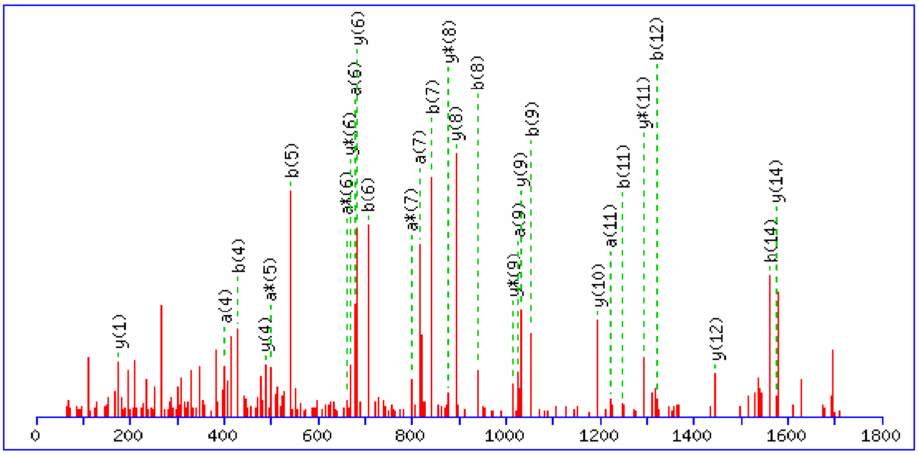
Supplemental Fig. S1 illustrates MALDI-TOF-TOF MS/MS spectra of ions from the changed proteins that are listed in Table 1, and the detailed information of mascot search results.

1 OAT_MOUSE

MS/MS Fragmentation of **YGAHNYHPLPVALER**

Found in **P29758**, OAT_MOUSE Ornithine aminotransferase, mitochondrial precursor - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 1735.88

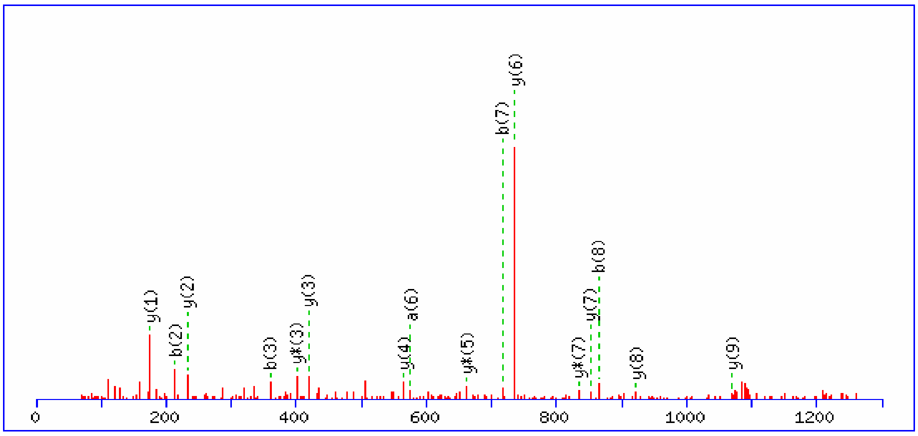
Fixed modifications: Carbamidomethyl (C)

Ions Score: 41

Matches (Bold Red): 29/76 fragment ions using 69 most intense peaks

MS/MS Fragmentation of **IVFADGNFWGR**

Found in **P29758**, OAT_MOUSE Ornithine aminotransferase, mitochondrial precursor - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 1280.63

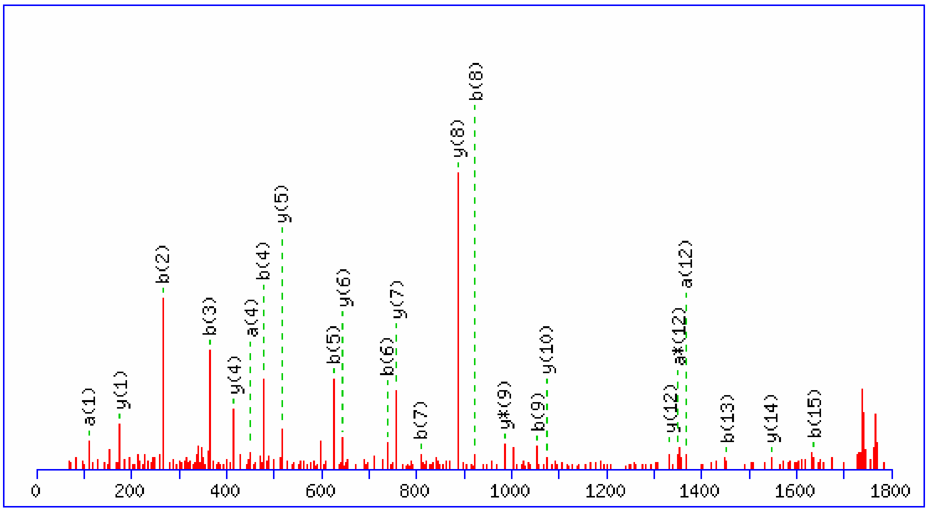
Fixed modifications: Carbamidomethyl (C)

Ions Score: 42

Matches (Bold Red): 16/48 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **HQVLFIADEIQTGLAR**

Found in **P29758**, OAT_MOUSE Ornithine aminotransferase, mitochondrial precursor - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 1809.97

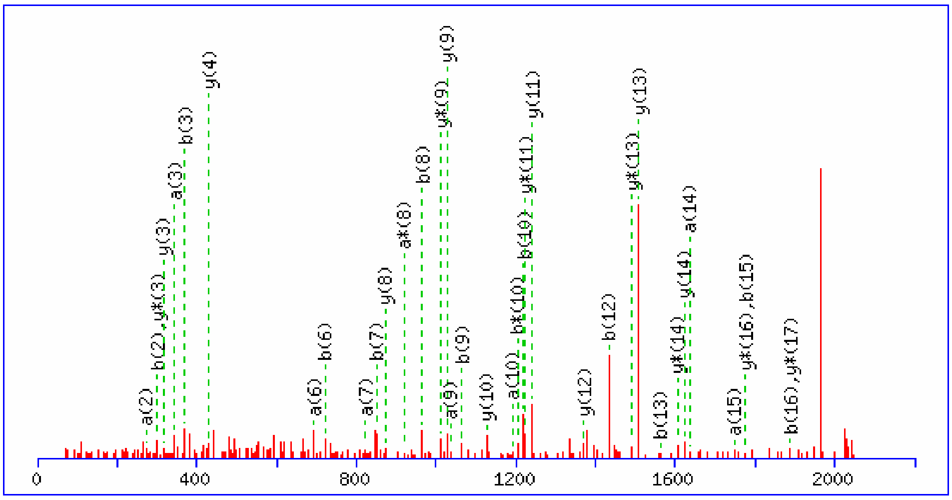
Fixed modifications: Carbamidomethyl (C)

Ions Score: 73

Matches (Bold Red): 24/88 fragment ions using 42 most intense peaks

MS/MS Fragmentation of **WLAVDHENVRPDMVLLGK**

Found in **P29758**, OAT_MOUSE Ornithine aminotransferase, mitochondrial precursor - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 2091.09

Fixed modifications: Carbamidomethyl (C)

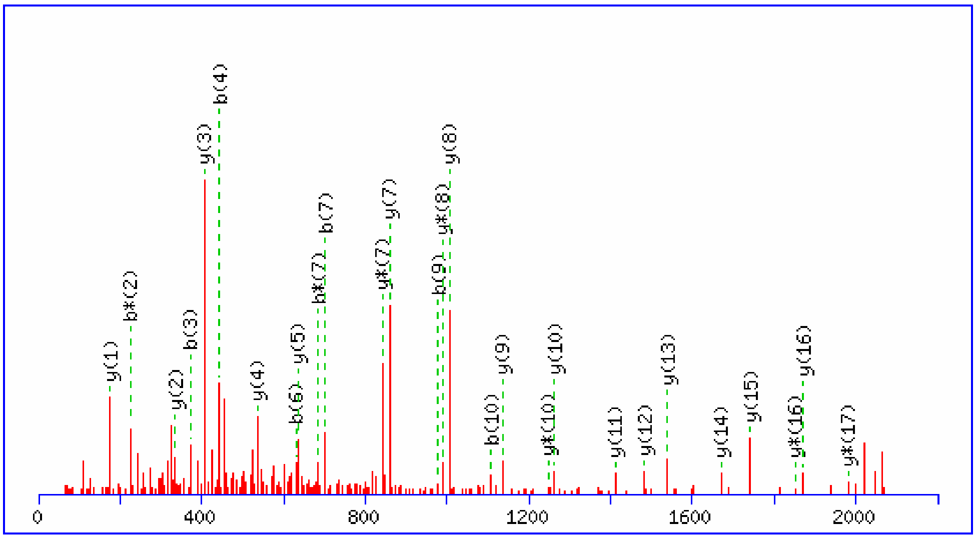
Ions Score: 39

Matches (Bold Red): 37/88 fragment ions using 101 most intense peaks

2 HACL1_MOUSE

MS/MS Fragmentation of **NQEAMGAFQEFPQVEACR**

Found in **Q9QXE0**, HACL1_MOUSE 2-hydroxyacyl-CoA lyase 1 - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 2110.92

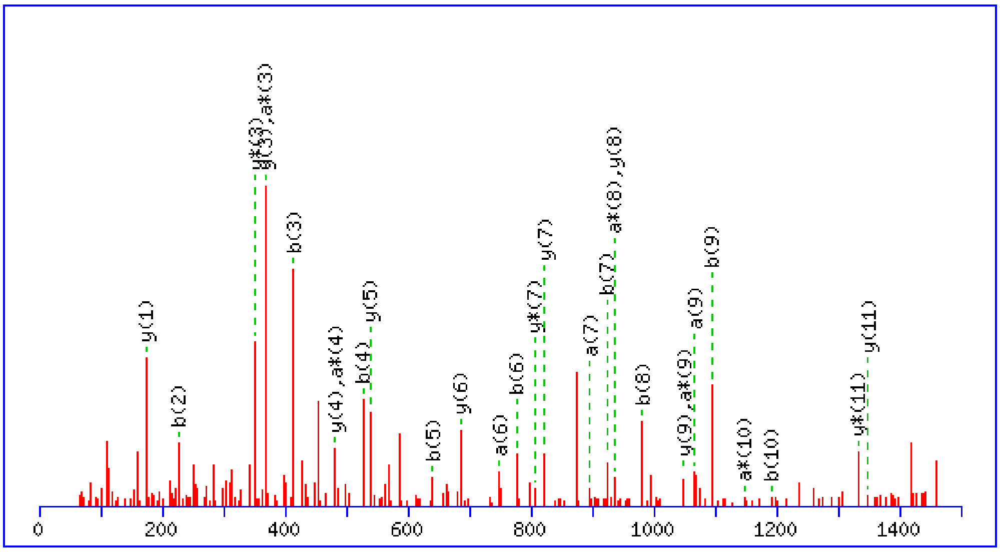
Fixed modifications: Carbamidomethyl (C)

Ions Score: 114

Matches (Bold Red): 28/102 fragment ions using 46 most intense peaks

MS/MS Fragmentation of **LNWILHFGLPPR**

Found in **Q9QXE0**, HACL1_MOUSE 2-hydroxyacyl-CoA lyase 1 - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 1461.82

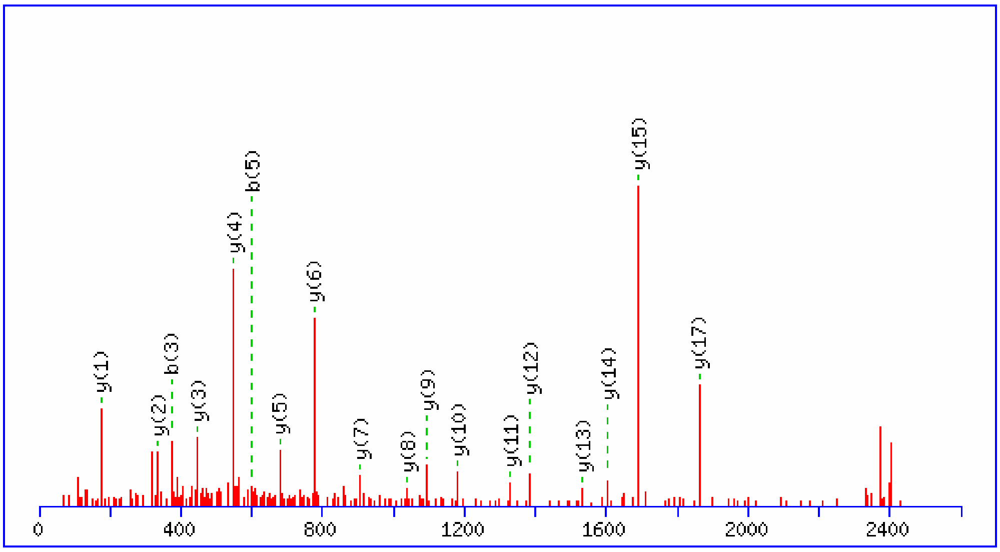
Fixed modifications: Carbamidomethyl (C)

Ions Score: 48

Matches (Bold Red): 29/64 fragment ions using 57 most intense peaks

MS/MS Fragmentation of **VICVEGDSAFGFSGMEVETICR**

Found in **Q9QXE0**, HACL1_MOUSE 2-hydroxyacyl-CoA lyase 1 - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 2462.09

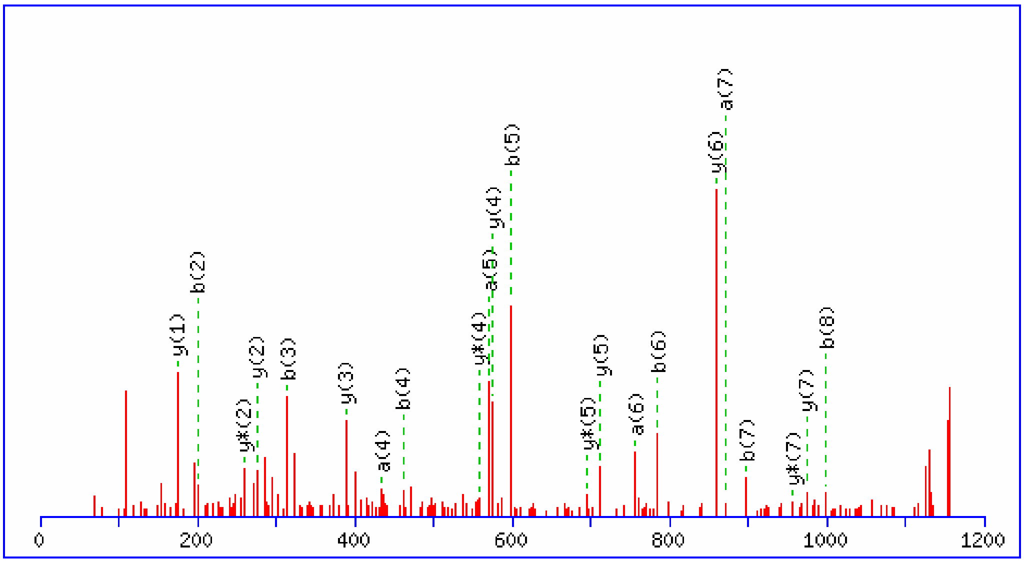
Fixed modifications: Carbamidomethyl (C)

Ions Score: 134

Matches (Bold Red): 18/84 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **AQDFHWLTR**

Found in **Q9QXE0**, HACL1_MOUSE 2-hydroxyacyl-CoA lyase 1 - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 1172.57

Fixed modifications: Carbamidomethyl (C)

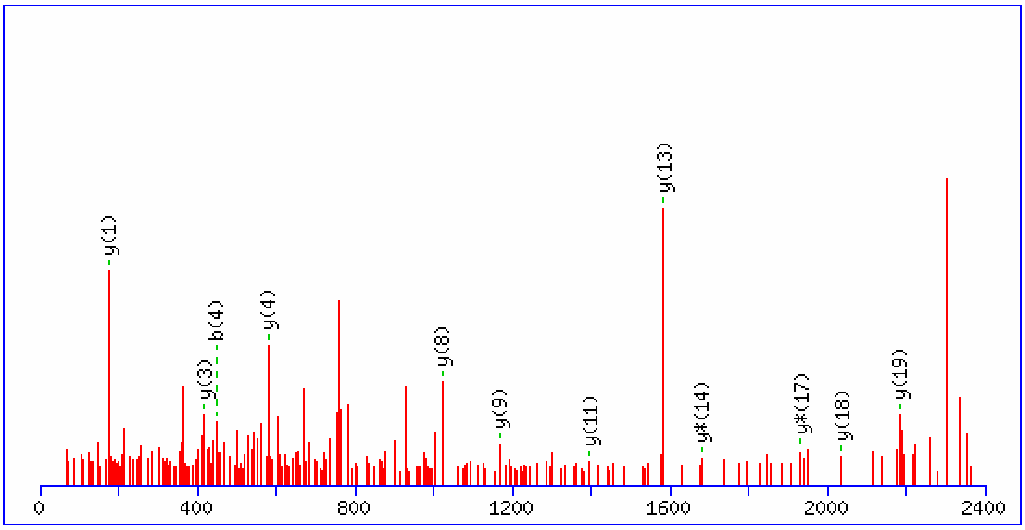
Ions Score: 38

Matches (Bold Red): 22/46 fragment ions using 44 most intense peaks

3 HMCS2_MOUSE

MS/MS Fragmentation of **VNFSPPGDTSNLFPGTWYLER**

Found in **P54869**, HMCS2_MOUSE Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 2396.14

Fixed modifications: Carbamidomethyl (C)

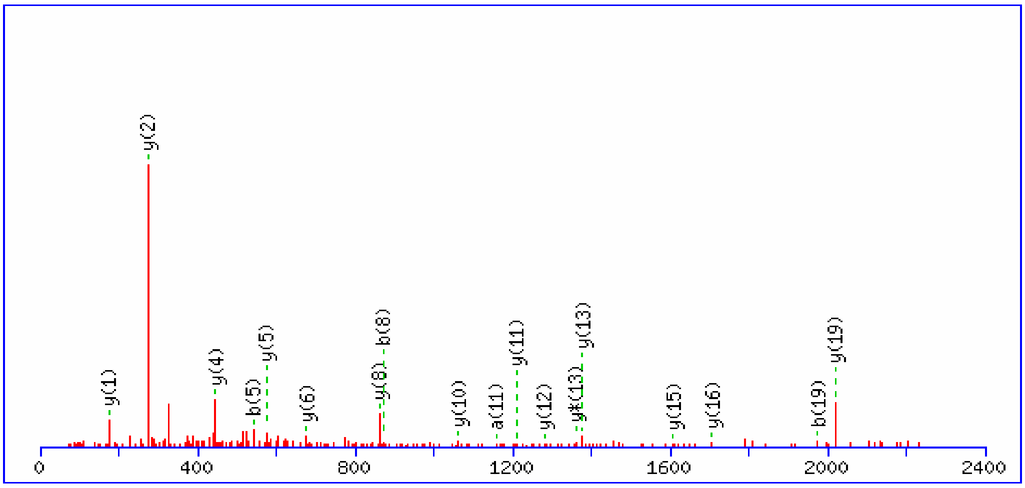
Ions Score: 39

Matches (Bold Red): 12/118 fragment ions using 27 most intense peaks

4 ODO2_MOUSE

MS/MS Fragmentation of **NDVITVQTPAFAESVTEGDVR**

Found in **Q9D2G2**, ODO2_MOUSE Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase



Monoisotopic mass of neutral peptide Mr(calc): 2247.10

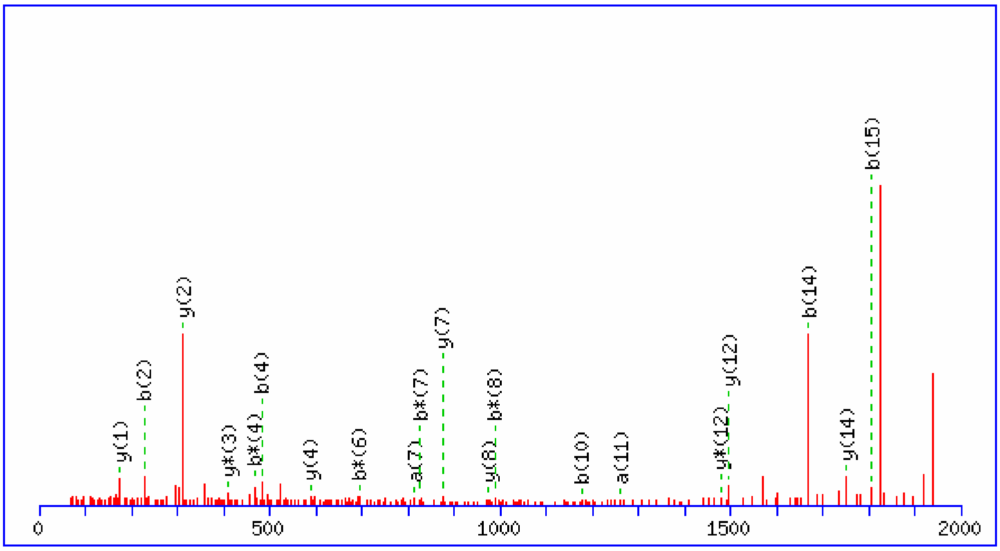
Fixed modifications: Carbamidomethyl (C)

Ions Score: 93

Matches (Bold Red): 18/120 fragment ions using 30 most intense peaks

MS/MS Fragmentation of **VEVRPMMYVALTYDHR**

Found in **Q9D2G2**, ODO2_MOUSE Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase



Monoisotopic mass of neutral peptide Mr(calc): 1978.98

Fixed modifications: Carbamidomethyl (C)

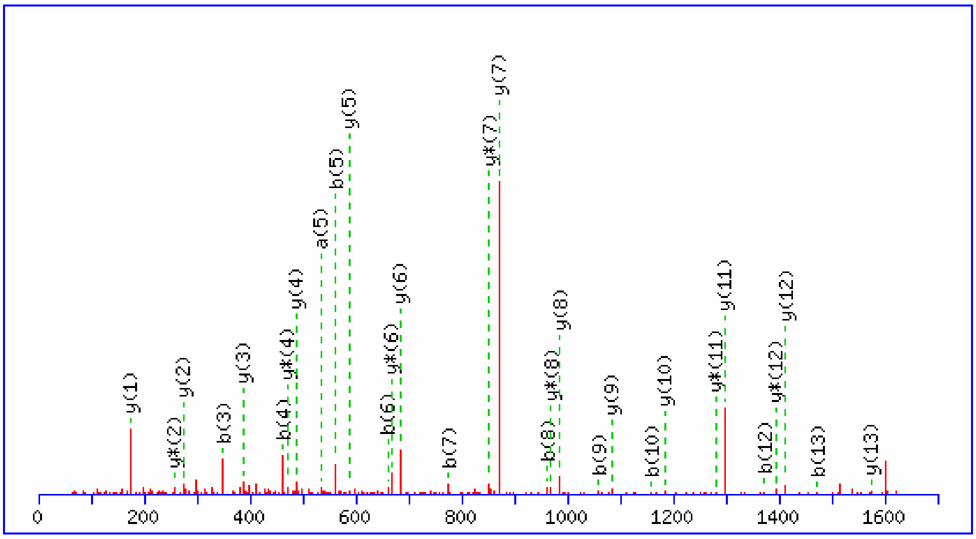
Ions Score: 23

Matches (Bold Red): 20/84 fragment ions using 47 most intense peaks

5 NDUBA_MOUSE

MS/MS Fragmentation of **AYDLVVDWPVTLVR**

Found in **Q9DCS9**, NDUBA_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 1644.89

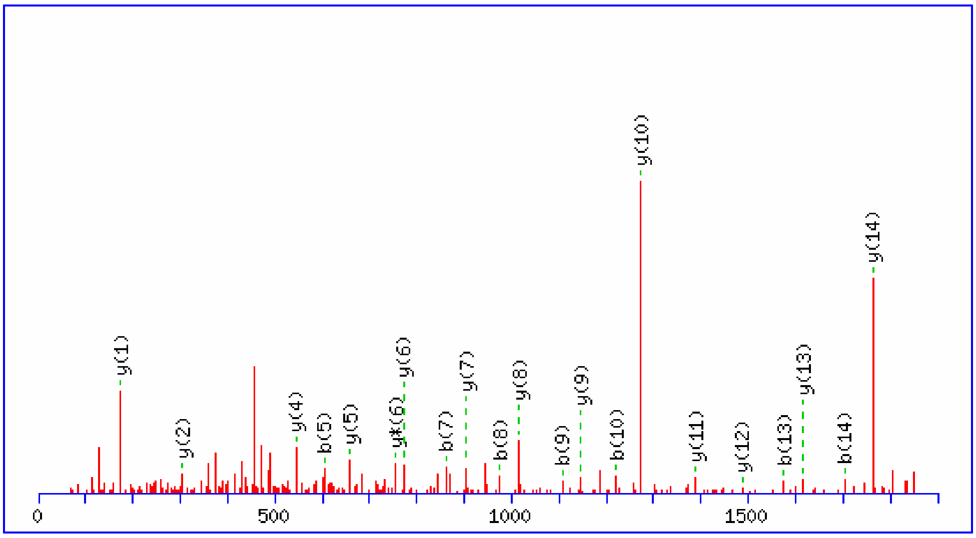
Fixed modifications: Carbamidomethyl (C)

Ions Score: 83

Matches (Bold Red): 31/52 fragment ions using 66 most intense peaks

MS/MS Fragmentation of **DFKVDQEIMNIIQER**

Found in **Q9DCS9**, NDUBA_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 1876.94

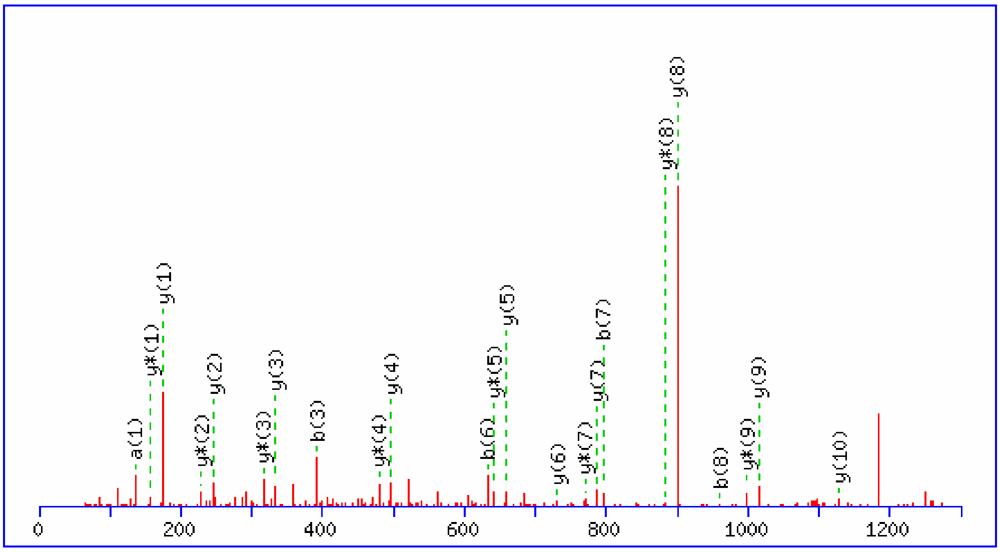
Fixed modifications: Carbamidomethyl (C)

Ions Score: 96

Matches (Bold Red): 21/80 fragment ions using 36 most intense peaks

MS/MS Fragmentation of **YLDLGAYYSAR**

Found in **Q9DCS9**, NDUBA_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 - Mus musculus (Mouse)



Monoisotopic mass of neutral peptide Mr(calc): 1290.62

Fixed modifications: Carbamidomethyl (C)

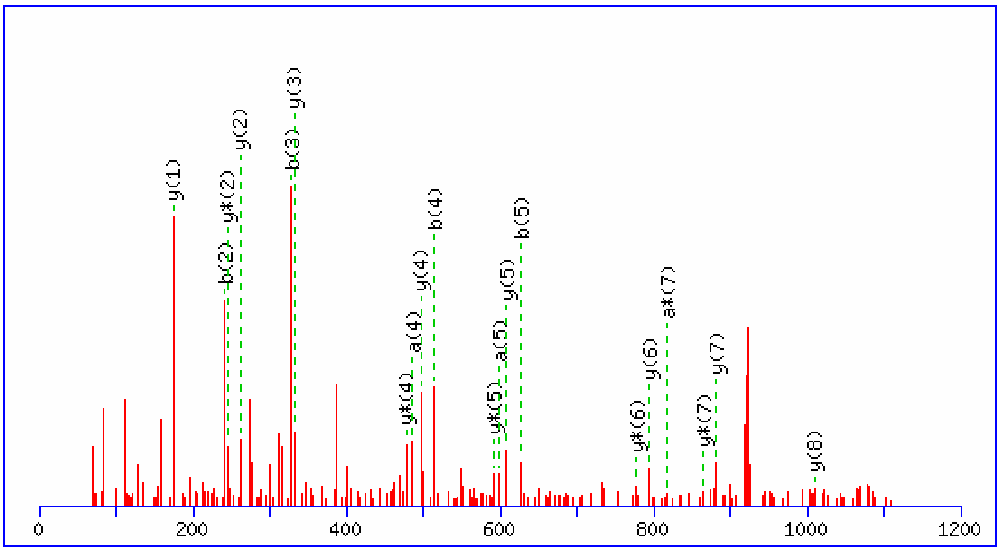
Ions Score: 76

Matches (Bold Red): 23/40 fragment ions using 39 most intense peaks

6 NDUAA_MOUSE

MS/MS Fragmentation of **LQSWLYASR**

Found in **Q99LC3**, NDUAA_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1122.58

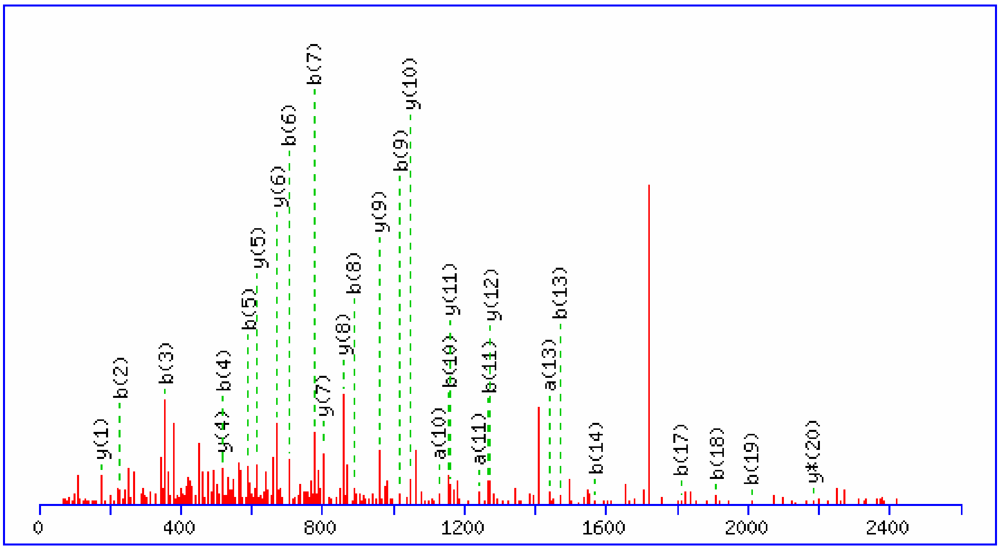
Fixed modifications: Carbamidomethyl (C)

Ions Score: 40

Matches (Bold Red): 20/46 fragment ions using 48 most intense peaks

MS/MS Fragmentation of **LLQYADALEHLLSTGQGVVLER**

Found in **Q99LC3**, NDUAA_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 2424.30

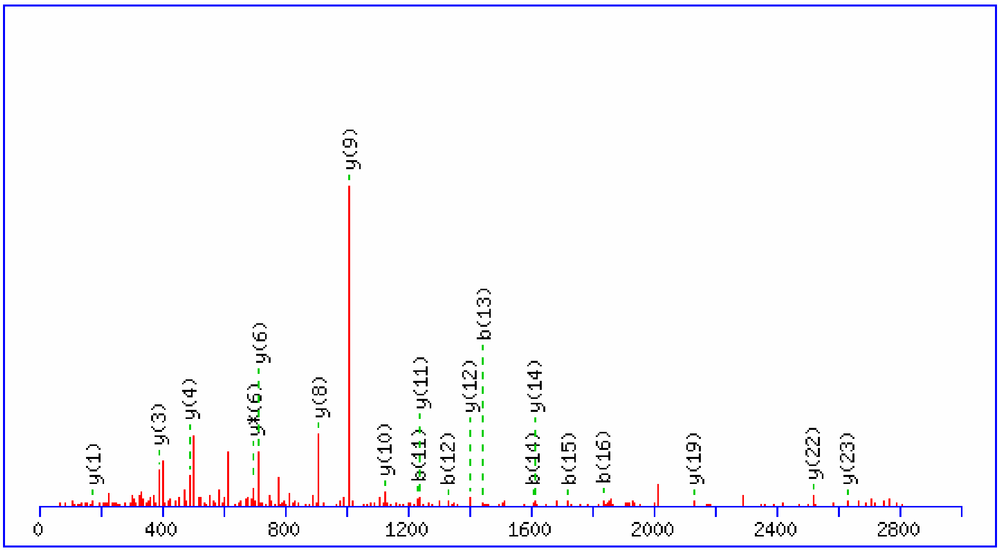
Fixed modifications: Carbamidomethyl (C)

Ions Score: 44

Matches (Bold Red): 29/122 fragment ions using 114 most intense peaks

MS/MS Fragmentation of **LTLPEYLPPHAVIYIDVPVPEVQSR**

Found in **Q99LC3**, NDUAA_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 2844.54

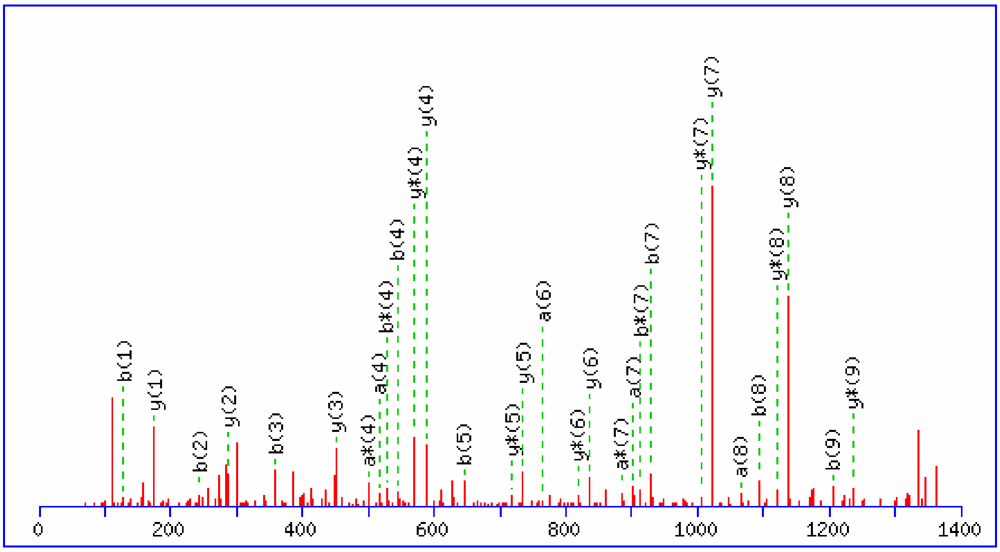
Fixed modifications: Carbamidomethyl (C)

Ions Score: 52

Matches (Bold Red): 20/100 fragment ions using 56 most intense peaks

MS/MS Fragmentation of **QDDWTFHYLR**

Found in **Q99LC3**, NDUAA_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1379.63

Fixed modifications: Carbamidomethyl (C)

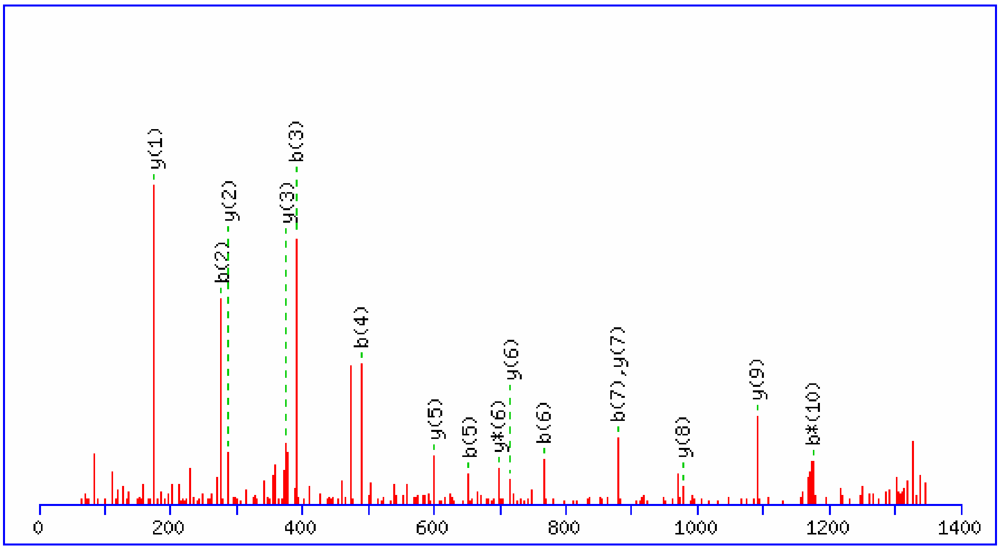
Ions Score: 49

Matches (Bold Red): 30/54 fragment ions using 54 most intense peaks

7 NDUS3_MOUSE

MS/MS Fragmentation of **FEIVYNLLSLR**

Found in **Q9DCT2**, NDUS3_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1365.77

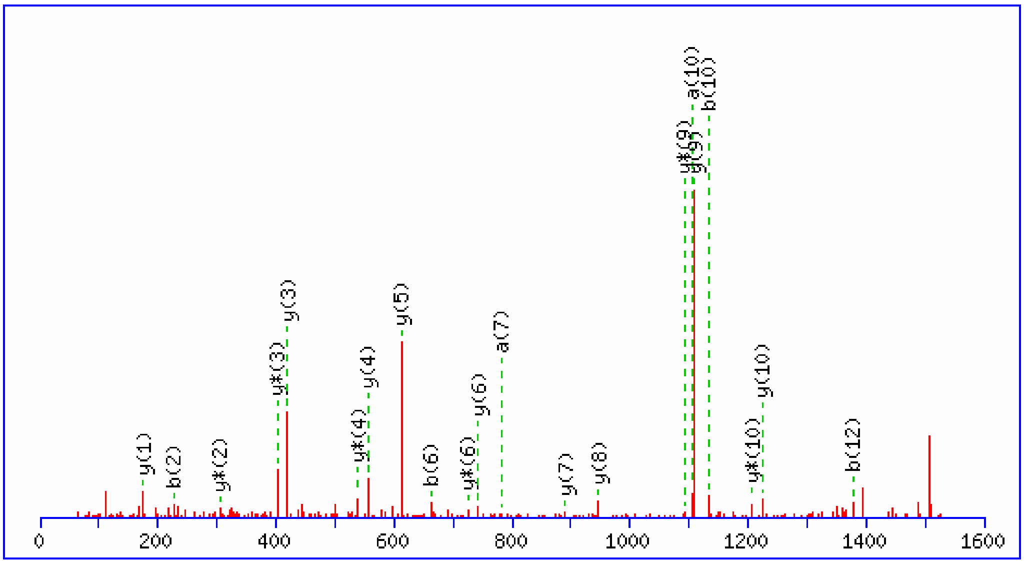
Fixed modifications: Carbamidomethyl (C)

Ions Score: 53

Matches (Bold Red): 16/50 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **ILTDYGFEGHPFR**

Found in **Q9DCT2**, NDUS3_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1550.75

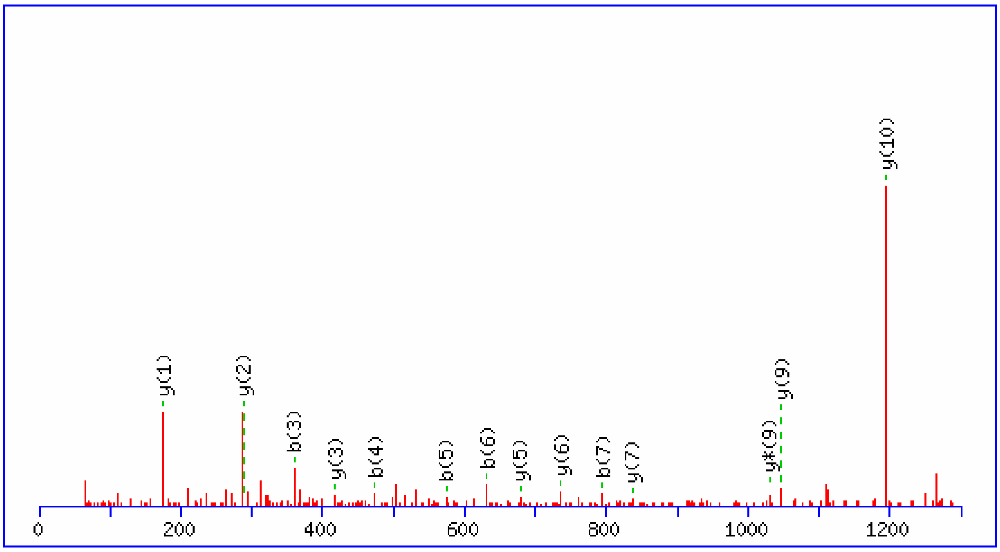
Fixed modifications: Carbamidomethyl (C)

Ions Score: 66

Matches (Bold Red): 21/48 fragment ions using 36 most intense peaks

MS/MS Fragmentation of **DFPLTGYVELR**

Found in **Q9DCT2**, NDUS3_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1308.67

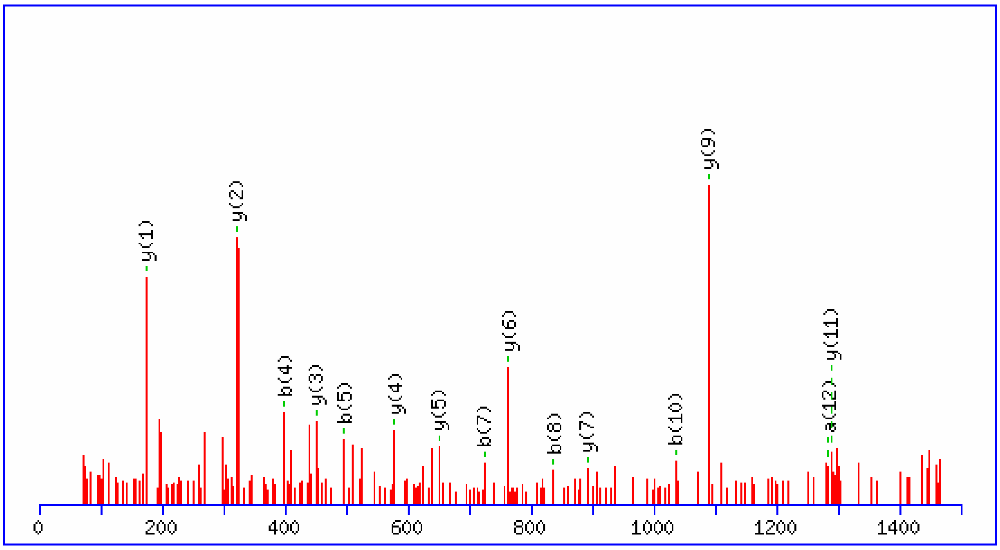
Fixed modifications: Carbamidomethyl (C)

Ions Score: 50

Matches (Bold Red): 14/40 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **VVAEPVELAQEFR**

Found in **Q9DCT2**, NDUS3_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1485.78

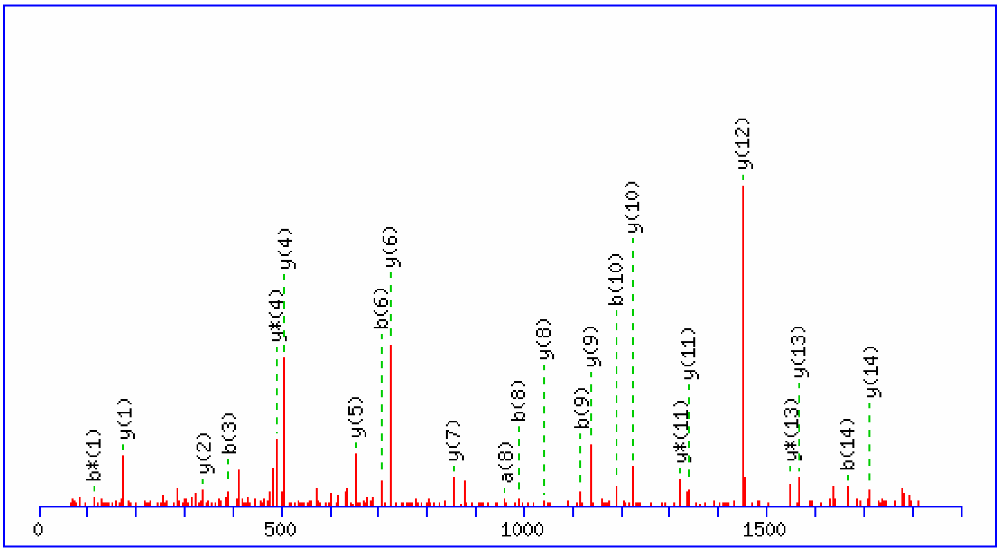
Fixed modifications: Carbamidomethyl (C)

Ions Score: 54

Matches (Bold Red): 15/54 fragment ions using 31 most intense peaks

MS/MS Fragmentation of **KFDLNSPWEAFPAYR**

Found in **Q9DCT2**, NDUS3_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1839.89

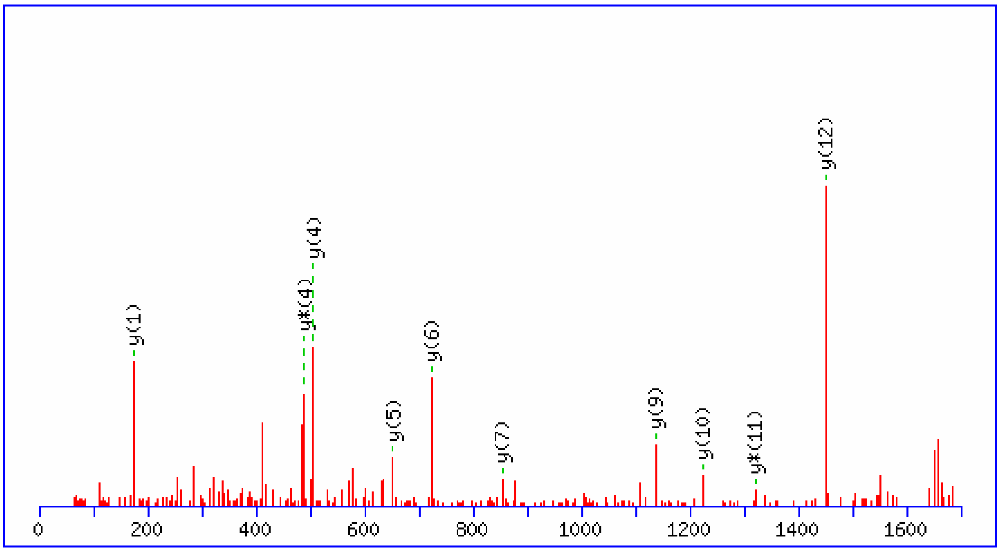
Fixed modifications: Carbamidomethyl (C)

Ions Score: 103

Matches (Bold Red): 24/84 fragment ions using 37 most intense peaks

MS/MS Fragmentation of **FDLNSPWEAFPAYR**

Found in **Q9DCT2**, NDUS3_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1711.80

Fixed modifications: Carbamidomethyl (C)

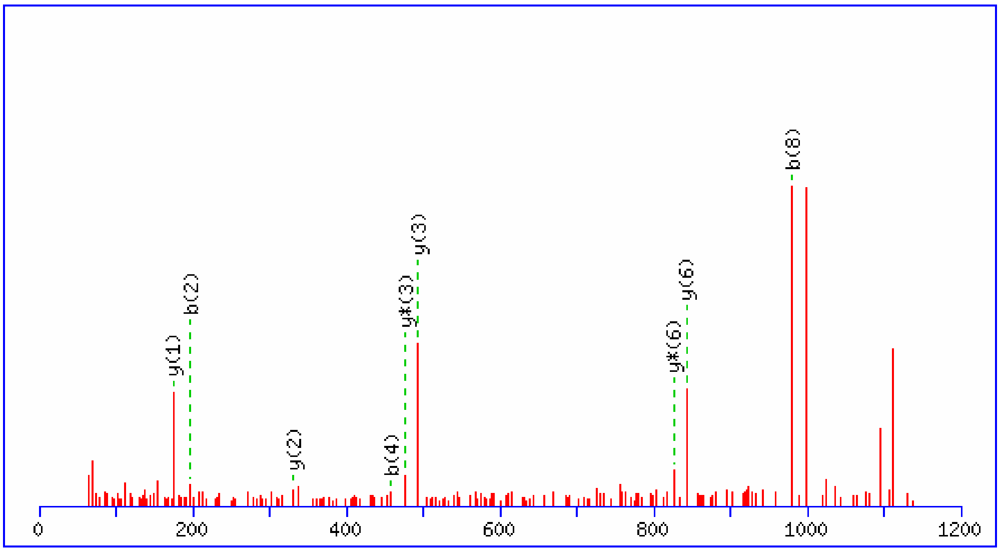
Ions Score: 49

Matches (Bold Red): 10/72 fragment ions using 20 most intense peaks

8 UCRI_MOUSE

MS/MS Fragmentation of **VPDFSDYRR**

Found in **Q9CR68**, UCRI_MOUSE Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1153.55

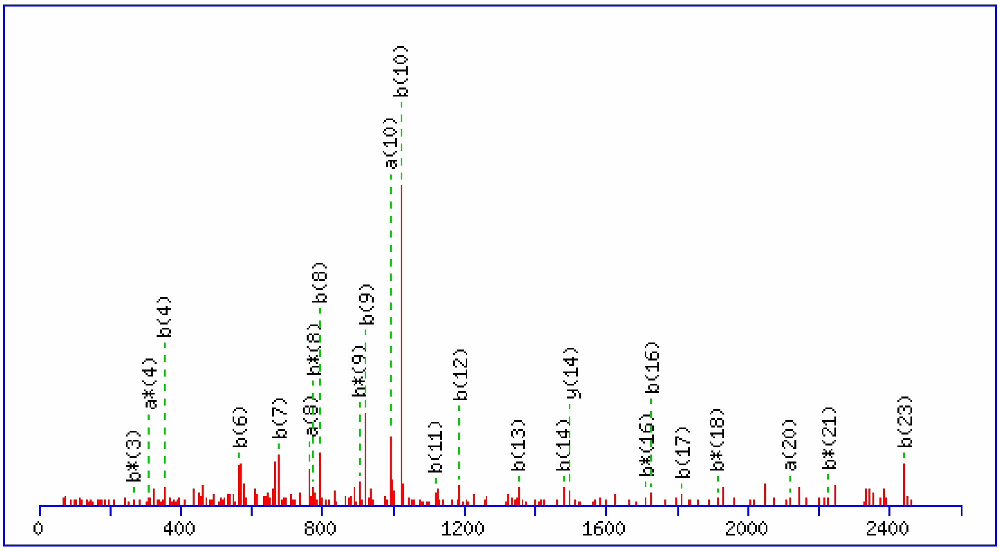
Fixed modifications: Carbamidomethyl (C)

Ions Score: 17

Matches (Bold Red): 9/34 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **KGPAPLNLEVPAYEFTSDDVVVVG**

Found in **Q9CR68**, UCRI_MOUSE Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 2515.28

Fixed modifications: Carbamidomethyl (C)

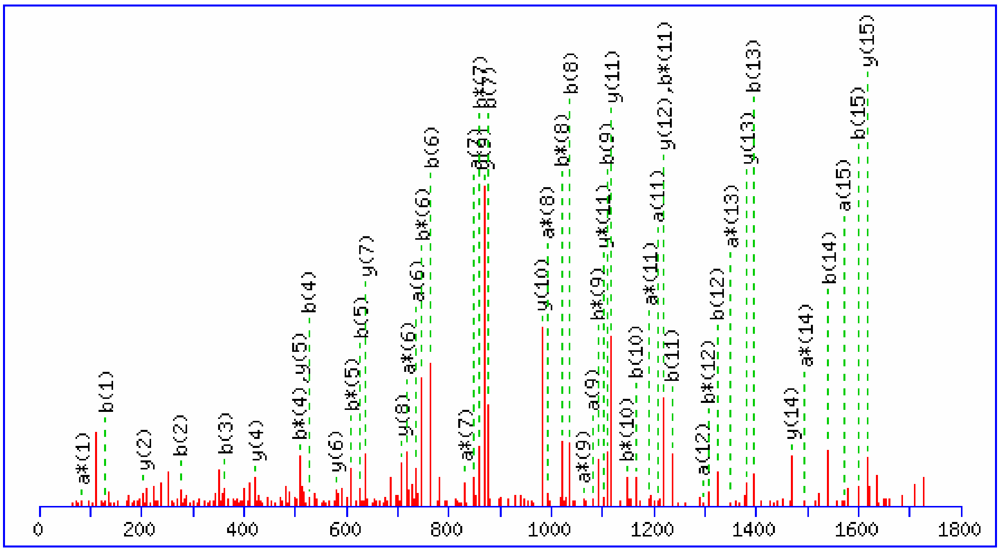
Ions Score: 66

Matches (Bold Red): 24/121 fragment ions using 54 most intense peaks

9 ETFA_MOUSE

MS/MS Fragmentation of **QFSYTHICAGASAFGK**

Found in **Q99LC5**, ETFA_MOUSE Electron transfer flavoprotein subunit alpha, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1743.80

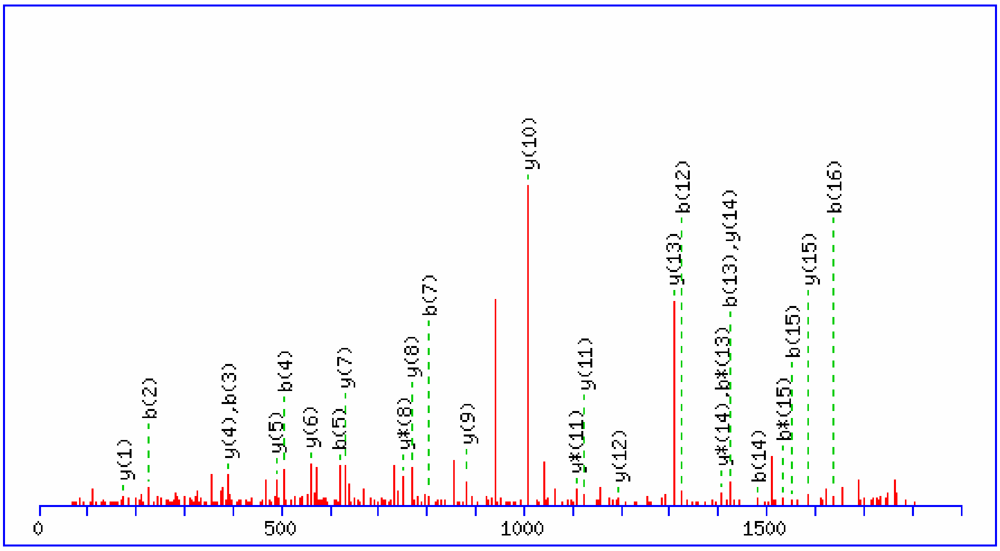
Fixed modifications: Carbamidomethyl (C)

Ions Score: 89

Matches (Bold Red): 52/90 fragment ions using 116 most intense peaks

MS/MS Fragmentation of **LLYDLADQLHAAVGASR**

Found in **Q99LC5**, ETFA_MOUSE Electron transfer flavoprotein subunit alpha, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1811.95

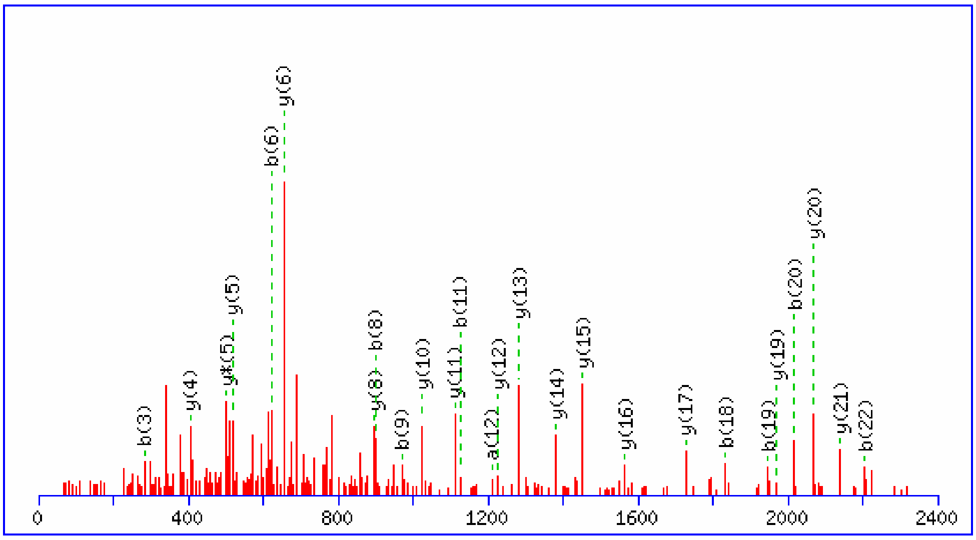
Fixed modifications: Carbamidomethyl (C)

Ions Score: 62

Matches (Bold Red): 28/82 fragment ions using 70 most intense peaks

MS/MS Fragmentation of **IVAPELYIAVGISGAIQHLAGMK**

Found in **Q99LC5**, ETFA_MOUSE Electron transfer flavoprotein subunit alpha, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 2350.31

Fixed modifications: Carbamidomethyl (C)

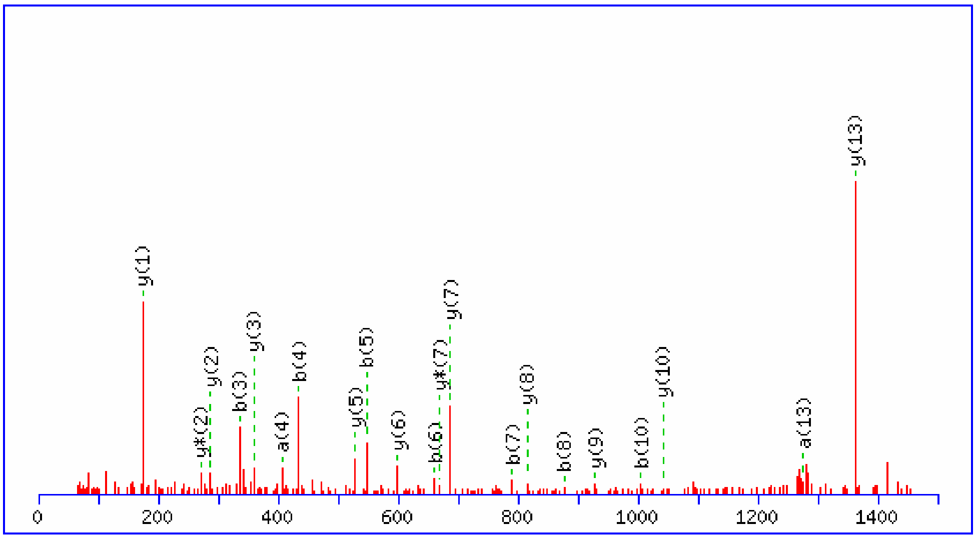
Ions Score: 98

Matches (Bold Red): 26/100 fragment ions using 48 most intense peaks

10 PRDX3_MOUSE

MS/MS Fragmentation of **DYGVLLESAGIALR**

Found in **P20108**, PRDX3_MOUSE Thioredoxin-dependent peroxide reductase, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1475.80

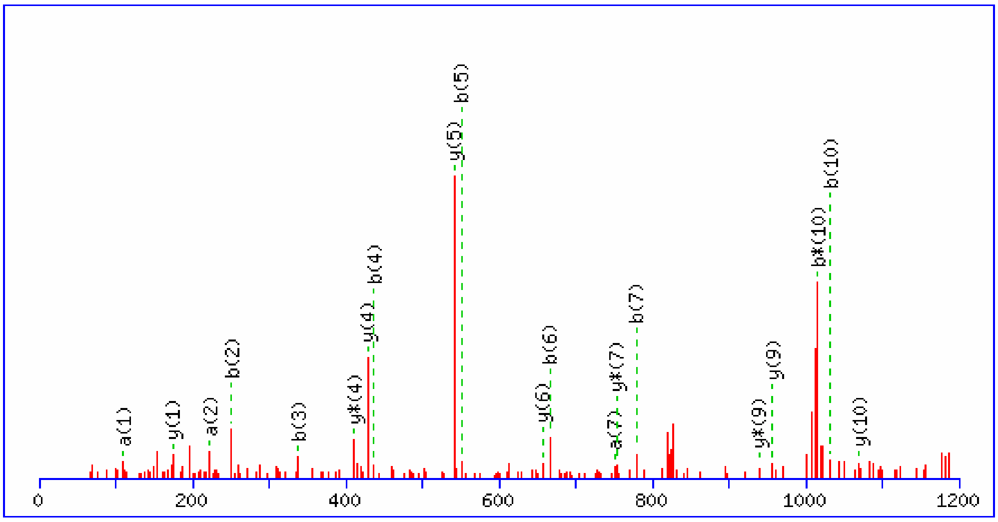
Fixed modifications: Carbamidomethyl (C)

Ions Score: 66

Matches (Bold Red): 21/52 fragment ions using 34 most intense peaks

MS/MS Fragmentation of **HLSVNDLPVGR**

Found in **P20108**, PRDX3_MOUSE Thioredoxin-dependent peroxide reductase, mitochondrial precursor



Monoisotopic mass of neutral peptide Mr(calc): 1205.65

Fixed modifications: Carbamidomethyl (C)

Ions Score: 28

Matches (Bold Red): 20/52 fragment ions using 54 most intense peaks