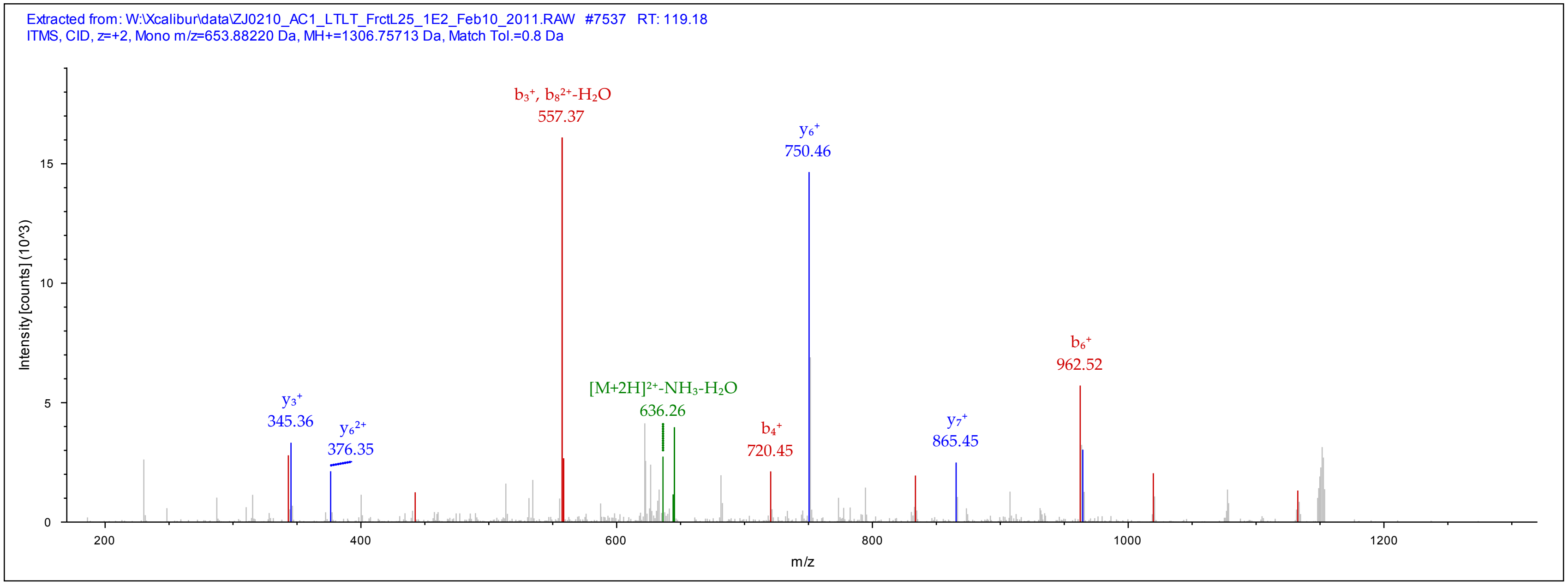
Identified with: Mascot (v1.16); IonScore:34, Exp Value:4.6E-002, Ions matched by search engine: 7/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Hcp beta-lactamase-like protein C1orf163



IPI:IPI00332453.1

Sequence: LQLVVLR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 535.36847 Da (+0.07 mmu/+0.13 ppm),   MH+: 1069.72966 Da,   RT: 109.57 min,

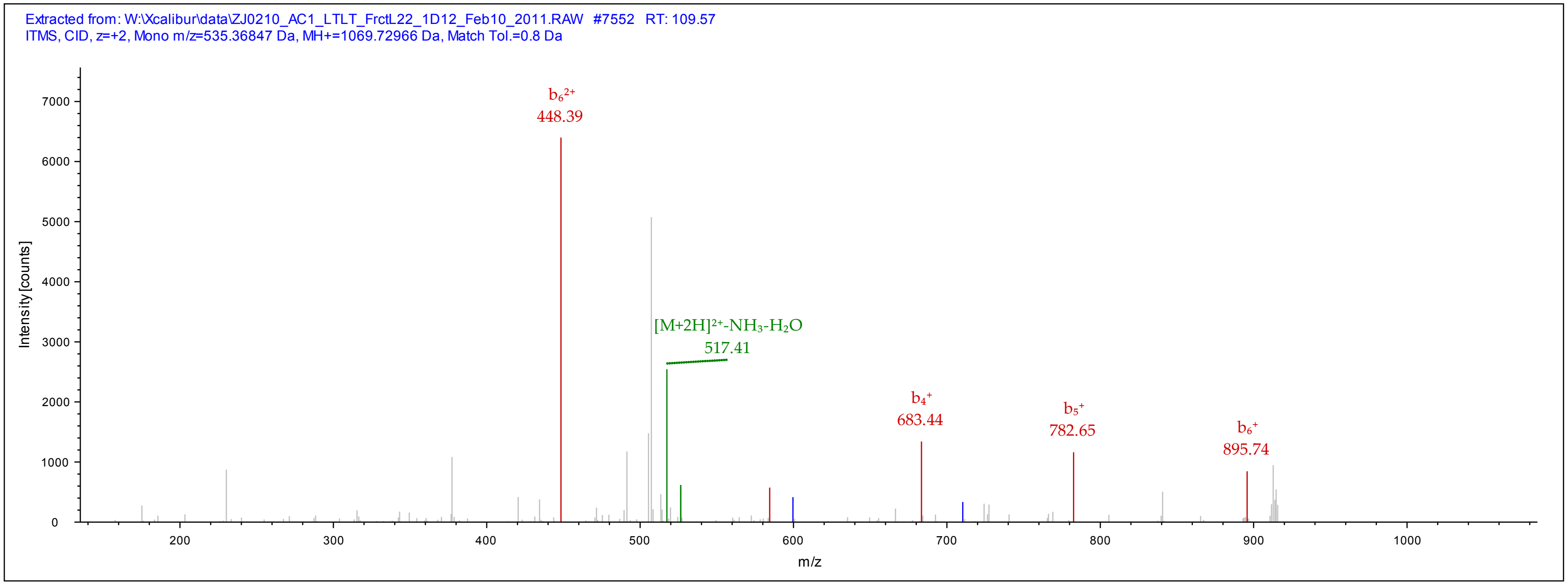
Identified with: Mascot (v1.16); IonScore:32, Exp Value:7.2E-003, Ions matched by search engine: 5/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (9):

- Isoform A1 of Tight junction protein ZO-2
- tight junction protein ZO-2 isoform 2
- Isoform A3 of Tight junction protein ZO-2
- Isoform C1 of Tight junction protein ZO-2 lng=1167



IPI:IPI00332936.1

Sequence: ASLEDAPVDDLTR, A1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 815.92950 Da (+1.56 mmu/+1.91 ppm),   MH+: 1630.85173 Da,   RT: 97.16 min,

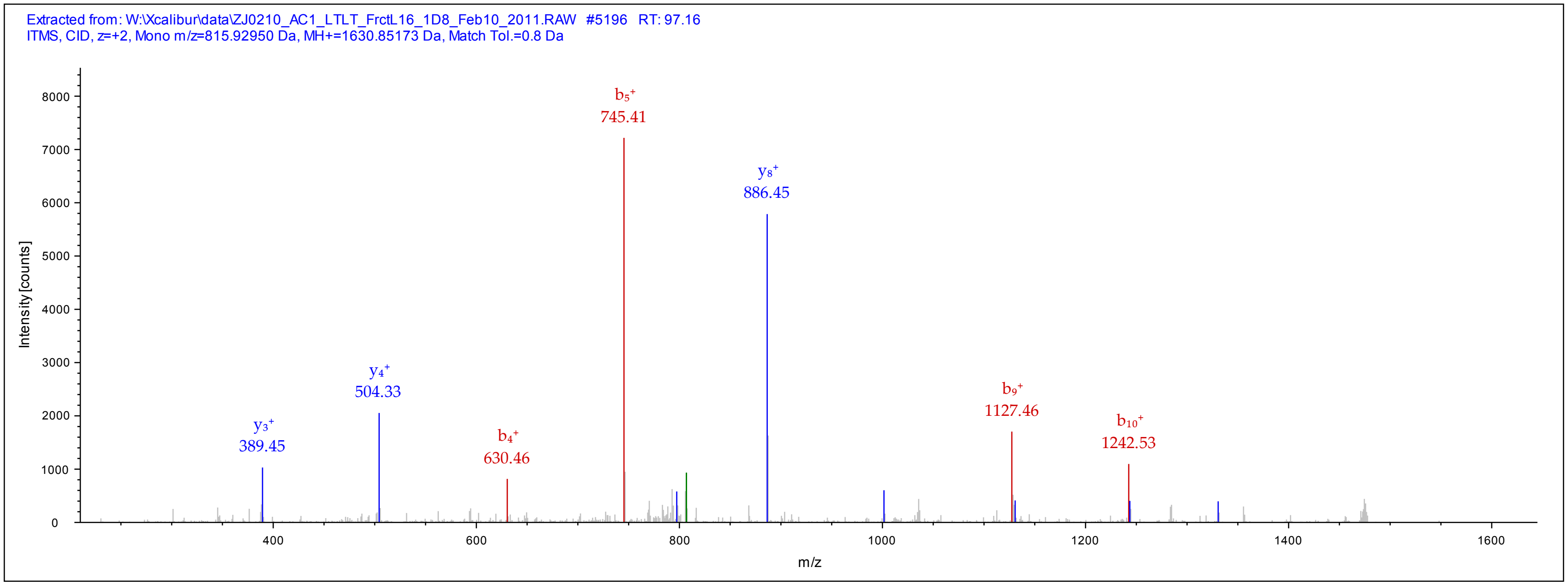
Identified with: Mascot (v1.16); IonScore:44, Exp Value:4.1E-003, Ions matched by search engine: 6/116

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 2 of Zinc finger CCCH-type antiviral protein 1
- Isoform 1 of Zinc finger CCCH-type antiviral protein 1
- Uncharacterized protein



IPI:IPI00333699.5

Sequence: TTVISAVGTIVK, T1-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 824.02740 Da (+0.9 mmu/+1.09 ppm),   MH+: 1647.04753 Da,   RT: 111.87 min,

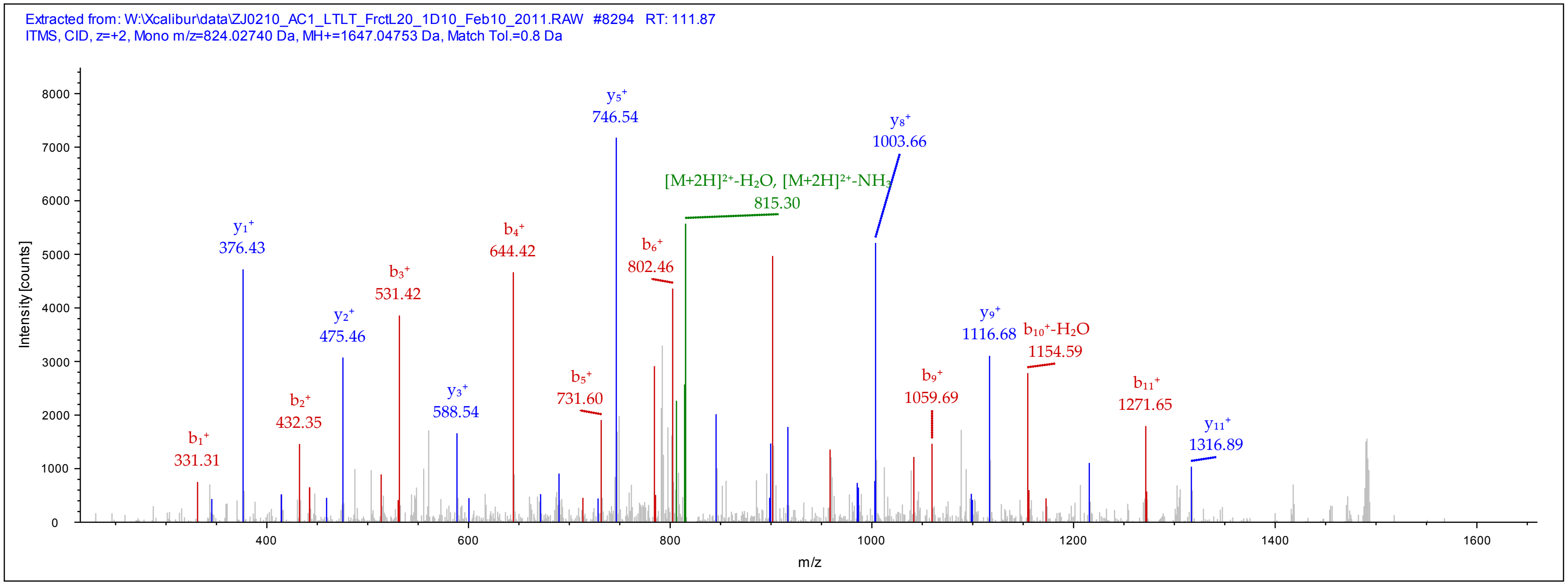
Identified with: Mascot (v1.16); IonScore:72, Exp Value:2.8E-006, Ions matched by search engine: 11/104

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; $b-H_2O$; $b-NH_3$; y; $y-H_2O$; $y-NH_3$

Protein references (2):

- Isoform 1 of SAP30-binding protein
- Isoform 2 of SAP30-binding protein



IPI:IPI00339238.1

Sequence: AVLQEFGR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 574.83472 Da (-0.21 mmu/-0.36 ppm), MH+: 1148.66216 Da, RT: 89.12 min,

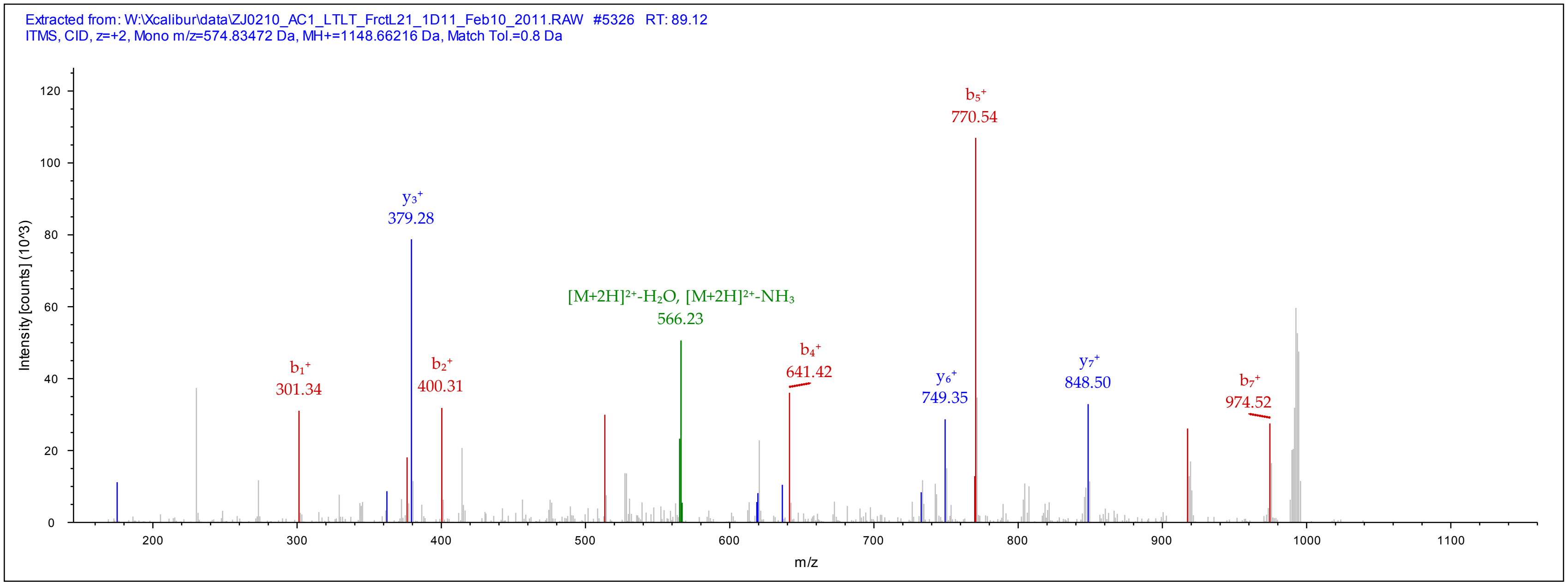
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.3E-002, Ions matched by search engine: 6/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Dehydrogenase/reductase SDR family member 7
- Isoform 2 of Dehydrogenase/reductase SDR family member 7
- Putative uncharacterized protein DKFZp564H1664



IPI00377233.1

Sequence: AQDEAFALQDVPLSSVVR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 1087.58704 Da (+0.62 mmu/+0.57 ppm), MH+: 2174.16680 Da, RT: 120.09 min,

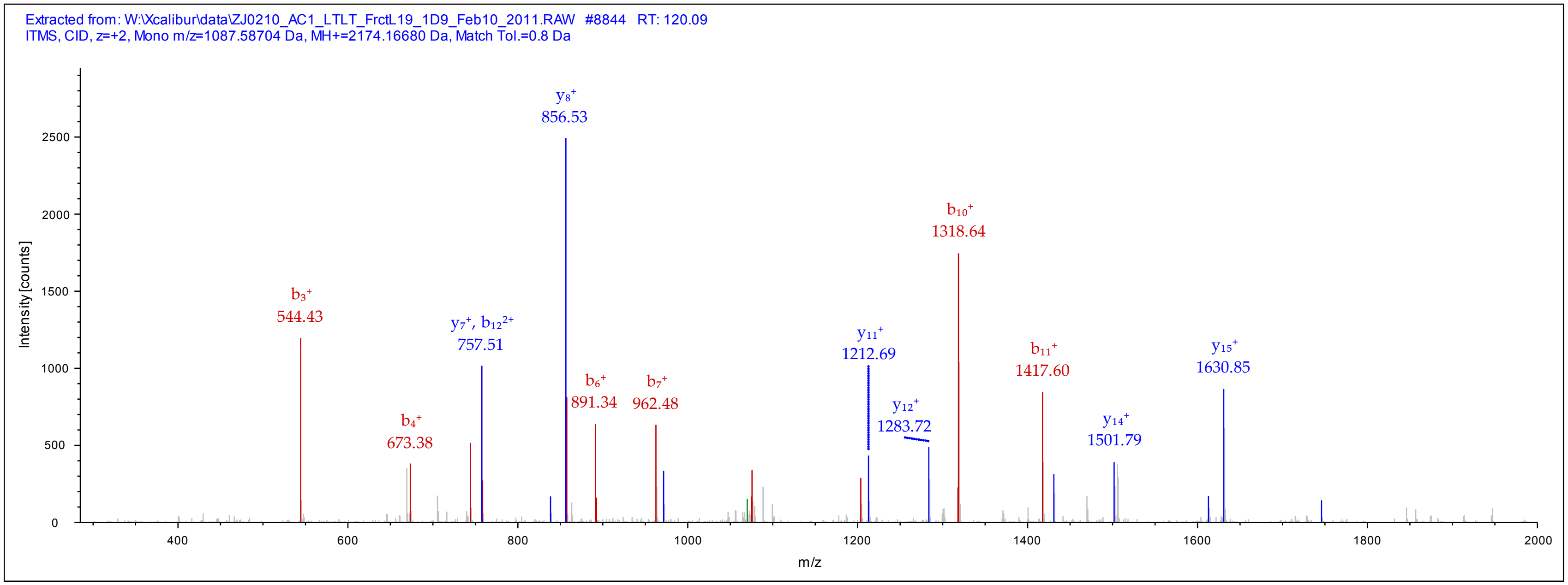
Identified with: Mascot (v1.16); IonScore:69, Exp Value:1.9E-005, Ions matched by search engine: 22/192

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- 39S ribosomal protein L11, mitochondrial lng=192
- 39S ribosomal protein L11, mitochondrial isoform c
- mitochondrial ribosomal protein L11 isoform b lng=166



IPI00382844.1

Sequence: VAGILTVK, V1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 629.92810 Da (-0.5 mmu/-0.79 ppm),   MH+: 1258.84892 Da,   RT: 102.22 min,

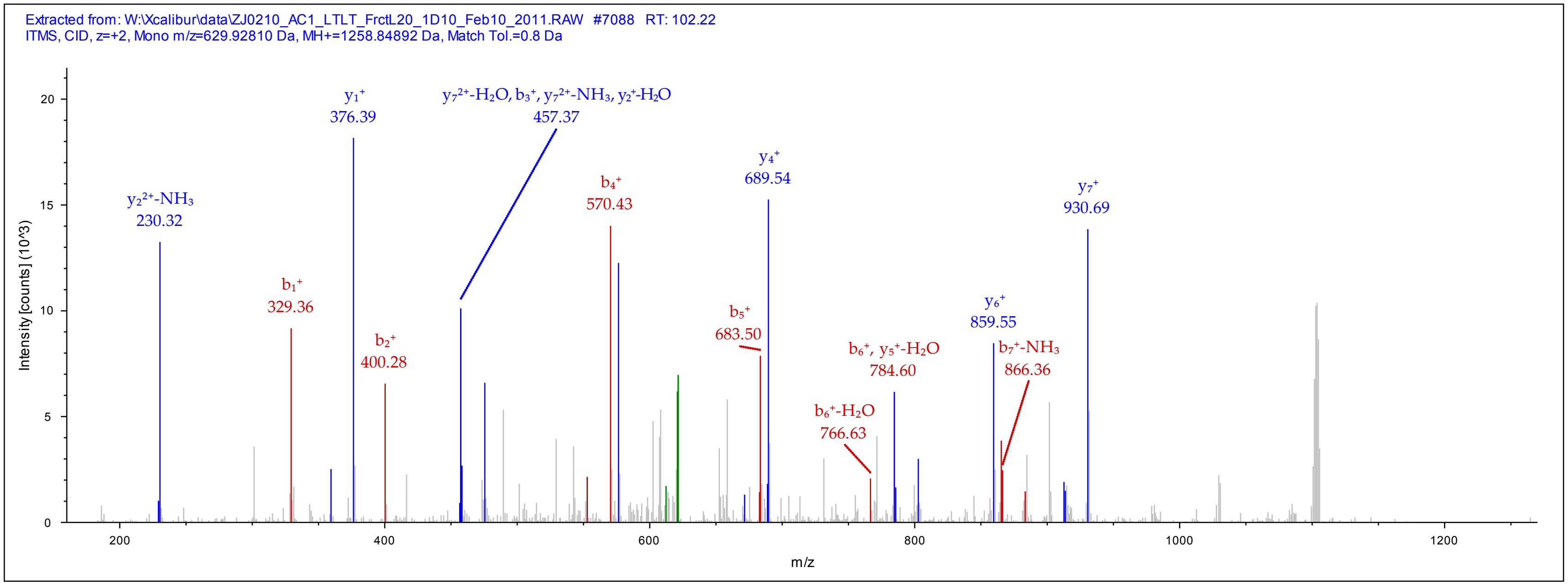
Identified with: Mascot (v1.16); IonScore:43, Exp Value:2.2E-003, Ions matched by search engine: 11/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Aconitate hydratase, mitochondrial
- Aconitase (Fragment) lng=600
- Aconitase 2, mitochondrial lng=805



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL20_1D10_Feb10_2011.RAW   #7088   RT: 102.22
ITMS, CID, z=+2, Mono m/z=629.92810 Da, MH+=1258.84892 Da, Match Tol.=0.8 Da

IPI00384901.2

Sequence: ELTELR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 495.29742 Da (+2.33 mmu/+4.71 ppm), MH+: 989.58757 Da, RT: 79.31 min,

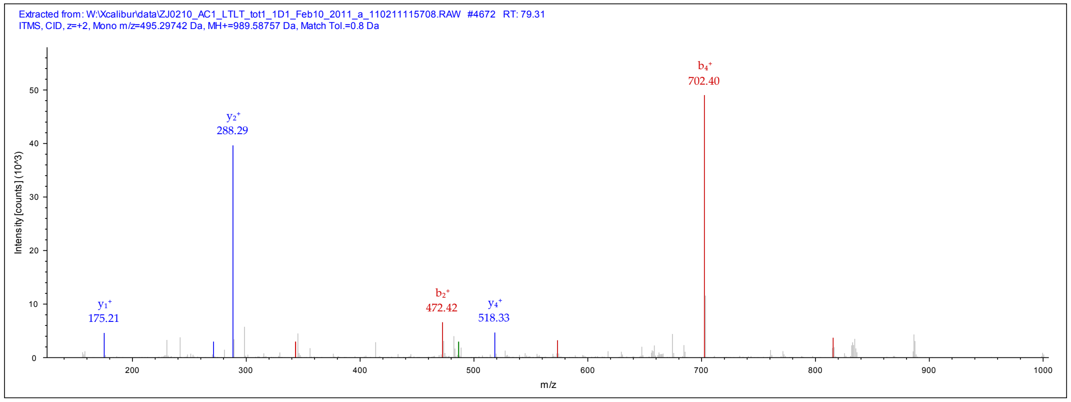
Identified with: Mascot (v1.16); IonScore:30, Exp Value:5.7E-002, Ions matched by search engine: 4/46

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (11):

- Isoform 1 of Serine/threonine-protein kinase TNNI3K
- Isoform 1 of Calcium-binding and coiled-coil domain-containing protein 1
- Isoform 2 of Serine/threonine-protein kinase TNNI3K
- Putative uncharacterized protein DKFZp686A11272 lng=392
- Isoform 4 of Serine/threonine-protein kinase TNNI3K
- Isoform 3 of Serine/threonine-protein kinase TNNI3K
- Isoform 2 of Calcium-binding and coiled-coil domain-containing protein 1
- cDNA FLJ35469 fis, clone SMINT2006205, highly similar to Homo sapiens calcium binding and coiled-coil domain 1 (CALCOCO1), mRNA lng=629
- Isoform 3 of Calcium-binding and coiled-coil domain-containing protein 1
- calcium-binding and coiled-coil domain-containing protein 1 isoform 2
- cDNA FLJ16315 fis, clone SPLEN2032112, highly similar to Homo sapiens calcium binding and coiled-coil domain 1 (CALCOCO1), mRNA lng=606



IPI00385082.1

Sequence: LIEIENFK, L1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 732.44720 Da (-0.15 mmu/-0.21 ppm),   MH+: 1463.88713 Da,   RT: 116.19 min,

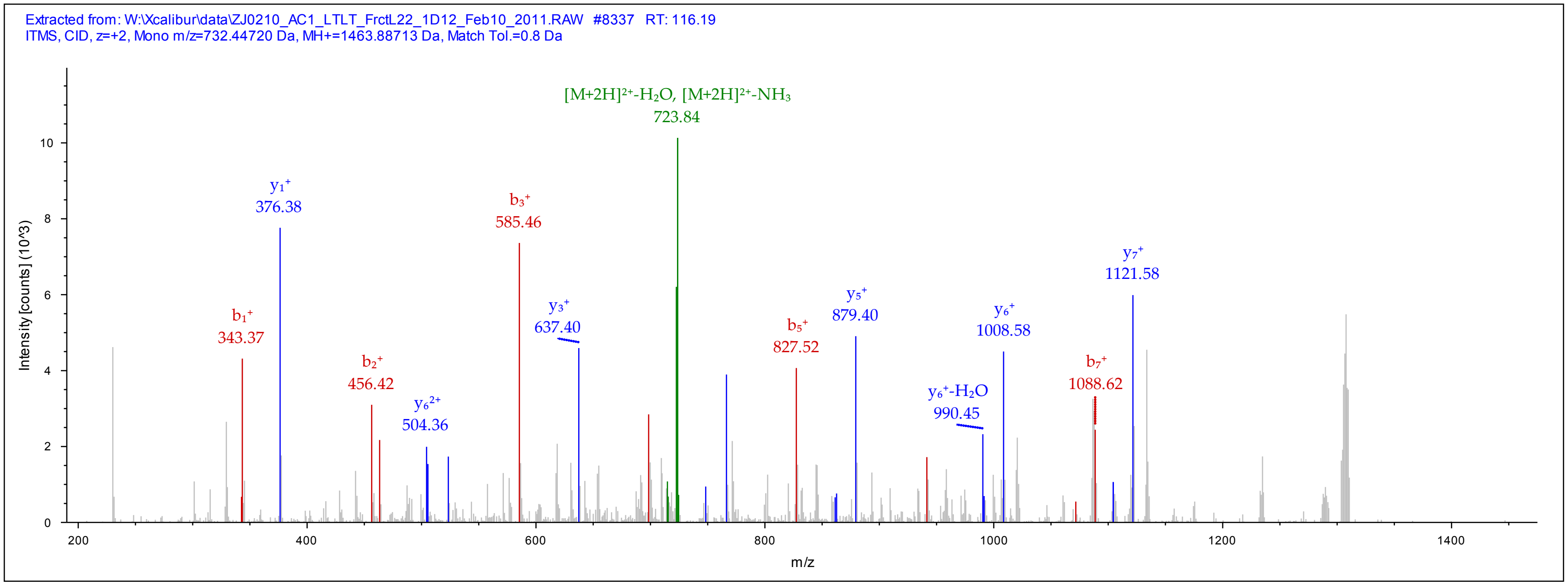
Identified with: Mascot (v1.16); IonScore:34, Exp Value:2.6E-002, Ions matched by search engine: 12/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; $b-H_2O$; $b-NH_3$; y; $y-H_2O$; $y-NH_3$

Protein references (3):

- Structural maintenance of chromosomes protein 1A
- MSTP142 lng=205
- cDNA FLJ50250, highly similar to Structural maintenance of chromosome 1-like 1 protein lng=516



IPI:IPI00956685.1

Sequence: IYAPQGLLLTDPIER, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 964.55658 Da (+0.19 mmu/+0.2 ppm), MH+: 1928.10588 Da, RT: 123.39 min,

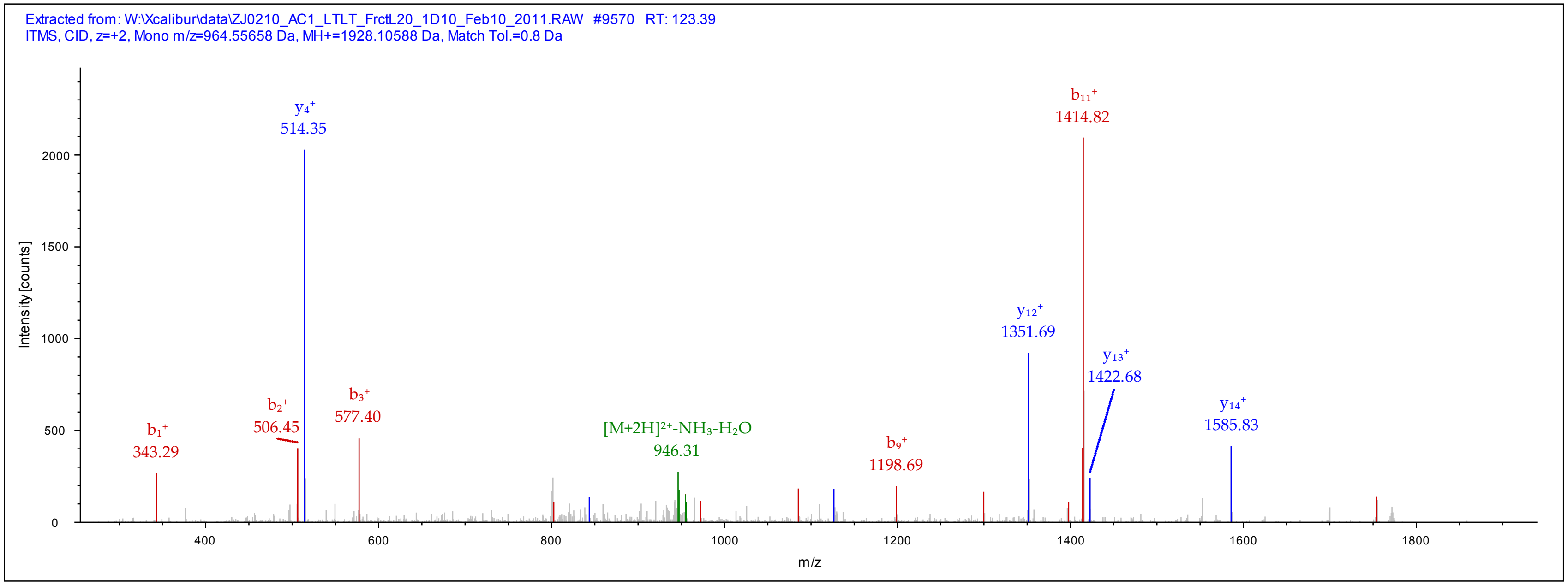
Identified with: Mascot (v1.16); IonScore:51, Exp Value:7.3E-004, Ions matched by search engine: 11/140

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Golgin subfamily A member 7
- golgin subfamily A member 7 isoform b



IPI00385260.1

Sequence: DFAPVIVEAFK, D1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 847.50159 Da (+1.46 mmu/+1.72 ppm),   MH+: 1693.99590 Da,   RT: 131.21 min,

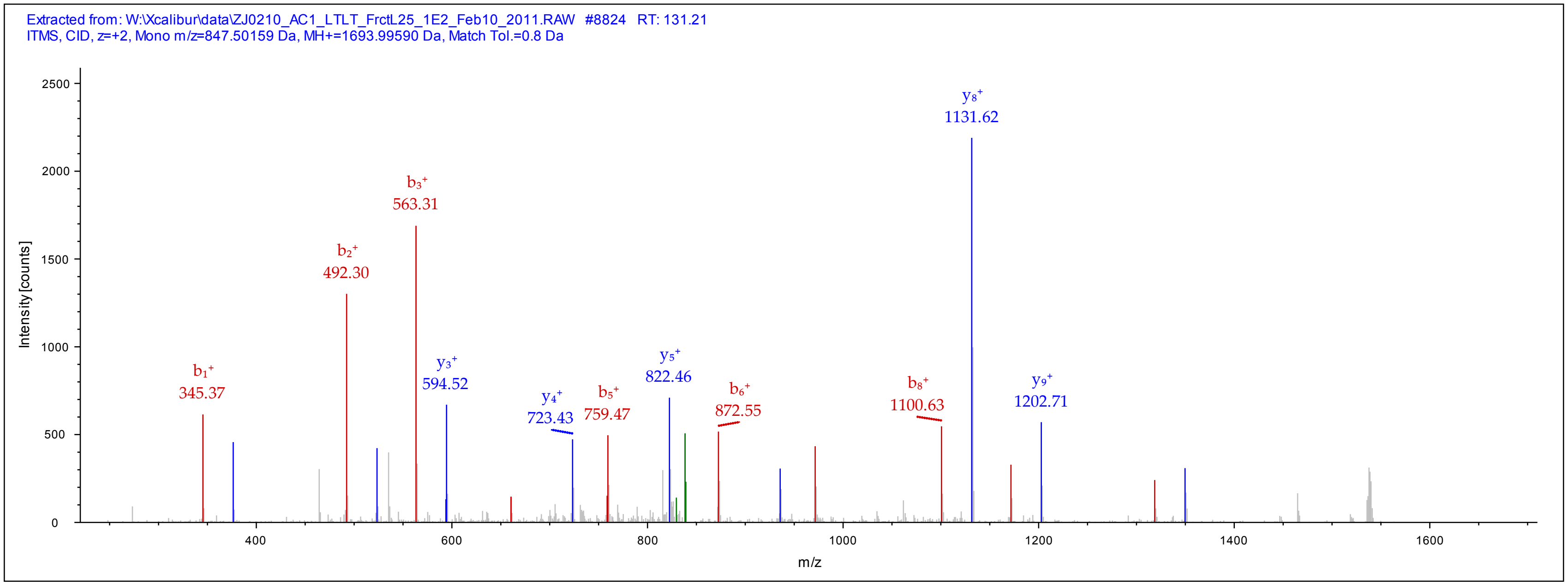
Identified with: Mascot (v1.16); IonScore:60, Exp Value:1.0E-004, Ions matched by search engine: 9/94

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Regulation of nuclear pre-mRNA domain-containing protein 1A
- Isoform 2 of Regulation of nuclear pre-mRNA domain-containing protein 1A
- Isoform 3 of Regulation of nuclear pre-mRNA domain-containing protein 1A lng=276



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL25_1E2_Feb10_2011.RAW   #8824   RT: 131.21
ITMS, CID, z=+2, Mono m/z=847.50159 Da, MH+=1693.99590 Da, Match Tol.=0.8 Da

IPI00385529.3

Sequence: AQGTLIR, A1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 494.30646 Da (-4.63 mmu/-9.36 ppm),   MH+: 987.60564 Da,   RT: 132.30 min,

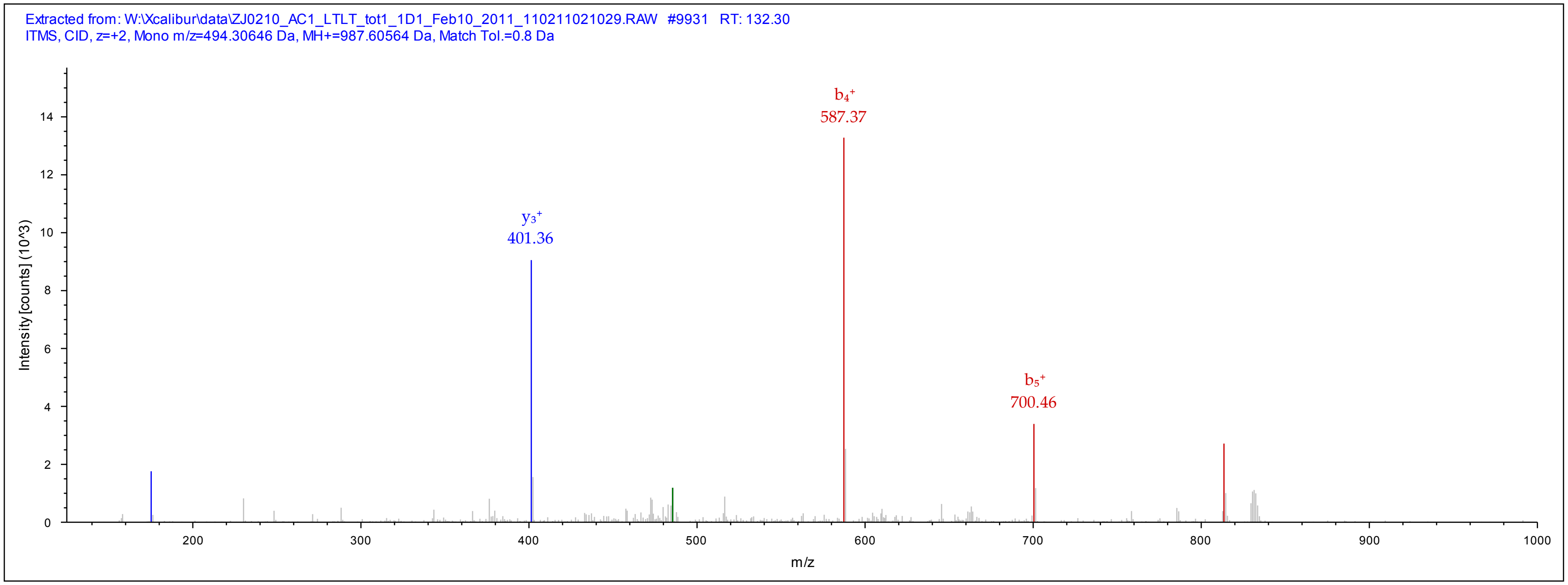
Identified with: Mascot (v1.16); IonScore:31, Exp Value:5.5E-002, Ions matched by search engine: 4/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- PADI-H protein lng=214
- Protein-arginine deiminase type-4



IPI:IPI00386115.2

Sequence: VLELAR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 465.30249 Da (-0.23 mmu/-0.51 ppm), MH+: 929.59770 Da, RT: 79.13 min,

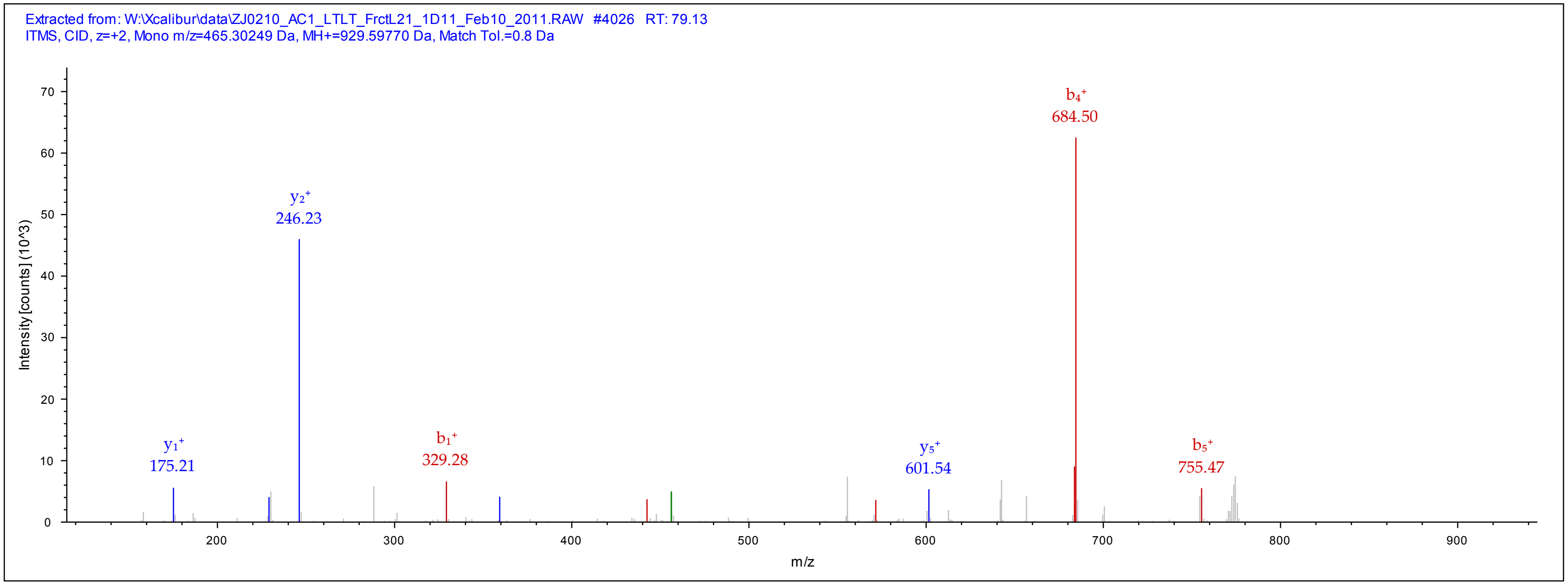
Identified with: Mascot (v1.16); IonScore:31, Exp Value:2.6E-002, Ions matched by search engine: 5/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of Metal transporter CNNM3
- Teneurin-4
- Isoform 2 of Metal transporter CNNM3
- Isoform 3 of Metal transporter CNNM3



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL21_1D11_Feb10_2011.RAW #4026 RT: 79.13
ITMS, CID, z=+2, Mono m/z=465.30249 Da, MH+=929.59770 Da, Match Tol.=0.8 Da

IPI:IPI00852972.1

Sequence: AAAAAAAK, A1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 551.85425 Da (+1.35 mmu/+2.45 ppm),   MH+: 1102.70122 Da,   RT: 68.57 min,

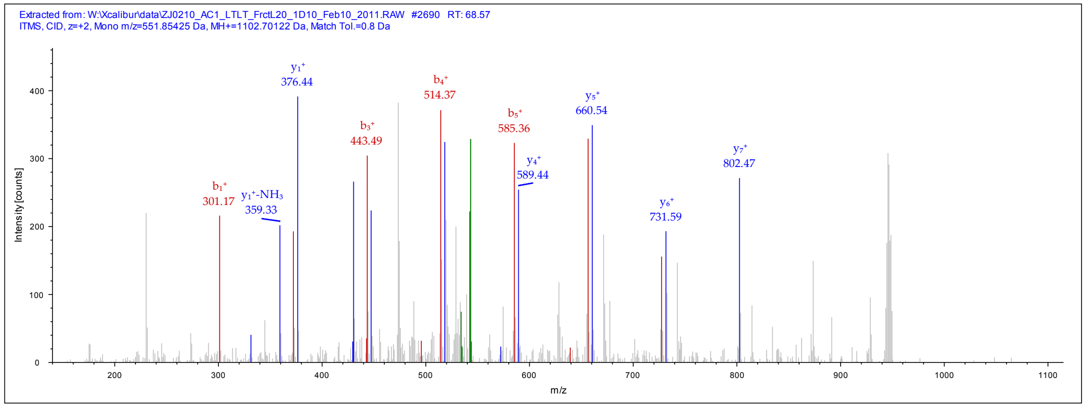
Identified with: Mascot (v1.16); IonScore:31, Exp Value:4.6E-002, Ions matched by search engine: 7/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (12):

- Isoform 1 of Tudor domain-containing protein PHF20L1
- Isoform 2 of Tudor domain-containing protein PHF20L1
- Uncharacterized protein
- PHD finger protein 20-like protein 1 isoform 2
- PHD finger protein 20-like protein 1 isoform 1
- Uncharacterized protein
- Uncharacterized protein
- cDNA FLJ60980, highly similar to Cell division cycle 2-related protein kinase 7 lng=1273
- Isoform 2 of Cell division protein kinase 12
- Uncharacterized protein
- cDNA FLJ13649 fis, clone PLACE1011399, weakly similar to Homo sapiens CGI-72 protein mRNA
- Isoform 1 of Cell division protein kinase 12



IPI:IPI00386908.3

Sequence: VLIDWINDVLVGER, V1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 935.53699 Da (+1.52 mmu/+1.63 ppm),   MH+: 1870.06670 Da,   RT: 222.63 min,

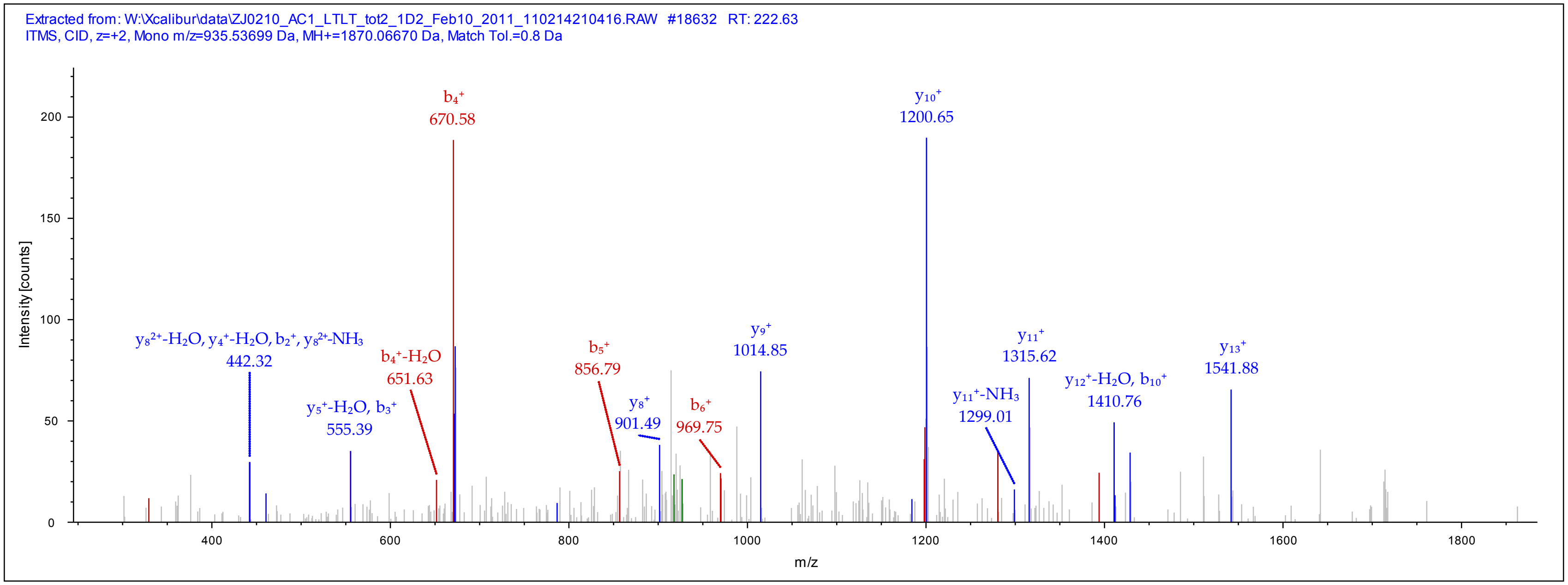
Identified with: Mascot (v1.16); IonScore:30, Exp Value:9.0E-002, Ions matched by search engine: 11/136

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Alpha-parvin
- Isoform 2 of Alpha-parvin
- cDNA FLJ54827, highly similar to Alpha-parvin lng=290



IPI00394837.2

Sequence: YLECSALTQR, Y1-TMT6plex (229.16293 Da), C4-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 735.38464 Da (0 mmu/0 ppm),   MH+: 1469.76201 Da,   RT: 84.82 min,

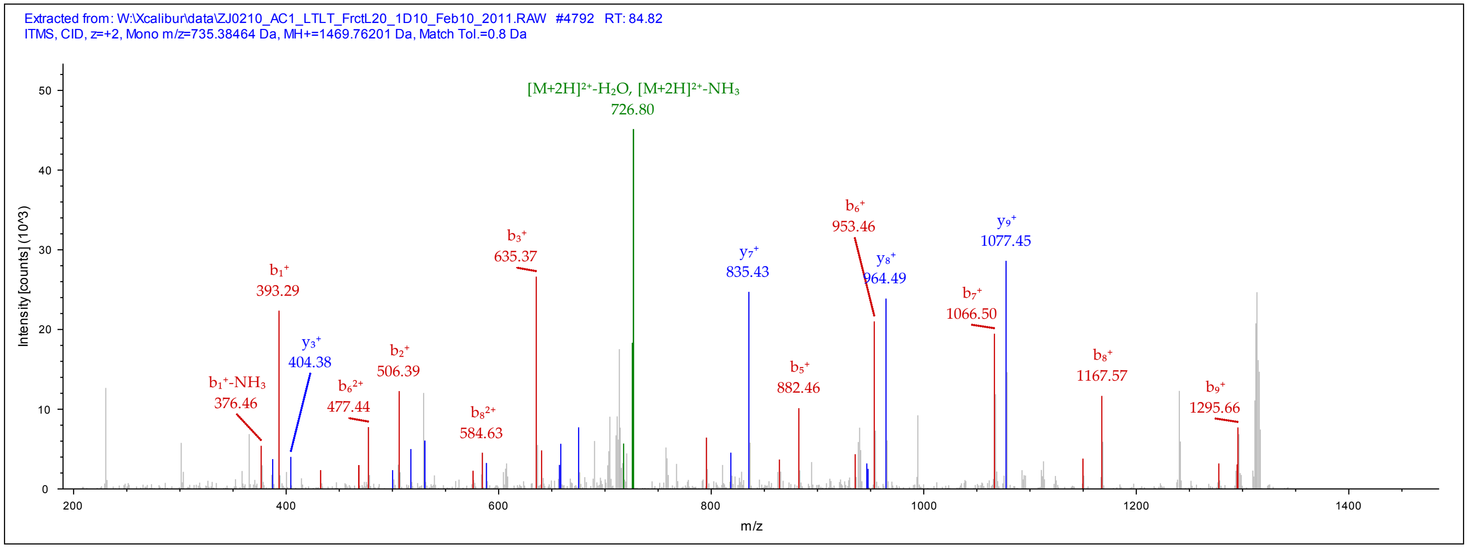
Identified with: Mascot (v1.16); IonScore:49, Exp Value:1.0E-003, Ions matched by search engine: 8/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (8):

- Ras-related C3 botulinum toxin substrate 2
- Isoform A of Ras-related C3 botulinum toxin substrate 1
- Ras-related C3 botulinum toxin substrate 3
- Isoform B of Ras-related C3 botulinum toxin substrate 1
- Ras-related C3 botulinum toxin substrate 1 (Rho family, small GTP binding protein Rac1), isoform CRA_b lng=148
- Ras-related C3 botulinum toxin substrate 2 (Rho family, small GTP binding protein Rac2), isoform CRA_c lng=185
- Ras-related C3 botulinum toxin substrate 2 lng=148
- Ras-related C3 botulinum toxin substrate 2 lng=166


Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL20_1D10_Feb10_2011.RAW   #4792   RT: 84.82

ITMS, CID, z=+2, Mono m/z=735.38464 Da, MH+=1469.76201 Da, Match Tol.=0.8 Da

IPI00883762.1

Sequence: LMDEVAGIVAAR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 737.41833 Da (-0.18 mmu/-0.24 ppm), MH+: 1473.82939 Da, RT: 119.53 min,

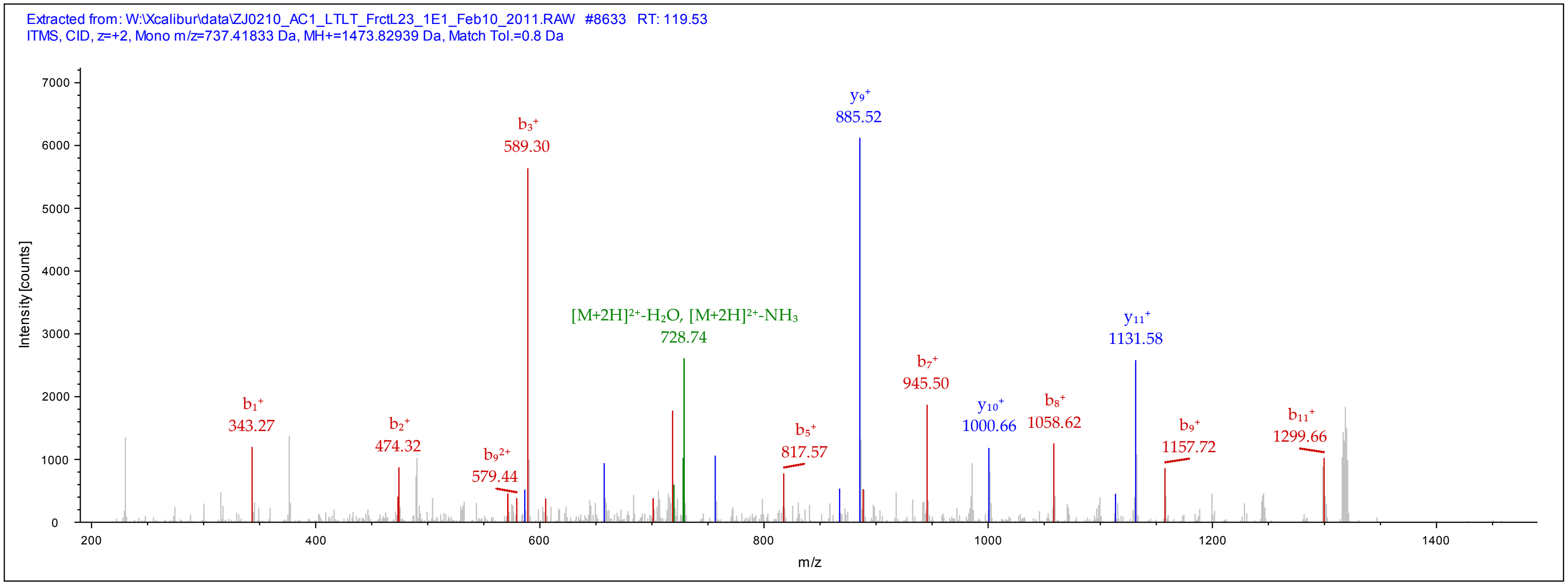
Identified with: Mascot (v1.16); IonScore:43, Exp Value:5.1E-003, Ions matched by search engine: 10/90

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform 1 of Cytosolic acyl coenzyme A thioester hydrolase
- Isoform 5 of Cytosolic acyl coenzyme A thioester hydrolase
- Isoform 6 of Cytosolic acyl coenzyme A thioester hydrolase
- Isoform 2 of Cytosolic acyl coenzyme A thioester hydrolase lng=246
- cytosolic acyl coenzyme A thioester hydrolase isoform hBACHa
- Isoform 3 of Cytosolic acyl coenzyme A thioester hydrolase lng=283



IPI:IPI00396018.1

Sequence: LLLEDLVK, L1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 700.96185 Da (+1.75 mmu/+2.5 ppm), MH+: 1400.91643 Da, RT: 131.10 min,

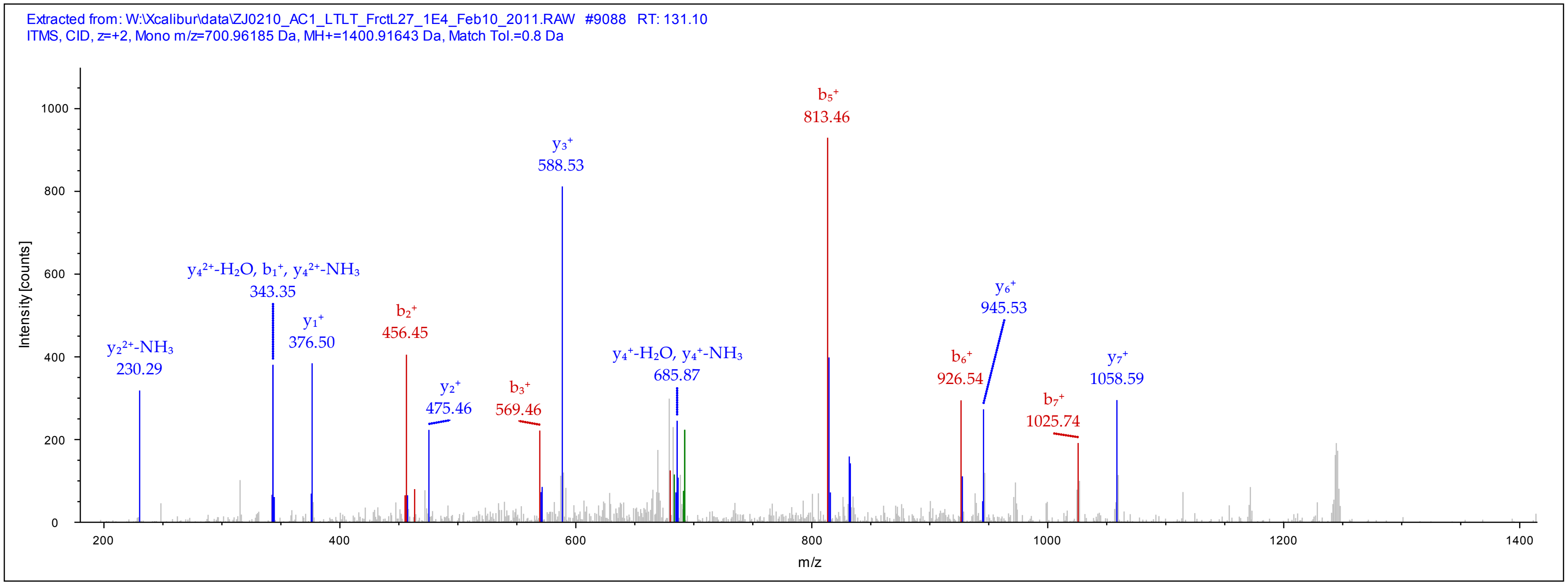
Identified with: Mascot (v1.16); IonScore:35, Exp Value:1.1E-002, Ions matched by search engine: 6/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H$_2$O; b-NH$_3$; y; y-H$_2$O; y-NH$_3$

Protein references (6):

- Isoform 1 of Acetyl-CoA carboxylase 1
- Isoform 2 of Acetyl-CoA carboxylase 1
- Isoform 3 of Acetyl-CoA carboxylase 1
- Isoform 4 of Acetyl-CoA carboxylase 1
- 265 kDa protein lng=2344
- 268 kDa protein lng=2370



IPI:IPI00397700.5

Sequence: AEFGDFDIK, A1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 750.41052 Da (-0.45 mmu/-0.6 ppm), MH+: 1499.81377 Da, RT: 106.10 min,

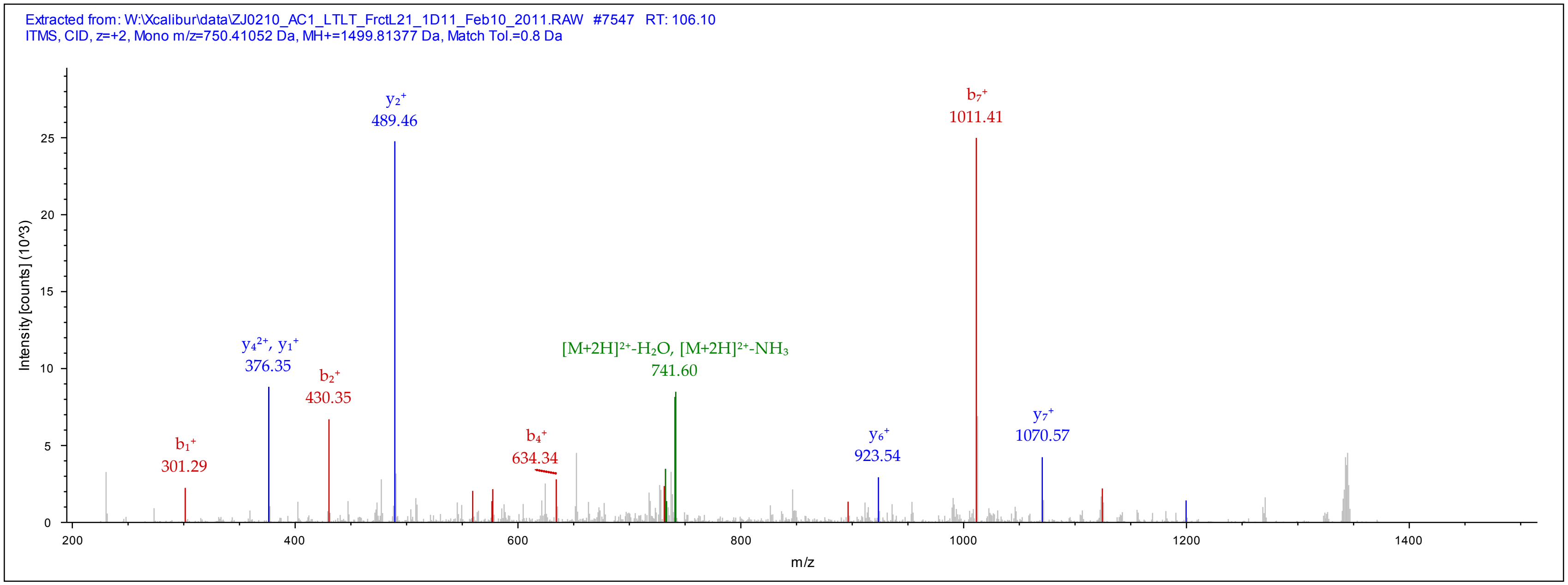
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.3E-002, Ions matched by search engine: 7/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of PHD finger protein 6
- Isoform 2 of PHD finger protein 6
- PHD finger protein 6, isoform CRA_d lng=366
- cDNA FLJ60207, highly similar to PHD finger protein 6 lng=331



IPI:IPI00401162.1

Sequence: ILELER, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 501.31326 Da (-0.03 mmu/-0.05 ppm), MH+: 1001.61925 Da, RT: 96.97 min,

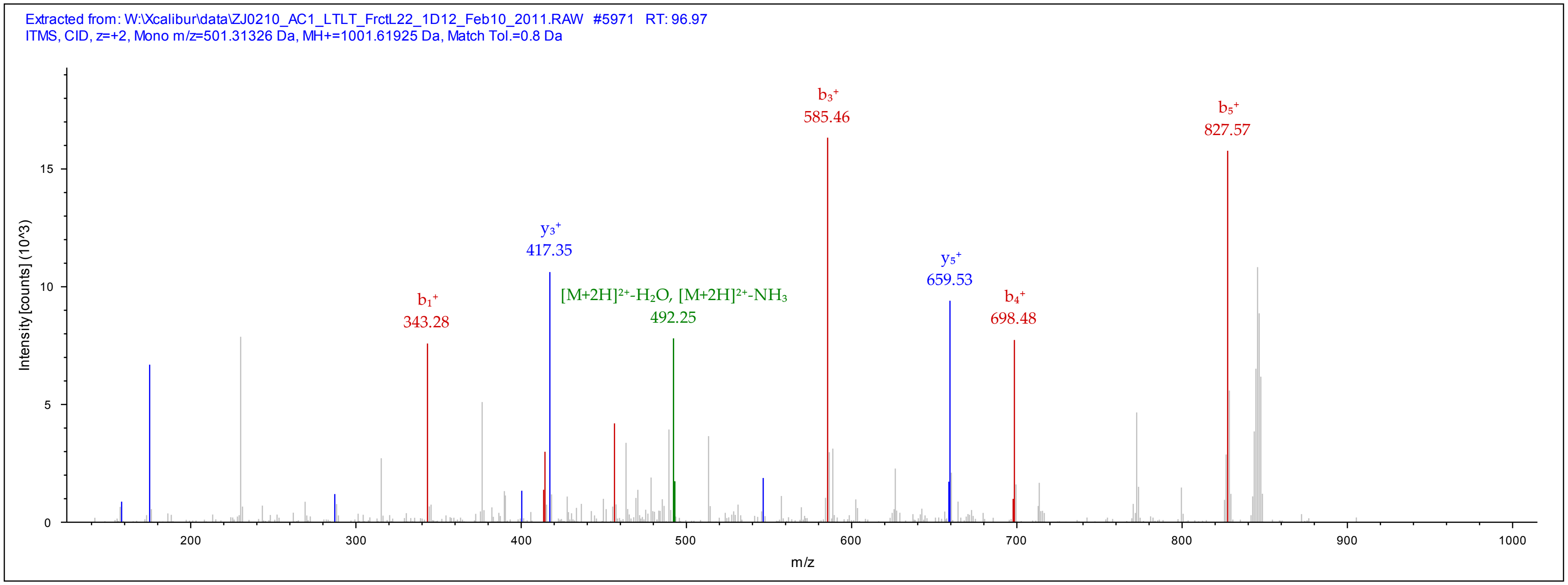
Identified with: Mascot (v1.16); IonScore:29, Exp Value:5.4E-002, Ions matched by search engine: 5/44

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Testis-specific serine kinase substrate
- Isoform 2 of Testis-specific serine kinase substrate
- Uncharacterized protein



IPI:IPI00410134.1

Sequence: VADLLYWK, V1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 733.44739 Da (+2.78 mmu/+3.79 ppm), MH+: 1465.88750 Da, RT: 128.96 min,

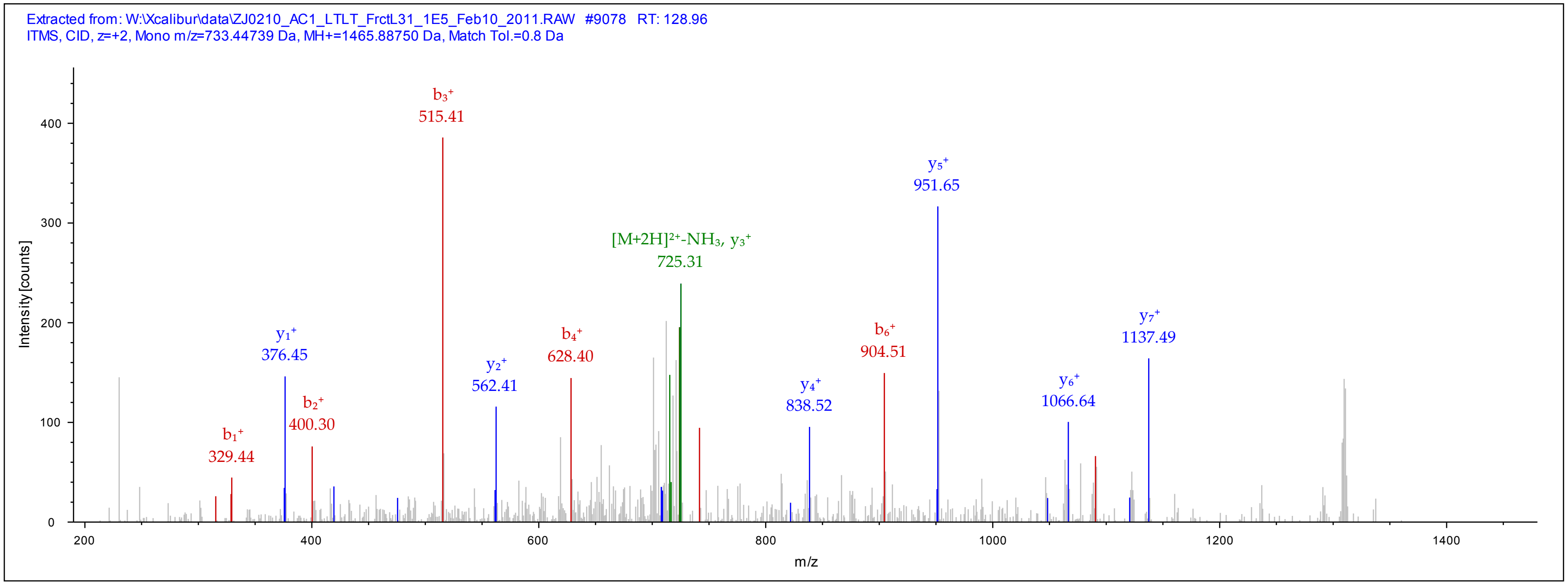
Identified with: Mascot (v1.16); IonScore:36, Exp Value:1.6E-002, Ions matched by search engine: 7/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform RTN2-A of Reticulon-2
- Isoform RTN2-C of Reticulon-2



IPI:IPI00410157.4

Sequence: SLDLIESLLR, S1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 694.42389 Da (+2.33 mmu/+3.35 ppm), MH+: 1387.84050 Da, RT: 183.68 min,

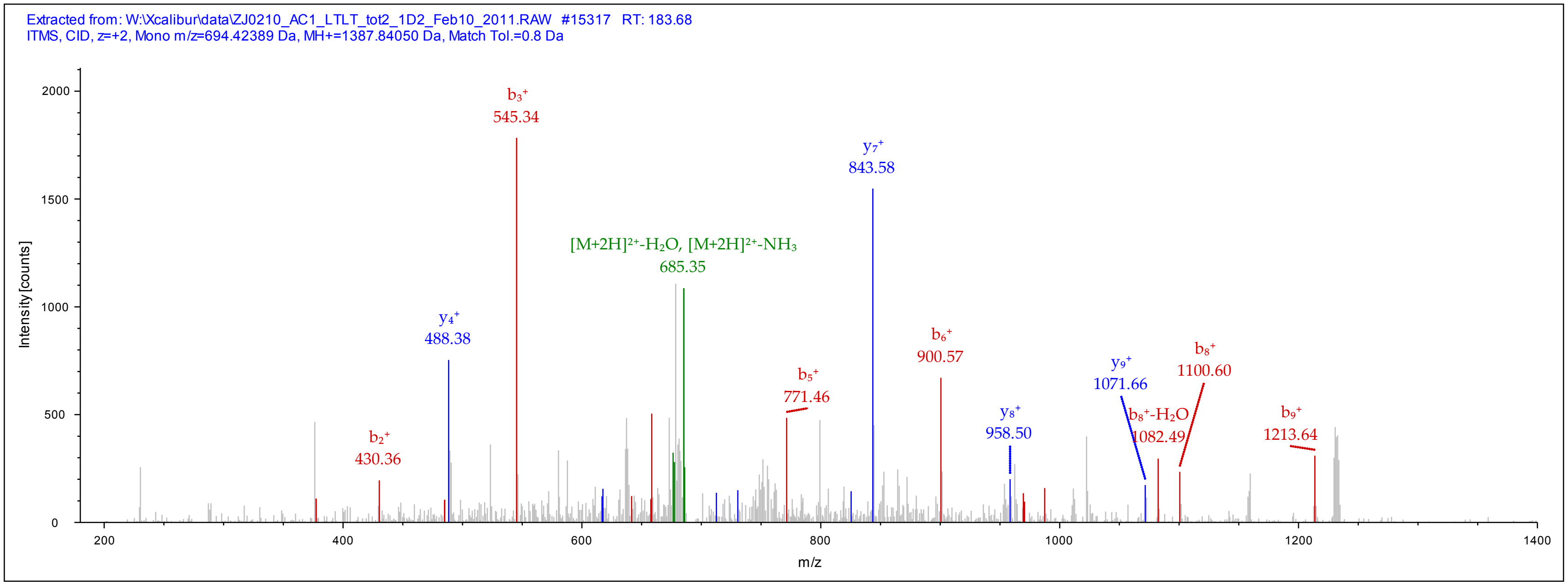
Identified with: Mascot (v1.16); IonScore:34, Exp Value:3.3E-002, Ions matched by search engine: 9/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of CCR4-NOT transcription complex subunit 1
- Isoform 4 of CCR4-NOT transcription complex subunit 1
- Isoform 3 of CCR4-NOT transcription complex subunit 1
- Isoform 2 of CCR4-NOT transcription complex subunit 1



IPI:IPI00873810.2

Sequence: GVQVETISPGDGR, G1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 772.41956 Da (+2.01 mmu/+2.6 ppm), MH+: 1543.83183 Da, RT: 84.62 min,

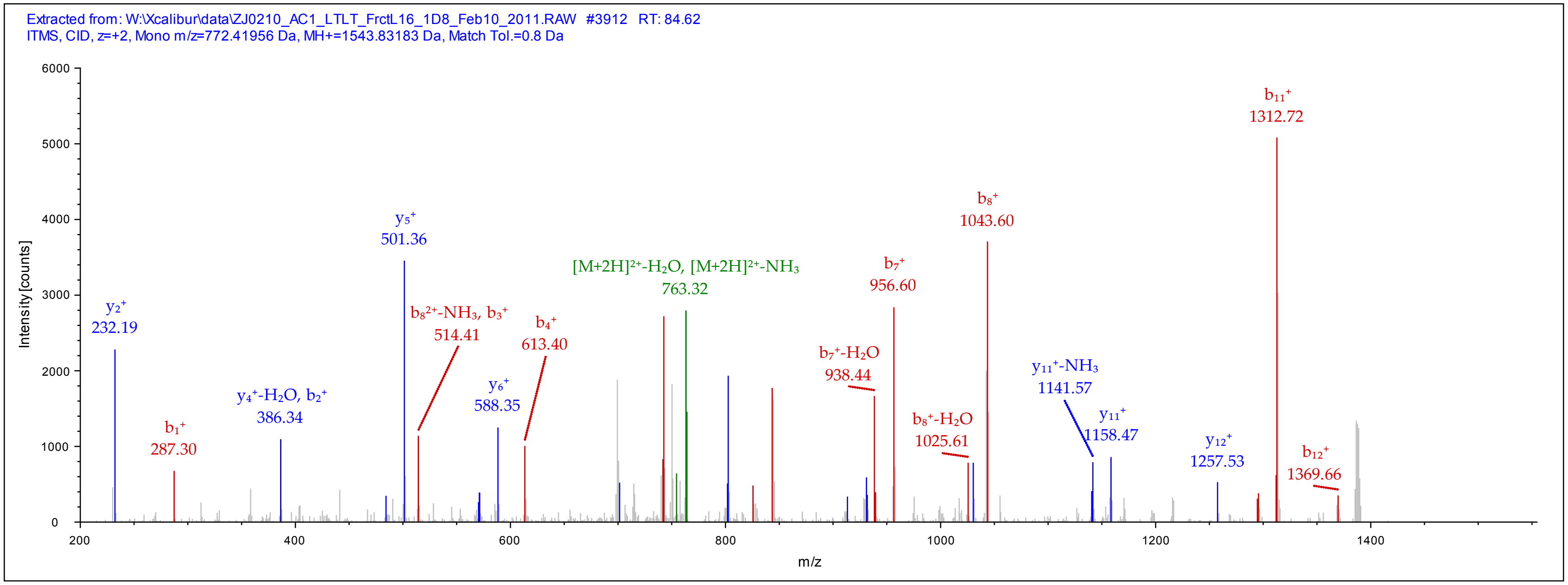
Identified with: Mascot (v1.16); IonScore:67, Exp Value:2.1E-005, Ions matched by search engine: 10/128

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- FK506 binding protein12
- FK506 binding protein12 lng=89



IPI:IPI00427741.1

Sequence: ELPEQFFQLVK, E1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 918.53998 Da (+2.74 mmu/+2.98 ppm), MH+: 1836.07268 Da, RT: 133.70 min,

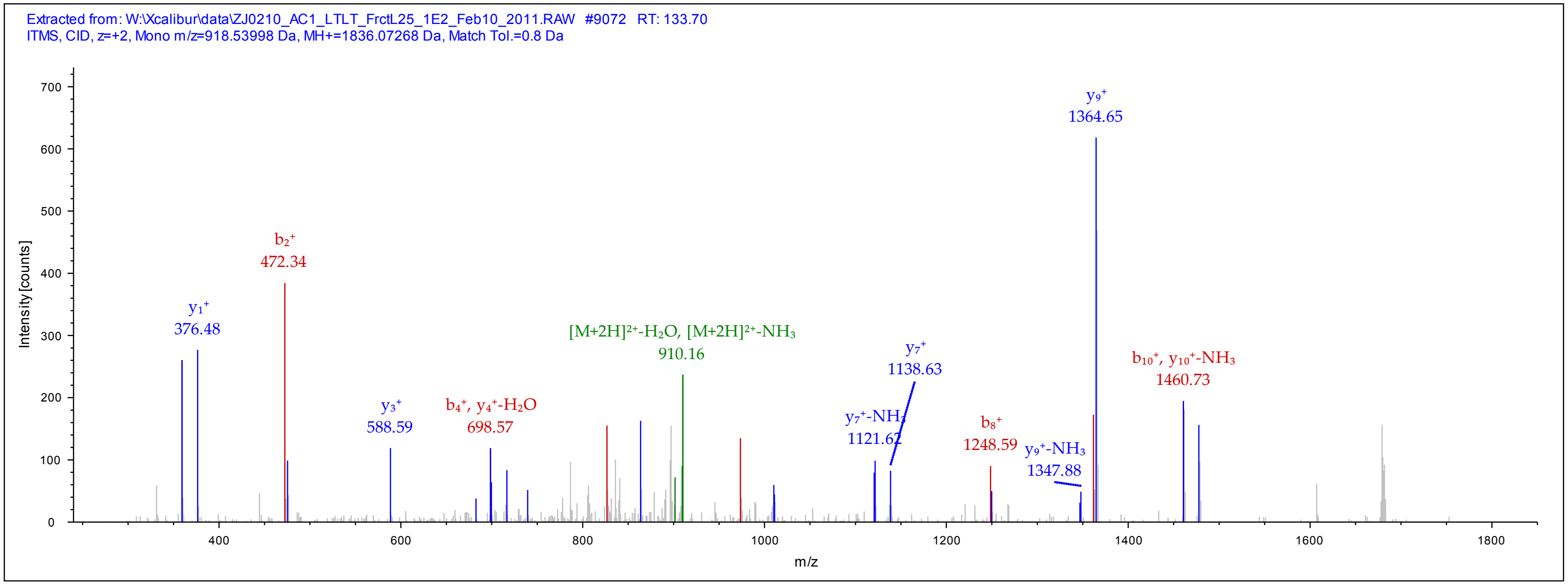
Identified with: Mascot (v1.16); IonScore:58, Exp Value:1.5E-004, Ions matched by search engine: 9/98

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Leucine-rich repeat-containing protein 1
- Isoform 2 of Leucine-rich repeat-containing protein 1



IPI:IPI00430772.3

Sequence: ALLLVGDVAQAADVAIEHR, A1-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 730.75409 Da (+1.07 mmu/+1.47 ppm), MH+: 2190.24771 Da, RT: 189.78 min,

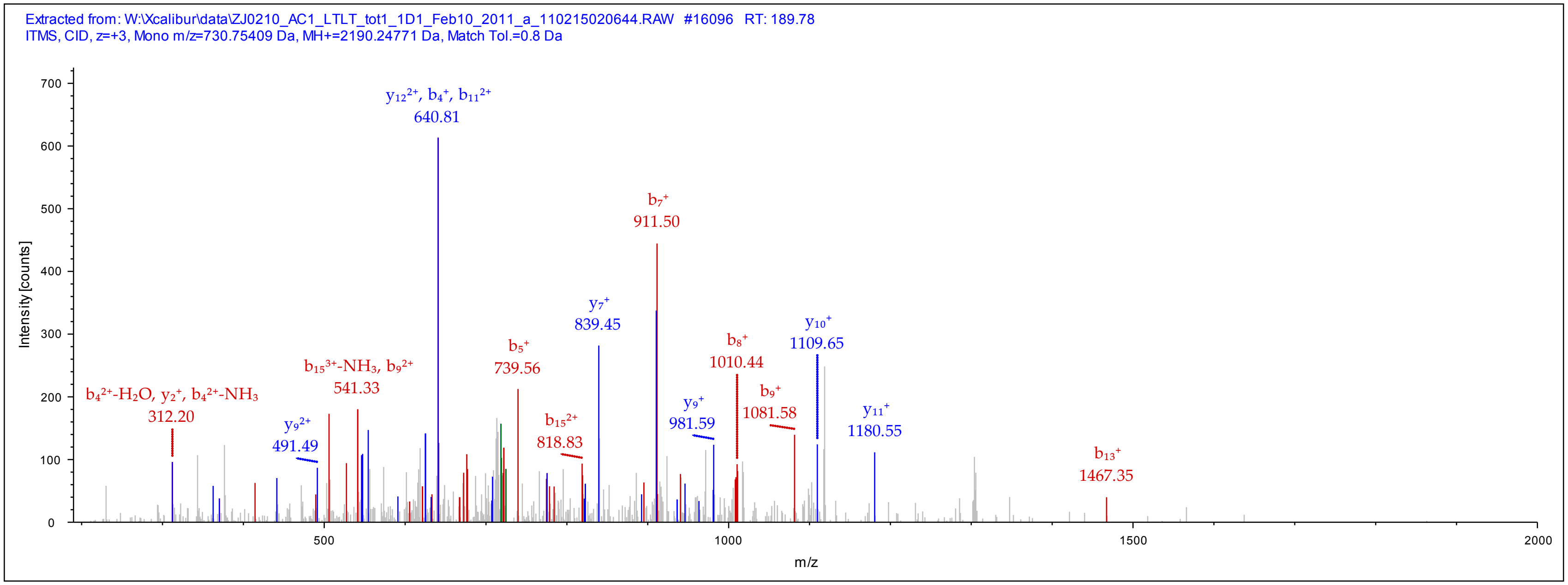
Identified with: Mascot (v1.16); IonScore:53, Exp Value:5.8E-004, Ions matched by search engine: 13/182

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Vacuolar protein sorting-associated protein 16 homolog
- Isoform 2 of Vacuolar protein sorting-associated protein 16 homolog
- Vacuolar protein sorting 16 homolog



IPI00443657.1

Sequence: GFGFVTFENIDDAK, G1-TMT6plex (229.16293 Da), K14-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 1009.53522 Da (-0.22 mmu/-0.22 ppm),   MH+: 2018.06316 Da,   RT: 125.10 min,

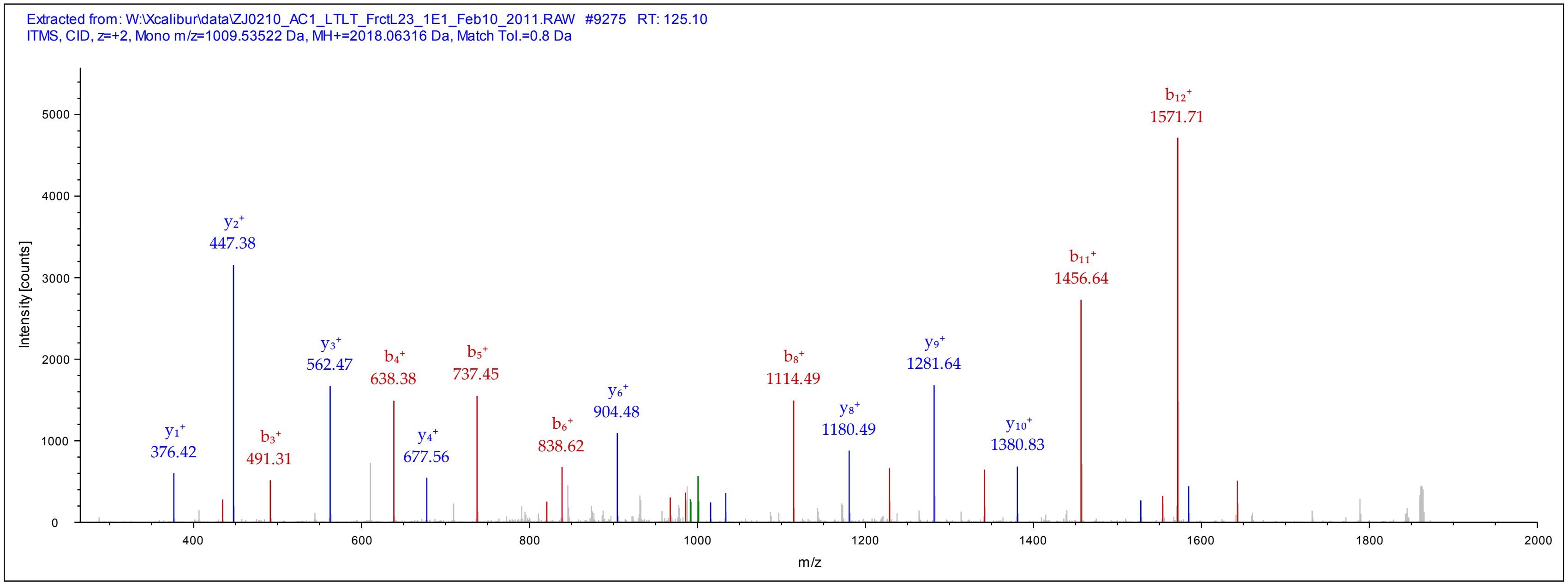
Identified with: Mascot (v1.16); IonScore:101, Exp Value:1.1E-008, Ions matched by search engine: 13/126

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

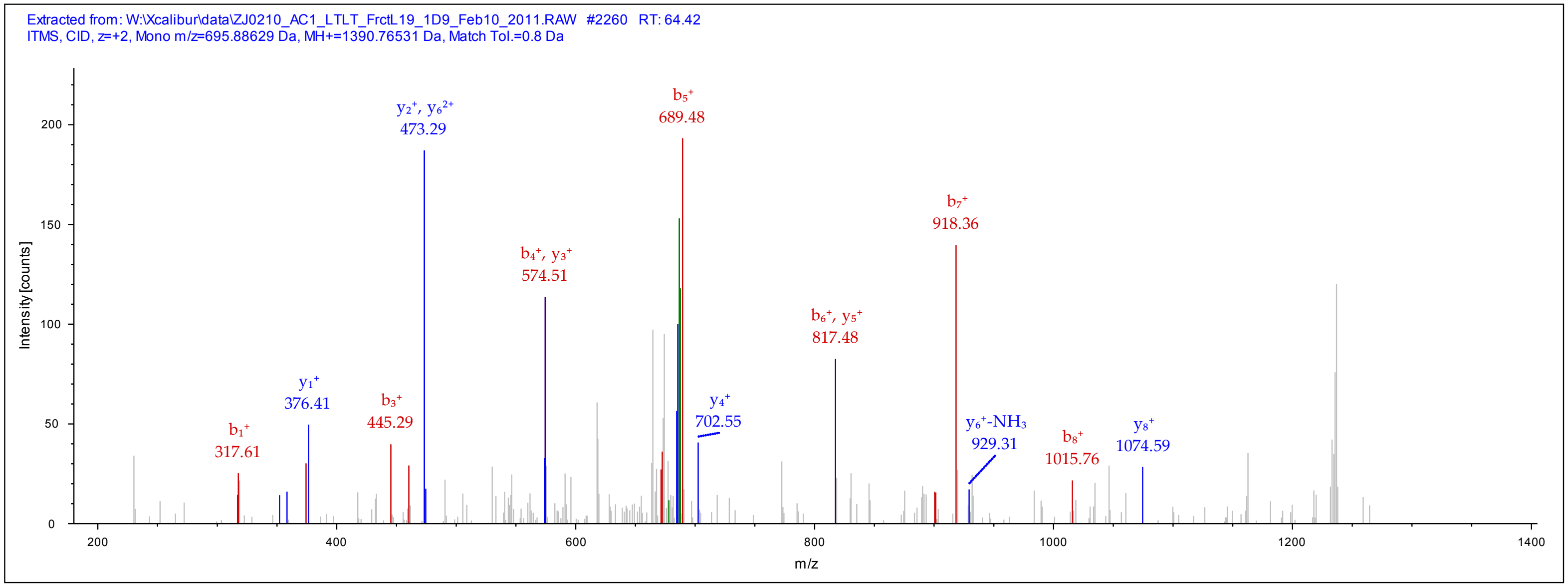
Protein references (6):

- Cold-inducible RNA-binding protein
- cDNA FLJ46566 fis, clone THYMU3040829, moderately similar to Cold-inducible RNA-binding protein lng=135
- cDNA FLJ37462 fis, clone BRAWH2011343, highly similar to COLD-INDUCIBLE RNA-BINDING PROTEIN lng=297
- 18 kDa protein lng=168
- cDNA FLJ52850, moderately similar to Cold-inducible RNA-binding protein lng=263
- cDNA FLJ52834, moderately similar to Cold-inducible RNA-binding protein lng=142



IPI:IPI00445166.1
Sequence: SGAEDQTPK, S1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)
Charge: +2,   Monoisotopic m/z: 695.88629 Da (+3.72 mmu/+5.34 ppm),   MH+: 1390.76531 Da,   RT: 64.42 min,
Identified with: Mascot (v1.16); IonScore:48, Exp Value:1.4E-003, Ions matched by search engine: 8/82
Fragment match tolerance used for search: 0.8 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (8):
- Isoform TGN51 of Trans-Golgi network integral membrane protein 2
- Isoform 6 of Trans-Golgi network integral membrane protein 2
- Isoform TGN48 of Trans-Golgi network integral membrane protein 2
- Isoform TGN46 of Trans-Golgi network integral membrane protein 2
- Isoform 4 of Trans-Golgi network integral membrane protein 2
- Isoform 5 of Trans-Golgi network integral membrane protein 2
- Uncharacterized protein
- Trans-golgi network protein 2, isoform CRA_b



IPI:IPI00446669.1

Sequence: EALLAALGYK, E1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 753.97028 Da (+1.82 mmu/+2.42 ppm),   MH+: 1506.93328 Da,   RT: 124.25 min,

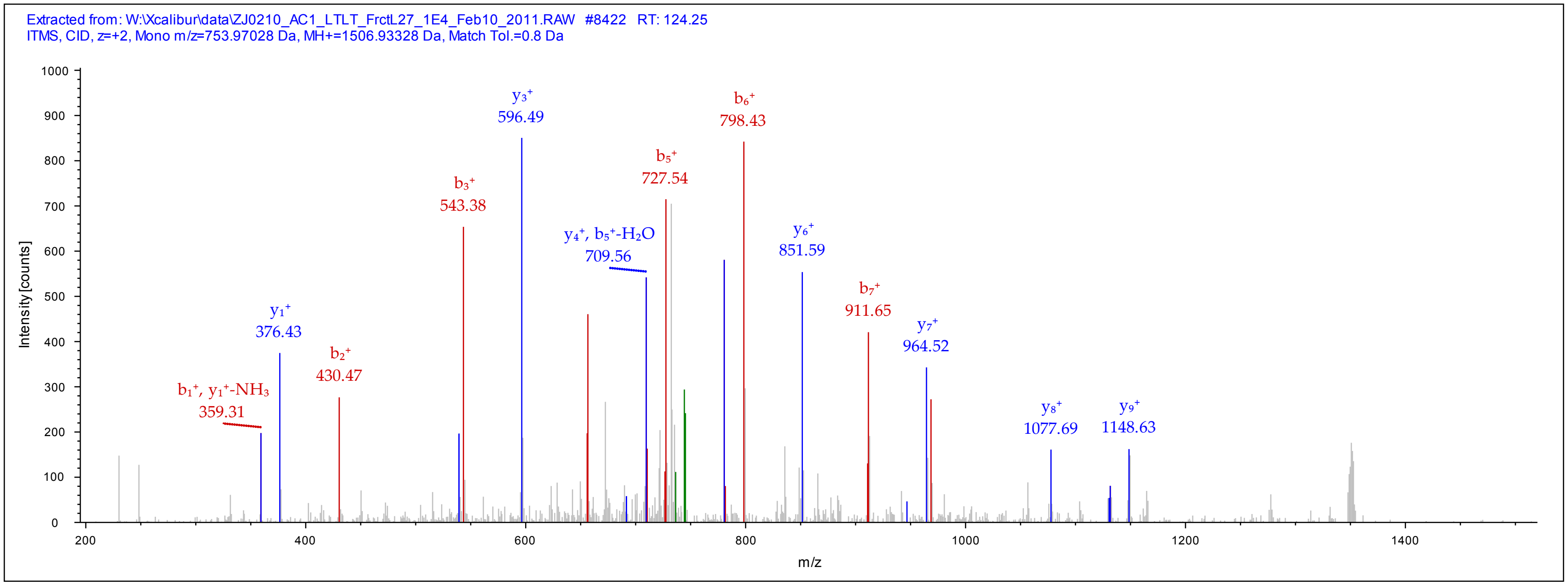
Identified with: Mascot (v1.16); IonScore:52, Exp Value:4.0E-004, Ions matched by search engine: 9/72

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of Multiple myeloma tumor-associated protein 2
- Isoform 2 of Multiple myeloma tumor-associated protein 2
- Isoform 4 of Multiple myeloma tumor-associated protein 2
- Isoform 3 of Multiple myeloma tumor-associated protein 2



IPI00446670.1

Sequence: LEVTLR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 480.30853 Da (+0.53 mmu/+1.1 ppm), MH+: 959.60979 Da, RT: 88.04 min,

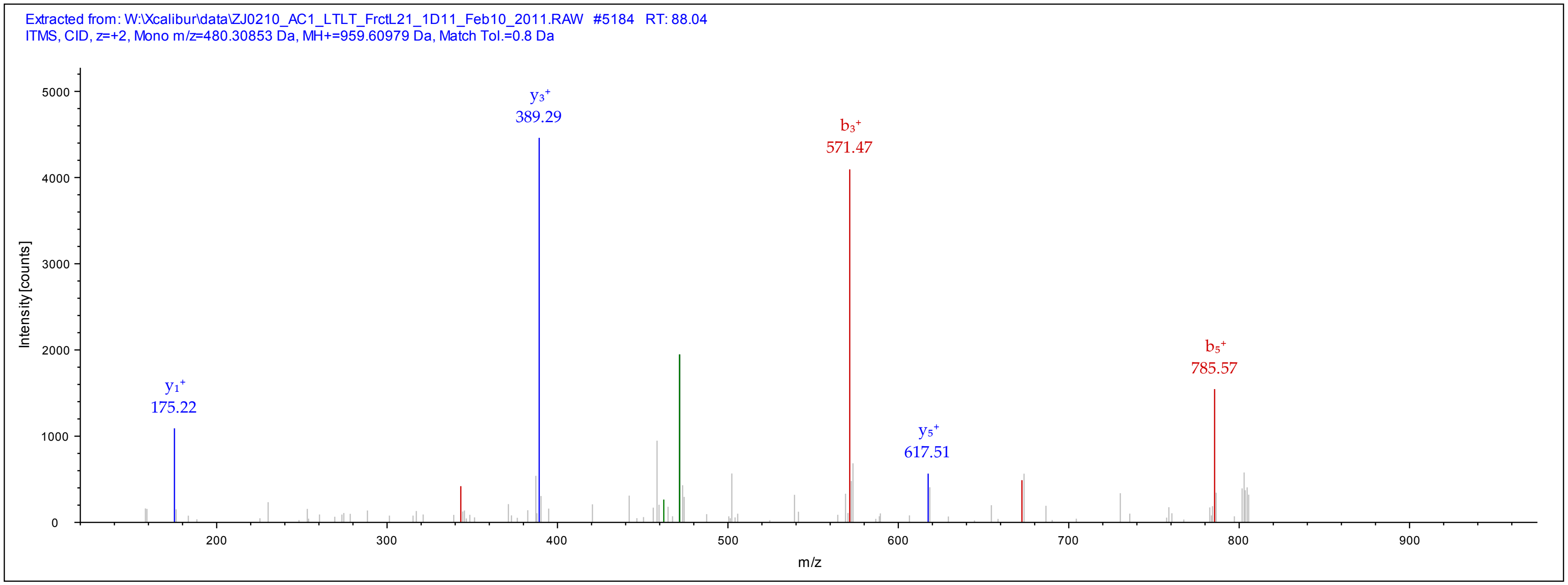
Identified with: Mascot (v1.16); IonScore:34, Exp Value:1.9E-002, Ions matched by search engine: 4/44

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- cDNA FLJ41377 fis, clone BRCAN2008528 lng=306



IPI:IPI00449669.2

Sequence: GTEDFIVESLDASFR, G1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 957.98572 Da (-0.28 mmu/-0.29 ppm), MH+: 1914.96416 Da, RT: 169.05 min,

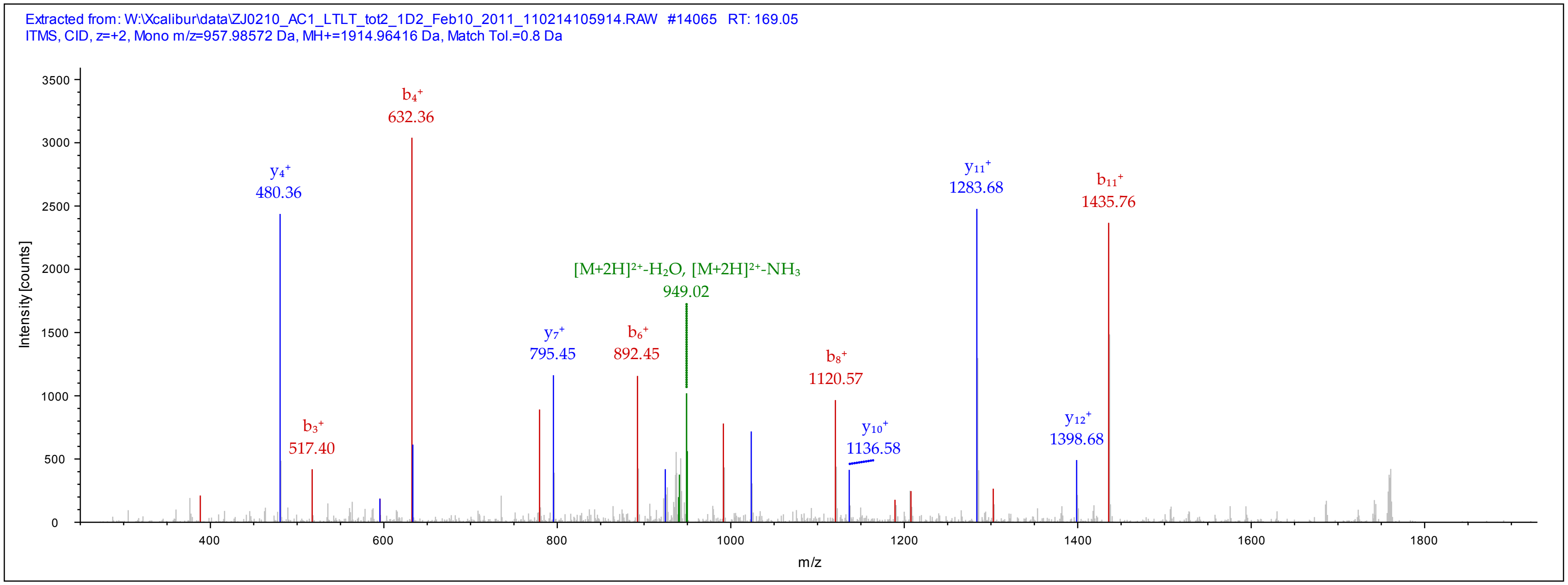
Identified with: Mascot (v1.16); IonScore:62, Exp Value:9.0E-005, Ions matched by search engine: 21/134

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform 1 of Translocon-associated protein subunit alpha
- Isoform 2 of Translocon-associated protein subunit alpha
- Uncharacterized protein
- Uncharacterized protein
- Uncharacterized protein
- cDNA, FLJ93042, highly similar to Homo sapiens signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA



IPI:IPI00456683.1

Sequence: VWQWDEK, V1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 724.90063 Da (+0.06 mmu/+0.09 ppm),   MH+: 1448.79399 Da,   RT: 102.08 min,

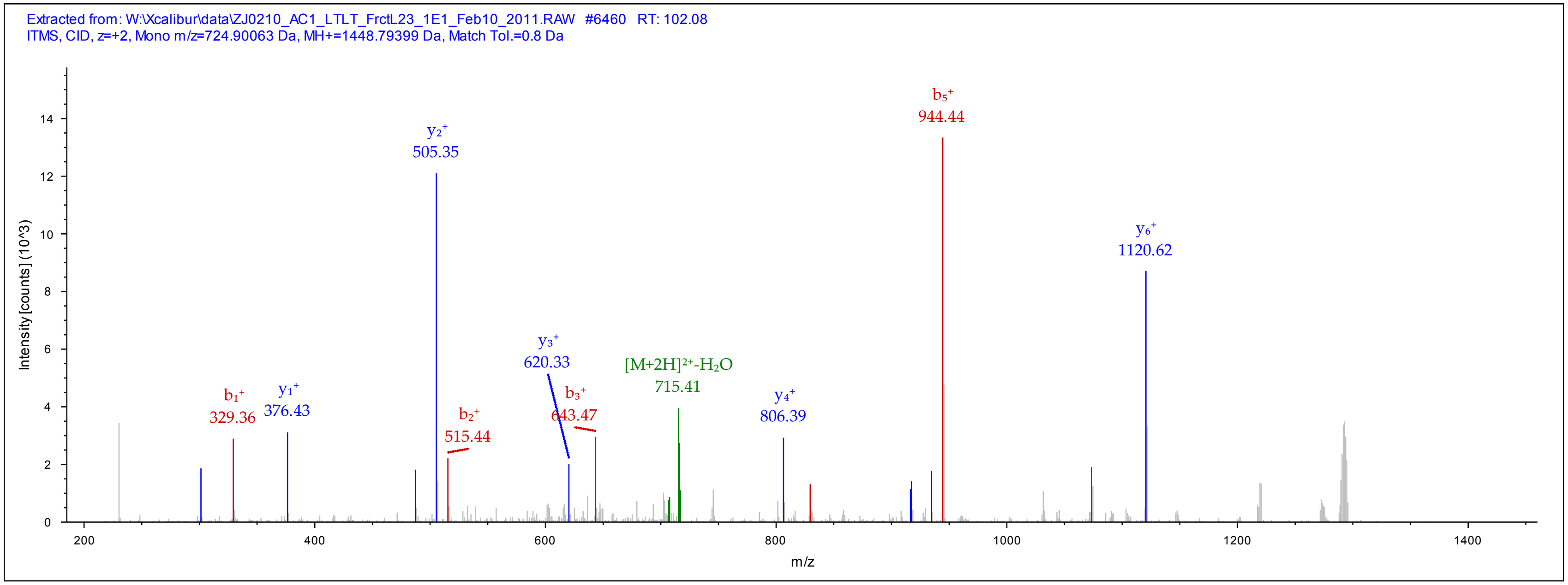
Identified with: Mascot (v1.16); IonScore:33, Exp Value:5.3E-002, Ions matched by search engine: 6/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Transcription elongation factor SPT6
- Isoform 3 of Transcription elongation factor SPT6



IPI00844008.1

Sequence: DQLLAAIR, D1-TMT6plex (229.16293 Da)

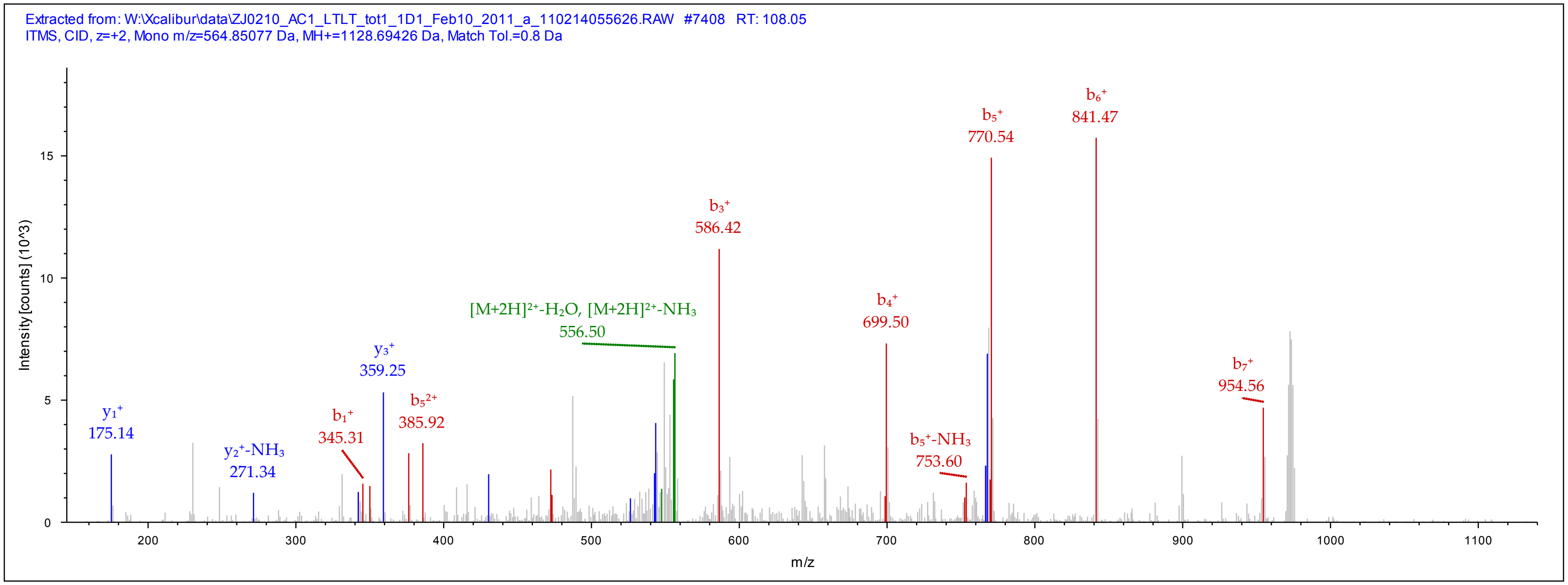
Charge: +2, Monoisotopic m/z: 564.85077 Da (+0.19 mmu/+0.34 ppm), MH+: 1128.69426 Da, RT: 108.05 min,

Identified with: Mascot (v1.16); IonScore:30, Exp Value:5.2E-002, Ions matched by search engine: 6/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):
- Isoform 1 of Leiomodin-1
- LMOD1 protein lng=269
- leiomodin-1
- cDNA FLJ44510 fis, clone UTERU3001652, highly similar to Leiomodin-1 lng=491
- cDNA FLJ53443, highly similar to Leiomodin-1 lng=549
- cDNA FLJ54257, highly similar to Leiomodin-1 lng=507



IPI:IPI00472951.1

Sequence: SLLQILR, S1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 536.35785 Da (-0.18 mmu/-0.34 ppm), MH+: 1071.70842 Da, RT: 111.07 min,

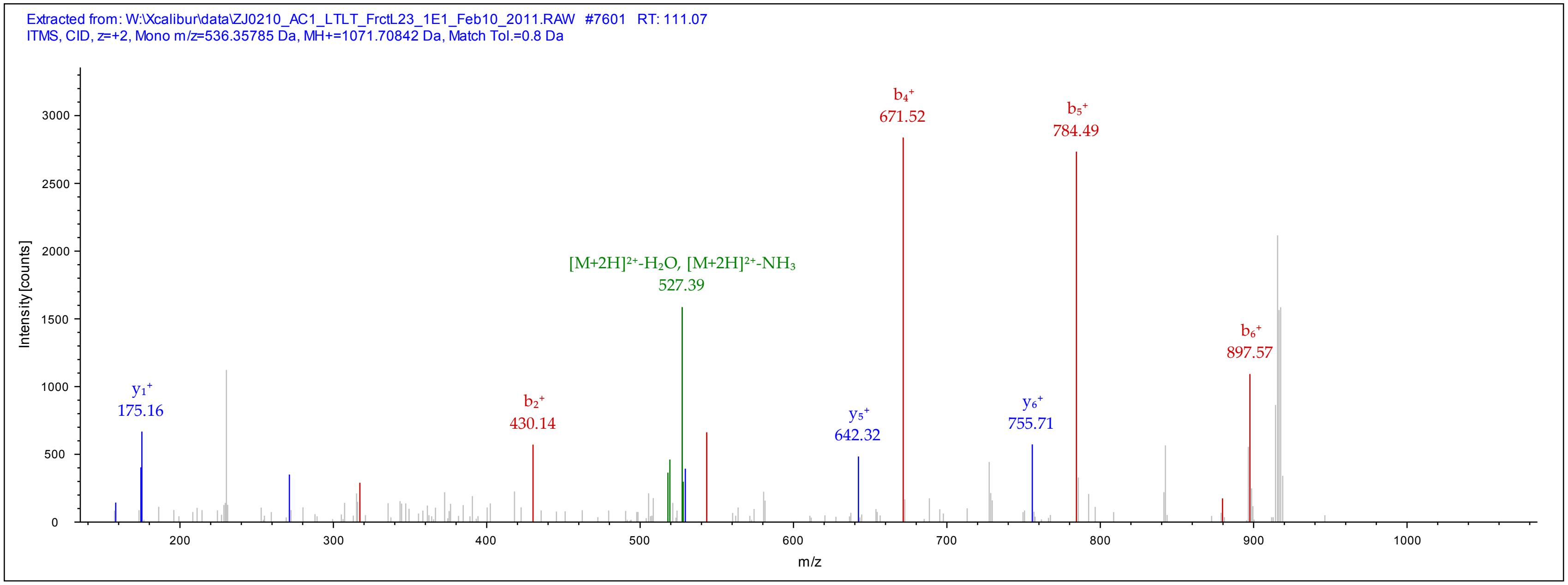
Identified with: Mascot (v1.16); IonScore:31, Exp Value:2.6E-002, Ions matched by search engine: 5/54

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Low-density lipoprotein receptor-related protein 10
- Isoform 2 of Low-density lipoprotein receptor-related protein 10



IPI:IPI00478723.3

Sequence: GSILSFLR, G1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 561.34790 Da (+0.24 mmu/+0.42 ppm),   MH+: 1121.68852 Da,   RT: 122.09 min,

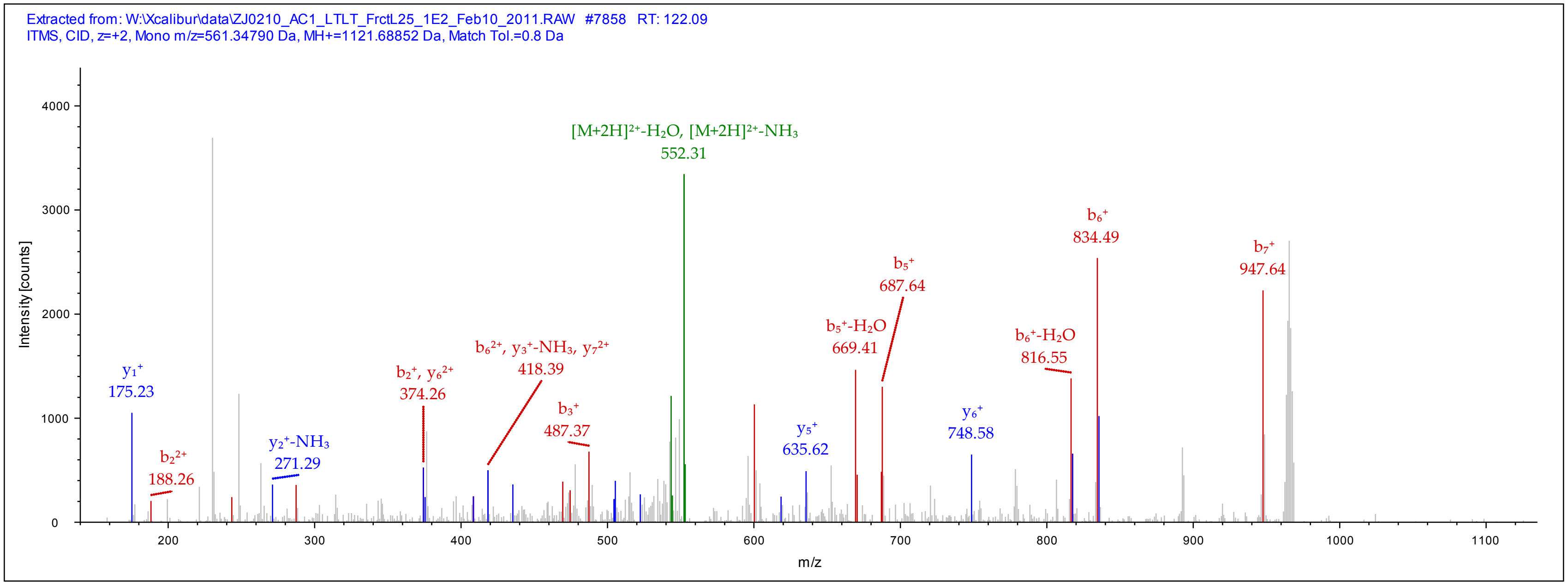
Identified with: Mascot (v1.16); IonScore:29, Exp Value:6.3E-002, Ions matched by search engine: 6/62

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- nardilysin isoform a
- nardilysin isoform b
- Isoform 2 of Nardilysin lng=1218



IPI:IPI00479595.3

Sequence: FGMLPLDEPAILVSEFLDR, F1-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 797.76776 Da (+1.82 mmu/+2.29 ppm), MH+: 2391.28873 Da, RT: 241.15 min,

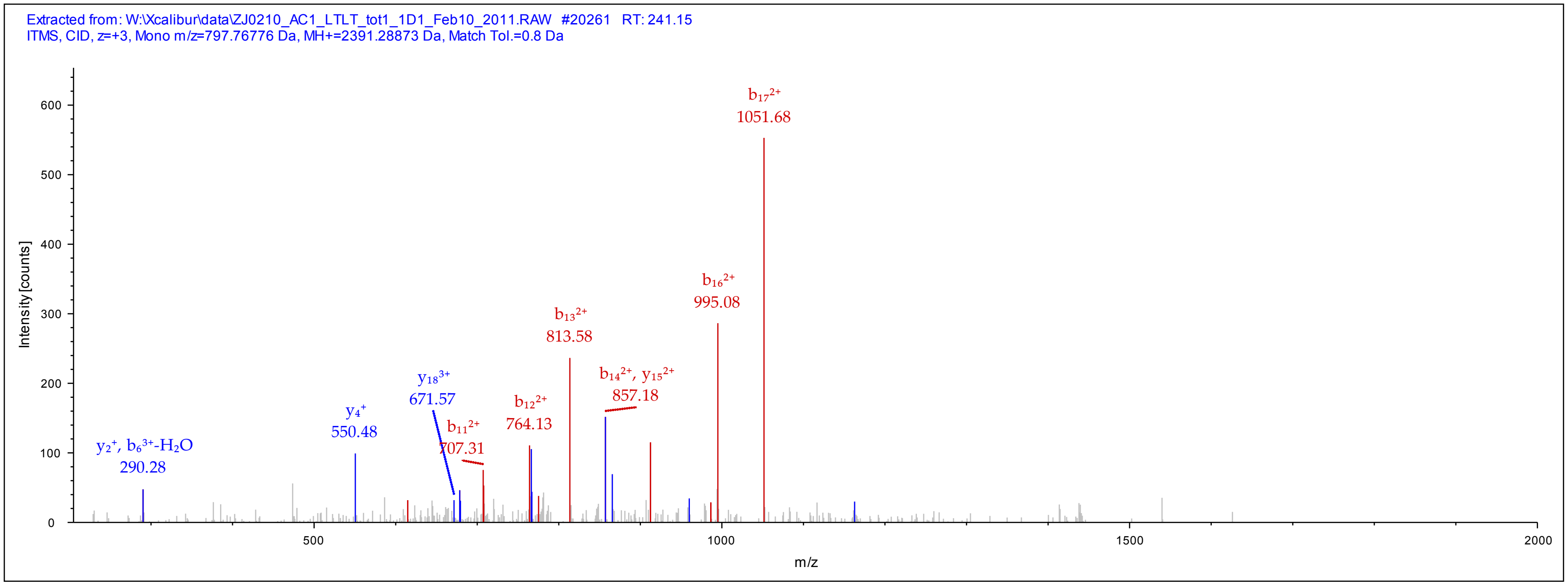
Identified with: Mascot (v1.16); IonScore:32, Exp Value:8.4E-002, Ions matched by search engine: 9/166

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of Nuclear-interacting partner of ALK
- Isoform 2 of Nuclear-interacting partner of ALK lng=481
- Isoform 3 of Nuclear-interacting partner of ALK
- Putative uncharacterized protein ZC3HC1 lng=459



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_tot1_1D1_Feb10_2011.RAW #20261 RT: 241.15
ITMS, CID, z=+3, Mono m/z=797.76776 Da, MH+=2391.28873 Da, Match Tol.=0.8 Da

IPI:IPI00479877.4

Sequence: ILLEAAR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 507.82935 Da (+0.24 mmu/+0.46 ppm), MH+: 1014.65141 Da, RT: 89.27 min,

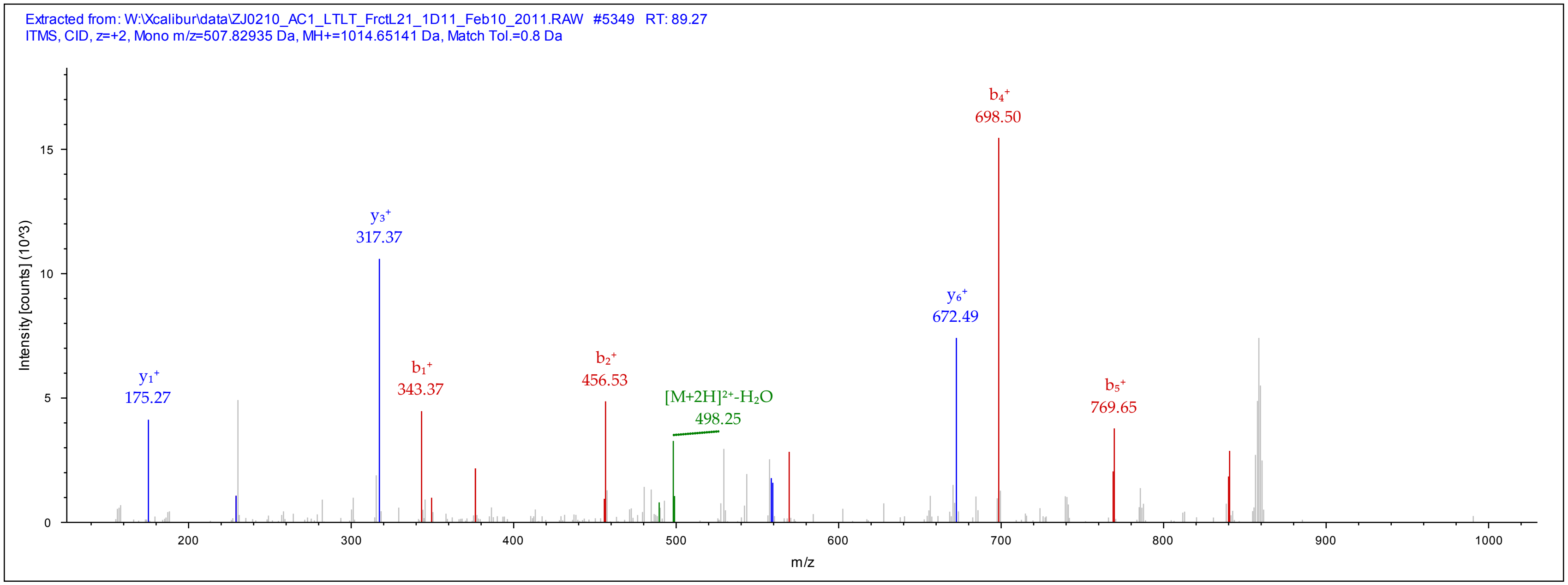
Identified with: Mascot (v1.16); IonScore:40, Exp Value:4.0E-003, Ions matched by search engine: 6/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 4-trimethylaminobutyraldehyde dehydrogenase



IPI:IPI00513721.2

Sequence: IQEEER, I1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 516.78192 Da (+2.11 mmu/+4.09 ppm),   MH+: 1032.55657 Da,   RT: 65.60 min,

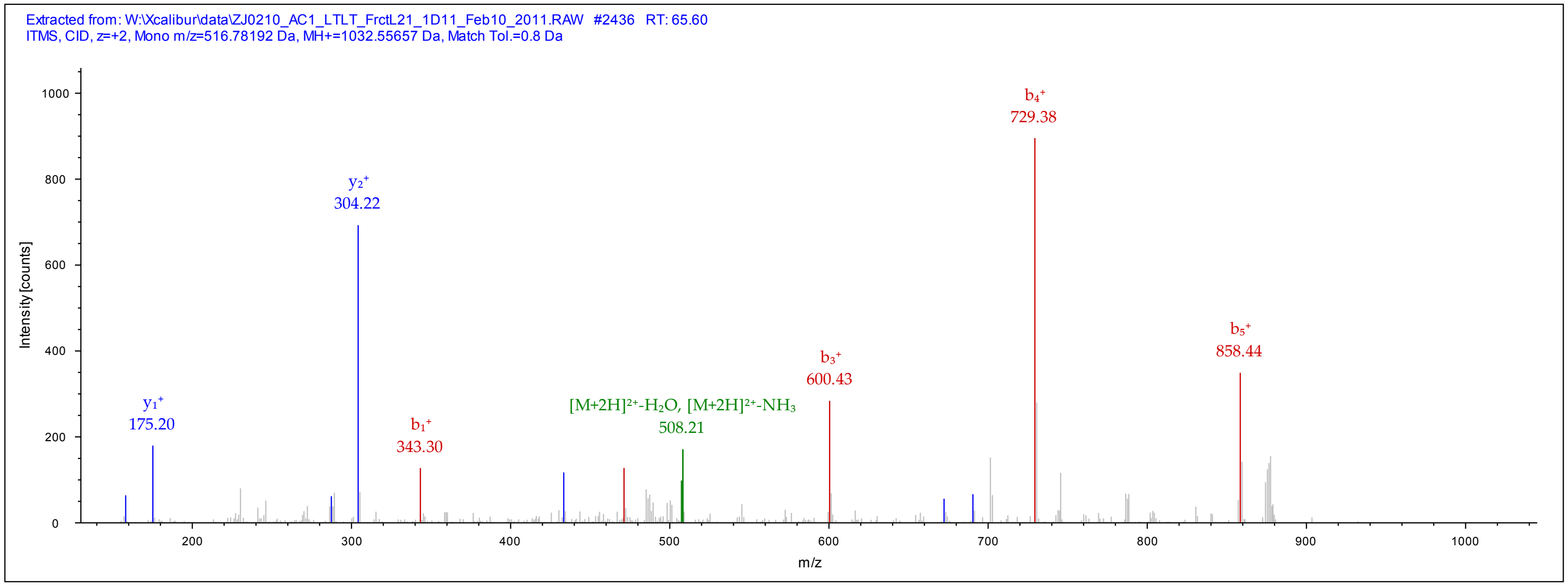
Identified with: Mascot (v1.16); IonScore:30, Exp Value:7.3E-002, Ions matched by search engine: 5/52

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Putative uncharacterized protein ITSN2
- Isoform 2 of Intersectin-2
- Isoform 1 of Intersectin-2
- Protein
- Isoform 3 of Intersectin-2
- Isoform 4 of Intersectin-2
- Putative uncharacterized protein ITSN2



IPI00513782.3

Sequence: QTQVSVLPEGGETPLFK, Q1-TMT6plex (229.16293 Da), K17-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 763.43927 Da (+4.32 mmu/+5.66 ppm), MH+: 2288.30326 Da, RT: 115.43 min,

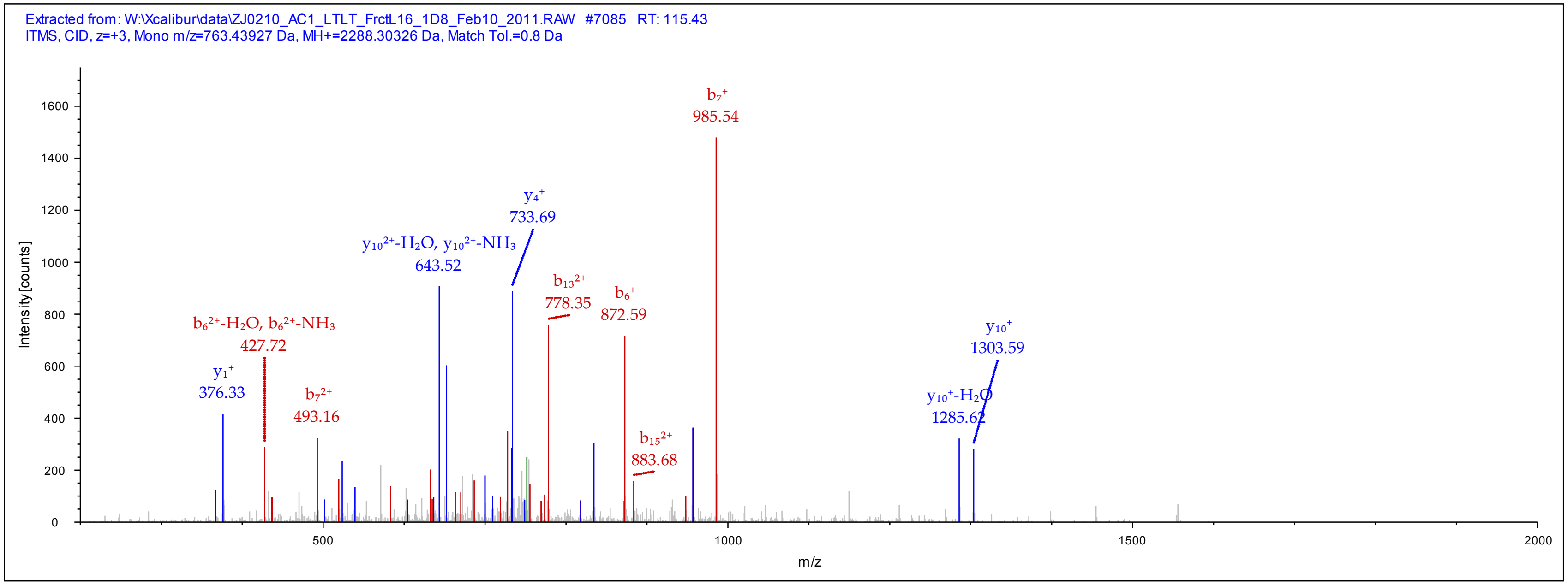
Identified with: Mascot (v1.16); IonScore:42, Exp Value:6.3E-003, Ions matched by search engine: 12/182

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of Gelsolin
- cDNA FLJ35478 fis, clone SMINT2007796, highly similar to Gelsolin lng=485
- Isoform 2 of Gelsolin
- gelsolin isoform c
- cDNA FLJ53327, highly similar to Gelsolin lng=705



IPI00515040.1

Sequence: LLLPLFR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 550.87488 Da (+1.56 mmu/+2.83 ppm),   MH+: 1100.74248 Da,   RT: 137.20 min,

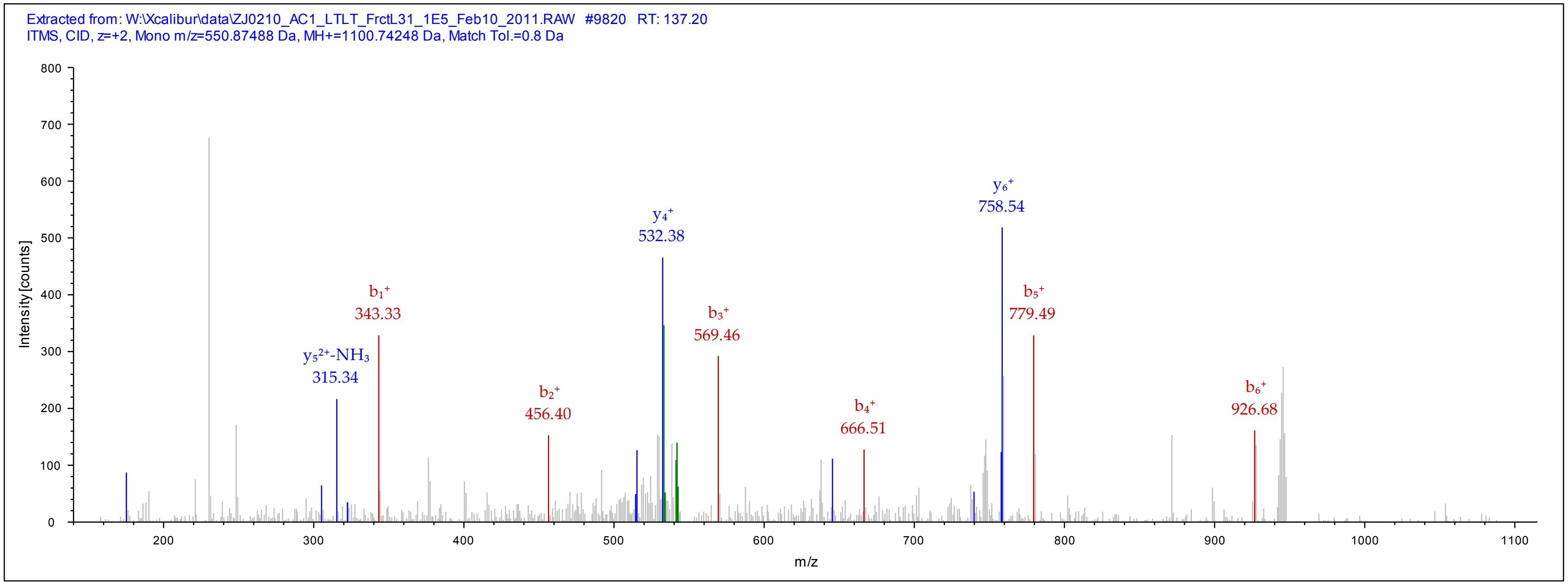
Identified with: Mascot (v1.16); IonScore:30, Exp Value:7.9E-003, Ions matched by search engine: 6/50

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- cDNA FLJ51938 lng=145
- Protein of unknown function DUF858, methyltransferase-like family protein lng=224



IPI:IPI00152849.2

Sequence: TEEAAITK, T1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 660.89288 Da (+0.47 mmu/+0.72 ppm), MH+: 1320.77849 Da, RT: 116.34 min,

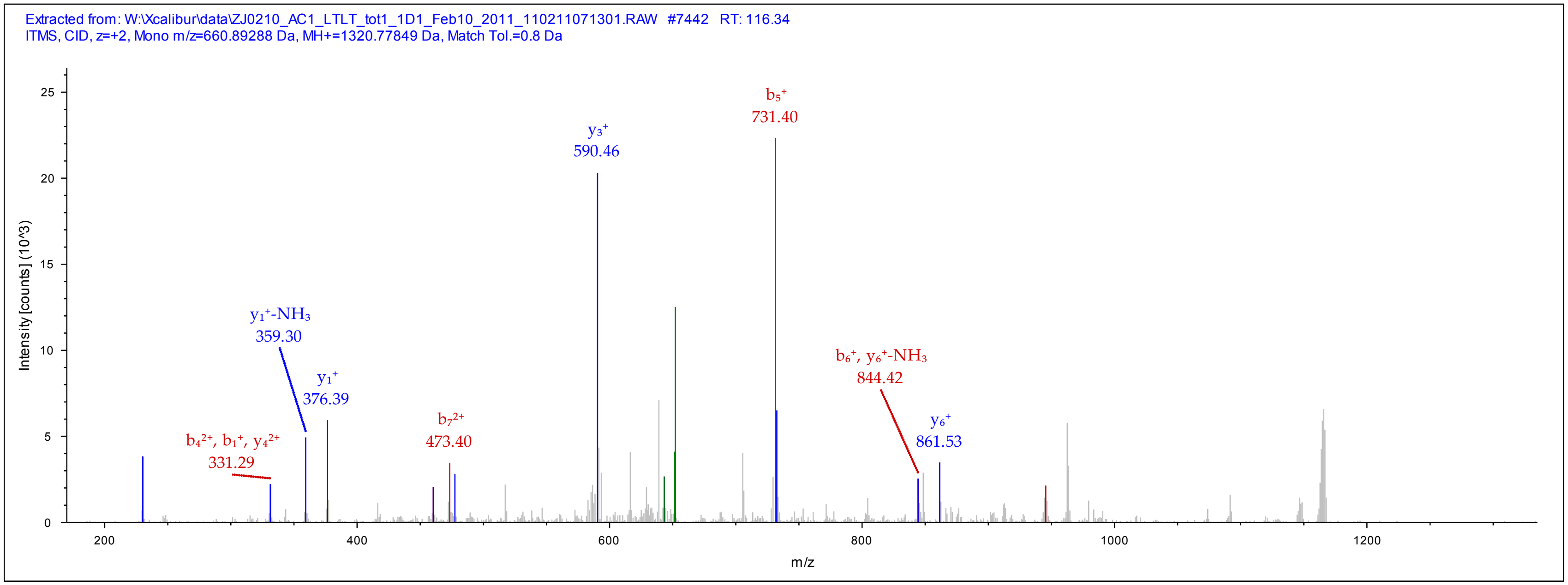
Identified with: Mascot (v1.16); IonScore:32, Exp Value:5.9E-002, Ions matched by search engine: 6/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Isoform 1 of G2/mitotic-specific cyclin-B3



IPI:IPI00552206.1

Sequence: LISVLK, L1-TMT6plex (229.16293 Da), K6-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 565.89960 Da (+0.29 mmu/+0.52 ppm), MH+: 1130.79192 Da, RT: 109.63 min,

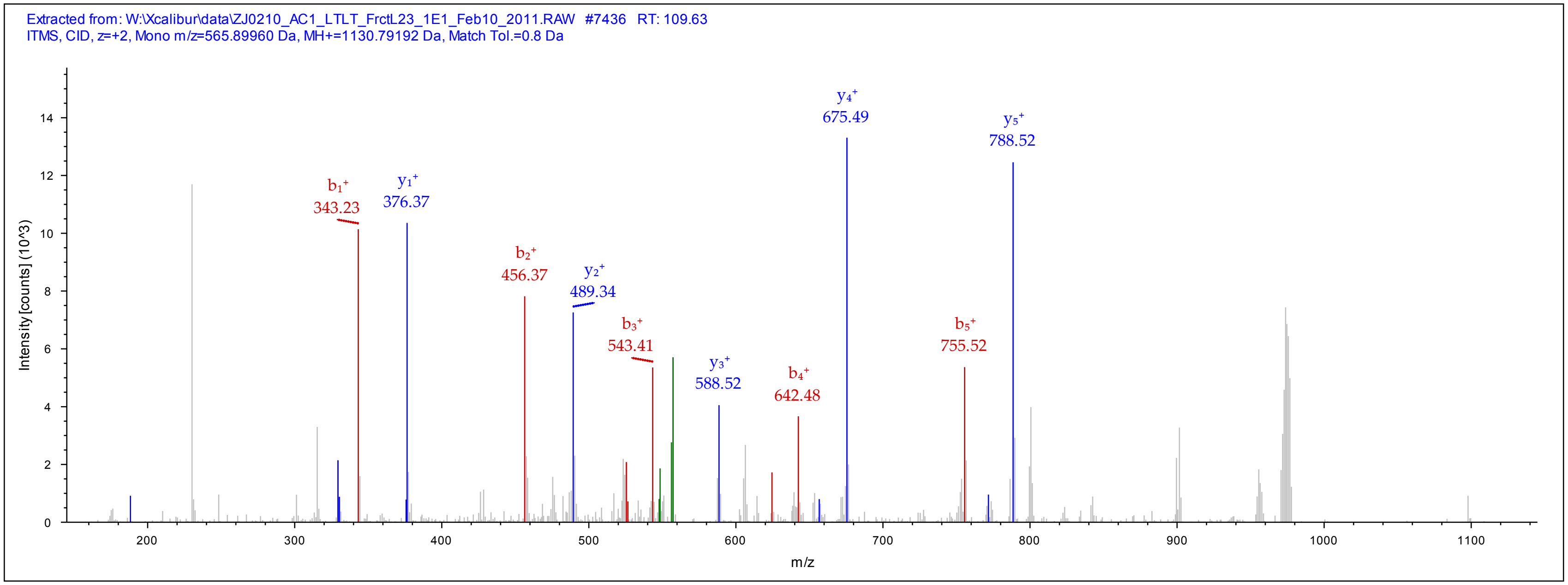
Identified with: Mascot (v1.16); IonScore:31, Exp Value:1.4E-002, Ions matched by search engine: 5/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of TATA box-binding protein-associated factor RNA polymerase I subunit A
- Isoform 2 of TATA box-binding protein-associated factor RNA polymerase I subunit A
- TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa



IPI00552255.1

Sequence: LMDPLK, L1-TMT6plex (229.16293 Da), M2-Oxidation (15.99492 Da), K6-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 595.87354 Da (+8.93 mmu/+14.99 ppm), MH+: 1190.73979 Da, RT: 82.11 min,

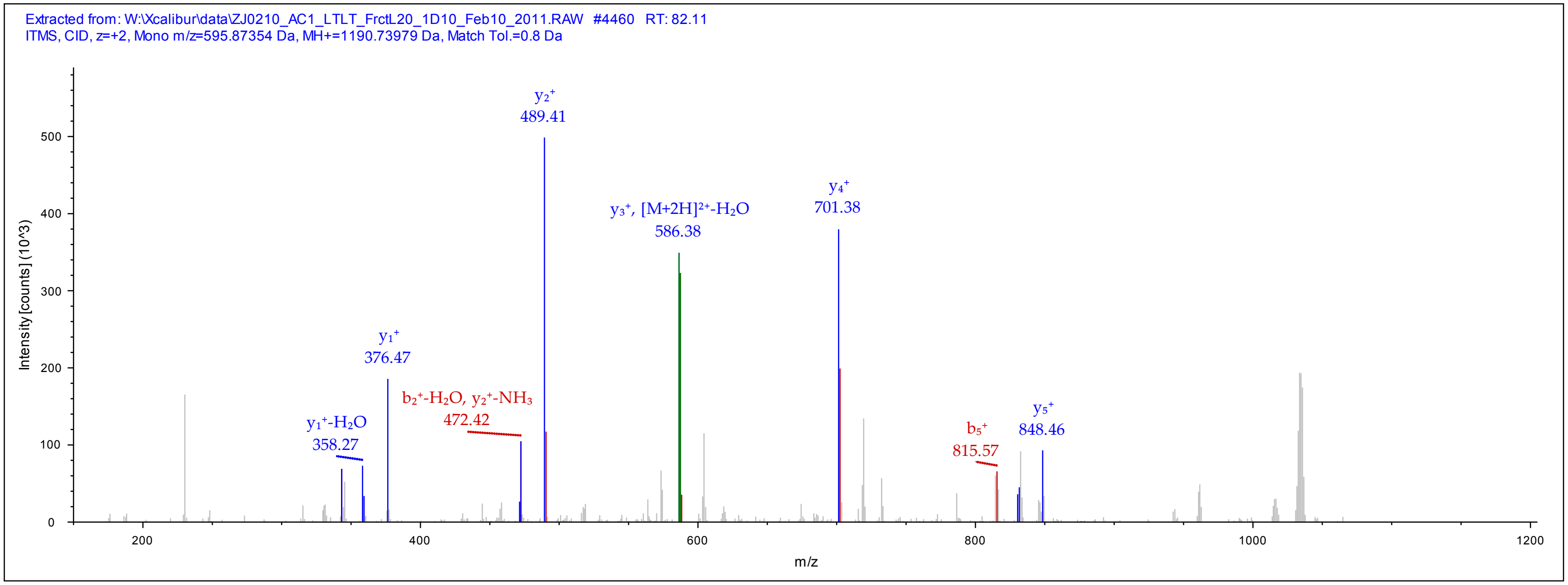
Identified with: Mascot (v1.16); IonScore:34, Exp Value:3.4E-002, Ions matched by search engine: 5/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Tubulin tyrosine ligase-like family, member 11 lng=451
- tubulin tyrosine ligase-like family, member 11 a lng=800



IPI:IPI00552588.1

Sequence: LYLAVLSDR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 639.88464 Da (+0.03 mmu/+0.05 ppm),   MH+: 1278.76201 Da,   RT: 117.69 min,

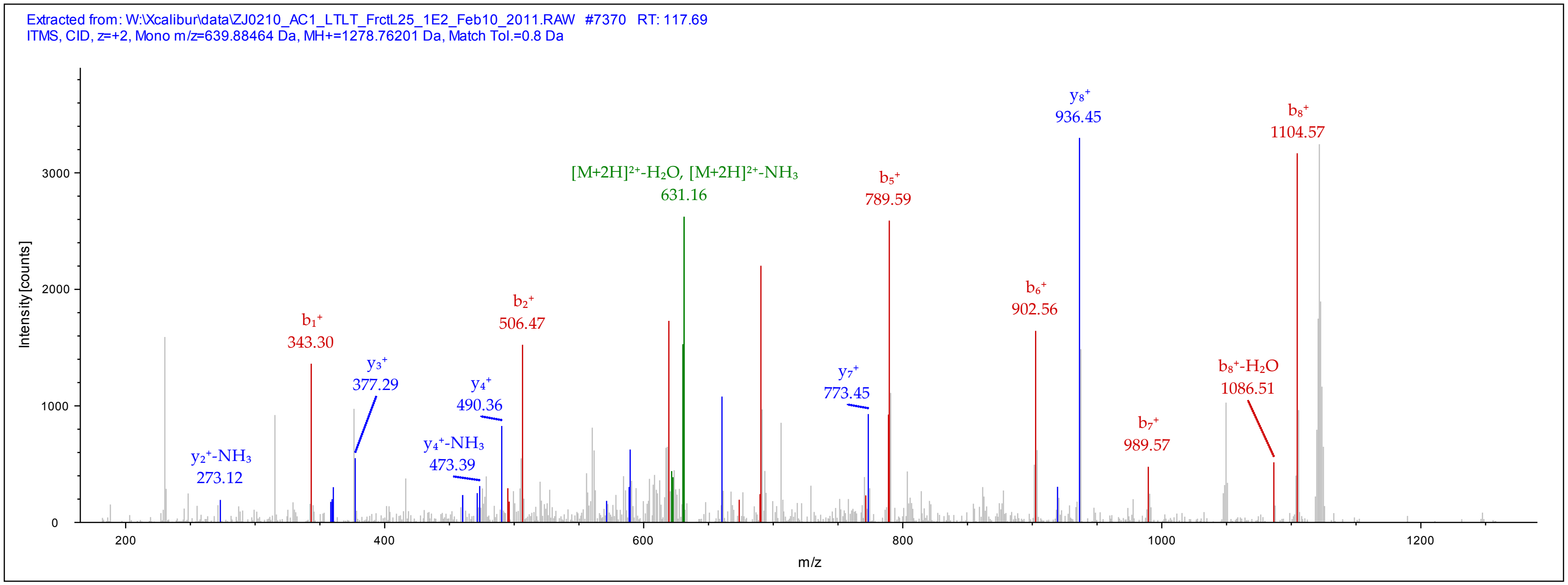
Identified with: Mascot (v1.16); IonScore:50, Exp Value:6.5E-004, Ions matched by search engine: 8/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of F-box/LRR-repeat protein 18
- Isoform 2 of F-box/LRR-repeat protein 18
- Isoform 4 of F-box/LRR-repeat protein 18
- Isoform 3 of F-box/LRR-repeat protein 18



IPI:IPI00552934.2

Sequence: IGALGVK, I1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 558.38110 Da (-0.18 mmu/-0.33 ppm),   MH+: 1115.75493 Da,   RT: 88.77 min,

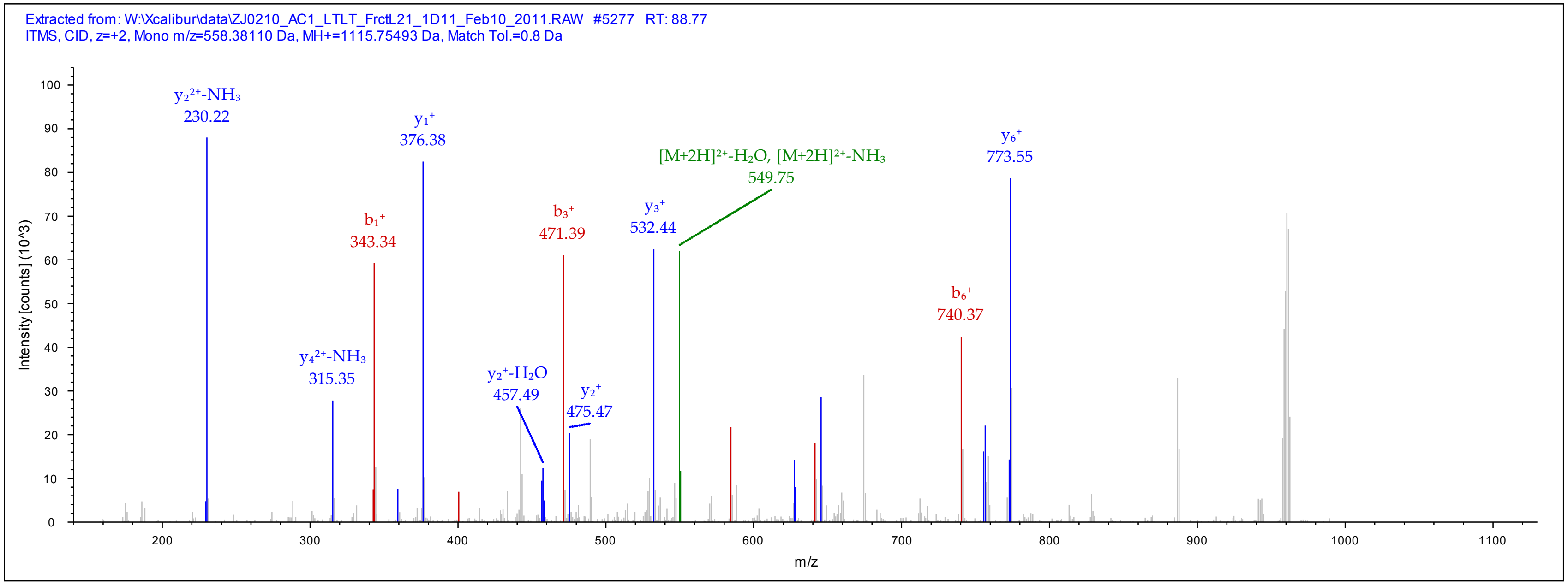
Identified with: Mascot (v1.16); IonScore:30, Exp Value:4.2E-002, Ions matched by search engine: 4/50

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Uncharacterized protein KIAA1755
- Novel protein



IPI:IPI00554618.2

Sequence: VAYLDPLELSEGK, V1-TMT6plex (229.16293 Da), K13-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 946.54279 Da (+0.06 mmu/+0.07 ppm), MH+: 1892.07829 Da, RT: 121.03 min,

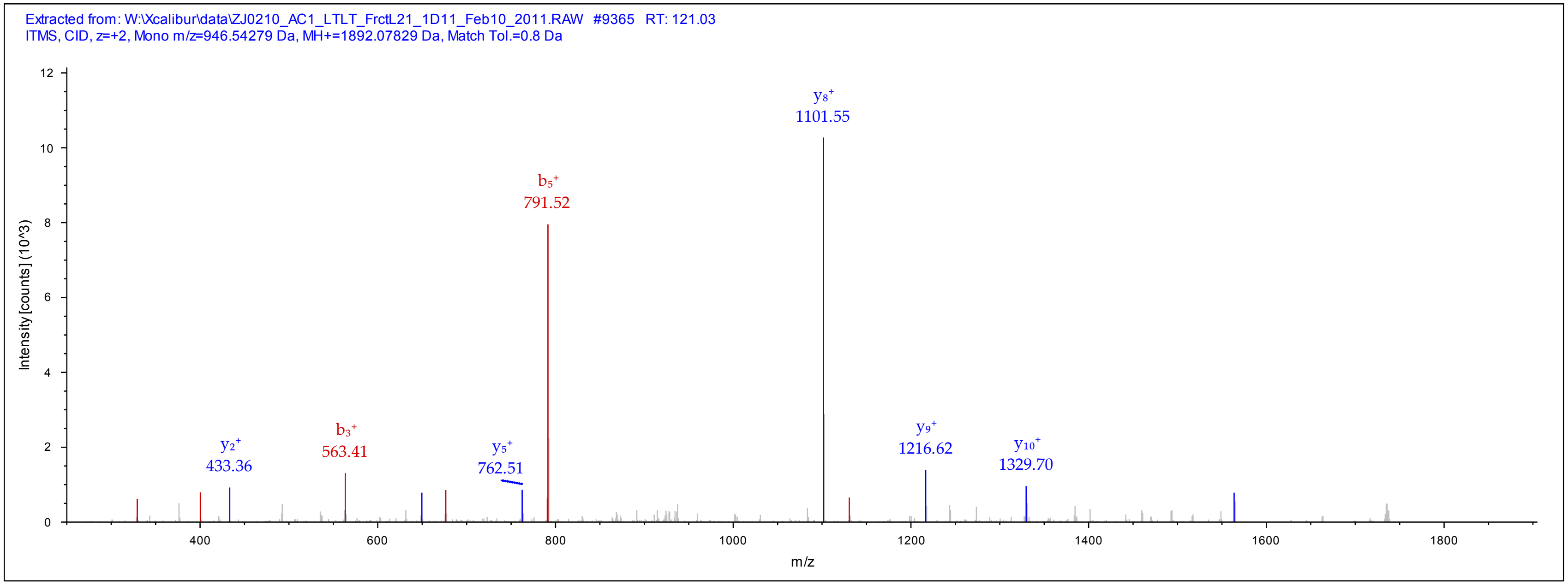
Identified with: Mascot (v1.16); IonScore:66, Exp Value:2.8E-005, Ions matched by search engine: 12/108

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Basal cell adhesion molecule
- basal cell adhesion molecule isoform 2 precursor



IPI:IPI00737652.7

Sequence: VQLLQDLQDFFR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 875.98944 Da (+1.3 mmu/+1.49 ppm), MH+: 1750.97161 Da, RT: 207.94 min,

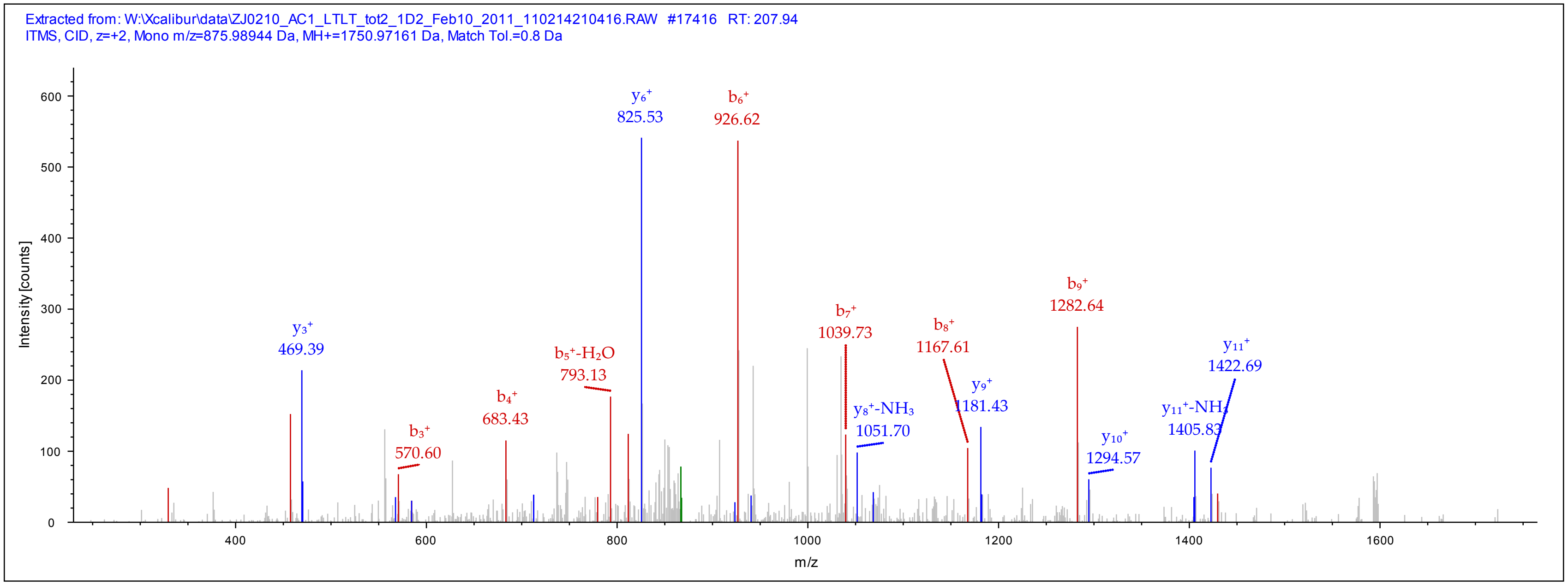
Identified with: Mascot (v1.16); IonScore:38, Exp Value:2.0E-002, Ions matched by search engine: 9/114

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Isoform 1 of SLIT-ROBO Rho GTPase-activating protein 1
- SLIT-ROBO Rho GTPase-activating protein 2
- Isoform 2 of SLIT-ROBO Rho GTPase-activating protein 1 lng=1062
- Novel protein similar to SLIT-ROBO Rho GTPase activating protein 2 SRGAP2
- SLIT-ROBO Rho GTPase-activating protein 2 isoform b
- 62 kDa protein lng=519



IPI:IPI00555553.1

Sequence: TPVTQVNEVTGTLR, T1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 872.49487 Da (+1.09 mmu/+1.25 ppm), MH+: 1743.98247 Da, RT: 98.08 min,

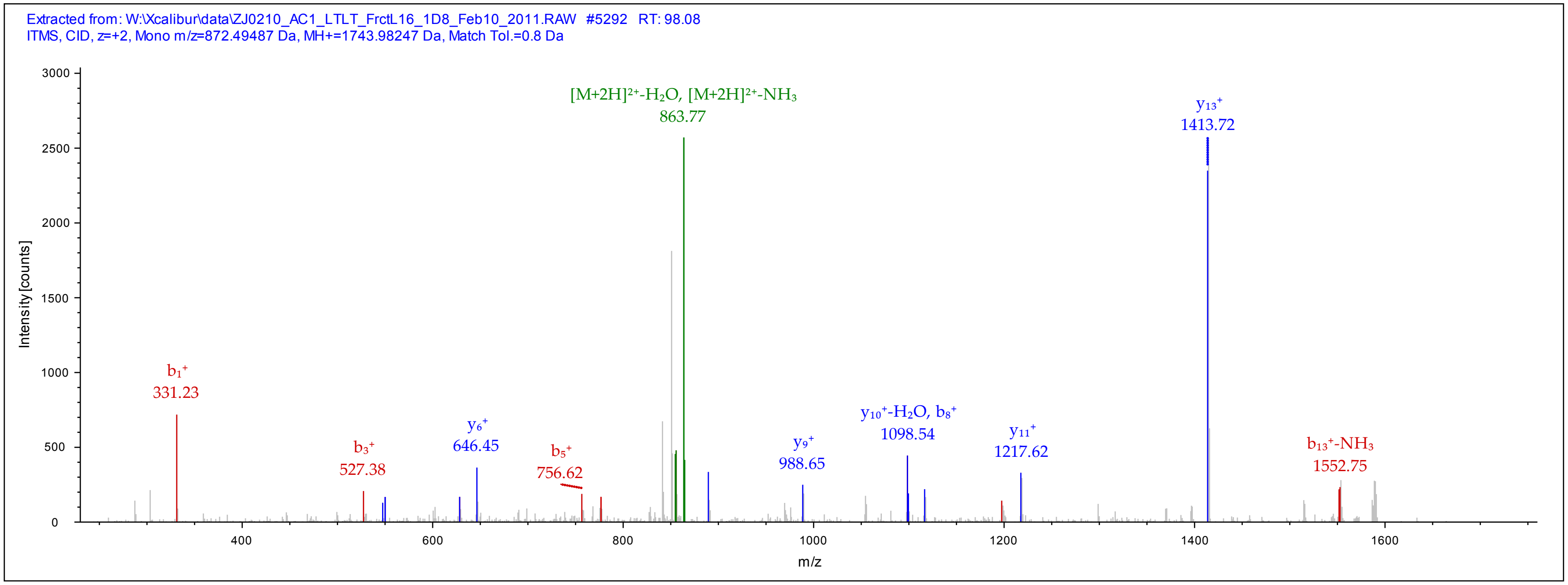
Identified with: Mascot (v1.16); IonScore:47, Exp Value:2.3E-003, Ions matched by search engine: 17/144

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

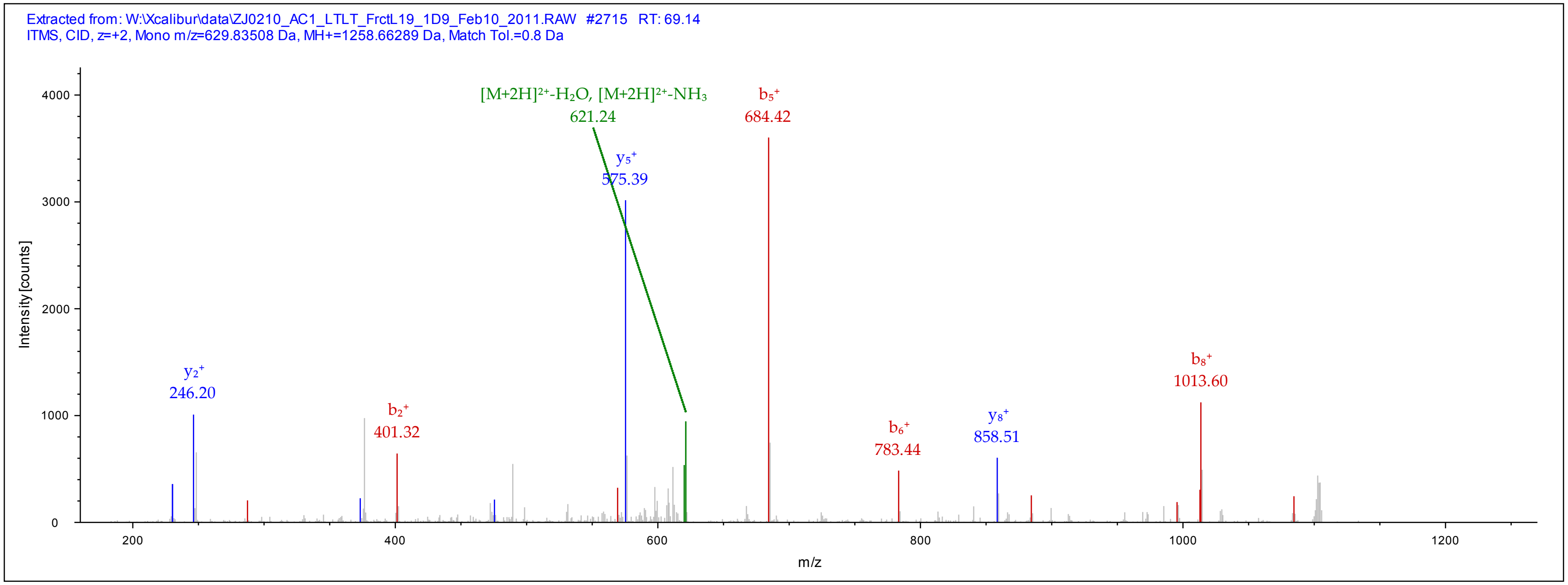
Protein references (2):

- 39S ribosomal protein L49, mitochondrial
- Mitochondrial ribosomal protein L49 variant (Fragment)



IPI:IPI00556105.1
Sequence: GNPADVTEAR, G1-TMT6plex (229.16293 Da)
Charge: +2, Monoisotopic m/z: 629.83508 Da (+1.97 mmu/+3.13 ppm), MH+: 1258.66289 Da, RT: 69.14 min,
Identified with: Mascot (v1.16); IonScore:47, Exp Value:1.6E-003, Ions matched by search engine: 8/94
Fragment match tolerance used for search: 0.8 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):
- Isoform 1 of Lipid phosphate phosphohydrolase 2
- Isoform 2 of Lipid phosphate phosphohydrolase 2
- lipid phosphate phosphohydrolase 2 isoform 2
- Phosphatidic acid phosphatase type 2C isoform 3 variant (Fragment)



IPI:IPI00556252.2

Sequence: WLEVLEK, W1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 687.92590 Da (+2.39 mmu/+3.47 ppm),   MH+: 1374.84453 Da,   RT: 125.64 min,

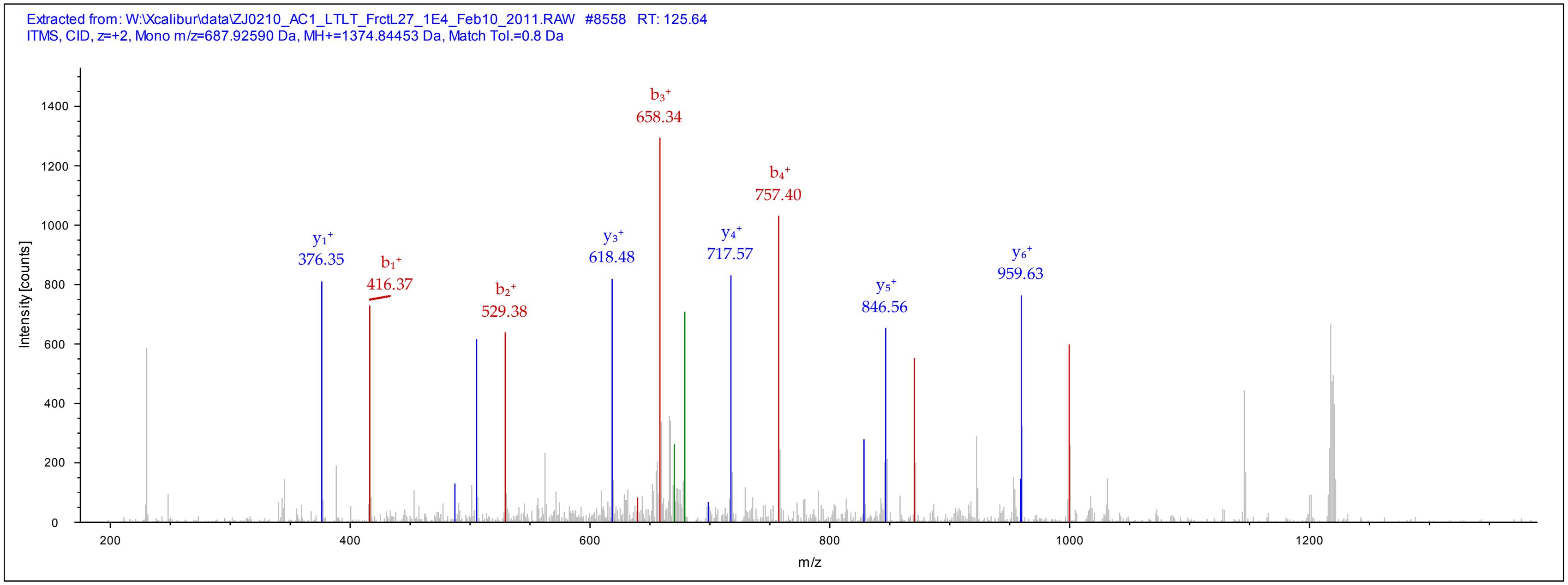
Identified with: Mascot (v1.16); IonScore:34, Exp Value:2.5E-002, Ions matched by search engine: 12/54

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Golgi-associated PDZ and coiled-coil motif-containing protein
- Isoform 3 of Golgi-associated PDZ and coiled-coil motif-containing protein
- Isoform 2 of Golgi-associated PDZ and coiled-coil motif-containing protein



IPI00917915.1

Sequence: ISFEEFCAVVGGLDIHK, I1-TMT6plex (229.16293 Da), C7-Carbamidomethyl (57.02146 Da), K17-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 793.76556 Da (+1.26 mmu/+1.58 ppm),   MH+: 2379.28214 Da,   RT: 182.99 min,

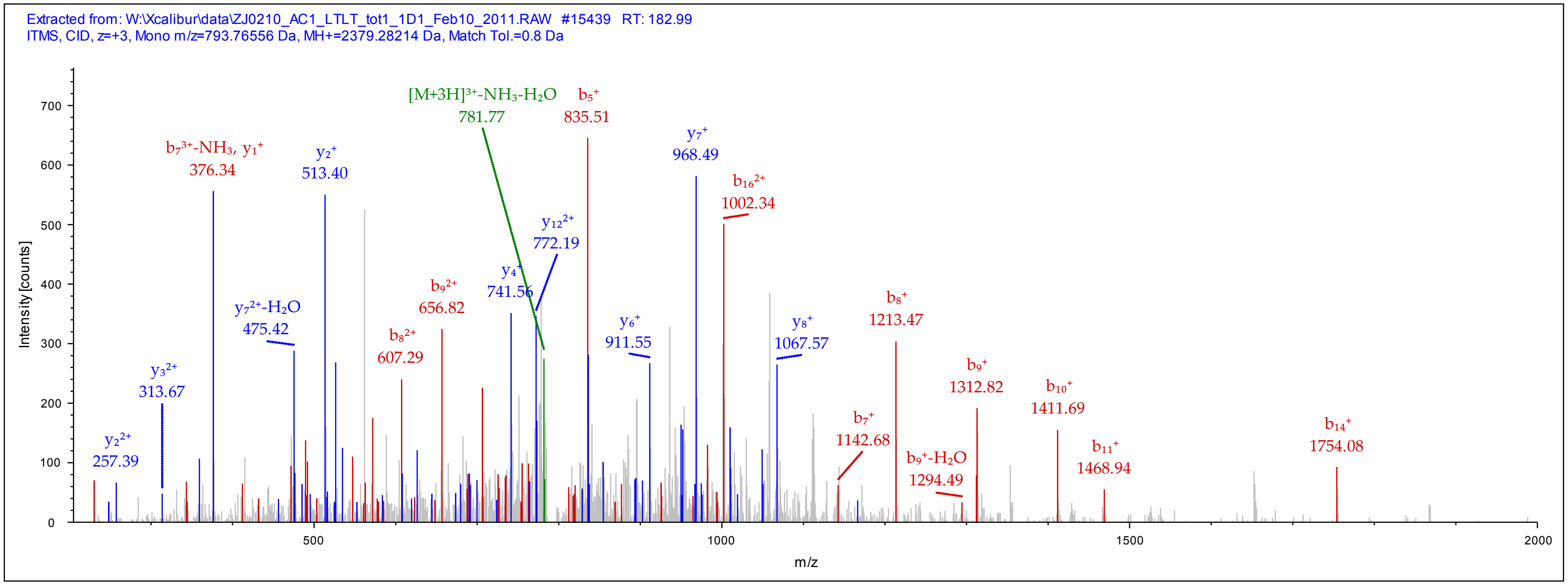
Identified with: Mascot (v1.16); IonScore:43, Exp Value:7.6E-003, Ions matched by search engine: 9/152

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Calcineurin subunit B type 1
- 18 kDa protein lng=160
- 21 kDa protein lng=189



IPI:IPI00607625.1

Sequence: VIQELGLDK, V1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 736.95789 Da (-0.21 mmu/-0.28 ppm), MH+: 1472.90849 Da, RT: 107.30 min,

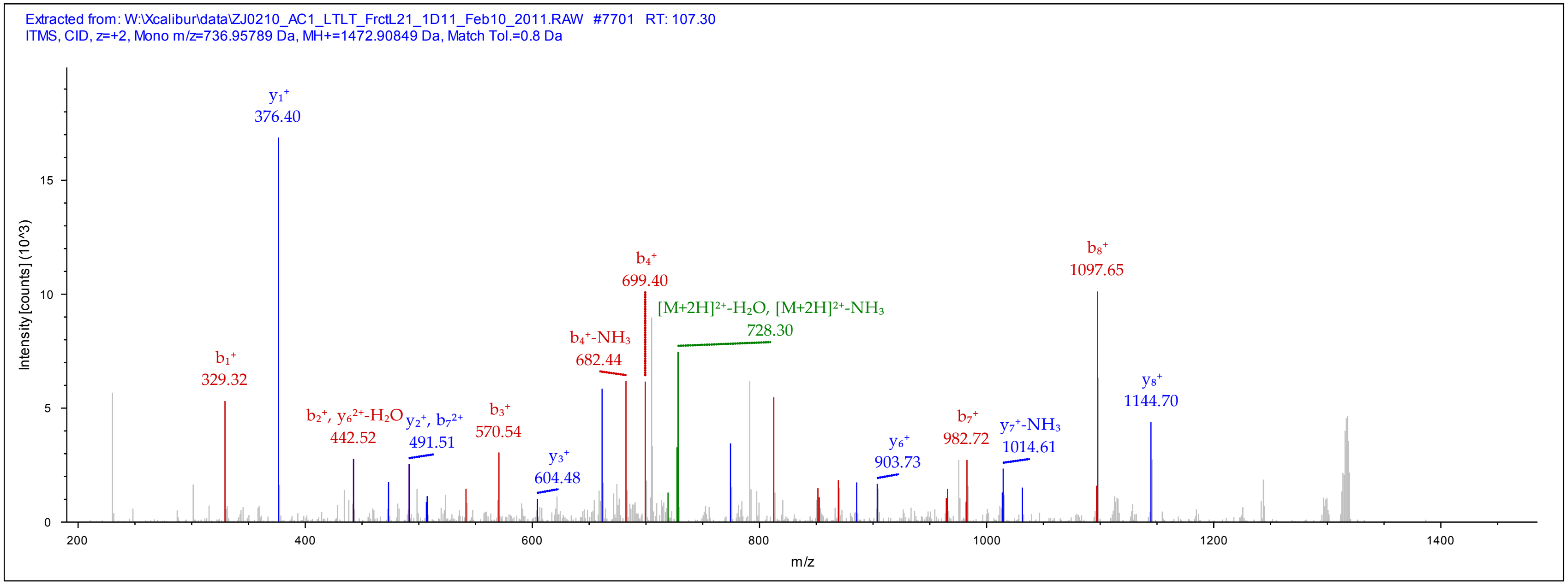
Identified with: Mascot (v1.16); IonScore:42, Exp Value:4.6E-003, Ions matched by search engine: 8/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of ATP-binding cassette sub-family G member 2
- Isoform 2 of ATP-binding cassette sub-family G member 2



IPI:IPI00306383.2

Sequence: TAAANAAAGAAENAFR, T1-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 569.29968 Da (+0.83 mmu/+1.46 ppm), MH+: 1705.88449 Da, RT: 92.46 min,

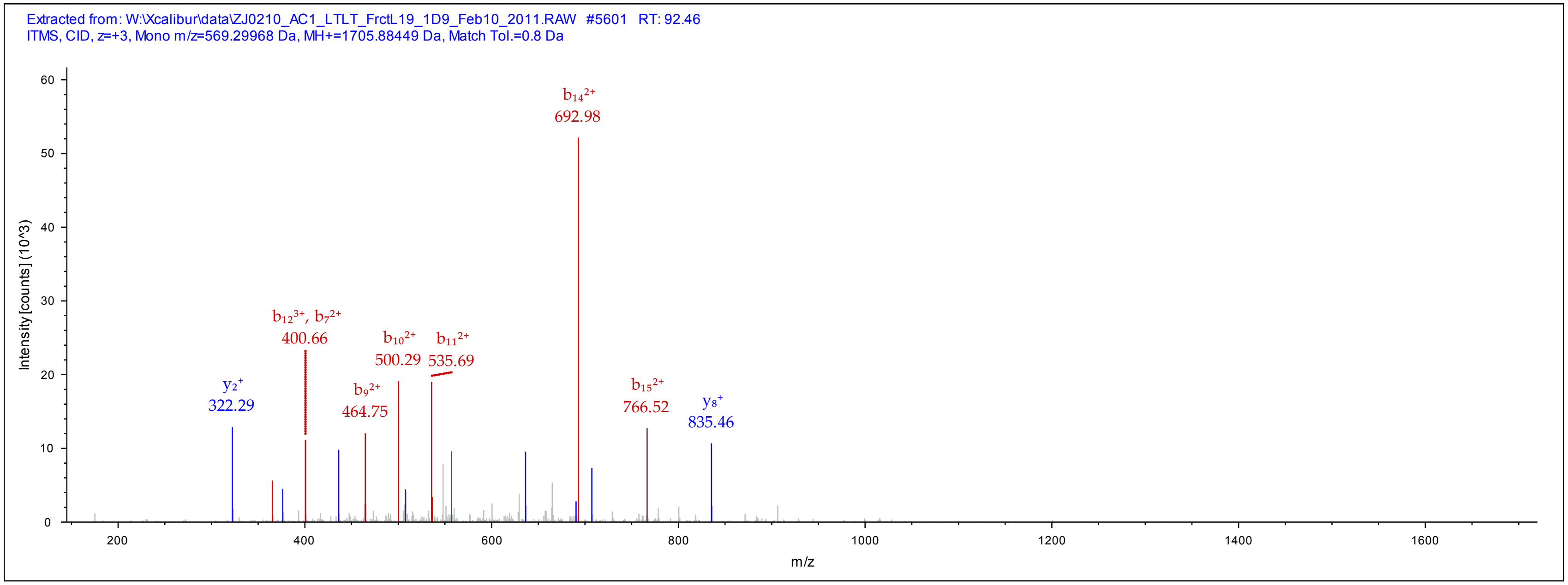
Identified with: Mascot (v1.16); IonScore:68, Exp Value:2.4E-005, Ions matched by search engine: 11/164

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Secretory carrier-associated membrane protein 3
- Isoform 2 of Secretory carrier-associated membrane protein 3



IPI00607714.1

Sequence: GFFWSTVPGAGR, G1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 755.90405 Da (+0.17 mmu/+0.23 ppm),   MH+: 1510.80083 Da,   RT: 112.65 min,

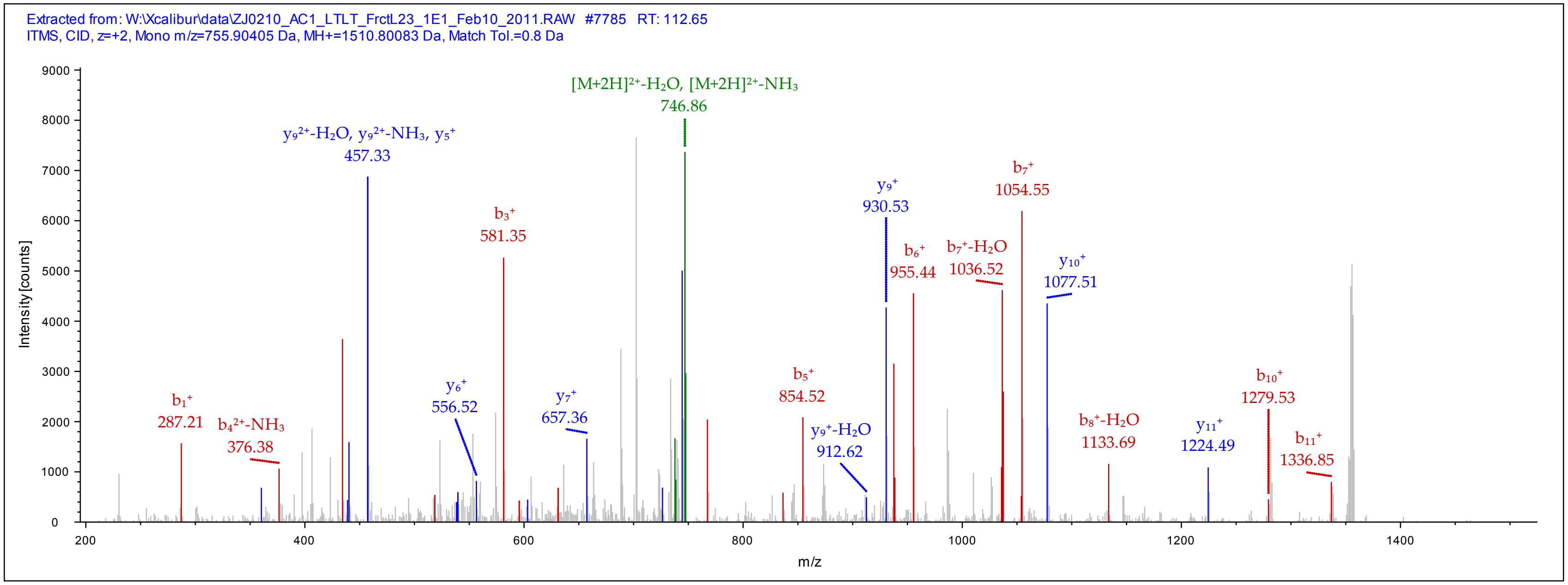
Identified with: Mascot (v1.16); IonScore:31, Exp Value:7.6E-002, Ions matched by search engine: 10/90

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of UPF0663 transmembrane protein C17orf28
- Isoform 2 of UPF0663 transmembrane protein C17orf28 lng=787



IPI:IPI00640188.1

Sequence: ALDDFVLGSAR, A1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 696.88733 Da (-0.57 mmu/-0.81 ppm),   MH+: 1392.76738 Da,   RT: 105.77 min,

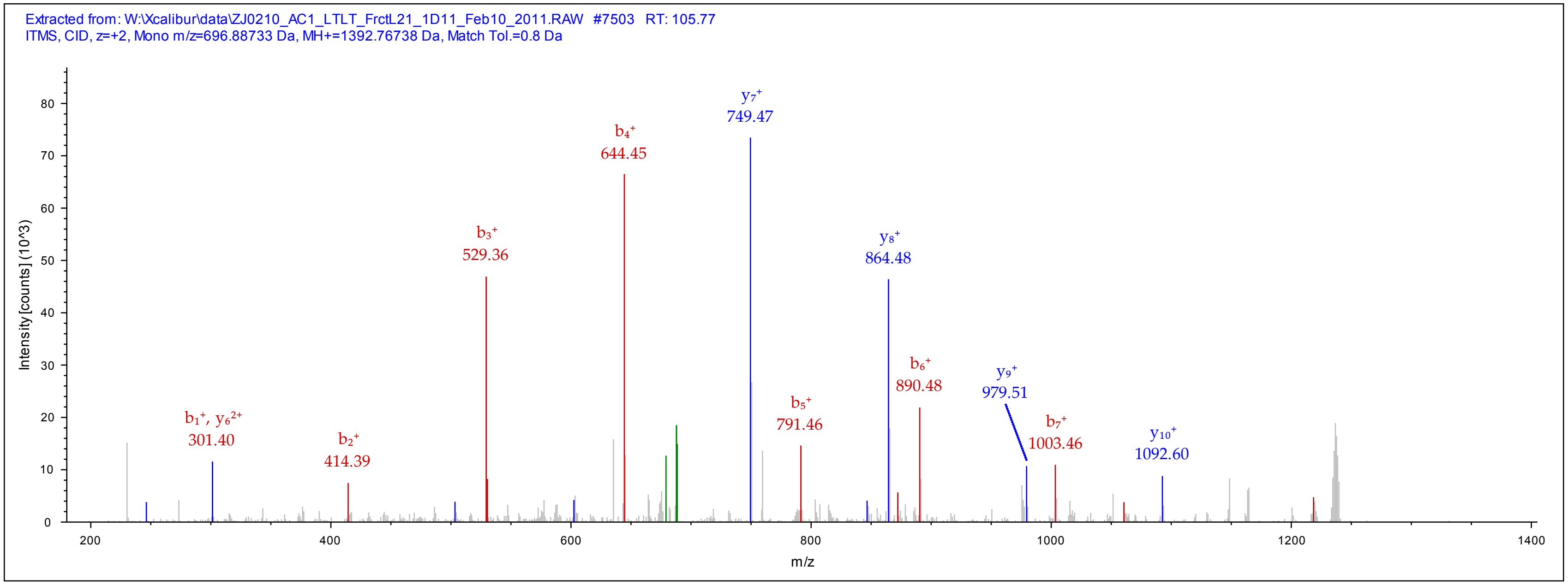
Identified with: Mascot (v1.16); IonScore:40, Exp Value:9.0E-003, Ions matched by search engine: 10/92

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- PRA1 family protein 2
- Uncharacterized protein



IPI00953423.1

Sequence: TLEEILLER, T1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 672.90009 Da (-0.38 mmu/-0.56 ppm), MH+: 1344.79289 Da, RT: 115.43 min,

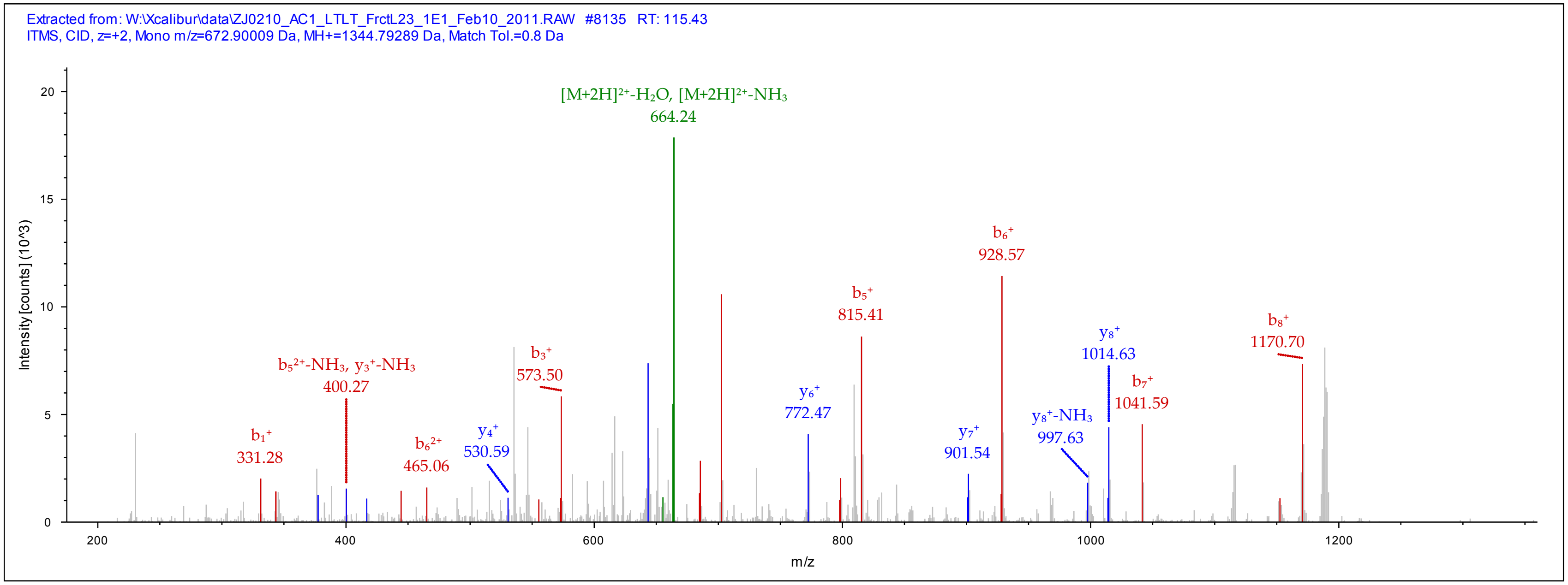
Identified with: Mascot (v1.16); IonScore:40, Exp Value:7.0E-003, Ions matched by search engine: 7/78

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Zinc finger CCCH domain-containing protein 11A
- ZC3H11A protein lng=515



IPI00641351.1

Sequence: VTVPLVR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 506.83948 Da (+0 mmu/+0.01 ppm), MH+: 1012.67168 Da, RT: 89.78 min,

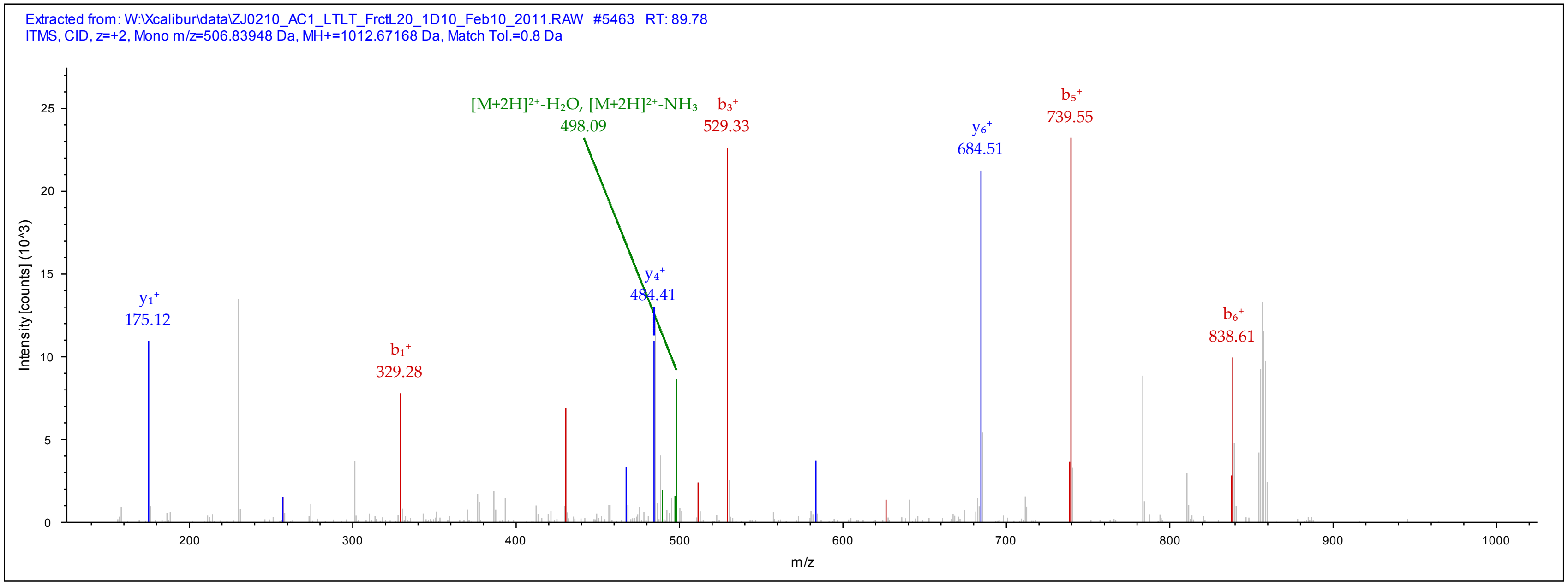
Identified with: Mascot (v1.16); IonScore:33, Exp Value:7.1E-003, Ions matched by search engine: 6/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- cDNA FLJ77422, highly similar to Homo sapiens RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse)), transcript variant 1, mRNA (Fragment)
- Isoform 1 of RNA-binding protein Raly
- RNA binding protein, autoantigenic lng=240
- RNA binding protein, autoantigenic lng=181
- RNA binding protein, autoantigenic lng=237



IPI00641437.1

Sequence: VNALLPTETFIPVIR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 956.57855 Da (+1.42 mmu/+1.49 ppm), MH+: 1912.14983 Da, RT: 135.14 min,

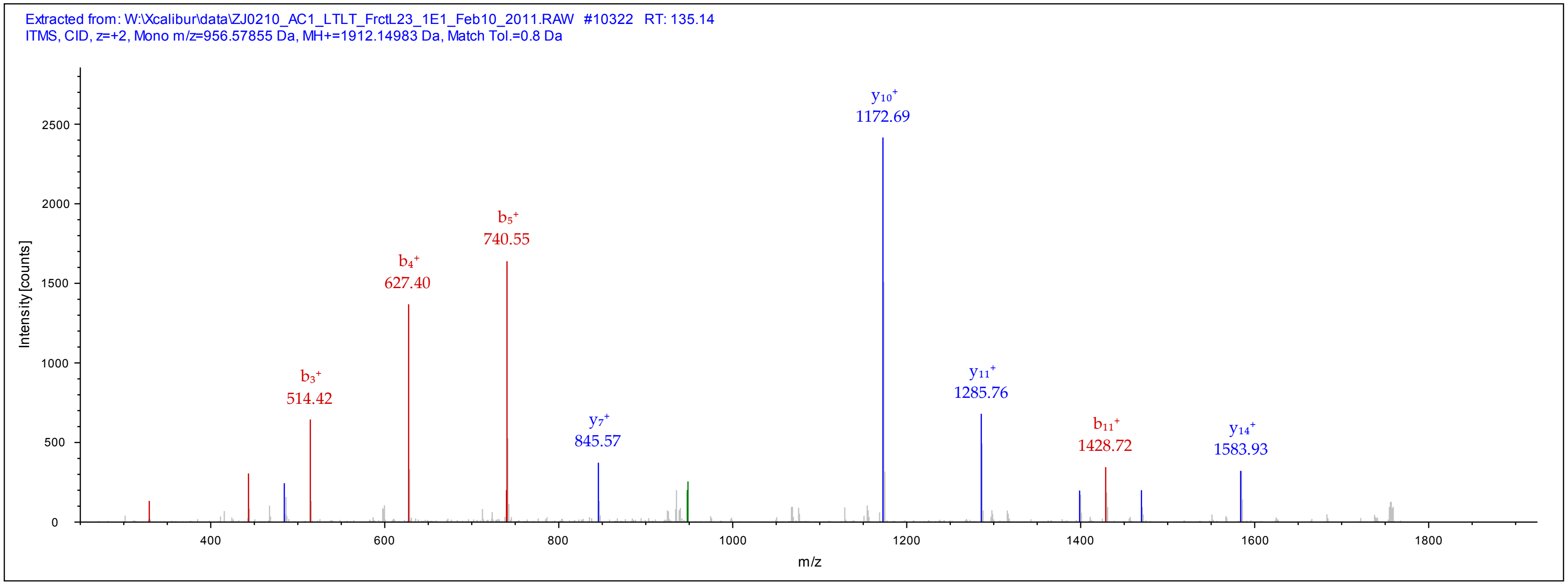
Identified with: Mascot (v1.16); IonScore:56, Exp Value:1.4E-004, Ions matched by search engine: 13/142

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- HEAT repeat-containing protein 1
- HEAT repeat containing 1 lng=2063



IPI:IPI00642935.1

Sequence: LLQLWEK, L1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 694.44116 Da (+1.83 mmu/+2.64 ppm),   MH+: 1387.87505 Da,   RT: 126.48 min,

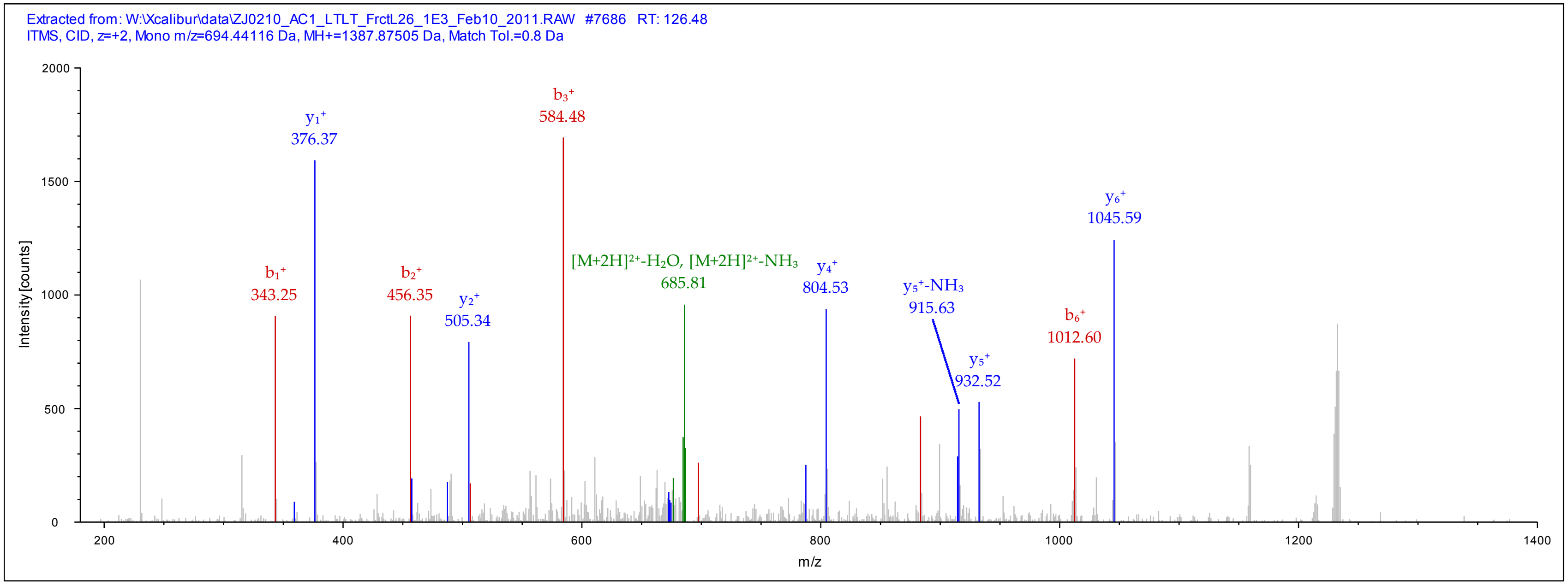
Identified with: Mascot (v1.16); IonScore:33, Exp Value:2.6E-002, Ions matched by search engine: 6/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Calcium homeostasis endoplasmic reticulum protein
- cDNA FLJ51519, highly similar to Homo sapiens calcium homeostasis endoplasmic reticulum protein (CHERP), mRNA



IPI:IPI00642957.1

Sequence: LDIIER, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 494.30573 Da (+0.26 mmu/+0.53 ppm), MH+: 987.60417 Da, RT: 85.48 min,

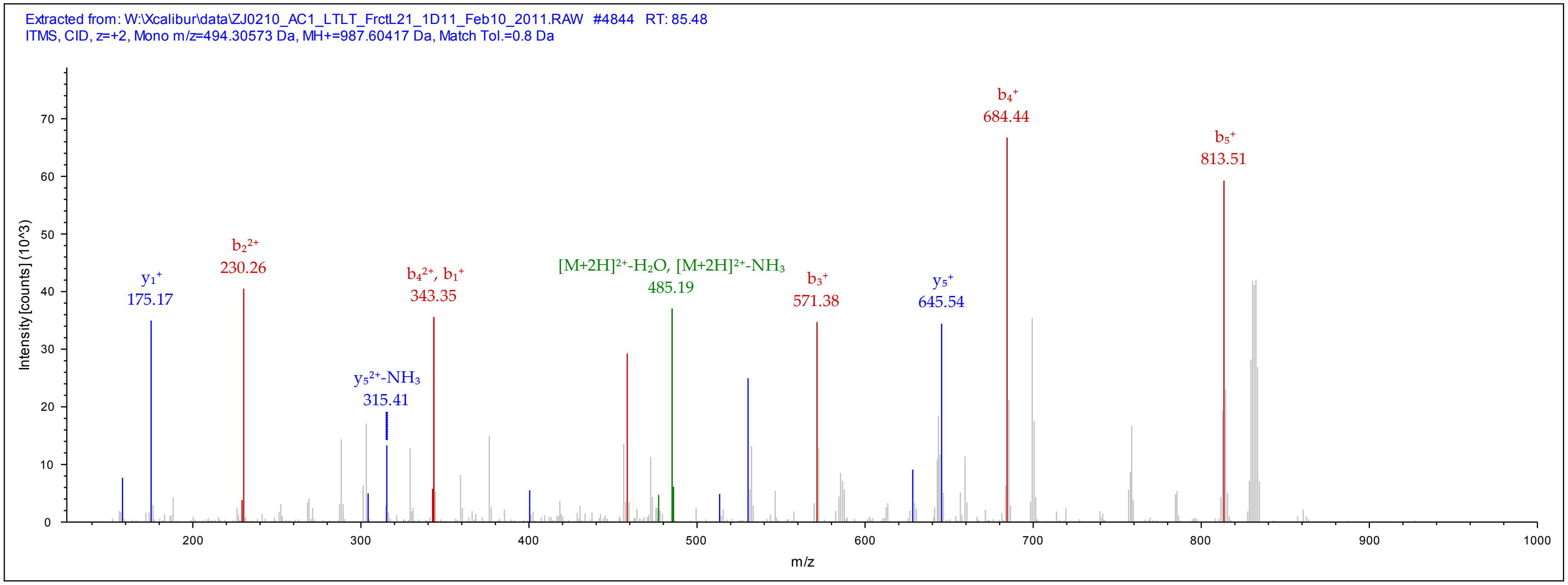
Identified with: Mascot (v1.16); IonScore:30, Exp Value:6.7E-002, Ions matched by search engine: 5/46

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Breast cancer anti-estrogen resistance protein 3
- Breast cancer anti-estrogen resistance 3, isoform CRA_c



IPI00643087.1

Sequence: VNILEVASGAVLR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 785.48291 Da (+2.96 mmu/+3.76 ppm), MH+: 1569.95854 Da, RT: 131.53 min,

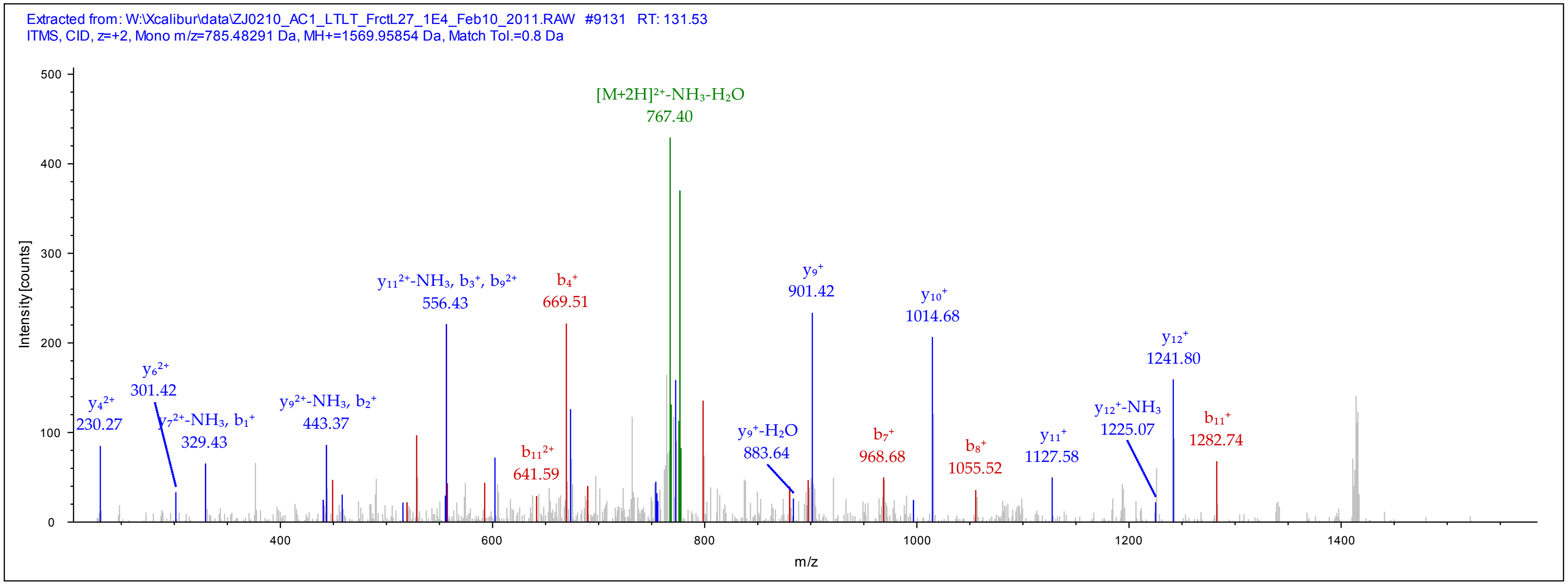
Identified with: Mascot (v1.16); IonScore:33, Exp Value:3.0E-002, Ions matched by search engine: 9/124

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Transducin beta-like protein 3
- 83 kDa protein lng=756



IPI00643317.3

Sequence: DVADYK, D1-TMT6plex (229.16293 Da), K6-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 584.83356 Da (-0.8 mmu/-1.37 ppm), MH+: 1168.65984 Da, RT: 74.63 min,

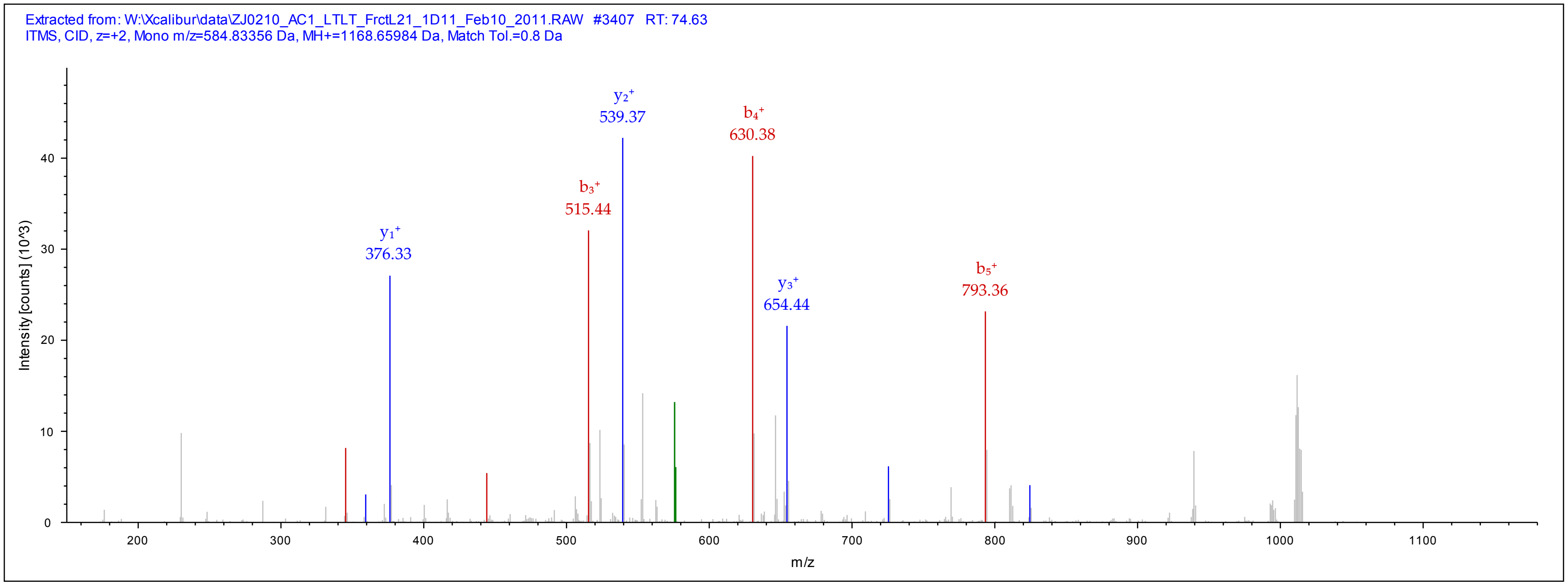
Identified with: Mascot (v1.16); IonScore:30, Exp Value:6.7E-002, Ions matched by search engine: 5/46

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- High mobility group protein B3
- similar to hCG1644442
- 22 kDa protein lng=193
- 21 kDa protein lng=188



IPI:IPI00643598.1

Sequence: LLPLYFPR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 624.38922 Da (-0.11 mmu/-0.17 ppm), MH+: 1247.77117 Da, RT: 127.21 min,

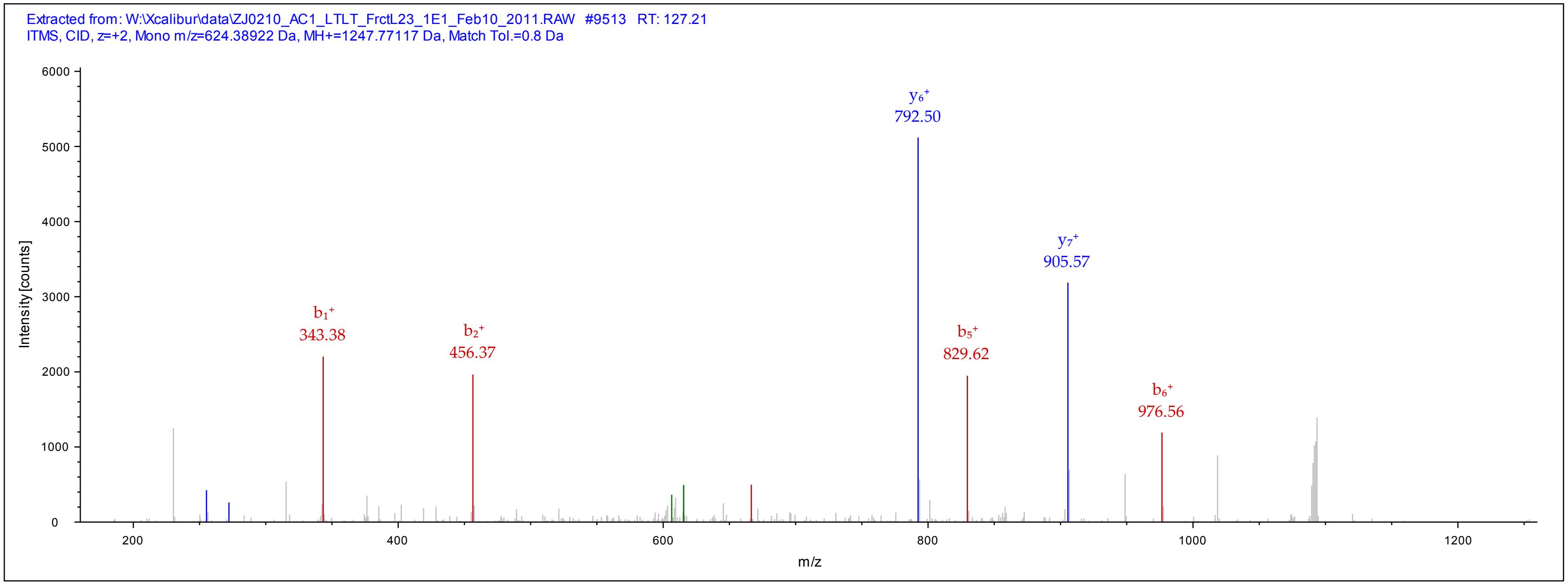
Identified with: Mascot (v1.16); IonScore:39, Exp Value:7.6E-003, Ions matched by search engine: 6/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Ganglioside-induced differentiation-associated protein 2
- Isoform 2 of Ganglioside-induced differentiation-associated protein 2



IPI:IPI00645138.1

Sequence: LSQILTDFPK, L1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 810.49268 Da (+0.38 mmu/+0.47 ppm), MH+: 1619.97807 Da, RT: 127.65 min,

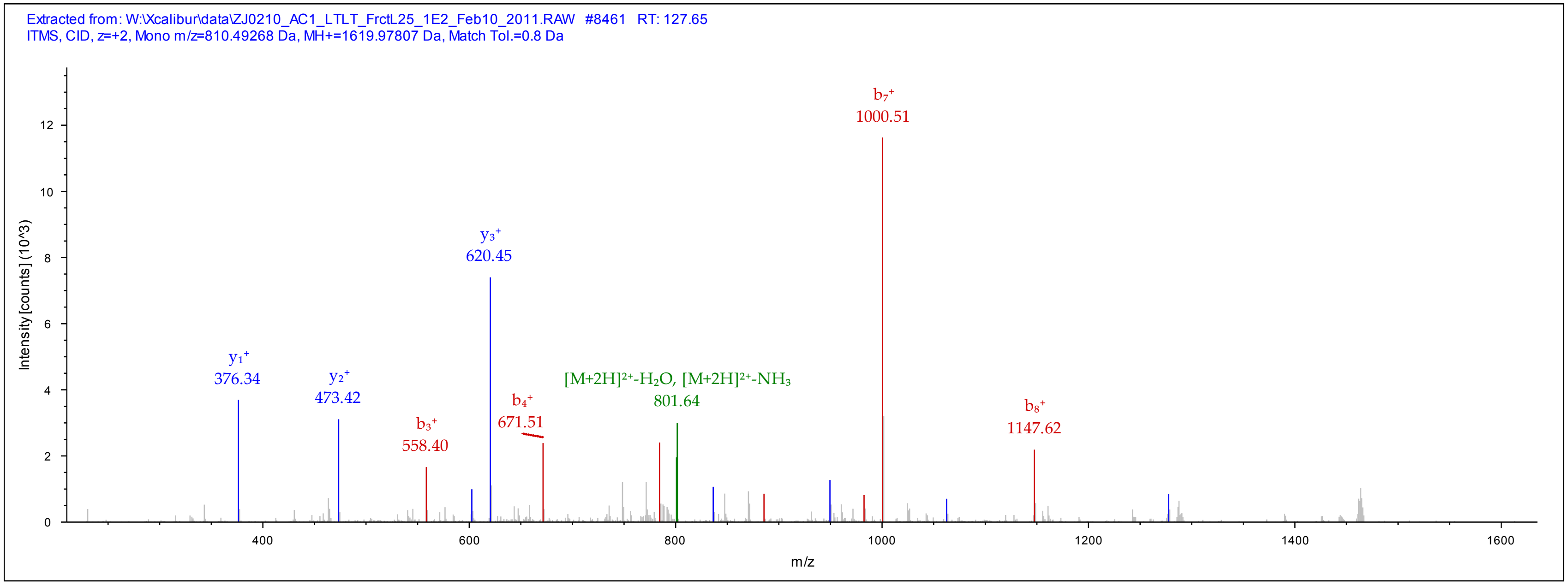
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.2E-002, Ions matched by search engine: 6/96

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Nucleolar GTP-binding protein 1
- GTP binding protein 4



IPI:IPI00217563.4

Sequence: WDTGENPIYK, W1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 840.95343 Da (-0.1 mmu/-0.12 ppm), MH+: 1680.89958 Da, RT: 96.08 min,

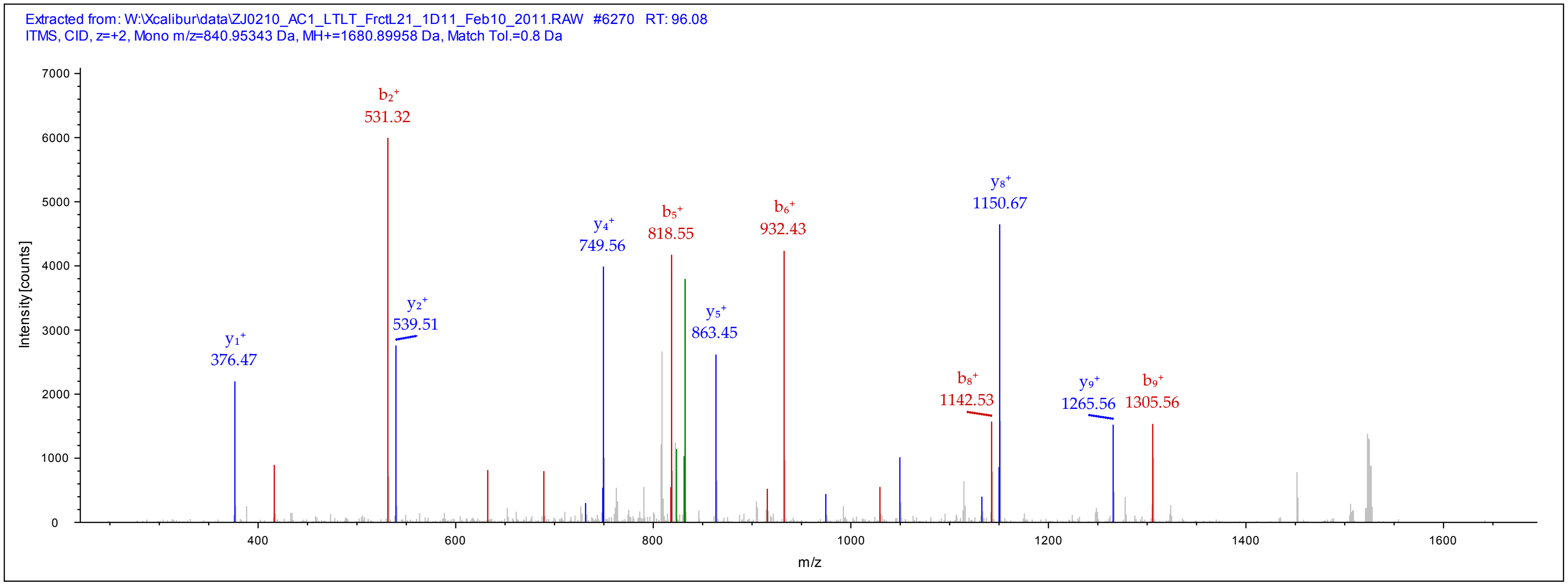
Identified with: Mascot (v1.16); IonScore:64, Exp Value:5.5E-005, Ions matched by search engine: 8/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Isoform Beta-1A of Integrin beta-1



IPI00645589.1

Sequence: YLTYLNAR, Y1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 621.85626 Da (+0.42 mmu/+0.68 ppm), MH+: 1242.70525 Da, RT: 96.31 min,

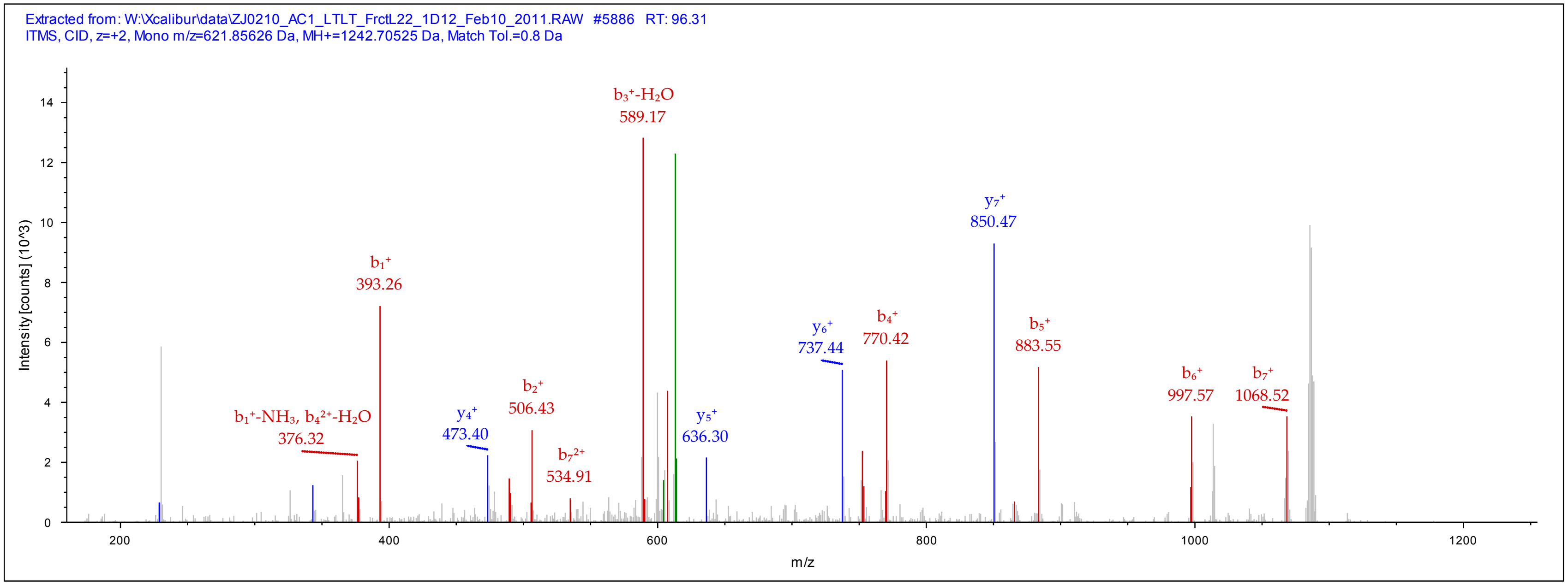
Identified with: Mascot (v1.16); IonScore:42, Exp Value:4.6E-003, Ions matched by search engine: 7/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 2 of Choline transporter-like protein 2 lng=709
- solute carrier family 44, member 2 isoform 2 lng=704
- Isoform 1 of Choline transporter-like protein 2



IPI:IPI00645795.1

Sequence: DIIFGR, D1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 475.28699 Da (-0.09 mmu/-0.18 ppm), MH+: 949.56670 Da, RT: 102.63 min,

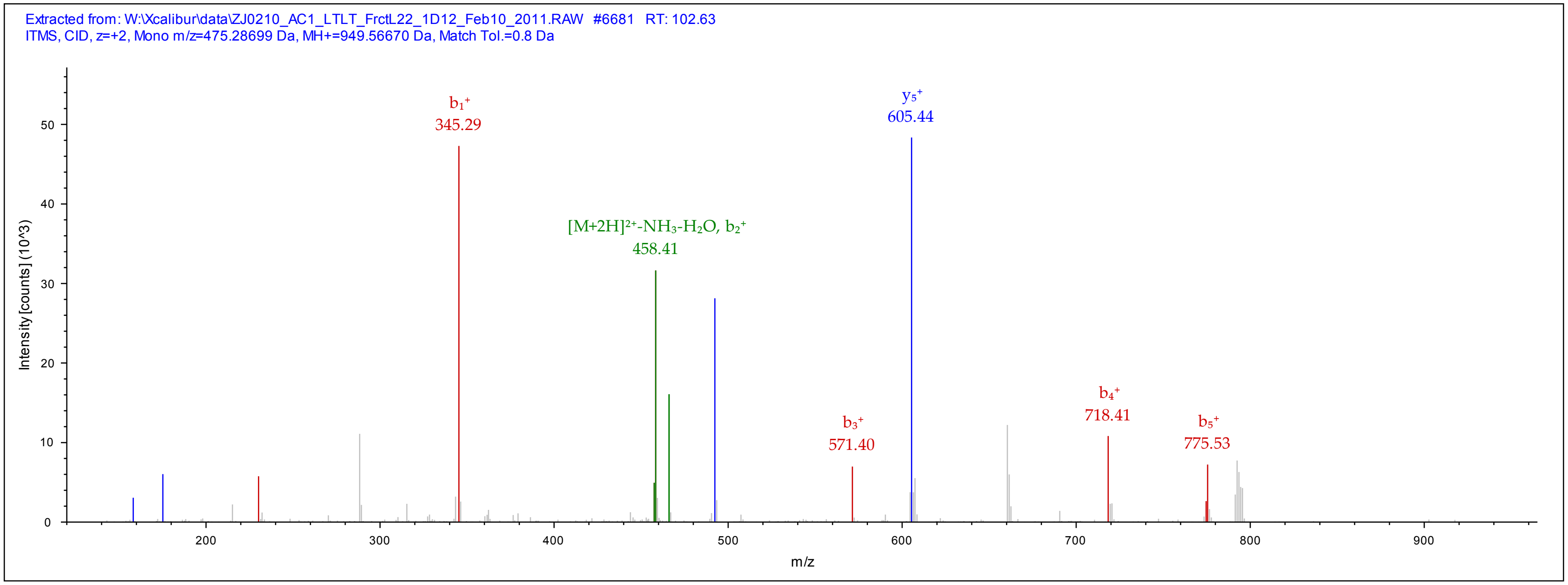
Identified with: Mascot (v1.16); IonScore:30, Exp Value:6.9E-002, Ions matched by search engine: 5/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Beta,beta-carotene 15,15'-monooxygenase
- 19 kDa protein



IPI00646239.1

Sequence: YDSYESCDSR, Y1-TMT6plex (229.16293 Da), C7-Carbamidomethyl (57.02146 Da)

Charge: +2, Monoisotopic m/z: 755.82135 Da (+1.82 mmu/+2.41 ppm), MH+: 1510.63542 Da, RT: 68.07 min,

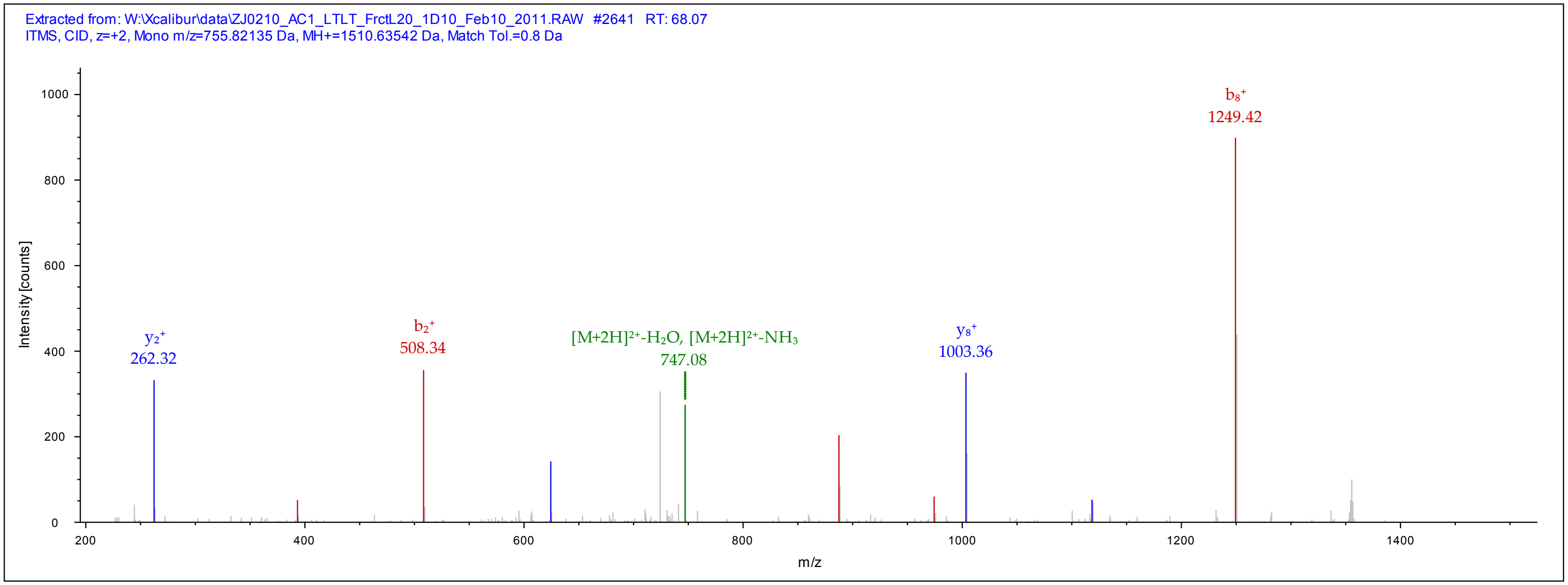
Identified with: Mascot (v1.16); IonScore:45, Exp Value:9.9E-004, Ions matched by search engine: 9/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- 47 kDa protein lng=431
- A kinase (PRKA) anchor protein 8-like, isoform CRA_d lng=386
- 39 kDa protein lng=358
- cDNA FLJ58398, highly similar to A-kinase anchor protein 8 lng=345
- A-kinase anchor protein 8-like
- 72 kDa protein lng=646



IPI:IPI00646783.1

Sequence: IVVAAVAR, I1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 514.34503 Da (+0.1 mmu/+0.2 ppm),   MH+: 1027.68279 Da,   RT: 82.77 min,

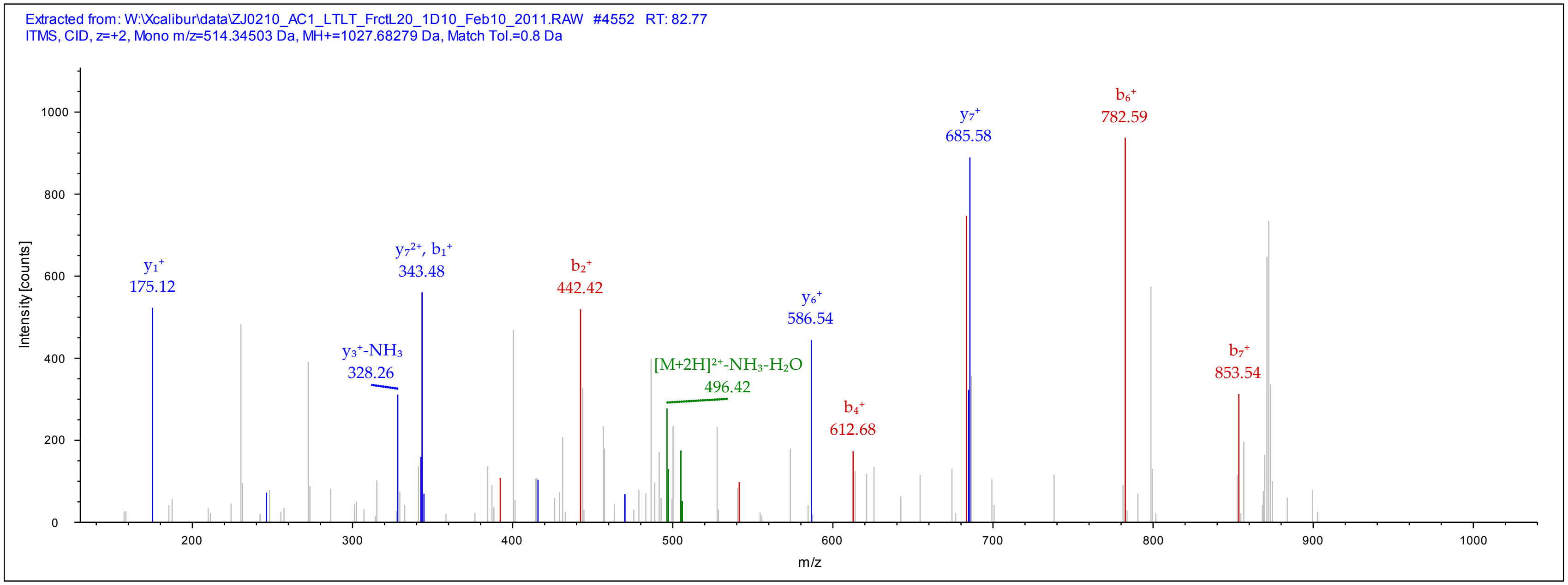
Identified with: Mascot (v1.16); IonScore:33, Exp Value:8.5E-003, Ions matched by search engine: 6/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of TRM1-like protein
- 24 kDa protein
- Isoform 2 of TRM1-like protein



IPI00646864.1

Sequence: FFDEESYSLLR, F1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 817.91663 Da (-0.21 mmu/-0.26 ppm),   MH+: 1634.82598 Da,   RT: 118.35 min,

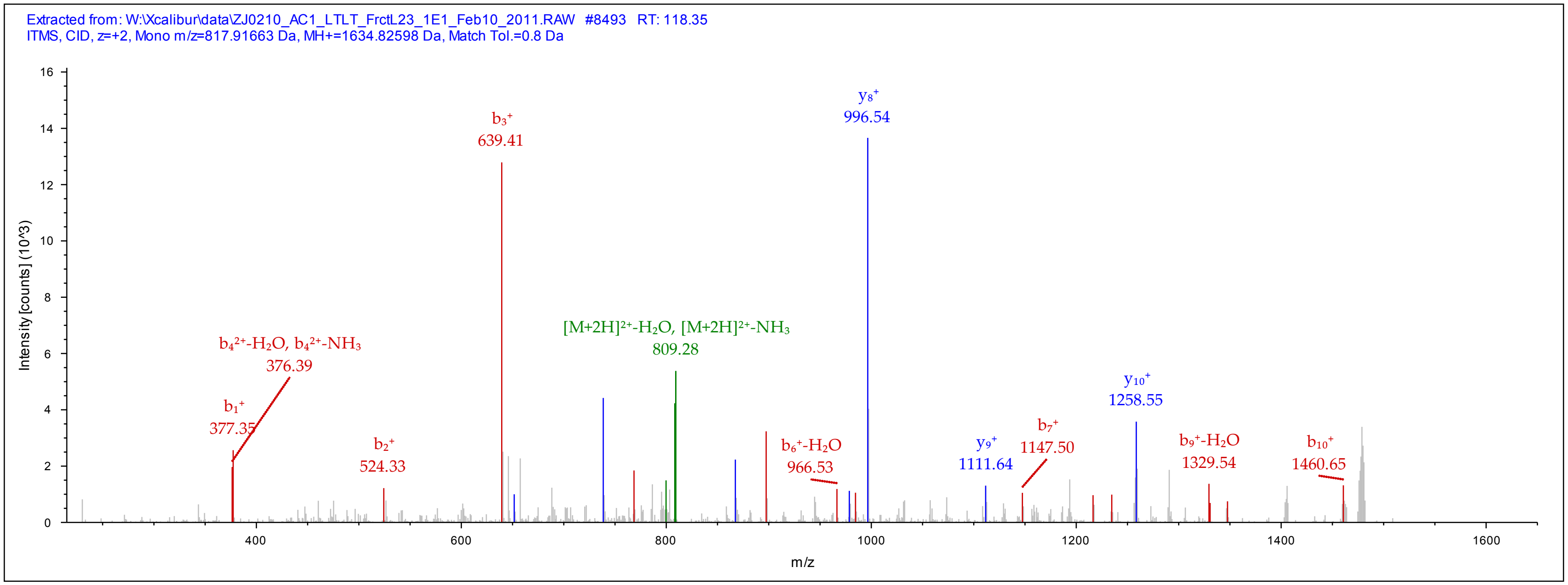
Identified with: Mascot (v1.16); IonScore:34, Exp Value:4.6E-002, Ions matched by search engine: 10/90

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Putative uncharacterized protein SSR4 lng=120
- Uncharacterized protein
- Translocon-associated protein subunit delta precursor



IPI00647481.1

Sequence: IIIIAR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 464.33136 Da (+0.07 mmu/+0.16 ppm), MH+: 927.65544 Da, RT: 102.84 min,

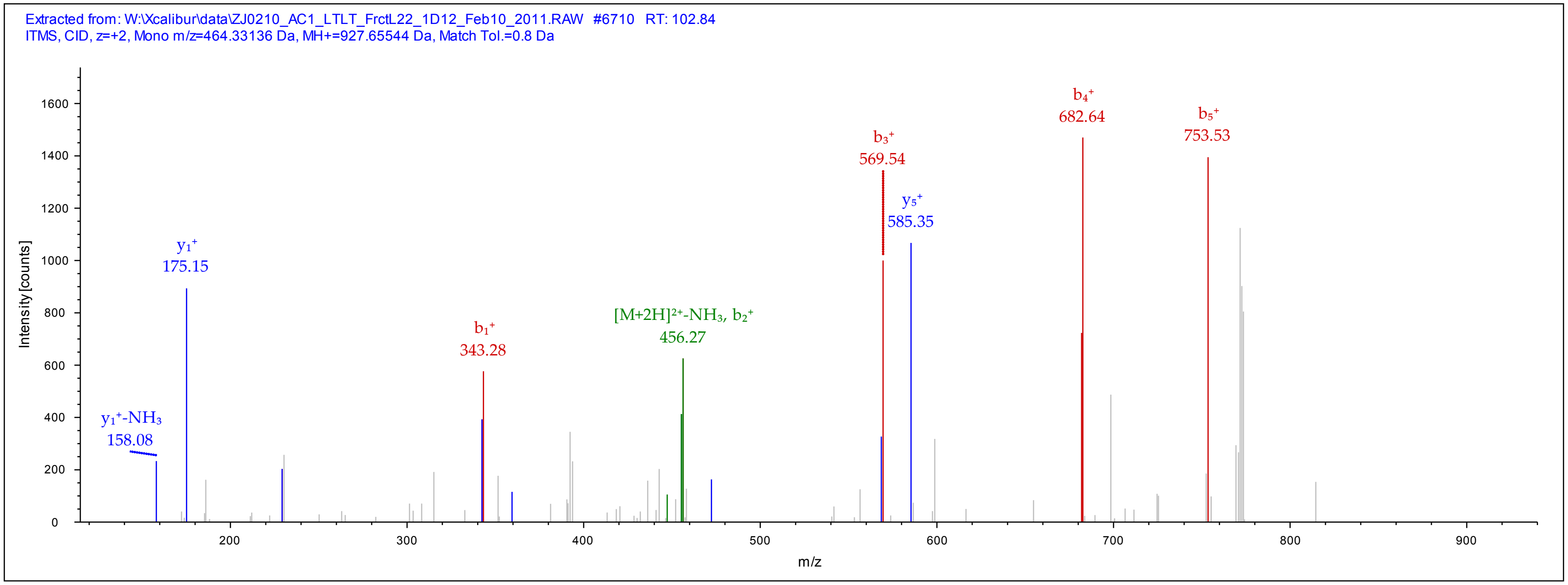
Identified with: Mascot (v1.16); IonScore:37, Exp Value:3.5E-004, Ions matched by search engine: 5/42

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Interferon-inducible protein AIM2
- Absent in melanoma 2 lng=167



IPI00651701.1

Sequence: TLSDATTK, T1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 647.88544 Da (+0.86 mmu/+1.32 ppm), MH+: 1294.76360 Da, RT: 76.65 min,

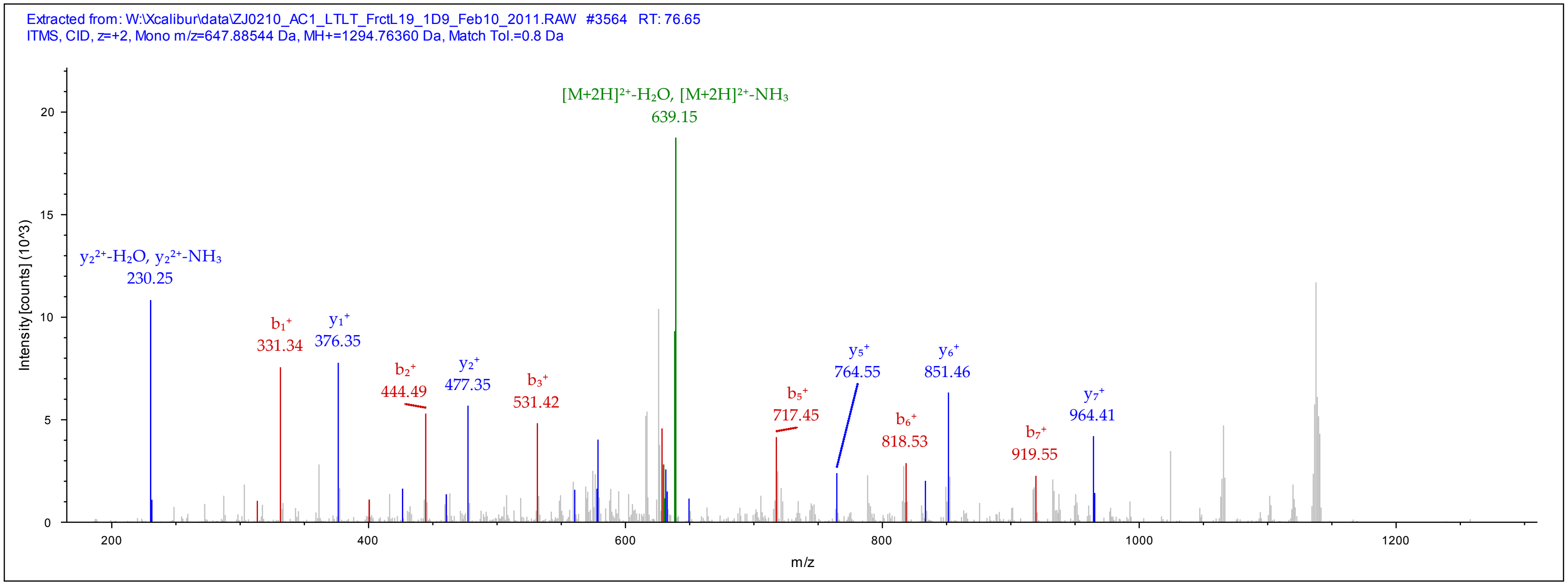
Identified with: Mascot (v1.16); IonScore:36, Exp Value:1.9E-002, Ions matched by search engine: 6/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Protein FAM49B
- Putative uncharacterized protein BM009 lng=220
- 33 kDa protein lng=286



IPI:IPI00658071.1

Sequence: QREPALR, Q1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 549.83978 Da (+7.07 mmu/+12.87 ppm), MH+: 1098.67229 Da, RT: 95.47 min,

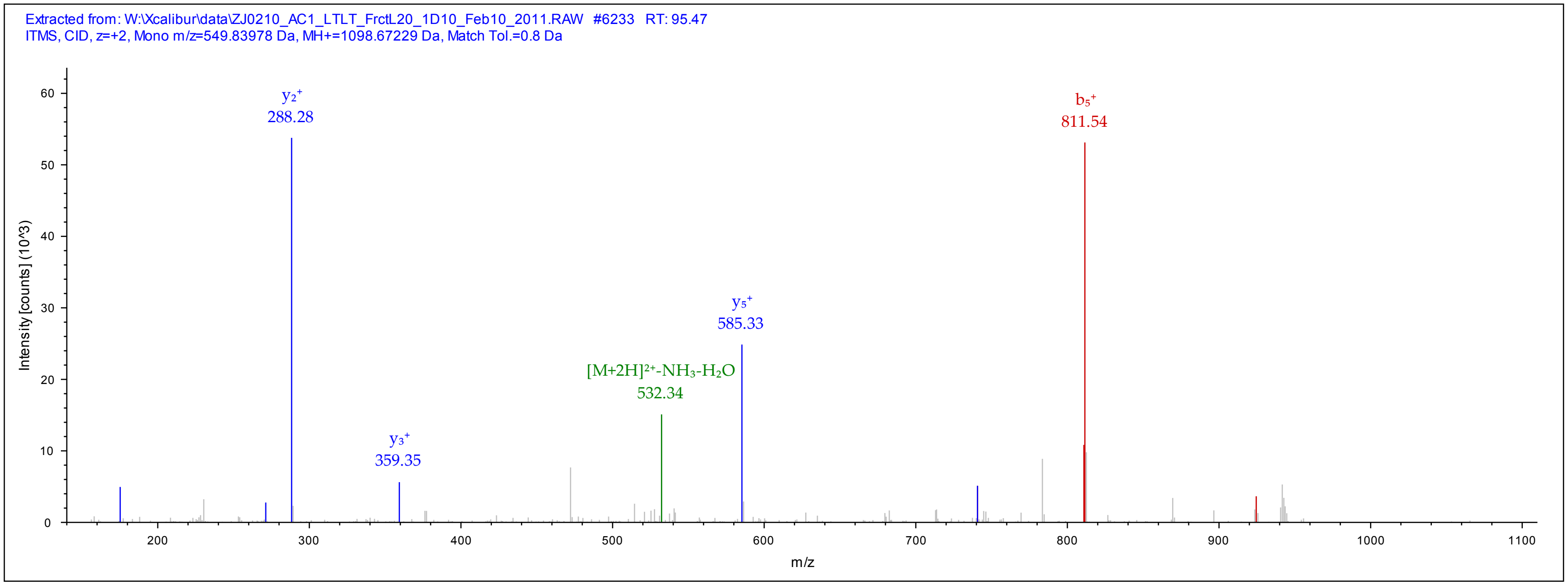
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.1E-002, Ions matched by search engine: 5/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Uncharacterized protein



IPI:IPI00719345.1

Sequence: QEIIEQLLSNIFHK, Q1-TMT6plex (229.16293 Da), K14-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 724.09546 Da (+2.72 mmu/+3.75 ppm),   MH+: 2170.27182 Da,   RT: 215.72 min,

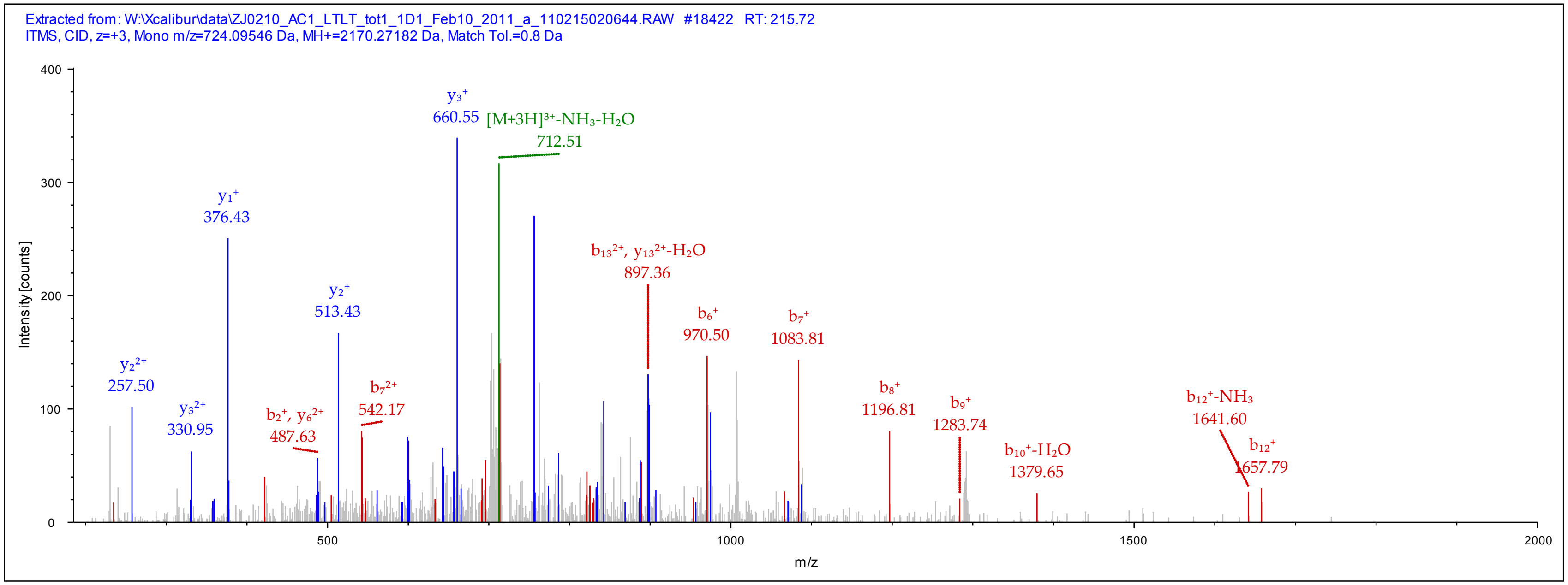
Identified with: Mascot (v1.16); IonScore:37, Exp Value:1.4E-002, Ions matched by search engine: 10/144

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform 1 of Serine/threonine-protein phosphatase 6 regulatory subunit 3
- Isoform 4 of Serine/threonine-protein phosphatase 6 regulatory subunit 3
- Isoform 6 of Serine/threonine-protein phosphatase 6 regulatory subunit 3
- Isoform 3 of Serine/threonine-protein phosphatase 6 regulatory subunit 3
- Isoform 2 of Serine/threonine-protein phosphatase 6 regulatory subunit 3
- Isoform 5 of Serine/threonine-protein phosphatase 6 regulatory subunit 3



IPI:IPI00736859.1

Sequence: INEEISVK, I1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 695.42108 Da (-0.25 mmu/-0.37 ppm),   MH+: 1389.83489 Da,   RT: 87.90 min,

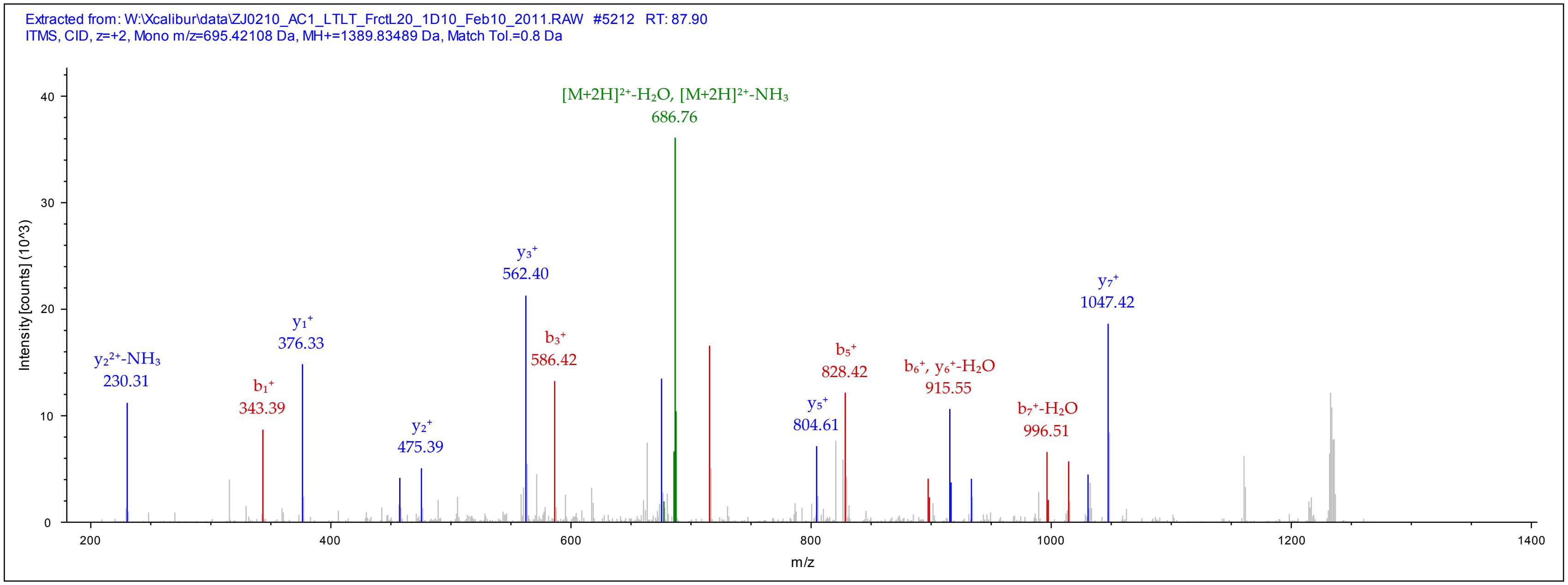
Identified with: Mascot (v1.16); IonScore:46, Exp Value:2.8E-003, Ions matched by search engine: 12/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Heterogeneous nuclear ribonucleoprotein U-like protein 1
- Isoform 2 of Heterogeneous nuclear ribonucleoprotein U-like protein 1
- Isoform 4 of Heterogeneous nuclear ribonucleoprotein U-like protein 1



IPI00943860.1

Sequence: LEWVQDNIR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 701.38806 Da (+0.01 mmu/+0.01 ppm),   MH+: 1401.76885 Da,   RT: 104.71 min,

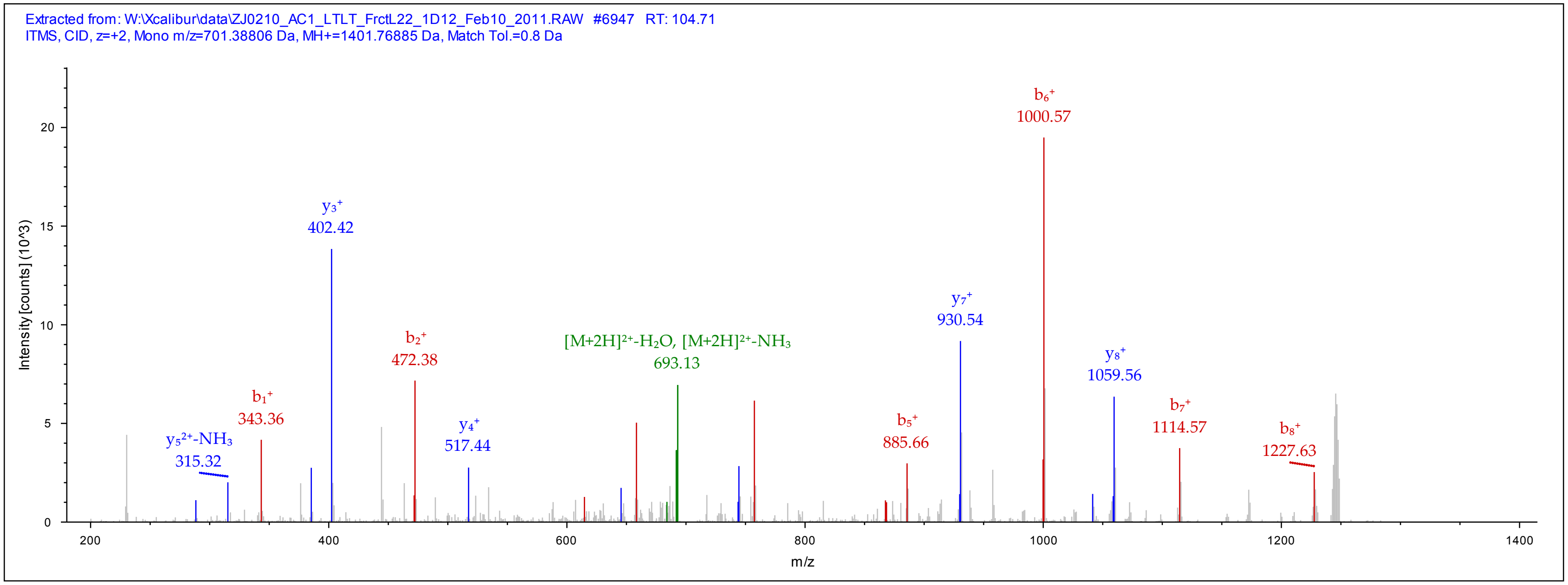
Identified with: Mascot (v1.16); IonScore:43, Exp Value:4.1E-003, Ions matched by search engine: 7/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Pre-mRNA-processing factor 6
- similar to U5 snRNP-associated 102 kDa protein lng=406



IPI00845444.1

Sequence: VLVTGATGLLGR, V1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 693.43695 Da (-0.6 mmu/-0.87 ppm),   MH+: 1385.86662 Da,   RT: 107.88 min,

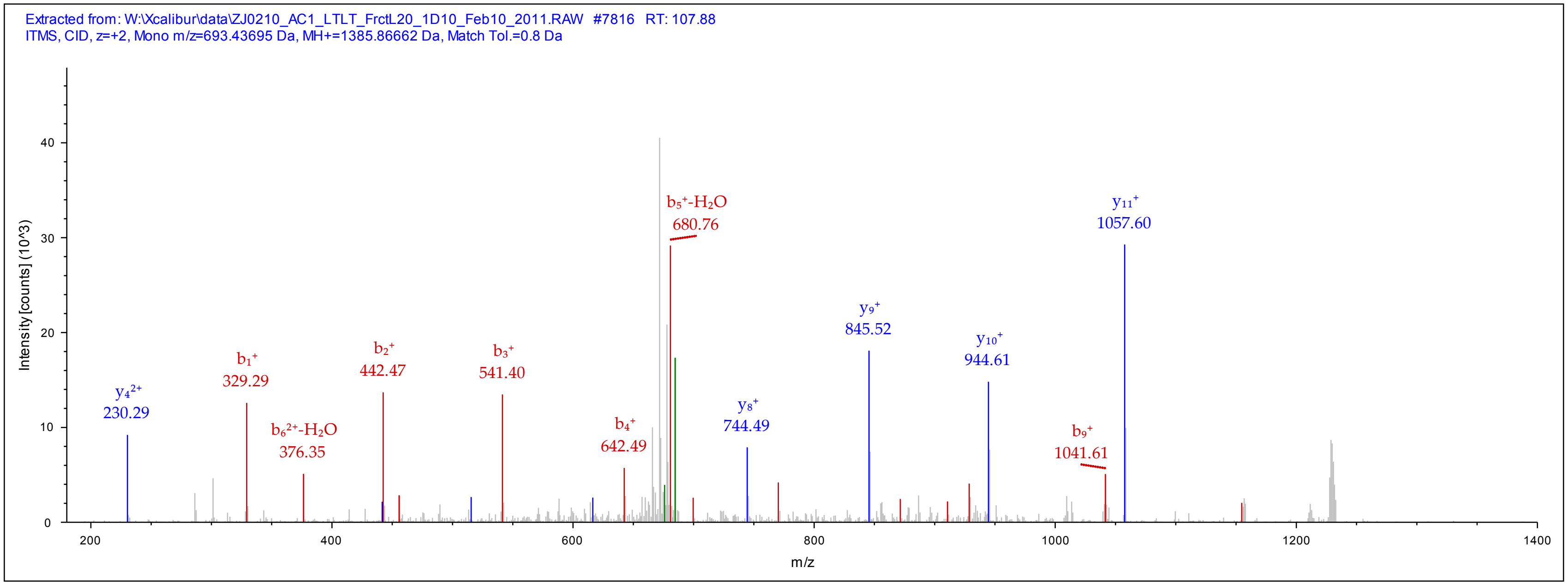
Identified with: Mascot (v1.16); IonScore:46, Exp Value:9.8E-004, Ions matched by search engine: 11/94

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform 1 of Methionine adenosyltransferase 2 subunit beta
- Isoform 2 of Methionine adenosyltransferase 2 subunit beta
- Isoform 3 of Methionine adenosyltransferase 2 subunit beta
- Isoform 5 of Methionine adenosyltransferase 2 subunit beta lng=83
- Isoform 4 of Methionine adenosyltransferase 2 subunit beta lng=306
- Putative uncharacterized protein MAT2B lng=83



IPI00741317.1

Sequence: GGPNIITLADIVK, G1-TMT6plex (229.16293 Da), K13-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 885.05103 Da (+0.5 mmu/+0.57 ppm), MH+: 1769.09477 Da, RT: 128.74 min,

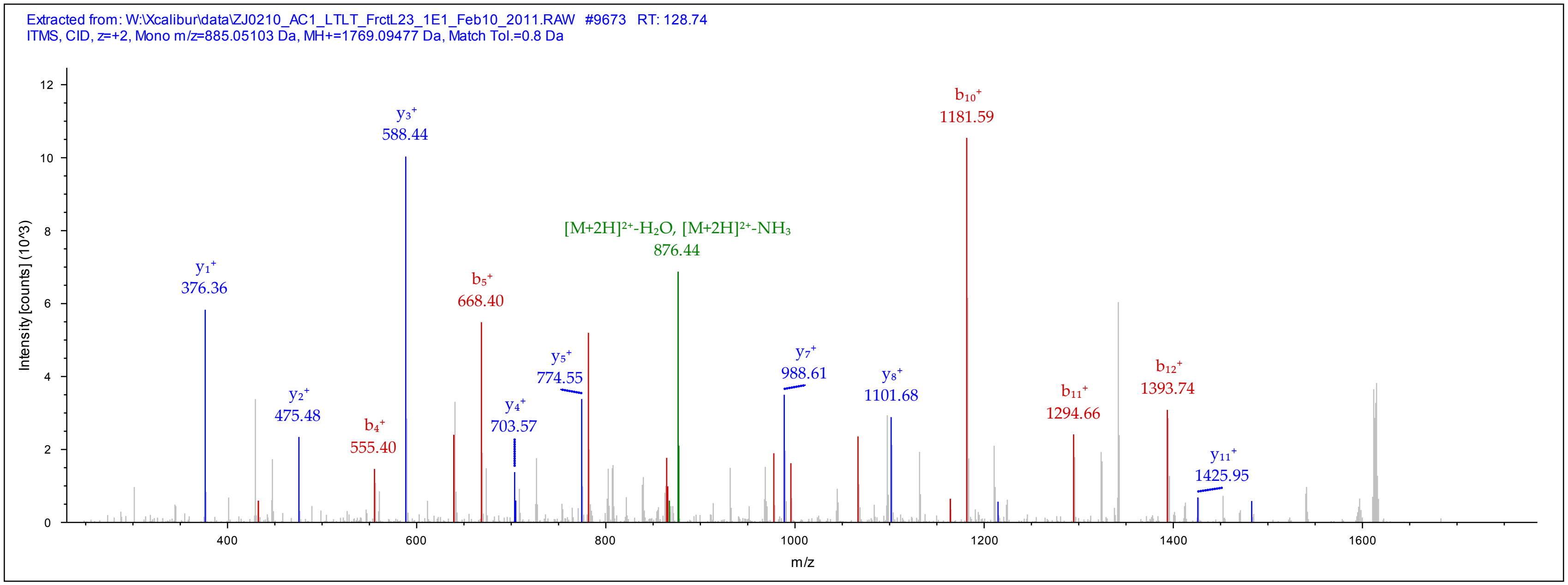
Identified with: Mascot (v1.16); IonScore:36, Exp Value:1.4E-002, Ions matched by search engine: 10/120

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Casein kinase II subunit alpha
- CSNK2A1 protein lng=397
- Casein kinase 2 alpha isoform lng=385
- HCG21984 lng=391



IPI:IPI00743364.1

Sequence: LLSPLLVR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 570.38922 Da (-0.11 mmu/-0.2 ppm),   MH+: 1139.77117 Da,   RT: 119.71 min,

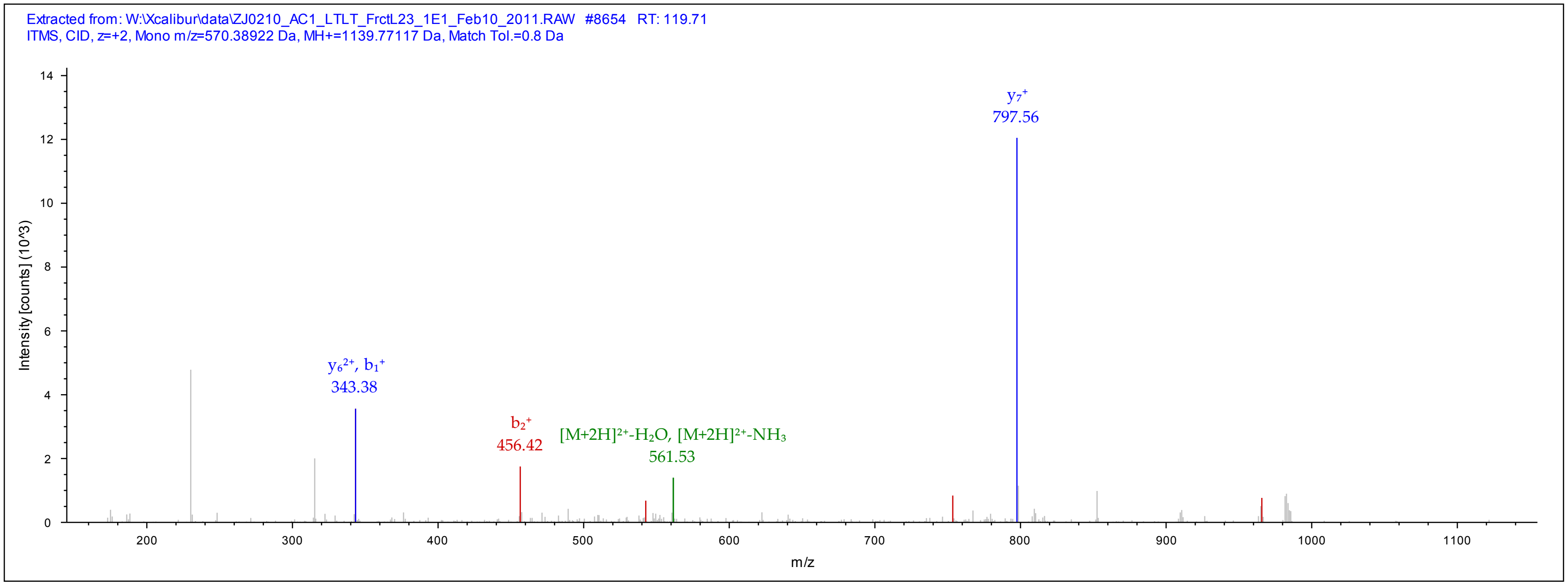
Identified with: Mascot (v1.16); IonScore:38, Exp Value:4.3E-004, Ions matched by search engine: 6/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Similar to Nuclear pore complex protein Nup153



IPI:IPI00749486.1

Sequence: EEPSNPFLAFVEK, E1-TMT6plex (229.16293 Da), K13-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 983.04095 Da (+0.6 mmu/+0.61 ppm), MH+: 1965.07463 Da, RT: 132.54 min,

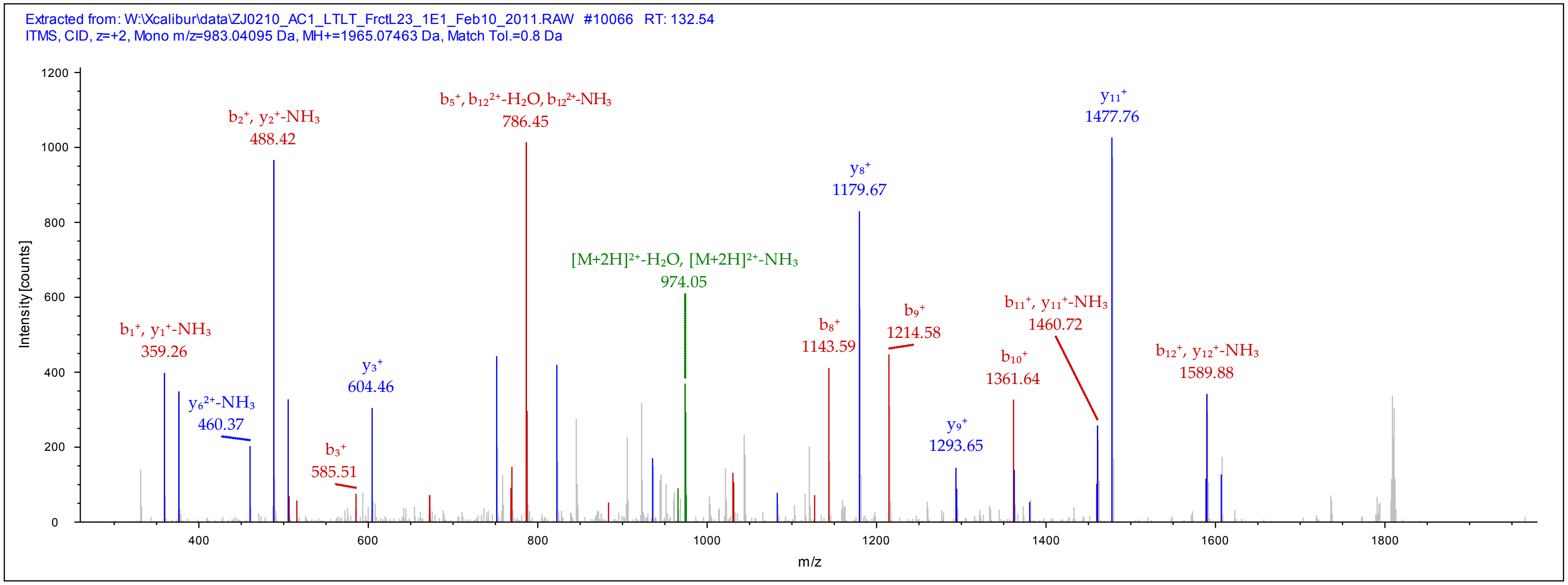
Identified with: Mascot (v1.16); IonScore:54, Exp Value:4.7E-004, Ions matched by search engine: 11/134

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 2 of Lysine-specific demethylase 3B
- Isoform 1 of Lysine-specific demethylase 3B



IPI:IPI00759539.1

Sequence: GALNPADITVLFK, G1-TMT6plex (229.16293 Da), K13-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 909.05267 Da (+2.15 mmu/+2.37 ppm),   MH+: 1817.09807 Da,   RT: 135.44 min,

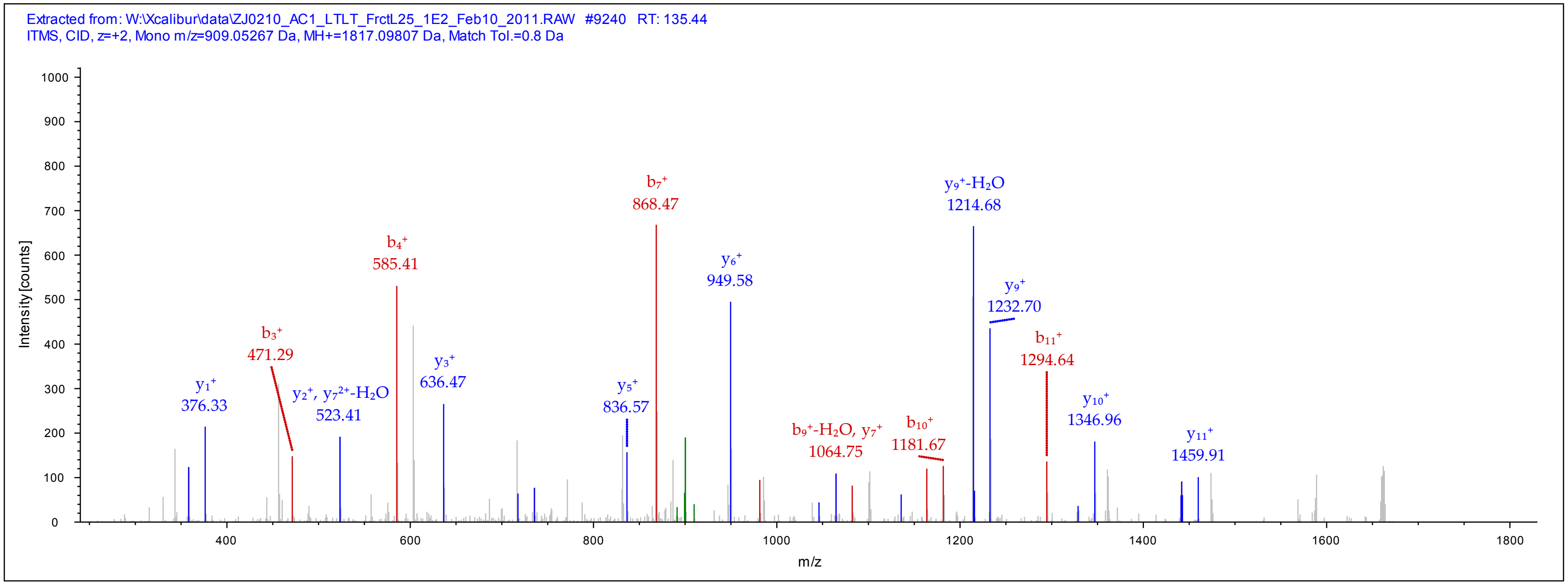
Identified with: Mascot (v1.16); IonScore:47, Exp Value:1.3E-003, Ions matched by search engine: 10/118

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform NELF-C of Negative elongation factor C/D
- Isoform NELF-D of Negative elongation factor C/D



IPI:IPI00000284.2

Sequence: DQNLRNPK, D1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 721.92297 Da (-4.68 mmu/-6.48 ppm),   MH+: 1442.83867 Da,   RT: 74.03 min,

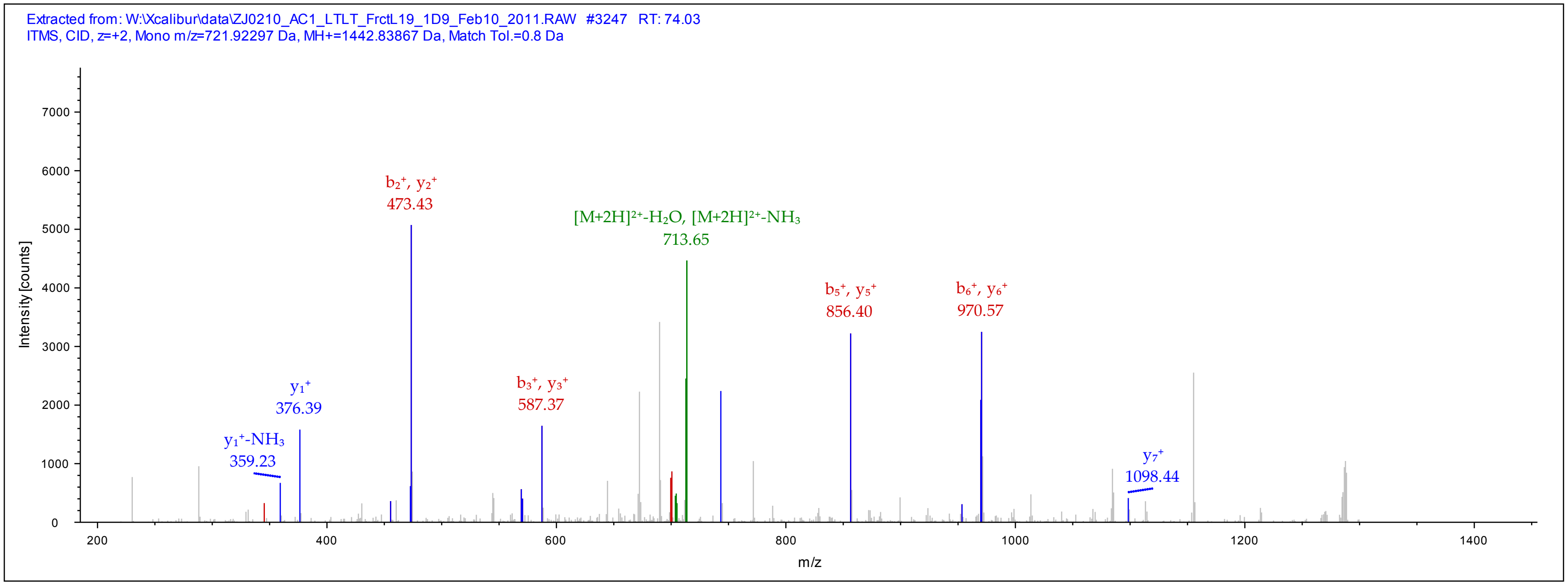
Identified with: Mascot (v1.16); IonScore:37, Exp Value:1.8E-002, Ions matched by search engine: 6/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Transcription factor HES-7
- hairy and enhancer of split 7 isoform 1 lng=230



IPI:IPI00003515.2

Sequence: ETLIAEIEELDR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 830.45679 Da (+2.99 mmu/+3.6 ppm),   MH+: 1659.90630 Da,   RT: 130.15 min,

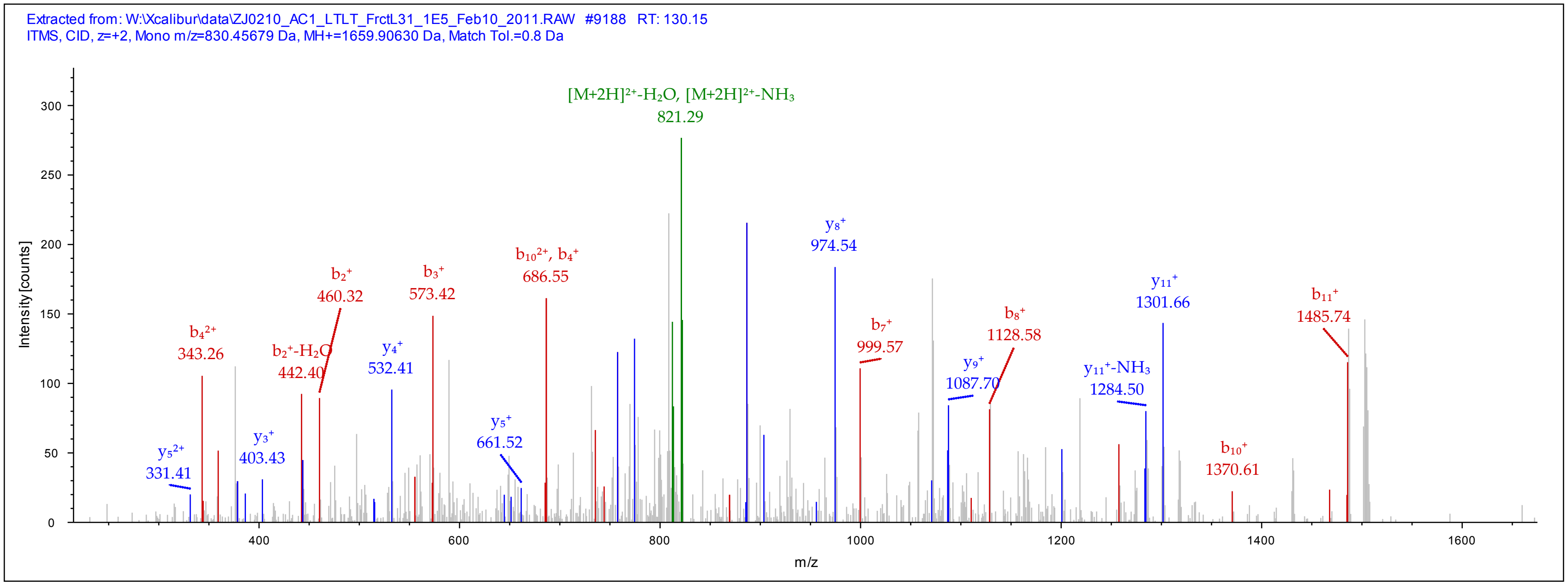
Identified with: Mascot (v1.16); IonScore:47, Exp Value:2.4E-003, Ions matched by search engine: 11/108

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Thyroid receptor-interacting protein 11



IPI00005416.5

Sequence: SSVATTSGK, S1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 648.38538 Da (+3.17 mmu/+4.89 ppm), MH+: 1295.76348 Da, RT: 67.66 min,

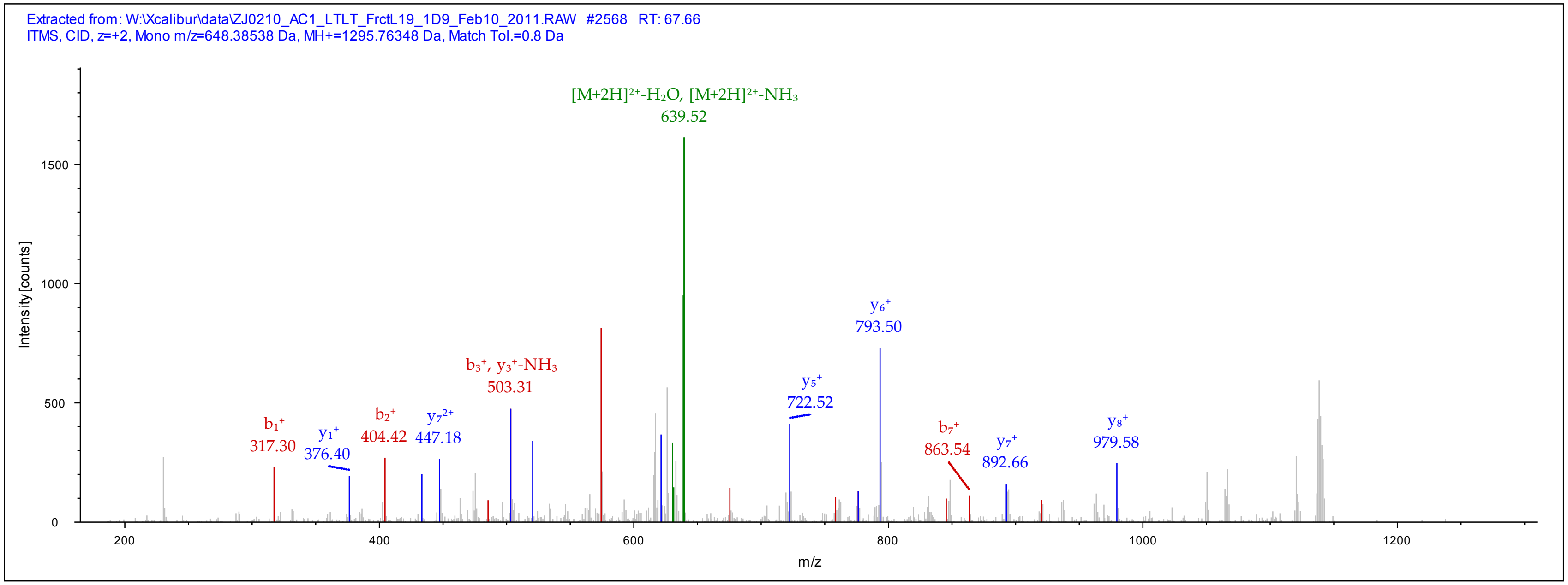
Identified with: Mascot (v1.16); IonScore:32, Exp Value:3.9E-002, Ions matched by search engine: 8/76

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of Ubiquitin-associated protein 2-like
- Isoform 2 of Ubiquitin-associated protein 2-like
- NICE-4 protein (Fragment) lng=408
- Isoform 3 of Ubiquitin-associated protein 2-like
- Isoform 4 of Ubiquitin-associated protein 2-like



IPI:IPI00005537.3

Sequence: LVESLPQEIK, L1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 807.49872 Da (+1.14 mmu/+1.41 ppm), MH+: 1613.99016 Da, RT: 106.36 min,

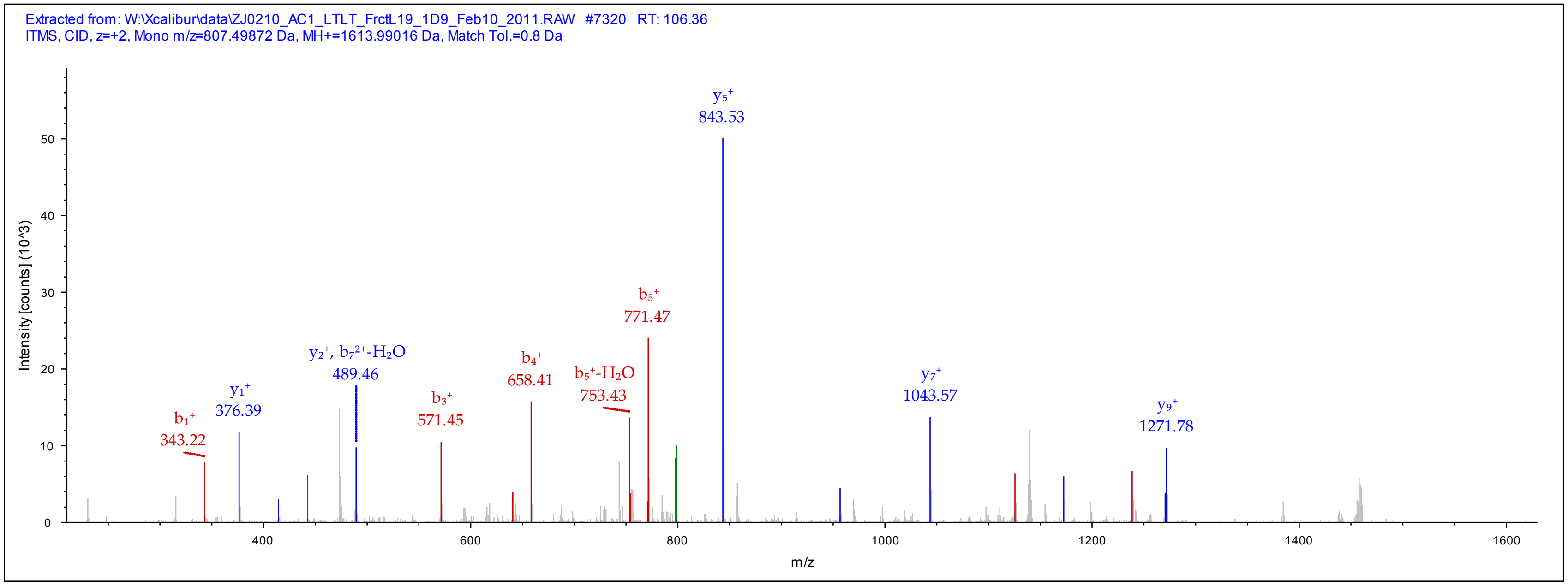
Identified with: Mascot (v1.16); IonScore:53, Exp Value:2.3E-004, Ions matched by search engine: 8/88

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier



IPI:IPI00021338.2

Sequence: DVPLGTPLCIIVEK, D1-TMT6plex (229.16293 Da), C9-Carbamidomethyl (57.02146 Da), K14-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 1006.59735 Da (+0.37 mmu/+0.37 ppm),   MH+: 2012.18743 Da,   RT: 129.04 min,

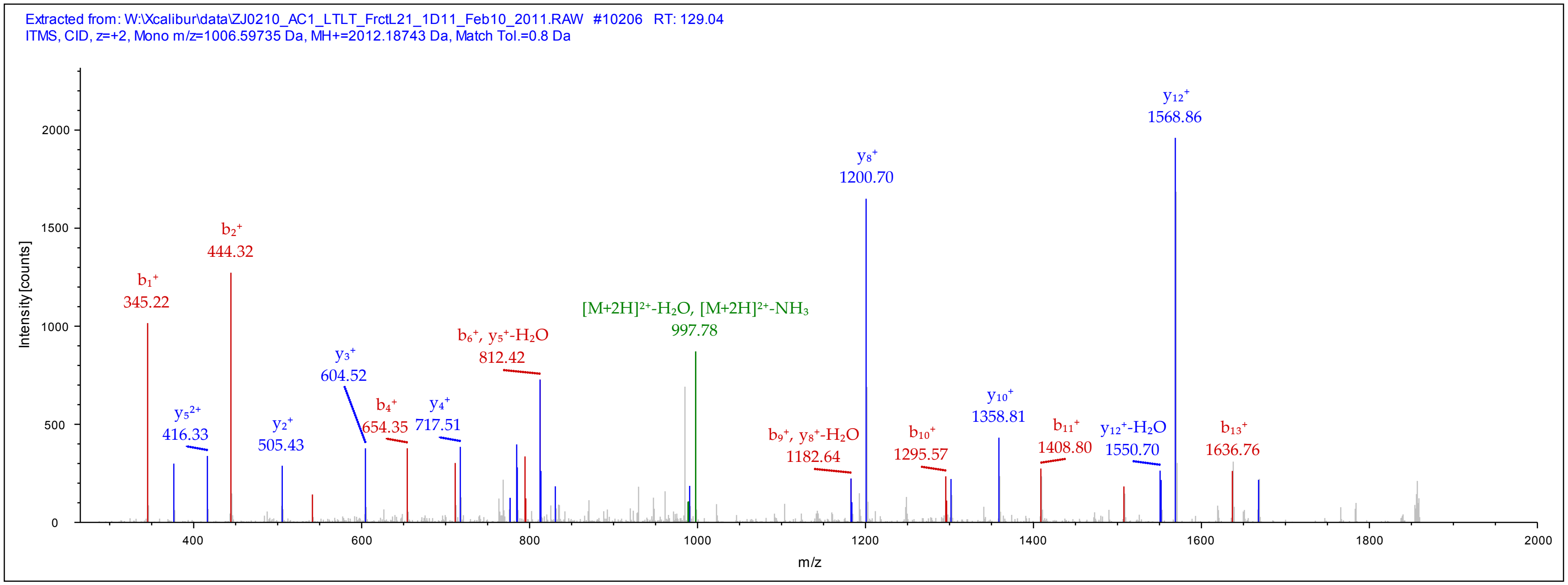
Identified with: Mascot (v1.16); IonScore:62, Exp Value:4.3E-005, Ions matched by search engine: 12/128

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial



IPI00100748.4

Sequence: ALFAISCLVR, A1-TMT6plex (229.16293 Da), C7-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 689.90875 Da (+1.18 mmu/+1.71 ppm),   MH+: 1378.81023 Da,   RT: 129.37 min,

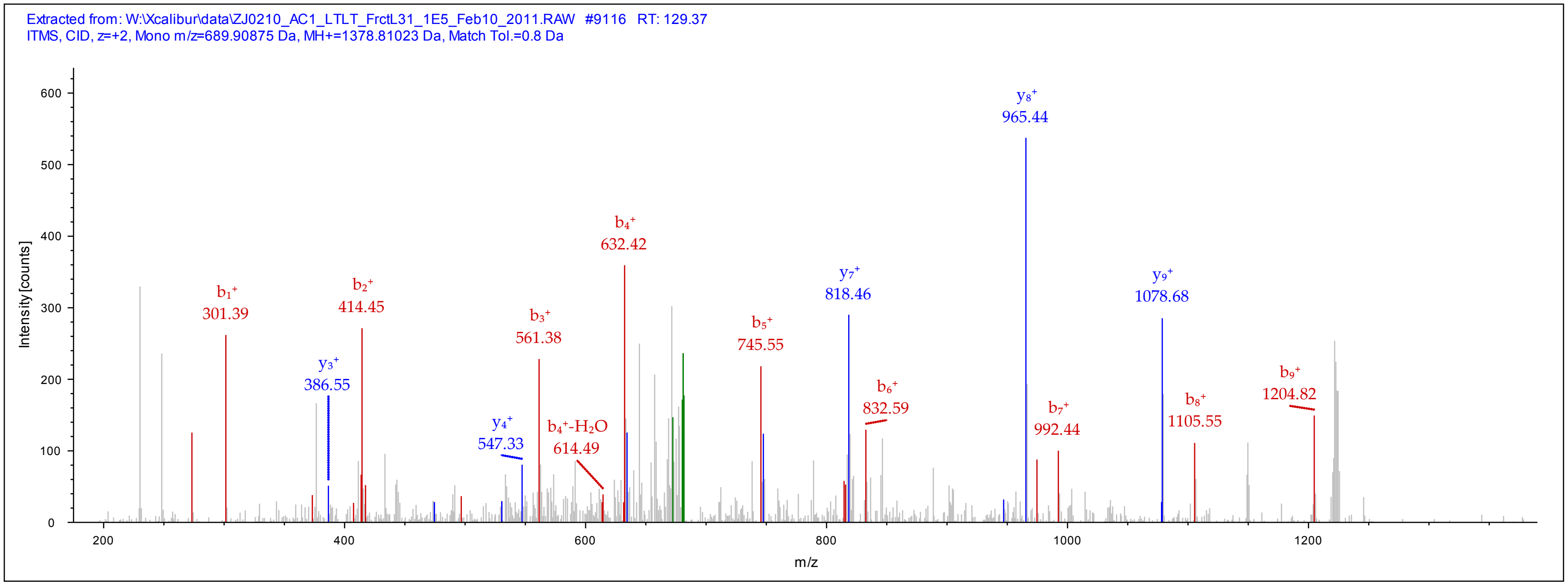
Identified with: Mascot (v1.16); IonScore:41, Exp Value:5.4E-003, Ions matched by search engine: 7/72

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- cDNA FLJ55382, highly similar to Hsp70-binding protein 1 lng=405



IPI:IPI00157928.2

Sequence: GIDYETVPINLIK, G1-TMT6plex (229.16293 Da), K13-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 967.07562 Da (+1.44 mmu/+1.49 ppm), MH+: 1933.14397 Da, RT: 121.71 min,

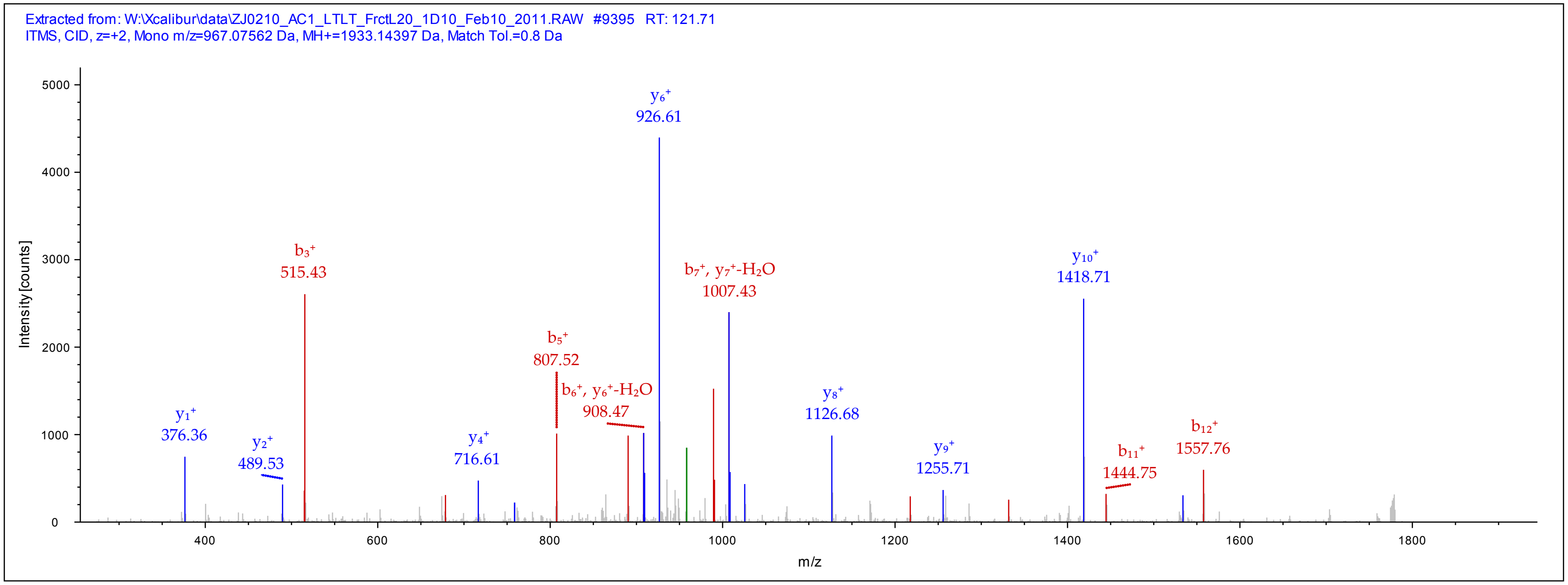
Identified with: Mascot (v1.16); IonScore:61, Exp Value:6.1E-005, Ions matched by search engine: 11/108

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- maleylacetoacetate isomerase isoform 1
- maleylacetoacetate isomerase isoform 2



IPI:IPI00168292.3

Sequence: NILETLLQMK, N1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 831.01025 Da (+2.99 mmu/+3.6 ppm), MH+: 1661.01323 Da, RT: 196.26 min,

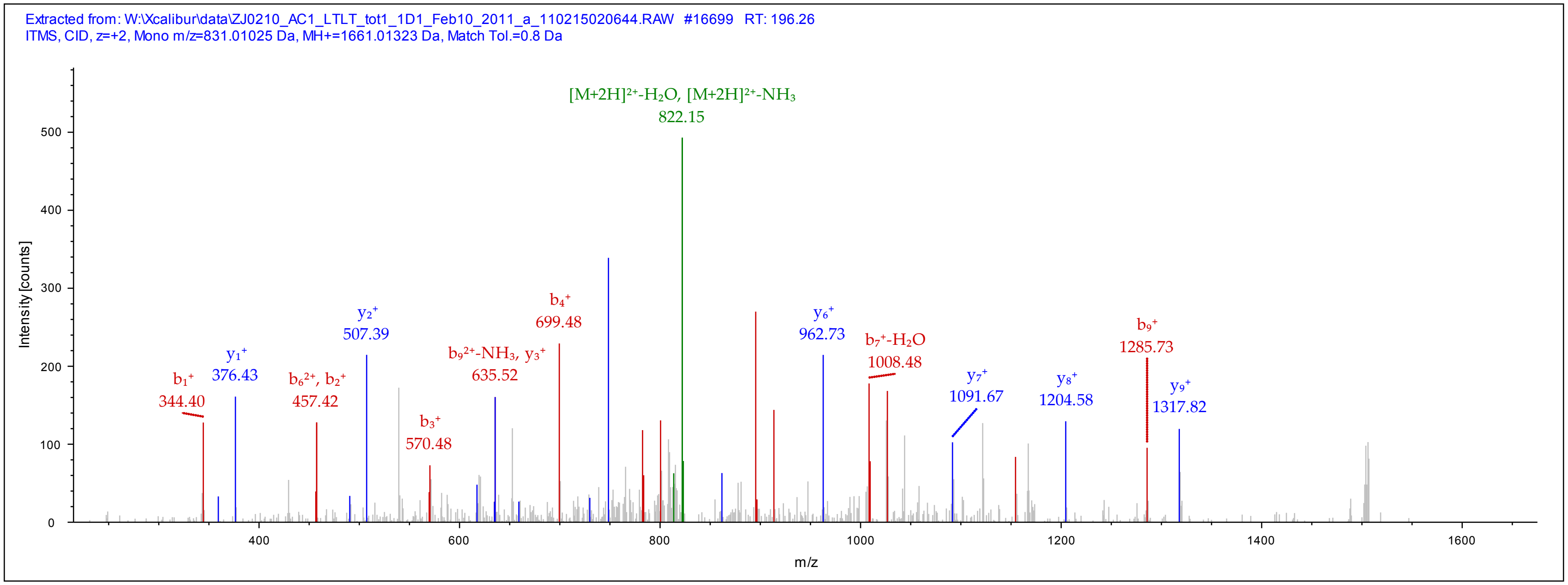
Identified with: Mascot (v1.16); IonScore:52, Exp Value:4.3E-004, Ions matched by search engine: 9/92

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of 28S ribosomal protein S35, mitochondrial
- Isoform 2 of 28S ribosomal protein S35, mitochondrial
- Uncharacterized protein



IPI00218848.5

Sequence: ELAEDDSILK, E1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 795.95416 Da (+0.96 mmu/+1.2 ppm),   MH+: 1590.90105 Da,   RT: 96.21 min,

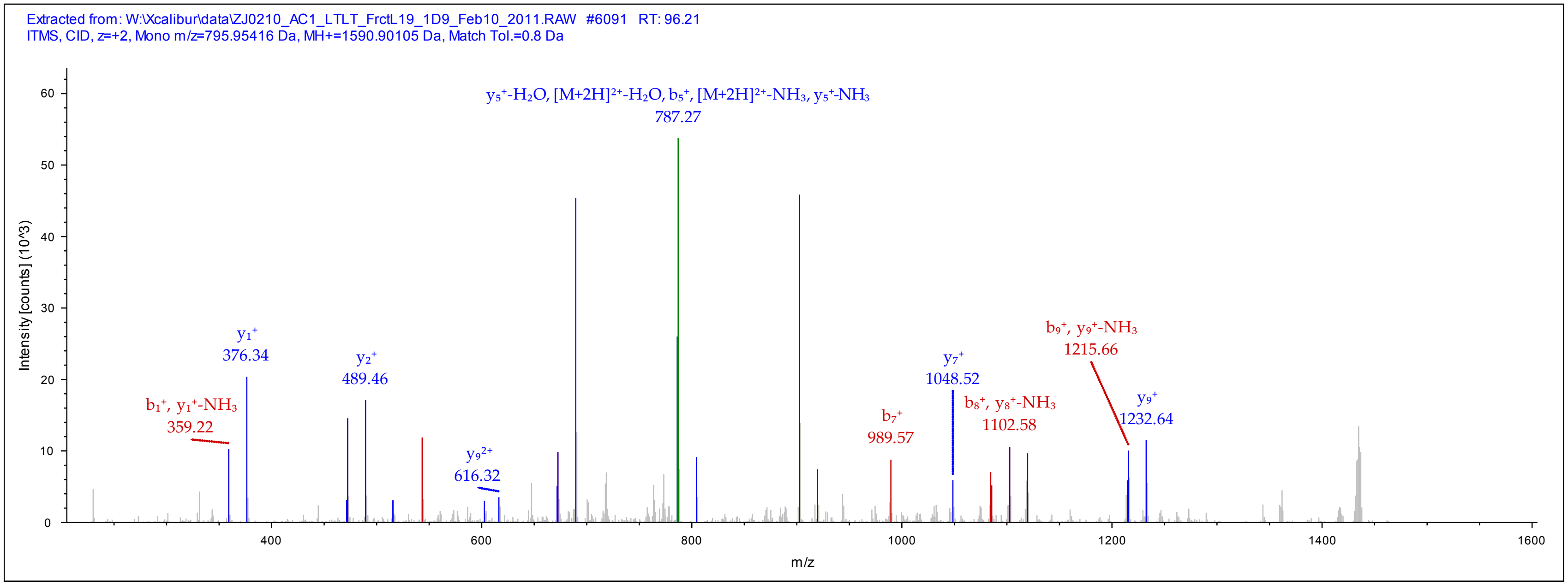
Identified with: Mascot (v1.16); IonScore:55, Exp Value:2.7E-004, Ions matched by search engine: 8/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E lng=72



IPI:IPI00291643.4

Sequence: SWVFTYAQR, S1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 693.87177 Da (-0.27 mmu/-0.38 ppm), MH+: 1386.73625 Da, RT: 102.25 min,

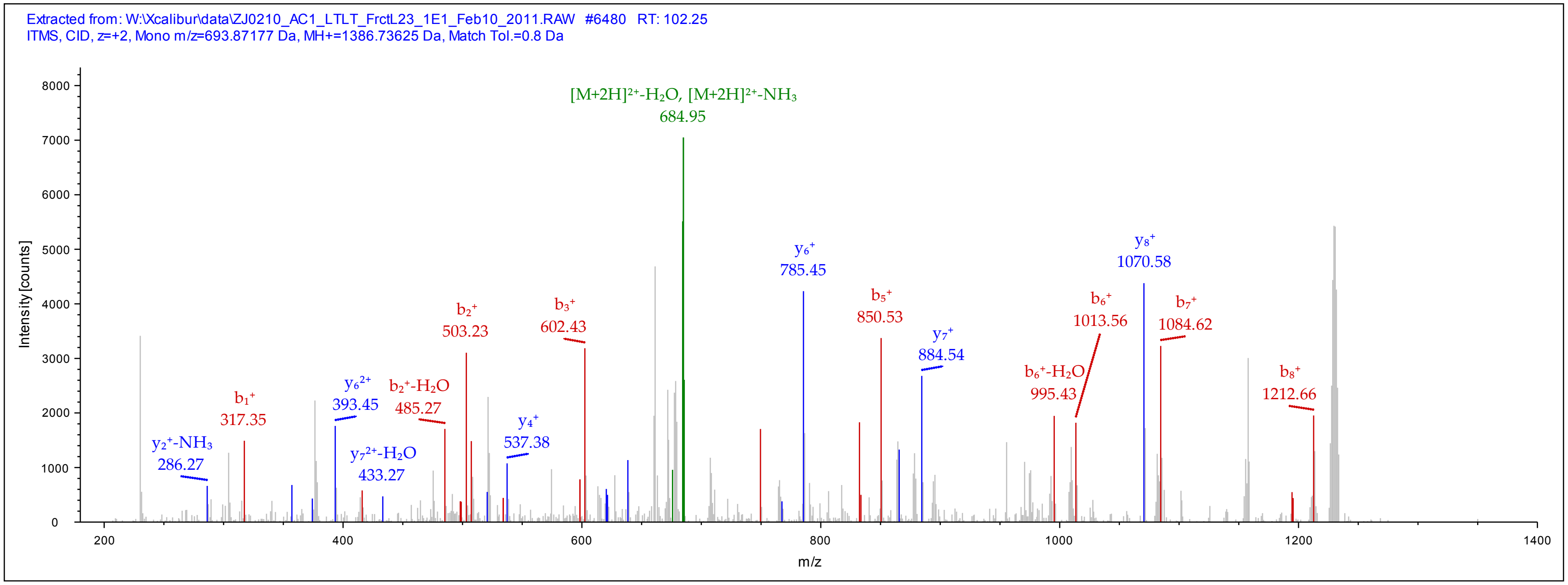
Identified with: Mascot (v1.16); IonScore:33, Exp Value:4.9E-002, Ions matched by search engine: 7/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- SPRY domain-containing protein 4



IPI:IPI00291783.4

Sequence: VYEAVELLK, V1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 761.47040 Da (+2.11 mmu/+2.78 ppm),   MH+: 1521.93352 Da,   RT: 122.74 min,

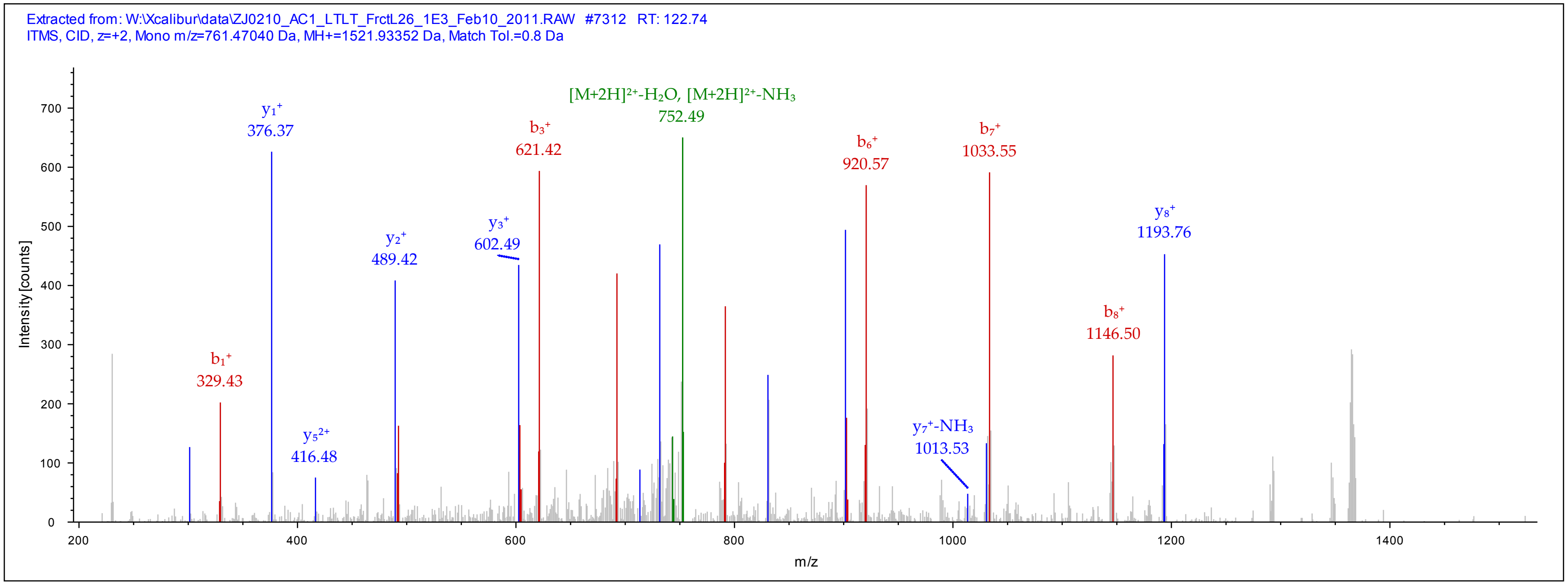
Identified with: Mascot (v1.16); IonScore:42, Exp Value:3.8E-003, Ions matched by search engine: 13/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Gem-associated protein 5



IPI:IPI00293680.4

Sequence: MAEAPPRR, M1-TMT6plex (229.16293 Da), M1-Oxidation (15.99492 Da)

Charge: +2,   Monoisotopic m/z: 586.83228 Da (+8.24 mmu/+14.04 ppm),   MH+: 1172.65727 Da,   RT: 62.80 min,

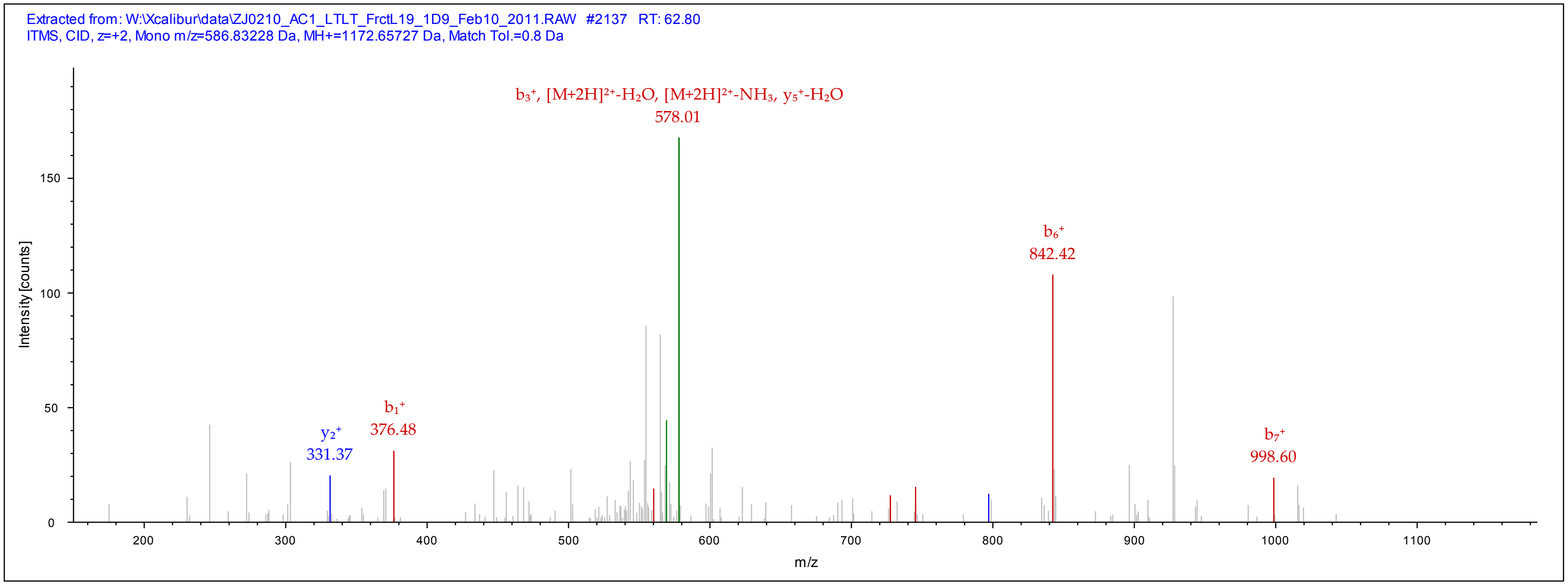
Identified with: Mascot (v1.16); IonScore:29, Exp Value:9.2E-002, Ions matched by search engine: 5/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Potassium voltage-gated channel subfamily KQT member 4
- Isoform 2 of Potassium voltage-gated channel subfamily KQT member 4



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL19_1D9_Feb10_2011.RAW #2137 RT: 62.80
ITMS, CID, z=+2, Mono m/z=586.83228 Da, MH+=1172.65727 Da, Match Tol.=0.8 Da

IPI:IPI00299506.9

Sequence: VIQQLEGAFALVFK, V1-TMT6plex (229.16293 Da), K14-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 1011.11755 Da (+3.9 mmu/+3.86 ppm),   MH+: 2021.22783 Da,   RT: 227.88 min,

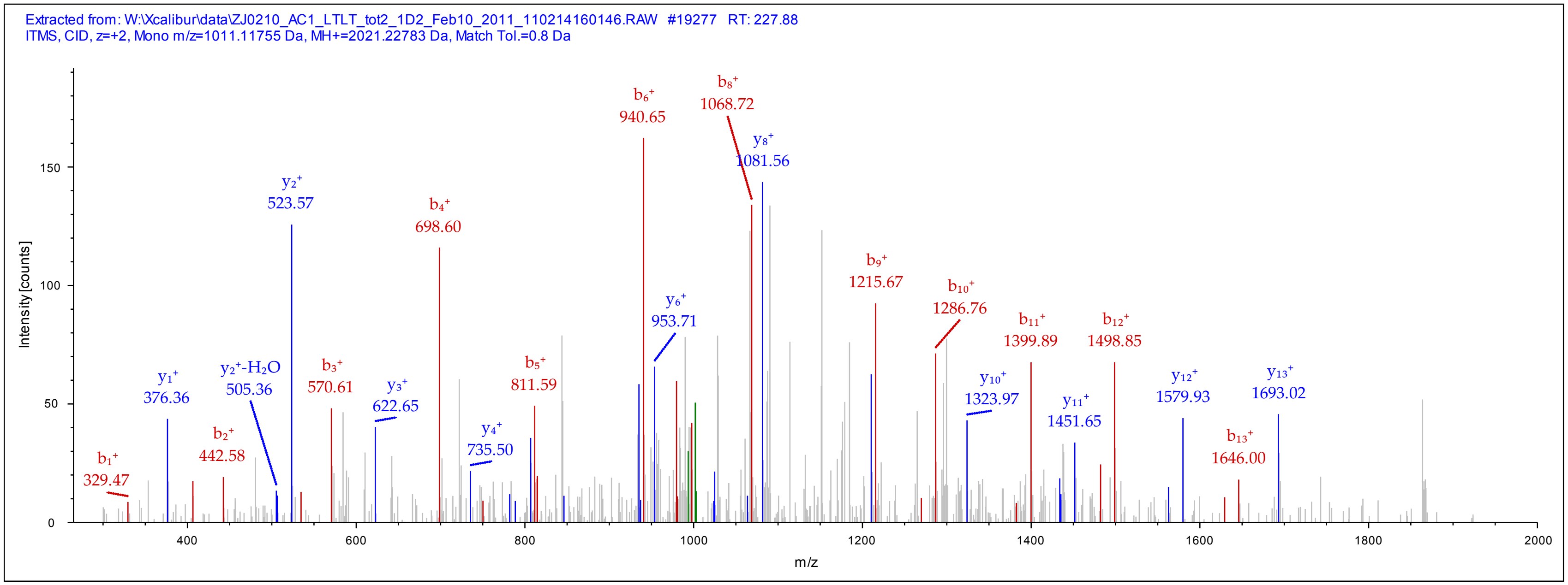
Identified with: Mascot (v1.16); IonScore:50, Exp Value:5.0E-004, Ions matched by search engine: 12/126

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 lng=699
- Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2
- Isoform 2 of Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1



IPI:IPI00301719.2

Sequence: EIGALLQQLR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 685.42188 Da (-0.02 mmu/-0.04 ppm), MH+: 1369.83647 Da, RT: 118.86 min,

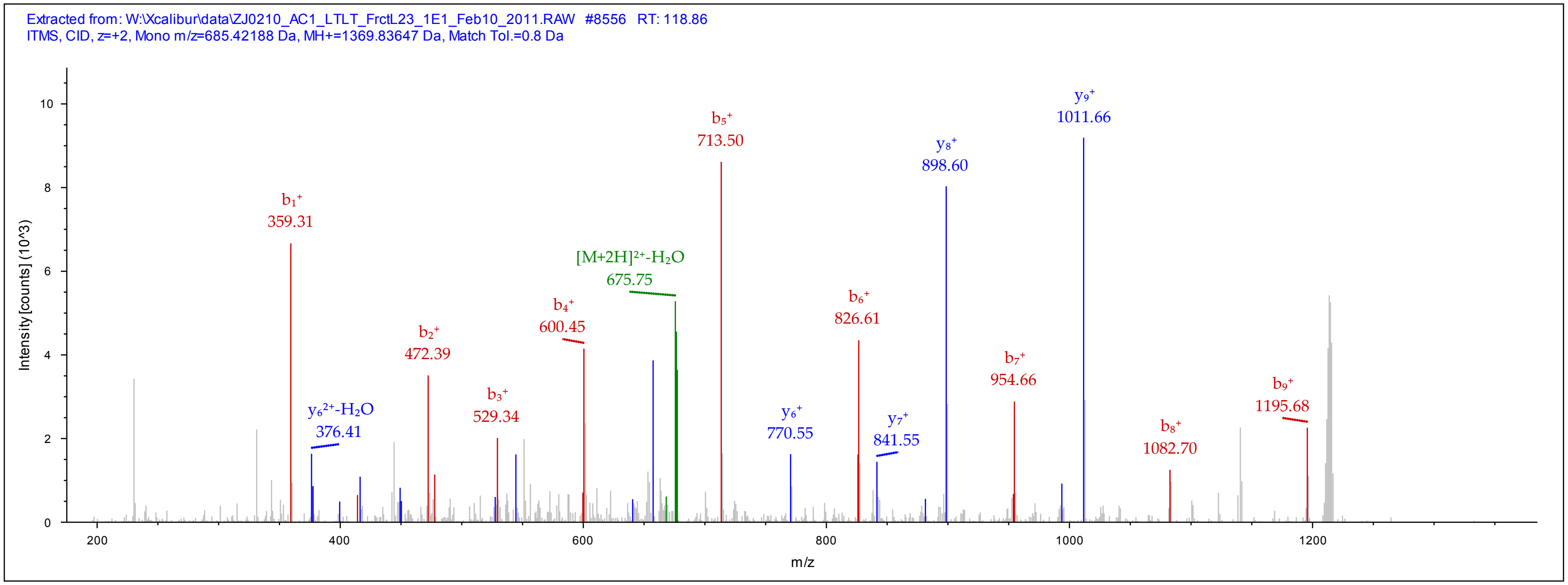
Identified with: Mascot (v1.16); IonScore:53, Exp Value:2.5E-004, Ions matched by search engine: 9/78

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of tRNA-nucleotidyltransferase 1, mitochondrial
- Isoform 2 of tRNA-nucleotidyltransferase 1, mitochondrial



IPI:IPI00333276.4

Sequence: NIADLR, N1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 465.77835 Da (-3.81 mmu/-8.18 ppm), MH+: 930.54943 Da, RT: 105.95 min,

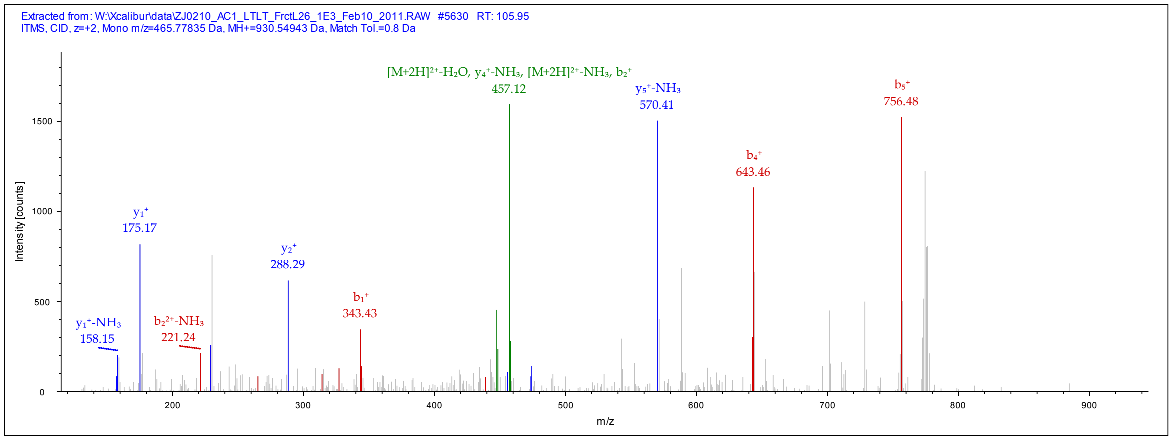
Identified with: Mascot (v1.16); IonScore:32, Exp Value:2.8E-002, Ions matched by search engine: 4/50

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (13):

- Isoform 1 of Neuron navigator 3
- Isoform 1 of Neuron navigator 2
- Isoform 3 of Neuron navigator 2
- Isoform 2 of Neuron navigator 3
- Isoform 3 of Neuron navigator 3
- Isoform 2 of Neuron navigator 2
- Isoform 13 of Neuron navigator 2
- Isoform 8 of Neuron navigator 2
- Isoform 9 of Neuron navigator 2
- Isoform 10 of Neuron navigator 2
- Isoform 12 of Neuron navigator 2



IPI:IPI00335824.5

Sequence: TVEEVTVER, T1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 645.86029 Da (+1.5 mmu/+2.32 ppm), MH+: 1290.71330 Da, RT: 77.90 min,

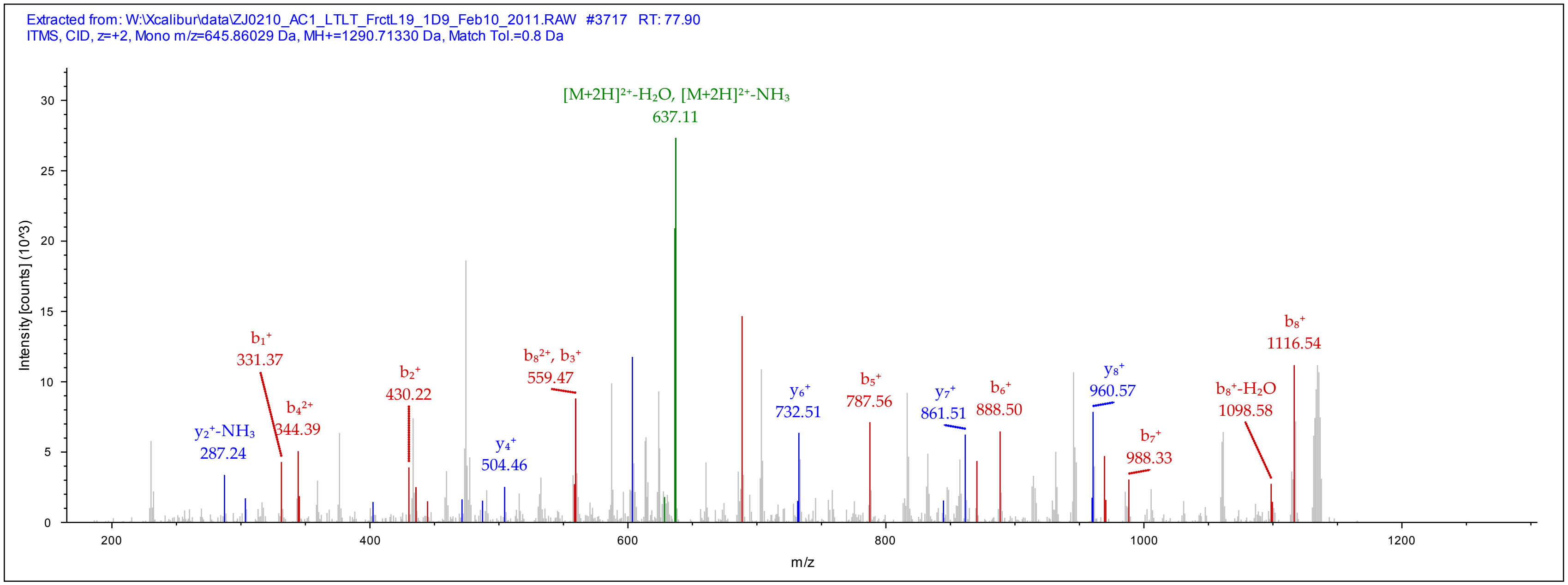
Identified with: Mascot (v1.16); IonScore:31, Exp Value:6.0E-002, Ions matched by search engine: 7/78

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform Long of Tight junction protein ZO-1
- Isoform Short of Tight junction protein ZO-1
- Putative uncharacterized protein DKFZp686A1195 lng=1692
- Tight junction protein ZO-1 lng=1727



IPI00383971.4

Sequence: VIEINPYLLGTMAGGAADCSFWER, V1-TMT6plex (229.16293 Da), C19-Carbamidomethyl (57.02146 Da)

Charge: +3, Monoisotopic m/z: 967.15192 Da (+3.02 mmu/+3.12 ppm), MH+: 2899.44120 Da, RT: 191.22 min,

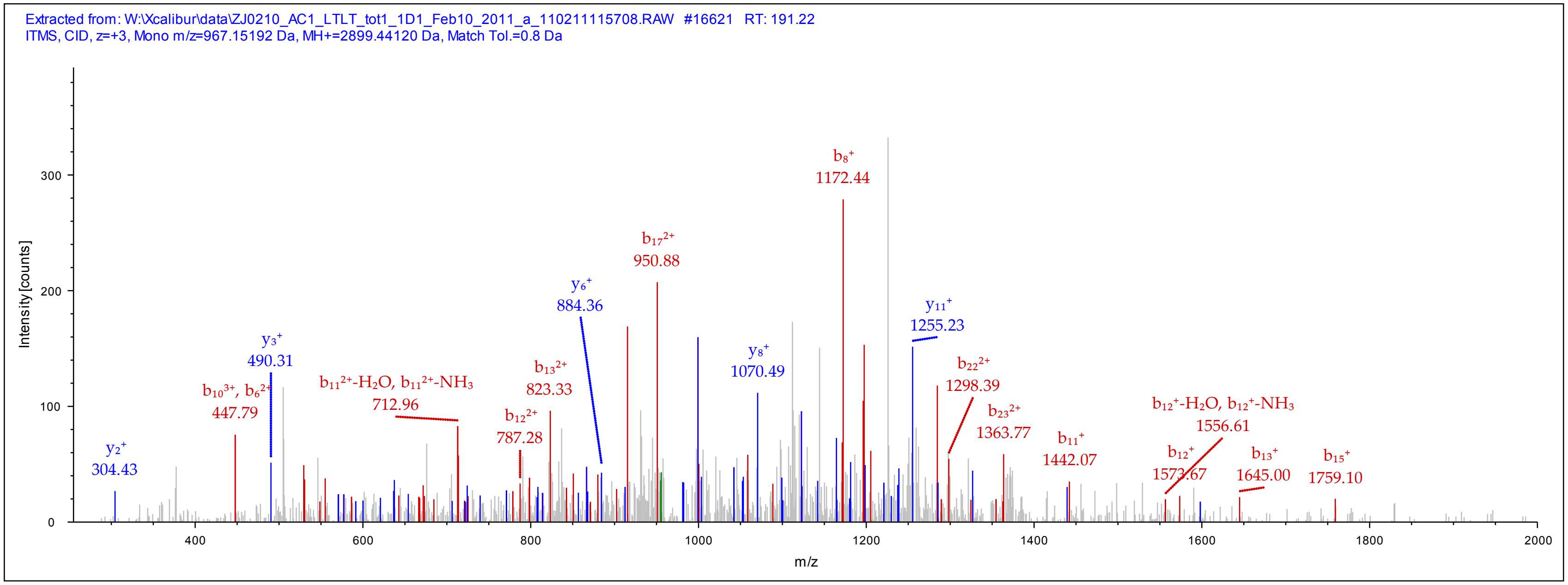
Identified with: Mascot (v1.16); IonScore:41, Exp Value:1.7E-002, Ions matched by search engine: 15/262

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Proteasome subunit beta type-5
- proteasome beta 5 subunit isoform 3 lng=203



IPI:IPI00385751.5

Sequence: DLVGELGTALR, D1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 686.90417 Da (+0.63 mmu/+0.92 ppm), MH+: 1372.80107 Da, RT: 111.09 min,

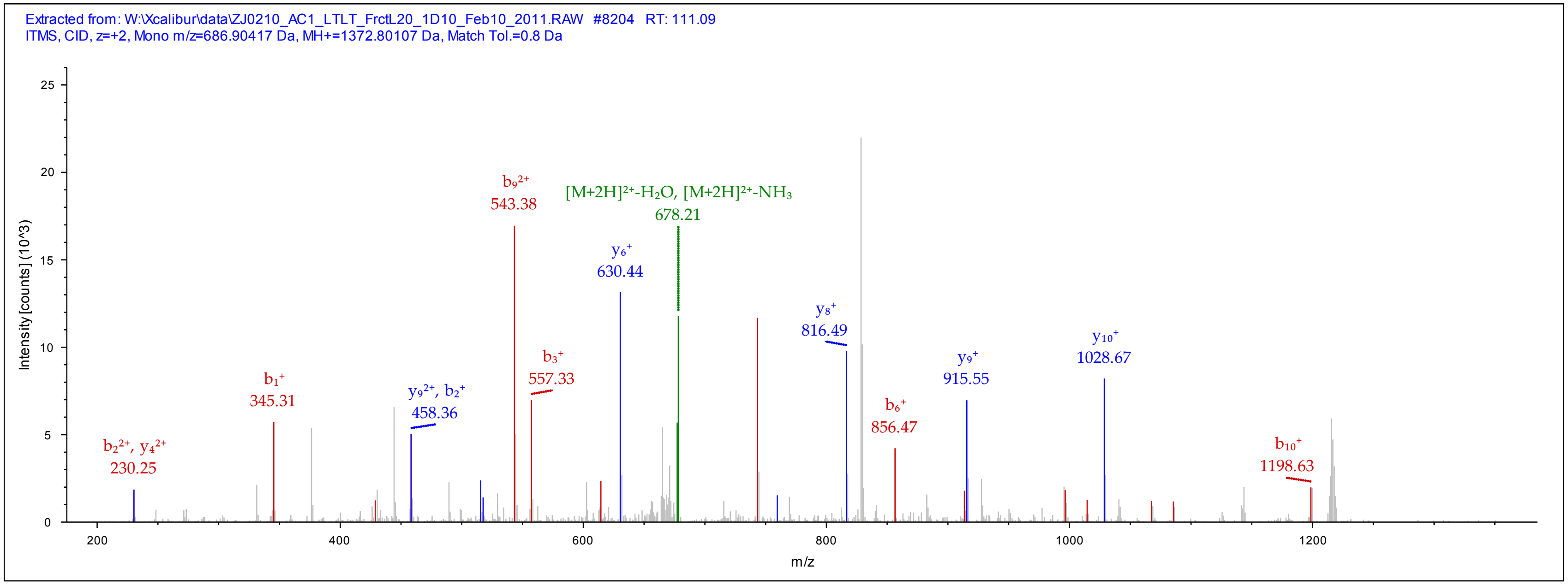
Identified with: Mascot (v1.16); IonScore:39, Exp Value:1.4E-002, Ions matched by search engine: 10/94

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Tissue alpha-L-fucosidase
- Uncharacterized protein



IPI00385756.2

Sequence: LYSIFIK, L1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 671.43335 Da (+2.39 mmu/+3.55 ppm),   MH+: 1341.85942 Da,   RT: 132.08 min,

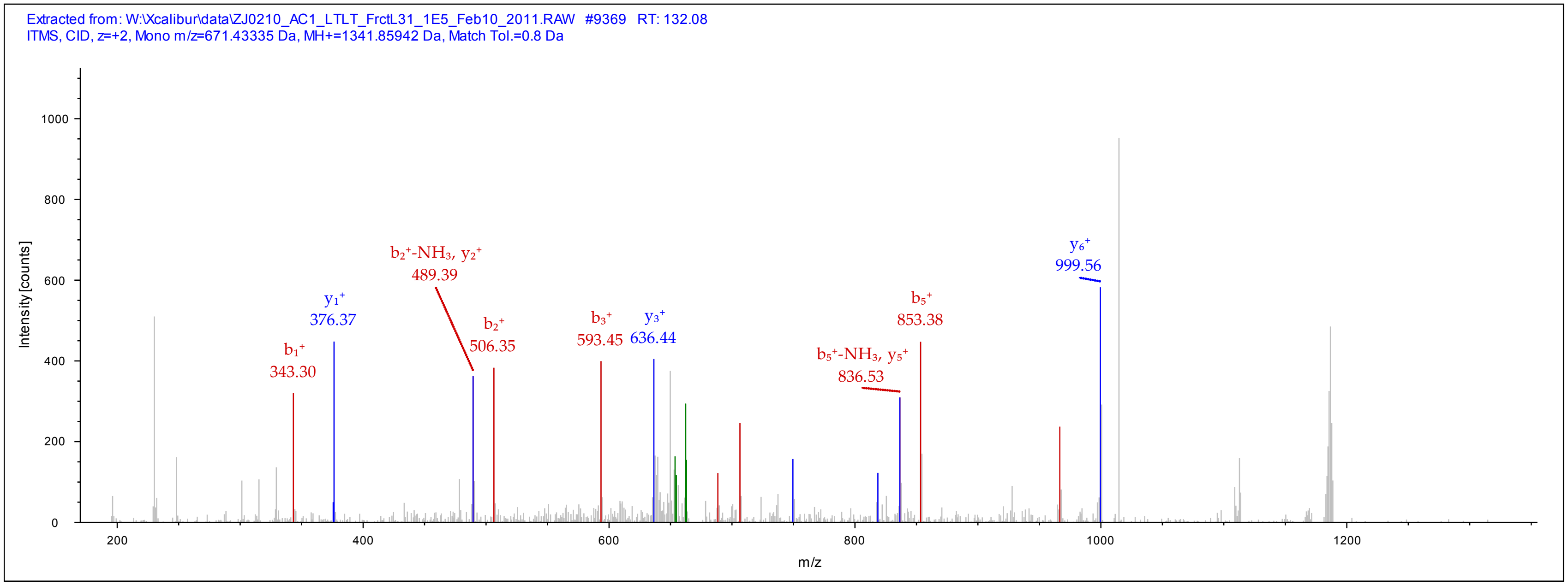
Identified with: Mascot (v1.16); IonScore:30, Exp Value:5.0E-002, Ions matched by search engine: 12/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- cDNA, FLJ79367, highly similar to Homo sapiens MAX dimerization protein 3 (MXD3), mRNA lng=388



IPI:IPI00395764.3

Sequence: EEIEATK, E1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 639.37238 Da (+1.07 mmu/+1.67 ppm), MH+: 1277.73747 Da, RT: 76.13 min,

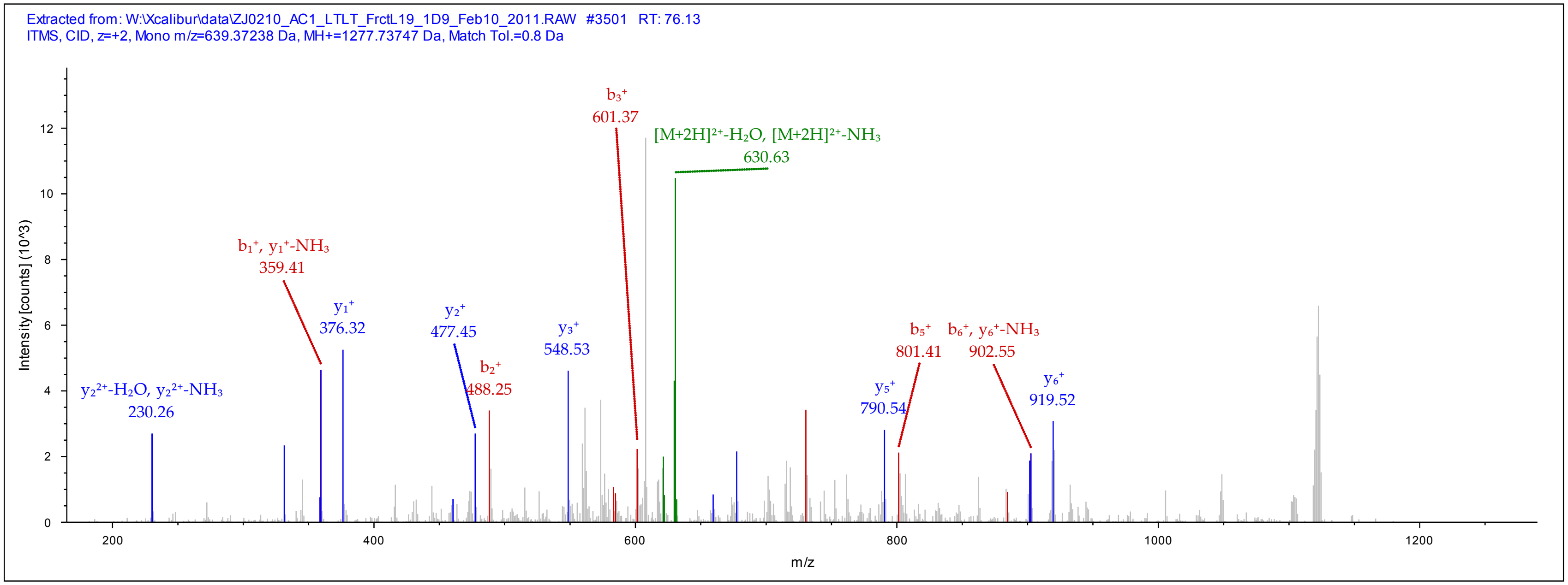
Identified with: Mascot (v1.16); IonScore:30, Exp Value:7.5E-002, Ions matched by search engine: 5/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- 39S ribosomal protein L37, mitochondrial
- Mitochondrial ribosomal protein L37
- Uncharacterized protein



IPI00401804.3

Sequence: AFNFLNEIK, A1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 777.45813 Da (-0.13 mmu/-0.16 ppm), MH+: 1553.90898 Da, RT: 125.58 min,

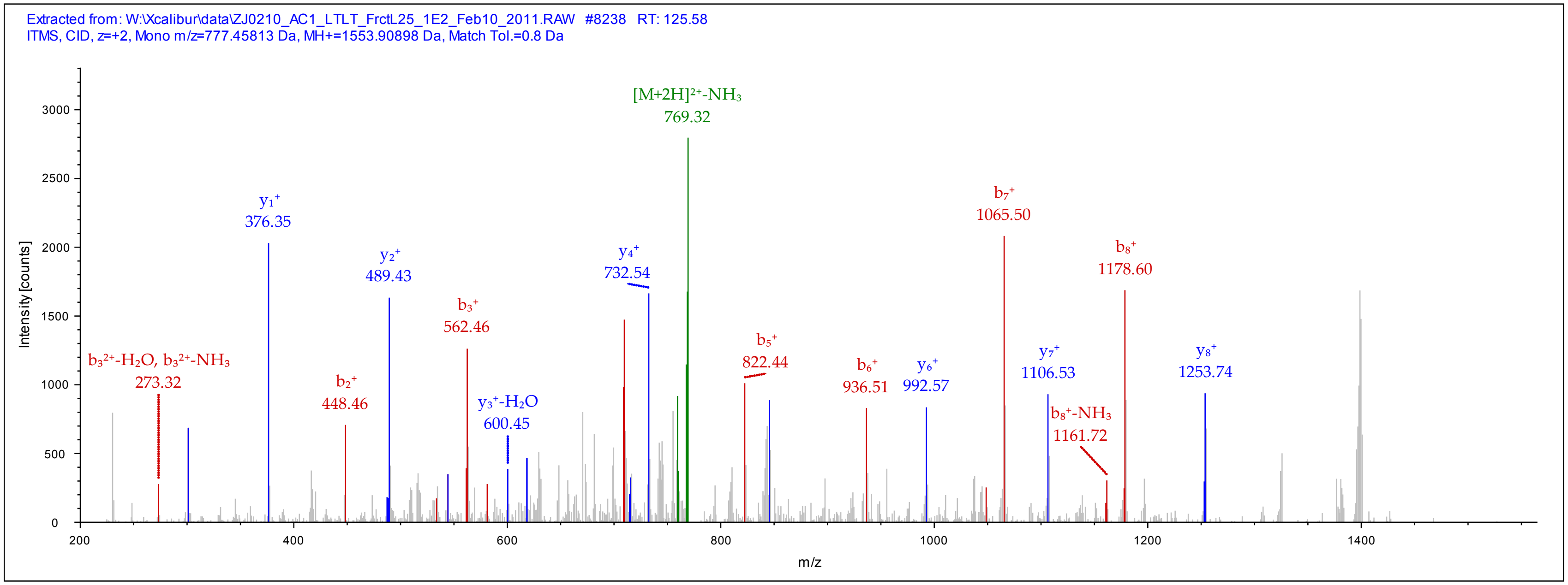
Identified with: Mascot (v1.16); IonScore:37, Exp Value:1.6E-002, Ions matched by search engine: 8/76

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Vesicle-associated membrane protein 7
- Isoform 2 of Vesicle-associated membrane protein 7
- Isoform 3 of Vesicle-associated membrane protein 7 lng=179



IPI00410226.3

Sequence: DLEAEHVEVEDTTLNR, D1-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 700.35535 Da (+2 mmu/+2.86 ppm), MH+: 2099.05149 Da, RT: 91.69 min,

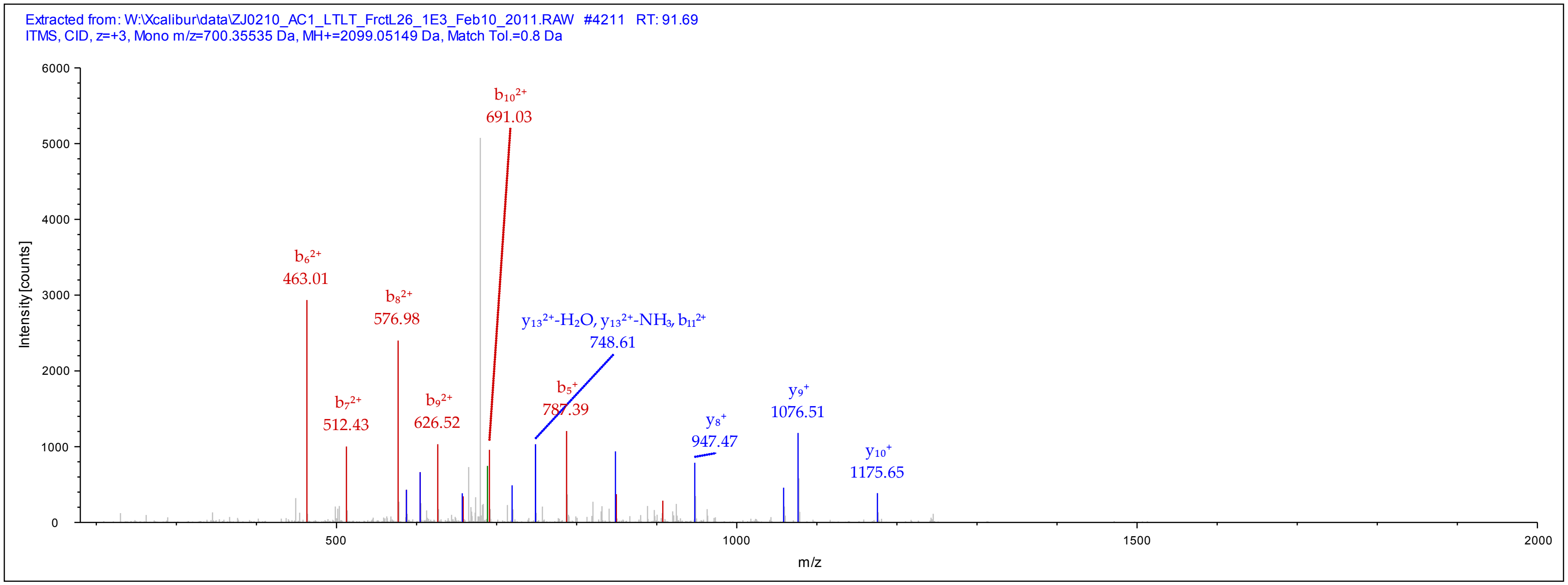
Identified with: Mascot (v1.16); IonScore:48, Exp Value:2.4E-003, Ions matched by search engine: 16/146

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of BolA-like protein 2 lng=86
- BolA-like protein 2 lng=152
- Isoform 2 of BolA-like protein 2 lng=58
- Putative uncharacterized protein BOLA2B lng=58



IPI:IPI00412448.4

Sequence: LHGARGLR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 554.84033 Da (-8.38 mmu/-15.1 ppm), MH+: 1108.67339 Da, RT: 112.51 min,

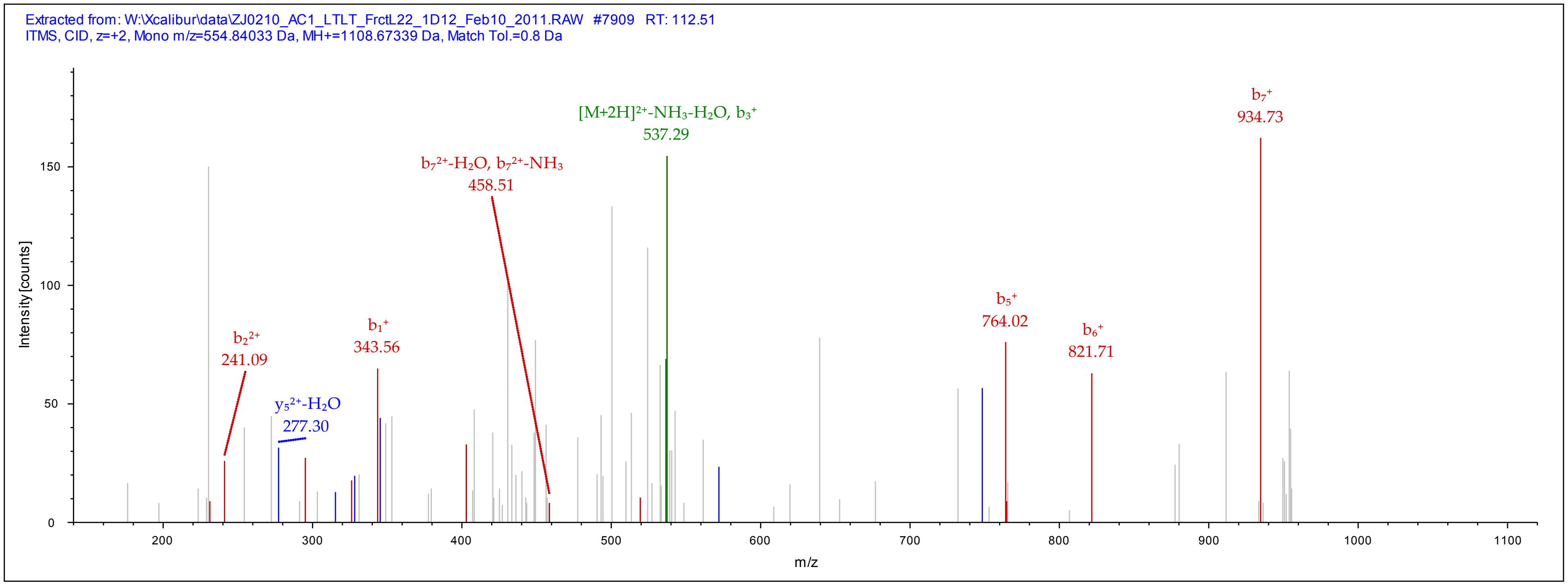
Identified with: Mascot (v1.16); IonScore:32, Exp Value:4.8E-002, Ions matched by search engine: 5/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

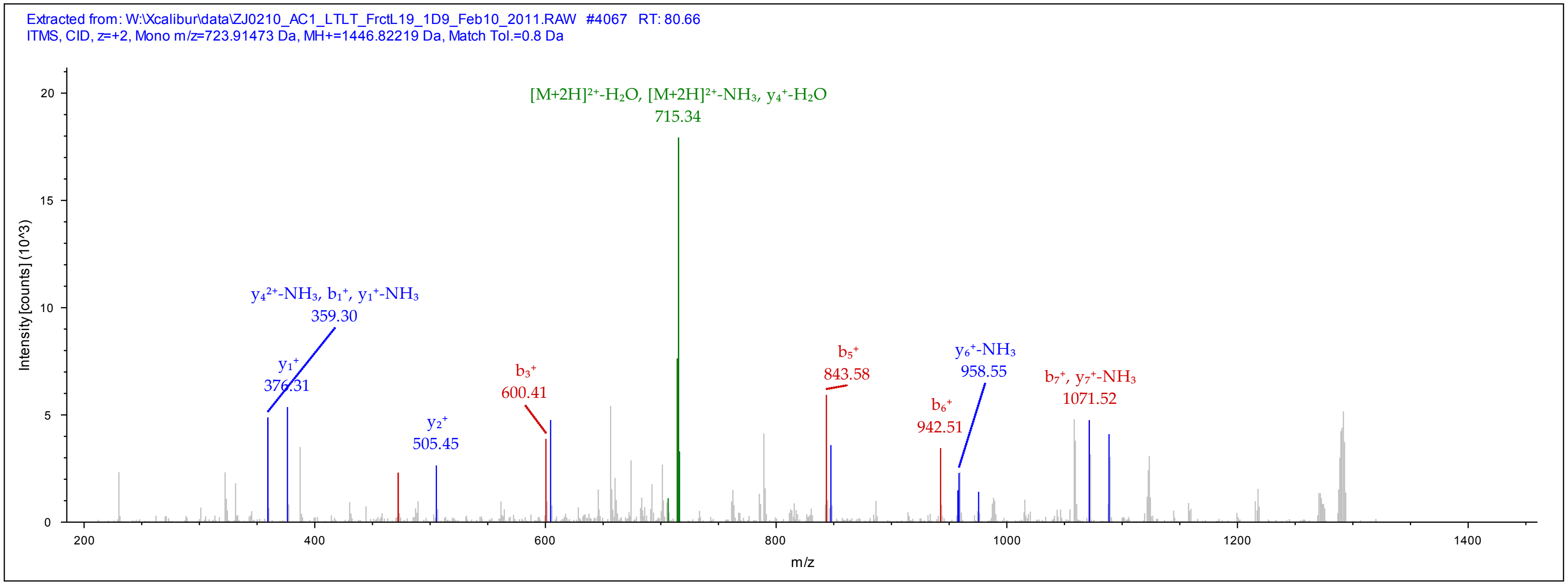
Protein references (4):

- Isoform 1 of Podocan-like protein 1
- Isoform 2 of Podocan-like protein 1
- cDNA FLJ51218, weakly similar to Mus musculus podocan (Podn), mRNA
- podocan-like protein 1 isoform 2



IPI00414963.2
Sequence: ELQNEVEK, E1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)
Charge: +2, Monoisotopic m/z: 723.91473 Da (+0.86 mmu/+1.19 ppm), MH+: 1446.82219 Da, RT: 80.66 min,
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.5E-002, Ions matched by search engine: 7/78
Fragment match tolerance used for search: 0.8 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):
- Isoform 1 of Polyadenylate-binding protein 2 lng=306
- Isoform 2 of Polyadenylate-binding protein 2 lng=296



IPI:IPI00419046.3

Sequence: LGAVGRAR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 514.83630 Da (+6.33 mmu/+12.3 ppm),   MH+: 1028.66533 Da,   RT: 102.98 min,

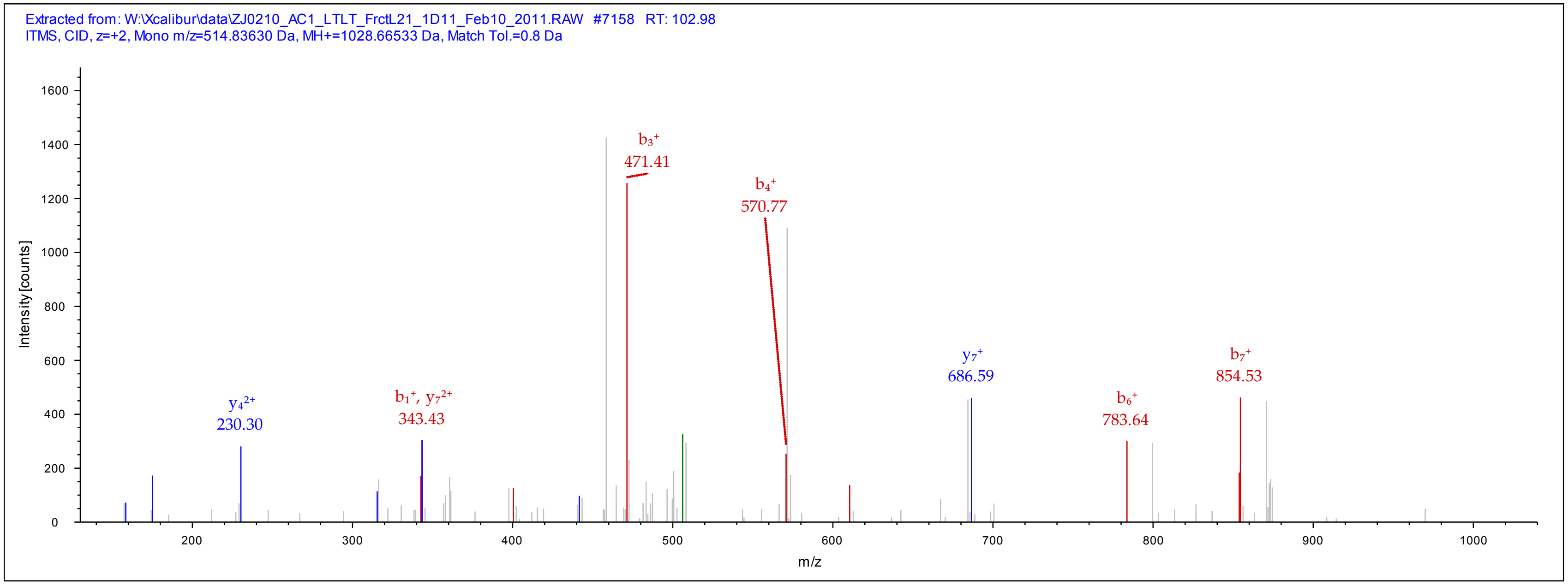
Identified with: Mascot (v1.16); IonScore:39, Exp Value:4.7E-003, Ions matched by search engine: 6/62

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Rho guanine nucleotide exchange factor 5
- Rho guanine nucleotide exchange factor 35



IPI:IPI00434390.2

Sequence: IDVLLDTFR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 660.89160 Da (+1.7 mmu/+2.58 ppm), MH+: 1320.77593 Da, RT: 134.31 min,

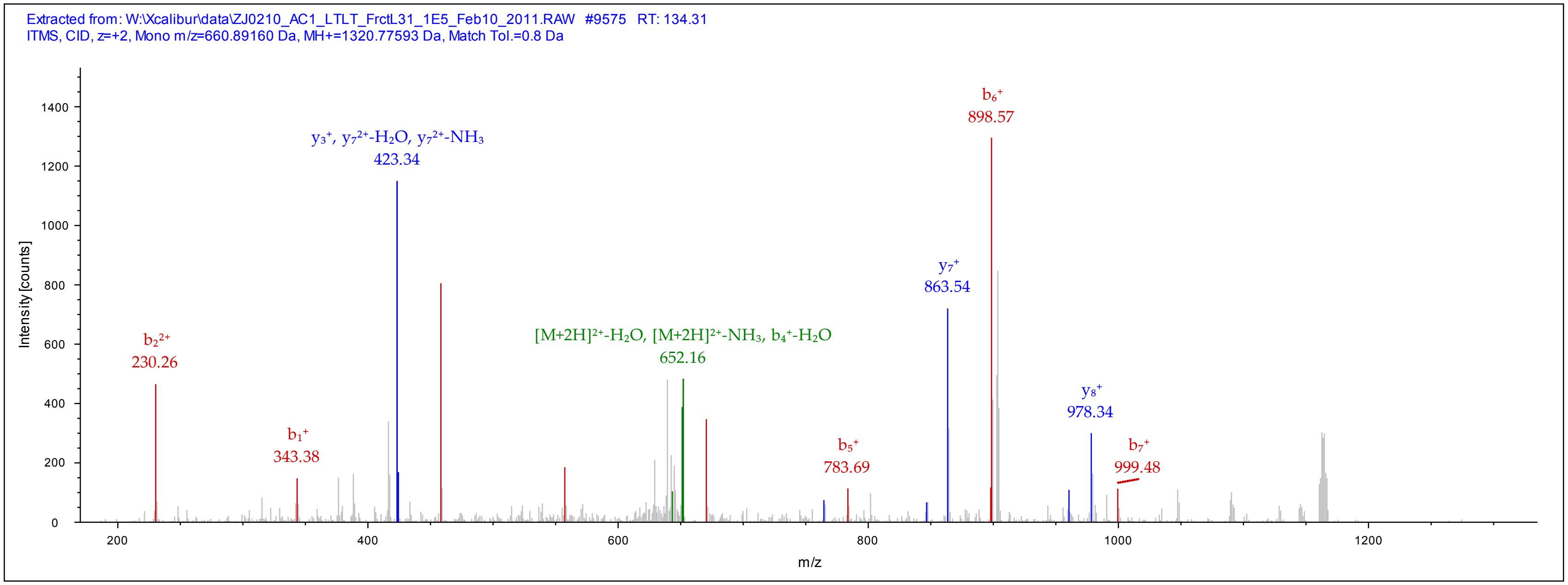
Identified with: Mascot (v1.16); IonScore:31, Exp Value:7.6E-002, Ions matched by search engine: 6/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Activating signal cointegrator 1 complex subunit 1
- cDNA FLJ55237, highly similar to Homo sapiens activating signal cointegrator 1 complex subunit 1 (ASCC1), mRNA



IPI:IPI00455359.2

Sequence: QIDDLK, Q1-TMT6plex (229.16293 Da), K6-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 595.36340 Da (+0.12 mmu/+0.2 ppm), MH+: 1189.71953 Da, RT: 82.08 min,

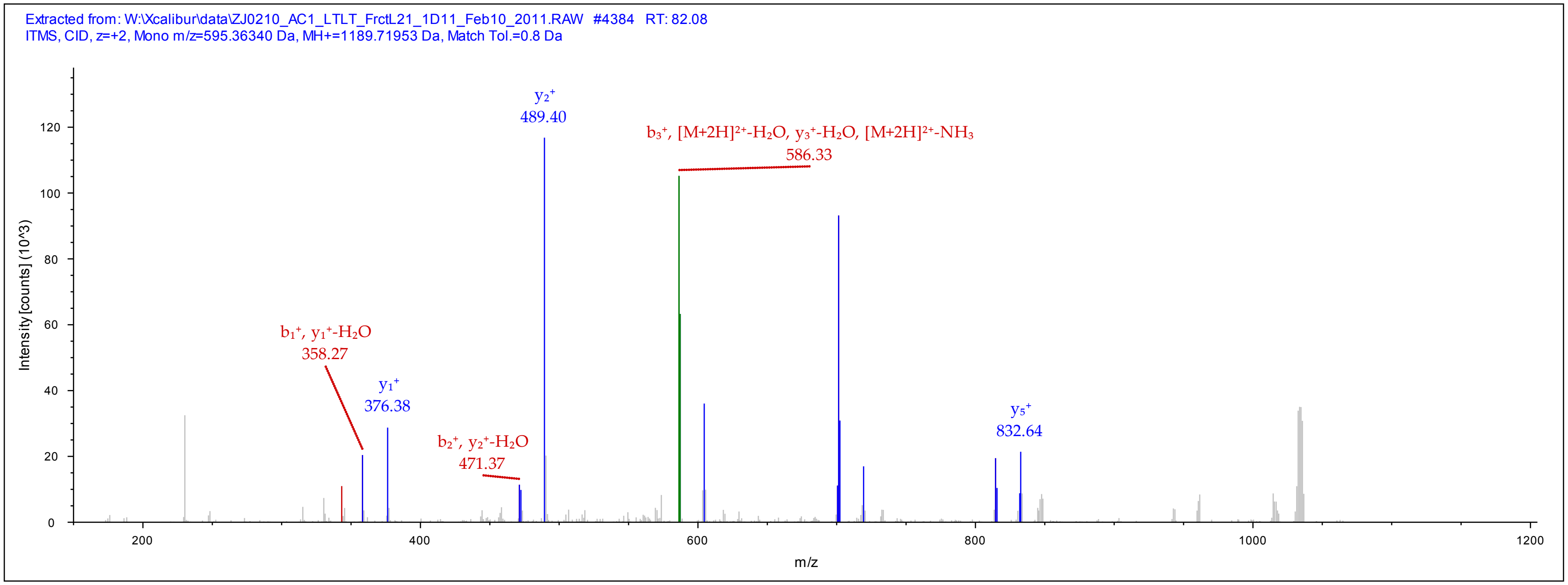
Identified with: Mascot (v1.16); IonScore:32, Exp Value:5.6E-002, Ions matched by search engine: 5/52

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of Ataxin-2
- Isoform 2 of Ataxin-2
- Isoform 4 of Ataxin-2



IPI00514131.6

Sequence: NLLQVDLTK, N1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 751.47131 Da (-0.05 mmu/-0.06 ppm),   MH+: 1501.93535 Da,   RT: 107.42 min,

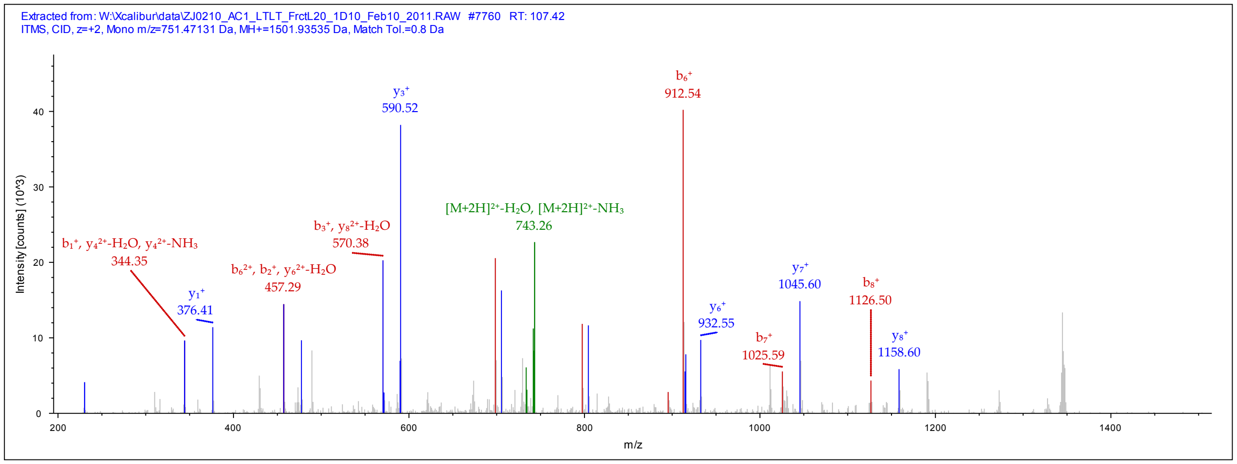
Identified with: Mascot (v1.16); IonScore:43, Exp Value:2.9E-003, Ions matched by search engine: 8/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (11):

- Isoform 1 of cAMP-dependent protein kinase catalytic subunit beta
- Isoform 1 of cAMP-dependent protein kinase catalytic subunit alpha
- Isoform 2 of cAMP-dependent protein kinase catalytic subunit alpha
- Isoform 2 of cAMP-dependent protein kinase catalytic subunit beta
- Putative uncharacterized protein PRKACB lng=322
- Isoform 5 of cAMP-dependent protein kinase catalytic subunit beta lng=354
- Isoform 7 of cAMP-dependent protein kinase catalytic subunit beta lng=355
- Isoform 4 of cAMP-dependent protein kinase catalytic subunit beta lng=338
- Isoform 3 of cAMP-dependent protein kinase catalytic subunit beta lng=339
- cDNA, FLJ79014, highly similar to cAMP-dependent protein kinase, beta-catalytic subunit lng=314
- cDNA FLJ52554, highly similar to cAMP-dependent protein kinase, beta-catalytic subunit lng=358



IPI:IPI00514944.4

Sequence: EAGLAPVPMIIFAK, E1-TMT6plex (229.16293 Da), K14-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 958.08112 Da (+2.88 mmu/+3.01 ppm),   MH+: 1915.15495 Da,   RT: 136.74 min,

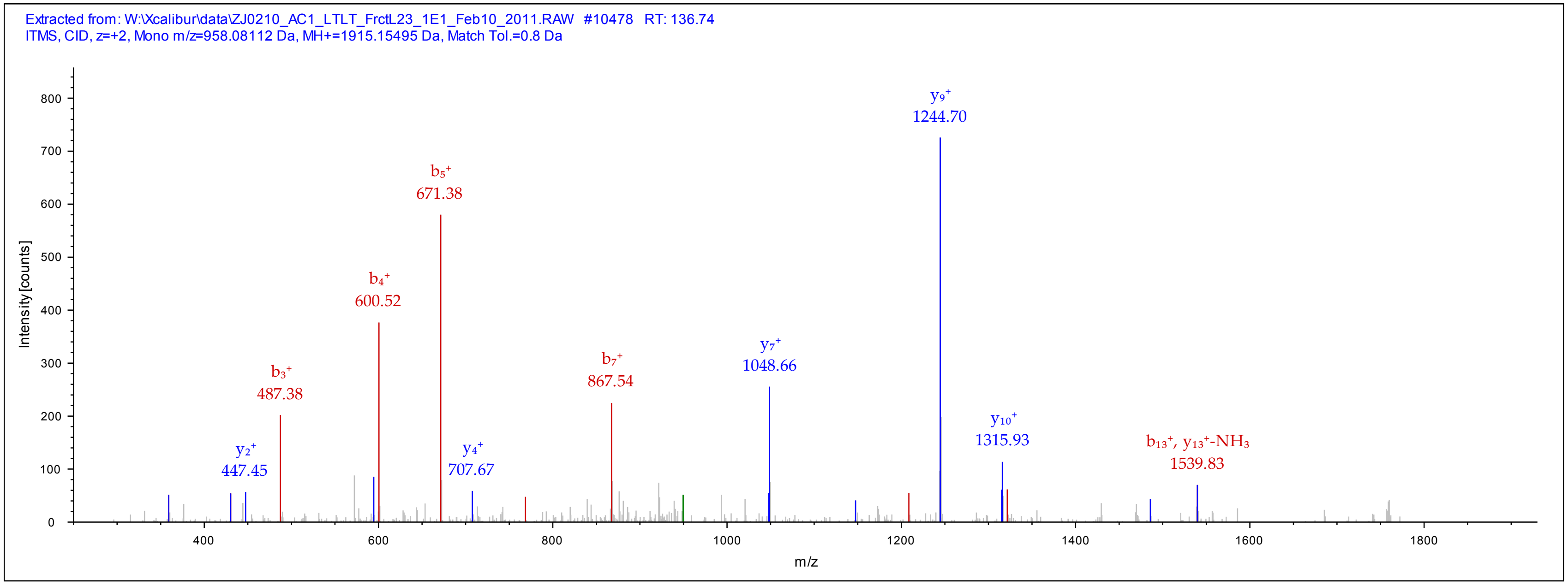
Identified with: Mascot (v1.16); IonScore:70, Exp Value:6.9E-006, Ions matched by search engine: 10/104

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Uroporphyrinogen decarboxylase
- Uroporphyrinogen decarboxylase



IPI:IPI00556201.3

Sequence: LTPLTVLLR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 627.92230 Da (+1.3 mmu/+2.08 ppm), MH+: 1254.83733 Da, RT: 131.46 min,

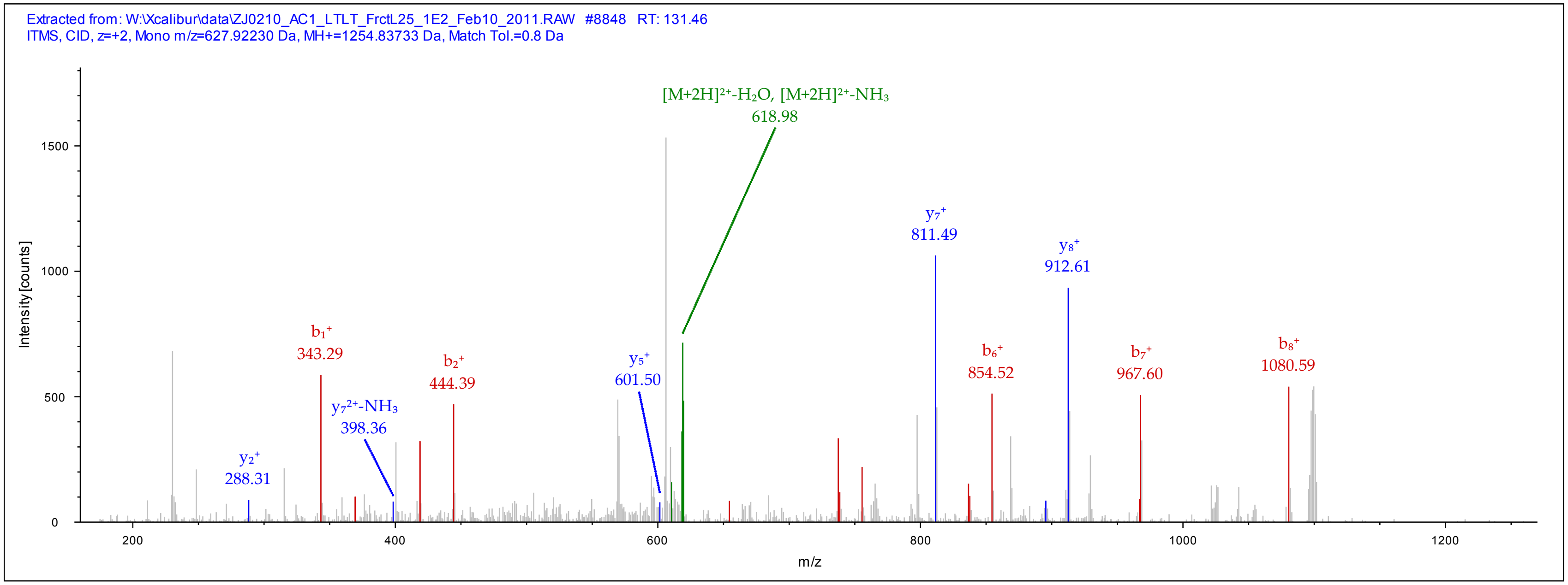
Identified with: Mascot (v1.16); IonScore:30, Exp Value:8.7E-003, Ions matched by search engine: 6/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Bromodomain-containing protein 1
- Bromodomain containing 1, isoform CRA_a lng=1189
- Bromodomain containing protein 1 variant
- cDNA FLJ61578, highly similar to Bromodomain-containing protein 1
- cDNA FLJ51191, highly similar to Bromodomain-containing protein 1 lng=784



IPI:IPI00604495.3

Sequence: ILEIEDLFSSLK, I1-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 933.05670 Da (+1.24 mmu/+1.33 ppm), MH+: 1865.10613 Da, RT: 208.11 min,

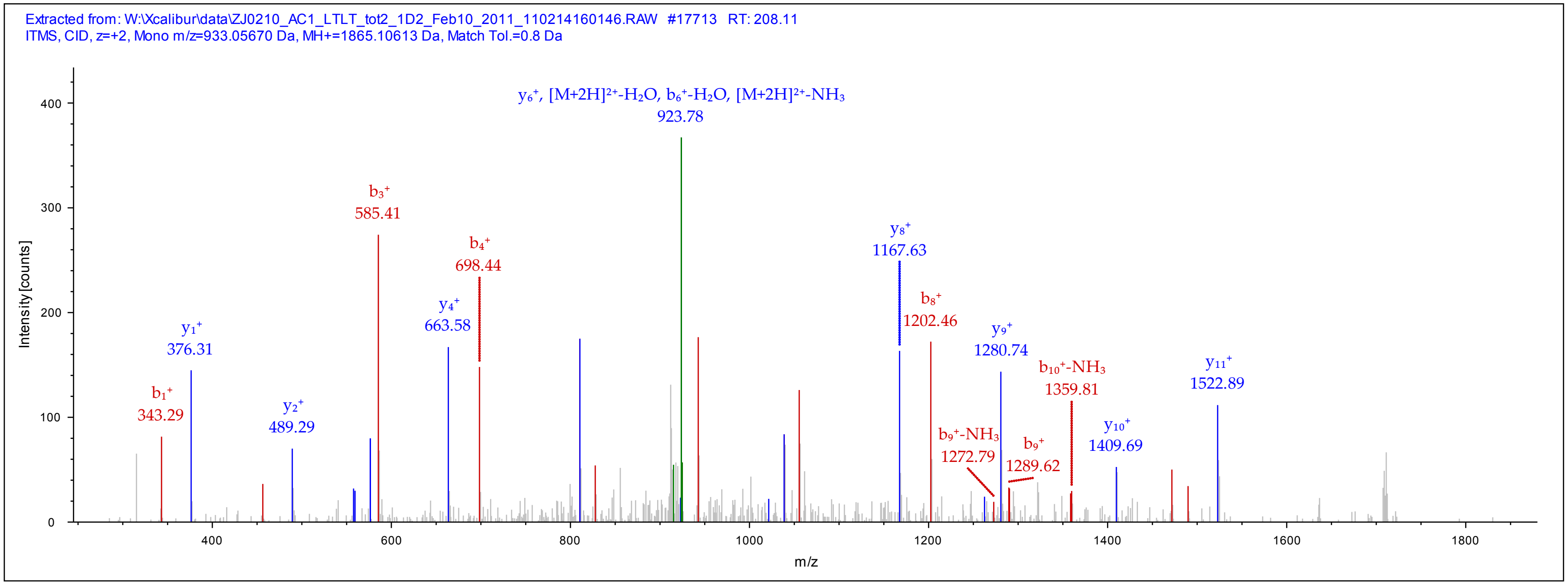
Identified with: Mascot (v1.16); IonScore:88, Exp Value:1.1E-007, Ions matched by search engine: 11/102

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of MAGUK p55 subfamily member 5
- Isoform 2 of MAGUK p55 subfamily member 5



IPI:IPI00607550.3

Sequence: LLEAISSLDGK, L1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 802.49017 Da (+2.96 mmu/+3.69 ppm), MH+: 1603.97307 Da, RT: 130.04 min,

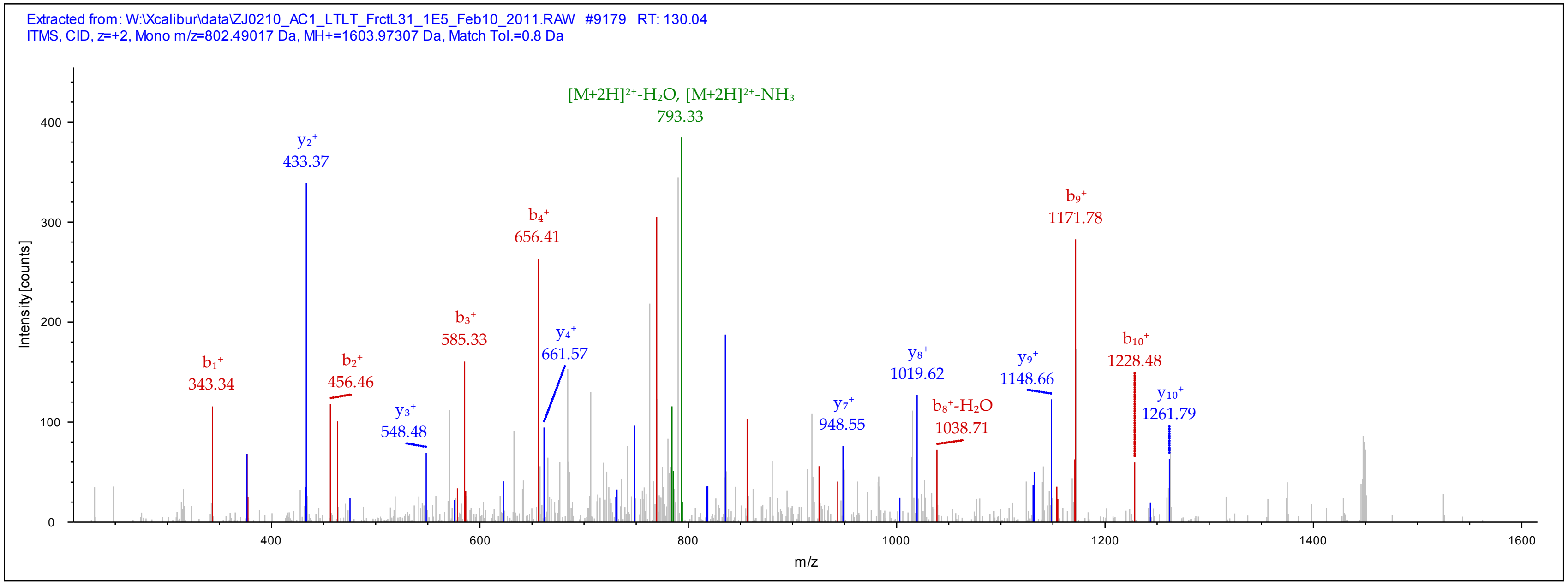
Identified with: Mascot (v1.16); IonScore:43, Exp Value:4.2E-003, Ions matched by search engine: 16/92

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of U3 small nucleolar RNA-associated protein 14 homolog A
- U3 small nucleolar RNA-associated protein 14 homolog A isoform 2



IPI00640930.2

Sequence: IDVLDPEELK, I1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 814.98010 Da (+0.88 mmu/+1.08 ppm), MH+: 1628.95293 Da, RT: 114.88 min,

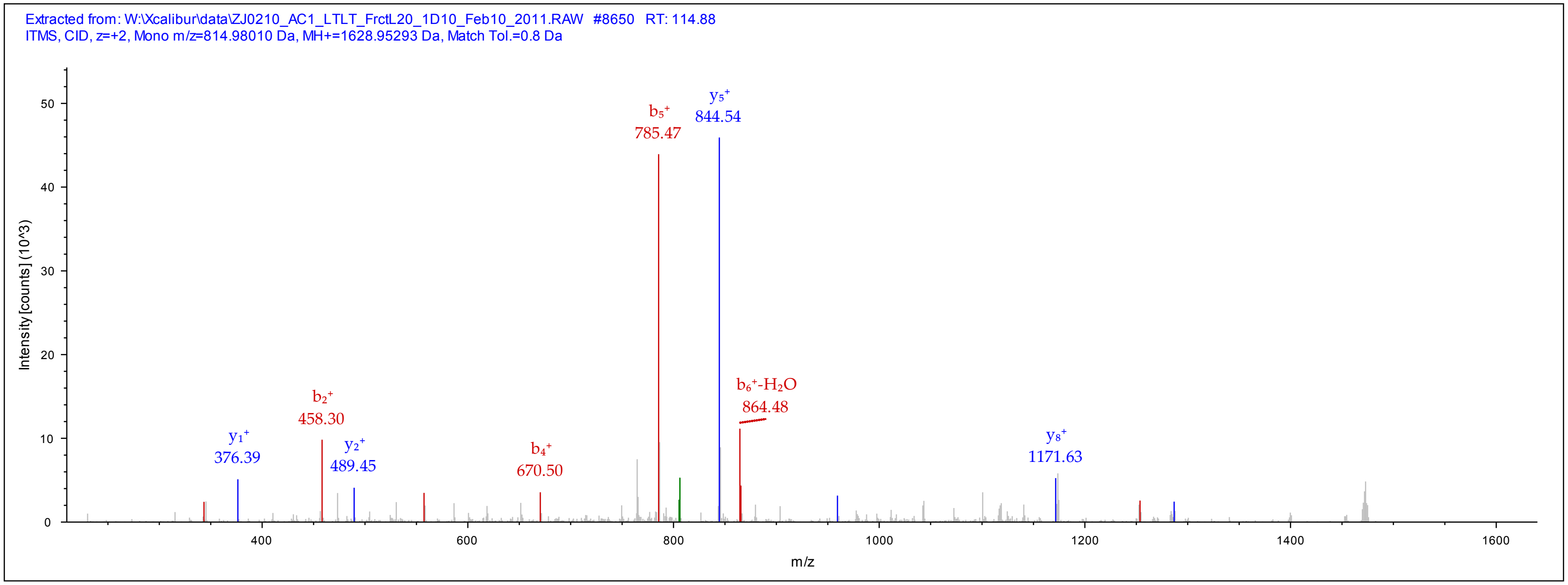
Identified with: Mascot (v1.16); IonScore:35, Exp Value:2.7E-002, Ions matched by search engine: 12/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- UPF0368 protein Cxorf26
- Putative uncharacterized protein CXorf26 lng=232



IPI00641692.3

Sequence: LYDVVAVFPK, L1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 804.99213 Da (+0.2 mmu/+0.24 ppm), MH+: 1608.97698 Da, RT: 126.50 min,

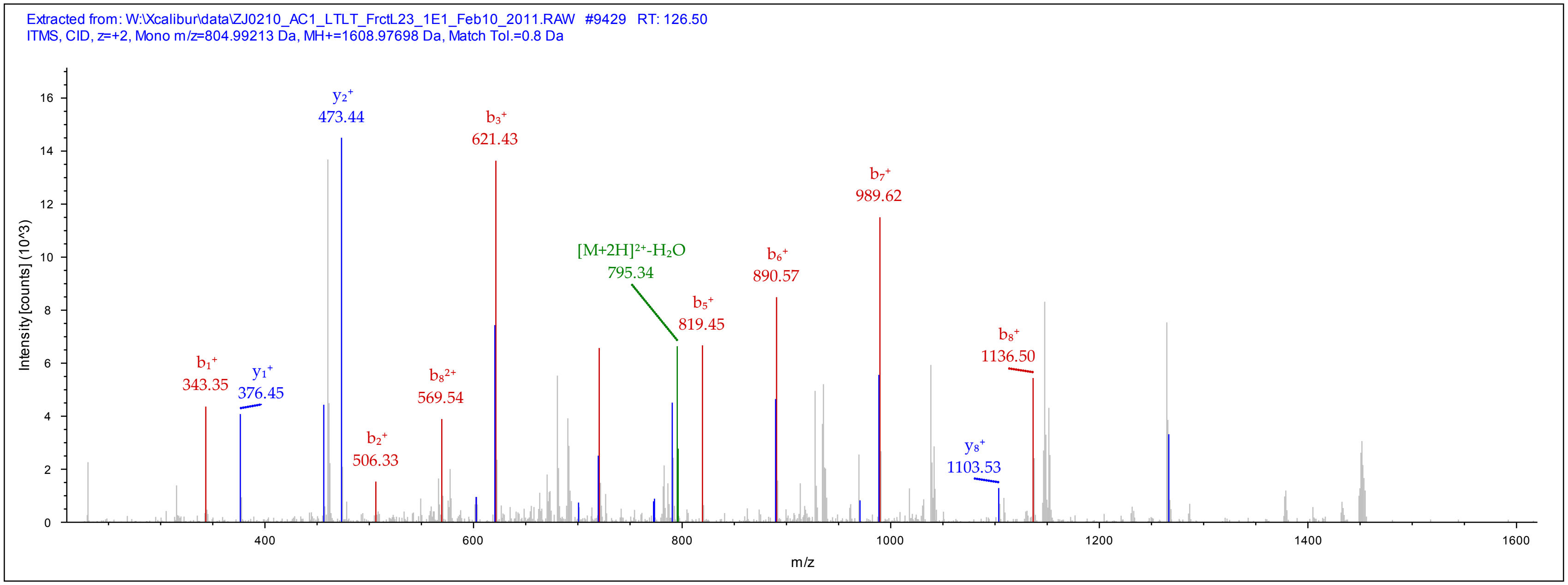
Identified with: Mascot (v1.16); IonScore:30, Exp Value:6.2E-002, Ions matched by search engine: 7/72

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Ribonuclease P protein subunit p30
- Ribonuclease P lng=344
- Ribonuclease P lng=212
- ribonuclease P protein subunit p30 isoform a
- cDNA FLJ57382, highly similar to Ribonuclease P protein subunit p30
- Putative uncharacterized protein RPP30 lng=312



IPI00642023.2

Sequence: SISADDDLQESSR, S1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 826.40521 Da (+2.92 mmu/+3.54 ppm), MH+: 1651.80315 Da, RT: 78.70 min,

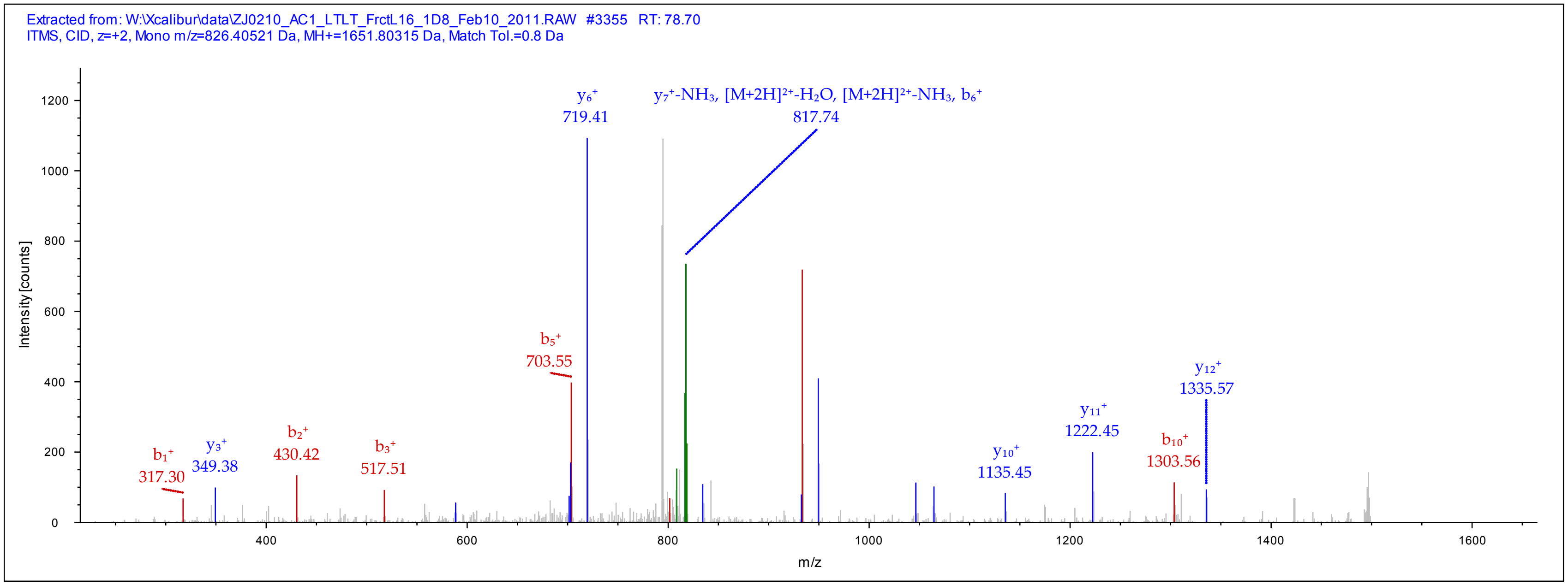
Identified with: Mascot (v1.16); IonScore:59, Exp Value:9.8E-005, Ions matched by search engine: 12/126

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Negative elongation factor E
- cDNA FLJ56180, highly similar to Negative elongation factor E lng=387
- RD RNA binding protein lng=159
- cDNA FLJ52247, highly similar to Negative elongation factor E lng=350



IPI00642338.3

Sequence: ADILLR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 465.30298 Da (+0.25 mmu/+0.55 ppm), MH+: 929.59868 Da, RT: 99.37 min,

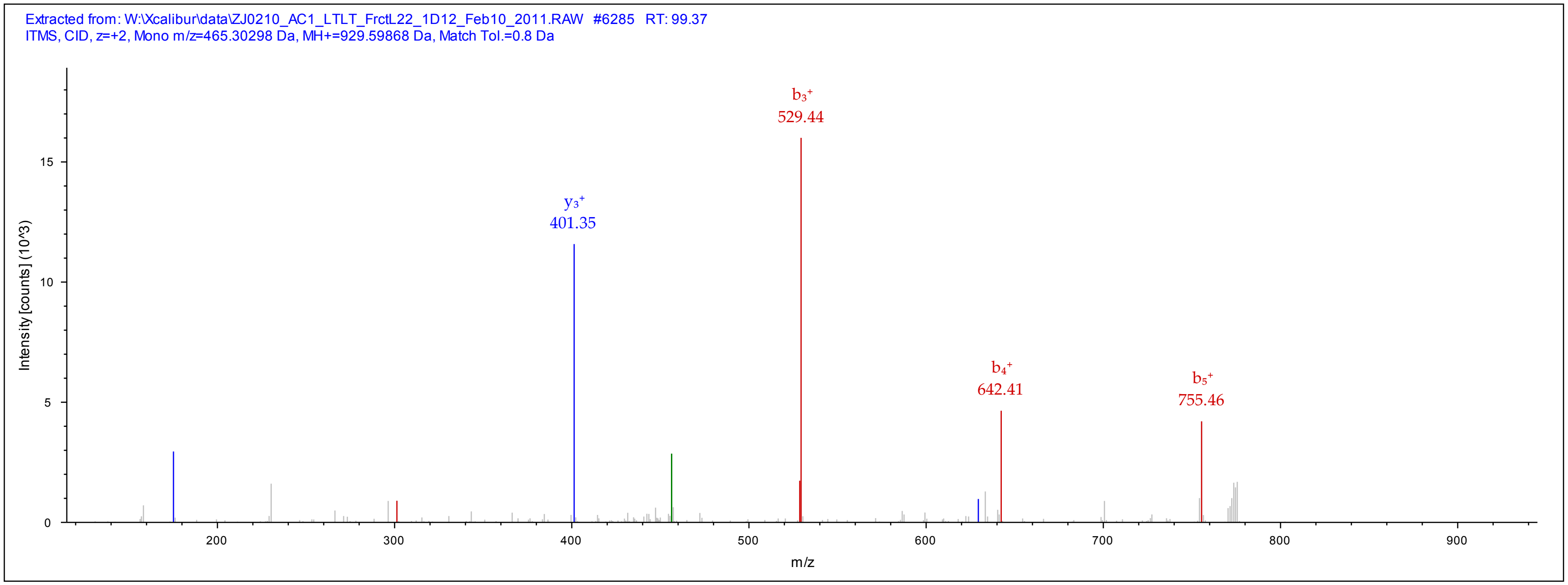
Identified with: Mascot (v1.16); IonScore:39, Exp Value:4.0E-003, Ions matched by search engine: 4/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- cDNA FLJ36622 fis, clone TRACH2016690, highly similar to Homo sapiens Vac14 homolog (VAC14), mRNA lng=214



IPI:IPI00642722.2

Sequence: IVEANPLLEAFGNAK, I1-TMT6plex (229.16293 Da), K15-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 1022.59674 Da (+0.91 mmu/+0.89 ppm), MH+: 2044.18620 Da, RT: 132.11 min,

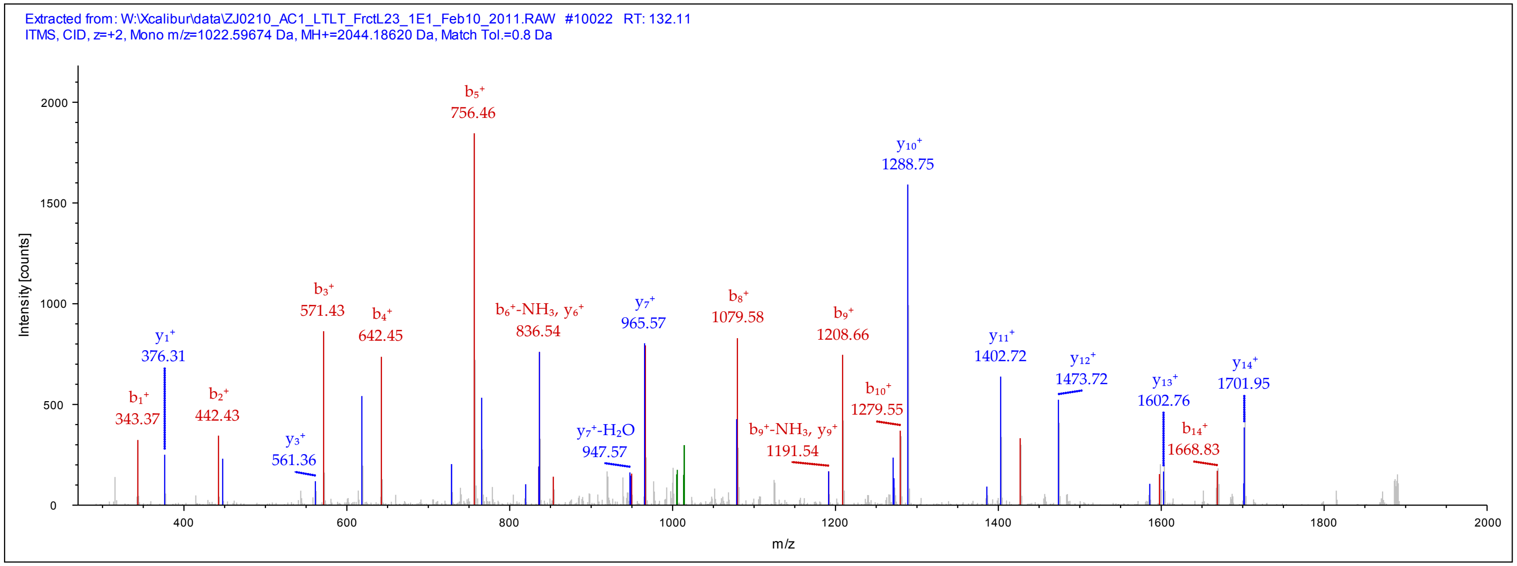
Identified with: Mascot (v1.16); IonScore:66, Exp Value:2.1E-005, Ions matched by search engine: 12/144

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Isoform 1 of Myosin-VI
- Isoform 2 of Myosin-VI
- Myosin lng=1253
- Isoform 5 of Myosin-VI
- Isoform 3 of Myosin-VI
- Isoform 4 of Myosin-VI
- 149 kDa protein lng=1286



IPI00643131.2

Sequence: NILIMAGDEASTIAEIIEECGGLEK, N1-TMT6plex (229.16293 Da), C20-Carbamidomethyl (57.02146 Da), K25-TMT6plex (229.16293 Da)

Charge: +4,   Monoisotopic m/z: 784.41791 Da (+3.28 mmu/+4.19 ppm),   MH+: 3134.64980 Da,   RT: 236.70 min,

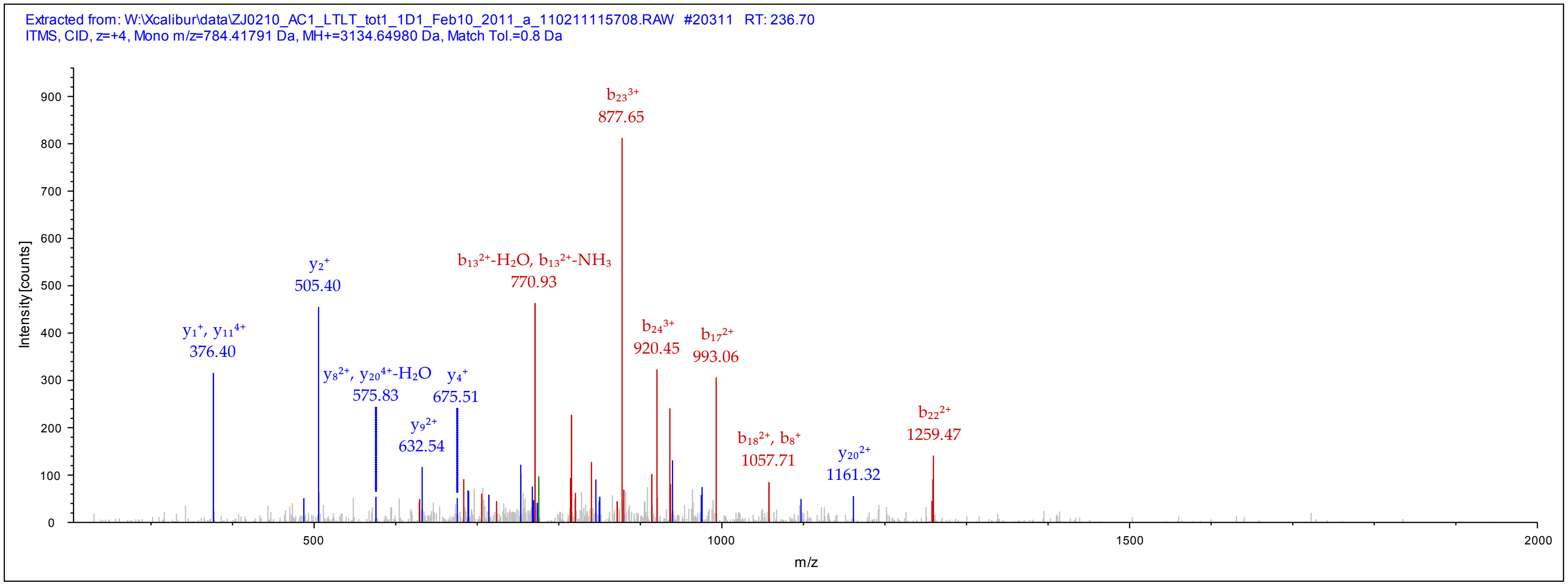
Identified with: Mascot (v1.16); IonScore:53, Exp Value:1.0E-003, Ions matched by search engine: 29/272

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Importin subunit alpha-3
- Karyopherin alpha 3 lng=150



IPI00643239.2

Sequence: LPEAVQLIEK, L1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 799.49988 Da (-0.25 mmu/-0.31 ppm),   MH+: 1597.99248 Da,   RT: 116.52 min,

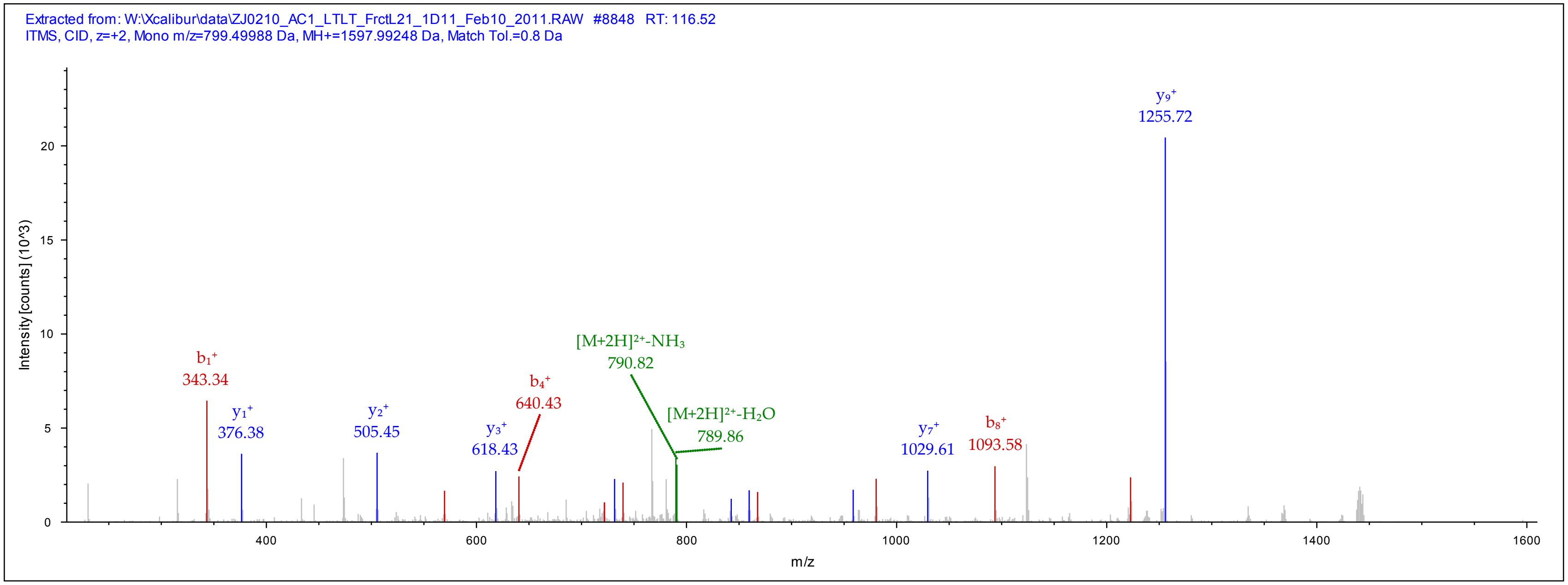
Identified with: Mascot (v1.16); IonScore:37, Exp Value:1.0E-002, Ions matched by search engine: 13/92

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Gamma-soluble NSF attachment protein
- cDNA FLJ61104, highly similar to Gamma-soluble NSF attachment protein lng=230



IPI00645811.2

Sequence: LAQLTLEQILEHLDNLR, L1-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 750.10175 Da (+1.45 mmu/+1.93 ppm),   MH+: 2248.29068 Da,   RT: 212.53 min,

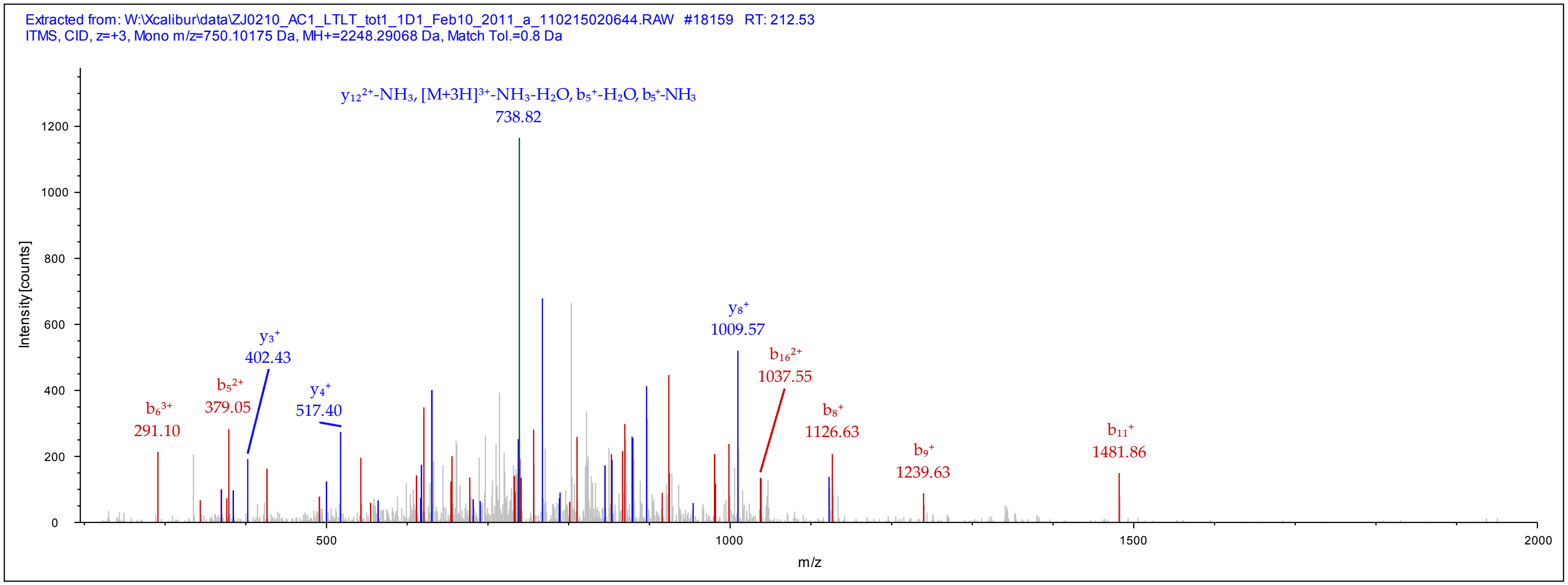
Identified with: Mascot (v1.16); IonScore:47, Exp Value:2.2E-003, Ions matched by search engine: 23/174

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of Integrator complex subunit 3
- Isoform 2 of Integrator complex subunit 3
- Isoform 3 of Integrator complex subunit 3 lng=902
- Isoform 4 of Integrator complex subunit 3 lng=555



IPI:IPI00645949.5

Sequence: LQVLLLAR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 577.89612 Da (+1.33 mmu/+2.31 ppm), MH+: 1154.78496 Da, RT: 123.55 min,

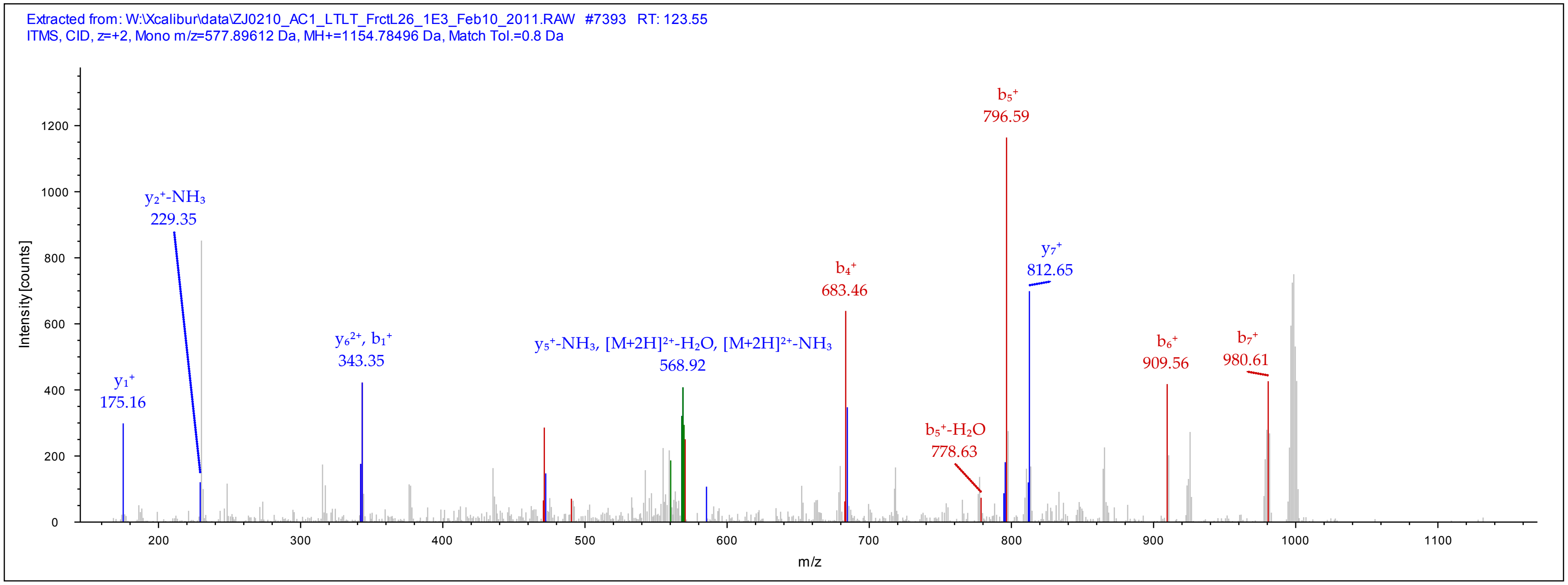
Identified with: Mascot (v1.16); IonScore:39, Exp Value:3.0E-004, Ions matched by search engine: 6/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Peroxisomal membrane protein 11B
- cDNA FLJ36854 fis, clone ASTRO2014561, highly similar to Peroxisomal membrane protein 11B



IPI:IPI00646620.2

Sequence: IQLFLAR, I1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 545.35199 Da (-0.76 mmu/-1.4 ppm),   MH+: 1089.69670 Da,   RT: 109.18 min,

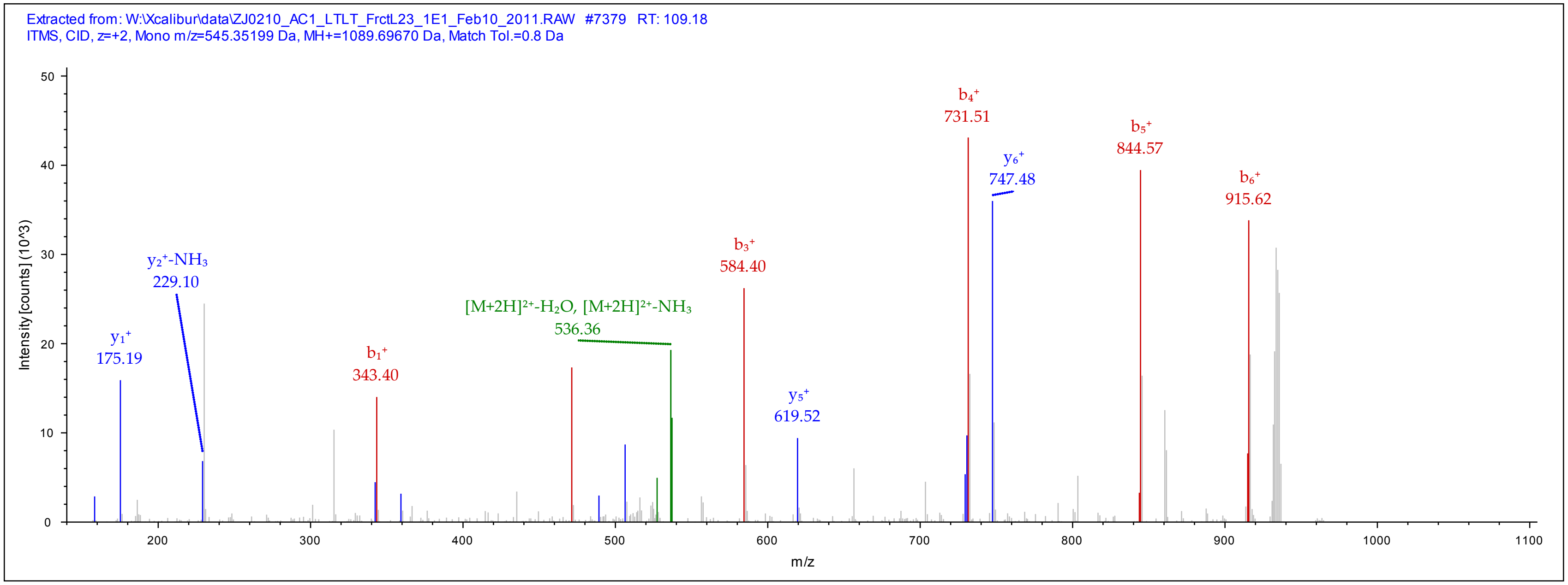
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.8E-002, Ions matched by search engine: 6/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of THO complex subunit 1
- Isoform 2 of THO complex subunit 1



IPI:IPI00647432.2

Sequence: EESESVLTLK, E1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 796.96149 Da (+0.46 mmu/+0.58 ppm),   MH+: 1592.91570 Da,   RT: 95.80 min,

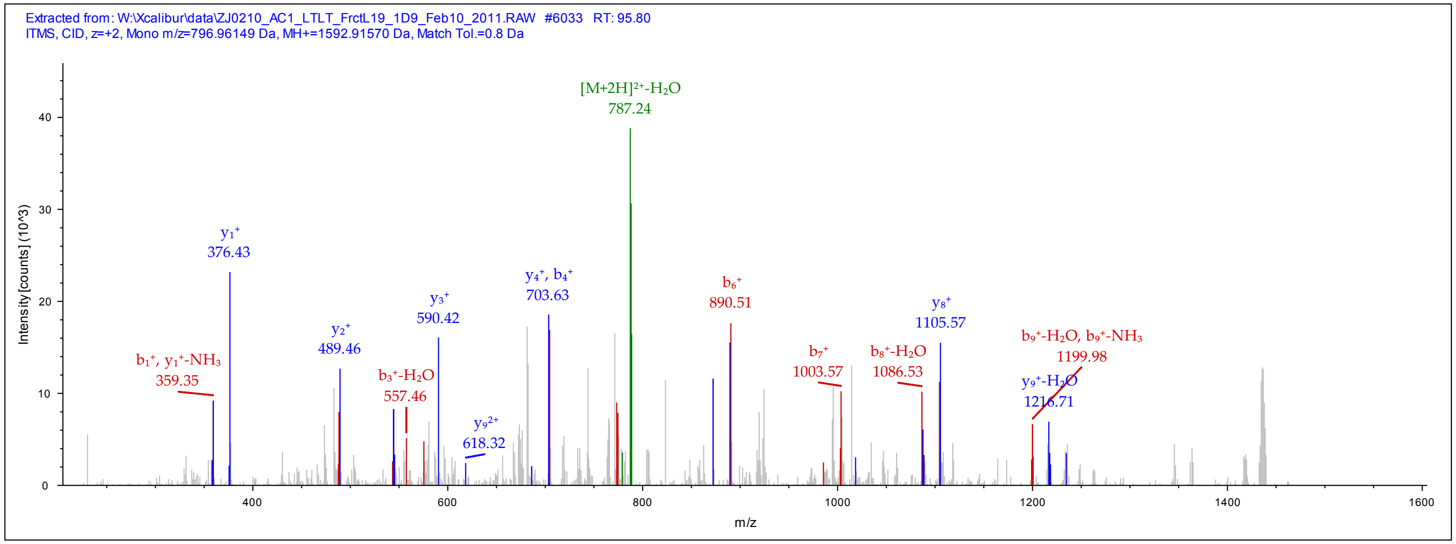
Identified with: Mascot (v1.16); IonScore:31, Exp Value:7.0E-002, Ions matched by search engine: 7/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (11):

- Isoform 1 of Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform
- Isoform 1 of Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform
- serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform a
- Isoform 2 of Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform
- Isoform 2 of Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform
- Serine/threonine-protein phosphatase
- serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform c
- Protein phosphatase 3 (Formerly 2B), catalytic subunit, beta isoform



IPI:IPI00737571.3

Sequence: DLLADLIGCQR, D1-TMT6plex (229.16293 Da), C9-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 751.91406 Da (+0.48 mmu/+0.63 ppm),   MH+: 1502.82085 Da,   RT: 124.83 min,

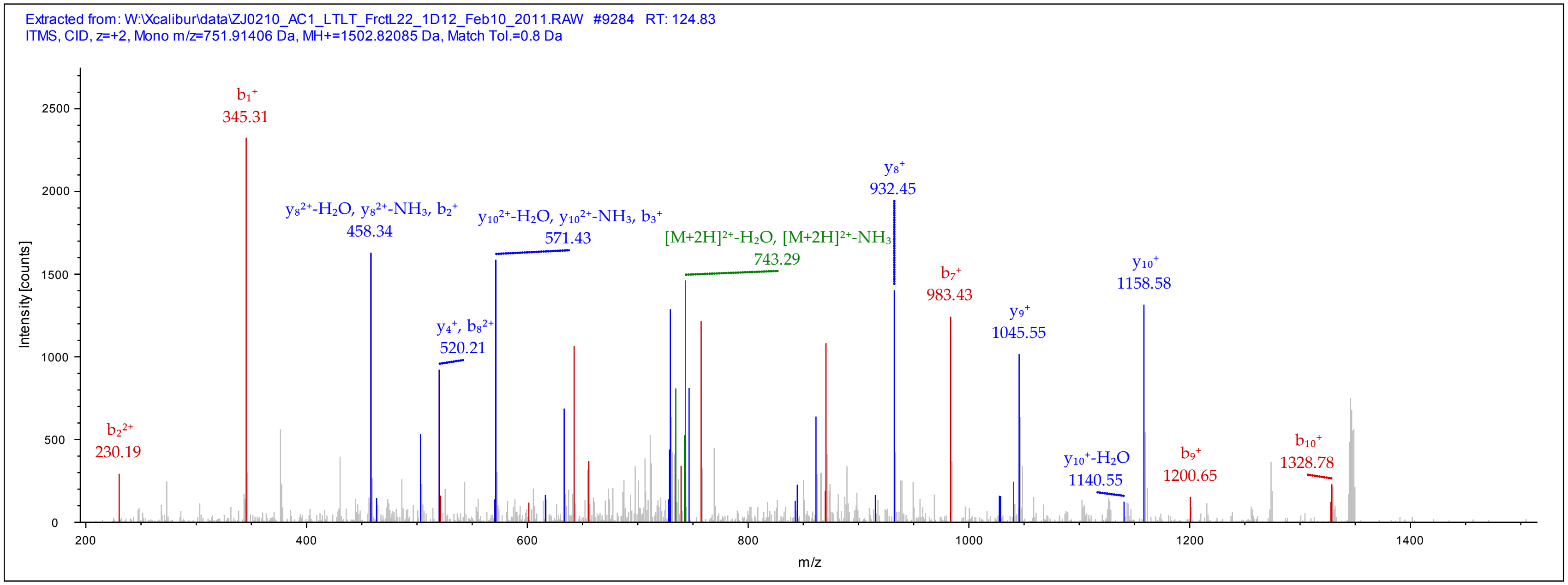
Identified with: Mascot (v1.16); IonScore:42, Exp Value:6.4E-003, Ions matched by search engine: 9/90

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Serine/threonine-protein kinase PRP4 homolog
- HCG1820375, isoform CRA_a



IPI00739847.3

Sequence: MAELNASRSEENNNPAPAEGSQGPGVVK, M1-TMT6plex (229.16293 Da), M1-Oxidation (15.99492 Da), S21-Phospho (79.96633 Da), K28-TMT6plex (229.16293 Da)

Charge: +4, Monoisotopic m/z: 852.66681 Da (+3.74 mmu/+4.39 ppm), MH+: 3407.64541 Da, RT: 205.77 min,

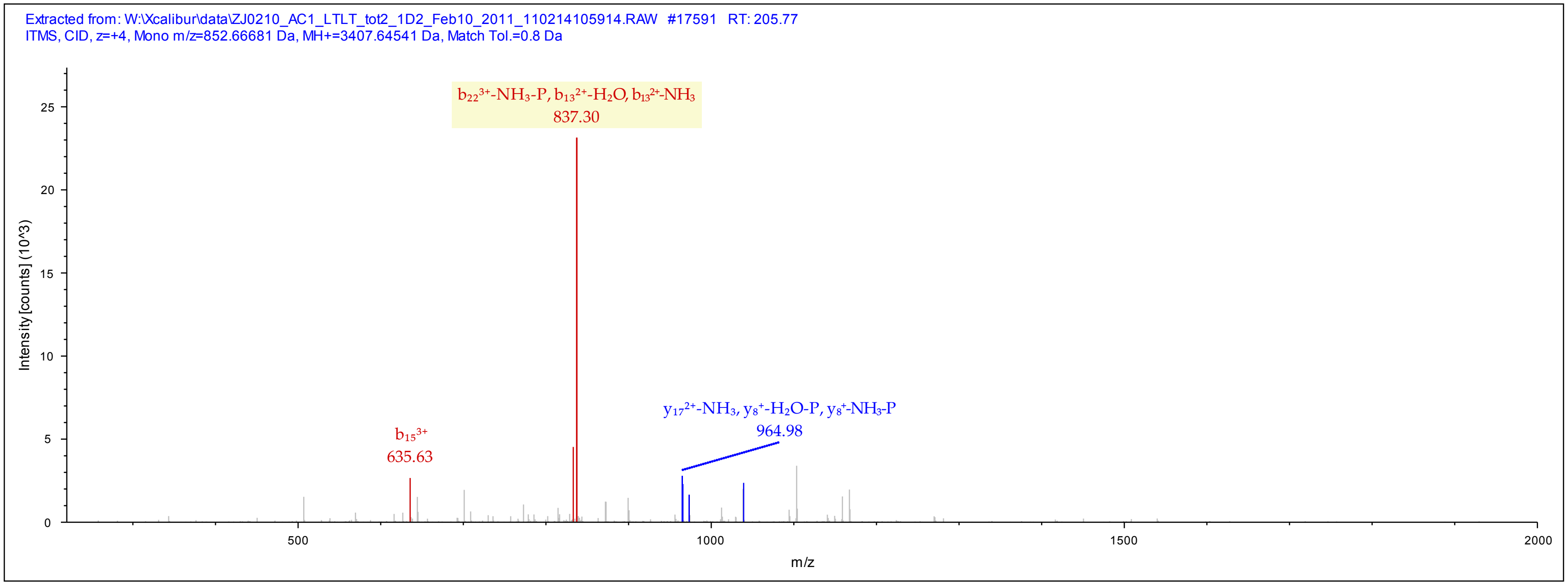
Identified with: Mascot (v1.16); IonScore:35, Exp Value:7.8E-002, Ions matched by search engine: 15/298

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- hypothetical protein XP_002343288 lng=89



IPI:IPI00783192.1

Sequence: AENLSVPVIGALLR, A1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 841.01556 Da (+1.4 mmu/+1.66 ppm),   MH+: 1681.02385 Da,   RT: 134.92 min,

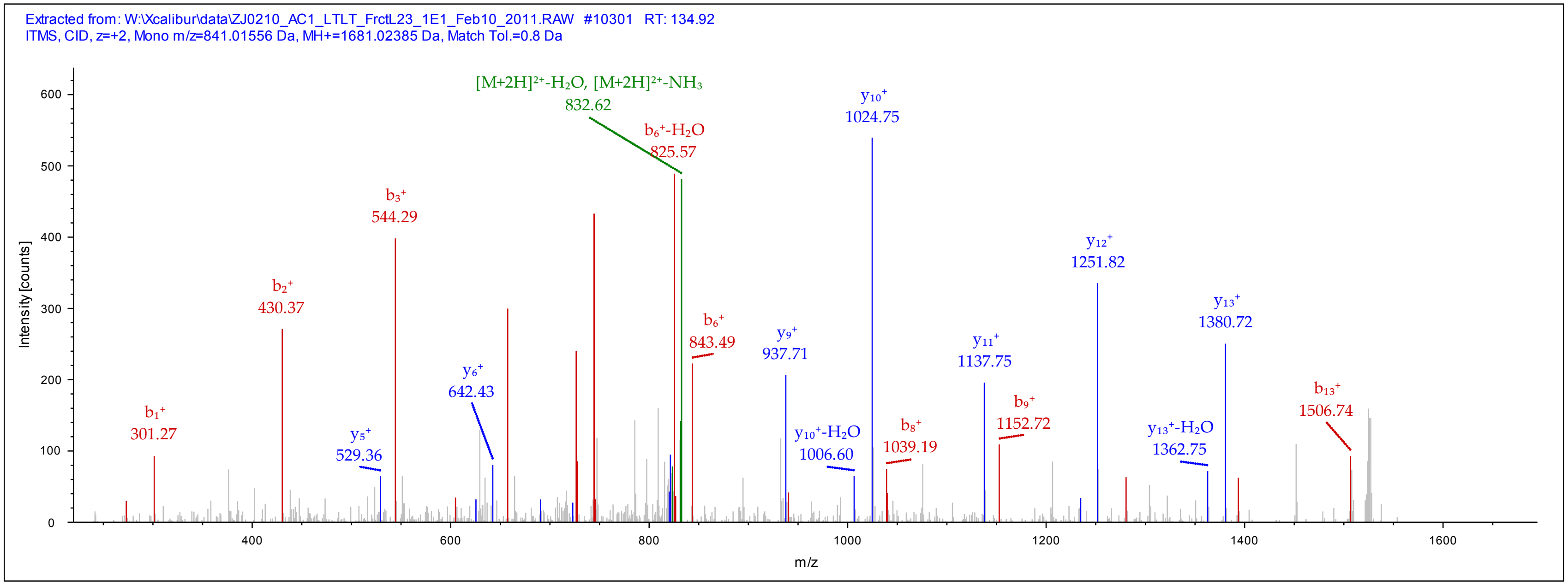
Identified with: Mascot (v1.16); IonScore:63, Exp Value:2.8E-005, Ions matched by search engine: 12/132

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Lysophospholipid acyltransferase LPCAT4
- Isoform 2 of Lysophospholipid acyltransferase LPCAT4



IPI:IPI00783568.3

Sequence: VLPQELVDLPLVK, V1-TMT6plex (229.16293 Da), K13-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 961.11237 Da (+1.79 mmu/+1.86 ppm), MH+: 1921.21745 Da, RT: 136.51 min,

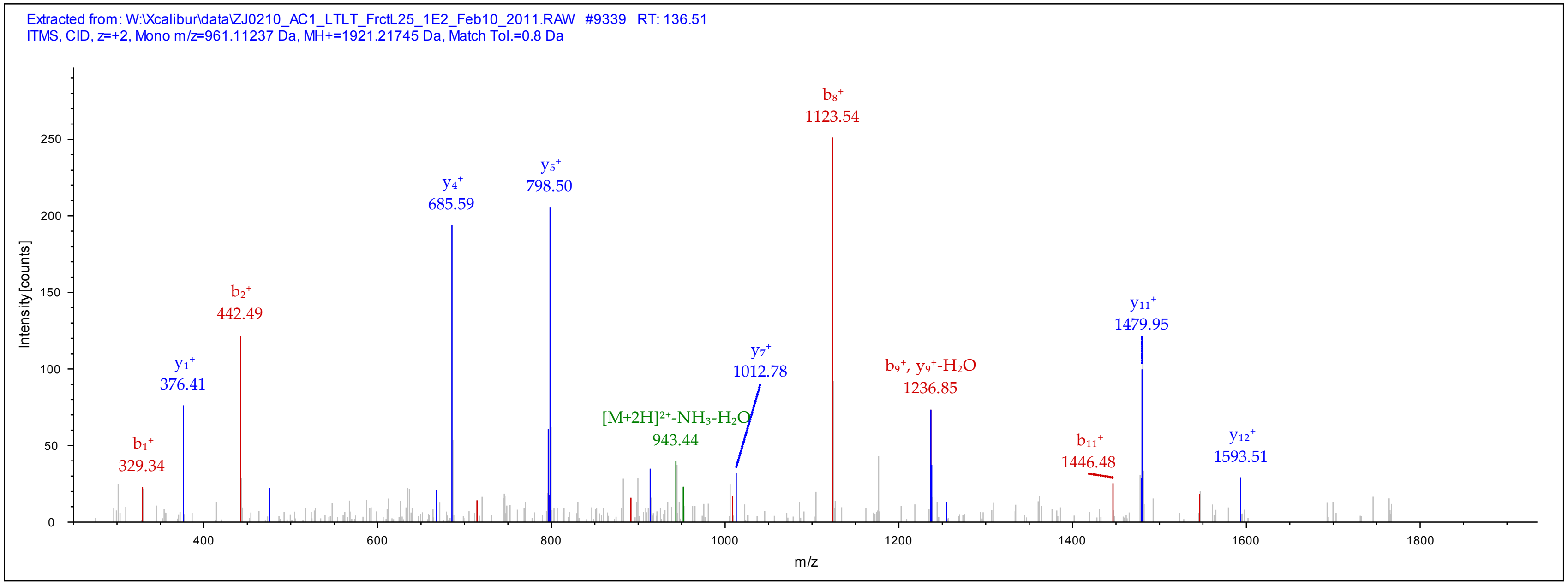
Identified with: Mascot (v1.16); IonScore:33, Exp Value:1.8E-002, Ions matched by search engine: 16/120

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- leucine-rich repeat and calponin homology domain-containing protein 1 isoform 1



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL25_1E2_Feb10_2011.RAW #9339 RT: 136.51
ITMS, CID, z=+2, Mono m/z=961.11237 Da, MH+=1921.21745 Da, Match Tol.=0.8 Da

IPI:IPI00783781.2

Sequence: LLDIEGLYSK, L1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 804.98218 Da (-2.12 mmu/-2.64 ppm),   MH+: 1608.95708 Da,   RT: 123.95 min,

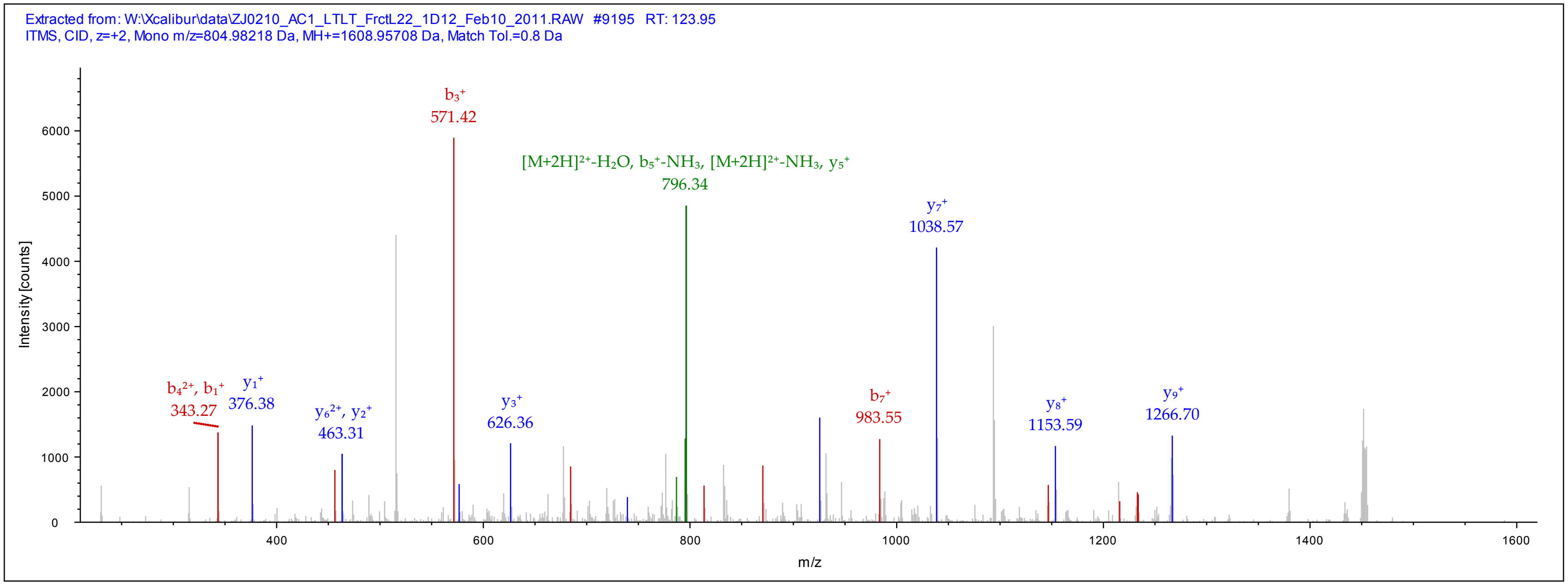
Identified with: Mascot (v1.16); IonScore:43, Exp Value:3.5E-003, Ions matched by search engine: 8/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Nuclear pore complex protein Nup205



IPI:IPI00784704.2

Sequence: IQQFLR, I1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 517.32147 Da (+0.03 mmu/+0.05 ppm),   MH+: 1033.63567 Da,   RT: 97.66 min,

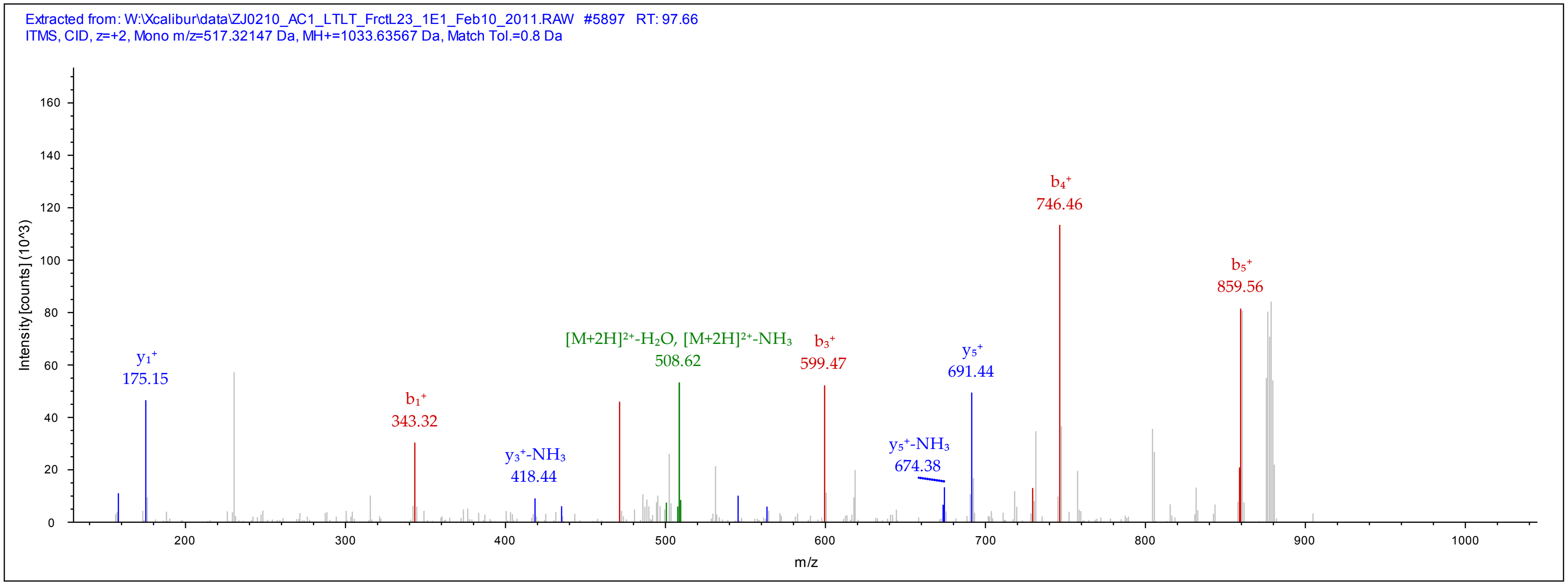
Identified with: Mascot (v1.16); IonScore:31, Exp Value:7.2E-002, Ions matched by search engine: 5/50

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Fanconi anemia group I protein
- Isoform 3 of Fanconi anemia group I protein
- Isoform 2 of Fanconi anemia group I protein



IPI00786894.1

Sequence: IVEIAR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 465.30353 Da (+0.8 mmu/+1.73 ppm), MH+: 929.59978 Da, RT: 120.21 min,

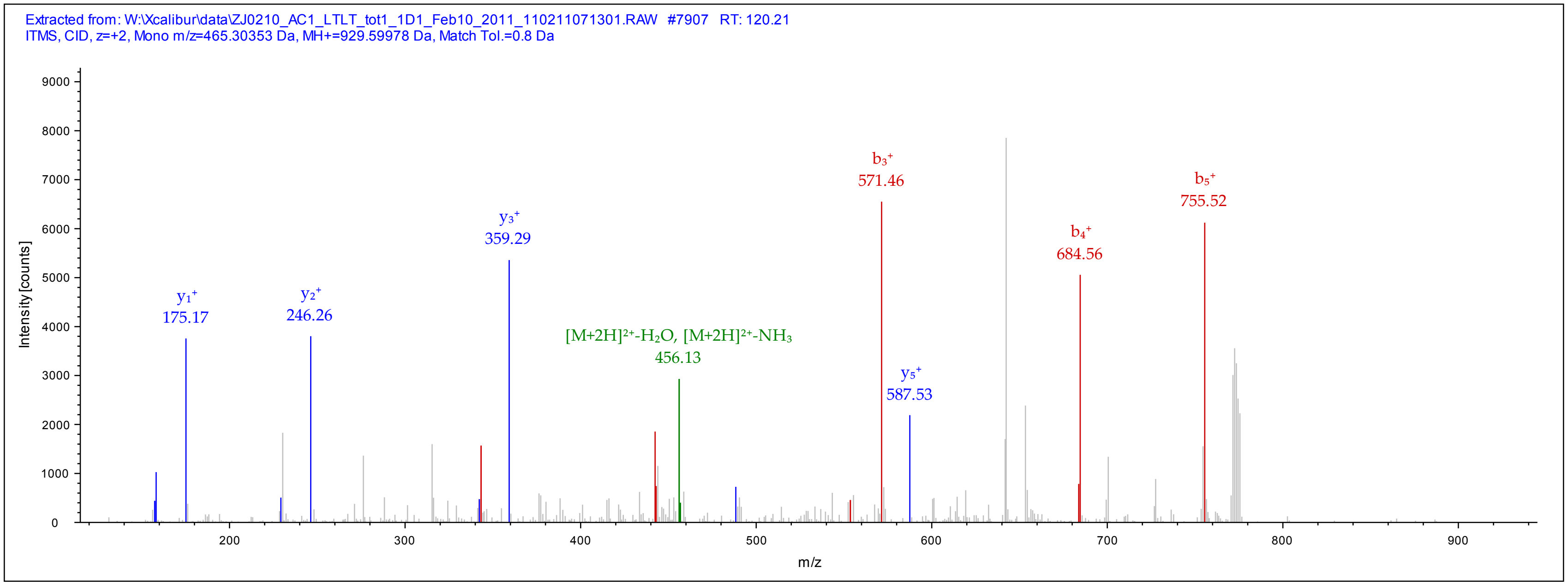
Identified with: Mascot (v1.16); IonScore:31, Exp Value:2.6E-002, Ions matched by search engine: 5/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of BTB/POZ domain-containing protein KCTD7 lng=289
- Isoform 2 of BTB/POZ domain-containing protein KCTD7 lng=288
- 42 kDa protein lng=379



IPI:IPI00787469.2

Sequence: VFSDEVQQQAQLSTIR, V1-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 693.37518 Da (+0.99 mmu/+1.43 ppm),   MH+: 2078.11100 Da,   RT: 101.01 min,

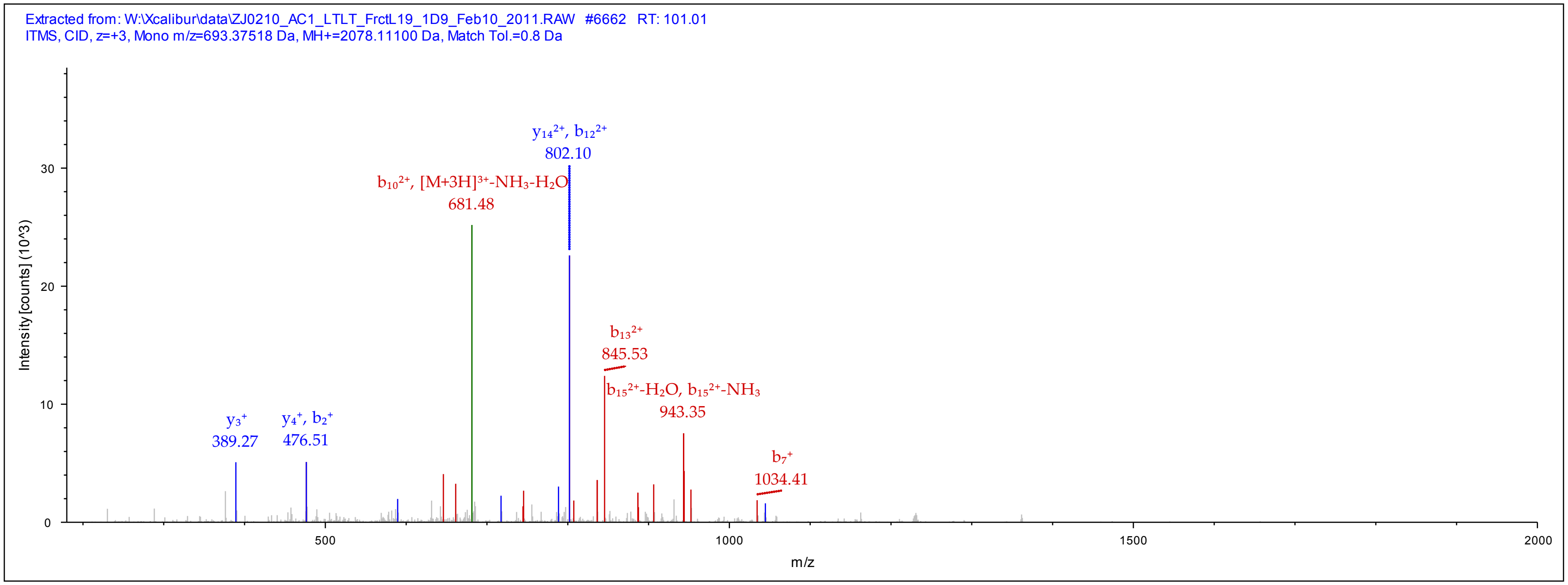
Identified with: Mascot (v1.16); IonScore:35, Exp Value:4.7E-002, Ions matched by search engine: 14/160

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Eukaryotic translation initiation factor 3 subunit L
- Eukaryotic translation initiation factor 3, subunit E interacting protein lng=607
- similar to eukaryotic translation initiation factor 3 subunit 6 interacting protein
- Eukaryotic translation initiation factor 3, subunit E interacting protein lng=466
- cDNA FLJ59381, highly similar to Eukaryotic translation initiation factor 3 subunit 6-interacting protein lng=531



IPI00787559.1

Sequence: GALIVLEGVDR, G1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 685.91382 Da (-0.1 mmu/-0.14 ppm), MH+: 1370.82036 Da, RT: 107.32 min,

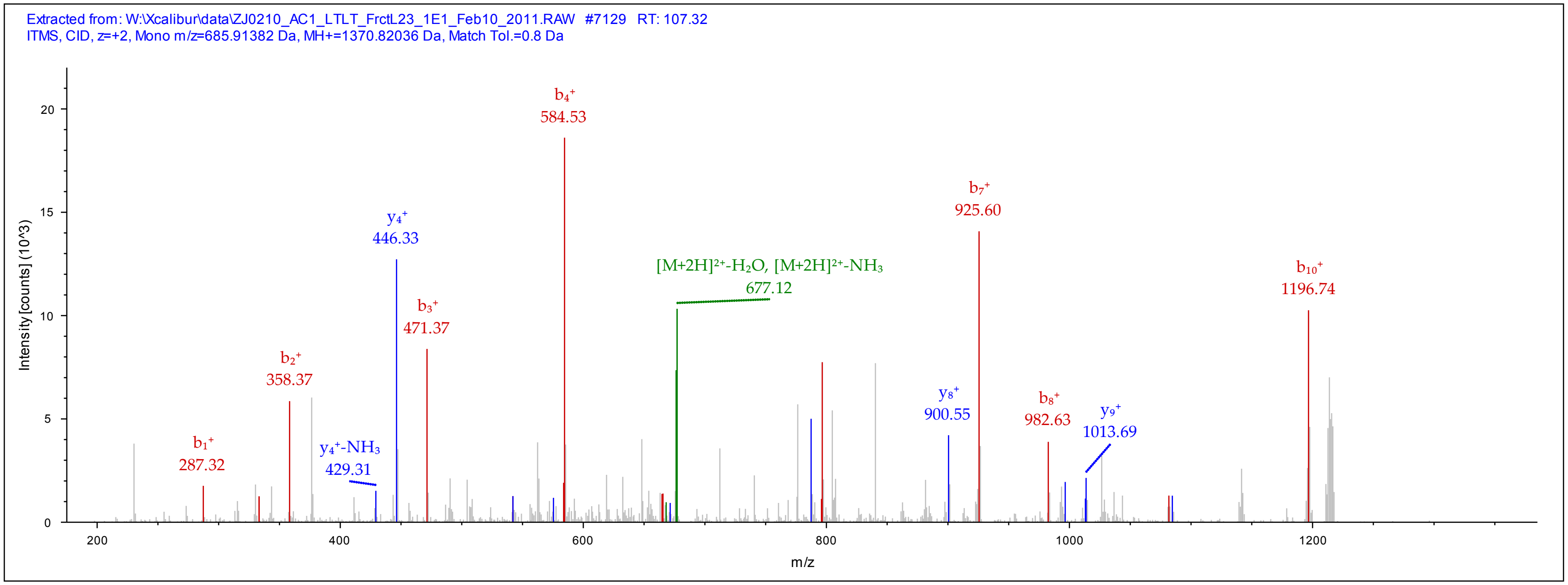
Identified with: Mascot (v1.16); IonScore:43, Exp Value:3.7E-003, Ions matched by search engine: 9/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Thymidylate kinase
- thymidylate kinase isoform 2 lng=188



IPI00788157.1

Sequence: VQMIMLAVGEVEDSIFK, V1-TMT6plex (229.16293 Da), K17-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 789.77789 Da (+4.07 mmu/+5.16 ppm), MH+: 2367.31913 Da, RT: 245.85 min,

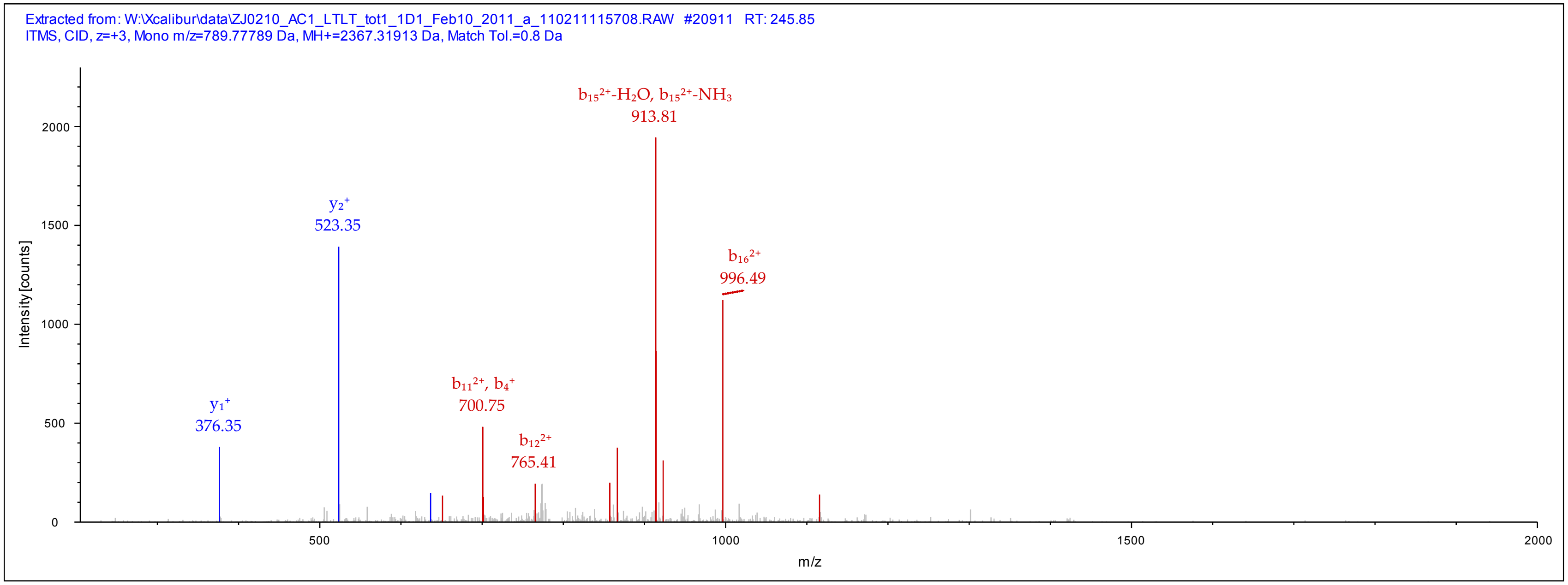
Identified with: Mascot (v1.16); IonScore:34, Exp Value:5.7E-002, Ions matched by search engine: 15/166

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of 5'-3' exoribonuclease 2
- Isoform 2 of 5'-3' exoribonuclease 2 lng=874



IPI00788741.1

Sequence: VVLISR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 458.31274 Da (-0.35 mmu/-0.76 ppm), MH+: 915.61821 Da, RT: 81.14 min,

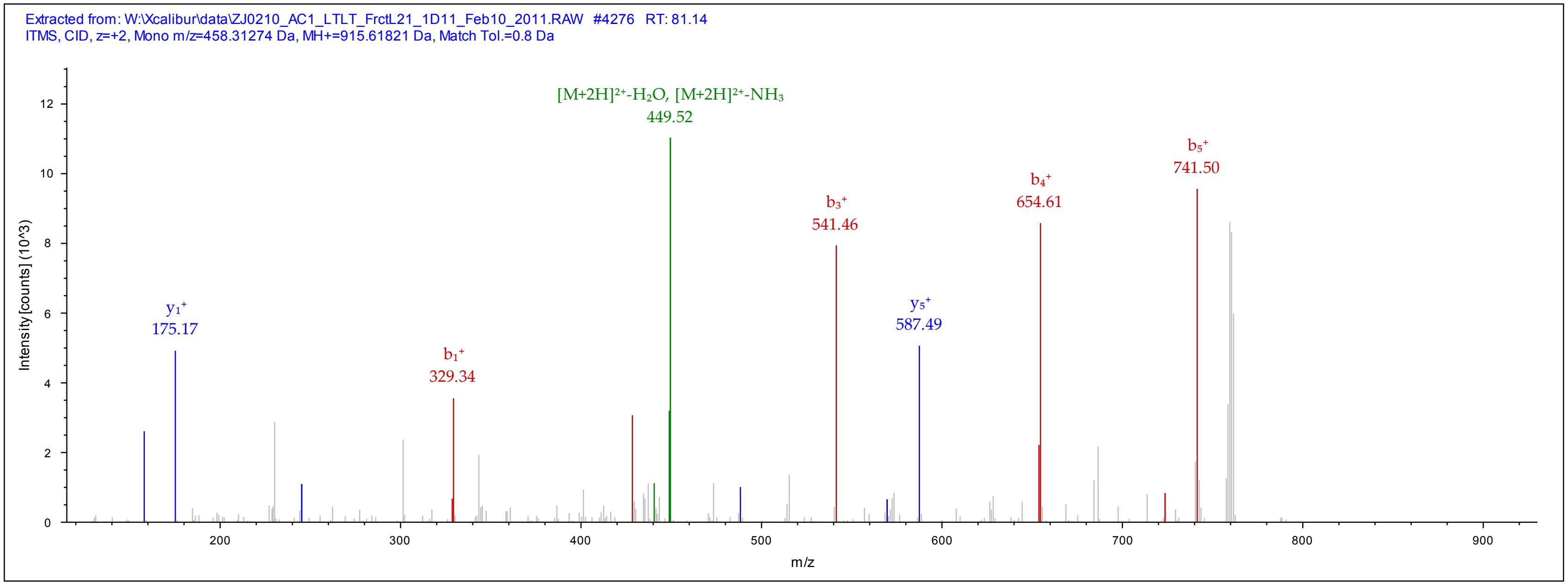
Identified with: Mascot (v1.16); IonScore:35, Exp Value:1.1E-002, Ions matched by search engine: 5/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Estradiol 17-beta-dehydrogenase 12
- Hydroxysteroid (17-beta) dehydrogenase 12, isoform CRA_g lng=98
- Hydroxysteroid (17-beta) dehydrogenase 12, isoform CRA_a



IPI00788826.1

Sequence: VIIYQEK, V1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 675.92371 Da (+0.2 mmu/+0.3 ppm),   MH+: 1350.84014 Da,   RT: 88.21 min,

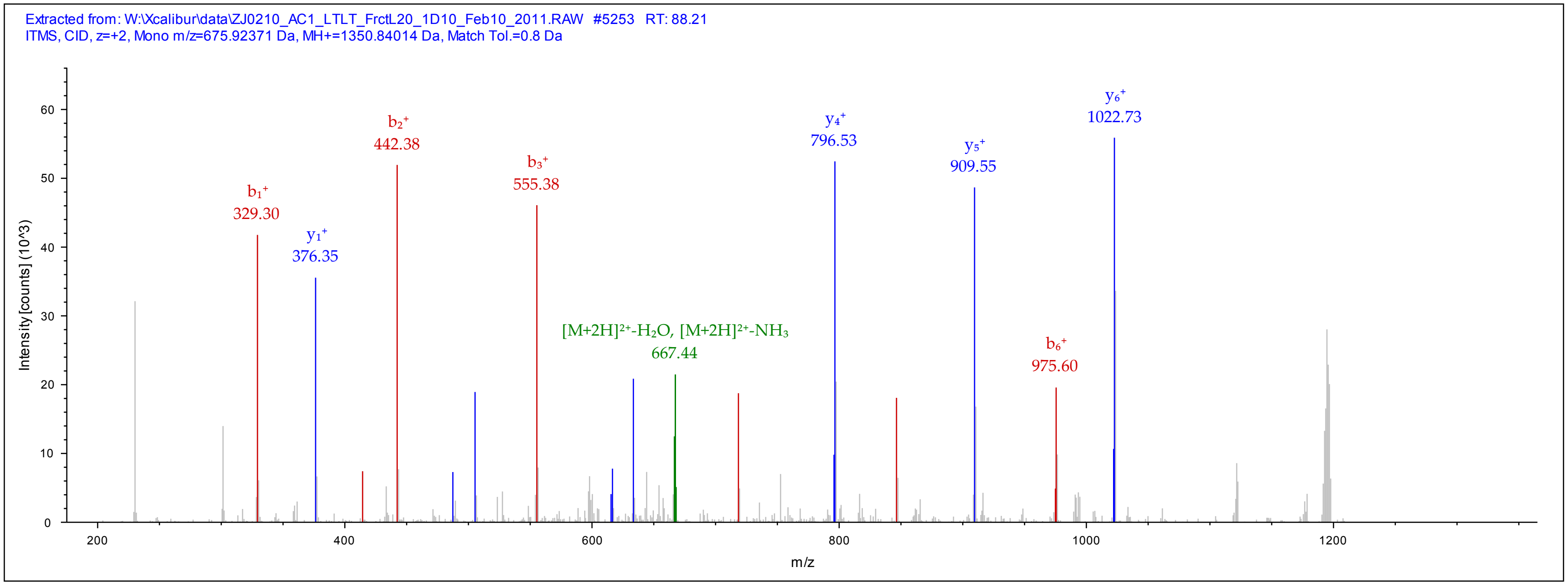
Identified with: Mascot (v1.16); IonScore:31, Exp Value:4.5E-002, Ions matched by search engine: 6/52

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform 1 of Poly(U)-binding-splicing factor PUF60
- Isoform 2 of Poly(U)-binding-splicing factor PUF60
- Isoform 4 of Poly(U)-binding-splicing factor PUF60 lng=499
- Isoform 3 of Poly(U)-binding-splicing factor PUF60
- Isoform 6 of Poly(U)-binding-splicing factor PUF60
- Isoform 5 of Poly(U)-binding-splicing factor PUF60



IPI:IPI00788871.1

Sequence: ETITAPVPFDFTHK, E1-TMT6plex (229.16293 Da), K14-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 687.71991 Da (+1 mmu/+1.46 ppm), MH+: 2061.14518 Da, RT: 115.52 min,

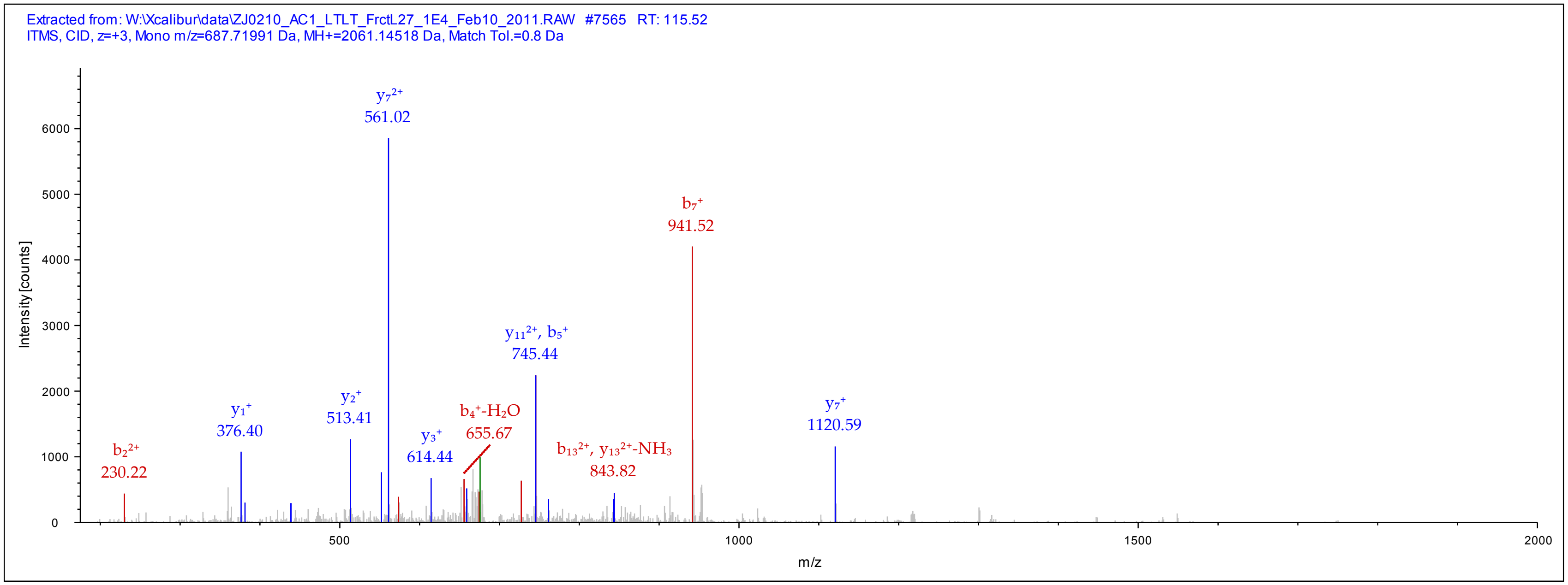
Identified with: Mascot (v1.16); IonScore:49, Exp Value:1.6E-003, Ions matched by search engine: 18/126

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of Elongation factor G, mitochondrial
- Uncharacterized protein
- 69 kDa protein
- Isoform 2 of Elongation factor G, mitochondrial



IPI:IPI00789225.3

Sequence: DSAQCAAIAER, D1-TMT6plex (229.16293 Da), C5-Carbamidomethyl (57.02146 Da)

Charge: +2, Monoisotopic m/z: 710.85815 Da (+1.89 mmu/+2.66 ppm), MH+: 1420.70903 Da, RT: 69.62 min,

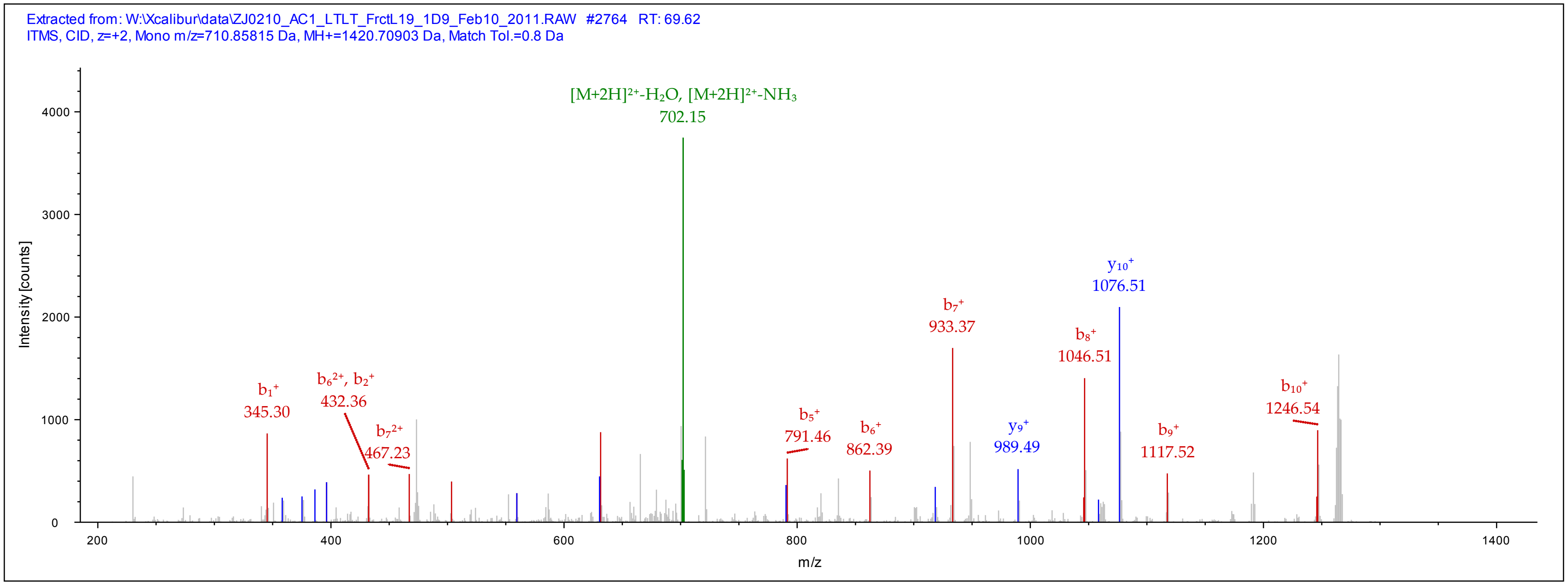
Identified with: Mascot (v1.16); IonScore:55, Exp Value:2.4E-004, Ions matched by search engine: 10/112

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 2 of NudC domain-containing protein 1
- Isoform 3 of NudC domain-containing protein 1
- Isoform 1 of NudC domain-containing protein 1



IPI00789396.1

Sequence: LCDVGEAIQEVMESYEVEIDGK, L1-TMT6plex (229.16293 Da), C2-Carbamidomethyl (57.02146 Da), K22-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 991.16296 Da (+2.05 mmu/+2.07 ppm), MH+: 2971.47434 Da, RT: 216.26 min,

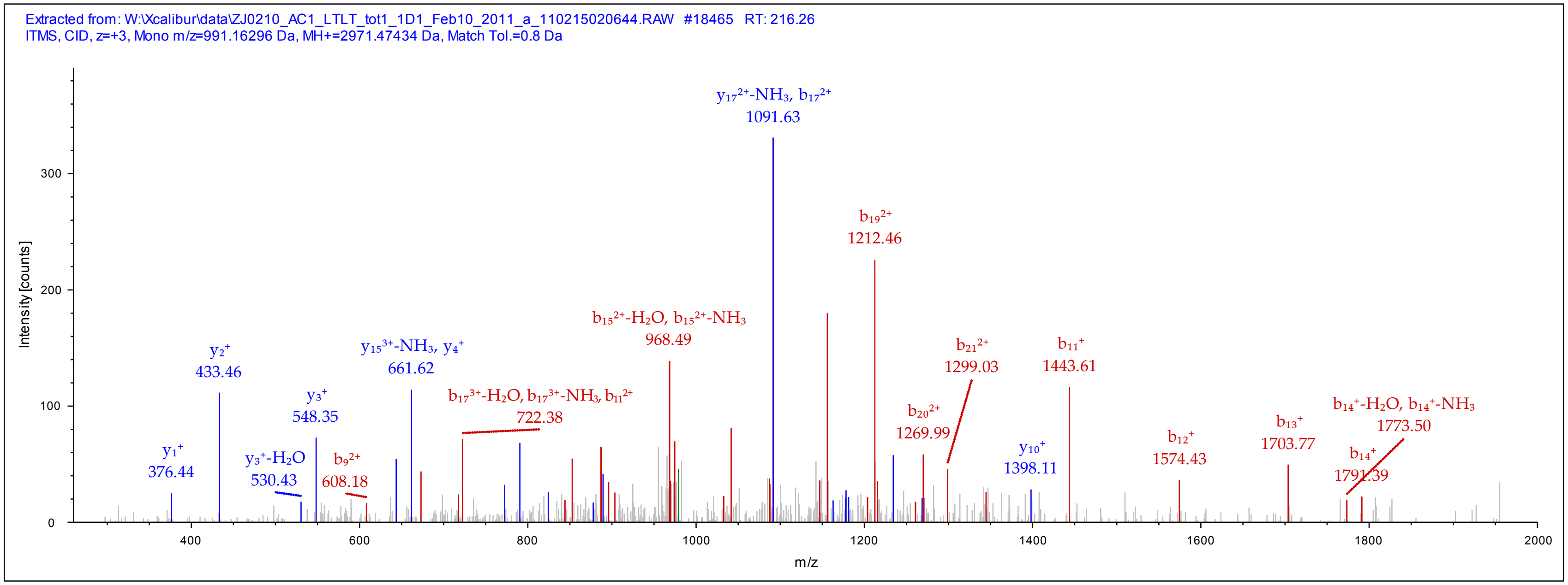
Identified with: Mascot (v1.16); IonScore:46, Exp Value:5.4E-003, Ions matched by search engine: 21/228

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Methionine aminopeptidase 2
- Methionine aminopeptidase lng=455
- Methionine aminopeptidase lng=436



IPI:IPI00789477.1

Sequence: YYGYTGAFR, Y1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 663.83679 Da (-0.85 mmu/-1.29 ppm),   MH+: 1326.66631 Da,   RT: 90.59 min,

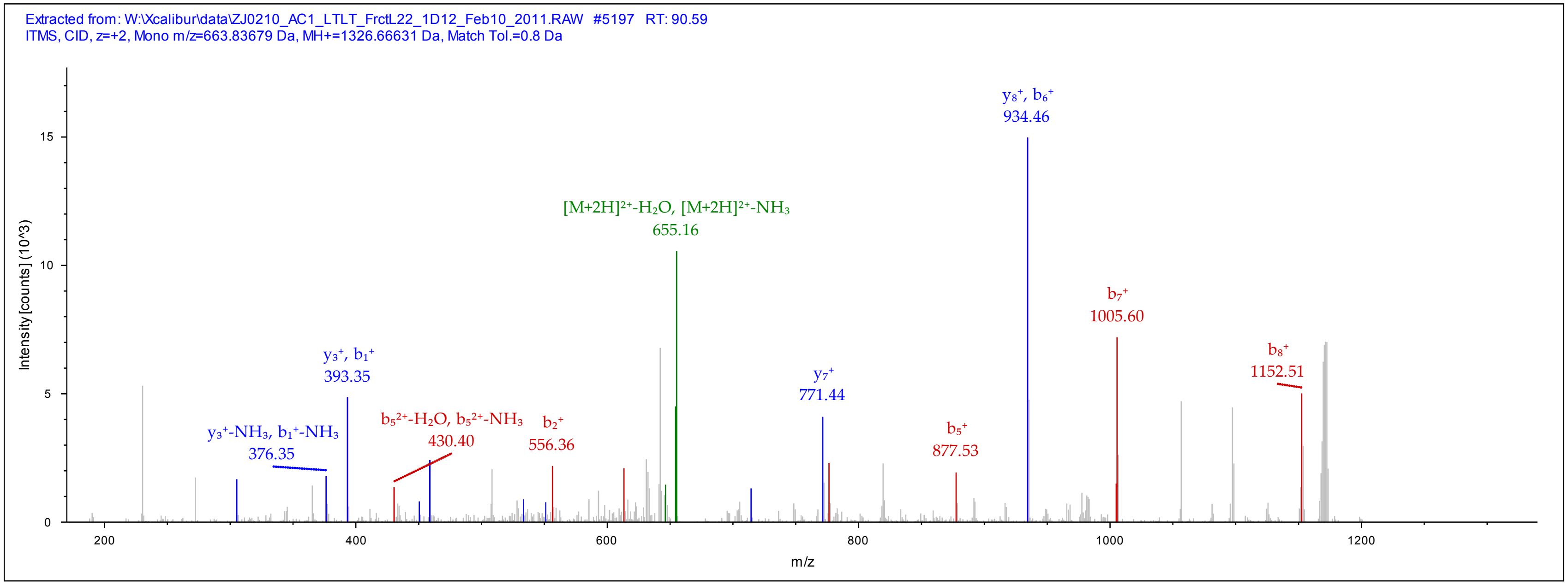
Identified with: Mascot (v1.16); IonScore:33, Exp Value:3.9E-002, Ions matched by search engine: 8/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- cDNA FLJ78440, highly similar to Human lactoferrin
- cDNA FLJ58679, highly similar to Lactotransferrin
- cDNA FLJ36533 fis, clone TRACH2004428, highly similar to Lactotransferrin (Fragment)



IPI00790097.1

Sequence: GLLGCNIIPLQR, G1-TMT6plex (229.16293 Da), C5-Carbamidomethyl (57.02146 Da)

Charge: +2, Monoisotopic m/z: 791.96906 Da (+0.36 mmu/+0.45 ppm), MH+: 1582.93083 Da, RT: 113.43 min,

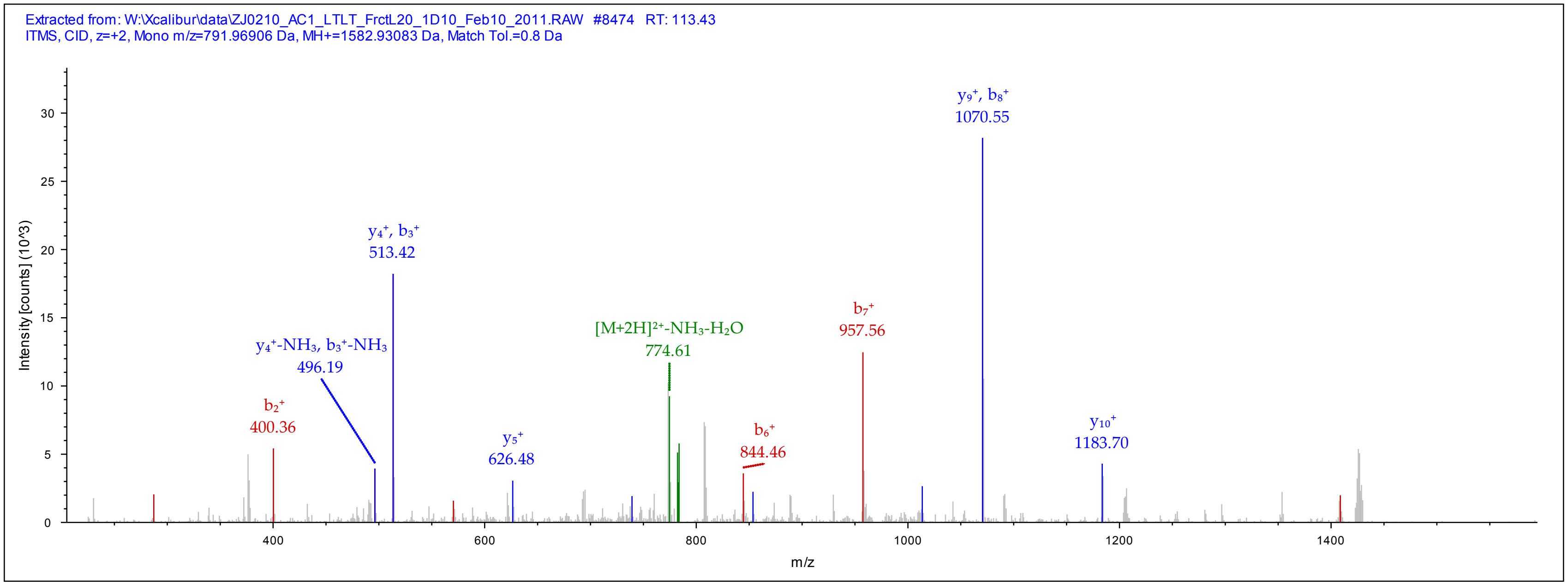
Identified with: Mascot (v1.16); IonScore:45, Exp Value:2.7E-003, Ions matched by search engine: 8/102

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform p27-L of 26S proteasome non-ATPase regulatory subunit 9
- 12 kDa protein lng=111
- 13 kDa protein lng=118



IPI00790135.1

Sequence: VVLPTFILEPR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 756.97339 Da (+2.16 mmu/+2.85 ppm), MH+: 1512.93950 Da, RT: 132.56 min,

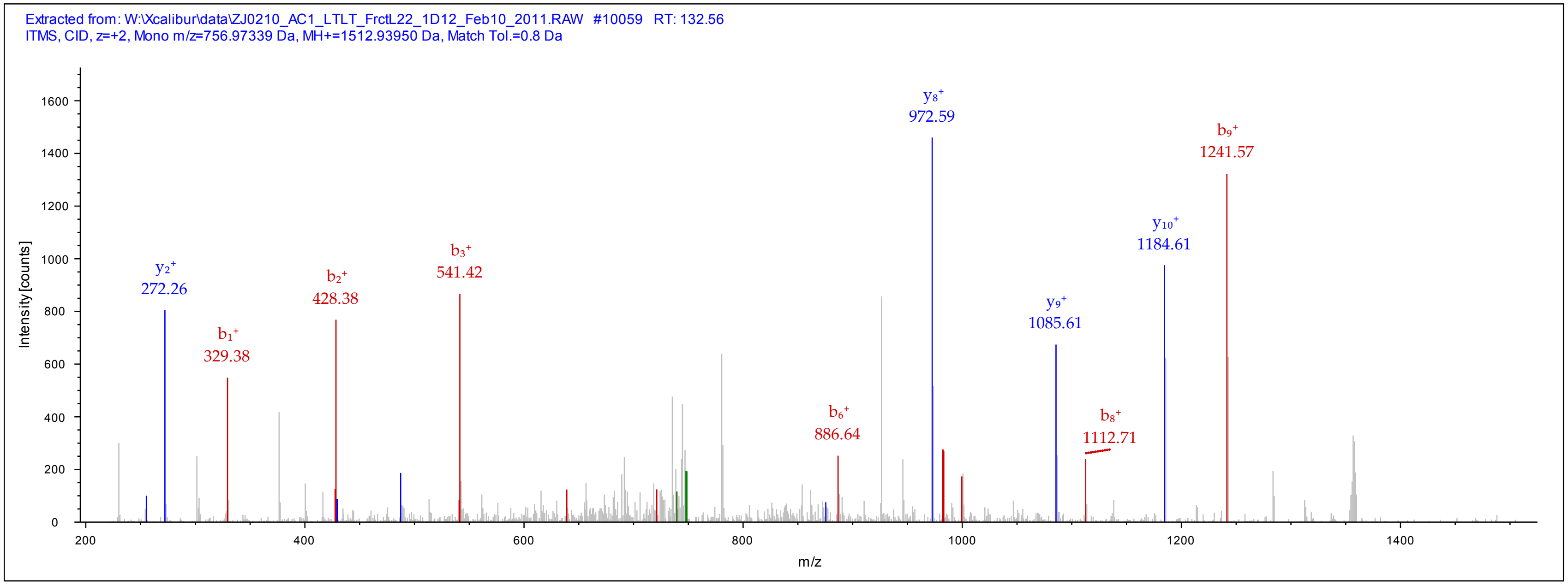
Identified with: Mascot (v1.16); IonScore:30, Exp Value:5.2E-002, Ions matched by search engine: 5/88

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Oxysterol-binding protein lng=890
- Isoform 2 of Oxysterol-binding protein-related protein 8 lng=874
- 79 kDa protein lng=695
- Oxysterol-binding protein lng=874



IPI:IPI00790316.1

Sequence: LDVDAPR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 507.80023 Da (+7.51 mmu/+14.8 ppm),   MH+: 1014.59319 Da,   RT: 97.10 min,

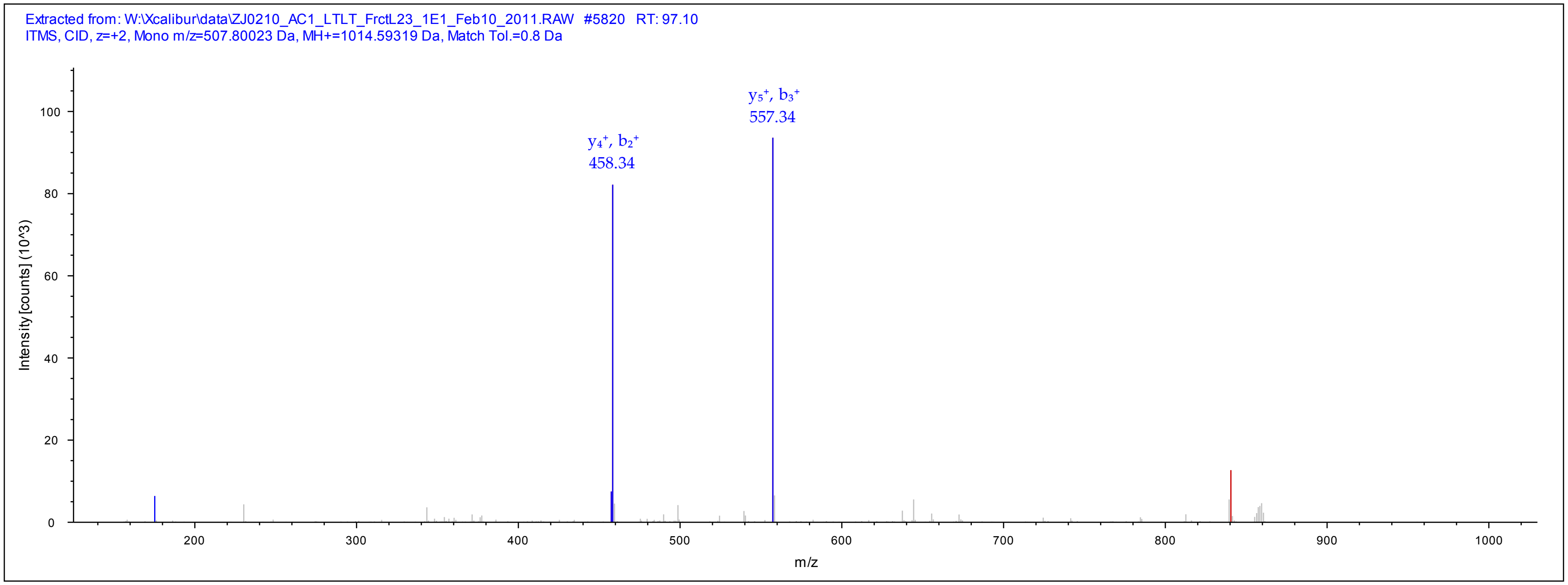
Identified with: Mascot (v1.16); IonScore:32, Exp Value:2.2E-002, Ions matched by search engine: 10/52

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- SEC14-like protein 1
- SEC14 (S. cerevisiae)-like 1 isoform a lng=715
- SEC14L1 protein
- SEC14 (S. cerevisiae)-like 1 isoform c lng=681
- 79 kDa protein lng=700
- cDNA FLJ59456, highly similar to SEC14-like protein 1 lng=696



IPI:IPI00790361.1

Sequence: IEGDETSTEAATR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 804.90234 Da (+2.96 mmu/+3.68 ppm), MH+: 1608.79741 Da, RT: 72.63 min,

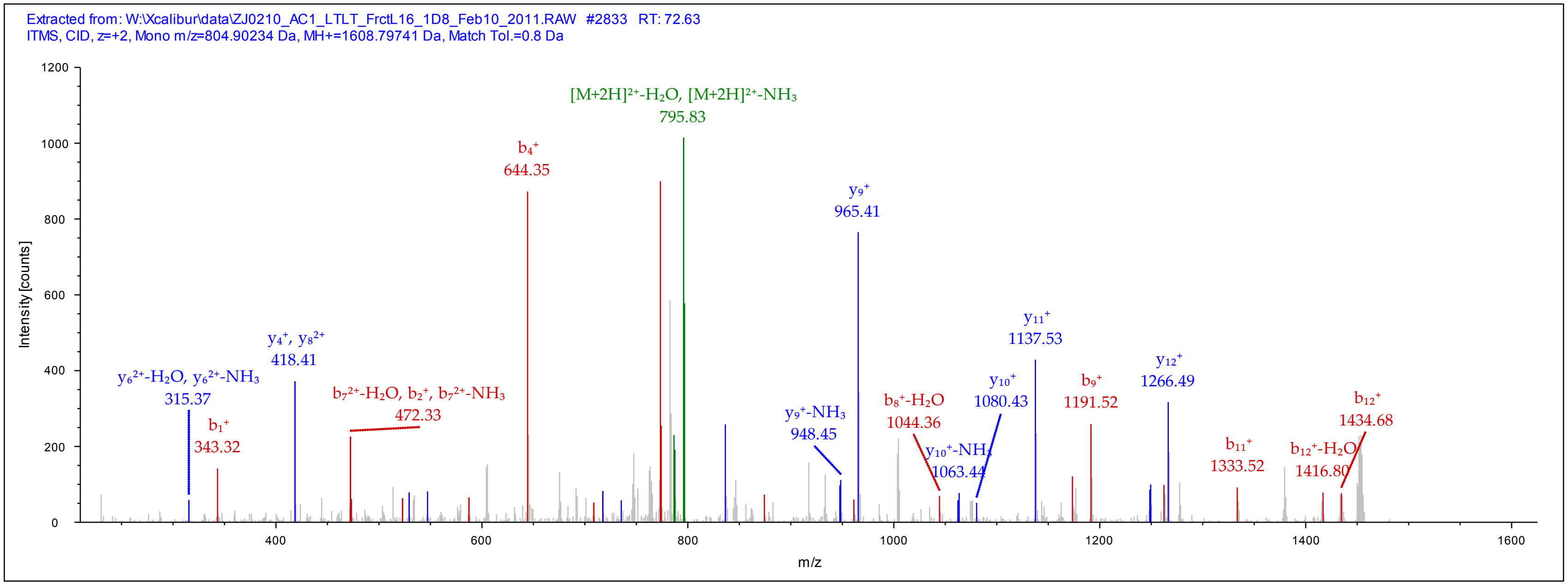
Identified with: Mascot (v1.16); IonScore:49, Exp Value:1.5E-003, Ions matched by search engine: 12/116

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- DNA-directed RNA polymerases I, II, and III subunit RPABC3
- Uncharacterized protein
- 5 kDa protein
- 9 kDa protein
- Uncharacterized protein
- Uncharacterized protein



IPI00791180.1

Sequence: AEEYEFLTPVEEAPK, A1-TMT6plex (229.16293 Da), K15-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 1105.58801 Da (+2.69 mmu/+2.44 ppm),   MH+: 2210.16875 Da,   RT: 112.80 min,

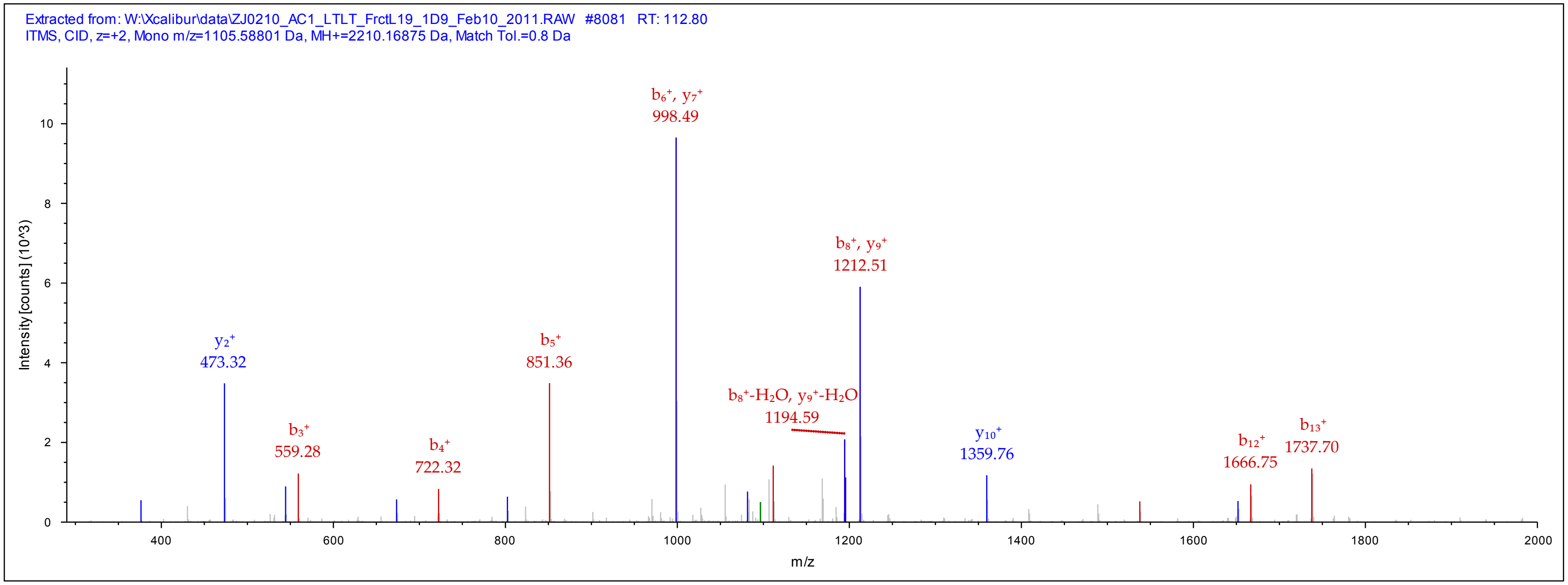
Identified with: Mascot (v1.16); IonScore:93, Exp Value:7.9E-008, Ions matched by search engine: 17/132

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Rho GDP-dissociation inhibitor 1
- 9 kDa protein lng=79
- 22 kDa protein lng=196
- 28 kDa protein lng=249
- 26 kDa protein lng=235



IPI00791243.1

Sequence: ALEAFETFK, A1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 757.43695 Da (-0.04 mmu/-0.05 ppm),   MH+: 1513.86662 Da,   RT: 113.43 min,

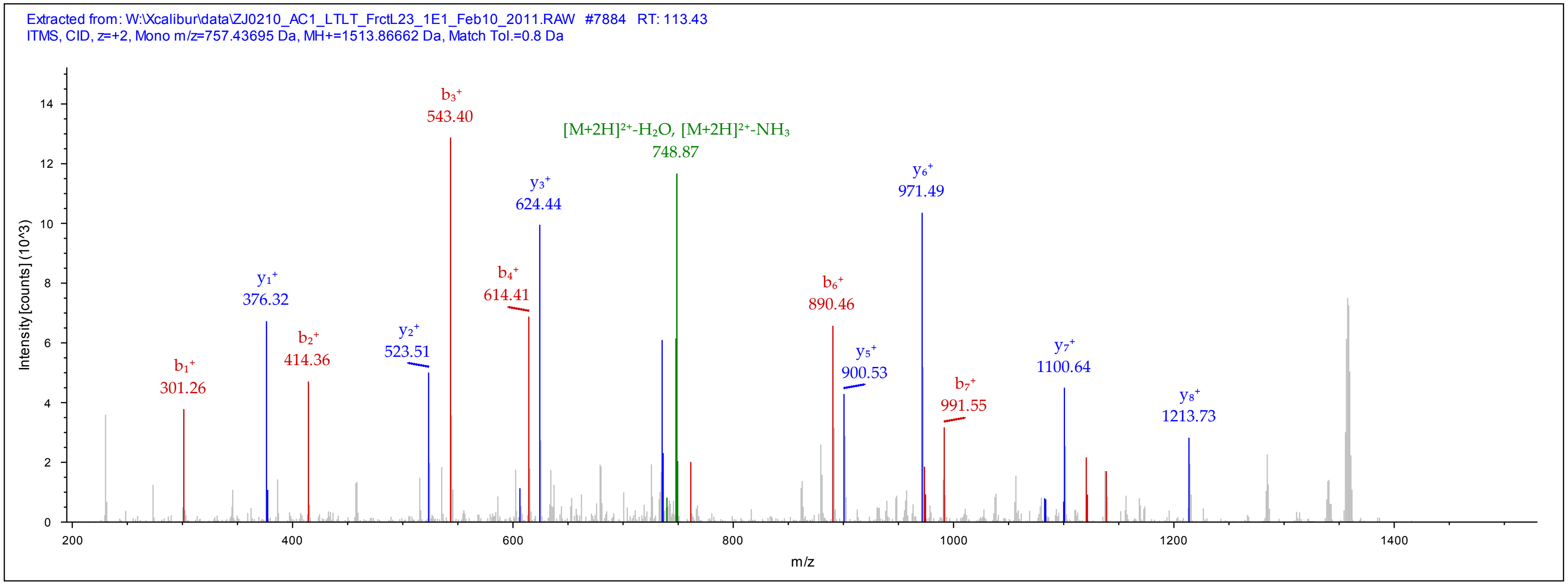
Identified with: Mascot (v1.16); IonScore:40, Exp Value:1.0E-002, Ions matched by search engine: 7/72

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Sorbitol dehydrogenase
- 11 kDa protein lng=105



IPI:IPI00791249.1

Sequence: QVPDTSVQETDR, Q1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 802.41266 Da (+2.75 mmu/+3.42 ppm), MH+: 1603.81804 Da, RT: 73.91 min,

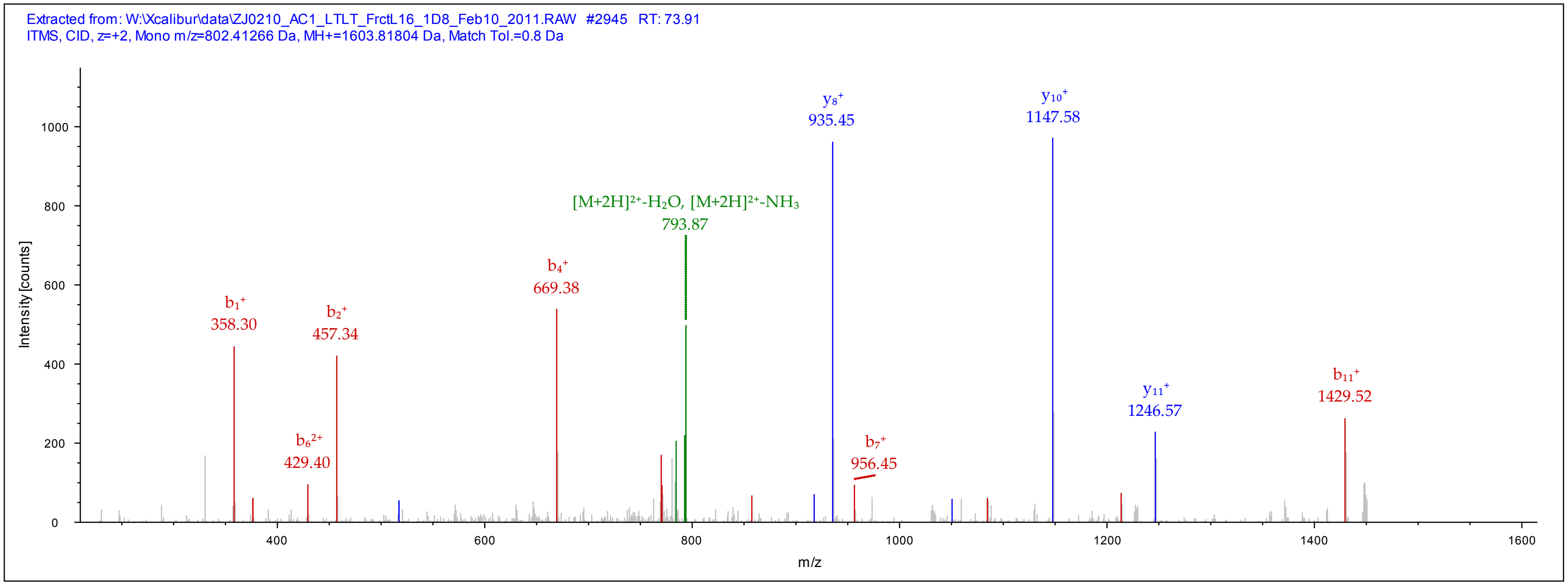
Identified with: Mascot (v1.16); IonScore:44, Exp Value:4.5E-003, Ions matched by search engine: 9/124

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Isoform 1 of Transmembrane protein 85
- Isoform 2 of Transmembrane protein 85
- 23 kDa protein lng=202
- 8 kDa protein
- Isoform 3 of Transmembrane protein 85
- 11 kDa protein



IPI00791618.1

Sequence: ENMAR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 425.22931 Da (+3.15 mmu/+7.41 ppm),   MH+: 849.45134 Da,   RT: 59.35 min,

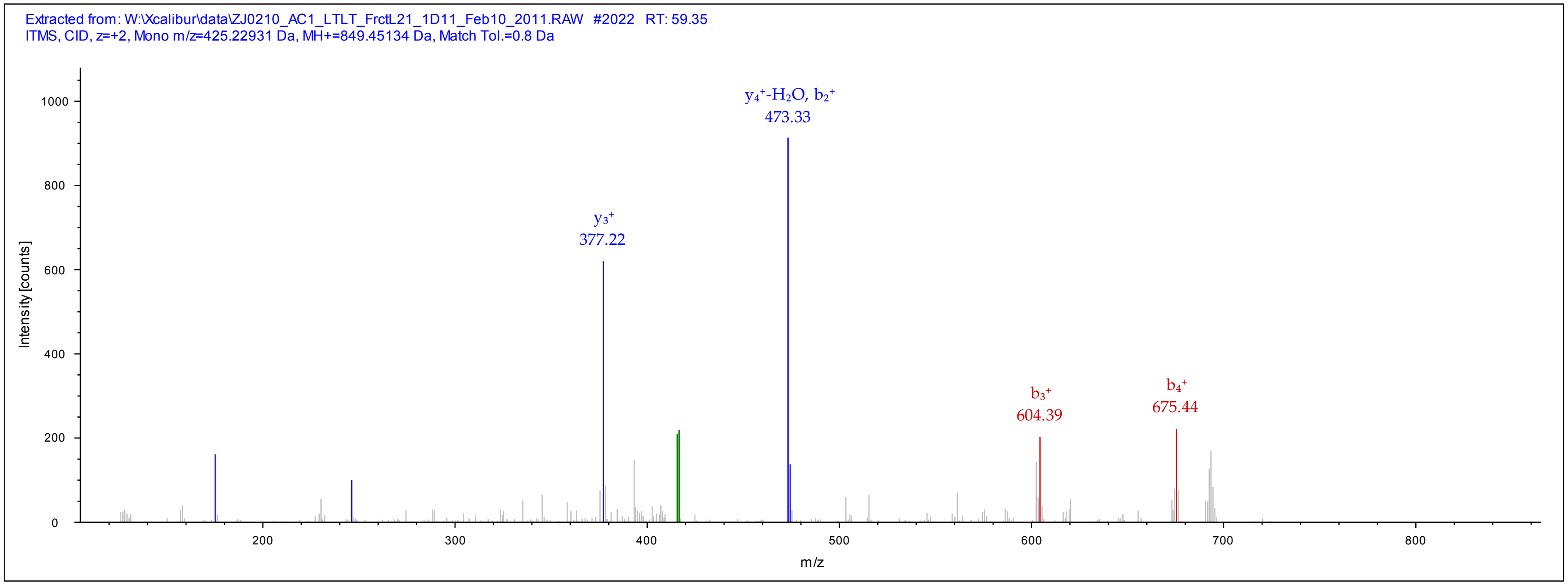
Identified with: Mascot (v1.16); IonScore:29, Exp Value:4.7E-002, Ions matched by search engine: 6/38

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Growth arrest-specific protein 1
- Bactericidal/permeability-increasing protein lng=123
- Bactericidal permeability-increasing protein



IPI:IPI00791716.1

Sequence: NFLELTELK, N1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 782.97150 Da (+0.3 mmu/+0.38 ppm), MH+: 1564.93572 Da, RT: 124.49 min,

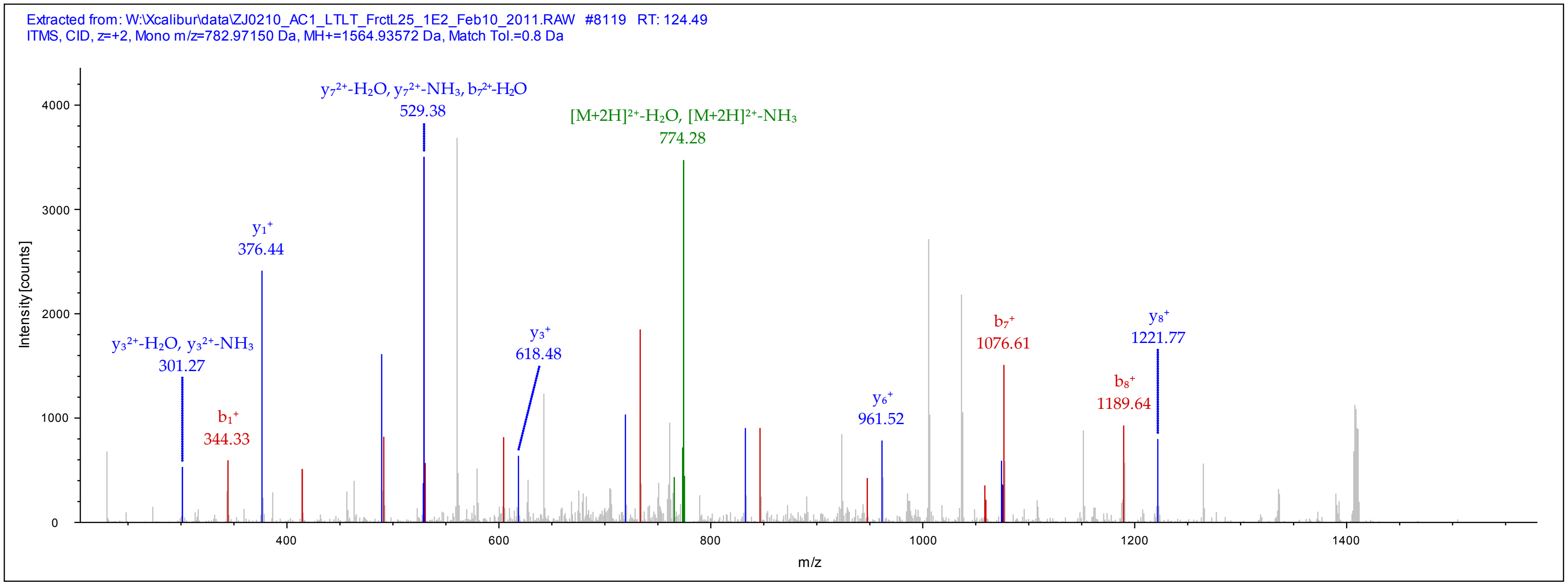
Identified with: Mascot (v1.16); IonScore:31, Exp Value:5.9E-002, Ions matched by search engine: 14/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of V-type proton ATPase 116 kDa subunit a isoform 1
- Isoform 2 of V-type proton ATPase 116 kDa subunit a isoform 1
- 27 kDa protein
- V-type proton ATPase 116 kDa subunit a isoform 1 isoform a



IPI:IPI00791751.1

Sequence: LISLPLSR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 564.37109 Da (-0.05 mmu/-0.08 ppm), MH+: 1127.73491 Da, RT: 108.84 min,

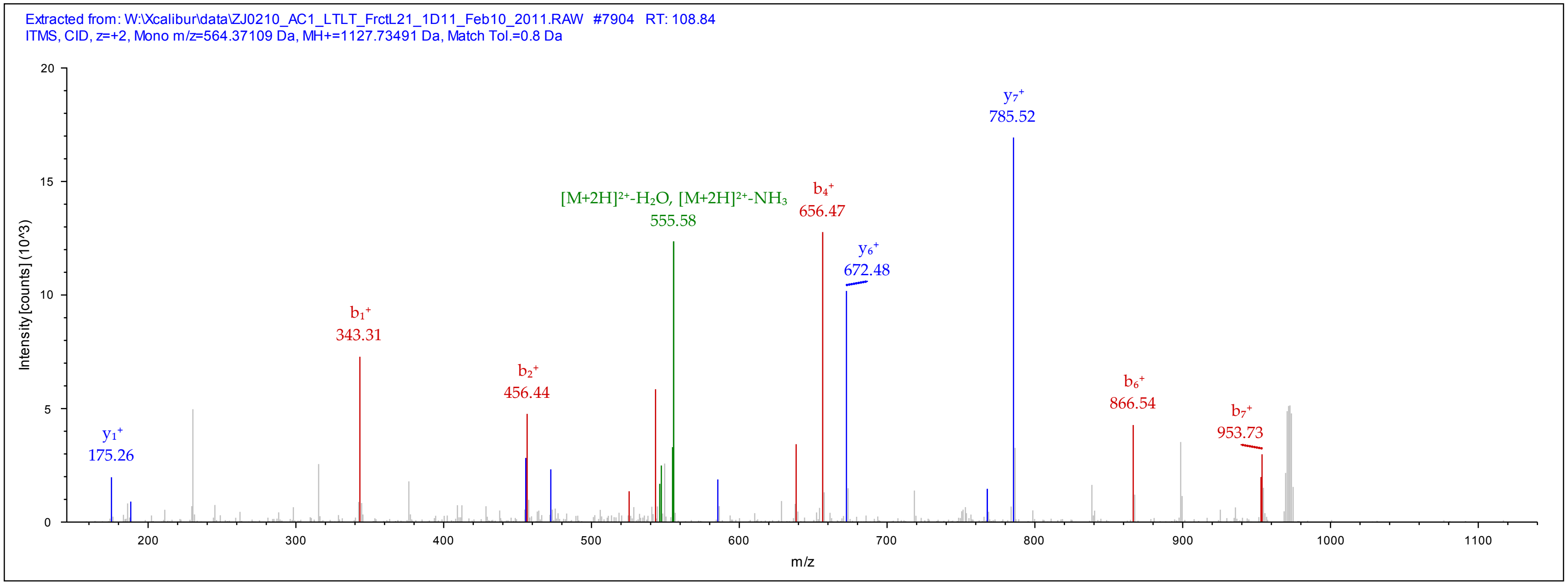
Identified with: Mascot (v1.16); IonScore:34, Exp Value:9.1E-003, Ions matched by search engine: 7/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Chromatin accessibility complex protein 1
- 6 kDa protein



IPI:IPI00791992.1

Sequence: VMSEFNNNFR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 743.86975 Da (+0.58 mmu/+0.77 ppm), MH+: 1486.73223 Da, RT: 118.52 min,

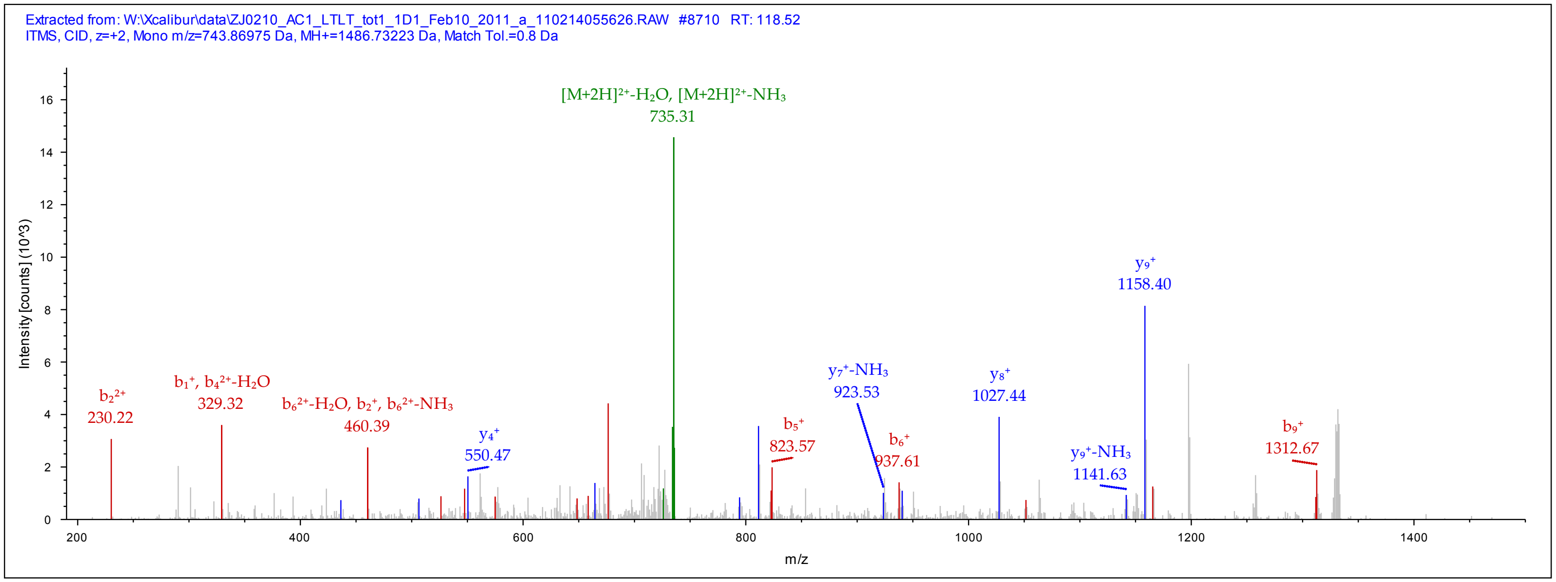
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.2E-002, Ions matched by search engine: 9/82

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- CD63 antigen
- Lysosome-associated membrane protein-3 variant lng=215
- CD63 antigen isoform B
- 14 kDa protein
- 14 kDa protein
- 15 kDa protein
- 13 kDa protein lng=120



IPI00792249.1

Sequence: NIAIEFLTLENEIFR, N1-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 684.38513 Da (+1.1 mmu/+1.61 ppm),   MH+: 2051.14084 Da,   RT: 226.05 min,

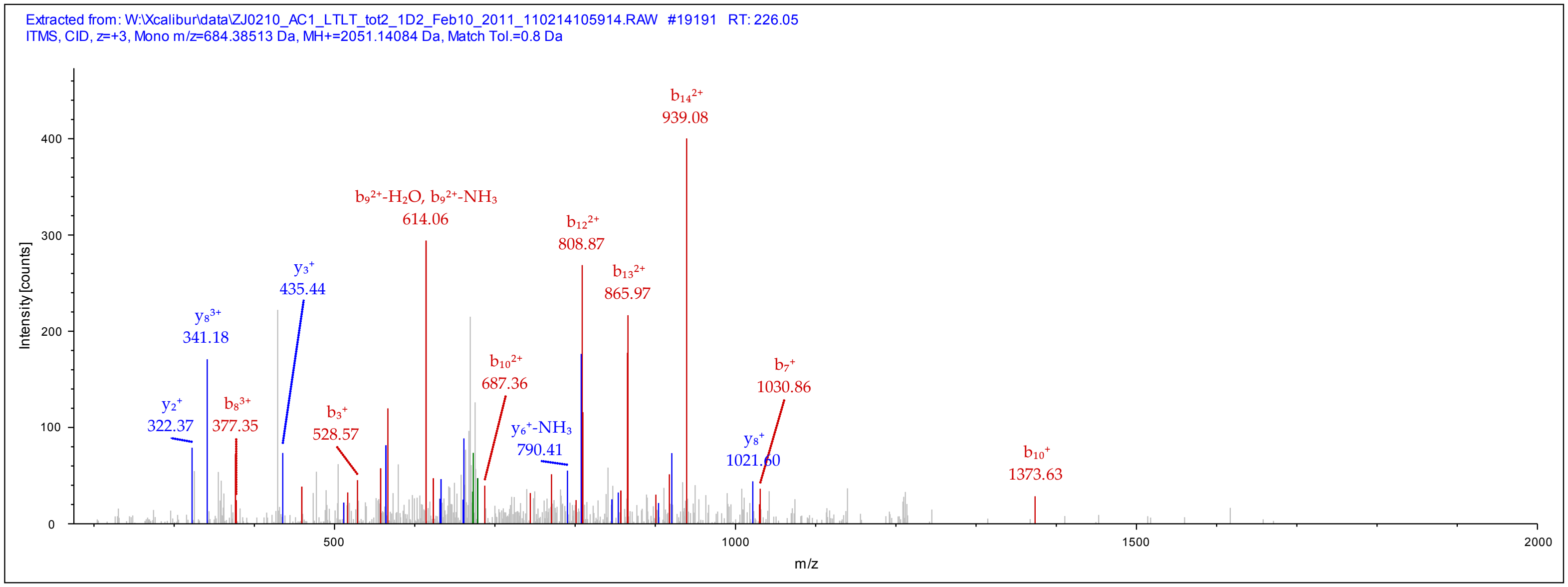
Identified with: Mascot (v1.16); IonScore:32, Exp Value:8.4E-002, Ions matched by search engine: 14/154

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Isoform 1 of Structural maintenance of chromosomes protein 4
- Isoform 2 of Structural maintenance of chromosomes protein 4
- 23 kDa protein lng=193
- 5 kDa protein lng=40
- cDNA FLJ16648 fis, clone TESTI4035508, highly similar to Structural maintenance of chromosomes 4-like 1 protein lng=1263
- SMC4 protein (Fragment) lng=423
- Putative uncharacterized protein SMC4 lng=423



IPI:IPI00792517.1

Sequence: ADLIEVVMNIEDMLCK, A1-TMT6plex (229.16293 Da), C15-Carbamidomethyl (57.02146 Da), K16-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 784.42133 Da (+2.28 mmu/+2.9 ppm), MH+: 2351.24942 Da, RT: 239.72 min,

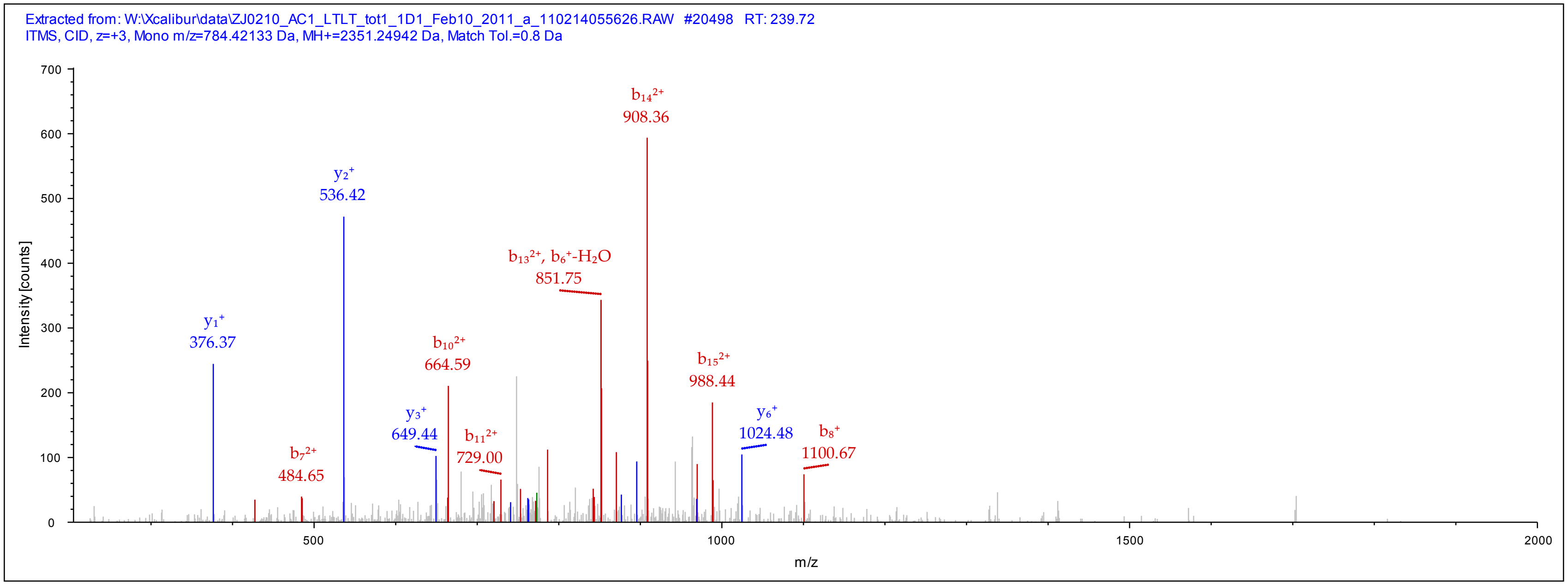
Identified with: Mascot (v1.16); IonScore:34, Exp Value:7.0E-002, Ions matched by search engine: 11/154

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Poly [ADP-ribose] polymerase 9
- Isoform 2 of Poly [ADP-ribose] polymerase 9
- poly [ADP-ribose] polymerase 9 isoform c



IPI:IPI00793212.1

Sequence: AWDVAR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 473.76907 Da (+0.02 mmu/+0.05 ppm), MH+: 946.53087 Da, RT: 78.37 min,

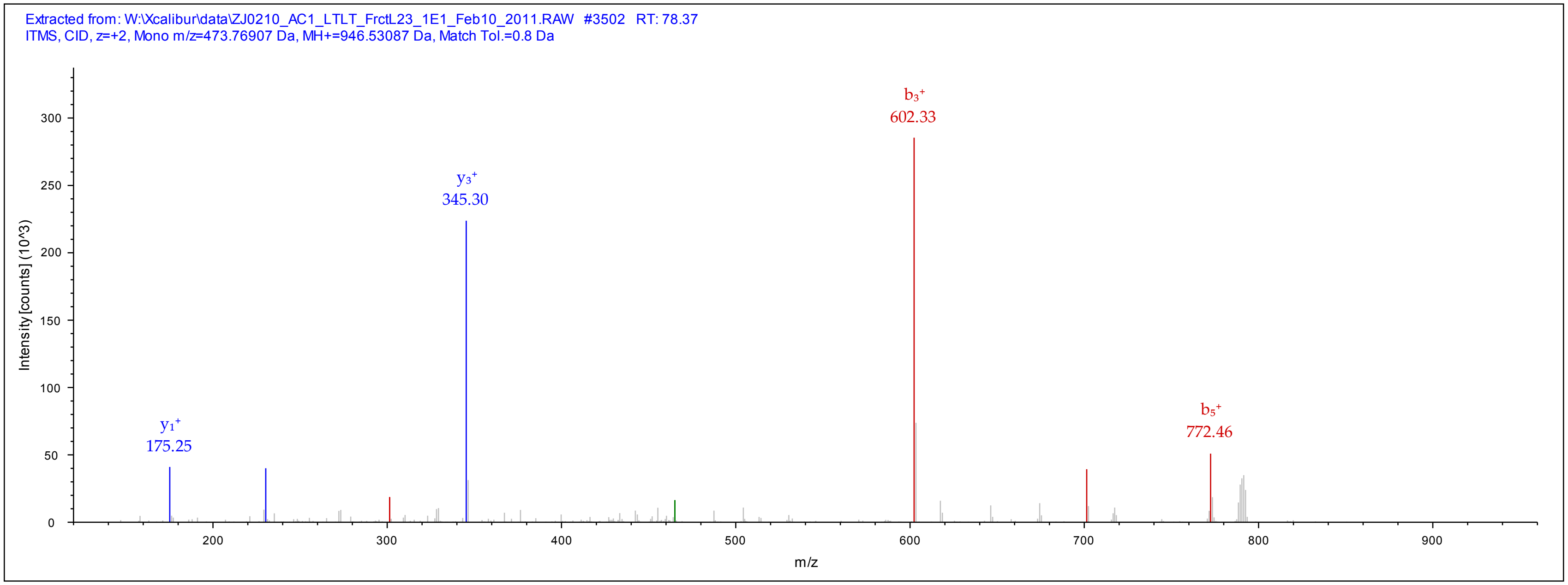
Identified with: Mascot (v1.16); IonScore:31, Exp Value:5.2E-002, Ions matched by search engine: 4/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Mevalonate kinase
- 28 kDa protein
- cDNA FLJ57879, highly similar to Mevalonate kinase



IPI:IPI00793420.1

Sequence: LLELIGR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 521.84479 Da (+0.03 mmu/+0.05 ppm),   MH+: 1042.68230 Da,   RT: 120.07 min,

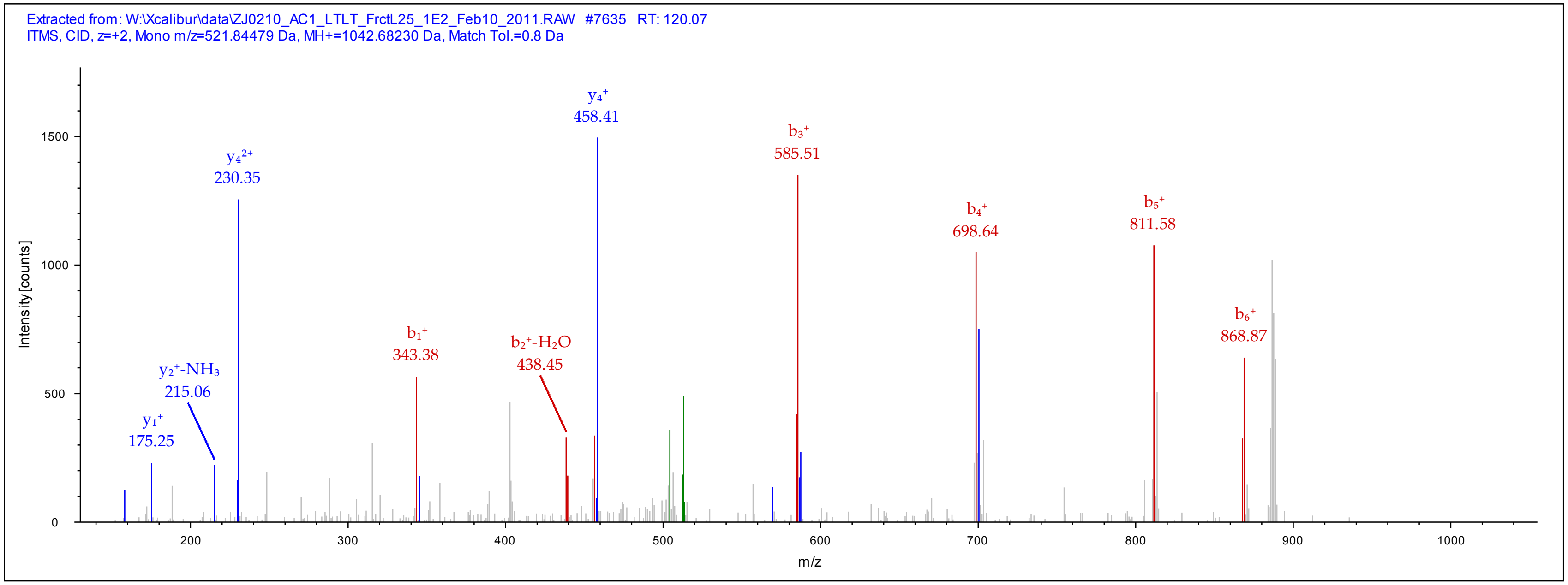
Identified with: Mascot (v1.16); IonScore:32, Exp Value:1.9E-002, Ions matched by search engine: 6/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Bone morphogenetic protein receptor type-2
- Bone morphogenic protein type II receptor



IPI00793819.1

Sequence: LVVLATPQVSDSMR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 872.99646 Da (+1.35 mmu/+1.54 ppm),   MH+: 1744.98564 Da,   RT: 109.27 min,

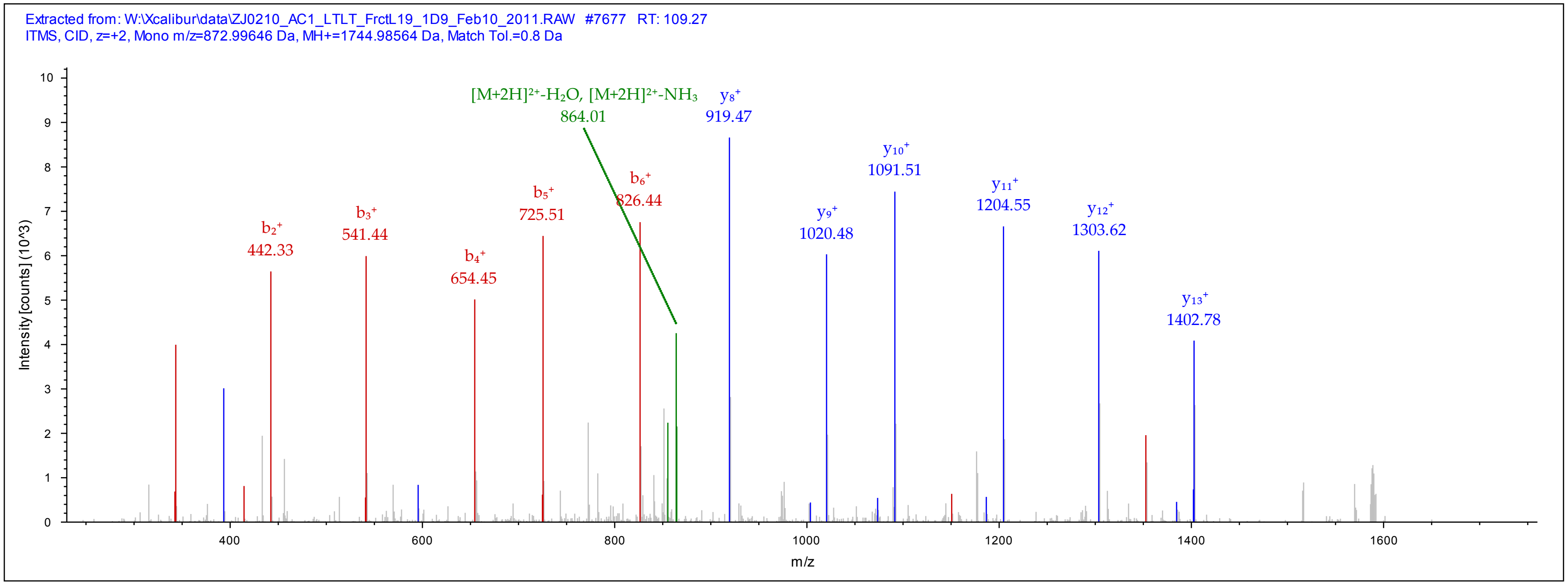
Identified with: Mascot (v1.16); IonScore:44, Exp Value:4.5E-003, Ions matched by search engine: 8/128

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform GN-1L of Glycogenin-1
- Isoform GN-1 of Glycogenin-1 lng=333
- cDNA FLJ57427, highly similar to Glycogenin-1 lng=193
- Isoform GN-1S of Glycogenin-1 lng=260
- Putative uncharacterized protein GYG1 lng=266



IPI00794141.1

Sequence: VGTSFSIPVVSDVR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 846.48126 Da (+1.11 mmu/+1.31 ppm), MH+: 1691.95525 Da, RT: 114.54 min,

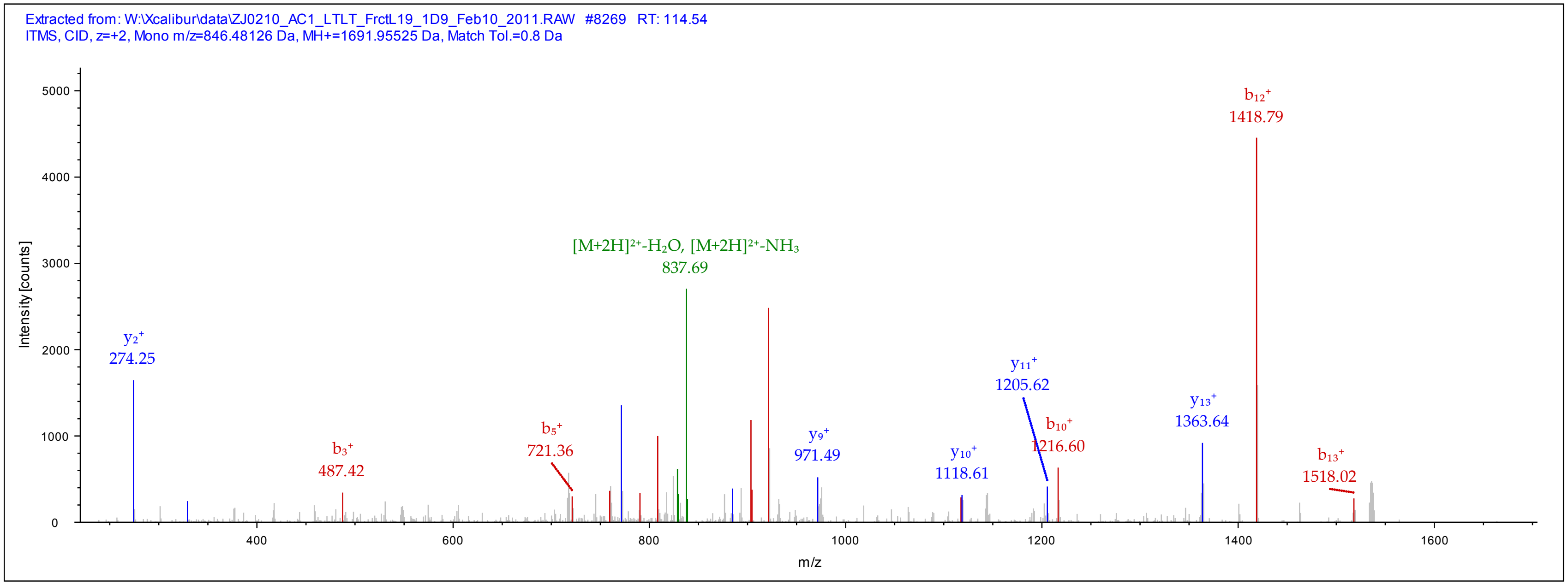
Identified with: Mascot (v1.16); IonScore:66, Exp Value:2.9E-005, Ions matched by search engine: 13/122

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Probable ribosome biogenesis protein NEP1
- cDNA FLJ60792, highly similar to Probable ribosome biogenesis protein NEP1 lng=222
- 15 kDa protein lng=142



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL19_1D9_Feb10_2011.RAW #8269 RT: 114.54
ITMS, CID, z=+2, Mono m/z=846.48126 Da, MH+=1691.95525 Da, Match Tol.=0.8 Da

IPI:IPI00794313.1

Sequence: SLLAGLLK, S1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 636.93701 Da (+0.59 mmu/+0.92 ppm), MH+: 1272.86675 Da, RT: 127.20 min,

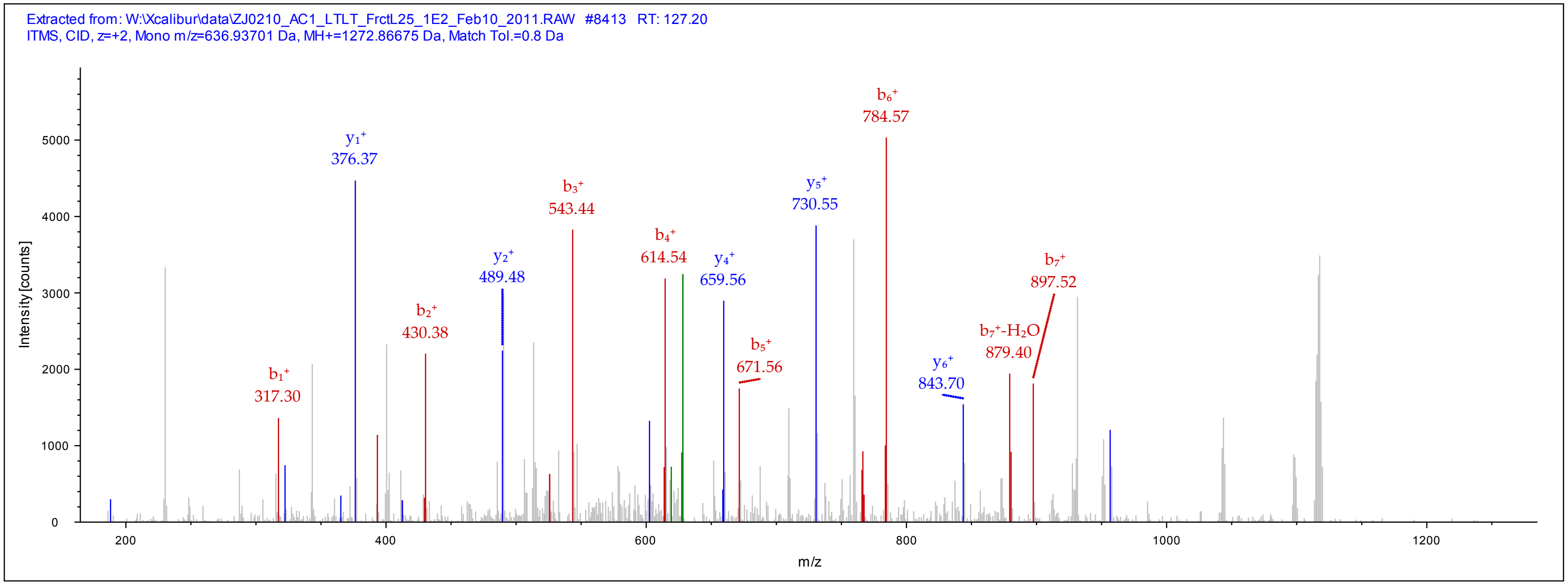
Identified with: Mascot (v1.16); IonScore:30, Exp Value:2.7E-002, Ions matched by search engine: 7/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- RAC-beta serine/threonine-protein kinase
- AKT2 protein
- Uncharacterized protein



IPI00794330.1

Sequence: DWIGIFR, D1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 568.32727 Da (+0.54 mmu/+0.94 ppm),   MH+: 1135.64726 Da,   RT: 120.39 min,

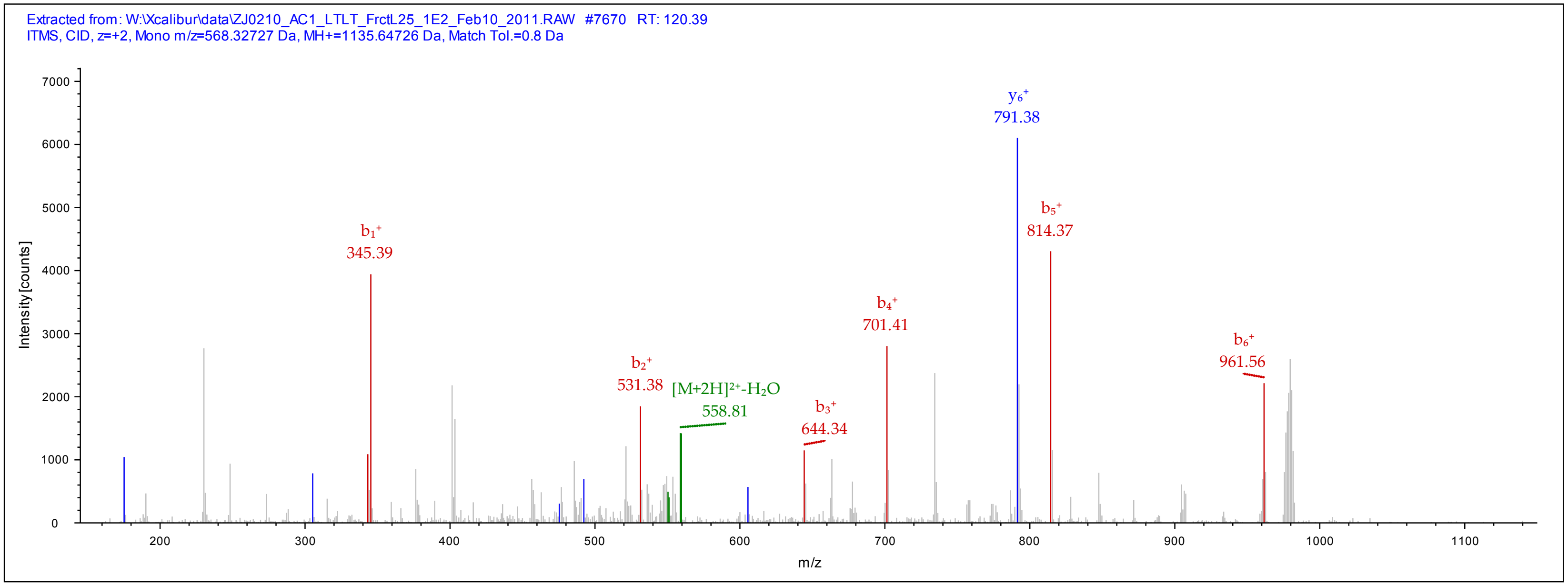
Identified with: Mascot (v1.16); IonScore:30, Exp Value:6.6E-002, Ions matched by search engine: 6/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (11):

- Calcium-binding and coiled-coil domain-containing protein 2
- 8 kDa protein lng=67
- 13 kDa protein lng=111
- cDNA FLJ52379, highly similar to Homo sapiens nuclear domain 10 protein (NDP52), mRNA lng=404
- cDNA FLJ55141, highly similar to Homo sapiens nuclear domain 10 protein (NDP52), mRNA lng=470
- Uncharacterized protein
- Uncharacterized protein



IPI00794418.1

Sequence: EISLLR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 480.30783 Da (-0.17 mmu/-0.36 ppm),   MH+: 959.60838 Da,   RT: 124.50 min,

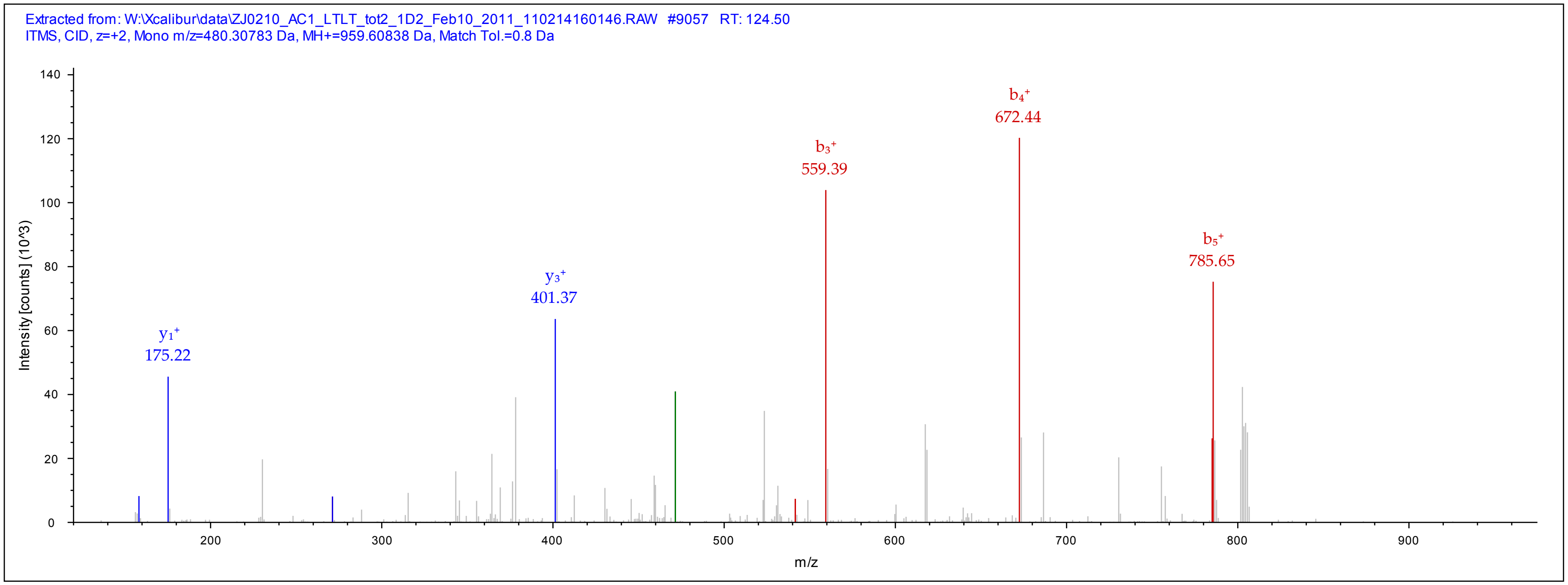
Identified with: Mascot (v1.16); IonScore:29, Exp Value:5.0E-002, Ions matched by search engine: 4/44

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 10 kDa protein lng=87



IPI:IPI00794545.1

Sequence: GNVGVVLFNFGK, G1-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 855.01178 Da (+0.58 mmu/+0.68 ppm), MH+: 1709.01628 Da, RT: 124.97 min,

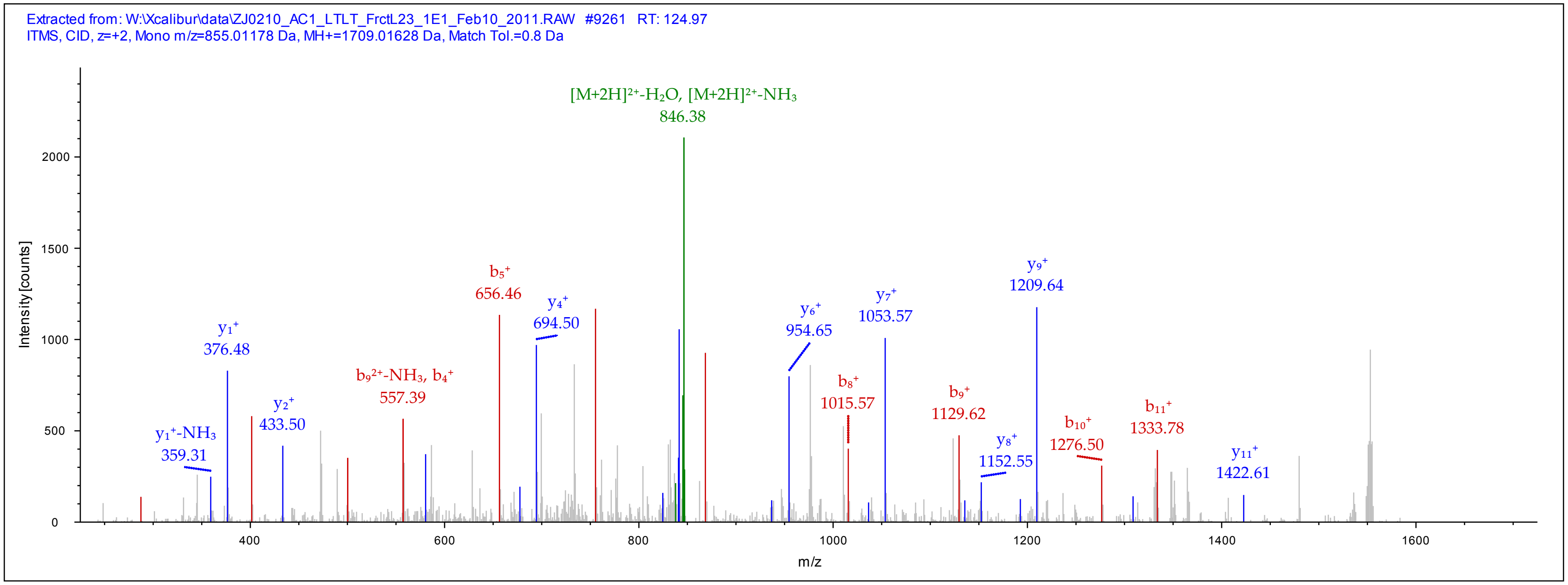
Identified with: Mascot (v1.16); IonScore:71, Exp Value:6.4E-006, Ions matched by search engine: 10/110

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial
- Isoform 2 of Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial
- Isoform 3 of Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial
- 24 kDa protein lng=229
- deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 3



IPI:IPI00794563.1

Sequence: AQICSLVELLATTLK, A1-TMT6plex (229.16293 Da), C4-Carbamidomethyl (57.02146 Da), K15-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 706.76129 Da (+2.81 mmu/+3.97 ppm),   MH+: 2118.26932 Da,   RT: 221.83 min,

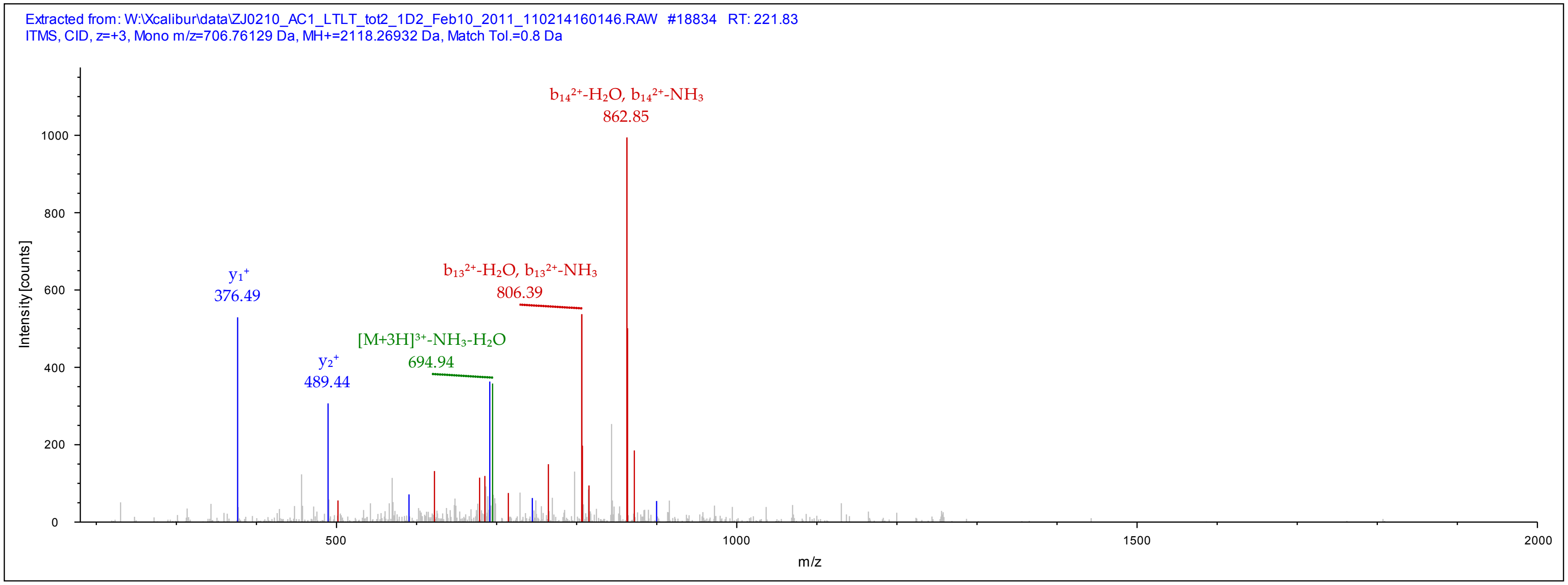
Identified with: Mascot (v1.16); IonScore:33, Exp Value:3.2E-002, Ions matched by search engine: 10/154

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Conserved oligomeric Golgi complex subunit 1
- COG1 protein



IPI:IPI00795434.1

Sequence: ACLDYPVTSVLPPASLCK, A1-TMT6plex (229.16293 Da), C2-Carbamidomethyl (57.02146 Da), C17-Carbamidomethyl (57.02146 Da), K18-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 1225.16882 Da (+3.39 mmu/+2.77 ppm), MH+: 2449.33037 Da, RT: 121.27 min,

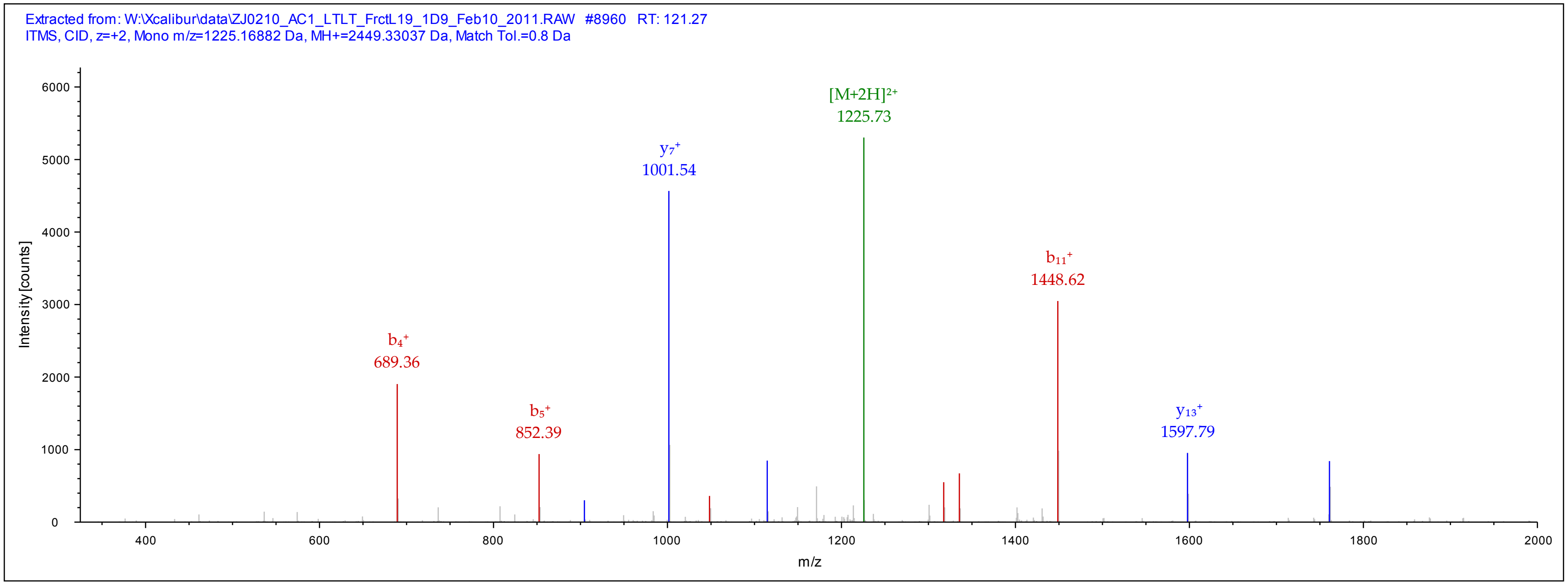
Identified with: Mascot (v1.16); IonScore:88, Exp Value:2.5E-007, Ions matched by search engine: 15/158

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Pituitary tumor-transforming gene 1 protein-interacting protein
- Putative uncharacterized protein PTTG1IP lng=159
- Uncharacterized protein



IPI:IPI00795592.1

Sequence: SDVEAIAK, S1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 645.88831 Da (+1.18 mmu/+1.82 ppm), MH+: 1290.76933 Da, RT: 82.88 min,

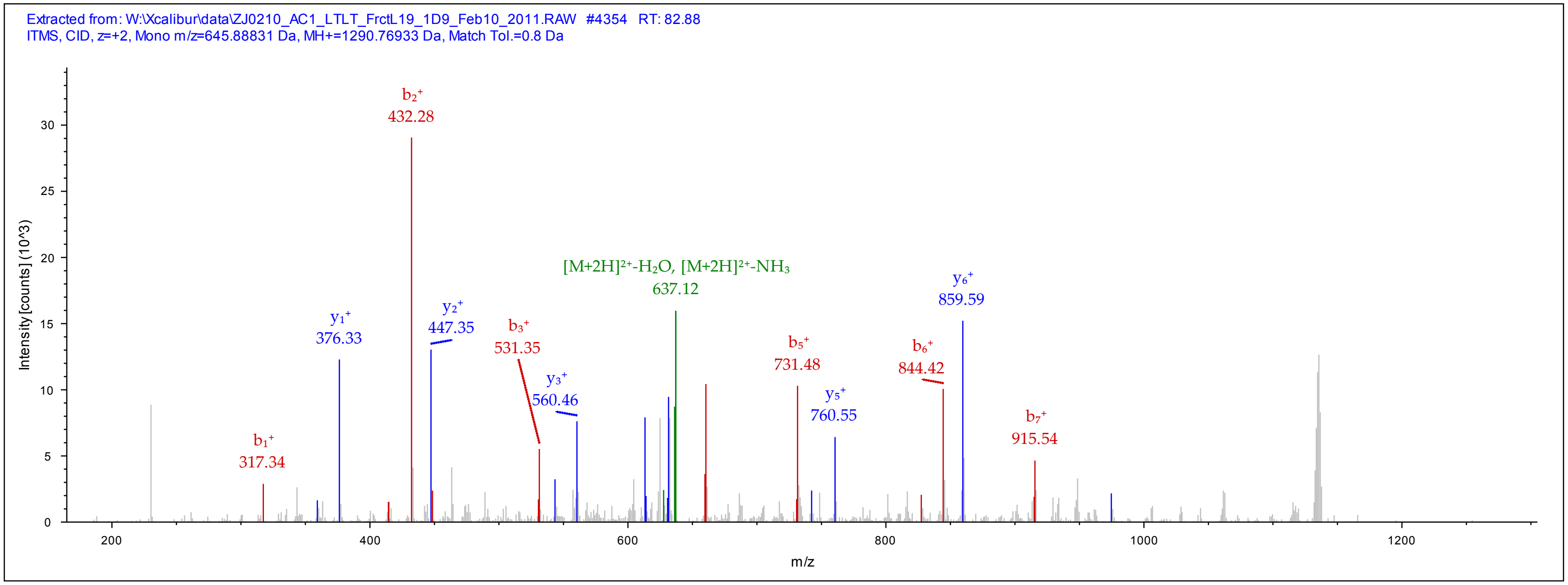
Identified with: Mascot (v1.16); IonScore:47, Exp Value:2.1E-003, Ions matched by search engine: 7/62

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Uncharacterized protein C17orf62
- hypothetical protein LOC79415 isoform b



IPI00796431.1

Sequence: VSAGEAVVNR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 615.85468 Da (+0.83 mmu/+1.34 ppm), MH+: 1230.70207 Da, RT: 74.95 min,

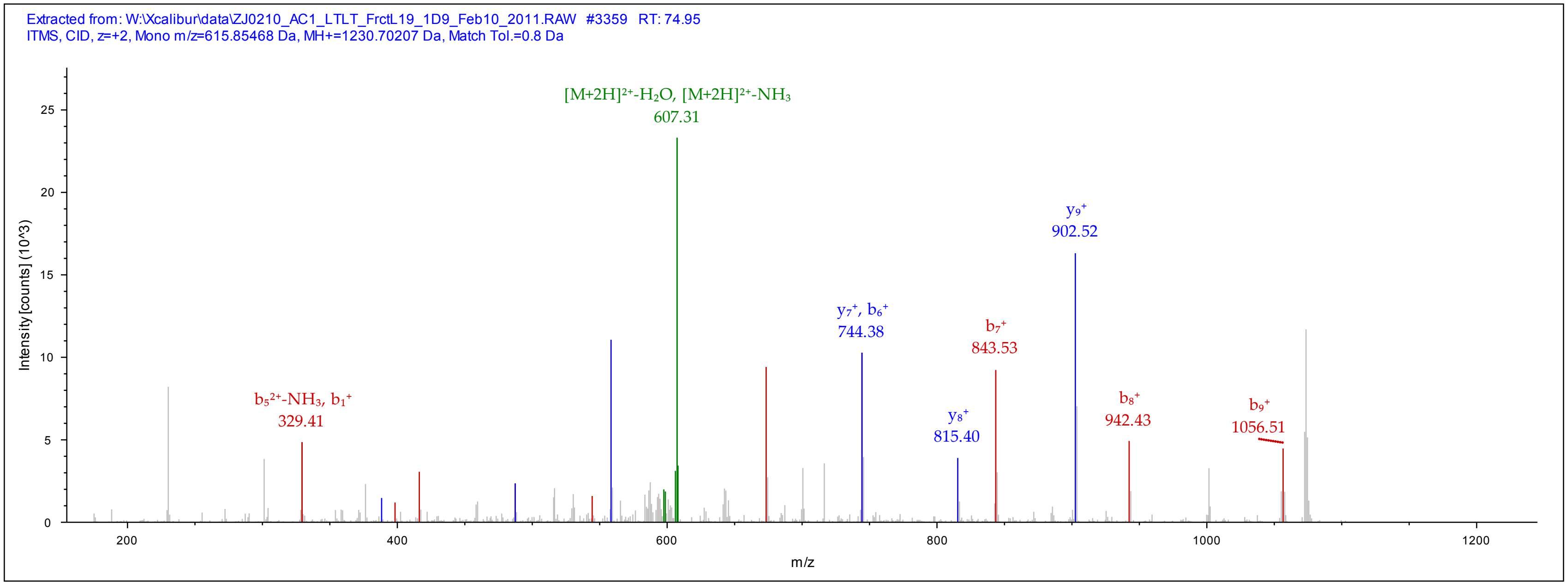
Identified with: Mascot (v1.16); IonScore:41, Exp Value:5.8E-003, Ions matched by search engine: 9/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform LMP2.L of Proteasome subunit beta type-9
- Isoform LMP2.S of Proteasome subunit beta type-9
- Proteasome (Prosome, macropain) subunit, beta type, 9 lng=131
- Proteasome (Prosome, macropain) subunit, beta type, 9 lng=131
- Proteasome subunit beta type lng=196
- Proteasome subunit beta type lng=219



IPI00796669.1

Sequence: WIPASQLR, W1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 600.35870 Da (+0.14 mmu/+0.23 ppm), MH+: 1199.71013 Da, RT: 99.74 min,

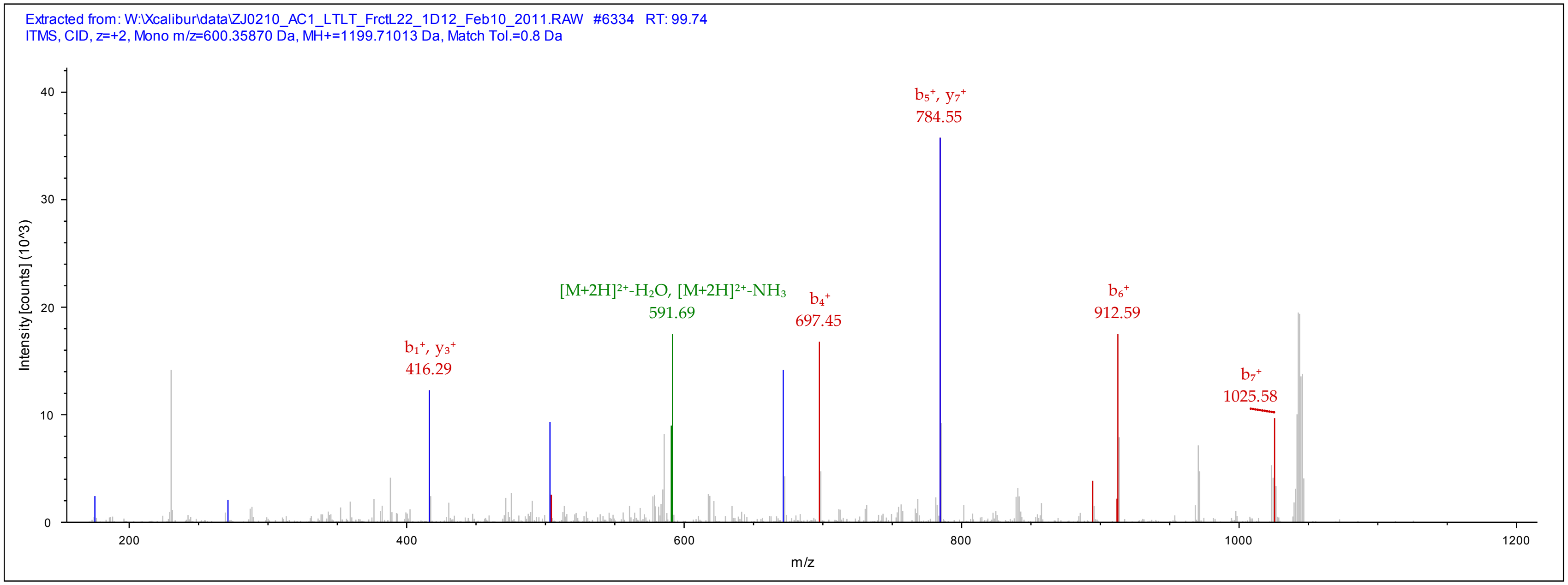
Identified with: Mascot (v1.16); IonScore:29, Exp Value:7.2E-002, Ions matched by search engine: 6/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- cDNA FLJ57852, highly similar to Cysteine-rich protein 2-binding protein lng=781
- Isoform 1 of Cysteine-rich protein 2-binding protein



IPI:IPI00796777.1

Sequence: LLASLLR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 507.84741 Da (+0.11 mmu/+0.22 ppm), MH+: 1014.68755 Da, RT: 122.29 min,

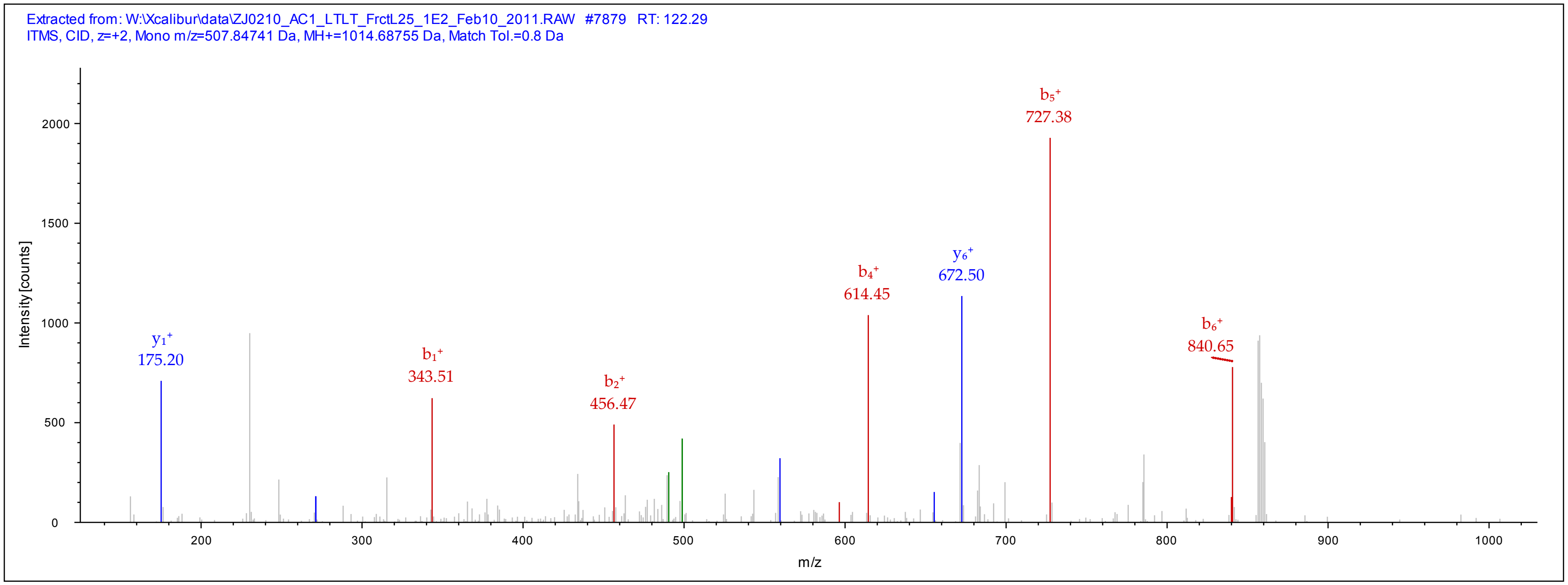
Identified with: Mascot (v1.16); IonScore:31, Exp Value:3.3E-002, Ions matched by search engine: 5/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 17 kDa protein



IPI:IPI00797108.1

Sequence: TLEVEIEPGVR, T1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 735.92218 Da (+0.25 mmu/+0.33 ppm), MH+: 1470.83708 Da, RT: 96.21 min,

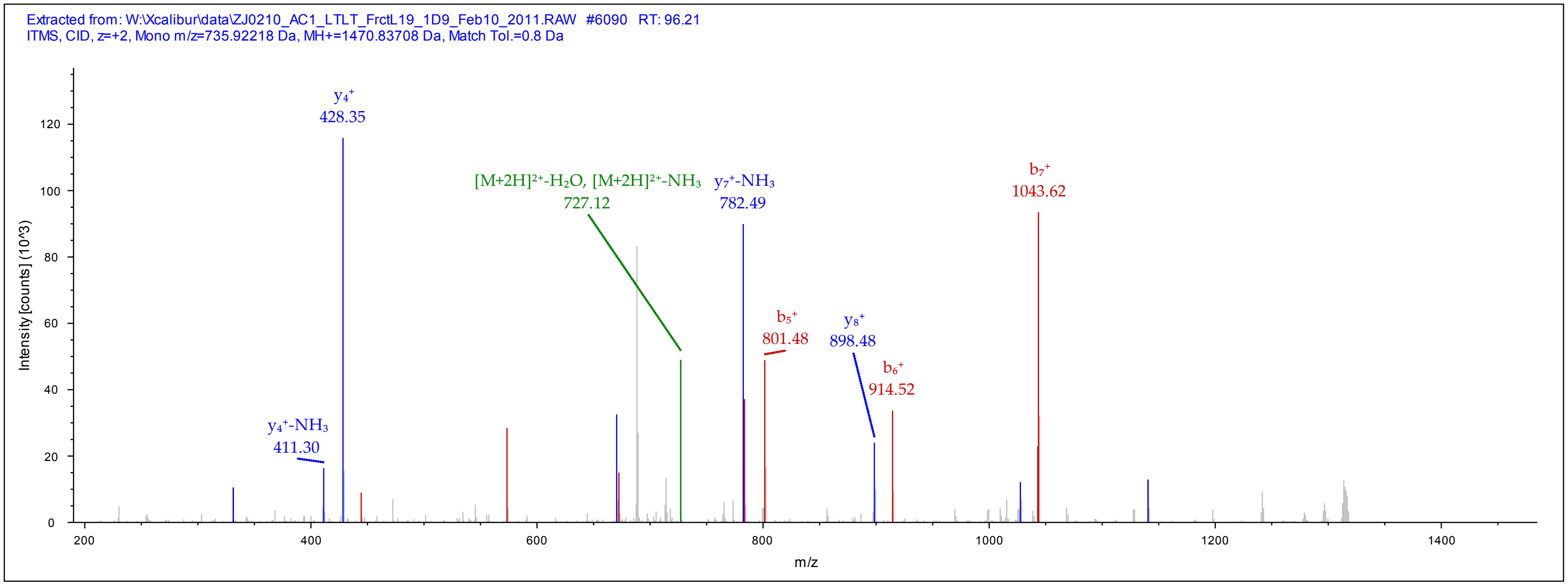
Identified with: Mascot (v1.16); IonScore:55, Exp Value:2.8E-004, Ions matched by search engine: 10/92

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- DnaJ homolog subfamily B member 11
- 19 kDa protein
- Protein



IPI00797778.1

Sequence: AALFLQTLK, A1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 731.97552 Da (+1.99 mmu/+2.71 ppm),   MH+: 1462.94377 Da,   RT: 124.38 min,

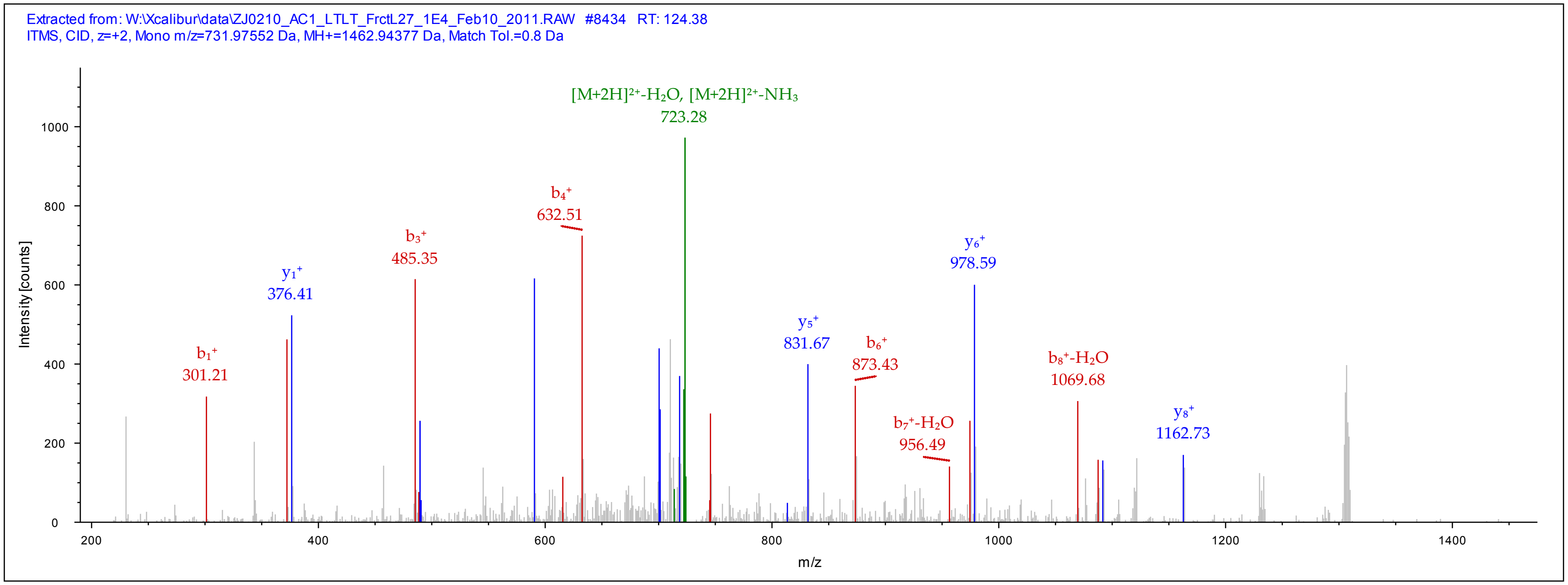
Identified with: Mascot (v1.16); IonScore:38, Exp Value:7.2E-003, Ions matched by search engine: 7/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Splicing factor, arginine/serine-rich 8
- SFRS8 protein lng=1003
- 91 kDa protein lng=825



IPI00798025.1

Sequence: NLSTFAVDGK, N1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 755.43805 Da (+0.53 mmu/+0.7 ppm), MH+: 1509.86882 Da, RT: 94.06 min,

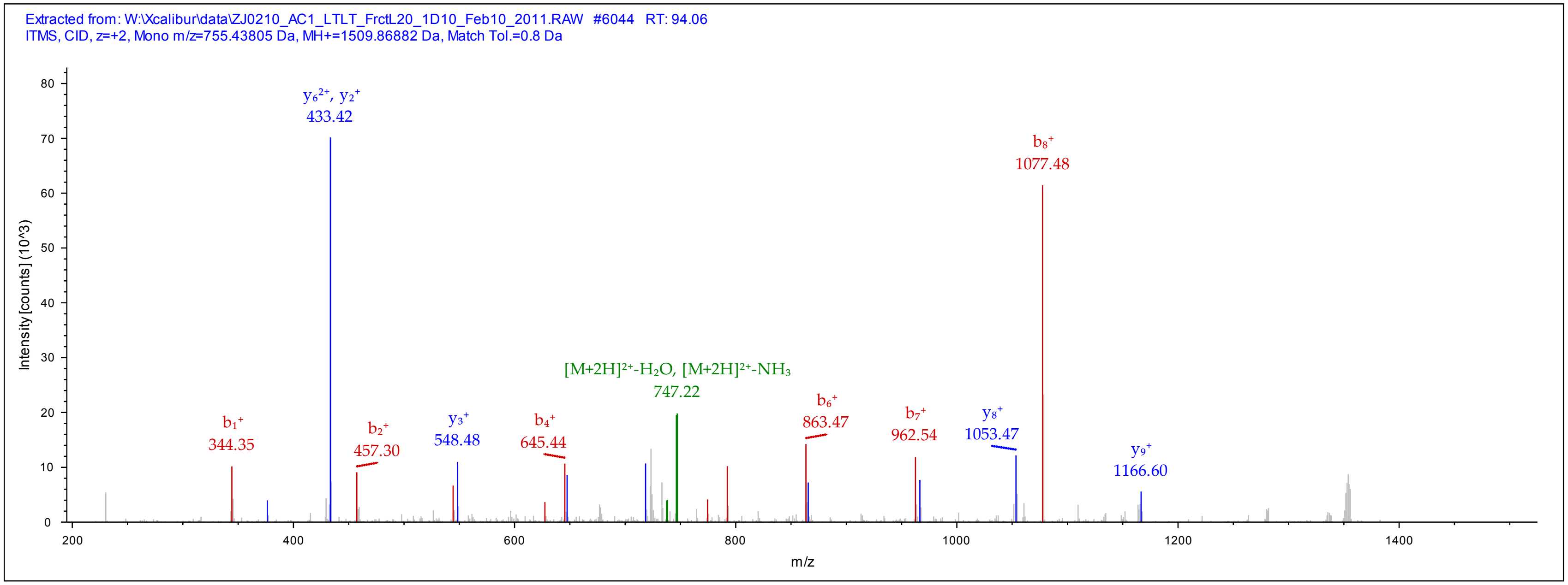
Identified with: Mascot (v1.16); IonScore:54, Exp Value:3.2E-004, Ions matched by search engine: 9/100

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

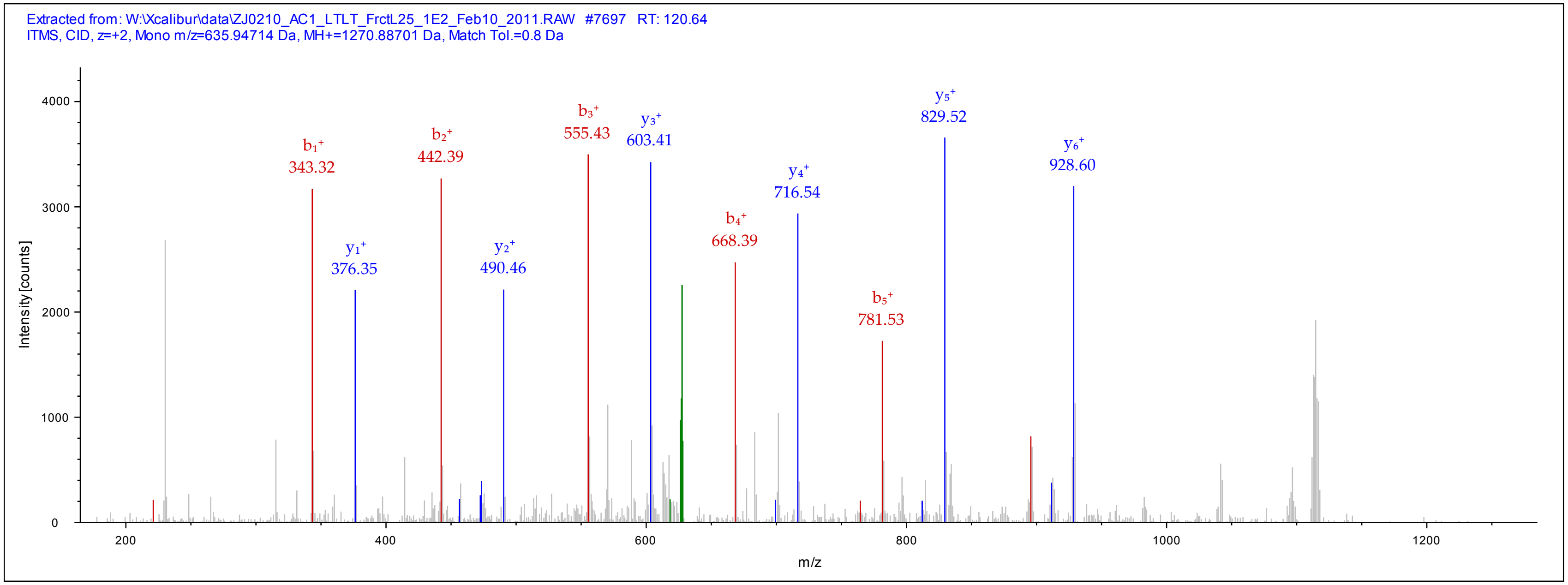
Protein references (5):

- Isoform Long of ES1 protein homolog, mitochondrial
- Putative uncharacterized protein C21orf33 lng=224
- 23 kDa protein lng=217
- Putative uncharacterized protein C21orf33 lng=191
- Putative uncharacterized protein PWP2 lng=205



IPI00798037.1
Sequence: LVLILNK, L1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)
Charge: +2,   Monoisotopic m/z: 635.94714 Da (+0.35 mmu/+0.55 ppm),   MH+: 1270.88701 Da,   RT: 120.64 min,
Identified with: Mascot (v1.16); IonScore:33, Exp Value:9.9E-004, Ions matched by search engine: 6/52
Fragment match tolerance used for search: 0.8 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):
- Isoform 1 of Guanine nucleotide-binding protein-like 3
- Isoform 2 of Guanine nucleotide-binding protein-like 3
- cDNA FLJ57535, highly similar to Guanine nucleotide-binding protein-like 3 lng=242



IPI:IPI00798394.1

Sequence: LWLLDDSK, L1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 724.43335 Da (+1.64 mmu/+2.27 ppm), MH+: 1447.85942 Da, RT: 124.31 min,

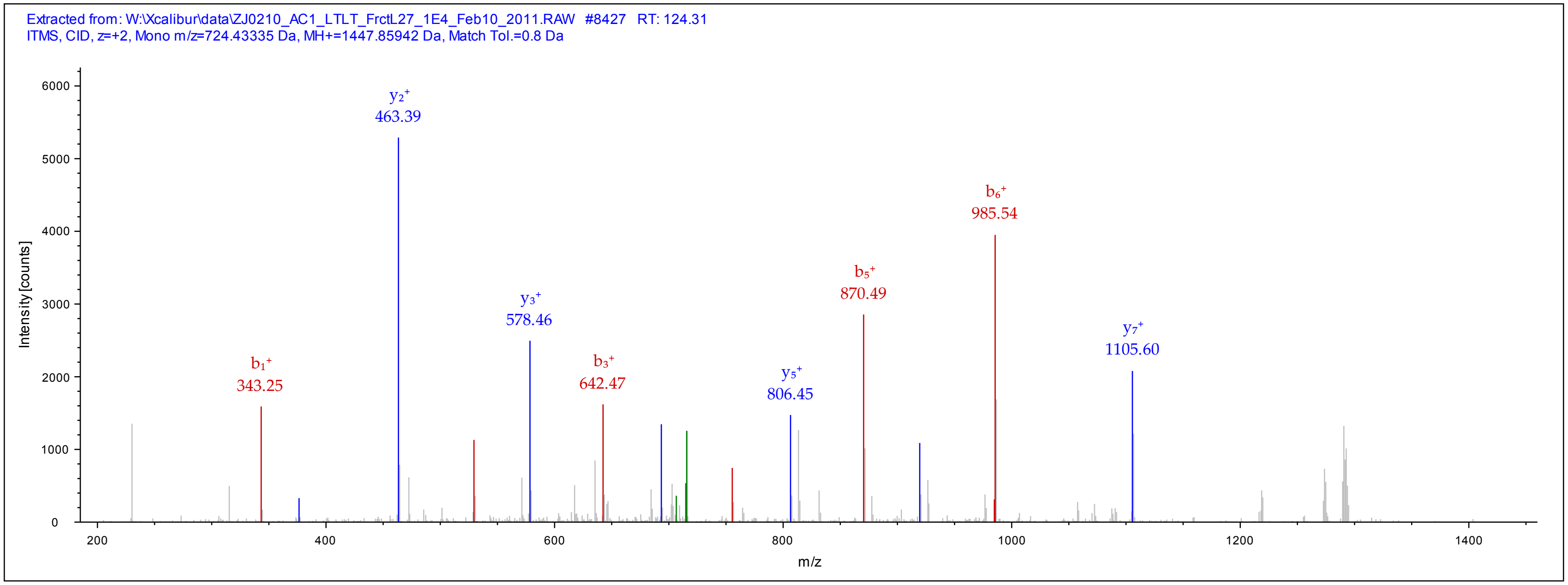
Identified with: Mascot (v1.16); IonScore:36, Exp Value:1.8E-002, Ions matched by search engine: 7/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (9):

- Cytoplasmic protein NCK1
- Cytoplasmic protein NCK2
- cytoplasmic protein NCK2 isoform B
- Uncharacterized protein
- Uncharacterized protein



IPI:IPI00807400.2

Sequence: IGIIVK, I1-TMT6plex (229.16293 Da), K6-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 550.89355 Da (-0.47 mmu/-0.86 ppm), MH+: 1100.77983 Da, RT: 107.19 min,

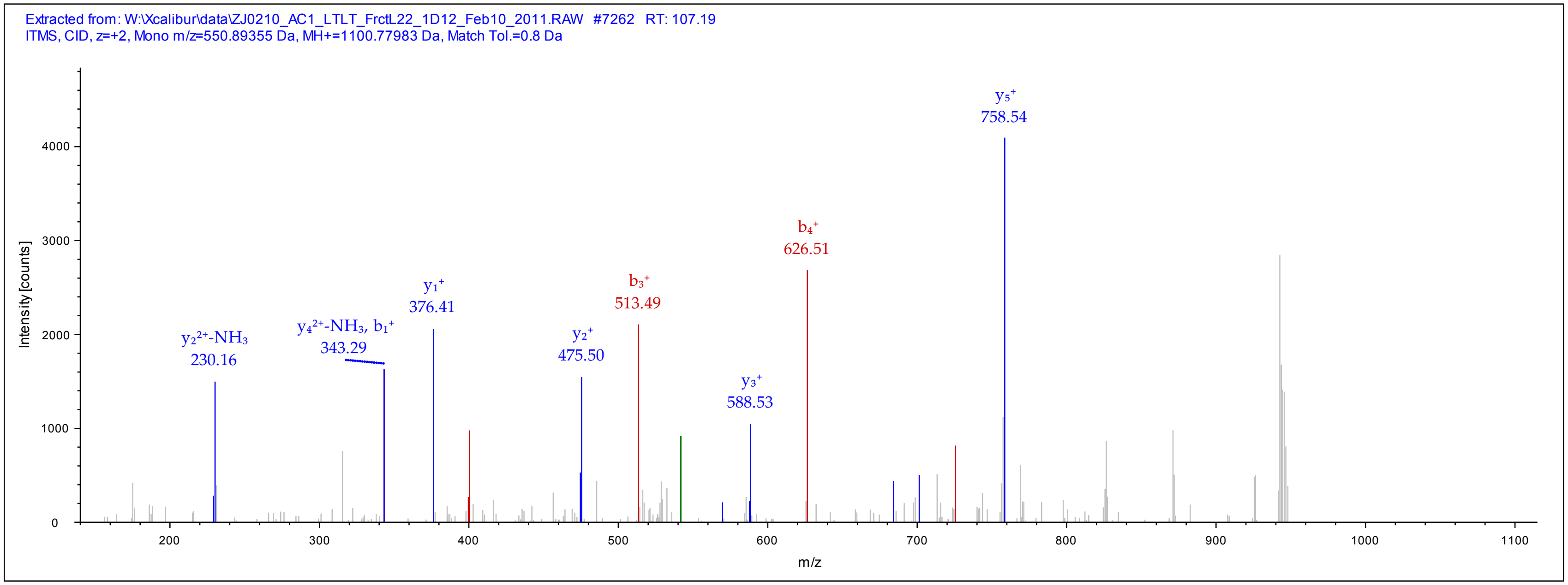
Identified with: Mascot (v1.16); IonScore:31, Exp Value:1.5E-002, Ions matched by search engine: 5/42

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Structural maintenance of chromosomes protein 1B
- Isoform 2 of Structural maintenance of chromosomes protein 1B
- Isoform 3 of Structural maintenance of chromosomes protein 1B



IPI00807611.1

Sequence: EFDPTITDASLSLPSR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 989.52362 Da (+3.42 mmu/+3.45 ppm),   MH+: 1978.03996 Da,   RT: 111.30 min,

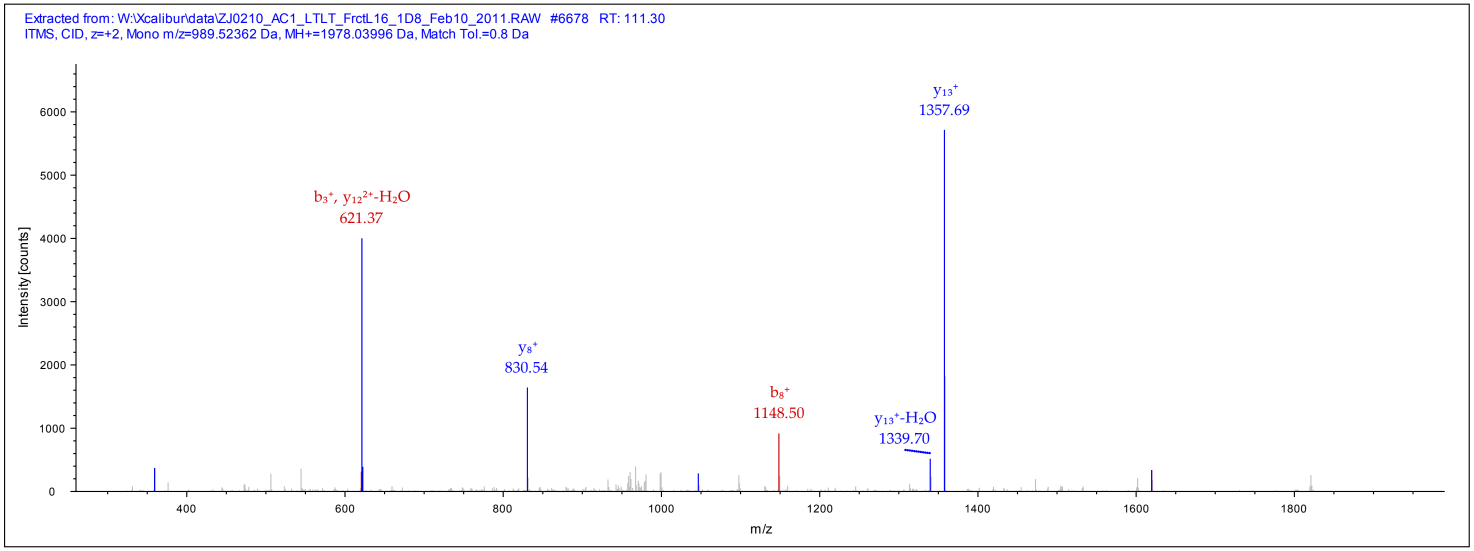
Identified with: Mascot (v1.16); IonScore:41, Exp Value:9.9E-003, Ions matched by search engine: 21/148

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (9):

- Isoform 1 of Caldesmon
- Isoform 2 of Caldesmon lng=564
- Isoform 3 of Caldesmon
- Isoform 5 of Caldesmon
- cDNA FLJ53193, highly similar to Homo sapiens caldesmon 1 (CALD1), transcript variant 5, mRNA lng=543
- CALD1 protein (Fragment) lng=153
- Putative uncharacterized protein DKFZp779D0769 lng=536
- caldesmon 1 isoform 3 lng=563
- Putative uncharacterized protein CALD1 lng=459



IPI00827813.1

Sequence: ADAEEEAATR, A1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 646.32550 Da (+5.46 mmu/+8.46 ppm),   MH+: 1291.64372 Da,   RT: 62.79 min,

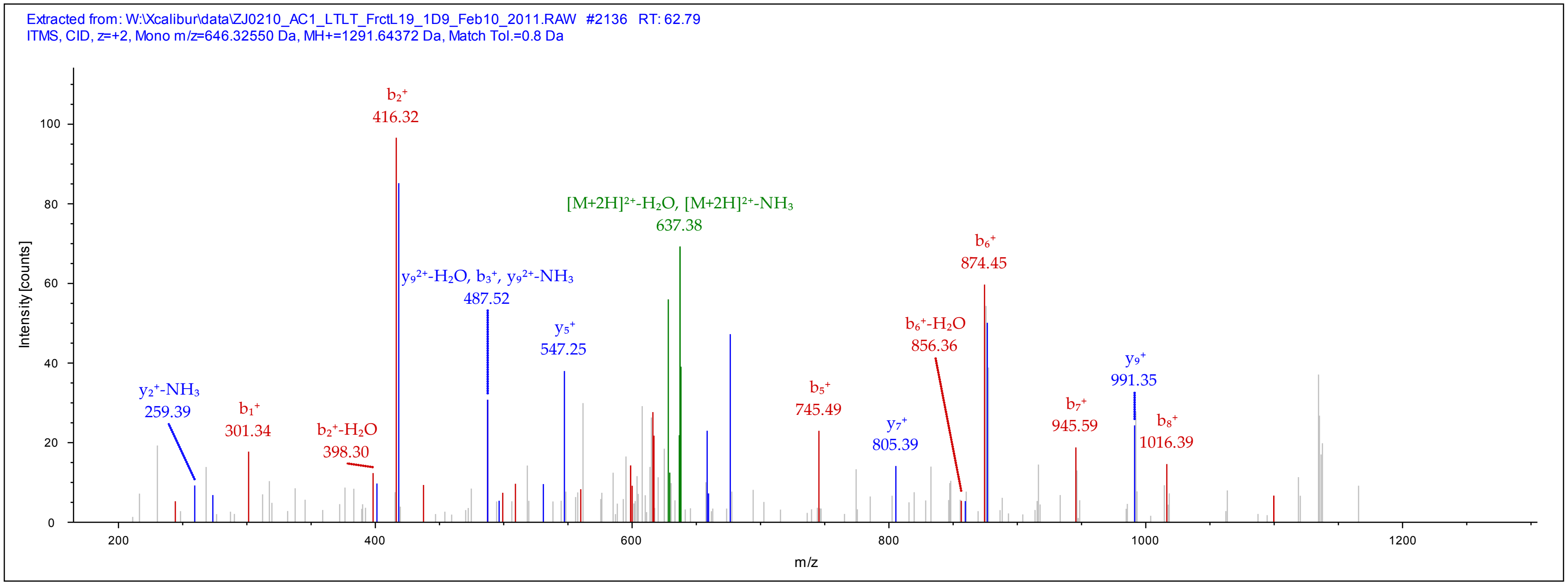
Identified with: Mascot (v1.16); IonScore:40, Exp Value:6.7E-003, Ions matched by search engine: 13/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform 2A of Cytoplasmic dynein 1 intermediate chain 2
- Isoform 2C of Cytoplasmic dynein 1 intermediate chain 2 lng=612
- Isoform 2B of Cytoplasmic dynein 1 intermediate chain 2 lng=632
- Isoform 2F of Cytoplasmic dynein 1 intermediate chain 2 lng=611
- Isoform 2E of Cytoplasmic dynein 1 intermediate chain 2
- cDNA, FLJ79018, highly similar to Cytoplasmic dynein 1 intermediate chain 2 lng=630



IPI00830086.1

Sequence: LLGLEEQLR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 650.39459 Da (-0.76 mmu/-1.17 ppm),   MH+: 1299.78191 Da,   RT: 108.70 min,

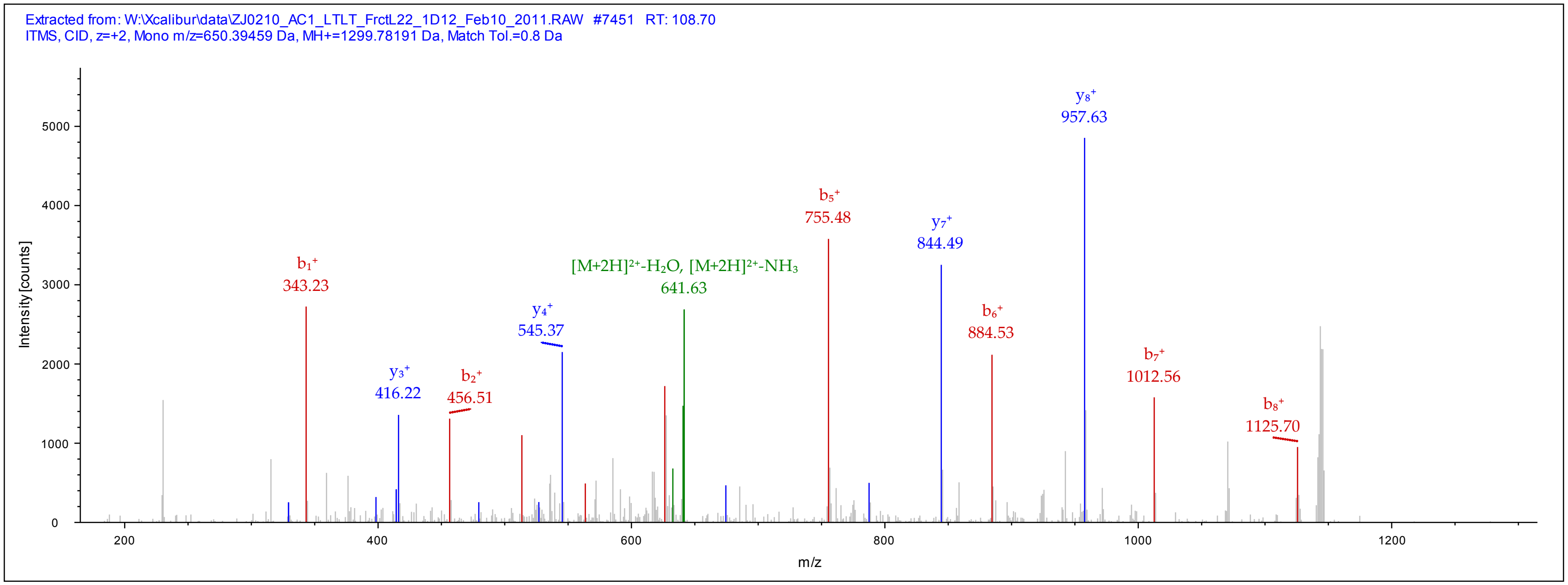
Identified with: Mascot (v1.16); IonScore:43, Exp Value:3.7E-003, Ions matched by search engine: 7/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of Sperm-specific antigen 2
- Isoform 3 of Sperm-specific antigen 2
- Isoform 2 of Sperm-specific antigen 2 lng=1106
- cDNA FLJ45996 fis, clone SKNSH2007306, highly similar to Homo sapiens sperm specific antigen 2 (SSFA2), mRNA lng=1237



IPI00844103.2

Sequence: LIEVTETICK, L1-TMT6plex (229.16293 Da), C9-Carbamidomethyl (57.02146 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 832.48865 Da (-0.25 mmu/-0.3 ppm),   MH+: 1663.97002 Da,   RT: 107.76 min,

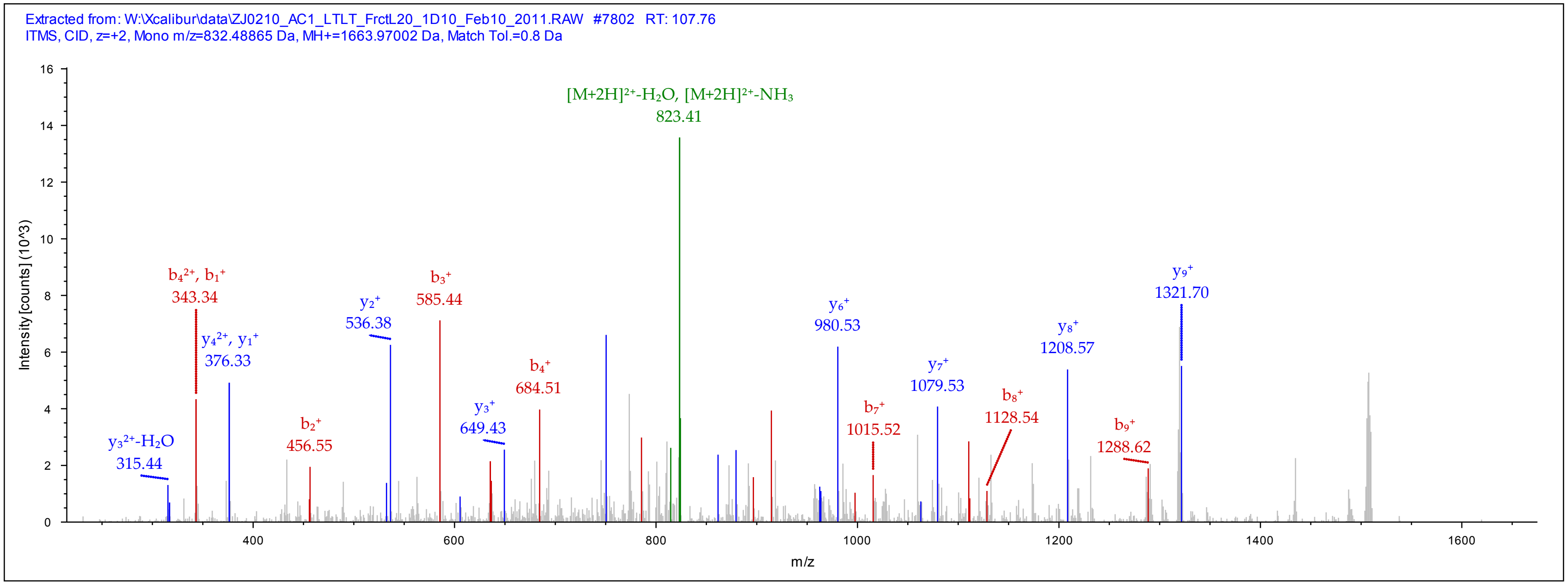
Identified with: Mascot (v1.16); IonScore:57, Exp Value:2.0E-004, Ions matched by search engine: 9/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Protein canopy homolog 3
- Putative uncharacterized protein CNPY3 lng=142



IPI00844363.2

Sequence: ALCYLVLK, A1-TMT6plex (229.16293 Da), C3-Carbamidomethyl (57.02146 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 719.44897 Da (+0.14 mmu/+0.19 ppm), MH+: 1437.89067 Da, RT: 115.99 min,

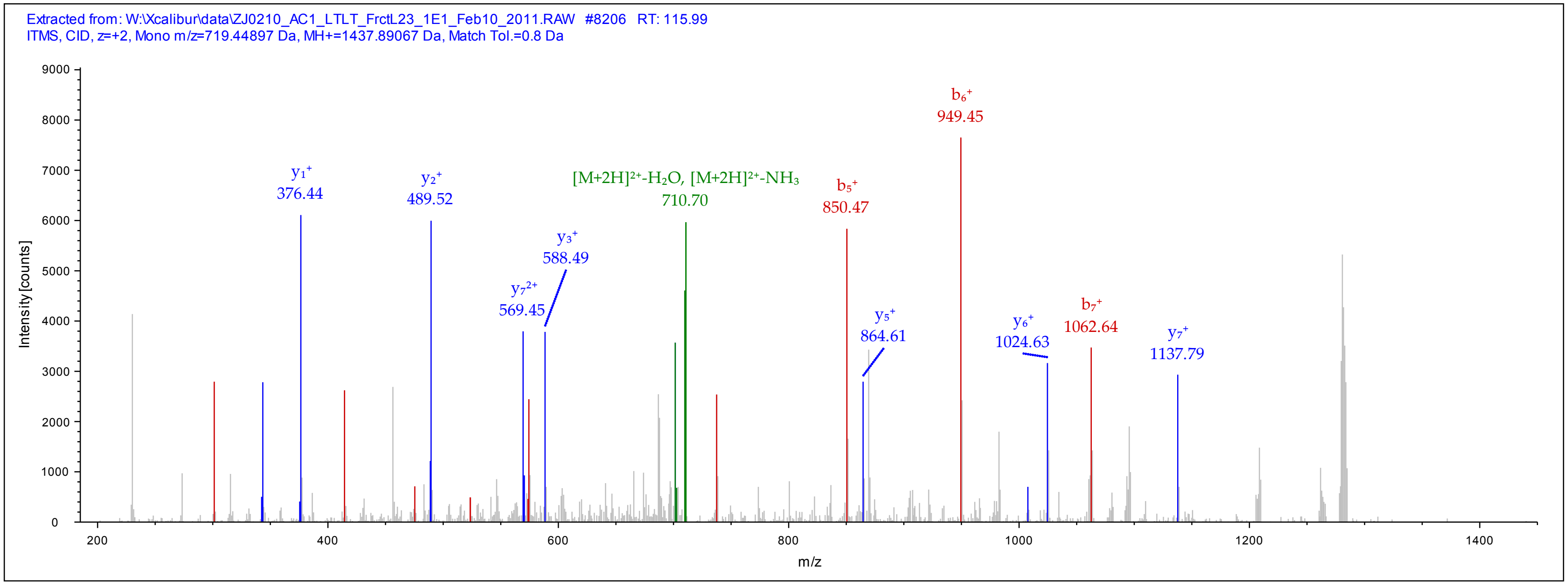
Identified with: Mascot (v1.16); IonScore:31, Exp Value:4.1E-002, Ions matched by search engine: 7/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Mitochondrial import receptor subunit TOM34
- cDNA FLJ26027 fis, clone PNC04328, highly similar to Homo sapiens translocase of outer mitochondrial membrane 34 lng=182



IPI:IPI00845230.1

Sequence: SETFLLLQPWPR, S1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 858.48956 Da (+1.79 mmu/+2.08 ppm),   MH+: 1715.97185 Da,   RT: 130.79 min,

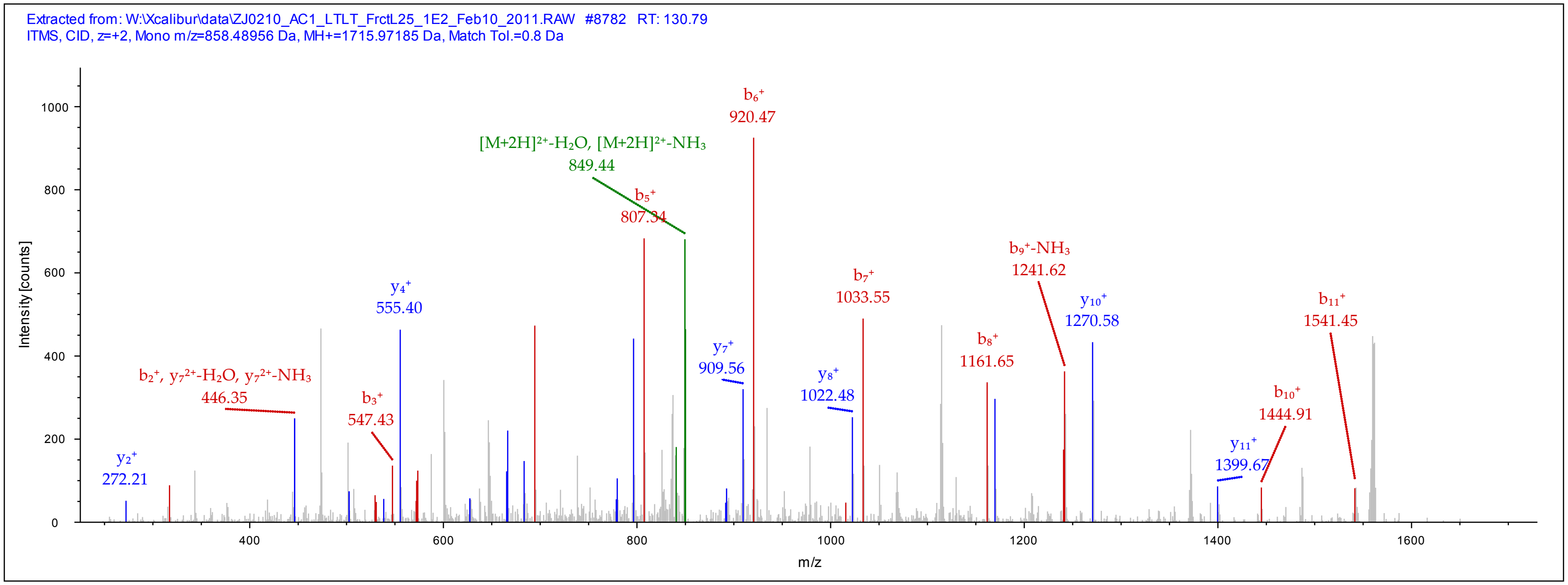
Identified with: Mascot (v1.16); IonScore:45, Exp Value:3.4E-003, Ions matched by search engine: 11/100

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Transmembrane protein 132A
- Isoform 2 of Transmembrane protein 132A
- Isoform 3 of Transmembrane protein 132A



IPI00852906.1

Sequence: EIDLVNR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 544.31989 Da (+0.78 mmu/+1.43 ppm),   MH+: 1087.63249 Da,   RT: 81.12 min,

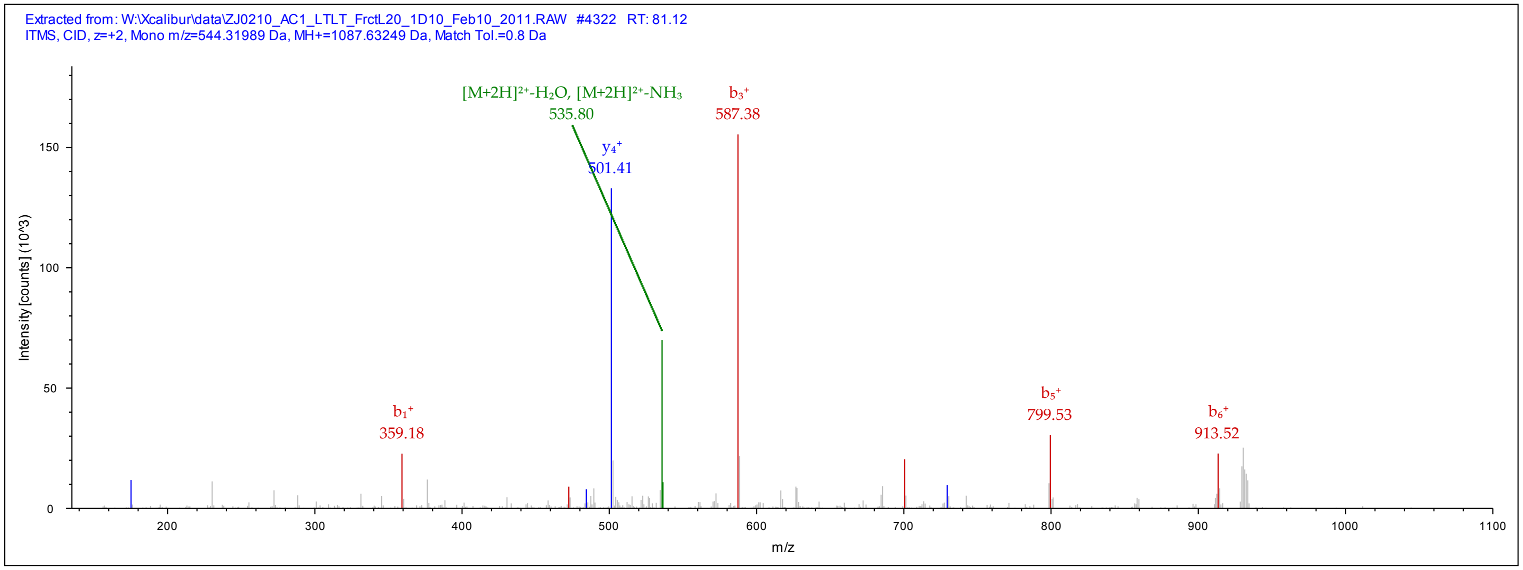
Identified with: Mascot (v1.16); IonScore:29, Exp Value:8.2E-002, Ions matched by search engine: 4/54

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Isoform Alpha of Caveolin-1
- Caveolin-3
- Caveolin (Fragment) lng=217
- Isoform Beta of Caveolin-1 lng=147
- Caveolin lng=150
- Putative uncharacterized protein CAV1 lng=138
- Caveolin lng=167



IPI00852988.1

Sequence: IIMPPSALDQLSR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 835.47943 Da (+0.33 mmu/+0.4 ppm), MH+: 1669.95159 Da, RT: 115.98 min,

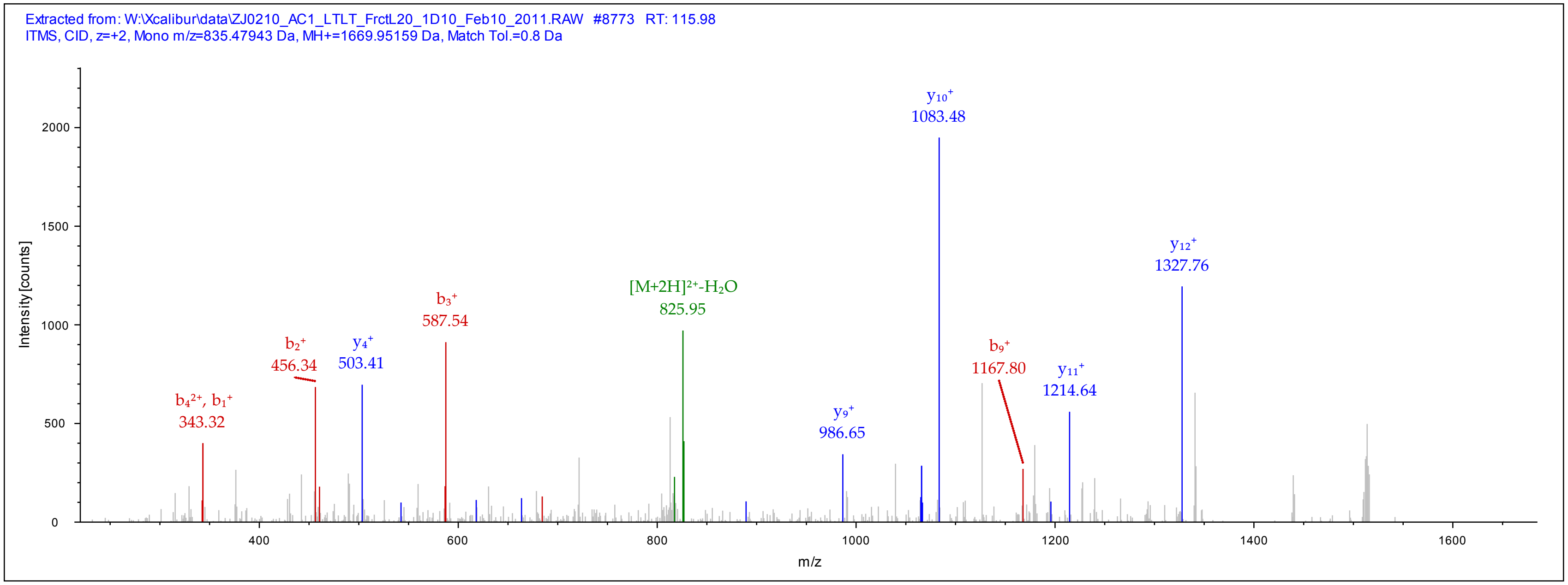
Identified with: Mascot (v1.16); IonScore:31, Exp Value:6.8E-002, Ions matched by search engine: 6/114

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform Short of Ubiquitin fusion degradation protein 1 homolog
- Isoform Long of Ubiquitin fusion degradation protein 1 homolog
- ubiquitin fusion degradation 1-like isoform B lng=266
- Putative uncharacterized protein UFD1L lng=343
- cDNA FLJ59614, highly similar to Ubiquitin fusion degradation protein 1 homolog lng=315



IPI:IPI00867529.1

Sequence: IDILTELR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 601.37164 Da (+0.3 mmu/+0.5 ppm), MH+: 1201.73601 Da, RT: 119.57 min,

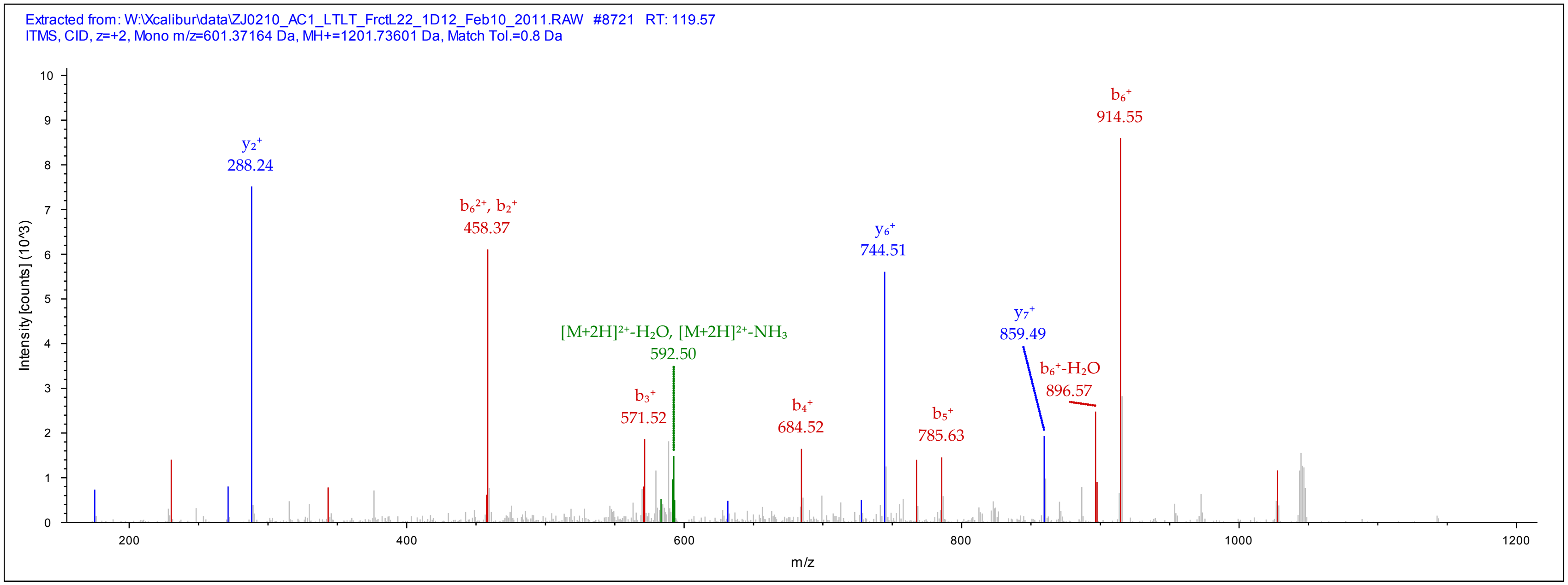
Identified with: Mascot (v1.16); IonScore:40, Exp Value:3.9E-003, Ions matched by search engine: 6/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 3 of Kinesin-like protein KIF2A
- Isoform 1 of Kinesin-like protein KIF2A
- Isoform 4 of Kinesin-like protein KIF2A
- Isoform 2 of Kinesin-like protein KIF2A



IPI:IPI00877909.1

Sequence: GLAFLDELR, G1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 631.86957 Da (+0.6 mmu/+0.95 ppm),   MH+: 1262.73186 Da,   RT: 122.48 min,

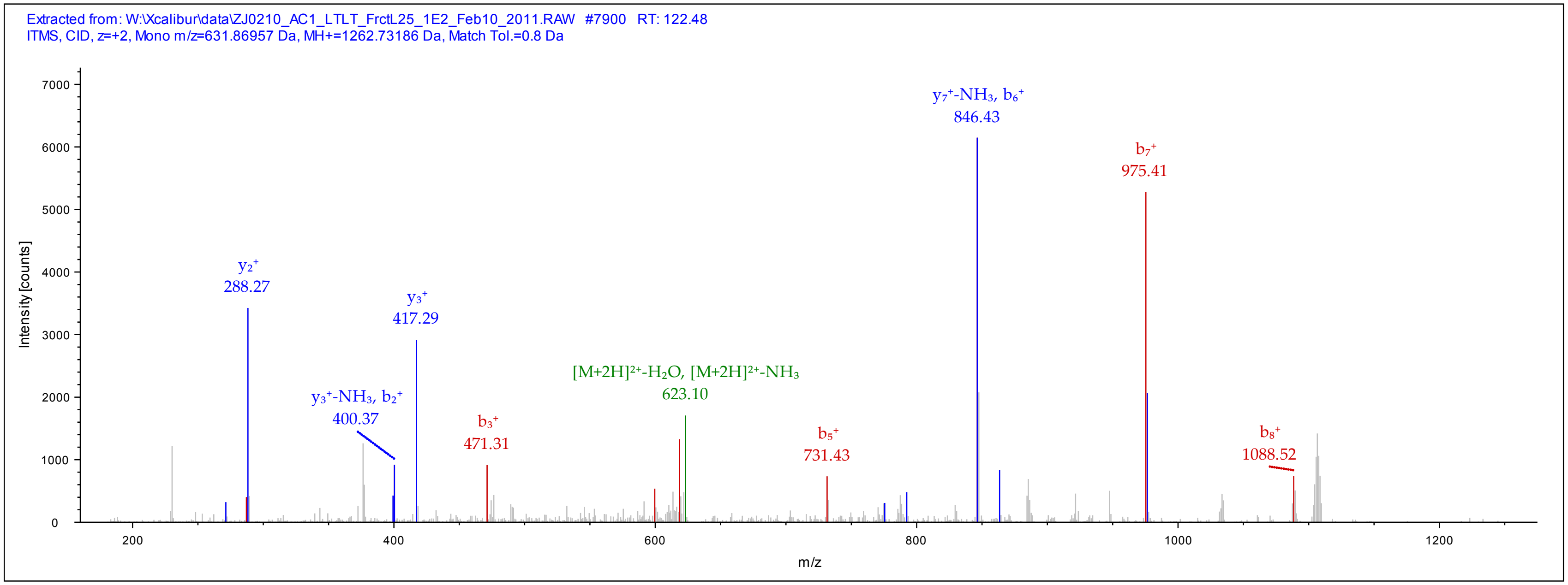
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.7E-002, Ions matched by search engine: 8/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of AT-rich interactive domain-containing protein 2
- Isoform 3 of AT-rich interactive domain-containing protein 2
- 11 kDa protein



IPI:IPI00878493.1

Sequence: LLAAFEER, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 589.34253 Da (-0.06 mmu/-0.09 ppm), MH+: 1177.67778 Da, RT: 106.99 min,

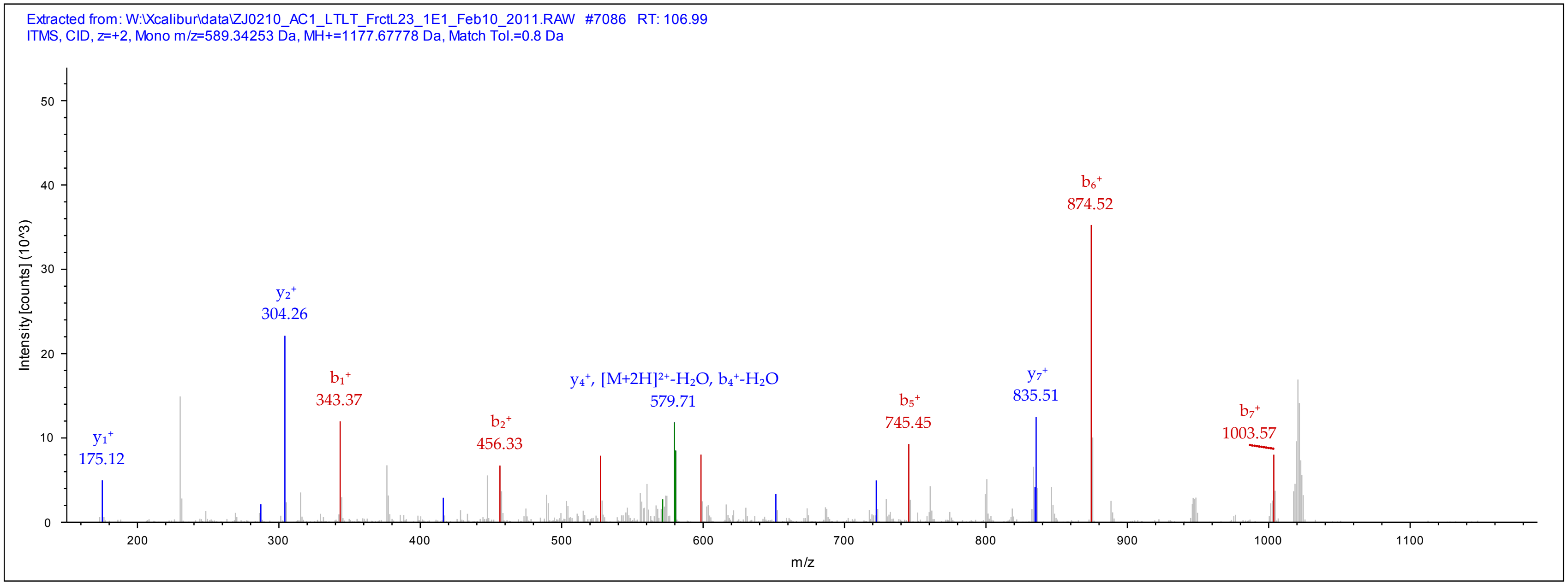
Identified with: Mascot (v1.16); IonScore:33, Exp Value:3.2E-002, Ions matched by search engine: 10/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Chromobox protein homolog 8
- Uncharacterized protein
- Uncharacterized protein



IPI:IPI00878721.2

Sequence: VDCEIDK, V1-TMT6plex (229.16293 Da), C3-Carbamidomethyl (57.02146 Da), K7-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 668.86285 Da (+0.06 mmu/+0.08 ppm), MH+: 1336.71843 Da, RT: 73.84 min,

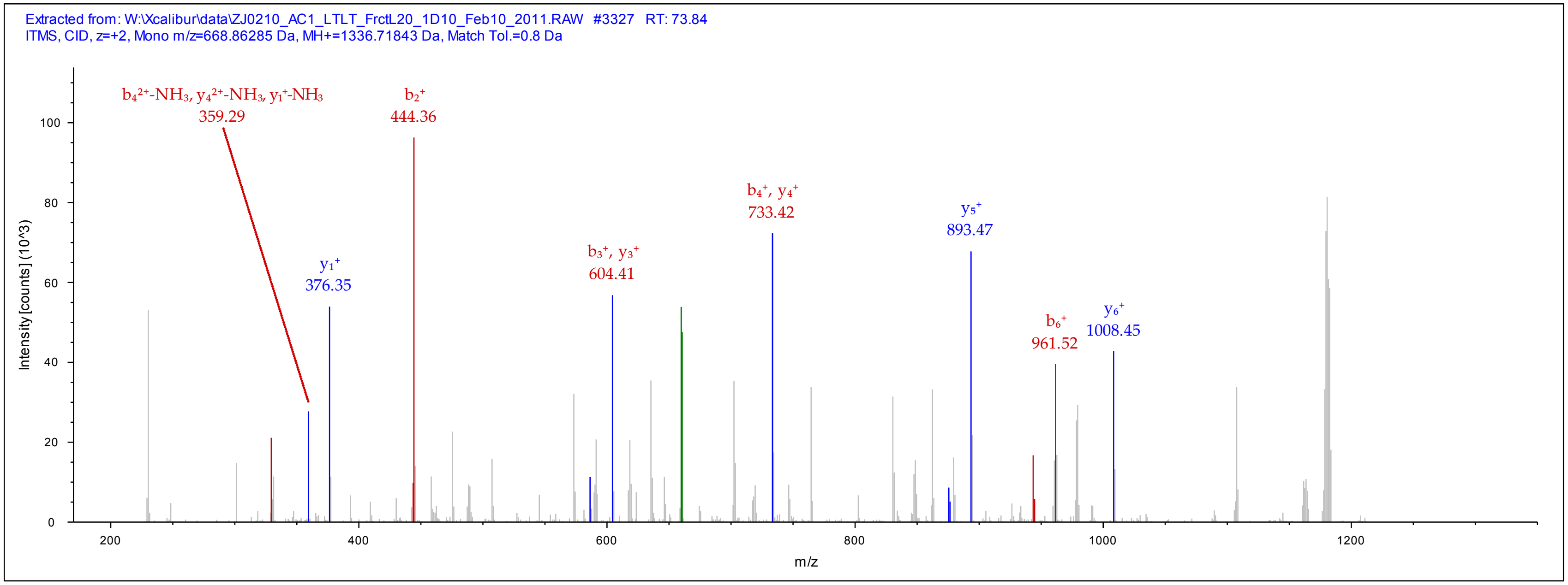
Identified with: Mascot (v1.16); IonScore:32, Exp Value:5.3E-002, Ions matched by search engine: 5/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Collagen alpha-6(VI) chain
- Isoform 2 of Collagen alpha-6(VI) chain



IPI00879168.1

Sequence: EDSGMVPLIIPVSVPVR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 1019.08734 Da (+2.87 mmu/+2.81 ppm), MH+: 2037.16741 Da, RT: 130.00 min,

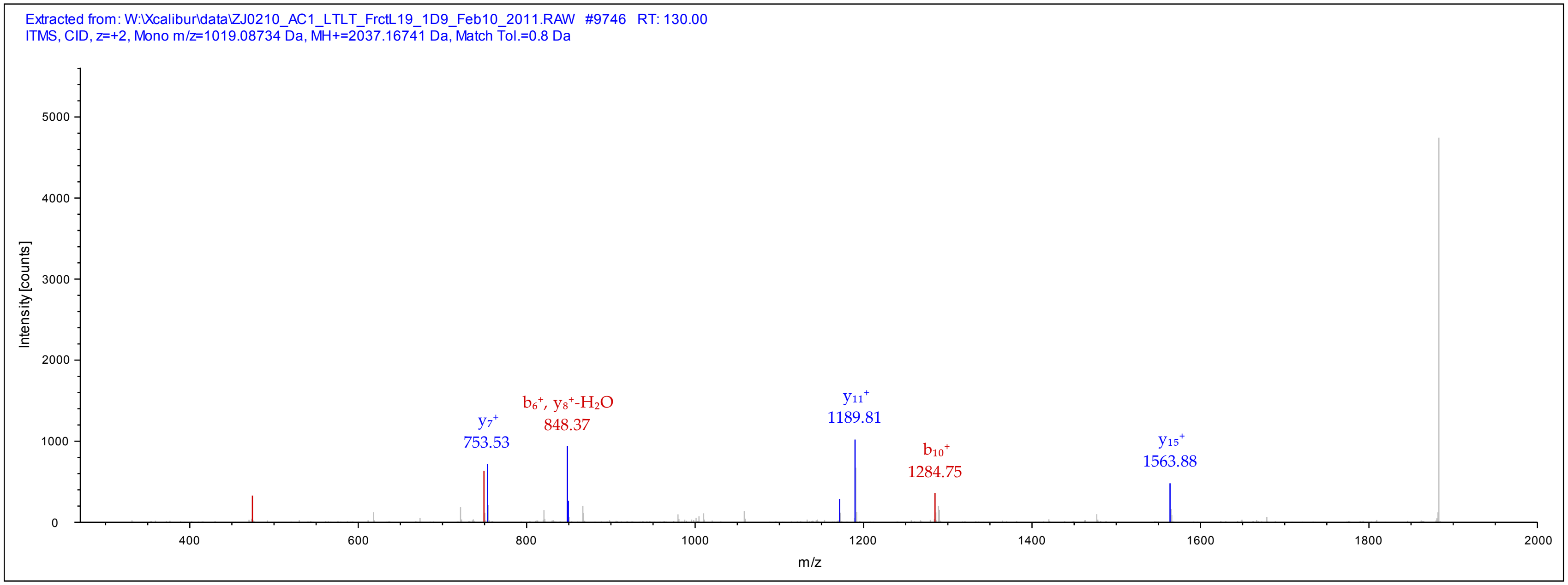
Identified with: Mascot (v1.16); IonScore:51, Exp Value:8.2E-004, Ions matched by search engine: 12/152

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Uncharacterized protein C14orf43
- C14orf43 protein (Fragment) lng=1025
- Putative uncharacterized protein C14orf43 lng=445



IPI00879681.2

Sequence: QVEVINFGDCLVR, Q1-TMT6plex (229.16293 Da), C10-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 889.47797 Da (+0.88 mmu/+0.99 ppm),   MH+: 1777.94866 Da,   RT: 113.57 min,

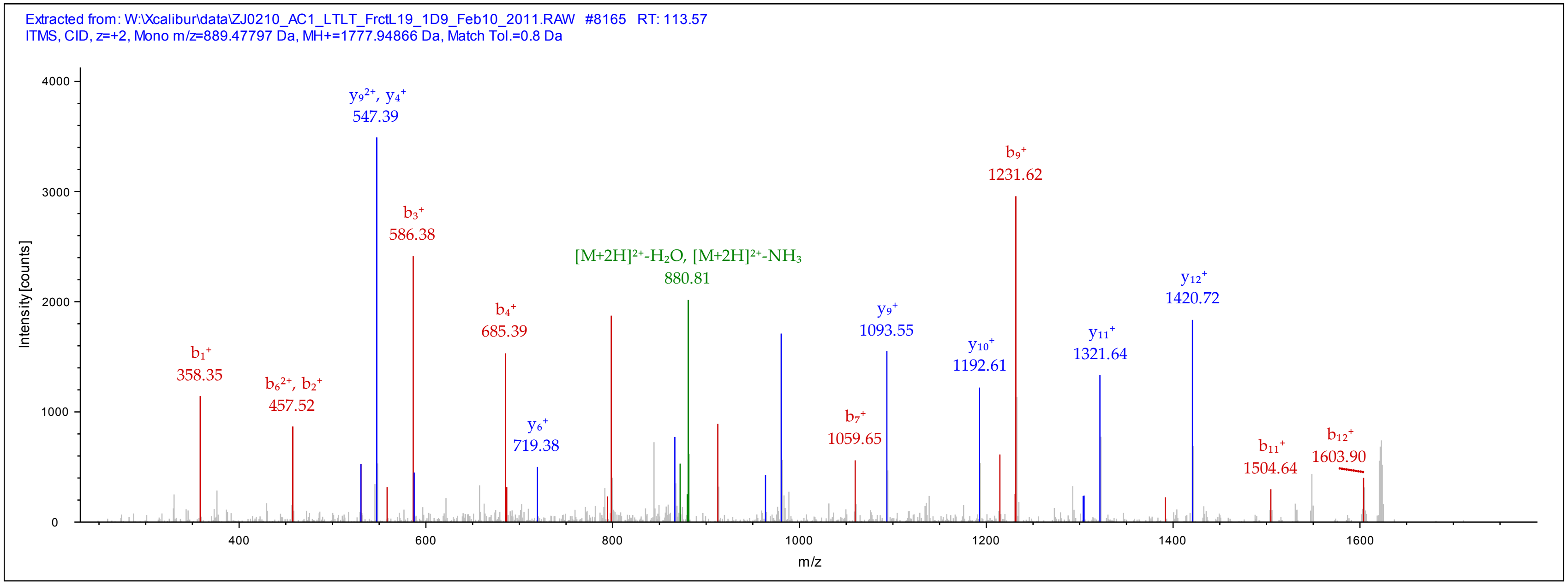
Identified with: Mascot (v1.16); IonScore:59, Exp Value:1.6E-004, Ions matched by search engine: 10/132

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Ran GTPase-activating protein 1
- Ran GTPase activating protein 1 lng=312



IPI00879747.1

Sequence: ISEIEDAAFLAR, I1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 782.43243 Da (-0.24 mmu/-0.3 ppm),   MH+: 1563.85759 Da,   RT: 115.76 min,

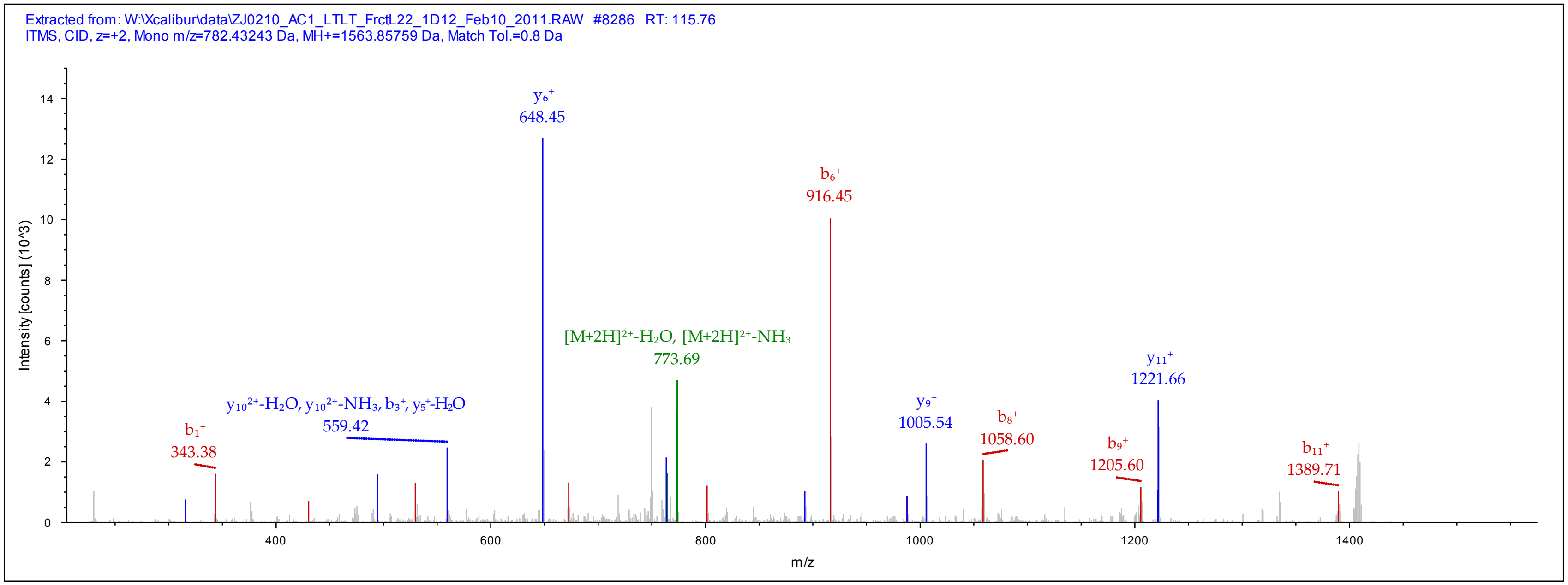
Identified with: Mascot (v1.16); IonScore:60, Exp Value:1.1E-004, Ions matched by search engine: 11/96

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of Erlin-2
- Erlin-1
- erlin-1
- ER lipid raft associated 1 lng=275



IPI:IPI00879893.1

Sequence: NVLLFLQDK, N1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 774.48352 Da (+1.79 mmu/+2.31 ppm), MH+: 1547.95976 Da, RT: 128.71 min,

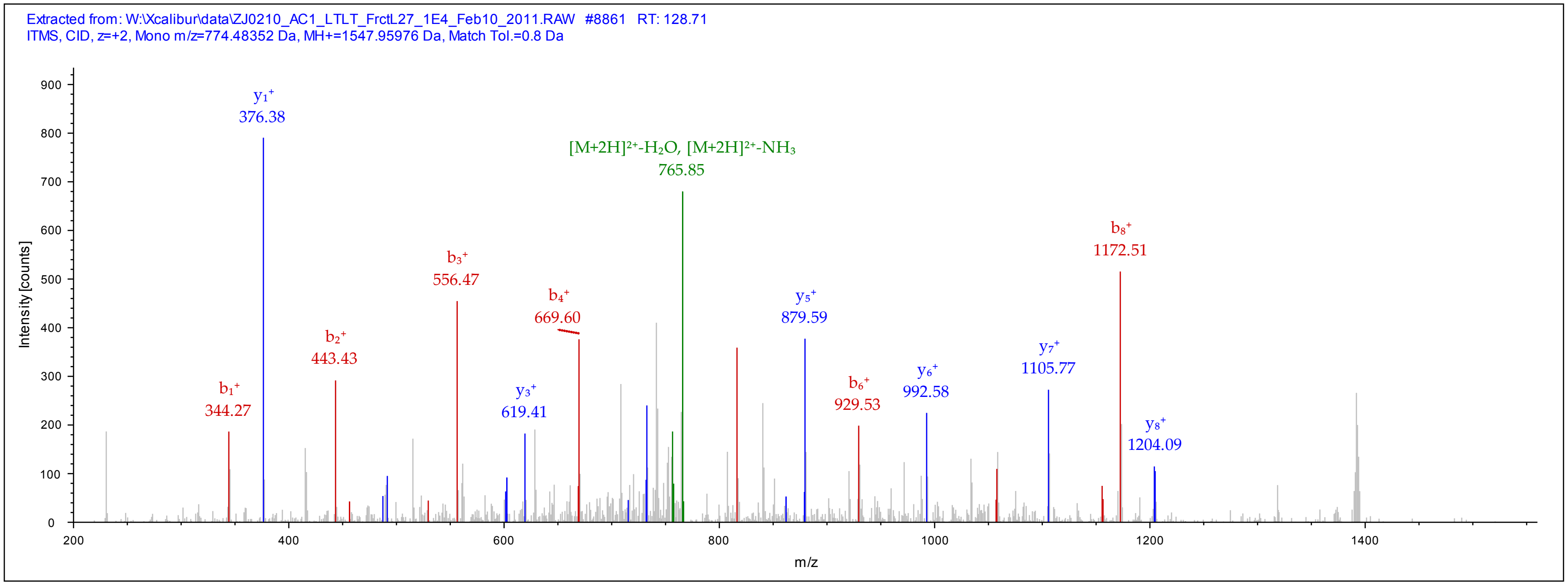
Identified with: Mascot (v1.16); IonScore:30, Exp Value:6.2E-002, Ions matched by search engine: 8/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- V-type proton ATPase subunit S1
- Uncharacterized protein
- ATPase, H+ transporting, lysosomal accessory protein 1
- Protein
- 14 kDa protein
- 14 kDa protein



IPI:IPI00880107.1

Sequence: LELFPVELEK, L1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 838.00824 Da (+0.45 mmu/+0.54 ppm), MH+: 1675.00920 Da, RT: 130.89 min,

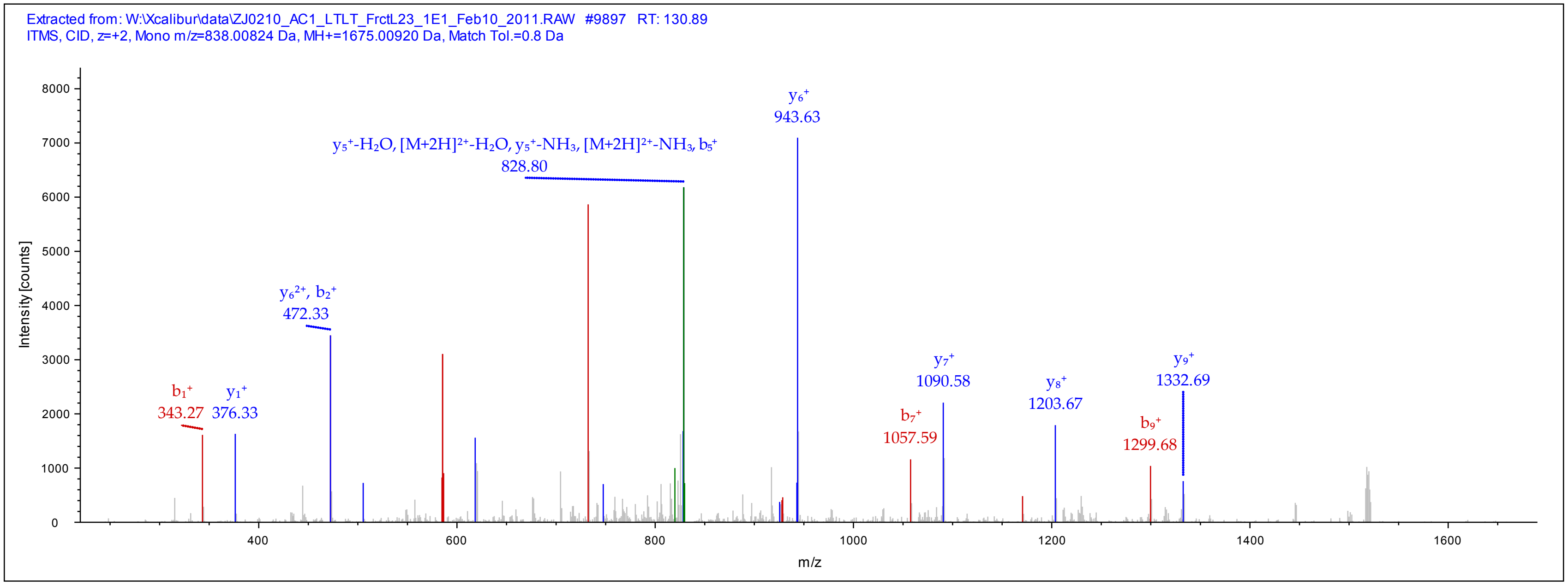
Identified with: Mascot (v1.16); IonScore:37, Exp Value:1.5E-002, Ions matched by search engine: 6/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Isoform 1 of Neurabin-1
- neurabin-2
- neurabin-1 isoform 2
- 20 kDa protein
- neurabin-1 isoform 1
- neurabin-1 isoform 5
- neurabin-1 isoform 3



IPI:IPI00885113.2

Sequence: DFLMSGLPDLLK, D1-TMT6plex (229.16293 Da), S5-Phospho (79.96633 Da), K12-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 944.00037 Da (-8.46 mmu/-8.97 ppm), MH+: 1886.99346 Da, RT: 81.95 min,

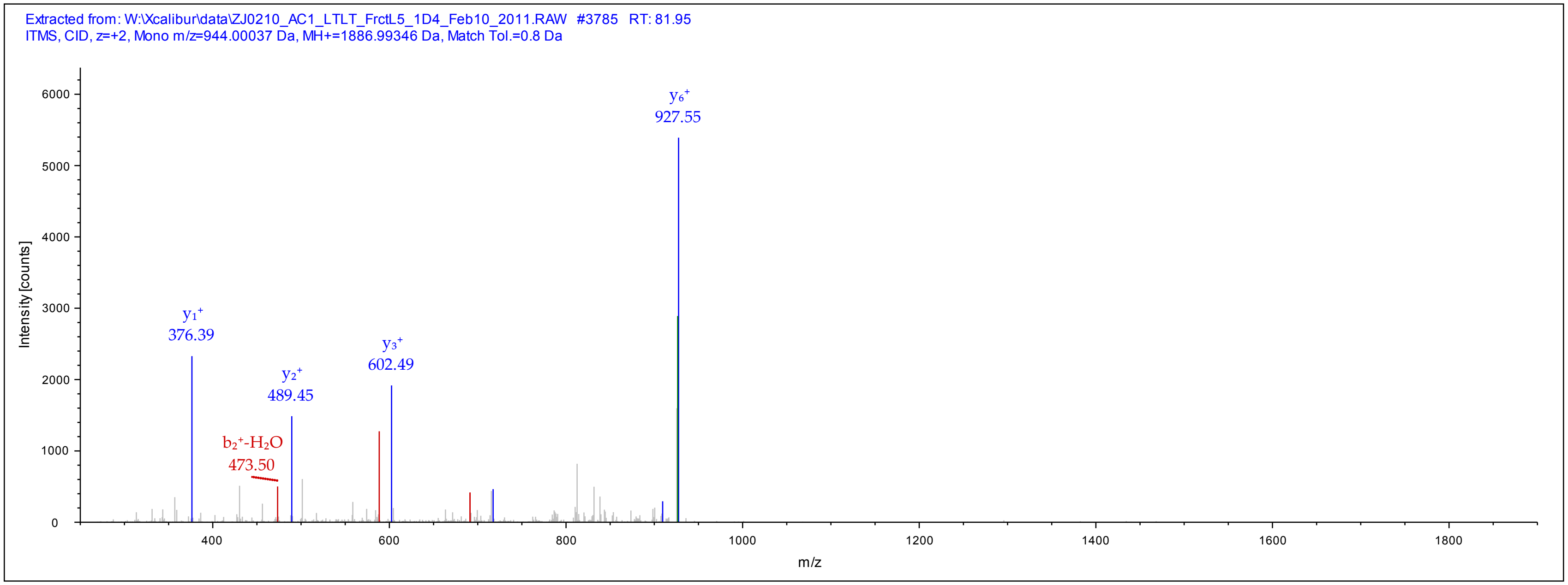
Identified with: Mascot (v1.16); IonScore:32, Exp Value:8.5E-002, Ions matched by search engine: 6/104

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of ATPase family AAA domain-containing protein 5
- Isoform 2 of ATPase family AAA domain-containing protein



IPI:IPI00887371.1

Sequence: RMGVRPAVPLLTQRGSGEAR, R1-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 794.11237 Da (-11.1 mmu/-13.98 ppm),   MH+: 2380.32254 Da,   RT: 227.78 min,

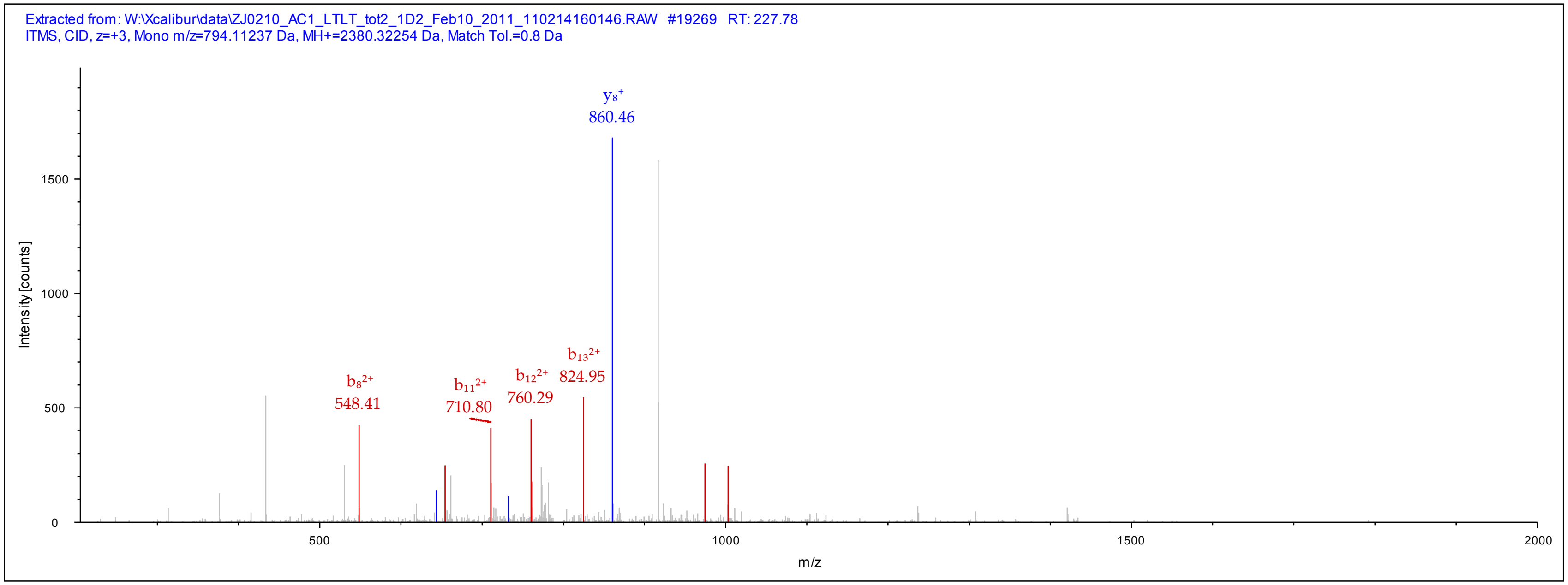
Identified with: Mascot (v1.16); IonScore:32, Exp Value:7.0E-002, Ions matched by search engine: 9/202

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Tubulin monoglycylase TTLL3
- Isoform 3 of Tubulin monoglycylase TTLL3



IPI:IPI00889667.1

Sequence: IDVESLSSASQLDQALR, I1-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 687.70691 Da (+1.19 mmu/+1.73 ppm),   MH+: 2061.10617 Da,   RT: 115.57 min,

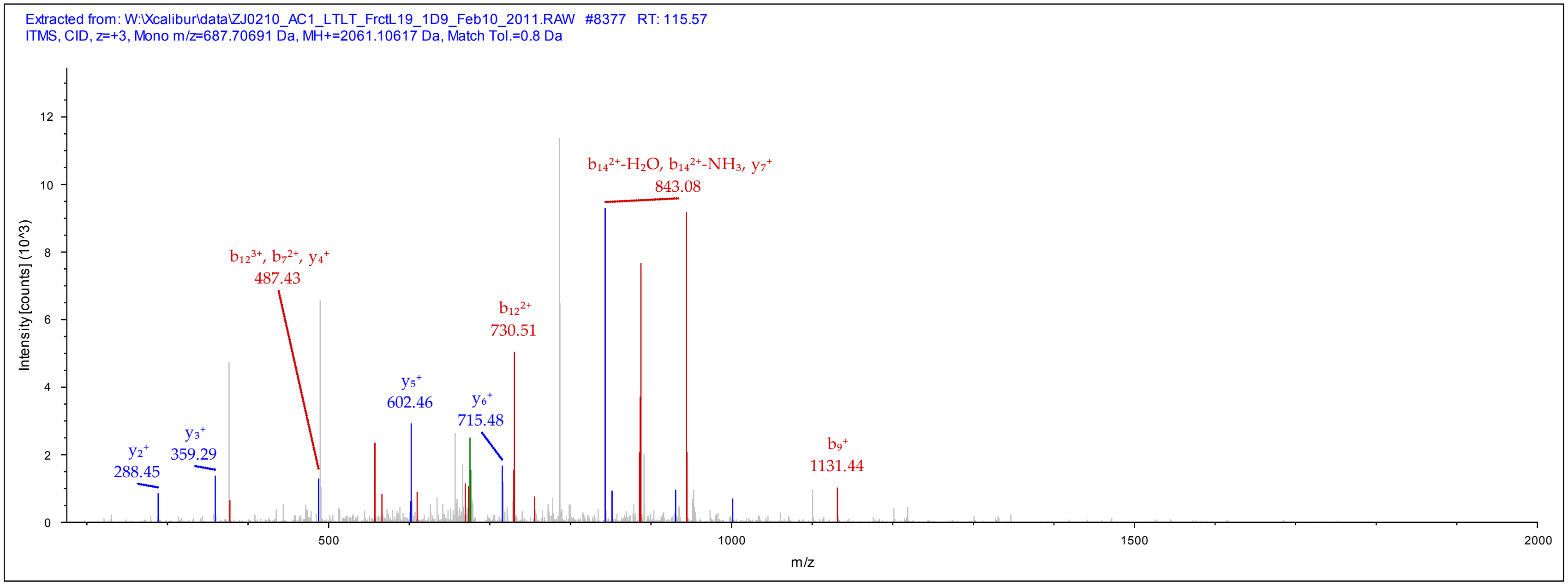
Identified with: Mascot (v1.16); IonScore:44, Exp Value:6.1E-003, Ions matched by search engine: 12/162

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Isoform 1 of Epithelial splicing regulatory protein 1
- Isoform 3 of Epithelial splicing regulatory protein 1
- Isoform 4 of Epithelial splicing regulatory protein 1
- Isoform 2 of Epithelial splicing regulatory protein 1
- epithelial splicing regulatory protein 1 isoform 5
- epithelial splicing regulatory protein 1 isoform 3
- 71 kDa protein



IPI00893087.1

Sequence: AMLDQLMGTSR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 726.38104 Da (-0.03 mmu/-0.04 ppm), MH+: 1451.75481 Da, RT: 107.98 min,

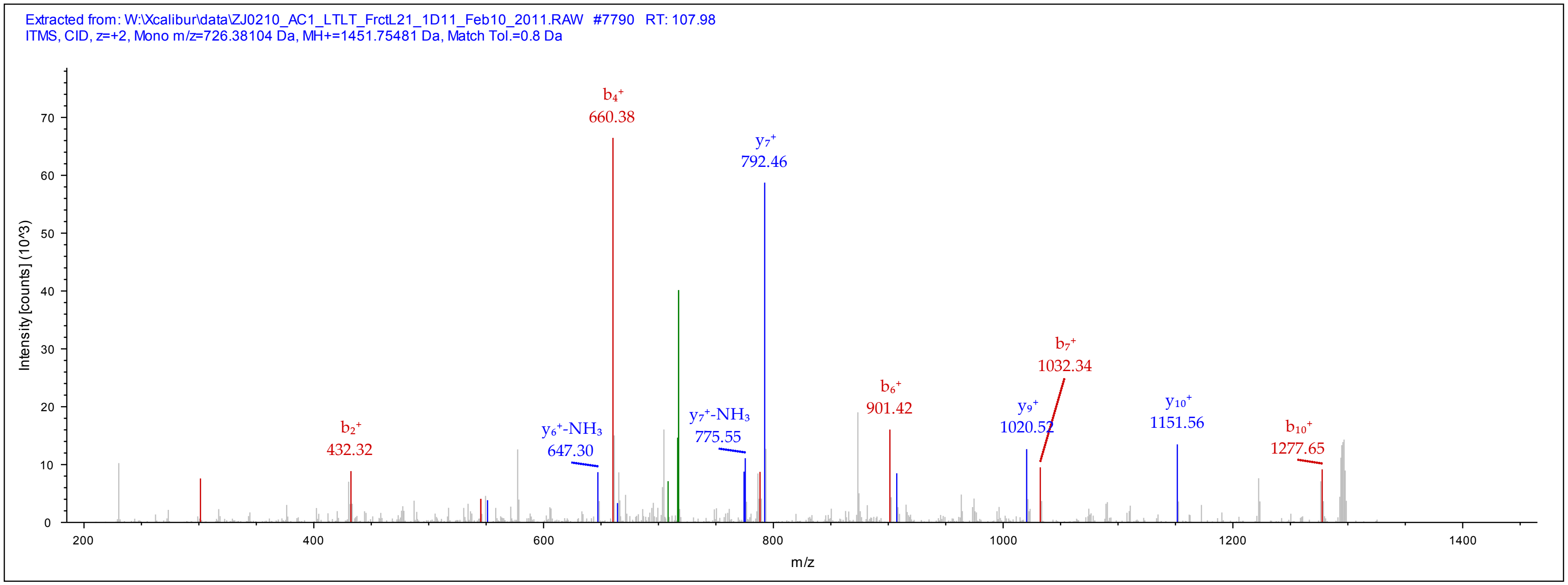
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.4E-002, Ions matched by search engine: 10/104

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Putative uncharacterized protein LUC7L2 lng=48
- Putative uncharacterized protein LUC7L2 lng=83



IPI00893683.1

Sequence: LAQEYSK, L1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 648.88202 Da (+0.18 mmu/+0.28 ppm),   MH+: 1296.75676 Da,   RT: 93.94 min,

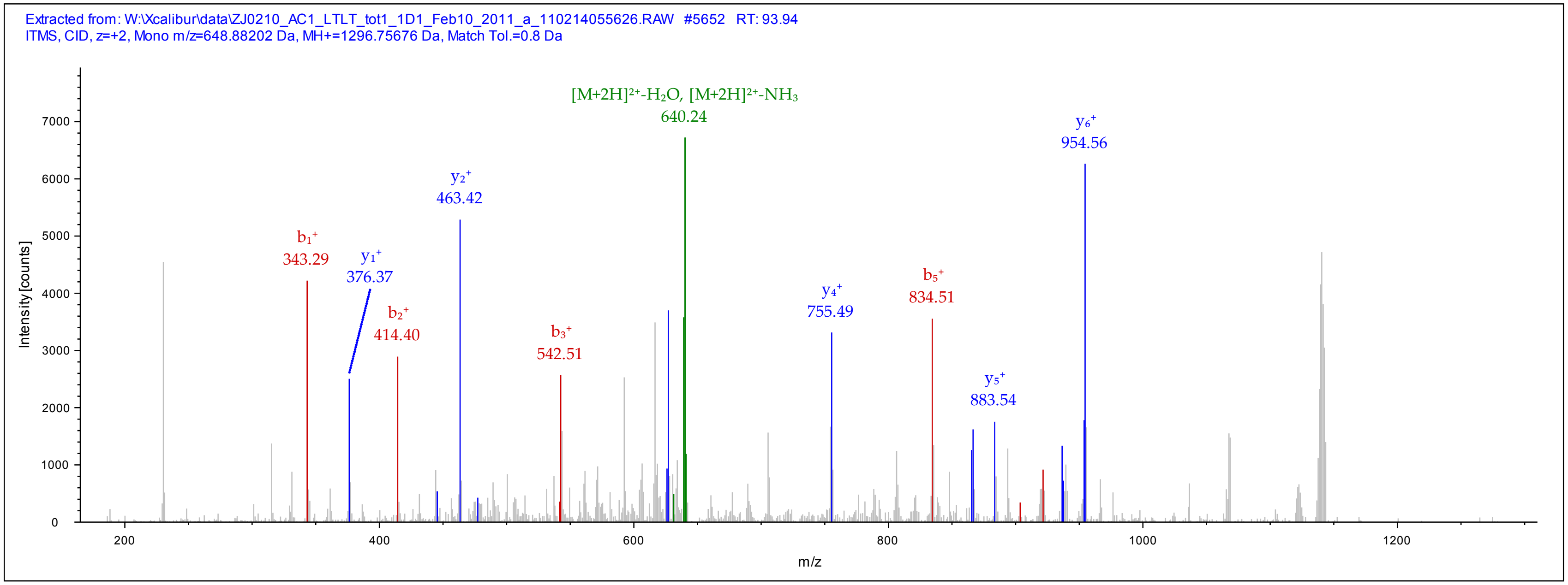
Identified with: Mascot (v1.16); IonScore:33, Exp Value:4.5E-002, Ions matched by search engine: 6/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of KLRAQ motif-containing protein 1
- Isoform 2 of KLRAQ motif-containing protein 1
- Isoform 3 of KLRAQ motif-containing protein 1
- Isoform 4 of KLRAQ motif-containing protein 1
- Putative uncharacterized protein KLRAQ1 lng=54



IPI:IPI00893778.1

Sequence: FLELLR, F1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 510.32745 Da (+1.25 mmu/+2.46 ppm), MH+: 1019.64763 Da, RT: 124.95 min,

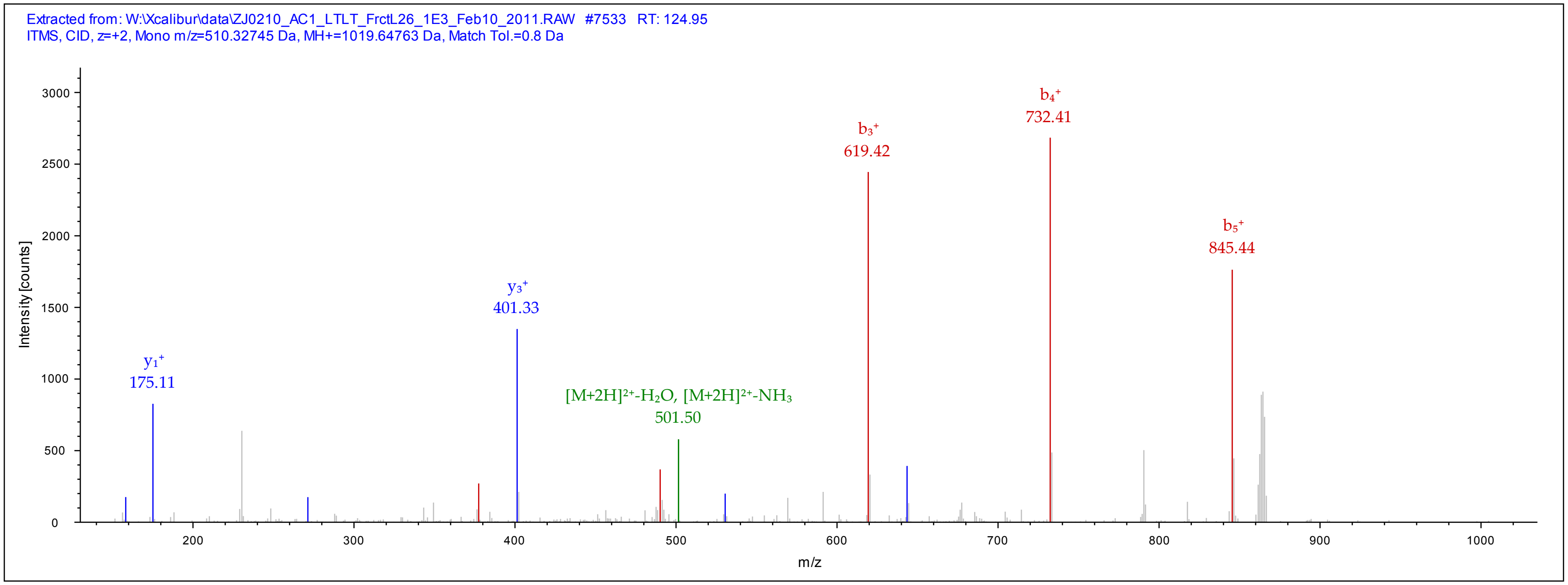
Identified with: Mascot (v1.16); IonScore:30, Exp Value:6.2E-002, Ions matched by search engine: 5/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Transmembrane protein 214
- transmembrane protein 214 isoform 2
- 25 kDa protein



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL26_1E3_Feb10_2011.RAW #7533 RT: 124.95
ITMS, CID, z=+2, Mono m/z=510.32745 Da, MH+=1019.64763 Da, Match Tol.=0.8 Da

IPI:IPI00894297.1

Sequence: LNLGGDFIK, L1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 717.93909 Da (-0.61 mmu/-0.86 ppm), MH+: 1434.87090 Da, RT: 110.06 min,

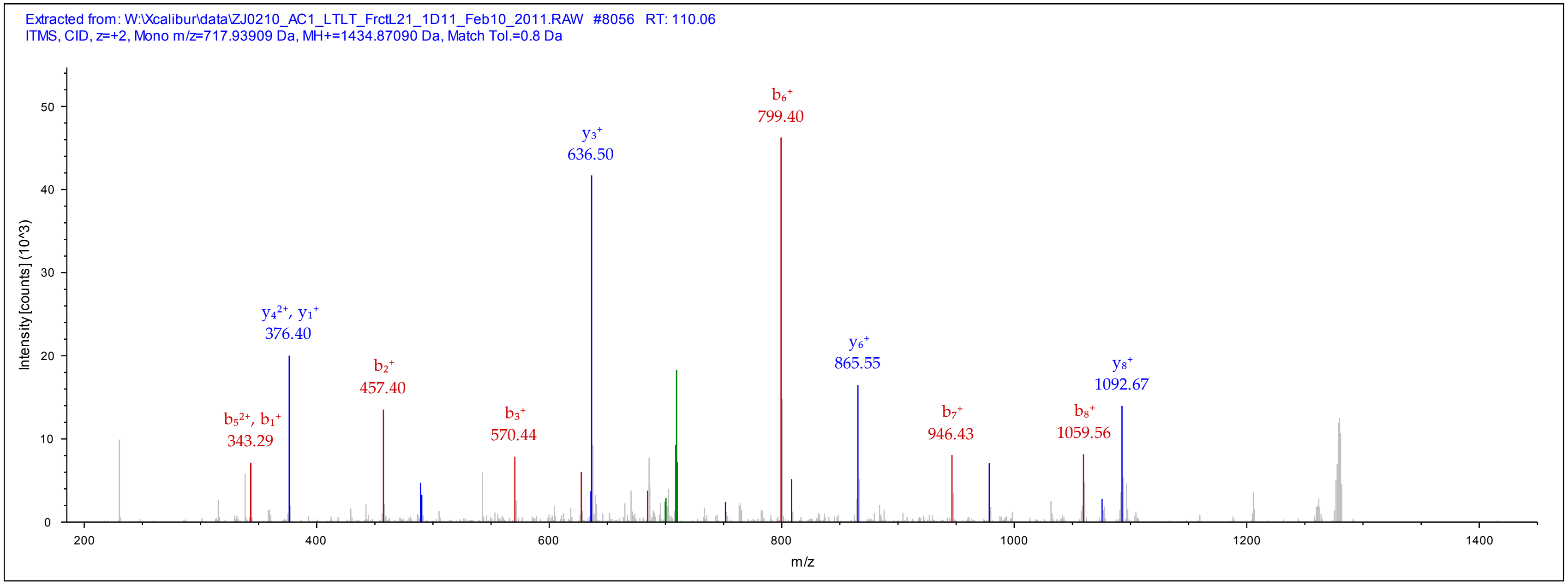
Identified with: Mascot (v1.16); IonScore:41, Exp Value:5.3E-003, Ions matched by search engine: 7/78

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Protein YIPF4
- 6 kDa protein



IPI00894420.1

Sequence: DIGAIAR, D1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 472.79446 Da (+4.48 mmu/+9.48 ppm), MH+: 944.58165 Da, RT: 46.20 min,

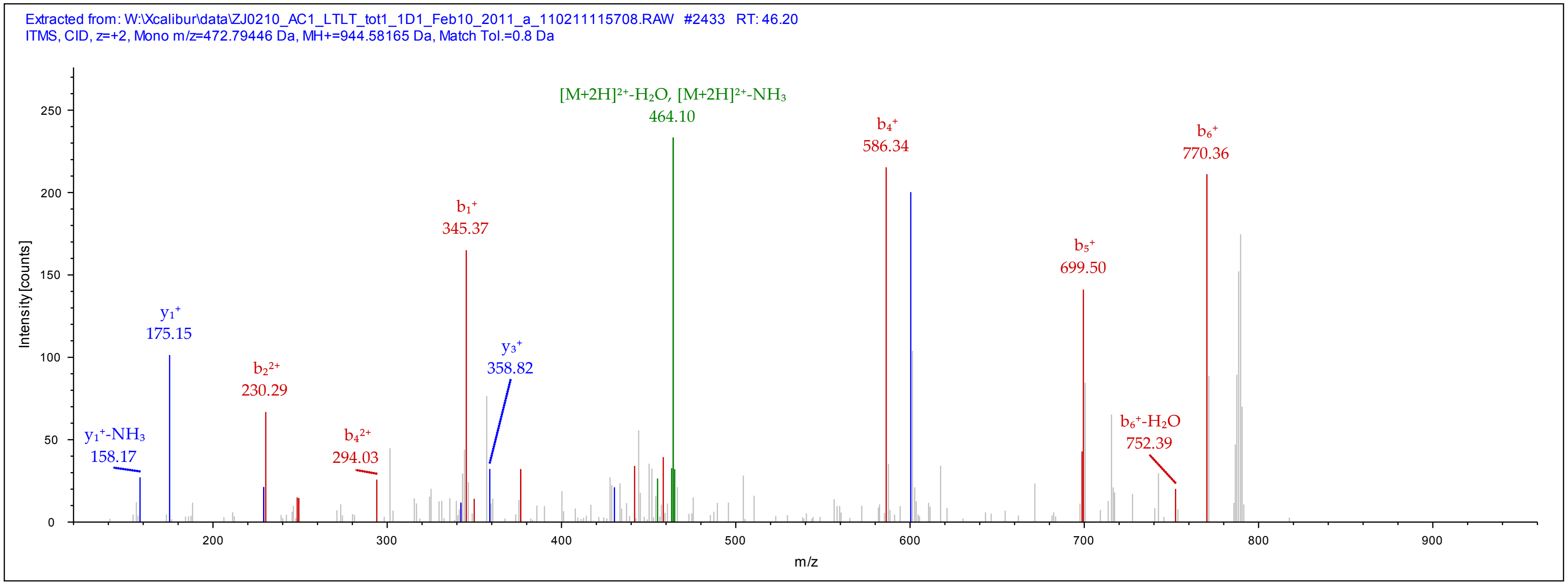
Identified with: Mascot (v1.16); IonScore:29, Exp Value:7.9E-002, Ions matched by search engine: 5/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Dihydropyrimidinase-related protein 5
- 21 kDa protein lng=190



IPI:IPI00894447.1

Sequence: FPVDIFYTK, F1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 794.46344 Da (+0.44 mmu/+0.55 ppm),   MH+: 1587.91960 Da,   RT: 131.61 min,

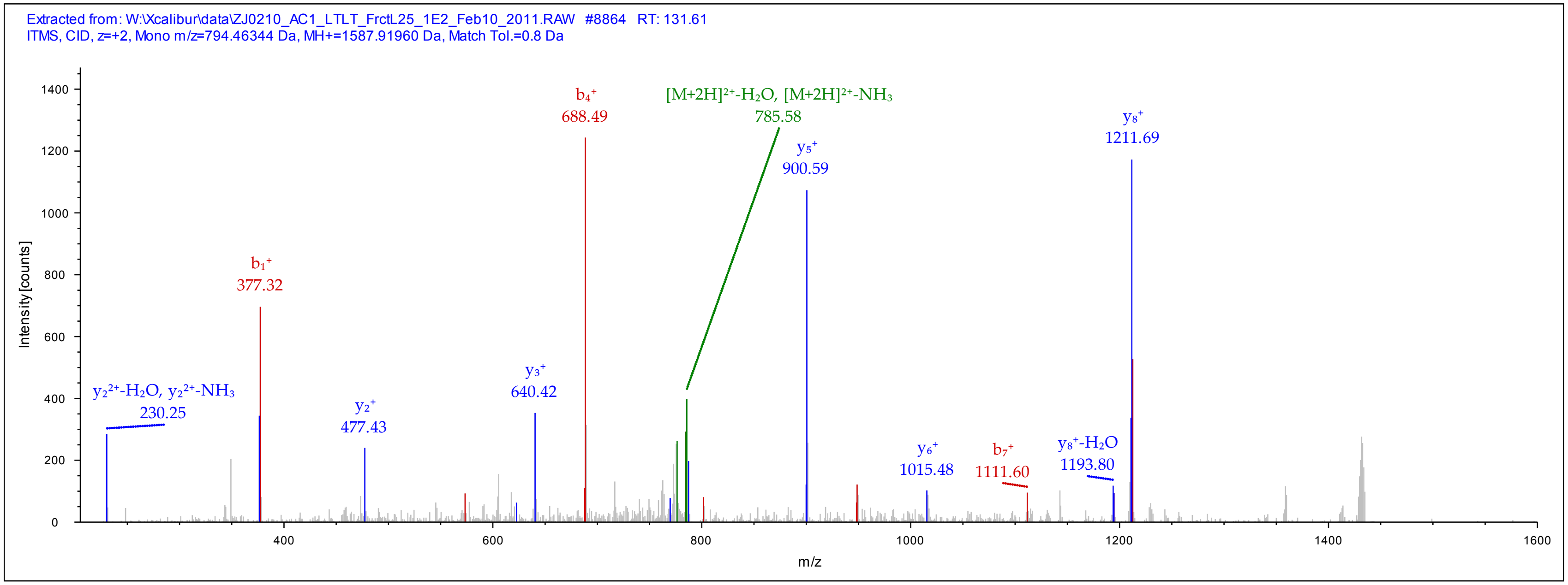
Identified with: Mascot (v1.16); IonScore:37, Exp Value:1.9E-002, Ions matched by search engine: 7/72

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16
- DEAH (Asp-Glu-Ala-His) box polypeptide 16
- 119 kDa protein lng=1041
- DEAH (Asp-Glu-Ala-His) box polypeptide 16, isoform CRA_a
- DEAH (Asp-Glu-Ala-His) box polypeptide 16 isoform 2 lng



IPI00896384.1

Sequence: ALESALK, A1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 595.38184 Da (+0.36 mmu/+0.6 ppm), MH+: 1189.75640 Da, RT: 85.08 min,

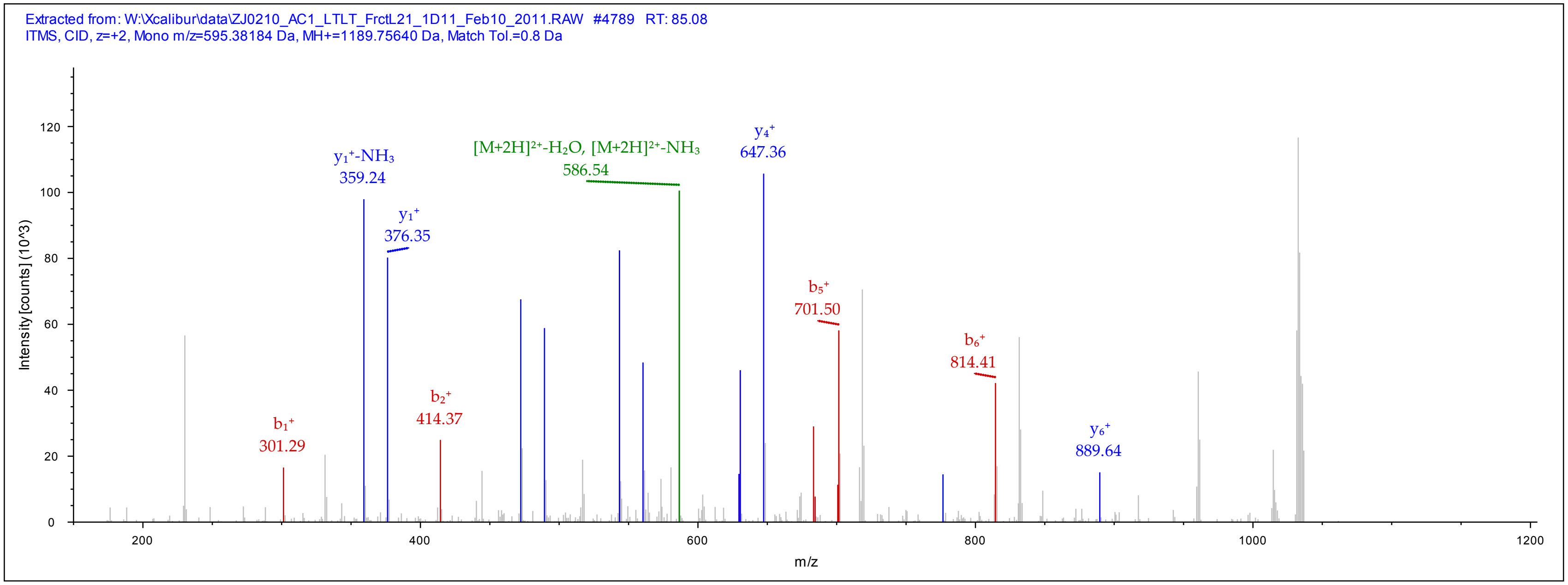
Identified with: Mascot (v1.16); IonScore:35, Exp Value:1.9E-002, Ions matched by search engine: 6/50

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Kinesin-1 heavy chain
- Isoform 1 of Kinesin heavy chain isoform 5C
- Isoform 2 of Kinesin heavy chain isoform 5C lng=725
- Kinesin heavy chain isoform 5C variant (Fragment) lng=265
- cDNA FLJ51288, highly similar to Kinesin heavy chain lng=438



IPI00902613.1

Sequence: FGIDDQDYLVSLTR, F1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 935.99133 Da (+0.26 mmu/+0.28 ppm),   MH+: 1870.97539 Da,   RT: 119.84 min,

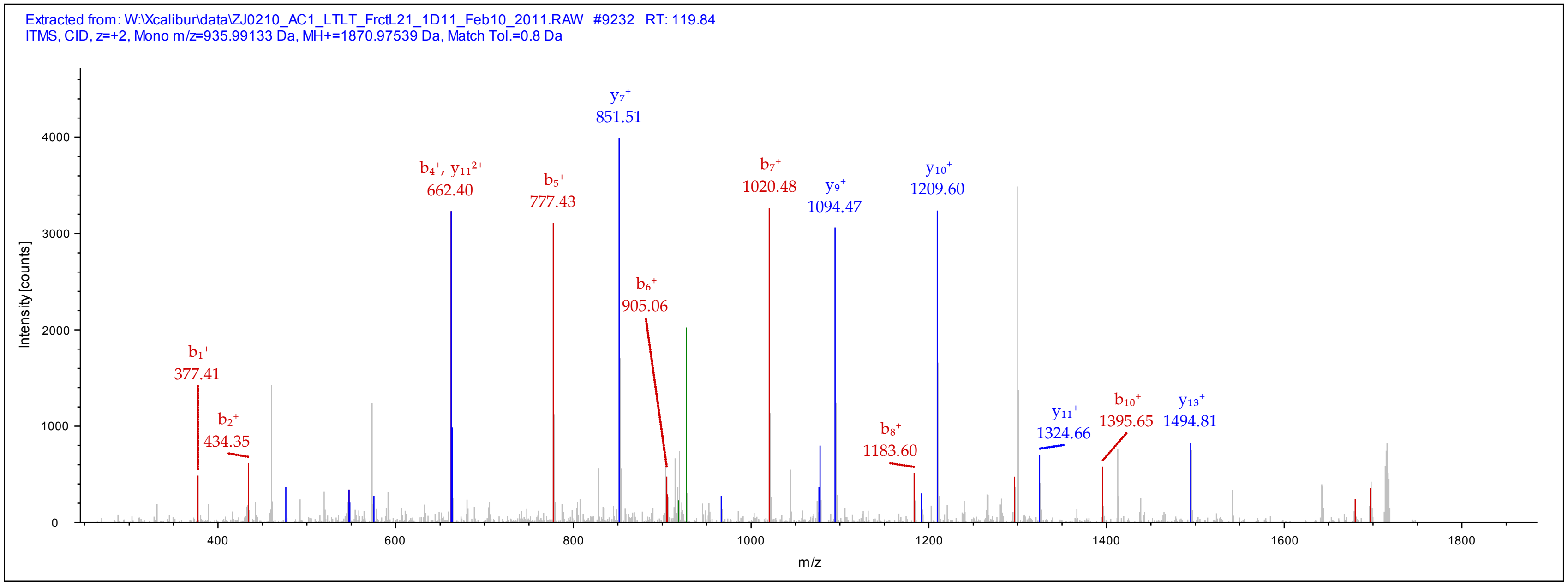
Identified with: Mascot (v1.16); IonScore:36, Exp Value:3.5E-002, Ions matched by search engine: 10/138

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Phosphatidylinositol-5-phosphate 4-kinase type-2 gamma
- cDNA PSEC0253 fis, clone NT2RP3003368, highly similar to Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, gamma (PIP5K2C), mRNA lng=265
- 1-phosphatidylinositol-5-phosphate 4-kinase C isoform b lng=403



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL21_1D11_Feb10_2011.RAW #9232 RT: 119.84
ITMS, CID, z=+2, Mono m/z=935.99133 Da, MH+=1870.97539 Da, Match Tol.=0.8 Da

IPI:IPI00903292.2

Sequence: LYSILGTTLK, L1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 783.99933 Da (+2.12 mmu/+2.71 ppm),   MH+: 1566.99138 Da,   RT: 127.52 min,

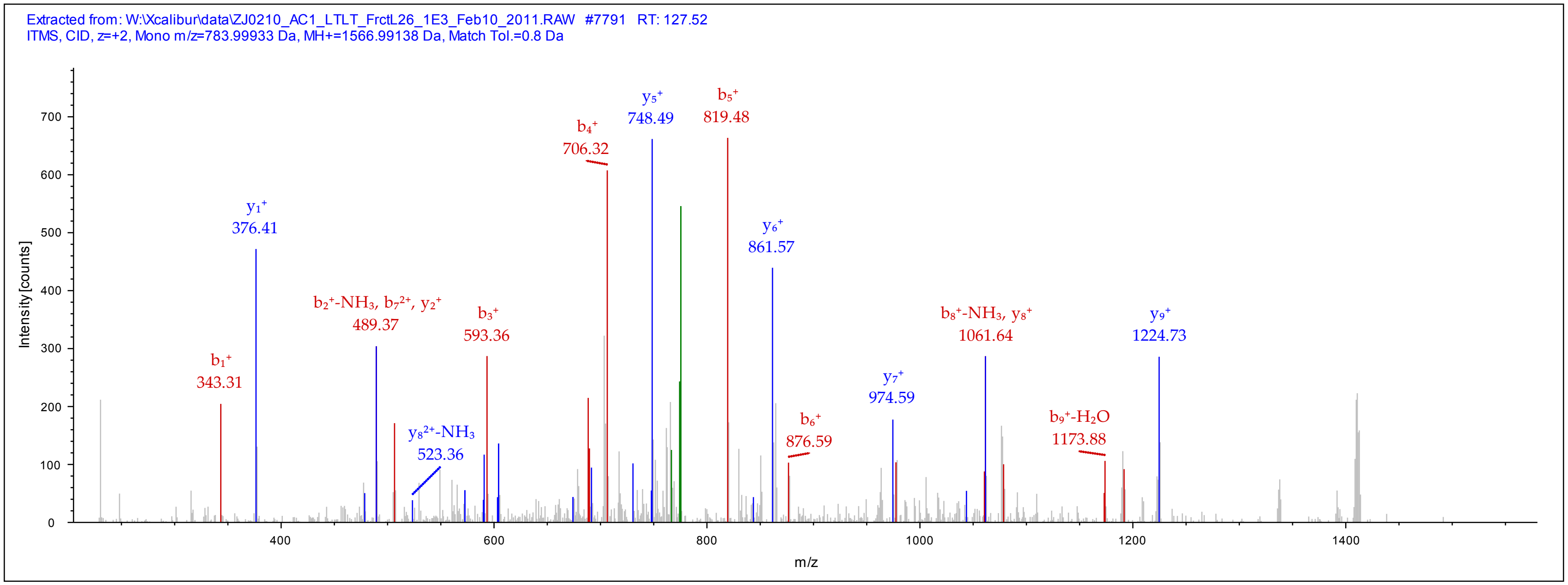
Identified with: Mascot (v1.16); IonScore:38, Exp Value:6.4E-003, Ions matched by search engine: 6/82

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of WD repeat-containing protein 1
- Putative uncharacterized protein WDR1 lng=607
- Isoform 2 of WD repeat-containing protein 1
- cDNA FLJ45763 fis, clone N1ESE2000698, highly similar to WD repeat protein 1 lng=572



IPI00908436.1

Sequence: IPELAINPLGDR, I1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 768.95160 Da (+0.57 mmu/+0.74 ppm),   MH+: 1536.89592 Da,   RT: 117.08 min,

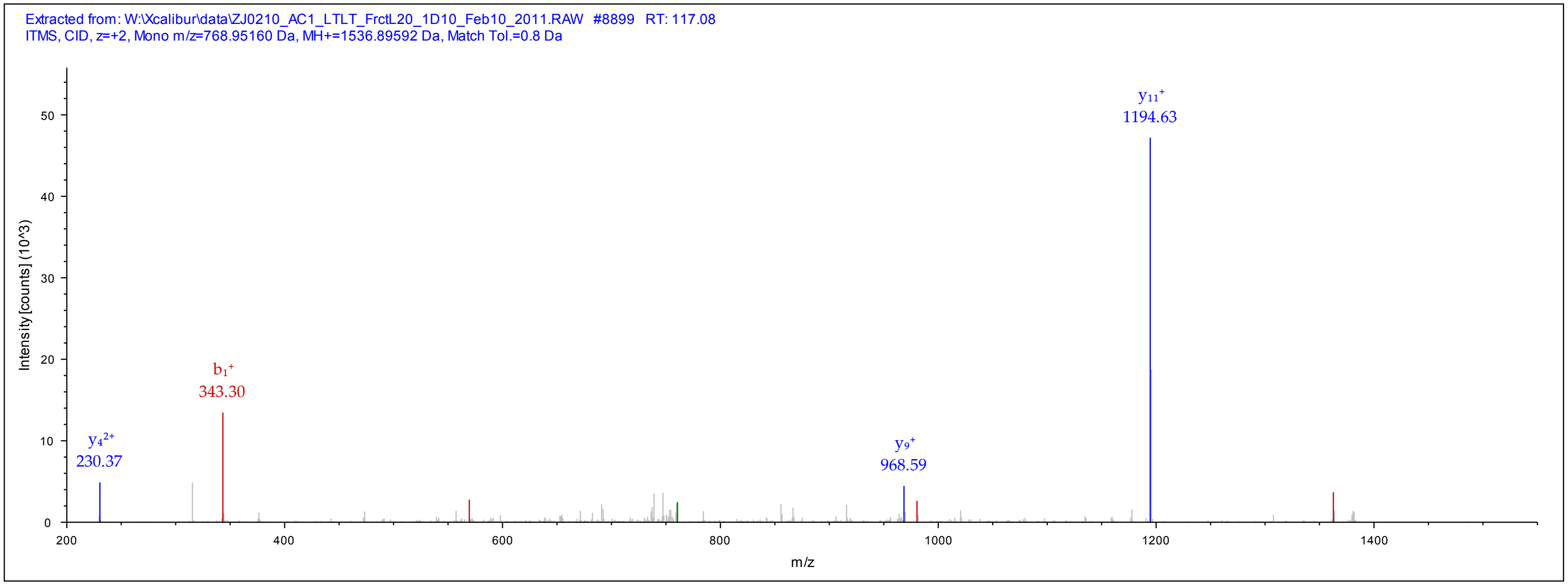
Identified with: Mascot (v1.16); IonScore:43, Exp Value:5.2E-003, Ions matched by search engine: 10/114

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Calcium-binding protein p22
- cDNA FLJ57188, highly similar to Calcium-binding protein p22 lng=128



IPI:IPI00908762.2

Sequence: SDLAVPSELALLK, S1-TMT6plex (229.16293 Da), K13-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 907.55591 Da (+0.27 mmu/+0.3 ppm), MH+: 1814.10454 Da, RT: 123.01 min,

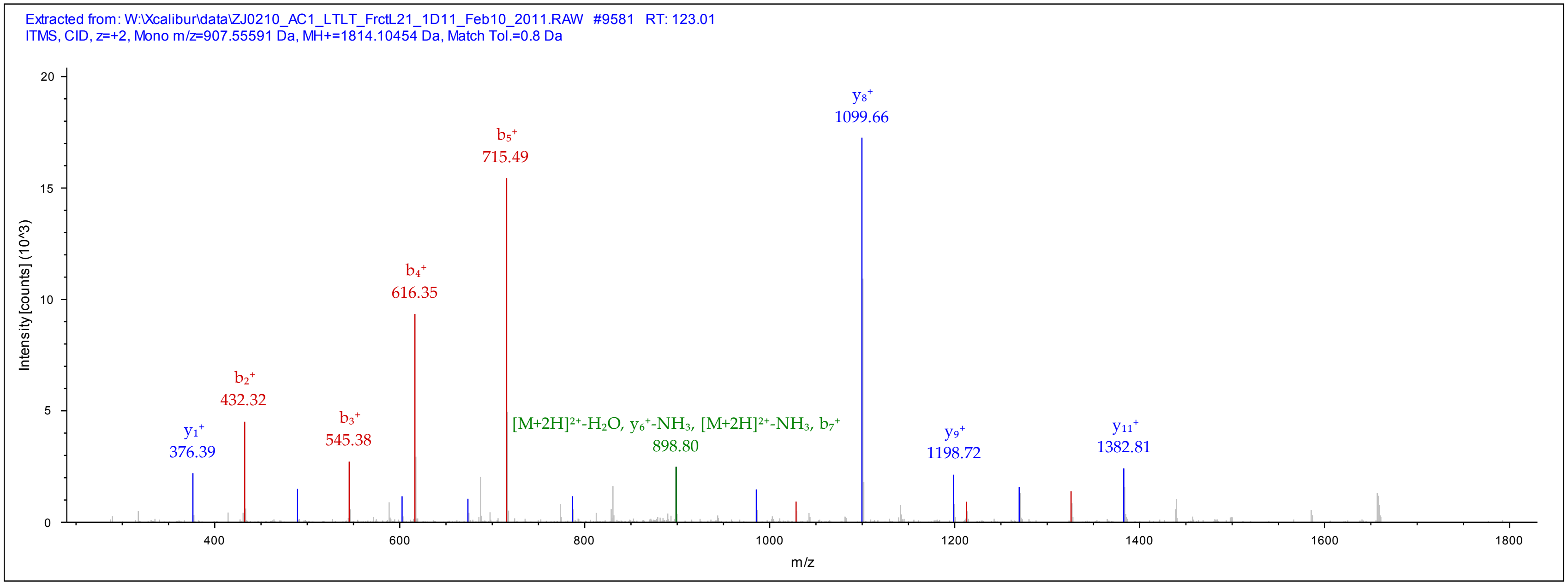
Identified with: Mascot (v1.16); IonScore:67, Exp Value:1.2E-005, Ions matched by search engine: 12/110

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Galectin-3-binding protein
- cDNA FLJ54583, highly similar to Galectin-3-binding protein
- cDNA FLJ53509, highly similar to Galectin-3-binding protein



IPI00909070.1

Sequence: AIIESDQEQGR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 737.88947 Da (+0.85 mmu/+1.15 ppm), MH+: 1474.77165 Da, RT: 74.15 min,

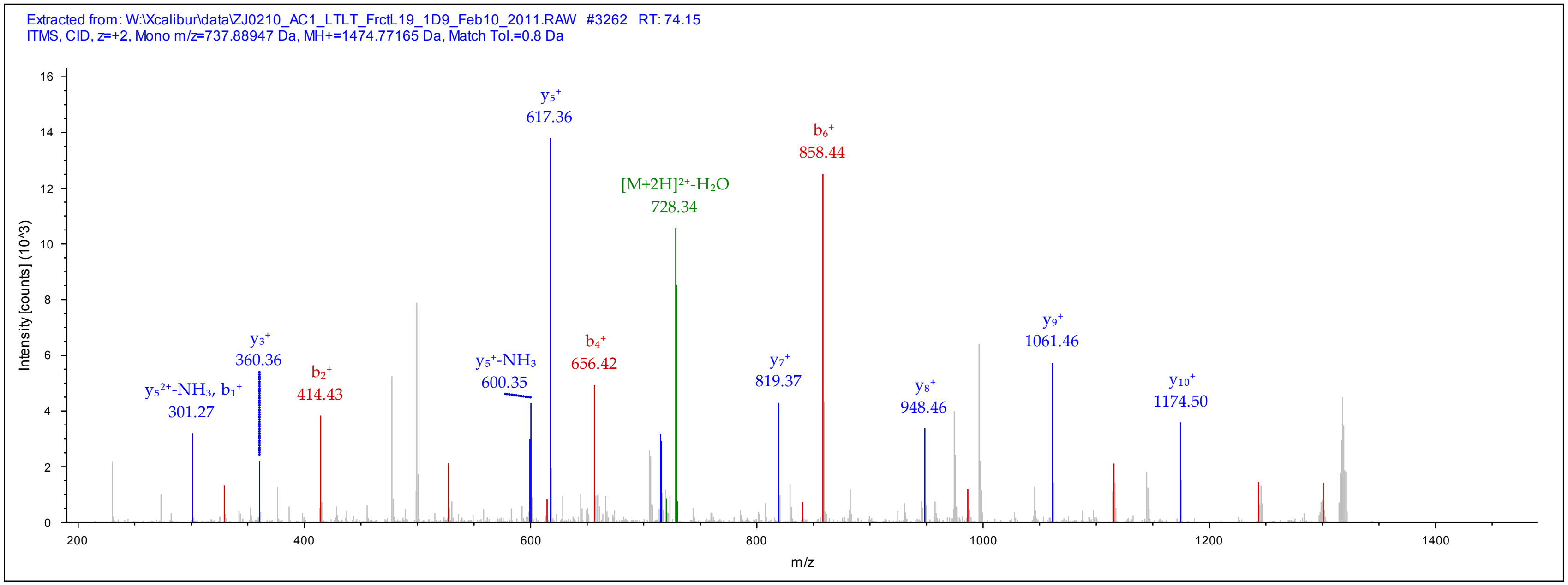
Identified with: Mascot (v1.16); IonScore:42, Exp Value:5.4E-003, Ions matched by search engine: 8/96

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Secernin-1
- secernin 1 isoform c lng=346
- cDNA FLJ51971, highly similar to Secernin-1 lng=240
- secernin 1 isoform b lng=434



IPI:IPI00909121.1

Sequence: IIIPPFLAYGEK, I1-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 910.06305 Da (+2.7 mmu/+2.97 ppm),   MH+: 1819.11882 Da,   RT: 139.86 min,

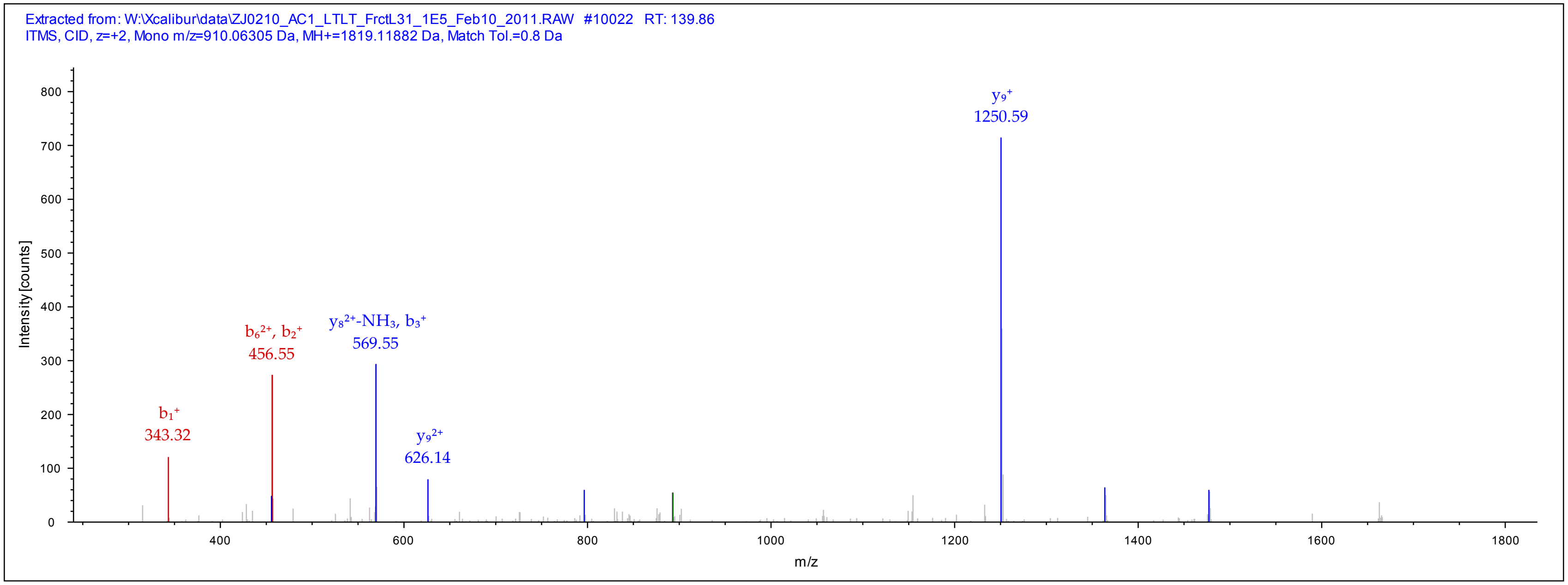
Identified with: Mascot (v1.16); IonScore:31, Exp Value:4.2E-002, Ions matched by search engine: 8/88

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Peptidyl-prolyl cis-trans isomerase FKBP10
- cDNA FLJ53423, highly similar to FK506-binding protein 10



IPI00909159.1

Sequence: EALDVLGAVLK, E1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 793.50201 Da (+1.88 mmu/+2.37 ppm),   MH+: 1585.99675 Da,   RT: 134.59 min,

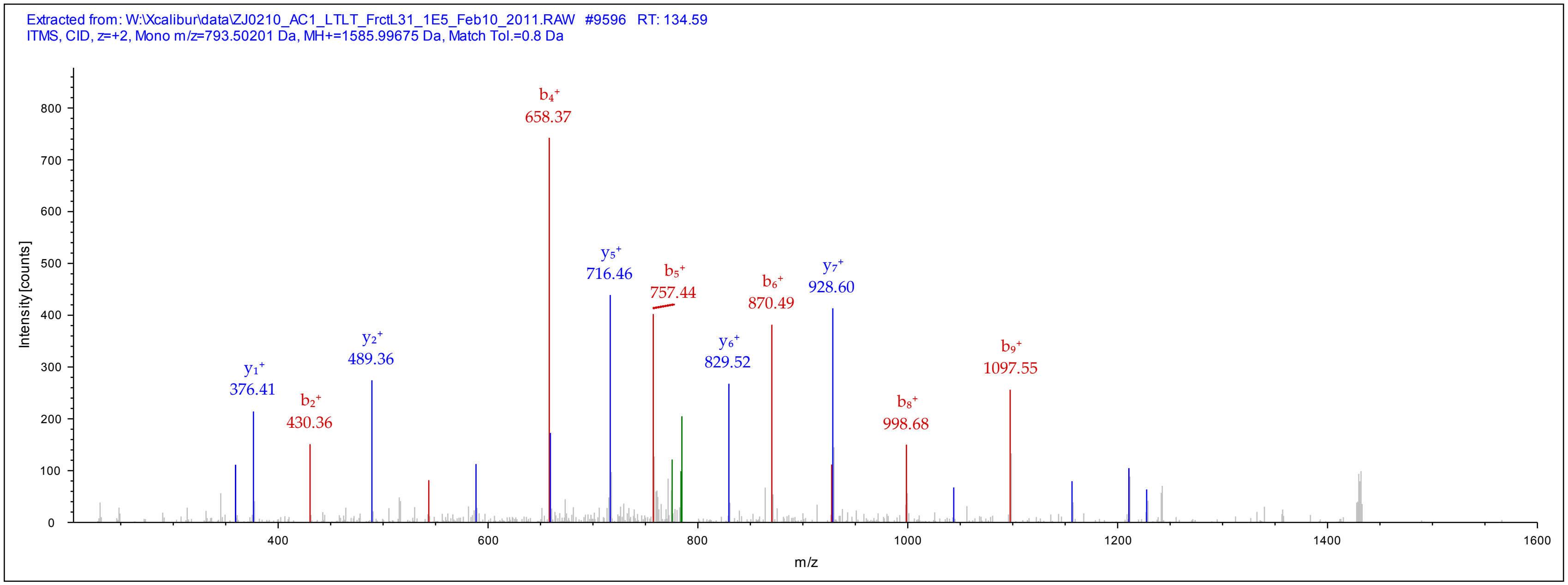
Identified with: Mascot (v1.16); IonScore:61, Exp Value:3.4E-005, Ions matched by search engine: 10/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- cDNA FLJ54536, highly similar to Mitochondrial 28S ribosomal protein S27 lng=428
- cDNA FLJ54799, highly similar to Mitochondrial 28S ribosomal protein S27 lng=195
- 28S ribosomal protein S27, mitochondrial
- Uncharacterized protein



IPI00909332.2

Sequence: DAVIEFLLDK, D1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 810.98480 Da (+0.49 mmu/+0.61 ppm),   MH+: 1620.96233 Da,   RT: 184.16 min,

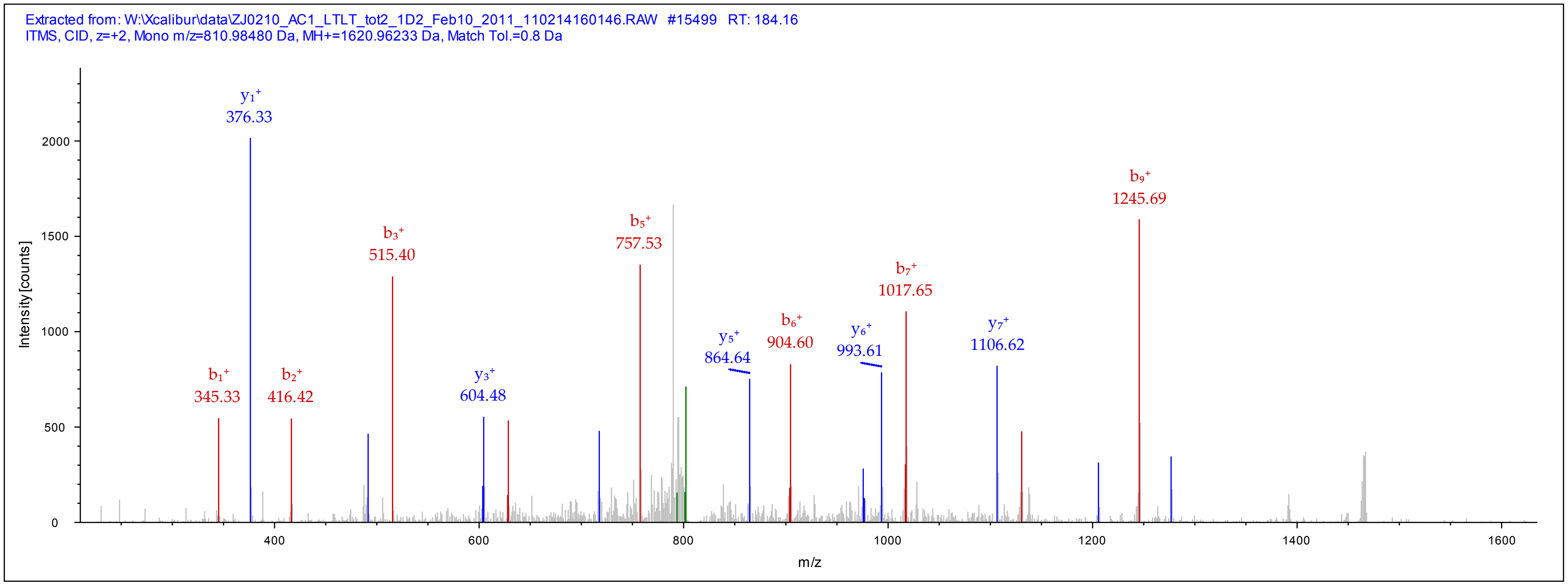
Identified with: Mascot (v1.16); IonScore:55, Exp Value:2.8E-004, Ions matched by search engine: 16/88

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- UPF0549 protein C20orf43
- Putative uncharacterized protein C20orf43 lng=336
- Chromosome 20 open reading frame 43 lng=230
- cDNA FLJ52477 lng=123



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ITMS, CID, z=+2, Mono m/z=810.98480 Da, MH+=1620.96233 Da, Match Tol.=0.8 Da

IPI:IPI00909461.1

Sequence: VPGDSQQEAK, V1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 758.92334 Da (+1.1 mmu/+1.46 ppm),   MH+: 1516.83940 Da,   RT: 72.23 min,

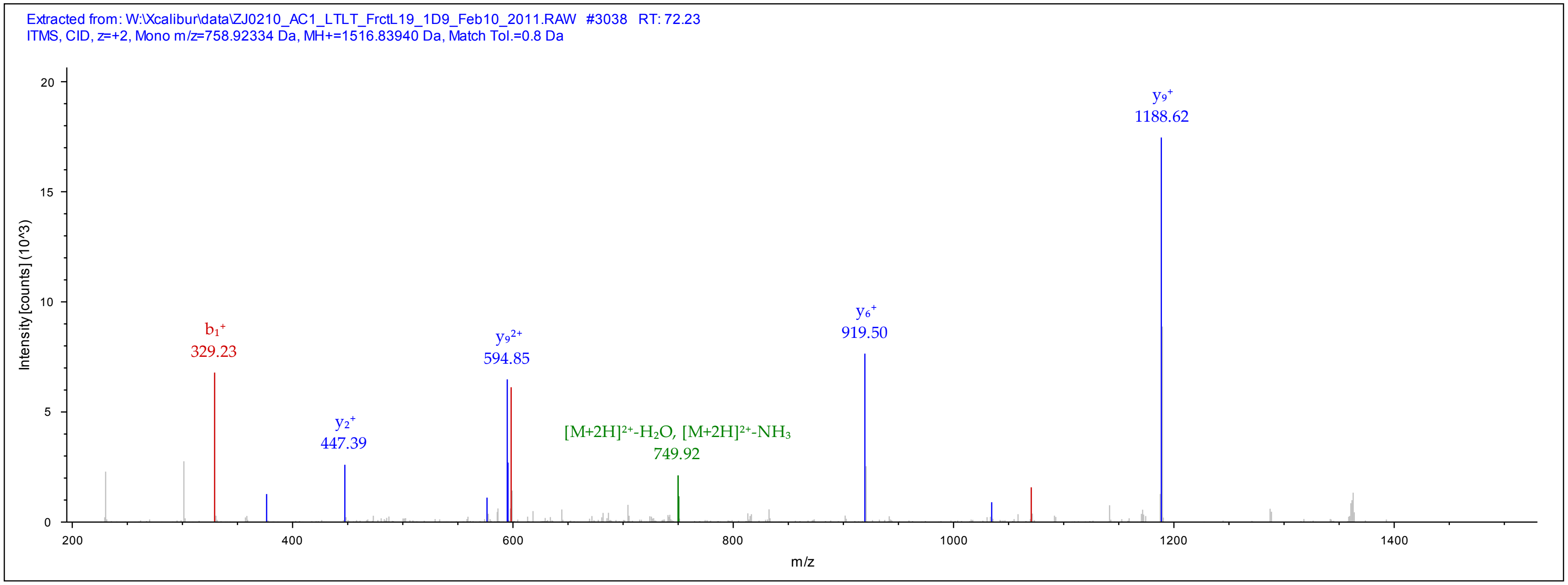
Identified with: Mascot (v1.16); IonScore:39, Exp Value:1.3E-002, Ions matched by search engine: 9/88

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of Breast carcinoma-amplified sequence 1
- Isoform 2 of Breast carcinoma-amplified sequence 1



IPI00909622.1

Sequence: IVDPEIALK, I1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 728.46295 Da (-0.06 mmu/-0.08 ppm),   MH+: 1455.91863 Da,   RT: 107.10 min,

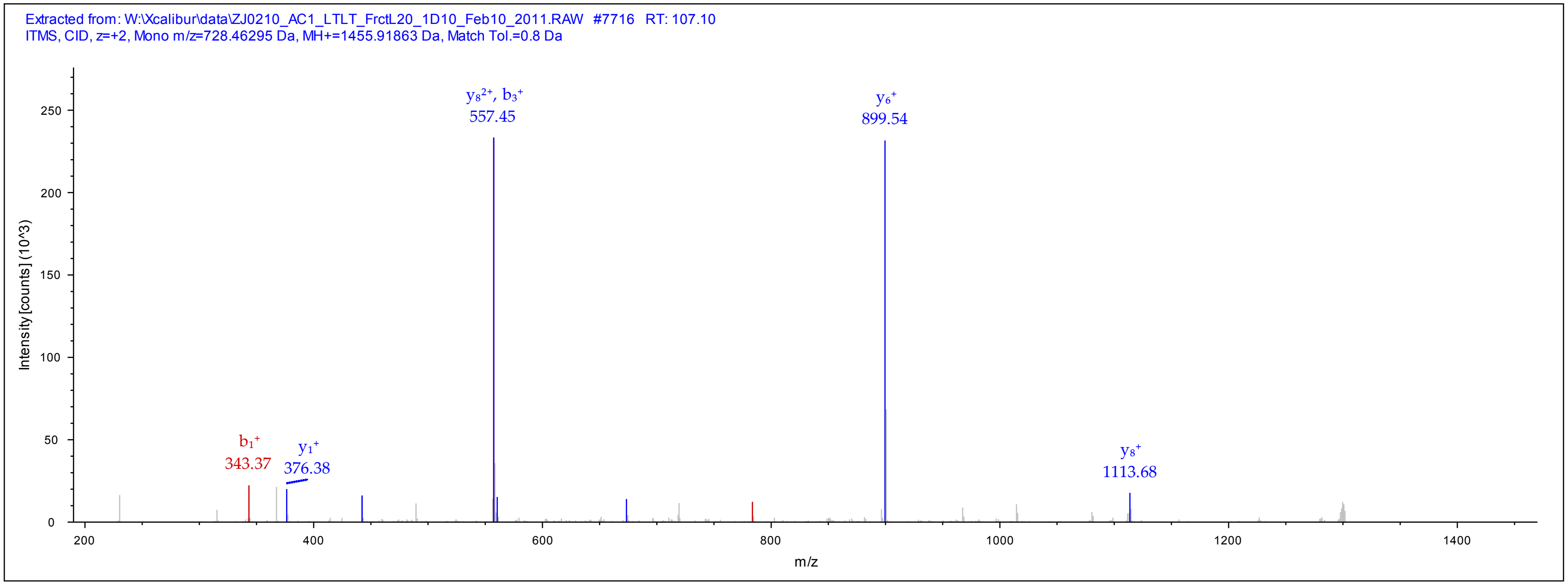
Identified with: Mascot (v1.16); IonScore:35, Exp Value:1.5E-002, Ions matched by search engine: 5/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of Cleavage stimulation factor subunit 2
- Isoform 2 of Cleavage stimulation factor 64 kDa subunit lng=560
- BetaCstF-64 variant 2 lng=597
- cDNA FLJ58787, highly similar to Cleavage stimulation factor 64 kDa subunit lng=553



IPI:IPI00909804.1

Sequence: LDEYIAIAK, L1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 747.45282 Da (+0.18 mmu/+0.25 ppm),   MH+: 1493.89836 Da,   RT: 109.11 min,

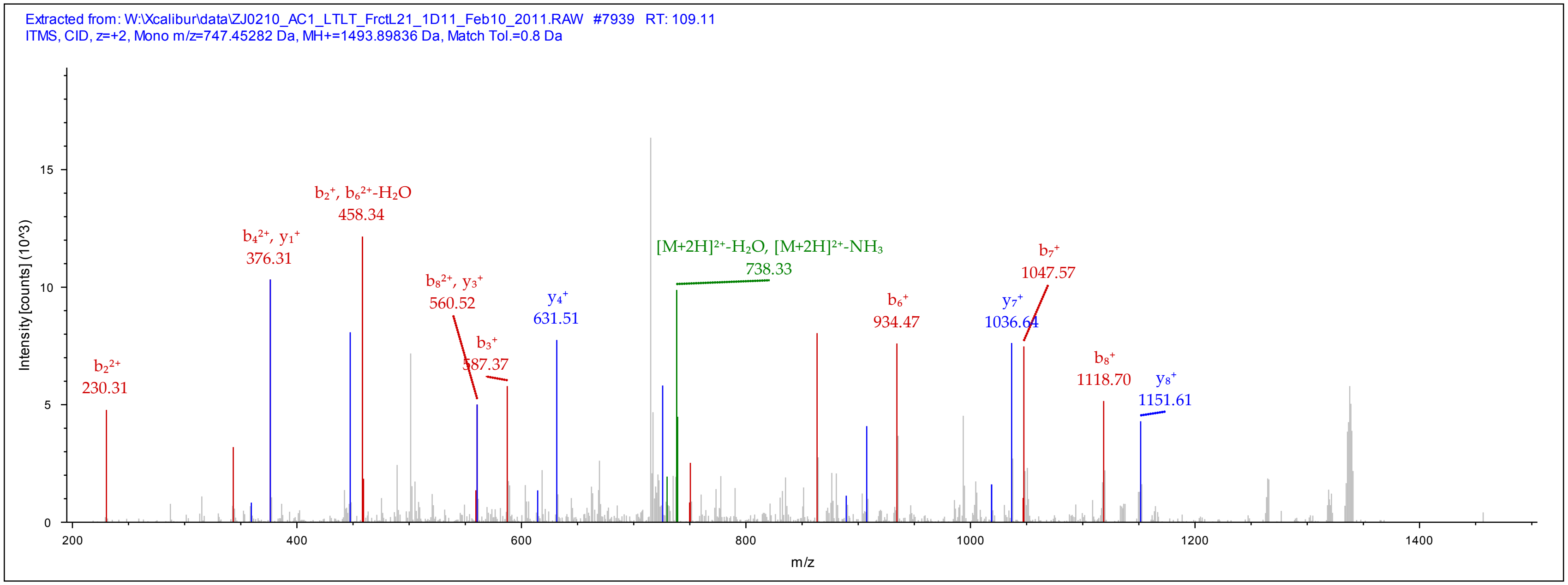
Identified with: Mascot (v1.16); IonScore:47, Exp Value:1.7E-003, Ions matched by search engine: 14/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- REST corepressor 1
- Isoform 1 of REST corepressor 3
- Isoform 2 of REST corepressor 3



IPI00910210.1

Sequence: LQPSIIFIDEIDSFLR, L1-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 712.40308 Da (-0.13 mmu/-0.18 ppm),   MH+: 2135.19468 Da,   RT: 227.04 min,

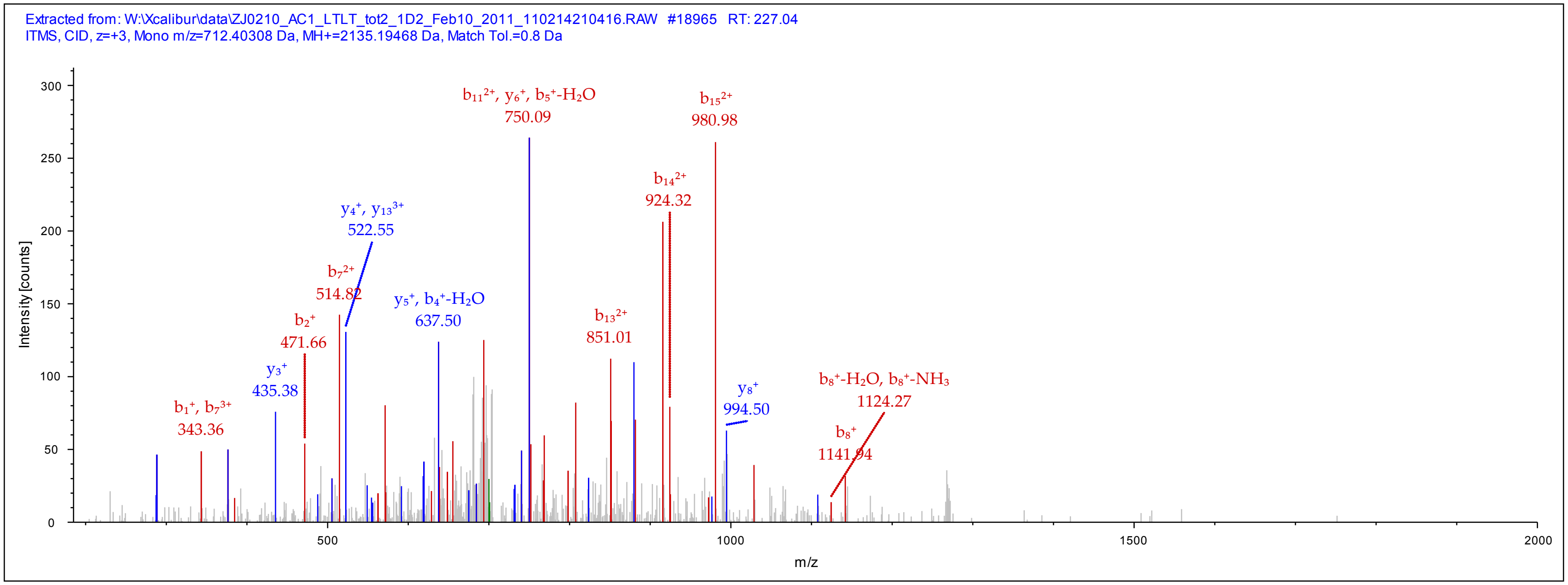
Identified with: Mascot (v1.16); IonScore:48, Exp Value:2.0E-003, Ions matched by search engine: 25/166

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of ATPase family AAA domain-containing protein 1
- cDNA FLJ54240, highly similar to ATPase family AAA domain-containing protein 1 lng=273
- Isoform 2 of ATPase family AAA domain-containing protein 1



IPI:IPI00910368.1

Sequence: GPDWILGEIK, G1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 793.47150 Da (+0.13 mmu/+0.16 ppm), MH+: 1585.93572 Da, RT: 122.58 min,

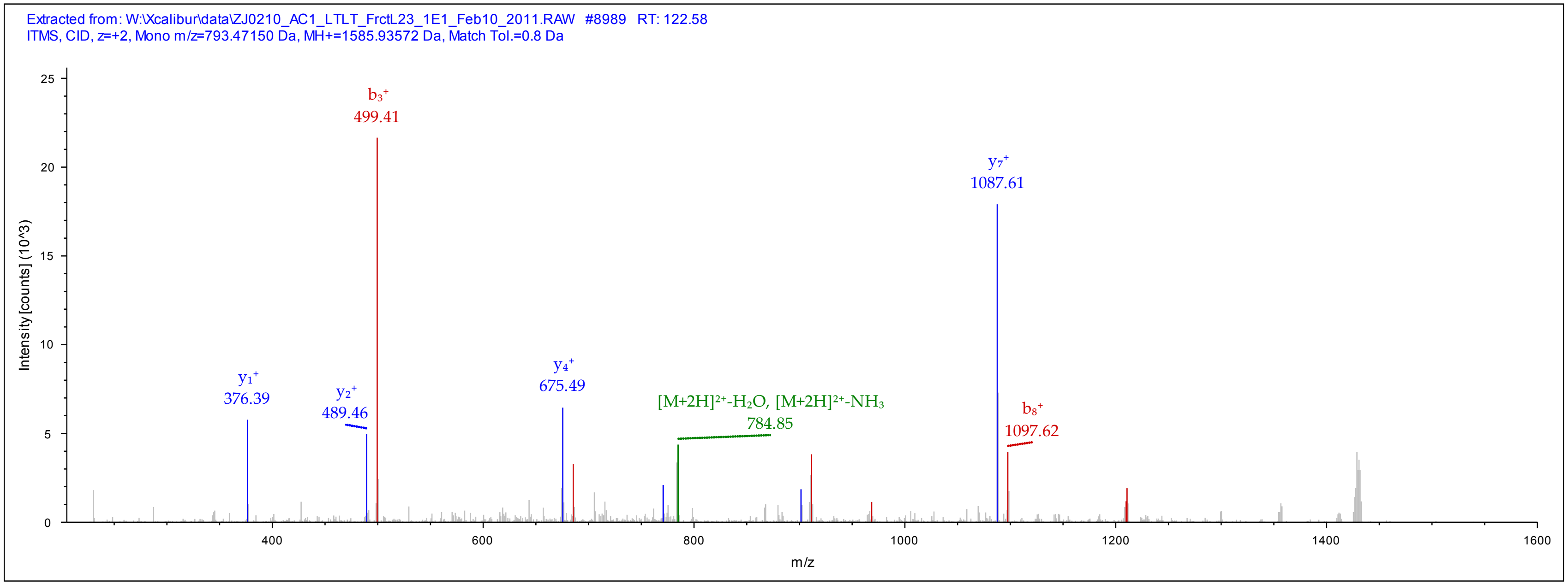
Identified with: Mascot (v1.16); IonScore:34, Exp Value:3.7E-002, Ions matched by search engine: 12/82

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial
- Isoform 2 of NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial
- cDNA FLJ57201, highly similar to NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial



IPI00910659.1

Sequence: EEAFLR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 497.28226 Da (+0.27 mmu/+0.54 ppm), MH+: 993.55724 Da, RT: 95.53 min,

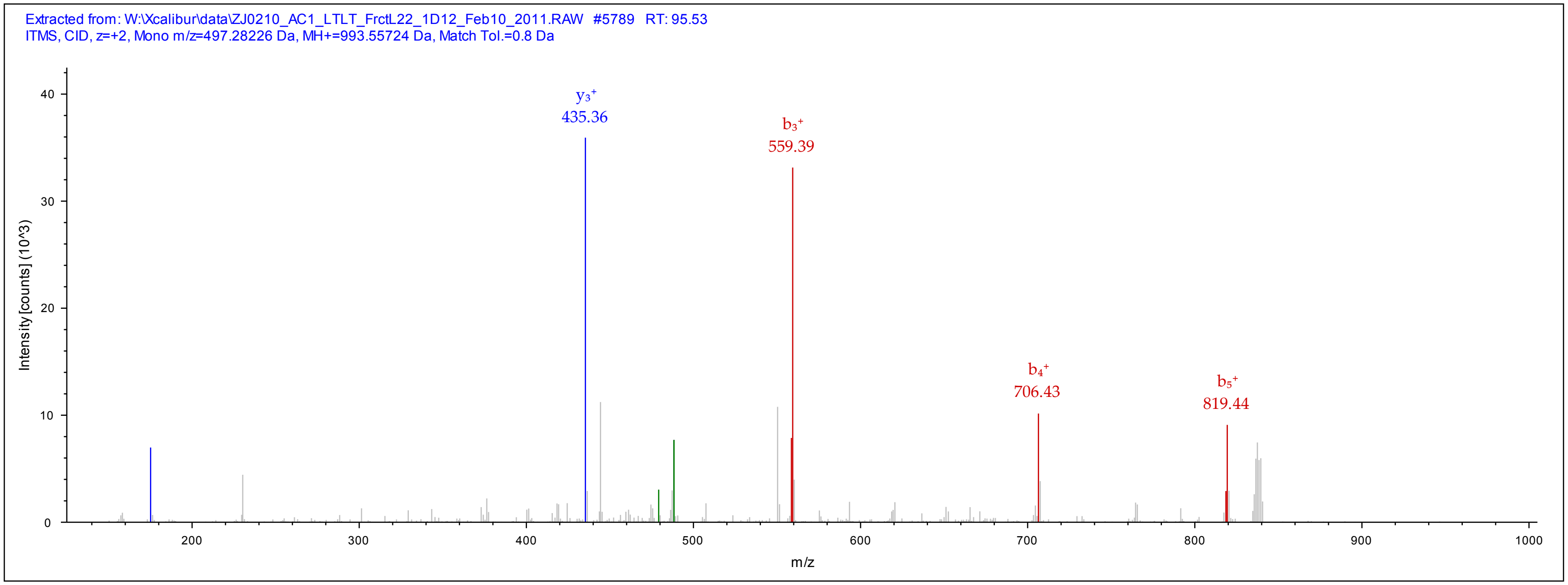
Identified with: Mascot (v1.16); IonScore:30, Exp Value:4.1E-002, Ions matched by search engine: 4/42

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Oxysterol-binding protein-related protein 5
- oxysterol-binding protein-related protein 5 isoform b
- Oxysterol-binding protein lng=621



IPI00910728.1

Sequence: VLTPEEQLADK, V1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 850.99603 Da (+0.63 mmu/+0.74 ppm),   MH+: 1700.98479 Da,   RT: 95.53 min,

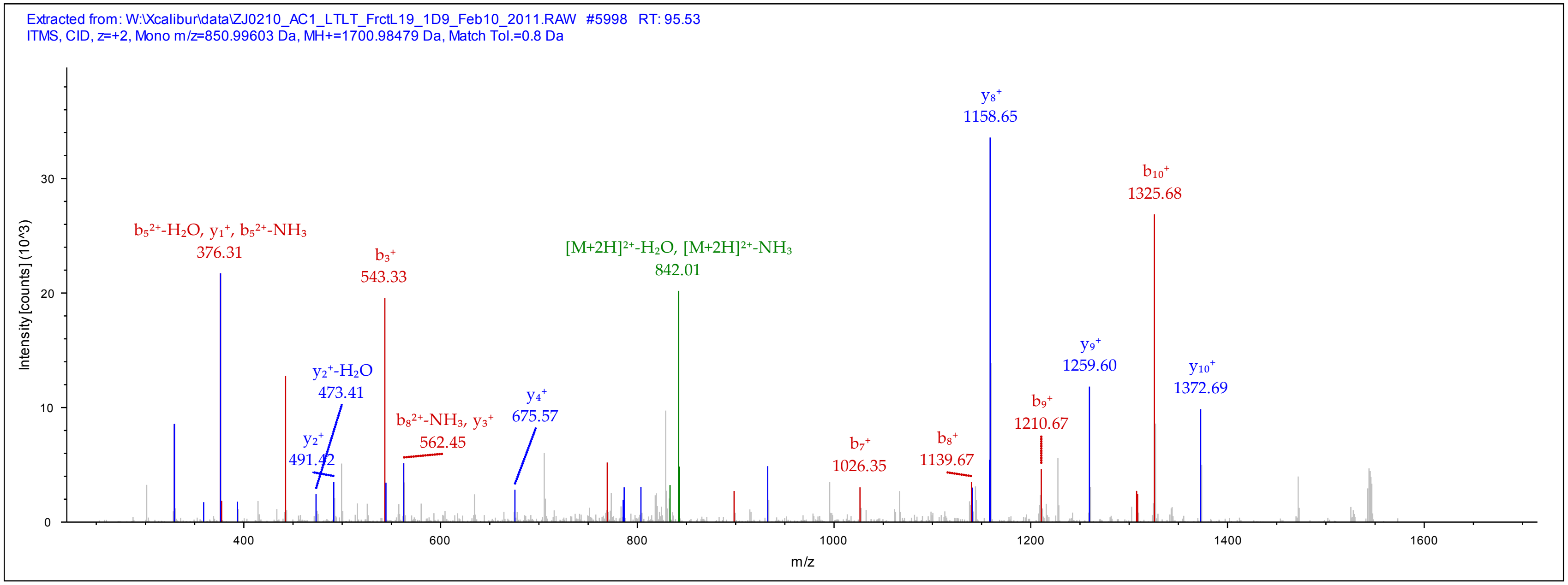
Identified with: Mascot (v1.16); IonScore:41, Exp Value:6.9E-003, Ions matched by search engine: 16/102

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Eukaryotic translation initiation factor 3 subunit J
- cDNA FLJ57599, moderately similar to Eukaryotic translation initiation factor 3 subunit 1 lng=204



IPI:IPI00910819.1

Sequence: AVSILPLLGHGVPR, A1-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 553.35040 Da (+1.7 mmu/+3.08 ppm), MH+: 1658.03666 Da, RT: 122.88 min,

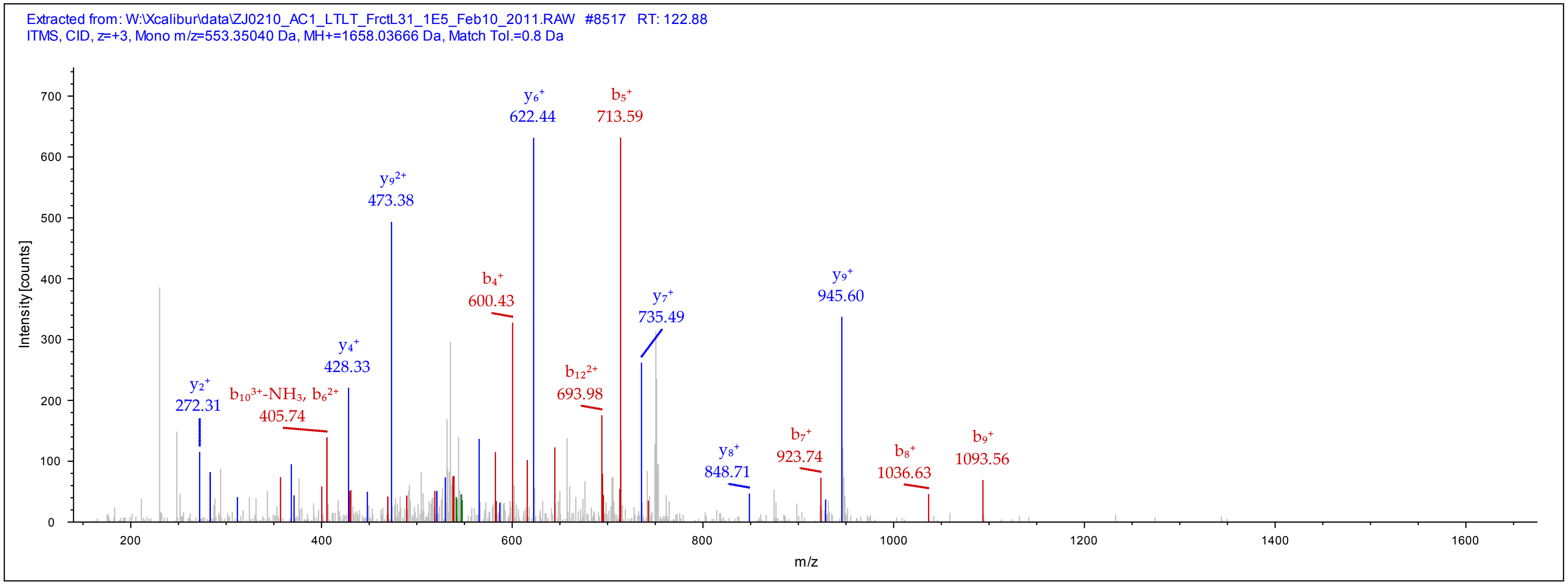
Identified with: Mascot (v1.16); IonScore:31, Exp Value:3.1E-002, Ions matched by search engine: 8/104

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- WW domain-binding protein 11
- cDNA FLJ60194, highly similar to WW domain-binding protein 11



IPI00910830.1

Sequence: YQIDPDACFSAK, Y1-TMT6plex (229.16293 Da), C8-Carbamidomethyl (57.02146 Da), K12-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 936.98328 Da (+1.31 mmu/+1.4 ppm), MH+: 1872.95928 Da, RT: 98.68 min,

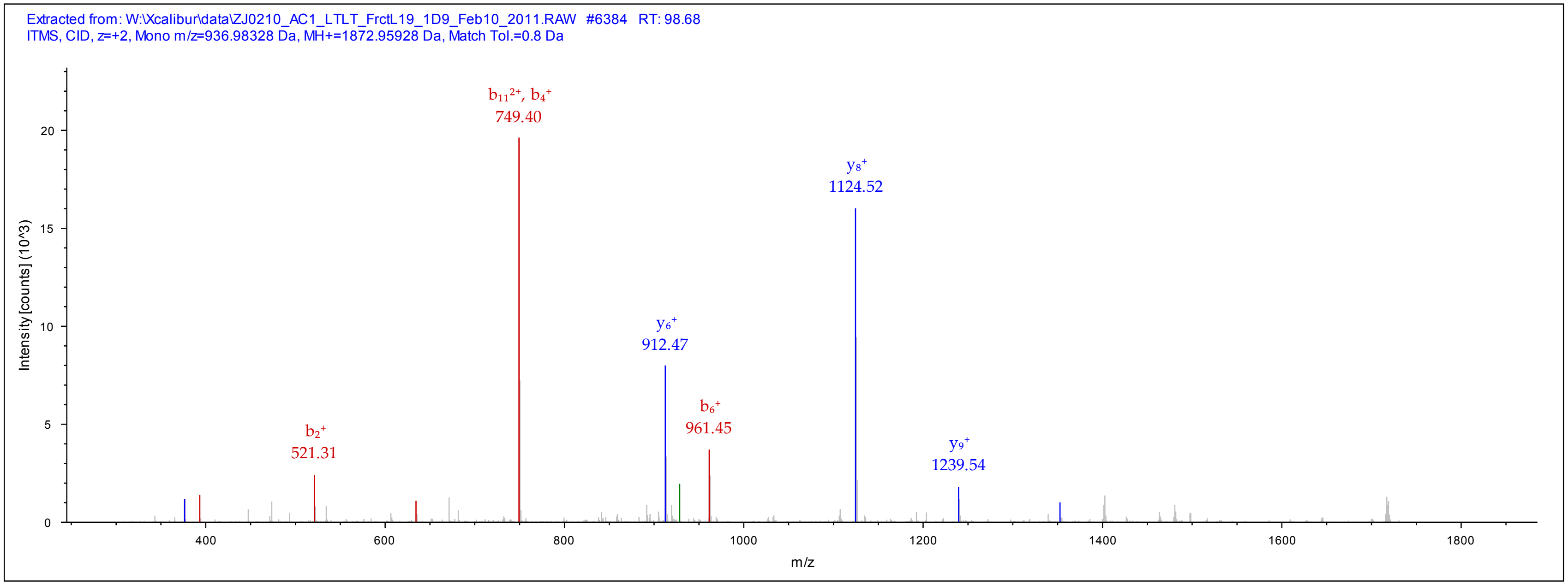
Identified with: Mascot (v1.16); IonScore:61, Exp Value:1.1E-004, Ions matched by search engine: 11/120

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Voltage-dependent anion-selective channel protein 1
- Similar to Voltage-dependent anion-selective channel protein 1 lng=251
- cDNA FLJ57715, highly similar to Voltage-dependent anion-selective channel protein 1 lng=156



IPI00910983.1

Sequence: VAPAQPSEEGPGR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 762.40729 Da (+2.84 mmu/+3.73 ppm), MH+: 1523.80730 Da, RT: 71.97 min,

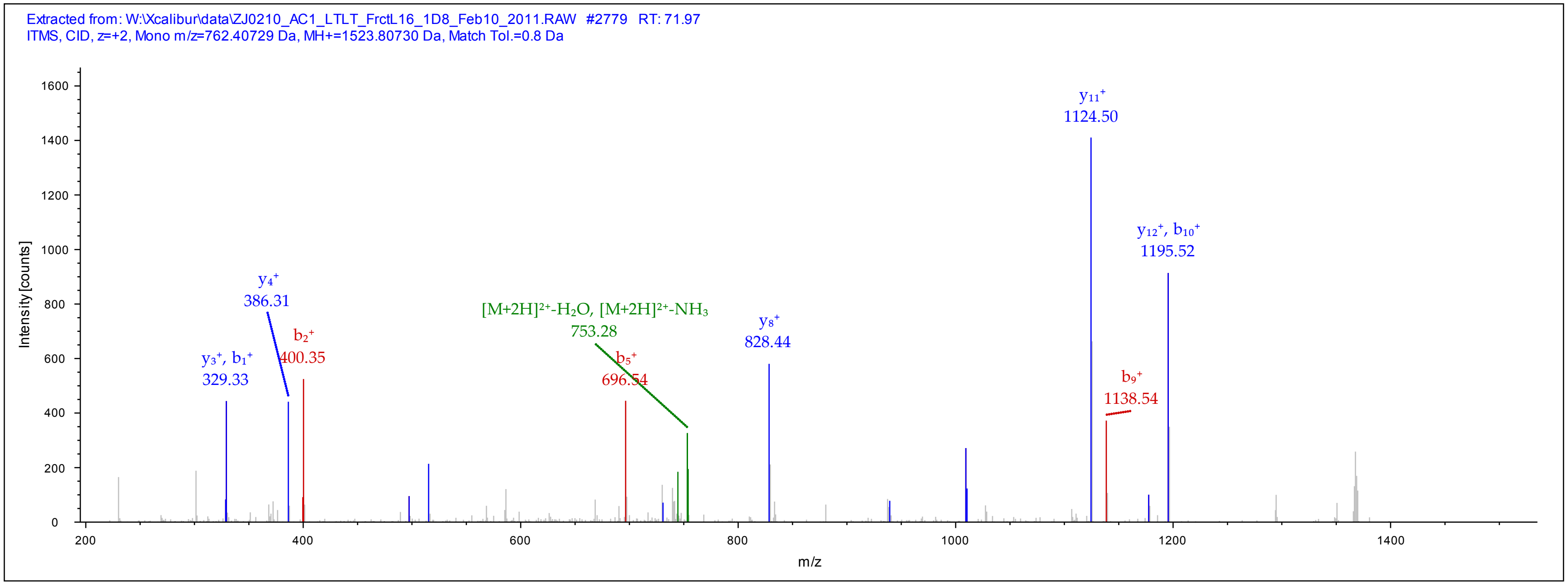
Identified with: Mascot (v1.16); IonScore:45, Exp Value:3.4E-003, Ions matched by search engine: 9/116

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- cDNA FLJ54492, highly similar to Eukaryotic translation initiation factor 4B
- cDNA FLJ59405, highly similar to Eukaryotic translation initiation factor 4B lng=572
- cDNA FLJ59206, highly similar to Eukaryotic translation initiation factor 4B lng=587
- cDNA FLJ59402, highly similar to Eukaryotic translation initiation factor 4B lng=368
- 70 kDa protein lng=616



IPI00913888.1

Sequence: AAWEAYLSR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 648.35034 Da (-0.59 mmu/-0.92 ppm), MH+: 1295.69341 Da, RT: 98.72 min,

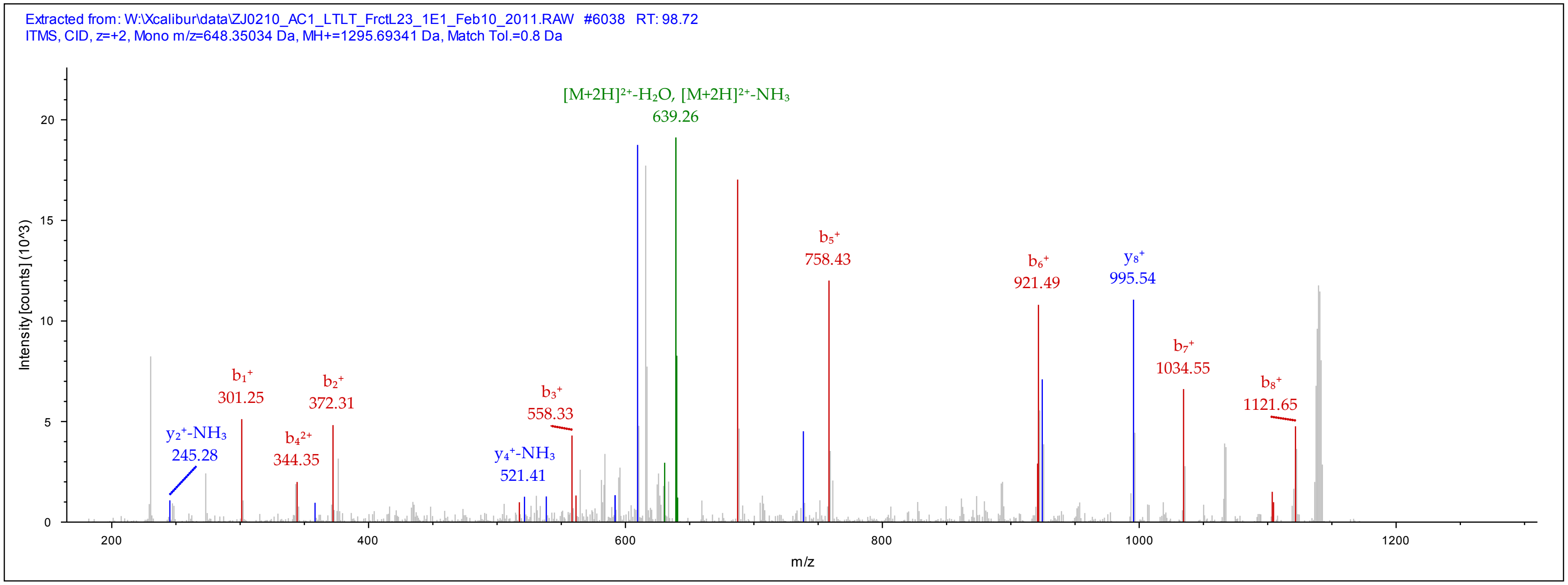
Identified with: Mascot (v1.16); IonScore:41, Exp Value:6.4E-003, Ions matched by search engine: 7/72

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of Uridine 5'-monophosphate synthase
- Isoform 2 of Uridine 5'-monophosphate synthase lng=302
- Orotidine 5'-phosphate decarboxylase lng=302



IPI:IPI00914908.1

Sequence: LTELQLR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 551.34467 Da (-0.45 mmu/-0.82 ppm), MH+: 1101.68205 Da, RT: 92.49 min,

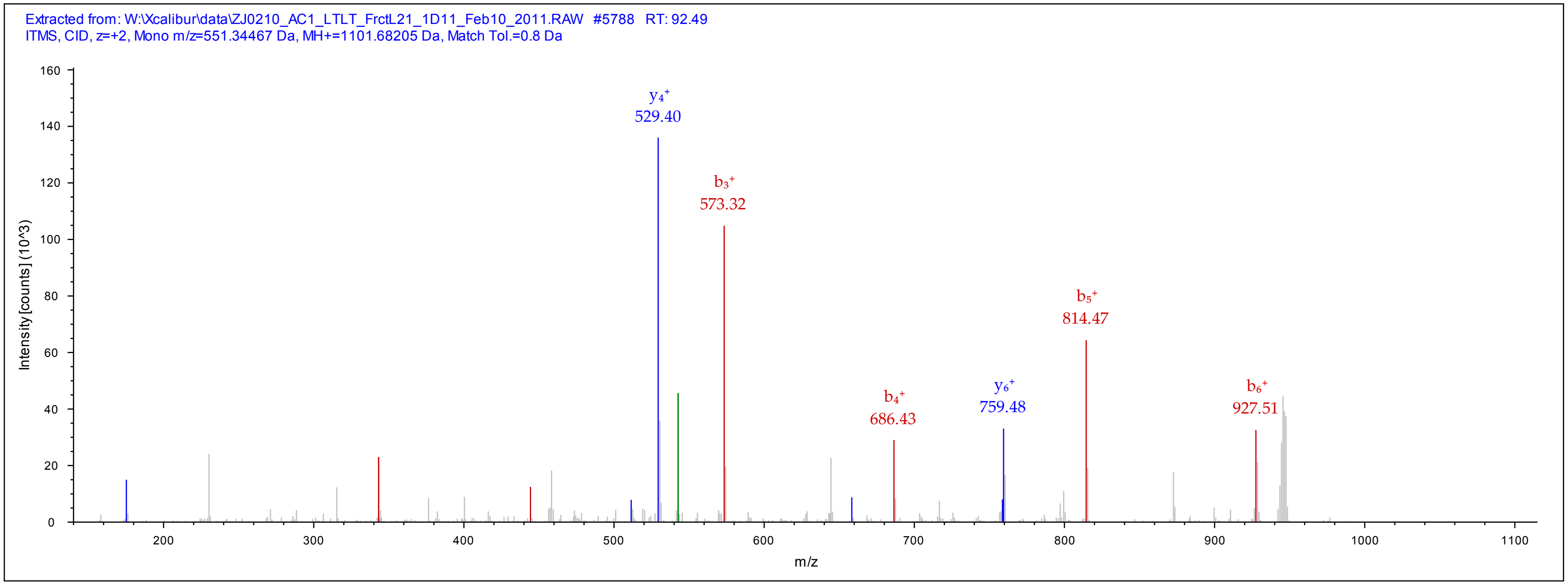
Identified with: Mascot (v1.16); IonScore:32, Exp Value:3.1E-002, Ions matched by search engine: 5/54

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of Transmembrane emp24 domain-containing protein 4
- 23 kDa protein
- Isoform 2 of Transmembrane emp24 domain-containing protein 4
- Isoform 3 of Transmembrane emp24 domain-containing protein 4



IPI00916298.1

Sequence: IICQGFTGK, I1-TMT6plex (229.16293 Da), C3-Carbamidomethyl (57.02146 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 741.43158 Da (+0.4 mmu/+0.54 ppm), MH+: 1481.85588 Da, RT: 92.26 min,

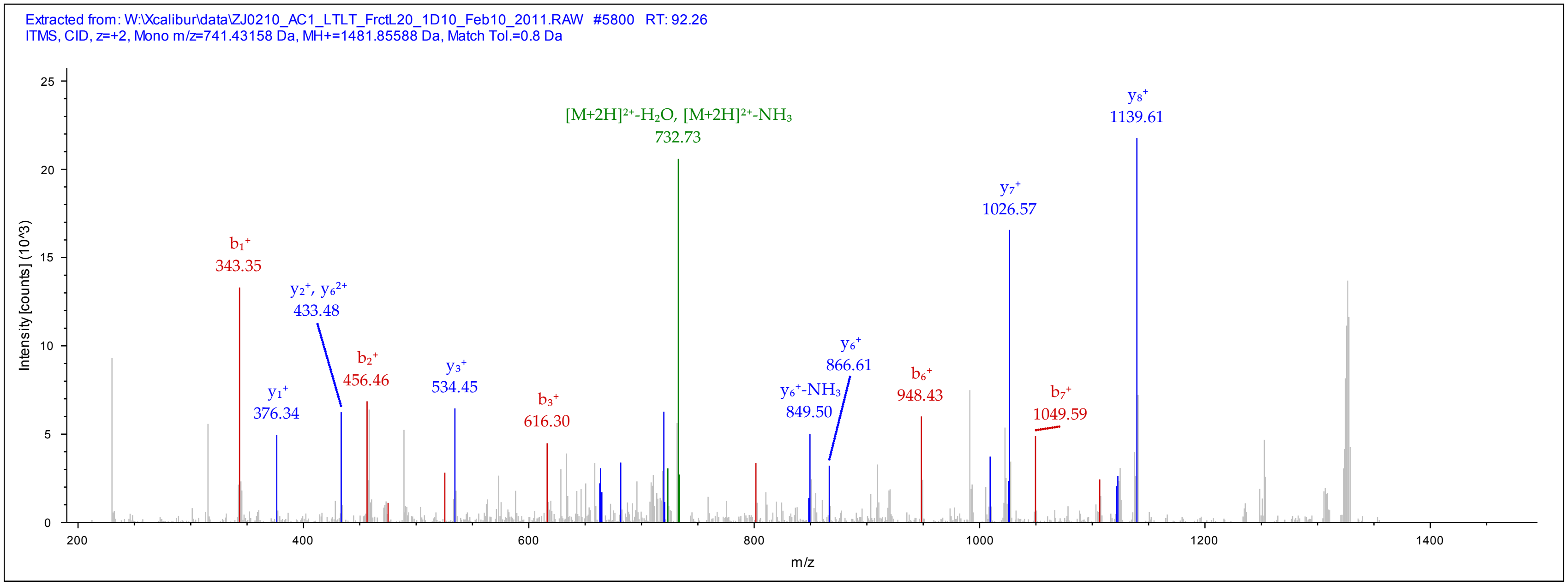
Identified with: Mascot (v1.16); IonScore:30, Exp Value:8.6E-002, Ions matched by search engine: 7/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial
- Putative uncharacterized protein tmp_locus_1 lng=333
- Putative uncharacterized protein SUCLG1 lng=105
- cDNA FLJ56352, highly similar to Succinyl-CoA ligase (GDP-forming) subunit alpha, mitochondrial lng=248



IPI:IPI00916535.1

Sequence: RPCTLSELE, R1-TMT6plex (229.16293 Da), C3-Carbamidomethyl (57.02146 Da)

Charge: +2, Monoisotopic m/z: 667.35333 Da (+0.51 mmu/+0.77 ppm), MH+: 1333.69939 Da, RT: 82.09 min,

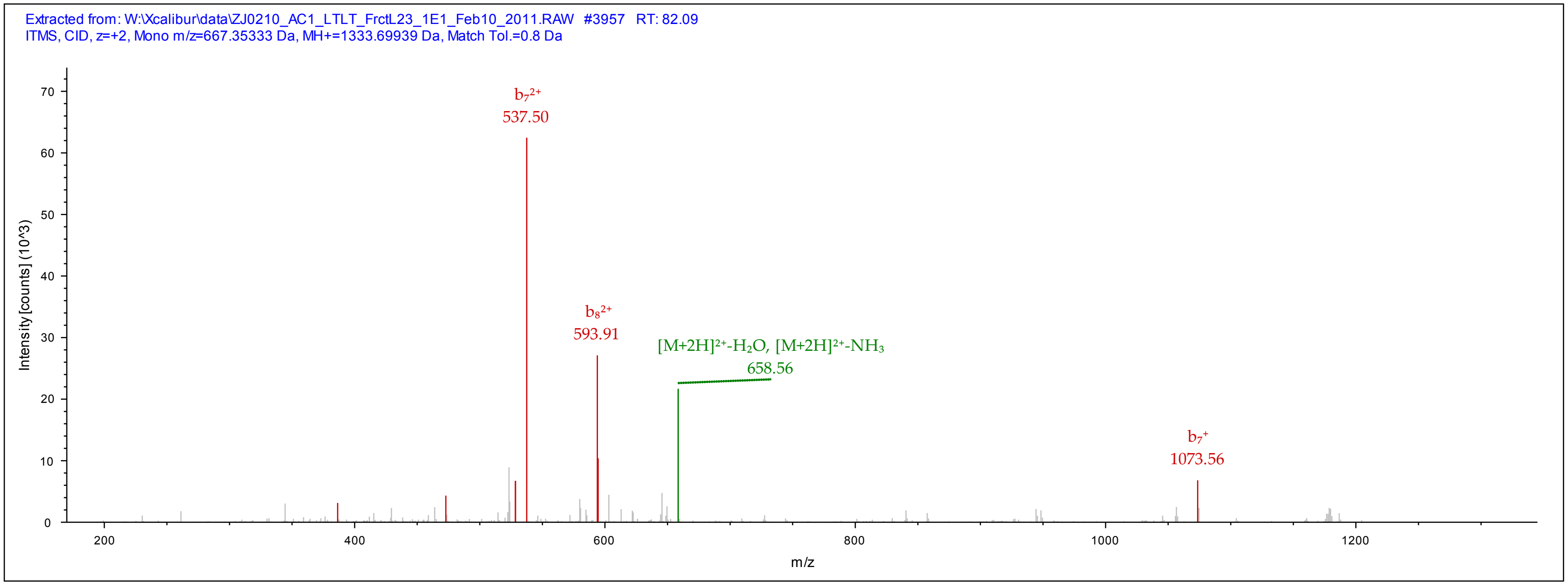
Identified with: Mascot (v1.16); IonScore:31, Exp Value:6.3E-002, Ions matched by search engine: 5/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Prolyl 4-hydroxylase subunit alpha-1
- Isoform 2 of Prolyl 4-hydroxylase subunit alpha-1
- prolyl 4-hydroxylase, alpha I subunit isoform 3 precursor



IPI00916623.2

Sequence: VAVLQALASTVNR, V1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 785.98004 Da (+2.47 mmu/+3.14 ppm),   MH+: 1570.95281 Da,   RT: 127.48 min,

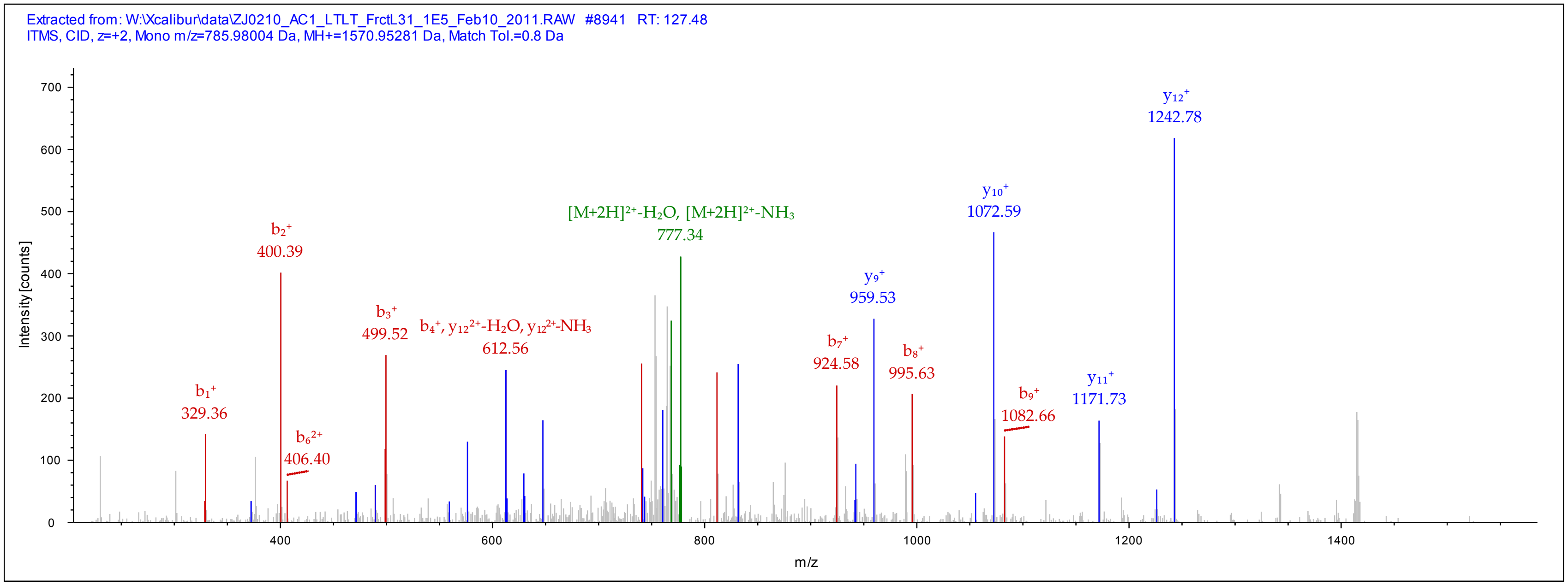
Identified with: Mascot (v1.16); IonScore:36, Exp Value:1.4E-002, Ions matched by search engine: 6/114

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of Pentatricopeptide repeat-containing protein 3, mitochondrial
- Putative uncharacterized protein PTCD3 lng=208
- 9 kDa protein lng=81
- Putative uncharacterized protein PTCD3 lng=149



IPI:IPI00916749.1

Sequence: ALEIITDFSGIVLEK, A1-TMT6plex (229.16293 Da), K15-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 702.75574 Da (+2.12 mmu/+3.01 ppm), MH+: 2106.25266 Da, RT: 208.19 min,

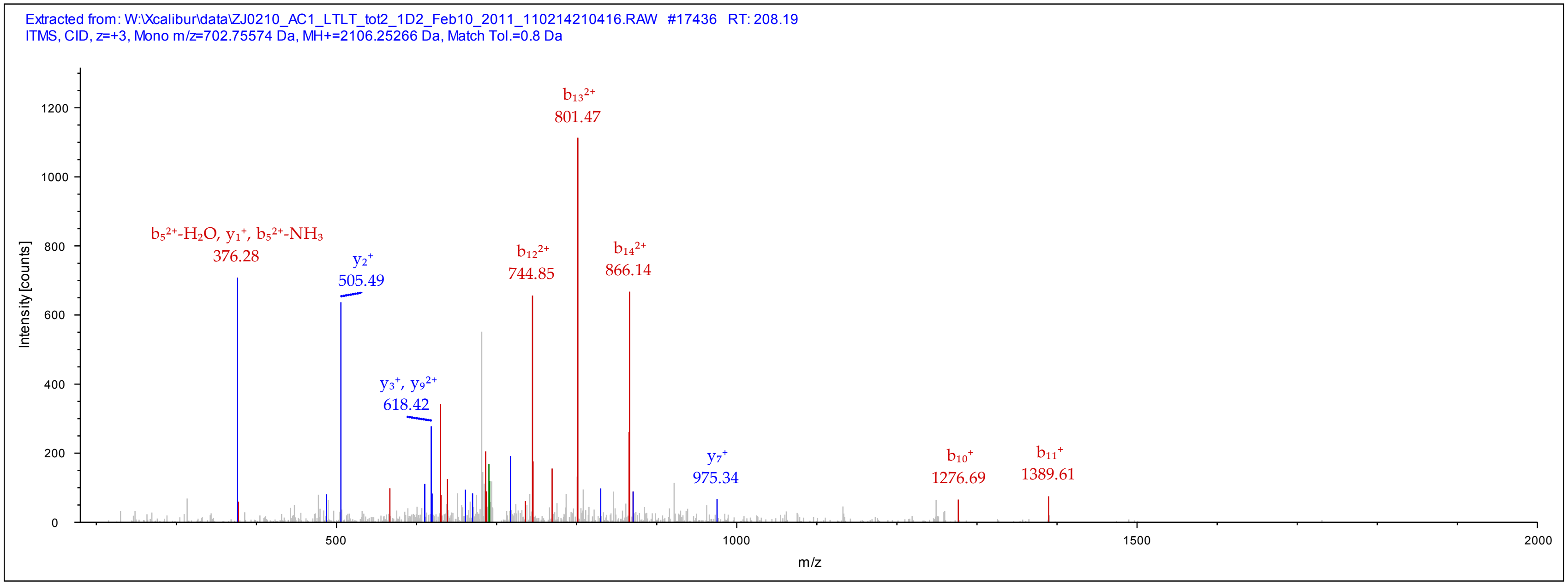
Identified with: Mascot (v1.16); IonScore:30, Exp Value:7.3E-002, Ions matched by search engine: 8/134

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of General transcription factor 3C polypeptide 3
- Isoform 2 of General transcription factor 3C polypeptide 3
- 18 kDa protein



IPI:IPI00917053.1

Sequence: IIFGKNSDR, I1-TMT6plex (229.16293 Da), K5-TMT6plex (229.16293 Da), S7-Phospho (79.96633 Da)

Charge: +2, Monoisotopic m/z: 794.42371 Da (-12.97 mmu/-16.33 ppm), MH+: 1587.84014 Da, RT: 116.93 min,

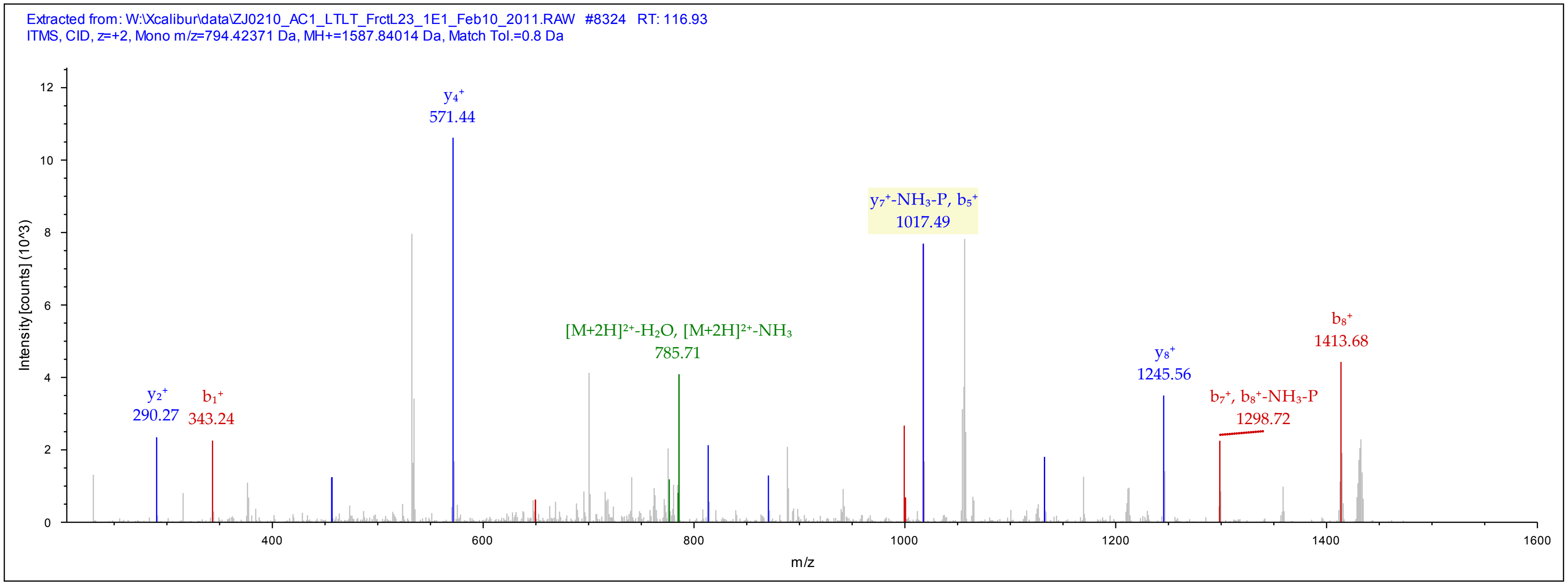
Identified with: Mascot (v1.16); IonScore:35, Exp Value:3.9E-002, Ions matched by search engine: 10/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Secernin-3
- Secernin-3
- Uncharacterized protein
- 13 kDa protein
- Uncharacterized protein
- Uncharacterized protein



IPI00917664.2

Sequence: VIPTLALLK, V1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 713.49622 Da (+2.11 mmu/+2.95 ppm),   MH+: 1425.98516 Da,   RT: 132.22 min,

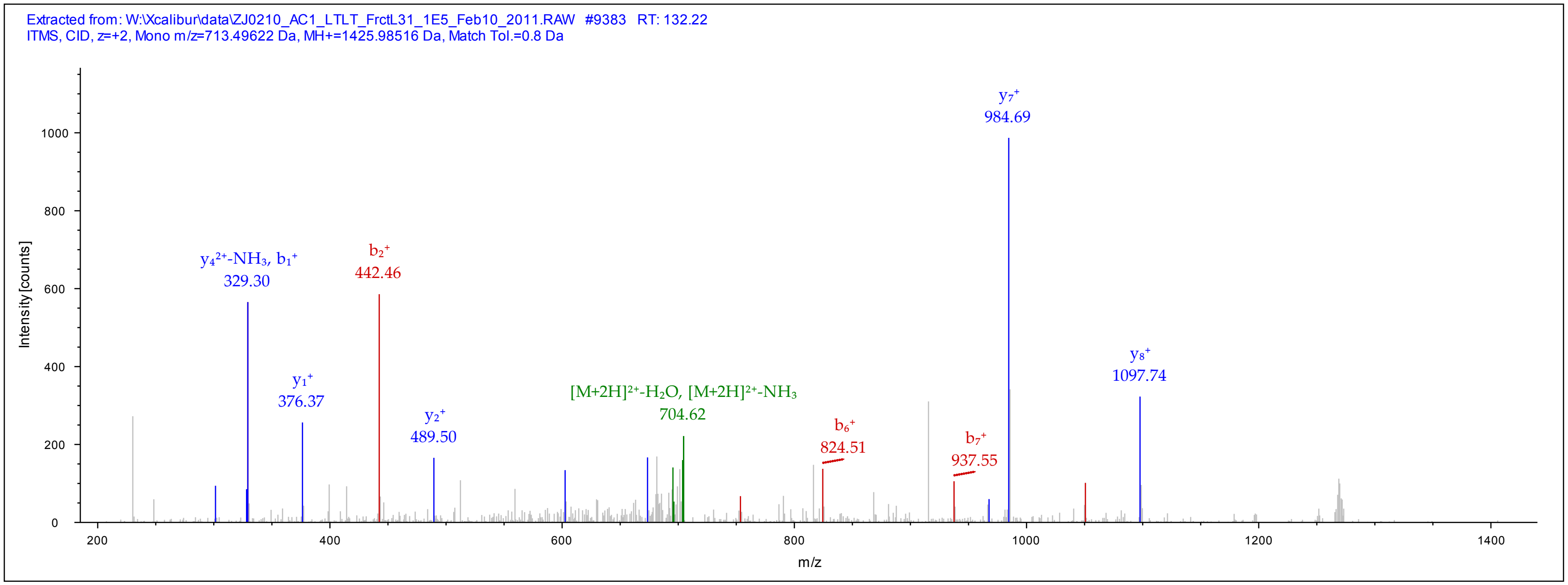
Identified with: Mascot (v1.16); IonScore:29, Exp Value:5.2E-003, Ions matched by search engine: 7/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Thioredoxin domain-containing protein 9
- cDNA FLJ55148, highly similar to Thioredoxin domain-containing protein 9 lng=208



IPI00917694.1

Sequence: ESSTVFELK, E1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 749.43201 Da (+0.11 mmu/+0.14 ppm),   MH+: 1497.85674 Da,   RT: 95.52 min,

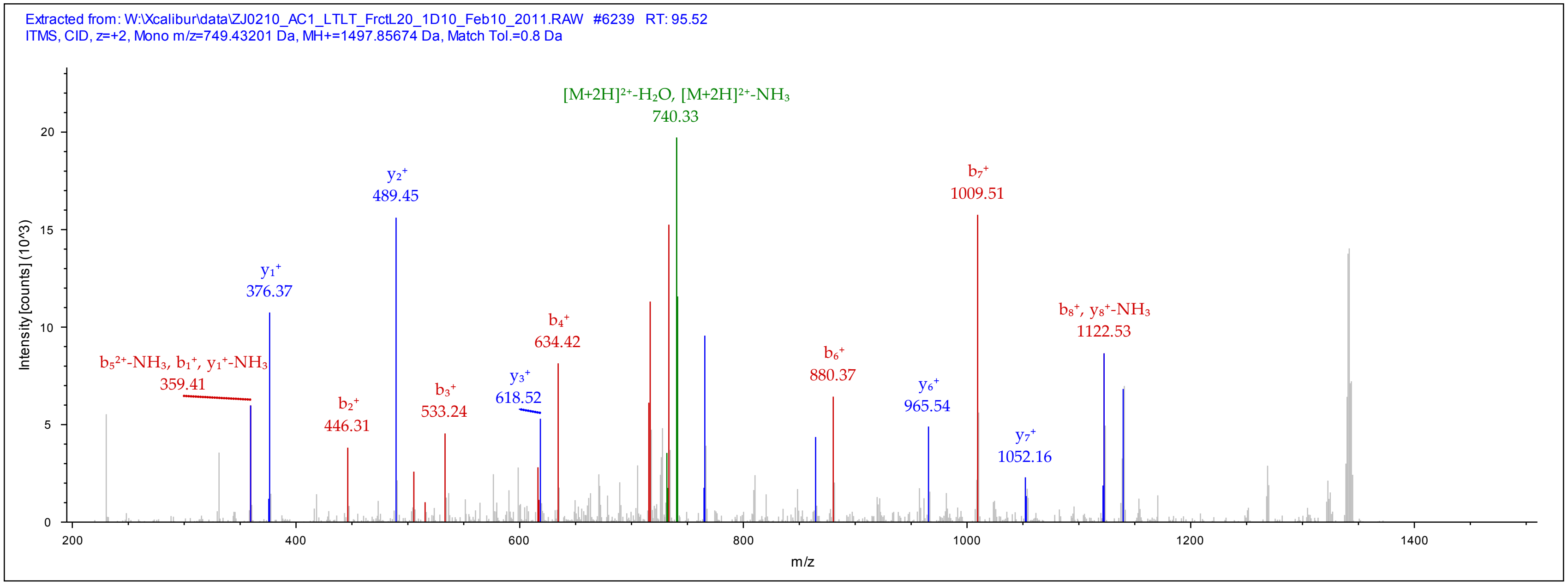
Identified with: Mascot (v1.16); IonScore:50, Exp Value:8.8E-004, Ions matched by search engine: 8/76

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Transcription elongation factor B polypeptide 2
- transcription elongation factor B polypeptide 2 isoform b
- Transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B), isoform CRA_b lng=113



IPI:IPI00921393.1

Sequence: RGAAAR, R1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 415.76855 Da (+7 mmu/+16.84 ppm), MH+: 830.52983 Da, RT: 79.99 min,

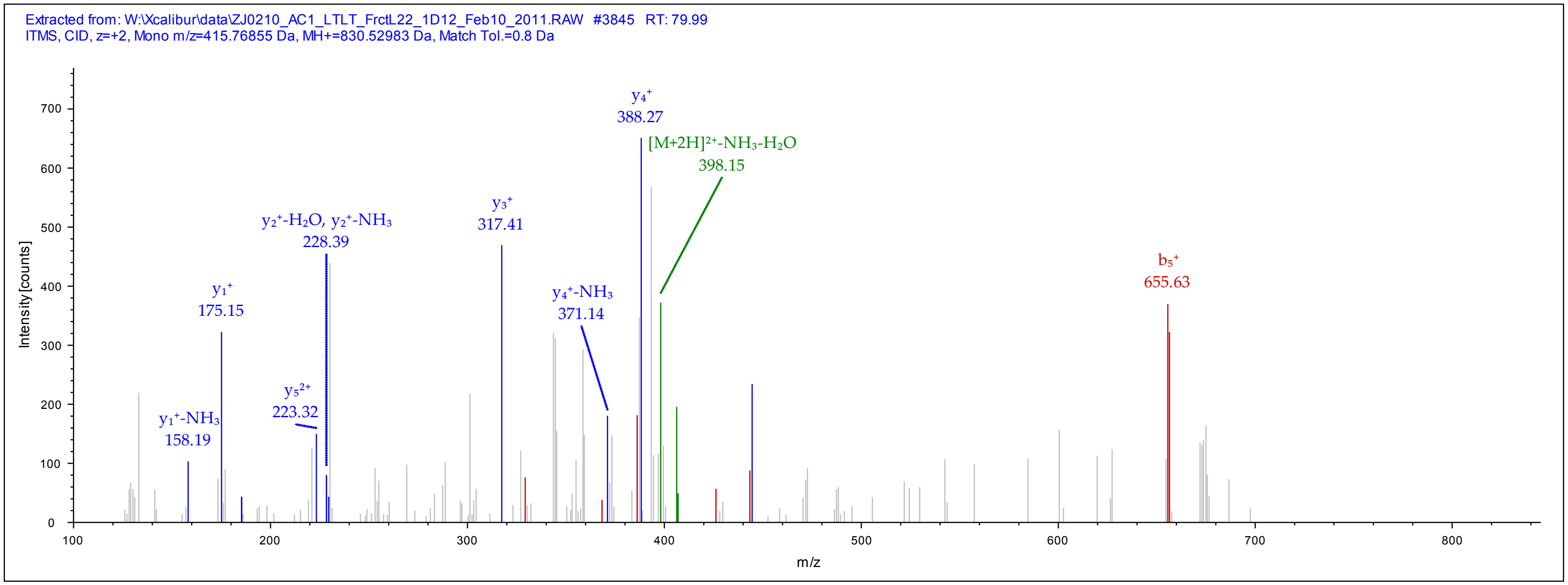
Identified with: Mascot (v1.16); IonScore:31, Exp Value:4.6E-002, Ions matched by search engine: 4/52

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- early growth response 4 lng=589
- Conserved hypothetical protein



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL22_1D12_Feb10_2011.RAW #3845 RT: 79.99
ITMS, CID, z=+2, Mono m/z=415.76855 Da, MH+=830.52983 Da, Match Tol.=0.8 Da

IPI00921944.1

Sequence: VPLLLEEQGVVDYFLR, V1-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 707.07312 Da (+1.56 mmu/+2.2 ppm),   MH+: 2119.20481 Da,   RT: 207.80 min,

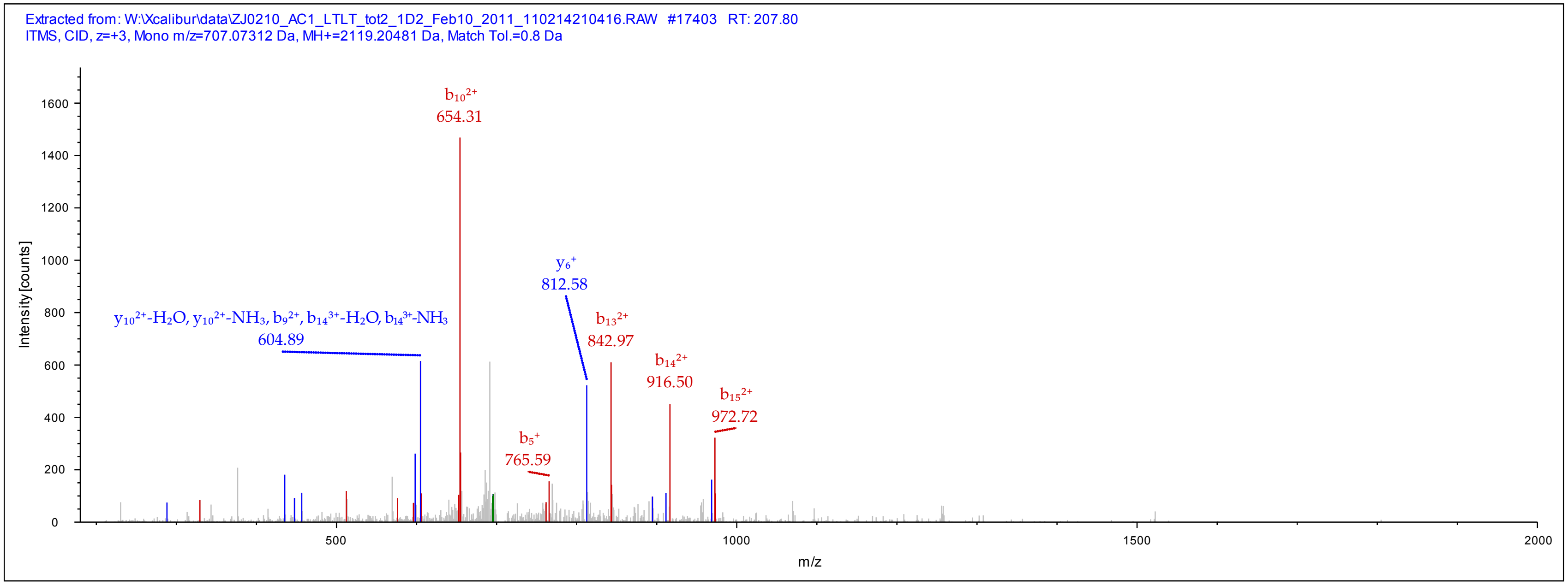
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.8E-002, Ions matched by search engine: 10/148

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- CTP synthase 1
- cDNA FLJ54863, highly similar to CTP synthase 1 lng=314


Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_tot2_1D2_Feb10_2011_110214210416.RAW   #17403   RT: 207.80
ITMS, CID, z=+3, Mono m/z=707.07312 Da, MH+=2119.20481 Da, Match Tol.=0.8 Da

IPI:IPI00921992.1

Sequence: QTIVPVCSYEER, Q1-TMT6plex (229.16293 Da), C7-Carbamidomethyl (57.02146 Da)

Charge: +2, Monoisotopic m/z: 855.44196 Da (+1.8 mmu/+2.1 ppm), MH+: 1709.87663 Da, RT: 91.79 min,

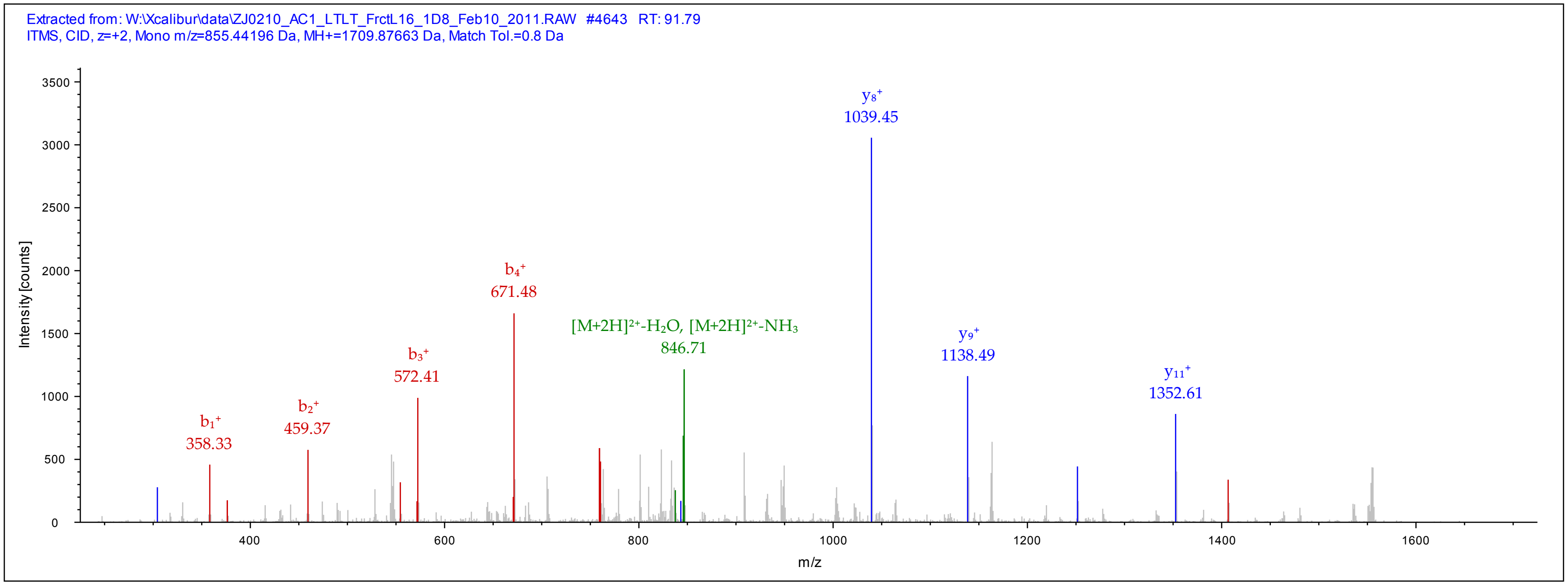
Identified with: Mascot (v1.16); IonScore:36, Exp Value:3.1E-002, Ions matched by search engine: 10/128

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of GDNF family receptor alpha-1
- Isoform 2 of GDNF family receptor alpha-1
- cDNA FLJ51412, highly similar to GDNF family receptor alpha-1



IPI:IPI00922108.1

Sequence: IYIGDDNPLTLIVK, I1-TMT6plex (229.16293 Da), K14-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 1016.60870 Da (+0.31 mmu/+0.3 ppm),   MH+: 2032.21013 Da,   RT: 183.94 min,

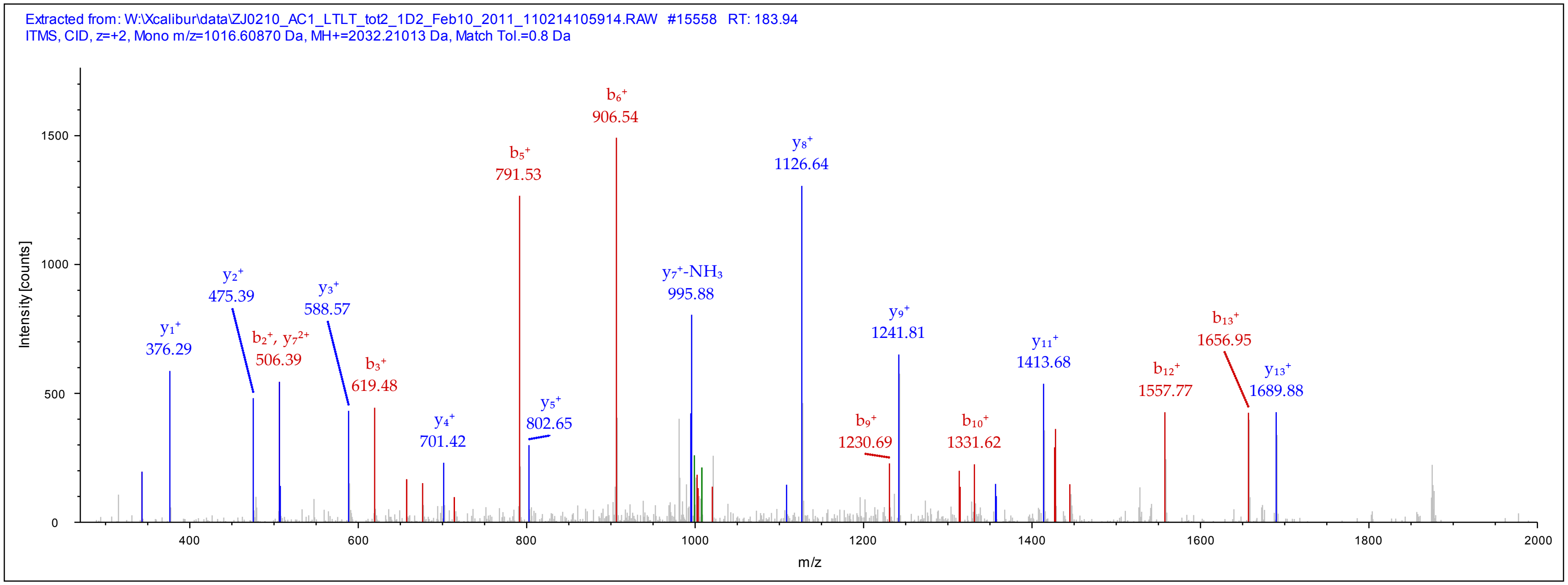
Identified with: Mascot (v1.16); IonScore:56, Exp Value:1.8E-004, Ions matched by search engine: 14/128

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Integrin alpha-V
- Isoform 2 of Integrin alpha-V
- integrin alpha-V isoform 2



IPI00922119.1

Sequence: ILLLEAGPK, I1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 706.47192 Da (+3.83 mmu/+5.42 ppm), MH+: 1411.93657 Da, RT: 268.32 min,

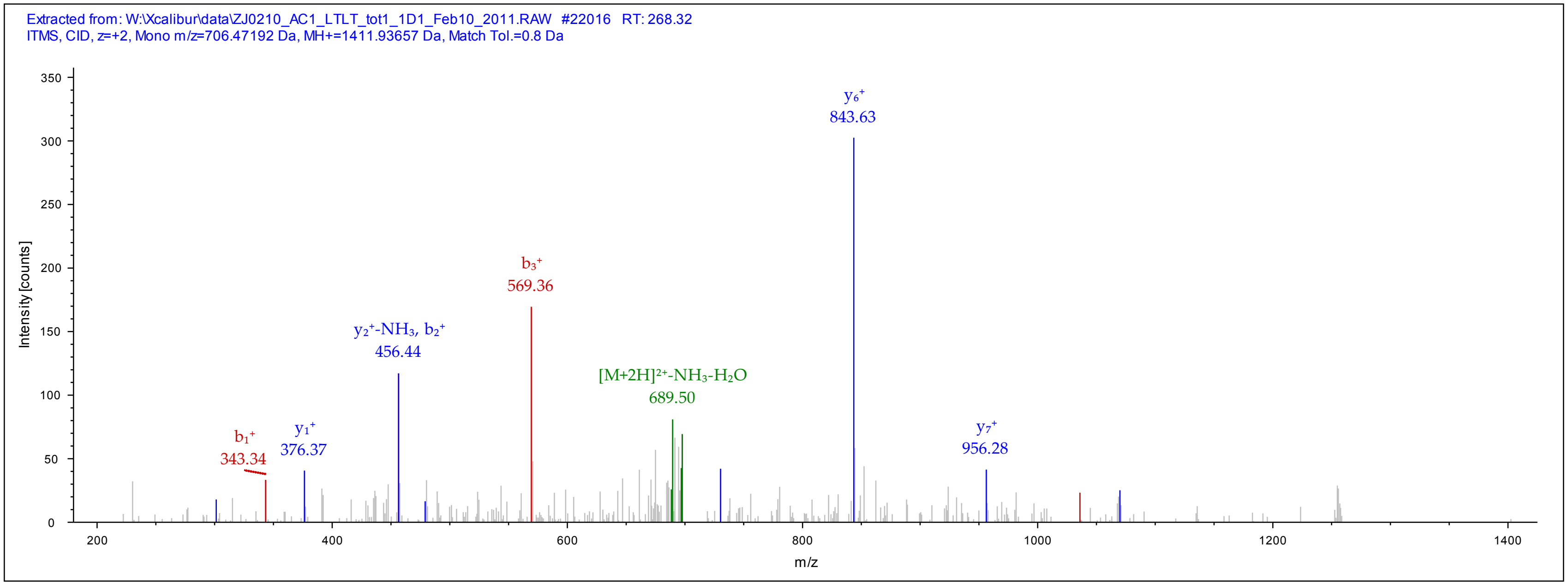
Identified with: Mascot (v1.16); IonScore:30, Exp Value:1.0E-002, Ions matched by search engine: 5/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Ubiquinone biosynthesis monooxygenase COQ6
- cDNA FLJ50973, highly similar to Ubiquinone biosynthesis monooxygenase COQ6 lng=443
- cDNA FLJ58993, highly similar to Ubiquinone biosynthesis monooxygenase COQ6 lng=233
- cDNA FLJ58904, highly similar to Ubiquinone biosynthesis monooxygenase COQ6 lng=146



IPI:IPI00922626.1

Sequence: LIPDDLSLLK, L1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 793.00311 Da (+0.61 mmu/+0.77 ppm), MH+: 1584.99895 Da, RT: 128.99 min,

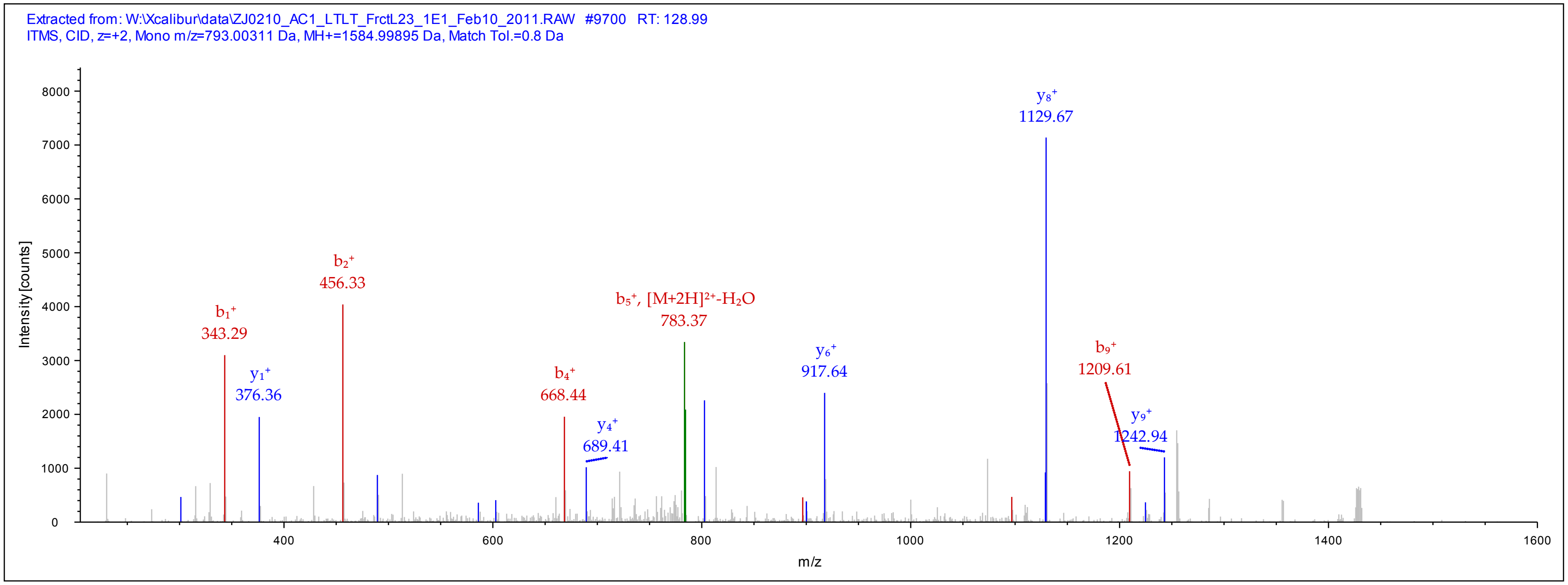
Identified with: Mascot (v1.16); IonScore:35, Exp Value:1.1E-002, Ions matched by search engine: 8/78

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of NFATC2-interacting protein
- cDNA FLJ57775, highly similar to Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein, mRNA



IPI:IPI00922847.1

Sequence: VFDVTK, V1-TMT6plex (229.16293 Da), K6-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 583.86340 Da (+0.48 mmu/+0.83 ppm), MH+: 1166.71953 Da, RT: 90.52 min,

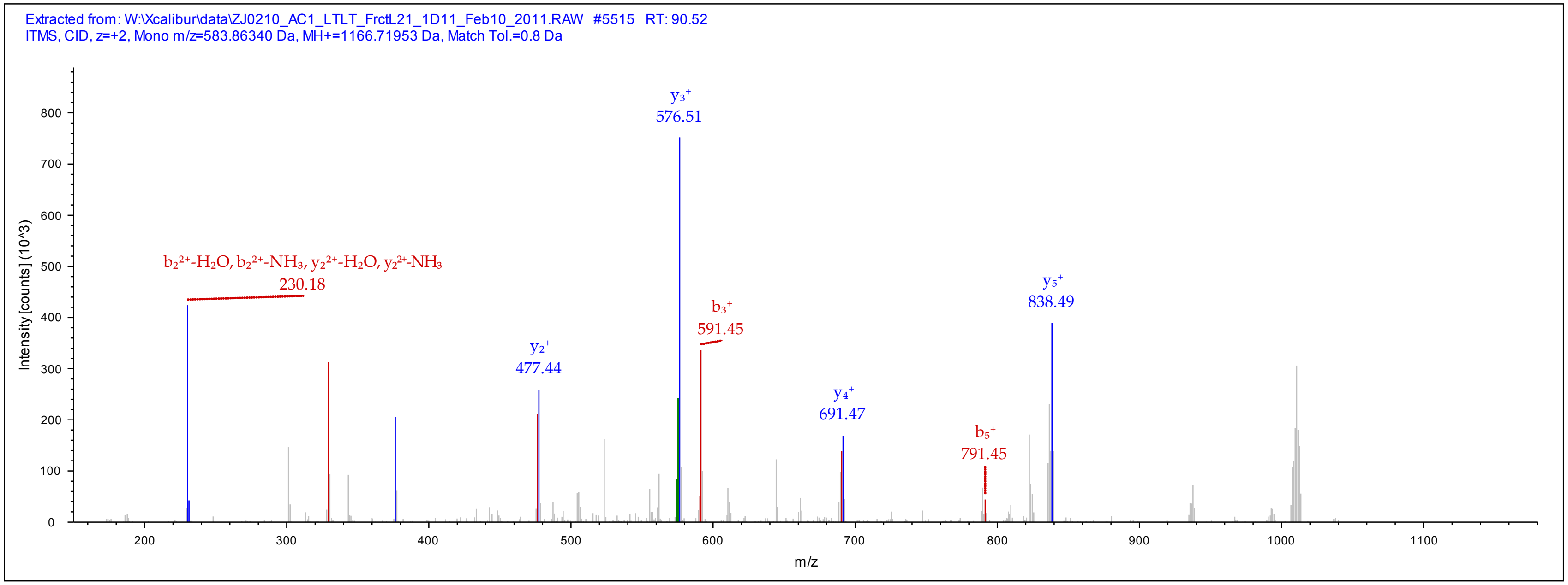
Identified with: Mascot (v1.16); IonScore:38, Exp Value:7.9E-003, Ions matched by search engine: 5/44

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Membrane-associated progesterone receptor component 1
- Membrane-associated progesterone receptor component 2 lng=247
- cDNA FLJ50115, moderately similar to Membrane-associated progesterone receptor component 1



IPI:IPI00924636.1

Sequence: LILEYVK, L1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 668.43628 Da (+0.03 mmu/+0.04 ppm), MH+: 1335.86528 Da, RT: 115.37 min,

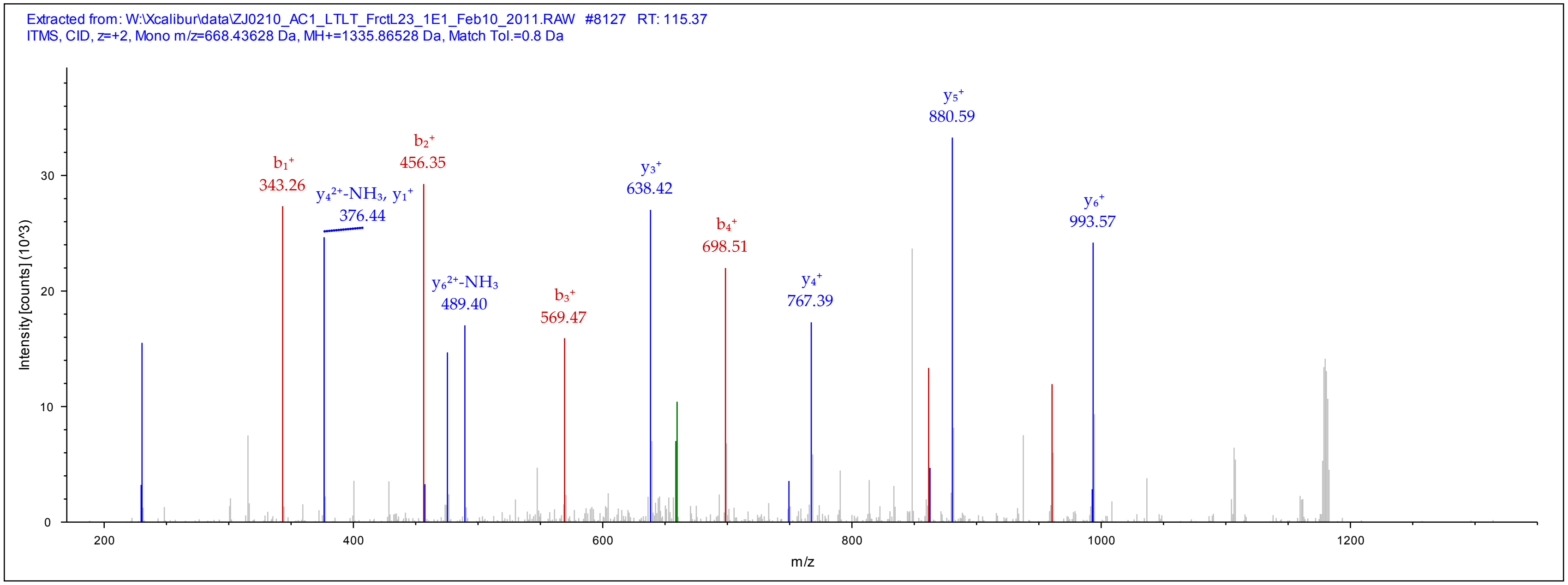
Identified with: Mascot (v1.16); IonScore:34, Exp Value:1.6E-002, Ions matched by search engine: 6/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- COP9 signalosome complex subunit 6
- cDNA, FLJ92300, Homo sapiens COP9 subunit 6 (MOV34 homolog, 34 kD) (COPS6), mRNA
- 36 kDa protein



IPI00924714.1

Sequence: IVDVIGEK, I1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 665.92108 Da (+0.11 mmu/+0.16 ppm), MH+: 1330.83489 Da, RT: 100.91 min,

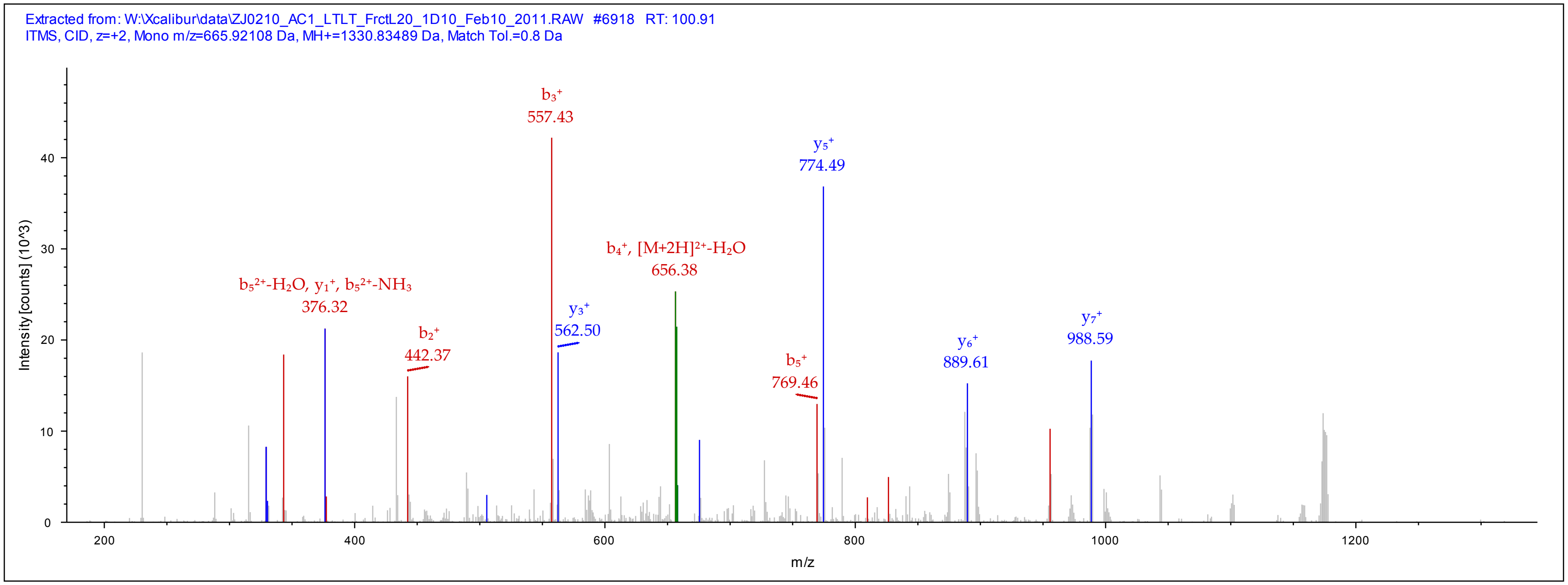
Identified with: Mascot (v1.16); IonScore:30, Exp Value:6.1E-002, Ions matched by search engine: 7/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- cAMP-dependent protein kinase type II-alpha regulatory subunit
- Protein kinase, cAMP-dependent, regulatory, type II, alpha, isoform CRA_b lng=382
- 38 kDa protein lng=337
- 36 kDa protein lng=315
- Putative uncharacterized protein PRKAR2A lng=99



IPI:IPI00924735.1

Sequence: DSTGTYTCVAR, D1-TMT6plex (229.16293 Da), C8-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 730.35730 Da (+1.21 mmu/+1.66 ppm),   MH+: 1459.70732 Da,   RT: 70.85 min,

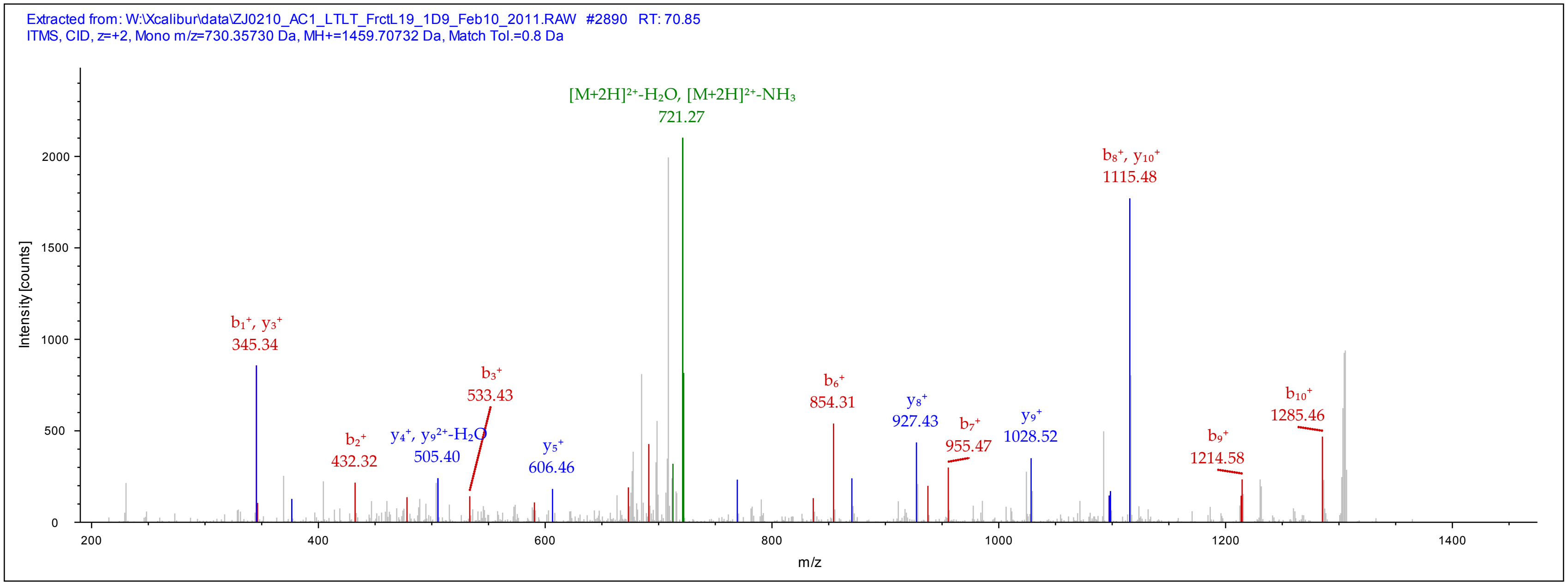
Identified with: Mascot (v1.16); IonScore:54, Exp Value:2.4E-004, Ions matched by search engine: 10/92

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Isoform 1 of Neuronal cell adhesion molecule
- Isoform 4 of Neuronal cell adhesion molecule
- Isoform 2 of Neuronal cell adhesion molecule
- Isoform 3 of Neuronal cell adhesion molecule
- Isoform 5 of Neuronal cell adhesion molecule
- NRCAM protein
- NRCAM protein



IPI00924931.1

Sequence: VSSIDLEIDSLSSLLDDMTK, V1-TMT6plex (229.16293 Da), K20-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 880.47833 Da (+3.4 mmu/+3.86 ppm), MH+: 2639.42044 Da, RT: 222.79 min,

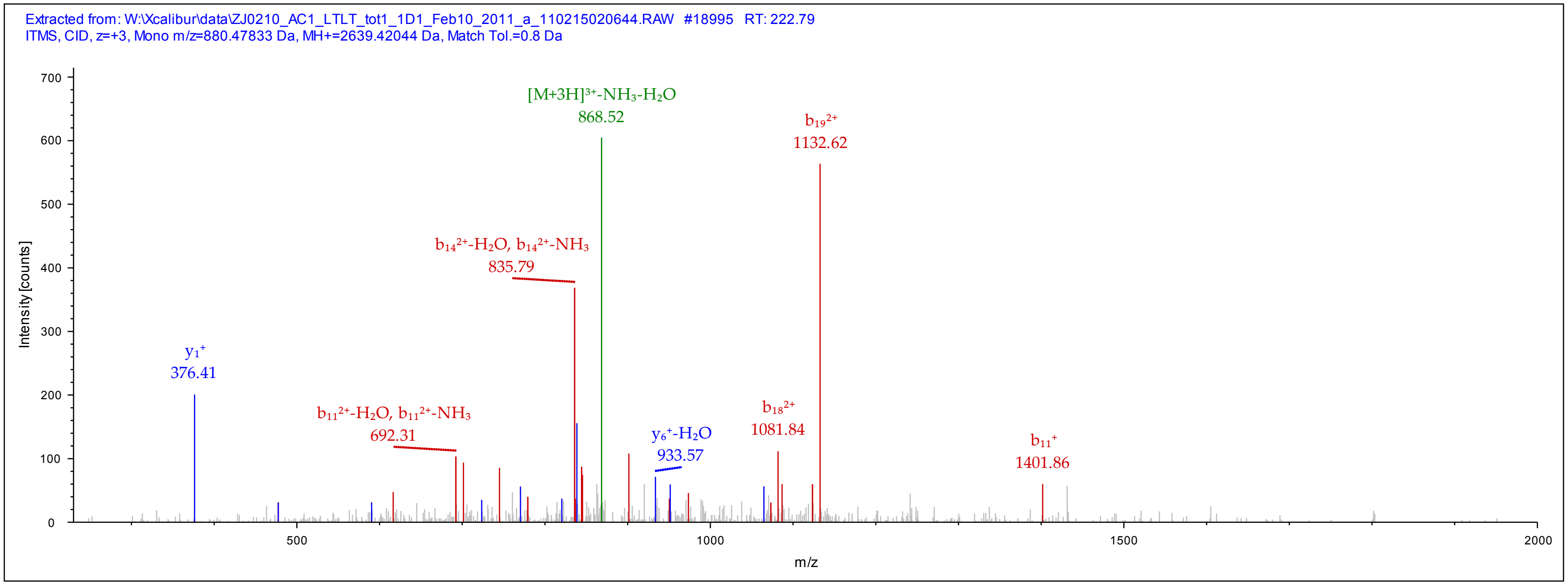
Identified with: Mascot (v1.16); IonScore:52, Exp Value:9.9E-004, Ions matched by search engine: 26/186

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Zyxin
- Putative uncharacterized protein ZYX lng=164
- 19 kDa protein



IPI00925248.1

Sequence: NAYVWTLK, N1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 726.93396 Da (-0.45 mmu/-0.61 ppm),   MH+: 1452.86064 Da,   RT: 106.71 min,

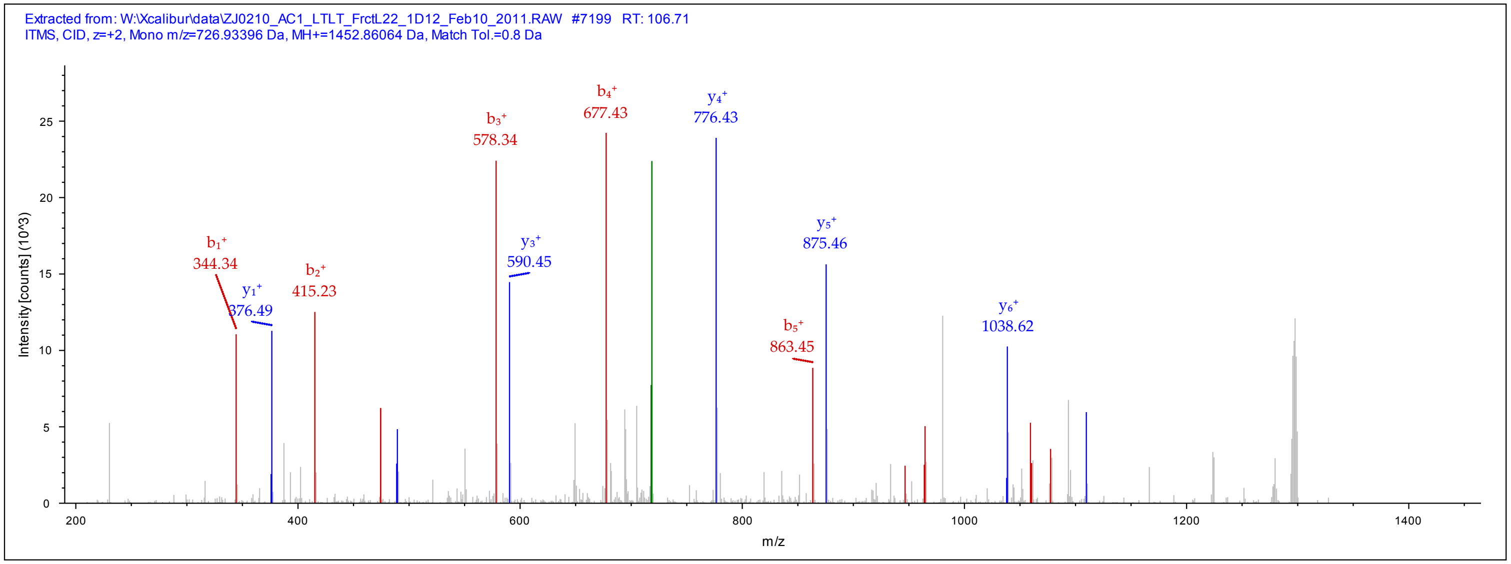
Identified with: Mascot (v1.16); IonScore:31, Exp Value:6.4E-002, Ions matched by search engine: 11/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (9):

- Actin-related protein 2/3 complex subunit 1B
- similar to actin related protein 2/3 complex subunit 1B lng=370
- Putative uncharacterized protein ARPC1B lng=130
- Putative uncharacterized protein ARPC1B lng=133
- Putative uncharacterized protein ARPC1B lng=83
- Putative uncharacterized protein ARPC1B lng=102
- Putative uncharacterized protein ARPC1B lng=213
- Putative uncharacterized protein ARPC1B lng=128



IPI:IPI00925369.1

Sequence: VVLPTFILEK, V1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 809.02441 Da (+1.18 mmu/+1.46 ppm), MH+: 1617.04155 Da, RT: 135.20 min,

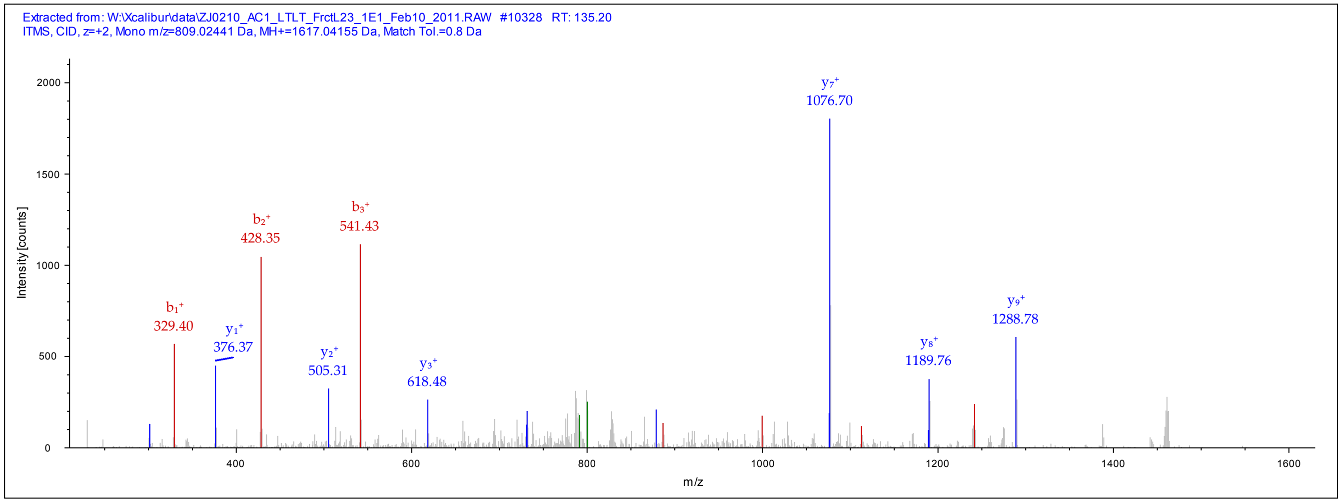
Identified with: Mascot (v1.16); IonScore:33, Exp Value:1.6E-002, Ions matched by search engine: 9/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Oxysterol-binding protein-related protein 11
- Oxysterol-binding protein-related protein 10
- Oxysterol-binding protein lng=745
- oxysterol-binding protein-like protein 10 isoform 2
- 20 kDa protein
- Oxysterol-binding protein



IPI00925852.1

Sequence: VIIDTLITK, V1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 737.48669 Da (+0.21 mmu/+0.29 ppm),   MH+: 1473.96611 Da,   RT: 124.36 min,

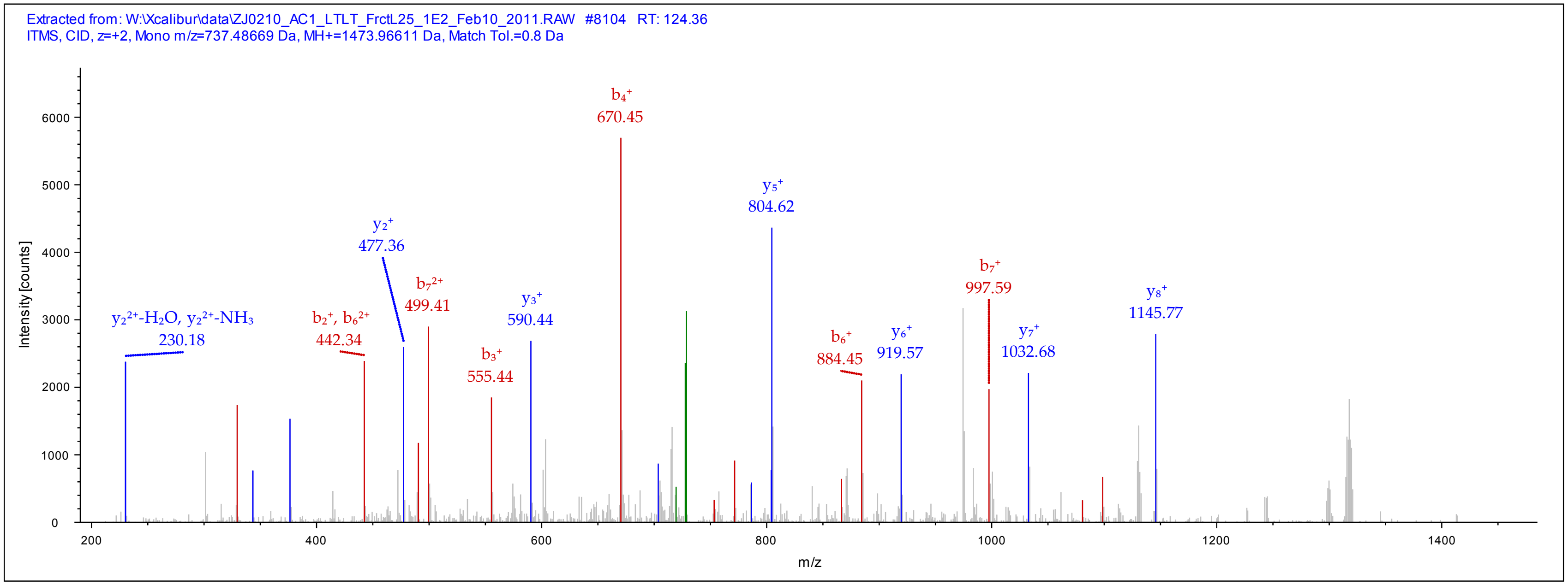
Identified with: Mascot (v1.16); IonScore:39, Exp Value:2.7E-003, Ions matched by search engine: 8/72

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform Long of Transcription intermediary factor 1-alpha
- Isoform Short of Transcription intermediary factor 1-alpha
- cDNA FLJ45687 fis, clone FCBBF3020030, highly similar to Transcription intermediary factor 1-alpha
- Putative uncharacterized protein TRIM24 lng=442



IPI00926412.1

Sequence: IIAALFK, I1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 617.42224 Da (+1.83 mmu/+2.97 ppm),   MH+: 1233.83721 Da,   RT: 132.23 min,

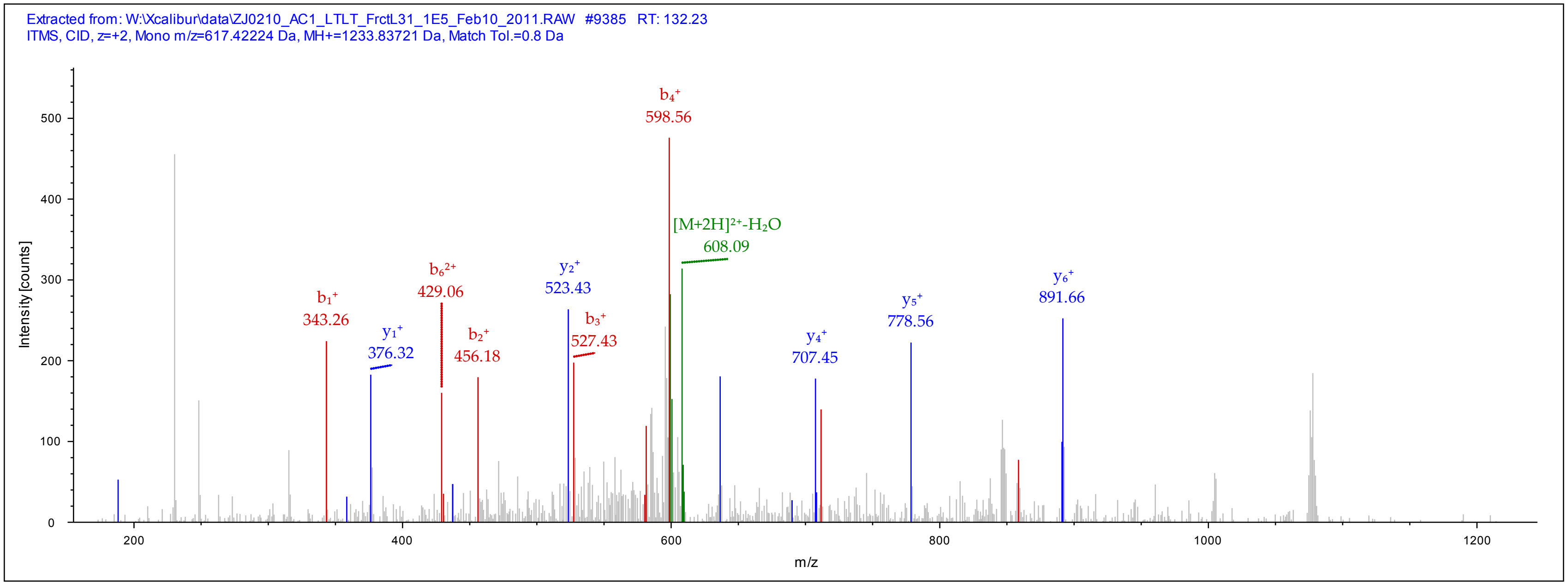
Identified with: Mascot (v1.16); IonScore:32, Exp Value:4.4E-002, Ions matched by search engine: 5/50

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 1 of Transformation/transcription domain-associated protein
- Isoform 2 of Transformation/transcription domain-associated protein
- 436 kDa protein lng=3848
- Transformation/transcription domain-associated protein variant lng=3588



IPI:IPI00927003.1

Sequence: IITGGAAAQDGR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 679.88605 Da (+2.9 mmu/+4.27 ppm), MH+: 1358.76482 Da, RT: 77.10 min,

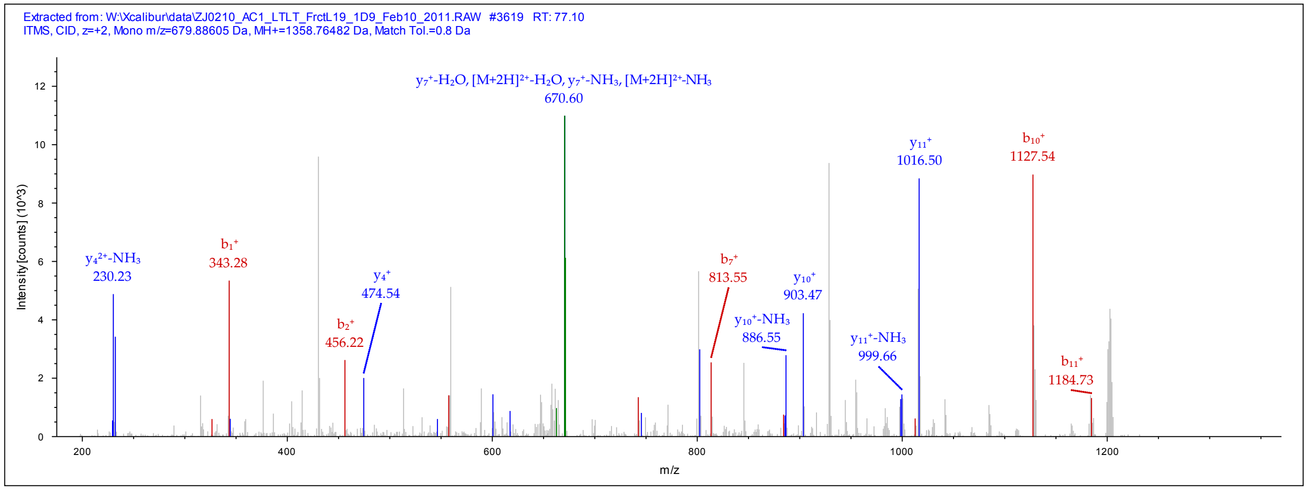
Identified with: Mascot (v1.16); IonScore:37, Exp Value:1.6E-002, Ions matched by search engine: 9/108

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (11):

- Isoform 1 of Disks large homolog 1
- Isoform 2 of Disks large homolog 1
- Isoform 6 of Disks large homolog 1
- Isoform 7 of Disks large homolog 1
- Isoform 4 of Disks large homolog 1
- Isoform 5 of Disks large homolog 1
- Isoform 3 of Disks large homolog 1
- cDNA FLJ50509, highly similar to Disks large homolog 1 lng=788
- cDNA FLJ58166, highly similar to Disks large homolog 1
- Uncharacterized protein
- 30 kDa protein



IPI00927476.1

Sequence: EVDILR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 487.29773 Da (+0.09 mmu/+0.18 ppm), MH+: 973.58818 Da, RT: 100.44 min,

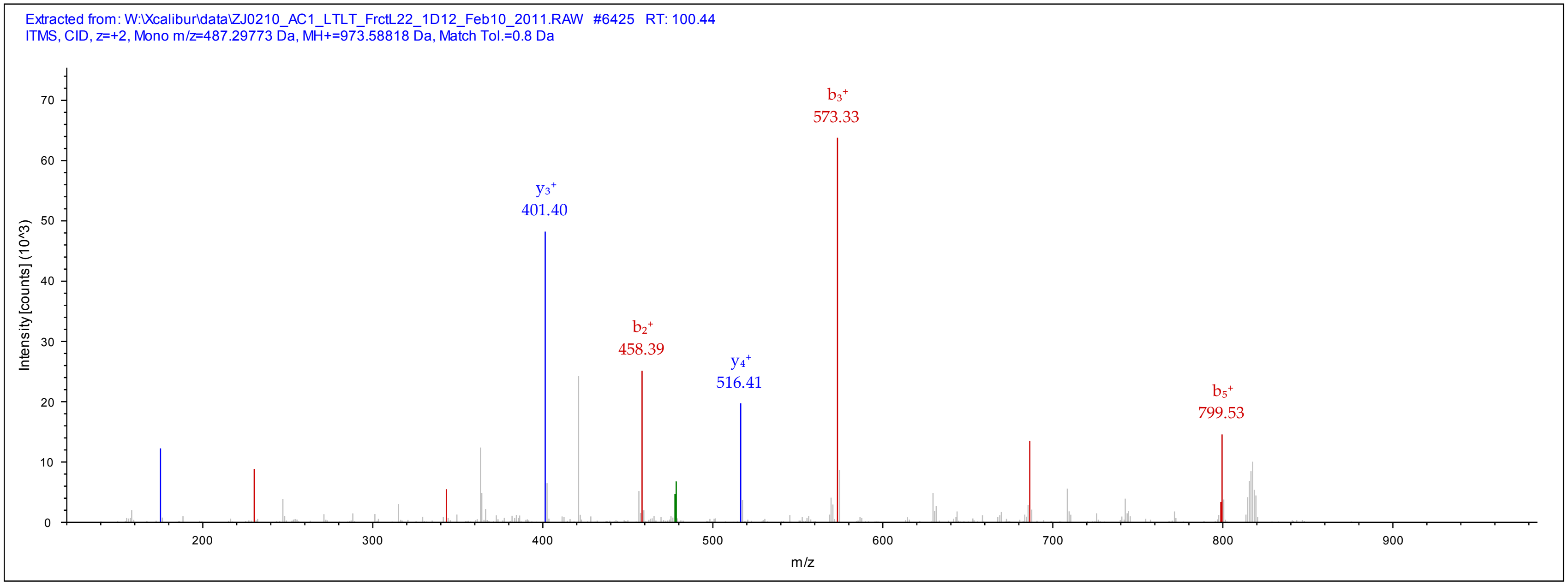
Identified with: Mascot (v1.16); IonScore:30, Exp Value:6.3E-002, Ions matched by search engine: 4/44

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- mRNA-decapping enzyme 1B
- PHKG1 protein lng=390
- 13 kDa protein lng=112
- 30 kDa protein lng=275
- mRNA-decapping enzyme 1B
- cDNA FLJ51787, highly similar to Phosphorylase b kinase gamma catalytic chain, skeletal muscle isoform lng=419



IPI00929107.1

Sequence: LVQIASR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 508.32718 Da (+0.45 mmu/+0.88 ppm),   MH+: 1015.64708 Da,   RT: 80.97 min,

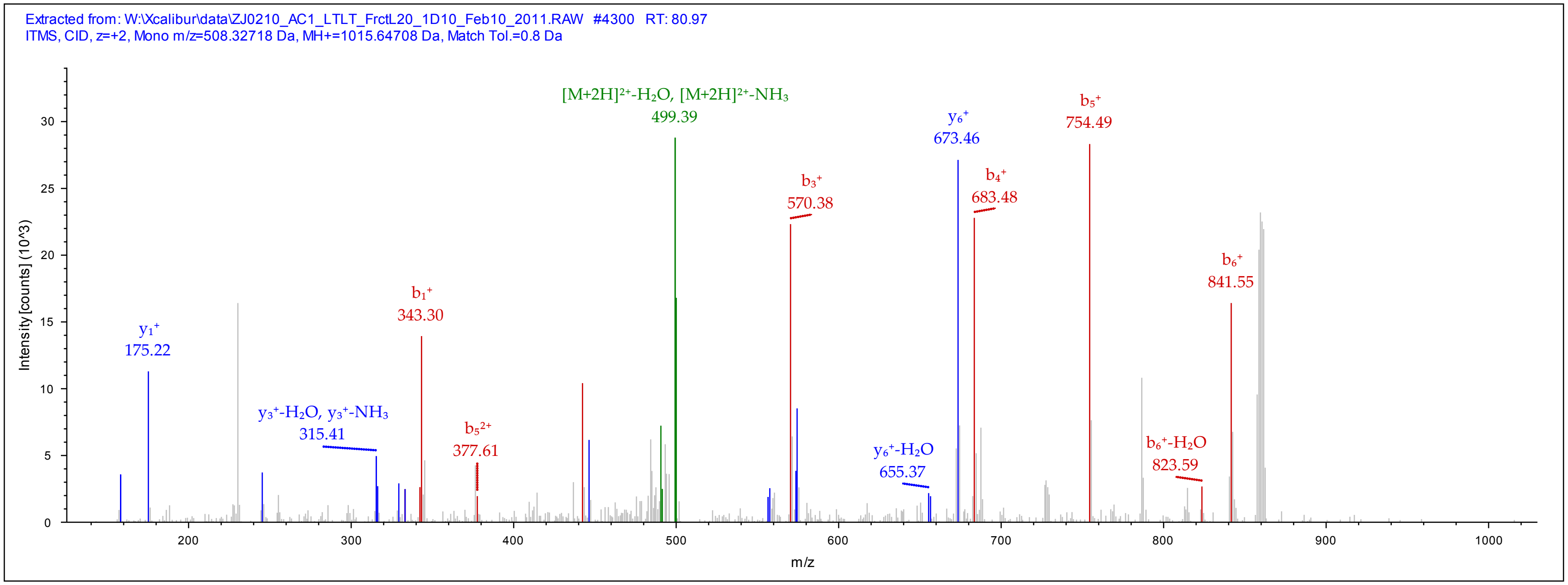
Identified with: Mascot (v1.16); IonScore:41, Exp Value:3.0E-003, Ions matched by search engine: 6/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Heterogeneous nuclear ribonucleoprotein U-like protein 2
- Seipin lng=746



IPI00929618.1

Sequence: DQVDAEAHPVR, D1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 733.38165 Da (-1.85 mmu/-2.53 ppm),   MH+: 1465.75603 Da,   RT: 79.07 min,

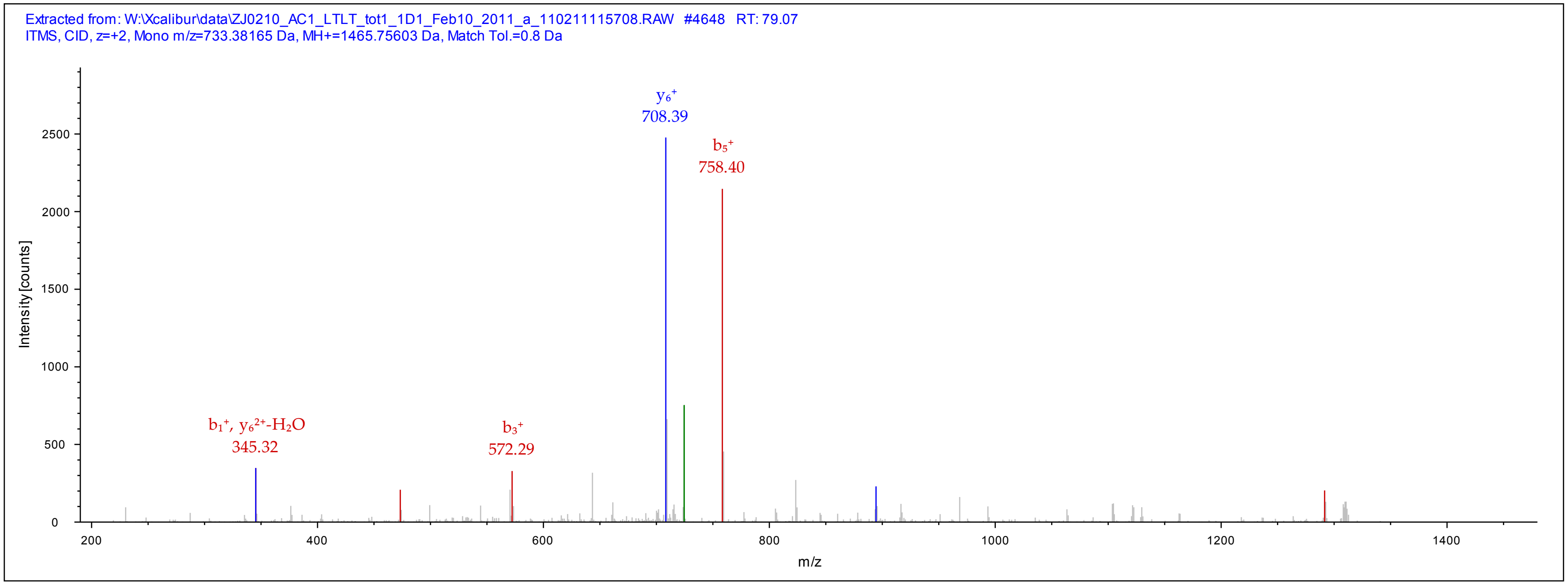
Identified with: Mascot (v1.16); IonScore:31, Exp Value:7.0E-002, Ions matched by search engine: 5/108

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Conserved hypothetical protein lng=48



IPI:IPI00929627.2

Sequence: DIELVMAQANVSR, D1-TMT6plex (229.16293 Da), M6-Oxidation (15.99492 Da)

Charge: +2,   Monoisotopic m/z: 845.95435 Da (+0.9 mmu/+1.06 ppm),   MH+: 1690.90141 Da,   RT: 103.26 min,

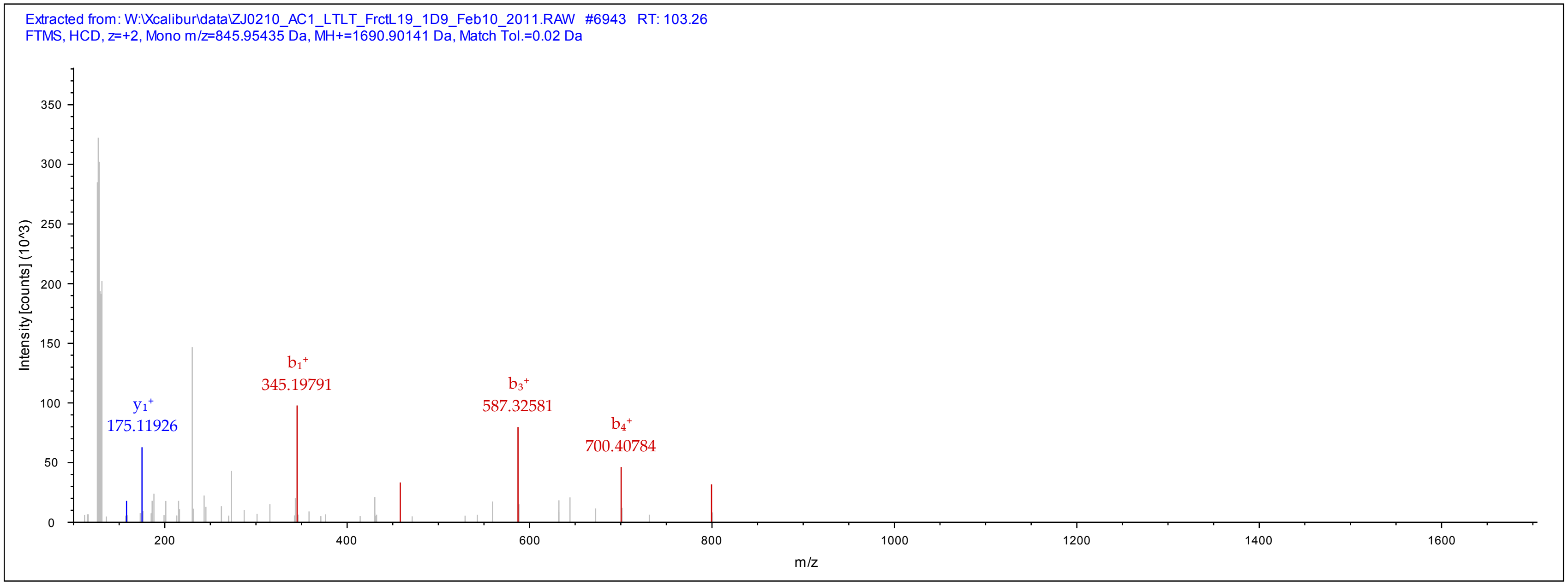
Identified with: Mascot (v1.16); IonScore:29, Exp Value:1.4E-001, Ions matched by search engine: 5/128

Fragment match tolerance used for search: 0.02 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- NAC-alpha domain-containing protein 1
- Similar to Nascent polypeptide-associated complex subunit alpha lng=2123



IPI:IPI00929742.1

Sequence: GFLVLEGK, G1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 660.91888 Da (+0.65 mmu/+0.98 ppm), MH+: 1320.83049 Da, RT: 114.61 min,

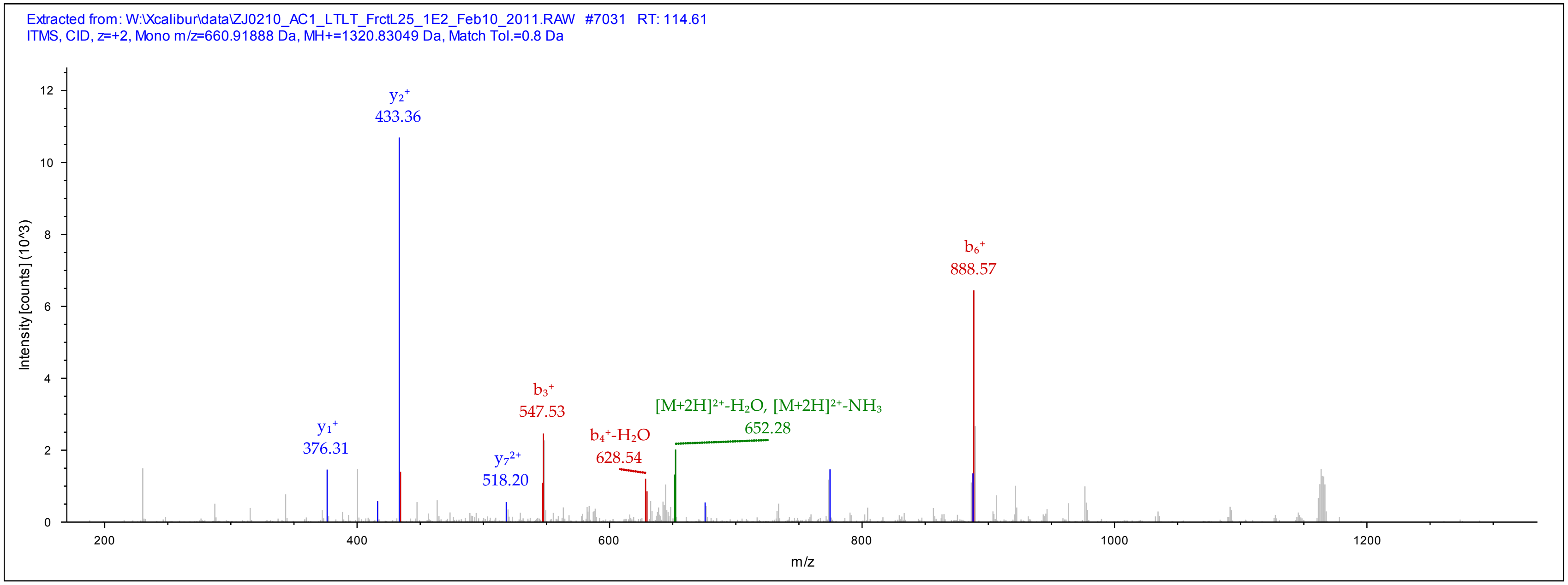
Identified with: Mascot (v1.16); IonScore:29, Exp Value:7.2E-002, Ions matched by search engine: 5/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Conserved hypothetical protein



IPI00930490.1

Sequence: LIELLAGK, L1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 657.94360 Da (+1.89 mmu/+2.88 ppm), MH+: 1314.87993 Da, RT: 130.27 min,

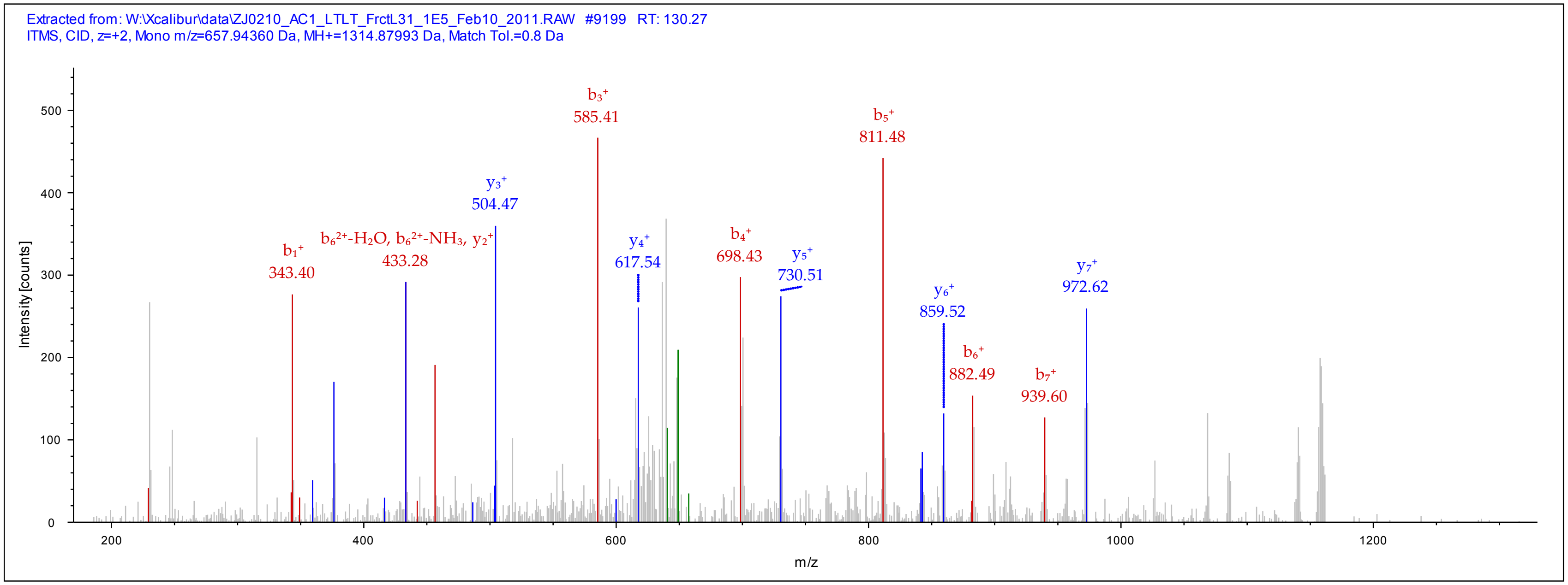
Identified with: Mascot (v1.16); IonScore:36, Exp Value:3.9E-003, Ions matched by search engine: 11/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- DNA-directed RNA polymerase III subunit RPC2
- DNA-directed RNA polymerase III B isoform 2 lng=1075



IPI00935732.1

Sequence: NIPMTLELLQSTR, N1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 872.99487 Da (-0.24 mmu/-0.27 ppm),   MH+: 1744.98247 Da,   RT: 123.85 min,

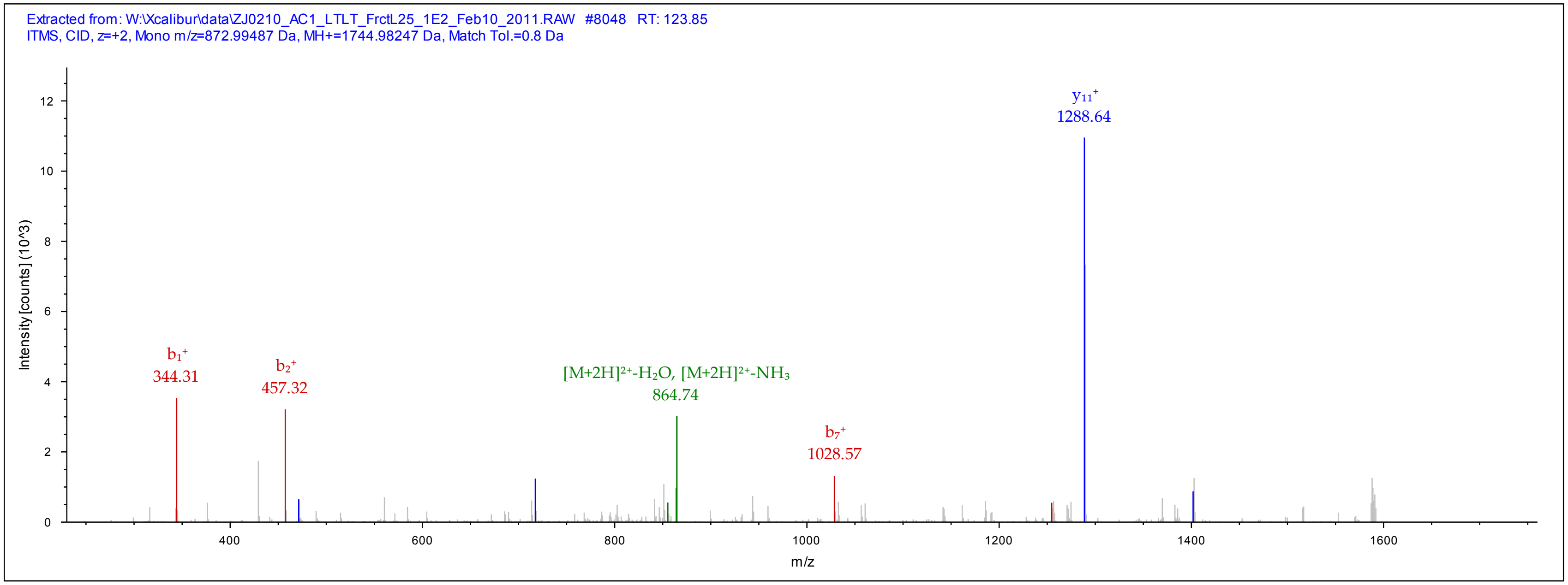
Identified with: Mascot (v1.16); IonScore:45, Exp Value:3.7E-003, Ions matched by search engine: 11/134

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Transcription elongation factor A protein 1
- hypothetical protein XP_002347041 lng=287
- 34 kDa protein lng=301



IPI:IPI00937554.1

Sequence: EVDAEYEAR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 655.82587 Da (+0.92 mmu/+1.4 ppm), MH+: 1310.64446 Da, RT: 71.97 min,

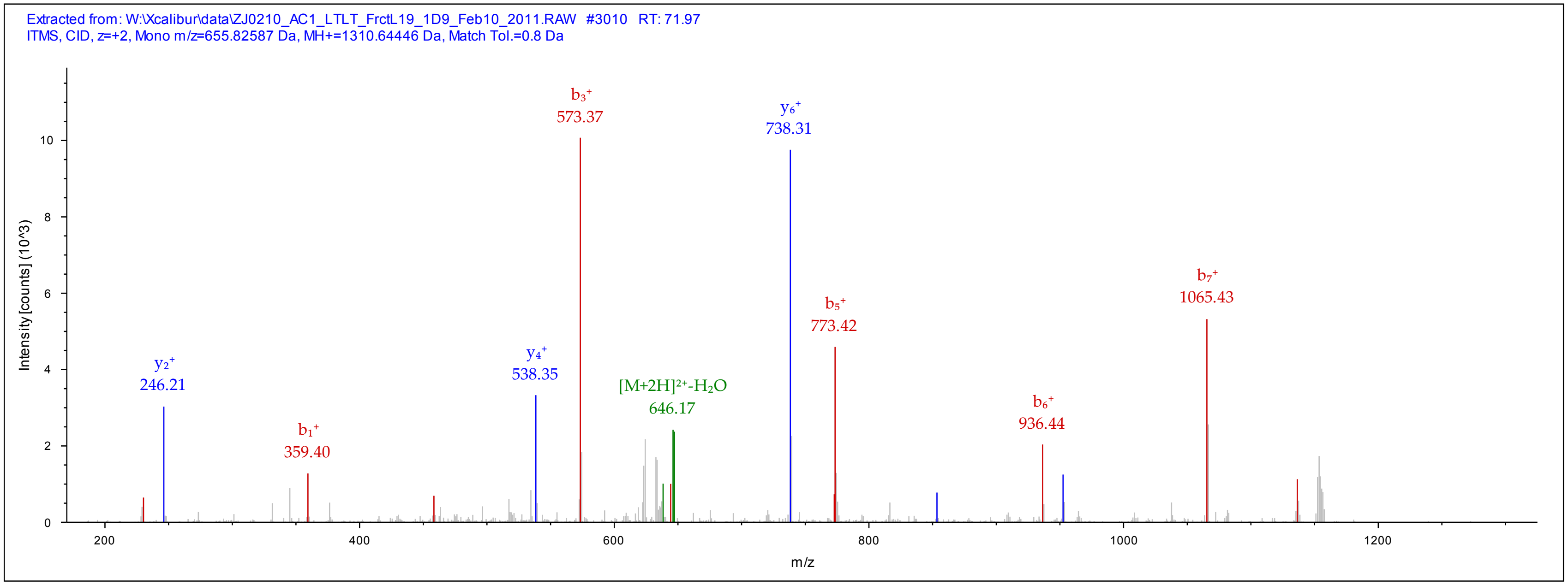
Identified with: Mascot (v1.16); IonScore:35, Exp Value:2.1E-002, Ions matched by search engine: 5/76

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- ADP-ribosylation factor GTPase-activating protein 2
- Putative uncharacterized protein ARFGAP2 lng=521
- cDNA FLJ41005 fis, clone UTERU2017613, highly similar to Homo sapiens zinc finger protein 289, ID1 regulated (ZNF289), mRNA
- cDNA FLJ58830, highly similar to Homo sapiens zinc finger protein 289, ID1 regulated (ZNF289), mRNA
- cDNA FLJ53674, highly similar to Homo sapiens zinc finger protein 289, ID1 regulated (ZNF289), mRNA



IPI00937682.1

Sequence: FFLEETLVR, F1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 691.89954 Da (+1.81 mmu/+2.62 ppm), MH+: 1382.79180 Da, RT: 125.79 min,

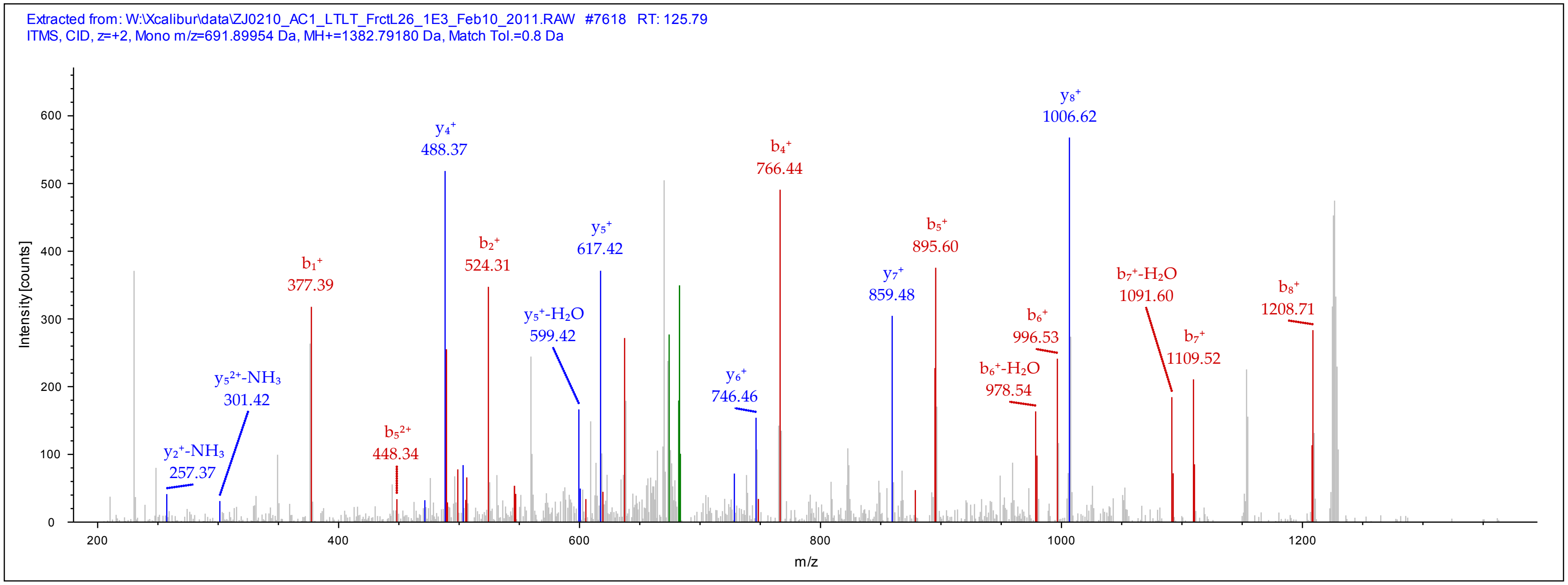
Identified with: Mascot (v1.16); IonScore:33, Exp Value:3.8E-002, Ions matched by search engine: 11/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of Opioid growth factor receptor
- Isoform 2 of Opioid growth factor receptor
- OGFR protein lng=513
- OGFR protein lng=660



IPI00937699.1

Sequence: DADLGIR, D1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 494.79239 Da (+7.5 mmu/+15.15 ppm), MH+: 988.57750 Da, RT: 97.00 min,

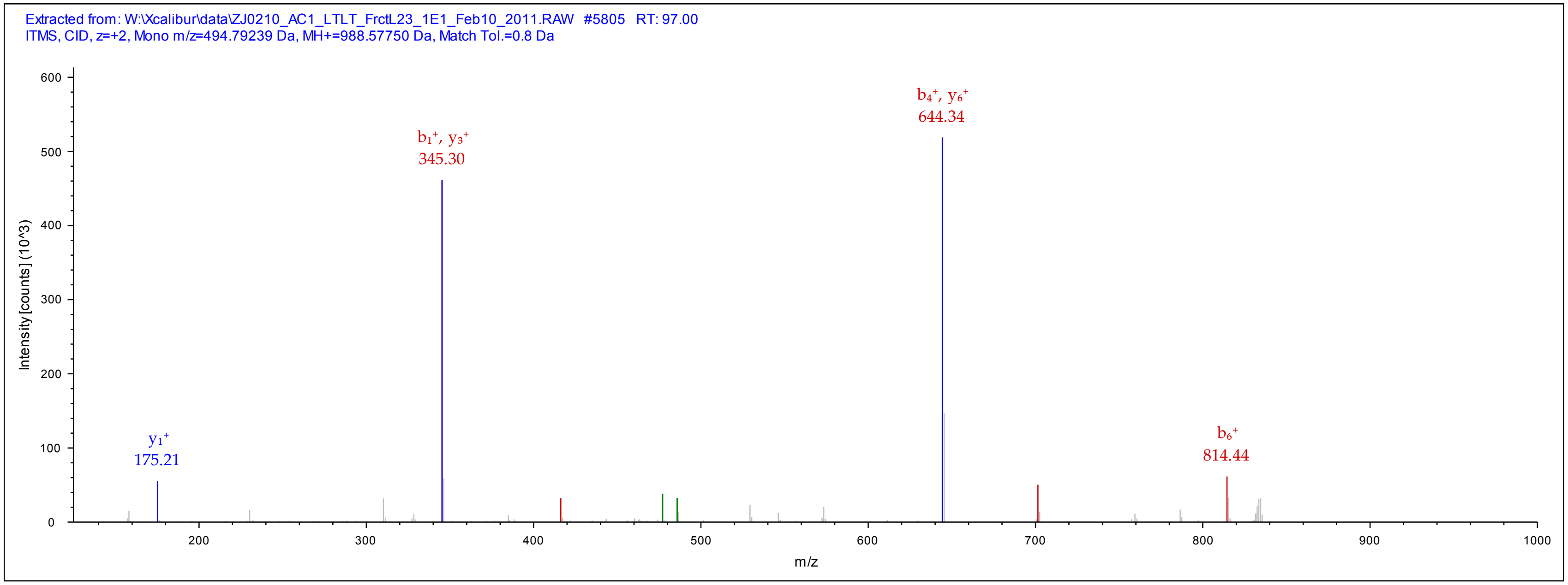
Identified with: Mascot (v1.16); IonScore:31, Exp Value:4.7E-002, Ions matched by search engine: 4/52

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- hypothetical protein XP_002343315 lng=219



IPI00939322.1

Sequence: ETAIEVGK, E1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 652.89563 Da (+0.67 mmu/+1.03 ppm), MH+: 1304.78398 Da, RT: 79.24 min,

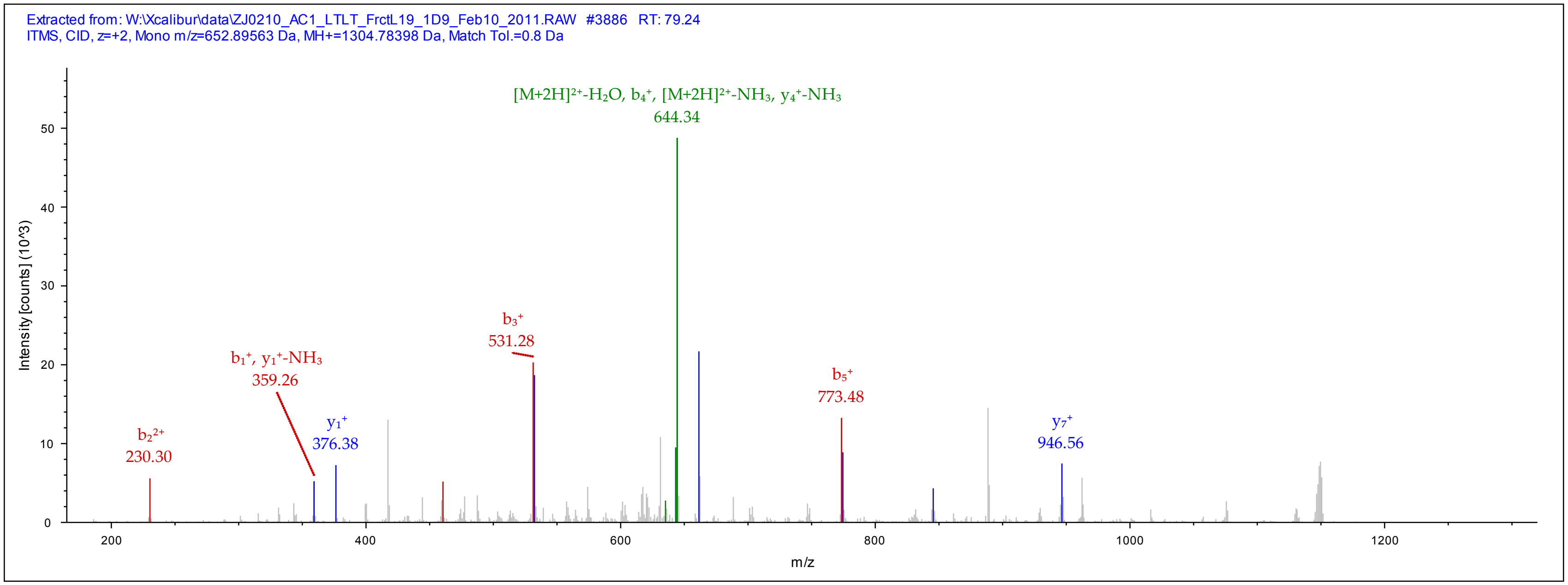
Identified with: Mascot (v1.16); IonScore:35, Exp Value:2.9E-002, Ions matched by search engine: 6/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Centrosomal protein POC5
- Isoform 3 of Centrosomal protein POC5
- Putative uncharacterized protein C5orf37 (Fragment) lng=549



IPI00939648.1

Sequence: TYDETYQR, T1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 652.82196 Da (+2.31 mmu/+3.54 ppm),   MH+: 1304.63664 Da,   RT: 67.13 min,

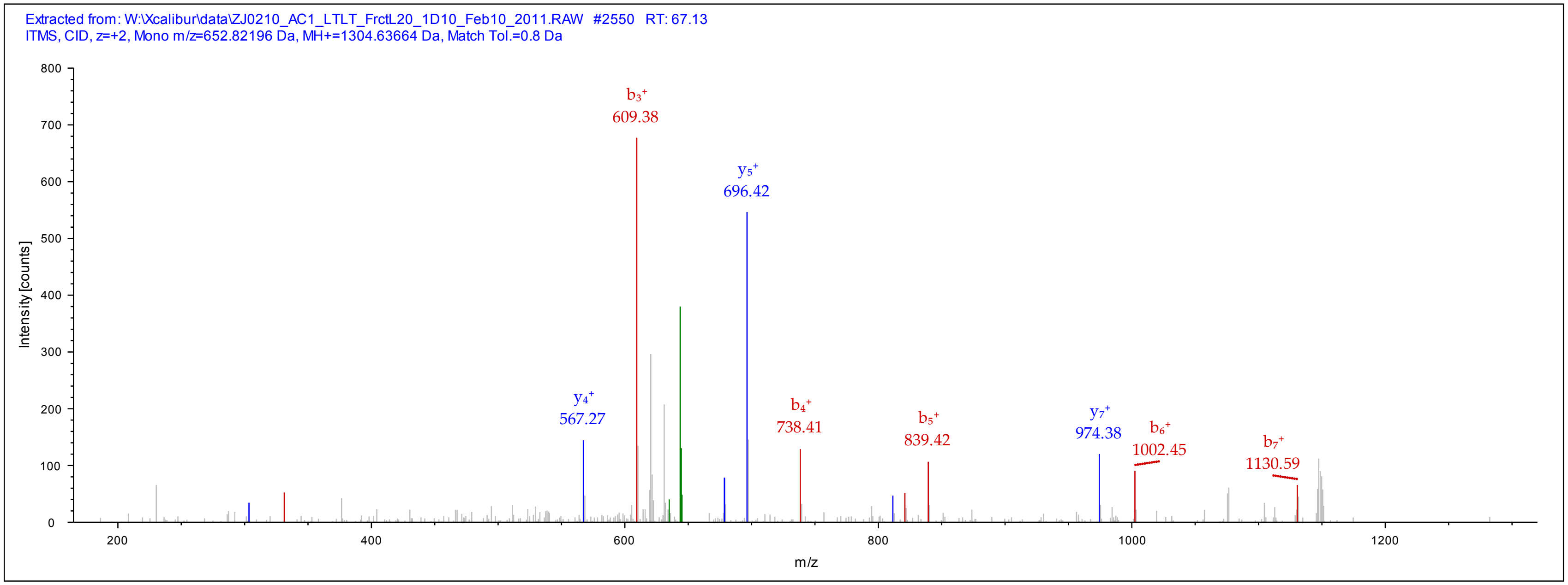
Identified with: Mascot (v1.16); IonScore:31, Exp Value:4.1E-002, Ions matched by search engine: 7/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of Protein phosphatase 1 regulatory subunit 12A
- Isoform 2 of Protein phosphatase 1 regulatory subunit 12A
- Isoform 4 of Protein phosphatase 1 regulatory subunit 12A
- Isoform 3 of Protein phosphatase 1 regulatory subunit 12A
- protein phosphatase 1, regulatory (inhibitor) subunit 12A isoform b lng=943



IPI00940107.1

Sequence: VVLLTEVDK, V1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 737.46918 Da (+0.89 mmu/+1.2 ppm),   MH+: 1473.93108 Da,   RT: 107.68 min,

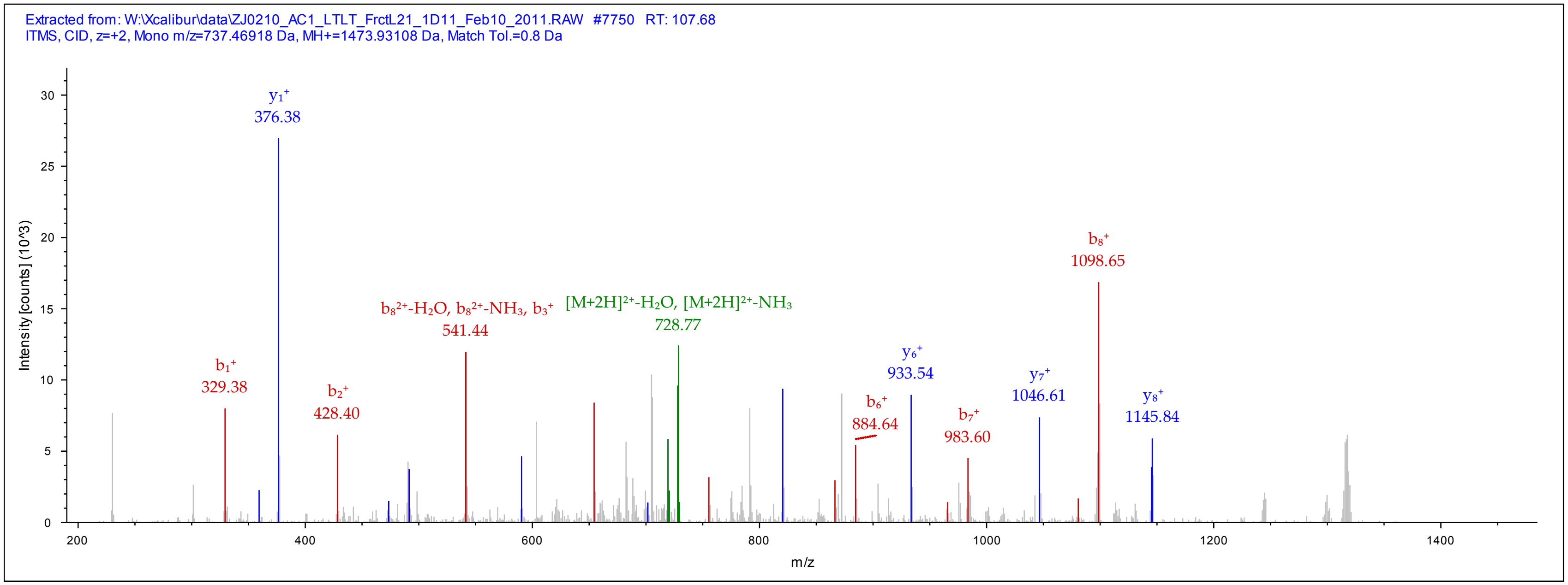
Identified with: Mascot (v1.16); IonScore:32, Exp Value:3.2E-002, Ions matched by search engine: 8/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Replication factor C subunit 3
- replication factor C subunit 3 isoform 2
- Putative uncharacterized protein RFC3 lng=300



IPI00940880.1

Sequence: LTSAVSSLPELLEK, L1-TMT6plex (229.16293 Da), K14-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 973.08728 Da (+2.53 mmu/+2.6 ppm),   MH+: 1945.16728 Da,   RT: 132.20 min,

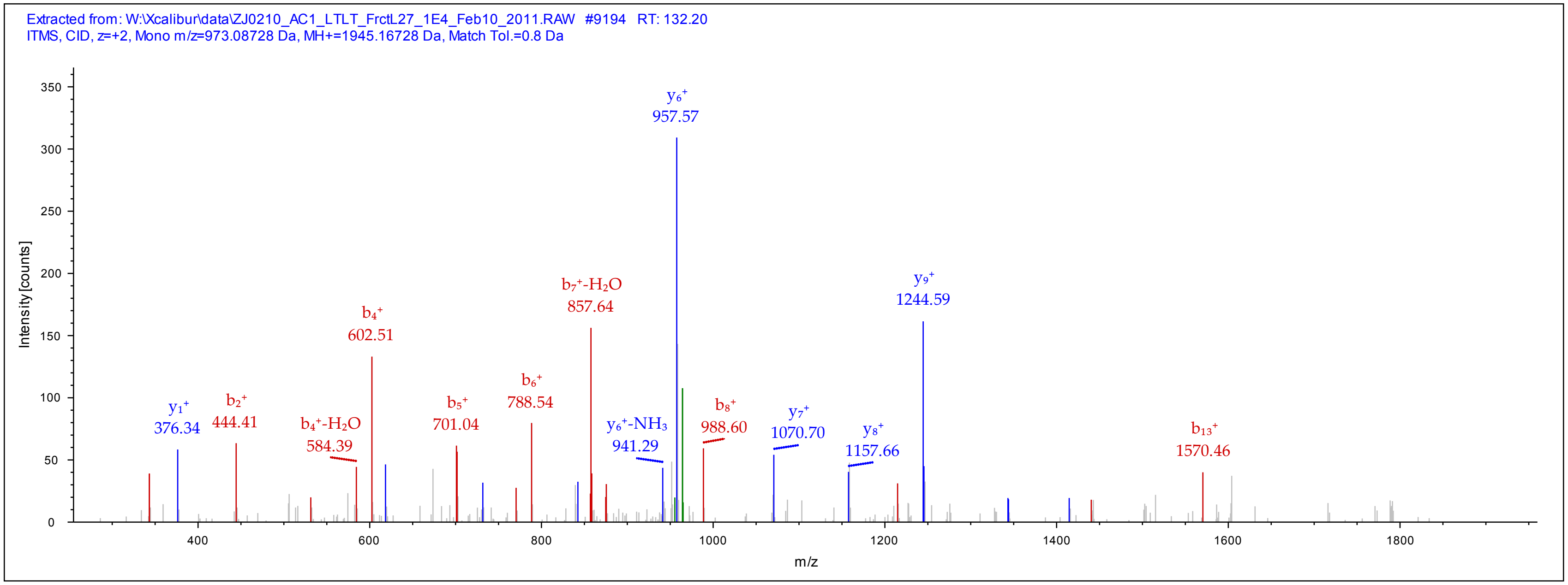
Identified with: Mascot (v1.16); IonScore:68, Exp Value:1.1E-005, Ions matched by search engine: 17/126

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Sec1 family domain-containing protein 1
- sec1 family domain-containing protein 1 isoform b
- Putative uncharacterized protein SCFD1 lng=642
- Putative uncharacterized protein SCFD1 (Fragment) lng=574



IPI:IPI00942956.1

Sequence: LVLCEVFK, L1-TMT6plex (229.16293 Da), C4-Carbamidomethyl (57.02146 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 733.44684 Da (+0.54 mmu/+0.73 ppm), MH+: 1465.88640 Da, RT: 122.64 min,

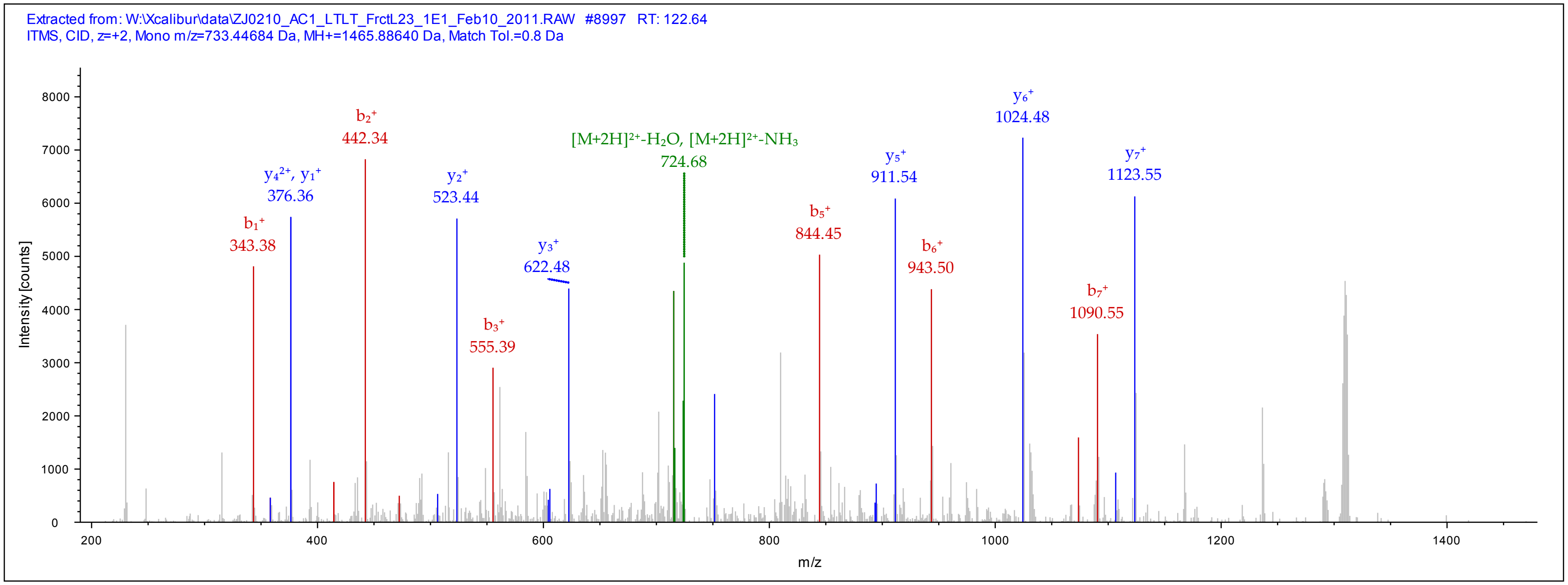
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.1E-002, Ions matched by search engine: 7/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Glutamine synthetase
- Proliferation-inducing protein 43


Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL23_1E1_Feb10_2011.RAW #8997 RT: 122.64
ITMS, CID, z=+2, Mono m/z=733.44684 Da, MH+=1465.88640 Da, Match Tol.=0.8 Da

IPI00943277.1

Sequence: LCDCPGLIFPSLLPR, L1-TMT6plex (229.16293 Da), C2-Carbamidomethyl (57.02146 Da), C4-Carbamidomethyl (57.02146 Da)

Charge: +2, Monoisotopic m/z: 994.03992 Da (+0.91 mmu/+0.92 ppm), MH+: 1987.07256 Da, RT: 135.42 min,

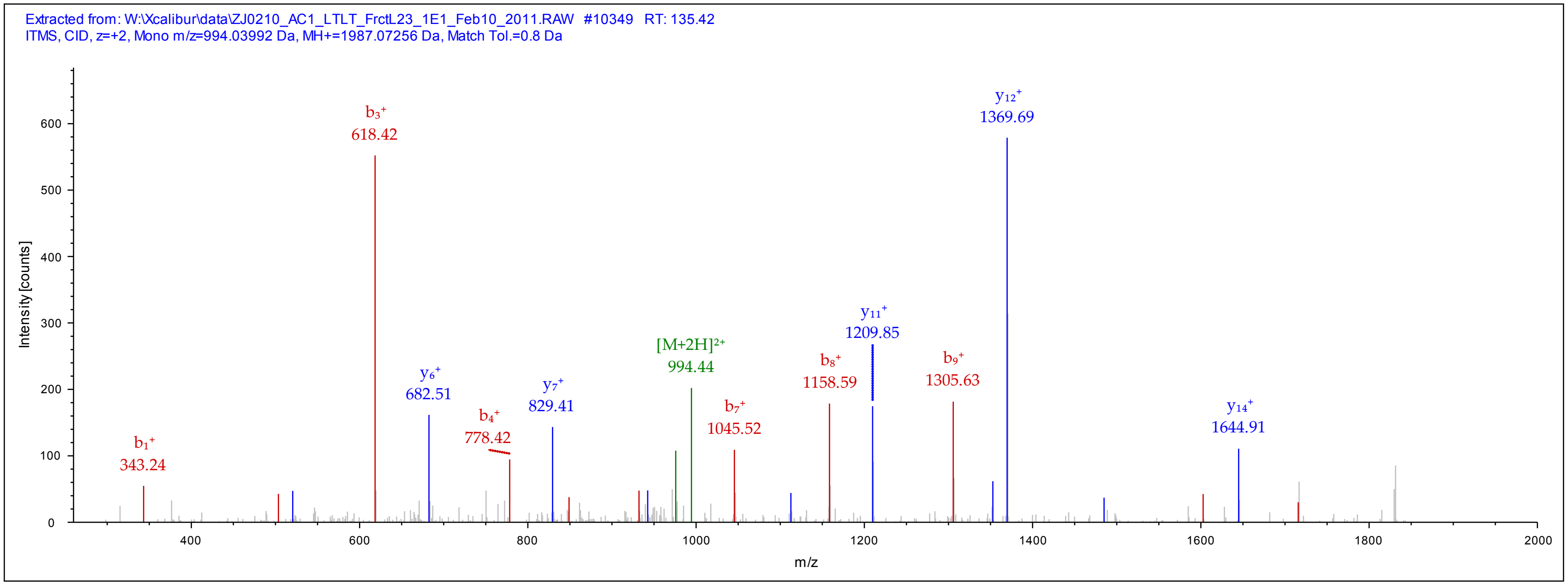
Identified with: Mascot (v1.16); IonScore:51, Exp Value:9.9E-004, Ions matched by search engine: 11/128

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Isoform 1 of Guanine nucleotide-binding protein-like 1
- HSR1 protein lng=561
- cDNA FLJ51011, highly similar to Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA lng=469
- Putative uncharacterized protein ENSP00000365787 lng=429
- cDNA FLJ52448, moderately similar to Guanine nucleotide-binding protein-like 1 lng=404



IPI00943293.1

Sequence: VIACFDSLK, V1-TMT6plex (229.16293 Da), C4-Carbamidomethyl (57.02146 Da), K9-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 755.93842 Da (-0.43 mmu/-0.57 ppm),   MH+: 1510.86955 Da,   RT: 108.94 min,

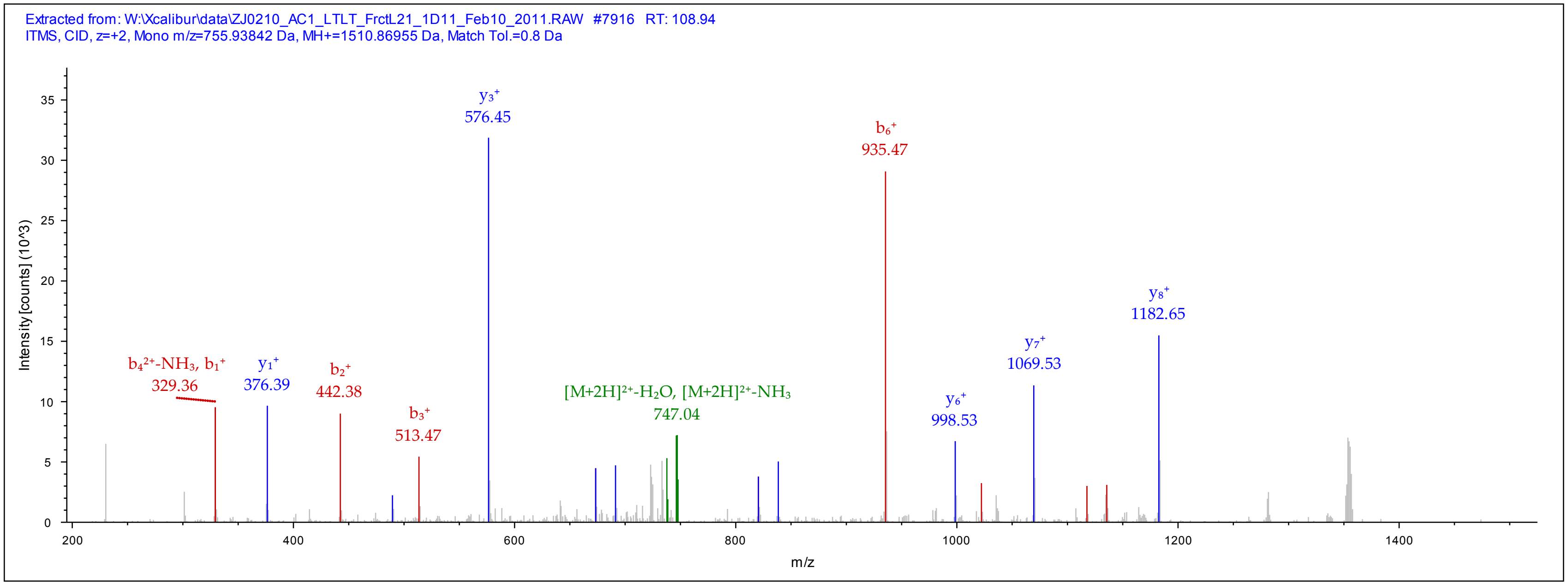
Identified with: Mascot (v1.16); IonScore:45, Exp Value:3.1E-003, Ions matched by search engine: 8/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (15):

- Isoform EXP42 of Muscleblind-like protein 1 lng=388
- Isoform 1 of Muscleblind-like protein 2
- muscleblind-like 1 isoform e lng=314
- Isoform 2 of Muscleblind-like protein 2
- Isoform EXP40 of Muscleblind-like protein 1 lng=370



IPI:IPI00943882.1

Sequence: QMAILPK, Q1-TMT6plex (229.16293 Da), M2-Oxidation (15.99492 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 637.89032 Da (-8.68 mmu/-13.6 ppm),   MH+: 1274.77336 Da,   RT: 107.20 min,

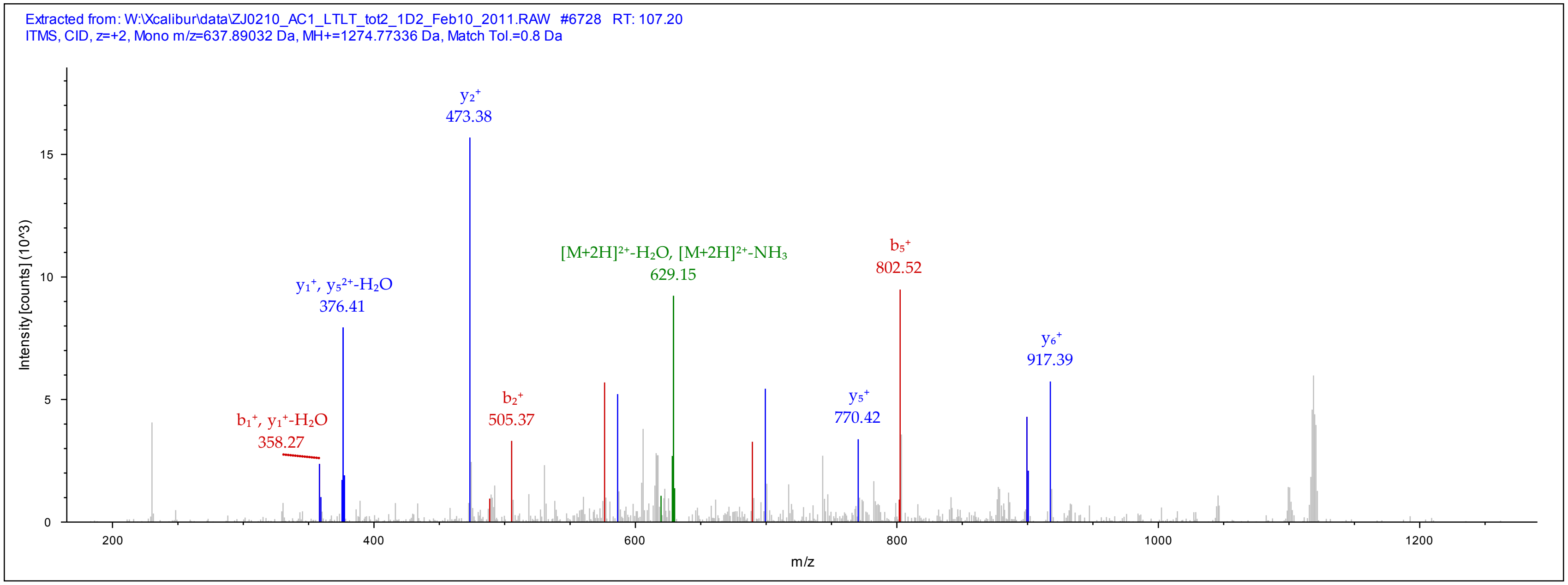
Identified with: Mascot (v1.16); IonScore:35, Exp Value:2.5E-002, Ions matched by search engine: 6/62

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- p150-like



IPI:IPI00944978.1

Sequence: GFGFVQFK, G1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 694.41064 Da (+0.07 mmu/+0.1 ppm),   MH+: 1387.81401 Da,   RT: 113.59 min,

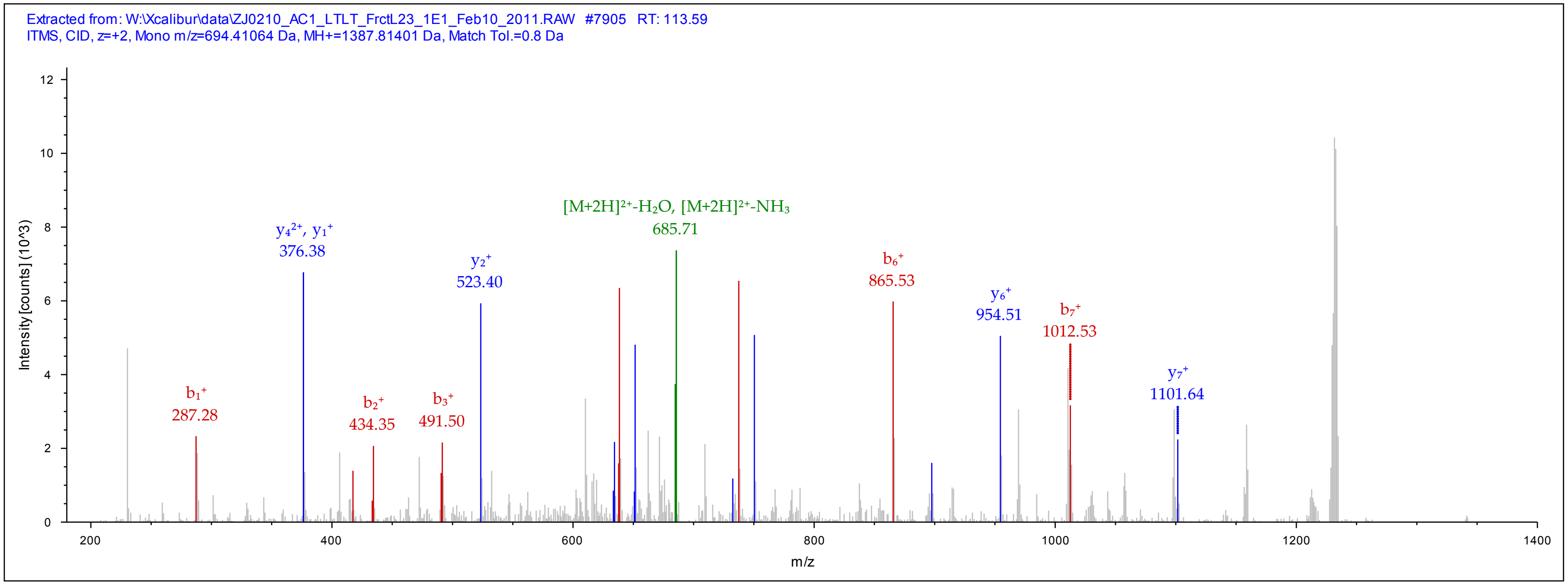
Identified with: Mascot (v1.16); IonScore:37, Exp Value:1.5E-002, Ions matched by search engine: 7/62

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- RNA-binding protein 28
- Uncharacterized protein
- cDNA FLJ51865, highly similar to RNA-binding protein 28



IPI00945384.1

Sequence: LFIYNPTTGEFLGR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 929.00940 Da (+0.33 mmu/+0.35 ppm), MH+: 1857.01152 Da, RT: 126.87 min,

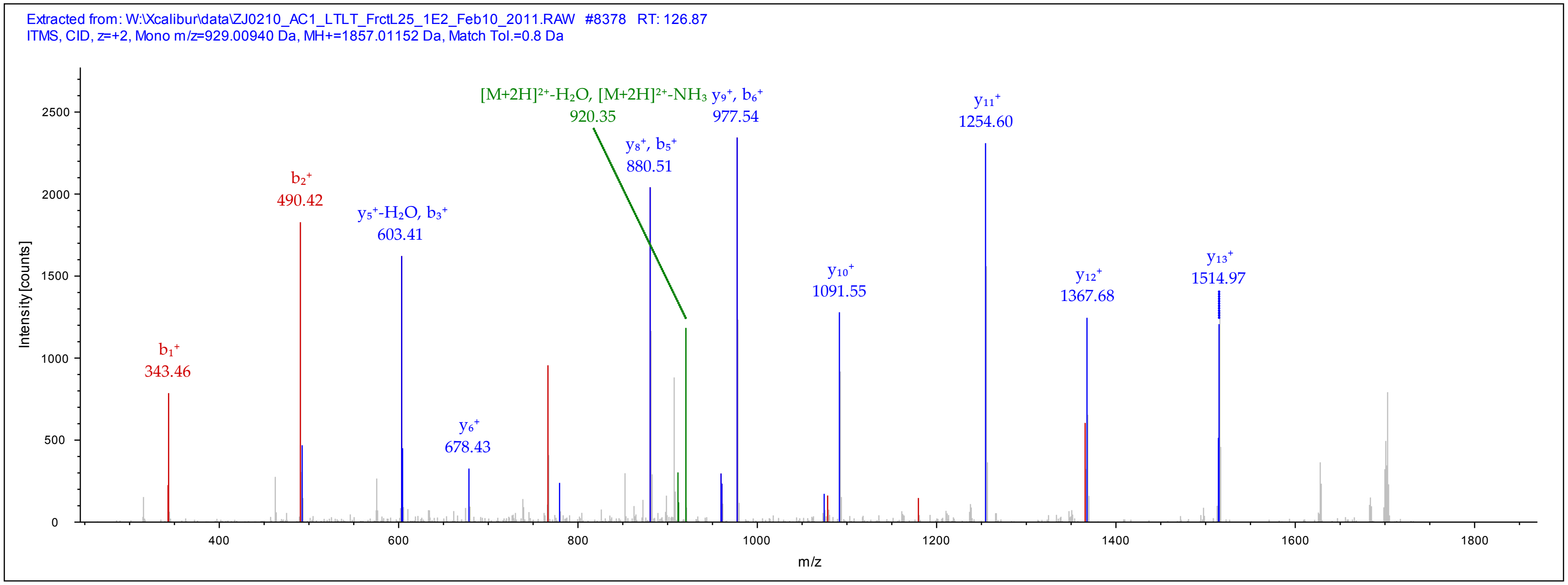
Identified with: Mascot (v1.16); IonScore:55, Exp Value:3.4E-004, Ions matched by search engine: 13/128

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Sodium/potassium-transporting ATPase subunit beta-3
- 16 kDa protein lng=138
- 15 kDa protein lng=131
- Putative uncharacterized protein ATP1B3 lng=44
- Putative uncharacterized protein ATP1B3 lng=43



IPI00945505.1

Sequence: LIDIAR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 465.30301 Da (+0.28 mmu/+0.61 ppm), MH+: 929.59874 Da, RT: 102.08 min,

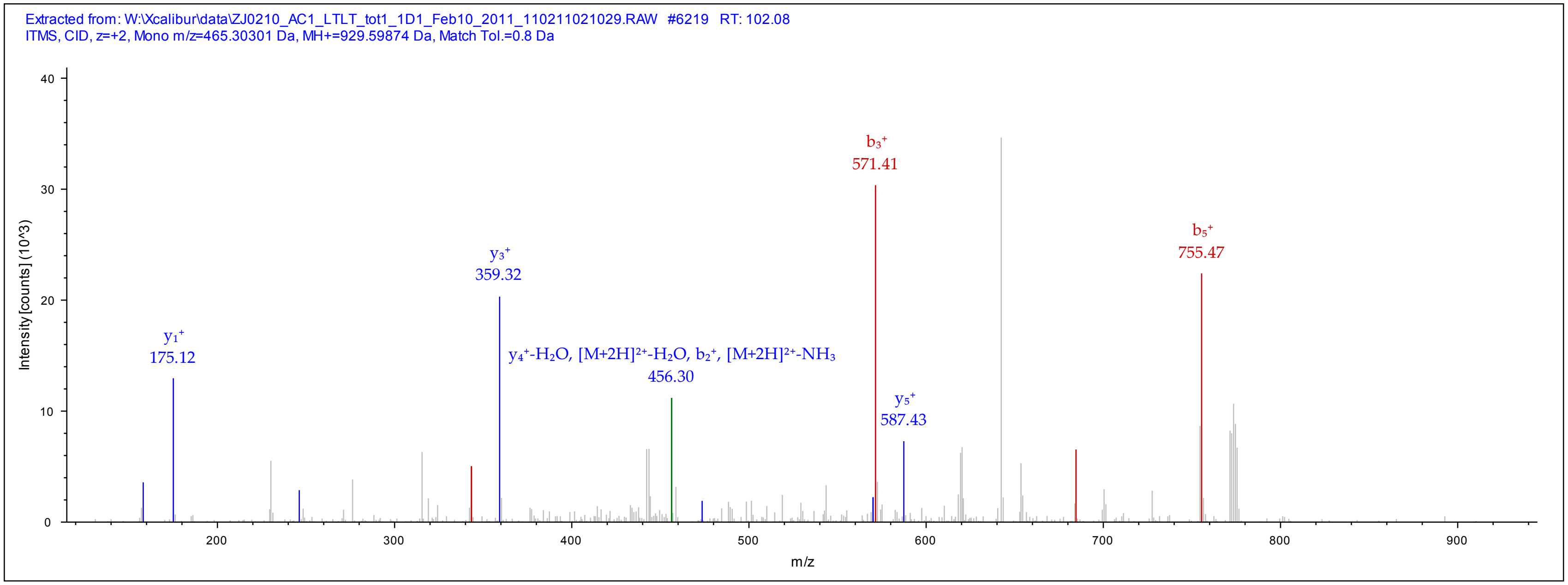
Identified with: Mascot (v1.16); IonScore:30, Exp Value:3.1E-002, Ions matched by search engine: 5/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Serine/threonine-protein kinase B-raf
- L-protein KIAA1549:BRAF 16_11 lng=2077
- L-protein KIAA1549:BRAF 16_9 lng=2135
- L-protein KIAA1549:BRAF 15_9 lng=2029



IPI:IPI00945578.1

Sequence: VDYFIASK, V1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 700.91296 Da (-0.18 mmu/-0.25 ppm), MH+: 1400.81865 Da, RT: 101.15 min,

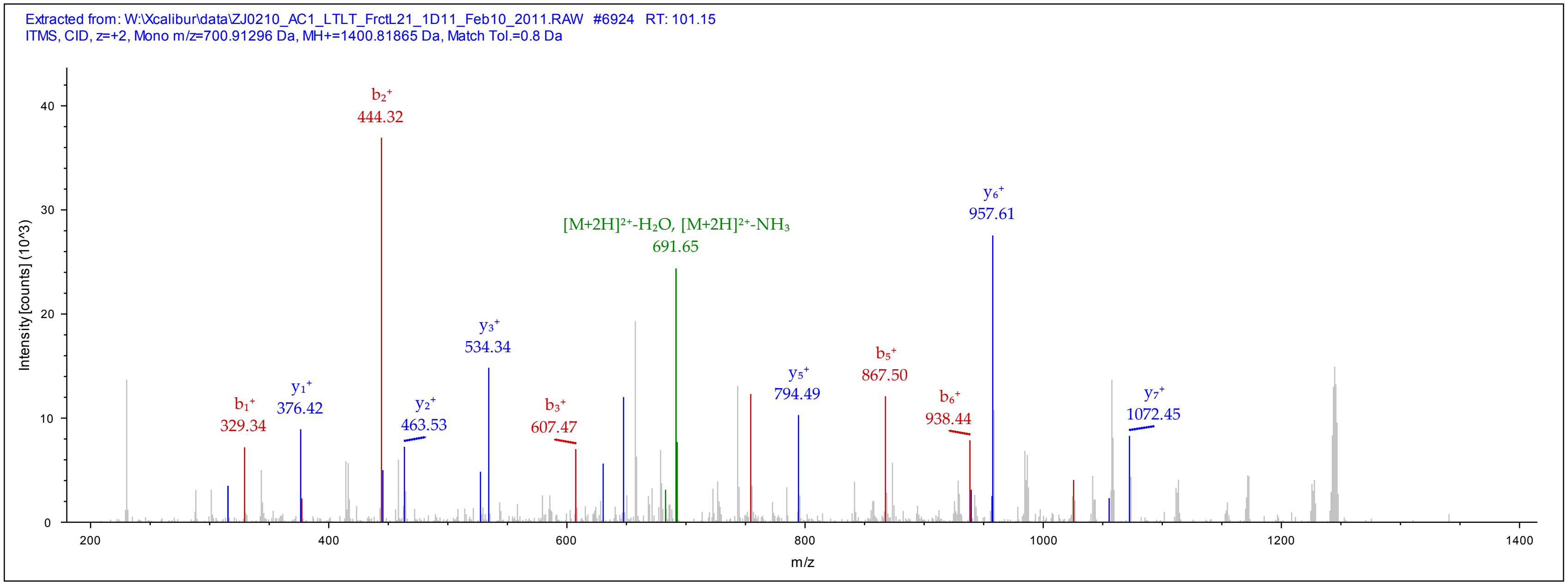
Identified with: Mascot (v1.16); IonScore:31, Exp Value:8.4E-002, Ions matched by search engine: 7/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Translocation protein SEC62
- 12 kDa protein
- SEC62 protein (Fragment)



IPI:IPI00945880.1

Sequence: LFSELPLAK, L1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 738.46545 Da (-0.1 mmu/-0.13 ppm), MH+: 1475.92363 Da, RT: 124.83 min,

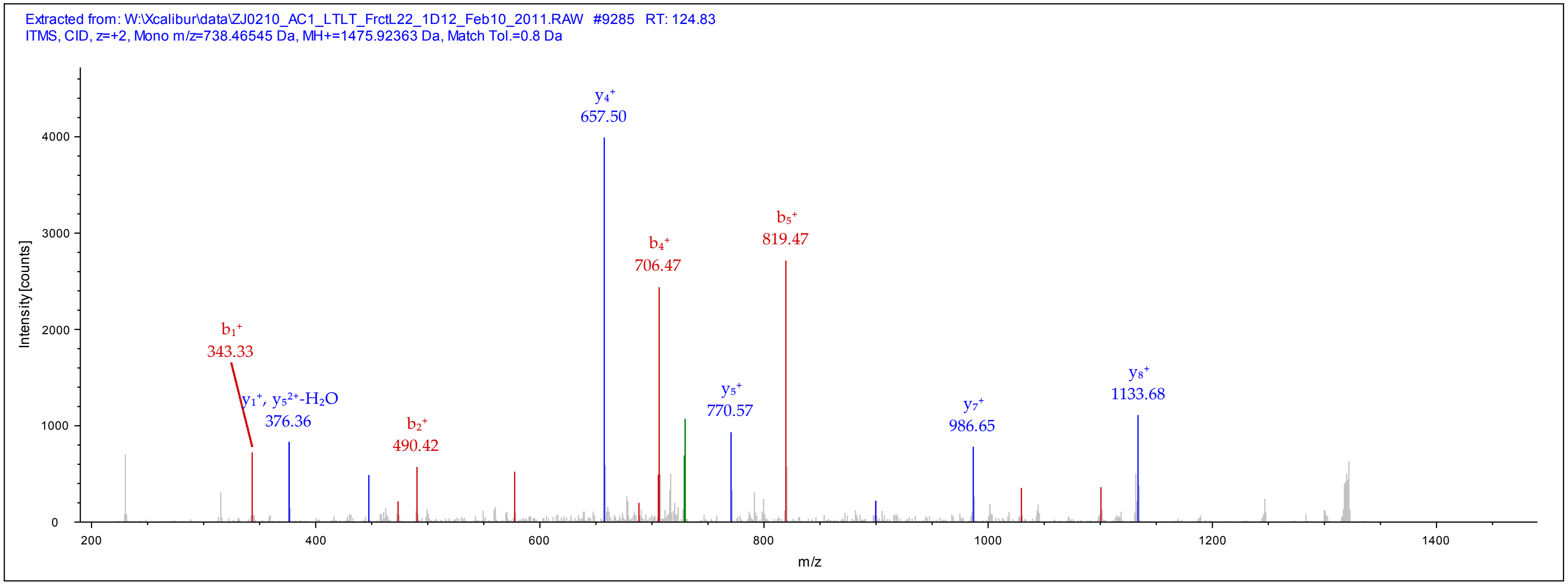
Identified with: Mascot (v1.16); IonScore:49, Exp Value:8.8E-004, Ions matched by search engine: 14/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- MRPS33 protein (Fragment)
- Uncharacterized protein



IPI:IPI00945995.1

Sequence: LALLTELSQNR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 743.94519 Da (+2 mmu/+2.68 ppm), MH+: 1486.88310 Da, RT: 123.49 min,

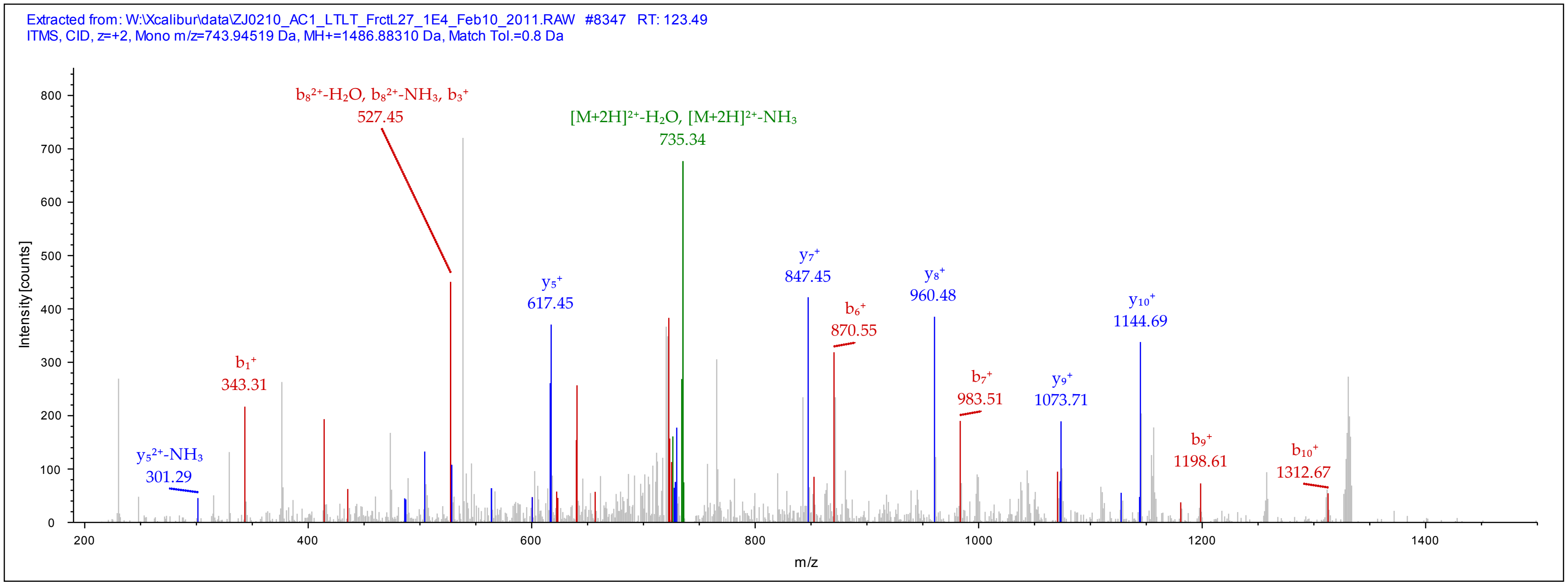
Identified with: Mascot (v1.16); IonScore:31, Exp Value:5.6E-002, Ions matched by search engine: 8/90

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- vacuolar protein sorting-associated protein 8 homolog isoform b
- Isoform 1 of Vacuolar protein sorting-associated protein 8 homolog
- Isoform 2 of Vacuolar protein sorting-associated protein 8 homolog
- 147 kDa protein



IPI00946081.1

Sequence: AVETPPLSSVNLLEGLSR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 1056.10083 Da (+1.67 mmu/+1.58 ppm), MH+: 2111.19438 Da, RT: 127.85 min,

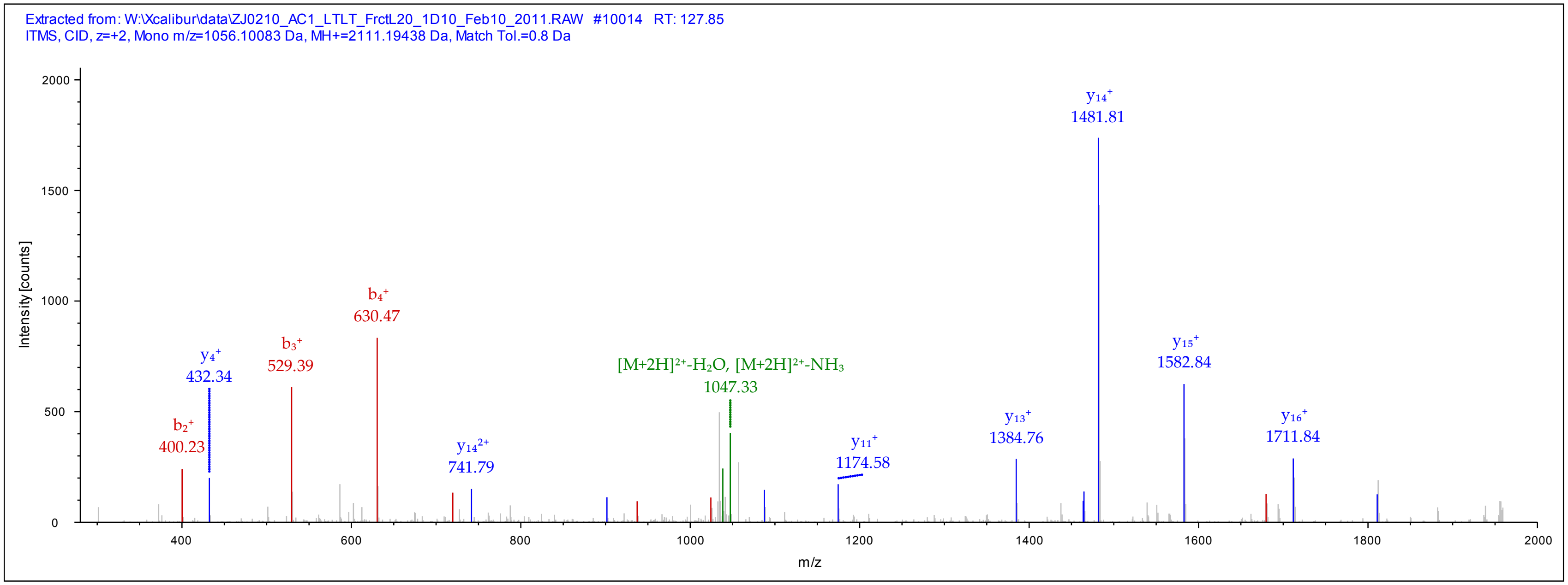
Identified with: Mascot (v1.16); IonScore:90, Exp Value:1.2E-007, Ions matched by search engine: 16/178

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (9):

- Isoform 1 of GTPase-activating protein and VPS9 domain-containing protein 1
- Isoform 6 of GTPase-activating protein and VPS9 domain-containing protein 1
- Isoform 5 of GTPase-activating protein and VPS9 domain-containing protein 1
- Isoform 3 of GTPase-activating protein and VPS9 domain-containing protein 1
- GTPase activating protein and VPS9 domains 1 lng=858
- Isoform 2 of GTPase-activating protein and VPS9 domain-containing protein 1



IPI00946242.1

Sequence: AGDNILAVLK, A1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 736.46912 Da (+3.03 mmu/+4.12 ppm), MH+: 1471.93096 Da, RT: 117.91 min,

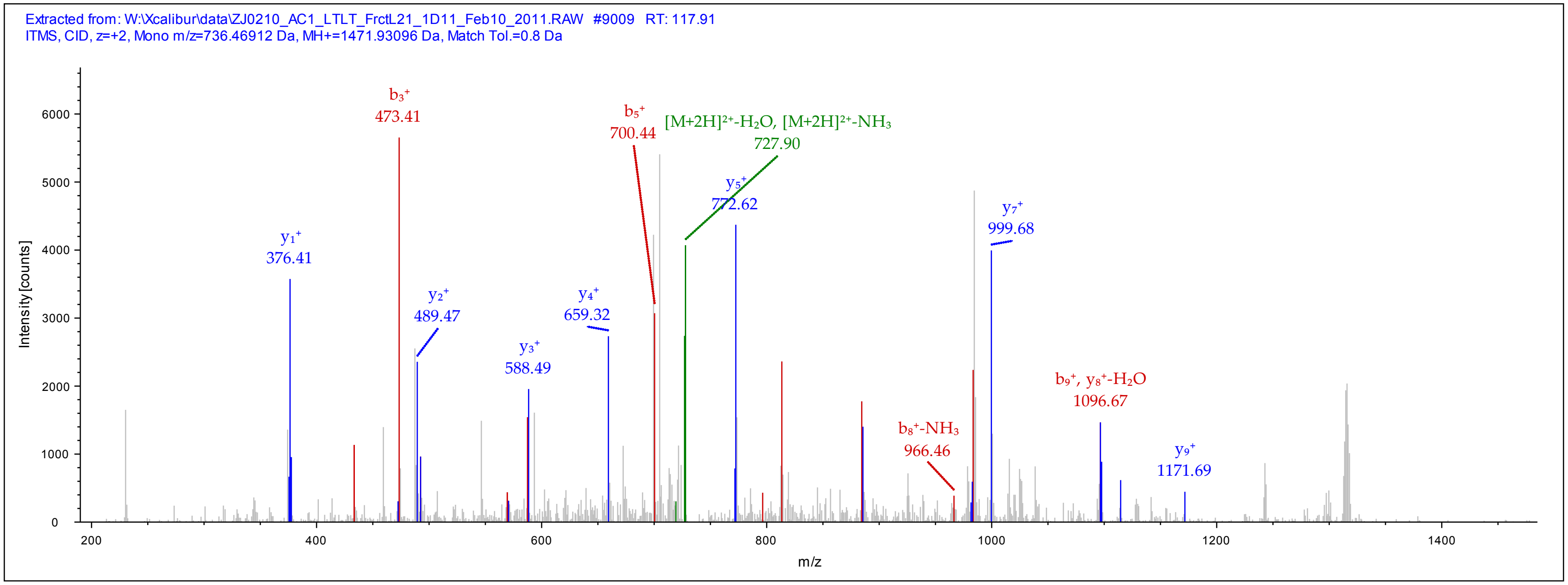
Identified with: Mascot (v1.16); IonScore:42, Exp Value:2.6E-003, Ions matched by search engine: 9/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Endoplasmic reticulum metallopeptidase 1
- 93 kDa protein lng=841



IPI00947007.1

Sequence: GVVVLAK, G1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 572.39758 Da (+0.65 mmu/+1.13 ppm),   MH+: 1143.78789 Da,   RT: 88.73 min,

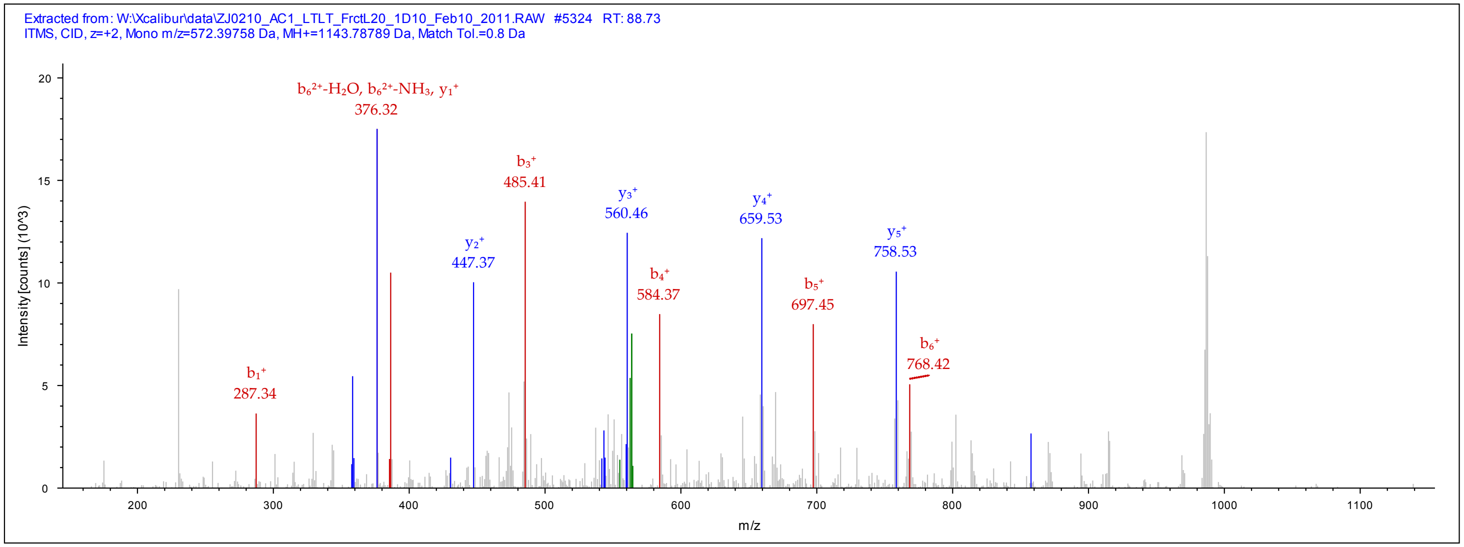
Identified with: Mascot (v1.16); IonScore:35, Exp Value:9.5E-003, Ions matched by search engine: 6/50

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (8):

- Aldo-keto reductase family 1 member C2
- Aldo-keto reductase family 1 member C1
- 35 kDa protein lng=302
- Aldo-keto reductase family 1, member C1 (Dihydrodiol dehydrogenase 1 lng=248
- cDNA FLJ52680, highly similar to Aldo-keto reductase family 1 member C2 lng=297
- Putative uncharacterized protein AKR1CL1 lng=148
- Aldo-keto reductase family 1 member C4
- Aldo-keto reductase family 1 member C3



IPI00947091.1

Sequence: FYNLVLLPR, F1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 682.41876 Da (+0.14 mmu/+0.21 ppm), MH+: 1363.83025 Da, RT: 127.59 min,

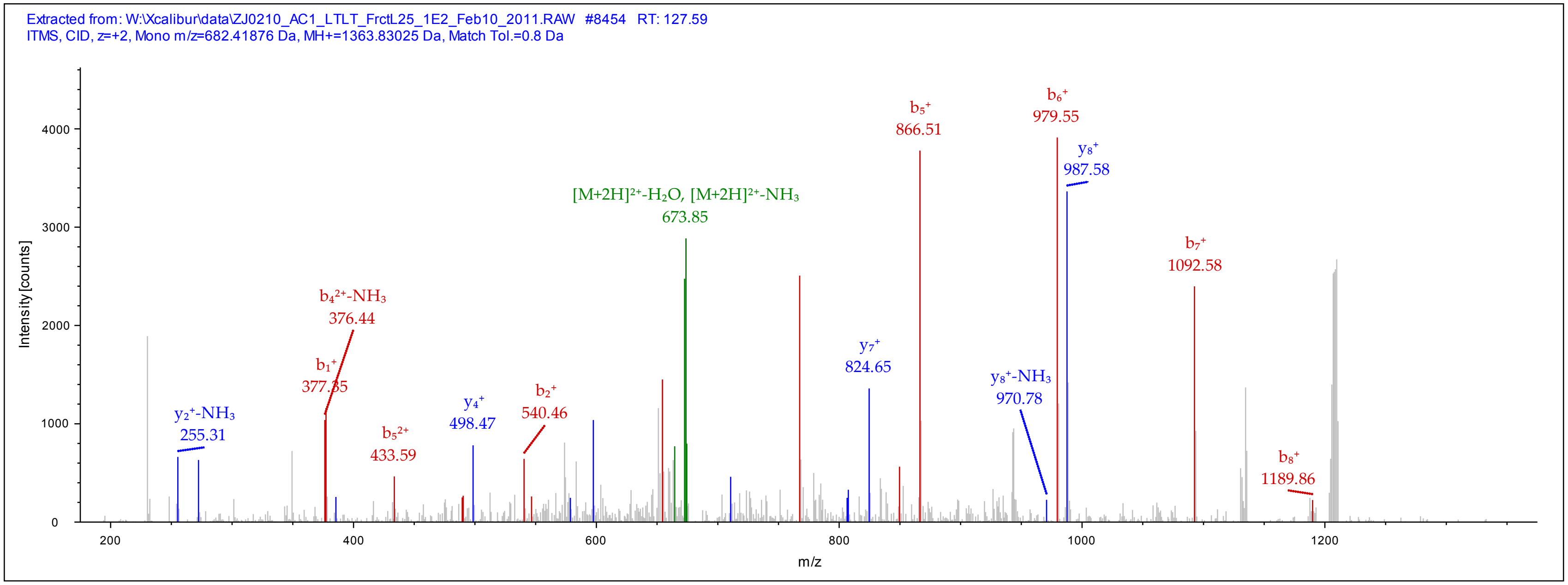
Identified with: Mascot (v1.16); IonScore:29, Exp Value:7.5E-002, Ions matched by search engine: 7/78

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Bystin
- Putative uncharacterized protein BYSL lng=183



IPI:IPI00947497.1

Sequence: FYLPILVPSAK, F1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 853.53973 Da (+3.23 mmu/+3.78 ppm), MH+: 1706.07219 Da, RT: 139.64 min,

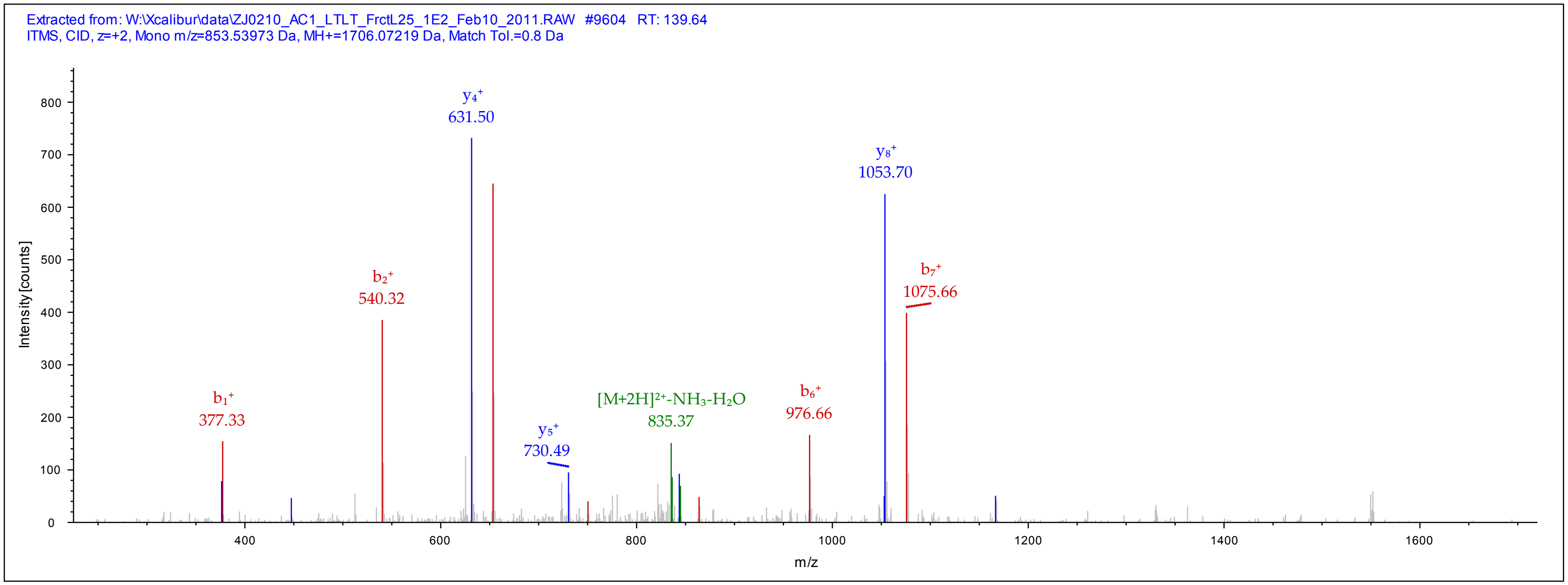
Identified with: Mascot (v1.16); IonScore:37, Exp Value:8.4E-003, Ions matched by search engine: 6/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of Glycosyltransferase 8 domain-containing protein 1
- Isoform 2 of Glycosyltransferase 8 domain-containing protein 1
- Uncharacterized protein
- Uncharacterized protein
- Uncharacterized protein



IPI:IPI00953363.1

equence: MLDLMLEAVNNIK, M1-TMT6plex (229.16293 Da), K13-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 981.56445 Da (+2.36 mmu/+2.41 ppm), MH+: 1962.12163 Da, RT: 207.11 min,

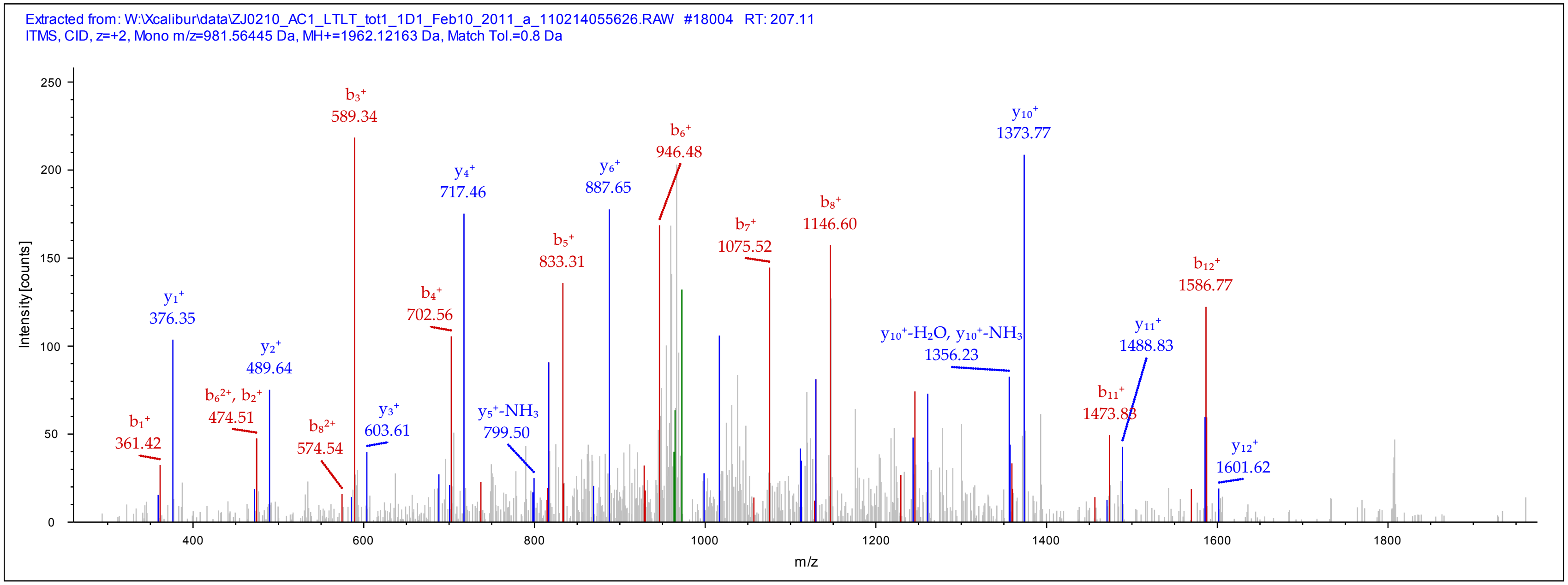
Identified with: Mascot (v1.16); IonScore:85, Exp Value:3.1E-007, Ions matched by search engine: 21/110

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Isoform 2 of Polypeptide N-acetylgalactosaminyltransferase 3
- Isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 3
- Uncharacterized protein
- Uncharacterized protein



IPI:IPI00954965.1

Sequence: QMYDMVVK, Q1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 736.41437 Da (+8.05 mmu/+10.93 ppm), MH+: 1471.82146 Da, RT: 122.05 min,

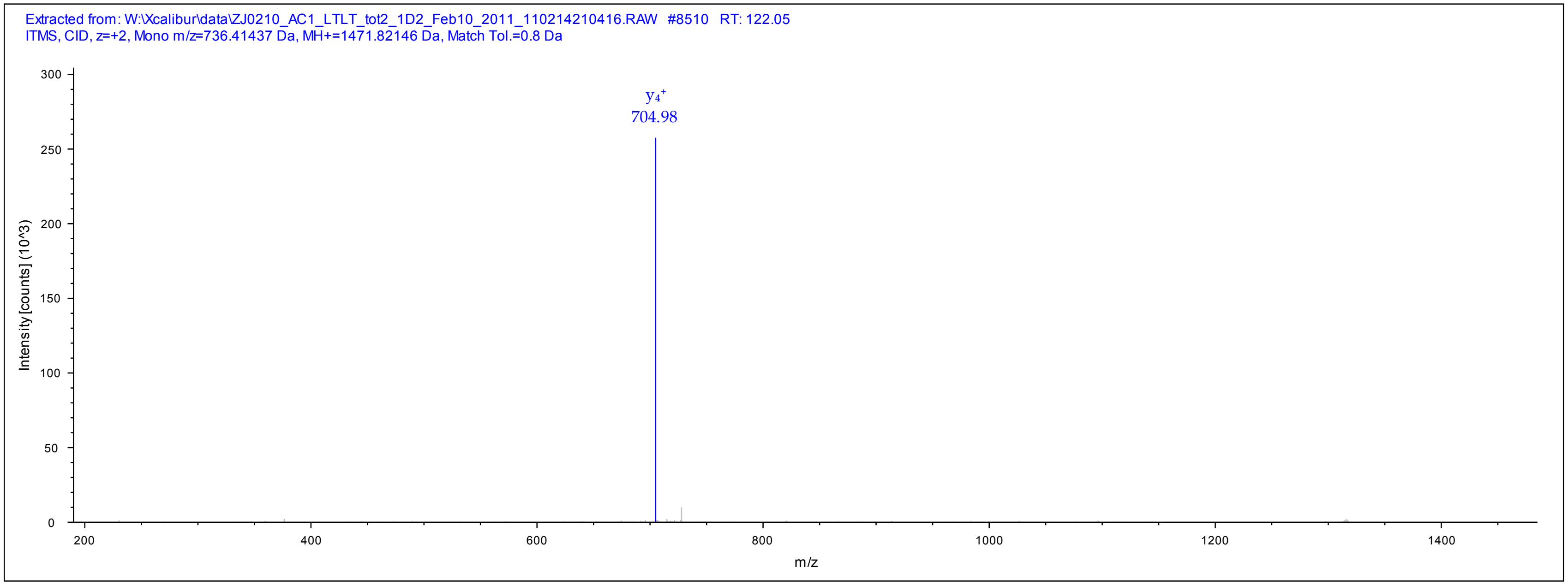
Identified with: Mascot (v1.16); IonScore:32, Exp Value:7.1E-002, Ions matched by search engine: 5/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Inner nuclear membrane protein Man1
- inner nuclear membrane protein Man1 isoform 2



IPI:IPI00955977.1

Sequence: SIFDFSALK, S1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 743.43970 Da (+0.17 mmu/+0.22 ppm), MH+: 1485.87212 Da, RT: 126.61 min,

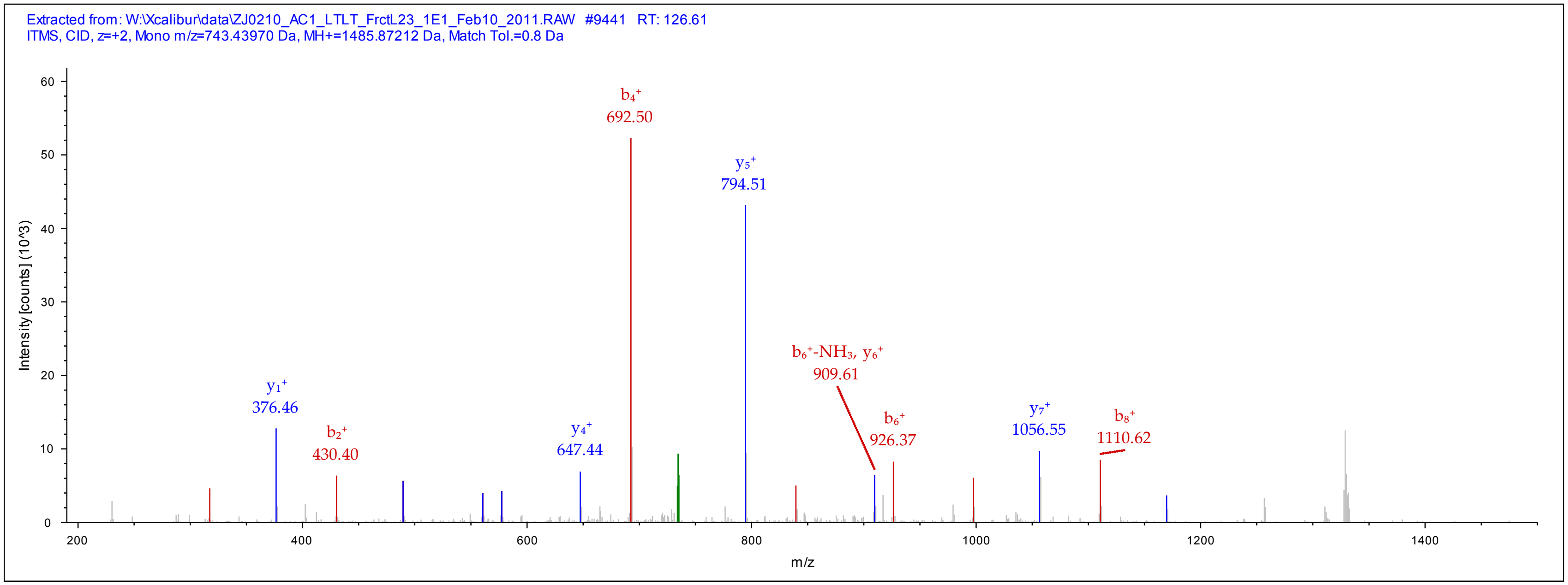
Identified with: Mascot (v1.16); IonScore:53, Exp Value:4.6E-004, Ions matched by search engine: 8/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Phosphoglucomutase-1
- Isoform 2 of Phosphoglucomutase-1 lng=580
- phosphoglucomutase-1 isoform 3



IPI:IPI00963963.1

Sequence: WDQSTFIGR, W1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 669.85394 Da (+0.1 mmu/+0.15 ppm), MH+: 1338.70061 Da, RT: 96.47 min,

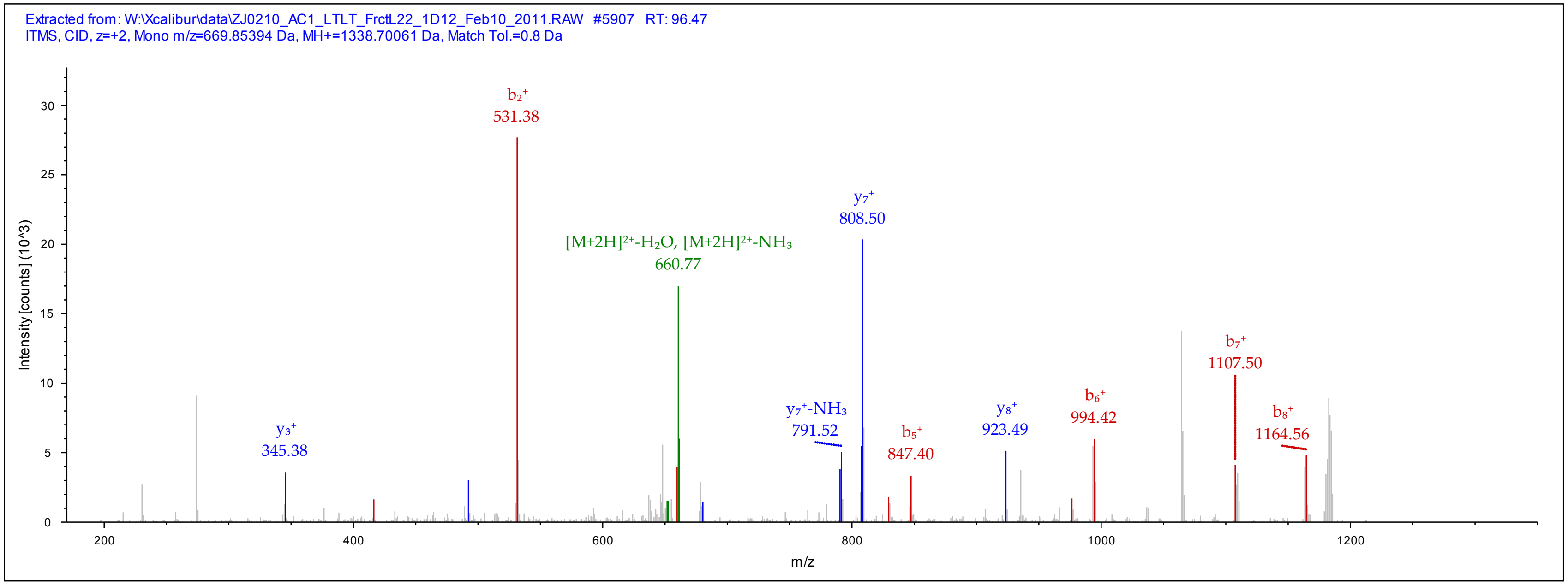
Identified with: Mascot (v1.16); IonScore:30, Exp Value:7.5E-002, Ions matched by search engine: 8/82

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- Sideroflexin-1
- Uncharacterized protein
- Uncharacterized protein
- Uncharacterized protein



IPI:IPI00964013.1

Sequence: GFQFVSSSLPDICYR, G1-TMT6plex (229.16293 Da), C13-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 1003.00641 Da (+0.21 mmu/+0.21 ppm),   MH+: 2005.00554 Da,   RT: 119.60 min,

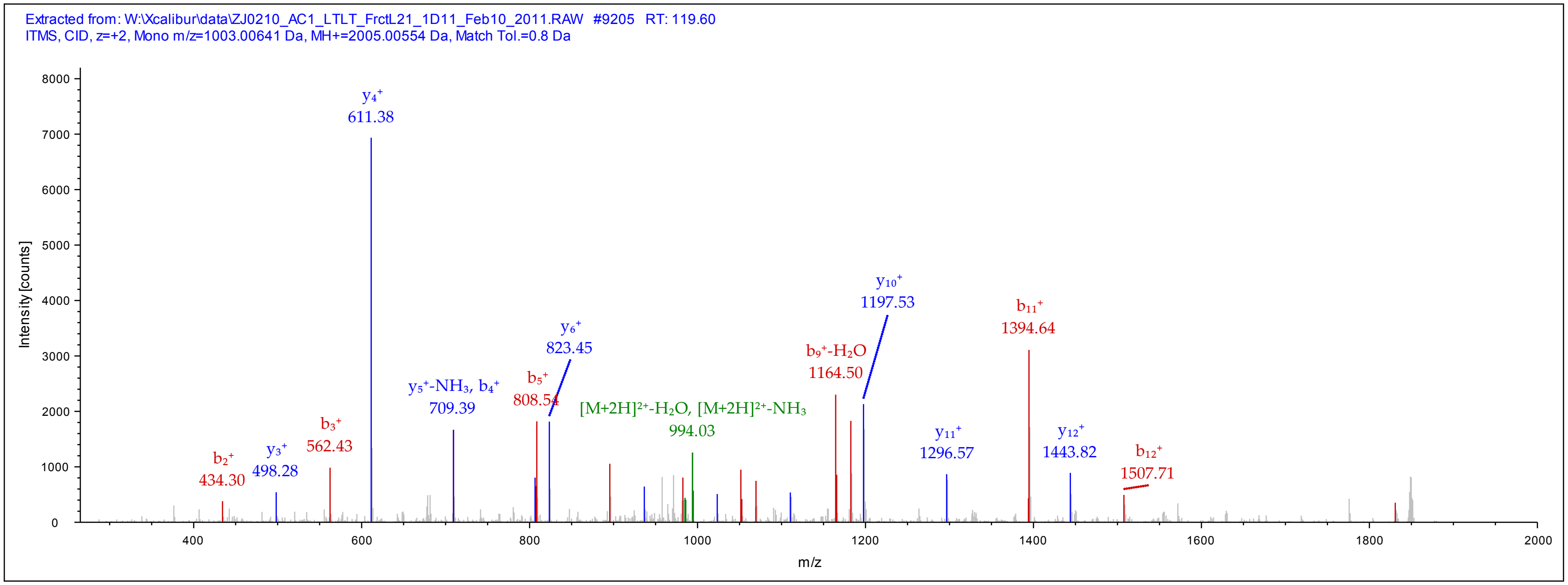
Identified with: Mascot (v1.16); IonScore:55, Exp Value:4.8E-004, Ions matched by search engine: 13/146

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- cellular nucleic acid-binding protein isoform 2
- Isoform 2 of Cellular nucleic acid-binding protein
- Isoform 1 of Cellular nucleic acid-binding protein
- cellular nucleic acid-binding protein isoform 1
- cellular nucleic acid-binding protein isoform 5



IPI:IPI00964251.1

Sequence: IISTEPLPGR, I1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 656.39667 Da (+1.32 mmu/+2.01 ppm),   MH+: 1311.78606 Da,   RT: 91.93 min,

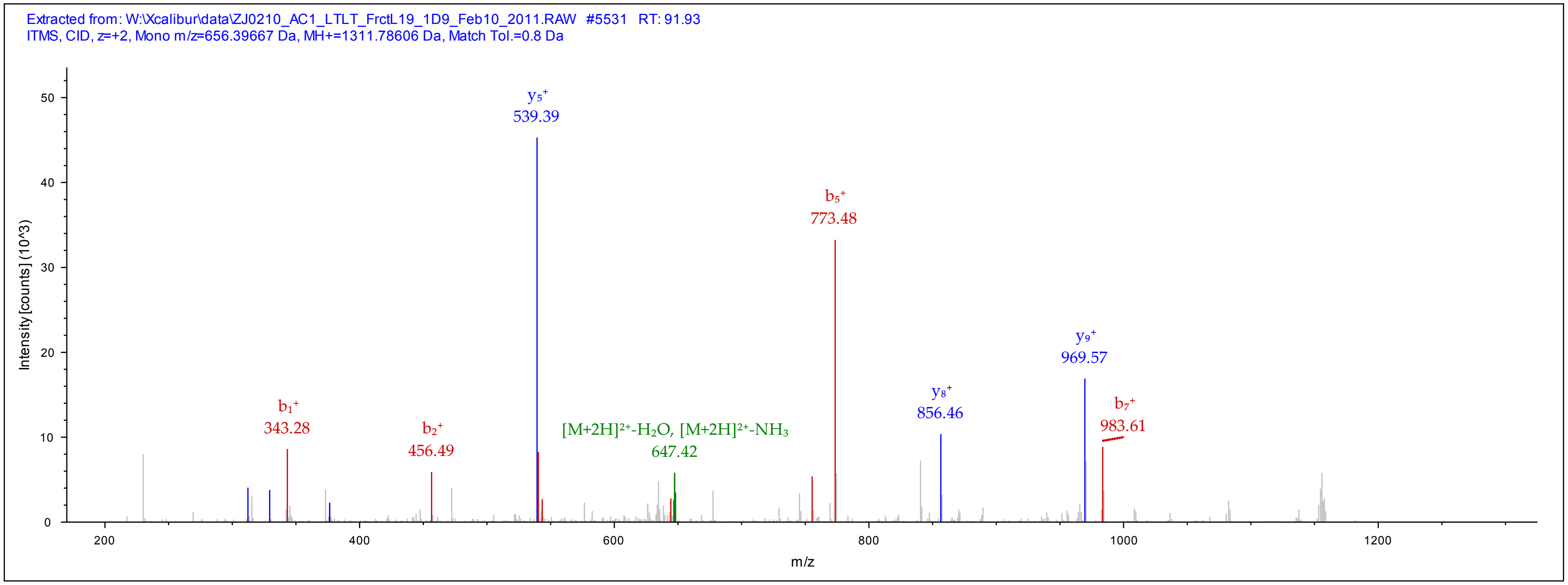
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.0E-002, Ions matched by search engine: 9/76

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; $b-H_2O$; $b-NH_3$; y; $y-H_2O$; $y-NH_3$

Protein references (4):

- Isoform 1 of La-related protein 7
- La-related protein 7 lng=589
- Uncharacterized protein
- Protein



IPI:IPI00964469.1

Sequence: ELIVLR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 486.32587 Da (-0.33 mmu/-0.69 ppm), MH+: 971.64446 Da, RT: 92.49 min,

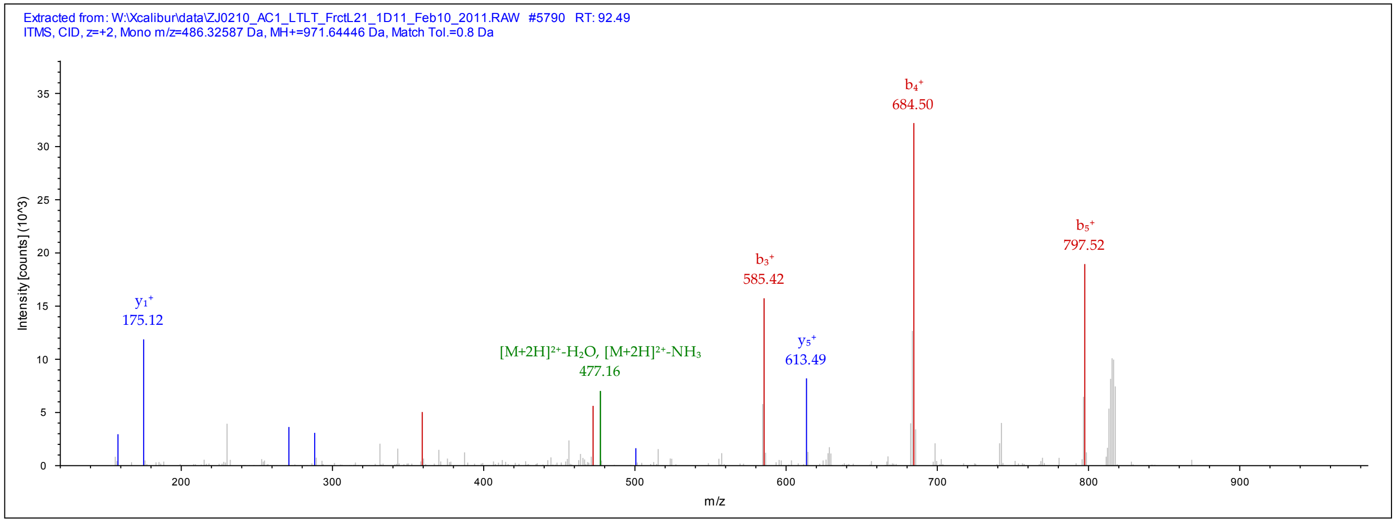
Identified with: Mascot (v1.16); IonScore:35, Exp Value:6.0E-003, Ions matched by search engine: 5/40

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (9):

- Ankyrin-3
- Ankyrin G119
- ankyrin-3 isoform 2
- 124 kDa protein lng=1128
- 475 kDa protein lng=4335
- cDNA FLJ44903 fis, clone BRAMY3005184, highly similar to Mus musculus ankyrin 3, epithelial lng=1101
- Protein
- Putative uncharacterized protein DKFZp686I225
- cDNA FLJ58990, highly similar to Ankyrin-3



IPI:IPI00964664.1

Sequence: AIVQQWLEYR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 767.93347 Da (+0.85 mmu/+1.1 ppm), MH+: 1534.85967 Da, RT: 118.27 min,

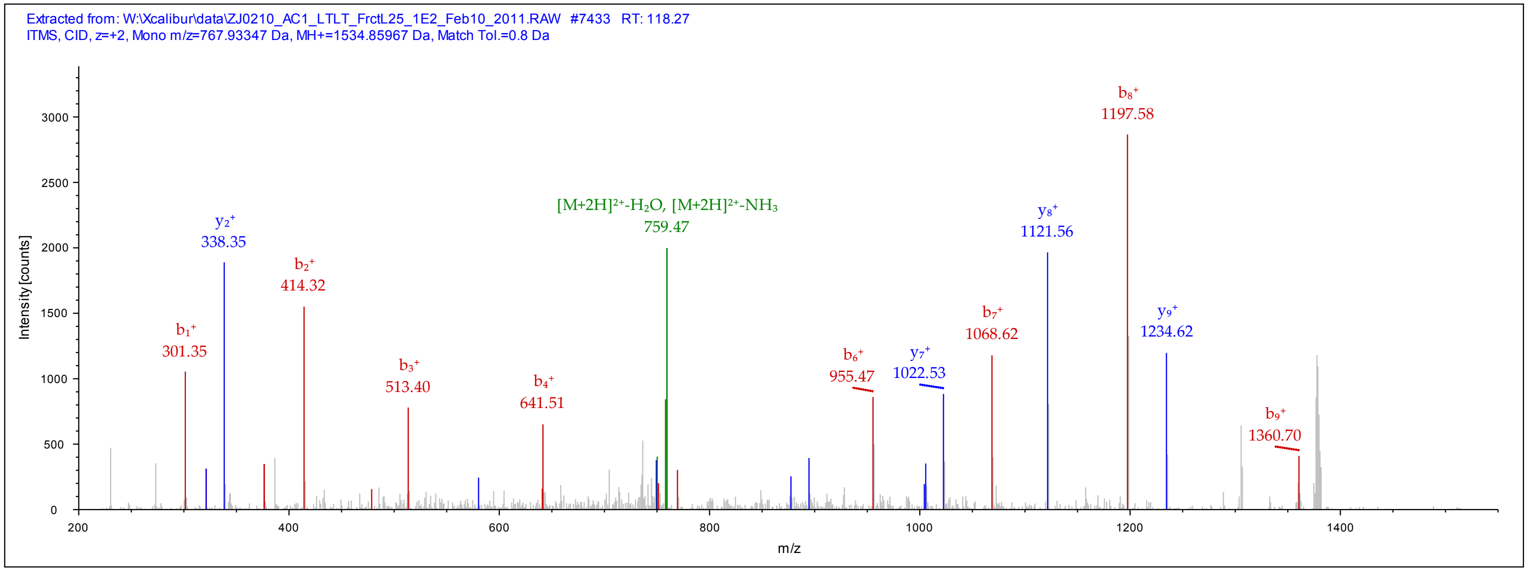
Identified with: Mascot (v1.16); IonScore:43, Exp Value:4.7E-003, Ions matched by search engine: 6/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Eukaryotic translation elongation factor 1 epsilon-1
- Uncharacterized protein
- eukaryotic translation elongation factor 1 epsilon-1 isoform 2
- Protein
- Uncharacterized protein
- Uncharacterized protein



IPI:IPI00964716.1

Sequence: LIAAVK, L1-TMT6plex (229.16293 Da), K6-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 536.87872 Da (+0.35 mmu/+0.65 ppm),   MH+: 1072.75017 Da,   RT: 89.32 min,

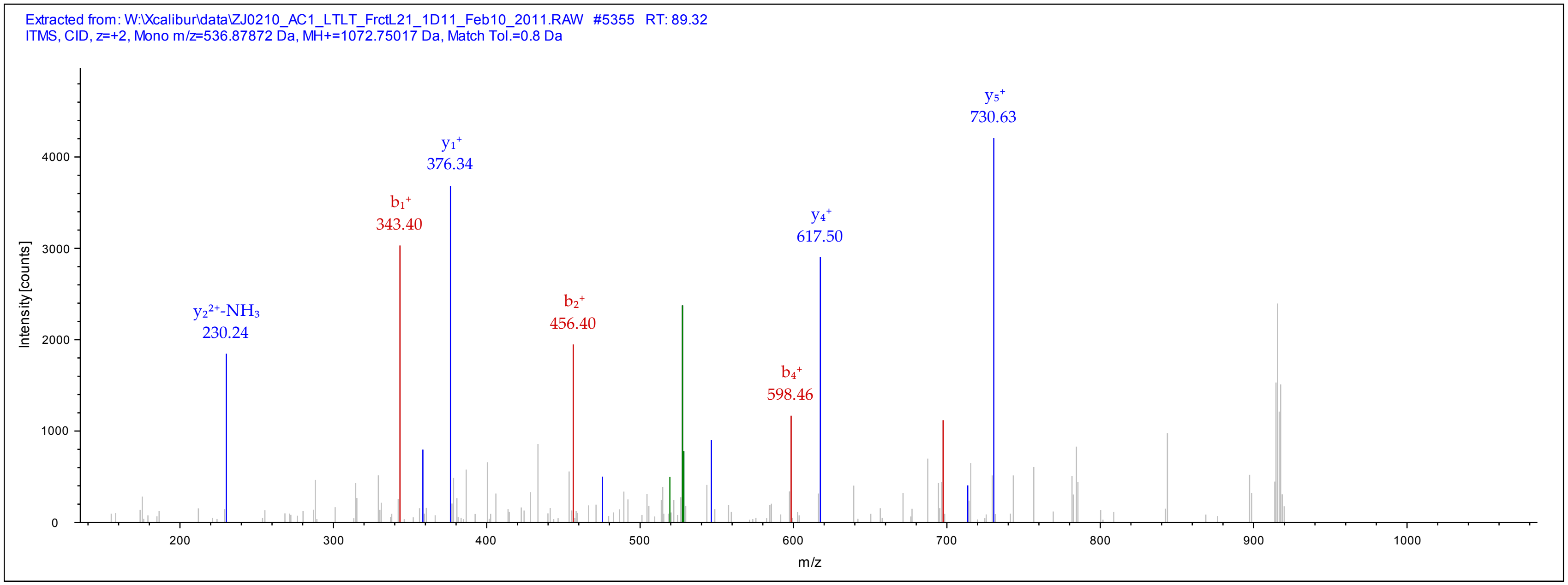
Identified with: Mascot (v1.16); IonScore:32, Exp Value:1.1E-002, Ions matched by search engine: 5/42

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Sorting nexin-2
- cDNA FLJ51799, highly similar to Sorting nexin-2



IPI:IPI00965192.1

Sequence: LVNTGLLTLR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 664.92657 Da (-0.24 mmu/-0.36 ppm), MH+: 1328.84587 Da, RT: 112.27 min,

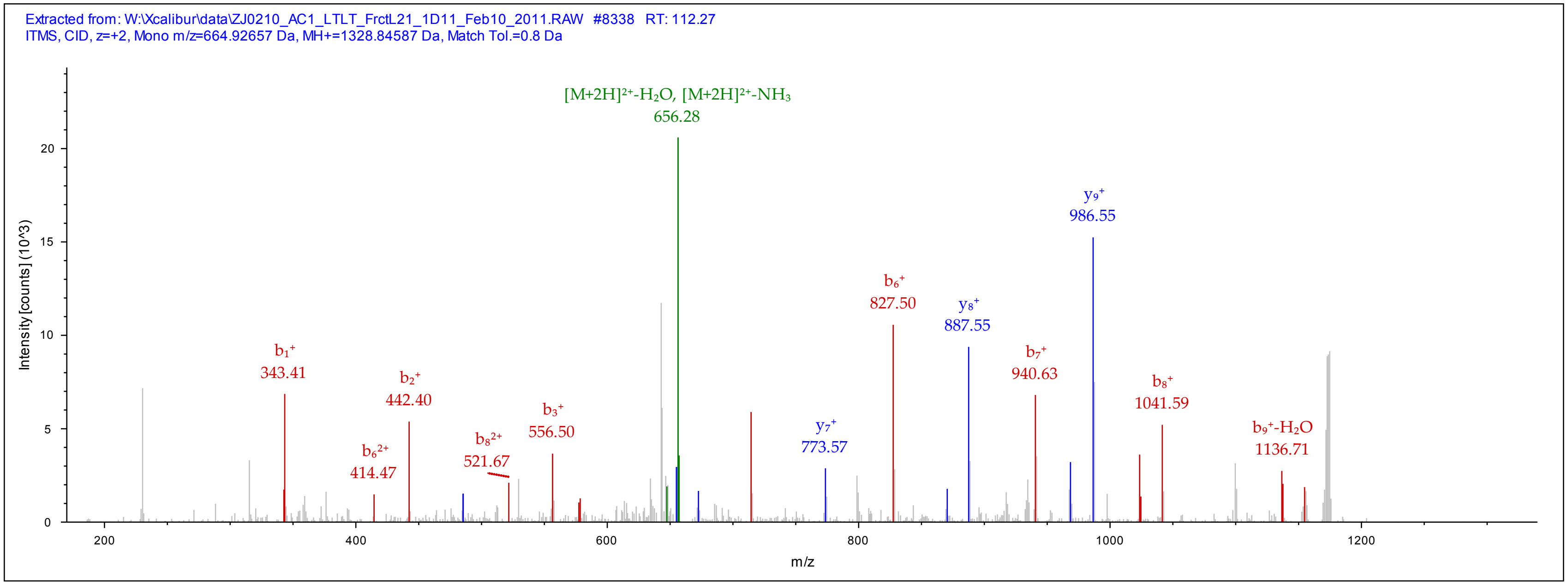
Identified with: Mascot (v1.16); IonScore:43, Exp Value:1.4E-003, Ions matched by search engine: 9/94

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Neurolysin, mitochondrial
- cDNA FLJ14696 fis, clone NT2RP2005775, highly similar to NEUROLYSIN
- Protein
- Putative uncharacterized protein DKFZp564F123
- 81 kDa protein



IPI:IPI00965611.1

Sequence: HSQGLR, H1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 463.76810 Da (-4.02 mmu/-8.67 ppm),   MH+: 926.52892 Da,   RT: 96.60 min,

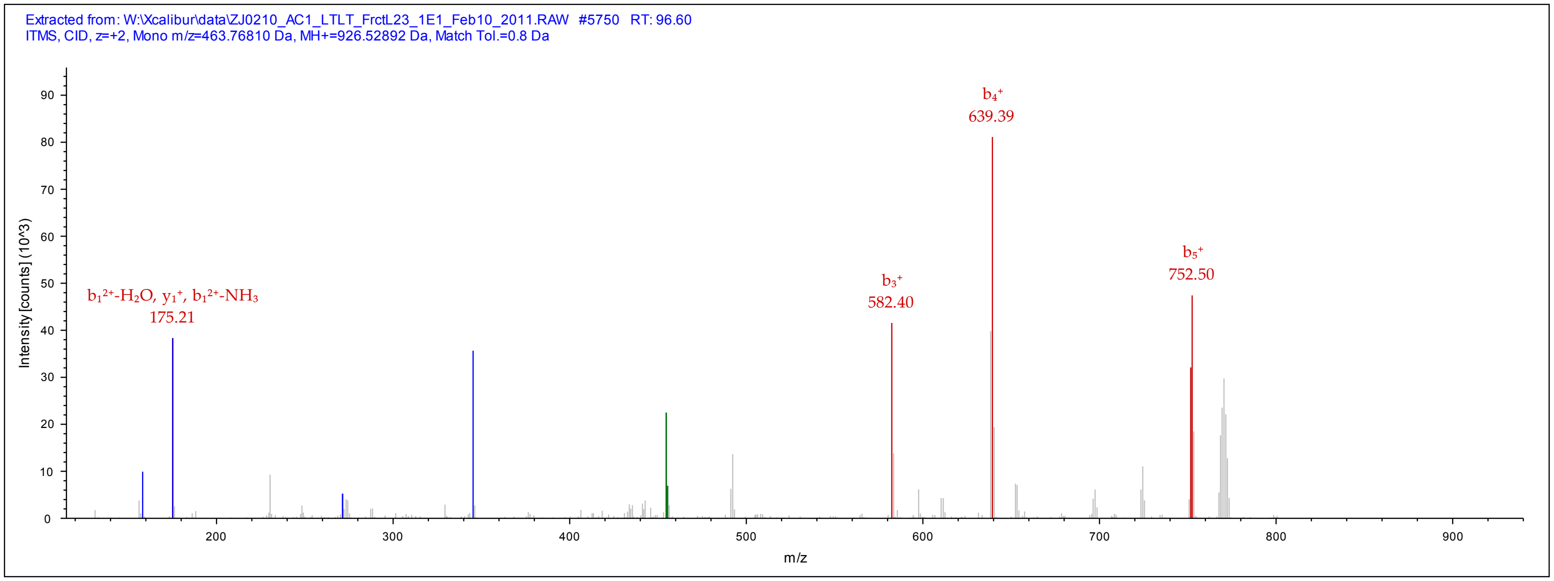
Identified with: Mascot (v1.16); IonScore:37, Exp Value:6.1E-003, Ions matched by search engine: 4/46

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Potassium voltage-gated channel subfamily D member 1
- Potassium voltage-gated channel subfamily D member 2
- Isoform 1 of Potassium voltage-gated channel subfamily D member 3
- Isoform 2 of Potassium voltage-gated channel subfamily D member 3
- Potassium channel, voltage dependent, Kv4.2 family protein
- SPARC-like protein 1
- cDNA FLJ52396, highly similar to SPARC-like protein 1



IPI:IPI00965871.1

Sequence: LLESMIPIK, L1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 751.47540 Da (+0.34 mmu/+0.45 ppm), MH+: 1501.94353 Da, RT: 127.34 min,

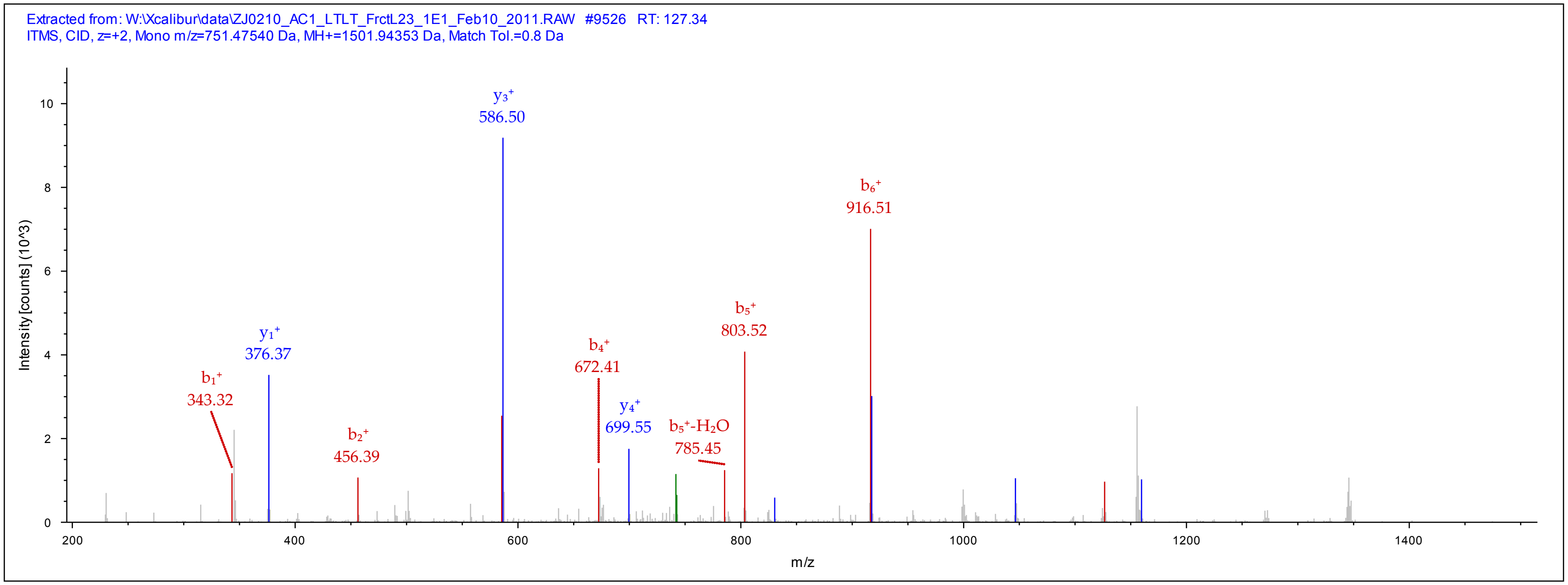
Identified with: Mascot (v1.16); IonScore:40, Exp Value:5.2E-003, Ions matched by search engine: 8/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Protein YIPF3
- Novel protein lng=225
- 34 kDa protein lng=303
- 39 kDa protein
- Protein
- Uncharacterized protein



IPI:IPI00966011.1

Sequence: SSPVVNDGVVR, S1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 679.38647 Da (+0.96 mmu/+1.41 ppm),   MH+: 1357.76567 Da,   RT: 77.35 min,

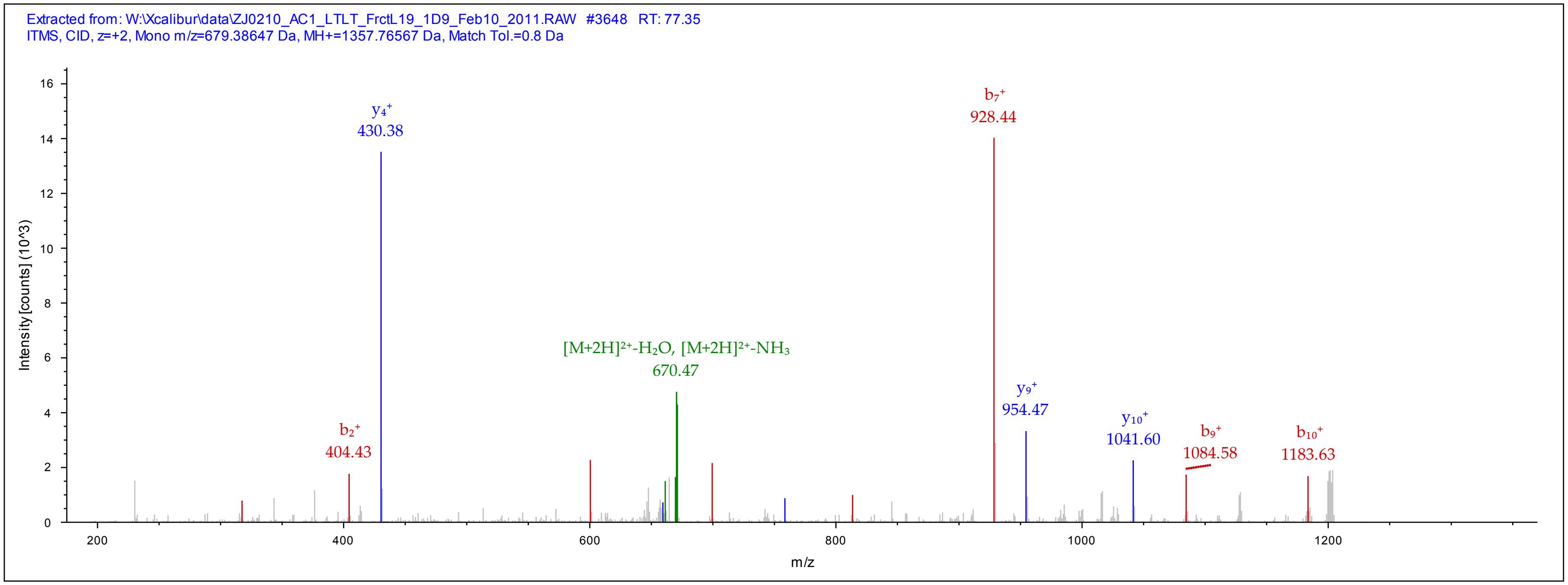
Identified with: Mascot (v1.16); IonScore:43, Exp Value:4.5E-003, Ions matched by search engine: 8/102

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- G-rich sequence factor 1
- G-rich sequence factor 1 isoform 2
- cDNA FLJ42130 fis, clone TESTI2014716, highly similar to G-rich sequence factor 1
- cDNA FLJ55466, highly similar to G-rich sequence factor 1 lng=448
- 51 kDa protein
- 13 kDa protein



IPI:IPI00966084.1

Sequence: ATTADGSSILDR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 718.38361 Da (+0.44 mmu/+0.61 ppm), MH+: 1435.75994 Da, RT: 80.54 min,

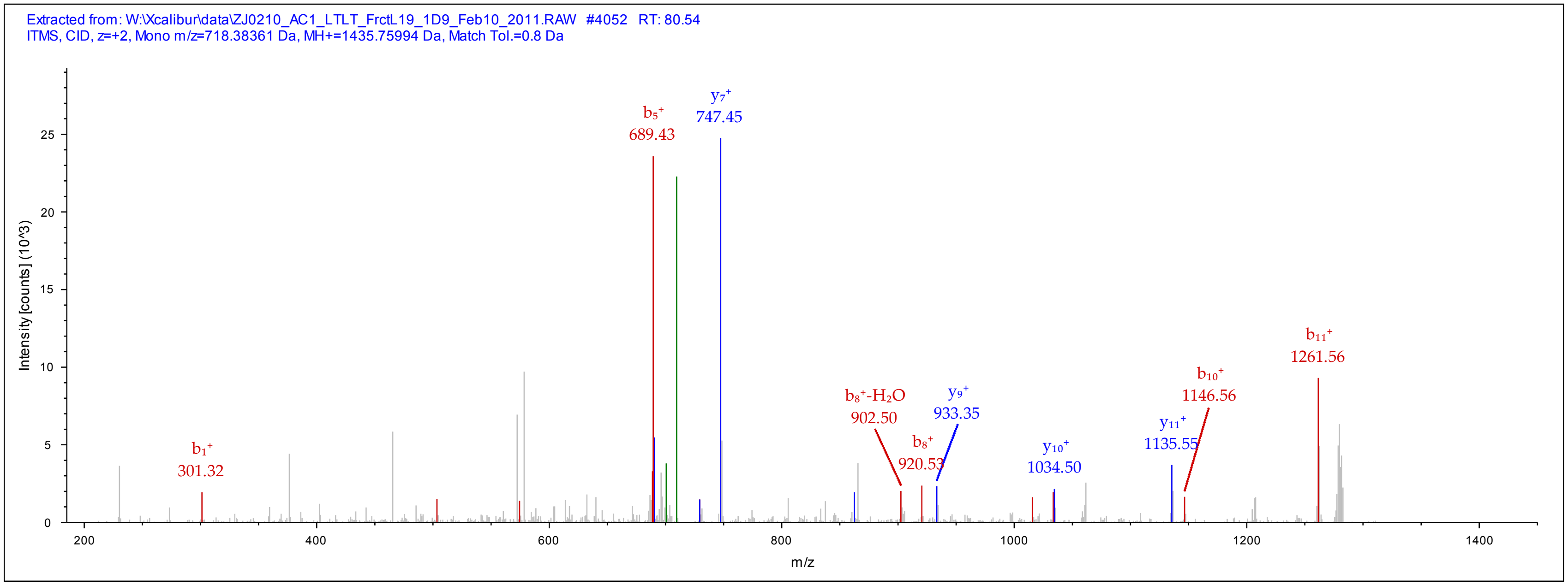
Identified with: Mascot (v1.16); IonScore:58, Exp Value:1.7E-004, Ions matched by search engine: 9/106

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- COP9 signalosome complex subunit 4
- Uncharacterized protein
- cDNA FLJ36919 fis, clone BRACE2003987, highly similar to COP9 signalosome complex subunit 4
- Uncharacterized protein



IPI:IPI00966426.1

Sequence: SAPFFIPTIPGLVPR, S1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 921.05133 Da (+3.32 mmu/+3.61 ppm), MH+: 1841.09538 Da, RT: 140.41 min,

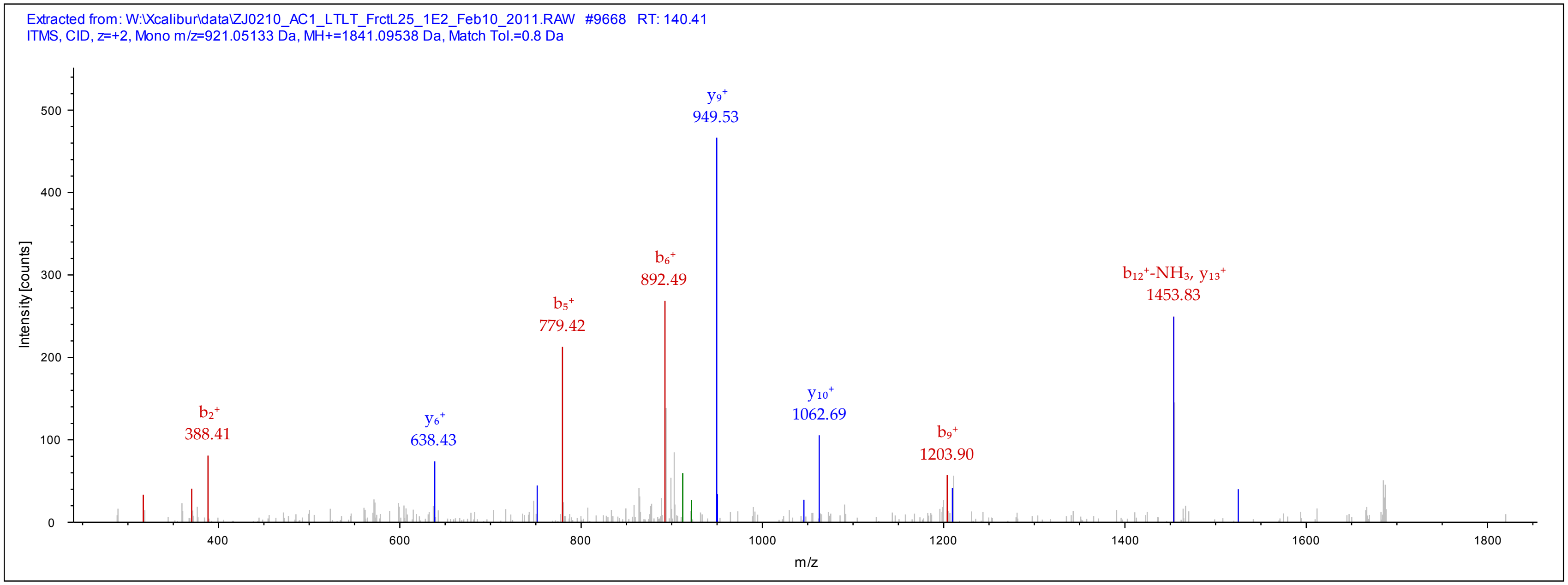
Identified with: Mascot (v1.16); IonScore:39, Exp Value:8.5E-003, Ions matched by search engine: 13/126

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- WD repeat-containing protein 36
- Uncharacterized protein
- Uncharacterized protein



IPI:IPI00966573.1

Sequence: AEFFADVVPAVR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 775.43262 Da (+0.14 mmu/+0.18 ppm), MH+: 1549.85796 Da, RT: 117.61 min,

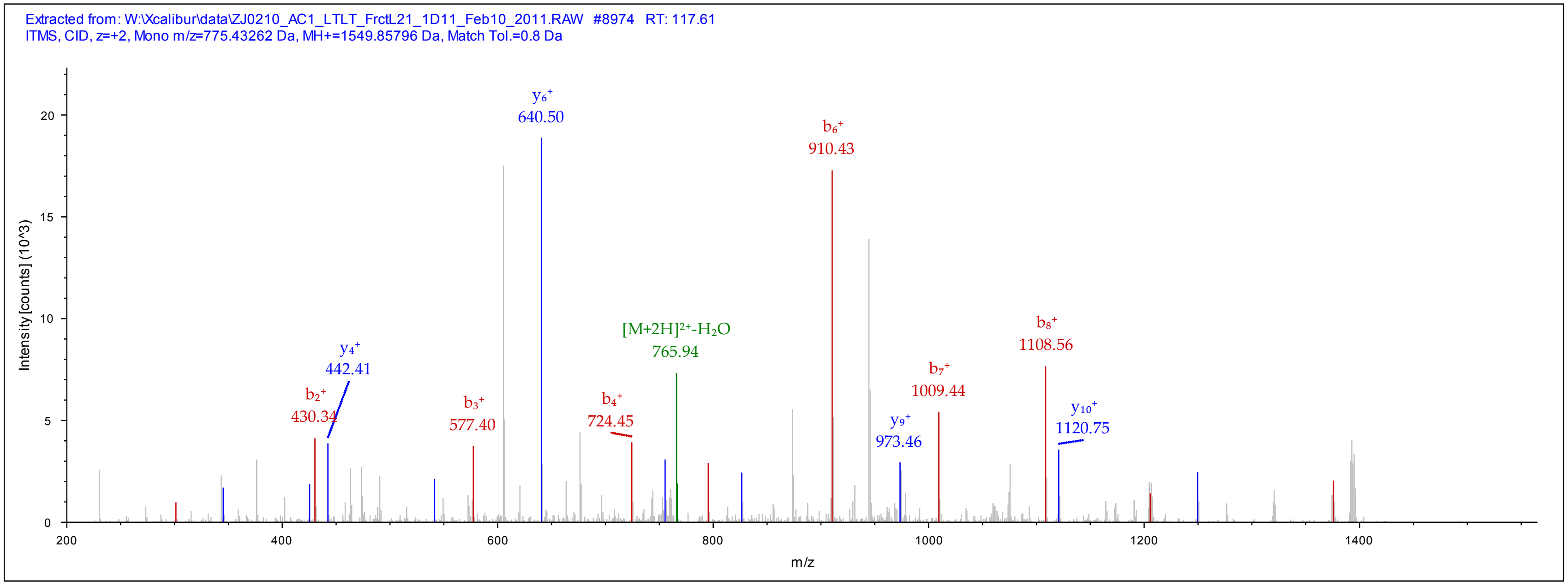
Identified with: Mascot (v1.16); IonScore:51, Exp Value:8.4E-004, Ions matched by search engine: 11/96

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Enolase-phosphatase E1
- MasA lng=210
- Uncharacterized protein



IPI:IPI00966700.1

Sequence: GIMVLAGDTLPIEVYCHLPVMCEDR, G1-TMT6plex (229.16293 Da), C16-Carbamidomethyl (57.02146 Da), C22-Carbamidomethyl (57.02146 Da)

Charge: +3, Monoisotopic m/z: 1039.85388 Da (+0.89 mmu/+0.86 ppm), MH+: 3117.54709 Da, RT: 189.88 min,

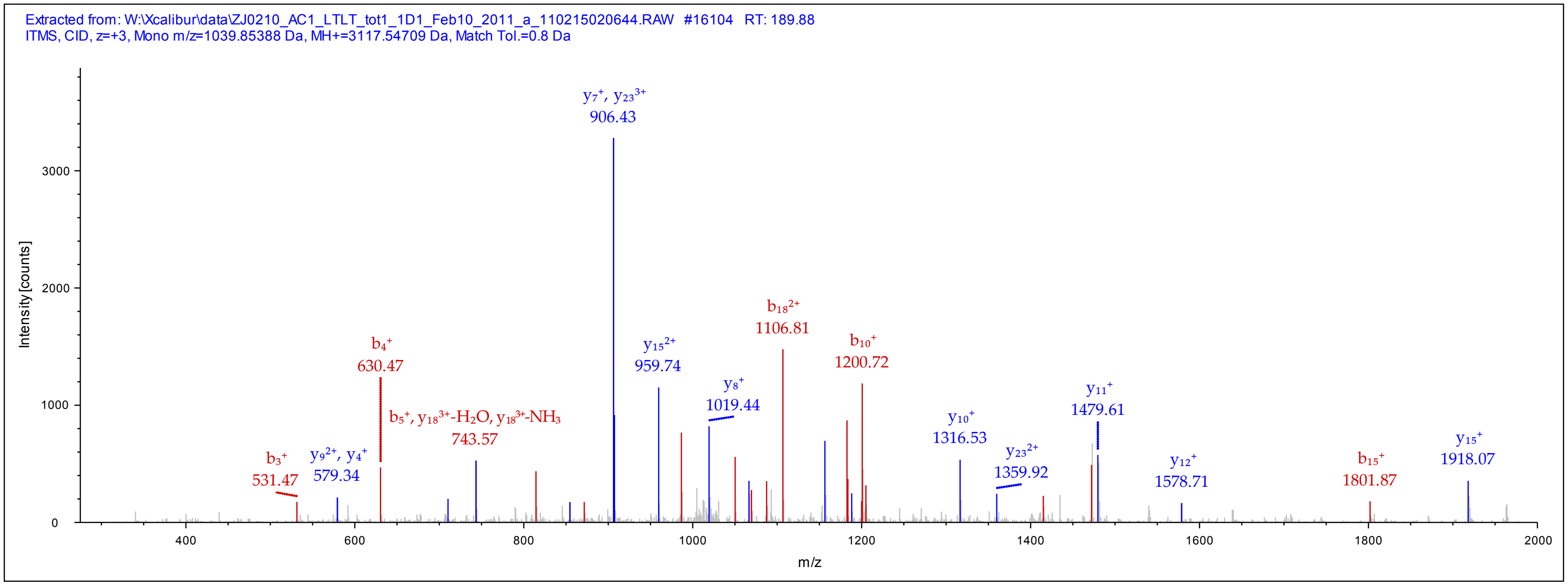
Identified with: Mascot (v1.16); IonScore:72, Exp Value:1.5E-005, Ions matched by search engine: 22/224

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- H/ACA ribonucleoprotein complex subunit 2
- Uncharacterized protein
- Uncharacterized protein



IPI:IPI00966744.1

Sequence: SQWSPALTISK, S1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 838.49359 Da (+0.77 mmu/+0.91 ppm), MH+: 1675.97991 Da, RT: 102.50 min,

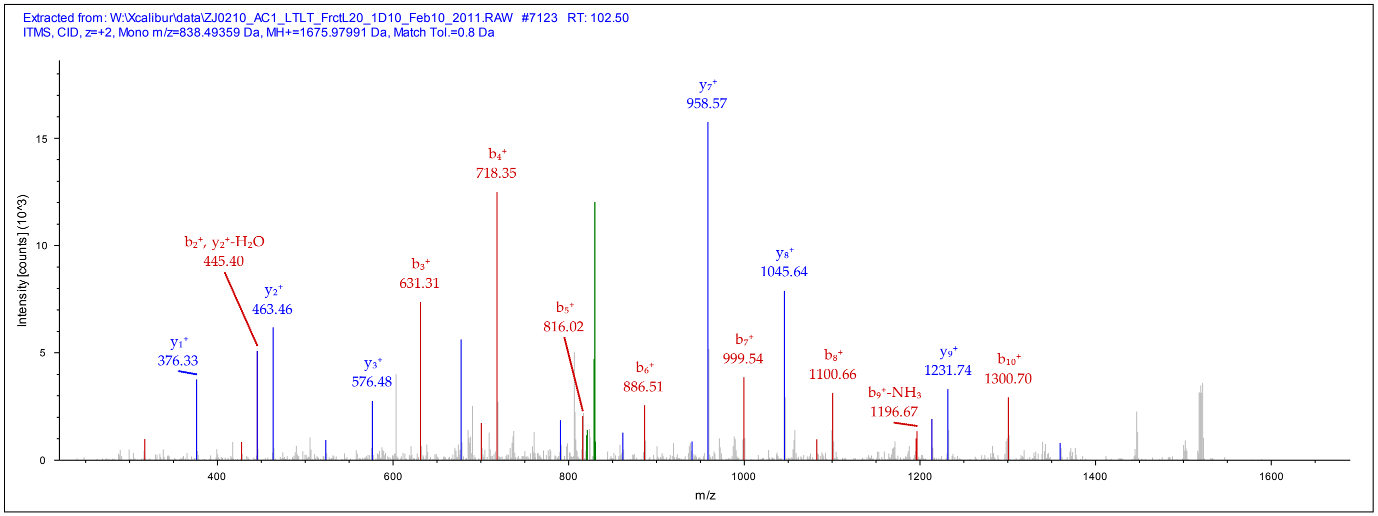
Identified with: Mascot (v1.16); IonScore:59, Exp Value:8.9E-005, Ions matched by search engine: 16/116

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (9):

- ubiquitin-conjugating enzyme E2D 2 isoform 2 lng=118
- Isoform 1 of Ubiquitin-conjugating enzyme E2 D3
- Isoform 2 of Ubiquitin-conjugating enzyme E2 D3
- Ubiquitin-conjugating enzyme E2 D2
- Isoform 3 of Ubiquitin-conjugating enzyme E2 D3
- 16 kDa protein
- Ubiquitin carrier protein



IPI:IPI00966747.1

Sequence: IEEFR, I1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 461.76328 Da (-0.15 mmu/-0.34 ppm),   MH+: 922.51927 Da,   RT: 82.73 min,

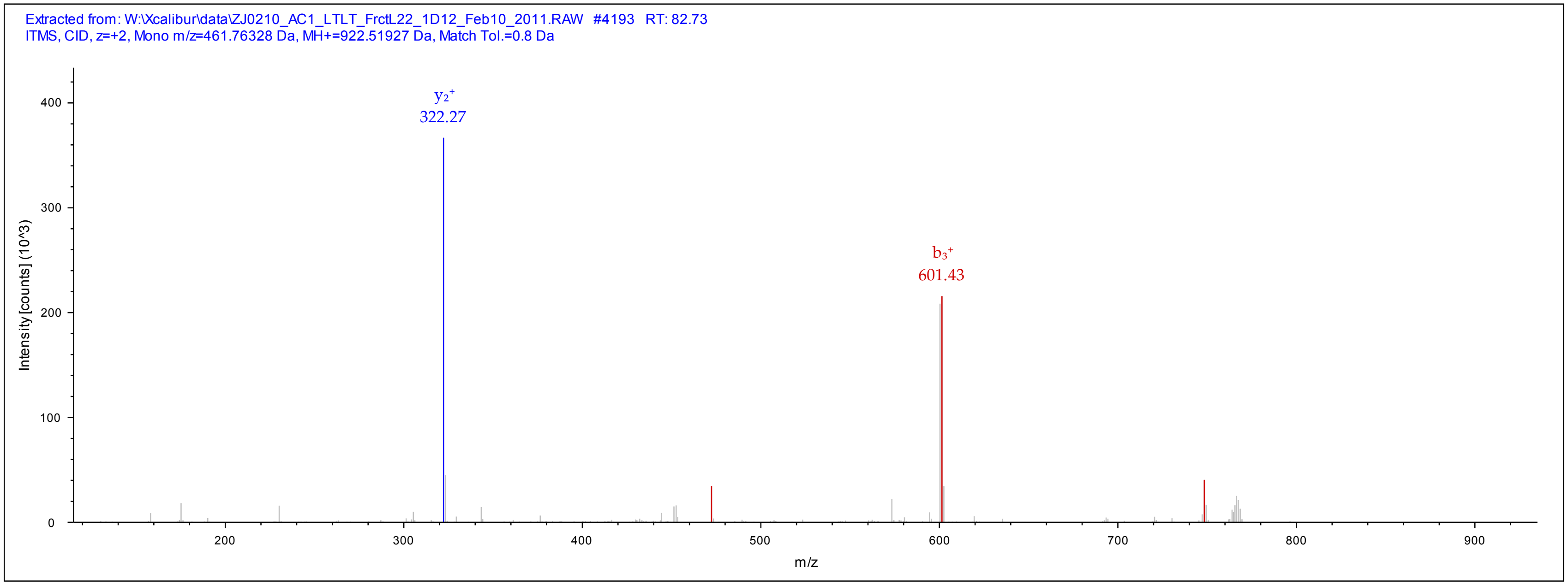
Identified with: Mascot (v1.16); IonScore:34, Exp Value:1.4E-002, Ions matched by search engine: 4/34

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform 1 of Centrosomal protein of 63 kDa
- Isoform 2 of Centrosomal protein of 63 kDa
- Isoform 4 of Centrosomal protein of 63 kDa
- Isoform 3 of Centrosomal protein of 63 kDa
- Uncharacterized protein



IPI:IPI00967665.1

Sequence: EYNEDEDPAAR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 769.35492 Da (+2.86 mmu/+3.71 ppm), MH+: 1537.70256 Da, RT: 67.88 min,

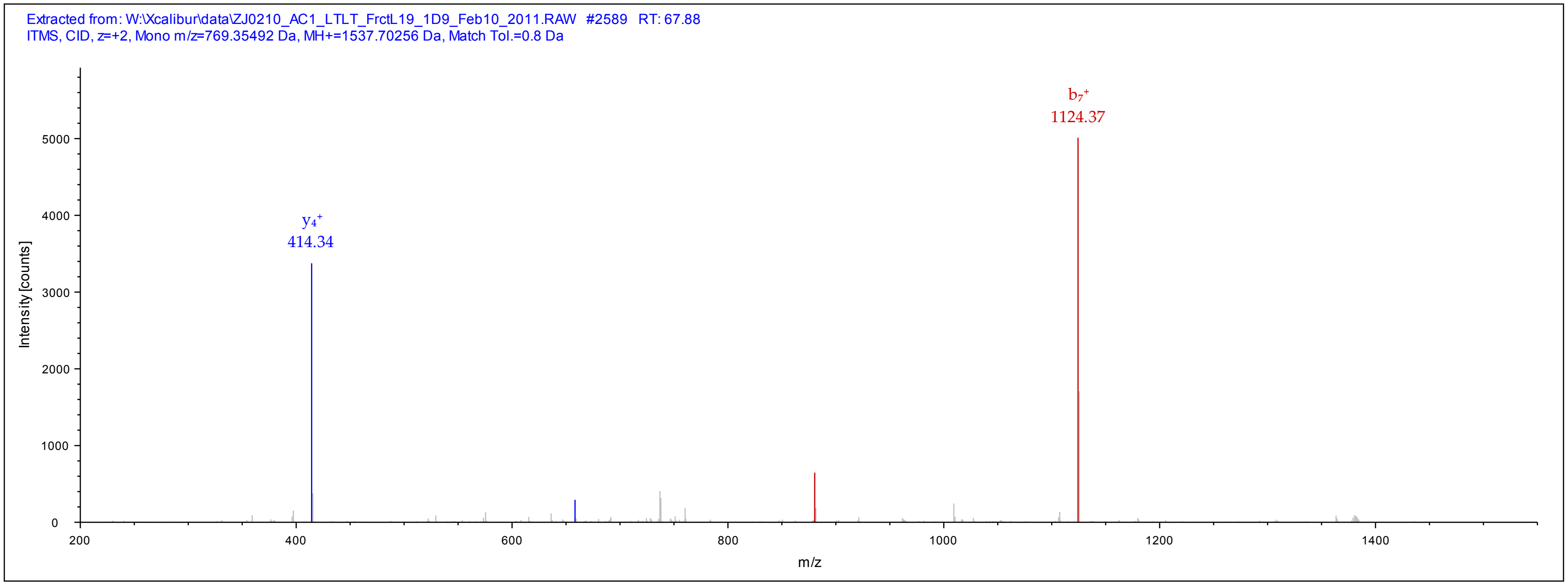
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.0E-002, Ions matched by search engine: 7/108

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Protein Red
- Chondrosarcoma-associated protein 2
- 66 kDa protein
- Uncharacterized protein
- Uncharacterized protein
- Uncharacterized protein



IPI:IPI00967791.1

Sequence: XSEILR, X1-TMT6plex (229.16293 Da), X1-MappingI (113.08407 Da)

Charge: +2,   Monoisotopic m/z: 480.30795 Da (-0.05 mmu/-0.11 ppm),   MH+: 959.60863 Da,   RT: 102.89 min,

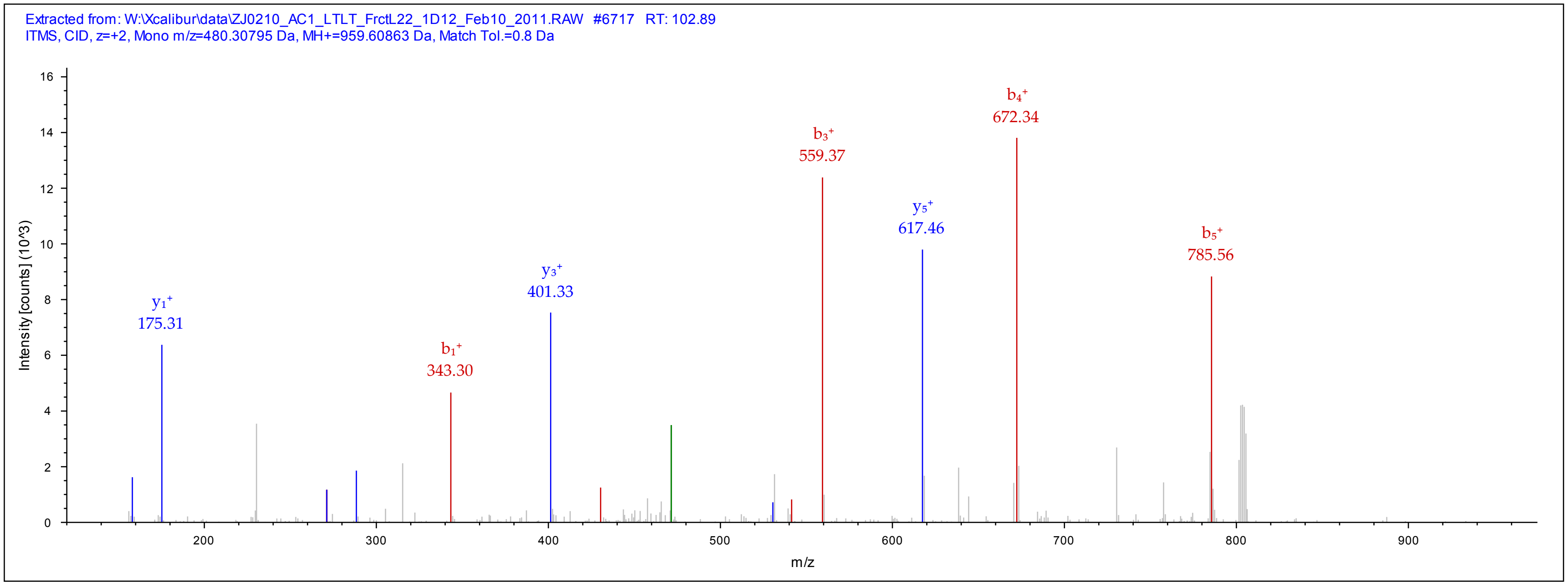
Identified with: Mascot (v1.16); IonScore:32, Exp Value:2.7E-002, Ions matched by search engine: 5/42

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Protein



IPI:IPI00967957.1

Sequence: ATIEDILFK, A1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 754.46216 Da (+1.69 mmu/+2.24 ppm), MH+: 1507.91704 Da, RT: 128.86 min,

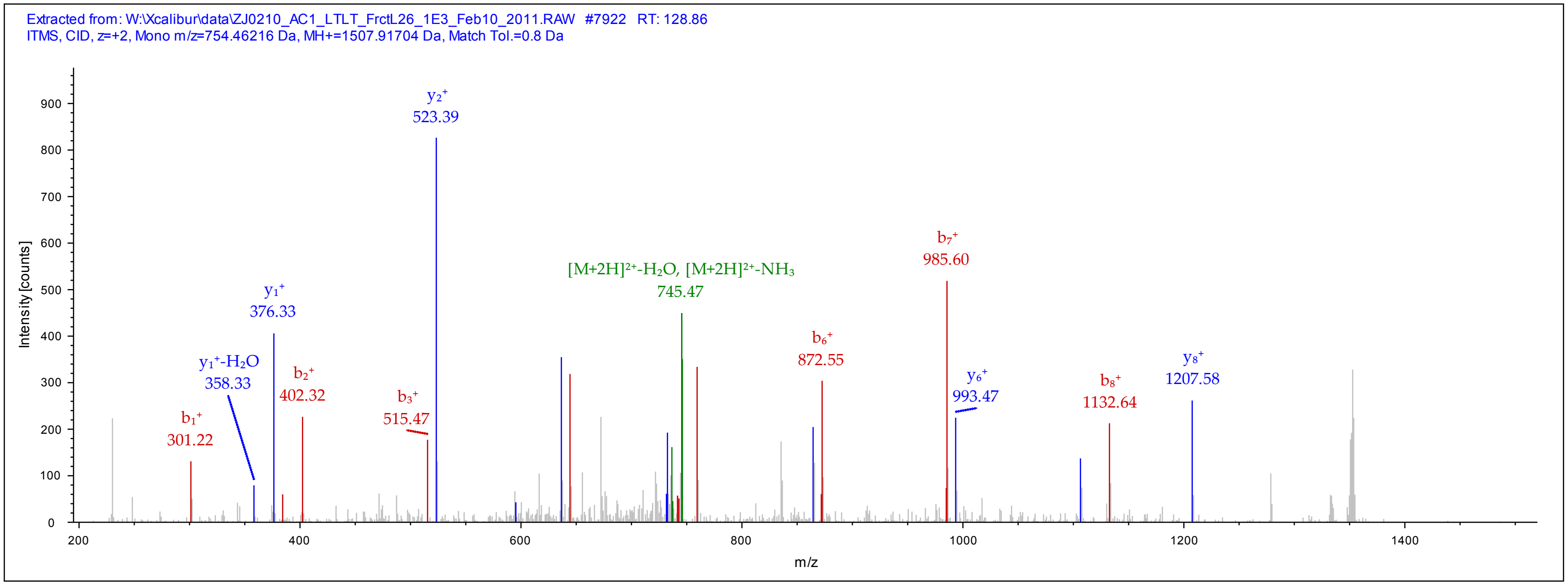
Identified with: Mascot (v1.16); IonScore:42, Exp Value:4.4E-003, Ions matched by search engine: 14/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (10):

- General transcription factor IIH subunit 2
- General transcription factor IIH subunit 2-like protein
- 19 kDa protein
- Uncharacterized protein
- Uncharacterized protein
- GTF2H2C protein



IPI:IPI00968032.1

Sequence: DLIDYVR, D1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 561.82166 Da (+0.18 mmu/+0.32 ppm),   MH+: 1122.63603 Da,   RT: 93.80 min,

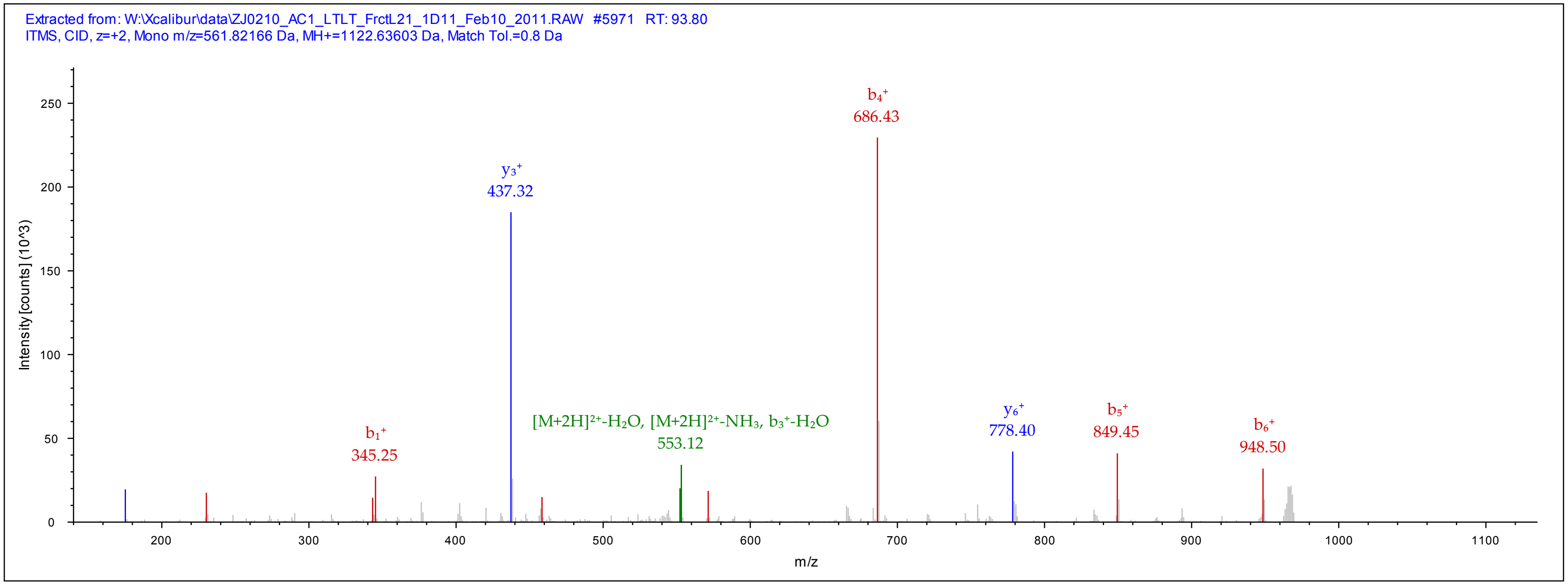
Identified with: Mascot (v1.16); IonScore:33, Exp Value:3.6E-002, Ions matched by search engine: 5/54

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Nucleolar protein 16
- HSPC185
- Putative uncharacterized protein HSPC111
- Uncharacterized protein
- Uncharacterized protein



IPI:IPI00969419.1

Sequence: FIAVGYVDDTQFVR, F1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 929.99835 Da (-0.35 mmu/-0.38 ppm),   MH+: 1858.98943 Da,   RT: 118.20 min,

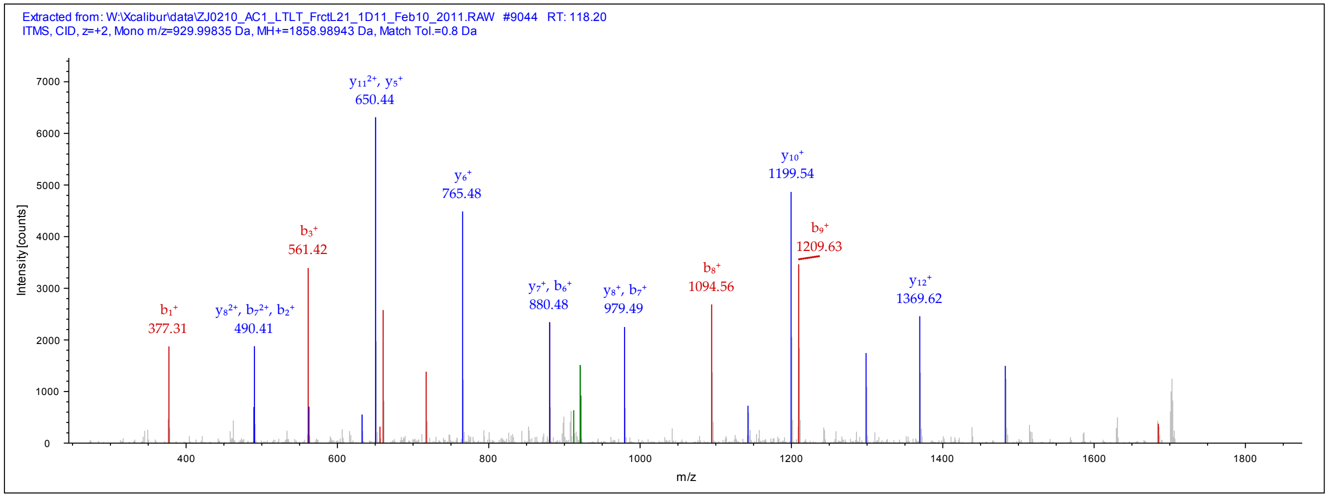
Identified with: Mascot (v1.16); IonScore:64, Exp Value:5.5E-005, Ions matched by search engine: 10/114

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (299):

- HLA class I histocompatibility antigen, A-1 alpha chain
- HLA class I histocompatibility antigen, A-33 alpha chain
- HLA class I histocompatibility antigen, B-59 alpha chain
- HLA class I histocompatibility antigen, B-58 alpha chain
- HLA class I histocompatibility antigen, A-23 alpha chain
- HLA class I histocompatibility antigen, A-74 alpha chain
- HLA class I histocompatibility antigen, B-54 alpha chain



IPI:IPI00011604.2

Sequence: SCYEDGWLIK, S1-TMT6plex (229.16293 Da), C2-Carbamidomethyl (57.02146 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 864.95605 Da (+0.84 mmu/+0.97 ppm),   MH+: 1728.90483 Da,   RT: 105.14 min,

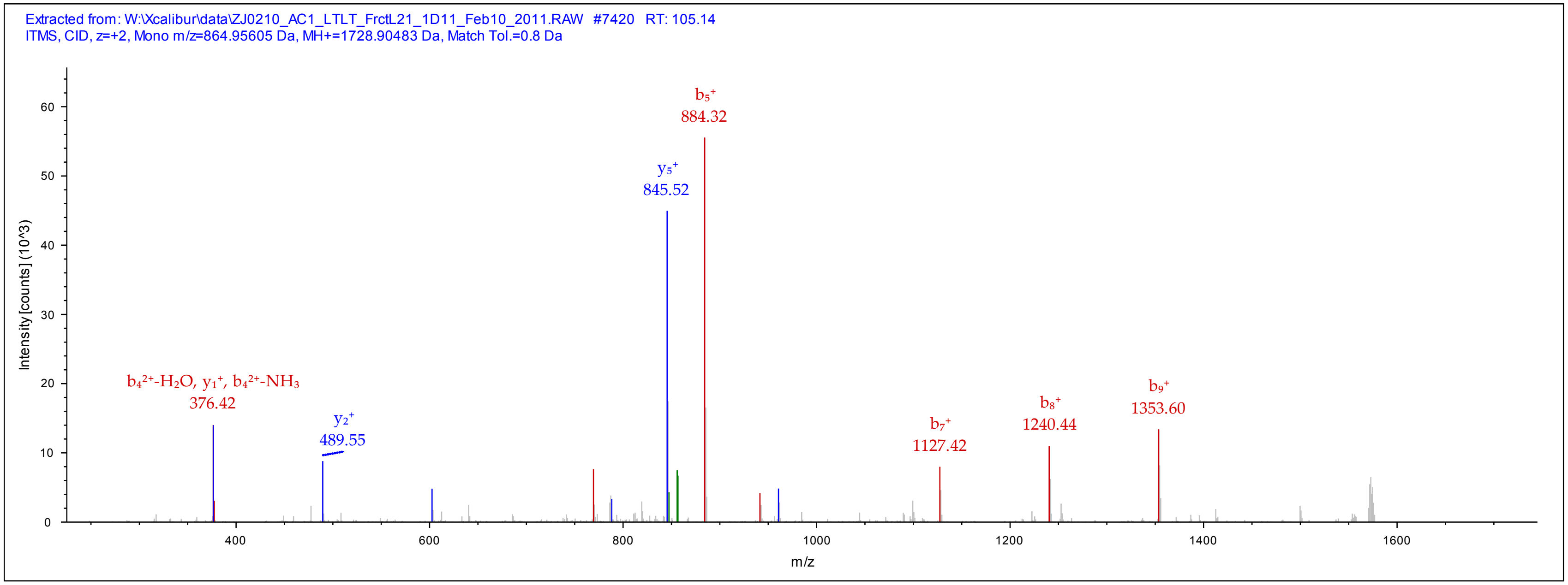
Identified with: Mascot (v1.16); IonScore:46, Exp Value:3.4E-003, Ions matched by search engine: 11/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Glycine cleavage system H protein, mitochondrial



IPI:IPI00000760.1

Sequence: LSDVTLVPVSCSELEK, L1-TMT6plex (229.16293 Da), C11-Carbamidomethyl (57.02146 Da), K16-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 1117.62512 Da (+3.74 mmu/+3.35 ppm),   MH+: 2234.24297 Da,   RT: 117.71 min,

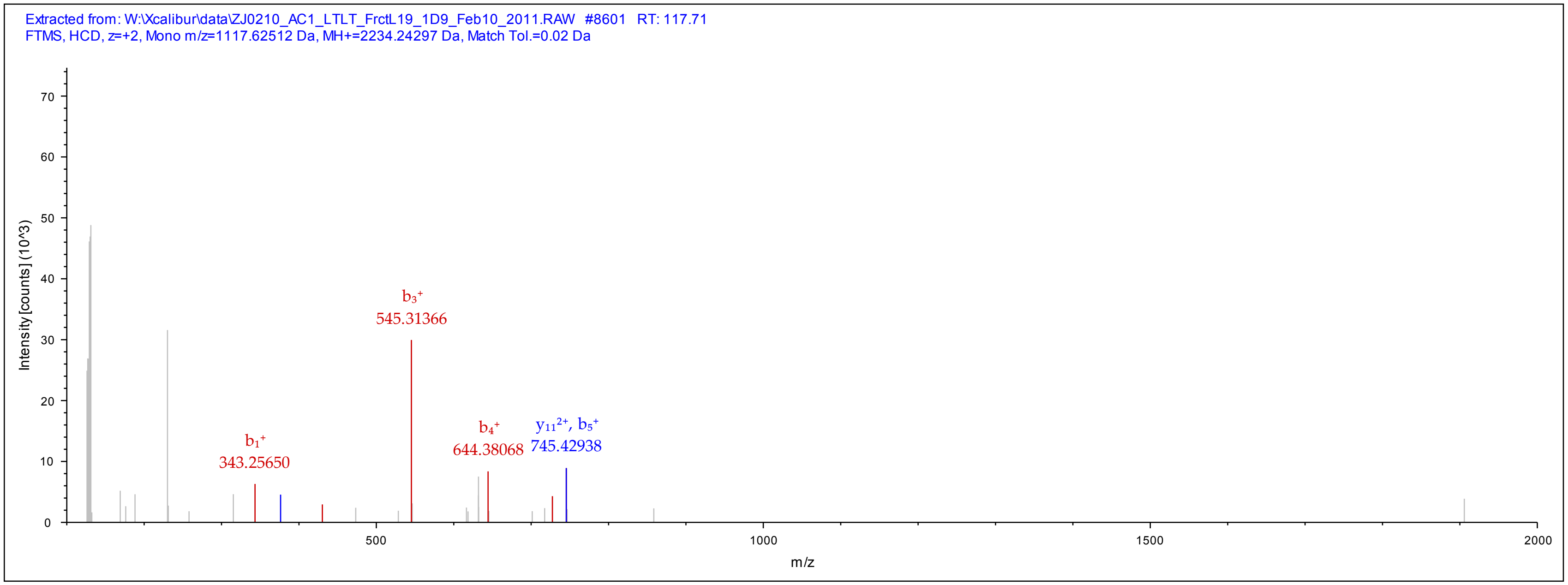
Identified with: Mascot (v1.16); IonScore:35, Exp Value:4.3E-001, Ions matched by search engine: 6/146

Fragment match tolerance used for search: 0.02 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- N(G),N(G)-dimethylarginine dimethylaminohydrolase 2



IPI:IPI00002214.1

Sequence: LLGASELPIVTPALR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 890.05164 Da (+0.89 mmu/+1 ppm),   MH+: 1779.09599 Da,   RT: 127.80 min,

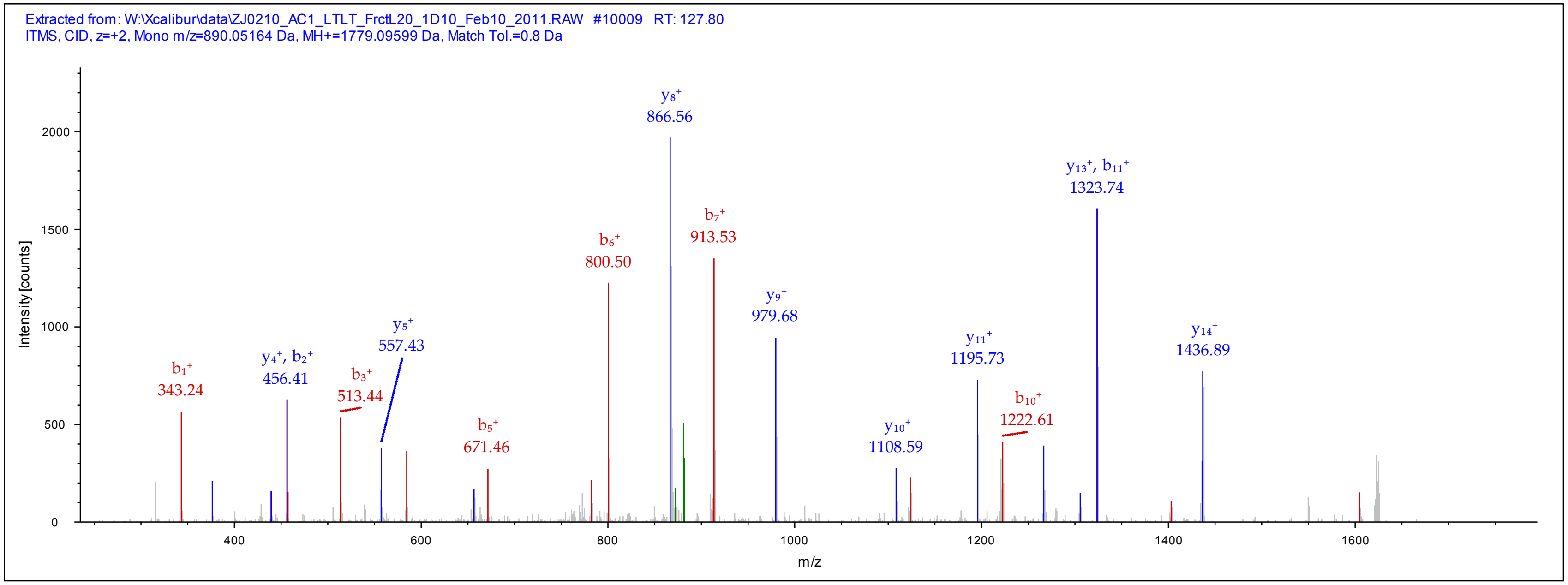
Identified with: Mascot (v1.16); IonScore:74, Exp Value:2.2E-006, Ions matched by search engine: 12/124

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Importin subunit alpha-2
- Karyopherin alpha 2 lng=529



IPI:IPI00002525.3

Sequence: ELEALDEVFTK, E1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 876.49512 Da (-0.12 mmu/-0.14 ppm), MH+: 1751.98296 Da, RT: 122.99 min,

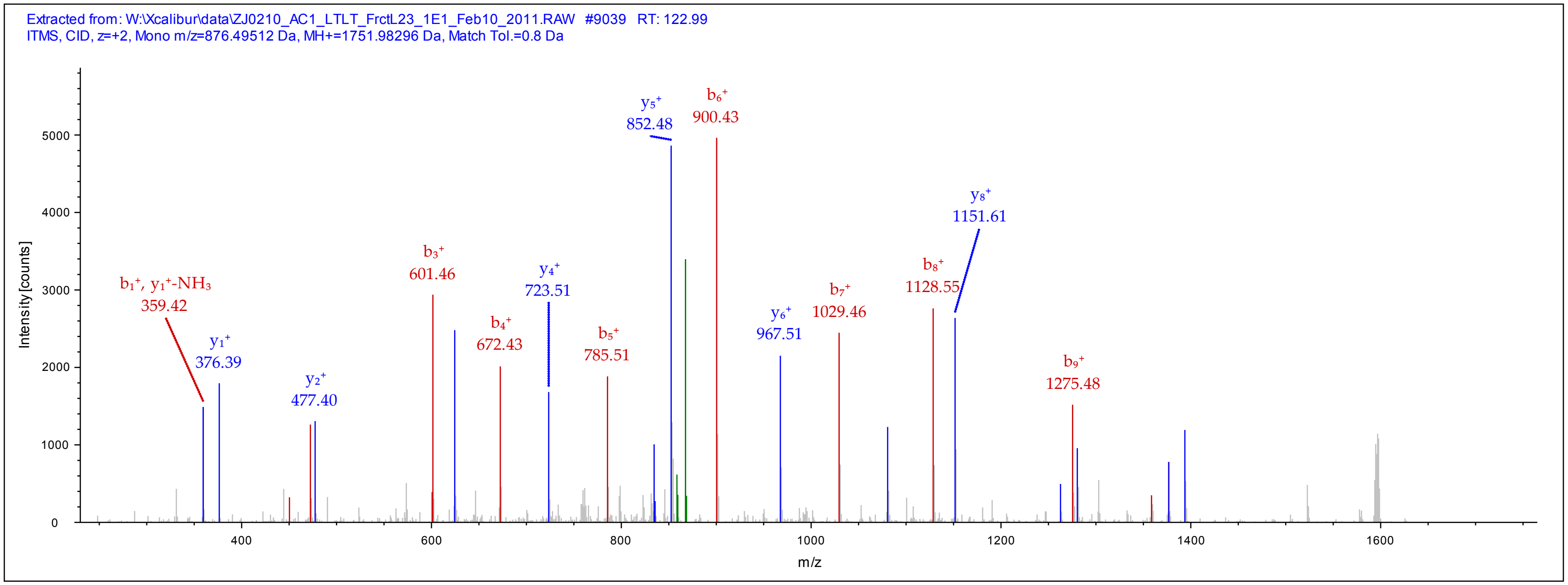
Identified with: Mascot (v1.16); IonScore:85, Exp Value:3.8E-007, Ions matched by search engine: 20/98

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Neudesin



IPI:IPI00002919.2

Sequence: LIVQIK, L1-TMT6plex (229.16293 Da), K6-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 586.41309 Da (+0.51 mmu/+0.86 ppm), MH+: 1171.81890 Da, RT: 107.82 min,

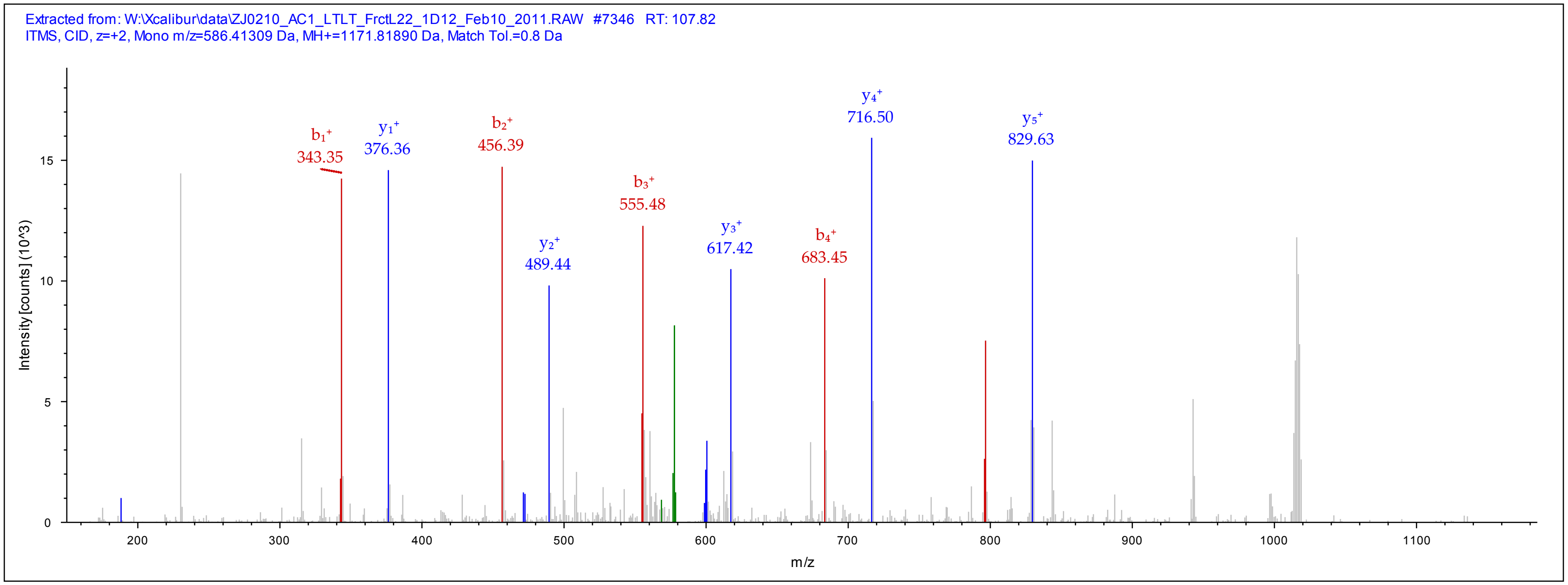
Identified with: Mascot (v1.16); IonScore:38, Exp Value:1.5E-002, Ions matched by search engine: 10/46

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- GTP-binding protein Di-Ras1



IPI00007163.1

Sequence: ESILDLSK, E1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 681.91534 Da (-0.54 mmu/-0.79 ppm),   MH+: 1362.82341 Da,   RT: 127.64 min,

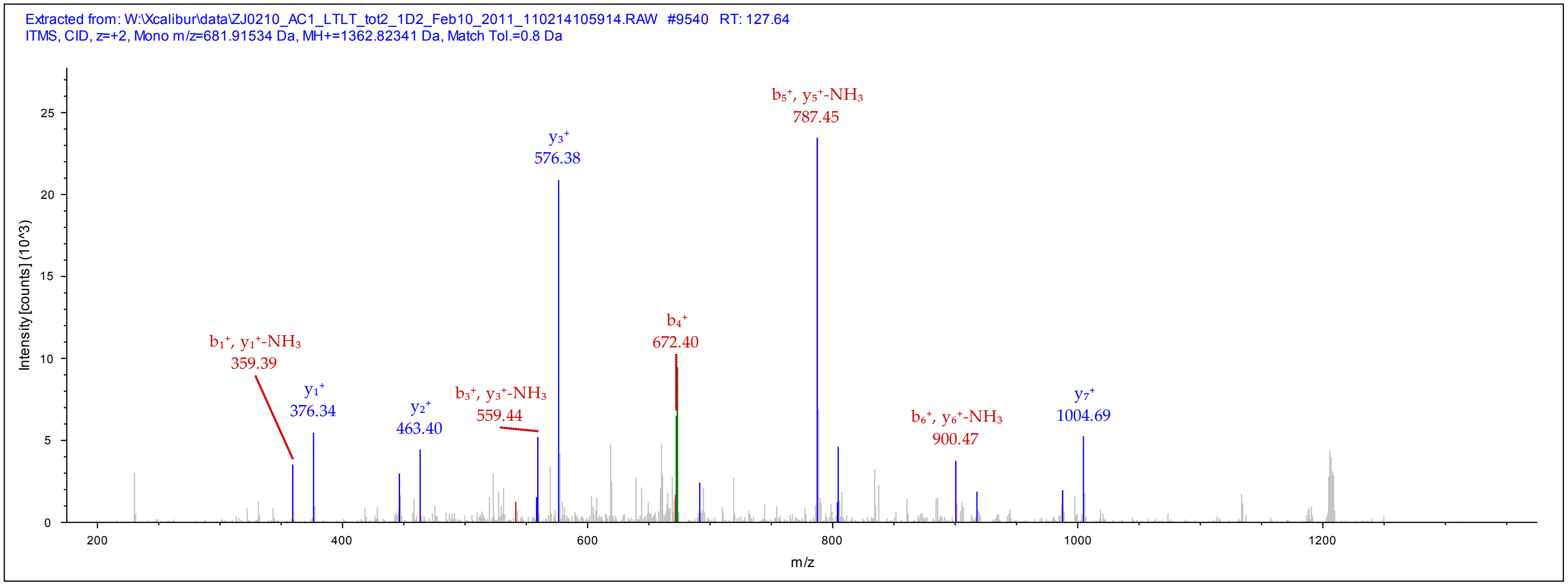
Identified with: Mascot (v1.16); IonScore:43, Exp Value:3.2E-003, Ions matched by search engine: 7/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- U6 snRNA-associated Sm-like protein LSm7 lng=103



IPI:IPI00007364.1

Sequence: STGPGASLGTGYDR, S1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 784.40039 Da (+1.04 mmu/+1.33 ppm), MH+: 1567.79350 Da, RT: 76.42 min,

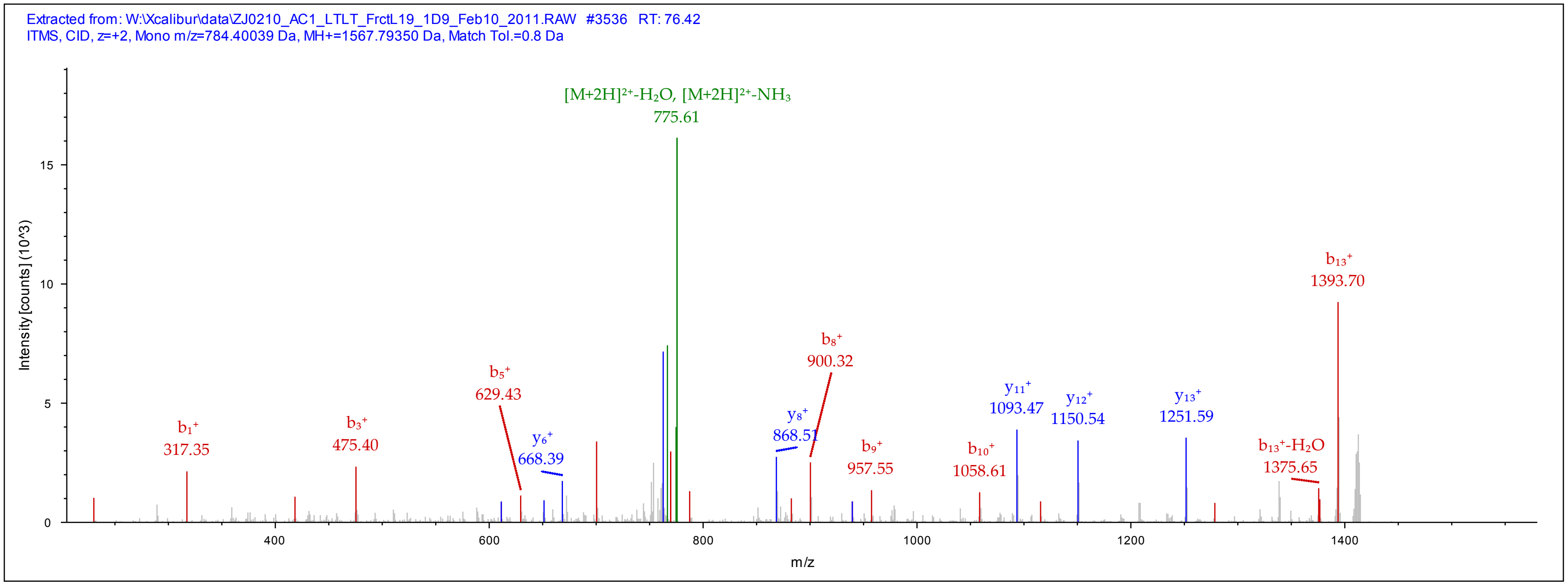
Identified with: Mascot (v1.16); IonScore:66, Exp Value:3.0E-005, Ions matched by search engine: 11/128

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Claudin-3



IPI:IPI00008552.6

Sequence: GELVGGLDIVK, G1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 779.48450 Da (+0.02 mmu/+0.02 ppm), MH+: 1557.96172 Da, RT: 109.23 min,

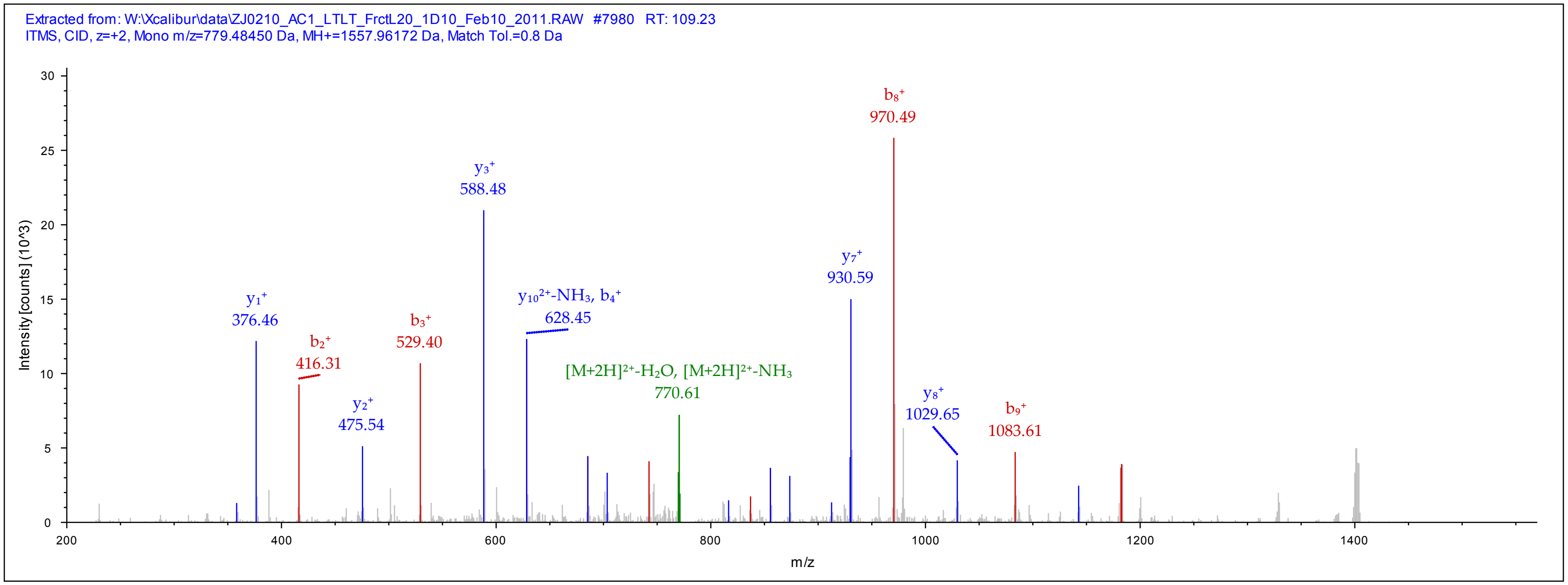
Identified with: Mascot (v1.16); IonScore:64, Exp Value:2.2E-005, Ions matched by search engine: 9/92

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Glutaredoxin-3



IPI:IPI00011603.2

Sequence: ELDTVTLEDIK, E1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 867.50134 Da (+0.82 mmu/+0.95 ppm), MH+: 1733.99541 Da, RT: 109.26 min,

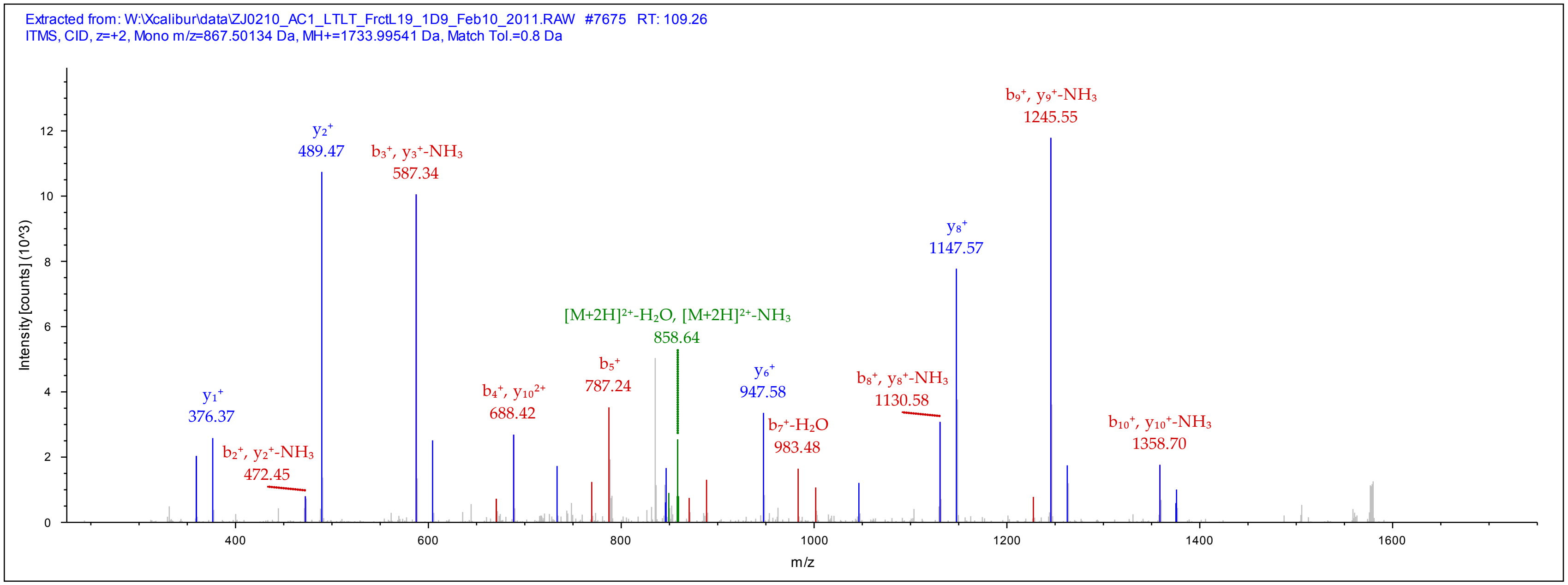
Identified with: Mascot (v1.16); IonScore:64, Exp Value:4.1E-005, Ions matched by search engine: 10/96

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 26S proteasome non-ATPase regulatory subunit 3



IPI:IPI00012795.3

Sequence: SYSSGGEDGYVR, S1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 753.35834 Da (+1.2 mmu/+1.59 ppm), MH+: 1505.70940 Da, RT: 70.75 min,

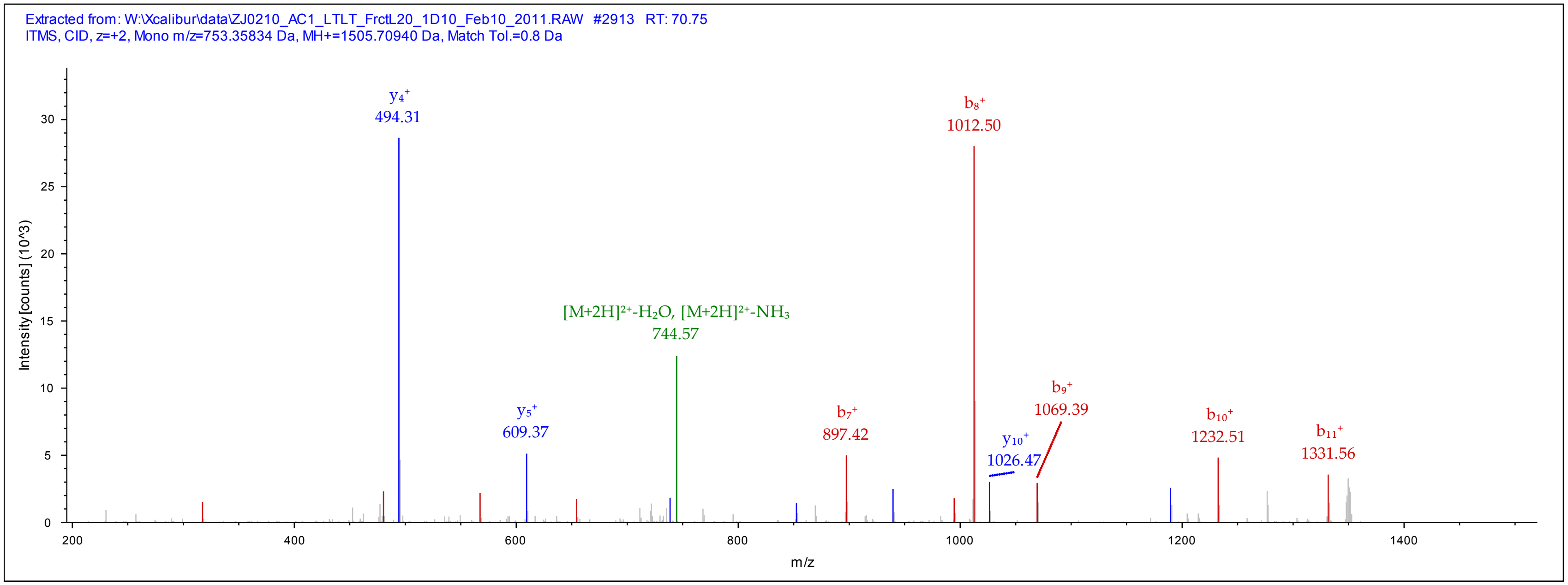
Identified with: Mascot (v1.16); IonScore:71, Exp Value:4.9E-006, Ions matched by search engine: 9/102

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Eukaryotic translation initiation factor 3 subunit I



IPI:IPI00013949.1

Sequence: TPPSEEDSAEAER, T1-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 549.59796 Da (+2.86 mmu/+5.2 ppm), MH+: 1646.77933 Da, RT: 65.90 min,

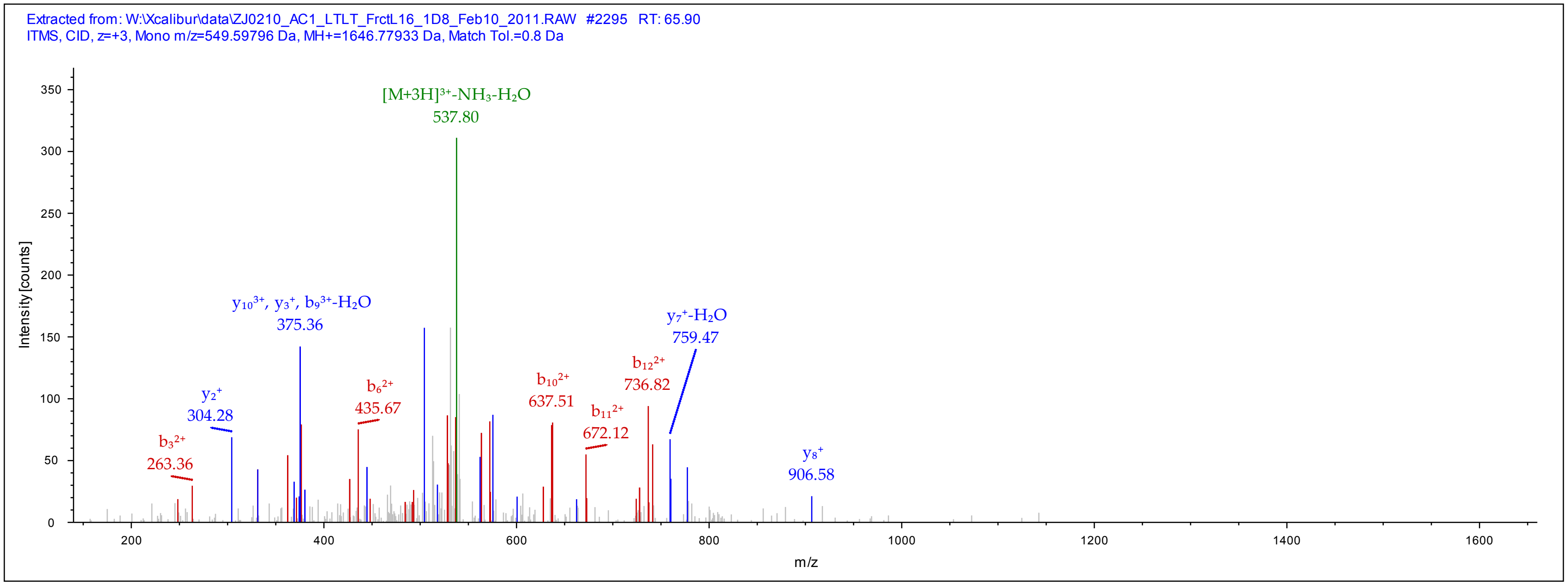
Identified with: Mascot (v1.16); IonScore:41, Exp Value:6.2E-003, Ions matched by search engine: 10/118

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Small glutamine-rich tetratricopeptide repeat-containing protein alpha



IPI:IPI00019018.3

Sequence: VAGLETISTATGR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 752.93188 Da (+1.6 mmu/+2.12 ppm), MH+: 1504.85649 Da, RT: 93.63 min,

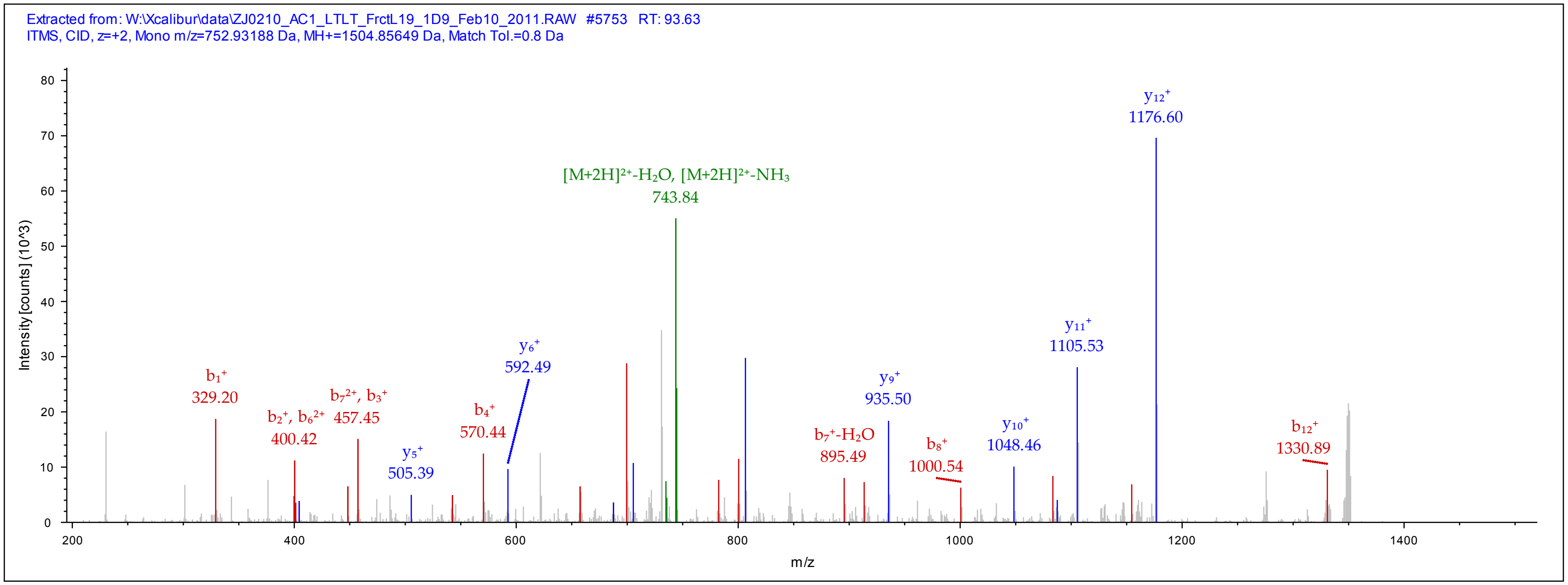
Identified with: Mascot (v1.16); IonScore:54, Exp Value:4.1E-004, Ions matched by search engine: 16/108

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Isoform 1 of Delta(14)-sterol reductase



IPI:IPI00019733.1

Sequence: GLIVYQLENQPSEFR, G1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 1011.54645 Da (-0.1 mmu/-0.1 ppm), MH+: 2022.08562 Da, RT: 112.25 min,

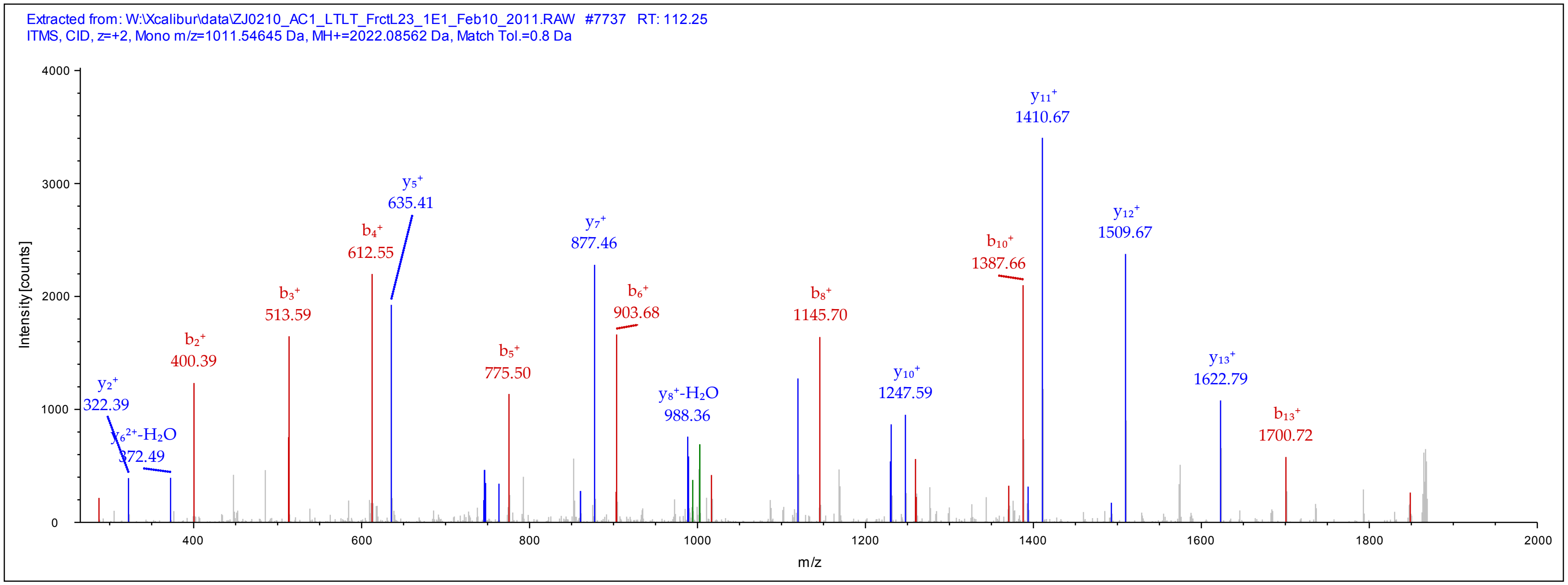
Identified with: Mascot (v1.16); IonScore:58, Exp Value:2.2E-004, Ions matched by search engine: 7/140

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- mRNA export factor



IPI:IPI00022283.1

Sequence: GCCFDDTVR, G1-TMT6plex (229.16293 Da), C2-Carbamidomethyl (57.02146 Da), C3-Carbamidomethyl (57.02146 Da)

Charge: +2, Monoisotopic m/z: 679.80560 Da (+0.42 mmu/+0.62 ppm), MH+: 1358.60393 Da, RT: 73.69 min,

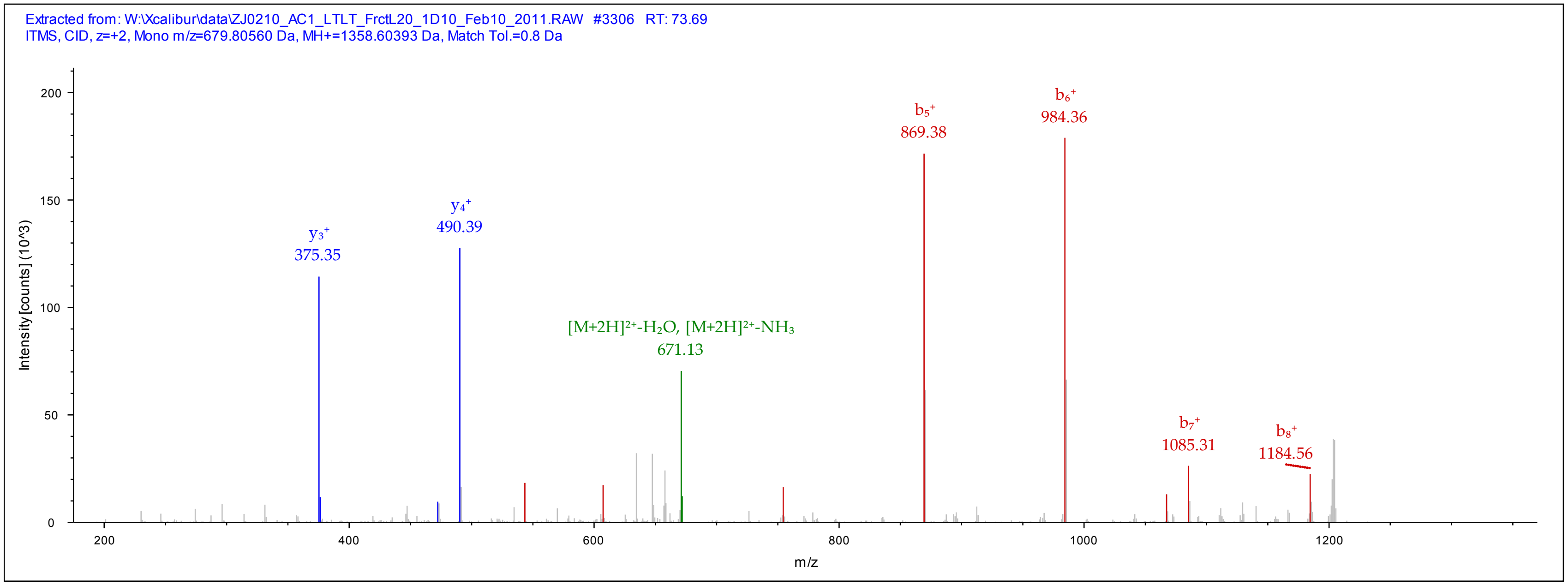
Identified with: Mascot (v1.16); IonScore:35, Exp Value:1.3E-002, Ions matched by search engine: 5/68

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Trefoil factor 1



IPI:IPI00024934.4

Sequence: ILFDGIPLEK, I1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 801.99847 Da (+1.25 mmu/+1.56 ppm), MH+: 1602.98967 Da, RT: 128.06 min,

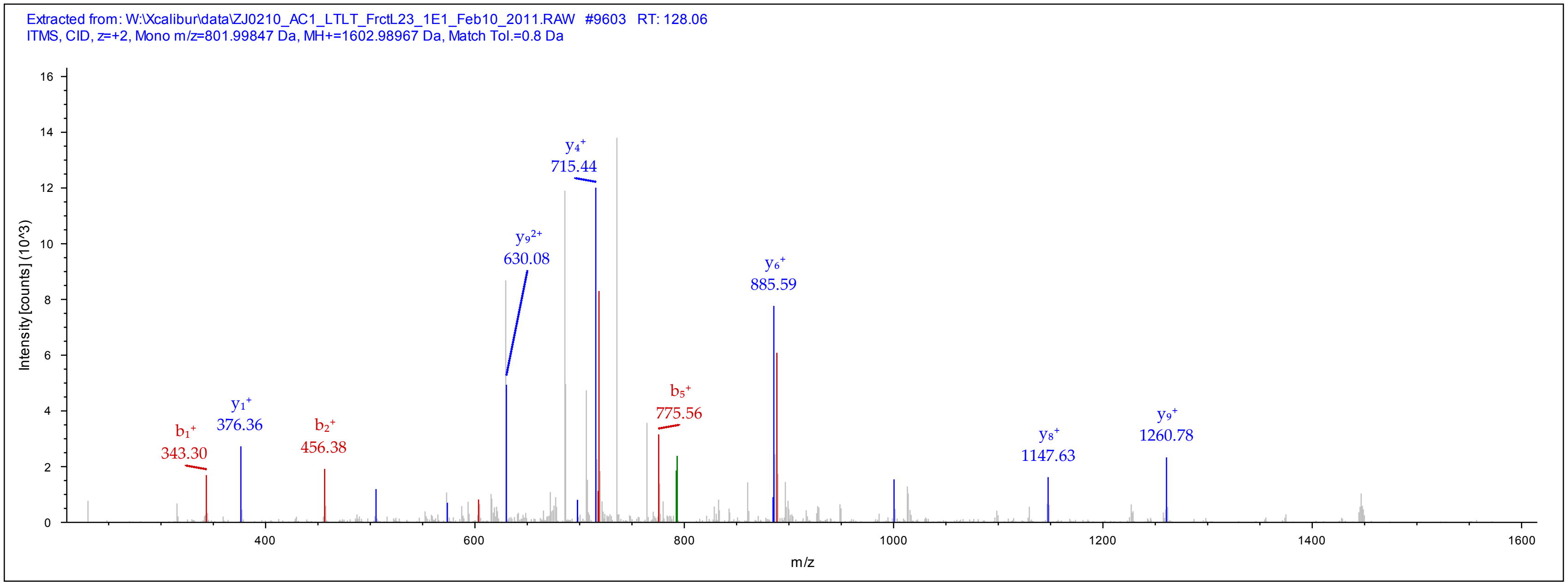
Identified with: Mascot (v1.16); IonScore:31, Exp Value:4.9E-002, Ions matched by search engine: 7/82

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Methylmalonyl-CoA mutase, mitochondrial



IPI:IPI00025084.3

Sequence: LFAQLAGDDMEVSATELMNILNK, L1-TMT6plex (229.16293 Da), K23-TMT6plex (229.16293 Da)

Charge: +4,   Monoisotopic m/z: 746.15021 Da (+1.52 mmu/+2.03 ppm),   MH+: 2981.57900 Da,   RT: 233.16 min,

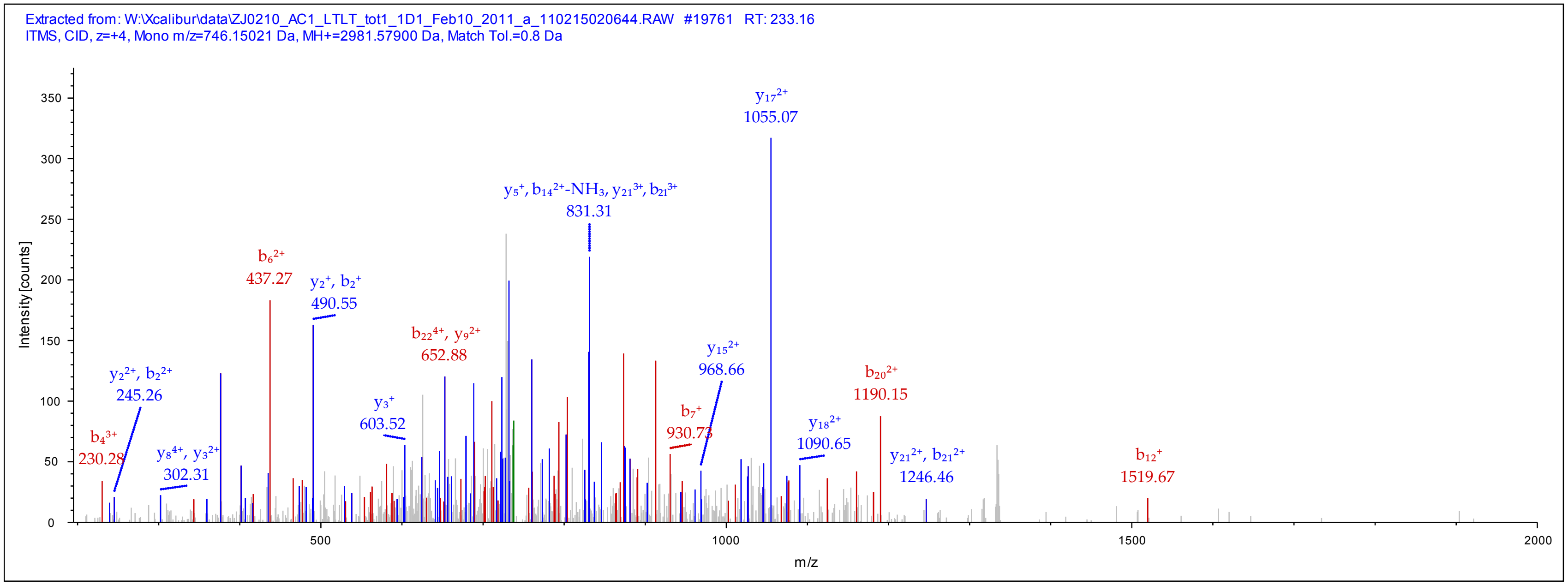
Identified with: Mascot (v1.16); IonScore:51, Exp Value:1.3E-003, Ions matched by search engine: 20/230

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Calpain small subunit 1



IPI:IPI00026530.4

Sequence: YVSSLTEEISK, Y1-TMT6plex (229.16293 Da), K11-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 857.48865 Da (+1.25 mmu/+1.45 ppm), MH+: 1713.97002 Da, RT: 102.50 min,

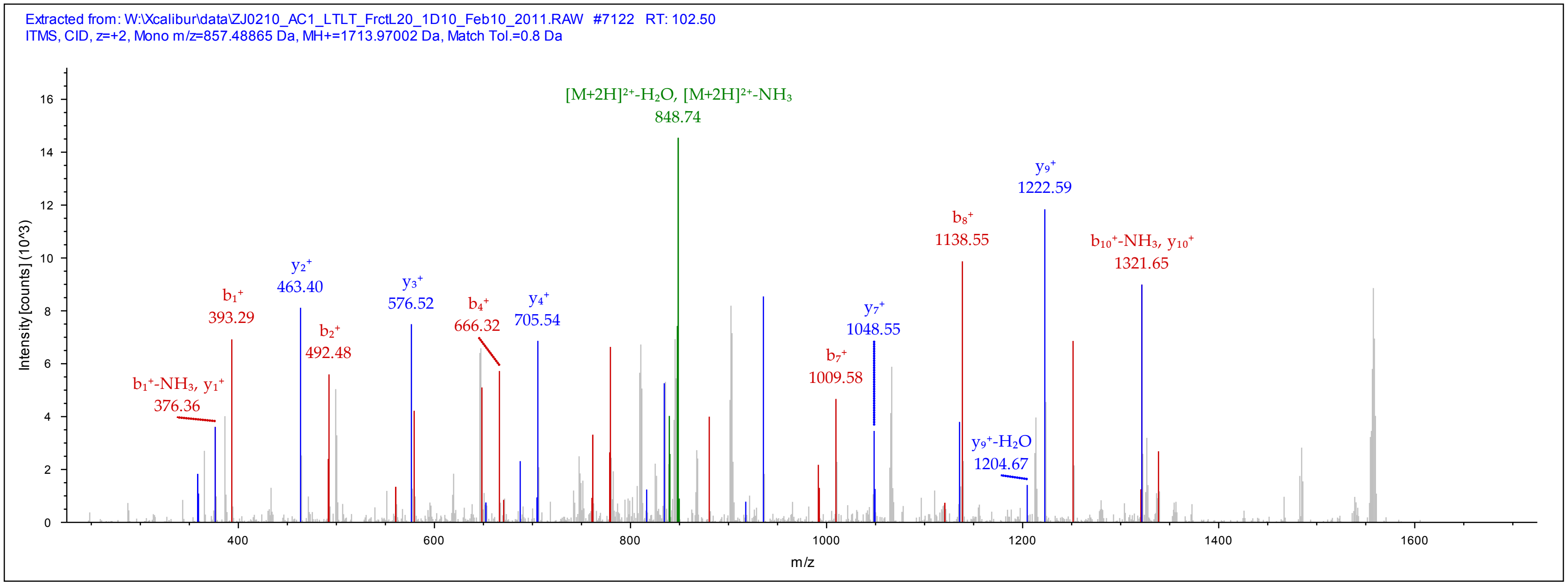
Identified with: Mascot (v1.16); IonScore:34, Exp Value:4.6E-002, Ions matched by search engine: 9/94

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Protein ERGIC-53



IPI:IPI00026952.1

Sequence: ILNPLLDR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 591.87451 Da (+0.46 mmu/+0.78 ppm), MH+: 1182.74175 Da, RT: 106.74 min,

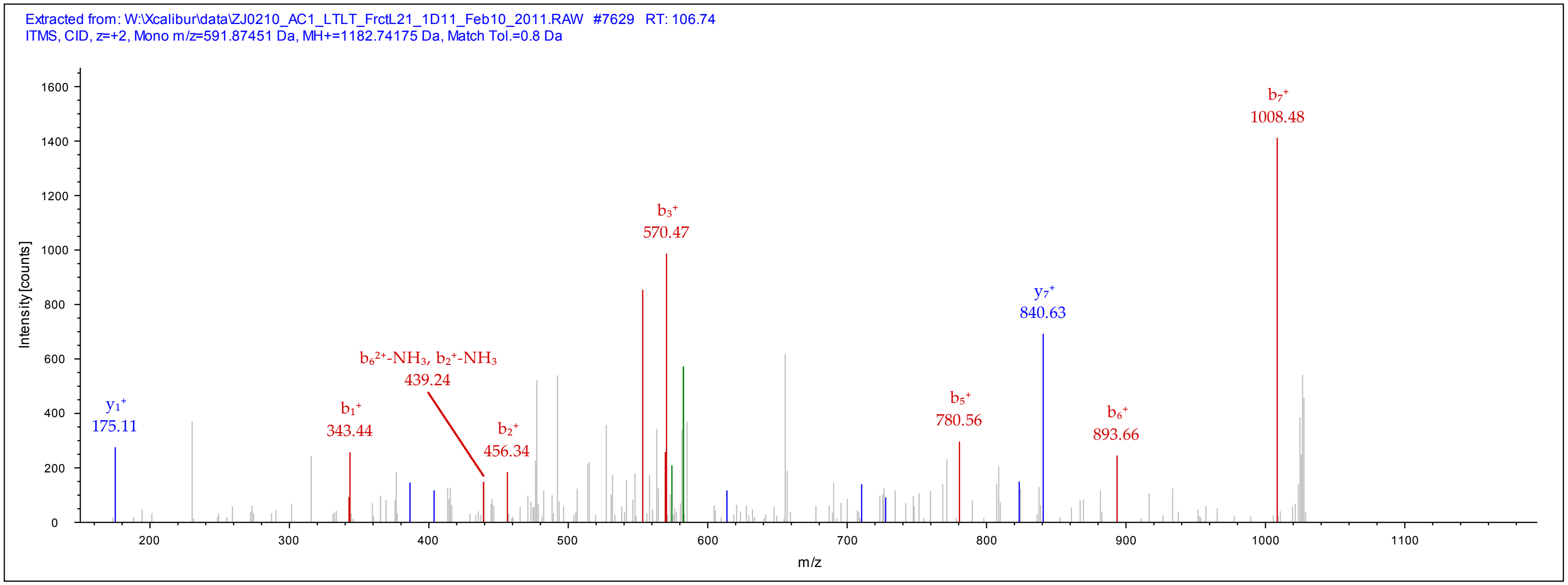
Identified with: Mascot (v1.16); IonScore:33, Exp Value:1.5E-002, Ions matched by search engine: 6/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Plakophilin-3



IPI:IPI00027378.5

Sequence: GEELGGGQDPVQLLSGFPR, G1-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 729.05487 Da (+1.63 mmu/+2.24 ppm),   MH+: 2185.15006 Da,   RT: 122.44 min,

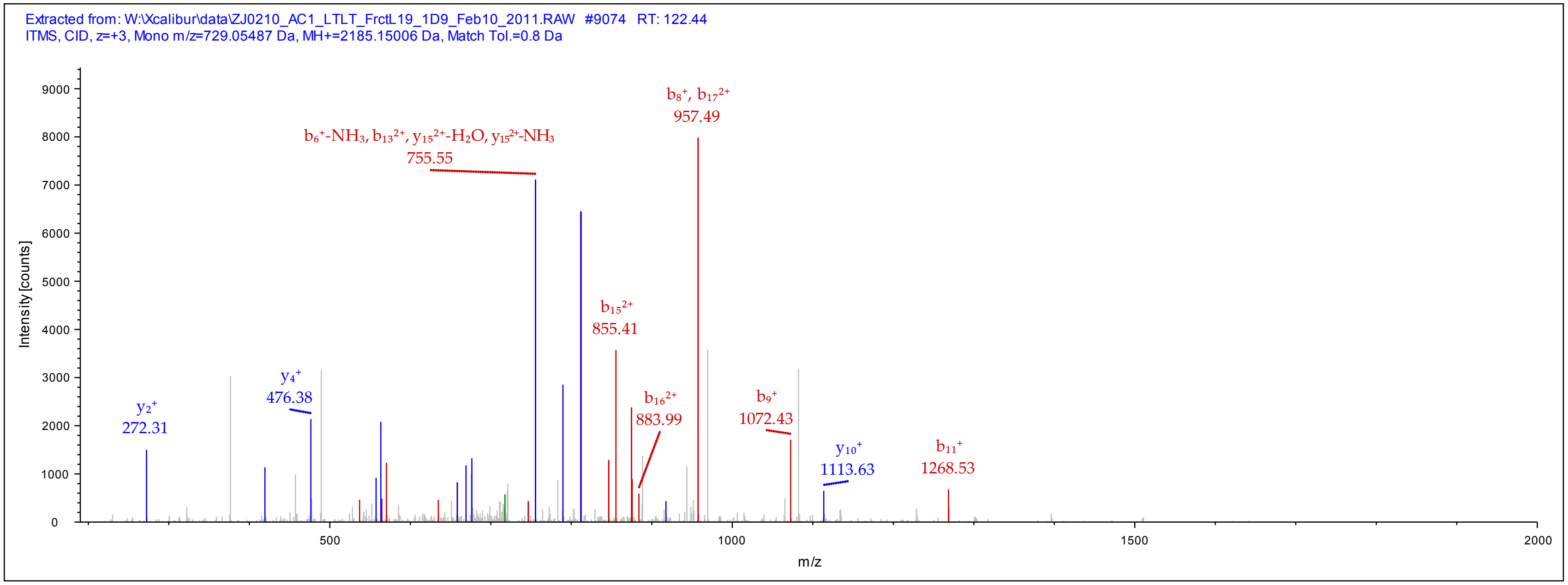
Identified with: Mascot (v1.16); IonScore:55, Exp Value:4.6E-004, Ions matched by search engine: 24/192

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of UBX domain-containing protein 1
- Isoform 2 of UBX domain-containing protein 1



IPI:IPI00029817.1

Sequence: GTLLAFAEAR, G1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 639.37372 Da (-0.7 mmu/-1.1 ppm),   MH+: 1277.74016 Da,   RT: 107.30 min,

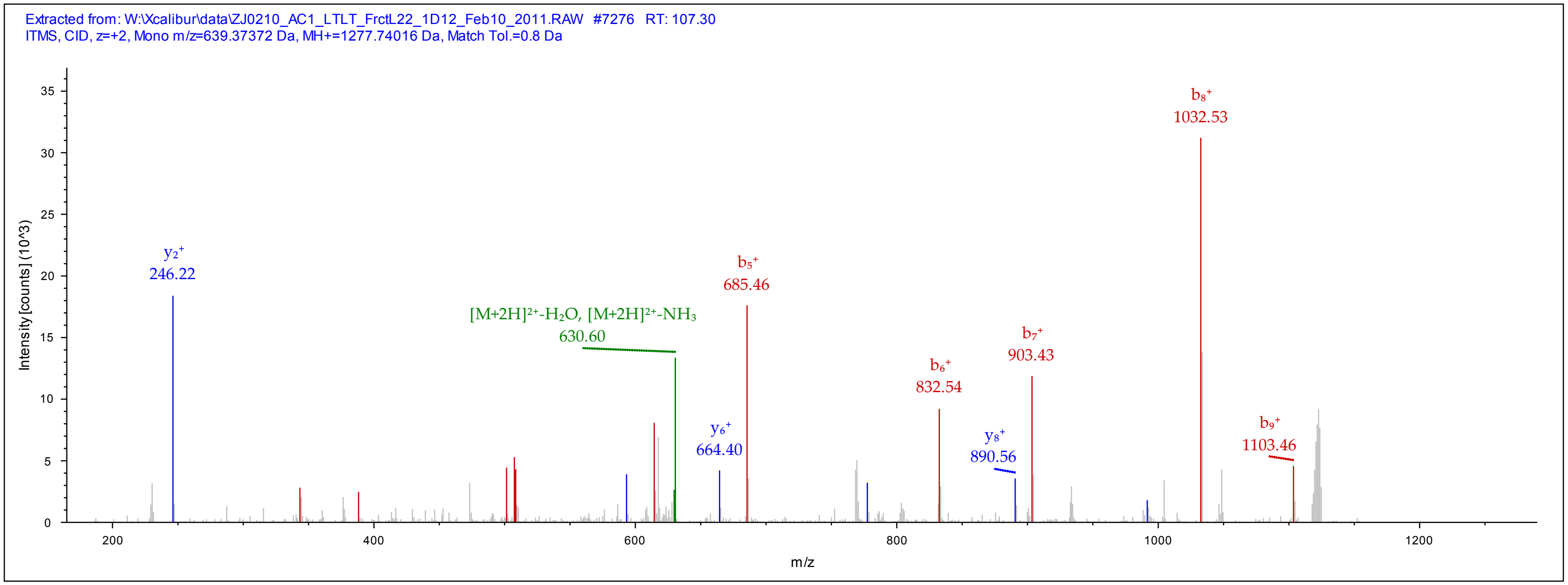
Identified with: Mascot (v1.16); IonScore:51, Exp Value:6.2E-004, Ions matched by search engine: 9/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Sialidase-1



IPI:IPI00030243.1

Sequence: TVESEAASYLDQISR, T1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 949.48914 Da (+0.24 mmu/+0.25 ppm),   MH+: 1897.97099 Da,   RT: 112.44 min,

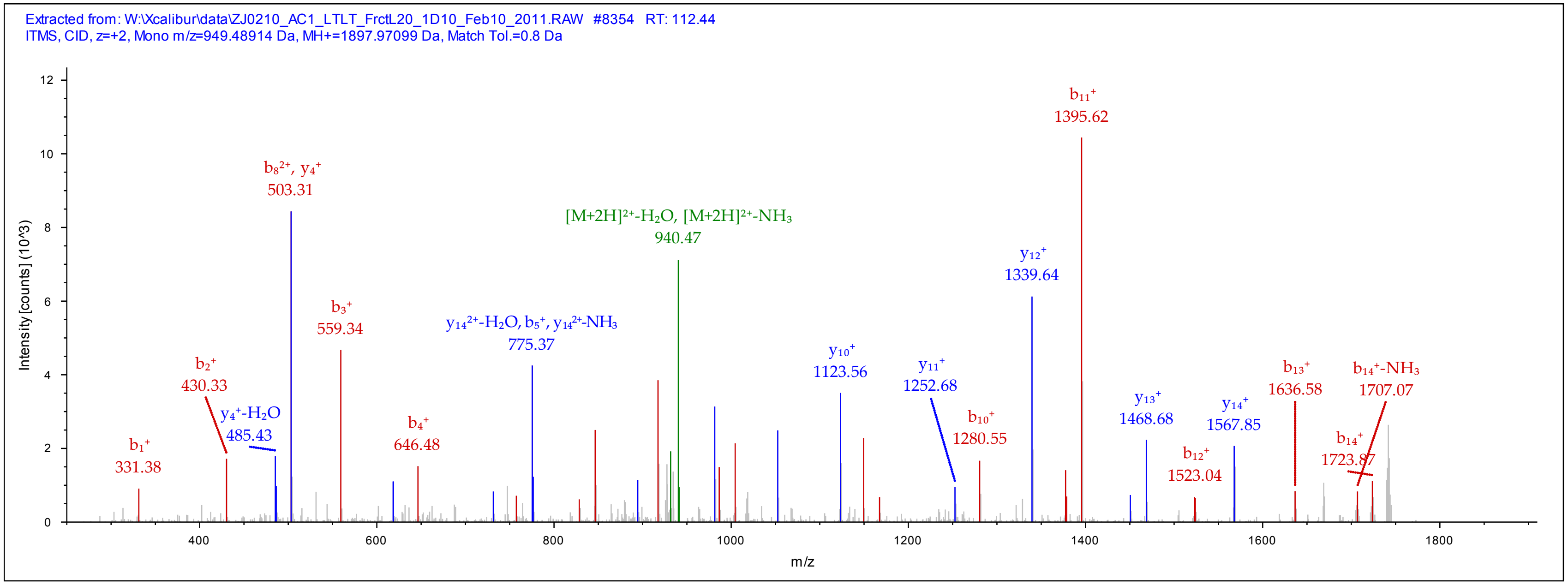
Identified with: Mascot (v1.16); IonScore:93, Exp Value:7.1E-008, Ions matched by search engine: 14/144

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Proteasome activator complex subunit 3
- Isoform 2 of Proteasome activator complex subunit 3



IPI:IPI00030362.1

Sequence: HTAAPTDPADGPV, H1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 739.37756 Da (-0.33 mmu/-0.44 ppm),   MH+: 1477.74785 Da,   RT: 72.58 min,

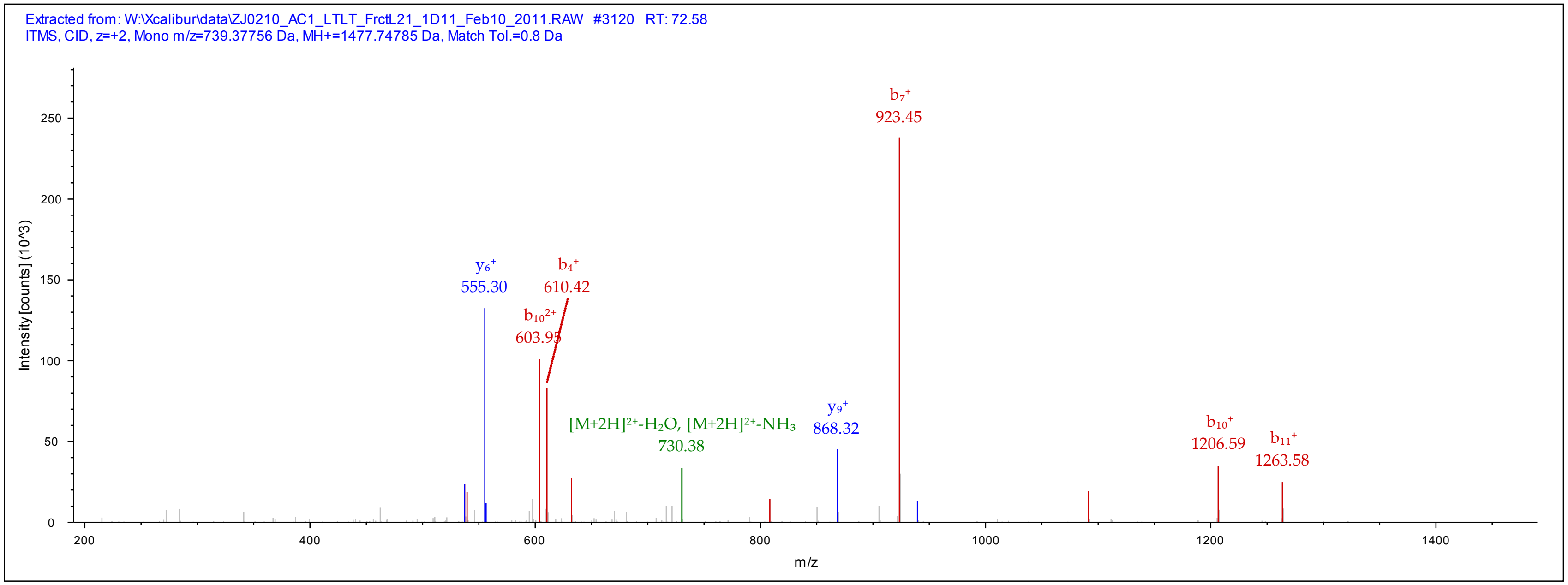
Identified with: Mascot (v1.16); IonScore:72, Exp Value:5.0E-006, Ions matched by search engine: 11/114

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Proteolipid protein 2



IPI00032409.1

Sequence: AQALVQYLEEPLTQVAAS, A1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 1080.59351 Da (+2.35 mmu/+2.17 ppm),   MH+: 2160.17974 Da,   RT: 138.83 min,

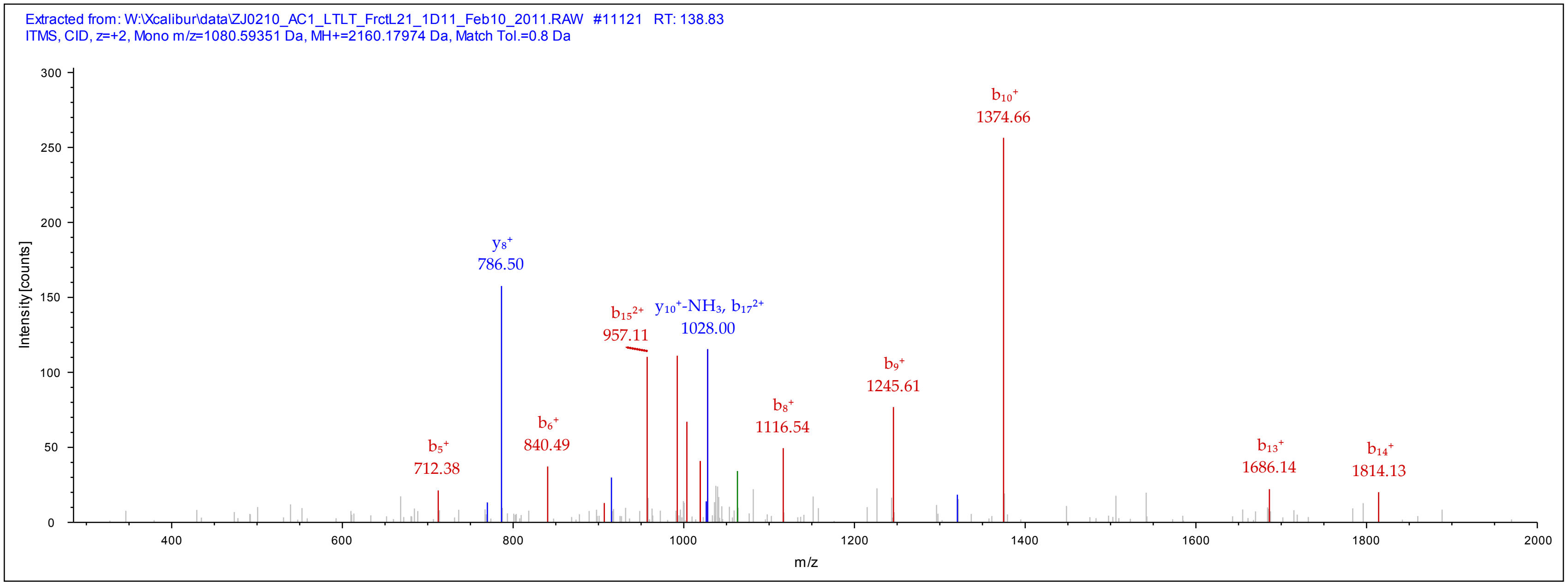
Identified with: Mascot (v1.16); IonScore:62, Exp Value:9.5E-005, Ions matched by search engine: 10/178

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Isoform 1 of Mitogen-activated protein-binding protein-interacting protein lng=125



IPI:IPI00056414.1

Sequence: VTLPAGPDILR, V1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 690.92511 Da (+0.83 mmu/+1.2 ppm), MH+: 1380.84294 Da, RT: 108.51 min,

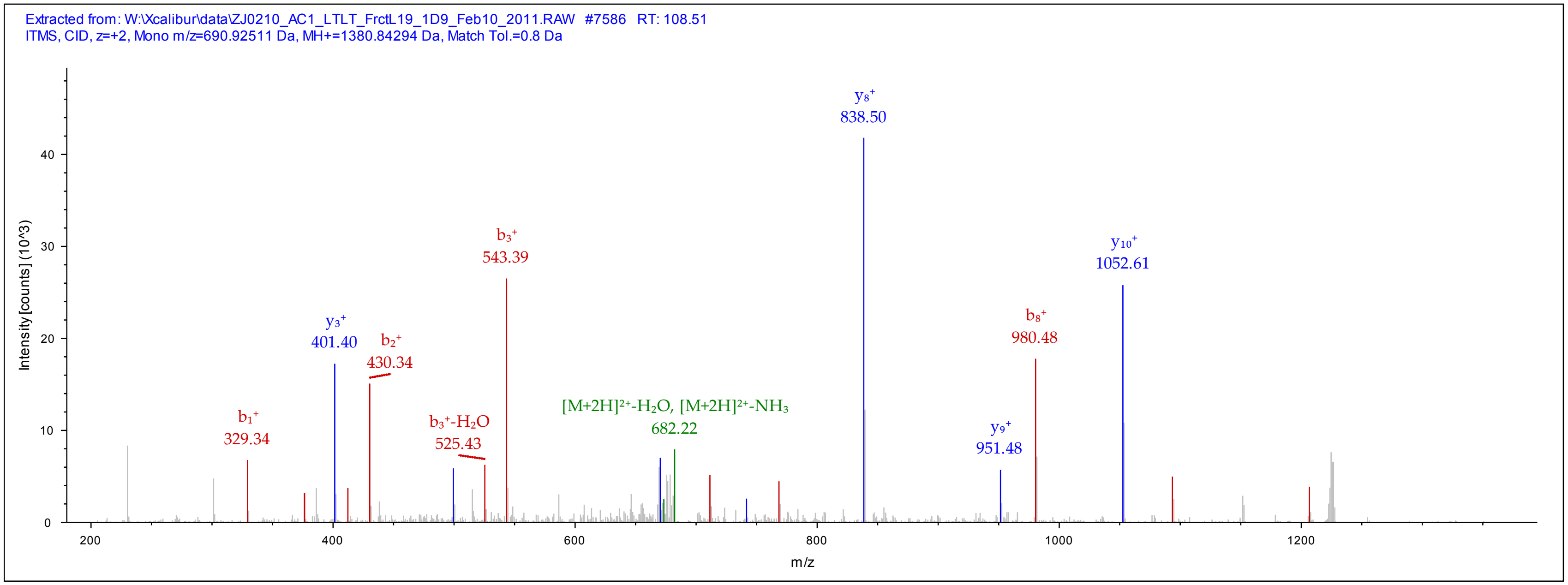
Identified with: Mascot (v1.16); IonScore:39, Exp Value:5.7E-003, Ions matched by search engine: 8/92

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

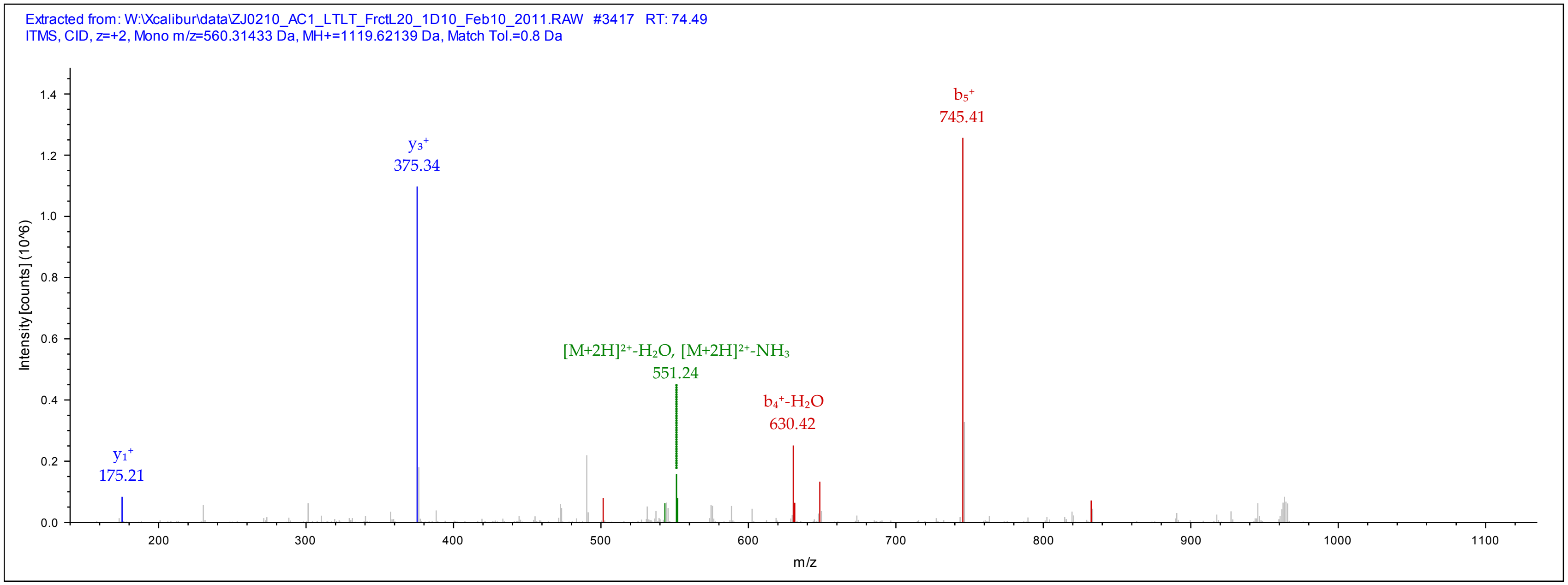
- Protein MAL2



IPI00062814.2

Sequence: AEAMPSLR, A1-TMT6plex (229.16293 Da), M4-Oxidation (15.99492 Da)
Charge: +2, Monoisotopic m/z: 560.31433 Da (+9.19 mmu/+16.4 ppm), MH+: 1119.62139 Da, RT: 74.49 min,
Identified with: Mascot (v1.16); IonScore:32, Exp Value:4.9E-002, Ions matched by search engine: 6/64
Fragment match tolerance used for search: 0.8 Da
Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):
- UPF0684 protein C5orf30 lng=206



IPI:IPI00093057.6

Sequence: EAEILEVLR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 650.88757 Da (+0.21 mmu/+0.33 ppm), MH+: 1300.76787 Da, RT: 111.84 min,

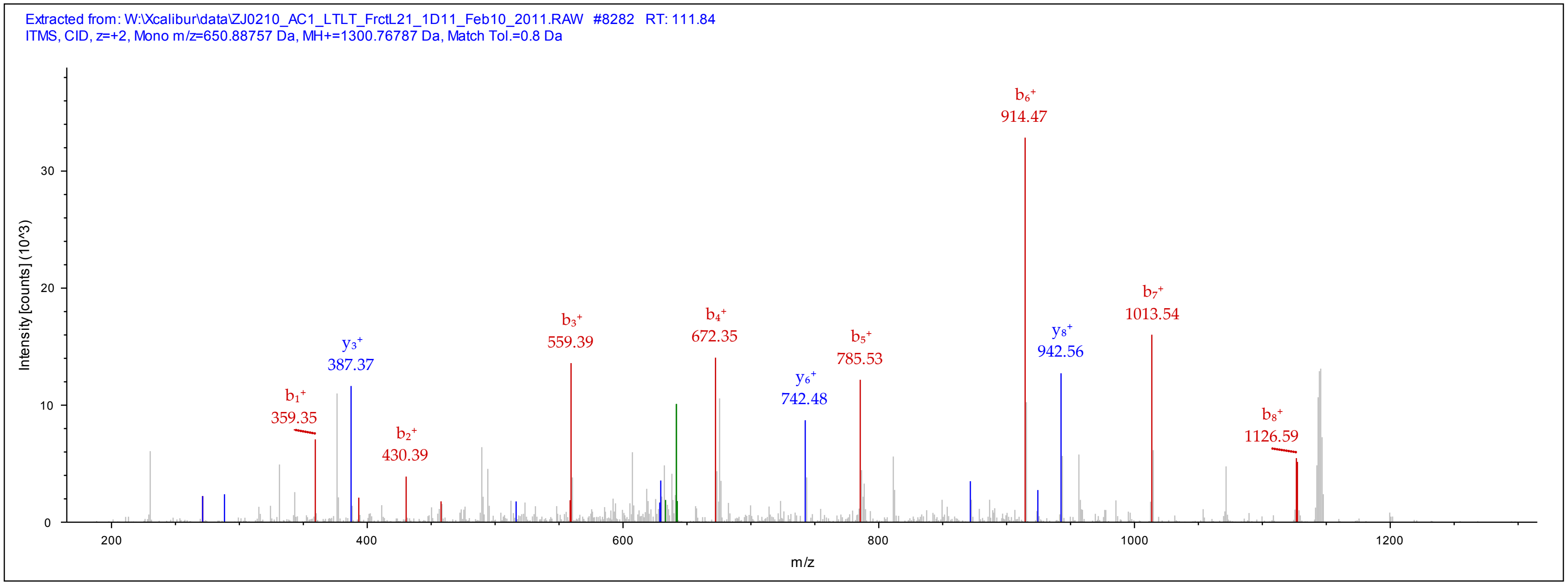
Identified with: Mascot (v1.16); IonScore:37, Exp Value:1.2E-002, Ions matched by search engine: 7/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Coproporphyrinogen-III oxidase, mitochondrial



IPI:IPI00166153.3

Sequence: NTDSDVNLVVPLEVIK, N1-TMT6plex (229.16293 Da), K16-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 1107.14673 Da (+3.39 mmu/+3.06 ppm), MH+: 2213.28618 Da, RT: 127.20 min,

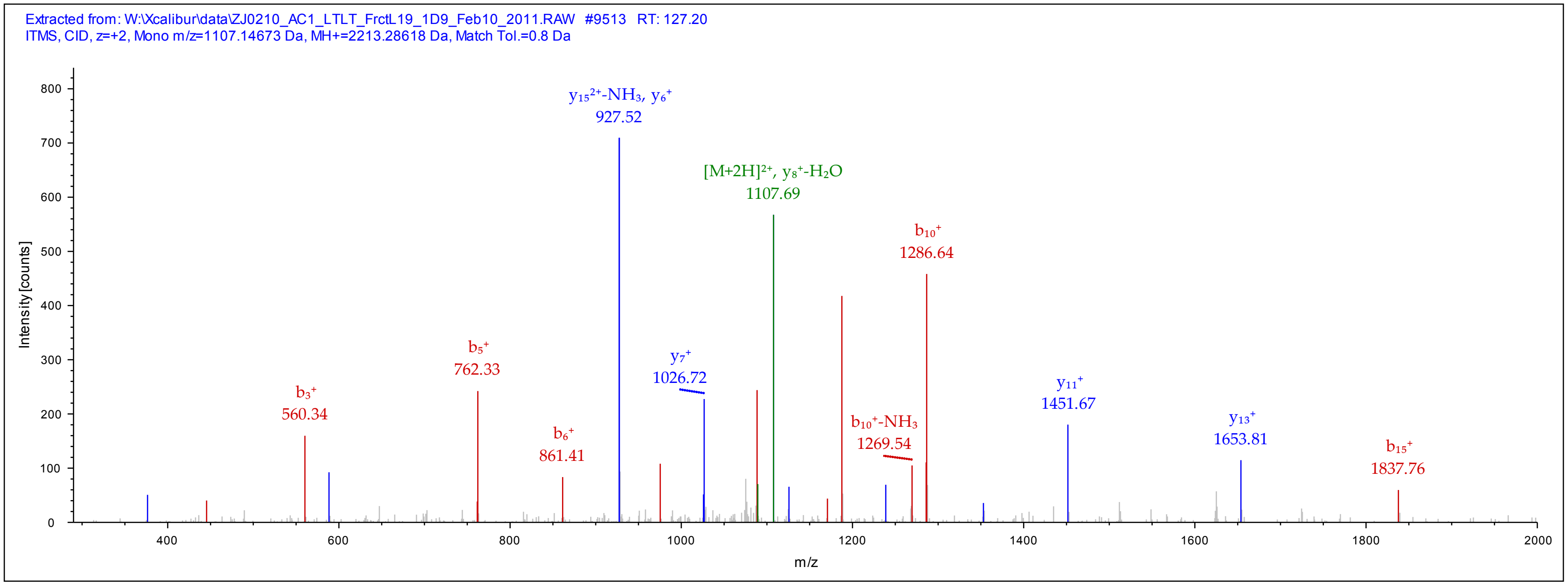
Identified with: Mascot (v1.16); IonScore:100, Exp Value:8.9E-009, Ions matched by search engine: 10/172

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1



IPI:IPI00167941.1

Sequence: QFPLHEK, Q1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 452.94043 Da (+0.9 mmu/+2 ppm), MH+: 1356.80674 Da, RT: 102.13 min,

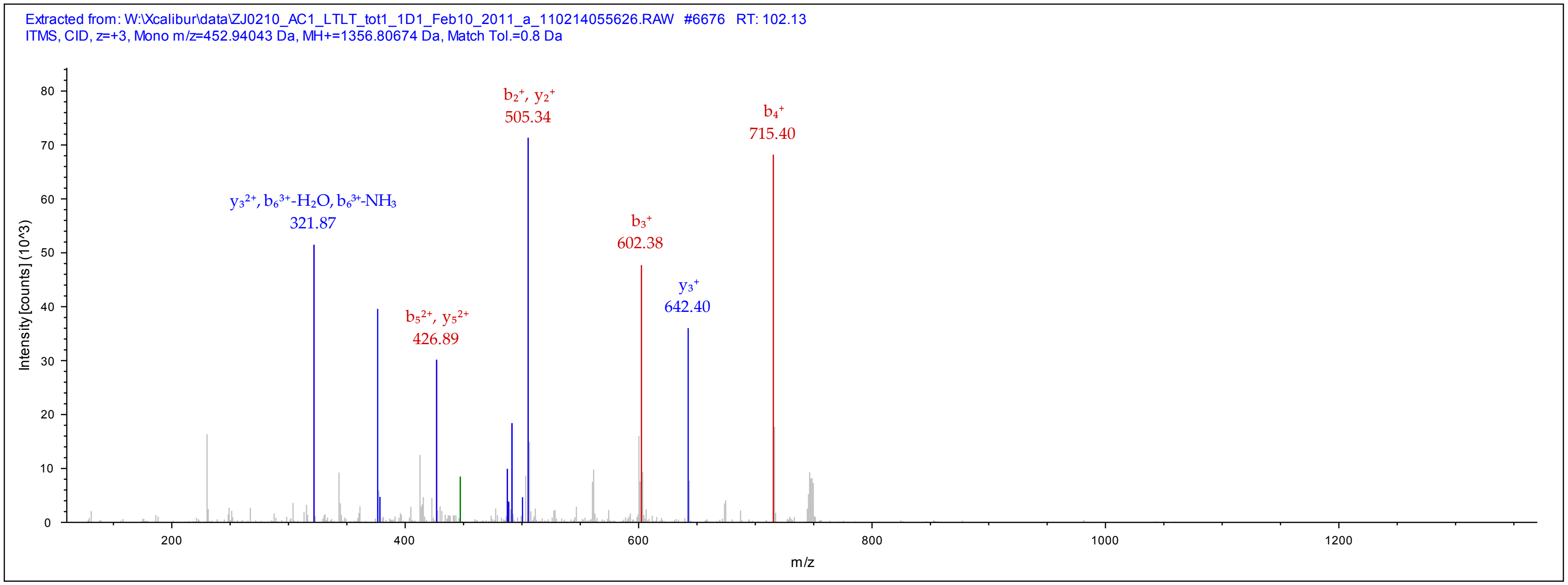
Identified with: Mascot (v1.16); IonScore:31, Exp Value:8.0E-002, Ions matched by search engine: 5/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Midasin



IPI:IPI00176702.4

Sequence: DRVVAR, D1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 472.79483 Da (-0.77 mmu/-1.63 ppm), MH+: 944.58238 Da, RT: 41.19 min,

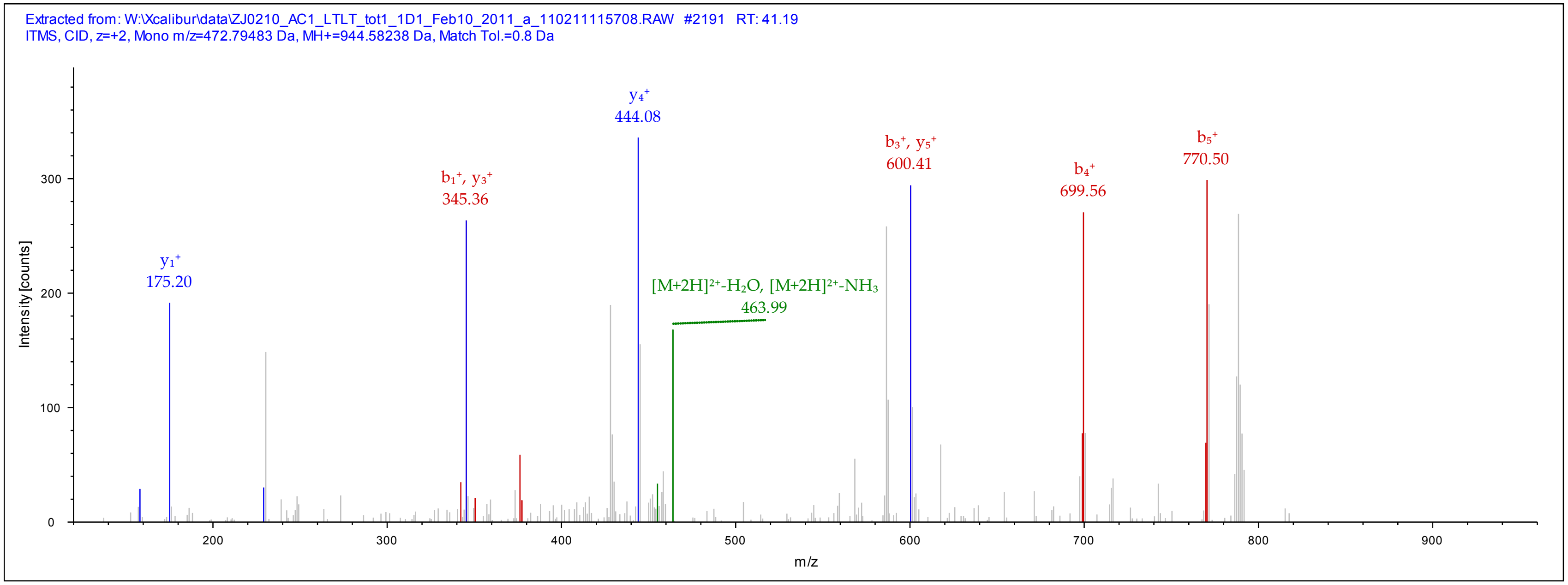
Identified with: Mascot (v1.16); IonScore:39, Exp Value:9.5E-003, Ions matched by search engine: 8/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Calmodulin-regulated spectrin-associated protein 3
- calmodulin-regulated spectrin-associated protein 3 isoform 1



IPI00217670.1

Sequence: SGAEVEAGDAAER, S1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 745.87085 Da (+2.96 mmu/+3.96 ppm),   MH+: 1490.73442 Da,   RT: 66.62 min,

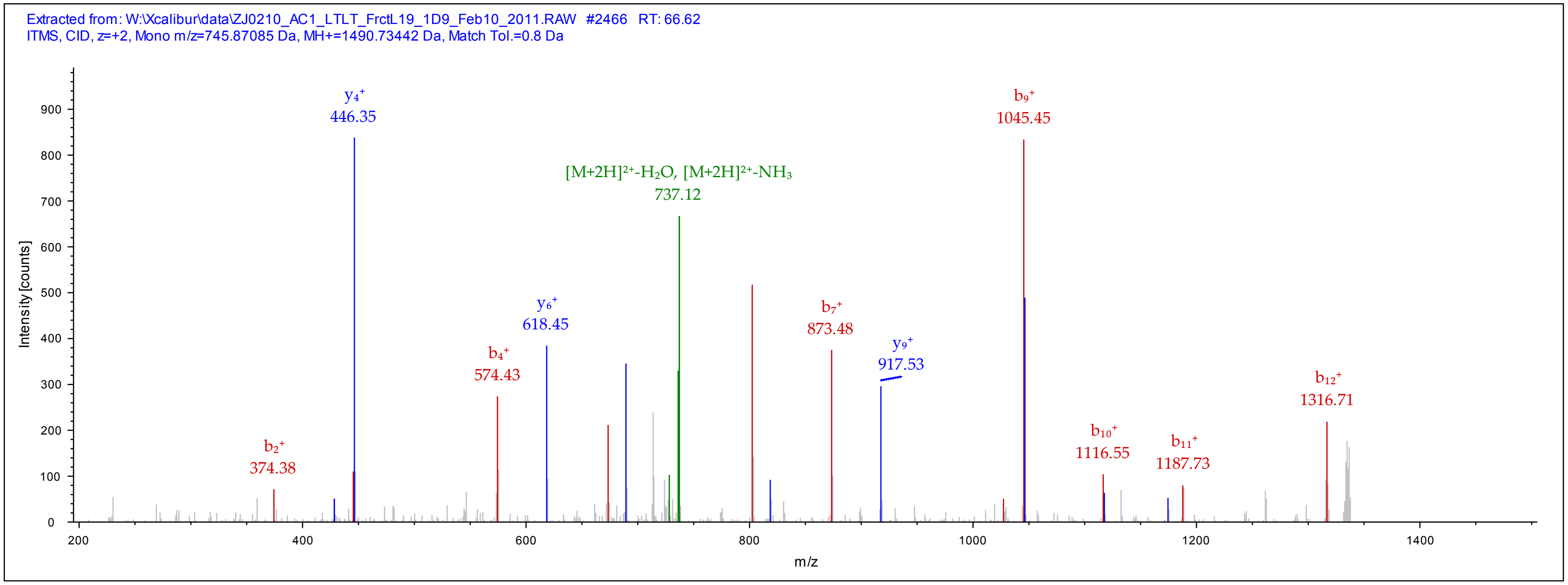
Identified with: Mascot (v1.16); IonScore:82, Exp Value:5.7E-007, Ions matched by search engine: 12/118

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Ribonucleoprotein PTB-binding 1 lng=606
- ribonucleoprotein PTB-binding 1



IPI:IPI00289819.4

Sequence: ATLITFLCDR, A1-TMT6plex (229.16293 Da), C8-Carbamidomethyl (57.02146 Da)

Charge: +2, Monoisotopic m/z: 719.90161 Da (+1.67 mmu/+2.32 ppm), MH+: 1438.79595 Da, RT: 124.24 min,

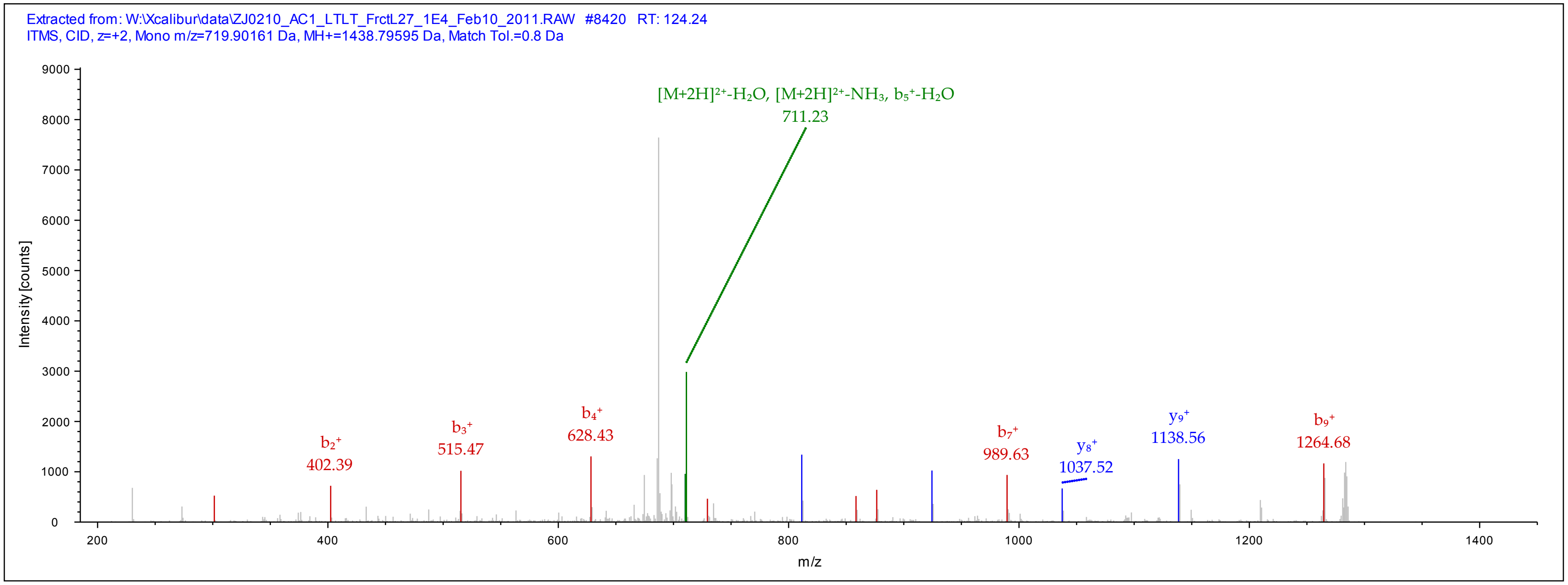
Identified with: Mascot (v1.16); IonScore:55, Exp Value:2.9E-004, Ions matched by search engine: 9/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Cation-independent mannose-6-phosphate receptor
- 274 kDa protein



IPI:IPI00291328.3

Sequence: DIEEIIDELK, D1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 837.98254 Da (+0.58 mmu/+0.69 ppm),   MH+: 1674.95781 Da,   RT: 179.02 min,

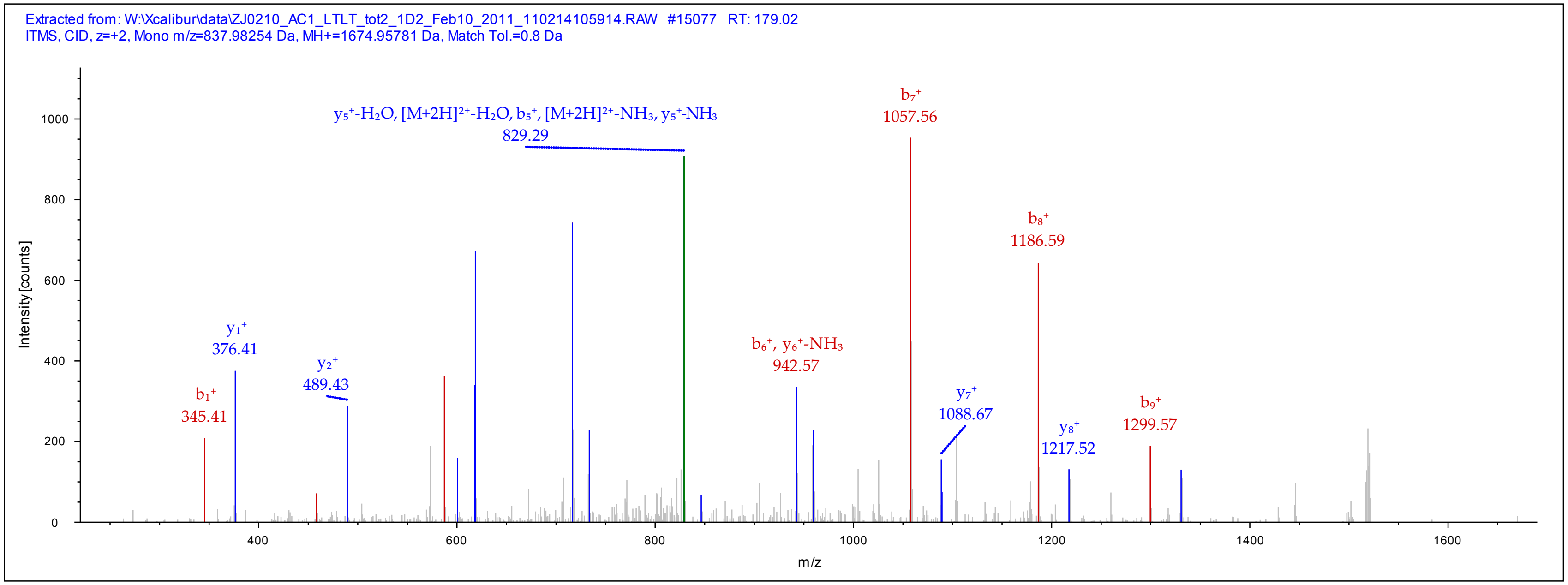
Identified with: Mascot (v1.16); IonScore:61, Exp Value:9.0E-005, Ions matched by search engine: 9/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial
- 28 kDa protein lng=252
- Putative uncharacterized protein ENSP00000343430 (Fragment) lng=249



IPI:IPI00940851.1

Sequence: ILQVSFK, I1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 646.92102 Da (+0.25 mmu/+0.39 ppm),   MH+: 1292.83476 Da,   RT: 139.08 min,

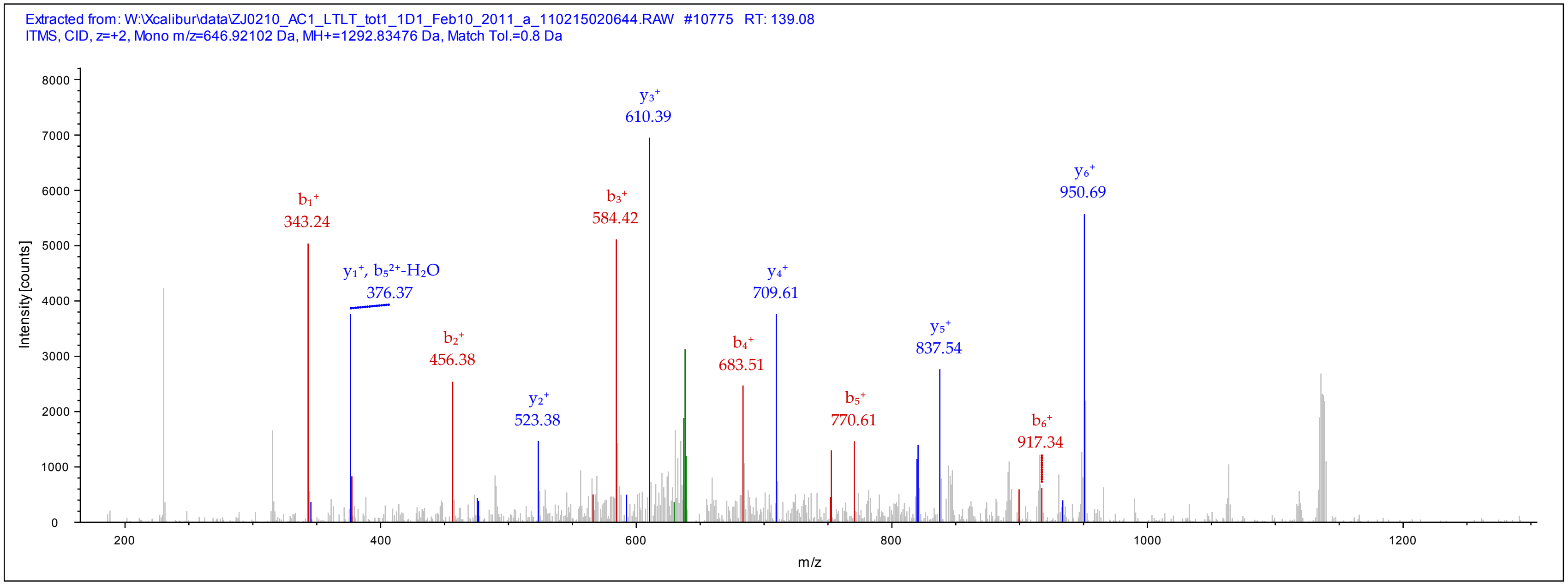
Identified with: Mascot (v1.16); IonScore:32, Exp Value:3.7E-002, Ions matched by search engine: 6/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- ELAV-like protein 1
- cDNA FLJ60076, highly similar to ELAV-like protein 1 lng=353



IPI:IPI00303722.5

Sequence: EALLSIGK, E1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 644.91534 Da (-0.35 mmu/-0.54 ppm),   MH+: 1288.82341 Da,   RT: 97.79 min,

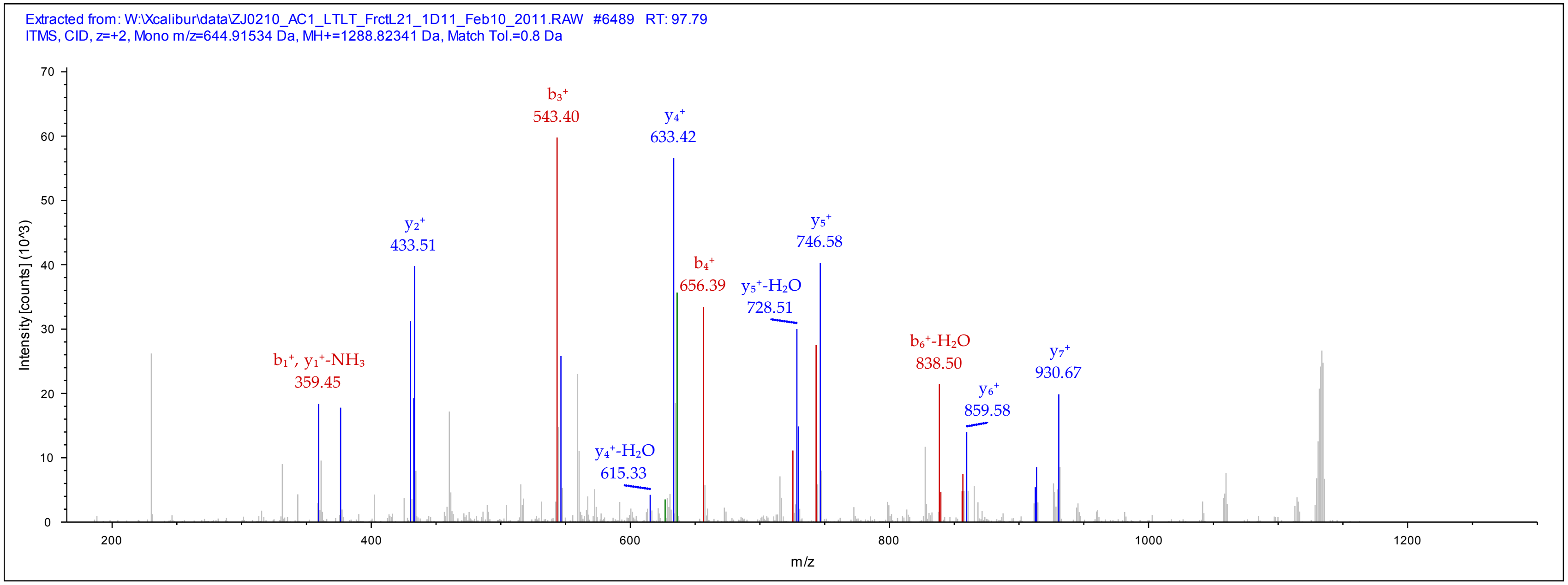
Identified with: Mascot (v1.16); IonScore:49, Exp Value:9.8E-004, Ions matched by search engine: 7/64

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Protein FAM136A
- 27 kDa protein lng=245



IPI:IPI00396411.4

Sequence: VSFCPLSLWR, V1-TMT6plex (229.16293 Da), C4-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 747.41089 Da (+0.41 mmu/+0.55 ppm),   MH+: 1493.81450 Da,   RT: 130.92 min,

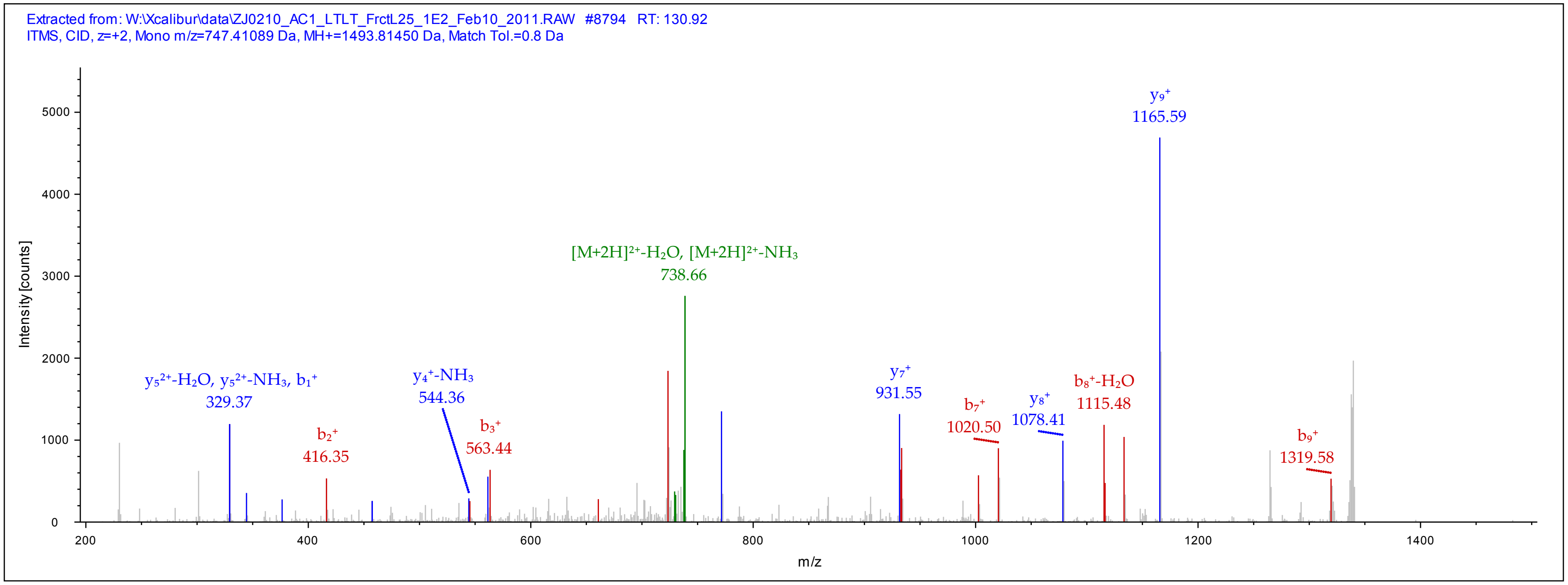
Identified with: Mascot (v1.16); IonScore:37, Exp Value:1.6E-002, Ions matched by search engine: 8/82

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Cleft lip and palate transmembrane protein 1
- Isoform 2 of Cleft lip and palate transmembrane protein 1



IPI:IPI00412224.2

Sequence: LATATGAK, L1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 595.87970 Da (+0.59 mmu/+1 ppm), MH+: 1190.75212 Da, RT: 82.70 min,

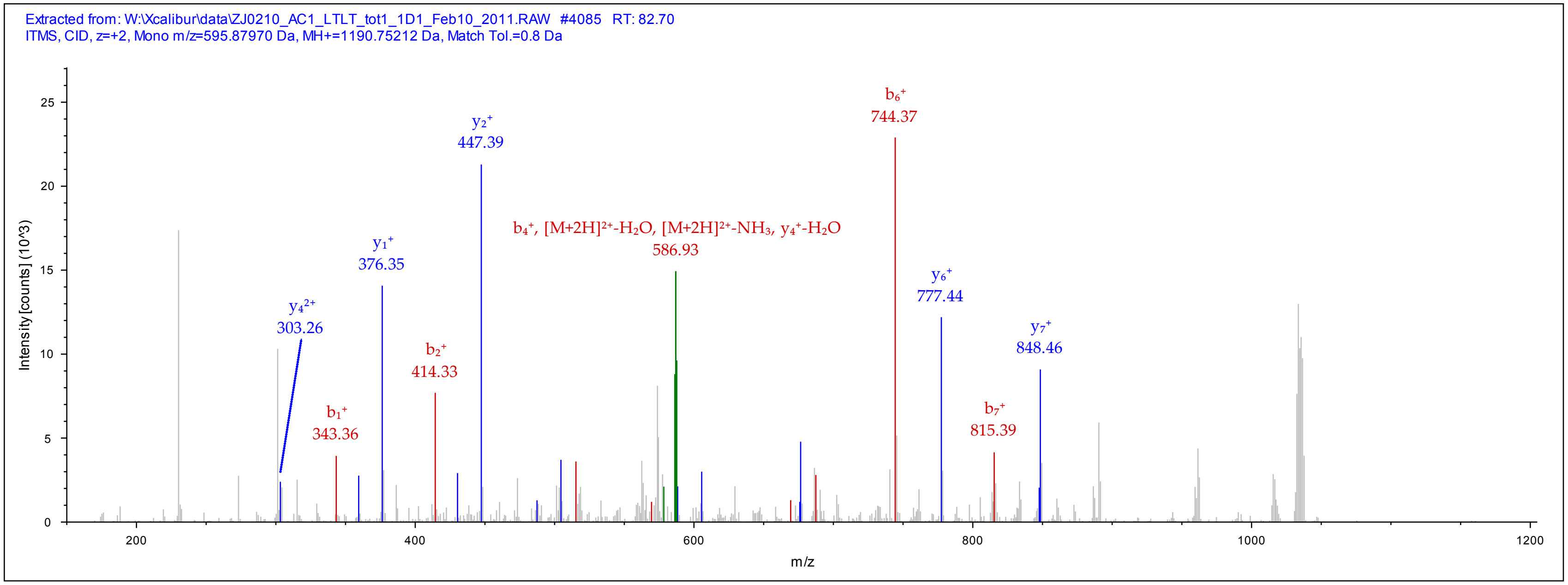
Identified with: Mascot (v1.16); IonScore:35, Exp Value:2.3E-002, Ions matched by search engine: 12/60

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- WD repeat-containing protein 11
- Putative uncharacterized protein BRWD2 lng=1224



IPI:IPI00549786.5

Sequence: SLPVSVPVWGFK, S1-TMT6plex (229.16293 Da), K12-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 887.53778 Da (+0.74 mmu/+0.83 ppm), MH+: 1774.06828 Da, RT: 130.07 min,

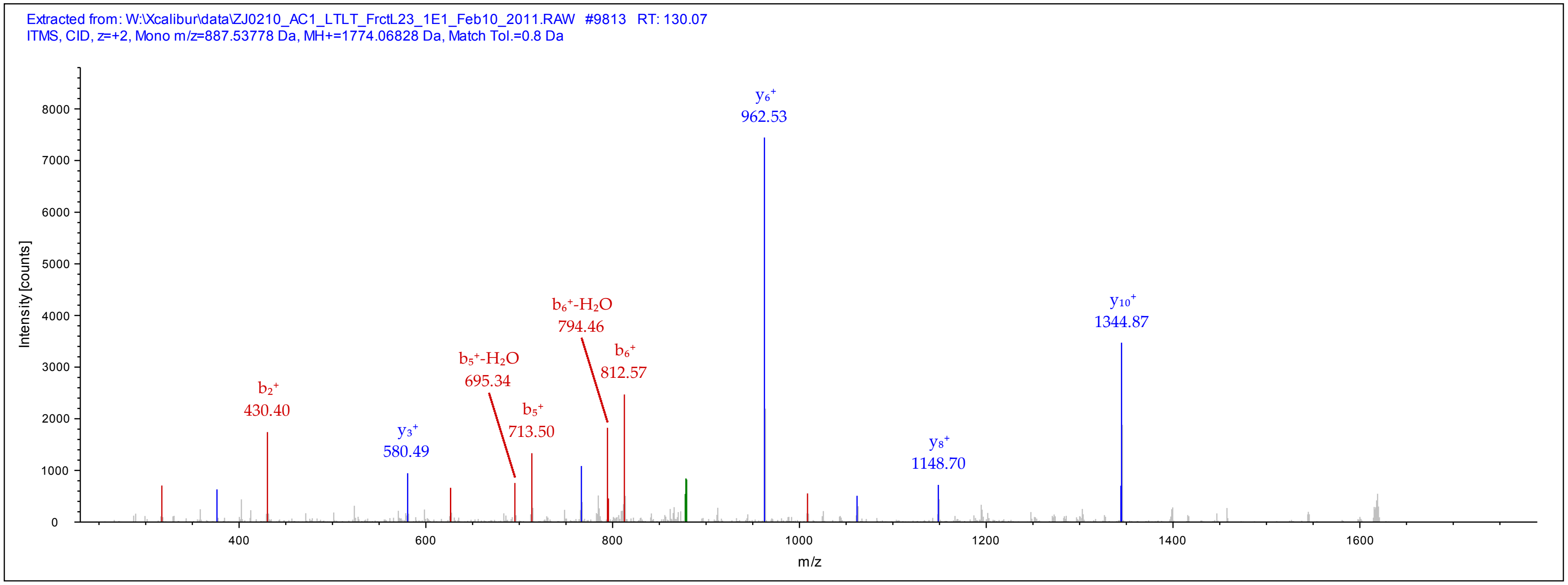
Identified with: Mascot (v1.16); IonScore:52, Exp Value:4.8E-004, Ions matched by search engine: 11/96

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Proline-rich AKT1 substrate 1
- Isoform 2 of Proline-rich AKT1 substrate 1 lng=276



IPI:IPI00329461.5

Sequence: IIDFGLAR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 567.34796 Da (+0.29 mmu/+0.51 ppm), MH+: 1133.68865 Da, RT: 116.06 min,

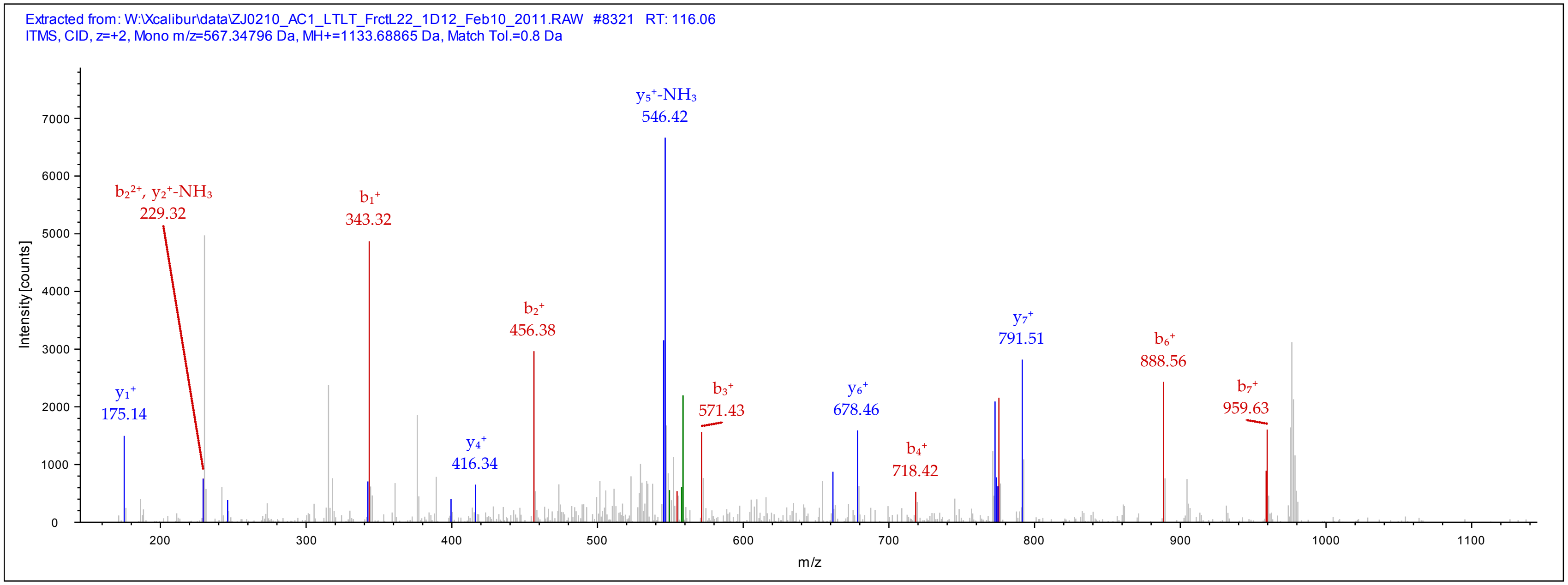
Identified with: Mascot (v1.16); IonScore:35, Exp Value:3.2E-002, Ions matched by search engine: 6/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Myosin light chain kinase family member 4
- Myosin light chain kinase 2, skeletal/cardiac muscle
- Putative myosin light chain kinase 3



IPI:IPI00747403.24

Sequence: SVLIGEFLEK, S1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 796.98834 Da (+1.49 mmu/+1.87 ppm),   MH+: 1592.96941 Da,   RT: 127.28 min,

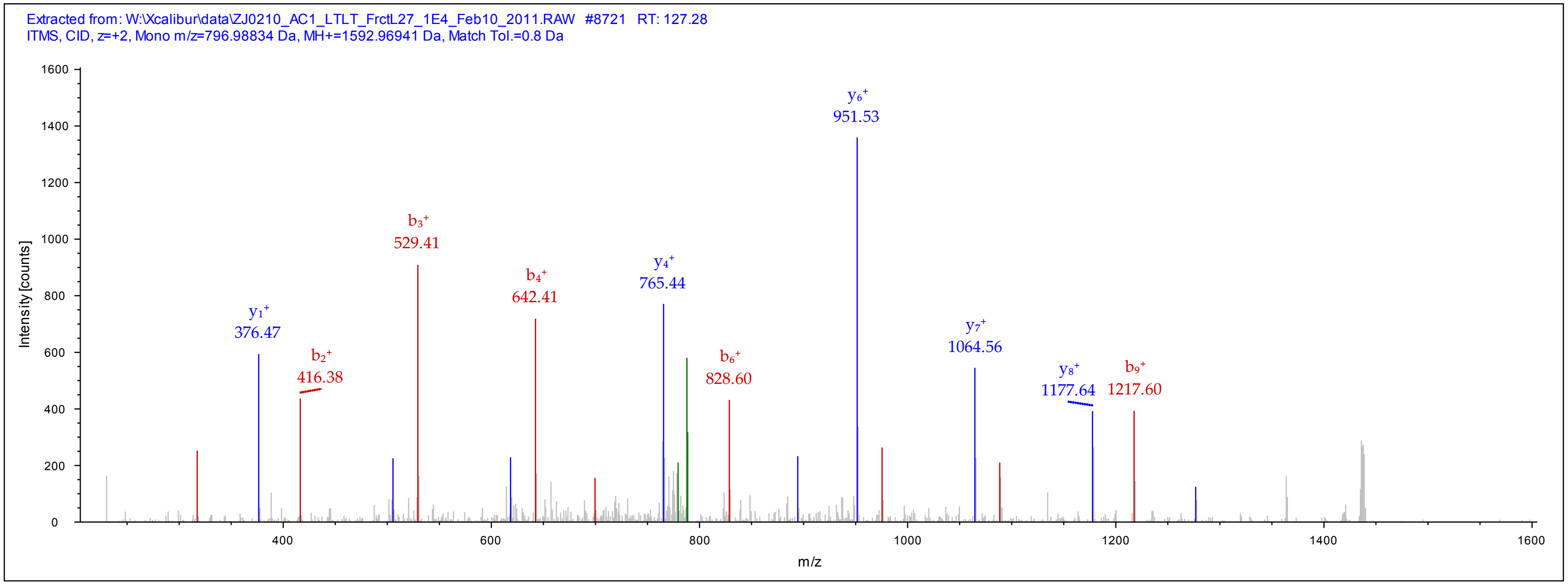
Identified with: Mascot (v1.16); IonScore:57, Exp Value:1.2E-004, Ions matched by search engine: 7/88

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of mRNA cap guanine-N7 methyltransferase
- Isoform 2 of mRNA cap guanine-N7 methyltransferase



IPI:IPI00027240.7

Sequence: VSQAAADLK, V1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 680.91412 Da (+0.44 mmu/+0.65 ppm), MH+: 1360.82097 Da, RT: 81.67 min,

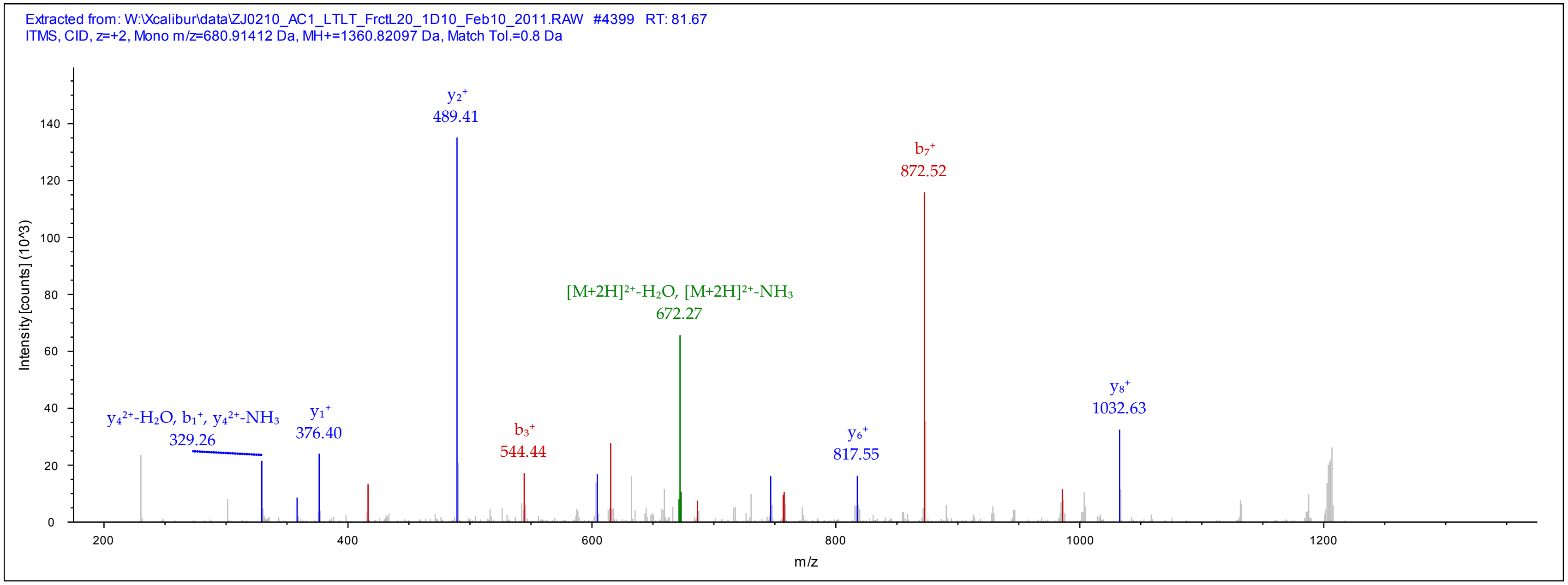
Identified with: Mascot (v1.16); IonScore:31, Exp Value:6.2E-002, Ions matched by search engine: 7/86

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- 7 kDa protein lng=68
- Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5



IPI:IPI00937974.1

Sequence: LAEVALAYAK, L1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 753.96875 Da (+0.29 mmu/+0.39 ppm), MH+: 1506.93022 Da, RT: 115.63 min,

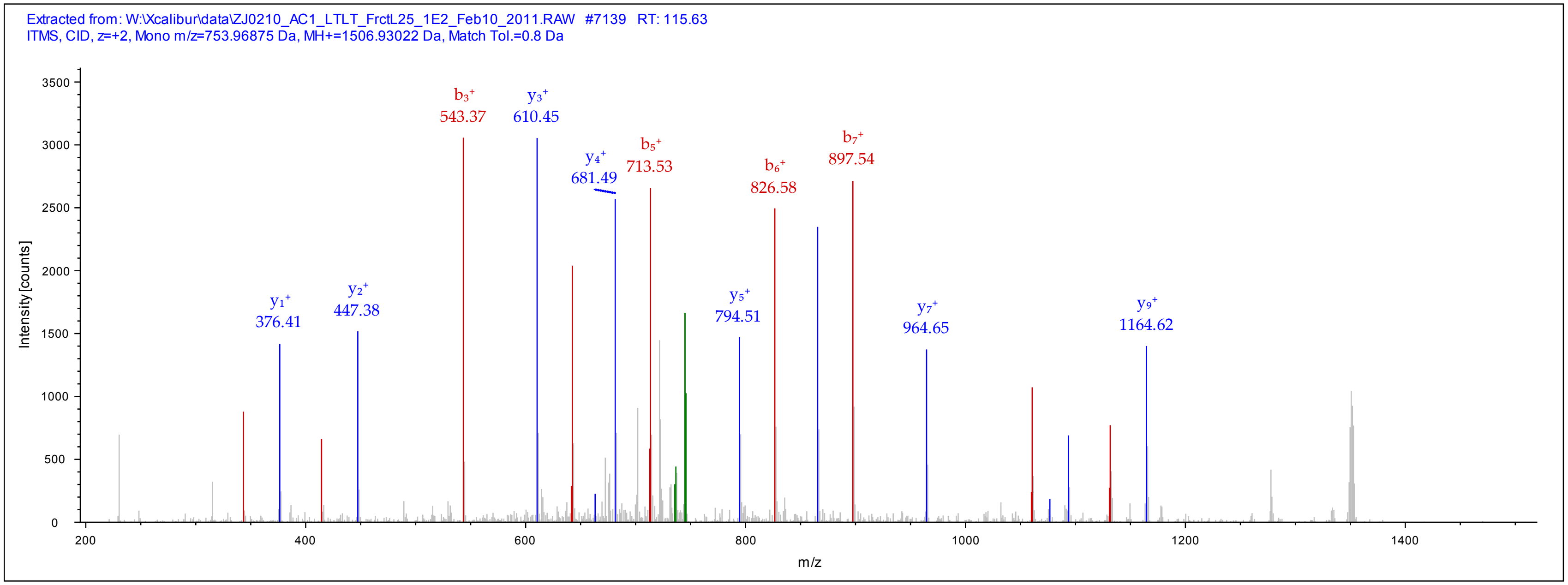
Identified with: Mascot (v1.16); IonScore:57, Exp Value:1.2E-004, Ions matched by search engine: 8/72

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Delta-aminolevulinic acid dehydratase
- Delta-aminolevulinic acid dehydratase lng=339
- Isoform 2 of Delta-aminolevulinic acid dehydratase lng=359



IPI:IPI00935516.1

Sequence: TVQDLTSVVQTLLQQMQDK, T1-TMT6plex (229.16293 Da), K19-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 878.49170 Da (+0.68 mmu/+0.77 ppm), MH+: 2633.46054 Da, RT: 227.41 min,

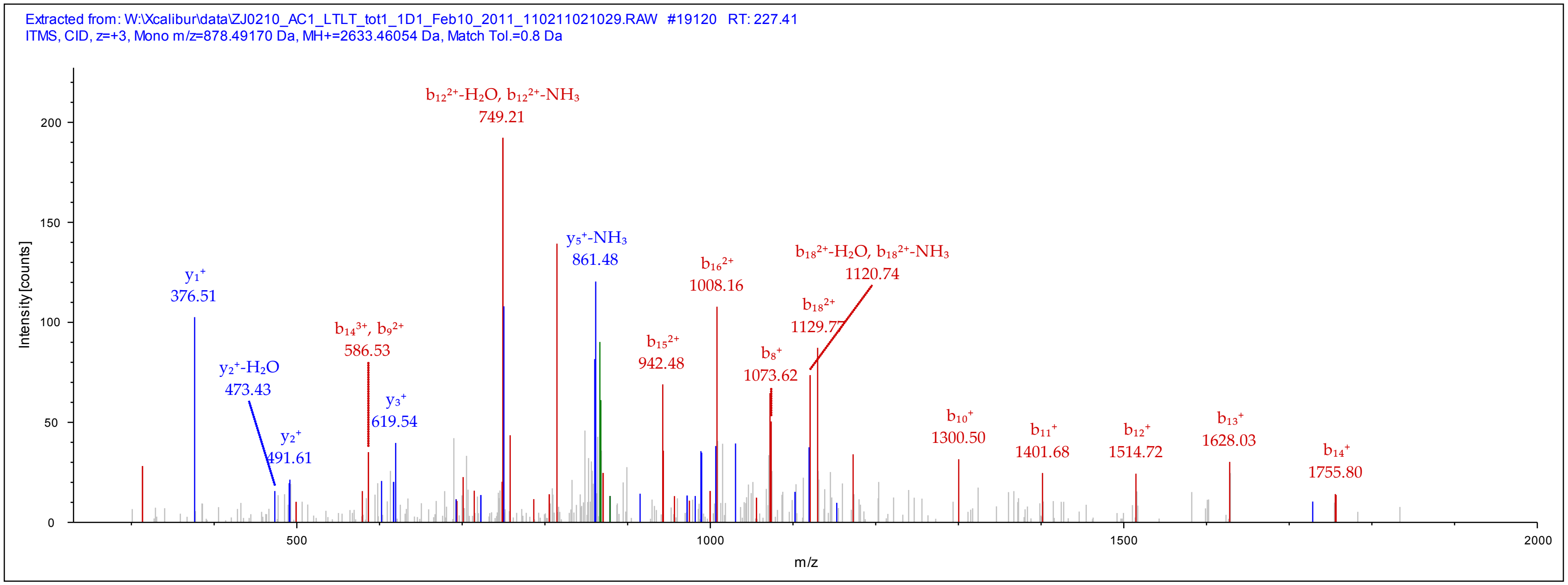
Identified with: Mascot (v1.16); IonScore:42, Exp Value:7.7E-003, Ions matched by search engine: 10/210

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Heat shock factor-binding protein 1



IPI:IPI00015947.5

Sequence: ILTIEVK, I1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 637.42987 Da (+1.44 mmu/+2.26 ppm), MH+: 1273.85246 Da, RT: 138.04 min,

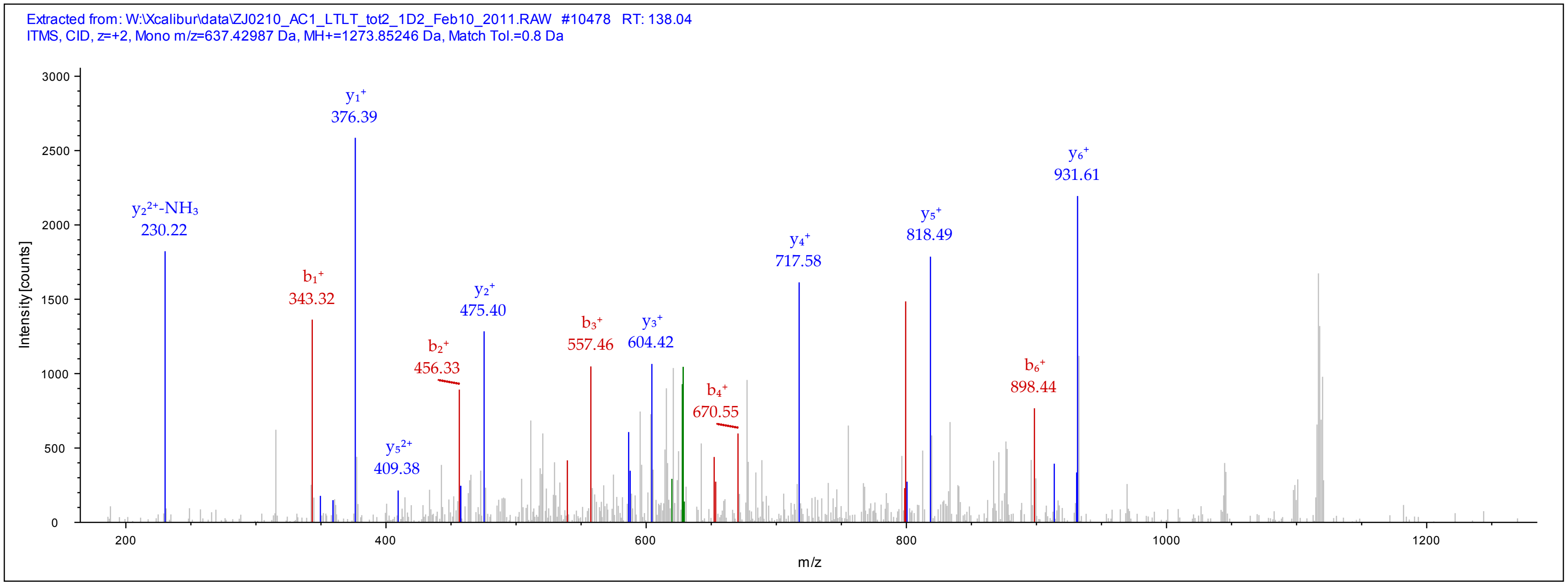
Identified with: Mascot (v1.16); IonScore:44, Exp Value:7.2E-004, Ions matched by search engine: 6/52

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- DnaJ homolog subfamily B member 1



IPI:IPI00219103.6

Sequence: LSLEEFIR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 618.36340 Da (-0.11 mmu/-0.18 ppm),   MH+: 1235.71953 Da,   RT: 118.52 min,

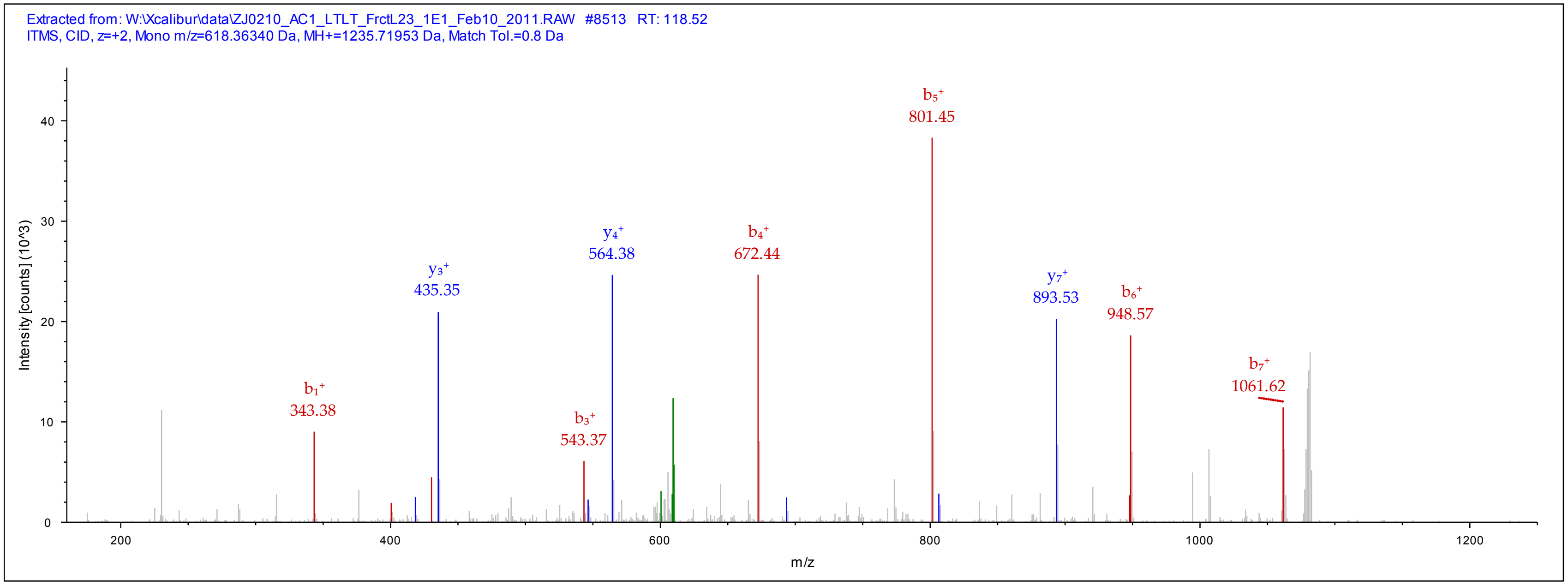
Identified with: Mascot (v1.16); IonScore:41, Exp Value:6.4E-003, Ions matched by search engine: 7/62

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Neurocalcin-delta
- Neuron-specific calcium-binding protein hippocalcin
- Hippocalcin-like protein 1



IPI:IPI00967375.1

Sequence: VVDLLVIK, V1-TMT6plex (229.16293 Da), K8-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 678.96527 Da (+0.09 mmu/+0.13 ppm), MH+: 1356.92327 Da, RT: 127.47 min,

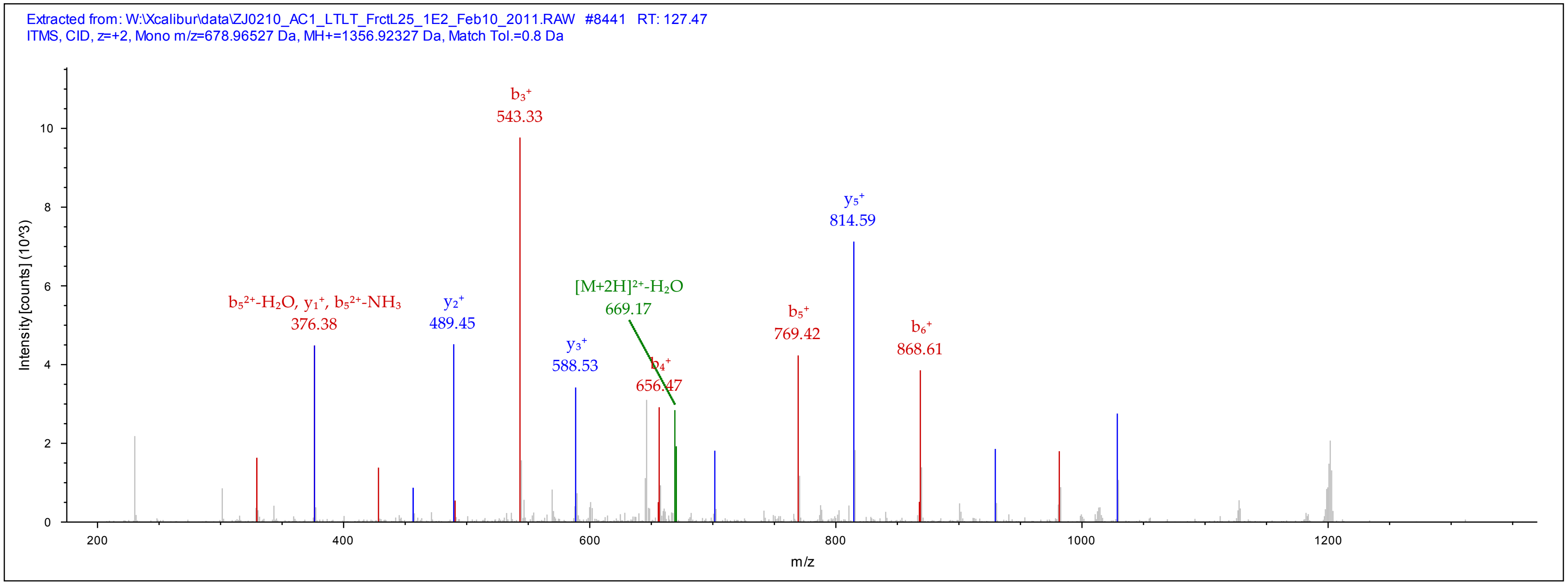
Identified with: Mascot (v1.16); IonScore:45, Exp Value:5.7E-004, Ions matched by search engine: 14/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
- NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6



IPI:IPI00290543.5

Sequence: VFGAPNVVEDEIDQYLSK, V1-TMT6plex (229.16293 Da), K18-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 827.78217 Da (+1.38 mmu/+1.66 ppm), MH+: 2481.33194 Da, RT: 188.51 min,

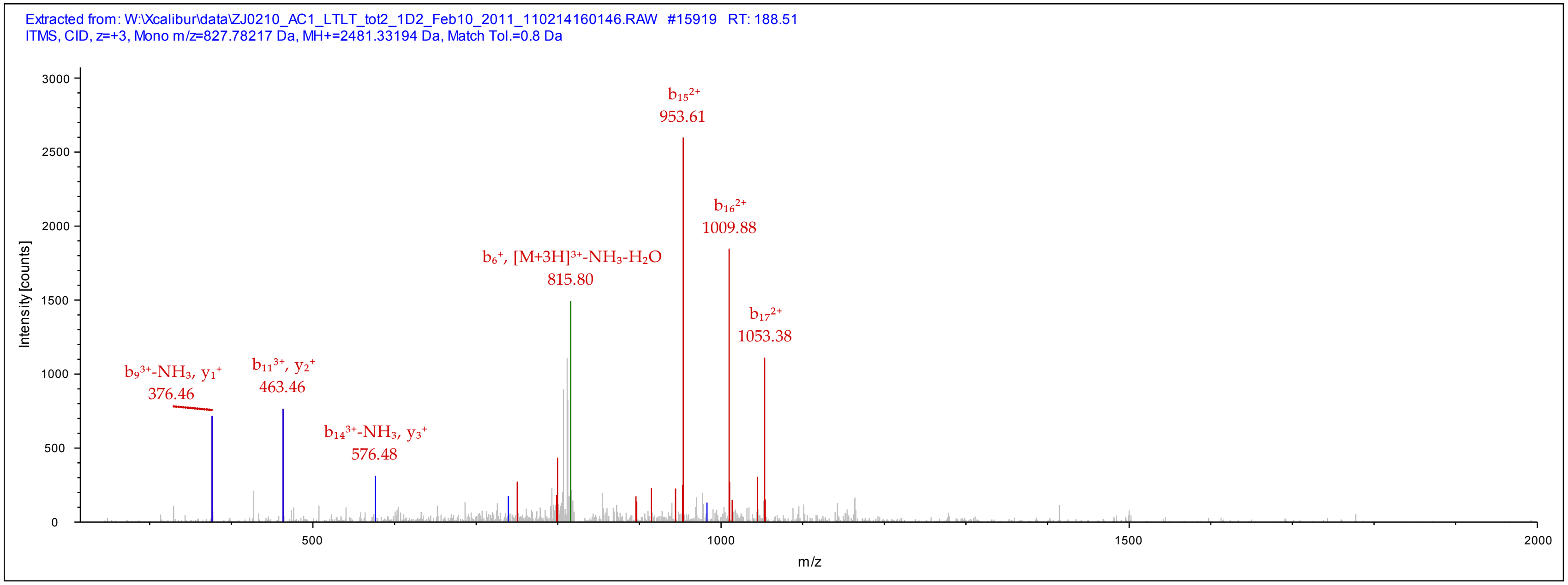
Identified with: Mascot (v1.16); IonScore:37, Exp Value:3.6E-002, Ions matched by search engine: 14/176

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Nuclear protein localization protein 4 homolog
- Isoform 2 of Nuclear protein localization protein 4 homolog



IPI:IPI00411680.10

Sequence: ELVDDSINNVR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 751.90509 Da (+0.82 mmu/+1.09 ppm),   MH+: 1502.80290 Da,   RT: 88.75 min,

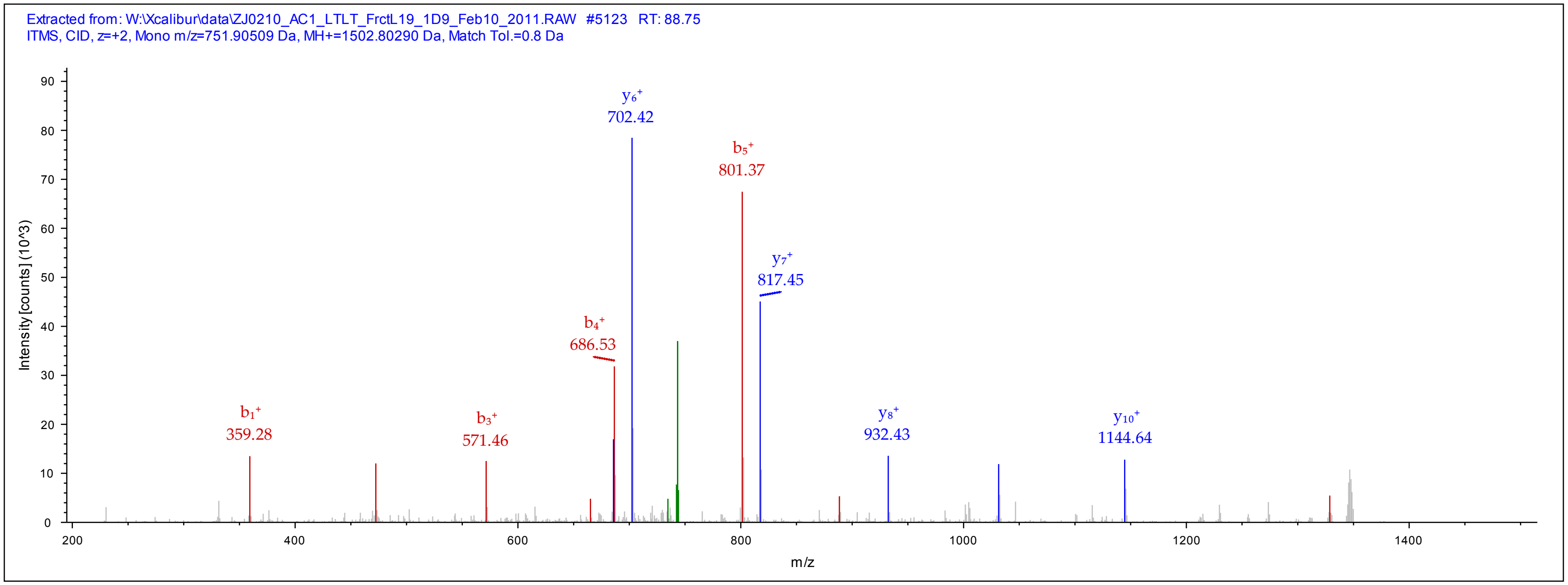
Identified with: Mascot (v1.16); IonScore:59, Exp Value:1.3E-004, Ions matched by search engine: 8/96

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Isoform 1 of Protein-L-isoaspartate(D-aspartate) O-methyltransferase



IPI:IPI00300078.6

Sequence: VLFDPFELDTSVTPGR, V1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 1011.54327 Da (+2.33 mmu/+2.3 ppm),   MH+: 2022.07927 Da,   RT: 136.54 min,

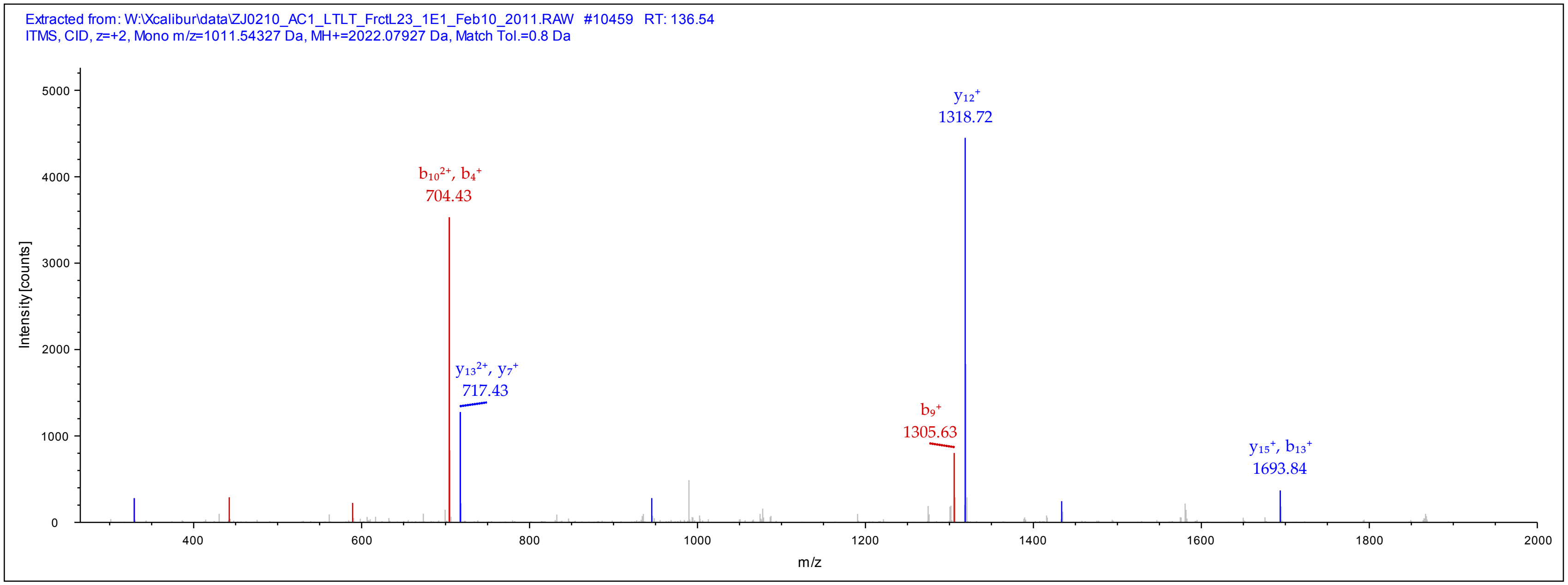
Identified with: Mascot (v1.16); IonScore:66, Exp Value:3.3E-005, Ions matched by search engine: 11/138

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Periodic tryptophan protein 2 homolog



IPI:IPI00025285.3

Sequence: EEAQAEIEQYR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 797.90076 Da (+1.58 mmu/+1.98 ppm), MH+: 1594.79424 Da, RT: 80.99 min,

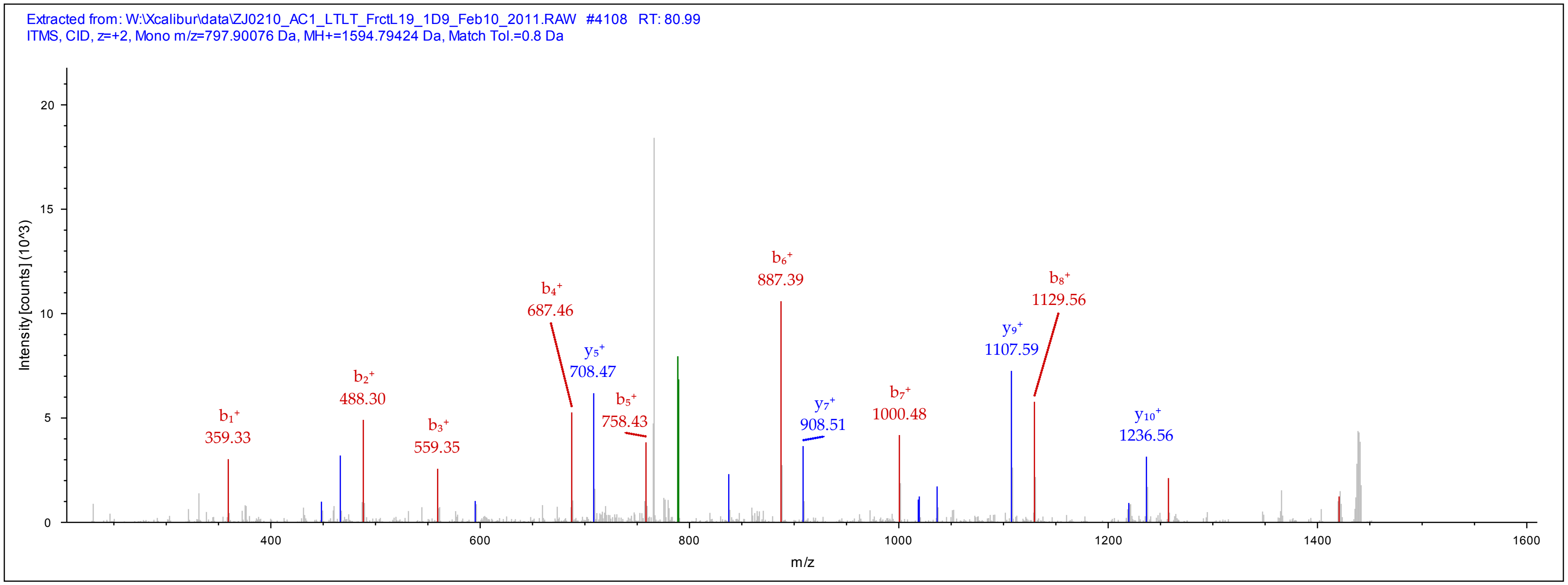
Identified with: Mascot (v1.16); IonScore:50, Exp Value:9.7E-004, Ions matched by search engine: 8/108

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- V-type proton ATPase subunit G 1



IPI:IPI00399130.5

Sequence: RVPLFSLR, R1-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 406.26212 Da (-0.33 mmu/-0.82 ppm), MH+: 1216.77179 Da, RT: 122.56 min,

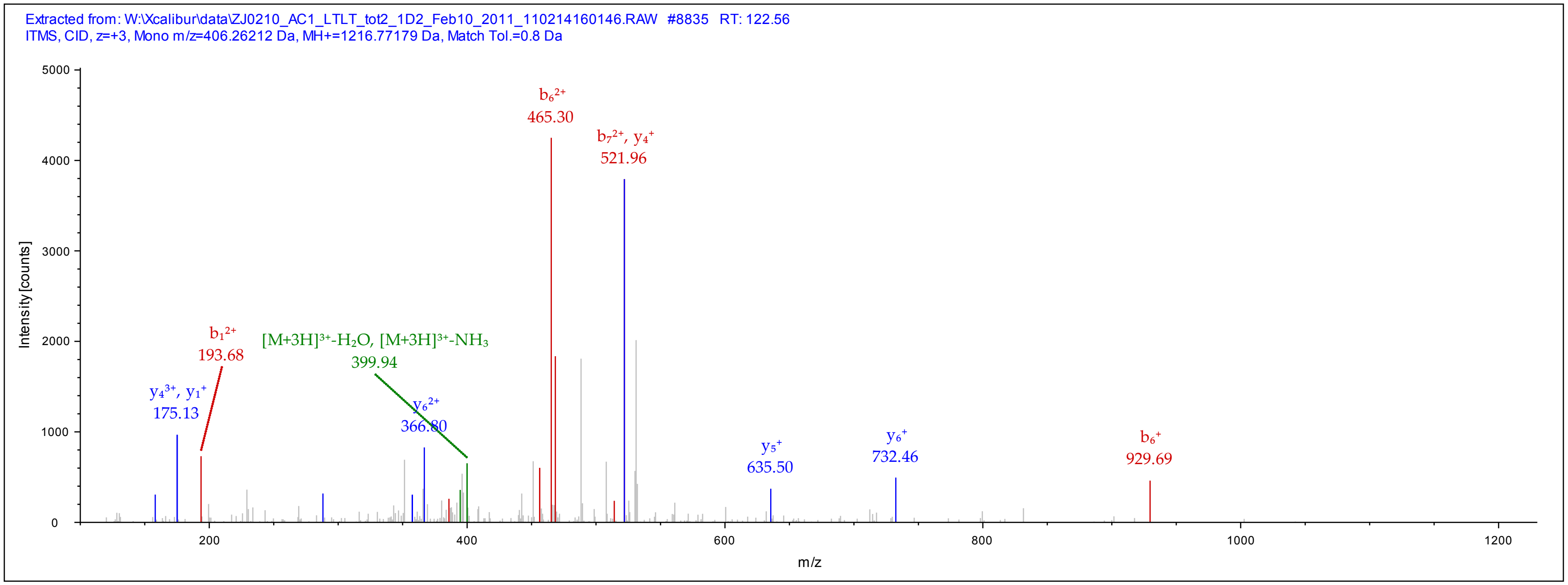
Identified with: Mascot (v1.16); IonScore:39, Exp Value:9.7E-003, Ions matched by search engine: 5/70

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- Putative uncharacterized protein FLJ37218



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_tot2_1D2_Feb10_2011_110214160146.RAW #8835 RT: 122.56
ITMS, CID, z=+3, Mono m/z=406.26212 Da, MH+=1216.77179 Da, Match Tol.=0.8 Da

IPI:IPI00020326.1

Sequence: LFEVIETEK, L1-TMT6plex (229.16293 Da), K9-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 783.46313 Da (-0.07 mmu/-0.09 ppm), MH+: 1565.91899 Da, RT: 116.16 min,

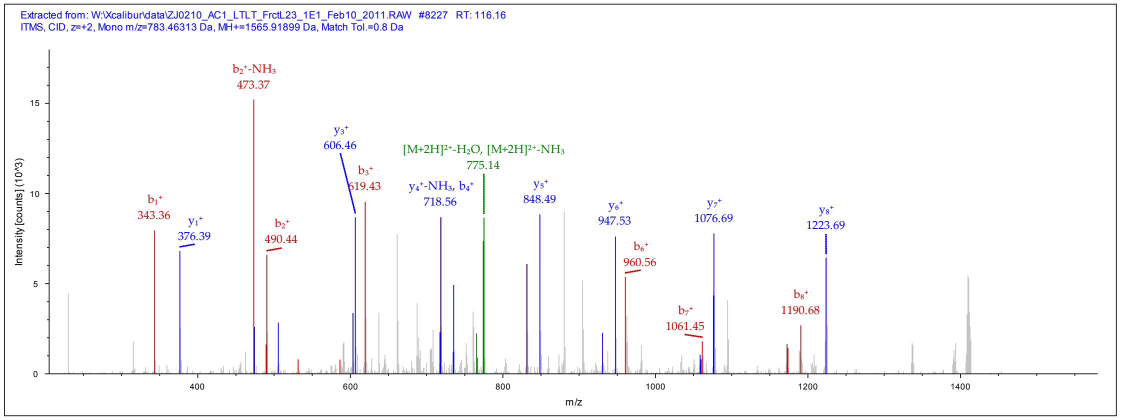
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.1E-002, Ions matched by search engine: 8/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (33):

- Isoform 1 of MAP/microtubule affinity-regulating kinase 4
- Isoform 1 of Serine/threonine-protein kinase MARK2
- Isoform 1 of Serine/threonine-protein kinase MARK1
- Isoform 1 of MAP/microtubule affinity-regulating kinase 3
- R31237_1 (Fragment)
- Isoform 7 of Serine/threonine-protein kinase MARK2 lng=692
- Isoform 2 of MAP/microtubule affinity-regulating kinase 4
- Isoform 10 of Serine/threonine-protein kinase MARK2 lng=686
- Isoform 4 of Serine/threonine-protein kinase MARK2
- Isoform 8 of Serine/threonine-protein kinase MARK2
- Isoform 11 of Serine/threonine-protein kinase MARK2



Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL23_1E1_Feb10_2011.RAW #8227 RT: 116.16
ITMS, CID, z=+2, Mono m/z=783.46313 Da, MH+=1565.91899 Da, Match Tol.=0.8 Da

IPI00181753.4

Sequence: EVVSAQPATFLAR, E1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 809.46271 Da (+0.95 mmu/+1.17 ppm), MH+: 1617.91814 Da, RT: 101.28 min,

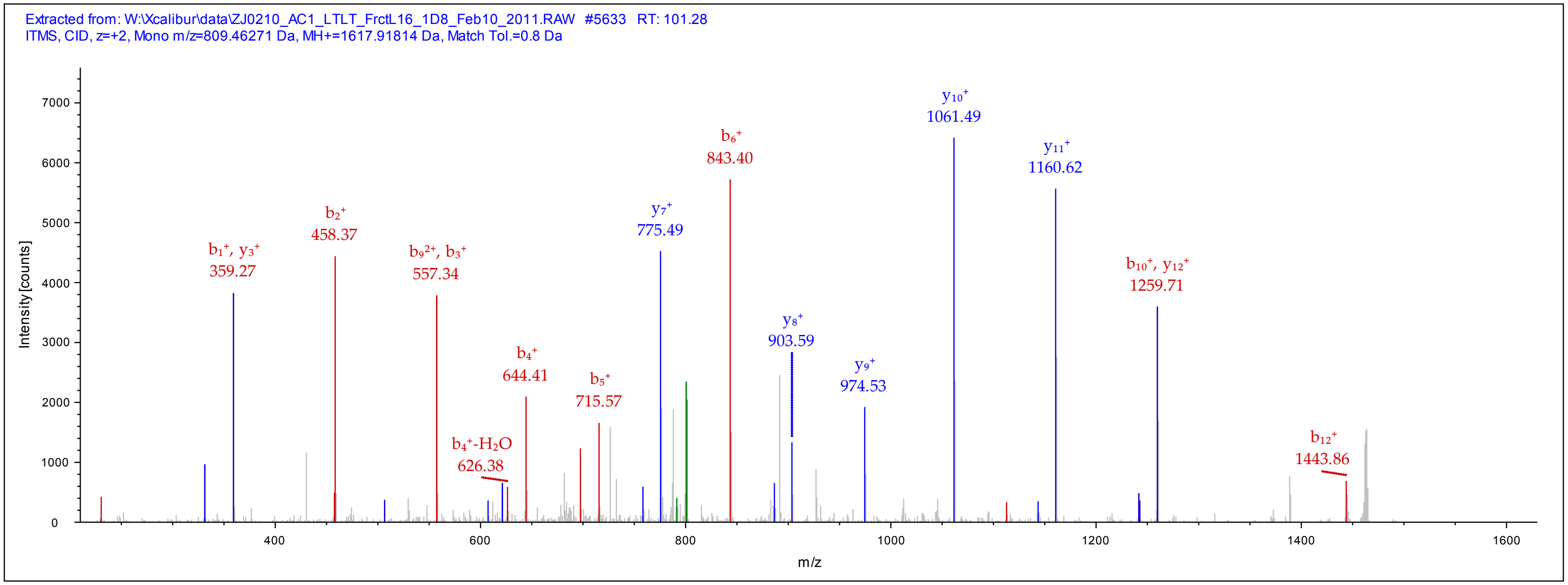
Identified with: Mascot (v1.16); IonScore:53, Exp Value:5.2E-004, Ions matched by search engine: 10/126

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Granulins
- cDNA FLJ13286 fis, clone OVARC1001154, highly similar to Homo sapiens clone 24720 epithelin 1 and 2 mRNA lng=413
- cDNA FLJ53692, moderately similar to Granulins



IPI00902743.1

Sequence: ISLISK, I1-TMT6plex (229.16293 Da), K6-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 559.88025 Da (-0.86 mmu/-1.54 ppm),   MH+: 1118.75322 Da,   RT: 95.34 min,

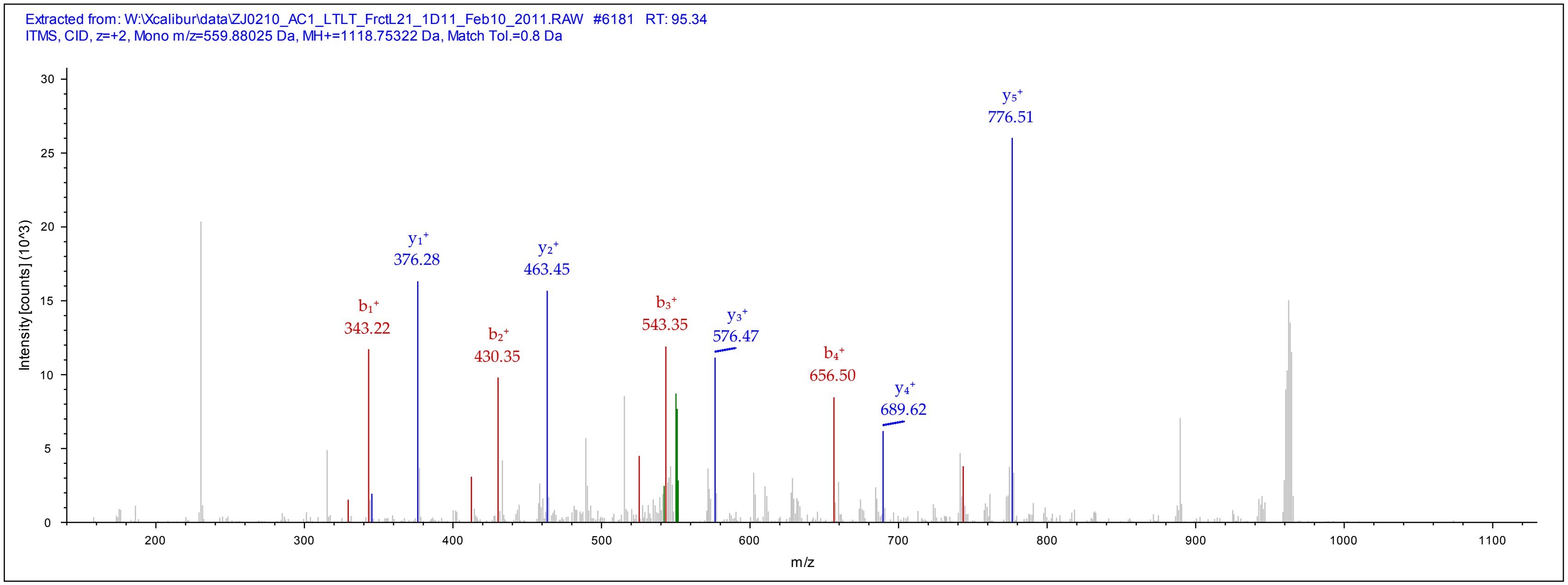
Identified with: Mascot (v1.16); IonScore:31, Exp Value:2.0E-002, Ions matched by search engine: 5/46

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (7):

- Isoform 1 of Protein LSM14 homolog B
- Isoform 1 of Protein LSM14 homolog A
- LSM14 homolog B lng=223
- Isoform 2 of Protein LSM14 homolog A



IPI:IPI00216529.1

Sequence: TECALLGLLLDLK, T1-TMT6plex (229.16293 Da), C3-Carbamidomethyl (57.02146 Da), K13-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 639.72321 Da (+1.83 mmu/+2.87 ppm),   MH+: 1917.15506 Da,   RT: 210.98 min,

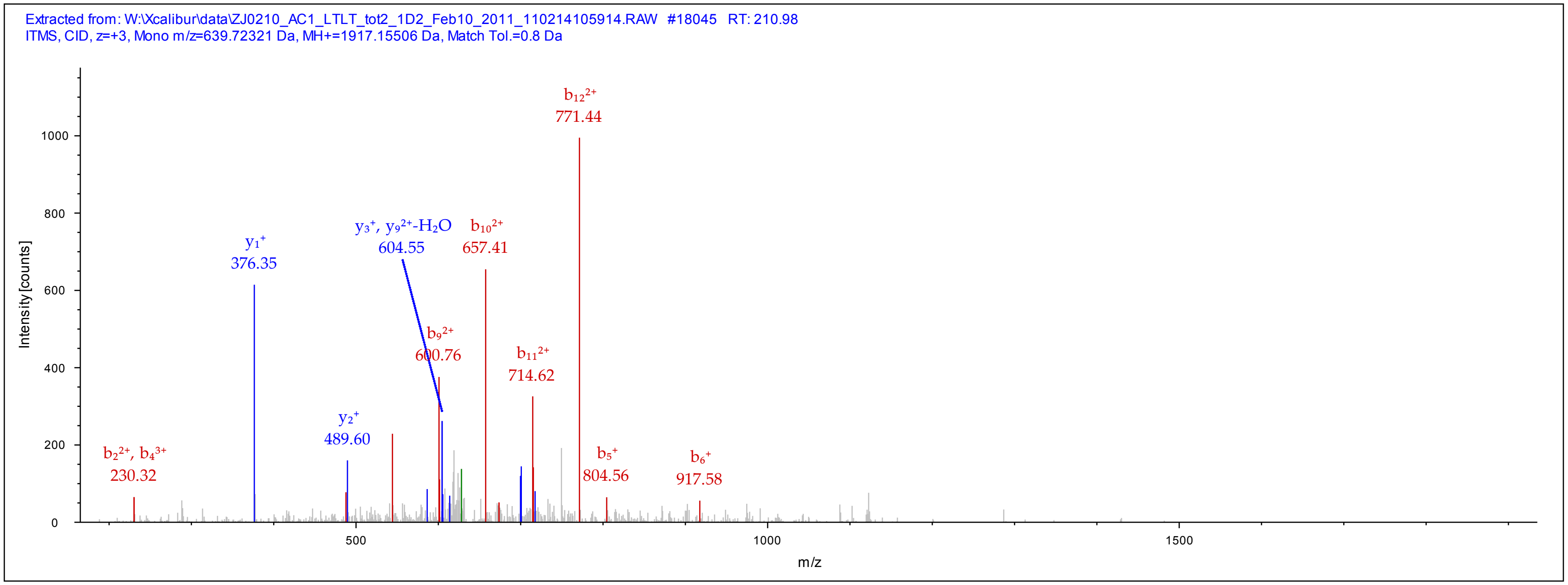
Identified with: Mascot (v1.16); IonScore:42, Exp Value:4.1E-003, Ions matched by search engine: 13/116

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform D of Plasma membrane calcium-transporting ATPase 1
- Isoform A of Plasma membrane calcium-transporting ATPase 1
- Isoform B of Plasma membrane calcium-transporting ATPase 1
- Isoform C of Plasma membrane calcium-transporting ATPase 1
- Isoform E of Plasma membrane calcium-transporting ATPase 1
- Isoform K of Plasma membrane calcium-transporting ATPase 1



IPI:IPI00218176.3

Sequence: VISLEDFMEK, V1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 834.96906 Da (+1.25 mmu/+1.5 ppm), MH+: 1668.93083 Da, RT: 129.65 min,

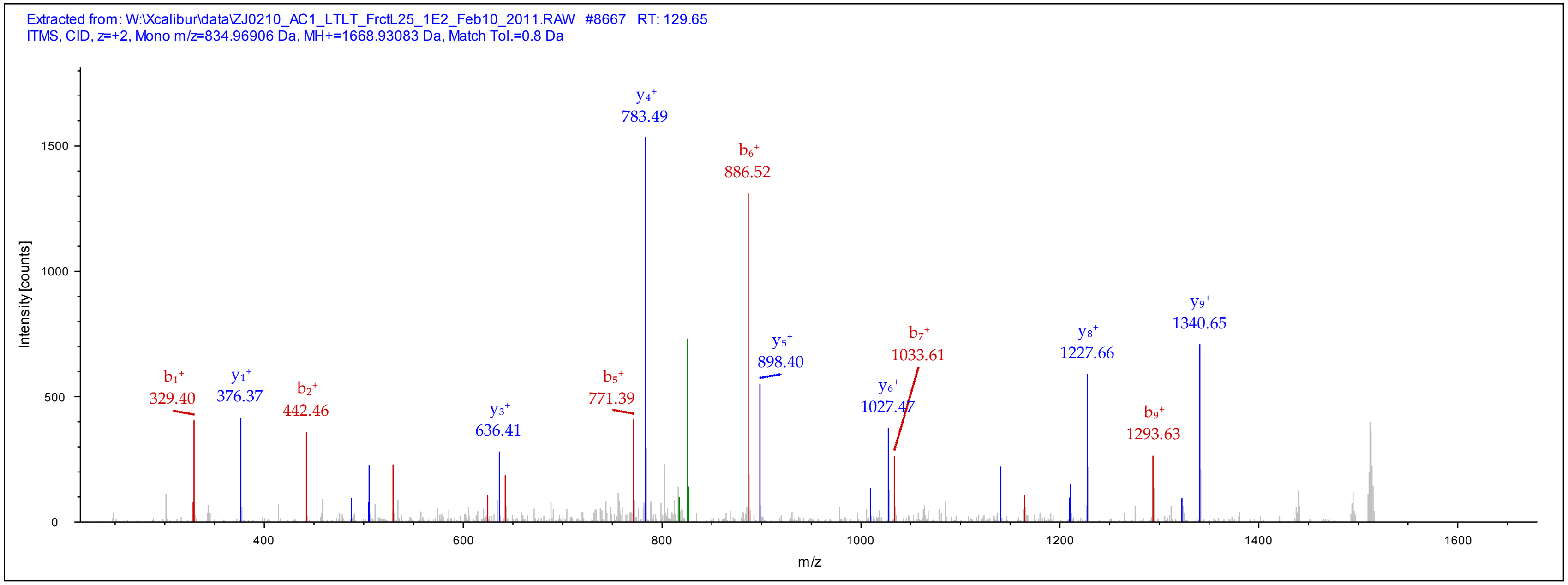
Identified with: Mascot (v1.16); IonScore:52, Exp Value:6.2E-004, Ions matched by search engine: 9/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of GDP-fucose protein O-fucosyltransferase 1
- Isoform 2 of GDP-fucose protein O-fucosyltransferase 1



IPI:IPI00218185.3

Sequence: DLILLIK, D1-TMT6plex (229.16293 Da), K7-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 643.44836 Da (+1.74 mmu/+2.7 ppm), MH+: 1285.88945 Da, RT: 130.21 min,

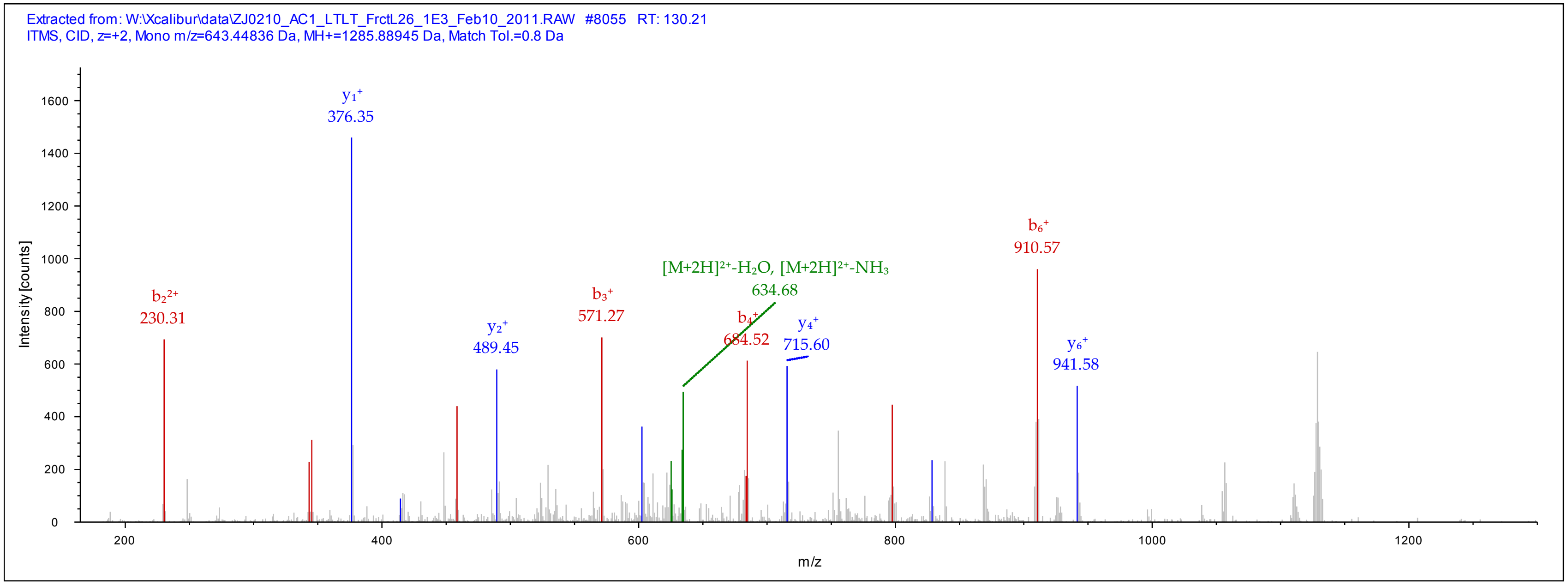
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.5E-003, Ions matched by search engine: 12/48

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform p71 of 2'-5'-oligoadenylate synthase 2
- Isoform p69 of 2'-5'-oligoadenylate synthase 2



IPI:IPI00339385.1

Sequence: LANILFTQELAR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 809.48236 Da (+2.41 mmu/+2.98 ppm), MH+: 1617.95745 Da, RT: 127.16 min,

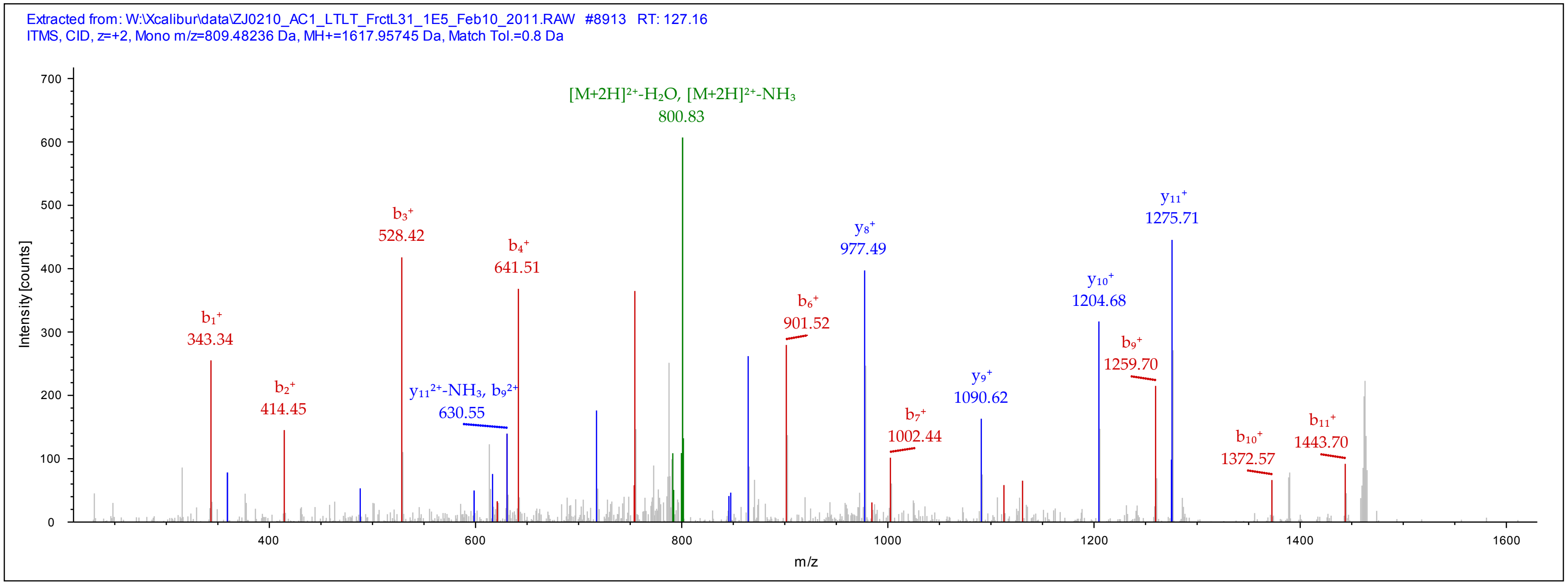
Identified with: Mascot (v1.16); IonScore:61, Exp Value:7.2E-005, Ions matched by search engine: 11/110

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform 1 of Retinol dehydrogenase 11
- Isoform 2 of Retinol dehydrogenase 11



IPI00398727.3

Sequence: LAGVTALSCWLPLR, L1-TMT6plex (229.16293 Da), C9-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 893.51685 Da (+0.83 mmu/+0.93 ppm),   MH+: 1786.02641 Da,   RT: 186.67 min,

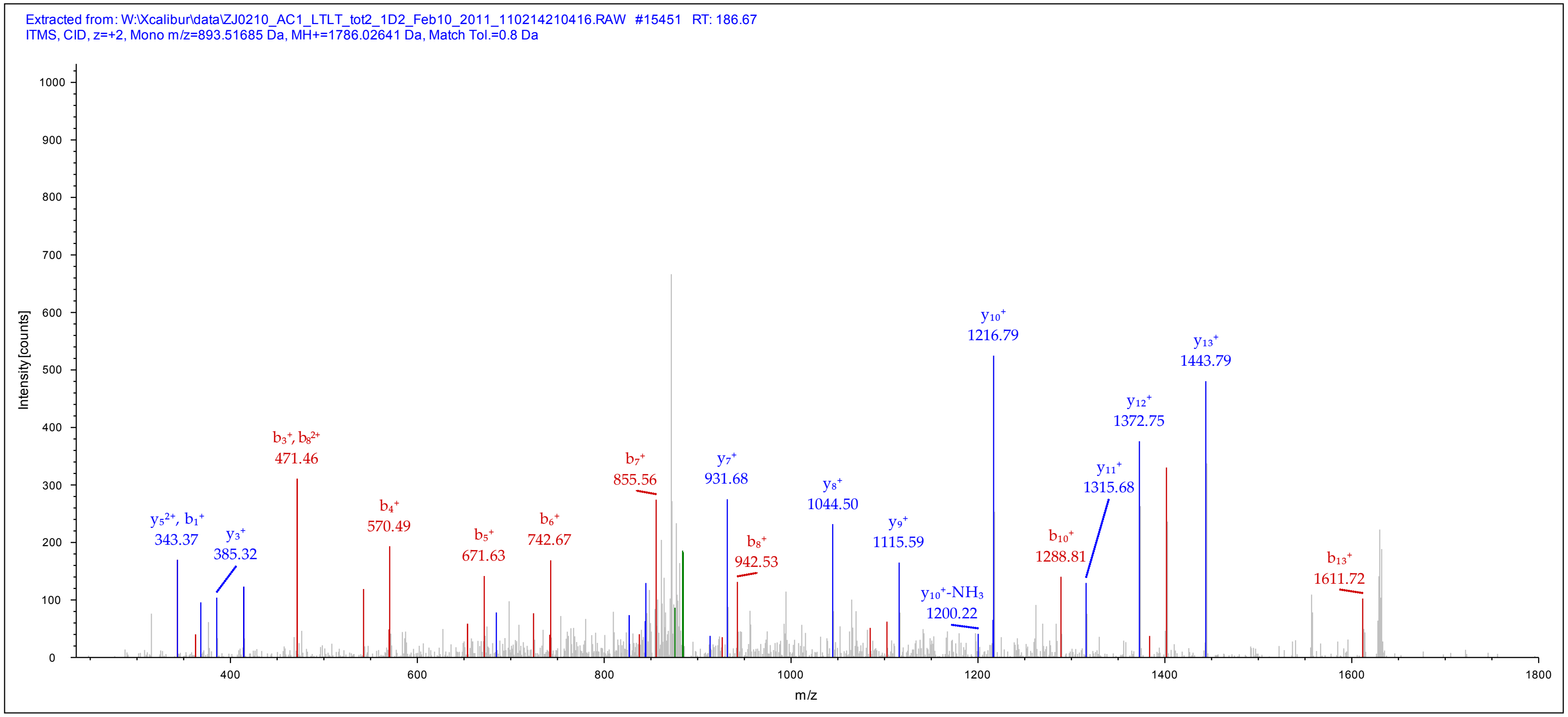
Identified with: Mascot (v1.16); IonScore:52, Exp Value:5.4E-004, Ions matched by search engine: 9/110

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Acyl-protein thioesterase 1
- Isoform 2 of Acyl-protein thioesterase 1 lng=214
- c**D**NA FLJ60607, highly similar to Acyl-protein thioesterase 1 lng=263



IPI:IPI00399318.1

Sequence: MQDLDEDATLTQLATAWVSLATGGEK, M1-TMT6plex (229.16293 Da), K26-TMT6plex (229.16293 Da)

Charge: +4,   Monoisotopic m/z: 806.42291 Da (+2.31 mmu/+2.87 ppm),   MH+: 3222.66982 Da,   RT: 227.25 min,

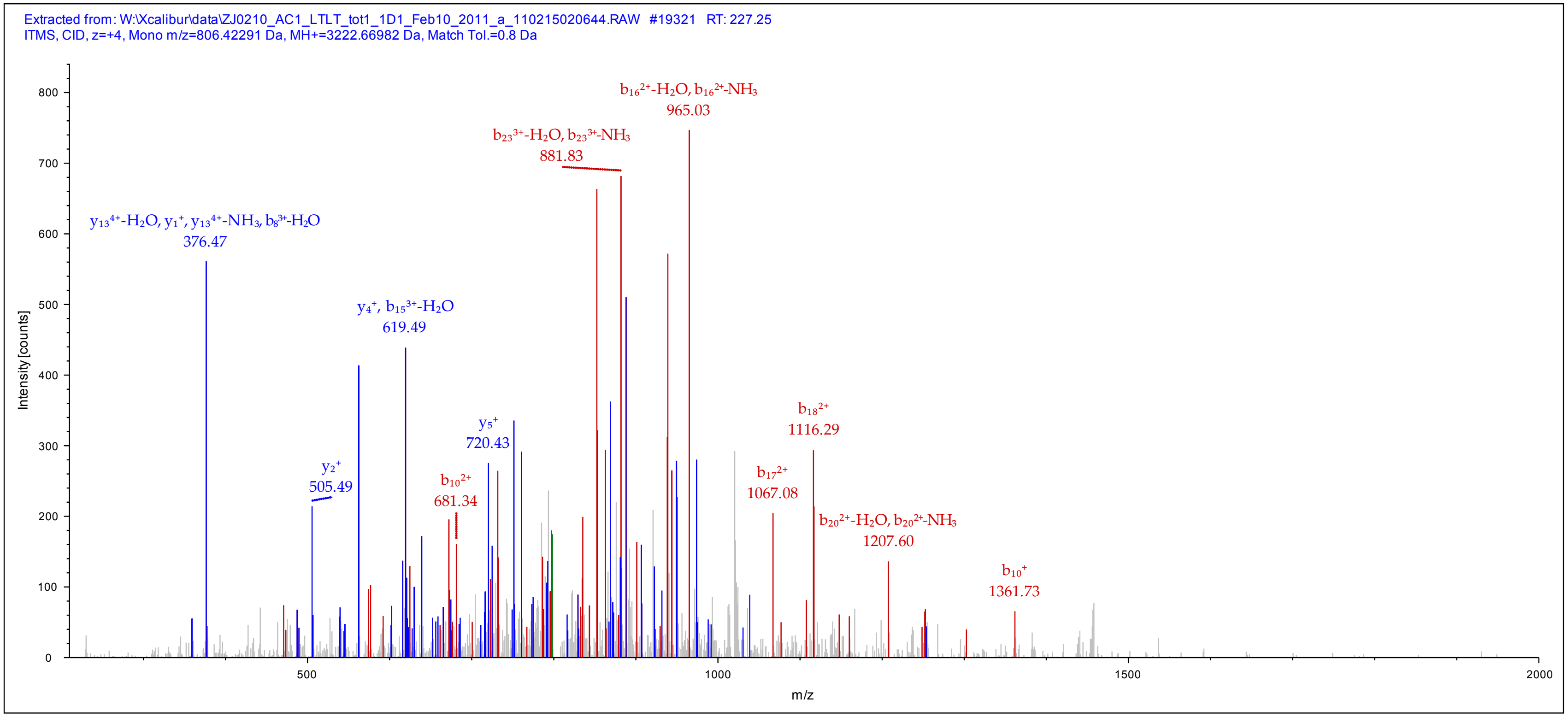
Identified with: Mascot (v1.16); IonScore:47, Exp Value:4.7E-003, Ions matched by search engine: 15/292

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Coatomer subunit epsilon
- coatomer subunit epsilon isoform b



IPI:IPI00414290.1

Sequence: LTDAFLLLR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 645.90332 Da (+0.51 mmu/+0.79 ppm), MH+: 1290.79936 Da, RT: 172.65 min,

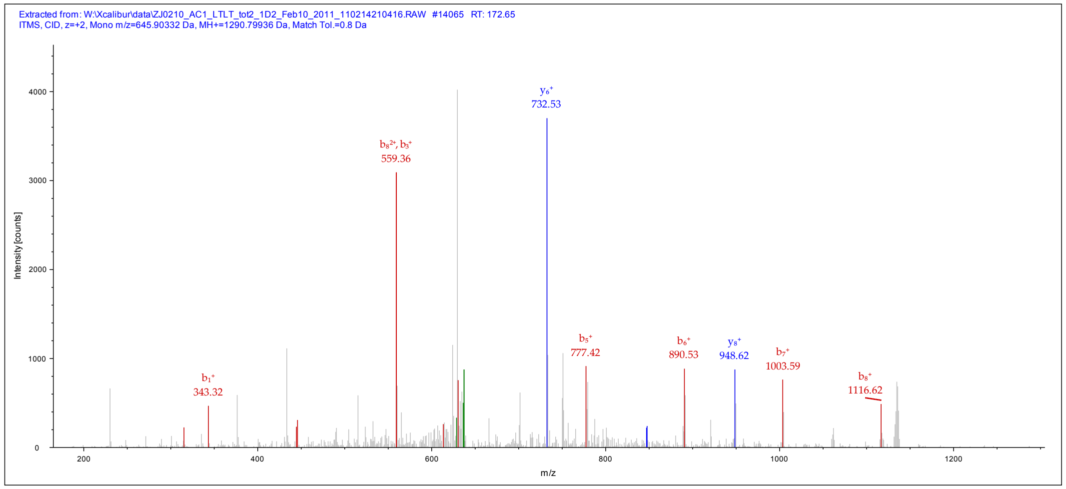
Identified with: Mascot (v1.16); IonScore:36, Exp Value:1.8E-002, Ions matched by search engine: 8/66

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (9):

- Isoform B of Syntaxin-16
- Isoform A of Syntaxin-16
- Isoform D of Syntaxin-16
- Isoform C of Syntaxin-16
- Syntaxin 16 isoform a variant (Fragment)
- 41 kDa protein
- 37 kDa protein
- syntaxin-16 isoform c
- Uncharacterized protein



IPI:IPI00400849.2

Sequence: GDIPDLSQAPSSLLDALEQHLASLEGK, G1-TMT6plex (229.16293 Da), K27-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 1088.25916 Da (+1.89 mmu/+1.74 ppm),   MH+: 3262.76291 Da,   RT: 214.79 min,

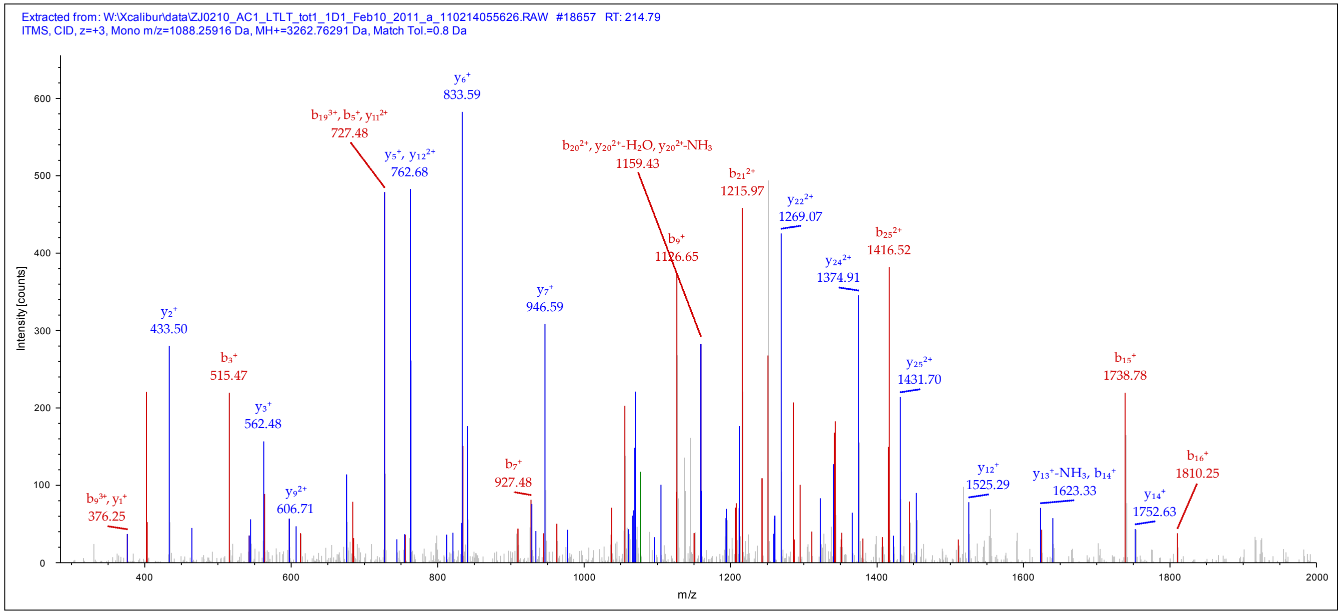
Identified with: Mascot (v1.16); IonScore:79, Exp Value:1.9E-006, Ions matched by search engine: 18/292

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform 1 of Phosphatidylinositol-binding clathrin assembly protein
- Isoform 3 of Phosphatidylinositol-binding clathrin assembly protein
- Isoform 2 of Phosphatidylinositol-binding clathrin assembly protein
- Putative uncharacterized protein PICALM lng=632
- Putative uncharacterized protein PICALM lng=660
- Putative uncharacterized protein PICALM lng=652



IPI00553155.1

Sequence: LEEGPPVTTVLTR, L1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 820.97601 Da (+1.31 mmu/+1.6 ppm), MH+: 1640.94475 Da, RT: 104.51 min,

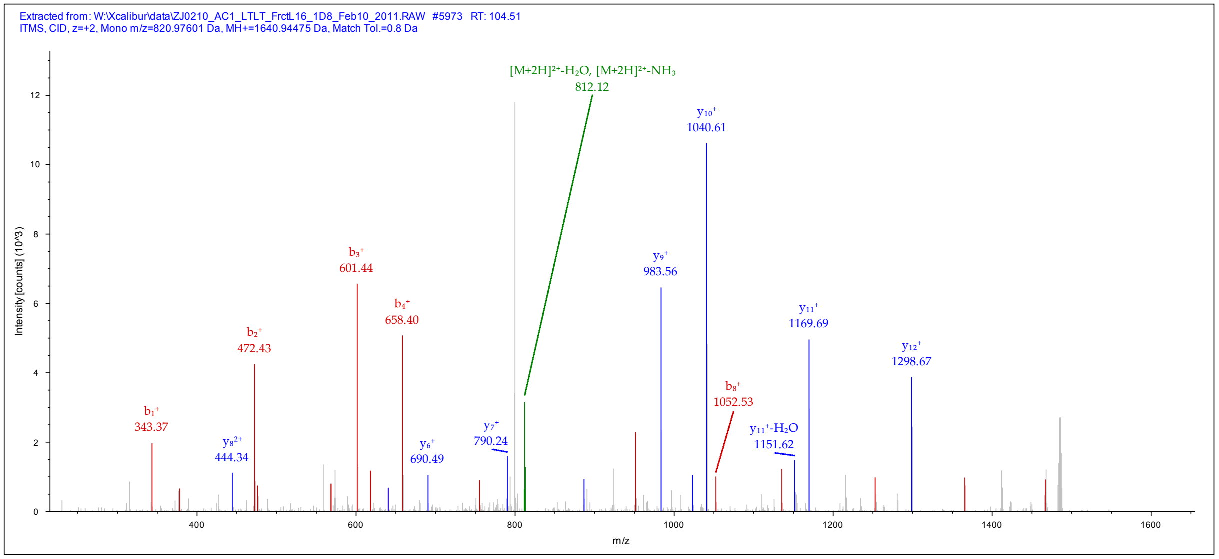
Identified with: Mascot (v1.16); IonScore:58, Exp Value:1.6E-004, Ions matched by search engine: 12/116

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial
- Pyruvate dehydrogenase (Lipoamide) alpha 1 lng=121
- Pyruvate dehydrogenase (Lipoamide) alpha 1
- Mitochondrial PDHA1 lng=428
- pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial isoform 3 precursor
- cDNA FLJ52314, highly similar to Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial lng=359



IPI00940890.1

Sequence: AEDAVEAIR, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 601.83313 Da (+0.55 mmu/+0.91 ppm), MH+: 1202.65898 Da, RT: 81.42 min,

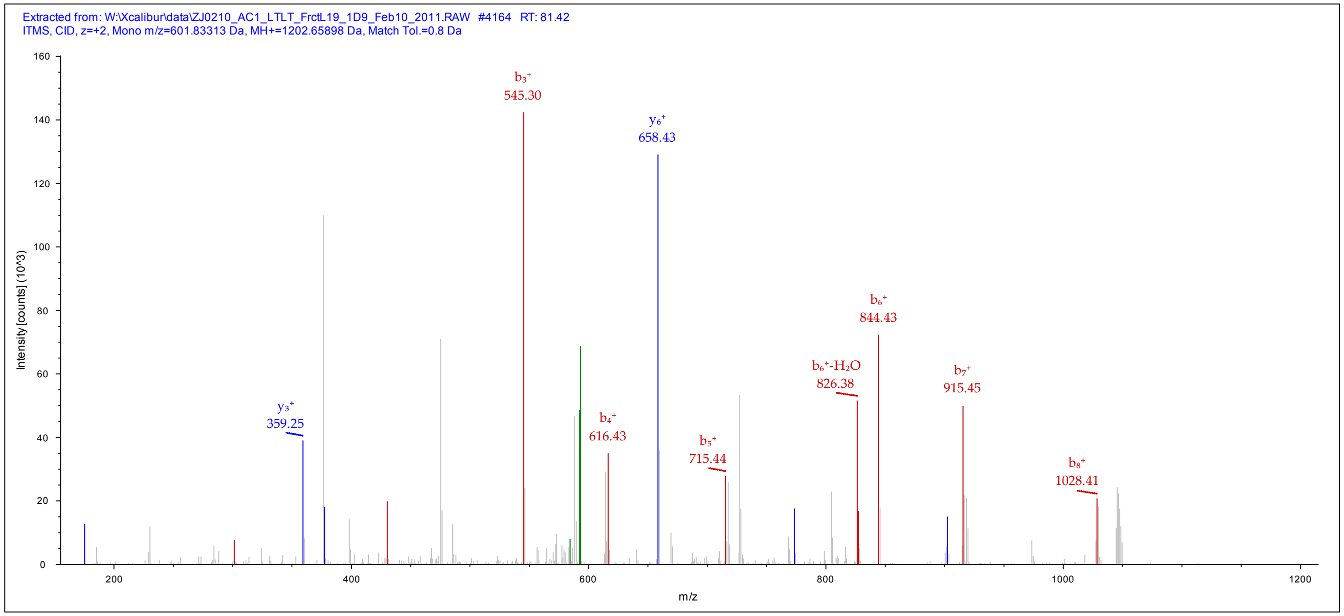
Identified with: Mascot (v1.16); IonScore:34, Exp Value:3.2E-002, Ions matched by search engine: 7/72

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (6):

- Isoform 1 of RNA-binding protein 4
- RNA-binding protein 4B
- Isoform 2 of RNA-binding protein 4 lng=177
- Isoform 3 of RNA-binding protein 4 lng=143
- cDNA FLJ59148, highly similar to RNA-binding protein 4 lng=173
- Uncharacterized protein



IPI:IPI00641801.2

Sequence: FWDASGVCLR, F1-TMT6plex (229.16293 Da), C8-Carbamidomethyl (57.02146 Da)

Charge: +2,   Monoisotopic m/z: 720.36841 Da (-0.4 mmu/-0.56 ppm),   MH+: 1439.72954 Da,   RT: 106.39 min,

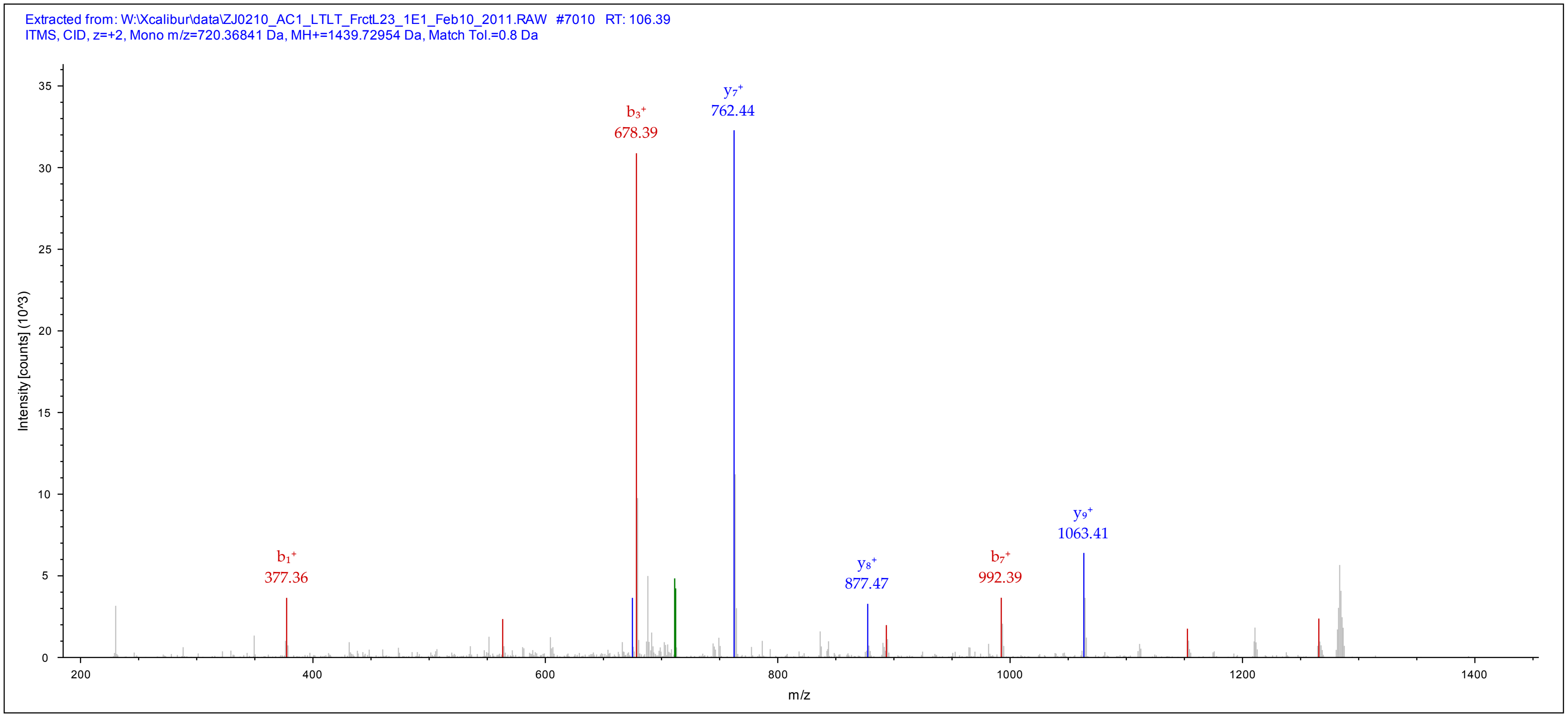
Identified with: Mascot (v1.16); IonScore:36, Exp Value:2.3E-002, Ions matched by search engine: 9/76

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Isoform C of Lethal(2) giant larvae protein homolog 2
- Isoform A of Lethal(2) giant larvae protein homolog 2



IPI:IPI00641968.1

Sequence: FYPPDPAQLTEDITR, F1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 996.51855 Da (+1.1 mmu/+1.1 ppm),   MH+: 1992.02983 Da,   RT: 122.77 min,

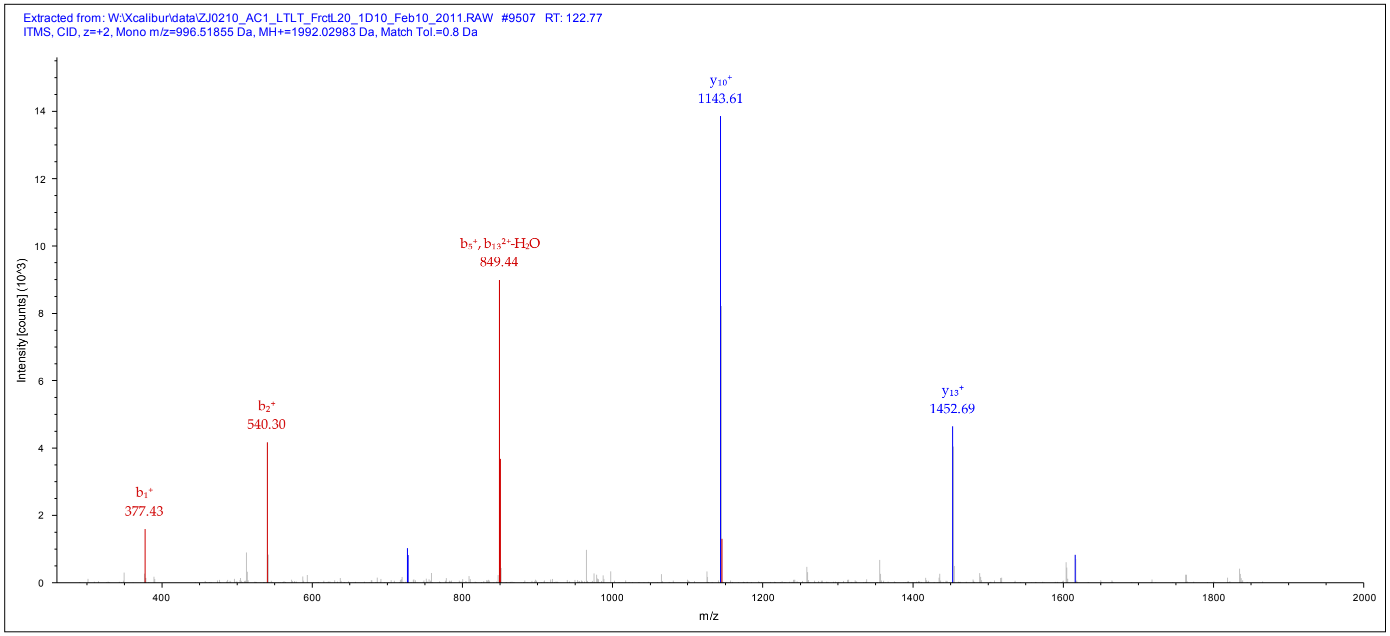
Identified with: Mascot (v1.16); IonScore:41, Exp Value:1.0E-002, Ions matched by search engine: 11/144

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (15):

- Isoform 1 of Protein 4.1
- Isoform 1 of Band 4.1-like protein 1
- Isoform 2 of Protein 4.1
- Isoform 3 of Protein 4.1
- Isoform 4 of Protein 4.1
- Isoform 5 of Protein 4.1
- Isoform 6 of Protein 4.1
- protein 4.1 isoform 3
- Erythrocyte membrane protein band 4.1-like 1
- cDNA FLJ61657, highly similar to Band 4.1-like protein 1
- Isoform 2 of Band 4.1-like protein 1
- Isoform 3 of Band 4.1-like protein
- Isoform 4 of Band 4.1-like protein 1
- cDNA FLJ50645
- EPB41 protein



IPI00644458.1

Sequence: YFSLPFCVGSK, Y1-TMT6plex (229.16293 Da), C7-Carbamidomethyl (57.02146 Da), K11-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 881.98383 Da (+0.05 mmu/+0.05 ppm), MH+: 1762.96037 Da, RT: 126.62 min,

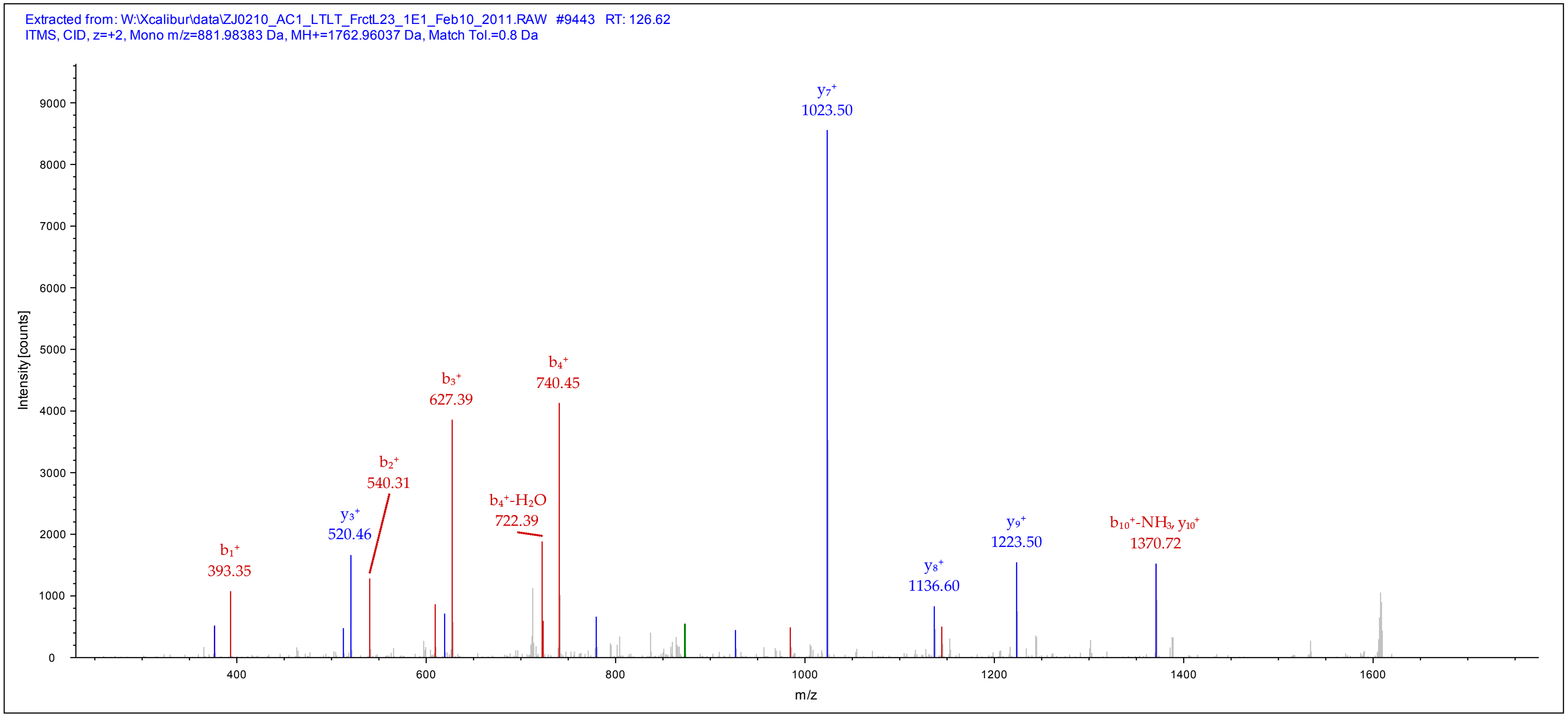
Identified with: Mascot (v1.16); IonScore:62, Exp Value:7.3E-005, Ions matched by search engine: 10/94

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; $b-H_2O$; $b-NH_3$; y; $y-H_2O$; $y-NH_3$

Protein references (2):

- Transmembrane 9 superfamily member 3
- SM-11044 binding protein lng=254



IPI00645320.1

Sequence: FVDILGLR, F1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 581.36334 Da (+0.02 mmu/+0.04 ppm), MH+: 1161.71941 Da, RT: 126.08 min,

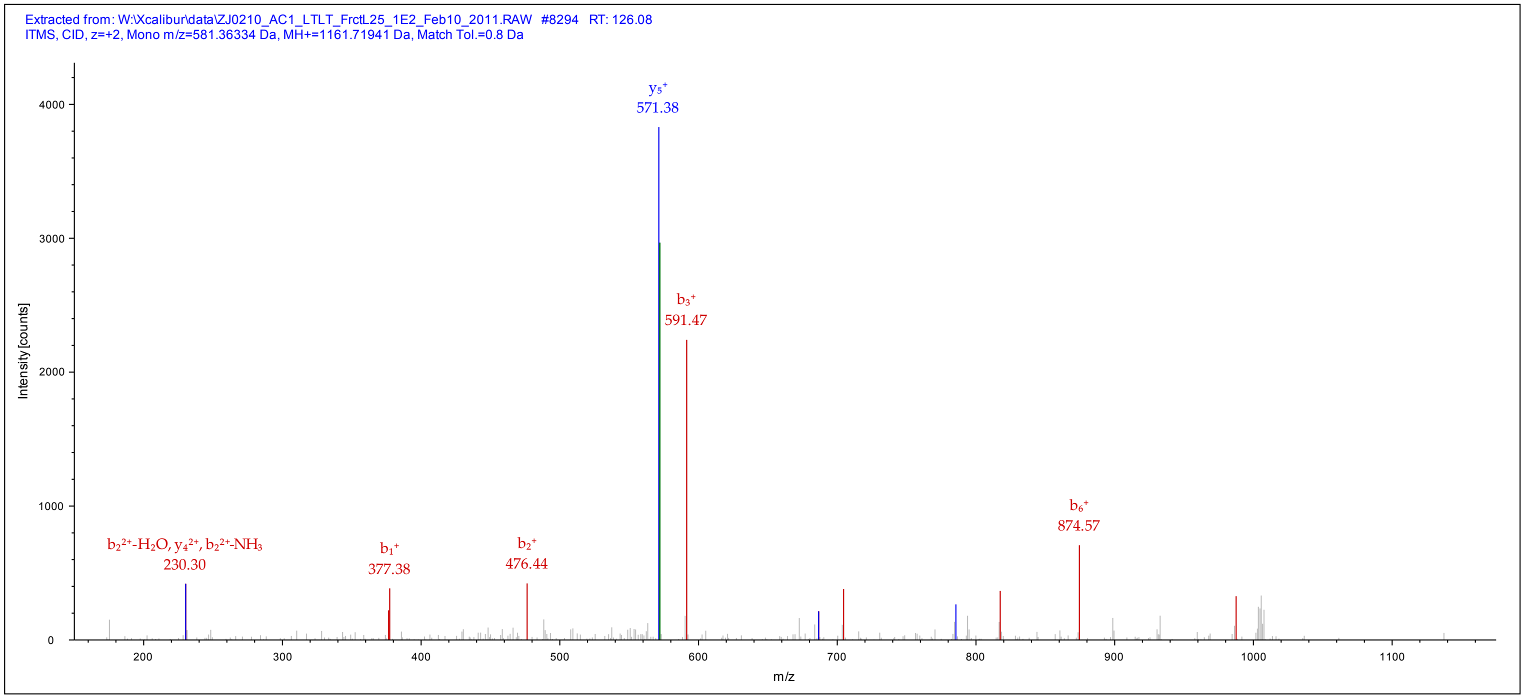
Identified with: Mascot (v1.16); IonScore:46, Exp Value:2.6E-003, Ions matched by search engine: 6/56

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Isoform 1 of Beta-catenin-like protein 1
- Isoform 2 of Beta-catenin-like protein 1 lng=376
- Isoform 3 of Beta-catenin-like protein 1 lng=311



IPI00645960.1

Sequence: DAGLLDEVIQEFHQELVETMR, D1-TMT6plex (229.16293 Da)

Charge: +3, Monoisotopic m/z: 901.12933 Da (+0.96 mmu/+1.06 ppm), MH+: 2701.37345 Da, RT: 231.00 min,

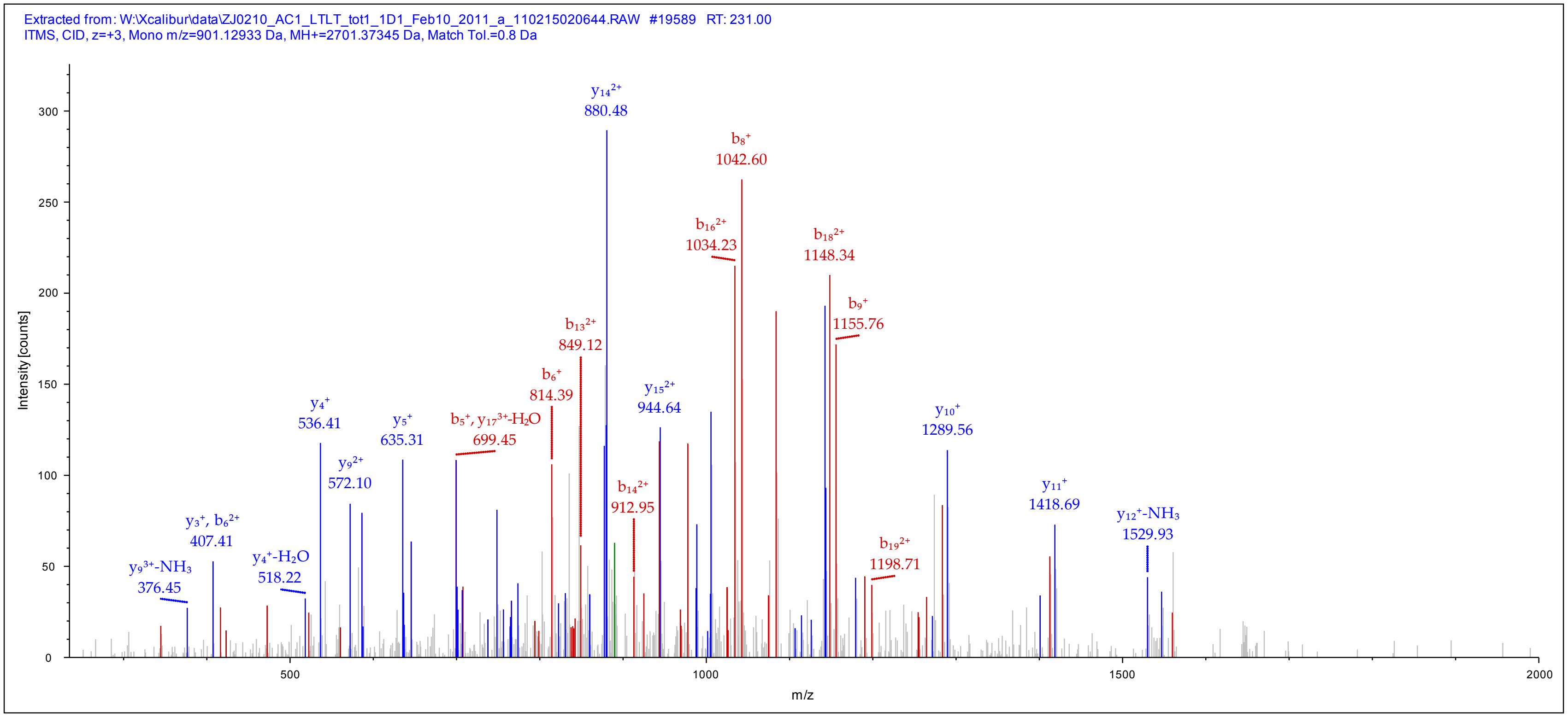
Identified with: Mascot (v1.16); IonScore:74, Exp Value:8.9E-006, Ions matched by search engine: 23/218

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- Glucocorticoid modulatory element-binding protein 2
- Glucocorticoid modulatory element binding protein 2, isoform CRA_a lng=479



IPI00647089.1

Sequence: LIEDFLAR, L1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 603.35870 Da (+0.47 mmu/+0.78 ppm),   MH+: 1205.71013 Da,   RT: 123.73 min,

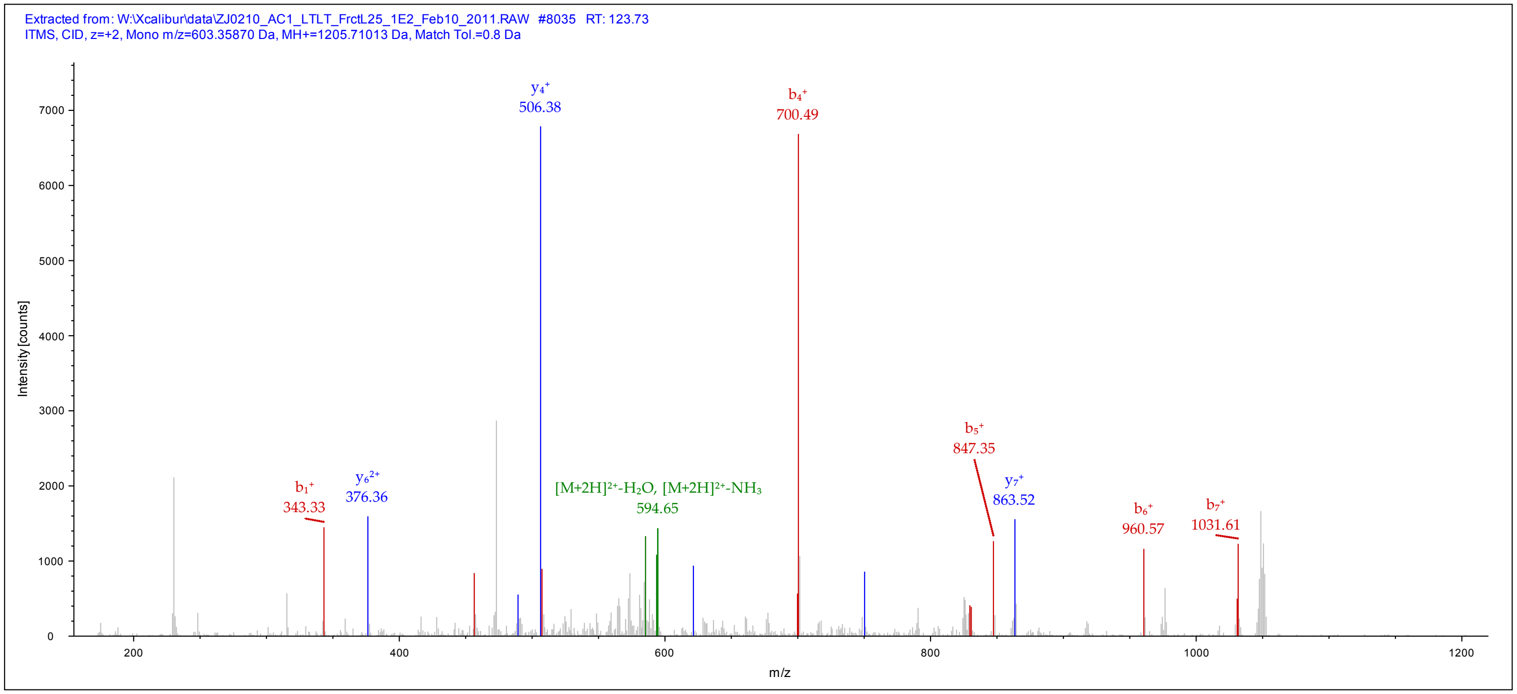
Identified with: Mascot (v1.16); IonScore:35, Exp Value:4.4E-002, Ions matched by search engine: 7/58

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Trafficking protein particle complex subunit 3
- Trafficking protein particle complex 3, isoform CRA_a lng=134
- Putative uncharacterized protein TRAPPC3 lng=118



IPI:IPI00815947.1

Sequence: LLVVYPWTQR, L1-TMT6plex (229.16293 Da)

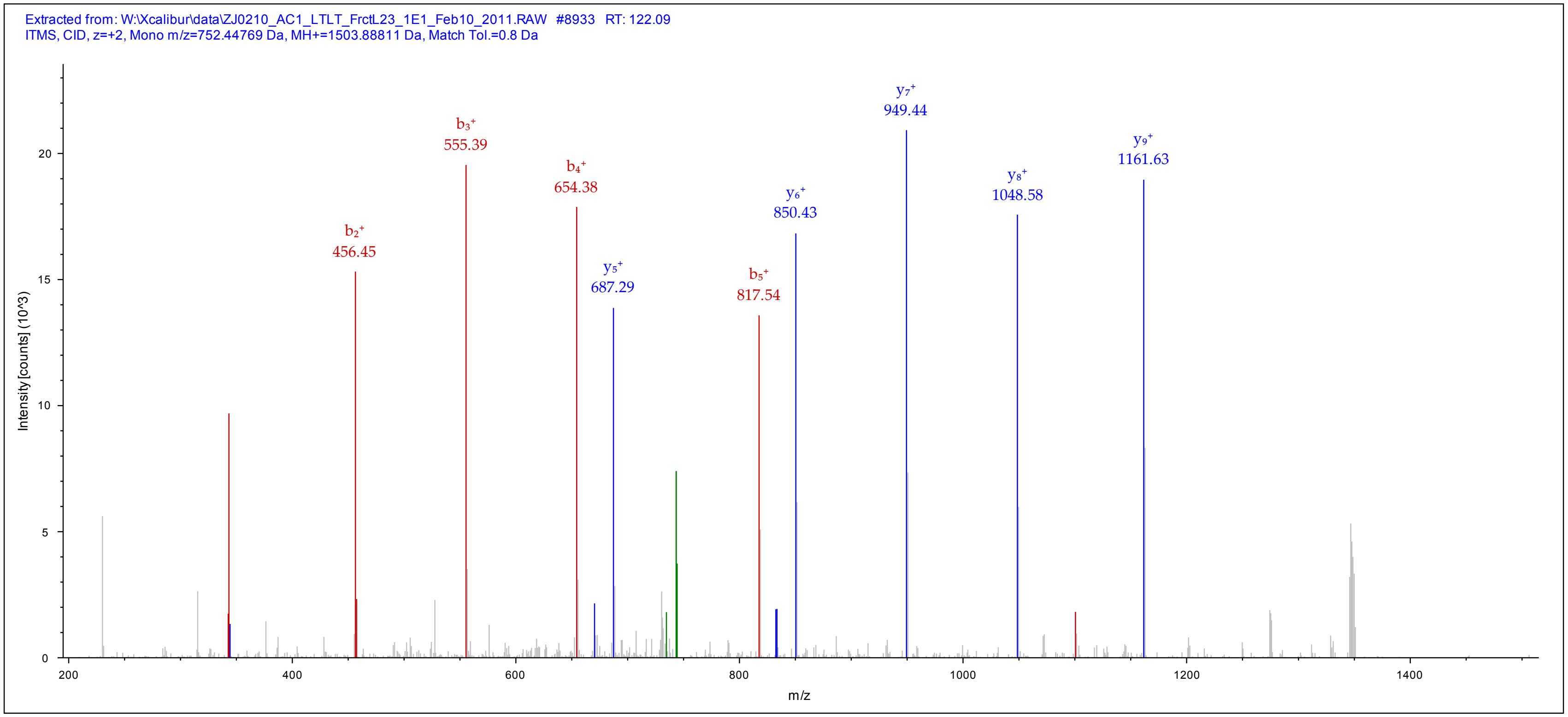
Charge: +2,   Monoisotopic m/z: 752.44769 Da (-0.22 mmu/-0.29 ppm),   MH+: 1503.88811 Da,   RT: 122.09 min,

Identified with: Mascot (v1.16); IonScore:34, Exp Value:3.5E-002, Ions matched by search engine: 8/74

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (20):
- Hemoglobin subunit beta
- Hemoglobin subunit delta
- Hemoglobin subunit epsilon
- Hemoglobin subunit gamma-1
- Hemoglobin subunit gamma-2
- Beta-globin gene from a thalassemia patient
- Delta-globin B2 variant
- Gamma-globin
- Hemoglobin Lepore-Baltimore (Fragment)
- Truncated beta-globin (Fragment)
- 17 kDa protein
- Gamma-G globin
- Delta-hemoglobin
- Hemoglobin (Fragment)
- Uncharacterized protein
- Hbbm fused globin protein (Fragment)
- G-gamma globin Paulinia variant
- A-gamma globin Osilo variant
- Truncated beta-globin
- 17 kDa protein


Extracted from: W:\Xcalibur\data\ZJ0210_AC1_LTLT_FrctL23_1E1_Feb10_2011.RAW #8933 RT: 122.09
ITMS, CID, z=+2, Mono m/z=752.44769 Da, MH+=1503.88811 Da, Match Tol.=0.8 Da
Intensity [counts] (10^3)
0
5
10
15
20
200
400
600
800
1000
1200
1400
m/z
b_2^+ 456.45
b_3^+ 555.39
b_4^+ 654.38
y_5^+ 687.29
b_5^+ 817.54
y_6^+ 850.43
y_7^+ 949.44
y_8^+ 1048.58
y_9^+ 1161.63

IPI:IPI00106668.5

Sequence: AQEALLQLSQVLSLMETVK, A1-TMT6plex (229.16293 Da), K19-TMT6plex (229.16293 Da)

Charge: +3,   Monoisotopic m/z: 853.83533 Da (+2.72 mmu/+3.18 ppm),   MH+: 2559.49143 Da,   RT: 230.44 min,

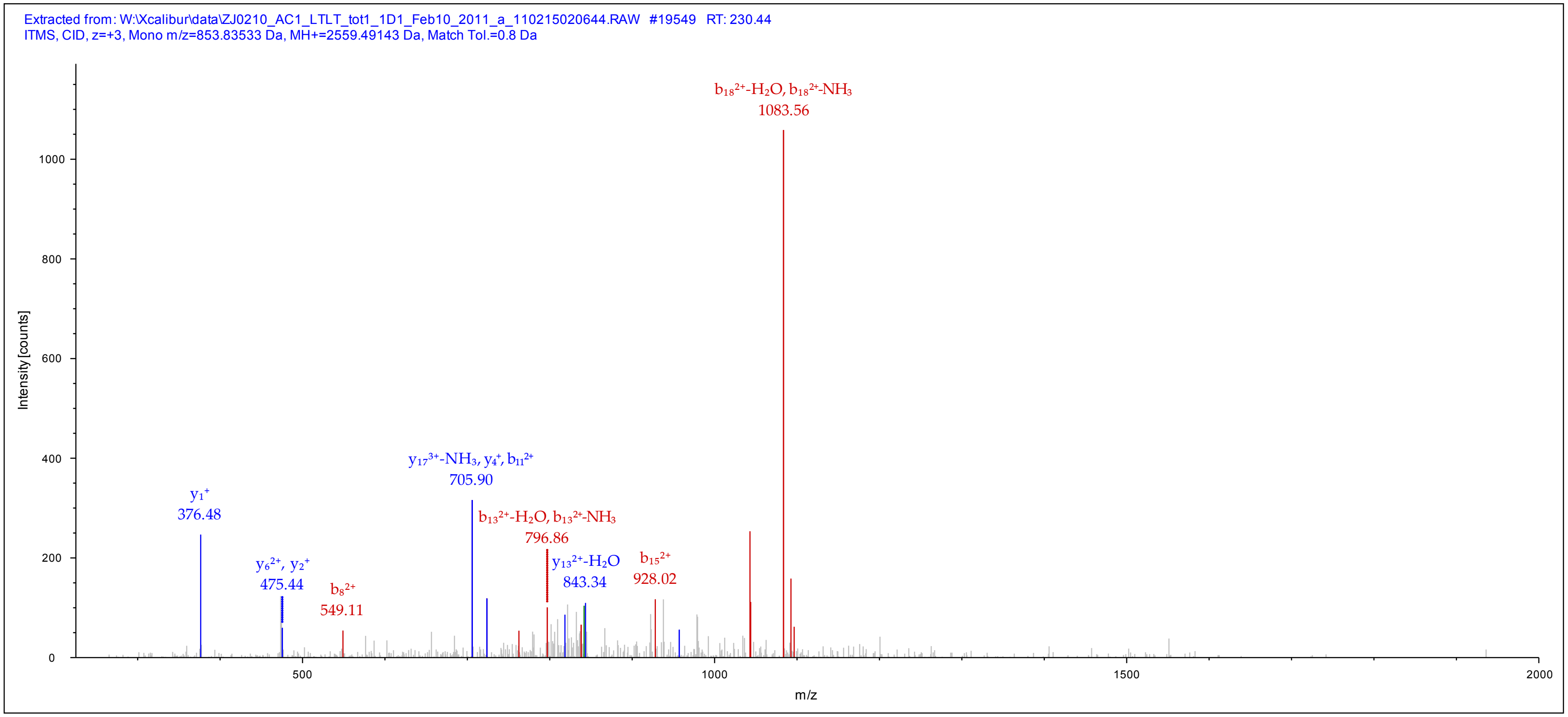
Identified with: Mascot (v1.16); IonScore:30, Exp Value:6.8E-002, Ions matched by search engine: 16/206

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (2):

- perilipin-3 isoform 3
- mannose 6 phosphate receptor binding protein 1 isoform 2 lng=433



IPI:IPI00384497.3

Sequence: AAVAATAAAK, A1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 651.91199 Da (+1.04 mmu/+1.6 ppm),   MH+: 1302.81670 Da,   RT: 76.76 min,

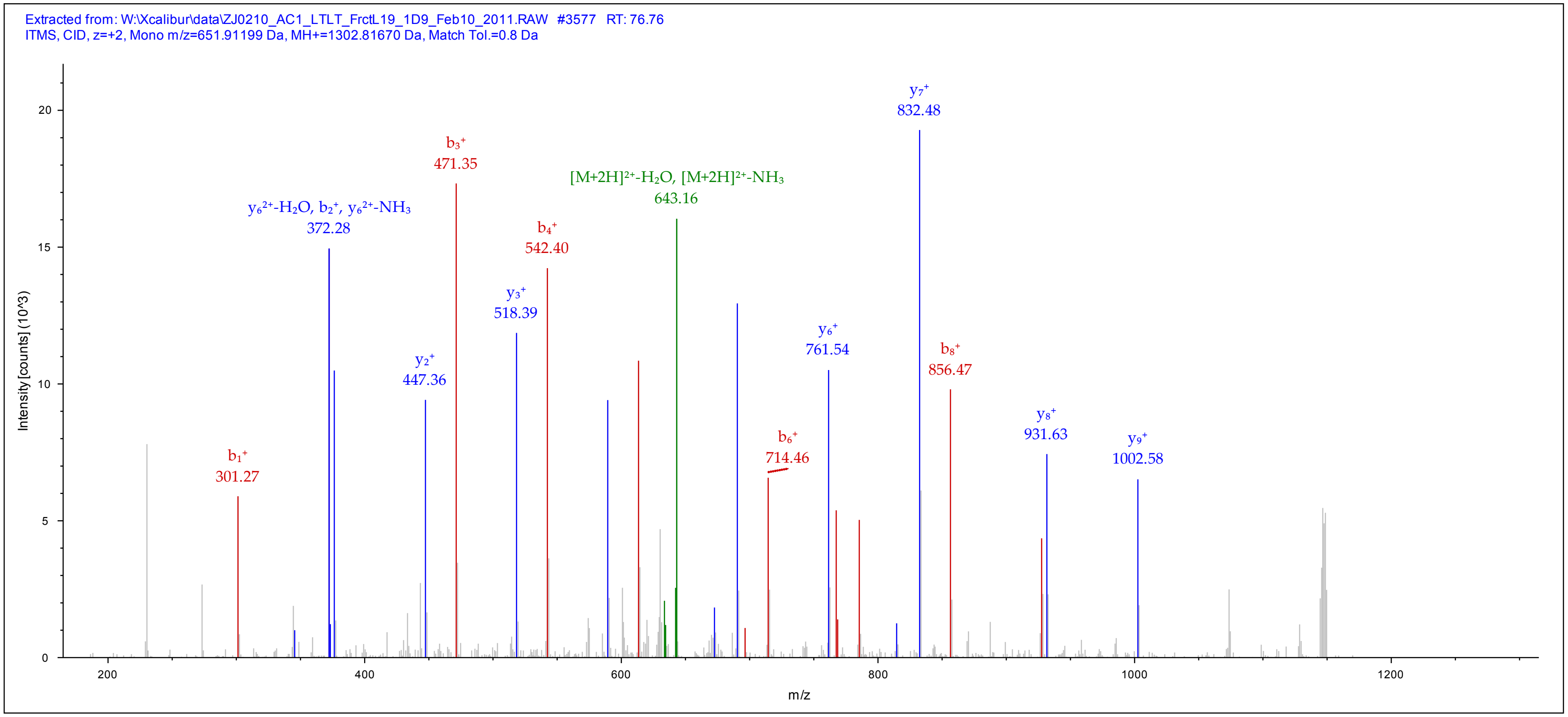
Identified with: Mascot (v1.16); IonScore:67, Exp Value:1.2E-005, Ions matched by search engine: 8/72

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- 3-hydroxyacyl-CoA dehydratase 2



IPI00654820.2

Sequence: LITTQQWLIK, L1-TMT6plex (229.16293 Da), K10-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 851.53766 Da (+0.62 mmu/+0.73 ppm),   MH+: 1702.06804 Da,   RT: 120.98 min,

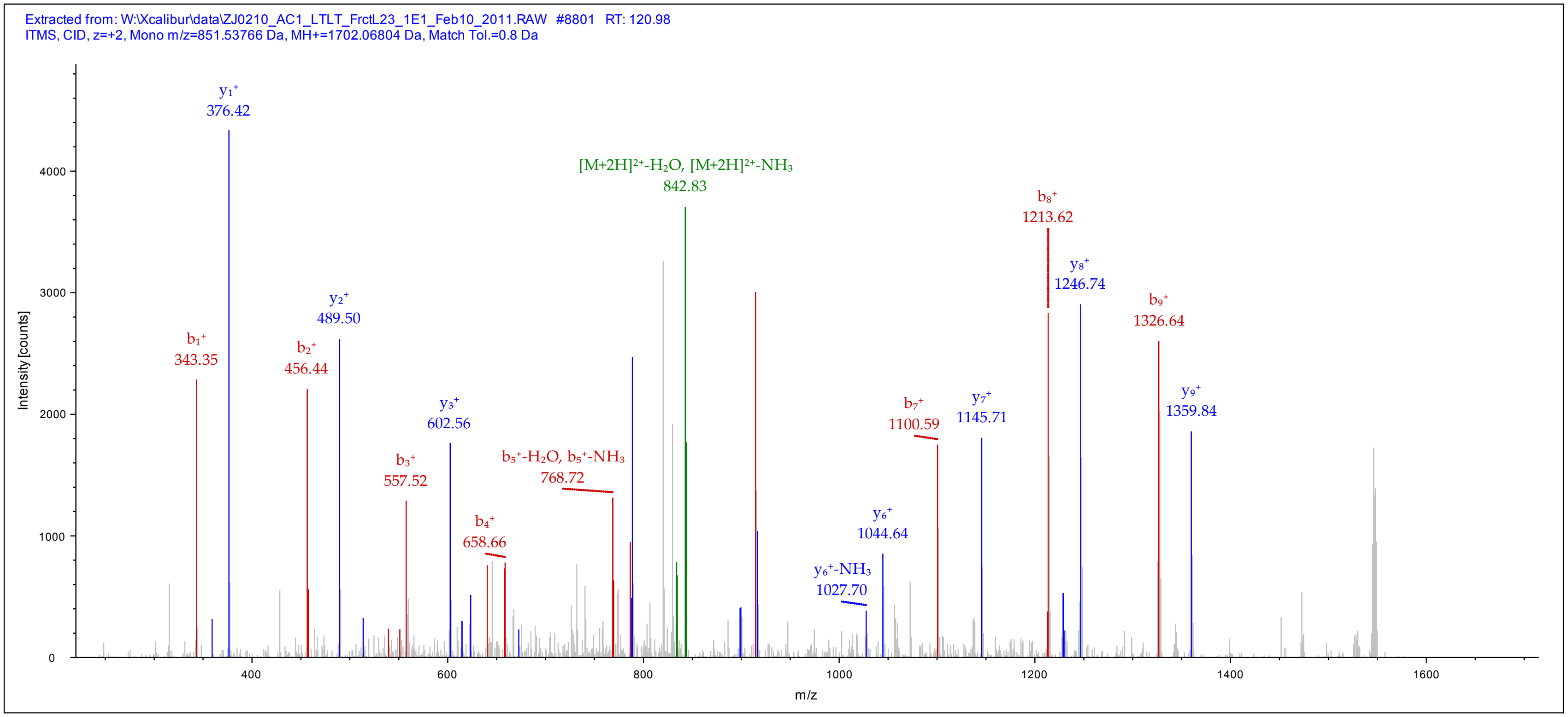
Identified with: Mascot (v1.16); IonScore:46, Exp Value:1.1E-003, Ions matched by search engine: 8/84

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (1):

- ATP synthase subunit a lng=236



IPI00788670.1

Sequence: ETIDAVPNAIPGR, E1-TMT6plex (229.16293 Da)

Charge: +2,   Monoisotopic m/z: 791.44543 Da (+1.87 mmu/+2.36 ppm),   MH+: 1581.88359 Da,   RT: 93.91 min,

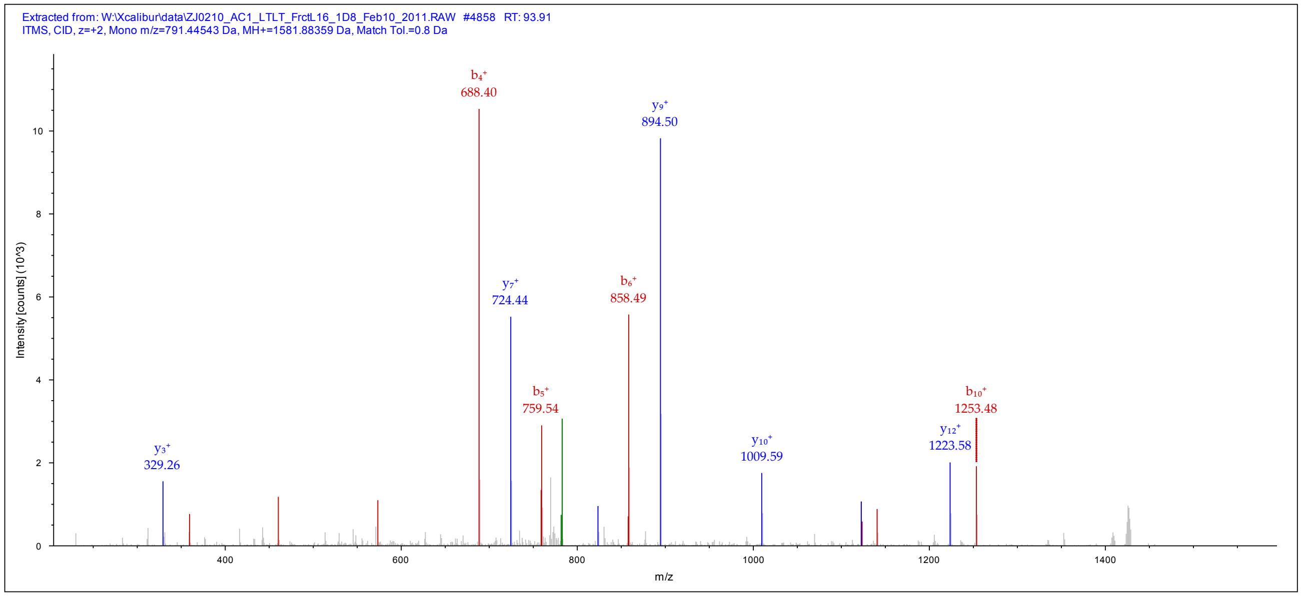
Identified with: Mascot (v1.16); IonScore:61, Exp Value:7.5E-005, Ions matched by search engine: 8/112

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (5):

- Isoform 1 of Zinc finger protein 207
- Isoform 2 of Zinc finger protein 207
- zinc finger protein 207 isoform c
- Putative uncharacterized protein ZNF207 lng=447
- Zinc finger, C2H2-type domain containing protein lng=493



IPI00789072.1

Sequence: TLAGDVHIVR, T1-TMT6plex (229.16293 Da)

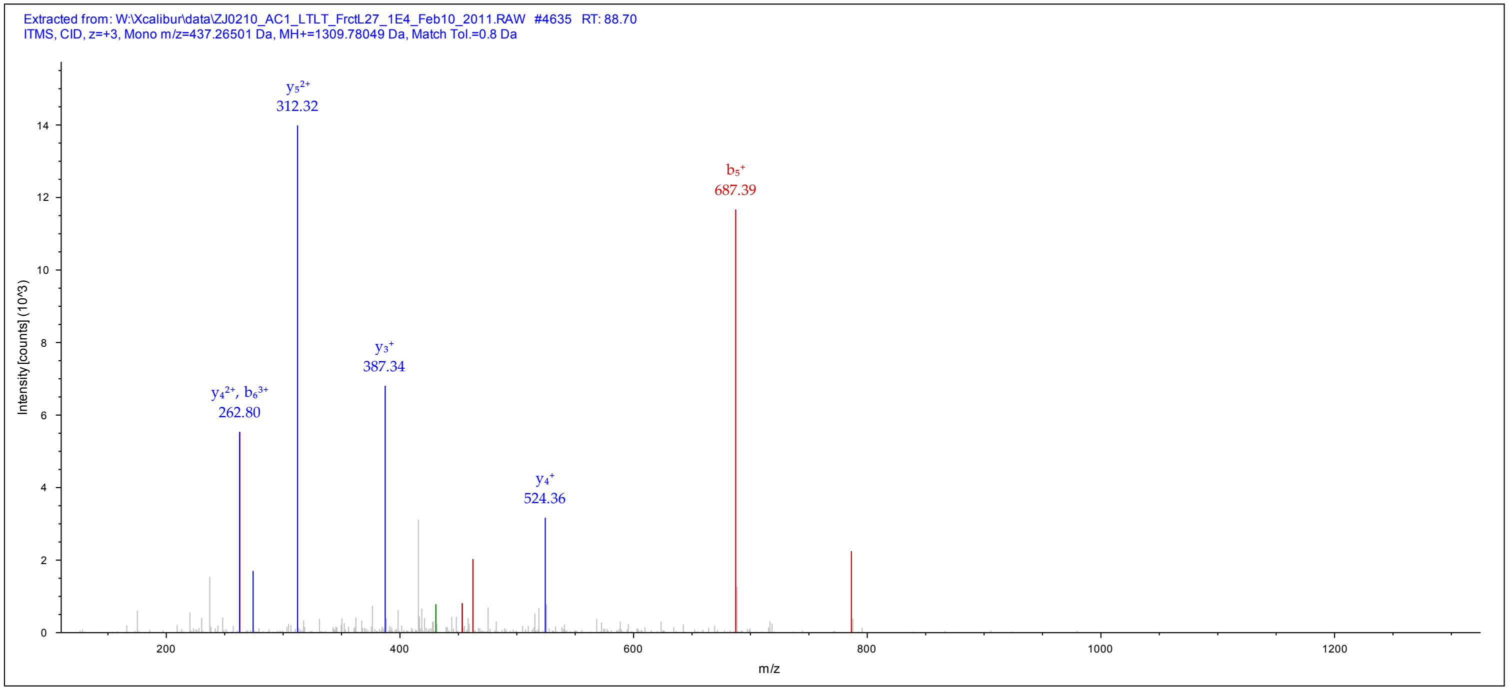
Charge: +3, Monoisotopic m/z: 437.26501 Da (+0.5 mmu/+1.14 ppm), MH+: 1309.78049 Da, RT: 88.70 min,

Identified with: Mascot (v1.16); IonScore:62, Exp Value:3.2E-005, Ions matched by search engine: 8/80

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):
- Isoform 1 of Vacuolar protein sorting-associated protein 29
- Isoform 2 of Vacuolar protein sorting-associated protein 29
- 10 kDa protein lng=91
- 26 kDa protein lng=226



IPI00789460.1

Sequence: AESEQEAYLRED, A1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 834.90082 Da (+1.44 mmu/+1.72 ppm), MH+: 1668.79436 Da, RT: 76.93 min,

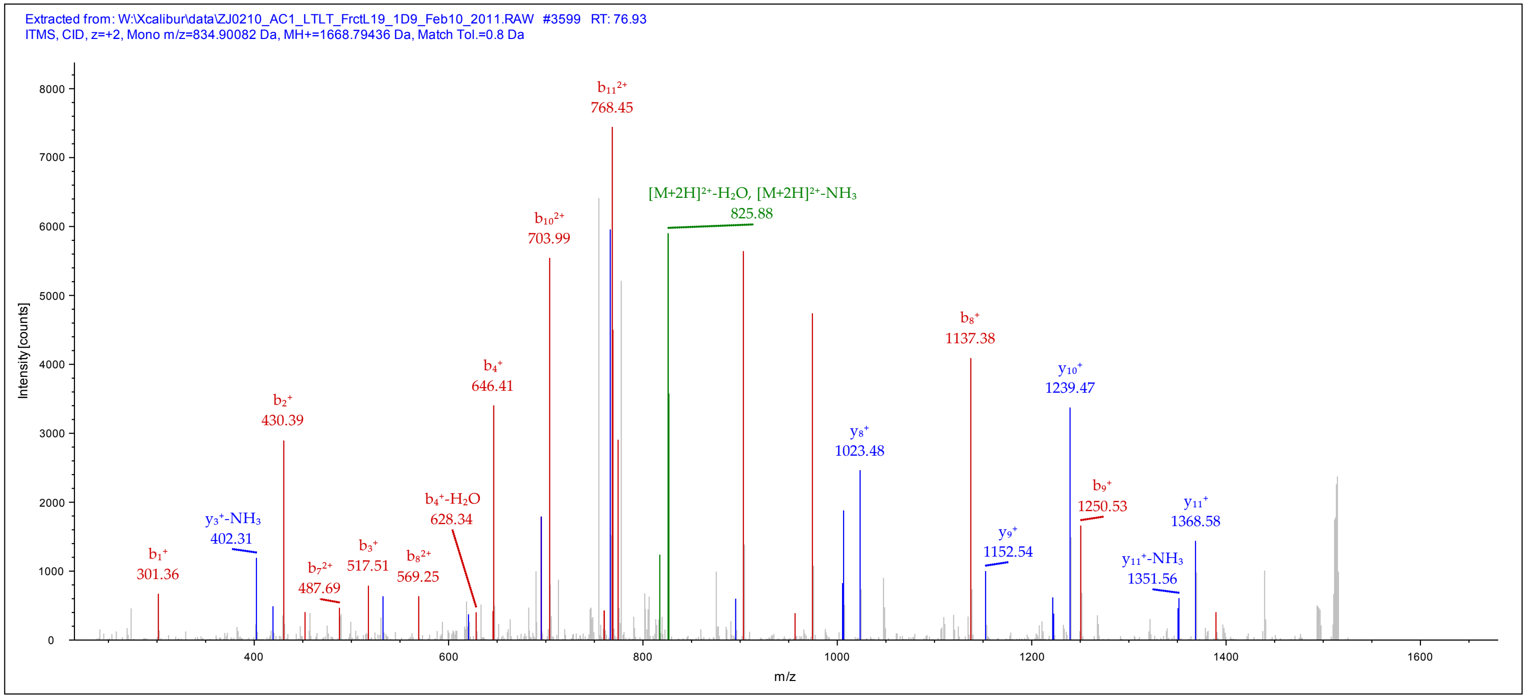
Identified with: Mascot (v1.16); IonScore:49, Exp Value:9.5E-004, Ions matched by search engine: 9/118

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (4):

- diablo isoform 3 precursor
- Isoform 2 of Diablo homolog, mitochondrial lng=186
- Diablo homolog, mitochondrial precursor lng=315
- 19 kDa protein lng=166



IPI:IPI00792829.1

Sequence: IQIEAIPLALQGR, I1-TMT6plex (229.16293 Da)

Charge: +2, Monoisotopic m/z: 826.00922 Da (+0.34 mmu/+0.41 ppm), MH+: 1651.01116 Da, RT: 121.29 min,

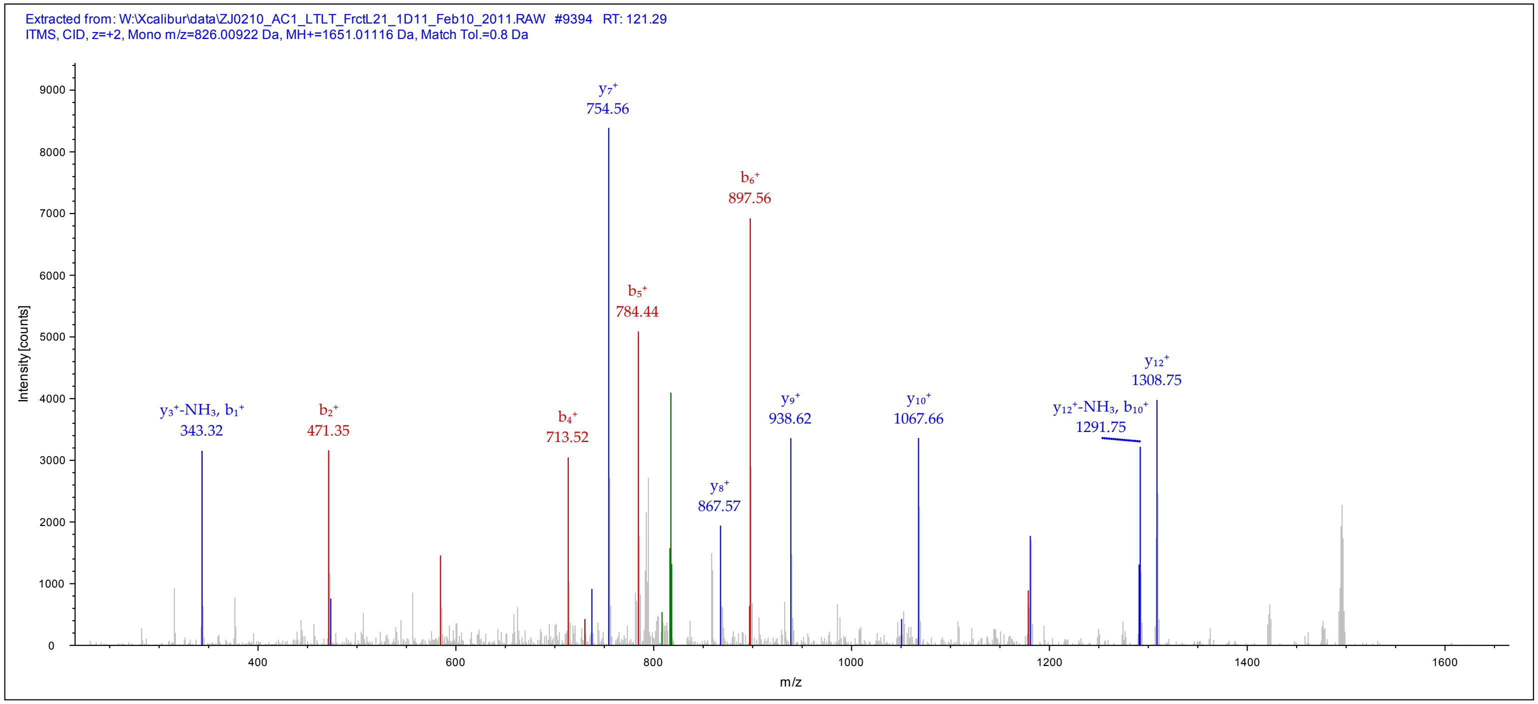
Identified with: Mascot (v1.16); IonScore:33, Exp Value:2.8E-002, Ions matched by search engine: 10/118

Fragment match tolerance used for search: 0.8 Da

Fragments used for search: b; b-H_2O; b-NH_3; y; y-H_2O; y-NH_3

Protein references (3):

- Probable ATP-dependent RNA helicase DDX47
- probable ATP-dependent RNA helicase DDX47 isoform 2
- cDNA FLJ57094, highly similar to Probable ATP-dependent RNA helicase DDX47



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ITMS, CID, z=+2, Mono m/z=826.00922 Da, MH+=1651.01116 Da, Match Tol.=0.8 Da