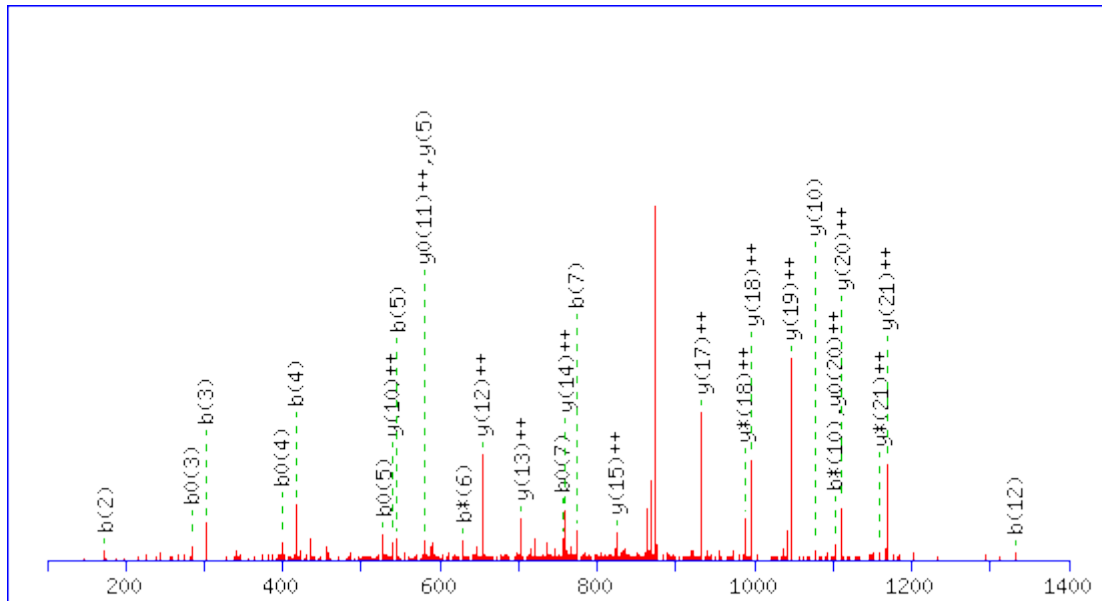


Supplemental Table 2. Annotated spectra for proteins identified on the basis of one unique peptide spectrum

Proteins identified in cytoplasmic fraction

MS/MS Fragmentation of **DGEDQTQDTELVETRPAGDGTQK**

Found in **1C07_HUMAN**, HLA class I histocompatibility antigen, Cw-7 alpha chain
 OS=Homo sapiens GN=HLA-C PE=1 SV=3



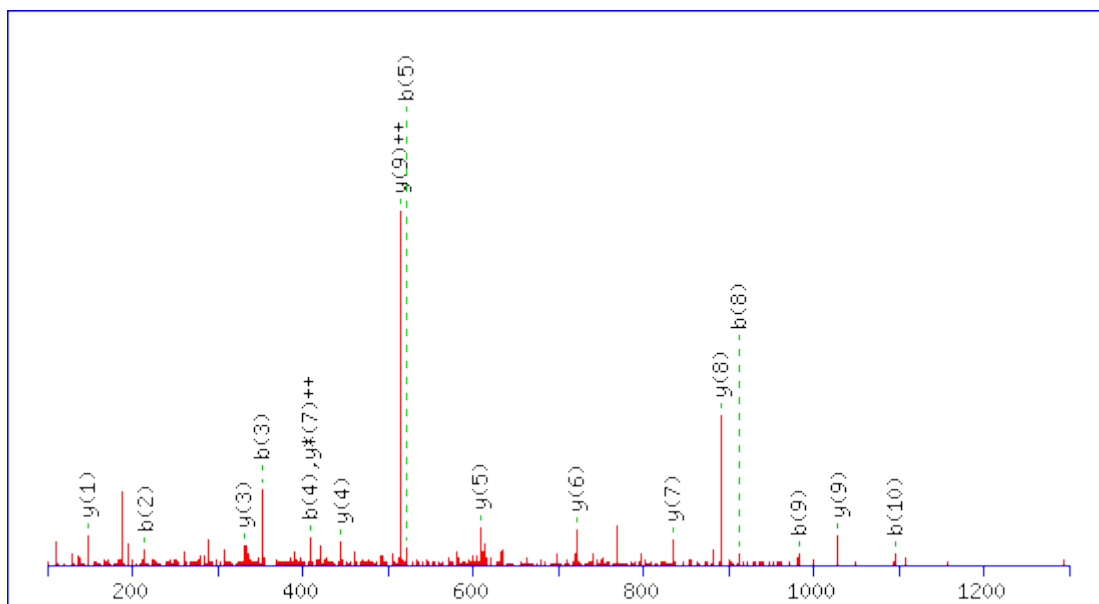
Monoisotopic mass of neutral peptide Mr(calc): 2636.1838

Ions Score: 63 Expect: 0.00021

Matches (Bold Red): 28/262 fragment ions using 42 most intense peaks

MS/MS Fragmentation of **TIHGLIYNALK**

Found in **2A5D_HUMAN**, Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo sapiens GN=PPP2R5D PE=1 SV=1



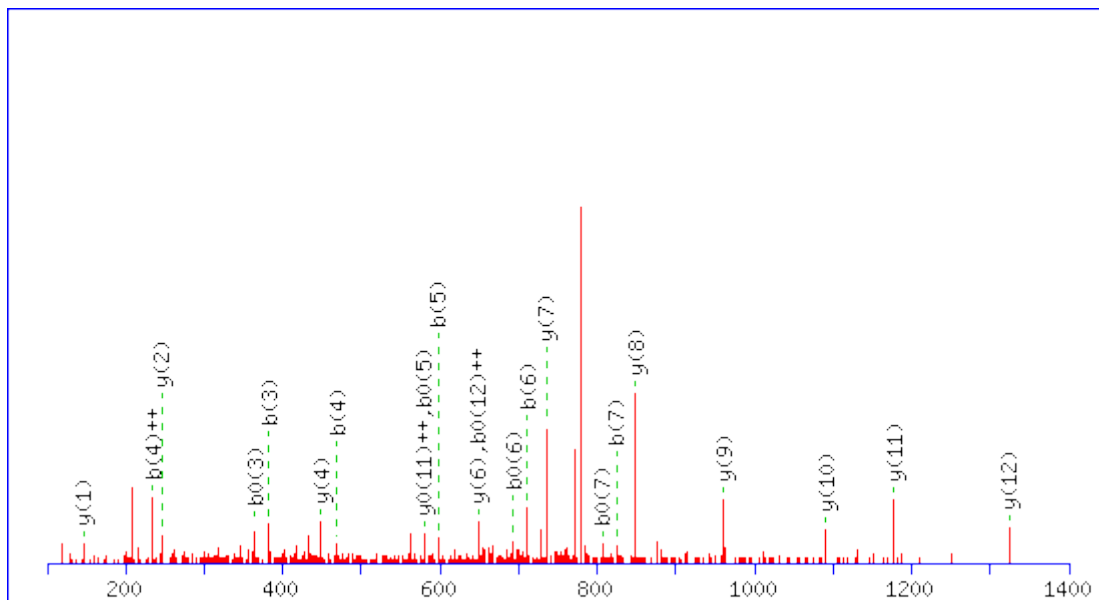
Monoisotopic mass of neutral peptide Mr(calc): 1241.7132

Ions Score: 68 Expect: 4.3e-005

Matches (Bold Red): 17/86 fragment ions using 25 most intense peaks

MS/MS Fragmentation of **SFFSEIISISDVK**

Found in **2ABD_HUMAN**, Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform OS=Homo sapiens GN=PPP2R2D PE=1 SV=1



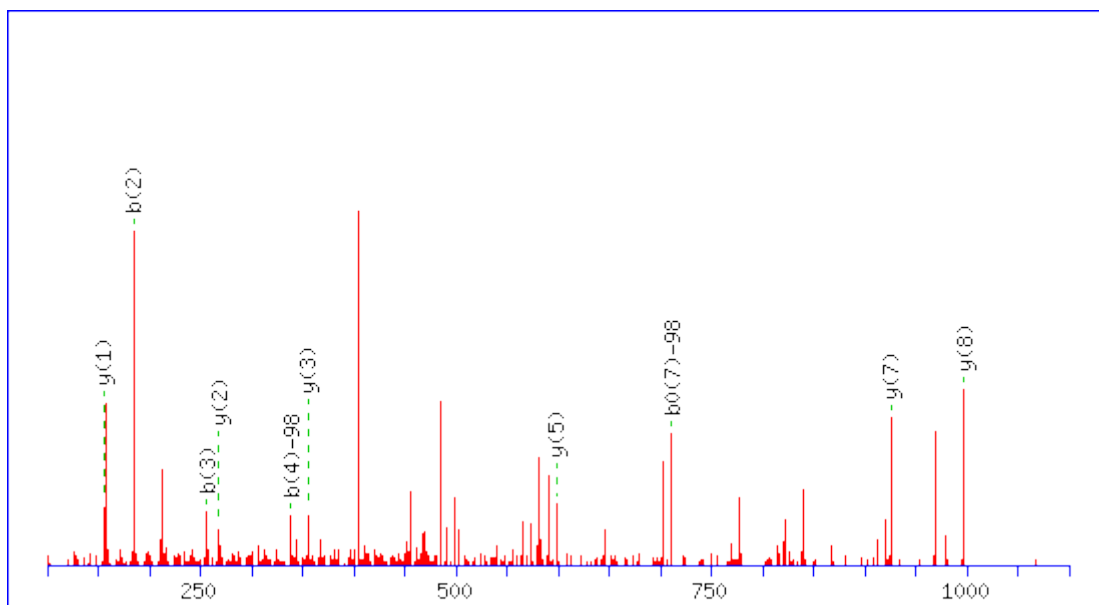
Monoisotopic mass of neutral peptide Mr(calc): 1557.7926

Ions Score: 69 Expect: 4e-005

Matches (Bold Red): 23/126 fragment ions using 38 most intense peaks

MS/MS Fragmentation of **AIATFWGSLK**

Found in **ABCAD_HUMAN**, ATP-binding cassette sub-family A member 13 OS=Homo sapiens
GN=ABCA13 PE=2 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1180.5773

Variable modifications:

T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

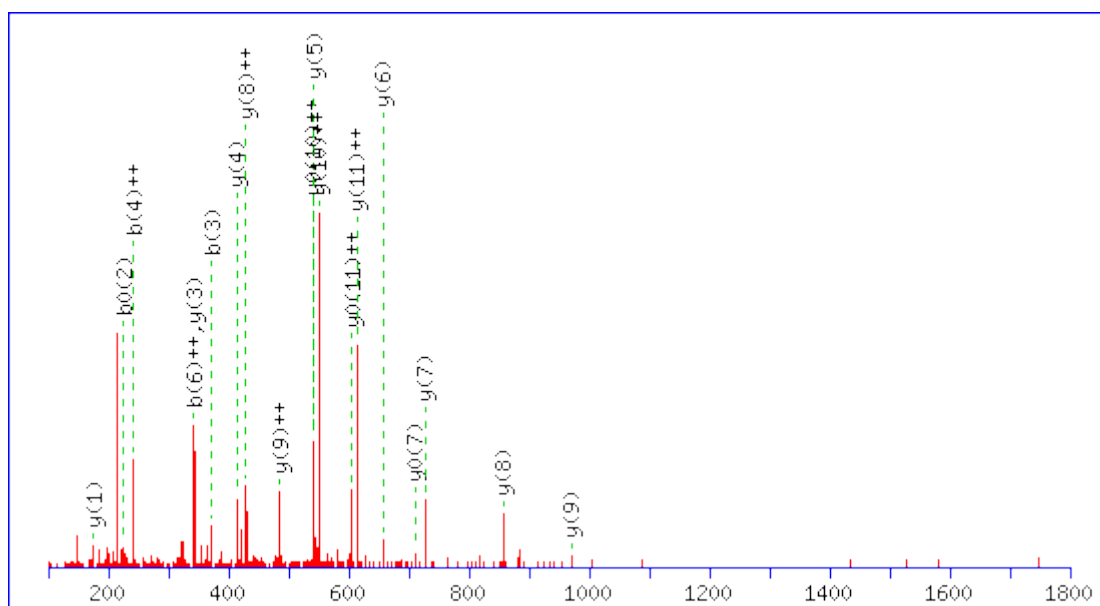
K10 : Label:13C(6)15N(2) (K)

Ions Score: 22 **Expect:** 1.6

Matches (Bold Red): 10/122 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **LEEIEADKAPAR**

Found in **ABCF3_HUMAN**, ATP-binding cassette sub-family F member 3 OS=Homo sapiens
GN=ABCF3 PE=1 SV=2



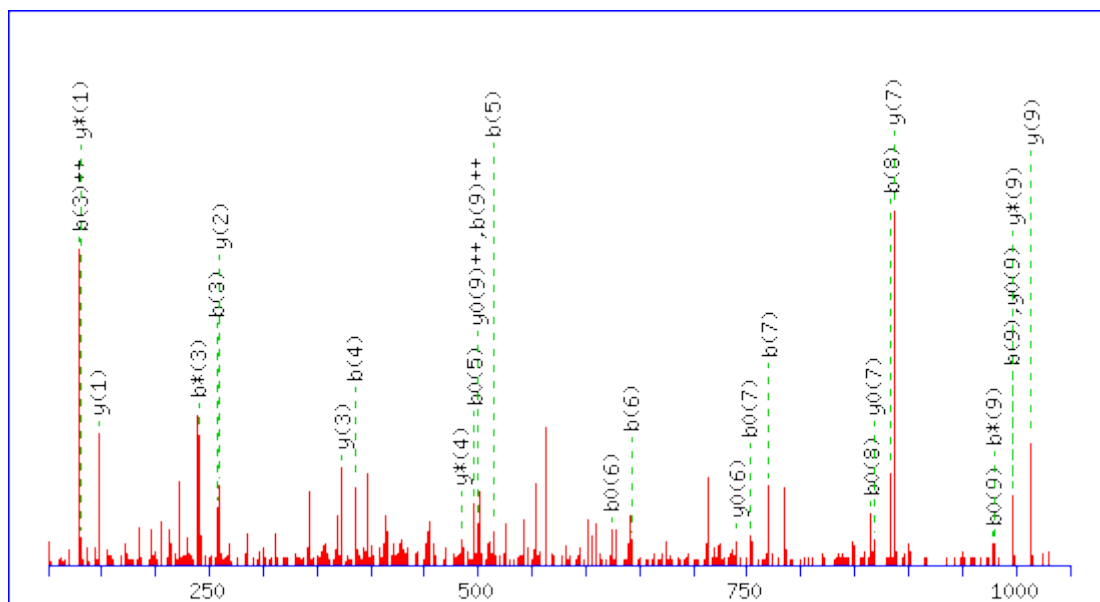
Monoisotopic mass of neutral peptide Mr(calc): 1340.6935

Ions Score: 55 Expect: 0.00082

Matches (**Bold Red**): 20/106 fragment ions using 32 most intense peaks

MS/MS Fragmentation of **QGAKEKQLLK**

Found in **ABHD8_HUMAN**, Abhydrolase domain-containing protein 8 OS=Homo sapiens
GN=ABHD8 PE=2 SV=1



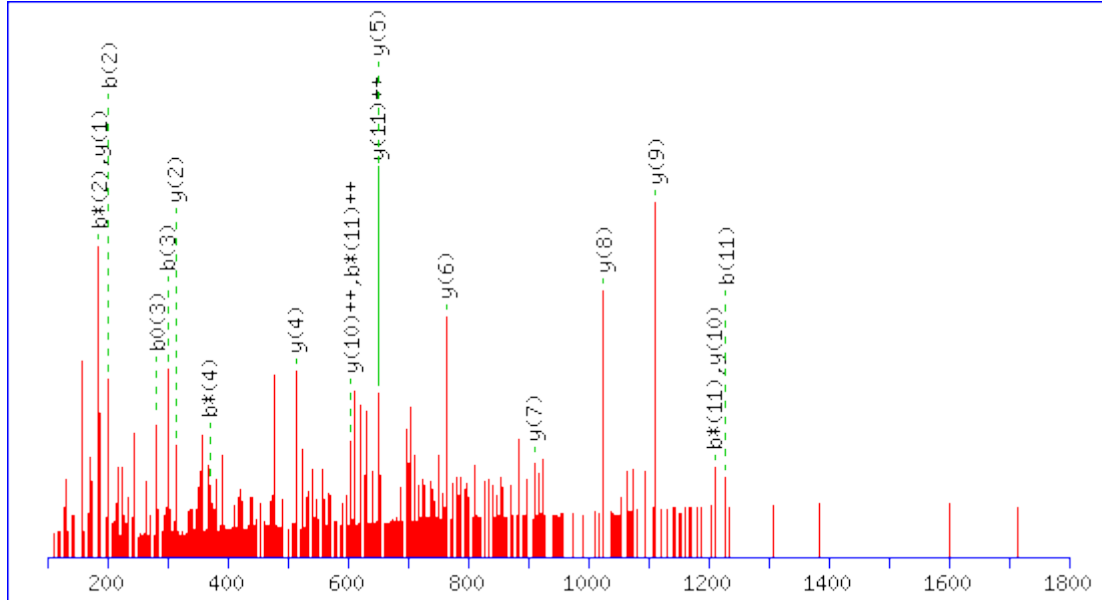
Monoisotopic mass of neutral peptide Mr(calc): 1141.6819

Ions Score: 39 Expect: 0.03

Matches (**Bold Red**): 29/90 fragment ions using 69 most intense peaks

MS/MS Fragmentation of **NSVSNFLHSLER**

Found in **ACACA_HUMAN**, Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1411.7083

Variable modifications:

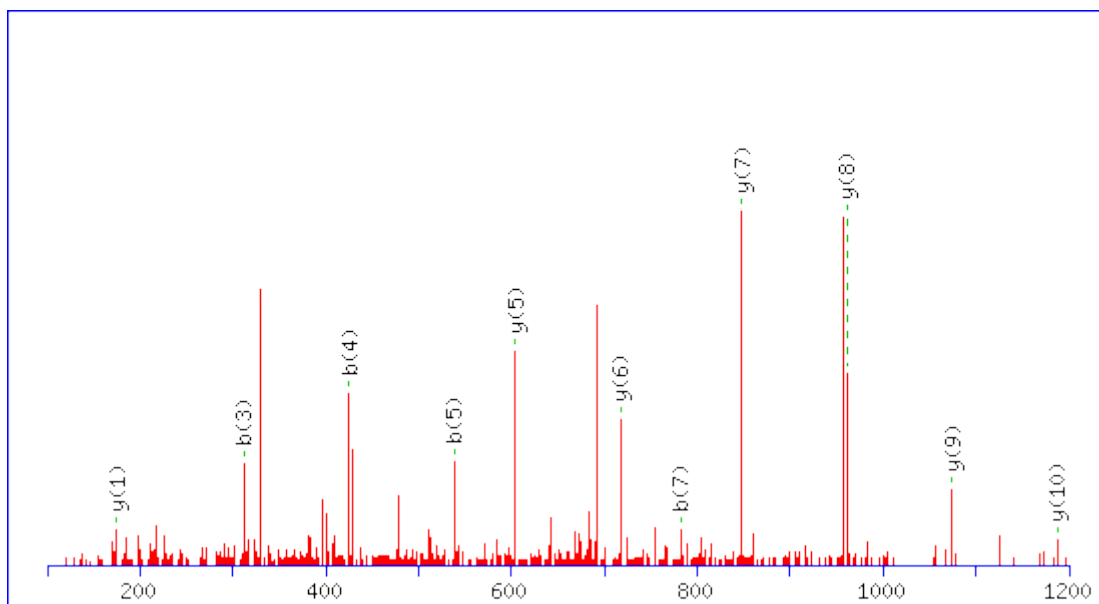
R12 : Label:13C(6)15N(4) (R)

Ions Score: 47 Expect: 0.0045

Matches (**Bold Red**): 19/128 fragment ions using 35 most intense peaks

MS/MS Fragmentation of **TPLLLMLGQEDR**

Found in **ACPH_HUMAN**, Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH
PE=1 SV=4



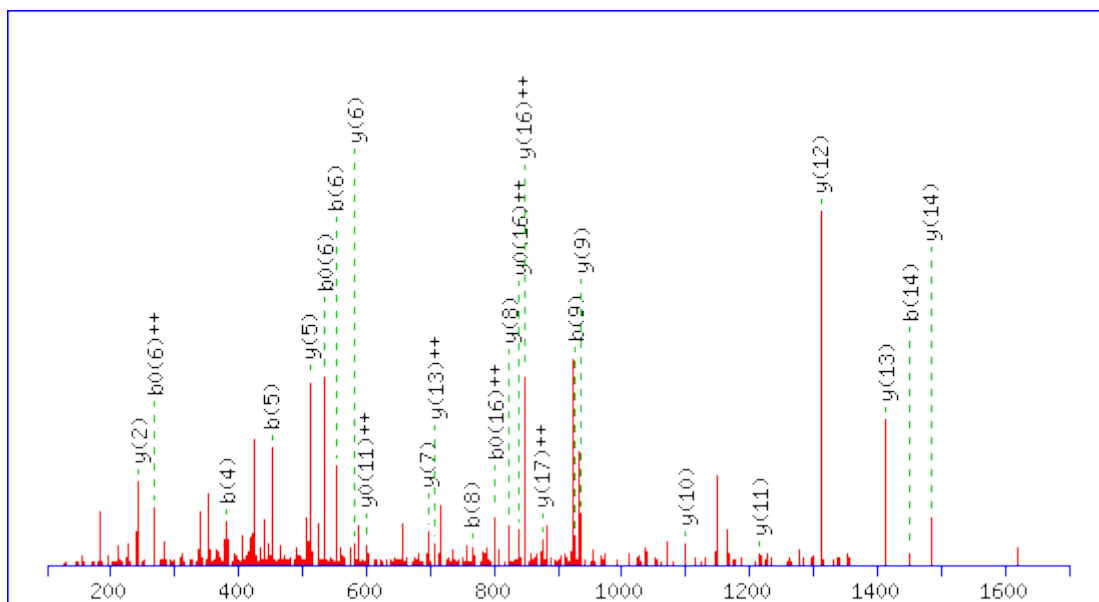
Monoisotopic mass of neutral peptide Mr(calc): 1384.7384

Ions Score: 39 Expect: 0.034

Matches (Bold Red): 11/114 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **IGPIATPDYIQNAPGLPK**

Found in **ACSA_HUMAN**, Acetyl-coenzyme A synthetase, cytoplasmic OS=Homo sapiens
GN=ACSS2 PE=1 SV=1



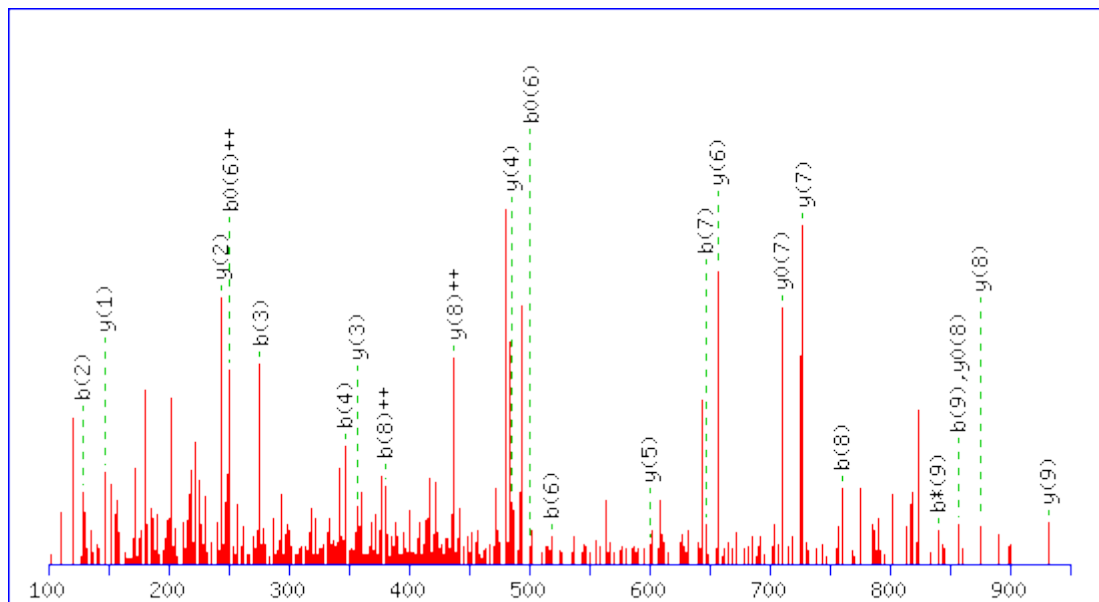
Monoisotopic mass of neutral peptide Mr(calc): 1864.0094

Ions Score: 46 Expect: 0.0079

Matches (**Bold Red**): 26/154 fragment ions using 71 most intense peaks

MS/MS Fragmentation of **AGFAGDQIPK**

Found in **ACTY_HUMAN**, Beta-actin OS=Homo sapiens GN=ACTR1B PE=1 SV=1



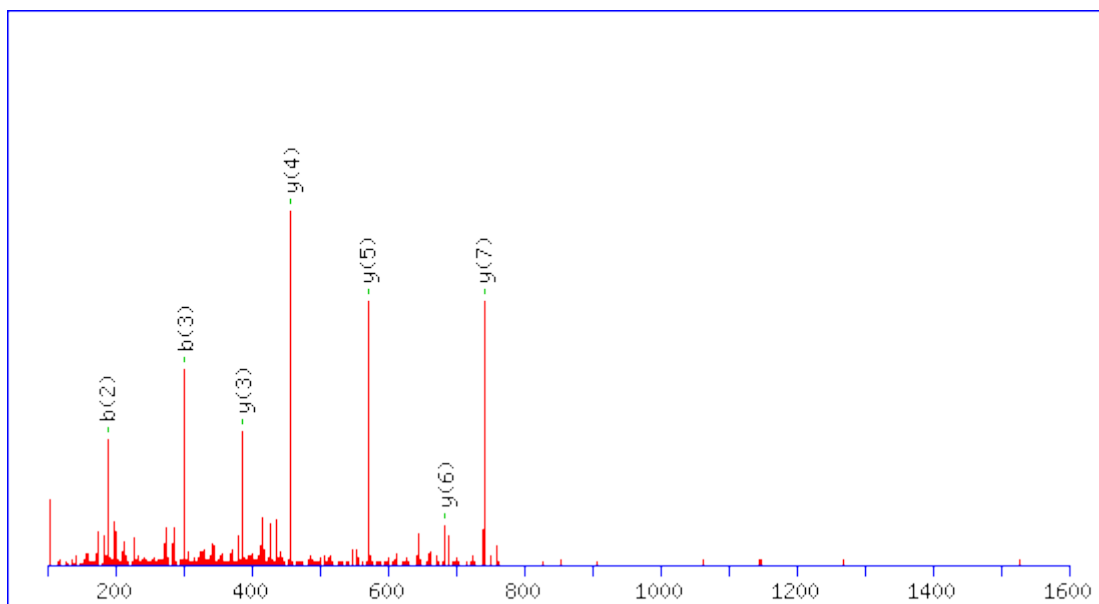
Monoisotopic mass of neutral peptide Mr(calc): 1002.5134

Ions Score: 40 Expect: 0.02

Matches (**Bold Red**): 23/78 fragment ions using 77 most intense peaks

MS/MS Fragmentation of **MGLLAVLR**

Found in **AGM1_HUMAN**, Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1



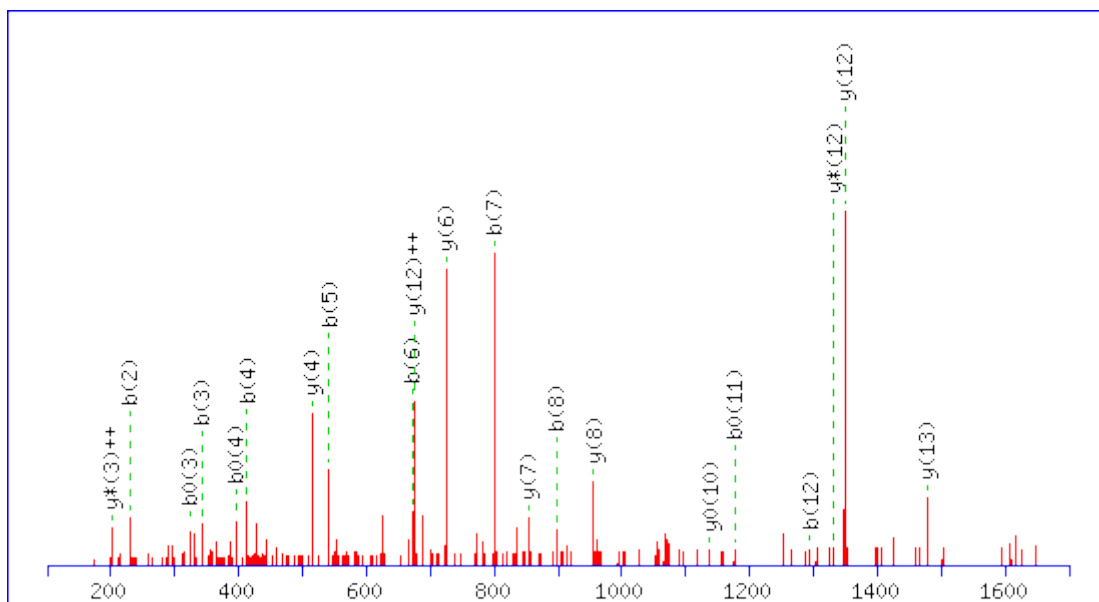
Monoisotopic mass of neutral peptide Mr(calc): 871.5313

Ions Score: 54 Expect: 0.00089

Matches (Bold Red): 7/42 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **EVI~~A~~EEEEPPPTVTEPLPENR**

Found in **AKA12_HUMAN**, A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=4



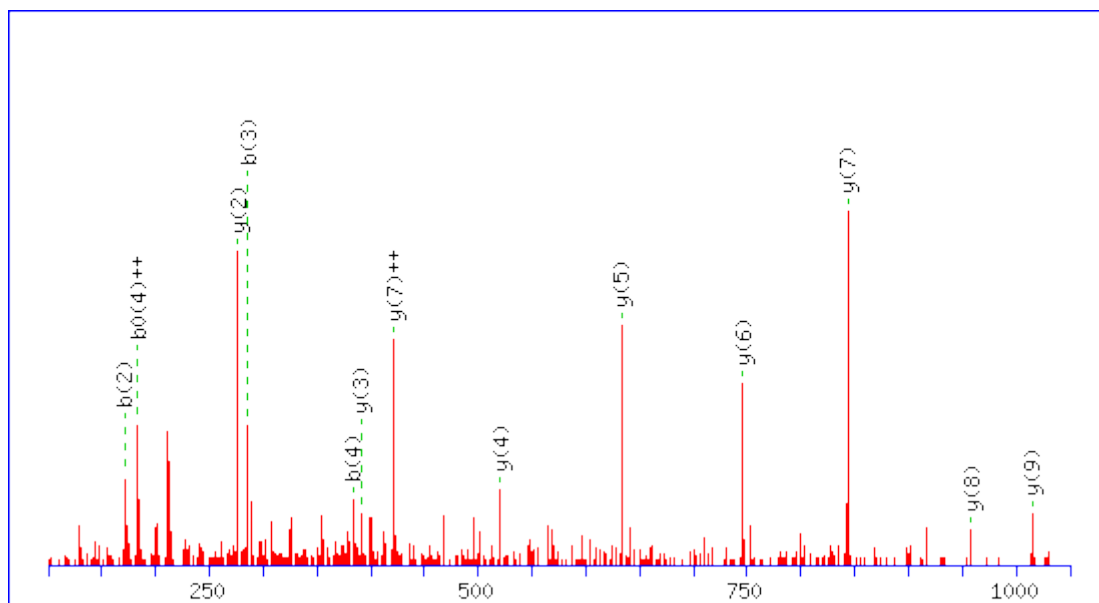
Monoisotopic mass of neutral peptide Mr(calc): 2148.0586

Ions Score: 50 Expect: 0.004

Matches (Bold Red): 21/178 fragment ions using 42 most intense peaks

MS/MS Fragmentation of **IGDPLLEDTR**

Found in **AL9A1_HUMAN**, 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3



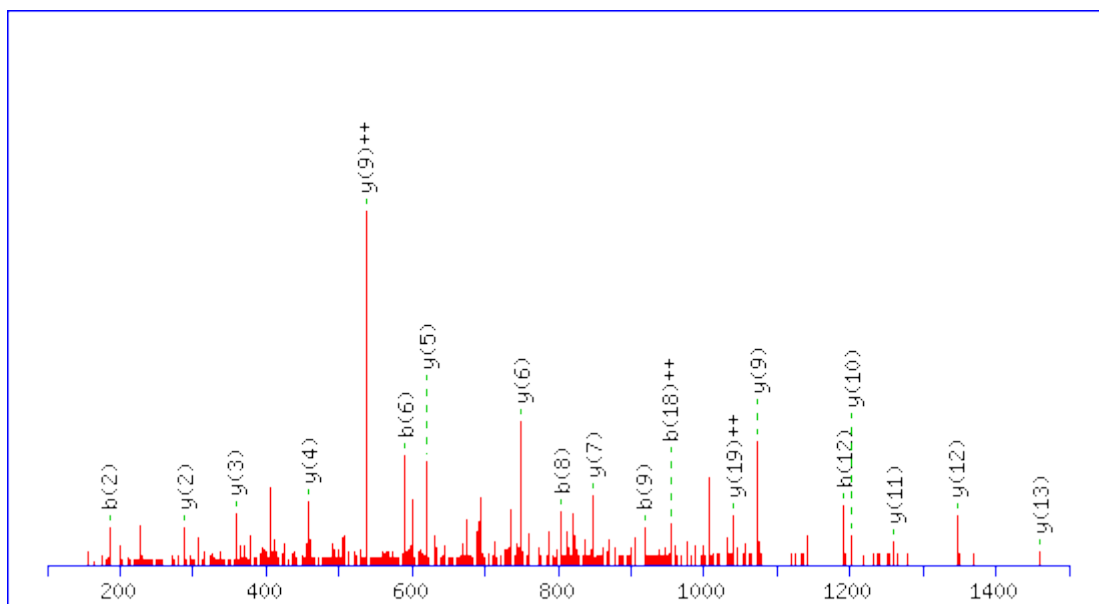
Monoisotopic mass of neutral peptide Mr(calc): 1127.5822

Ions Score: 61 **Expect:** 0.00016

Matches (Bold Red): 13/84 fragment ions using 20 most intense peaks

MS/MS Fragmentation of **LAPPLVTLLSGEPEVQYVALR**

Found in **AP2B1_HUMAN**, AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1



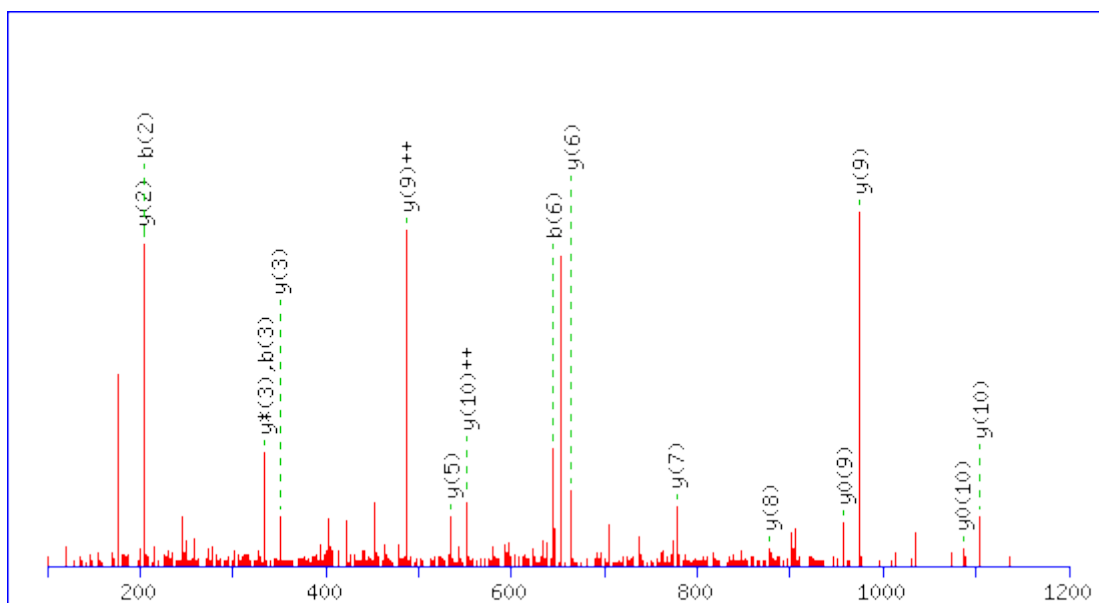
Monoisotopic mass of neutral peptide Mr(calc): 2264.2780

Ions Score: 80 Expect: 3.6e-006

Matches (Bold Red): 19/184 fragment ions using 26 most intense peaks

MS/MS Fragmentation of **GFEPTLEALFGK**

Found in **APOB_HUMAN**, Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2



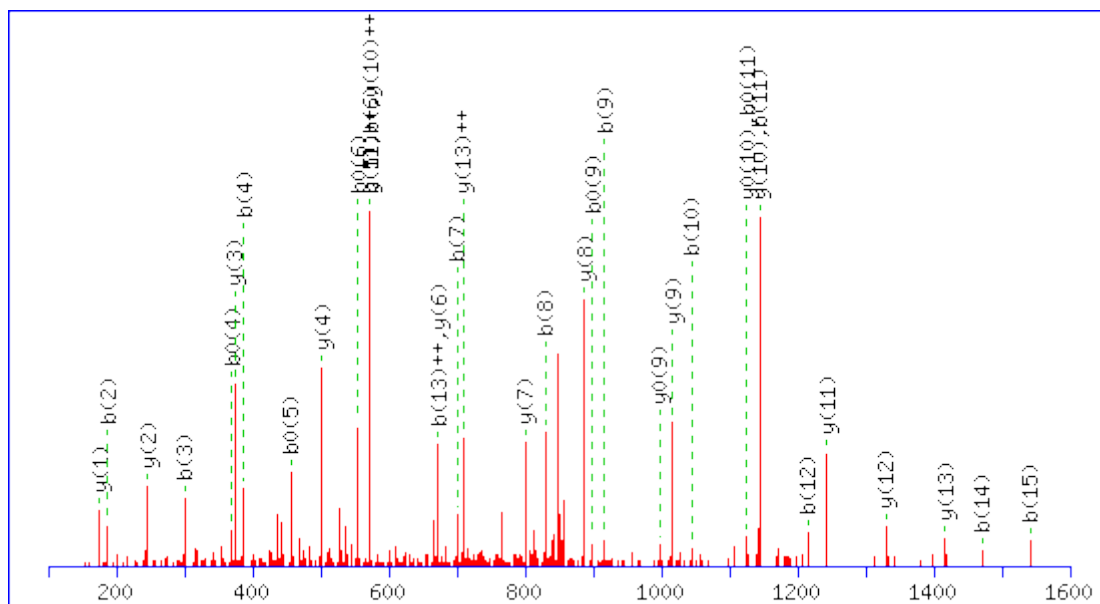
Monoisotopic mass of neutral peptide Mr(calc): 1307.6761

Ions Score: 45 Expect: 0.0081

Matches (**Bold Red**): 16/96 fragment ions using 36 most intense peaks

MS/MS Fragmentation of **DALSSVQESQVAQQAR**

Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1



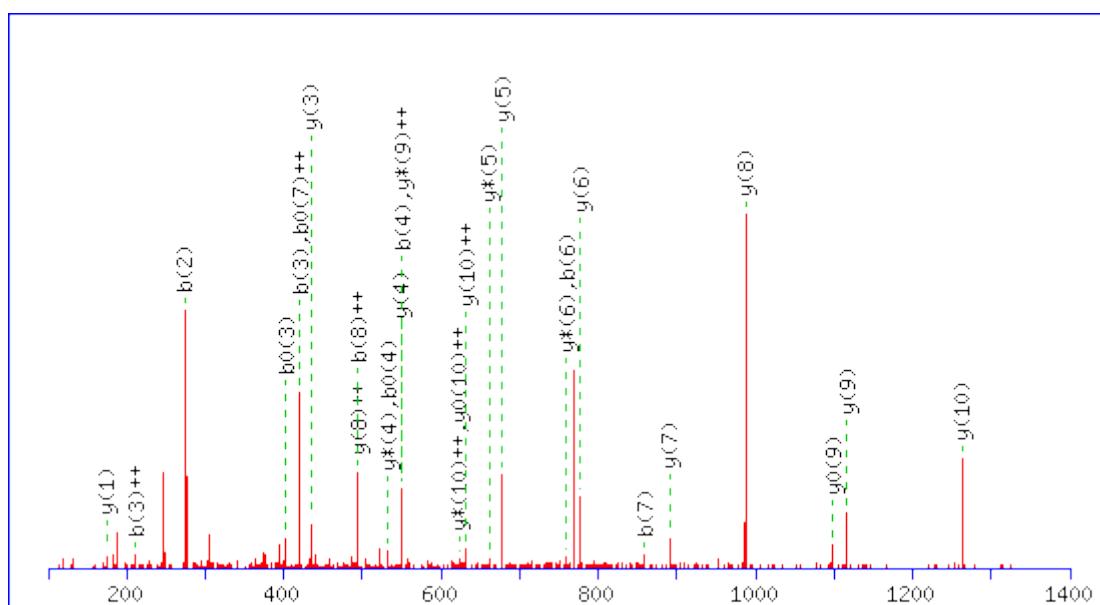
Monoisotopic mass of neutral peptide Mr(calc): 1715.8438

Ions Score: 109 Expect: 3.8e-009

Matches (**Bold Red**): 36/154 fragment ions using 48 most intense peaks

MS/MS Fragmentation of **SWFEPLVEDMQR**

Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1



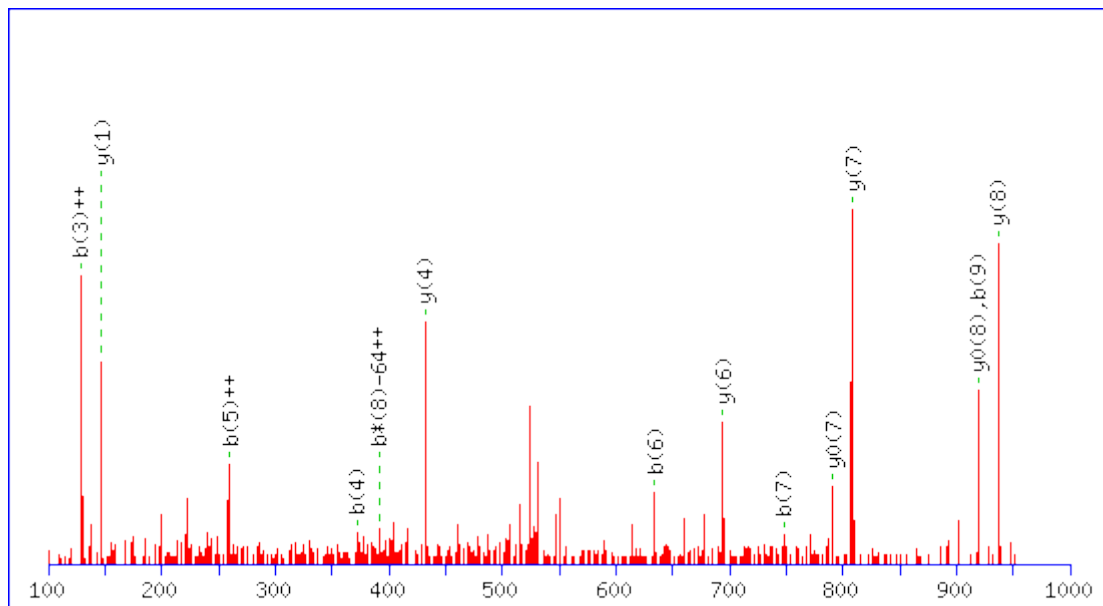
Monoisotopic mass of neutral peptide Mr(calc): 1535.7079

Ions Score: 49 Expect: 0.0024

Matches (Bold Red): 28/106 fragment ions using 55 most intense peaks

MS/MS Fragmentation of **GAQDMDNNGK**

Found in **ARI4B_HUMAN**, AT-rich interactive domain-containing protein 4B OS=Homo sapiens GN=ARID4B PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1064.4193

Variable modifications:

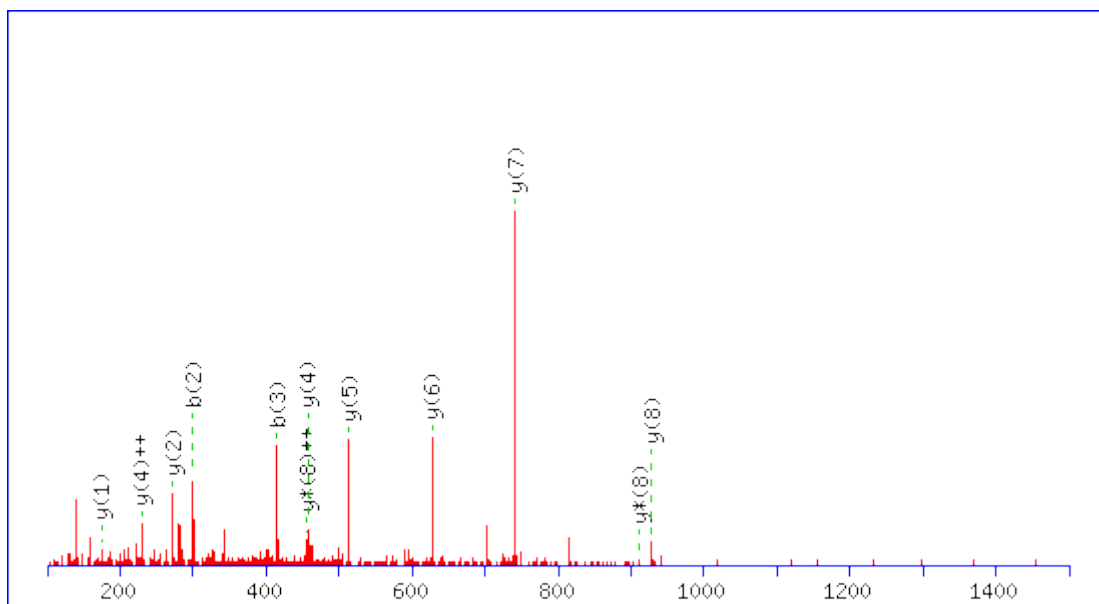
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 40 Expect: 0.018

Matches (Bold Red): 15/144 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **LWDIGGQPR**

Found in **ARL8A_HUMAN**, ADP-ribosylation factor-like protein 8A OS=Homo sapiens GN=ARL8A PE=1 SV=1



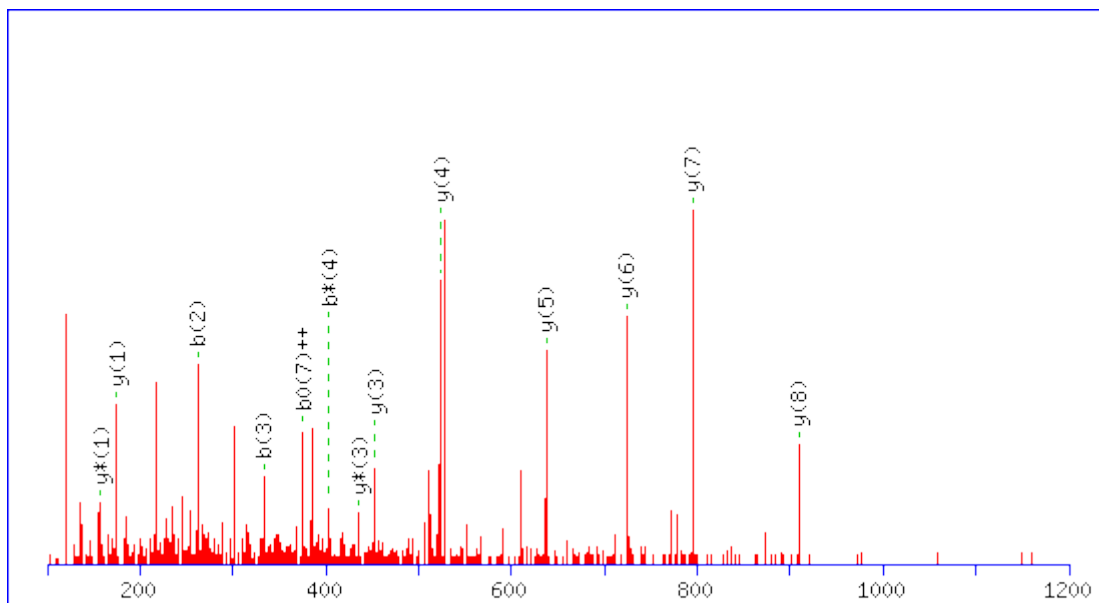
Monoisotopic mass of neutral peptide Mr(calc): 1040.5403

Ions Score: 38 Expect: 0.03

Matches (Bold Red): 12/68 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **FNASIAYDR**

Found in **ARLY_HUMAN**, Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4



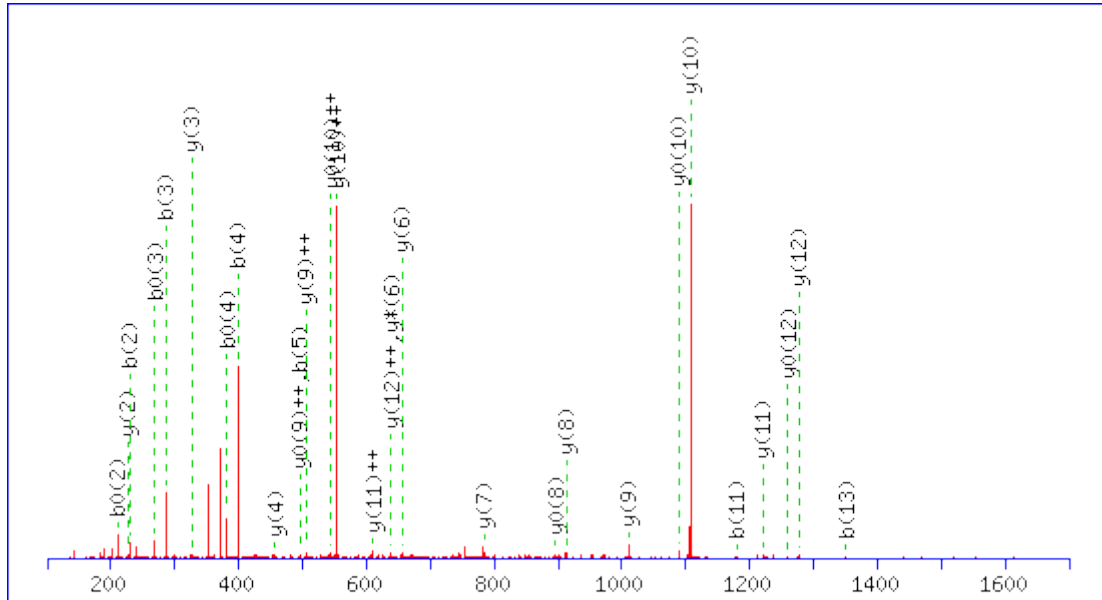
Monoisotopic mass of neutral peptide Mr(calc): 1055.5036

Ions Score: 44 Expect: 0.0073

Matches (**Bold Red**): 13/86 fragment ions using 31 most intense peaks

MS/MS Fragmentation of **EVGIPPEQSLETAK**

Found in **ARP3B_HUMAN**, Actin-related protein 3B OS=Homo sapiens GN=ACTR3B PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1504.7864

Variable modifications:

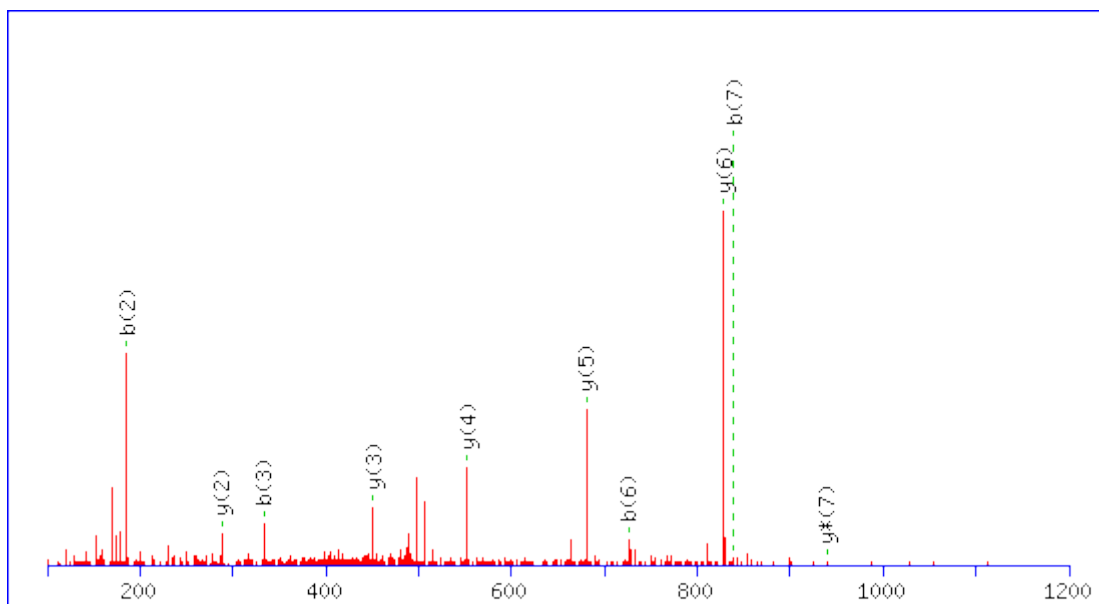
K14 : Label:13C(6)15N(2) (K)

Ions Score: 42 Expect: 0.021

Matches (**Bold Red**): 29/138 fragment ions using 90 most intense peaks

MS/MS Fragmentation of **GQFETYLK**

Found in **ASAHI_HUMAN**, Acid ceramidase OS=Homo sapiens GN=ASAHI PE=1 SV=5



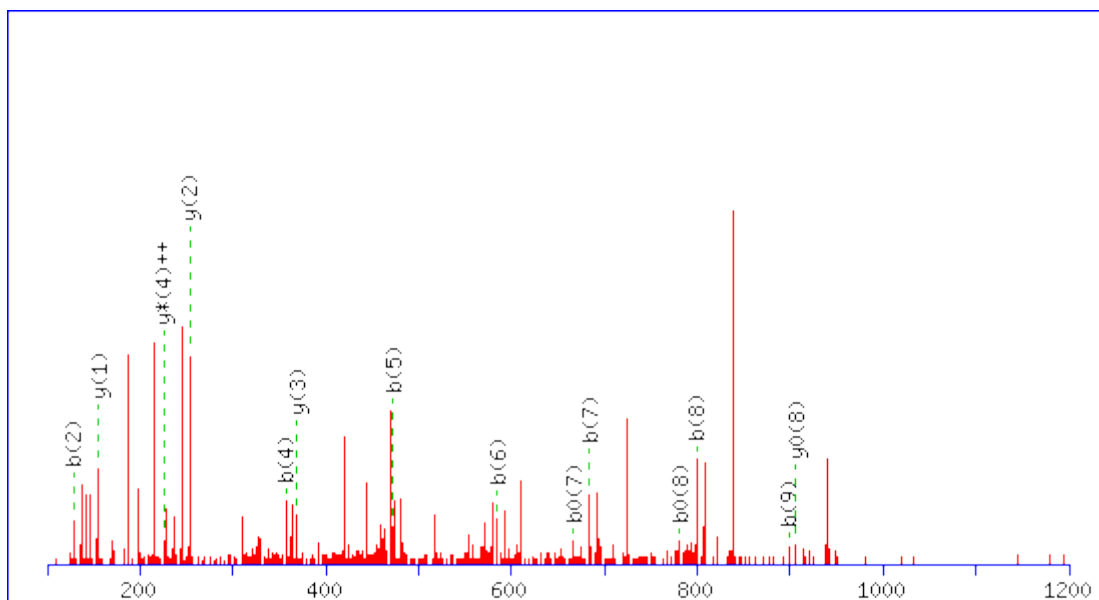
Monoisotopic mass of neutral peptide Mr(calc): 1012.4978

Ions Score: 38 Expect: 0.028

Matches (Bold Red): 10/70 fragment ions using 21 most intense peaks

MS/MS Fragmentation of **GAEVDLVDVK**

Found in **ASB1_HUMAN**, Ankyrin repeat and SOCS box protein 1 OS=Homo sapiens GN=ASB1
PE=1 SV=1



Variable modifications:

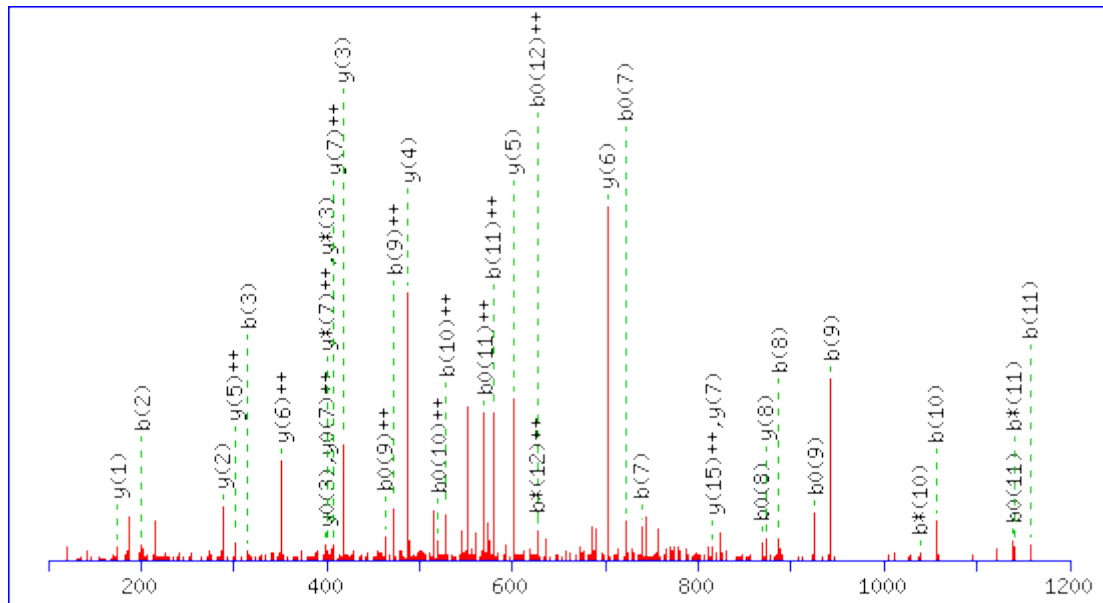
K10 : Label:13C(6)15N(2) (K)

Ions Score: 16 Expect: 4.7

Matches (**Bold Red**): 14/82 fragment ions using 68 most intense peaks

MS/MS Fragmentation of **EANHDGDFGITLAELR**

Found in **AT2B1_HUMAN**, Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1 PE=1 SV=3



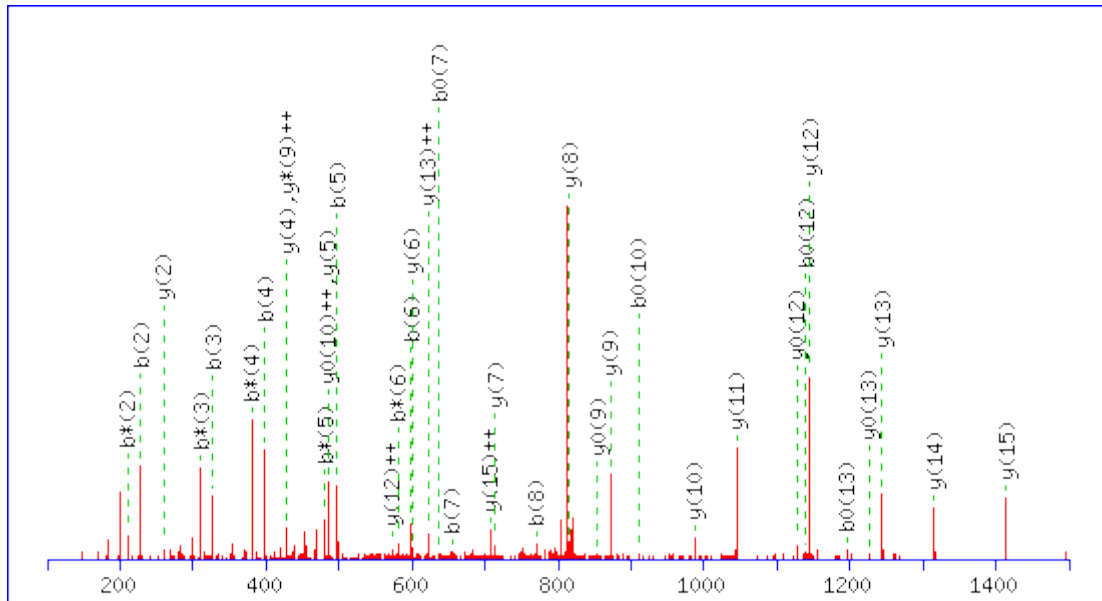
Monoisotopic mass of neutral peptide Mr(calc): 1756.8380

Ions Score: 46 Expect: 0.0077

Matches (**Bold Red**): 37/172 fragment ions using 66 most intense peaks

MS/MS Fragmentation of **QVVAVTGDGTNDGPALK**

Found in **AT2B3_HUMAN**, Plasma membrane calcium-transporting ATPase 3 OS=Homo sapiens GN=ATP2B3 PE=1 SV=3



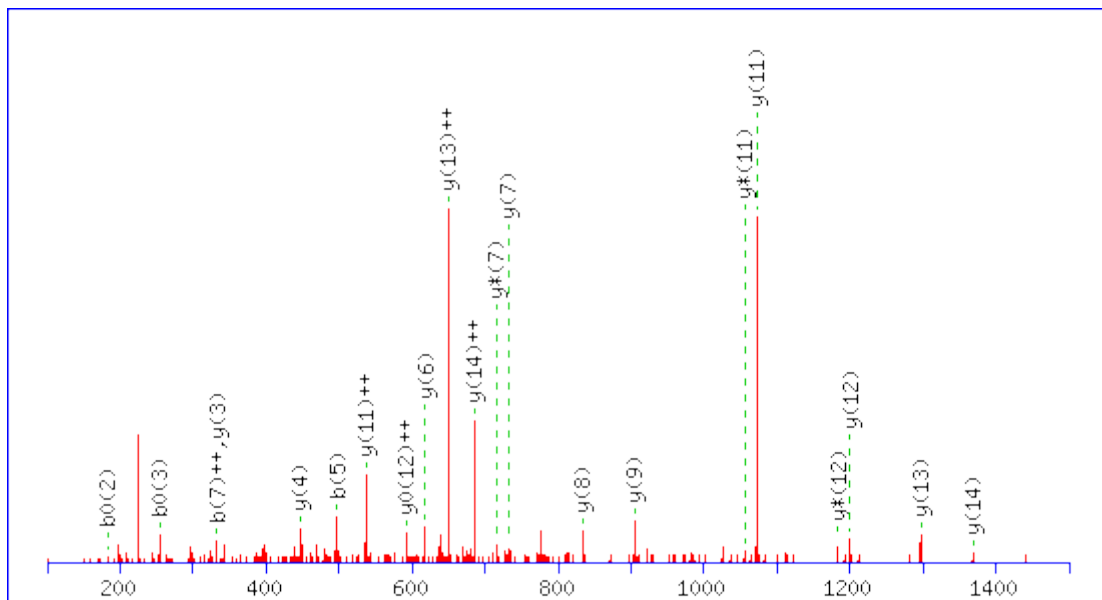
Monoisotopic mass of neutral peptide Mr(calc): 1640.8370

Ions Score: 80 Expect: 3.4e-006

Matches (Bold Red): 37/172 fragment ions using 82 most intense peaks

MS/MS Fragmentation of **VTAPQPAATNGDLASR**

Found in **AT2C1_HUMAN**, Calcium-transporting ATPase type 2C member 1 OS=Homo sapiens GN=ATP2C1 PE=1 SV=3

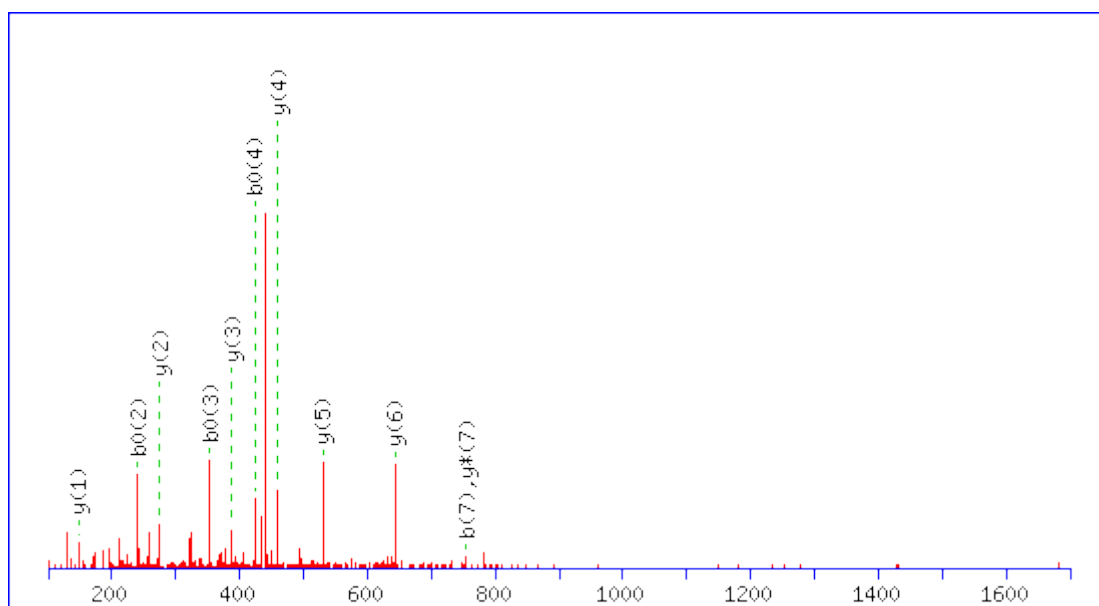


Ions Score: 55 Expect: 0.00093

Matches (Bold Red): 21/168 fragment ions using 46 most intense peaks

MS/MS Fragmentation of **EQLAALKK**

Found in **ATIF1_HUMAN**, ATPase inhibitor, mitochondrial OS=Homo sapiens GN=ATPIF1
PE=1 SV=1



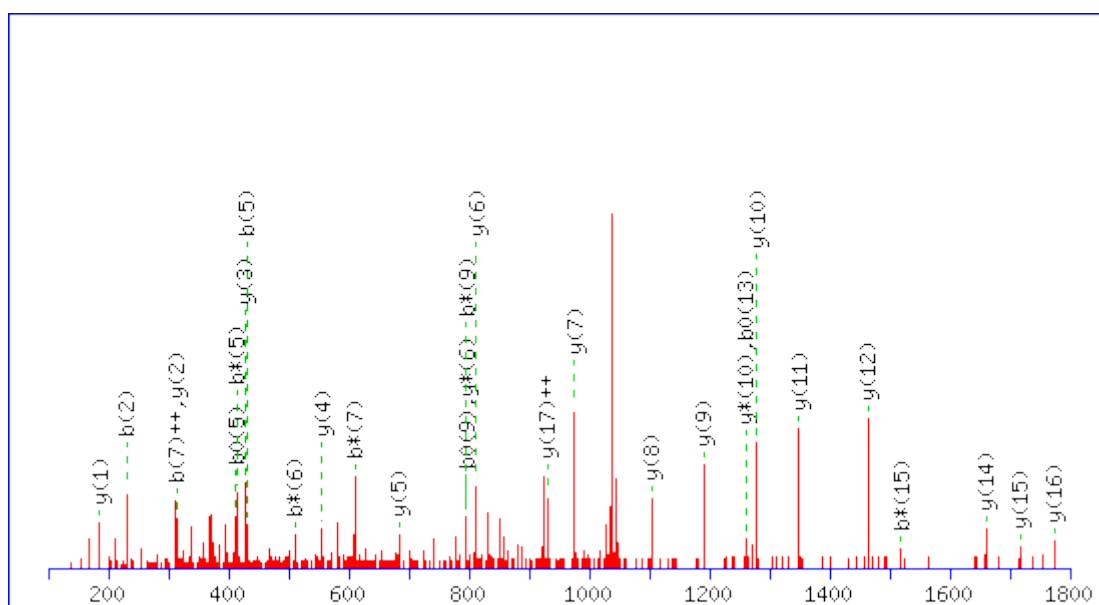
Monoisotopic mass of neutral peptide Mr(calc): 899.5440

Ions Score: 41 Expect: 0.017

Matches (Bold Red): 11/68 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **QTSGGPVDASSEYQQELER**

Found in **ATP5J_HUMAN**, ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 2089.9428

Variable modifications:

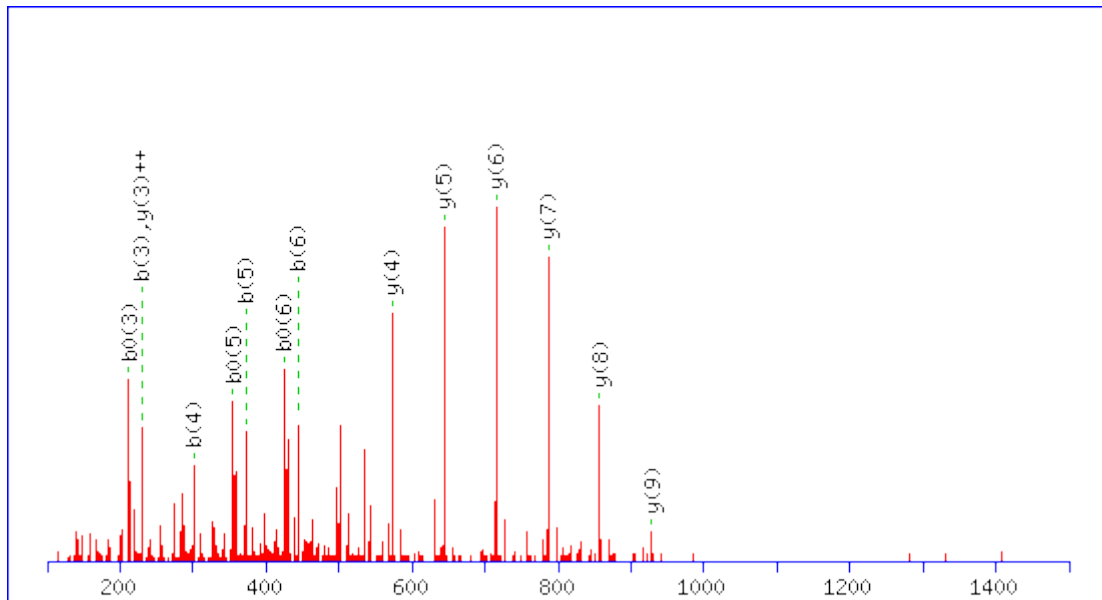
R19 : Label:13C(6)15N(4) (R)

Ions Score: 94 **Expect:** 1.3e-007

Matches (Bold Red): 29/212 fragment ions using 46 most intense peaks

MS/MS Fragmentation of **SAAAAAANRKR**

Found in **ATP9B_HUMAN**, Probable phospholipid-transporting ATPase IIB OS=Homo sapiens GN=ATP9B PE=2 SV=4



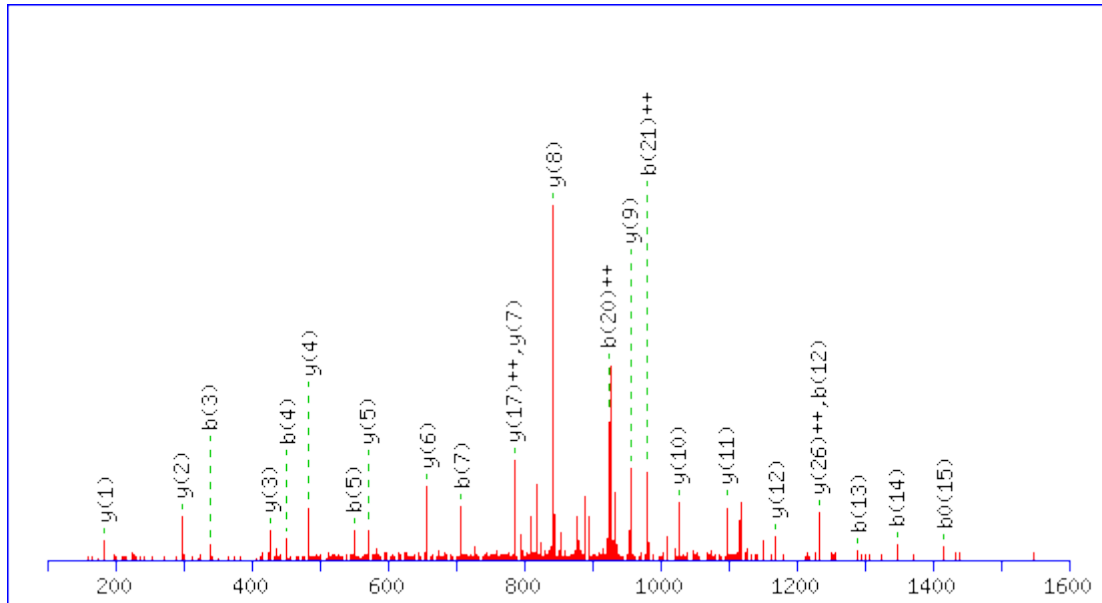
Monoisotopic mass of neutral peptide Mr(calc): 1085.6053

Ions Score: 48 **Expect:** 0.004

Matches (Bold Red): 14/86 fragment ions using 20 most intense peaks

MS/MS Fragmentation of **LPQLVGVSTPLQGGSNSAAAIGQSSGELR**

Found in **B4GT1_HUMAN**, Beta-1,4-galactosyltransferase 1 OS=Homo sapiens GN=B4GALT1 PE=1 SV=5



Monoisotopic mass of neutral peptide Mr(calc): 2803.4704

Variable modifications:

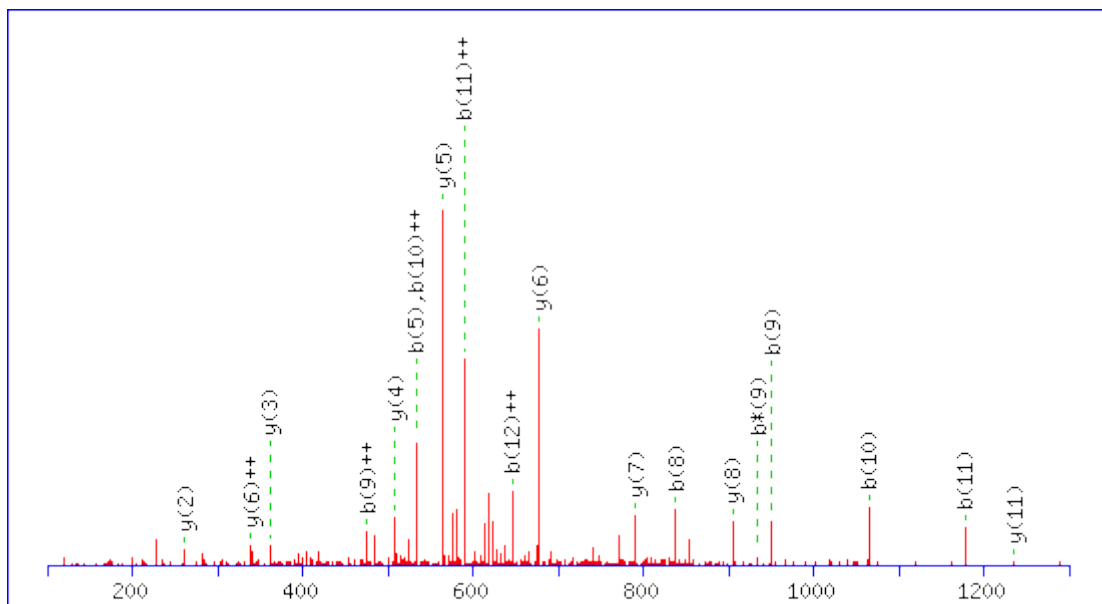
R29 : Label:13C(6)15N(4) (R)

Ions Score: 89 Expect: 5.4e-007

Matches (Bold Red): 24/314 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **NPHPSSAFLNLIGFVSR**

Found in **BIEA_HUMAN**, Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2



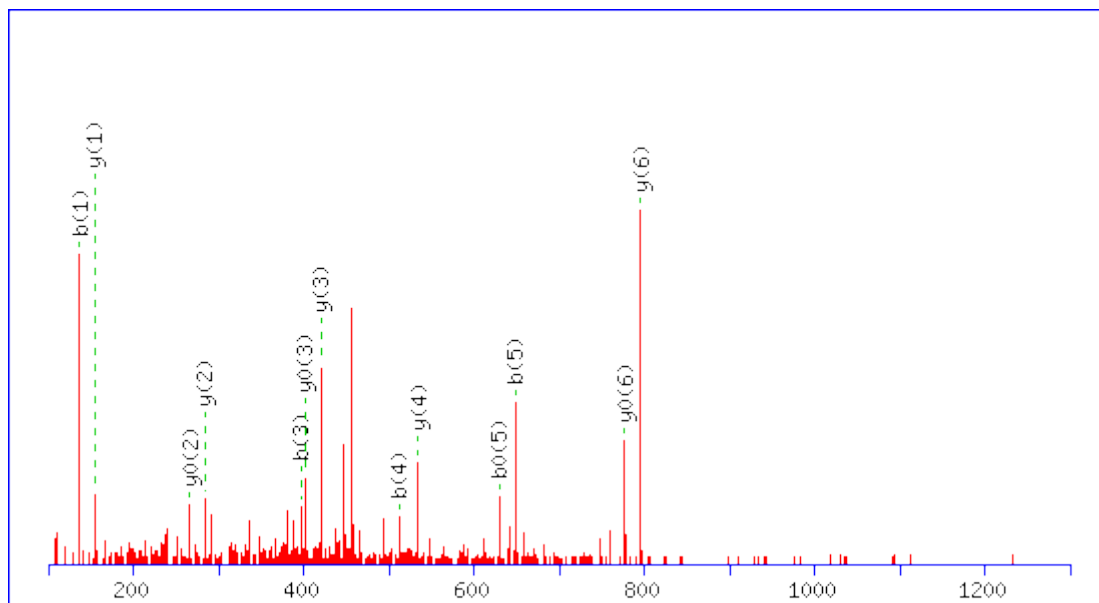
Monoisotopic mass of neutral peptide Mr(calc): 1854.9741

Ions Score: 54 Expect: 0.0014

Matches (Bold Red): 19/182 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **KMEDKEK**

Found in **BIN2_HUMAN**, Bridging integrator 2 OS=Homo sapiens GN=BIN2 PE=1 SV=3



Variable modifications:

K1 : Label:13C(6)15N(2) (K)

K5 : Label:13C(6)15N(2) (K)

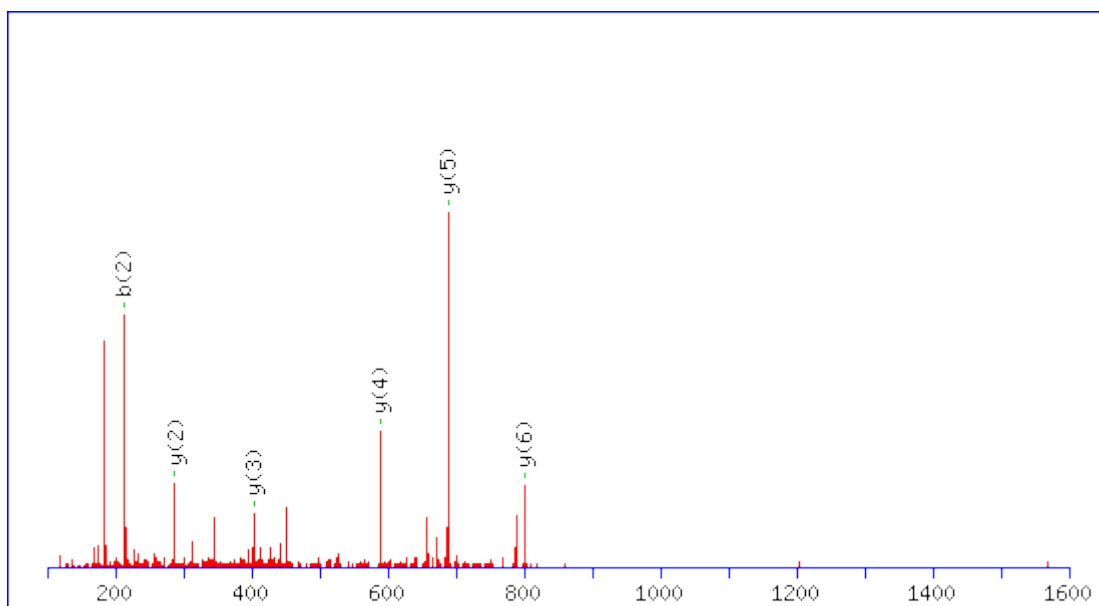
K7 : Label:13C(6)15N(2) (K)

Ions Score: 40 Expect: 0.017

Matches (Bold Red): 14/66 fragment ions using 33 most intense peaks

MS/MS Fragmentation of **VLVWDLR**

Found in **BUB3_HUMAN**, Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1



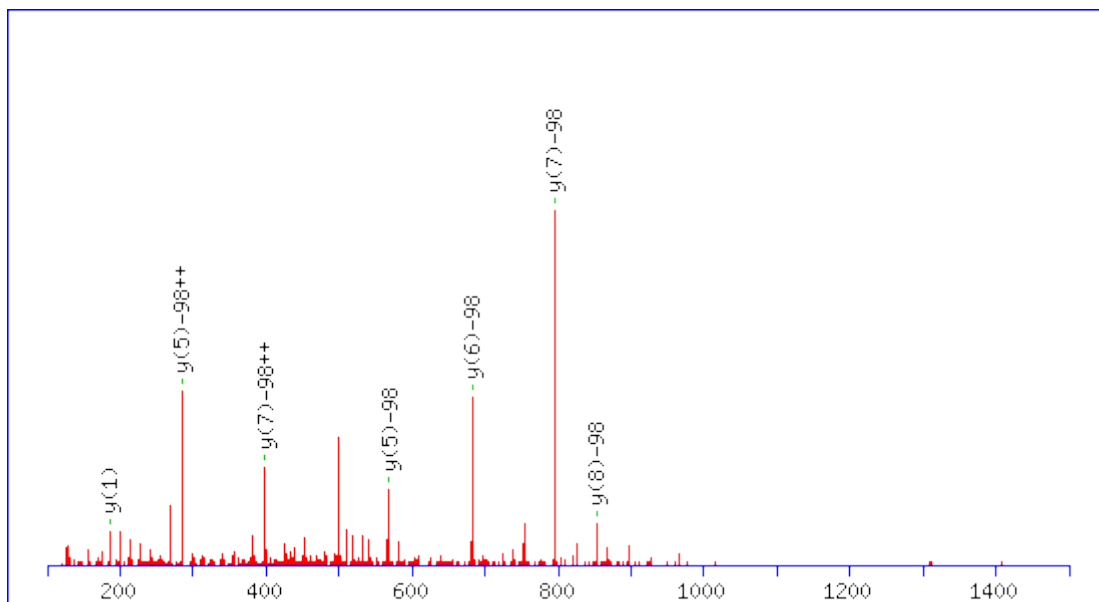
Monoisotopic mass of neutral peptide Mr(calc): 899.5229

Ions Score: 38 Expect: 0.03

Matches (Bold Red): 6/48 fragment ions using 11 most intense peaks

MS/MS Fragmentation of **EGILEESGR**

Found in **CCD38_HUMAN**, Coiled-coil domain-containing protein 38 OS=Homo sapiens
GN=CCDC38 PE=2 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1078.4571

Variable modifications:

S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

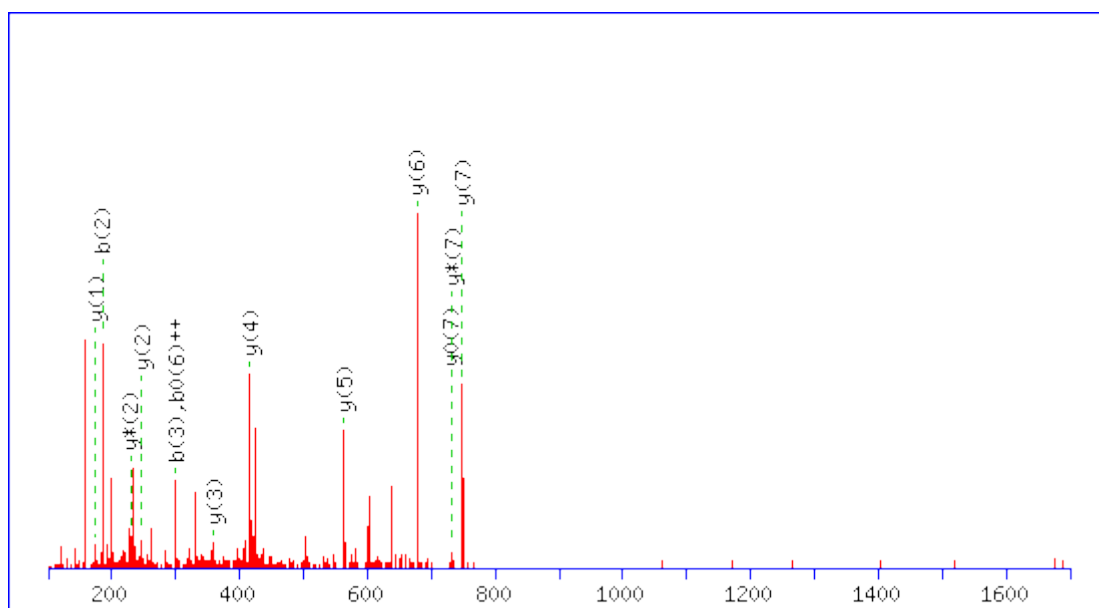
R9 : Label:13C(6)15N(4) (R)

Ions Score: 41 Expect: 0.019

Matches (Bold Red): 7/120 fragment ions using 13 most intense peaks

MS/MS Fragmentation of **LADFGLAR**

Found in **CDK5_HUMAN**, Cyclin-dependent kinase 5 OS=Homo sapiens GN=CDK5 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 861.4708

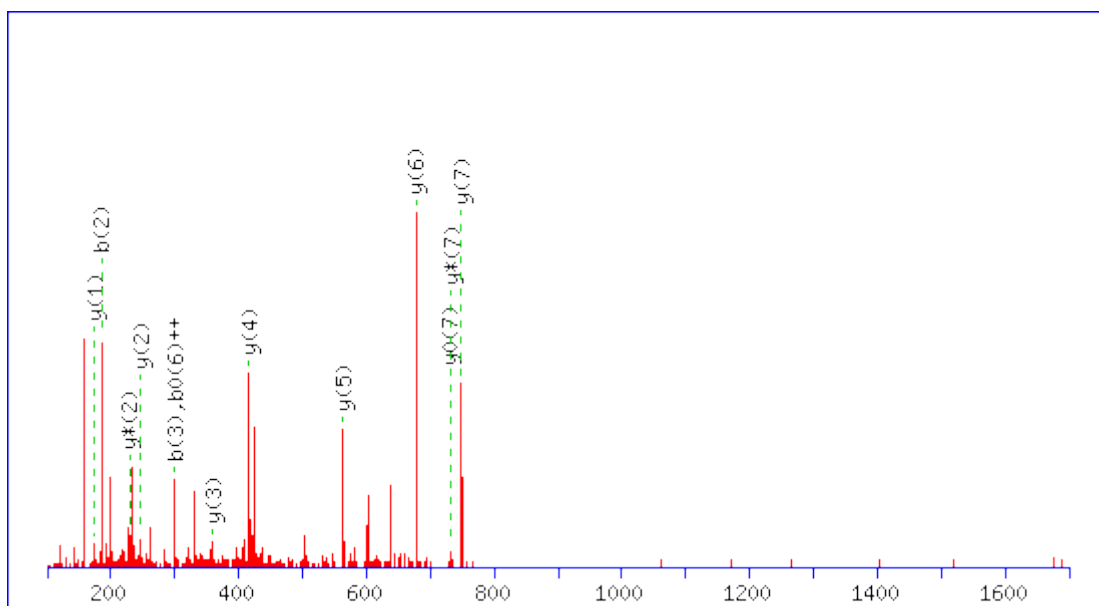
Ions Score: 37 Expect: 0.039

Matches (Bold Red): 13/56 fragment ions using 43 most intense peaks

MS/MS Fragmentation of **LADFGLAR**

Found in **CDK12_HUMAN**, Cyclin-dependent kinase 12 OS=Homo sapiens GN=CDK12 PE=1 SV=2

M



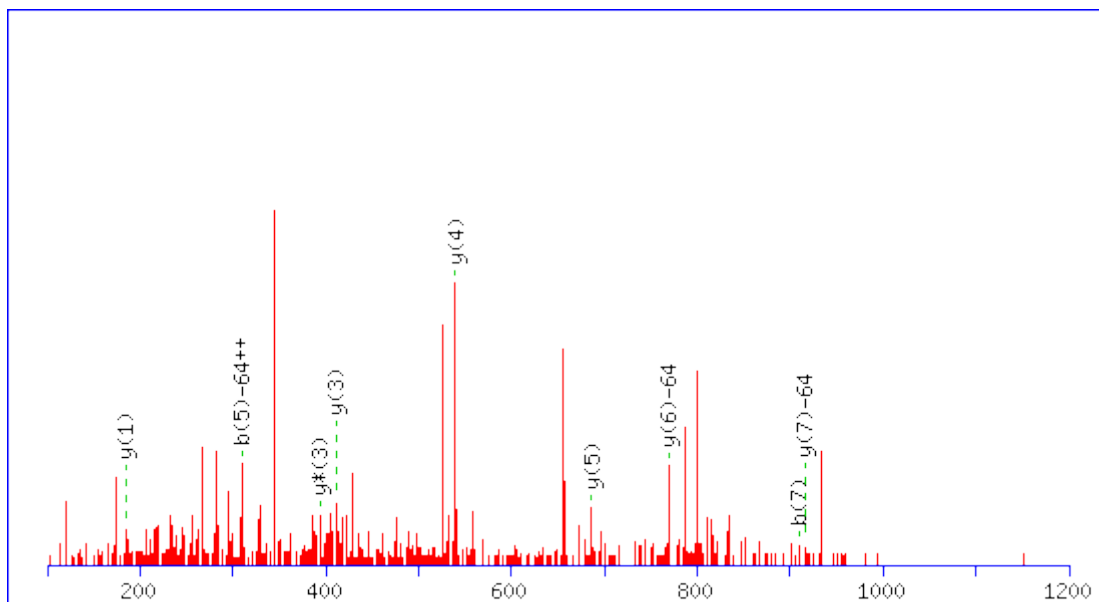
monoisotopic mass of neutral peptide Mr(calc): 861.4708

Ions Score: 37 Expect: 0.039

Matches (**Bold Red**): 13/56 fragment ions using 43 most intense peaks

MS/MS Fragmentation of **IFMFQLLR**

Found in **CDK18_HUMAN**, Cyclin-dependent kinase 18 OS=Homo sapiens GN=CDK18 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1092.6029

Variable modifications:

M3 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000

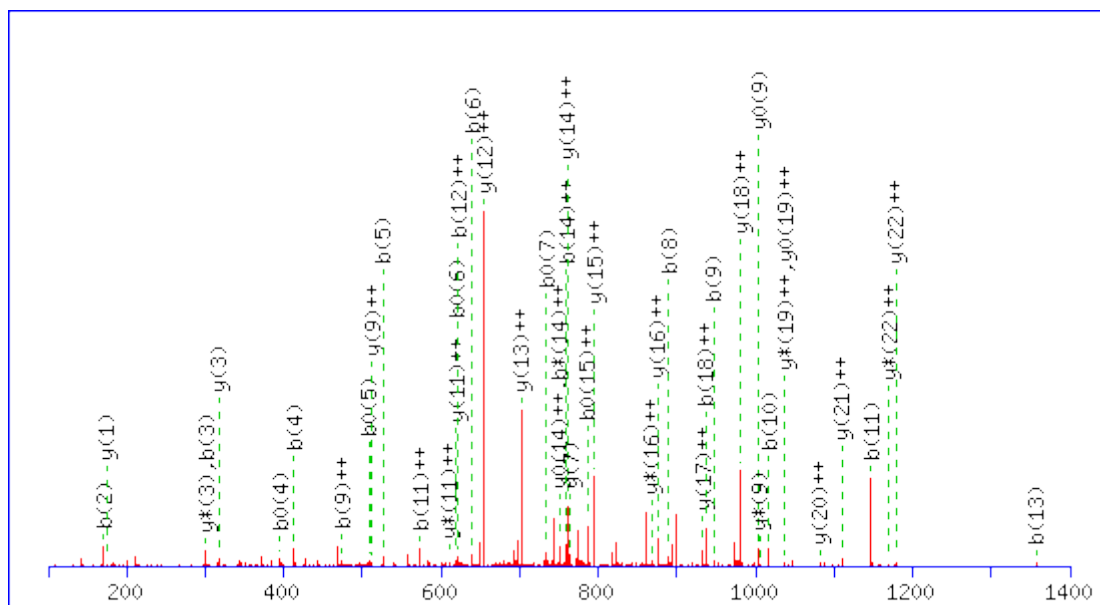
R8 : Label:13C(6)15N(4) (R)

Ions Score: 9 Expect: 27

Matches (Bold Red): 9/72 fragment ions using 44 most intense peaks

MS/MS Fragmentation of **VAELLLLHGAEPNCADPATLTRPVHDAAR**

Found in **CDN2B_HUMAN**, Cyclin-dependent kinase 4 inhibitor B OS=Homo sapiens
GN=CDKN2B PE=1 SV=1



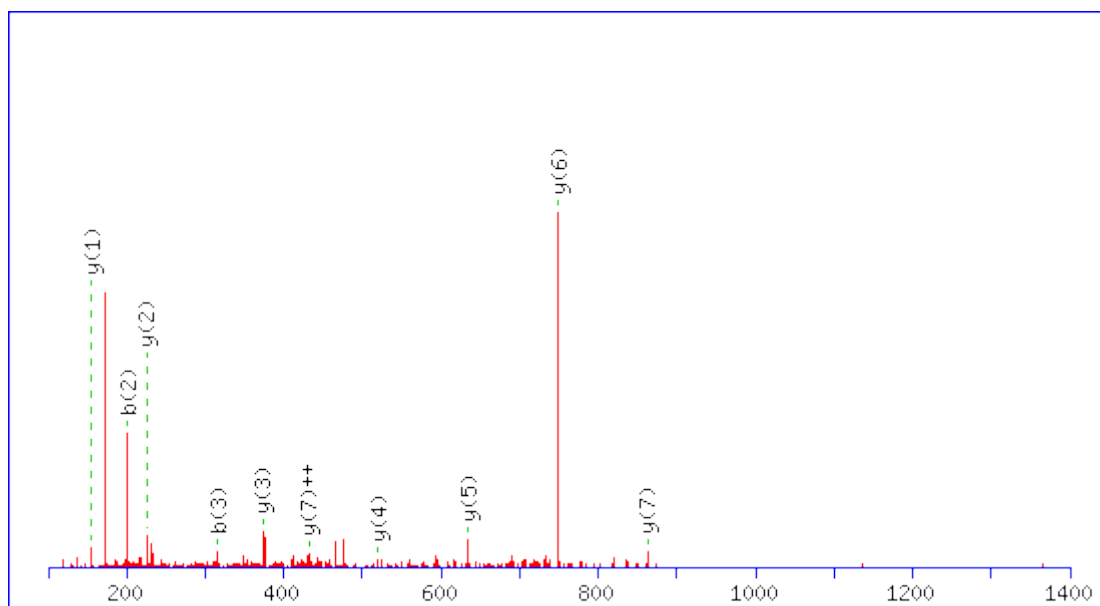
Monoisotopic mass of neutral peptide Mr(calc): 3106.5982

Ions Score: 42 Expect: 0.034

Matches (Bold Red): 45/302 fragment ions using 107 most intense peaks

MS/MS Fragmentation of **SLDNFFAK**

Found in **CDV3_HUMAN**, Protein CDV3 homolog OS=Homo sapiens GN=CDV3 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 948.4796

Variable modifications:

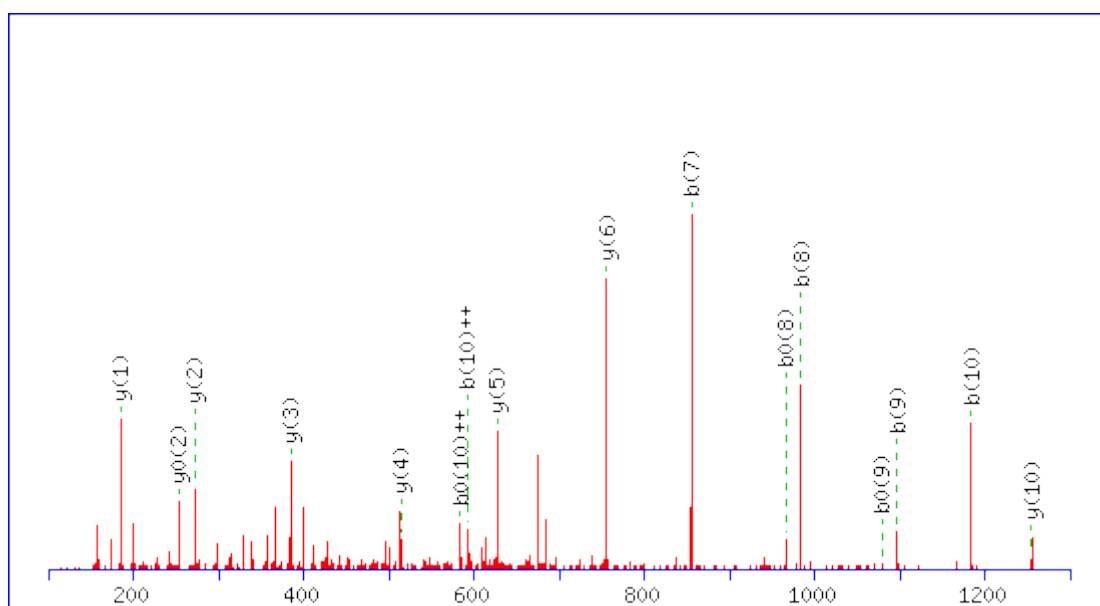
K8 : Label:¹³C(6)¹⁵N(2) (K)

Ions Score: 43 **Expect: 0.0088**

Matches (Bold Red): 10/68 fragment ions using 26 most intense peaks

MS/MS Fragmentation of **NQLEQELELSR**

Found in **CE128_HUMAN**, Centrosomal protein of 128 kDa OS=Homo sapiens GN=CEP128
PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1367.6920

Variable modifications:

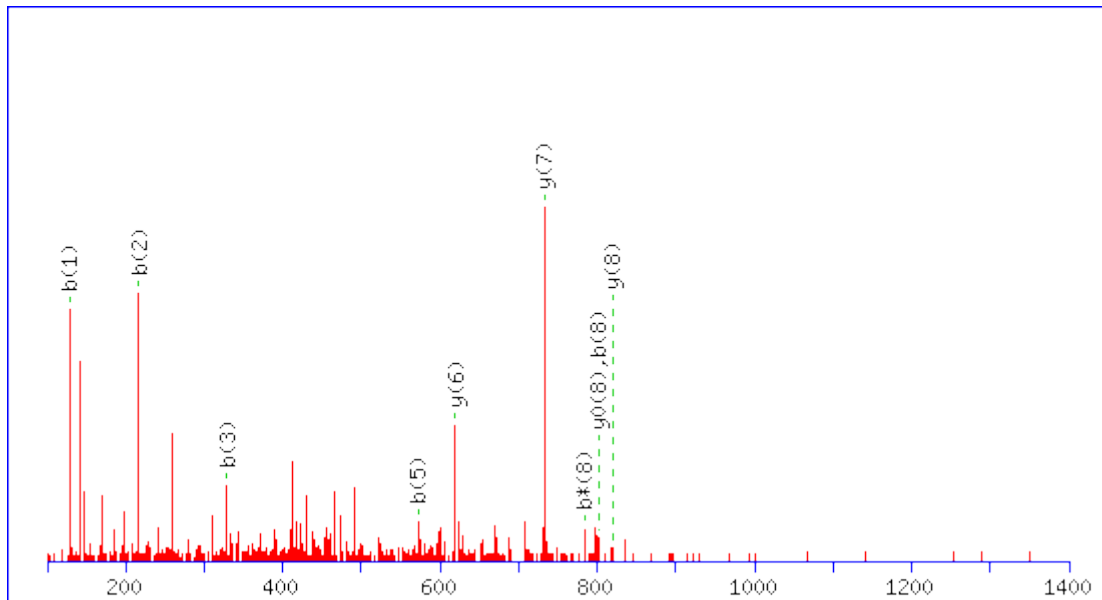
R11 : Label:13C(6)15N(4) (R)

Ions Score: 49 Expect: 0.0035

Matches (Bold Red): 16/112 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **QSIDKTAGK**

Found in **CE170_HUMAN**, Centrosomal protein of 170 kDa OS=Homo sapiens GN=CEP170
PE=1 SV=1



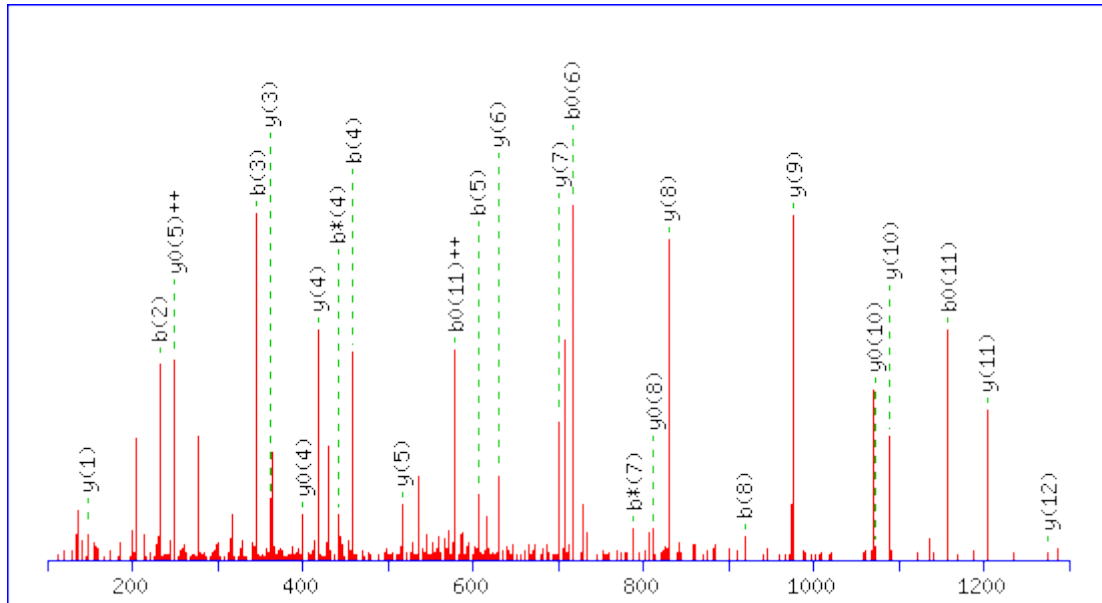
Monoisotopic mass of neutral peptide Mr(calc): 946.5083

Ions Score: 41 Expect: 0.015

Matches (Bold Red): 10/88 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **CANLFEALVGTLK**

Found in **CF115_HUMAN**, Costars family protein C6orf115 OS=Homo sapiens
GN=C6orf115 PE=1 SV=1



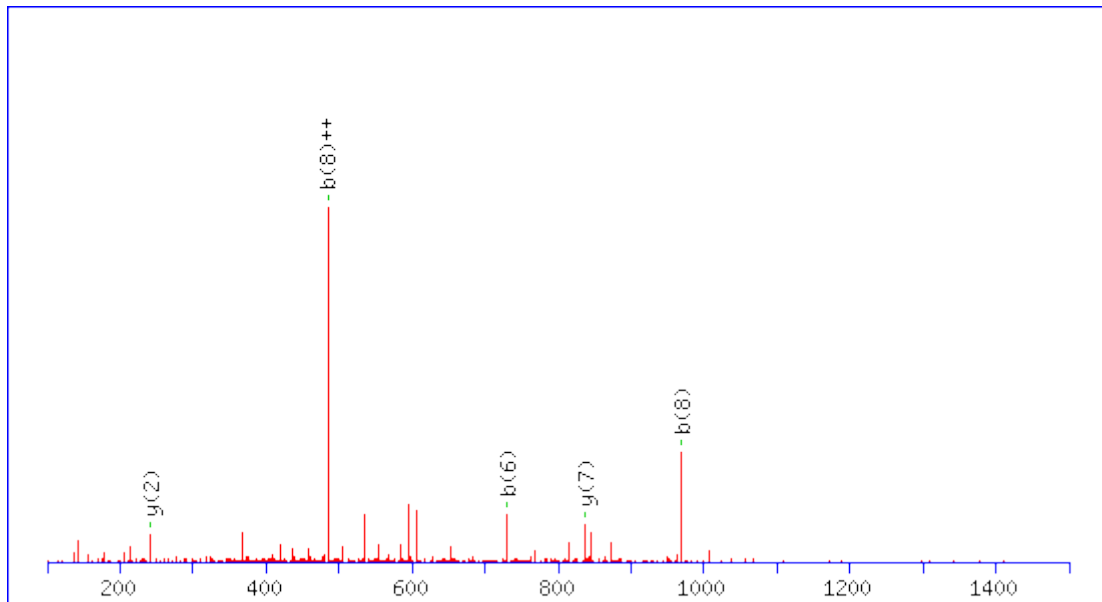
Monoisotopic mass of neutral peptide Mr(calc): 1434.7541

Ions Score: 67 Expect: 6e-005

Matches (Bold Red): 25/126 fragment ions using 60 most intense peaks

MS/MS Fragmentation of **YIPFLPGTGR**

Found in **CGNL1_HUMAN**, Cingulin-like protein 1 OS=Homo sapiens GN=CGNL1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1209.5823

Variable modifications:

T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

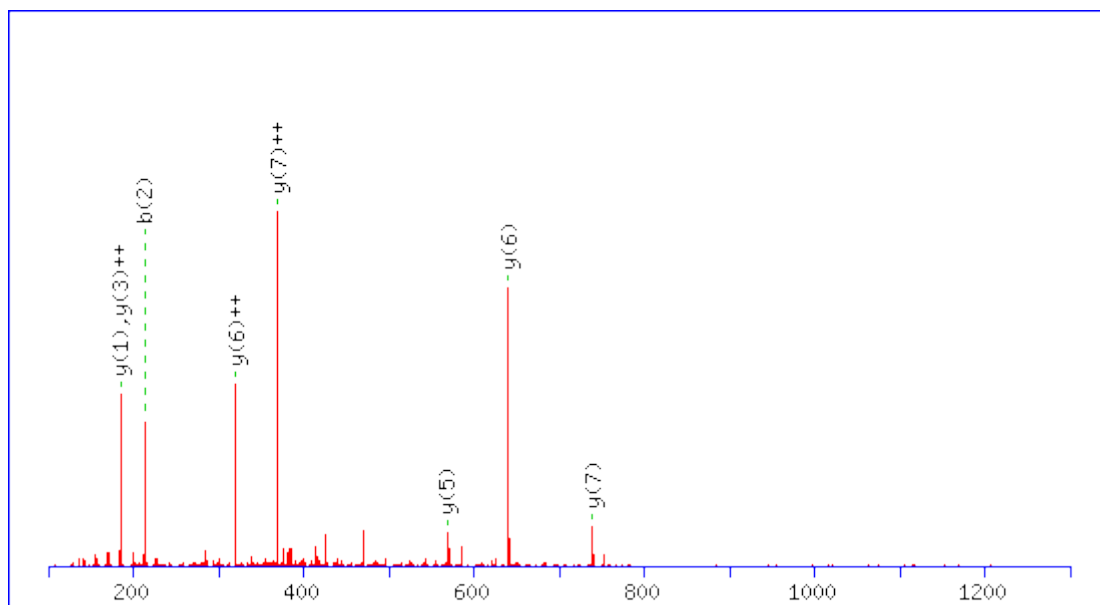
R10 : Label:13C(6)15N(4) (R)

Ions Score: 10 Expect: 24

Matches (Bold Red): 5/122 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **IVAEAIAR**

Found in **CHD8_HUMAN**, Chromodomain-helicase-DNA-binding protein 8 OS=Homo sapiens
GN=CHD8 PE=1 SV=5



Monoisotopic mass of neutral peptide Mr(calc): 851.5104

Variable modifications:

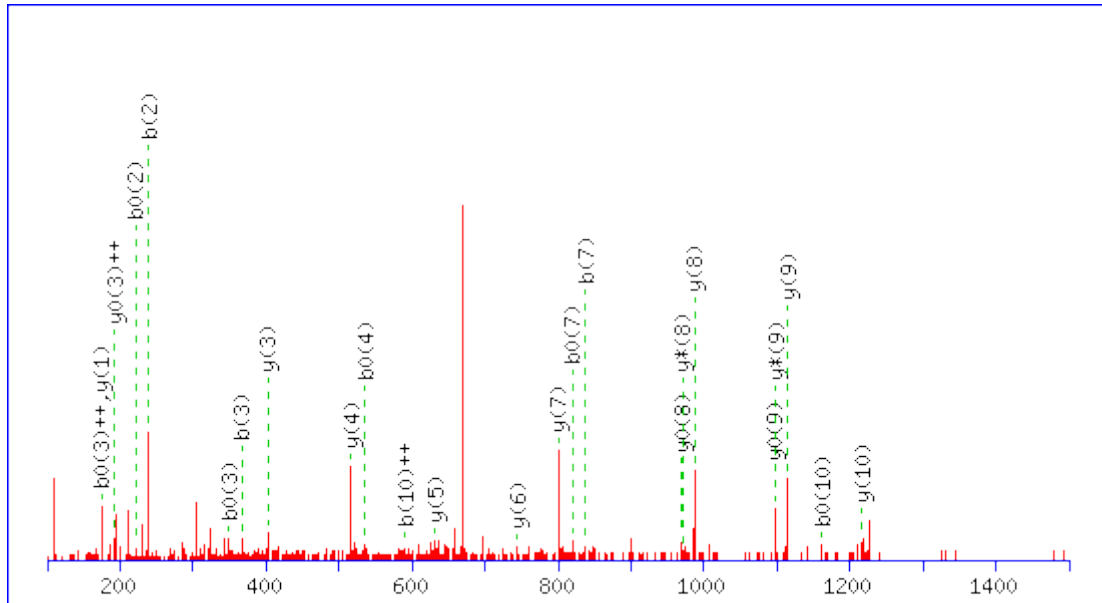
R8 : Label:13C(6)15N(4) (R)

Ions Score: 36 Expect: 0.043

Matches (Bold Red): 8/56 fragment ions using 8 most intense peaks

MS/MS Fragmentation of **HTQWGLDLLDR**

Found in **CIP4_HUMAN**, Cdc42-interacting protein 4 OS=Homo sapiens GN=TRIP10 PE=1
SV=3



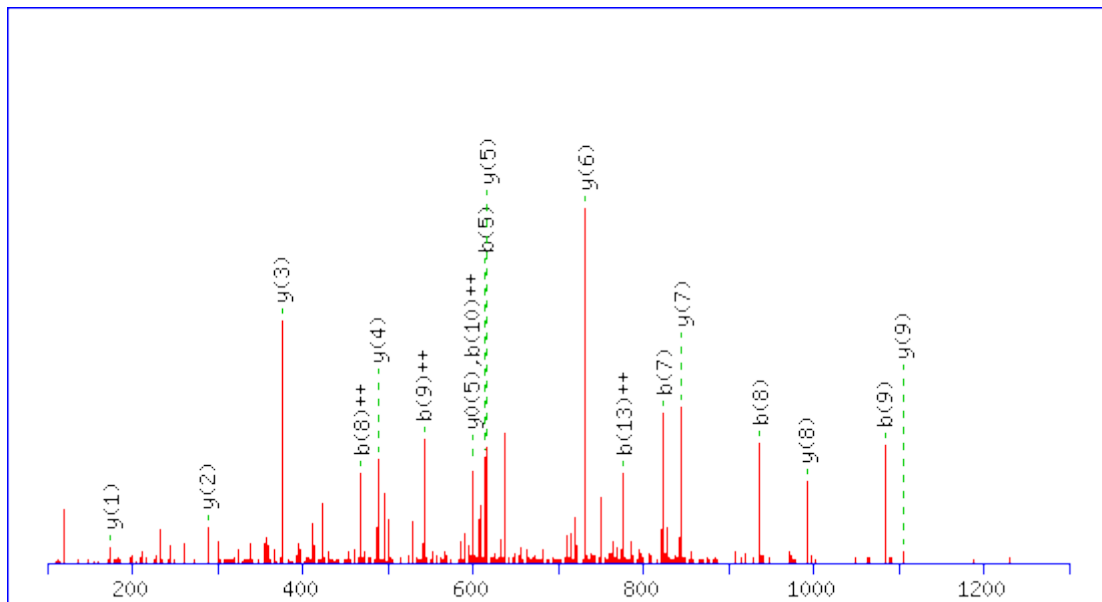
Monoisotopic mass of neutral peptide Mr(calc): 1352.6837

Ions Score: 40 Expect: 0.029

Matches (Bold Red): 24/112 fragment ions using 68 most intense peaks

MS/MS Fragmentation of **TVHYLPILFIDQLSNR**

Found in **CLP1L_HUMAN**, Cleft lip and palate transmembrane protein 1-like protein
OS=Homo sapiens GN=CLPTM1L PE=1 SV=1



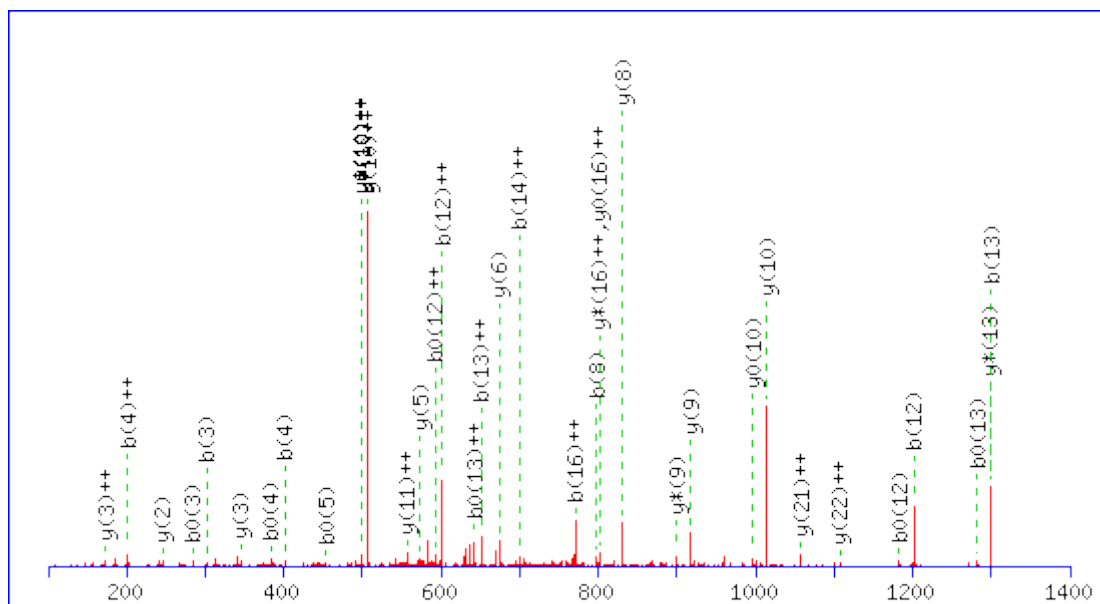
Monoisotopic mass of neutral peptide Mr(calc): 1928.0520

Ions Score: 68 Expect: 6.3e-005

Matches (**Bold Red**): 18/154 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **VTTVASHTSDSDVPSGVTEVVVK**

Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1



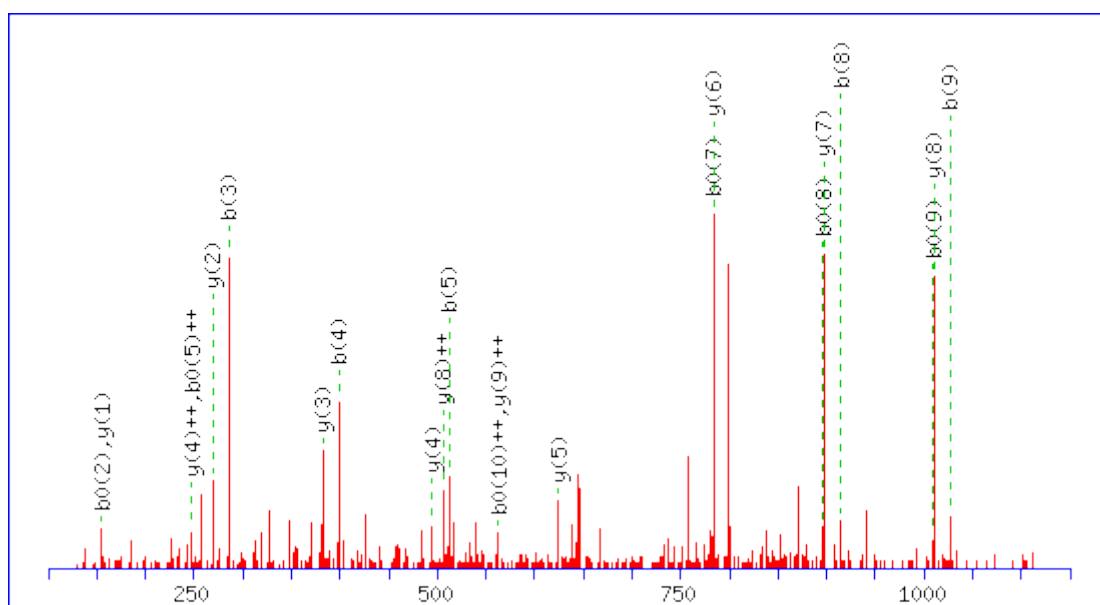
Monoisotopic mass of neutral peptide Mr(calc): 2313.1700

Ions Score: 42 Expect: 0.027

Matches (**Bold Red**): 37/210 fragment ions using 62 most intense peaks

MS/MS Fragmentation of **DGIILCELINK**

Found in **CNN3_HUMAN**, Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1294.7046

Variable modifications:

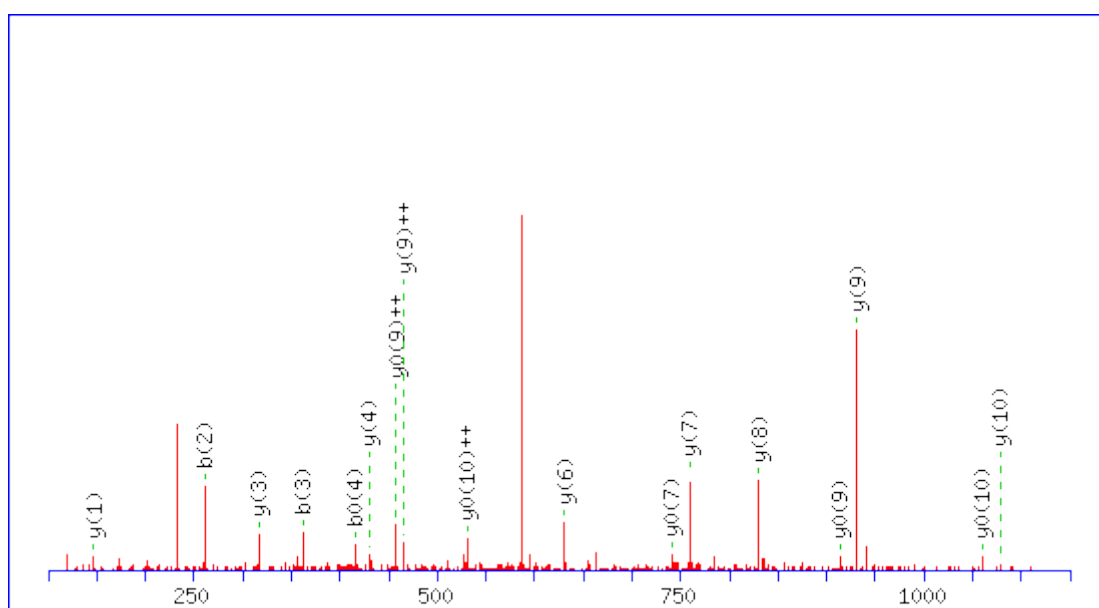
K11 : Label:13C(6)15N(2) (K)

Ions Score: 44 Expect: 0.01

Matches (**Bold Red**): 22/94 fragment ions using 41 most intense peaks

MS/MS Fragmentation of **LFTAESLIGLK**

Found in **COPD_HUMAN**, Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1



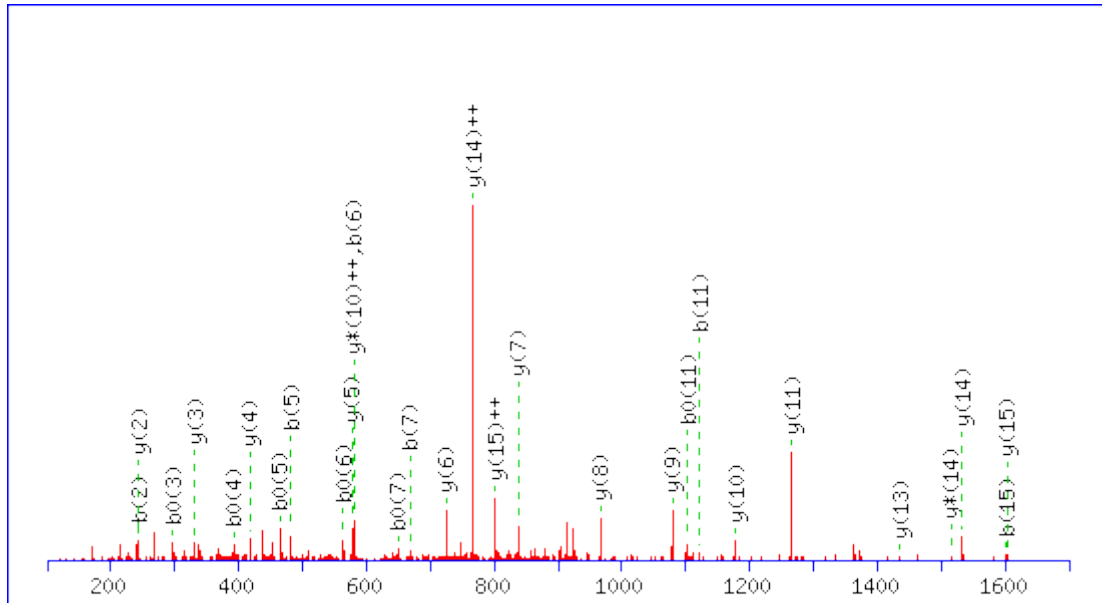
Monoisotopic mass of neutral peptide Mr(calc): 1190.6911

Ions Score: 58 Expect: 0.00038

Matches (**Bold Red**): 17/86 fragment ions using 30 most intense peaks

MS/MS Fragmentation of **ELAPAVSVLQLFCSSPK**

Found in **COPG_HUMAN**, Coatomer subunit gamma OS=Homo sapiens GN=COPG PE=1 SV=1



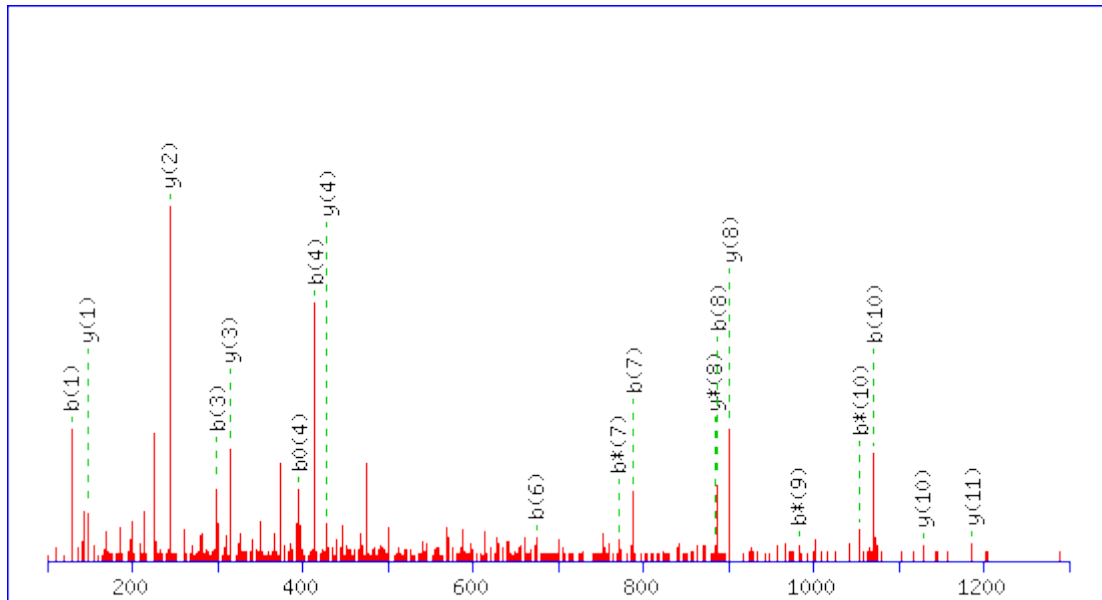
Monoisotopic mass of neutral peptide Mr(calc): 1844.9706

Ions Score: 79 Expect: 4.4e-006

Matches (Bold Red): 30/170 fragment ions using 63 most intense peaks

MS/MS Fragmentation of **KGLDPYNVLAPK**

Found in **COX5B_HUMAN**, Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2



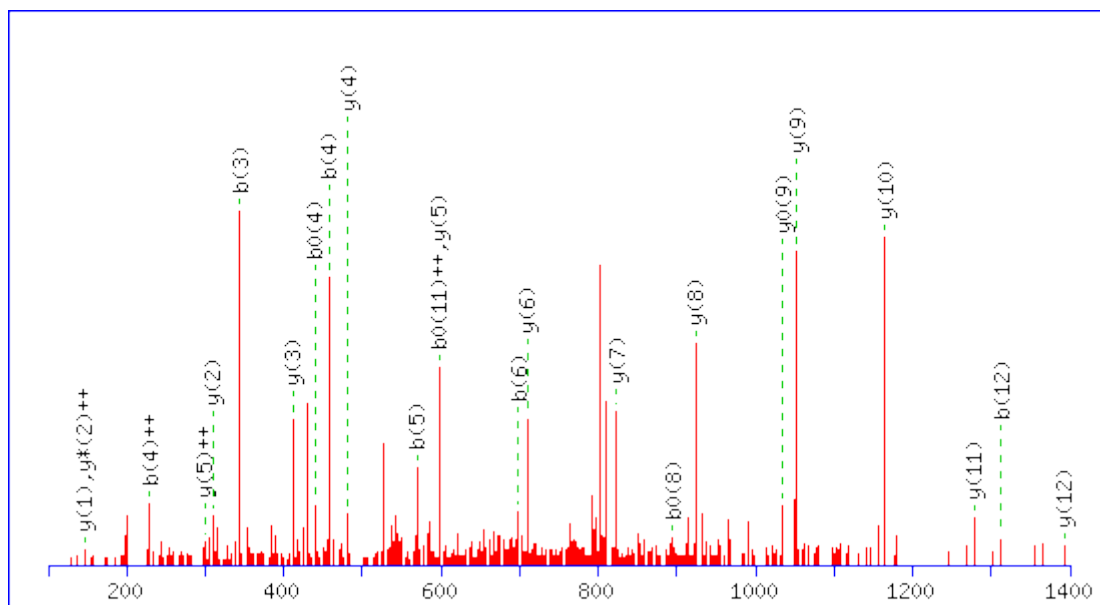
Monoisotopic mass of neutral peptide Mr(calc): 1313.7343

Ions Score: 51 Expect: 0.0023

Matches (**Bold Red**): 19/110 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **IDDILQTLLDATYK**

Found in **CP51A_HUMAN**, Lanosterol 14-alpha demethylase OS=Homo sapiens GN=CYP51A1
PE=1 SV=3



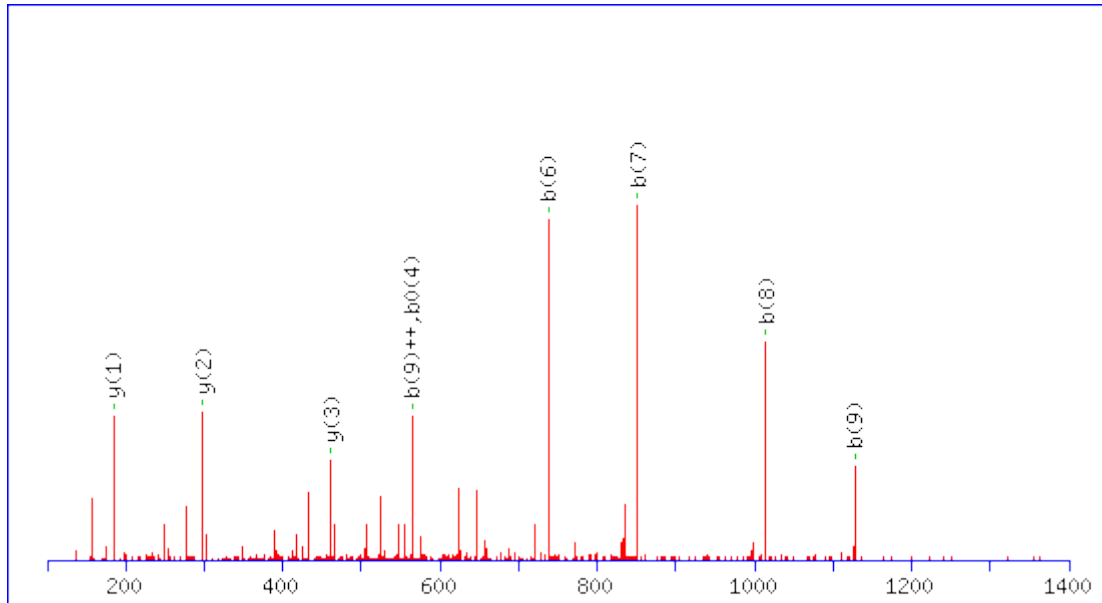
Monoisotopic mass of neutral peptide Mr(calc): 1620.8610

Ions Score: 63 Expect: 0.00015

Matches (**Bold Red**): 25/140 fragment ions using 68 most intense peaks

MS/MS Fragmentation of **TYMWGVIYLR**

Found in **CQ028_HUMAN**, UPF0663 transmembrane protein C17orf28 OS=Homo sapiens
GN=C17orf28 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1310.6721

Variable modifications:

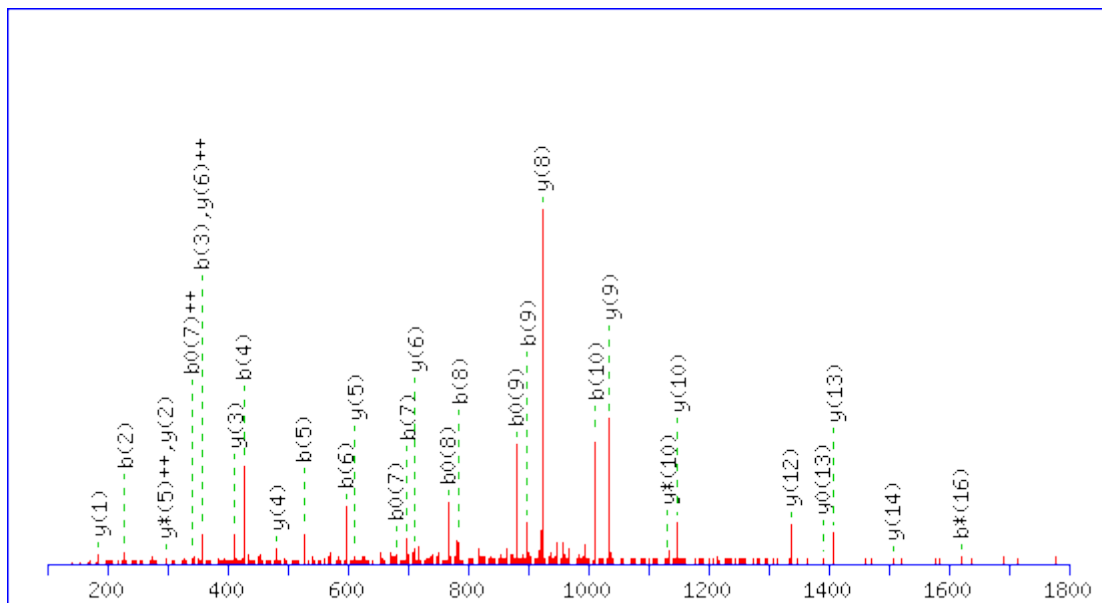
R10 : Label:13C(6)15N(4) (R)

Ions Score: 27 Expect: 0.54

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

MS/MS Fragmentation of **DIQAVATSLPLTEANLR**

Found in **CS066_HUMAN**, UPF0515 protein C19orf66 OS=Homo sapiens GN=C19orf66 PE=2 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1934.0712

Variable modifications:

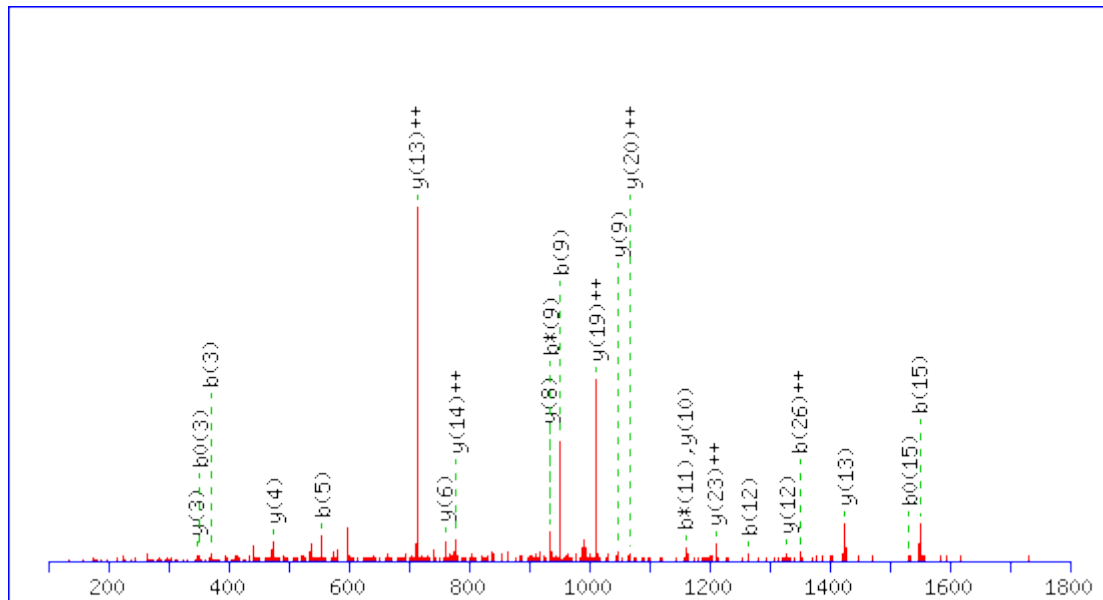
R18 : Label:13C(6)15N(4) (R)

Ions Score: 82 **Expect:** 1.9e-006

Matches (Bold Red): 30/192 fragment ions using 56 most intense peaks

MS/MS Fragmentation of **ELQNAPDAIPESGVEPPALDTAWVEATR**

Found in **CSN1_HUMAN**, COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1
PE=1 SV=4



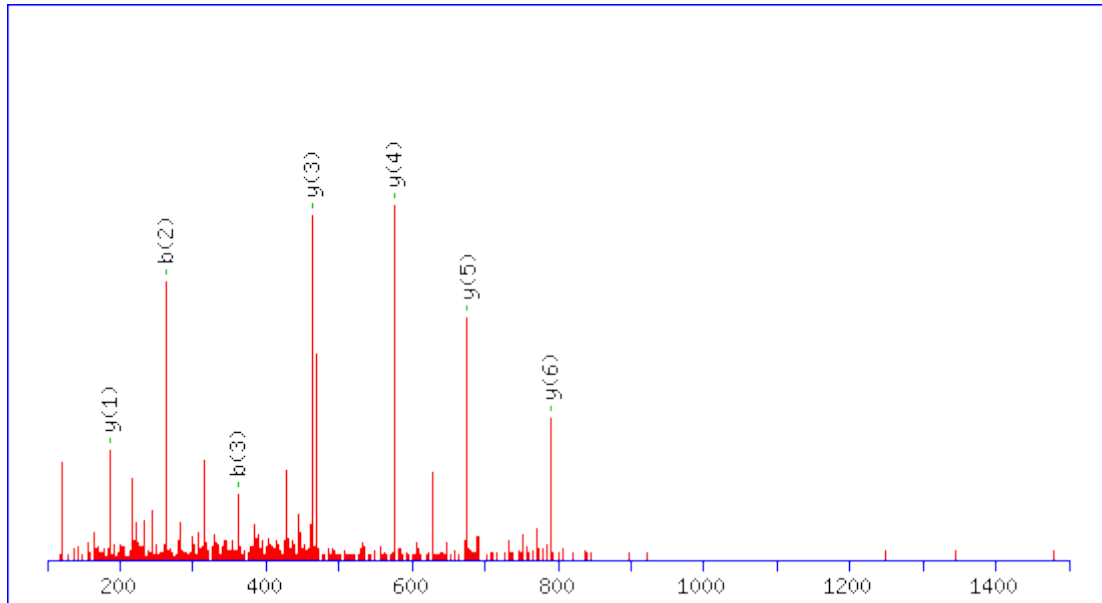
Monoisotopic mass of neutral peptide Mr(calc): 2975.4512

Ions Score: 41 **Expect:** 0.035

Matches (Bold Red): 23/318 fragment ions using 43 most intense peaks

MS/MS Fragmentation of **FNVLYDR**

Found in **CSN6_HUMAN**, COP9 signalosome complex subunit 6 OS=Homo sapiens GN=COPS6
PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 935.4740

Variable modifications:

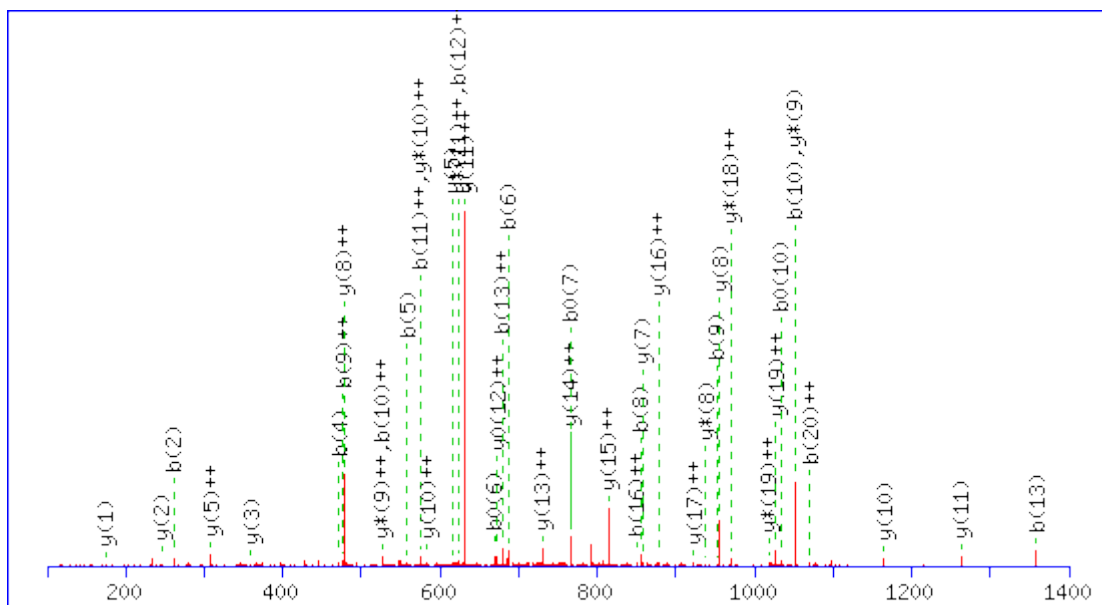
R7 : Label:13C(6)15N(4) (R)

Ions Score: 42 Expect: 0.011

Matches (Bold Red): 7/58 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **FIPLSEPAVPVPPIPNEQLAR**

Found in **CSN8_HUMAN**, COP9 signalosome complex subunit 8 OS=Homo sapiens GN=COPS8
PE=1 SV=1



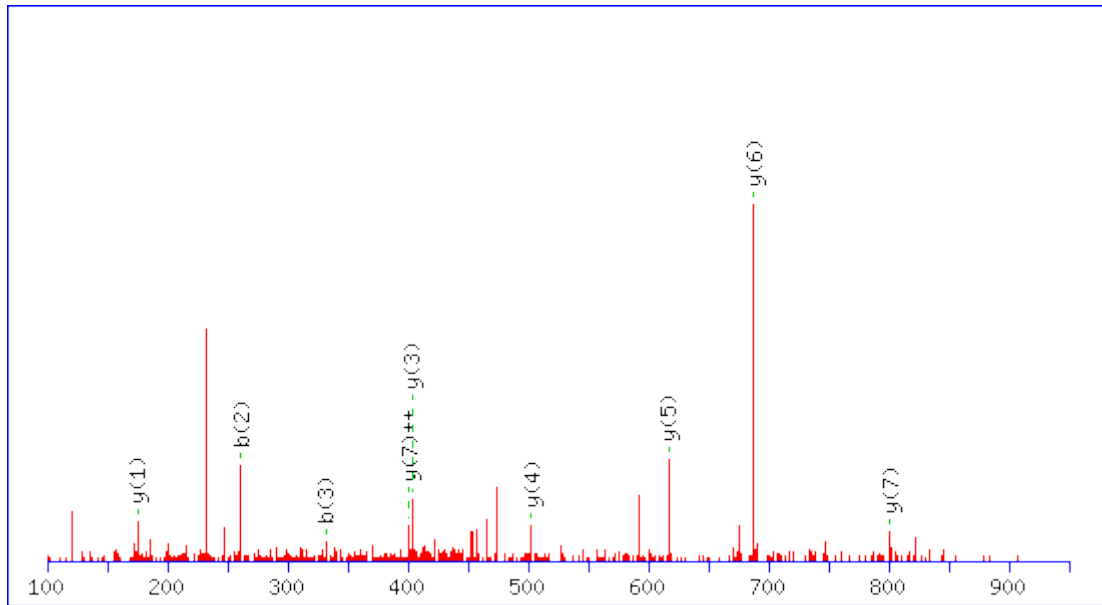
Monoisotopic mass of neutral peptide Mr(calc): 2312.2528

Ions Score: 48 Expect: 0.0069

Matches (Bold Red): 44/194 fragment ions using 93 most intense peaks

MS/MS Fragmentation of **FLANVNDR**

Found in **CTR1_HUMAN**, High affinity cationic amino acid transporter 1 OS=Homo sapiens GN=SLC7A1 PE=1 SV=1



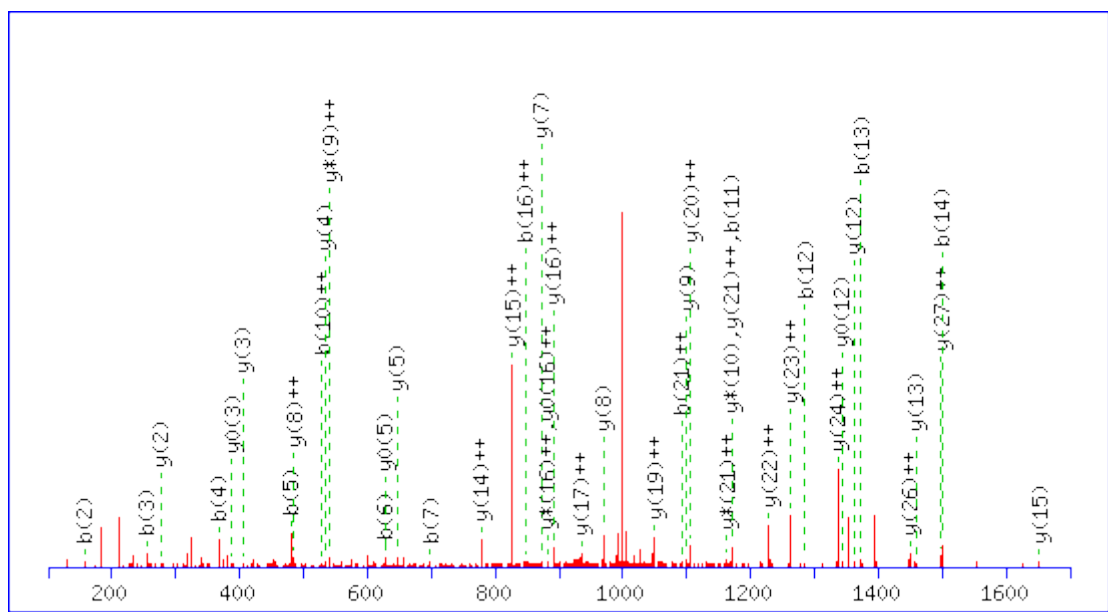
Monoisotopic mass of neutral peptide Mr(calc): 947.4825

Ions Score: 37 Expect: 0.036

Matches (Bold Red): 9/64 fragment ions using 26 most intense peaks

MS/MS Fragmentation of **GVPIIFADELDDSKPPSSSMPLILQEEK**

Found in **DAG1_HUMAN**, Dystroglycan OS=Homo sapiens GN=DAG1 PE=1 SV=2

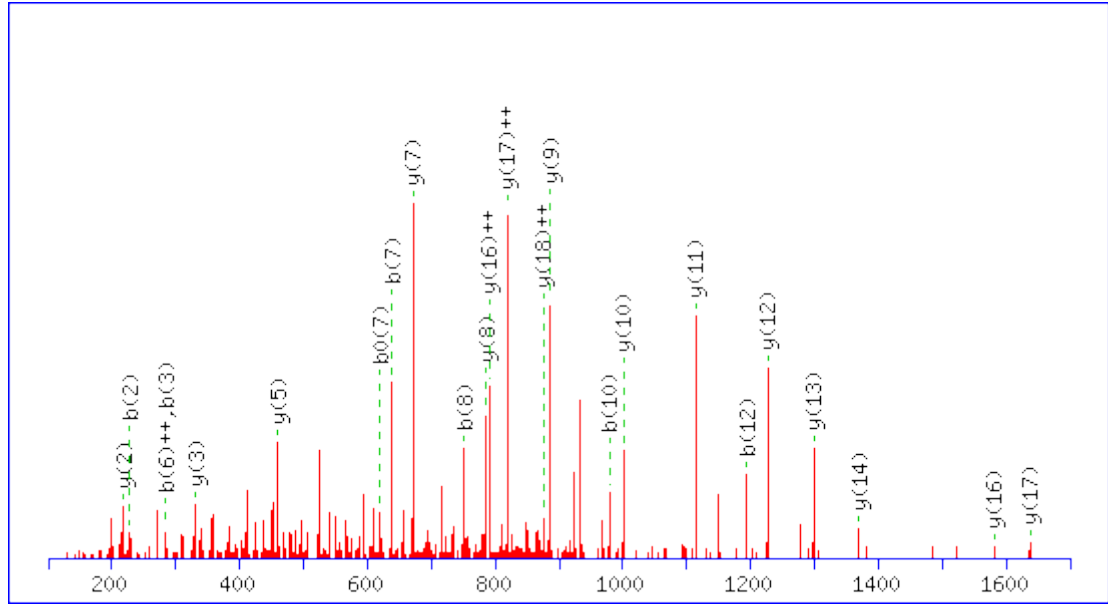


Monoisotopic mass of neutral peptide Mr(calc): 3151.5999

Ions Score: 41 Expect: 0.036

Matches (Bold Red): 44/294 fragment ions using 148 most intense peaks

MS/MS Fragmentation of **LLGPDAAINLTPDGALAK**
 Found in **DCTN2_HUMAN**, Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4



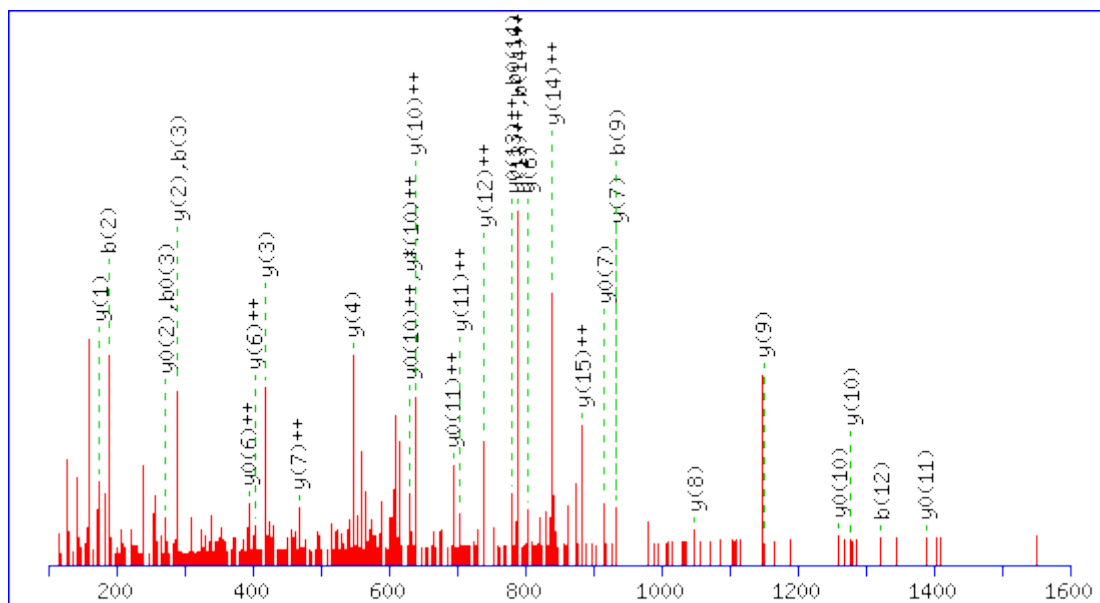
Monoisotopic mass of neutral peptide Mr(calc): 1863.9942

Ions Score: 86 Expect: 8.9e-007

Matches (**Bold Red**): 24/182 fragment ions using 45 most intense peaks

MS/MS Fragmentation of **TSTTAEKTDEEEKEDR**

Found in **DD19A_HUMAN**, ATP-dependent RNA helicase DDX19A OS=Homo sapiens
GN=DDX19A PE=1 SV=1



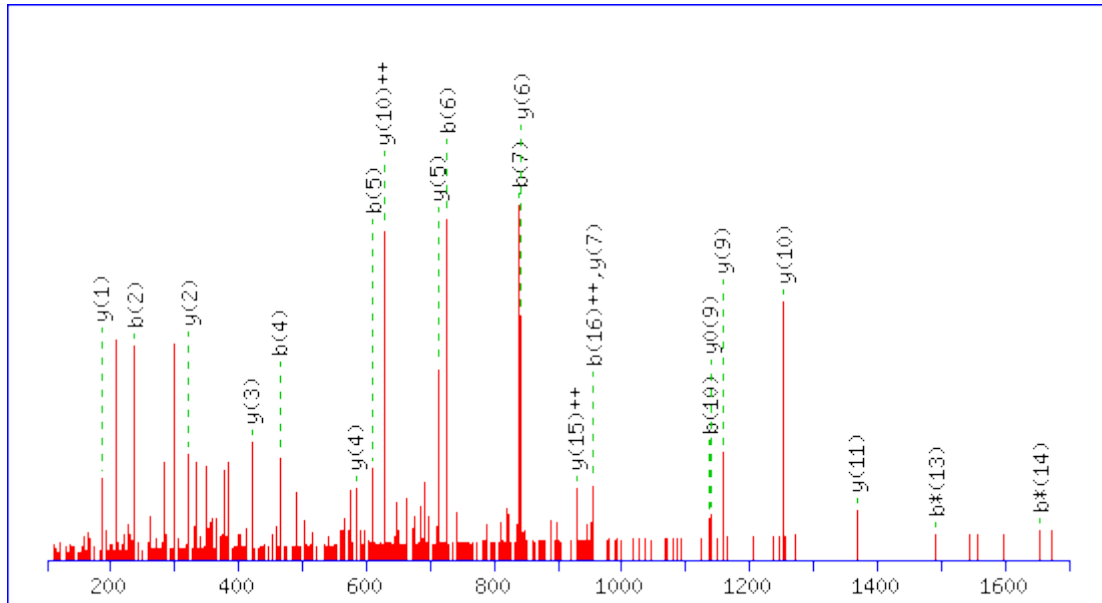
Monoisotopic mass of neutral peptide Mr(calc): 1867.8283

Ions Score: 43 Expect: 0.0097

Matches (**Bold Red**): 33/166 fragment ions using 68 most intense peaks

MS/MS Fragmentation of **HVINFDLPSDIEEYVHR**

Found in **DDX3Y_HUMAN**, ATP-dependent RNA helicase DDX3Y OS=Homo sapiens GN=DDX3Y
PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 2092.0253

Variable modifications:

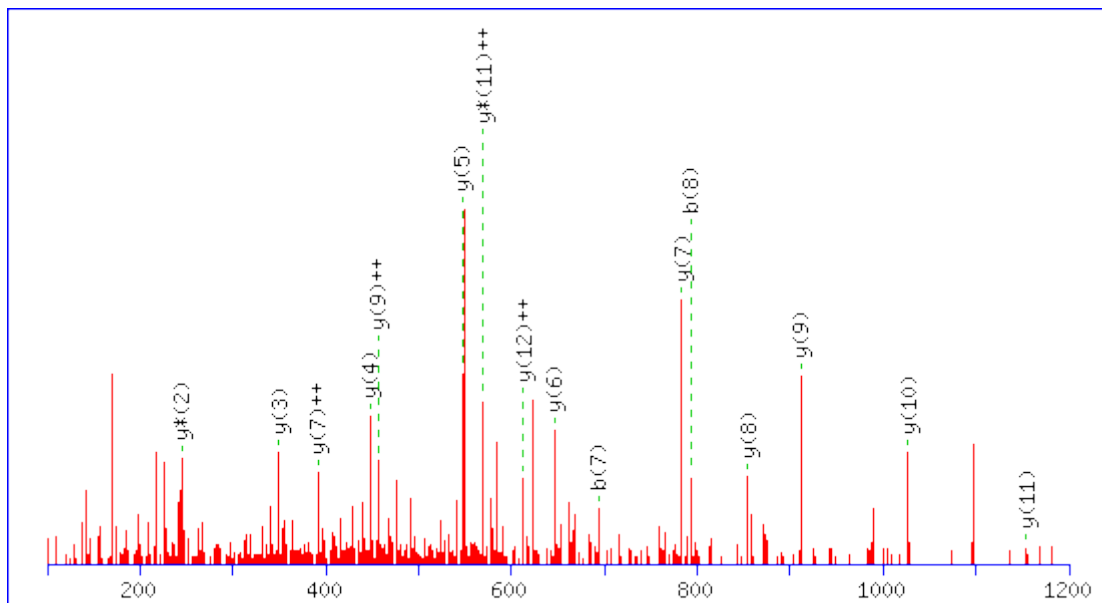
R17 : Label:13C(6)15N(4) (R)

Ions Score: 64 **Expect:** 0.00013

Matches (Bold Red): 22/168 fragment ions using 35 most intense peaks

MS/MS Fragmentation of **LAQDGAHVVSRR**

Found in **DHRS4_HUMAN**, Dehydrogenase/reductase SDR family member 4 OS=Homo sapiens GN=DHRS4 PE=1 SV=3



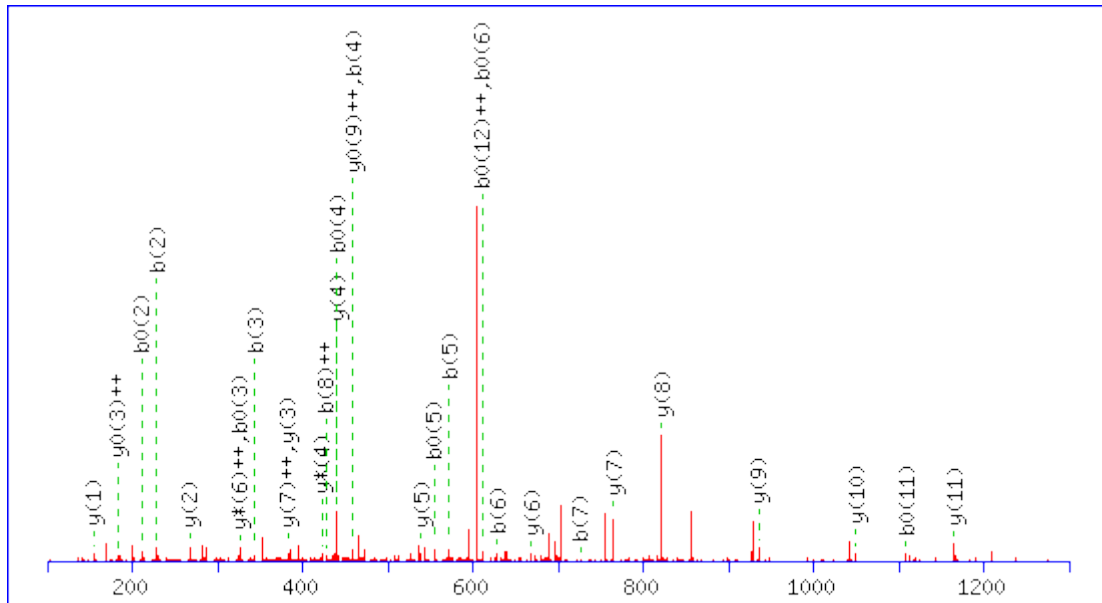
Monoisotopic mass of neutral peptide Mr(calc): 1337.7052

Ions Score: 50 Expect: 0.003

Matches (Bold Red): 16/132 fragment ions using 38 most intense peaks

MS/MS Fragmentation of **EVDDLGPVGDIK**

Found in **DHX15_HUMAN**, Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1392.6864

Variable modifications:

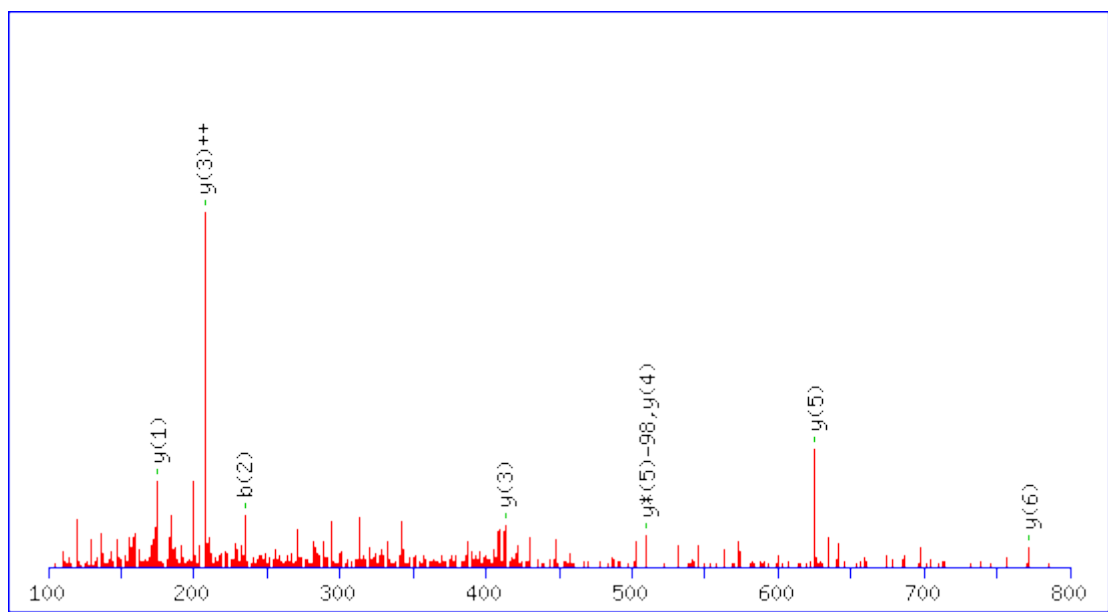
K13 : Label:13C(6)15N(2) (K)

Ions Score: 38 Expect: 0.04

Matches (Bold Red): 30/116 fragment ions using 105 most intense peaks

MS/MS Fragmentation of **SFDPSAR**

Found in **DIDO1_HUMAN**, Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5



Monoisotopic mass of neutral peptide Mr(calc): 858.3273

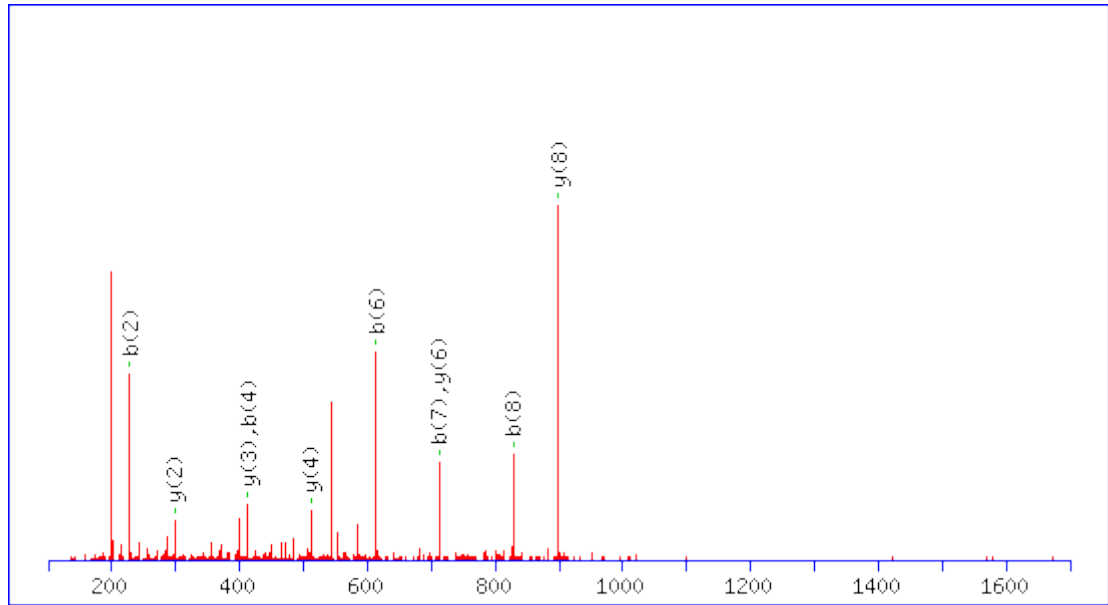
Variable modifications:

S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 46 Expect: 0.0047

Matches (Bold Red): 8/88 fragment ions using 11 most intense peaks

MS/MS Fragmentation of **IISVNSVDLR**
 Found in **DLG1_HUMAN**, Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1124.6429

Variable modifications:

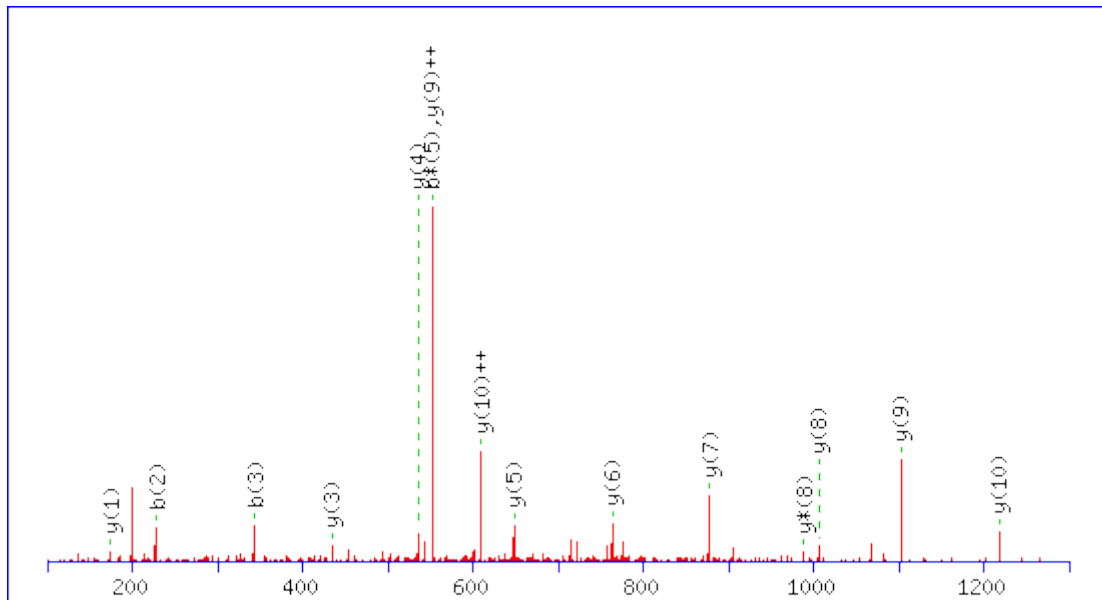
R10 : Label:13C(6)15N(4) (R)

Ions Score: 36 Expect: 0.059

Matches (Bold Red): 10/92 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **DIDPQNDLTFLR**

Found in **DLRB2_HUMAN**, Dynein light chain roadblock-type 2 OS=Homo sapiens
GN=DYNLRB2 PE=1 SV=1



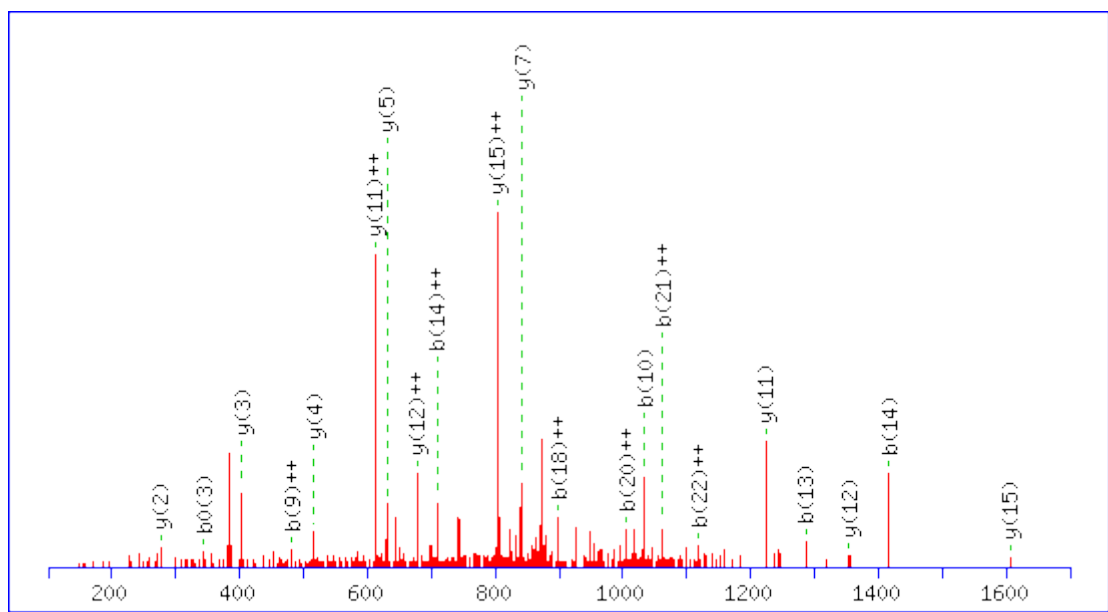
Monoisotopic mass of neutral peptide Mr(calc): 1445.7151

Ions Score: 67 Expect: 4.9e-005

Matches (Bold Red): 15/118 fragment ions using 26 most intense peaks

MS/MS Fragmentation of **ITFTGEADQAPGVEPGDIVLLLQEK**

Found in **DNJA2_HUMAN**, DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2
PE=1 SV=1



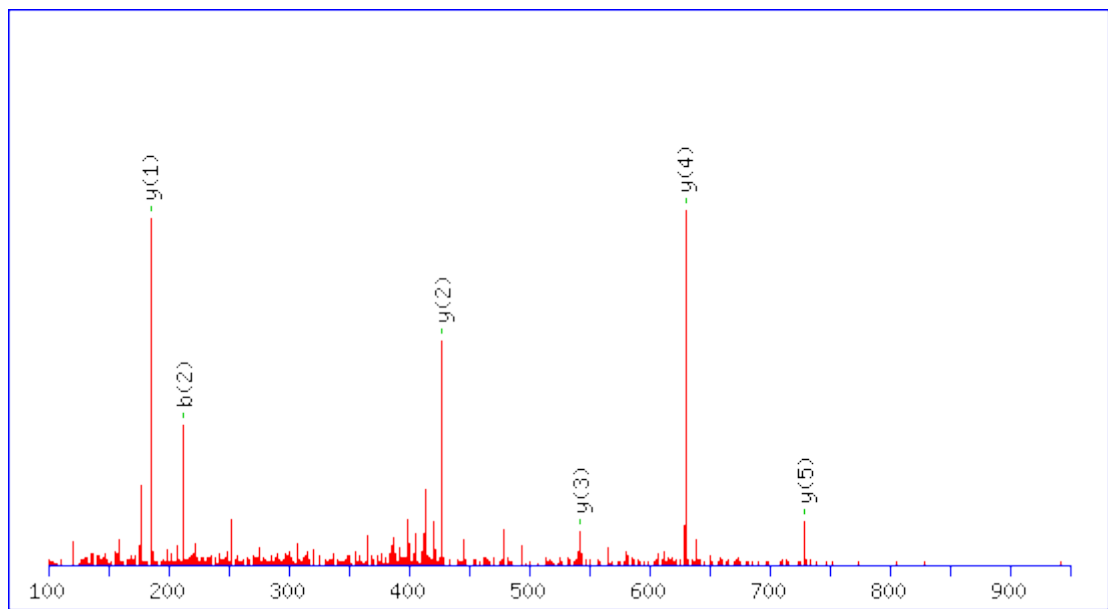
Monoisotopic mass of neutral peptide Mr(calc): 2639.3694

Ions Score: 46 Expect: 0.01

Matches (Bold Red): 21/268 fragment ions using 33 most intense peaks

MS/MS Fragmentation of **LVSDYR**

Found in **DOC10_HUMAN**, Dedicator of cytokinesis protein 10 OS=Homo sapiens
GN=DOCK10 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 841.3610

Variable modifications:

Y5 : Phospho (Y)

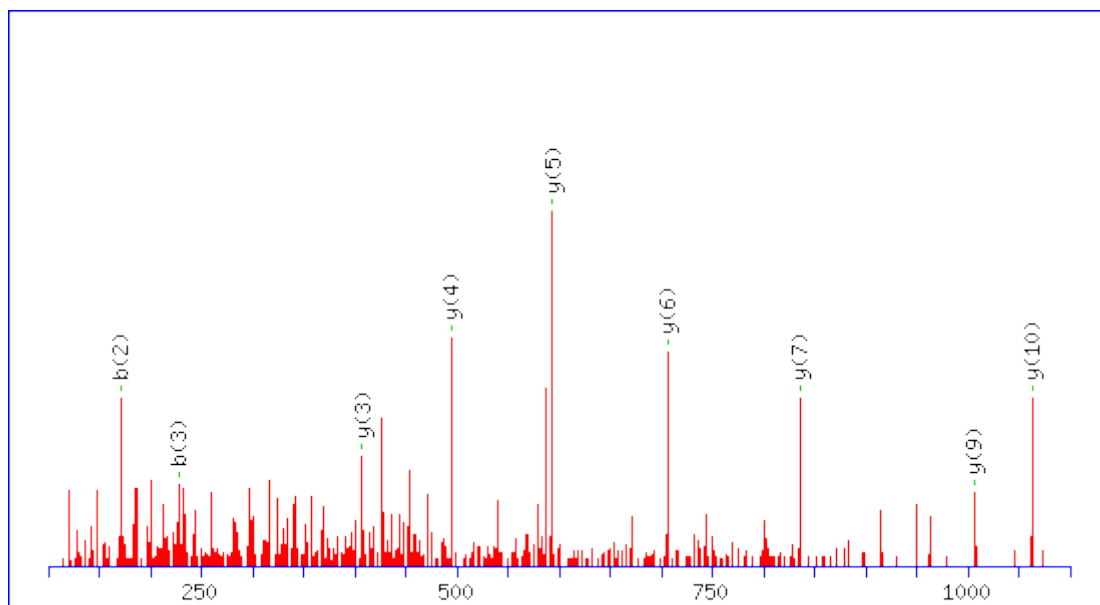
R6 : Label:13C(6)15N(4) (R)

Ions Score: 40 **Expect:** 0.015

Matches (Bold Red): 6/42 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **LGGNEIVSFLK**

Found in **DPM1_HUMAN**, Dolichol-phosphate mannosyltransferase OS=Homo sapiens
GN=DPM1 PE=1 SV=1



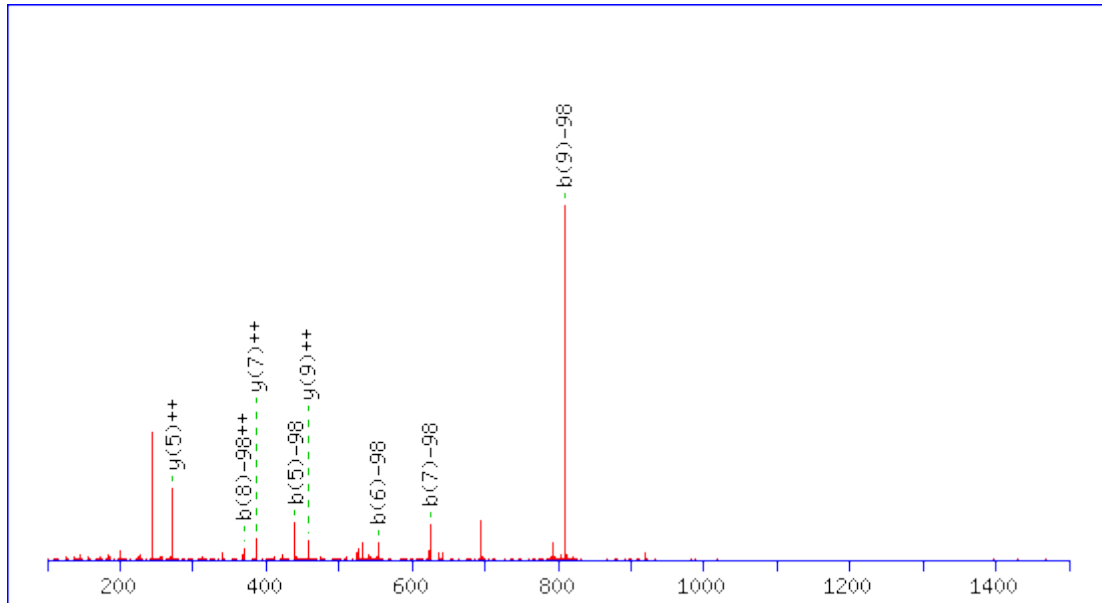
Monoisotopic mass of neutral peptide Mr(calc): 1175.6550

Ions Score: 67 **Expect:** 4.8e-005

Matches (Bold Red): 9/100 fragment ions using 13 most intense peaks

MS/MS Fragmentation of **SAADIILAR**

Found in **DPYL1_HUMAN**, Dihydropyrimidinase-related protein 1 OS=Homo sapiens
GN=CRMP1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1079.5376

Variable modifications:

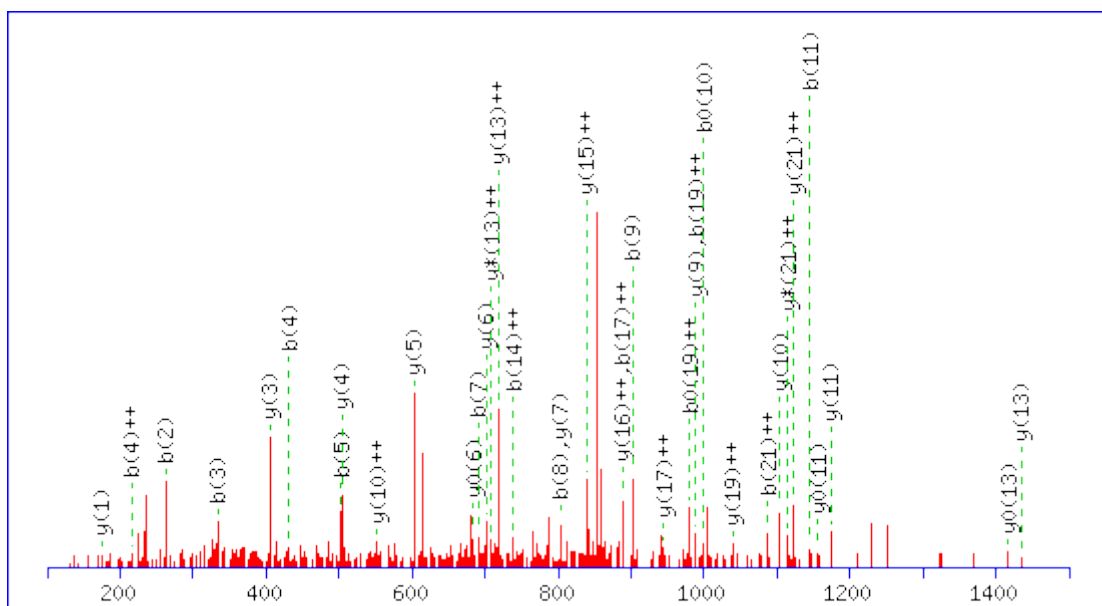
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 18 Expect: 3.4

Matches (Bold Red): 8/114 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **VYAPASTLVDQPYANEGTVVVTTER**

Found in **DSG2_HUMAN**, Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2



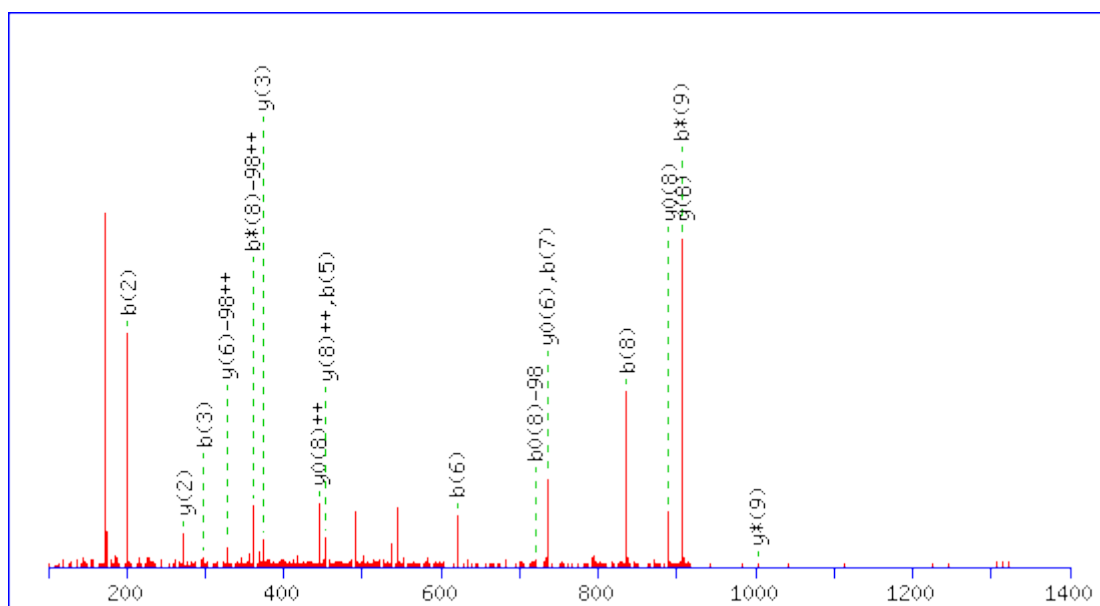
Monoisotopic mass of neutral peptide Mr(calc): 2578.2915

Ions Score: 41 Expect: 0.032

Matches (**Bold Red**): 37/244 fragment ions using 83 most intense peaks

MS/MS Fragmentation of **SIPGVSNTSR**

Found in **DTX4_HUMAN**, Protein deltex-4 OS=Homo sapiens GN=DTX4 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1106.4997

Variable modifications:

S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

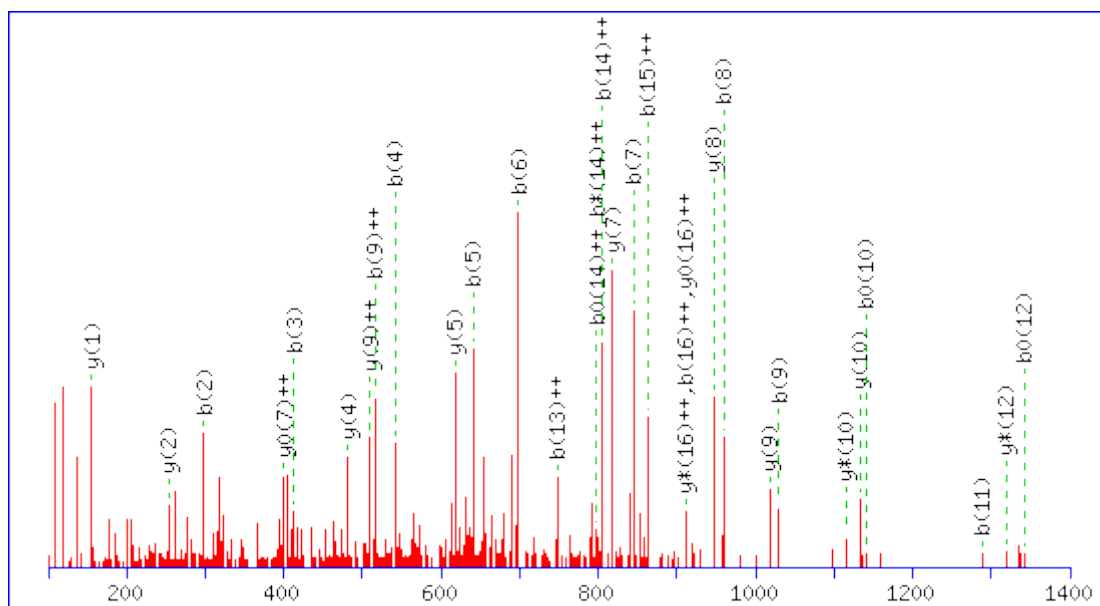
R10 : Label:13C(6)15N(4) (R)

Ions Score: 37 Expect: 0.032

Matches (**Bold Red**): 18/146 fragment ions using 39 most intense peaks

MS/MS Fragmentation of **HCDEVGFNAEEAHNIVK**

Found in **DYLT3_HUMAN**, Dynein light chain Tctex-type 3 OS=Homo sapiens GN=DYNLT3 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1975.8938

Variable modifications:

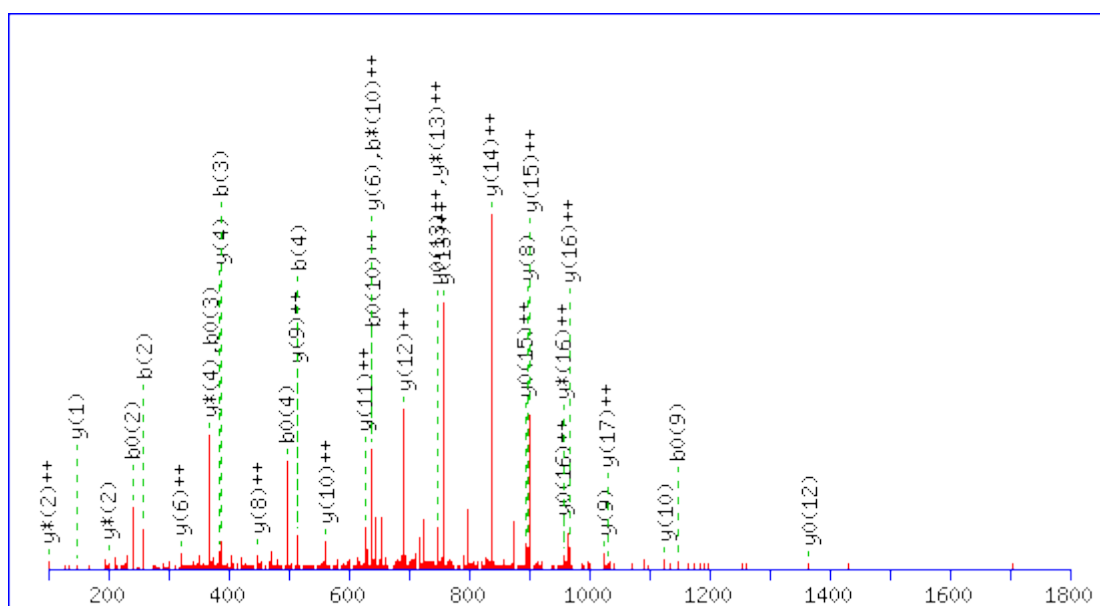
K17 : Label:13C(6)15N(2) (K)

Ions Score: 81 Expect: 2e-006

Matches (Bold Red): 32/162 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **EEQEYEEEEVEEPRPAAK**

Found in **E41L2_HUMAN**, Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1



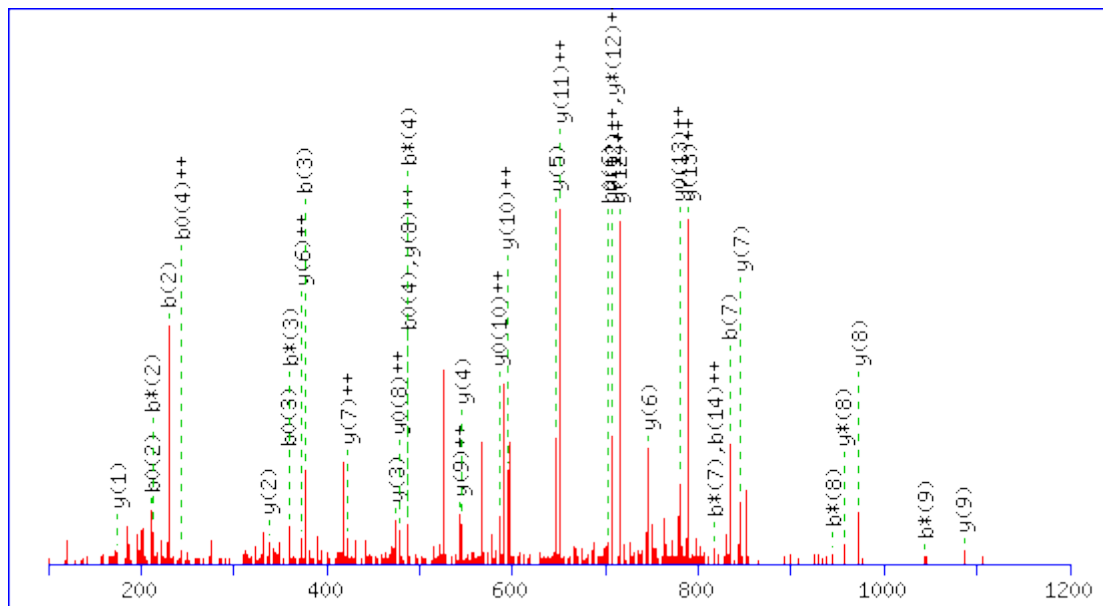
Monoisotopic mass of neutral peptide Mr(calc): 2189.9600

Ions Score: 52 Expect: 0.002

Matches (Bold Red): 35/188 fragment ions using 76 most intense peaks

MS/MS Fragmentation of **DNFQDTLQVVTAHYR**

Found in **ECE1_HUMAN**, Endothelin-converting enzyme 1 OS=Homo sapiens GN=ECE1 PE=1 SV=2



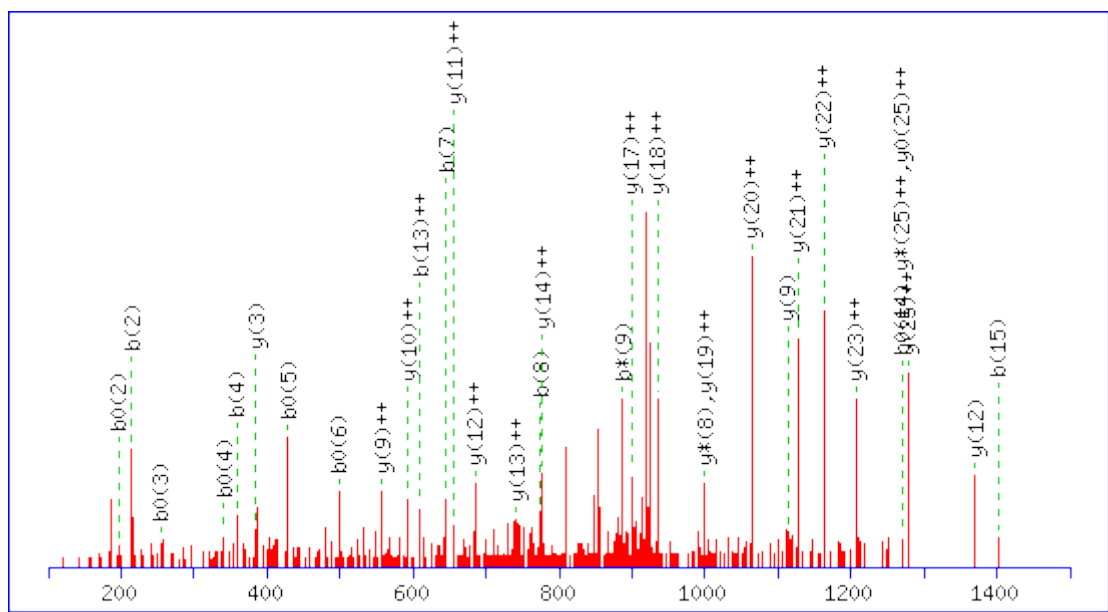
Monoisotopic mass of neutral peptide Mr(calc): 1805.8697

Ions Score: 39 Expect: 0.041

Matches (Bold Red): 38/158 fragment ions using 102 most intense peaks

MS/MS Fragmentation of **LTGSSAQEEASGVALGEAPDHSYESLR**

Found in **ECH1_HUMAN**, Delta(3, 5)-Delta(2, 4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 2770.2921

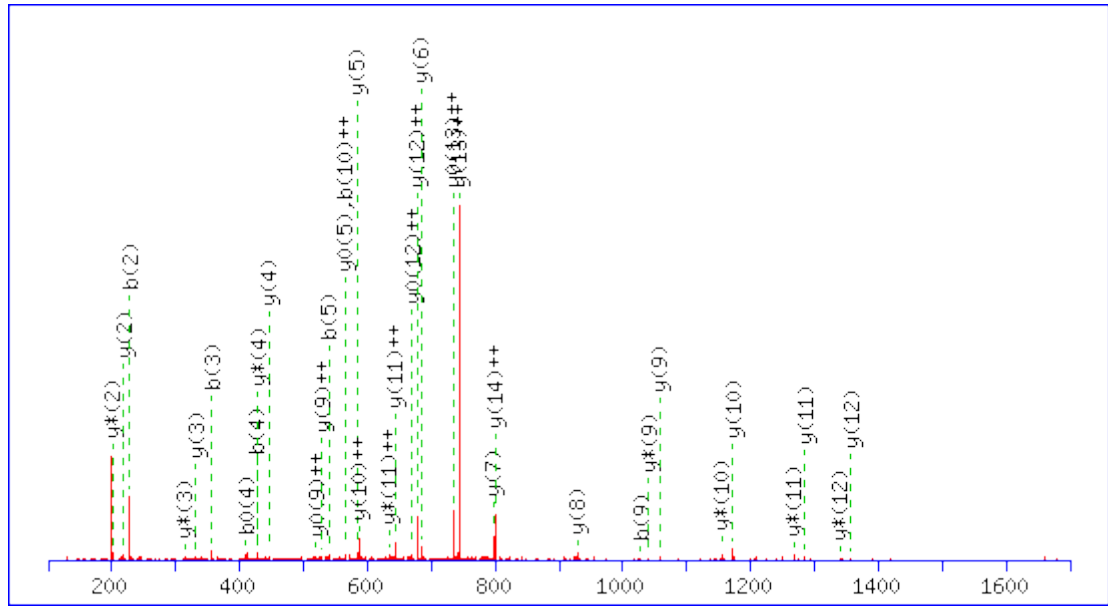
Variable modifications:

R27 : Label:13C(6)15N(4) (R)

Ions Score: 83 **Expect: 2.1e-006**

Matches (Bold Red): 33/294 fragment ions using 53 most intense peaks

MS/MS Fragmentation of **LLEALDEMLTHDIAK**
 Found in **EHD2_HUMAN**, EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2



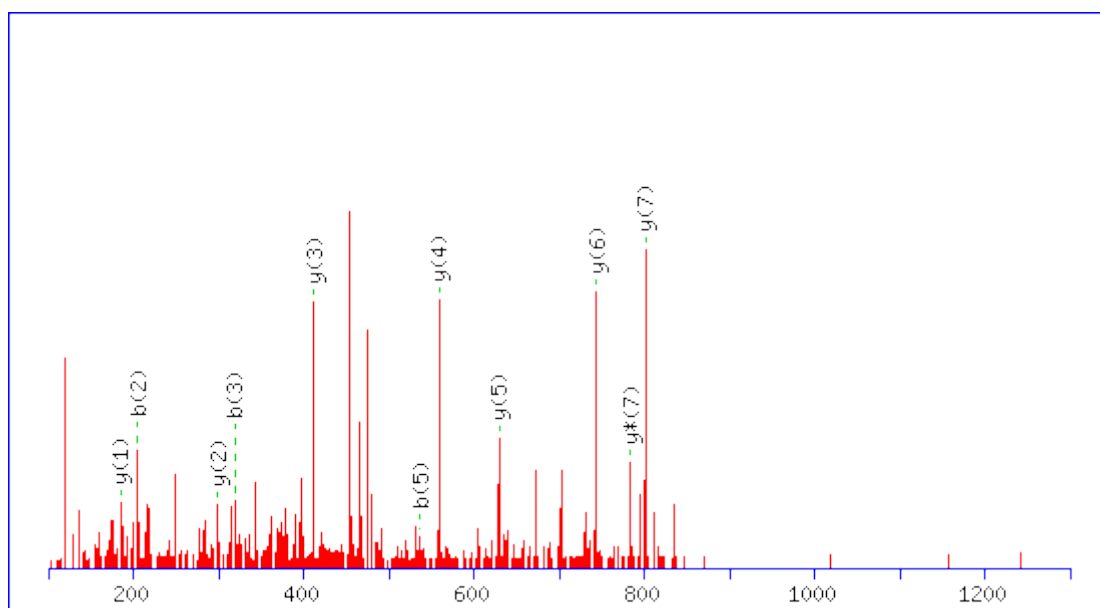
Monoisotopic mass of neutral peptide Mr(calc): 1710.8862

Ions Score: 57 Expect: 0.00068

Matches (Bold Red): 36/130 fragment ions using 88 most intense peaks

MS/MS Fragmentation of **FGNAFLNR**

Found in **EHD4_HUMAN**, EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 947.4853

Variable modifications:

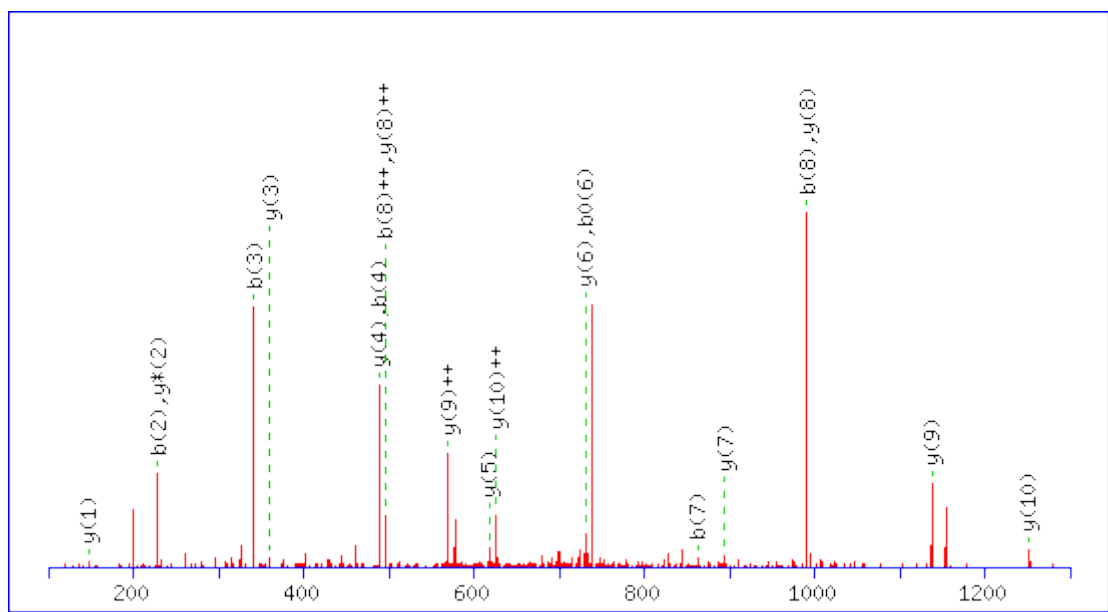
R8 : Label:13C(6)15N(4) (R)

Ions Score: 36 Expect: 0.04

Matches (Bold Red): 11/52 fragment ions using 33 most intense peaks

MS/MS Fragmentation of **DILFPYIEENVK**

Found in **ENOPH_HUMAN**, Enolase-phosphatase E1 OS=Homo sapiens GN=ENOPH1 PE=1 SV=1



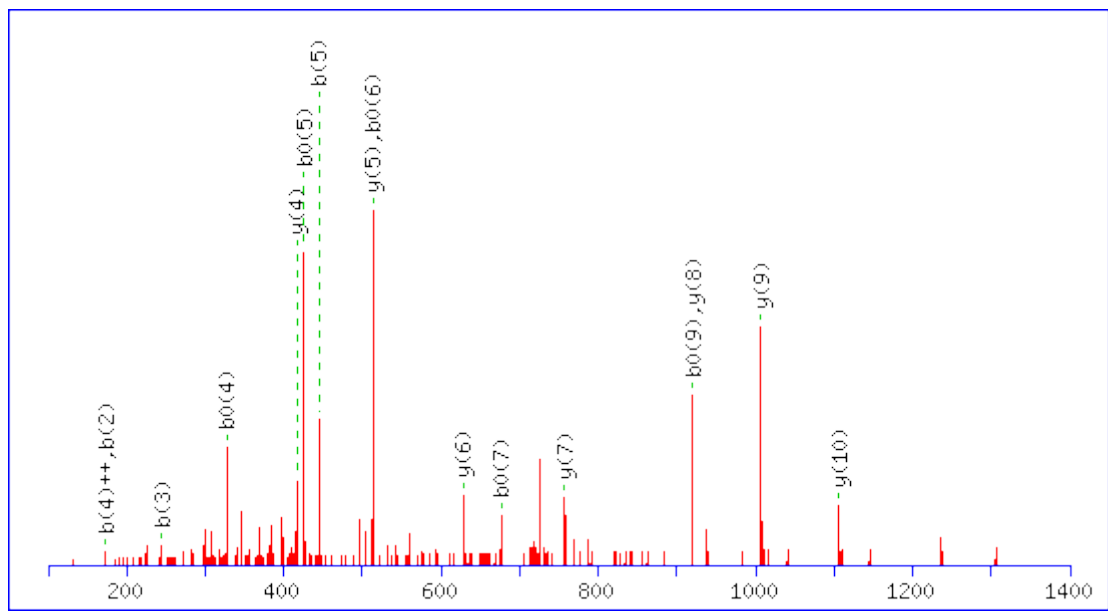
Monoisotopic mass of neutral peptide Mr(calc): 1478.7657

Ions Score: 39 Expect: 0.043

Matches (Bold Red): 20/108 fragment ions using 50 most intense peaks

MS/MS Fragmentation of **GDATVSYEDPPTAK**

Found in **EWS_HUMAN**, RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1



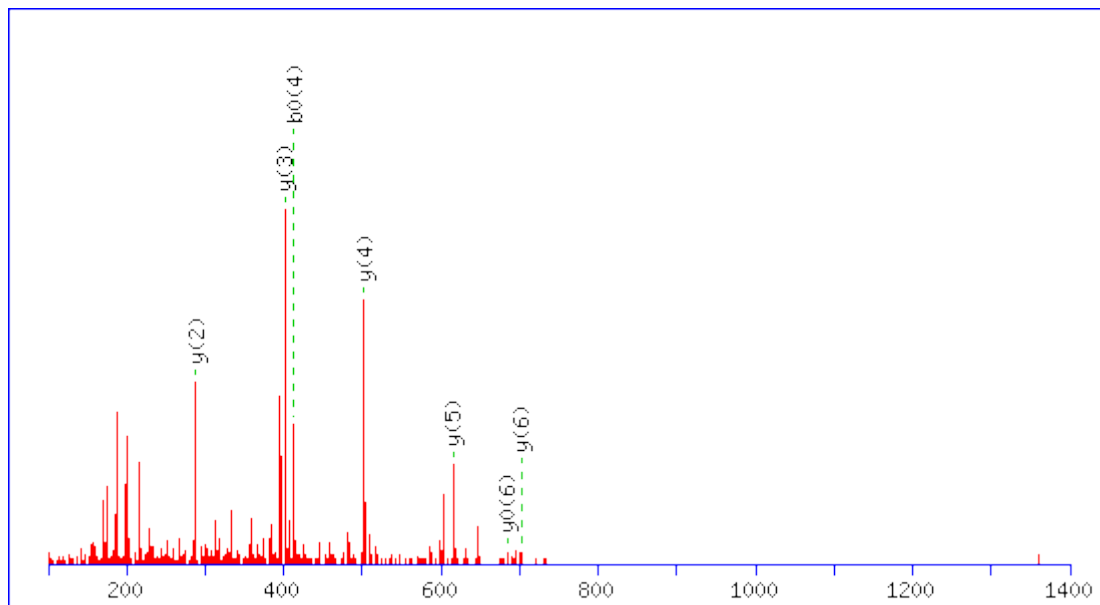
Monoisotopic mass of neutral peptide Mr(calc): 1449.6624

Ions Score: 39 Expect: 0.027

Matches (**Bold Red**): 16/124 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **ESLTLLR**

Found in **F105B_HUMAN**, Protein FAM105B OS=Homo sapiens GN=FAM105B PE=1 SV=3



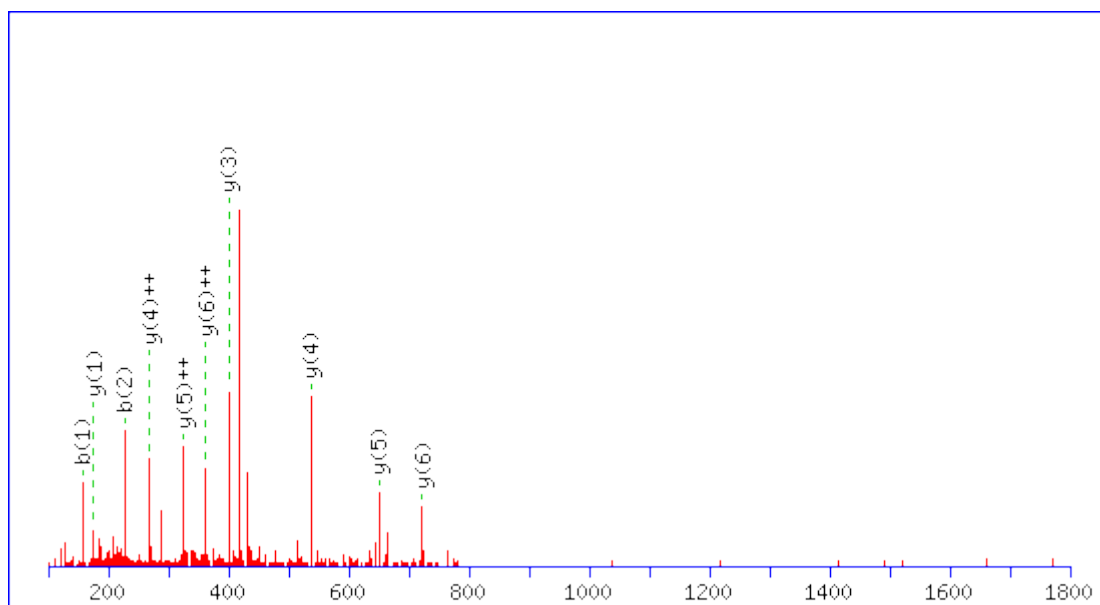
Monoisotopic mass of neutral peptide Mr(calc): 830.4861

Ions Score: 41 Expect: 0.017

Matches (**Bold Red**): 7/54 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **RALHPER**

Found in **F134C_HUMAN**, Protein FAM134C OS=Homo sapiens GN=FAM134C PE=1 SV=1



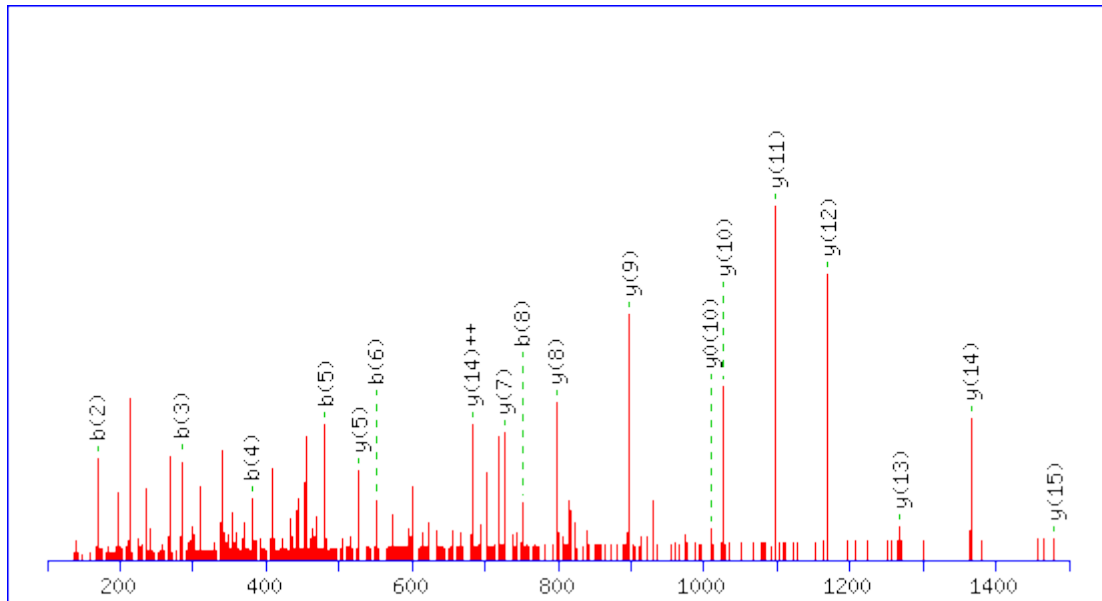
Monoisotopic mass of neutral peptide Mr(calc): 877.4882

Ions Score: 39 Expect: 0.017

Matches (**Bold Red**): 10/60 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **APDPVAAETAAQGTPR**

Found in **FADS1_HUMAN**, Fatty acid desaturase 1 OS=Homo sapiens GN=FADS1 PE=1 SV=1



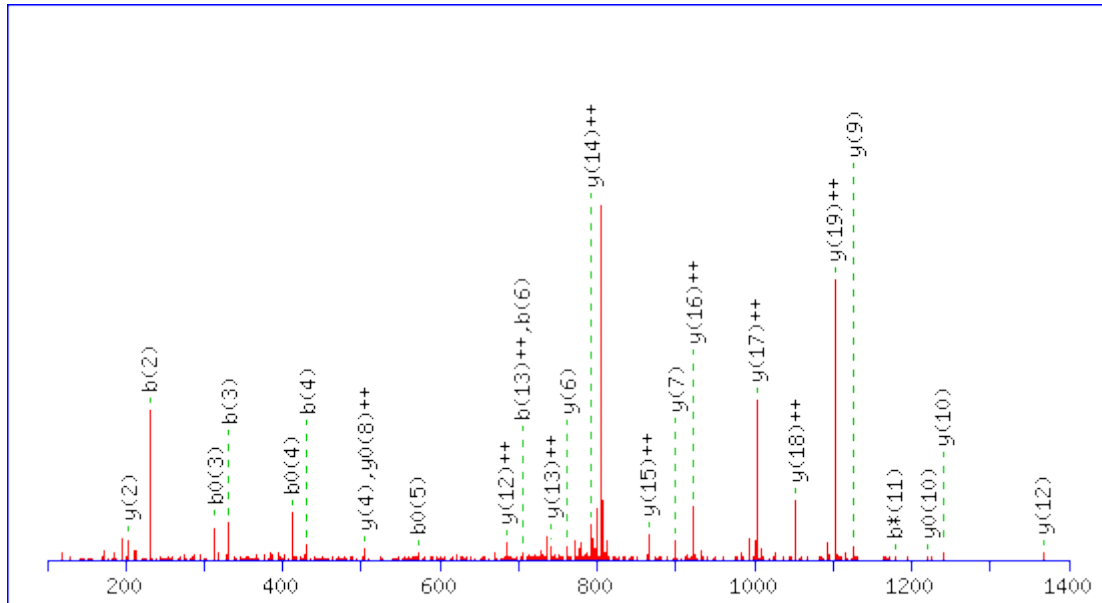
Monoisotopic mass of neutral peptide Mr(calc): 1647.8216

Ions Score: 52 Expect: 0.0023

Matches (**Bold Red**): 18/162 fragment ions using 45 most intense peaks

MS/MS Fragmentation of **TQTVCNFTDGALVQHQEWDGK**

Found in **FB5L3_HUMAN**, Putative fatty acid-binding protein 5-like protein 3 OS=Homo sapiens GN=FABP5P3 PE=5 SV=1



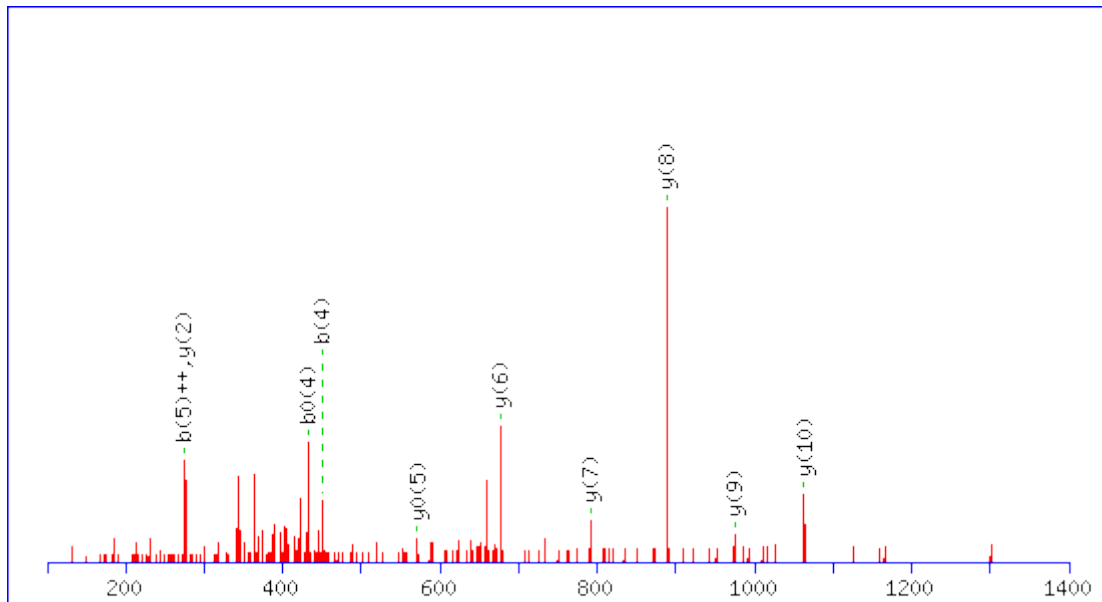
Monoisotopic mass of neutral peptide Mr(calc): 2433.1020

Ions Score: 60 Expect: 0.00036

Matches (Bold Red): 26/234 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **CDSSPDSAEDVR**

Found in **FETUA_HUMAN**, Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1



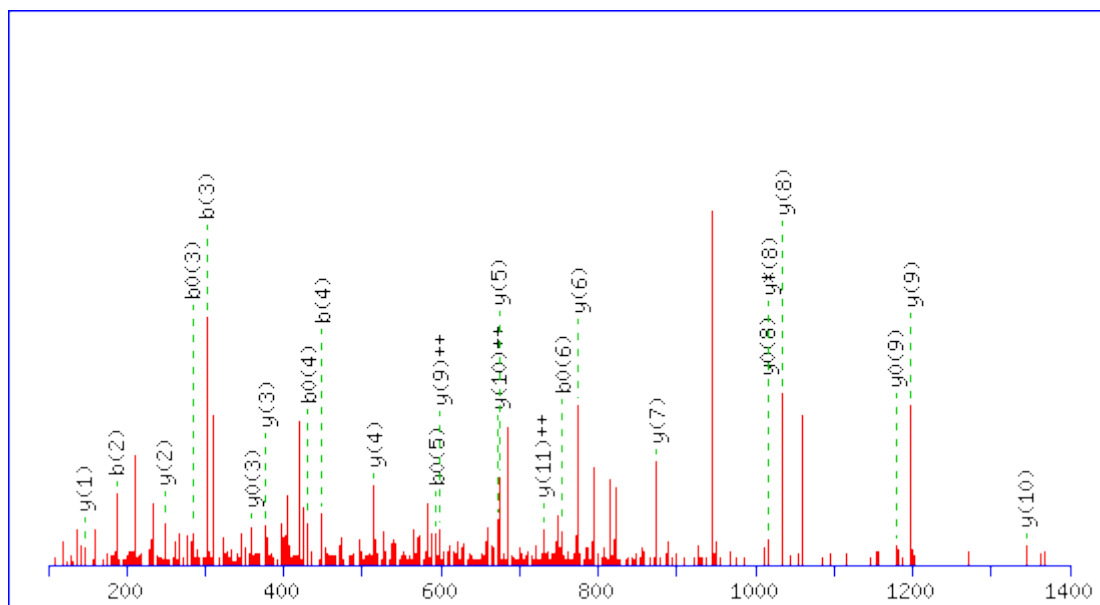
Monoisotopic mass of neutral peptide Mr(calc): 1336.5201

Ions Score: 39 Expect: 0.018

Matches (**Bold Red**): 10/104 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **GEDFYCVTCETK**

Found in **FHL1_HUMAN**, Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1
PE=1 SV=4



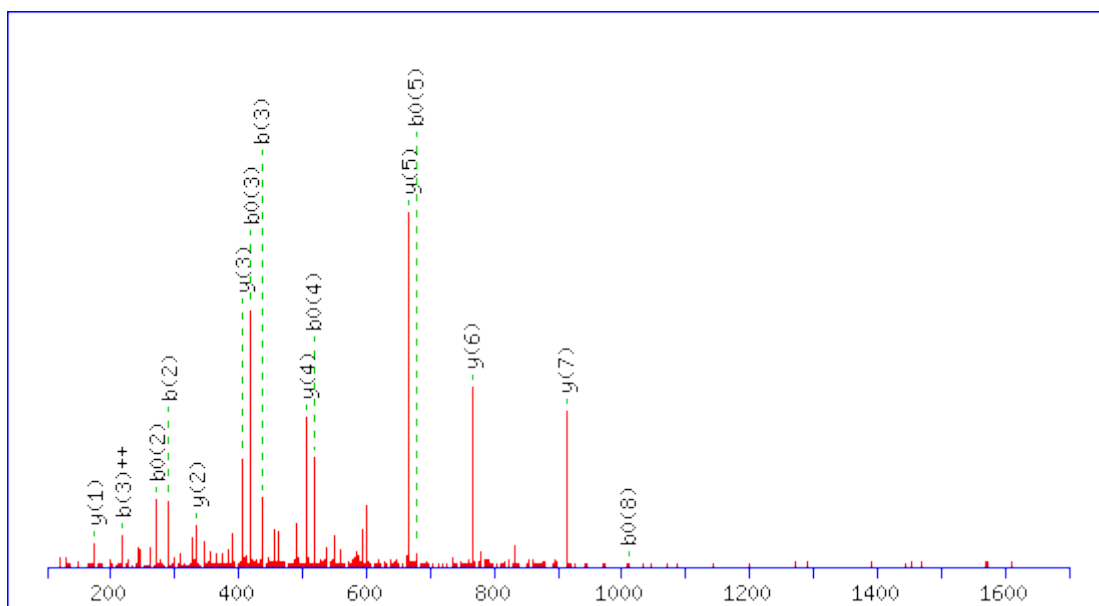
Monoisotopic mass of neutral peptide Mr(calc): 1644.6549

Ions Score: 39 Expect: 0.028

Matches (**Bold Red**): 24/116 fragment ions using 72 most intense peaks

MS/MS Fragmentation of **ECFVCTACR**

Found in **FHL2_HUMAN**, Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2
PE=1 SV=3



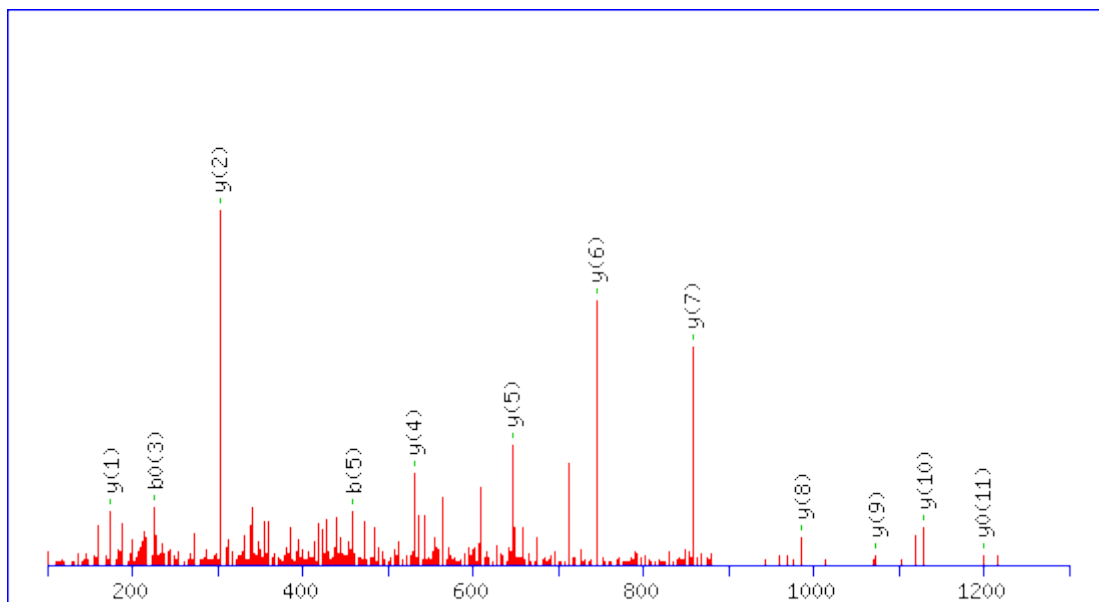
Monoisotopic mass of neutral peptide Mr(calc): 1201.4679

Ions Score: 41 Expect: 0.0086

Matches (Bold Red): 15/74 fragment ions using 41 most intense peaks

MS/MS Fragmentation of **VSGSQIVDIDKR**

Found in **GBRL2_HUMAN**, Gamma-aminobutyric acid receptor-associated protein-like 2 OS=Homo sapiens GN=GABARAPL2 PE=1 SV=1



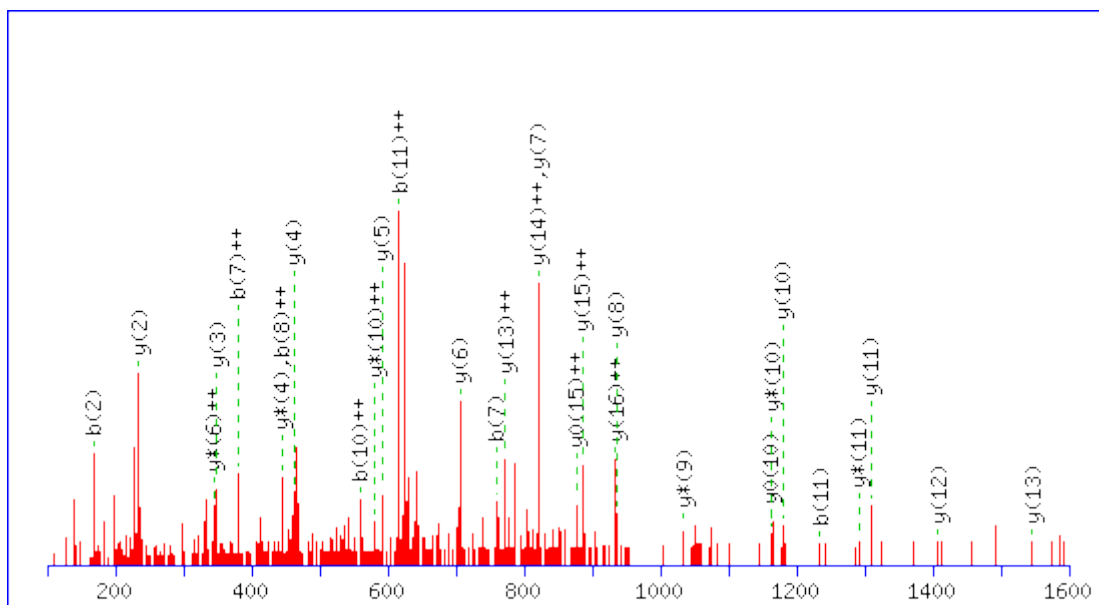
Monoisotopic mass of neutral peptide Mr(calc): 1315.7096

Ions Score: 84 Expect: 1e-006

Matches (**Bold Red**): 12/118 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **APEPHVEEDDDDELDSK**

Found in **GDIR2_HUMAN**, Rho GDP-dissociation inhibitor 2 OS=Homo sapiens
GN=ARHGDIB PE=1 SV=3



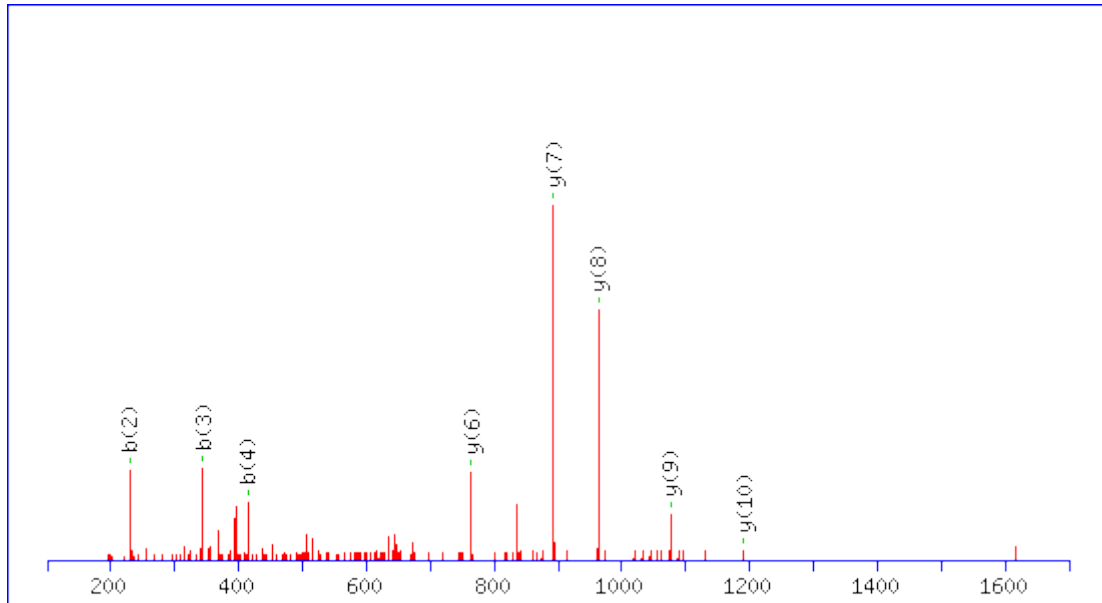
Monoisotopic mass of neutral peptide Mr(calc): 1938.7967

Ions Score: 57 Expect: 0.00042

Matches (**Bold Red**): 30/154 fragment ions using 64 most intense peaks

MS/MS Fragmentation of **DNLAQDLATVR**

Found in **GFAP_HUMAN**, Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1
SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1304.6001

Variable modifications:

T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

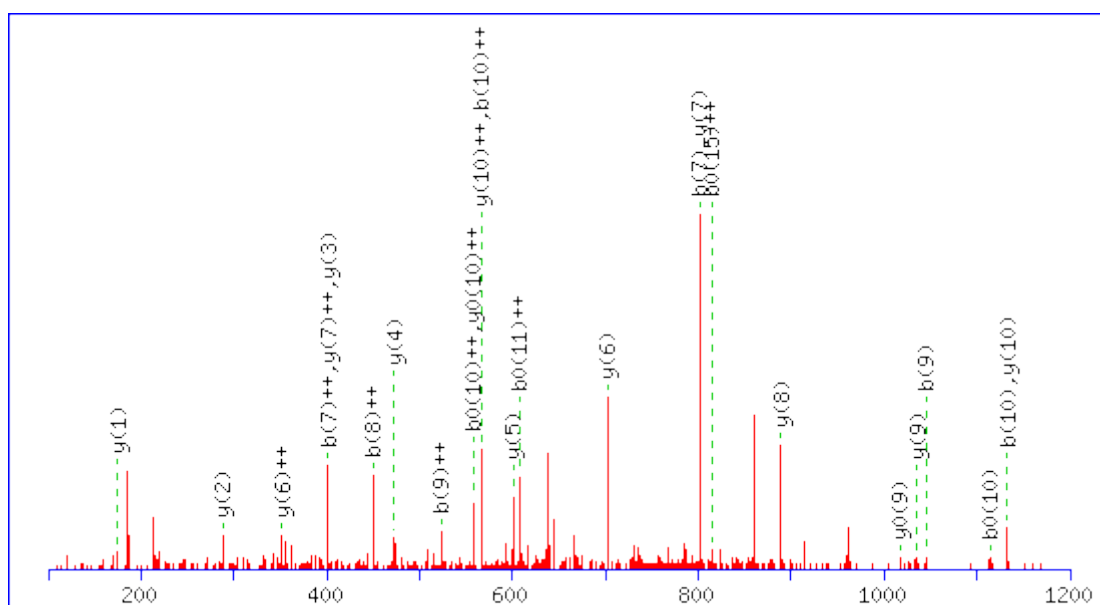
R11 : Label:13C(6)15N(4) (R)

Ions Score: 43 **Expect:** 0.013

Matches (Bold Red): 8/174 fragment ions using 12 most intense peaks

MS/MS Fragmentation of **RPSANCDPFSVTEALIR**

Found in **GLNA_HUMAN**, Glutamine synthetase OS=Homo sapiens GN=GLUL PE=1 SV=4



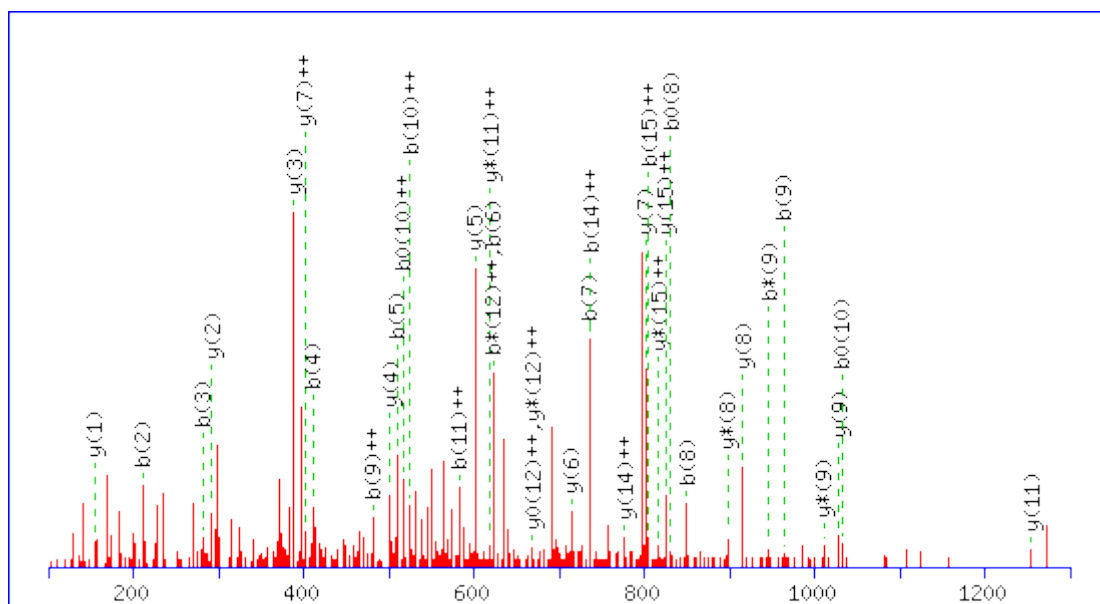
Monoisotopic mass of neutral peptide Mr(calc): 1931.9523

Ions Score: 63 Expect: 0.00018

Matches (**Bold Red**): 26/180 fragment ions using 35 most intense peaks

MS/MS Fragmentation of **IPAEVLILNSIVLPHK**

Found in **GMPPA_HUMAN**, Mannose-1-phosphate guanylttransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1763.0800

Variable modifications:

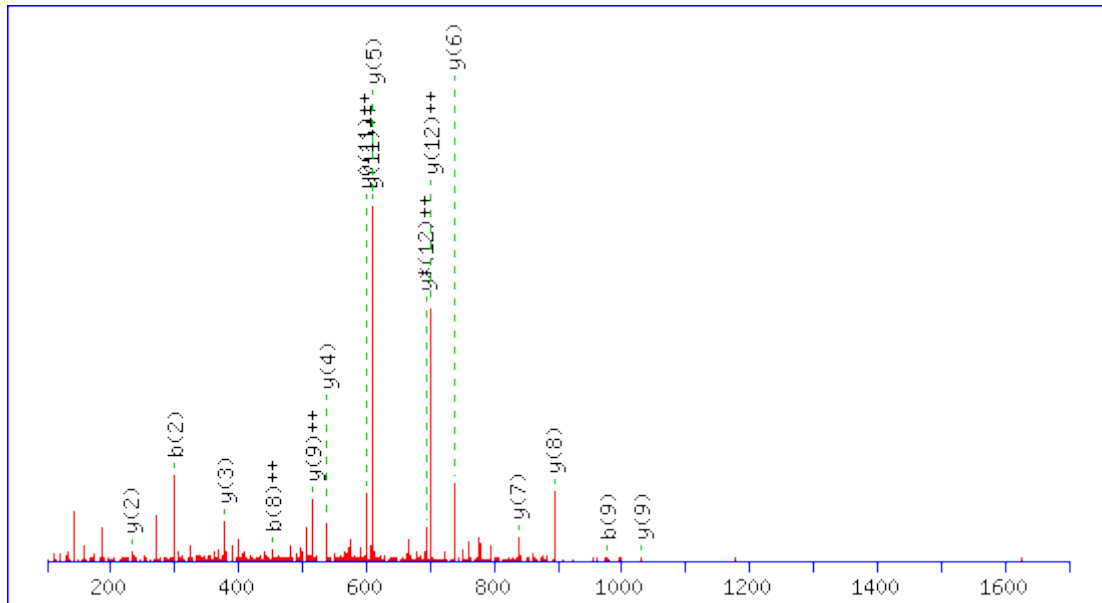
K16 : Label:13C(6)15N(2) (K)

Ions Score: 47 **Expect:** 0.0051

Matches (Bold Red): 37/146 fragment ions using 95 most intense peaks

MS/MS Fragmentation of **LWADHGVQACFGR**

Found in **GNAI2_HUMAN**, Guanine nucleotide-binding protein G(i) subunit alpha-2
OS=Homo sapiens GN=GNAI2 PE=1 SV=3



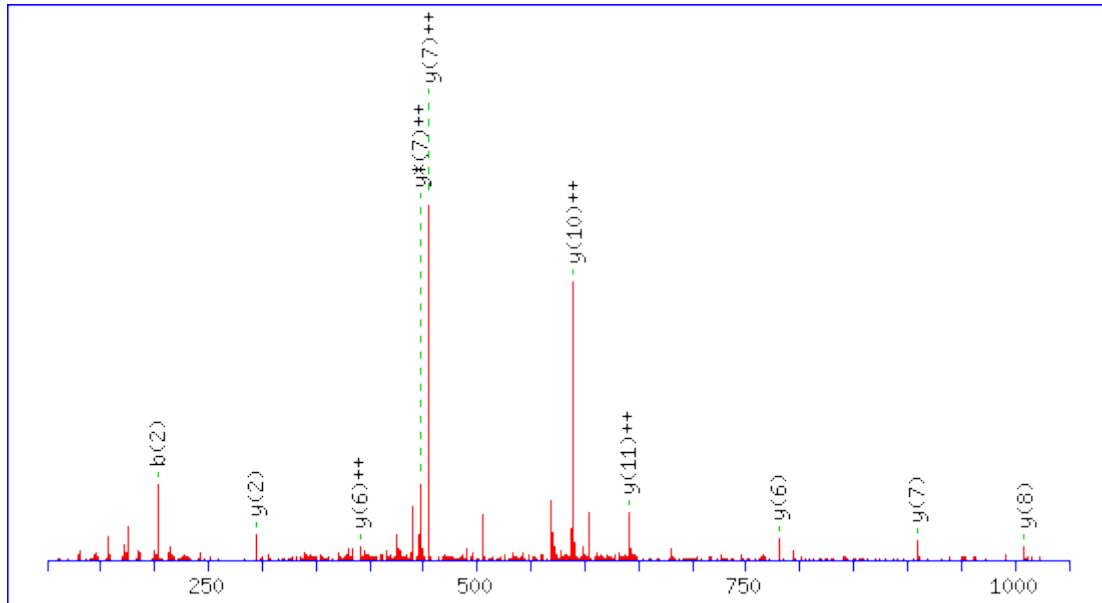
Monoisotopic mass of neutral peptide Mr(calc): 1515.7041

Ions Score: 48 **Expect:** 0.0032

Matches (Bold Red): 16/106 fragment ions using 35 most intense peaks

MS/MS Fragmentation of **TTGIVETHFTFK**

Found in **GNAO1_HUMAN**, Guanine nucleotide-binding protein G(o) subunit alpha
OS=Homo sapiens GN=GNAO1 PE=1 SV=4



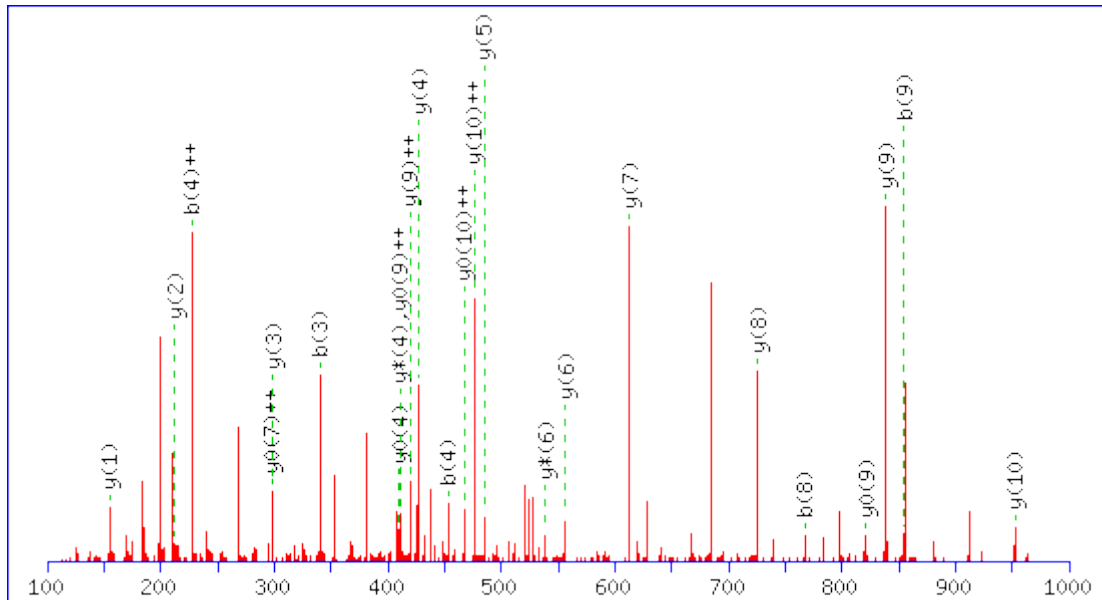
Monoisotopic mass of neutral peptide Mr(calc): 1379.7085

Ions Score: 38 Expect: 0.047

Matches (Bold Red): 10/106 fragment ions using 18 most intense peaks

MS/MS Fragmentation of **LLLLGAGESGK**

Found in **GNAS1_HUMAN**, Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1064.6321

Variable modifications:

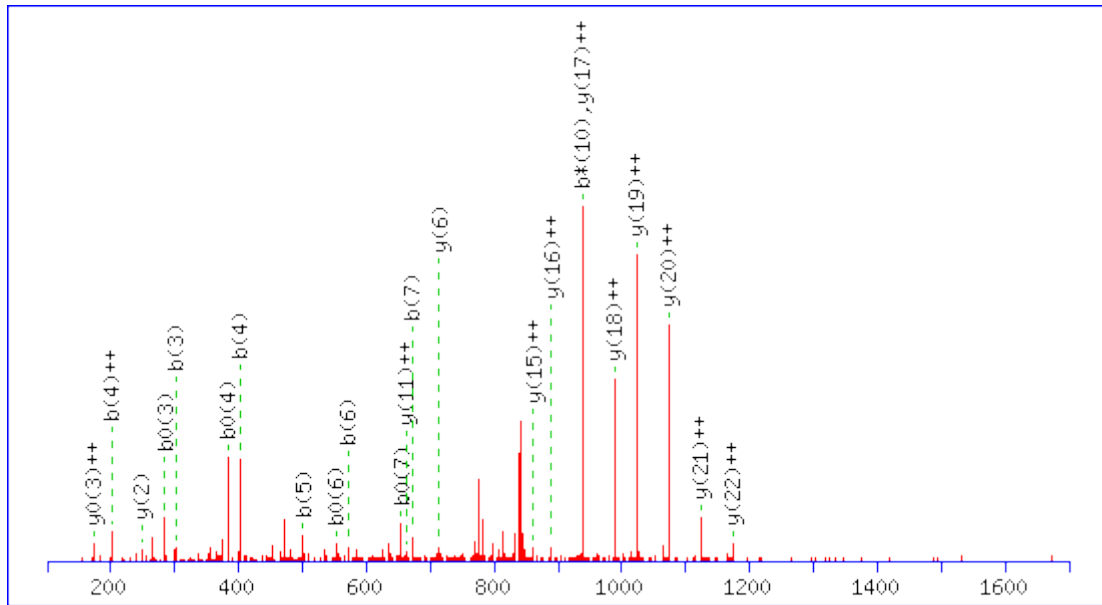
K11 : Label:13C(6)15N(2) (K)

Ions Score: 50 **Expect:** 0.0021

Matches (Bold Red): 25/82 fragment ions using 70 most intense peaks

MS/MS Fragmentation of **VTTVVATPGQGPD RPQEVSYTDTK**

Found in **GSK3B_HUMAN**, Glycogen synthase kinase-3 beta OS=Homo sapiens GN=GSK3B
PE=1 SV=2



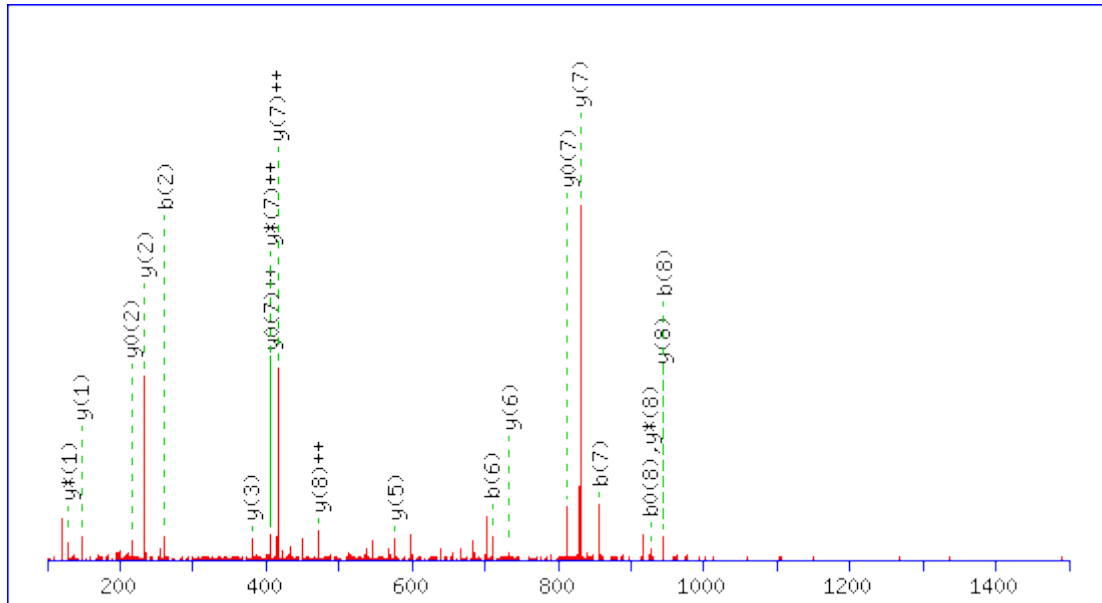
Monoisotopic mass of neutral peptide Mr(calc): 2545.2661

Ions Score: 43 **Expect:** 0.021

Matches (Bold Red): 24/254 fragment ions using 45 most intense peaks

MS/MS Fragmentation of **FLPRPVFSK**

Found in **GSTM1_HUMAN**, Glutathione S-transferase Mu 1 OS=Homo sapiens GN=GSTM1
PE=1 SV=3



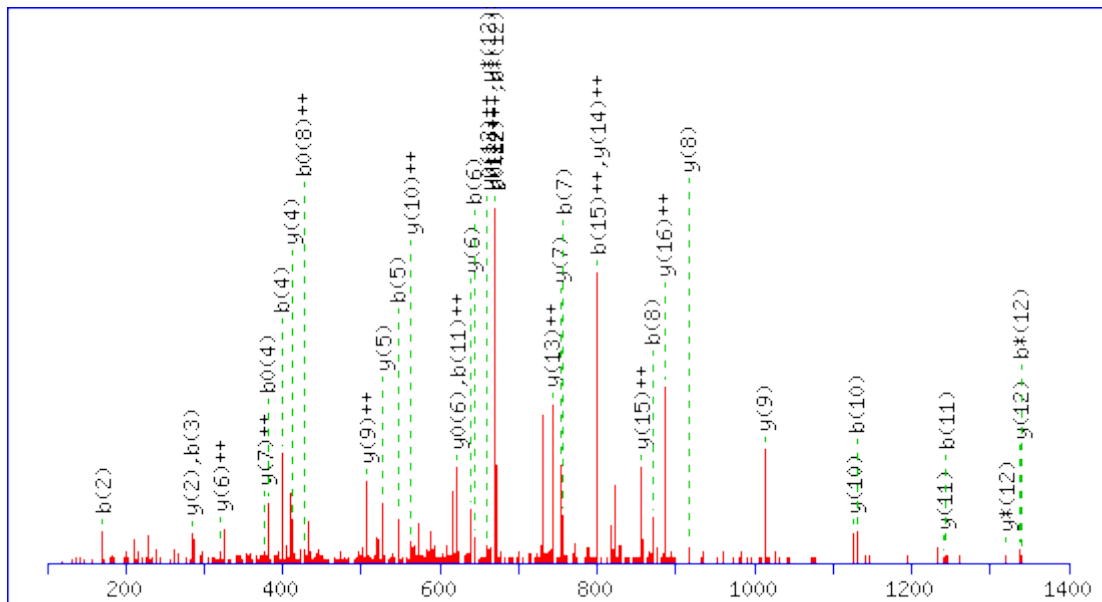
Monoisotopic mass of neutral peptide Mr(calc): 1089.6335

Ions Score: 38 Expect: 0.032

Matches (**Bold Red**): 20/74 fragment ions using 50 most intense peaks

MS/MS Fragmentation of **LGLDFPNLPYLIDGAHK**

Found in **GSTM4_HUMAN**, Glutathione S-transferase Mu 4 OS=Homo sapiens GN=GSTM4
PE=1 SV=3



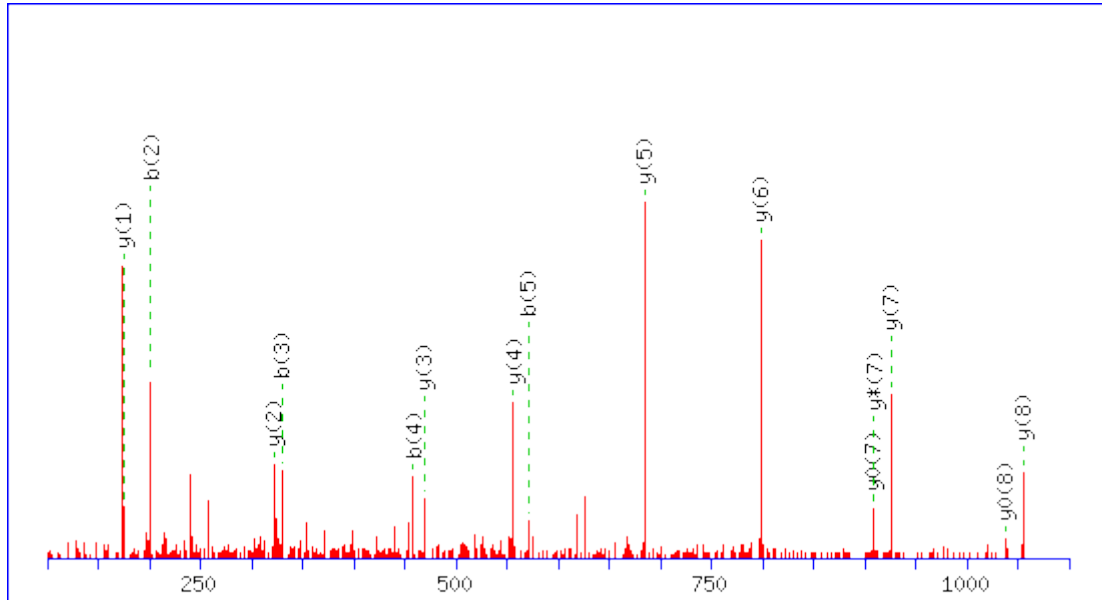
Monoisotopic mass of neutral peptide Mr(calc): 1881.9989

Ions Score: 49 Expect: 0.0042

Matches (Bold Red): 39/166 fragment ions using 92 most intense peaks

MS/MS Fragmentation of **SLEQIESFFR**

Found in **GTR6_HUMAN**, Solute carrier family 2, facilitated glucose transporter member 6 OS=Homo sapiens GN=SLC2A6 PE=1 SV=2



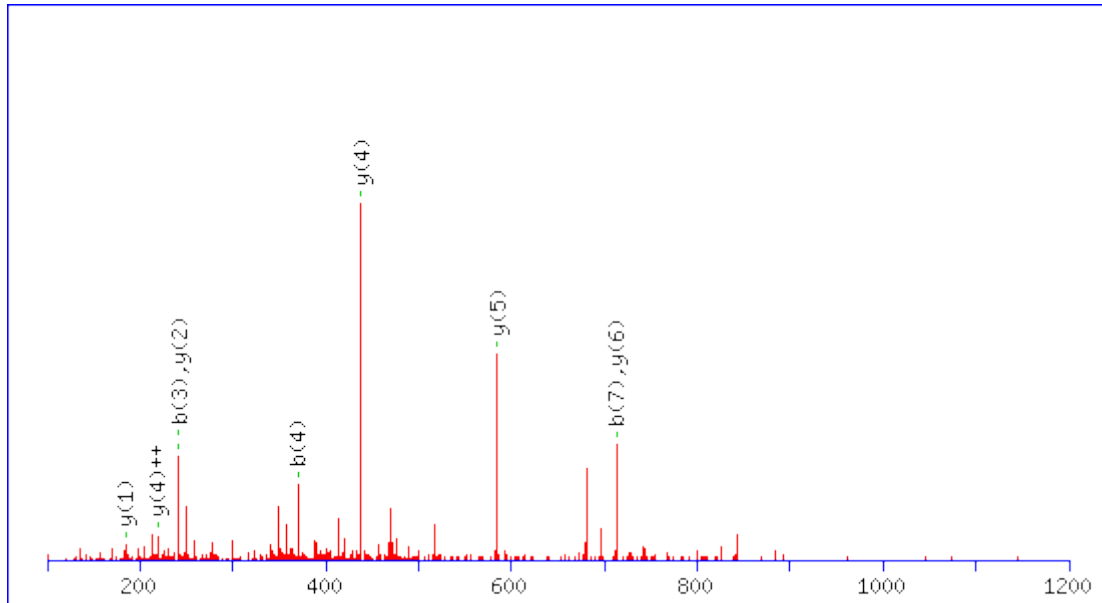
Monoisotopic mass of neutral peptide Mr(calc): 1254.6244

Ions Score: 65 **Expect:** 7e-005

Matches (Bold Red): 15/96 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **AGLQFPVGR**

Found in **H2A2C_HUMAN**, Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4



Monoisotopic mass of neutral peptide Mr(calc): 953.5322

Variable modifications:

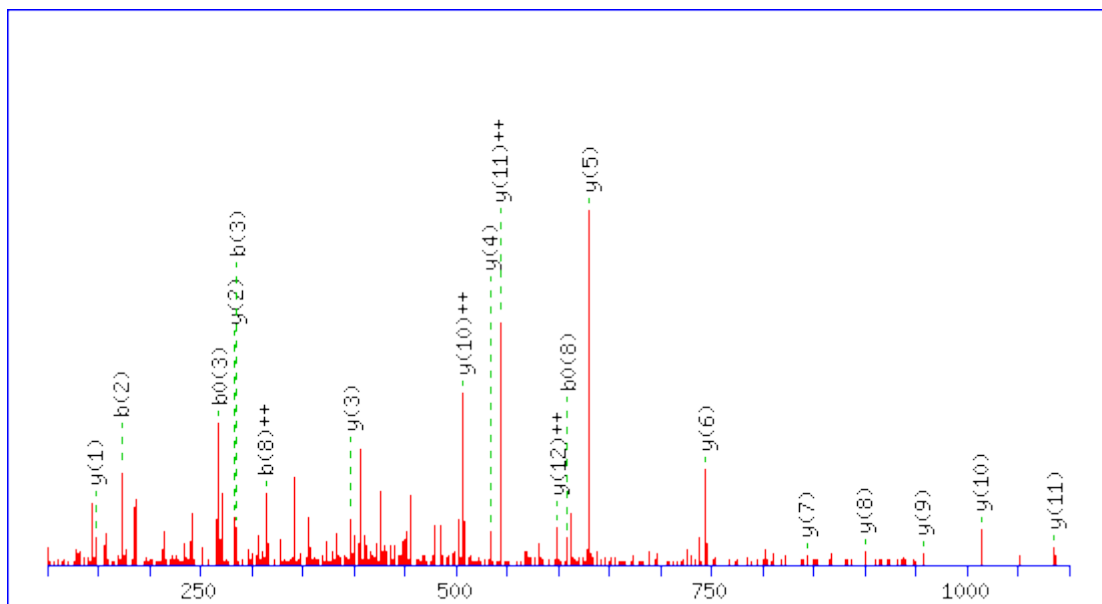
R9 : Label:13C(6)15N(4) (R)

Ions Score: 42 Expect: 0.013

Matches (Bold Red): 9/58 fragment ions using 10 most intense peaks

MS/MS Fragmentation of **ATIAGGGVIPHIHK**

Found in **H2AV_HUMAN**, Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3



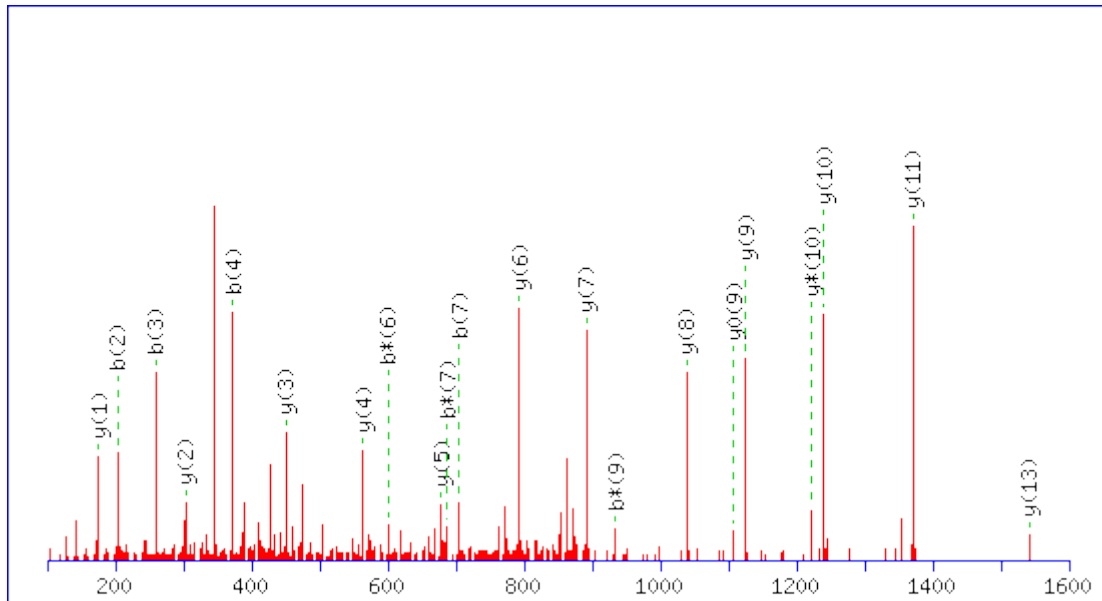
Monoisotopic mass of neutral peptide Mr(calc): 1369.7830

Ions Score: 45 Expect: 0.0076

Matches (**Bold Red**): 19/104 fragment ions using 58 most intense peaks

MS/MS Fragmentation of **AMGIMNSFVNDIFER**

Found in **H2B3B_HUMAN**, Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3



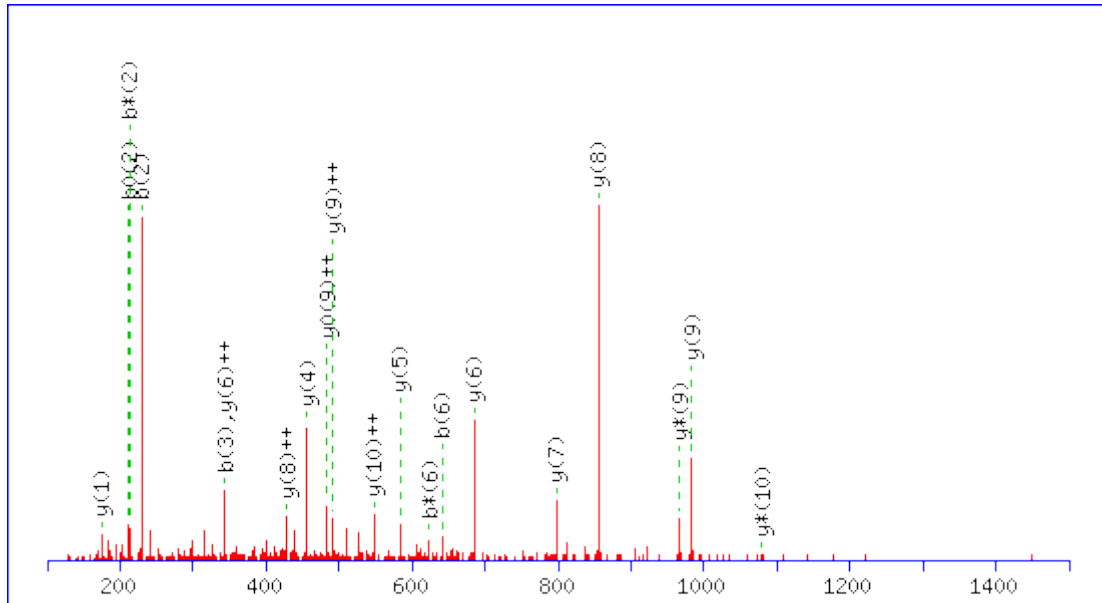
Monoisotopic mass of neutral peptide Mr(calc): 1742.8120

Ions Score: 97 Expect: 5.7e-008

Matches (**Bold Red**): 21/144 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **DNIQGITKPAIR**

Found in **H4_HUMAN**, Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2



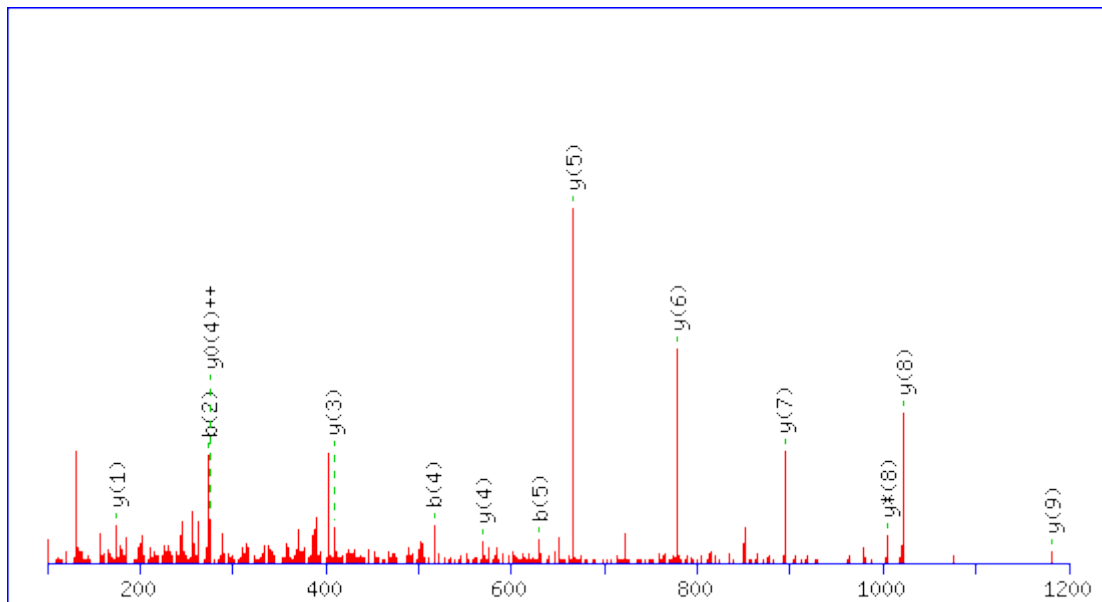
Monoisotopic mass of neutral peptide Mr(calc): 1324.7463

Ions Score: 45 Expect: 0.0088

Matches (Bold Red): 20/120 fragment ions using 35 most intense peaks

MS/MS Fragmentation of **LCQDLPCFSR**

Found in **HAT1_HUMAN**, Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1



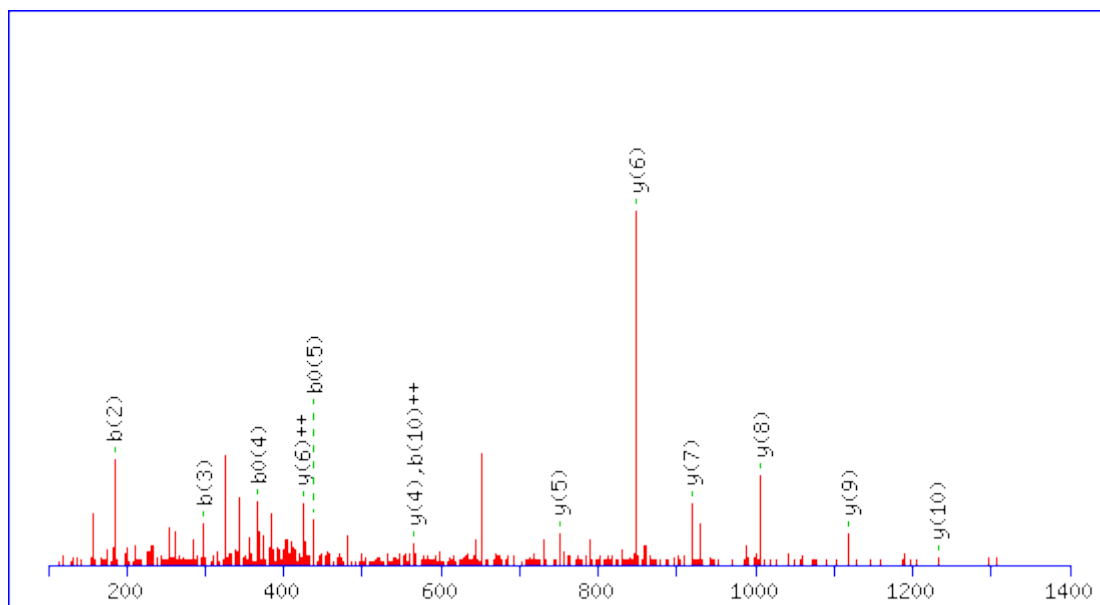
Monoisotopic mass of neutral peptide Mr(calc): 1294.5798

Ions Score: 51 Expect: 0.0011

Matches (**Bold Red**): 13/96 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **ALLSAPWYLNR**

Found in **HEXA_HUMAN**, Beta-hexosaminidase subunit alpha OS=Homo sapiens GN=HEXA
PE=1 SV=2



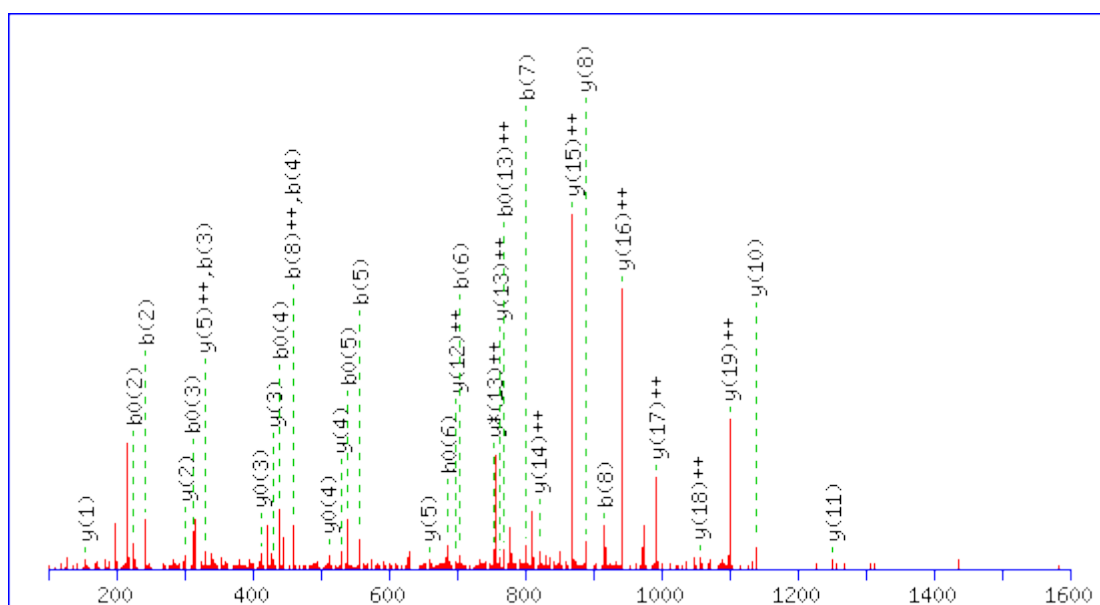
Monoisotopic mass of neutral peptide Mr(calc): 1302.7084

Ions Score: 38 Expect: 0.043

Matches (**Bold Red**): 13/82 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **EISEVFPDQFIHLGGDEVEFK**

Found in **HEXB_HUMAN**, Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB
PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 2442.1835

Variable modifications:

K21 : Label:13C(6)15N(2) (K)

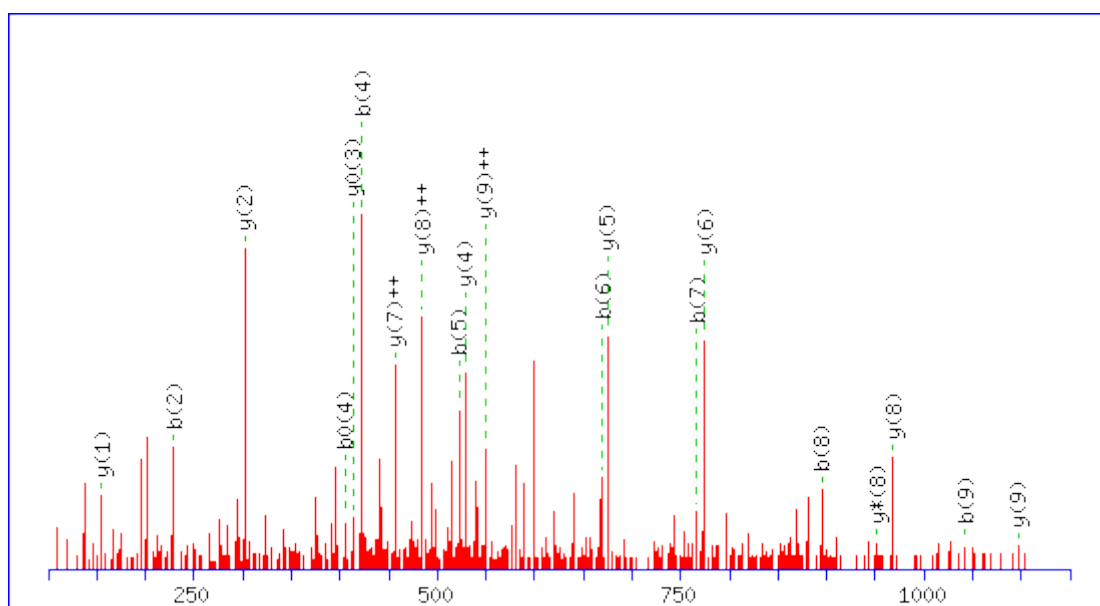
Ions Score: 39 Expect: 0.054

Matches (Bold Red): 34/220 fragment ions using 93 most intense peaks

MS/MS Fragmentation of **VEGHVFPFEK**

Found in **HGS_HUMAN**, Hepatocyte growth factor-regulated tyrosine kinase substrate

OS=Homo sapiens GN=HGS PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1195.6117

Variable modifications:

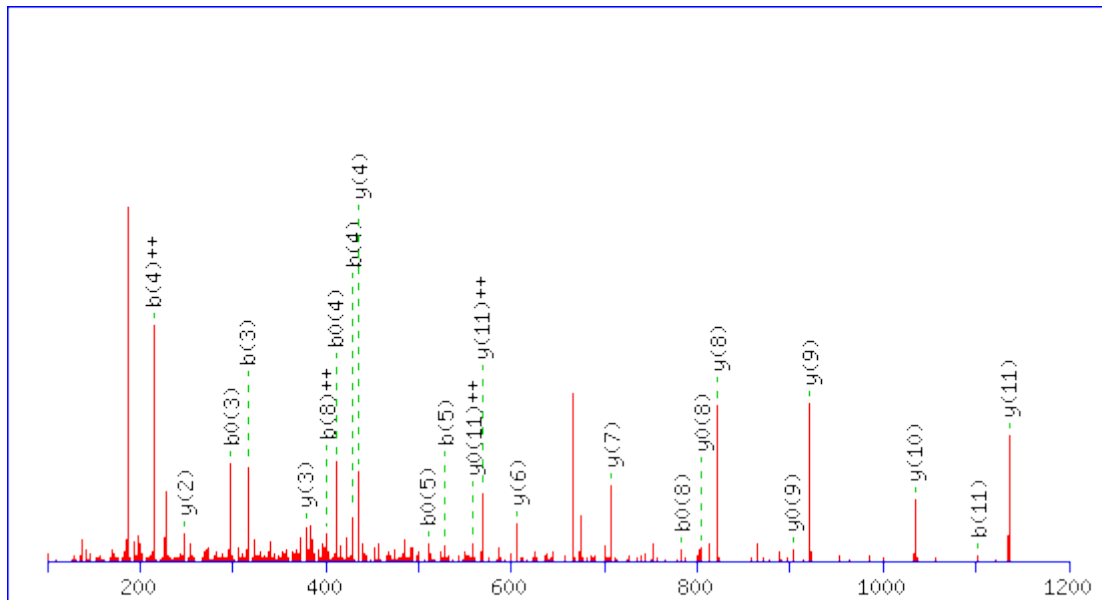
K10 : Label:13C(6)15N(2) (K)

Ions Score: 39 Expect: 0.036

Matches (Bold Red): 20/84 fragment ions using 41 most intense peaks

MS/MS Fragmentation of **TLTIVDTGIGMTK**

Found in **HS904_HUMAN**, Putative heat shock protein HSP 90-alpha A4 OS=Homo sapiens
GN=HSP90AA4P PE=5 SV=1



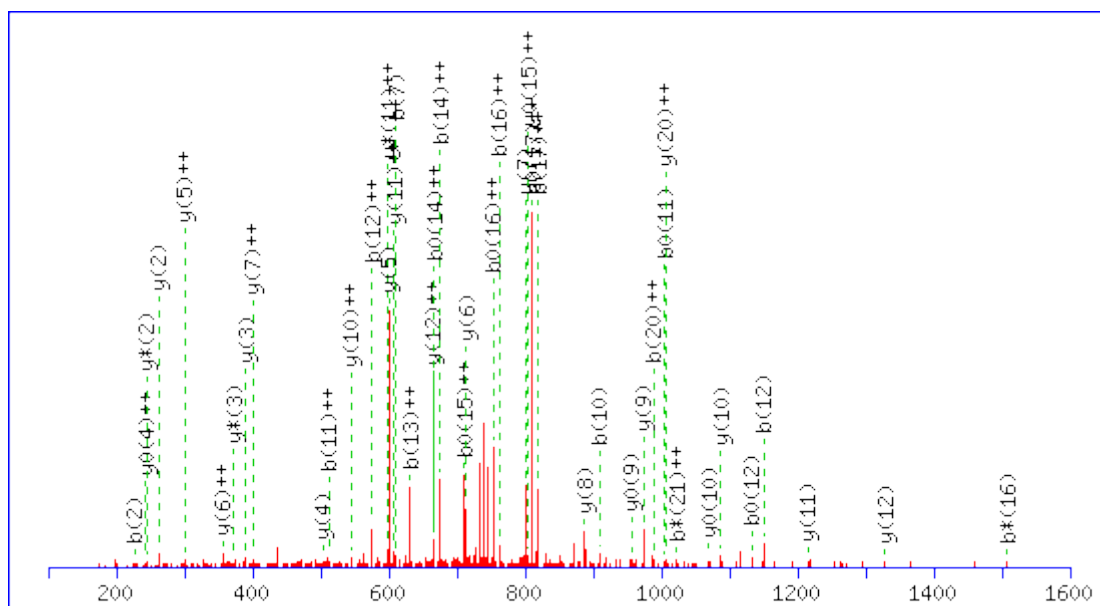
Monoisotopic mass of neutral peptide Mr(calc): 1348.7272

Ions Score: 53 Expect: 0.0014

Matches (Bold Red): 24/118 fragment ions using 46 most intense peaks

MS/MS Fragmentation of **LLGPSAAADILQLSSSLPLQSR**

Found in **HUWE1_HUMAN**, E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1
PE=1 SV=3



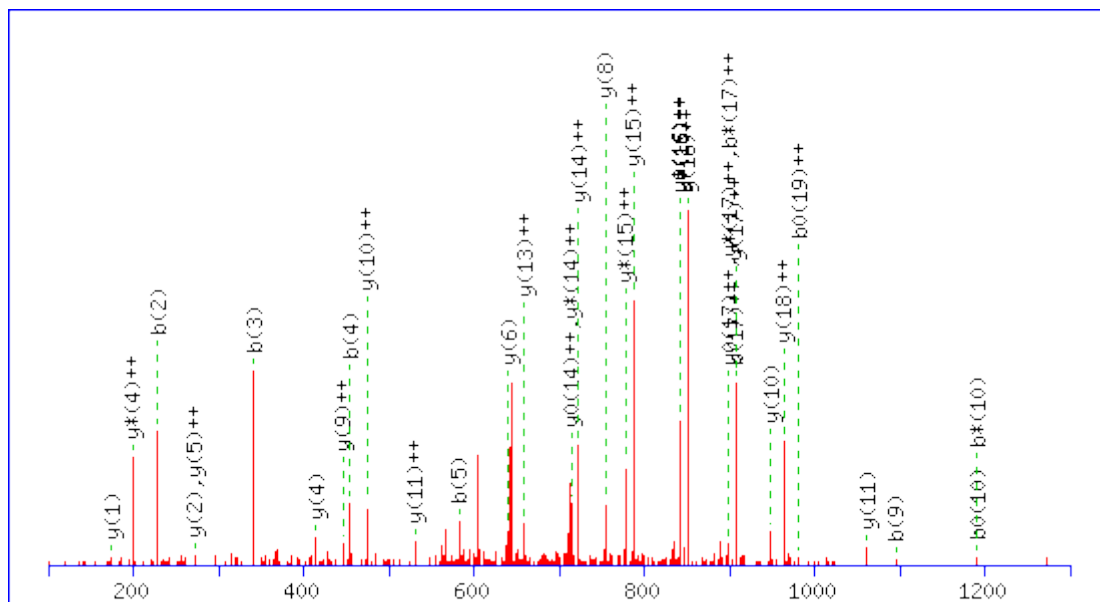
Monoisotopic mass of neutral peptide Mr(calc): 2236.2427

Ions Score: 39 Expect: 0.044

Matches (**Bold Red**): 44/220 fragment ions using 103 most intense peaks

MS/MS Fragmentation of **DILLQQQQQLGHGGPEAAPR**

Found in **I2BP2_HUMAN**, Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2 PE=1 SV=2



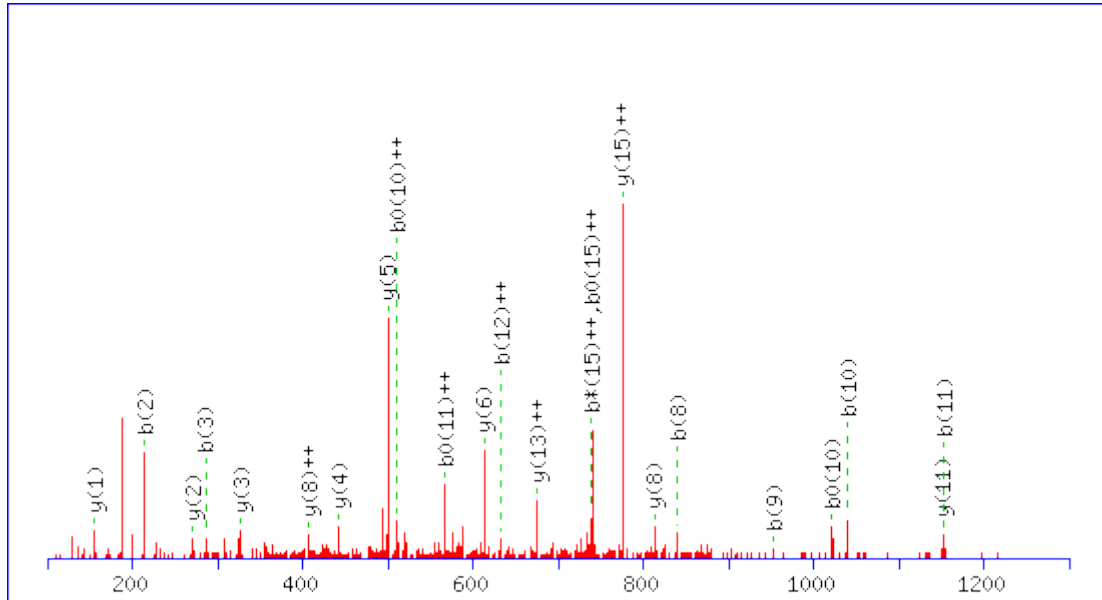
Monoisotopic mass of neutral peptide Mr(calc): 2155.1134

Ions Score: 51 Expect: 0.003

Matches (**Bold Red**): 35/212 fragment ions using 67 most intense peaks

MS/MS Fragmentation of **DVAEAKPELSLLGDDH**

Found in **IAH1_HUMAN**, Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1



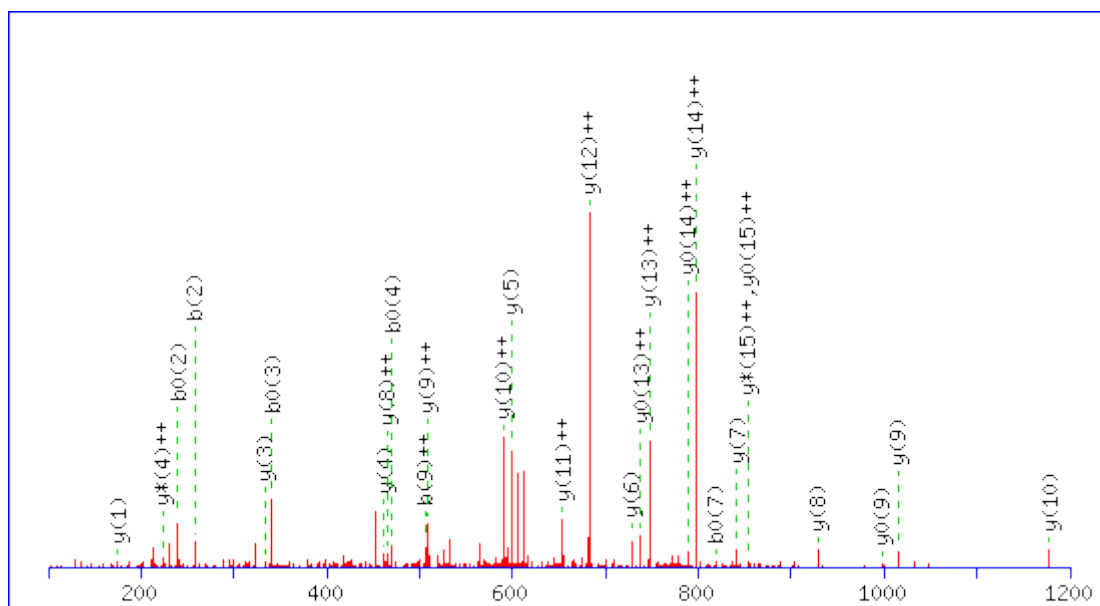
Monoisotopic mass of neutral peptide Mr(calc): 1764.8530

Ions Score: 59 Expect: 0.00047

Matches (**Bold Red**): 23/158 fragment ions using 38 most intense peaks

MS/MS Fragmentation of **EQTEGEYSSLEHESAR**

Found in **IDH3B_HUMAN**, Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B PE=1 SV=2



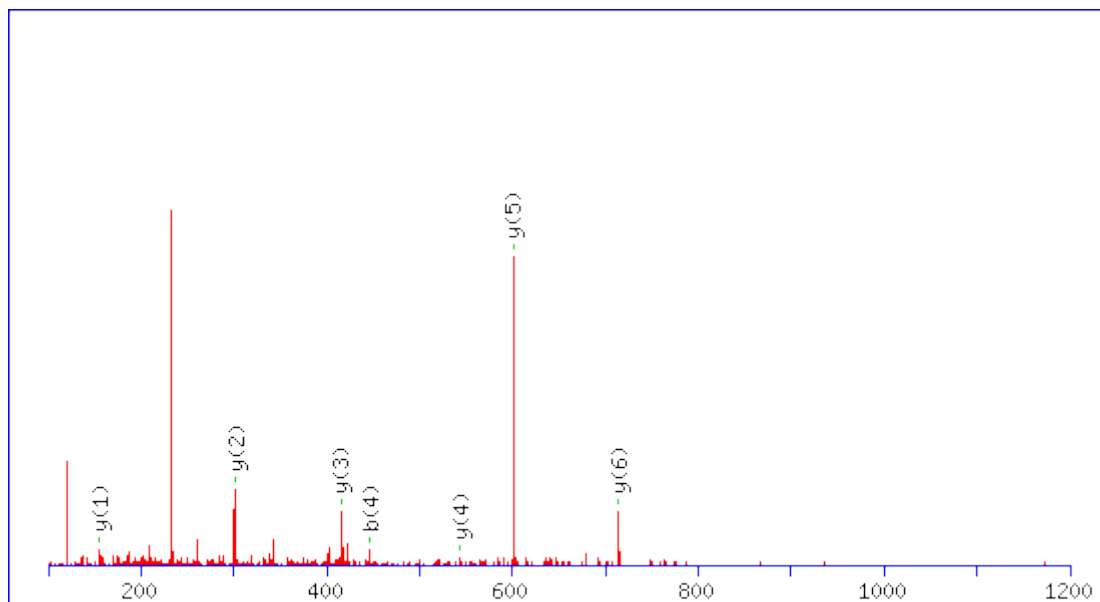
Monoisotopic mass of neutral peptide Mr(calc): 1850.7918

Ions Score: 43 Expect: 0.01

Matches (Bold Red): 28/174 fragment ions using 62 most intense peaks

MS/MS Fragmentation of **FIGELFK**

Found in **IF4G3_HUMAN**, Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 860.4887

Variable modifications:

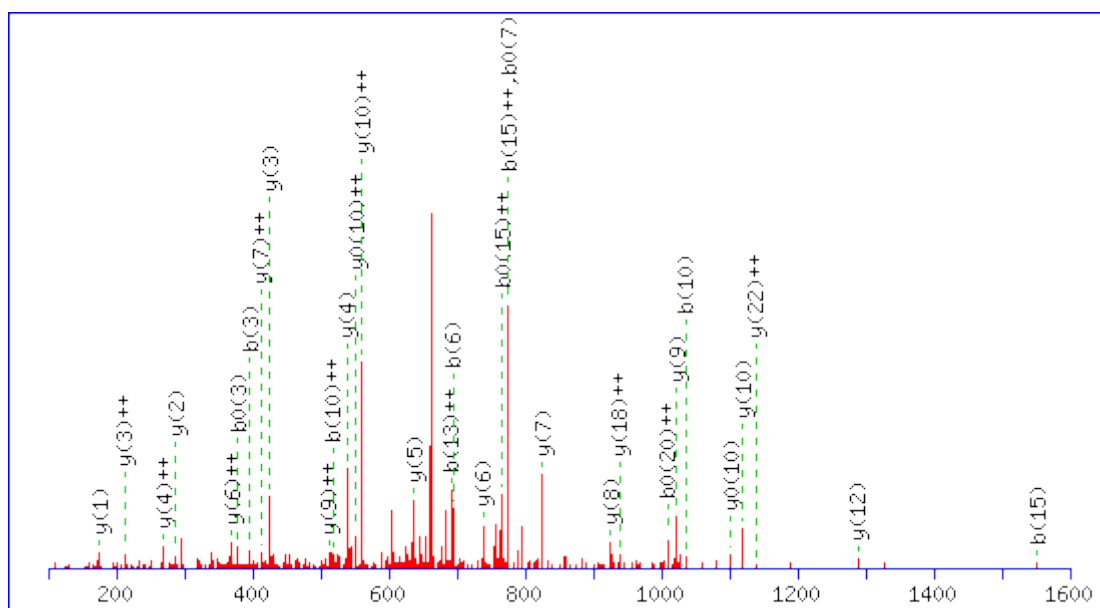
K7 : Label:13C(6)15N(2) (K)

Ions Score: 42 **Expect:** 0.013

Matches (Bold Red): 7/48 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **EEHEVAVLGAPHNPAPPTSTVIHIR**

Found in **IFM3_HUMAN**, Interferon-induced transmembrane protein 3 OS=Homo sapiens
GN=IFITM3 PE=1 SV=2



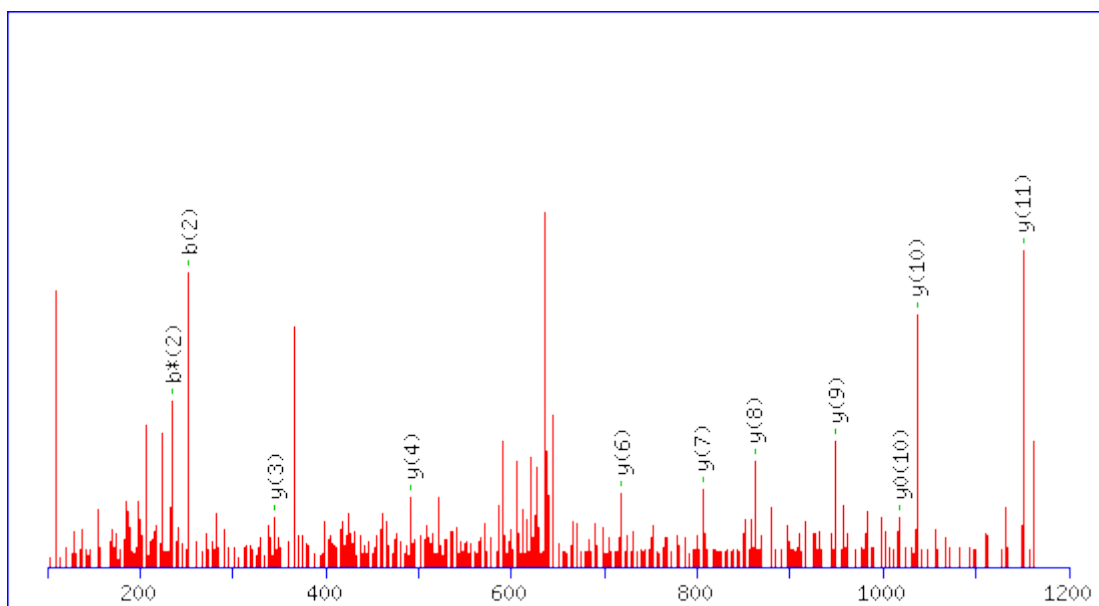
Monoisotopic mass of neutral peptide Mr(calc): 2670.3878

Ions Score: 60 **Expect:** 0.00044

Matches (Bold Red): 32/254 fragment ions using 51 most intense peaks

MS/MS Fragmentation of **HNSSGSILFLGR**

Found in **ILEU_HUMAN**, Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1
PE=1 SV=1



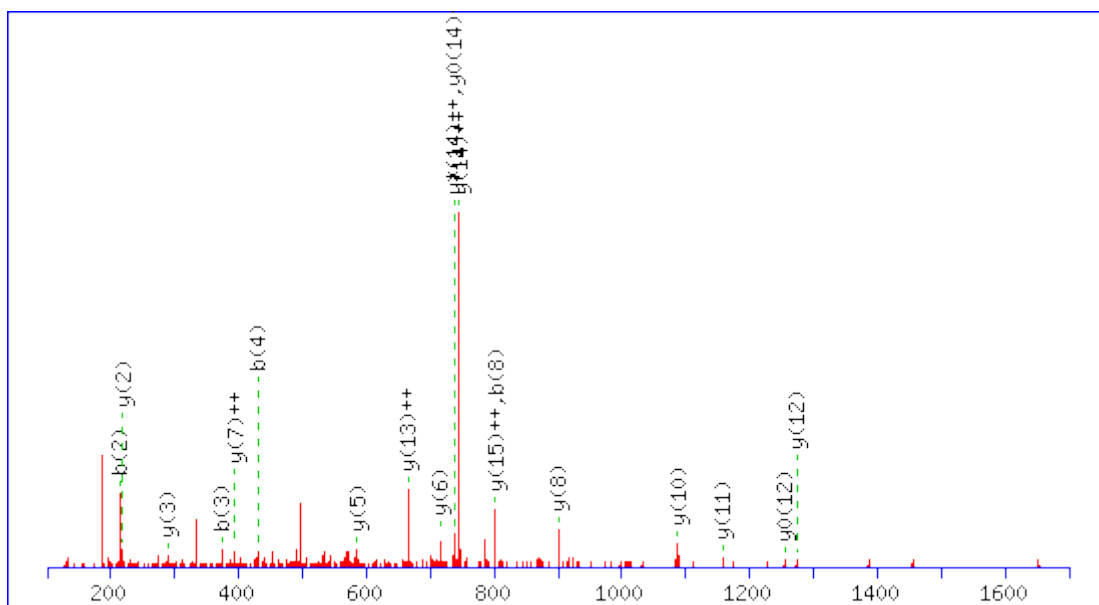
Monoisotopic mass of neutral peptide Mr(calc): 1286.6731

Ions Score: 51 Expect: 0.0022

Matches (**Bold Red**): 11/114 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **VLCGDAGEDAECHAAK**

Found in **IPO8_HUMAN**, Importin-8 OS=Homo sapiens GN=IPO8 PE=1 SV=2



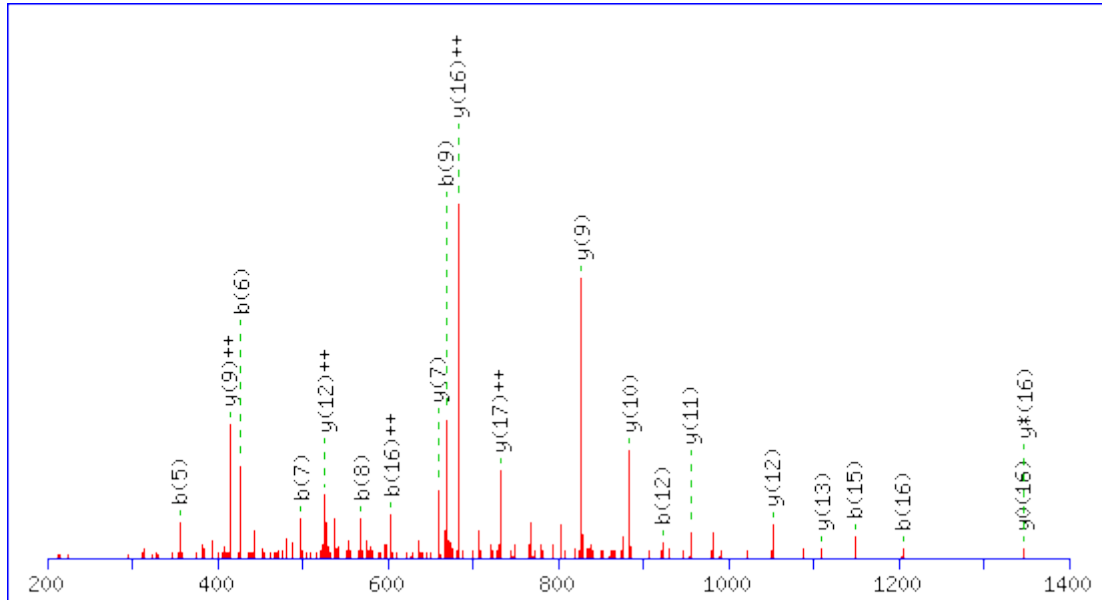
Monoisotopic mass of neutral peptide Mr(calc): 1701.7087

Ions Score: 41 Expect: 0.013

Matches (**Bold Red**): 19/132 fragment ions using 43 most intense peaks

MS/MS Fragmentation of **AAAAAAAAVPSAGPAGPAP TSAAGR**

Found in **IRS2_HUMAN**, Insulin receptor substrate 2 OS=Homo sapiens GN=IRS2 PE=1 SV=2



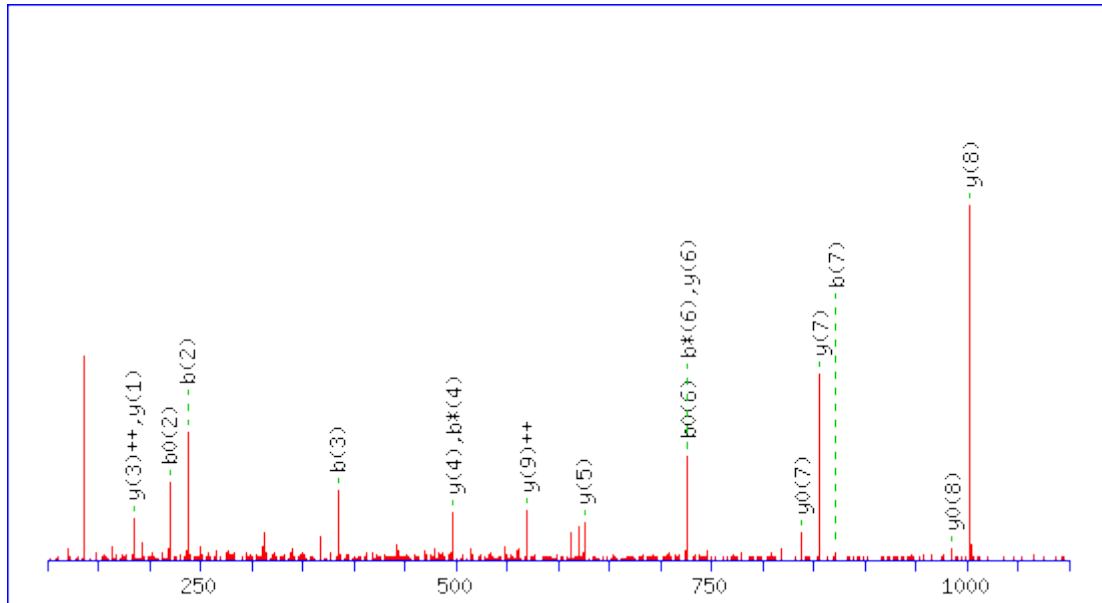
Monoisotopic mass of neutral peptide Mr(calc): 2031.0497

Ions Score: 51 Expect: 0.0034

Matches (**Bold Red**): 21/212 fragment ions using 32 most intense peaks

MS/MS Fragmentation of **TKFETEQALR**

Found in **K1C17_HUMAN**, Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1239.6578

Variable modifications:

K2 : Label:13C(6)15N(2) (K)

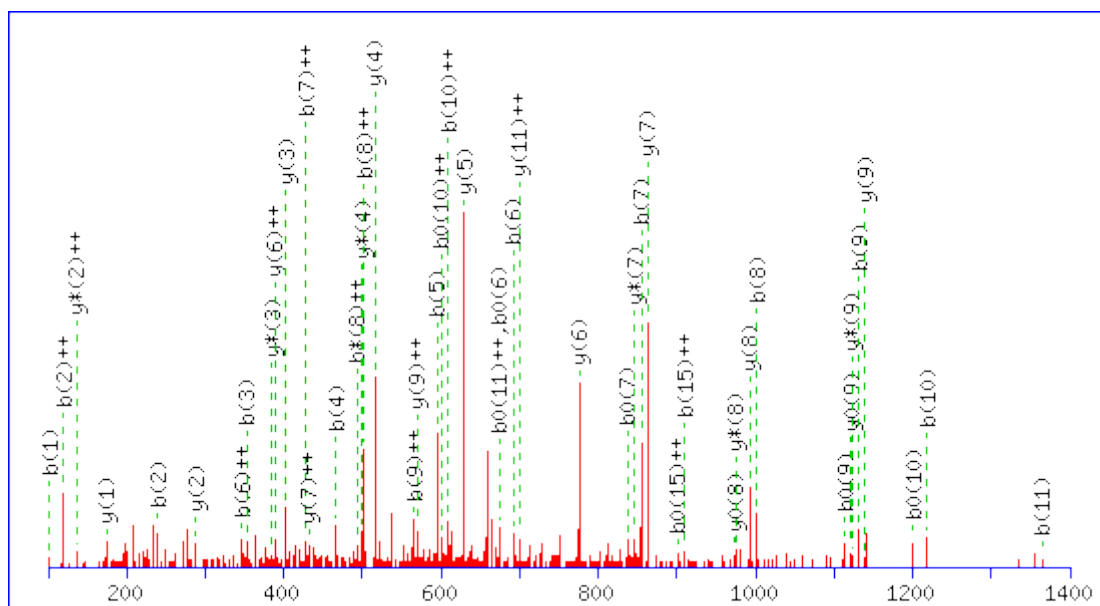
R10 : Label:13C(6)15N(4) (R)

Ions Score: 40 Expect: 0.024

Matches (Bold Red): 17/98 fragment ions using 21 most intense peaks

MS/MS Fragmentation of **THNLEPYFESFINLR**

Found in **K2C1_HUMAN**, Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6



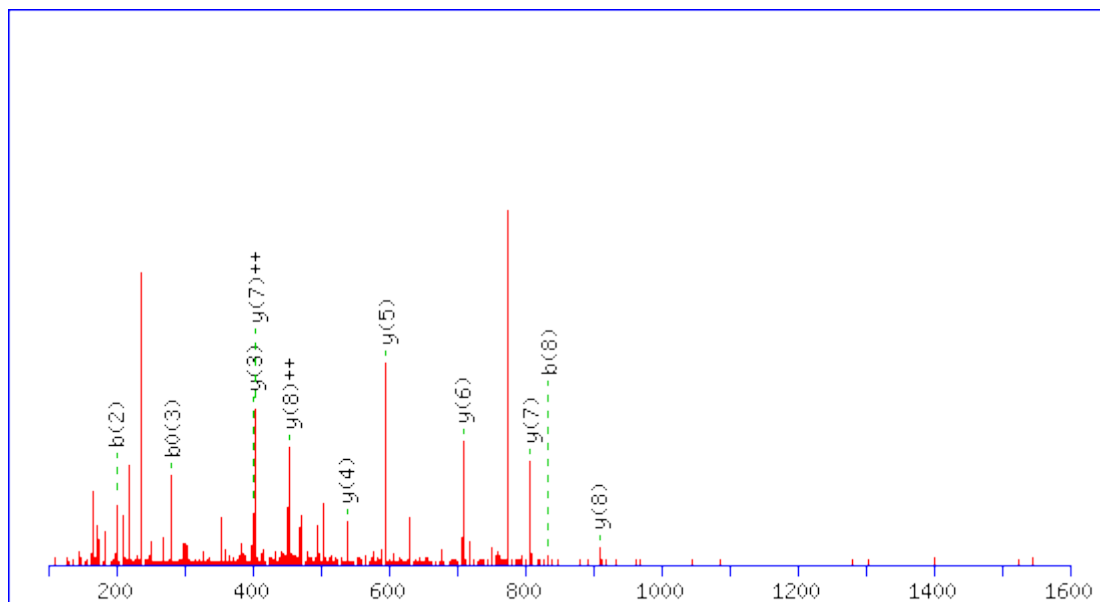
Monoisotopic mass of neutral peptide Mr(calc): 1992.9693

Ions Score: 61 **Expect:** 0.00027

Matches (Bold Red): 47/164 fragment ions using 95 most intense peaks

MS/MS Fragmentation of **VTVLGHVQR**

Found in **K6PL_HUMAN**, 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL
PE=1 SV=6



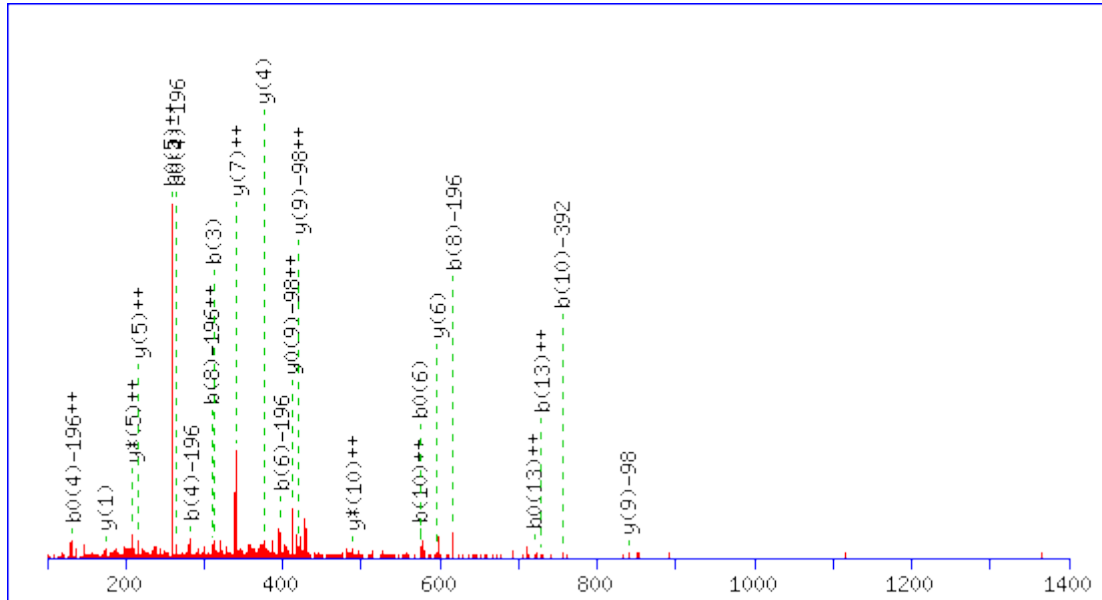
Monoisotopic mass of neutral peptide Mr(calc): 1007.5876

Ions Score: 40 **Expect:** 0.021

Matches (**Bold Red**): 11/66 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **GSSSGGYSSGSSSYGSGGR**

Found in **K22E_HUMAN**, Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens
GN=KRT2 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 2139.5299

Variable modifications:

S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

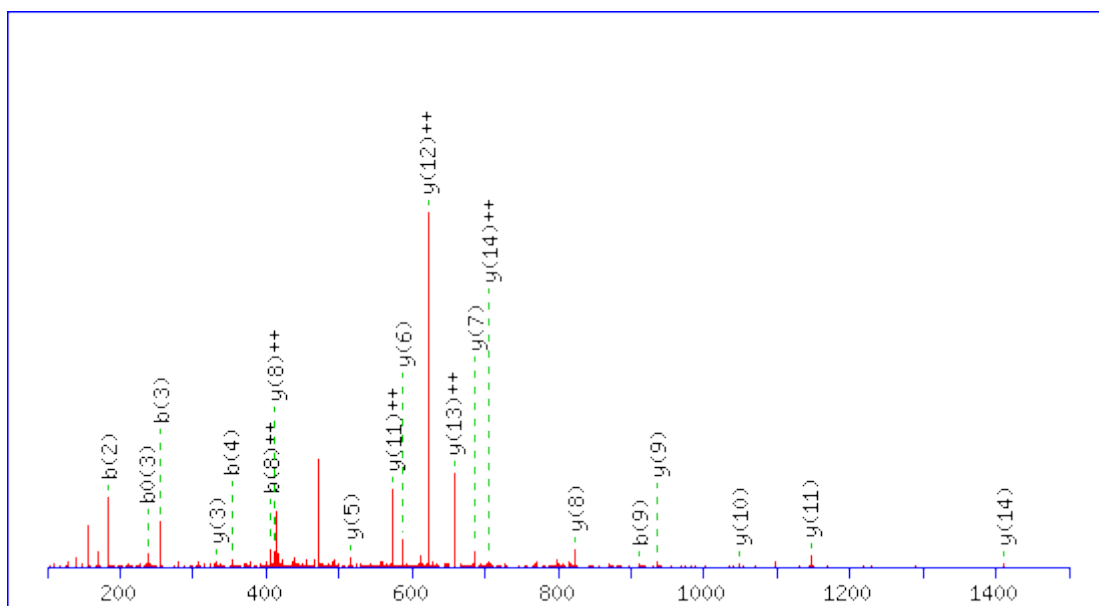
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 4 Expect: 8.9

Matches (**Bold Red**): 23/316 fragment ions using 76 most intense peaks

MS/MS Fragmentation of **SPAPLLHVAALGQK**

Found in **K1967_HUMAN**, Protein KIAA1967 OS=Homo sapiens GN=KIAA1967 PE=1 SV=2



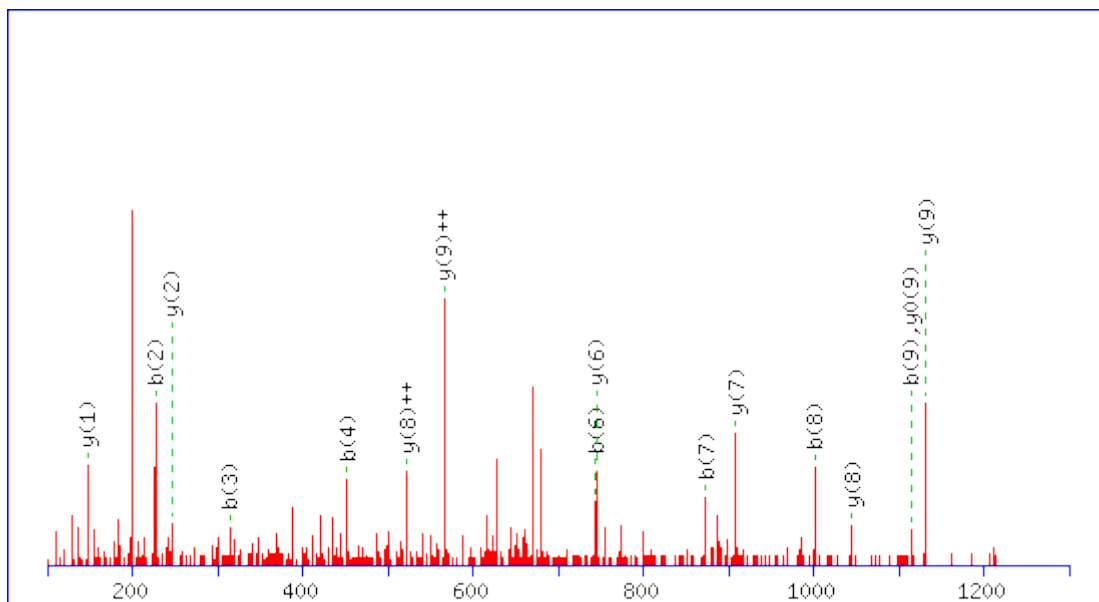
Monoisotopic mass of neutral peptide Mr(calc): 1497.8667

Ions Score: 51 Expect: 0.0022

Matches (Bold Red): 20/114 fragment ions using 43 most intense peaks

MS/MS Fragmentation of **NISHYEEQLVK**

Found in **KAP2_HUMAN**, cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2



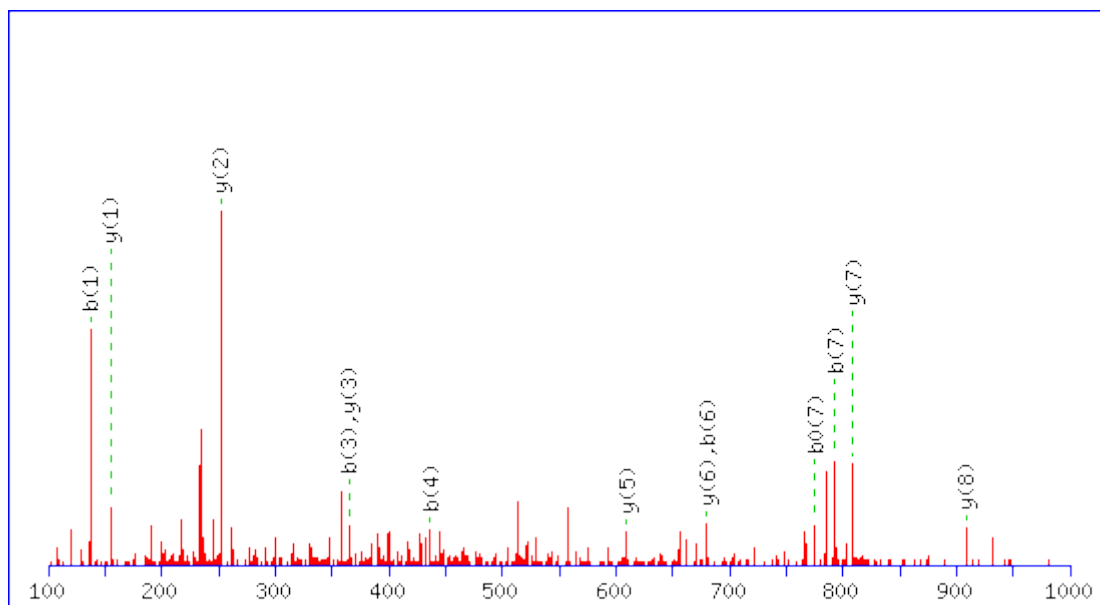
Monoisotopic mass of neutral peptide Mr(calc): 1358.6830

Ions Score: 48 Expect: 0.0038

Matches (Bold Red): 16/108 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **KVEAPFIPK**

Found in **KAPCA_HUMAN**, cAMP-dependent protein kinase catalytic subunit alpha
OS=Homo sapiens GN=PRKACA PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1043.6350

Variable modifications:

K1 : Label:13C(6)15N(2) (K)

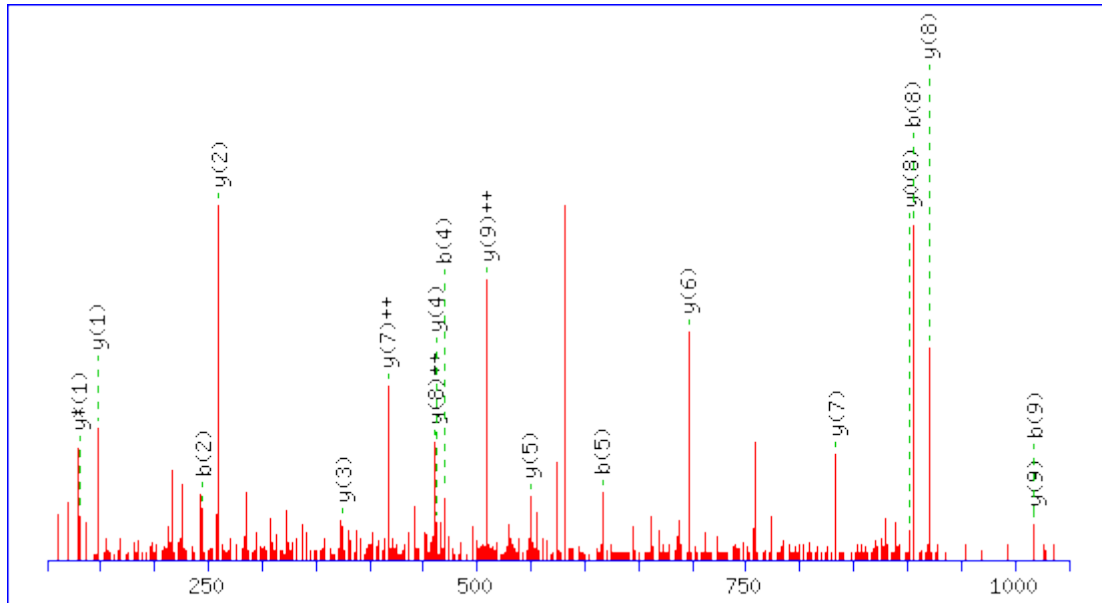
K9 : Label:13C(6)15N(2) (K)

Ions Score: 40 **Expect:** 0.02

Matches (Bold Red): 13/80 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **FPSHFSSDLK**

Found in **KAPCB_HUMAN**, cAMP-dependent protein kinase catalytic subunit beta
OS=Homo sapiens GN=PRKACB PE=1 SV=2



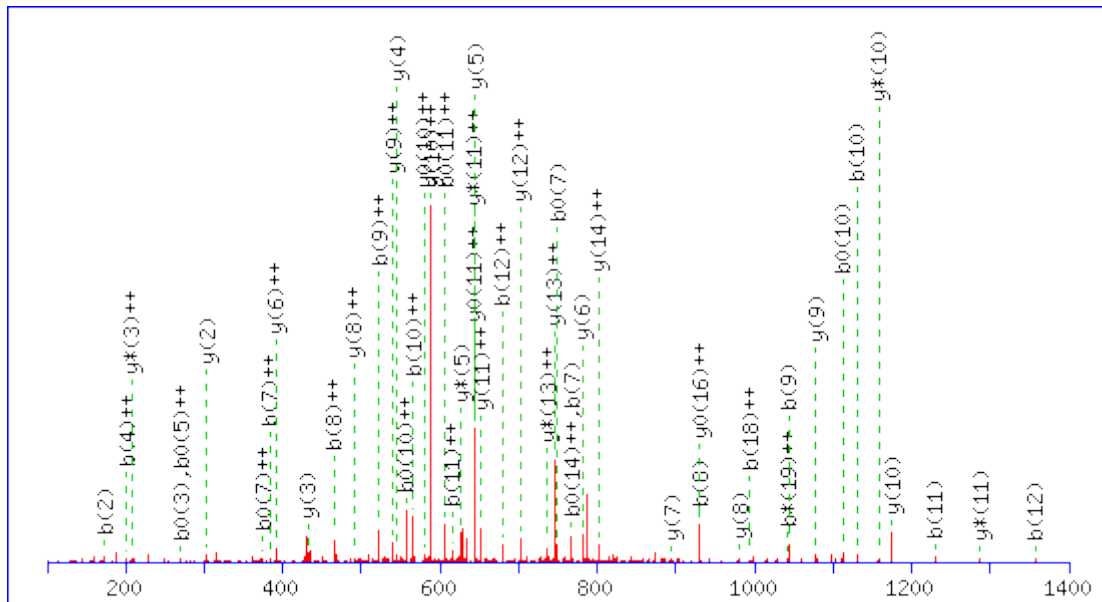
Monoisotopic mass of neutral peptide Mr(calc): 1163.5611

Ions Score: 44 Expect: 0.0073

Matches (**Bold Red**): 19/82 fragment ions using 59 most intense peaks

MS/MS Fragmentation of **ATDLRPIYISVQPPSLHVLEQR**

Found in **KGUA_HUMAN**, Guanylate kinase OS=Homo sapiens GN=GUK1 PE=1 SV=2



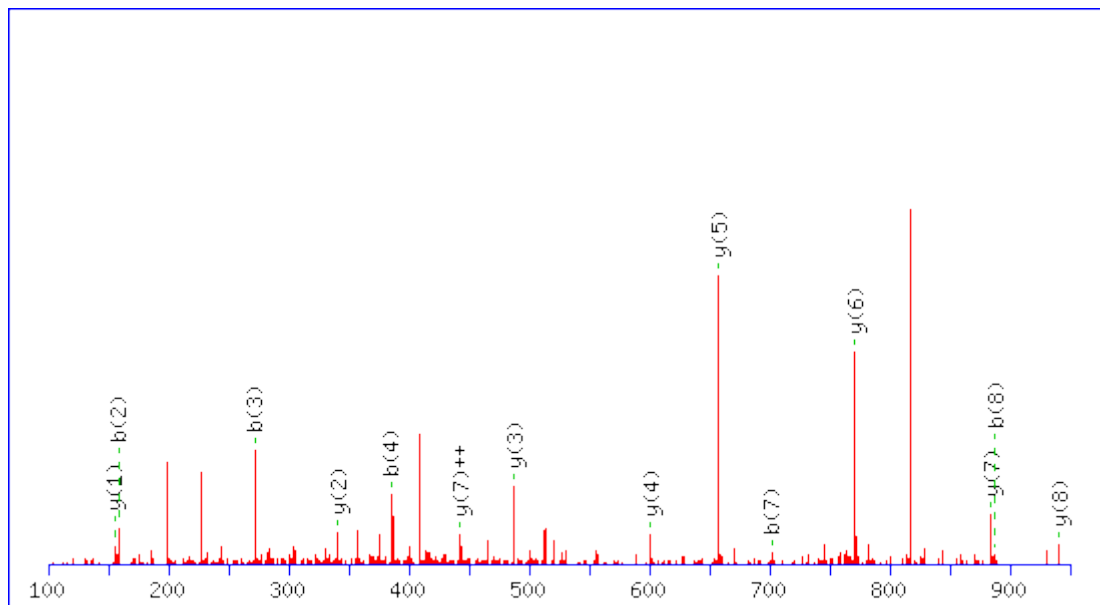
Monoisotopic mass of neutral peptide Mr(calc): 2531.3860

Ions Score: 42 Expect: 0.027

Matches (Bold Red): 50/238 fragment ions using 113 most intense peaks

MS/MS Fragmentation of **TGLLGIFWK**

Found in **KISHA_HUMAN**, Protein kish-A OS=Homo sapiens GN=TMEM167A PE=2 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1041.6103

Variable modifications:

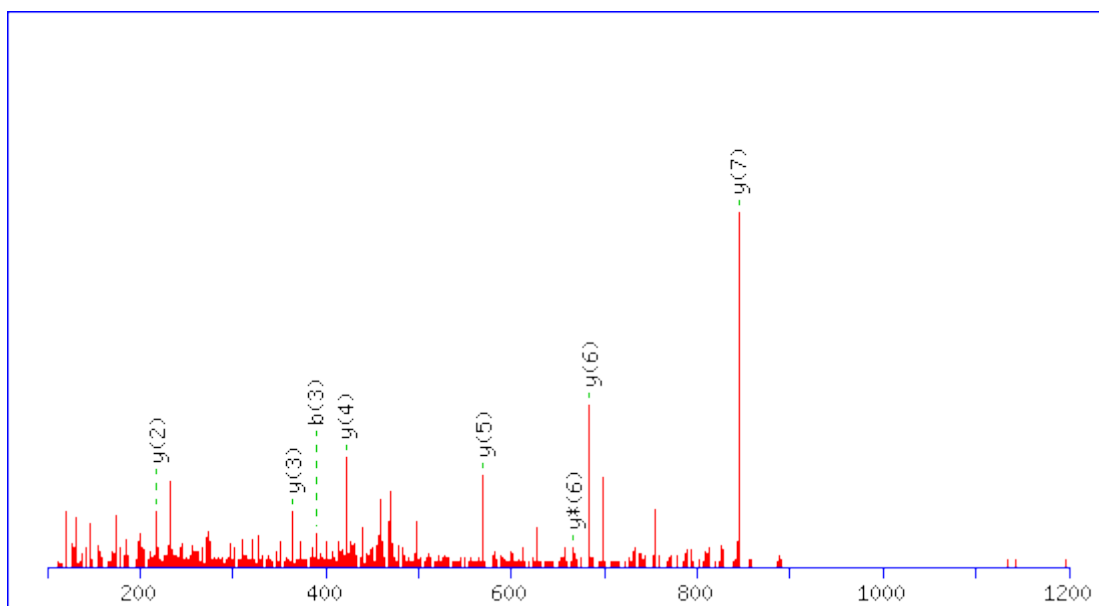
K9 : Label:13C(6)15N(2) (K)

Ions Score: 45 **Expect:** 0.0065

Matches (Bold Red): 14/64 fragment ions using 39 most intense peaks

MS/MS Fragmentation of **ICDFGFAK**

Found in **KS6A3_HUMAN**, Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens
GN=RPS6KA3 PE=1 SV=1



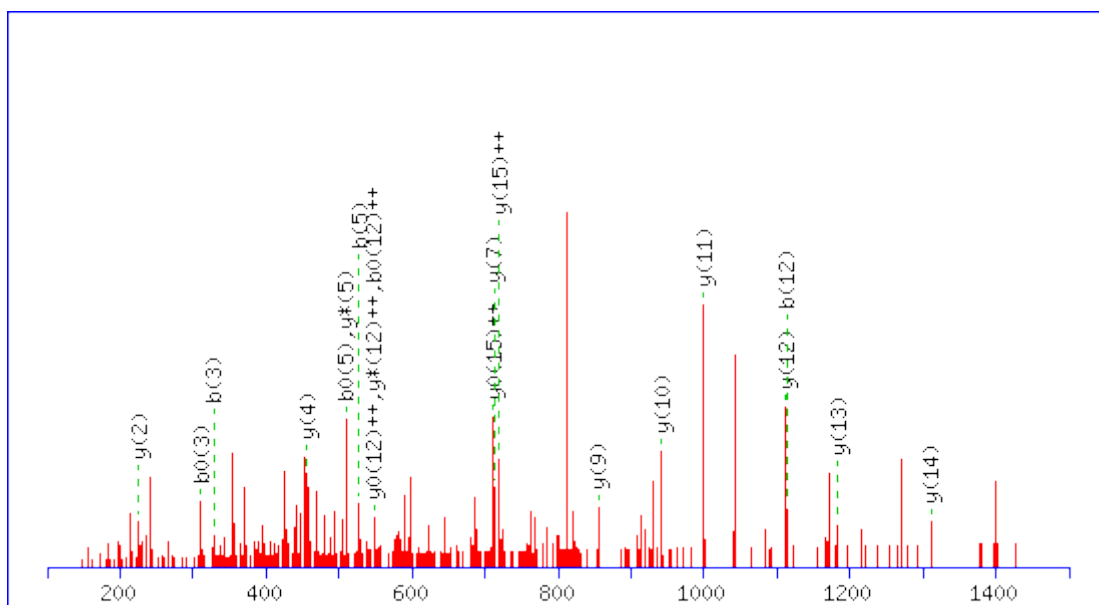
Monoisotopic mass of neutral peptide Mr(calc): 956.4426

Ions Score: 39 Expect: 0.024

Matches (**Bold Red**): 8/56 fragment ions using 20 most intense peaks

MS/MS Fragmentation of **EAQQALGSAAADATEAK**

Found in **LAMC1_HUMAN**, Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1638.7940

Variable modifications:

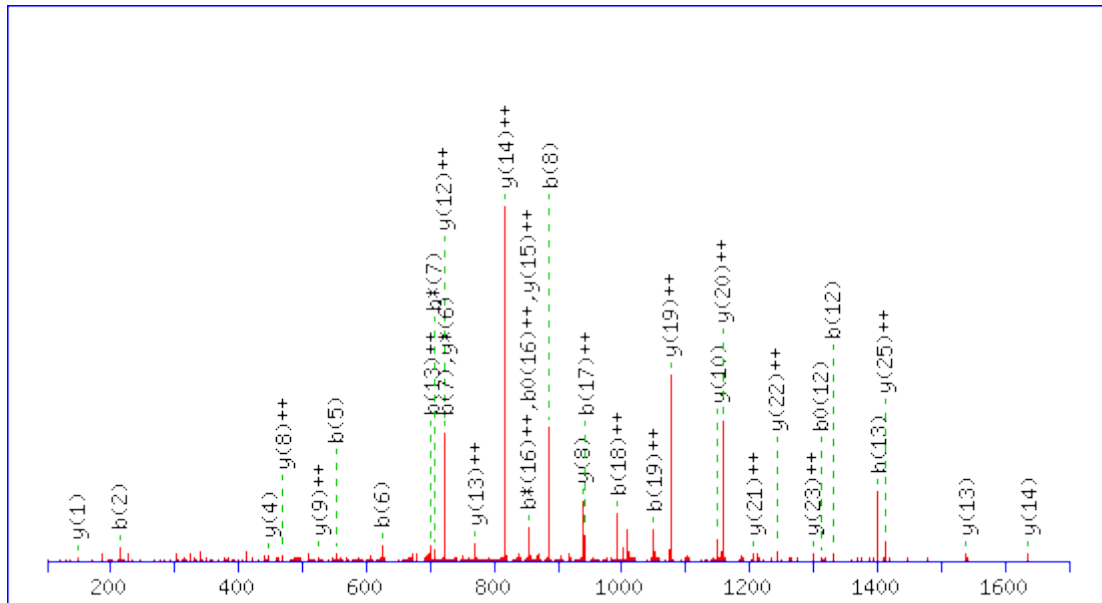
K17 : Label:13C(6)15N(2) (K)

Ions Score: 44 **Expect:** 0.014

Matches (Bold Red): 20/184 fragment ions using 41 most intense pea

MS/MS Fragmentation of **NVPEIAVYPAFEAPPQYVLPTYEMAVK**

Found in **LAP4A_HUMAN**, Lysosomal-associated transmembrane protein 4A OS=Homo sapiens GN=LAPTM4A PE=1 SV=1



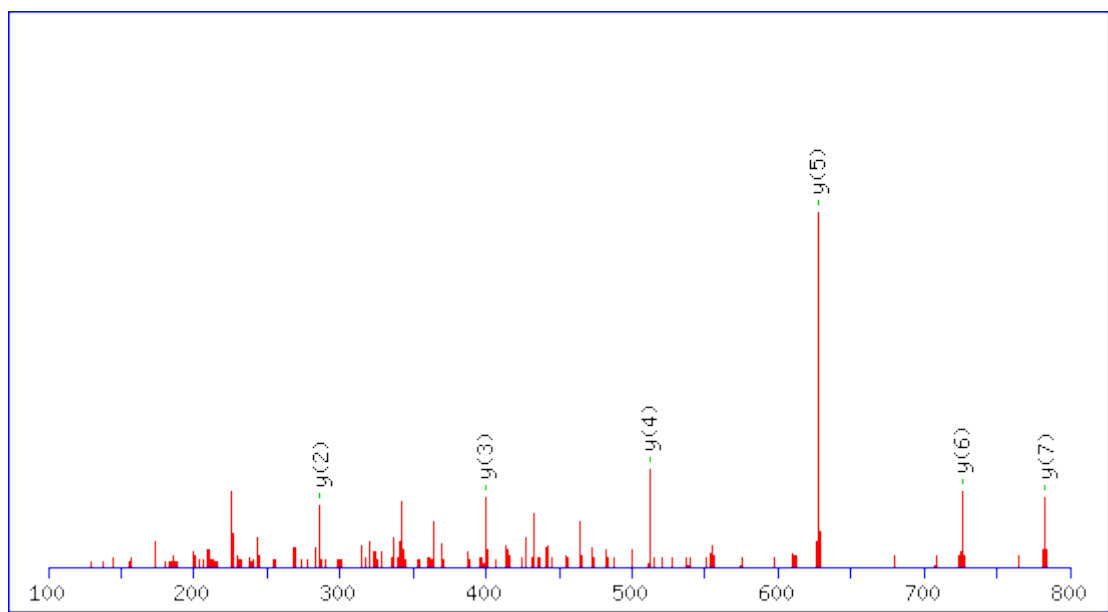
Monoisotopic mass of neutral peptide Mr(calc): 3035.5354

Ions Score: 78 **Expect:** 6.8e-006

Matches (Bold Red): 34/298 fragment ions using 47 most intense peaks

MS/MS Fragmentation of **DGVDLITR**

Found in **LCA5_HUMAN**, Lebercilin OS=Homo sapiens GN=LCA5 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 897.4795

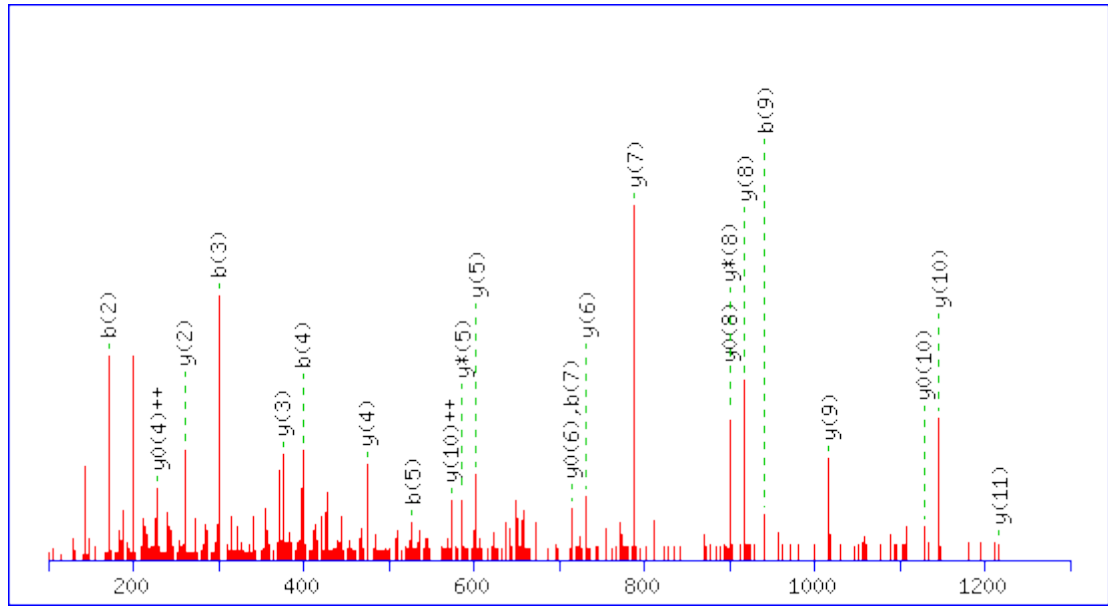
Variable modifications:

R8 : Label:13C(6)15N(4) (R)

Ions Score: 58 Expect: 0.00028

Matches (Bold Red): 6/68 fragment ions using 8 most intense peaks

MS/MS Fragmentation of **VAEVEGEQVDNK**
 Found in **LETM1_HUMAN**, LETM1 and EF-hand domain-containing protein 1,
 mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1



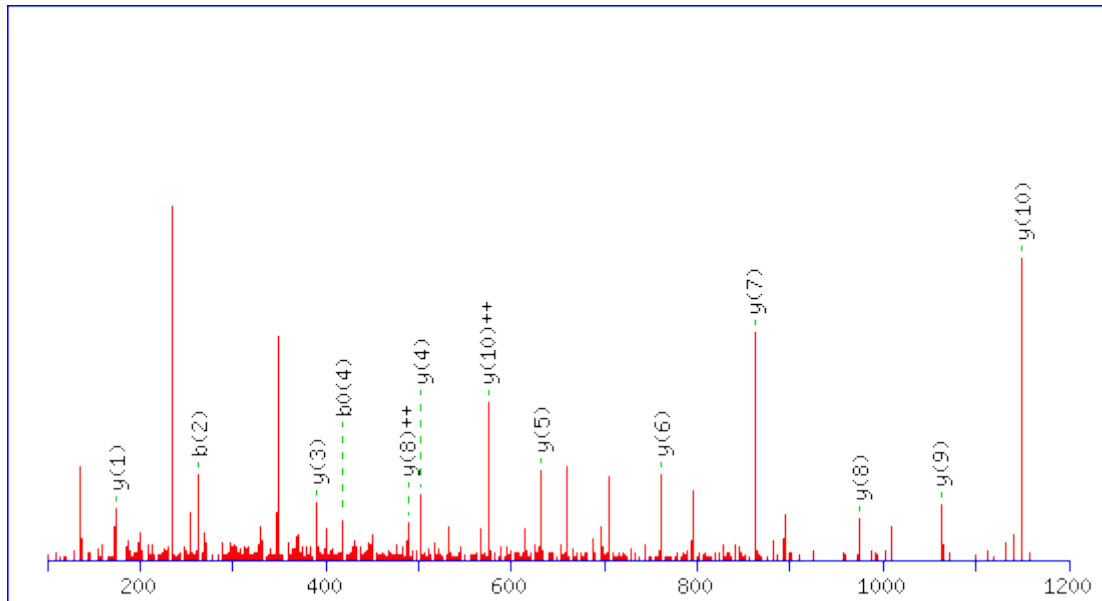
Monoisotopic mass of neutral peptide Mr(calc): 1315.6256

Ions Score: 76 **Expect:** 5.8e-006

Matches (Bold Red): 23/110 fragment ions using 37 most intense peaks

MS/MS Fragmentation of **YVSSLTEEISKR**

Found in **LMAN1_HUMAN**, Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2



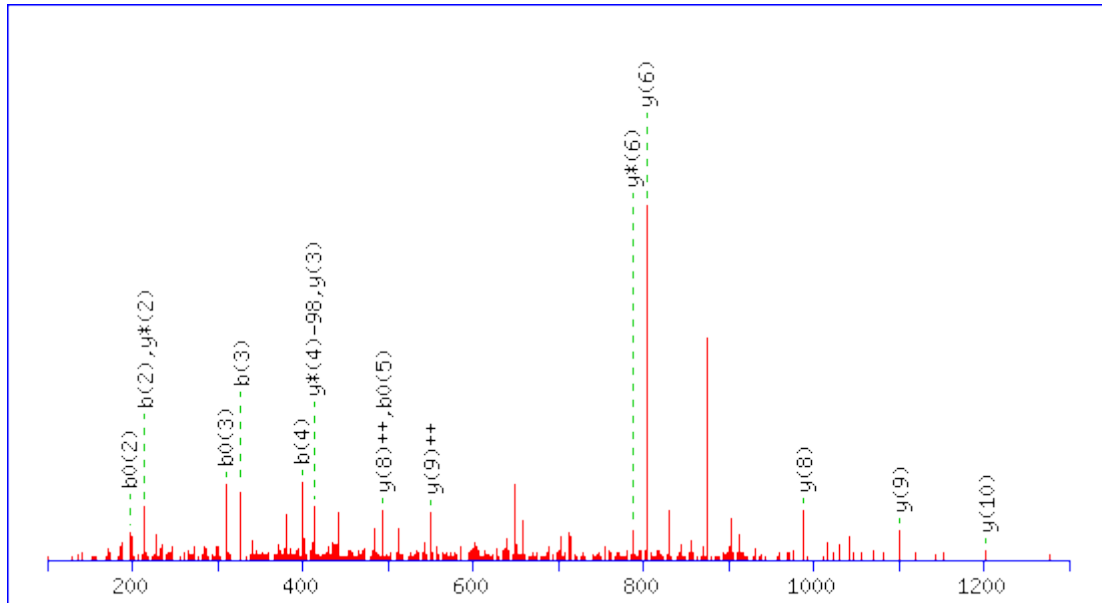
Monoisotopic mass of neutral peptide Mr(calc): 1410.7354

Ions Score: 60 **Expect:** 0.00028

Matches (Bold Red): 13/104 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **ITLALMEDTGR**

Found in **LMLN_HUMAN**, Leishmanolysin-like peptidase OS=Homo sapiens GN=LMLN PE=2 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1314.5891

Variable modifications:

M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

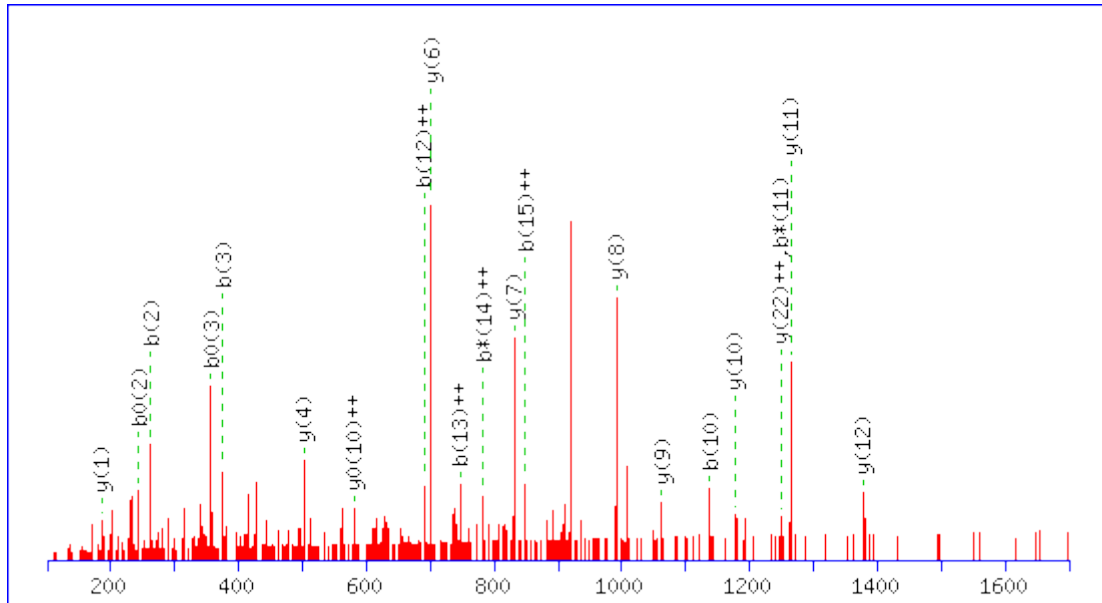
Ions Score: 41 Expect: 0.02

Matches (Bold Red): 16/238 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **CTLPEHESPSQDISDACEAESTER**

Found in **LRRF1_HUMAN**, Leucine-rich repeat flightless-interacting protein 1

OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 2757.1369

Variable modifications:

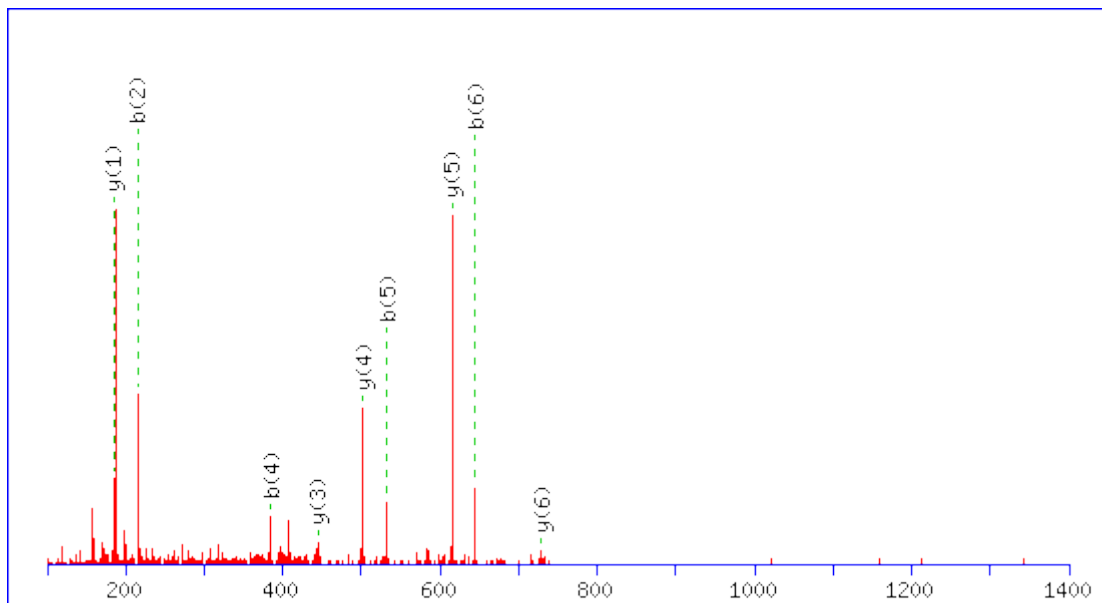
R24 : Label: $^{13}\text{C}(6)^{15}\text{N}(4)$ (R)

Ions Score: 48 **Expect: 0.0039**

Matches (Bold Red): 21/252 fragment ions using 38 most intense peaks

MS/MS Fragmentation of **TLIGFLR**

Found in **LSM1_HUMAN**, U6 snRNA-associated Sm-like protein LSM1 OS=Homo sapiens
GN=LSM1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 828.5097

Variable modifications:

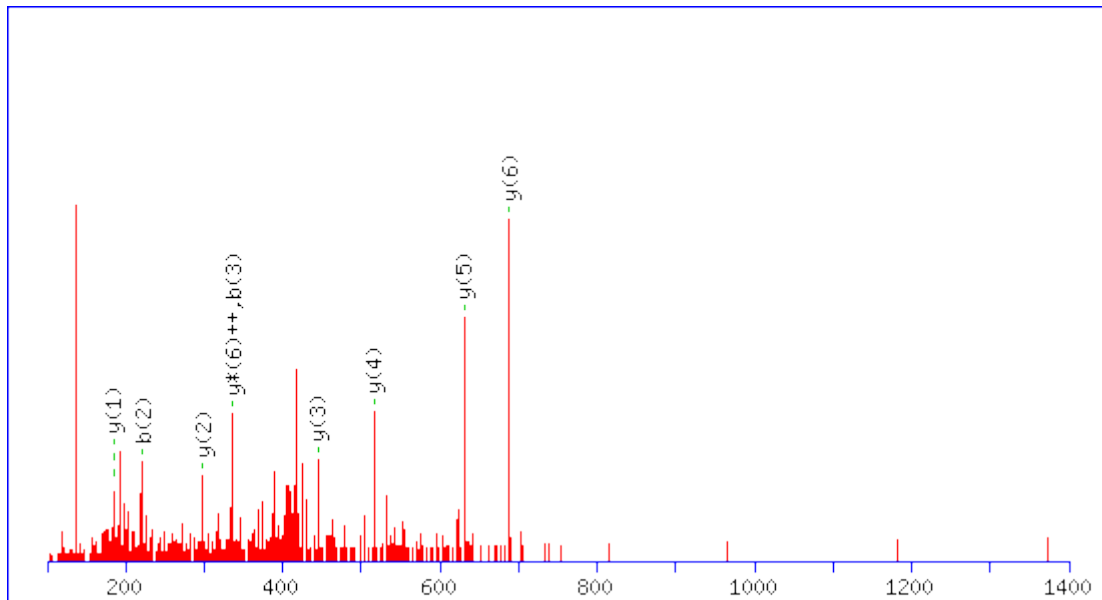
R7 : Label:13C(6)15N(4) (R)

Ions Score: 42 Expect: 0.013

Matches (Bold Red): 9/48 fragment ions using 14 most intense peaks

MS/MS Fragmentation of **YGDAFIR**

Found in **LSM6_HUMAN**, U6 snRNA-associated Sm-like protein LSM6 OS=Homo sapiens
GN=LSM6 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 850.4213

Variable modifications:

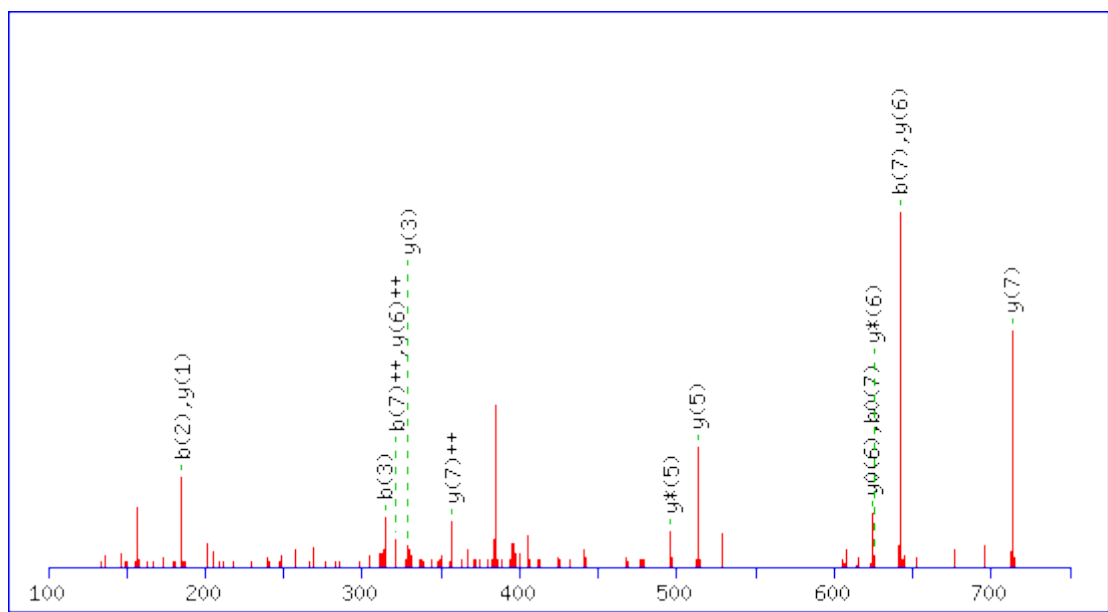
R7 : Label:13C(6)15N(4) (R)

Ions Score: 38 Expect: 0.025

Matches (Bold Red): 9/48 fragment ions using 25 most intense peaks

MS/MS Fragmentation of **LAELAGSR**

Found in **MALT1_HUMAN**, Mucosa-associated lymphoid tissue lymphoma translocation
protein 1 OS=Homo sapiens GN=MALT1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 825.4584

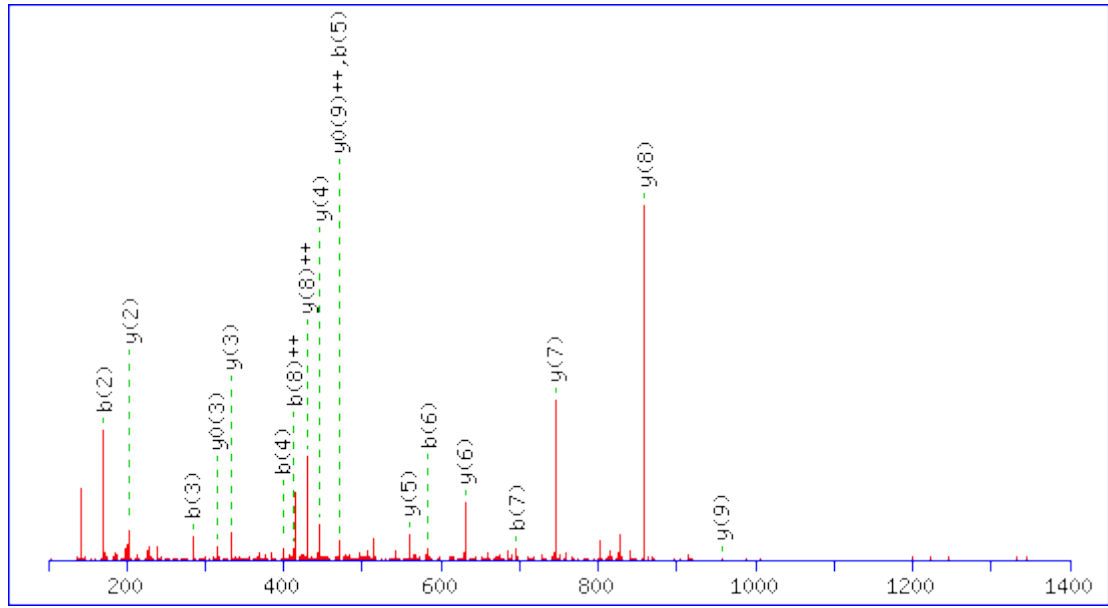
Variable modifications:

R8 : Label:13C(6)15N(4) (R)

Ions Score: 39 Expect: 0.022

Matches (Bold Red): 15/64 fragment ions using 20 most intense peaks

MS/MS Fragmentation of **AVLDALLEGK**
 Found in **MAP1A_HUMAN**, Microtubule-associated protein 1A OS=Homo sapiens GN=MAP1A
 PE=1 SV=6



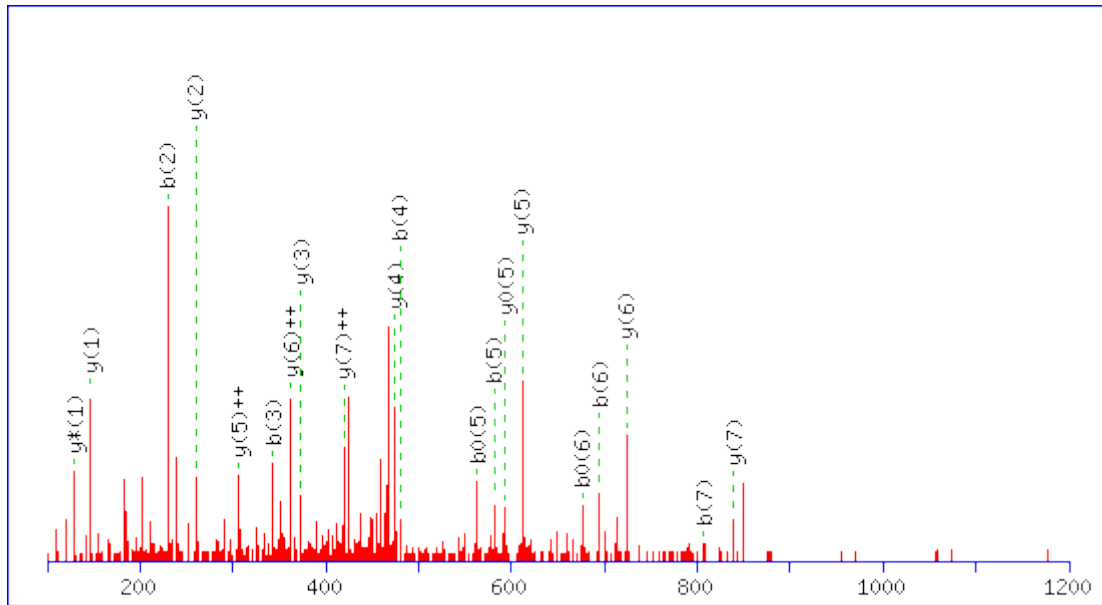
Monoisotopic mass of neutral peptide Mr(calc): 1027.5913

Ions Score: 50 Expect: 0.0021

Matches (Bold Red): 18/80 fragment ions using 44 most intense peaks

MS/MS Fragmentation of **NDIHTLLK**

Found in **MCA3_HUMAN**, Eukaryotic translation elongation factor 1 epsilon-1 OS=Homo sapiens GN=EEF1E1 PE=1 SV=1



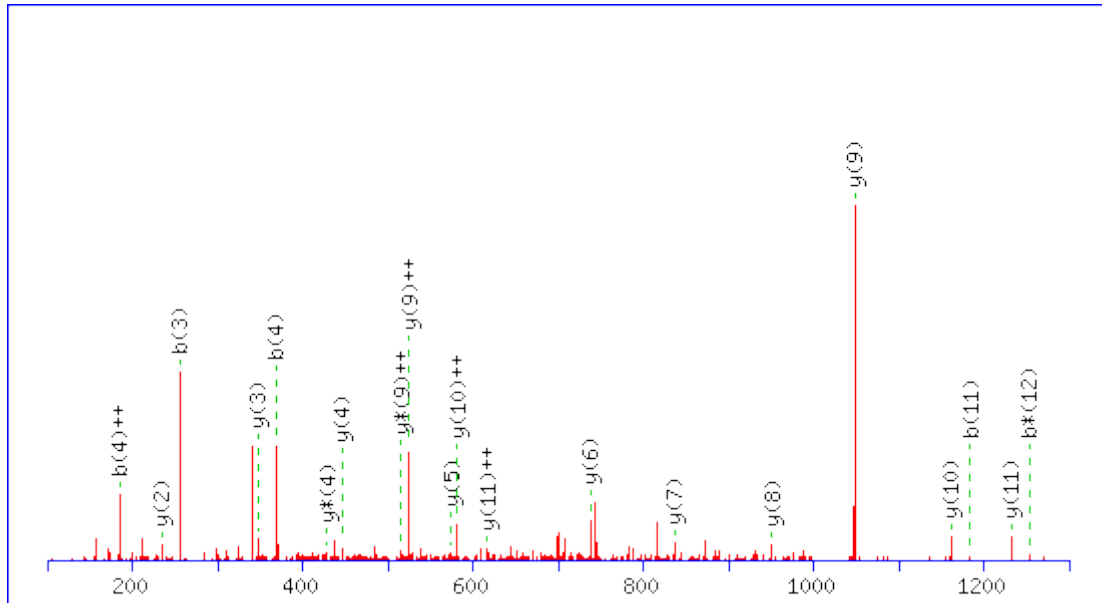
Monoisotopic mass of neutral peptide Mr(calc): 952.5342

Ions Score: 49 Expect: 0.0024

Matches (Bold Red): 20/76 fragment ions using 37 most intense peaks

MS/MS Fragmentation of **LAALPNVYEVISK**

Found in **MCM5_HUMAN**, DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5



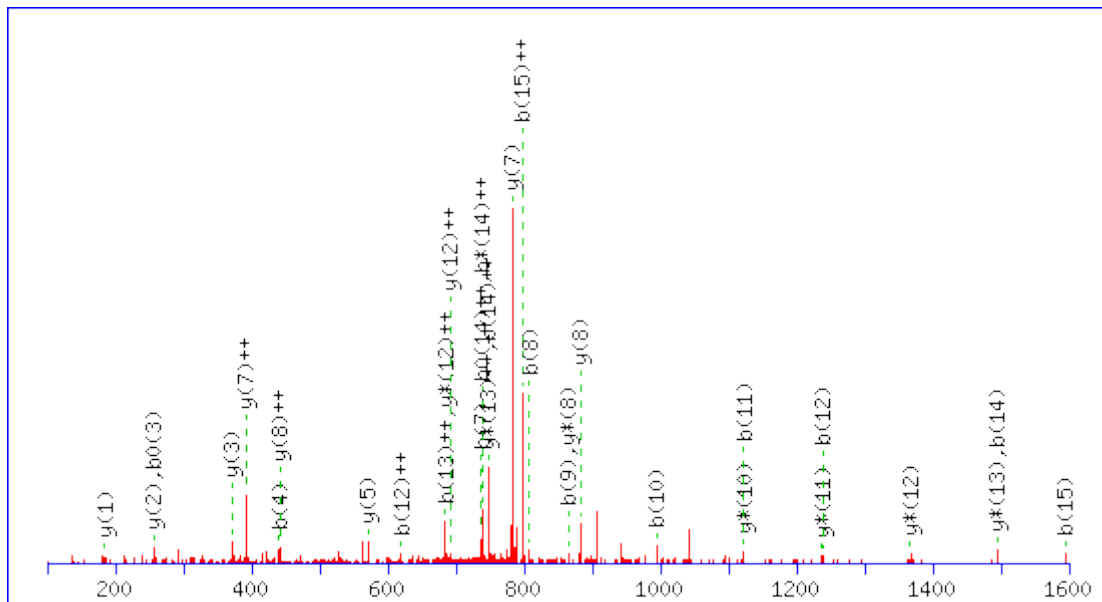
Monoisotopic mass of neutral peptide Mr(calc): 1415.8024

Ions Score: 43 Expect: 0.014

Matches (Bold Red): 21/116 fragment ions using 71 most intense peaks

MS/MS Fragmentation of **SGERPVTAGEEDEQVPDSIDAR**

Found in **MIP18_HUMAN**, Mitotic spindle-associated MMXD complex subunit MIP18
 OS=Homo sapiens GN=FAM96B PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 2376.0944

Variable modifications:

R4 : Label:13C(6)15N(4) (R)

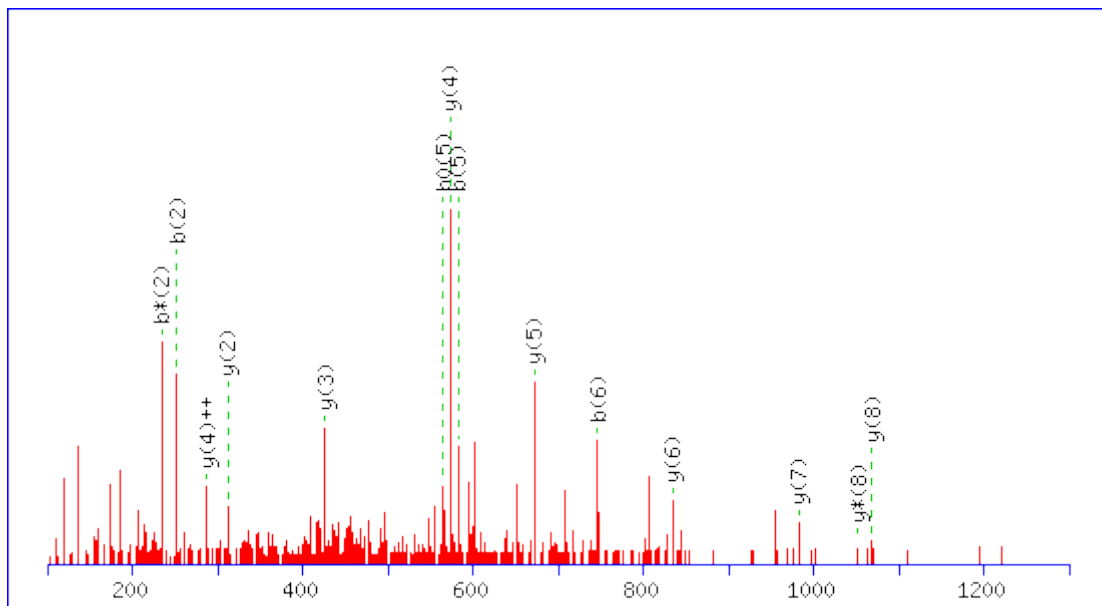
R22 : Label:13C(6)15N(4) (R)

Ions Score: 46 **Expect:** 0.0084

Matches (Bold Red): 32/242 fragment ions using 52 most intense peaks

MS/MS Fragmentation of **NHPSFYVFNHR**

Found in **MMGT1_HUMAN**, Membrane magnesium transporter 1 OS=Homo sapiens GN=MMGT1
PE=1 SV=1



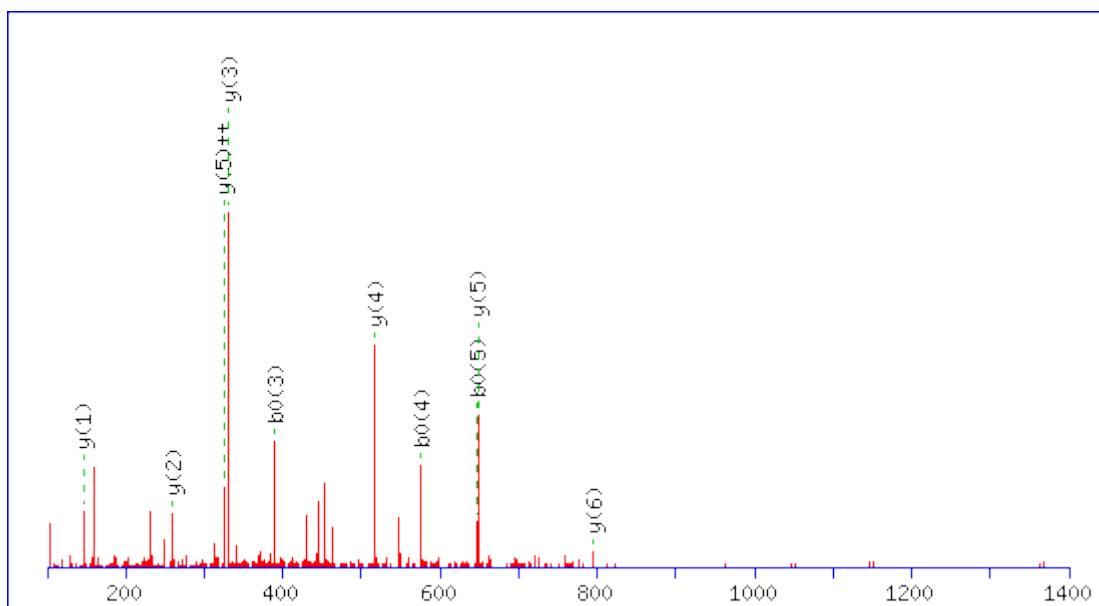
Monoisotopic mass of neutral peptide Mr(calc): 1416.6687

Ions Score: 40 **Expect:** 0.02

Matches (Bold Red): 14/100 fragment ions using 26 most intense peaks

MS/MS Fragmentation of **EFMWALK**

Found in **MTPN_HUMAN**, Myotrophin OS=Homo sapiens GN=MTPN PE=1 SV=2



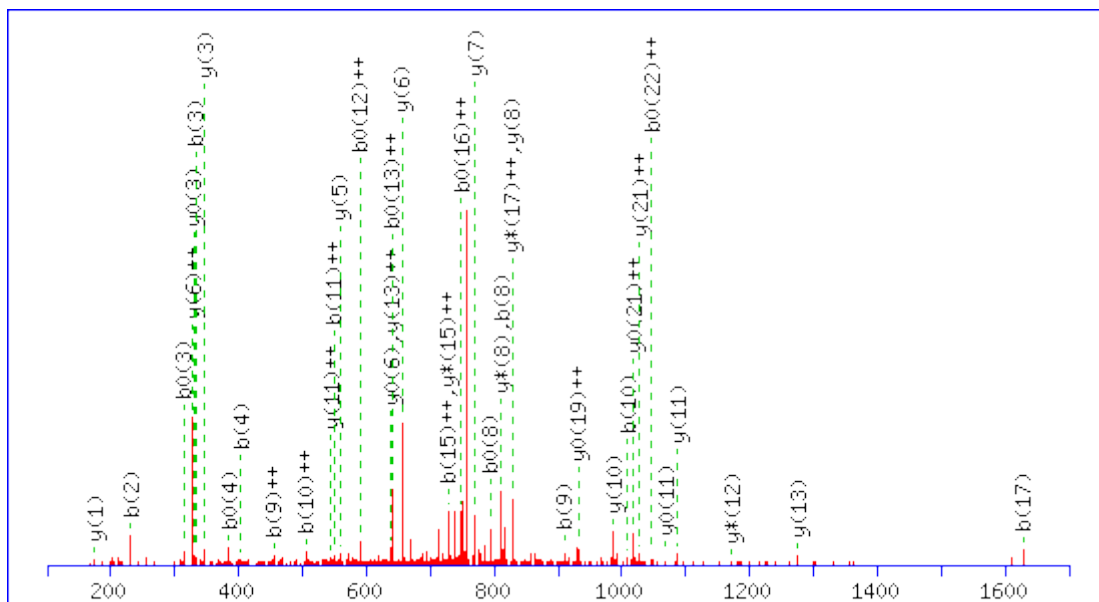
Monoisotopic mass of neutral peptide Mr(calc): 923.4575

Ions Score: 38 Expect: 0.025

Matches (Bold Red): 10/48 fragment ions using 24 most intense peaks

MS/MS Fragmentation of **TETAPLVVVVSTGTGDPPDTAR**

Found in **MTRR_HUMAN**, Methionine synthase reductase OS=Homo sapiens GN=MTRR PE=1 SV=3



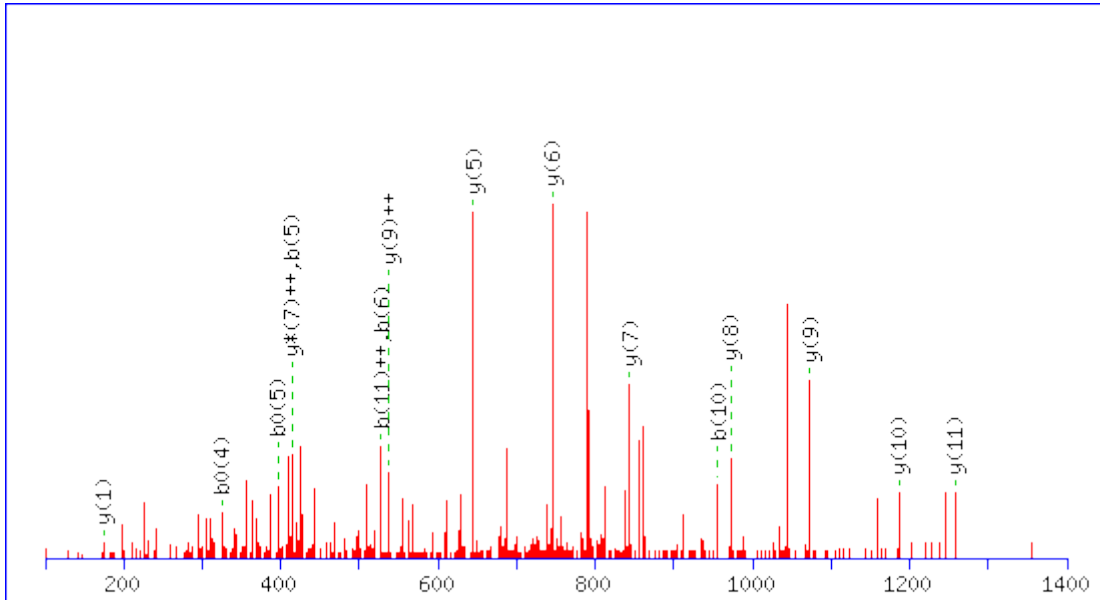
Monoisotopic mass of neutral peptide Mr(calc): 2283.1595

Ions Score: 50 Expect: 0.0047

Matches (**Bold Red**): 40/216 fragment ions using 74 most intense peaks

MS/MS Fragmentation of **GATLALTQVTPQDER**

Found in **MUC18_HUMAN**, Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM
PE=1 SV=2



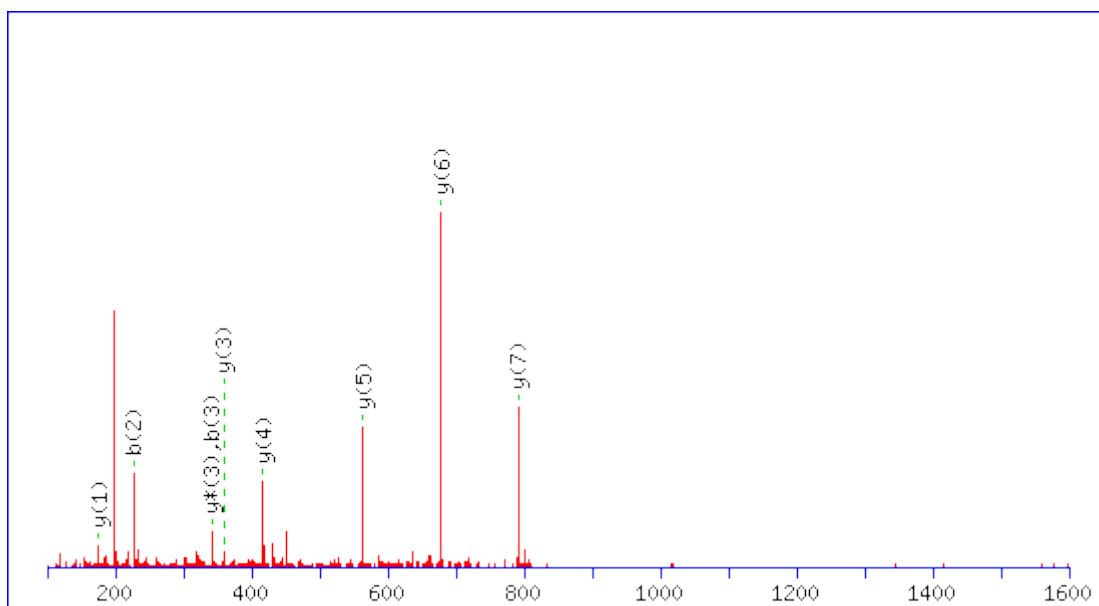
Monoisotopic mass of neutral peptide Mr(calc): 1598.8264

Ions Score: 43 Expect: 0.015

Matches (**Bold Red**): 16/148 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **IIDFGLAR**

Found in **MYLK3_HUMAN**, Putative myosin light chain kinase 3 OS=Homo sapiens
GN=MYLK3 PE=2 SV=3



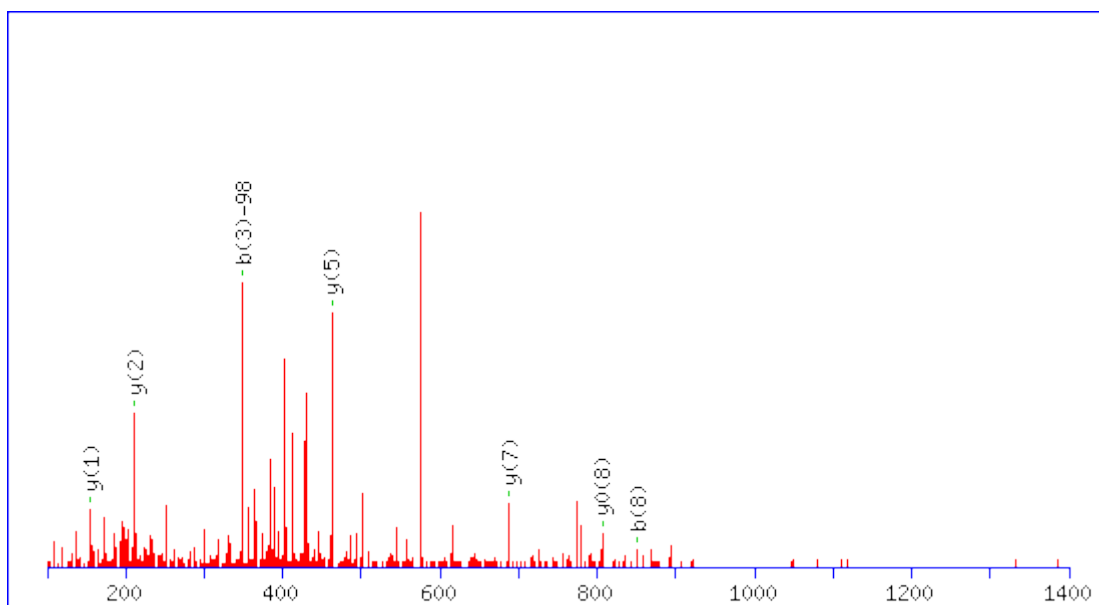
Monoisotopic mass of neutral peptide Mr(calc): 903.5178

Ions Score: 40 Expect: 0.019

Matches (Bold Red): 9/56 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **TKEPGGKGK**

Found in **MY09B_HUMAN**, Myosin-IXb OS=Homo sapiens GN=MY09B PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1004.5118

Variable modifications:

T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

K2 : Label:13C(6)15N(2) (K)

K7 : Label:13C(6)15N(2) (K)

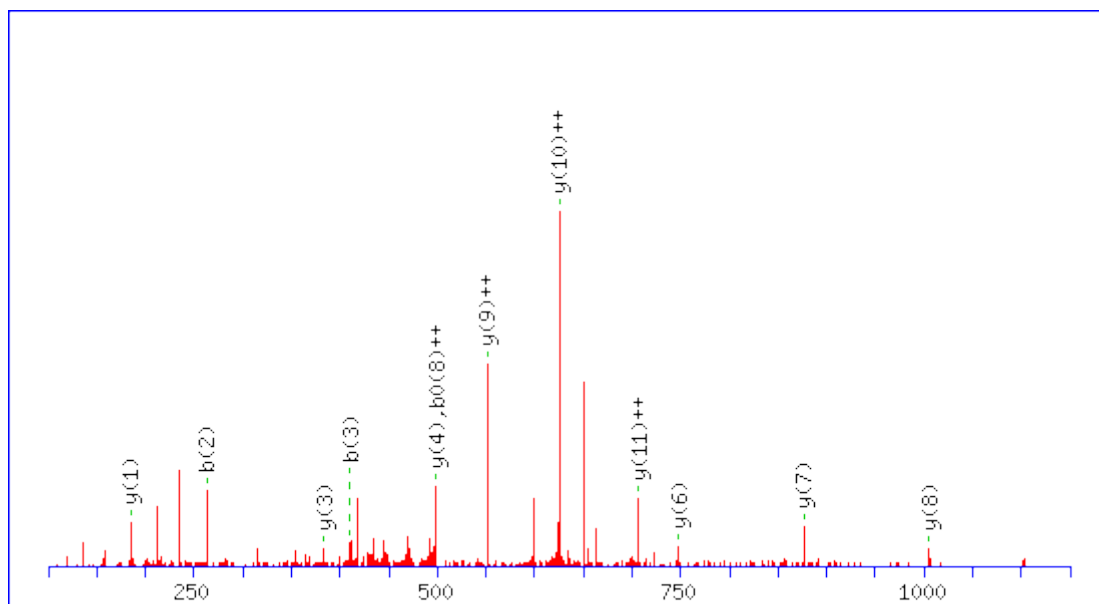
K9 : Label:13C(6)15N(2) (K)

Ions Score: 21 Expect: 1.7

Matches (**Bold Red**): 7/128 fragment ions using 22 most intense peaks

MS/MS Fragmentation of **VYFPEQIHDVVR**

Found in **NCEH1_HUMAN**, Neutral cholesterol ester hydrolase 1 OS=Homo sapiens
GN=NCEH1 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1510.7808

Variable modifications:

R12 : Label:13C(6)15N(4) (R)

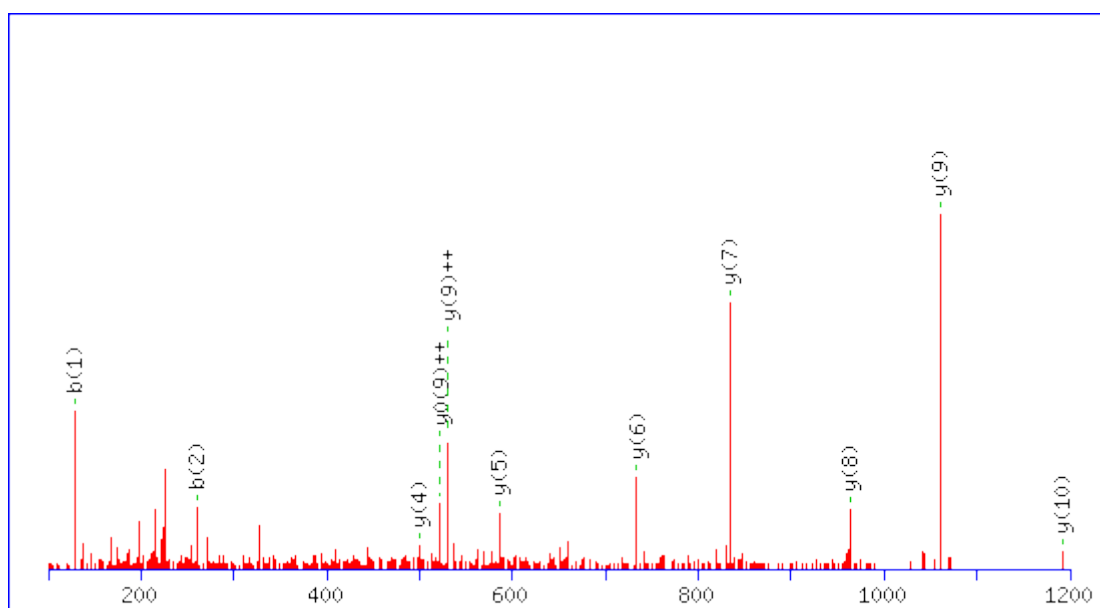
Ions Score: 47 Expect: 0.006

Matches (**Bold Red**): 12/108 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **KMPETFSNLPR**

Found in **NFIP1_HUMAN**, NEDD4 family-interacting protein 1 OS=Homo sapiens

GN=NDFIP1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1318.6703

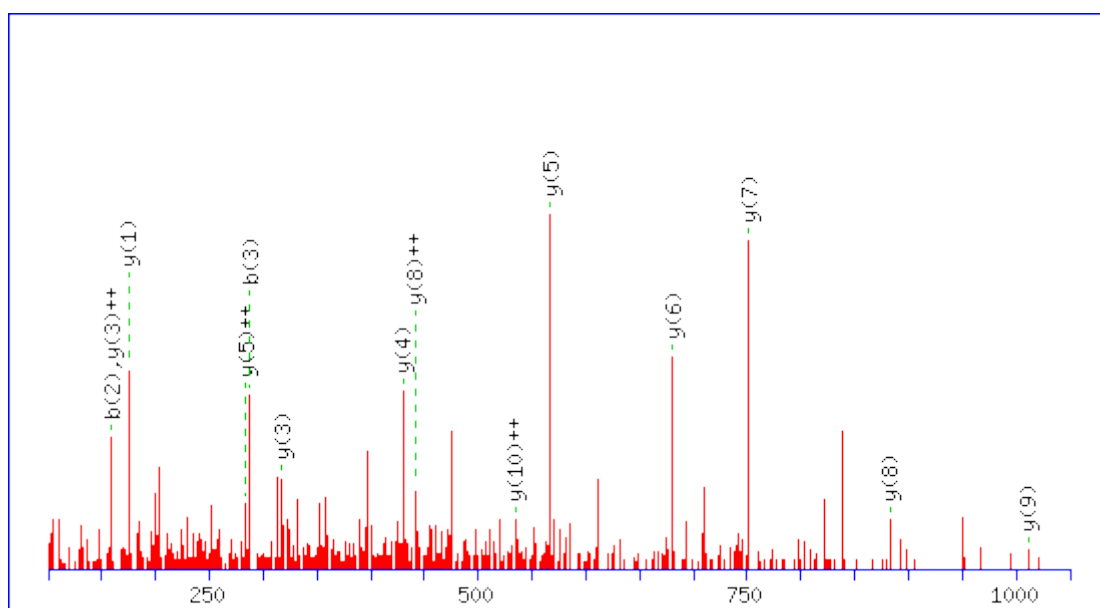
Ions Score: 39 Expect: 0.032

Matches (Bold Red): 11/106 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **TGEMALHLAAR**

Found in **NOTC2_HUMAN**, Neurogenic locus notch homolog protein 2 OS=Homo sapiens

GN=NOTCH2 PE=1 SV=3



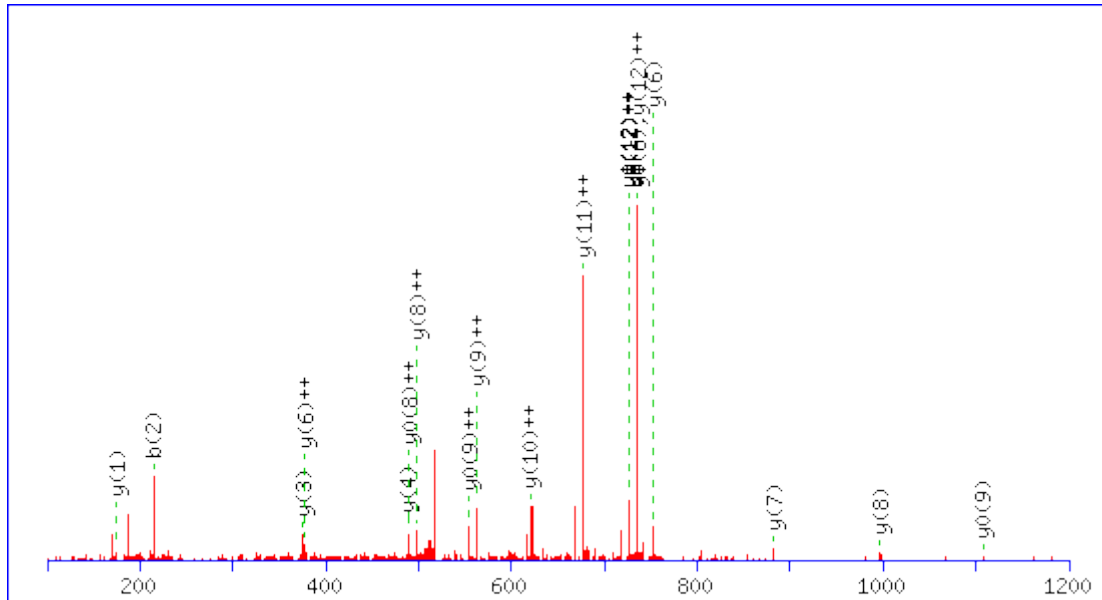
Monoisotopic mass of neutral peptide Mr(calc): 1168.6022

Ions Score: 48 Expect: 0.0039

Matches (**Bold Red**): 14/84 fragment ions using 31 most intense peaks

MS/MS Fragmentation of **VDNDENEHQLSLR**

Found in **NPM_HUMAN**, Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2



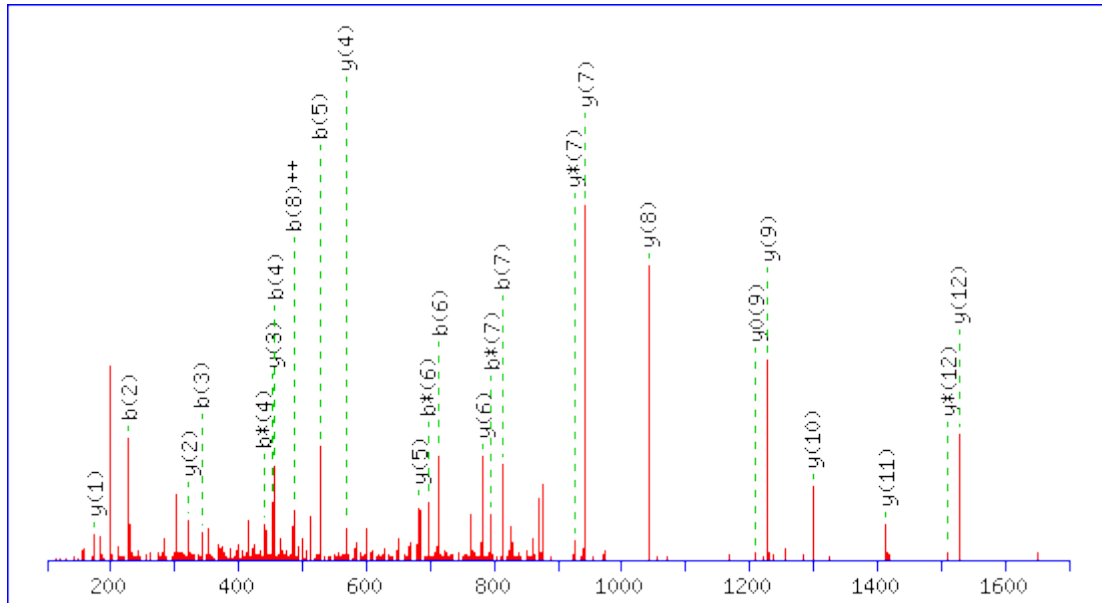
Monoisotopic mass of neutral peptide Mr(calc): 1567.7226

Ions Score: 40 Expect: 0.02

Matches (**Bold Red**): 20/134 fragment ions using 35 most intense peaks

MS/MS Fragmentation of **NINDAWVCTNDMFR**

Found in **NTF2_HUMAN**, Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1



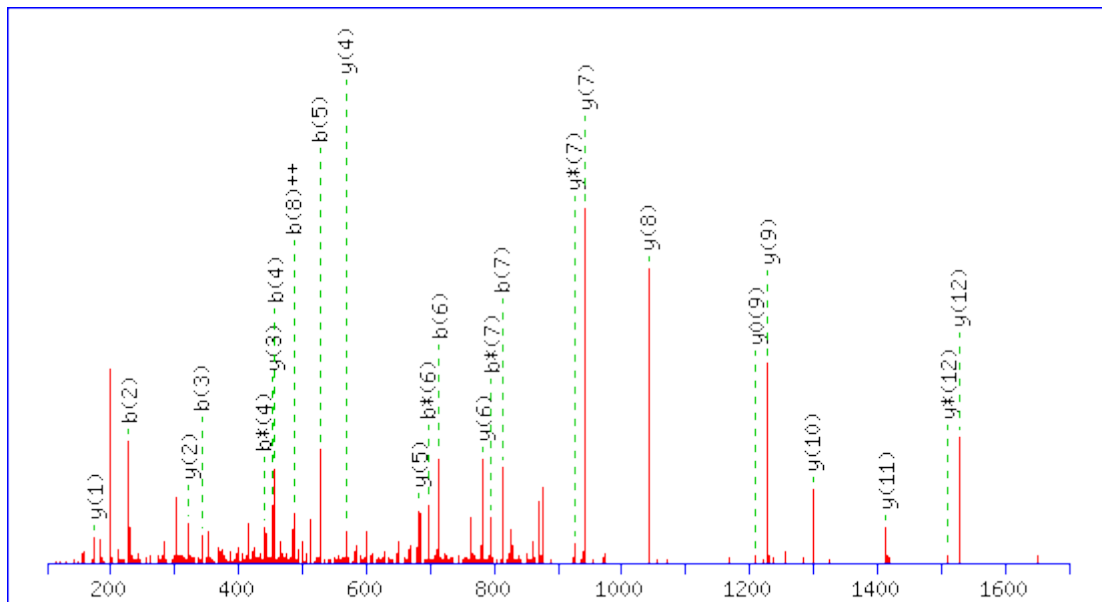
Monoisotopic mass of neutral peptide Mr(calc): 1754.7505

Ions Score: 87 Expect: 3.7e-007

Matches (Bold Red): 25/144 fragment ions using 48 most intense peaks

MS/MS Fragmentation of **LLLPLFR**

Found in **NTM1A_HUMAN**, Alpha N-terminal protein methyltransferase 1A OS=Homo sapiens GN=METTL11A PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 880.5774

Variable modifications:

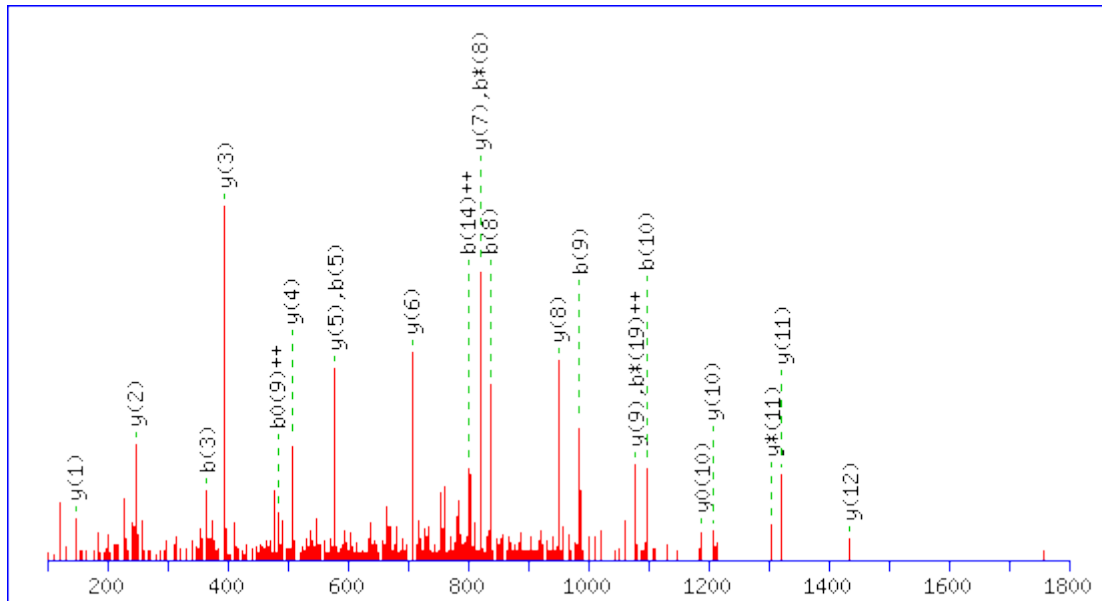
R7 : Label:13C(6)15N(4) (R)

Ions Score: 38 **Expect:** 0.02

Matches (Bold Red): 9/36 fragment ions using 14 most intense peaks

MS/MS Fragmentation of **LHDVNSDGLDEQEALFTK**

Found in **NUCB2_HUMAN**, Nucleobindin-2 OS=Homo sapiens GN=NUCB2 PE=1 SV=2



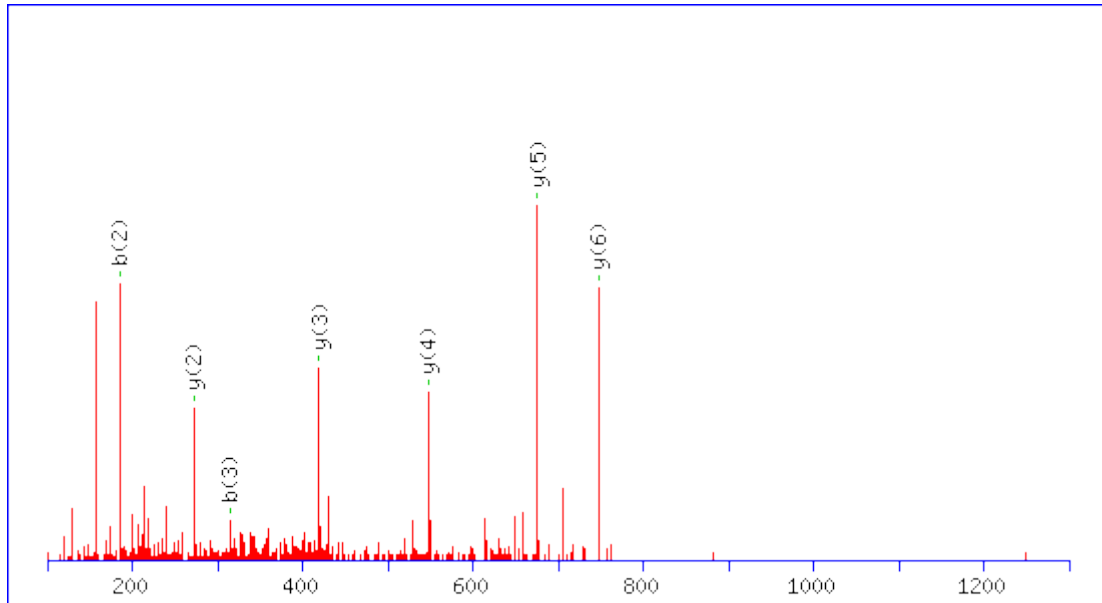
Monoisotopic mass of neutral peptide Mr(calc): 2419.1543

Ions Score: 88 **Expect:** 5.8e-007

Matches (Bold Red): 23/226 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **LAEQMPR**

Found in **NWD1_HUMAN**, NACHT and WD repeat domain-containing protein 1 OS=Homo sapiens GN=NWD1 PE=2 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 859.4222

Variable modifications:

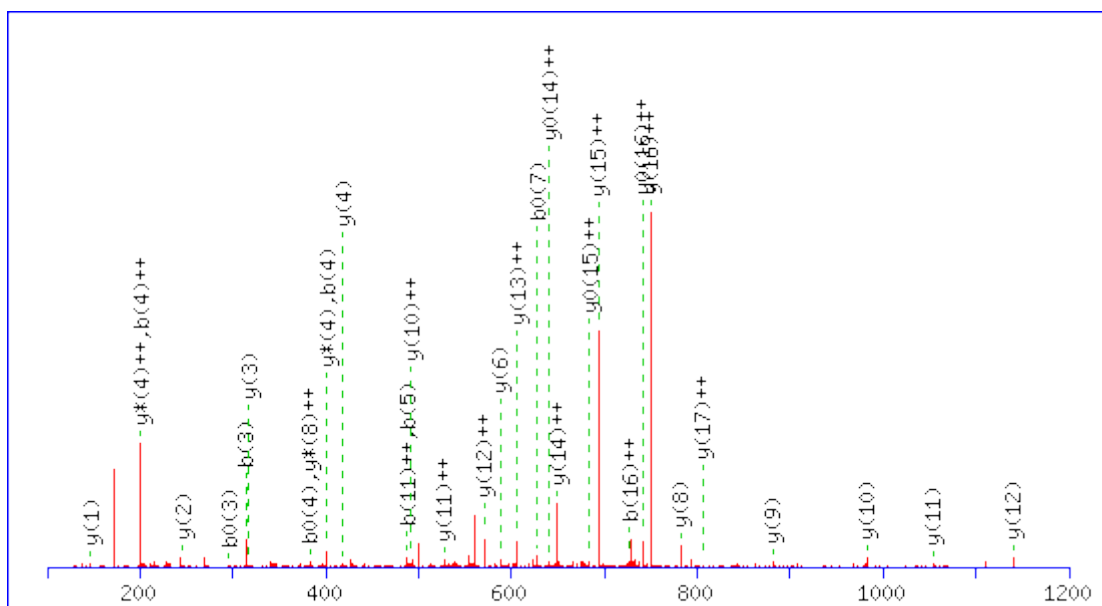
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 53 **Expect:** 0.00097

Matches (Bold Red): 7/86 fragment ions using 7 most intense peaks

MS/MS Fragmentation of **SLLSSASATVGHGLTAVK**

Found in **NXP20_HUMAN**, Protein NOXP20 OS=Homo sapiens GN=FAM114A1 PE=1 SV=2



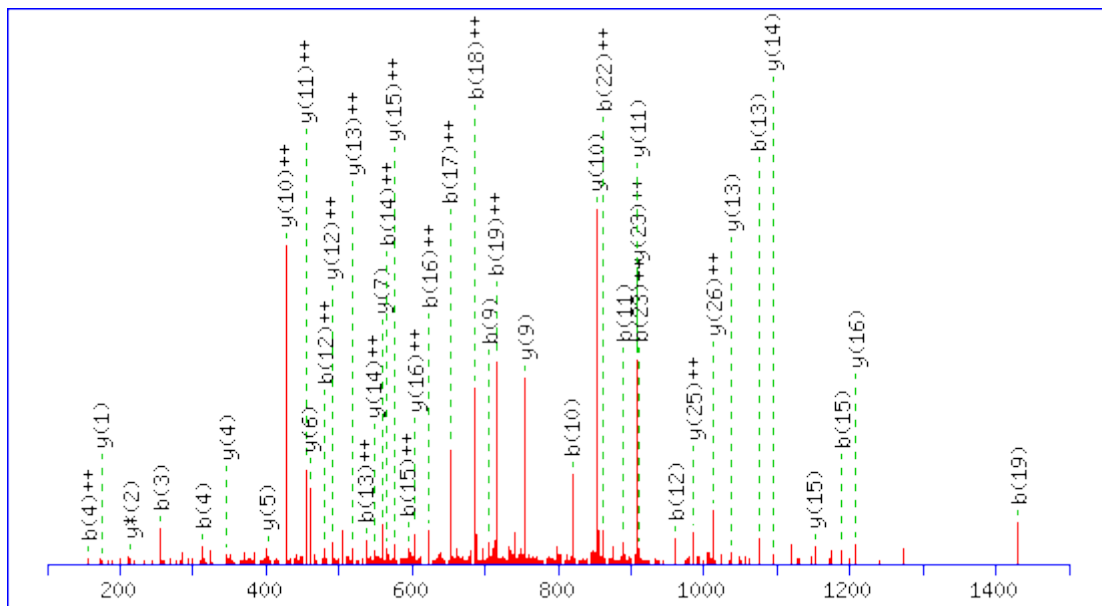
Monoisotopic mass of neutral peptide Mr(calc): 1697.9312

Ions Score: 44 Expect: 0.012

Matches (**Bold Red**): 34/164 fragment ions using 82 most intense peaks

MS/MS Fragmentation of **GVVGPAAIAALGGGGAGPPVVGGGGGR**

Found in **OSBP1_HUMAN**, Oxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=



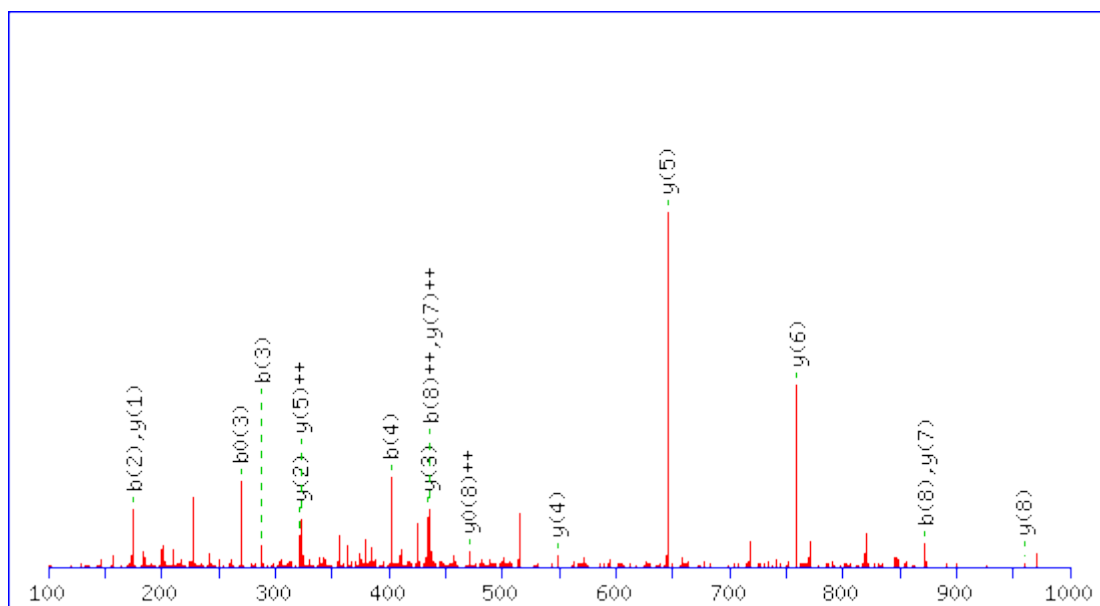
Monoisotopic mass of neutral peptide Mr(calc): 2281.2292

Ions Score: 70 Expect: 4.5e-005

Matches (**Bold Red**): 44/168 fragment ions using 89 most intense peaks

MS/MS Fragmentation of **SSLNPILFR**

Found in **OST48_HUMAN**, Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4



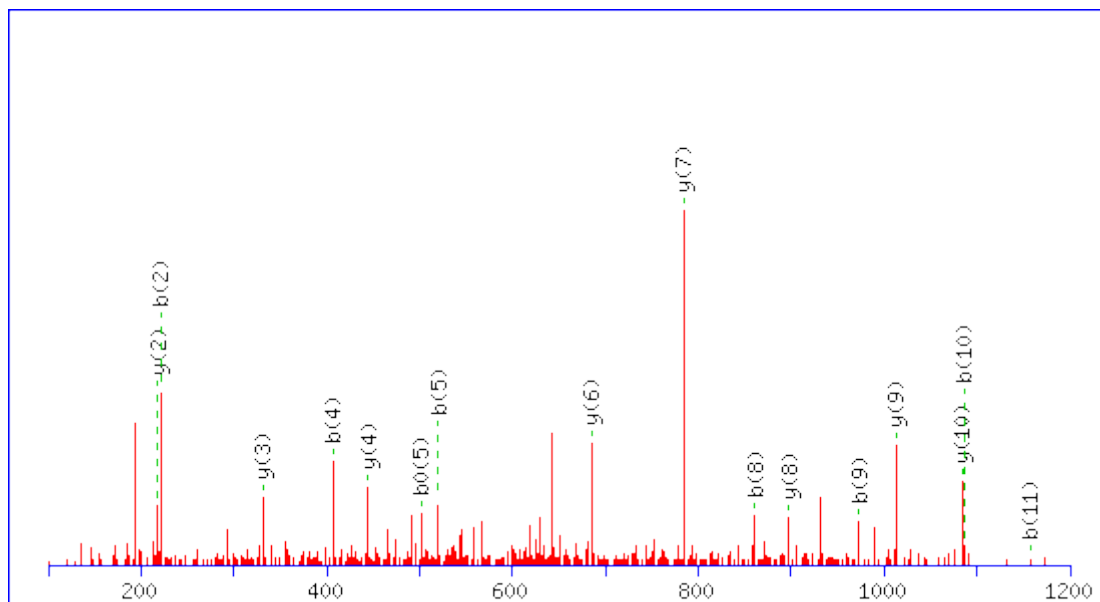
Monoisotopic mass of neutral peptide Mr(calc): 1045.5920

Ions Score: 59 Expect: 0.00029

Matches (Bold Red): 17/76 fragment ions using 36 most intense peaks

MS/MS Fragmentation of **GYADIVQLLLAK**

Found in **OSTF1_HUMAN**, Osteoclast-stimulating factor 1 OS=Homo sapiens GN=OSTF1
PE=1 SV=2



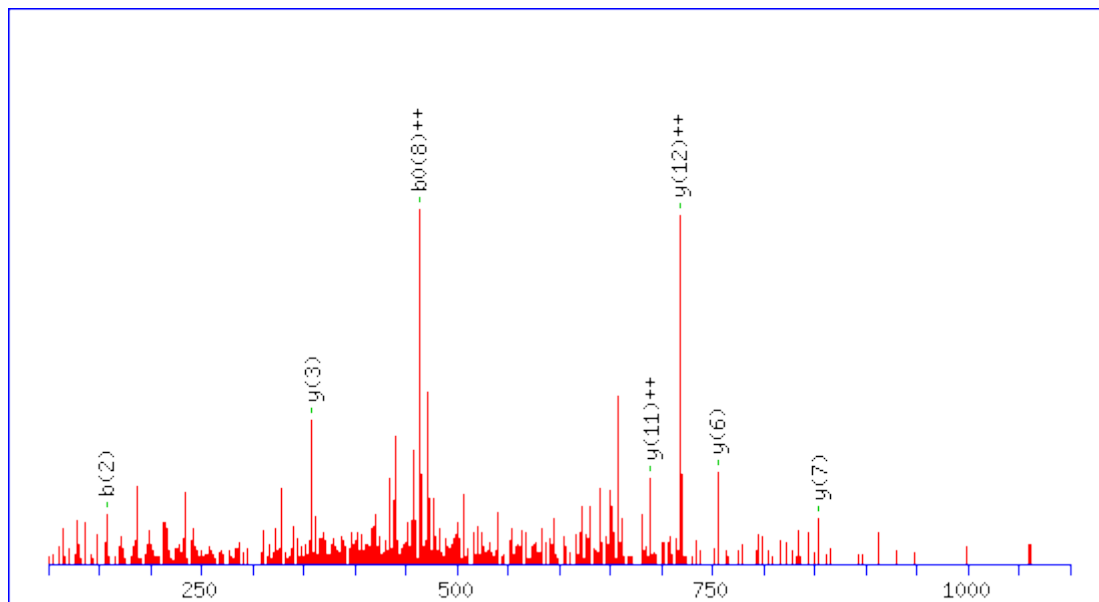
Monoisotopic mass of neutral peptide Mr(calc): 1302.7547

Ions Score: 65 Expect: 8.1e-005

Matches (**Bold Red**): 16/98 fragment ions using 24 most intense peaks

MS/MS Fragmentation of **VGEEHVYSFPNK**

Found in **PAXI_HUMAN**, Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3



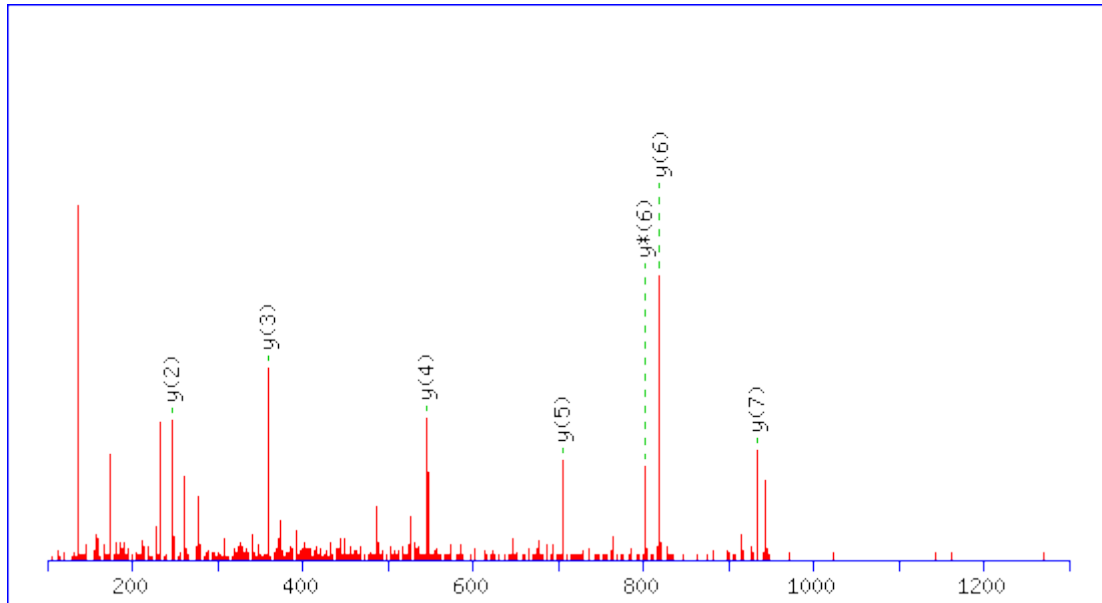
Monoisotopic mass of neutral peptide Mr(calc): 1533.7100

Ions Score: 3 Expect: 1.6e+002

Matches (**Bold Red**): 7/110 fragment ions using 25 most intense peaks

MS/MS Fragmentation of **YNNCWLAR**

Found in **PCKGM_HUMAN**, Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=



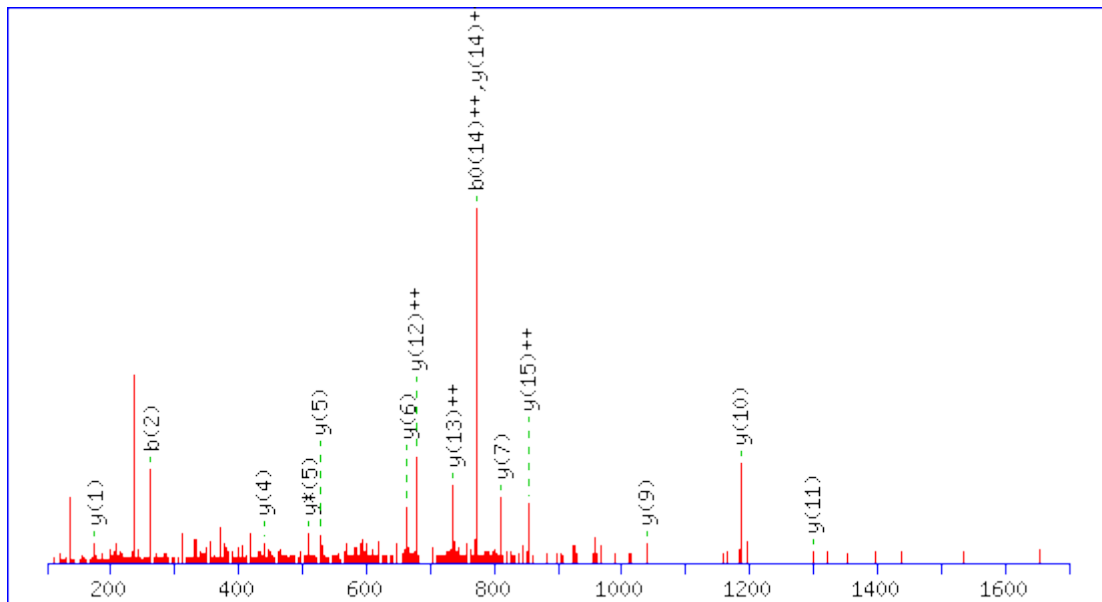
Monoisotopic mass of neutral peptide Mr(calc): 1095.4920

Ions Score: 48 Expect: 0.0025

Matches (Bold Red): 7/54 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **VYADGIFDLFHSGHAR**

Found in **PCY1A_HUMAN**, Choline-phosphate cytidyltransferase A OS=Homo sapiens
GN=PCYT1A PE=1 SV=2



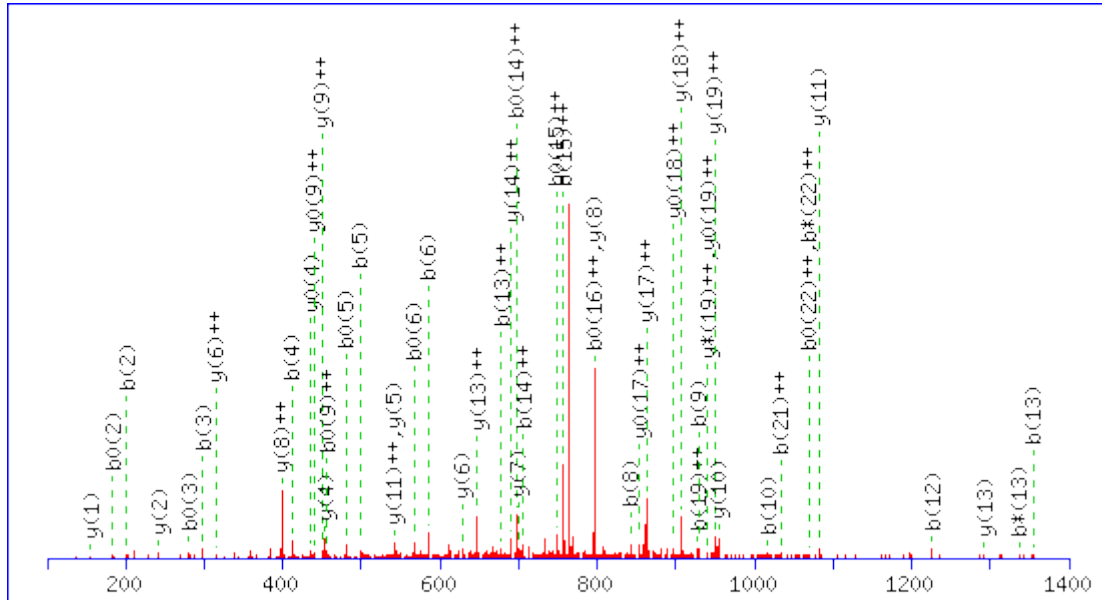
Monoisotopic mass of neutral peptide Mr(calc): 1803.8693

Ions Score: 46 Expect: 0.0074

Matches (Bold Red): 15/136 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **ISPLSSPCSSPLQGTPASSLVSK**

Found in **PDE3A_HUMAN**, cGMP-inhibited 3',5'-cyclic phosphodiesterase A OS=Homo sapiens GN=PDE3A PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 2307.1872

Variable modifications:

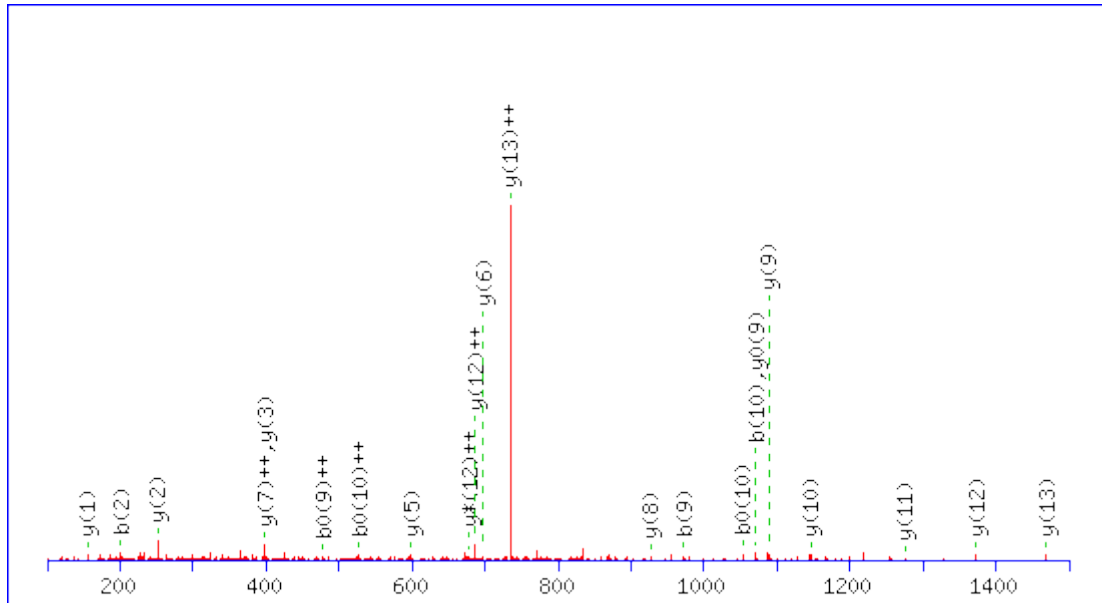
K23 : Label:13C(6)15N(2) (K)

Ions Score: 50 **Expect:** 0.0044

Matches (Bold Red): 51/236 fragment ions using 115 most intense peaks

MS/MS Fragmentation of **VTPPEGYEVVTVFPK**

Found in **PDLI1_HUMAN**, PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4



Monoisotopic mass of neutral peptide Mr(calc): 1668.8855

Variable modifications:

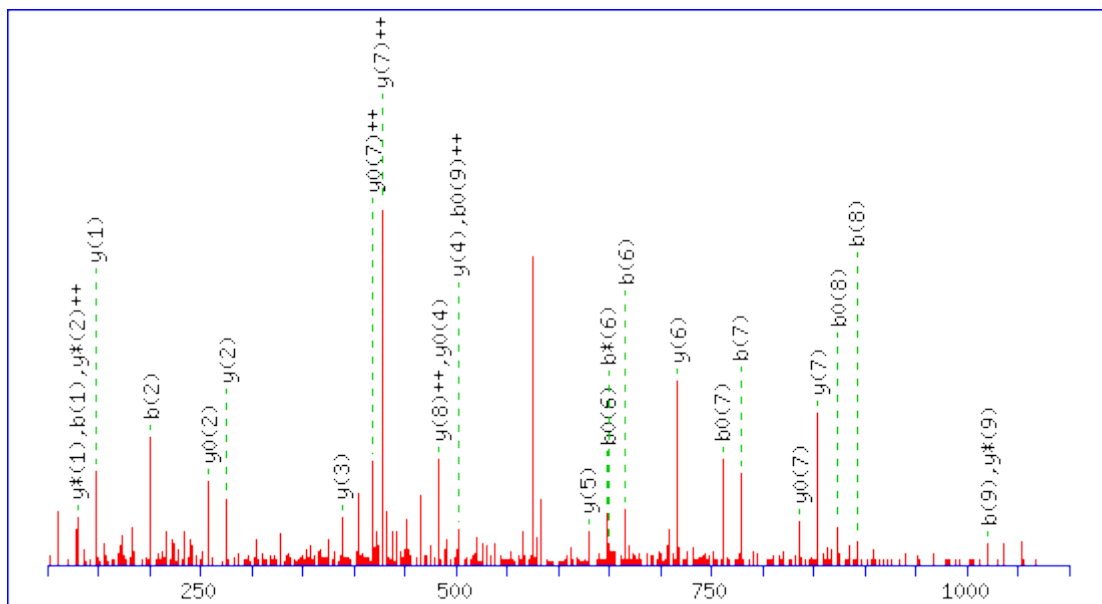
K15 : Label:13C(6)15N(2) (K)

Ions Score: 61 Expect: 0.00029

Matches (Bold Red): 22/130 fragment ions using 53 most intense peaks

MS/MS Fragmentation of **EAIHSQLEK**

Found in **PFD1_HUMAN**, Prefoldin subunit 1 OS=Homo sapiens GN=PFDN1 PE=1 SV=2



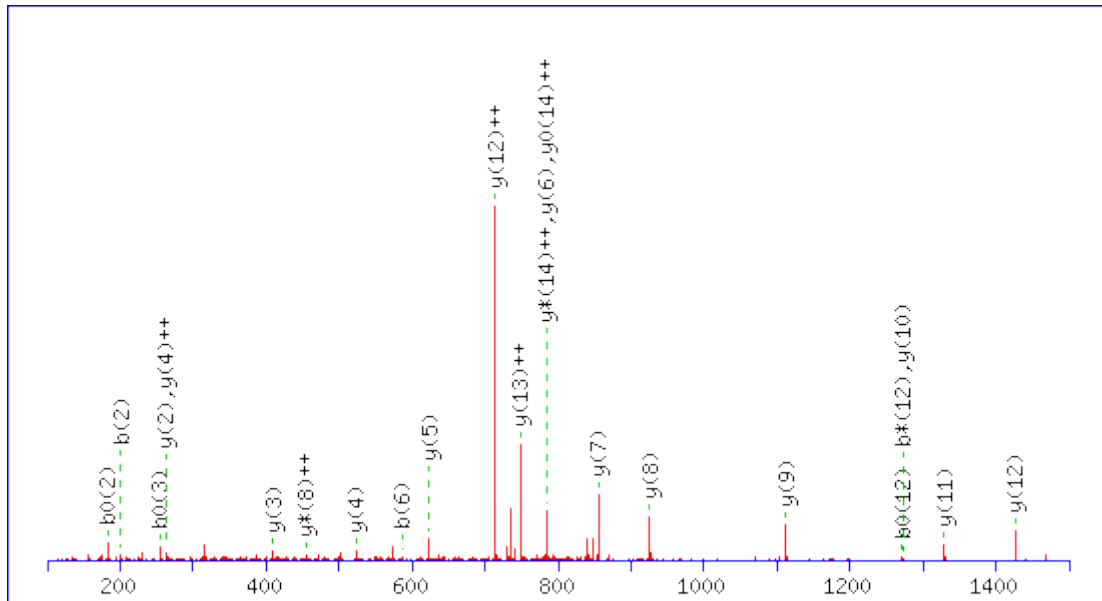
Monoisotopic mass of neutral peptide Mr(calc): 1166.6295

Ions Score: 47 Expect: 0.0046

Matches (**Bold Red**): 27/96 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **LSAPGCWAACTNFSR**

Found in **PLP2_HUMAN**, Proteolipid protein 2 OS=Homo sapiens GN=PLP2 PE=1 SV=1



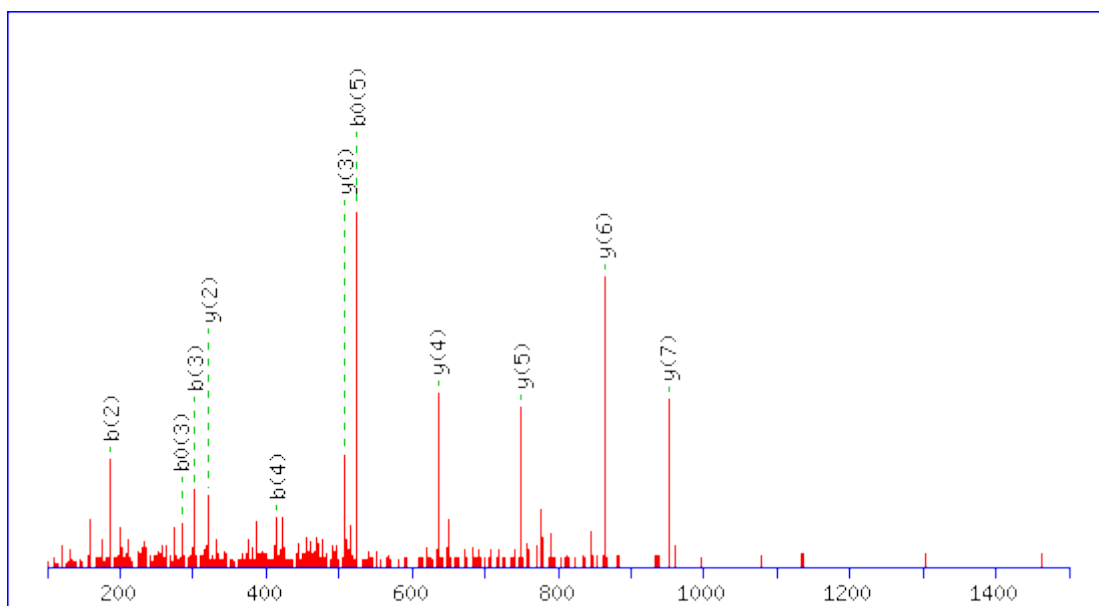
Monoisotopic mass of neutral peptide Mr(calc): 1696.7450

Ions Score: 69 Expect: 2e-005

Matches (**Bold Red**): 23/142 fragment ions using 44 most intense peaks

MS/MS Fragmentation of **VSDIQWFR**

Found in **PMVK_HUMAN**, Phosphomevalonate kinase OS=Homo sapiens GN=PMVK PE=1 SV=3



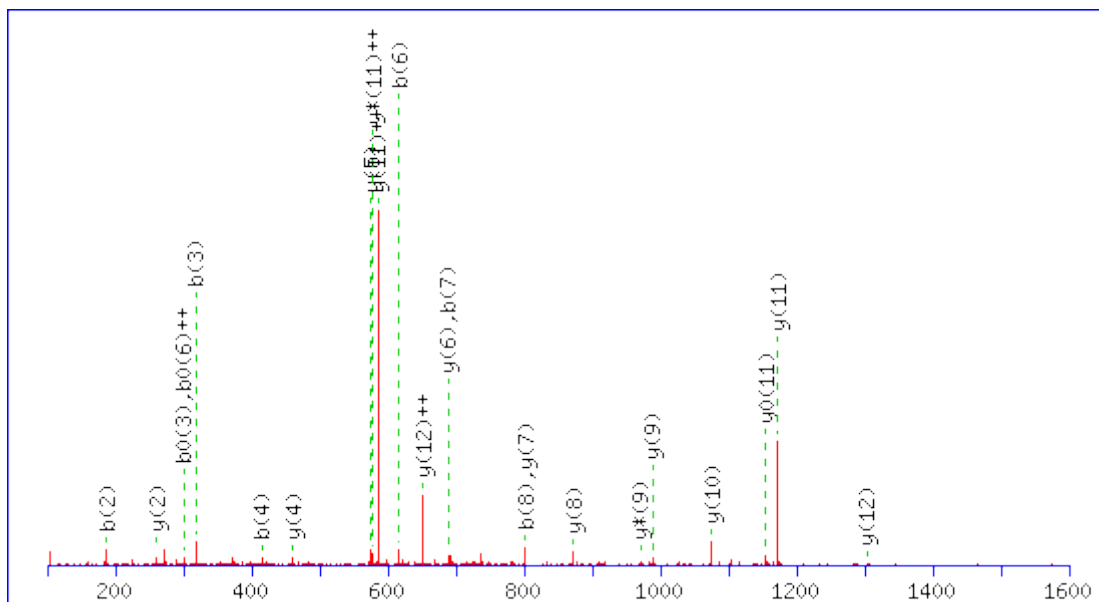
Monoisotopic mass of neutral peptide Mr(calc): 1049.5294

Ions Score: 42 Expect: 0.013

Matches (Bold Red): 11/64 fragment ions using 18 most intense peaks

MS/MS Fragmentation of **DAMPSDANLNSINK**

Found in **PP2BA_HUMAN**, Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Homo sapiens GN=PPP3CA PE=1 SV=1



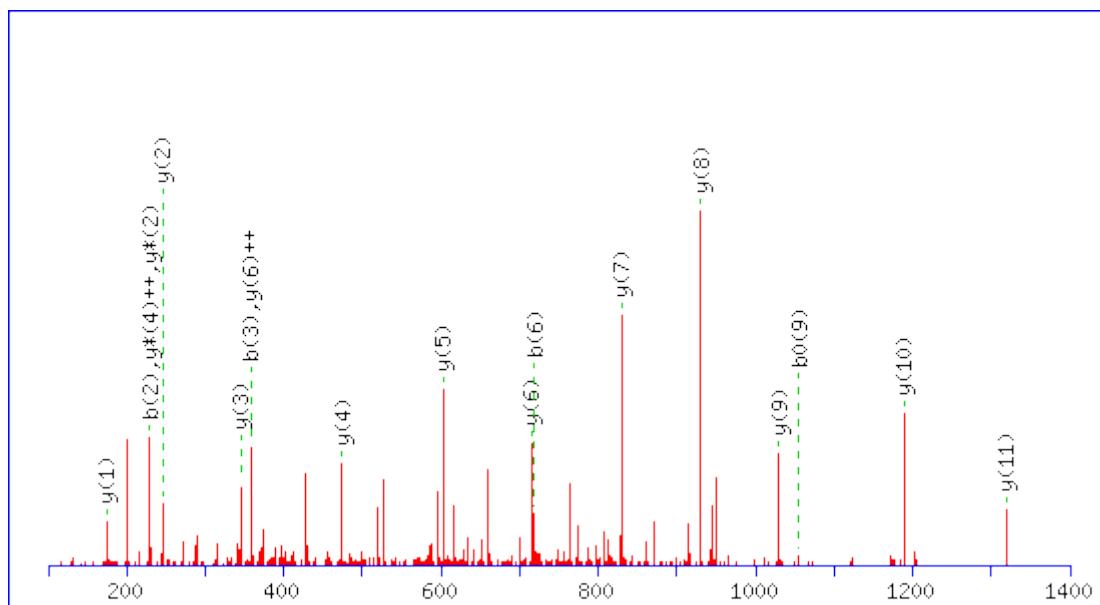
Monoisotopic mass of neutral peptide Mr(calc): 1488.6878

Ions Score: 69 Expect: 3.2e-005

Matches (**Bold Red**): 23/136 fragment ions using 43 most intense peaks

MS/MS Fragmentation of **DLECVTNLQEVAR**

Found in **PPGB_HUMAN**, Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2



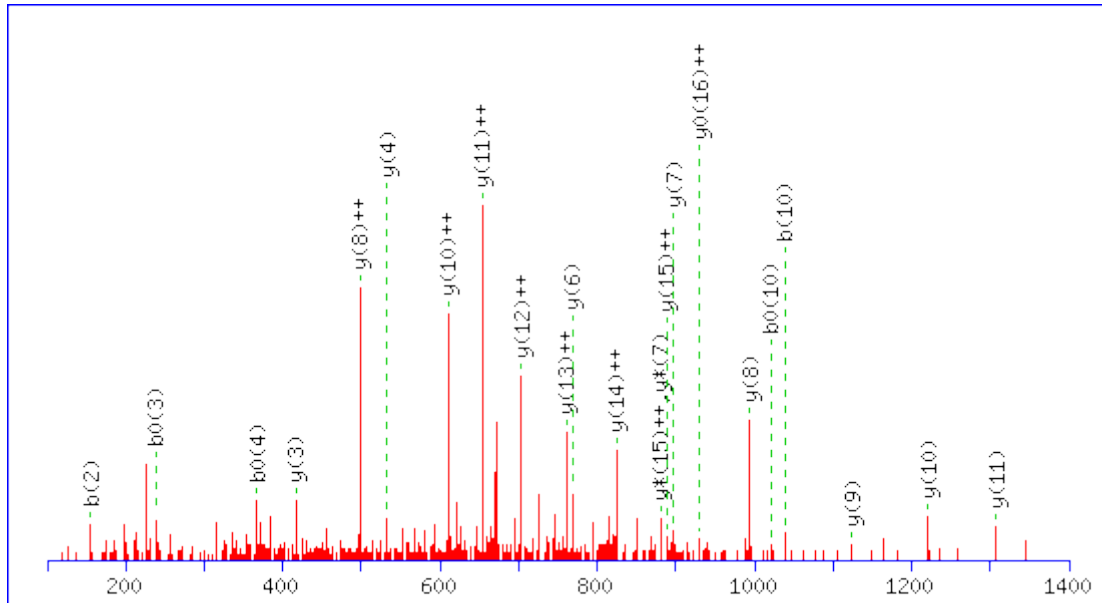
Monoisotopic mass of neutral peptide Mr(calc): 1545.7457

Ions Score: 97 Expect: 6.3e-008

Matches (**Bold Red**): 18/126 fragment ions using 24 most intense peaks

MS/MS Fragmentation of **GPTEQLVSPEPEVHDIER**

Found in **PPM1A_HUMAN**, Protein phosphatase 1A OS=Homo sapiens GN=PPM1A PE=1 SV=1



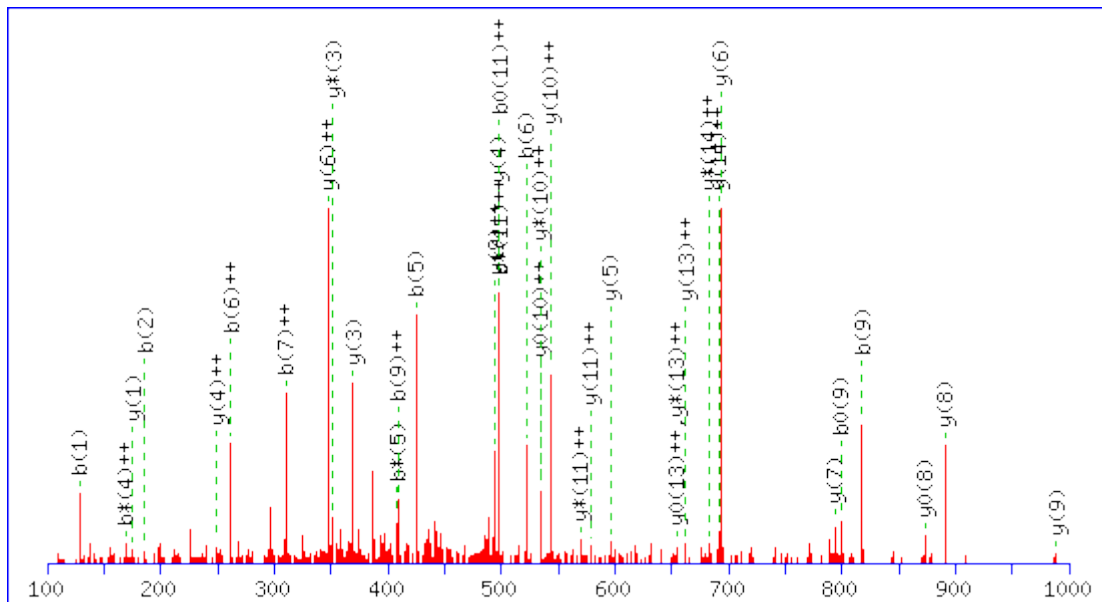
Monoisotopic mass of neutral peptide Mr(calc): 2030.9909

Ions Score: 57 **Expect:** 0.00083

Matches (Bold Red): 23/190 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **KGPAAPPPTPVKPPR**

Found in **PRDBP_HUMAN**, Protein kinase C delta-binding protein OS=Homo sapiens
GN=PRKCDBP PE=1 SV=3



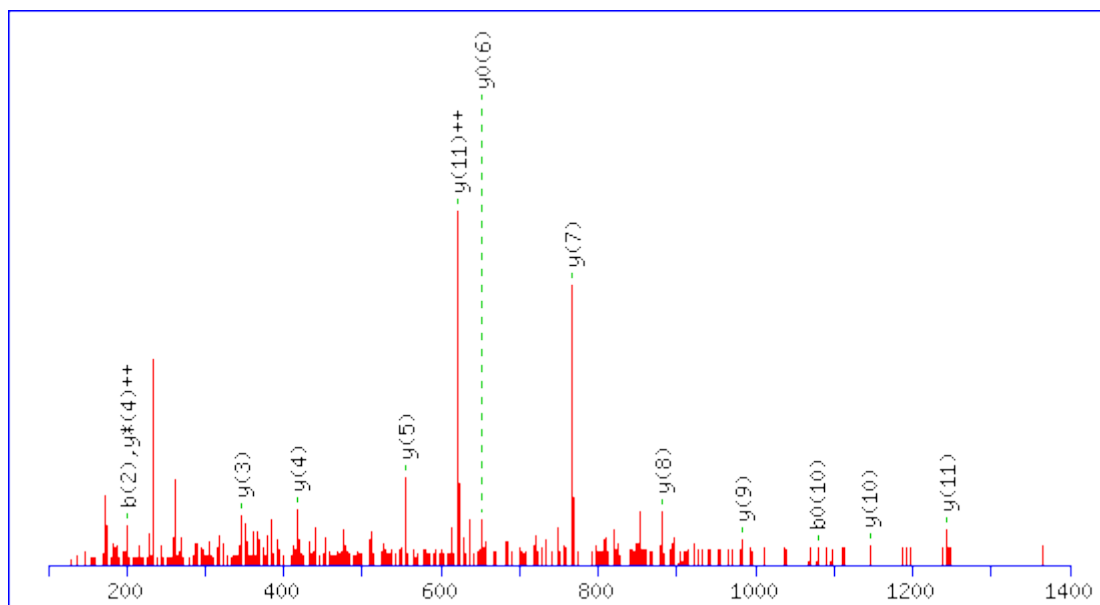
Monoisotopic mass of neutral peptide Mr(calc): 1508.8827

Ions Score: 51 **Expect:** 0.0022

Matches (**Bold Red**): 37/140 fragment ions using 70 most intense peaks

MS/MS Fragmentation of **TVPYTDPDHASLK**

Found in **PREP_HUMAN**, Presequence protease, mitochondrial OS=Homo sapiens
GN=PITRM1 PE=1 SV=2



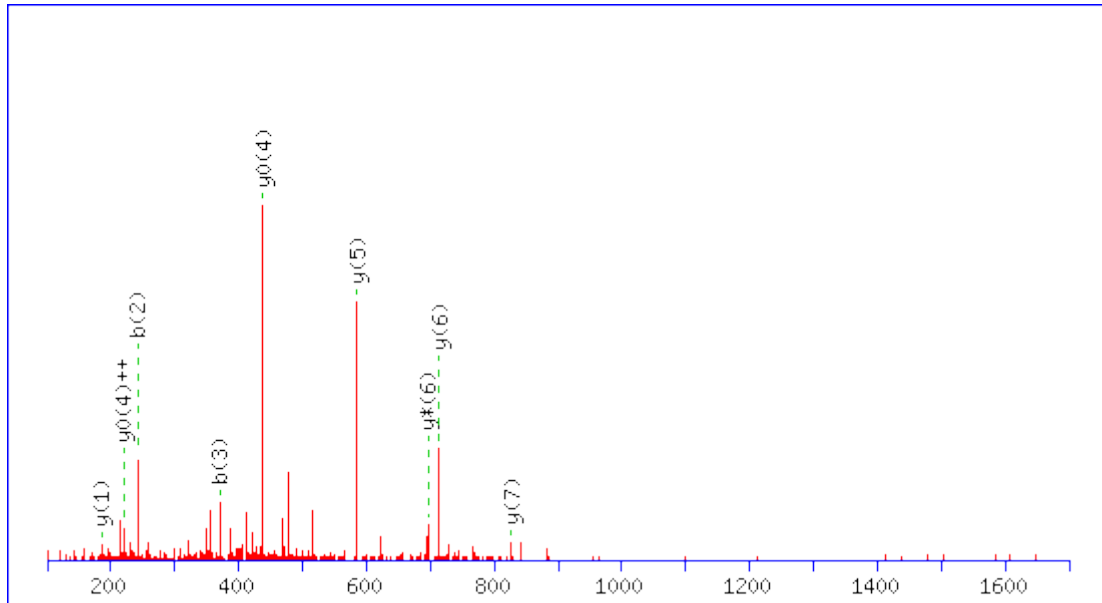
Monoisotopic mass of neutral peptide Mr(calc): 1442.7042

Ions Score: 40 Expect: 0.028

Matches (**Bold Red**): 13/116 fragment ions using 32 most intense peaks

MS/MS Fragmentation of **QLQEEAAR**

Found in **PRIP1_HUMAN**, ProSAP-interacting protein 1 OS=Homo sapiens GN=PROSAP1P1
PE=2 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 953.4805

Variable modifications:

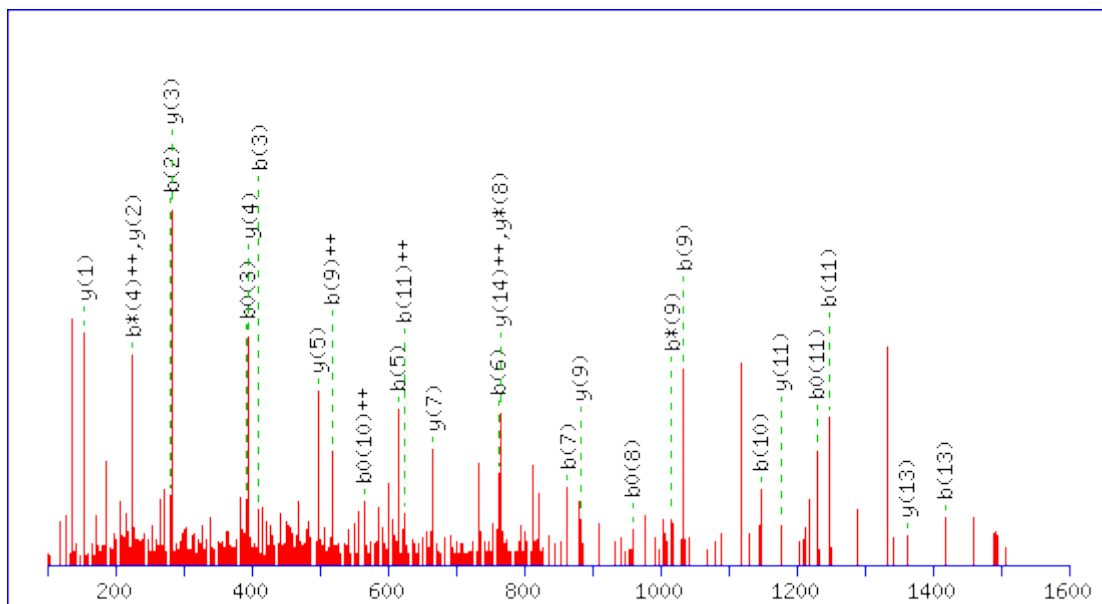
R8 : Label:13C(6)15N(4) (R)

Ions Score: 39 Expect: 0.027

Matches (Bold Red): 9/72 fragment ions using 11 most intense peaks

MS/MS Fragmentation of **DREGFFTNGTLGAK**

Found in **PROF2_HUMAN**, Profilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1642.8434

Variable modifications:

R2 : Label:13C(6)15N(4) (R)

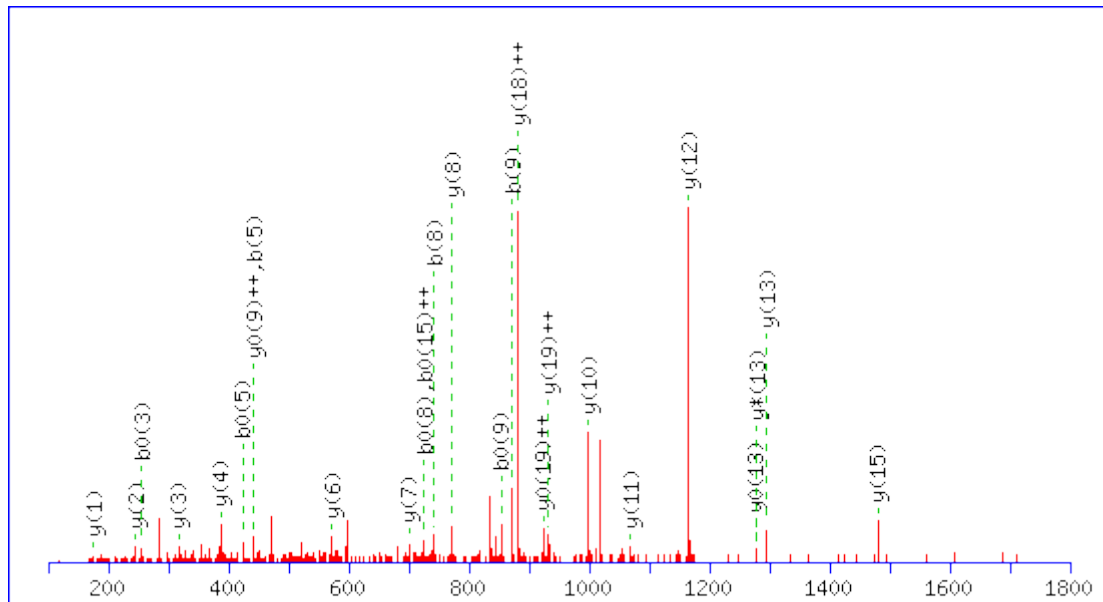
K15 : Label:13C(6)15N(2) (K)

Ions Score: 53 Expect: 0.0018

Matches (Bold Red): 28/158 fragment ions using 59 most intense peaks

MS/MS Fragmentation of **ATTPADGEEPAPAEALAAAR**

Found in **PRPK_HUMAN**, TP53-regulating kinase OS=Homo sapiens GN=TP53RK PE=1 SV=2



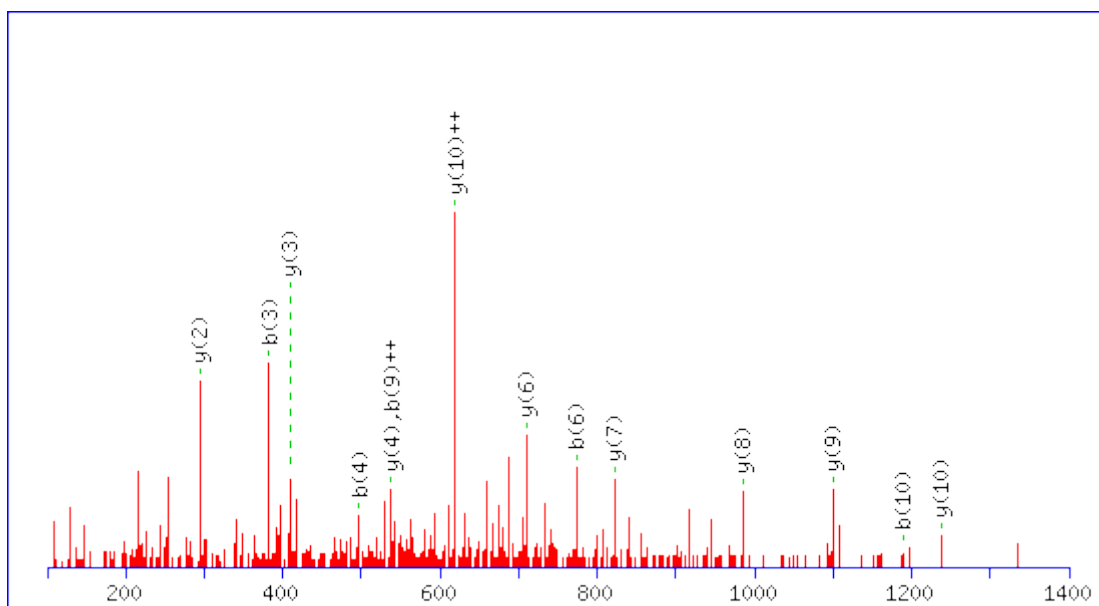
Monoisotopic mass of neutral peptide Mr(calc): 2036.9650

Ions Score: 53 Expect: 0.002

Matches (Bold Red): 26/186 fragment ions using 65 most intense peaks

MS/MS Fragmentation of **MLHDYIGDKDFK**

Found in **PSAL_HUMAN**, Puromycin-sensitive aminopeptidase-like protein OS=Homo sapiens GN=NPEPPSL1 PE=2 SV=3



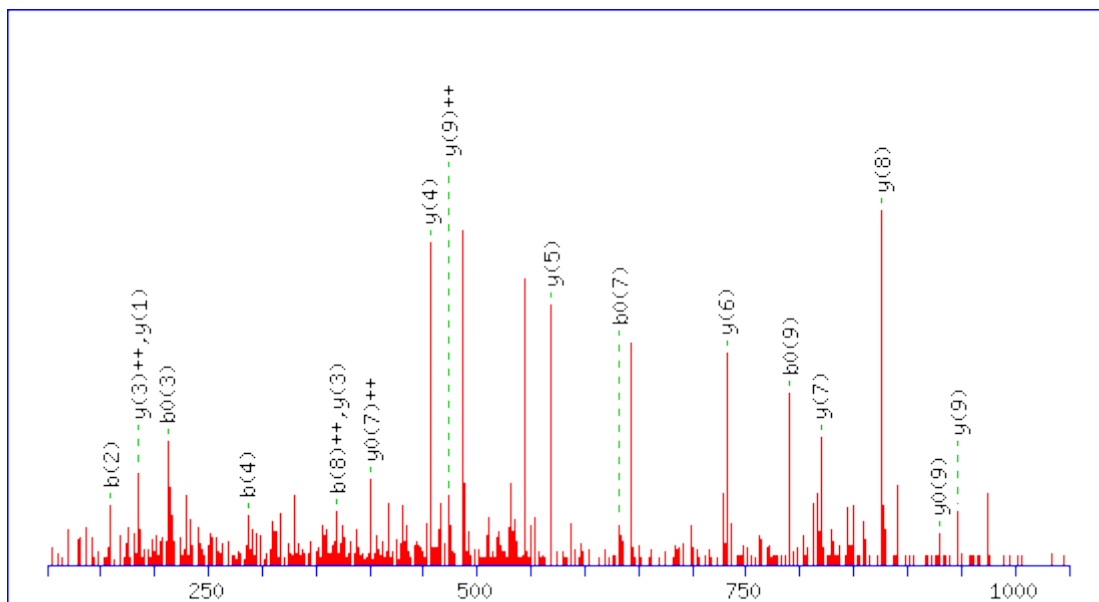
Monoisotopic mass of neutral peptide Mr(calc): 1480.7020

Ions Score: 47 Expect: 0.0057

Matches (**Bold Red**): 14/106 fragment ions using 25 most intense peaks

MS/MS Fragmentation of **ASAGSYISALR**

Found in **PSB8_HUMAN**, Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1104.5803

Variable modifications:

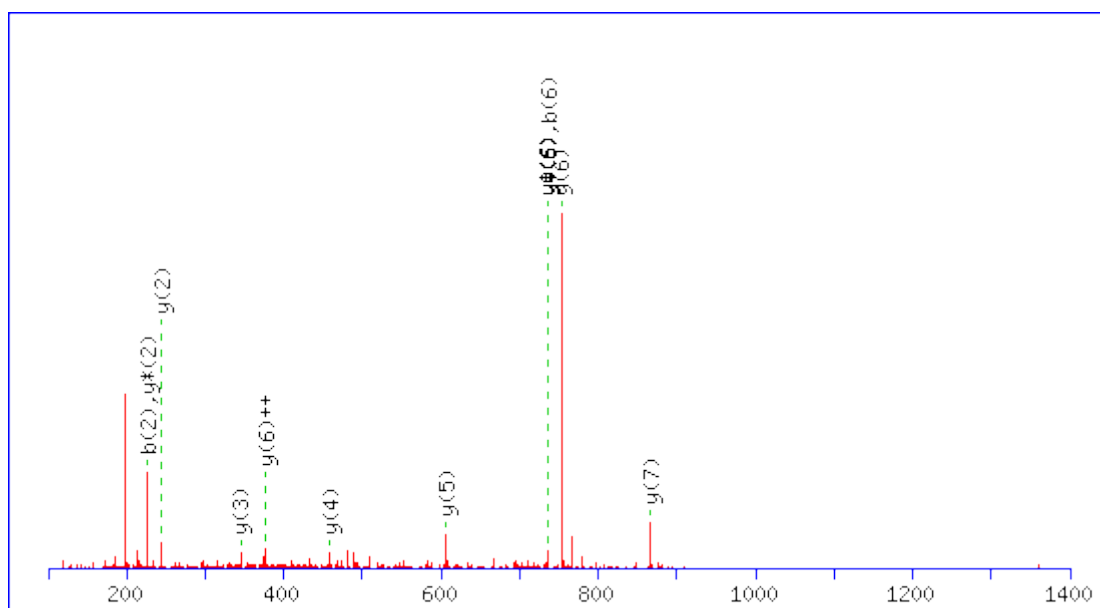
R11 : Label:13C(6)15N(4) (R)

Ions Score: 44 **Expect:** 0.0097

Matches (Bold Red): 18/92 fragment ions using 41 most intense peaks

MS/MS Fragmentation of **ILFFNTPK**

Found in **PSMD8_HUMAN**, 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2



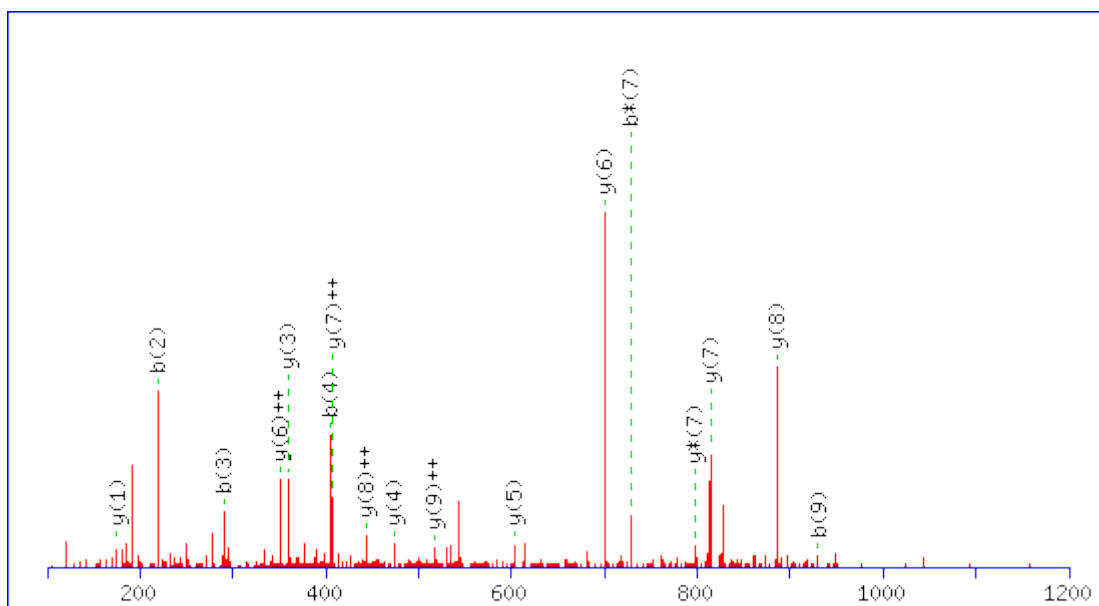
Monoisotopic mass of neutral peptide Mr(calc): 978.5538

Ions Score: 43 **Expect:** 0.011

Matches (Bold Red): 12/62 fragment ions using 20 most intense peaks

MS/MS Fragmentation of **AFANPEDALR**

Found in **PTGES_HUMAN**, Prostaglandin E synthase OS=Homo sapiens GN=PTGES PE=1 SV=2



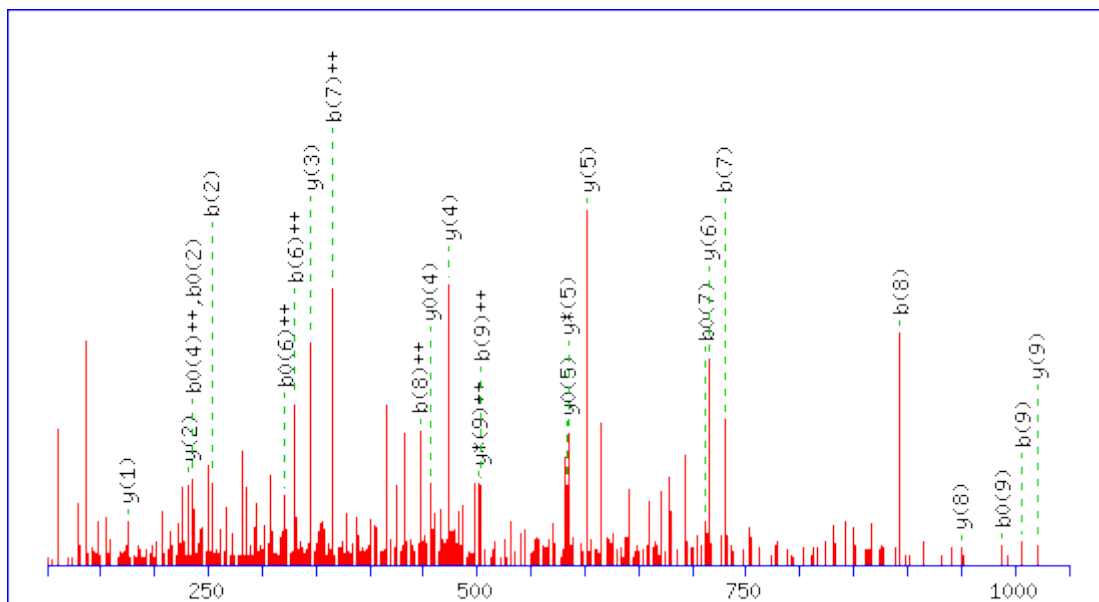
Monoisotopic mass of neutral peptide Mr(calc): 1102.5407

Ions Score: 42 Expect: 0.014

Matches (Bold Red): 17/86 fragment ions using 43 most intense peaks

MS/MS Fragmentation of **DHPHTAAYLQELGR**

Found in **PTRD1_HUMAN**, Putative peptidyl-tRNA hydrolase PTRHD1 OS=Homo sapiens
GN=PTRHD1 PE=1 SV=1



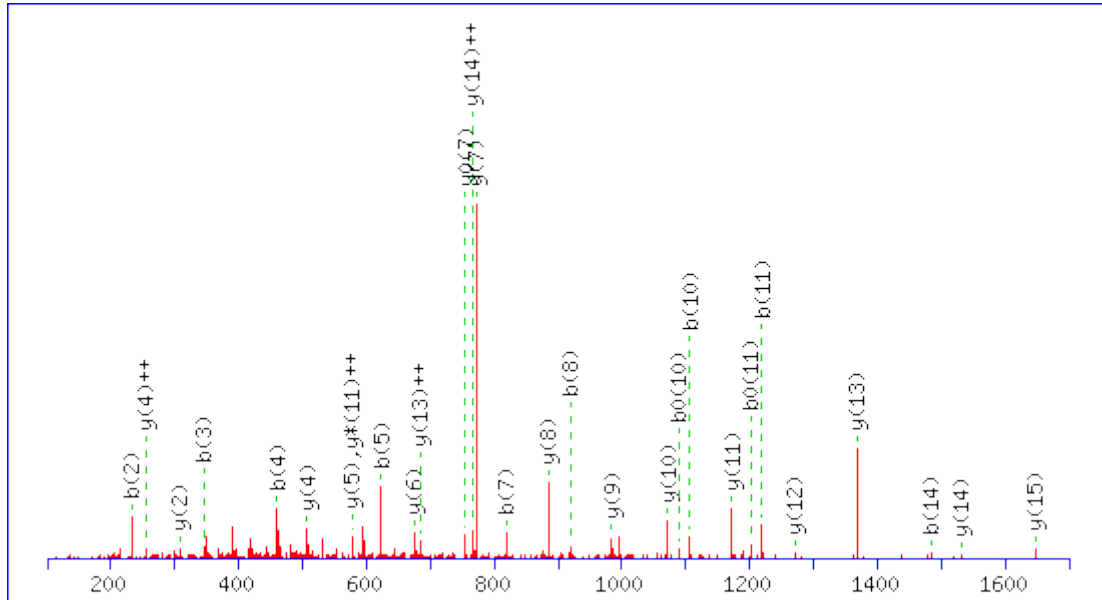
Monoisotopic mass of neutral peptide Mr(calc): 1606.7852

Ions Score: 39 Expect: 0.039

Matches (**Bold Red**): 25/132 fragment ions using 50 most intense peaks

MS/MS Fragmentation of **ACLDYPVTSVLPPASLCK**

Found in **PTTG_HUMAN**, Pituitary tumor-transforming gene 1 protein-interacting protein OS=Homo sapiens GN=PTTG1IP PE=1 SV=1



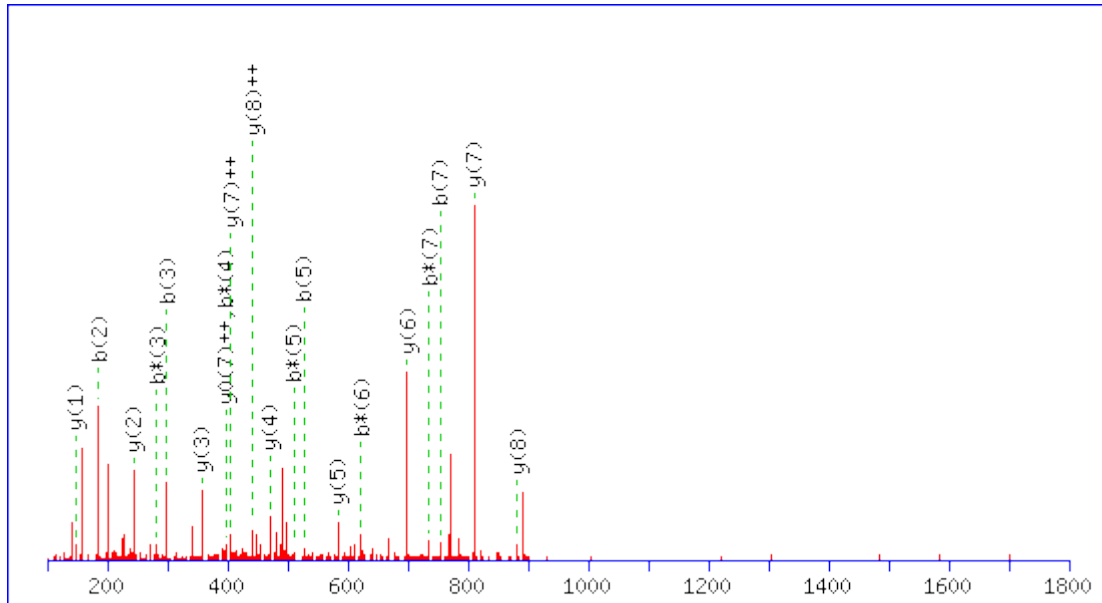
Monoisotopic mass of neutral peptide Mr(calc): 1989.9904

Ions Score: 94 Expect: 1.5e-007

Matches (**Bold Red**): 29/158 fragment ions using 49 most intense peaks

MS/MS Fragmentation of **NALDLLLPK**

Found in **PUR8_HUMAN**, Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2



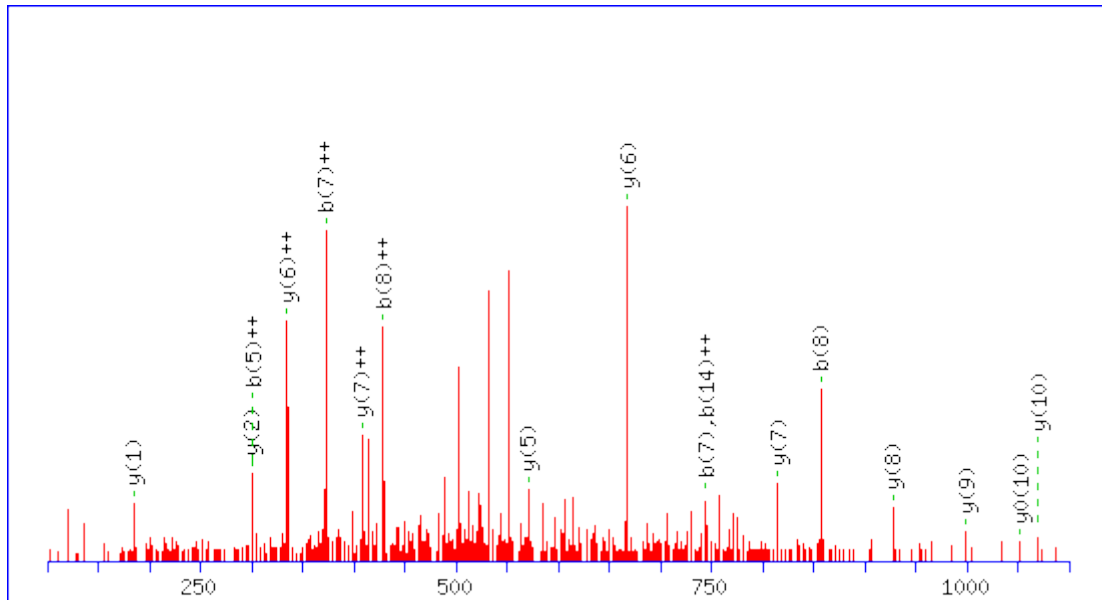
Monoisotopic mass of neutral peptide Mr(calc): 995.6015

Ions Score: 46 Expect: 0.0048

Matches (Bold Red): 20/80 fragment ions using 57 most intense peaks

MS/MS Fragmentation of **HLDHVAALFPGDVDR**

Found in **PYGB_HUMAN**, Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB
PE=1 SV=5



Monoisotopic mass of neutral peptide Mr(calc): 1670.8404

Variable modifications:

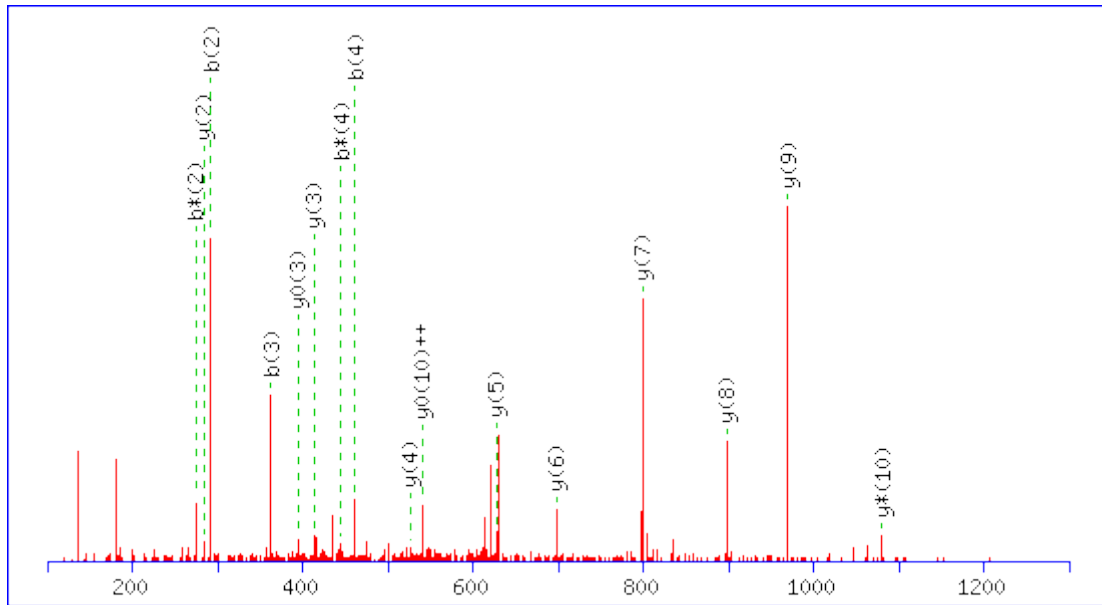
R15 : Label:13C(6)15N(4) (R)

Ions Score: 49 **Expect:** 0.004

Matches (Bold Red): 17/134 fragment ions using 22 most intense peaks

MS/MS Fragmentation of **YQAVTATLEEK**

Found in **R13AX_HUMAN**, Putative 60S ribosomal protein L13a-like MGC87657 OS=Homo sapiens PE=5 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1259.6489

Variable modifications:

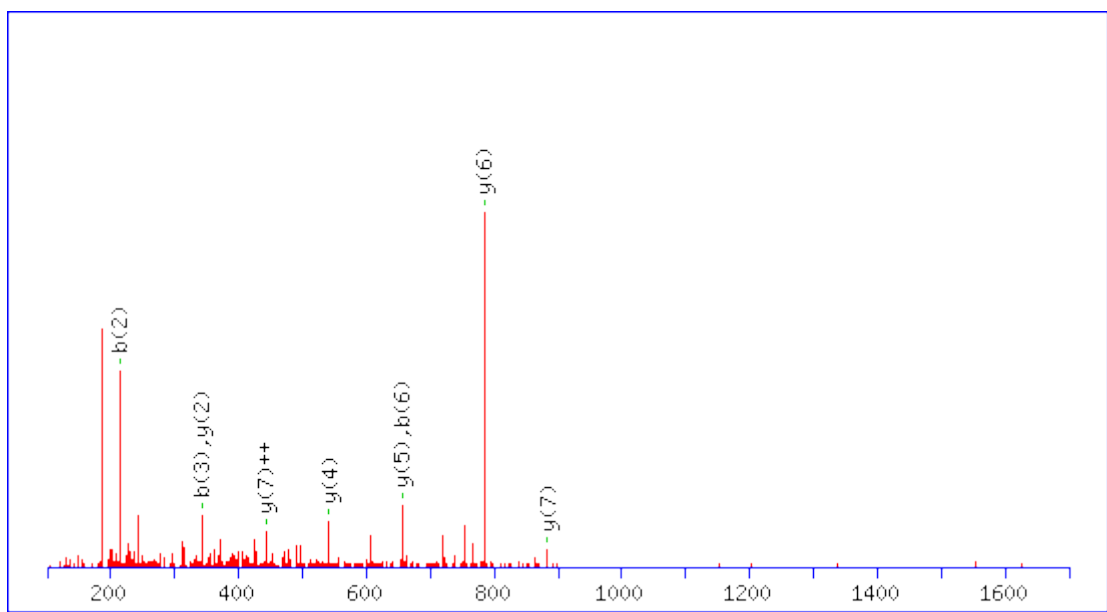
K11 : Label:13C(6)15N(2) (K)

Ions Score: 45 **Expect:** 0.0082

Matches (Bold Red): 16/108 fragment ions using 46 most intense peaks

MS/MS Fragmentation of **LVEIAESR**

Found in **RA51B_HUMAN**, DNA repair protein RAD51 homolog 2 OS=Homo sapiens GN=RAD51L1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 995.4688

Variable modifications:

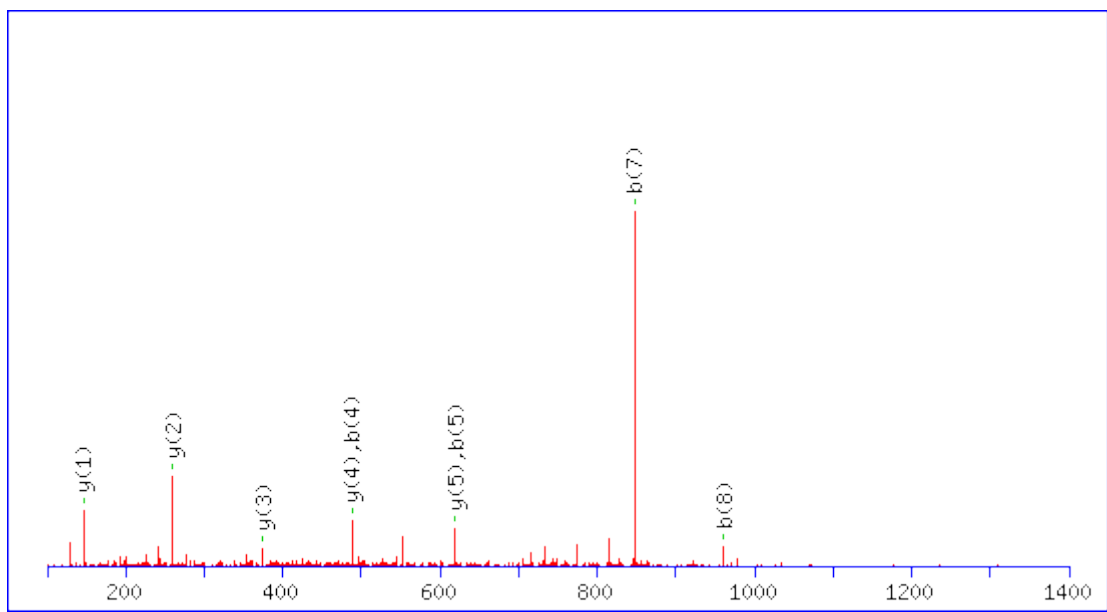
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 45 Expect: 0.0062

Matches (Bold Red): 9/104 fragment ions using 10 most intense peaks

MS/MS Fragmentation of **SREDMIDIK**

Found in **RAB6A_HUMAN**, Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3



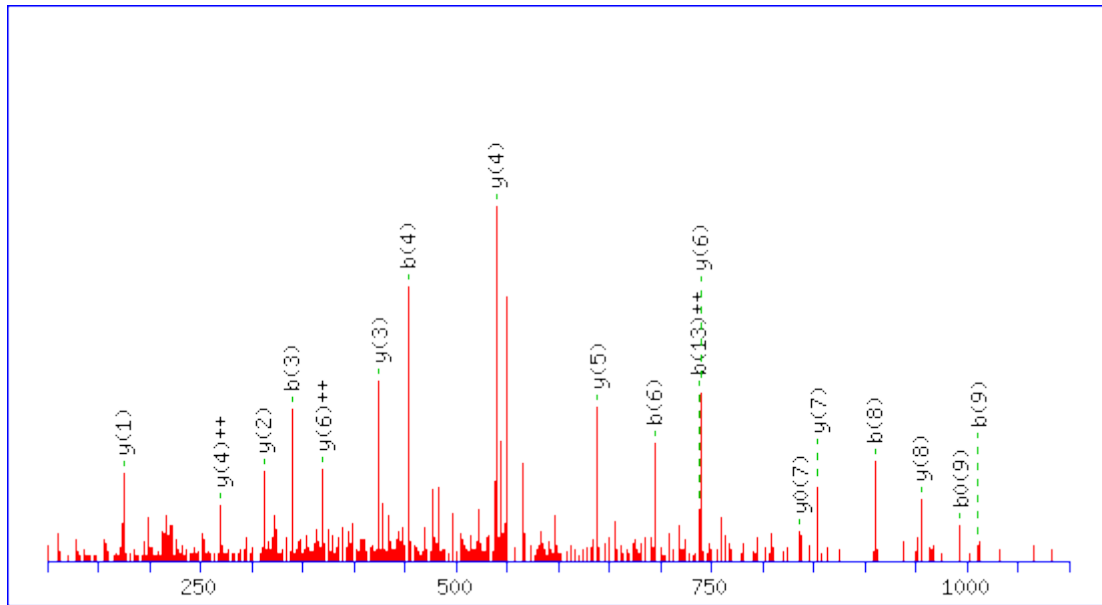
Monoisotopic mass of neutral peptide Mr(calc): 1105.5437

Ions Score: 39 Expect: 0.033

Matches (Bold Red): 9/90 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **SDHLIQDDEVNLHR**

Found in **RAB9A_HUMAN**, Ras-related protein Rab-9A OS=Homo sapiens GN=RAB9A PE=1 SV=1



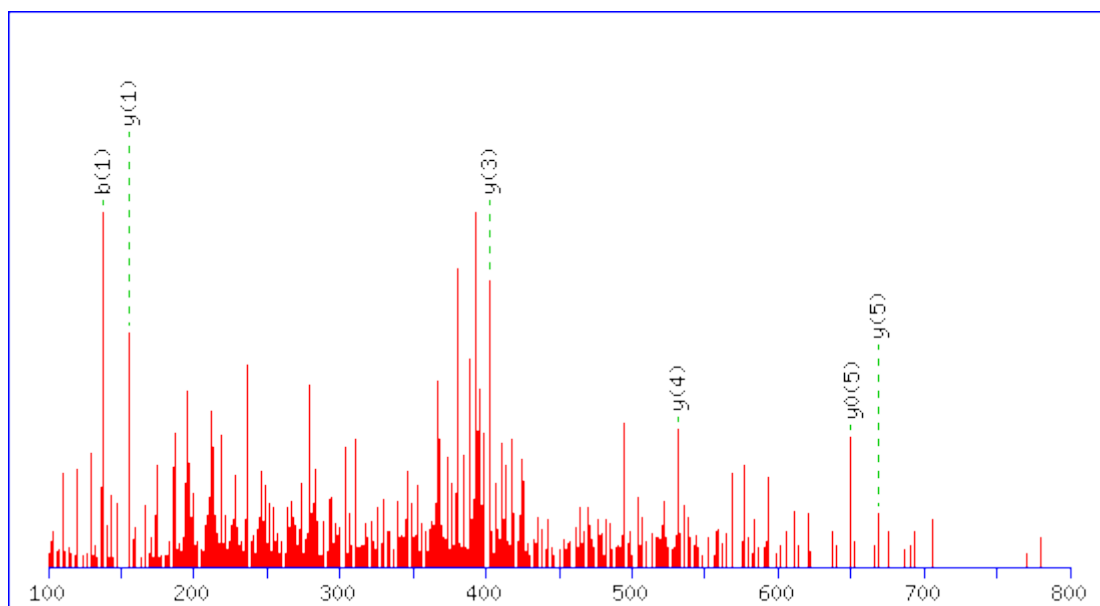
Monoisotopic mass of neutral peptide Mr(calc): 1647.8329

Ions Score: 55 Expect: 0.0012

Matches (Bold Red): 18/136 fragment ions using 24 most intense peaks

MS/MS Fragmentation of **KHECSK**

Found in **RAI1_HUMAN**, Retinoic acid-induced protein 1 OS=Homo sapiens GN=RAI1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 803.3931

Variable modifications:

K1 : Label:13C(6)15N(2) (K)

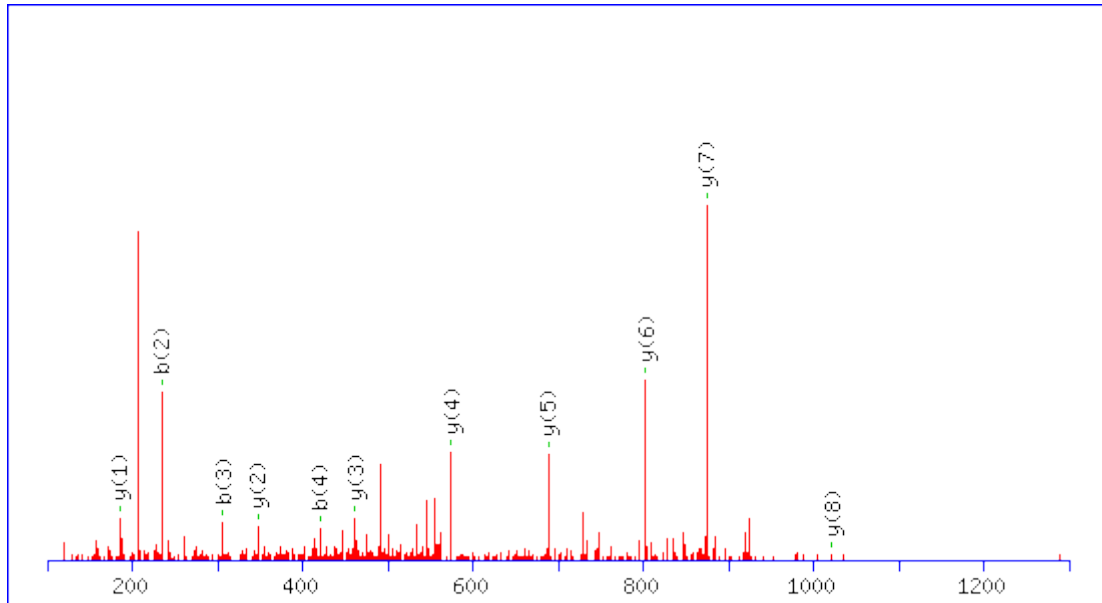
K6 : Label:13C(6)15N(2) (K)

Ions Score: 14 **Expect:** 6

Matches (Bold Red): 7/54 fragment ions using 12 most intense peaks

MS/MS Fragmentation of **SFADINLYR**

Found in **RASN_HUMAN**, GTPase NRas OS=Homo sapiens GN=NRAS PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1107.5588

Variable modifications:

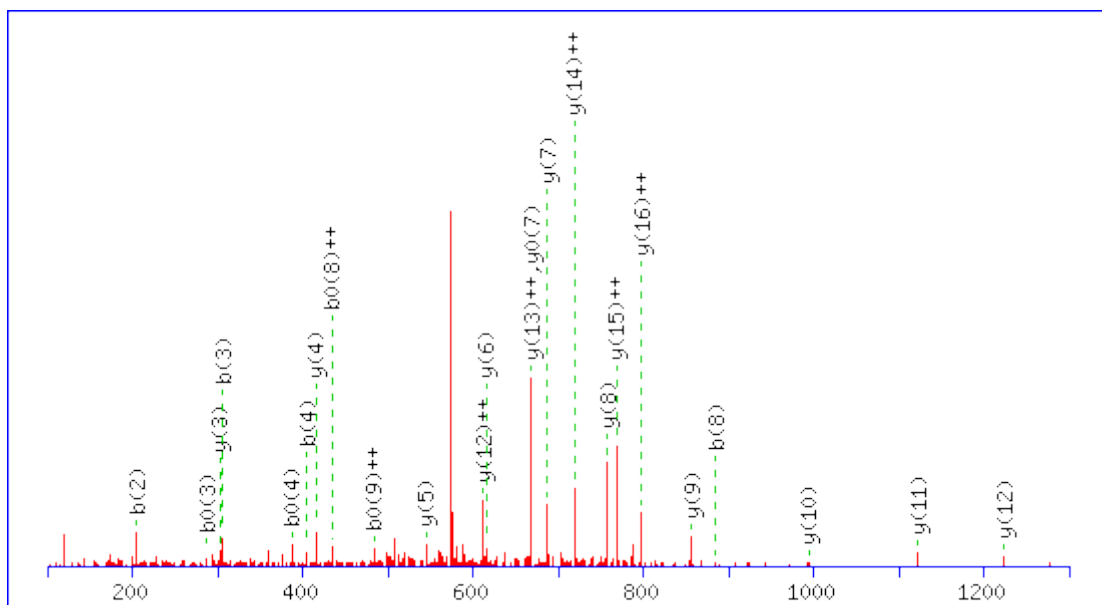
R9 : Label:13C(6)15N(4) (R)

Ions Score: 58 Expect: 0.00039

Matches (Bold Red): 11/76 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **FGTVLTEHVAAAELGAR**

Found in **RCL_HUMAN**, Deoxyribonucleoside 5'-monophosphate N-glycosidase OS=Homo sapiens GN=RCL PE=1 SV=1



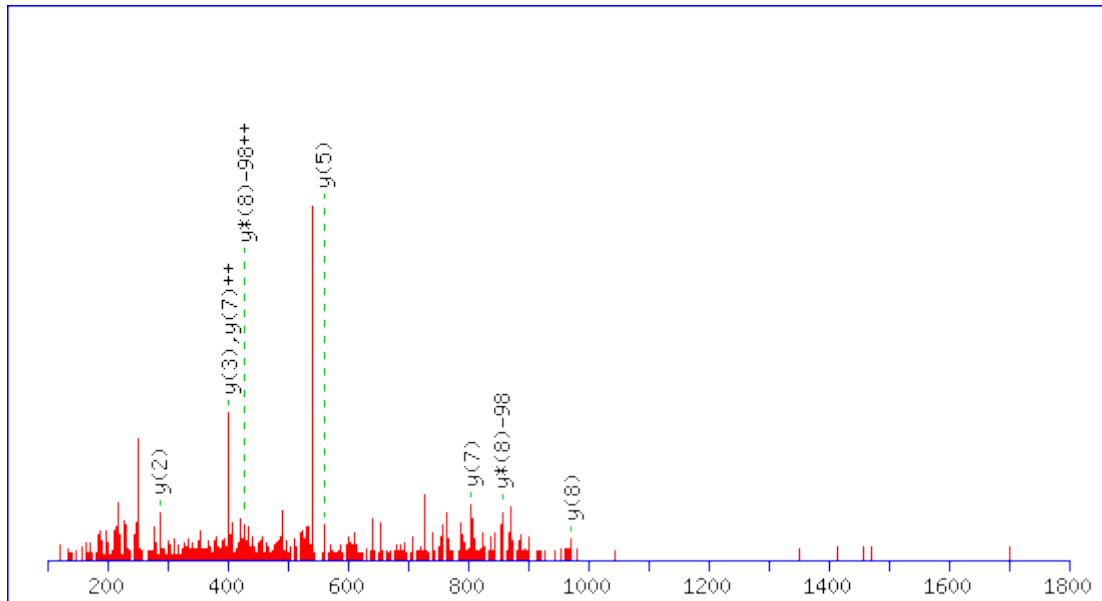
Monoisotopic mass of neutral peptide Mr(calc): 1740.9159

Ions Score: 67 Expect: 7.1e-005

Matches (Bold Red): 24/148 fragment ions using 42 most intense peaks

MS/MS Fragmentation of **ISPFASDIR**

Found in **RD3_HUMAN**, Protein RD3 OS=Homo sapiens GN=RD3 PE=2 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1084.4954

Variable modifications:

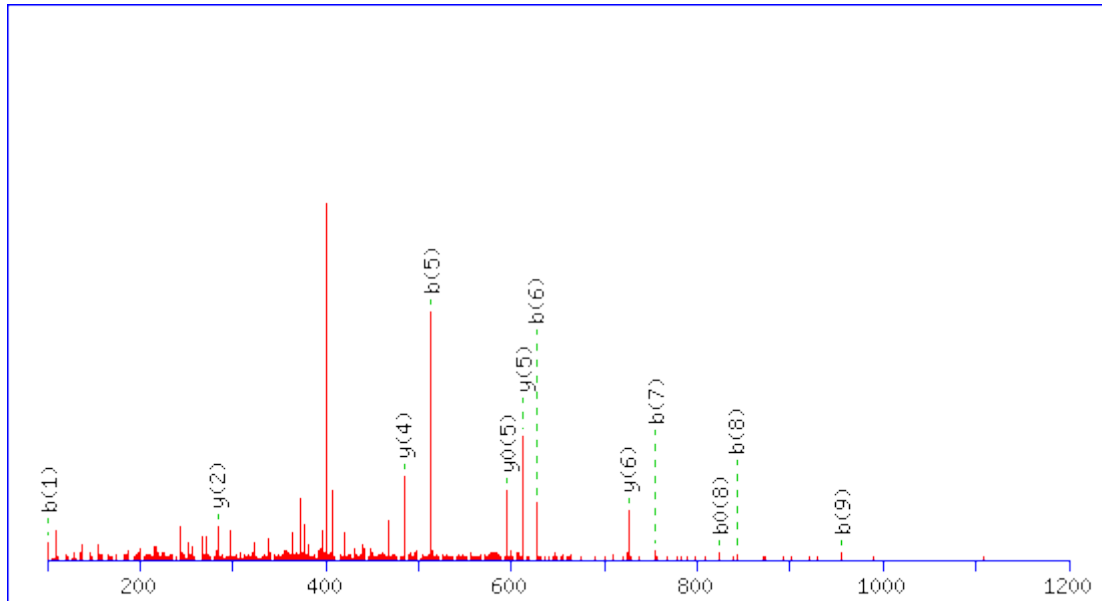
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 7 Expect: 45

Matches (Bold Red): 8/108 fragment ions using 38 most intense peaks

MS/MS Fragmentation of **TPVTNLESLEK**

Found in **RDH1_HUMAN**, 11-cis retinol dehydrogenase OS=Homo sapiens GN=RDH5 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1237.6645

Variable modifications:

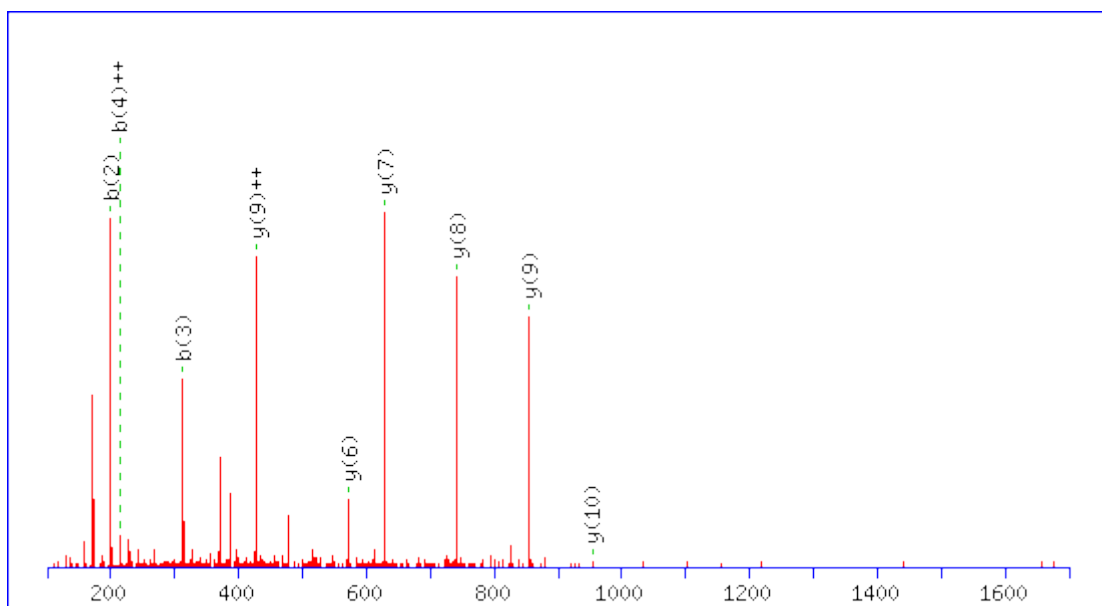
K11 : Label:¹³C(6)¹⁵N(2) (K)

Ions Score: 38 Expect: 0.035

Matches (Bold Red): 12/110 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **VLLGDPGVGK**

Found in **REM1_HUMAN**, GTP-binding protein REM 1 OS=Homo sapiens GN=REM1 PE=1 SV=2



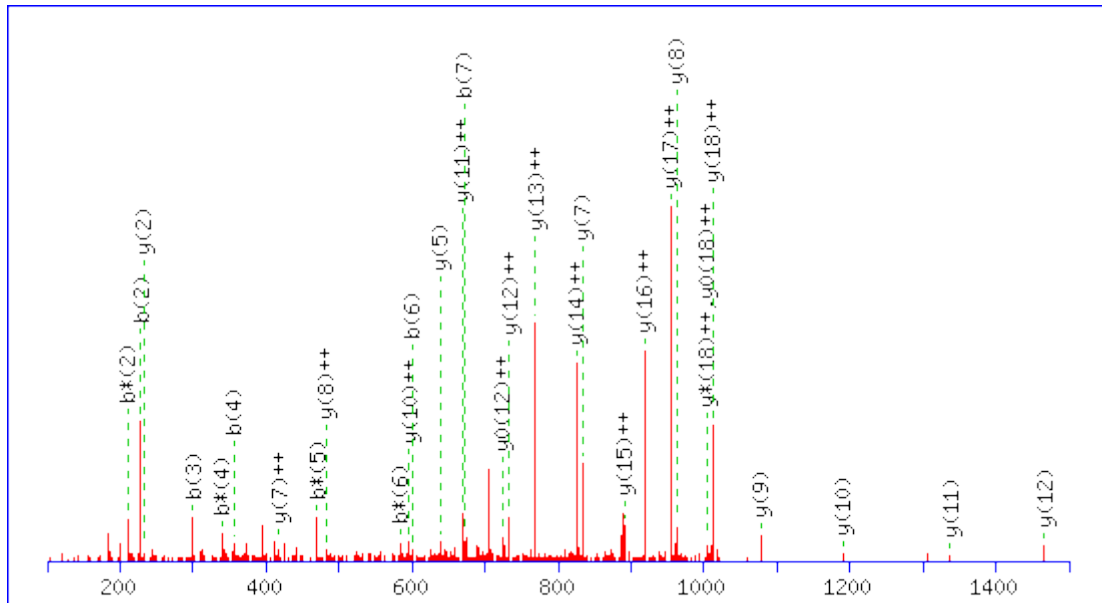
Monoisotopic mass of neutral peptide Mr(calc): 1052.6230

Ions Score: 38 **Expect:** 0.037

Matches (Bold Red): 9/80 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **INAGMLAQFIDKPVCVGR**

Found in **RFA3_HUMAN**, Replication protein A 14 kDa subunit OS=Homo sapiens GN=RPA3
PE=1 SV=1



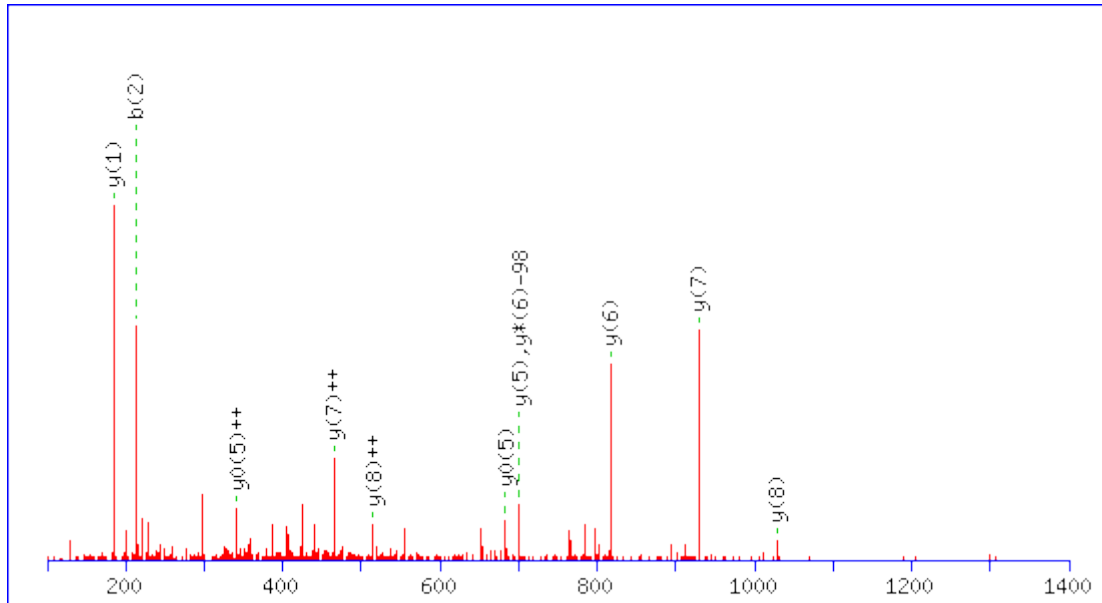
Monoisotopic mass of neutral peptide Mr(calc): 2135.1020

Ions Score: 63 **Expect:** 0.00022

Matches (Bold Red): 31/178 fragment ions using 58 most intense peaks

MS/MS Fragmentation of **LVLDMSSR**

Found in **RHG44_HUMAN**, Rho GTPase-activating protein 44 OS=Homo sapiens
GN=ARHGAP44 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1140.4762

Variable modifications:

M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

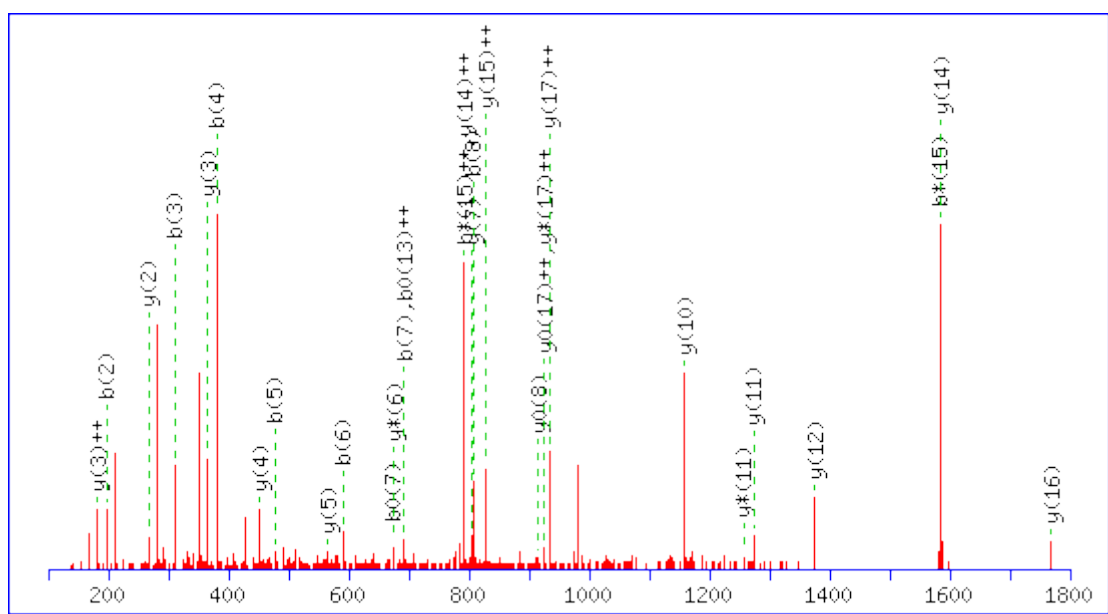
R9 : Label:13C(6)15N(4) (R)

Ions Score: 41 Expect: 0.02

Matches (Bold Red): 11/186 fragment ions using 13 most intense peaks

MS/MS Fragmentation of **VPLAPITDPQQLQLSPLK**

Found in **RIR2_HUMAN**, Ribonucleoside-diphosphate reductase subunit M2 OS=Homo sapiens GN=RRM2 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1965.1390

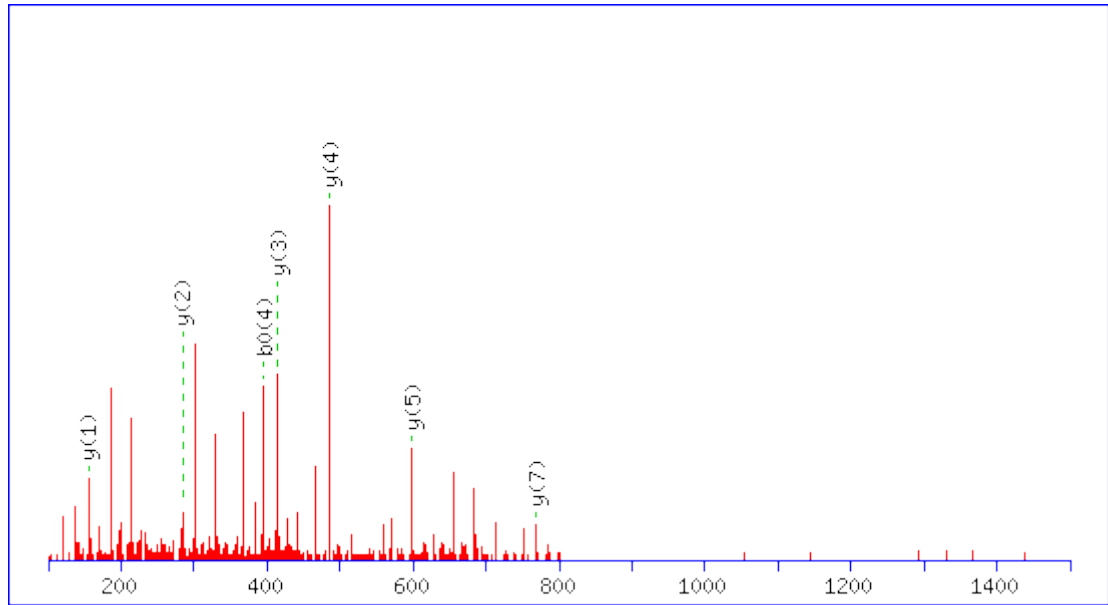
Variable modifications:

K18 : Label:13C(6)15N(2) (K)

Ions Score: 51 **Expect: 0.0027**

Matches (Bold Red): 30/168 fragment ions using 62 most intense peaks

MS/MS Fragmentation of **EAVLAMEK**
 Found in **RIT1_HUMAN**, GTP-binding protein Rit1 OS=Homo sapiens GN=RIT1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 897.4721

Variable modifications:

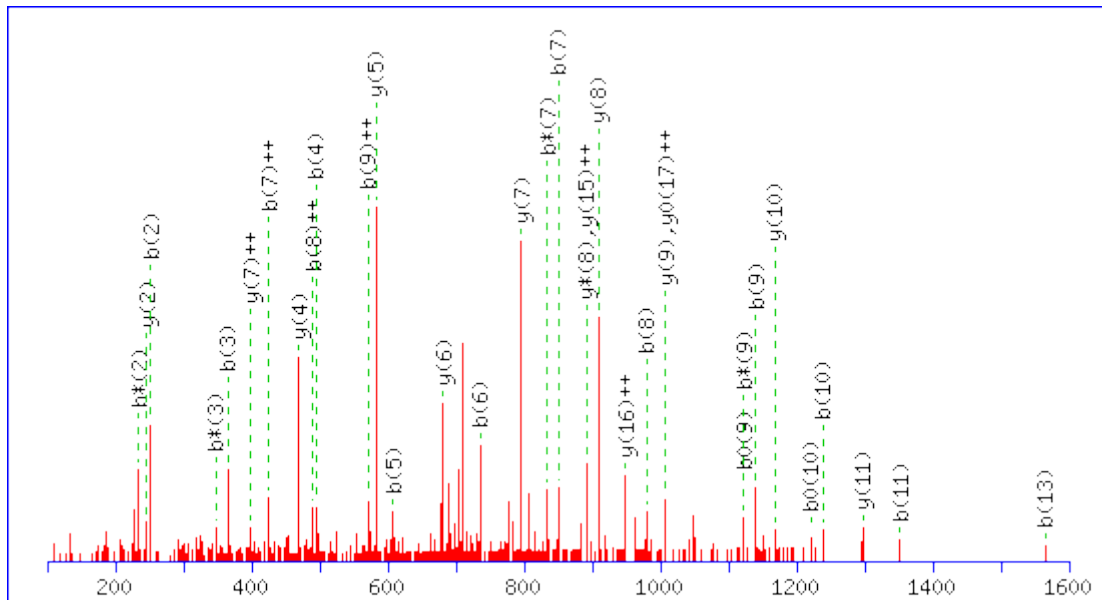
K8 : Label:13C(6)15N(2) (K)

Ions Score: 35 **Expect:** 0.053

Matches (Bold Red): 7/68 fragment ions using 14 most intense peaks

MS/MS Fragmentation of **NHIENQDECVLNVISHAR**

Found in **RM37_HUMAN**, 39S ribosomal protein L37, mitochondrial OS=Homo sapiens
GN=MRPL37 PE=1 SV=2



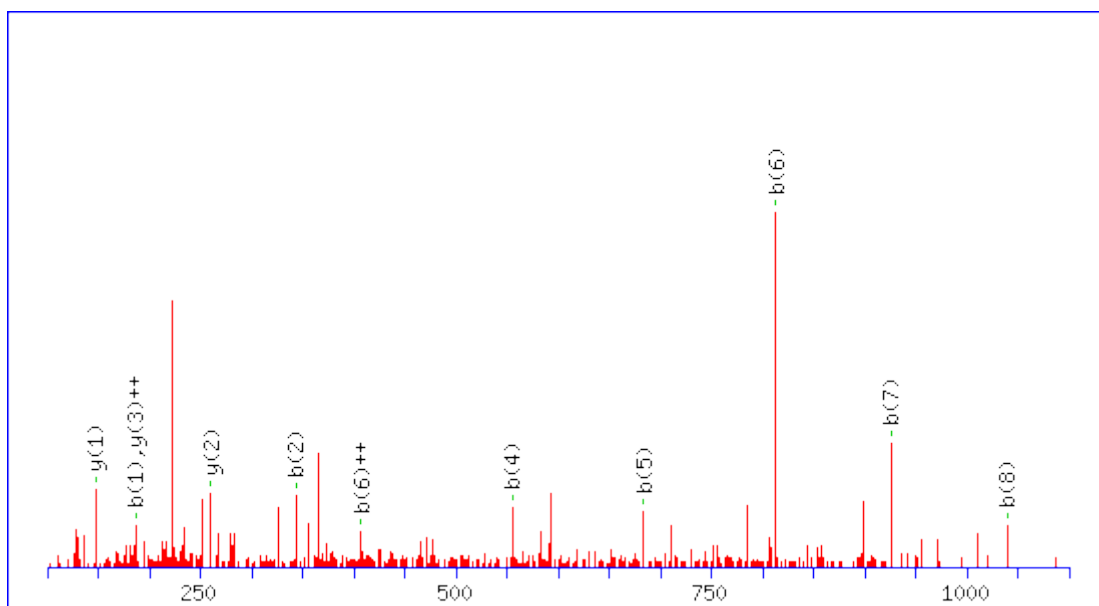
Monoisotopic mass of neutral peptide Mr(calc): 2147.0178

Ions Score: 76 **Expect:** 7.8e-006

Matches (Bold Red): 34/192 fragment ions using 51 most intense peaks

MS/MS Fragmentation of **WRPDEEILK**

Found in **RO60_HUMAN**, 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2
PE=1 SV=2



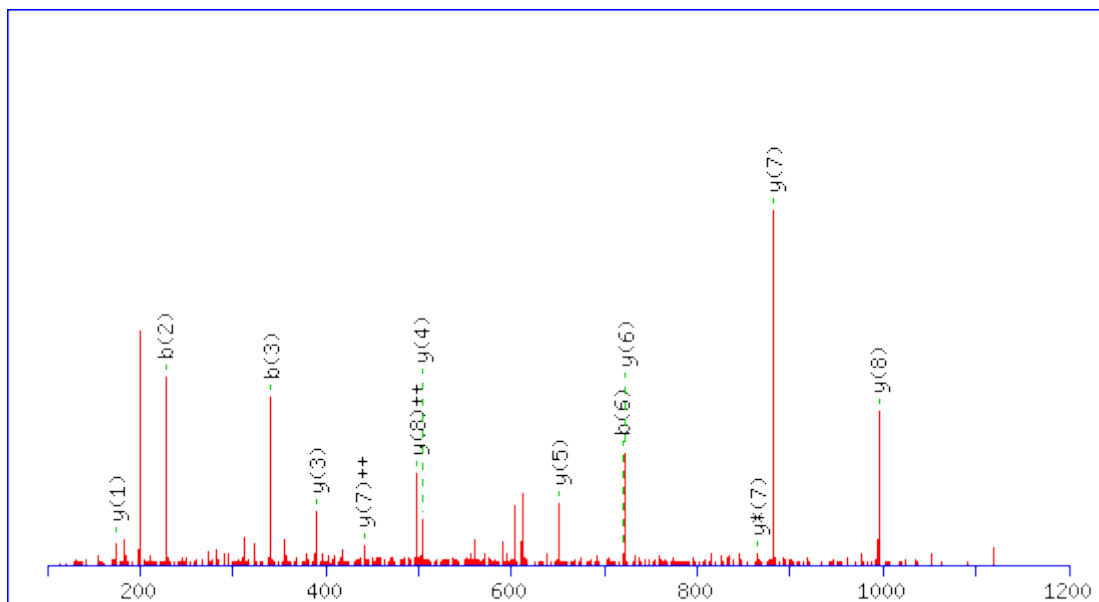
Monoisotopic mass of neutral peptide Mr(calc): 1184.6189

Ions Score: 40 Expect: 0.022

Matches (Bold Red): 11/82 fragment ions using 21 most intense peaks

MS/MS Fragmentation of **NLICAFLTDR**

Found in **ROCK1_HUMAN**, Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1
PE=1 SV=1



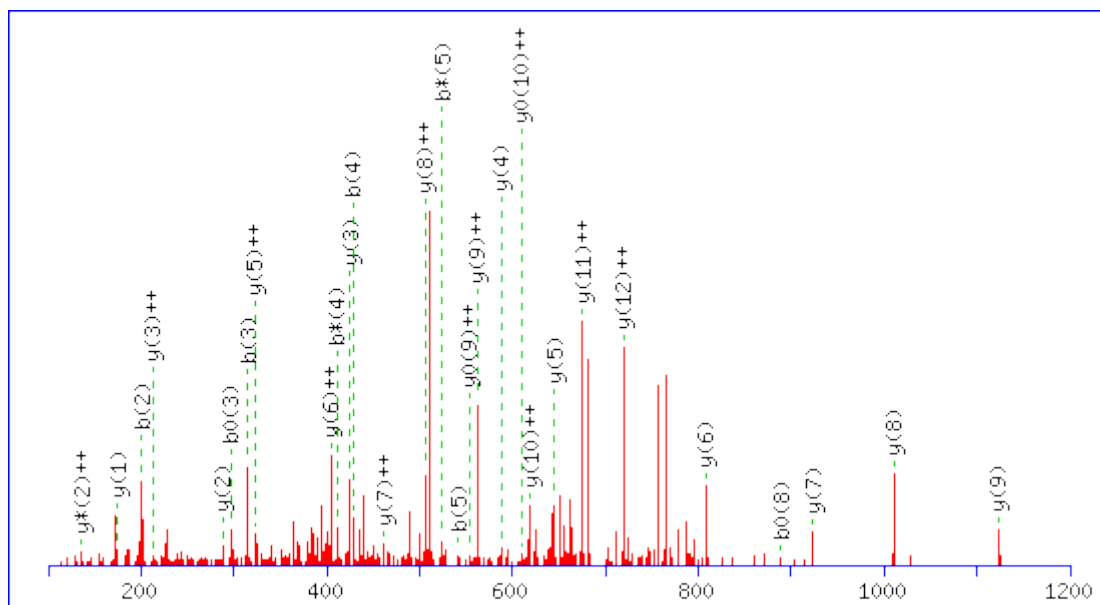
Monoisotopic mass of neutral peptide Mr(calc): 1221.6176

Ions Score: 37 Expect: 0.047

Matches (**Bold Red**): 13/92 fragment ions using 35 most intense peaks

MS/MS Fragmentation of **ISNLLSDYGYHLR**

Found in **RPB2_HUMAN**, DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens
GN=POLR2B PE=1 SV=1



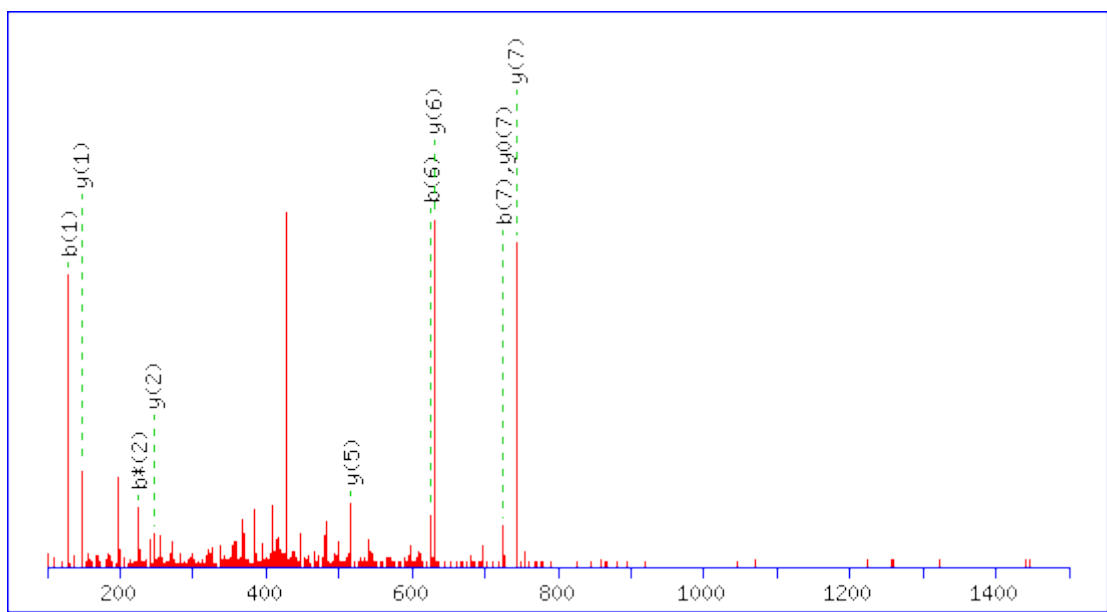
Monoisotopic mass of neutral peptide Mr(calc): 1549.7889

Ions Score: 40 Expect: 0.028

Matches (**Bold Red**): 29/126 fragment ions using 83 most intense peaks

MS/MS Fragmentation of **QLLISAVK**

Found in **RPP14_HUMAN**, Ribonuclease P protein subunit p14 OS=Homo sapiens GN=RPP14
PE=1 SV=3



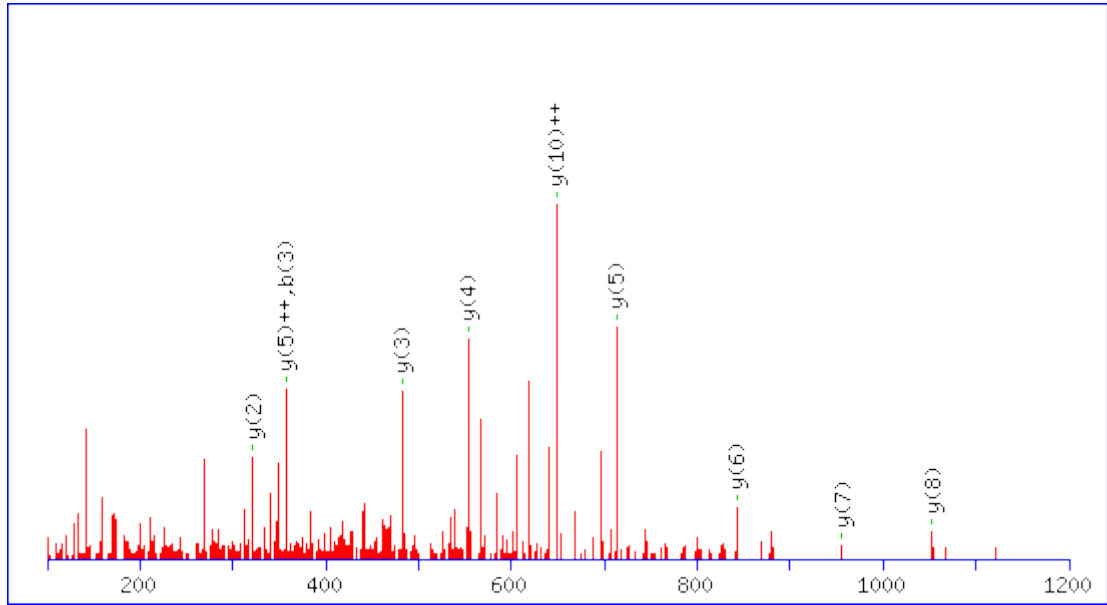
Monoisotopic mass of neutral peptide Mr(calc): 870.5538

Ions Score: 36 Expect: 0.034

Matches (Bold Red): 10/70 fragment ions using 26 most intense peaks

MS/MS Fragmentation of **LSRPLECACFR**

Found in **RRAGA_HUMAN**, Ras-related GTP-binding protein A OS=Homo sapiens GN=RRAGA
PE=1 SV=1



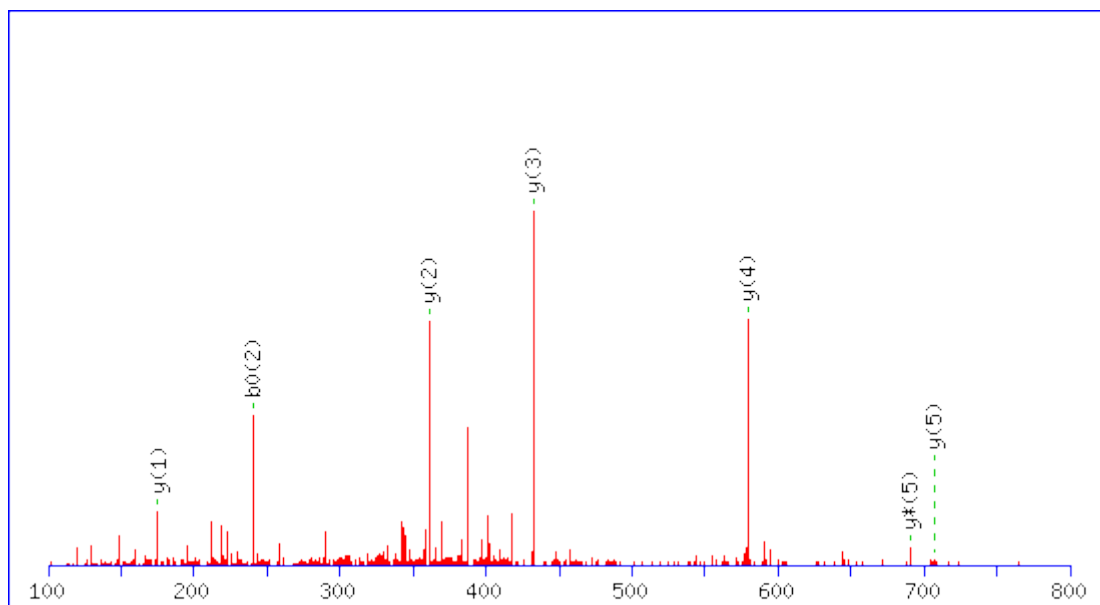
Monoisotopic mass of neutral peptide Mr(calc): 1407.6751

Ions Score: 44 Expect: 0.0087

Matches (Bold Red): 10/104 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **EQFAWR**

Found in **RS10L_HUMAN**, Putative 40S ribosomal protein S10-like OS=Homo sapiens
GN=RPS10P5 PE=5 SV=1



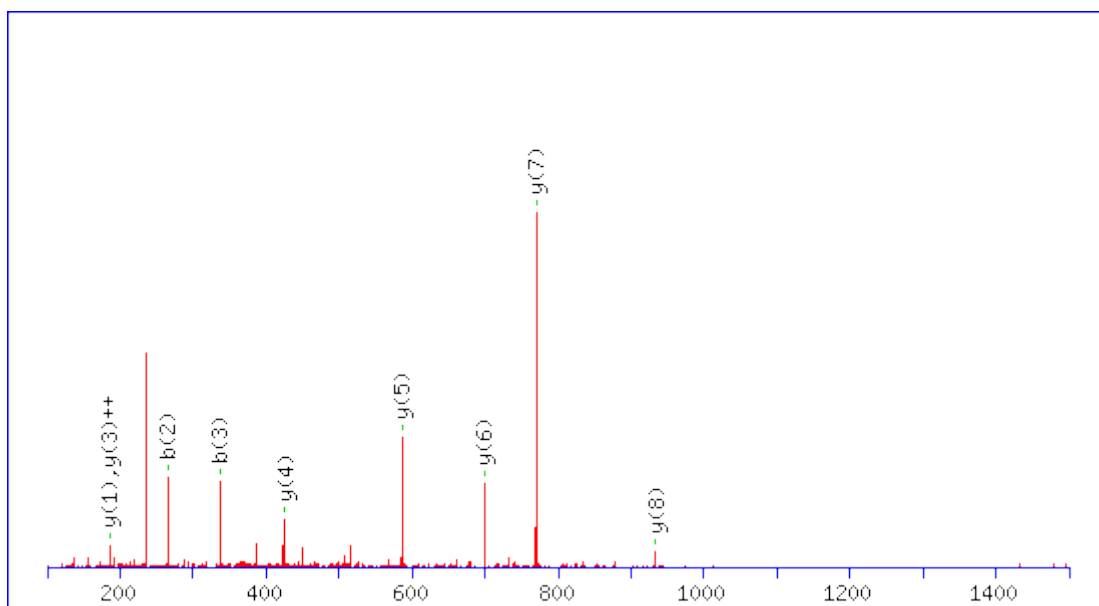
Monoisotopic mass of neutral peptide Mr(calc): 835.3977

Ions Score: 47 **Expect:** 0.0026

Matches (Bold Red): 7/48 fragment ions using 8 most intense peaks

MS/MS Fragmentation of **TYAICGAIR**

Found in **RS21_HUMAN**, 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1033.5254

Variable modifications:

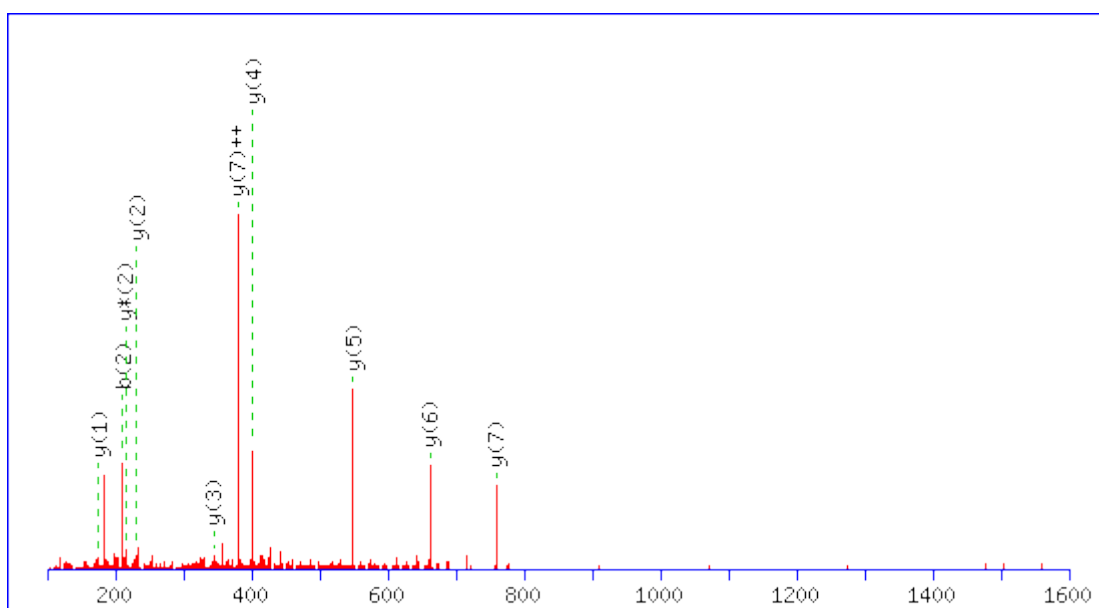
R9 : Label:¹³C(6)¹⁵N(4) (R)

Ions Score: 46 Expect: 0.0053

Matches (Bold Red): 9/64 fragment ions using 18 most intense peaks

MS/MS Fragmentation of **LPLFGLGR**

Found in **RT34_HUMAN**, 28S ribosomal protein S34, mitochondrial OS=Homo sapiens
GN=MRPS34 PE=1 SV=2



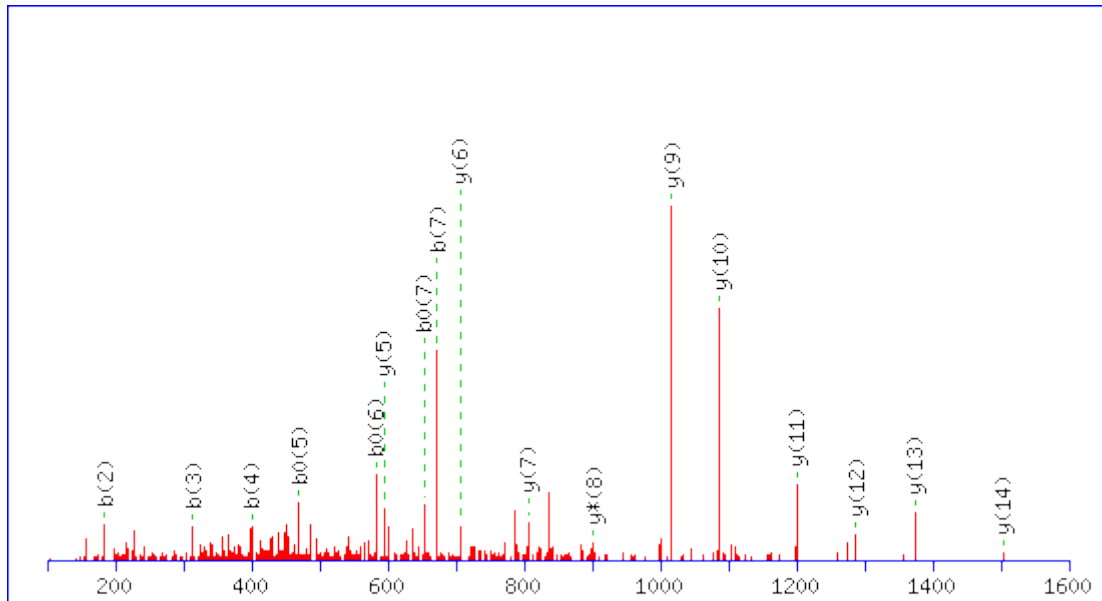
Monoisotopic mass of neutral peptide Mr(calc): 871.5280

Ions Score: 38 Expect: 0.033

Matches (Bold Red): 10/42 fragment ions using 30 most intense peaks

MS/MS Fragmentation of **ALESSIPIVIFASNR**

Found in **RUVB1_HUMAN**, RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1



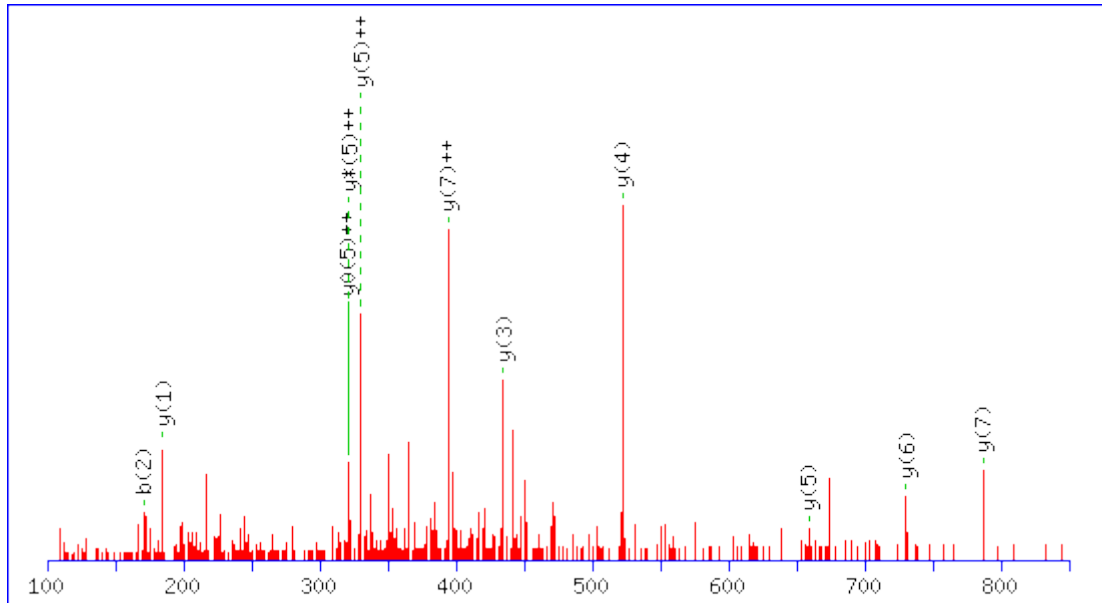
Monoisotopic mass of neutral peptide Mr(calc): 1686.9304

Ions Score: 62 Expect: 0.00022

Matches (Bold Red): 17/144 fragment ions using 31 most intense peaks

MS/MS Fragmentation of **IGAHSIR**

Found in **RUVB2_HUMAN**, RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 899.4965

Variable modifications:

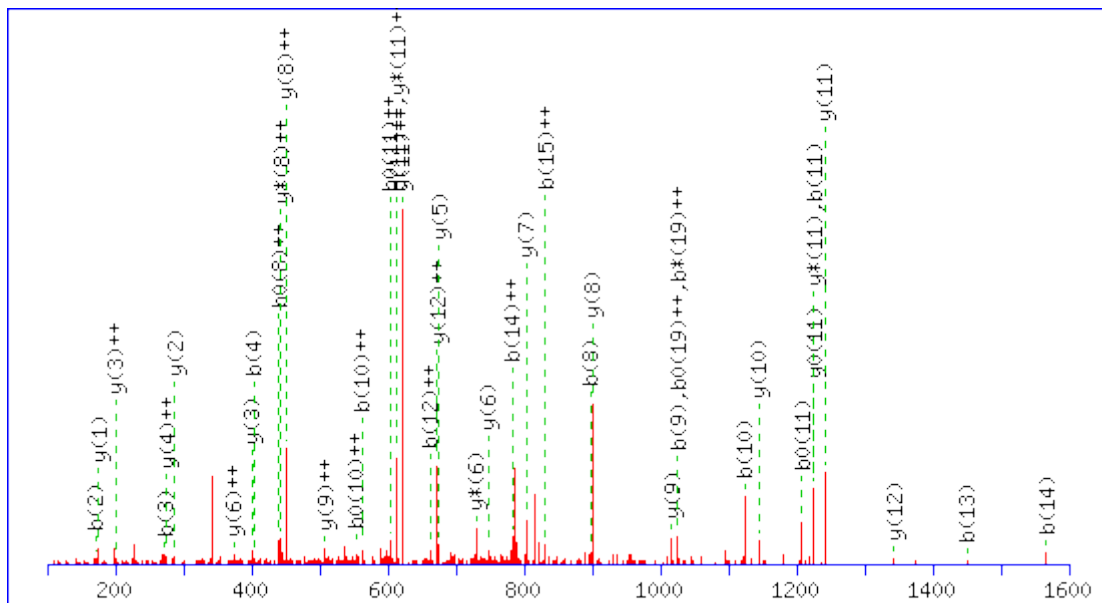
R8 : Label:13C(6)15N(4) (R)

Ions Score: 42 Expect: 0.012

Matches (Bold Red): 11/56 fragment ions using 25 most intense peaks

MS/MS Fragmentation of **GLTMLDHEQVTPEDPGAQFLIR**

Found in **SAE1_HUMAN**, SUMO-activating enzyme subunit 1 OS=Homo sapiens GN=SAE1
PE=1 SV=1



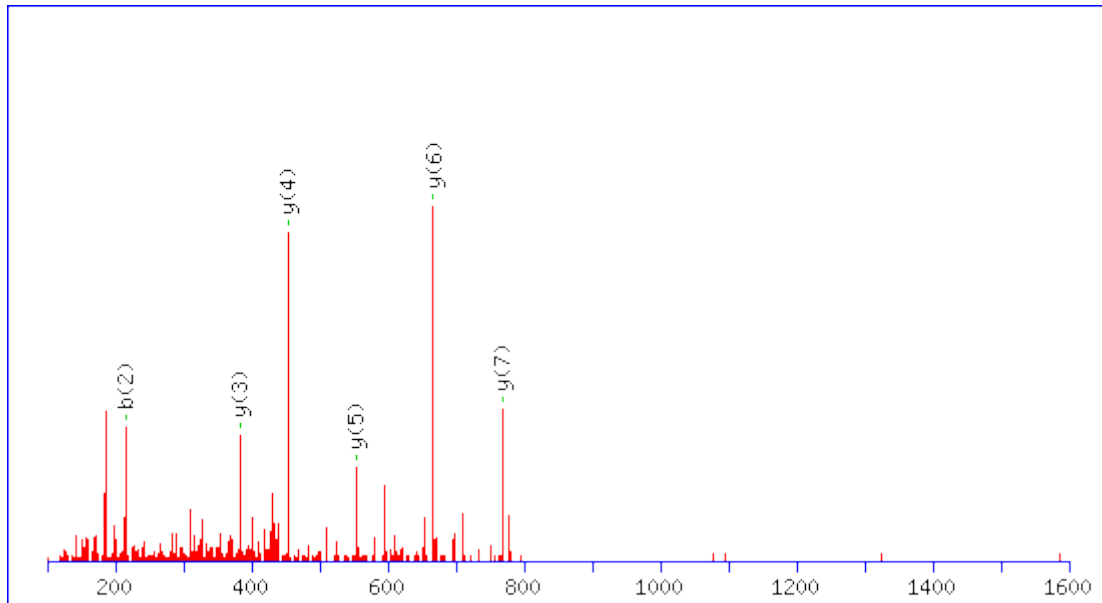
Monoisotopic mass of neutral peptide Mr(calc): 2466.2213

Ions Score: 57 Expect: 0.0009

Matches (Bold Red): 44/216 fragment ions using 90 most intense peaks

MS/MS Fragmentation of **LTNVAVVR**

Found in **SBDS_HUMAN**, Ribosome maturation protein SBDS OS=Homo sapiens GN=SBDS
PE=1 SV=4



Monoisotopic mass of neutral peptide Mr(calc): 880.5370

Variable modifications:

R8 : Label:13C(6)15N(4) (R)

Ions Score: 47 Expect: 0.0038

Matches (Bold Red): 6/66 fragment ions using 7 most intense peaks

MS/MS Fragmentation of **LPPEEASPYVDHGESGPLR**

Found in **SEC24C_HUMAN**, Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C
PE=1 SV=3

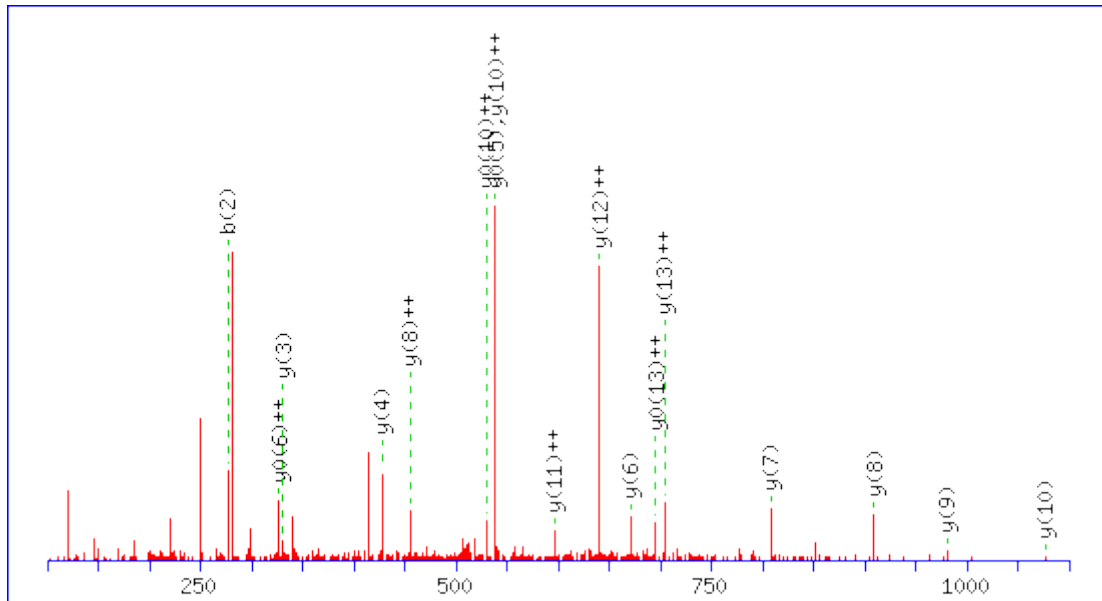
Monoisotopic mass of neutral peptide Mr(calc): 2151.0556

Ions Score: 96 Expect: 1.1e-007

Matches (**Bold Red**): 44/246 fragment ions using 60 most intense peaks

MS/MS Fragmentation of **FESDPATHNEPGVR**

Found in **SEP11_HUMAN**, Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3



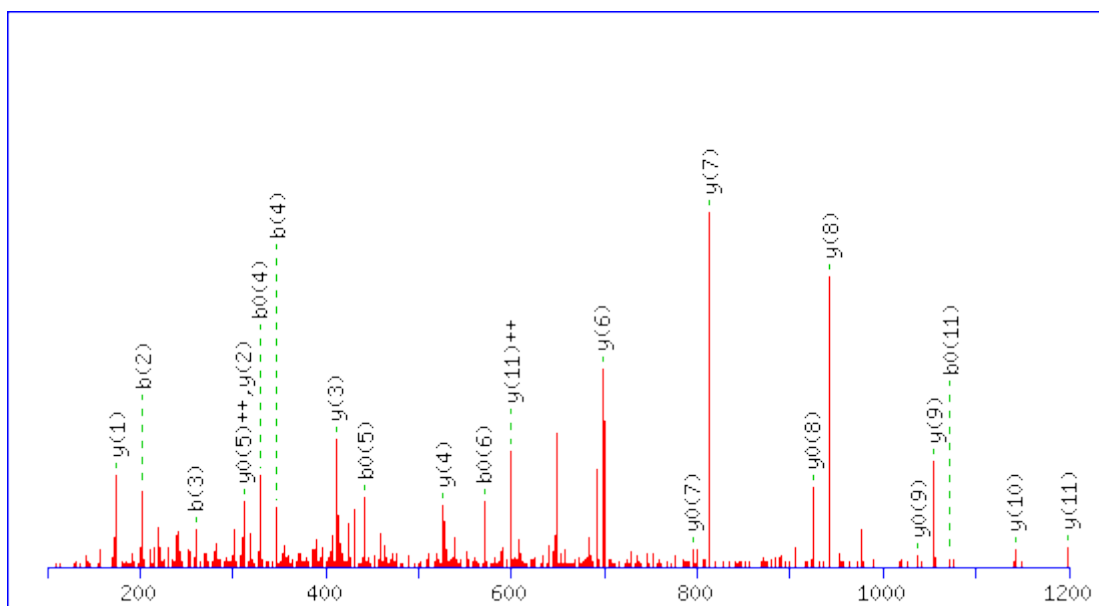
Monoisotopic mass of neutral peptide Mr(calc): 1554.7063

Ions Score: 45 Expect: 0.0061

Matches (**Bold Red**): 17/130 fragment ions using 30 most intense peaks

MS/MS Fragmentation of **SDGSLEDGDDVHR**

Found in **SERC1_HUMAN**, Serine incorporator 1 OS=Homo sapiens GN=SERINC1 PE=1 SV=1



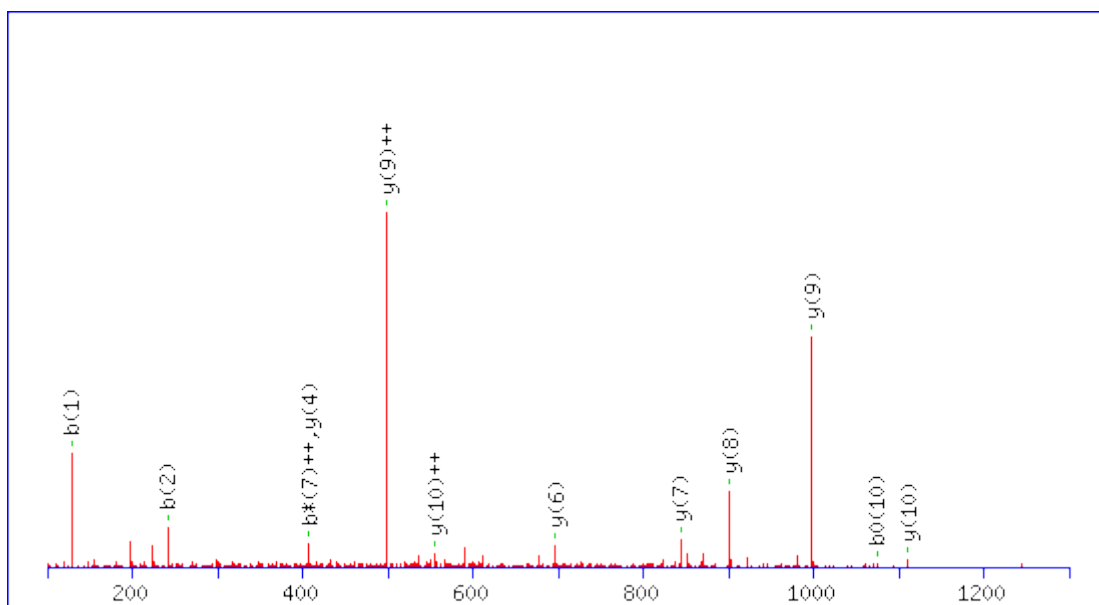
Monoisotopic mass of neutral peptide Mr(calc): 1400.5804

Ions Score: 73 Expect: 7.3e-006

Matches (Bold Red): 22/114 fragment ions using 38 most intense peaks

MS/MS Fragmentation of **KIPGFCEGGFK**

Found in **SERC3_HUMAN**, Serine incorporator 3 OS=Homo sapiens GN=SERINC3 PE=1 SV=2



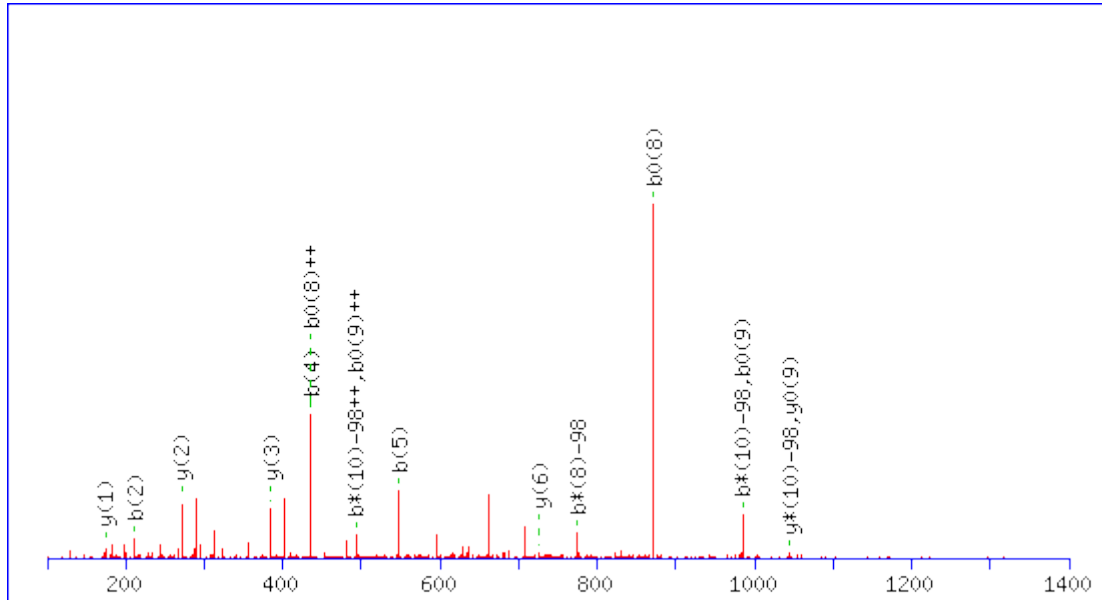
Monoisotopic mass of neutral peptide Mr(calc): 1238.6118

Ions Score: 38 Expect: 0.045

Matches (**Bold Red**): 12/100 fragment ions using 26 most intense peaks

MS/MS Fragmentation of **LPGSLRKGIPR**

Found in **SHAN3_HUMAN**, SH3 and multiple ankyrin repeat domains protein 3 OS=Homo sapiens GN=SHANK3 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1272.7067

Variable modifications:

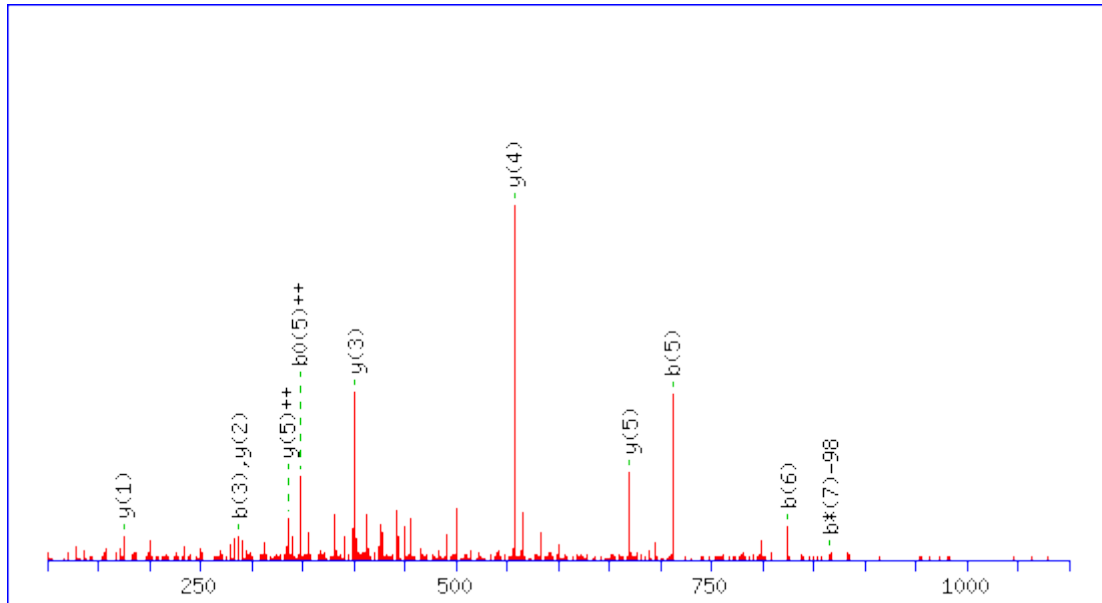
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 14 Expect: 9.7

Matches (**Bold Red**): 16/146 fragment ions using 39 most intense peaks

MS/MS Fragmentation of **LSSYTLRILR**

Found in **SLAF6_HUMAN**, SLAM family member 6 OS=Homo sapiens GN=SLAMF6 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1380.6567

Variable modifications:

Y4 : Phospho (Y)

T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

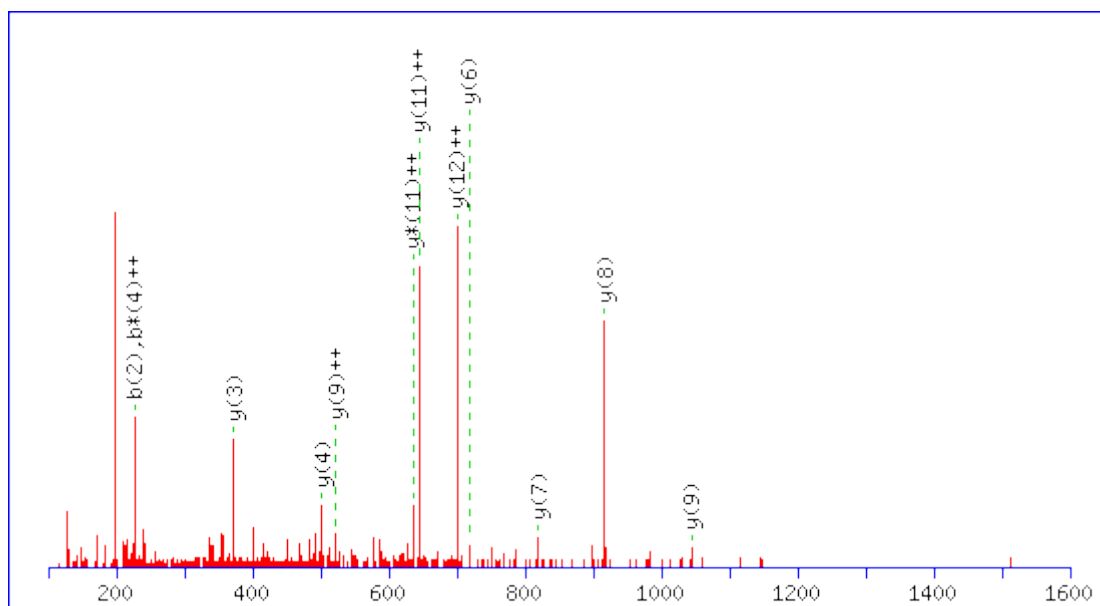
Ions Score: 38 Expect: 0.044

Matches (Bold Red): 11/134 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **ILNEKPTTDEPEK**

Found in **SLK_HUMAN**, STE20-like serine/threonine-protein kinase OS=Homo sapiens

GN=SLK PE=1 SV=1



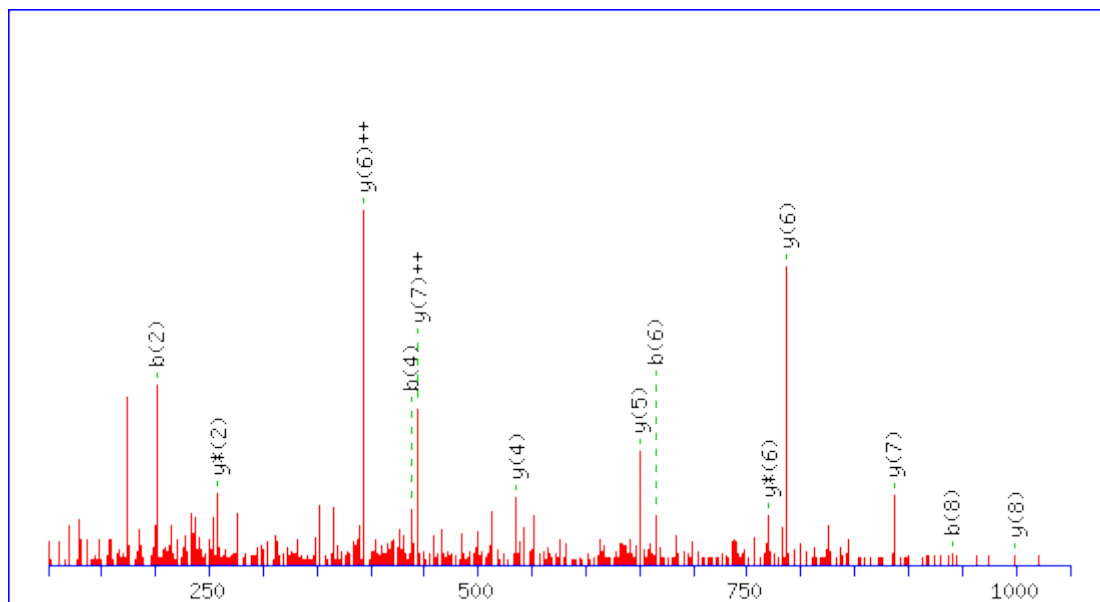
Monoisotopic mass of neutral peptide Mr(calc): 1512.7671

Ions Score: 40 Expect: 0.028

Matches (Bold Red): 12/132 fragment ions using 18 most intense peaks

MS/MS Fragmentation of **SLVHDLFQK**

Found in **SMC4_HUMAN**, Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2



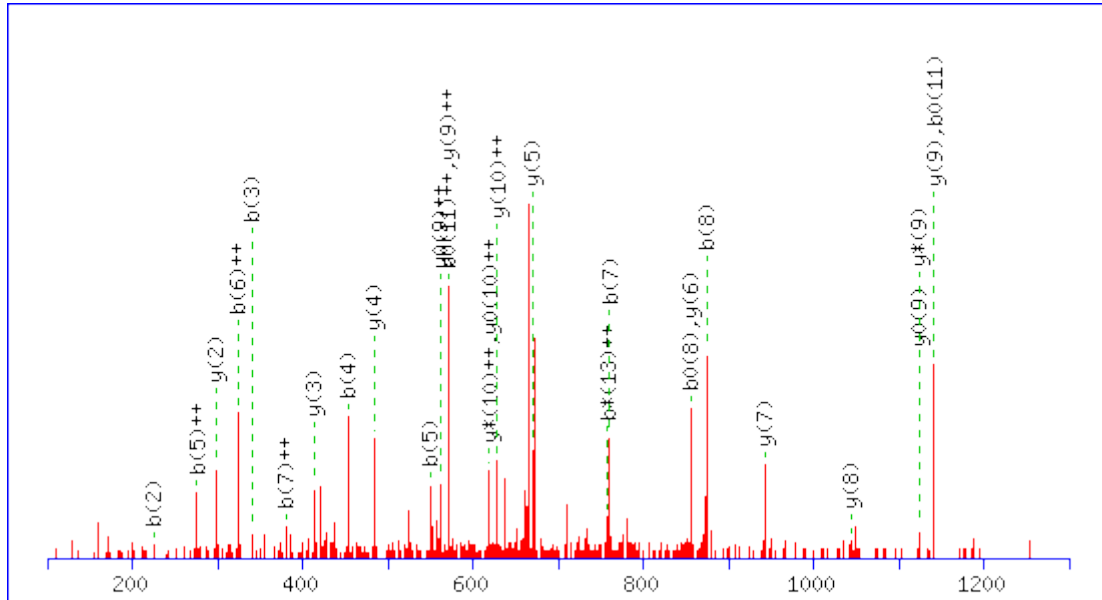
Monoisotopic mass of neutral peptide Mr(calc): 1085.5869

Ions Score: 39 Expect: 0.031

Matches (**Bold Red**): 13/74 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **HSDLPPLNPTSWWADLR**

Found in **SPNS1_HUMAN**, Protein spinster homolog 1 OS=Homo sapiens GN=SPNS1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 2013.9936

Variable modifications:

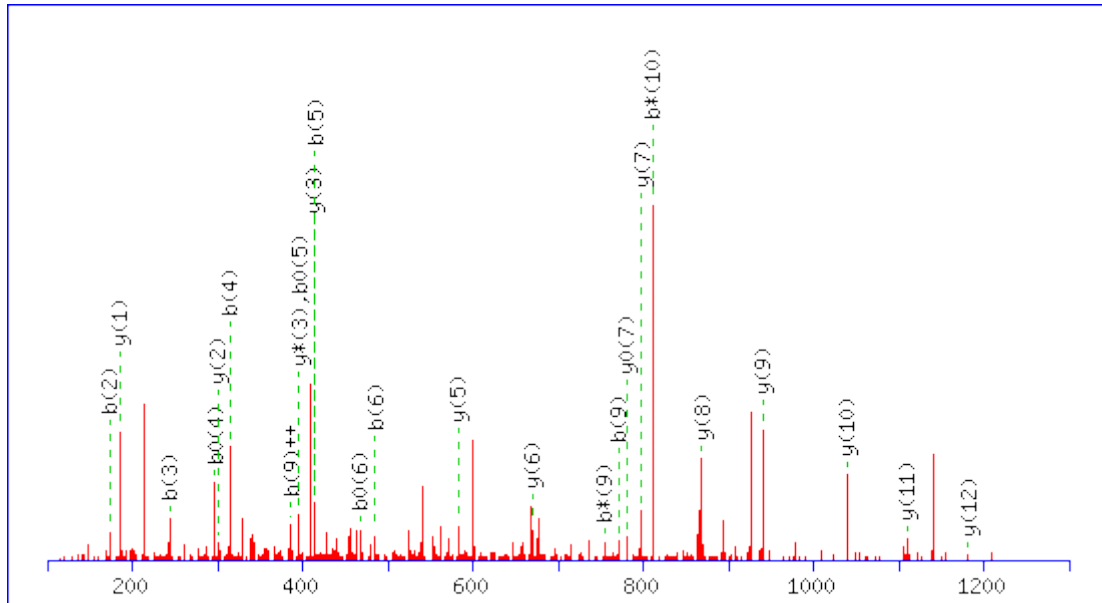
R17 : Label:13C(6)15N(4) (R)

Ions Score: 42 Expect: 0.021

Matches (**Bold Red**): 28/172 fragment ions using 56 most intense peaks

MS/MS Fragmentation of **TAAAVAAQSGILDR**

Found in **SQRD_HUMAN**, Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1352.7287

Variable modifications:

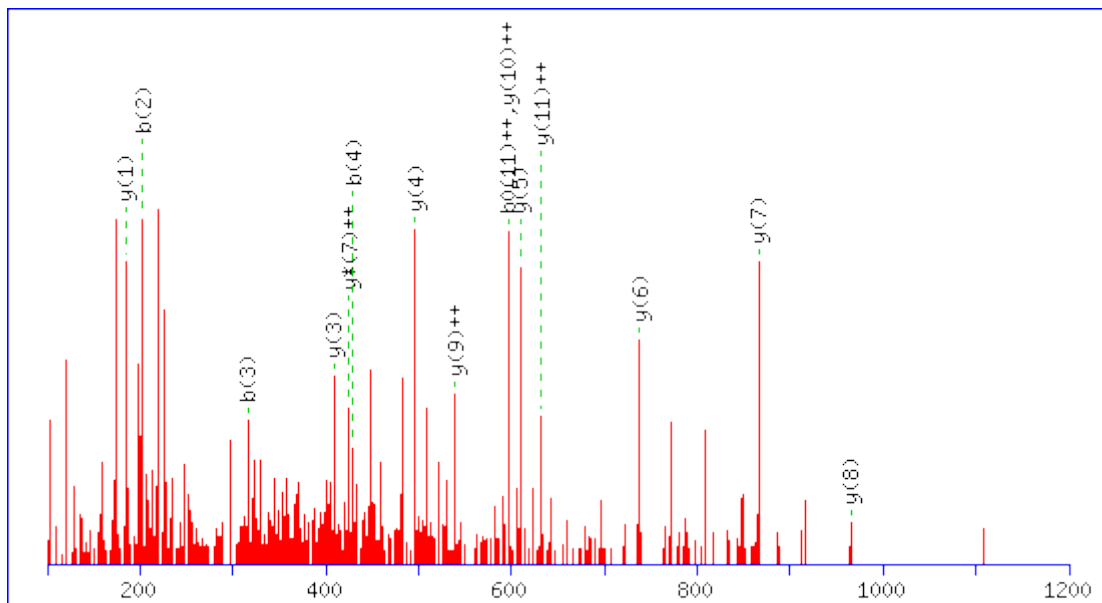
R14 : Label: $^{13}\text{C}(6)^{15}\text{N}(4)$ (R)

Ions Score: 50 Expect: 0.003

Matches (Bold Red): 25/140 fragment ions using 78 most intense peaks

MS/MS Fragmentation of **MALLVQELSSHR**

Found in **SRA1_HUMAN**, Steroid receptor RNA activator 1 OS=Homo sapiens GN=SRA1
PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1392.7423

Variable modifications:

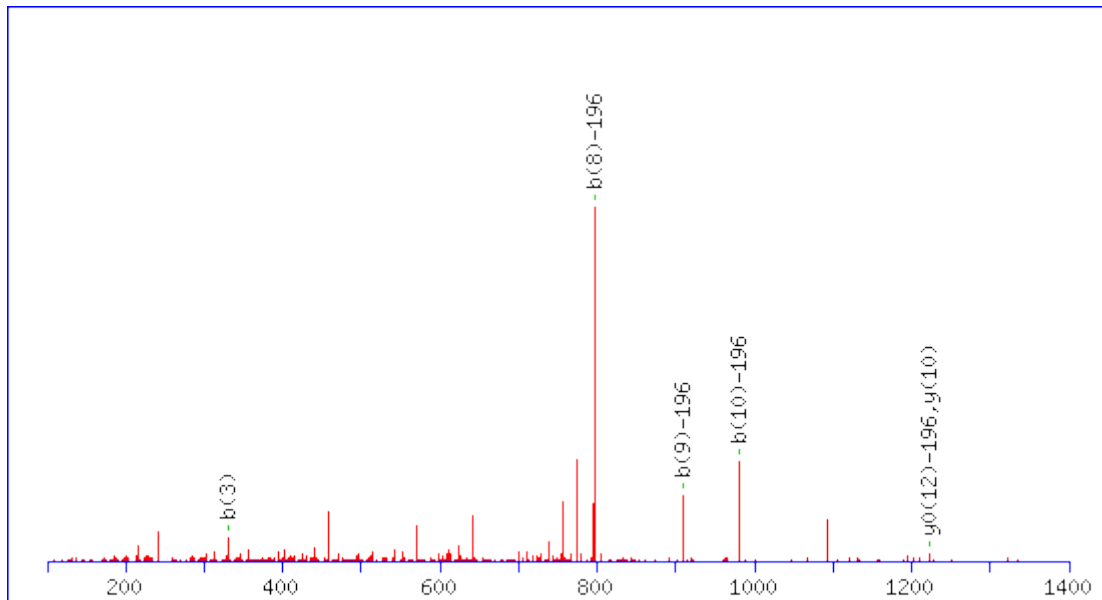
R12 : Label:13C(6)15N(4) (R)

Ions Score: 38 Expect: 0.04

Matches (Bold Red): 15/106 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **DITTSADQIAEVK**

Found in **SSH2_HUMAN**, Protein phosphatase Slingshot homolog 2 OS=Homo sapiens
GN=SSH2 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1549.6314

Variable modifications:

T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

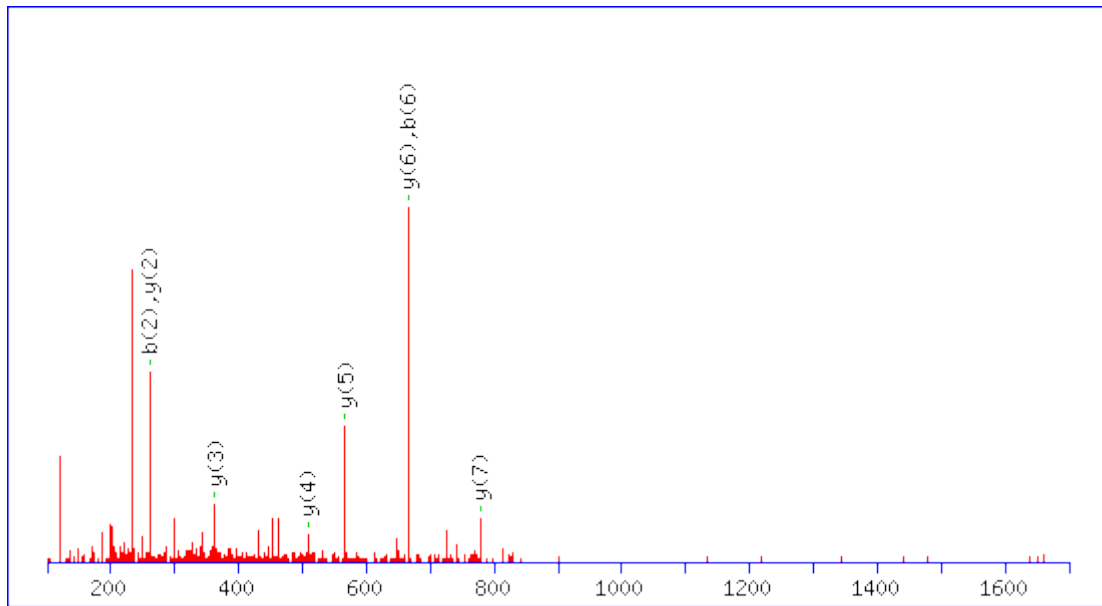
Ions Score: 13 Expect: 11

Matches (Bold Red): 6/196 fragment ions using 18 most intense peaks

MS/MS Fragmentation of **FLVGFTNK**

Found in **SSRA_HUMAN**, Translocon-associated protein subunit alpha OS=Homo sapiens

GN=SSR1 PE=1 SV=3



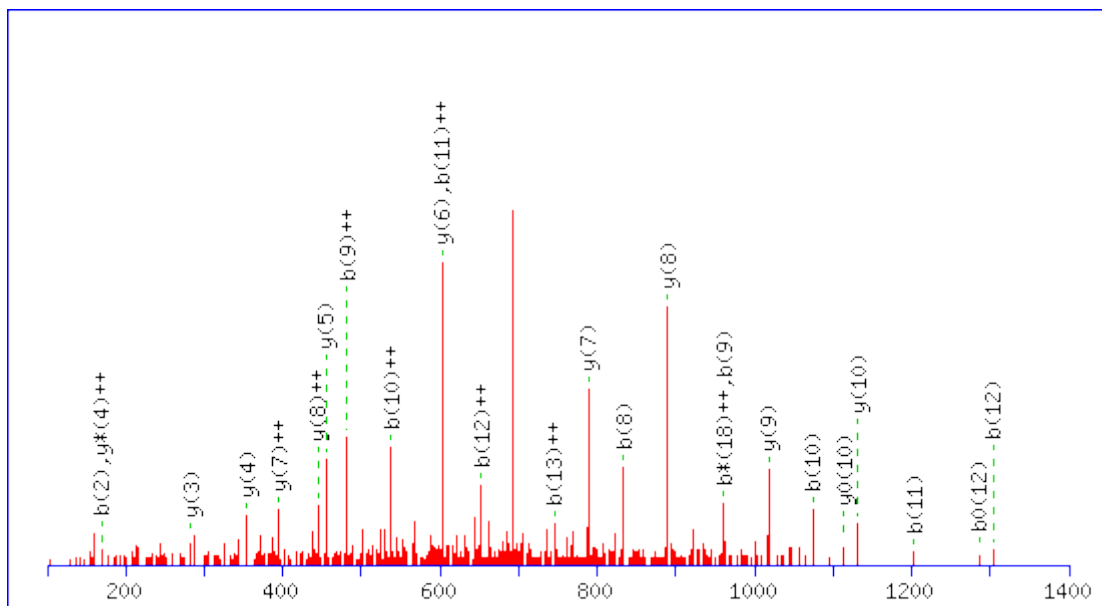
Monoisotopic mass of neutral peptide Mr(calc): 924.5069

Ions Score: 37 Expect: 0.045

Matches (Bold Red): 8/58 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **APIDHGLEQLETWFTAGAK**

Found in **STAT2_HUMAN**, Signal transducer and activator of transcription 2 OS=Homo sapiens GN=STAT2 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 2091.0517

Variable modifications:

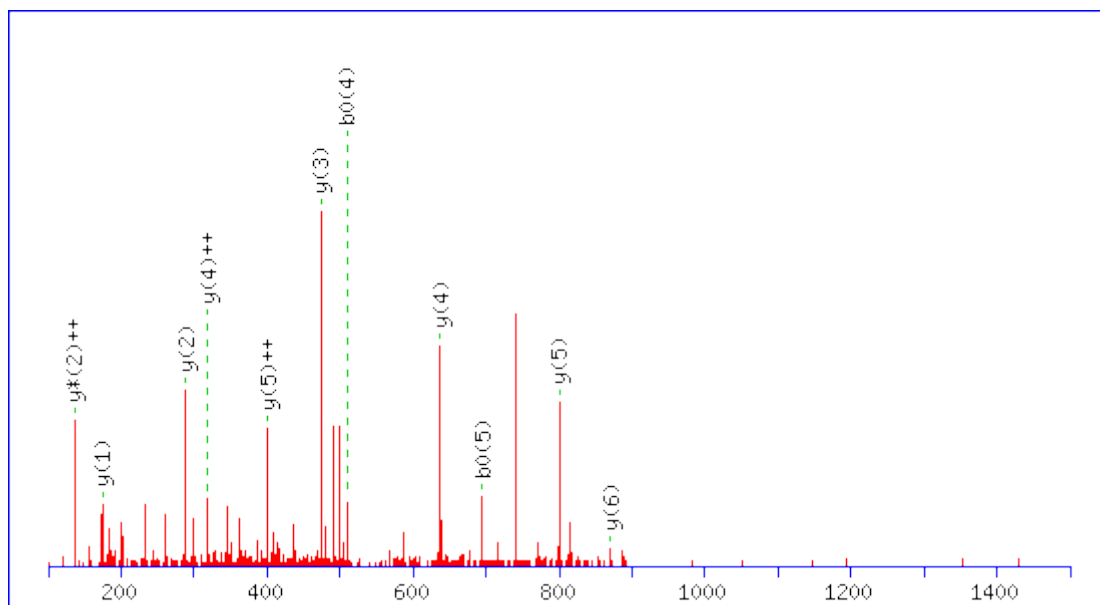
K19 : Label:13C(6)15N(2) (K)

Ions Score: 58 **Expect: 0.00057**

Matches (Bold Red): 25/186 fragment ions using 31 most intense peaks

MS/MS Fragmentation of **EAYYWLR**

Found in **STT3A_HUMAN**, Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=



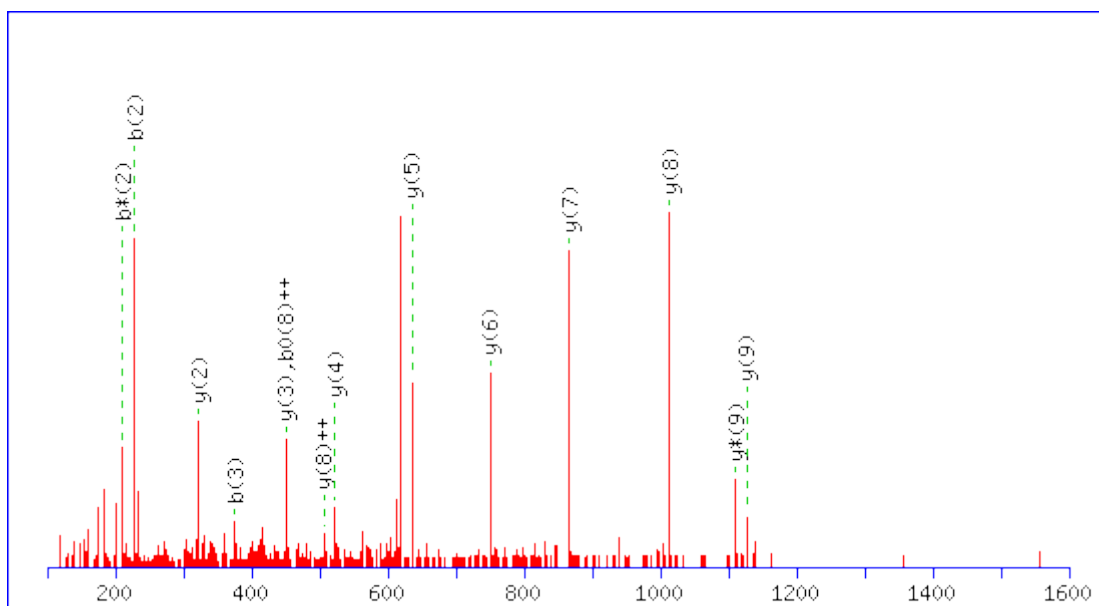
Monoisotopic mass of neutral peptide Mr(calc): 999.4814

Ions Score: 41 **Expect: 0.012**

Matches (Bold Red): 11/48 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **INFDDNAEFR**

Found in **SUCB2_HUMAN**, Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2



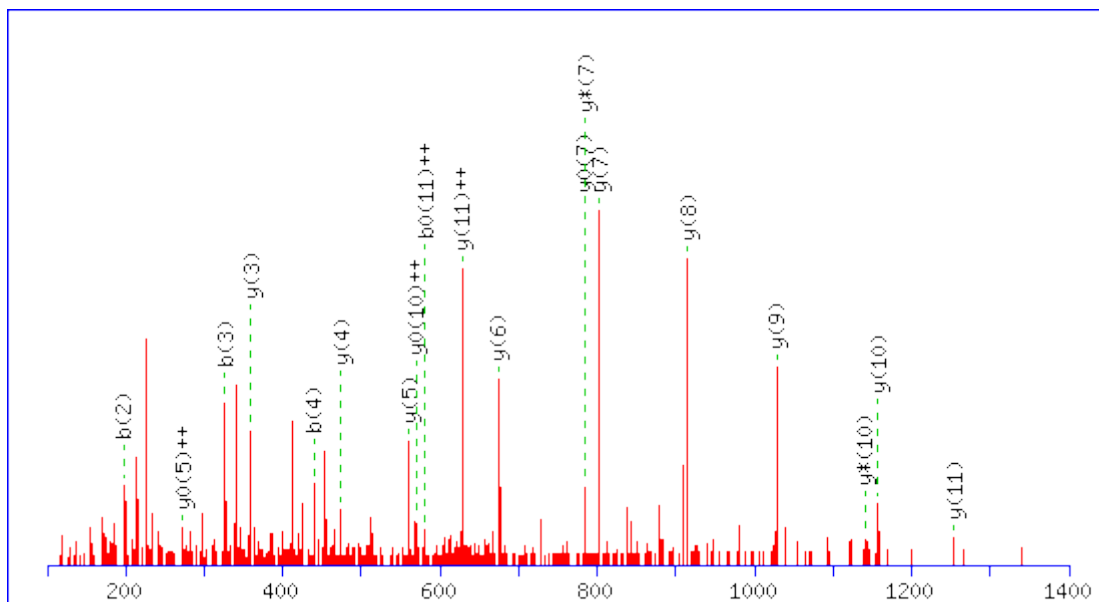
Monoisotopic mass of neutral peptide Mr(calc): 1239.5520

Ions Score: 58 Expect: 0.00035

Matches (Bold Red): 14/96 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **VPEILQLSDALR**

Found in **SYCC_HUMAN**, Cysteinyl-tRNA synthetase, cytoplasmic OS=Homo sapiens
GN=CARS PE=1 SV=3



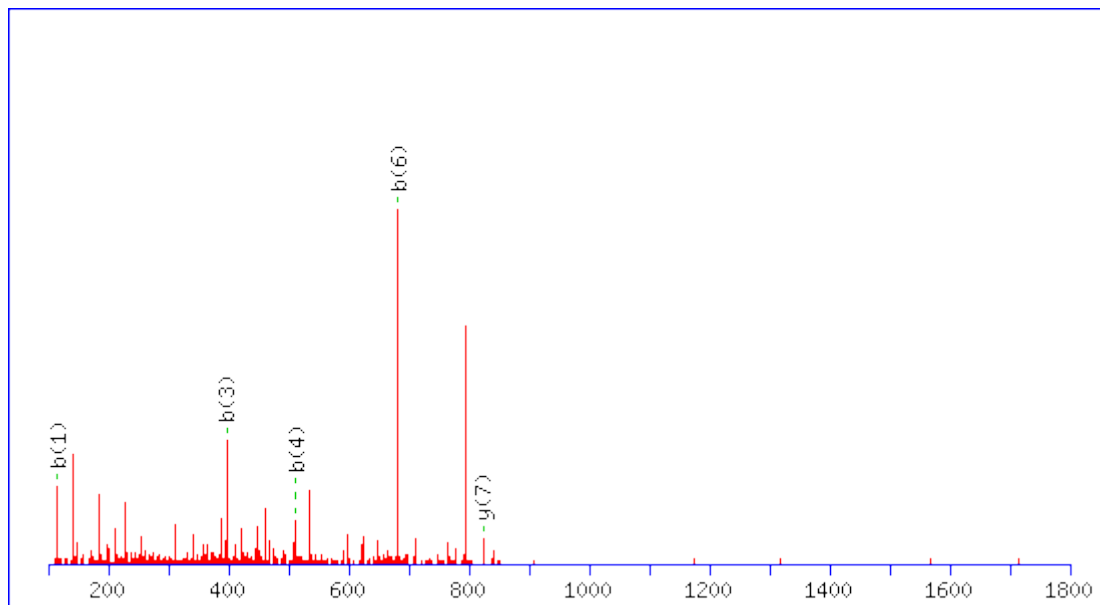
Monoisotopic mass of neutral peptide Mr(calc): 1352.7663

Ions Score: 45 Expect: 0.0096

Matches (Bold Red): 19/112 fragment ions using 47 most intense peaks

MS/MS Fragmentation of **NFKNVATK**

Found in **SYNE1_HUMAN**, Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 936.5364

Variable modifications:

K3 : Label:13C(6)15N(2) (K)

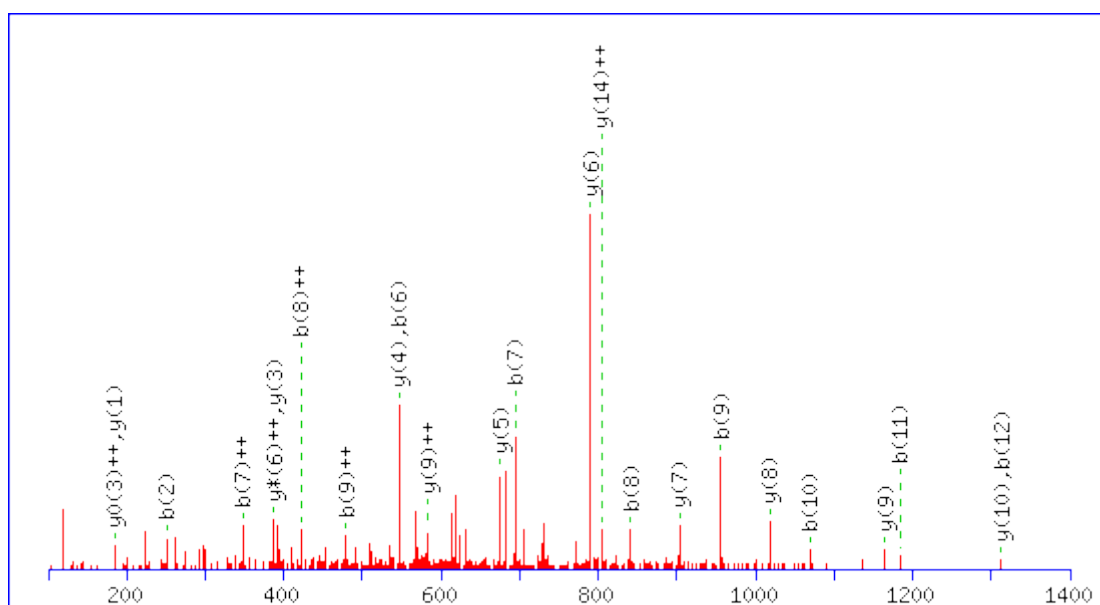
K8 : Label:13C(6)15N(2) (K)

Ions Score: 11 **Expect:** 14

Matches (Bold Red): 5/70 fragment ions using 18 most intense peaks

MS/MS Fragmentation of **HIPGAFFDIDQCSDR**

Found in **THTM_HUMAN**, 3-mercaptopyruvate sulfurtransferase OS=Homo sapiens
GN=MPST PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1857.8344

Variable modifications:

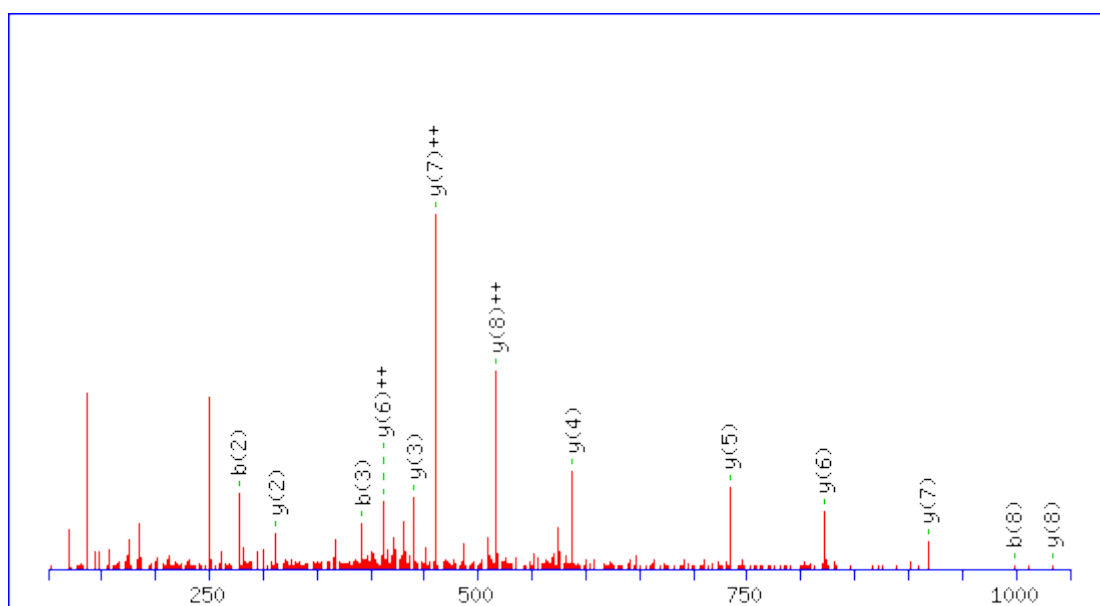
R16 : Label:13C(6)15N(4) (R)

Ions Score: 58 **Expect: 0.00035**

Matches (Bold Red): 24/140 fragment ions using 37 most intense peaks

MS/MS Fragmentation of **YLDPSFFQHR**

Found in **TM9S3_HUMAN**, Transmembrane 9 superfamily member 3 OS=Homo sapiens
GN=TM9SF3 PE=1 SV=2



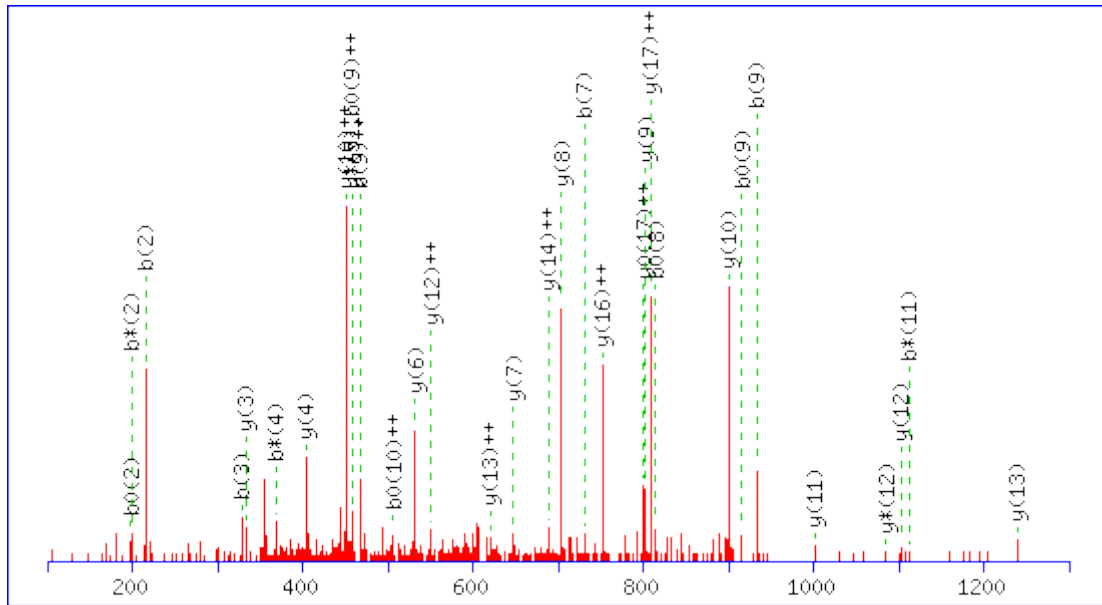
Monoisotopic mass of neutral peptide Mr(calc): 1308.6251

Ions Score: 48 Expect: 0.0037

Matches (**Bold Red**): 13/80 fragment ions using 24 most intense peaks

MS/MS Fragmentation of **SQLGAHHTPVGDGAAGTR**

Found in **TM41B_HUMAN**, Transmembrane protein 41B OS=Homo sapiens GN=TMEM41B PE=1 SV=1



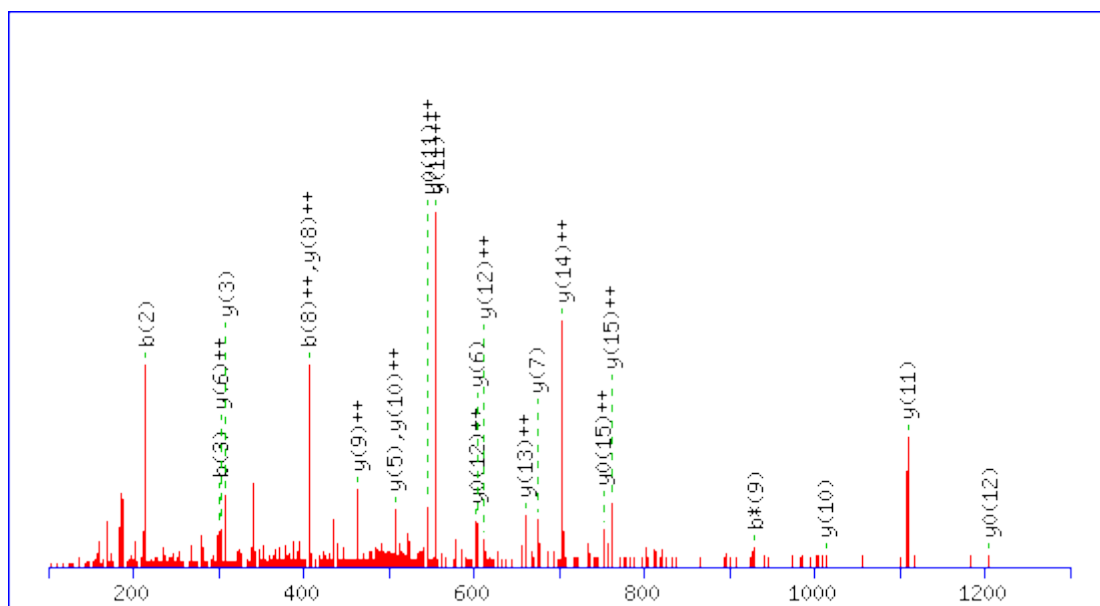
Monoisotopic mass of neutral peptide Mr(calc): 1831.8925

Ions Score: 45 Expect: 0.011

Matches (**Bold Red**): 32/212 fragment ions using 69 most intense peaks

MS/MS Fragmentation of **VDSPLPSDKAPTPPGK**

Found in **TM115_HUMAN**, Transmembrane protein 115 OS=Homo sapiens GN=TMEM115 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1620.8694

Variable modifications:

K9 : Label:13C(6)15N(2) (K)

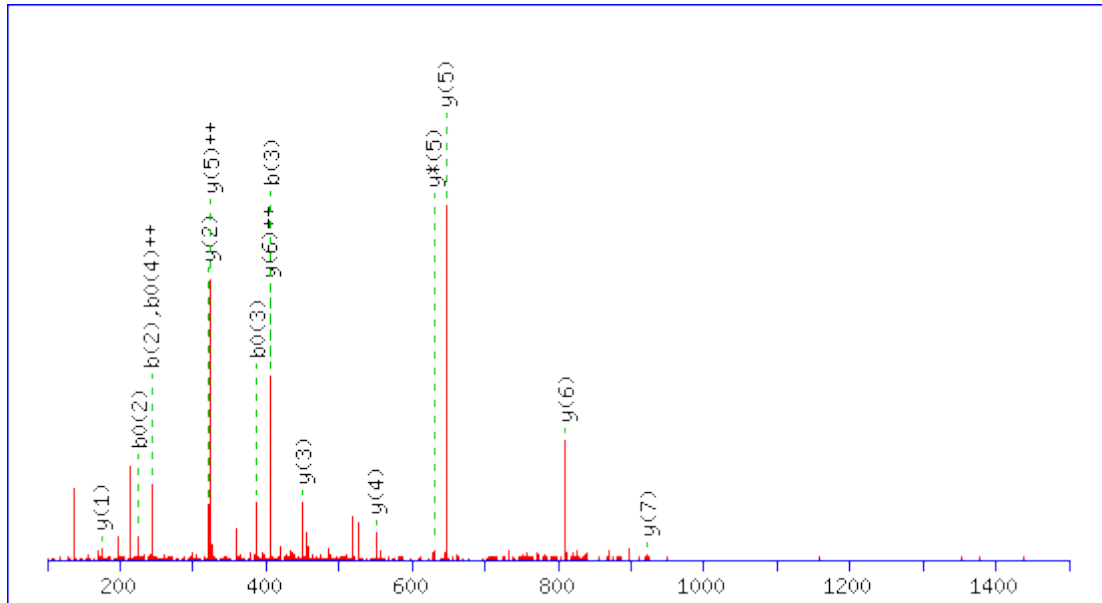
K16 : Label:13C(6)15N(2) (K)

Ions Score: 45 Expect: 0.01

Matches (Bold Red): 24/154 fragment ions using 47 most intense peaks

MS/MS Fragmentation of **ELYPVEFR**

Found in **TMM97_HUMAN**, Transmembrane protein 97 OS=Homo sapiens GN=TMEM97 PE=1 SV=1



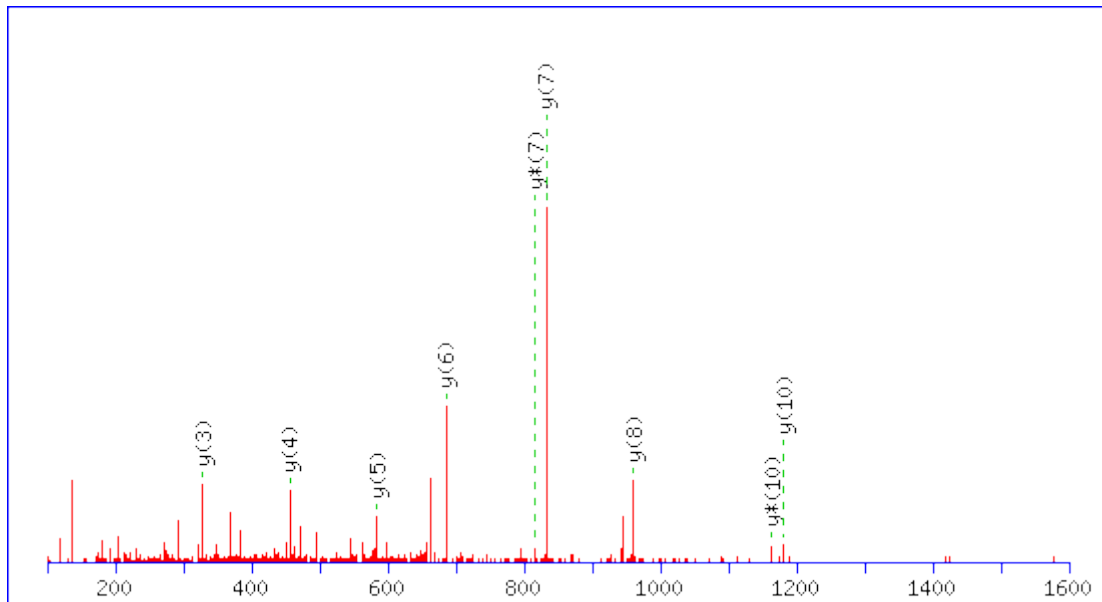
Monoisotopic mass of neutral peptide Mr(calc): 1051.5338

Ions Score: 48 Expect: 0.0034

Matches (Bold Red): 15/66 fragment ions using 32 most intense peaks

MS/MS Fragmentation of **FGYQFTKQGPR**

Found in **TMOD2_HUMAN**, Tropomodulin-2 OS=Homo sapiens GN=TMOD2 PE=1 SV=1



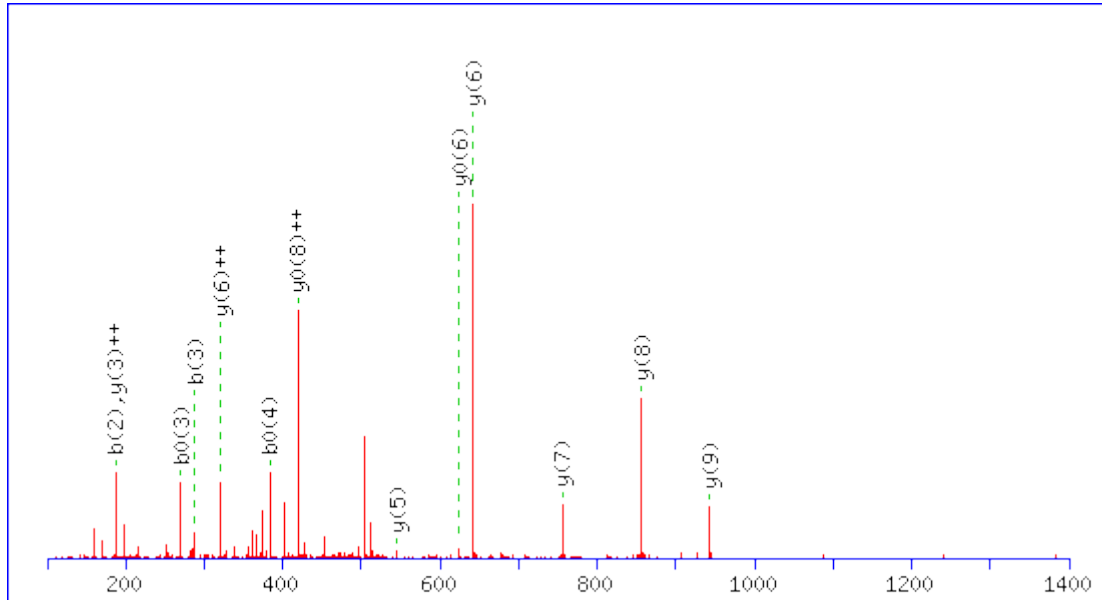
Monoisotopic mass of neutral peptide Mr(calc): 1327.6673

Ions Score: 54 Expect: 0.00096

Matches (Bold Red): 9/94 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **VSTLPATSTR**

Found in **TPPC9_HUMAN**, Trafficking protein particle complex subunit 9 OS=Homo sapiens GN=TRAPPC9 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1041.5694

Variable modifications:

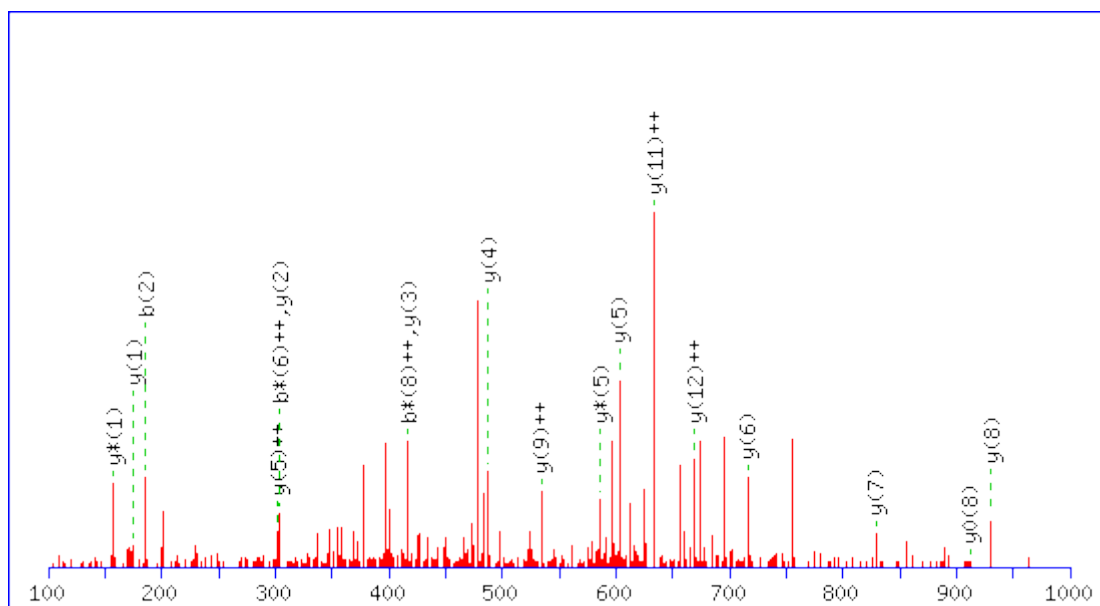
R10 : Label:13C(6)15N(4) (R)

Ions Score: 42 **Expect:** 0.014

Matches (Bold Red): 13/86 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **NASIHTLLDALER**

Found in **TR10A_HUMAN**, Tumor necrosis factor receptor superfamily member 10A OS=Homo sapiens GN=TNFRSF10A PE=1 SV=3



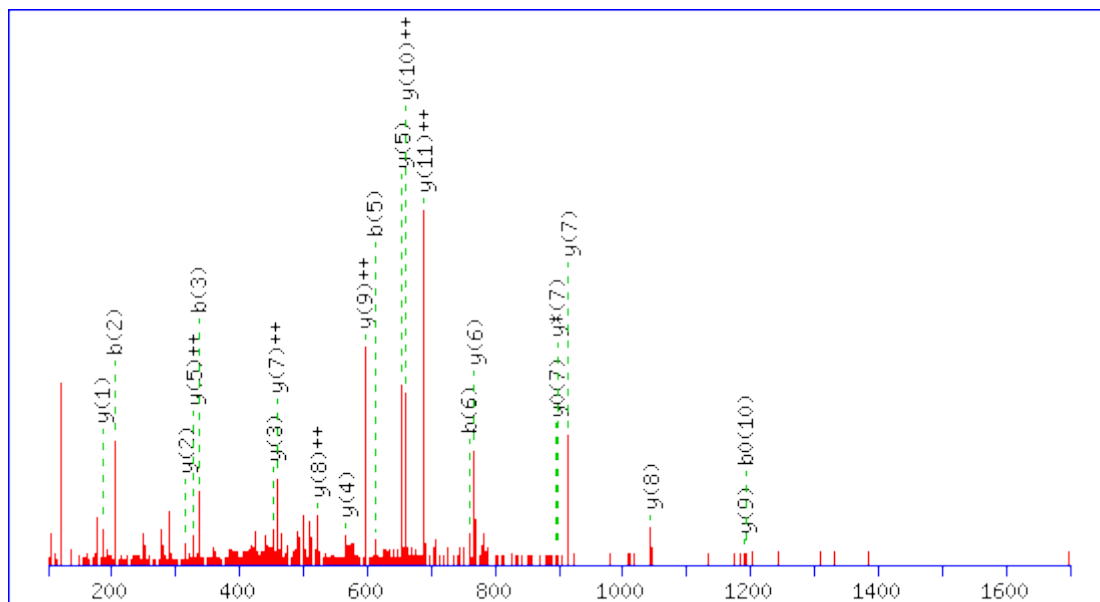
Monoisotopic mass of neutral peptide Mr(calc): 1451.7732

Ions Score: 42 Expect: 0.018

Matches (Bold Red): 18/138 fragment ions using 37 most intense peaks

MS/MS Fragmentation of **FGMFEFLSNHMR**

Found in **TXTP_HUMAN**, Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1524.6881

Variable modifications:

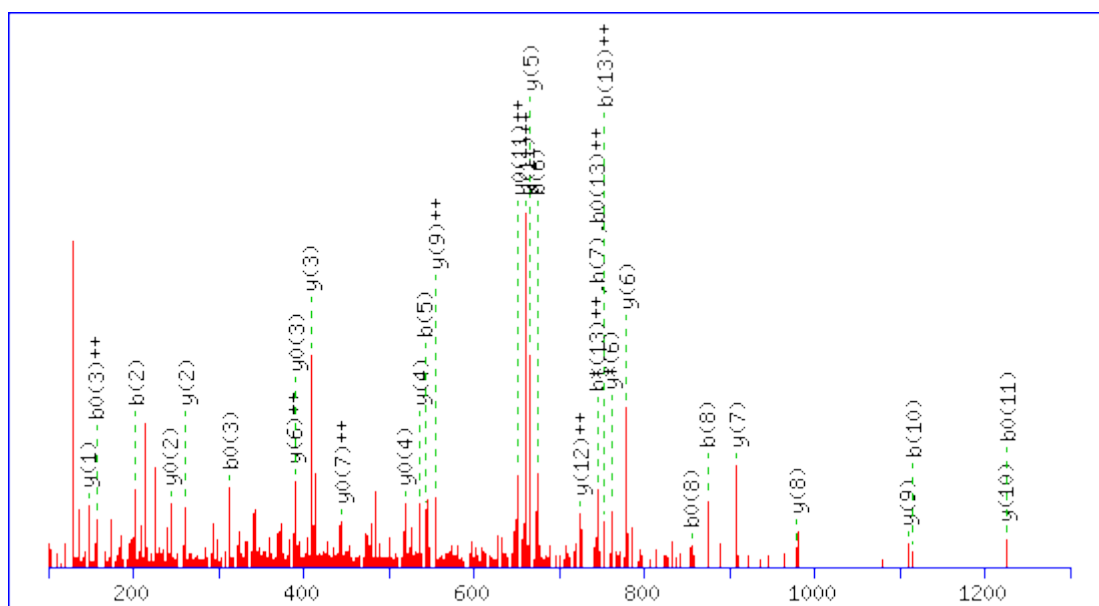
R12 : Label:13C(6)15N(4) (R)

Ions Score: 46 Expect: 0.005

Matches (**Bold Red**): 22/100 fragment ions using 53 most intense peaks

MS/MS Fragmentation of **SDKPDMAEIEKFDK**

Found in **TYB4_HUMAN**, Thymosin beta-4 OS=Homo sapiens GN=TMSB4X PE=1 SV=2



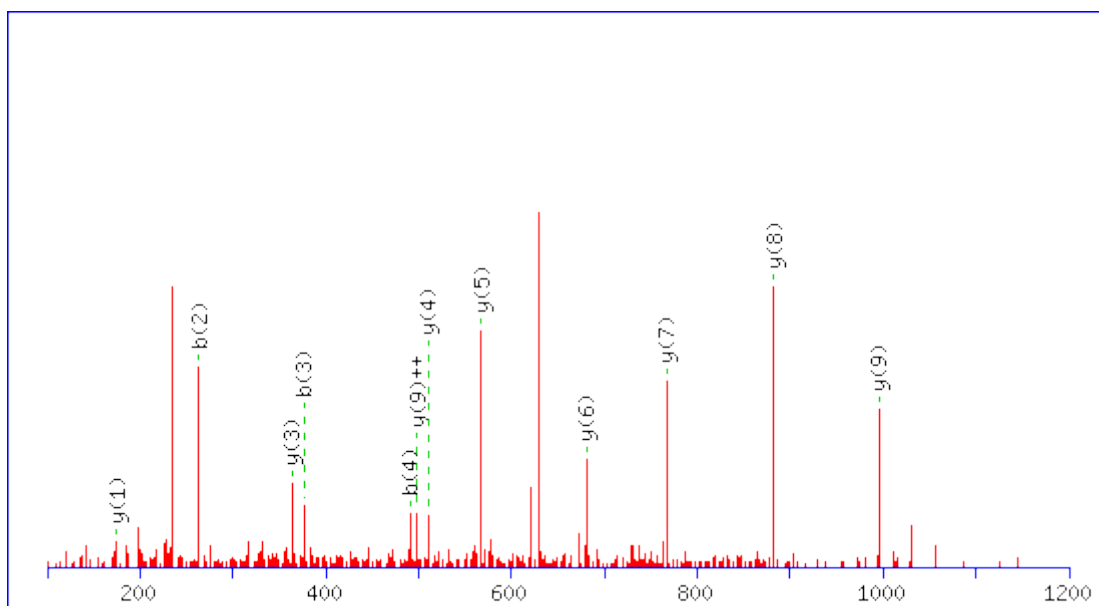
Monoisotopic mass of neutral peptide Mr(calc): 1651.7763

Ions Score: 66 Expect: 6.5e-005

Matches (**Bold Red**): 33/150 fragment ions using 53 most intense peaks

MS/MS Fragmentation of **DFLDSLGFSTR**

Found in **TYSY_HUMAN**, Thymidylate synthase OS=Homo sapiens GN=TYMS PE=1 SV=3



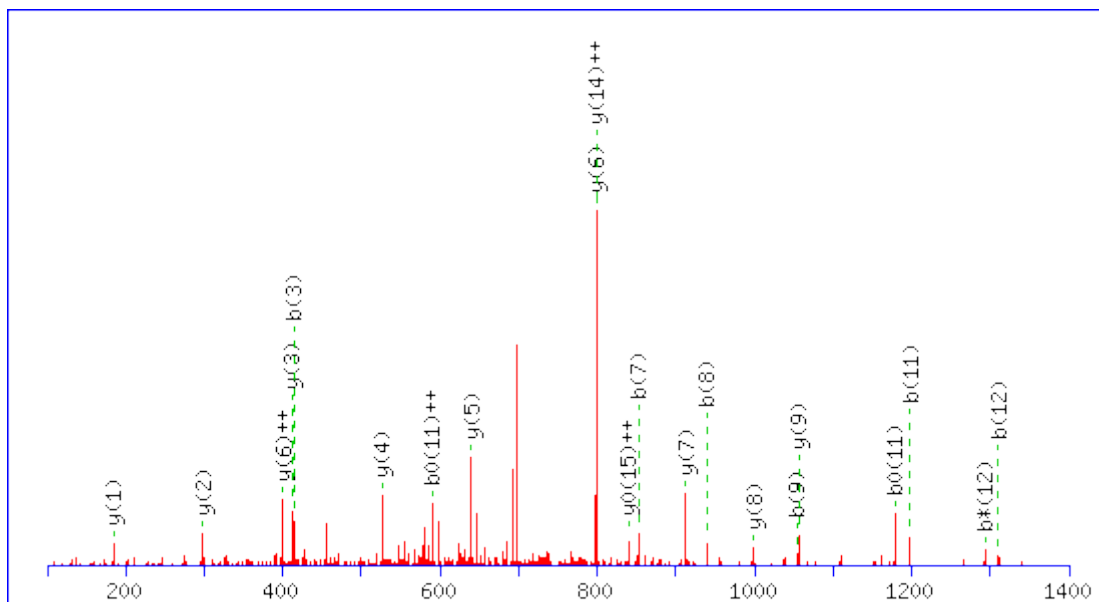
Monoisotopic mass of neutral peptide Mr(calc): 1256.6037

Ions Score: 52 Expect: 0.0013

Matches (**Bold Red**): 12/98 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **IYHPNINSNGSICLDILR**

Found in **UB2D1_HUMAN**, Ubiquitin-conjugating enzyme E2 D1 OS=Homo sapiens
GN=UBE2D1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 2108.0712

Variable modifications:

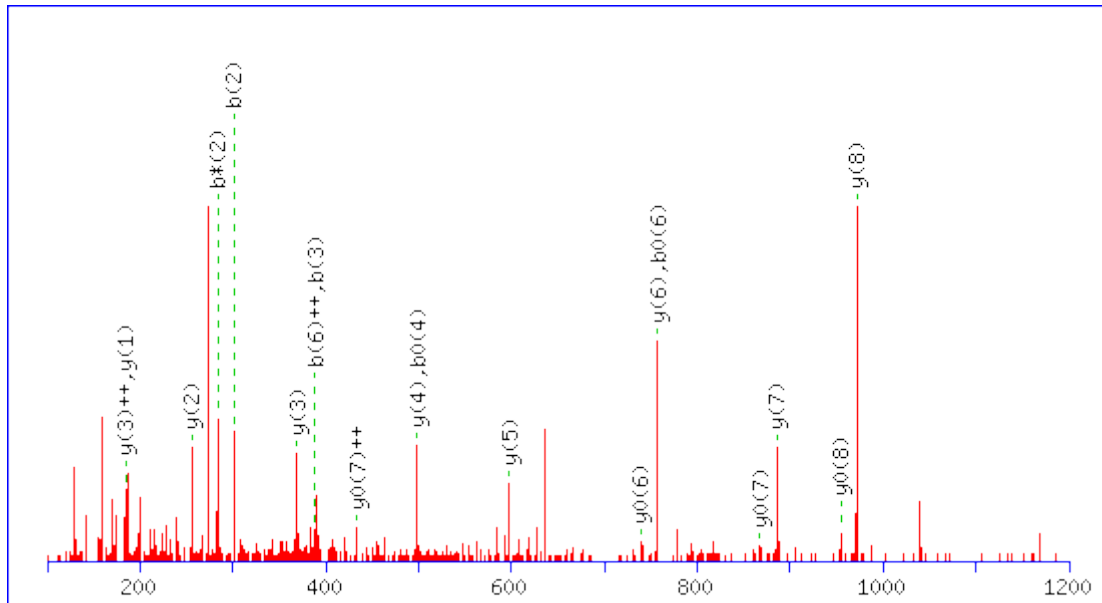
R18 : Label:13C(6)15N(4) (R)

Ions Score: 59 **Expect:** 0.00046

Matches (Bold Red): 21/176 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **NWSQCVELAR**

Found in **UBA6_HUMAN**, Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens
GN=UBA6 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1271.5956

Variable modifications:

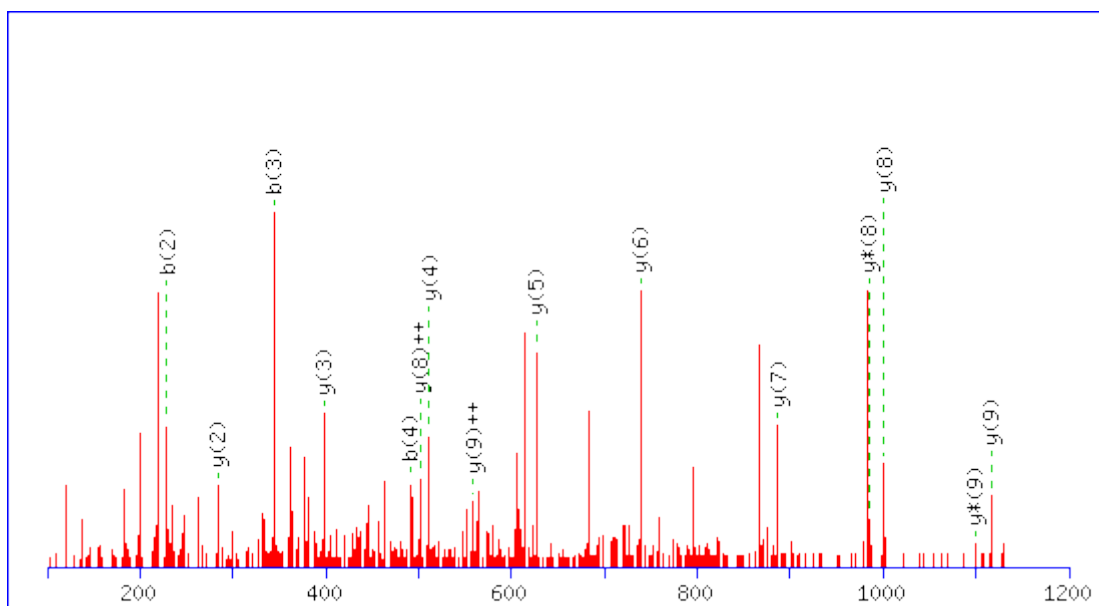
R10 : Label:13C(6)15N(4) (R)

Ions Score: 40 **Expect:** 0.023

Matches (Bold Red): 19/98 fragment ions using 45 most intense peaks

MS/MS Fragmentation of **LDDFLDLNHK**

Found in **UBCP1_HUMAN**, Ubiquitin-like domain-containing CTD phosphatase 1 OS=Homo sapiens
GN=UBLCP1 PE=1 SV=2



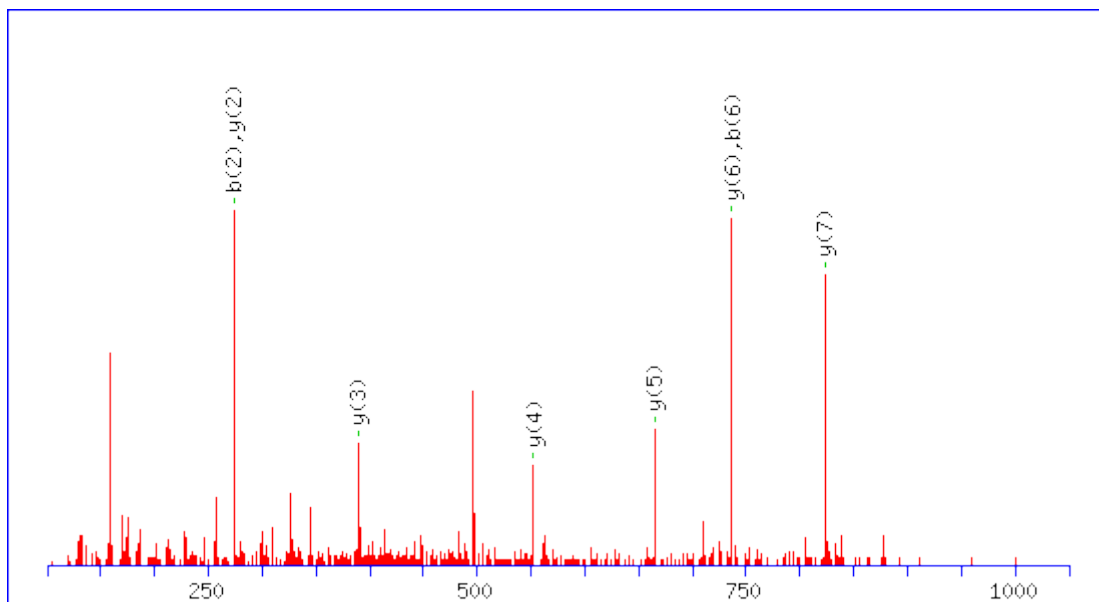
Monoisotopic mass of neutral peptide Mr(calc): 1228.6088

Ions Score: 43 Expect: 0.012

Matches (Bold Red): 15/84 fragment ions using 36 most intense peaks

MS/MS Fragmentation of **WSALYDVR**

Found in **UBE2C_HUMAN**, Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C
PE=1 SV=1



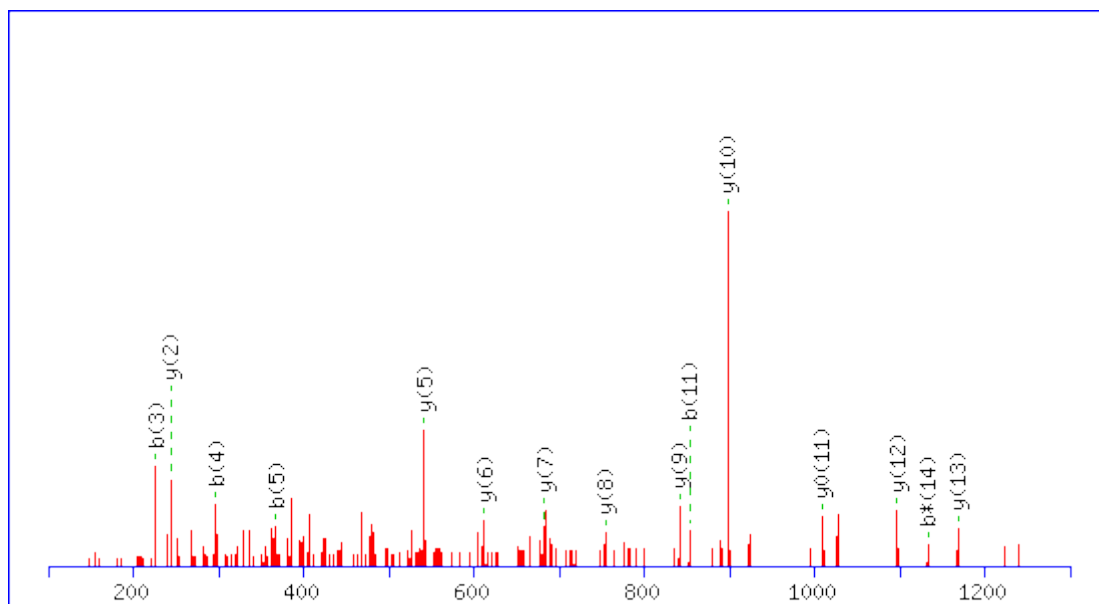
Monoisotopic mass of neutral peptide Mr(calc): 1008.5029

Ions Score: 53 Expect: 0.00092

Matches (**Bold Red**): 8/64 fragment ions using 18 most intense peaks

MS/MS Fragmentation of **GPAAAQGSAAAPAEPK**

Found in **UBQL2_HUMAN**, Ubiquilin-2 OS=Homo sapiens GN=UBQLN2 PE=1 SV=2



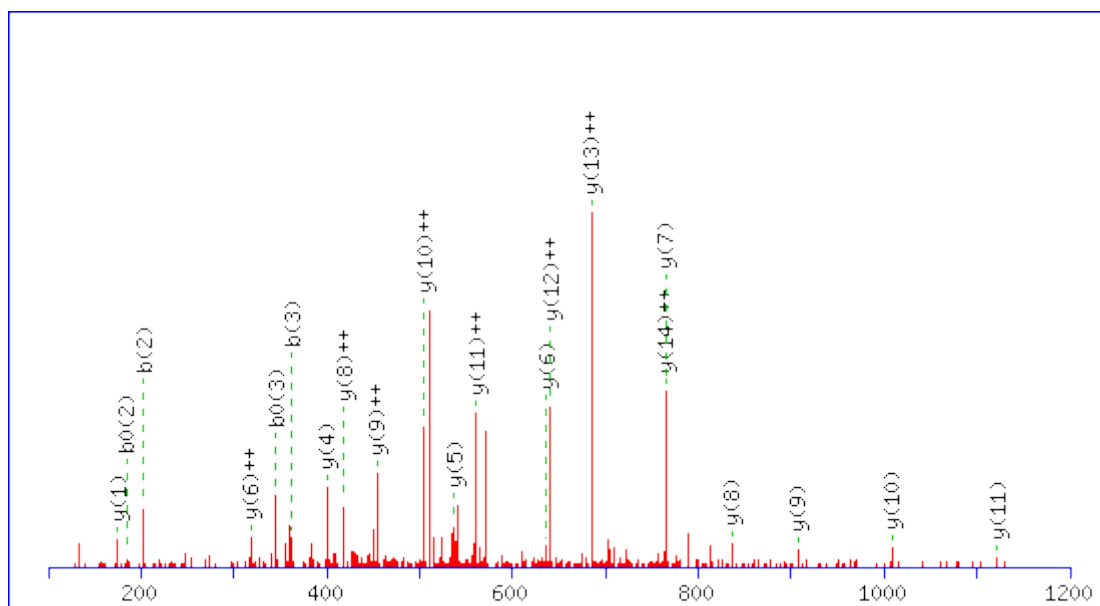
Monoisotopic mass of neutral peptide Mr(calc): 1392.6997

Ions Score: 63 Expect: 0.00013

Matches (**Bold Red**): 15/152 fragment ions using 25 most intense peaks

MS/MS Fragmentation of **DSCSCLTAAEVHPAGR**

Found in **UFO_HUMAN**, Tyrosine-protein kinase receptor UFO OS=Homo sapiens GN=AXL PE=1 SV=3



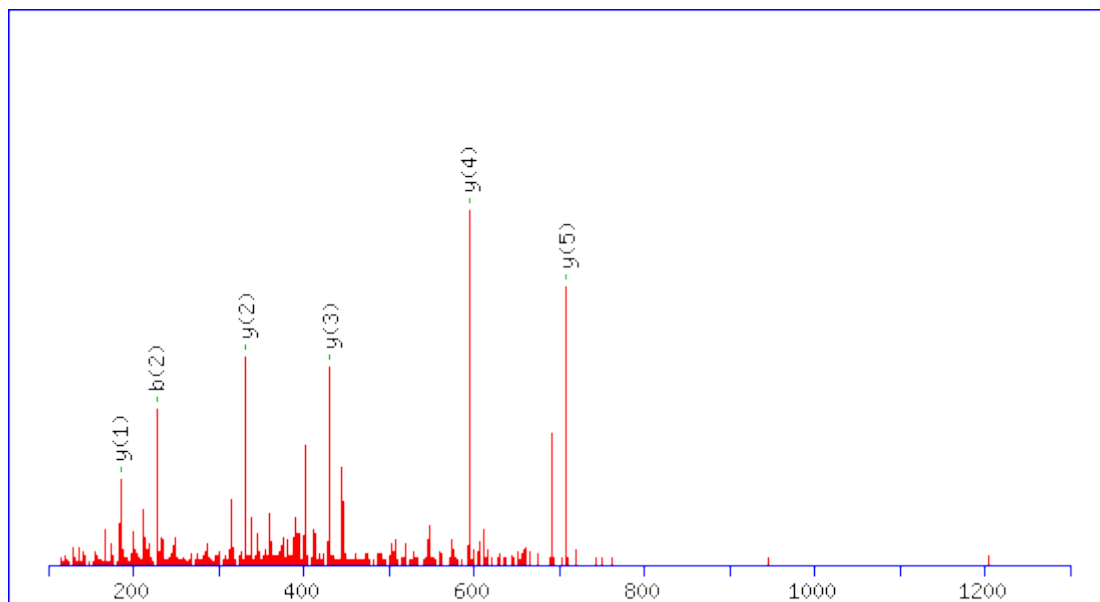
Monoisotopic mass of neutral peptide Mr(calc): 1729.7512

Ions Score: 48 Expect: 0.0037

Matches (**Bold Red**): 21/138 fragment ions using 52 most intense peaks

MS/MS Fragmentation of **INyVFR**

Found in **UGGG1_HUMAN**, UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 820.4471

Variable modifications:

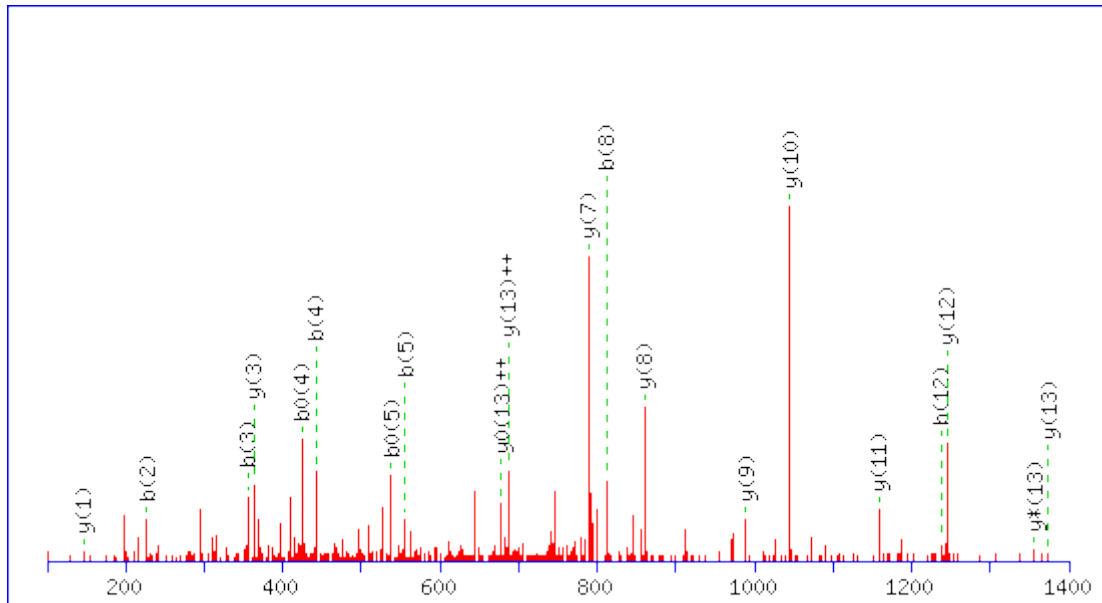
R6 : Label:13C(6)15N(4) (R)

Ions Score: 47 **Expect:** 0.0037

Matches (Bold Red): 6/38 fragment ions using 8 most intense peaks

MS/MS Fragmentation of **LLSIGQAPESISEK**

Found in **ULA1_HUMAN**, NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens GN=NAE1 PE=1 SV=1



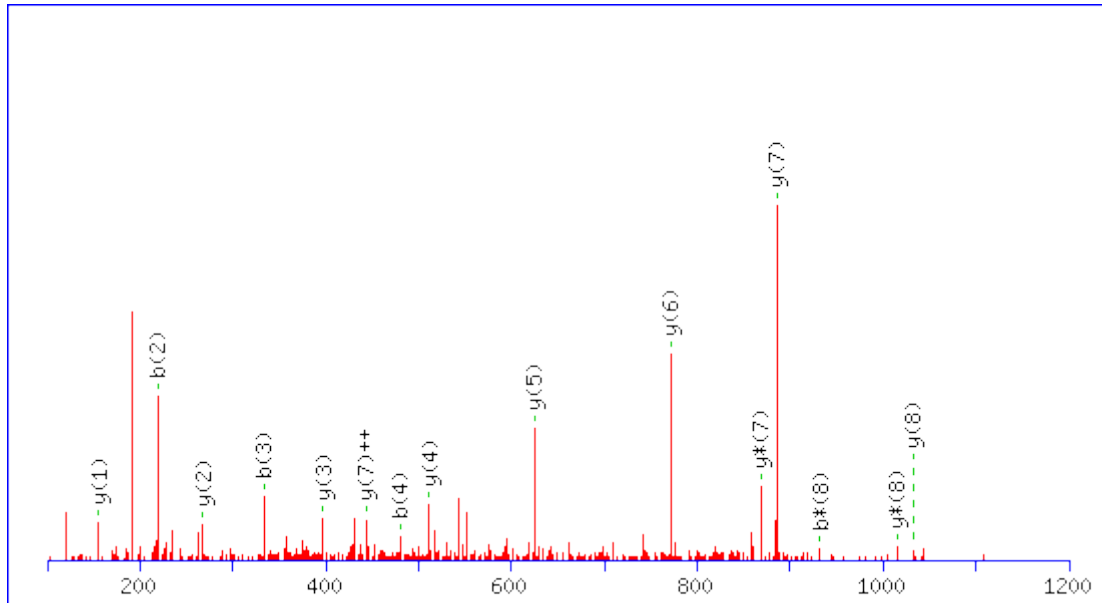
Monoisotopic mass of neutral peptide Mr(calc): 1598.8515

Ions Score: 52 **Expect:** 0.0023

Matches (Bold Red): 20/156 fragment ions using 39 most intense peaks

MS/MS Fragmentation of **AFNFLNEIK**

Found in **VAMP7_HUMAN**, Vesicle-associated membrane protein 7 OS=Homo sapiens GN=VAMP7 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1102.5902

Variable modifications:

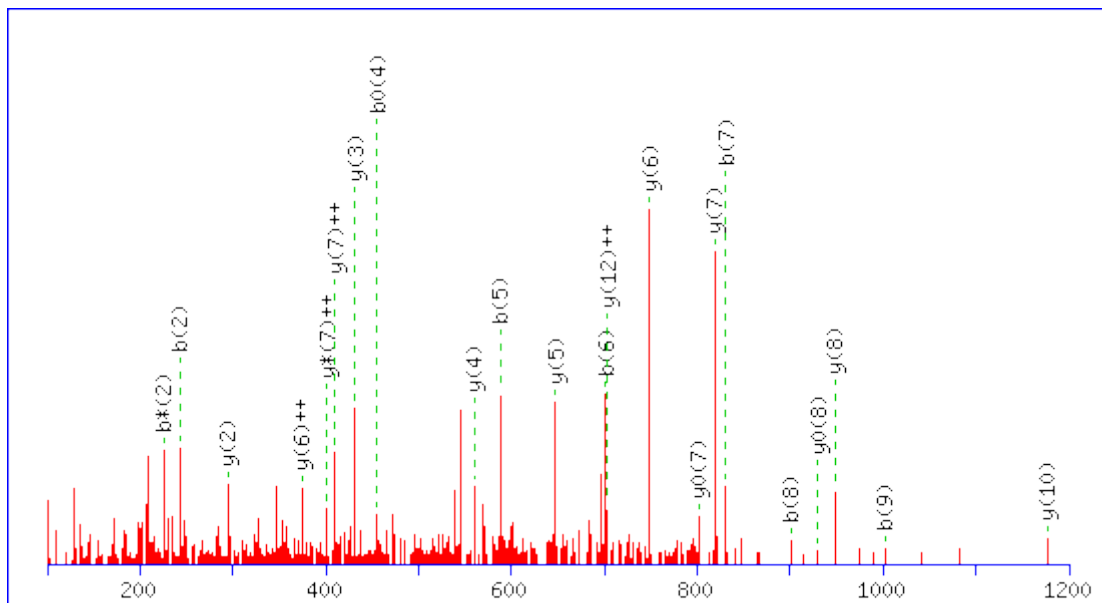
K9 : Label:13C(6)15N(2) (K)

Ions Score: 54 Expect: 0.00089

Matches (Bold Red): 15/76 fragment ions using 37 most intense peaks

MS/MS Fragmentation of **NKTEDLEATSEHFK**

Found in **VAMP8_HUMAN**, Vesicle-associated membrane protein 8 OS=Homo sapiens
GN=VAMP8 PE=1 SV=1



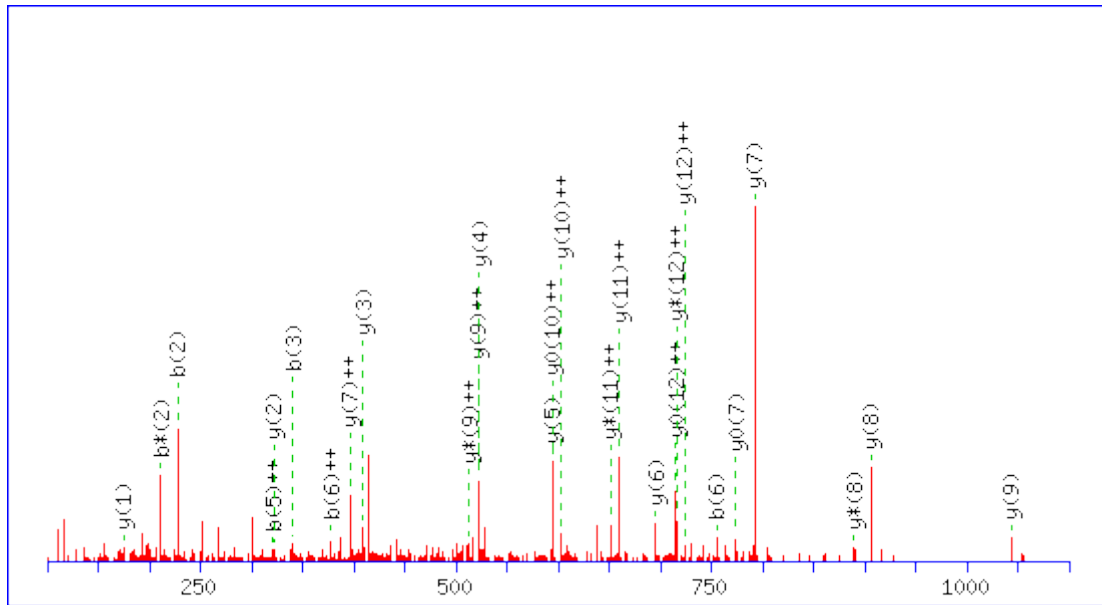
Monoisotopic mass of neutral peptide Mr(calc): 1647.7740

Ions Score: 45 Expect: 0.0075

Matches (Bold Red): 22/146 fragment ions using 38 most intense peaks

MS/MS Fragmentation of **VQIYHNPTANSFR**

Found in **VASP_HUMAN**, Vasodilator-stimulated phosphoprotein OS=Homo sapiens
GN=VASP PE=1 SV=3



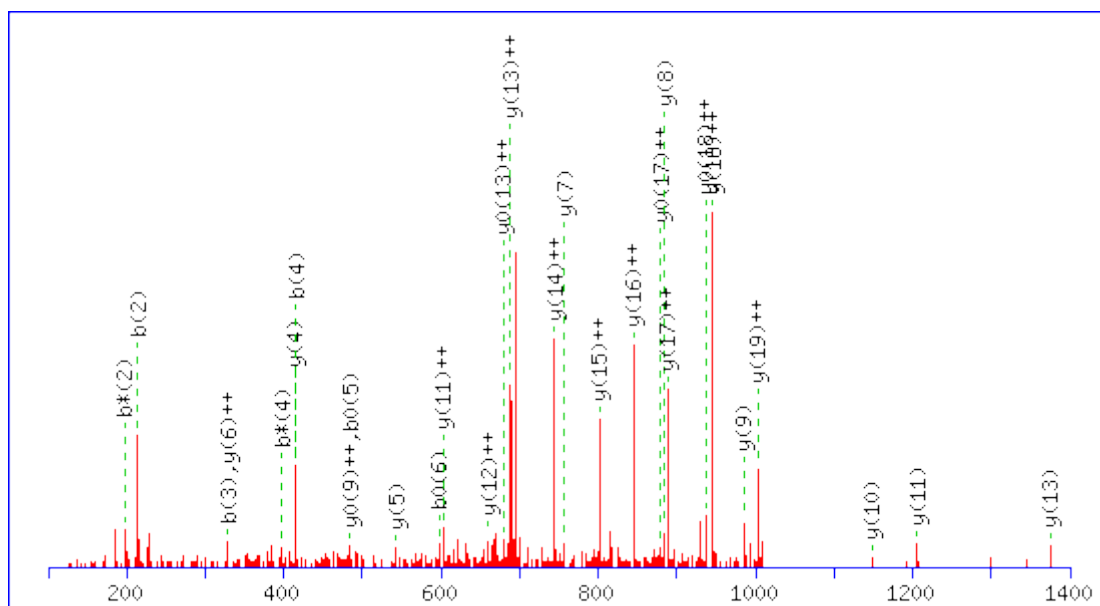
Monoisotopic mass of neutral peptide Mr(calc): 1545.7688

Ions Score: 40 Expect: 0.029

Matches (Bold Red): 27/124 fragment ions using 71 most intense peaks

MS/MS Fragmentation of **VNSSLIGLGYTLKPGIK**

Found in **VDAC1_HUMAN**, Voltage-dependent anion-selective channel protein 1
OS=Homo sapiens GN=VDAC1 PE=1 SV=2



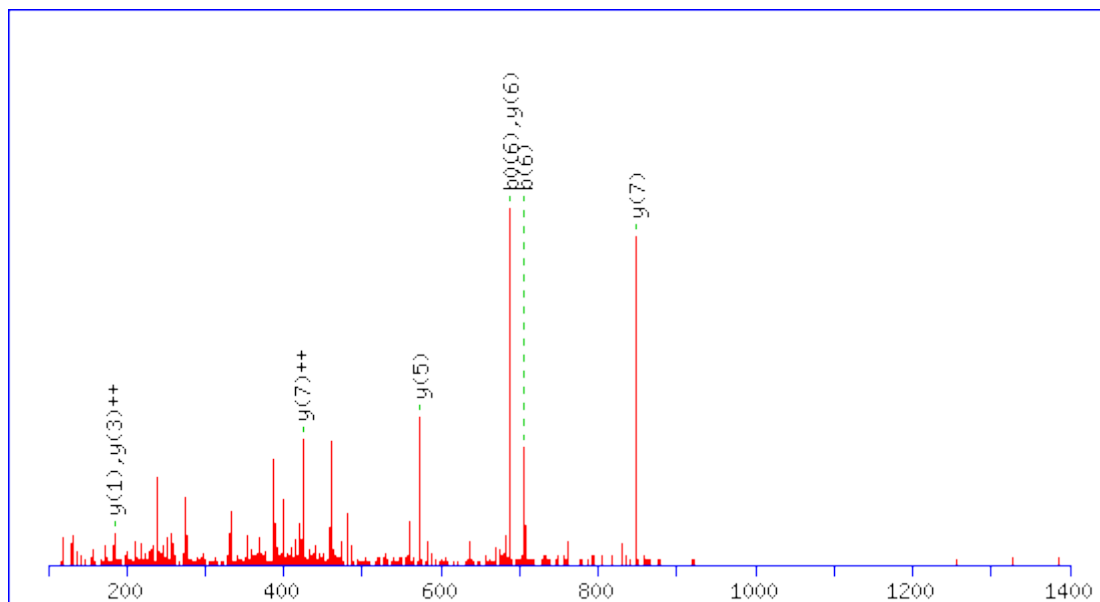
Monoisotopic mass of neutral peptide Mr(calc): 2102.1735

Ions Score: 55 Expect: 0.0011

Matches (Bold Red): 29/208 fragment ions using 62 most intense peaks

MS/MS Fragmentation of **ICDFGLAR**

Found in **VGFR1_HUMAN**, Vascular endothelial growth factor receptor 1 OS=Homo sapiens GN=FLT1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 960.4727

Variable modifications:

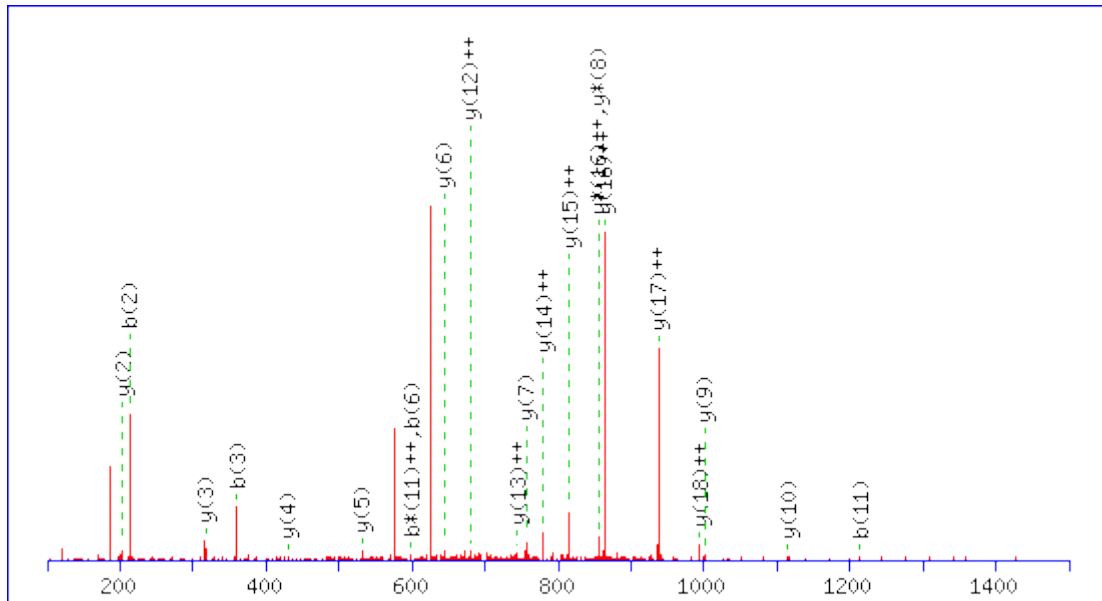
R8 : Label:13C(6)15N(4) (R)

Ions Score: 24 Expect: 0.86

Matches (**Bold Red**): 8/56 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **VIFPAAEDKDQLITIIGK**

Found in **VIGLN_HUMAN**, Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2



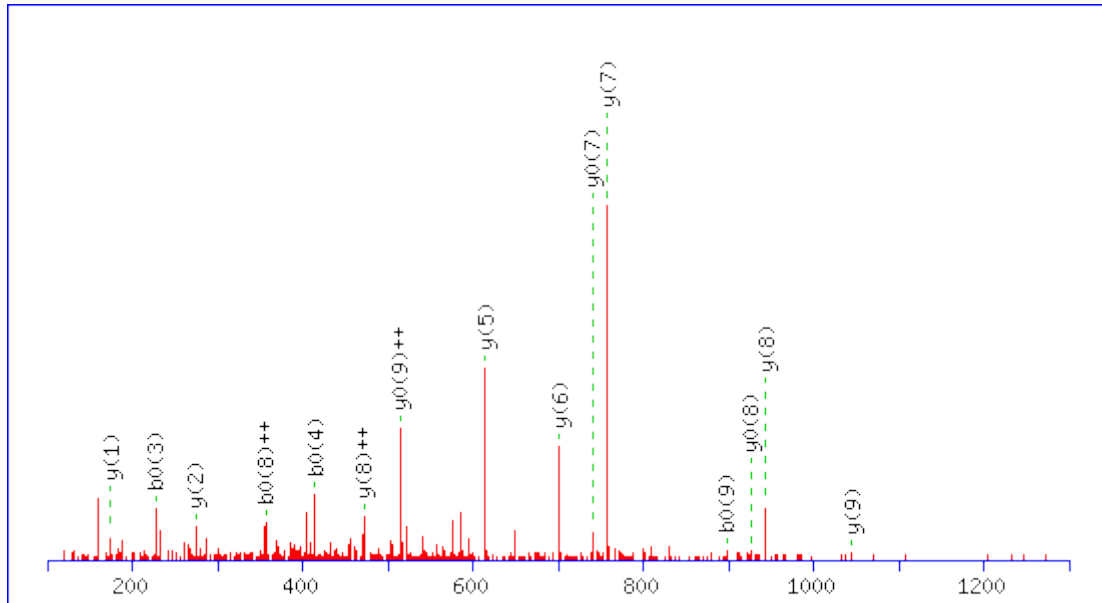
Monoisotopic mass of neutral peptide Mr(calc): 2085.1358

Ions Score: 52 Expect: 0.0026

Matches (**Bold Red**): 22/180 fragment ions using 51 most intense peaks

MS/MS Fragmentation of **GSTWGSPGWVR**

Found in **VKOR1_HUMAN**, Vitamin K epoxide reductase complex subunit 1 OS=Homo sapiens GN=VKORC1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1188.5676

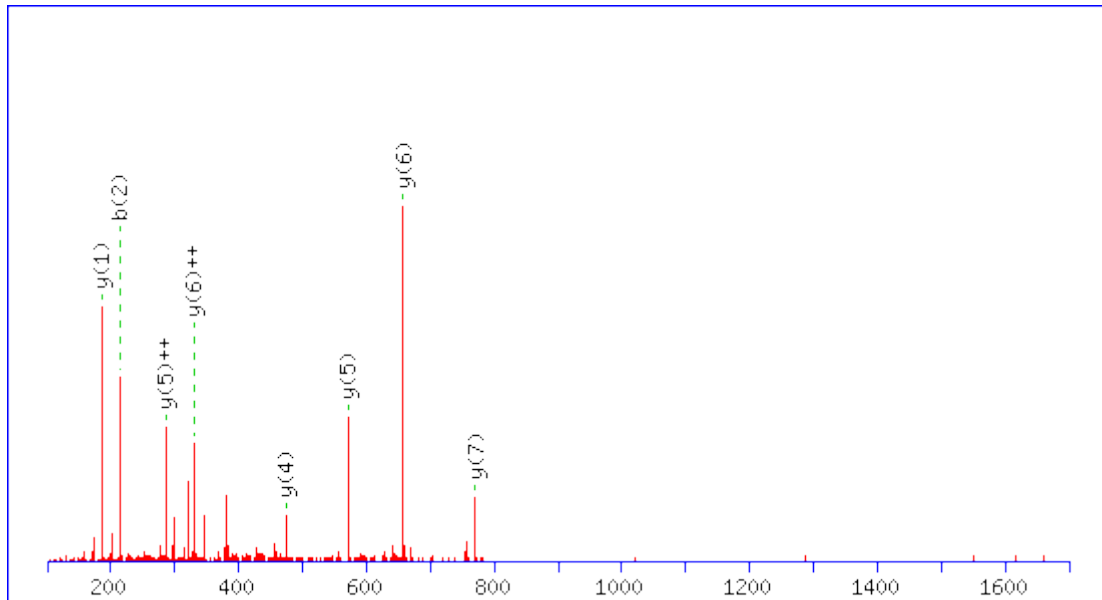
Ions Score: 48 Expect: 0.0035

Matches (Bold Red): 15/88 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **VLSPTTSR**

Found in **VWCE_HUMAN**, von Willebrand factor C and EGF domain-containing protein

OS=Homo sapiens GN=VWCE PE=2 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 869.4846

Variable modifications:

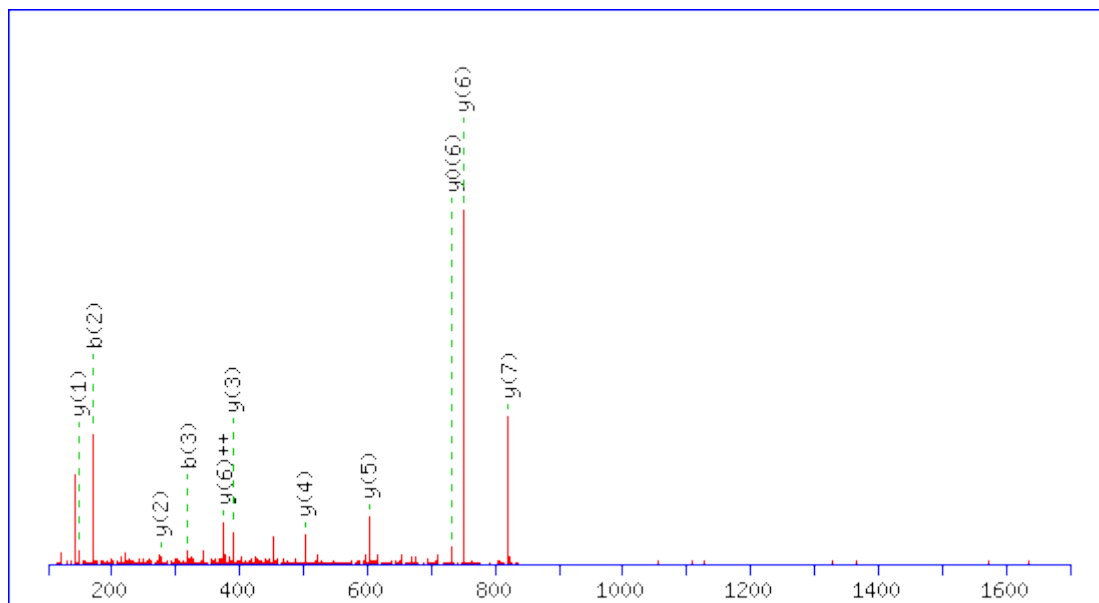
R8 : Label:13C(6)15N(4) (R)

Ions Score: 54 **Expect:** 0.00073

Matches (Bold Red): 8/64 fragment ions using 9 most intense peaks

MS/MS Fragmentation of **VAFTLLEK**

Found in **YKT6_HUMAN**, Synaptobrevin homolog YKT6 OS=Homo sapiens GN=YKT6 PE=1 SV=1



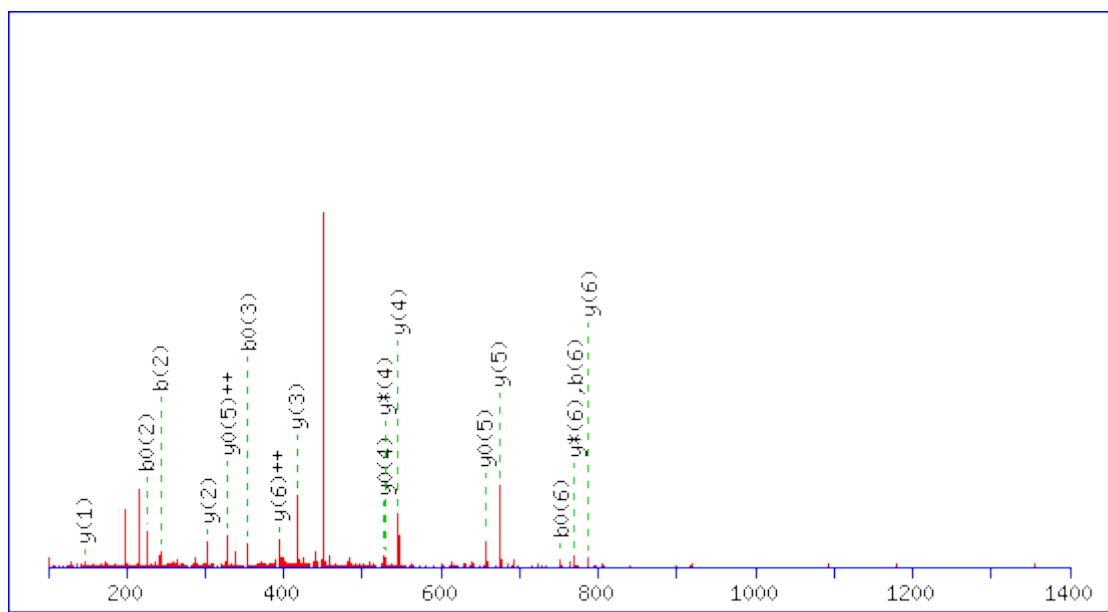
Monoisotopic mass of neutral peptide Mr(calc): 919.5379

Ions Score: 42 **Expect:** 0.012

Matches (Bold Red): 11/62 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **ELEELRK**

Found in **ZC3H6_HUMAN**, Zinc finger CCCH domain-containing protein 6 OS=Homo sapiens GN=ZC3H6 PE=2 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 915.5025

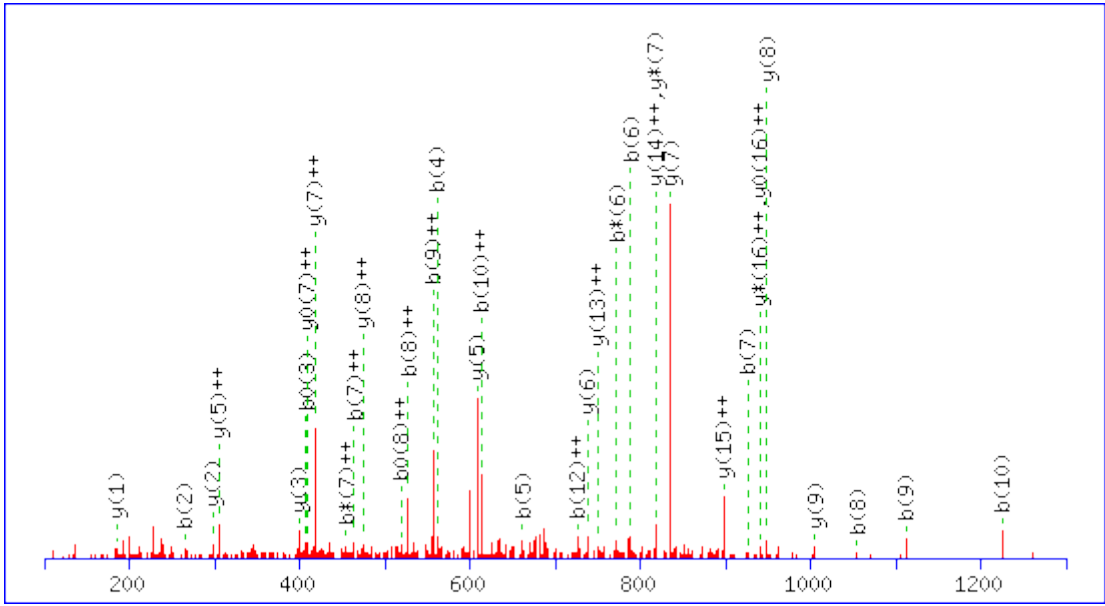
Ions Score: 38 Expect: 0.033

Matches (Bold Red): 17/56 fragment ions using 37 most intense peaks

Proteins identified in nuclear fraction

MS/MS Fragmentation of **YTCHVQHEGLPEPLTLR**

Found in **1C04_HUMAN**, HLA class I histocompatibility antigen, Cw-4 alpha chain
OS=Homo sapiens GN=HLA-C PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 2059.0185

Variable modifications:

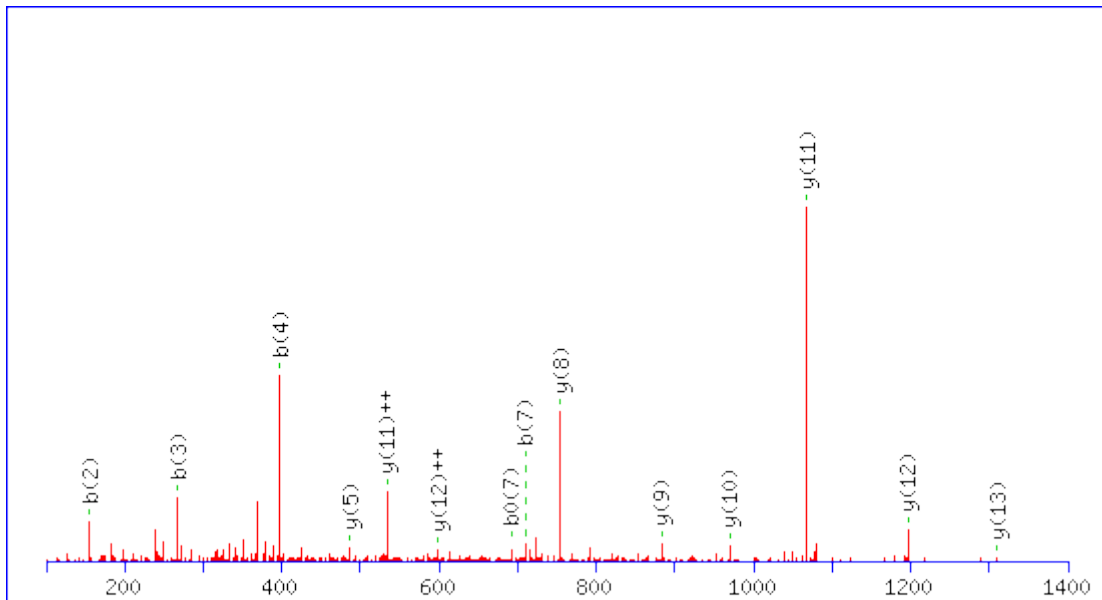
R17 : Label:13C(6)15N(4) (R)

Ions Score: 40 Expect: 0.034

Matches (Bold Red): 35/176 fragment ions using 81 most intense peaks

MS/MS Fragmentation of **GPLEPSEPAVVAAAR**

Found in **3MG_HUMAN**, DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG
PE=1 SV=3



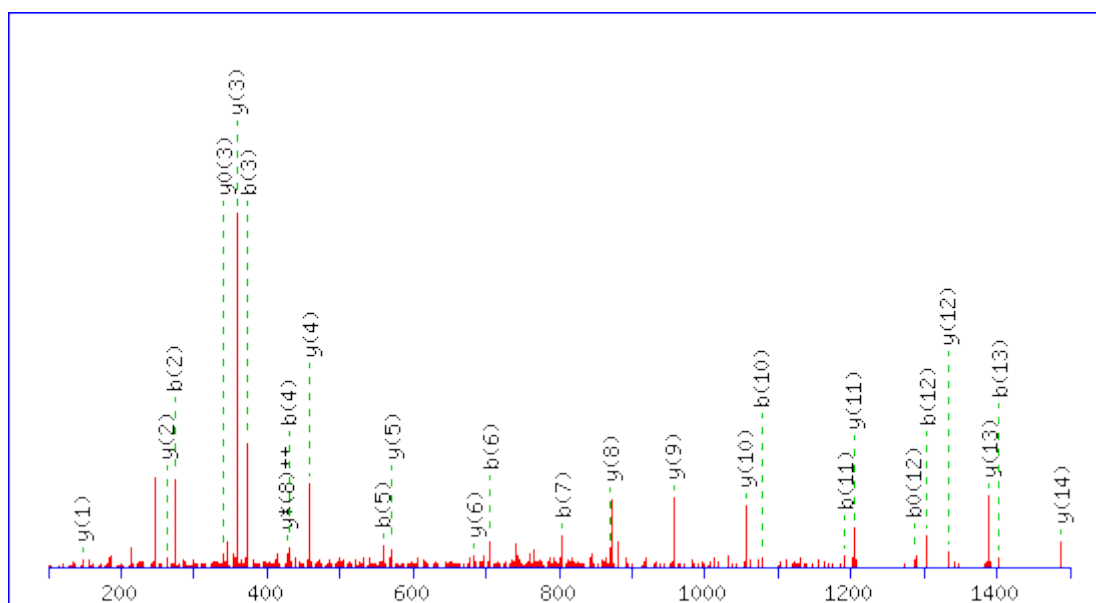
Monoisotopic mass of neutral peptide Mr(calc): 1462.7780

Ions Score: 60 Expect: 0.00027

Matches (Bold Red): 14/118 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **CLVGEFVSDALLVPDK**

Found in **A4_HUMAN**, Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=3



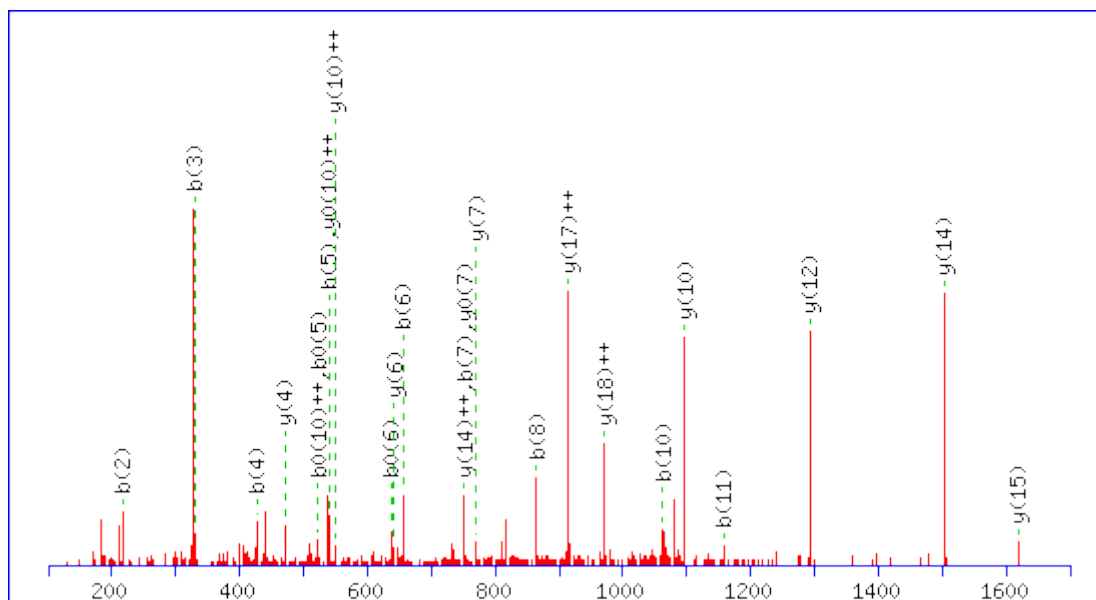
Monoisotopic mass of neutral peptide Mr(calc): 1760.9019

Ions Score: 85 Expect: 1.1e-006

Matches (Bold Red): 26/140 fragment ions using 55 most intense peaks

MS/MS Fragmentation of **SELPLDPLVPTEEGNPLLK**

Found in **AAAT_HUMAN**, Neutral amino acid transporter B(0) OS=Homo sapiens
GN=SLC1A5 PE=1 SV=2



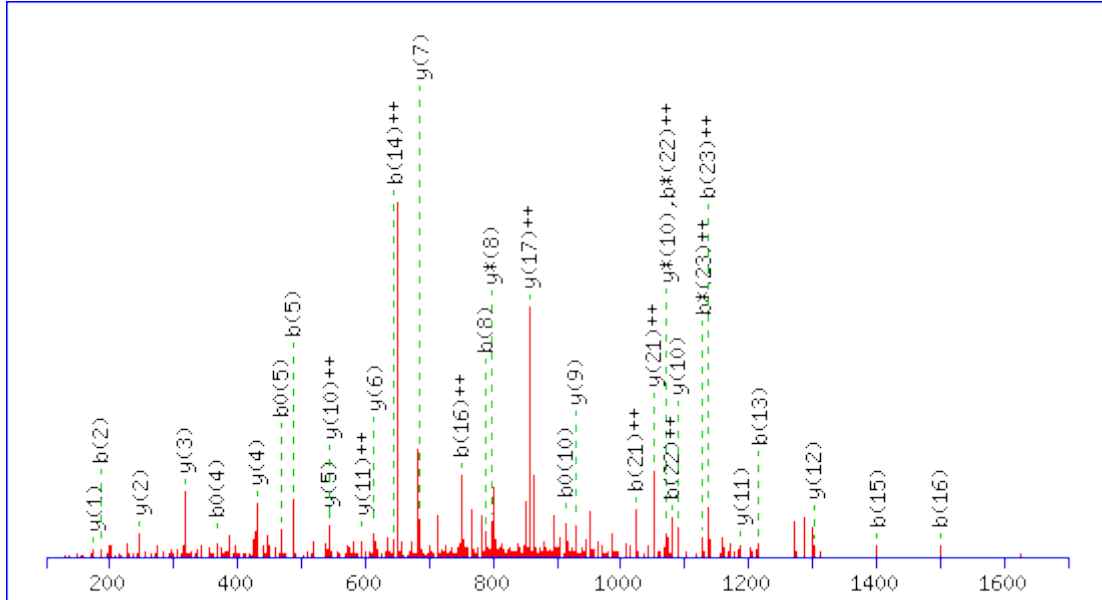
Monoisotopic mass of neutral peptide Mr(calc): 2157.1569

Ions Score: 49 Expect: 0.0044

Matches (**Bold Red**): 25/186 fragment ions using 46 most intense peaks

MS/MS Fragmentation of **LASLTPGFSGADVANCNEAALIAAR**

Found in **AFG32_HUMAN**, AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2



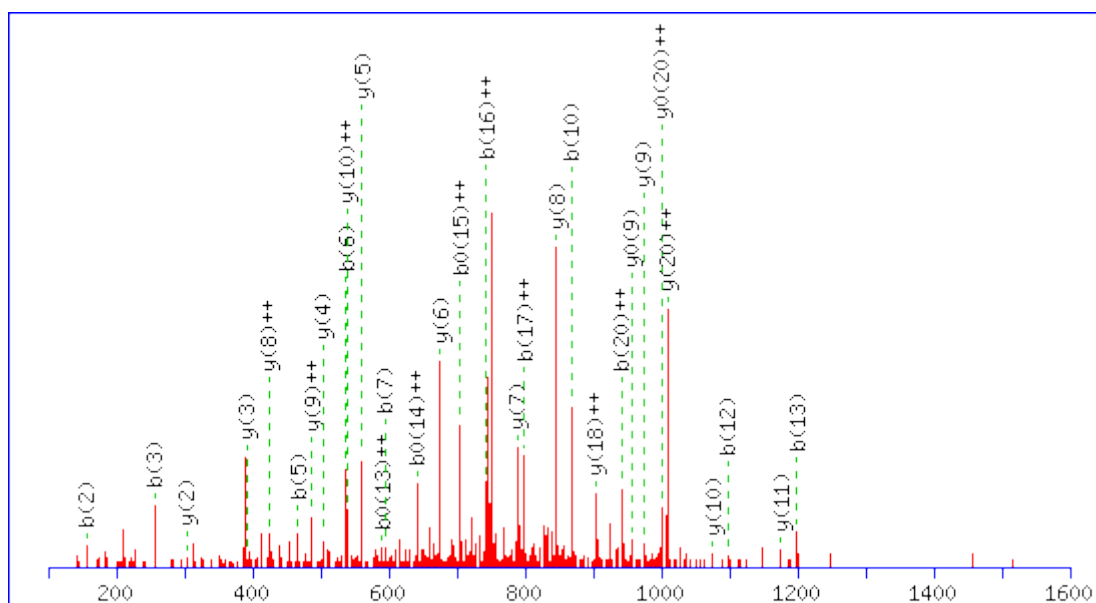
Monoisotopic mass of neutral peptide Mr(calc): 2587.3064

Ions Score: 41 Expect: 0.035

Matches (**Bold Red**): 33/254 fragment ions using 75 most intense peaks

MS/MS Fragmentation of **GVVPLAGTDGETTTQGLDGLSER**

Found in **ALDOC_HUMAN**, Fructose-bisphosphatealdolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 2272.1183

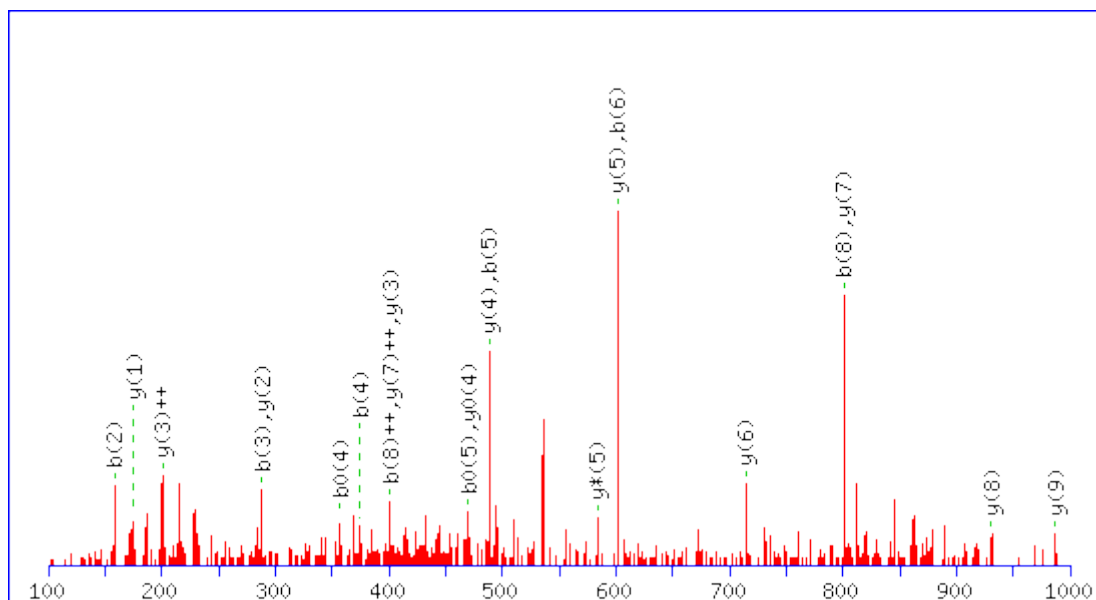
Ions Score: 54 Expect: 0.0018

Matches (Bold Red): 31/220 fragment ions using 72 most intense peaks

MS/MS Fragmentation of **TGESILSLLR**

Found in **ALG3_HUMAN**, Do1-P-Man:Man(5)GlcNAc(2)-PP-Do1

alpha-1,3-mannosyltransferase OS=Homo sapiens GN=ALG3 PE=1 SV=1



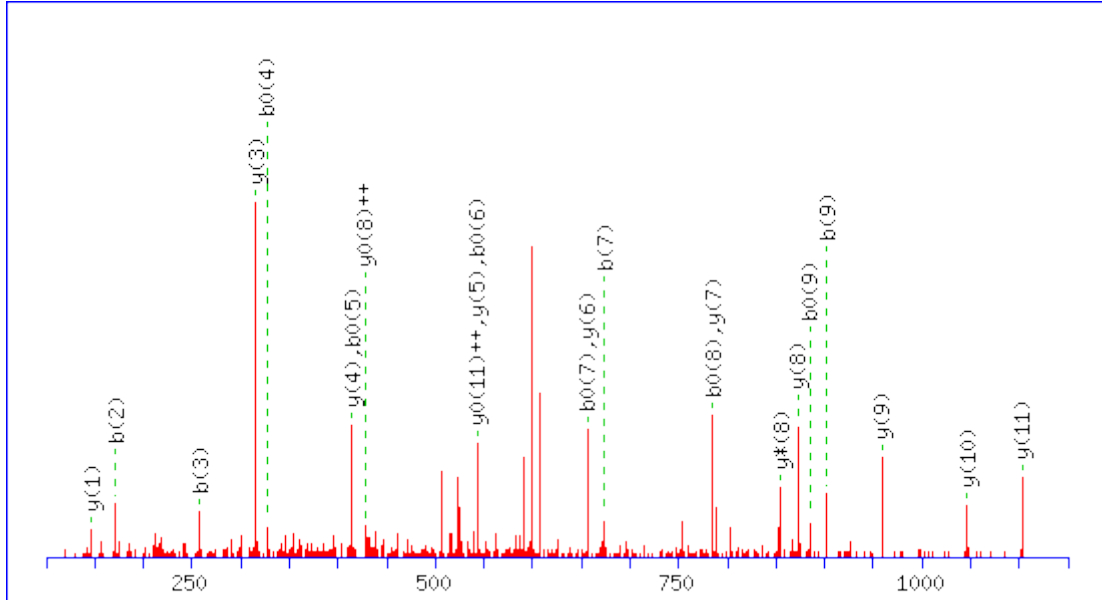
Monoisotopic mass of neutral peptide Mr(calc): 1087.6237

Ions Score: 53 Expect: 0.0011

Matches (**Bold Red**): 22/84 fragment ions using 45 most intense peaks

MS/MS Fragmentation of **LGSSEIEVPAK**

Found in **APOOL_HUMAN**, Apolipoprotein O-like OS=Homo sapiens GN=APOOL PE=1 SV=1



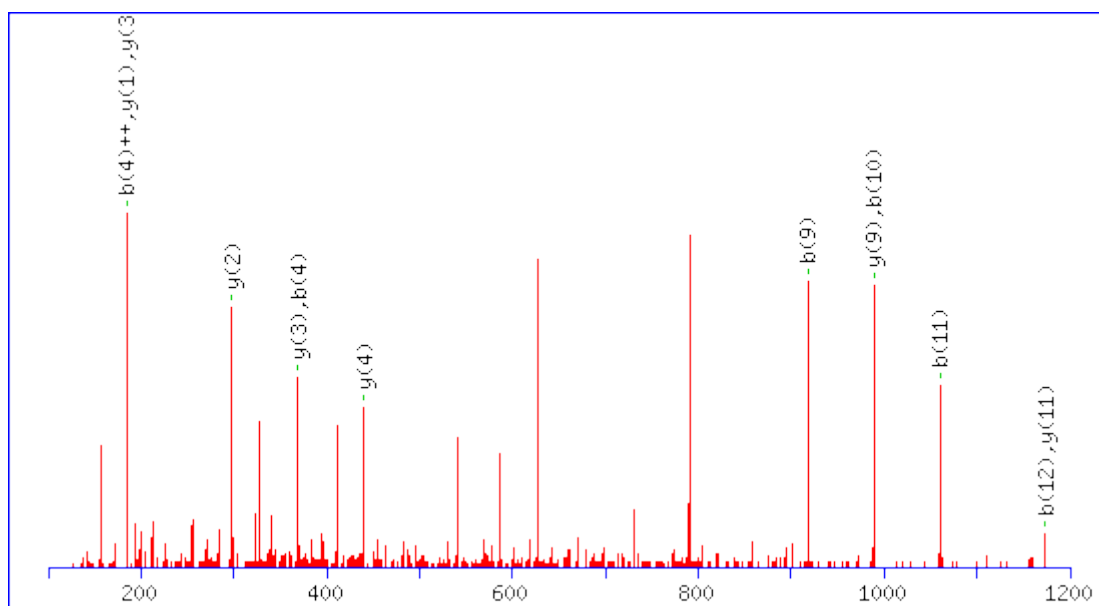
Monoisotopic mass of neutral peptide Mr(calc): 1215.6347

Ions Score: 84 Expect: 1e-006

Matches (**Bold Red**): 23/98 fragment ions using 25 most intense peaks

MS/MS Fragmentation of **ALALDLGSPAALR**

Found in **ARH40_HUMAN**, Rho guanine nucleotide exchange factor 40 OS=Homo sapiens
GN=ARHGEF40 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1356.7041

Variable modifications:

S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

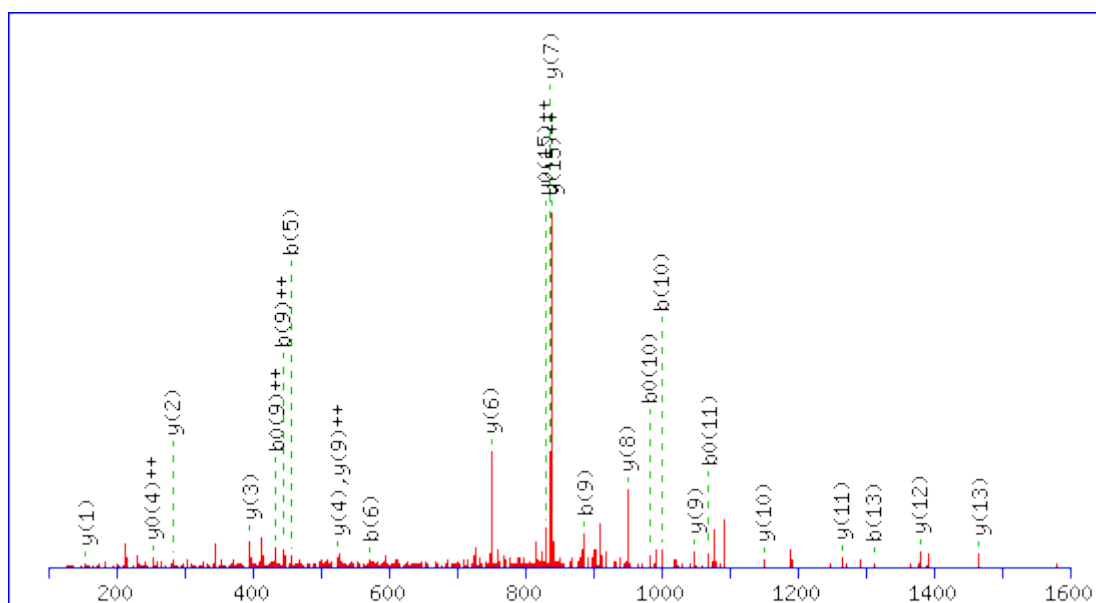
R13 : Label:13C(6)15N(4) (R)

Ions Score: 48 **Expect:** 0.0041

Matches (Bold Red): 14/164 fragment ions using 11 most intense peaks

MS/MS Fragmentation of **ASPNSDDTVLSPQELQK**

Found in **ARMX3_HUMAN**, Armadillo repeat-containing X-linked protein 3 OS=Homo sapiens GN=ARMCX3 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1835.8992

Variable modifications:

K17 : Label:13C(6)15N(2) (K)

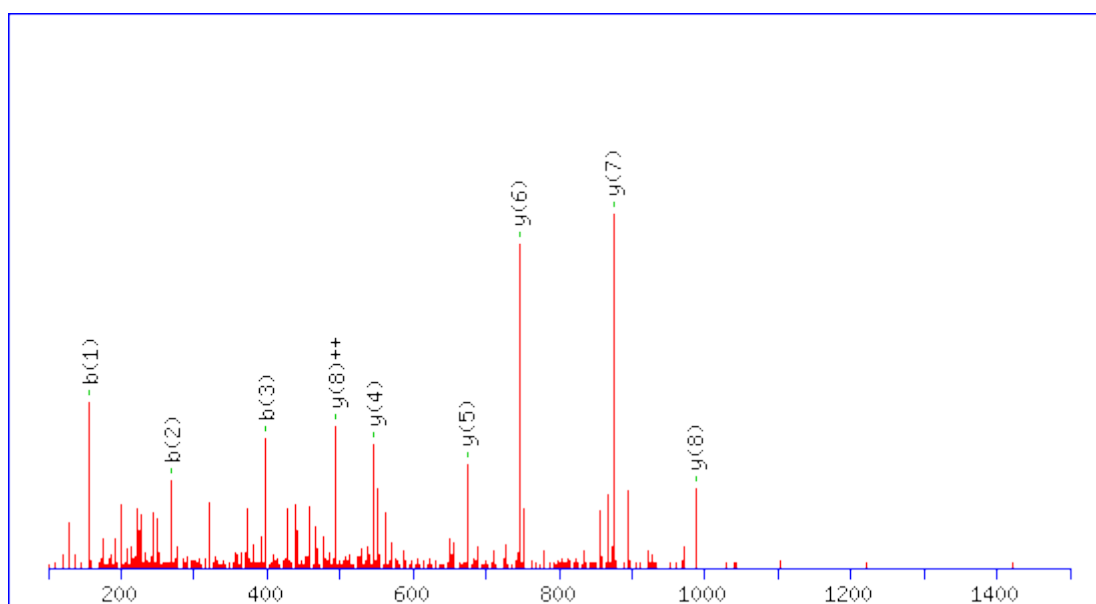
Ions Score: 54 Expect: 0.0014

Matches (Bold Red): 25/178 fragment ions using 70 most intense peaks

MS/MS Fragmentation of **RLEAQNQER**

Found in **ARP21_HUMAN**, cAMP-regulated phosphoprotein 21 OS=Homo sapiens

GN=ARPP21 PE=1 SV=2



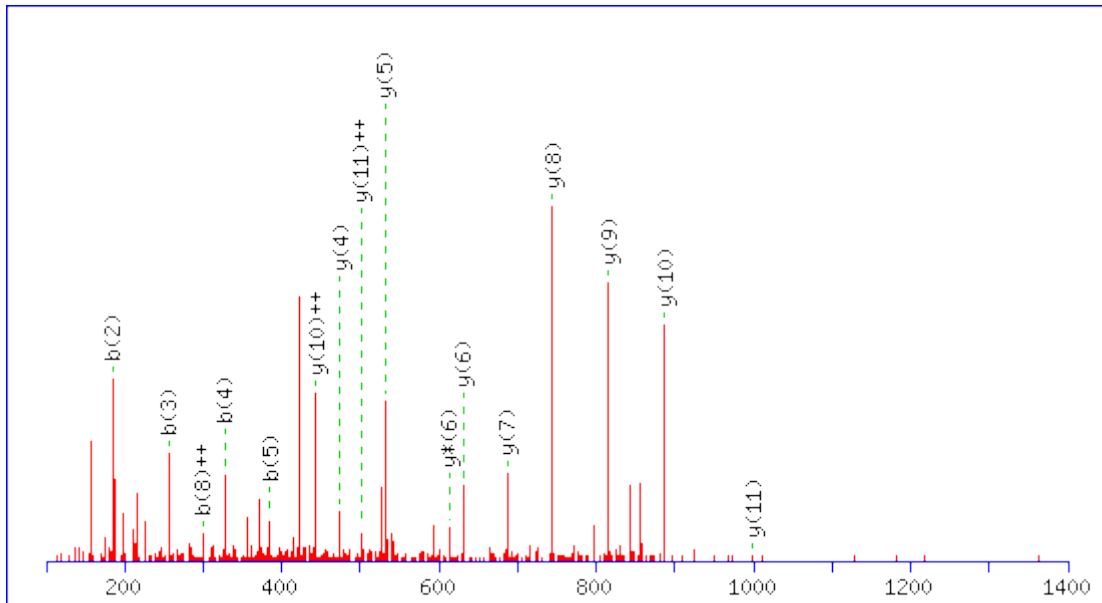
Monoisotopic mass of neutral peptide Mr(calc): 1142.5792

Ions Score: 37 Expect: 0.054

Matches (Bold Red): 9/90 fragment ions using 11 most intense peaks

MS/MS Fragmentation of **ALAAGGVGSIVR**

Found in **ARPC5_HUMAN**, Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3



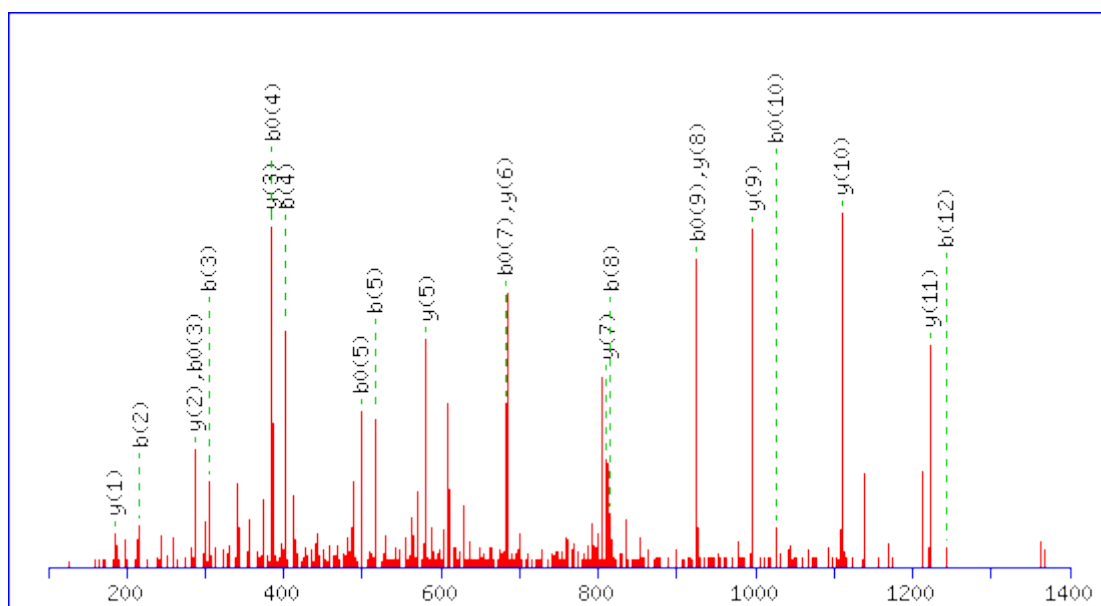
Monoisotopic mass of neutral peptide Mr(calc): 1069.6244

Ions Score: 44 Expect: 0.0082

Matches (Bold Red): 16/88 fragment ions using 41 most intense peaks

MS/MS Fragmentation of **TDSVIIADQTPTPTR**

Found in **ATF7_HUMAN**, Cyclic AMP-dependent transcription factor ATF-7 OS=Homo sapiens GN=ATF7 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1623.8344

Variable modifications:

R15 : Label:13C(6)15N(4) (R)

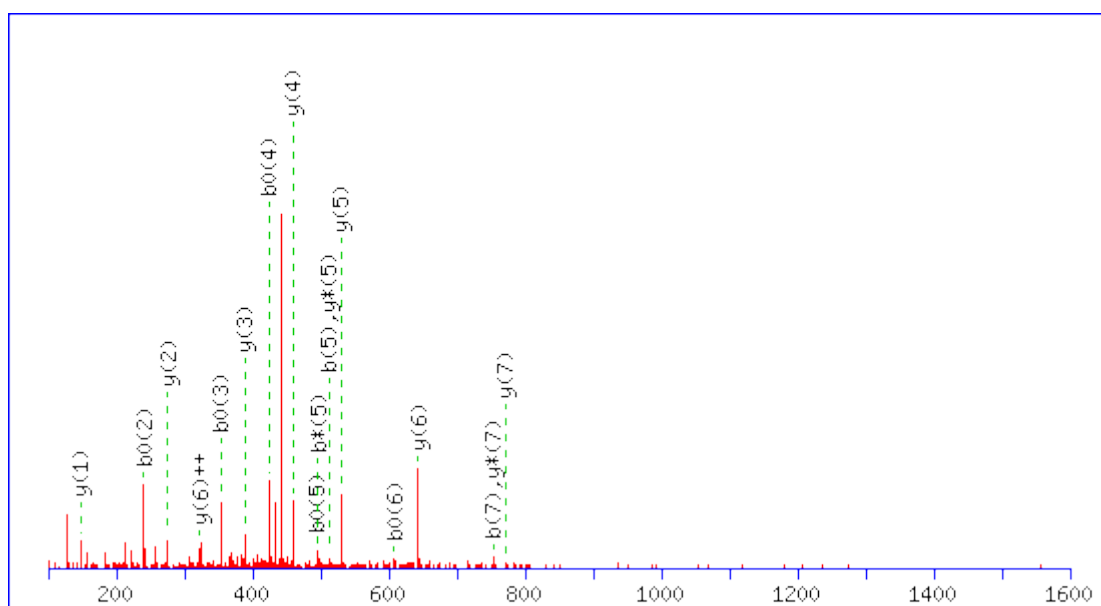
Ions Score: 70 Expect: 3.1e-005

Matches (Bold Red): 22/150 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **EQLAALKK**

Found in **ATIF1_HUMAN**, ATPase inhibitor, mitochondrial OS=Homo sapiens

GN=ATPIF1 PE=1 SV=1



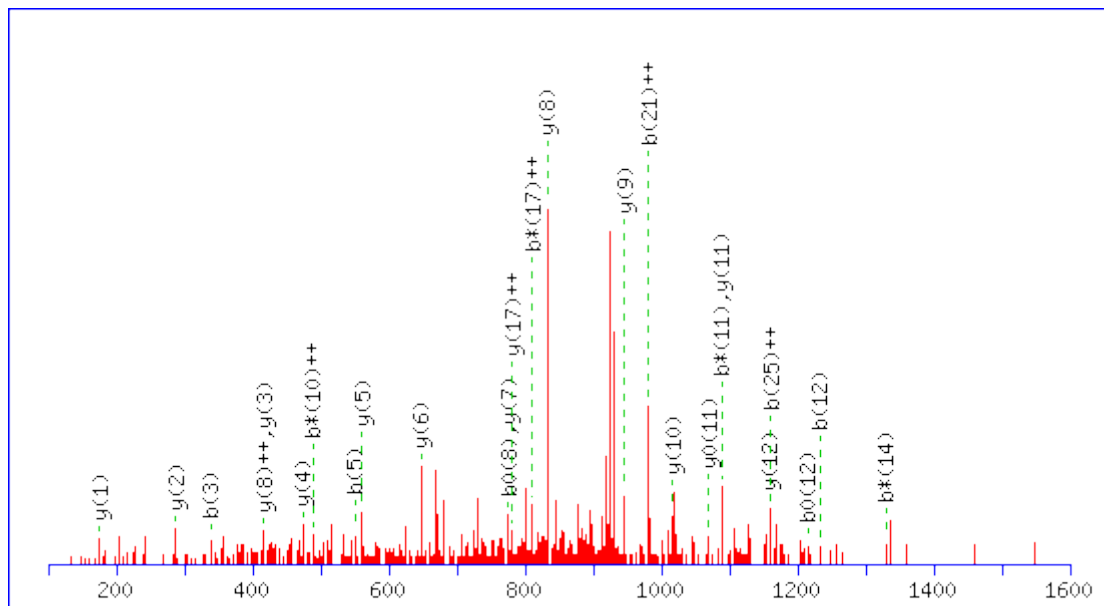
Monoisotopic mass of neutral peptide Mr(calc): 899.5440

Ions Score: 44 Expect: 0.0071

Matches (Bold Red): 18/68 fragment ions using 47 most intense peaks

MS/MS Fragmentation of **LPQLVGVSTPLQGGSNSAAAIGQSSGELR**

Found in **B4GT1_HUMAN**, Beta-1,4-galactosyltransferase 1 OS=Homo sapiens
GN=B4GALT1 PE=1 SV=5



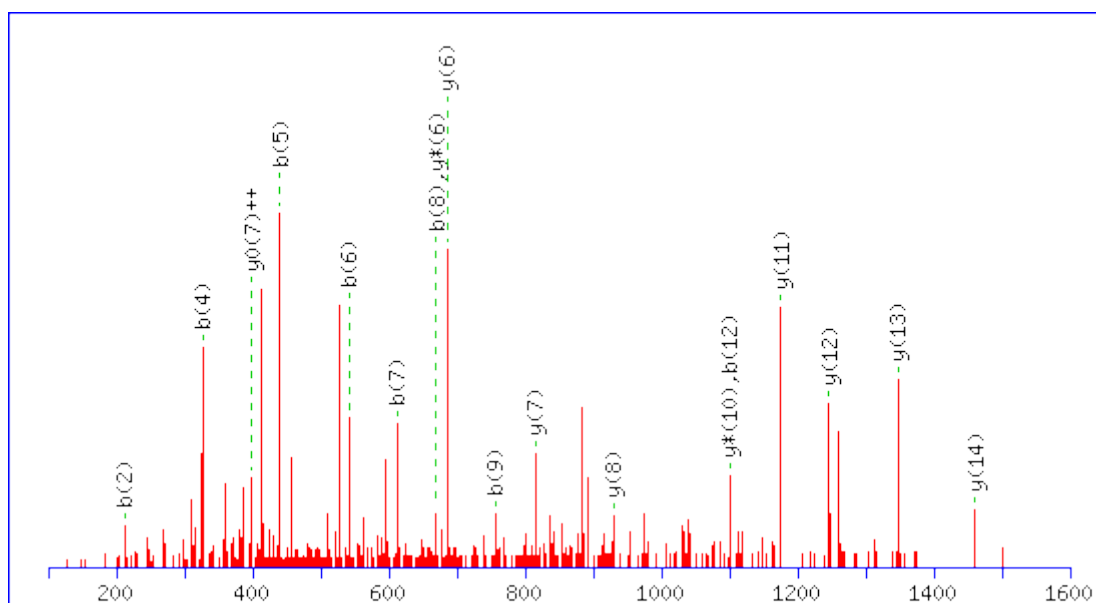
Monoisotopic mass of neutral peptide Mr(calc): 2793.4621

Ions Score: 46 Expect: 0.012

Matches (Bold Red): 26/314 fragment ions using 58 most intense peaks

MS/MS Fragmentation of **DPGGITAGSTDEPPMLTK**

Found in **BCL7C_HUMAN**, B-cell CLL/lymphoma 7 protein family member C OS=Homo sapiens
GN=BCL7C PE=1 SV=3



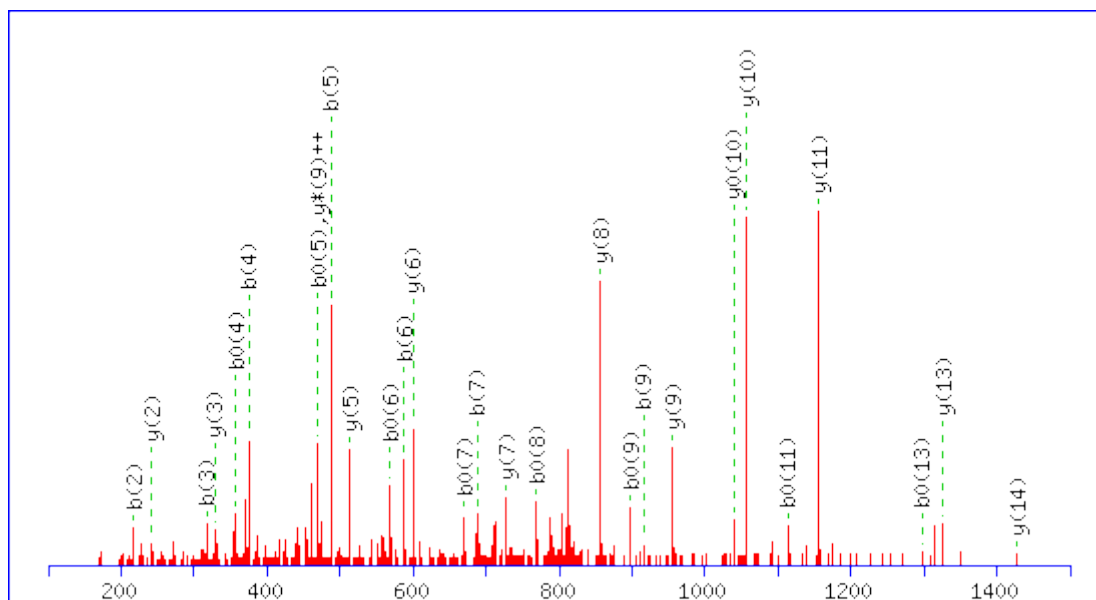
Monoisotopic mass of neutral peptide Mr(calc): 1785.8455

Ions Score: 55 Expect: 0.0012

Matches (Bold Red): 18/168 fragment ions using 31 most intense peaks

MS/MS Fragmentation of **TDTGIVTVEQSPSSSK**

Found in **BOD1L_HUMAN**, Biorientation of chromosomes in cell division protein 1-like OS=Homo sapiens GN=BOD1L PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1642.8141

Variable modifications:

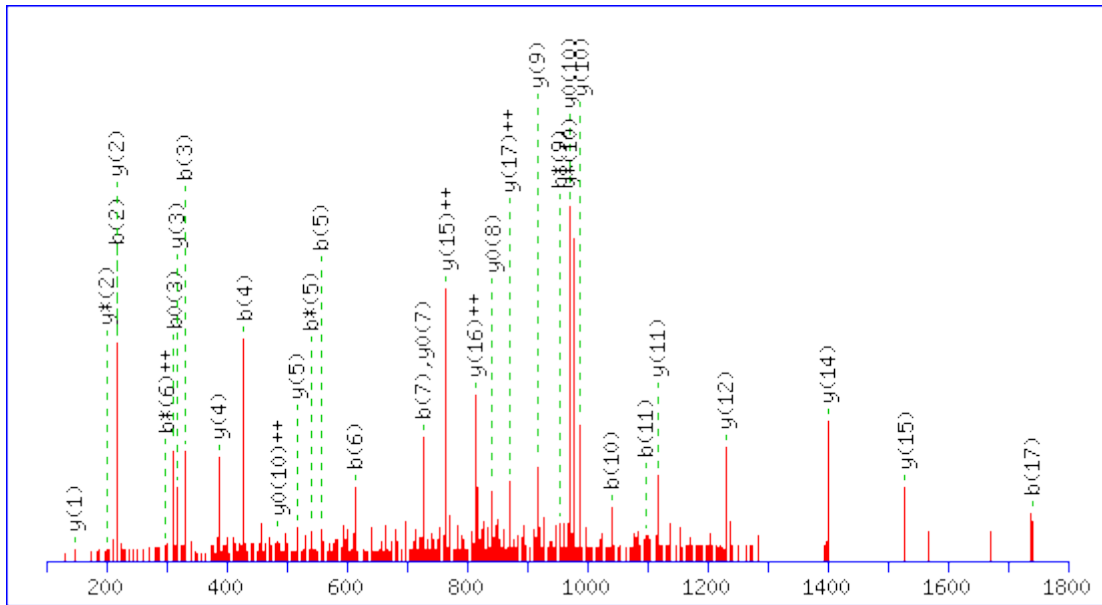
K16 : Label:13C(6)15N(2) (K)

Ions Score: 89 **Expect:** 4.4e-007

Matches (Bold Red): 28/160 fragment ions using 39 most intense peaks

MS/MS Fragmentation of **DTLVQGLNEAGDDLEAVAK**

Found in **BZW2_HUMAN**, Basic leucine zipper and W2 domain-containing protein 2
OS=Homo sapiens GN=BZW2 PE=1 SV=1



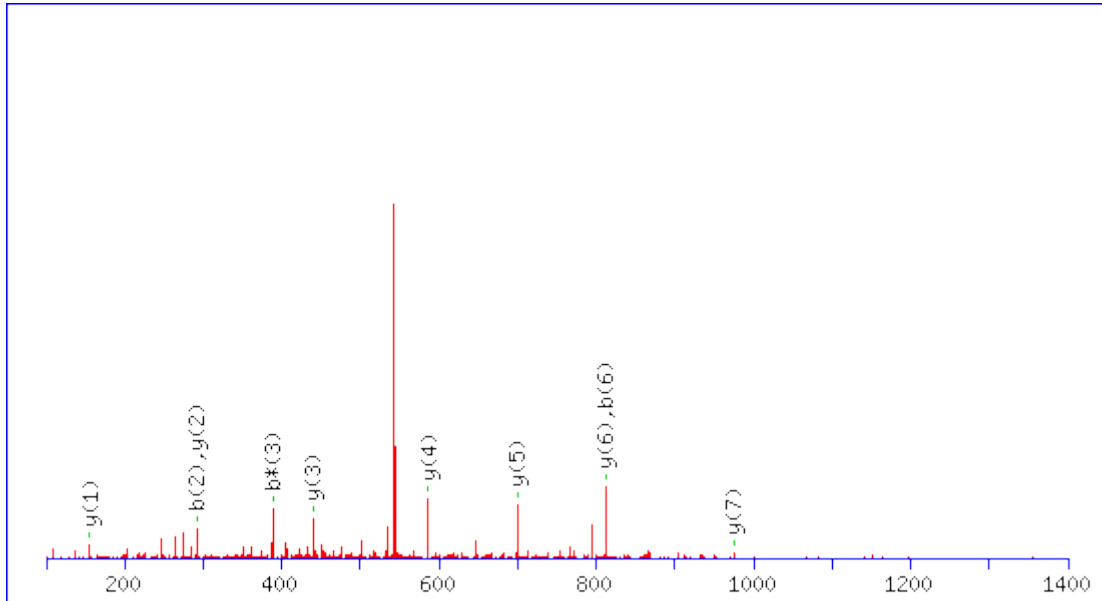
Monoisotopic mass of neutral peptide Mr(calc): 1956.9640

Ions Score: 56 **Expect:** 0.00095

Matches (Bold Red): 35/200 fragment ions using 82 most intense peaks

MS/MS Fragmentation of **QYLLFFHK**

Found in **C109A_HUMAN**, Coiled-coil domain-containing protein 109A OS=Homo sapiens GN=CCDC109A PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1102.6055

Variable modifications:

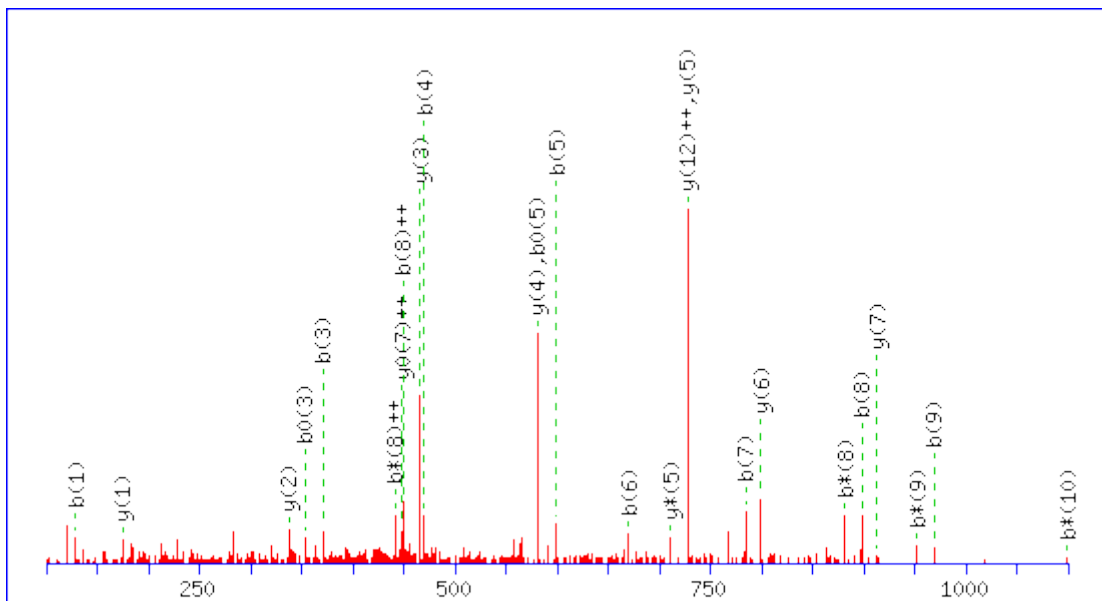
K8 : Label:13C(6)15N(2) (K)

Ions Score: 49 Expect: 0.0025

Matches (Bold Red): 10/56 fragment ions using 21 most intense peaks

MS/MS Fragmentation of **KLEVEANNAFDQYR**

Found in **CAPZB_HUMAN**, F-actin-capping protein subunit beta OS=Homo sapiens
GN=CAPZB PE=1 SV=4



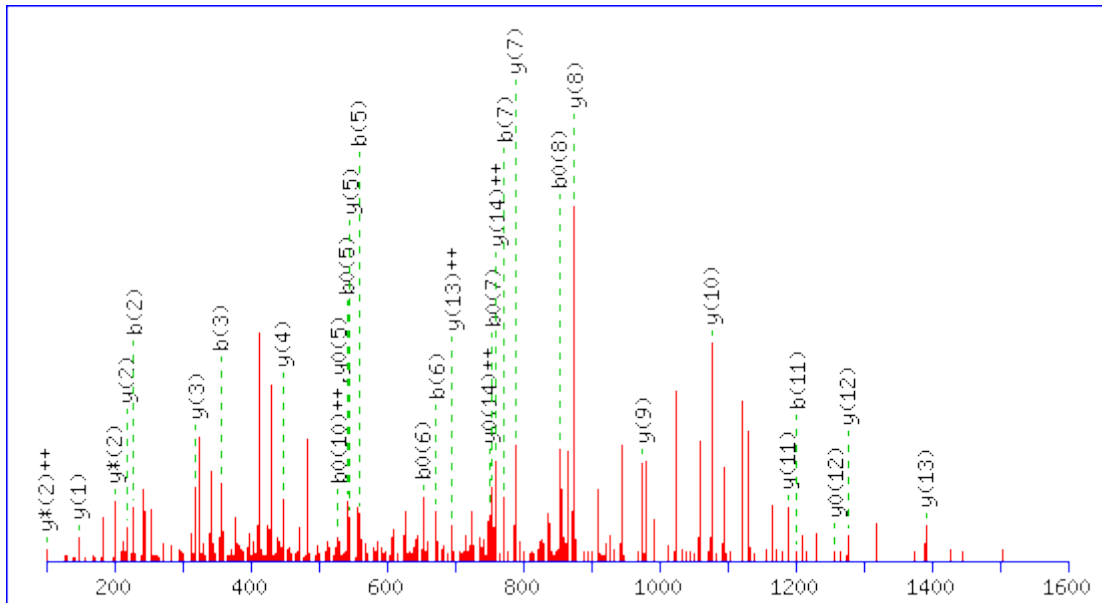
Monoisotopic mass of neutral peptide Mr(calc): 1695.8216

Ions Score: 68 Expect: 5.1e-005

Matches (Bold Red): 25/146 fragment ions using 34 most intense peaks

MS/MS Fragmentation of **DIQDSLTVSNEVQTAK**

Found in **CAZA2_HUMAN**, F-actin-capping protein subunit alpha-2 OS=Homo sapiens
GN=CAPZA2 PE=1 SV=3



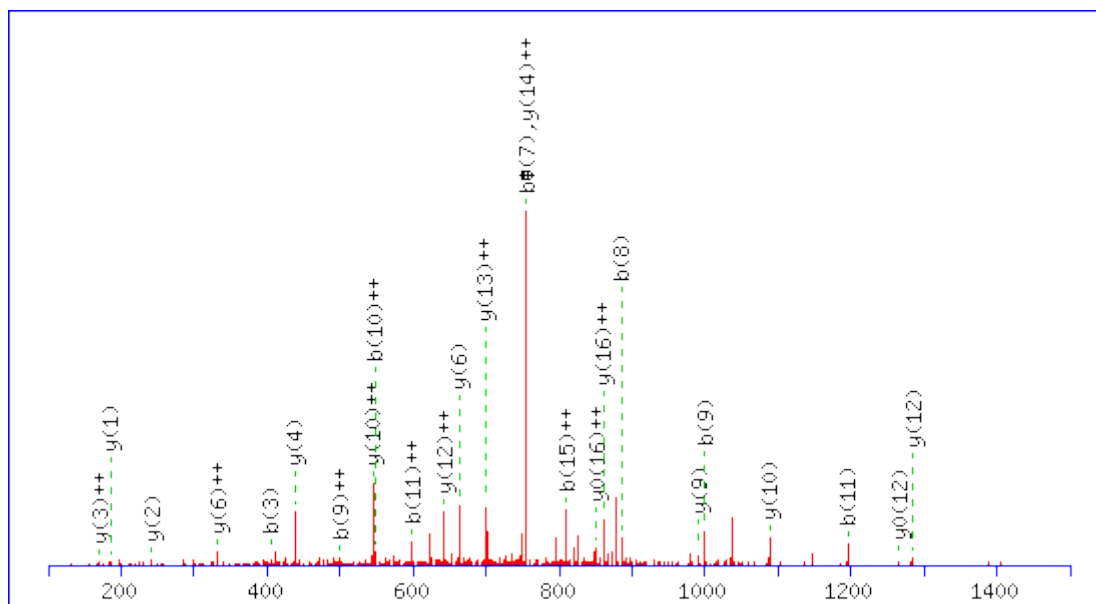
Monoisotopic mass of neutral peptide Mr(calc): 1746.8636

Ions Score: 53 Expect: 0.0016

Matches (Bold Red): 30/172 fragment ions using 81 most intense peaks

MS/MS Fragmentation of **EFQASPLLLPVPTQVPQPVGR**

Found in **CCD22_HUMAN**, Coiled-coil domain-containing protein 22 OS=Homo sapiens
GN=CCDC22 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 2282.2662

Variable modifications:

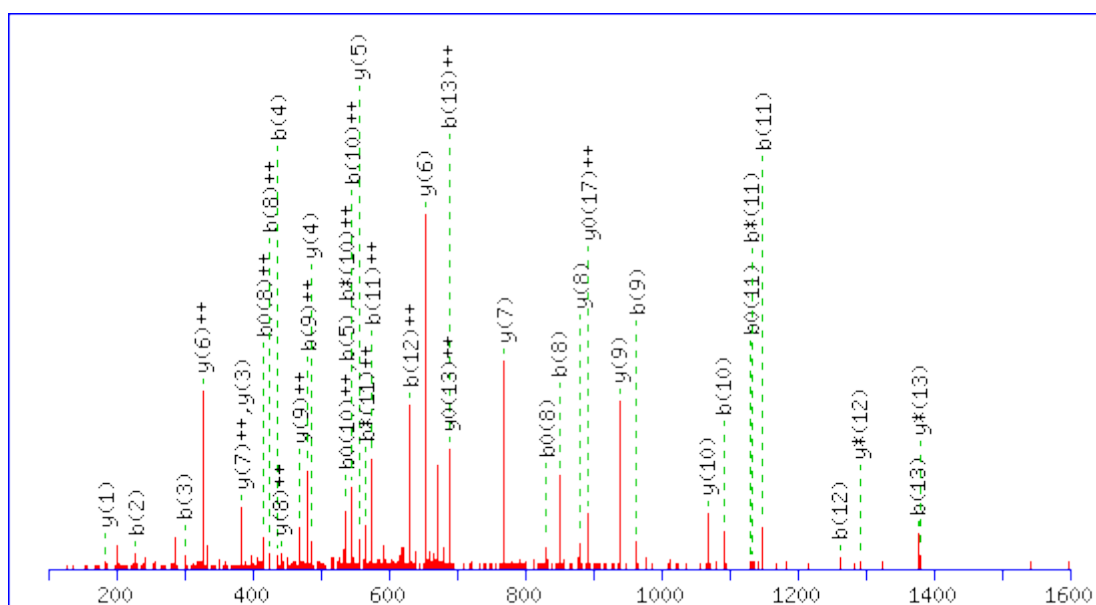
R21 : Label:13C(6)15N(4) (R)

Ions Score: 39 Expect: 0.039

Matches (Bold Red): 26/220 fragment ions using 53 most intense peaks

MS/MS Fragmentation of **DLAHTPSQLEGLDPATEAR**

Found in **CCNK_HUMAN**, Cyclin-K OS=Homo sapiens GN=CCNK PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 2029.9944

Variable modifications:

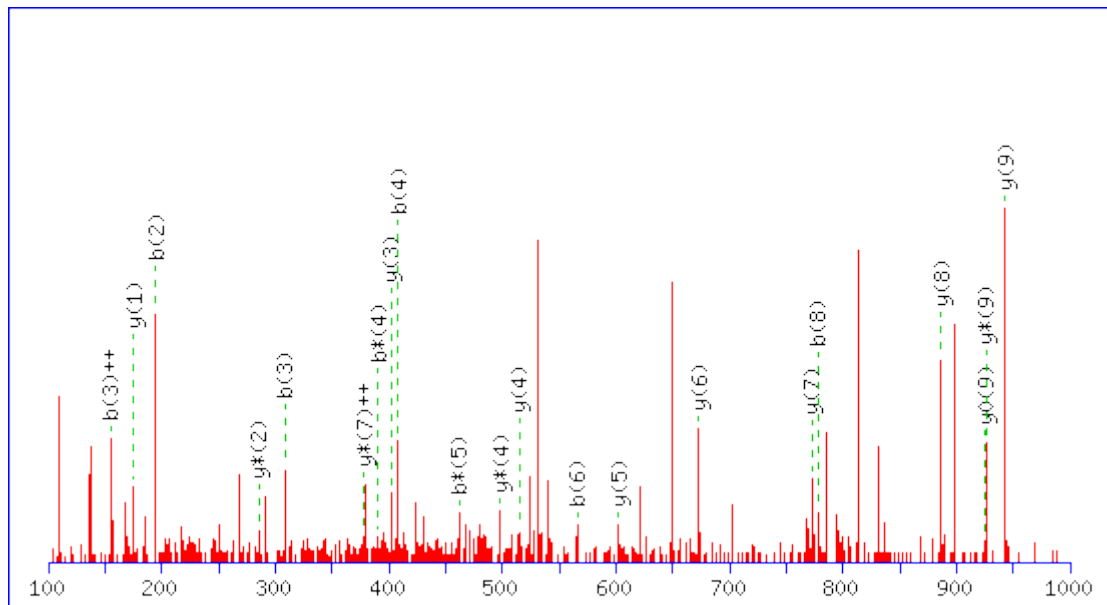
R19 : Label:13C(6)15N(4) (R)

Ions Score: 54 Expect: 0.0015

Matches (**Bold Red**): 40/198 fragment ions using 74 most intense peaks

MS/MS Fragmentation of **HGNVASLVQR**

Found in **CD2AP_HUMAN**, CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1



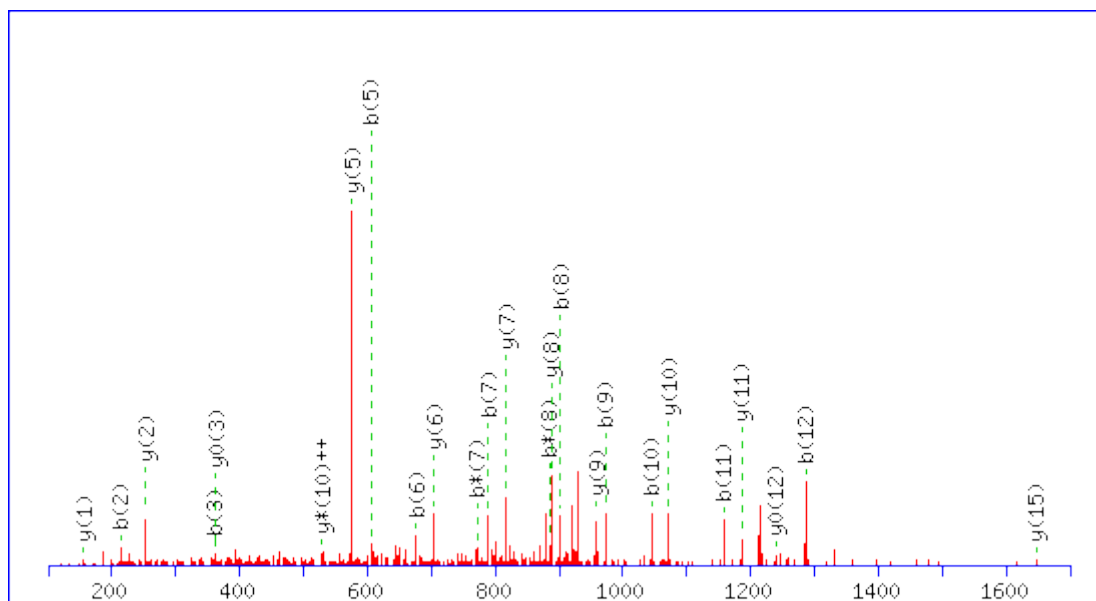
Monoisotopic mass of neutral peptide Mr(calc): 1079.5836

Ions Score: 36 Expect: 0.053

Matches (**Bold Red**): 21/86 fragment ions using 63 most intense peaks

MS/MS Fragmentation of **NVFDEAILAALEPPEPK**

Found in **CDC42_HUMAN**, Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1859.9760

Variable modifications:

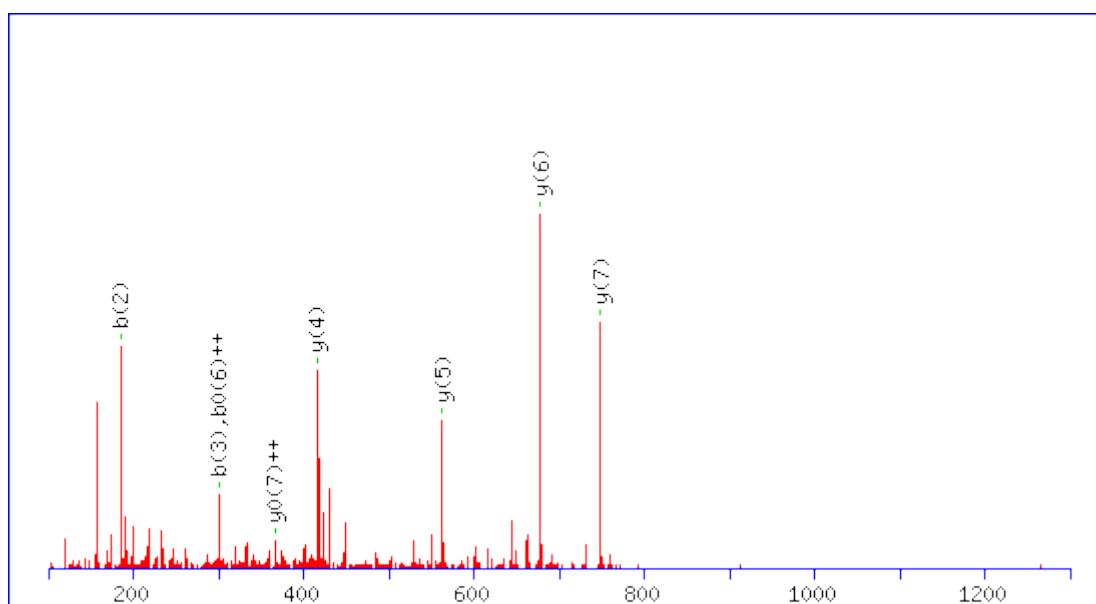
K17 : Label:13C(6)15N(2) (K)

Ions Score: 53 Expect: 0.0017

Matches (Bold Red): 25/182 fragment ions using 64 most intense peaks

MS/MS Fragmentation of **LADFGLAR**

Found in **CDK16_HUMAN**, Cyclin-dependent kinase 16 OS=Homo sapiens GN=CDK16 PE=1 SV=1



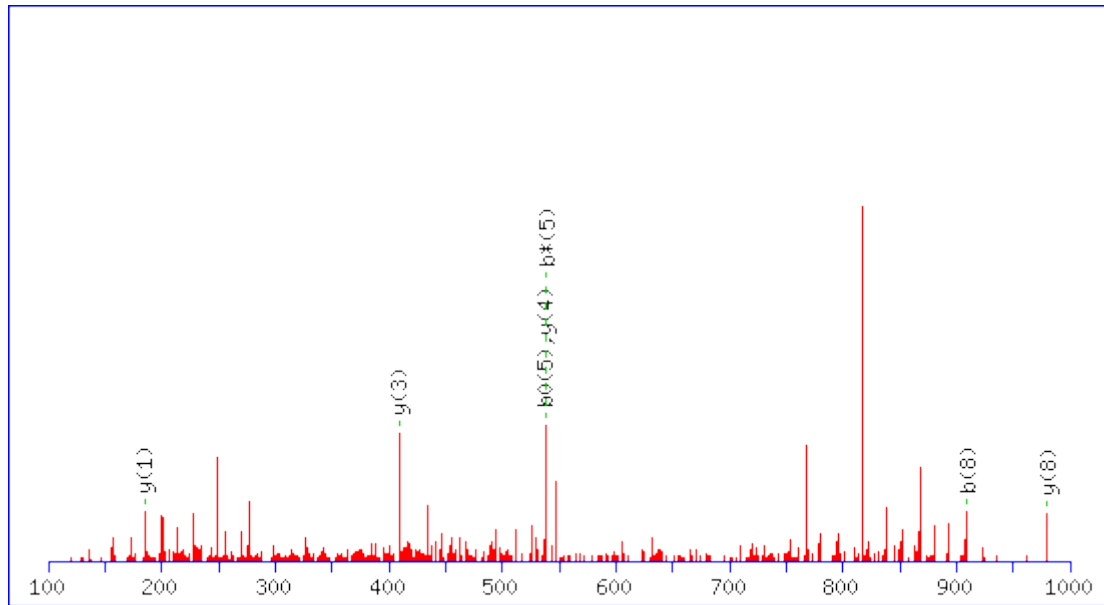
Monoisotopic mass of neutral peptide Mr(calc): 861.4708

Ions Score: 40 Expect: 0.022

Matches (Bold Red): 8/56 fragment ions using 7 most intense peaks

MS/MS Fragmentation of **LLNQSEGSR**

Found in **CE128_HUMAN**, Centrosomal protein of 128 kDa OS=Homo sapiens GN=CEP128
PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1092.4840

Variable modifications:

S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

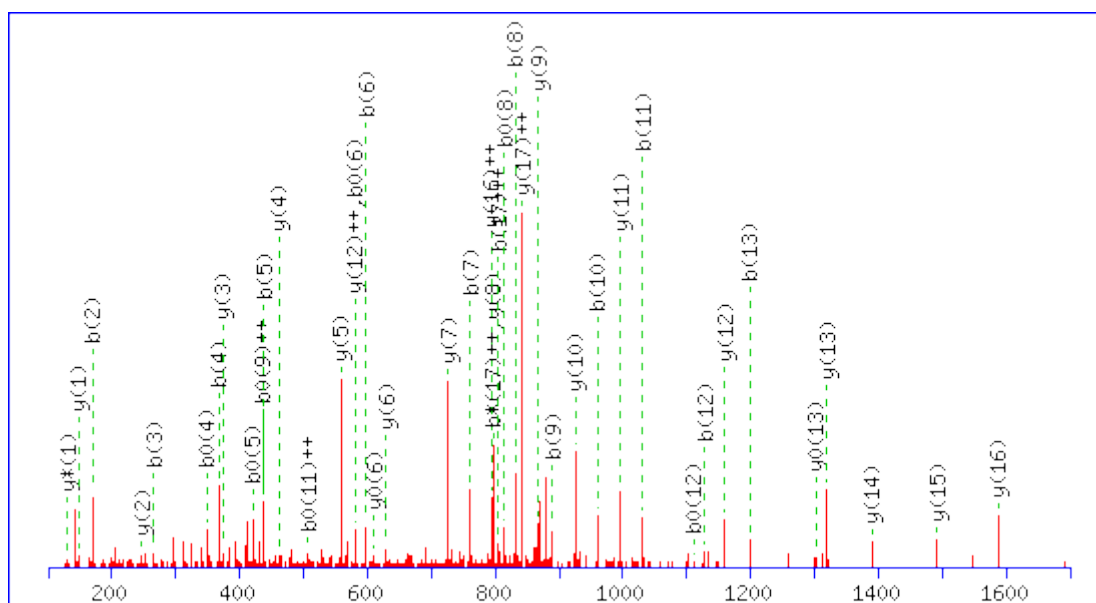
R9 : Label:13C(6)15N(4) (R)

Ions Score: 16 Expect: 5.4

Matches (Bold Red): 7/130 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **APPTACYAGAAPAPSQVK**

Found in **CEBPB_HUMAN**, CCAAT/enhancer-binding protein beta OS=Homo sapiens
GN=CEBPB PE=1 SV=2



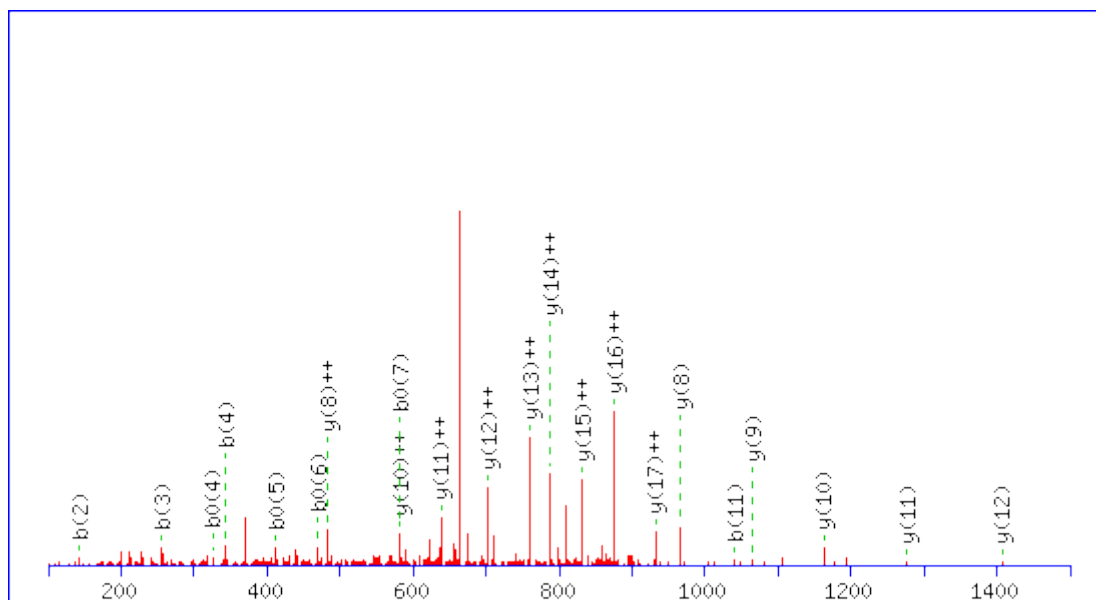
Monoisotopic mass of neutral peptide Mr(calc): 1755.8614

Ions Score: 87 Expect: 7.6e-007

Matches (Bold Red): 43/162 fragment ions using 113 most intense peaks

MS/MS Fragmentation of **AAISSGIEDPVPTLHLTER**

Found in **CNOT3_HUMAN**, CCR4-NOT transcription complex subunit 3 OS=Homo sapiens
GN=CNOT3 PE=1 SV=1



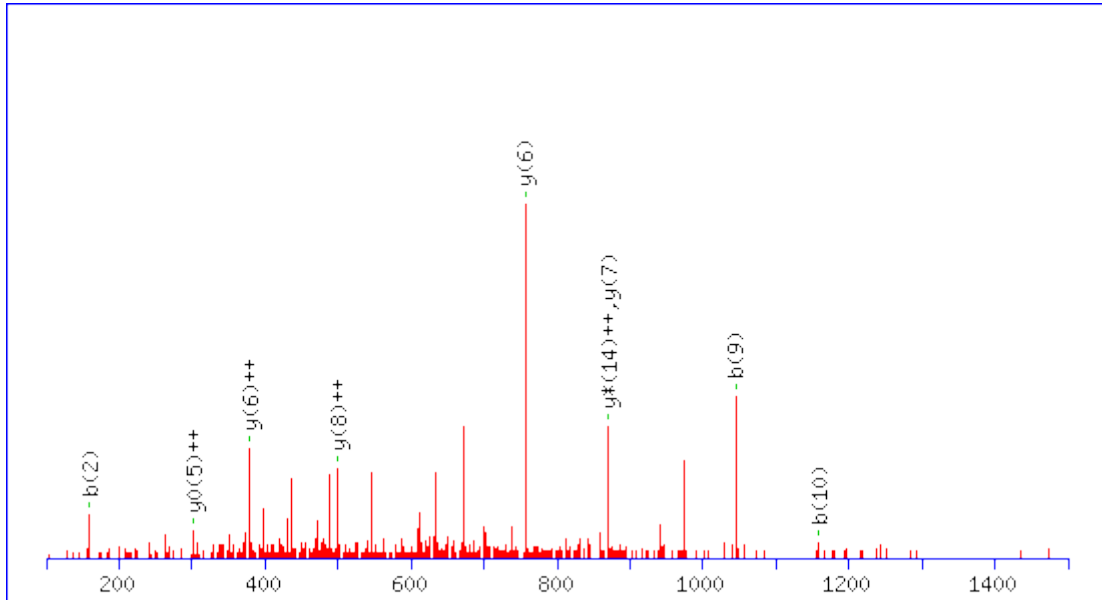
Monoisotopic mass of neutral peptide Mr(calc): 2005.0480

Ions Score: 42 Expect: 0.023

Matches (**Bold Red**): 22/172 fragment ions using 53 most intense peaks

MS/MS Fragmentation of **SATDRDLMELKAEHVR**

Found in **CP250_HUMAN**, Centrosome-associated protein CEP250 OS=Homo sapiens
GN=CEP250 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1913.9623

Variable modifications:

R5 : Label:13C(6)15N(4) (R)

M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

K11 : Label:13C(6)15N(2) (K)

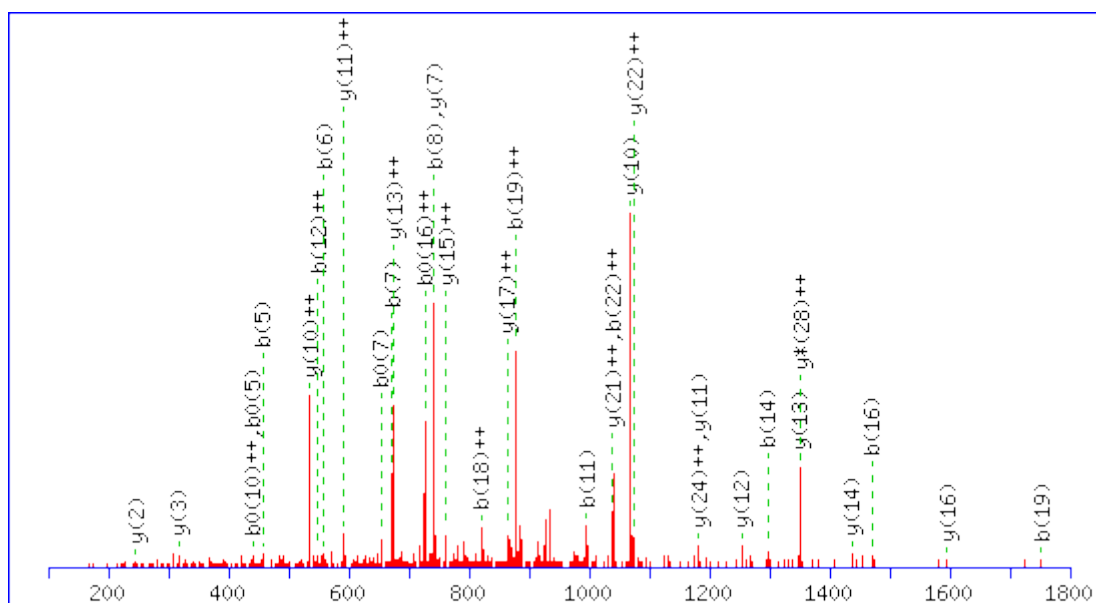
R16 : Label:13C(6)15N(4) (R)

Ions Score: 12 Expect: 26

Matches (**Bold Red**): 9/256 fragment ions using 13 most intense peaks

MS/MS Fragmentation of **TAPTSTIAPGVVMASSPALPTQPAEEAAR**

Found in **CREB1_HUMAN**, Cyclic AMP-responsive element-binding protein 1 OS=Homo sapiens
GN=CREB1 PE=1 SV=2



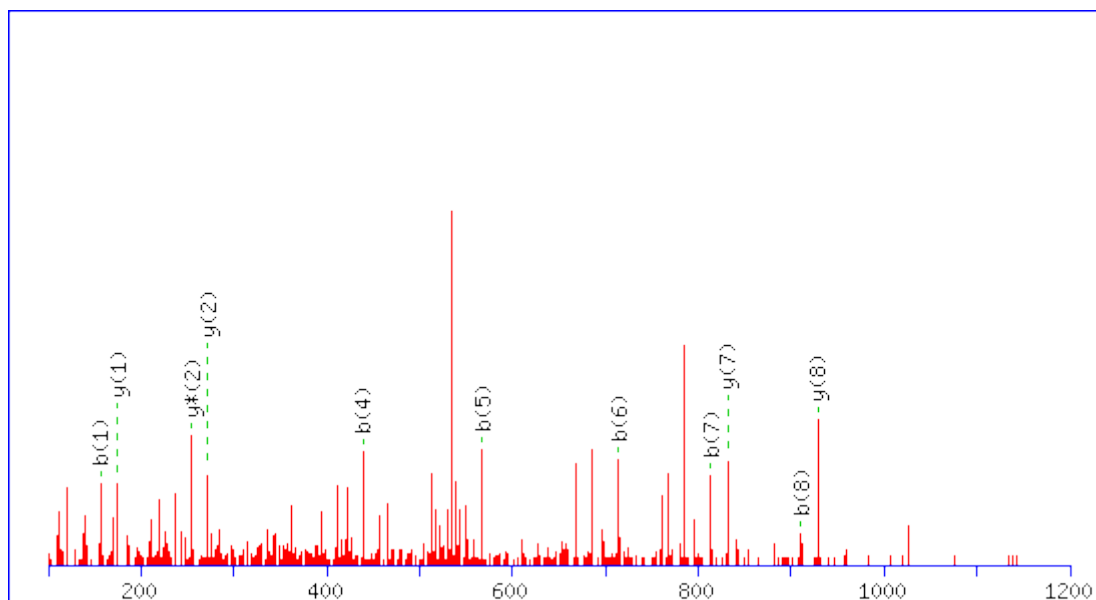
Monoisotopic mass of neutral peptide Mr(calc): 2820.4327

Ions Score: 56 Expect: 0.001

Matches (Bold Red): 34/288 fragment ions using 53 most intense peaks

MS/MS Fragmentation of **RPANQFVPR**

Found in **CSK2B_HUMAN**, Casein kinase II subunit beta OS=Homo sapiens GN=CSNK2B
PE=1 SV=1



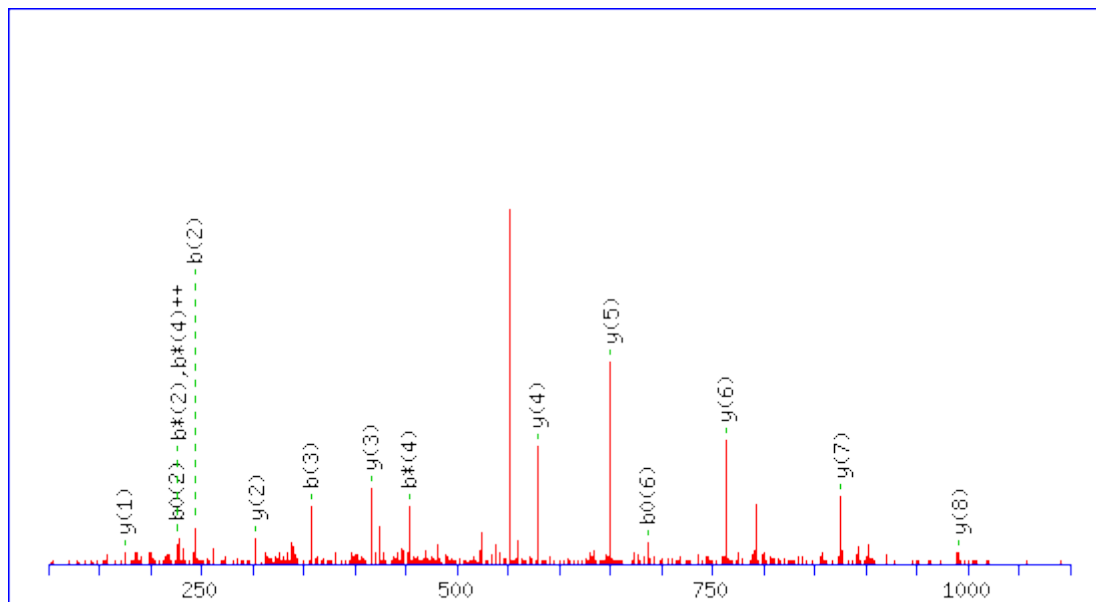
Monoisotopic mass of neutral peptide Mr(calc): 1083.5938

Ions Score: 39 Expect: 0.03

Matches (**Bold Red**): 11/64 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **QDLLAYLQR**

Found in **CTNA2_HUMAN**, Catenin alpha-2 OS=Homo sapiens GN=CTNNA2 PE=1 SV=5



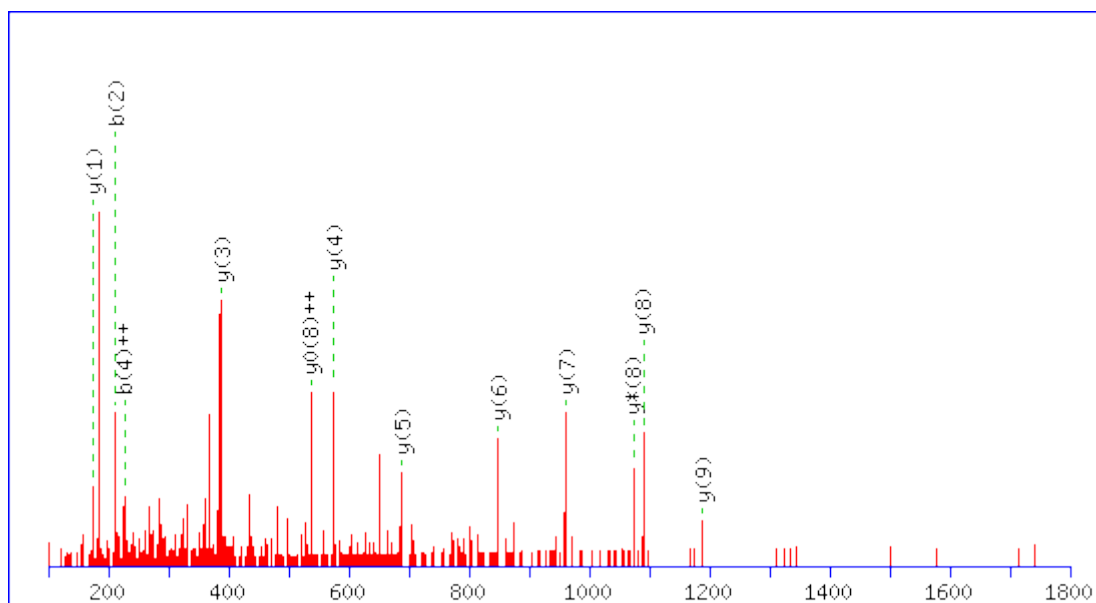
Monoisotopic mass of neutral peptide Mr(calc): 1118.6084

Ions Score: 65 Expect: 7.7e-005

Matches (**Bold Red**): 15/80 fragment ions using 22 most intense peaks

MS/MS Fragmentation of **LVQNCLWTLR**

Found in **CTNB1_HUMAN**, Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1



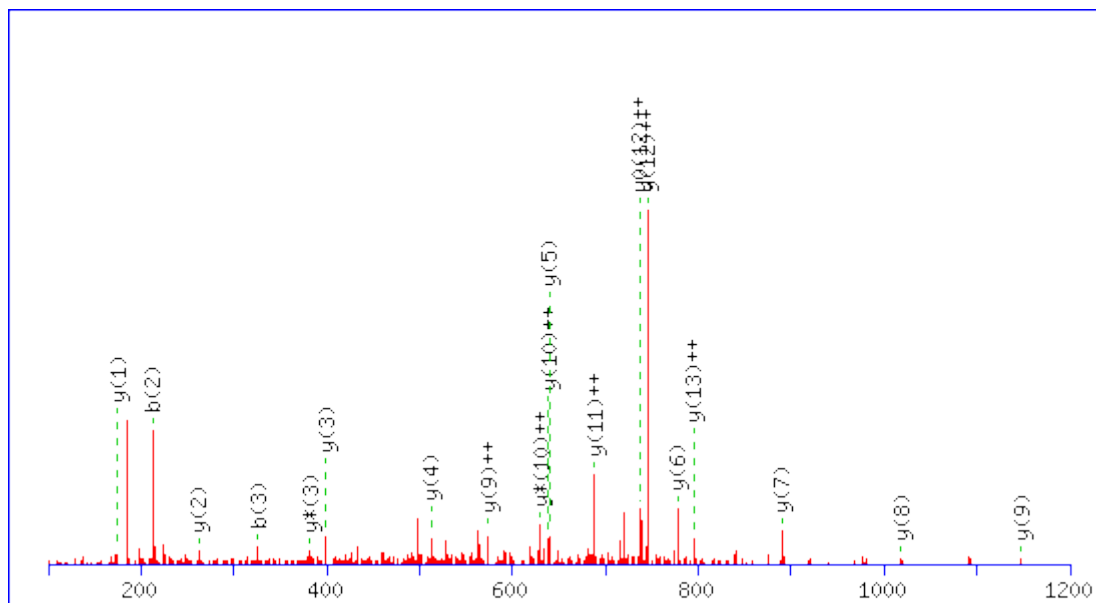
Monoisotopic mass of neutral peptide Mr(calc): 1301.6914

Ions Score: 48 Expect: 0.0043

Matches (**Bold Red**): 12/86 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **LVLTQEQLHQLHSR**

Found in **DCTN1_HUMAN**, Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3



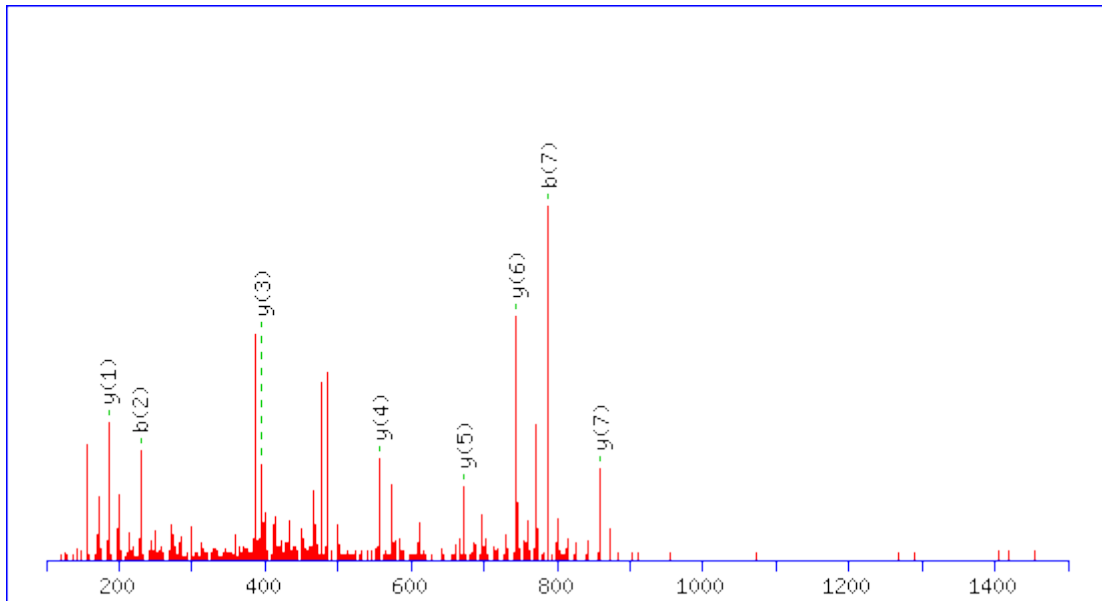
Monoisotopic mass of neutral peptide Mr(calc): 1700.9322

Ions Score: 45 Expect: 0.011

Matches (**Bold Red**): 19/140 fragment ions using 43 most intense peaks

MS/MS Fragmentation of **LDADYPLR**

Found in **DENR_HUMAN**, Density-regulated protein OS=Homo sapiens GN=DENR PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 971.4951

Variable modifications:

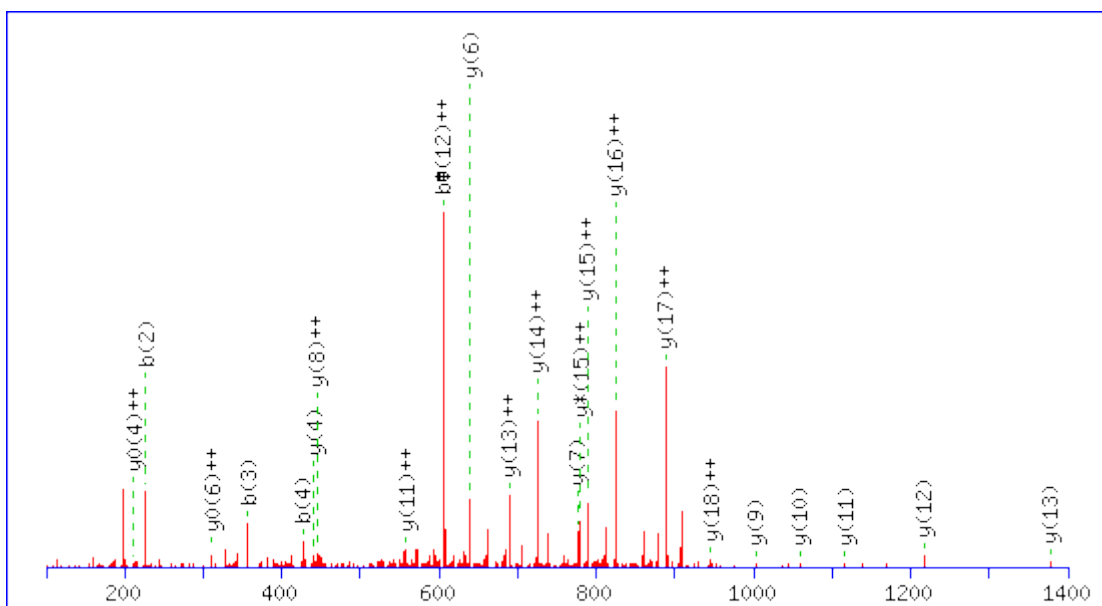
R8 : Label:13C(6)15N(4) (R)

Ions Score: 42 Expect: 0.014

Matches (Bold Red): 8/60 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **LLEAQTGGIIHPTTGQK**

Found in **DESP_HUMAN**, Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 2002.0397

Variable modifications:

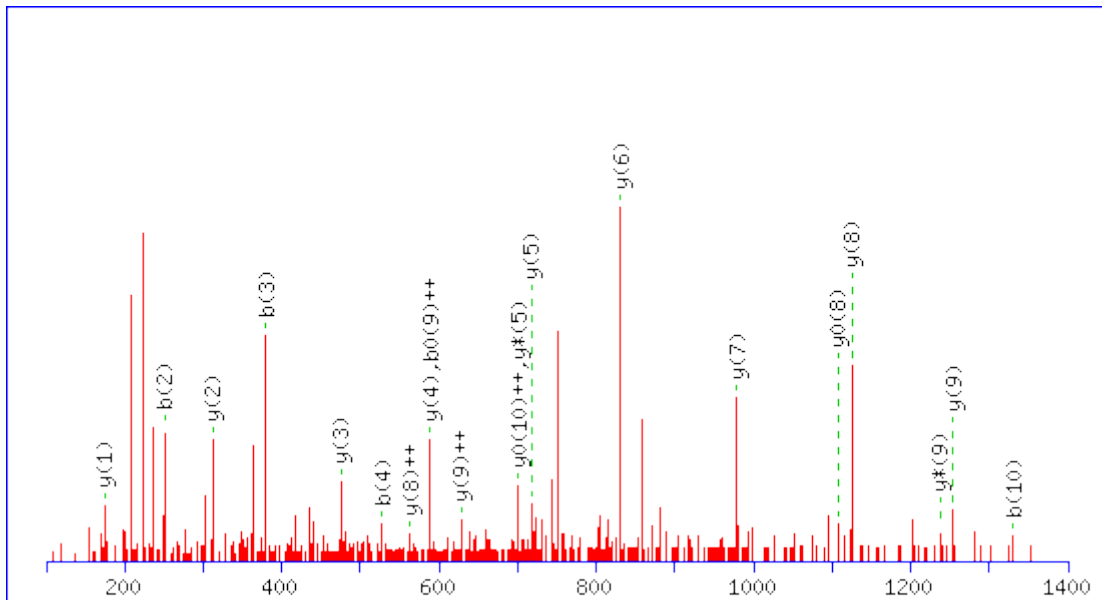
K19 : Label:13C(6)15N(2) (K)

Ions Score: 50 **Expect:** 0.0036

Matches (Bold Red): 24/198 fragment ions using 59 most intense peaks

MS/MS Fragmentation of **SYEFFNELYHR**

Found in **DJC13_HUMAN**, DnaJ homolog subfamily C member 13 OS=Homo sapiens
GN=DNAJC13 PE=1 SV=5



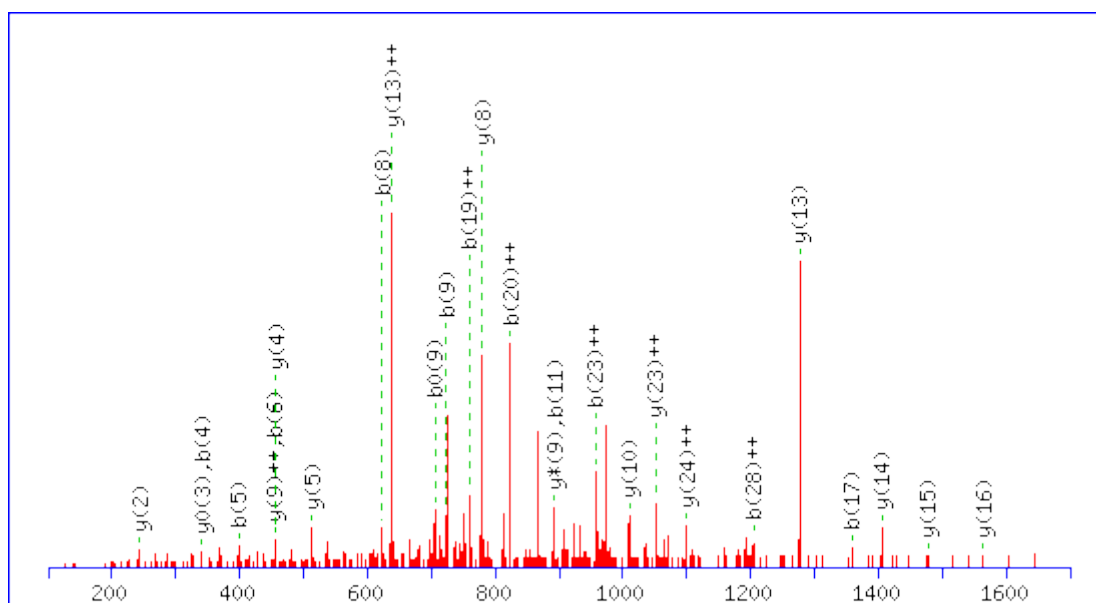
Monoisotopic mass of neutral peptide Mr(calc): 1503.6783

Ions Score: 50 **Expect:** 0.0033

Matches (Bold Red): 20/102 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **AGVLGGPATPASGPGPASAEPVTEPGLGDPK**

Found in **DMAP1_HUMAN**, DNA methyltransferase 1-associated protein 1 OS=Homo sapiens GN=DMAP1 PE=1 SV=1



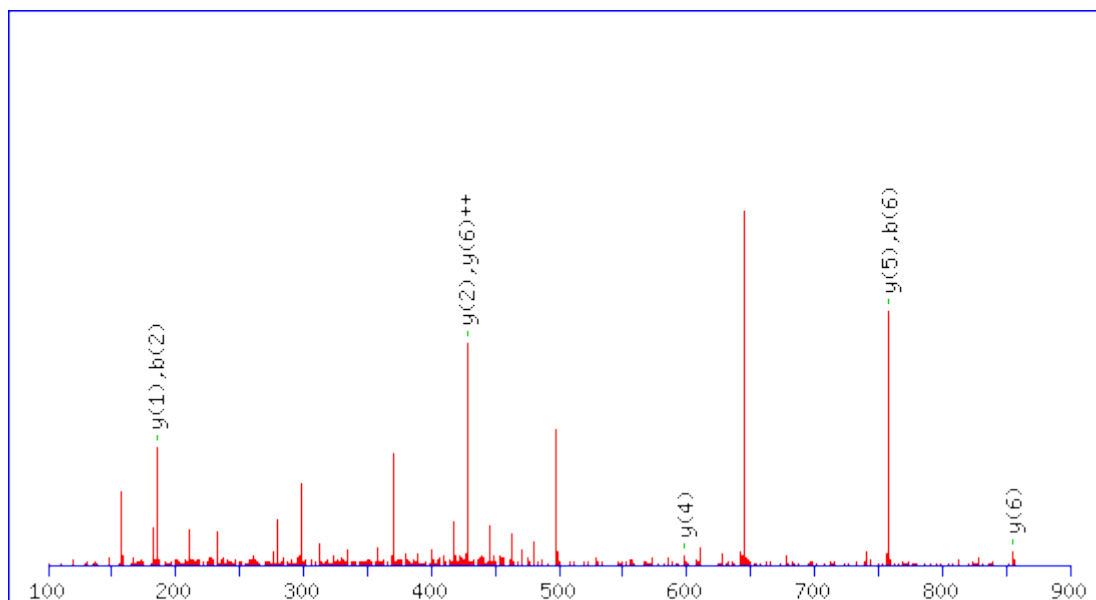
Monoisotopic mass of neutral peptide Mr(calc): 2921.4771

Ions Score: 40 Expect: 0.045

Matches (Bold Red): 27/300 fragment ions using 52 most intense peaks

MS/MS Fragmentation of **SPCGLYR**

Found in **DOXA1_HUMAN**, Dual oxidase maturation factor 1 OS=Homo sapiens
GN=DUOXA1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 941.3706

Variable modifications:

Y6 : Phospho (Y)

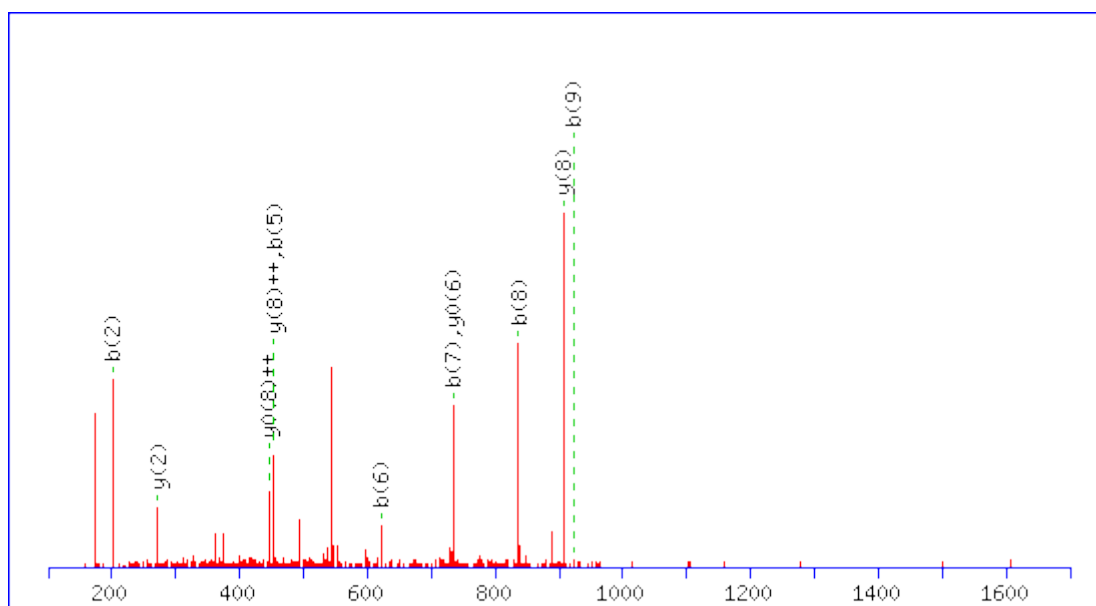
R7 : Label:13C(6)15N(4) (R)

Ions Score: 36 **Expect:** 0.046

Matches (Bold Red): 8/48 fragment ions using 22 most intense peaks

MS/MS Fragmentation of **SIPGVSNTSR**

Found in **DTX4_HUMAN**, Protein deltex-4 OS=Homo sapiens GN=DTX4 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1106.4997

Variable modifications:

S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

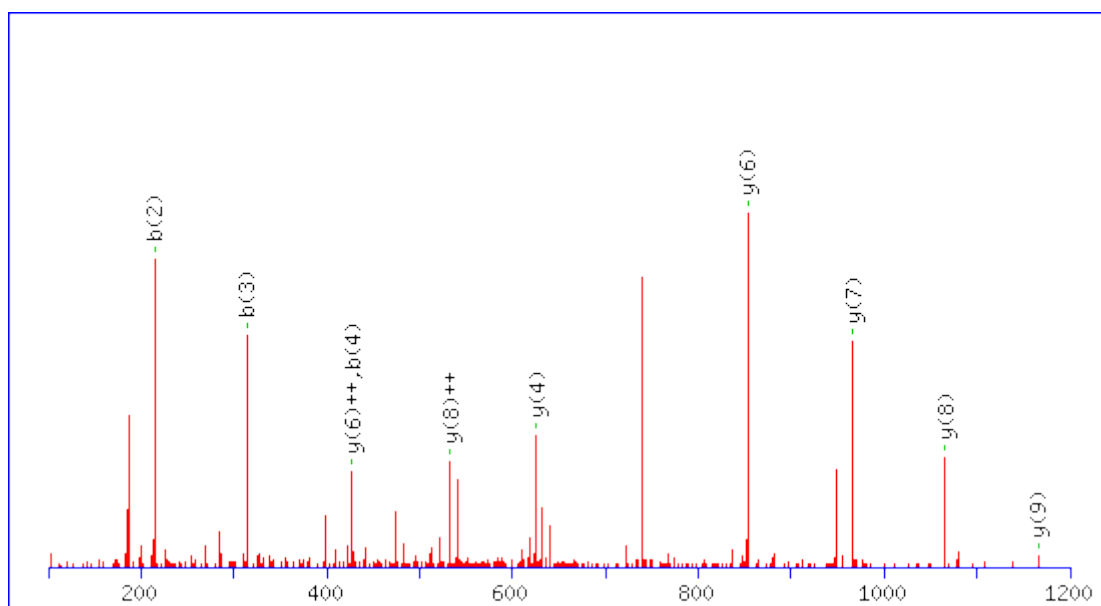
R10 : Label:13C(6)15N(4) (R)

Ions Score: 42 **Expect:** 0.011

Matches (Bold Red): 11/146 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **ITVLDLISCR**

Found in **DUS10_HUMAN**, Dual specificity protein phosphatase 10 OS=Homo sapiens GN=DUSP10 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1278.6282

Variable modifications:

S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

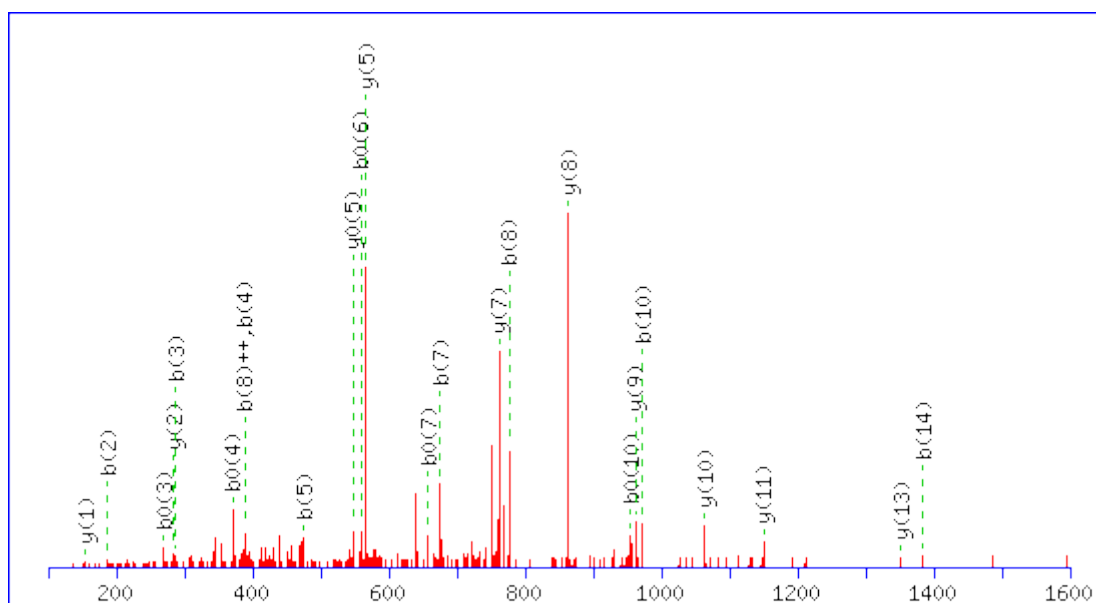
R10 : Label:¹³C(6)¹⁵N(4) (R)

Ions Score: 39 Expect: 0.032

Matches (Bold Red): 10/134 fragment ions using 12 most intense peaks

MS/MS Fragmentation of **ADTTSTVTPVPGQEK**

Found in **EHMT1_HUMAN**, Histone-lysine N-methyltransferase EHMT1 OS=Homo sapiens
GN=EHMT1 PE=1 SV=4



Monoisotopic mass of neutral peptide Mr(calc): 1537.7715

Variable modifications:

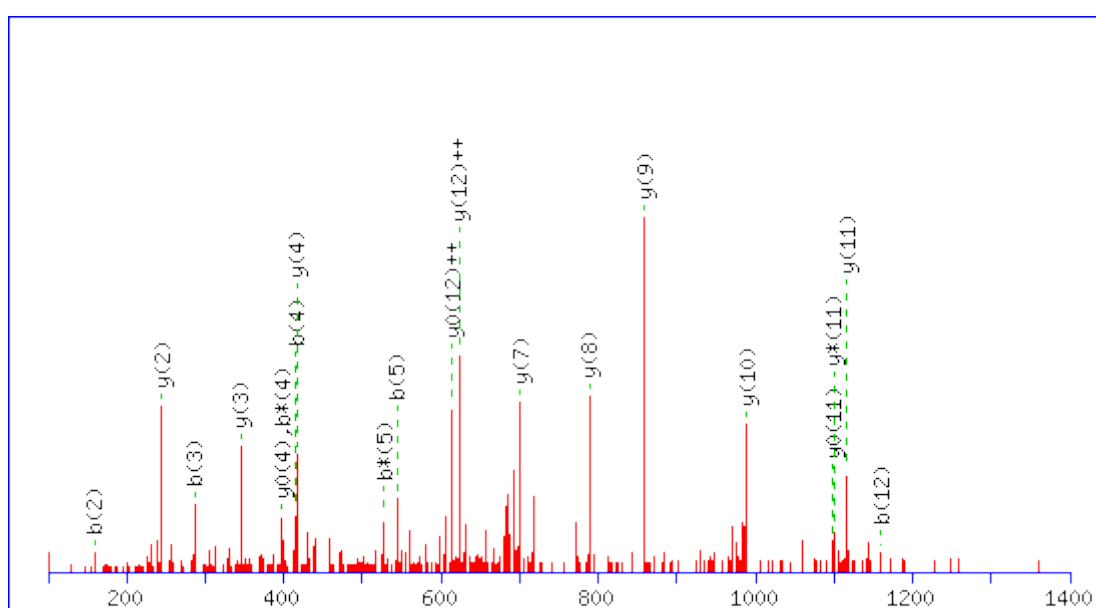
K15 : Label:13C(6)15N(2) (K)

Ions Score: 61 Expect: 0.00028

Matches (Bold Red): 24/140 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **SAQQEASADVATPK**

Found in **ELYS_HUMAN**, Protein ELYS OS=Homo sapiens GN=AHCTF1 PE=1 SV=3



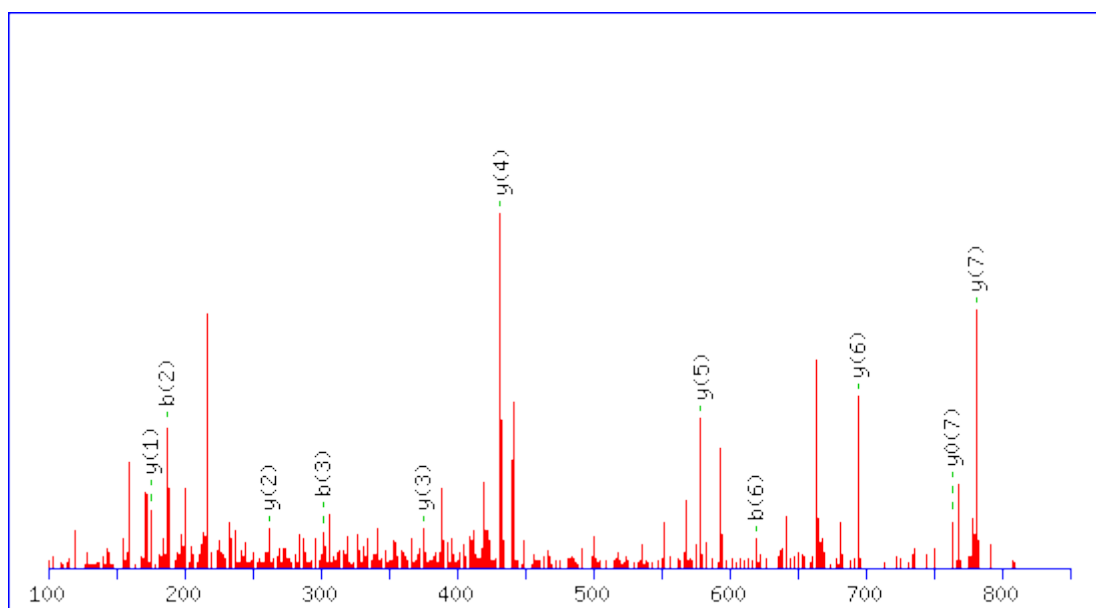
Monoisotopic mass of neutral peptide Mr(calc): 1401.6736

Ions Score: 58 Expect: 0.00047

Matches (Bold Red): 20/148 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **VSDFGLSR**

Found in **EPHB3_HUMAN**, Ephrin type-B receptor 3 OS=Homo sapiens GN=EPHB3 PE=1 SV=2



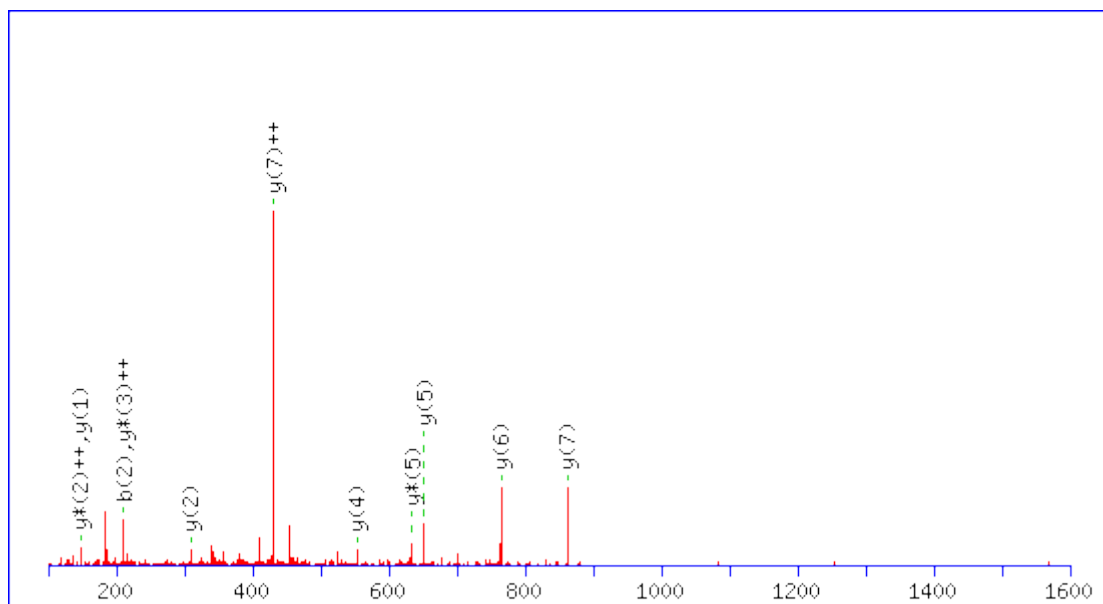
Monoisotopic mass of neutral peptide Mr(calc): 879.4450

Ions Score: 30 Expect: 0.2

Matches (Bold Red): 11/66 fragment ions using 46 most intense peaks

MS/MS Fragmentation of **LPIVDKYK**

Found in **ERF3A_HUMAN**, Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 PE=1 SV=1



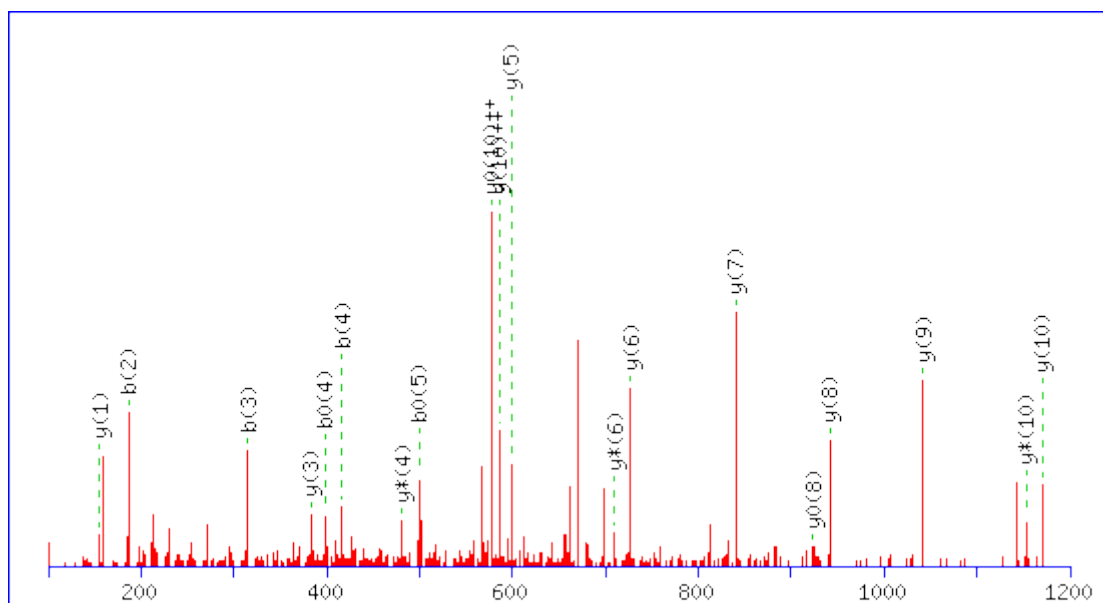
Monoisotopic mass of neutral peptide Mr(calc): 974.5800

Ions Score: 41 Expect: 0.018

Matches (Bold Red): 11/60 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **SVQTTLTDEVK**

Found in **ERLN1_HUMAN**, Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1355.7024

Variable modifications:

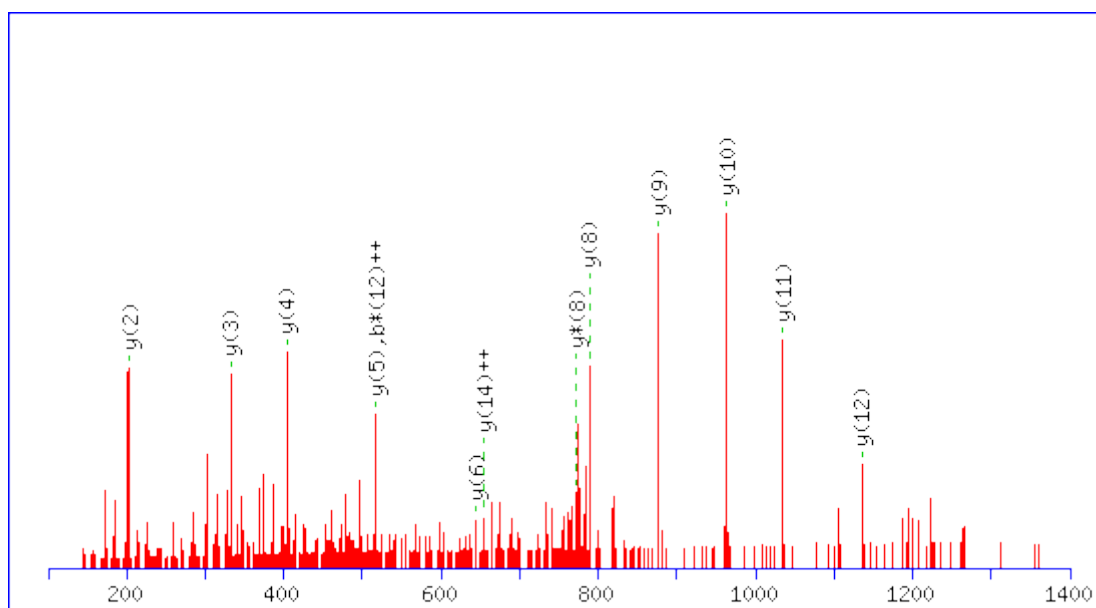
K12 : Label:13C(6)15N(2) (K)

Ions Score: 53 **Expect: 0.0015**

Matches (Bold Red): 19/124 fragment ions using 35 most intense peaks

MS/MS Fragmentation of **AEGSSTASSGSQLAEGK**

Found in **F120A_HUMAN**, Constitutive coactivator of PPAR-gamma-like protein 1
OS=Homo sapiens GN=FAM120A PE=1 SV=2



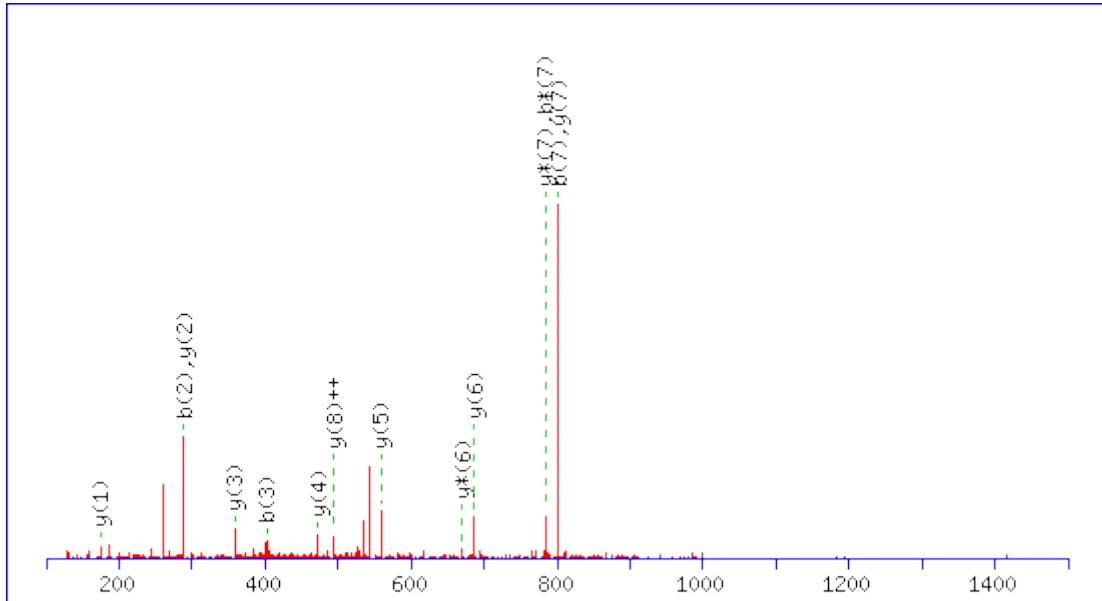
Monoisotopic mass of neutral peptide Mr(calc): 1565.7169

Ions Score: 54 **Expect: 0.0012**

Matches (Bold Red): 13/164 fragment ions using 22 most intense peaks

MS/MS Fragmentation of **TWNQSIALR**

Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4



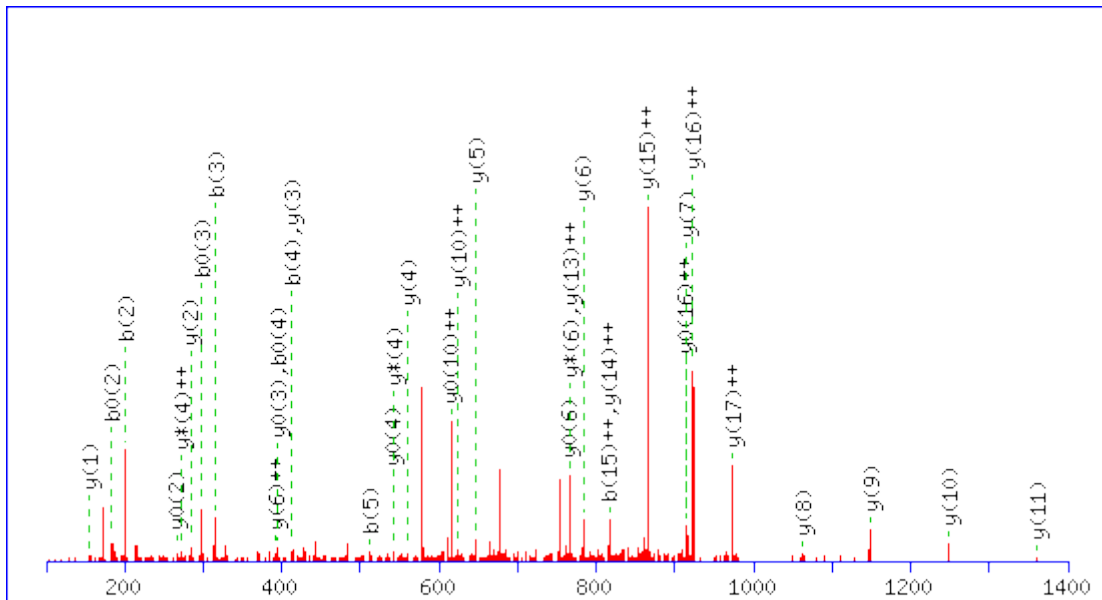
Monoisotopic mass of neutral peptide Mr(calc): 1087.5774

Ions Score: 51 Expect: 0.002

Matches (**Bold Red**): 14/84 fragment ions using 22 most intense peaks

MS/MS Fragmentation of **VTDPVGDIVSFMHSFEEL**

Found in **FAF2_HUMAN**, FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 2043.9703

Variable modifications:

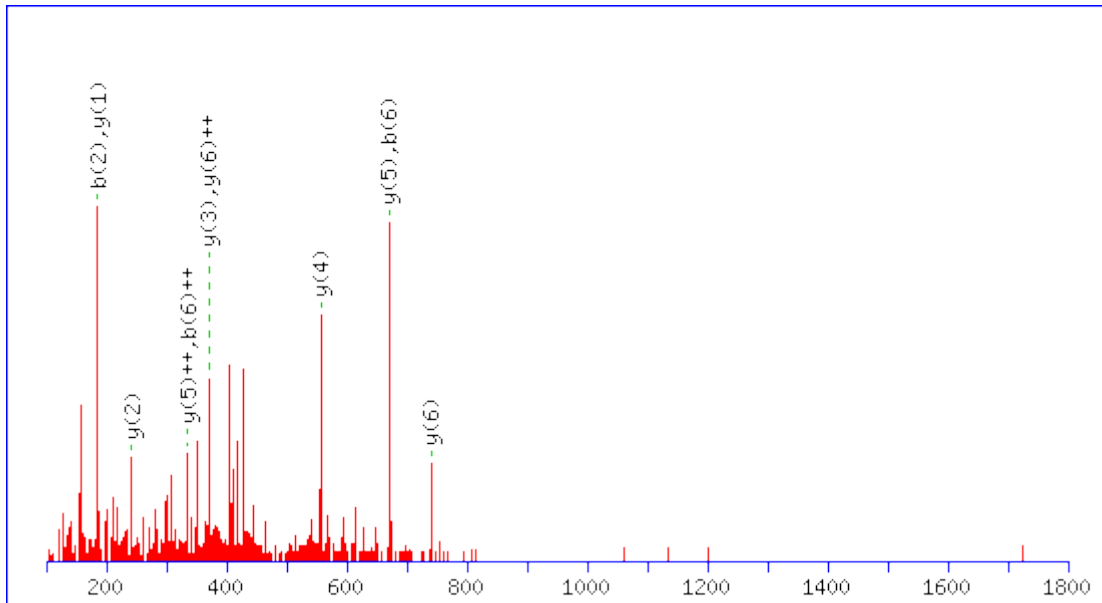
K18 : Label:13C(6)15N(2) (K)

Ions Score: 38 **Expect: 0.06**

Matches (Bold Red): 35/166 fragment ions using 98 most intense peaks

MS/MS Fragmentation of **LALWEGR**

Found in **FARP1_HUMAN**, FERM, RhoGEF and pleckstrin domain-containing protein
1 OS=Homo sapiens GN=FARP1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 853.4685

Variable modifications:

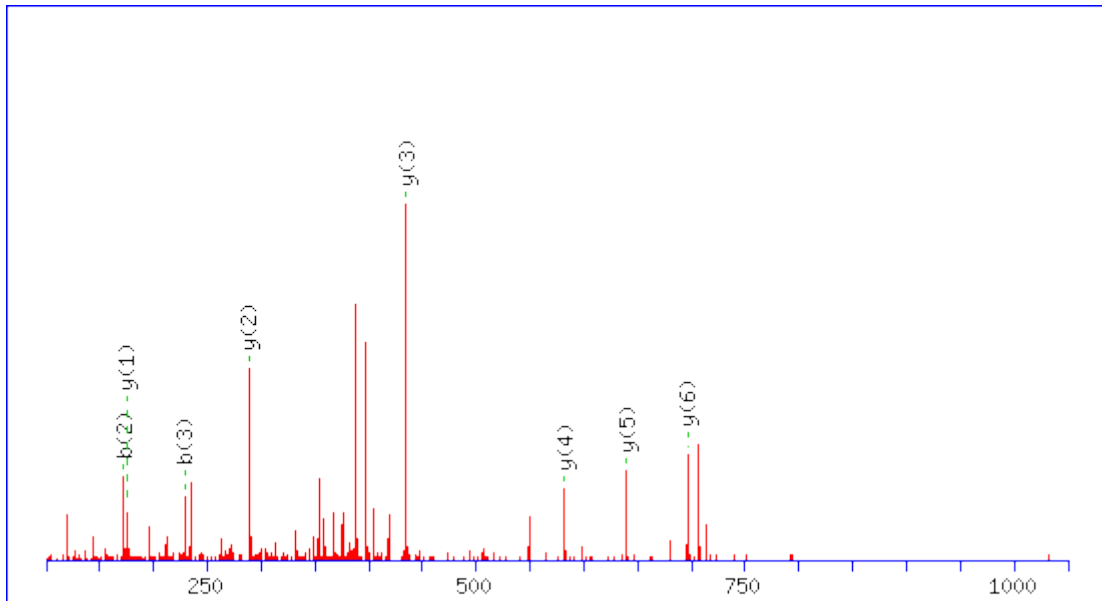
R7 : Label:13C(6)15N(4) (R)

Ions Score: 55 **Expect: 0.00063**

Matches (Bold Red): 11/48 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **NGGFLLR**

Found in **FGF2_HUMAN**, Heparin-binding growth factor 2 OS=Homo sapiens GN=FGF2
PE=1 SV=3



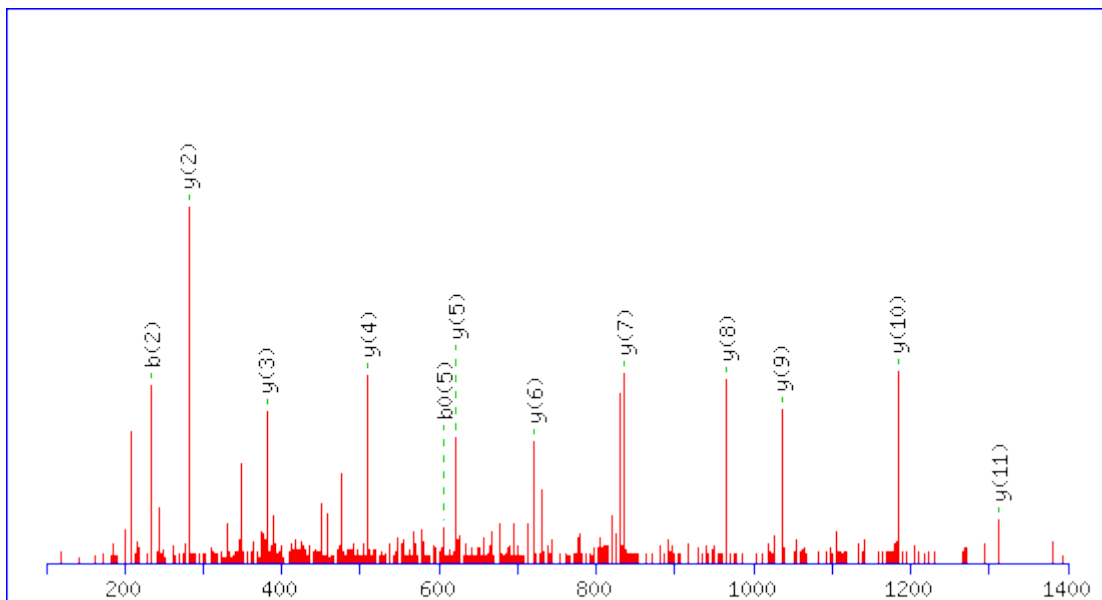
Monoisotopic mass of neutral peptide Mr(calc): 809.4184

Ions Score: 43 Expect: 0.0096

Matches (Bold Red): 8/48 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **SFLEFAEDVIQVPR**

Found in **FMR1_HUMAN**, Fragile X mental retardation 1 protein OS=Homo sapiens
GN=FMR1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1658.8543

Variable modifications:

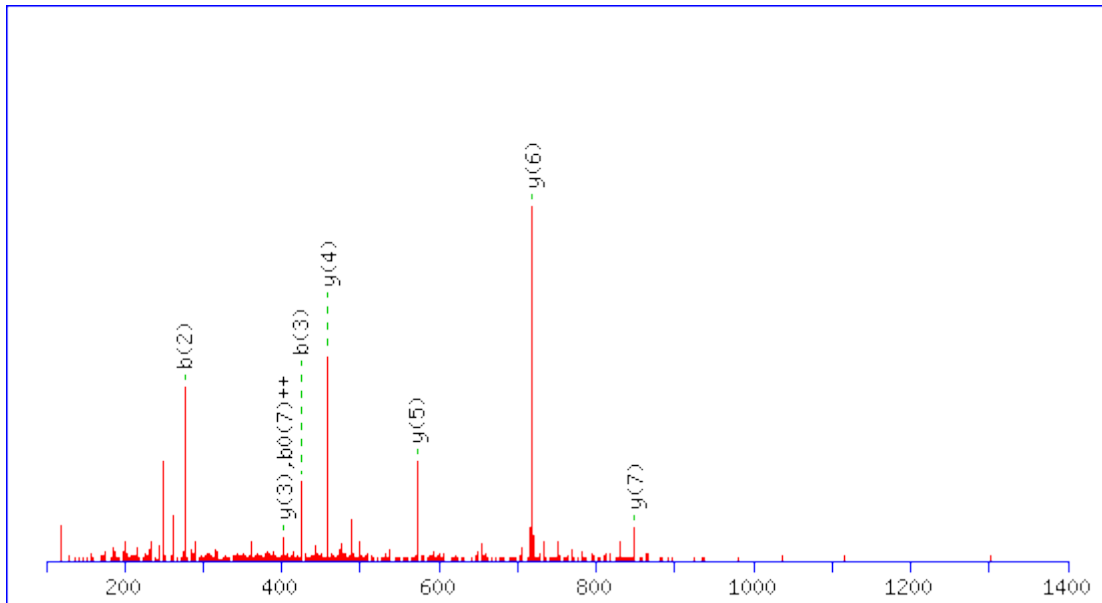
R14 : Label:13C(6)15N(4) (R)

Ions Score: 74 **Expect:** 1.3e-005

Matches (Bold Red): 12/124 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **FEFLGINR**

Found in **FBNP4_HUMAN**, Formin-binding protein 4 OS=Homo sapiens GN=FBNP4 PE=1 SV=3



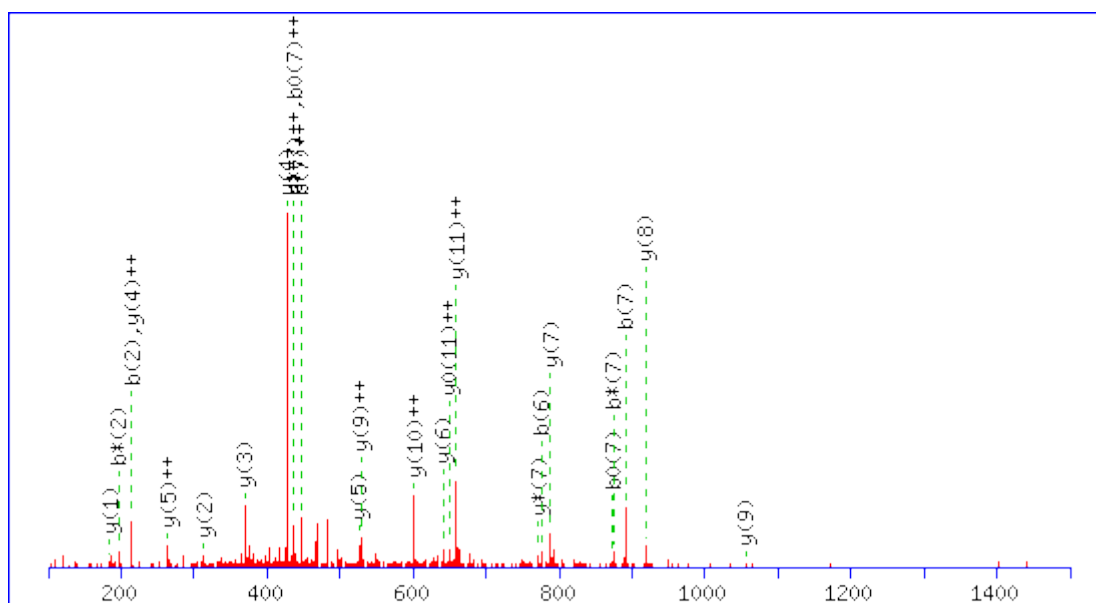
Monoisotopic mass of neutral peptide Mr(calc): 994.5236

Ions Score: 39 **Expect:** 0.026

Matches (Bold Red): 8/58 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **VNFHMFVGGQR**

Found in **GNAL_HUMAN**, Guanine nucleotide-binding protein G(olf) subunit alpha OS=Homo sapiens GN=GNAL PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1415.6644

Variable modifications:

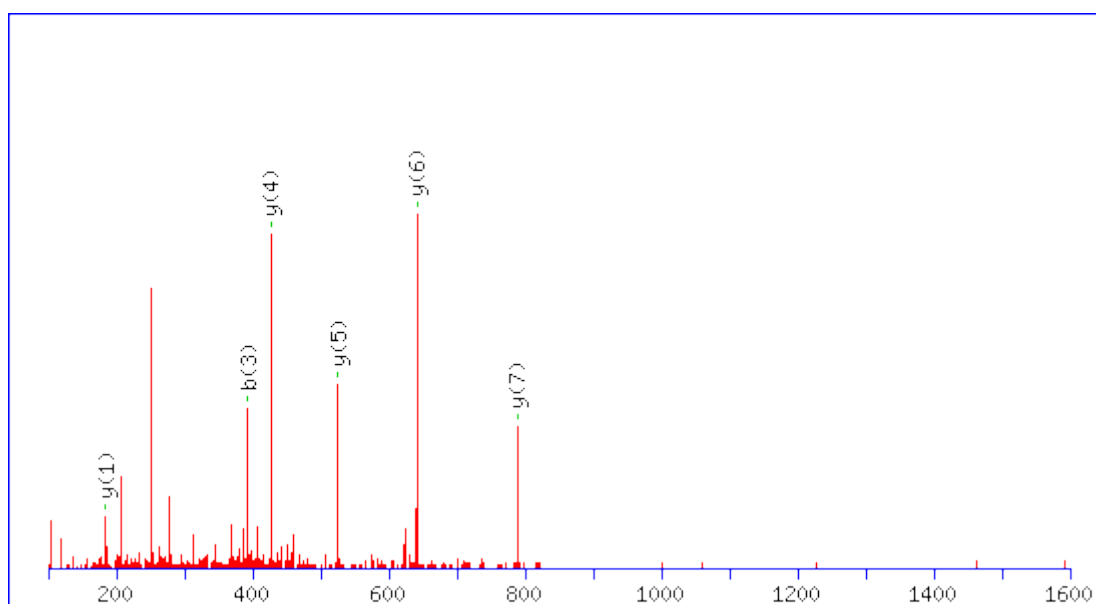
R12 : Label:13C(6)15N(4) (R)

Ions Score: 42 Expect: 0.016

Matches (Bold Red): 25/108 fragment ions using 62 most intense peaks

MS/MS Fragmentation of **MFDVGGQR**

Found in **GNAT1_HUMAN**, Guanine nucleotide-binding protein G(t) subunit alpha-1
 OS=Homo sapiens GN=GNAT1 PE=1 SV=5



Monoisotopic mass of neutral peptide Mr(calc): 918.4257

Variable modifications:

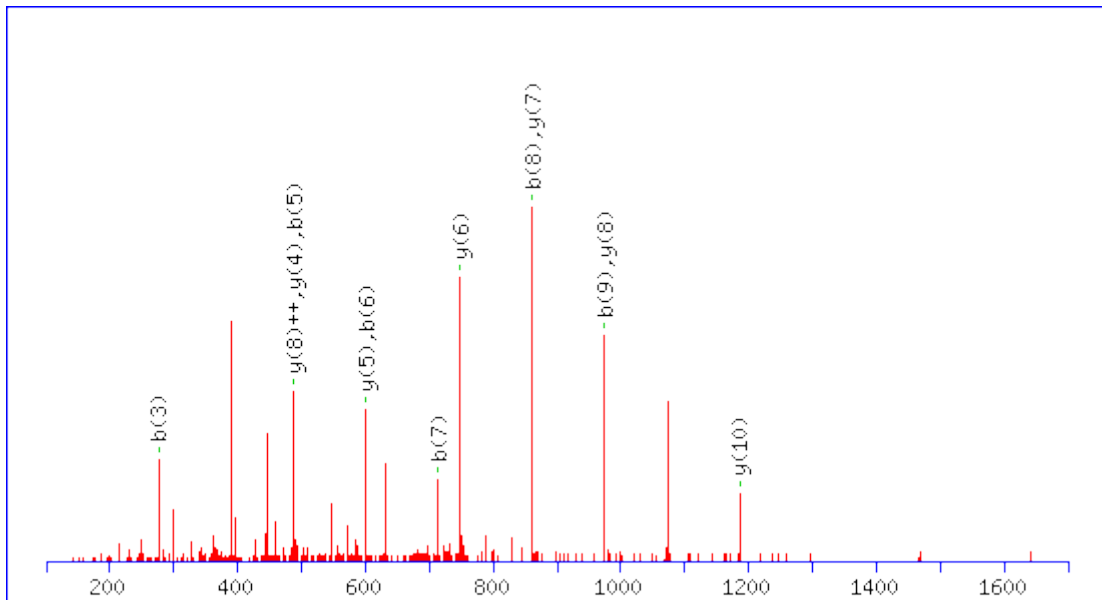
R8 : Label:13C(6)15N(4) (R)

Ions Score: 38 Expect: 0.02

Matches (Bold Red): 6/58 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **SSTDPIIFLLDK**

Found in **GPR82_HUMAN**, Probable G-protein coupled receptor 82 OS=Homo sapiens
GN=GPR82 PE=2 SV=1



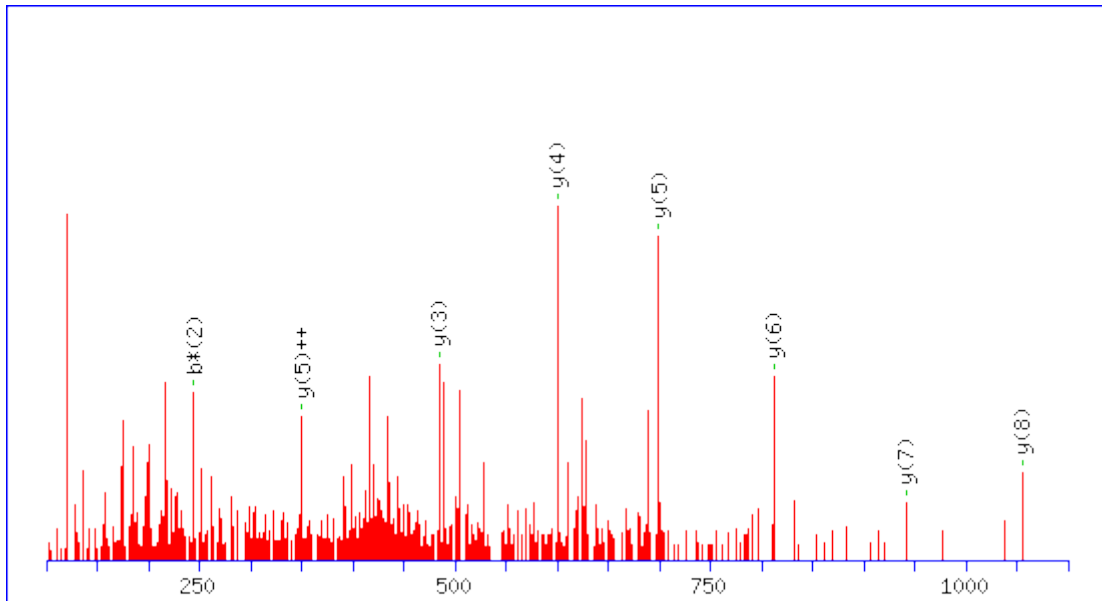
Monoisotopic mass of neutral peptide Mr(calc): 1460.8126

Ions Score: 42 Expect: 0.02

Matches (Bold Red): 13/118 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **FNSLNELVDFYR**

Found in **GRAP_HUMAN**, GRB2-related adapter protein OS=Homo sapiens GN=GRAP PE=1
SV=1



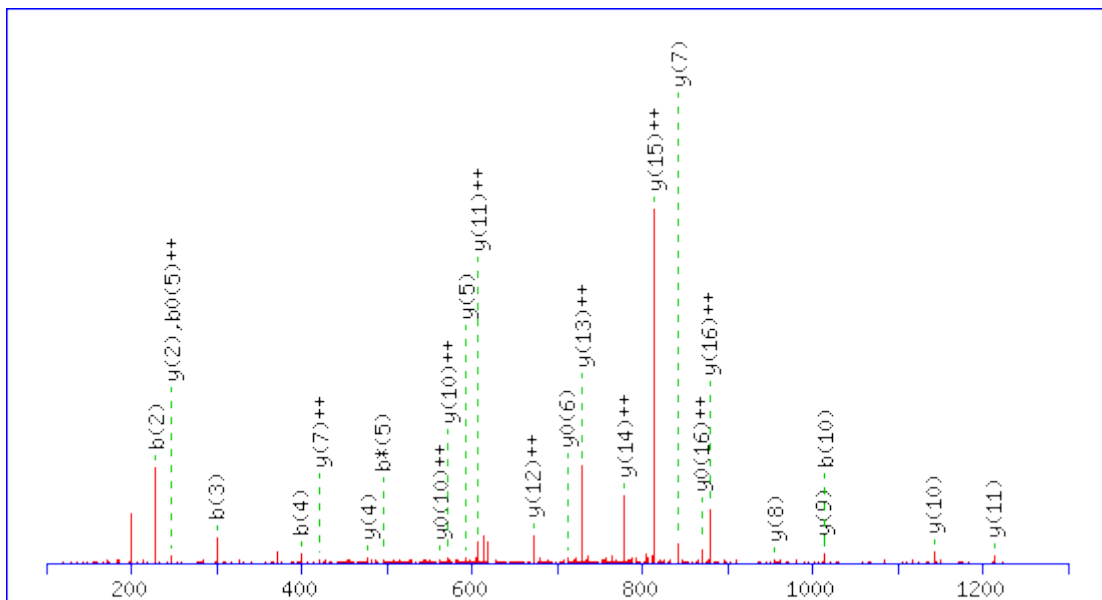
Monoisotopic mass of neutral peptide Mr(calc): 1515.7358

Ions Score: 37 Expect: 0.064

Matches (Bold Red): 8/120 fragment ions using 14 most intense peaks

MS/MS Fragmentation of **VEAVNMAEGIIHDTETK**

Found in **GRP75_HUMAN**, Stress-70 protein, mitochondrial OS=Homo sapiens
GN=HSPA9 PE=1 SV=2



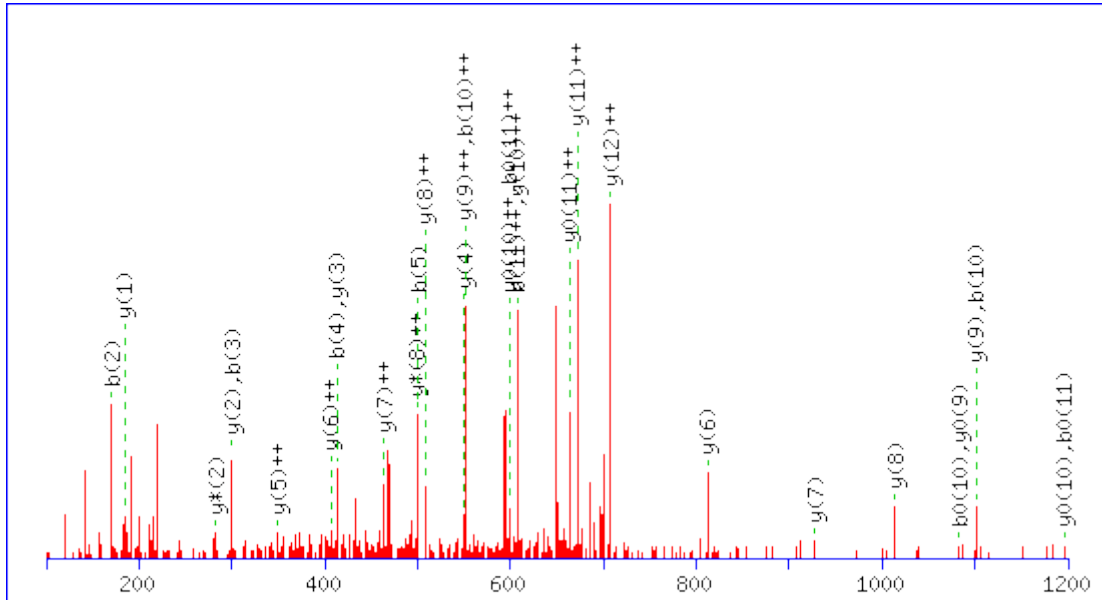
Monoisotopic mass of neutral peptide Mr(calc): 1855.8986

Ions Score: 60 Expect: 0.00038

Matches (**Bold Red**): 25/180 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **VAELSSDDFHLDR**

Found in **GSLG1_HUMAN**, Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1512.7084

Variable modifications:

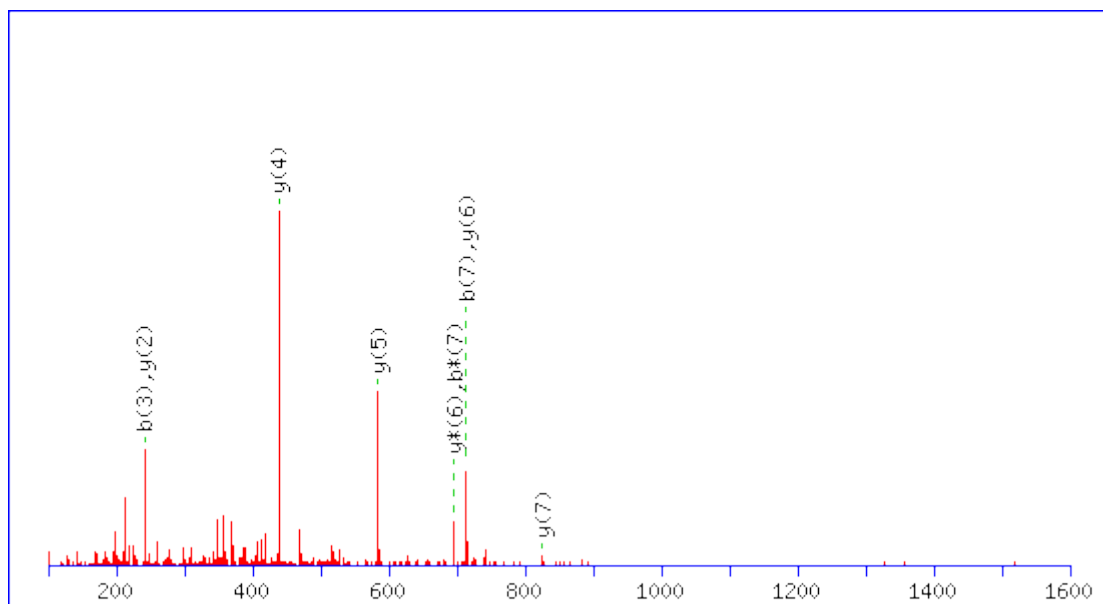
R13 : Label:13C(6)15N(4) (R)

Ions Score: 40 Expect: 0.025

Matches (**Bold Red**): 32/114 fragment ions using 67 most intense peaks

MS/MS Fragmentation of **AGLQFPVGR**

Found in **H2AJ_HUMAN**, Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 953.5322

Variable modifications:

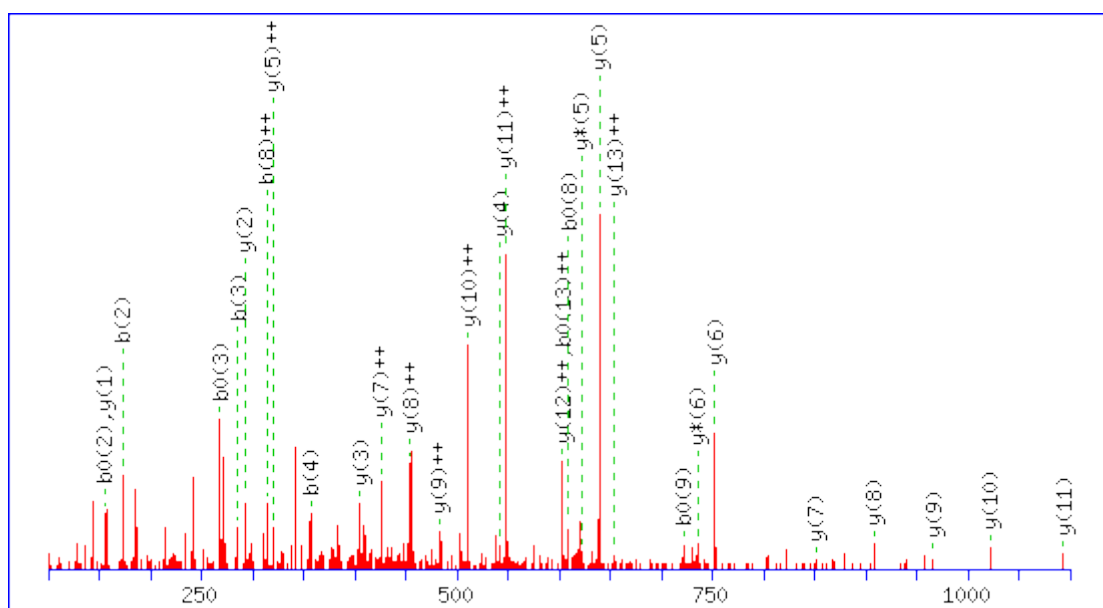
R9 : Label:13C(6)15N(4) (R)

Ions Score: 42 Expect: 0.014

Matches (Bold Red): 9/58 fragment ions using 12 most intense peaks

MS/MS Fragmentation of **ATIAGGGVIPHIHK**

Found in **H2AV_HUMAN**, Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1377.7972

Variable modifications:

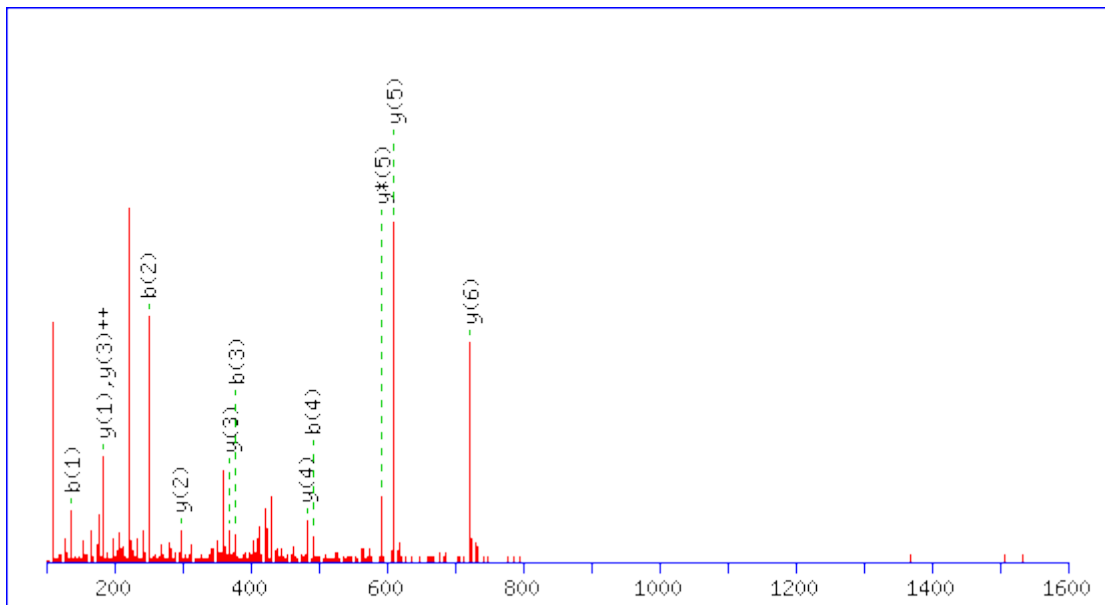
K14 : Label:13C(6)15N(2) (K)

Ions Score: 57 Expect: 0.00049

Matches (**Bold Red**): 30/104 fragment ions using 69 most intense peaks

MS/MS Fragmentation of **HLQLAIR**

Found in **H2AX_HUMAN**, Histone H2A.x OS=Homo sapiens GN=H2AFX PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 859.5267

Variable modifications:

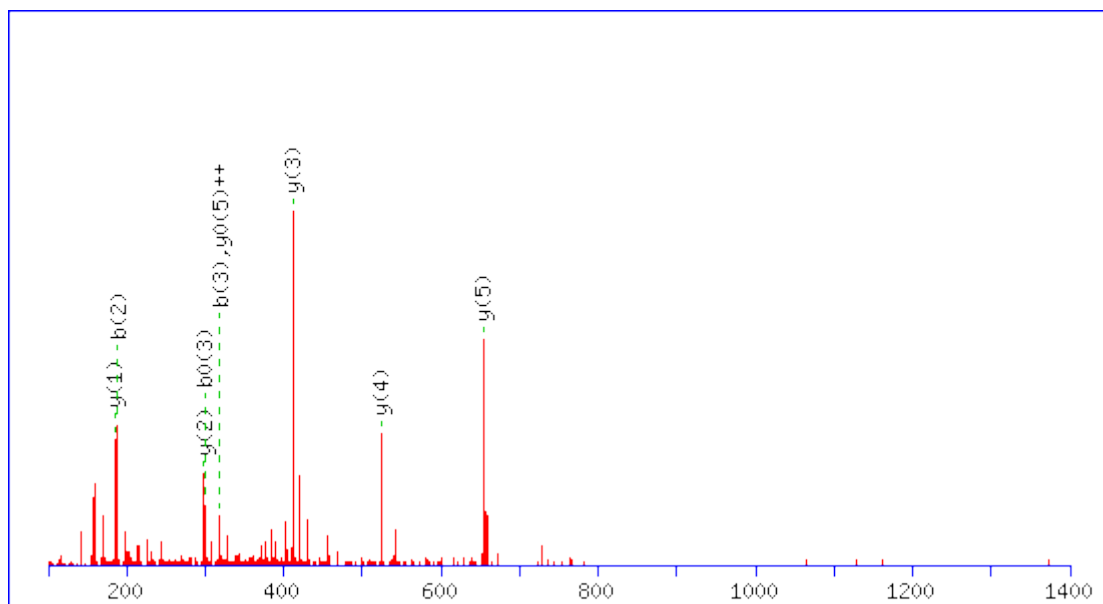
R7 : Label:13C(6)15N(4) (R)

Ions Score: 40 Expect: 0.013

Matches (**Bold Red**): 12/44 fragment ions using 24 most intense peaks

MS/MS Fragmentation of **STELLIR**

Found in **H3C_HUMAN**, Histone H3.3C OS=Homo sapiens GN=H3F3C PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 840.4944

Variable modifications:

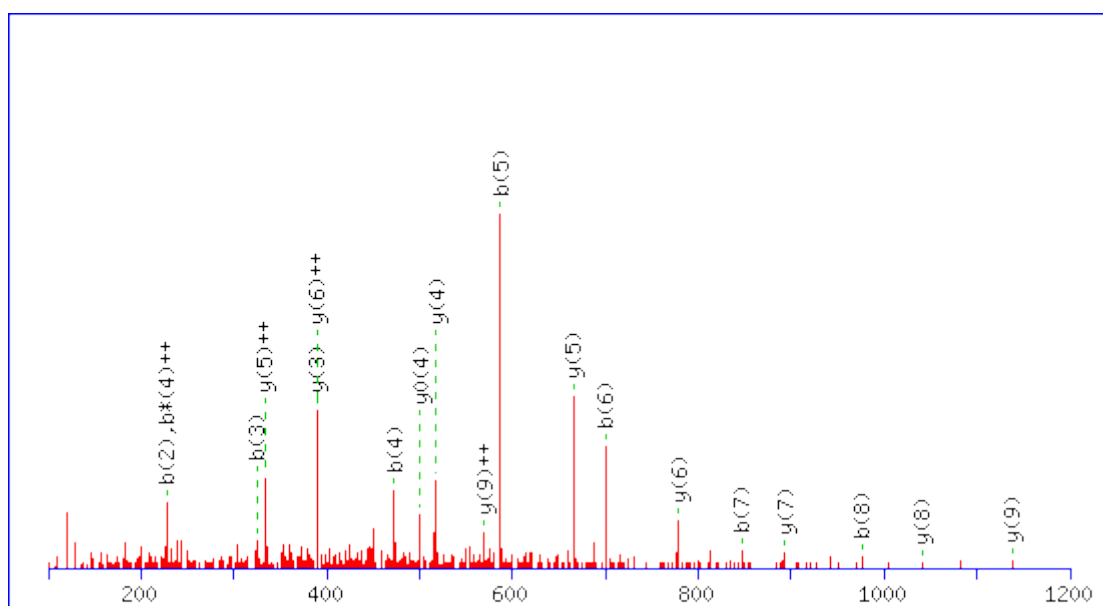
R7 : Label: $^{13}\text{C}(6)^{15}\text{N}(4)$ (R)

Ions Score: 38 Expect: 0.028

Matches (Bold Red): 9/52 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **RAPFDLFENKK**

Found in **H90B3_HUMAN**, Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens
GN=HSP90AB3P PE=5 SV=1



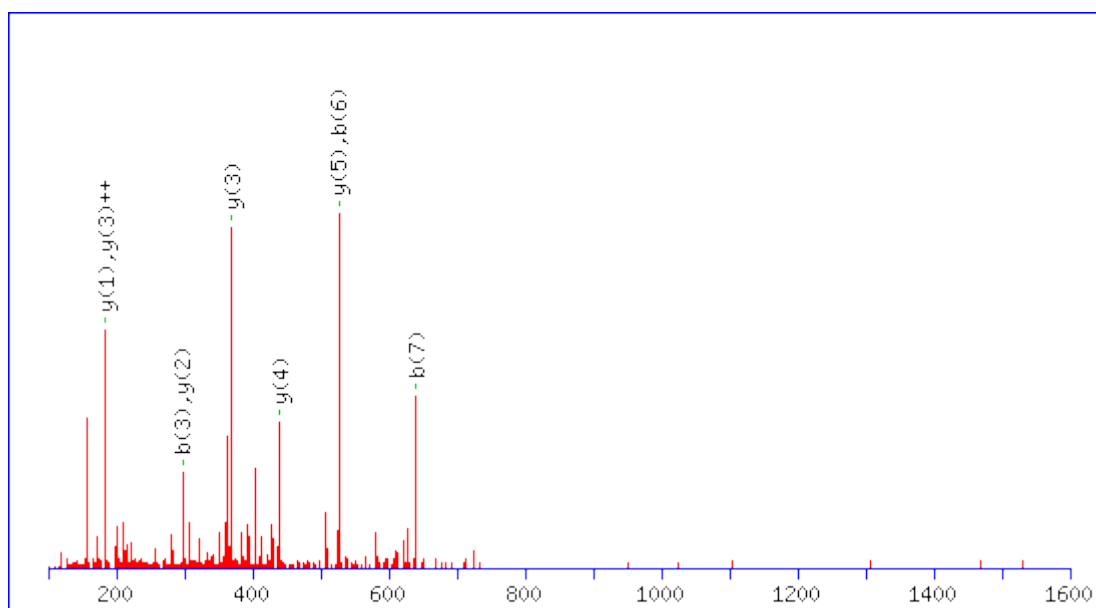
Monoisotopic mass of neutral peptide Mr(calc): 1363.7248

Ions Score: 40 Expect: 0.025

Matches (Bold Red): 19/106 fragment ions using 33 most intense peaks

MS/MS Fragmentation of **ISPSAALR**

Found in **HIPK4_HUMAN**, Homeodomain-interacting protein kinase 4 OS=Homo sapiens
GN=HIPK4 PE=2 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 823.4791

Variable modifications:

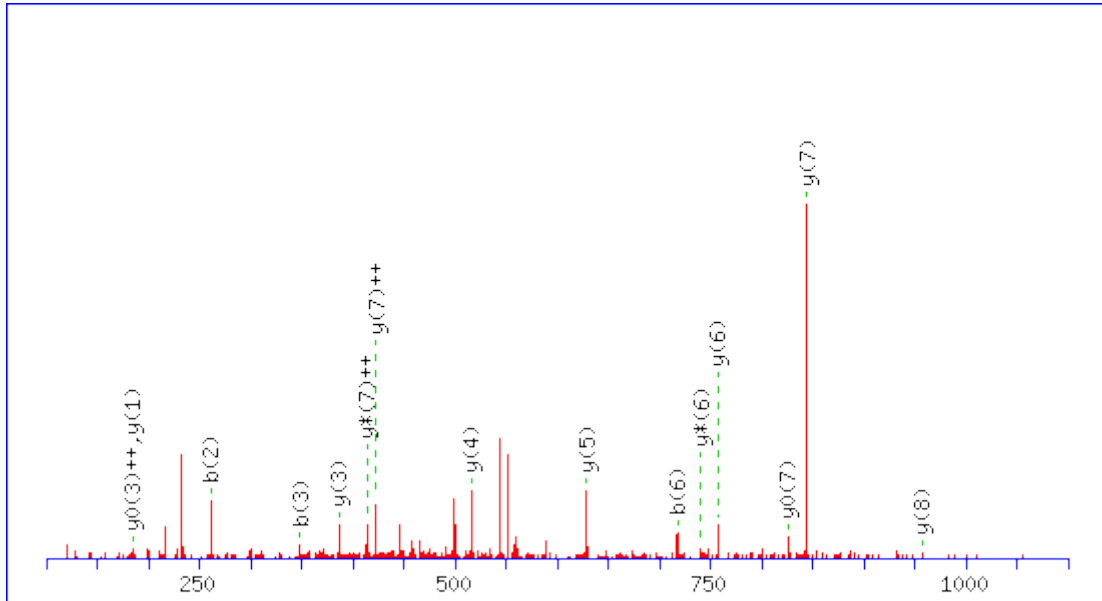
R8 : Label:13C(6)15N(4) (R)

Ions Score: 48 Expect: 0.0028

Matches (Bold Red): 9/60 fragment ions using 8 most intense peaks

MS/MS Fragmentation of **FLSQIESDR**

Found in **HKDC1_HUMAN**, Putative hexokinase HKDC1 OS=Homo sapiens GN=HKDC1 PE=2
SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1103.5486

Variable modifications:

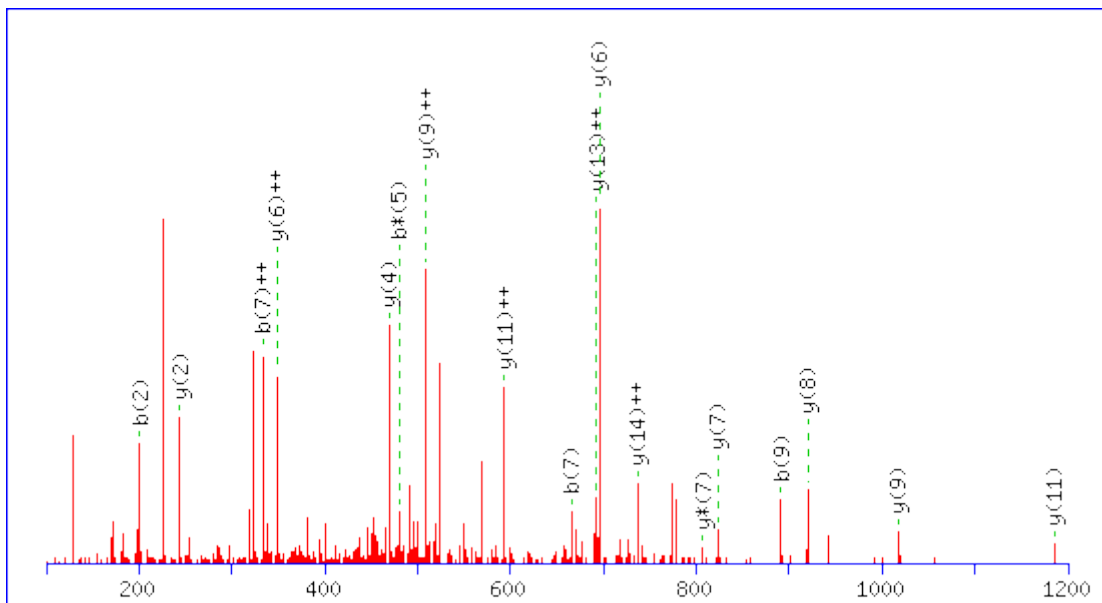
R9 : Label:13C(6)15N(4) (R)

Ions Score: 44 Expect: 0.0093

Matches (Bold Red): 15/84 fragment ions using 32 most intense peaks

MS/MS Fragmentation of **LSAKPAPPKPEPKPK**

Found in **HMGN2_HUMAN**, Non-histone chromosomal protein HMG-17 OS=Homo sapiens
GN=HMGN2 PE=1 SV=3



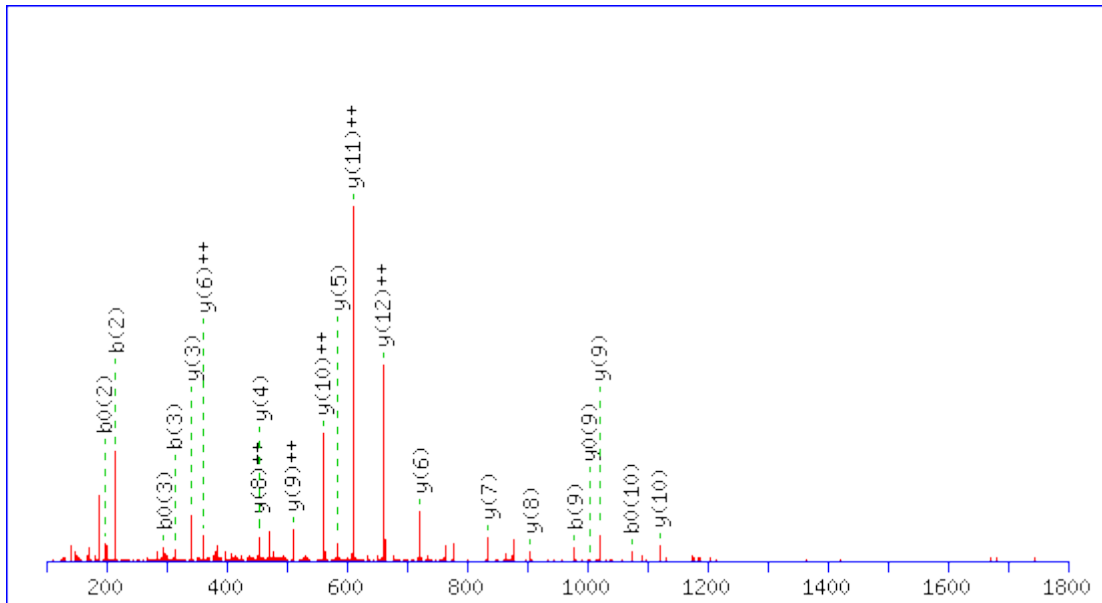
Monoisotopic mass of neutral peptide Mr(calc): 1583.9399

Ions Score: 40 Expect: 0.019

Matches (Bold Red): 18/152 fragment ions using 31 most intense peaks

MS/MS Fragmentation of **ITVVDALHEIPVK**

Found in **IBP7_HUMAN**, Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1



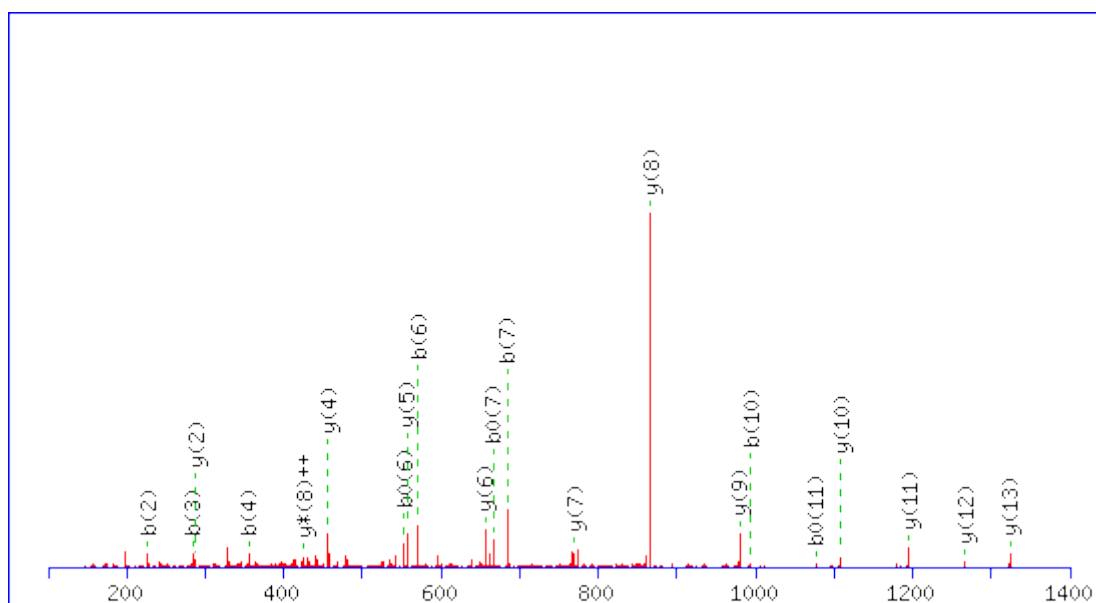
Monoisotopic mass of neutral peptide Mr(calc): 1432.8290

Ions Score: 45 Expect: 0.0089

Matches (Bold Red): 21/110 fragment ions using 50 most intense peaks

MS/MS Fragmentation of **LLGASELPITPALR**

Found in **IMA2_HUMAN**, Importin subunit alpha-2 OS=Homo sapiens GN=KPNA2 PE=1 SV=1



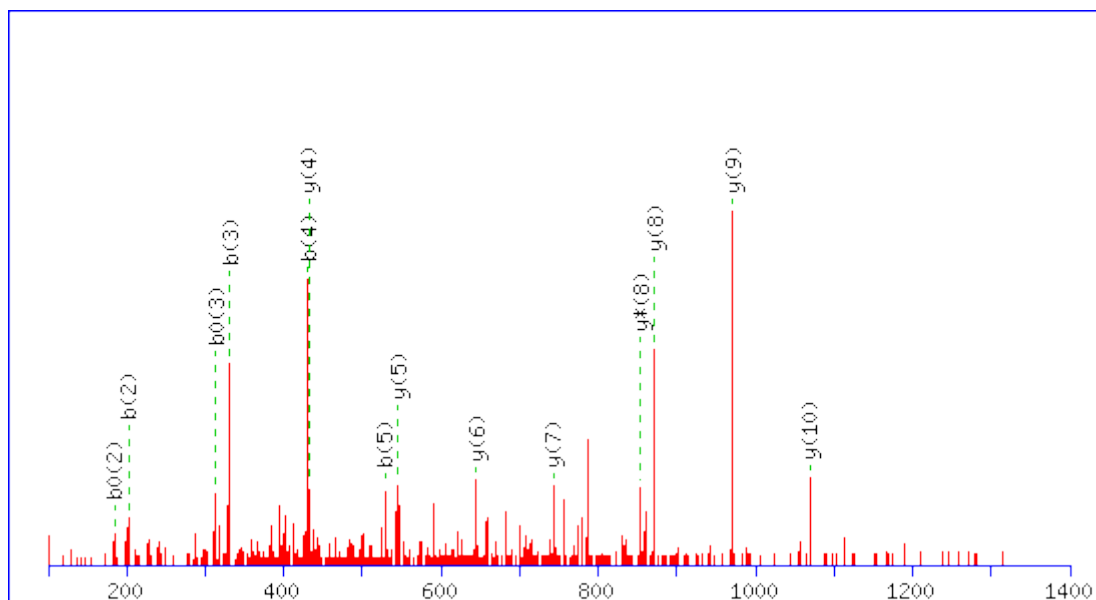
Monoisotopic mass of neutral peptide Mr(calc): 1548.9239

Ions Score: 82 Expect: 1.2e-006

Matches (Bold Red): 21/124 fragment ions using 36 most intense peaks

MS/MS Fragmentation of **DSQVVQVLDGLK**

Found in **IMA3_HUMAN**, Importin subunit alpha-3 OS=Homo sapiens GN=KPNA3 PE=1 SV=2



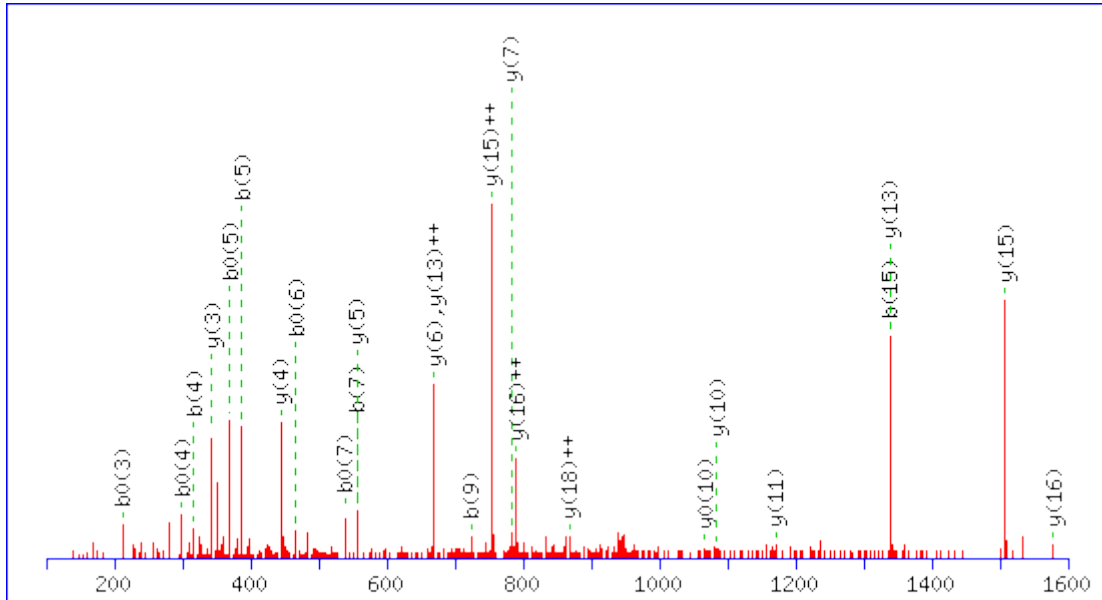
Monoisotopic mass of neutral peptide Mr(calc): 1398.7719

Ions Score: 44 Expect: 0.011

Matches (**Bold Red**): 14/134 fragment ions using 25 most intense peaks

MS/MS Fragmentation of **ASASAPAPASATEILLTPAR**

Found in **ITM2C_HUMAN**, Integral membrane protein 2C OS=Homo sapiens GN=ITM2C
PE=1 SV=1



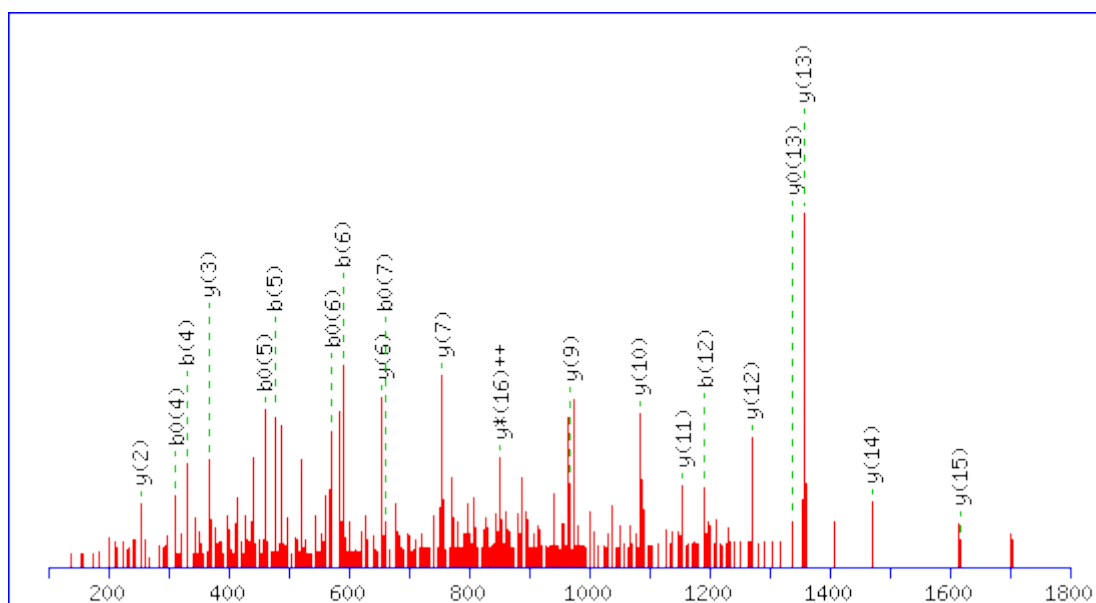
Monoisotopic mass of neutral peptide Mr(calc): 1894.0159

Ions Score: 58 Expect: 0.00051

Matches (**Bold Red**): 25/182 fragment ions using 48 most intense peaks

MS/MS Fragmentation of **DGGTFISDADDVVSAMIVK**

Found in **IWS1_HUMAN**, Protein IWS1 homolog OS=Homo sapiens GN=IWS1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1946.9387

Variable modifications:

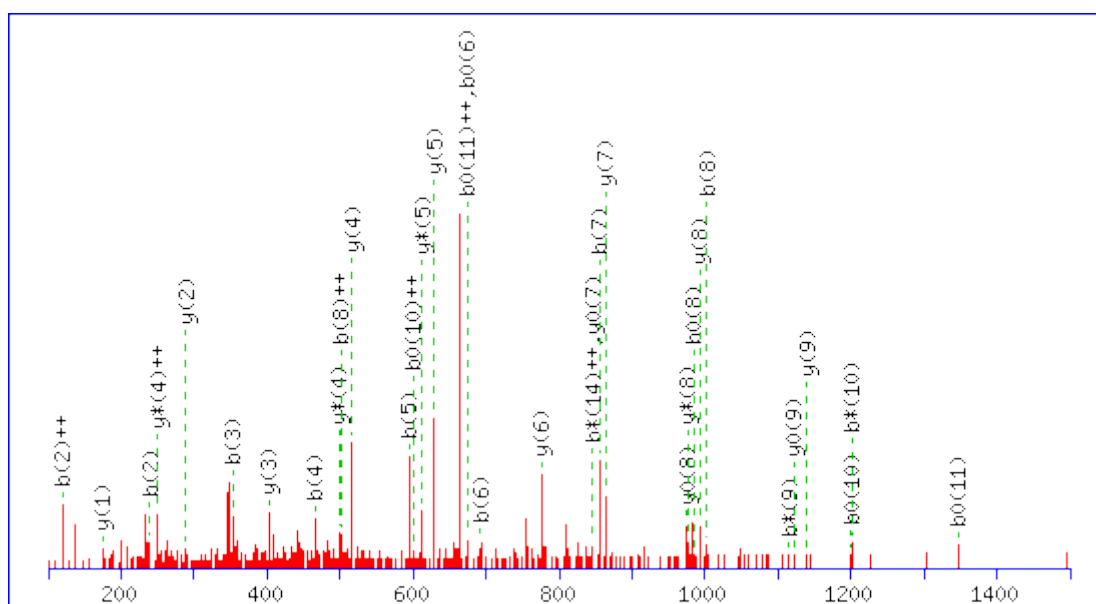
K19 : Label:13C(6)15N(2) (K)

Ions Score: 57 **Expect: 0.00079**

Matches (Bold Red): 21/170 fragment ions using 51 most intense peaks

MS/MS Fragmentation of **THNLEPYFESFINNLR**

Found in **K2C1_HUMAN**, Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1
PE=1 SV=6



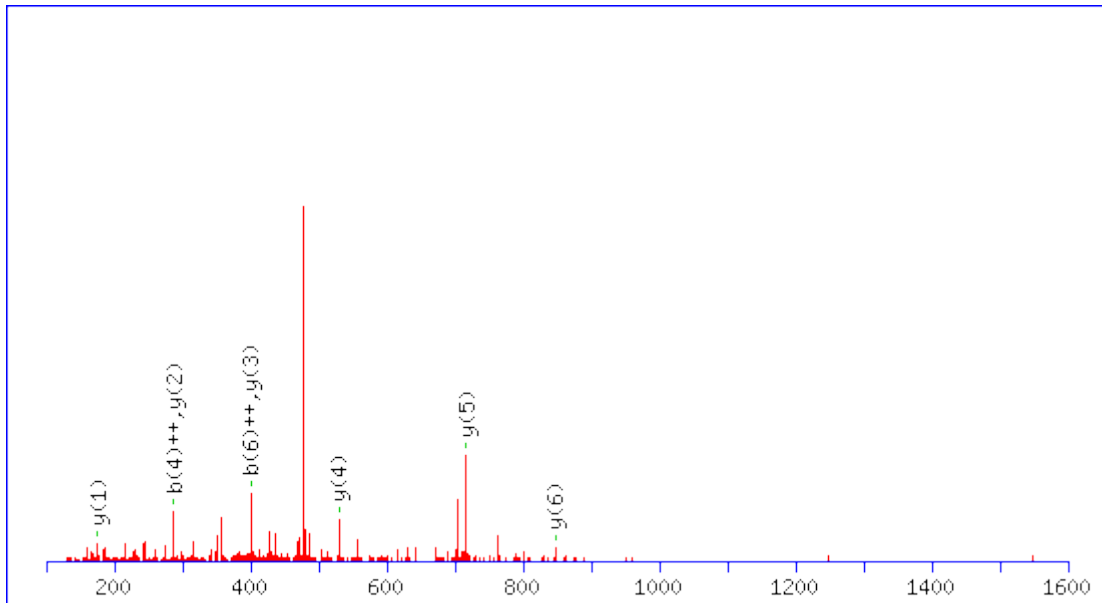
Monoisotopic mass of neutral peptide Mr(calc): 1992.9693

Ions Score: 41 Expect: 0.027

Matches (Bold Red): 34/164 fragment ions using 81 most intense peaks

MS/MS Fragmentation of **QMWEILR**

Found in **K0020_HUMAN**, Pumilio domain-containing protein KIAA0020 OS=Homo sapiens GN=KIAA0020 PE=1 SV=3



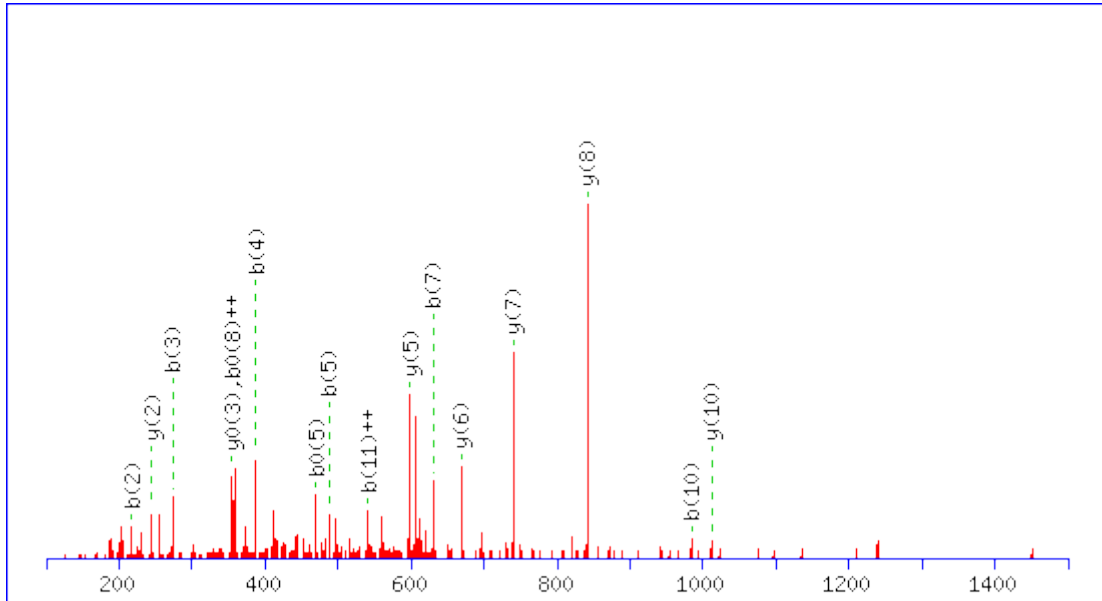
Monoisotopic mass of neutral peptide Mr(calc): 974.5007

Ions Score: 55 Expect: 0.00069

Matches (Bold Red): 8/60 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **DTGLTAAPQEPK**

Found in **K1211_HUMAN**, Uncharacterized protein KIAA1211 OS=Homo sapiens GN=KIAA1211 PE=1 SV=3



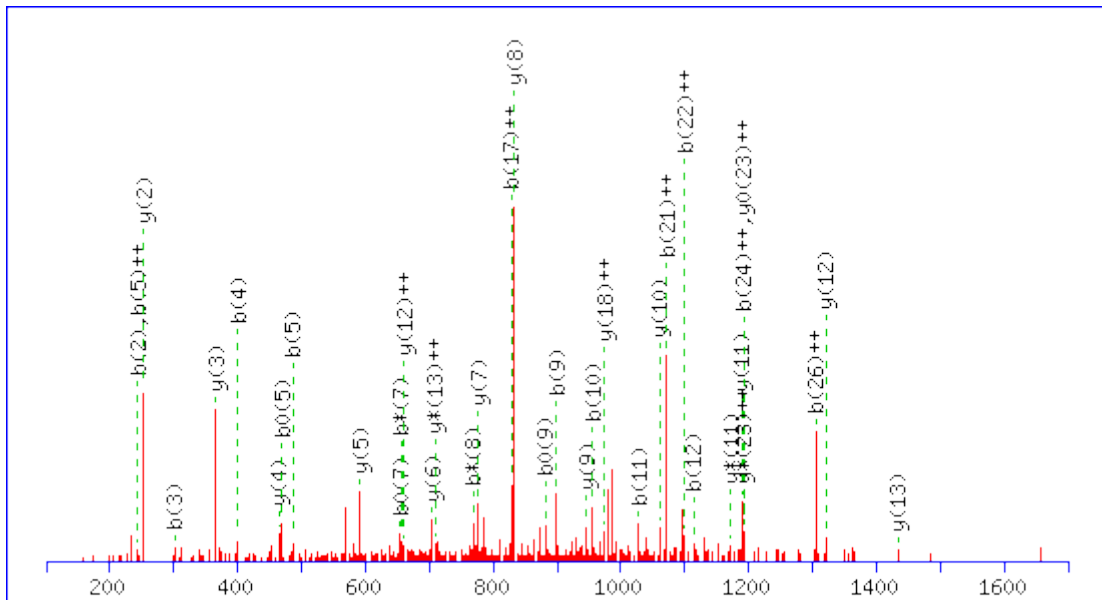
Monoisotopic mass of neutral peptide Mr(calc): 1226.6143

Ions Score: 43 Expect: 0.012

Matches (**Bold Red**): 17/112 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **NEGVSSVLLGASNADQLMENIGAIQVLPK**

Found in **KCAB2_HUMAN**, Voltage-gated potassium channel subunit beta-2 OS=Homo sapiens GN=KCNA2 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 2974.5525

Variable modifications:

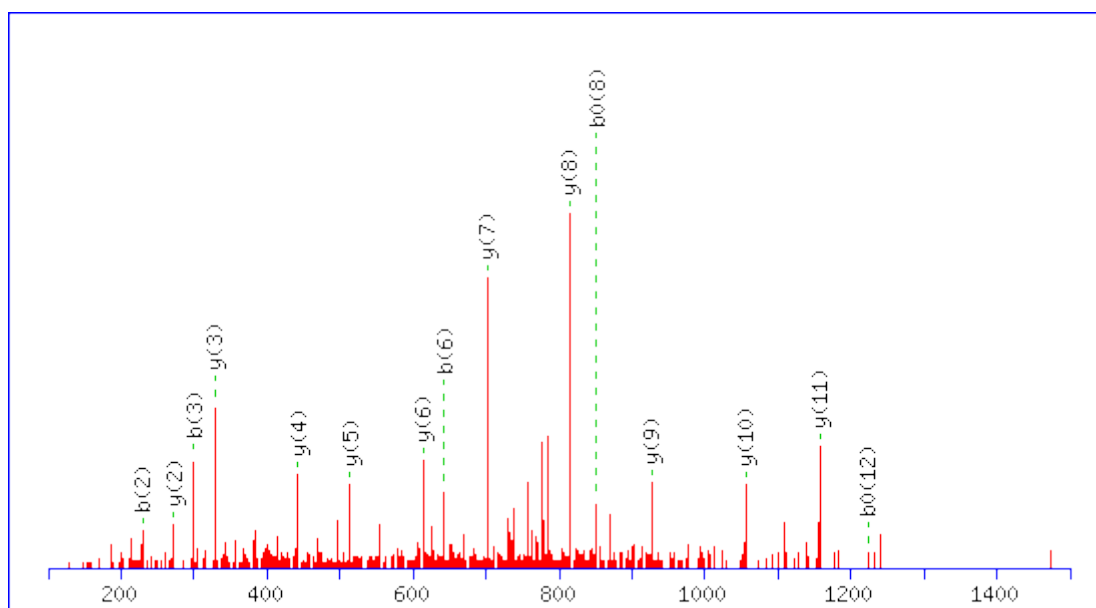
K29 : Label:13C(6)15N(2) (K)

Ions Score: 80 **Expect:** 4.6e-006

Matches (Bold Red): 37/314 fragment ions using 62 most intense peaks

MS/MS Fragmentation of **LDALTELLSTALGPR**

Found in **KCNN4_HUMAN**, Intermediate conductance calcium-activated potassium channel protein 4 OS=Homo sapiens GN=KCNN4 PE=1 SV=1



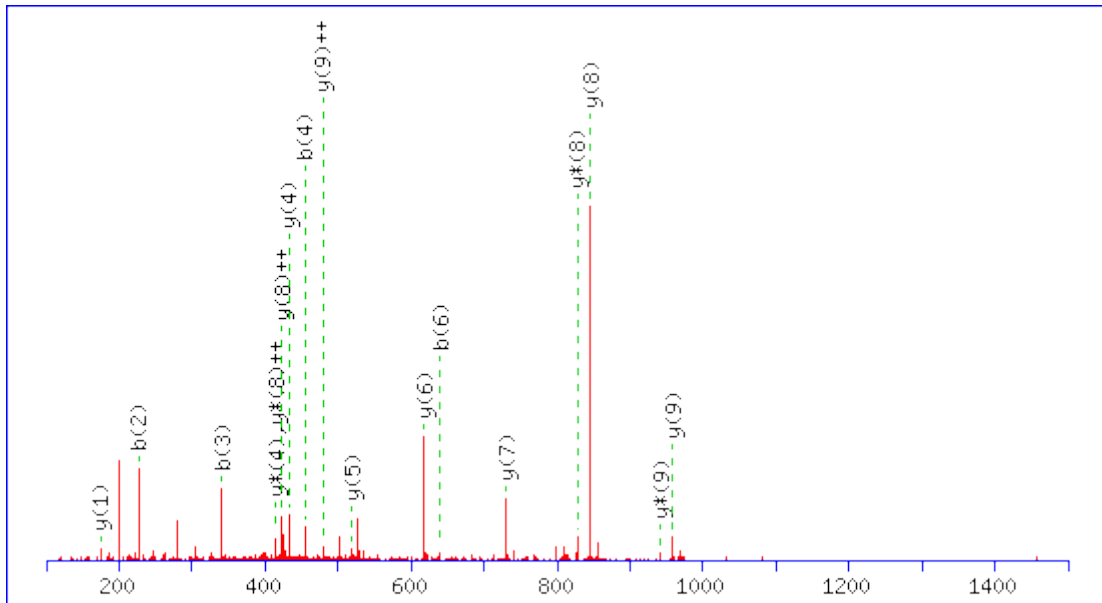
Monoisotopic mass of neutral peptide Mr(calc): 1568.8774

Ions Score: 67 **Expect:** 4.9e-005

Matches (Bold Red): 15/128 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **LLNIVSVTGR**

Found in **KDIS_HUMAN**, Kinase D-interacting substrate of 220 kDa OS=Homo sapiens GN=KIDINS220 PE=1 SV=3



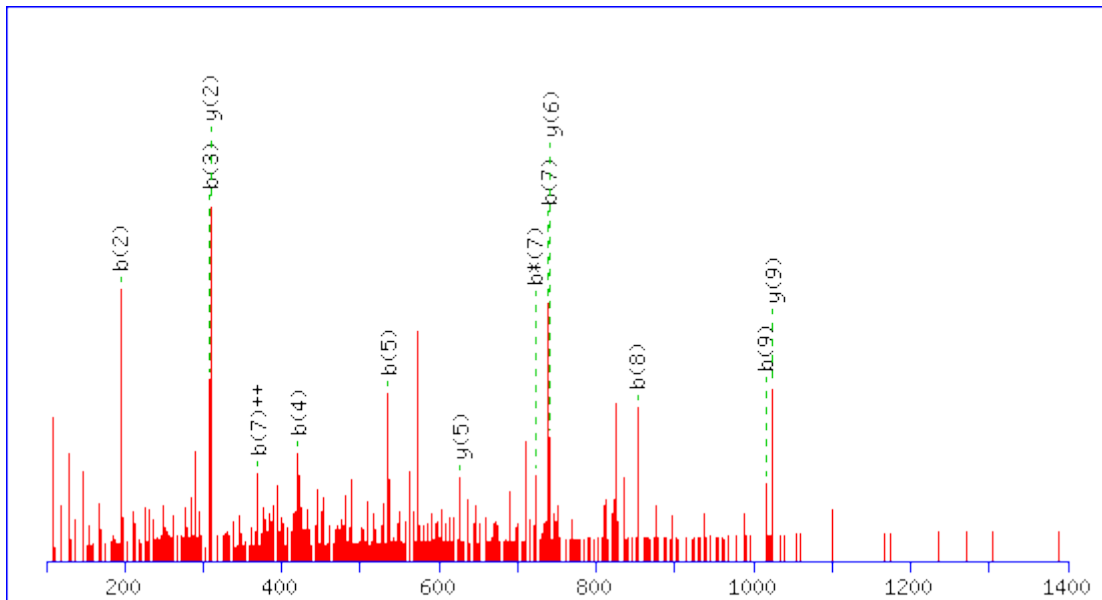
Monoisotopic mass of neutral peptide Mr(calc): 1070.6448

Ions Score: 46 Expect: 0.005

Matches (Bold Red): 17/90 fragment ions using 33 most intense peaks

MS/MS Fragmentation of **HGLINFGIYK**

Found in **KDM1A_HUMAN**, Lysine-specific histone demethylase 1A OS=Homo sapiens
GN=KDM1A PE=1 SV=2



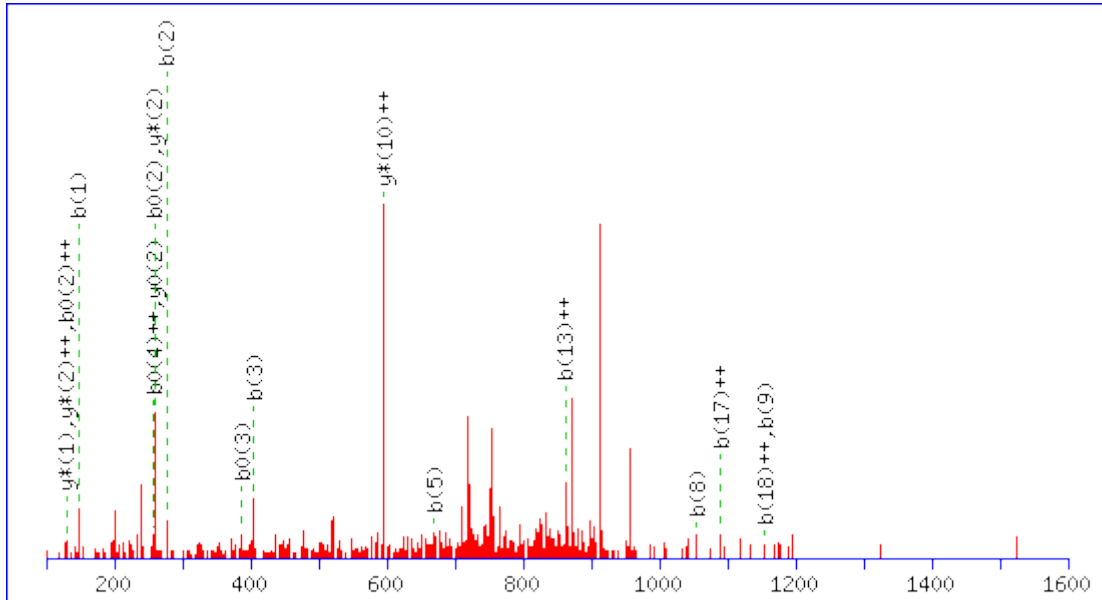
Monoisotopic mass of neutral peptide Mr(calc): 1160.6342

Ions Score: 46 Expect: 0.0066

Matches (Bold Red): 13/64 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **MEQQHQEKVLYLVSQLQESQMAEK**

Found in **KIF4B_HUMAN**, Chromosome-associated kinesin KIF4B OS=Homo sapiens
GN=KIF4B PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 3015.3718

Variable modifications:

M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Y11 : Phospho (Y)

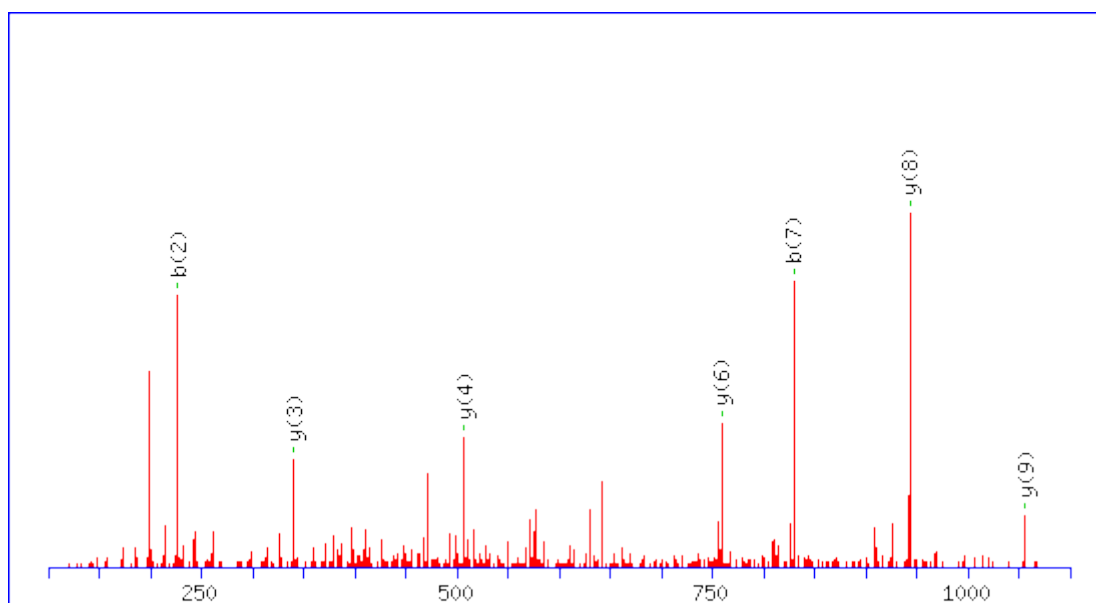
M21 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 4 **Expect:** 1.8e+002

Matches (Bold Red): 18/520 fragment ions using 50 most intense peaks

MS/MS Fragmentation of **LIALTASANK**

Found in **KNTC1_HUMAN**, Kinetochore-associated protein 1 OS=Homo sapiens
GN=KNTC1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1168.5385

Variable modifications:

T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

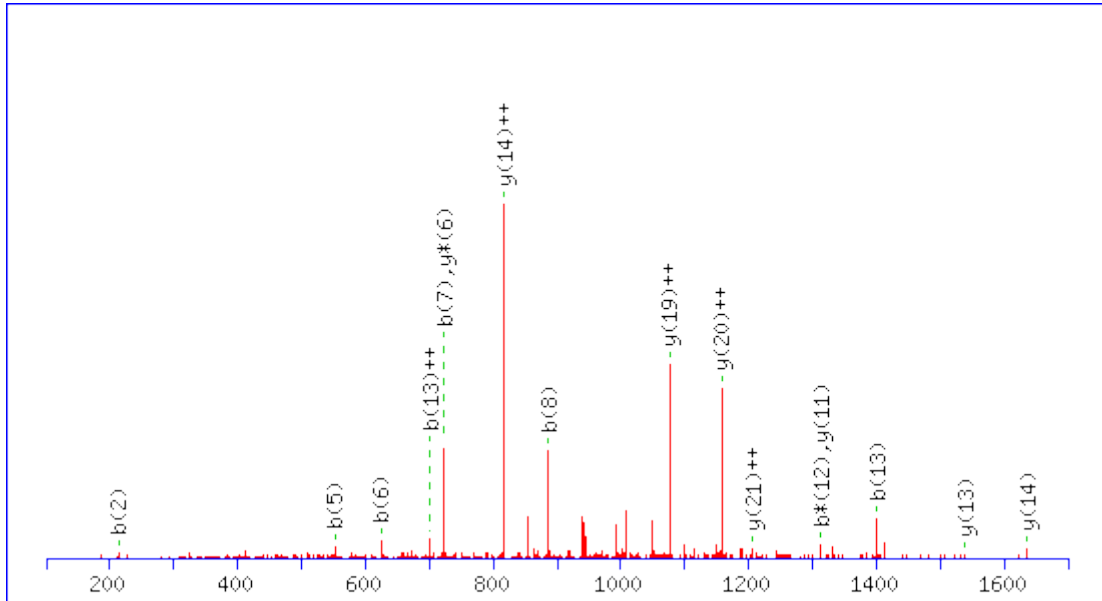
K10 : Label:13C(6)15N(2) (K)

Ions Score: 39 Expect: 0.027

Matches (Bold Red): 7/136 fragment ions using 10 most intense peaks

MS/MS Fragmentation of **NVPEIAVYPAFEAPPQYVLPTYEMAVK**

Found in **LAP4A_HUMAN**, Lysosomal-associated transmembrane protein 4A OS=Homo sapiens GN=LAPTM4A PE=1 SV=1



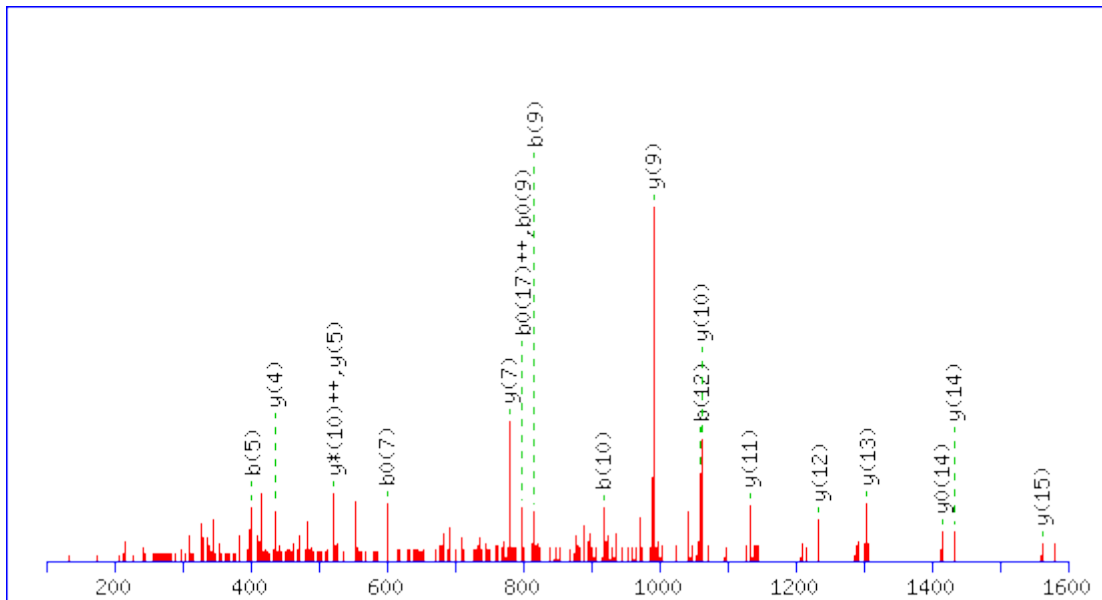
Monoisotopic mass of neutral peptide Mr(calc): 3035.5354

Ions Score: 42 Expect: 0.029

Matches (Bold Red): 16/298 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **DSGAASEQATAAPNPCSSSR**

Found in **LMF2_HUMAN**, Lipase maturation factor 2 OS=Homo sapiens GN=LMF2 PE=1 SV=2



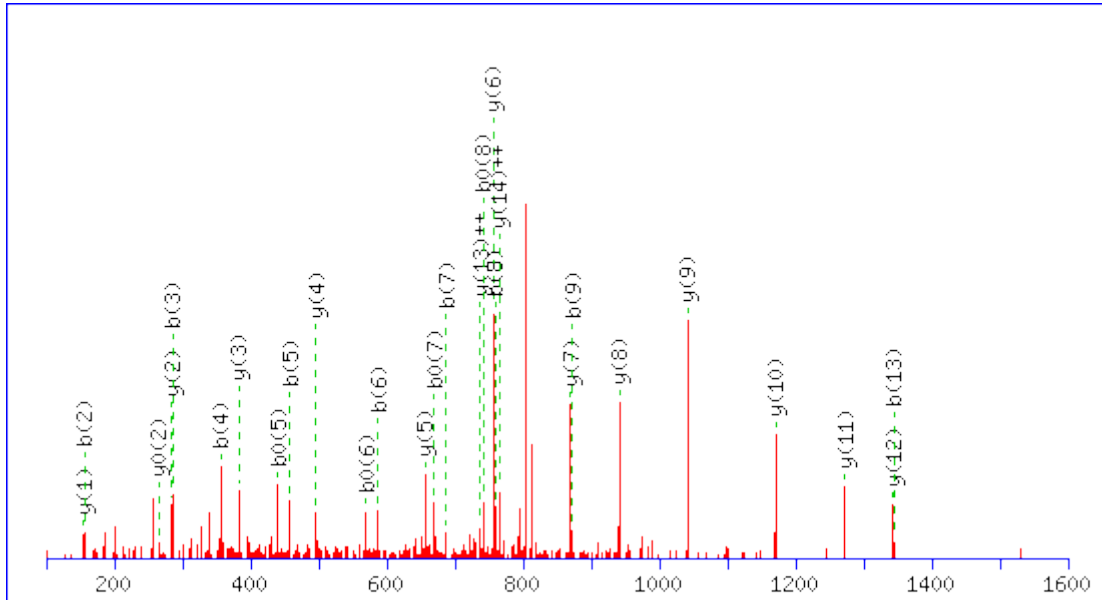
Monoisotopic mass of neutral peptide Mr(calc): 2049.8658

Ions Score: 58 Expect: 0.00053

Matches (Bold Red): 19/224 fragment ions using 32 most intense peaks

MS/MS Fragmentation of **VGEATETALTCLVEK**

Found in **AT2A3_HUMAN**, Sarcoplasmic/endoplasmic reticulum calcium ATPase 3
OS=Homo sapiens GN=ATP2A3 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1627.8218

Variable modifications:

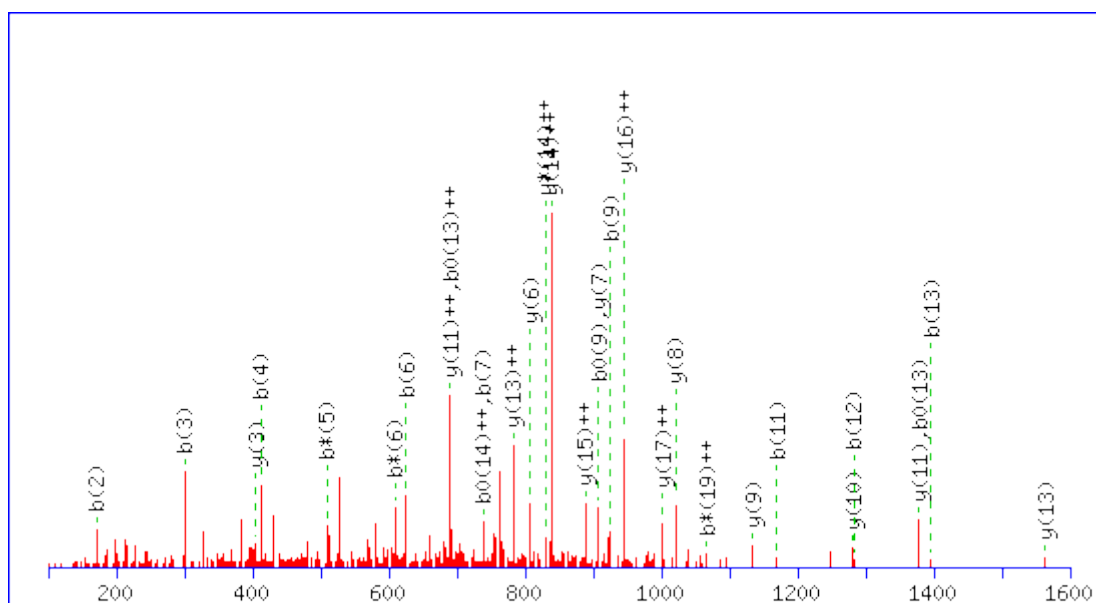
K15 : Label:13C(6)15N(2) (K)

Ions Score: 83 **Expect:** 1.6e-006

Matches (Bold Red): 28/134 fragment ions using 54 most intense peaks

MS/MS Fragmentation of **LGEINVIGEPFLNVNCEHIK**

Found in **MCM4_HUMAN**, DNA replication licensing factor MCM4 OS=Homo sapiens
GN=MCM4 PE=1 SV=5



Monoisotopic mass of neutral peptide Mr(calc): 2302.1871

Variable modifications:

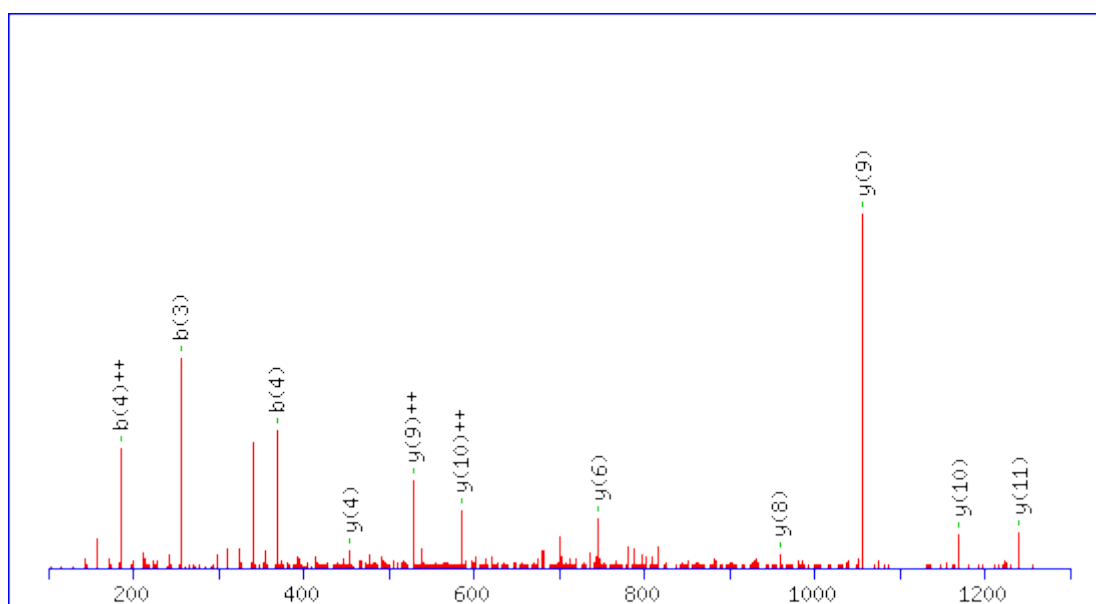
K20 : Label:13C(6)15N(2) (K)

Ions Score: 53 Expect: 0.002

Matches (Bold Red): 31/210 fragment ions using 49 most intense peaks

MS/MS Fragmentation of **LAALPNVYEISK**

Found in **MCM5_HUMAN**, DNA replication licensing factor MCM5 OS=Homo sapiens
GN=MCM5 PE=1 SV=5



Monoisotopic mass of neutral peptide Mr(calc): 1423.8166

Variable modifications:

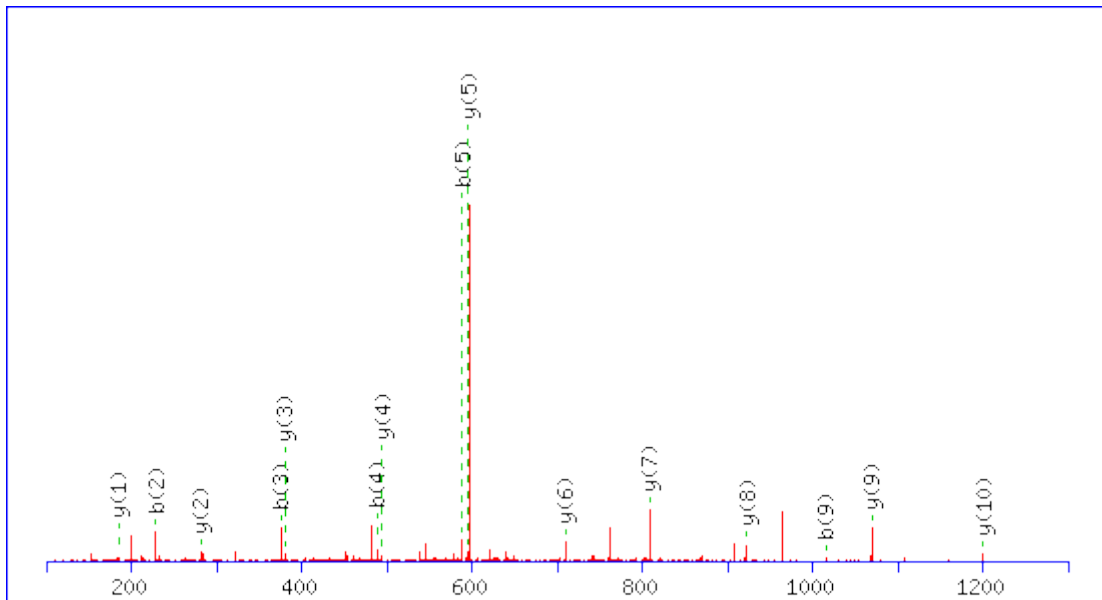
K13 : Label:13C(6)15N(2) (K)

Ions Score: 46 Expect: 0.0054

Matches (Bold Red): 12/116 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **PMFIVNTNVPR**

Found in **MIF_HUMAN**, Macrophage migration inhibitory factor OS=Homo sapiens
GN=MIF PE=1 SV=4



Monoisotopic mass of neutral peptide Mr(calc): 1296.6888

Variable modifications:

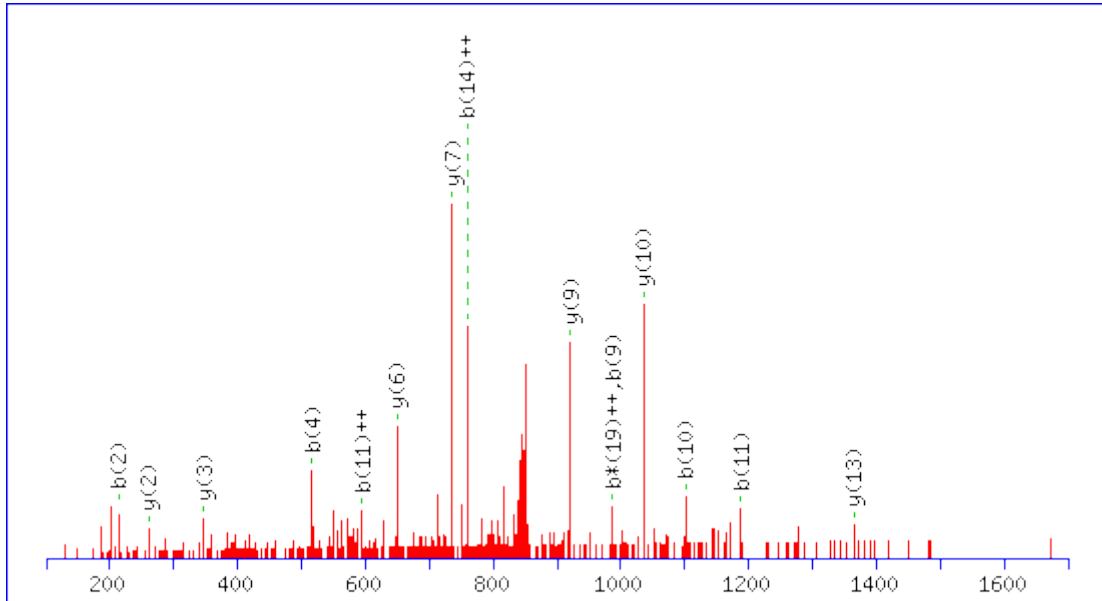
R11 : Label:13C(6)15N(4) (R)

Ions Score: 42 Expect: 0.017

Matches (Bold Red): 15/90 fragment ions using 62 most intense peaks

MS/MS Fragmentation of **VLFRPSDTANSSNQDALSSNTSLK**

Found in **MMGT1_HUMAN**, Membrane magnesium transporter 1 OS=Homo sapiens GN=MMGT1
PE=1 SV=1



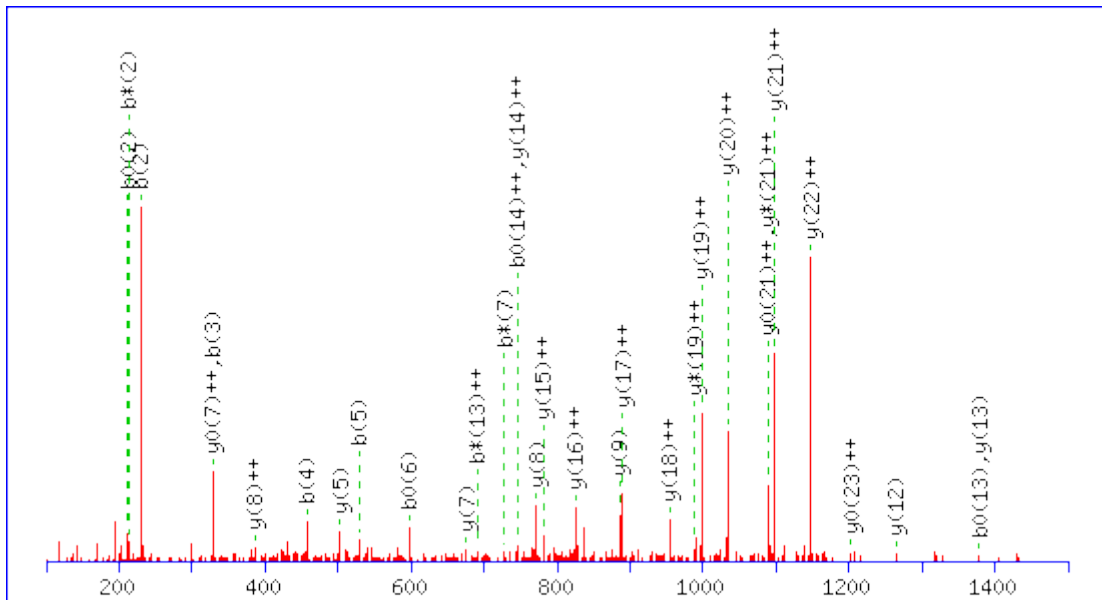
Monoisotopic mass of neutral peptide Mr(calc): 2551.2514

Ions Score: 40 Expect: 0.041

Matches (Bold Red): 15/256 fragment ions using 18 most intense peaks

MS/MS Fragmentation of **TQVEASEESALNHLQNPGDAAEGR**

Found in **MOFA1_HUMAN**, MORF4 family-associated protein 1 OS=Homo sapiens
GN=MRFAP1 PE=1 SV=1



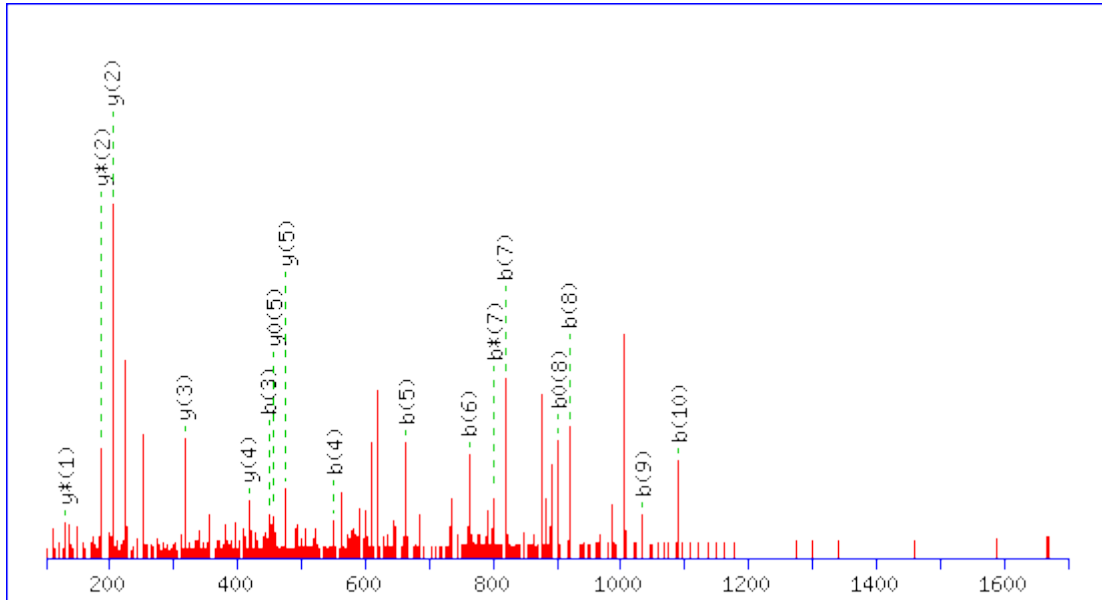
Monoisotopic mass of neutral peptide Mr(calc): 2522.1633

Ions Score: 68 Expect: 6.8e-005

Matches (**Bold Red**): 32/270 fragment ions using 47 most intense peaks

MS/MS Fragmentation of **RYETLVGTIGK**

Found in **MPH6_HUMAN**, M-phase phosphoprotein 6 OS=Homo sapiens GN=MPHOSPH6 PE=1 SV=2



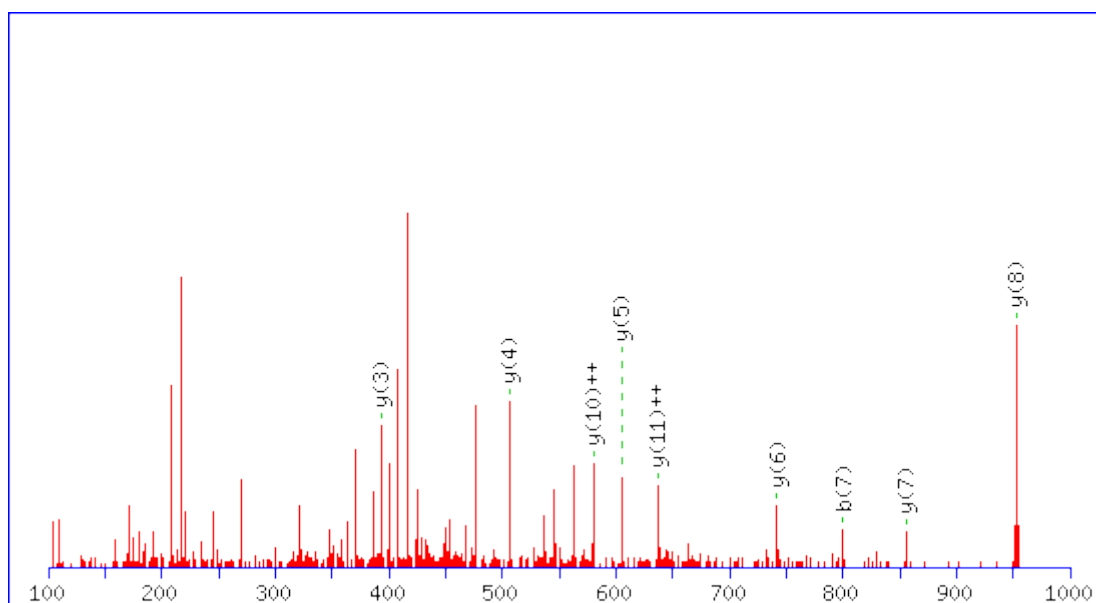
Monoisotopic mass of neutral peptide Mr(calc): 1235.6874

Ions Score: 39 Expect: 0.032

Matches (**Bold Red**): 17/110 fragment ions using 51 most intense peaks

MS/MS Fragmentation of **MLAHPLHVISM R**

Found in **MTCH1_HUMAN**, Mitochondrial carrier homolog 1 OS=Homo sapiens GN=MTCH1 PE=1 SV=1



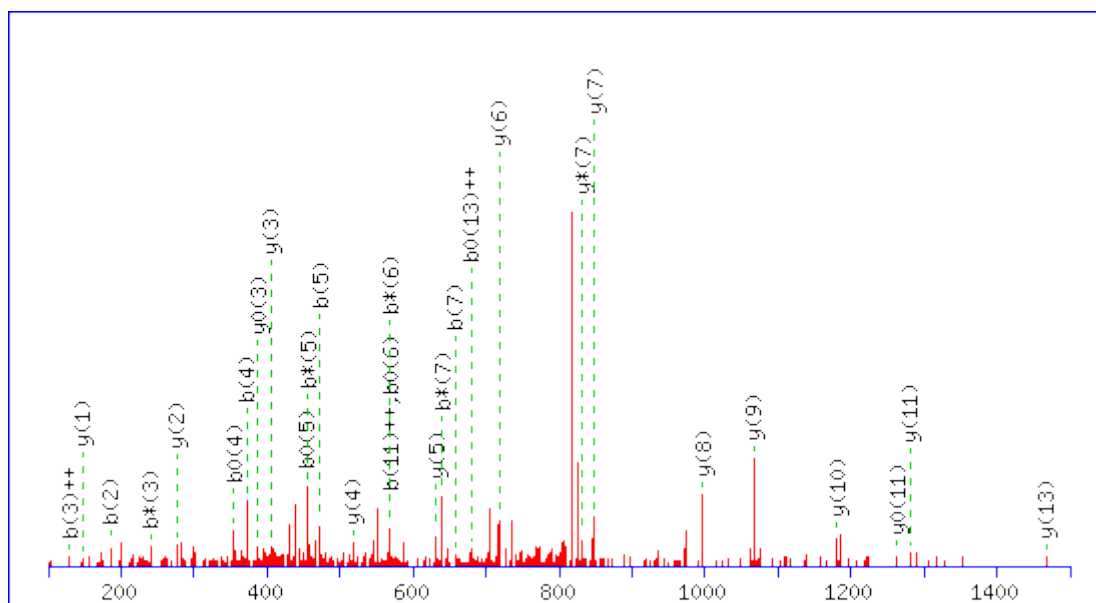
Monoisotopic mass of neutral peptide Mr(calc): 1403.7530

Ions Score: 41 Expect: 0.026

Matches (Bold Red): 9/88 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **QGADTLAFMSLLEEK**

Found in **MTX1_HUMAN**, Metaxin-1 OS=Homo sapiens GN=MTX1 PE=1 SV=2



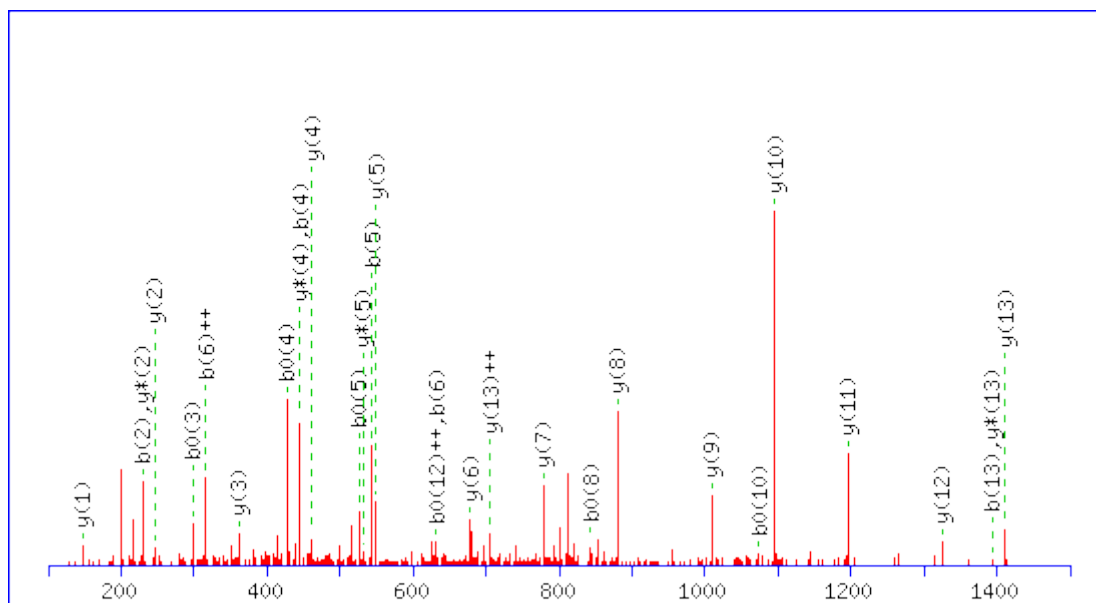
Monoisotopic mass of neutral peptide Mr(calc): 1651.8127

Ions Score: 48 Expect: 0.0049

Matches (**Bold Red**): 30/160 fragment ions using 84 most intense peaks

MS/MS Fragmentation of **DLSEVSETTESTDVK**

Found in **NAA10_HUMAN**, N-alpha-acetyltransferase 10, NatA catalytic subunit
OS=Homo sapiens GN=NAA10 PE=1 SV=1



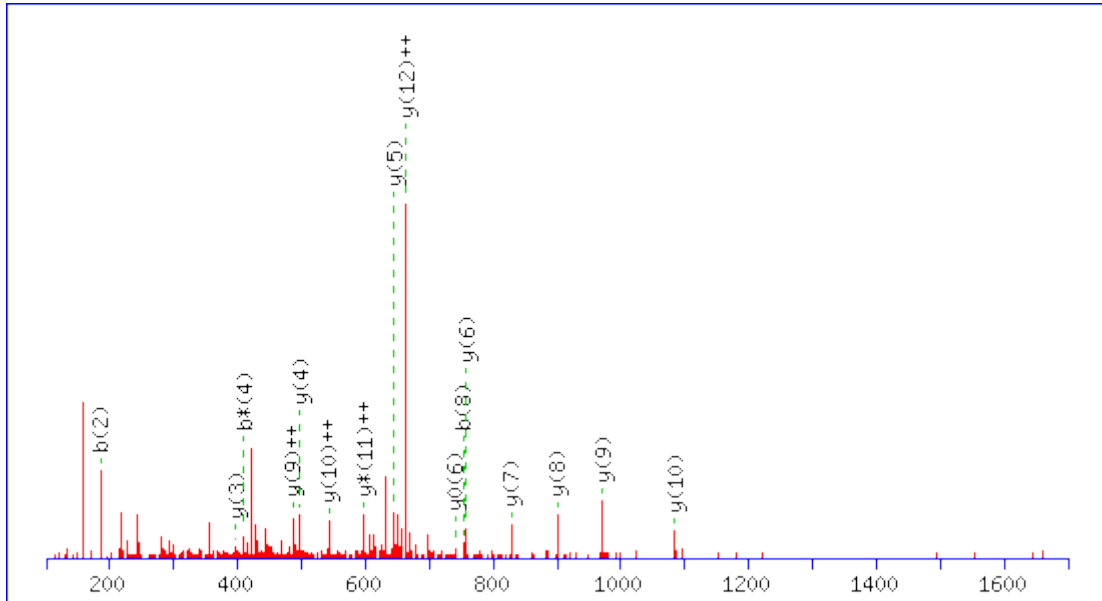
Monoisotopic mass of neutral peptide Mr(calc): 1638.7472

Ions Score: 96 Expect: 8.1e-008

Matches (**Bold Red**): 31/136 fragment ions using 54 most intense peaks

MS/MS Fragmentation of **AINQIAAALFTIHK**

Found in **NCKP1_HUMAN**, Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1
SV=1



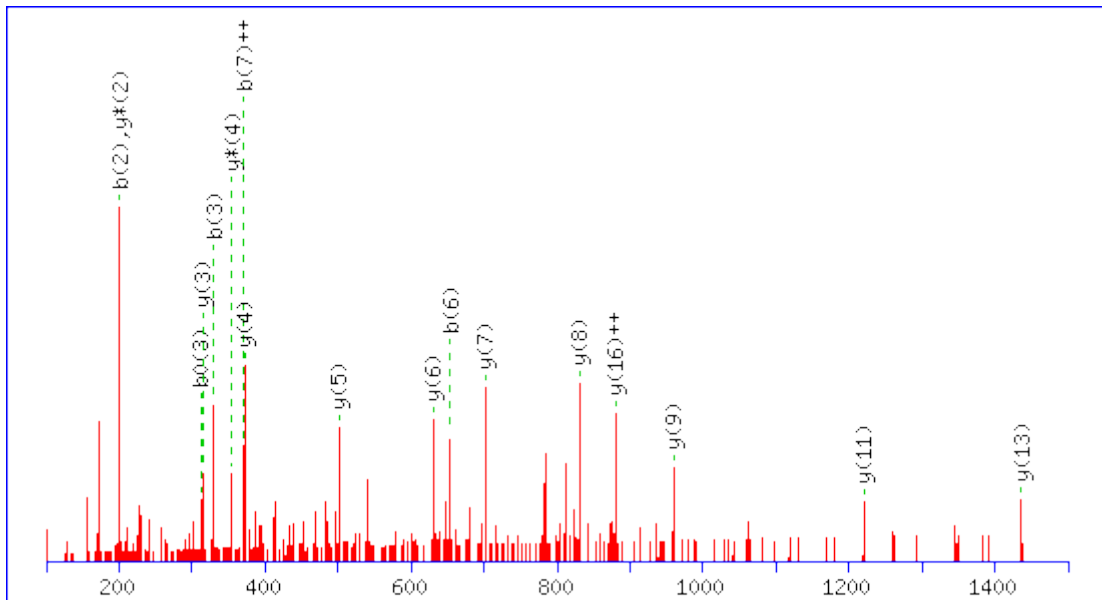
Monoisotopic mass of neutral peptide Mr(calc): 1509.8667

Ions Score: 42 Expect: 0.02

Matches (Bold Red): 16/126 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **AEEPVKSECTEEAEEGPAK**

Found in **NCOR2_HUMAN**, Nuclear receptor corepressor 2 OS=Homo sapiens GN=NCOR2
PE=1 SV=2



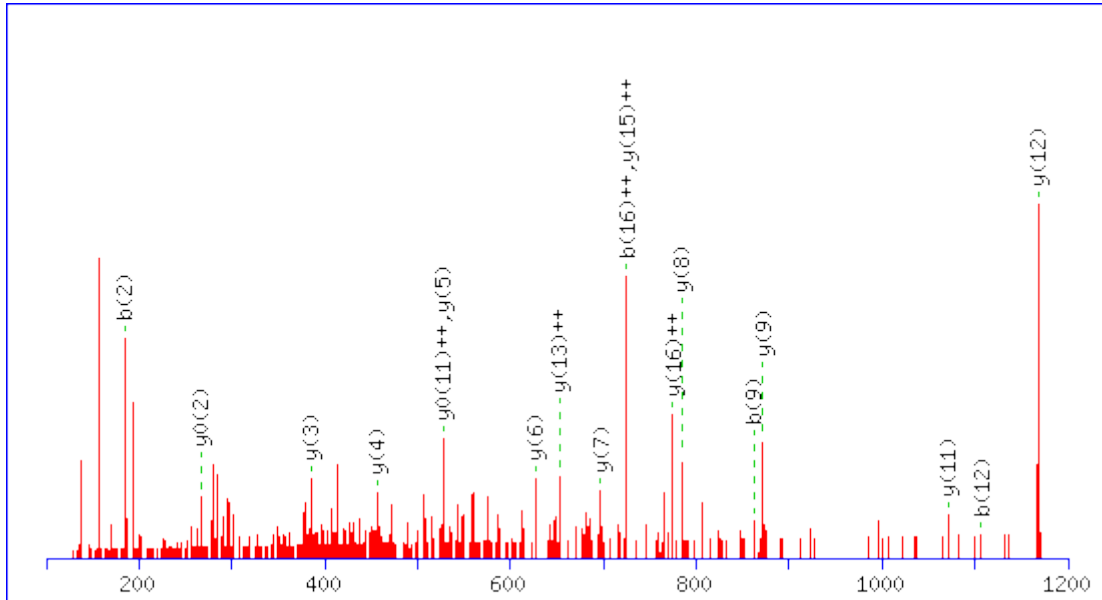
Monoisotopic mass of neutral peptide Mr(calc): 2088.9157

Ions Score: 39 Expect: 0.048

Matches (Bold Red): 17/196 fragment ions using 24 most intense peaks

MS/MS Fragmentation of **ALVSGKPAESSAVAATEK**

Found in **NDUA7_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 OS=Homo sapiens GN=NDUFA7 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1730.9385

Variable modifications:

K6 : Label:13C(6)15N(2) (K)

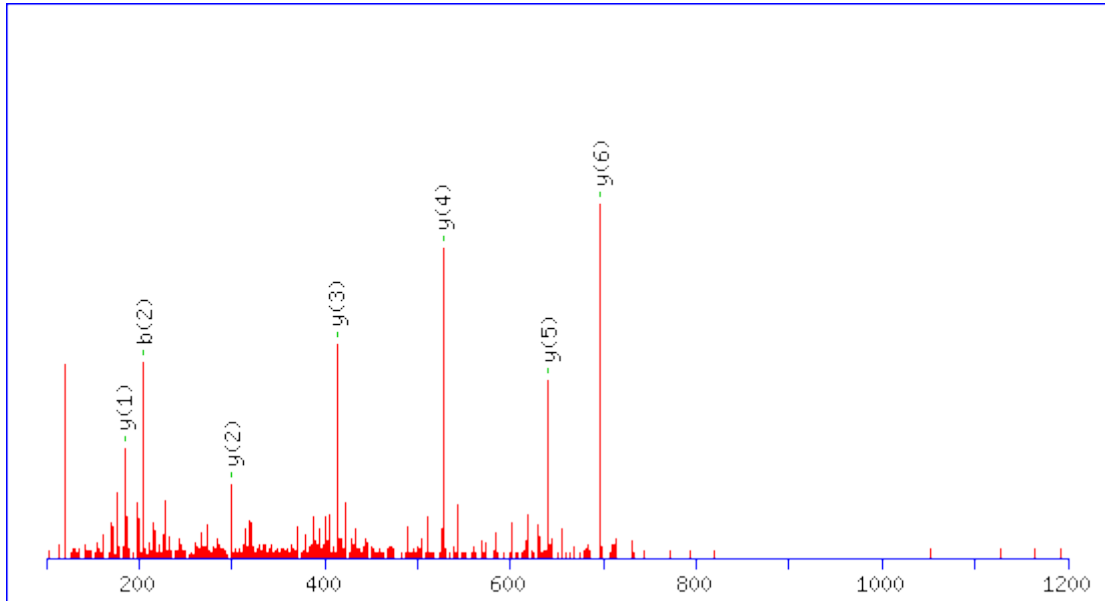
K18 : Label:13C(6)15N(2) (K)

Ions Score: 46 **Expect:** 0.0073

Matches (Bold Red): 18/186 fragment ions using 42 most intense peaks

MS/MS Fragmentation of **FGLNIDR**

Found in **NDUS5_HUMAN**, NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 OS=Homo sapiens GN=NDUFS5 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 843.4478

Variable modifications:

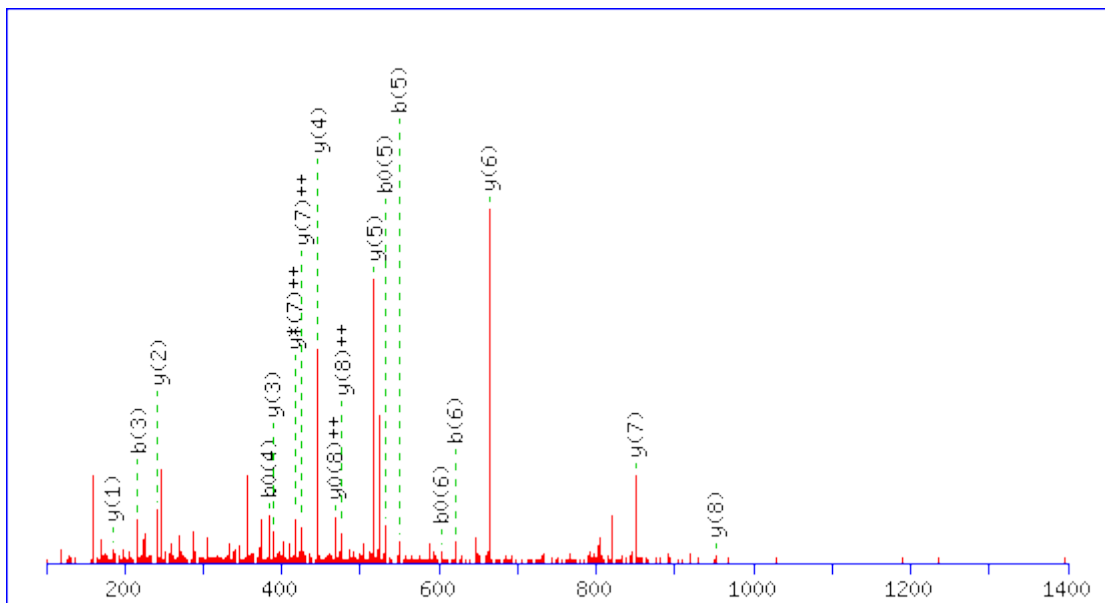
R7 : Label:13C(6)15N(4) (R)

Ions Score: 38 Expect: 0.032

Matches (Bold Red): 7/54 fragment ions using 21 most intense peaks

MS/MS Fragmentation of **GGTWFAFGFR**

Found in **NDUV1_HUMAN**, NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Homo sapiens GN=NDUFV1 PE=1 SV=4



Monoisotopic mass of neutral peptide Mr(calc): 1064.5068

Variable modifications:

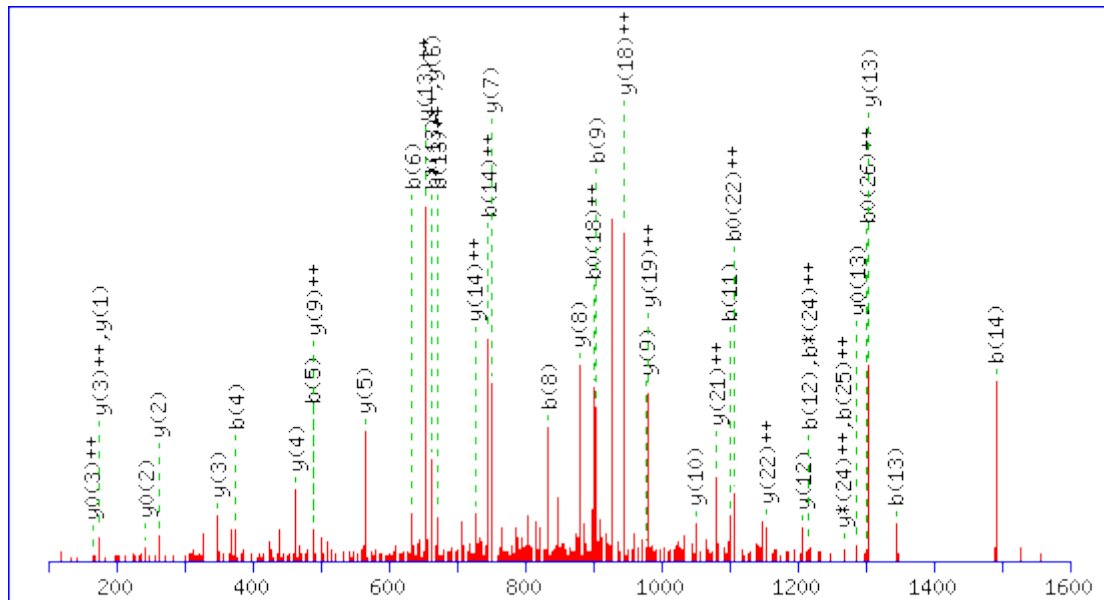
R10 : Label:13C(6)15N(4) (R)

Ions Score: 48 **Expect:** 0.0034

Matches (Bold Red): 18/72 fragment ions using 47 most intense peaks

MS/MS Fragmentation of **TSGELFAQAPVDQFPGTAVESVTDSSR**

Found in **NECP2_HUMAN**, Adaptin ear-binding coat-associated protein 2 OS=Homo sapiens GN=NECAP2 PE=1 SV=1



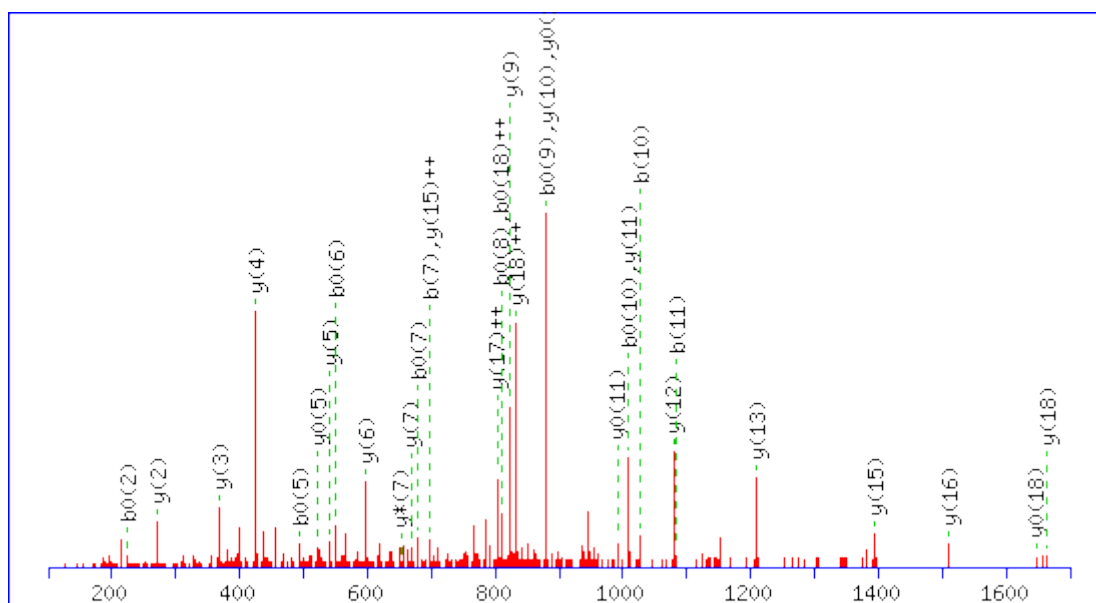
Monoisotopic mass of neutral peptide Mr(calc): 2795.3250

Ions Score: 83 **Expect:** 2.2e-006

Matches (Bold Red): 41/296 fragment ions using 65 most intense peaks

MS/MS Fragmentation of **ELGPDGEEAEGPGAGDGPPR**

Found in **NELFE_HUMAN**, Negative elongation factor E OS=Homo sapiens GN=RDBP PE=1 SV=3



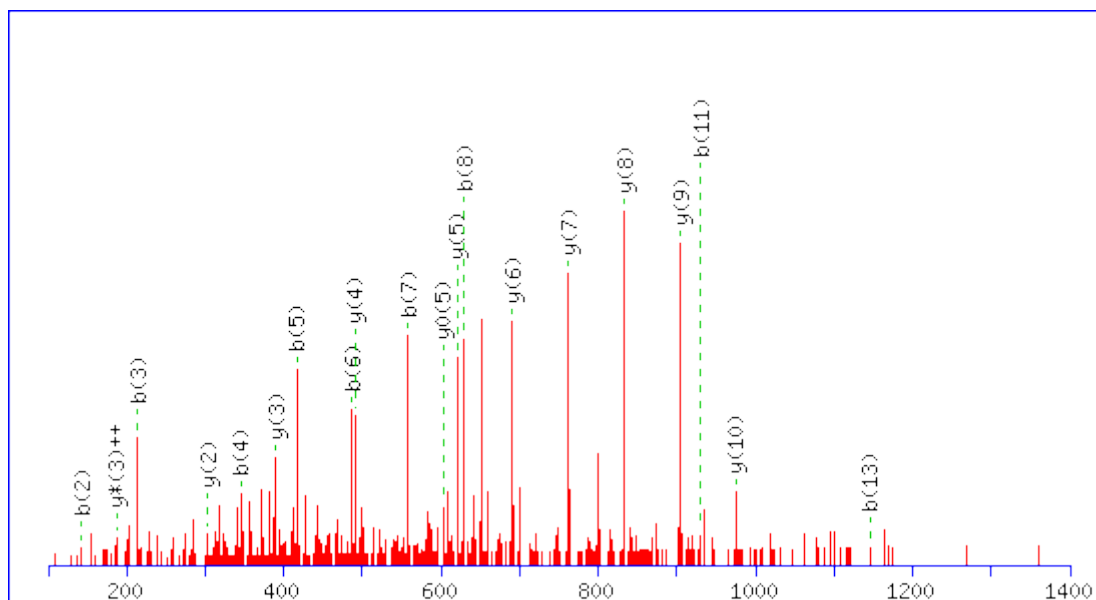
Monoisotopic mass of neutral peptide Mr(calc): 1905.8341

Ions Score: 76 Expect: 7.8e-006

Matches (Bold Red): 33/182 fragment ions using 71 most intense peaks

MS/MS Fragmentation of **AAAMAAAAETSQR**

Found in **NFIP2_HUMAN**, NEDD4 family-interacting protein 2 OS=Homo sapiens
GN=NDFIP2 PE=1 SV=2



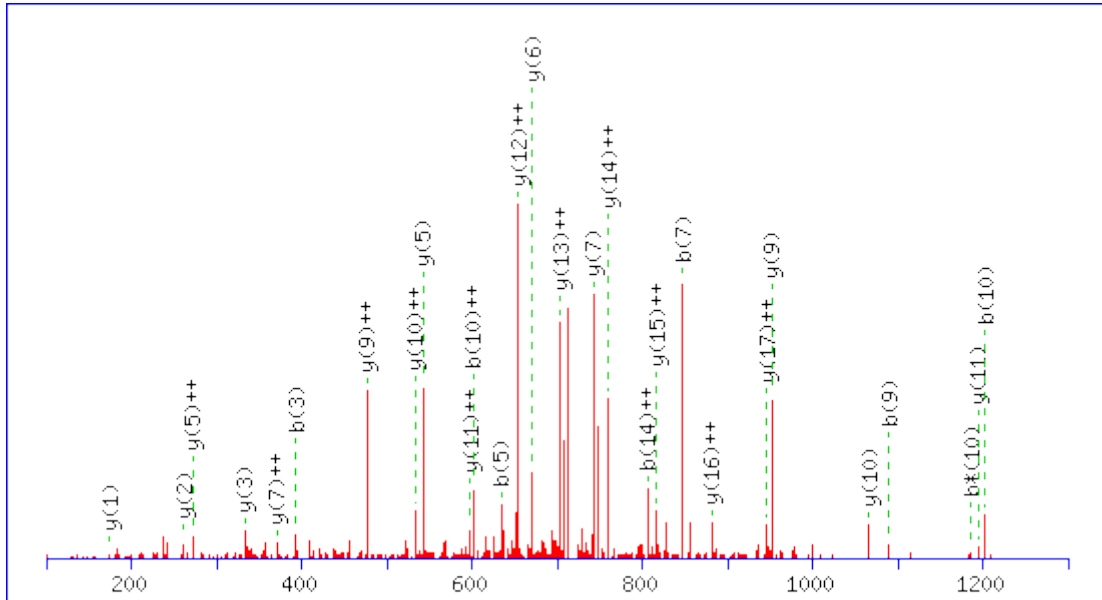
Monoisotopic mass of neutral peptide Mr(calc): 1318.6299

Ions Score: 46 Expect: 0.008

Matches (**Bold Red**): 20/110 fragment ions using 71 most intense peaks

MS/MS Fragmentation of **TYQELLVNQNPIAQPLASR**

Found in **NHP2_HUMAN**, H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens
GN=NHP2 PE=1 SV=1



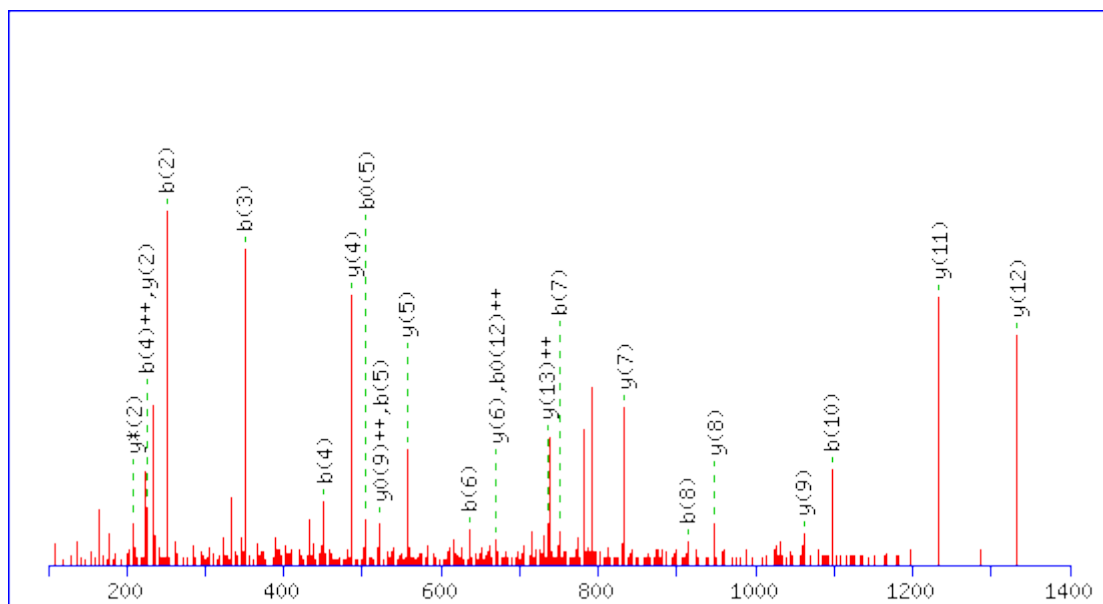
Monoisotopic mass of neutral peptide Mr(calc): 2154.1433

Ions Score: 81 Expect: 2.9e-006

Matches (**Bold Red**): 28/210 fragment ions using 52 most intense peaks

MS/MS Fragmentation of **LHVTALDYLAPYAK**

Found in **NIP7_HUMAN**, 60S ribosome subunit biogenesis protein NIP7 homolog
OS=Homo sapiens GN=NIP7 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1581.8646

Variable modifications:

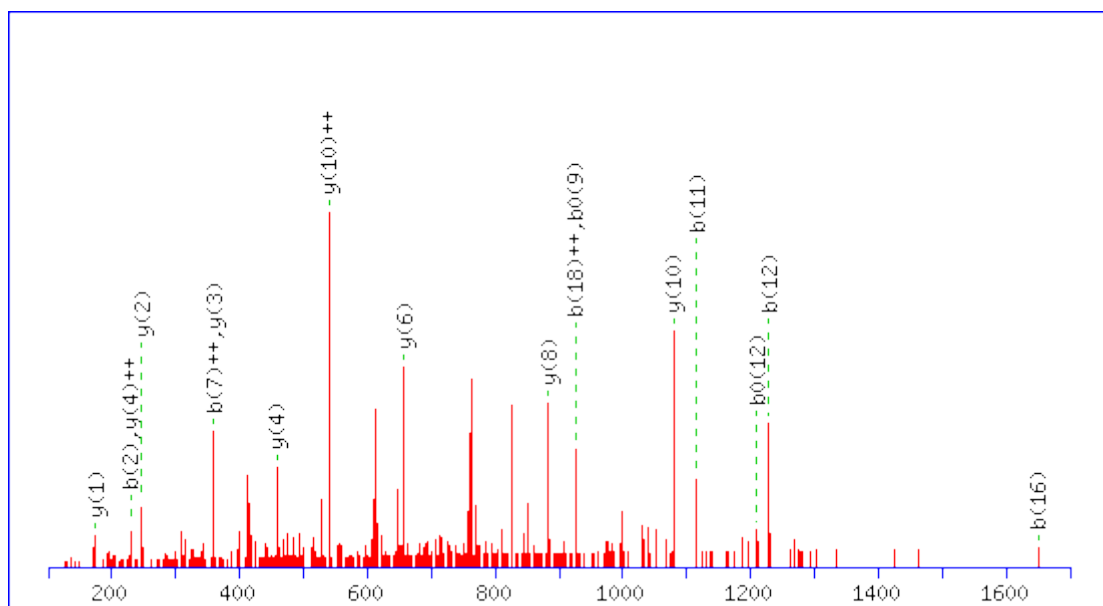
K14 : Label:13C(6)15N(2) (K)

Ions Score: 57 Expect: 0.00058

Matches (Bold Red): 23/110 fragment ions using 37 most intense peaks

MS/MS Fragmentation of **DNLGSDDPEGDIPVLLQAVLAR**

Found in **NIPBL_HUMAN**, Nipped-B-like protein OS=Homo sapiens GN=NIPBL PE=1 SV=2



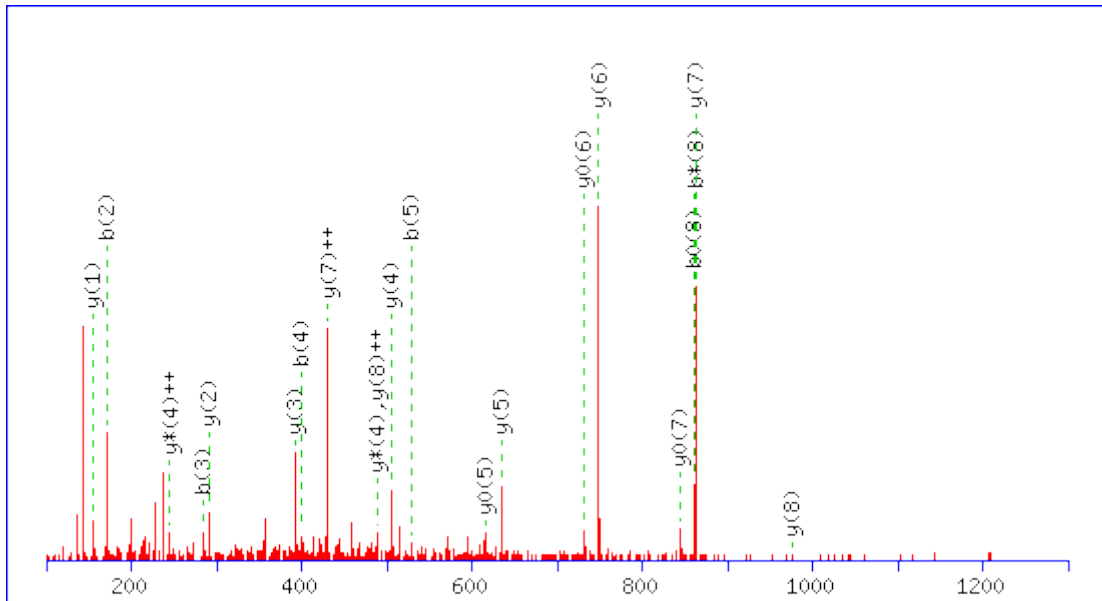
Monoisotopic mass of neutral peptide Mr(calc): 2306.1754

Ions Score: 42 Expect: 0.026

Matches (**Bold Red**): 17/228 fragment ions using 20 most intense peaks

MS/MS Fragmentation of **GLIDEITKK**

Found in **NMI_HUMAN**, N-myc-interactor OS=Homo sapiens GN=NMI PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1031.6198

Variable modifications:

K8 : Label:13C(6)15N(2) (K)

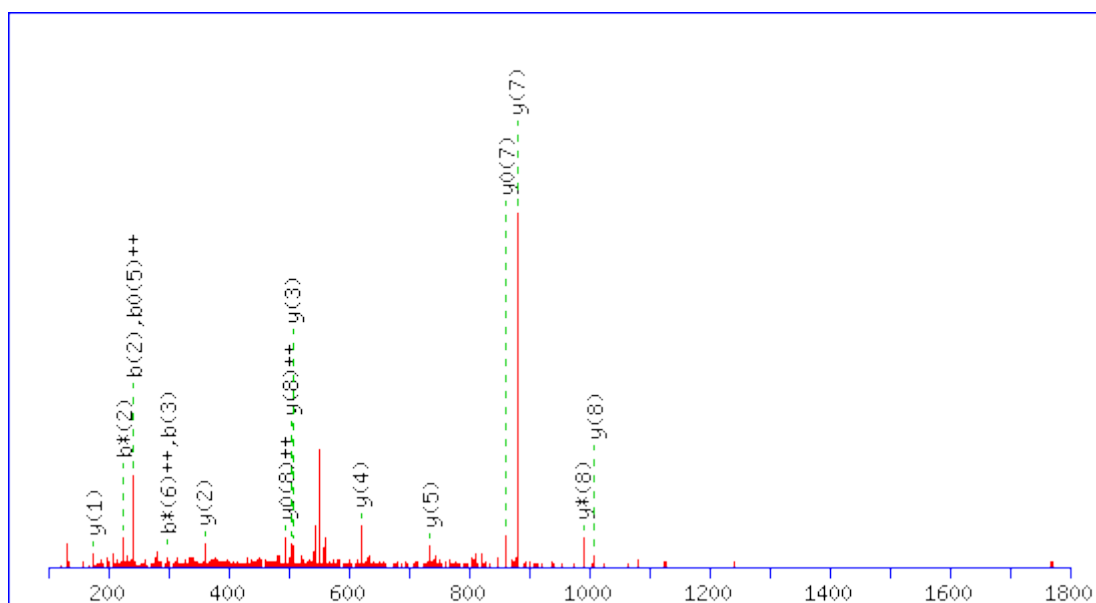
K9 : Label:13C(6)15N(2) (K)

Ions Score: 45 Expect: 0.0049

Matches (**Bold Red**): 21/72 fragment ions using 57 most intense peaks

MS/MS Fragmentation of **LQGSDLFWR**

Found in **NOL8_HUMAN**, Nucleolar protein 8 OS=Homo sapiens GN=NOL8 PE=1 SV=1



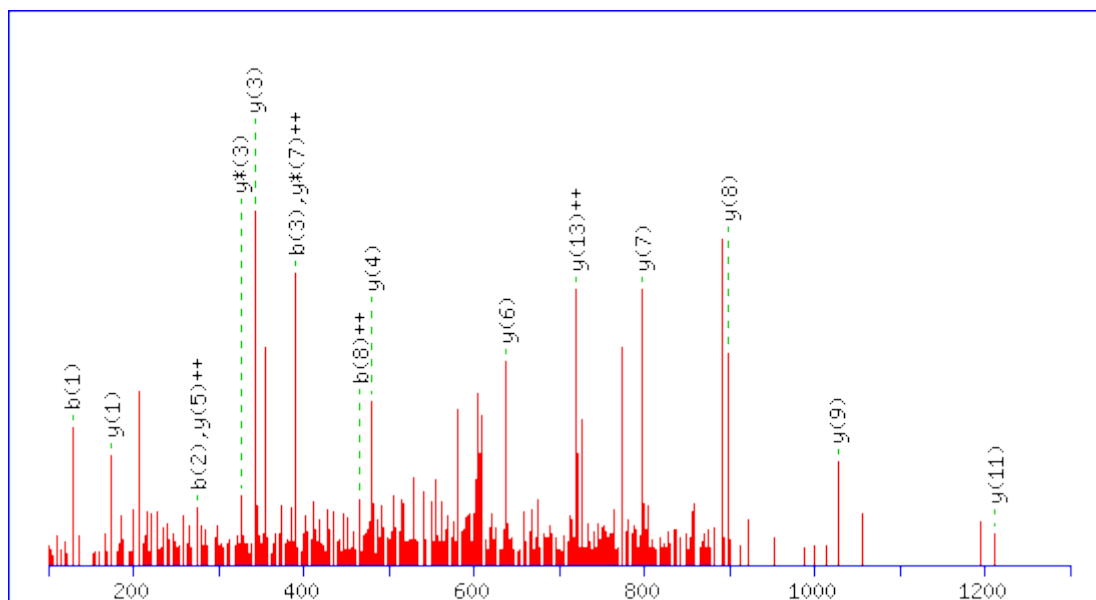
Monoisotopic mass of neutral peptide Mr(calc): 1120.5665

Ions Score: 37 Expect: 0.052

Matches (Bold Red): 16/80 fragment ions using 35 most intense peaks

MS/MS Fragmentation of **KFDPMGQQTCSAHPAR**

Found in **NOP10_HUMAN**, H/ACA ribonucleoprotein complex subunit 3 OS=Homo sapiens
GN=NOP10 PE=1 SV=1



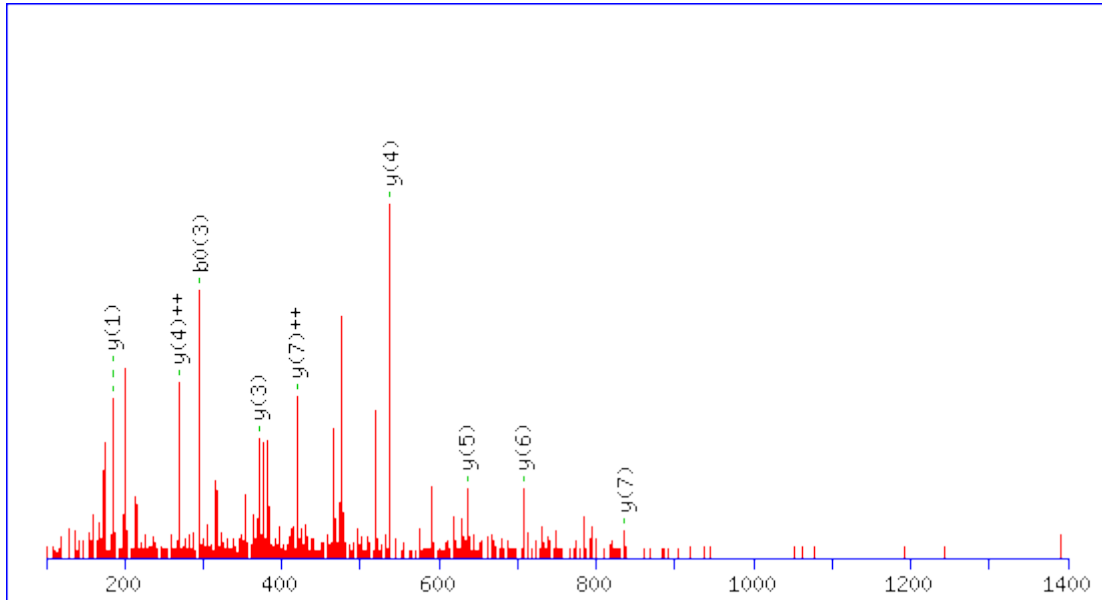
Monoisotopic mass of neutral peptide Mr(calc): 1829.8301

Ions Score: 46 Expect: 0.0079

Matches (Bold Red): 16/166 fragment ions using 23 most intense peaks

MS/MS Fragmentation of **LEAVRADR**

Found in **NR5A2_HUMAN**, Nuclear receptor subfamily 5 group A member 2 OS=Homo sapiens GN=NR5A2 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 948.5255

Variable modifications:

R5 : Label:13C(6)15N(4) (R)

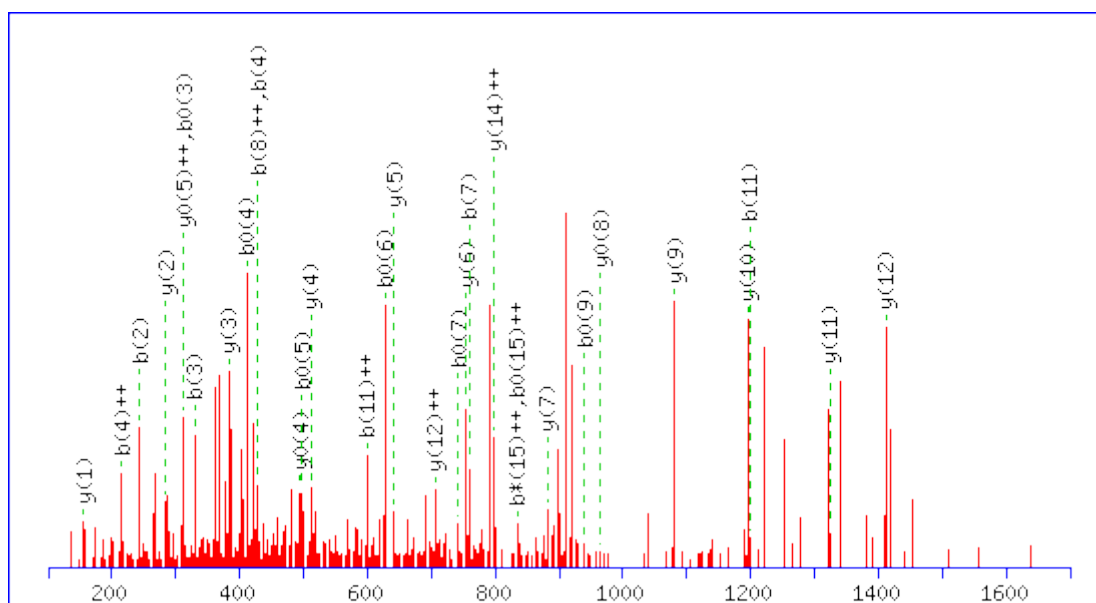
R8 : Label:13C(6)15N(4) (R)

Ions Score: 47 **Expect:** 0.004

Matches (Bold Red): 9/72 fragment ions using 25 most intense peaks

MS/MS Fragmentation of **LESVSEDPTQLEEVEK**

Found in **NTKL_HUMAN**, N-terminal kinase-like protein OS=Homo sapiens GN=SCYL1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1838.8876

Variable modifications:

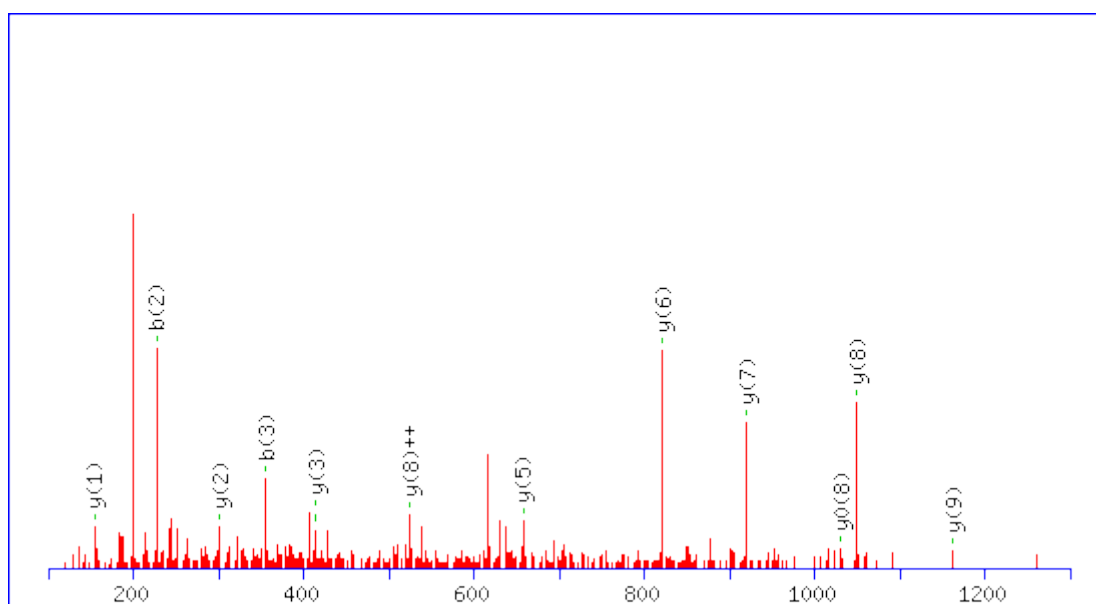
K16 : Label:13C(6)15N(2) (K)

Ions Score: 38 Expect: 0.056

Matches (Bold Red): 32/158 fragment ions using 91 most intense peaks

MS/MS Fragmentation of **LLEVYDQLFK**

Found in **NU155_HUMAN**, Nuclear pore complex protein Nup155 OS=Homo sapiens
GN=NUP155 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1274.7002

Variable modifications:

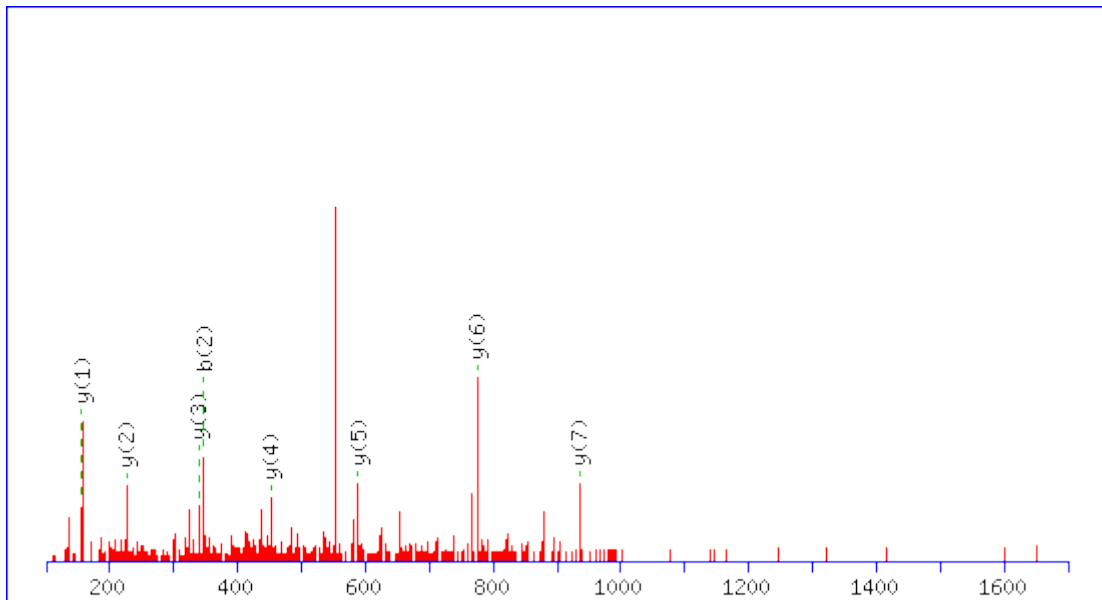
K10 : Label:13C(6)15N(2) (K)

Ions Score: 39 Expect: 0.029

Matches (Bold Red): 12/84 fragment ions using 36 most intense peaks

MS/MS Fragmentation of **WCWHLAK**

Found in **OAS2_HUMAN**, 2'-5'-oligoadenylate synthase 2 OS=Homo sapiens GN=OAS2
PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1120.5732

Variable modifications:

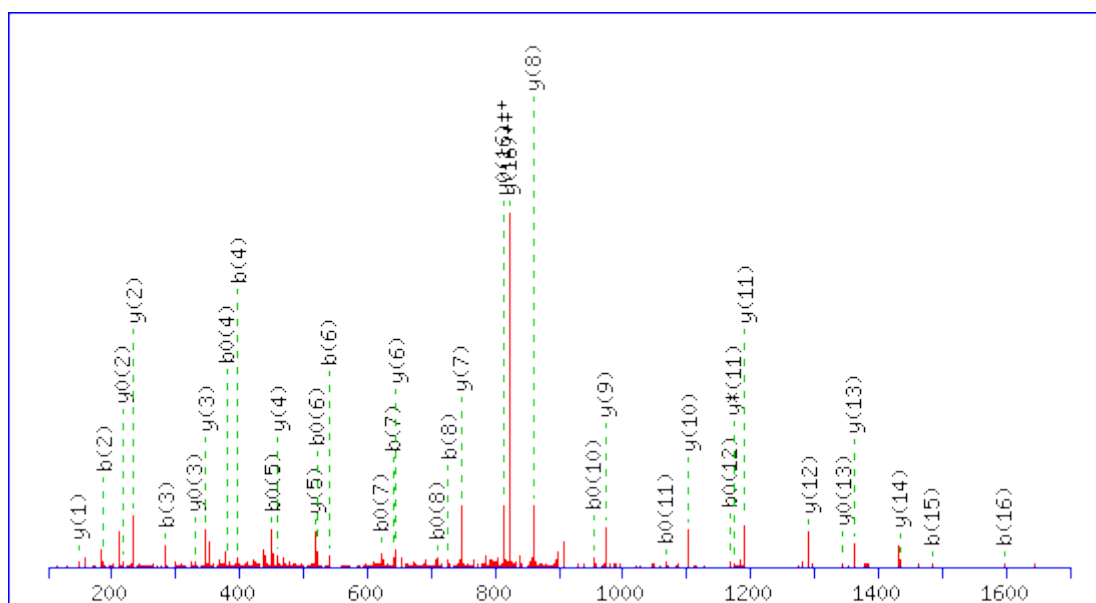
K8 : Label:13C(6)15N(2) (K)

Ions Score: 43 Expect: 0.011

Matches (Bold Red): 8/42 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **SVPLAATSMITQGLISK**

Found in **OCAD1_HUMAN**, OCIA domain-containing protein 1 OS=Homo sapiens
GN=OCAD1 PE=1 SV=1



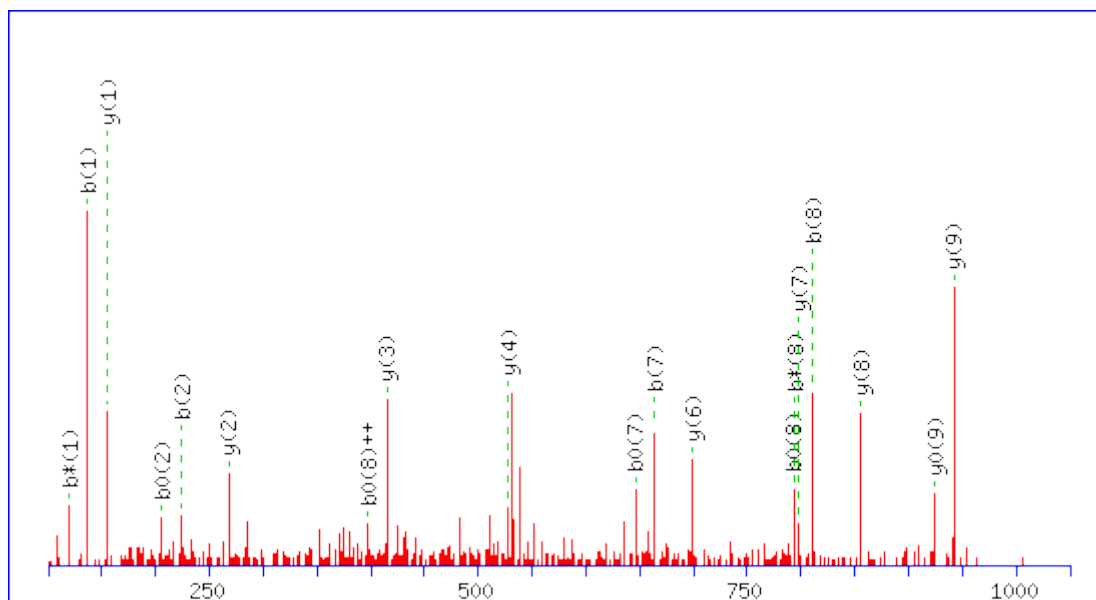
Monoisotopic mass of neutral peptide Mr(calc): 1829.0332

Ions Score: 85 Expect: 8.7e-007

Matches (Bold Red): 36/178 fragment ions using 75 most intense peaks

MS/MS Fragmentation of **KSGVGNIFIK**

Found in **PAP1L_HUMAN**, Polyadenylate-binding protein 1-like OS=Homo sapiens
GN=PABPC1L PE=2 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1077.6517

Variable modifications:

K1 : Label:13C(6)15N(2) (K)

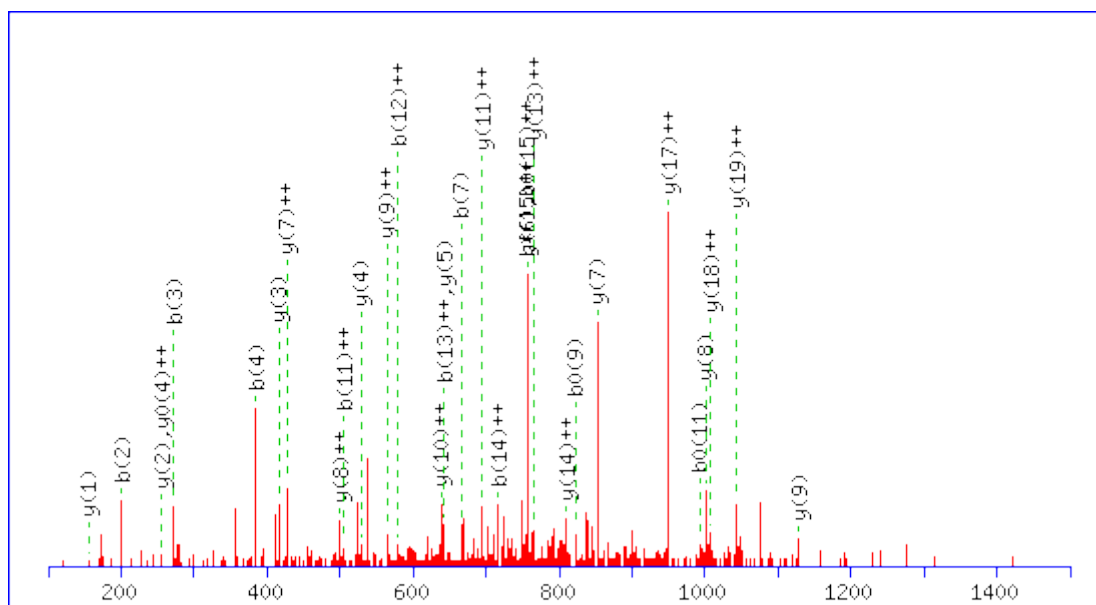
K10 : Label:13C(6)15N(2) (K)

Ions Score: 68 Expect: 2.6e-005

Matches (Bold Red): 20/90 fragment ions using 32 most intense peaks

MS/MS Fragmentation of **TVAIPALSSGIFQFPLNLCTK**

Found in **PARP9_HUMAN**, Poly [ADP-ribose] polymerase 9 OS=Homo sapiens GN=PARP9
PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 2284.2381

Variable modifications:

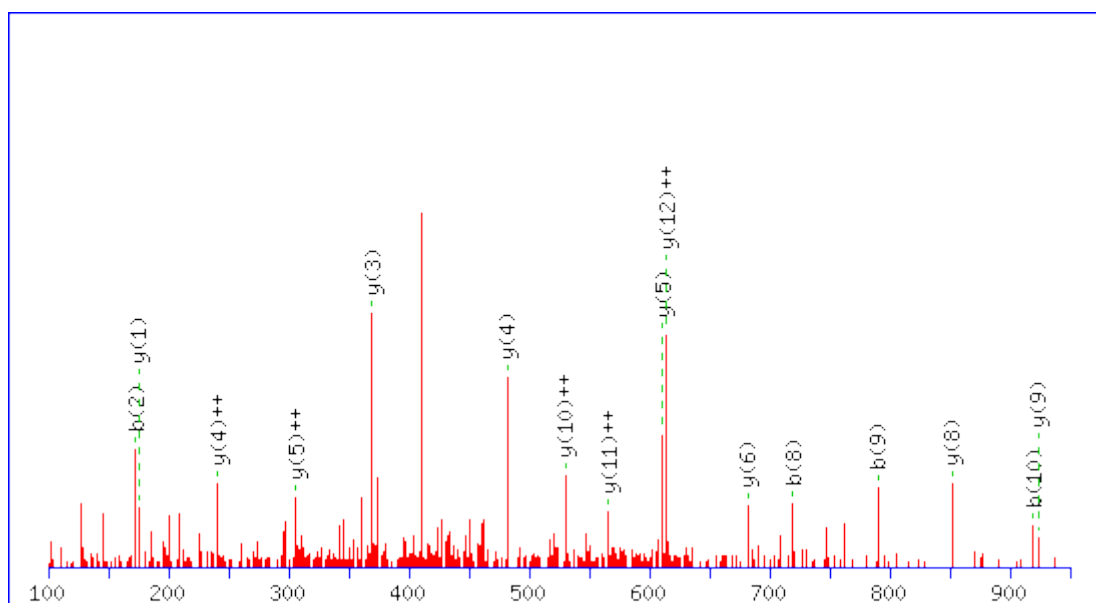
K21 : Label:13C(6)15N(2) (K)

Ions Score: 40 Expect: 0.035

Matches (Bold Red): 32/214 fragment ions using 109 most intense peaks

MS/MS Fragmentation of **GDPAHAGLAELGHR**

Found in **PBIP1_HUMAN**, Pre-B-cell leukemia transcription factor-interacting
protein 1 OS=Homo sapiens GN=PBXIP1 PE=1 SV=1



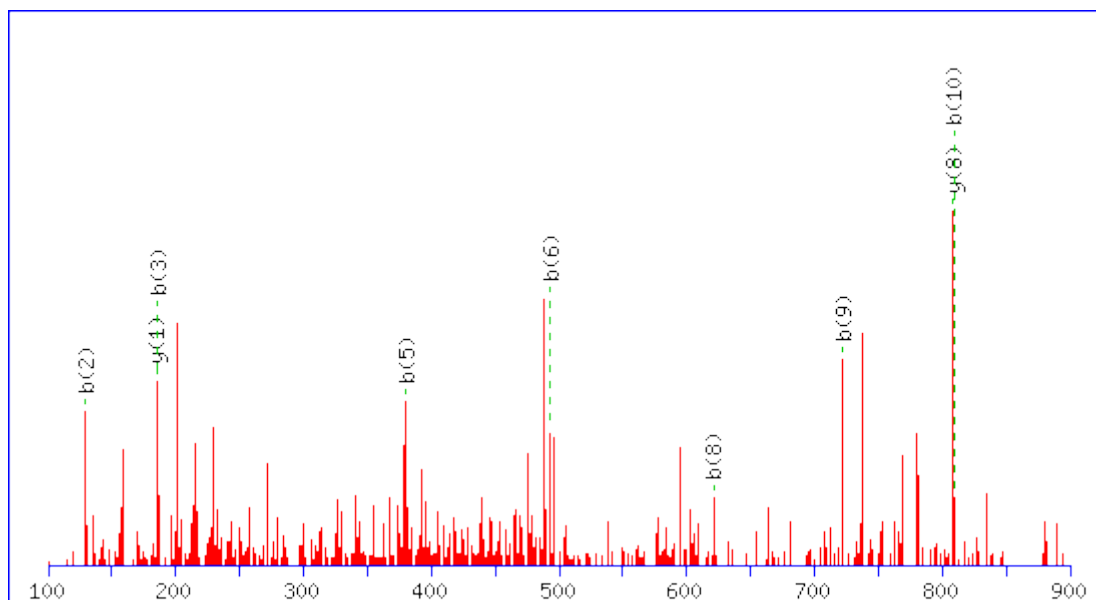
Monoisotopic mass of neutral peptide Mr(calc): 1399.6956

Ions Score: 48 Expect: 0.0041

Matches (Bold Red): 16/120 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **GAGPPLAGTSR**

Found in **PERQ1_HUMAN**, PERQ amino acid-rich with GYF domain-containing protein
1 OS=Homo sapiens GN=GIGYF1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 992.5279

Variable modifications:

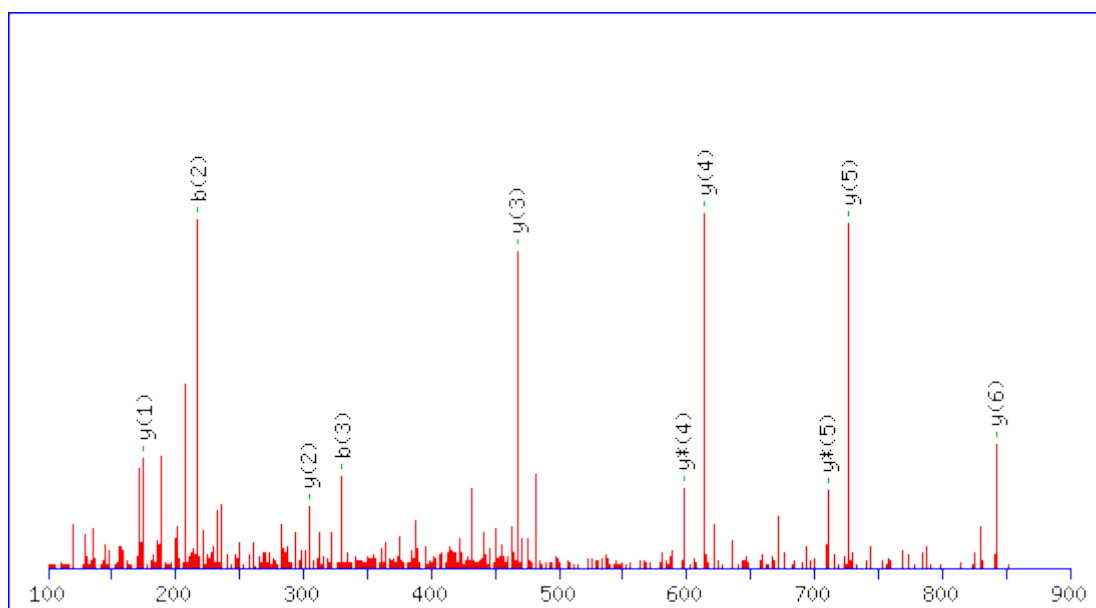
R11 : Label:13C(6)15N(4) (R)

Ions Score: 37 **Expect:** 0.045

Matches (Bold Red): 9/82 fragment ions using 25 most intense peaks

MS/MS Fragmentation of **TDLFYER**

Found in **PHF5A_HUMAN**, PHD finger-like domain-containing protein 5A OS=Homo sapiens GN=PHF5A PE=1 SV=1



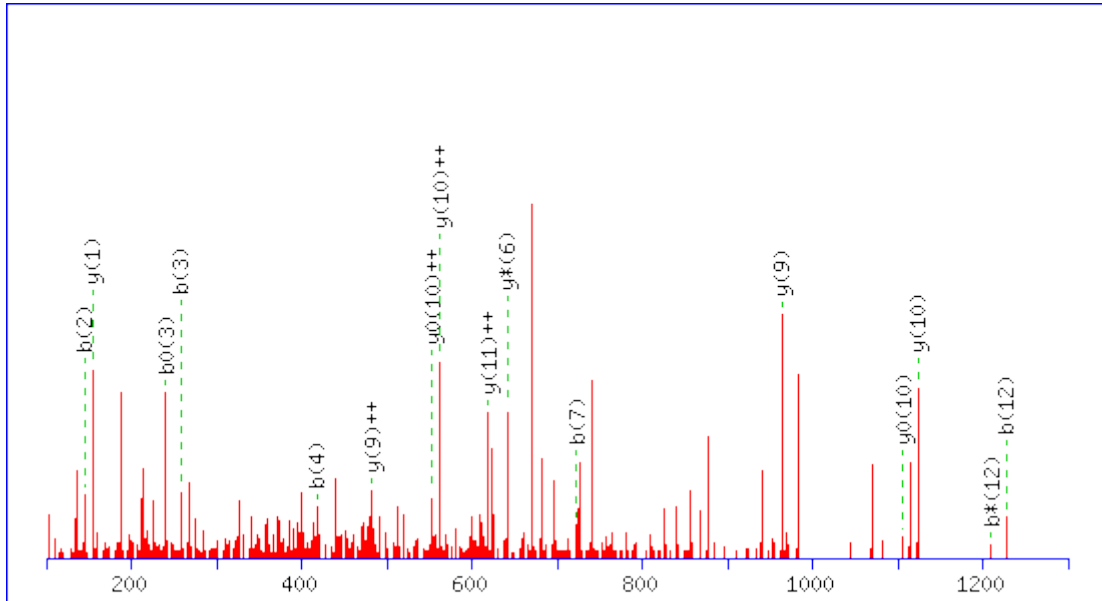
Monoisotopic mass of neutral peptide Mr(calc): 942.4447

Ions Score: 45 **Expect:** 0.0058

Matches (Bold Red): 10/58 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **GSLCMSSGIKTPK**

Found in **PKHD1_HUMAN**, Fibrocystin OS=Homo sapiens GN=PKHD1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1380.7076

Variable modifications:

K10 : Label:13C(6)15N(2) (K)

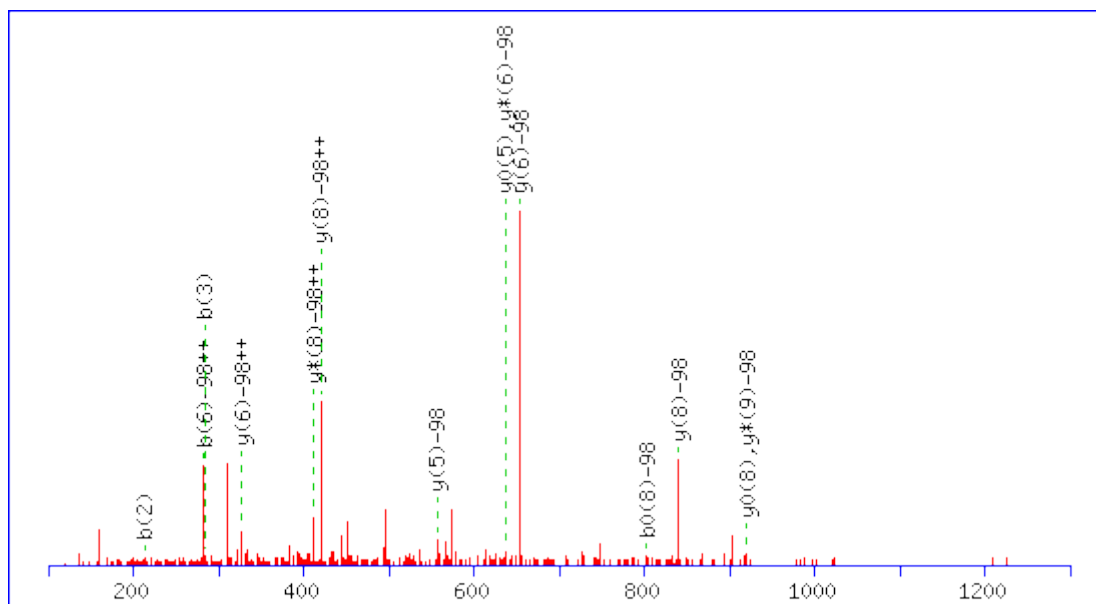
K13 : Label:13C(6)15N(2) (K)

Ions Score: 11 Expect: 24

Matches (Bold Red): 16/120 fragment ions using 49 most intense peaks

MS/MS Fragmentation of **DPADPSQQGR**

Found in **PKHG3_HUMAN**, Pleckstrin homology domain-containing family G member 3 OS=Homo sapiens GN=PLEKHG3 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1149.4452

Variable modifications:

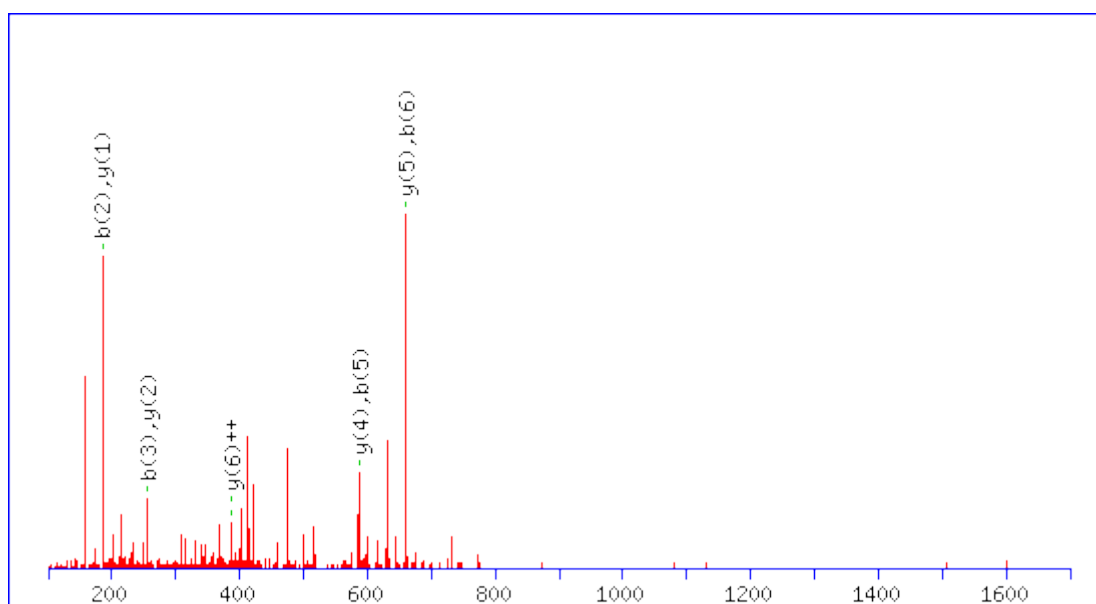
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 4 Expect: 90

Matches (Bold Red): 14/140 fragment ions using 46 most intense peaks

MS/MS Fragmentation of **AIASRAR**

Found in **PLCH2_HUMAN**, 1-phosphatidylinositol-4,5-bisphosphate
phosphodiesterase eta-2 OS=Homo sapiens GN=PLCH2 PE=2 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 843.4230

Variable modifications:

S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

R5 : Label:13C(6)15N(4) (R)

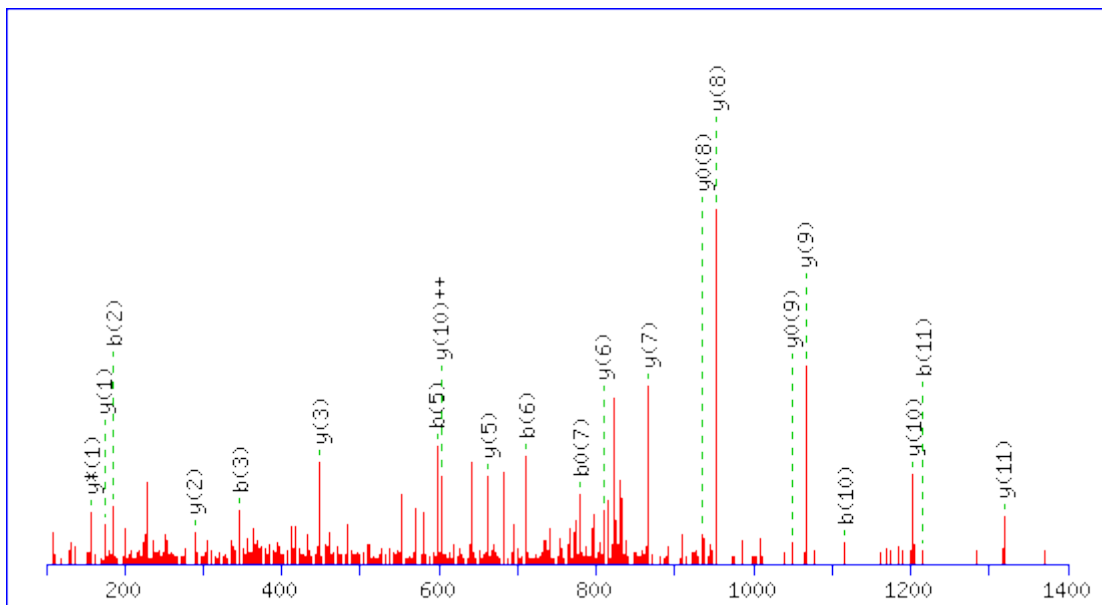
R7 : Label:13C(6)15N(4) (R)

Ions Score: 36 Expect: 0.045

Matches (Bold Red): 9/86 fragment ions using 11 most intense peaks

MS/MS Fragmentation of **NACDHLSGFNVCNR**

Found in **PM14_HUMAN**, Pre-mRNA branch site protein p14 OS=Homo sapiens GN=SF3B14
PE=1 SV=1



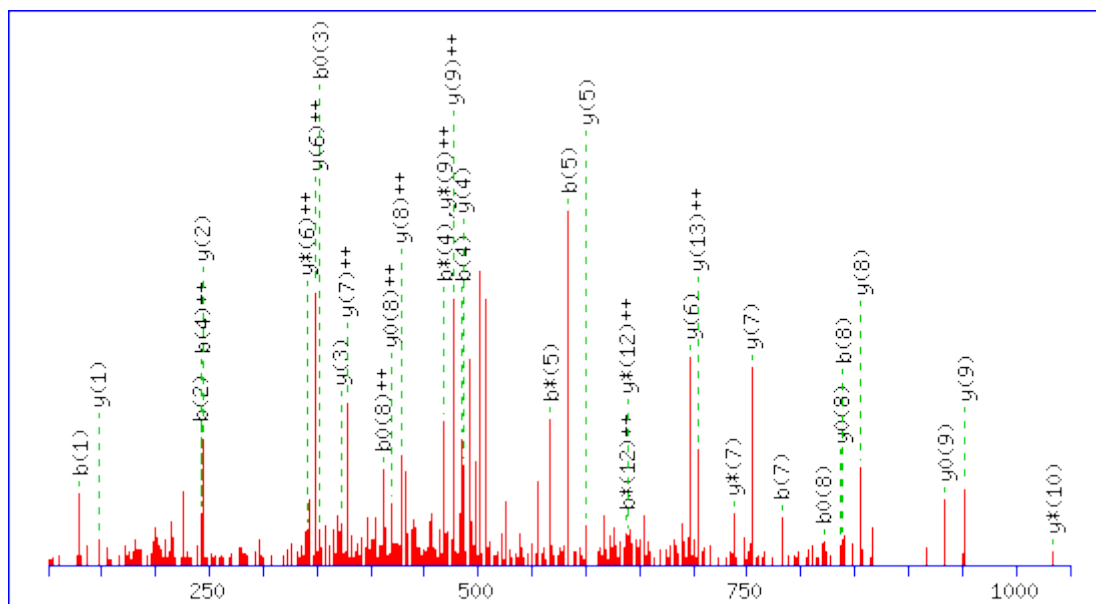
Monoisotopic mass of neutral peptide Mr(calc): 1662.6991

Ions Score: 64 Expect: 0.00012

Matches (Bold Red): 21/136 fragment ions using 42 most intense peaks

MS/MS Fragmentation of **KIENVPTGPNNKPK**

Found in **PPIH_HUMAN**, Peptidyl-prolylcis-trans isomerase H OS=Homo sapiens
GN=PPIH PE=1 SV=1



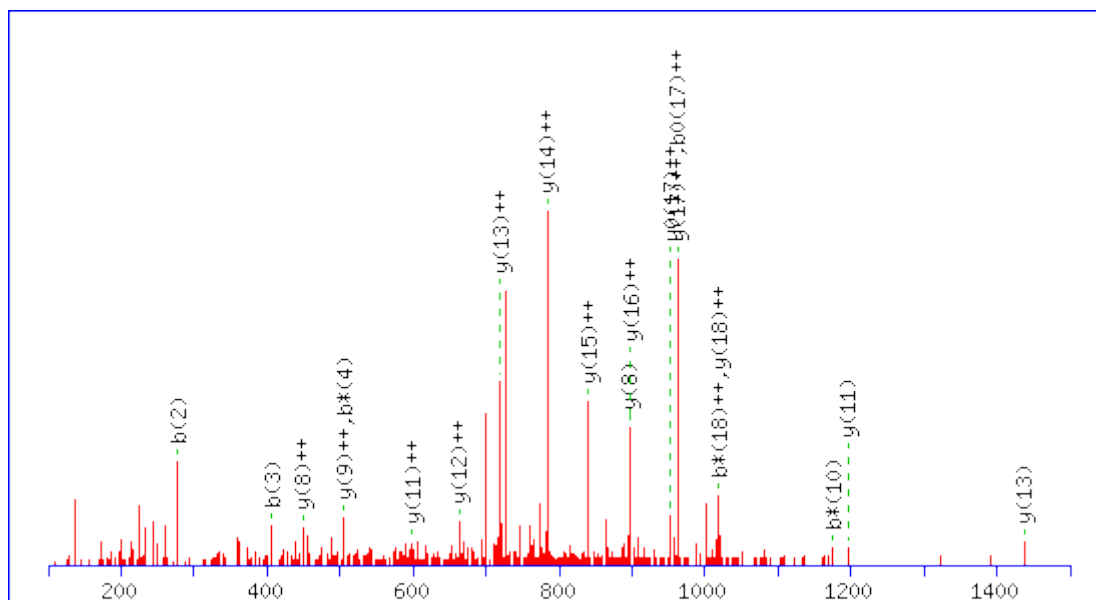
Monoisotopic mass of neutral peptide Mr(calc): 1534.8467

Ions Score: 41 Expect: 0.023

Matches (**Bold Red**): 35/138 fragment ions using 83 most intense peaks

MS/MS Fragmentation of **YNEDLEDAIHTAILTK**

Found in **PSA2_HUMAN**, Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2
PE=1 SV=2



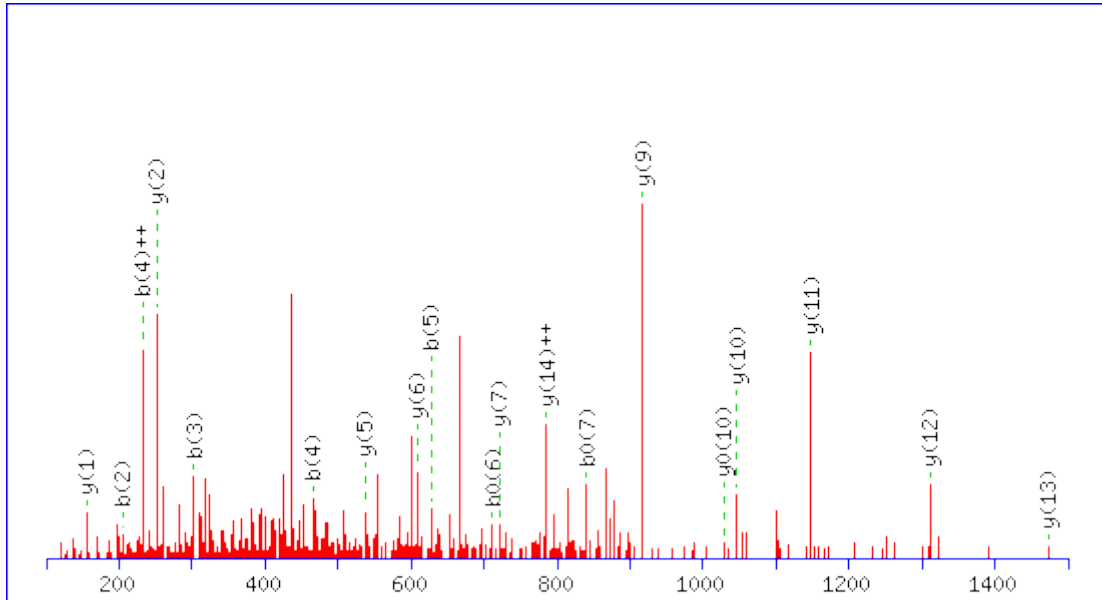
Monoisotopic mass of neutral peptide Mr(calc): 2200.1263

Ions Score: 51 Expect: 0.0028

Matches (Bold Red): 20/206 fragment ions using 38 most intense peaks

MS/MS Fragmentation of **FGPYYTEPVIAGLDPK**

Found in **PSB3_HUMAN**, Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3
PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1773.9069

Variable modifications:

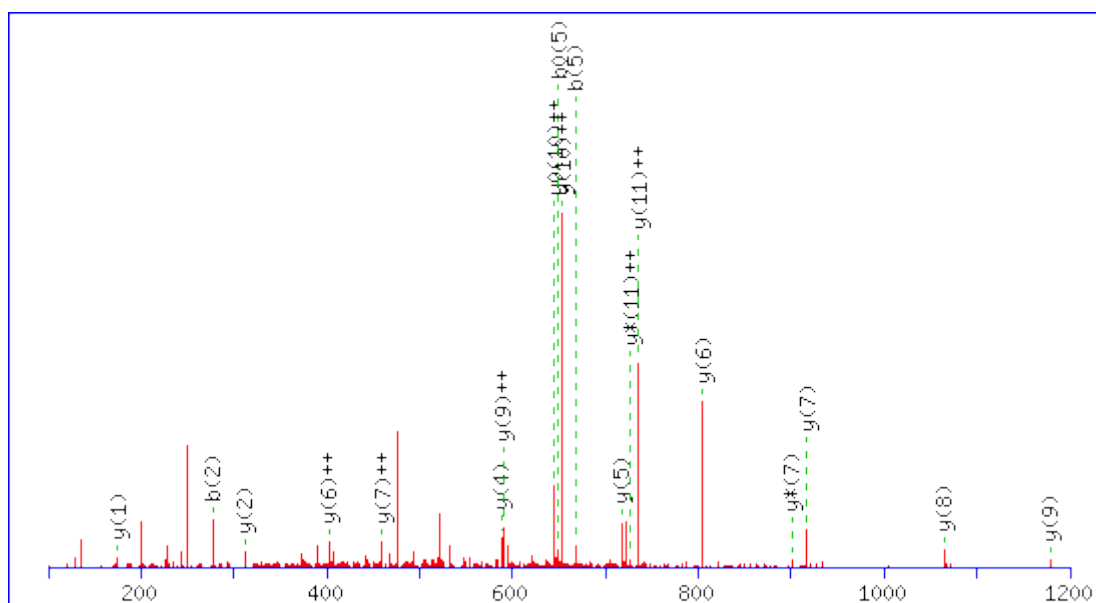
K16 : Label:13C(6)15N(2) (K)

Ions Score: 41 **Expect:** 0.029

Matches (Bold Red): 19/136 fragment ions using 55 most intense peaks

MS/MS Fragmentation of **LYENFISEFEHR**

Found in **PSD13_HUMAN**, 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2



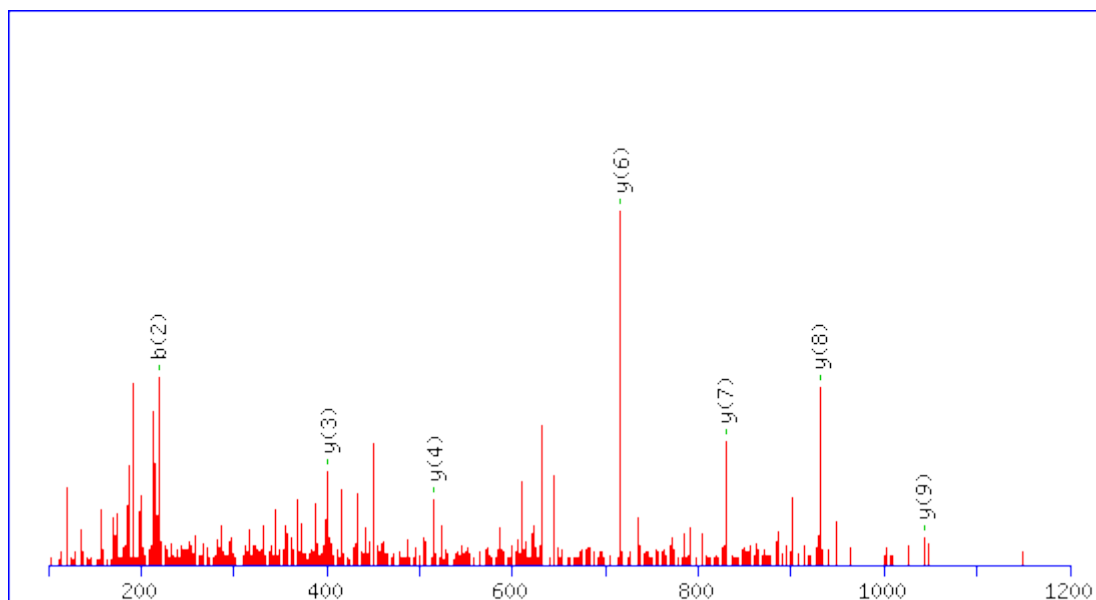
Monoisotopic mass of neutral peptide Mr(calc): 1582.7416

Ions Score: 39 Expect: 0.037

Matches (Bold Red): 19/118 fragment ions using 41 most intense peaks

MS/MS Fragmentation of **AFLTAEILR**

Found in **RAB10_HUMAN**, Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1



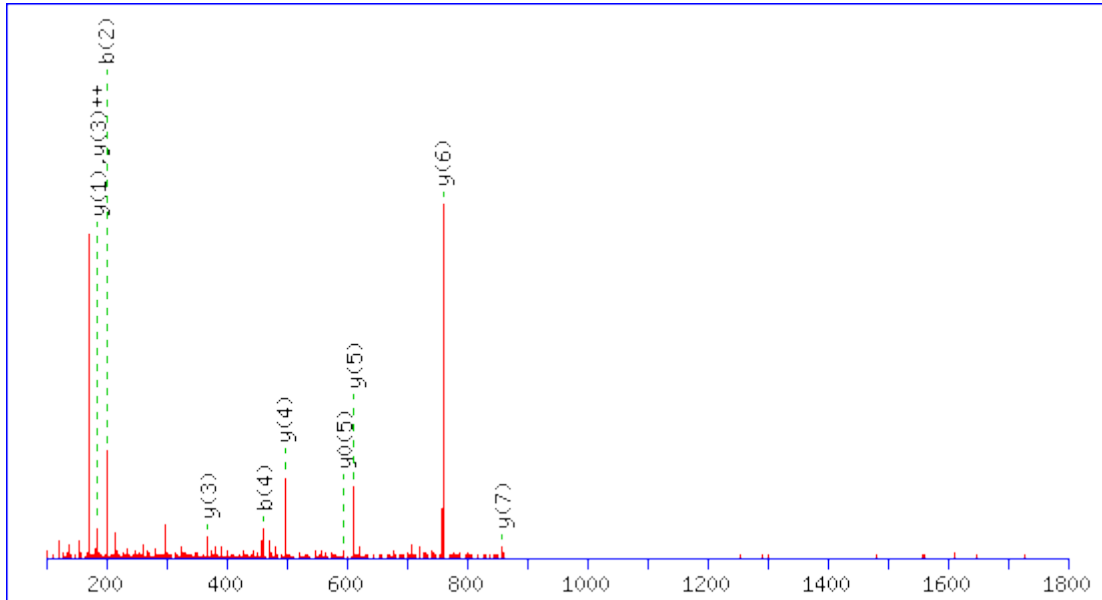
Monoisotopic mass of neutral peptide Mr(calc): 1260.7078

Ions Score: 37 Expect: 0.051

Matches (Bold Red): 7/88 fragment ions using 14 most intense peaks

MS/MS Fragmentation of **TVFDEAIR**

Found in **RAC2_HUMAN**, Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens
GN=RAC2 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 959.4952

Variable modifications:

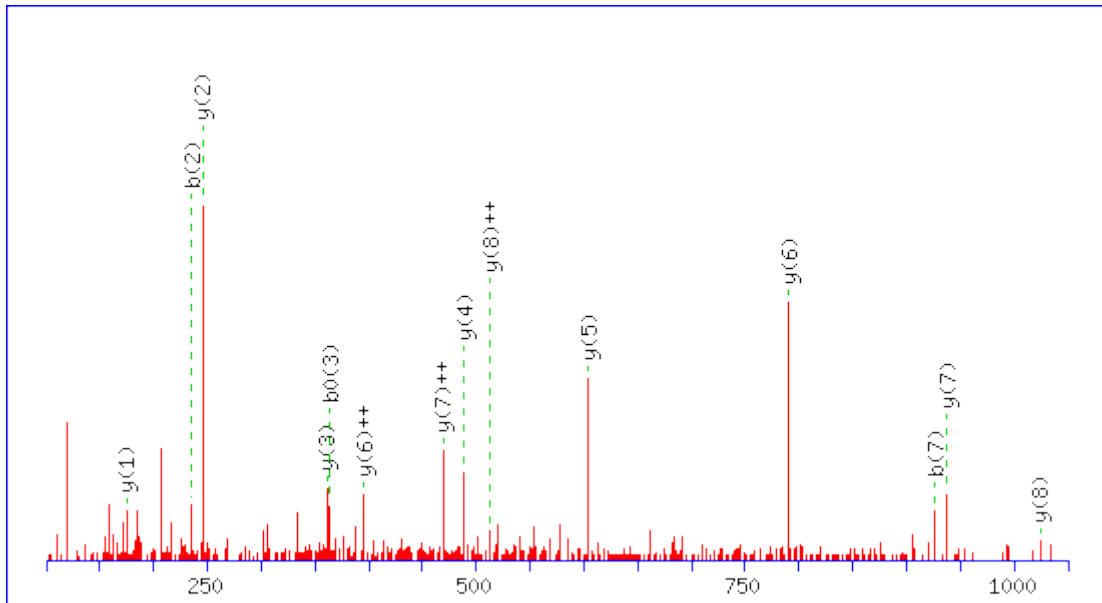
R8 : Label:13C(6)15N(4) (R)

Ions Score: 42 **Expect:** 0.012

Matches (Bold Red): 10/64 fragment ions using 20 most intense peaks

MS/MS Fragmentation of **FSFWDKDAR**

Found in **RAE1L_HUMAN**, mRNA export factor OS=Homo sapiens GN=RAE1 PE=1 SV=1



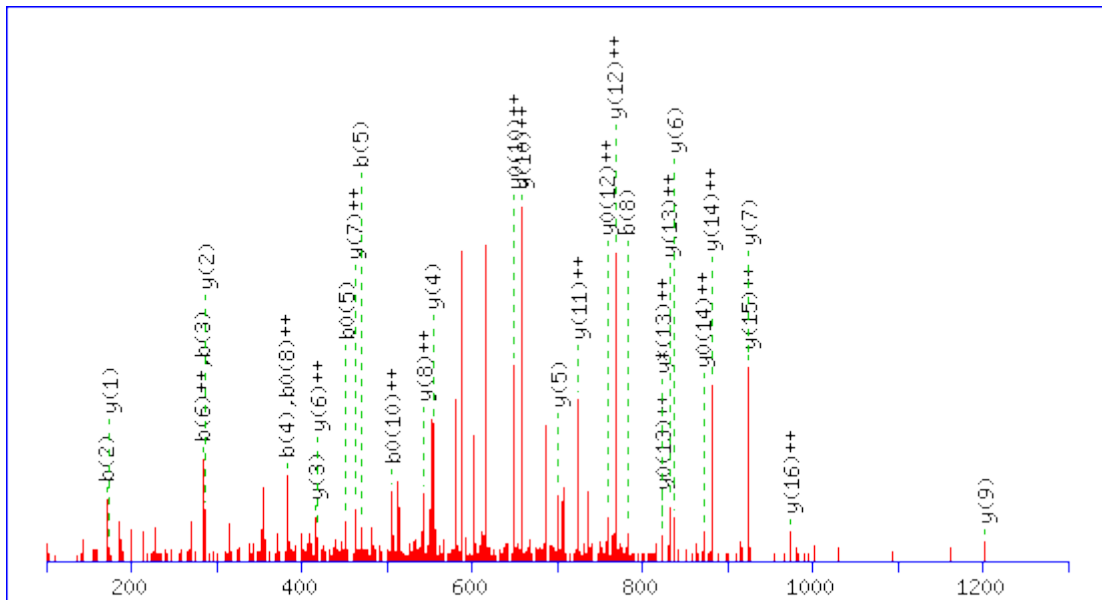
Monoisotopic mass of neutral peptide Mr(calc): 1170.5458

Ions Score: 49 Expect: 0.0031

Matches (**Bold Red**): 14/80 fragment ions using 35 most intense peaks

MS/MS Fragmentation of **LGLVSPESMDNYSHFELR**

Found in **RAI14_HUMAN**, Ankyrin OS=Homo sapiens GN=RAI14 PE=1 SV=2



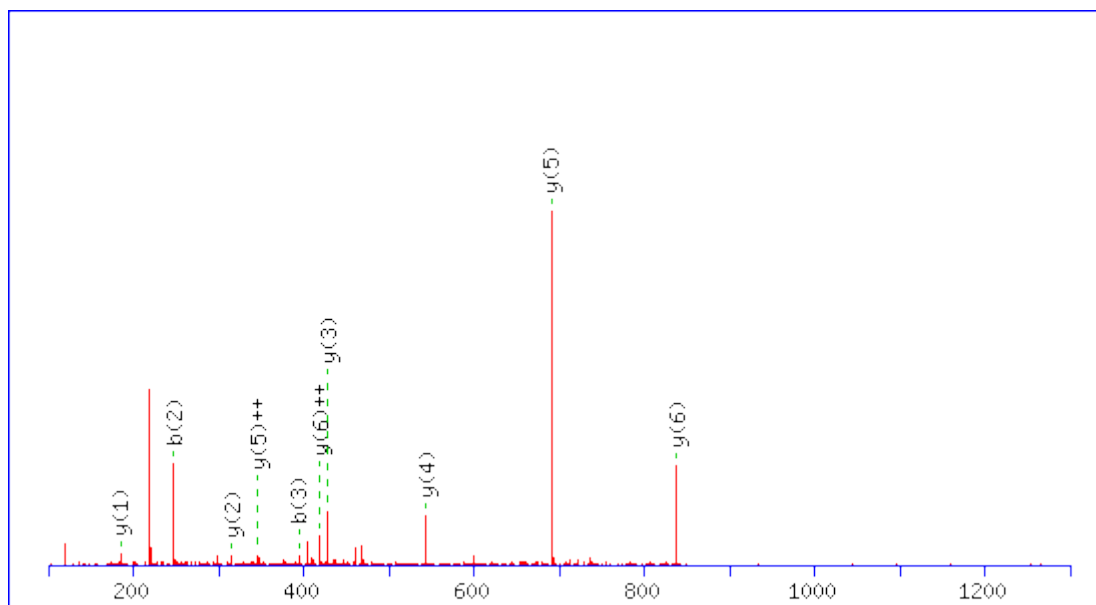
Monoisotopic mass of neutral peptide Mr(calc): 2230.0477

Ions Score: 46 Expect: 0.0097

Matches (Bold Red): 32/184 fragment ions using 86 most intense peaks

MS/MS Fragmentation of **VFFDLMR**

Found in **RALA_HUMAN**, Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 936.4767

Variable modifications:

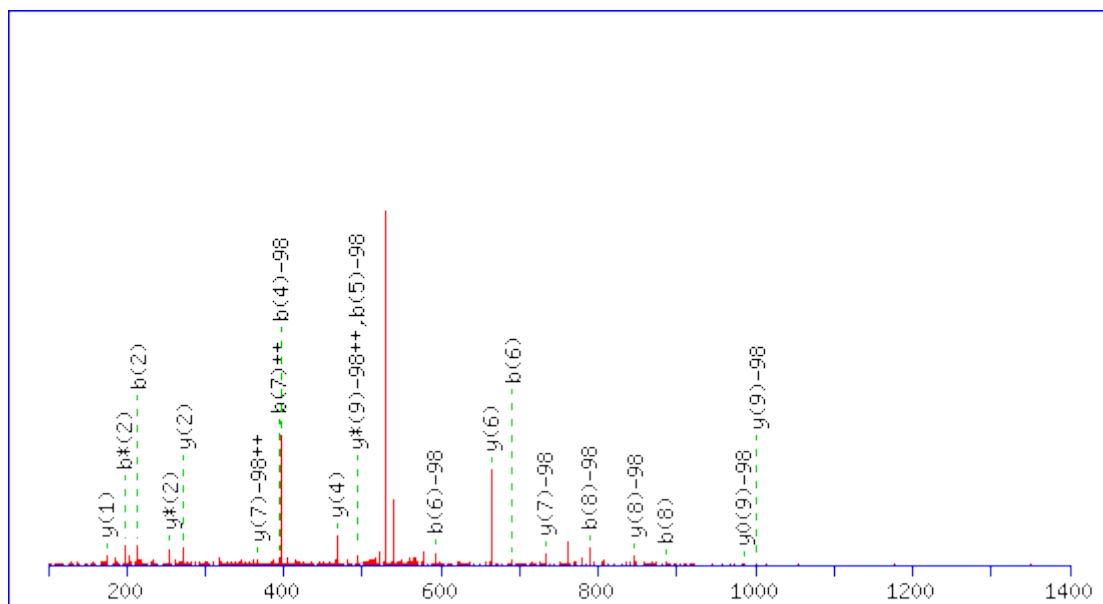
R7 : Label:13C(6)15N(4) (R)

Ions Score: 36 **Expect:** 0.04

Matches (Bold Red): 10/48 fragment ions using 36 most intense peaks

MS/MS Fragmentation of **GRLSPVPVPR**

Found in **RALY_HUMAN**, RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1156.6118

Variable modifications:

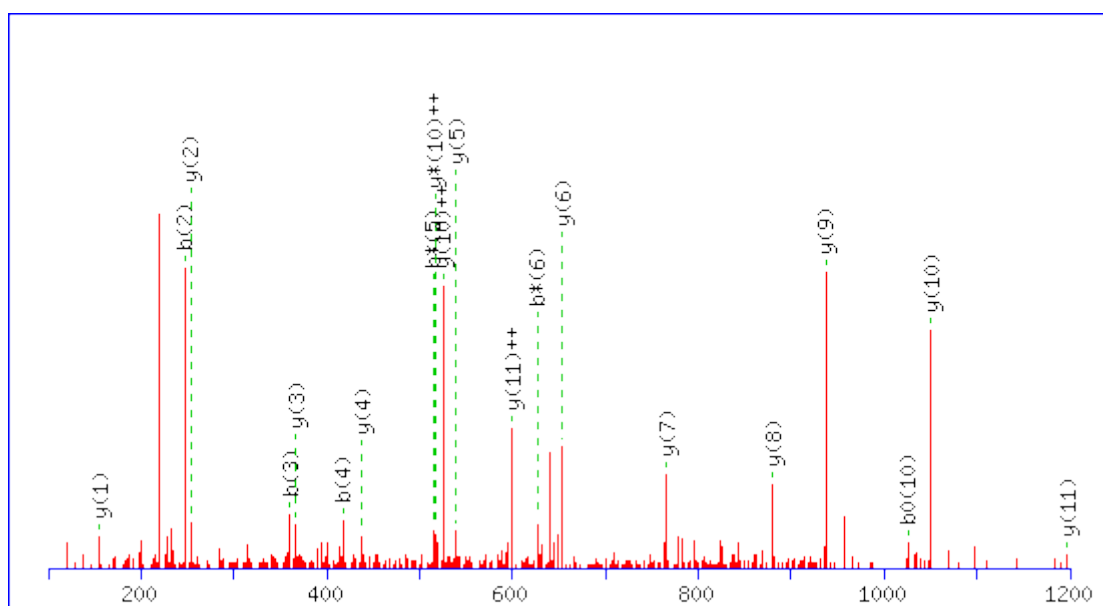
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 37 Expect: 0.05

Matches (Bold Red): 20/142 fragment ions using 43 most intense peaks

MS/MS Fragmentation of **VFIGNLNTAIVK**

Found in **RALYL_HUMAN**, RNA-binding Raly-like protein OS=Homo sapiens GN=RALYL
PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1295.7693

Variable modifications:

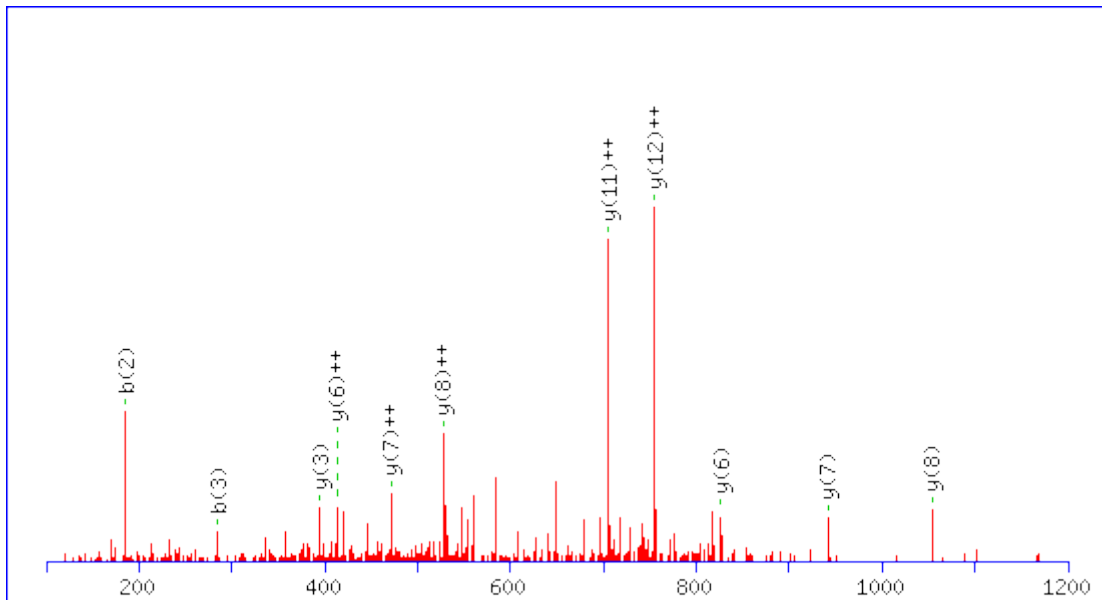
K12 : Label:13C(6)15N(2) (K)

Ions Score: 95 Expect: 6.7e-008

Matches (Bold Red): 20/102 fragment ions using 36 most intense peaks

MS/MS Fragmentation of **ANVNEILDFFHGYR**

Found in **RB12B_HUMAN**, RNA-binding protein 12B OS=Homo sapiens GN=RBM12B PE=1 SV=2



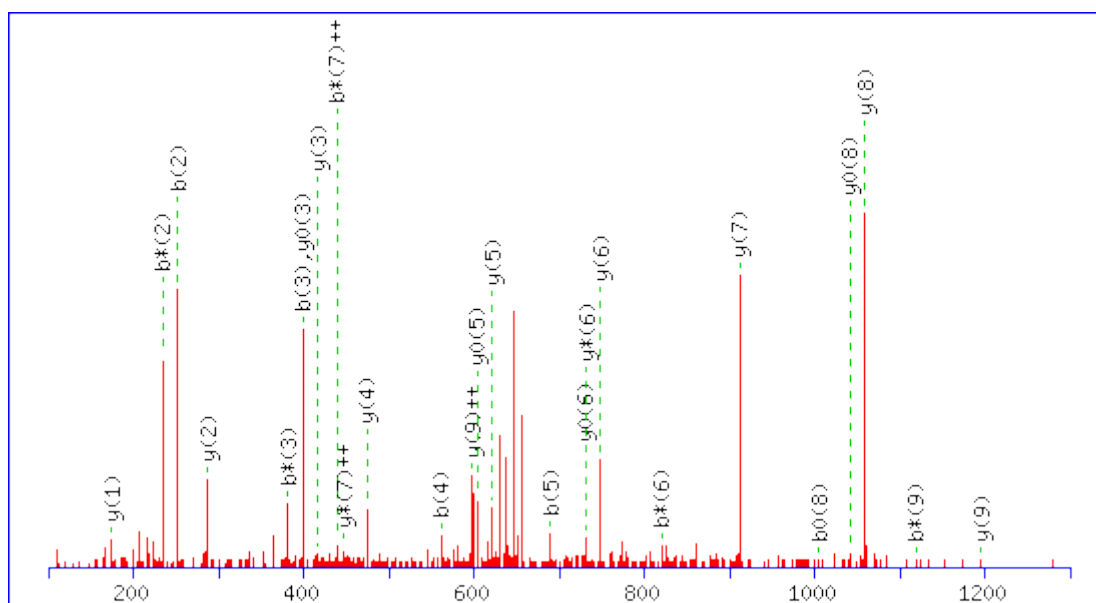
Monoisotopic mass of neutral peptide Mr(calc): 1693.8212

Ions Score: 39 Expect: 0.04

Matches (Bold Red): 11/134 fragment ions using 15 most intense peaks

MS/MS Fragmentation of **NHFYQFGEIR**

Found in **RBM22_HUMAN**, Pre-mRNA-splicing factor RBM22 OS=Homo sapiens GN=RBM22 PE=1 SV=1



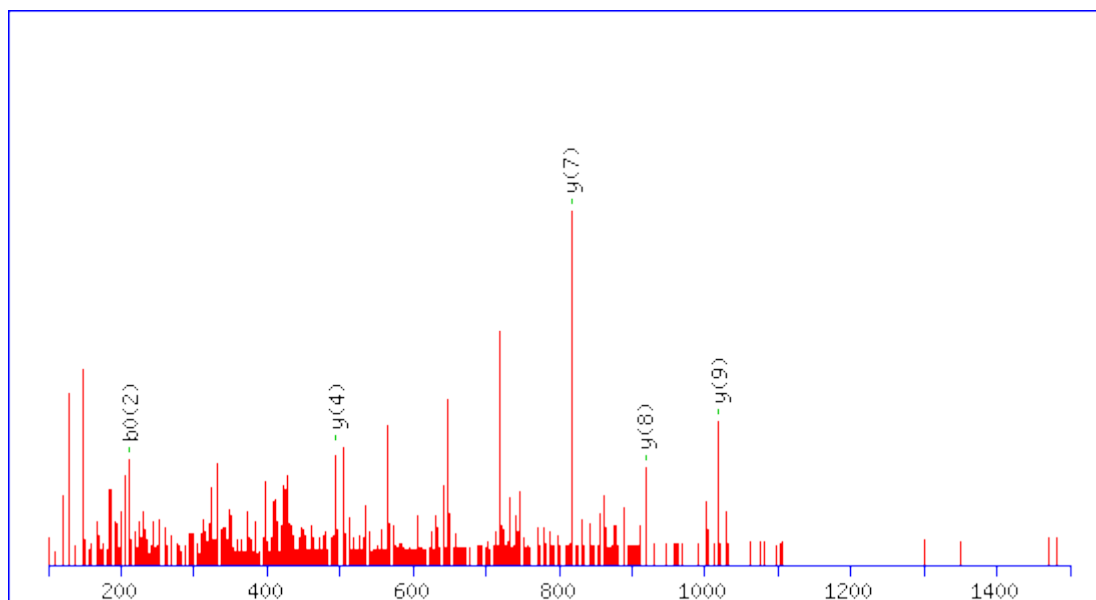
Monoisotopic mass of neutral peptide Mr(calc): 1309.6204

Ions Score: 49 Expect: 0.0029

Matches (Bold Red): 26/90 fragment ions using 66 most intense peaks

MS/MS Fragmentation of **KTTPLLSFLK**

Found in **REN3B_HUMAN**, Regulator of nonsense transcripts 3B OS=Homo sapiens
GN=UPF3B PE=1 SV=1



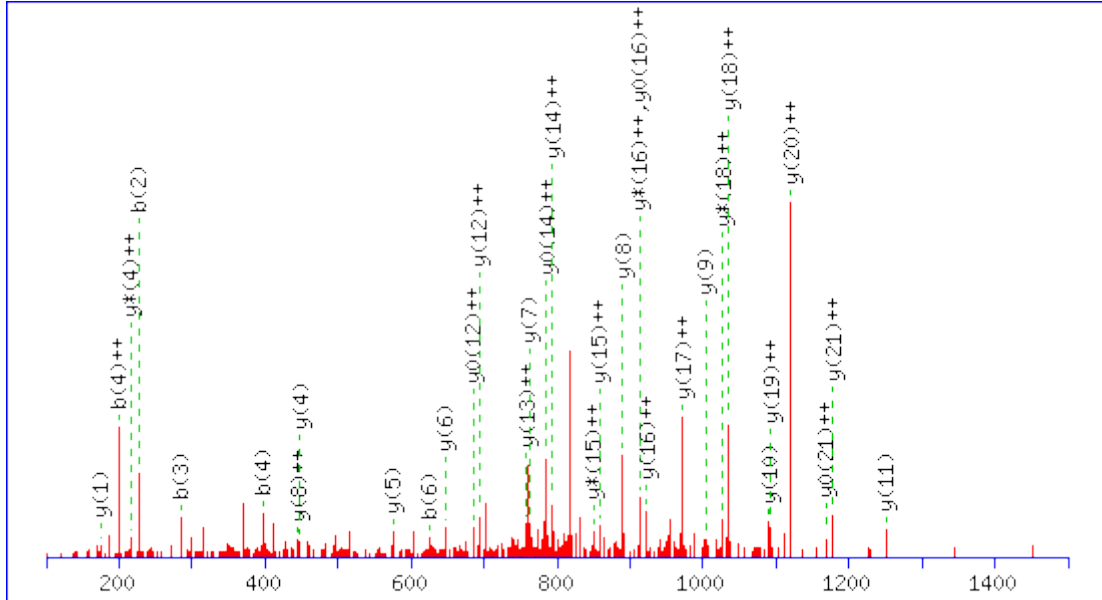
Monoisotopic mass of neutral peptide Mr(calc): 1146.7012

Ions Score: 15 Expect: 5.9

Matches (**Bold Red**): 5/100 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **ILGLQVQQA**EHCSIQDAQAAMR

Found in **REX04_HUMAN**, RNA exonuclease 4 OS=Homo sapiens GN=REX04 PE=1 SV=2



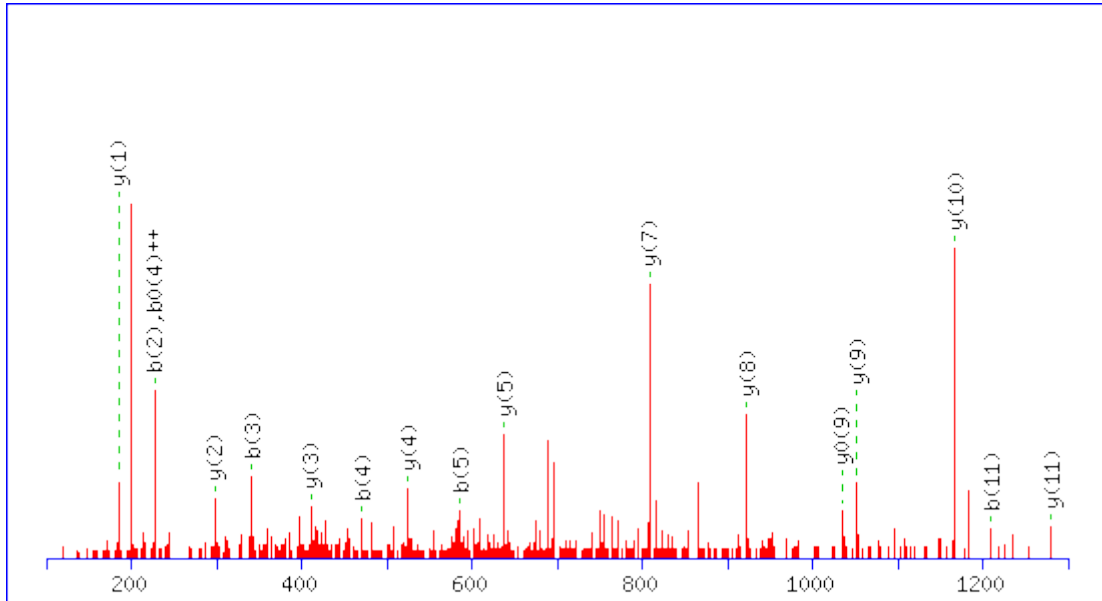
Monoisotopic mass of neutral peptide Mr(calc): 2466.2107

Ions Score: 55 Expect: 0.0014

Matches (**Bold Red**): 33/214 fragment ions using 96 most intense peaks

MS/MS Fragmentation of **IIDEDGLLN**LIR

Found in **RFC1_HUMAN**, Replication factor C subunit 1 OS=Homo sapiens GN=RFC1 PE=1 SV=4



Monoisotopic mass of neutral peptide Mr(calc): 1392.7852

Variable modifications:

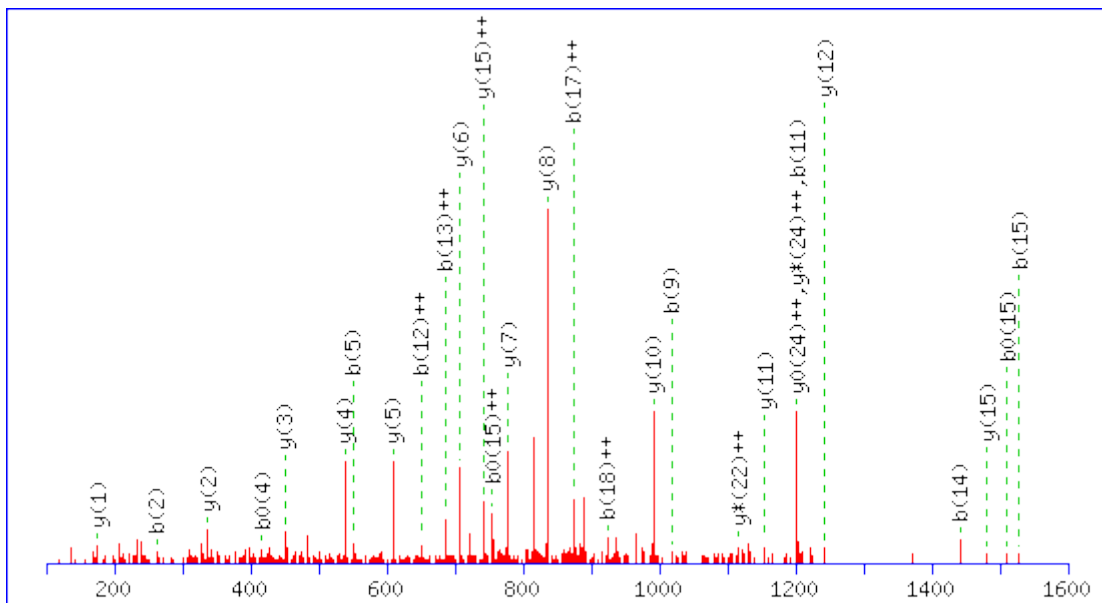
R12 : Label:13C(6)15N(4) (R)

Ions Score: 82 **Expect: 1.3e-006**

Matches (Bold Red): 17/98 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **VYTADPYHALAPAASYGVGAVASLYR**

Found in **RFOX2_HUMAN**, RNA binding protein fox-1 homolog 2 OS=Homo sapiens
GN=RBF0X2 PE=1 SV=3



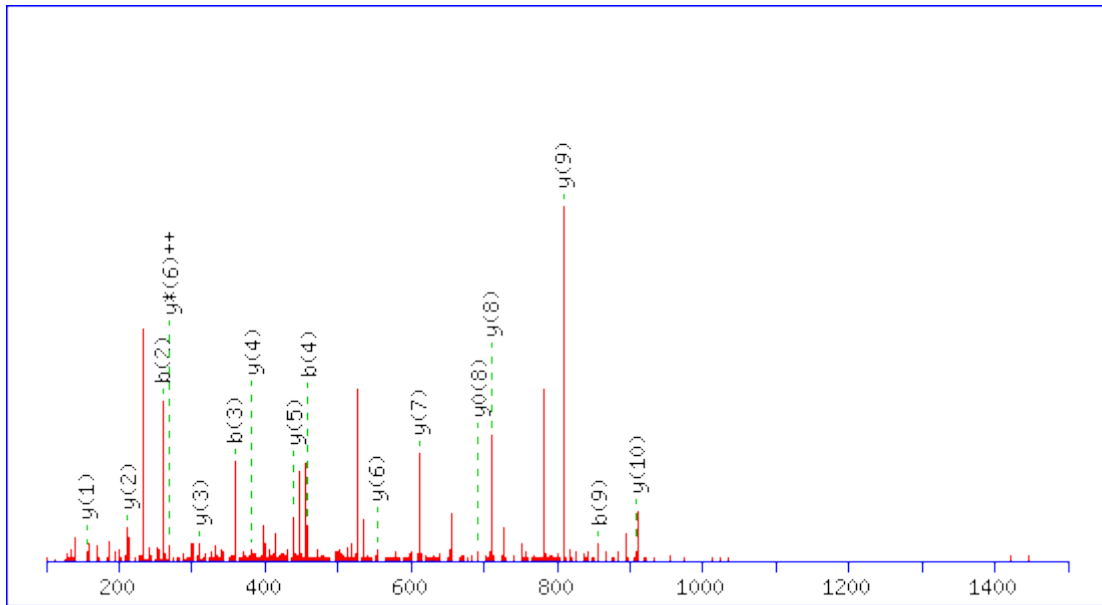
Monoisotopic mass of neutral peptide Mr(calc): 2682.3442

Ions Score: 59 Expect: 0.00049

Matches (Bold Red): 29/240 fragment ions using 55 most intense peaks

MS/MS Fragmentation of **CVVVGDAVGK**

Found in **RHOJ_HUMAN**, Rho-related GTP-binding protein RhoJ OS=Homo sapiens
GN=RHOJ PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1067.5525

Variable modifications:

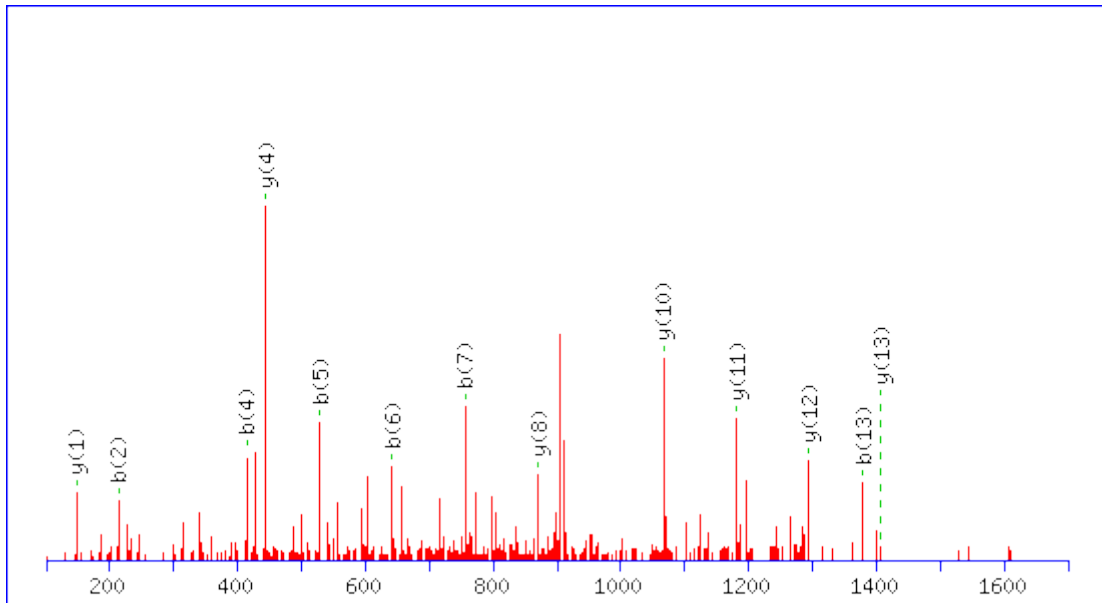
K11 : Label:13C(6)15N(2) (K)

Ions Score: 49 Expect: 0.0026

Matches (Bold Red): 16/80 fragment ions using 69 most intense peaks

MS/MS Fragmentation of **LVSDIIDPVALEIPLSK**

Found in **RIF1_HUMAN**, Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1
PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1821.0499

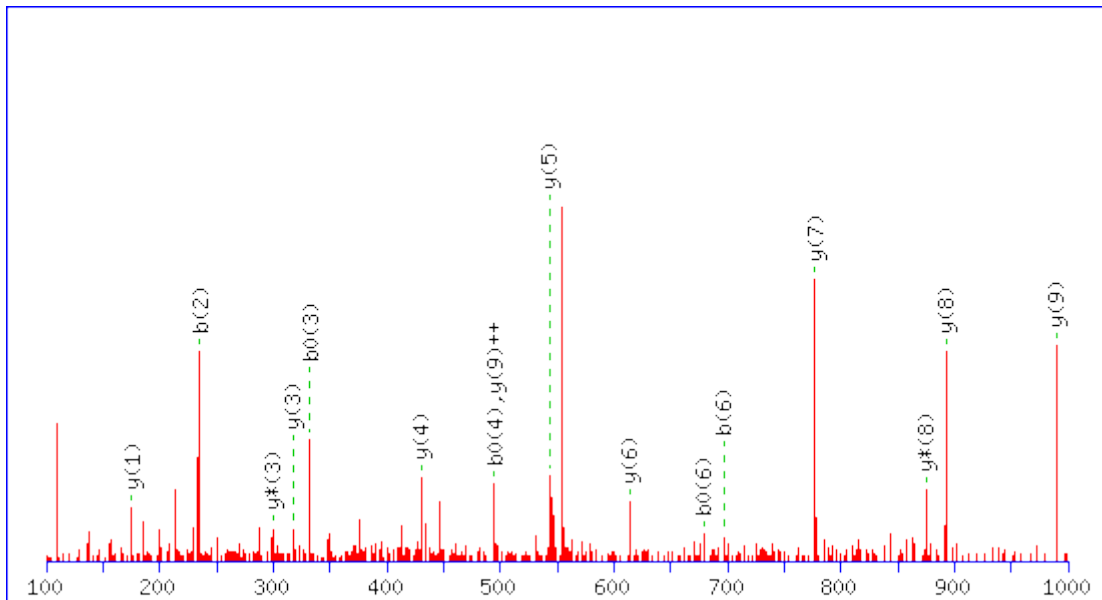
Ions Score: 50 Expect: 0.0024

Matches (Bold Red): 13/154 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **HPDYAILAAR**

Found in **RIR1_HUMAN**, Ribonucleoside-diphosphatereductase large subunit

OS=Homo sapiens GN=RRM1 PE=1 SV=1



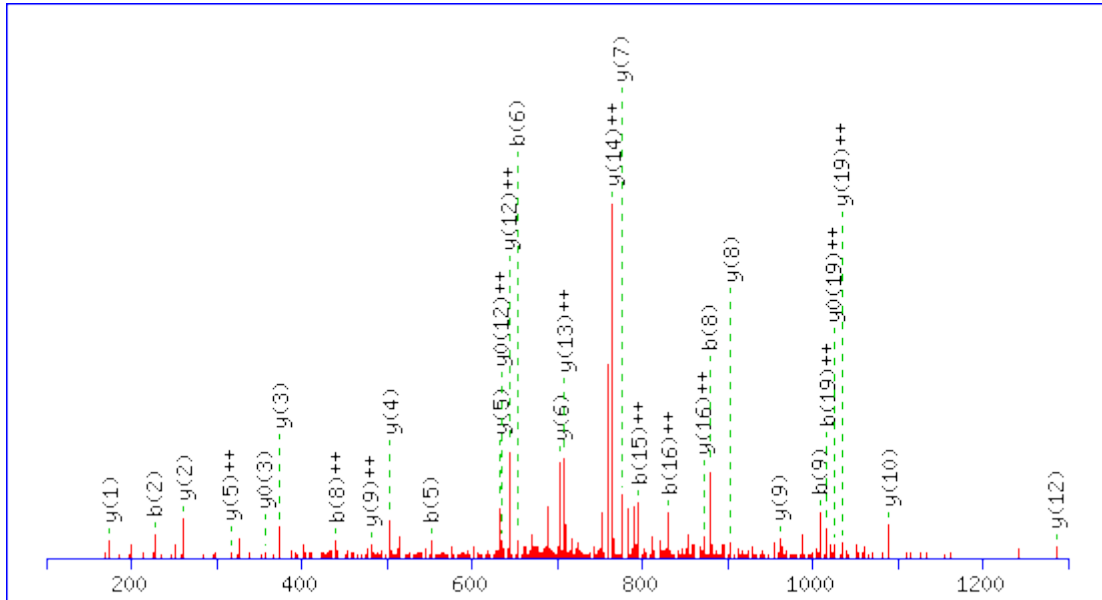
Monoisotopic mass of neutral peptide Mr(calc): 1125.5931

Ions Score: 60 Expect: 0.00022

Matches (**Bold Red**): 16/72 fragment ions using 29 most intense peaks

MS/MS Fragmentation of **LLPDITLLEPVEGEAAEELSR**

Found in **RPAC1_HUMAN**, DNA-directed RNA polymerases I and III subunit RPAC1
OS=Homo sapiens GN=POLR1C PE=1 SV=1



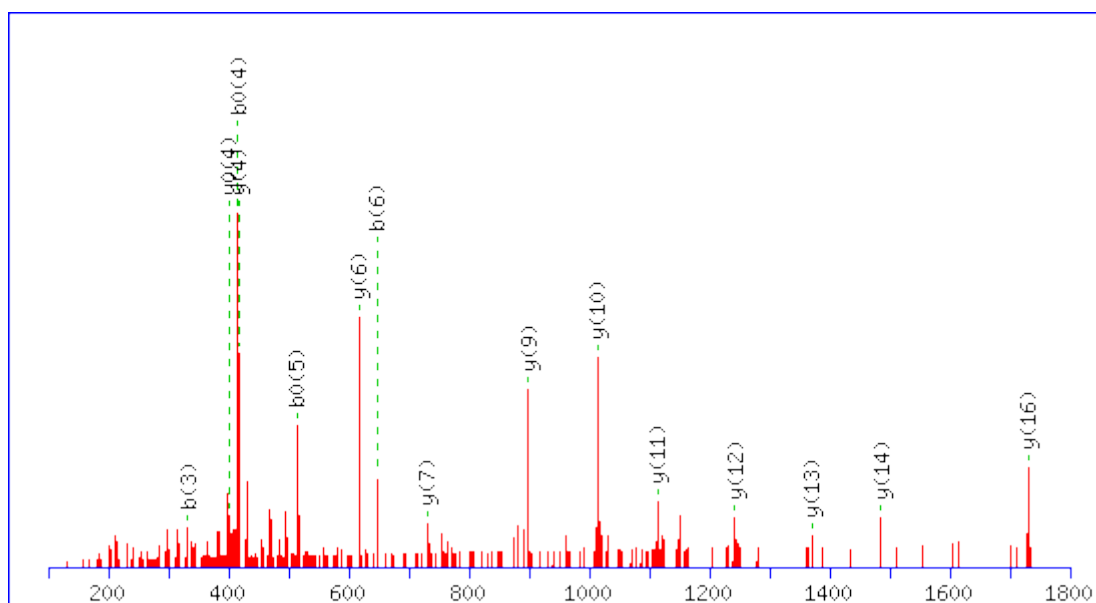
Monoisotopic mass of neutral peptide Mr(calc): 2293.2053

Ions Score: 69 Expect: 5e-005

Matches (**Bold Red**): 30/192 fragment ions using 59 most intense peaks

MS/MS Fragmentation of **DSETVDEDEEVDPALTVGTIK**

Found in **RRP5_HUMAN**, Protein RRP5 homolog OS=Homo sapiens GN=PCDC11 PE=1 SV=3



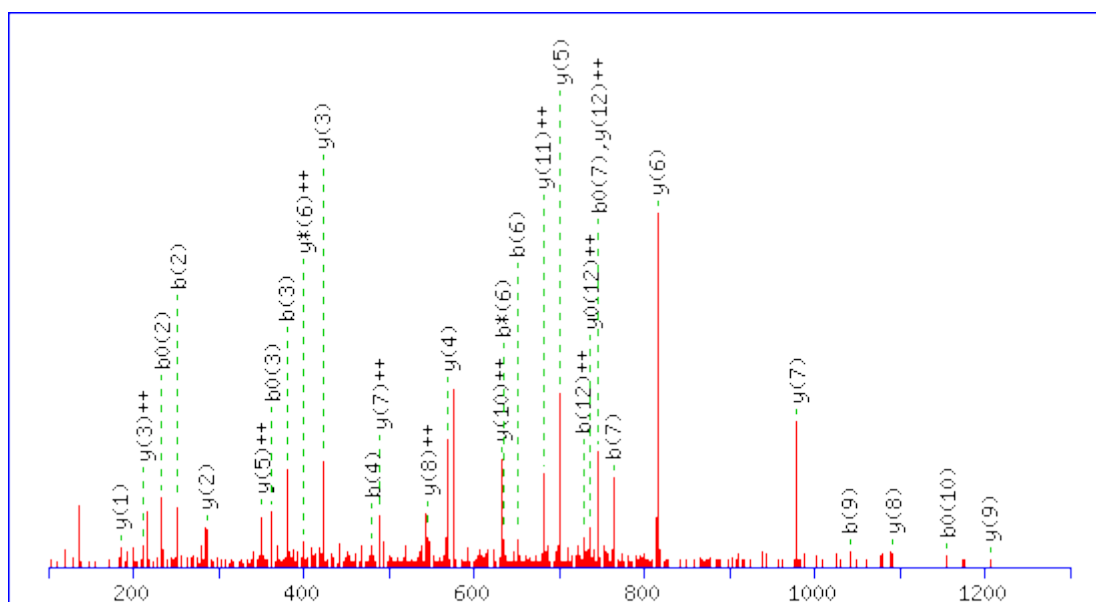
Monoisotopic mass of neutral peptide Mr(calc): 2261.0435

Ions Score: 54 **Expect:** 0.0018

Matches (Bold Red): 15/196 fragment ions using 21 most intense peaks

MS/MS Fragmentation of **DKEVG~~N~~LYDMFHTR**

Found in **SAMH1_HUMAN**, SAM domain and HD domain-containing protein 1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1741.8213

Variable modifications:

K2 : Label:13C(6)15N(2) (K)

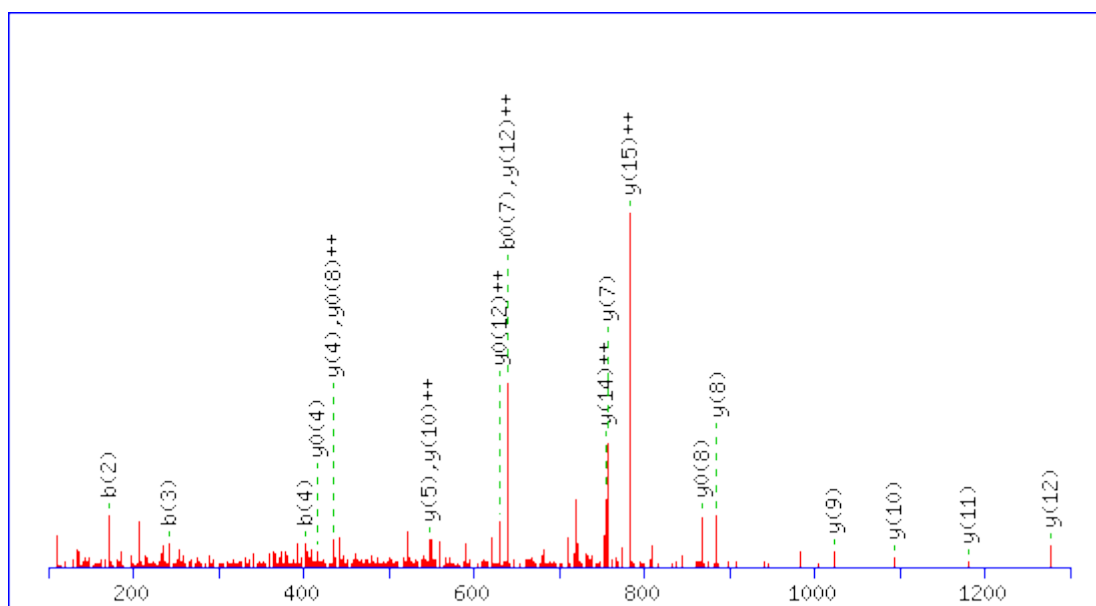
R14 : Label:13C(6)15N(4) (R)

Ions Score: 46 **Expect:** 0.0076

Matches (Bold Red): 30/152 fragment ions using 66 most intense peaks

MS/MS Fragmentation of **IGACPSAHKPLLGTEK**

Found in **SAP_HUMAN**, Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2



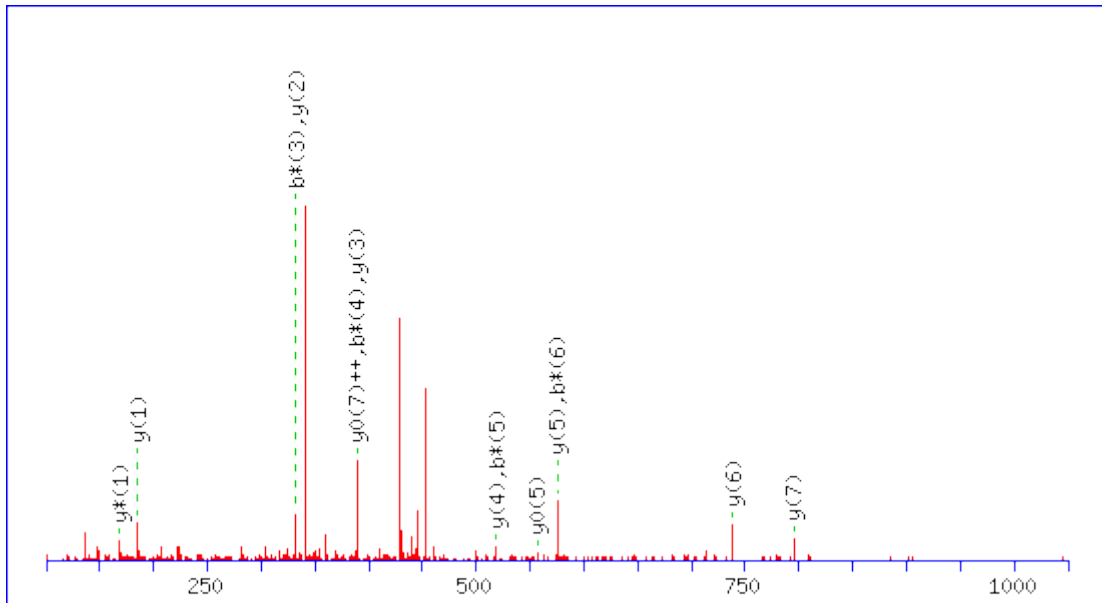
Monoisotopic mass of neutral peptide Mr(calc): 1677.8872

Ions Score: 44 **Expect:** 0.012

Matches (Bold Red): 20/152 fragment ions using 32 most intense peaks

MS/MS Fragmentation of **QGYGEGFR**

Found in **SAR1A_HUMAN**, GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 922.4173

Variable modifications:

R8 : Label: $^{13}\text{C}(6)^{15}\text{N}(4)$ (R)

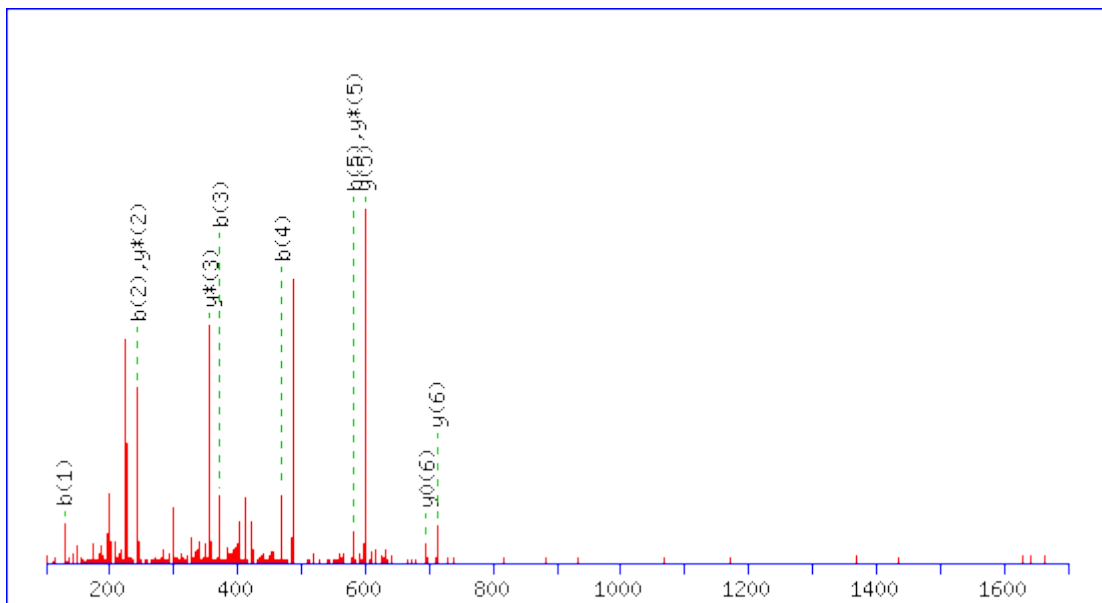
Ions Score: 41 Expect: 0.013

Matches (Bold Red): 14/70 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **KNEPIIK**

Found in **SC31B_HUMAN**, Protein transport protein Sec31B OS=Homo sapiens

GN=SEC31B PE=1 SV=1



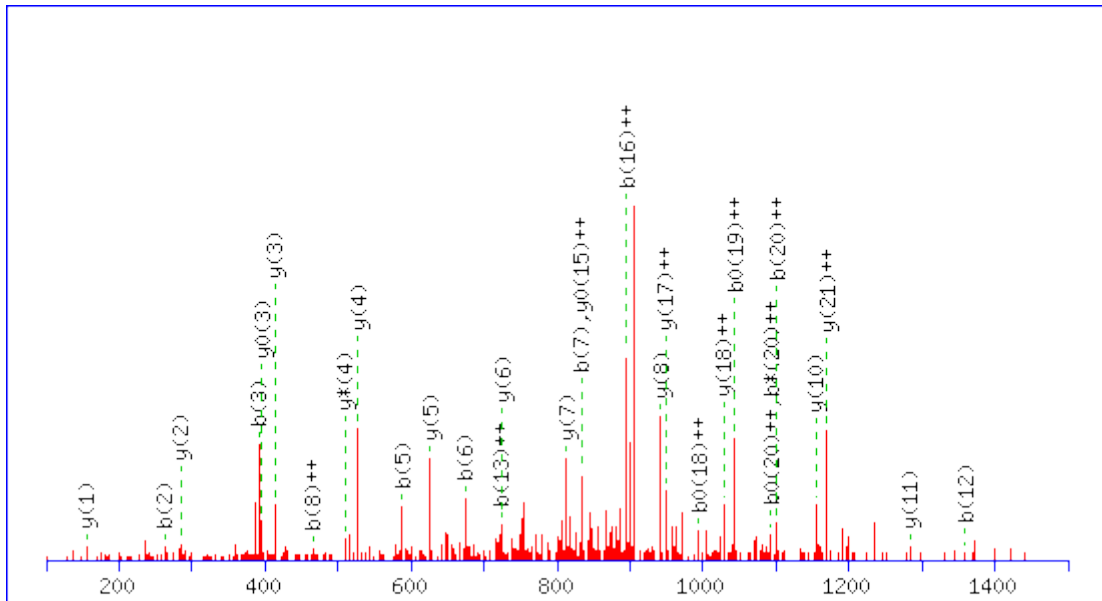
Monoisotopic mass of neutral peptide Mr(calc): 840.5069

Ions Score: 38 Expect: 0.025

Matches (**Bold Red**): 12/60 fragment ions using 31 most intense peaks

MS/MS Fragmentation of **VYQPVSCPLSDLSENVESVVNEEK**

Found in **SCAFB_HUMAN**, Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 2728.2993

Variable modifications:

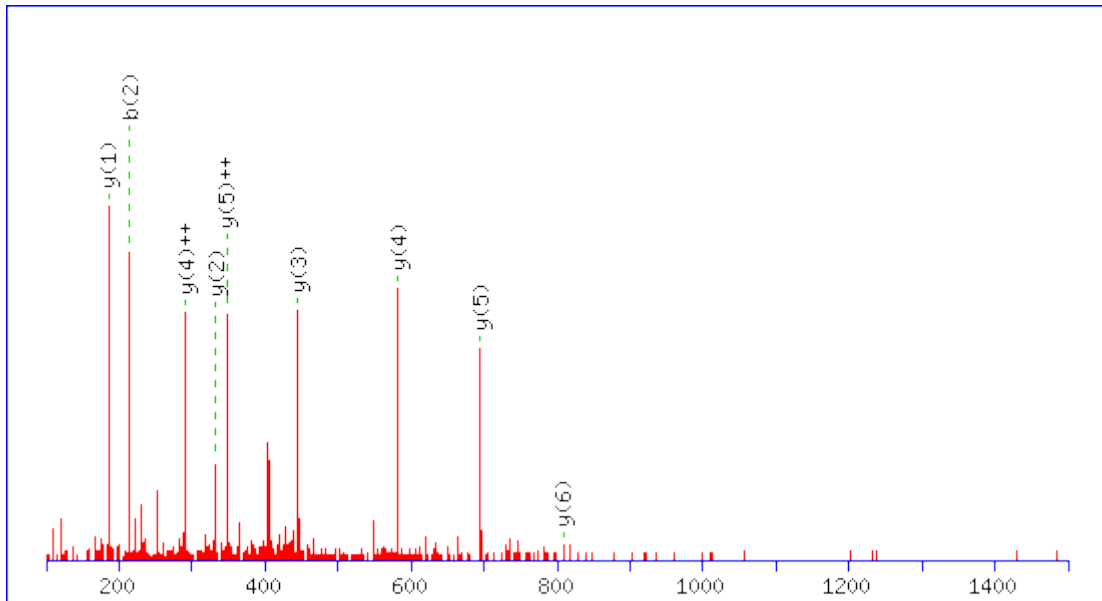
K24 : Label:13C(6)15N(2) (K)

Ions Score: 55 Expect: 0.0016

Matches (**Bold Red**): 30/260 fragment ions using 57 most intense peaks

MS/MS Fragmentation of **TLIHLFR**

Found in **SDA1_HUMAN**, Protein SDA1 homolog OS=Homo sapiens GN=SDAD1 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 908.5471

Variable modifications:

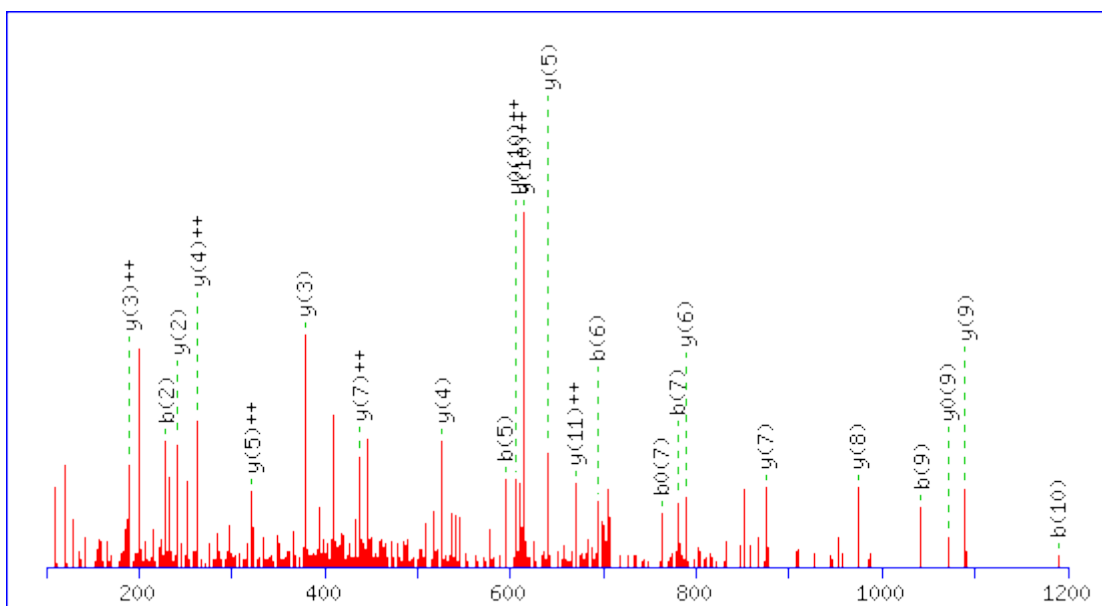
R7 : Label:13C(6)15N(4) (R)

Ions Score: 38 Expect: 0.026

Matches (Bold Red): 9/48 fragment ions using 31 most intense peaks

MS/MS Fragmentation of **DLIHDVSFDFHGR**

Found in **SEH1_HUMAN**, Nucleoporin SEH1 OS=Homo sapiens GN=SEH1L PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1566.7455

Variable modifications:

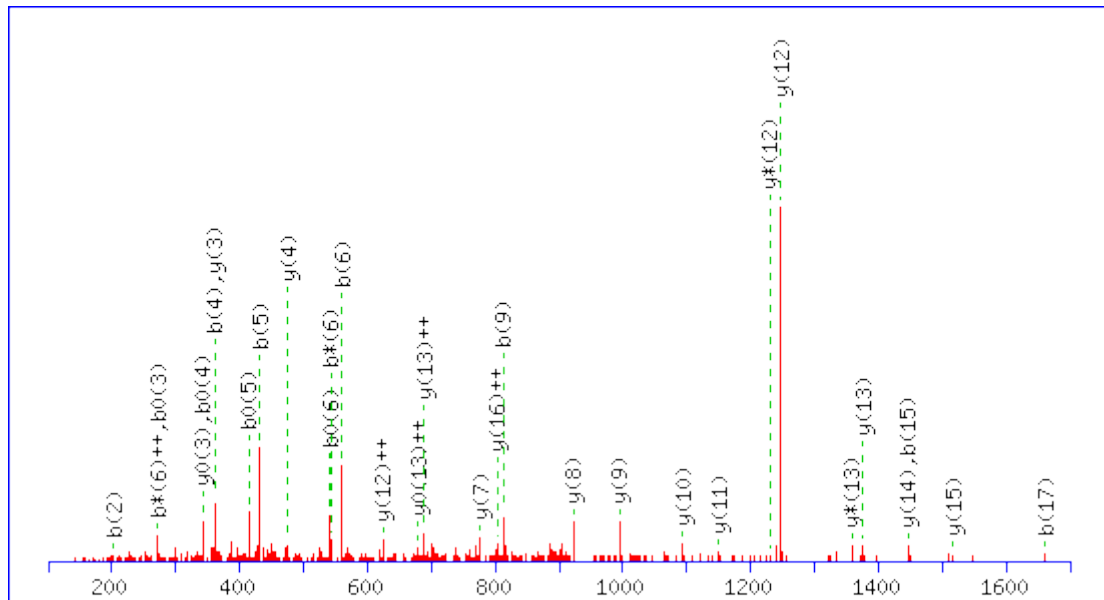
R13 : Label:13C(6)15N(4) (R)

Ions Score: 58 Expect: 0.00046

Matches (Bold Red): 23/112 fragment ions using 34 most intense peaks

MS/MS Fragmentation of **DSSAAQPGVAFSVDNTIK**

Found in **SHOC2_HUMAN**, Leucine-rich repeat protein SHOC-2 OS=Homo sapiens
GN=SHOC2 PE=1 SV=2



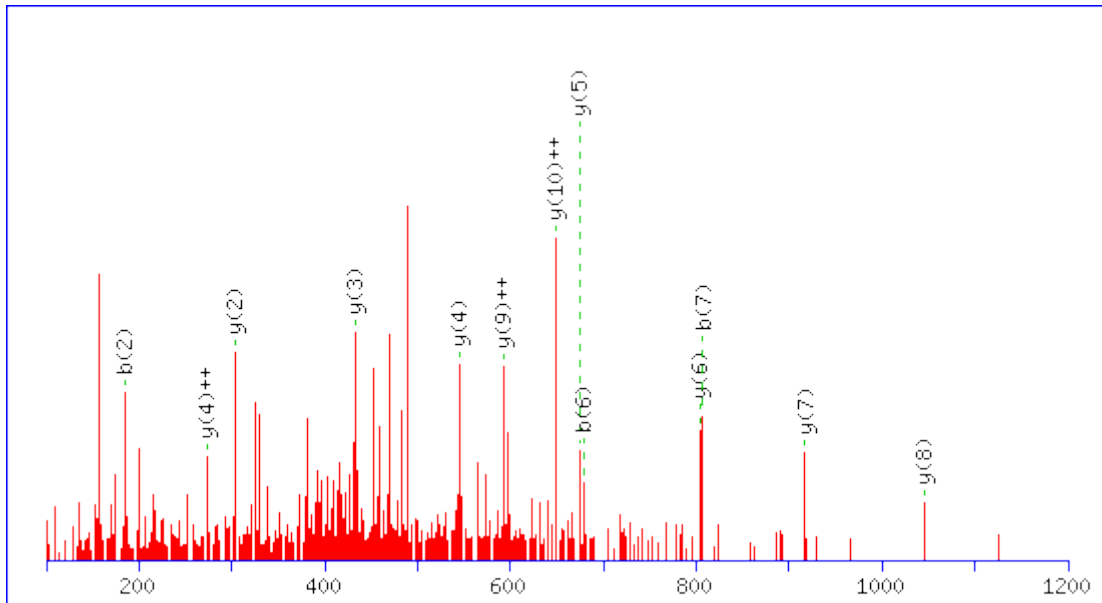
Monoisotopic mass of neutral peptide Mr(calc): 1805.8796

Ions Score: 59 Expect: 0.00043

Matches (Bold Red): 31/190 fragment ions using 60 most intense peaks

MS/MS Fragmentation of **ALNHEIEELEKR**

Found in **SMC2_HUMAN**, Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2



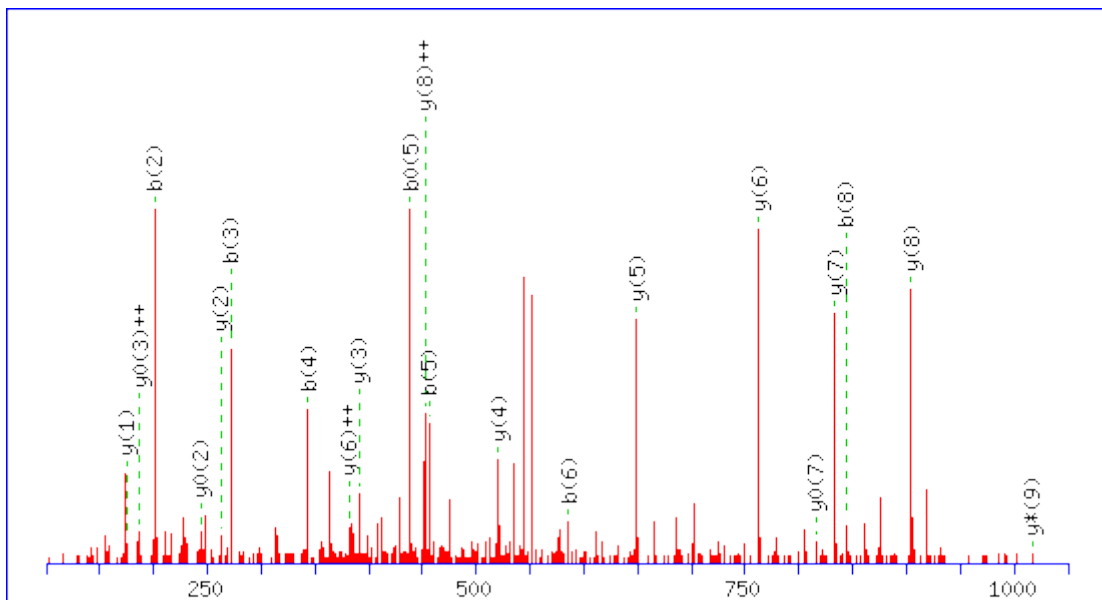
Monoisotopic mass of neutral peptide Mr(calc): 1479.7681

Ions Score: 43 Expect: 0.015

Matches (Bold Red): 13/116 fragment ions using 22 most intense peaks

MS/MS Fragmentation of **AEAALEEESR**

Found in **SMCE1_HUMAN**, SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens GN=SMARCE1 PE=1 SV=2



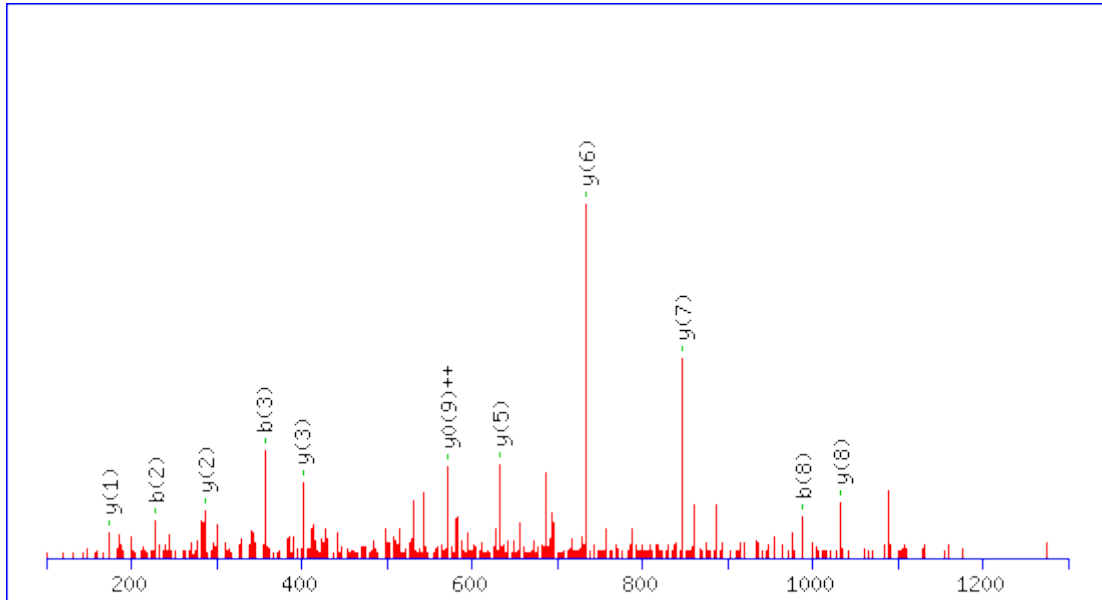
Monoisotopic mass of neutral peptide Mr(calc): 1103.5094

Ions Score: 39 Expect: 0.031

Matches (Bold Red): 21/86 fragment ions using 66 most intense peaks

MS/MS Fragmentation of **LDQWLTMLLR**

Found in **SNAB_HUMAN**, Beta-soluble NSF attachment protein OS=Homo sapiens
GN=NAPB PE=1 SV=2



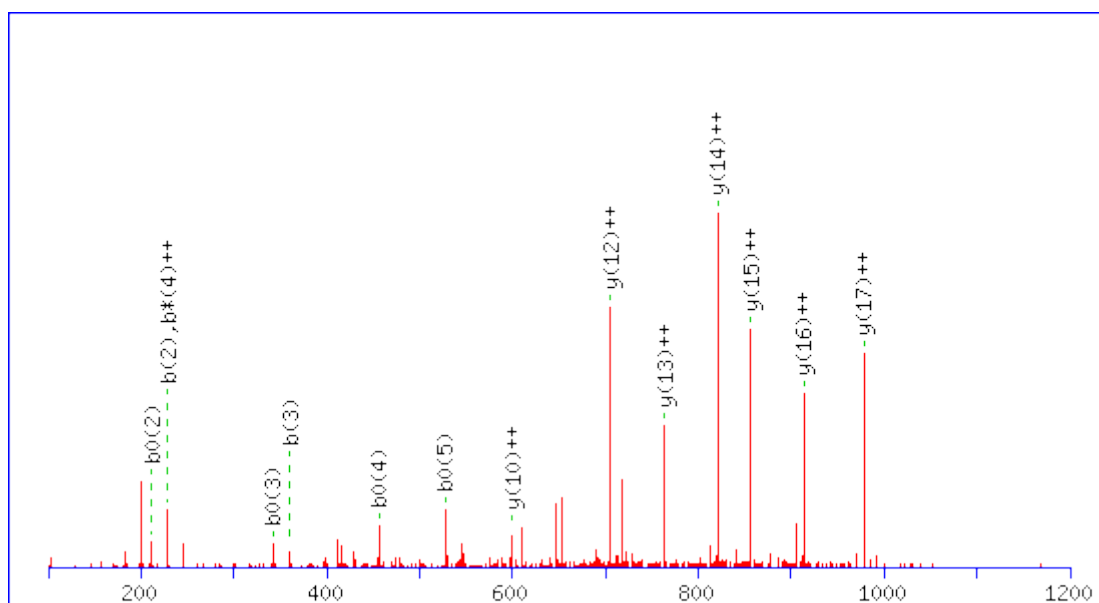
Monoisotopic mass of neutral peptide Mr(calc): 1388.7486

Ions Score: 45 **Expect:** 0.0099

Matches (Bold Red): 11/106 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **EVMNADDPDLQRPDEEAIK**

Found in **SNW1_HUMAN**, SNW domain-containing protein 1 OS=Homo sapiens GN=SNW1
PE=1 SV=1



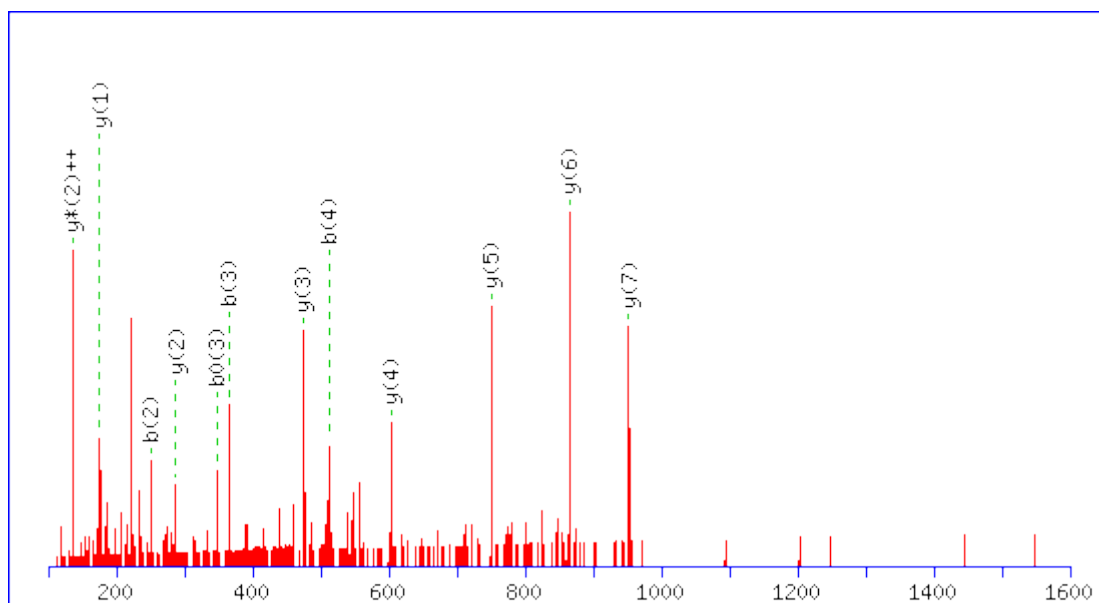
Monoisotopic mass of neutral peptide Mr(calc): 2184.0004

Ions Score: 41 Expect: 0.032

Matches (Bold Red): 14/204 fragment ions using 25 most intense peaks

MS/MS Fragmentation of **YSDFEWLR**

Found in **SNX3_HUMAN**, Sorting nexin-3 OS=Homo sapiens GN=SNX3 PE=1 SV=3



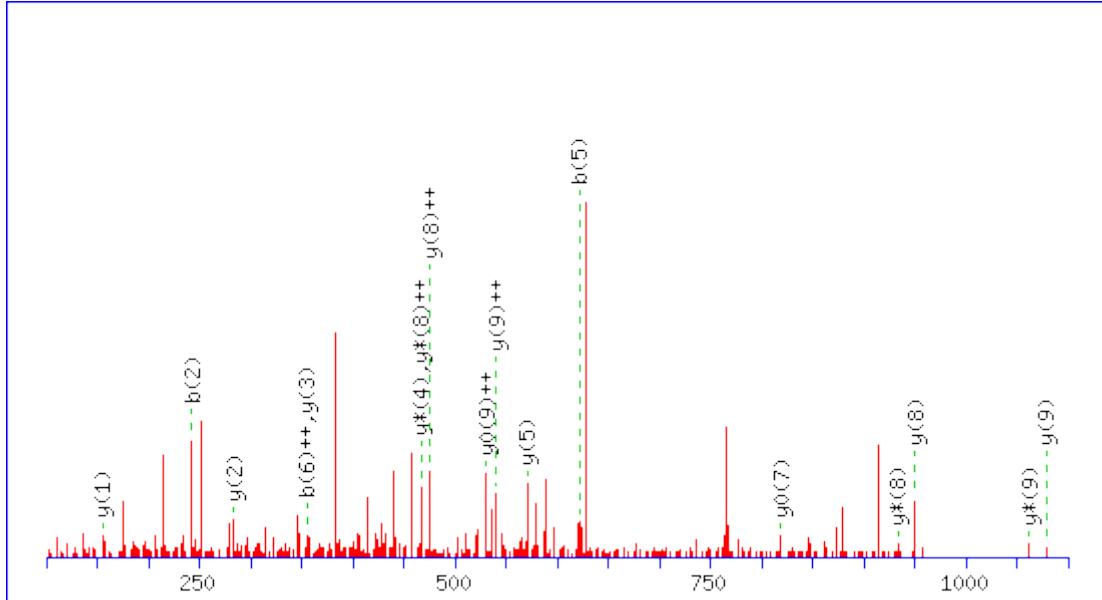
Monoisotopic mass of neutral peptide Mr(calc): 1114.5083

Ions Score: 38 Expect: 0.028

Matches (Bold Red): 12/62 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **IEISVSEAEK**

Found in **SNX4_HUMAN**, Sorting nexin-4 OS=Homo sapiens GN=SNX4 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1191.5515

Variable modifications:

S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

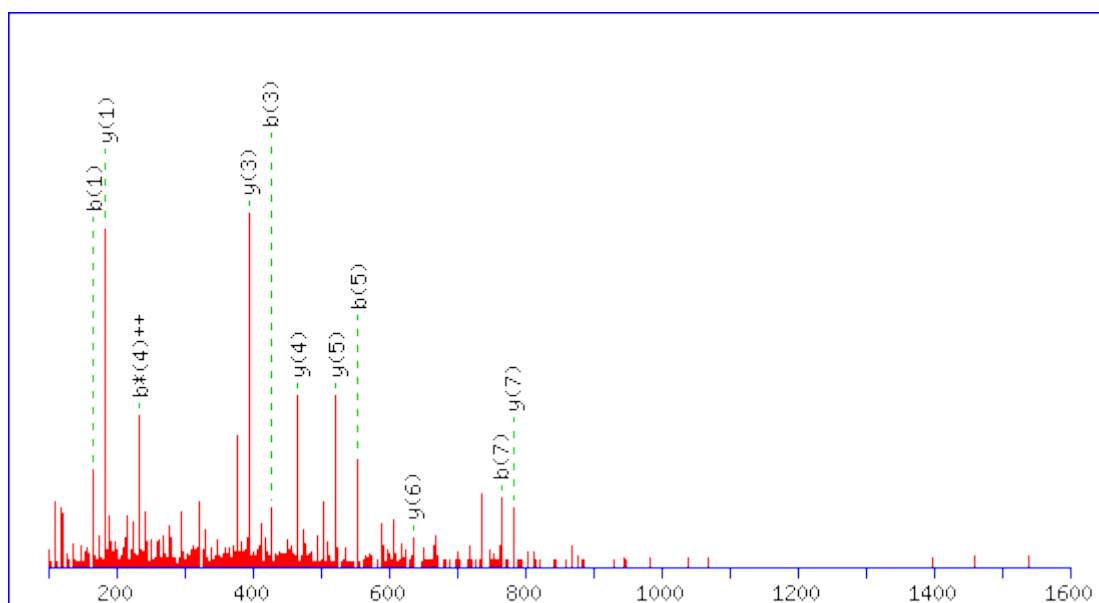
K10 : Label:13C(6)15N(2) (K)

Ions Score: 19 **Expect:** 3.5

Matches (Bold Red): 17/128 fragment ions using 48 most intense peaks

MS/MS Fragmentation of **RMLGAPLR**

Found in **SOCS1_HUMAN**, Suppressor of cytokine signaling 1 OS=Homo sapiens
GN=SOCS1 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 948.5442

Variable modifications:

R1 : Label:13C(6)15N(4) (R)

M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

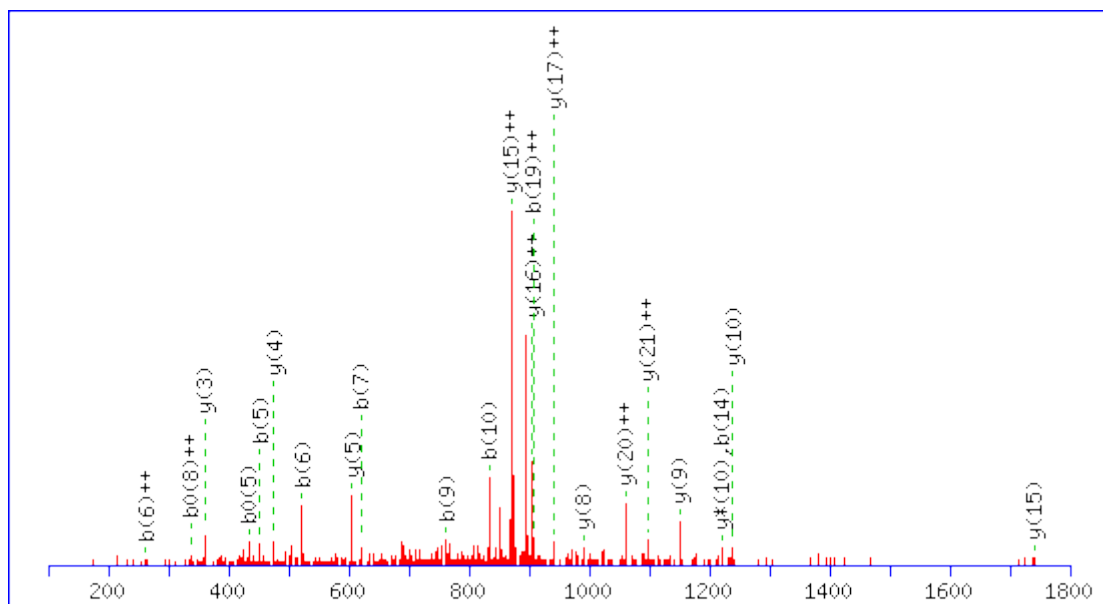
R8 : Label:13C(6)15N(4) (R)

Ions Score: 35 Expect: 0.075

Matches (Bold Red): 11/84 fragment ions using 34 most intense peaks

MS/MS Fragmentation of **EGPPAAPAAAPGYGQSCCLIEDGER**

Found in **SP30L_HUMAN**, Histone deacetylase complex subunit SAP30L OS=Homo sapiens GN=SAP30L PE=1 SV=1



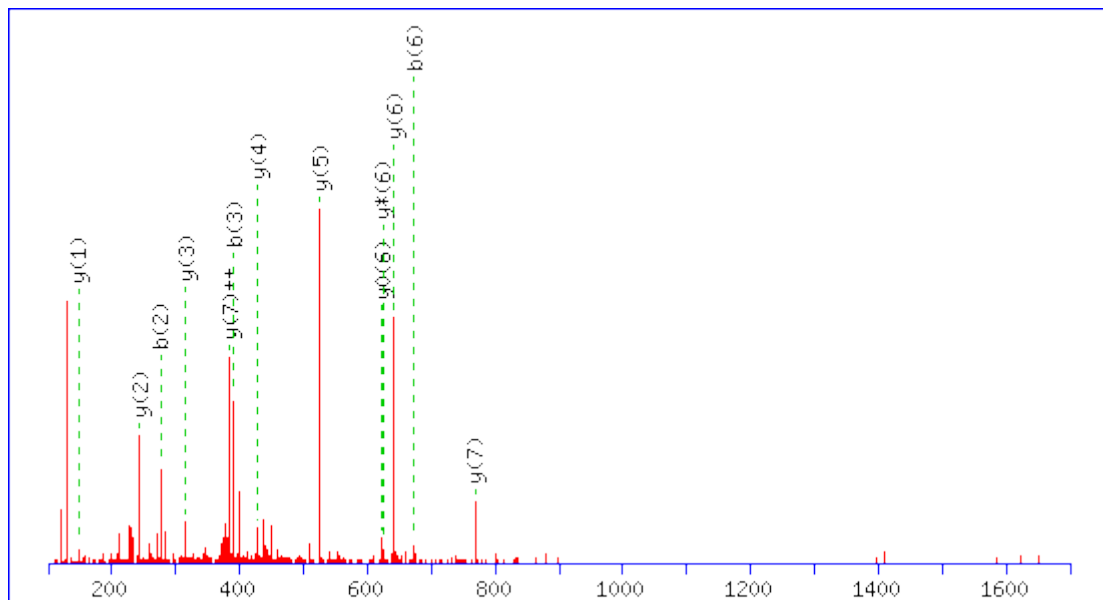
Monoisotopic mass of neutral peptide Mr(calc): 2643.1693

Ions Score: 55 Expect: 0.0015

Matches (Bold Red): 23/268 fragment ions using 34 most intense peaks

MS/MS Fragmentation of **FKDPNAPK**

Found in **SP100_HUMAN**, Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 915.4814

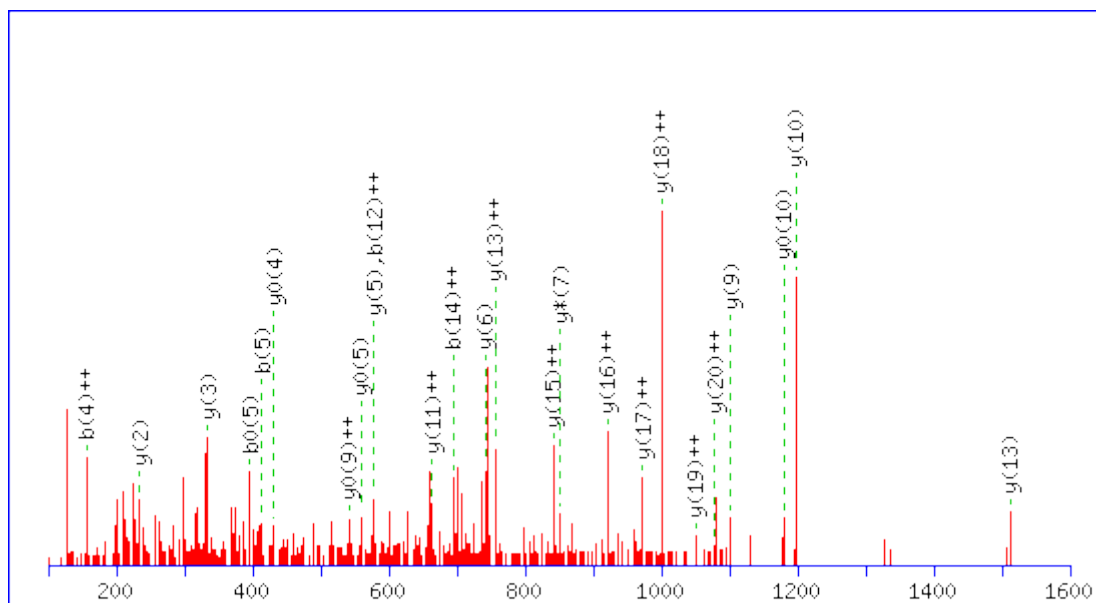
Ions Score: 44 Expect: 0.0087

Matches (**Bold Red**): 13/68 fragment ions using 39 most intense peaks

MS/MS Fragmentation of **VGVGTCGIADKPMTQYQDTSK**

Found in **SPF30_HUMAN**, Survival of motor neuron-related-splicing factor 30

OS=Homo sapiens GN=SMNDC1 PE=1 SV=1



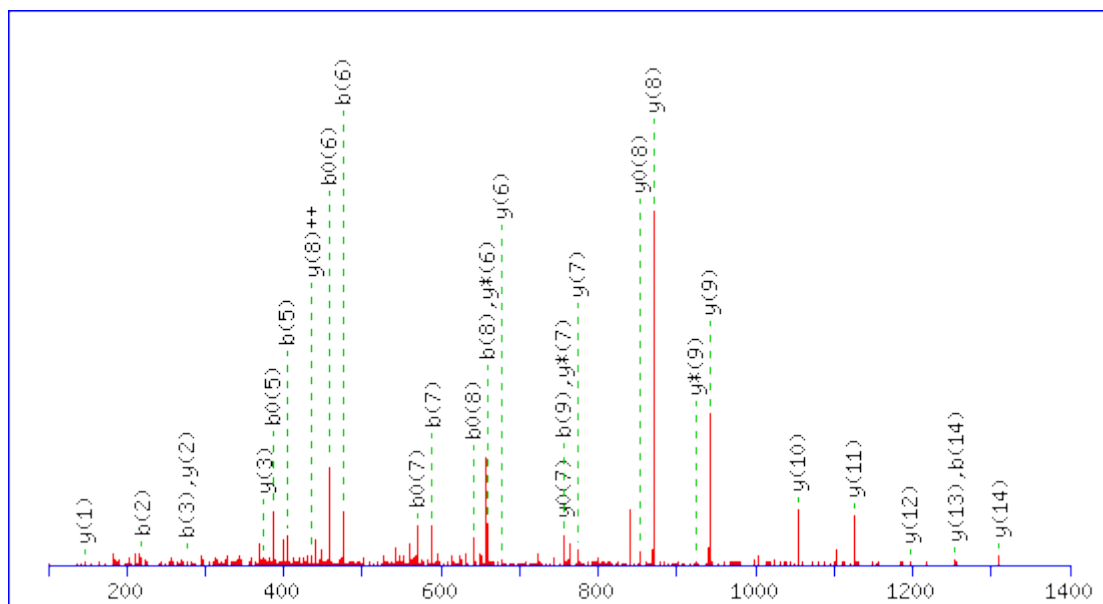
Monoisotopic mass of neutral peptide Mr(calc): 2255.0562

Ions Score: 52 Expect: 0.0029

Matches (**Bold Red**): 26/210 fragment ions using 50 most intense peaks

MS/MS Fragmentation of **SMGGAAIAPPTSLVEK**

Found in **SPF45_HUMAN**, Splicing factor 45 OS=Homo sapiens GN=RBM17 PE=1 SV=1



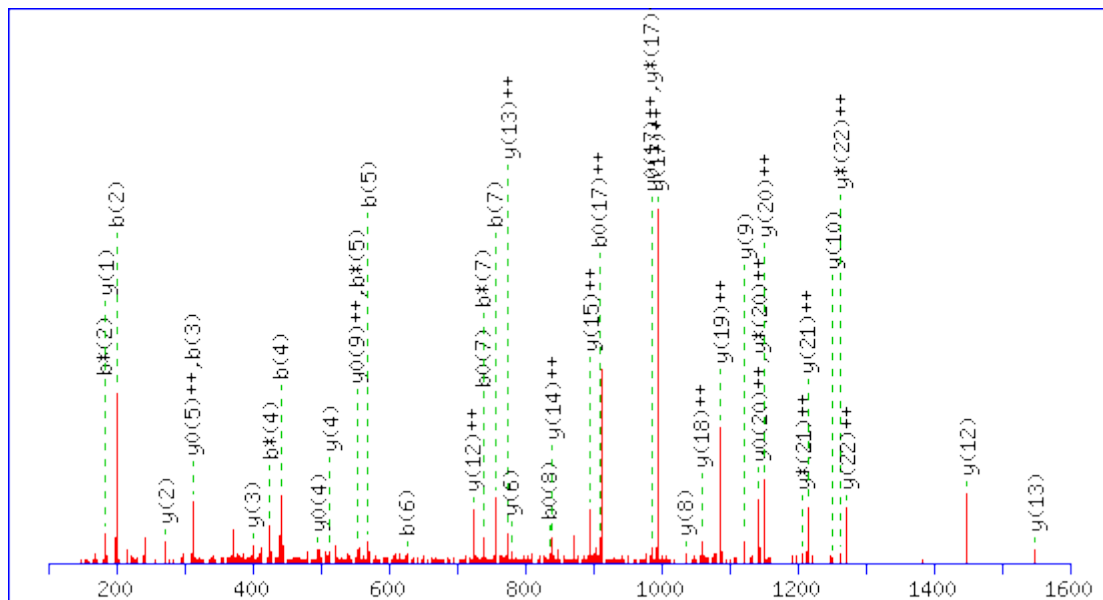
Monoisotopic mass of neutral peptide Mr(calc): 1527.7967

Ions Score: 39 Expect: 0.044

Matches (**Bold Red**): 30/148 fragment ions using 114 most intense peaks

MS/MS Fragmentation of **AQLEQGEPVLETPVESQQHEIESR**

Found in **STAT2_HUMAN**, Signal transducer and activator of transcription 2
OS=Homo sapiens GN=STAT2 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 2742.3336

Variable modifications:

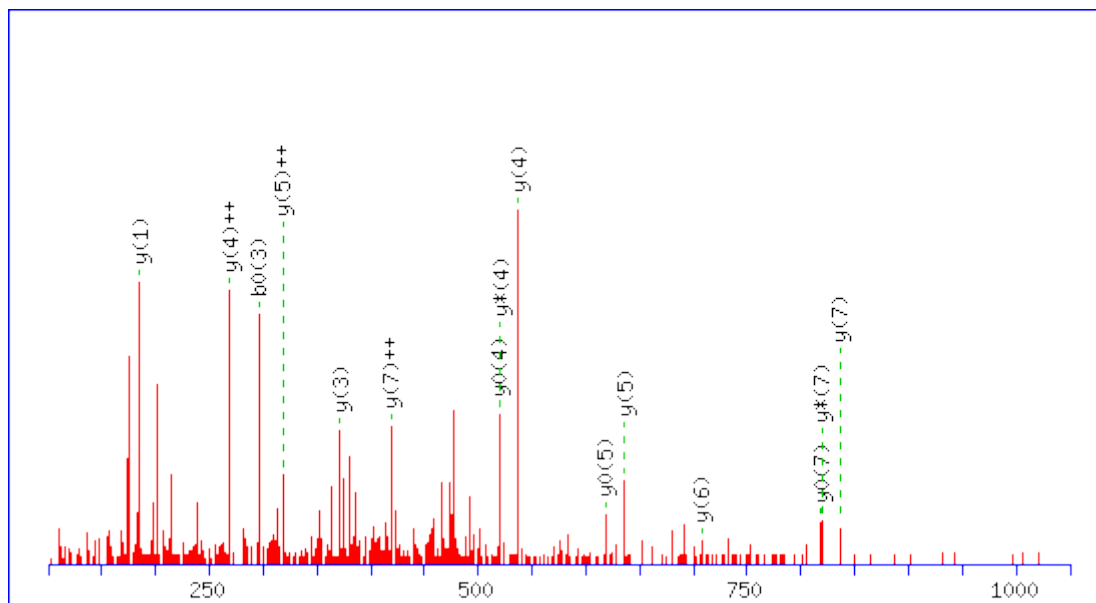
R24 : Label:13C(6)15N(4) (R)

Ions Score: 70 **Expect:** 4.1e-005

Matches (Bold Red): 42/266 fragment ions using 74 most intense peaks

MS/MS Fragmentation of **LEAVRADR**

Found in **STF1_HUMAN**, Steroidogenic factor 1 OS=Homo sapiens GN=NR5A1 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 948.5255

Variable modifications:

R5 : Label:13C(6)15N(4) (R)

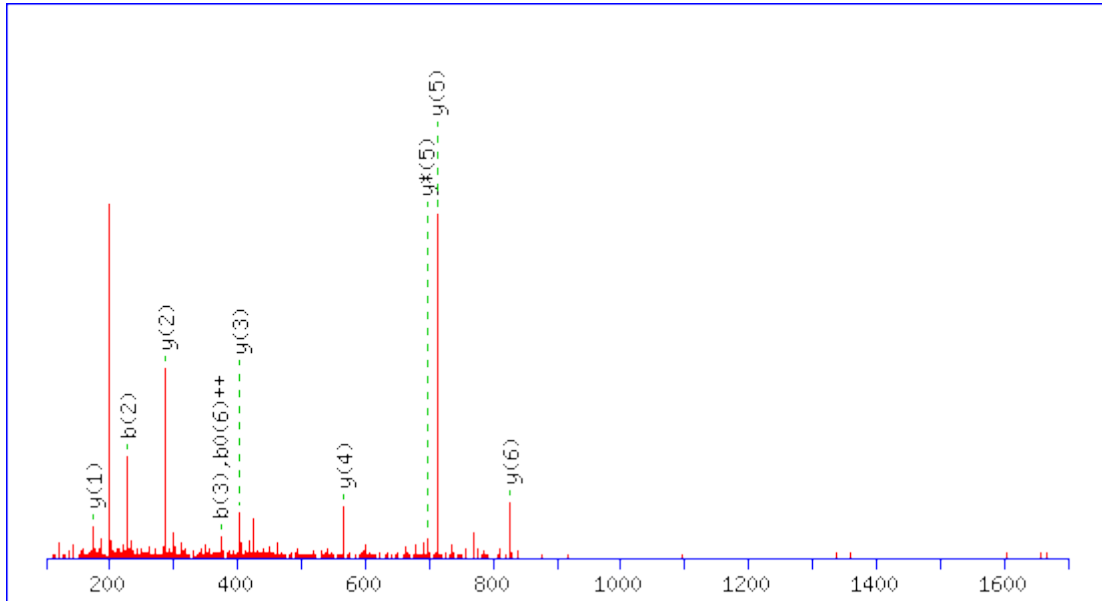
R8 : Label:13C(6)15N(4) (R)

Ions Score: 38 **Expect:** 0.018

Matches (Bold Red): 15/72 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **LIFYDLR**

Found in **SYK_HUMAN**, Lysyl-tRNA synthetase OS=Homo sapiens GN=KARS PE=1 SV=3



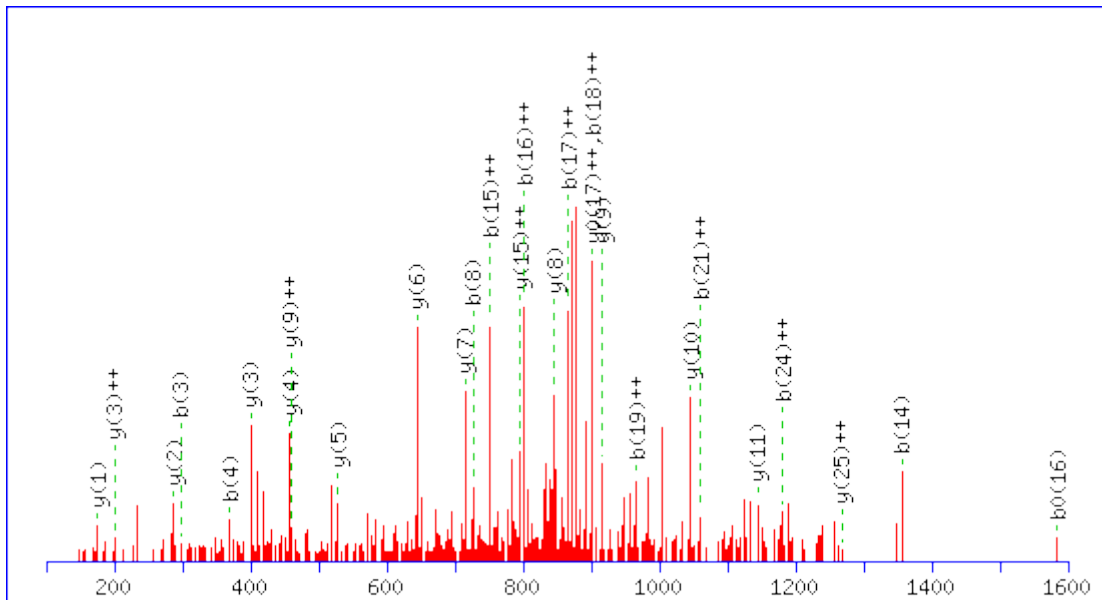
Monoisotopic mass of neutral peptide Mr(calc): 938.5225

Ions Score: 43 Expect: 0.0093

Matches (Bold Red): 10/48 fragment ions using 28 most intense peaks

MS/MS Fragmentation of **LALADAGDTVEDANFVEAMADAGILR**

Found in **SYLC_HUMAN**, Leucyl-tRNA synthetase, cytoplasmic OS=Homo sapiens
GN=LARS PE=1 SV=2



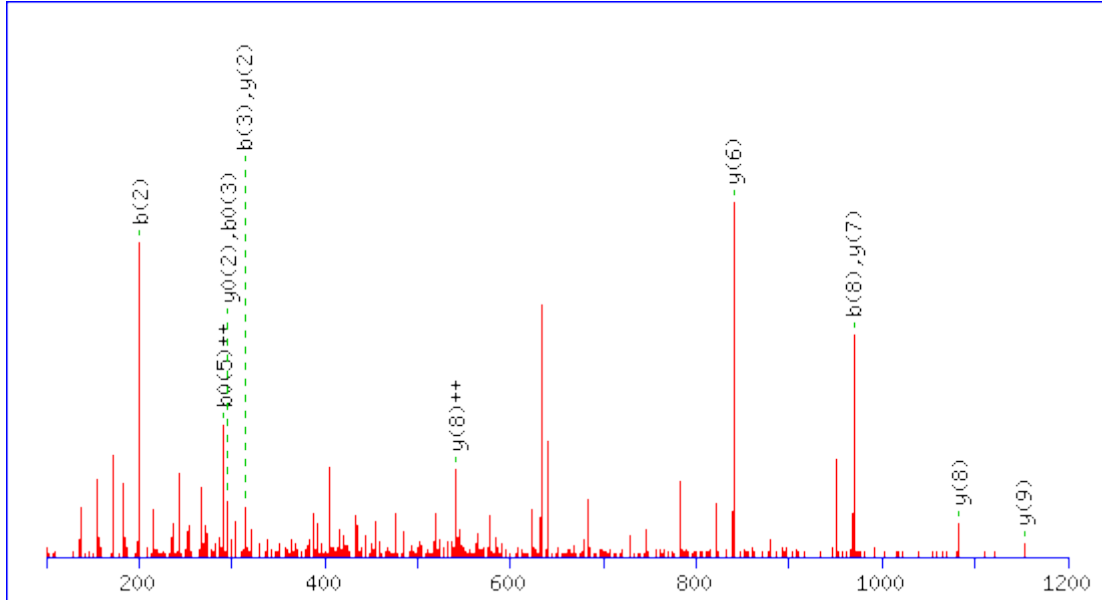
Monoisotopic mass of neutral peptide Mr(calc): 2647.2799

Ions Score: 44 Expect: 0.016

Matches (Bold Red): 28/256 fragment ions using 53 most intense peaks

MS/MS Fragmentation of **EALERLEQSK**

Found in **SYNE2_HUMAN**, Nesprin-2 OS=Homo sapiens GN=SYNE2 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1281.5965

Variable modifications:

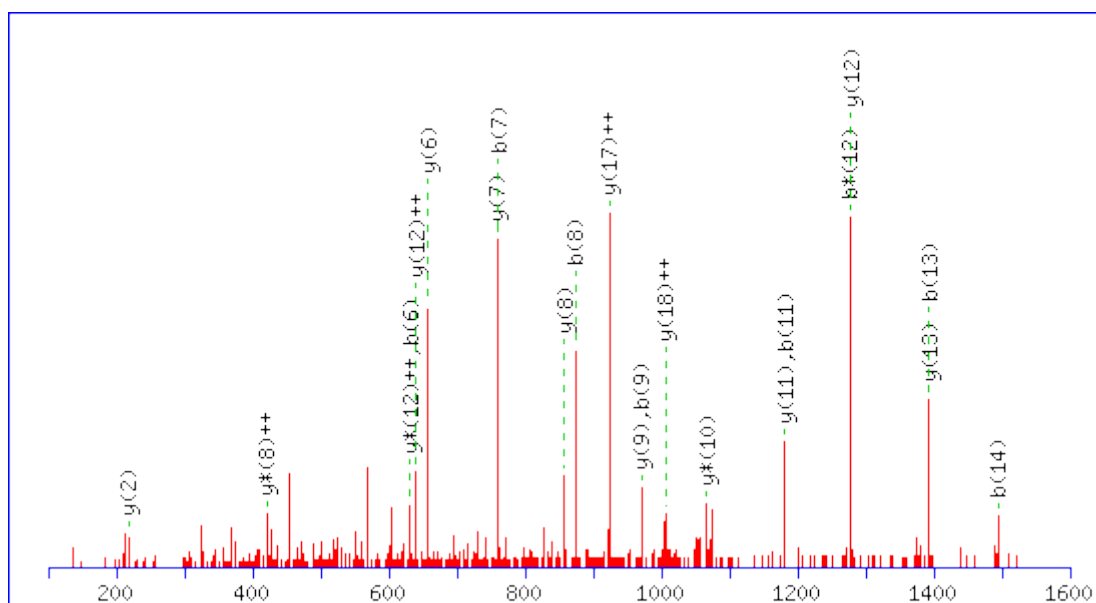
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 38 **Expect:** 0.037

Matches (Bold Red): 12/152 fragment ions using 13 most intense peaks

MS/MS Fragmentation of **AAYPDLENPPLLVTSPQAK**

Found in **SYRC_HUMAN**, Arginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens
GN=RARS PE=1 SV=2



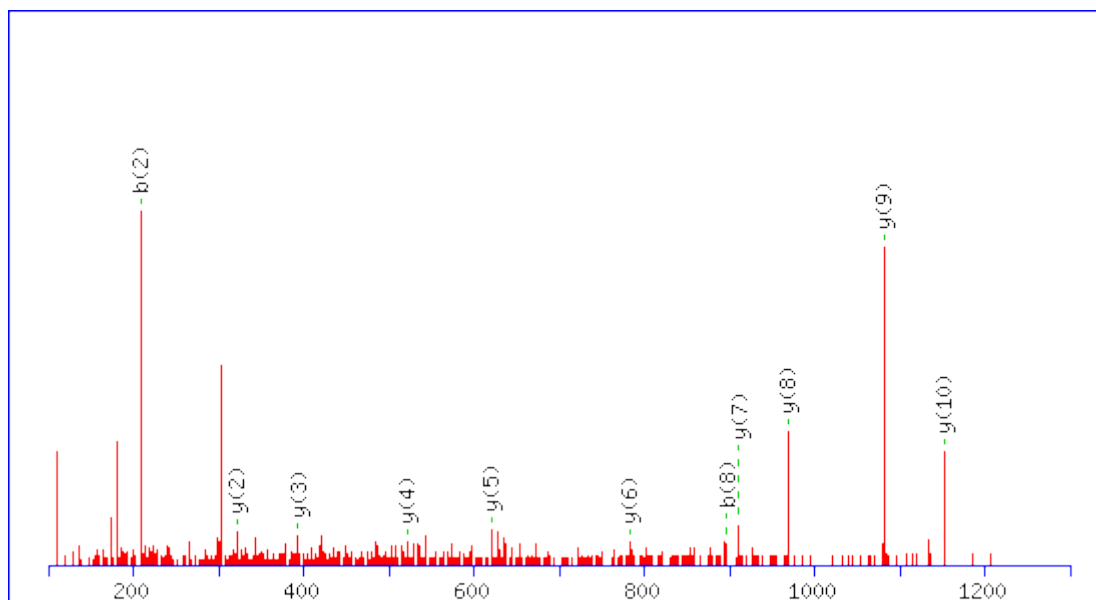
Monoisotopic mass of neutral peptide Mr(calc): 2151.1212

Ions Score: 44 Expect: 0.014

Matches (Bold Red): 22/198 fragment ions using 30 most intense peaks

MS/MS Fragmentation of **HALGQYVQAFR**

Found in **TF3C3_HUMAN**, General transcription factor 3C polypeptide 3 OS=Homo sapiens GN=GTF3C3 PE=1 SV=1



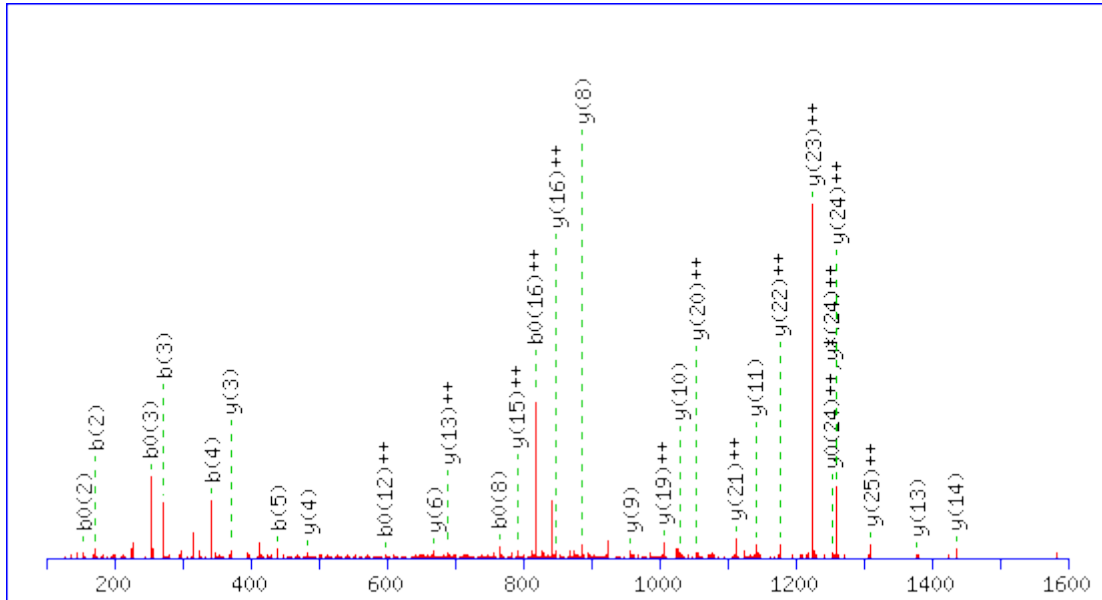
Monoisotopic mass of neutral peptide Mr(calc): 1288.6676

Ions Score: 63 Expect: 0.00014

Matches (**Bold Red**): 13/72 fragment ions using 24 most intense peaks

MS/MS Fragmentation of **ATVAPEDVSEVIFGHVLAAGCGQNPVR**

Found in **THIC_HUMAN**, Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens
GN=ACAT2 PE=1 SV=2



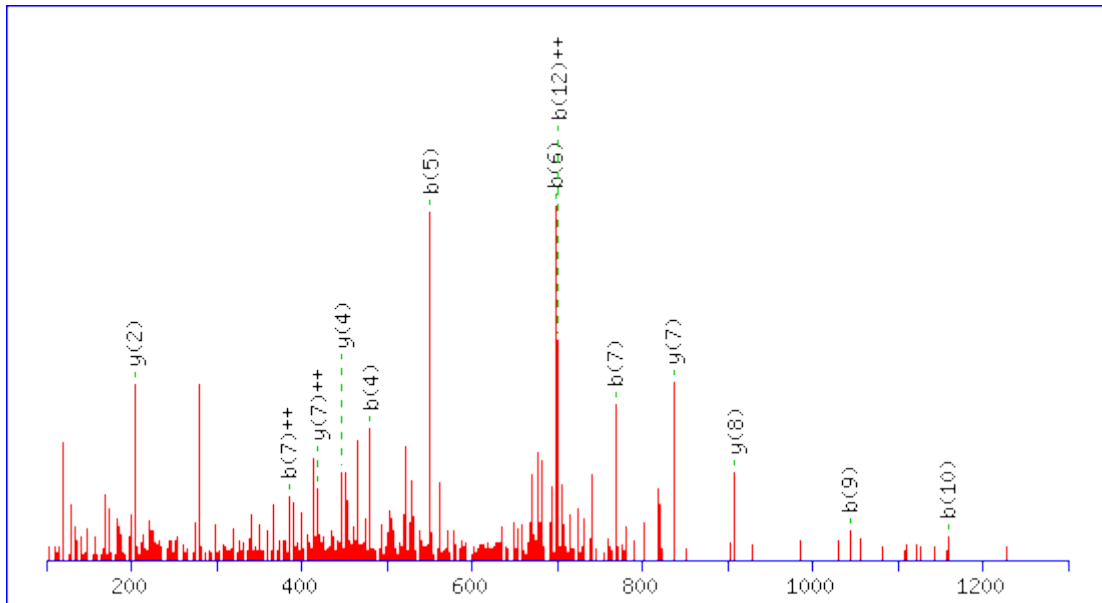
Monoisotopic mass of neutral peptide Mr(calc): 2792.3916

Ions Score: 63 Expect: 0.00023

Matches (**Bold Red**): 30/232 fragment ions using 71 most intense peaks

MS/MS Fragmentation of **RPLLAACDDKDGK**

Found in **THOC3_HUMAN**, THO complex subunit 3 OS=Homo sapiens GN=THOC3 PE=1 SV=1



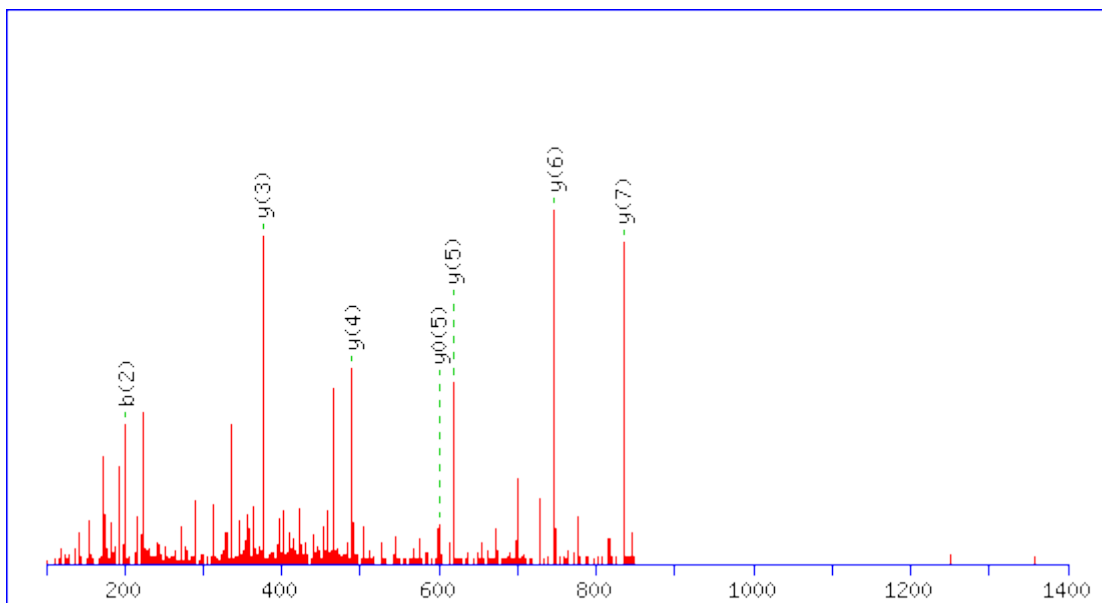
Monoisotopic mass of neutral peptide Mr(calc): 1604.7981

Ions Score: 42 Expect: 0.02

Matches (Bold Red): 13/136 fragment ions using 19 most intense peaks

MS/MS Fragmentation of **ISEEITKK**

Found in **TITIN_HUMAN**, Titin OS=Homo sapiens GN=TTN PE=1 SV=2



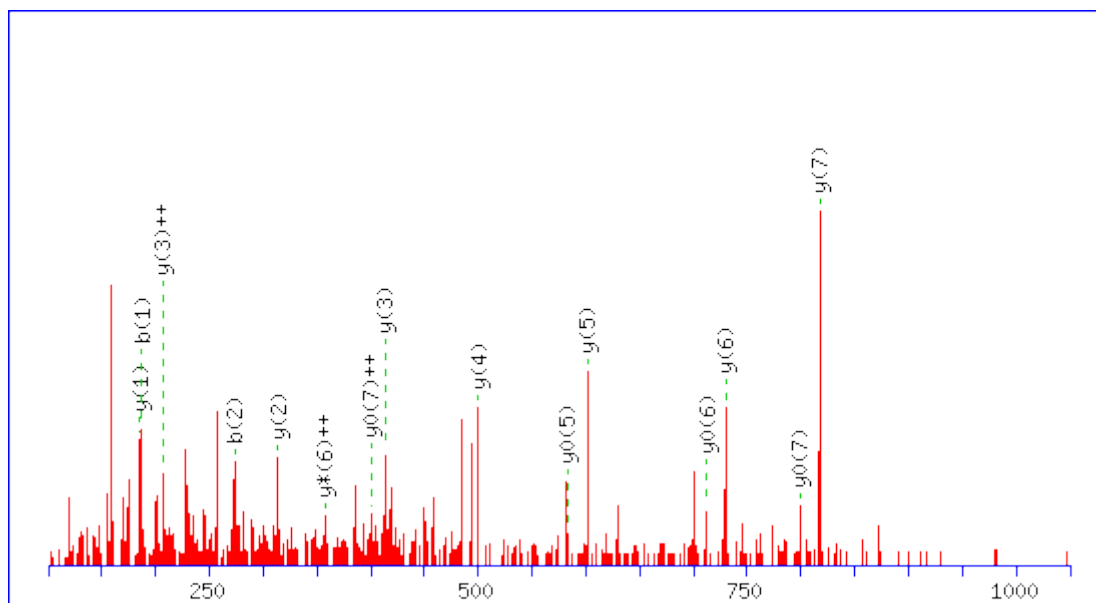
Monoisotopic mass of neutral peptide Mr(calc): 946.5335

Ions Score: 41 Expect: 0.016

Matches (Bold Red): 7/66 fragment ions using 9 most intense peaks

MS/MS Fragmentation of **WSETSVVER**

Found in **TM9S1_HUMAN**, Transmembrane 9 superfamily member 1 OS=Homo sapiens
GN=TM9SF1 PE=2 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1002.4646

Variable modifications:

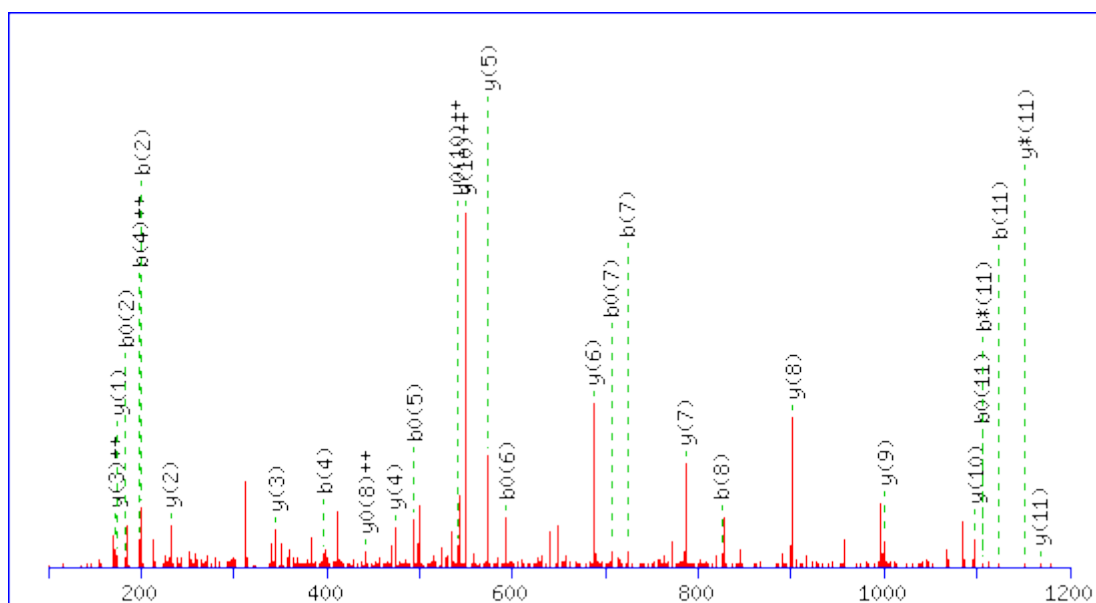
R8 : Label:13C(6)15N(4) (R)

Ions Score: 37 **Expect:** 0.042

Matches (Bold Red): 15/66 fragment ions using 37 most intense peaks

MS/MS Fragmentation of **EAPVDVLTQIGR**

Found in **TM109_HUMAN**, Transmembrane protein 109 OS=Homo sapiens GN=TMEM109 PE=1
SV=1



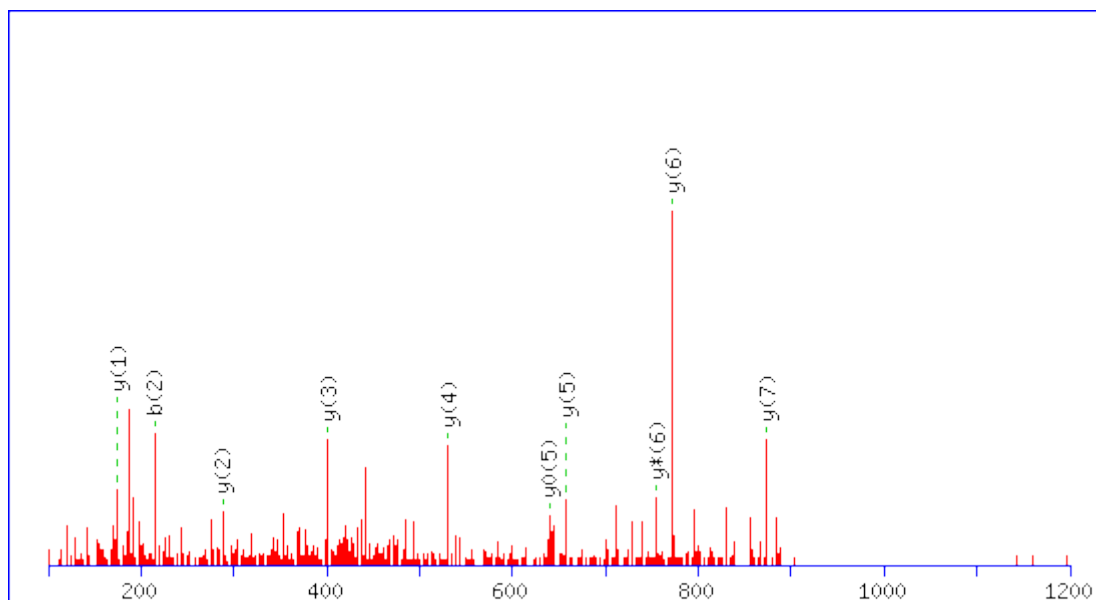
Monoisotopic mass of neutral peptide Mr(calc): 1296.7038

Ions Score: 51 Expect: 0.0019

Matches (Bold Red): 28/108 fragment ions using 88 most intense peaks

MS/MS Fragmentation of **LTNQELLR**

Found in **TM214_HUMAN**, Transmembrane protein 214 OS=Homo sapiens GN=TMEM214 PE=1 SV=2



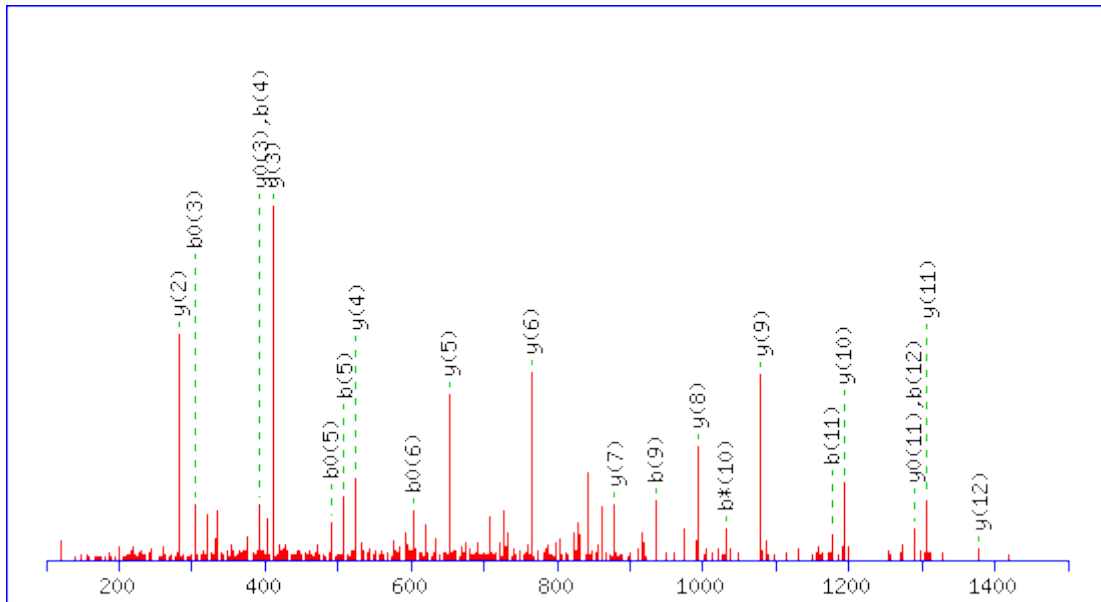
Monoisotopic mass of neutral peptide Mr(calc): 985.5556

Ions Score: 51 Expect: 0.0018

Matches (Bold Red): 10/72 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **SSFADISNLLQIEPR**

Found in **TOM34_HUMAN**, Mitochondrial import receptor subunit TOM34 OS=Homo sapiens GN=TOMM34 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1698.8816

Variable modifications:

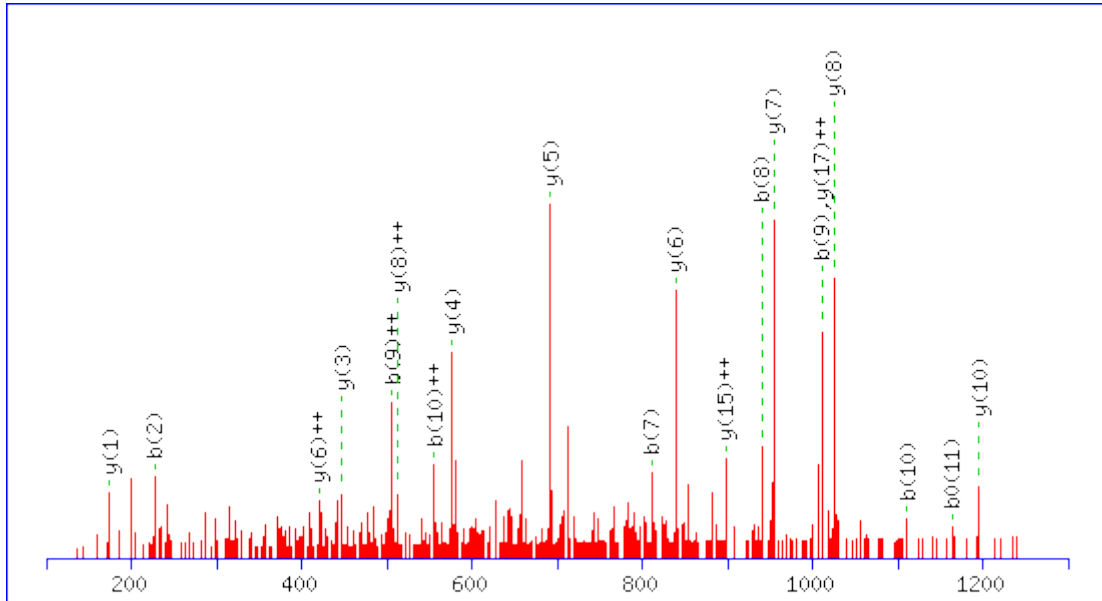
R15 : Label:13C(6)15N(4) (R)

Ions Score: 100 **Expect:** 3.3e-008

Matches (Bold Red): 22/150 fragment ions using 27 most intense peaks

MS/MS Fragmentation of **ILLDQVEEAVADFDECIR**

Found in **TOM70_HUMAN**, Mitochondrial import receptor subunit TOM70 OS=Homo sapiens GN=TOMM70A PE=1 SV=1



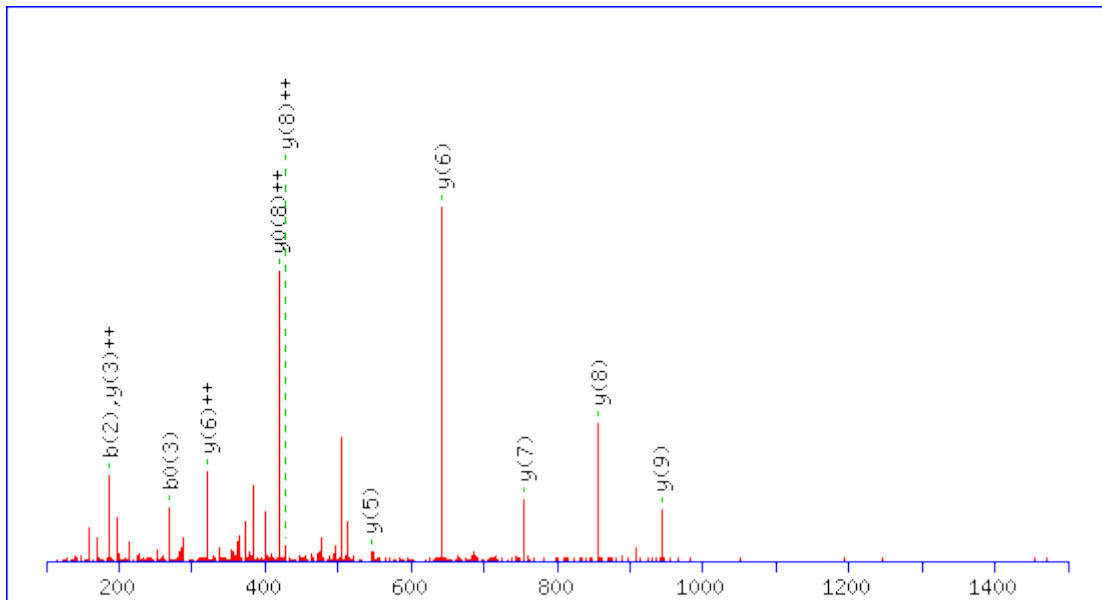
Monoisotopic mass of neutral peptide Mr(calc): 2134.0252

Ions Score: 38 Expect: 0.059

Matches (Bold Red): 20/184 fragment ions using 39 most intense peaks

MS/MS Fragmentation of **VSTLPATSTR**

Found in **TPPC9_HUMAN**, Trafficking protein particle complex subunit 9 OS=Homo sapiens GN=TRAPPC9 PE=1 SV=2



Monoisotopic mass of neutral peptide Mr(calc): 1041.5694

Variable modifications:

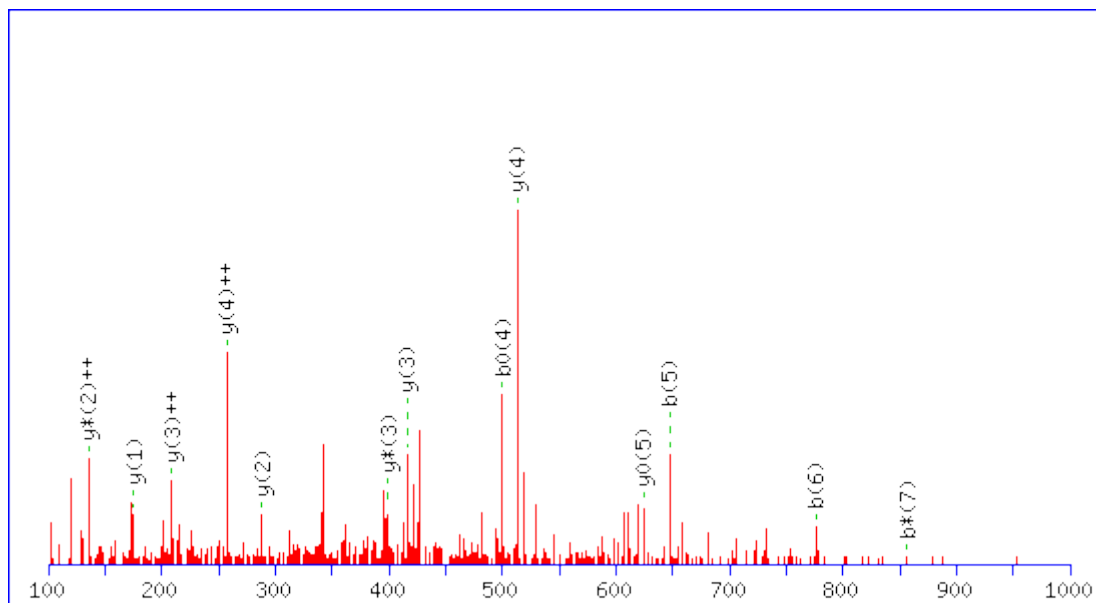
R10 : Label:13C(6)15N(4) (R)

Ions Score: 46 **Expect:** 0.0037

Matches (Bold Red): 11/86 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **KFLEEEPQLR**

Found in **TRHY_HUMAN**, Trichohyalin OS=Homo sapiens GN=TCHH PE=1 SV=2



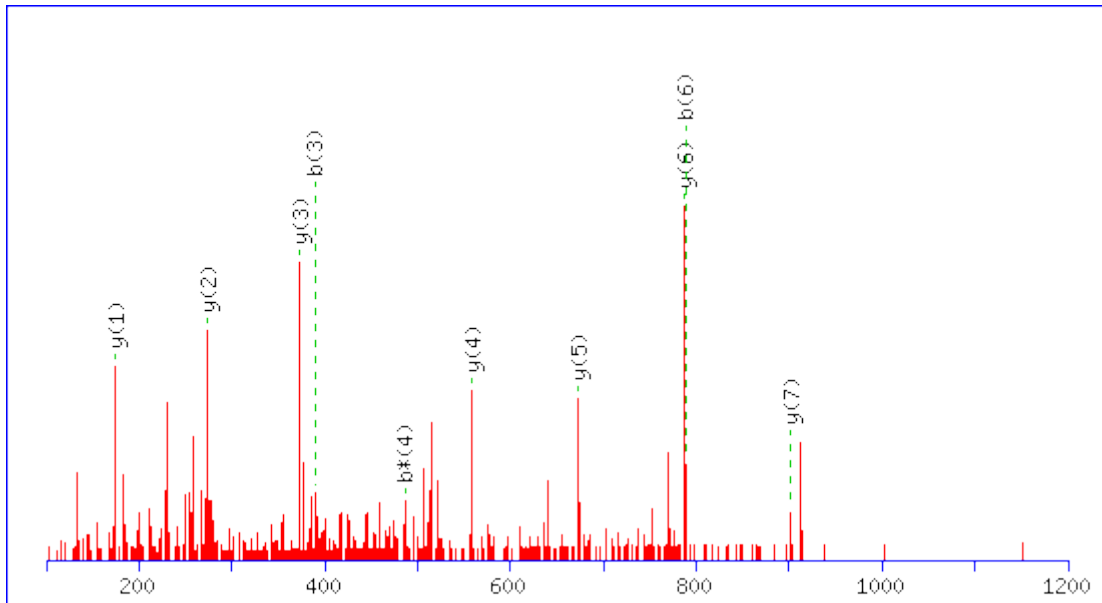
Monoisotopic mass of neutral peptide Mr(calc): 1287.6823

Ions Score: 11 **Expect:** 24

Matches (Bold Red): 13/94 fragment ions using 36 most intense peaks

MS/MS Fragmentation of **CNNNWVVR**

Found in **TRI18_HUMAN**, Midline-1 OS=Homo sapiens GN=MID1 PE=1 SV=1



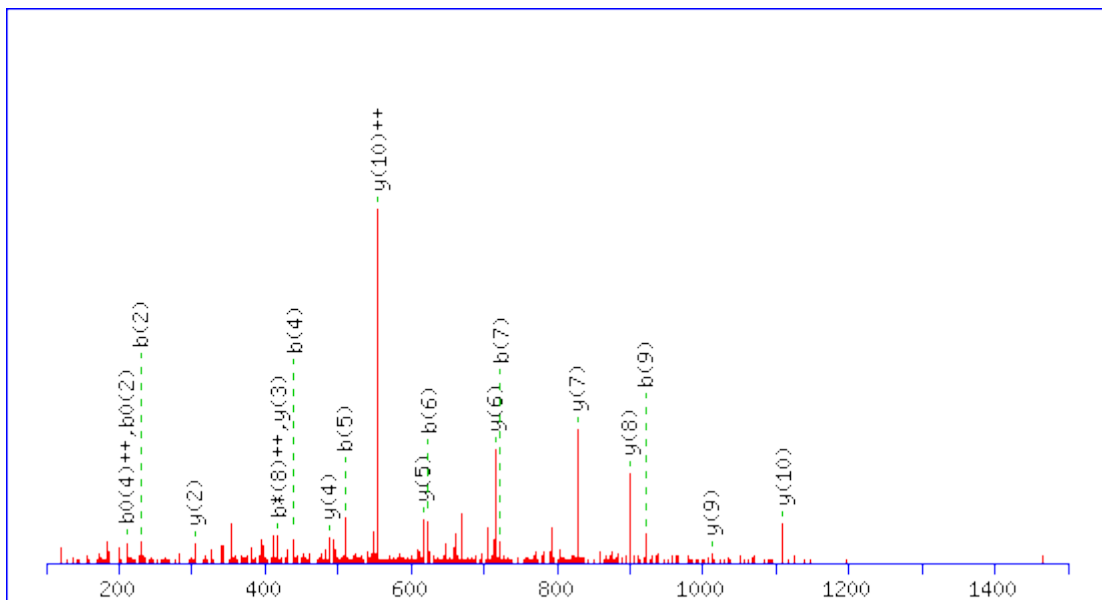
Monoisotopic mass of neutral peptide Mr(calc): 1060.4872

Ions Score: 64 Expect: 8.6e-005

Matches (Bold Red): 10/54 fragment ions using 17 most intense peaks

MS/MS Fragmentation of **IDPLALVQAIER**

Found in **TRIPC_HUMAN**, Probable E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1



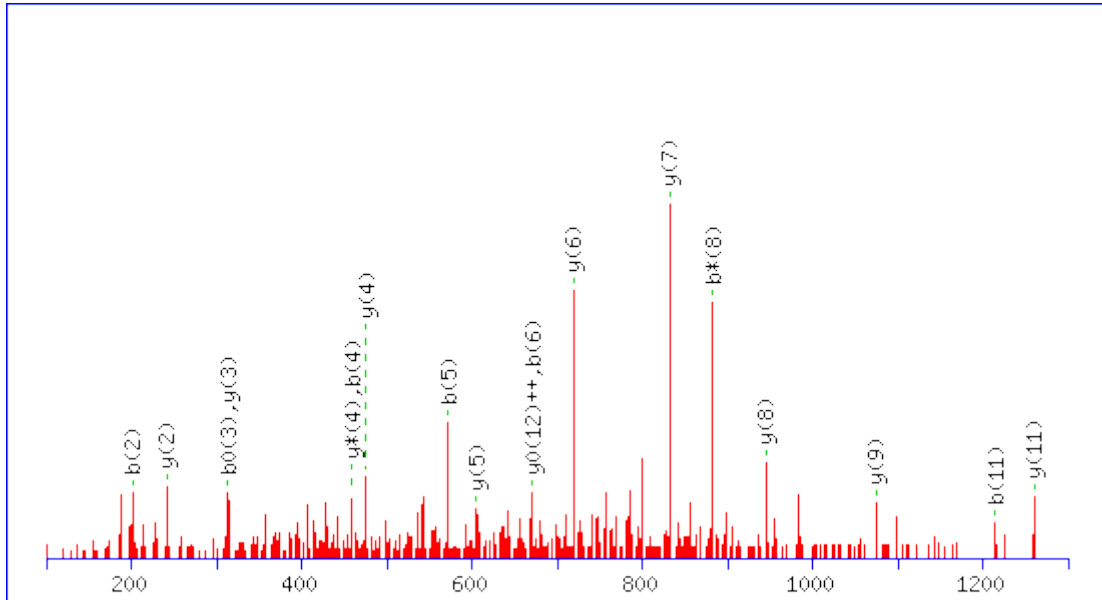
Monoisotopic mass of neutral peptide Mr(calc): 1336.7714

Ions Score: 56 Expect: 0.00056

Matches (Bold Red): 19/114 fragment ions using 34 most intense peaks

MS/MS Fragmentation of **NSEQIVEVGEELINEYASK**

Found in **TTC35_HUMAN**, Tetratricopeptide repeat protein 35 OS=Homo sapiens
GN=TTC35 PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 2158.0521

Variable modifications:

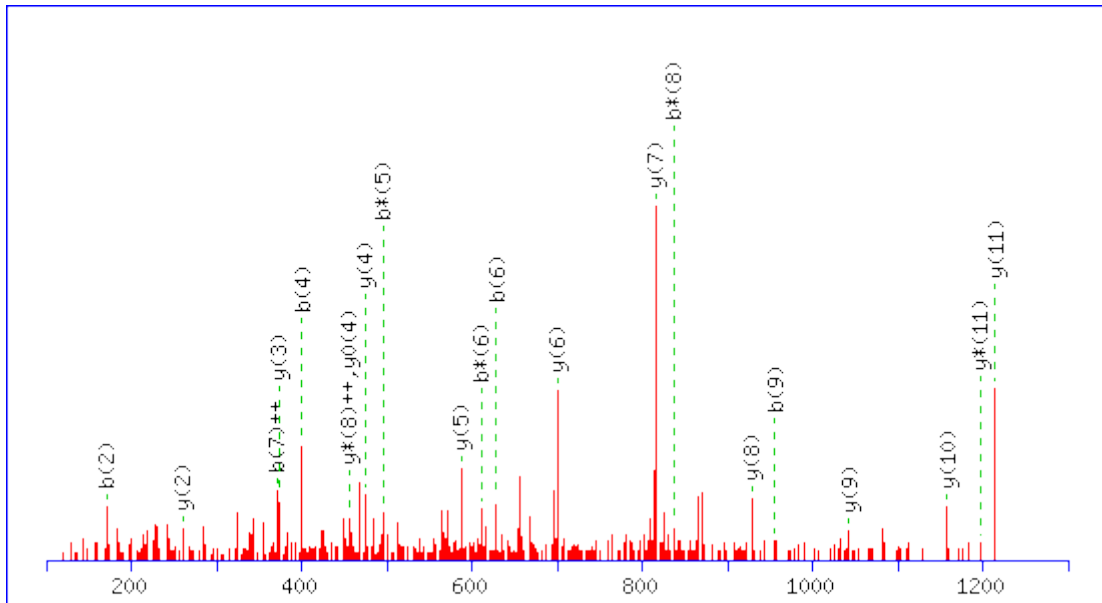
K19 : Label:13C(6)15N(2) (K)

Ions Score: 66 **Expect:** 0.00011

Matches (Bold Red): 18/212 fragment ions using 24 most intense peaks

MS/MS Fragmentation of **IGDNLIDILTLK**

Found in **UACA_HUMAN**, Uvealautoantigen with coiled-coil domains and ankyrin repeats OS=Homo sapiens GN=UACA PE=1 SV=2



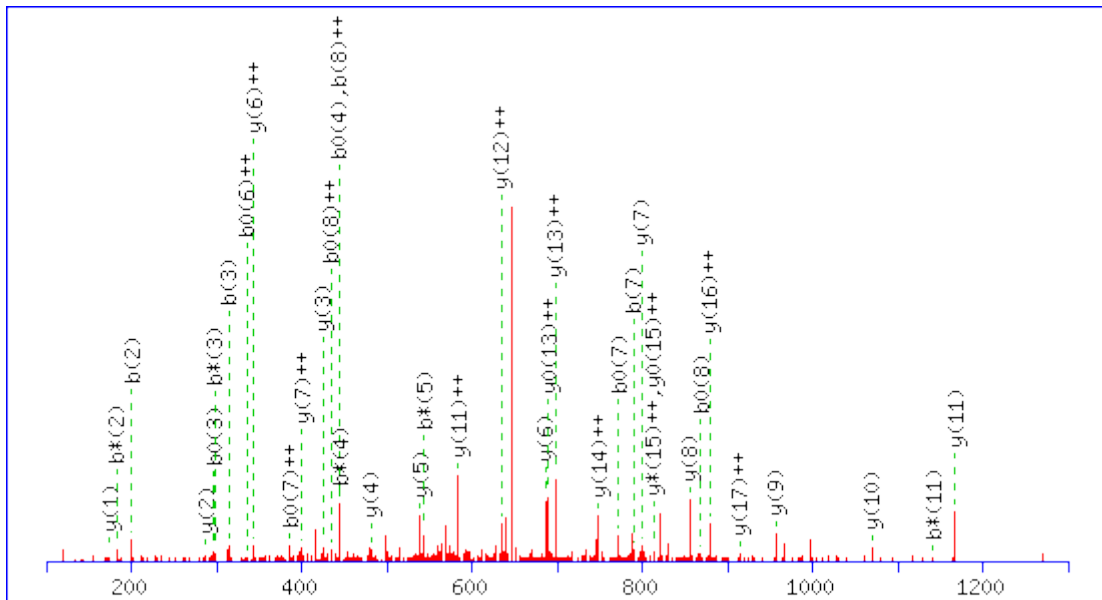
Monoisotopic mass of neutral peptide Mr(calc): 1326.7758

Ions Score: 52 Expect: 0.0015

Matches (Bold Red): 21/116 fragment ions using 55 most intense peaks

MS/MS Fragmentation of **QADFVQTPITGIFGGHIR**

Found in **UBP10_HUMAN**, Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens
GN=USP10 PE=1 SV=2



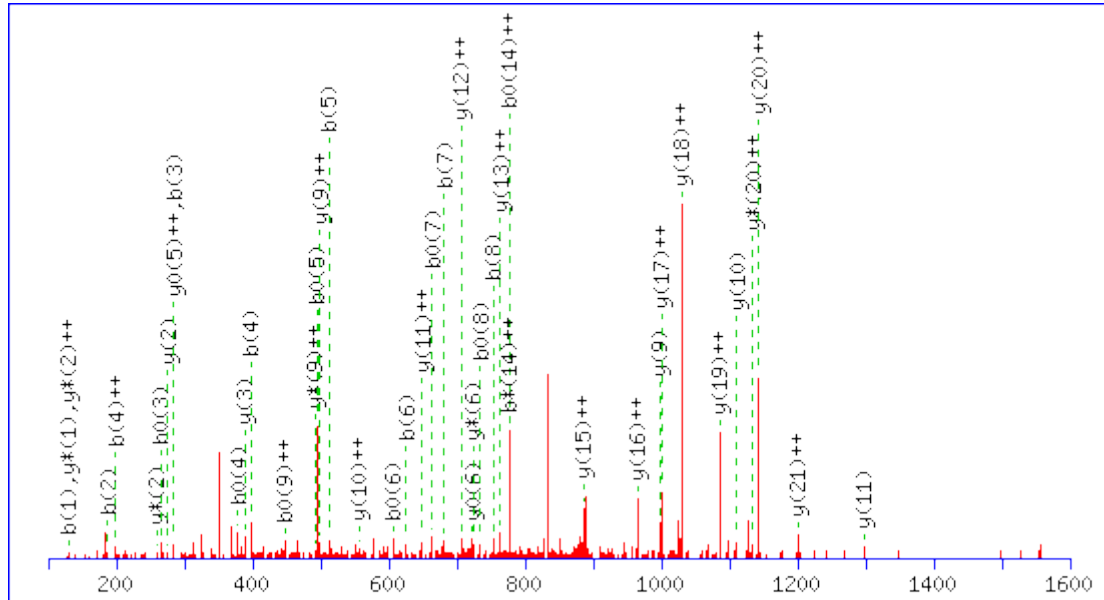
Monoisotopic mass of neutral peptide Mr(calc): 1956.0218

Ions Score: 53 Expect: 0.002

Matches (**Bold Red**): 38/184 fragment ions using 97 most intense peaks

MS/MS Fragmentation of **EGPIDLGACNQDDWISAVRPVIEK**

Found in **UCLH5_HUMAN**, Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Homo sapiens GN=UCLH5 PE=1 SV=3



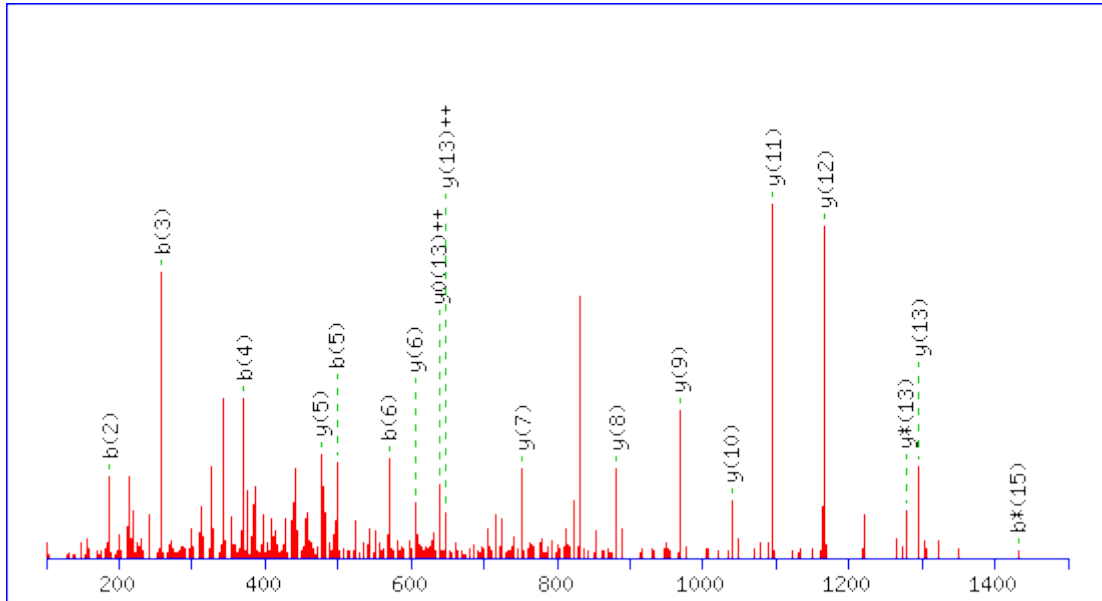
Monoisotopic mass of neutral peptide Mr(calc): 2681.3119

Ions Score: 42 Expect: 0.025

Matches (**Bold Red**): 43/256 fragment ions using 98 most intense peaks

MS/MS Fragmentation of **ADALQAGASQFETSAAK**

Found in **VAMP2_HUMAN**, Vesicle-associated membrane protein 2 OS=Homo sapiens GN=VAMP2 PE=1 SV=3



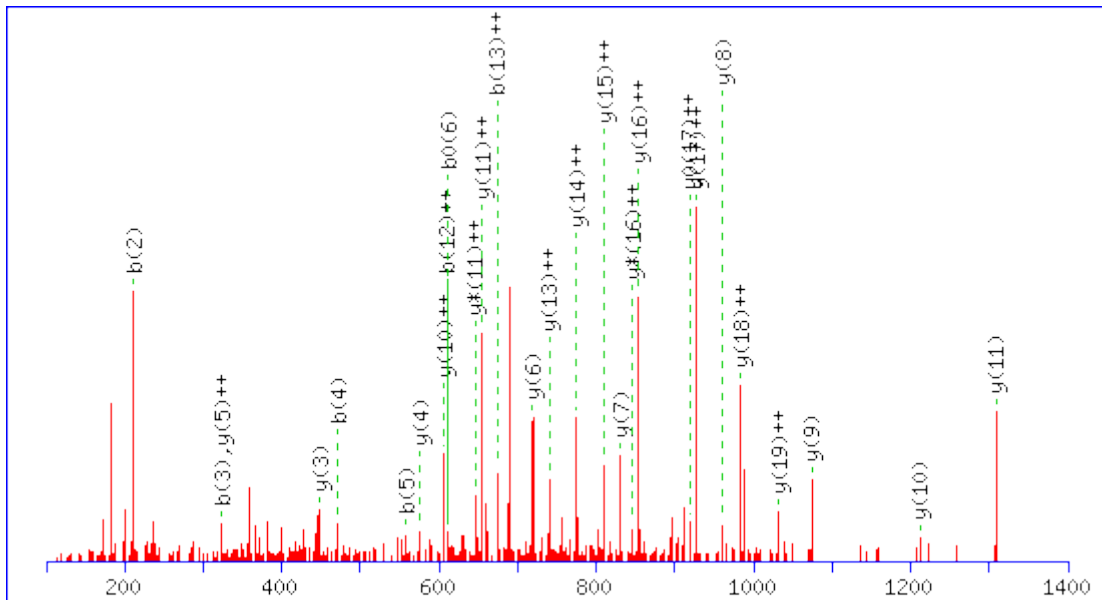
Monoisotopic mass of neutral peptide Mr(calc): 1664.8006

Ions Score: 60 Expect: 0.00037

Matches (Bold Red): 18/176 fragment ions using 30 most intense peaks

MS/MS Fragmentation of **IPIFSAAGLPHNEIAAQICR**

Found in **VATB1_HUMAN**, V-type proton ATPase subunit B, kidney isoform OS=Homo sapiens GN=ATP6V1B1 PE=1 SV=3



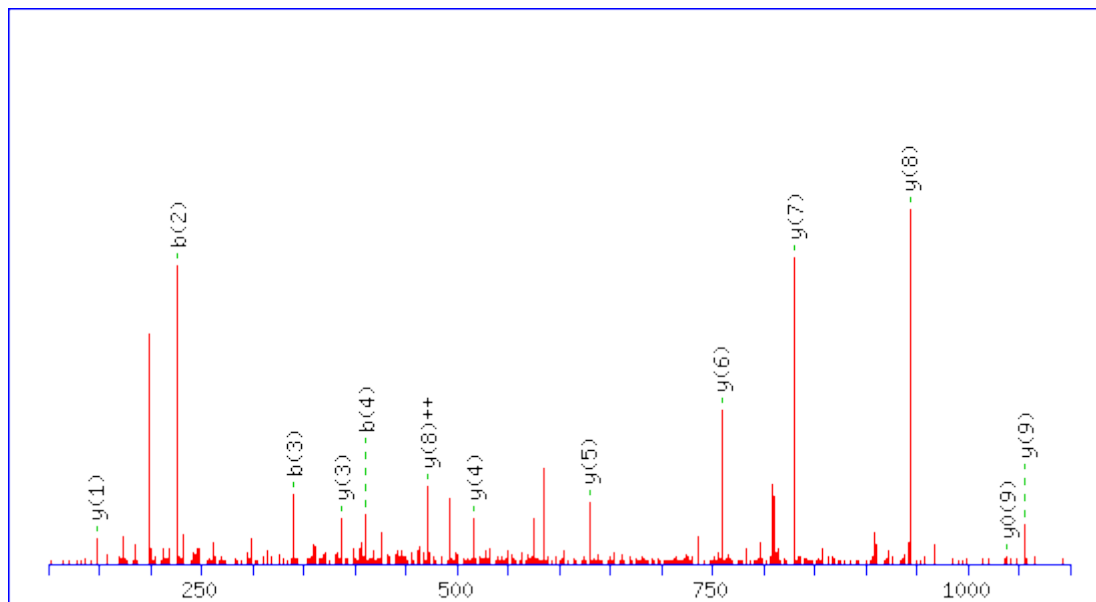
Monoisotopic mass of neutral peptide Mr(calc): 2177.1415

Ions Score: 60 Expect: 0.00037

Matches (Bold Red): 28/184 fragment ions using 61 most intense peaks

MS/MS Fragmentation of **ILLAELEQLK**

Found in **VIME_HUMAN**, Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4



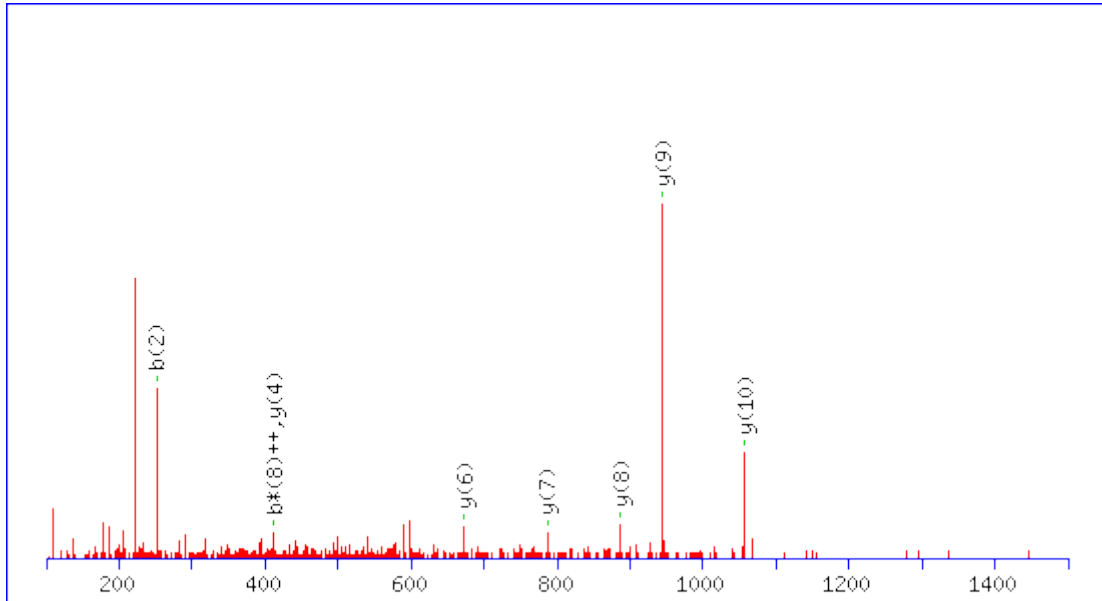
Monoisotopic mass of neutral peptide Mr(calc): 1168.7067

Ions Score: 48 **Expect:** 0.0033

Matches (Bold Red): 13/80 fragment ions using 31 most intense peaks

MS/MS Fragmentation of **HLGTLNFGGIR**

Found in **VPP1_HUMAN**, V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3



Monoisotopic mass of neutral peptide Mr(calc): 1193.6545

Variable modifications:

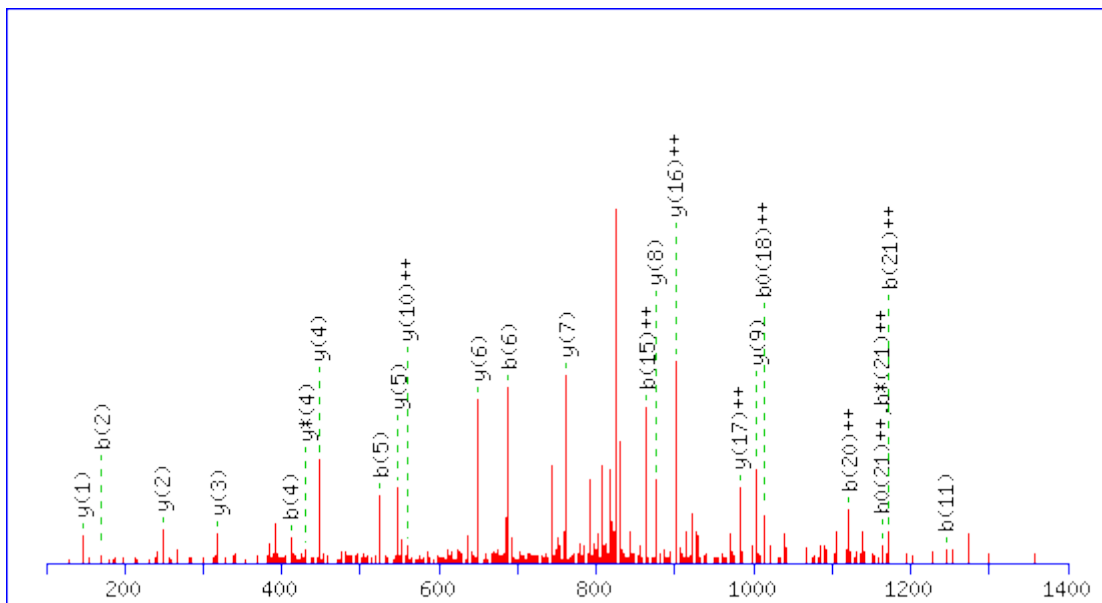
R11 : Label:13C(6)15N(4) (R)

Ions Score: 39 Expect: 0.033

Matches (Bold Red): 8/90 fragment ions using 21 most intense peaks

MS/MS Fragmentation of **AVLQLYPENSEQLELITTQATK**

Found in **WBS22_HUMAN**, Uncharacterized methyltransferase WBSR22 OS=Homo sapiens GN=WBSR22 PE=1 SV=2



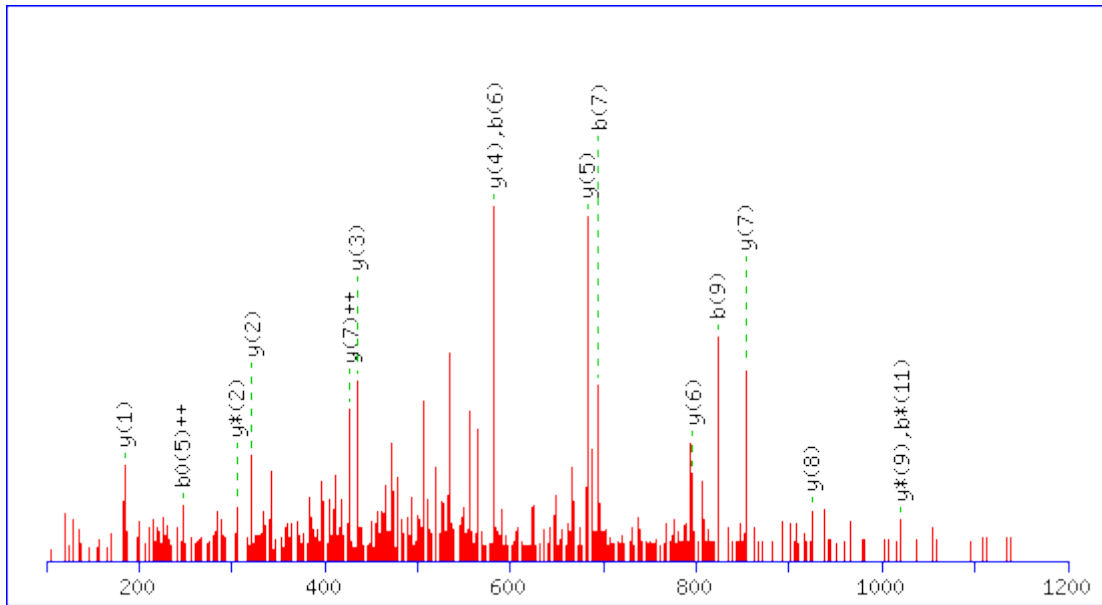
Monoisotopic mass of neutral peptide Mr(calc): 2488.3060

Ions Score: 58 Expect: 0.00061

Matches (Bold Red): 24/230 fragment ions using 40 most intense peaks

MS/MS Fragmentation of **NAHSTAIAGLTFLHR**

Found in **WDR36_HUMAN**, WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36
PE=1 SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1617.8615

Variable modifications:

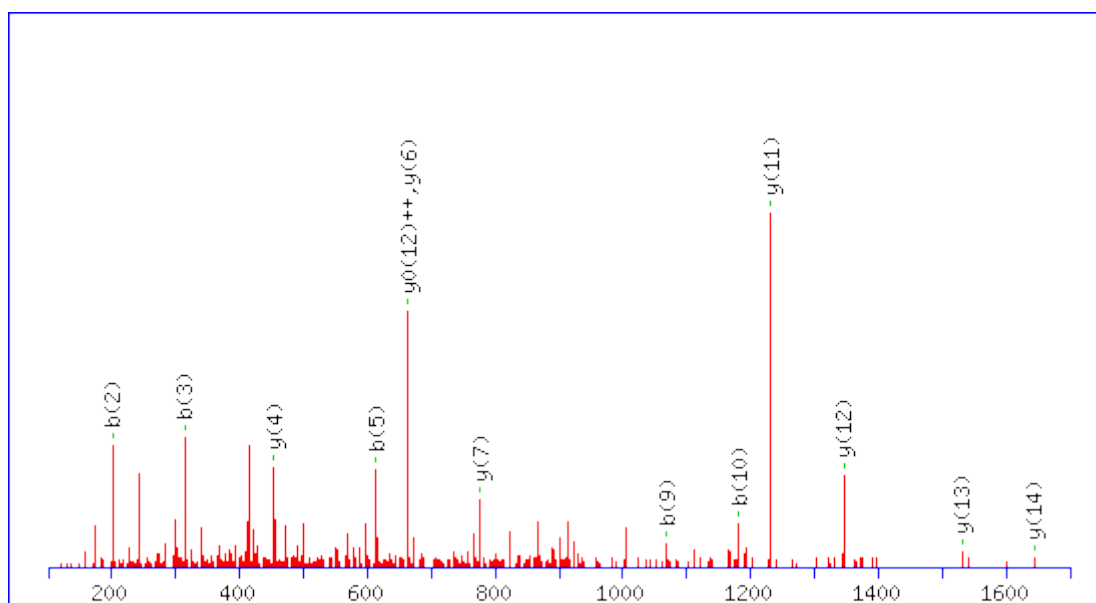
R15 : Label:13C(6)15N(4) (R)

Ions Score: 50 Expect: 0.003

Matches (Bold Red): 16/154 fragment ions using 24 most intense peaks

MS/MS Fragmentation of **TVLWNPEDLIPLIPK**

Found in **ZC3H4_HUMAN**, Zinc finger CCCH domain-containing protein 4 OS=Homo sapiens GN=ZC3H4 PE=1 SV=3



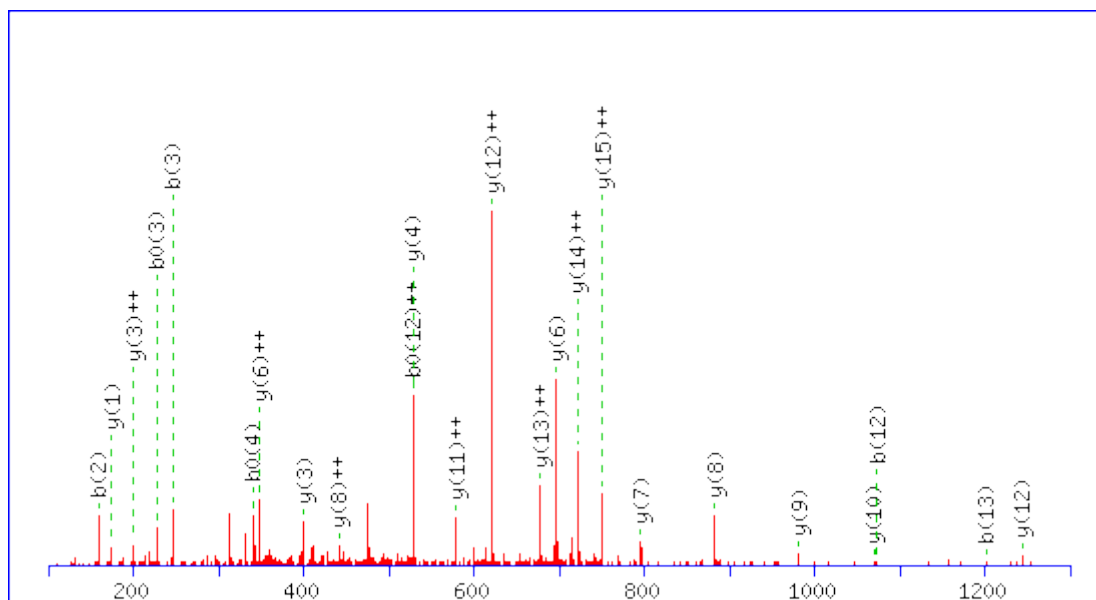
Monoisotopic mass of neutral peptide Mr(calc): 1844.0448

Ions Score: 57 Expect: 0.0006

Matches (Bold Red): 13/156 fragment ions using 16 most intense peaks

MS/MS Fragmentation of **TGSISSVSVPKPER**

Found in **ZC3HE_HUMAN**, Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1



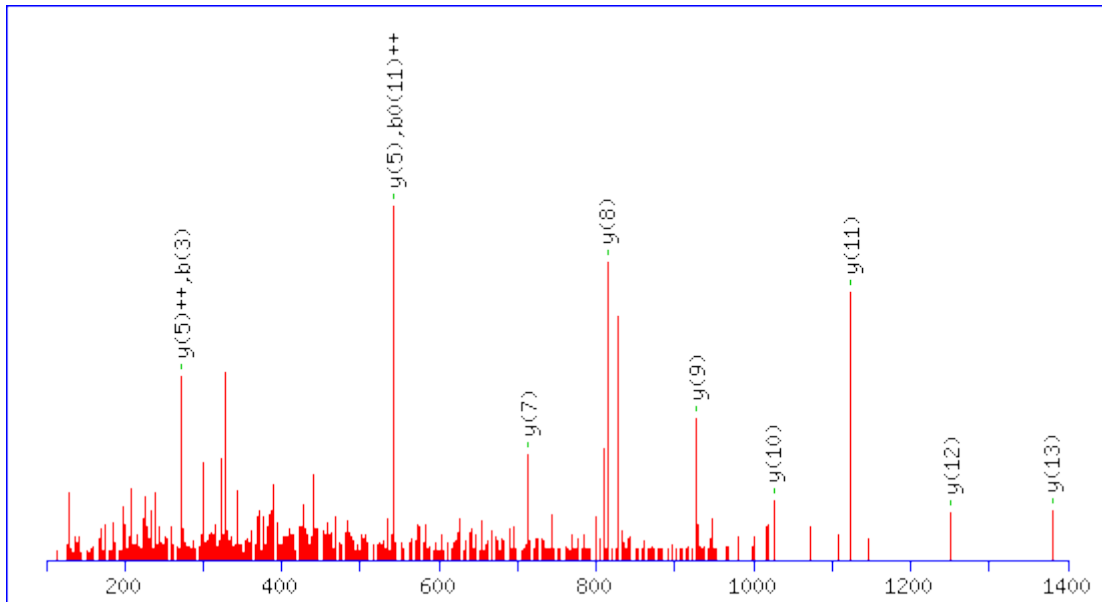
Monoisotopic mass of neutral peptide Mr(calc): 1600.8420

Ions Score: 65 Expect: 9.3e-005

Matches (Bold Red): 24/154 fragment ions using 51 most intense peaks

MS/MS Fragmentation of **GDVASCNTQVAEKPVLTAVPGITR**

Found in **ZC11A_HUMAN**, Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens GN=ZC3H11A PE=1 SV=3



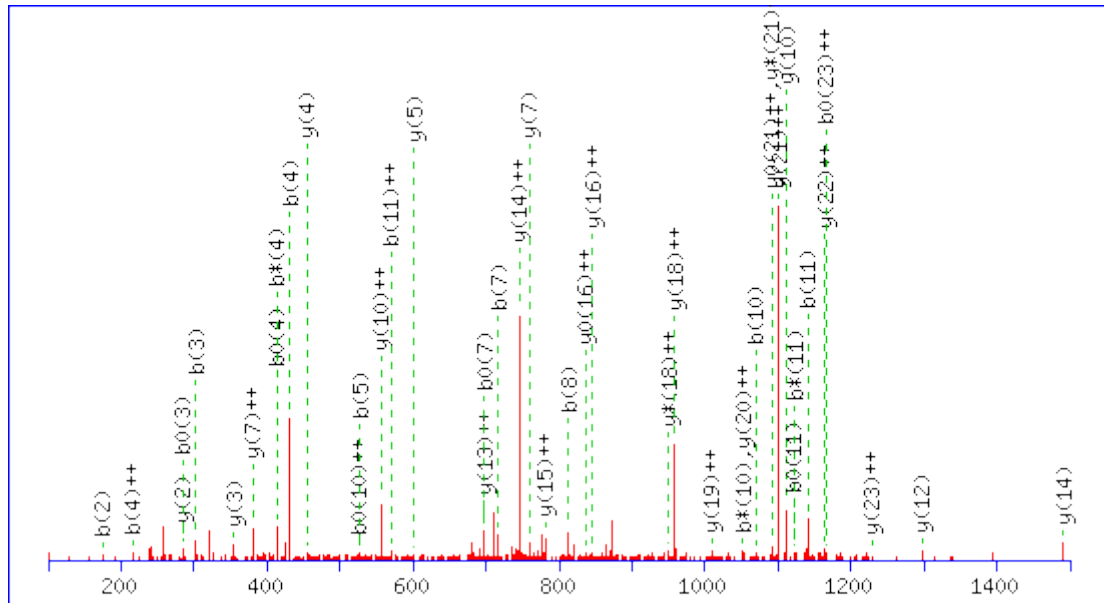
Monoisotopic mass of neutral peptide Mr(calc): 2482.2850

Ions Score: 49 **Expect:** 0.0051

Matches (Bold Red): 11/260 fragment ions using 14 most intense peaks

MS/MS Fragmentation of **SSQQPSTPQQAPPGQPQQGTFVAHK**

Found in **ZCH18_HUMAN**, Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens GN=ZC3H18 PE=1 SV=2



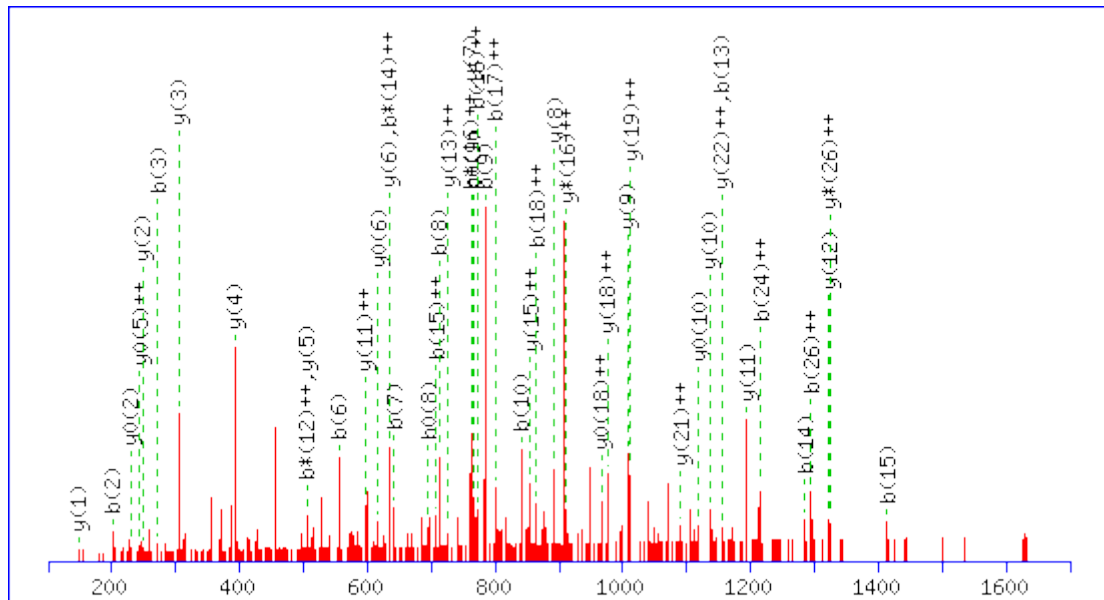
Monoisotopic mass of neutral peptide Mr(calc): 2630.2838

Ions Score: 44 Expect: 0.018

Matches (**Bold Red**): 43/274 fragment ions using 106 most intense peaks

MS/MS Fragmentation of **AEAGPESAAGGQEEEEGEDEEELSGTK**

Found in **ZGPAT_HUMAN**, Zinc finger CCCH-type with G patch domain-containing protein OS=Homo sapiens GN=ZGPAT PE=1 SV=3



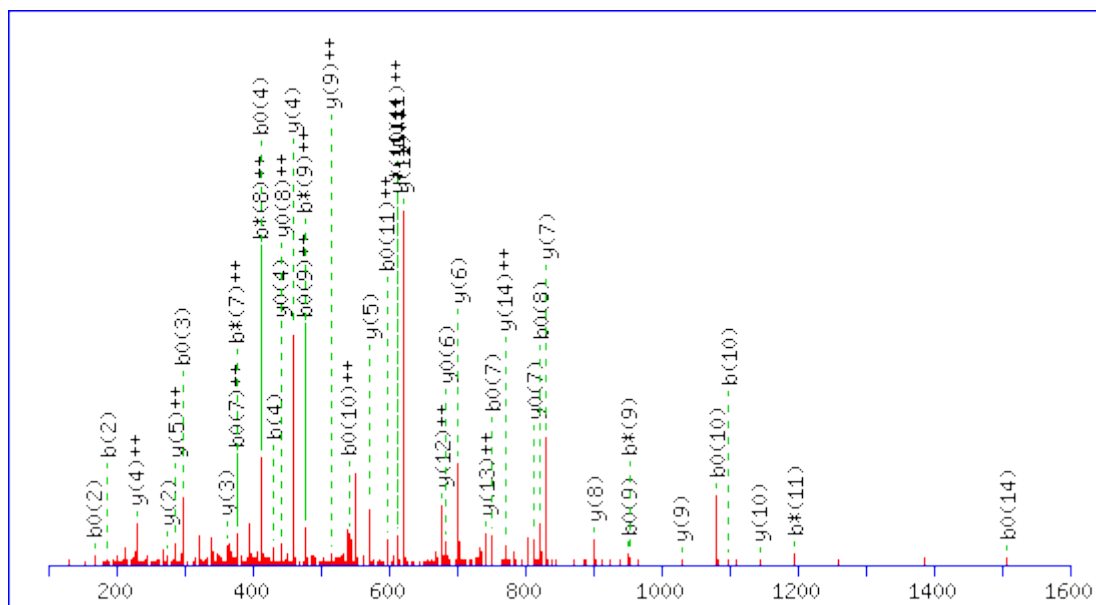
Monoisotopic mass of neutral peptide Mr(calc): 2734.1213

Ions Score: 59 Expect: 0.00052

Matches (**Bold Red**): 47/286 fragment ions using 107 most intense peaks

MS/MS Fragmentation of **EGEDPNKAEELPSEK**

Found in **ZN622_HUMAN**, Zinc finger protein 622 OS=Homo sapiens GN=ZNF622 PE=1
SV=1



Monoisotopic mass of neutral peptide Mr(calc): 1670.7635

Ions Score: 49 Expect: 0.0031

Matches (**Bold Red**): 42/156 fragment ions using 93 most intense peaks
