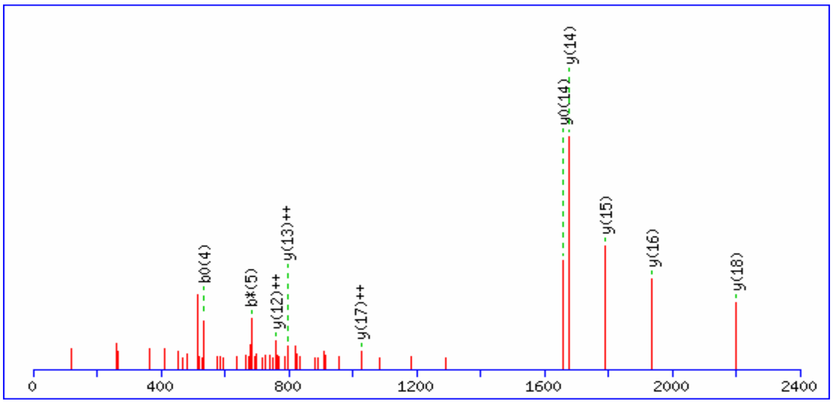
Supplemental Fig. S2 illustrates ESI-FTICR mass spectra of ICAT-labeled peptides from the changed proteins that are listed in Table 2, and the detailed information of Mascot search results.

1 OAT_MOUSE

MS/MS Fragmentation of **QYFDFLSAYGAVSQGHCHPK**
Found in **P29758**, OAT_MOUSE Ornithine aminotransferase, mitochondrial precursor

Variable modifications: C17 : ICAT_heavy

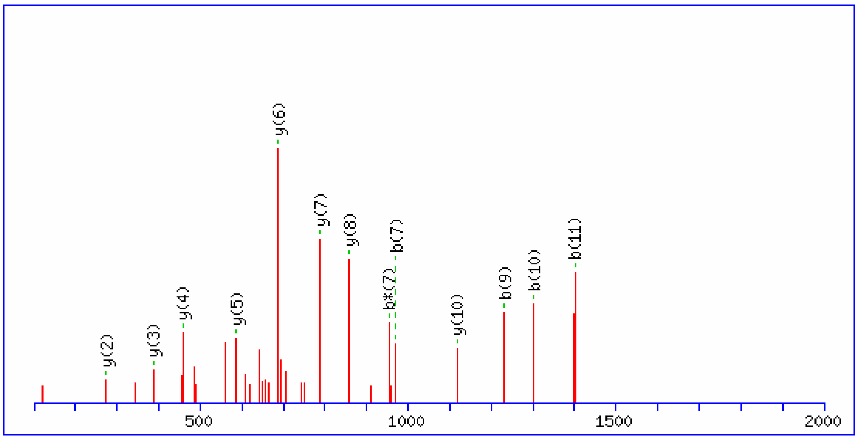


Monoisotopic mass of neutral peptide Mr(calc): 2490.18
Ions Score: 14
Matches (Bold Red): 10/208 fragment ions using 23 most intense peaks

2 GLNA_MOUSE

MS/MS Fragmentation of **RPSANCDPYAVTEAIVR**
Found in **P15105**, GLNA_MOUSE Glutamine synthetase - Mus musculus (Mouse)

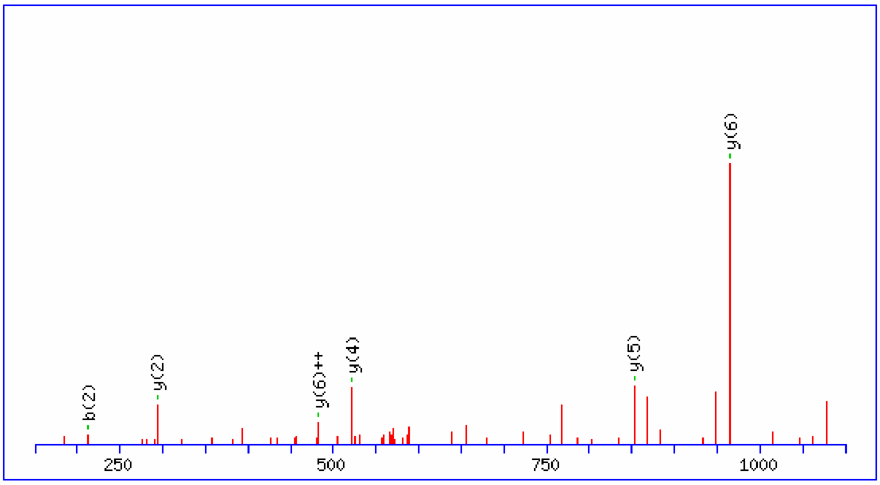
Variable modifications: C6 : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 2088.04
Ions Score: 73
Matches (Bold Red): 13/180 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **LVLCEVFK**
Found in **P15105**, GLNA_MOUSE Glutamine synthetase - Mus musculus (Mouse)

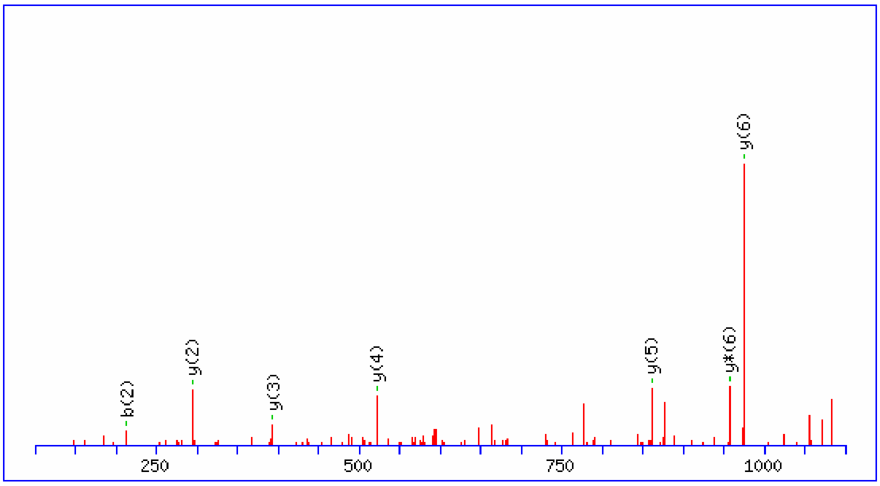
Variable modifications: C4 : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 1176.66
Ions Score: 27
Matches (Bold Red): 6/56 fragment ions using 11 most intense peaks

MS/MS Fragmentation of **LVLCEVFK**
Found in **P15105**, GLNA_MOUSE Glutamine synthetase - Mus musculus (Mouse)

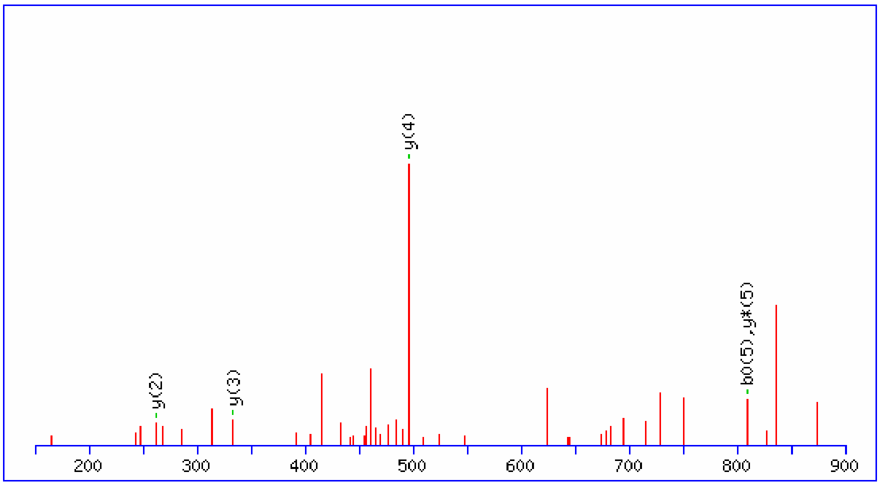
Variable modifications: C4 : ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 1185.69
Ions Score: 34
Matches (Bold Red): 7/56 fragment ions using 14 most intense peaks

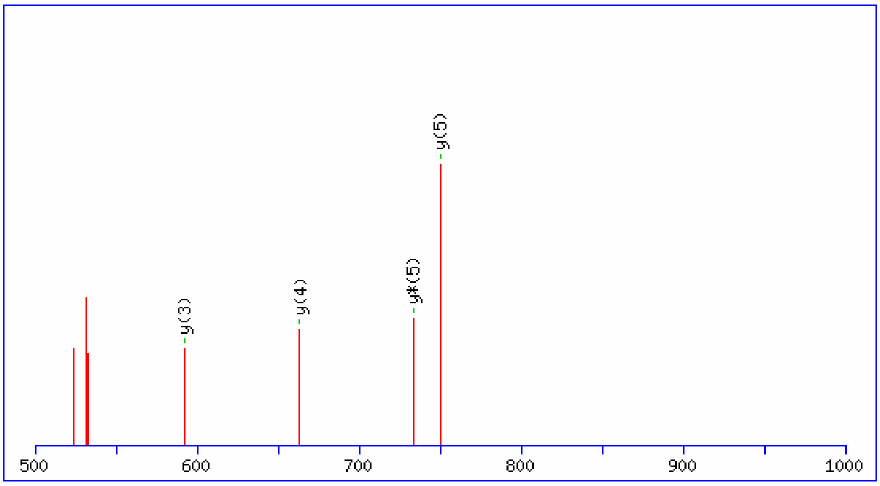
3 AL4A1_MOUSE

MS/MS Fragmentation of **FCYADK**
Found in **Q8CHT0**, AL4A1_MOUSE Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial precursor
Variable modifications: C2 : ICAT_light



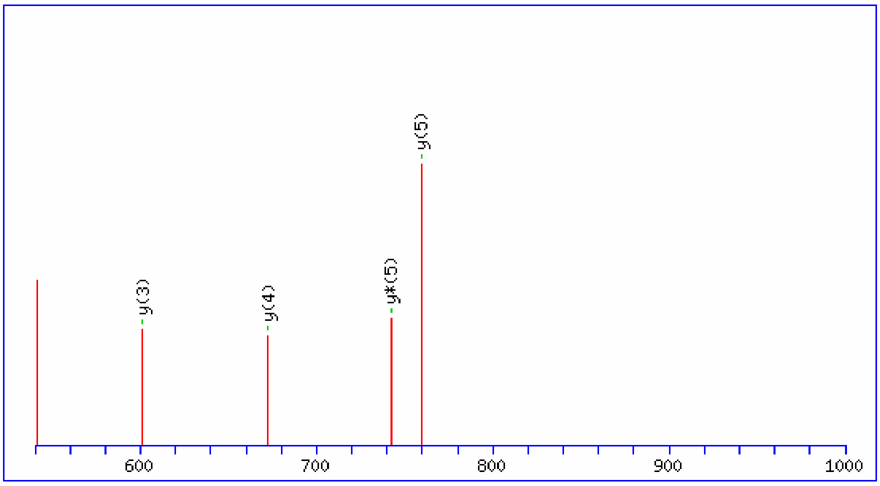
Monoisotopic mass of neutral peptide Mr(calc): 972.44
Ions Score: 18
Matches (Bold Red): 5/40 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **CSACSR**
Found in **Q8CHT0**, AL4A1_MOUSE Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial precursor
Variable modifications: C1 : ICAT_light **C4 :** ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 1079.49
Ions Score: 21
Matches (Bold Red): 4/46 fragment ions using 9 most intense peaks

MS/MS Fragmentation of **CSACSR**
Found in **Q8CHT0**, AL4A1_MOUSE Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial precursor
Variable modifications: C1 : ICAT_heavy **C4 :** ICAT_heavy

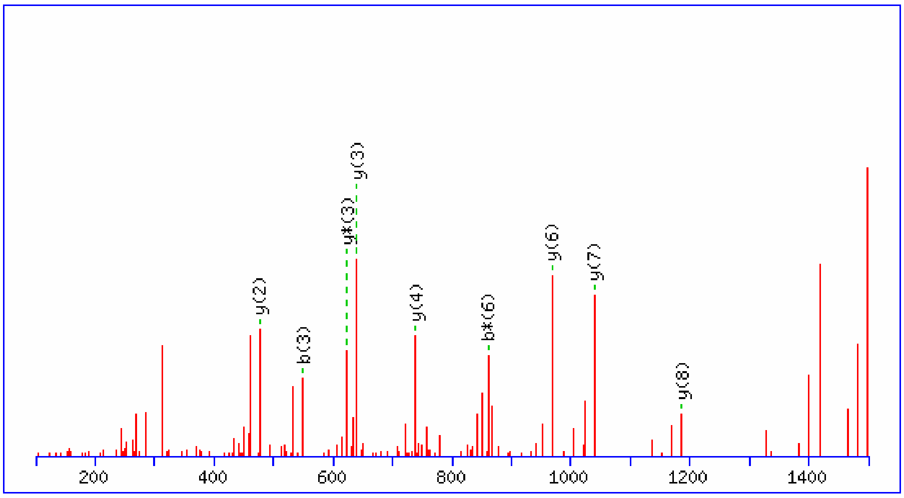


Monoisotopic mass of neutral peptide Mr(calc): 1097.55
Ions Score: 29
Matches (Bold Red): 4/46 fragment ions using 6 most intense peaks

4 URIC_MOUSE

MS/MS Fragmentation of **CFATQVYCK**
Found in **P25688**, URIC_MOUSE Uricase - Mus musculus (Mouse)

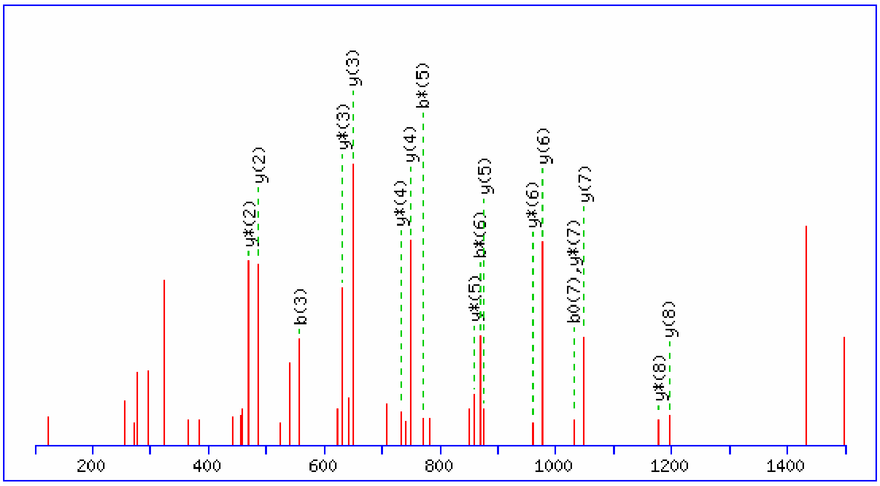
Variable modifications: C1 : ICAT_light **C8 :** ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 1515.72
Ions Score: 42
Matches (Bold Red): 9/72 fragment ions using 22 most intense peaks

MS/MS Fragmentation of **CFATQVYCK**
Found in **P25688**, URIC_MOUSE Uricase - Mus musculus (Mouse)

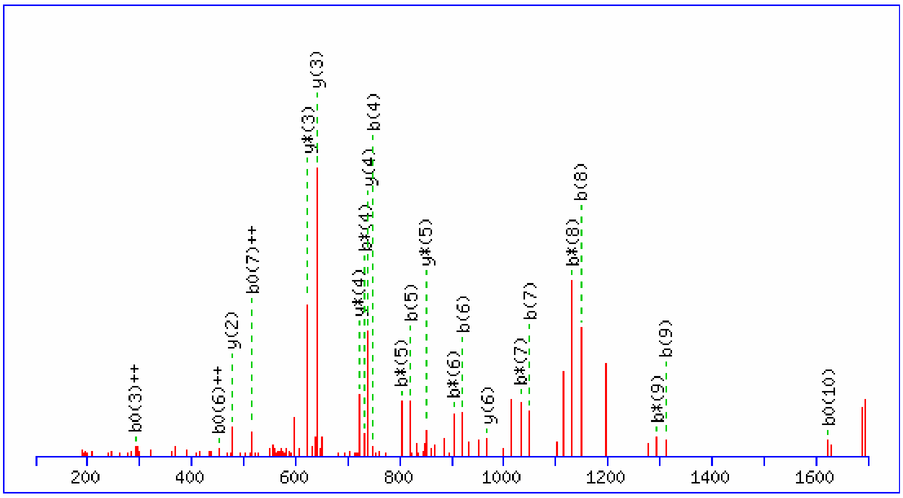
Variable modifications: C1 : ICAT_heavy **C8 :** ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 1533.78
Ions Score: 42
Matches (Bold Red): 18/72 fragment ions using 39 most intense peaks

MS/MS Fragmentation of **DRCFATQVYCK**
Found in **P25688**, URIC_MOUSE Uricase - Mus musculus (Mouse)

Variable modifications: C3 : ICAT_light **C10 :** ICAT_light

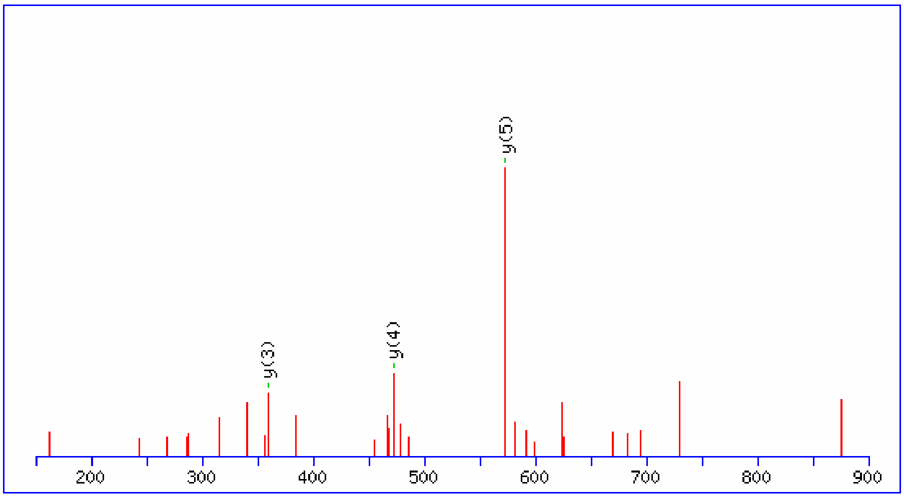


Monoisotopic mass of neutral peptide Mr(calc): 1786.85
Ions Score: 23
Matches (Bold Red): 23/108 fragment ions using 51 most intense peaks

5 ACOX1_MOUSE

MS/MS Fragmentation of **ACTIAIR**
Found in **Q9R0H0**, ACOX1_MOUSE Acyl-coenzyme A oxidase 1

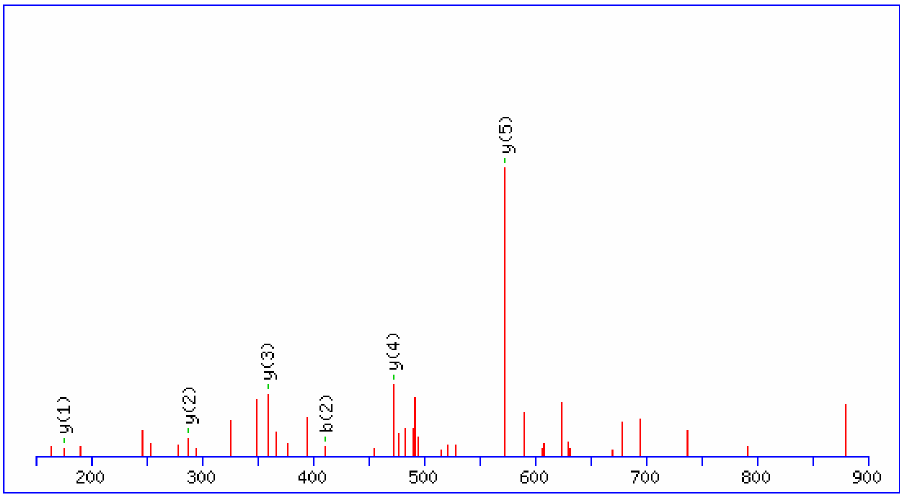
Variable modifications: C2 : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 973.54
Ions Score: 17
Matches (Bold Red): 3/48 fragment ions using 10 most intense peaks

MS/MS Fragmentation of **ACTIAIR**
Found in **Q9R0H0**, ACOX1_MOUSE Acyl-coenzyme A oxidase 1

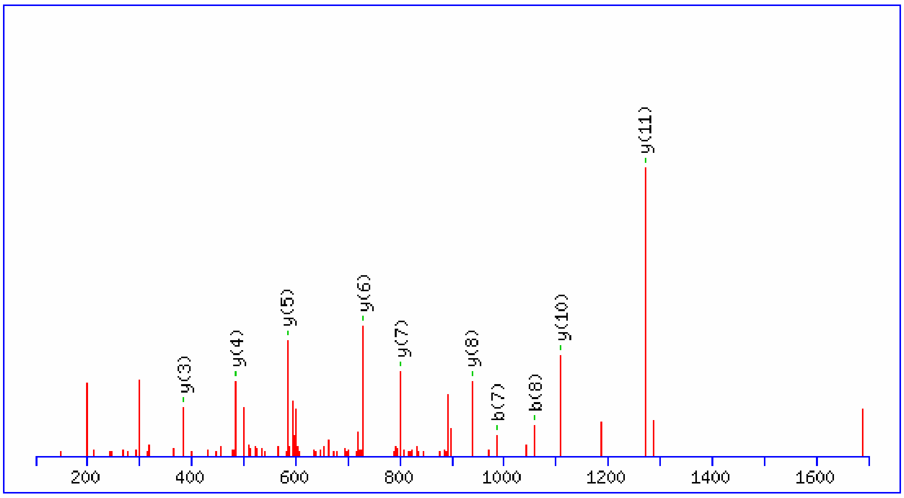
Variable modifications: C2 : ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 982.57
Ions Score: 16
Matches (Bold Red): 6/48 fragment ions using 36 most intense peaks

MS/MS Fragmentation of **GECYGLHAFVVPIR**
Found in **Q9R0H0**, ACOX1_MOUSE Acyl-coenzyme A oxidase 1

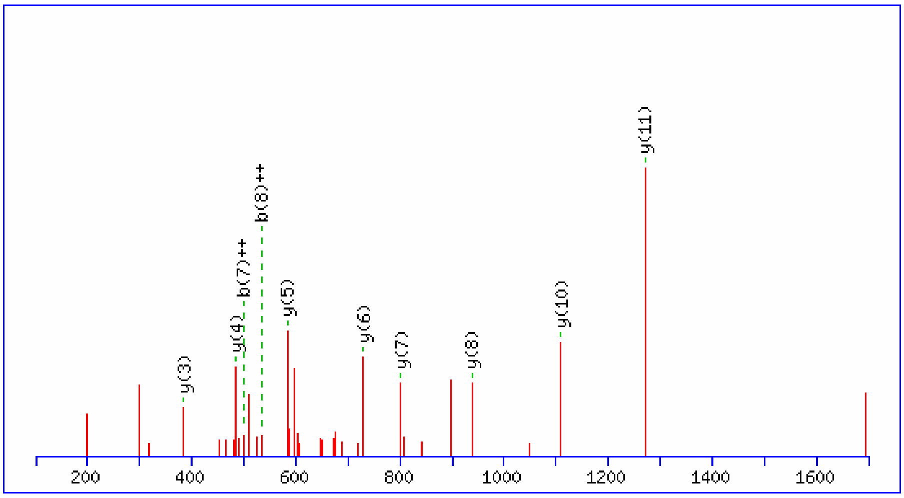
Variable modifications: C3 : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 1786.92
Ions Score: 62
Matches (Bold Red): 10/104 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **GECYGLHAFVVPIR**
Found in **Q9R0H0**, ACOX1_MOUSE Acyl-coenzyme A oxidase 1

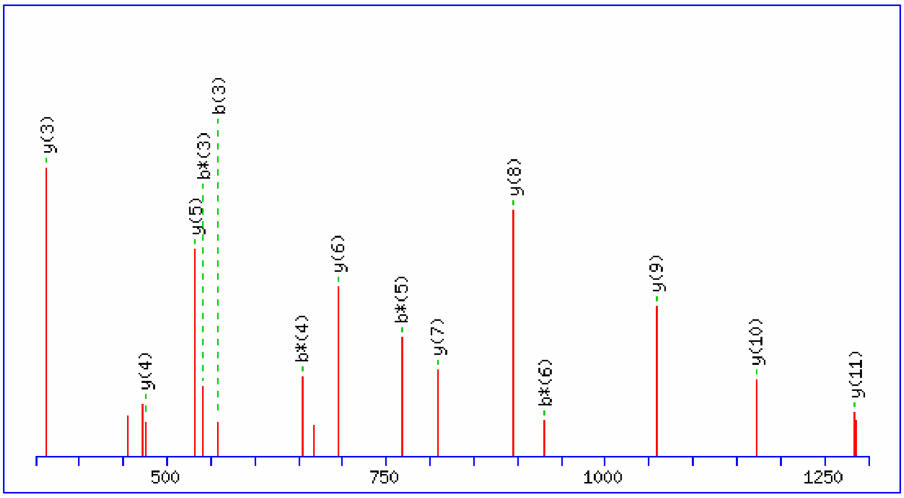
Variable modifications: C3 : ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 1795.95
Ions Score: 45
Matches (Bold Red): 10/104 fragment ions using 26 most intense peaks

MS/MS Fragmentation of **NLCLLYSLYGISQK**
Found in **Q9R0H0**, ACOX1_MOUSE Acyl-coenzyme A oxidase 1

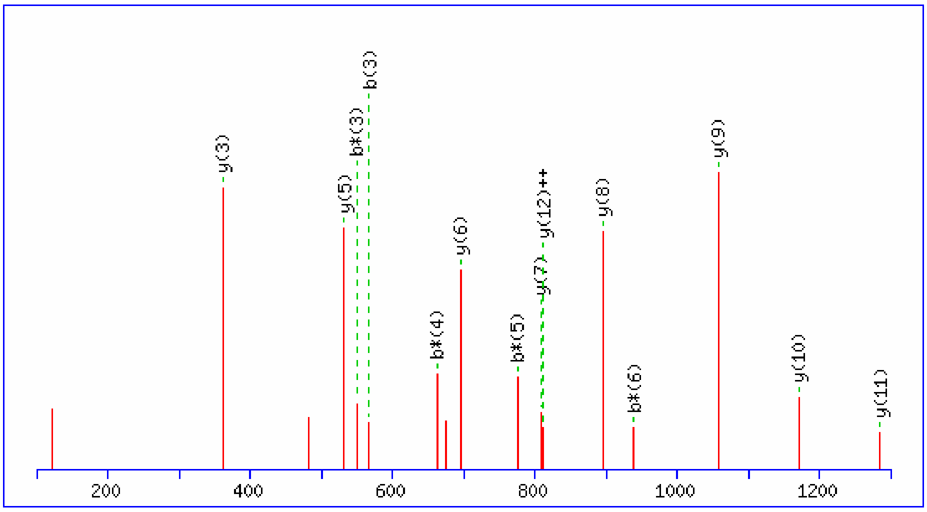
Variable modifications: C3 : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 1840.98
Ions Score: 71
Matches (Bold Red): 14/140 fragment ions using 20 most intense peaks

MS/MS Fragmentation of **NLCLLYSLYGISQK**
Found in **Q9R0H0**, ACOX1_MOUSE Acyl-coenzyme A oxidase 1

Variable modifications: C3 : ICAT_heavy

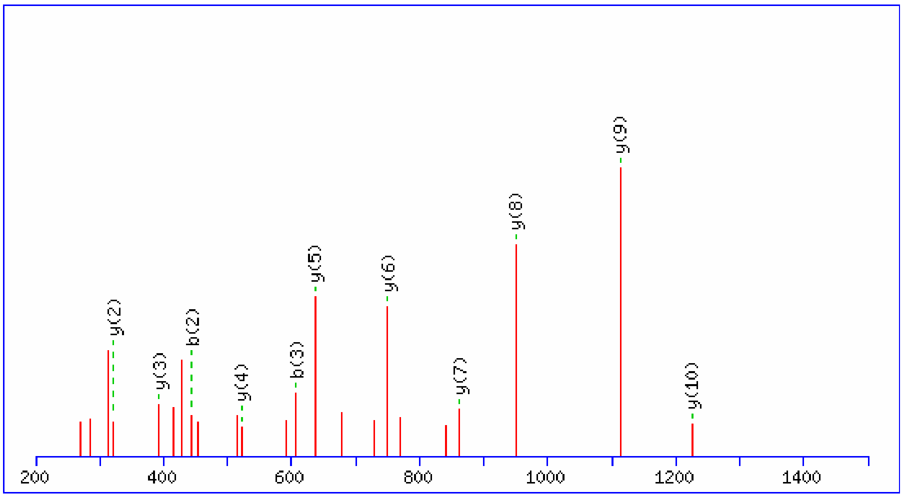


Monoisotopic mass of neutral peptide Mr(calc): 1850.01
Ions Score: 66
Matches (Bold Red): 14/140 fragment ions using 18 most intense peaks

6 ECHP_MOUSE

MS/MS Fragmentation of **CLYSLINEAFR**
Found in **Q9DBM2**, ECHP_MOUSE Peroxisomal bifunctional enzyme

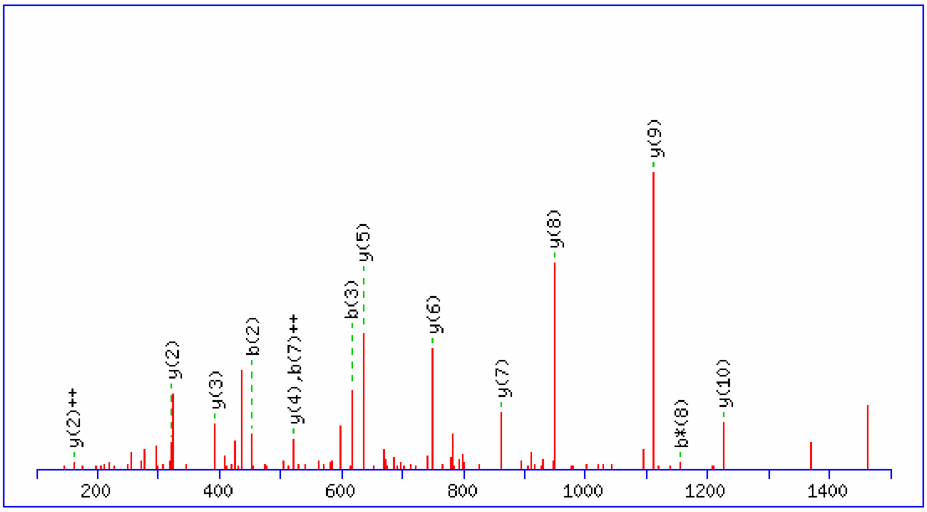
Variable modifications: C1 : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 1554.79
Ions Score: 64
Matches (Bold Red): 11/96 fragment ions using 22 most intense peaks

MS/MS Fragmentation of **CLYSLINEAFR**
Found in **Q9DBM2**, ECHP_MOUSE Peroxisomal bifunctional enzyme

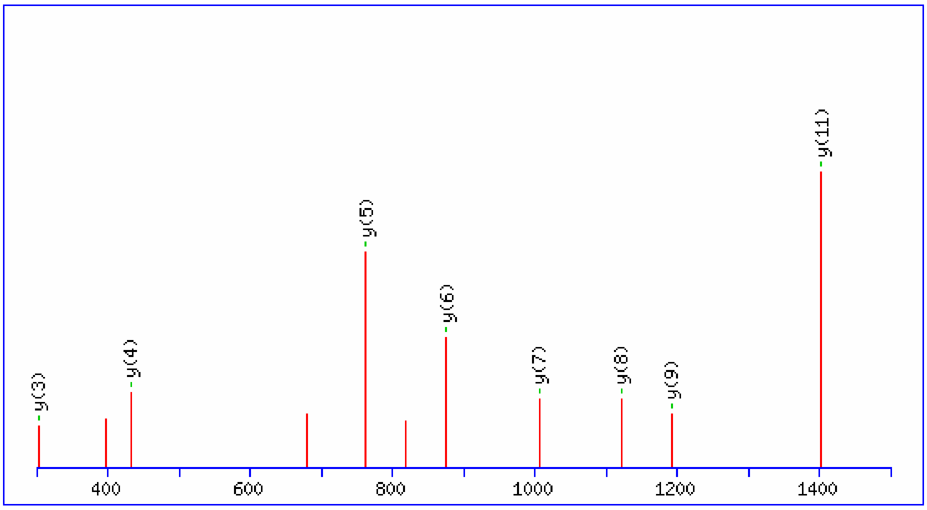
Variable modifications: C1 : ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 1563.82
Ions Score: 59
Matches (Bold Red): 14/96 fragment ions using 39 most intense peaks

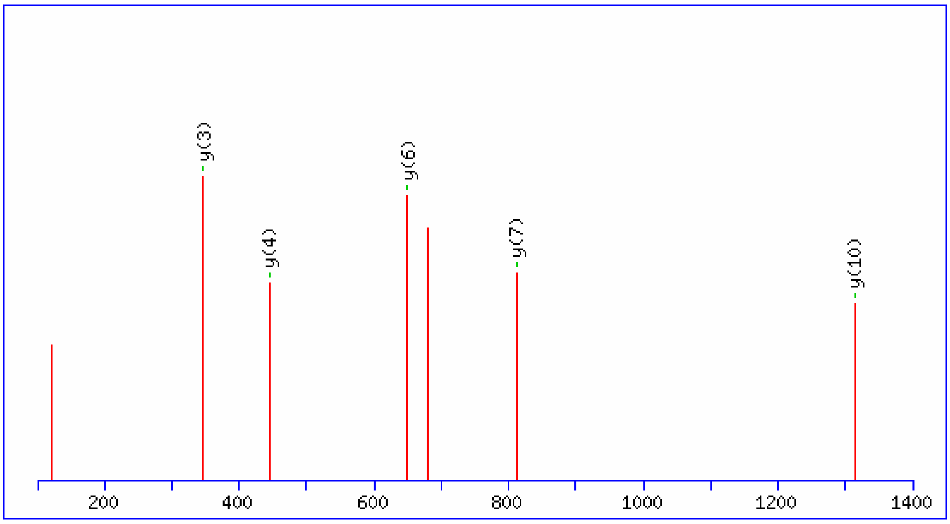
MS/MS Fragmentation of **YSPIADMLCEAGR**
Found in **Q9DBM2**, ECHP_MOUSE Peroxisomal bifunctional enzyme

Variable modifications: C9 : ICAT_light



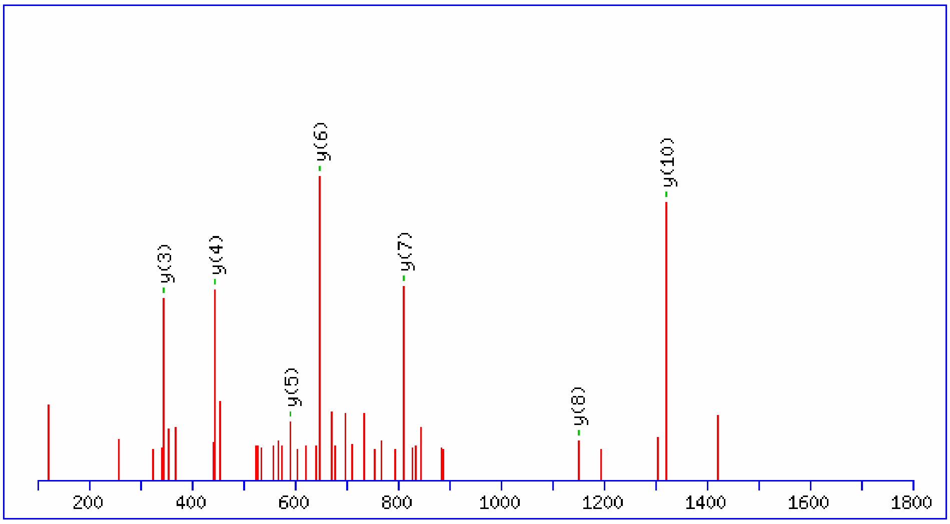
Monoisotopic mass of neutral peptide Mr(calc): 1651.77
Ions Score: 65
Matches (Bold Red): 8/112 fragment ions using 12 most intense peaks

MS/MS Fragmentation of **IGVVVGNCYGFVGNR**
Found in **Q9DBM2**, ECHP_MOUSE Peroxisomal bifunctional enzyme
Variable modifications: C8 : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 1779.91
Ions Score: 41
Matches (Bold Red): 5/100 fragment ions using 7 most intense peaks

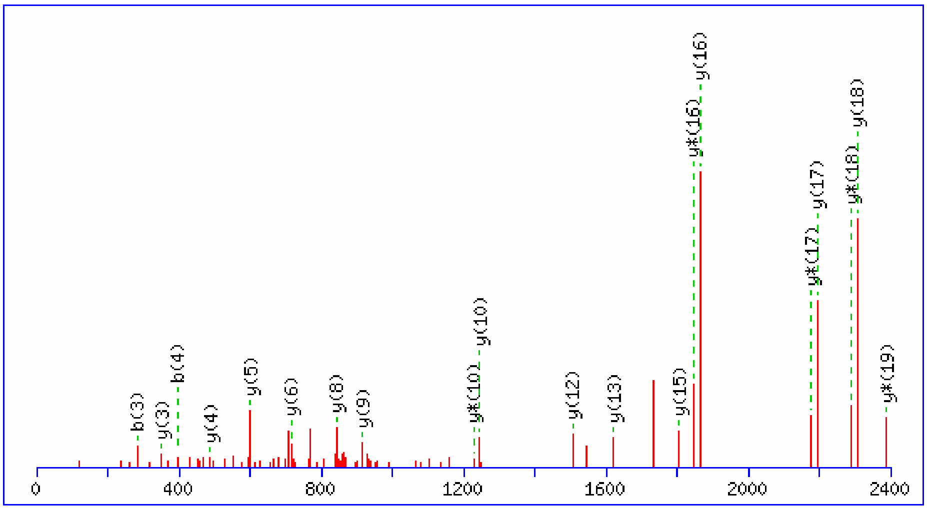
MS/MS Fragmentation of **IGVVVGNCYGFVGNR**
Found in **Q9DBM2**, ECHP_MOUSE Peroxisomal bifunctional enzyme
Variable modifications: C8 : ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 1788.94
Ions Score: 49
Matches (Bold Red): 7/100 fragment ions using 12 most intense peaks

MS/MS Fragmentation of **AIVICGANDNFCAGADIHGFK**
Found in **Q9DBM2**, ECHP_MOUSE Peroxisomal bifunctional enzyme

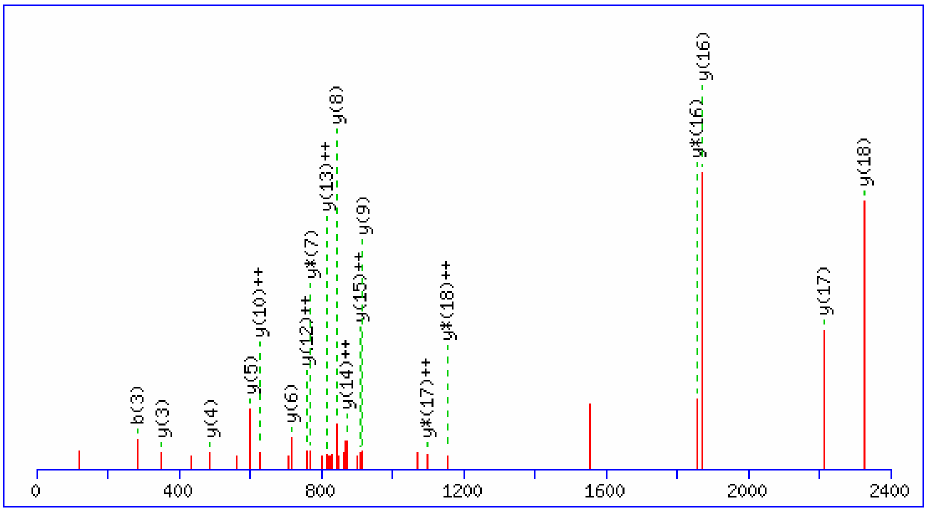
Variable modifications: C5 : ICAT_light **C12 :** ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 2589.25
Ions Score: 91
Matches (Bold Red): 21/200 fragment ions using 42 most intense peaks

MS/MS Fragmentation of **AIVICGANDNFCAGADIHGFK**
Found in **Q9DBM2**, ECHP_MOUSE Peroxisomal bifunctional enzyme

Variable modifications: C5 : ICAT_heavy **C12 :** ICAT_heavy

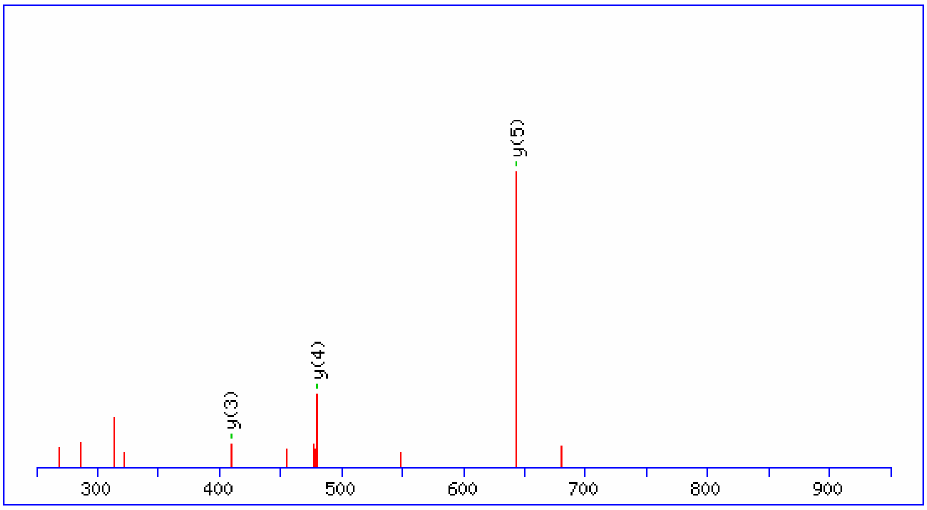


Monoisotopic mass of neutral peptide Mr(calc): 2607.31
Ions Score: 60
Matches (Bold Red): 20/200 fragment ions using 42 most intense peaks

7 HMCS2_MOUSE

MS/MS Fragmentation of **CYAAYR**
Found in **P54869**, HMCS2_MOUSE Hydroxymethylglutaryl-CoA synthase

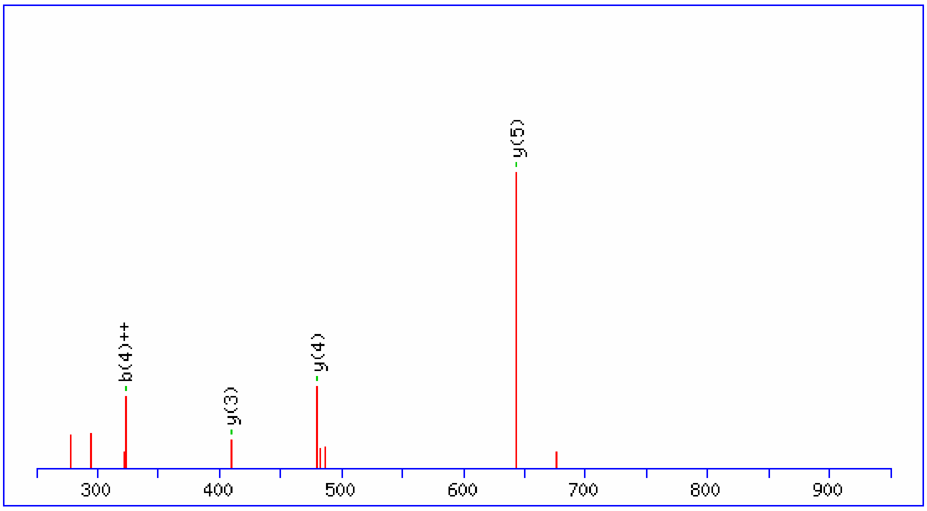
Variable modifications: C1 : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 972.45
Ions Score: 21
Matches (Bold Red): 3/30 fragment ions using 6 most intense peaks

MS/MS Fragmentation of **CYAAYR**
Found in **P54869**, HMCS2_MOUSE Hydroxymethylglutaryl-CoA synthase

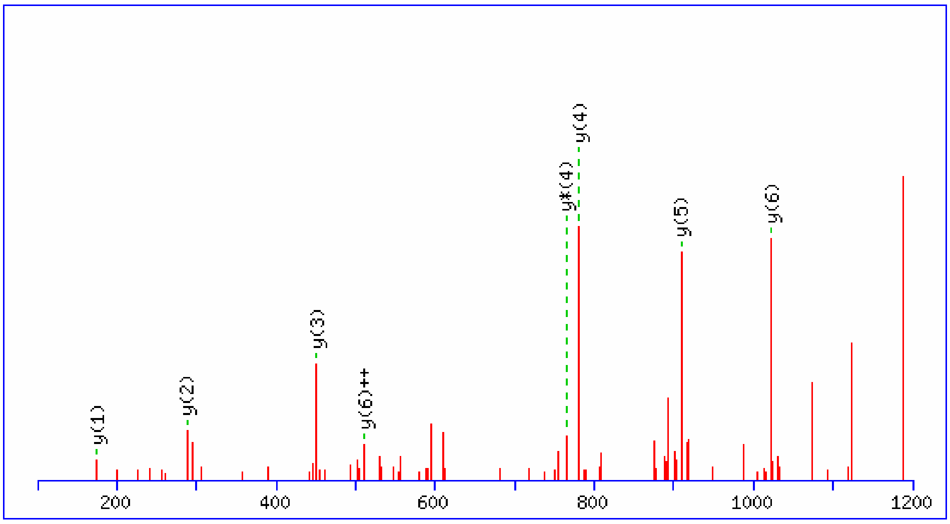
Variable modifications: C1 : ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 981.48
Ions Score: 29
Matches (Bold Red): 4/30 fragment ions using 4 most intense peaks

MS/MS Fragmentation of **LSIQCYLR**
Found in **P54869**, HMCS2_MOUSE Hydroxymethylglutaryl-CoA synthase

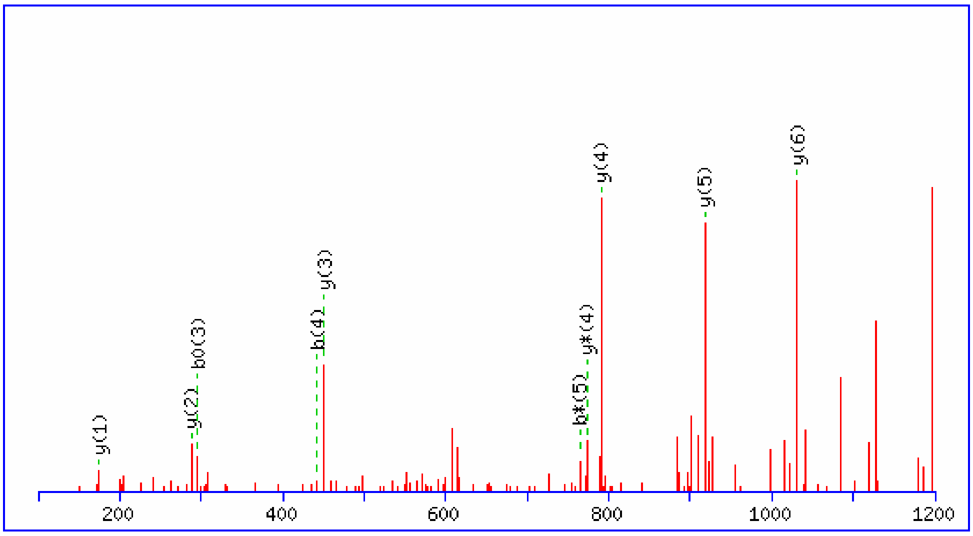
Variable modifications: C5 : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 1221.65
Ions Score: 51
Matches (Bold Red): 8/64 fragment ions using 14 most intense peaks

MS/MS Fragmentation of **LSIQCYLR**
Found in **P54869**, HMCS2_MOUSE Hydroxymethylglutaryl-CoA synthase

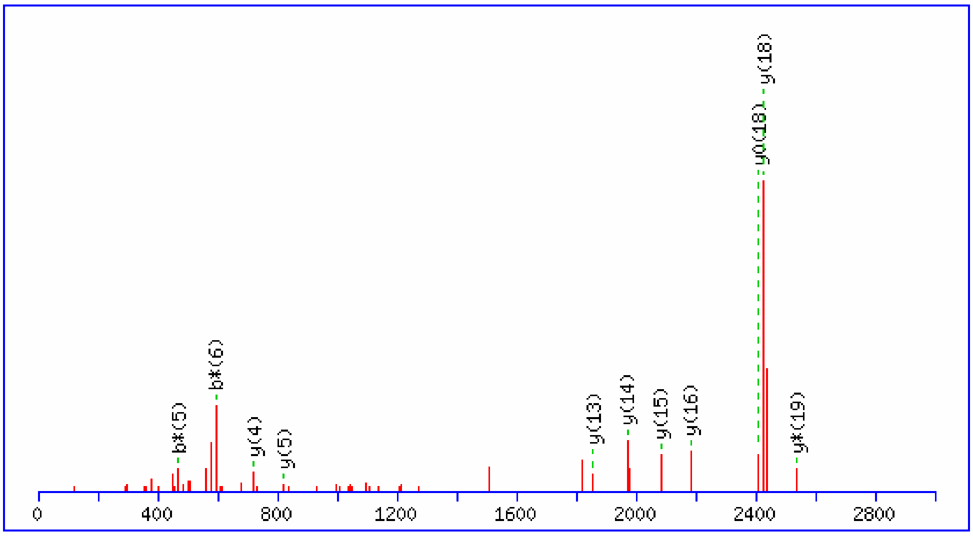
Variable modifications: **C5** **:** ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 1230.68
Ions Score: 51
Matches (Bold Red): 10/64 fragment ions using 22 most intense peaks

MS/MS Fragmentation of **QAGNNQPFTLDDVQYMIFHTPFCK**
Found in **P54869**, HMCS2_MOUSE Hydroxymethylglutaryl-CoA synthase

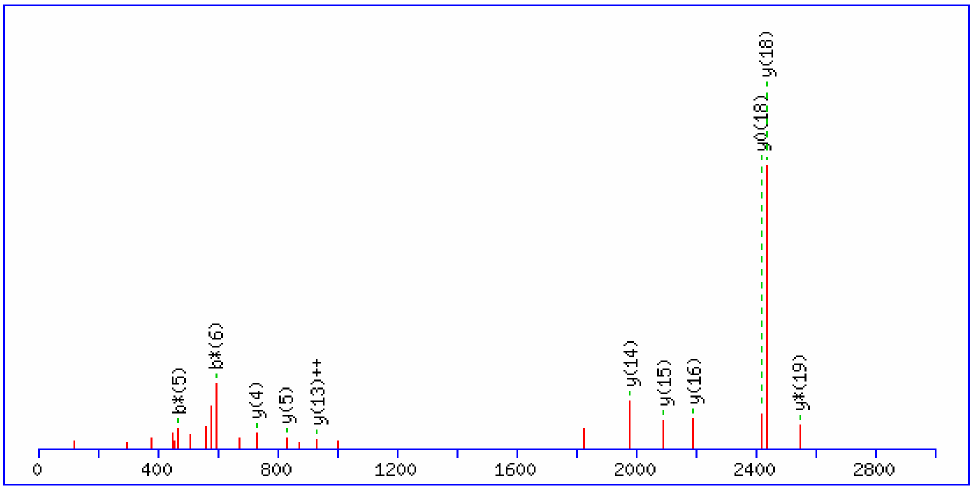
Variable modifications: **C23** **:** ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 3040.42
Ions Score: 29
Matches (Bold Red): 11/252 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **QAGNNQPFTLDDVQYMIFHTPFCK**
Found in **P54869**, HMCS2_MOUSE Hydroxymethylglutaryl-CoA synthase

Variable modifications: C23 : ICAT_heavy

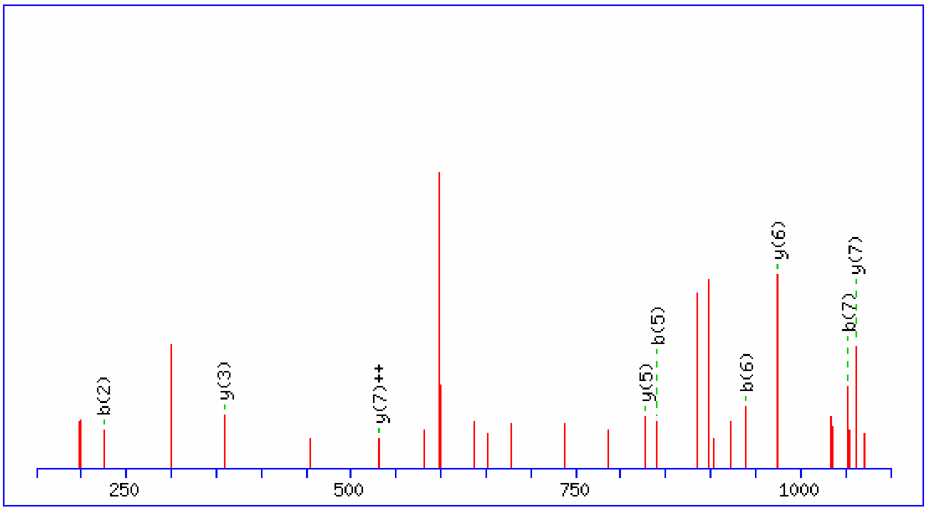


Monoisotopic mass of neutral peptide Mr(calc): 3049.45
Ions Score: 29
Matches (Bold Red): 11/252 fragment ions using 21 most intense peaks

8 NDUS1_MOUSE

MS/MS Fragmentation of **HSFCEVLK**
Found in **Q91VD9**, NDUS1_MOUSE NADH-ubiquinone oxidoreductase 75 kDa subunit

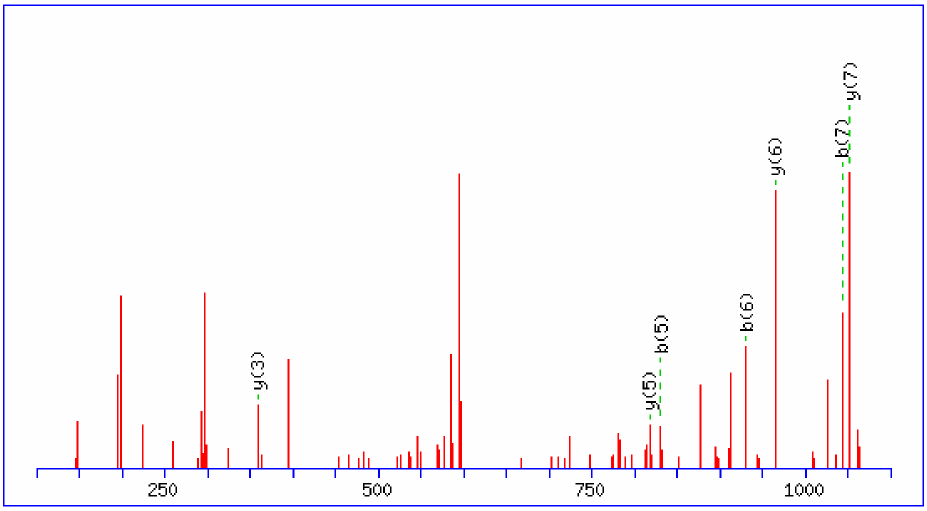
Variable modifications: C4 : ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 1197.63
Ions Score: 23
Matches (Bold Red): 9/62 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **HSFCEVLK**
Found in **Q91VD9**, NDUS1_MOUSE NADH-ubiquinone oxidoreductase 75 kDa subunit

Variable modifications: C4 : ICAT_light

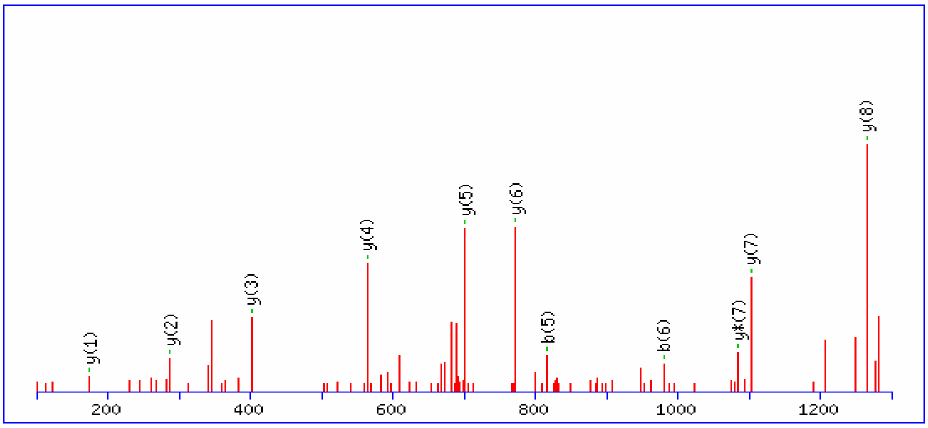


Monoisotopic mass of neutral peptide Mr(calc): 1188.60
Ions Score: 20
Matches (Bold Red): 7/62 fragment ions using 33 most intense peaks

9 NDUB7_MOUSE

MS/MS Fragmentation of **DYCAHYLIR**
Found in **Q9CR61**, NDUB7_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

Variable modifications: C3 : ICAT_light

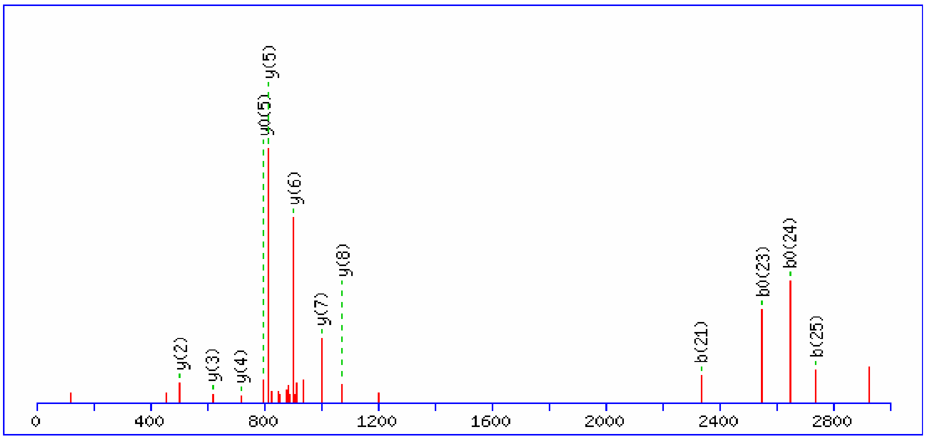


Monoisotopic mass of neutral peptide Mr(calc): 1379.67
Ions Score: 62
Matches (Bold Red): 11/64 fragment ions using 16 most intense peak

10 NDUV1_MOUSE

MS/MS Fragmentation of **LKPPFPADVGVFGCPTTVANVETVAVSPTICR**
Found in **Q91YT0**, NDUV1_MOUSE NADH dehydrogenase [ubiquinone] flavoprotein 1

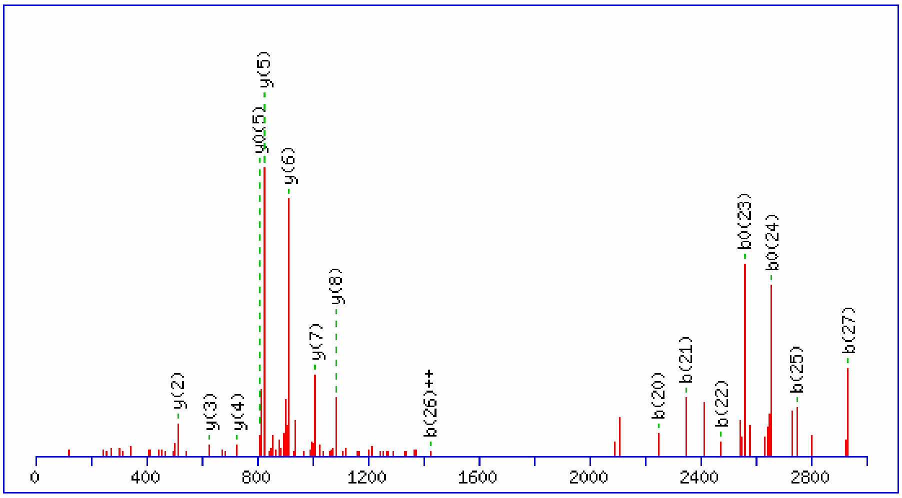
Variable modifications: C14 : ICAT_light **C31 :** ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 3738.95
Ions Score: 46
Matches (Bold Red): 12/350 fragment ions using 18 most intense peaks

MS/MS Fragmentation of **LKPPFPADVGVFGCPTTVANVETVAVSPTICR**
Found in **Q91YT0**, NDUV1_MOUSE NADH dehydrogenase [ubiquinone] flavoprotein 1

Variable modifications: C14 : ICAT_heavy **C31 :** ICAT_heavy

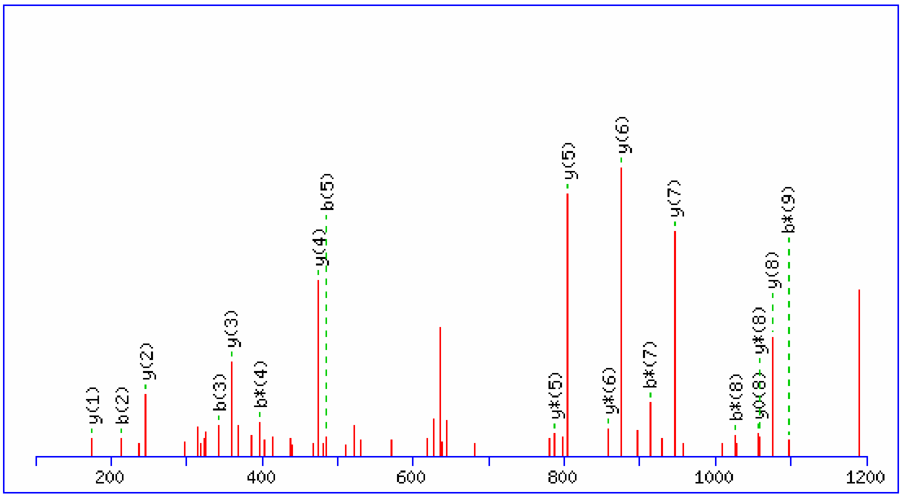


Monoisotopic mass of neutral peptide Mr(calc): 3757.01
Ions Score: 27
Matches (Bold Red): 16/350 fragment ions using 33 most intense peak

11 BHMT1_MOUSE

MS/MS Fragmentation of **VNEAACDIAR**
Found in **O35490**, BHMT1_MOUSE Betaine--homocysteine S-methyltransferase 1

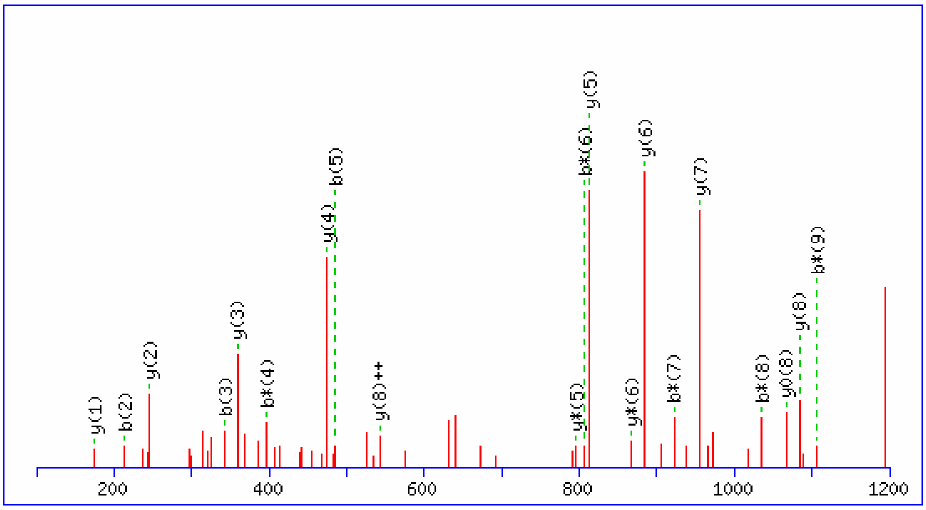
Variable modifications: C6 : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 1287.62
Ions Score: 64
Matches (Bold Red): 19/96 fragment ions using 32 most intense peaks

MS/MS Fragmentation of **VNEAACDIAR**
Found in **O35490**, BHMT1_MOUSE Betaine--homocysteine S-methyltransferase 1

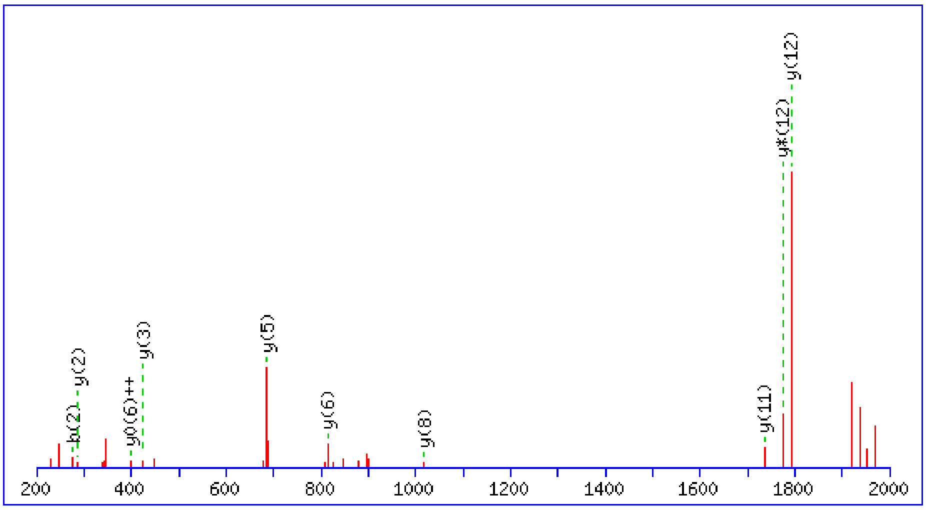
Variable modifications: C6 : ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 1296.65
Ions Score: 61
Matches (Bold Red): 20/96 fragment ions using 39 most intense peaks

MS/MS Fragmentation of **YIGGCCGFEPYHIR**
Found in **O35490**, BHMT1_MOUSE Betaine--homocysteine S-methyltransferase 1

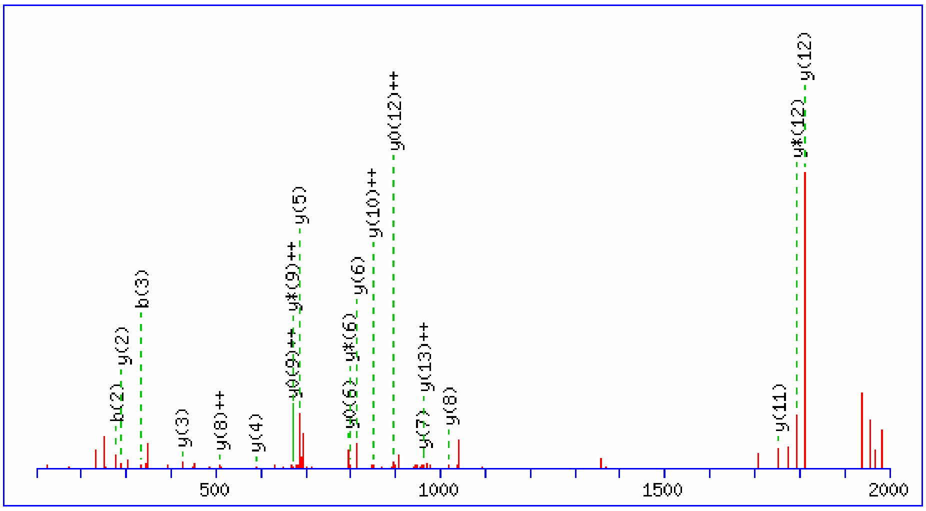
Variable modifications: C5 : ICAT_light **C6 :** ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 2067.97
Ions Score: 21
Matches (Bold Red): 10/104 fragment ions using 37 most intense peaks

MS/MS Fragmentation of **YIGGCCGFEPYHIR**
Found in **O35490**, BHMT1_MOUSE Betaine--homocysteine S-methyltransferase 1

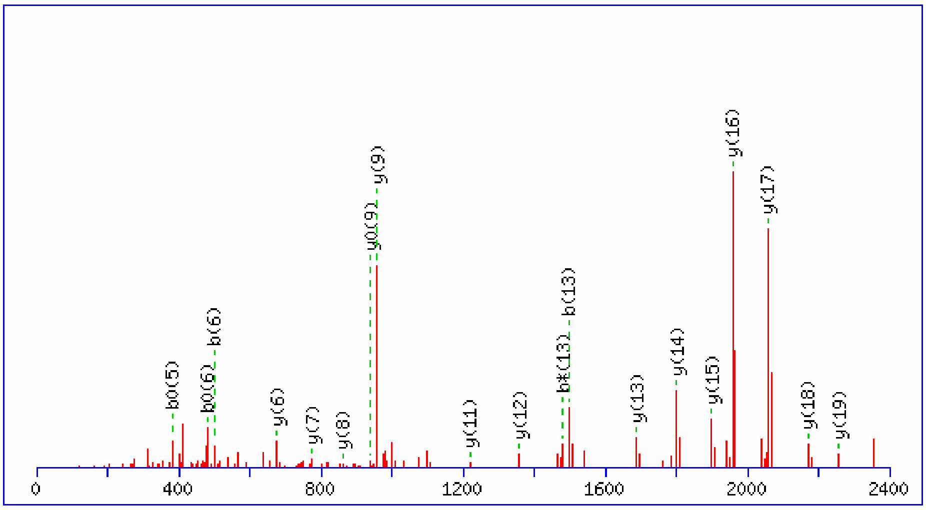
Variable modifications: C5 : ICAT_heavy **C6 :** ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 2086.03
Ions Score: 27
Matches (Bold Red): 20/104 fragment ions using 76 most intense peaks

MS/MS Fragmentation of **AGASIVGVNCHFDPSVSLQTVK**
Found in **O35490**, BHMT1_MOUSE Betaine--homocysteine S-methyltransferase

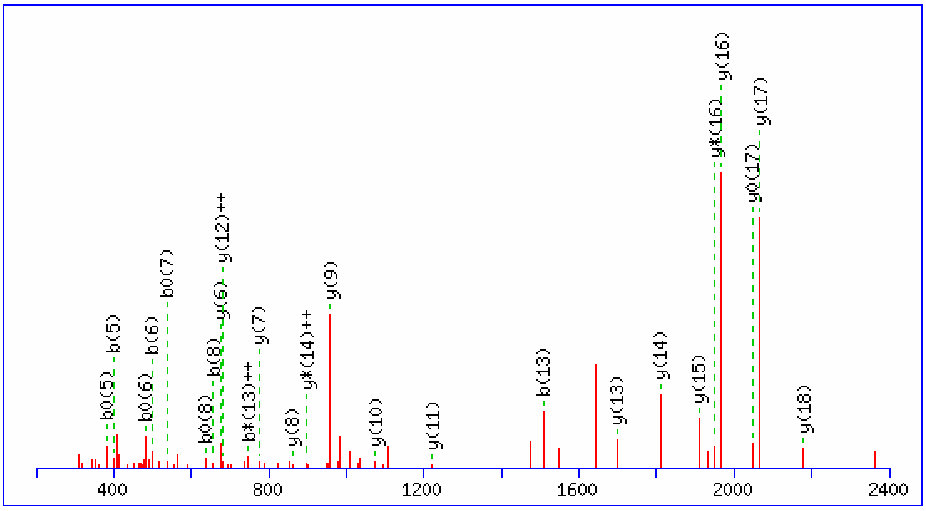
Variable modifications: C10 : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 2455.25
Ions Score: 104
Matches (Bold Red): 19/226 fragment ions using 41 most intense peaks

MS/MS Fragmentation of **AGASIVGVNCHFDPSVSLQTVK**
Found in **O35490**, BHMT1_MOUSE Betaine--homocysteine S-methyltransferase 1

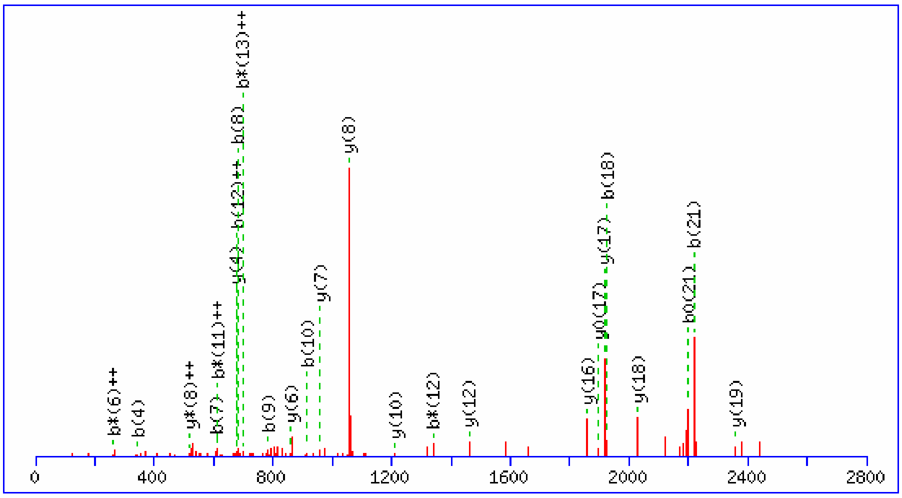
Variable modifications: C10 : ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 2464.28
Ions Score: 67
Matches (Bold Red): 25/226 fragment ions using 53 most intense peaks

MS/MS Fragmentation of **ASGKPVAATMCIGPEGDLHGVPPGECAVR**
Found in **O35490**, BHMT1_MOUSE Betaine--homocysteine S-methyltransferase 1

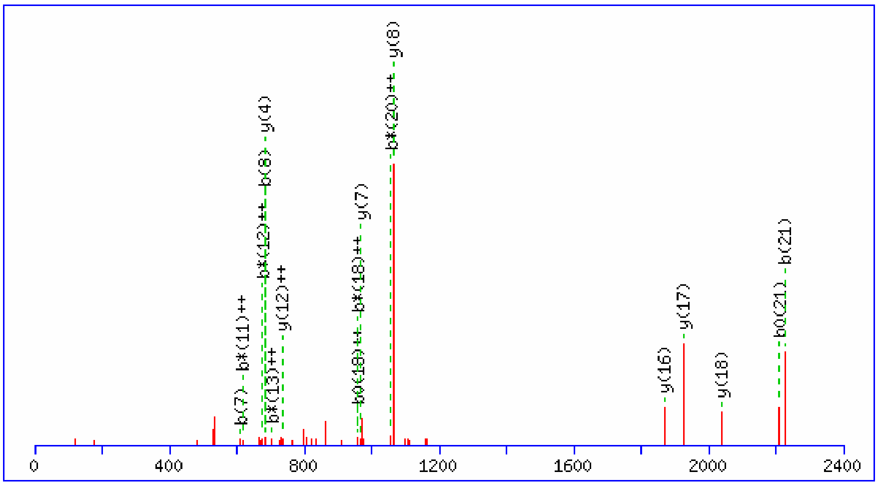
Variable modifications: **C11** **:** ICAT_light **C26** **:** ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 3272.61
Ions Score: 41
Matches (Bold Red): 25/320 fragment ions using 64 most intense peaks

MS/MS Fragmentation of **ASGKPVAATMCIGPEGDLHGVPPGECAVR**
Found in **O35490**, BHMT1_MOUSE Betaine--homocysteine S-methyltransferase

Variable modifications: **C11** **:** ICAT_heavy **C26** **:** ICAT_heavy

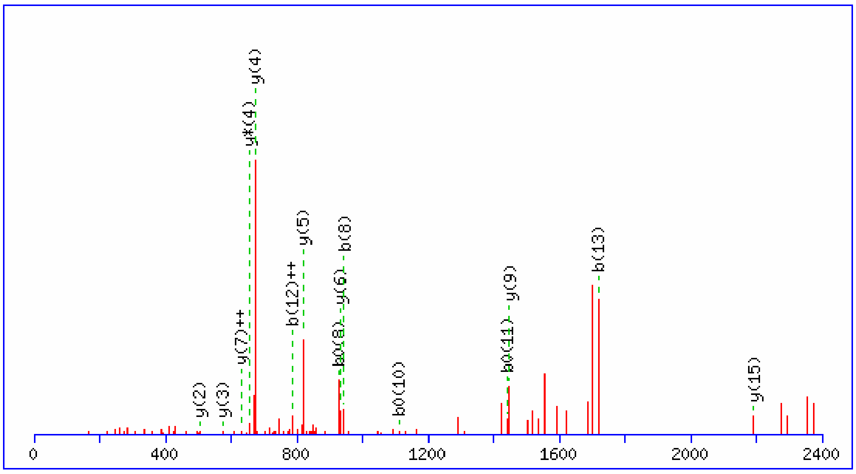


Monoisotopic mass of neutral peptide Mr(calc): 3290.67
Ions Score: 16
Matches (Bold Red): 17/320 fragment ions using 42 most intense peaks

12 CAH3_MOUSE

MS/MS Fragmentation of **EAPFTHFDPSCLFPACR**
Found in **P16015**, CAH3_MOUSE Carbonic anhydrase 3

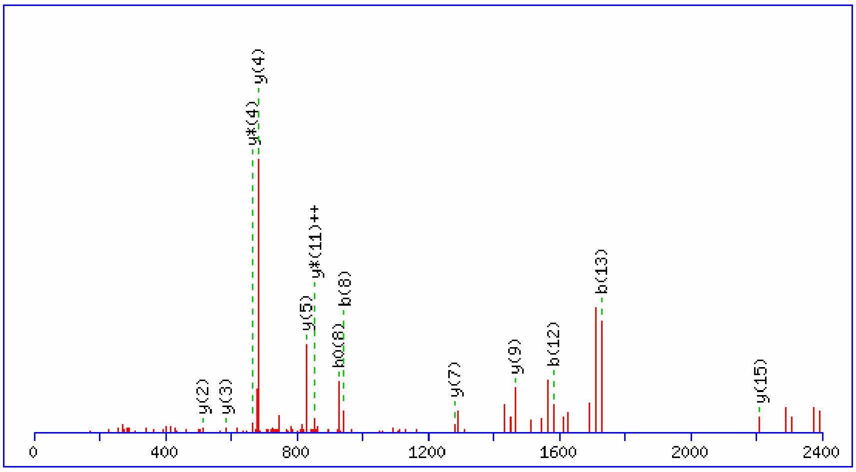
Variable modifications: C11 : ICAT_light **C16** : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 2391.11
Ions Score: 19
Matches (Bold Red): 15/146 fragment ions using 51 most intense peaks

MS/MS Fragmentation of **EAPFTHFDPSCLFPACR**
Found in **P16015**, CAH3_MOUSE Carbonic anhydrase 3

Variable modifications: C11 : ICAT_heavy **C16 :** ICAT_heavy

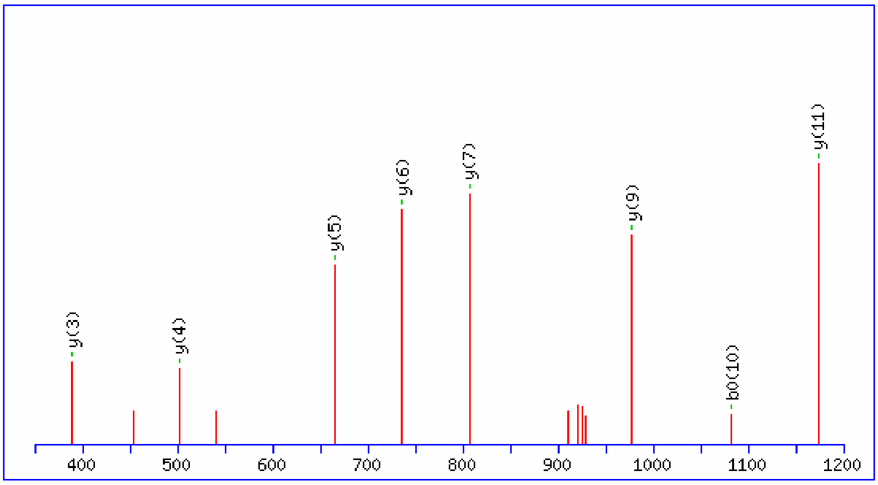


Monoisotopic mass of neutral peptide Mr(calc): 2409.17
Ions Score: 26
Matches (Bold Red): 13/146 fragment ions using 39 most intense peaks

13   HYEP_MOUSE

MS/MS Fragmentation of **ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK**
Found in **Q9D379**, HYEP_MOUSE Epoxide hydrolase 1

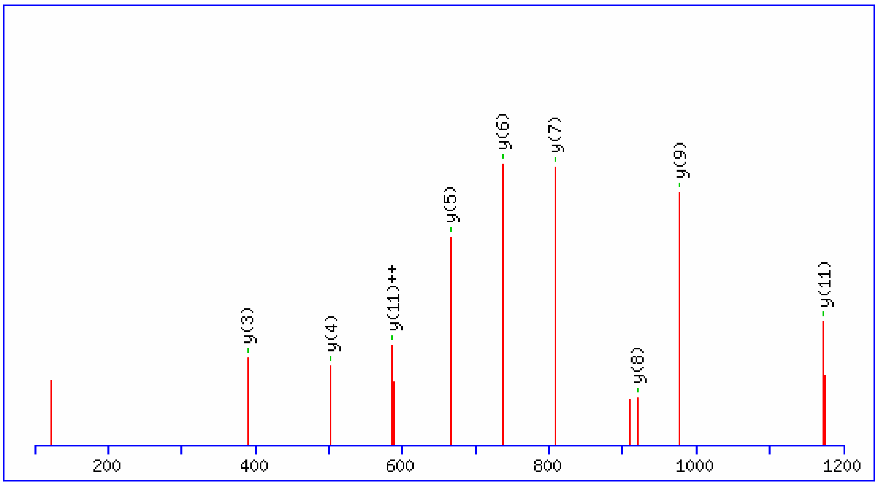
Variable modifications: C17   : ICAT_light



Monoisotopic mass of neutral peptide Mr(calc): 3699.88
Ions Score: 54
Matches (Bold Red): 8/368 fragment ions using 8 most intense peaks

MS/MS Fragmentation of **ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK**
Found in **Q9D379**, HYEP_MOUSE Epoxide hydrolase 1

Variable modifications: C17   : ICAT_heavy



Monoisotopic mass of neutral peptide Mr(calc): 3708.91
Ions Score: 53
Matches (Bold Red): 9/368 fragment ions using 10 most intense peaks