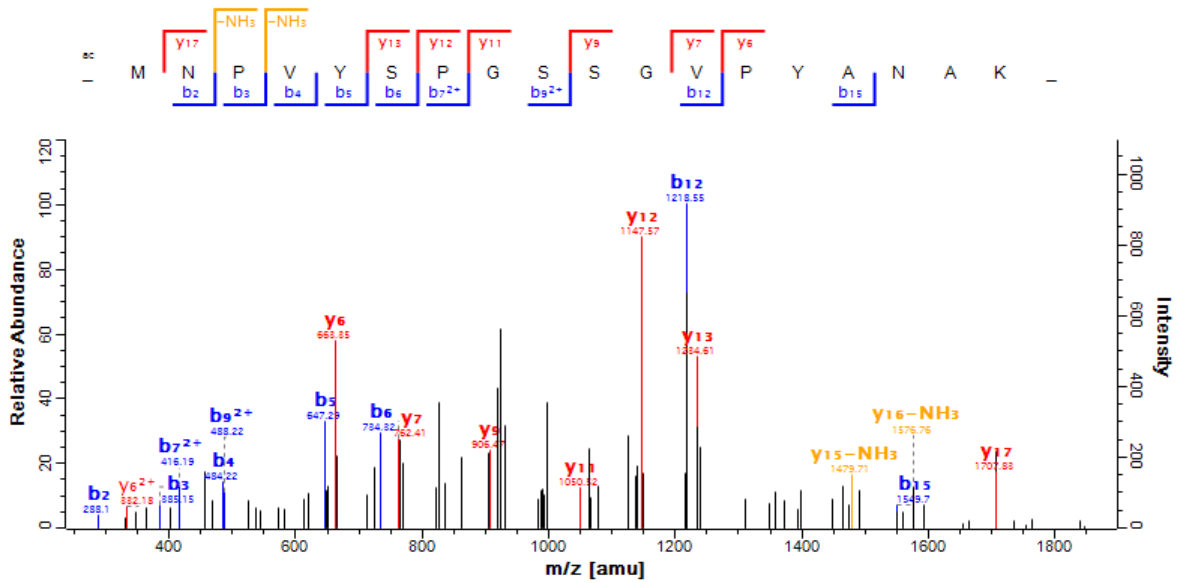


Supplemental Fig. 5. Annotated spectra for single peptide identifications in the protein fractionation-free workflow in addition to those presented in supplemental Fig. 3. Where multiple spectra match the peptide sequence, the annotated spectrum corresponding to the best match is reported.

Protein Group ID: 6
Protein Accession Numbers: A1KXE4; A1KXE4-2
Gene Names: FAM168B
Peptide Sequence: MNPVYSPGSSGVYANAK
Total Number of Spectra: 3
Number of Replicates (out of 8): 2
Best Match Score: 86.455
Best Match Posterior Error Probability: 0.00074526
Best Match Spectrum:

Scan number 47303 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** FAM168B



Protein Group ID: 9

Protein Accession Numbers: A1L3X0; D6RBM2; D6RBR5; D6RE10

Gene Names: ELOVL7

Peptide Sequence: TVHLYDNWIK

Total Number of Spectra: 4

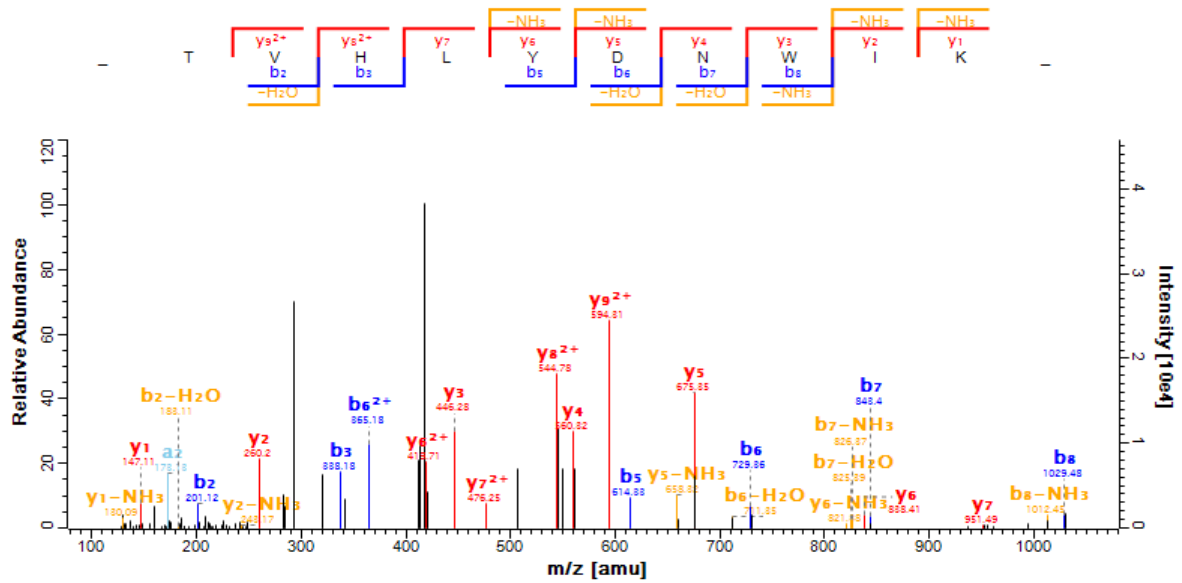
Number of Replicates (out of 8): 4

Best Match Score: 207.83

Best Match Posterior Error Probability: 2.84E-19

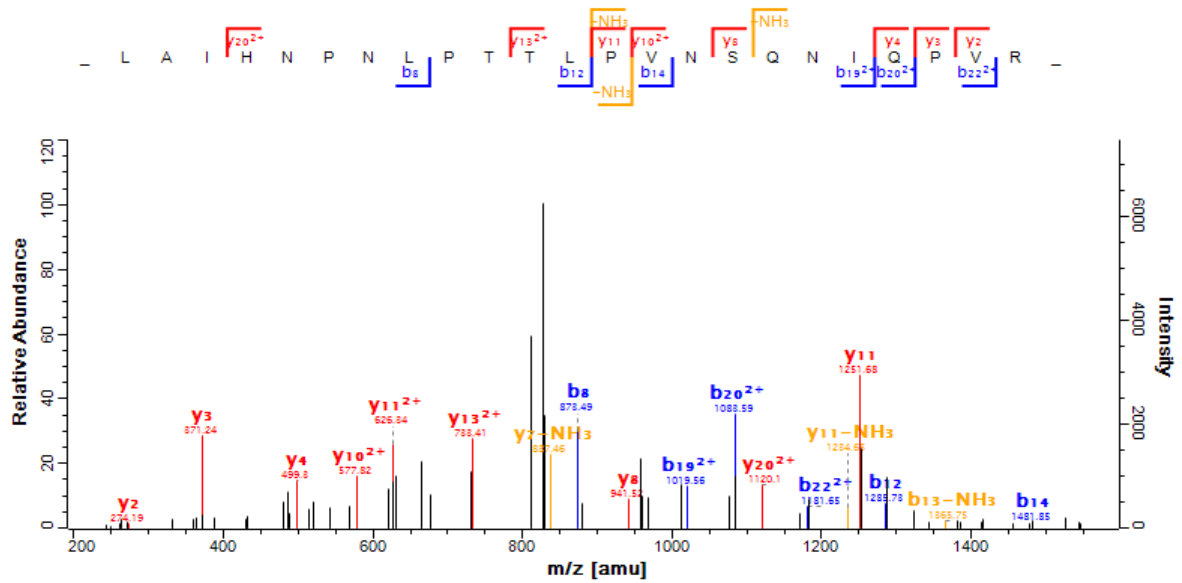
Best Match Spectrum:

Scan number 44590 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ELOVL7



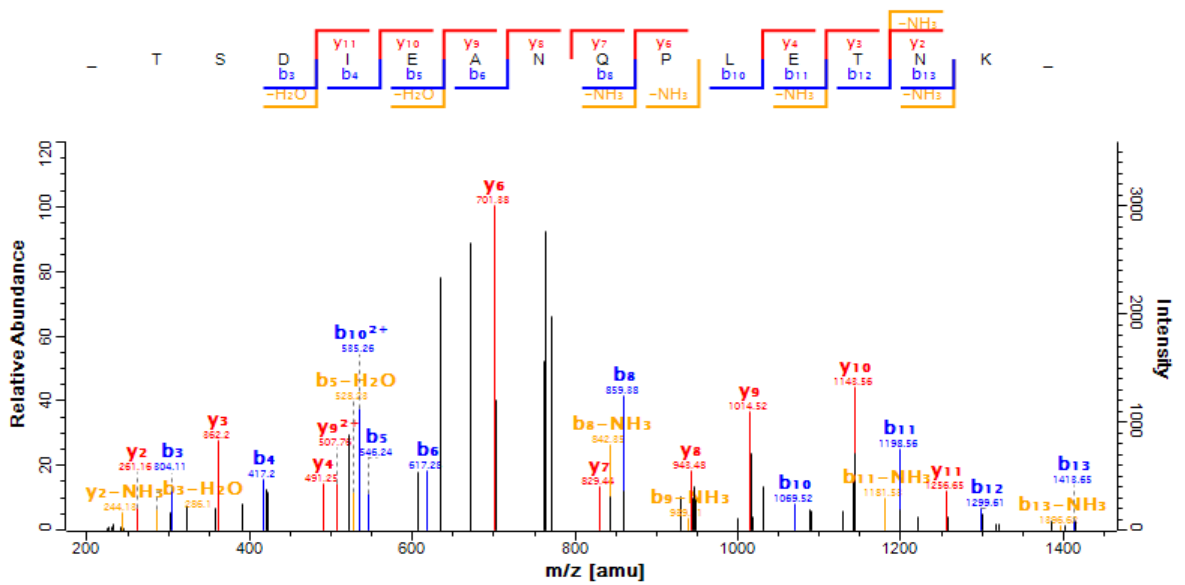
Protein Group ID: 24
Protein Accession Numbers: Q13887; A2TJX0
Gene Names: KLF5
Peptide Sequence: LAIHNPNTLPTLPVNSQNIQPVR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 62.966
Best Match Posterior Error Probability: 0.0016494
Best Match Spectrum:

Scan number 54133 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** KLF5



Protein Group ID: 29
Protein Accession Numbers: A4D104; C9J7I0
Gene Names: LOC401307
Peptide Sequence: TSDIEANQPLETNK
Total Number of Spectra: 7
Number of Replicates (out of 8): 6
Best Match Score: 133.48
Best Match Posterior Error Probability: 4.32E-05
Best Match Spectrum:

Scan number 18008 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** LOC401307



Protein Group ID: 34

Protein Accession Numbers: H0YE88; P28347; H0YEJ9; A4FUP2; E9PKB7

Gene Names: TEAD1

Peptide Sequence: ALQHMAAMSSAQIVSATAIHNK

Total Number of Spectra: 2

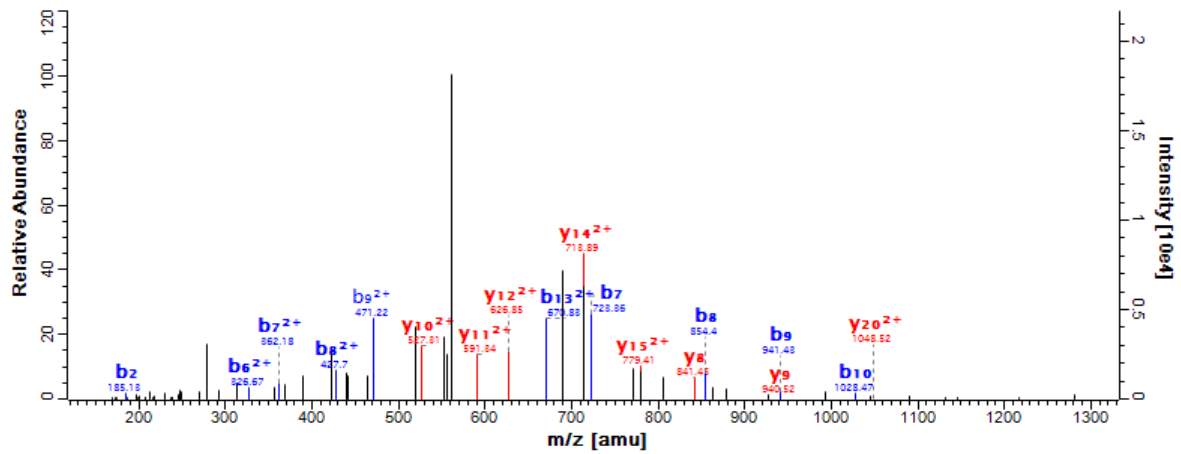
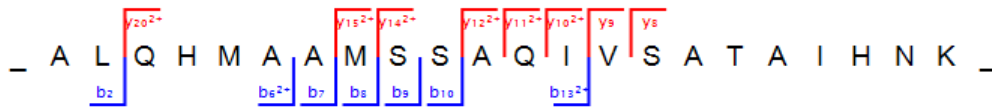
Number of Replicates (out of 8): 2

Best Match Score: 61.096

Best Match Posterior Error Probability: 0.0030914

Best Match Spectrum:

Scan number	42005	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	TEAD1



Protein Group ID: 35

Protein Accession Numbers: Q9UNL4; Q9UNL4-2; Q9UNL4-6; Q9UNL4-5; Q9UNL4-7; Q9UNL4-4; Q9UNL4-8; A4KYM5; E9PJ14

Gene Names: ING4

Peptide Sequence: AAGMYLEHLSIENLPLFELQR

Total Number of Spectra: 5

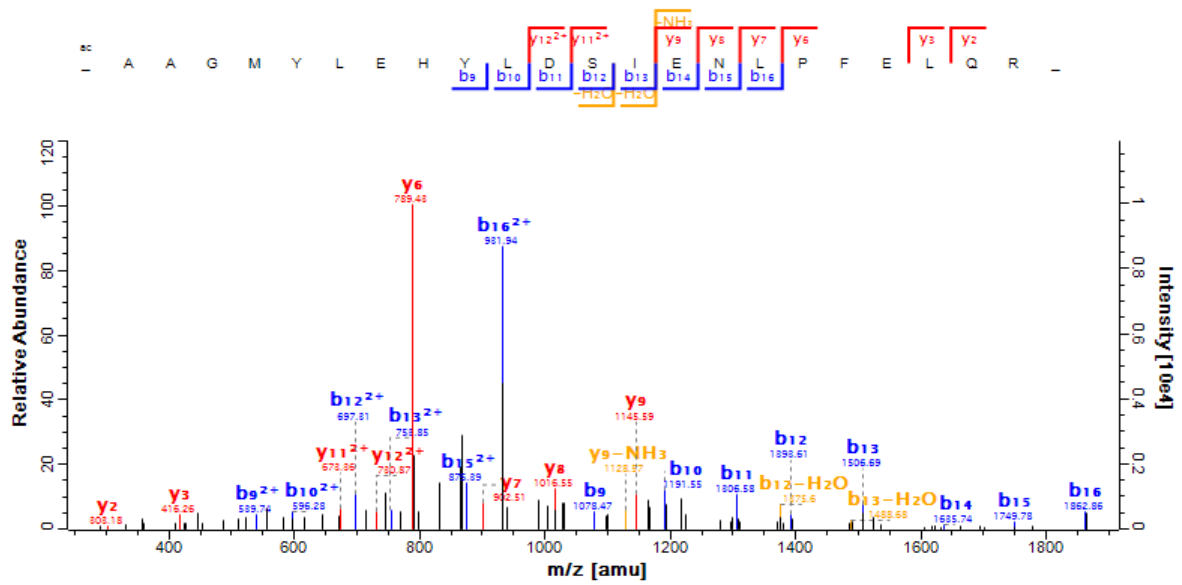
Number of Replicates (out of 8): 5

Best Match Score: 122.57

Best Match Posterior Error Probability: 1.25E-08

Best Match Spectrum:

Scan number	94262	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	ING4



Protein Group ID: 41

Protein Accession Numbers: Q9Y5U2; Q9Y5U2-2; C9JJV1; C9JHT9; E9PME3; A6NCC9

Gene Names: TSSC4

Peptide Sequence: RAPSSVAHTSMSDNGGFK

Total Number of Spectra: 3

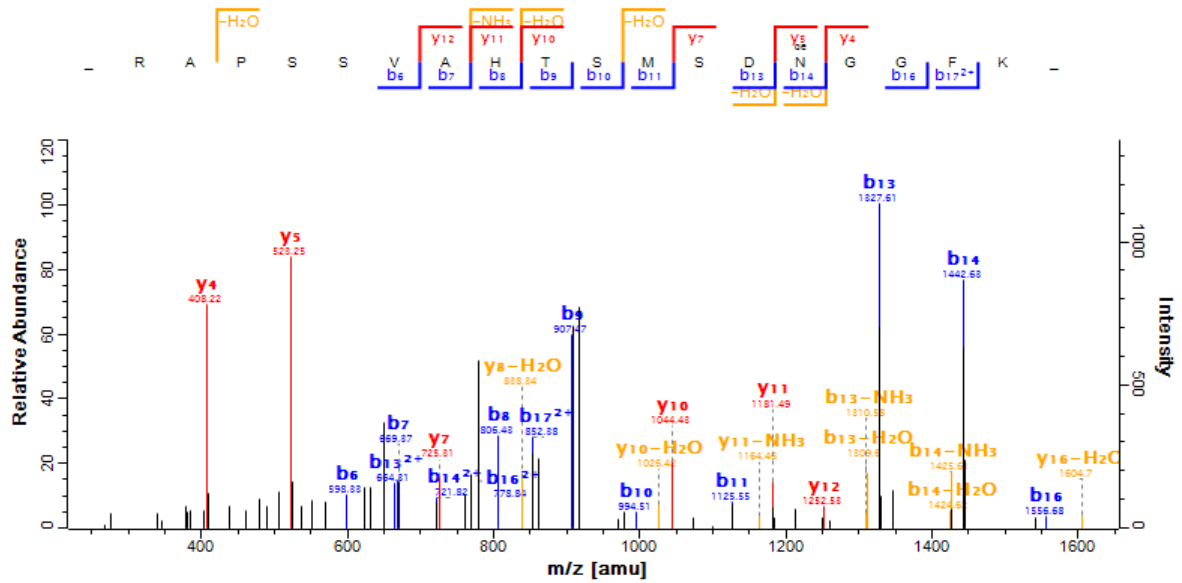
Number of Replicates (out of 8): 3

Best Match Score: 106.93

Best Match Posterior Error Probability: 0.00063748

Best Match Spectrum:

Scan number 15009 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** TSSC4



Protein Group ID: 42

Protein Accession Numbers: A6NCE7; Q9GZQ8; H3BTL1

Gene Names: MAP1LC3B2;MAP1LC3B

Peptide Sequence: FLVPDHVNS ELIK

Total Number of Spectra: 8

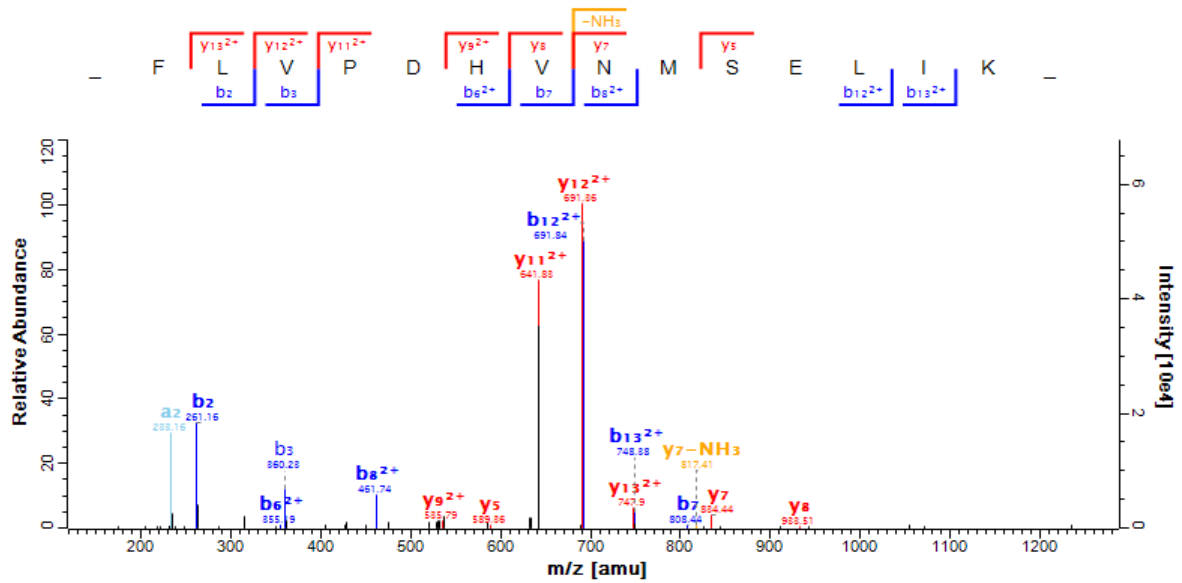
Number of Replicates (out of 8): 7

Best Match Score: 103.91

Best Match Posterior Error Probability: 0.0002713

Best Match Spectrum:

Scan number	61760	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	MAP1LC3B2;MAP1LC3B



Protein Group ID: 43

Protein Accession Numbers: A6NCI0; Q9Y6G3; J3KPP0

Gene Names: MRPL42

Peptide Sequence: VEHLEEGPMIEQLSK

Total Number of Spectra: 6

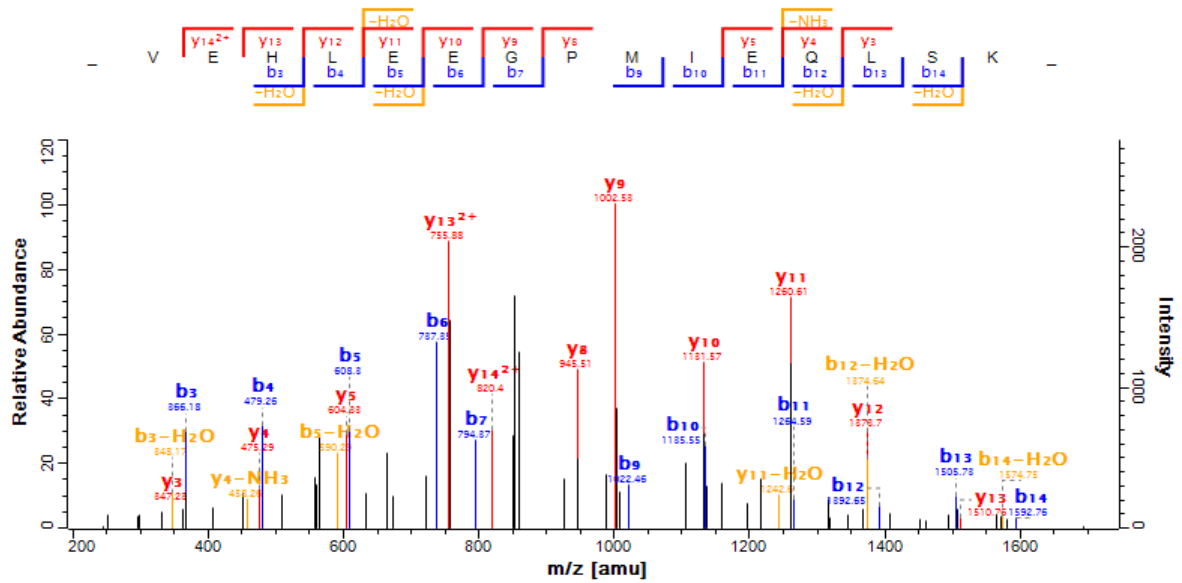
Number of Replicates (out of 8): 5

Best Match Score: 156.17

Best Match Posterior Error Probability: 8.58E-08

Best Match Spectrum:

Scan number 41509 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** MRPL42



Protein Group ID: 44

Protein Accession Numbers: Q7LGA3; A6ND99; Q7LGA3-2; Q7LGA3-3; K7EP71

Gene Names: HS2ST1

Peptide Sequence: PGFYHGVSYLDFAK

Total Number of Spectra: 3

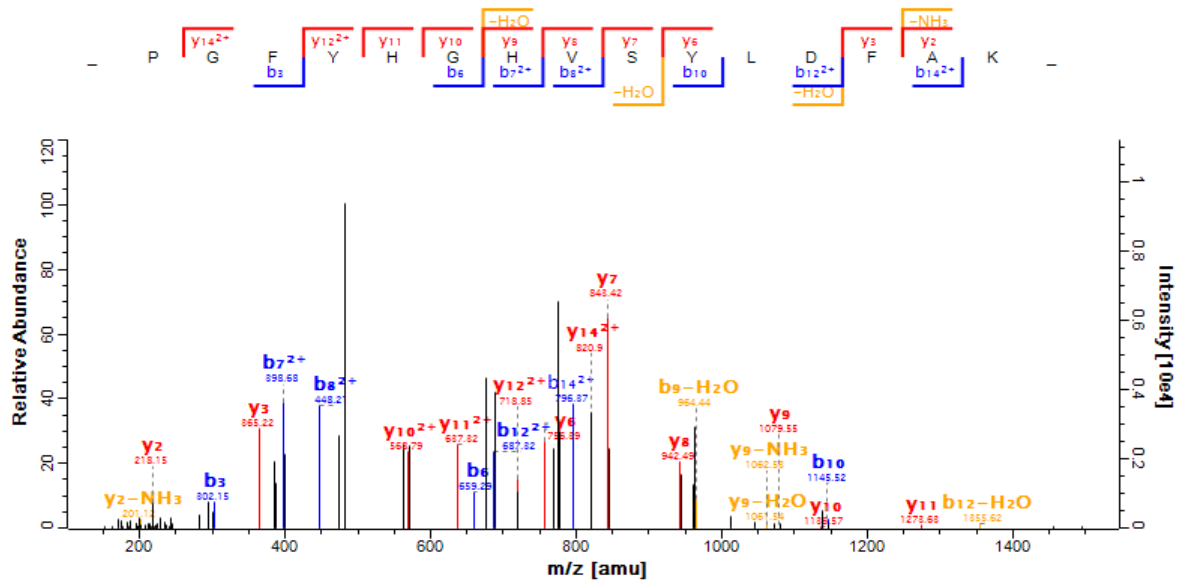
Number of Replicates (out of 8): 2

Best Match Score: 105.95

Best Match Posterior Error Probability: 0.00015957

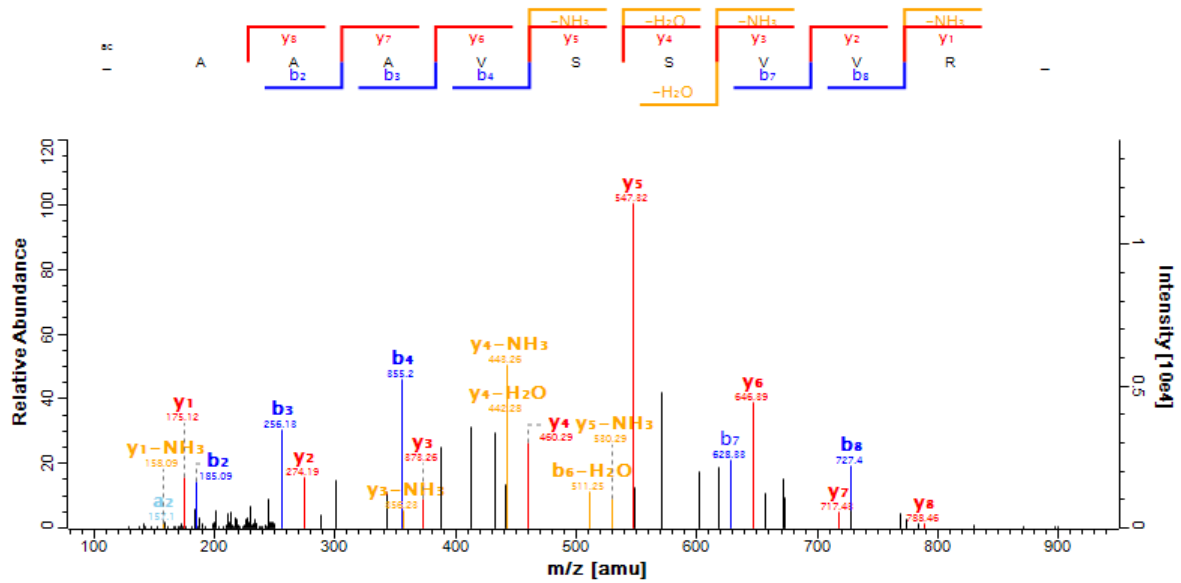
Best Match Spectrum:

Scan number	46120	Raw file	A549-US-WT-top20CID-Elite-2ug-811
Method	ITMS; CID	Genenames	HS2ST1



Protein Group ID: 46
Protein Accession Numbers: A6NDU8
Gene Names: C5orf51
Peptide Sequence: AAAVSSVVR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 109.29
Best Match Posterior Error Probability: 0.0014792
Best Match Spectrum:

Scan number 35375 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** C5orf51



Protein Group ID: 51

Protein Accession Numbers: P45983; P45983-4; P45983-2; P45983-3; Q308M2; A6NF29; C9J762

Gene Names: MAPK8

Peptide Sequence: NIIGLLNVFTPQK

Total Number of Spectra: 2

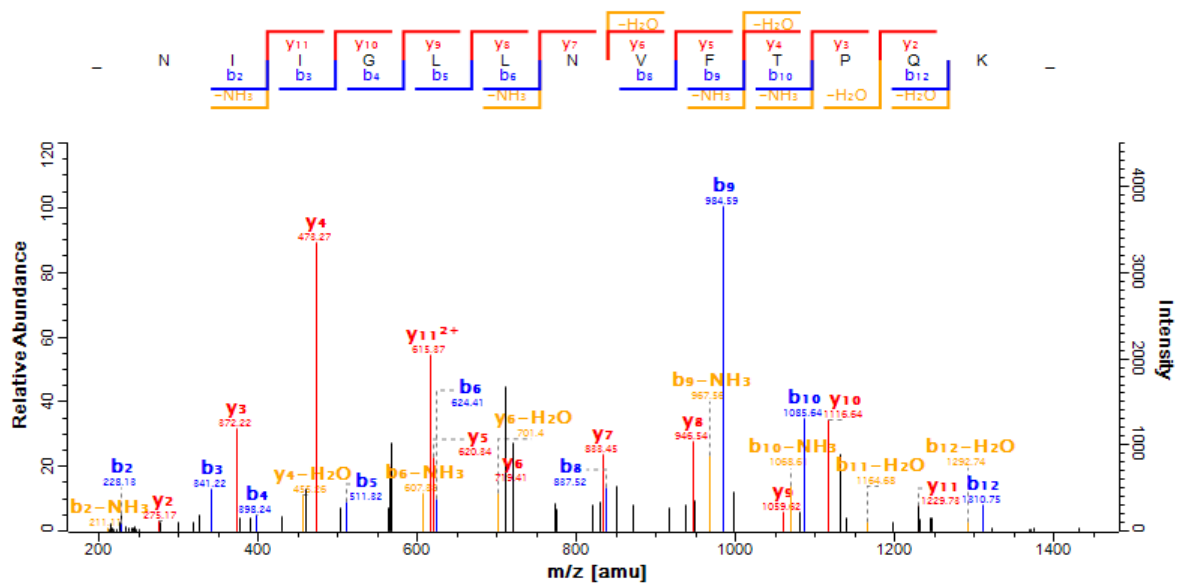
Number of Replicates (out of 8): 2

Best Match Score: 162.72

Best Match Posterior Error Probability: 1.68E-09

Best Match Spectrum:

Scan number 83355 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MAPK8



Protein Group ID: 55

Protein Accession Numbers: A6NFV8; Q96EV8; Q96EV8-2; D6RCT8; D6RAX1

Gene Names: DTNBP1

Peptide Sequence: LLSVQQDFTSGLK

Total Number of Spectra: 1

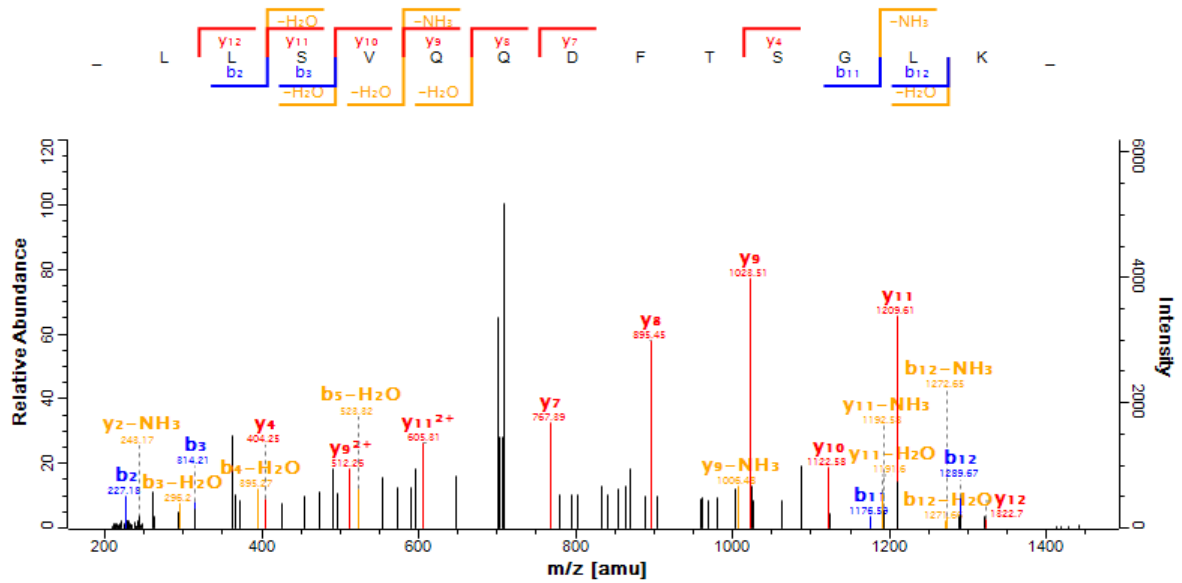
Number of Replicates (out of 8): 1

Best Match Score: 97.463

Best Match Posterior Error Probability: 0.00066916

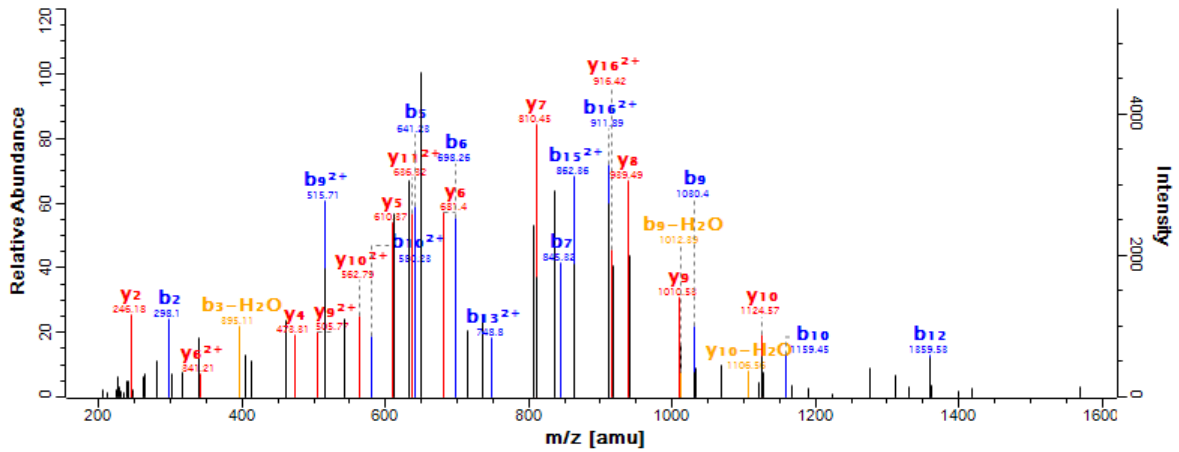
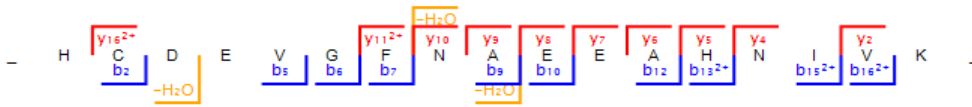
Best Match Spectrum:

Scan number 51124 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** DTNBP1



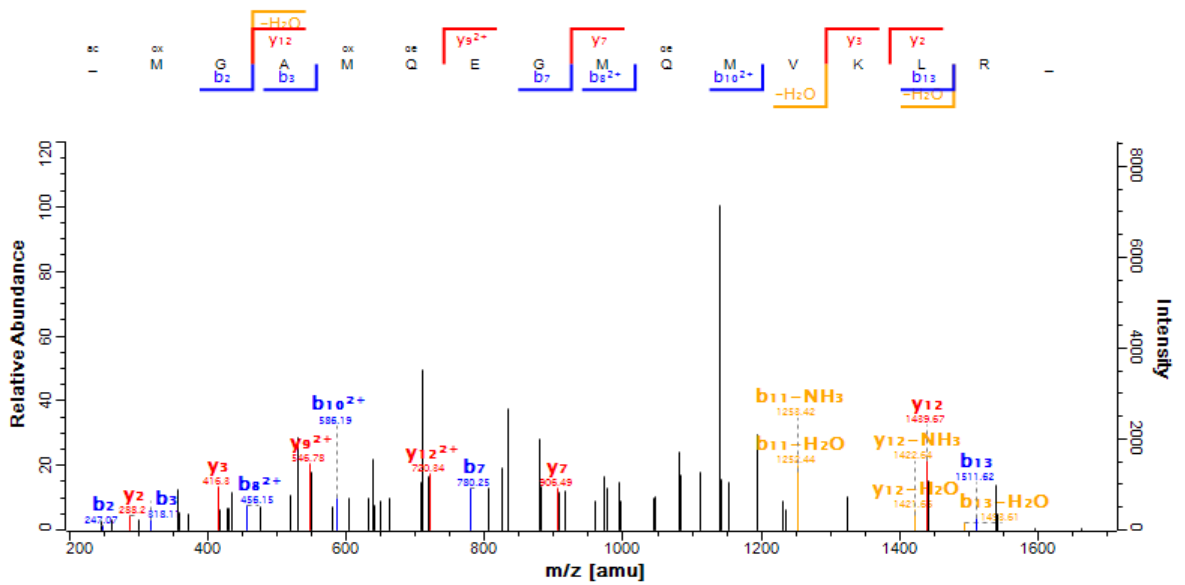
Protein Group ID: 60
Protein Accession Numbers: A6NGJ0; P51808
Gene Names: DYNLT3
Peptide Sequence: HCDEVGFNAEEAHNIVK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 139.66
Best Match Posterior Error Probability: 3.90E-05
Best Match Spectrum:

Scan number 31442 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** DYNLT3



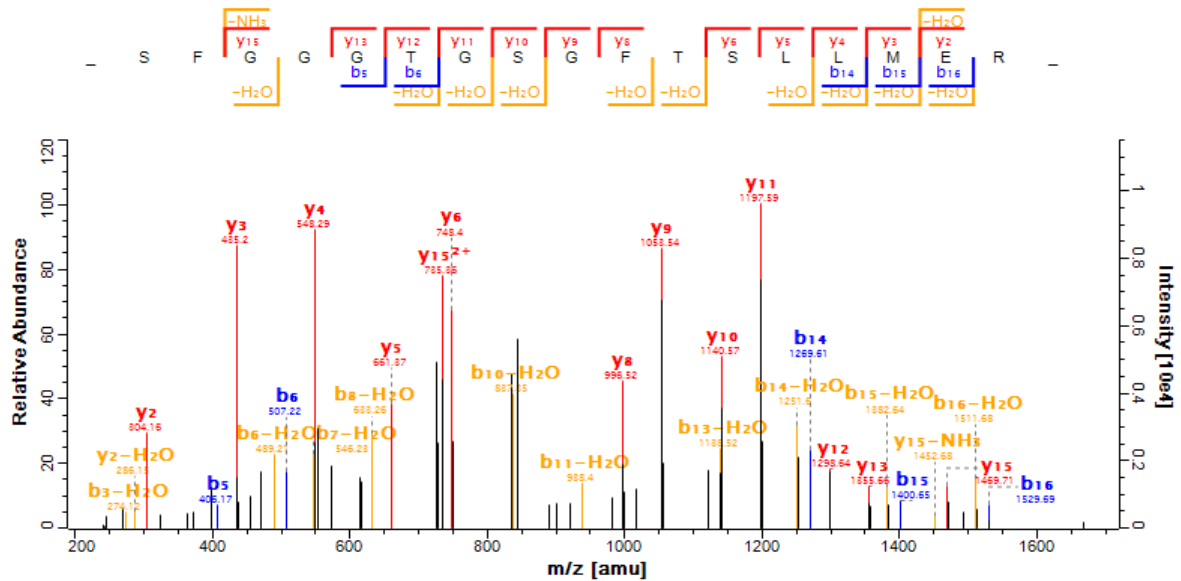
Protein Group ID: 62
Protein Accession Numbers: A6NGX9; O75038-5
Gene Names: PLCH2
Peptide Sequence: MGAMQEGMQMKLR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 68.676
Best Match Posterior Error Probability: 0.0053147
Best Match Spectrum:

Scan number 37851 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** PLCH2



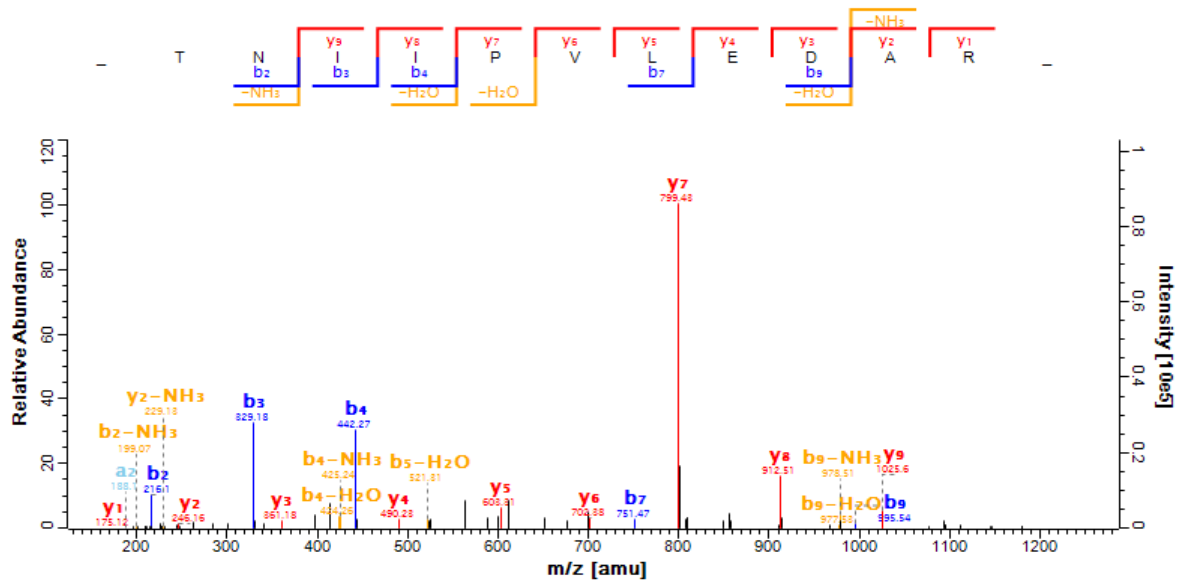
Protein Group ID: 63
Protein Accession Numbers: A6NHL2; A6NHL2-2
Gene Names: TUBAL3
Peptide Sequence: SFGGGTGSFGFTSLLMER
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 132.47
Best Match Posterior Error Probability: 8.22E-05
Best Match Spectrum:

Scan number 65109 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TUBAL3



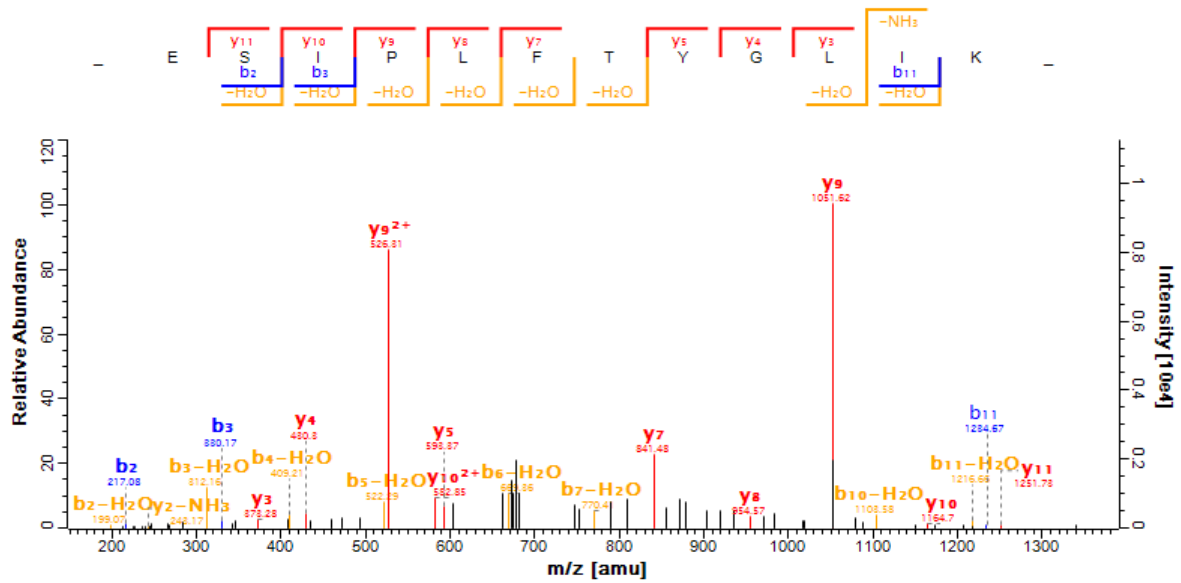
Protein Group ID: 64
Protein Accession Numbers: A6NHQ2
Gene Names: FBLL1
Peptide Sequence: TNIPVLEDAR
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 98.902
Best Match Posterior Error Probability: 0.00055543
Best Match Spectrum:

Scan number 48555 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** FBLL1



Protein Group ID: 66
Protein Accession Numbers: A6NHX0
Gene Names: GATSL2
Peptide Sequence: ESIPLFYGLIK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 102.4
Best Match Posterior Error Probability: 0.00045333
Best Match Spectrum:

Scan number 74712 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** GATSL2



Protein Group ID: 70

Protein Accession Numbers: Q9GZM8-2; Q9NXR1; Q9GZM8; Q9NXR1-2; J3QT32; A6NIZ0; J3QRZ1; J3QSD2; I3L522; I3L2R9; I3L533; I3L2T8; I3L2R3

Gene Names: NDE1;NDEL1

Peptide Sequence: ISALNIVGDLLR

Total Number of Spectra: 4

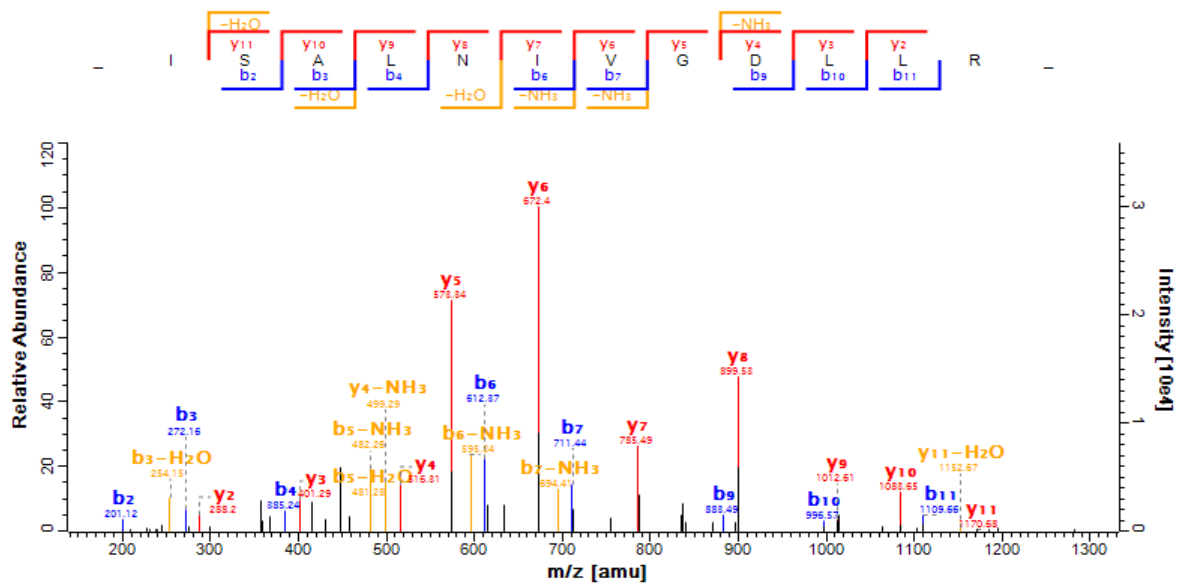
Number of Replicates (out of 8): 4

Best Match Score: 151.99

Best Match Posterior Error Probability: 2.85E-06

Best Match Spectrum:

Scan number	88294	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS: CID	Genenames	NDE1;NDEL1



Protein Group ID: 75

Protein Accession Numbers: J3KNE0; A6NKT7; J3KKNY6; Q7Z3J3

Gene Names: RGPD3;RGPD4

Peptide Sequence: ILDDSDSNLSVVK

Total Number of Spectra: 11

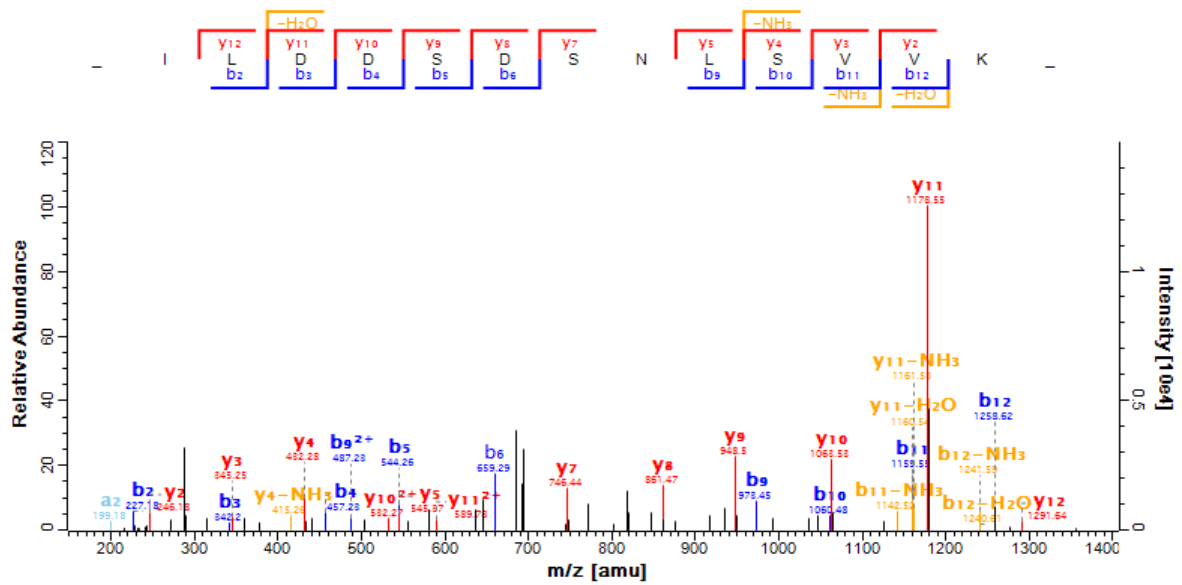
Number of Replicates (out of 8): 8

Best Match Score: 178.67

Best Match Posterior Error Probability: 2.30E-14

Best Match Spectrum:

Scan number 30795 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** RGPD3;RGPD4



Protein Group ID: 77

Protein Accession Numbers: Q8IY57; A6NL56; J3KNM5; Q8IY57-2; Q8IY57-3

Gene Names: YAF2

Peptide Sequence: SPPASSAASADQHSQSGSSSDNTER

Total Number of Spectra: 7

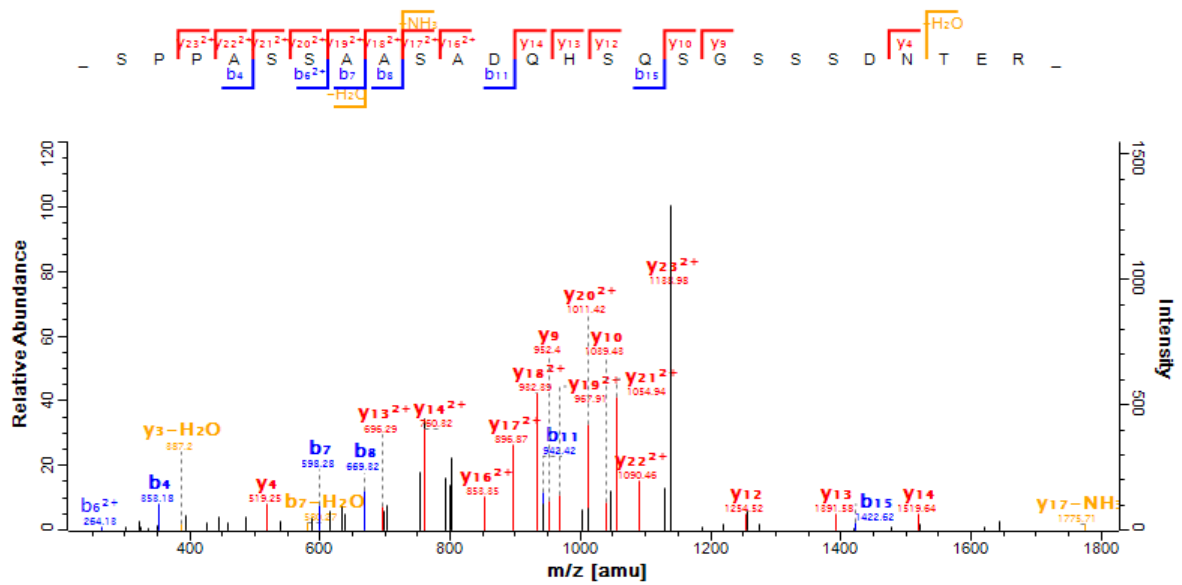
Number of Replicates (out of 8): 5

Best Match Score: 94.837

Best Match Posterior Error Probability: 5.28E-06

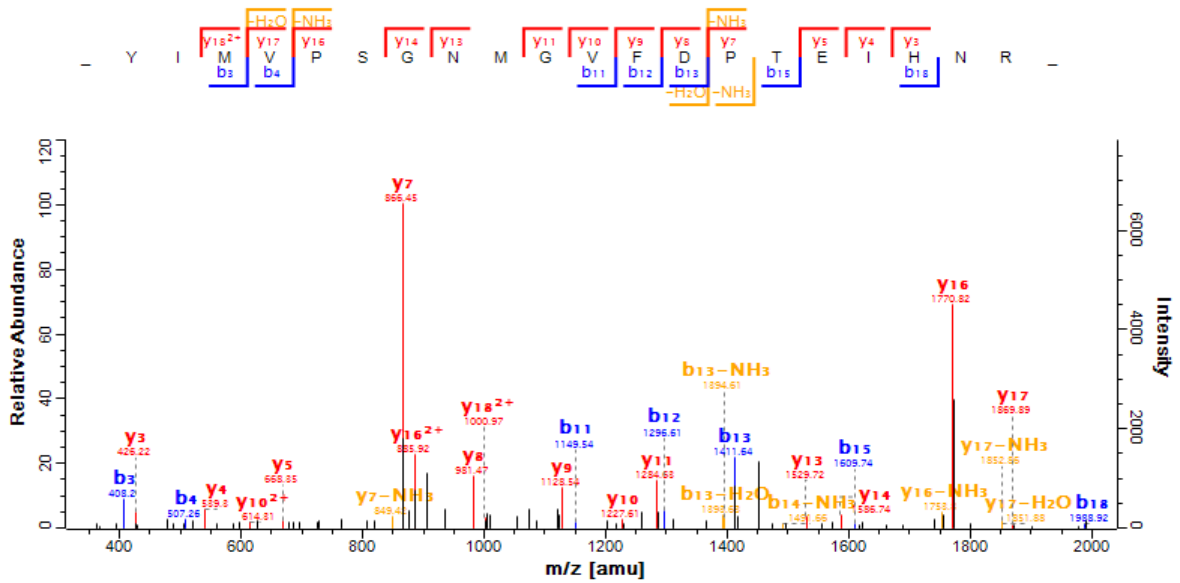
Best Match Spectrum:

Scan number 3272 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** YAF2



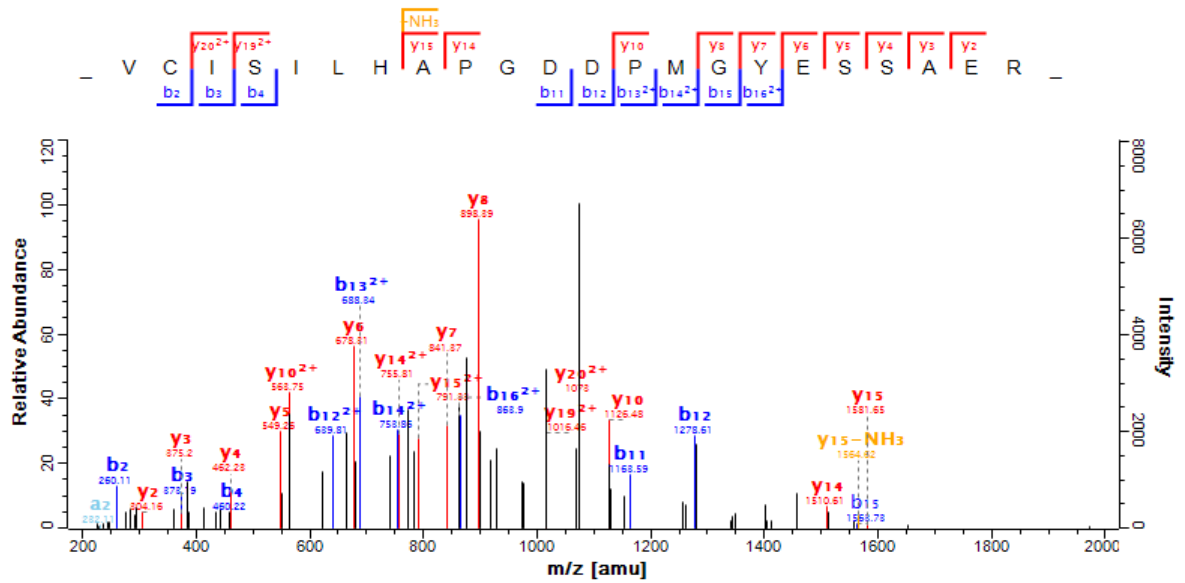
Protein Group ID: 78
Protein Accession Numbers: Q9P003; A6NLH6
Gene Names: CNIH4
Peptide Sequence: YIMVPSGNMGVFDPTIHN R
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 137.61
Best Match Posterior Error Probability: 1.03E-06
Best Match Spectrum:

Scan number 60907 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CNIH4



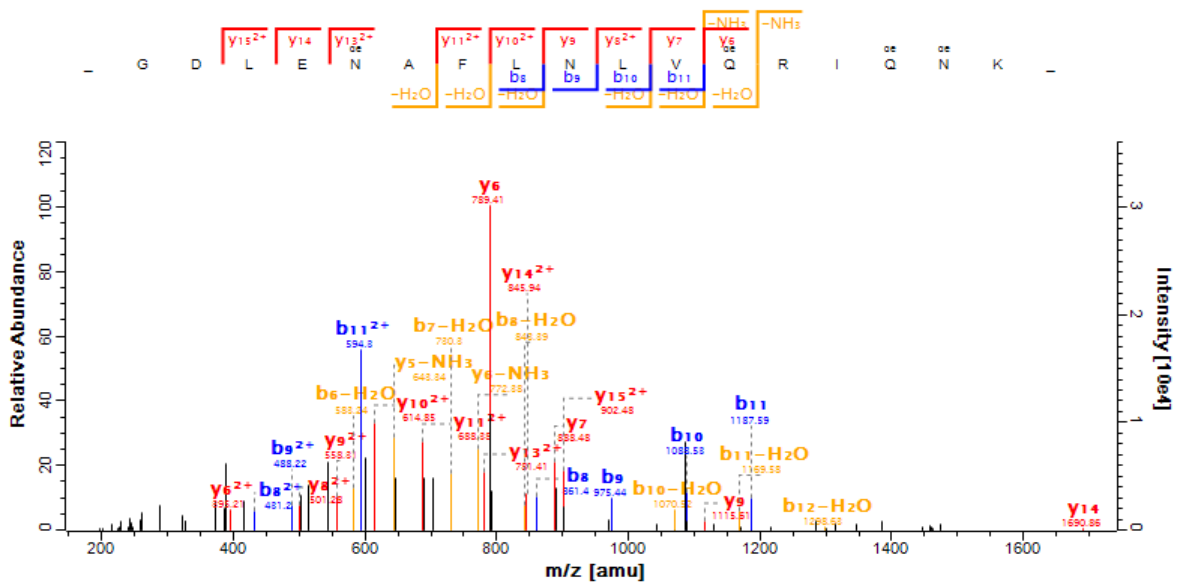
Protein Group ID: 86
Protein Accession Numbers: P60604; A6NMQ7
Gene Names: UBE2G2
Peptide Sequence: VCISILHAPGGDDPMGYESSASAEER
Total Number of Spectra: 10
Number of Replicates (out of 8): 8
Best Match Score: 112.55
Best Match Posterior Error Probability: 3.44E-07
Best Match Spectrum:

Scan number 53052 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** UBE2G2



Protein Group ID: 87
Protein Accession Numbers: A6NMY6
Gene Names: ANXA2P2
Peptide Sequence: GDLENAFLNLVQRIQNK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 115.06
Best Match Posterior Error Probability: 0.0063144
Best Match Spectrum:

Scan number 92185 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ANXA2P2



Protein Group ID: 91

Protein Accession Numbers: P24001; F8VSD2; F8VVN4; F8W1V1; E9PIV2; P24001-2; A6NNM0; P24001-3; P24001-5; E9PK07; P24001-4

Gene Names: IL32

Peptide Sequence: EGYLETVAAYYEEQHPELTPLEEK

Total Number of Spectra: 1

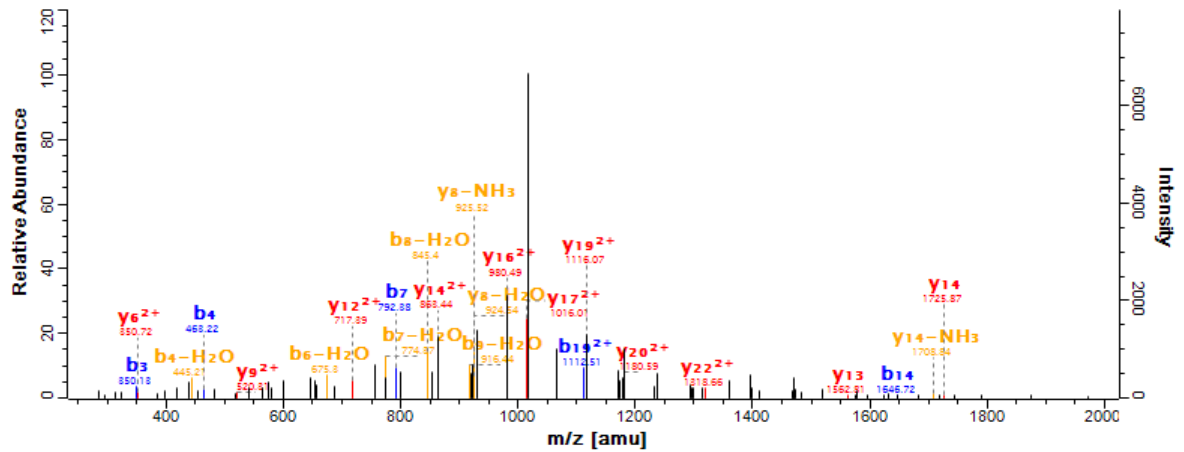
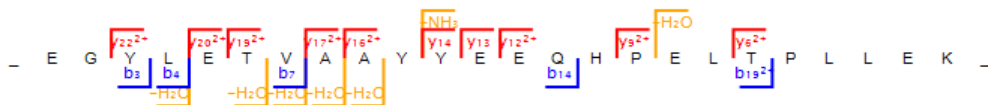
Number of Replicates (out of 8): 1

Best Match Score: 68.639

Best Match Posterior Error Probability: 0.00059479

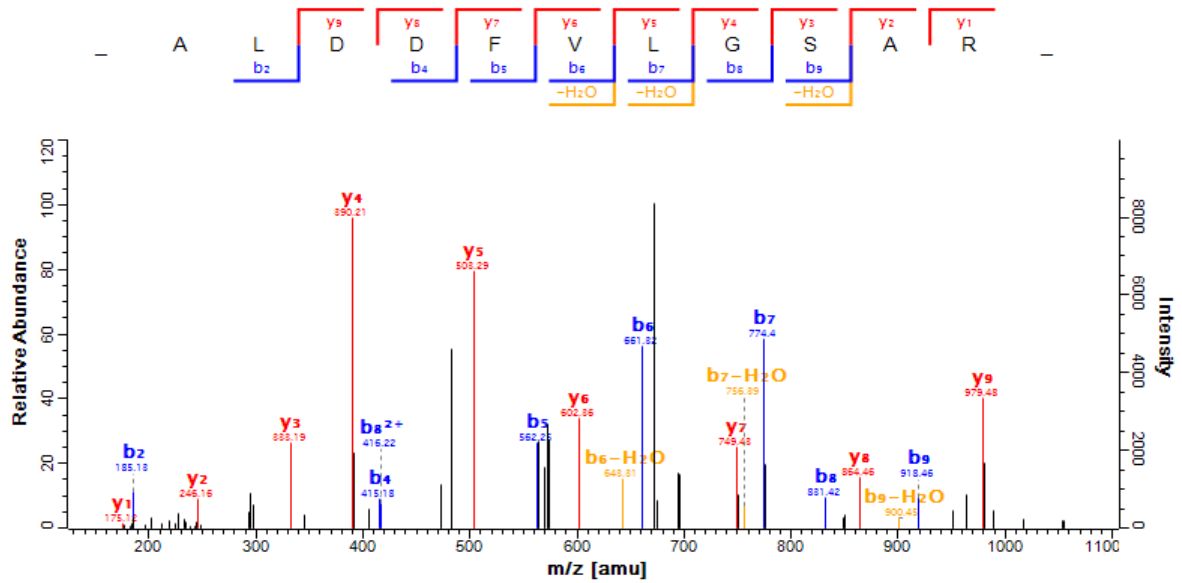
Best Match Spectrum:

Scan number	81206	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	IL32



Protein Group ID: 93
Protein Accession Numbers: O60831; A6NP52
Gene Names: PRAF2
Peptide Sequence: ALDDFVLGSAR
Total Number of Spectra: 2
Number of Replicates (out of 8): 1
Best Match Score: 125.97
Best Match Posterior Error Probability: 4.33E-05
Best Match Spectrum:

Scan number 49115 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** PRAF2



Protein Group ID: 95

Protein Accession Numbers: Q6UXH1-5; Q6UXH1-6; Q6UXH1; Q6UXH1-4; Q6UXH1-2; Q6UXH1-3; A6PWM2

Gene Names: CRELD2

Peptide Sequence: NFGGGNTAWEK

Total Number of Spectra: 7

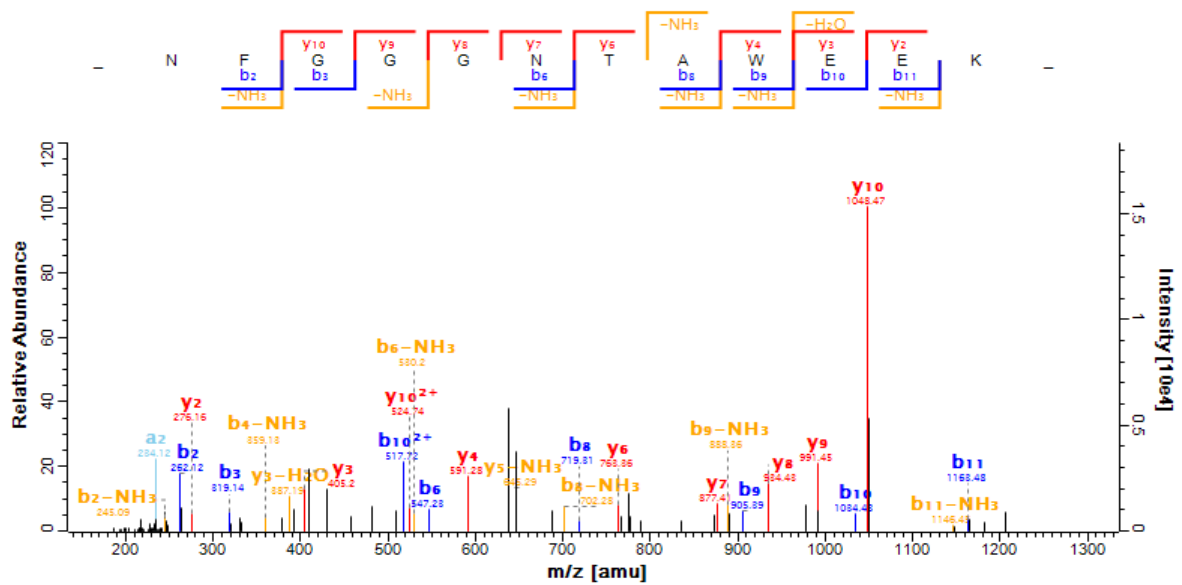
Number of Replicates (out of 8): 7

Best Match Score: 135.02

Best Match Posterior Error Probability: 8.76E-05

Best Match Spectrum:

Scan number	24552	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	CRELD2



Protein Group ID: 96

Protein Accession Numbers: A6ZKI3; Q17RB0; Q9BWD3

Gene Names: FAM127A;FAM127C;FAM127B

Peptide Sequence: RVFGWEEEDF

Total Number of Spectra: 3

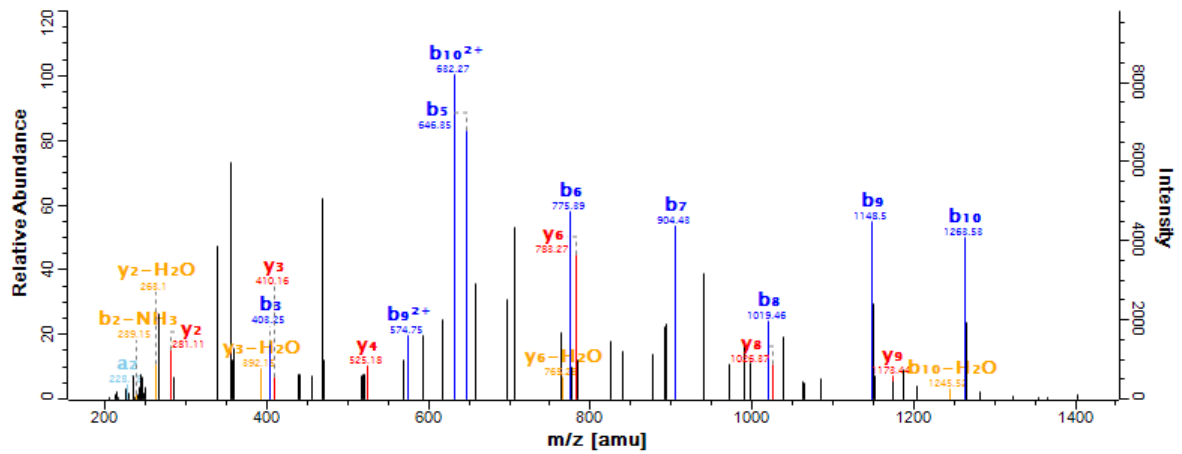
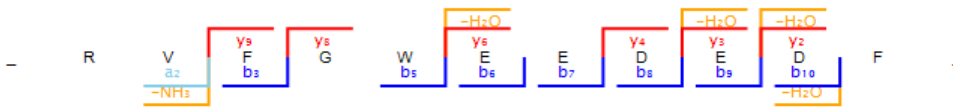
Number of Replicates (out of 8): 3

Best Match Score: 119.27

Best Match Posterior Error Probability: 0.00015874

Best Match Spectrum:

Scan number 54901 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** FAM127A;FAM127C;FAM127B



Protein Group ID: 99

Protein Accession Numbers: A8CTX8; A8CTY3; B4DTM2; E7ERJ0; Q15811-3; E7ERJ1; A7Y322; A8DCP3

Gene Names: ITSN1

Peptide Sequence: SHDEITIQPGDIVMVD E S Q T G E P G W L G G E L K

Total Number of Spectra: 1

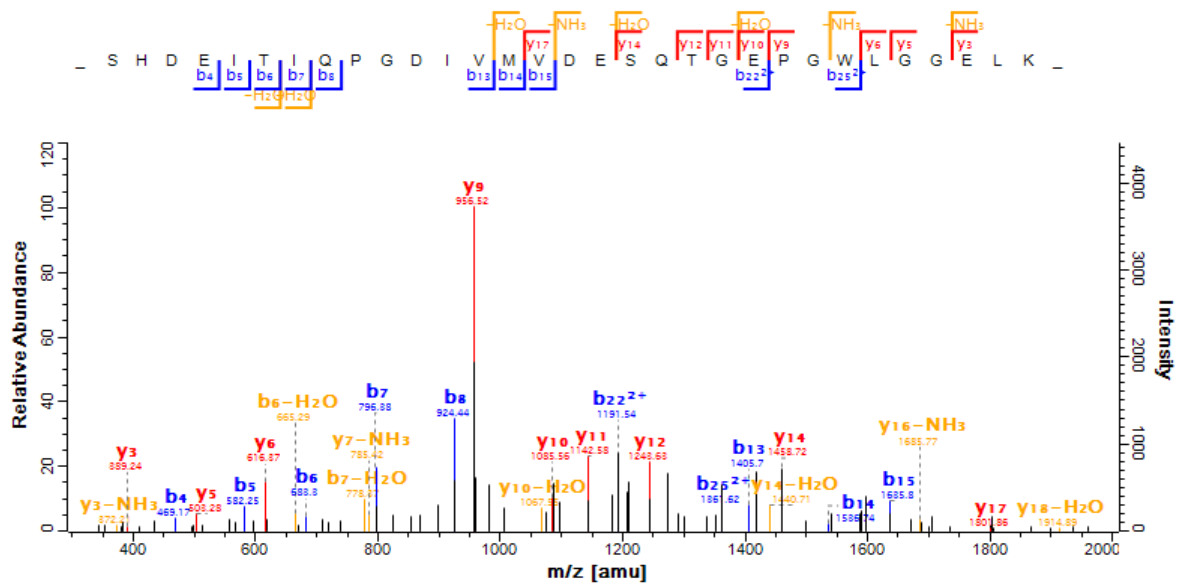
Number of Replicates (out of 8): 1

Best Match Score: 80.439

Best Match Posterior Error Probability: 1.97E-06

Best Match Spectrum:

Scan number	73820	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS: CID	Genenames	ITSN1



Protein Group ID: 102

Protein Accession Numbers: Q9Y6D0; A8K0M9; F8WAX7

Gene Names: SELK

Peptide Sequence: VYISNGQVLDSR

Total Number of Spectra: 1

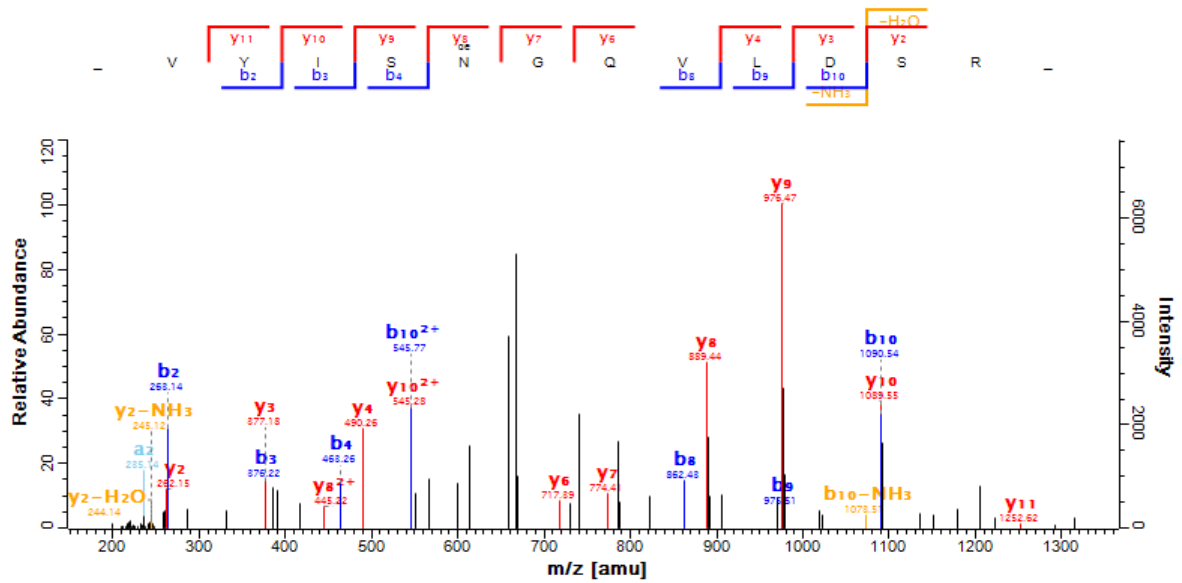
Number of Replicates (out of 8): 1

Best Match Score: 113.99

Best Match Posterior Error Probability: 0.0010492

Best Match Spectrum:

Scan number	32617	Raw file	A549-US-WT-top20CID-Elite-2ug-813
Method	ITMS; CID	Genenames	SELK



Protein Group ID: 105

Protein Accession Numbers: I3L448; Q5TC12; A8MRA7; I3L1W9; B7Z7I6; H0YD21; B7Z7D6; H0YEW4

Gene Names: ATPAF1

Peptide Sequence: YMSVIAELEQSGGLGAE LK

Total Number of Spectra: 6

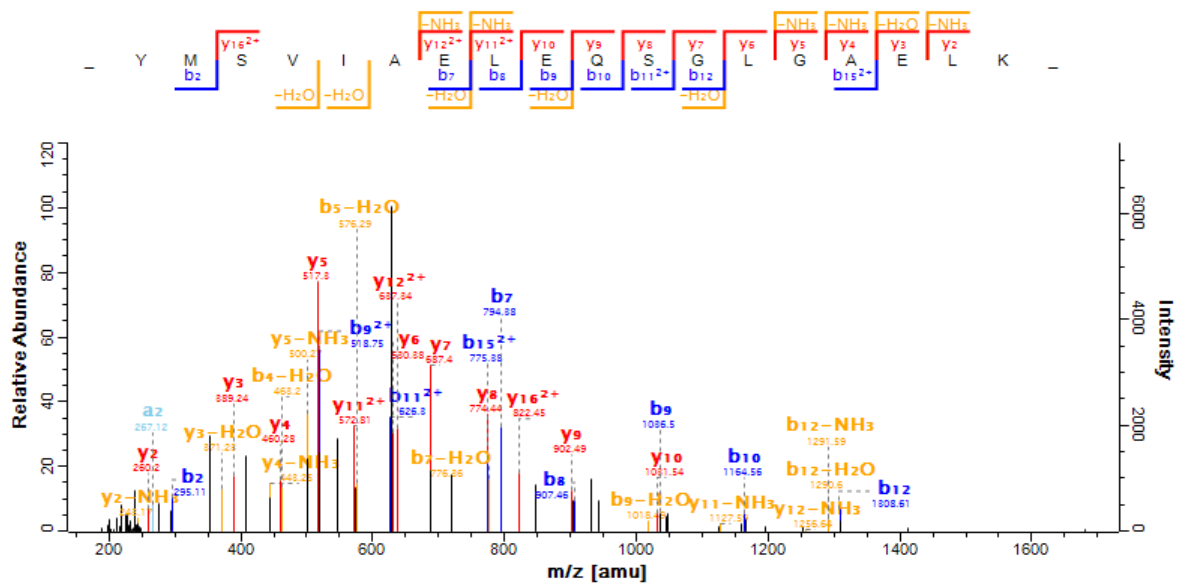
Number of Replicates (out of 8): 6

Best Match Score: 147.7

Best Match Posterior Error Probability: 9.50E-07

Best Match Spectrum:

Scan number 83879 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS: CID **Genenames** ATPAF1



Protein Group ID: 122

Protein Accession Numbers: P53801; A8MXQ1; A8MZH8

Gene Names: PTTG1IP

Peptide Sequence: ACLDYPVTSVLPPASLCK

Total Number of Spectra: 1

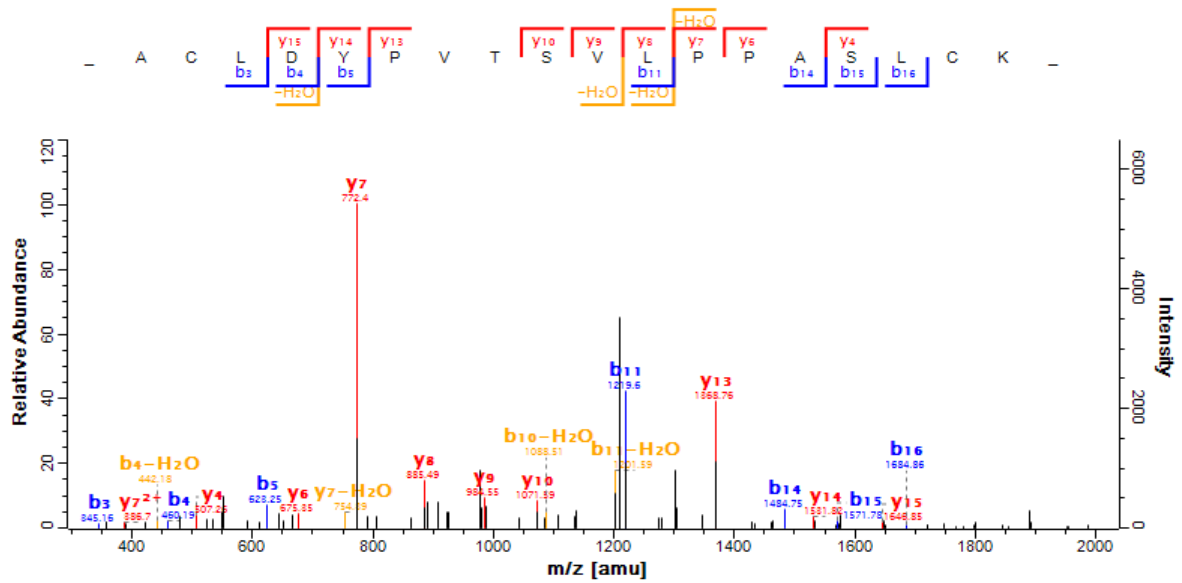
Number of Replicates (out of 8): 1

Best Match Score: 85.362

Best Match Posterior Error Probability: 0.00064535

Best Match Spectrum:

Scan number	62605	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	PTTG1IP



Protein Group ID: 125

Protein Accession Numbers: O14874; A8MY43; Q96G95; H3BS02; H3BTL2

Gene Names: BCKDK

Peptide Sequence: DVVTLLAEGLR

Total Number of Spectra: 1

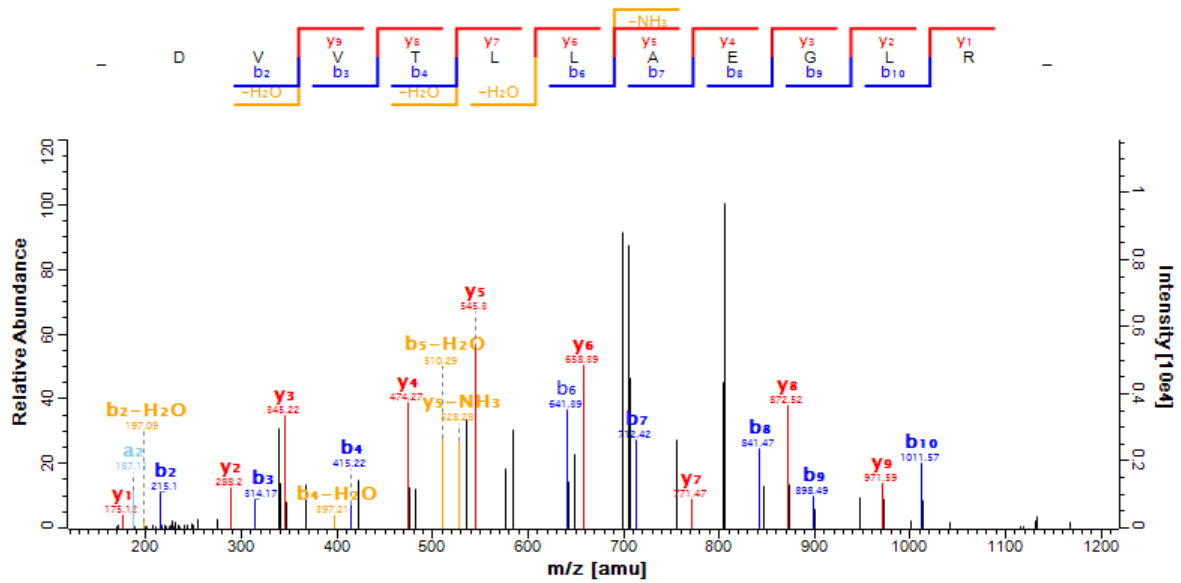
Number of Replicates (out of 8): 1

Best Match Score: 144.1

Best Match Posterior Error Probability: 1.35E-05

Best Match Spectrum:

Scan number	72566	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	BCKDK



Protein Group ID: 131

Protein Accession Numbers: B4DUM7; A9UHW6-2; J3QLJ5; A9UHW6; J3QRZ6; J3KSB8; J3QKW3; J3KSU6; J3QLD1; J3QLN4

Gene Names: MIF4GD

Peptide Sequence: IQSFDAETQQLK

Total Number of Spectra: 2

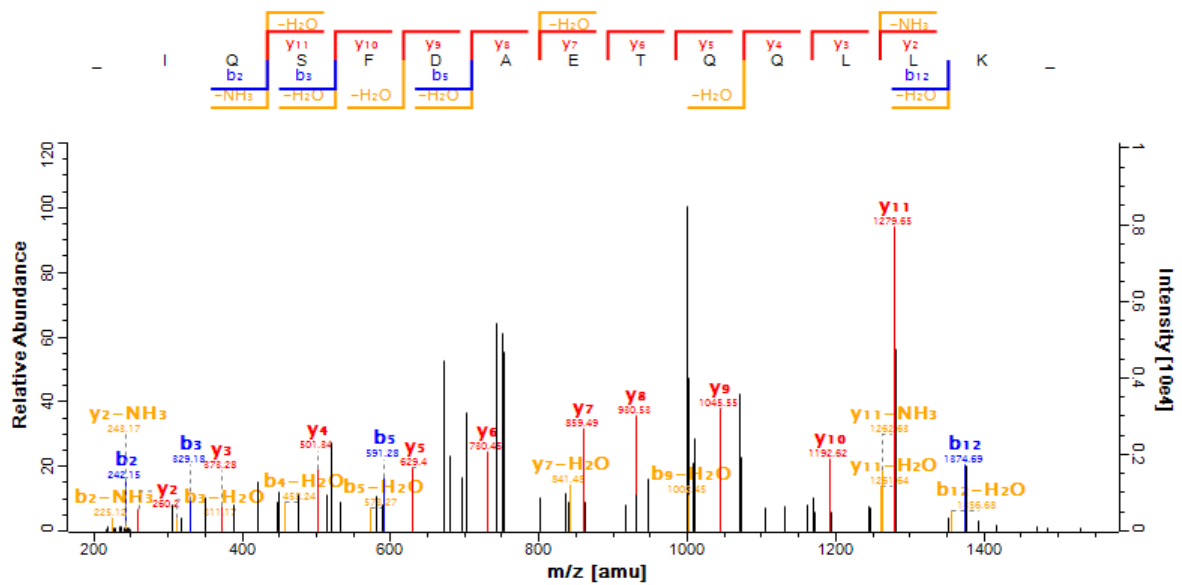
Number of Replicates (out of 8): 2

Best Match Score: 127.71

Best Match Posterior Error Probability: 7.62E-05

Best Match Spectrum:

Scan number	49586	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS: CID	Genenames	MIF4GD



Protein Group ID: 133

Protein Accession Numbers: O60238; H0YBC7; B0AZS9

Gene Names: BNIP3L

Peptide Sequence: DHSSQSEEEVVEGEK

Total Number of Spectra: 1

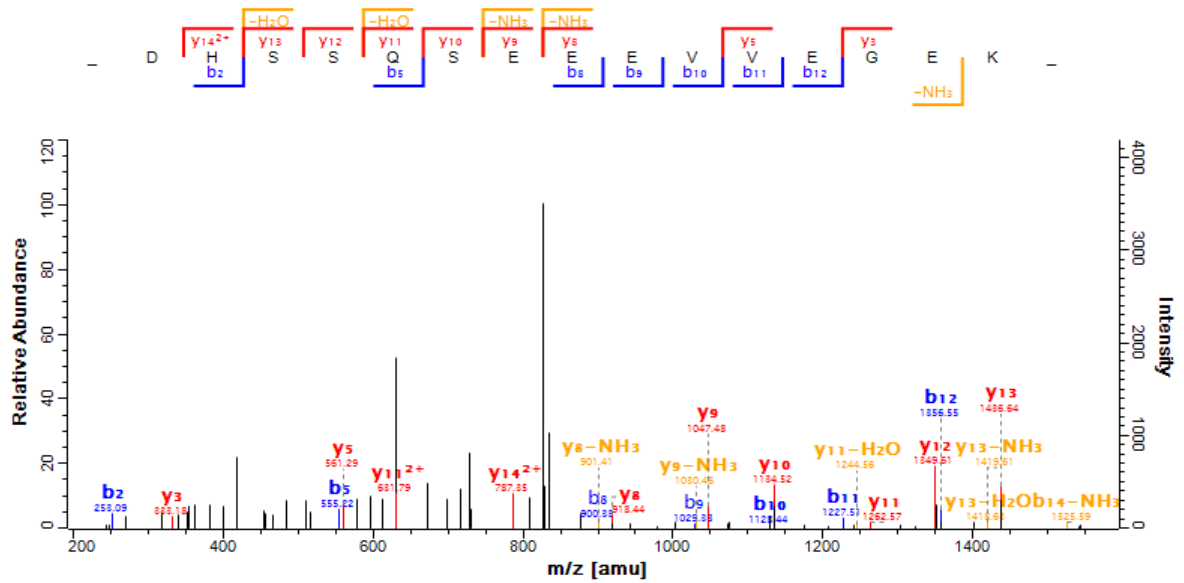
Number of Replicates (out of 8): 1

Best Match Score: 95.236

Best Match Posterior Error Probability: 0.00046119

Best Match Spectrum:

Scan number 11238 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** BNIP3L



Protein Group ID: 136

Protein Accession Numbers: Q8N3F8; Q68D58; B0QY91

Gene Names: MICALL1;DKFZp686M2226

Peptide Sequence: VLMQELVTLEIQR

Total Number of Spectra: 4

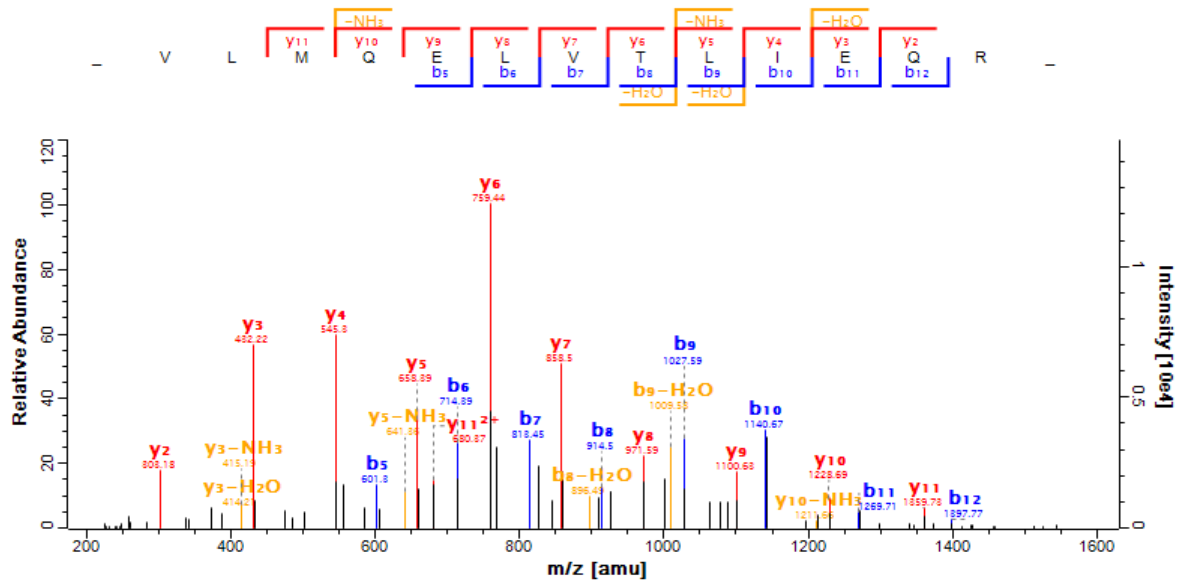
Number of Replicates (out of 8): 4

Best Match Score: 134.9

Best Match Posterior Error Probability: 3.98E-05

Best Match Spectrum:

Scan number	89334	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	MICALL1;DKFZp686M2226



Protein Group ID: 137

Protein Accession Numbers: P02144; B0QYF8; F2Z2F1; Q8WVH6; B0QYF7

Gene Names: MB

Peptide Sequence: HGATVLTALGGILK

Total Number of Spectra: 3

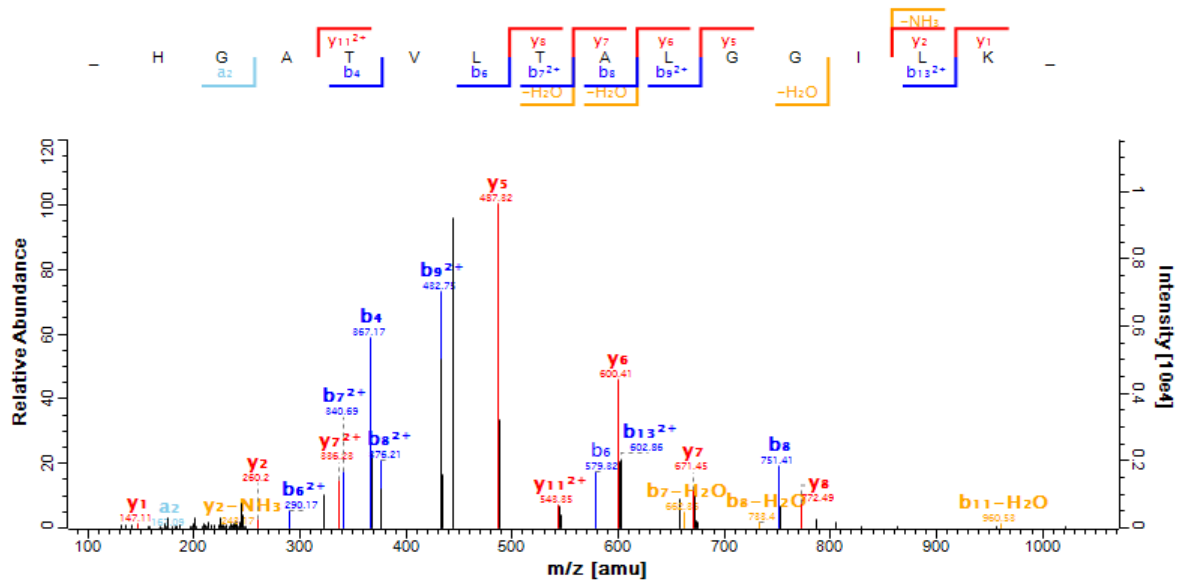
Number of Replicates (out of 8): 3

Best Match Score: 95.094

Best Match Posterior Error Probability: 0.00071244

Best Match Spectrum:

Scan number	64598	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	MB



Protein Group ID: 138

Protein Accession Numbers: Q8WUA7; B0QYI3; Q8WUA7-3; F8WDP1

Gene Names: TBC1D22A

Peptide Sequence: S Q L P H S A T V T L G G T S D P S T L S S A L S E R

Total Number of Spectra: 2

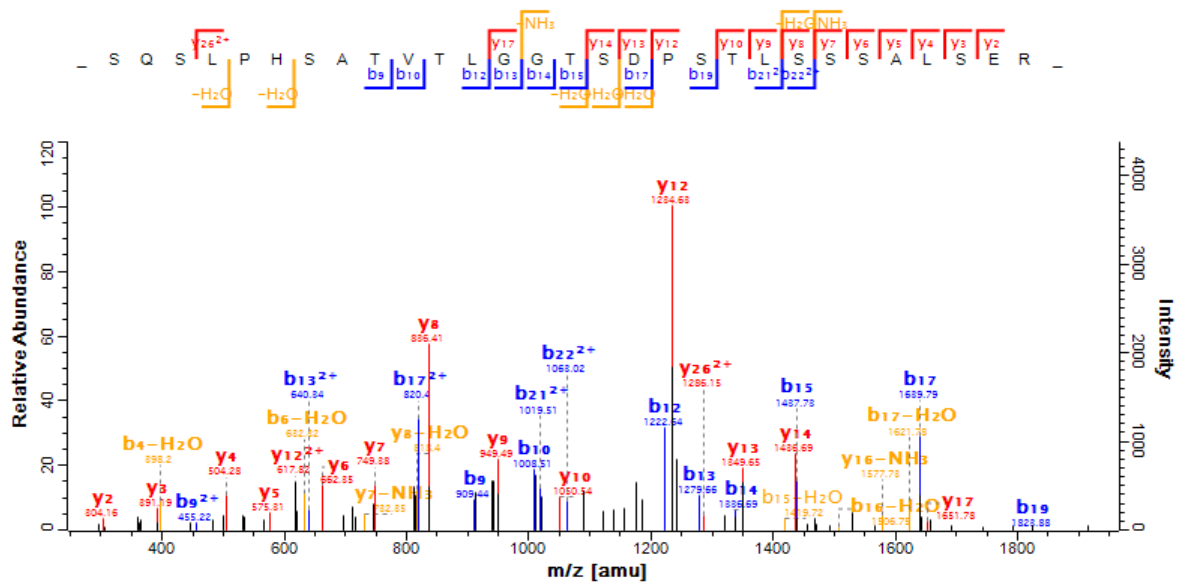
Number of Replicates (out of 8): 2

Best Match Score: 99.753

Best Match Posterior Error Probability: 2.66E-09

Best Match Spectrum:

Scan number 45987 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TBC1D22A



Protein Group ID: 140

Protein Accession Numbers: Q9HBI1-2; Q9HBI1; B0QYM8; B0QYP8

Gene Names: PARVB

Peptide Sequence: LNVAEVTQSEIGQK

Total Number of Spectra: 4

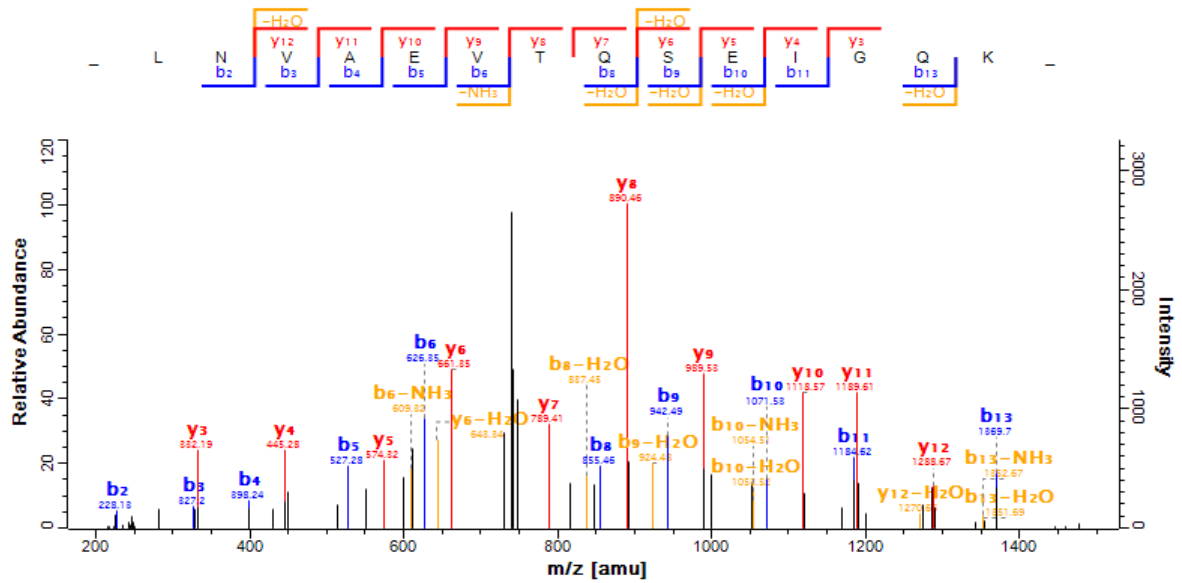
Number of Replicates (out of 8): 4

Best Match Score: 179.56

Best Match Posterior Error Probability: 1.92E-15

Best Match Spectrum:

Scan number 39533 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PARVB



Protein Group ID: 141

Protein Accession Numbers: F8VZG9; O43251-8; O43251-6; B7Z1U7; Q9NWB1-2; J3KNW3; O43251-7; Q9NWB1; Q9NWB1-5; Q9NWB1-4; O43251; O43251-2; O43251-10; O43251-5; B0QYY4; O43251-4; Q9NWB1-3; O43251-9; B0QYV1; F8VZY7; F8VR27; B0QYY7; I3L1D4

Gene Names: RBFOX1;RBFOX2;RBM9

Peptide Sequence: GFGFVTFENSADADR

Total Number of Spectra: 4

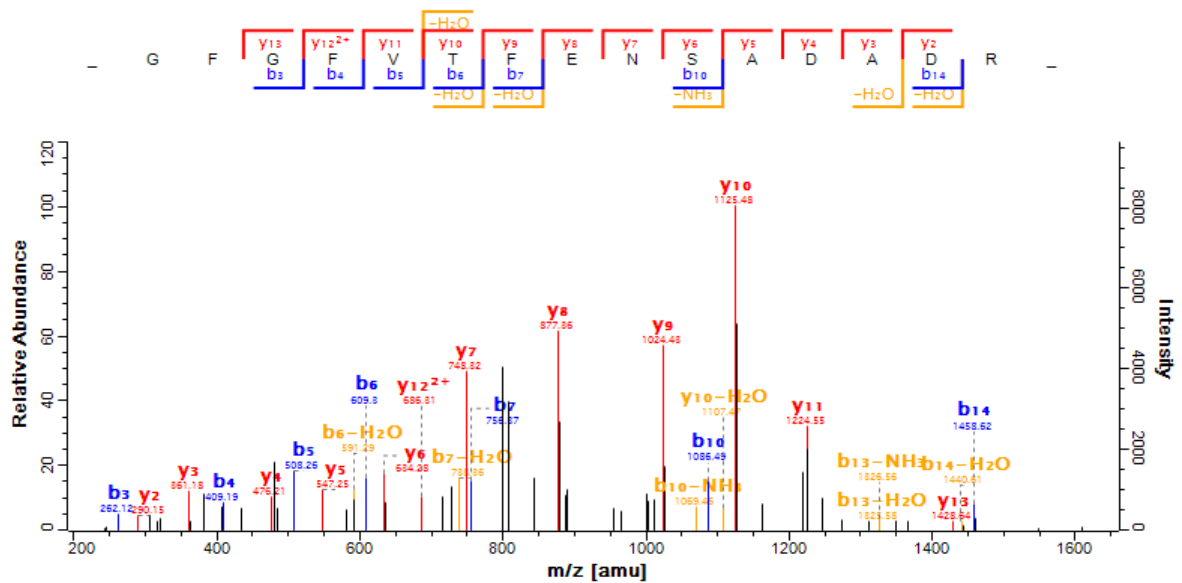
Number of Replicates (out of 8): 3

Best Match Score: 130.72

Best Match Posterior Error Probability: 3.15E-05

Best Match Spectrum:

Scan number 55404 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS: CID **Genenames** RBFOX1;RBFOX2;RBM9



Protein Group ID: 142

Protein Accession Numbers: B0S7P1; P25440-2; H0Y5T9; H0Y6K2; P25440; F8VXF8; Q658Y7; B0V073; H0Y602; B0V072; E9PIQ3; H0Y799; H0Y801

Gene Names: BRD2;DKFZp313H139

Peptide Sequence: VASMPQEEQLVVTIPK

Total Number of Spectra: 2

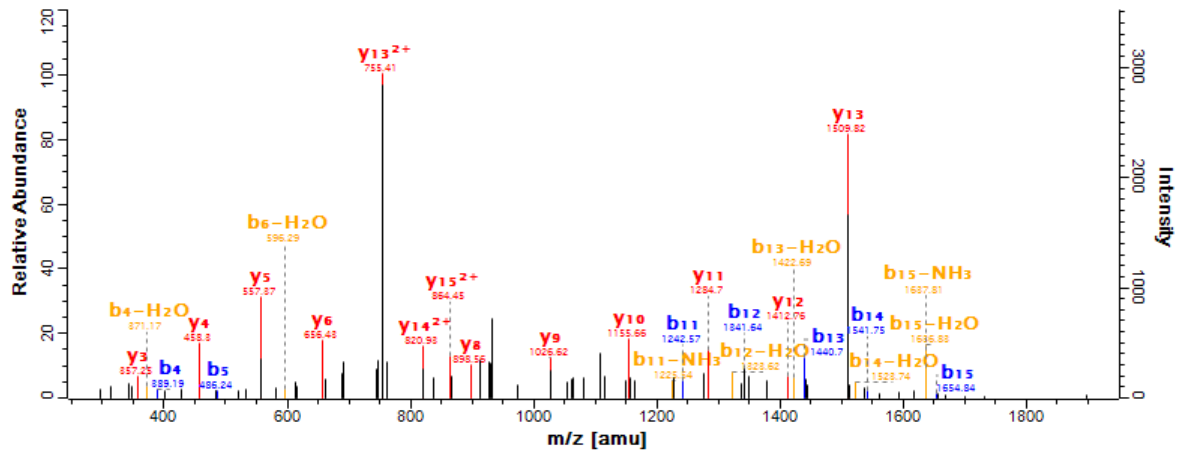
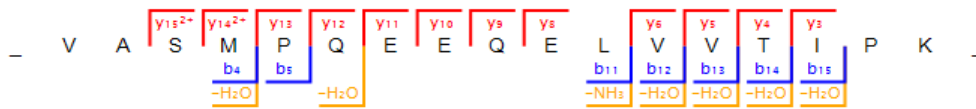
Number of Replicates (out of 8): 2

Best Match Score: 124.68

Best Match Posterior Error Probability: 0.00011291

Best Match Spectrum:

Scan number	54323	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS: CID	Genenames	BRD2;DKFZp313H139



Protein Group ID: 144

Protein Accession Numbers: Q14657; B0S8I7

Gene Names: LAGE3

Peptide Sequence: GGVDTAAPAGGAPPAHAPGPGR

Total Number of Spectra: 11

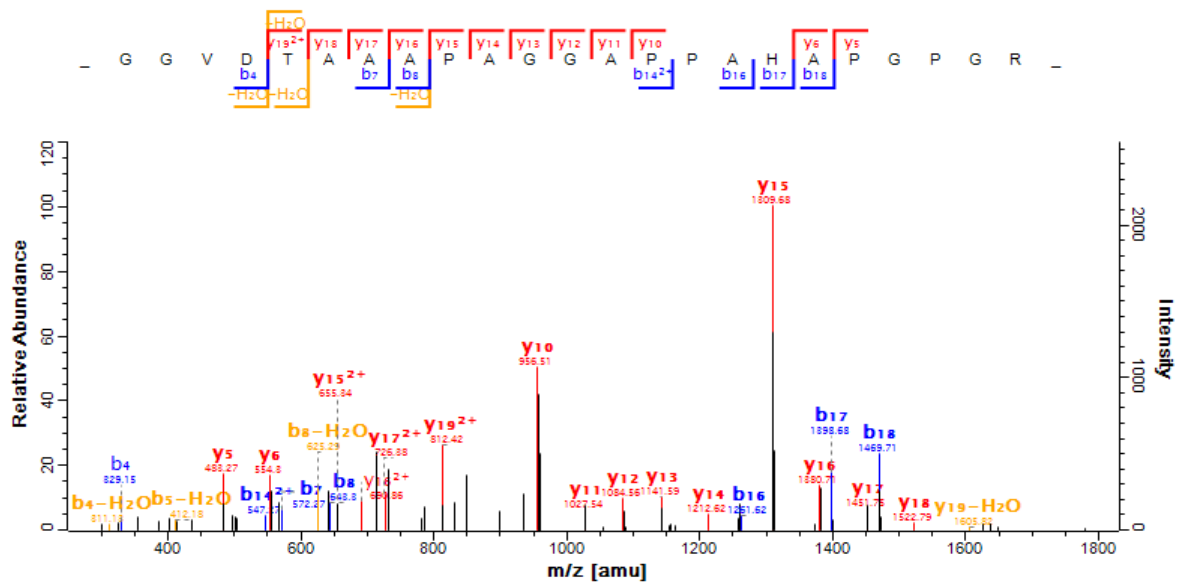
Number of Replicates (out of 8): 6

Best Match Score: 88.176

Best Match Posterior Error Probability: 1.41E-05

Best Match Spectrum:

Scan number 17688 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** LAGE3



Protein Group ID: 146

Protein Accession Numbers: B0UXB6; O95870; F2Z3H2

Gene Names: BAT5;ABHD16A

Peptide Sequence: APASVPETPTAVTAPHSSSWDTYYQPR

Total Number of Spectra: 2

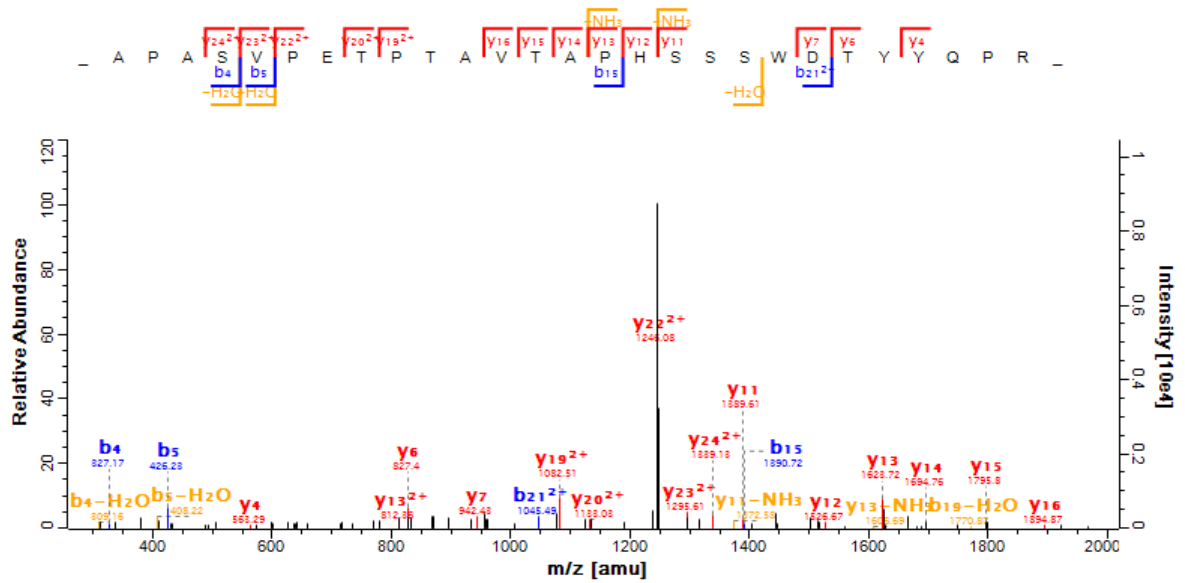
Number of Replicates (out of 8): 2

Best Match Score: 73.11

Best Match Posterior Error Probability: 0.00014838

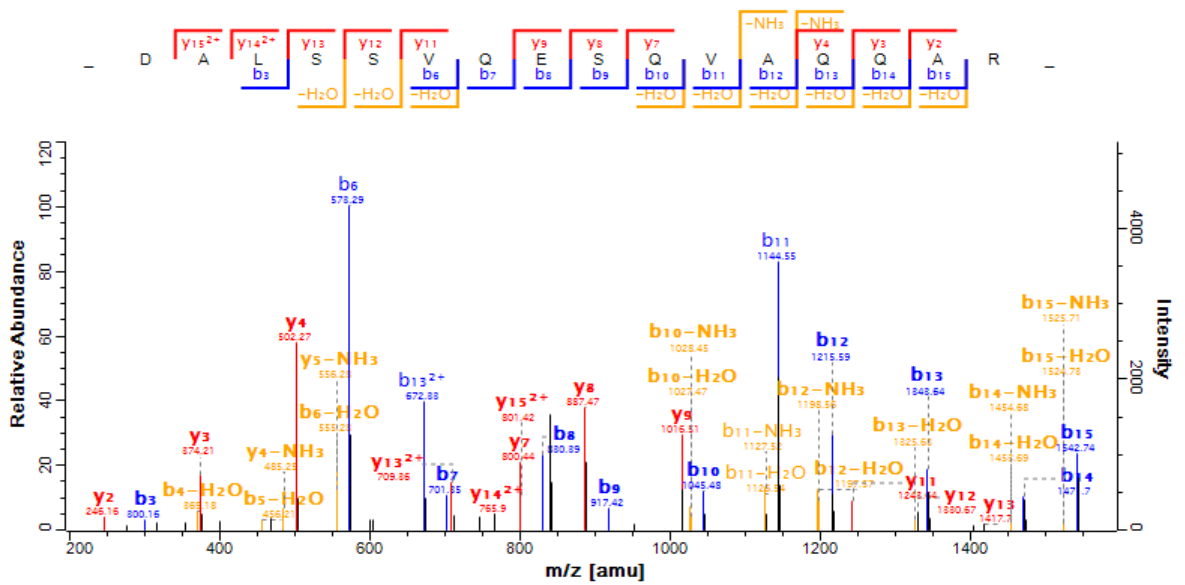
Best Match Spectrum:

Scan number 47877 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** BAT5;ABHD16A



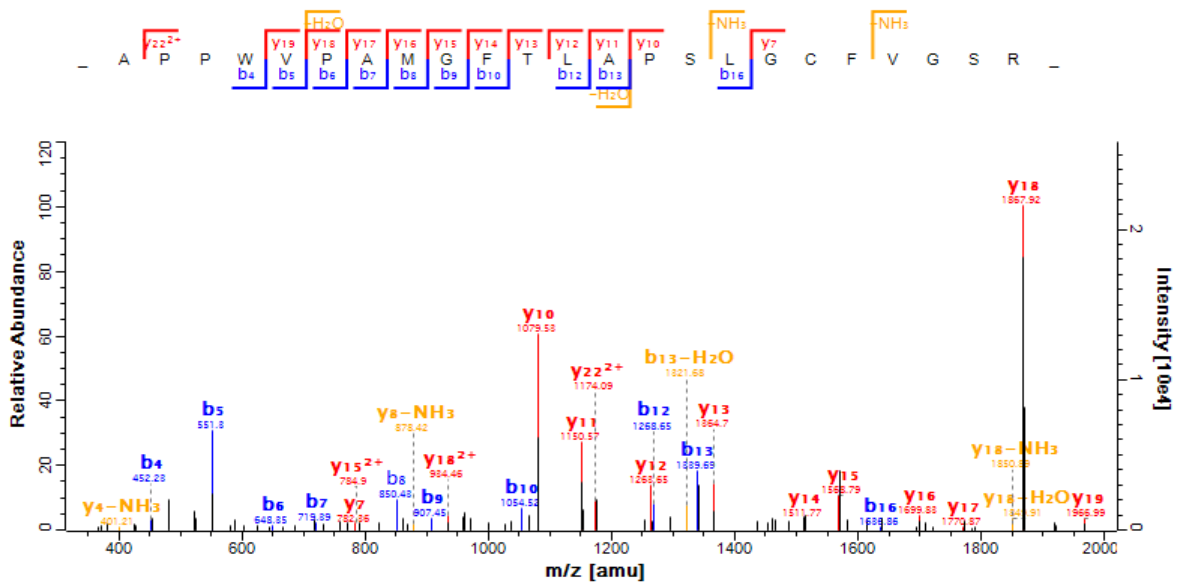
Protein Group ID: 149
Protein Accession Numbers: B0YIW2; P02656
Gene Names: APOC3
Peptide Sequence: DALSSVQESQVAQQAR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 231.71
Best Match Posterior Error Probability: 1.45E-63
Best Match Spectrum:

Scan number 29967 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** APOC3



Protein Group ID: 150
Protein Accession Numbers: P30536; B1AH87
Gene Names: TSPO
Peptide Sequence: APPWVPAMGFTLAPSLGCFVGSR
Total Number of Spectra: 16
Number of Replicates (out of 8): 8
Best Match Score: 125.23
Best Match Posterior Error Probability: 2.81E-11
Best Match Spectrum:

Scan number 87976 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TSPO



Protein Group ID: 154

Protein Accession Numbers: Q9UH03; Q9UH03-2; B1AHR1; B7Z686

Gene Names: Sep-03

Peptide Sequence: PLDLEFMK

Total Number of Spectra: 7

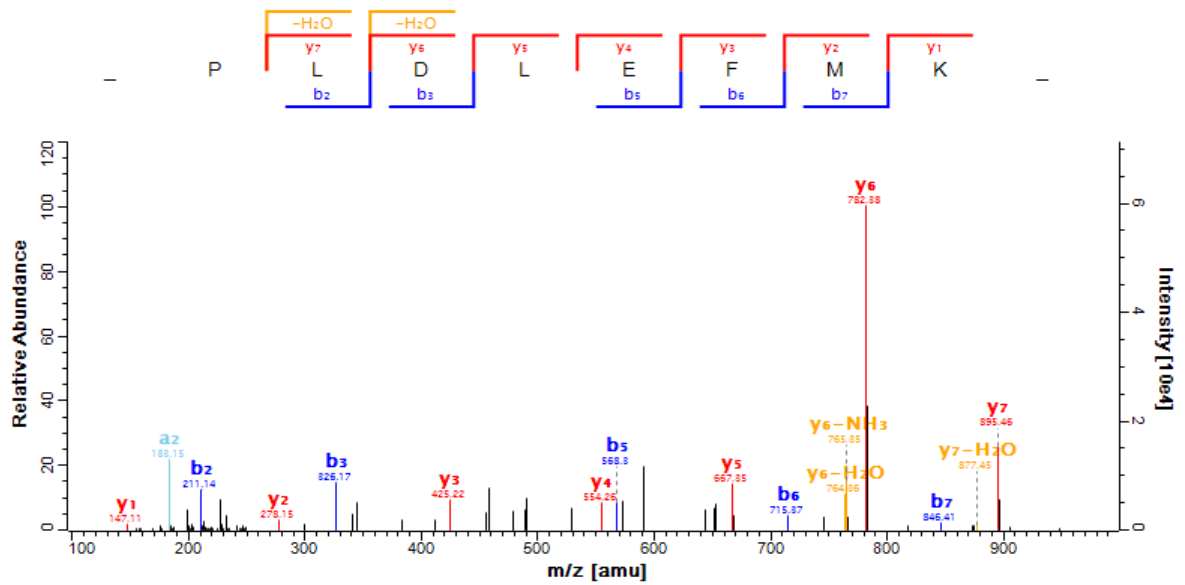
Number of Replicates (out of 8): 7

Best Match Score: 135.83

Best Match Posterior Error Probability: 0.00085718

Best Match Spectrum:

Scan number	51600	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	SEPT3



Protein Group ID: 158

Protein Accession Numbers: Q9HAF1-3; B1AK64; Q9HAF1; Q9HAF1-2; B1AK63

Gene Names: Clorf149;MEAF6

Peptide Sequence: SSVTSAAAVSALAGVQDLIEK

Total Number of Spectra: 1

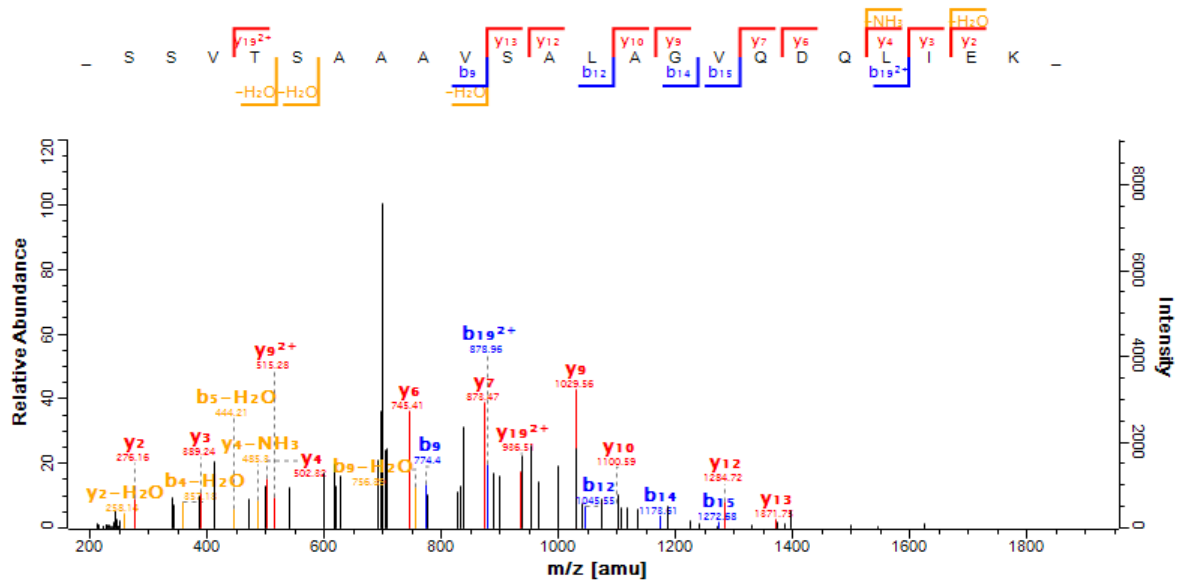
Number of Replicates (out of 8): 1

Best Match Score: 67.251

Best Match Posterior Error Probability: 0.0011892

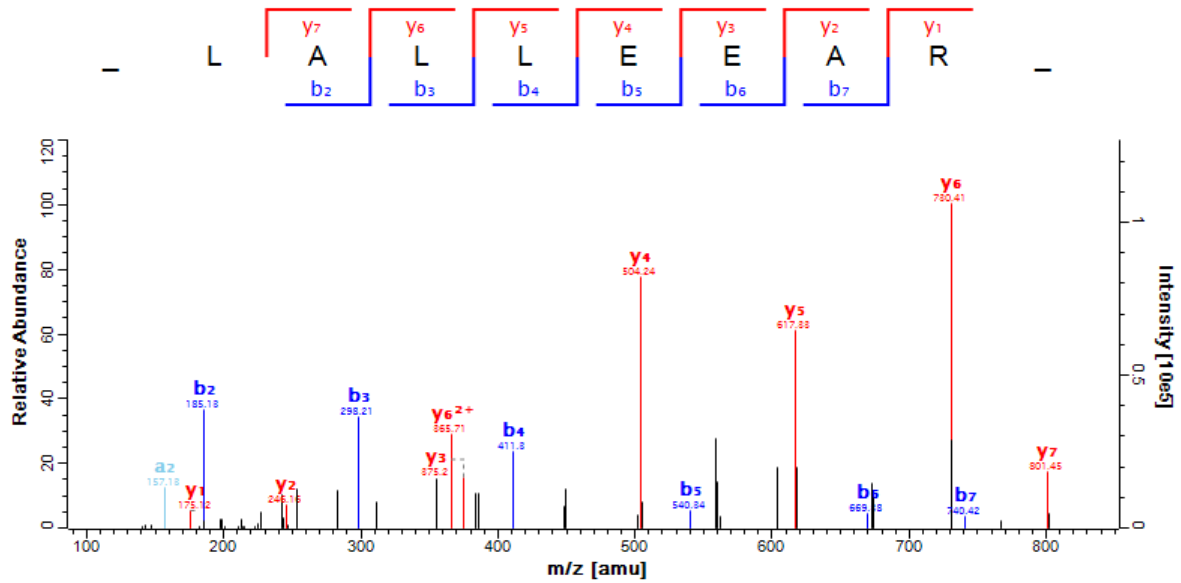
Best Match Spectrum:

Scan number 65970 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** Clorf149;MEAF6



Protein Group ID: 160
Protein Accession Numbers: Q5TZA2; B1AKD8; Q5TZA2-2
Gene Names: CROCC
Peptide Sequence: LALLEEAR
Total Number of Spectra: 8
Number of Replicates (out of 8): 8
Best Match Score: 112.84
Best Match Posterior Error Probability: 0.0026712
Best Match Spectrum:

Scan number 32663 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CROCC



Protein Group ID: 163

Protein Accession Numbers: Q12857; Q12857-2; B1AKN5; B1AKN7; B1AKN6

Gene Names: NFIA

Peptide Sequence: MYSPLCLTQDEFHPFIEALLPHVR

Total Number of Spectra: 1

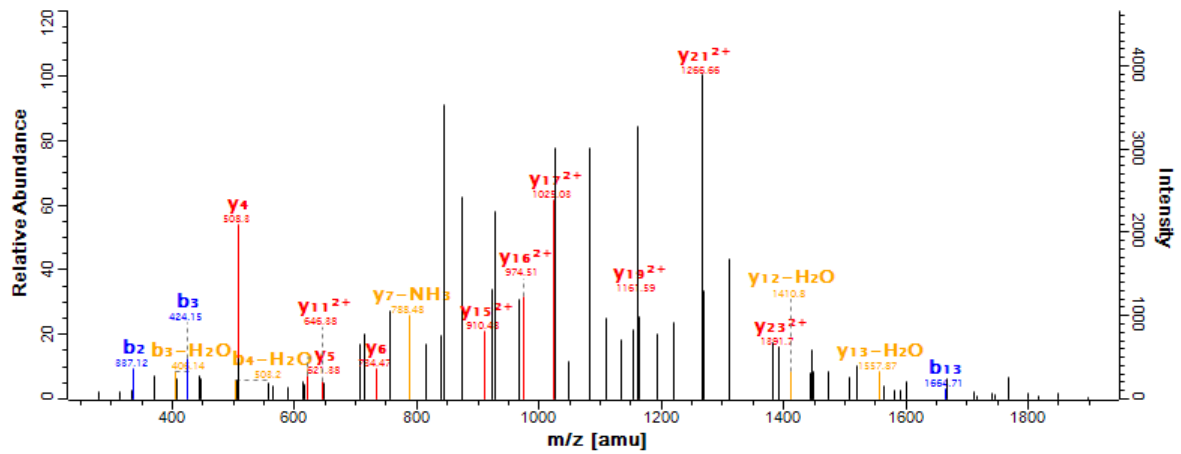
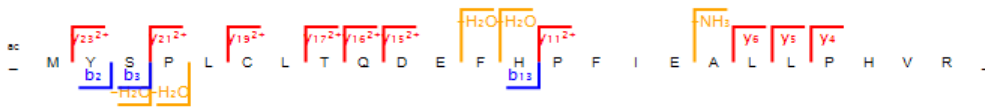
Number of Replicates (out of 8): 1

Best Match Score: 76.155

Best Match Posterior Error Probability: 0.00019868

Best Match Spectrum:

Scan number 93326 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** NFIA



Protein Group ID: 164

Protein Accession Numbers: Q92845; B1AKU4; Q92845-2

Gene Names: KIFAP3

Peptide Sequence: LNEVEQLLYLQNR

Total Number of Spectra: 1

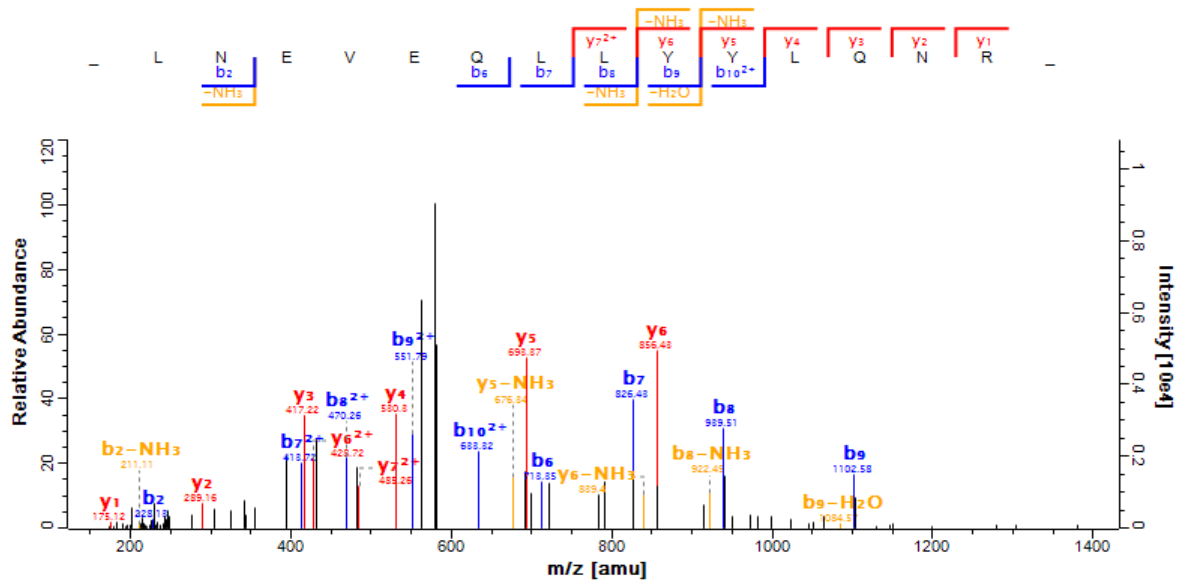
Number of Replicates (out of 8): 1

Best Match Score: 102.97

Best Match Posterior Error Probability: 0.00028661

Best Match Spectrum:

Scan number 90825 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** KIFAP3



Protein Group ID: 165

Protein Accession Numbers: Q9NVA1; Q9NVA1-2; Q9NVA1-4; Q9NVA1-5; B1AKV4; B7Z314; H7BYA2; Q9NVA1-3; B7Z7J8; B7Z1C6

Gene Names: UQCC

Peptide Sequence: PHSPTYNDEGL

Total Number of Spectra: 2

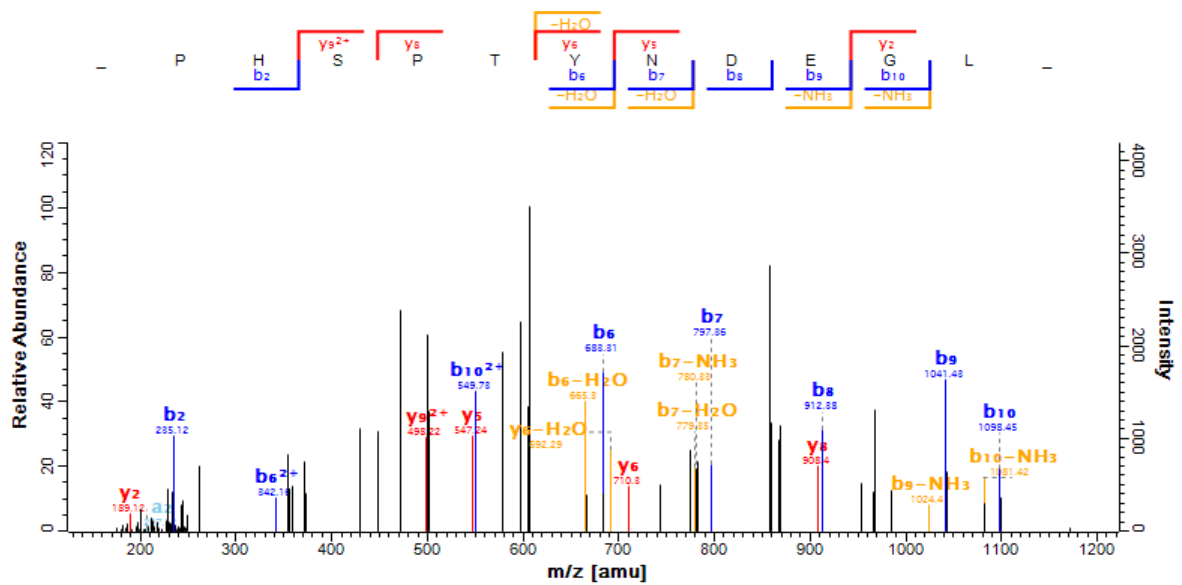
Number of Replicates (out of 8): 2

Best Match Score: 114.89

Best Match Posterior Error Probability: 0.00010499

Best Match Spectrum:

Scan number	20393	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	UQCC



Protein Group ID: 168

Protein Accession Numbers: Q9BPZ7; Q9BPZ7-2; Q9BPZ7-3; Q9BPZ7-6; Q9BPZ7-5; B1AMB2; B1AMB1

Gene Names: MAPKAP1

Peptide Sequence: AFLDNPTIILAHIR

Total Number of Spectra: 2

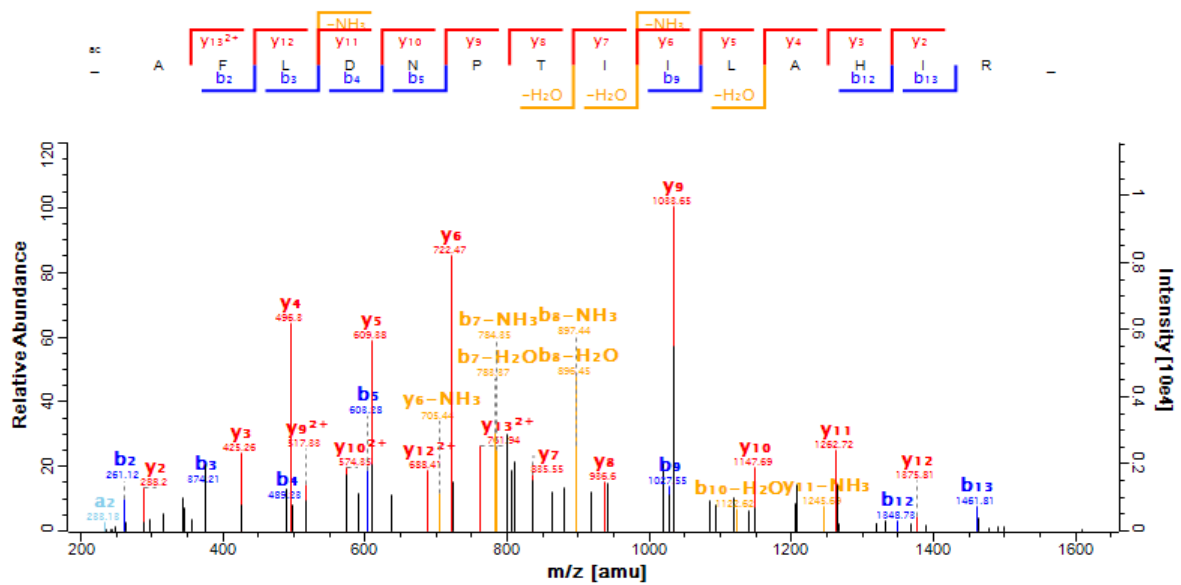
Number of Replicates (out of 8): 2

Best Match Score: 162.93

Best Match Posterior Error Probability: 1.69E-09

Best Match Spectrum:

Scan number	89248	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS: CID	Genenames	MAPKAP1



Protein Group ID: 171

Protein Accession Numbers: P19256; P19256-3; B1AMW1; P19256-2; H0YDI1

Gene Names: CD58

Peptide Sequence: VAELENSFR

Total Number of Spectra: 2

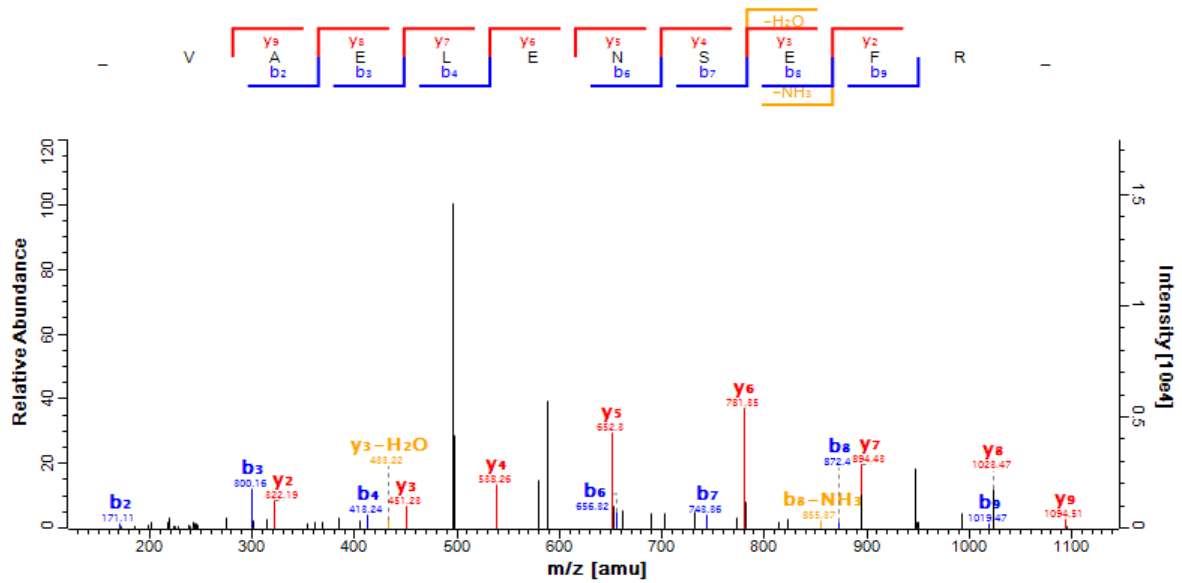
Number of Replicates (out of 8): 2

Best Match Score: 96.604

Best Match Posterior Error Probability: 0.0011276

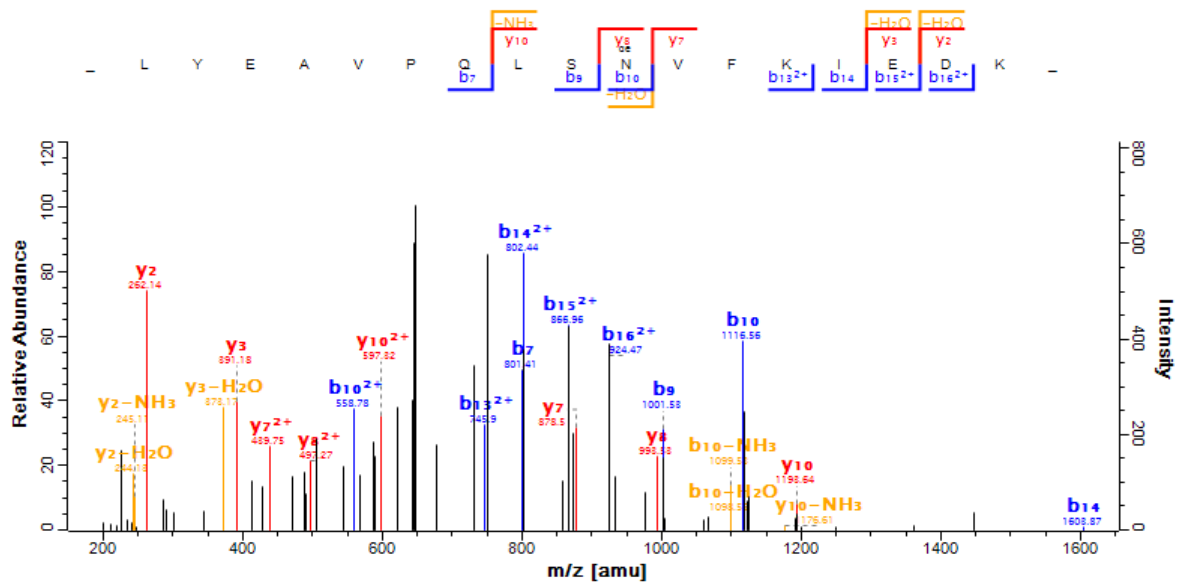
Best Match Spectrum:

Scan number 25529 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CD58



Protein Group ID: 172
Protein Accession Numbers: O00311; B1AMW7
Gene Names: CDC7
Peptide Sequence: LYEAVPQLS^{NS}VNFKIEDK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 113.4
Best Match Posterior Error Probability: 0.0010543
Best Match Spectrum:

Scan number 1688 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CDC7



Protein Group ID: 179

Protein Accession Numbers: Q8TAG9; E7EW84; B1AP46

Gene Names: EXOC6

Peptide Sequence: AENSESLGTVPEHER

Total Number of Spectra: 8

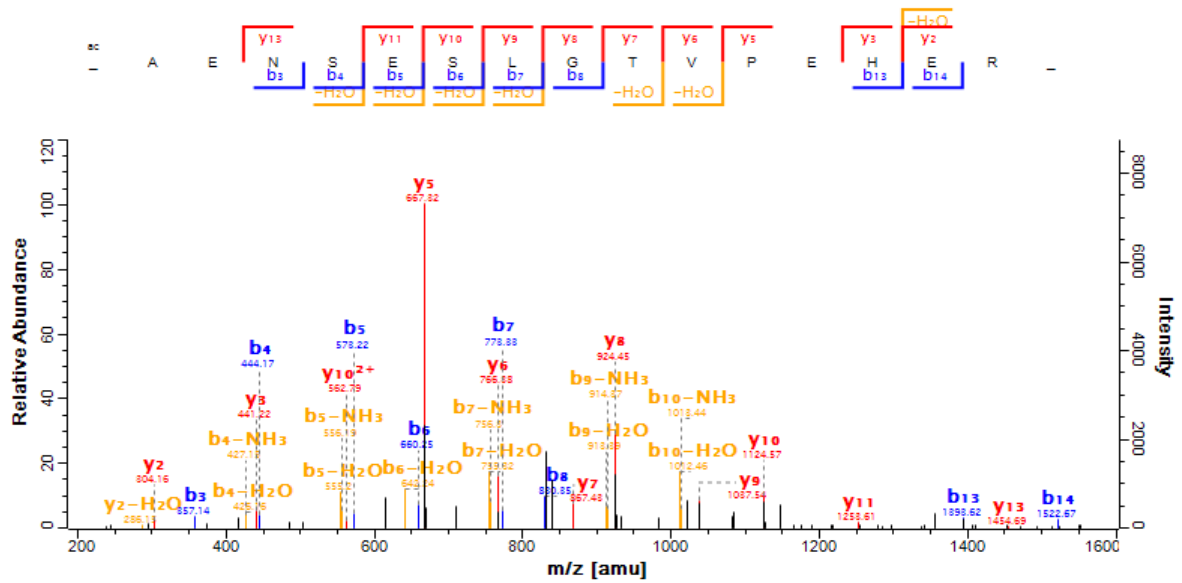
Number of Replicates (out of 8): 5

Best Match Score: 140.22

Best Match Posterior Error Probability: 1.92E-05

Best Match Spectrum:

Scan number	22733	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	EXOC6



Protein Group ID: 181

Protein Accession Numbers: Q9BYP7; Q9BYP7-2; Q9BYP7-4; Q9BYP7-3; B1AQN8

Gene Names: WNK3

Peptide Sequence: VDKLPSNVLR

Total Number of Spectra: 2

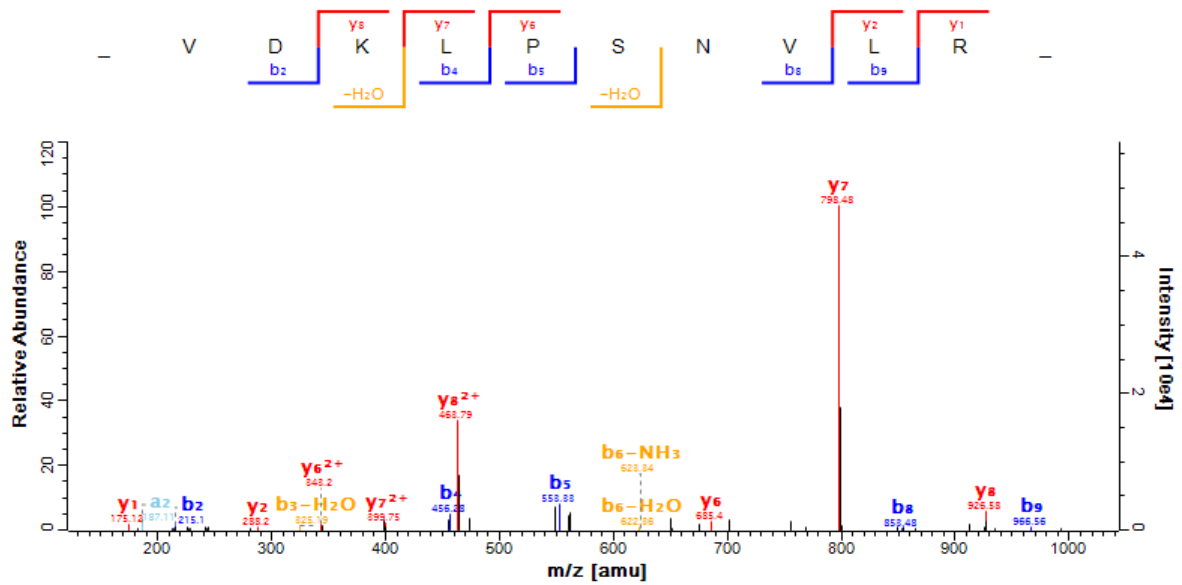
Number of Replicates (out of 8): 2

Best Match Score: 104.79

Best Match Posterior Error Probability: 0.002608

Best Match Spectrum:

Scan number	21578	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	WNK3



Protein Group ID: 185

Protein Accession Numbers: Q5HYJ3; F5GX09; B2R9C2; Q5HYJ3-2

Gene Names: FAM76B

Peptide Sequence: SSATIQNETPK

Total Number of Spectra: 3

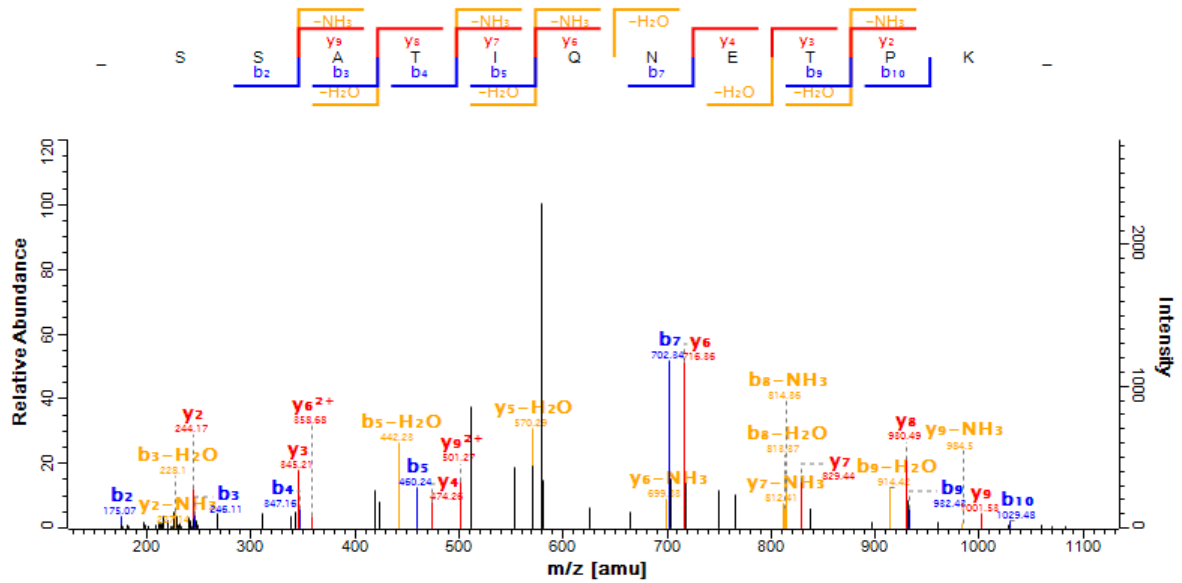
Number of Replicates (out of 8): 2

Best Match Score: 146.16

Best Match Posterior Error Probability: 1.14E-05

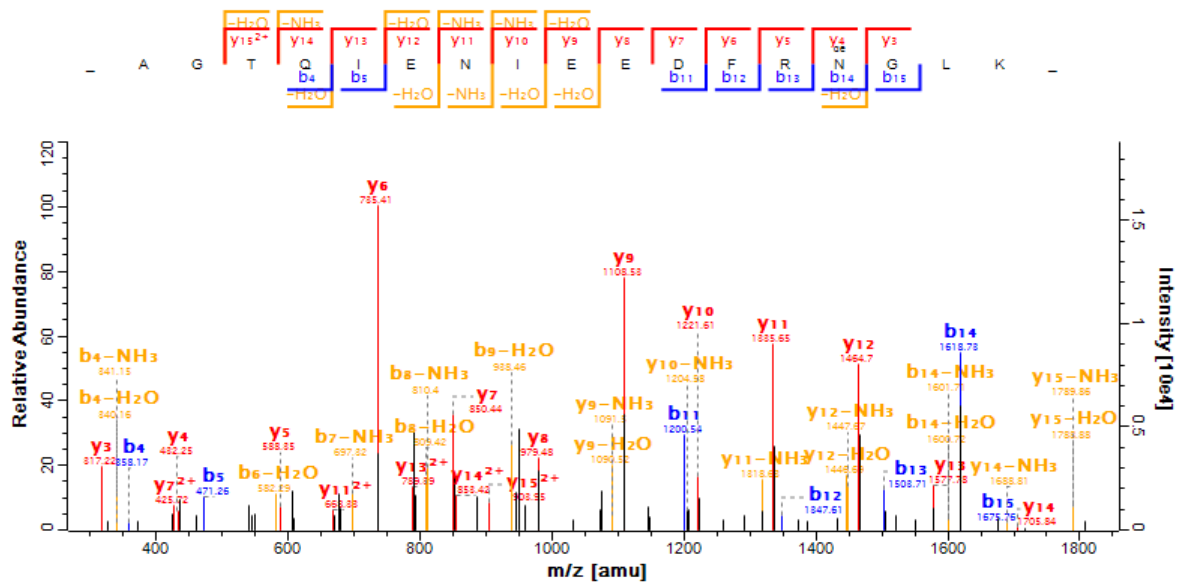
Best Match Spectrum:

Scan number 7116 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** FAM76B



Protein Group ID: 186
Protein Accession Numbers: B2RCS5; P35609
Gene Names: ACTN2
Peptide Sequence: AGTQIENIEEDFRNGLK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 211.9
Best Match Posterior Error Probability: 1.67E-38
Best Match Spectrum:

Scan number 61537 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ACTN2



Protein Group ID: 191

Protein Accession Numbers: I3NI25; Q96NB1; I3L269; B3KPU9

Gene Names: FOPNL

Peptide Sequence: STNIEDLHVSQAVNR

Total Number of Spectra: 2

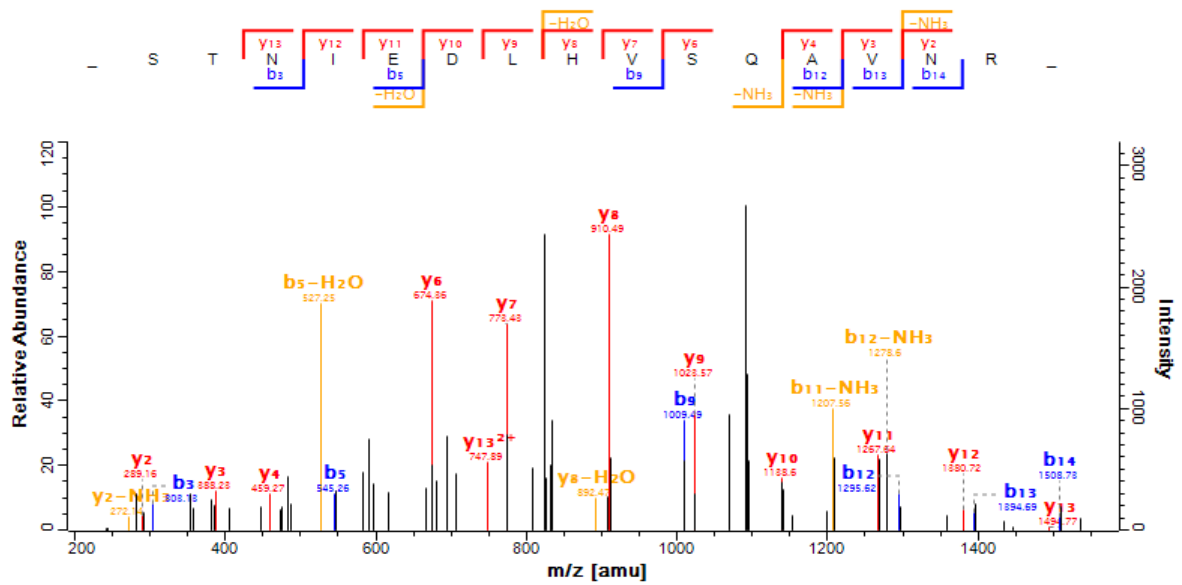
Number of Replicates (out of 8): 2

Best Match Score: 94.569

Best Match Posterior Error Probability: 0.00050687

Best Match Spectrum:

Scan number	29262	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	FOPNL



Protein Group ID: 197

Protein Accession Numbers: Q9UPY3; Q9UPY3-2; B3KRG4

Gene Names: DICER1

Peptide Sequence: AVSPELFHVIDDFVQFQYLK

Total Number of Spectra: 1

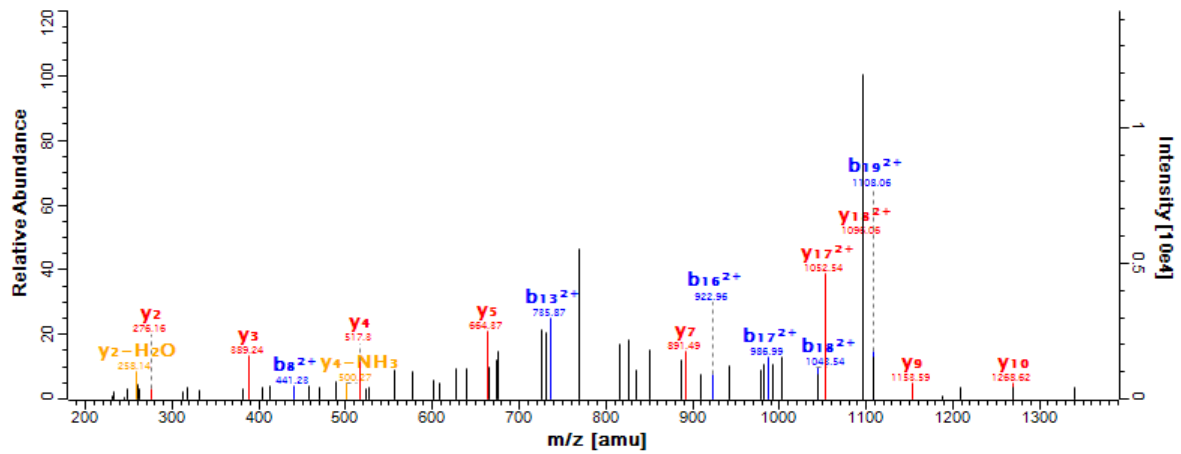
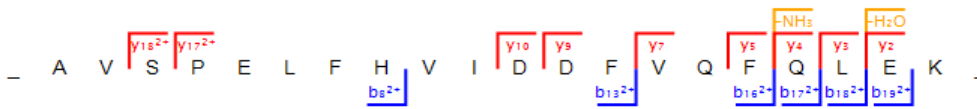
Number of Replicates (out of 8): 1

Best Match Score: 69.188

Best Match Posterior Error Probability: 0.002106

Best Match Spectrum:

Scan number	93411	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	DICER1



Protein Group ID: 199

Protein Accession Numbers: P07992; P07992-2; B3KRR0

Gene Names: ERCC1

Peptide Sequence: LFDVLHEPFLK

Total Number of Spectra: 6

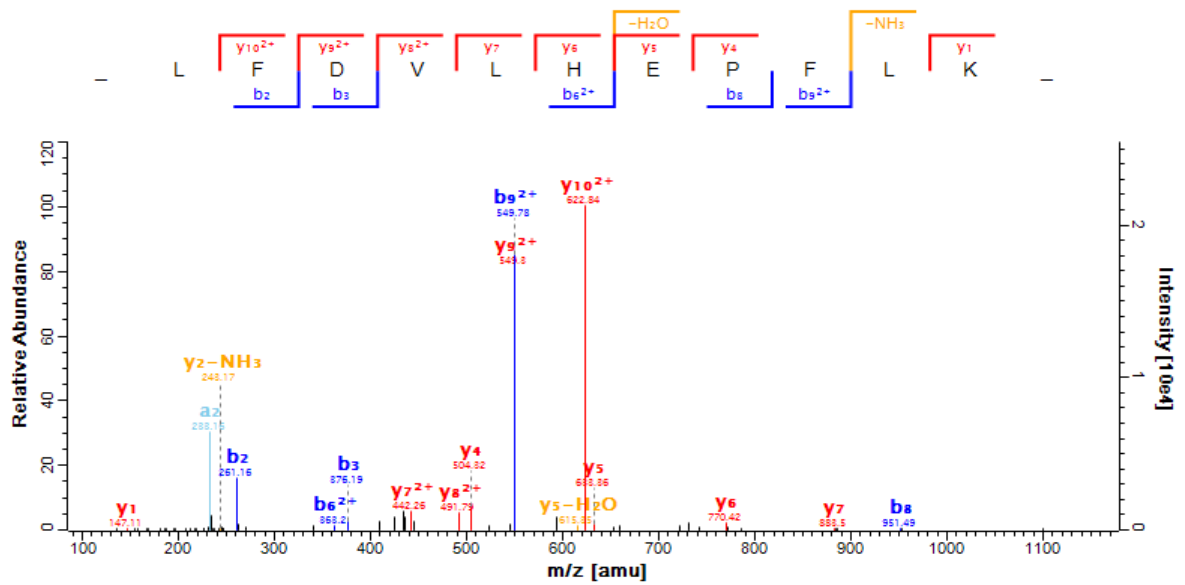
Number of Replicates (out of 8): 6

Best Match Score: 112.75

Best Match Posterior Error Probability: 0.00012314

Best Match Spectrum:

Scan number 64379 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ERCC1



Protein Group ID: 203

Protein Accession Numbers: Q9NQ48; B3KSI9; F5GWL8; H7C488

Gene Names: LZTFL1

Peptide Sequence: ALQDLQLDQGNQK

Total Number of Spectra: 2

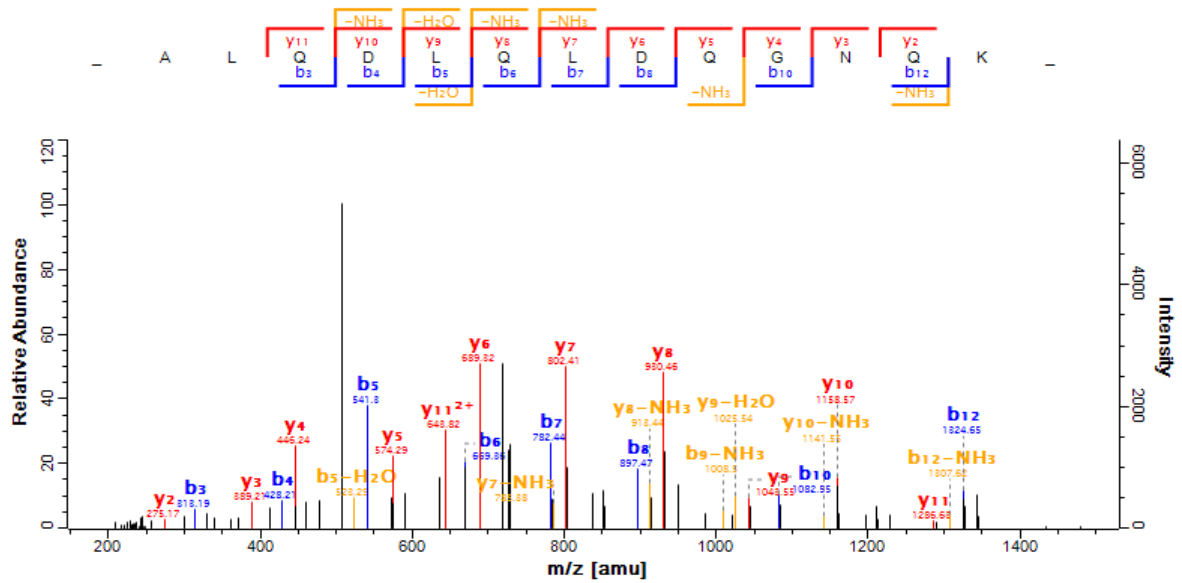
Number of Replicates (out of 8): 1

Best Match Score: 155.43

Best Match Posterior Error Probability: 2.83E-07

Best Match Spectrum:

Scan number 28871 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** LZTFL1



Protein Group ID: 213

Protein Accession Numbers: B3KY94; O14735; H3BTV1

Gene Names: CDIPT

Peptide Sequence: NMAALDAADR

Total Number of Spectra: 4

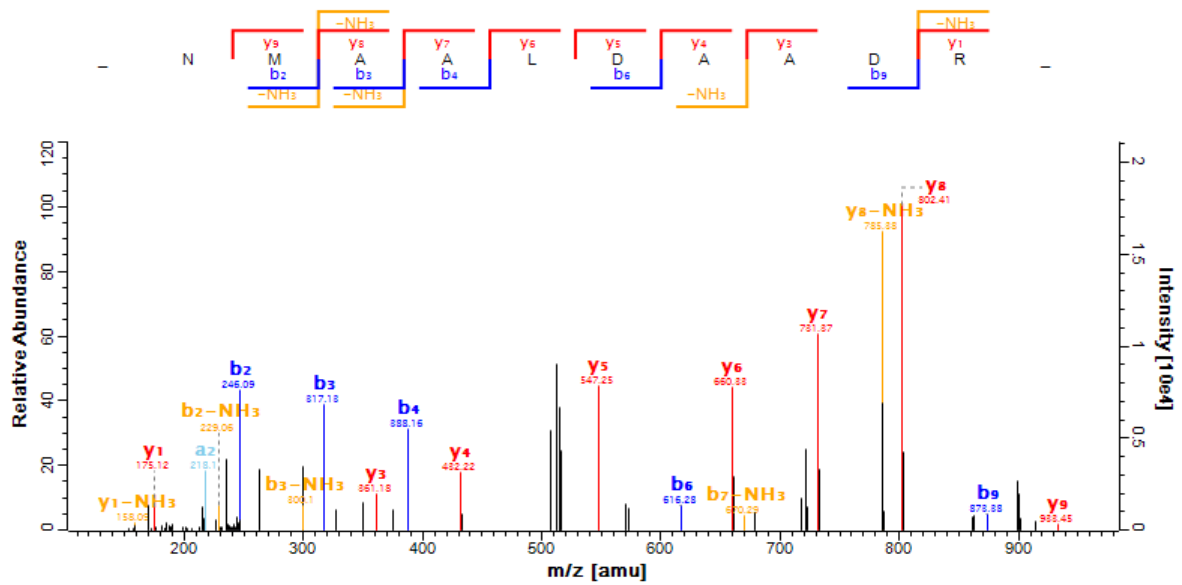
Number of Replicates (out of 8): 4

Best Match Score: 111.86

Best Match Posterior Error Probability: 0.00029194

Best Match Spectrum:

Scan number	18414	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	CDIPT



Protein Group ID: 214

Protein Accession Numbers: B3KYA7; Q13188; E5RFQ9

Gene Names: STK3

Peptide Sequence: DLITEAMEIK

Total Number of Spectra: 4

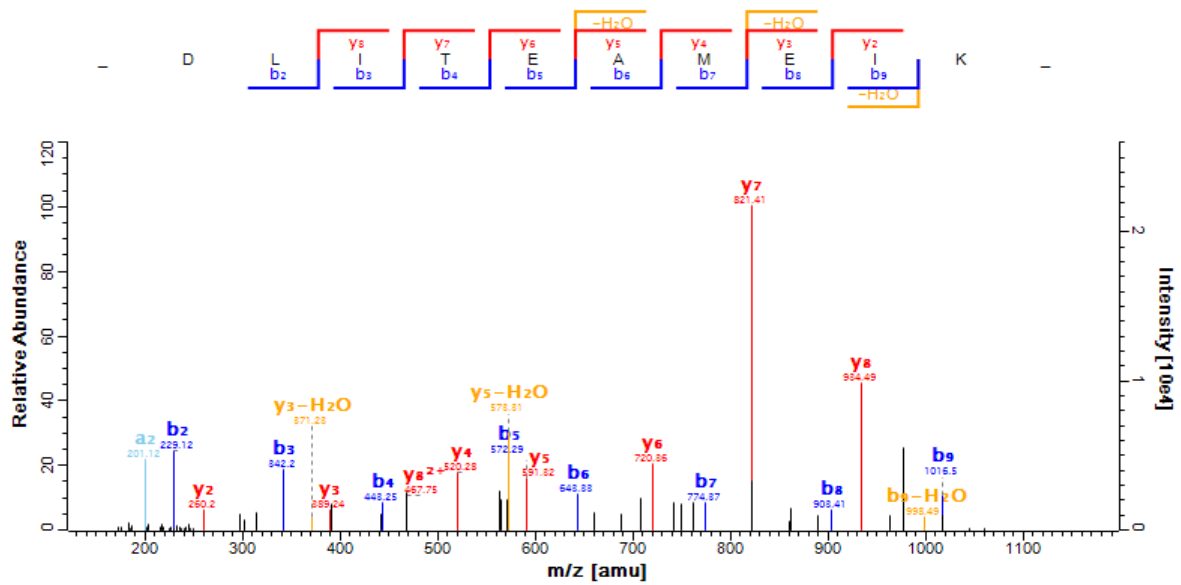
Number of Replicates (out of 8): 4

Best Match Score: 141.88

Best Match Posterior Error Probability: 1.42E-05

Best Match Spectrum:

Scan number 64050 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** STK3



Protein Group ID: 217

Protein Accession Numbers: B4E171; B4DEA5; B4DDG0; P41732; B4DEB8

Gene Names: TSPAN7

Peptide Sequence: TYTDAMQTYNGNDER

Total Number of Spectra: 5

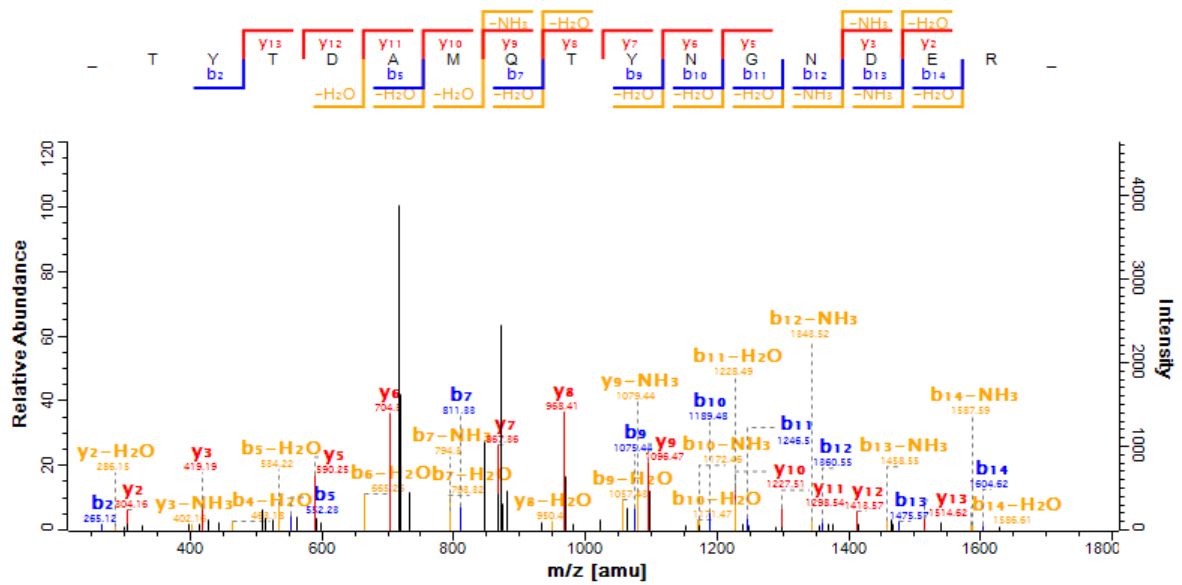
Number of Replicates (out of 8): 5

Best Match Score: 217.48

Best Match Posterior Error Probability: 2.42E-48

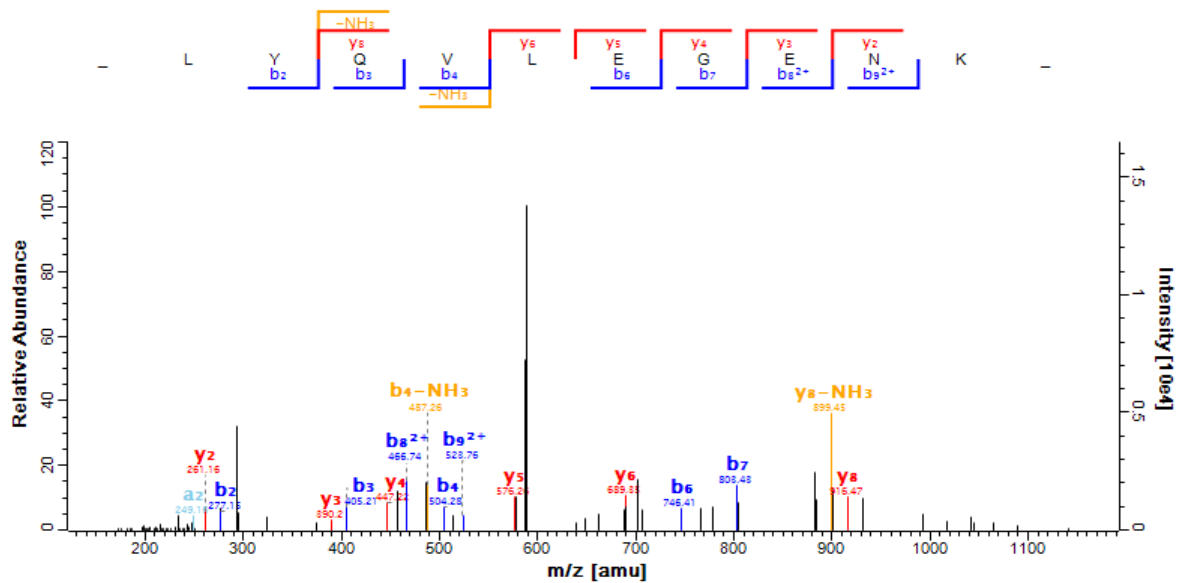
Best Match Spectrum:

Scan number 22379 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TSPAN7



Protein Group ID: 224
Protein Accession Numbers: Q68CZ6; B4DF64
Gene Names: HAUS3
Peptide Sequence: LYQVLEGENK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 89.171
Best Match Posterior Error Probability: 0.0020853
Best Match Spectrum:

Scan number 27062 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** HAUS3



Protein Group ID: 226

Protein Accession Numbers: E9PAV7; J3KQN8; Q13772; B4DF87; B4DZ85

Gene Names: NCOA4

Peptide Sequence: MGNLSQLSSGEDK

Total Number of Spectra: 1

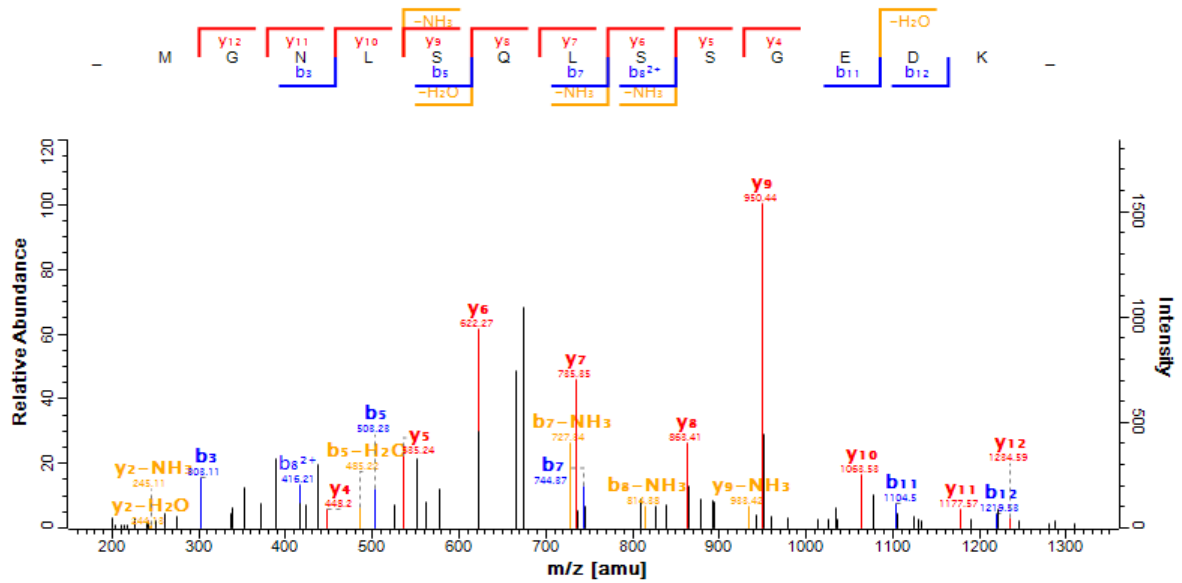
Number of Replicates (out of 8): 1

Best Match Score: 80.706

Best Match Posterior Error Probability: 0.0031517

Best Match Spectrum:

Scan number 23868 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** NCOA4



Protein Group ID: 231

Protein Accession Numbers: Q6PD74; B4DG44; H0YL49

Gene Names: AAGAB

Peptide Sequence: HGFELVELSELP EELP EEDD DDFPESTGVK

Total Number of Spectra: 12

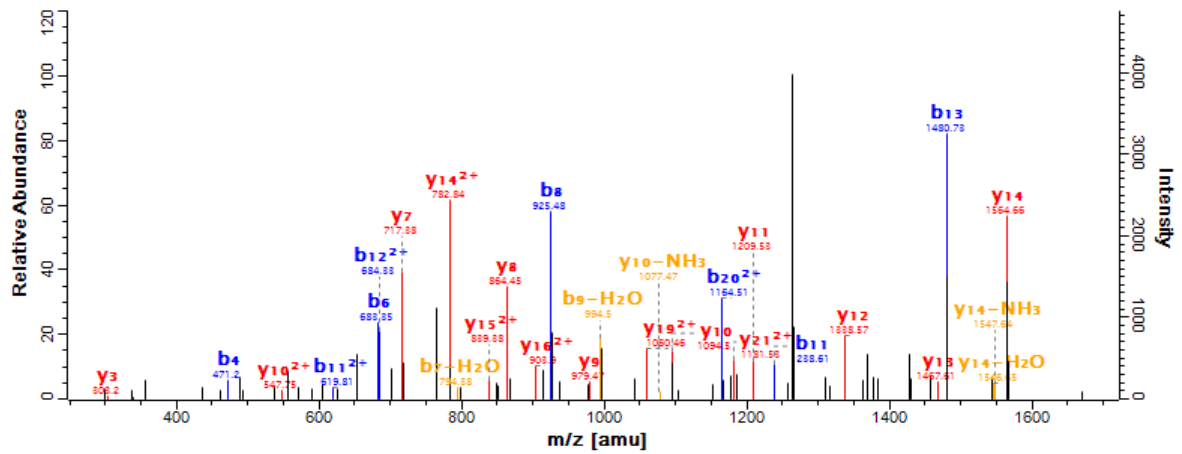
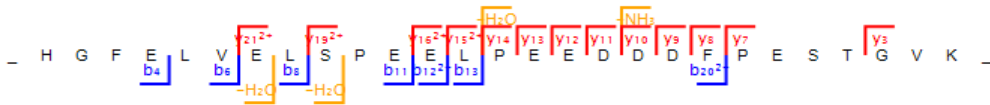
Number of Replicates (out of 8): 7

Best Match Score: 83.31

Best Match Posterior Error Probability: 4.62E-05

Best Match Spectrum:

Scan number	69303	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	AAGAB



Protein Group ID: 236

Protein Accession Numbers: P48426; B4DGX2; Q5JUT3

Gene Names: PIP4K2A;PIP5K2A

Peptide Sequence: FGIDDQDFQNSLTR

Total Number of Spectra: 8

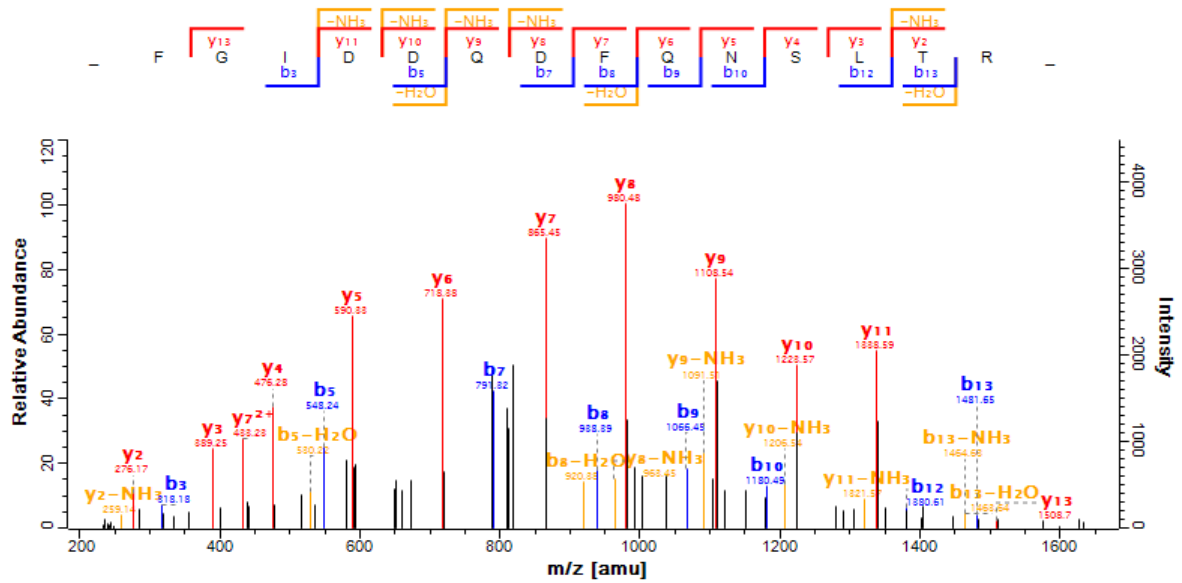
Number of Replicates (out of 8): 8

Best Match Score: 177.88

Best Match Posterior Error Probability: 8.74E-15

Best Match Spectrum:

Scan number 51377 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PIP4K2A;PIP5K2A



Protein Group ID: 238

Protein Accession Numbers: B4DSS8; Q9UKA9-3; Q9UKA9-4; Q9UKA9-2; Q9UKA9; Q9UKA9-6; Q9UKA9-5; B4DI28

Gene Names: PTBP2

Peptide Sequence: NQAFLELATEEEA A A I T M V N Y Y S A V T P H L R

Total Number of Spectra: 1

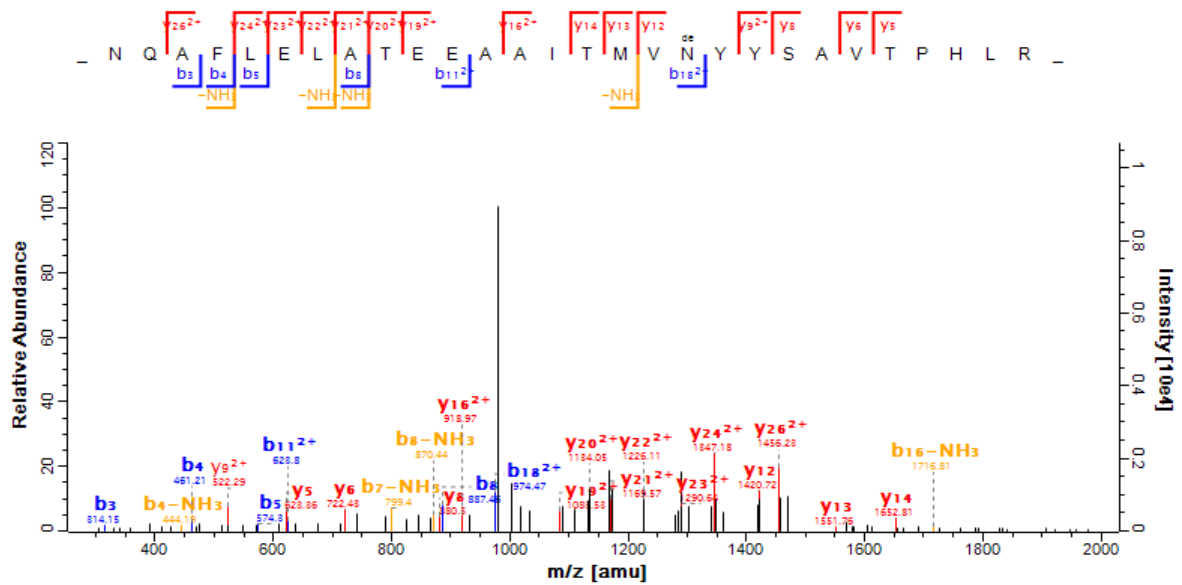
Number of Replicates (out of 8): 1

Best Match Score: 81.477

Best Match Posterior Error Probability: 0.0001648

Best Match Spectrum:

Scan number	91535	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	PTBP2



Protein Group ID: 241

Protein Accession Numbers: Q9NYJ8; B4DIR9; Q9NYJ8-2

Gene Names: TAB2

Peptide Sequence: TSSTSSSVNSQTLNR

Total Number of Spectra: 5

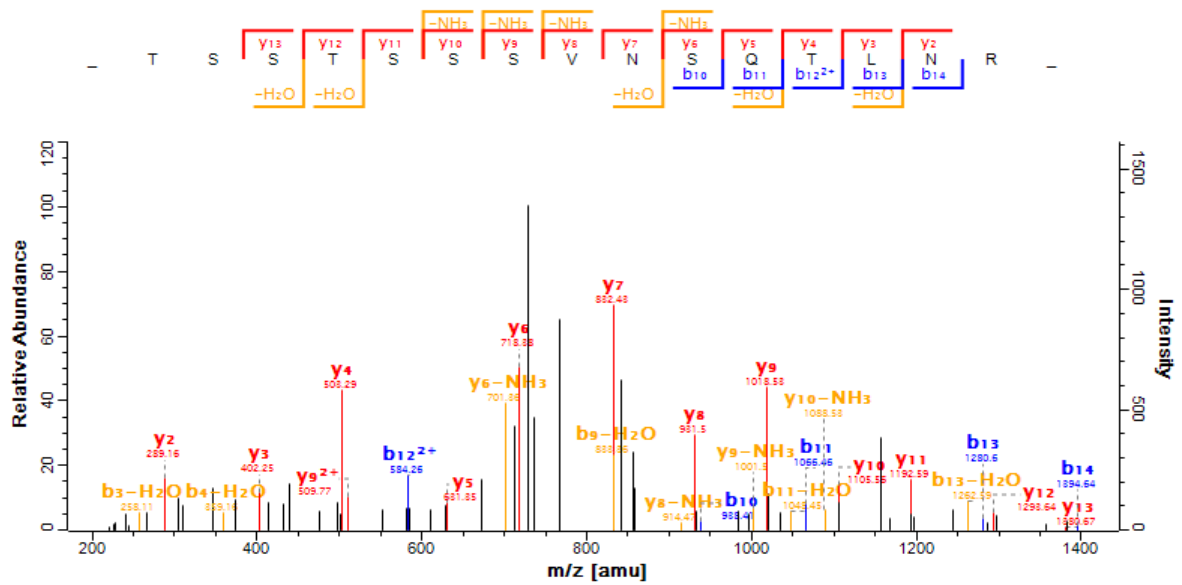
Number of Replicates (out of 8): 5

Best Match Score: 118.19

Best Match Posterior Error Probability: 6.76E-05

Best Match Spectrum:

Scan number	8455	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	TAB2



Protein Group ID: 242

Protein Accession Numbers: B4DIY7; C9J2U4; Q96BW9

Gene Names: TAMM41

Peptide Sequence: SPEGQFTQLMTPK

Total Number of Spectra: 2

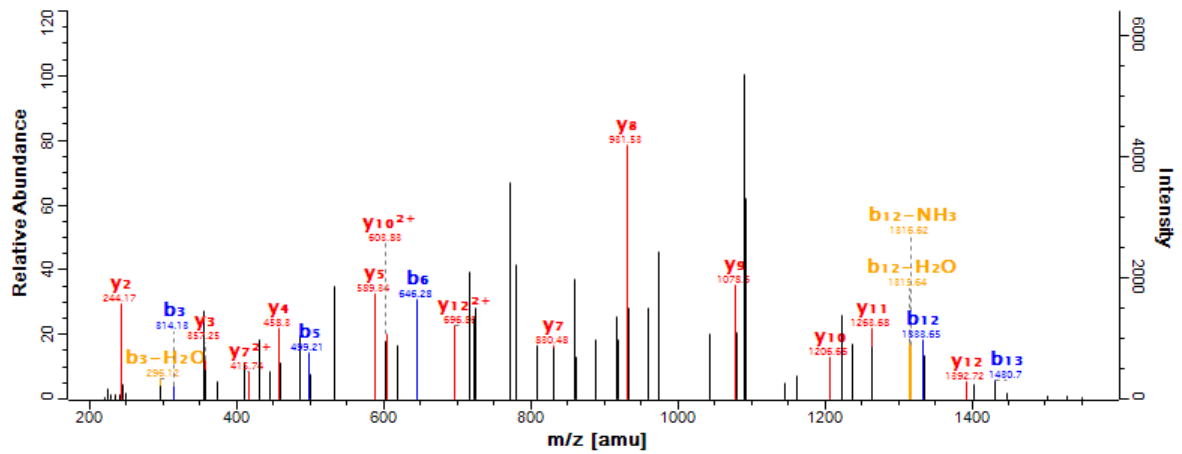
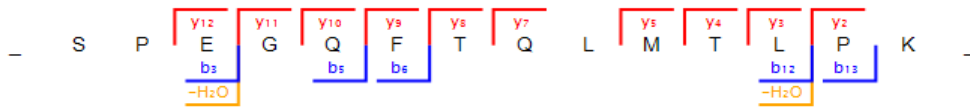
Number of Replicates (out of 8): 2

Best Match Score: 107.35

Best Match Posterior Error Probability: 0.00021525

Best Match Spectrum:

Scan number	61825	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	TAMM41



Protein Group ID: 244

Protein Accession Numbers: O75376; E7EVK1; B4DJ25

Gene Names: NCOR1

Peptide Sequence: SAAVSEQQLEQK

Total Number of Spectra: 4

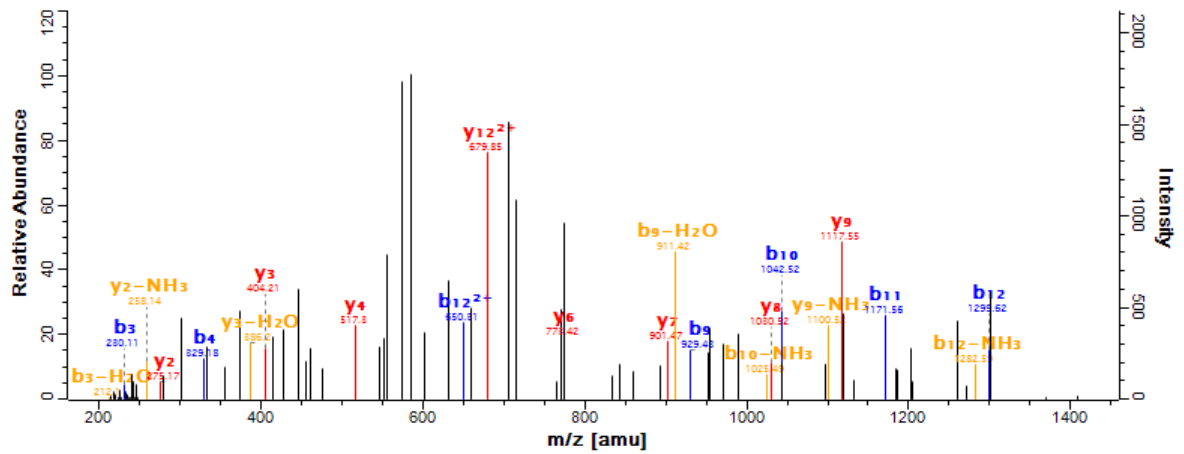
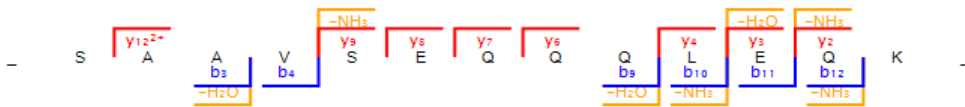
Number of Replicates (out of 8): 4

Best Match Score: 105.95

Best Match Posterior Error Probability: 0.00039873

Best Match Spectrum:

Scan number	10957	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	NCOR1



Protein Group ID: 245

Protein Accession Numbers: O15374; G3V175; B4DJ67; E7EPY8

Gene Names: SLC16A4

Peptide Sequence: GSSLSAHGPEAHATEETHCHETEEESTIK

Total Number of Spectra: 3

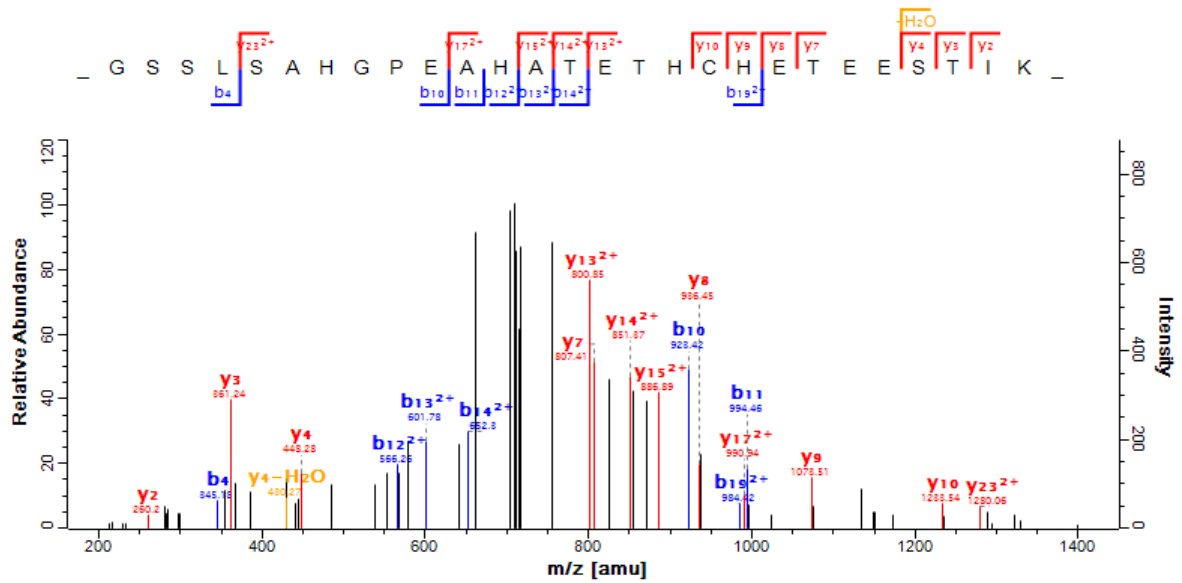
Number of Replicates (out of 8): 3

Best Match Score: 64.488

Best Match Posterior Error Probability: 0.00029726

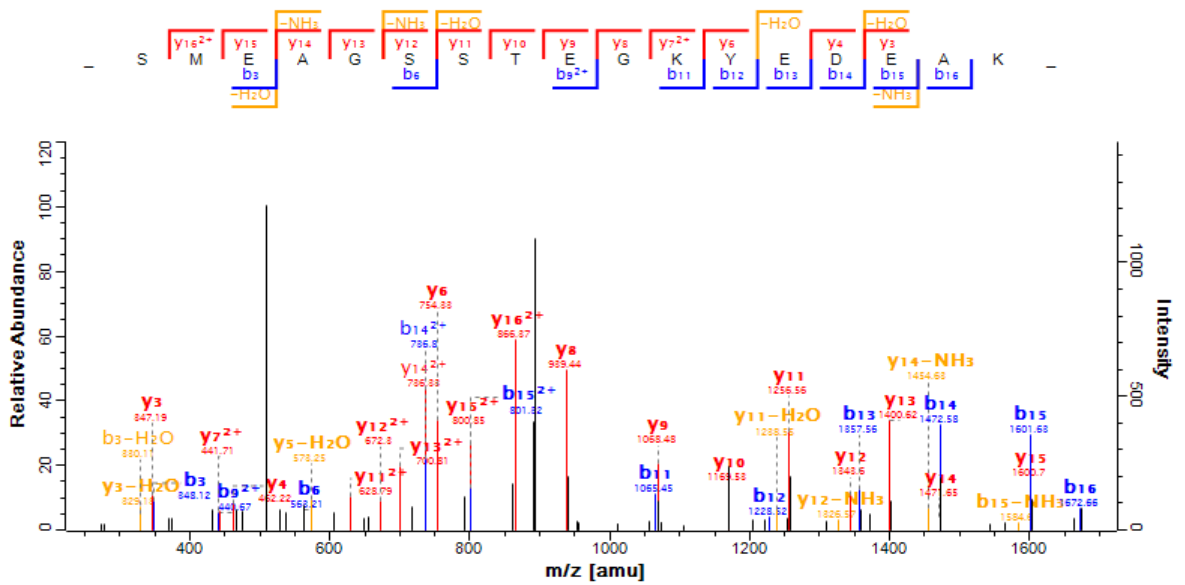
Best Match Spectrum:

Scan number	11934	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	SLC16A4



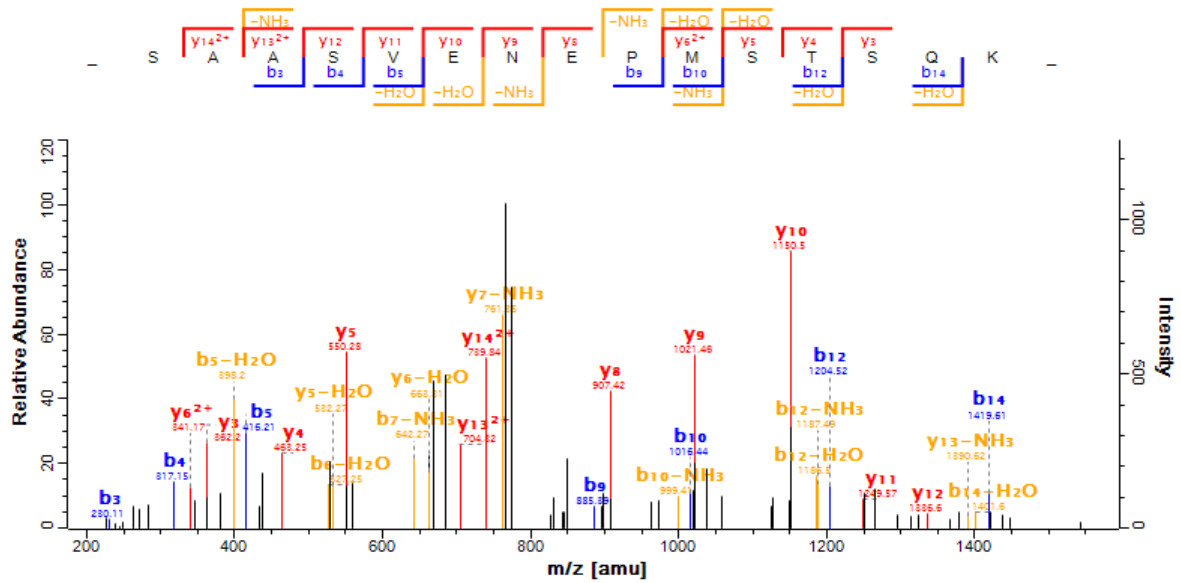
Protein Group ID: 251
Protein Accession Numbers: Q9UGH3; B4DJZ1
Gene Names: SLC23A2
Peptide Sequence: SMEAGSSTEGKYEDEAK
Total Number of Spectra: 10
Number of Replicates (out of 8): 7
Best Match Score: 213.49
Best Match Posterior Error Probability: 1.52E-39
Best Match Spectrum:

Scan number 11013 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** SLC23A2



Protein Group ID: 261
Protein Accession Numbers: B4DLE8
Gene Names: CRYBG3
Peptide Sequence: SAASVENEPMSTSQK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 115.1
Best Match Posterior Error Probability: 0.00085612
Best Match Spectrum:

Scan number 11964 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CRYBG3



Protein Group ID: 263

Protein Accession Numbers: Q96RN5; Q96RN5-2; G3V1P5; Q96RN5-3; F5GZU5; H7C308; B4DM43

Gene Names: MED15

Peptide Sequence: LHHQNQQQIQQQQQQLQR

Total Number of Spectra: 4

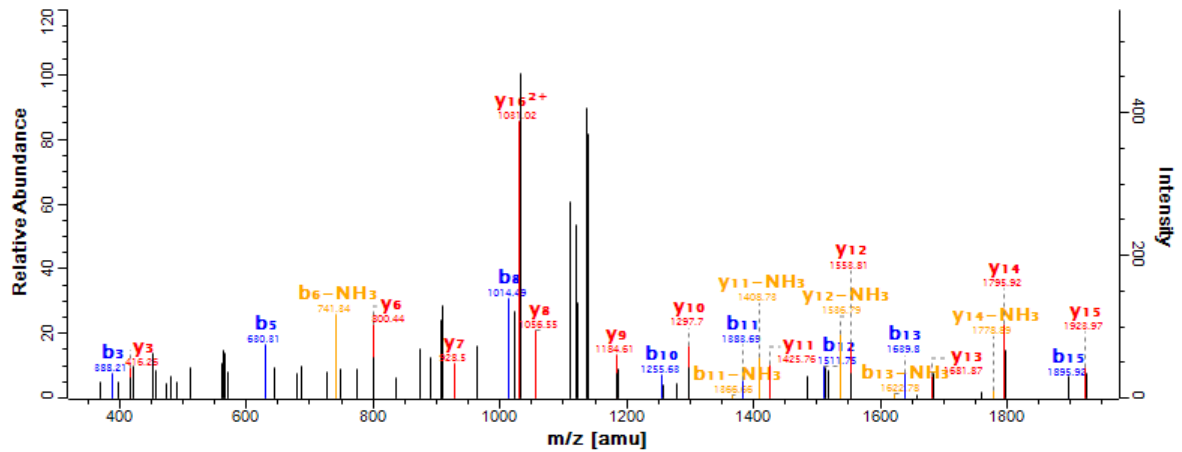
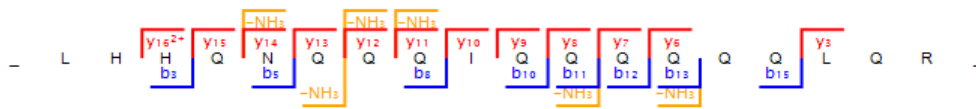
Number of Replicates (out of 8): 3

Best Match Score: 138.19

Best Match Posterior Error Probability: 2.05E-05

Best Match Spectrum:

Scan number	9115	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS: CID	Genenames	MED15



Protein Group ID: 265

Protein Accession Numbers: E9PN70; Q9Y296; J3KP27; E9PQE8; B4DME1; E9PKS9; G5EA23; G3V1A0

Gene Names: TRAPPC4

Peptide Sequence: AGGLIYQLDSYAPR

Total Number of Spectra: 3

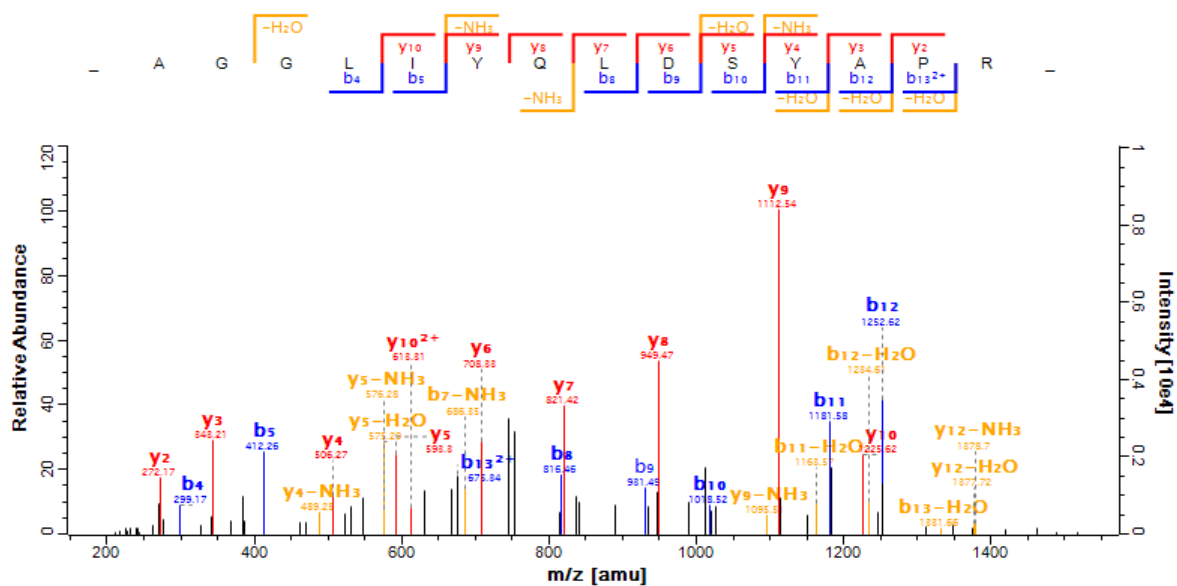
Number of Replicates (out of 8): 3

Best Match Score: 153.39

Best Match Posterior Error Probability: 3.70E-11

Best Match Spectrum:

Scan number	60216	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	TRAPPC4



Protein Group ID: 269

Protein Accession Numbers: Q06136; B4DMX0; K7EQS7

Gene Names: KDSR

Peptide Sequence: E I E M H S I N D K

Total Number of Spectra: 2

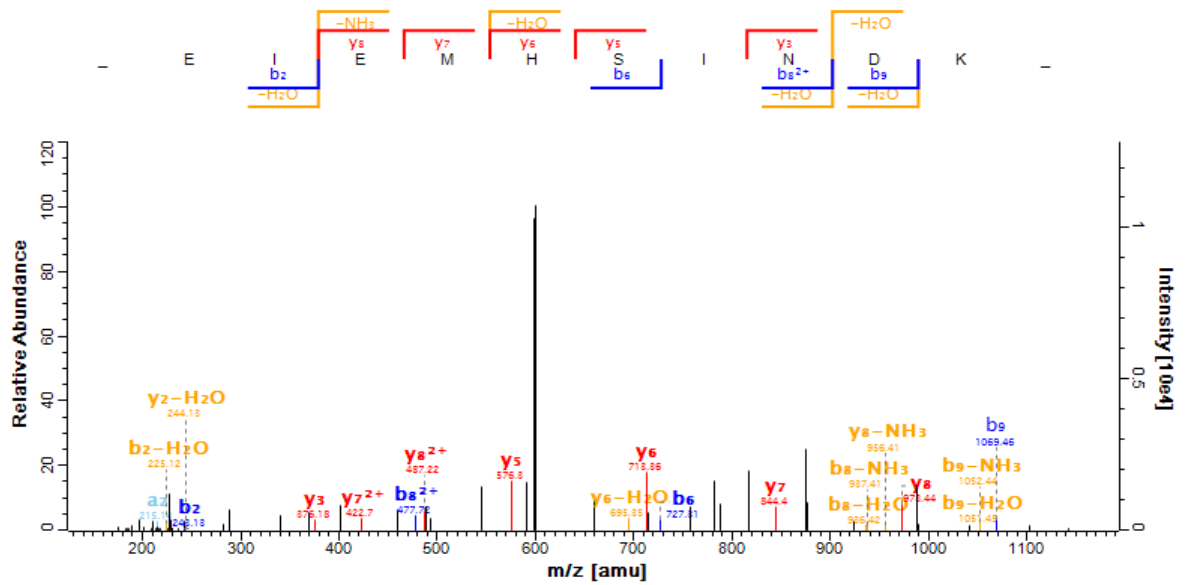
Number of Replicates (out of 8): 2

Best Match Score: 83.499

Best Match Posterior Error Probability: 0.0037103

Best Match Spectrum:

Scan number 14151 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** KDSR



Protein Group ID: 277

Protein Accession Numbers: Q9NVM9; B4DNK1; H0YH12

Gene Names: Asun;ASUN

Peptide Sequence: GPVSLLSLWSNR

Total Number of Spectra: 2

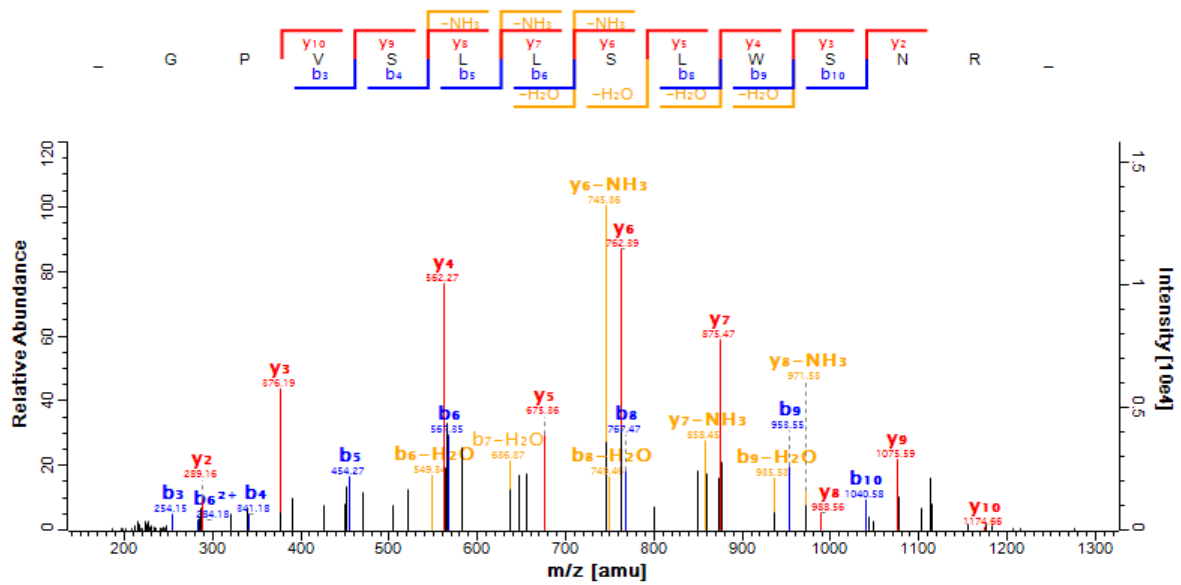
Number of Replicates (out of 8): 2

Best Match Score: 142.97

Best Match Posterior Error Probability: 2.47E-05

Best Match Spectrum:

Scan number	74073	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	Asun;ASUN



Protein Group ID: 278

Protein Accession Numbers: J9JID1; Q96GD4; Q96GD4-2; B4DNM4; J3QLN8; J3KTD6; J3QR41; Q96GD4-3; J3KRF8; J3KRJ2

Gene Names: AURKB

Peptide Sequence: VMENSSGTPDILTR

Total Number of Spectra: 2

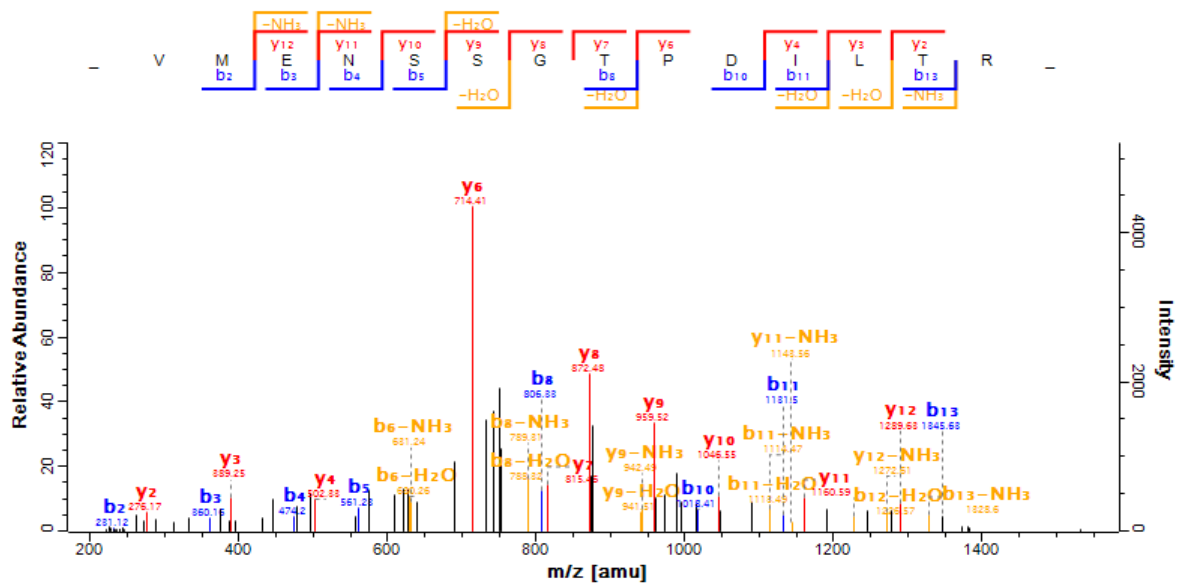
Number of Replicates (out of 8): 2

Best Match Score: 139.66

Best Match Posterior Error Probability: 2.22E-05

Best Match Spectrum:

Scan number	32040	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	AURKB



Protein Group ID: 294

Protein Accession Numbers: Q8IW45-2; Q8IW45; Q8IW45-4; B4DQR1; Q8IW45-3

Gene Names: CAR KD

Peptide Sequence: LSQALGNVTVVQK

Total Number of Spectra: 3

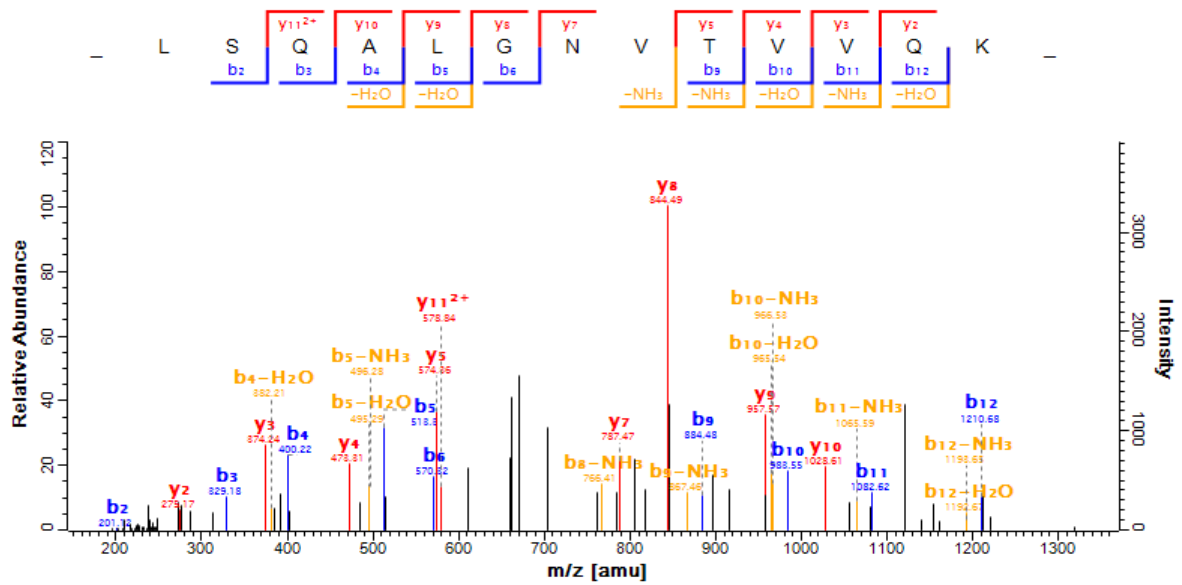
Number of Replicates (out of 8): 3

Best Match Score: 142.1

Best Match Posterior Error Probability: 1.37E-05

Best Match Spectrum:

Scan number	30514	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	CAR KD



Protein Group ID: 295

Protein Accession Numbers: B4DR52; Q5QNW6-2; O60814; P57053; P58876; P62807; Q5QNW6; Q93079; Q99877; Q99879; Q99880

Gene Names:

HIST2H2BF; HIST1H2BK; H2BFS; HIST1H2BD; HIST1H2BC; HIST1H2BH; HIST1H2BN; HIST1H2BM; HIST1H2BL

Peptide Sequence: KESYSVYVYK

Total Number of Spectra: 6

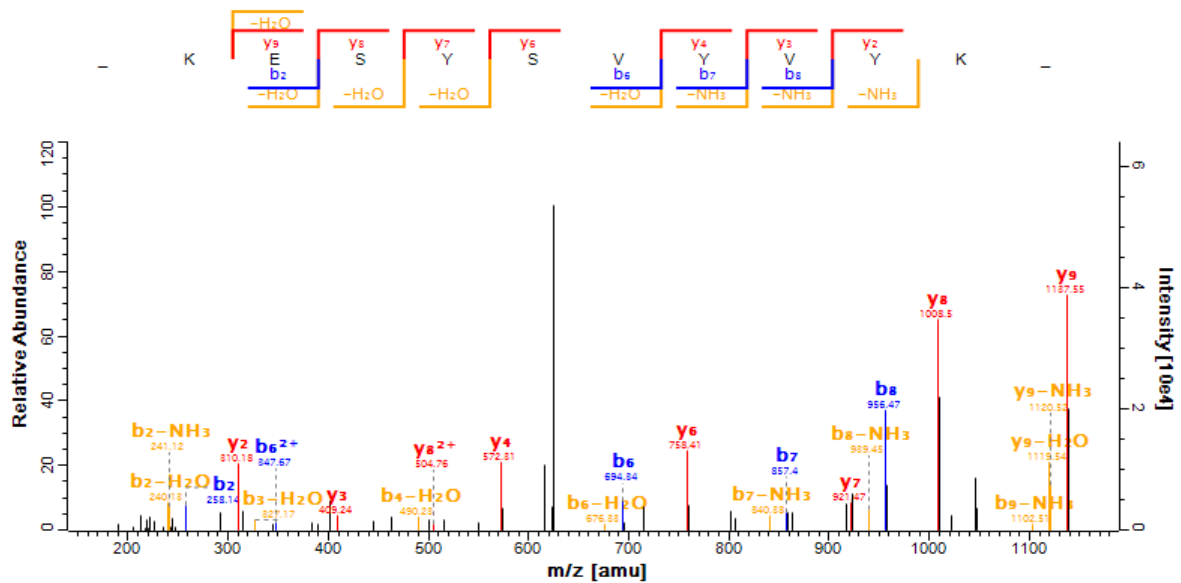
Number of Replicates (out of 8): 6

Best Match Score: 132.25

Best Match Posterior Error Probability: 3.75E-05

Best Match Spectrum:

Scan number 23082 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS: CID **Genenames** HIST2H2BF; HIST1H2BK; H2BFS; HIST1H2BD; HIST1H2BC; HIST1H2BH; HIST1H2BN; HIST1H2BM; HIST1H2BL



Protein Group ID: 301

Protein Accession Numbers: Q5W0Z9; Q5W0Z9-3; Q2TB82; B4DRN8

Gene Names: ZDHHC20

Peptide Sequence: LVGMDEQASVTNNEYAR

Total Number of Spectra: 2

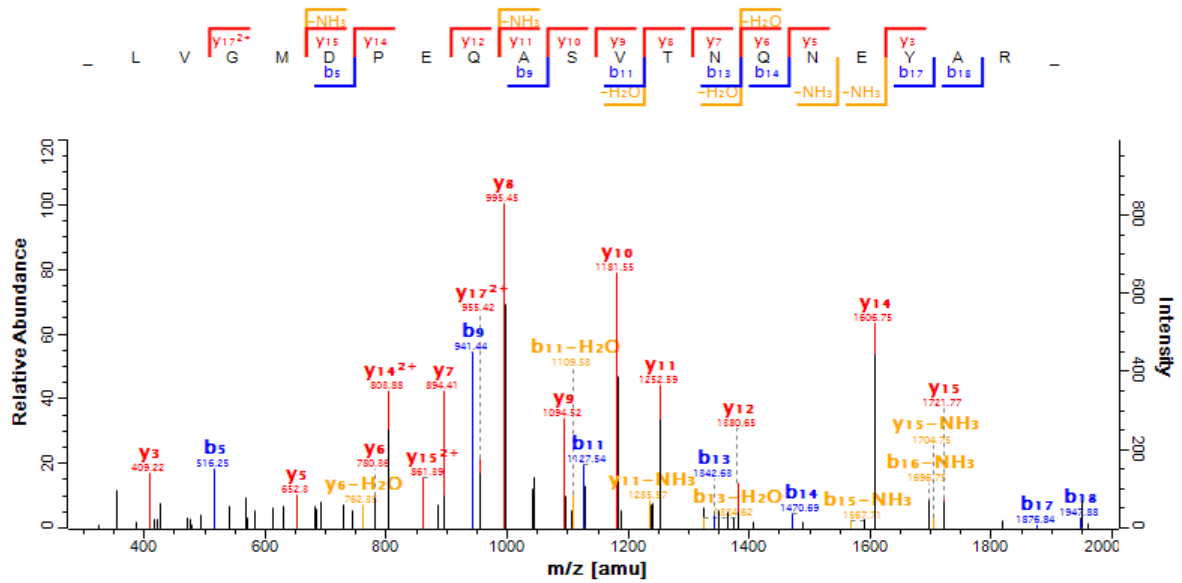
Number of Replicates (out of 8): 2

Best Match Score: 120.92

Best Match Posterior Error Probability: 9.41E-08

Best Match Spectrum:

Scan number 35621 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ZDHHC20



Protein Group ID: 303

Protein Accession Numbers: Q96J42; H0Y997; Q96J42-2; B4DS52; D6RB48; D6RBD9

Gene Names: TXNDC15

Peptide Sequence: VSSEPSGVTCGAGGAEDSR

Total Number of Spectra: 10

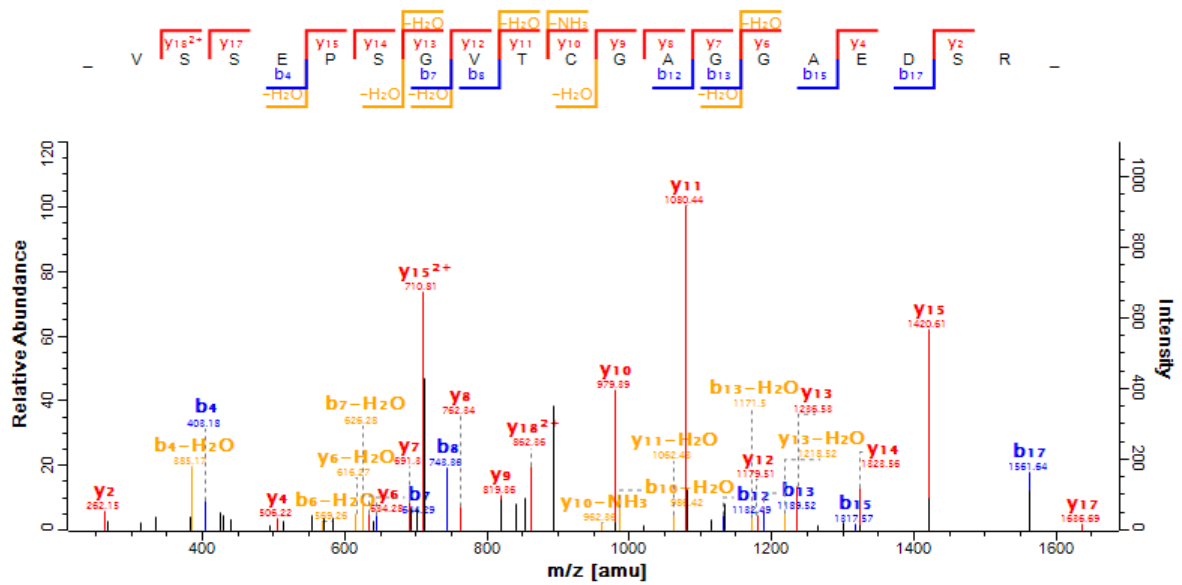
Number of Replicates (out of 8): 6

Best Match Score: 172.97

Best Match Posterior Error Probability: 3.29E-16

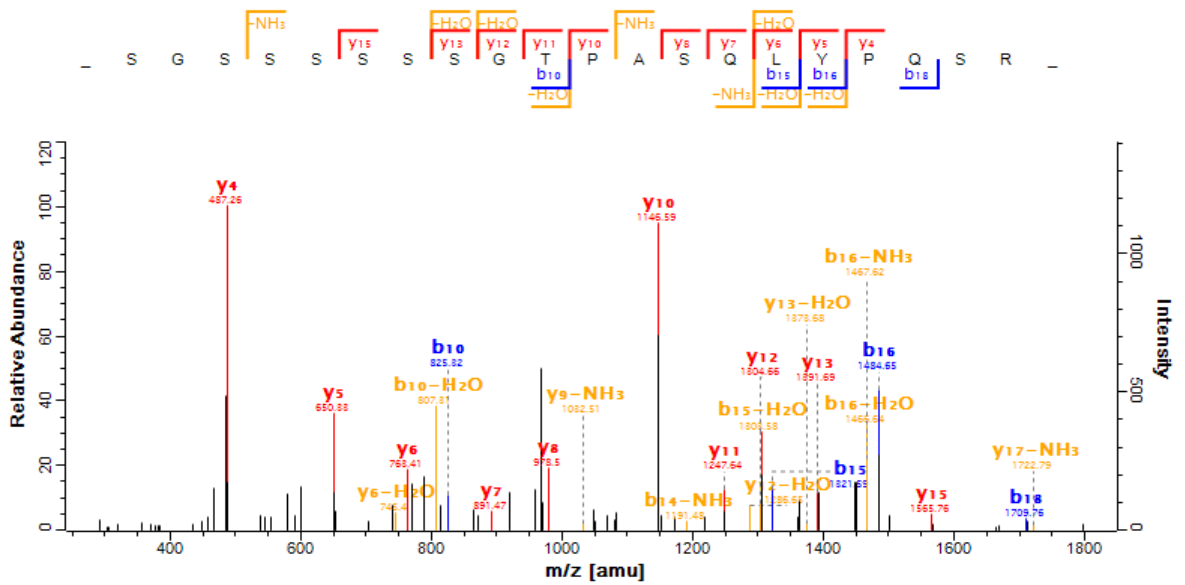
Best Match Spectrum:

Scan number 11788 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TXNDC15



Protein Group ID: 306
Protein Accession Numbers: O15066; B4DSR5
Gene Names: KIF3B
Peptide Sequence: SGSSSSSGTTPASQLYPQSR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 77.391
Best Match Posterior Error Probability: 0.00066478
Best Match Spectrum:

Scan number 22397 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** KIF3B



Protein Group ID: 308

Protein Accession Numbers: Q9HAD4; B4DT55; H0Y9Z3

Gene Names: WDR41

Peptide Sequence: LVAPTEGSLLEWDLILVEVK

Total Number of Spectra: 7

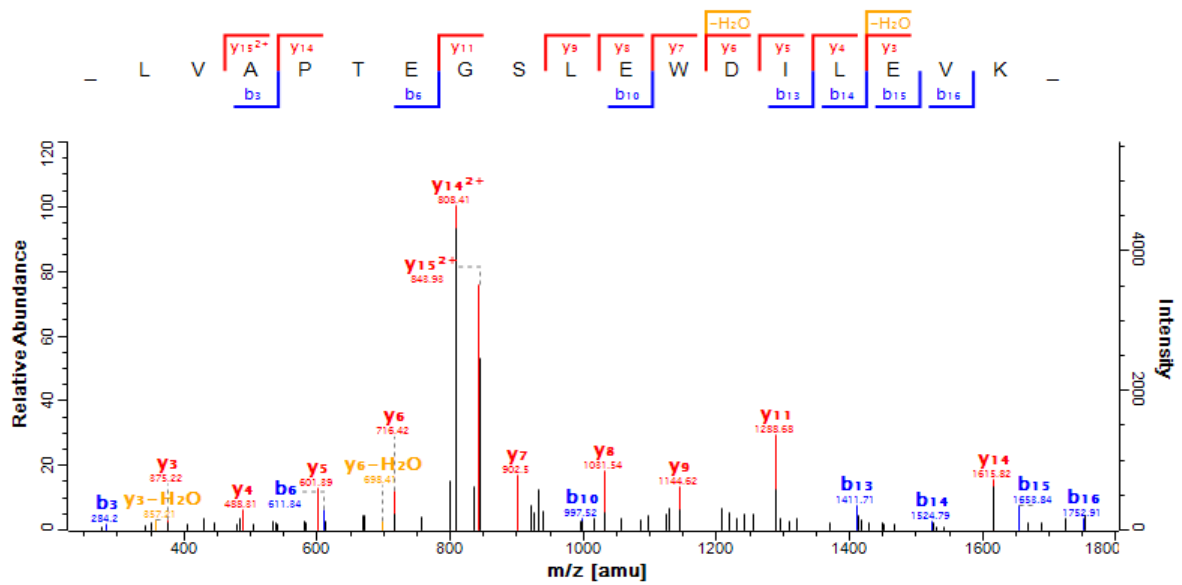
Number of Replicates (out of 8): 7

Best Match Score: 114.59

Best Match Posterior Error Probability: 0.00010548

Best Match Spectrum:

Scan number	76997	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	WDR41



Protein Group ID: 311

Protein Accession Numbers: O15162; C9J7K9; C9J9P4; B4DTE8; H7C5I5

Gene Names: PLSCR1

Peptide Sequence: SLDEQC**V**VGK

Total Number of Spectra: 1

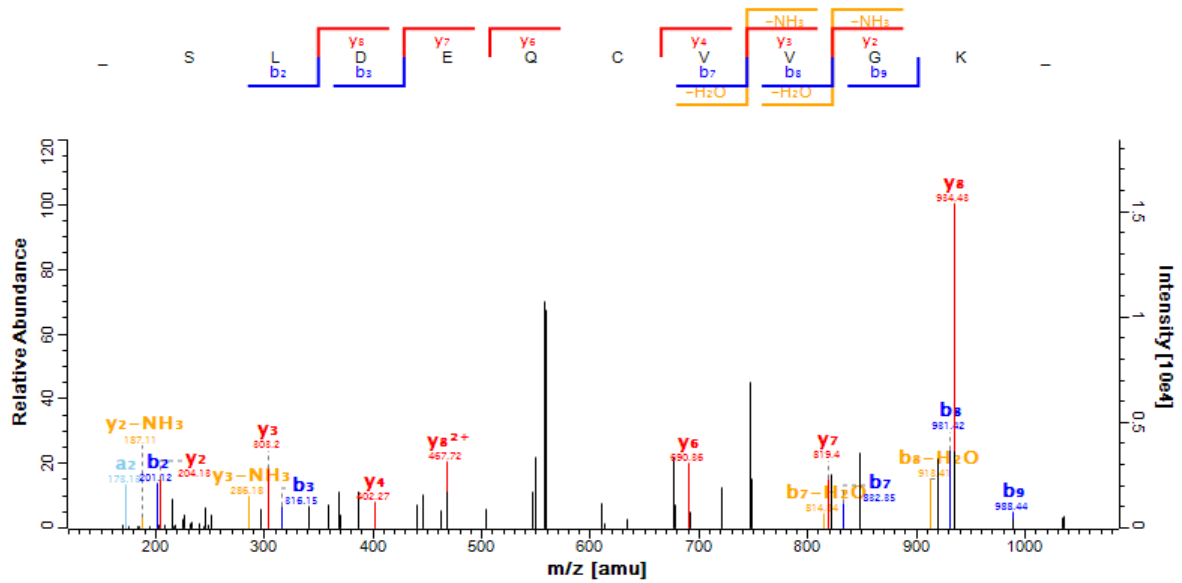
Number of Replicates (out of 8): 1

Best Match Score: 99.973

Best Match Posterior Error Probability: 0.0029173

Best Match Spectrum:

Scan number	15966	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	PLSCR1



Protein Group ID: 318

Protein Accession Numbers: Q9P2K3-3; Q9P2K3; Q9P2K3-4; Q9P2K3-2; B4DV59; E9PQE5; E9PR63

Gene Names: RCOR3

Peptide Sequence: HGYNVEQALGMLFWHK

Total Number of Spectra: 4

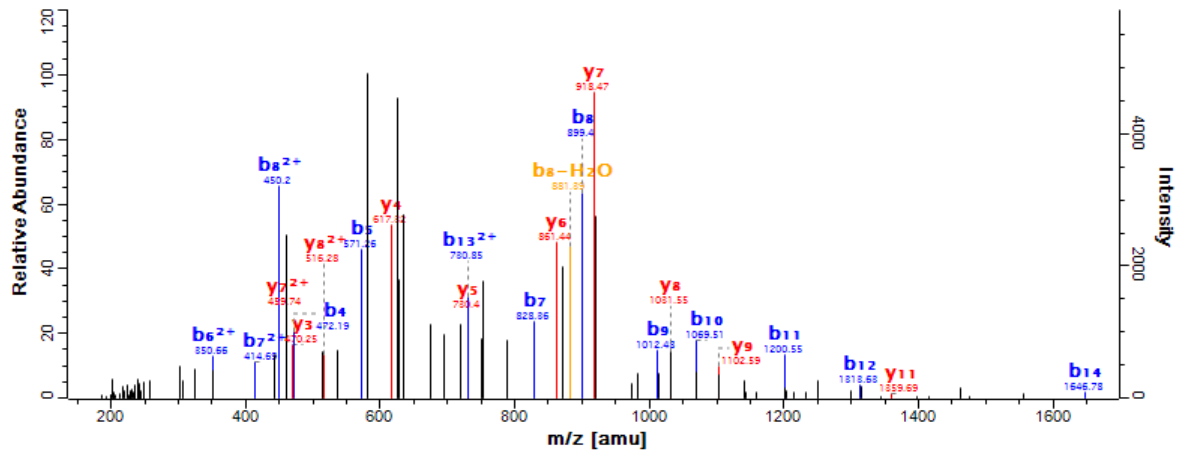
Number of Replicates (out of 8): 4

Best Match Score: 129.01

Best Match Posterior Error Probability: 6.25E-05

Best Match Spectrum:

Scan number	79717	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	RCOR3



Protein Group ID: 323

Protein Accession Numbers: Q96F24; B4DWS0

Gene Names: NRBF2

Peptide Sequence: DAAHLQTSHKPSAEAEQGSPLEYSQK

Total Number of Spectra: 1

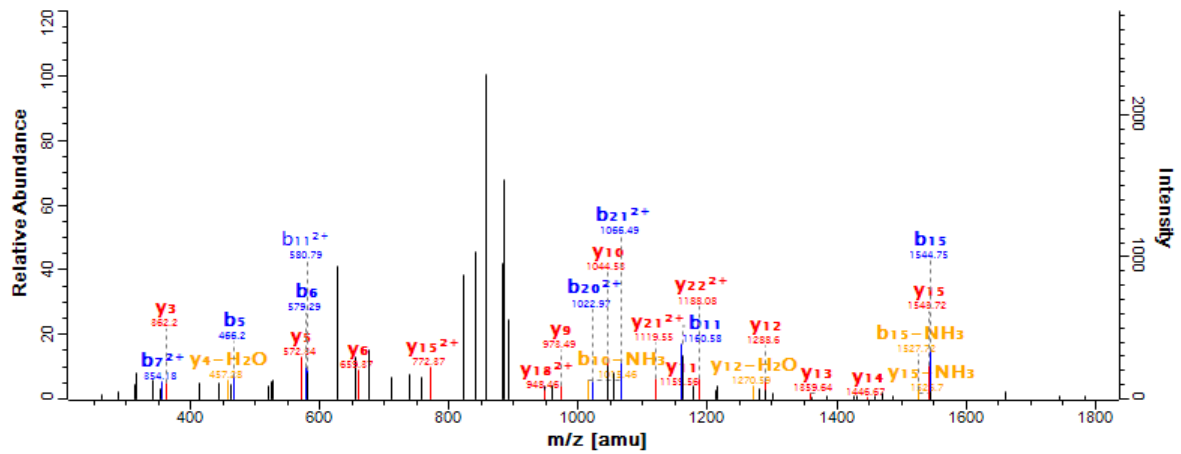
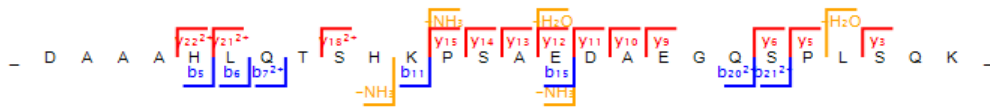
Number of Replicates (out of 8): 1

Best Match Score: 76.744

Best Match Posterior Error Probability: 0.00054698

Best Match Spectrum:

Scan number 20267 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** NRBF2



Protein Group ID: 325

Protein Accession Numbers: Q9Y5B8; Q9Y5B8-2; B4DXC8; E9PNU1

Gene Names: NME7

Peptide Sequence: YDNLHLEDLFIGNK

Total Number of Spectra: 5

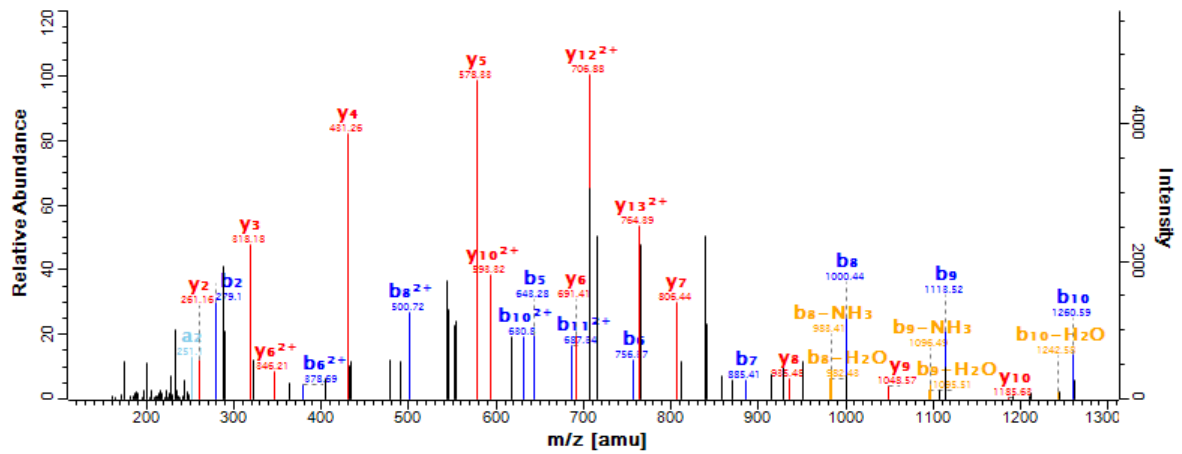
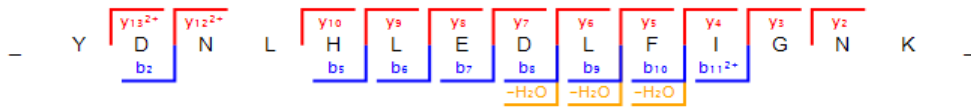
Number of Replicates (out of 8): 5

Best Match Score: 183.89

Best Match Posterior Error Probability: 4.06E-19

Best Match Spectrum:

Scan number 62501 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** NME7



Protein Group ID: 330

Protein Accession Numbers: P36897-2; P36897; B4DY26; P36897-3

Gene Names: TGFBR1

Peptide Sequence: TLSQLSQQEGIK

Total Number of Spectra: 1

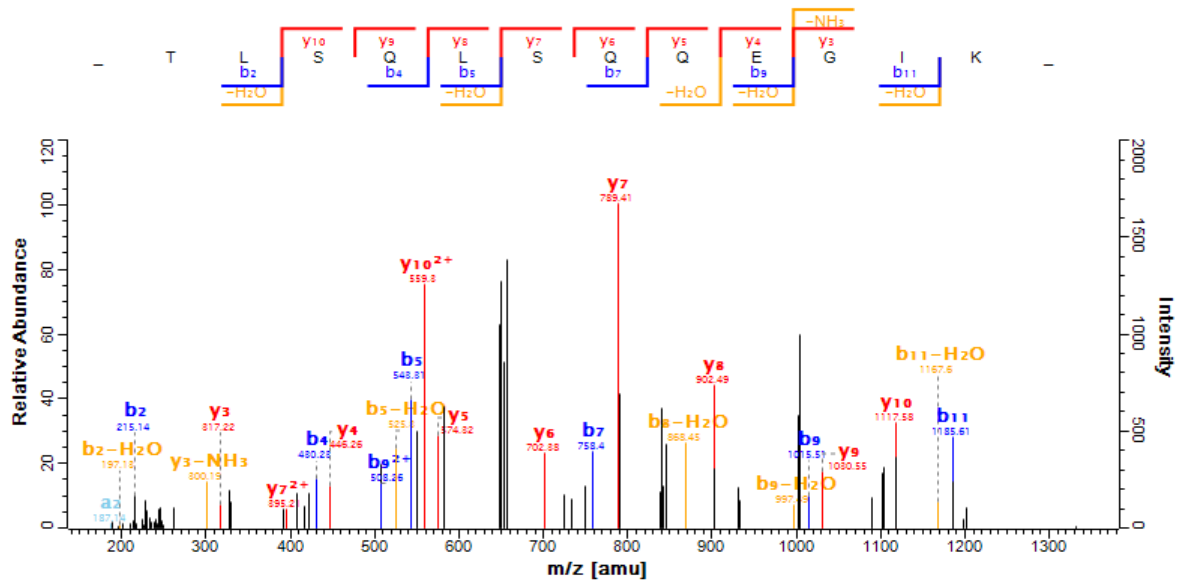
Number of Replicates (out of 8): 1

Best Match Score: 112.44

Best Match Posterior Error Probability: 0.00023048

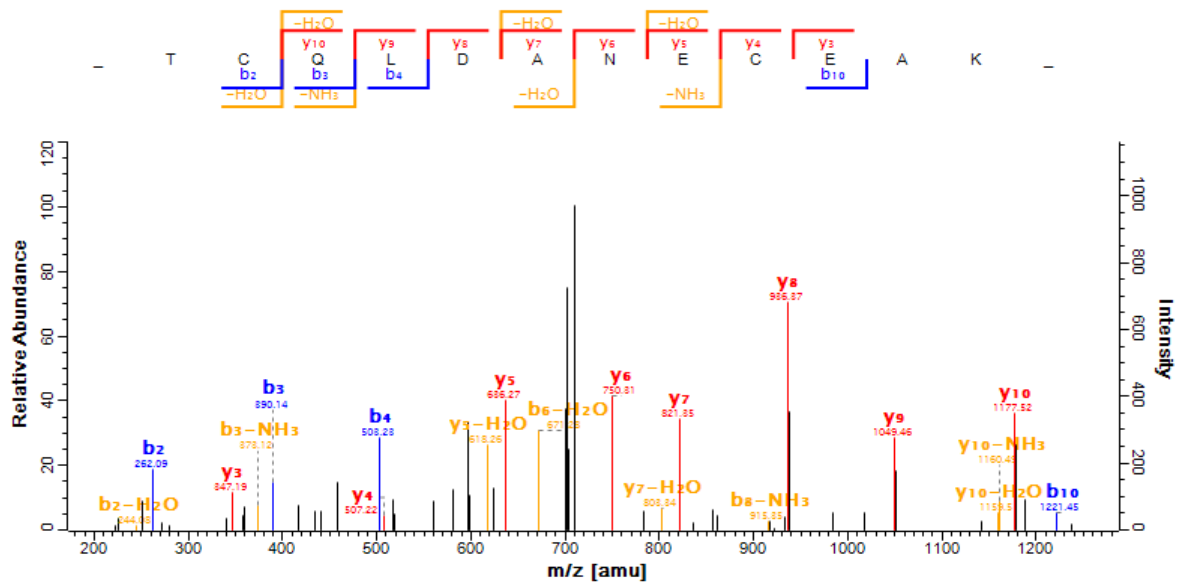
Best Match Spectrum:

Scan number	25095	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	TGFBR1



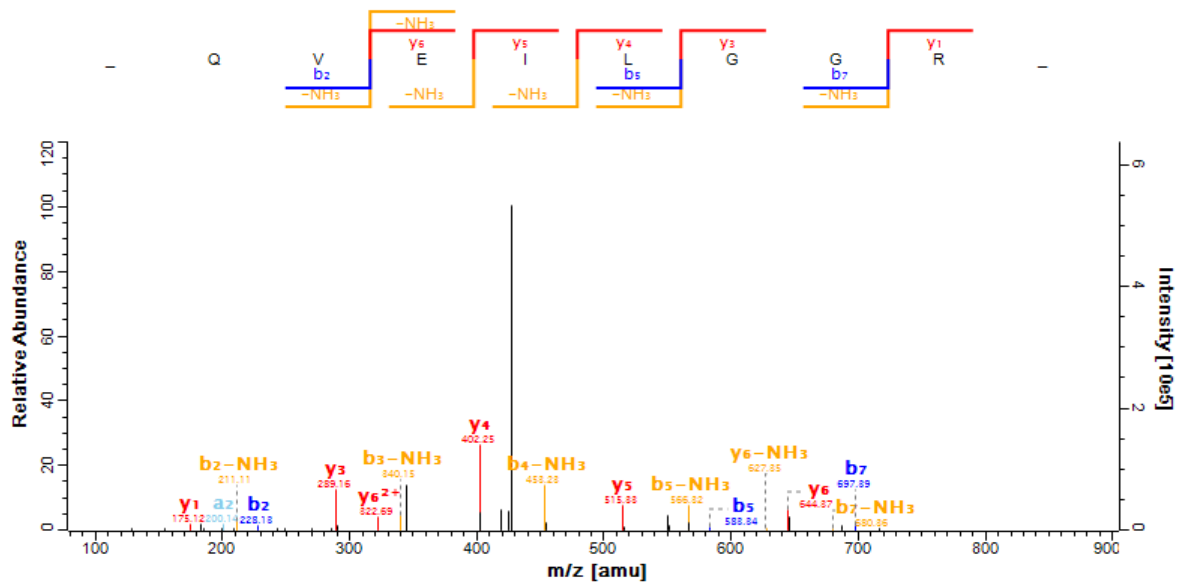
Protein Group ID: 332
Protein Accession Numbers: P78504; B4DYR1
Gene Names: JAG1
Peptide Sequence: TCQLDANECEAK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 92.039
Best Match Posterior Error Probability: 0.0012267
Best Match Spectrum:

Scan number 8577 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** JAG1



Protein Group ID: 333
Protein Accession Numbers: Q8IYM0; B4DZ15
Gene Names: FAM186B
Peptide Sequence: QVEILGGR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 106.36
Best Match Posterior Error Probability: 0.003812
Best Match Spectrum:

Scan number 18081 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** FAM186B



Protein Group ID: 337

Protein Accession Numbers: B4E040; P11234; Q6ZS74; C9J6B1

Gene Names: RALB

Peptide Sequence: AEEWGVQYVETSAK

Total Number of Spectra: 8

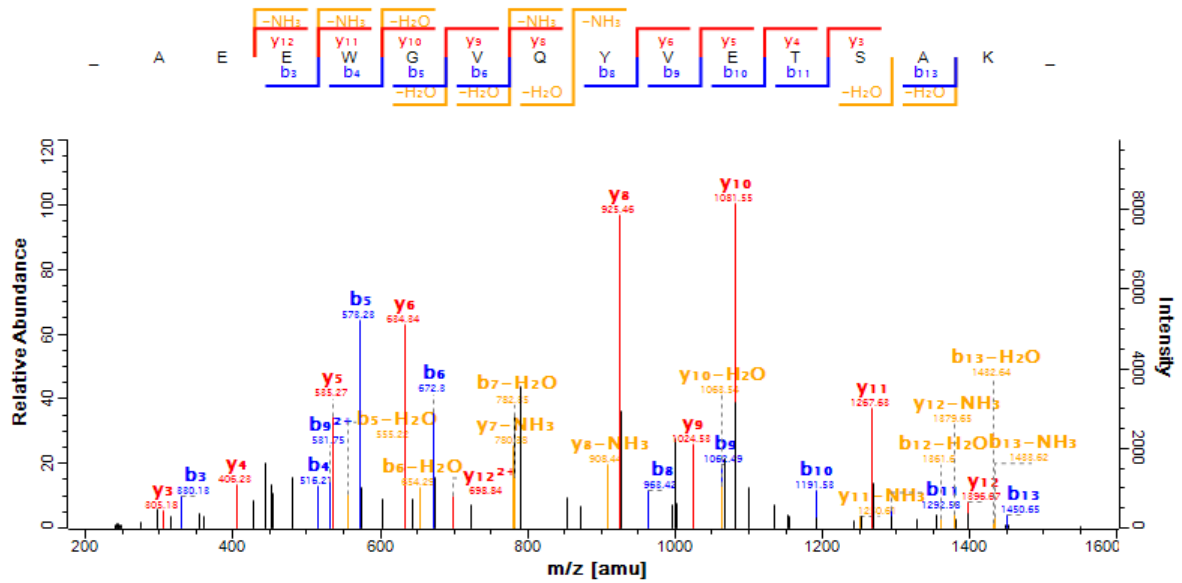
Number of Replicates (out of 8): 8

Best Match Score: 157.35

Best Match Posterior Error Probability: 2.39E-09

Best Match Spectrum:

Scan number 43249 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** RALB



Protein Group ID: 338

Protein Accession Numbers: Q9NVF7; E9PEM8; B4E0H5

Gene Names: FBXO28

Peptide Sequence: MAEEGGGGQGDGGSSLASGSTQR

Total Number of Spectra: 4

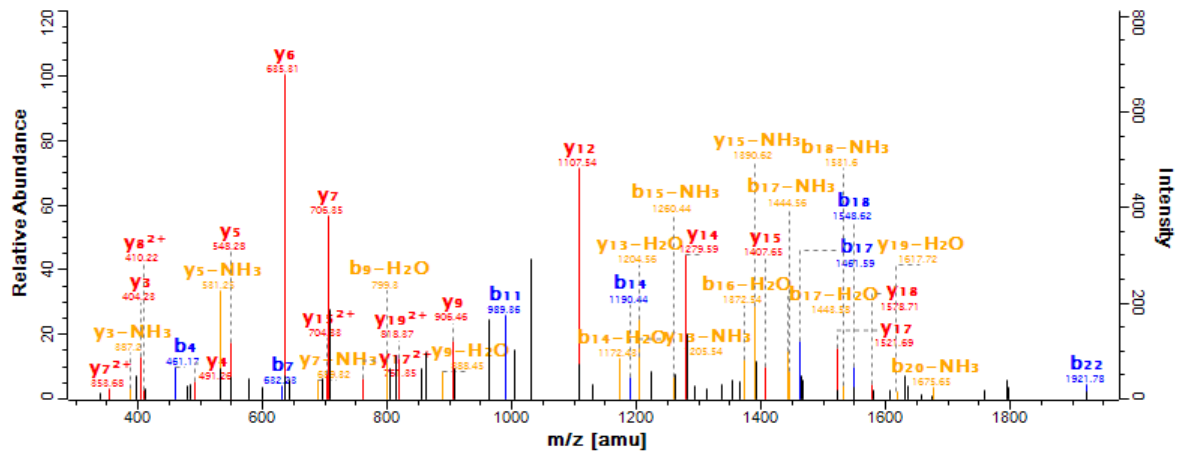
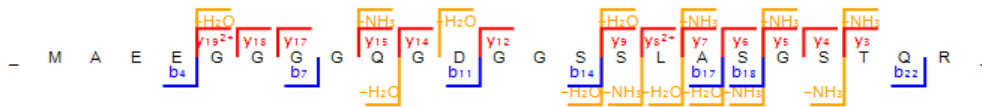
Number of Replicates (out of 8): 3

Best Match Score: 158.52

Best Match Posterior Error Probability: 6.38E-19

Best Match Spectrum:

Scan number	11372	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	FBXO28



Protein Group ID: 342

Protein Accession Numbers: Q9BUN8; Q9BUN8-2; B4E1G1; E5RGY0

Gene Names: DERL1

Peptide Sequence: NFLSTPQFLYR

Total Number of Spectra: 8

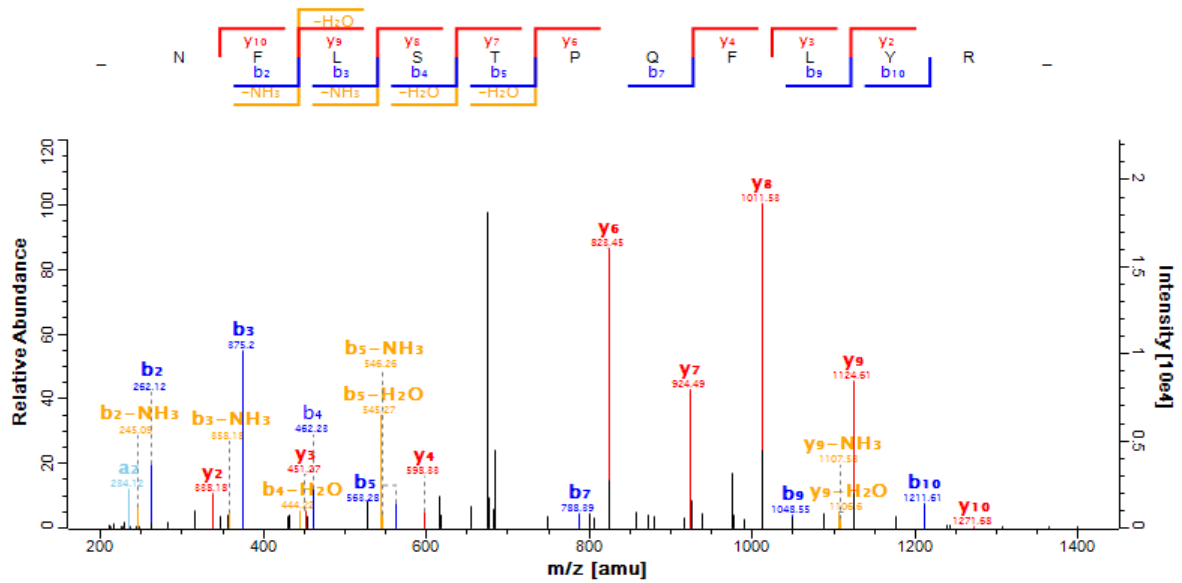
Number of Replicates (out of 8): 8

Best Match Score: 164.04

Best Match Posterior Error Probability: 8.91E-06

Best Match Spectrum:

Scan number 63624 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** DERL1



Protein Group ID: 349

Protein Accession Numbers: Q9BVC5; B4E2G9; C9J4K0

Gene Names: C2orf49

Peptide Sequence: SCTDSELLHPELLSQEFLLLTLEQK

Total Number of Spectra: 1

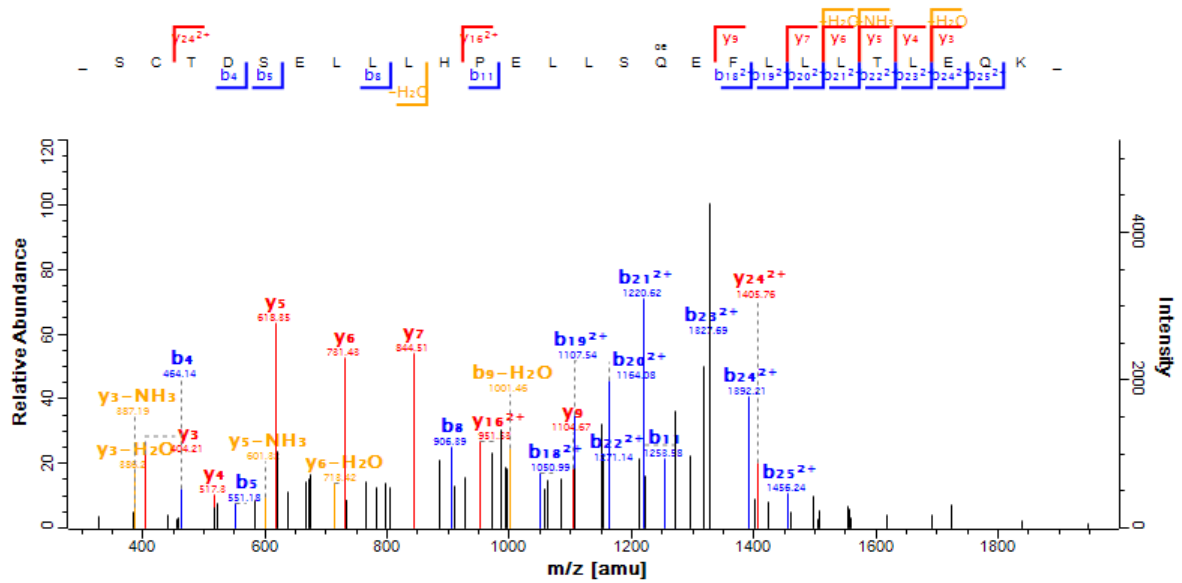
Number of Replicates (out of 8): 1

Best Match Score: 103.27

Best Match Posterior Error Probability: 4.80E-06

Best Match Spectrum:

Scan number	89797	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	C2orf49



Protein Group ID: 351

Protein Accession Numbers: B4E2P2; Q9UNL2; C9JA28

Gene Names: SSR3

Peptide Sequence: QQSEEDLLLQDFSR

Total Number of Spectra: 9

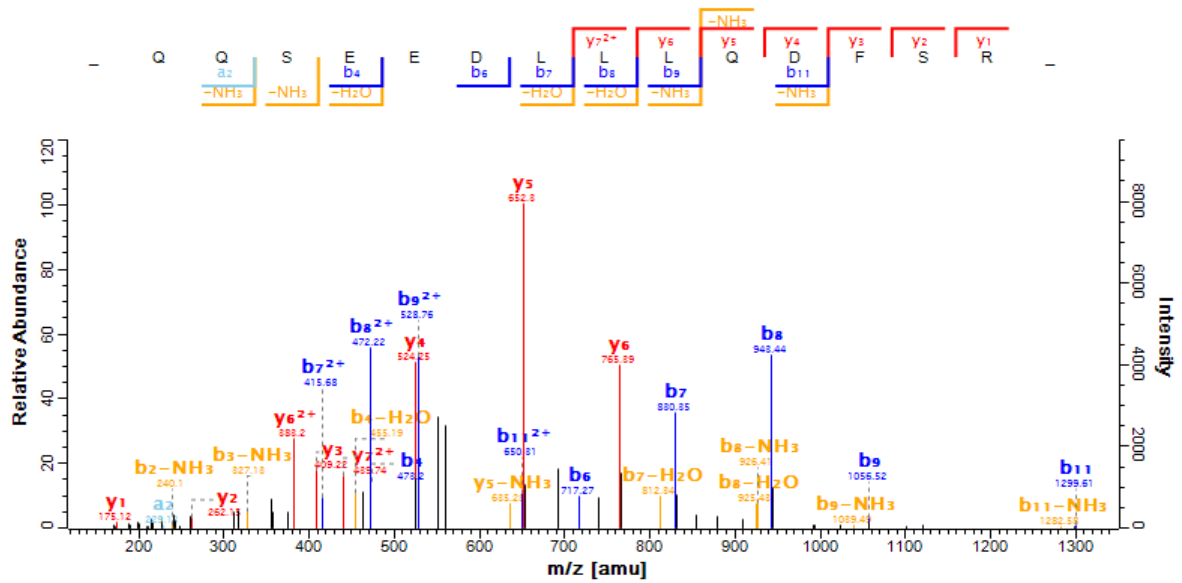
Number of Replicates (out of 8): 7

Best Match Score: 137.62

Best Match Posterior Error Probability: 2.93E-05

Best Match Spectrum:

Scan number 60142 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** SSR3



Protein Group ID: 356

Protein Accession Numbers: G5E9D4; Q96EB1-2; B4E3W0; Q96EB1

Gene Names: ELP4

Peptide Sequence: LNNLICDESDVK

Total Number of Spectra: 1

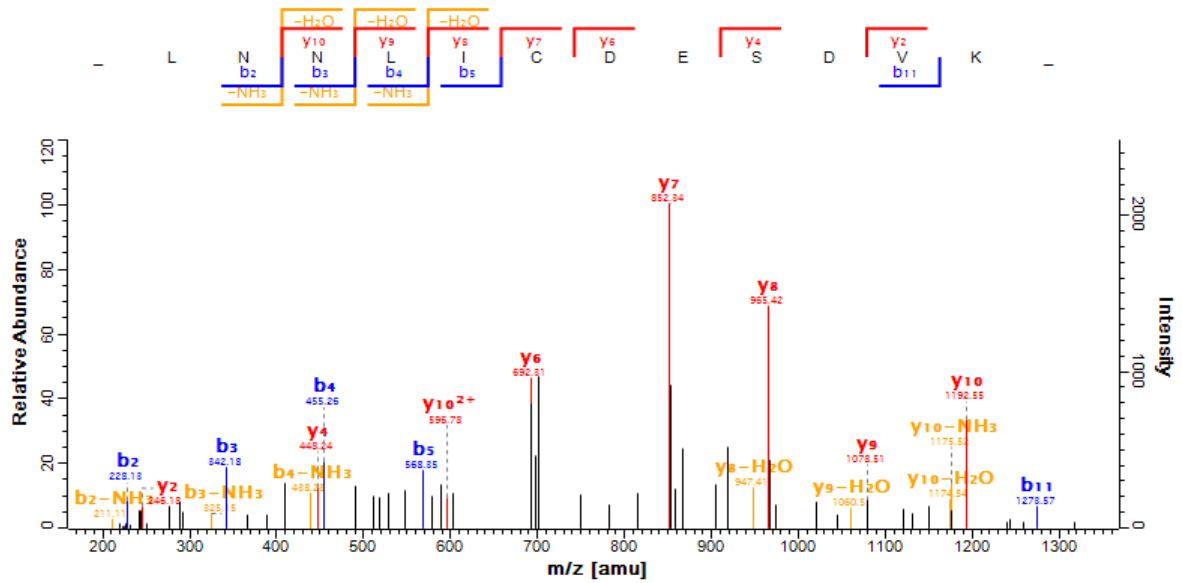
Number of Replicates (out of 8): 1

Best Match Score: 110.31

Best Match Posterior Error Probability: 0.00026024

Best Match Spectrum:

Scan number 30697 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ELP4



Protein Group ID: 357

Protein Accession Numbers: O94864; O94864-2; B4E3W3

Gene Names: SUPT7L

Peptide Sequence: LGQTPFPDVMEQVFHEVGI G S V L S L Q K

Total Number of Spectra: 2

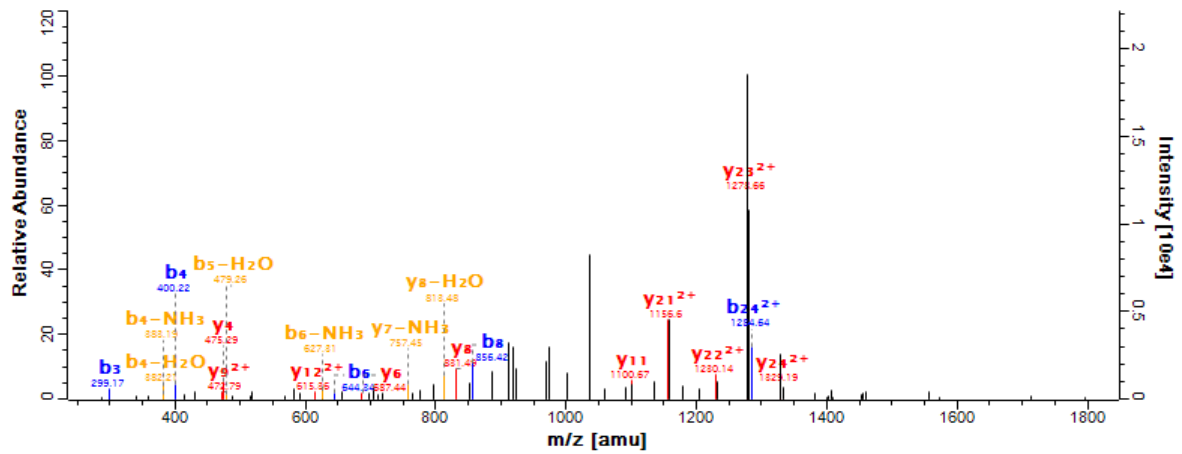
Number of Replicates (out of 8): 2

Best Match Score: 51.39

Best Match Posterior Error Probability: 0.0036284

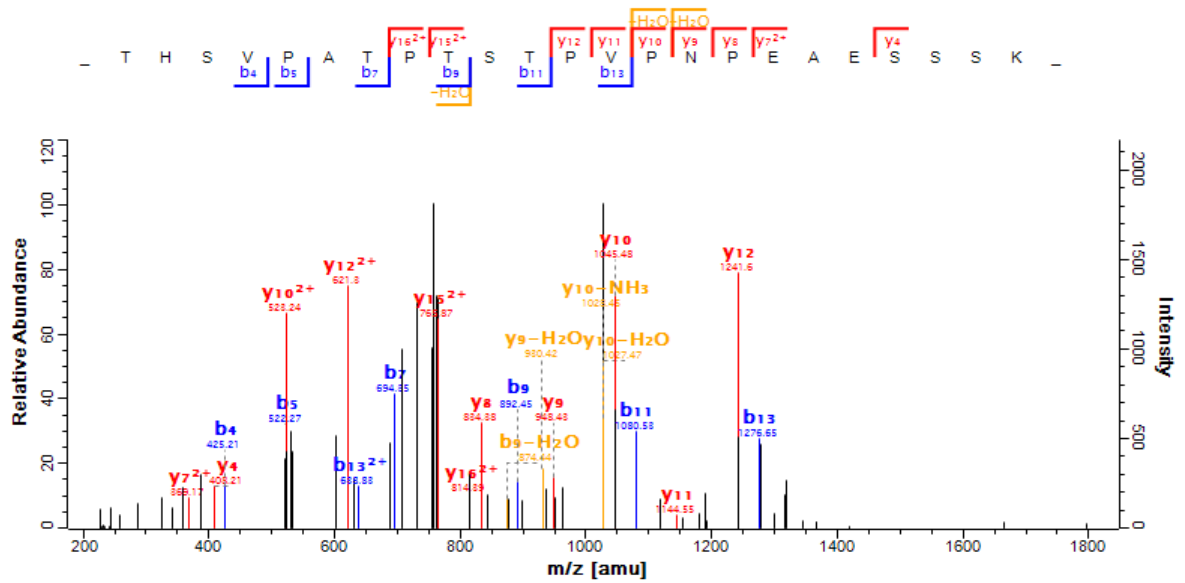
Best Match Spectrum:

Scan number 92179 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** SUPT7L



Protein Group ID: 358
Protein Accession Numbers: B5MBX0; Q96FF9
Gene Names: CDCA5
Peptide Sequence: THSVPATPTSTPVPNPEAESSK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 87.654
Best Match Posterior Error Probability: 1.46E-05
Best Match Spectrum:

Scan number 26126 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CDCA5



Protein Group ID: 360

Protein Accession Numbers: P05231; B5MCZ3; B5MC21

Gene Names: IL6

Peptide Sequence: LQAQNQLQDMTTHLIR

Total Number of Spectra: 3

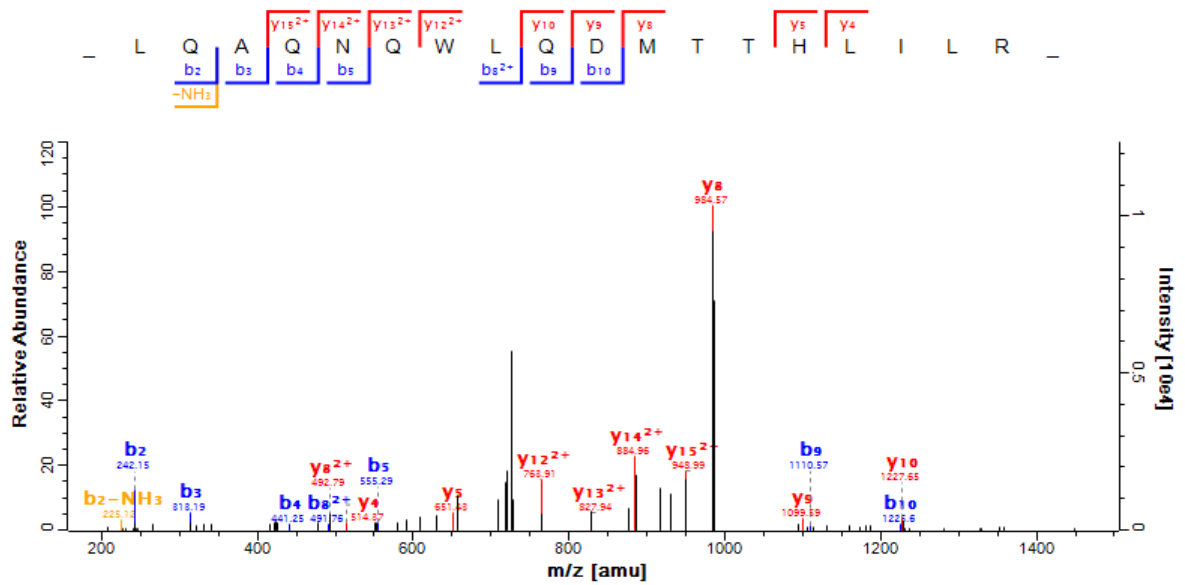
Number of Replicates (out of 8): 2

Best Match Score: 70.41

Best Match Posterior Error Probability: 0.0034301

Best Match Spectrum:

Scan number 79106 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** IL6



Protein Group ID: 361

Protein Accession Numbers: B5MC40; Q86YP4; Q86YP4-2; C9JJK9; C9JHD7; C9JGN4; C9JMI3; C9JVV3

Gene Names: GATAD2A

Peptide Sequence: GEGLVGDGPVDMR

Total Number of Spectra: 1

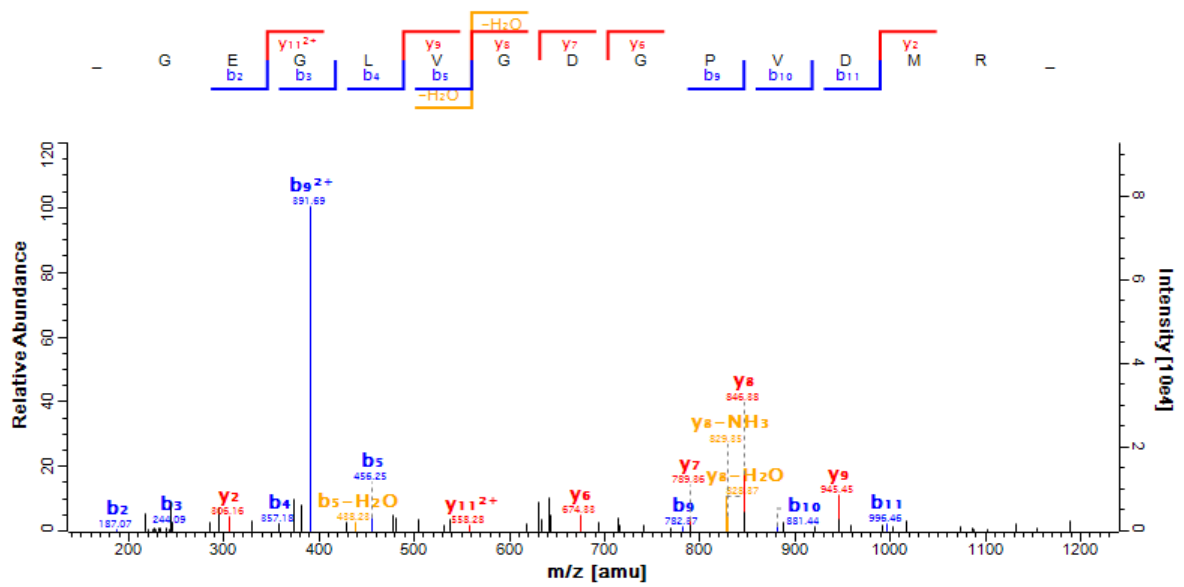
Number of Replicates (out of 8): 1

Best Match Score: 80.318

Best Match Posterior Error Probability: 0.0032393

Best Match Spectrum:

Scan number	34393	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS: CID	Genenames	GATAD2A



Protein Group ID: 367

Protein Accession Numbers: Q8N465; B5MCV2; H7BZ32; H7C0N1

Gene Names: D2HGDH

Peptide Sequence: LYDIVTDLR

Total Number of Spectra: 2

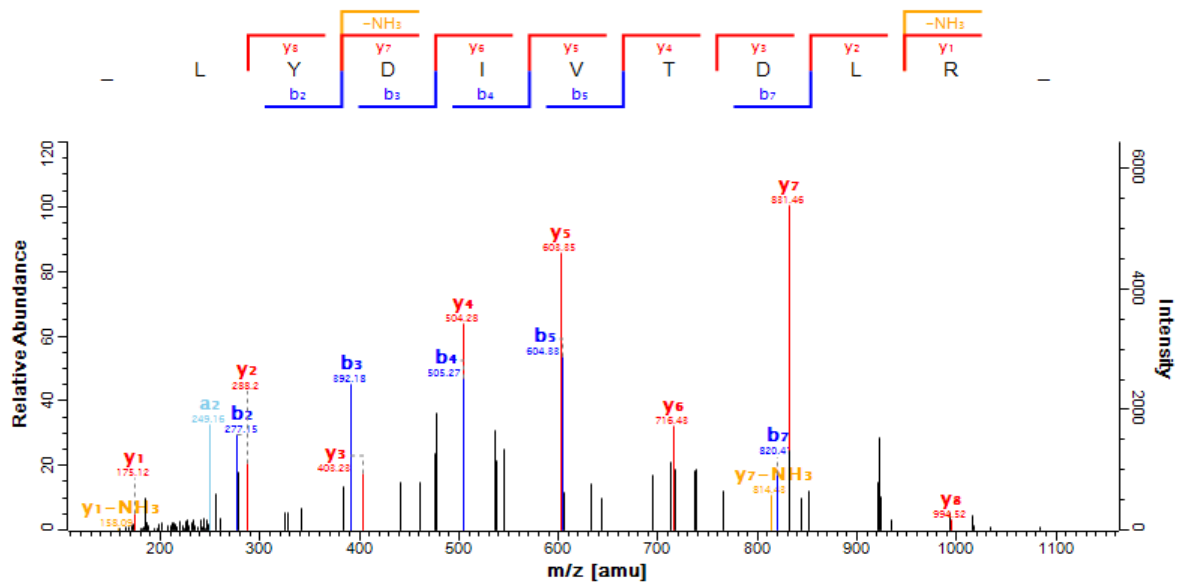
Number of Replicates (out of 8): 2

Best Match Score: 112.75

Best Match Posterior Error Probability: 0.00082265

Best Match Spectrum:

Scan number	50328	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	D2HGDH



Protein Group ID: 377

Protein Accession Numbers: B7WPE2; Q32P44; G3V195; H7C355

Gene Names: EML3

Peptide Sequence: VLGAGGAGPAPATPSR

Total Number of Spectra: 6

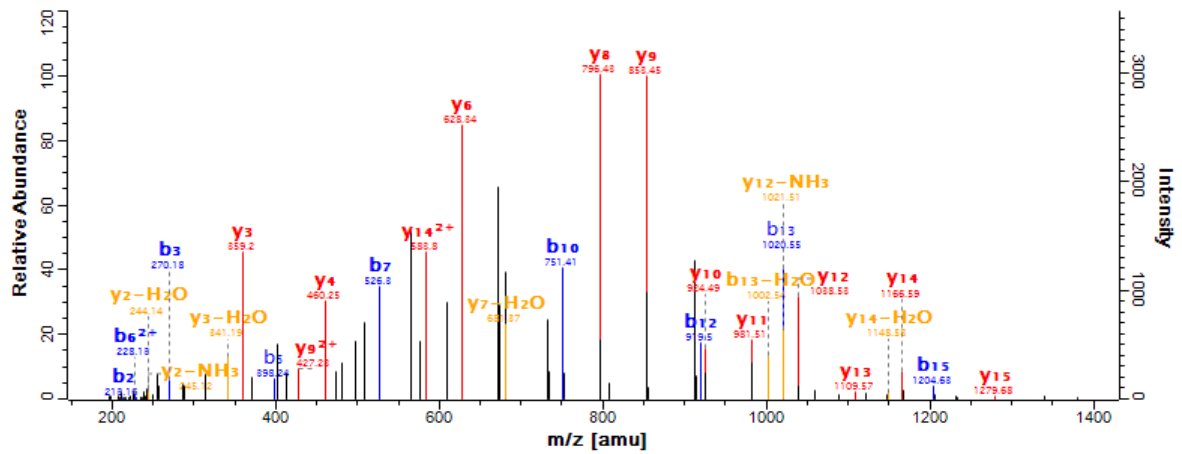
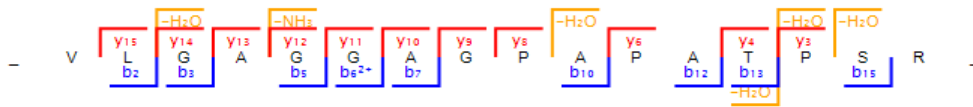
Number of Replicates (out of 8): 5

Best Match Score: 144.68

Best Match Posterior Error Probability: 4.47E-06

Best Match Spectrum:

Scan number 18647 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** EML3



Protein Group ID: 380

Protein Accession Numbers: P78310; B7WPI3; P78310-2; D3YHP0; P78310-5

Gene Names: CXADR

Peptide Sequence: EGSLPLQYEWQK

Total Number of Spectra: 2

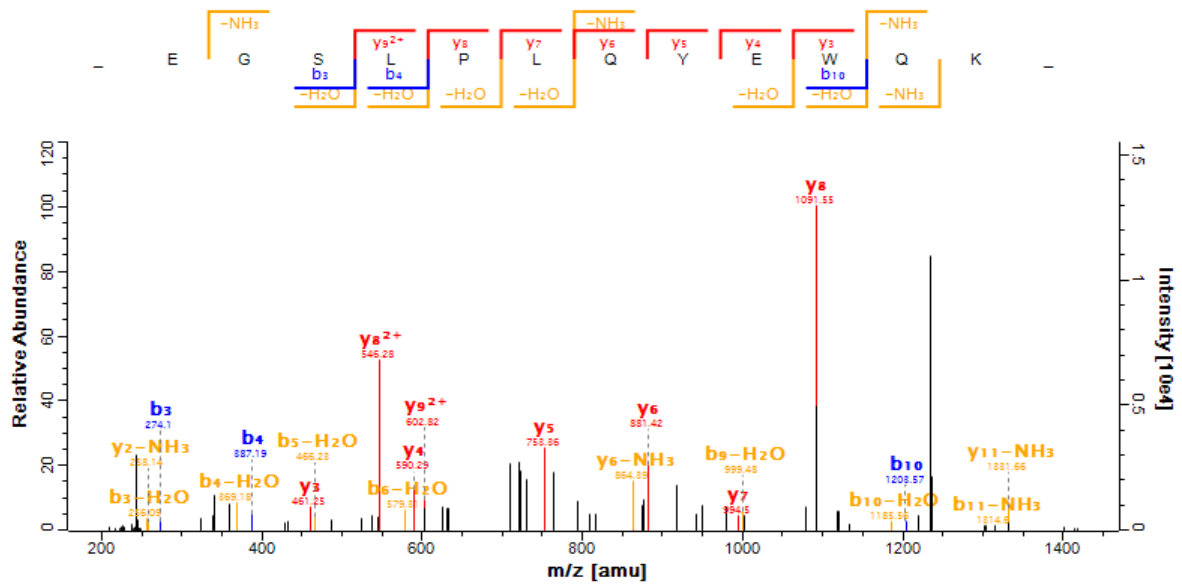
Number of Replicates (out of 8): 2

Best Match Score: 84.605

Best Match Posterior Error Probability: 0.0023153

Best Match Spectrum:

Scan number 48493 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CXADR



Protein Group ID: 381

Protein Accession Numbers: Q8NB37-2; Q8NB37; Q8NB37-3; B7Z1J9; H0YF25; H0YE25; H0YER3

Gene Names: PDDC1

Peptide Sequence: LPLVVEDFVK

Total Number of Spectra: 2

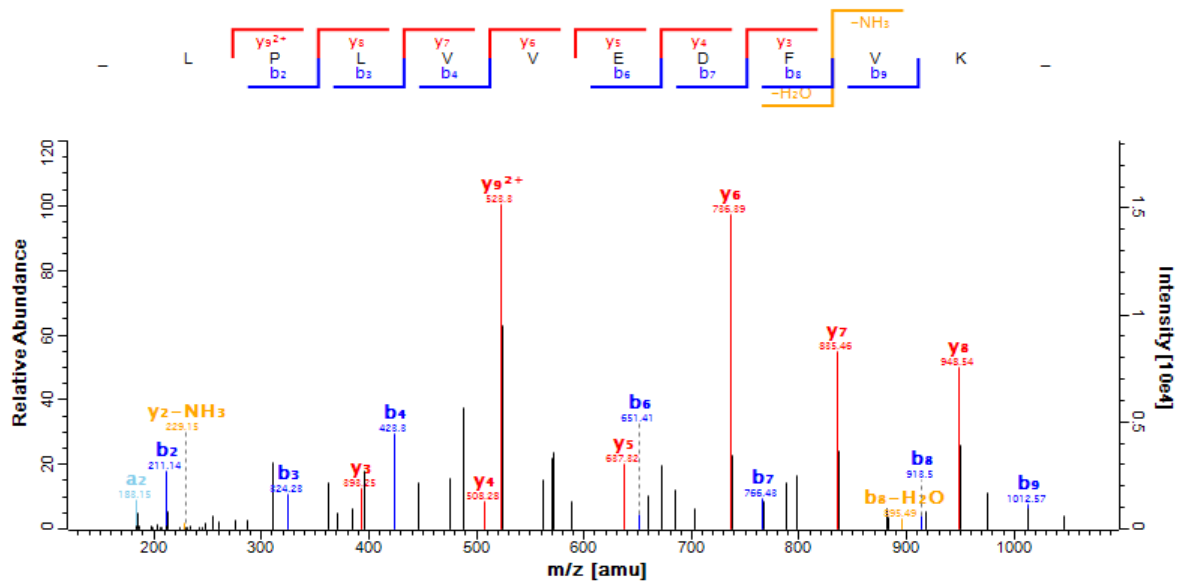
Number of Replicates (out of 8): 2

Best Match Score: 103.26

Best Match Posterior Error Probability: 0.00064102

Best Match Spectrum:

Scan number	65345	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	PDDC1



Protein Group ID: 382

Protein Accession Numbers: B7Z1P2; Q9H4M3; Q9H4M3-2

Gene Names: FBXO44

Peptide Sequence: AVGNINLELPENILLELFTHVPAAR

Total Number of Spectra: 1

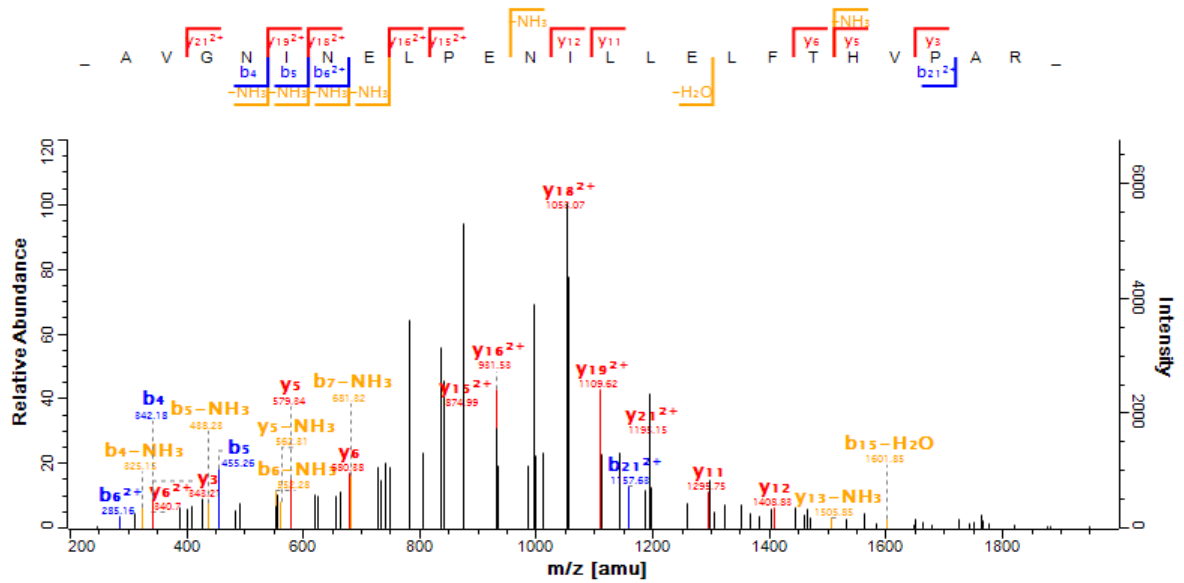
Number of Replicates (out of 8): 1

Best Match Score: 64.2

Best Match Posterior Error Probability: 0.0011815

Best Match Spectrum:

Scan number 93143 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** FBXO44



Protein Group ID: 383

Protein Accession Numbers: O00258; B7Z1T1; O00258-2; H7BYE5

Gene Names: WRB

Peptide Sequence: QELSTVNMMDEFAR

Total Number of Spectra: 2

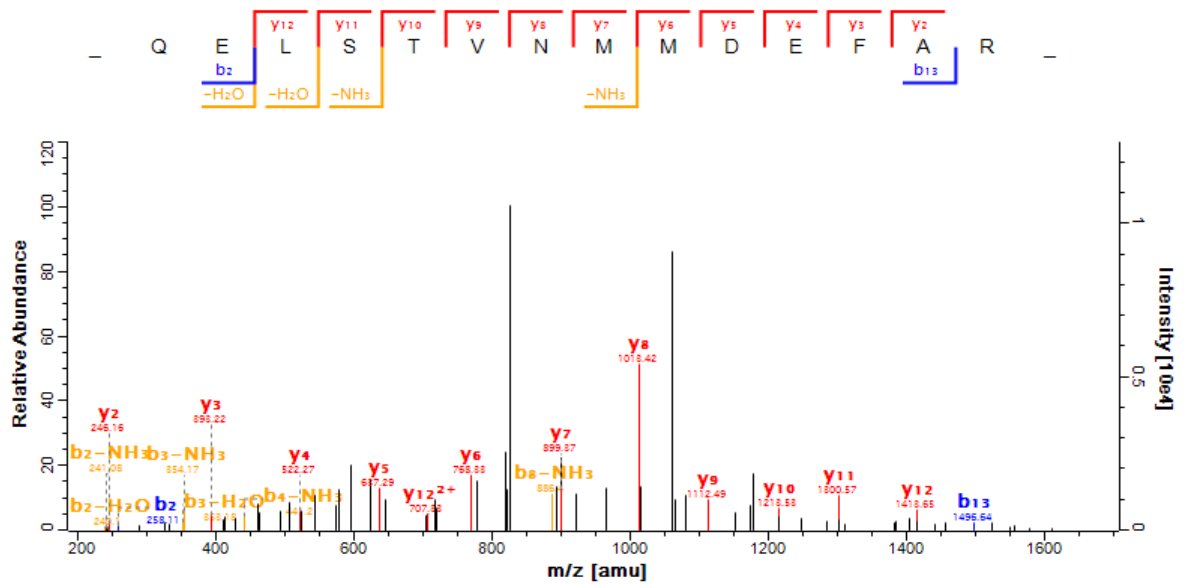
Number of Replicates (out of 8): 2

Best Match Score: 80.706

Best Match Posterior Error Probability: 0.0030738

Best Match Spectrum:

Scan number 58673 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** WRB



Protein Group ID: 384

Protein Accession Numbers: P06746; H0YBJ0; B7Z1W5; E5RHZ4

Gene Names: POLB

Peptide Sequence: GFTINEYTI RLPGLV TGVAGEPLVDSEK

Total Number of Spectra: 2

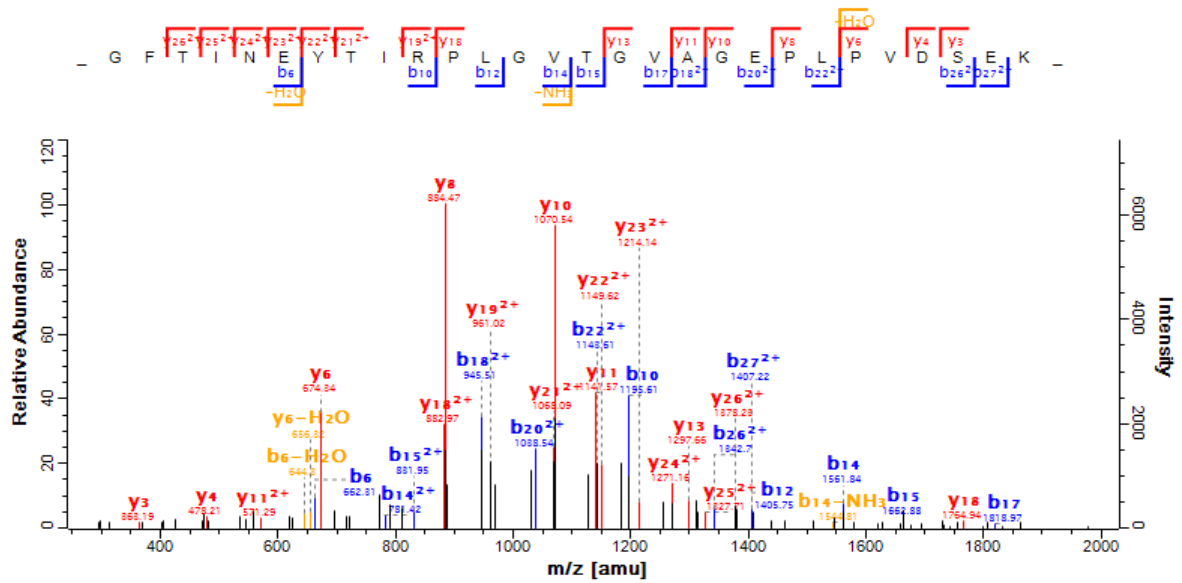
Number of Replicates (out of 8): 2

Best Match Score: 129.29

Best Match Posterior Error Probability: 7.06E-18

Best Match Spectrum:

Scan number 68518 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** POLB



Protein Group ID: 387

Protein Accession Numbers: Q93050-3; F5H569; Q93050; Q93050-1; B7Z2A9; B7Z641; K7EN36; K7EM24; K7ELZ6

Gene Names: ATP6V0A1

Peptide Sequence: ANIPIMDTGENPEVPFPR

Total Number of Spectra: 7

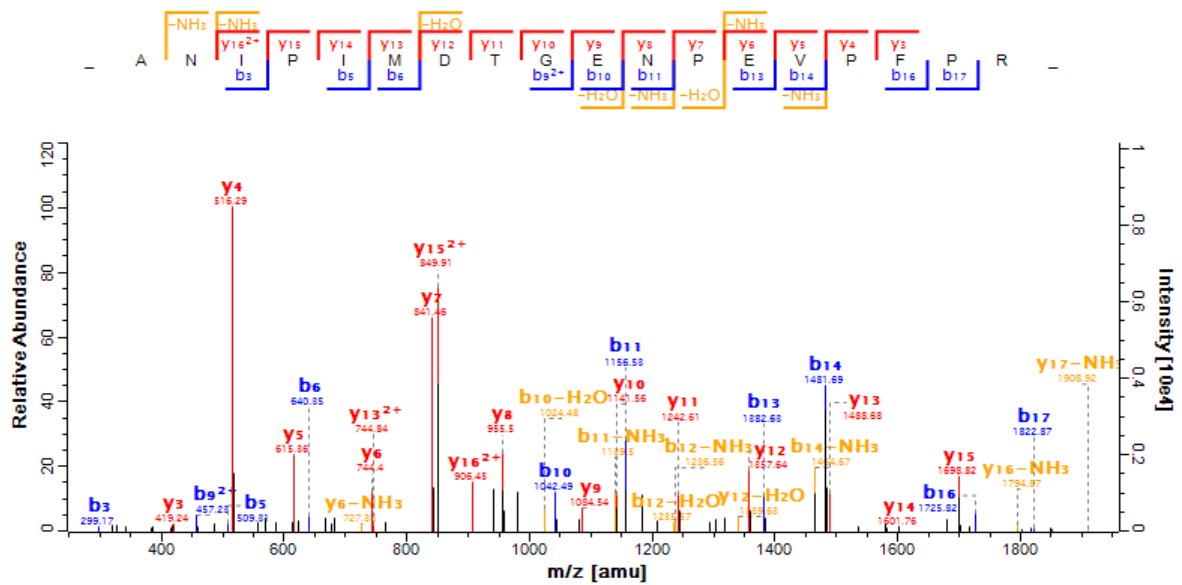
Number of Replicates (out of 8): 6

Best Match Score: 171.98

Best Match Posterior Error Probability: 1.01E-14

Best Match Spectrum:

Scan number	61511	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS: CID	Genenames	ATP6V0A1



Protein Group ID: 390

Protein Accession Numbers: J3KQA6; O43739; Q99418; O43739-2; Q99418-2; B7Z2V9; G5E9B7; F8W8E2

Gene Names: CYTH3;CYTH2

Peptide Sequence: GINEGGDLPEELLR

Total Number of Spectra: 1

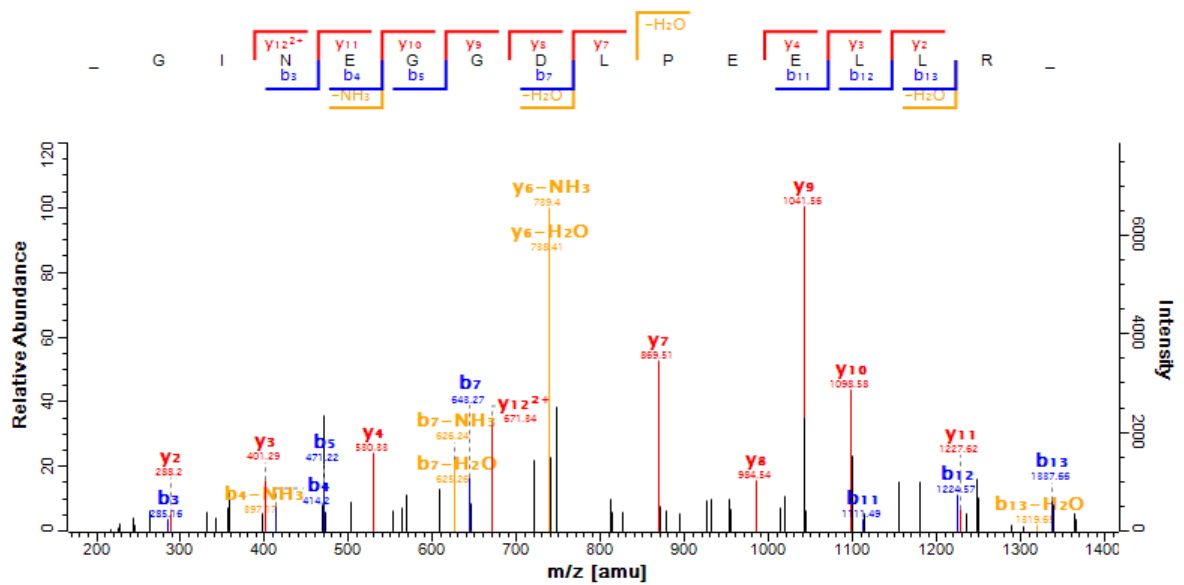
Number of Replicates (out of 8): 1

Best Match Score: 91.076

Best Match Posterior Error Probability: 0.0010949

Best Match Spectrum:

Scan number	56248	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS: CID	Genenames	CYTH3;CYTH2



Protein Group ID: 392

Protein Accession Numbers: Q8NCE0; Q8NCE0-2; B7Z355; C9IZI7; C9J7Z4

Gene Names: TSEN2

Peptide Sequence: EAAPNEELVQR

Total Number of Spectra: 3

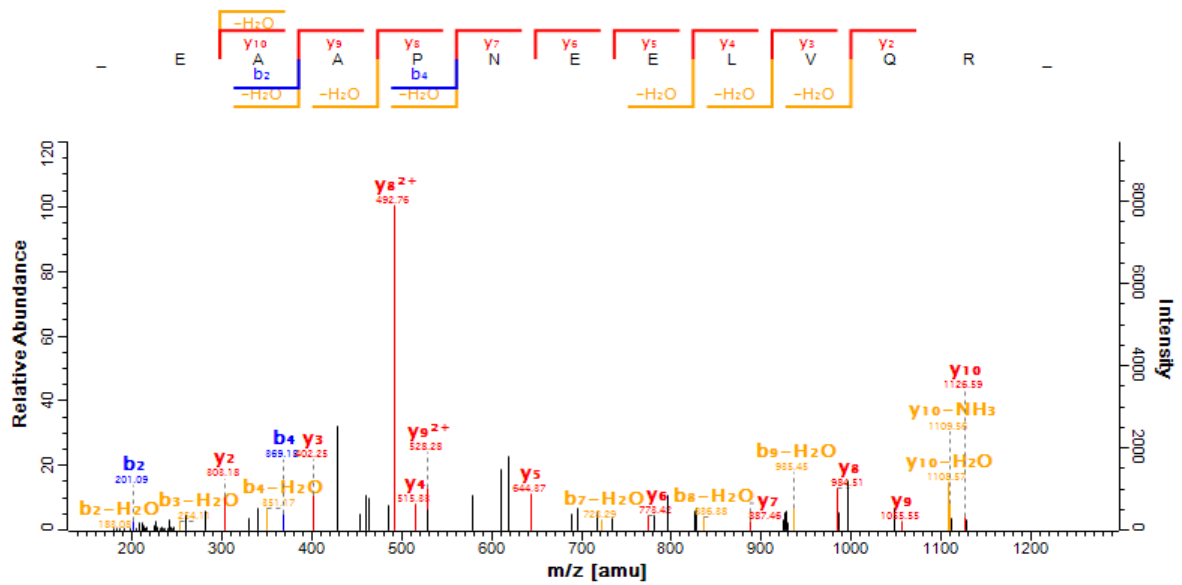
Number of Replicates (out of 8): 3

Best Match Score: 90.653

Best Match Posterior Error Probability: 0.0014098

Best Match Spectrum:

Scan number 17027 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** TSEN2



Protein Group ID: 393

Protein Accession Numbers: P13716-2; P13716; B7Z3I9

Gene Names: ALAD

Peptide Sequence: AGCQVVAPSDMMDGR

Total Number of Spectra: 1

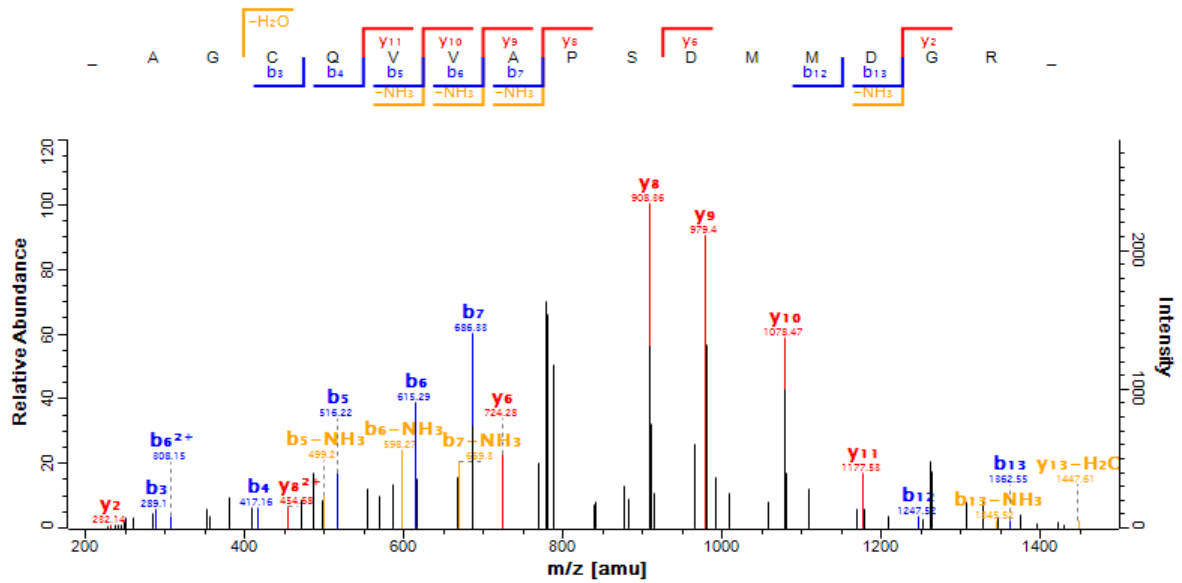
Number of Replicates (out of 8): 1

Best Match Score: 82.925

Best Match Posterior Error Probability: 0.0019569

Best Match Spectrum:

Scan number 33658 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ALAD



Protein Group ID: 396

Protein Accession Numbers: Q9NZ52; Q9NZ52-2; J3KRN0; J3KSS7; B7Z456; Q9NZ52-3; J3QS87; J3KTR5; J3KRM3

Gene Names: GGA3

Peptide Sequence: LQPPSGTELSPFSP I QPPAAITQVMLLANPLK

Total Number of Spectra: 1

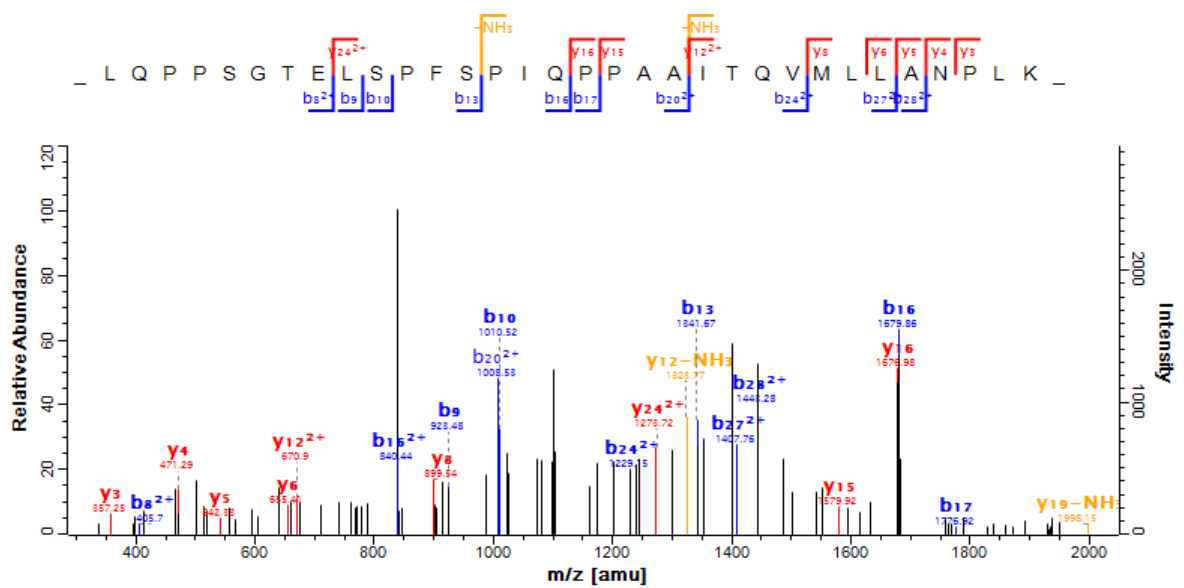
Number of Replicates (out of 8): 1

Best Match Score: 55.153

Best Match Posterior Error Probability: 0.00054089

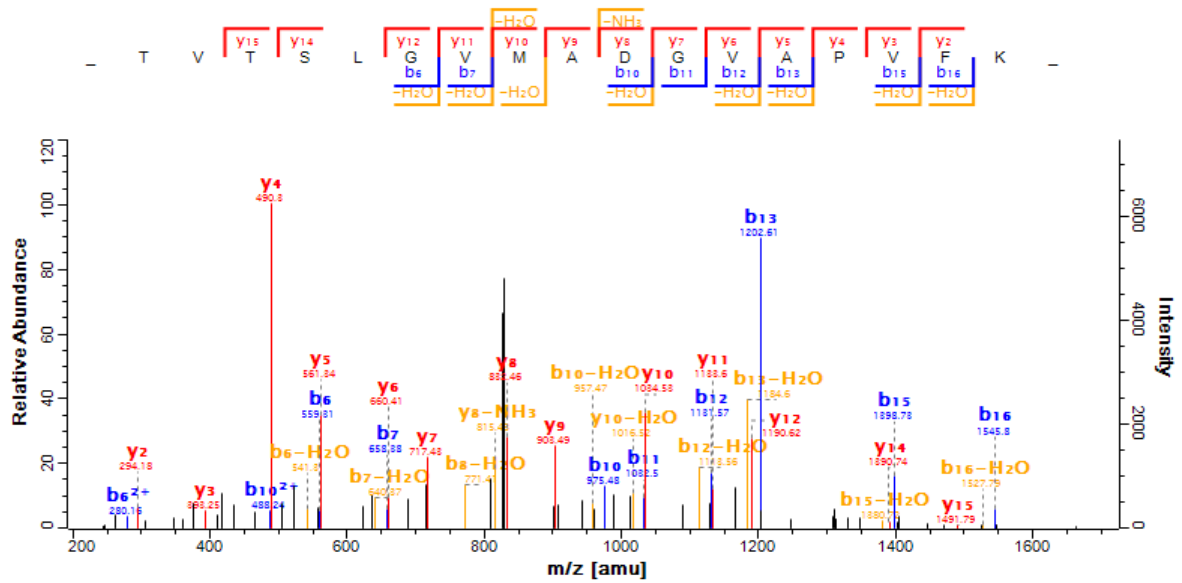
Best Match Spectrum:

Scan number	93563	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS: CID	Genenames	GGA3



Protein Group ID: 400
Protein Accession Numbers: O75554; B7Z4M2
Gene Names: WBP4
Peptide Sequence: TVTSLGVMADGVAPVFK
Total Number of Spectra: 8
Number of Replicates (out of 8): 8
Best Match Score: 188.59
Best Match Posterior Error Probability: 3.08E-21
Best Match Spectrum:

Scan number 64833 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** WBP4



Protein Group ID: 403

Protein Accession Numbers: Q5VTE6; F5H476; Q5VTE6-2; B7Z5T0

Gene Names: ANGEL2

Peptide Sequence: LTQLAMLLAEISSVAHQK

Total Number of Spectra: 2

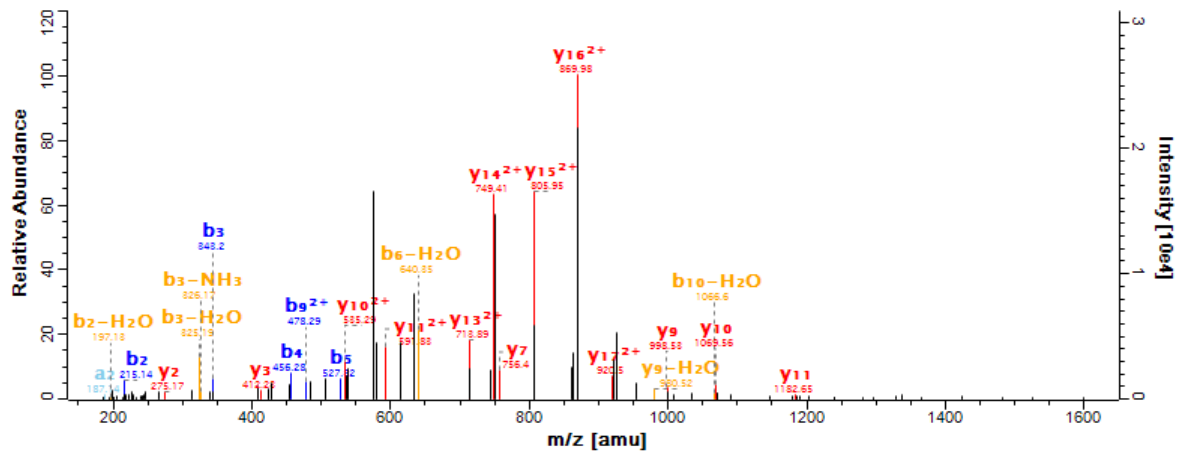
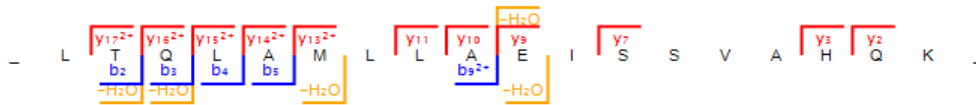
Number of Replicates (out of 8): 2

Best Match Score: 87.138

Best Match Posterior Error Probability: 0.0004486

Best Match Spectrum:

Scan number 91860 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ANGEL2



Protein Group ID: 410

Protein Accession Numbers: P51854; P51854-1; Q5TYJ8; B7Z7M4

Gene Names: TKTL1

Peptide Sequence: IGGLAESNINIIGSHCGVSVGDDGASQMALEDAIMFR

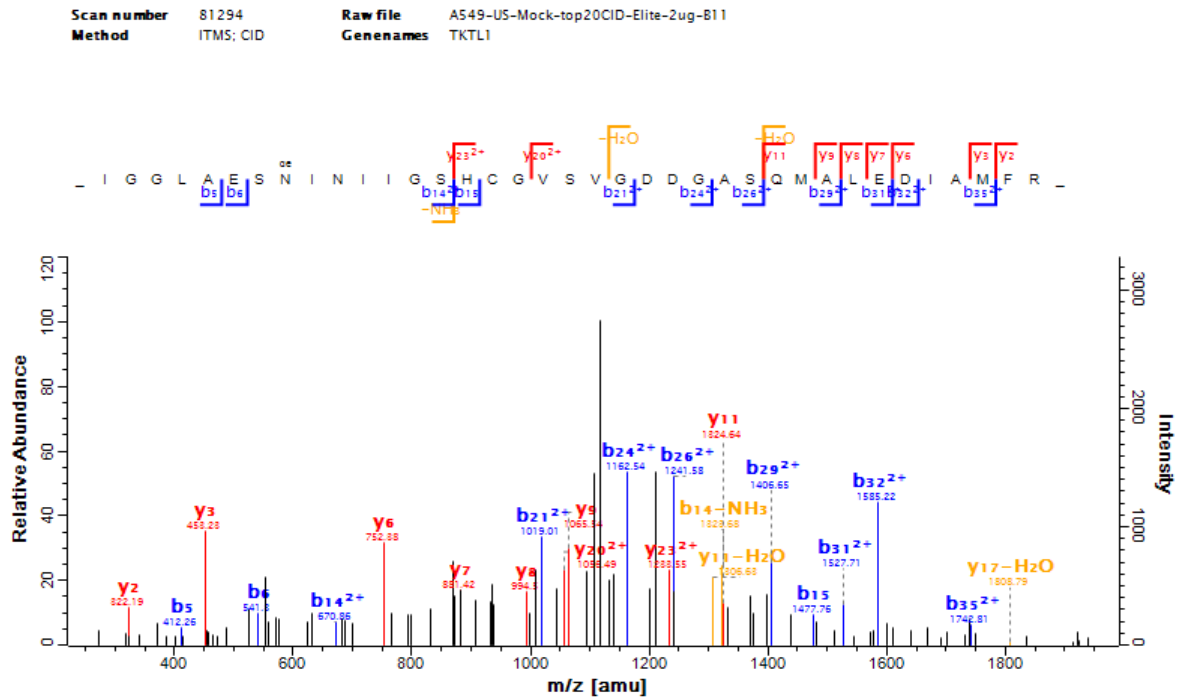
Total Number of Spectra: 1

Number of Replicates (out of 8): 1

Best Match Score: 55.442

Best Match Posterior Error Probability: 0.00034025

Best Match Spectrum:



Protein Group ID: 411

Protein Accession Numbers: Q14139-2; Q14139; B7Z7P0

Gene Names: UBE4A

Peptide Sequence: DAQQSSSPAADNLR

Total Number of Spectra: 1

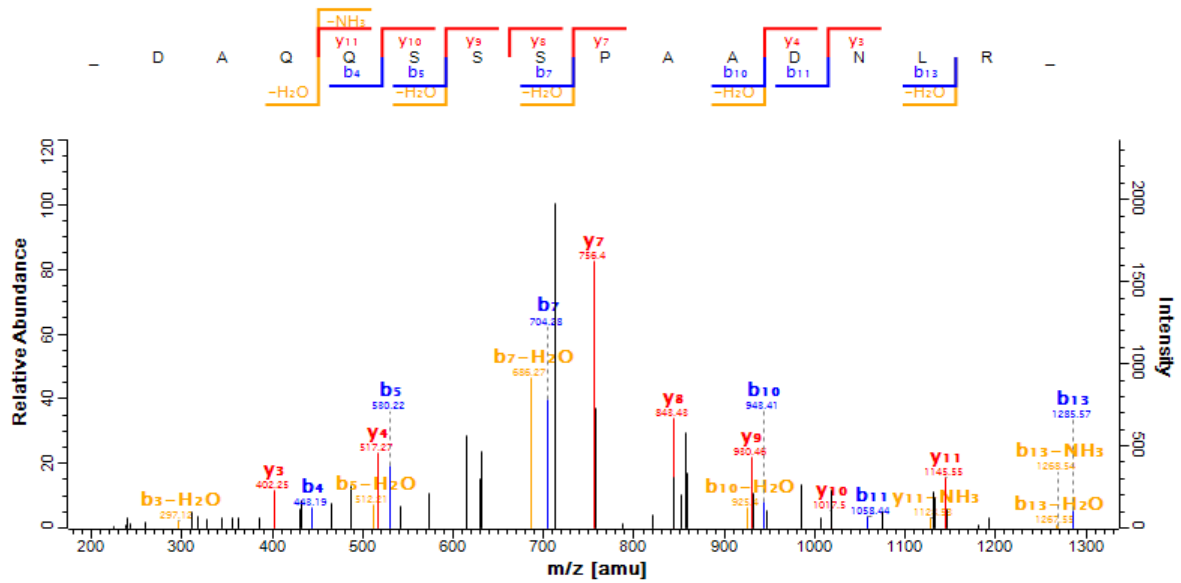
Number of Replicates (out of 8): 1

Best Match Score: 93.478

Best Match Posterior Error Probability: 0.00086622

Best Match Spectrum:

Scan number 9211 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** UBE4A



Protein Group ID: 414

Protein Accession Numbers: Q502W6-6; Q502W6; Q502W6-8; Q502W6-2; B7Z7Q7; H0YF54

Gene Names: VWA3B

Peptide Sequence: IIQFIQEQLK

Total Number of Spectra: 3

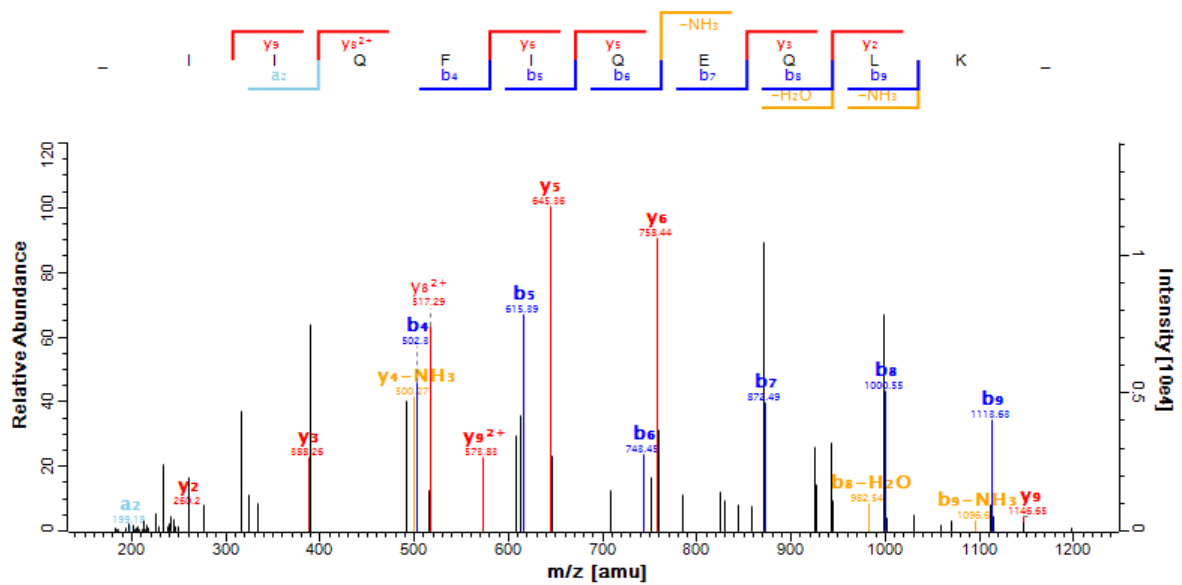
Number of Replicates (out of 8): 3

Best Match Score: 86.014

Best Match Posterior Error Probability: 0.0027897

Best Match Spectrum:

Scan number 63958 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** VWA3B



Protein Group ID: 420

Protein Accession Numbers: Q8NEY8; Q8NEY8-3; F8W0Q9; Q8NEY8-2; Q8NEY8-8; F8W6A0; E9PAX8; B7Z8L1; Q8NEY8-6; F8WF16; Q8NEY8-5; F8VWU8; F8VPY7

Gene Names: PPHLN1

Peptide Sequence: SFYSSHYAR

Total Number of Spectra: 3

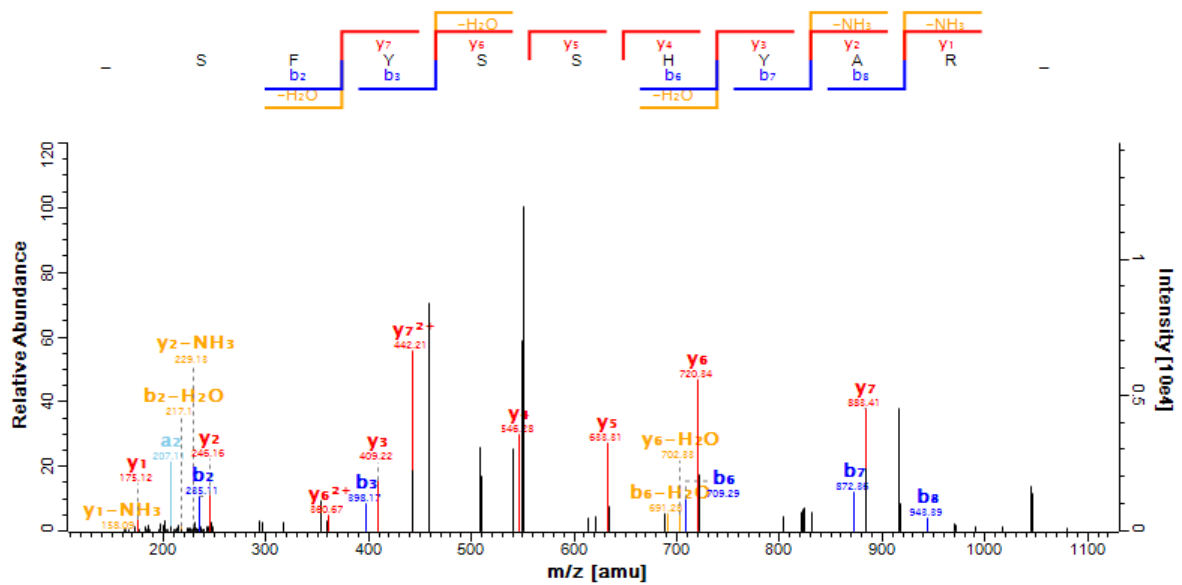
Number of Replicates (out of 8): 3

Best Match Score: 113.62

Best Match Posterior Error Probability: 0.0007746

Best Match Spectrum:

Scan number	13075	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	PPHLN1



Protein Group ID: 421

Protein Accession Numbers: Q4G0N4; Q4G0N4-2; B7Z8V7; Q4G0N4-3

Gene Names: NADKD1

Peptide Sequence: VTNEYNESLLYSPEEPK

Total Number of Spectra: 2

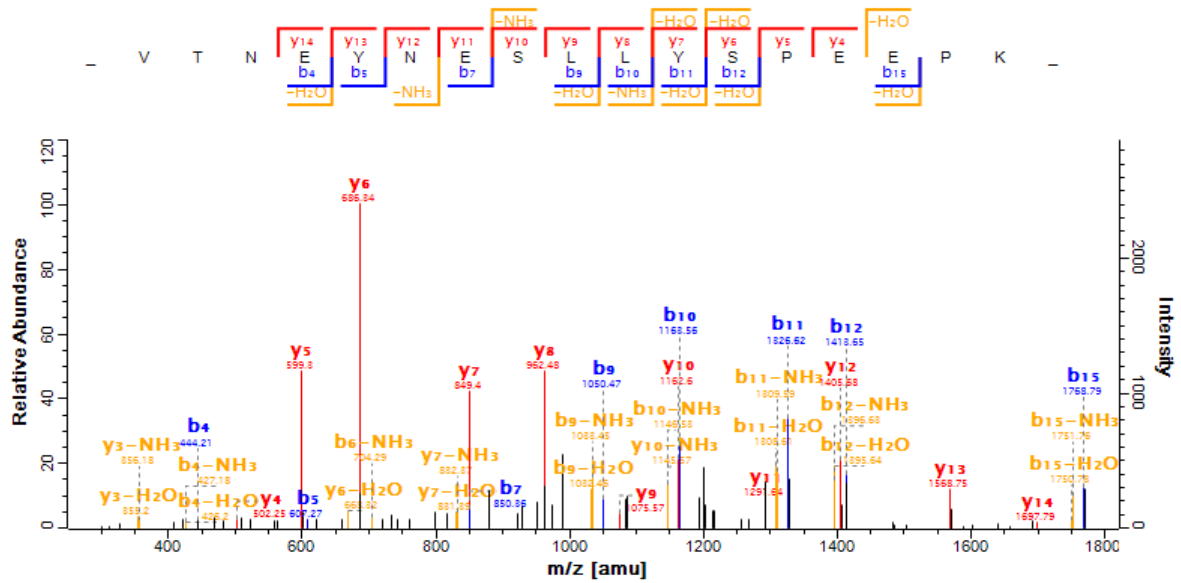
Number of Replicates (out of 8): 2

Best Match Score: 178

Best Match Posterior Error Probability: 8.09E-15

Best Match Spectrum:

Scan number 42372 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** NADKD1



Protein Group ID: 427

Protein Accession Numbers: Q9UPQ7; F5H8I9; B7ZAG0; Q9UPQ7-3; E7ENB6; C9JWE6; H7C566

Gene Names: PDZRN3

Peptide Sequence: IIQINGIEVQNR

Total Number of Spectra: 1

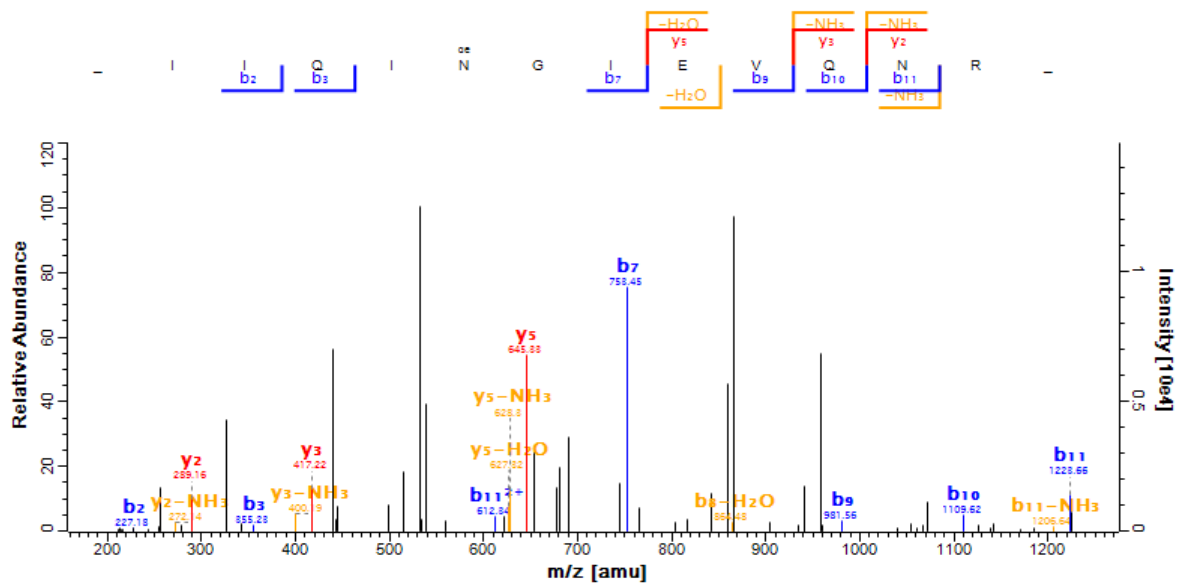
Number of Replicates (out of 8): 1

Best Match Score: 87.184

Best Match Posterior Error Probability: 0.0086204

Best Match Spectrum:

Scan number	92076	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	PDZRN3



Protein Group ID: 428

Protein Accession Numbers: F5H8B1; Q99447; I3L1R7; B7ZAS0; Q99447-2; I3L2Q1; I3L1C4; I3L1F9

Gene Names: PCYT2

Peptide Sequence: WVDEVVPAAPYVTTLETLDK

Total Number of Spectra: 1

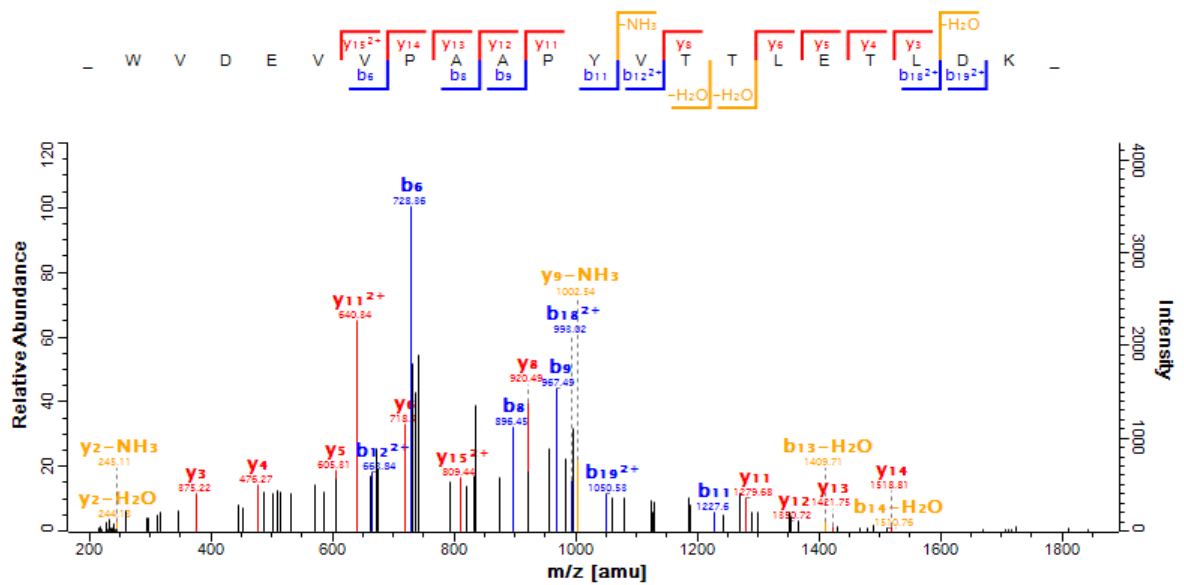
Number of Replicates (out of 8): 1

Best Match Score: 64.2

Best Match Posterior Error Probability: 0.0031511

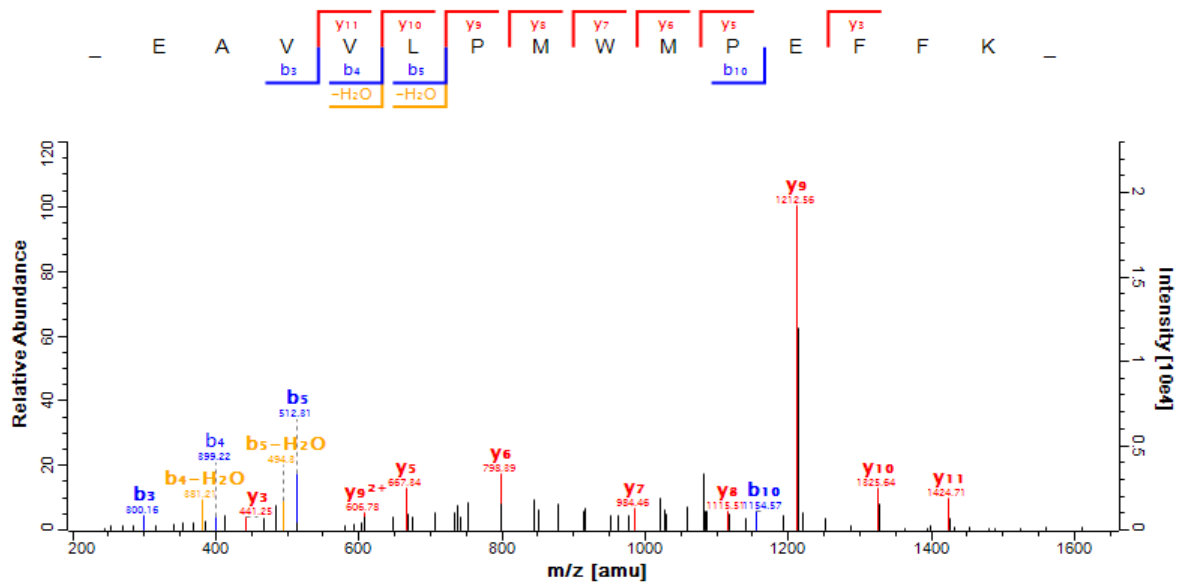
Best Match Spectrum:

Scan number	80388	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	PCYT2



Protein Group ID: 430
Protein Accession Numbers: O75449; B7ZBC8
Gene Names: KATNA1
Peptide Sequence: EAVVLPMWMPFFK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 96.591
Best Match Posterior Error Probability: 0.00056989
Best Match Spectrum:

Scan number 91438 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** KATNA1



Protein Group ID: 441

Protein Accession Numbers: Q17RY0; Q17RY0-2; B7ZLQ8; E5RJM0; E5RFP2; Q17RY0-3

Gene Names: CPEB4

Peptide Sequence: FGPLIVDWPBK

Total Number of Spectra: 1

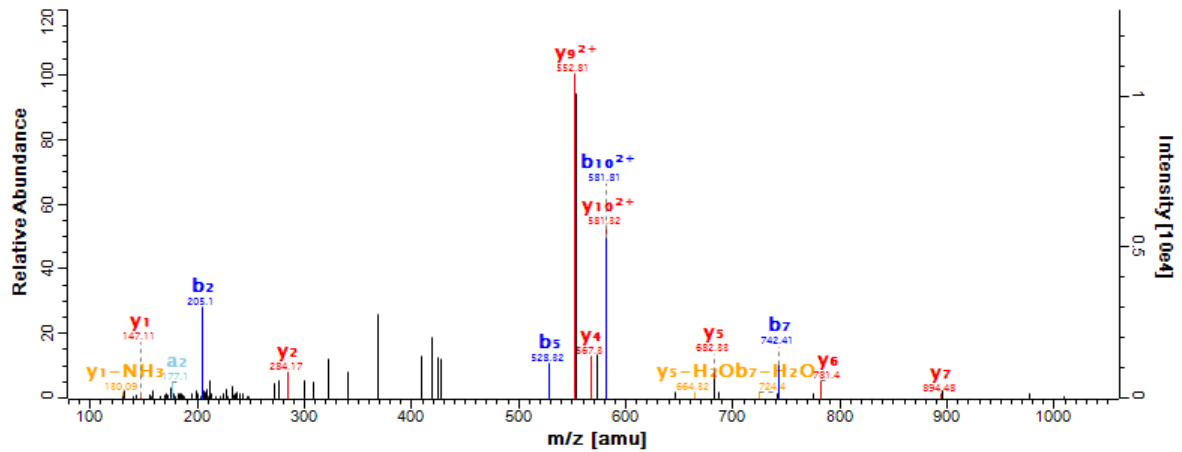
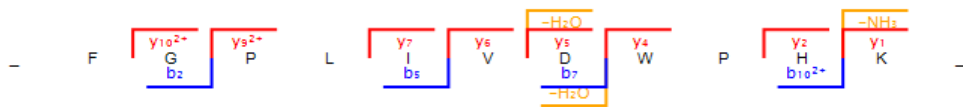
Number of Replicates (out of 8): 1

Best Match Score: 83.869

Best Match Posterior Error Probability: 0.0027702

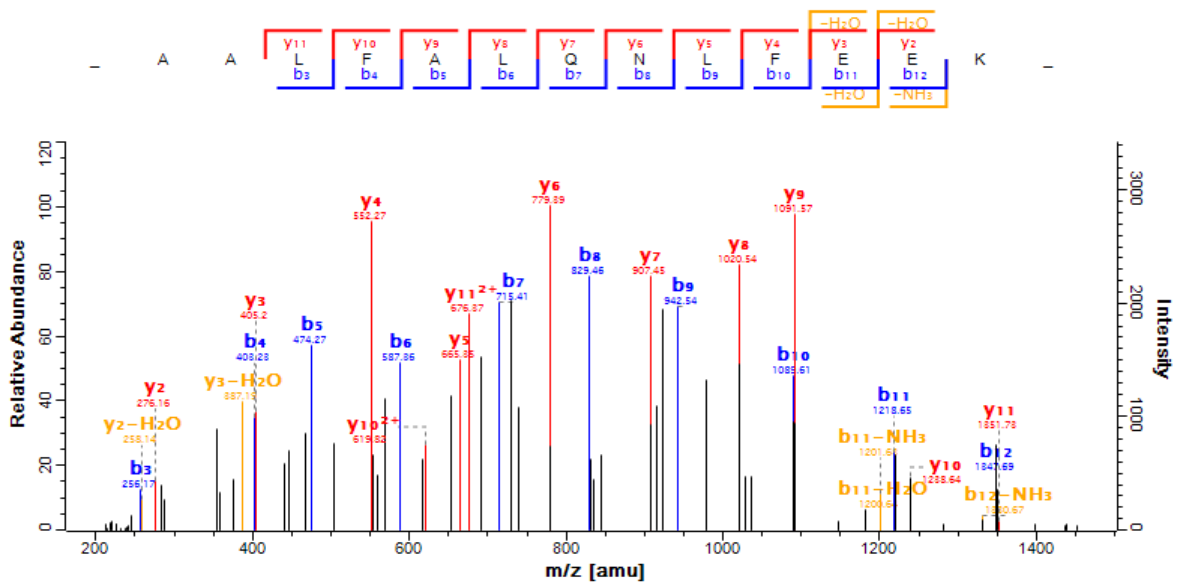
Best Match Spectrum:

Scan number	59237	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	CPEB4



Protein Group ID: 442
Protein Accession Numbers: Q99707; B7ZLW7
Gene Names: MTR
Peptide Sequence: AALFALQNLFE EK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 156.08
Best Match Posterior Error Probability: 1.53E-07
Best Match Spectrum:

Scan number 80668 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MTR



Protein Group ID: 445

Protein Accession Numbers: E9PGC5; B7ZMG0; Q5TG12; F5GXI4; Q15262-3; Q15262-2; Q15262; H0YDP9

Gene Names: PTPRK

Peptide Sequence: LWHLDPDTEYEIR

Total Number of Spectra: 1

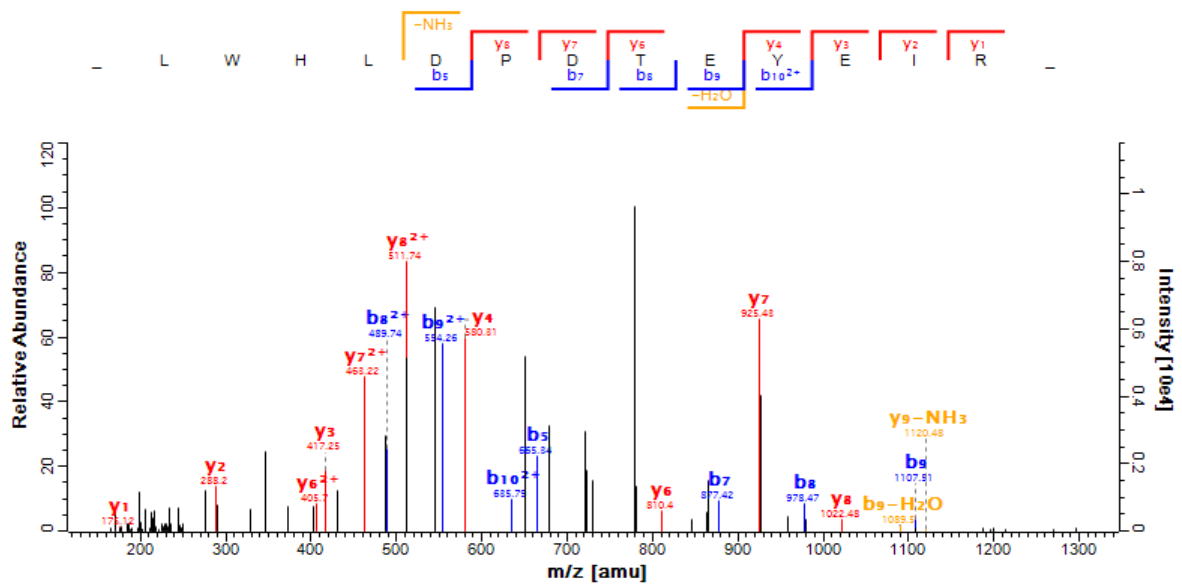
Number of Replicates (out of 8): 1

Best Match Score: 92.19

Best Match Posterior Error Probability: 0.0011858

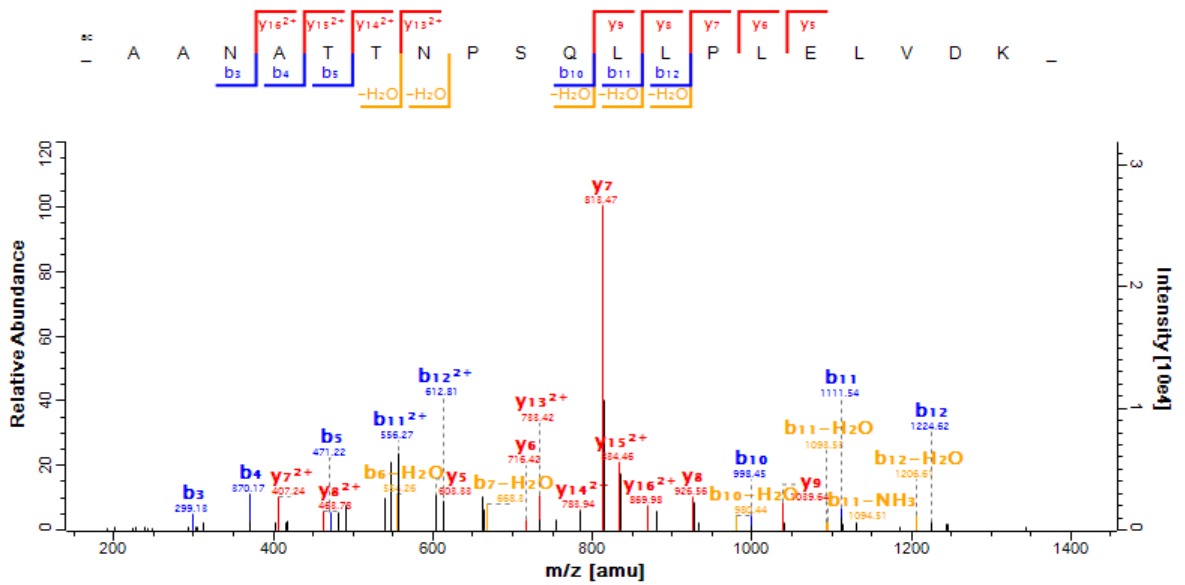
Best Match Spectrum:

Scan number	51633	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	PTPRK



Protein Group ID: 453
Protein Accession Numbers: Q9Y4Y9; B8ZZF8
Gene Names: LSM5
Peptide Sequence: AANATTNPSQLLPLELVDK
Total Number of Spectra: 8
Number of Replicates (out of 8): 6
Best Match Score: 112.3
Best Match Posterior Error Probability: 3.66E-05
Best Match Spectrum:

Scan number 77200 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** LSM5



Protein Group ID: 458

Protein Accession Numbers: Q8TCC3-2; Q8TCC3; Q8TCC3-3; B8ZZV5

Gene Names: MRPL30

Peptide Sequence: VFQASPEDHEK

Total Number of Spectra: 11

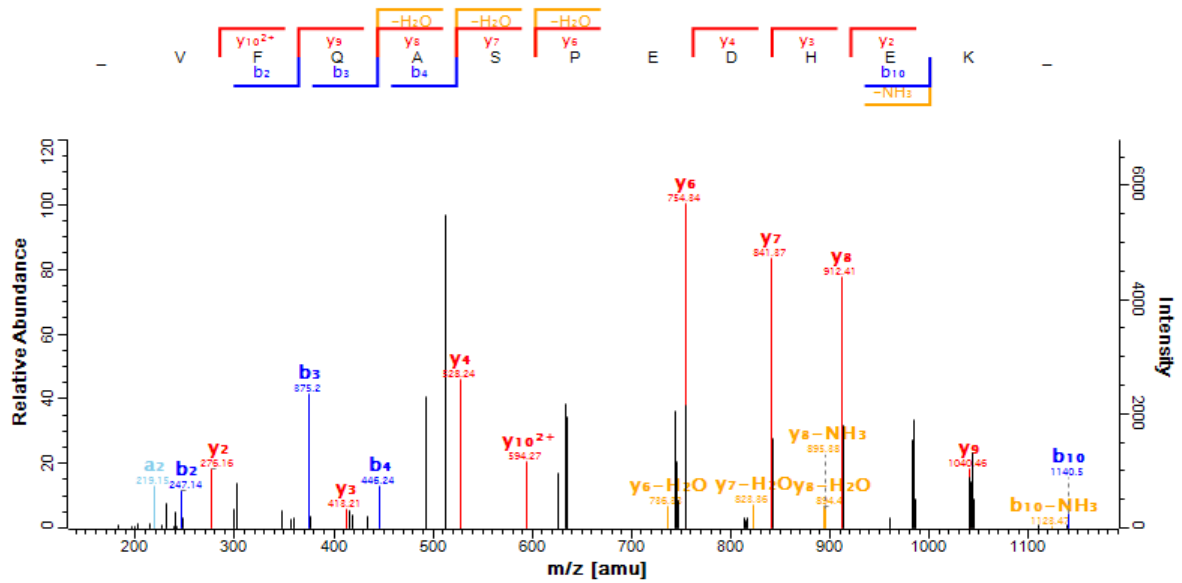
Number of Replicates (out of 8): 7

Best Match Score: 116.55

Best Match Posterior Error Probability: 9.10E-05

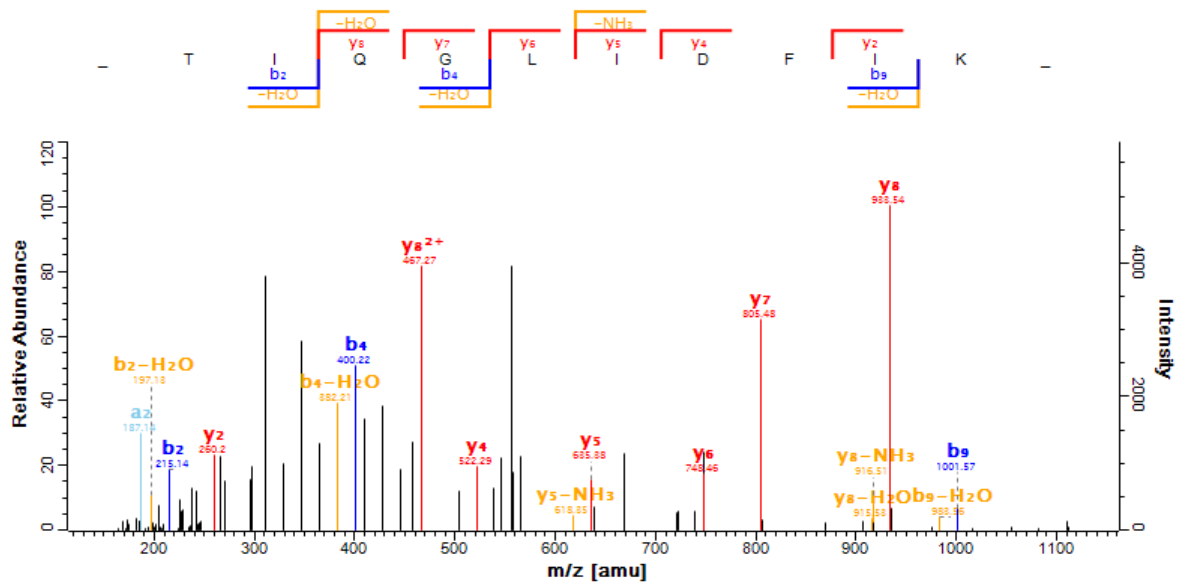
Best Match Spectrum:

Scan number 7138 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** MRPL30



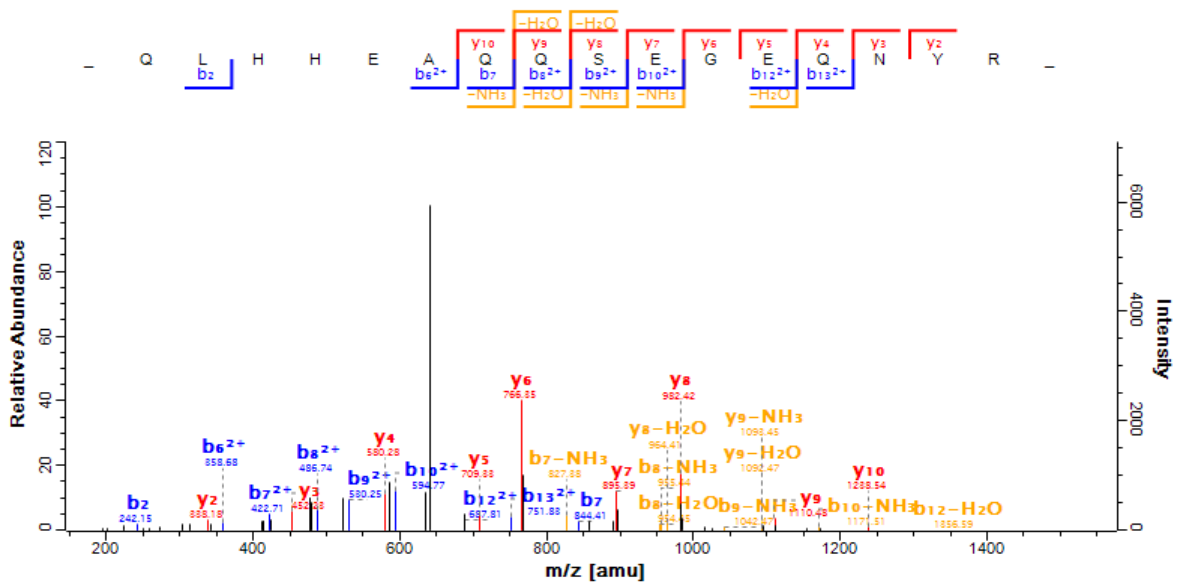
Protein Group ID: 465
Protein Accession Numbers: C1IDX9; O94817
Gene Names: ATG12
Peptide Sequence: TIQGLIDFIK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 115.78
Best Match Posterior Error Probability: 0.00021181
Best Match Spectrum:

Scan number 69458 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ATG12



Protein Group ID: 474
Protein Accession Numbers: P54278; I3L0B5; C9J167
Gene Names: PMS2
Peptide Sequence: QLHHEAQQSEGEQNYR
Total Number of Spectra: 8
Number of Replicates (out of 8): 6
Best Match Score: 104.55
Best Match Posterior Error Probability: 0.00013992
Best Match Spectrum:

Scan number 3254 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** PMS2



Protein Group ID: 477

Protein Accession Numbers: P52747; E7ER34; E7EN86; P52747-2; C9JTC5; E9PJF2; E9PMY8; E9PS81; E9PLN4; C9JRS3; E9PPB0; E9PLS7; C9JCG1; C9J2G7

Gene Names: ZNF143

Peptide Sequence: MLLAQINR

Total Number of Spectra: 1

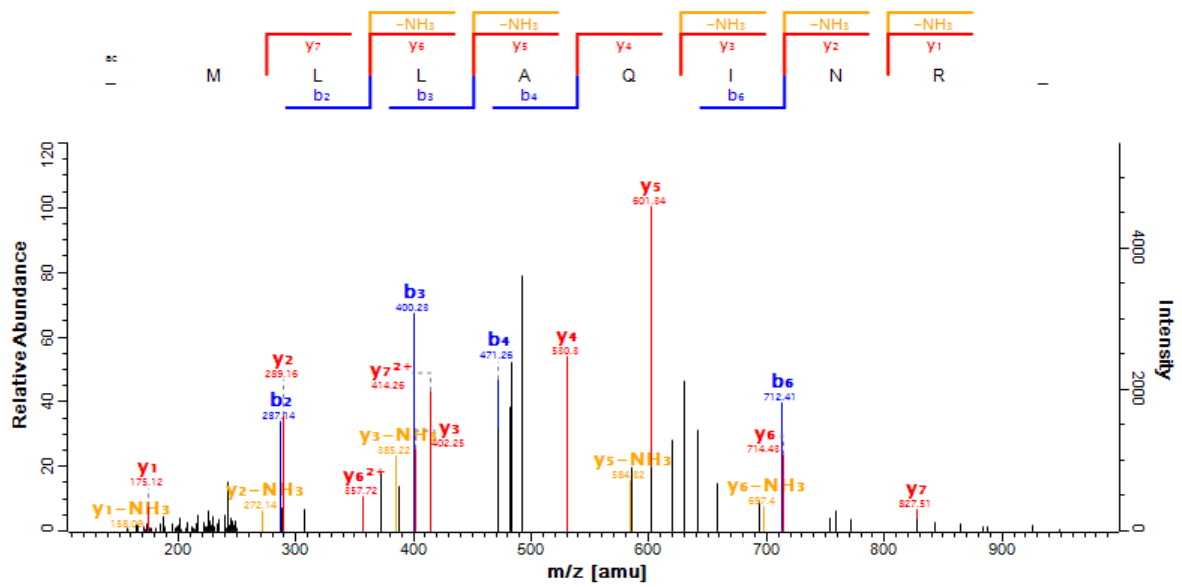
Number of Replicates (out of 8): 1

Best Match Score: 145.04

Best Match Posterior Error Probability: 0.0014018

Best Match Spectrum:

Scan number	61594	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	ZNF143



Protein Group ID: 479

Protein Accession Numbers: P51965; C9J8K2; H7C061; C9J2P0

Gene Names: UBE2E1

Peptide Sequence: ELADITLDPPPNC SAGPK

Total Number of Spectra: 7

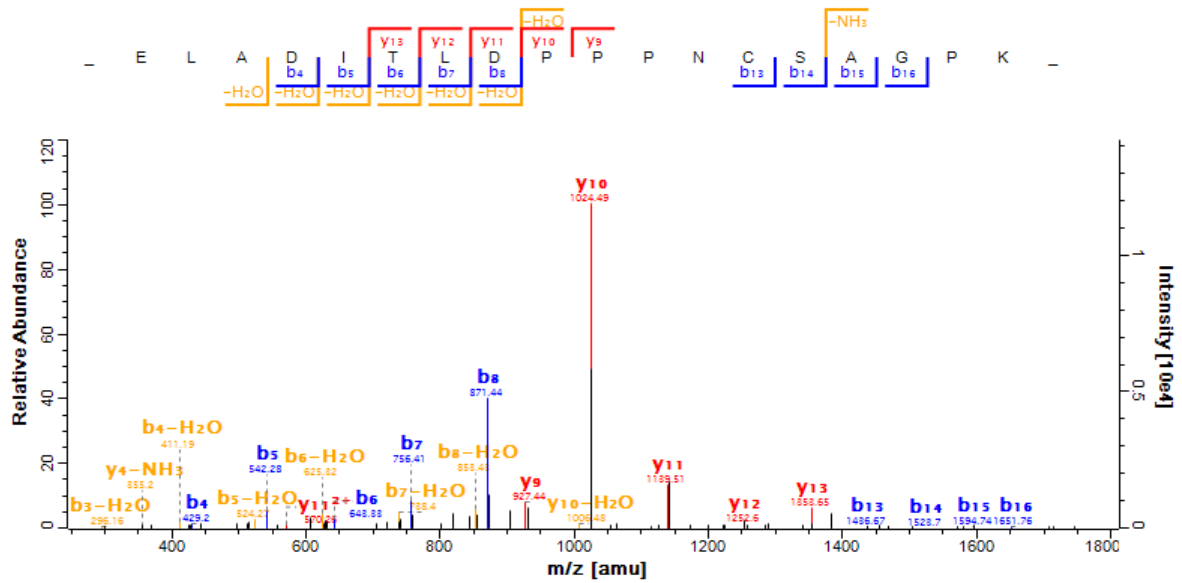
Number of Replicates (out of 8): 7

Best Match Score: 125.52

Best Match Posterior Error Probability: 4.86E-05

Best Match Spectrum:

Scan number 43966 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** UBE2E1



Protein Group ID: 488

Protein Accession Numbers: P10145-2; P10145; C9J4T6

Gene Names: IL8

Peptide Sequence: VIESGPHCANTEIIVK

Total Number of Spectra: 4

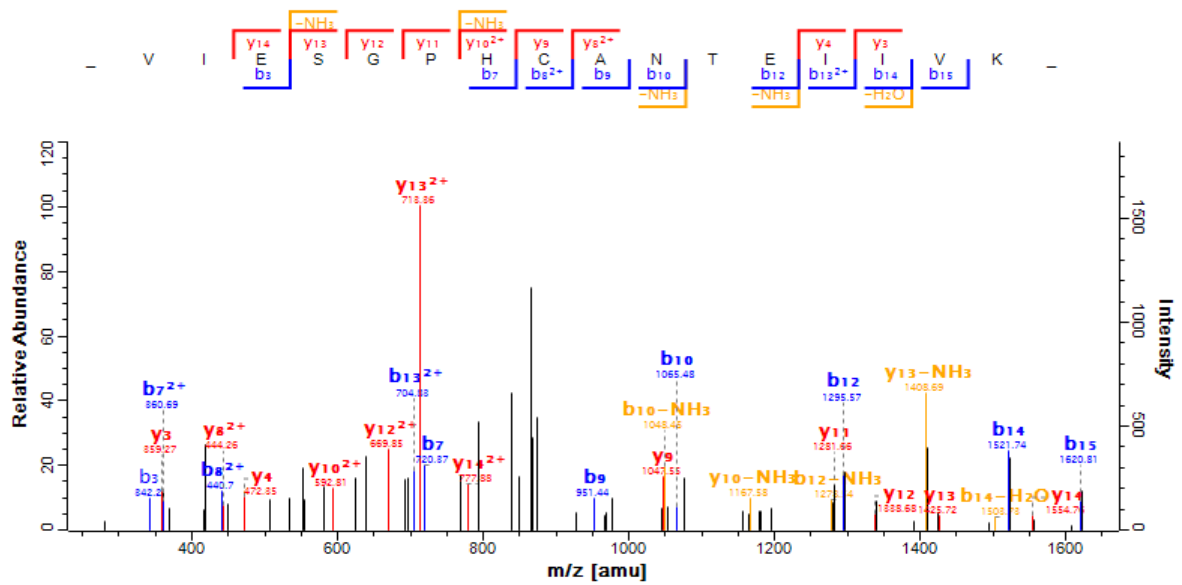
Number of Replicates (out of 8): 4

Best Match Score: 138.73

Best Match Posterior Error Probability: 2.89E-05

Best Match Spectrum:

Scan number	26563	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	IL8



Protein Group ID: 490

Protein Accession Numbers: Q96S97; C9JC07; C9J5M0; C9JZL8; C9JJV6

Gene Names: MYADM

Peptide Sequence: TTITTTTSSSGLGSPMIVGSPR

Total Number of Spectra: 11

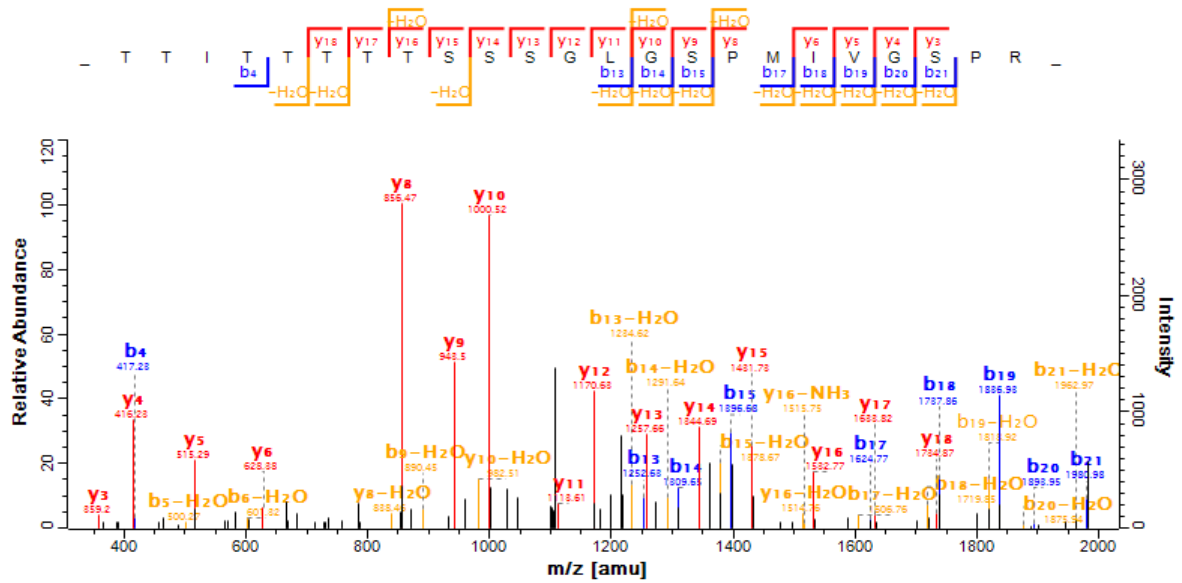
Number of Replicates (out of 8): 8

Best Match Score: 179.03

Best Match Posterior Error Probability: 9.43E-26

Best Match Spectrum:

Scan number 44761 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MYADM



Protein Group ID: 492

Protein Accession Numbers: Q9UI15; C9J5W6; H7C5N2

Gene Names: TAGLN3

Peptide Sequence: TTDIFQTVDLWEGK

Total Number of Spectra: 2

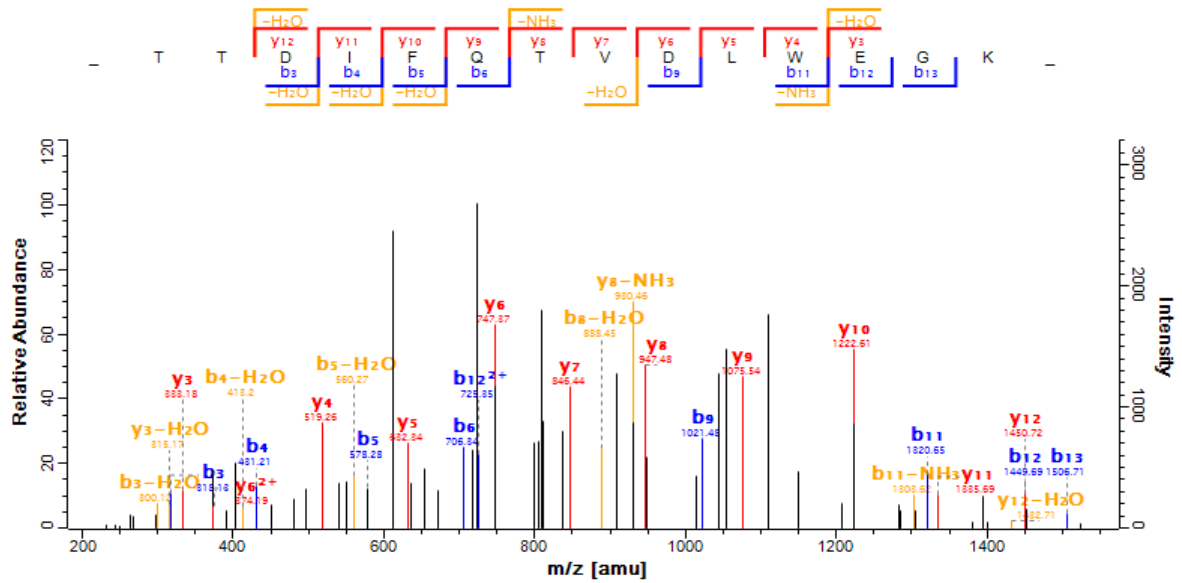
Number of Replicates (out of 8): 2

Best Match Score: 139.66

Best Match Posterior Error Probability: 2.22E-05

Best Match Spectrum:

Scan number 73030 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TAGLN3



Protein Group ID: 496

Protein Accession Numbers: Q9NQS3; E9PFR0; Q9NQS3-2; H7C4L0; C9JMW3; C9J795

Gene Names: PVRL3

Peptide Sequence: SSQTVAVHHPQYGFSVQGEYQGR

Total Number of Spectra: 3

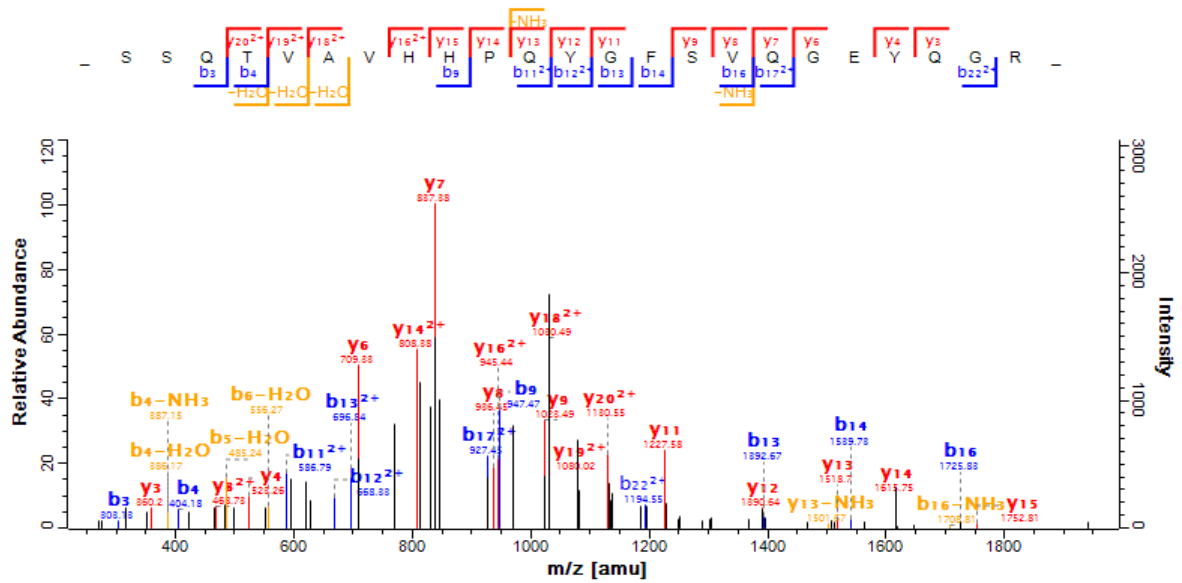
Number of Replicates (out of 8): 3

Best Match Score: 145.02

Best Match Posterior Error Probability: 4.40E-14

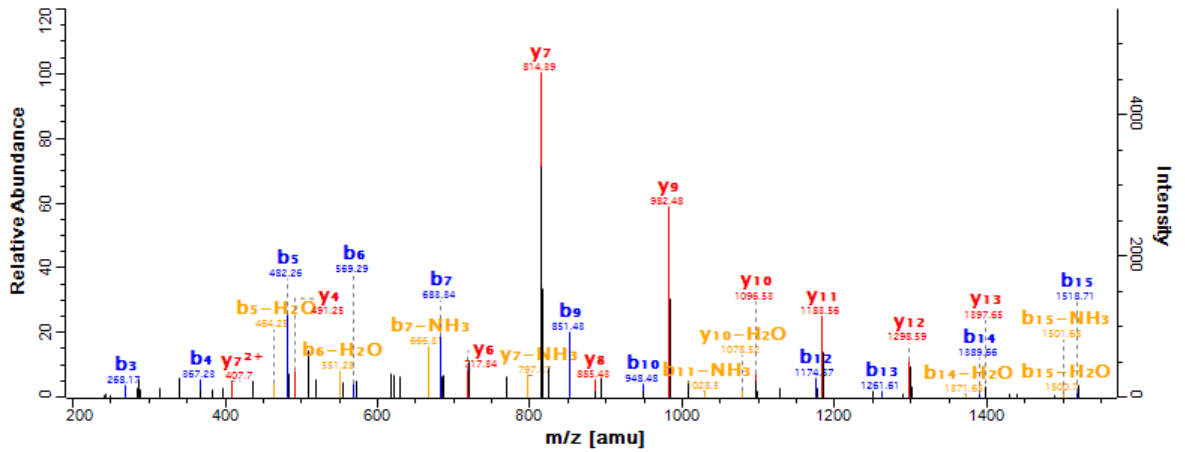
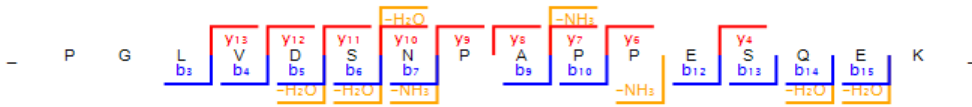
Best Match Spectrum:

Scan number 31426 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** PVRL3



Protein Group ID: 500
Protein Accession Numbers: C9J8T6; Q14061
Gene Names: COX17
Peptide Sequence: PGLVDSNPAPPESQEK
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 147.64
Best Match Posterior Error Probability: 1.71E-06
Best Match Spectrum:

Scan number 21109 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** COX17



Protein Group ID: 502

Protein Accession Numbers: E7EUN2; Q96P47-4; Q96P47-2; Q96P47; Q9UPQ3; Q9UPQ3-2; E7ESL9; Q9UPQ3-3; E9PAL8; Q96P47-3; C9J975; H7C4F1; C9J8Z2

Gene Names: AGAP1;AGAP3

Peptide Sequence: YLTGTYYVQEQESPEGR

Total Number of Spectra: 1

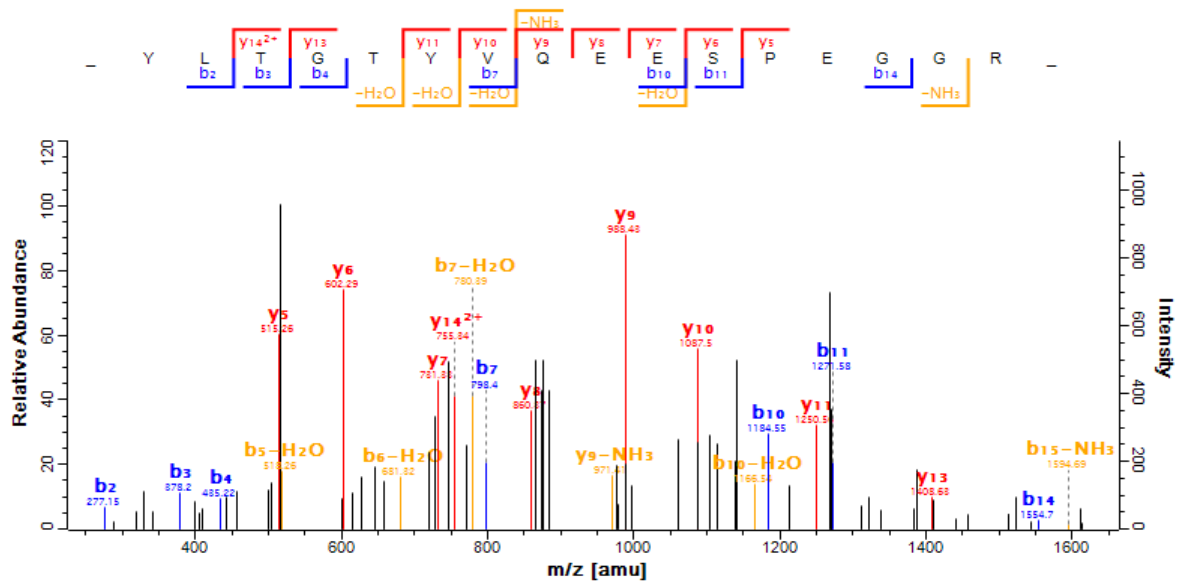
Number of Replicates (out of 8): 1

Best Match Score: 76.341

Best Match Posterior Error Probability: 0.0027146

Best Match Spectrum:

Scan number	29452	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	AGAP1;AGAP3



Protein Group ID: 504

Protein Accession Numbers: P51668; Q9Y2X8; C9J9H9; Q9UQL0; H0YGA2

Gene Names: UBE2D1;UBE2D4

Peptide Sequence: SQWSPALTVSK

Total Number of Spectra: 1

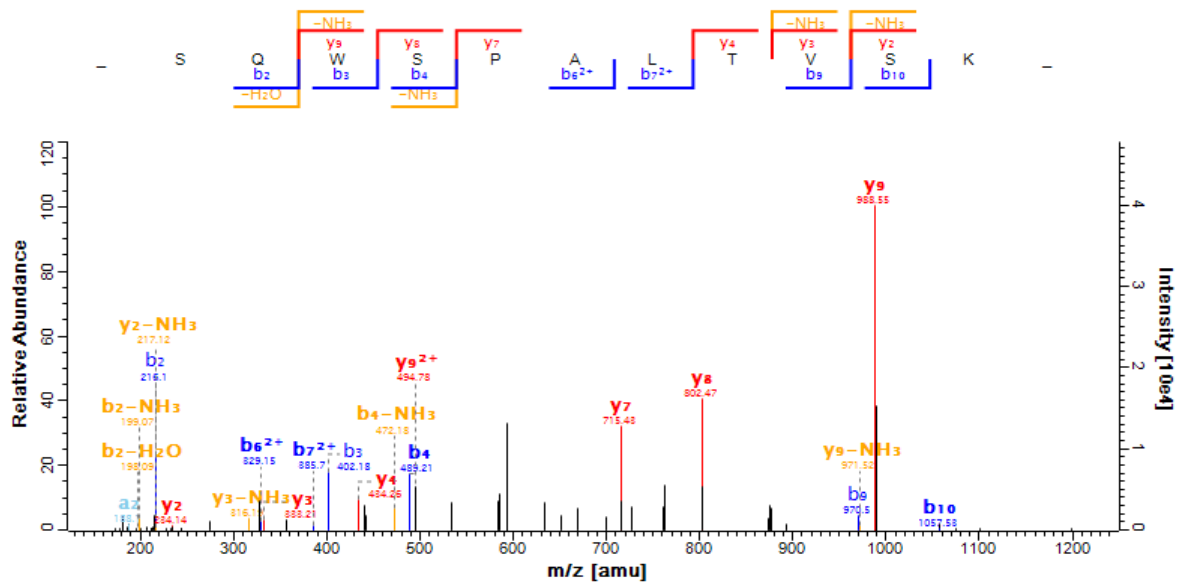
Number of Replicates (out of 8): 1

Best Match Score: 92.247

Best Match Posterior Error Probability: 0.0012443

Best Match Spectrum:

Scan number 35233 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** UBE2D1;UBE2D4



Protein Group ID: 507

Protein Accession Numbers: P18564; E9PEE8; C9JA97

Gene Names: ITGB6

Peptide Sequence: LGFGSFVEK

Total Number of Spectra: 8

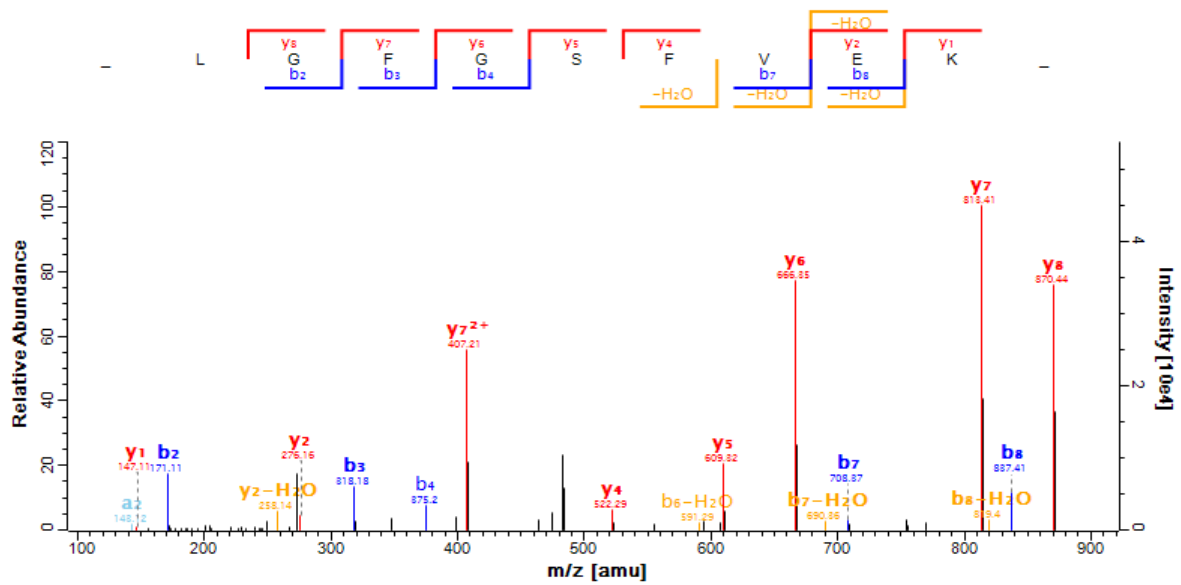
Number of Replicates (out of 8): 8

Best Match Score: 132.01

Best Match Posterior Error Probability: 9.50E-05

Best Match Spectrum:

Scan number	43640	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	ITGB6



Protein Group ID: 511

Protein Accession Numbers: Q6H3X3; Q5VY80; Q9BZM5; C9JAK3; Q6H3X3-2

Gene Names: RAET1G;RAET1L;ULBP2

Peptide Sequence: WCAVQGGVDEK

Total Number of Spectra: 1

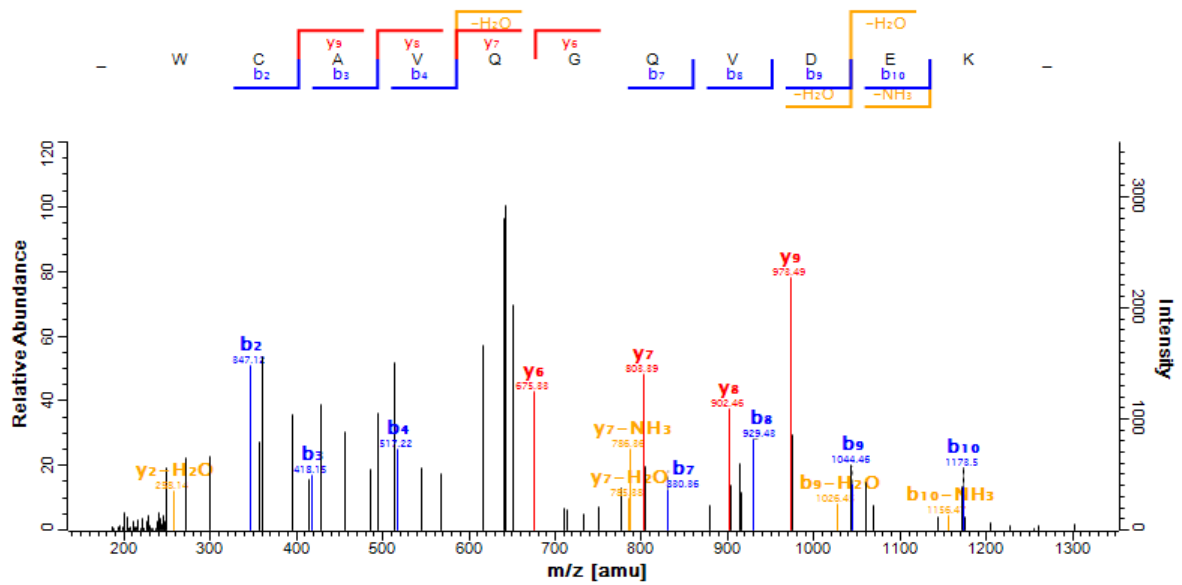
Number of Replicates (out of 8): 1

Best Match Score: 79.659

Best Match Posterior Error Probability: 0.0040191

Best Match Spectrum:

Scan number 18989 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** RAET1G;RAET1L;ULBP2



Protein Group ID: 512

Protein Accession Numbers: C9JNU6; Q9Y241; C9JAW5

Gene Names: HIGD1A

Peptide Sequence: STDTGVSLPSYEEDQGSK

Total Number of Spectra: 6

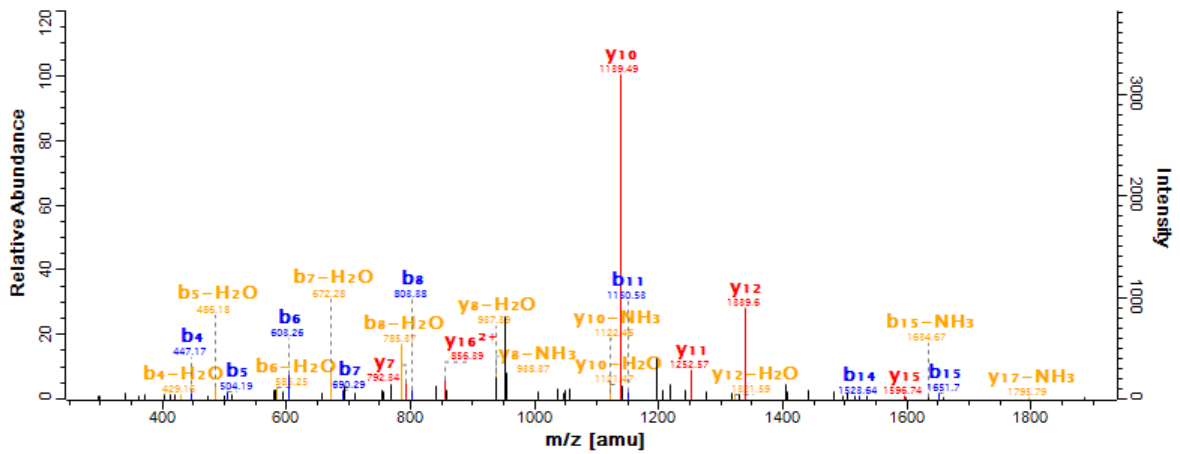
Number of Replicates (out of 8): 6

Best Match Score: 123.42

Best Match Posterior Error Probability: 7.49E-05

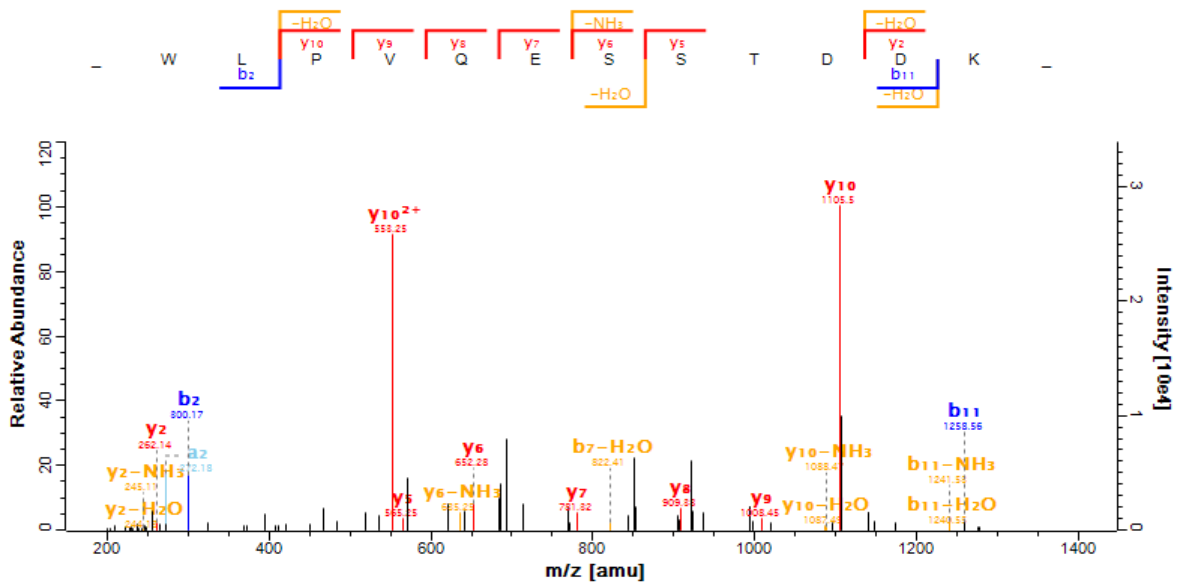
Best Match Spectrum:

Scan number 39668 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** HIGD1A



Protein Group ID: 516
Protein Accession Numbers: Q9Y6A9; C9JBL1
Gene Names: SPCS1
Peptide Sequence: WLPVQESSTDDK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 78.903
Best Match Posterior Error Probability: 0.0036177
Best Match Spectrum:

Scan number 28921 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** SPCS1



Protein Group ID: 521

Protein Accession Numbers: Q9BVT8; C9JCW7; C9JE12

Gene Names: TMUB1

Peptide Sequence: HRGQAAQPEPSTGFTATPPAPDPSPEPLVLR

Total Number of Spectra: 7

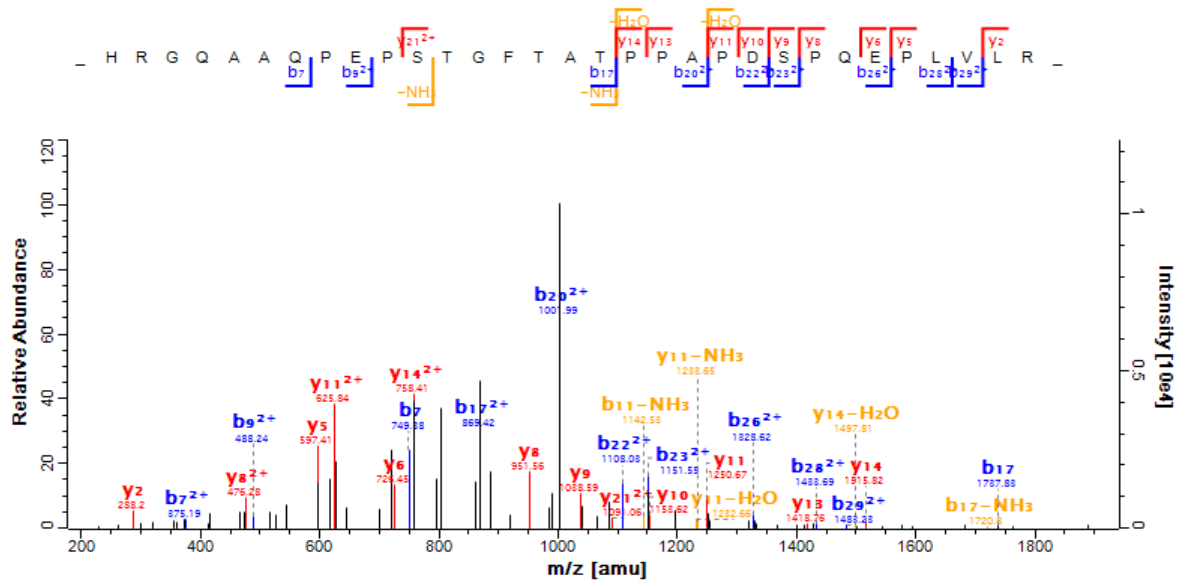
Number of Replicates (out of 8): 7

Best Match Score: 94.72

Best Match Posterior Error Probability: 3.32E-07

Best Match Spectrum:

Scan number 46131 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TMUB1



Protein Group ID: 522

Protein Accession Numbers: Q8WW22-2; Q8WW22; E9PDM9; F5H170; C9JDE6

Gene Names: DNAJA4

Peptide Sequence: NVVHQLSVTLEDL YGVTK

Total Number of Spectra: 1

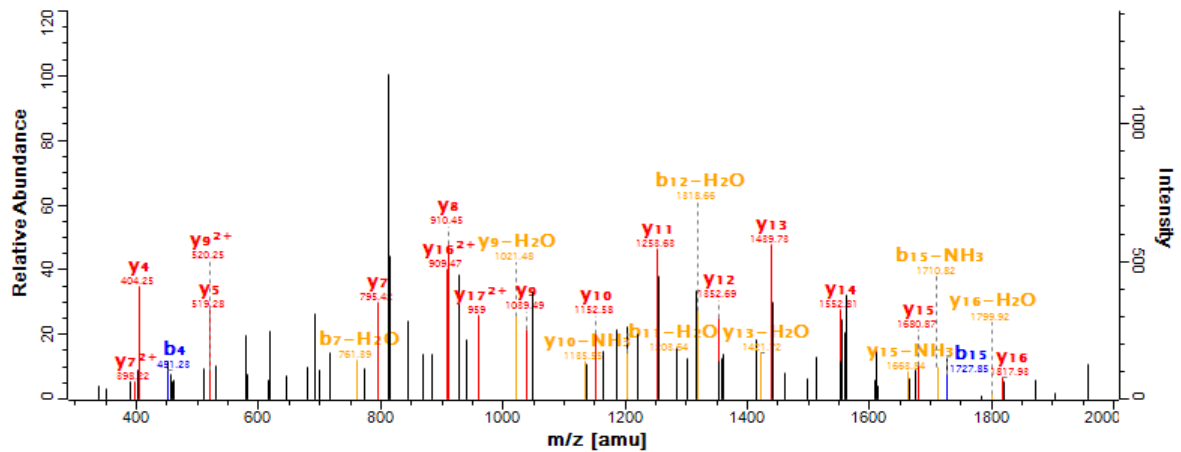
Number of Replicates (out of 8): 1

Best Match Score: 103.88

Best Match Posterior Error Probability: 0.00058402

Best Match Spectrum:

Scan number	69374	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	DNAJA4



Protein Group ID: 528

Protein Accession Numbers: Q8IX18; Q8IX18-2; C9JEW8; Q8IX18-3; C9JR60; F5H625

Gene Names: DHX40

Peptide Sequence: LGLDILEVVPISK

Total Number of Spectra: 4

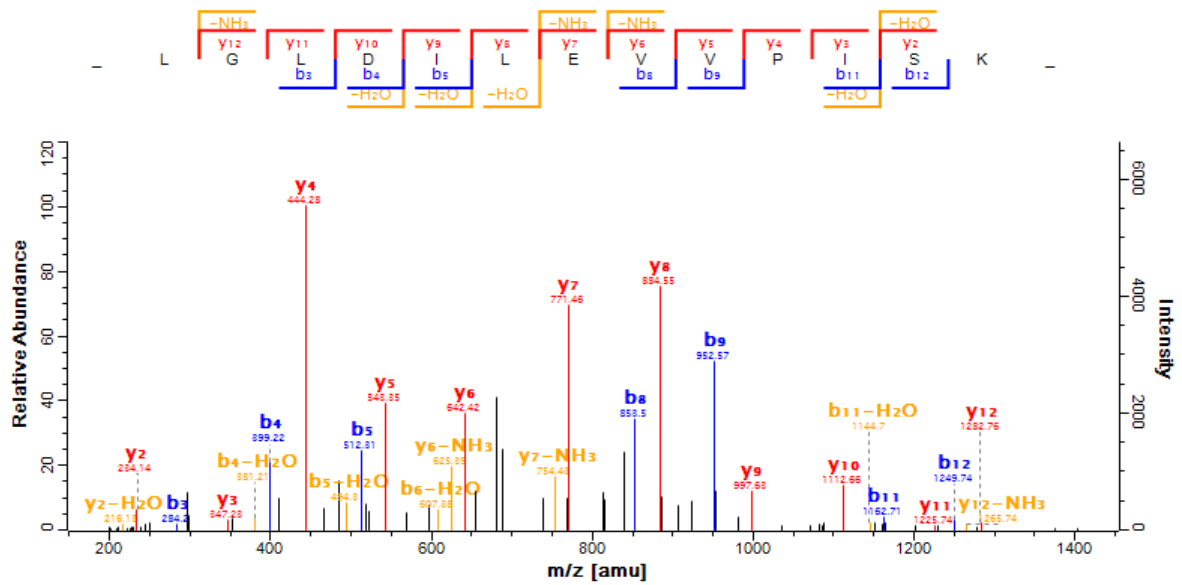
Number of Replicates (out of 8): 3

Best Match Score: 161.21

Best Match Posterior Error Probability: 2.12E-09

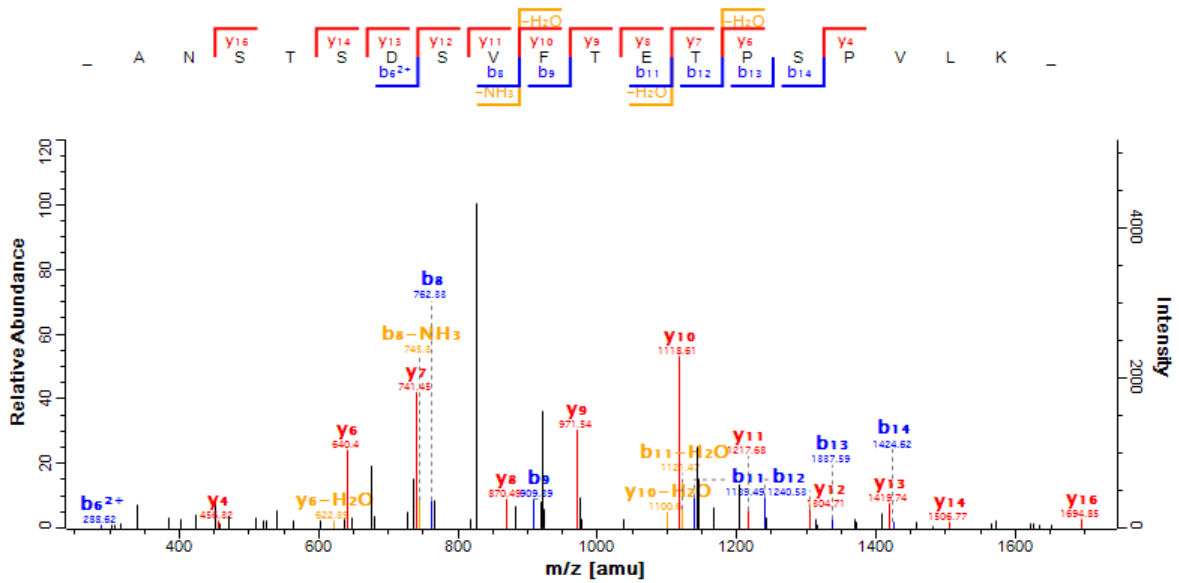
Best Match Spectrum:

Scan number 79266 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** DHX40



Protein Group ID: 529
Protein Accession Numbers: Q9UKI2; C9JEZ4
Gene Names: CDC42EP3
Peptide Sequence: ANSTSDSVFTETPSPVLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 77.969
Best Match Posterior Error Probability: 0.0014644
Best Match Spectrum:

Scan number 44766 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CDC42EP3



Protein Group ID: 536

Protein Accession Numbers: P30039; C9JIM0; F8W7D0

Gene Names: PBLD

Peptide Sequence: LPIFIADAFTAR

Total Number of Spectra: 1

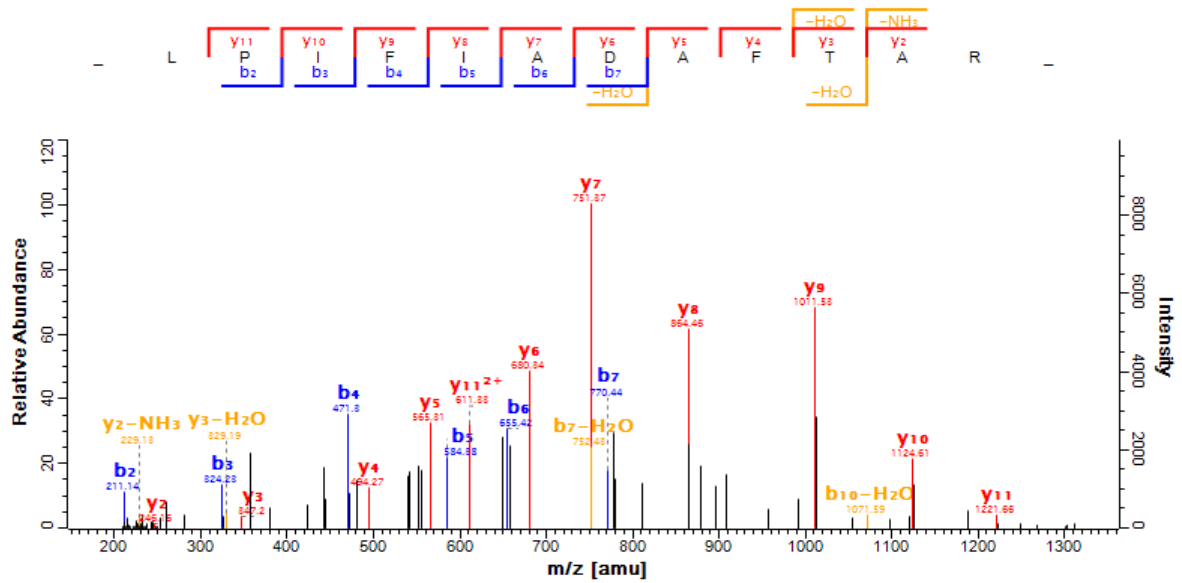
Number of Replicates (out of 8): 1

Best Match Score: 111.94

Best Match Posterior Error Probability: 0.0011698

Best Match Spectrum:

Scan number	76033	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	PBLD



Protein Group ID: 540

Protein Accession Numbers: Q9NVE5-3; Q9NVE5; C9JK14

Gene Names: USP40

Peptide Sequence: EALFSLGPEELGLFEDK

Total Number of Spectra: 1

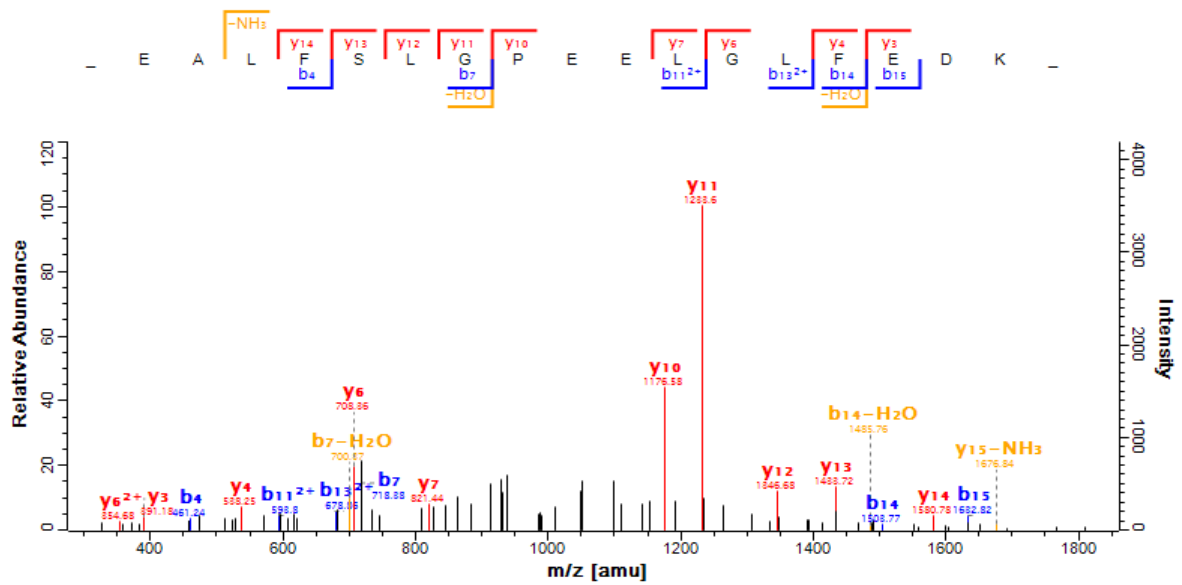
Number of Replicates (out of 8): 1

Best Match Score: 74.12

Best Match Posterior Error Probability: 0.0028163

Best Match Spectrum:

Scan number 85096 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** USP40



Protein Group ID: 541

Protein Accession Numbers: Q9Y4F3; Q9Y4F3-5; Q9Y4F3-4; Q9Y4F3-3; G8JLP4; C9JKX0; F8VVB8

Gene Names: KIAA0430

Peptide Sequence: AVVQMENLQDAIGAVNSLHR

Total Number of Spectra: 1

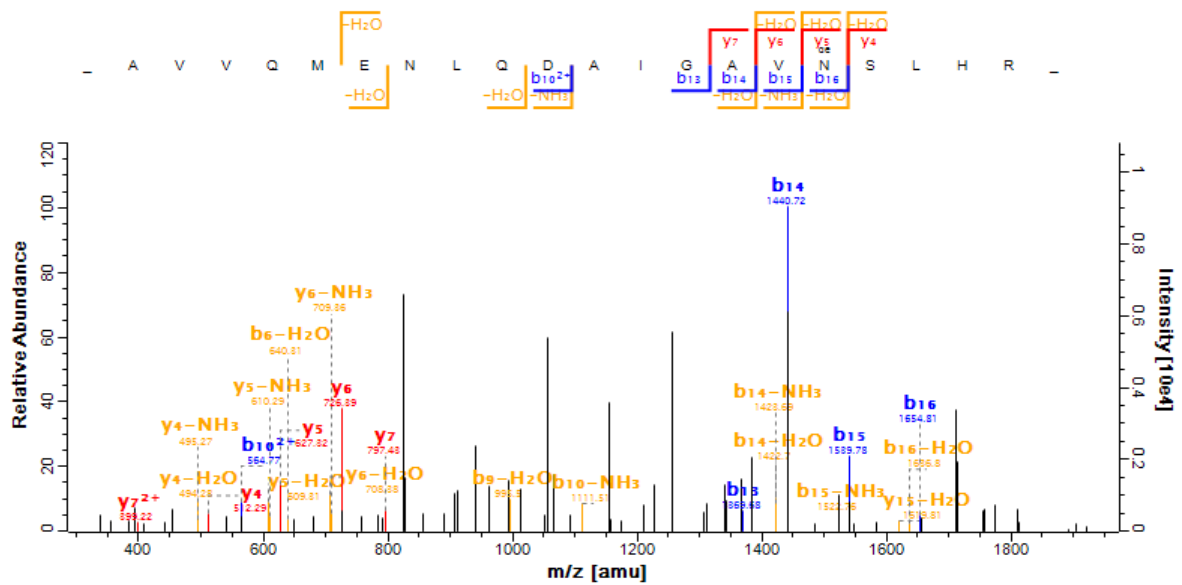
Number of Replicates (out of 8): 1

Best Match Score: 72.207

Best Match Posterior Error Probability: 0.0073584

Best Match Spectrum:

Scan number 66911 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** KIAA0430



Protein Group ID: 545

Protein Accession Numbers: Q9BQ15; C9JMP5; C9JT95

Gene Names: OBFC2B

Peptide Sequence: IGEFCMVYSEVPNFSEVPNPEYSTQQAQAPNK

Total Number of Spectra: 3

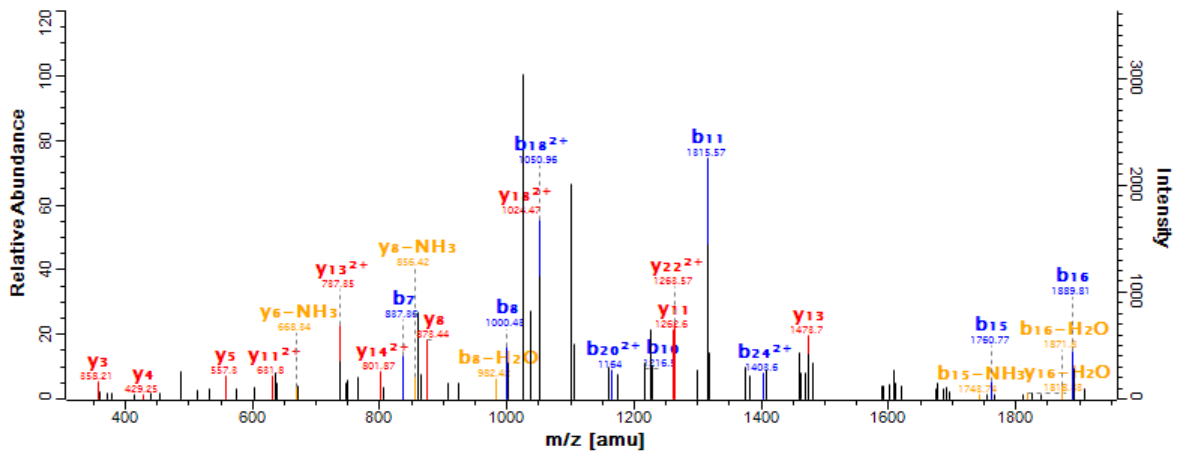
Number of Replicates (out of 8): 2

Best Match Score: 72.302

Best Match Posterior Error Probability: 3.40E-05

Best Match Spectrum:

Scan number 68077 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** OBFC2B



Protein Group ID: 549

Protein Accession Numbers: Q96IW7; C9JNZ0; C9JRY4

Gene Names: SEC22A

Peptide Sequence: INLSDMQTEIK

Total Number of Spectra: 2

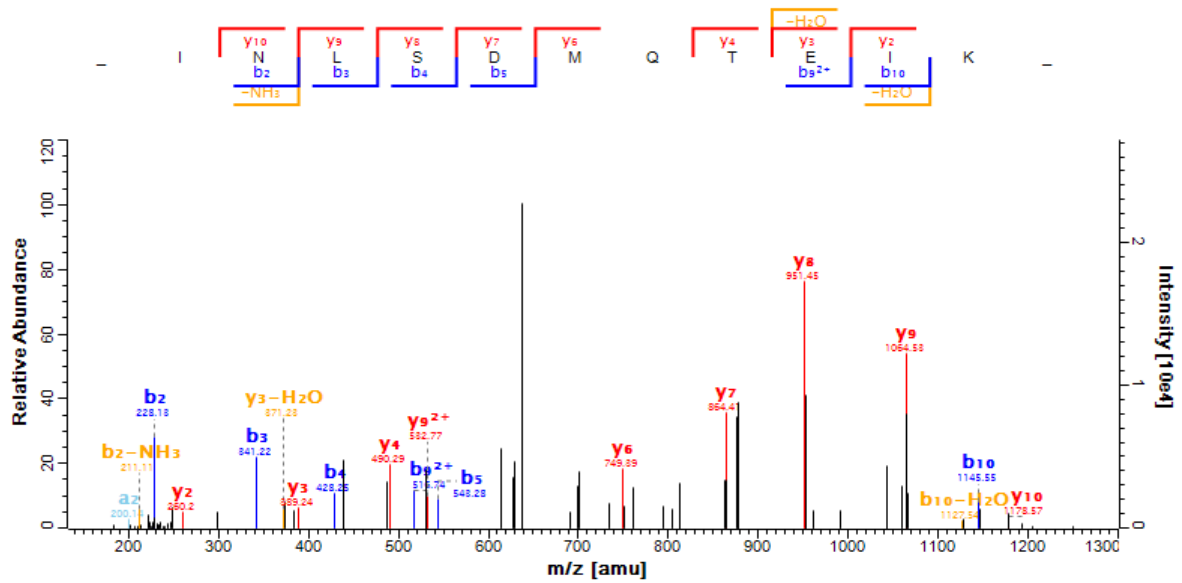
Number of Replicates (out of 8): 2

Best Match Score: 100.04

Best Match Posterior Error Probability: 0.00051486

Best Match Spectrum:

Scan number	43478	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	SEC22A



Protein Group ID: 551

Protein Accession Numbers: H7BXP1; Q9NYR9; C9JPP2; Q9NYR9-2; K7ERG2; Q9NYR9-3

Gene Names: NKIRAS2

Peptide Sequence: SLLEPFVYLSK

Total Number of Spectra: 2

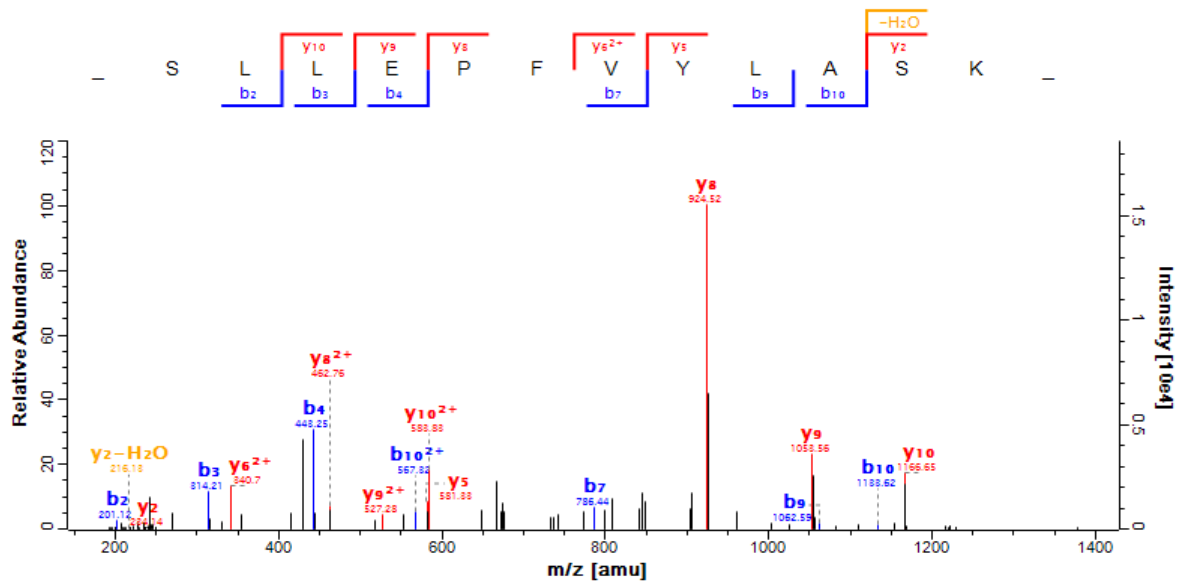
Number of Replicates (out of 8): 2

Best Match Score: 87.001

Best Match Posterior Error Probability: 0.0017681

Best Match Spectrum:

Scan number	76608	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	NKIRAS2



Protein Group ID: 559

Protein Accession Numbers: C9JRZ8

Gene Names: AKR1B15

Peptide Sequence: VLQMEPQVNSTNNFHHQGPLDQPVGPLTGLK

Total Number of Spectra: 1

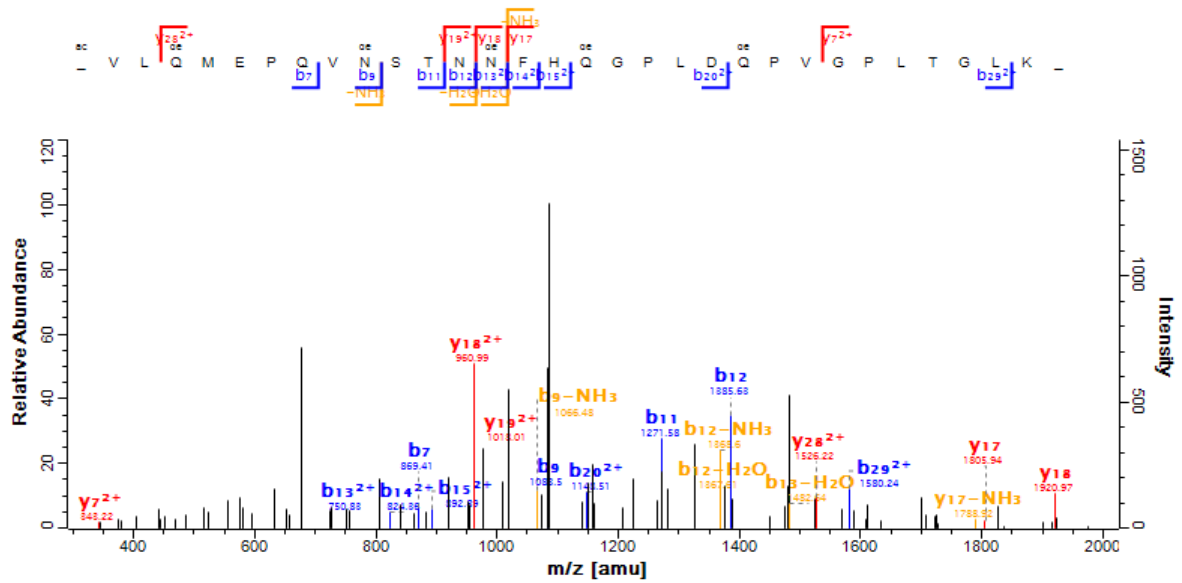
Number of Replicates (out of 8): 1

Best Match Score: 55.526

Best Match Posterior Error Probability: 0.010706

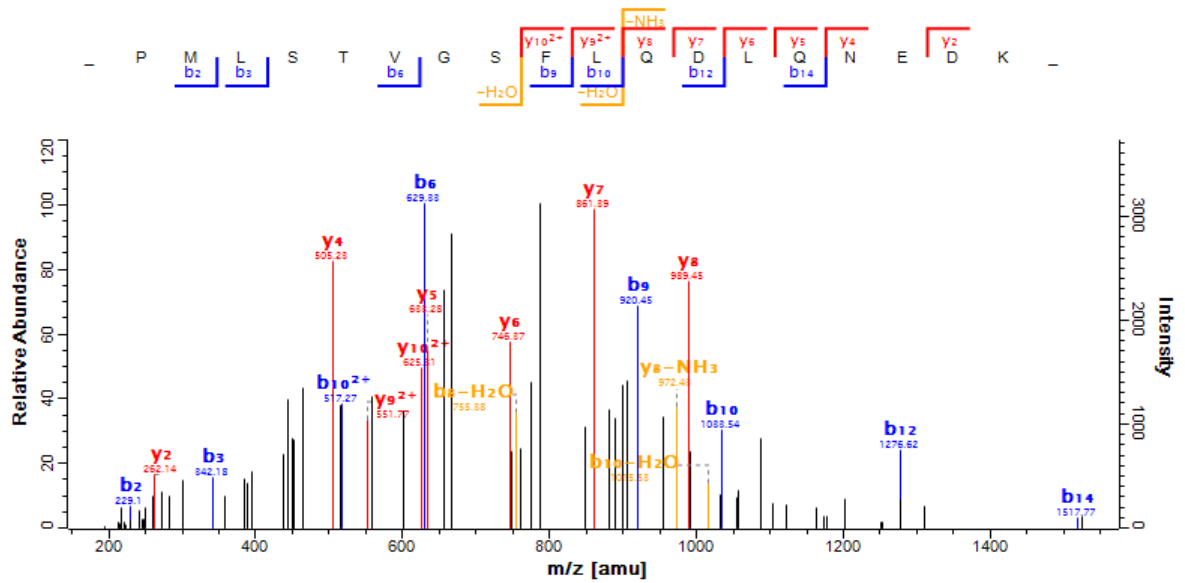
Best Match Spectrum:

Scan number 31724 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** AKR1B15



Protein Group ID: 560
Protein Accession Numbers: Q9NWR8; C9JTJ6
Gene Names: CCDC109B
Peptide Sequence: PMLSTVGSFLQLQNK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 74.428
Best Match Posterior Error Probability: 0.0021238
Best Match Spectrum:

Scan number 84990 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CCDC109B



Protein Group ID: 562

Protein Accession Numbers: P08962; C9JV86; F8VWK8; F8W022; P08962-2; F8VZE2; F8VV56; F8VNT9

Gene Names: CD63

Peptide Sequence: VMSEFNNFR

Total Number of Spectra: 6

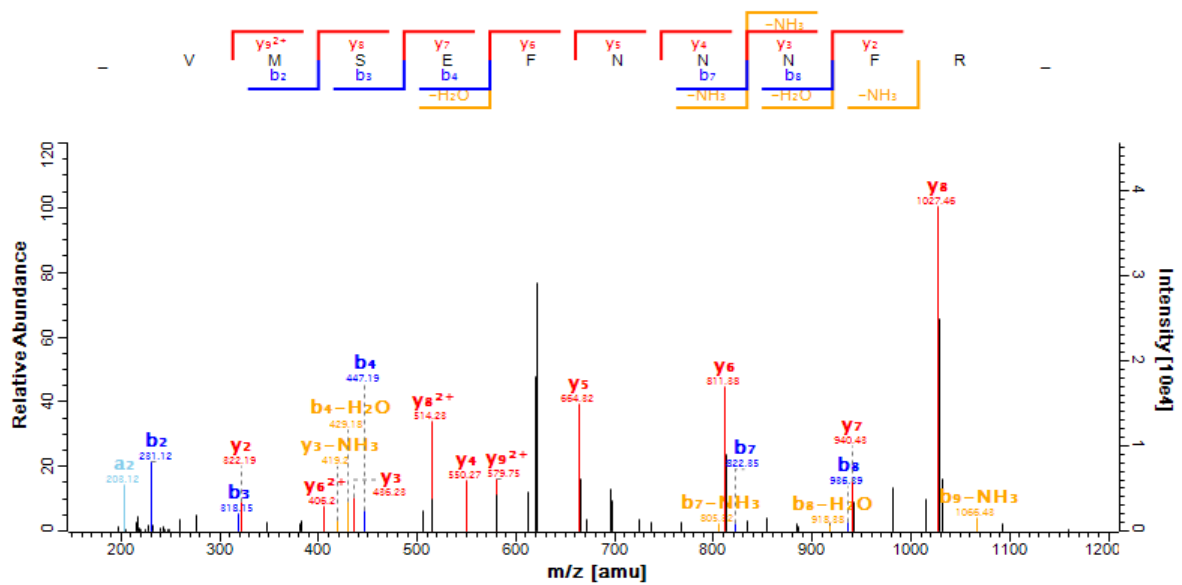
Number of Replicates (out of 8): 5

Best Match Score: 135.43

Best Match Posterior Error Probability: 8.38E-06

Best Match Spectrum:

Scan number	30622	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS: CID	Genenames	CD63



Protein Group ID: 563

Protein Accession Numbers: Q9BQE9; C9JWD3; Q9BQE9-2

Gene Names: BCL7B

Peptide Sequence: RFCVDQPTVPQTASES

Total Number of Spectra: 1

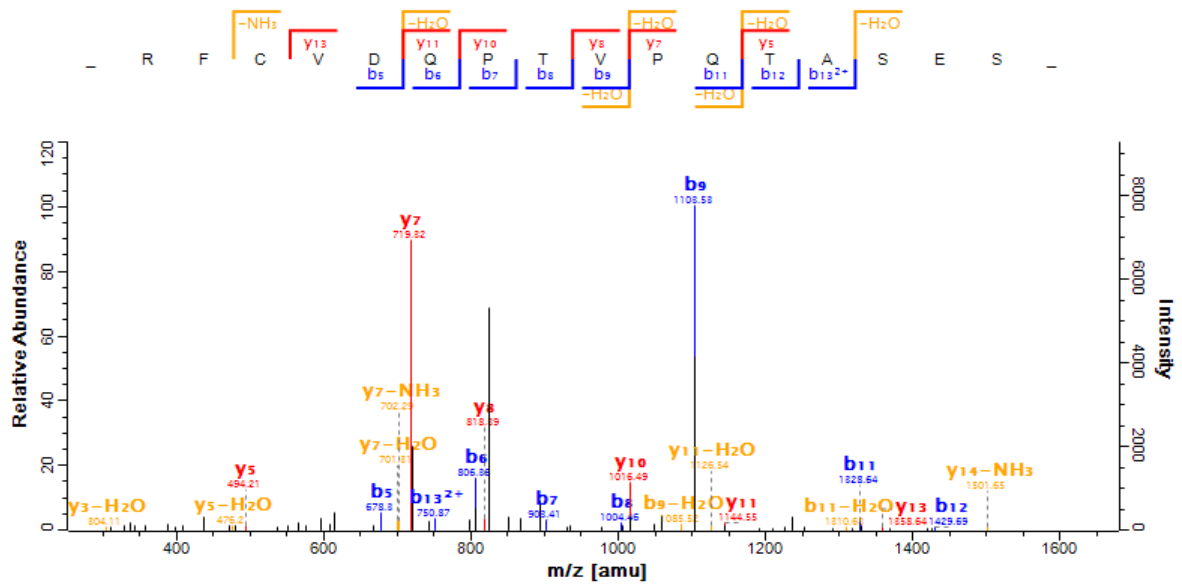
Number of Replicates (out of 8): 1

Best Match Score: 85.988

Best Match Posterior Error Probability: 0.0021846

Best Match Spectrum:

Scan number 33032 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** BCL7B



Protein Group ID: 568

Protein Accession Numbers: O95168; O95168-2; C9JXQ9; F2Z3P9

Gene Names: NDUFB4

Peptide Sequence: TLPETLDPAEYNISPETR

Total Number of Spectra: 9

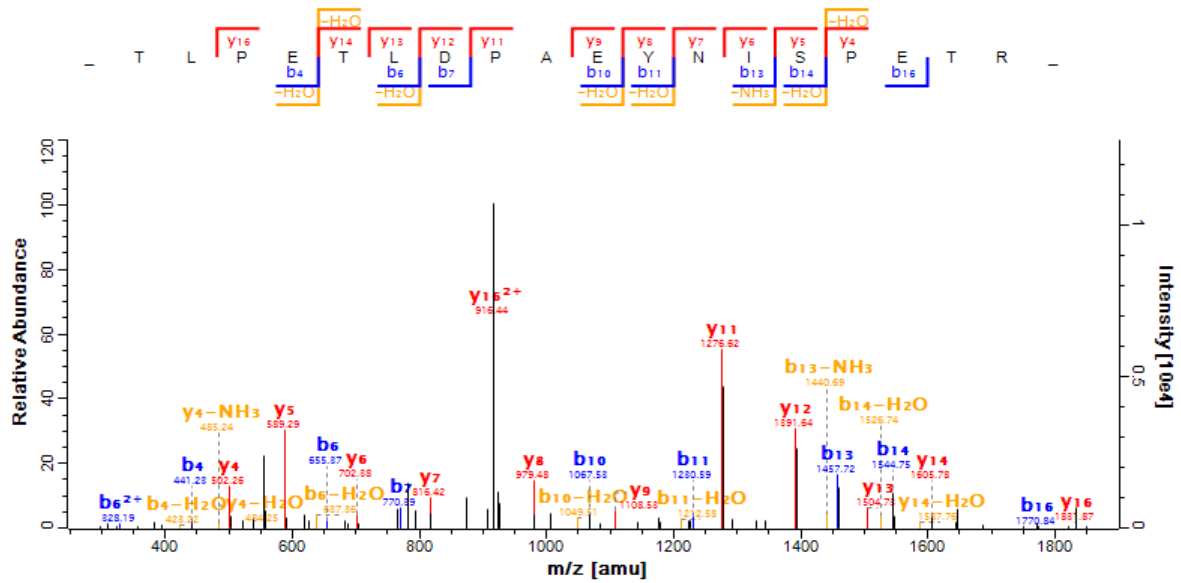
Number of Replicates (out of 8): 8

Best Match Score: 142.35

Best Match Posterior Error Probability: 9.11E-06

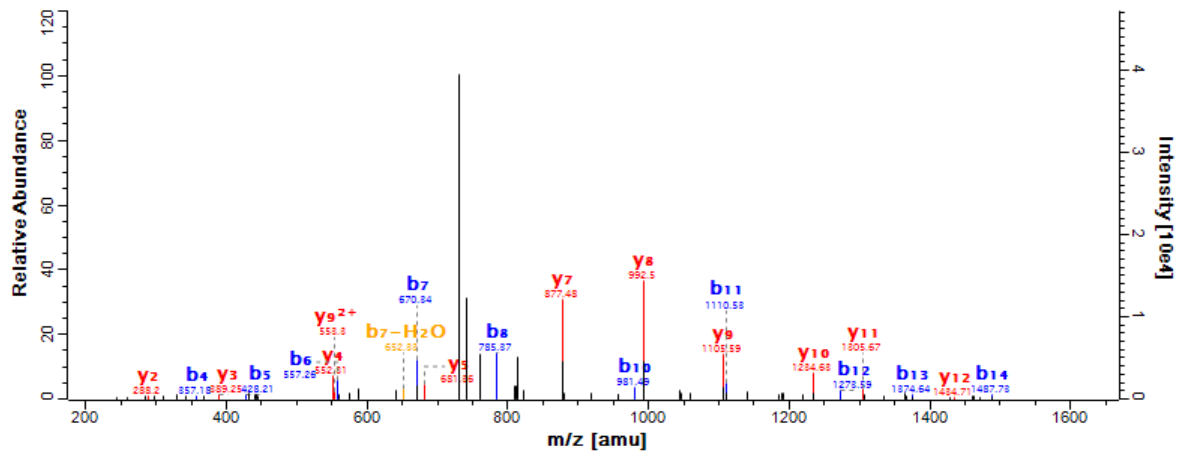
Best Match Spectrum:

Scan number 54306 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** NDUFB4



Protein Group ID: 569
Protein Accession Numbers: O75817; C9JYM0
Gene Names: POP7
Peptide Sequence: GAVEALDPVEYTLR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 119.45
Best Match Posterior Error Probability: 0.00025611
Best Match Spectrum:

Scan number 55508 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** POP7



Protein Group ID: 571

Protein Accession Numbers: Q96ET8; C9JYS5; Q9NYZ1; J3KS67; Q96ET8-3; Q96ET8-2; E5RGC5; I3L376; E5RIS5

Gene Names: FAM18B2;FAM18B1

Peptide Sequence: MLQQDSNDDTVDVSLFDEEETTRPR

Total Number of Spectra: 6

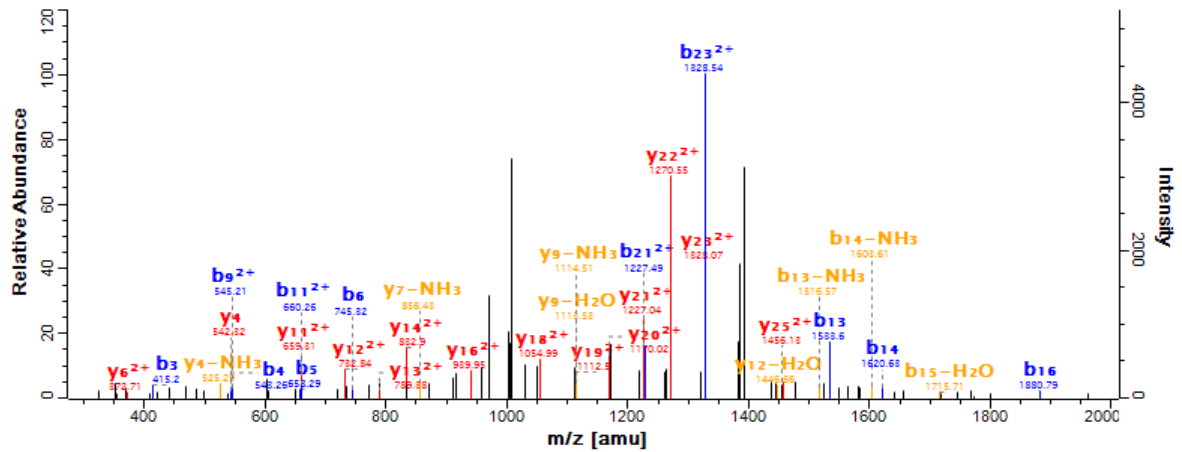
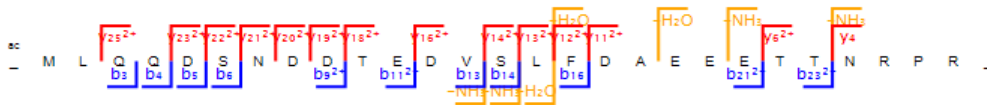
Number of Replicates (out of 8): 4

Best Match Score: 110.67

Best Match Posterior Error Probability: 3.97E-11

Best Match Spectrum:

Scan number	61534	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS: CID	Genenames	FAM18B2;FAM18B1



Protein Group ID: 573

Protein Accession Numbers: Q7Z2E3; Q7Z2E3-7; Q7Z2E3-8; Q7Z2E3-11; Q7Z2E3-10; Q7Z2E3-9; Q7Z2E3-5; Q7Z2E3-3; Q7Z2E3-4; C9JZ40; F8W6G5; Q7Z2E3-2; Q7Z2E3-6

Gene Names: APTX

Peptide Sequence: YHWLVPTSISLK

Total Number of Spectra: 6

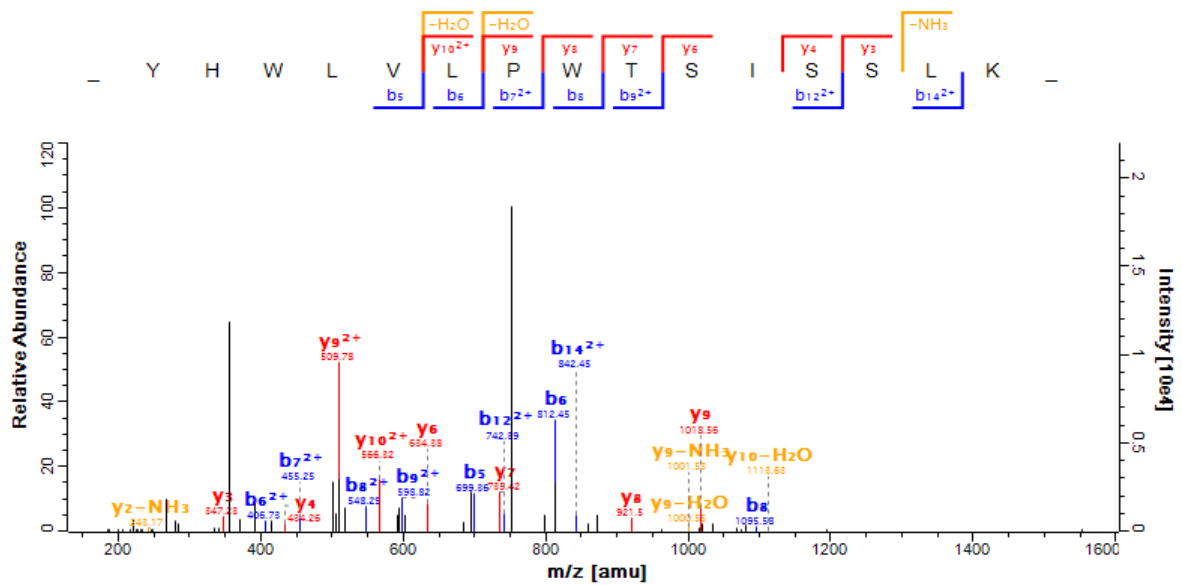
Number of Replicates (out of 8): 5

Best Match Score: 105.65

Best Match Posterior Error Probability: 0.00016181

Best Match Spectrum:

Scan number	82207	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS: CID	Genenames	APTX



Protein Group ID: 579

Protein Accession Numbers: J3KR78; Q9H974; Q9H974-3; Q9H974-2; C9K0B6

Gene Names: QTRTD1

Peptide Sequence: SVIGVIEGGDVMEEER

Total Number of Spectra: 1

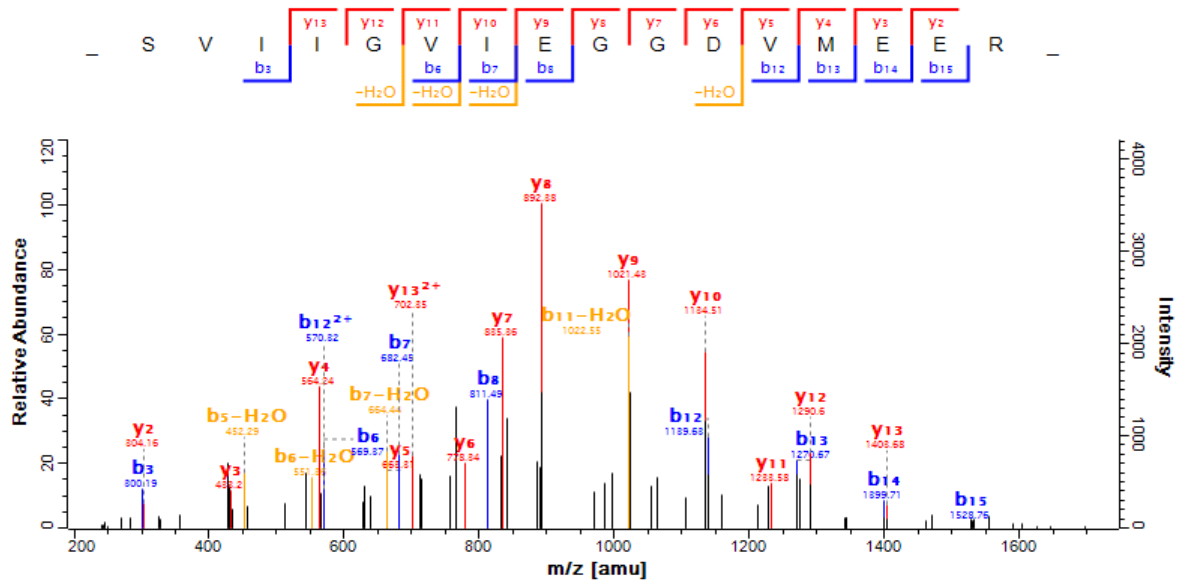
Number of Replicates (out of 8): 1

Best Match Score: 120.63

Best Match Posterior Error Probability: 8.50E-05

Best Match Spectrum:

Scan number 58752 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** QTRTD1



Protein Group ID: 581

Protein Accession Numbers: CON__A2I7N3

Gene Names:

Peptide Sequence: FSISSHYQLK

Total Number of Spectra: 4

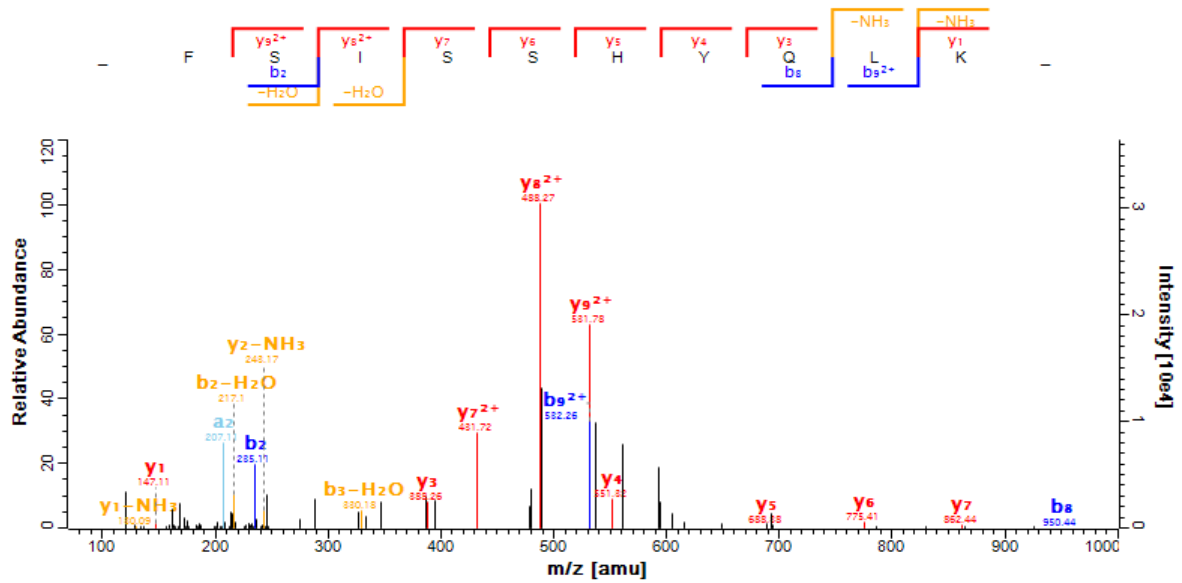
Number of Replicates (out of 8): 4

Best Match Score: 89.08

Best Match Posterior Error Probability: 0.0020971

Best Match Spectrum:

Scan number 32370 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Pepti...** 89.08



Protein Group ID: 582

Protein Accession Numbers: CON__ENSEMBL:ENSBTAP00000007350; CON__P01030

Gene Names:

Peptide Sequence: ALVALGAVDTALYAVGGK

Total Number of Spectra: 1

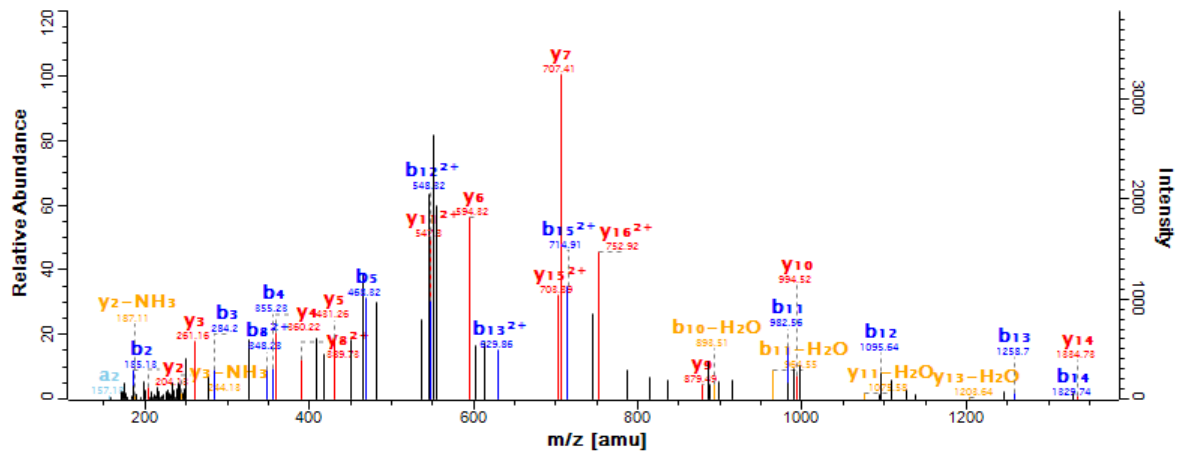
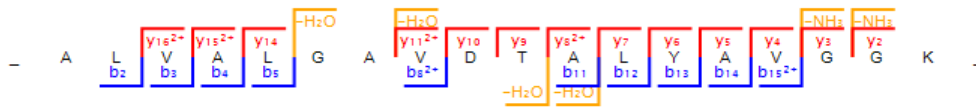
Number of Replicates (out of 8): 1

Best Match Score: 130.47

Best Match Posterior Error Probability: 3.90E-05

Best Match Spectrum:

Scan number 78122 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Pepti...** 130.47



Protein Group ID: 587

Protein Accession Numbers: CON__ENSEMBL:ENSBTAP00000034412

Gene Names:

Peptide Sequence: ALCQKPEISNGK

Total Number of Spectra: 1

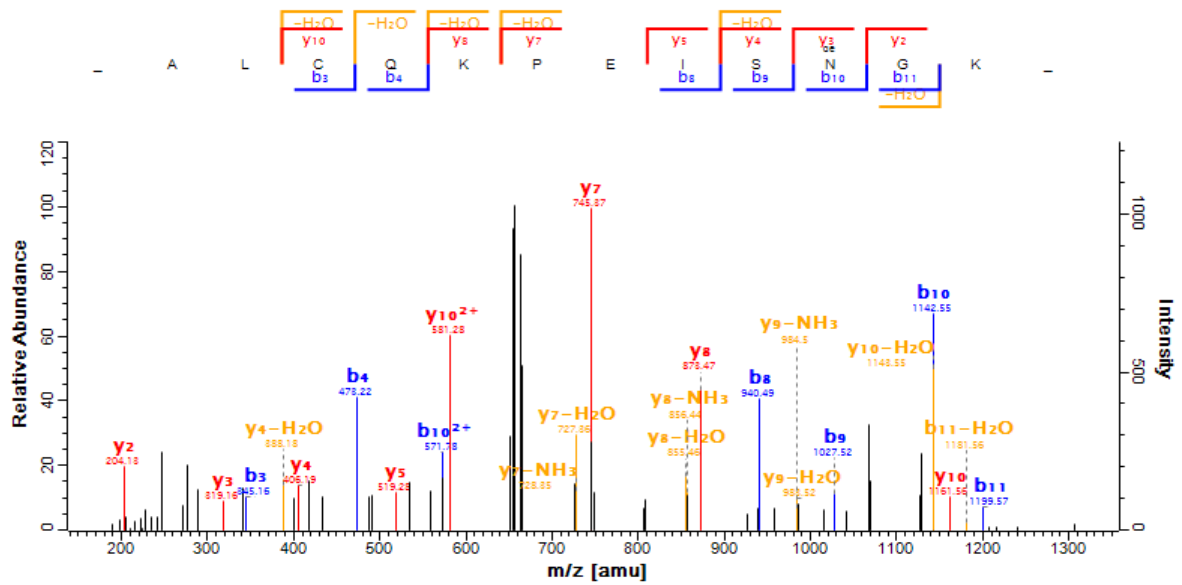
Number of Replicates (out of 8): 1

Best Match Score: 131.17

Best Match Posterior Error Probability: 0.0022658

Best Match Spectrum:

Scan number 9304 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Peptide...** 131.17



Protein Group ID: 588

Protein Accession Numbers: CON__ENSEMBL:ENSBTAP00000038329

Gene Names:

Peptide Sequence: LPENVTPPEEQHK

Total Number of Spectra: 1

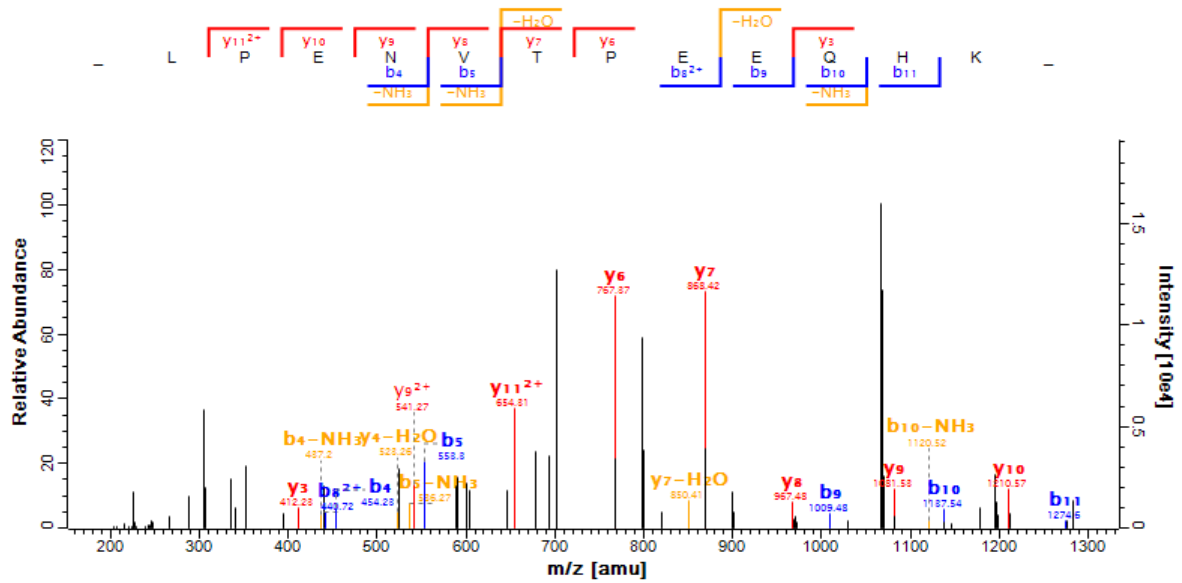
Number of Replicates (out of 8): 1

Best Match Score: 100.22

Best Match Posterior Error Probability: 0.00050652

Best Match Spectrum:

Scan number 11939 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Pepti...** 100.22



Protein Group ID: 589

Protein Accession Numbers: CON__H-INV:HIT000292931

Gene Names:

Peptide Sequence: QLYEKEIRELELQSQISQISDTSVVLSDNSR

Total Number of Spectra: 1

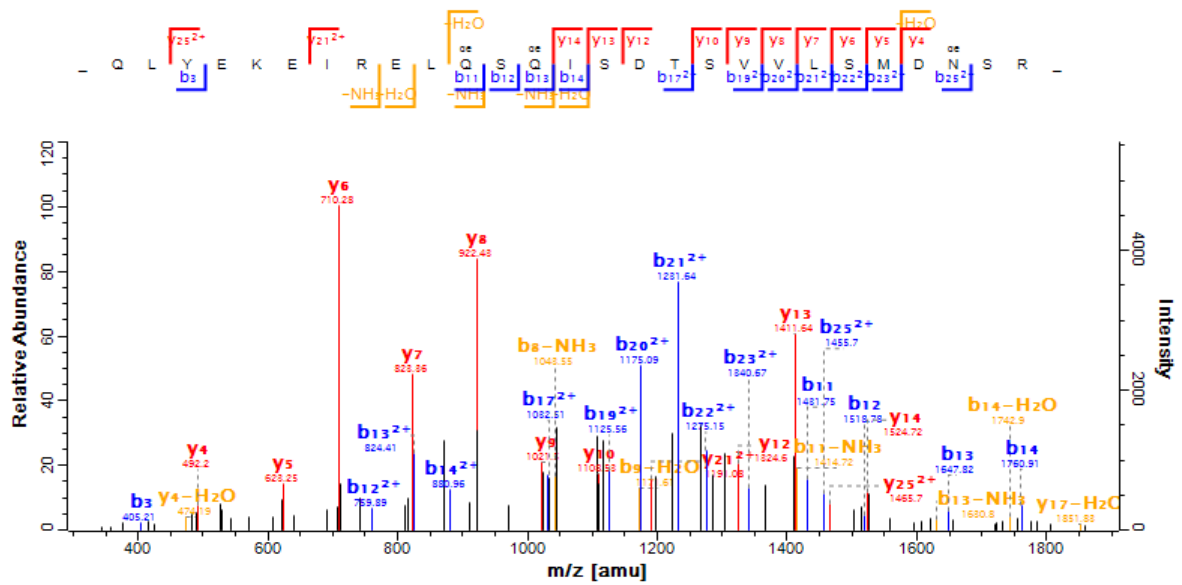
Number of Replicates (out of 8): 1

Best Match Score: 132.36

Best Match Posterior Error Probability: 3.01E-15

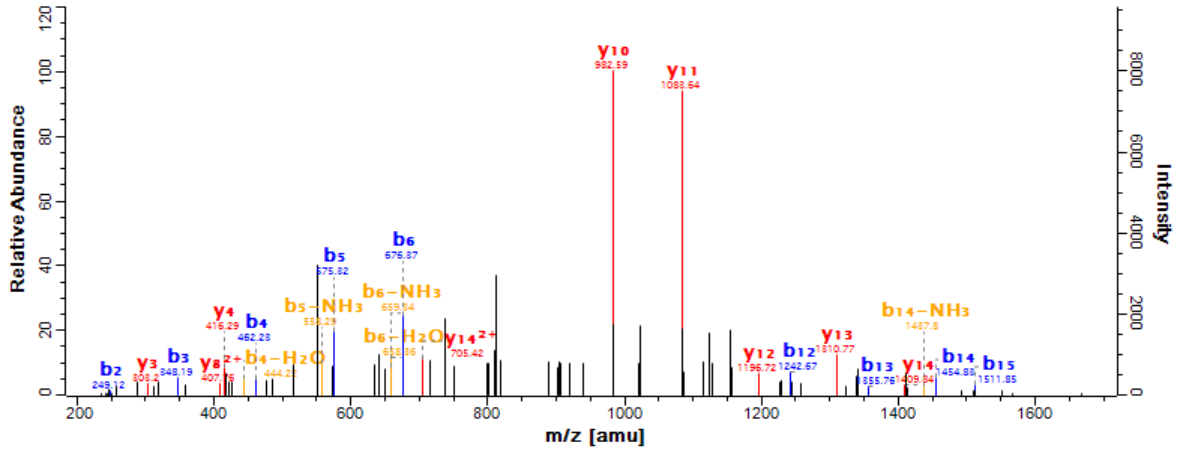
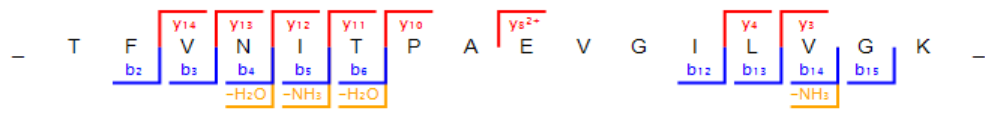
Best Match Spectrum:

Scan number 85553 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Pepti...** 132.36



Protein Group ID: 595
Protein Accession Numbers: CON__P02584
Gene Names:
Peptide Sequence: T F V N I T P A E V G I L V G K
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 99.747
Best Match Posterior Error Probability: 0.00016539
Best Match Spectrum:

Scan number 75867 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Pepti...** 99.75



Protein Group ID: 599

Protein Accession Numbers: CON__P04259; CON__P48668; P48668; P04259

Gene Names: KRT6C;KRT6B

Peptide Sequence: SGFSSISVSR

Total Number of Spectra: 1

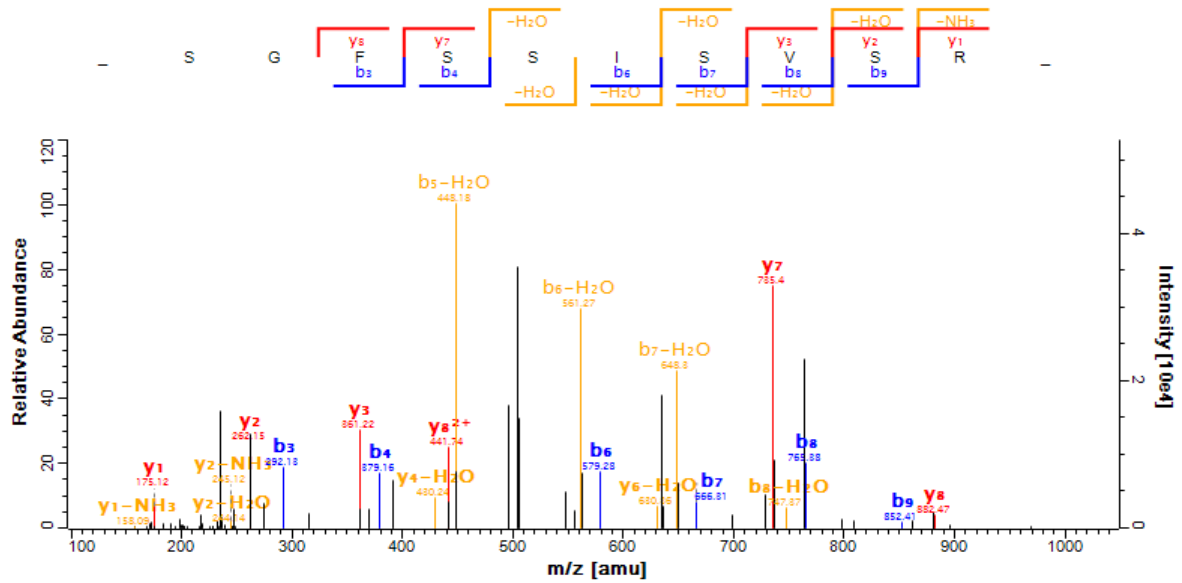
Number of Replicates (out of 8): 1

Best Match Score: 100.69

Best Match Posterior Error Probability: 0.00051002

Best Match Spectrum:

Scan number 26164 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** KRT6C;KRT6B



Protein Group ID: 603

Protein Accession Numbers: E7EQ64; CON__P07477; P07477; H0Y8D1

Gene Names: PRSS1

Peptide Sequence: TLNNDIMLIK

Total Number of Spectra: 10

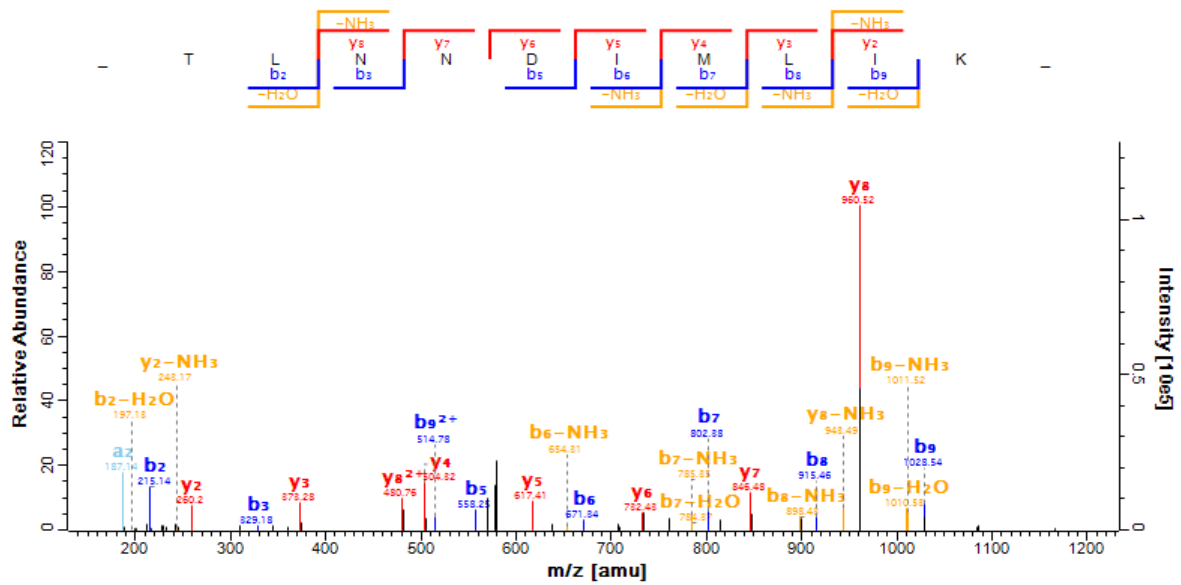
Number of Replicates (out of 8): 7

Best Match Score: 179.57

Best Match Posterior Error Probability: 5.46E-07

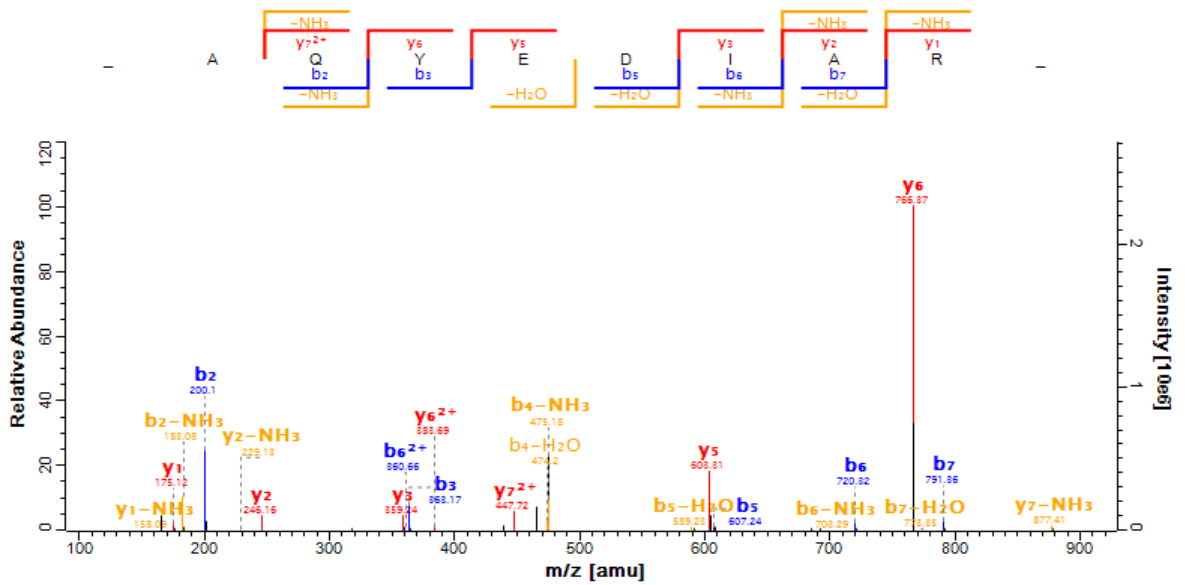
Best Match Spectrum:

Scan number 47582 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PRSS1



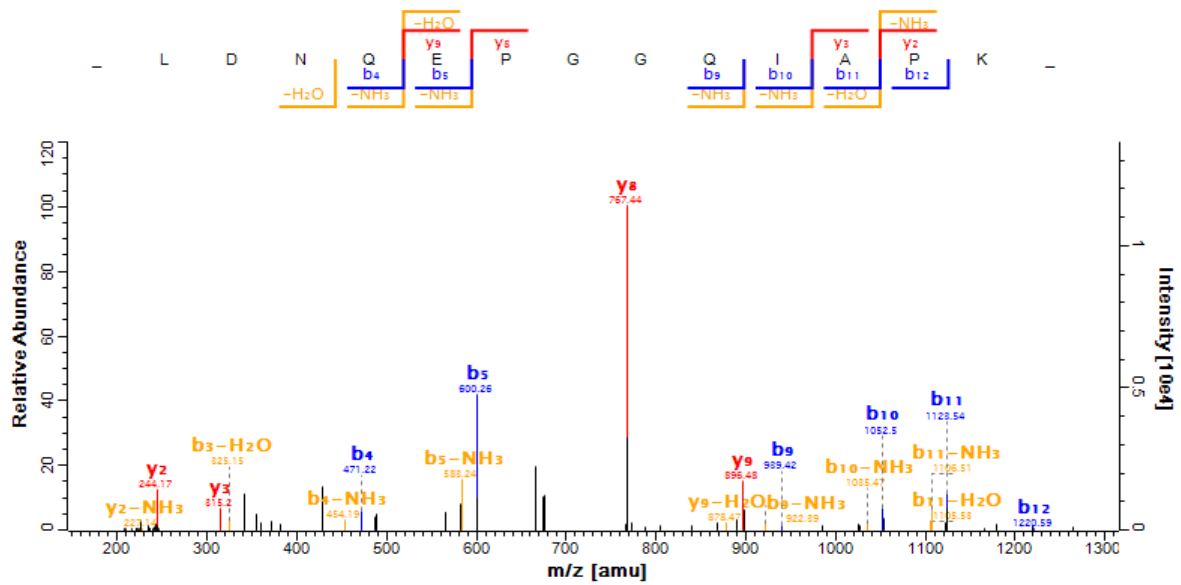
Protein Group ID: 604
Protein Accession Numbers: CON__P07744
Gene Names:
Peptide Sequence: AQYEDIAR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 141.2
Best Match Posterior Error Probability: 0.0025953
Best Match Spectrum:

Scan number 14389 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Pepti...** 141.2



Protein Group ID: 613
Protein Accession Numbers: CON__P28800
Gene Names:
Peptide Sequence: LDNQEPGGQIAPK
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 90.793
Best Match Posterior Error Probability: 0.0013227
Best Match Spectrum:

Scan number 14466 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Pepti...** 90.79



Protein Group ID: 616

Protein Accession Numbers: CON__P35908

Gene Names:

Peptide Sequence: GGGFGGGSGFGGGSGFGGGSGFSGGGFGGGGFGGGR

Total Number of Spectra: 2

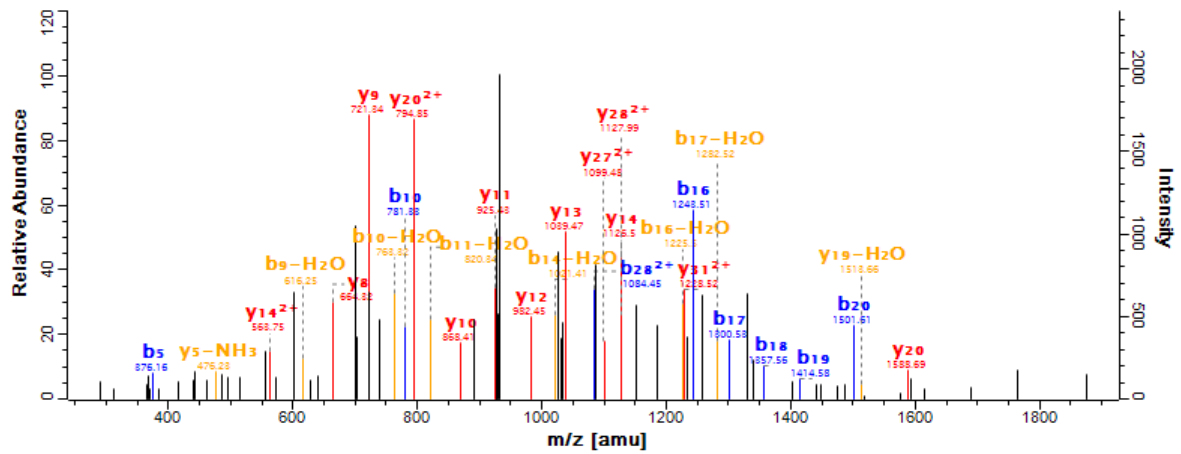
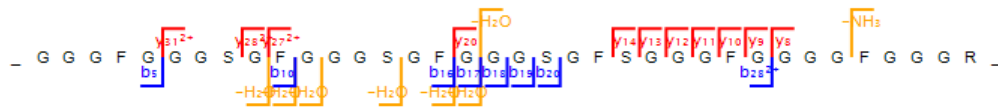
Number of Replicates (out of 8): 2

Best Match Score: 70.701

Best Match Posterior Error Probability: 3.79E-07

Best Match Spectrum:

Scan number 62840 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Pepti...** 70.7



Protein Group ID: 618

Protein Accession Numbers: CON__P60712; P60709; E7EVS6; G5E9R0; C9JZR7; C9JTX5

Gene Names: ACTB

Peptide Sequence: DDDIAALVVDNNGSGMCK

Total Number of Spectra: 65

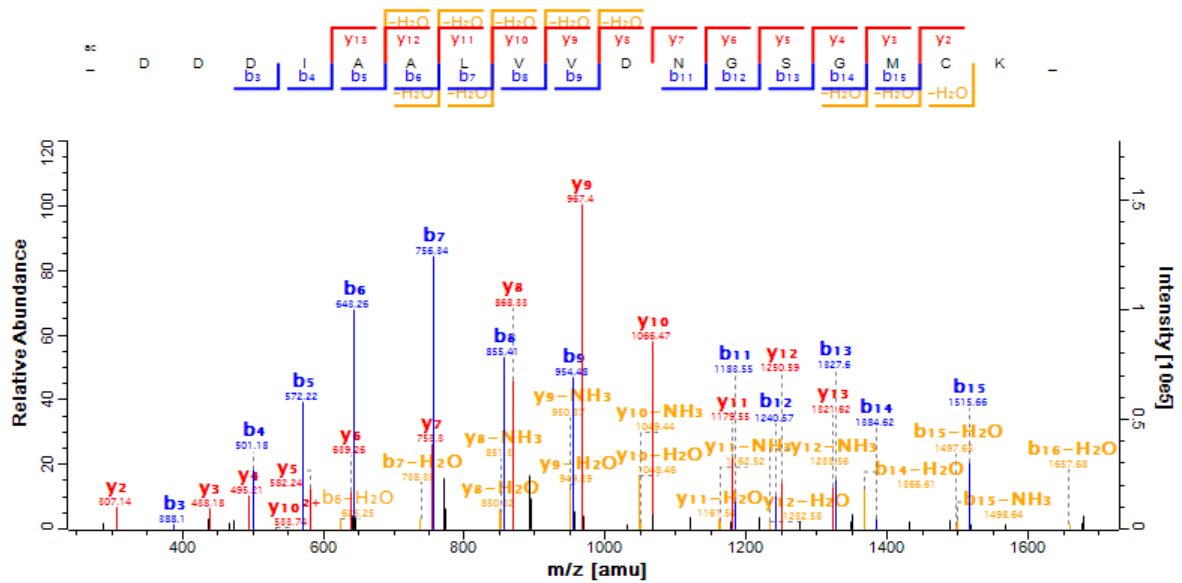
Number of Replicates (out of 8): 8

Best Match Score: 239.58

Best Match Posterior Error Probability: 1.41E-80

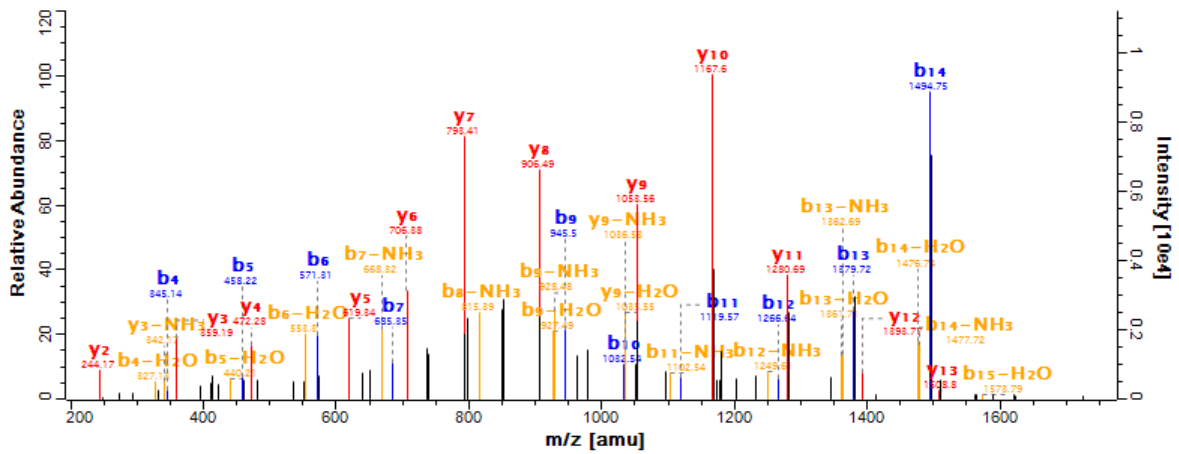
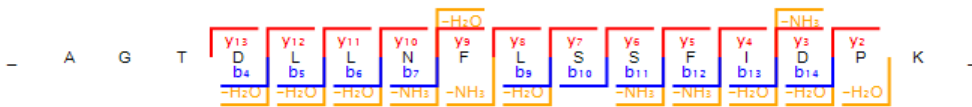
Best Match Spectrum:

Scan number 66196 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS: CID **Genenames** ACTB



Protein Group ID: 619
Protein Accession Numbers: CON__P81644
Gene Names:
Peptide Sequence: AGTDLLNFLSSFIDPK
Total Number of Spectra: 9
Number of Replicates (out of 8): 8
Best Match Score: 227.67
Best Match Posterior Error Probability: 2.37E-63
Best Match Spectrum:

Scan number 96790 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Pepti...** 227.67



Protein Group ID: 620

Protein Accession Numbers: CON_Q04695; Q04695; CON_Q9QWL7; K7EPJ9;
CON_Q99PS0; CON_Q9C075; Q9C075; J3QR55

Gene Names: KRT17;KRT23

Peptide Sequence: ATMQNLNDR

Total Number of Spectra: 2

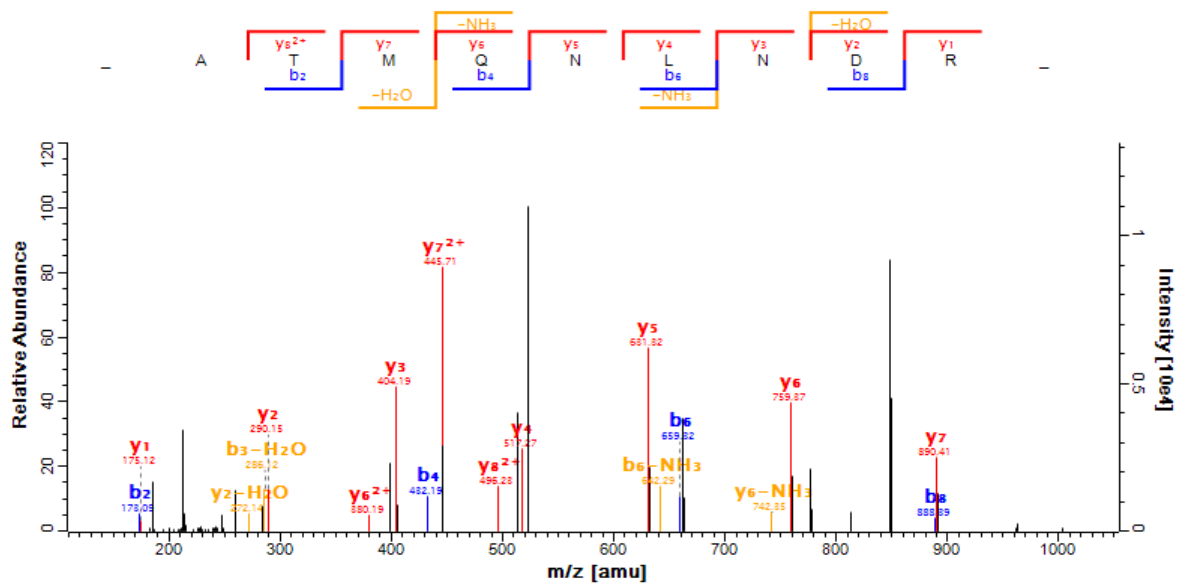
Number of Replicates (out of 8): 2

Best Match Score: 99.973

Best Match Posterior Error Probability: 0.001775

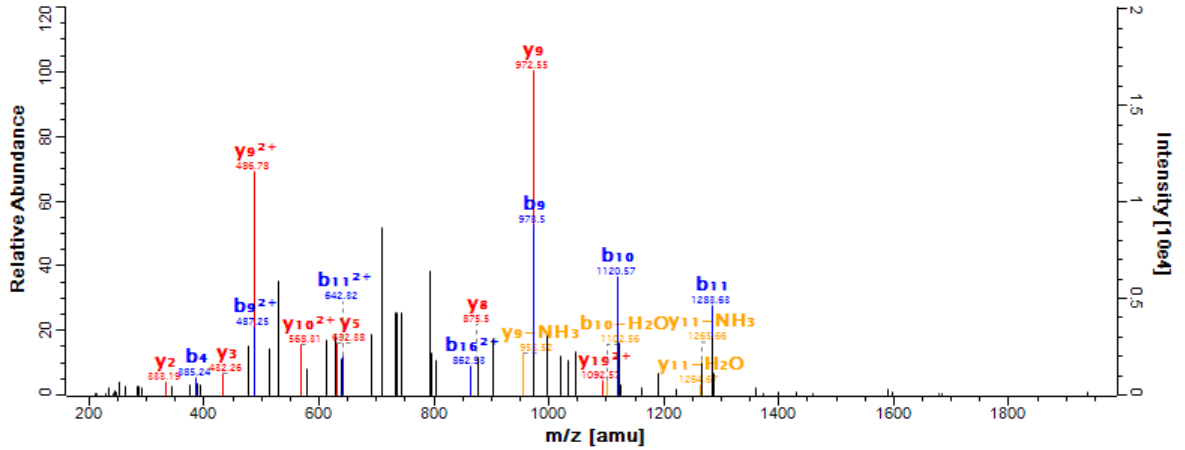
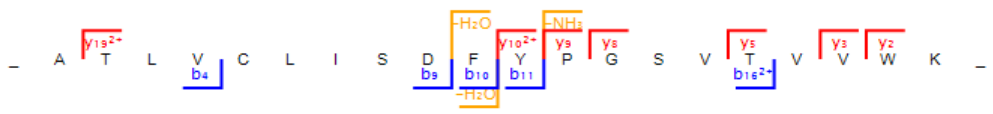
Best Match Spectrum:

Scan number	7549	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS: CID	Genenames	KRT17;KRT23



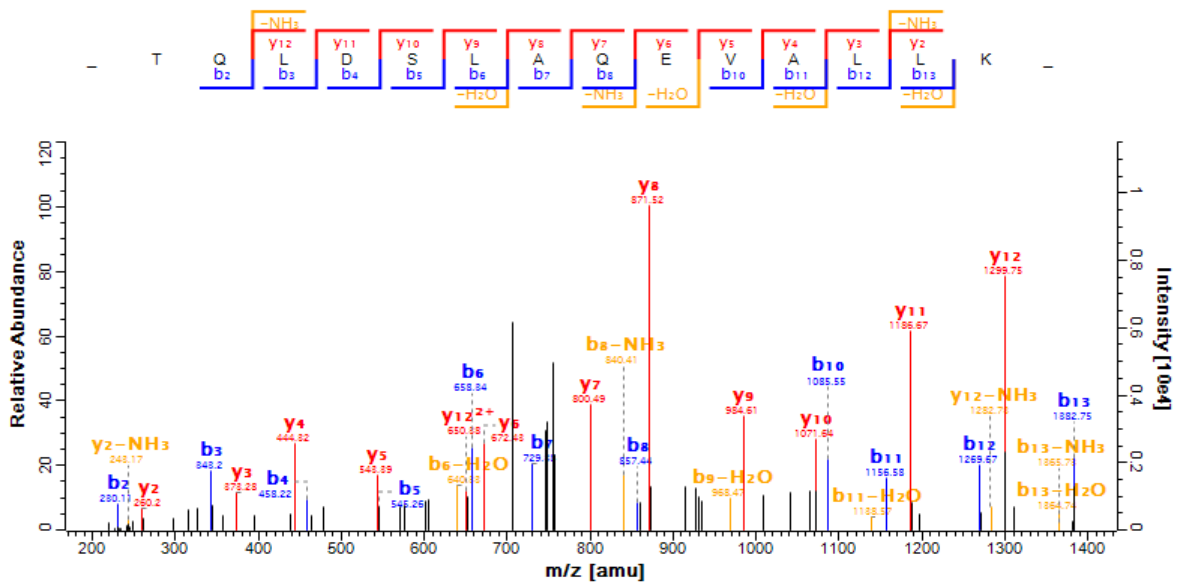
Protein Group ID: 624
Protein Accession Numbers: CON_Q1RMN8
Gene Names:
Peptide Sequence: ATLVCLISDFYPGSVTVVWK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 73.498
Best Match Posterior Error Probability: 0.0012031
Best Match Spectrum:

Scan number 92794 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Pepti...** 73.5



Protein Group ID: 625
Protein Accession Numbers: CON__Q2KIS7
Gene Names:
Peptide Sequence: TQLDSLAEVALLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 167.69
Best Match Posterior Error Probability: 1.61E-10
Best Match Spectrum:

Scan number 71050 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Pepti...** 167.69



Protein Group ID: 628

Protein Accession Numbers: CON_Q2YDI2; O43929; F5H069; O43929-2; Q53SE3

Gene Names: ORC4;ORC4L

Peptide Sequence: VFGSFAENLSFLLEALK

Total Number of Spectra: 2

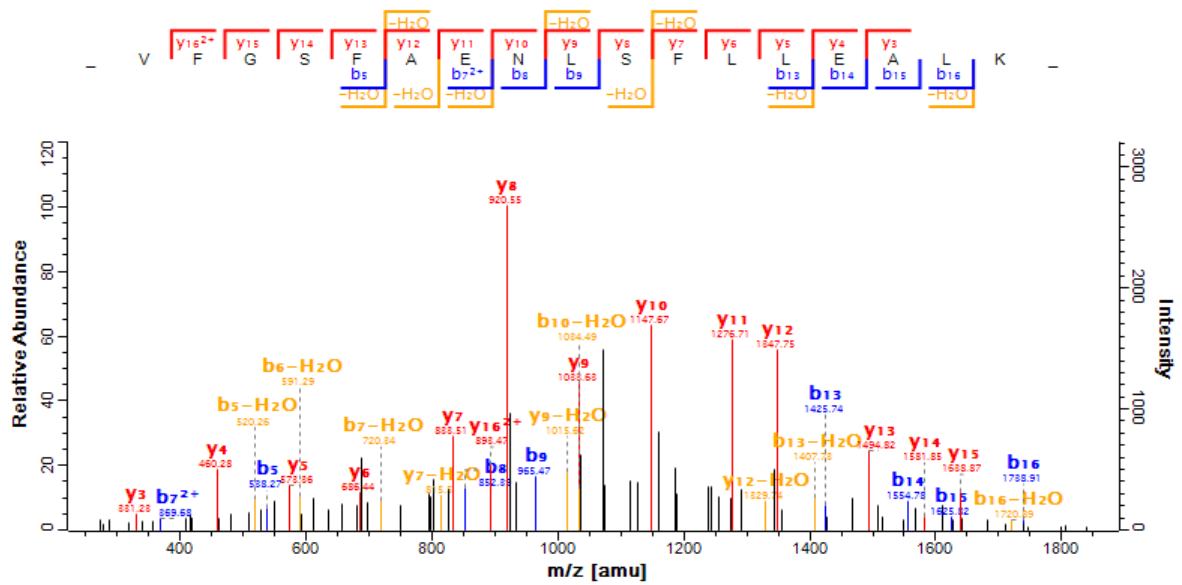
Number of Replicates (out of 8): 2

Best Match Score: 137.45

Best Match Posterior Error Probability: 1.02E-08

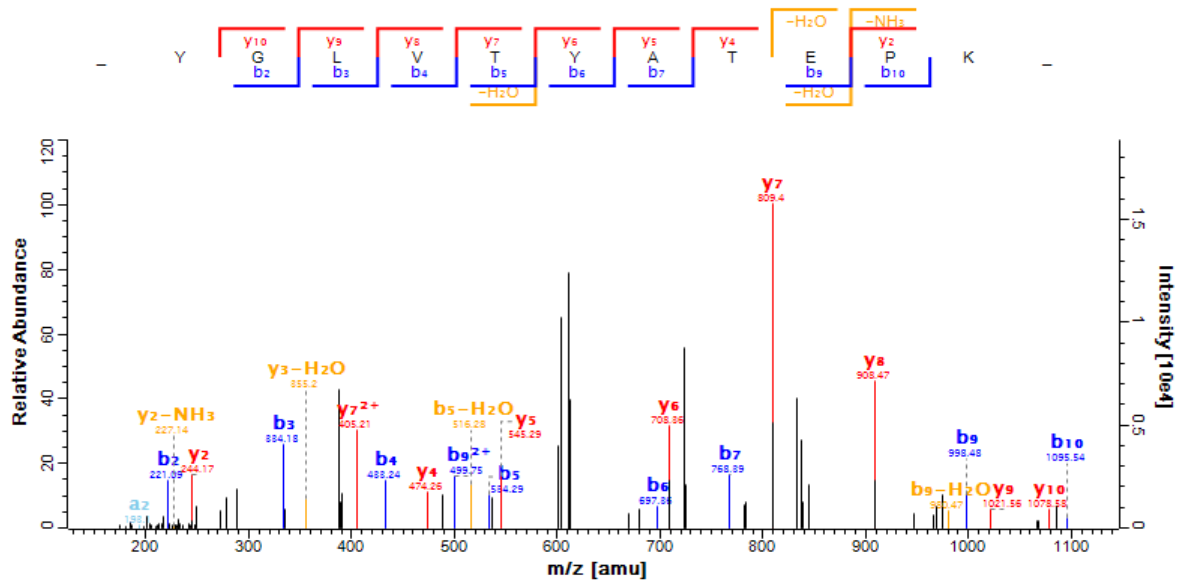
Best Match Spectrum:

Scan number	95495	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	ORC4;ORC4L



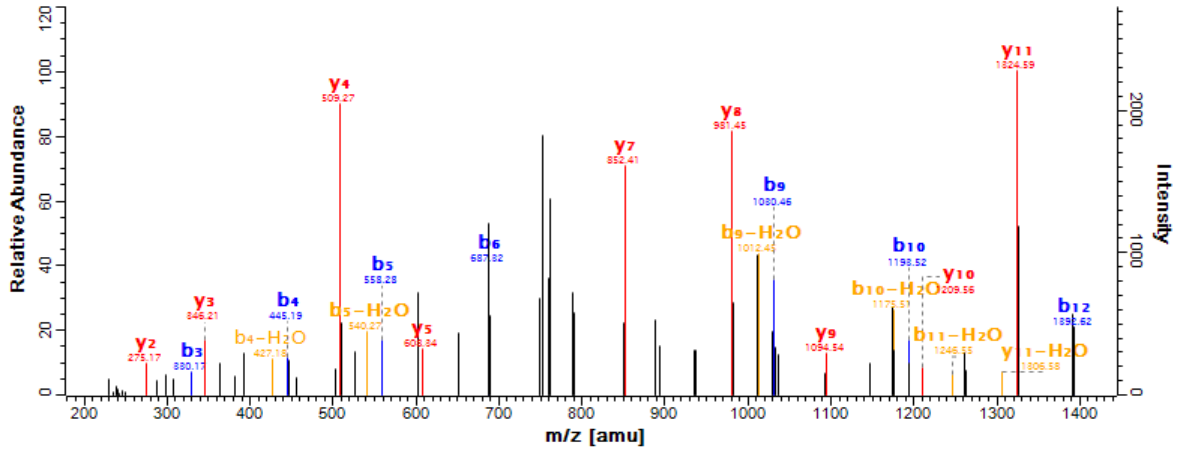
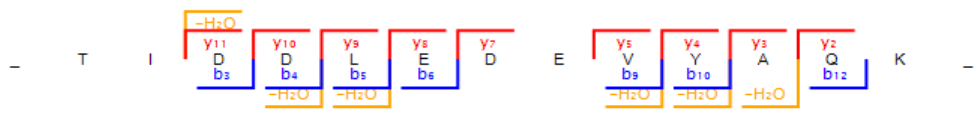
Protein Group ID: 630
Protein Accession Numbers: CON_Q3KUS7
Gene Names:
Peptide Sequence: YGLVTYATEPK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 141.08
Best Match Posterior Error Probability: 2.15E-05
Best Match Spectrum:

Scan number 34019 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Pepti...** 141.08



Protein Group ID: 633
Protein Accession Numbers: CON_Q3SX28
Gene Names:
Peptide Sequence: TIDDLEDEVYAQK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 112.44
Best Match Posterior Error Probability: 0.00027861
Best Match Spectrum:

Scan number 42603 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Pepti...** 112.44



Protein Group ID: 639

Protein Accession Numbers: CON_Q3ZBD7

Gene Names:

Peptide Sequence: KIEPELDGSSSPVTSHDSSSTNGLINFIK

Total Number of Spectra: 1

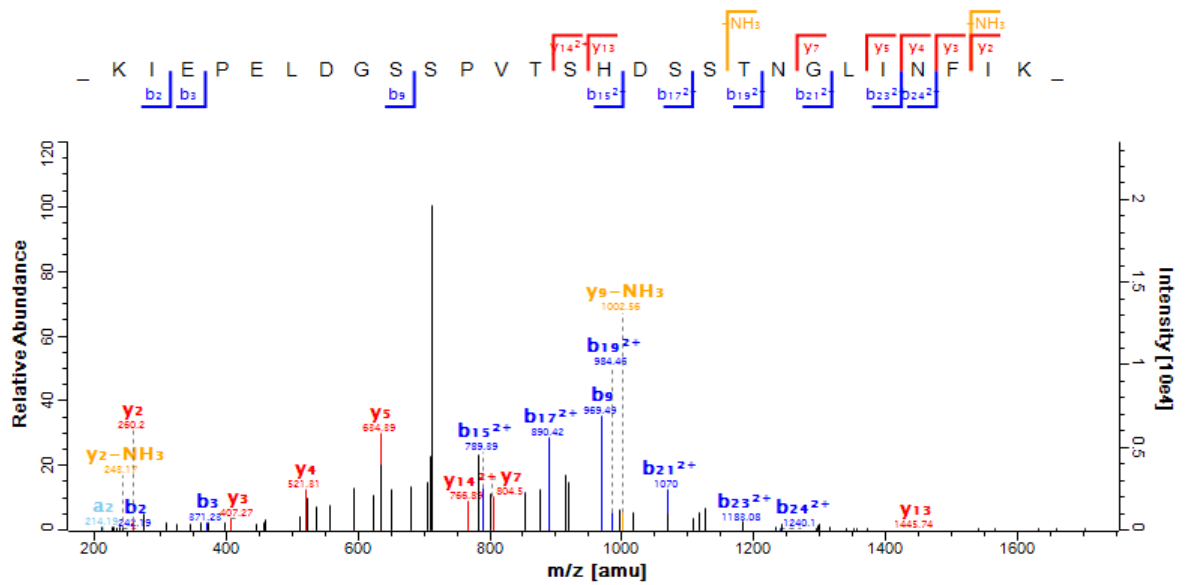
Number of Replicates (out of 8): 1

Best Match Score: 50.029

Best Match Posterior Error Probability: 0.012666

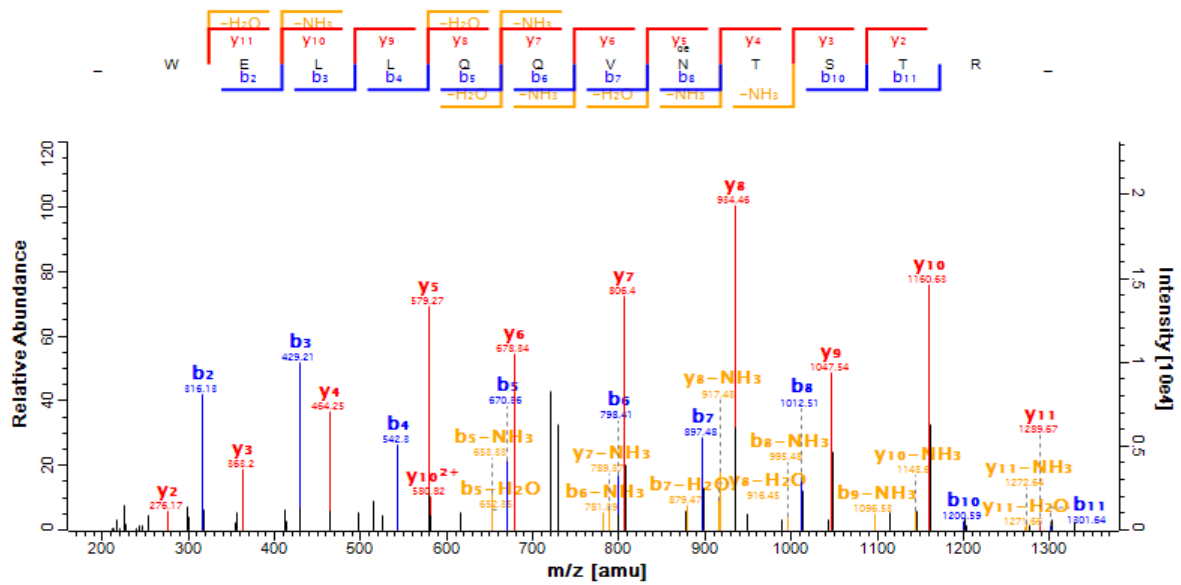
Best Match Spectrum:

Scan number 58997 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Pepti...** 50.03



Protein Group ID: 643
Protein Accession Numbers: CON_Q6IFZ6
Gene Names:
Peptide Sequence: WELLQQVNTSTR
Total Number of Spectra: 8
Number of Replicates (out of 8): 8
Best Match Score: 192.65
Best Match Posterior Error Probability: 1.40E-17
Best Match Spectrum:

Scan number 52094 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Pepti...** 192.65



Protein Group ID: 644

Protein Accession Numbers: CON_Q7Z794; Q7Z794; F5GY66

Gene Names: KRT77

Peptide Sequence: YQELQITAGR

Total Number of Spectra: 3

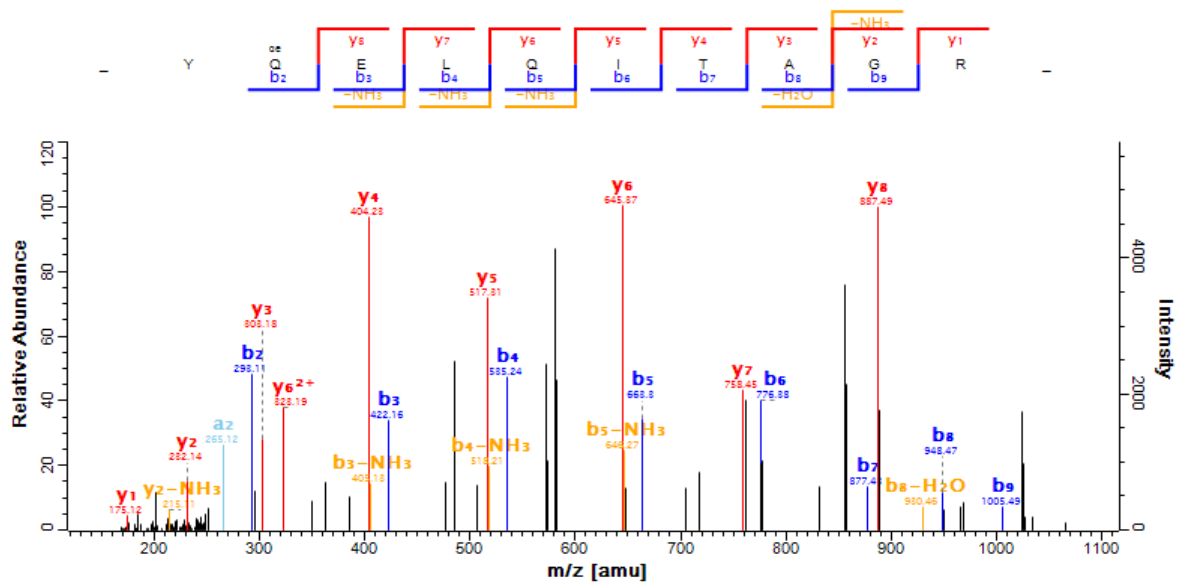
Number of Replicates (out of 8): 3

Best Match Score: 144.1

Best Match Posterior Error Probability: 0.0012543

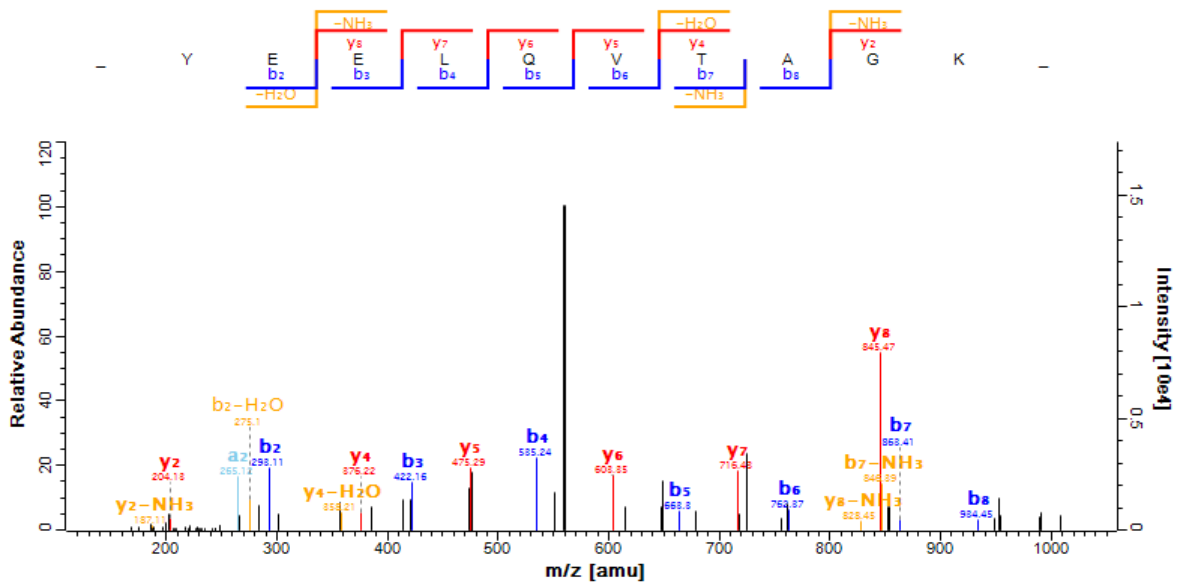
Best Match Spectrum:

Scan number 29112 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** KRT77



Protein Group ID: 646
Protein Accession Numbers: CON_Q8VED5
Gene Names:
Peptide Sequence: YEELQVTAGK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 107.03
Best Match Posterior Error Probability: 0.0004732
Best Match Spectrum:

Scan number 28866 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Pepti...** 107.03



Protein Group ID: 647

Protein Accession Numbers: CON_Q95121

Gene Names:

Peptide Sequence: SGESPTANVLLSPLSVATALSLGAEQR

Total Number of Spectra: 6

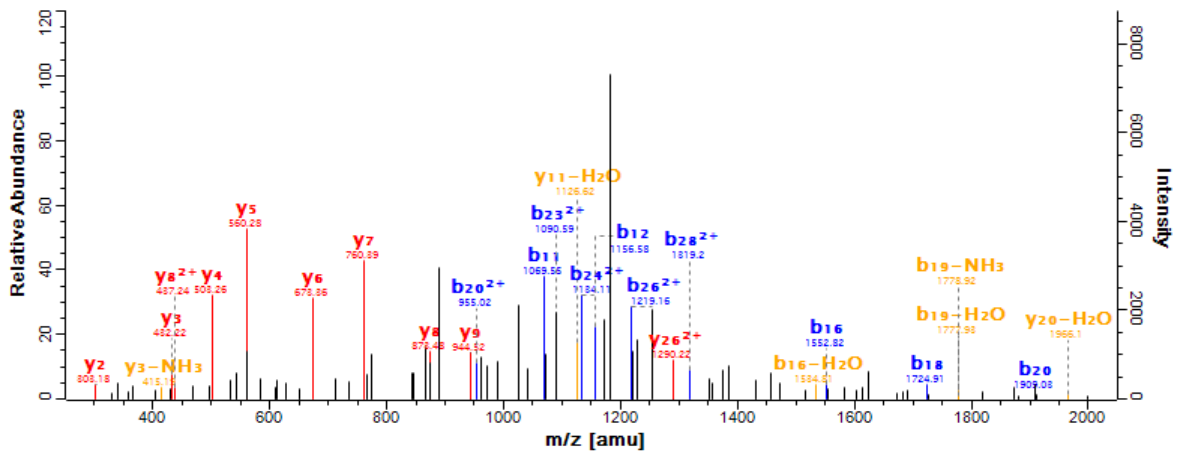
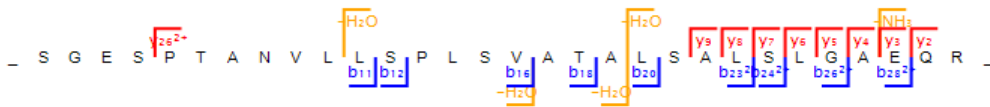
Number of Replicates (out of 8): 4

Best Match Score: 71.882

Best Match Posterior Error Probability: 2.53E-05

Best Match Spectrum:

Scan number	95647	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Pepti...	71.88



Protein Group ID: 650

Protein Accession Numbers: CON_REFSEQ:XP_001252647

Gene Names:

Peptide Sequence: IFTSDADFSGITNDHK

Total Number of Spectra: 5

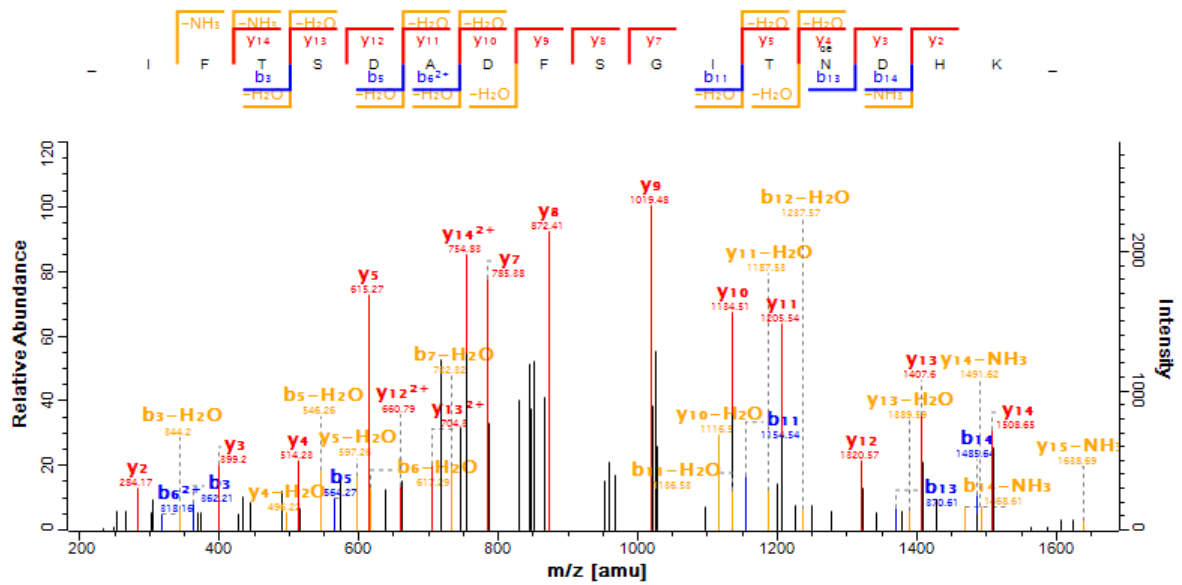
Number of Replicates (out of 8): 4

Best Match Score: 181.58

Best Match Posterior Error Probability: 1.21E-19

Best Match Spectrum:

Scan number 42159 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Pepti...** 181.58



Protein Group ID: 652

Protein Accession Numbers: D2X2H5; Q8N2Q7; Q8N2Q7-2

Gene Names: nlg1;NLGN1

Peptide Sequence: KNSVPVTSAFPTAK

Total Number of Spectra: 1

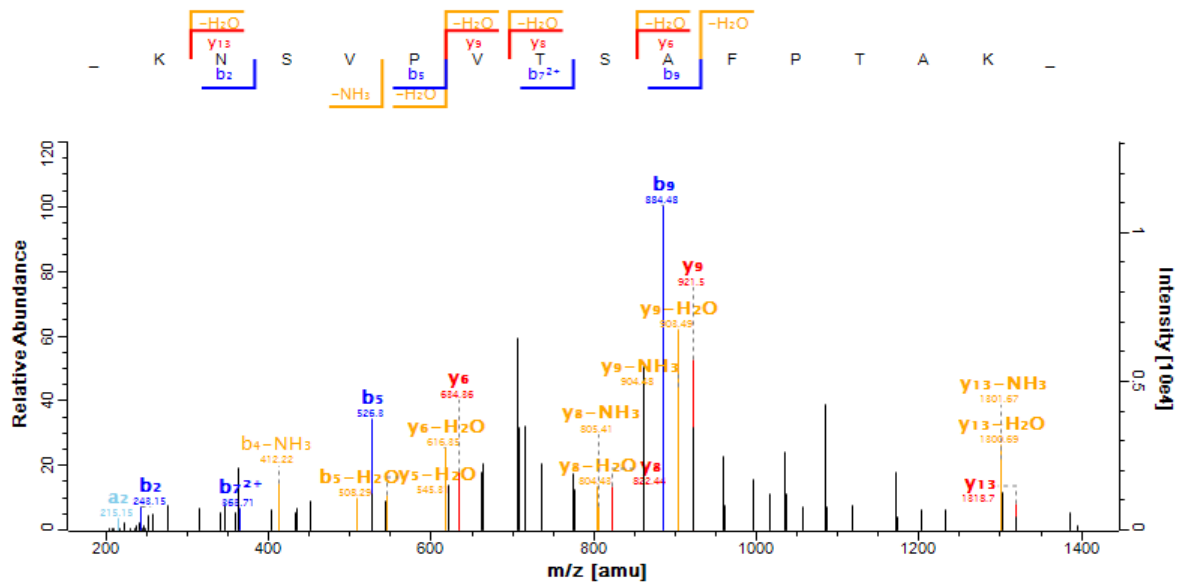
Number of Replicates (out of 8): 1

Best Match Score: 97.463

Best Match Posterior Error Probability: 0.0011377

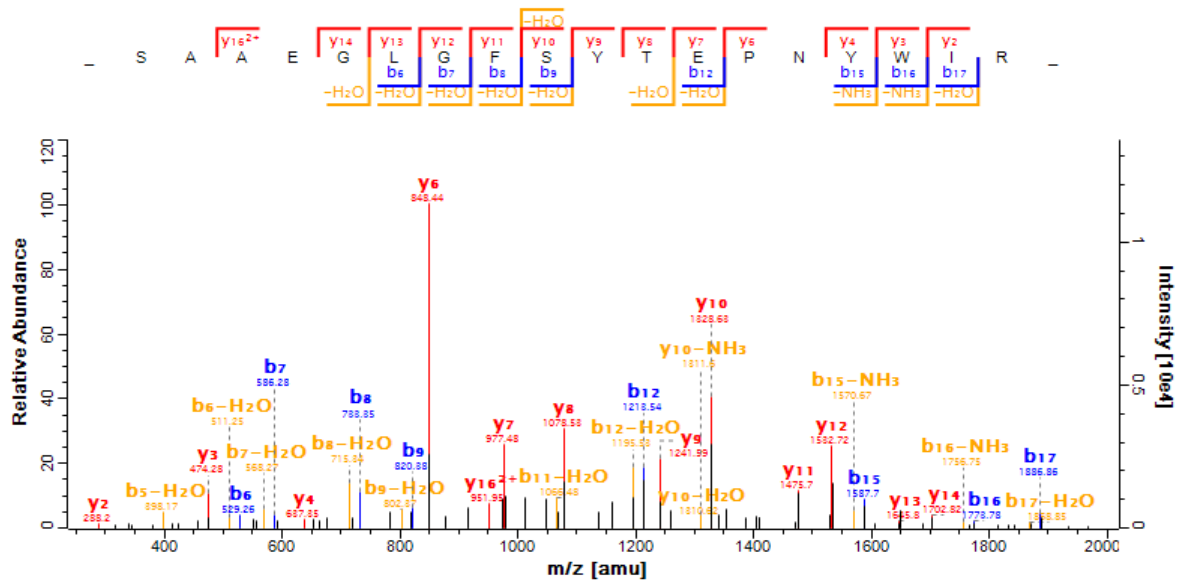
Best Match Spectrum:

Scan number	43836	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	nlg1;NLGN1



Protein Group ID: 653
Protein Accession Numbers: Q8IVL5; D3DNV8
Gene Names: LEPREL1
Peptide Sequence: SAAEGLGFSYTEPNIYR
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 180.64
Best Match Posterior Error Probability: 3.42E-21
Best Match Spectrum:

Scan number 69996 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** LEPREL1



Protein Group ID: 662

Protein Accession Numbers: D3YTE6; H0YN69; Q6PKH6-2; Q6PKH6; E9PFL3; F5H660; Q6E0Y0

Gene Names: DHRS4L2

Peptide Sequence: LHGGIDILVSNAAVNPFFGSLMDVTEEVWWDK

Total Number of Spectra: 1

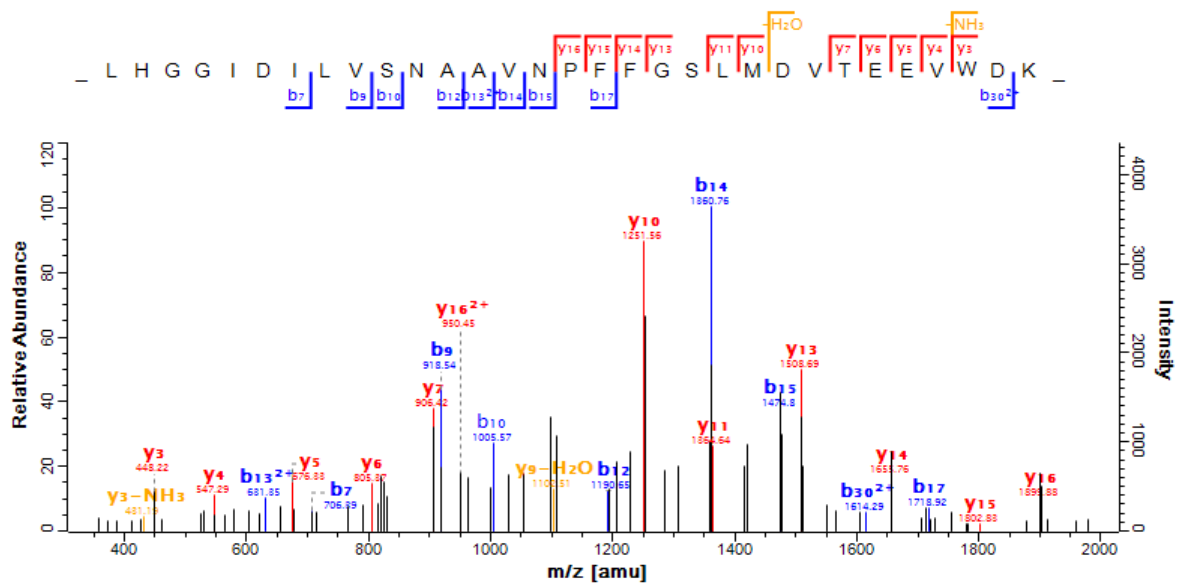
Number of Replicates (out of 8): 1

Best Match Score: 63.724

Best Match Posterior Error Probability: 6.71E-05

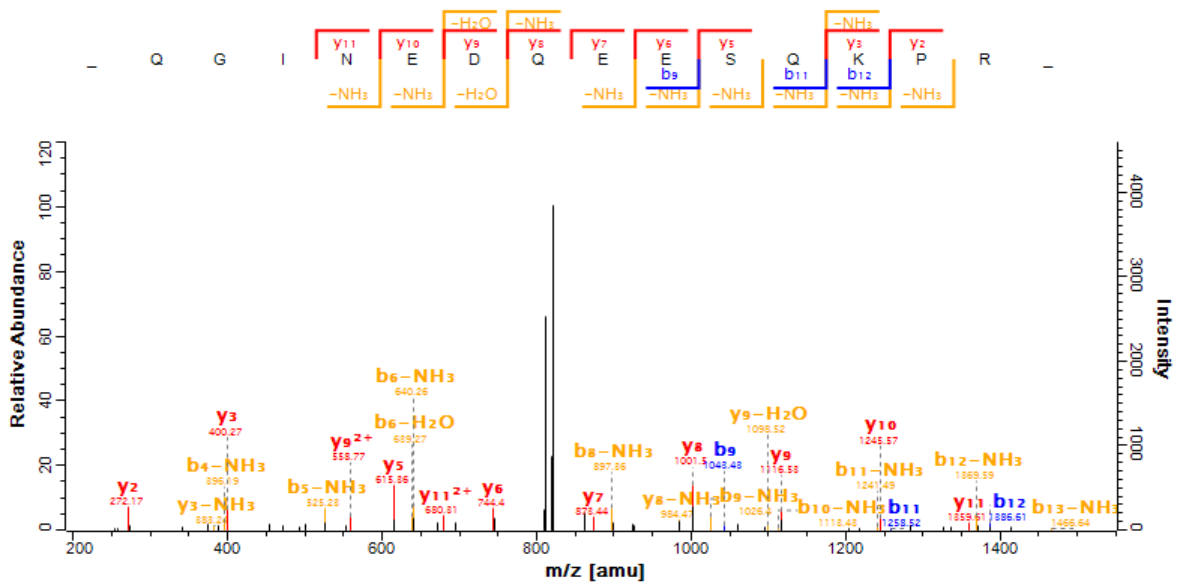
Best Match Spectrum:

Scan number	94731	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	DHRS4L2



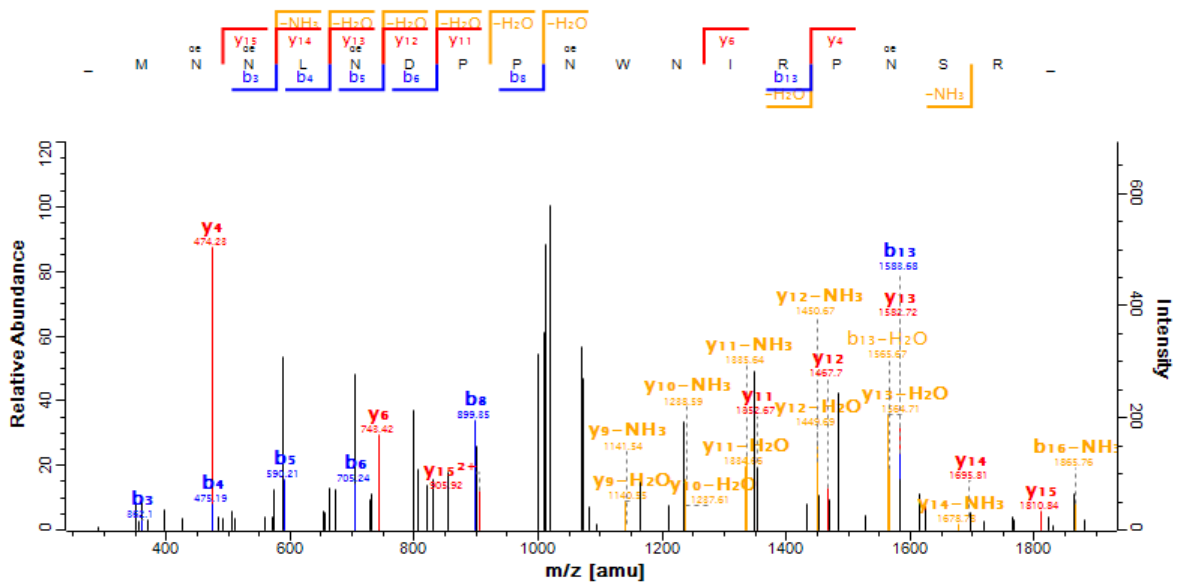
Protein Group ID: 665
Protein Accession Numbers: Q8TBZ6; D6R954
Gene Names: RG9MTD2
Peptide Sequence: QGINEDQEESQKPR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 113.76
Best Match Posterior Error Probability: 0.00057829
Best Match Spectrum:

Scan number 4401 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** RG9MTD2



Protein Group ID: 670
Protein Accession Numbers: Q96BQ5; D6R9R2
Gene Names: CCDC127
Peptide Sequence: MNNLNDPPNWNIRPNSR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 107.5
Best Match Posterior Error Probability: 0.0004282
Best Match Spectrum:

Scan number 21898 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CCDC127



Protein Group ID: 671

Protein Accession Numbers: Q8NEC7; Q8NEC7-3; D6R9W2

Gene Names: GSTCD

Peptide Sequence: VHTQETSEGLDSSSK

Total Number of Spectra: 1

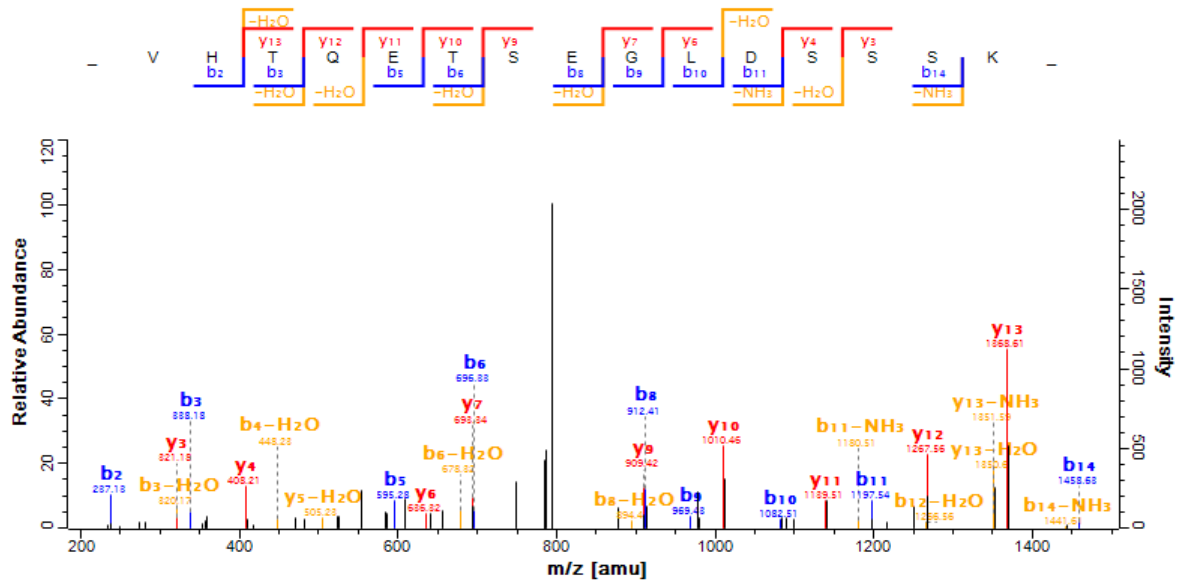
Number of Replicates (out of 8): 1

Best Match Score: 115.38

Best Match Posterior Error Probability: 8.87E-05

Best Match Spectrum:

Scan number 4511 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** GSTCD



Protein Group ID: 672

Protein Accession Numbers: D6RE79; Q14728; D6RA47; D6RIZ4

Gene Names: MFSD10

Peptide Sequence: DAADLLSPLALLR

Total Number of Spectra: 4

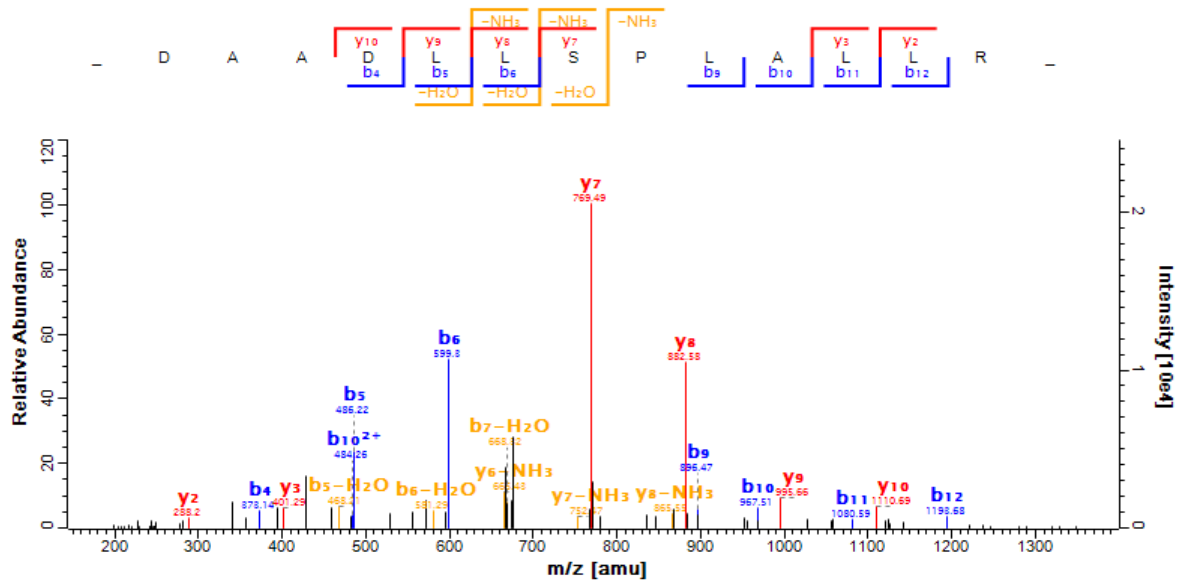
Number of Replicates (out of 8): 4

Best Match Score: 100.38

Best Match Posterior Error Probability: 0.00050349

Best Match Spectrum:

Scan number	88858	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	MFSD10



Protein Group ID: 683

Protein Accession Numbers: Q9BVS4; D6RDI3; H0Y919

Gene Names: RIOK2

Peptide Sequence: GQVVENNSVTEFSEEK

Total Number of Spectra: 7

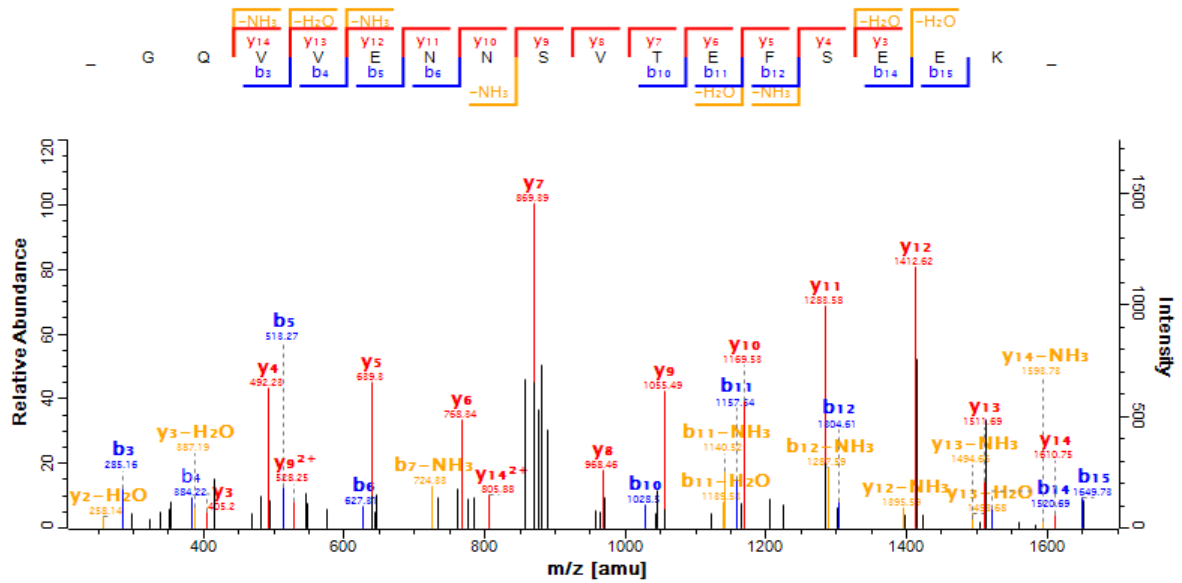
Number of Replicates (out of 8): 5

Best Match Score: 180.64

Best Match Posterior Error Probability: 2.64E-20

Best Match Spectrum:

Scan number 29618 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** RIOK2



Protein Group ID: 684

Protein Accession Numbers: Q709F0; Q709F0-2; Q709F0-3; D6RDI8

Gene Names: ACAD11

Peptide Sequence: VEGLWNLFLPAVSGLSLHVDYALIAEETGK

Total Number of Spectra: 2

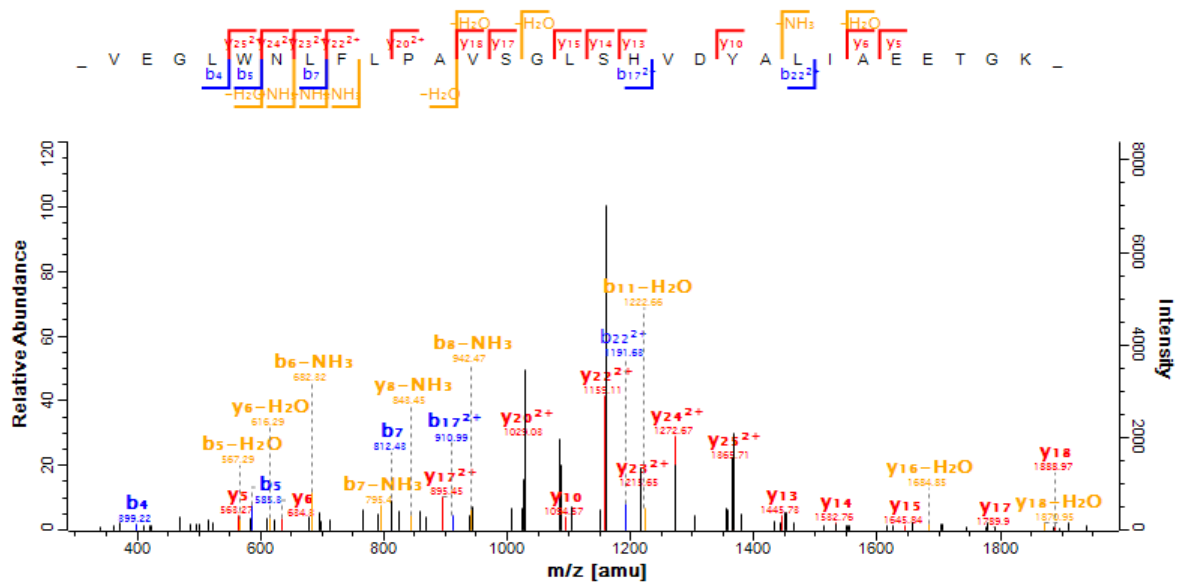
Number of Replicates (out of 8): 2

Best Match Score: 61.417

Best Match Posterior Error Probability: 0.00033224

Best Match Spectrum:

Scan number 93990 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ACAD11



Protein Group ID: 686

Protein Accession Numbers: Q9NP73; Q9NP73-3; D6RE84; Q9NP73-2

Gene Names: ALG13

Peptide Sequence: LMNNHQLELAK

Total Number of Spectra: 1

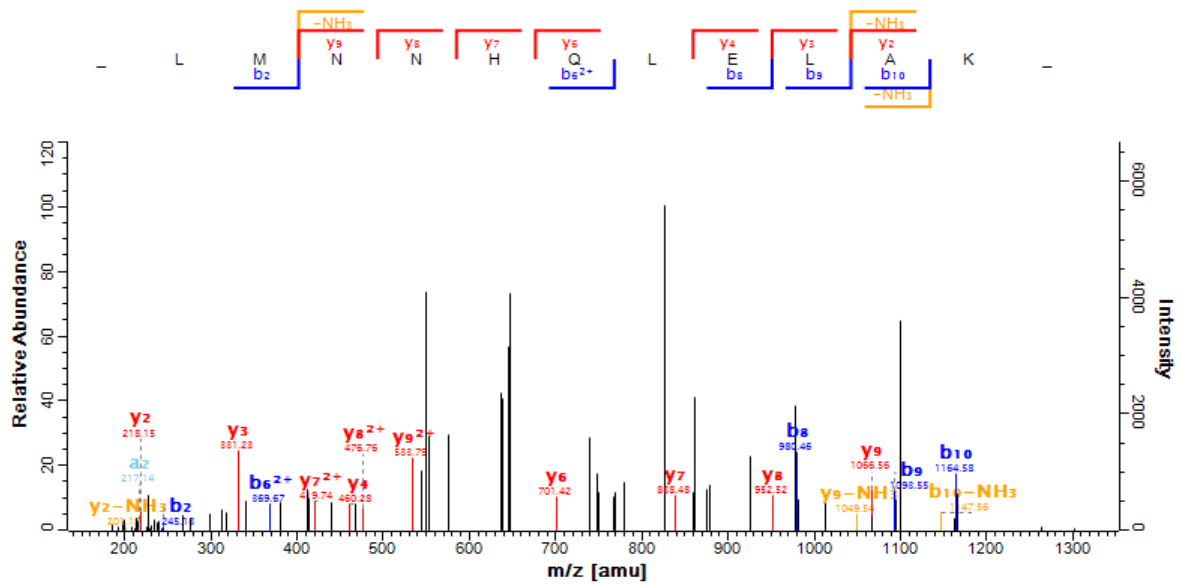
Number of Replicates (out of 8): 1

Best Match Score: 89.266

Best Match Posterior Error Probability: 0.0015539

Best Match Spectrum:

Scan number	22556	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	ALG13



Protein Group ID: 688

Protein Accession Numbers: O00584; D6RHI9; D6REQ6; H0YAE9

Gene Names: RNASET2

Peptide Sequence: HGTCAAQVDALNSQK

Total Number of Spectra: 4

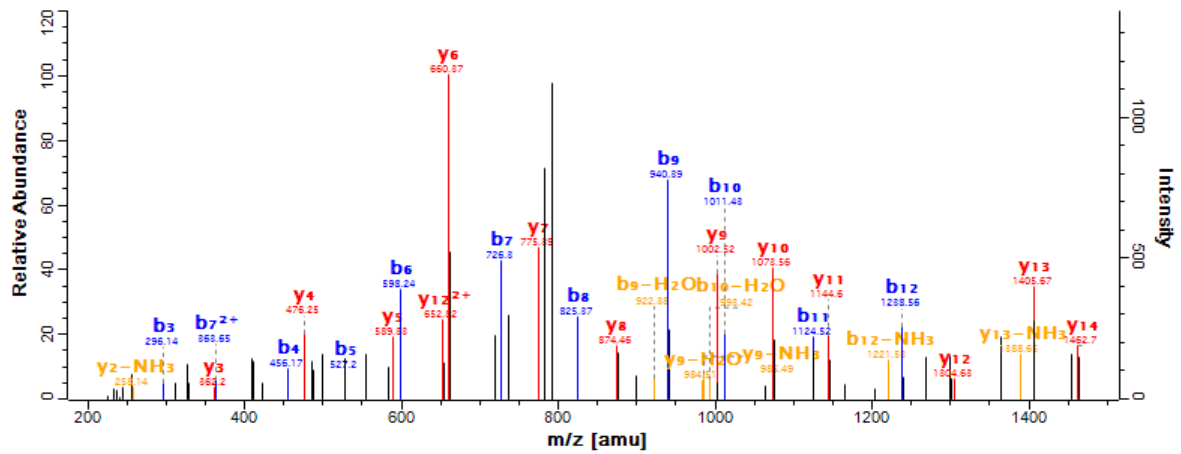
Number of Replicates (out of 8): 3

Best Match Score: 149.99

Best Match Posterior Error Probability: 8.66E-07

Best Match Spectrum:

Scan number 11730 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** RNASET2



Protein Group ID: 692

Protein Accession Numbers: P55285; P55285-2; D6RF86

Gene Names: CDH6

Peptide Sequence: VEASNPYVEPR

Total Number of Spectra: 6

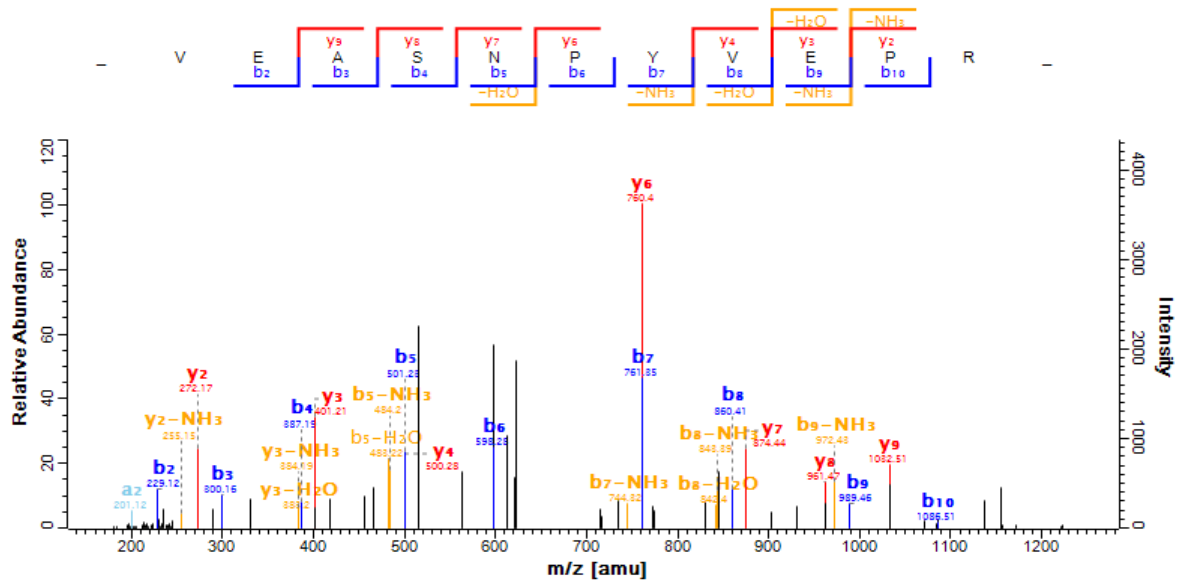
Number of Replicates (out of 8): 5

Best Match Score: 162.49

Best Match Posterior Error Probability: 1.17E-05

Best Match Spectrum:

Scan number	16540	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	CDH6



Protein Group ID: 697

Protein Accession Numbers: Q13888; Q6P1K8; F5GZM1; J3KQC7; D6RID8; D6RJD3; D6RGC9; D6RIT7

Gene Names: GTF2H2;GTF2H2C

Peptide Sequence: TMEDQDLKPNR

Total Number of Spectra: 7

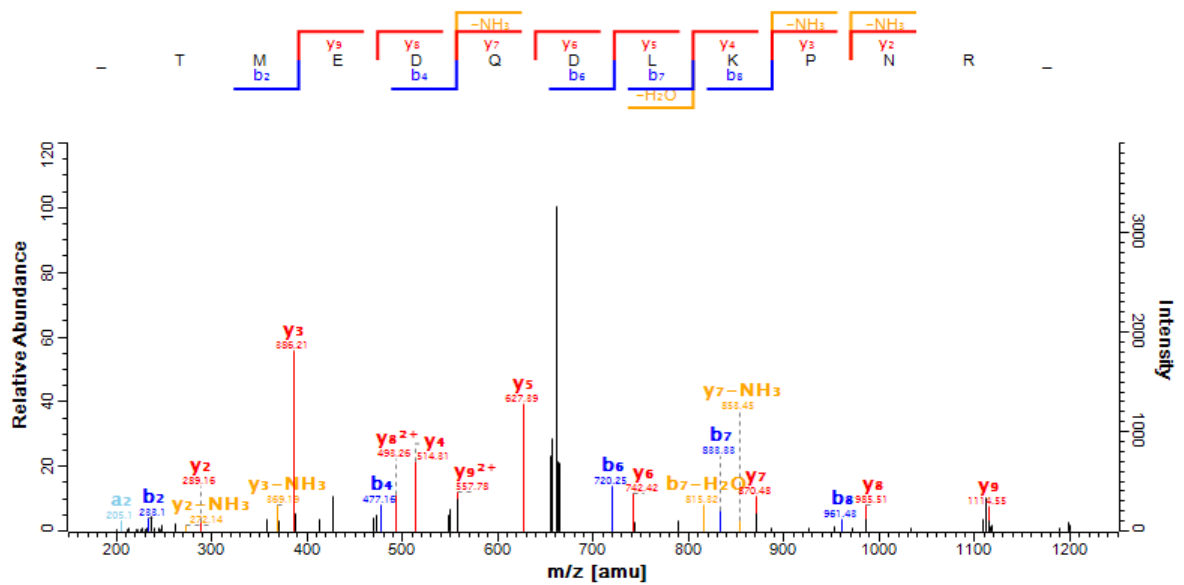
Number of Replicates (out of 8): 6

Best Match Score: 133.07

Best Match Posterior Error Probability: 6.24E-06

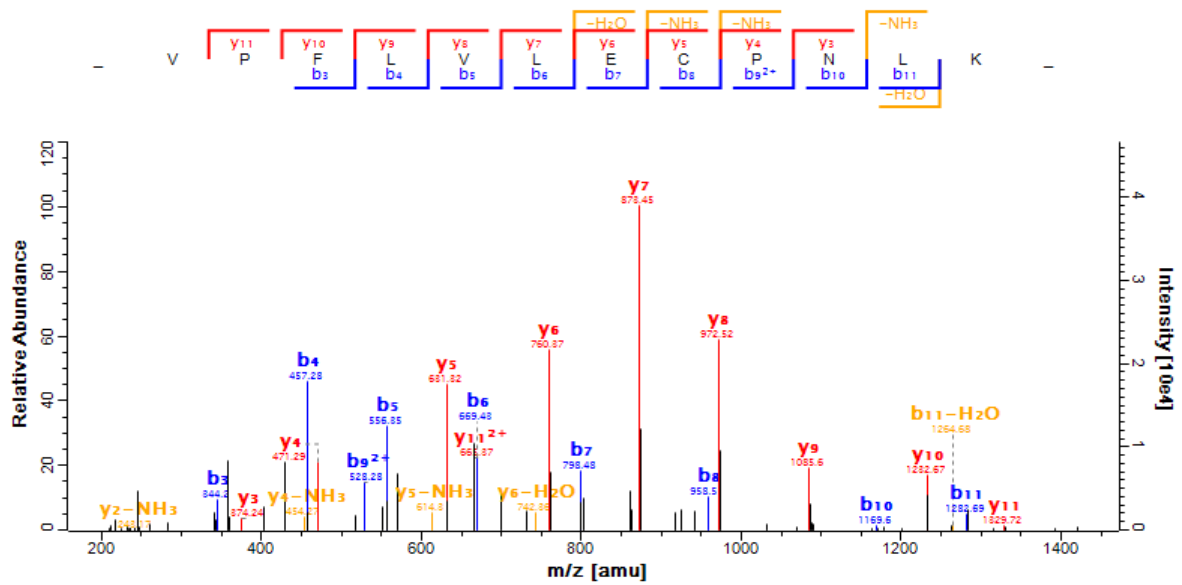
Best Match Spectrum:

Scan number	9062	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS: CID	Genenames	GTF2H2;GTF2H2C



Protein Group ID: 699
Protein Accession Numbers: D6RH22; Q9NRPO
Gene Names: OSTC
Peptide Sequence: VPFLVLECPNLK
Total Number of Spectra: 11
Number of Replicates (out of 8): 8
Best Match Score: 136.53
Best Match Posterior Error Probability: 7.56E-05
Best Match Spectrum:

Scan number 65301 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** OSTC



Protein Group ID: 703

Protein Accession Numbers: P35680; H0YL84; P35680-2; E0YMJ9; P35680-3

Gene Names: HNF1B

Peptide Sequence: ELQALNTEEEAAEQR

Total Number of Spectra: 2

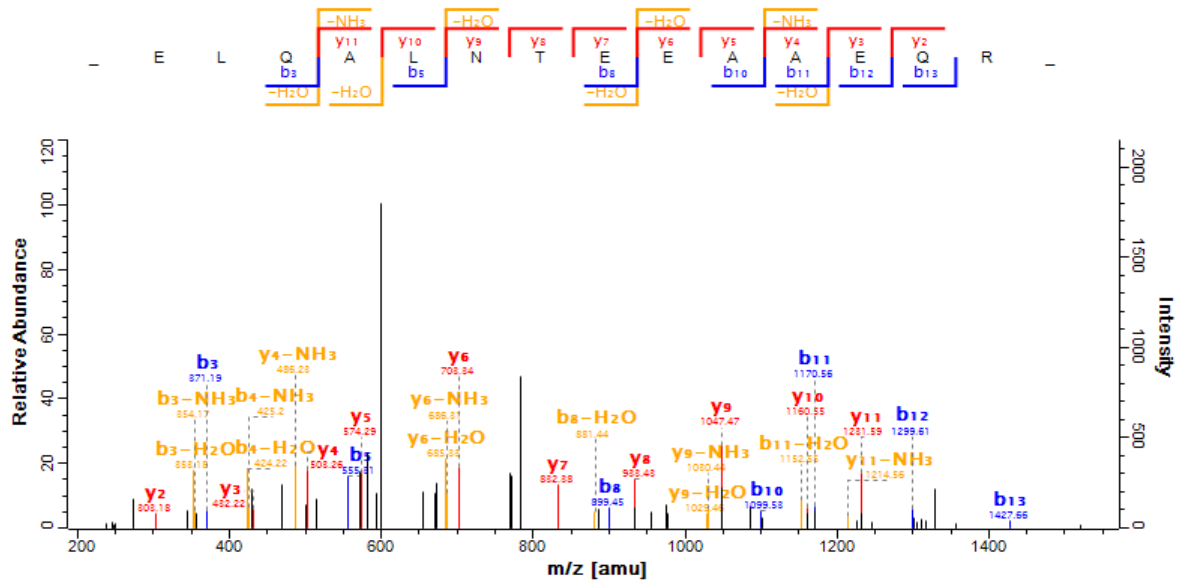
Number of Replicates (out of 8): 2

Best Match Score: 158.93

Best Match Posterior Error Probability: 2.05E-09

Best Match Spectrum:

Scan number	25933	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	HNF1B



Protein Group ID: 705

Protein Accession Numbers: F6SH78; Q9NYP7; E2QRH7

Gene Names: ELOVL5

Peptide Sequence: DHQNGSMAAVNGHTNSFSPLENNVK

Total Number of Spectra: 2

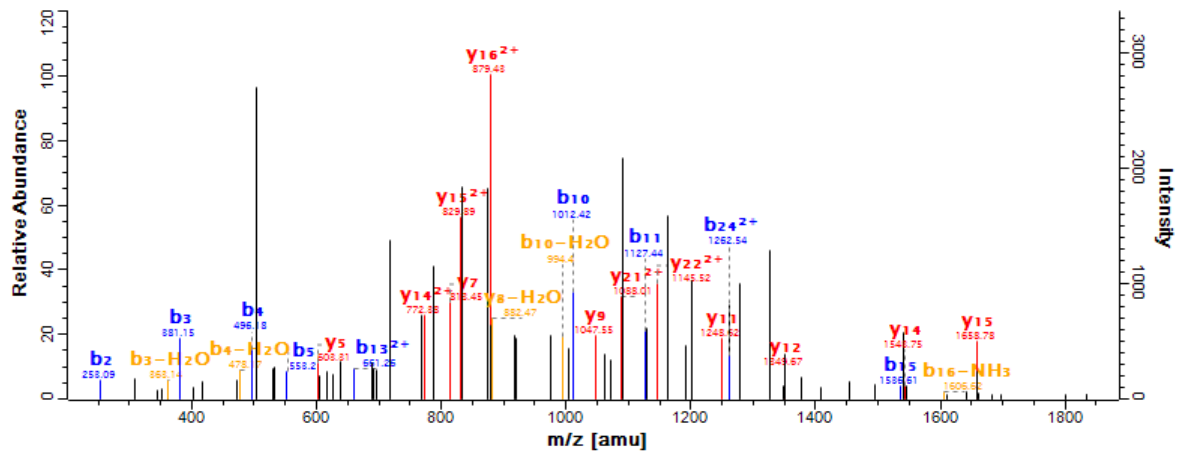
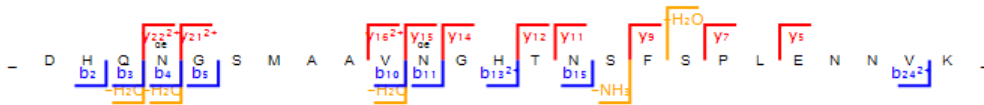
Number of Replicates (out of 8): 2

Best Match Score: 83.602

Best Match Posterior Error Probability: 0.00073784

Best Match Spectrum:

Scan number 37718 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ELOVL5



Protein Group ID: 707

Protein Accession Numbers: O75330-3; O75330; O75330-2; O75330-4; E3W978

Gene Names: HMMR

Peptide Sequence: NAEDVQHQLATISSNQEYVR

Total Number of Spectra: 1

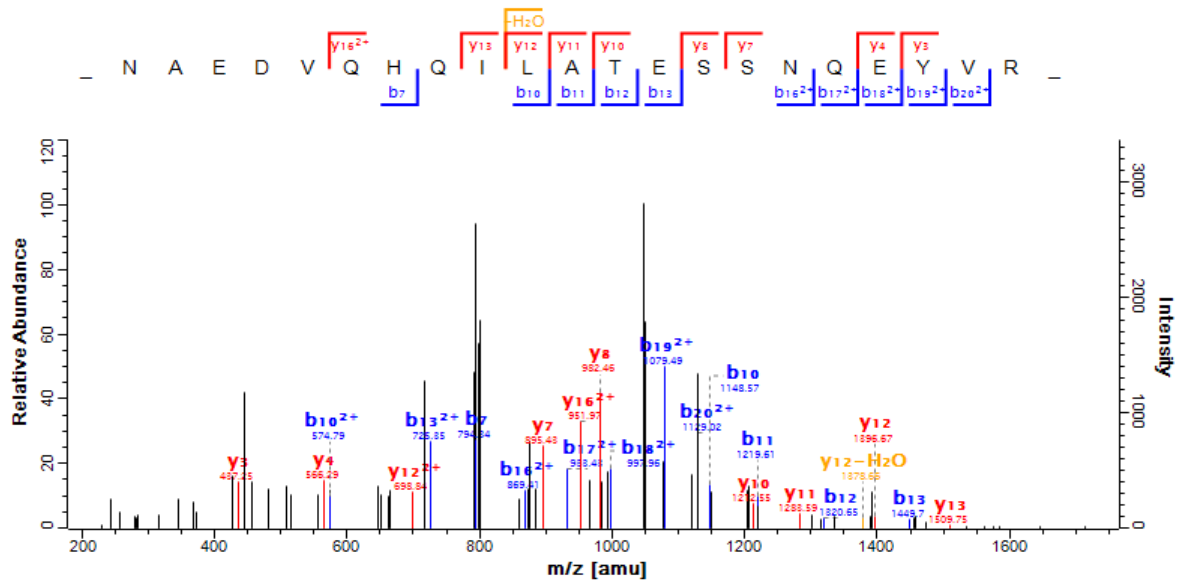
Number of Replicates (out of 8): 1

Best Match Score: 88.574

Best Match Posterior Error Probability: 9.80E-05

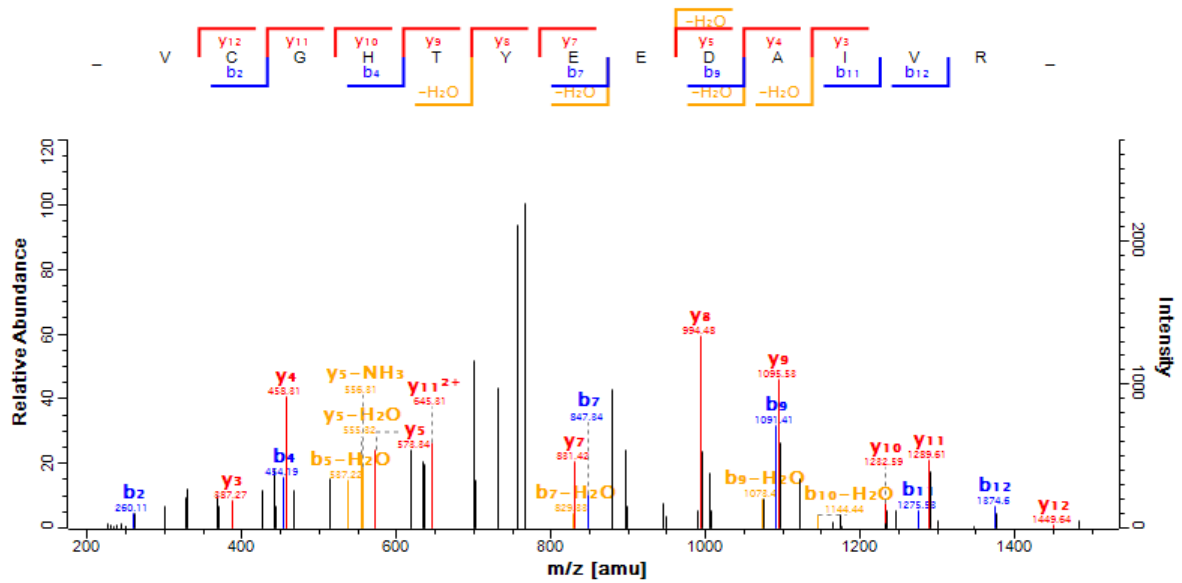
Best Match Spectrum:

Scan number	40126	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	HMMR



Protein Group ID: 710
Protein Accession Numbers: Q96MF7; E5RFJ1
Gene Names: NSMCE2
Peptide Sequence: VCGHTYEEDAIVR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 113.99
Best Match Posterior Error Probability: 0.00025087
Best Match Spectrum:

Scan number 19542 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** NSMCE2



Protein Group ID: 712

Protein Accession Numbers: Q75QN2; Q75QN2-2; J3KNV5; E5RG48; E5RIN8; H0YBQ1; E5RJF0; E5RJL5

Gene Names: INTS8

Peptide Sequence: PGPPQLSVMNQMEK

Total Number of Spectra: 1

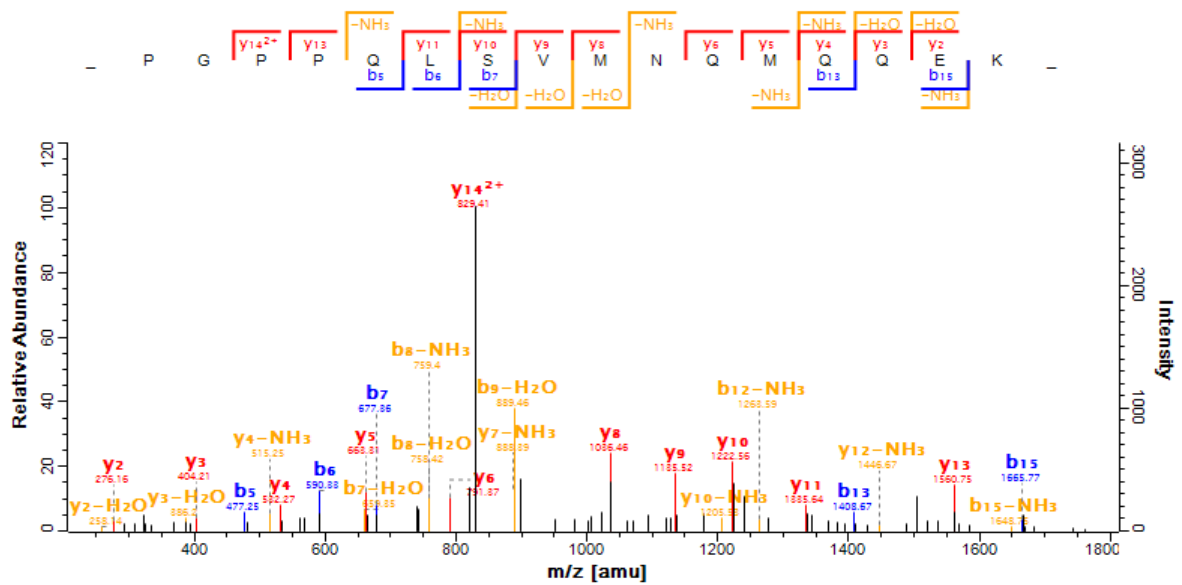
Number of Replicates (out of 8): 1

Best Match Score: 118.47

Best Match Posterior Error Probability: 0.00017722

Best Match Spectrum:

Scan number 42584 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS: CID **Genenames** INTS8



Protein Group ID: 714

Protein Accession Numbers: Q9BRU9; E5RGP0; Q9BRU9-2; G3XAM4

Gene Names: UTP23

Peptide Sequence: YLMGETQLCTTR

Total Number of Spectra: 1

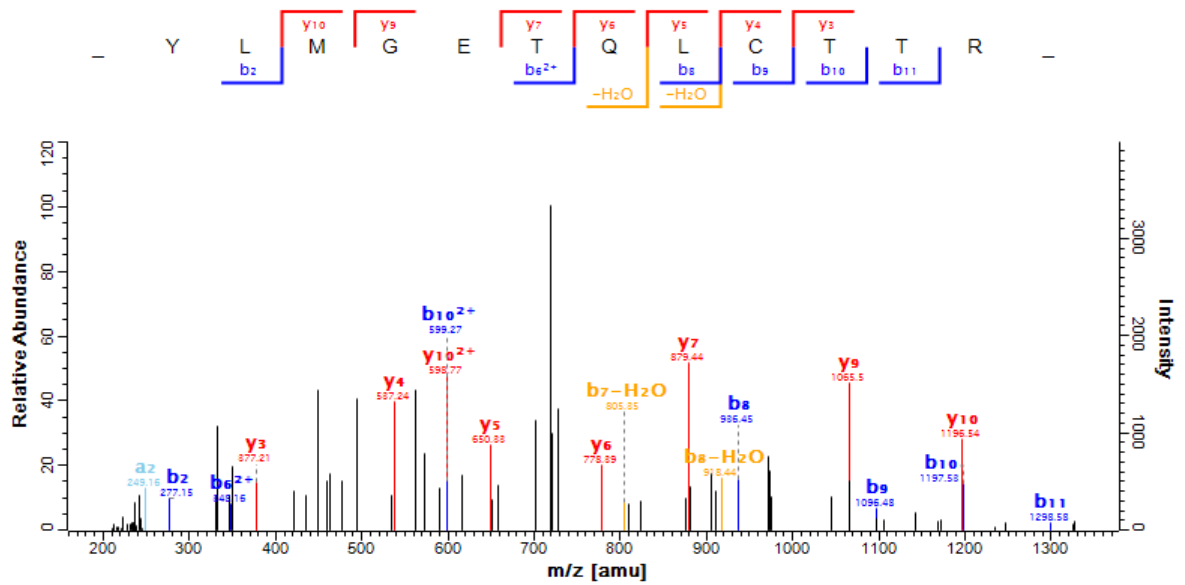
Number of Replicates (out of 8): 1

Best Match Score: 90.731

Best Match Posterior Error Probability: 0.0013583

Best Match Spectrum:

Scan number 34827 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** UTP23



Protein Group ID: 715

Protein Accession Numbers: Q9H6H4; E5RGS2; E5RJV5; Q9H6H4-2

Gene Names: REEP4

Peptide Sequence: EIDAYIVQAK

Total Number of Spectra: 2

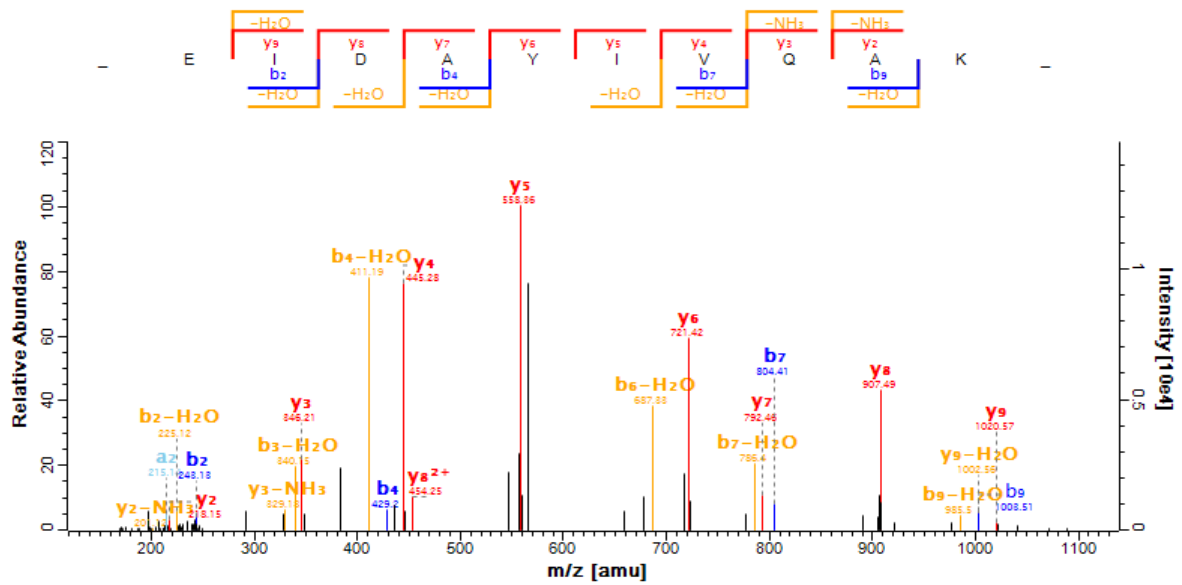
Number of Replicates (out of 8): 2

Best Match Score: 137.95

Best Match Posterior Error Probability: 1.07E-05

Best Match Spectrum:

Scan number 32954 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** REEP4



Protein Group ID: 718

Protein Accession Numbers: Q93045-2; Q93045; E5RGX5

Gene Names: STMN2

Peptide Sequence: ALEENNNFSK

Total Number of Spectra: 16

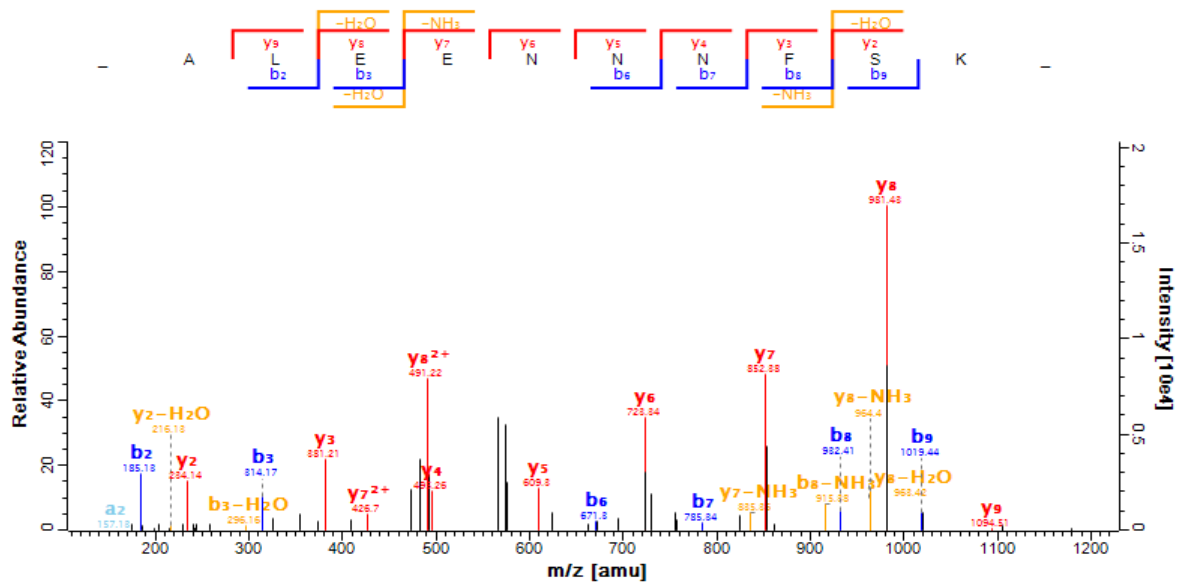
Number of Replicates (out of 8): 8

Best Match Score: 134.3

Best Match Posterior Error Probability: 7.36E-06

Best Match Spectrum:

Scan number 9765 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** STMN2



Protein Group ID: 721

Protein Accession Numbers: Q9Y5V0; E5RHR6; H0YAP1; E5RHV4

Gene Names: ZNF706

Peptide Sequence: AALIYTCTVCR

Total Number of Spectra: 2

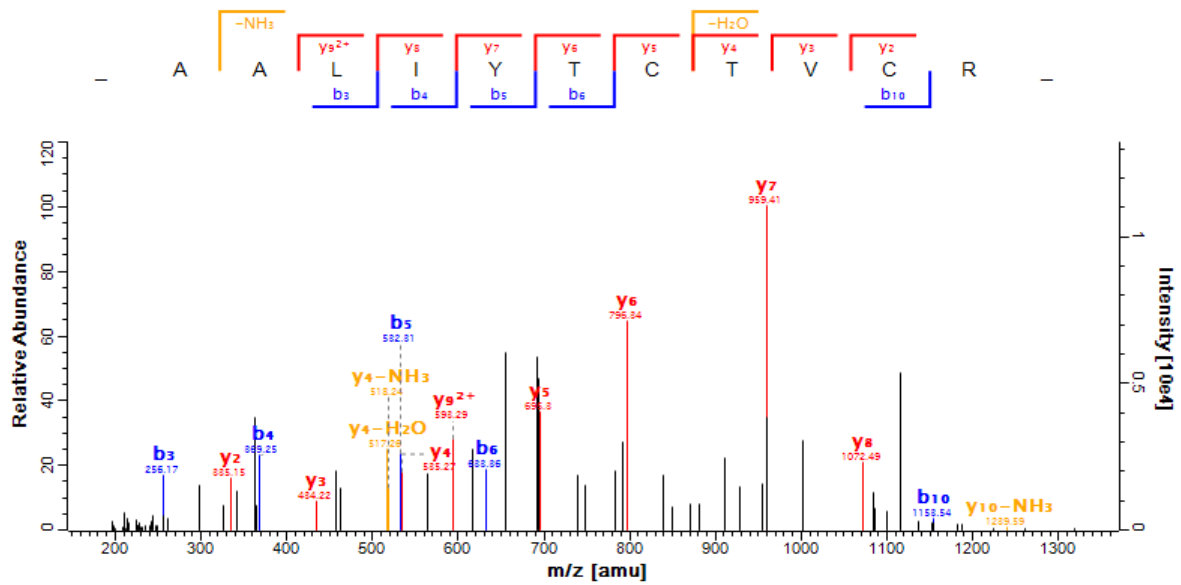
Number of Replicates (out of 8): 2

Best Match Score: 87.568

Best Match Posterior Error Probability: 0.0017303

Best Match Spectrum:

Scan number 32018 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ZNF706



Protein Group ID: 724

Protein Accession Numbers: Q9NPA8; E5RHX8; G3V117

Gene Names: ENY2

Peptide Sequence: GLEHVTVDLVAEITPK

Total Number of Spectra: 6

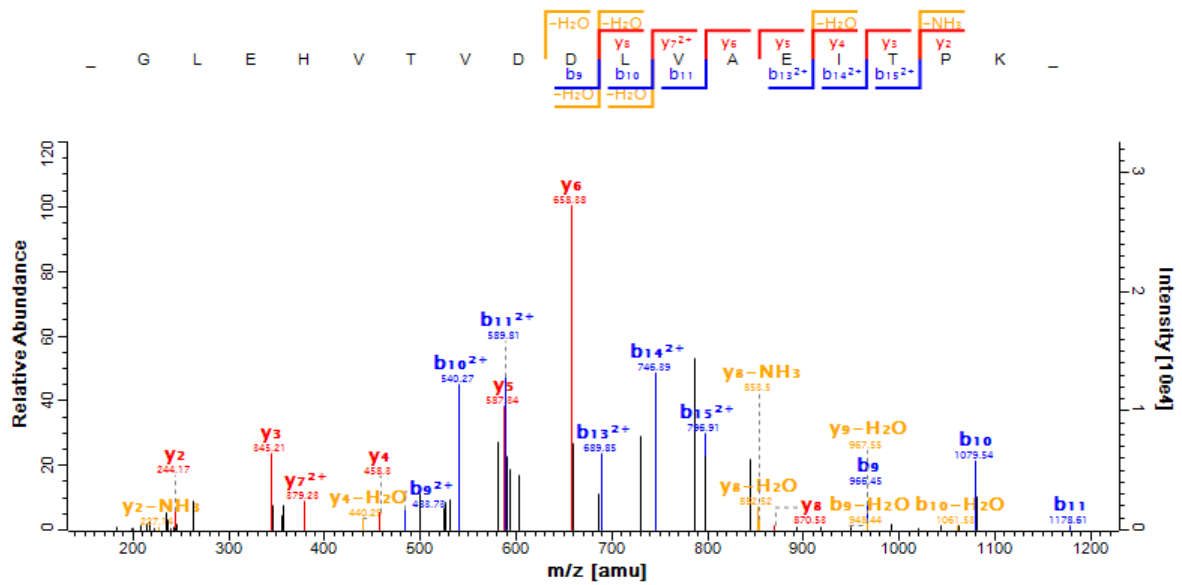
Number of Replicates (out of 8): 6

Best Match Score: 118.52

Best Match Posterior Error Probability: 0.00011484

Best Match Spectrum:

Scan number 69846 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ENY2



Protein Group ID: 726

Protein Accession Numbers: E9PFX0; Q96D42; E5RIF6

Gene Names: HAVCR1

Peptide Sequence: VGGEAGPSVTLPLCHYSGAVTSMCWNR

Total Number of Spectra: 6

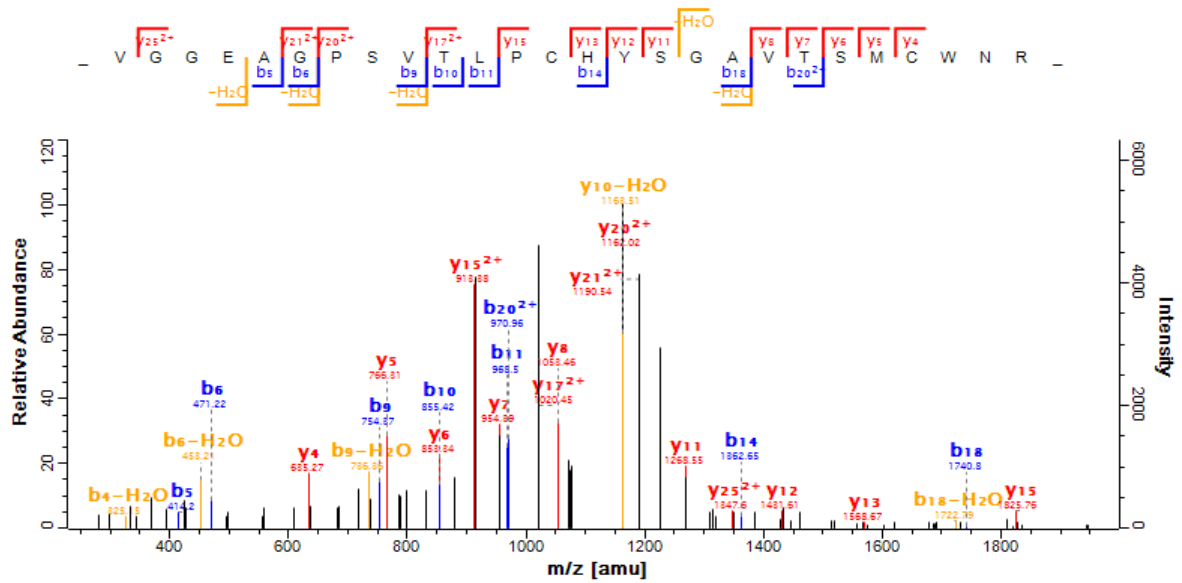
Number of Replicates (out of 8): 5

Best Match Score: 91.238

Best Match Posterior Error Probability: 1.21E-05

Best Match Spectrum:

Scan number 53849 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** HAVCR1



Protein Group ID: 732

Protein Accession Numbers: Q15390; E5RJS5; E7EP84; H0YBZ4

Gene Names: MTFR1

Peptide Sequence: SRPPLQDDLLFFEK

Total Number of Spectra: 1

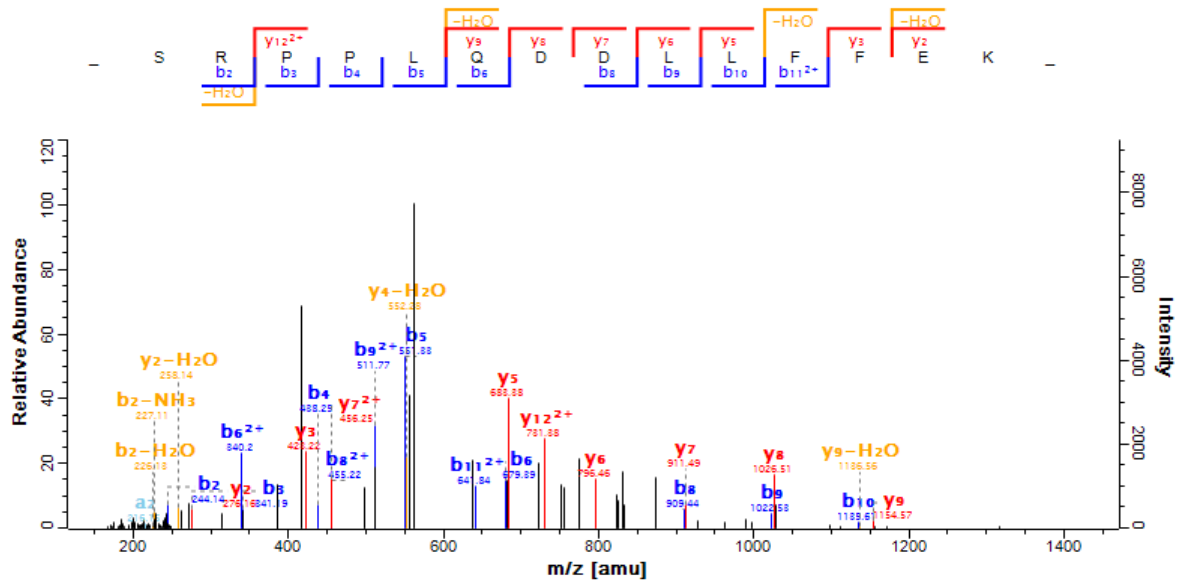
Number of Replicates (out of 8): 1

Best Match Score: 123.76

Best Match Posterior Error Probability: 0.00015484

Best Match Spectrum:

Scan number	63939	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	MTFR1



Protein Group ID: 736

Protein Accession Numbers: Q99952; E7EMB8; Q99952-2

Gene Names: PTPN18

Peptide Sequence: RGAPAGASGTQTGTGTGTGAR

Total Number of Spectra: 1

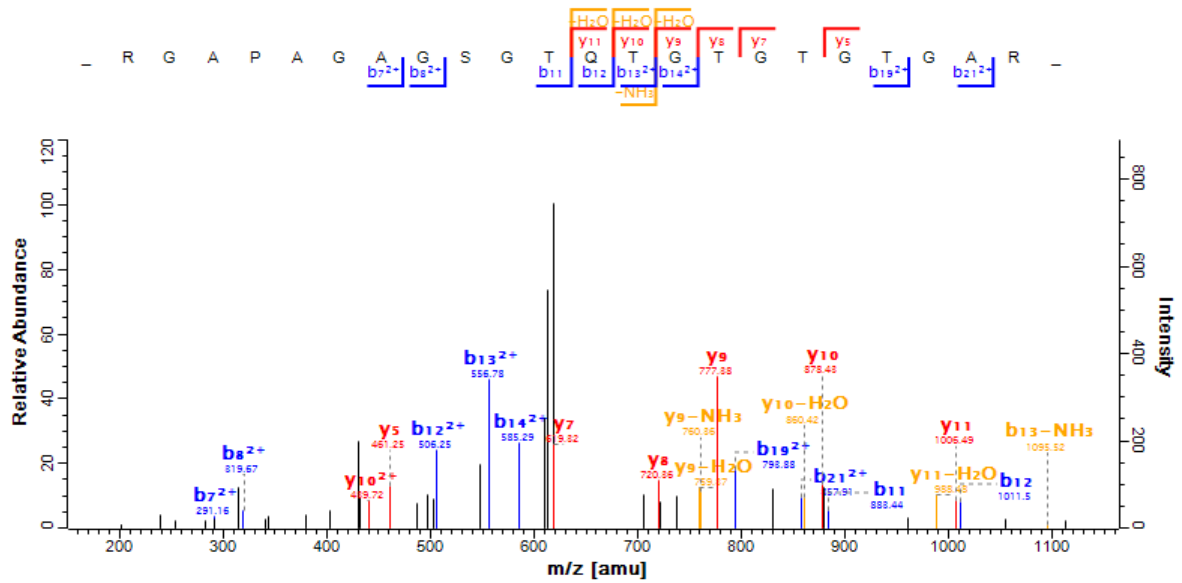
Number of Replicates (out of 8): 1

Best Match Score: 65.085

Best Match Posterior Error Probability: 0.0033715

Best Match Spectrum:

Scan number	3597	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	PTPN18



Protein Group ID: 737

Protein Accession Numbers: O95208; E9PBC2; O95208-2; I3L2B2; E7EMC3; E9PBC1; F6PQP6; J3QLN2; J3KSC7; J3KSA6; J3QRG9; J3KTF6; J3KSF8

Gene Names: EPN2

Peptide Sequence: NIVNNYSEAEIK

Total Number of Spectra: 3

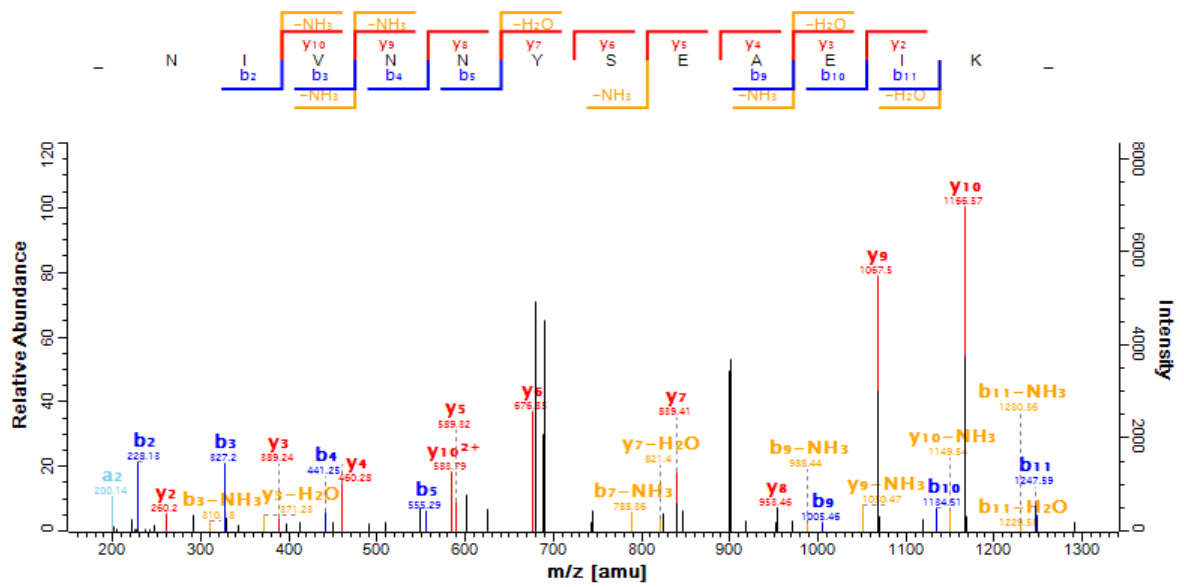
Number of Replicates (out of 8): 3

Best Match Score: 155.86

Best Match Posterior Error Probability: 6.66E-07

Best Match Spectrum:

Scan number 31161 Raw file A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS: CID Genenames EPN2



Protein Group ID: 738

Protein Accession Numbers: Q96PM5; Q96PM5-2; E7ETW5; J3KPI0; E7EMC8

Gene Names: RCHY1

Peptide Sequence: ICESYNTAQAGGR

Total Number of Spectra: 2

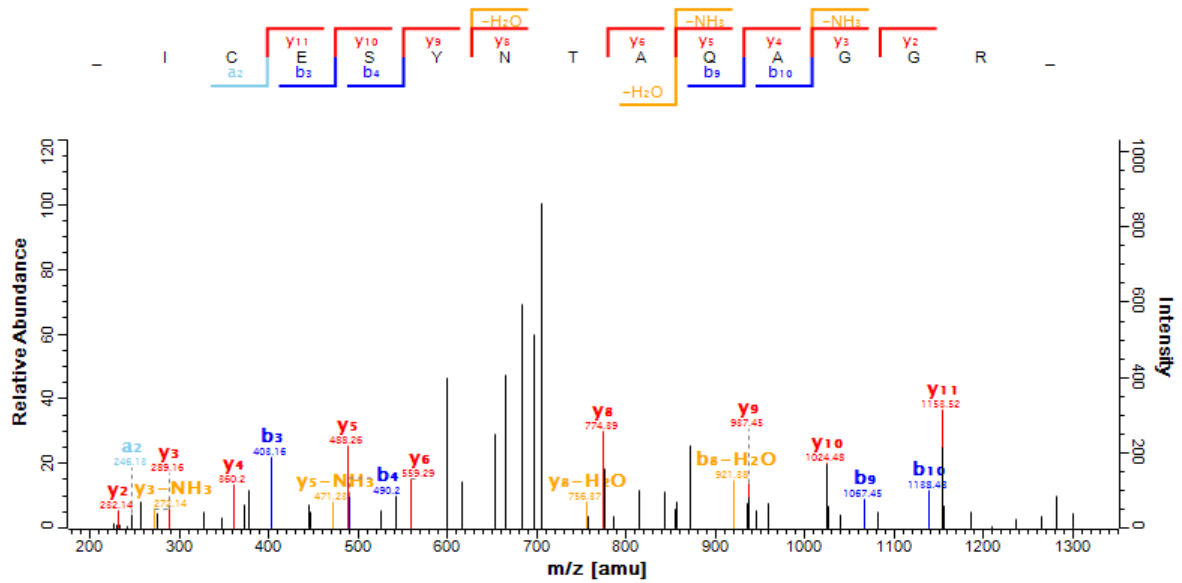
Number of Replicates (out of 8): 2

Best Match Score: 111.12

Best Match Posterior Error Probability: 0.00030214

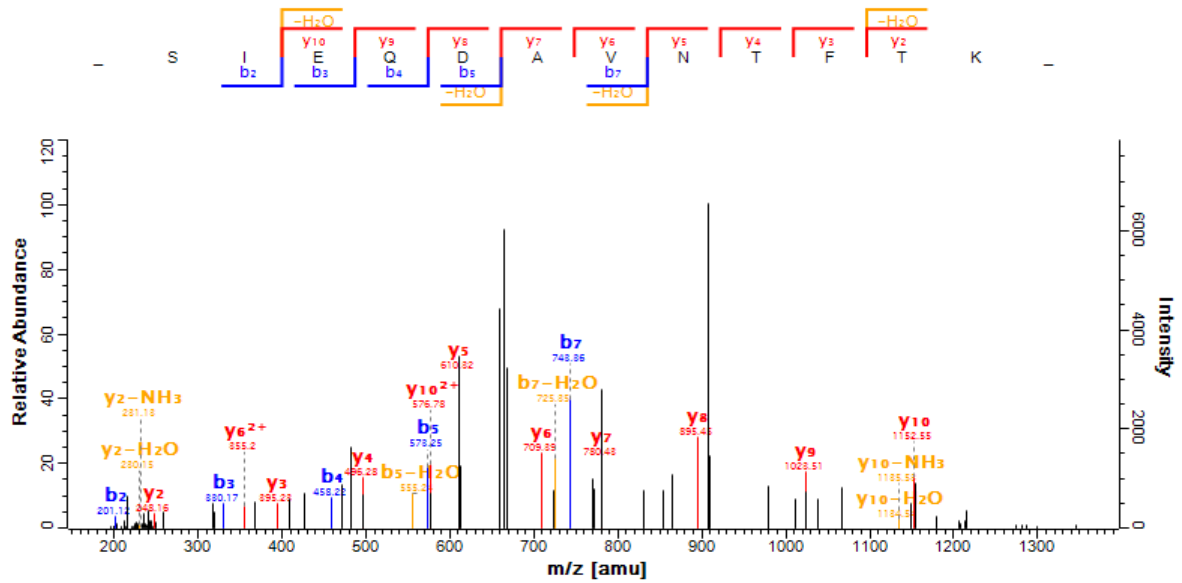
Best Match Spectrum:

Scan number 10162 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** RCHY1



Protein Group ID: 739
Protein Accession Numbers: O43572; E7EMD6
Gene Names: AKAP10
Peptide Sequence: SIEQDAVNTFTK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 98.337
Best Match Posterior Error Probability: 0.00059274
Best Match Spectrum:

Scan number 43127 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** AKAP10



Protein Group ID: 749

Protein Accession Numbers: Q8TB03; E7EN46; Q8TB03-2

Gene Names: CXorf38

Peptide Sequence: IEQLLTSDWAVHIPEEDQR

Total Number of Spectra: 2

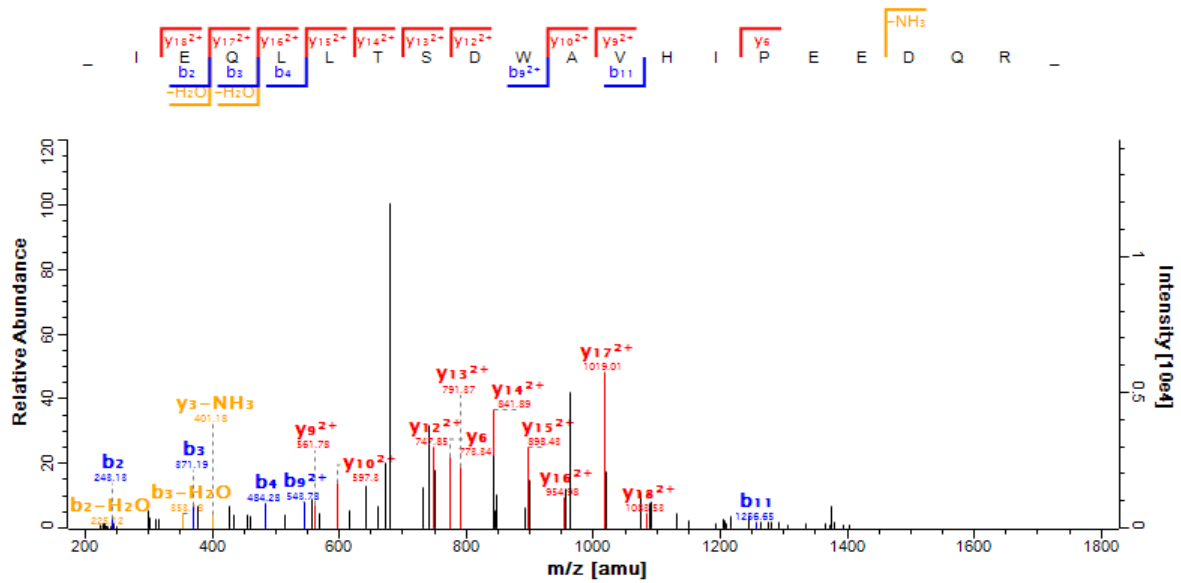
Number of Replicates (out of 8): 1

Best Match Score: 67.646

Best Match Posterior Error Probability: 0.0033773

Best Match Spectrum:

Scan number 64719 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CXorf38



Protein Group ID: 751

Protein Accession Numbers: P28290; P28290-3; E9PHV5; P28290-2; E7END2; E7EUL7

Gene Names: SSFA2

Peptide Sequence: RVMEHDGQSLVK

Total Number of Spectra: 1

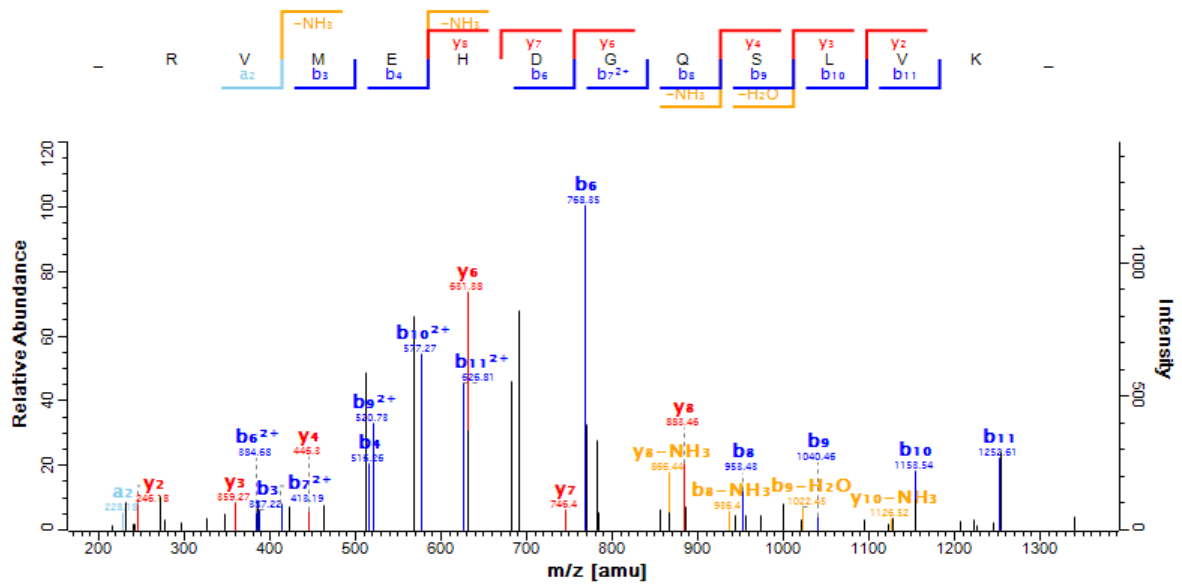
Number of Replicates (out of 8): 1

Best Match Score: 127.56

Best Match Posterior Error Probability: 0.00023681

Best Match Spectrum:

Scan number	8741	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	SSFA2



Protein Group ID: 754

Protein Accession Numbers: Q68CP9; Q68CP9-3; F8WCU9; F8W108; E7ENG3

Gene Names: ARID2

Peptide Sequence: KIEVMENPSCR

Total Number of Spectra: 1

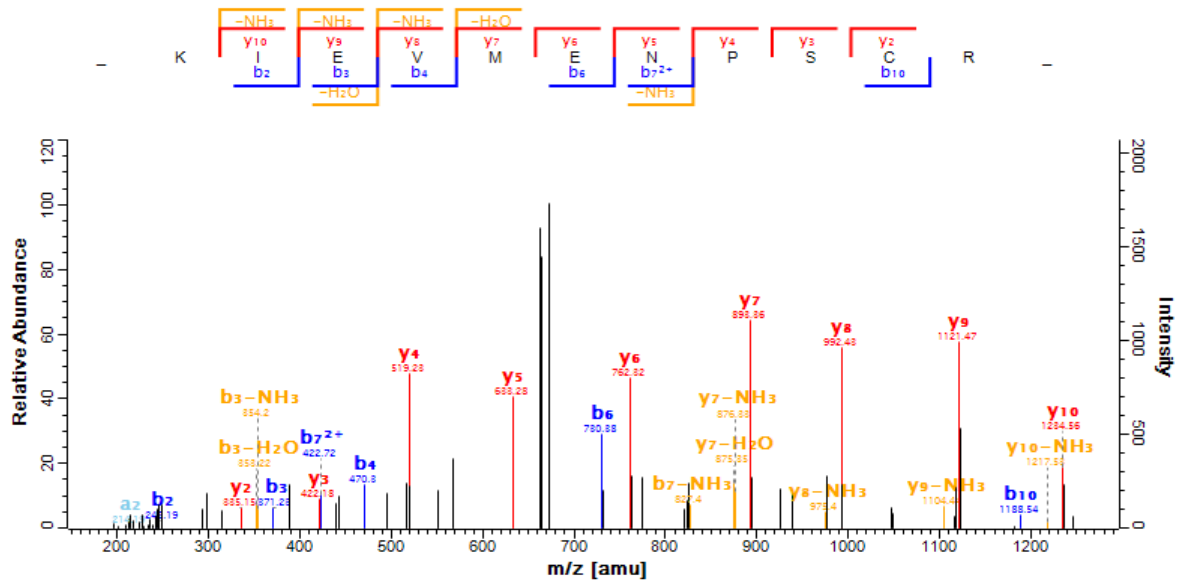
Number of Replicates (out of 8): 1

Best Match Score: 114.24

Best Match Posterior Error Probability: 0.00025825

Best Match Spectrum:

Scan number 16164 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ARID2



Protein Group ID: 756

Protein Accession Numbers: Q8NF91; E9PEL9; Q8NF91-4; E7ENN3; Q8NF91-2; Q8NF91-8

Gene Names: SYNE1

Peptide Sequence: VLFTSLADNK

Total Number of Spectra: 1

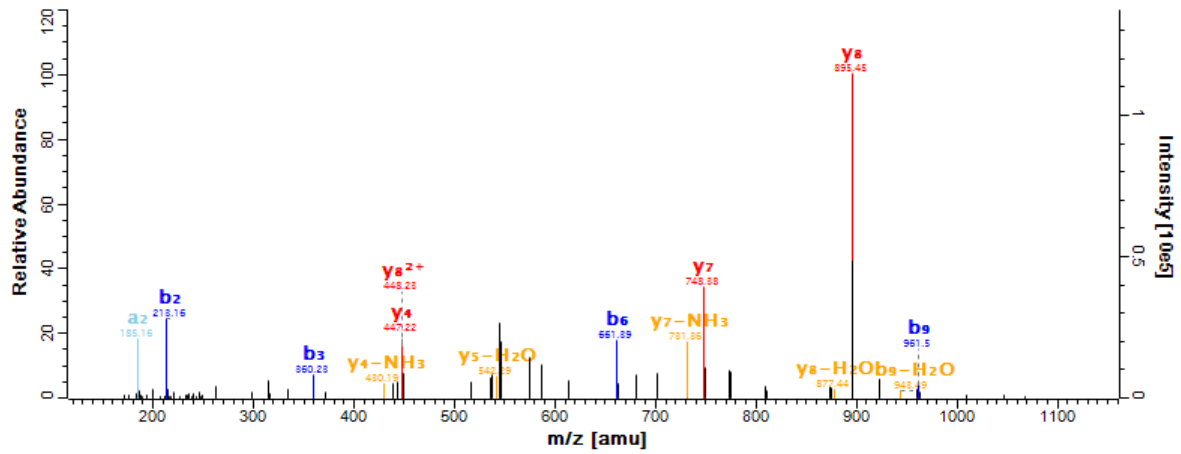
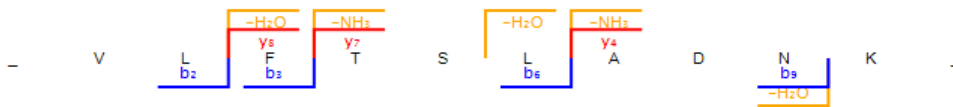
Number of Replicates (out of 8): 1

Best Match Score: 89.247

Best Match Posterior Error Probability: 0.0020755

Best Match Spectrum:

Scan number	34645	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	SYNE1



Protein Group ID: 760

Protein Accession Numbers: J3KNB2; Q9NYB9; Q9NYB9-4; E7EP65; E7EW77; Q9NYB9-2; E9PEZ7; F8WEB9; F8WAQ3; F8WBL5

Gene Names: ABI2

Peptide Sequence: VADYCENNYIQSADK

Total Number of Spectra: 1

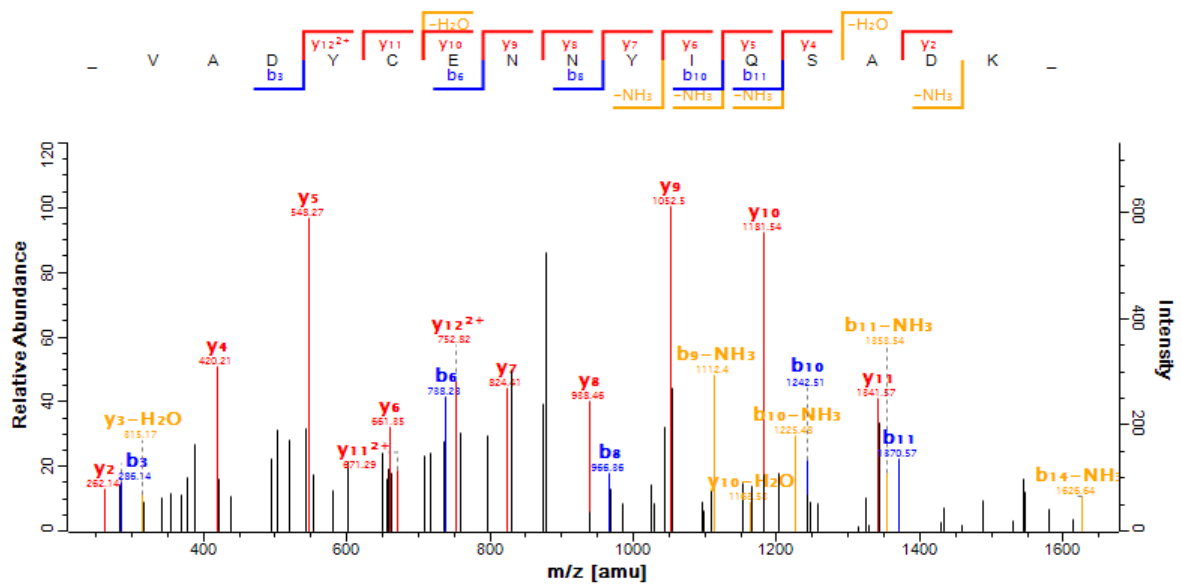
Number of Replicates (out of 8): 1

Best Match Score: 97.836

Best Match Posterior Error Probability: 0.00028316

Best Match Spectrum:

Scan number	27808	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	ABI2



Protein Group ID: 765

Protein Accession Numbers: E7EPH8; J3KNL5; Q3KR37; Q3KR37-2; E9PRD6

Gene Names: GRAMD1B

Peptide Sequence: SPSTPEQGVQR

Total Number of Spectra: 3

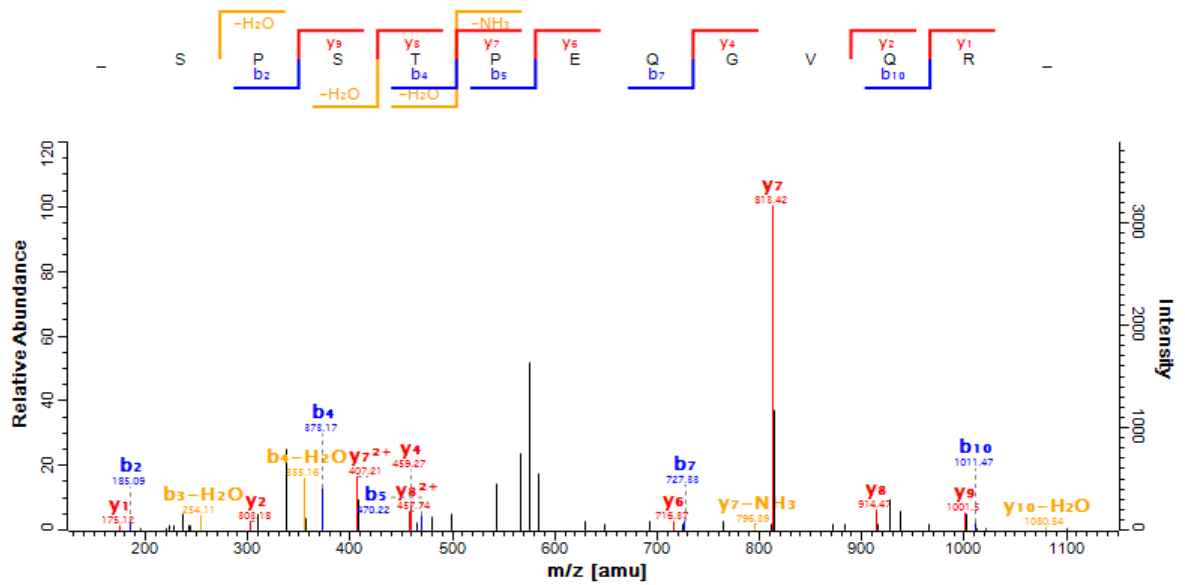
Number of Replicates (out of 8): 3

Best Match Score: 94.767

Best Match Posterior Error Probability: 0.00098239

Best Match Spectrum:

Scan number 5048 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** GRAMD1B



Protein Group ID: 779

Protein Accession Numbers: E7EQP8; F8W9Q9; Q96PV6-2; Q96PV6; E7EWC7

Gene Names: LENG8

Peptide Sequence: R P F A V T T Q S F G S N A E G Q H S G F G P Q P N P E K

Total Number of Spectra: 2

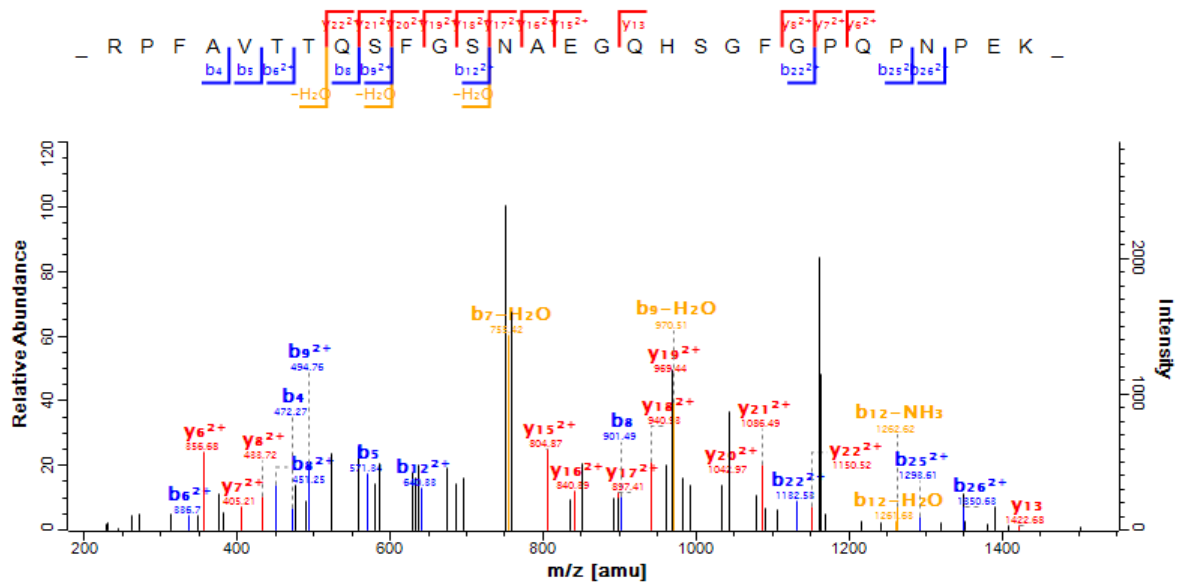
Number of Replicates (out of 8): 2

Best Match Score: 64.069

Best Match Posterior Error Probability: 0.00020283

Best Match Spectrum:

Scan number 38631 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** LENG8



Protein Group ID: 792

Protein Accession Numbers: Q5R3I4; E7ES35; H7C089

Gene Names: TTC38

Peptide Sequence: DASESPGENCQHLLAR

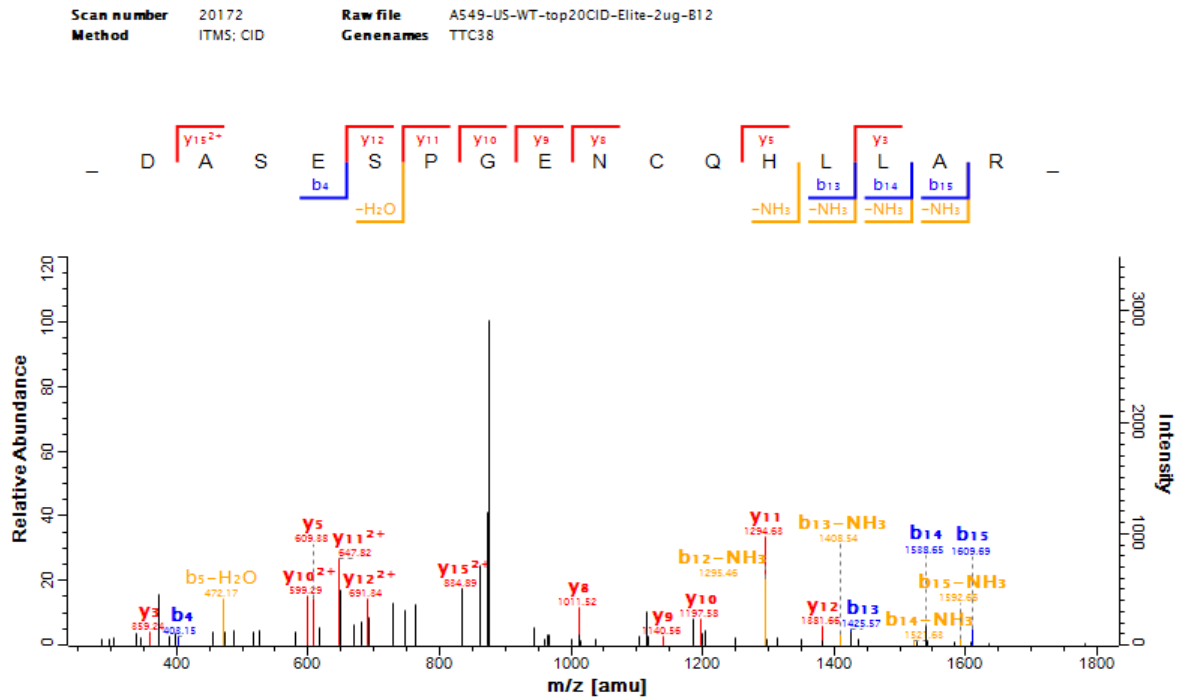
Total Number of Spectra: 1

Number of Replicates (out of 8): 1

Best Match Score: 88.561

Best Match Posterior Error Probability: 0.0006397

Best Match Spectrum:



Protein Group ID: 794

Protein Accession Numbers: F2Z2Y1; O95677; O95677-4; E9PLN6; O95677-2; O95677-5; E7ESD5; O95677-3

Gene Names: EYA4

Peptide Sequence: TCTESDVSQSQNSR

Total Number of Spectra: 6

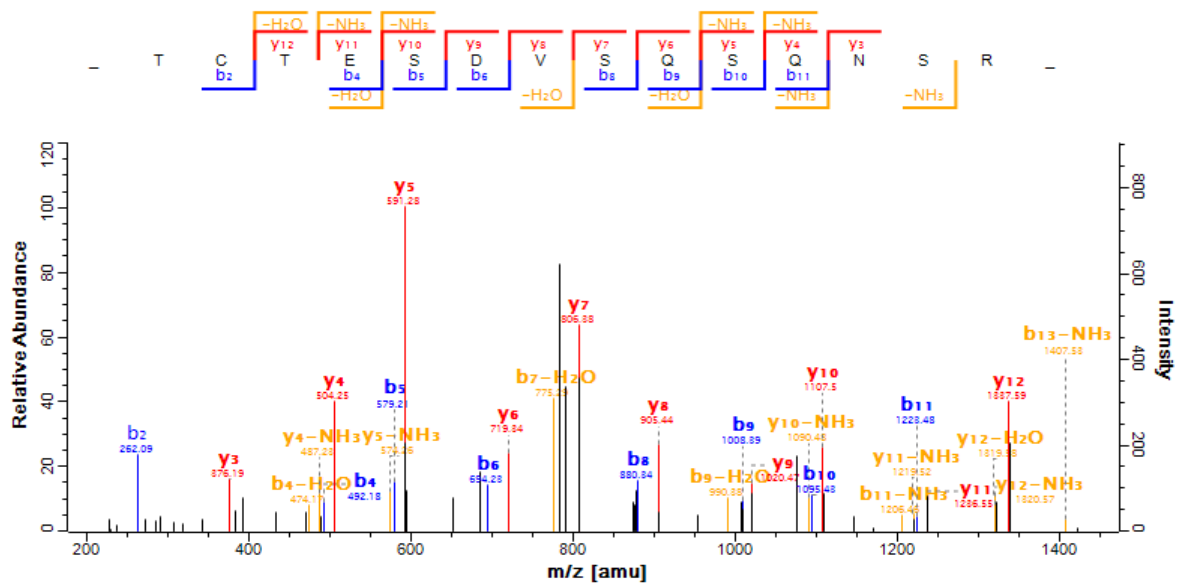
Number of Replicates (out of 8): 6

Best Match Score: 155.57

Best Match Posterior Error Probability: 2.78E-07

Best Match Spectrum:

Scan number 2822 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS: CID **Genenames** EYA4



Protein Group ID: 796

Protein Accession Numbers: G3V5T9; P24941; P24941-2; E7ESI2

Gene Names: CDK2

Peptide Sequence: SYLFQLLQGLAFCHSR

Total Number of Spectra: 2

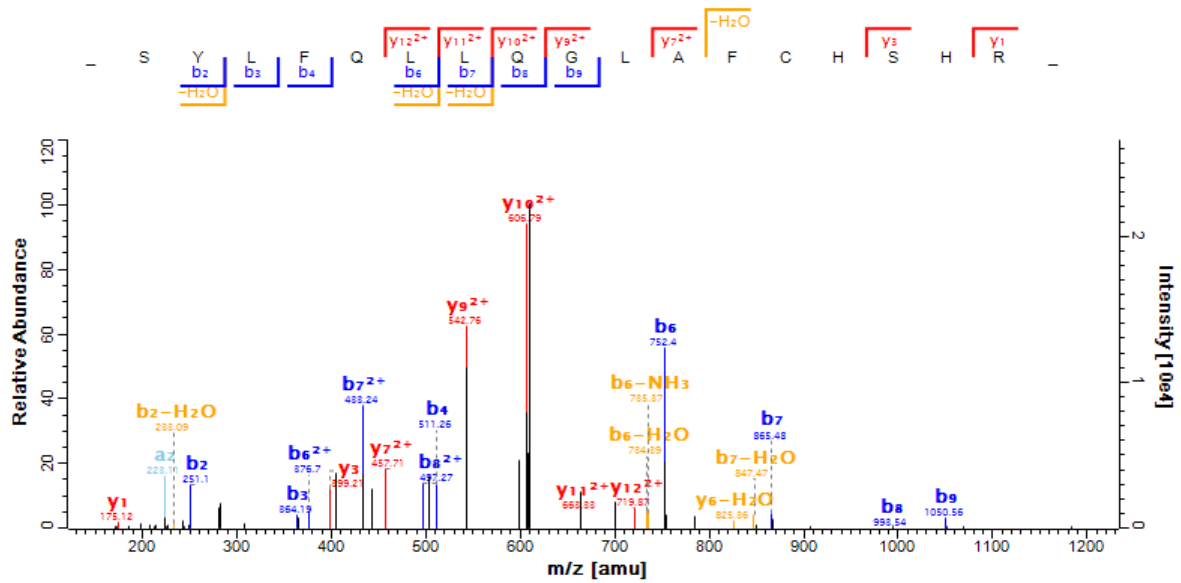
Number of Replicates (out of 8): 2

Best Match Score: 101.2

Best Match Posterior Error Probability: 0.00016455

Best Match Spectrum:

Scan number 86935 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CDK2



Protein Group ID: 806

Protein Accession Numbers: E7ETS8; Q07864; F5H1D6; F5H7H6

Gene Names: POLE

Peptide Sequence: AFHELSTREEQAK

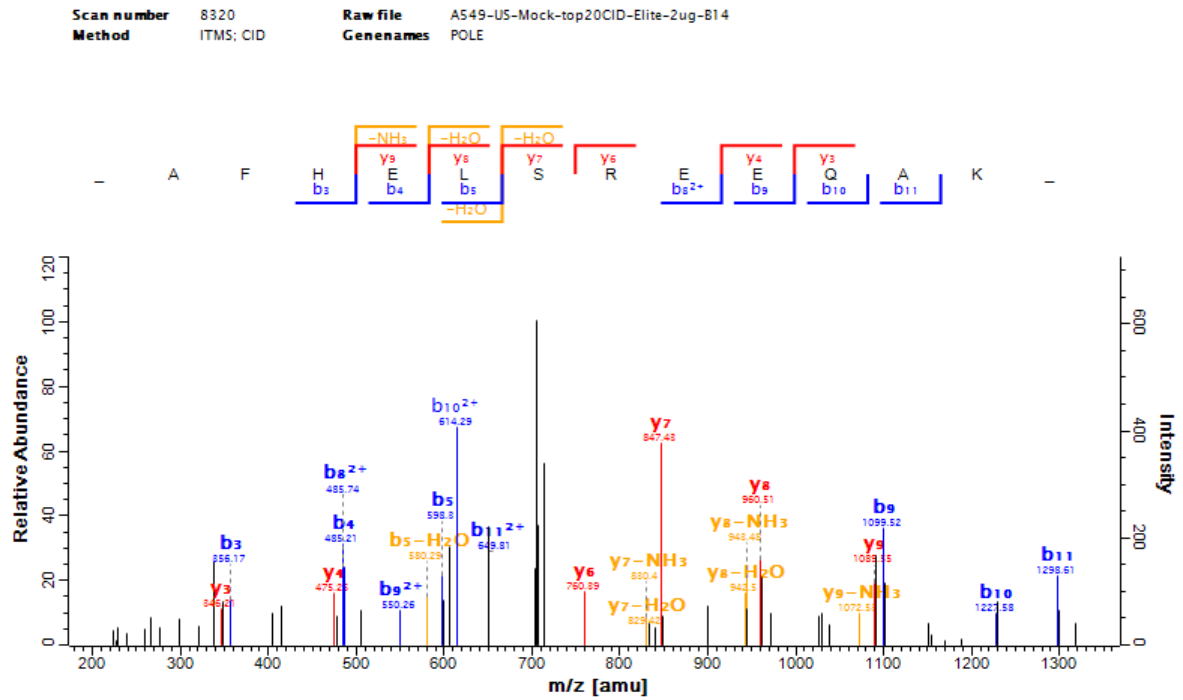
Total Number of Spectra: 1

Number of Replicates (out of 8): 1

Best Match Score: 134.98

Best Match Posterior Error Probability: 0.00040035

Best Match Spectrum:



Protein Group ID: 813

Protein Accession Numbers: P13688; P13688-10; P13688-8; P13688-5; P13688-6; P13688-2; P13688-9; P13688-11; E7EUB1; P13688-4; P13688-3; P13688-7

Gene Names: CEACAM1

Peptide Sequence: EVLLVHNLPPQLFGYSWK

Total Number of Spectra: 1

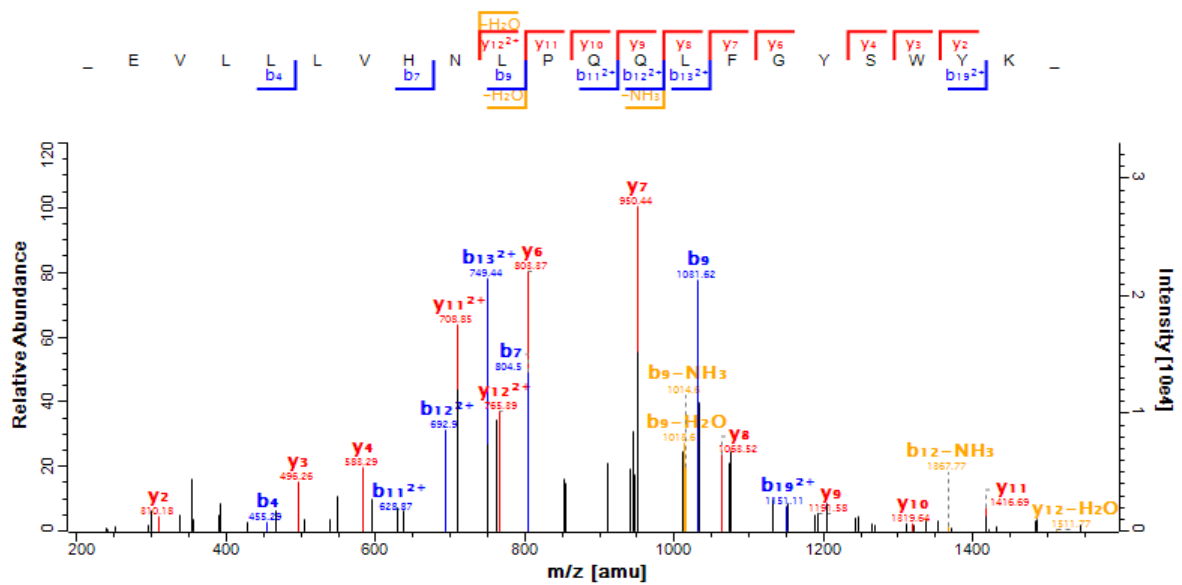
Number of Replicates (out of 8): 1

Best Match Score: 73.918

Best Match Posterior Error Probability: 0.0011151

Best Match Spectrum:

Scan number 90226 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS: CID **Genenames** CEACAM1



Protein Group ID: 818

Protein Accession Numbers: E7EUT7; P38571; P38571-2; Q5T073; Q5T770

Gene Names: LIPA

Peptide Sequence: TGQEQVYYVGHSGTITIGFIAFSQIPELAK

Total Number of Spectra: 2

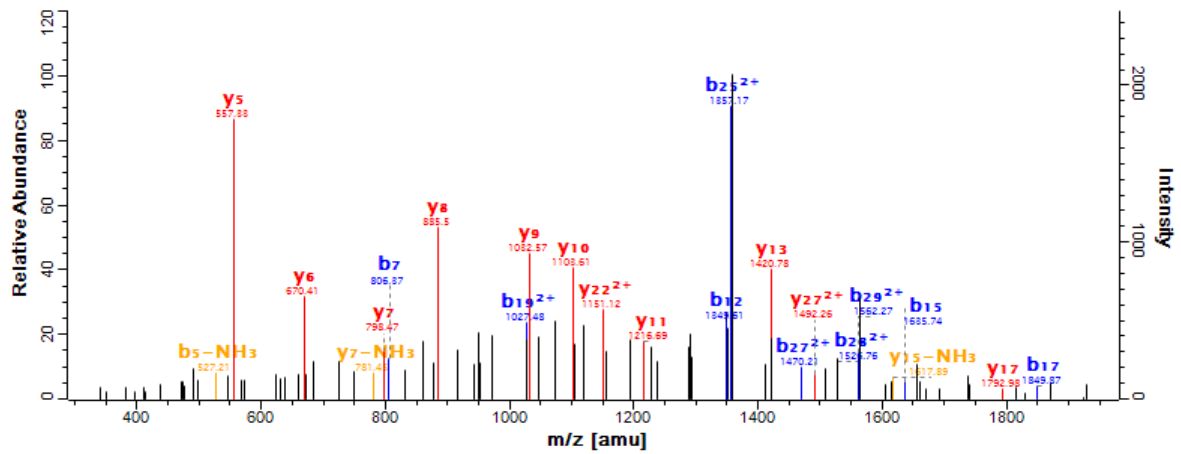
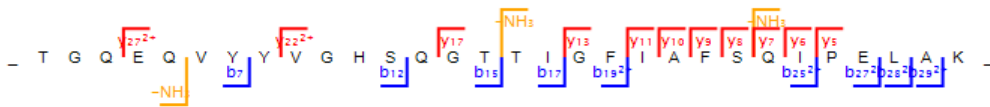
Number of Replicates (out of 8): 2

Best Match Score: 71.085

Best Match Posterior Error Probability: 2.91E-05

Best Match Spectrum:

Scan number 80728 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** LIPA



Protein Group ID: 825

Protein Accession Numbers: Q5VV67; Q5VV67-2; E7EVG6

Gene Names: PPRC1

Peptide Sequence: EGLSLNSEEK

Total Number of Spectra: 1

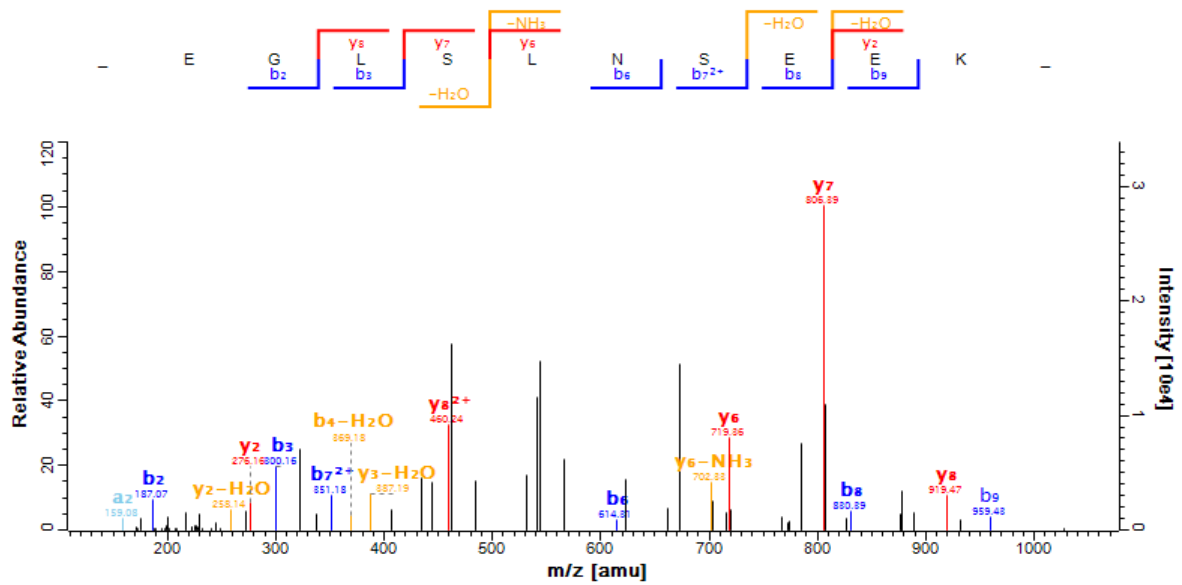
Number of Replicates (out of 8): 1

Best Match Score: 96.015

Best Match Posterior Error Probability: 0.0012035

Best Match Spectrum:

Scan number 17741 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PPRC1



Protein Group ID: 826

Protein Accession Numbers: Q9H490; E7EVL4; Q9H490-2

Gene Names: PIGU

Peptide Sequence: LLELDQYAPDVAELIR

Total Number of Spectra: 12

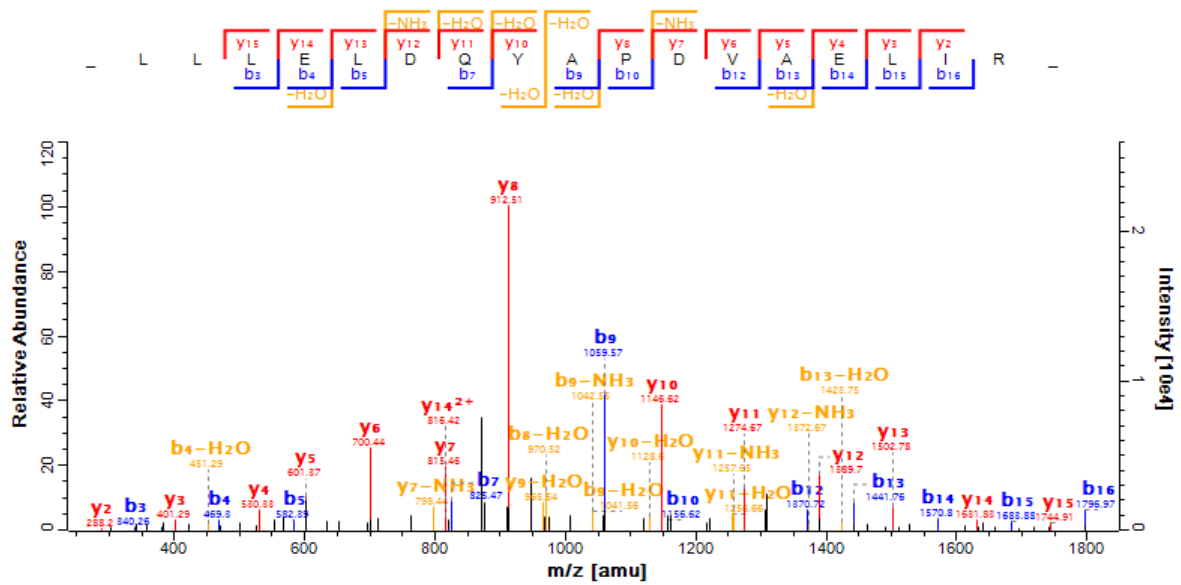
Number of Replicates (out of 8): 8

Best Match Score: 203.59

Best Match Posterior Error Probability: 2.83E-39

Best Match Spectrum:

Scan number 88804 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** PIGU



Protein Group ID: 832

Protein Accession Numbers: Q13576; E7EWC2; D6R939

Gene Names: IQGAP2

Peptide Sequence: IGGILANELSVDEAAALHAAVIAIINEAVEK

Total Number of Spectra: 11

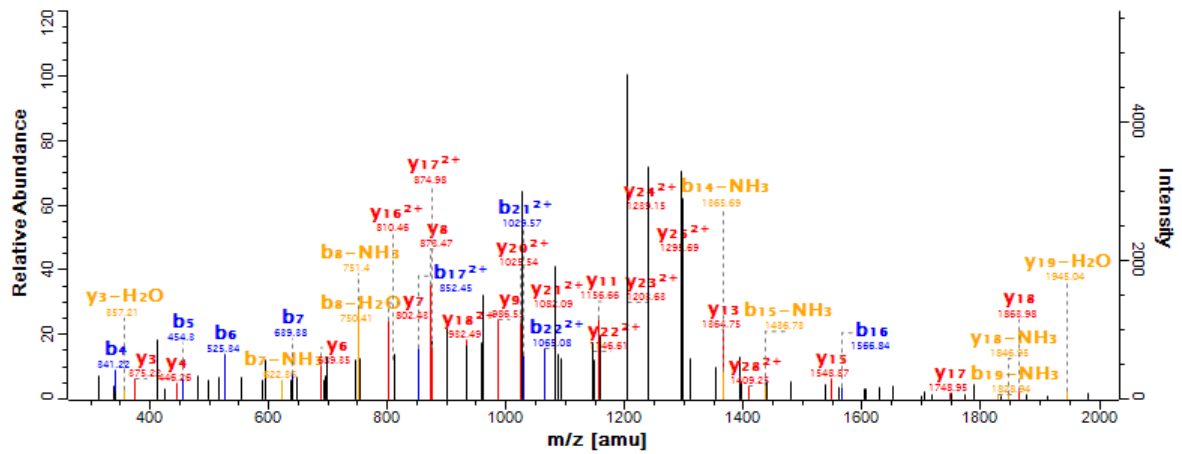
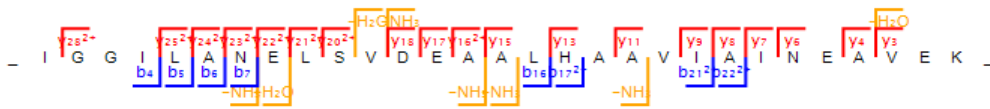
Number of Replicates (out of 8): 8

Best Match Score: 120.54

Best Match Posterior Error Probability: 2.11E-14

Best Match Spectrum:

Scan number 94262 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** IQGAP2



Protein Group ID: 833

Protein Accession Numbers: E7EWD9; O95718; O95718-2; O95718-3; P11474; P11474-2; HOYGT3

Gene Names: ESRRB;ESRRA

Peptide Sequence: LLLTLPLLR

Total Number of Spectra: 1

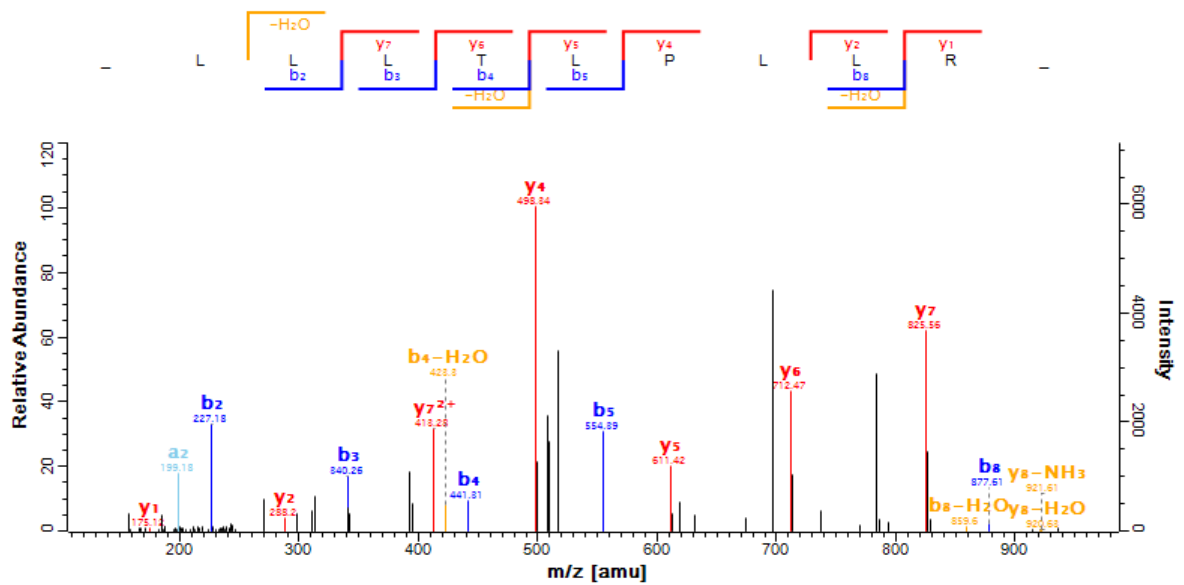
Number of Replicates (out of 8): 1

Best Match Score: 96.948

Best Match Posterior Error Probability: 0.0022423

Best Match Spectrum:

Scan number	80587	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	ESRRB;ESRRA



Protein Group ID: 836

Protein Accession Numbers: F8WAQ9; O15021; J3QT34; E7EWQ5; O15021-1; O15021-3; O15021-2; H7C1I9

Gene Names: MAST4

Peptide Sequence: SPGTVMESNPQQR

Total Number of Spectra: 1

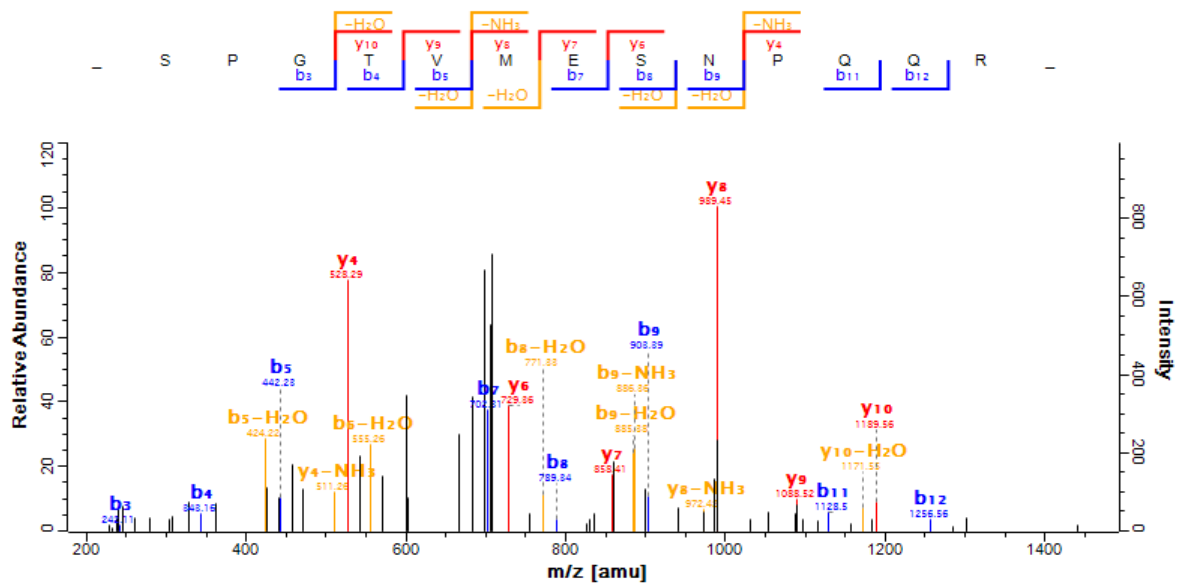
Number of Replicates (out of 8): 1

Best Match Score: 107.53

Best Match Posterior Error Probability: 0.0025113

Best Match Spectrum:

Scan number 10646 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS: CID **Genenames** MAST4



Protein Group ID: 837

Protein Accession Numbers: Q9UNS1; Q9UNS1-2; E7EWS5

Gene Names: TIMELESS

Peptide Sequence: SADFAEVLRL

Total Number of Spectra: 2

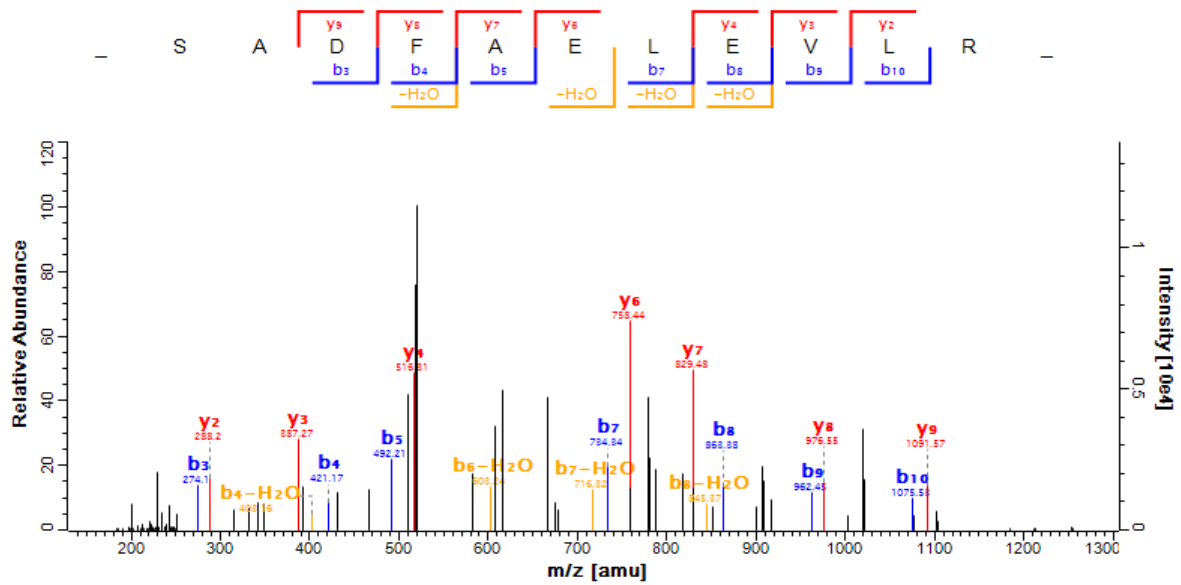
Number of Replicates (out of 8): 2

Best Match Score: 99.752

Best Match Posterior Error Probability: 0.00052505

Best Match Spectrum:

Scan number	56221	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	TIMELESS



Protein Group ID: 841

Protein Accession Numbers: Q5QPH3; Q9NR19; E7EWU3

Gene Names: ACSS2

Peptide Sequence: IGPIATPDYIQNAPGLPK

Total Number of Spectra: 9

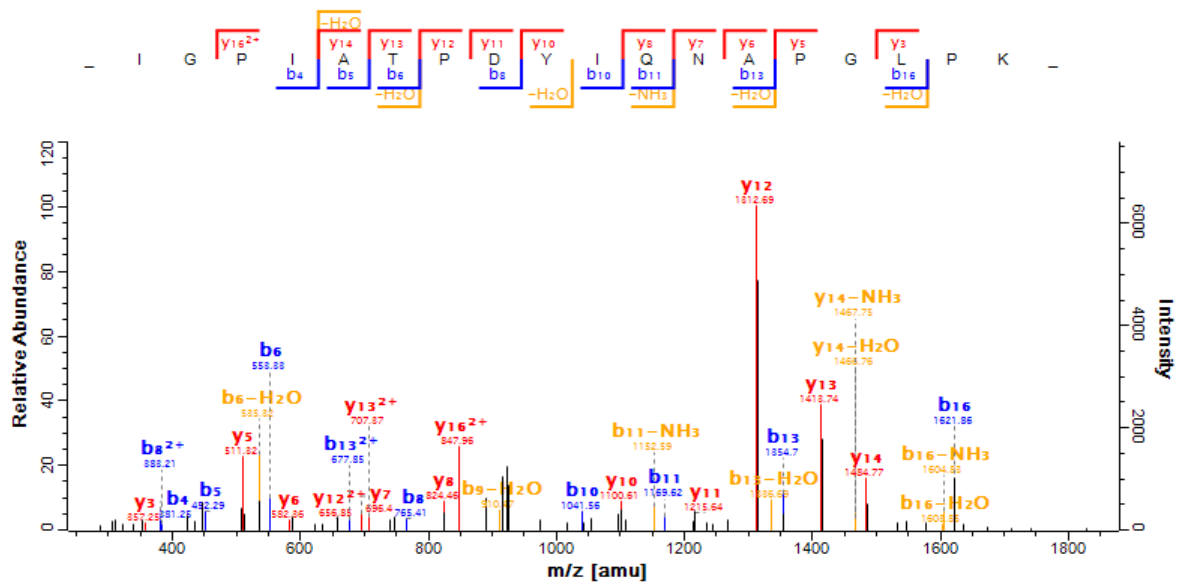
Number of Replicates (out of 8): 7

Best Match Score: 159.18

Best Match Posterior Error Probability: 7.86E-10

Best Match Spectrum:

Scan number 57542 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ACSS2



Protein Group ID: 856

Protein Accession Numbers: O43516-3; O43516; O43516-2; E9PB87

Gene Names: WIPF1

Peptide Sequence: NLSLSSSTPPLPSPGR

Total Number of Spectra: 1

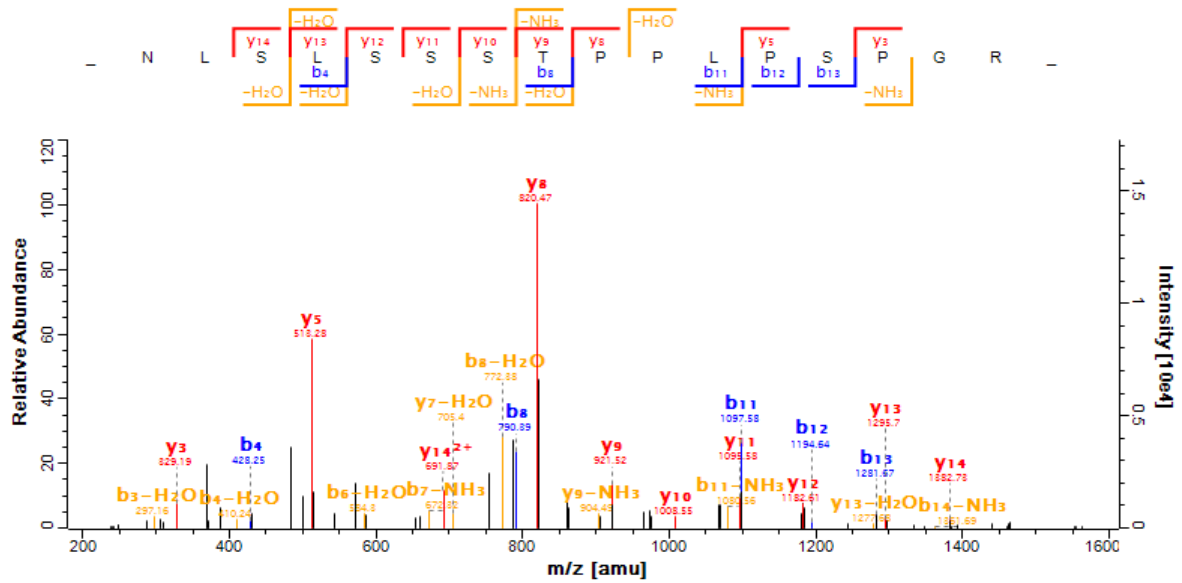
Number of Replicates (out of 8): 1

Best Match Score: 77.191

Best Match Posterior Error Probability: 0.0025577

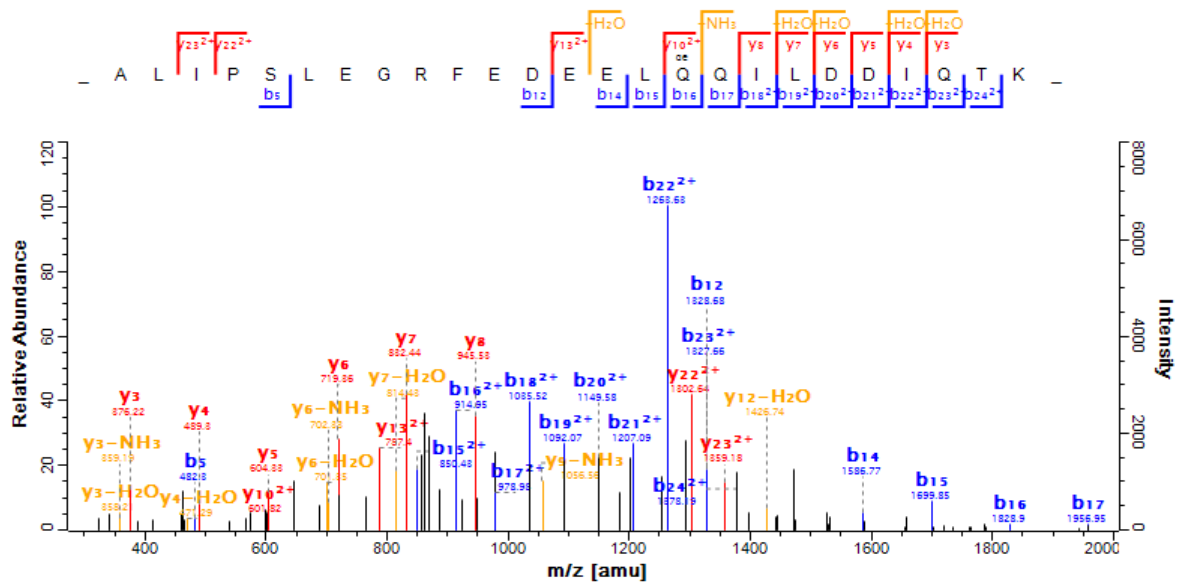
Best Match Spectrum:

Scan number 45390 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** WIPF1



Protein Group ID: 857
Protein Accession Numbers: O15514; E9PB93
Gene Names: POLR2D
Peptide Sequence: ALIPSLEGRFEDELQQLIDDIQTK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 135.21
Best Match Posterior Error Probability: 7.12E-16
Best Match Spectrum:

Scan number 87286 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** POLR2D



Protein Group ID: 859

Protein Accession Numbers: Q5SNT2; E9PBR6; Q5SNT2-2

Gene Names: TMEM201

Peptide Sequence: MEGVSALLAR

Total Number of Spectra: 4

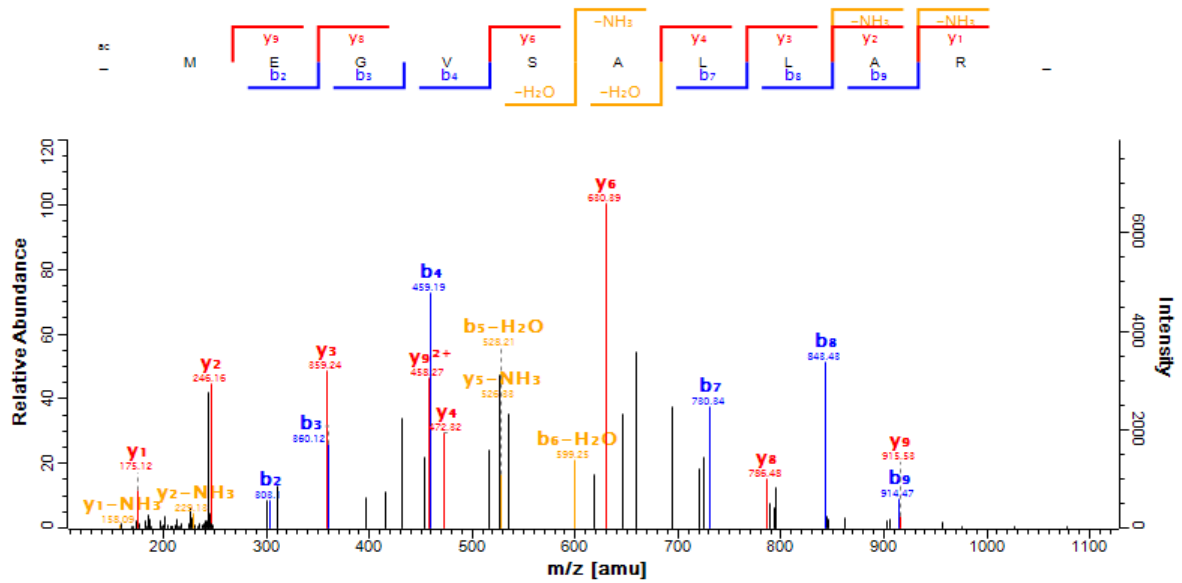
Number of Replicates (out of 8): 4

Best Match Score: 119.16

Best Match Posterior Error Probability: 0.0002032

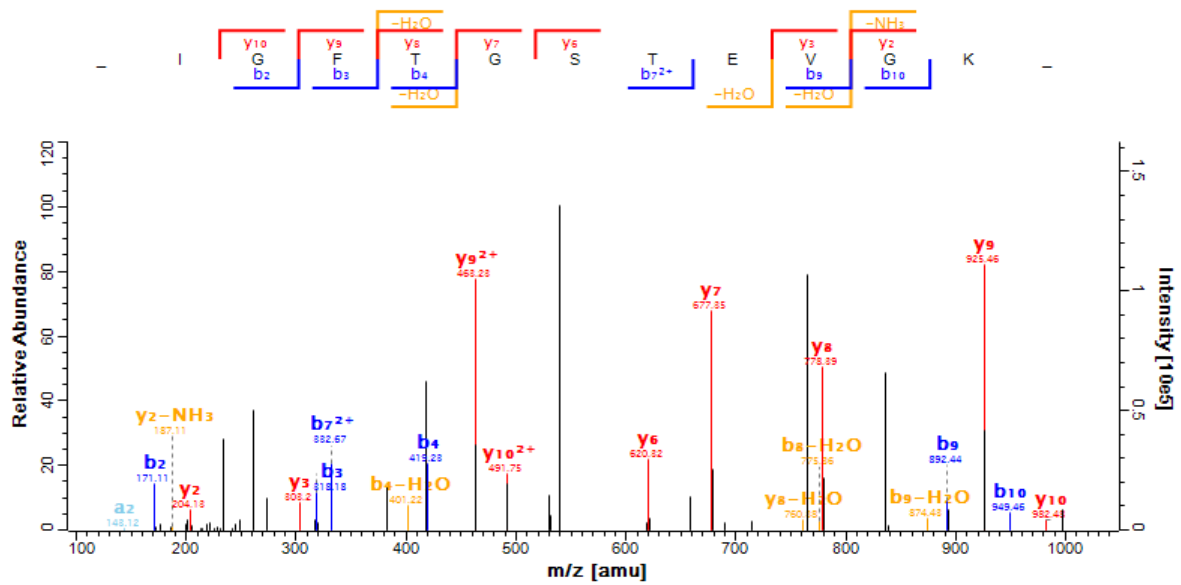
Best Match Spectrum:

Scan number 68842 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TMEM201



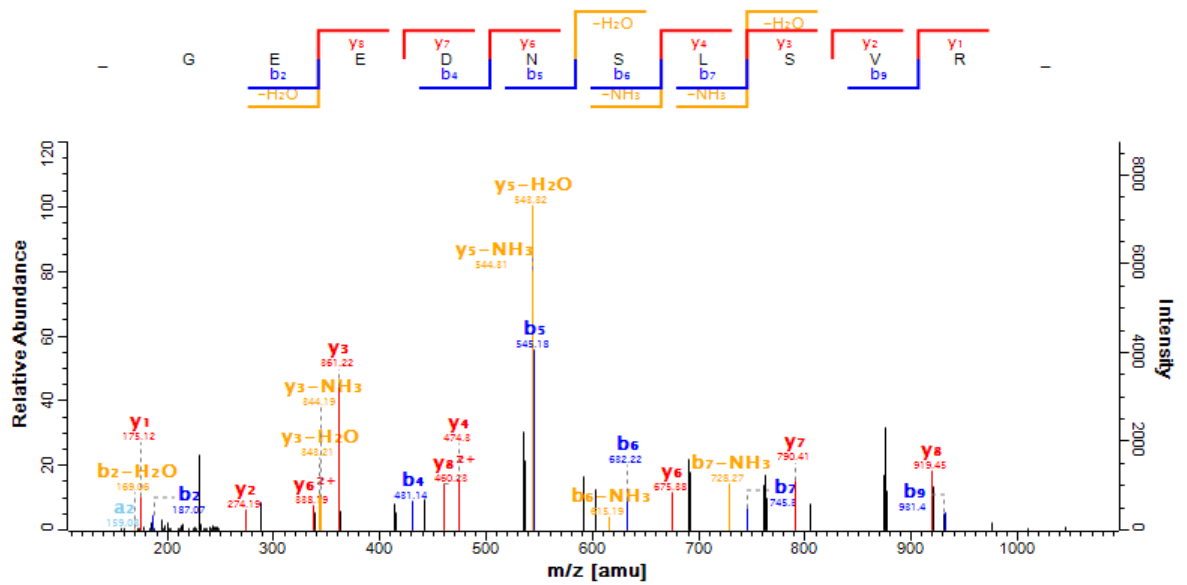
Protein Group ID: 860
Protein Accession Numbers: O75891; E9PBX3
Gene Names: ALDH1L1
Peptide Sequence: IGFTGSTEVGK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 117.52
Best Match Posterior Error Probability: 8.28E-05
Best Match Spectrum:

Scan number 18249 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ALDH1L1



Protein Group ID: 863
Protein Accession Numbers: P27701; E9PC70
Gene Names: CD82
Peptide Sequence: GEEDNSLSVR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 111.86
Best Match Posterior Error Probability: 0.00029194
Best Match Spectrum:

Scan number 10143 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CD82



Protein Group ID: 872

Protein Accession Numbers: P37275-2; P37275; E9PCM7; Q5VZ84; F5H4I8; G3V1R3

Gene Names: ZEB1

Peptide Sequence: VGESSEQVSEEK

Total Number of Spectra: 5

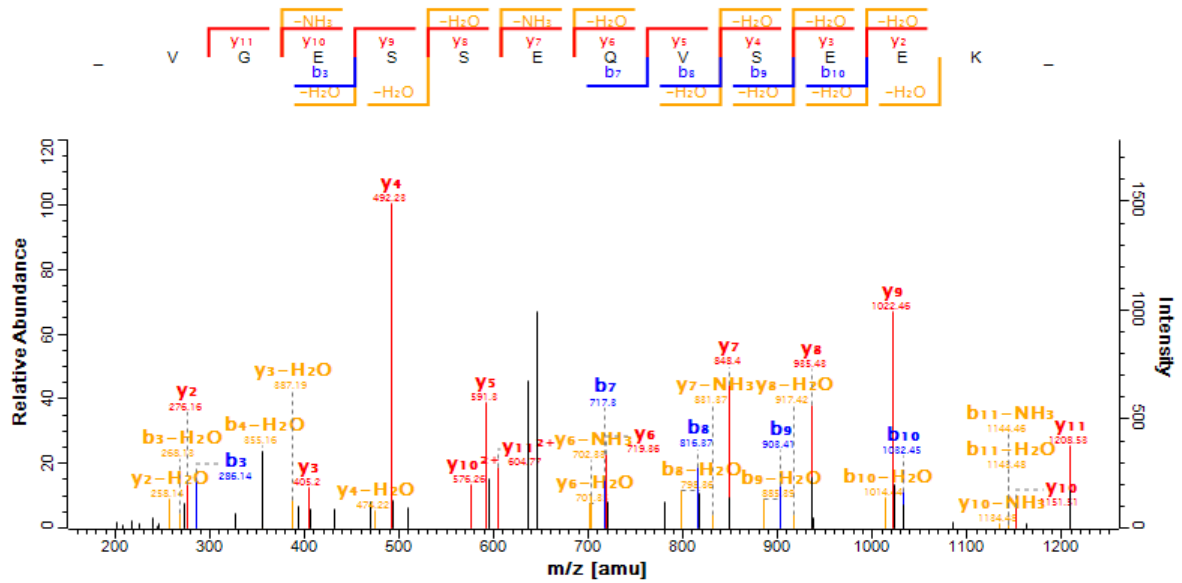
Number of Replicates (out of 8): 5

Best Match Score: 184.34

Best Match Posterior Error Probability: 4.10E-13

Best Match Spectrum:

Scan number 4614 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ZEB1



Protein Group ID: 873

Protein Accession Numbers: P51636; P51636-2; E9PCT3

Gene Names: CAV2

Peptide Sequence: LGFEDVIAEPVTTHSFDK

Total Number of Spectra: 6

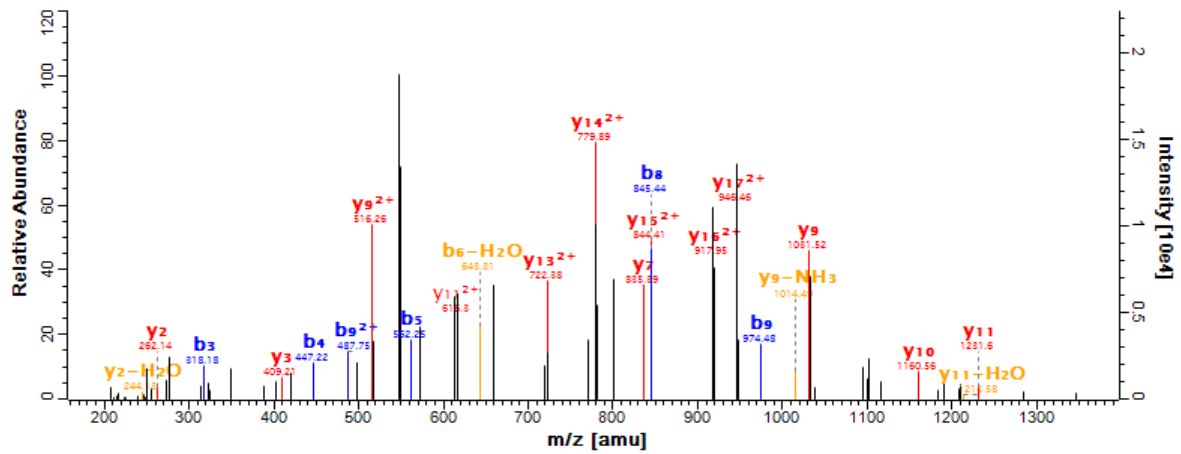
Number of Replicates (out of 8): 6

Best Match Score: 93.909

Best Match Posterior Error Probability: 0.00028903

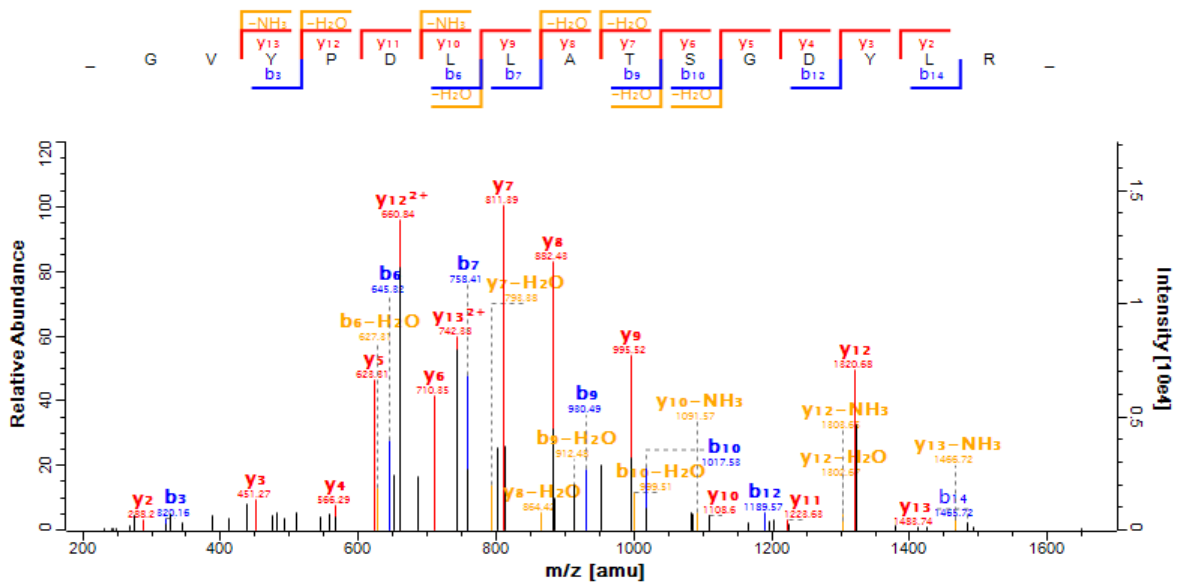
Best Match Spectrum:

Scan number 59799 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CAV2



Protein Group ID: 876
Protein Accession Numbers: P61962; E9PCY4
Gene Names: DCAF7
Peptide Sequence: GVYPDLLATSGDYLR
Total Number of Spectra: 10
Number of Replicates (out of 8): 8
Best Match Score: 171.26
Best Match Posterior Error Probability: 4.33E-14
Best Match Spectrum:

Scan number 64049 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** DCAF7



Protein Group ID: 877

Protein Accession Numbers: H0YL70; H0YKN8; H0YKT5; Q04726; Q04726-4; E9PD64; Q6PI57; F8W8S3; Q04726-3; F8W964; Q04726-2; H0YNT2; F5H7D6; H0YLI3; H0YWL9; H0YKH0

Gene Names: TLE3

Peptide Sequence: NDAPTPGTSTTPGLR

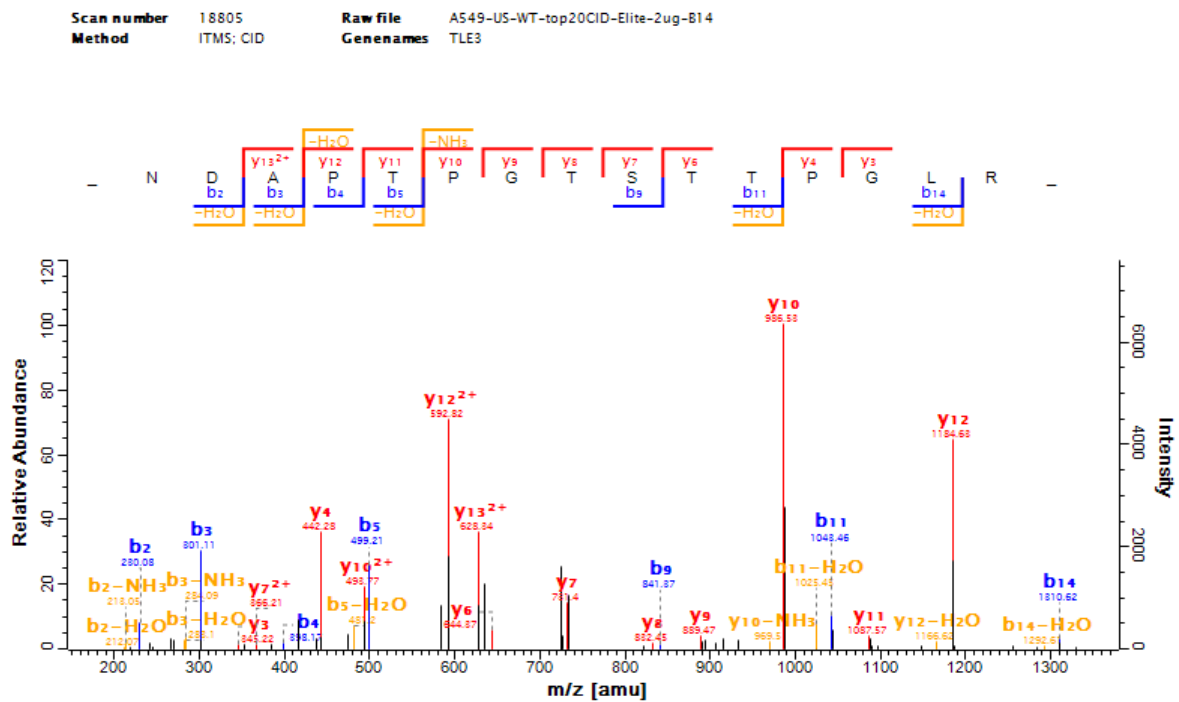
Total Number of Spectra: 7

Number of Replicates (out of 8): 7

Best Match Score: 170.11

Best Match Posterior Error Probability: 4.90E-14

Best Match Spectrum:



Protein Group ID: 883

Protein Accession Numbers: H3BNE9; Q9H1H9; E9PDX3; Q9H1H9-2; Q9H1H9-4; Q9H1H9-3; H0Y307

Gene Names: KIF13A

Peptide Sequence: LAYSSQTAQQK

Total Number of Spectra: 5

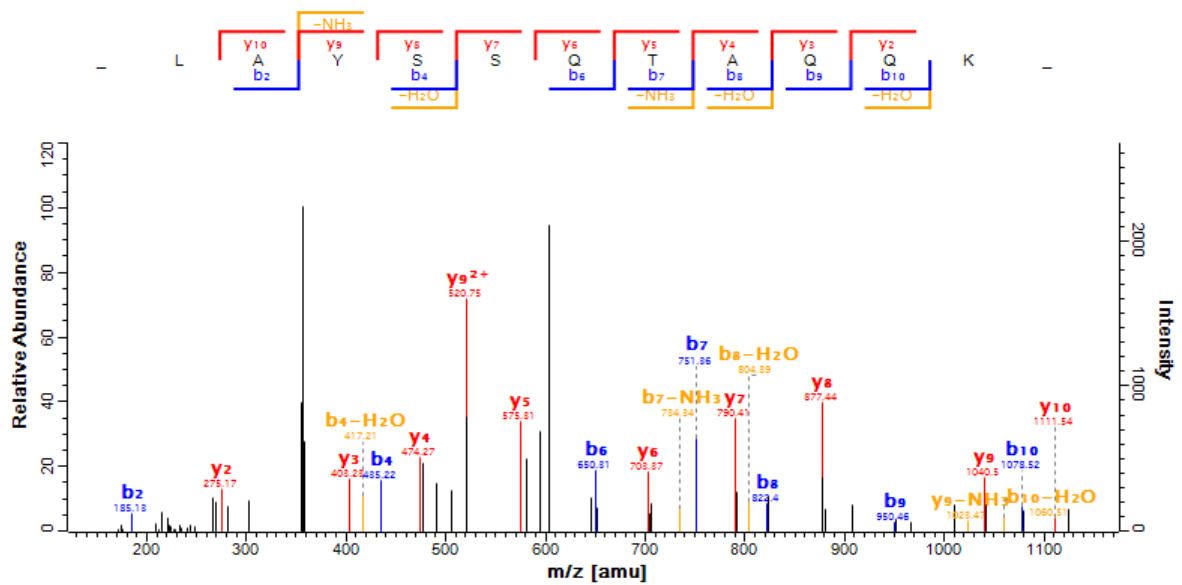
Number of Replicates (out of 8): 5

Best Match Score: 129.34

Best Match Posterior Error Probability: 4.24E-05

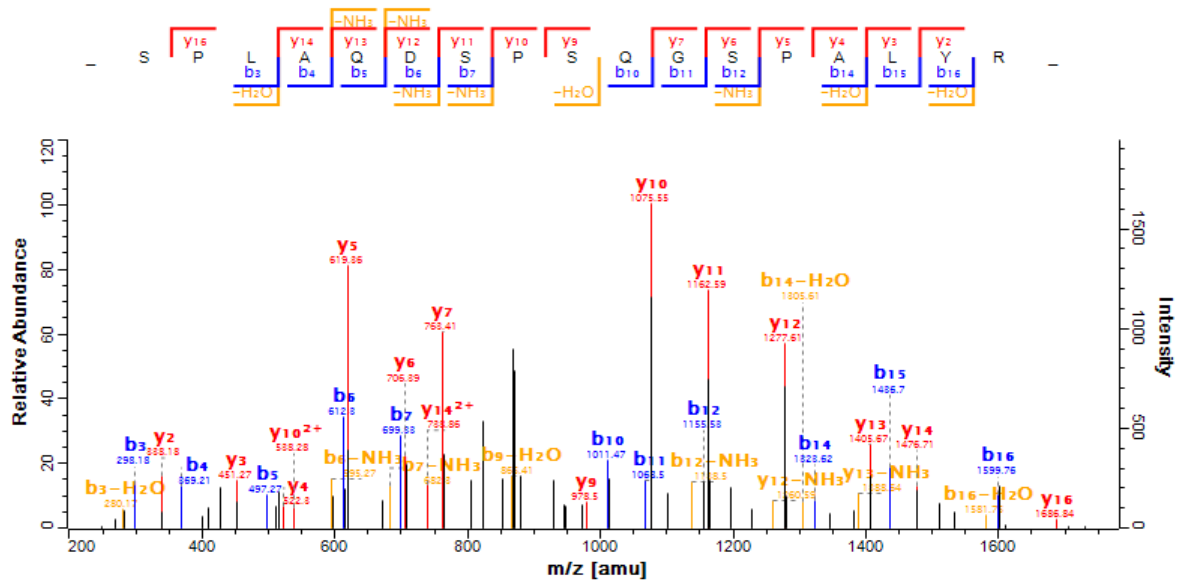
Best Match Spectrum:

Scan number	5792	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS: CID	Genenames	KIF13A



Protein Group ID: 888
Protein Accession Numbers: Q69YH5; E9PEI0
Gene Names: CDCA2
Peptide Sequence: SPLAQDSPSQGSPALYR
Total Number of Spectra: 6
Number of Replicates (out of 8): 4
Best Match Score: 182.31
Best Match Posterior Error Probability: 9.45E-21
Best Match Spectrum:

Scan number 30432 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CDCA2



Protein Group ID: 897

Protein Accession Numbers: F5GXA0; Q8NBK3-3; Q8NBK3; E9PGL0; G5E9B0; E9PF05

Gene Names: SUMF1

Peptide Sequence: EANAPGPVPGER

Total Number of Spectra: 1

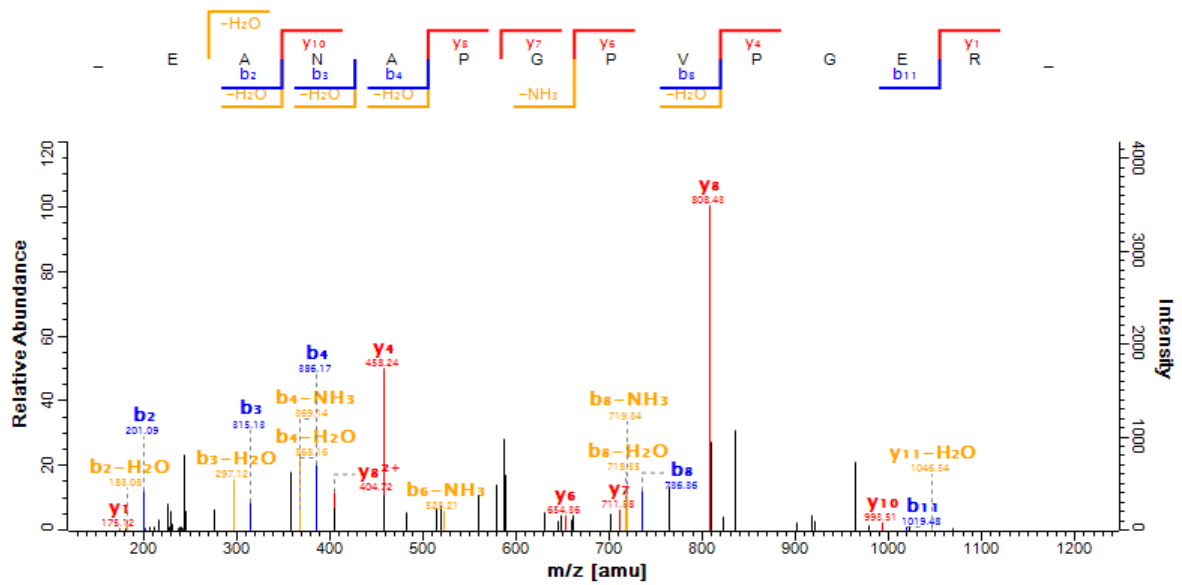
Number of Replicates (out of 8): 1

Best Match Score: 86.772

Best Match Posterior Error Probability: 0.0018203

Best Match Spectrum:

Scan number	10437	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	SUMF1



Protein Group ID: 899

Protein Accession Numbers: P49754; E9PF36; P49754-2

Gene Names: VPS41

Peptide Sequence: ILDIGLAYINHLVER

Total Number of Spectra: 4

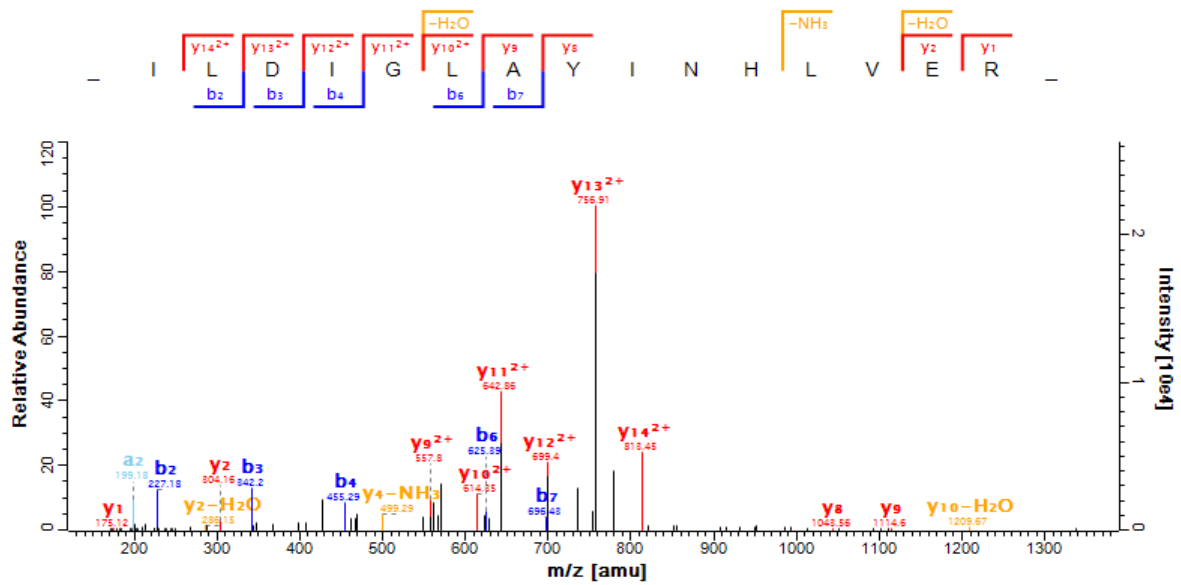
Number of Replicates (out of 8): 3

Best Match Score: 92.856

Best Match Posterior Error Probability: 0.00062416

Best Match Spectrum:

Scan number	79397	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	VPS41



Protein Group ID: 905

Protein Accession Numbers: P25054; P25054-2; E9PFT7

Gene Names: APC

Peptide Sequence: TEHMSSSSSENTSTPSSNAK

Total Number of Spectra: 5

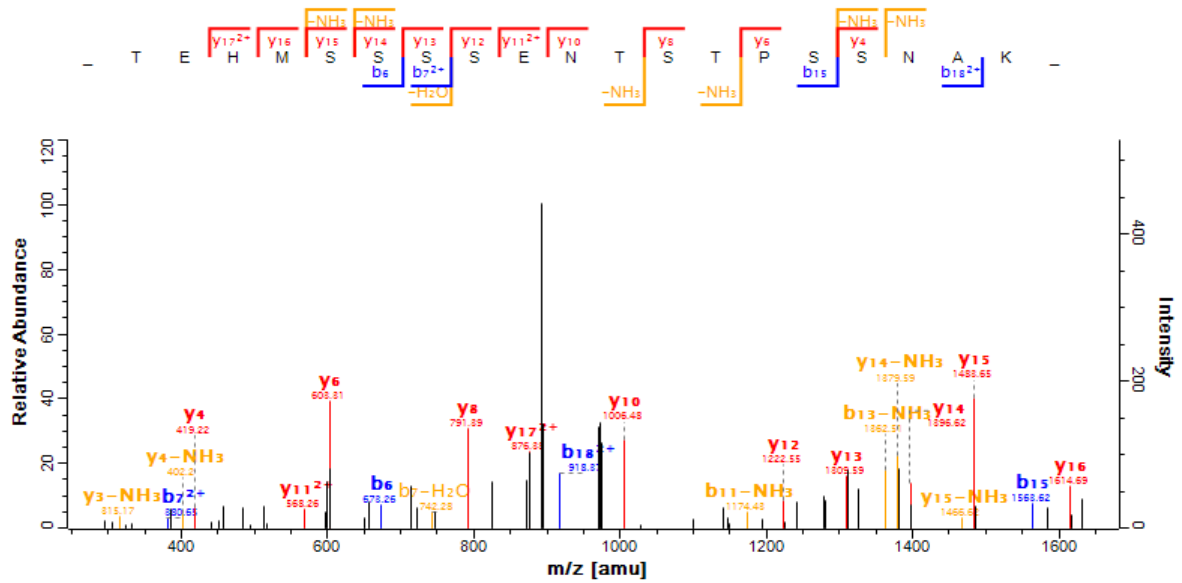
Number of Replicates (out of 8): 5

Best Match Score: 90.385

Best Match Posterior Error Probability: 0.00028065

Best Match Spectrum:

Scan number 3167 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** APC



Protein Group ID: 909

Protein Accession Numbers: Q6P4A7; E9PGB5; Q6P4A7-2

Gene Names: SFXN4

Peptide Sequence: LFRPAAFLPFMAPTVFLSMTPLK

Total Number of Spectra: 2

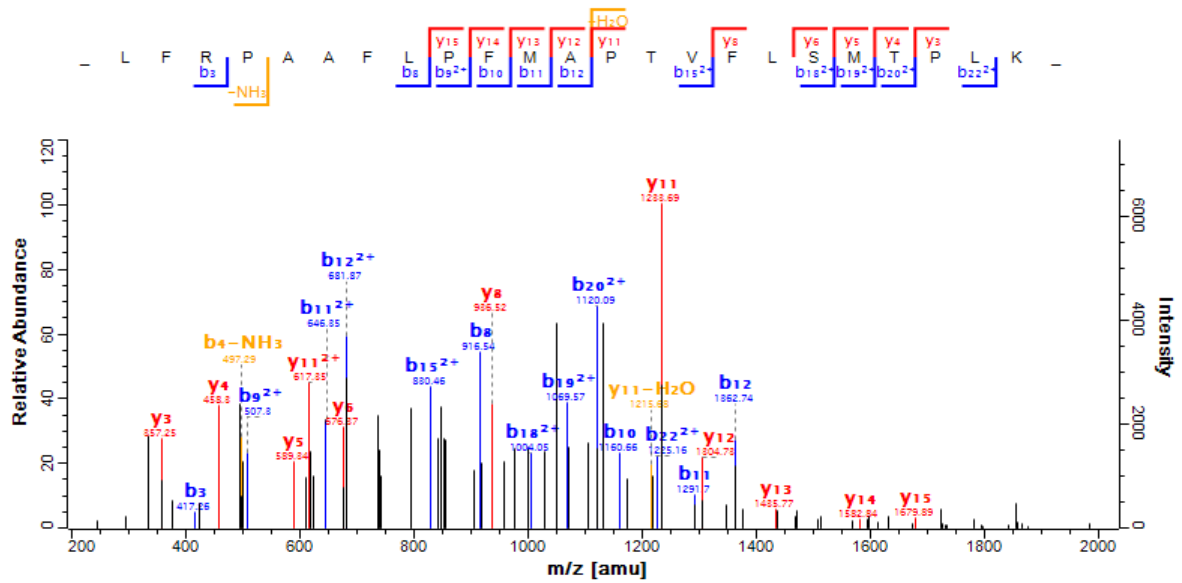
Number of Replicates (out of 8): 2

Best Match Score: 108.71

Best Match Posterior Error Probability: 2.36E-06

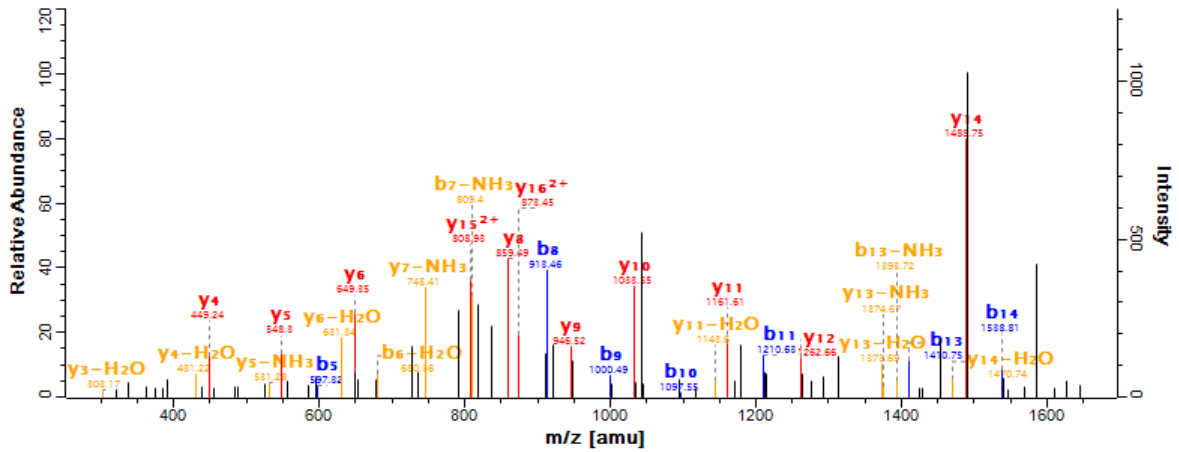
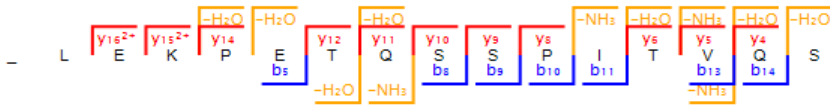
Best Match Spectrum:

Scan number 94009 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** SFXN4



Protein Group ID: 910
Protein Accession Numbers: Q96CB8; E9PGI3
Gene Names: INTS12
Peptide Sequence: LEKPETQSSPITVQSSK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 123.4
Best Match Posterior Error Probability: 0.00053732
Best Match Spectrum:

Scan number 19504 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** INTS12



Protein Group ID: 912

Protein Accession Numbers: Q96RU3; Q96RU3-2; E9PGQ4; Q96RU3-3; H0Y7W6; Q96RU3-4

Gene Names: FNBP1

Peptide Sequence: SGFEPPGDIEFEDYTQPMK

Total Number of Spectra: 2

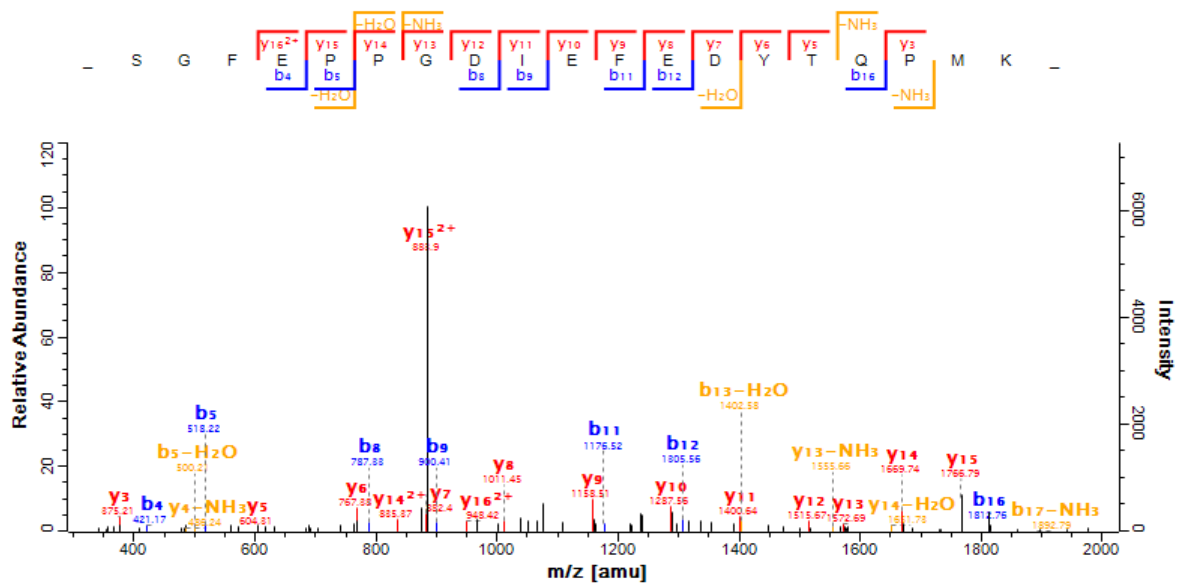
Number of Replicates (out of 8): 1

Best Match Score: 106.57

Best Match Posterior Error Probability: 7.12E-05

Best Match Spectrum:

Scan number 61315 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** FNBP1



Protein Group ID: 915

Protein Accession Numbers: Q15418-2; Q15418; E9PGT3; E9PRI4; Q15418-3

Gene Names: RPS6KA1

Peptide Sequence: LGMPQFLSTEAQSLLR

Total Number of Spectra: 6

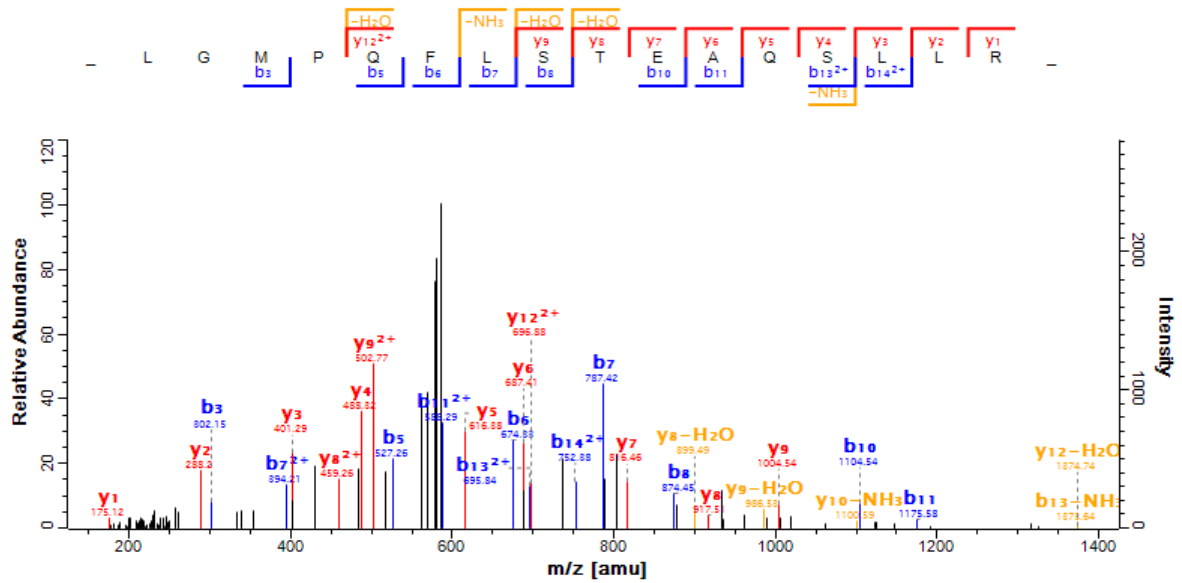
Number of Replicates (out of 8): 5

Best Match Score: 122.63

Best Match Posterior Error Probability: 8.01E-05

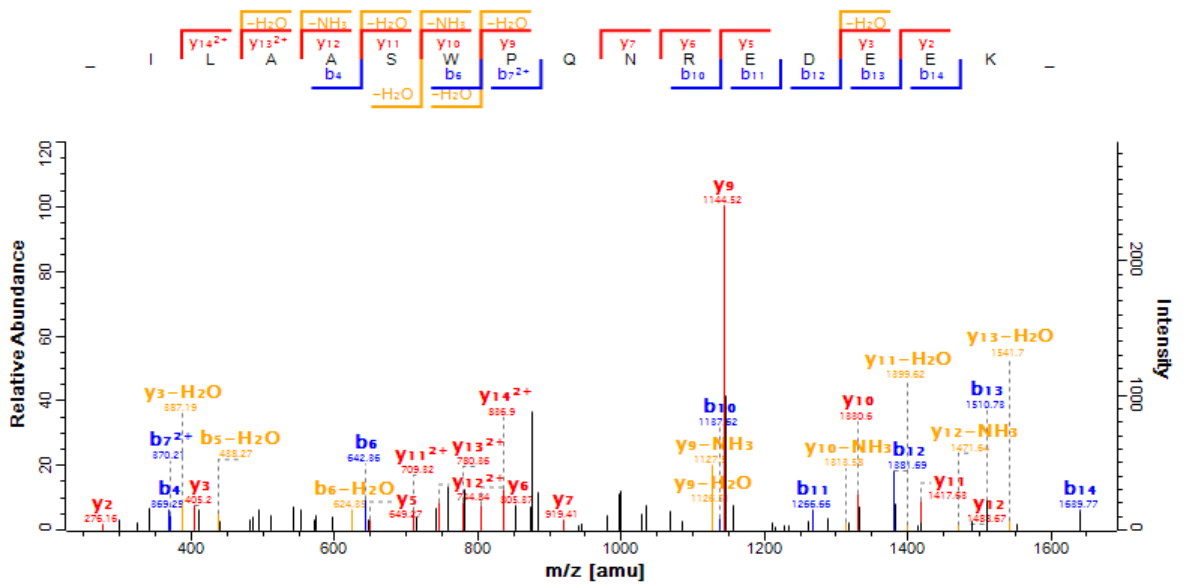
Best Match Spectrum:

Scan number	86104	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	RPS6KA1



Protein Group ID: 922
Protein Accession Numbers: Q01831; E9PH69
Gene Names: XPC
Peptide Sequence: ILAASWPQNREDEEK
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 149.3
Best Match Posterior Error Probability: 4.34E-06
Best Match Spectrum:

Scan number 28535 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** XPC



Protein Group ID: 927

Protein Accession Numbers: Q9UPV0; Q9UPV0-2; E9PI34

Gene Names: CEP164

Peptide Sequence: EHTLLQSNQQLR

Total Number of Spectra: 2

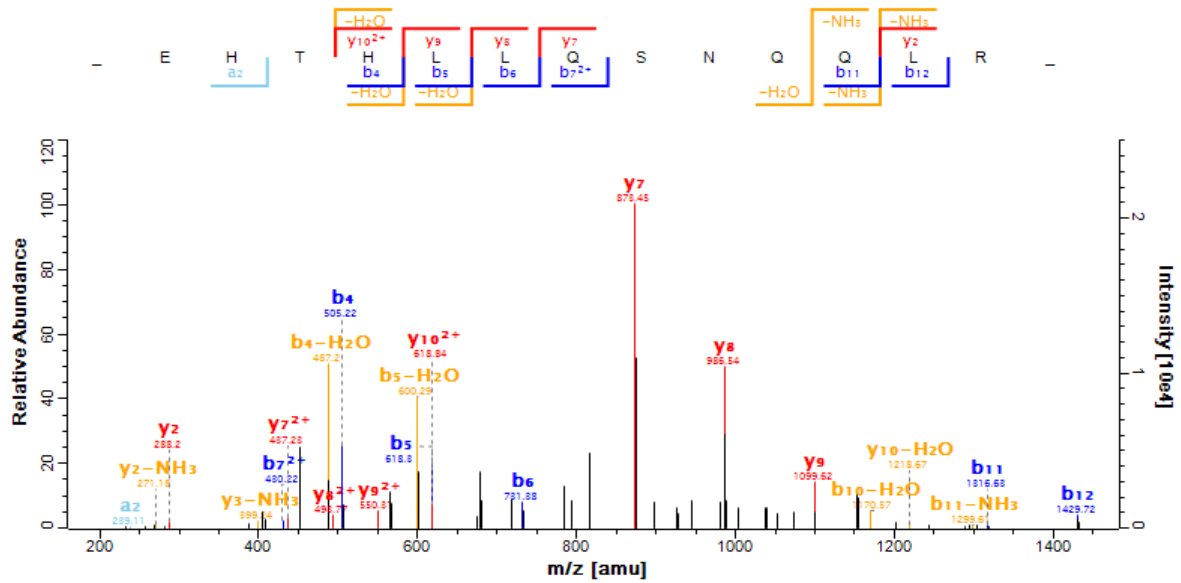
Number of Replicates (out of 8): 2

Best Match Score: 92.247

Best Match Posterior Error Probability: 0.0011802

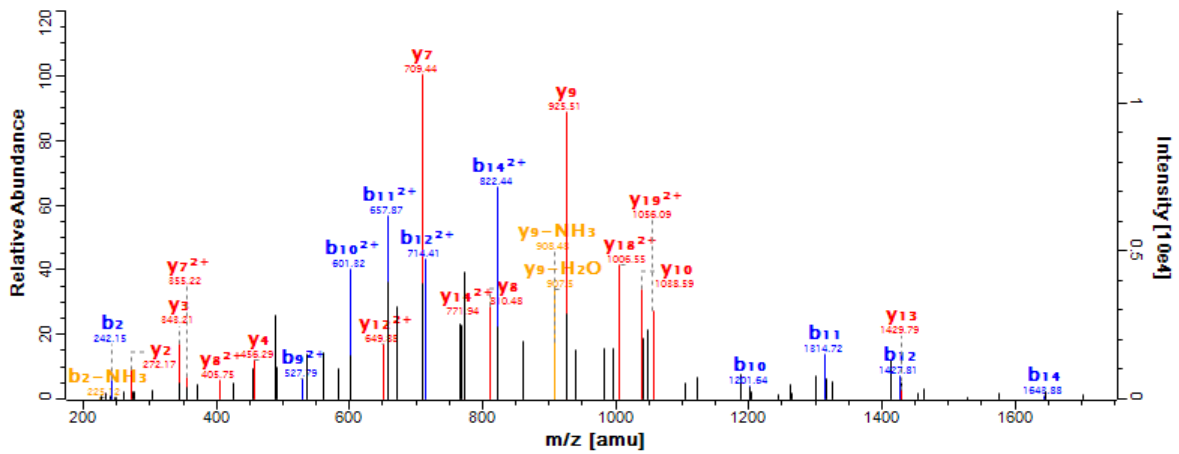
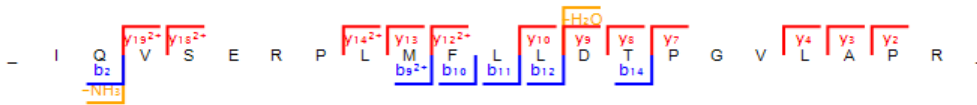
Best Match Spectrum:

Scan number	92676	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	CEP164



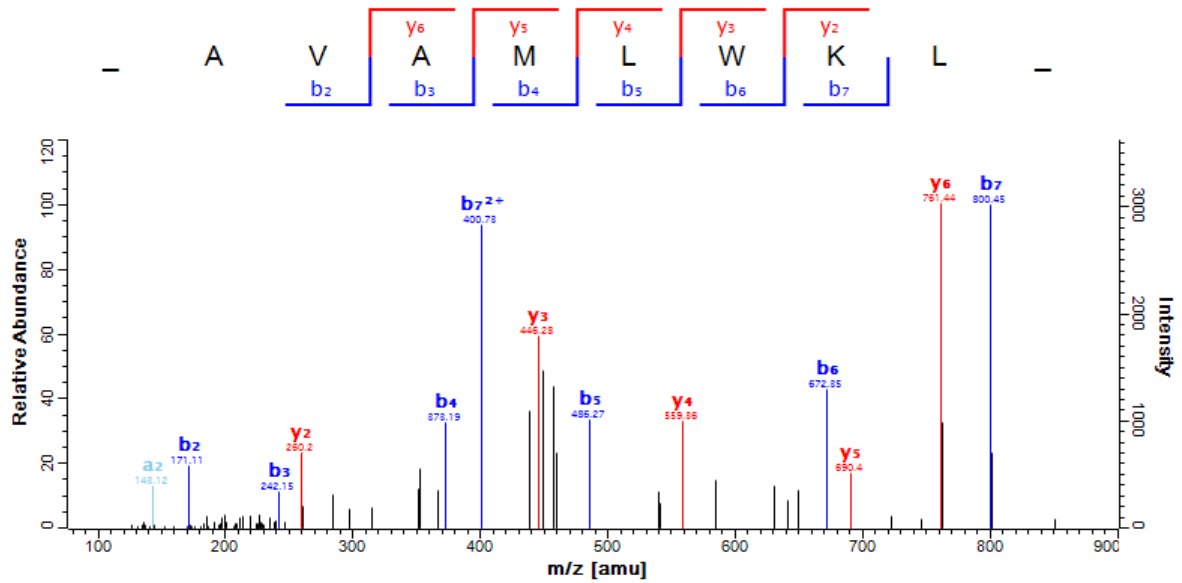
Protein Group ID: 928
Protein Accession Numbers: E9PI62; Q9BT17
Gene Names: MTG1
Peptide Sequence: IQVSERPLMFLLDTPGVLR
Total Number of Spectra: 4
Number of Replicates (out of 8): 3
Best Match Score: 145.61
Best Match Posterior Error Probability: 1.16E-09
Best Match Spectrum:

Scan number 87984 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MTG1



Protein Group ID: 932
Protein Accession Numbers: O14521; E9PIC0
Gene Names: SDHD
Peptide Sequence: AVAMLWKL
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 140.53
Best Match Posterior Error Probability: 0.0028284
Best Match Spectrum:

Scan number 63991 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** SDHD



Protein Group ID: 933

Protein Accession Numbers: E9PPM1; O14683; E9PKZ4; E9PIK4; E9PIN5; E9PQ46; E9PMW4; E9PMY0; E9PS55; E9PKN9; E9PNB3; E9PN66

Gene Names: TP53I11

Peptide Sequence: ILGVGGEDDDGEVHR

Total Number of Spectra: 3

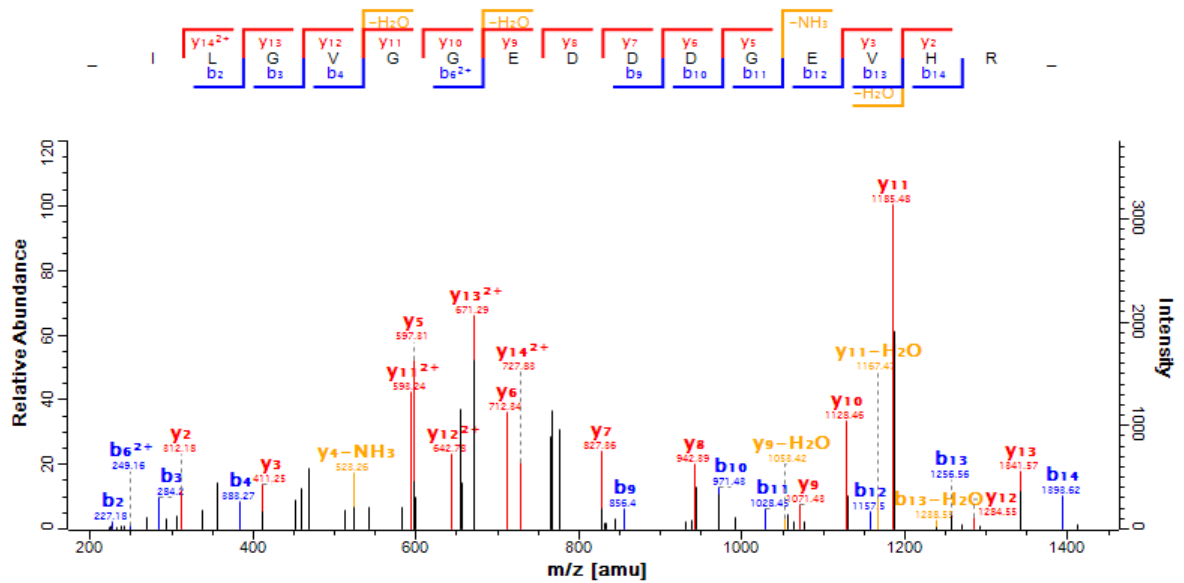
Number of Replicates (out of 8): 3

Best Match Score: 154.72

Best Match Posterior Error Probability: 2.69E-07

Best Match Spectrum:

Scan number	23898	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	TP53I11



Protein Group ID: 935

Protein Accession Numbers: Q3B7T1; Q3B7T1-5; Q3B7T1-3; Q3B7T1-4; E9PJ07

Gene Names: EDRF1;C10orf137

Peptide Sequence: EAGAEGPPAGAAAR

Total Number of Spectra: 8

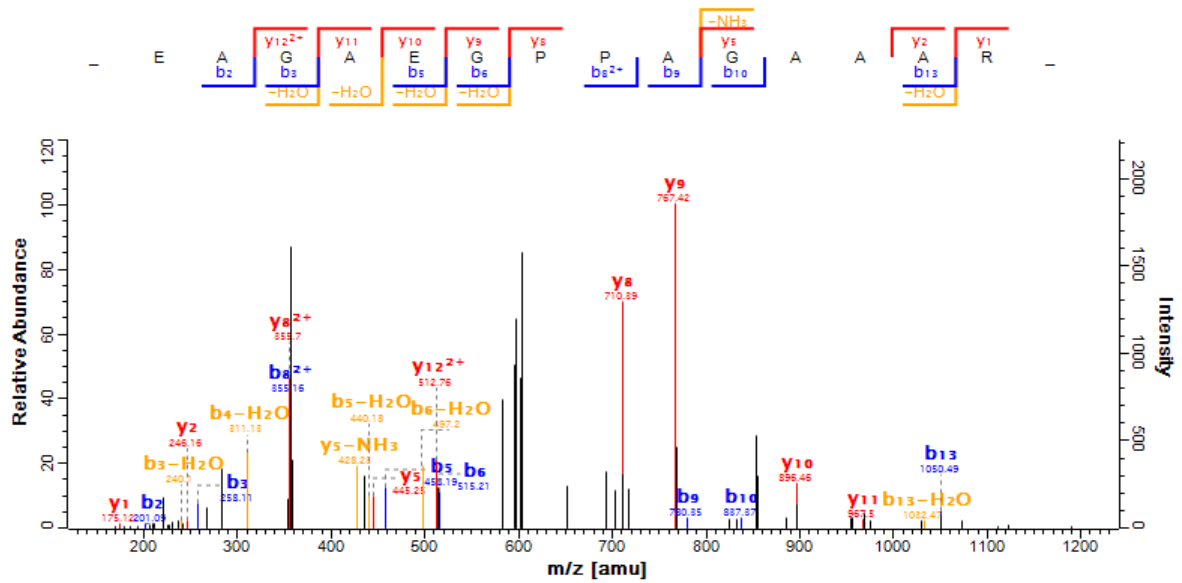
Number of Replicates (out of 8): 7

Best Match Score: 115.57

Best Match Posterior Error Probability: 0.00010623

Best Match Spectrum:

Scan number	5330	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	EDRF1;C10orf137



Protein Group ID: 937

Protein Accession Numbers: Q5BJD5; E9PJ42; Q5BJD5-2; Q5BJD5-3

Gene Names: TMEM41B

Peptide Sequence: SQLGAHHTTPVGDGAAGTR

Total Number of Spectra: 12

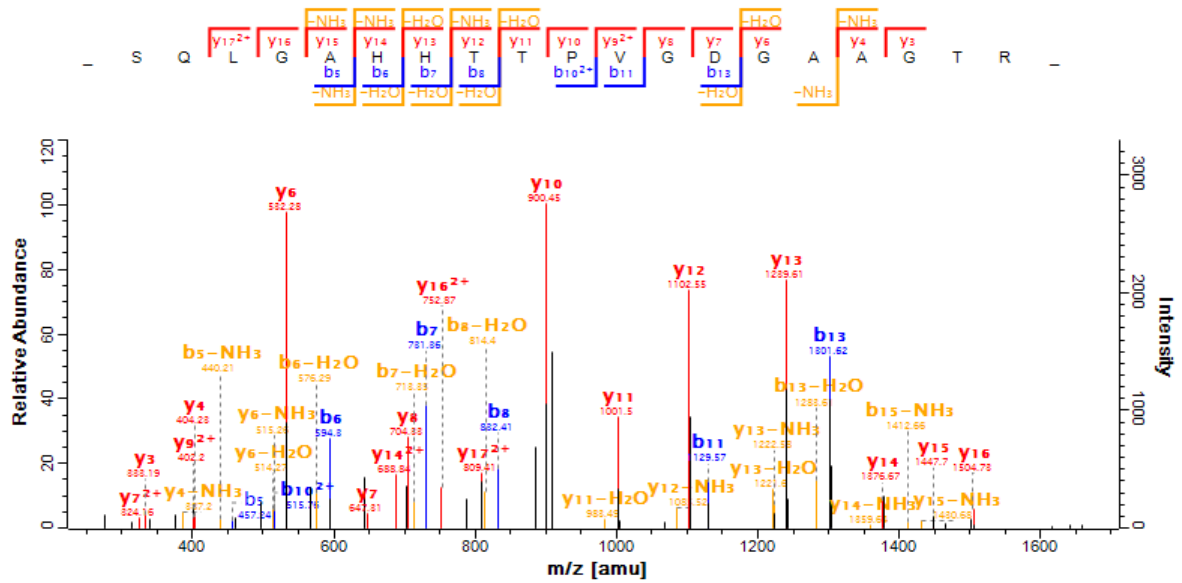
Number of Replicates (out of 8): 8

Best Match Score: 206.62

Best Match Posterior Error Probability: 1.86E-42

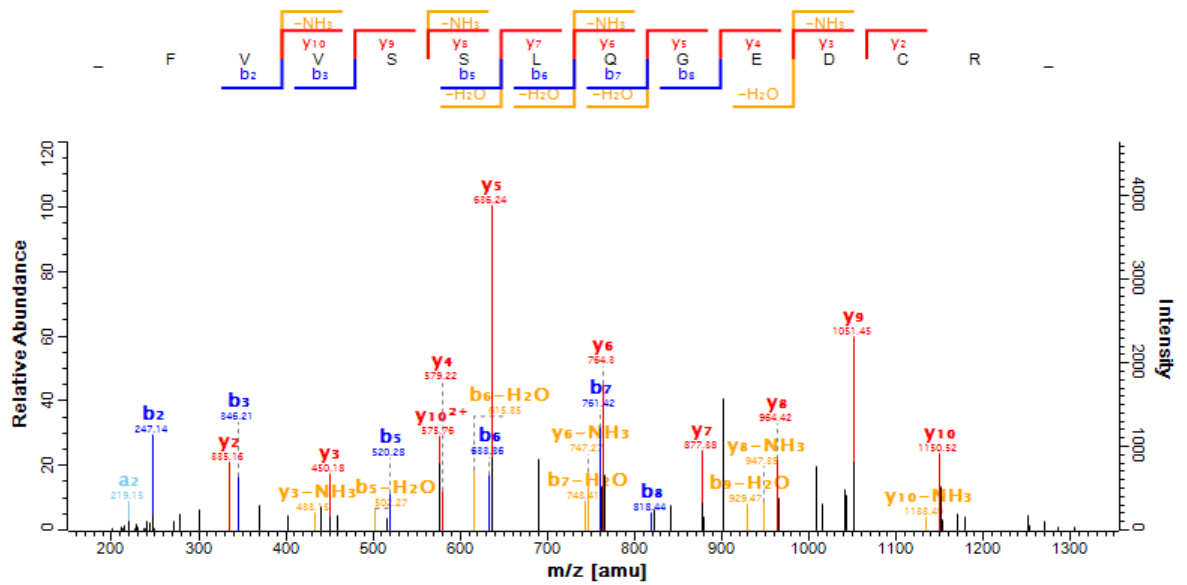
Best Match Spectrum:

Scan number 8566 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** TMEM41B



Protein Group ID: 942
Protein Accession Numbers: Q9GZQ3; E9PJE4
Gene Names: COMMD5
Peptide Sequence: FVVSSLQGEDCR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 154.36
Best Match Posterior Error Probability: 1.52E-06
Best Match Spectrum:

Scan number 30098 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** COMMD5



Protein Group ID: 943

Protein Accession Numbers: Q8N9N2; Q8N9N2-2; E9PQZ6; E9PR40; E9PKM6; E9PL92; E9PJM2; E9PQ44

Gene Names: ASCC1

Peptide Sequence: MEVLRPQLIR

Total Number of Spectra: 1

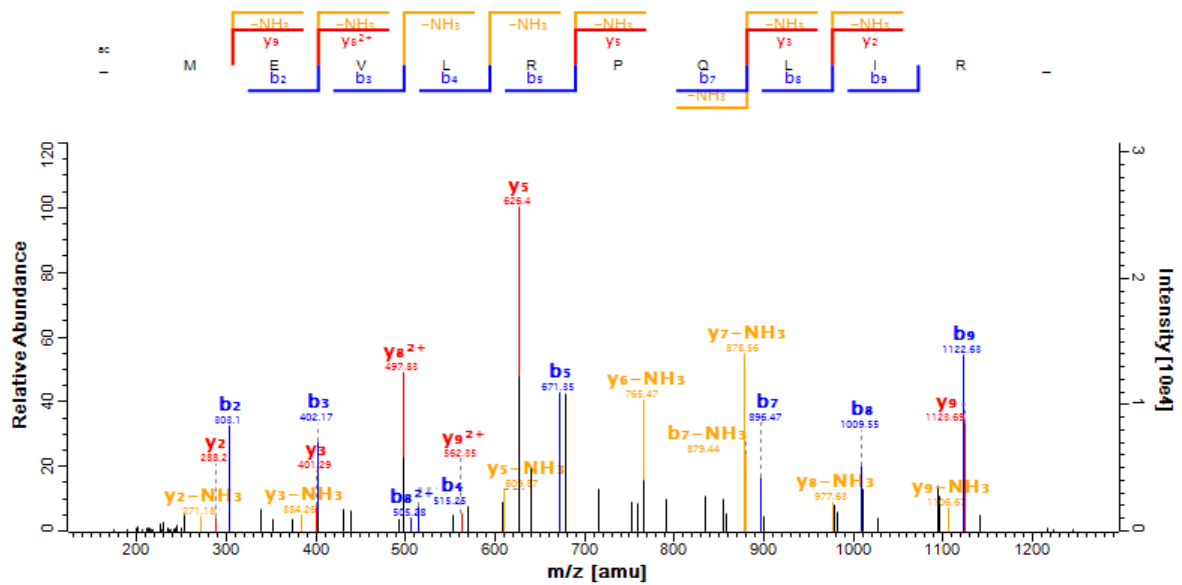
Number of Replicates (out of 8): 1

Best Match Score: 135.55

Best Match Posterior Error Probability: 5.50E-05

Best Match Spectrum:

Scan number 58755 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS: CID **Genenames** ASCC1



Protein Group ID: 944

Protein Accession Numbers: E9PL17; Q92989; Q92989-2; E9PJM4

Gene Names: CLP1

Peptide Sequence: VMVVGPTDVGK

Total Number of Spectra: 1

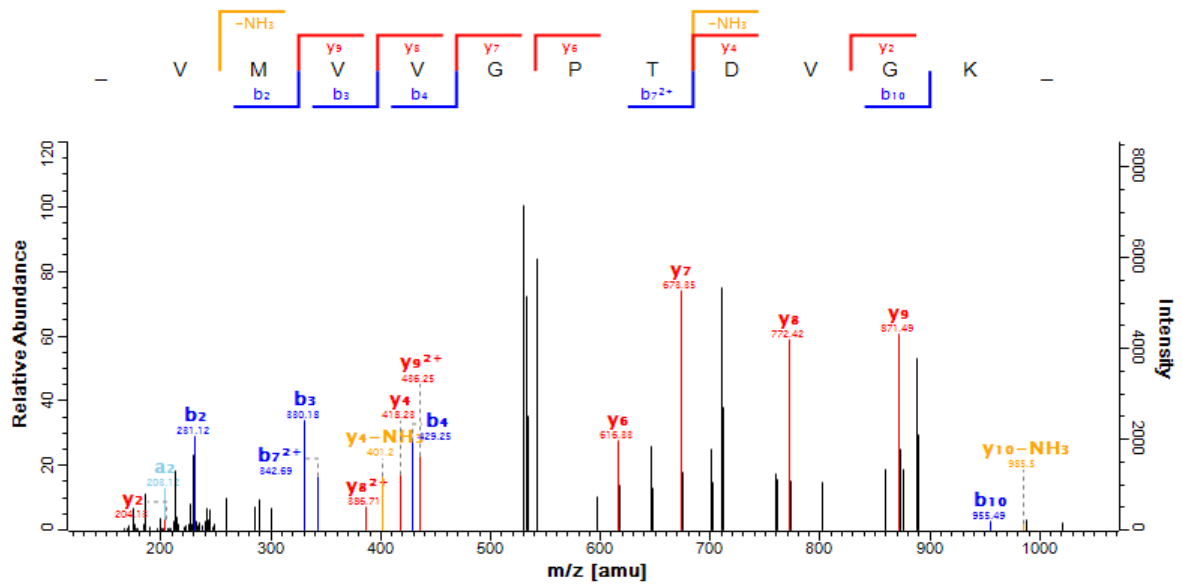
Number of Replicates (out of 8): 1

Best Match Score: 82.417

Best Match Posterior Error Probability: 0.003201

Best Match Spectrum:

Scan number 27304 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CLP1



Protein Group ID: 946

Protein Accession Numbers: Q7Z5B4; Q7Z5B4-5; E9PK46; F5GZ89

Gene Names: RIC3

Peptide Sequence: ITSFELAK

Total Number of Spectra: 3

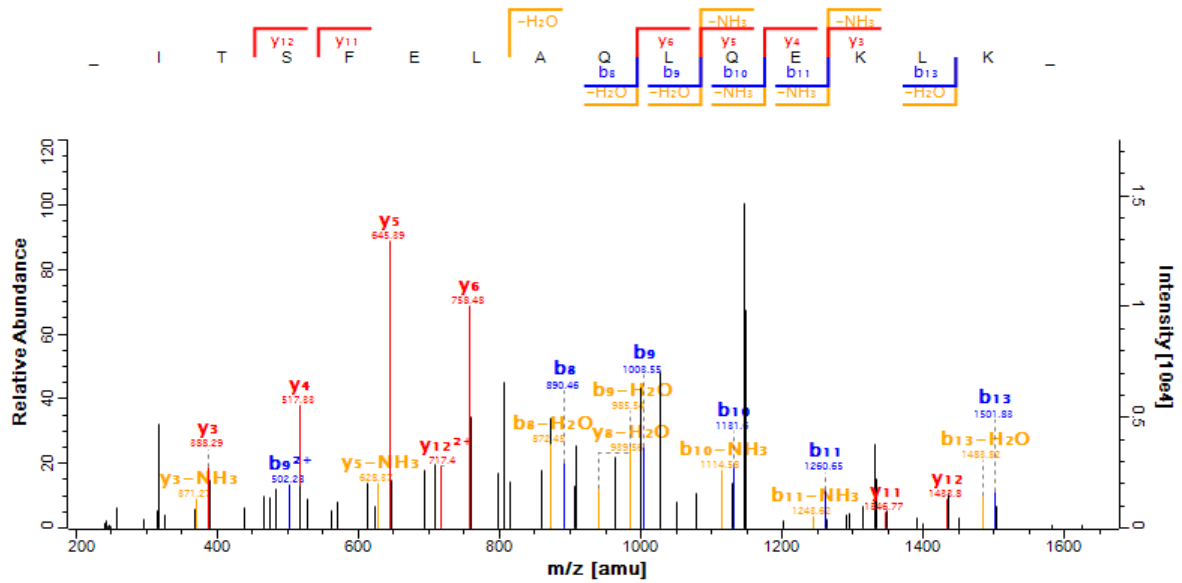
Number of Replicates (out of 8): 3

Best Match Score: 115.12

Best Match Posterior Error Probability: 0.00050755

Best Match Spectrum:

Scan number 88608 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** RIC3



Protein Group ID: 949

Protein Accession Numbers: O94830; E9PKE6

Gene Names: DDHD2

Peptide Sequence: LMVHYQPVAGSDDWGSTPTEQGRPR

Total Number of Spectra: 1

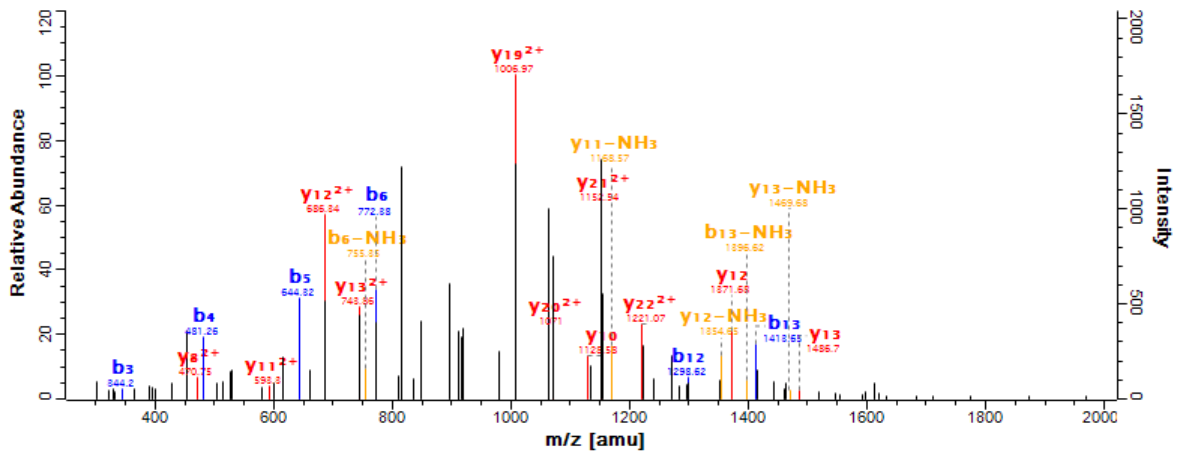
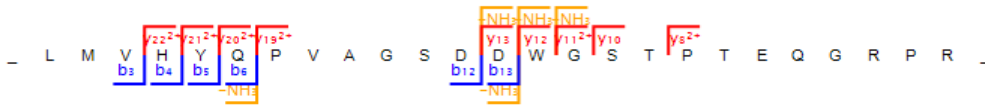
Number of Replicates (out of 8): 1

Best Match Score: 72.09

Best Match Posterior Error Probability: 0.0013593

Best Match Spectrum:

Scan number 39655 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** DDHD2



Protein Group ID: 953

Protein Accession Numbers: P42695; G3V1A9; E9PKK4

Gene Names: NCAPD3

Peptide Sequence: SALQVLVSILK

Total Number of Spectra: 1

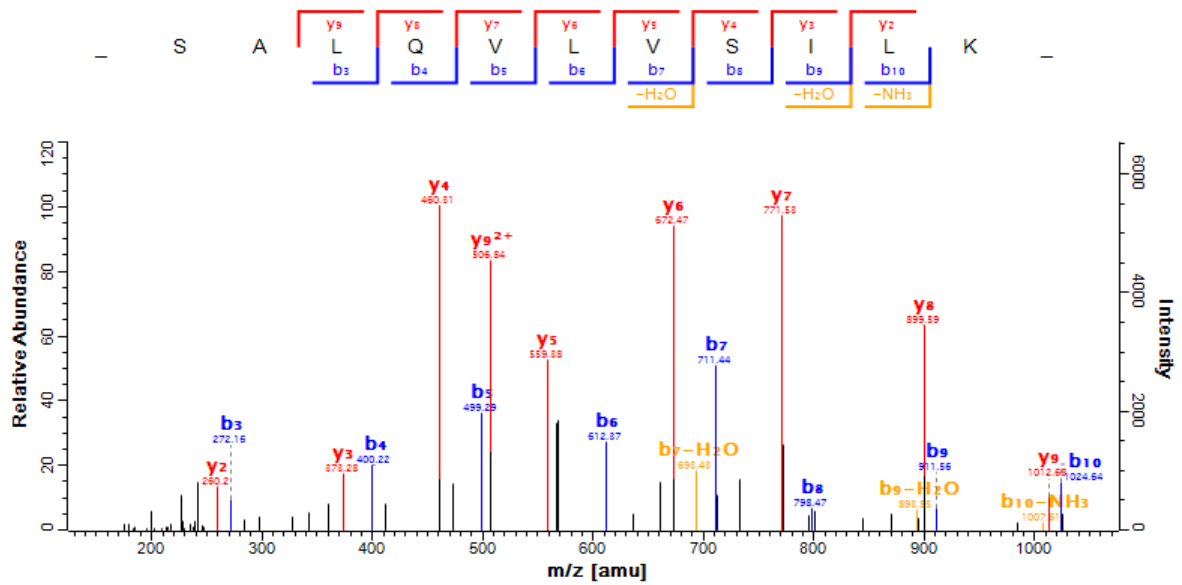
Number of Replicates (out of 8): 1

Best Match Score: 120.87

Best Match Posterior Error Probability: 5.44E-05

Best Match Spectrum:

Scan number 88219 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** NCAPD3



Protein Group ID: 954

Protein Accession Numbers: E9PN81; Q8TDP1; Q8TDP1-2; H0YEF3; H0YCP5; H0YE52; E9PKP0

Gene Names: RNASEH2C

Peptide Sequence: FTLWGLETIPGPDAK

Total Number of Spectra: 1

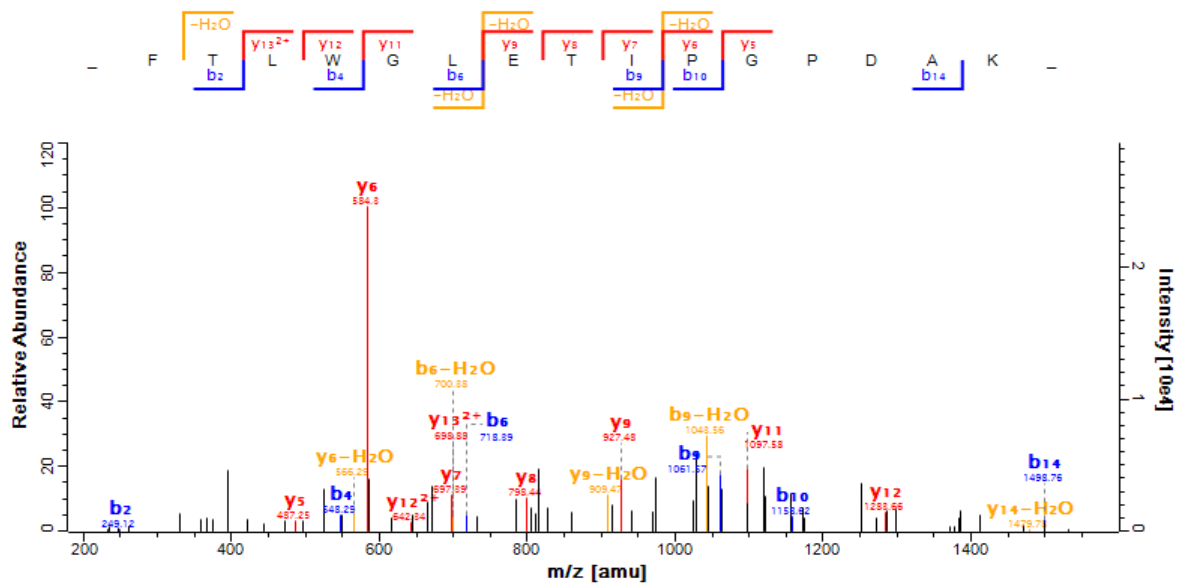
Number of Replicates (out of 8): 1

Best Match Score: 81.703

Best Match Posterior Error Probability: 0.0022241

Best Match Spectrum:

Scan number	74423	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	RNASEH2C



Protein Group ID: 956

Protein Accession Numbers: Q9Y5Q0; E9PS00; E9PKP8; H0YED5; H0YCN1

Gene Names: FADS3

Peptide Sequence: PFLTALVDIVR

Total Number of Spectra: 2

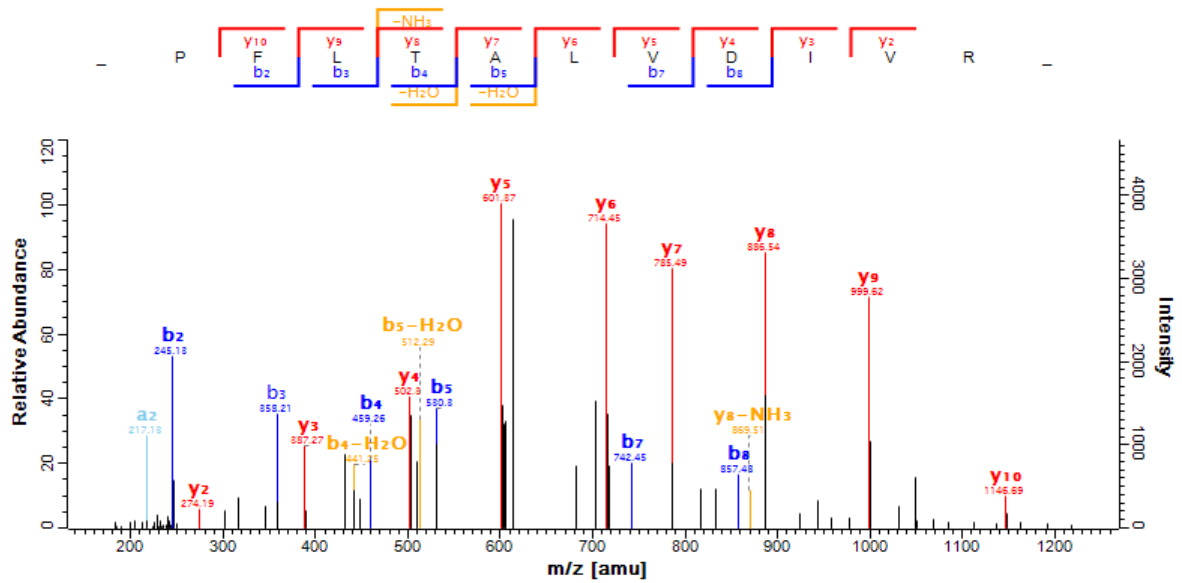
Number of Replicates (out of 8): 2

Best Match Score: 113.22

Best Match Posterior Error Probability: 0.00011911

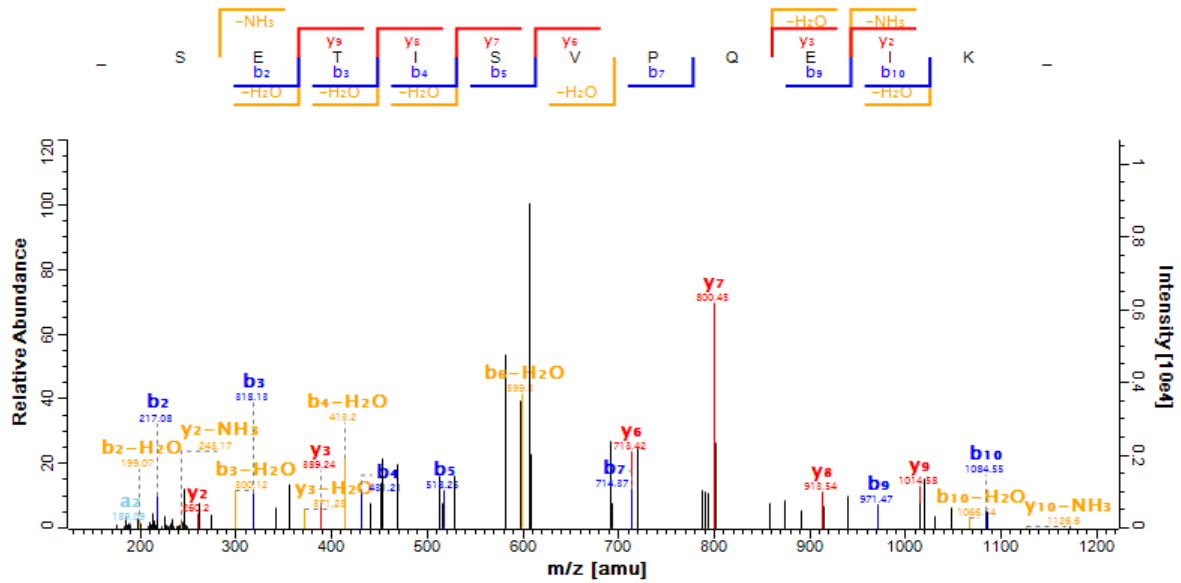
Best Match Spectrum:

Scan number 83986 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** FADS3



Protein Group ID: 958
Protein Accession Numbers: O96033; E9PKT9
Gene Names: MOCS2
Peptide Sequence: SETISVPQEIK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 86.114
Best Match Posterior Error Probability: 0.002104
Best Match Spectrum:

Scan number 32866 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** MOCS2



Protein Group ID: 960

Protein Accession Numbers: P48509; E9PMR4; E9PRJ3; E9PL82

Gene Names: CD151

Peptide Sequence: TVVALCGQR

Total Number of Spectra: 8

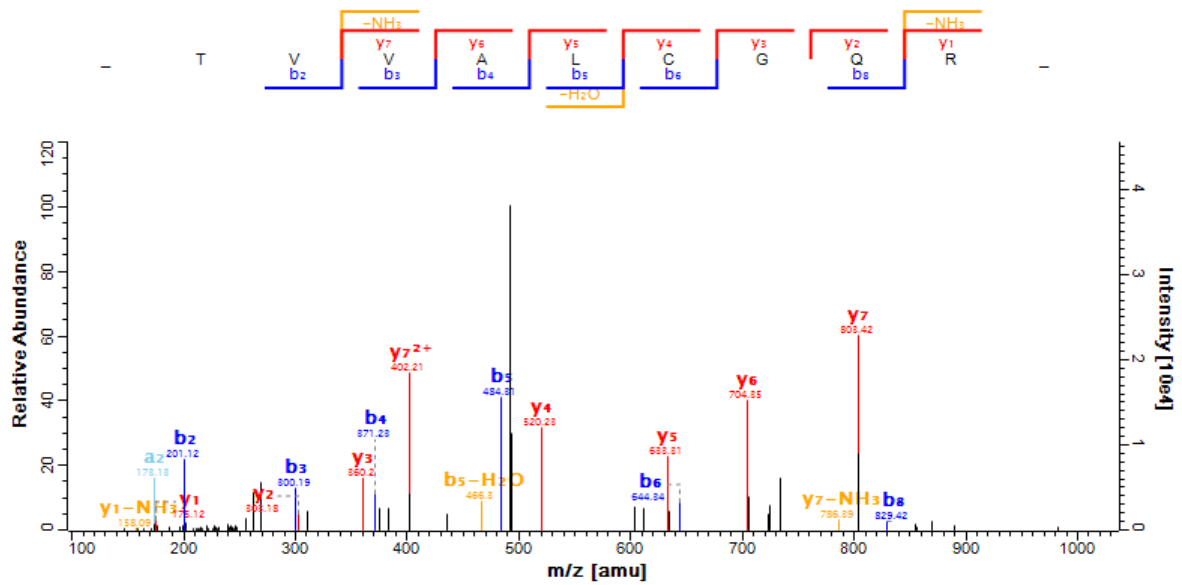
Number of Replicates (out of 8): 8

Best Match Score: 125.82

Best Match Posterior Error Probability: 0.00022929

Best Match Spectrum:

Scan number	15563	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	CD151



Protein Group ID: 964

Protein Accession Numbers: E9PQA6; Q96EY5; Q96EY5-3; E9PLL0

Gene Names: FAM125A

Peptide Sequence: IGDMGGFAIWCK

Total Number of Spectra: 1

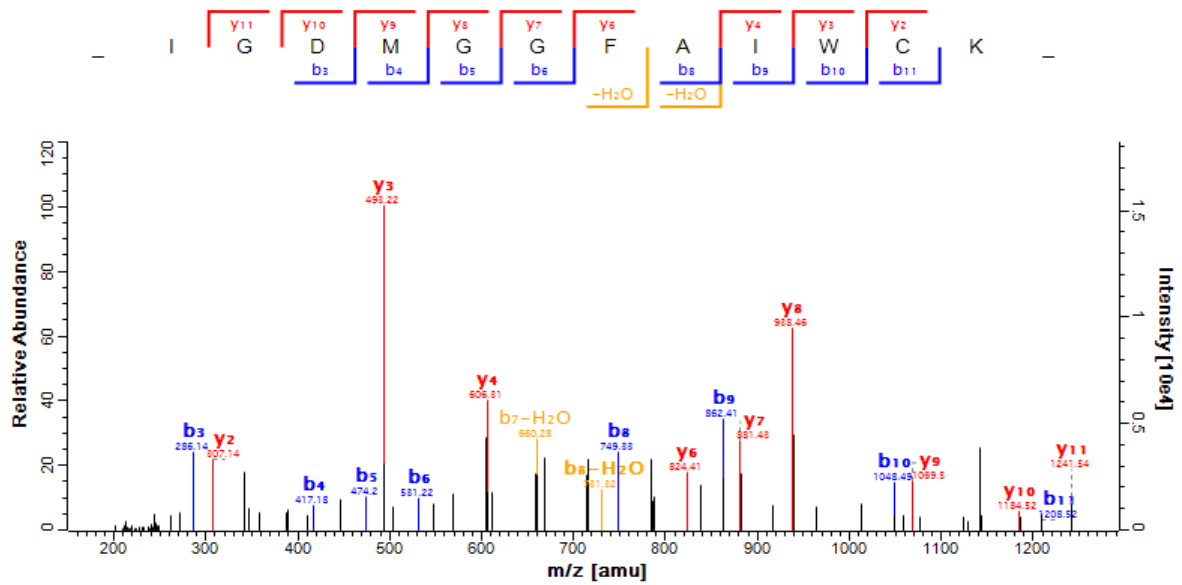
Number of Replicates (out of 8): 1

Best Match Score: 105.17

Best Match Posterior Error Probability: 0.00038567

Best Match Spectrum:

Scan number	61721	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	FAM125A



Protein Group ID: 966

Protein Accession Numbers: E9PLN8; Q9BQB6; Q9BQB6-2; F8W9H0; I3L3B4; Q9BQB6-3

Gene Names: VKORC1

Peptide Sequence: ALCDVGTAISCSR

Total Number of Spectra: 6

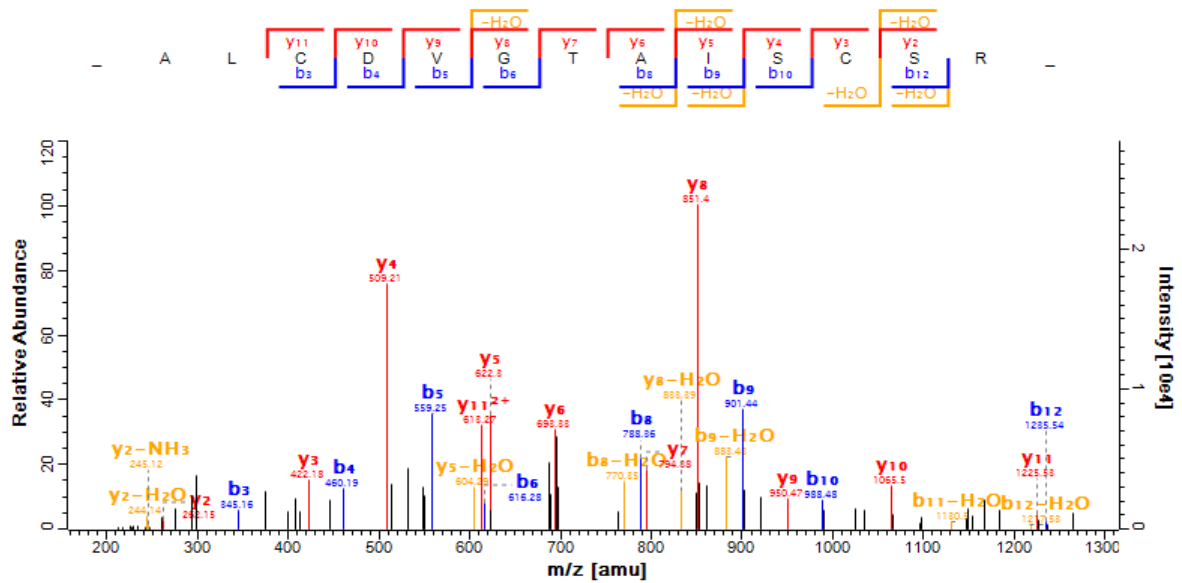
Number of Replicates (out of 8): 5

Best Match Score: 147.73

Best Match Posterior Error Probability: 1.82E-06

Best Match Spectrum:

Scan number 30094 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS: CID **Genenames** VKORC1



Protein Group ID: 968

Protein Accession Numbers: Q9Y5Y5-2; Q9Y5Y5; E9PP98; E9PMM3; E9PLS4

Gene Names: PEX16

Peptide Sequence: TLQNTPSLHSR

Total Number of Spectra: 7

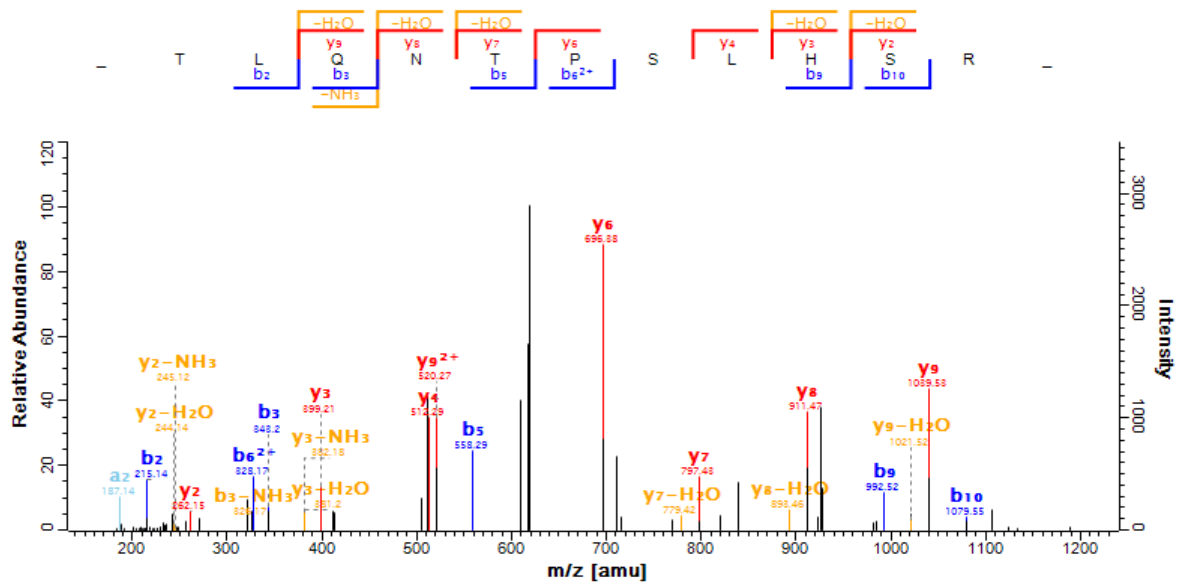
Number of Replicates (out of 8): 6

Best Match Score: 119.74

Best Match Posterior Error Probability: 6.40E-05

Best Match Spectrum:

Scan number 11148 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PEX16



Protein Group ID: 969

Protein Accession Numbers: O43292; O43292-2; E9PPZ9; E9PLV6

Gene Names: GPAA1

Peptide Sequence: YMVSGTNVYGILR

Total Number of Spectra: 3

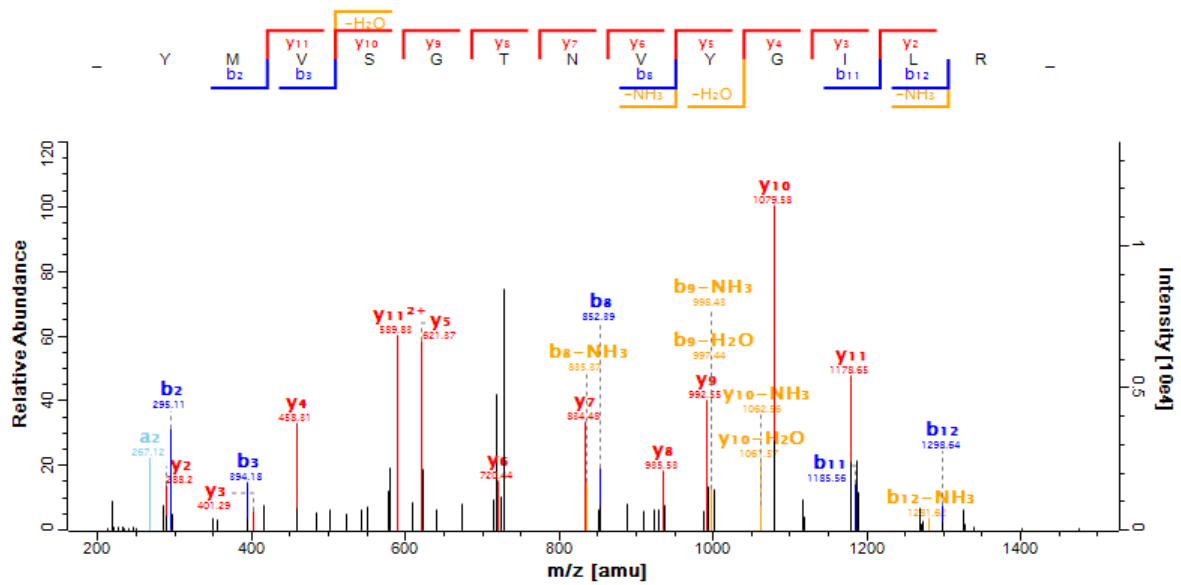
Number of Replicates (out of 8): 3

Best Match Score: 144.57

Best Match Posterior Error Probability: 4.74E-06

Best Match Spectrum:

Scan number 55170 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** GPAA1



Protein Group ID: 970

Protein Accession Numbers: Q8N573; Q8N573-8; Q8N573-5; Q8N573-2; H0YC07; Q8N573-6; Q8N573-4; Q8N573-7; E9PLW2

Gene Names: OXR1

Peptide Sequence: DSDGQVFGALASEPLK

Total Number of Spectra: 1

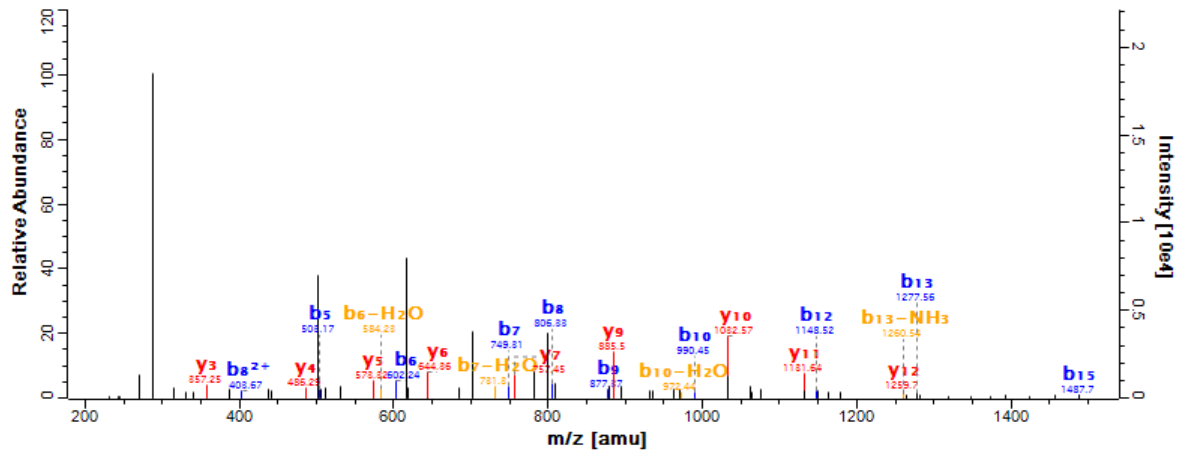
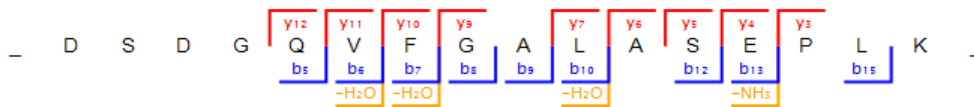
Number of Replicates (out of 8): 1

Best Match Score: 91.518

Best Match Posterior Error Probability: 0.00050492

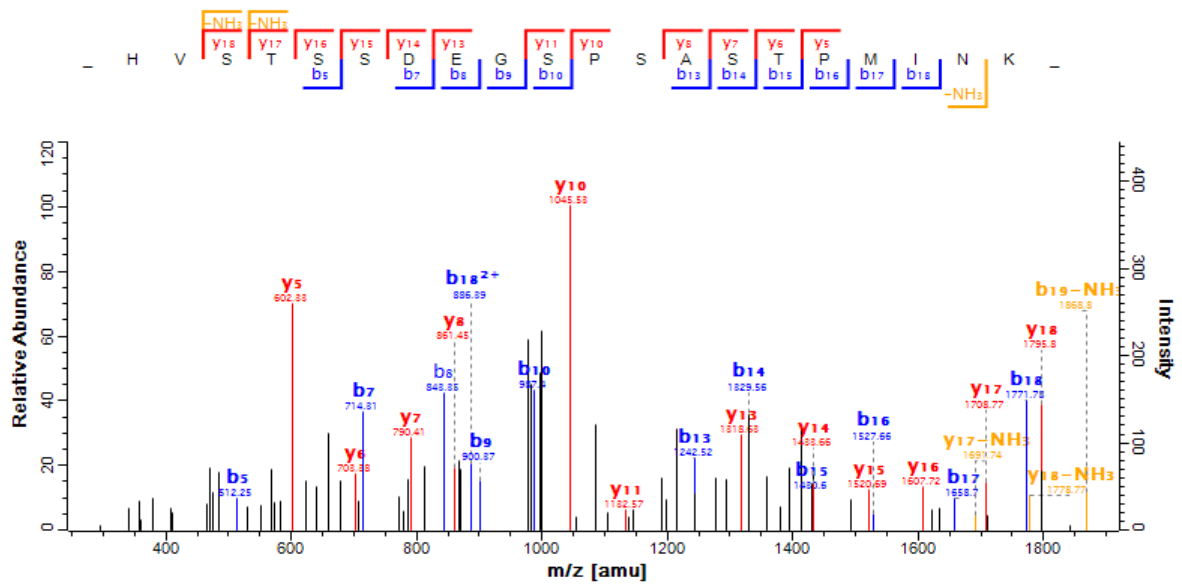
Best Match Spectrum:

Scan number	55341	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS: CID	Genenames	OXR1



Protein Group ID: 974
Protein Accession Numbers: Q7L1W4; E9PMF9
Gene Names: LRRC8D
Peptide Sequence: HVSTSSDEGSPSASTPMINK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 107.41
Best Match Posterior Error Probability: 6.11E-05
Best Match Spectrum:

Scan number 16677 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** LRRC8D



Protein Group ID: 979

Protein Accession Numbers: P49662; P49662-2; E9PMT1

Gene Names: CASP4

Peptide Sequence: ERAEEIYPIK

Total Number of Spectra: 1

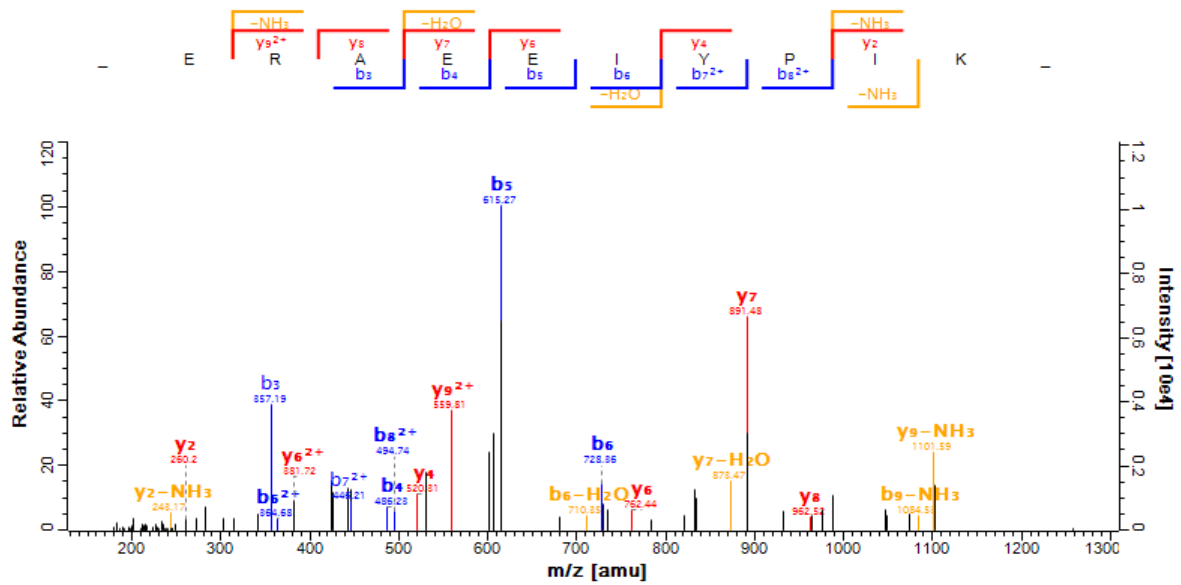
Number of Replicates (out of 8): 1

Best Match Score: 110.84

Best Match Posterior Error Probability: 0.0014245

Best Match Spectrum:

Scan number 22265 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CASP4



Protein Group ID: 981

Protein Accession Numbers: O00214-2; O00214; F6V2D4; E9PN19; H7BXD8

Gene Names: LGALS8

Peptide Sequence: DIALHLNPR

Total Number of Spectra: 2

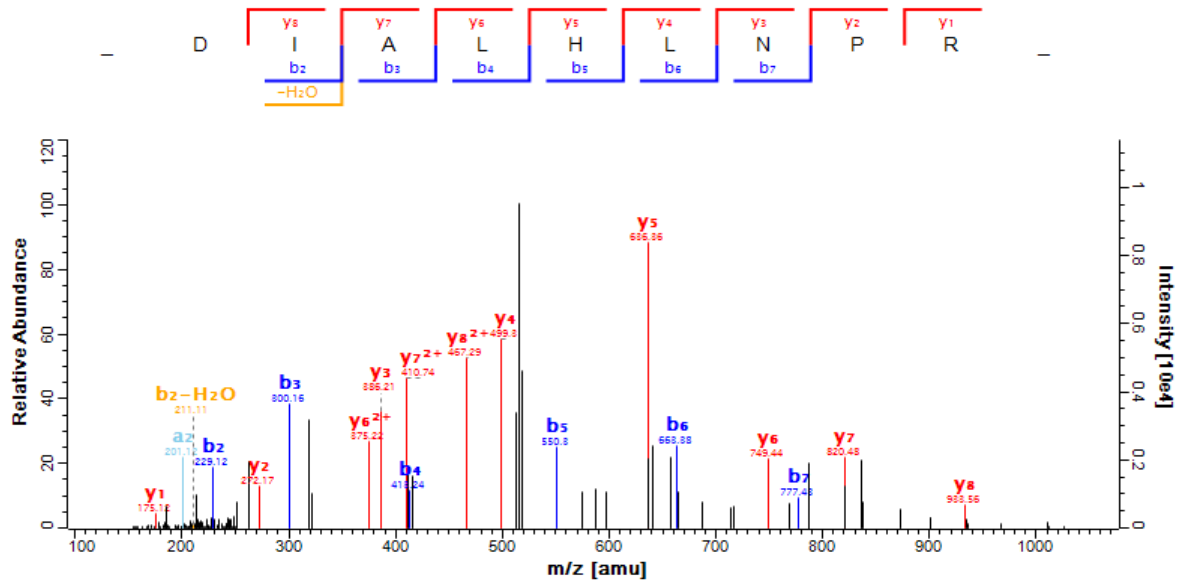
Number of Replicates (out of 8): 2

Best Match Score: 122.28

Best Match Posterior Error Probability: 0.00030596

Best Match Spectrum:

Scan number	30588	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	LGALS8



Protein Group ID: 982

Protein Accession Numbers: Q01433; H0Y360; Q01433-4; Q01433-2; E9PNG0; Q01433-3

Gene Names: AMPD2

Peptide Sequence: FQMHVLLNEMK

Total Number of Spectra: 1

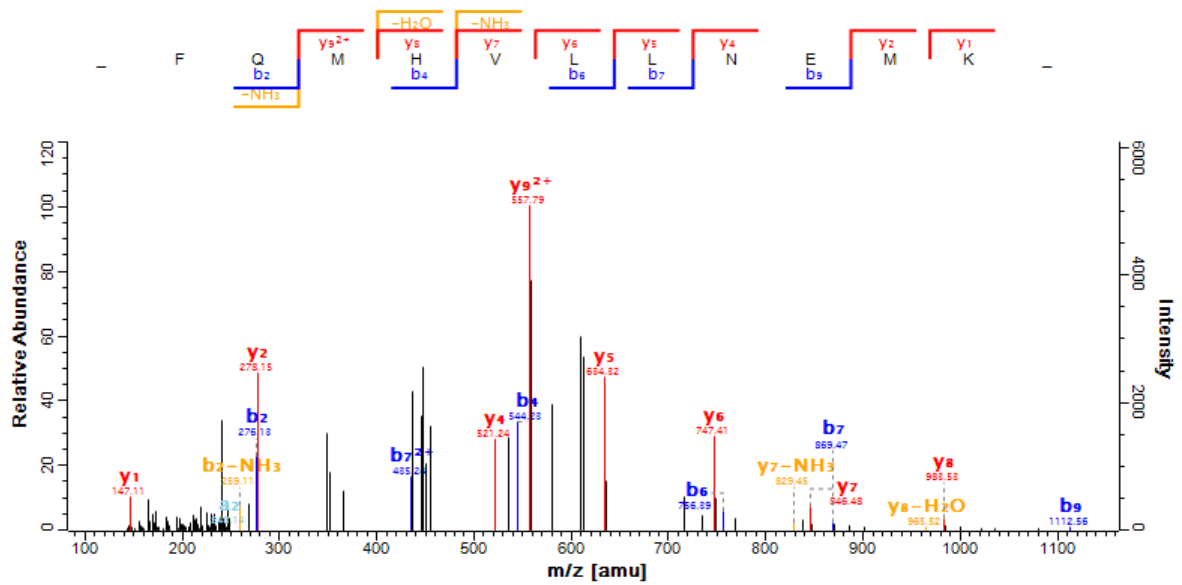
Number of Replicates (out of 8): 1

Best Match Score: 87.667

Best Match Posterior Error Probability: 0.00172

Best Match Spectrum:

Scan number 49330 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** AMPD2



Protein Group ID: 985

Protein Accession Numbers: Q96PZ2; E9PR18; E9PNQ0

Gene Names: FAM111A

Peptide Sequence: KNPEDQTPMQNR

Total Number of Spectra: 3

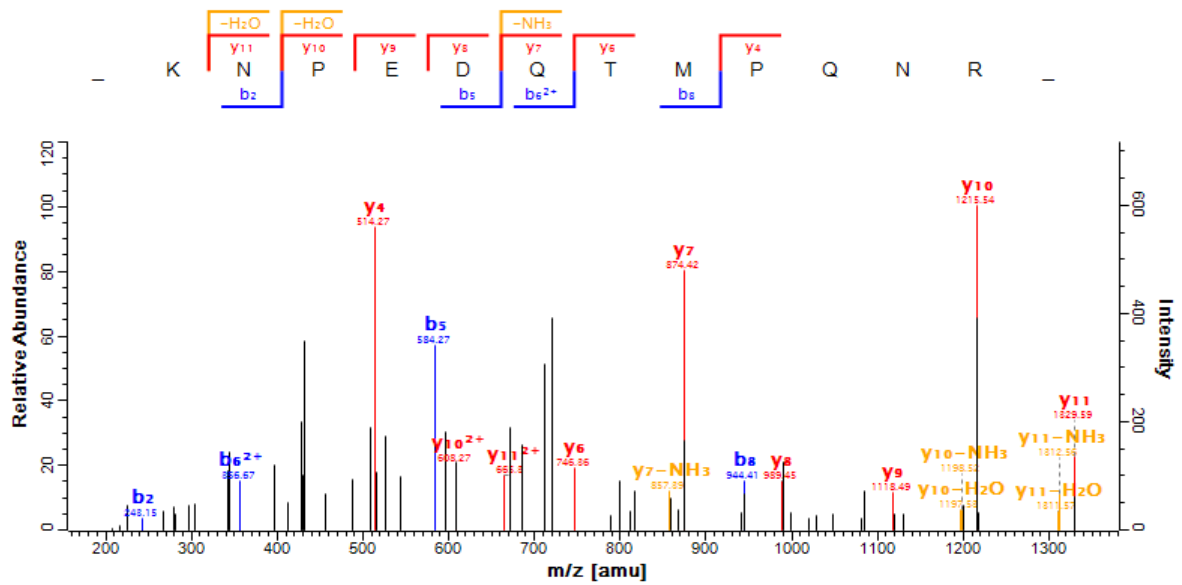
Number of Replicates (out of 8): 3

Best Match Score: 105.03

Best Match Posterior Error Probability: 0.00090905

Best Match Spectrum:

Scan number 5228 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** FAM111A



Protein Group ID: 988

Protein Accession Numbers: Q96K19; Q96K19-2; Q96K19-3; Q96K19-5; E9PP55

Gene Names: RNF170

Peptide Sequence: EQLQTEQDAPAATR

Total Number of Spectra: 9

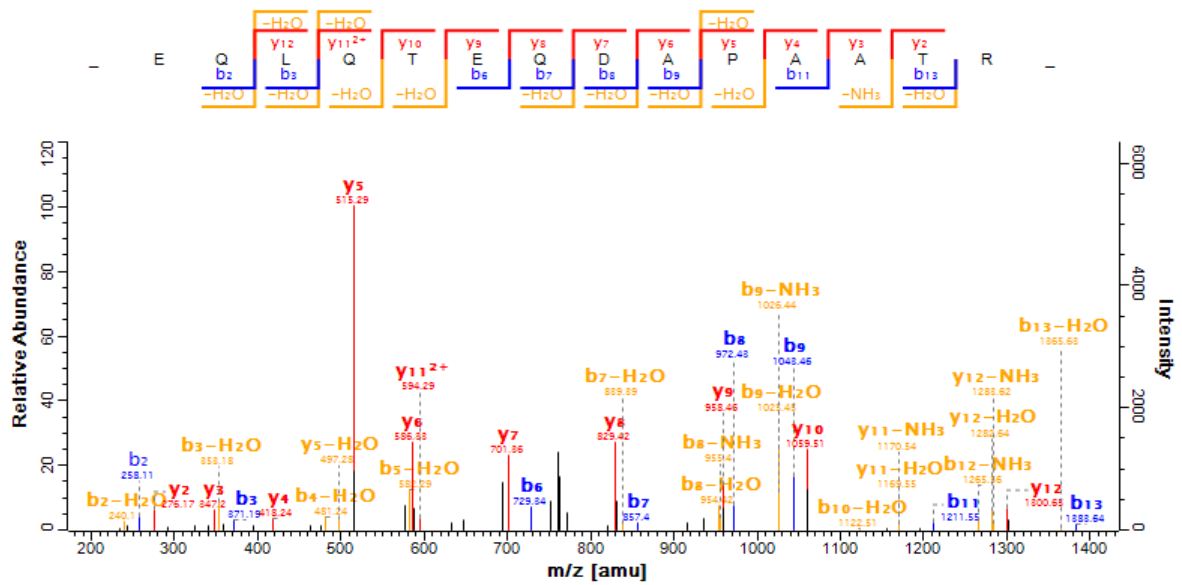
Number of Replicates (out of 8): 7

Best Match Score: 181.58

Best Match Posterior Error Probability: 5.27E-19

Best Match Spectrum:

Scan number 12207 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** RNF170



Protein Group ID: 998

Protein Accession Numbers: E9PSH4; Q9H063; E9PR76

Gene Names: MAF1

Peptide Sequence: SQGGEEEGPLSDK

Total Number of Spectra: 2

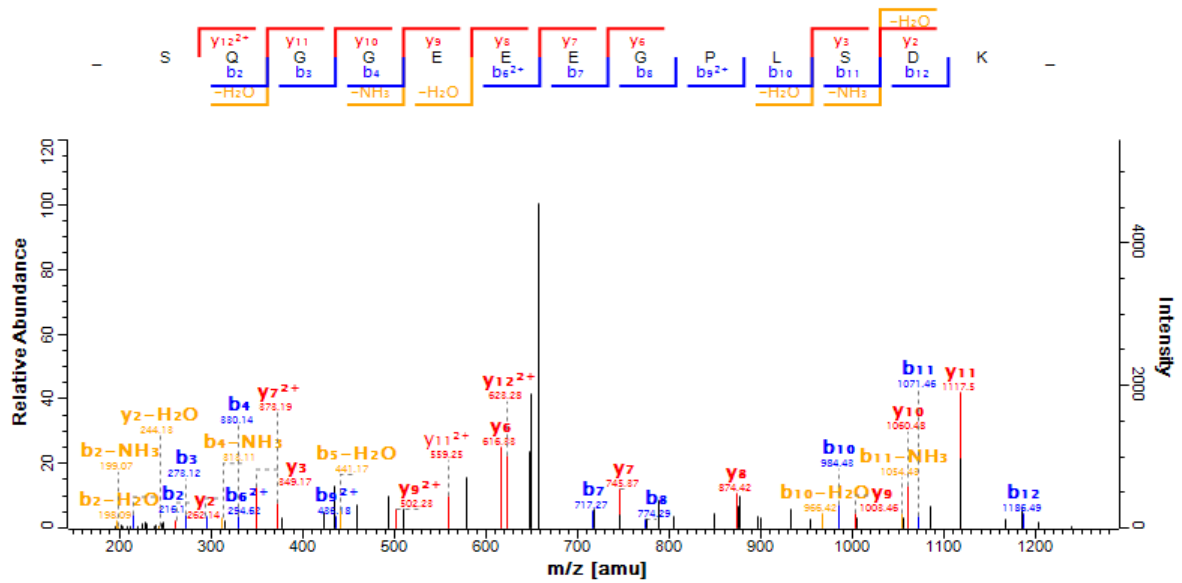
Number of Replicates (out of 8): 2

Best Match Score: 135.14

Best Match Posterior Error Probability: 3.89E-05

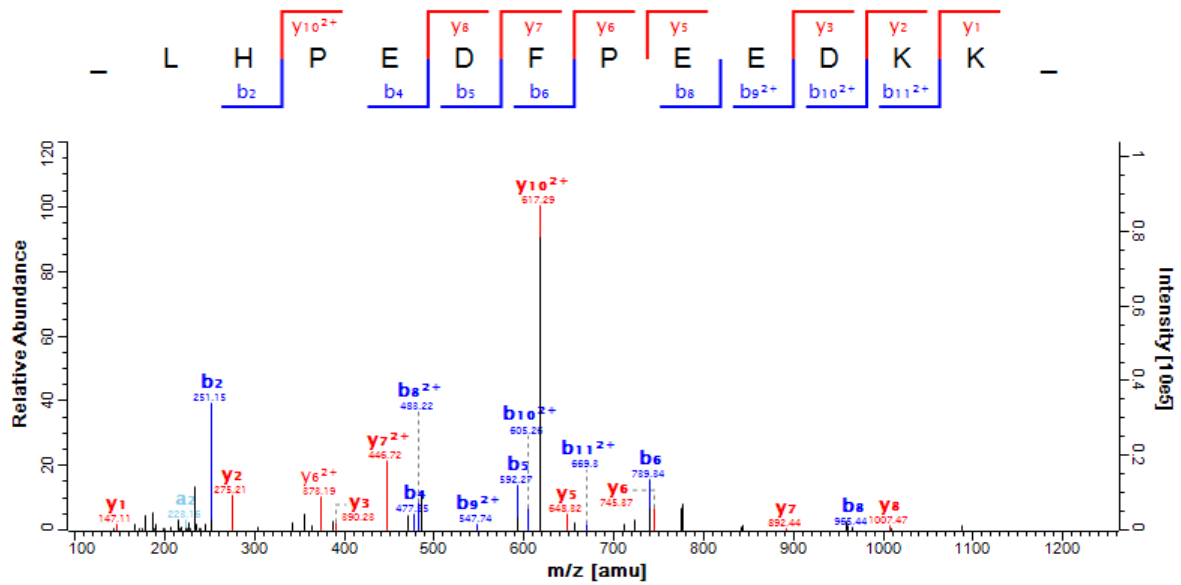
Best Match Spectrum:

Scan number 10053 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MAF1



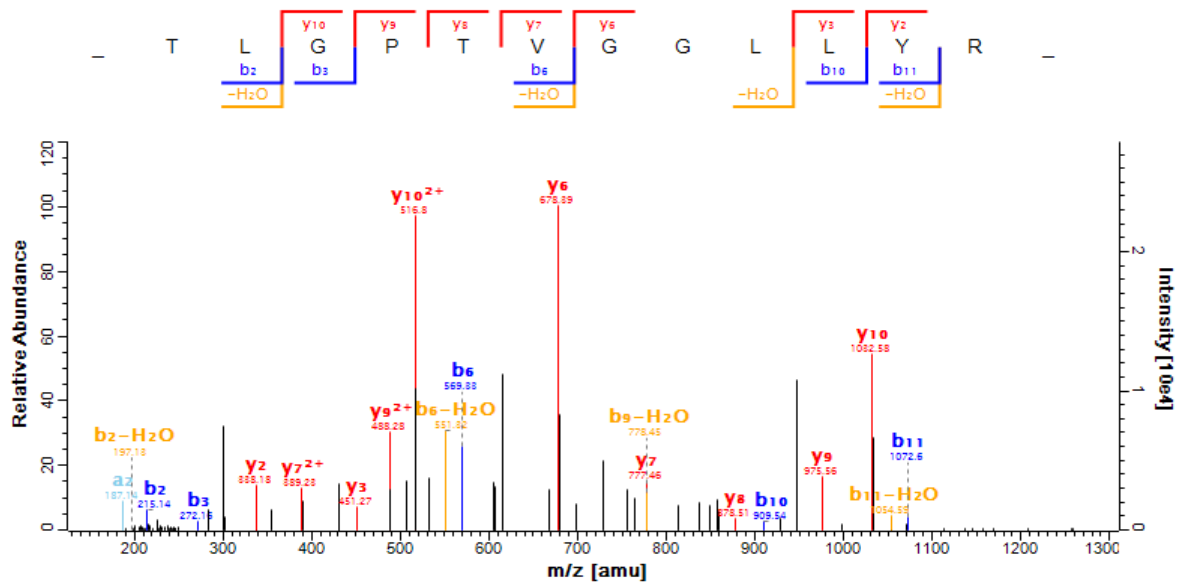
Protein Group ID: 999
Protein Accession Numbers: O95298; E9PRB2
Gene Names: NDUFC2
Peptide Sequence: LHPEDFPEEDKK
Total Number of Spectra: 9
Number of Replicates (out of 8): 6
Best Match Score: 129.82
Best Match Posterior Error Probability: 0.00023425
Best Match Spectrum:

Scan number 15118 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** NDUFC2



Protein Group ID: 1000
Protein Accession Numbers: Q96BI1; E9PRM7
Gene Names: SLC22A18
Peptide Sequence: TLGPTVGGLLYR
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 110.08
Best Match Posterior Error Probability: 0.00026584
Best Match Spectrum:

Scan number 51194 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** SLC22A18



Protein Group ID: 1008

Protein Accession Numbers: E9PSI1; O15321; E9PMQ9; O15321-2; E9PJM1; E9PL78; E9PS99; E9PQY7; E9PJC4

Gene Names: TM9SF1

Peptide Sequence: VGPYHNSETPYHQYLYQLPVCPCPEK

Total Number of Spectra: 3

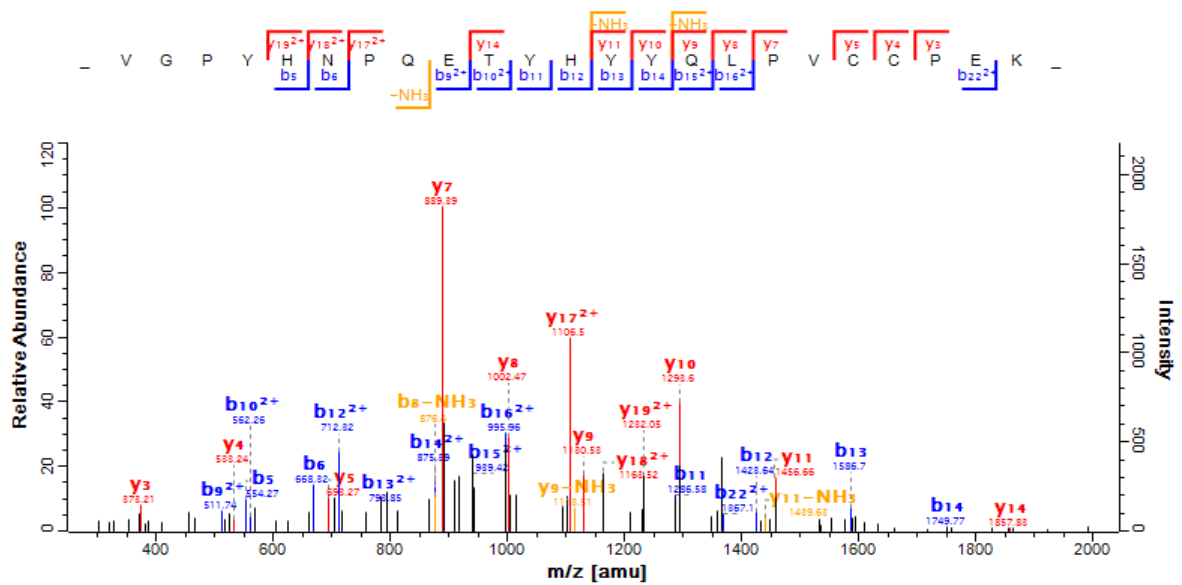
Number of Replicates (out of 8): 3

Best Match Score: 123.19

Best Match Posterior Error Probability: 2.21E-09

Best Match Spectrum:

Scan number 42201 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS: CID **Genenames** TM9SF1



Protein Group ID: 1015

Protein Accession Numbers: P07902; G3V4G9; F2Z2X9; G3V223; G3V3U5

Gene Names: GALT

Peptide Sequence: QQASEADAAAATFR

Total Number of Spectra: 1

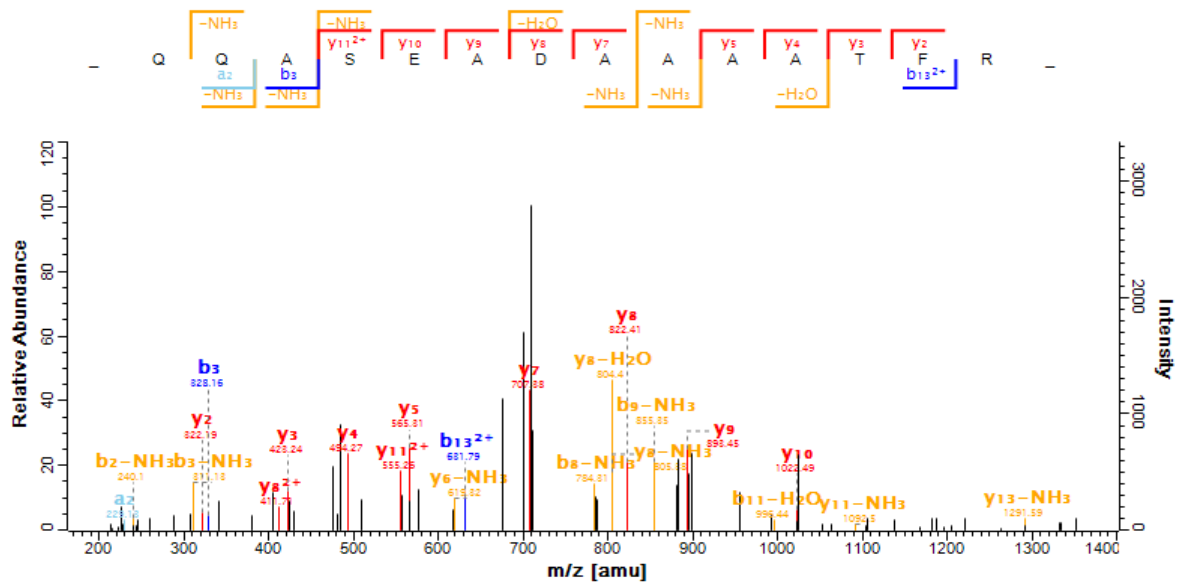
Number of Replicates (out of 8): 1

Best Match Score: 82.069

Best Match Posterior Error Probability: 0.0027382

Best Match Spectrum:

Scan number 22770 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** GALT



Protein Group ID: 1017

Protein Accession Numbers: J3QSS6; J3KPC5; P47736-3; P47736-2; P47736; G3V1A7; F2Z357

Gene Names: RAP1GAP

Peptide Sequence: DDVPPFFGPPLPDPAVR

Total Number of Spectra: 3

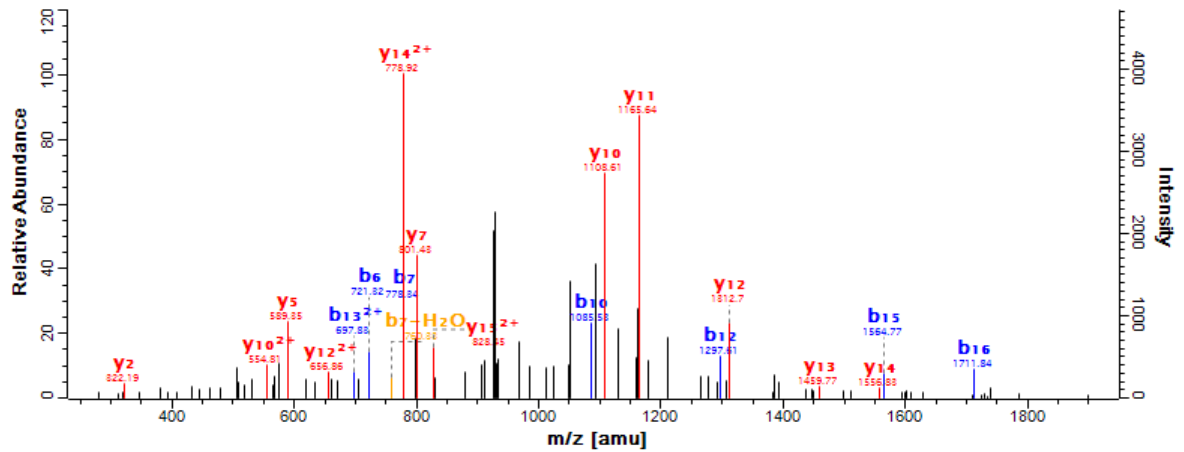
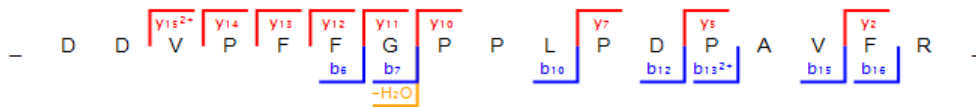
Number of Replicates (out of 8): 3

Best Match Score: 107.07

Best Match Posterior Error Probability: 0.00012085

Best Match Spectrum:

Scan number	84379	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS: CID	Genenames	RAP1GAP



Protein Group ID: 1018

Protein Accession Numbers: P42766; F2Z388; H0Y3A0

Gene Names: RPL35

Peptide Sequence: VLTVINQTQK

Total Number of Spectra: 11

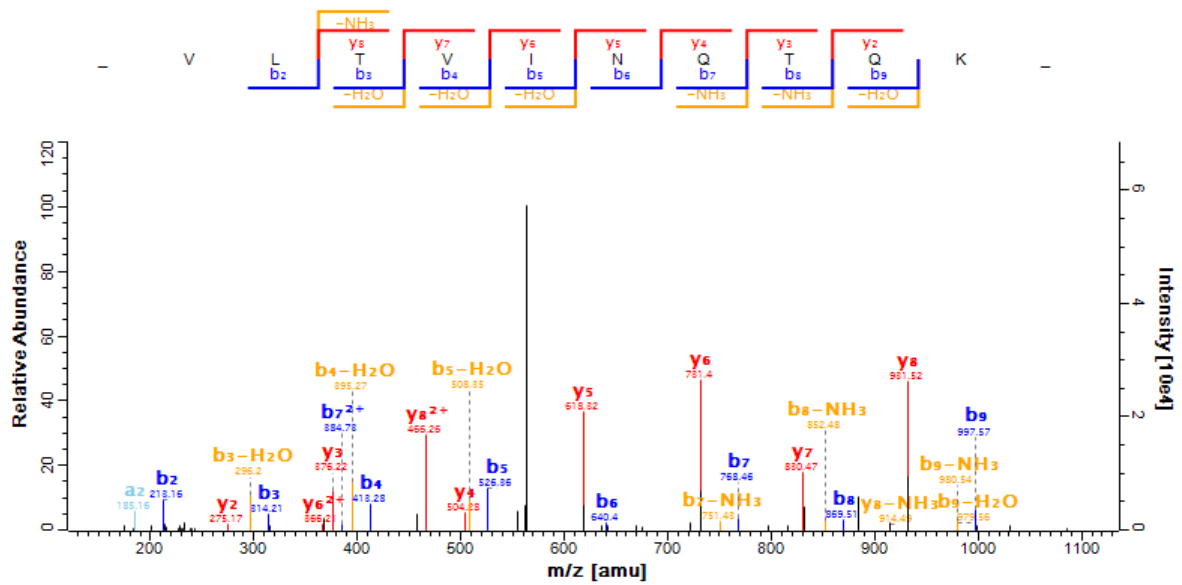
Number of Replicates (out of 8): 8

Best Match Score: 195.51

Best Match Posterior Error Probability: 5.83E-13

Best Match Spectrum:

Scan number 19901 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** RPL35



Protein Group ID: 1019

Protein Accession Numbers: Q9HBM0; F2Z3A6; F8W8C2; Q9HBM0-2

Gene Names: VEZT

Peptide Sequence: ALLNEVILIEDLEK

Total Number of Spectra: 3

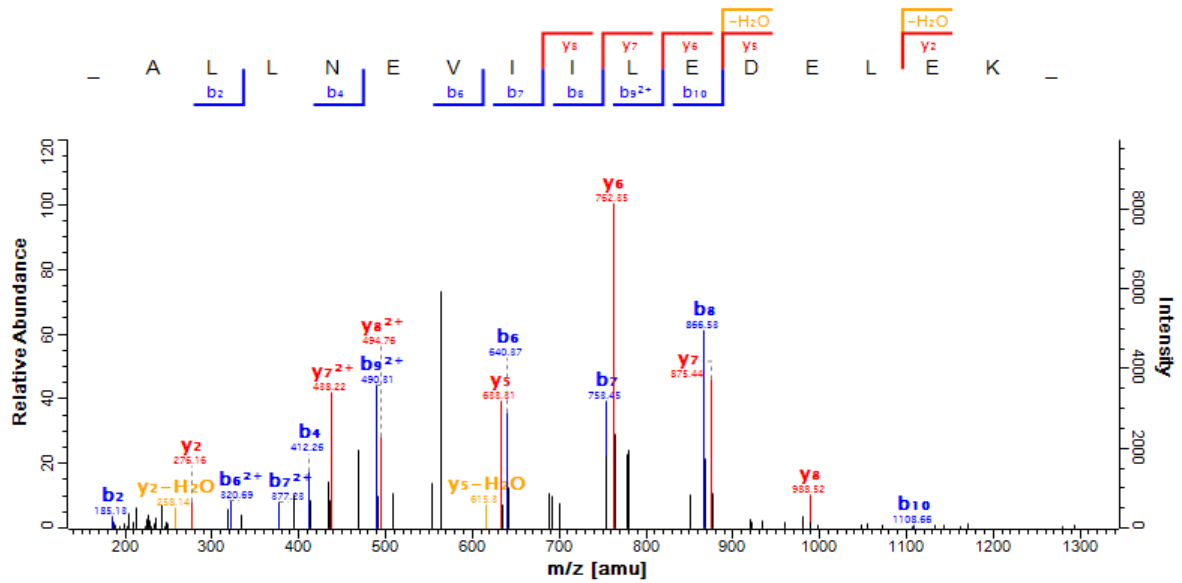
Number of Replicates (out of 8): 3

Best Match Score: 92.939

Best Match Posterior Error Probability: 0.00061849

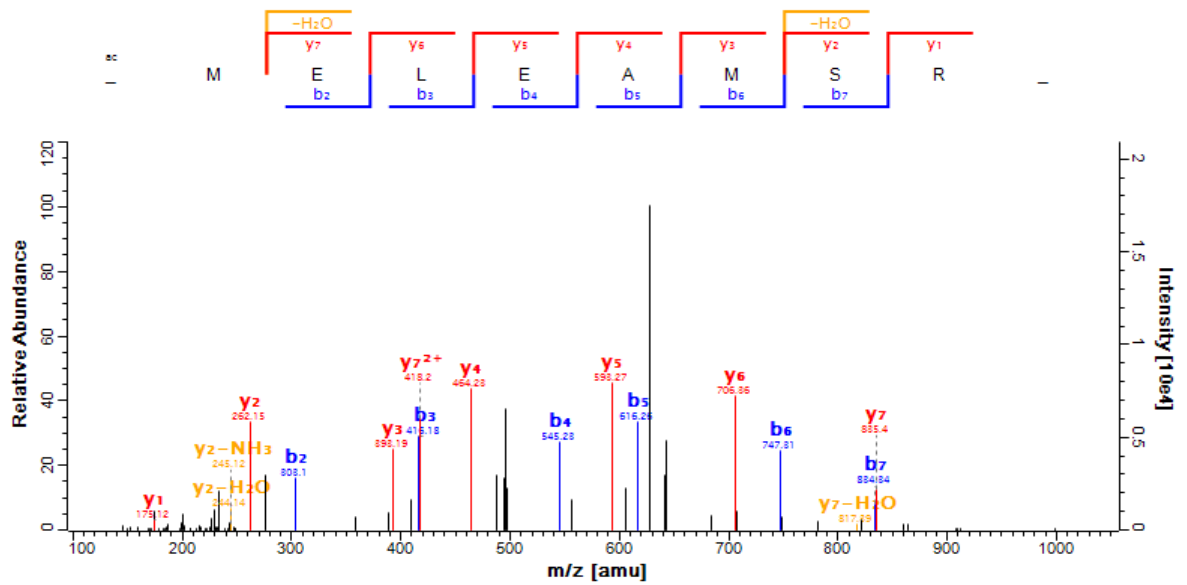
Best Match Spectrum:

Scan number	89693	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	VEZT



Protein Group ID: 1020
Protein Accession Numbers: P61165; F5GWH5
Gene Names: C11orf10
Peptide Sequence: MELEAMSR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 118.18
Best Match Posterior Error Probability: 0.0031312
Best Match Spectrum:

Scan number 44920 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** C11orf10



Protein Group ID: 1028

Protein Accession Numbers: Q6NXE6; Q6NXE6-2; F5H4P3; F5GWV0; F5H2K4; F5H2X2; F5H052

Gene Names: ARMC6

Peptide Sequence: VSADGSQEP¹THDILQLML²SLDLQESVASSR³PQEVSA⁴YLTR⁵

Total Number of Spectra: 1

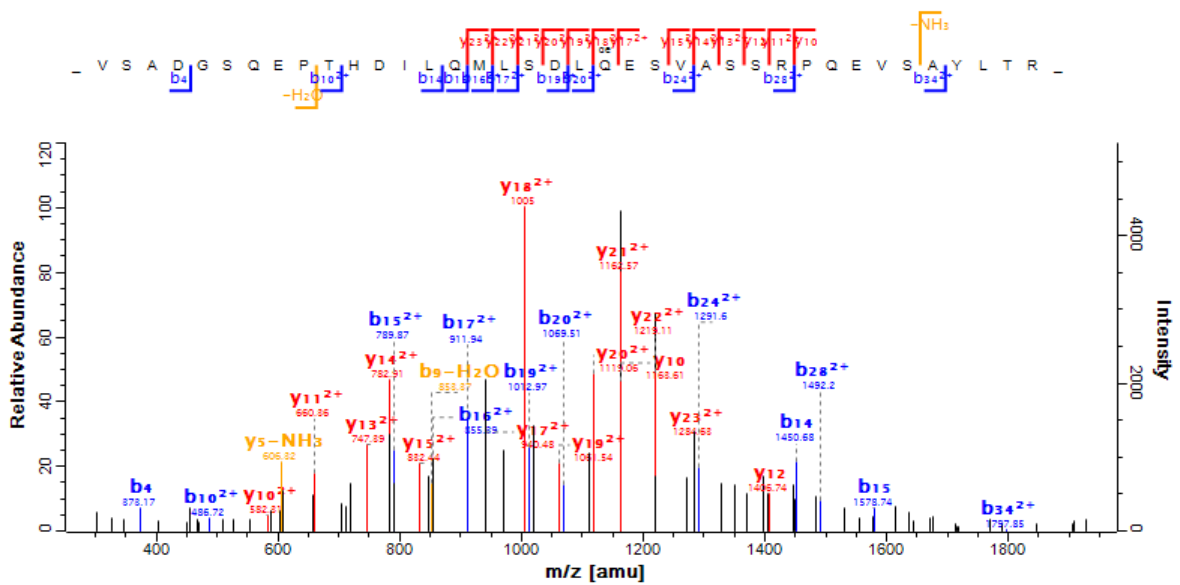
Number of Replicates (out of 8): 1

Best Match Score: 61.525

Best Match Posterior Error Probability: 0.0038862

Best Match Spectrum:

Scan number	92890	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS: CID	Genenames	ARMC6



Protein Group ID: 1033

Protein Accession Numbers: Q8TB96; F5GXC5; H3BUJ1

Gene Names: ITFG1

Peptide Sequence: NDFAIHTLK

Total Number of Spectra: 1

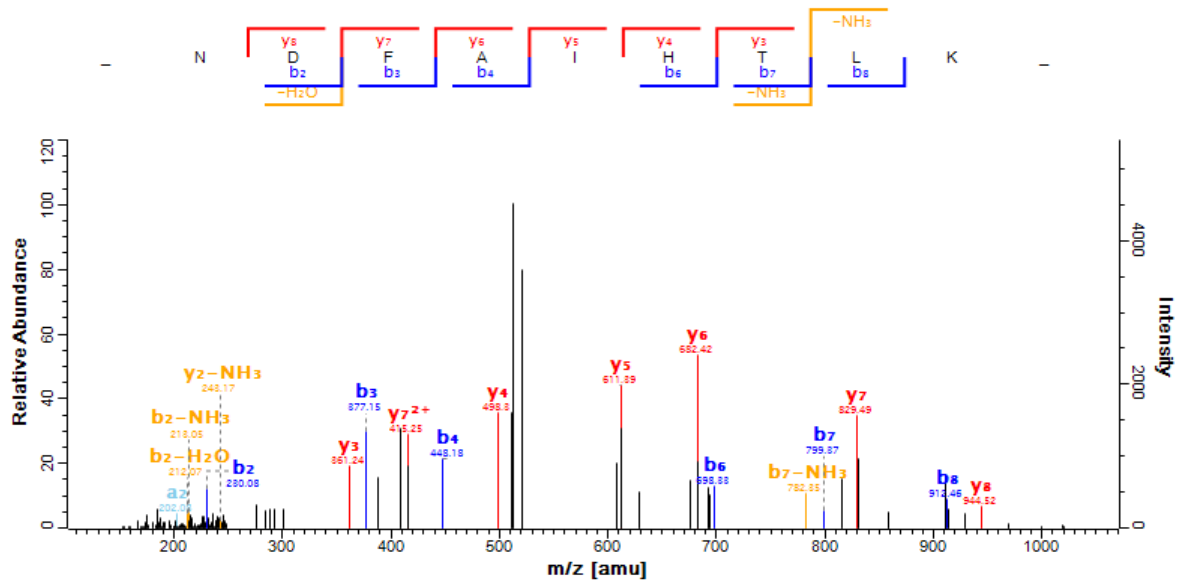
Number of Replicates (out of 8): 1

Best Match Score: 104.82

Best Match Posterior Error Probability: 0.0013927

Best Match Spectrum:

Scan number	25417	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	ITFG1



Protein Group ID: 1038

Protein Accession Numbers: F5GXR3; P20962; F5H7R9

Gene Names: PTMS

Peptide Sequence: SVEAAAELSAK

Total Number of Spectra: 13

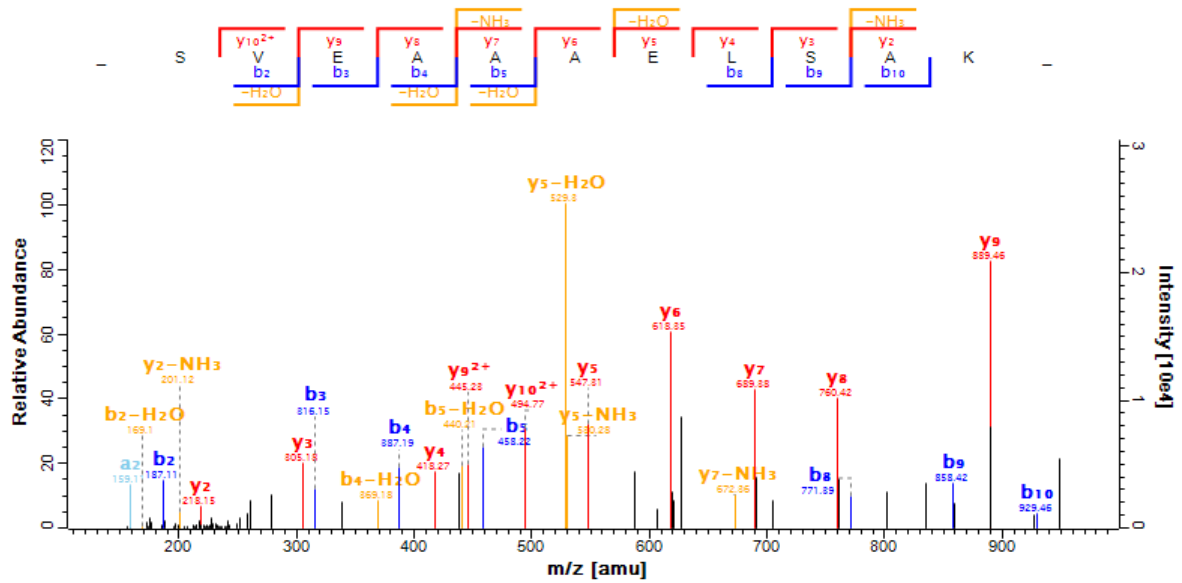
Number of Replicates (out of 8): 7

Best Match Score: 178.67

Best Match Posterior Error Probability: 5.88E-24

Best Match Spectrum:

Scan number	18256	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	PTMS



Protein Group ID: 1040

Protein Accession Numbers: H0Y599; Q8N1I0-3; Q8N1I0; Q8N1I0-2; H0Y7H7; F5GXW1

Gene Names: DOCK4

Peptide Sequence: EYILSHPEDGEK

Total Number of Spectra: 1

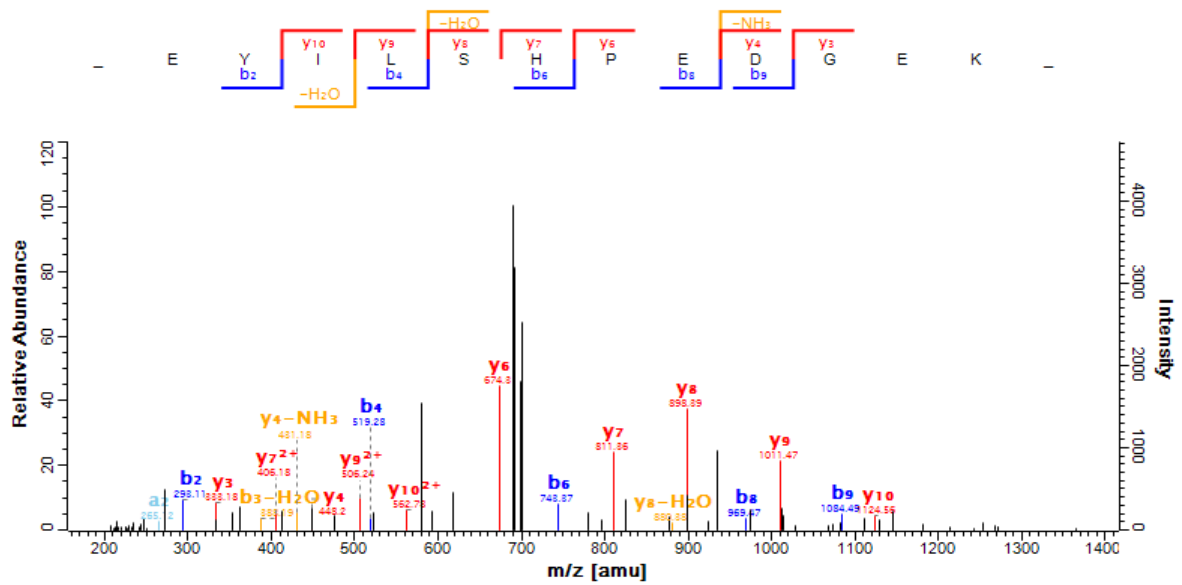
Number of Replicates (out of 8): 1

Best Match Score: 98.407

Best Match Posterior Error Probability: 0.0031807

Best Match Spectrum:

Scan number 17921 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** DOCK4



Protein Group ID: 1043

Protein Accession Numbers: P13051; P13051-2; F5GYA2; Q68DM5

Gene Names: UNG;DKFZp781L1143

Peptide Sequence: KAPAGQEEPGETPTSPSSPLSAELQDR

Total Number of Spectra: 3

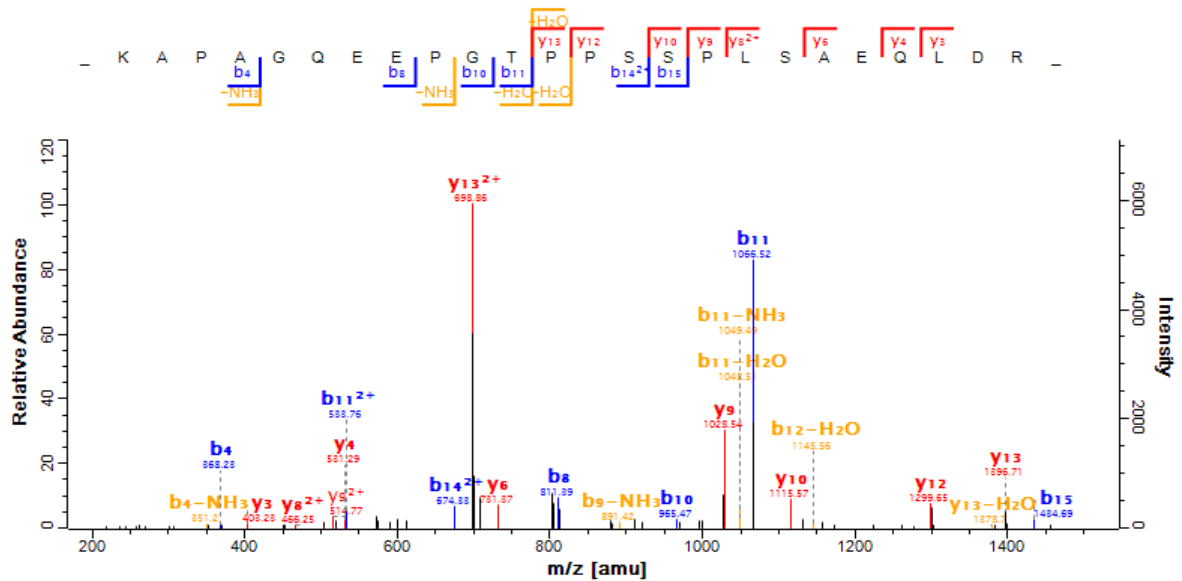
Number of Replicates (out of 8): 3

Best Match Score: 66.137

Best Match Posterior Error Probability: 0.0017634

Best Match Spectrum:

Scan number 33721 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** UNG;DKFZp781L1143



Protein Group ID: 1044

Protein Accession Numbers: O14519; F5GYA4; F5GZF0

Gene Names: CDK2AP1

Peptide Sequence: YAELLAIIIEELGK

Total Number of Spectra: 7

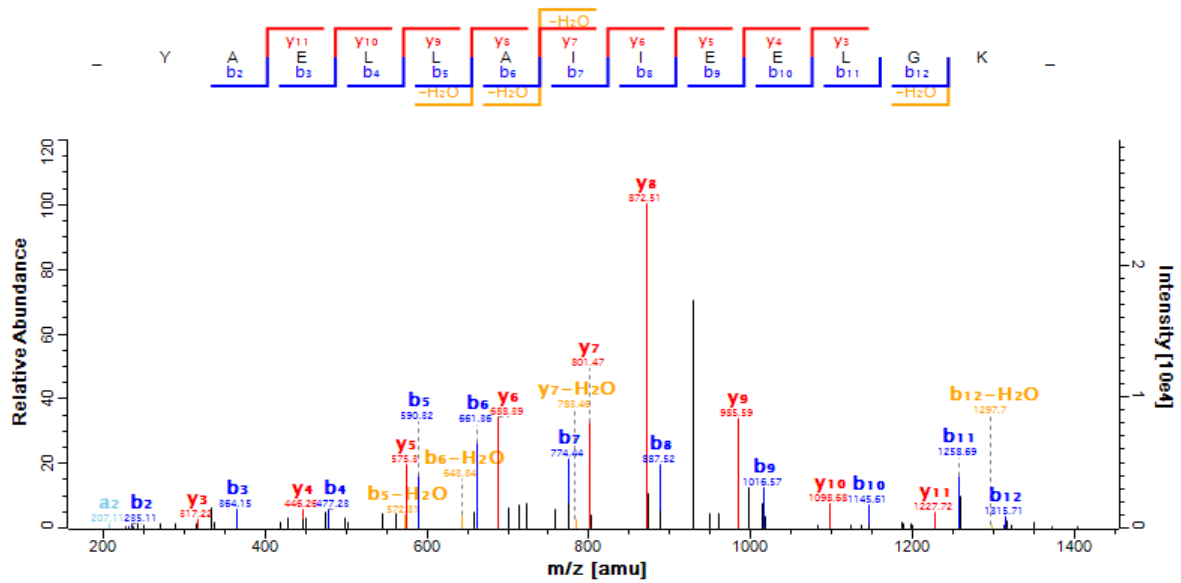
Number of Replicates (out of 8): 7

Best Match Score: 157.52

Best Match Posterior Error Probability: 3.20E-09

Best Match Spectrum:

Scan number	89717	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	CDK2AP1



Protein Group ID: 1052

Protein Accession Numbers: Q8N9N5; F5GZM0; Q8N9N5-5; Q8N9N5-4; Q8N9N5-2; Q8N9N5-6; J3QTH5; Q8N9N5-3

Gene Names: BANP

Peptide Sequence: EVQAVSNLSGQK

Total Number of Spectra: 1

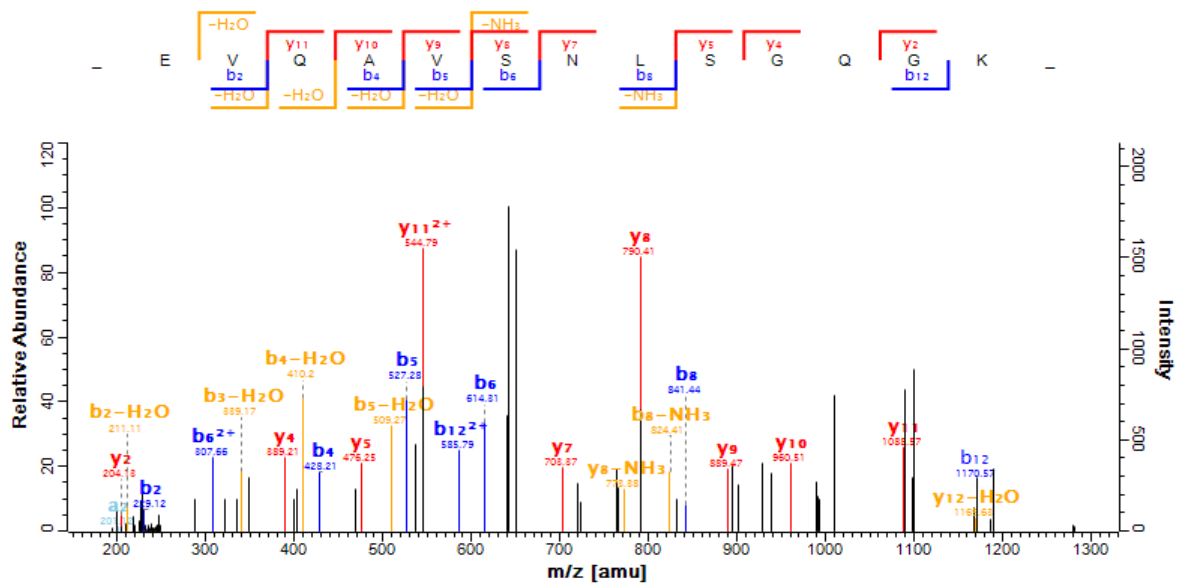
Number of Replicates (out of 8): 1

Best Match Score: 107.99

Best Match Posterior Error Probability: 0.0025157

Best Match Spectrum:

Scan number	14670	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	BANP



Protein Group ID: 1056

Protein Accession Numbers: Q06481; H7BXI4; Q06481-3; Q06481-2; Q06481-4; F5GZY0; F5H845; Q06481-5

Gene Names: APLP2

Peptide Sequence: MQNHGYENPTYK

Total Number of Spectra: 3

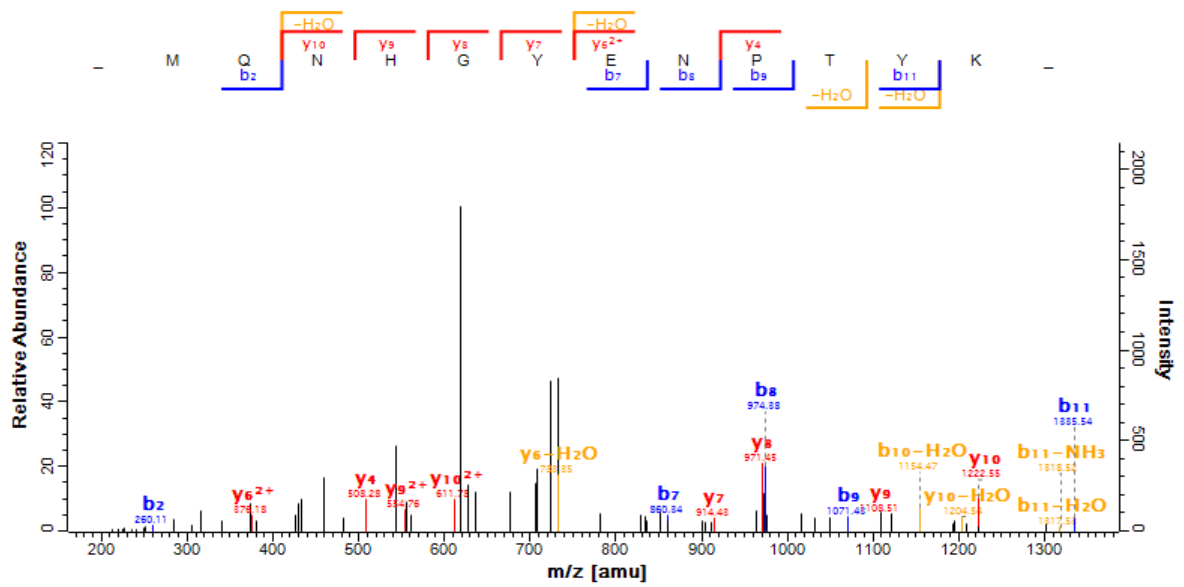
Number of Replicates (out of 8): 3

Best Match Score: 84.169

Best Match Posterior Error Probability: 0.0024149

Best Match Spectrum:

Scan number	9206	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS: CID	Genenames	APLP2



Protein Group ID: 1060

Protein Accession Numbers: O14576; O14576-2; G5E9K1; O14576-3; F5H050

Gene Names: DYNC111

Peptide Sequence: TPLSAAHTHPVYCVNVVGTQNAHNLITVSTDGK

Total Number of Spectra: 2

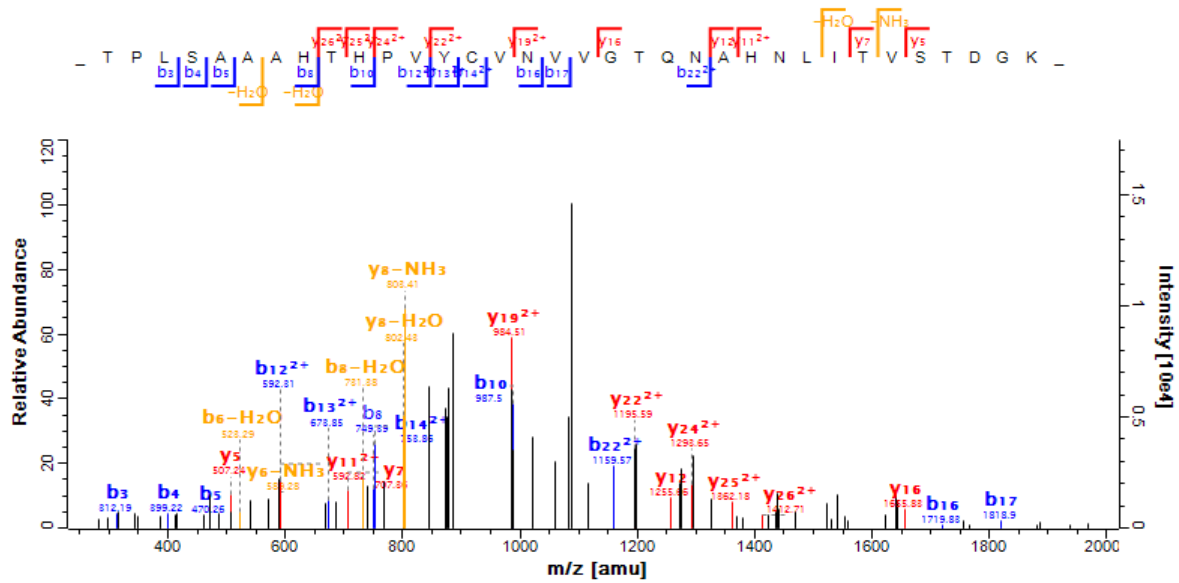
Number of Replicates (out of 8): 2

Best Match Score: 57.629

Best Match Posterior Error Probability: 0.00018633

Best Match Spectrum:

Scan number 53470 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** DYNC111



Protein Group ID: 1071

Protein Accession Numbers: J3KNJ9; Q2KHT4-6; Q2KHT4-7; G3XAB9; F5H0V9; F5H134

Gene Names: GSG1

Peptide Sequence: SDPSQLTQNVCLTQEMELSKAFSGQR

Total Number of Spectra: 2

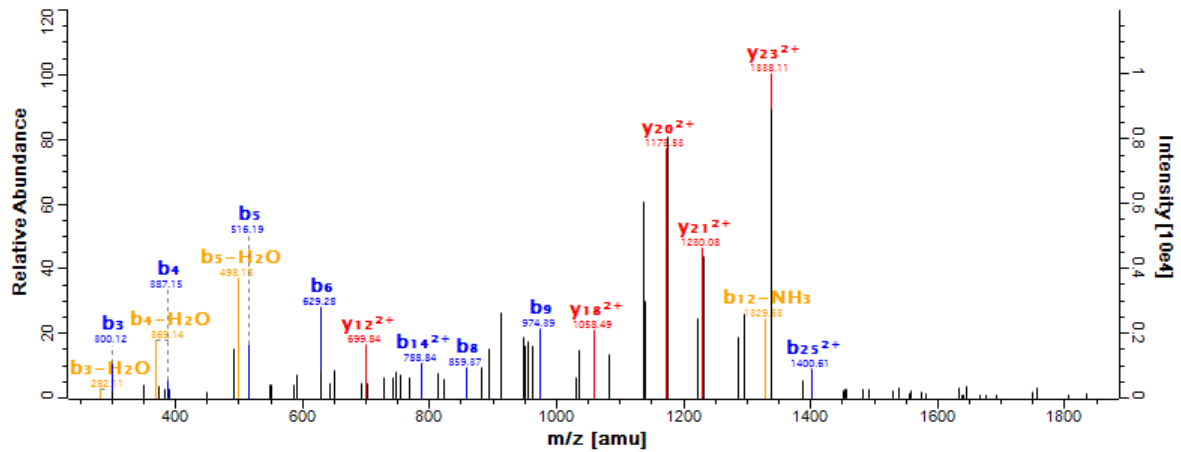
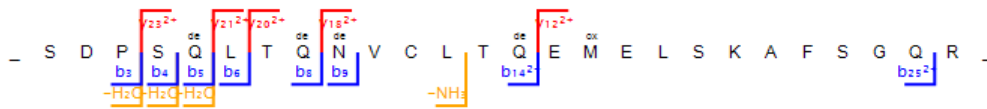
Number of Replicates (out of 8): 2

Best Match Score: 87.772

Best Match Posterior Error Probability: 0.00014004

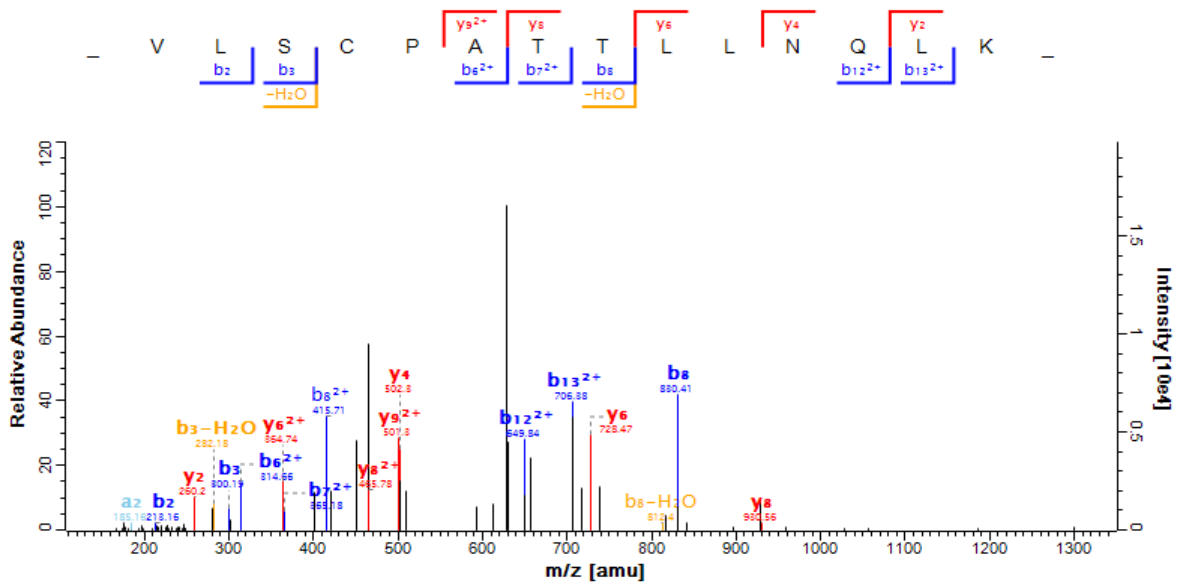
Best Match Spectrum:

Scan number	92065	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	GSG1



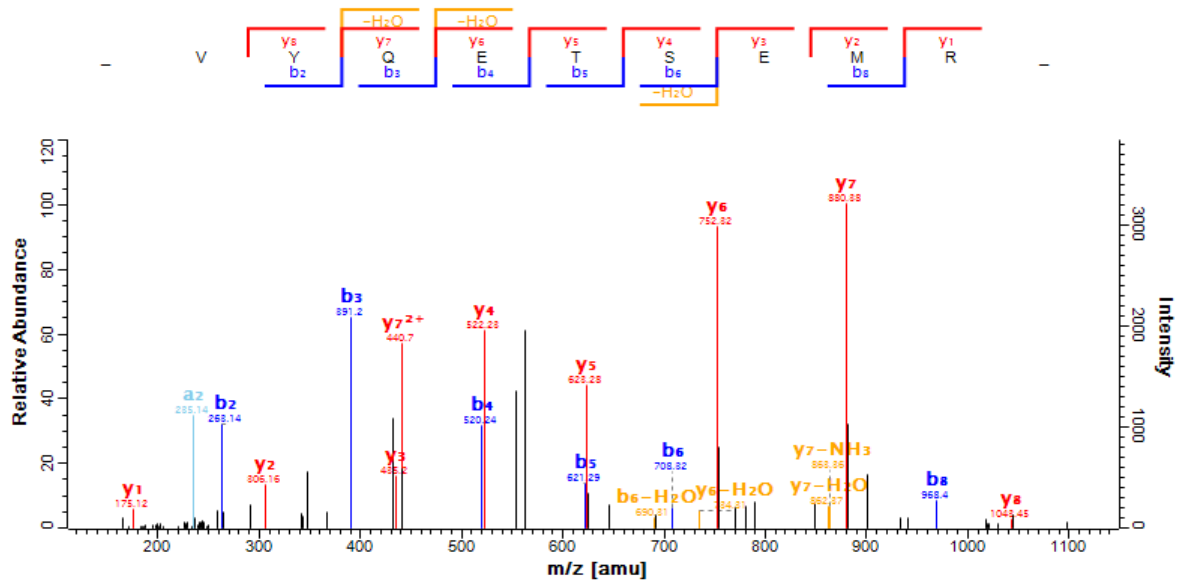
Protein Group ID: 1072
Protein Accession Numbers: F5H0X2; Q96MK2
Gene Names: FAM65C
Peptide Sequence: VLSCPATLLNQLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 103.91
Best Match Posterior Error Probability: 0.0024983
Best Match Spectrum:

Scan number 71385 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** FAM65C



Protein Group ID: 1073
Protein Accession Numbers: Q15773; F5H0Y3
Gene Names: MLF2
Peptide Sequence: VYQETSEMR
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 125.74
Best Match Posterior Error Probability: 0.00023104
Best Match Spectrum:

Scan number 8227 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** MLF2



Protein Group ID: 1077

Protein Accession Numbers: Q9H9H4; F5H4M0; F5H1F6

Gene Names: VPS37B

Peptide Sequence: IEEDTENMAEK

Total Number of Spectra: 6

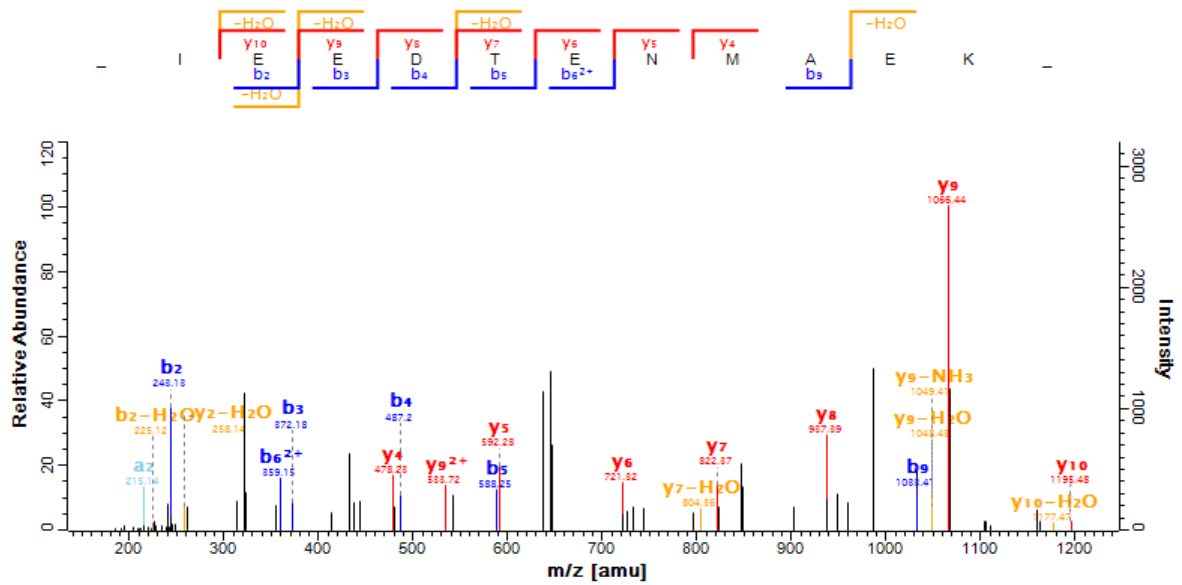
Number of Replicates (out of 8): 5

Best Match Score: 105.2

Best Match Posterior Error Probability: 0.00033027

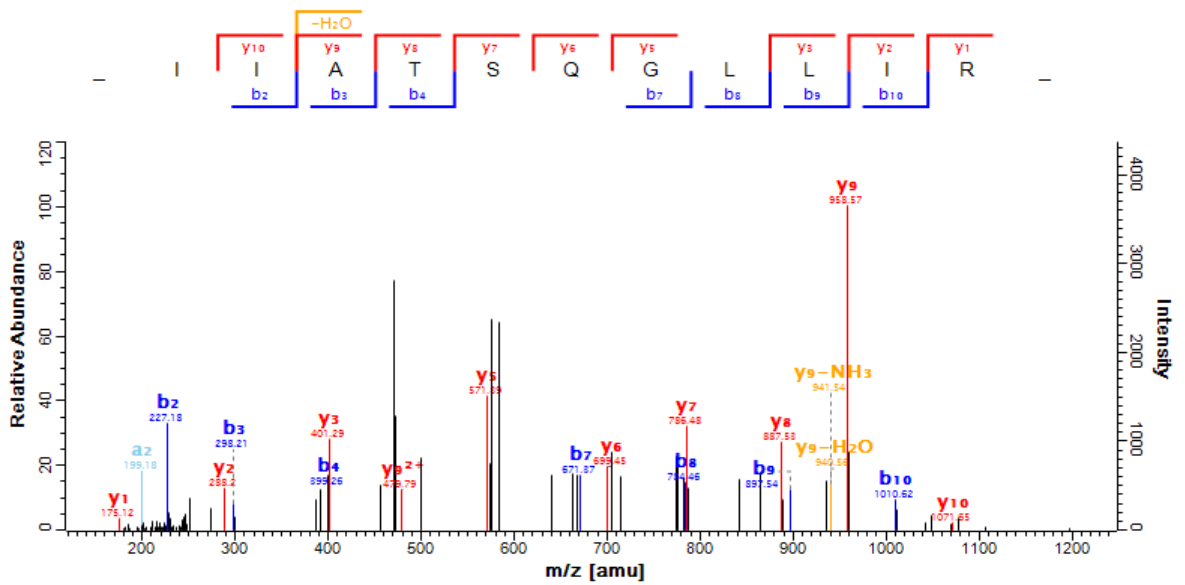
Best Match Spectrum:

Scan number	9516	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	VPS37B



Protein Group ID: 1086
Protein Accession Numbers: F5H1Z7; Q99985
Gene Names: SEMA3C
Peptide Sequence: IIATSQGLLIR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 111.52
Best Match Posterior Error Probability: 0.00013349
Best Match Spectrum:

Scan number 41637 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SEMA3C



Protein Group ID: 1093

Protein Accession Numbers: F5H301; Q9UDY2; Q9UDY2-3; F5H886

Gene Names: TJP2

Peptide Sequence: SNPSAVAGNETPGASTK

Total Number of Spectra: 1

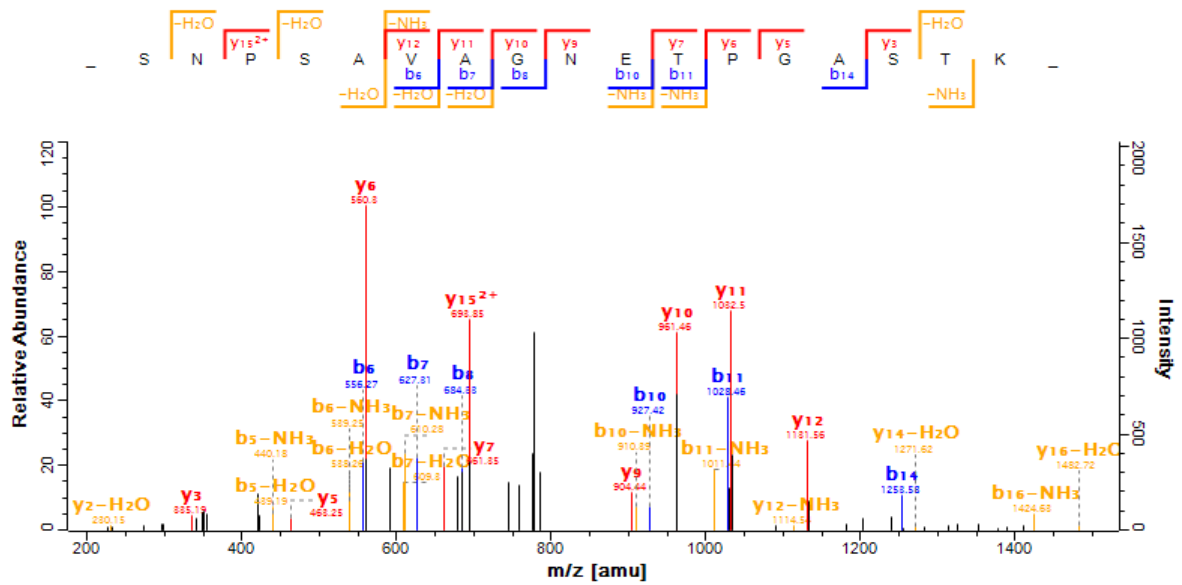
Number of Replicates (out of 8): 1

Best Match Score: 87.088

Best Match Posterior Error Probability: 0.00053445

Best Match Spectrum:

Scan number 9999 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TJP2



Protein Group ID: 1095

Protein Accession Numbers: P34059; F5H325; H3BP66

Gene Names: GALNS

Peptide Sequence: HGFDEWF⁺GSPNCHFGPYDNK

Total Number of Spectra: 4

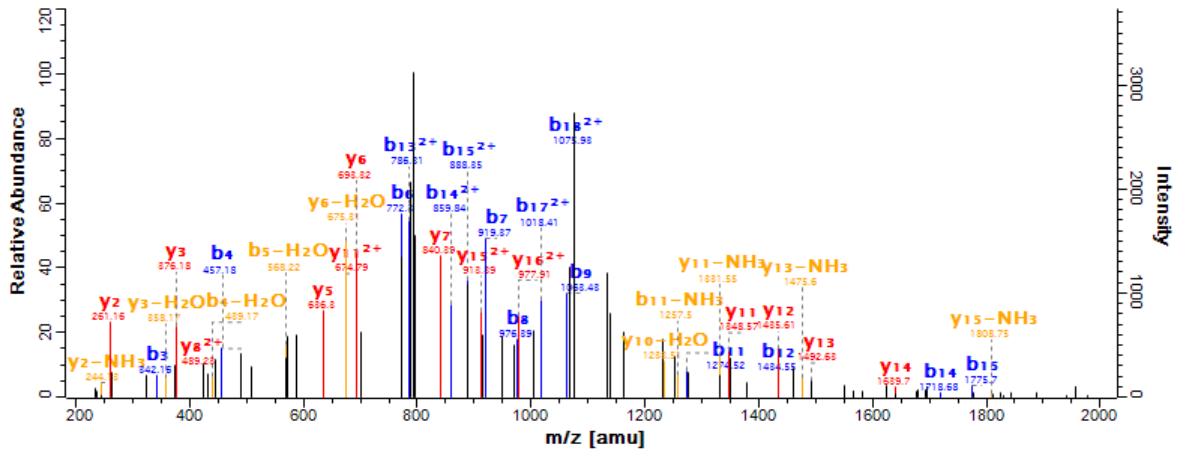
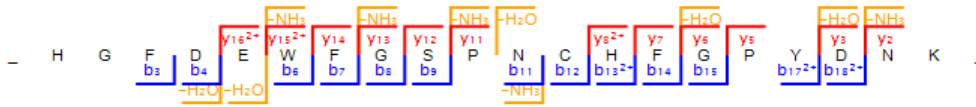
Number of Replicates (out of 8): 4

Best Match Score: 180.78

Best Match Posterior Error Probability: 8.97E-24

Best Match Spectrum:

Scan number 55075 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** GALNS



Protein Group ID: 1105

Protein Accession Numbers: Q8IVH8; Q8IVH8-2; Q8IVH8-3; F5H5A3

Gene Names: MAP4K3

Peptide Sequence: GHVAHLEDDEGDDDESK

Total Number of Spectra: 3

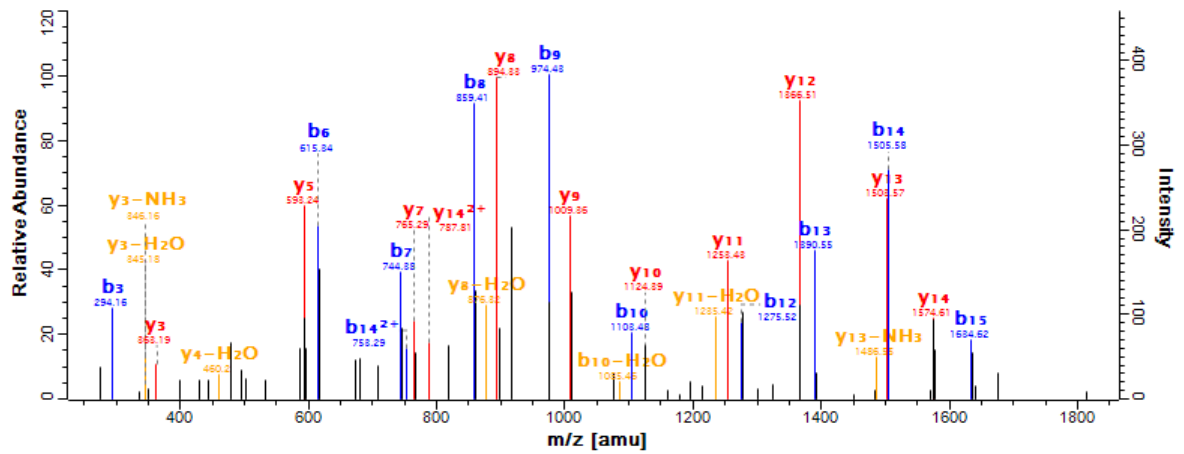
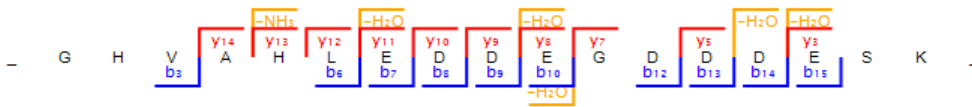
Number of Replicates (out of 8): 2

Best Match Score: 150.39

Best Match Posterior Error Probability: 1.84E-06

Best Match Spectrum:

Scan number 4979 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MAP4K3



Protein Group ID: 1110

Protein Accession Numbers: Q5VT25-6; Q5VT25-2; Q5VT25; Q5VT25-5; F5H5N0;
Q5VT25-4; Q5VT25-3; H0Y5V1; H0Y7V8; H0Y6V3; H0Y6R0

Gene Names: CDC42BPA

Peptide Sequence: VTASQLSASNNK

Total Number of Spectra: 1

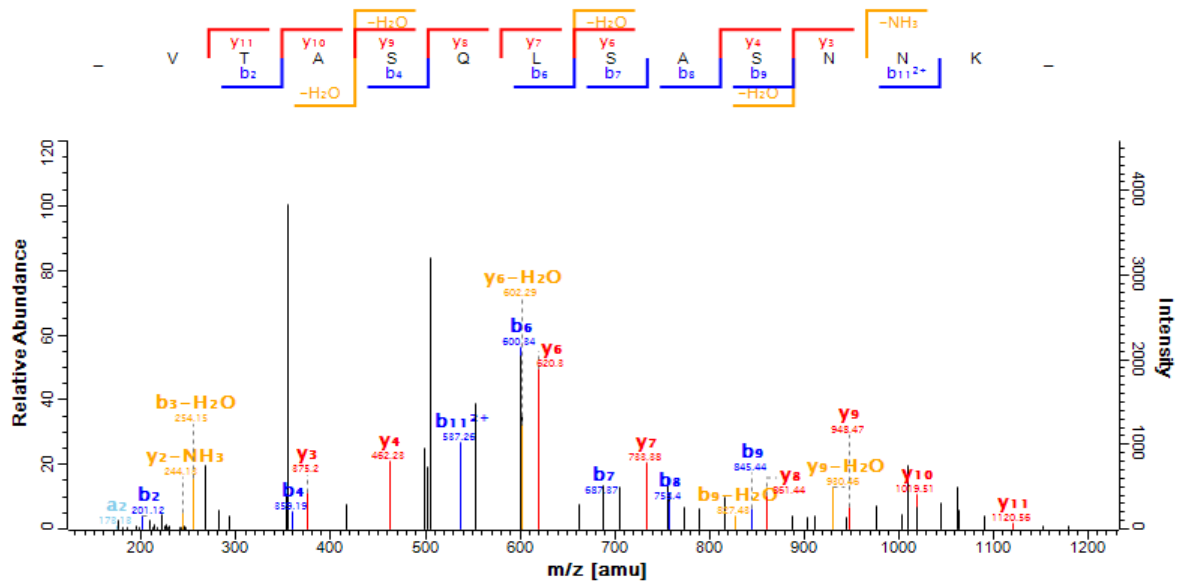
Number of Replicates (out of 8): 1

Best Match Score: 90.861

Best Match Posterior Error Probability: 0.0013453

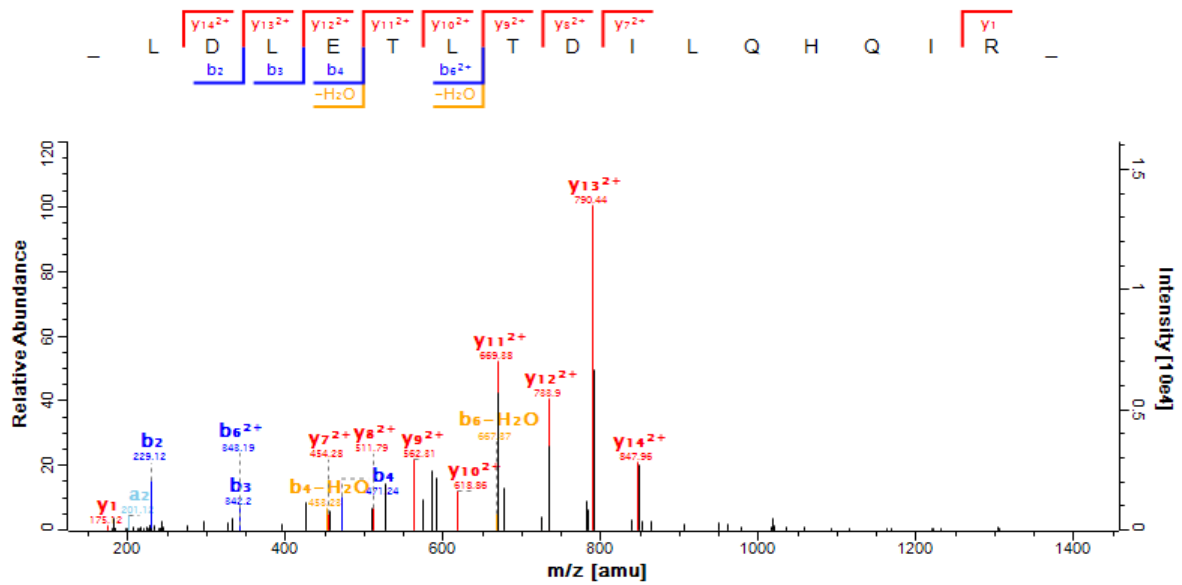
Best Match Spectrum:

Scan number	7403	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	CDC42BPA



Protein Group ID: 1112
Protein Accession Numbers: F5H5R8; P18440
Gene Names: NAT1
Peptide Sequence: LDLETLTDILQHQR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 87.001
Best Match Posterior Error Probability: 0.0010655
Best Match Spectrum:

Scan number	86793	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	NAT1



Protein Group ID: 1114

Protein Accession Numbers: F5H607; Q9NNX1; Q9NNX1-2; Q9NNX1-3

Gene Names: TUFT1

Peptide Sequence: SEVQYIQEAR

Total Number of Spectra: 1

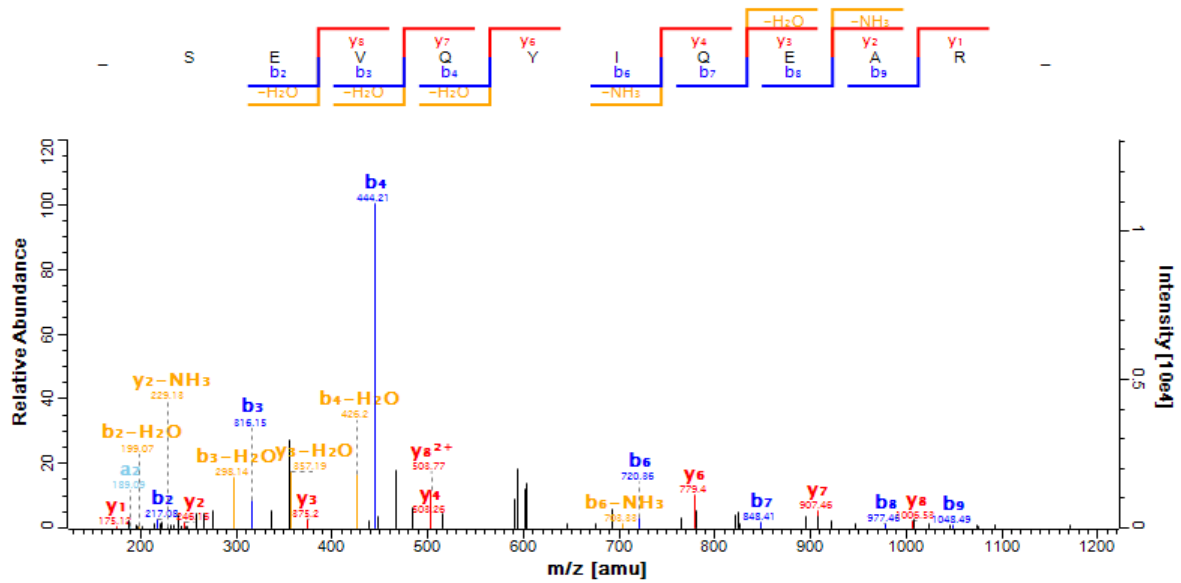
Number of Replicates (out of 8): 1

Best Match Score: 95.477

Best Match Posterior Error Probability: 0.0012728

Best Match Spectrum:

Scan number 20773 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TUFT1



Protein Group ID: 1124

Protein Accession Numbers: F5H759; Q9UHW5-2; Q9UHW5; H0YHZ5

Gene Names: GPN3

Peptide Sequence: FLDPDPMYSLLEDSTSDLR

Total Number of Spectra: 7

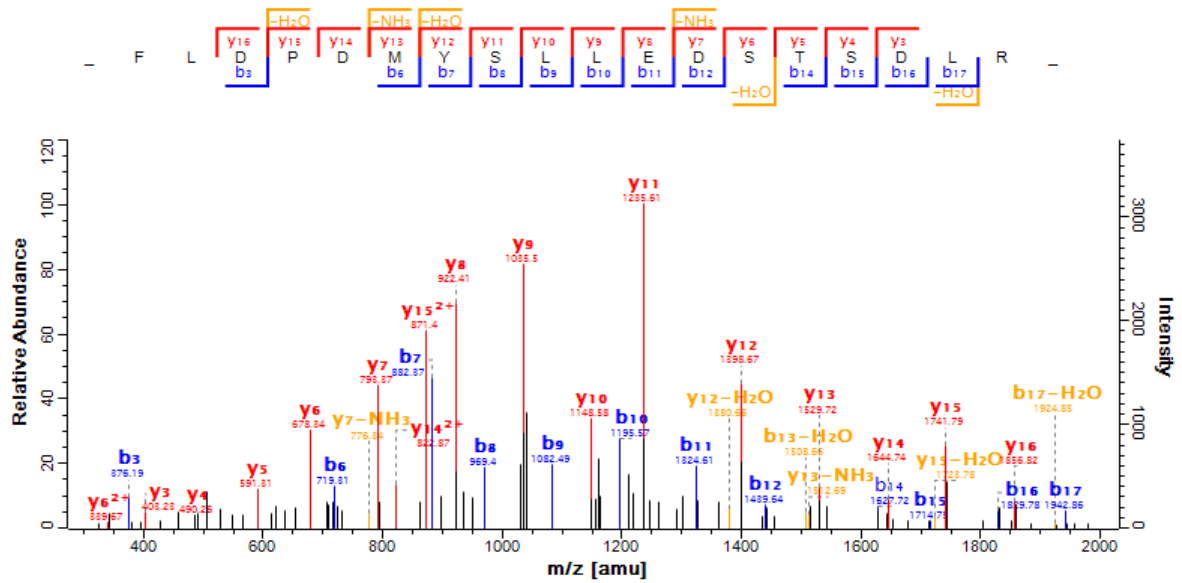
Number of Replicates (out of 8): 7

Best Match Score: 179.46

Best Match Posterior Error Probability: 7.09E-16

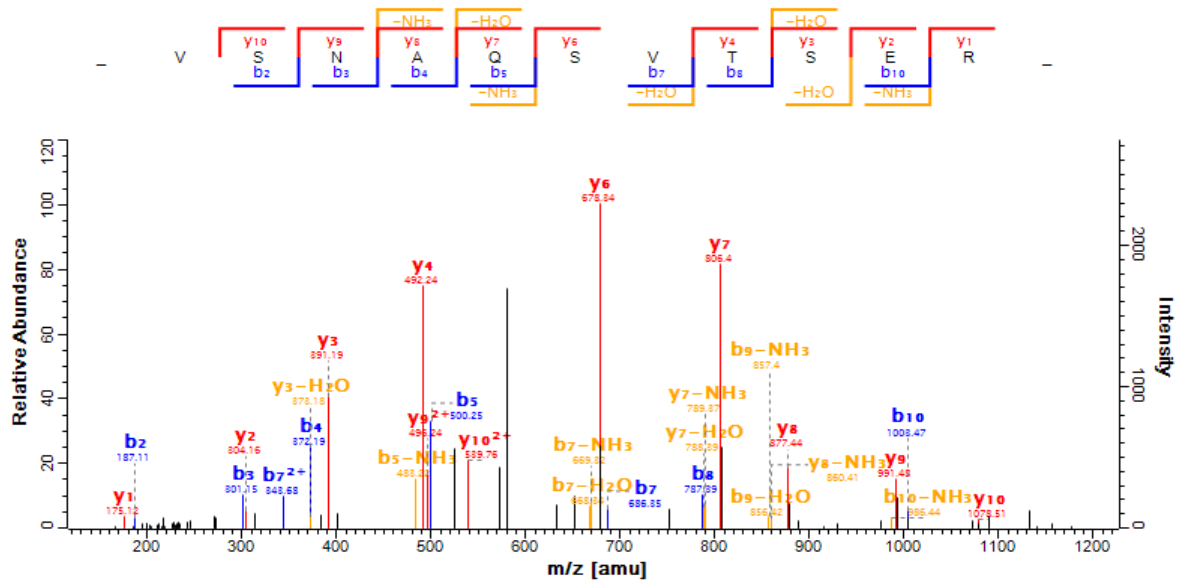
Best Match Spectrum:

Scan number 82974 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** GPN3



Protein Group ID: 1129
Protein Accession Numbers: O60669; F5H843
Gene Names: SLC16A7
Peptide Sequence: VSNAQSVTSER
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 168.98
Best Match Posterior Error Probability: 1.01E-06
Best Match Spectrum:

Scan number 4834 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** SLC16A7



Protein Group ID: 1133

Protein Accession Numbers: Q9Y2V7; Q9Y2V7-2; F5H8M2; H0YGX8

Gene Names: COG6

Peptide Sequence: SLAINEEFVSIFK

Total Number of Spectra: 1

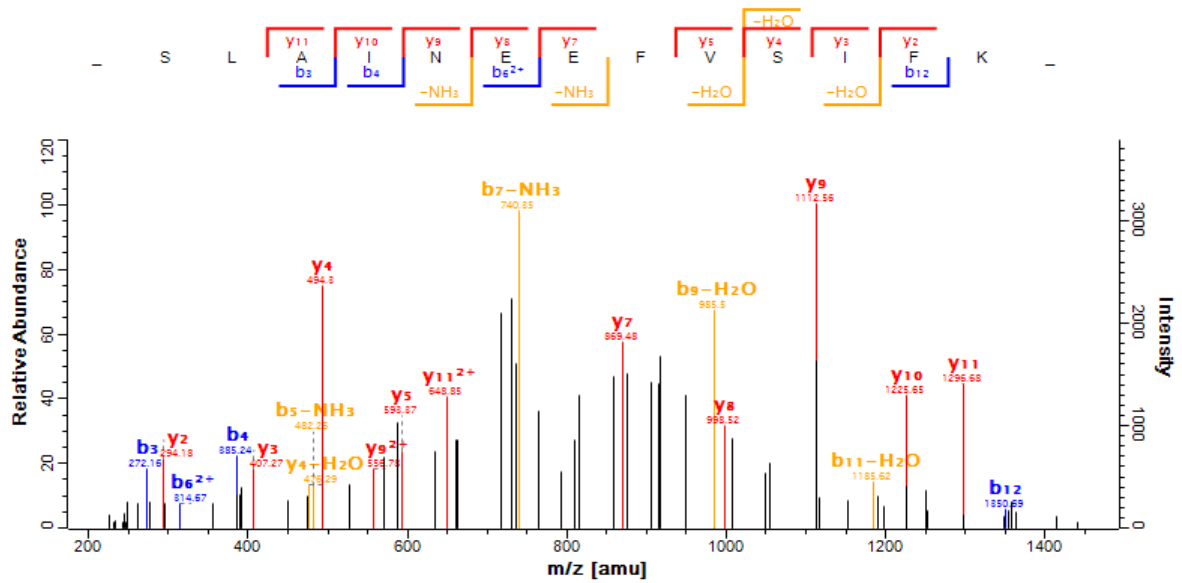
Number of Replicates (out of 8): 1

Best Match Score: 99.531

Best Match Posterior Error Probability: 0.00051937

Best Match Spectrum:

Scan number 79220 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** COG6



Protein Group ID: 1141

Protein Accession Numbers: P78537; F8VP73; P78537-2; F8W036; G8JLQ3; F8W606; F8W099

Gene Names: BLOC1S1

Peptide Sequence: TLQVQAQFAK

Total Number of Spectra: 2

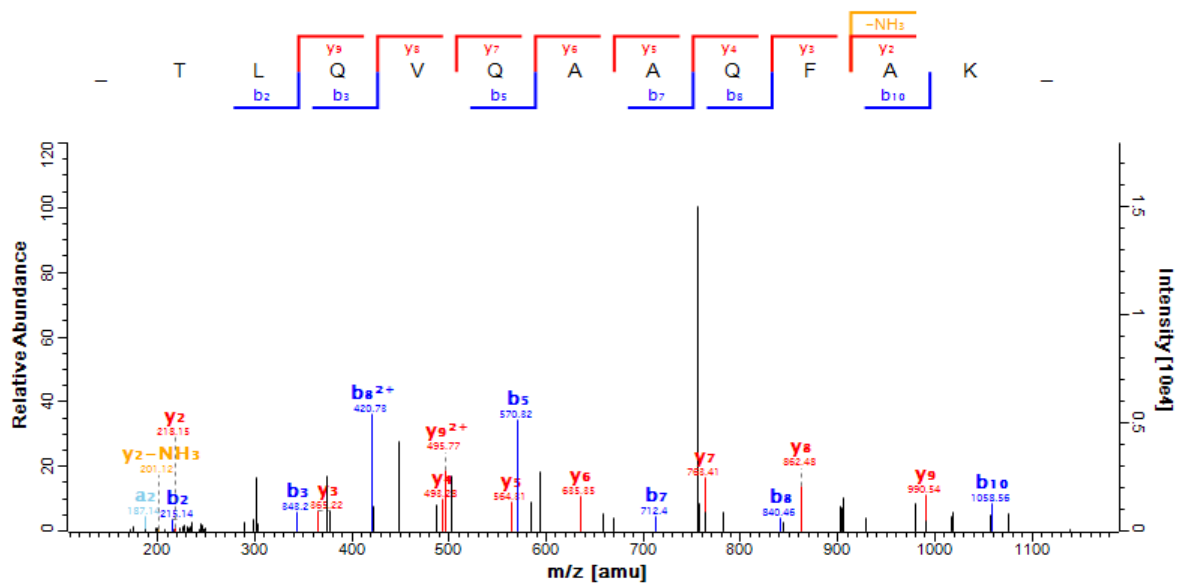
Number of Replicates (out of 8): 2

Best Match Score: 89.805

Best Match Posterior Error Probability: 0.001498

Best Match Spectrum:

Scan number	30825	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	BLOC1S1



Protein Group ID: 1148

Protein Accession Numbers: F8VQY2; Q96RL1; Q96RL1-3; Q96RL1-2; Q96RL1-4

Gene Names: UIMC1

Peptide Sequence: SDSGTAAQTSLDK

Total Number of Spectra: 3

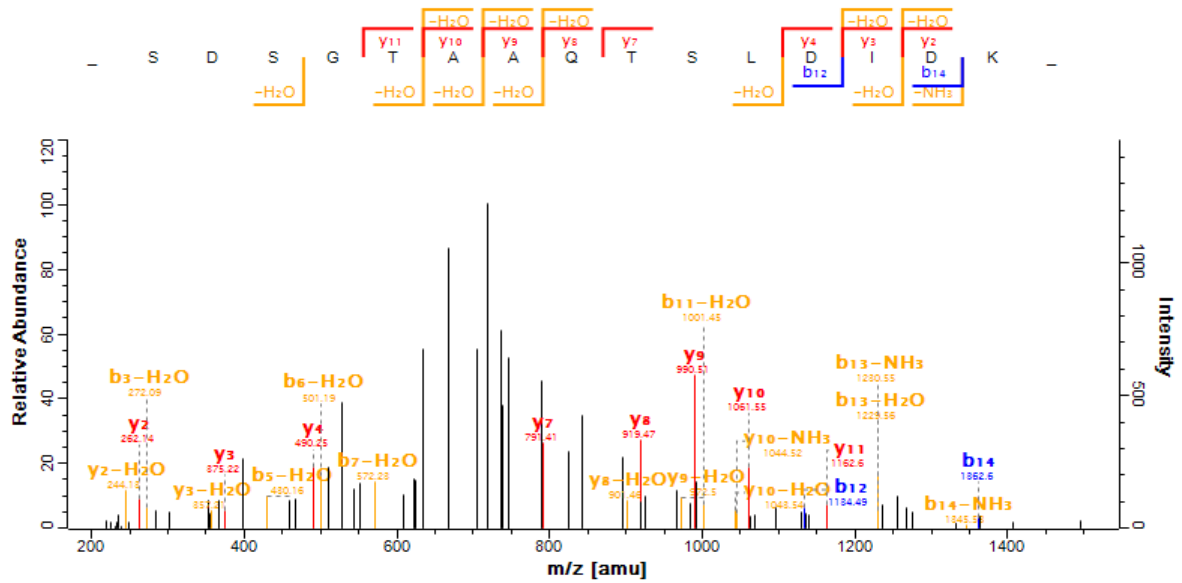
Number of Replicates (out of 8): 3

Best Match Score: 77.42

Best Match Posterior Error Probability: 0.0031607

Best Match Spectrum:

Scan number 20649 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** UIMC1



Protein Group ID: 1149

Protein Accession Numbers: J3KPX5; P51530; P51530-4; P51530-3; F8VR31; P51530-2

Gene Names: DNA2

Peptide Sequence: TVLSTGMDNR

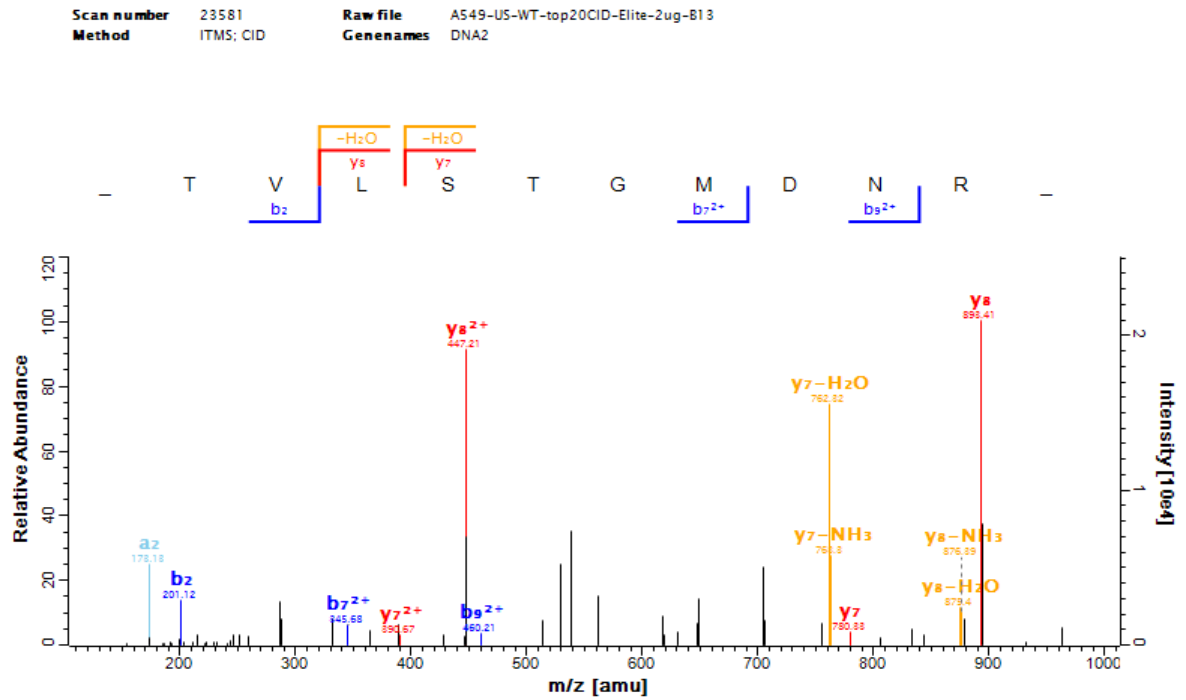
Total Number of Spectra: 1

Number of Replicates (out of 8): 1

Best Match Score: 89.355

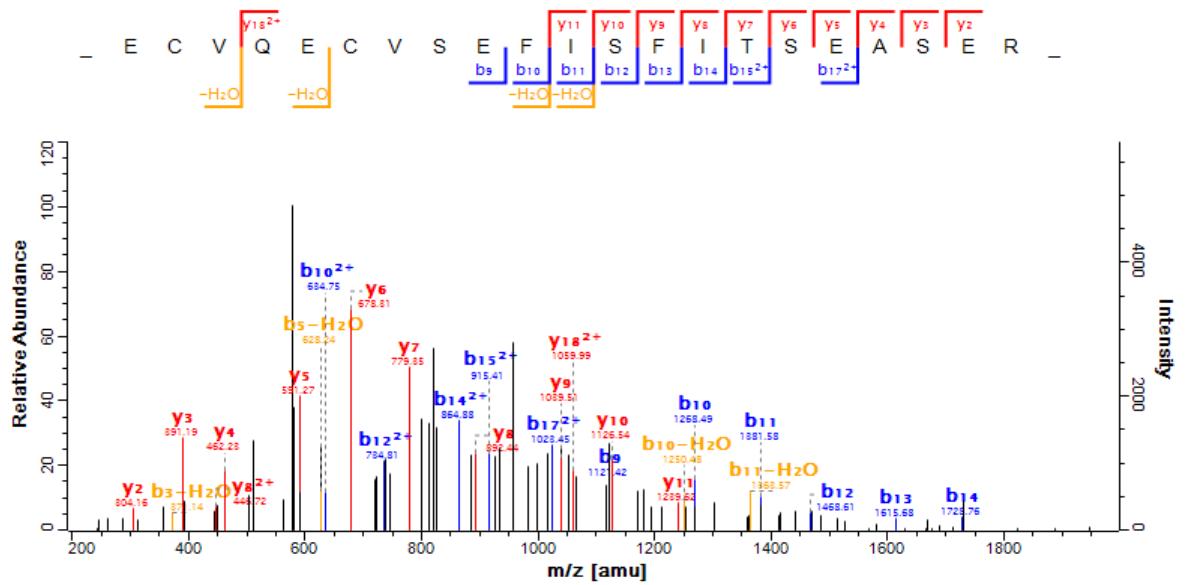
Best Match Posterior Error Probability: 0.0020617

Best Match Spectrum:



Protein Group ID: 1150
Protein Accession Numbers: P25208; F8VSL3
Gene Names: NFYB
Peptide Sequence: ECVQECVSEFISFITSEASER
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 100.28
Best Match Posterior Error Probability: 5.91E-05
Best Match Spectrum:

Scan number 92902 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** NFYB



Protein Group ID: 1152

Protein Accession Numbers: P11802; F8VWX7; F8VTV8; F8VYH9; F8W1L8; Q96BE9; F8VYY1

Gene Names: CDK4

Peptide Sequence: VPNGGGGGGLPISTVR

Total Number of Spectra: 1

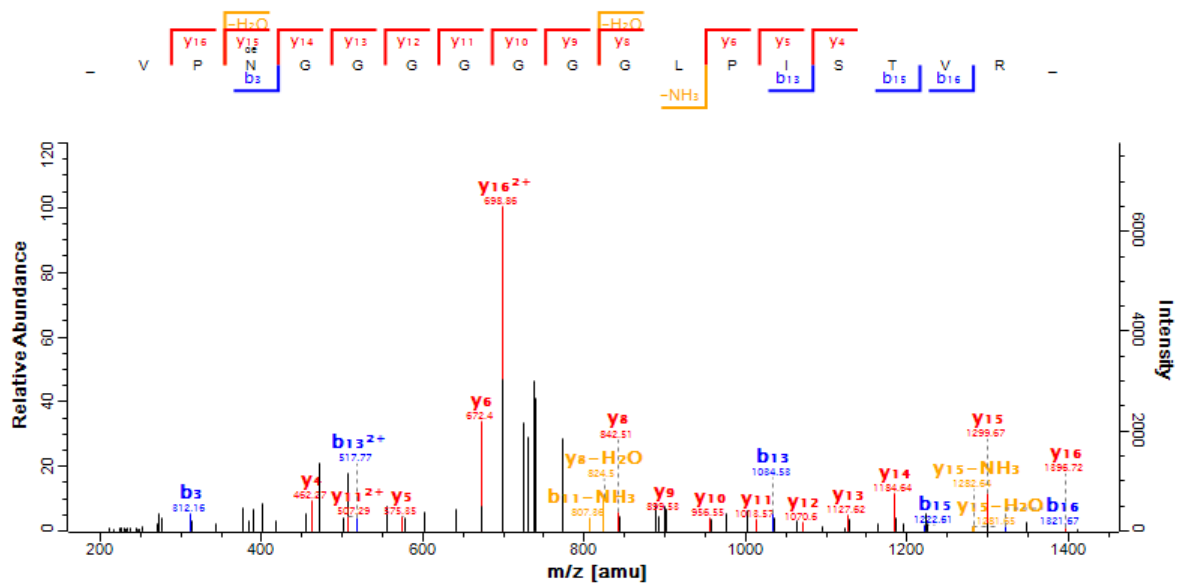
Number of Replicates (out of 8): 1

Best Match Score: 91.518

Best Match Posterior Error Probability: 0.0019387

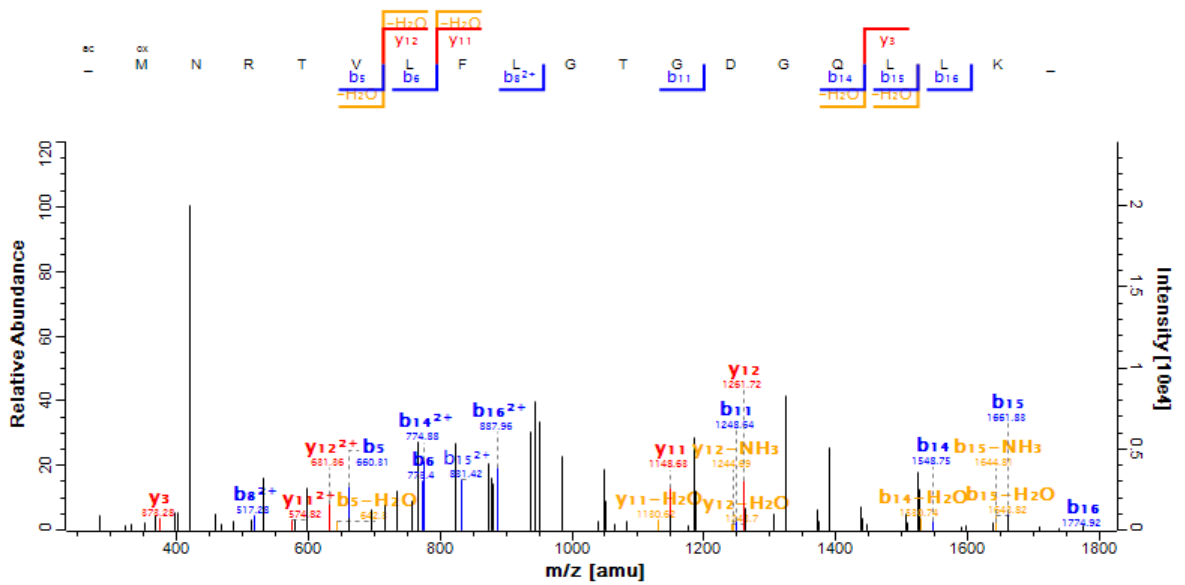
Best Match Spectrum:

Scan number 34356 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CDK4



Protein Group ID: 1158
Protein Accession Numbers: F8VUW4
Gene Names: PLXNC1
Peptide Sequence: MNRTVLFLGTGDGQLLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 103.88
Best Match Posterior Error Probability: 0.0034095
Best Match Spectrum:

Scan number 49042 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PLXNC1



Protein Group ID: 1159

Protein Accession Numbers: F8VX10; Q9H9L4; F8VXI8; H0YIQ8; Q9H9L4-4; F8VUX5; H0YID1

Gene Names: KANSL2

Peptide Sequence: TELGSQTPESSR

Total Number of Spectra: 3

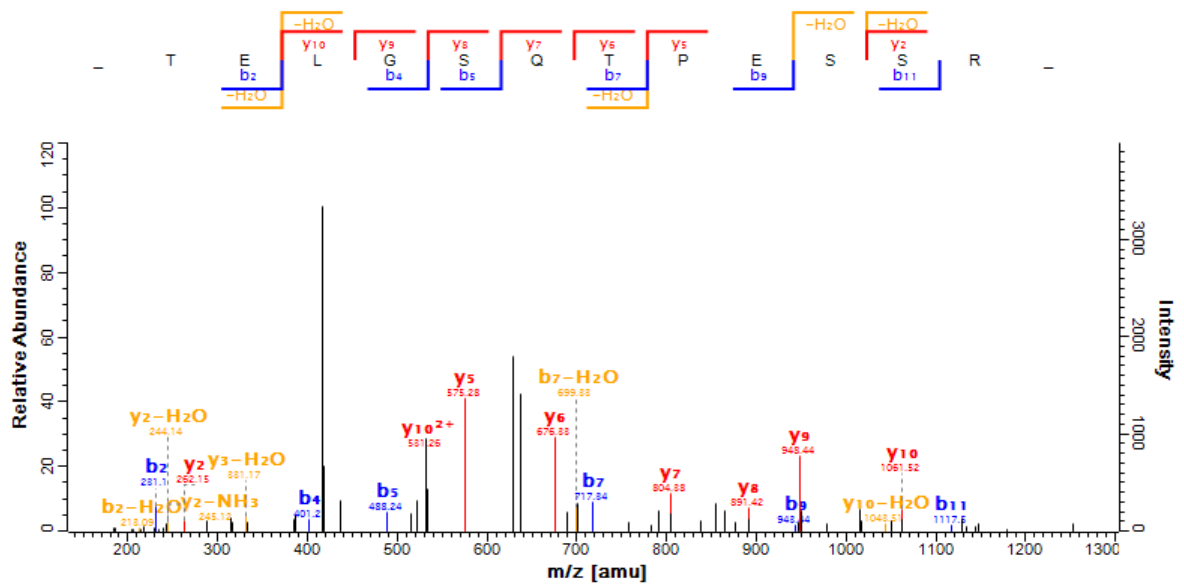
Number of Replicates (out of 8): 3

Best Match Score: 84.892

Best Match Posterior Error Probability: 0.0022498

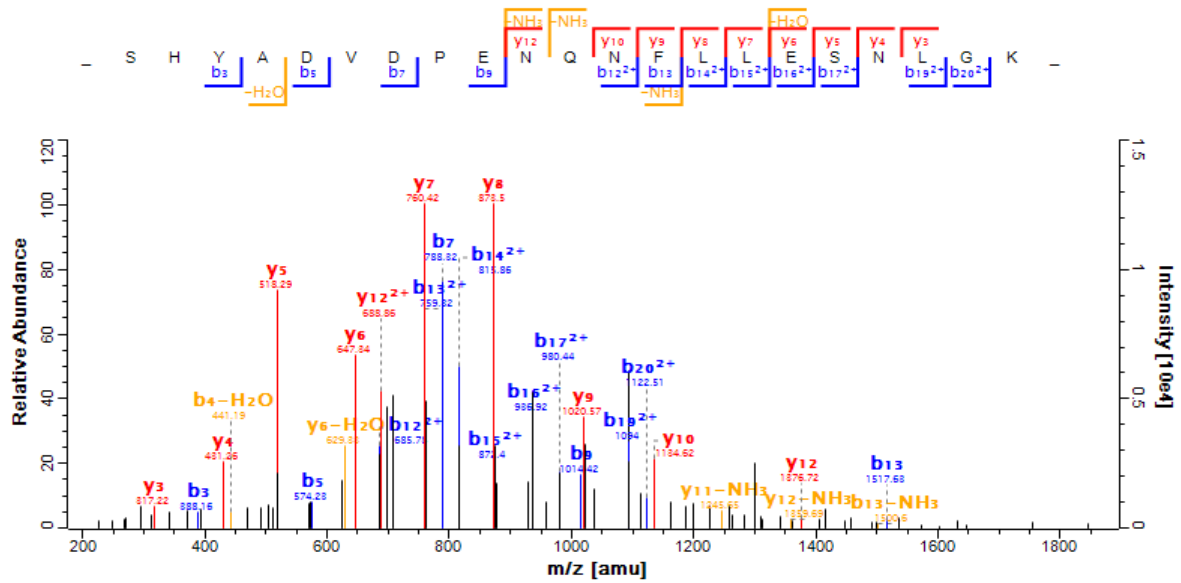
Best Match Spectrum:

Scan number 7647 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** KANSL2



Protein Group ID: 1160
Protein Accession Numbers: Q96QD8; F8VUY8
Gene Names: SLC38A2
Peptide Sequence: SHYADVDPENQNFLLLESNLGK
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 107.15
Best Match Posterior Error Probability: 2.15E-05
Best Match Spectrum:

Scan number 52264 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** SLC38A2



Protein Group ID: 1165

Protein Accession Numbers: F8VVS7; P55211; P55211-4; P55211-2; Q5JRU2

Gene Names: CASP9

Peptide Sequence: DHGFEVASTSPEDESPESNPEPDAATPFQEGLR

Total Number of Spectra: 1

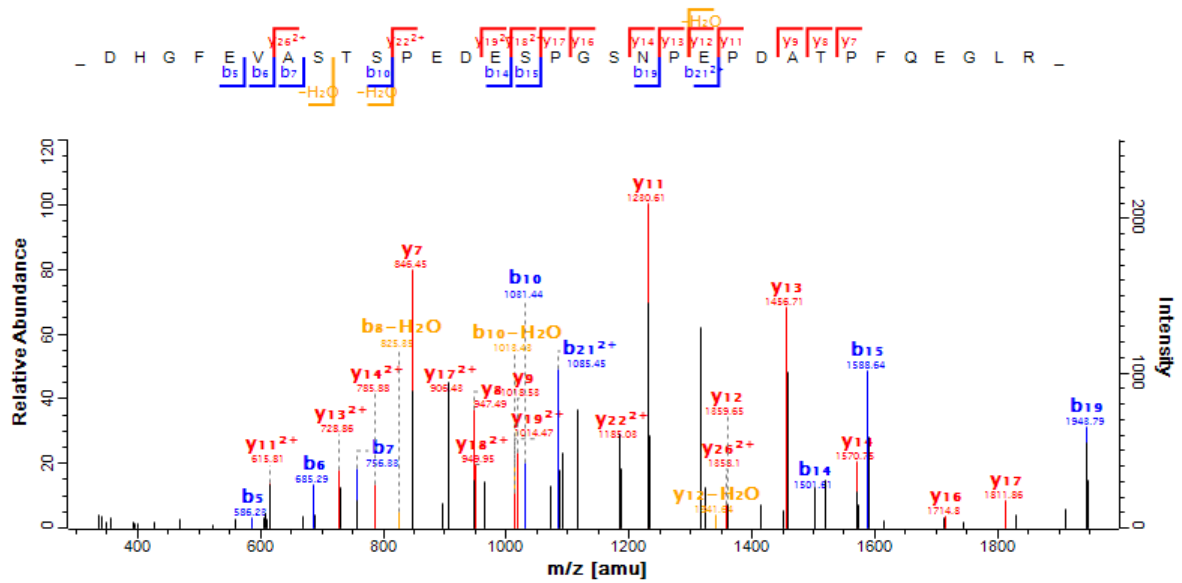
Number of Replicates (out of 8): 1

Best Match Score: 75.717

Best Match Posterior Error Probability: 9.07E-08

Best Match Spectrum:

Scan number 50822 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CASP9



Protein Group ID: 1171

Protein Accession Numbers: Q8TBF4; G3V1V1; F8VXY6

Gene Names: ZCRB1

Peptide Sequence: GVAFILFDK

Total Number of Spectra: 2

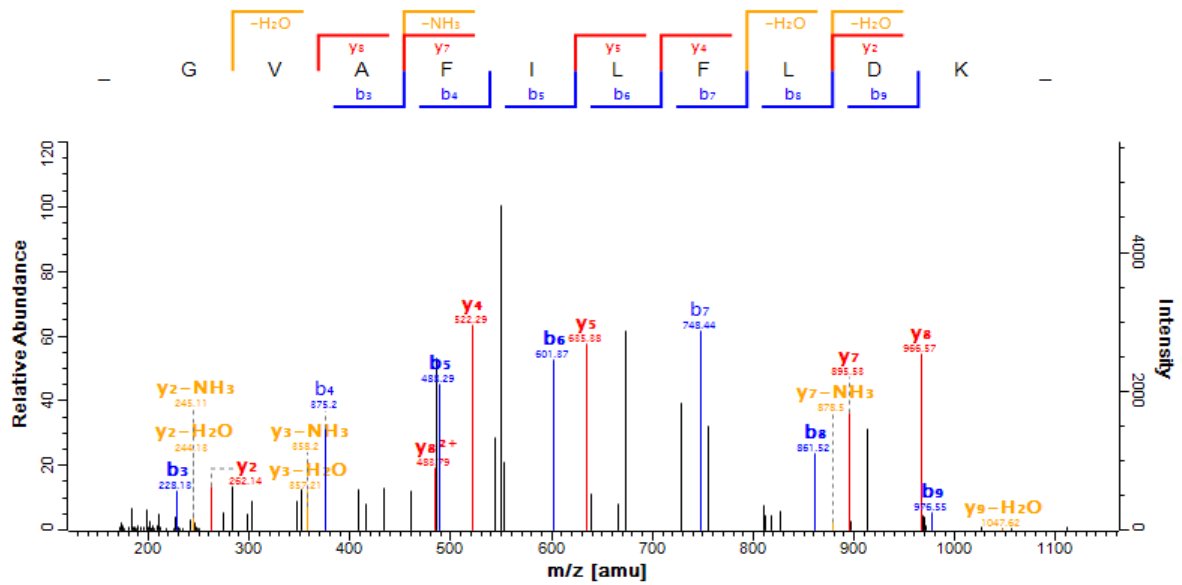
Number of Replicates (out of 8): 1

Best Match Score: 103.26

Best Match Posterior Error Probability: 0.0023218

Best Match Spectrum:

Scan number 77944 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ZCRB1



Protein Group ID: 1172

Protein Accession Numbers: Q6ZV73; Q6ZV73-2; F8VY01

Gene Names: FGD6

Peptide Sequence: SSQLGDTTTGHLSSGEQK

Total Number of Spectra: 1

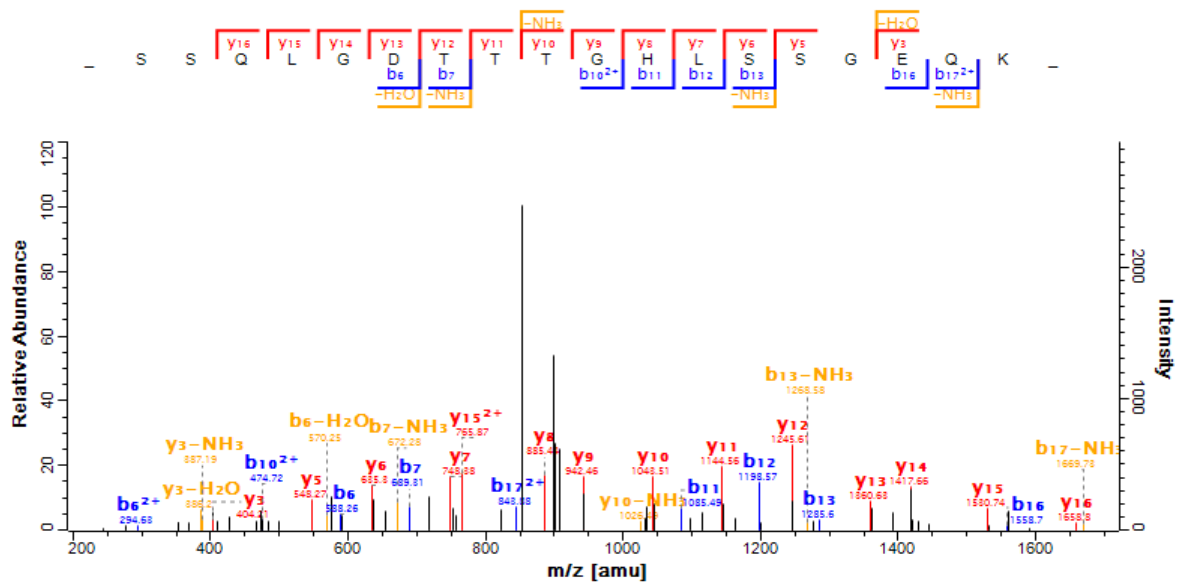
Number of Replicates (out of 8): 1

Best Match Score: 126.8

Best Match Posterior Error Probability: 4.61E-05

Best Match Spectrum:

Scan number 12941 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** FGD6



Protein Group ID: 1174

Protein Accession Numbers: F8VYC4; P0DJJ1; J3QTV4; P0DJJ0; E7ES93

Gene Names: RGPD1;RGPD2

Peptide Sequence: SNDSETSSVAQSGSESK

Total Number of Spectra: 3

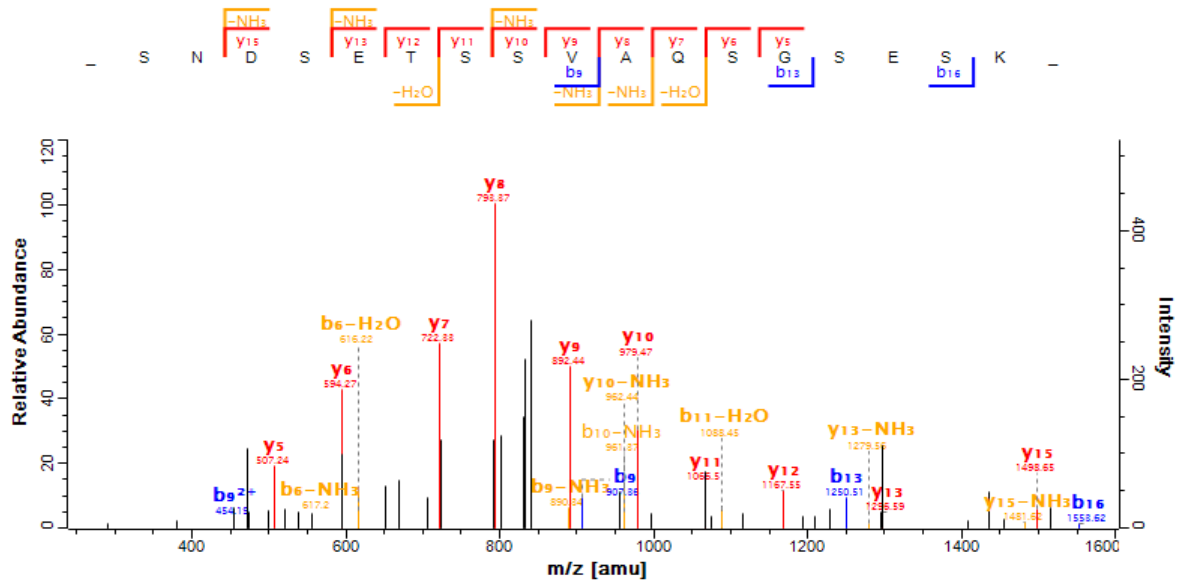
Number of Replicates (out of 8): 3

Best Match Score: 79.393

Best Match Posterior Error Probability: 0.0016748

Best Match Spectrum:

Scan number 2982 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** RGPD1;RGPD2



Protein Group ID: 1181

Protein Accession Numbers: Q8WYA0; H0YHE2; Q8WYA0-3; F8W1J4

Gene Names: IFT81

Peptide Sequence: MLSLLGILK

Total Number of Spectra: 5

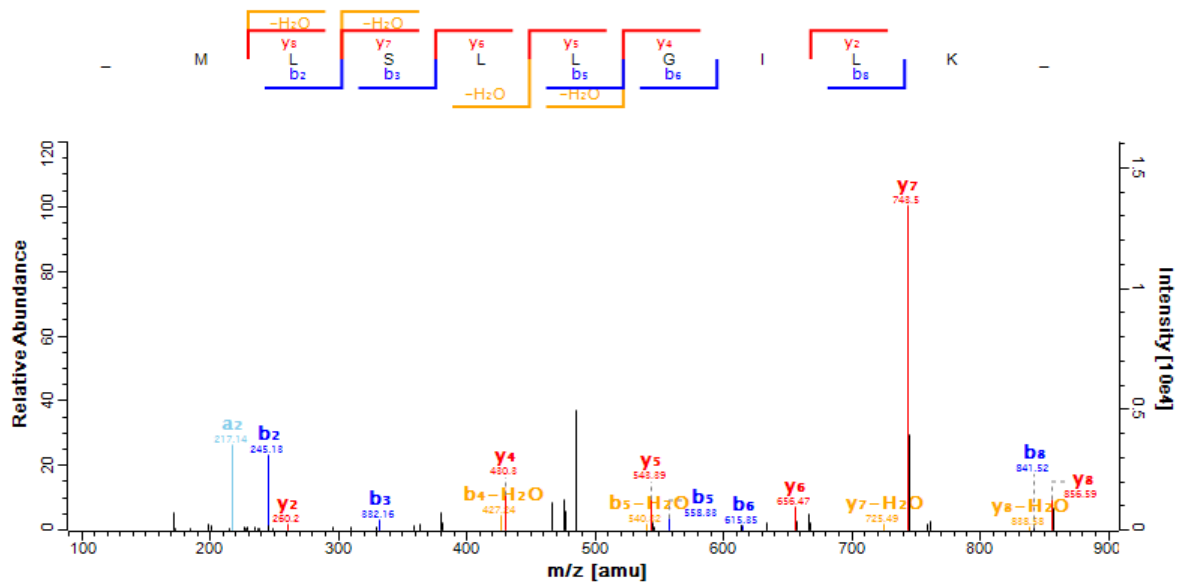
Number of Replicates (out of 8): 5

Best Match Score: 120.15

Best Match Posterior Error Probability: 0.00041533

Best Match Spectrum:

Scan number	78060	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	IFT81



Protein Group ID: 1183

Protein Accession Numbers: Q9UHY8-2; Q9UHY8; G3V0F5; F8W6C0; F8WB37

Gene Names: FEZ2

Peptide Sequence: TLHLLTLNLSEK

Total Number of Spectra: 1

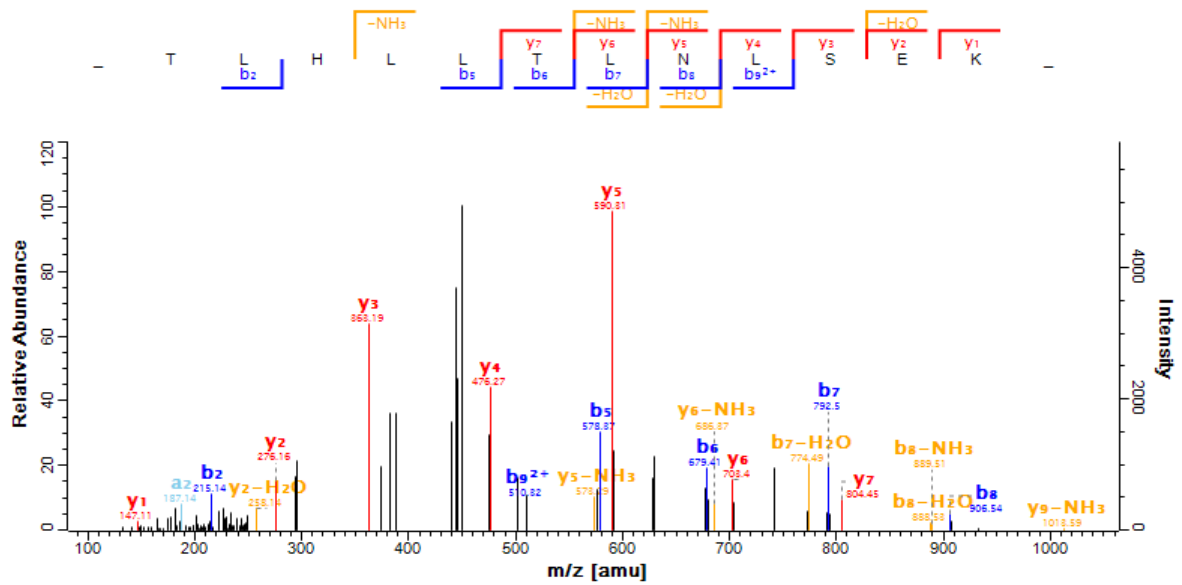
Number of Replicates (out of 8): 1

Best Match Score: 109.72

Best Match Posterior Error Probability: 0.00027452

Best Match Spectrum:

Scan number 55571 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** FEZ2



Protein Group ID: 1184

Protein Accession Numbers: Q9H2D6; Q9H2D6-2; Q9H2D6-3; F8W6V6; Q9H2D6-5

Gene Names: TRIOBP

Peptide Sequence: ELQVLSEQYSQK

Total Number of Spectra: 5

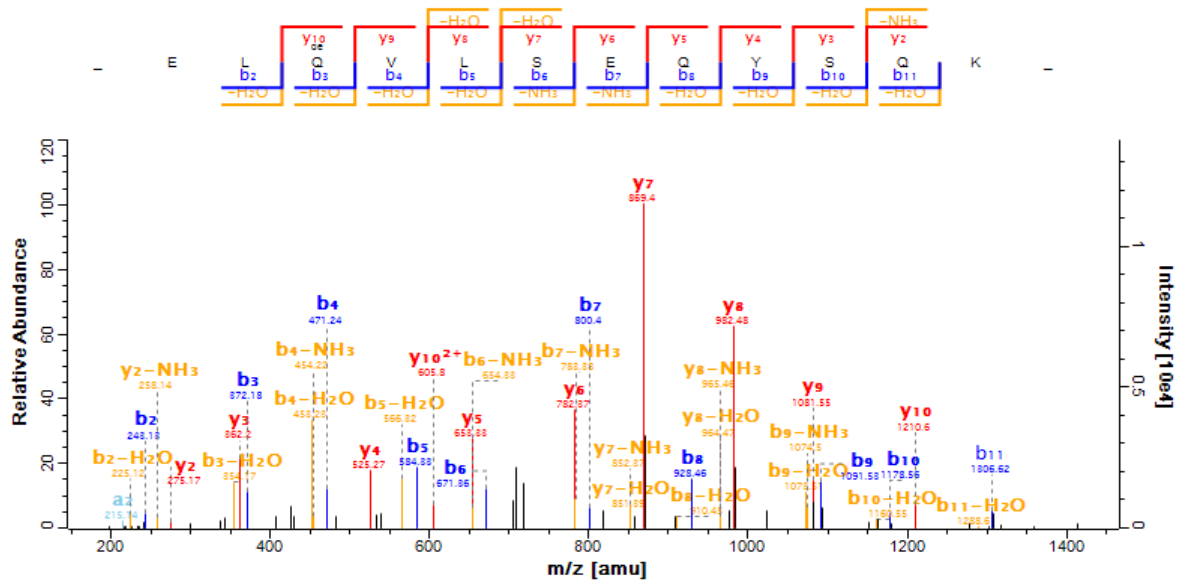
Number of Replicates (out of 8): 5

Best Match Score: 273.27

Best Match Posterior Error Probability: 9.76E-104

Best Match Spectrum:

Scan number 35203 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TRIOBP



Protein Group ID: 1187

Protein Accession Numbers: O75935; O75935-2; Q8NB28; F8W786; O75935-3

Gene Names: DCTN3

Peptide Sequence: YLDPEYIDR

Total Number of Spectra: 2

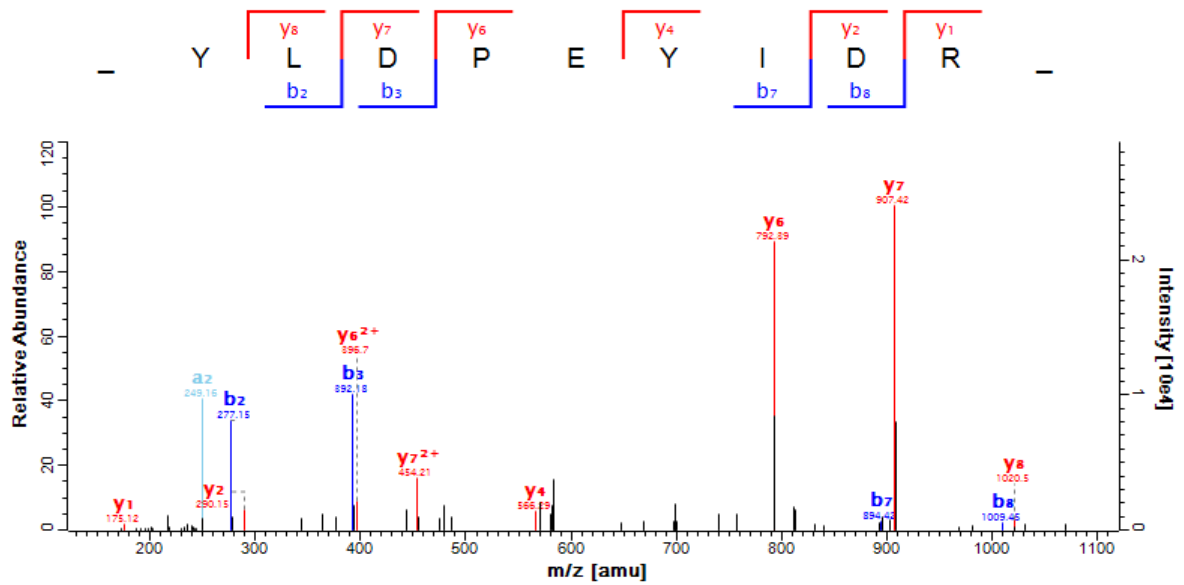
Number of Replicates (out of 8): 2

Best Match Score: 87.913

Best Match Posterior Error Probability: 0.0040334

Best Match Spectrum:

Scan number	33127	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	DCTN3



Protein Group ID: 1189

Protein Accession Numbers: Q6P2H3; Q6P2H3-2; F8W7K4; H7BZW2; Q6P2H3-3

Gene Names: CEP85

Peptide Sequence: ELSVQNQDLIEK

Total Number of Spectra: 1

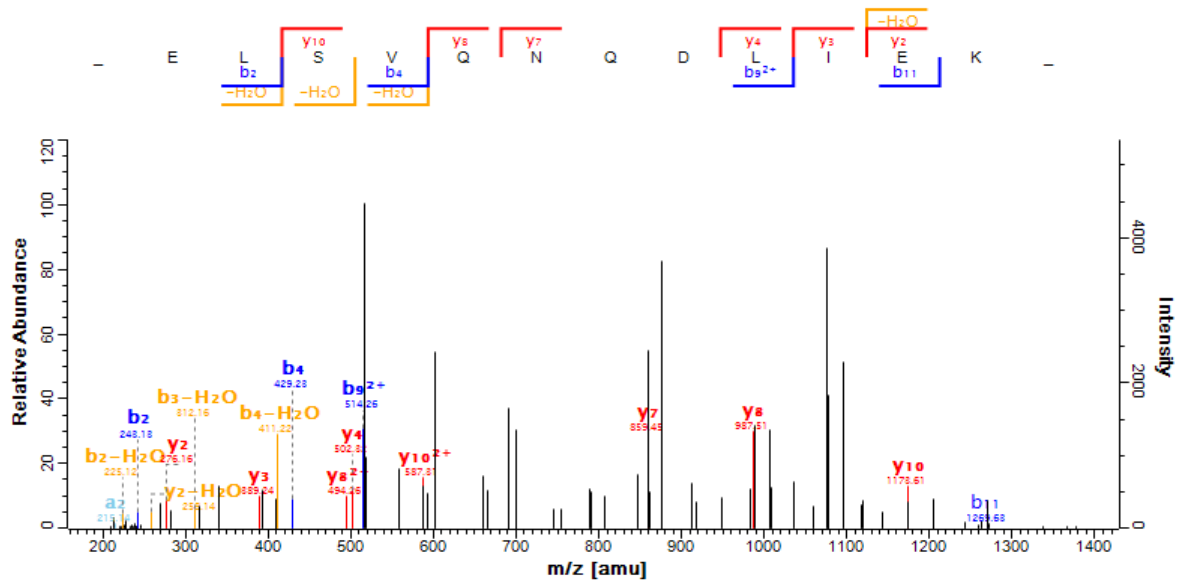
Number of Replicates (out of 8): 1

Best Match Score: 78.903

Best Match Posterior Error Probability: 0.0036177

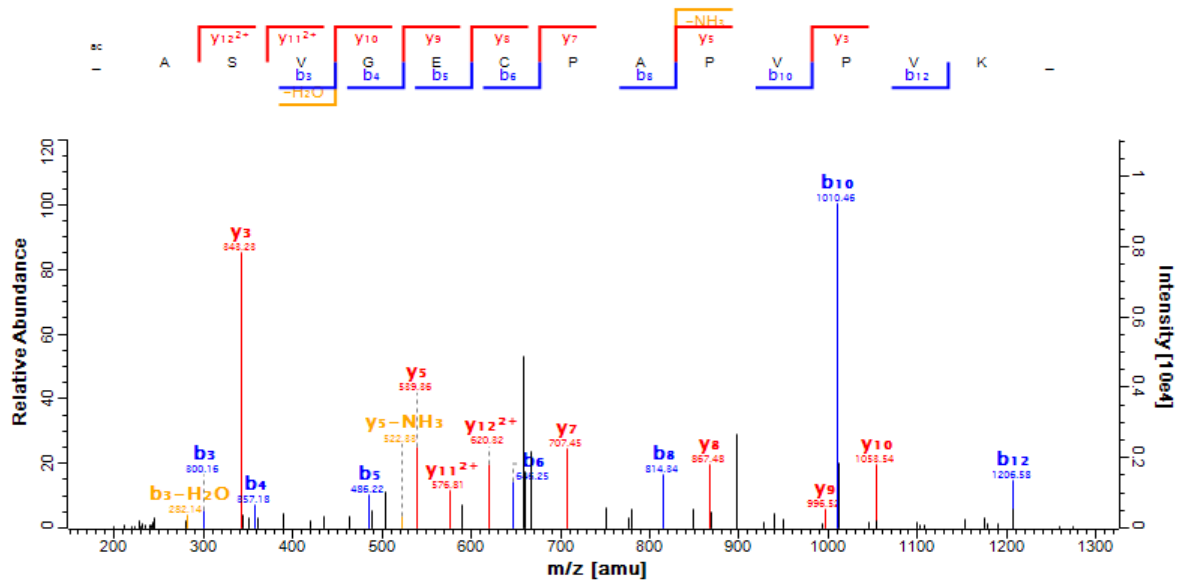
Best Match Spectrum:

Scan number	31930	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	CEP85



Protein Group ID: 1192
Protein Accession Numbers: P56134; F8W7V3
Gene Names: ATP5J2
Peptide Sequence: ASVGEC PAPVPVK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 105.17
Best Match Posterior Error Probability: 0.00058762
Best Match Spectrum:

Scan number 31941 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ATP5J2



Protein Group ID: 1197

Protein Accession Numbers: O15381; O15381-5; O15381-2; H0Y8B6; O15381-3; F8W938

Gene Names: NVL

Peptide Sequence: TLLAHAIAGELDLPIK

Total Number of Spectra: 3

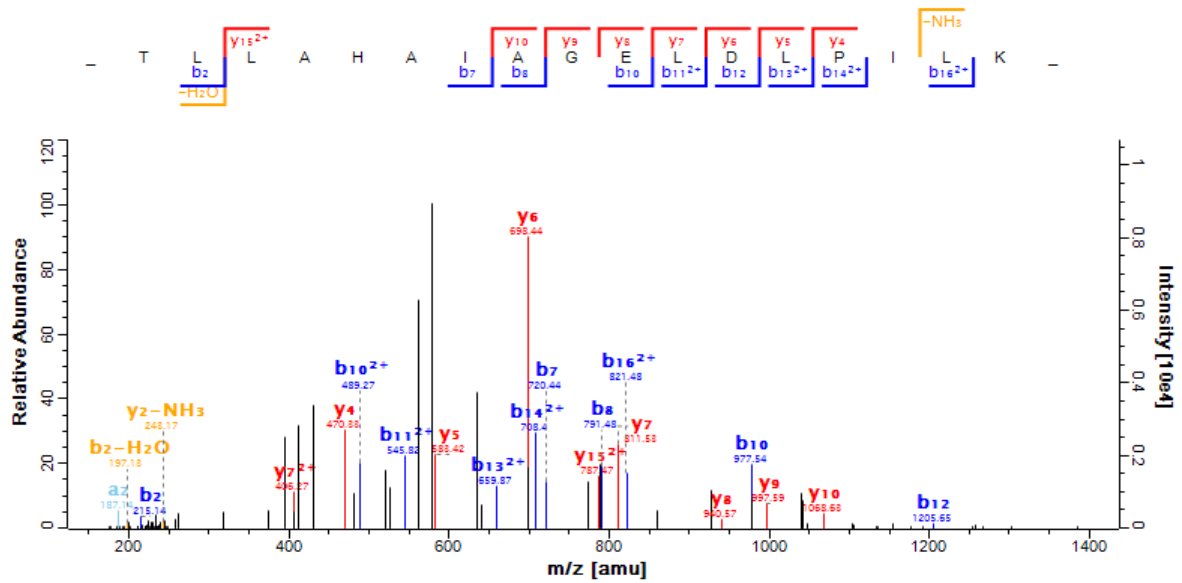
Number of Replicates (out of 8): 3

Best Match Score: 88.768

Best Match Posterior Error Probability: 0.00046545

Best Match Spectrum:

Scan number	79596	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	NVL



Protein Group ID: 1201

Protein Accession Numbers: F8W9H1; J3KPJ3; Q8N5S9-2; Q8N5S9

Gene Names: CAMKK1

Peptide Sequence: LAYNESEDR

Total Number of Spectra: 3

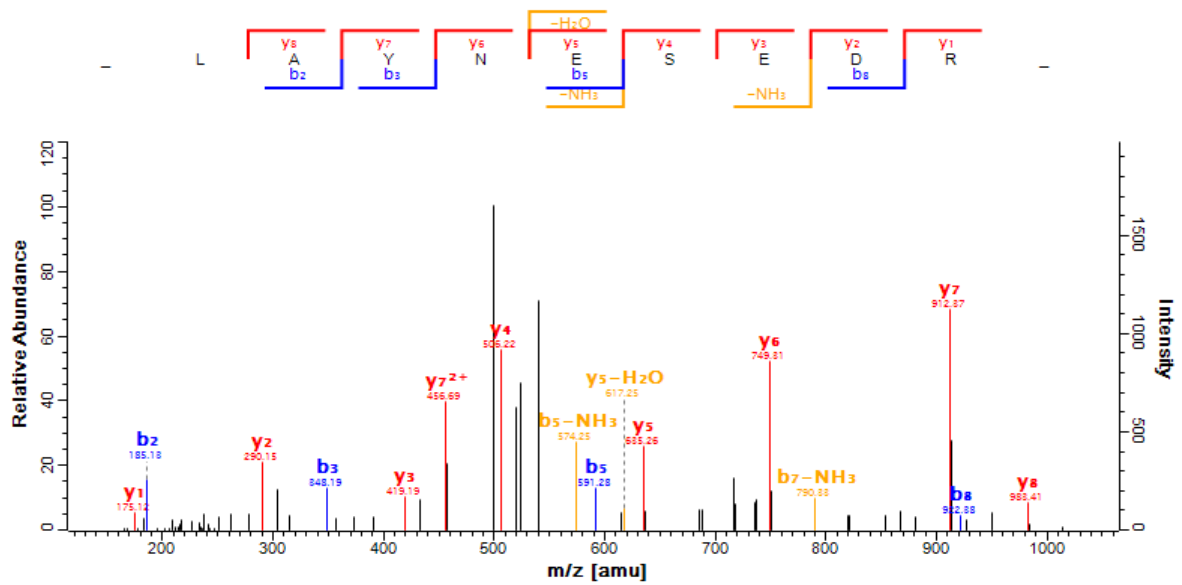
Number of Replicates (out of 8): 3

Best Match Score: 105.98

Best Match Posterior Error Probability: 0.001302

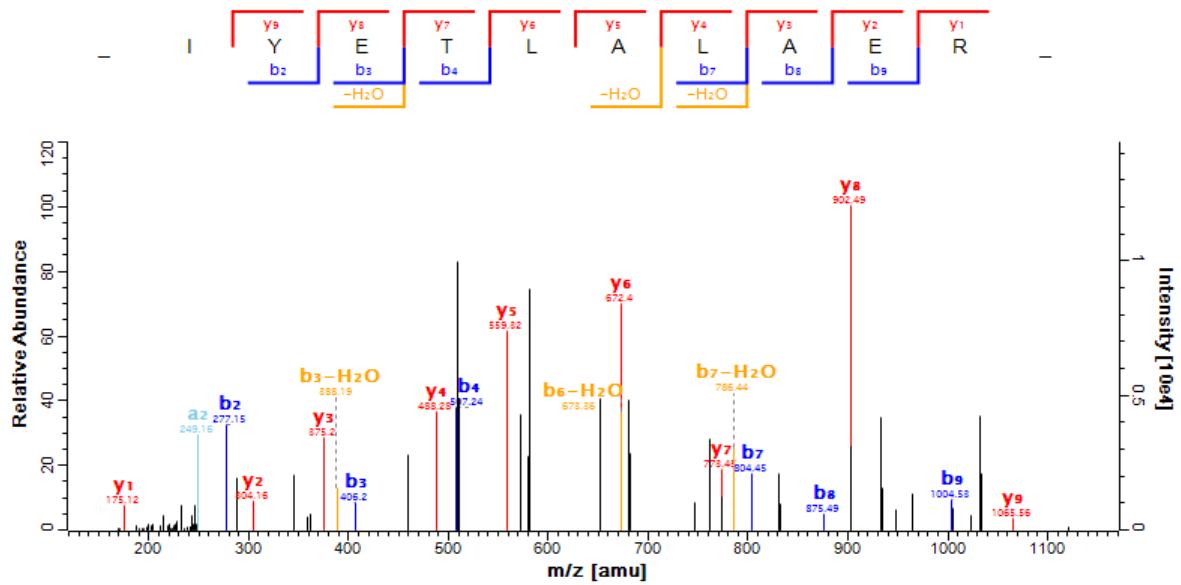
Best Match Spectrum:

Scan number 7673 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CAMKK1



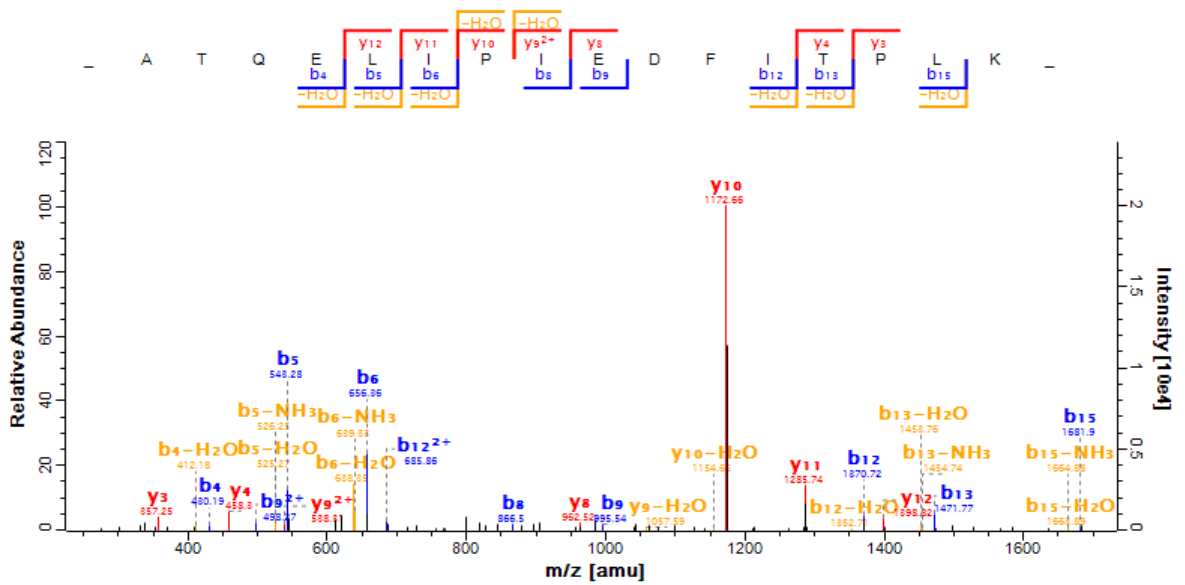
Protein Group ID: 1209
Protein Accession Numbers: Q9UK59; F8WAY1
Gene Names: DBR1
Peptide Sequence: IYETLALAEER
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 116.55
Best Match Posterior Error Probability: 0.0001962
Best Match Spectrum:

Scan number	37594	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	DBR1



Protein Group ID: 1212
Protein Accession Numbers: Q9NQ50; F8WBK5
Gene Names: MRPL40
Peptide Sequence: ATQELIPIEDFITPLK
Total Number of Spectra: 8
Number of Replicates (out of 8): 8
Best Match Score: 145.86
Best Match Posterior Error Probability: 2.04E-06
Best Match Spectrum:

Scan number 84064 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MRPL40



Protein Group ID: 1213

Protein Accession Numbers: Q6P6B7; F8WEI4; F8WBM1

Gene Names: ANKRD16

Peptide Sequence: NLGVIQELVEHGANPLLK

Total Number of Spectra: 4

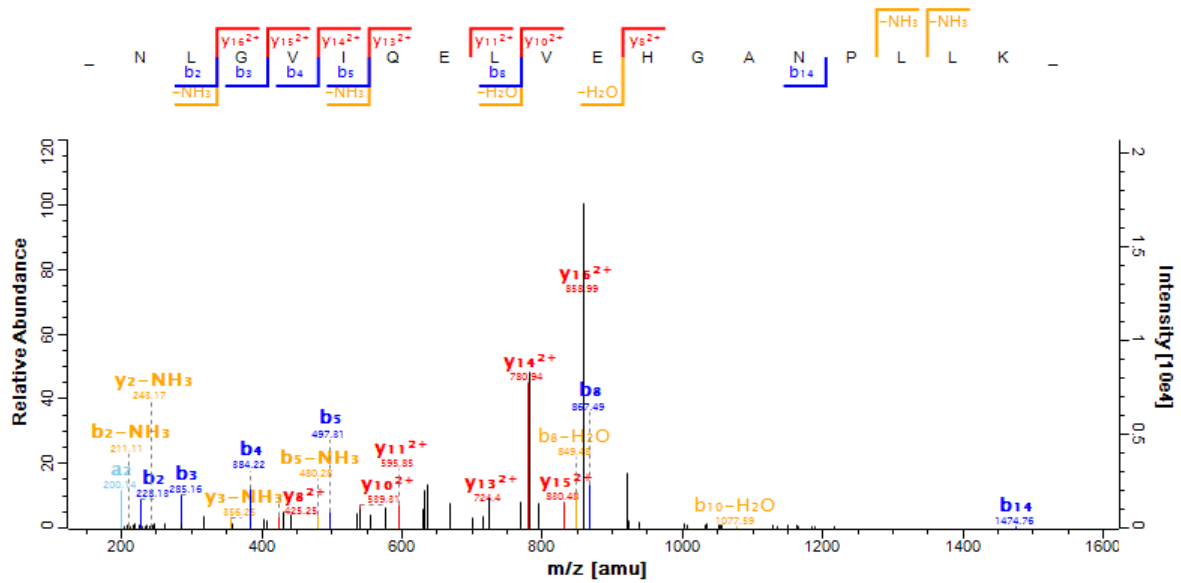
Number of Replicates (out of 8): 4

Best Match Score: 79.652

Best Match Posterior Error Probability: 0.001278

Best Match Spectrum:

Scan number	78454	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	ANKRD16



Protein Group ID: 1218

Protein Accession Numbers: Q8N1G0; Q8N1G0-2; F8WCX2; H0Y5I5

Gene Names: ZNF687

Peptide Sequence: TATGPSTGGGTVISR

Total Number of Spectra: 2

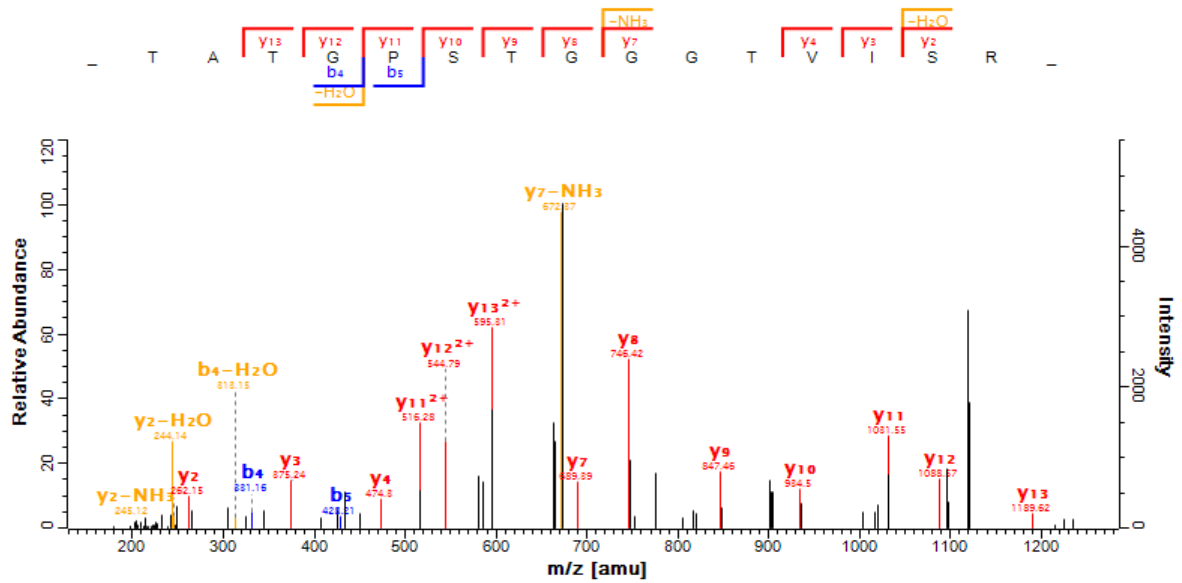
Number of Replicates (out of 8): 2

Best Match Score: 79.771

Best Match Posterior Error Probability: 0.0026466

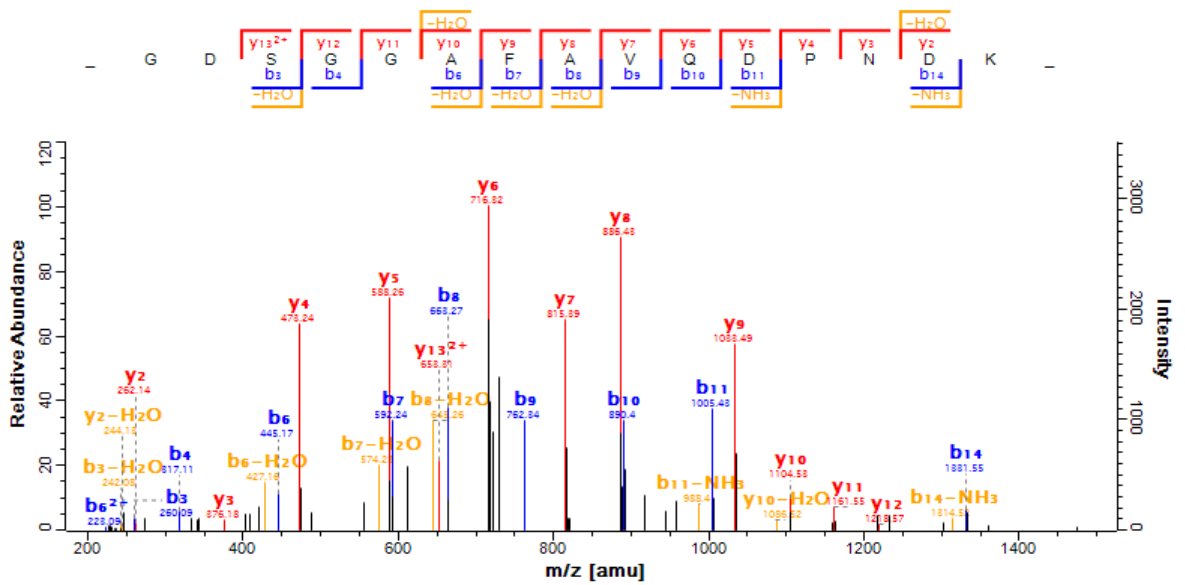
Best Match Spectrum:

Scan number	12963	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	ZNF687



Protein Group ID: 1220
Protein Accession Numbers: P09871; F8WCZ6
Gene Names: C1S
Peptide Sequence: GDSGGAFVQDPNDK
Total Number of Spectra: 5
Number of Replicates (out of 8): 4
Best Match Score: 142.91
Best Match Posterior Error Probability: 7.04E-06
Best Match Spectrum:

Scan number 19117 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** C1S



Protein Group ID: 1223

Protein Accession Numbers: Q92685; H7C0X4; F8WE30; H7BZZ2; F8WF93

Gene Names: ALG3

Peptide Sequence: SGSAAQAEG LCK

Total Number of Spectra: 9

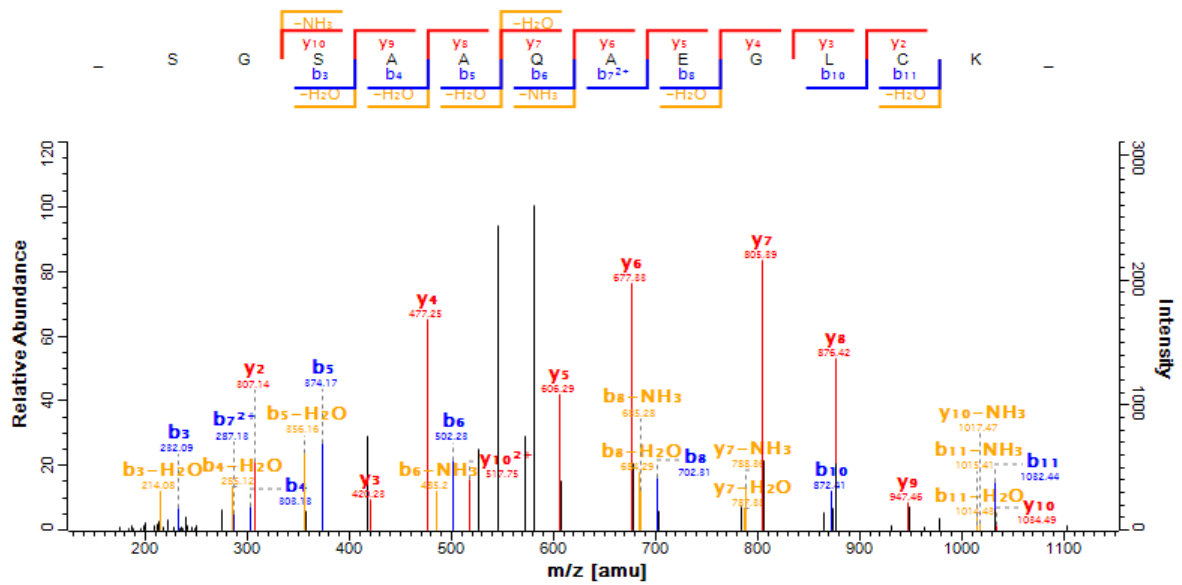
Number of Replicates (out of 8): 7

Best Match Score: 191.79

Best Match Posterior Error Probability: 3.03E-18

Best Match Spectrum:

Scan number 6899 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ALG3



Protein Group ID: 1224

Protein Accession Numbers: F8WEA9; Q8IVT5; Q8IVT5-3; J3QQL4

Gene Names: KSR1

Peptide Sequence: FGLGVLESSNPK

Total Number of Spectra: 1

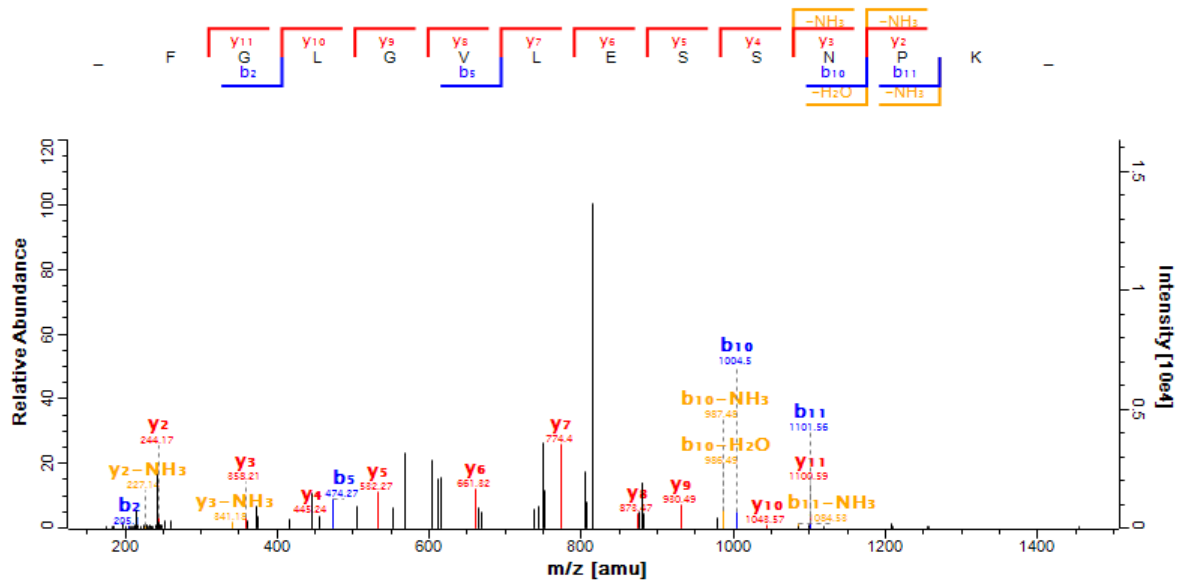
Number of Replicates (out of 8): 1

Best Match Score: 89.43

Best Match Posterior Error Probability: 0.0014893

Best Match Spectrum:

Scan number 46105 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** KSR1



Protein Group ID: 1225

Protein Accession Numbers: Q9UBF6; Q9UBF6-2; Q9UBF6-4; Q9UBF6-3; F8WEU8

Gene Names: RNF7

Peptide Sequence: ADVEDGEETCALASHSGSSGSK

Total Number of Spectra: 2

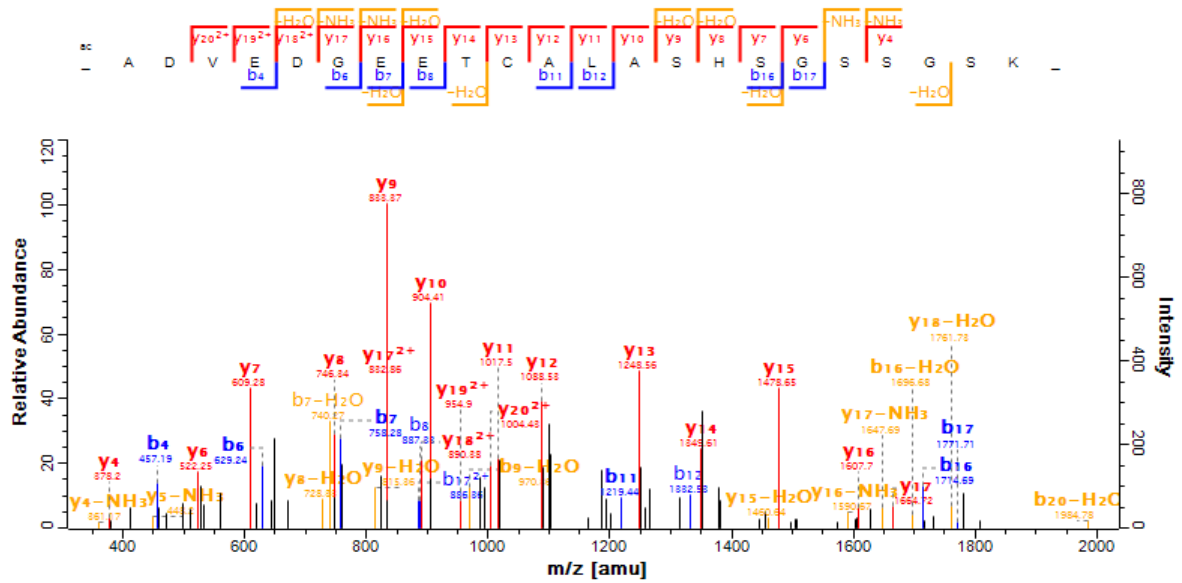
Number of Replicates (out of 8): 2

Best Match Score: 158.44

Best Match Posterior Error Probability: 2.46E-30

Best Match Spectrum:

Scan number 27217 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** RNF7



Protein Group ID: 1228

Protein Accession Numbers: P0DI81-3; G1K394; P0DI81; P0DI82

Gene Names: TRAPPC2;TRAPPC2P1

Peptide Sequence: FSMNPFYEPNSPIR

Total Number of Spectra: 1

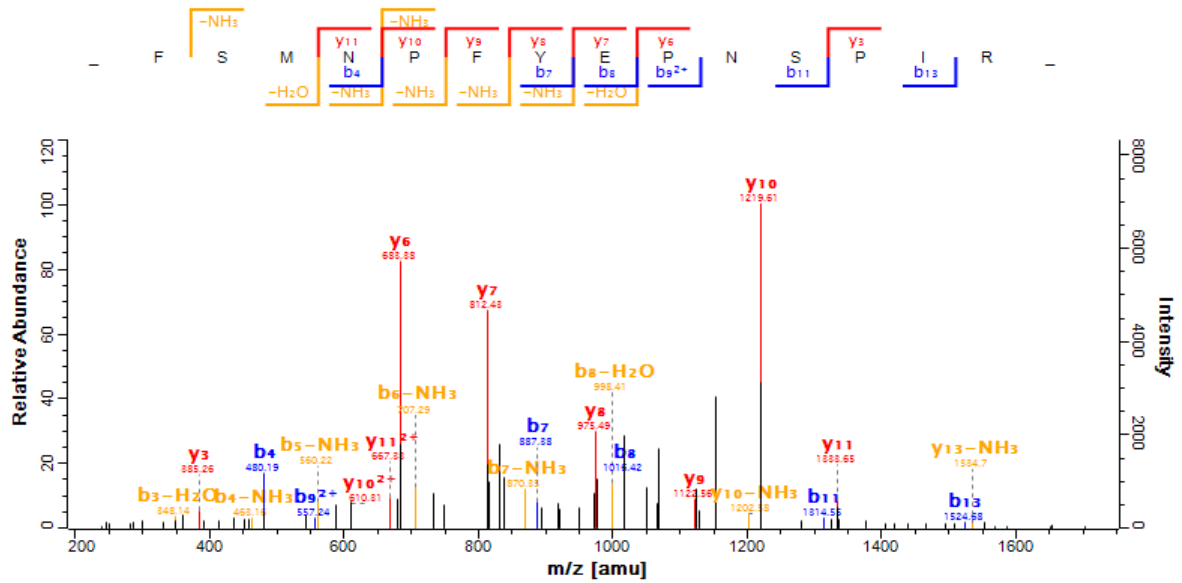
Number of Replicates (out of 8): 1

Best Match Score: 95.981

Best Match Posterior Error Probability: 0.00062797

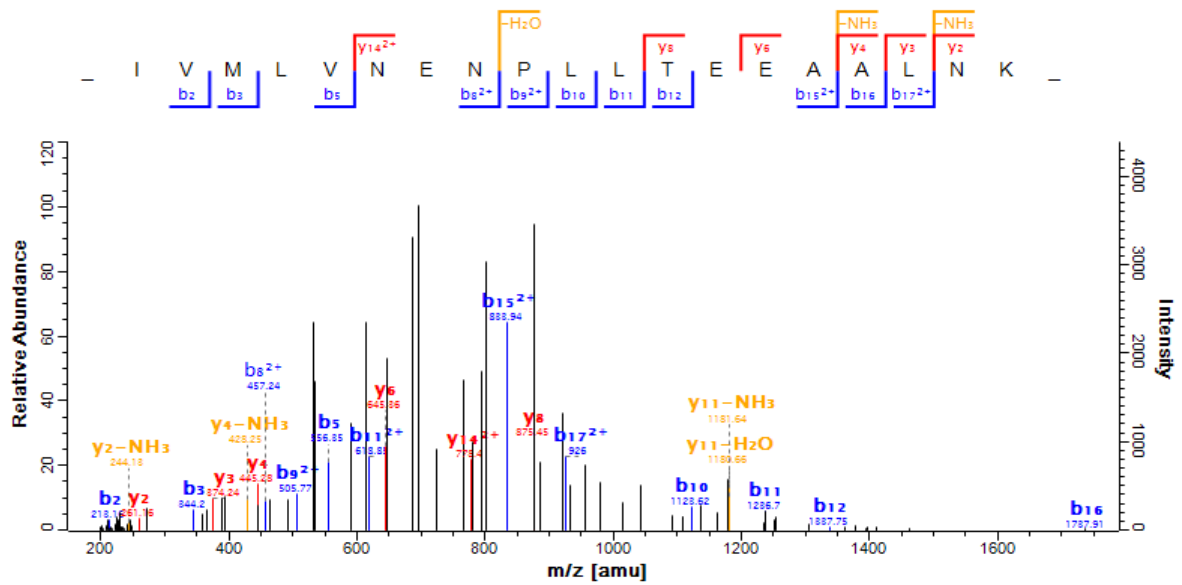
Best Match Spectrum:

Scan number 59801 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TRAPPC2;TRAPPC2P1



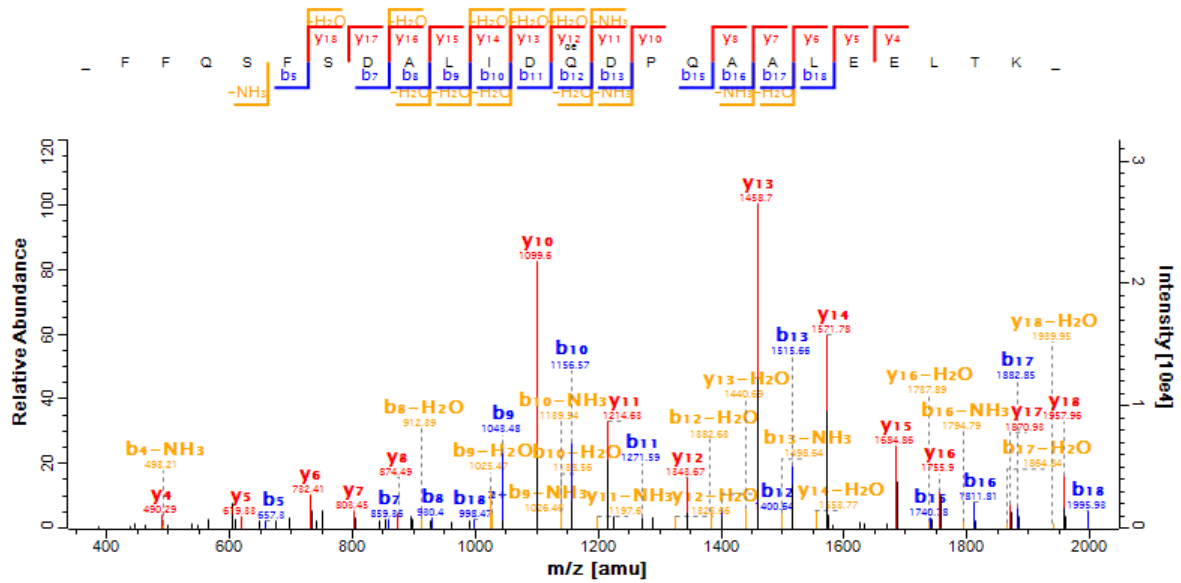
Protein Group ID: 1230
Protein Accession Numbers: Q8IV38; G3V0G5
Gene Names: ANKMY2
Peptide Sequence: IVMLVNENPLLTEEAALNK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 69.805
Best Match Posterior Error Probability: 0.0027986
Best Match Spectrum:

Scan number 74174 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ANKMY2



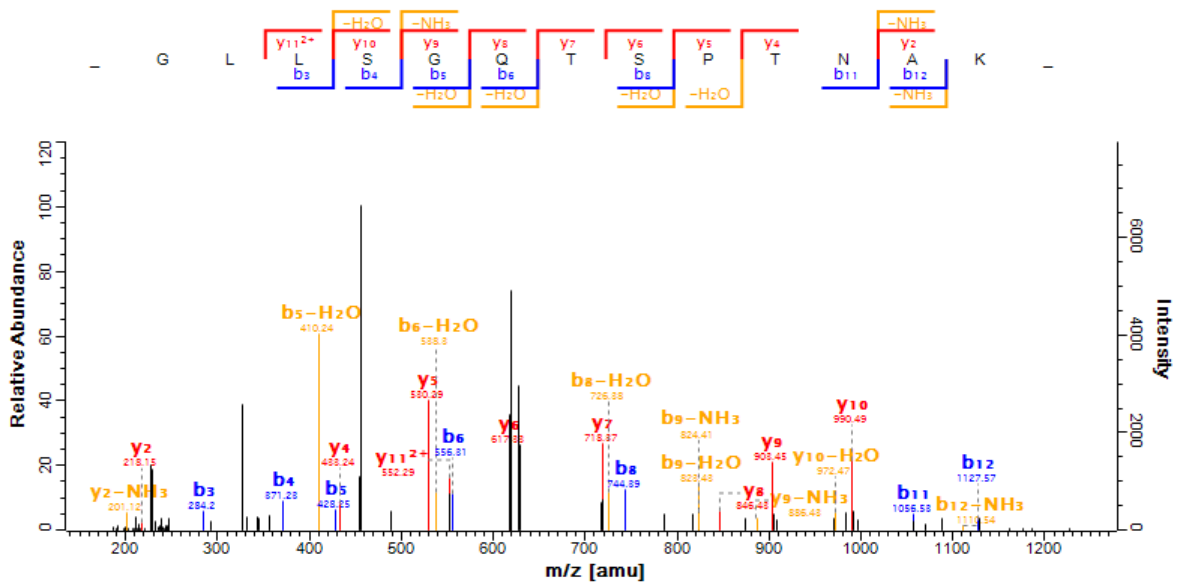
Protein Group ID: 1236
Protein Accession Numbers: G3V1B1
Gene Names: SUGT1P3
Peptide Sequence: FFQSFSDALIDQPQAAL EELTK
Total Number of Spectra: 15
Number of Replicates (out of 8): 8
Best Match Score: 193.42
Best Match Posterior Error Probability: 6.00E-40
Best Match Spectrum:

Scan number 89139 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** SUGT1P3



Protein Group ID: 1240
Protein Accession Numbers: Q969J3; G3V1P3
Gene Names: LOH12CR1
Peptide Sequence: GLLSGQTSPTNAK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 117.7
Best Match Posterior Error Probability: 0.00018435
Best Match Spectrum:

Scan number 18439 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** LOH12CR1



Protein Group ID: 1243

Protein Accession Numbers: G3V1X3; Q8WUH1; G3V214; Q8WUH1-2; H0YIM9

Gene Names: CHURC1;CHURC1-FNTB

Peptide Sequence: AEDTISILPDDR

Total Number of Spectra: 8

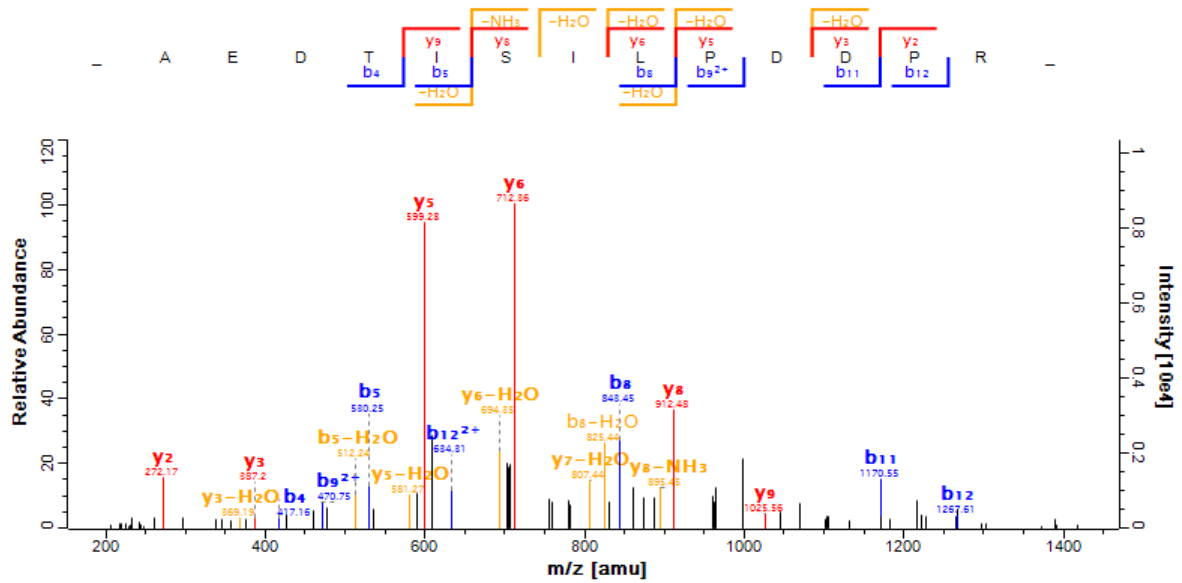
Number of Replicates (out of 8): 6

Best Match Score: 136.7

Best Match Posterior Error Probability: 3.33E-05

Best Match Spectrum:

Scan number 44247 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CHURC1;CHURC1-FNTB



Protein Group ID: 1248

Protein Accession Numbers: Q86SZ2; Q86SZ2-2; G3V2H7; G3V4C3

Gene Names: TRAPPC6B

Peptide Sequence: ADEALFLLHNEMVSGVYK

Total Number of Spectra: 6

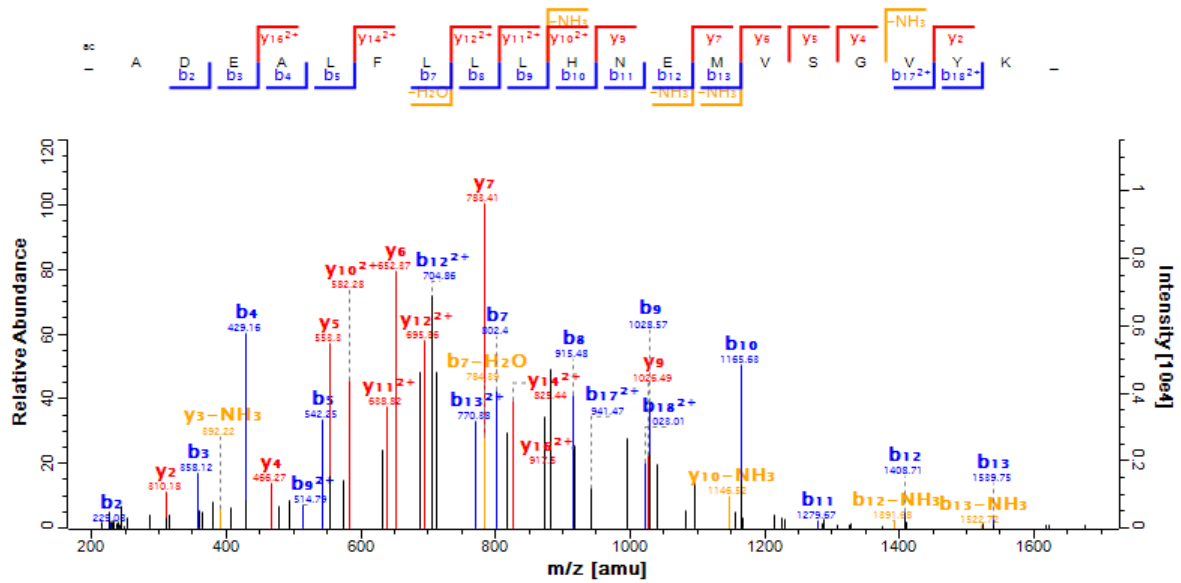
Number of Replicates (out of 8): 6

Best Match Score: 149.99

Best Match Posterior Error Probability: 1.67E-07

Best Match Spectrum:

Scan number 91749 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TRAPPC6B



Protein Group ID: 1250

Protein Accession Numbers: Q9H7H0-3; Q9H7H0; Q9H7H0-2; G3V2Q4; G3V4H5; G3V353; H0YJW8; G3V3X6; G3V4P2

Gene Names: METTL17

Peptide Sequence: FLENPDLSQTEEK

Total Number of Spectra: 4

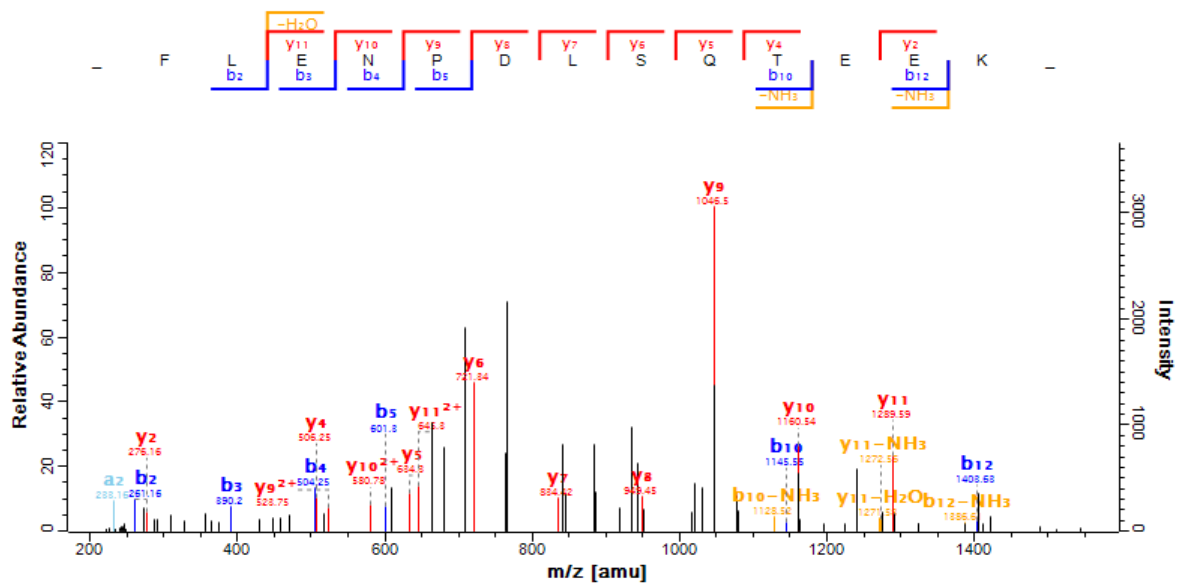
Number of Replicates (out of 8): 4

Best Match Score: 124.51

Best Match Posterior Error Probability: 9.33E-05

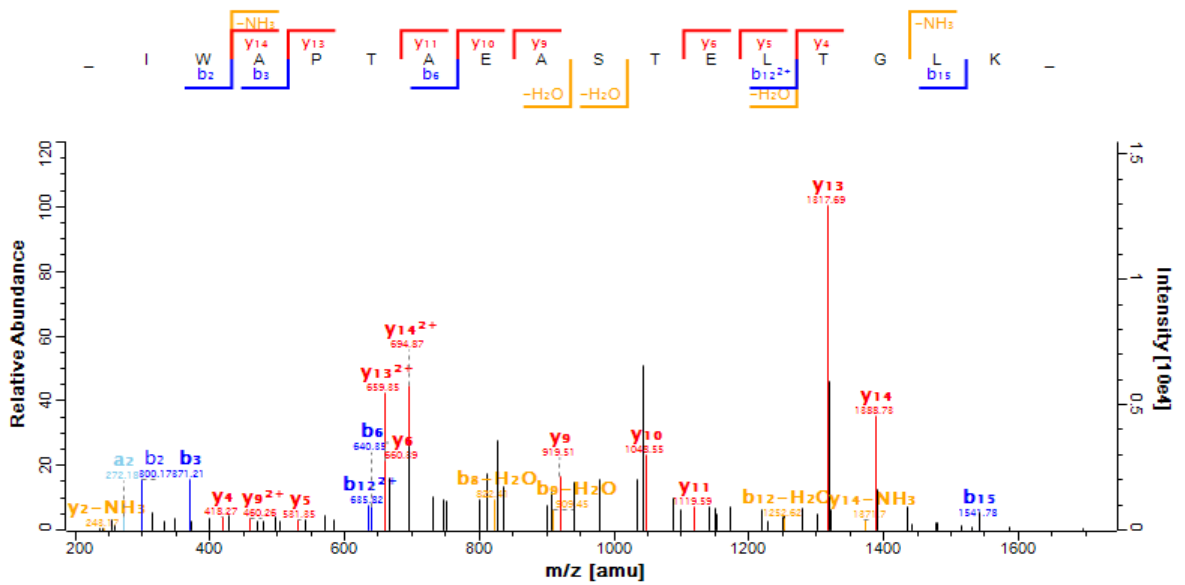
Best Match Spectrum:

Scan number	31044	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	METTL17



Protein Group ID: 1257
Protein Accession Numbers: G3V3G9; Q5TAQ9
Gene Names: DCAF8
Peptide Sequence: IWAPTAEASTELTGLK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 88.561
Best Match Posterior Error Probability: 0.0006397
Best Match Spectrum:

Scan number 56994 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** DCAF8



Protein Group ID: 1263

Protein Accession Numbers: P61244; P61244-2; G3V5L1; G3V570

Gene Names: MAX

Peptide Sequence: RQNALLEQQVR

Total Number of Spectra: 3

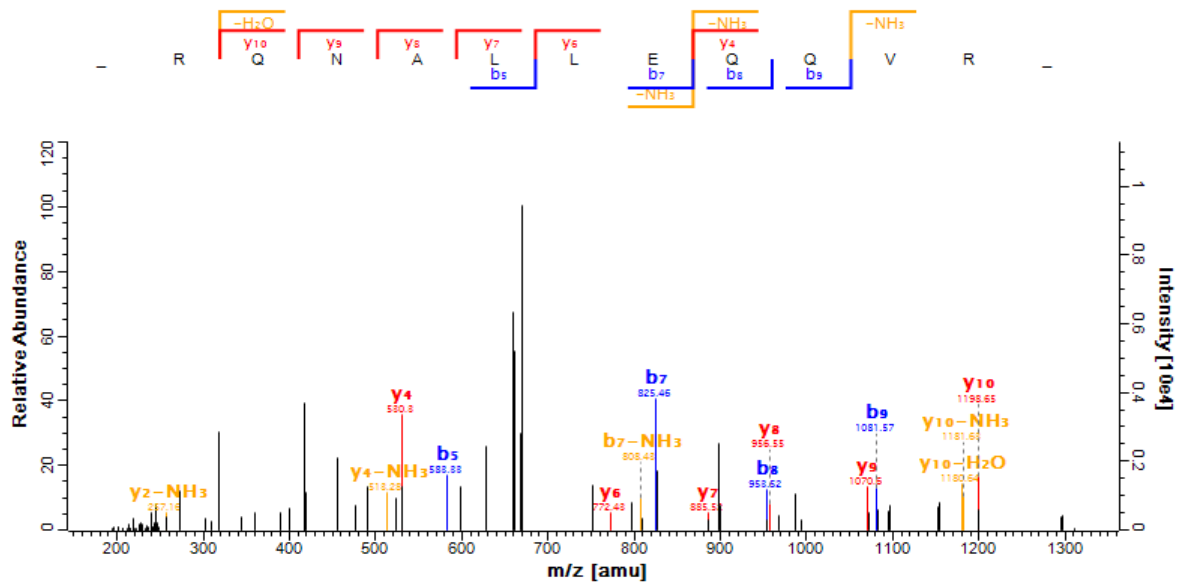
Number of Replicates (out of 8): 3

Best Match Score: 91.961

Best Match Posterior Error Probability: 0.0029766

Best Match Spectrum:

Scan number 16931 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MAX



Protein Group ID: 1267

Protein Accession Numbers: Q9NUM3; Q9NUM3-2; G3V5J8

Gene Names: SLC39A9

Peptide Sequence: HHQASETHNVIASDK

Total Number of Spectra: 3

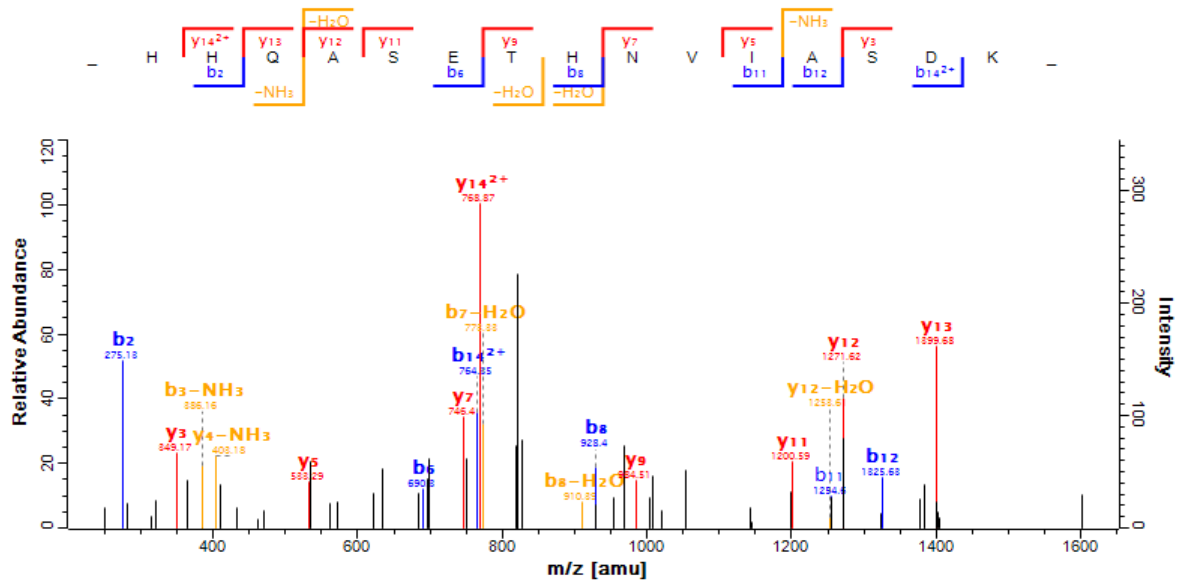
Number of Replicates (out of 8): 3

Best Match Score: 107.61

Best Match Posterior Error Probability: 0.00014713

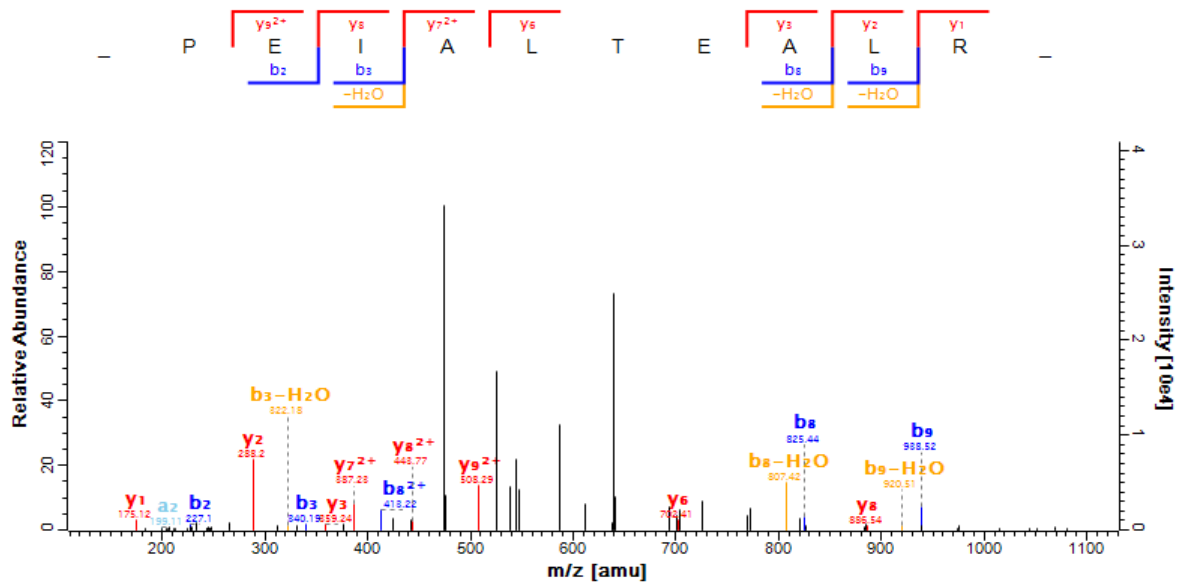
Best Match Spectrum:

Scan number	3121	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	SLC39A9



Protein Group ID: 1272
Protein Accession Numbers: G3XAE9; Q9Y4F4
Gene Names: FAM179B
Peptide Sequence: PEIALTEALR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 110.76
Best Match Posterior Error Probability: 0.00031437
Best Match Spectrum:

Scan number 75842 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** FAM179B



Protein Group ID: 1277

Protein Accession Numbers: O00754; G5E928; H7BZP0

Gene Names: MAN2B1

Peptide Sequence: LPVSEGVFVVK

Total Number of Spectra: 6

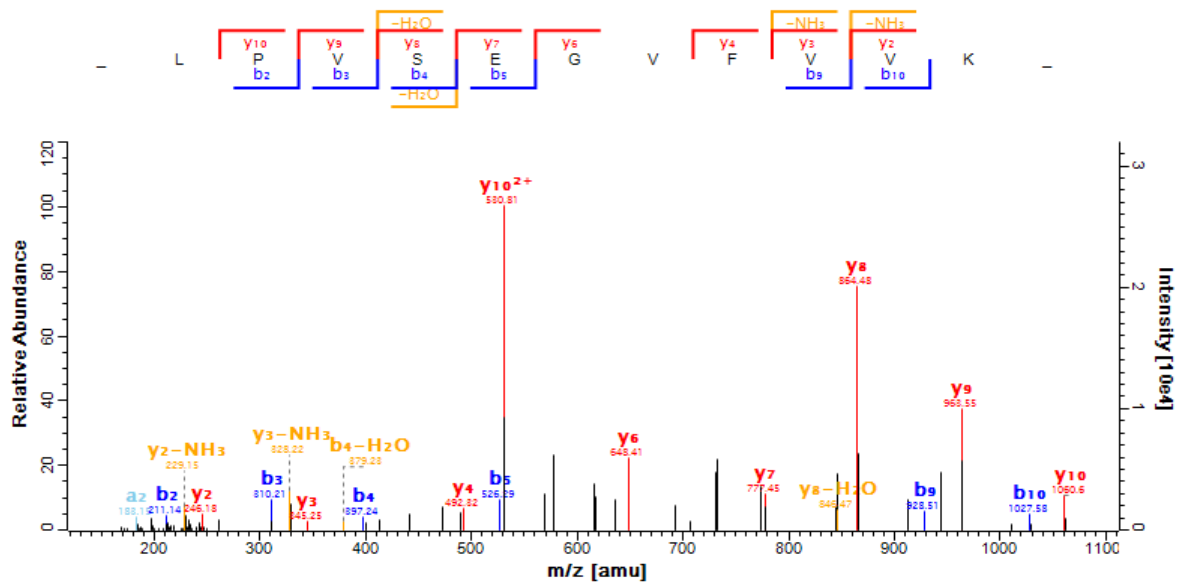
Number of Replicates (out of 8): 6

Best Match Score: 126.71

Best Match Posterior Error Probability: 4.31E-05

Best Match Spectrum:

Scan number	48562	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	MAN2B1



Protein Group ID: 1282

Protein Accession Numbers: Q15653; Q15653-2; G5E9C2; I3L4X3; I3L1A4

Gene Names: NFKB1B

Peptide Sequence: LQLEAENYEGHTPLHVAVIHK

Total Number of Spectra: 1

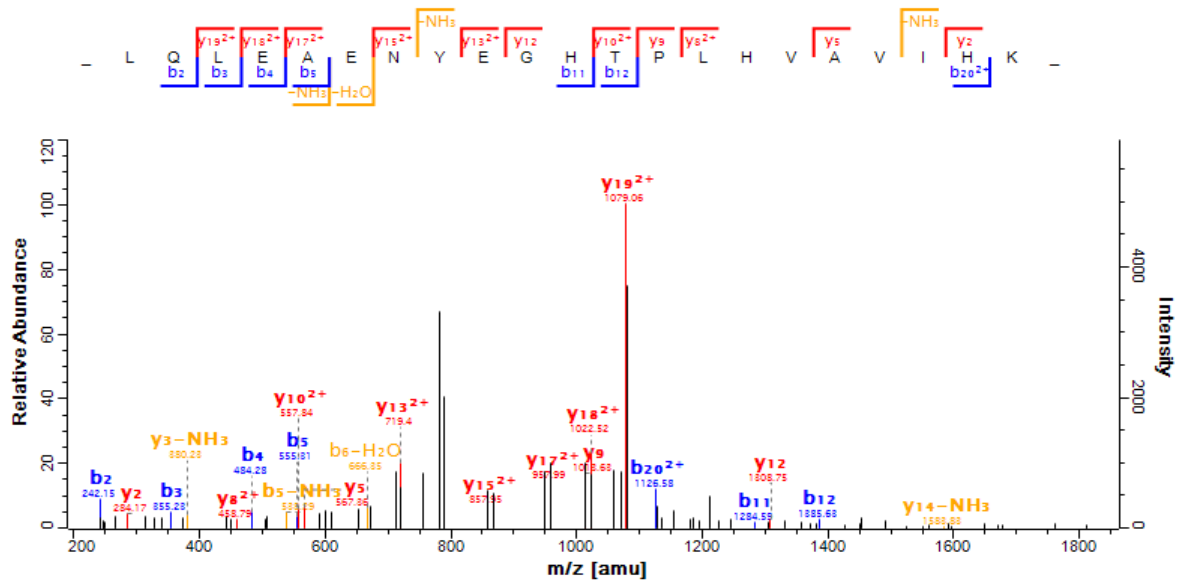
Number of Replicates (out of 8): 1

Best Match Score: 73.918

Best Match Posterior Error Probability: 0.0007318

Best Match Spectrum:

Scan number 42157 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** NFKB1B



Protein Group ID: 1288

Protein Accession Numbers: Q02833; Q02833-2; G5E9N9; H0YEI0

Gene Names: RASSF7

Peptide Sequence: LQALSAATAEAR

Total Number of Spectra: 2

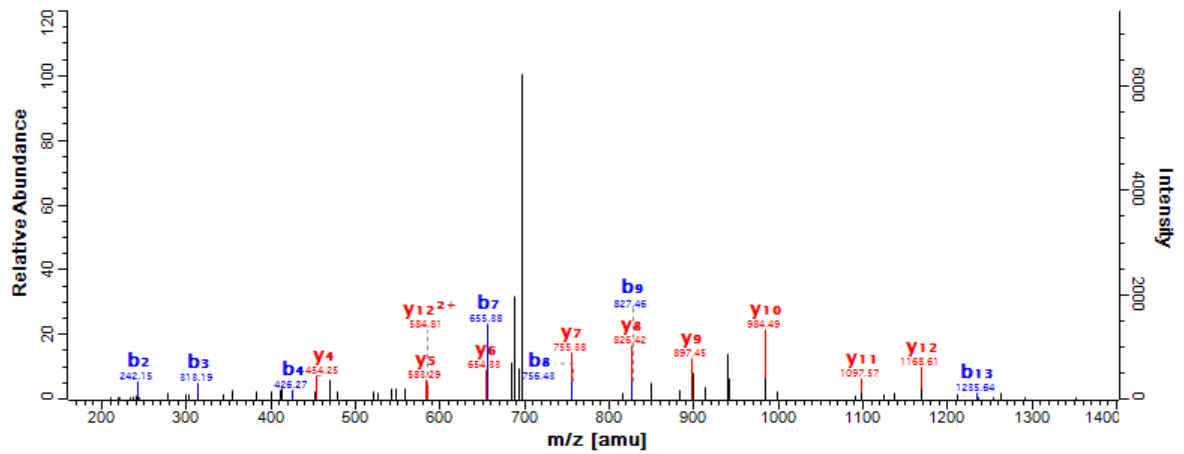
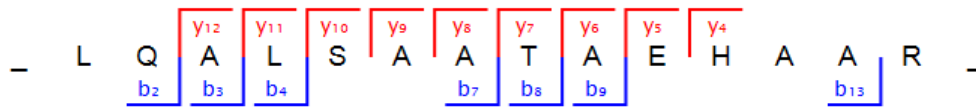
Number of Replicates (out of 8): 2

Best Match Score: 99.566

Best Match Posterior Error Probability: 0.00034211

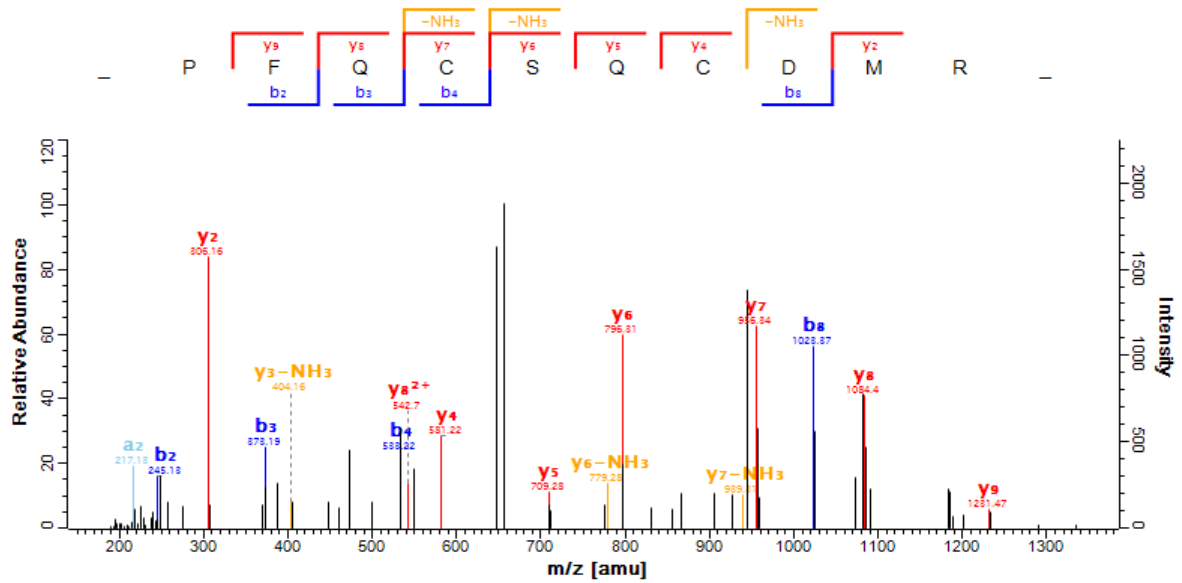
Best Match Spectrum:

Scan number	22061	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	RASSF7



Protein Group ID: 1293
Protein Accession Numbers: Q9UQR1; G5E9X2
Gene Names: ZNF148
Peptide Sequence: PFQCSQCDMR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 96.015
Best Match Posterior Error Probability: 0.0012035
Best Match Spectrum:

Scan number 12912 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ZNF148



Protein Group ID: 1295

Protein Accession Numbers: Q96KA5; Q96KA5-2; G5E9Z2

Gene Names: CLPTM1L

Peptide Sequence: TVHYLPILFIDQLSNR

Total Number of Spectra: 7

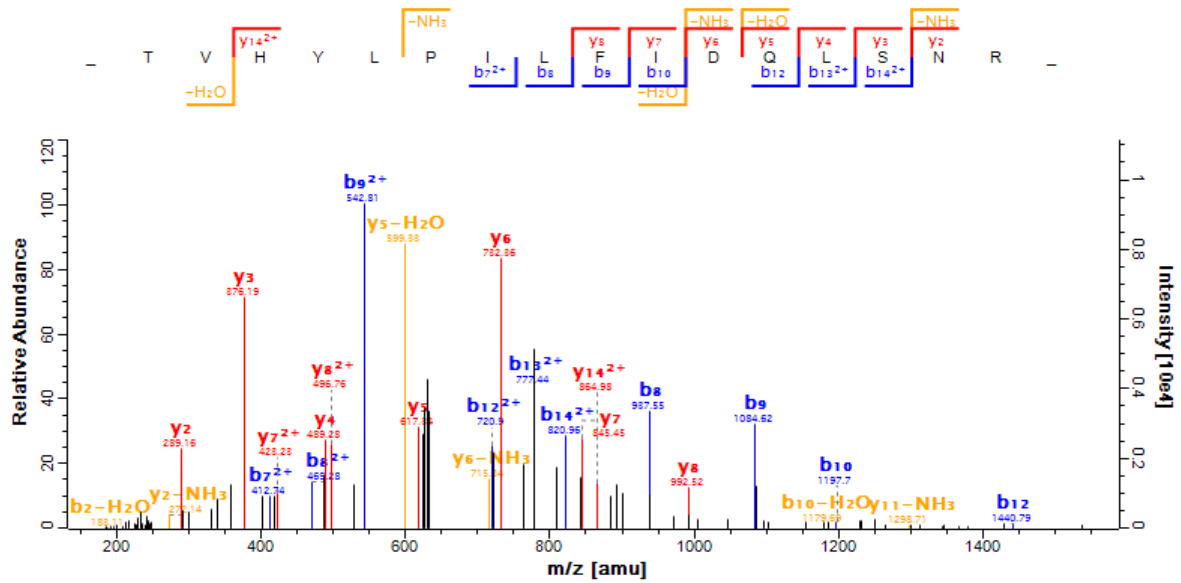
Number of Replicates (out of 8): 7

Best Match Score: 139.86

Best Match Posterior Error Probability: 2.42E-05

Best Match Spectrum:

Scan number 81607 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CLPTM1L



Protein Group ID: 1310

Protein Accession Numbers: J3KR72; P49848-3; P49848; G8JLM6

Gene Names: TAF6

Peptide Sequence: AQAALQAQQVNR

Total Number of Spectra: 1

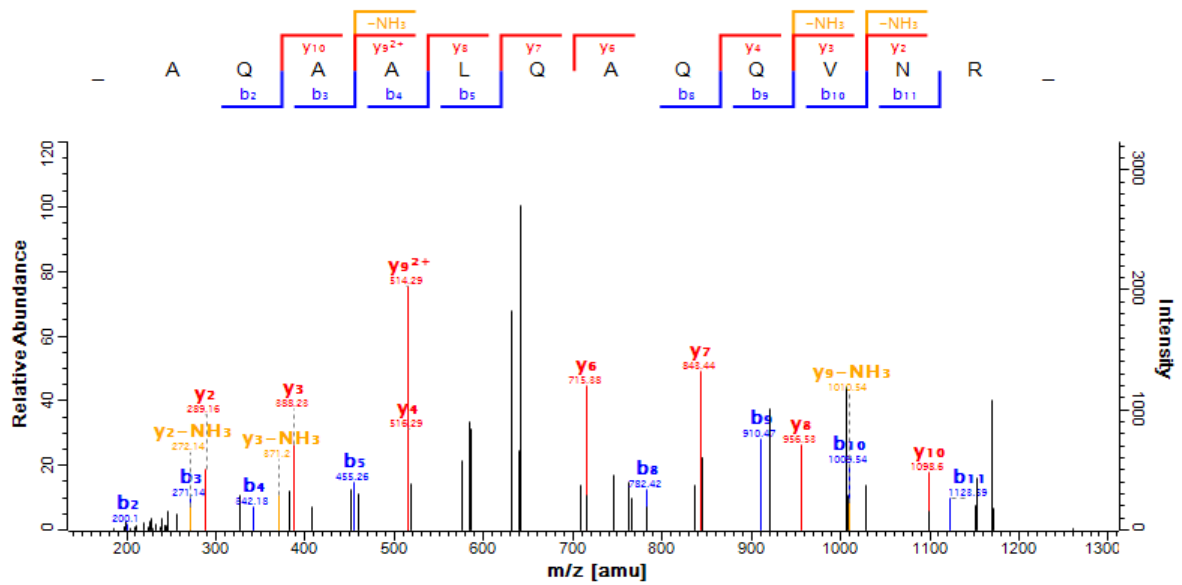
Number of Replicates (out of 8): 1

Best Match Score: 99.752

Best Match Posterior Error Probability: 0.00051802

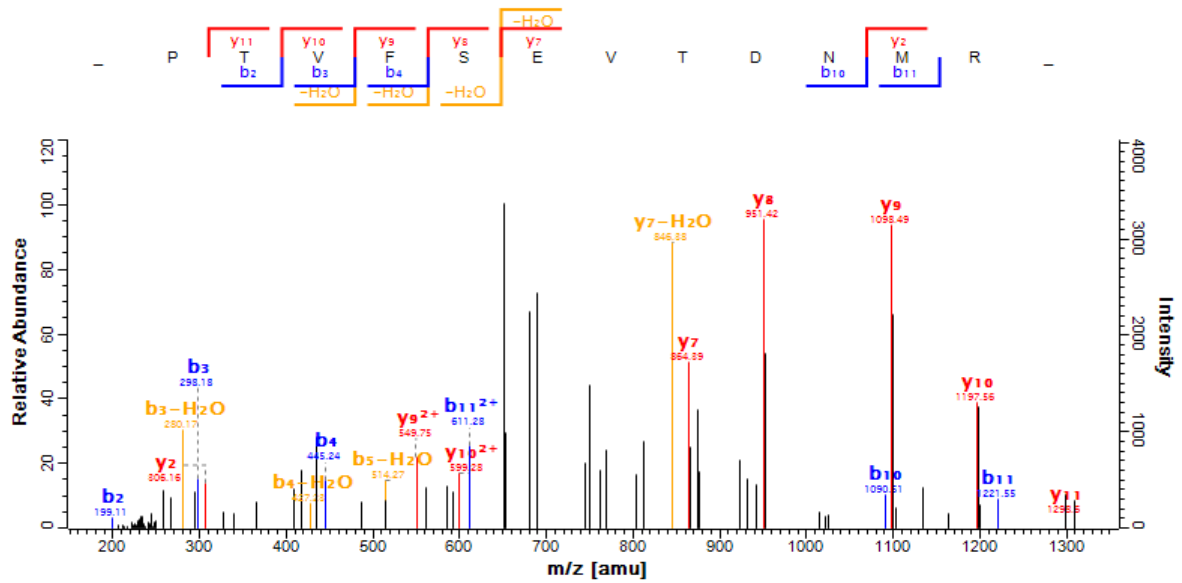
Best Match Spectrum:

Scan number	10112	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	TAF6



Protein Group ID: 1312
Protein Accession Numbers: P47895; H0Y2X5
Gene Names: ALDH1A3
Peptide Sequence: PTVFSEVTDNMR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 99.5
Best Match Posterior Error Probability: 0.00052417
Best Match Spectrum:

Scan number 68833 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ALDH1A3



Protein Group ID: 1315

Protein Accession Numbers: Q13371; H0Y3M0; H0Y5D3

Gene Names: PDCL

Peptide Sequence: QLETEQREEQCR

Total Number of Spectra: 1

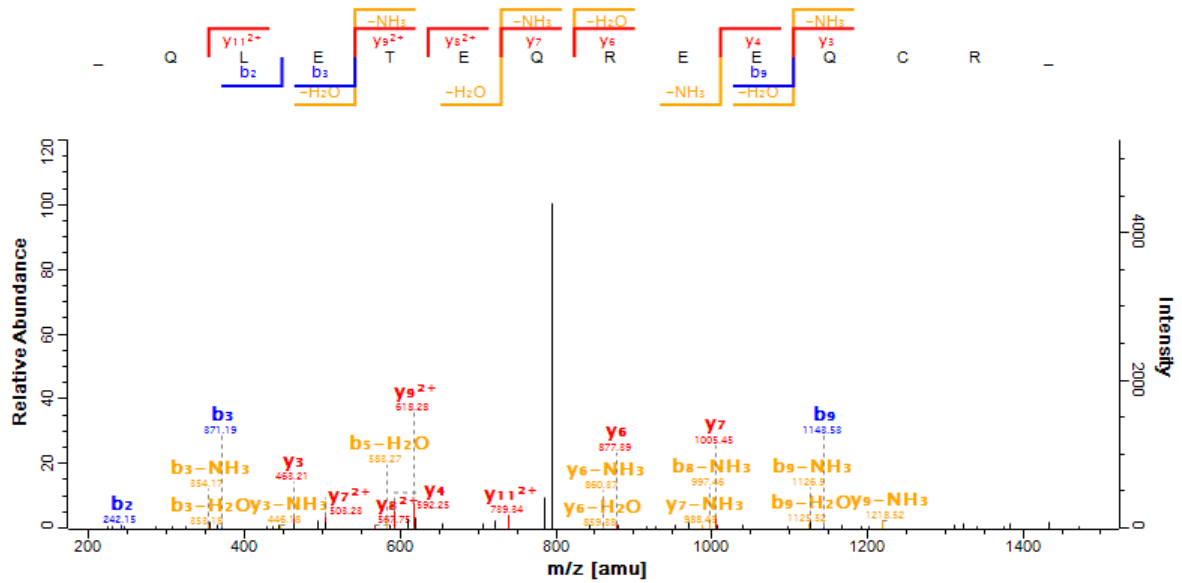
Number of Replicates (out of 8): 1

Best Match Score: 126.71

Best Match Posterior Error Probability: 0.00046359

Best Match Spectrum:

Scan number 3897 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** PDCL



Protein Group ID: 1316

Protein Accession Numbers: Q53EZ4; Q53EZ4-2; H0Y432

Gene Names: CEP55

Peptide Sequence: KPESGYLQEEK

Total Number of Spectra: 3

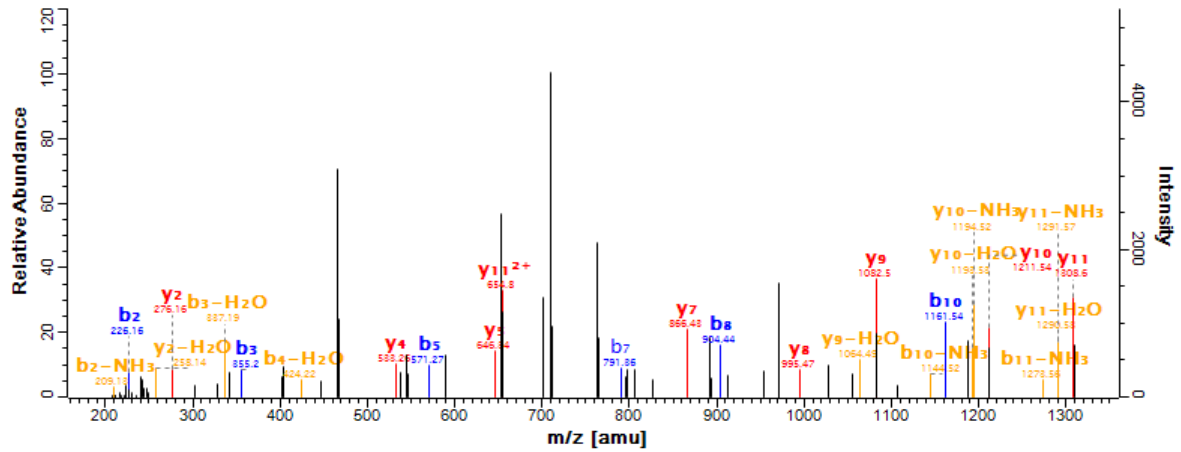
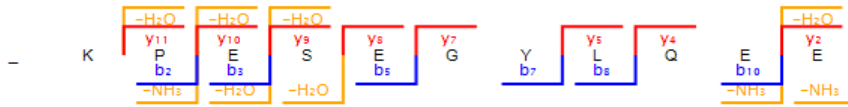
Number of Replicates (out of 8): 3

Best Match Score: 148.62

Best Match Posterior Error Probability: 1.11E-05

Best Match Spectrum:

Scan number 9937 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CEP55



Protein Group ID: 1319

Protein Accession Numbers: Q9Y4B6; Q9Y4B6-2; H0Y4P3; Q9Y4B6-3

Gene Names: VPRBP

Peptide Sequence: EADLPMTAASHSSAFTPTAAASPVSLPR

Total Number of Spectra: 5

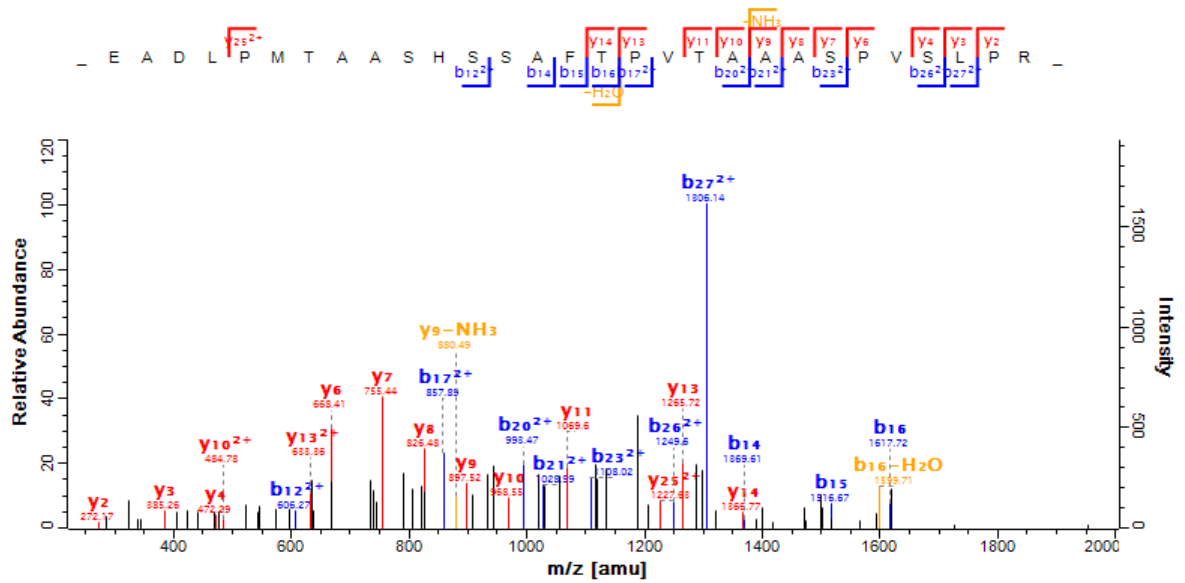
Number of Replicates (out of 8): 4

Best Match Score: 76.152

Best Match Posterior Error Probability: 1.23E-05

Best Match Spectrum:

Scan number	59697	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	VPRBP



Protein Group ID: 1321

Protein Accession Numbers: Q14687; Q14687-3; Q14687-2; H0Y613

Gene Names: GSE1; KIAA0182

Peptide Sequence: PQLHAAPTALWNPVSLMDNTLETR

Total Number of Spectra: 2

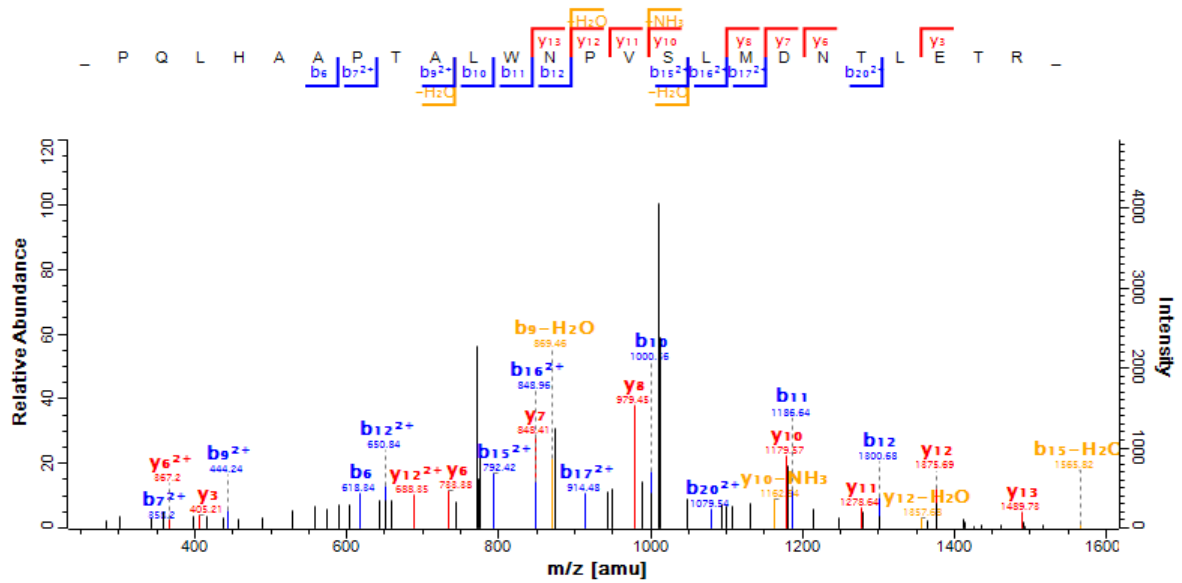
Number of Replicates (out of 8): 2

Best Match Score: 72.564

Best Match Posterior Error Probability: 0.00034403

Best Match Spectrum:

Scan number 82732 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** GSE1; KIAA0182



Protein Group ID: 1324

Protein Accession Numbers: Q02447; Q02447-2; H0Y7L6; Q02447-6; H0Y6K5; Q02447-5; Q02447-3; Q02447-4

Gene Names: SP3

Peptide Sequence: VQVVDEEGDQQHQEGK

Total Number of Spectra: 10

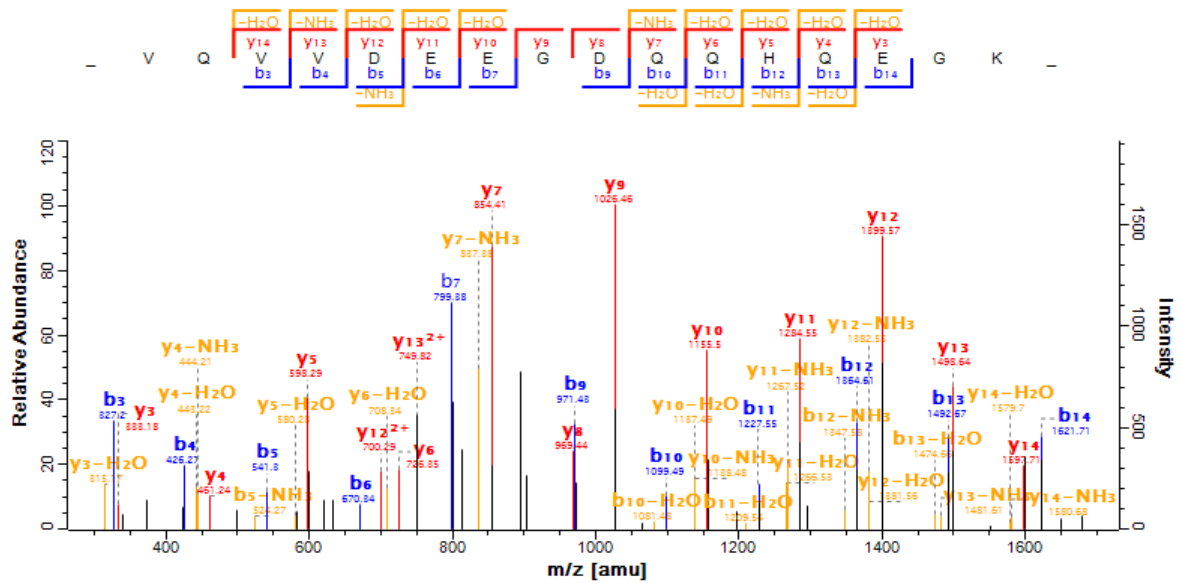
Number of Replicates (out of 8): 8

Best Match Score: 290.95

Best Match Posterior Error Probability: 8.34E-156

Best Match Spectrum:

Scan number	8241	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS: CID	Genenames	SP3



Protein Group ID: 1328

Protein Accession Numbers: Q6ZNJ1; Q6ZNJ1-3; Q6ZNJ1-2; H0Y764

Gene Names: NBEAL2

Peptide Sequence: YGVQFILDALR

Total Number of Spectra: 2

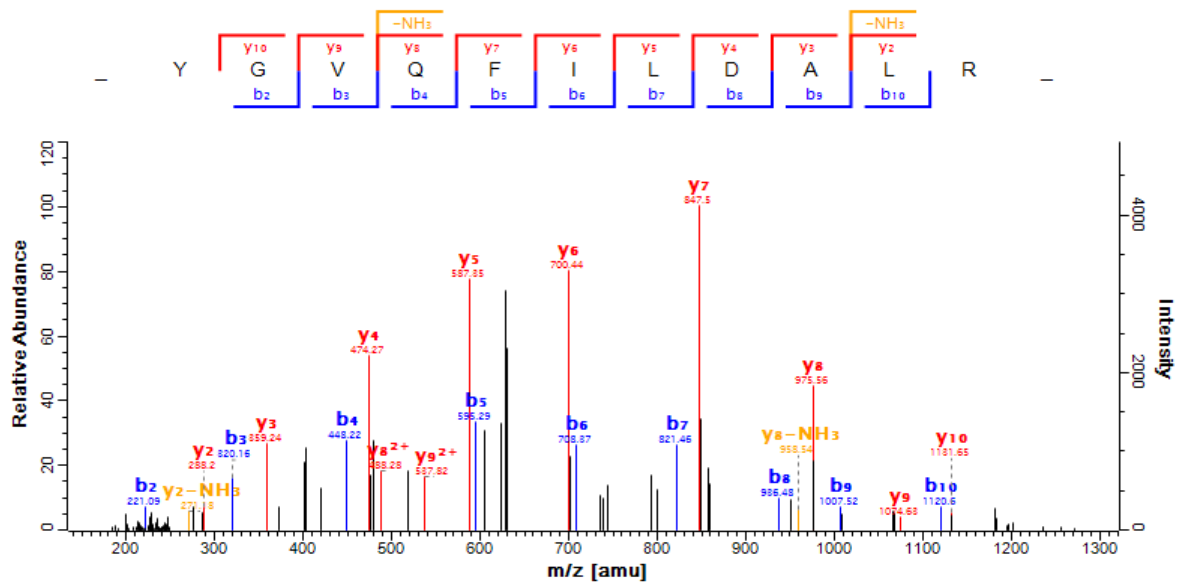
Number of Replicates (out of 8): 2

Best Match Score: 148.18

Best Match Posterior Error Probability: 1.34E-05

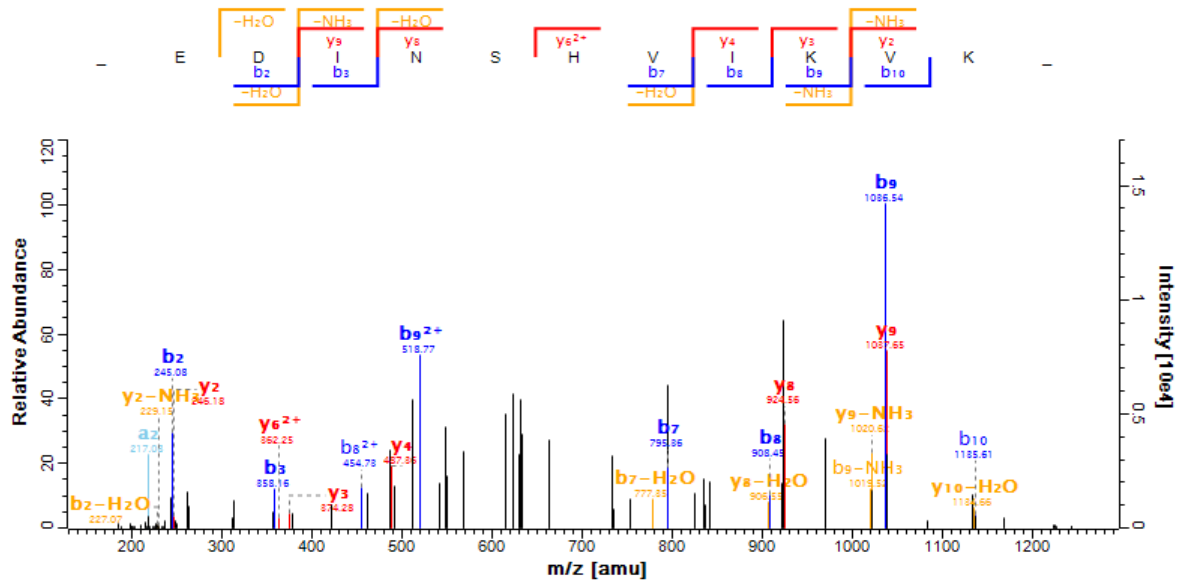
Best Match Spectrum:

Scan number 81756 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** NBEAL2



Protein Group ID: 1332
Protein Accession Numbers: Q7Z3E2; H0Y7V5
Gene Names: C10orf118
Peptide Sequence: EDINSHVIKVK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 100.69
Best Match Posterior Error Probability: 0.0022397
Best Match Spectrum:

Scan number 35019 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** C10orf118



Protein Group ID: 1333

Protein Accession Numbers: Q4LE39; Q4LE39-2; Q4LE39-3; Q4LE39-4; H7C5R6; H0Y7Y8

Gene Names: ARID4B

Peptide Sequence: EEQNSSSLLEENK

Total Number of Spectra: 1

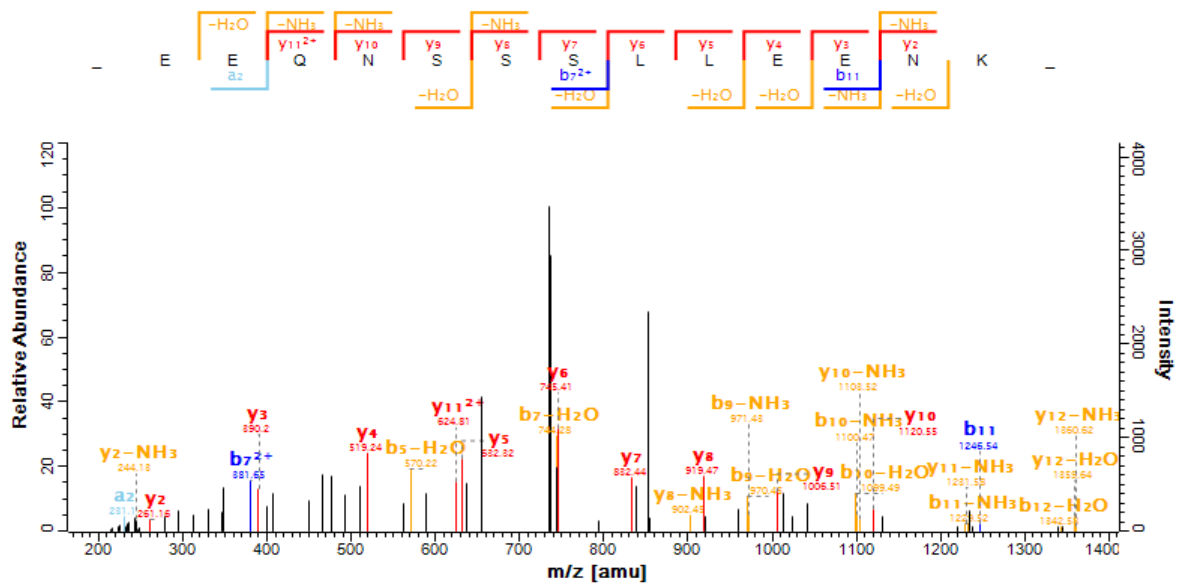
Number of Replicates (out of 8): 1

Best Match Score: 87.498

Best Match Posterior Error Probability: 0.0016454

Best Match Spectrum:

Scan number 16339 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS: CID **Genenames** ARID4B



Protein Group ID: 1339

Protein Accession Numbers: Q9Y2E5; Q9Y2E5-2; H0YA68

Gene Names: MAN2B2

Peptide Sequence: PPQDGVYPNMSEPVTPANINLYAEALVANVK

Total Number of Spectra: 1

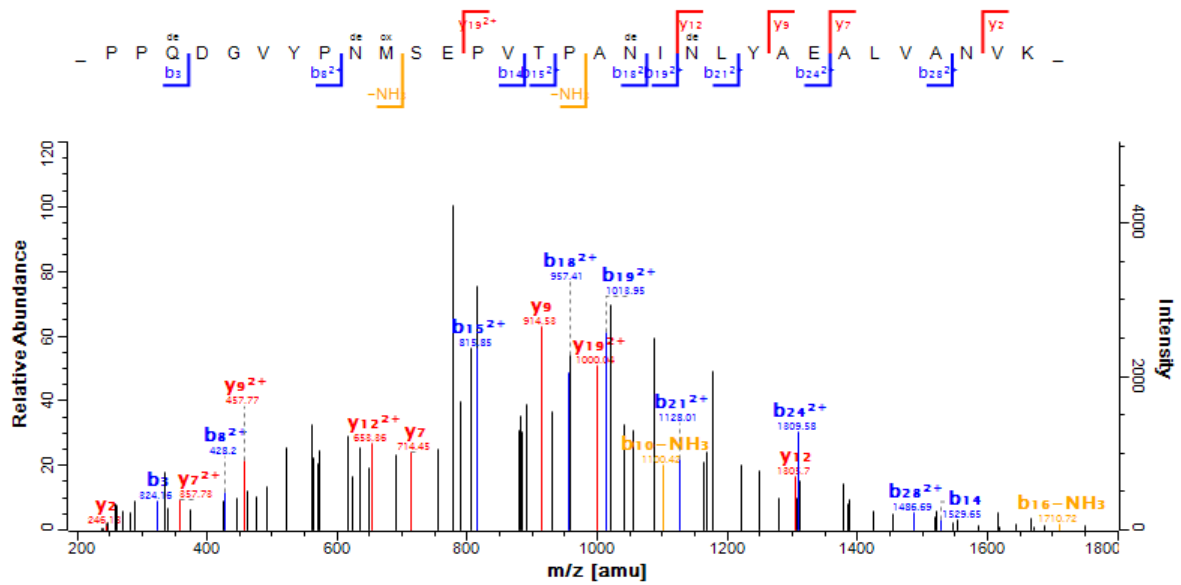
Number of Replicates (out of 8): 1

Best Match Score: 46.399

Best Match Posterior Error Probability: 0.0041571

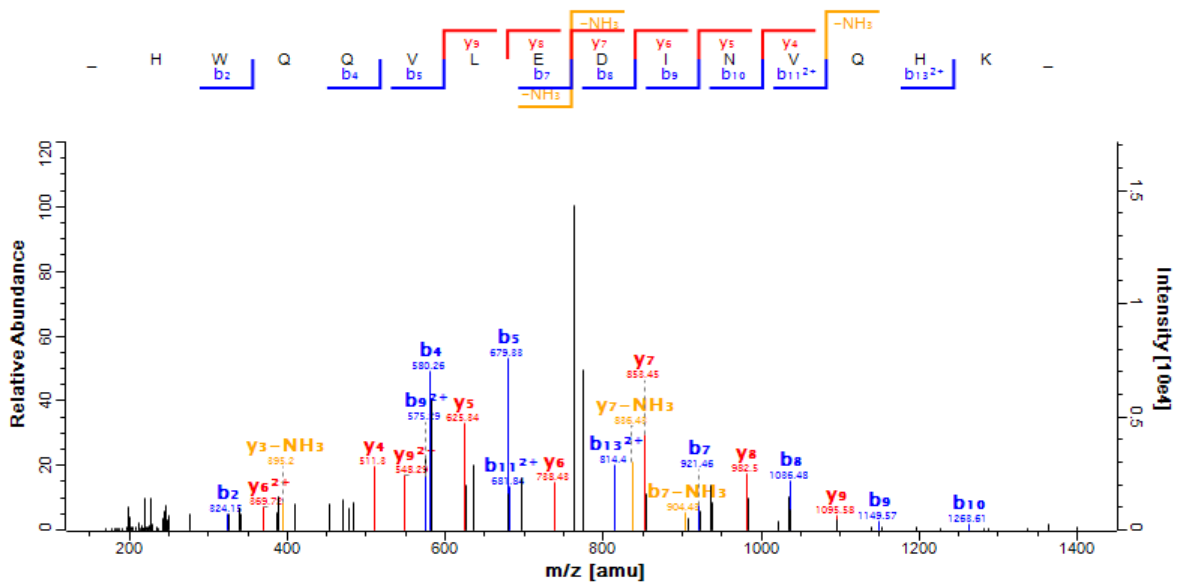
Best Match Spectrum:

Scan number 81397 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MAN2B2



Protein Group ID: 1340
Protein Accession Numbers: H0YAA8; Q9H204
Gene Names: MED28
Peptide Sequence: HWQQVLEDINVQHK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 96.866
Best Match Posterior Error Probability: 0.00054379
Best Match Spectrum:

Scan number 43400 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MED28



Protein Group ID: 1341

Protein Accession Numbers: Q7Z6I8; Q7Z6I8-2; H0YAE0

Gene Names: C5orf24

Peptide Sequence: AADQFDIYSSQSK

Total Number of Spectra: 1

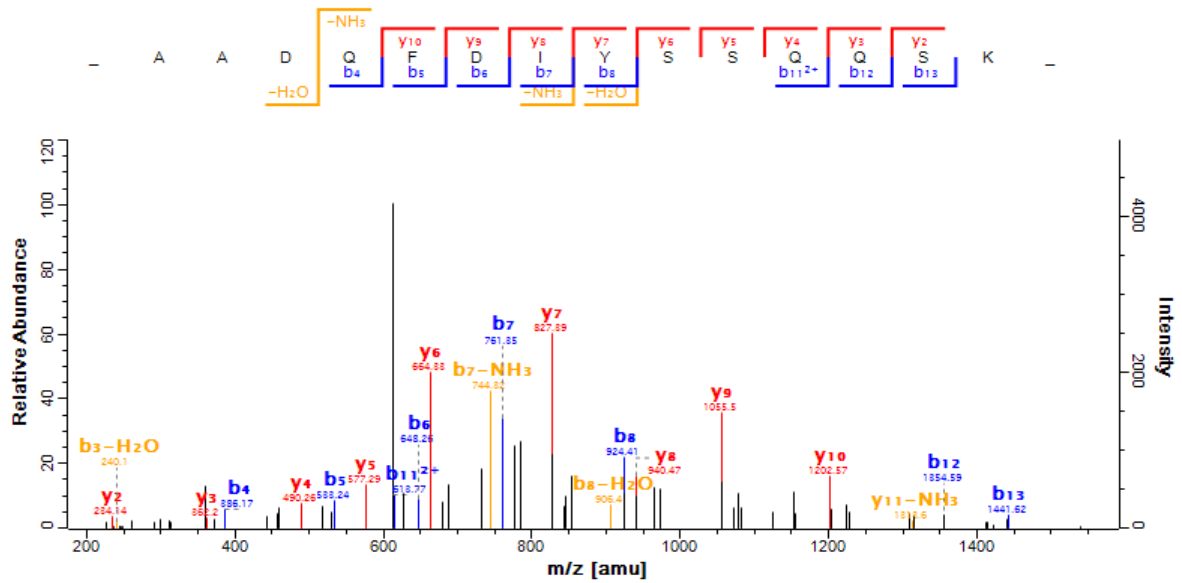
Number of Replicates (out of 8): 1

Best Match Score: 96.163

Best Match Posterior Error Probability: 0.0023271

Best Match Spectrum:

Scan number 30168 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** C5orf24



Protein Group ID: 1346

Protein Accession Numbers: Q8TEY7; Q8TEY7-2; Q8TEY7-3; H0YCV3; H0YD08

Gene Names: USP33

Peptide Sequence: ISTHVSFPLEGLDLPQLPFLAK

Total Number of Spectra: 1

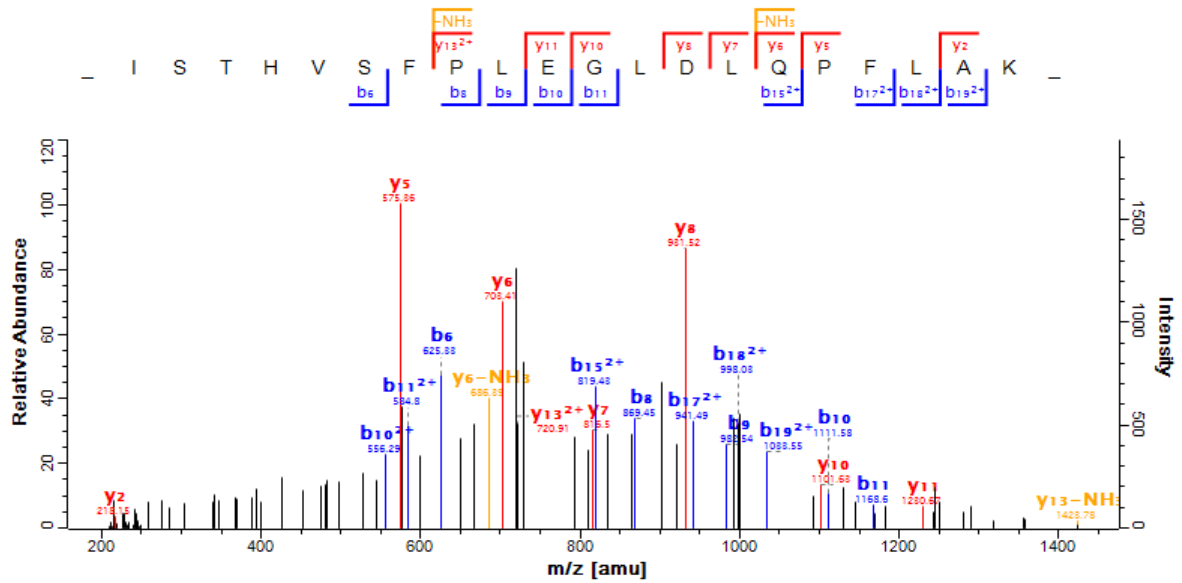
Number of Replicates (out of 8): 1

Best Match Score: 69.188

Best Match Posterior Error Probability: 0.002106

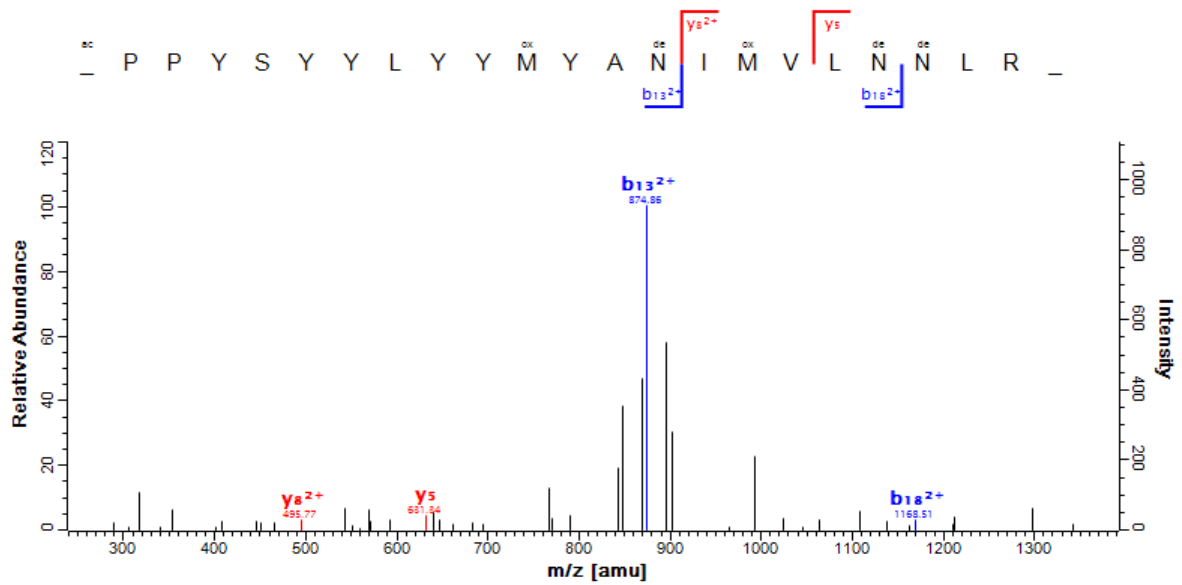
Best Match Spectrum:

Scan number 84050 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** USP33



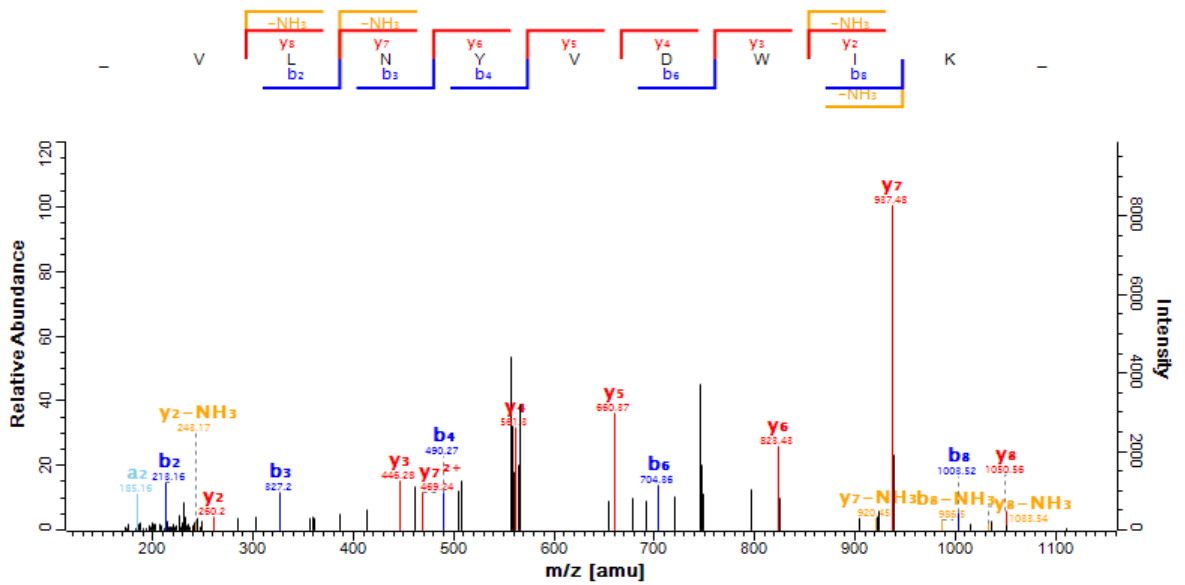
Protein Group ID: 1350
Protein Accession Numbers: H0YDY8
Gene Names: AMPD3
Peptide Sequence: PPYSYYLYYMYANIMVLLNNLR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 12.663
Best Match Posterior Error Probability: 0.0036502
Best Match Spectrum:

Scan number 12817 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** AMPD3



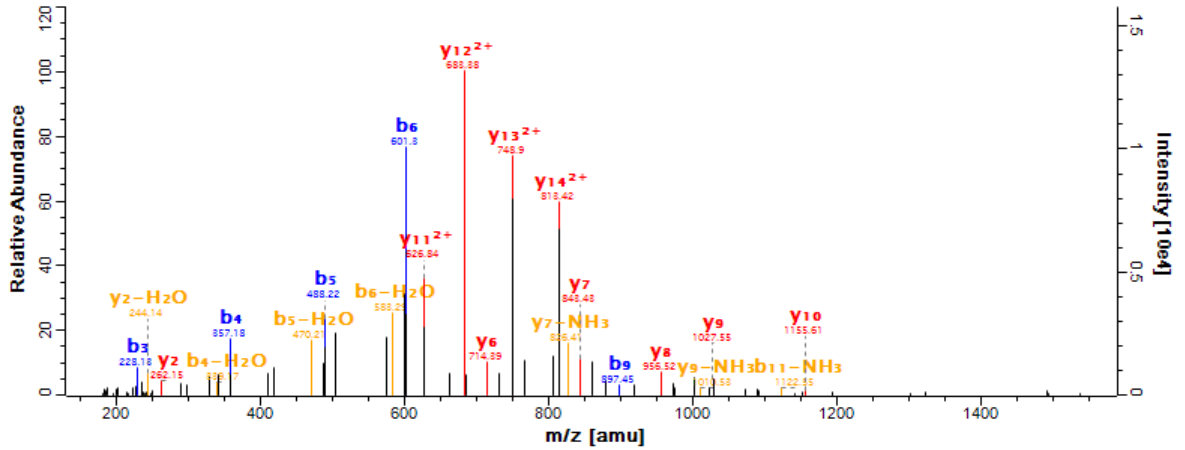
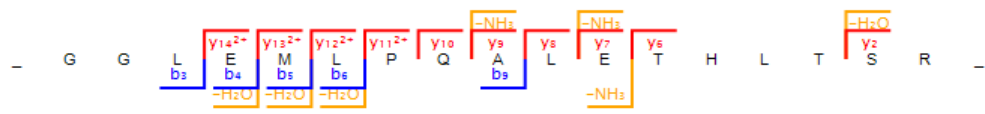
Protein Group ID: 1356
Protein Accession Numbers: P00736; H0YFH3
Gene Names: CIR
Peptide Sequence: VLNYVDWIK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 104.05
Best Match Posterior Error Probability: 0.0014539
Best Match Spectrum:

Scan number 59712 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CIR



Protein Group ID: 1357
Protein Accession Numbers: P50336; H0YFP3
Gene Names: PPOX
Peptide Sequence: GGLEMLPQALEHTSR
Total Number of Spectra: 9
Number of Replicates (out of 8): 6
Best Match Score: 101.42
Best Match Posterior Error Probability: 0.00016293
Best Match Spectrum:

Scan number 65295 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** PPOX



Protein Group ID: 1358

Protein Accession Numbers: Q9UJ78; H0YH25; Q9UJ78-5; Q9UJ78-1

Gene Names: ZMYM5

Peptide Sequence: QNFQPTAQQQLTKPAK

Total Number of Spectra: 1

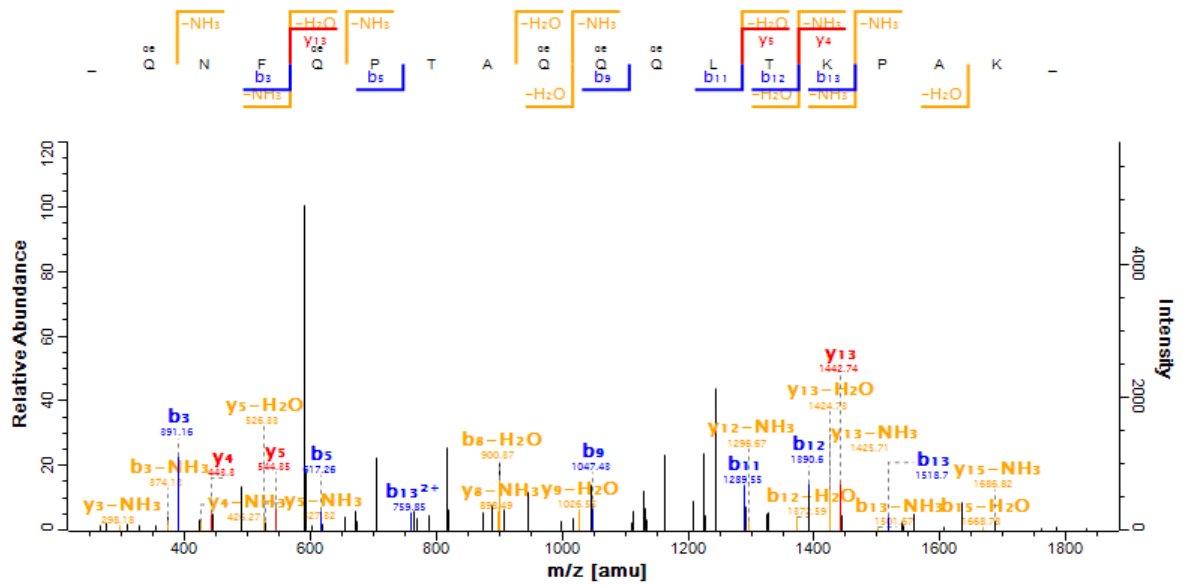
Number of Replicates (out of 8): 1

Best Match Score: 102.5

Best Match Posterior Error Probability: 0.0018186

Best Match Spectrum:

Scan number 29425 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ZMYM5



Protein Group ID: 1363

Protein Accession Numbers: P51948; H0YJF2; H0YJ92

Gene Names: MNAT1

Peptide Sequence: QAFLDELESSDLPVALLA QHK

Total Number of Spectra: 3

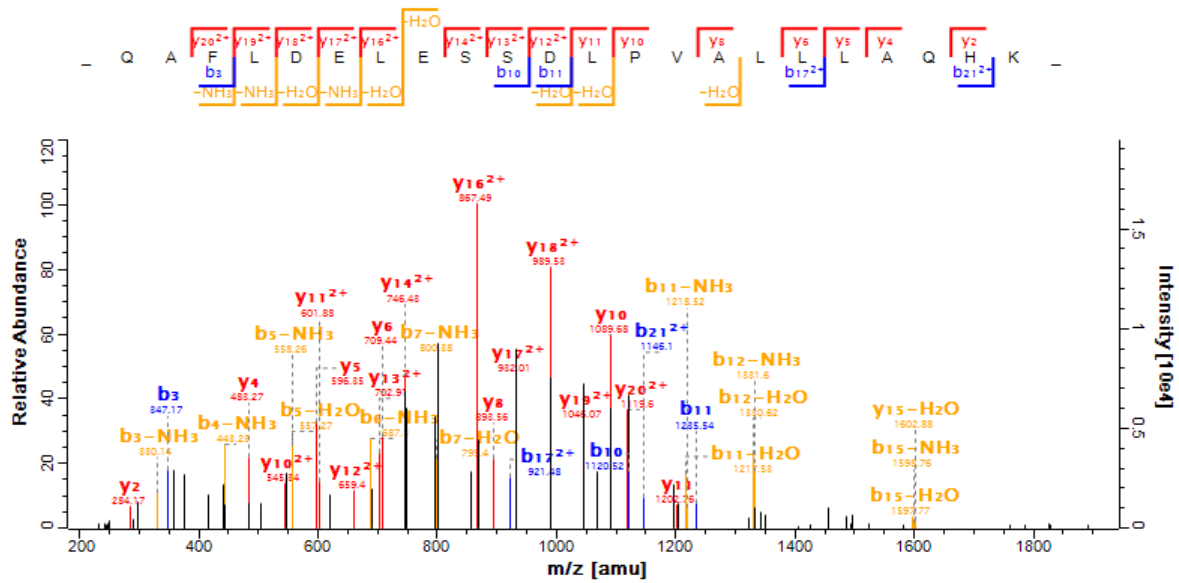
Number of Replicates (out of 8): 3

Best Match Score: 106.28

Best Match Posterior Error Probability: 4.57E-06

Best Match Spectrum:

Scan number	89158	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	MNAT1



Protein Group ID: 1366

Protein Accession Numbers: Q5J8M3; Q5J8M3-2; Q5J8M3-3; H0YLP8; H0YNK8; H0YNK0; H0YK61

Gene Names: TMEM85

Peptide Sequence: GSGQGDSLYPVGYLDK

Total Number of Spectra: 8

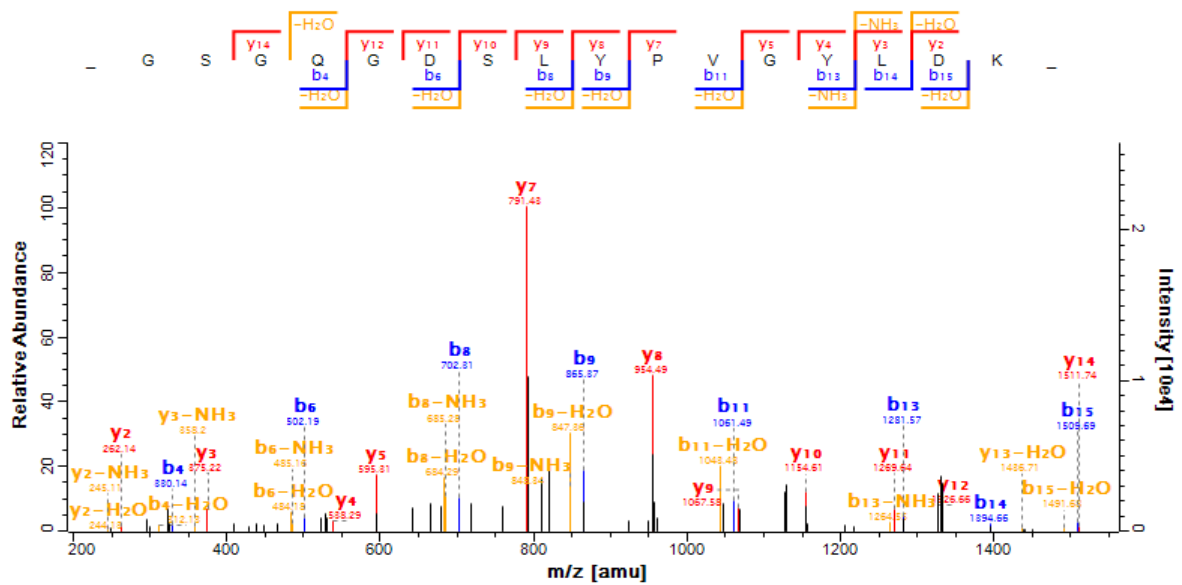
Number of Replicates (out of 8): 5

Best Match Score: 168.05

Best Match Posterior Error Probability: 8.24E-11

Best Match Spectrum:

Scan number 46791 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS: CID **Genenames** TMEM85



Protein Group ID: 1368

Protein Accession Numbers: Q9NZD8; H0YKB0; H0YMB7

Gene Names: SPG21

Peptide Sequence: VHLFGASLGGFLAQQK

Total Number of Spectra: 5

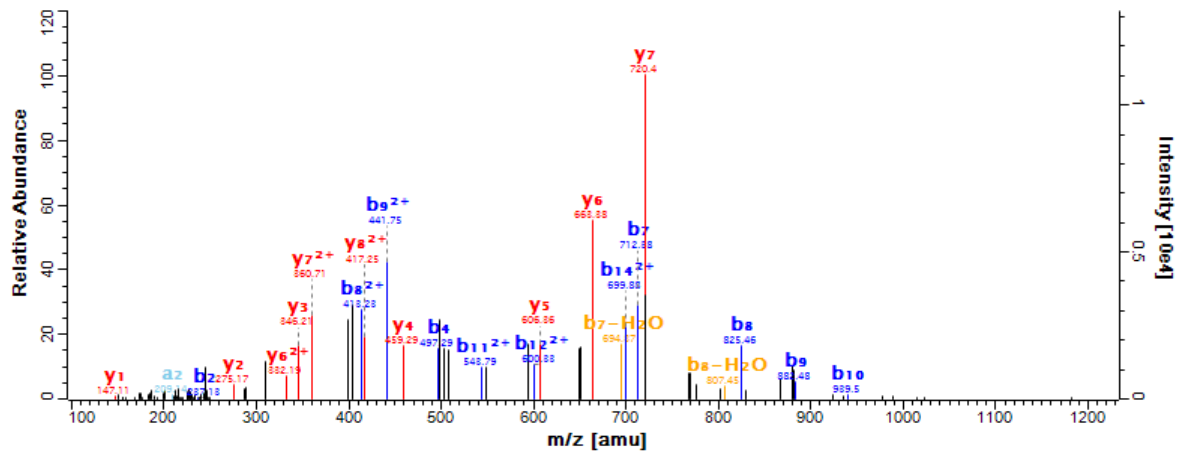
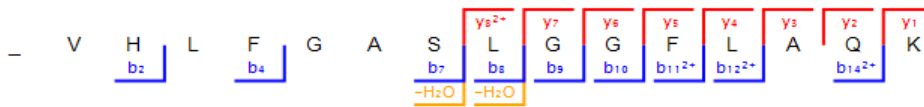
Number of Replicates (out of 8): 5

Best Match Score: 112.5

Best Match Posterior Error Probability: 0.0001104

Best Match Spectrum:

Scan number	64483	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	SPG21



Protein Group ID: 1370

Protein Accession Numbers: Q8N4P3; H0YKT9; H0YNP9; Q8N4P3-2

Gene Names: HDDC3

Peptide Sequence: RLQVEQAPHSSPGAK

Total Number of Spectra: 9

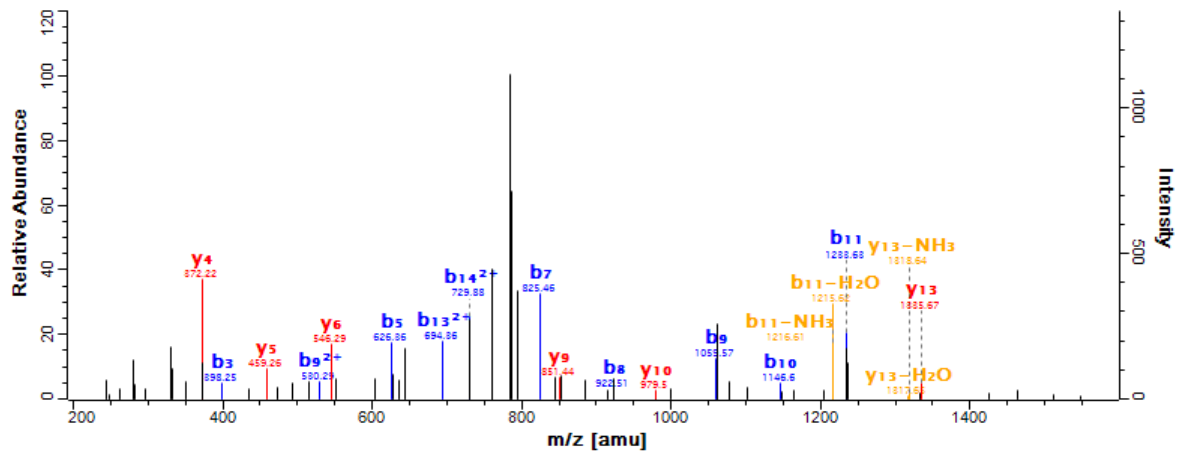
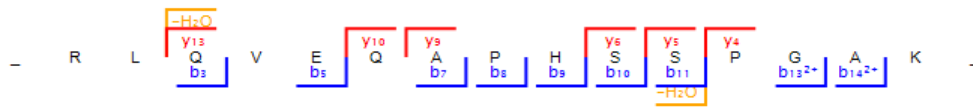
Number of Replicates (out of 8): 6

Best Match Score: 115.91

Best Match Posterior Error Probability: 0.000198

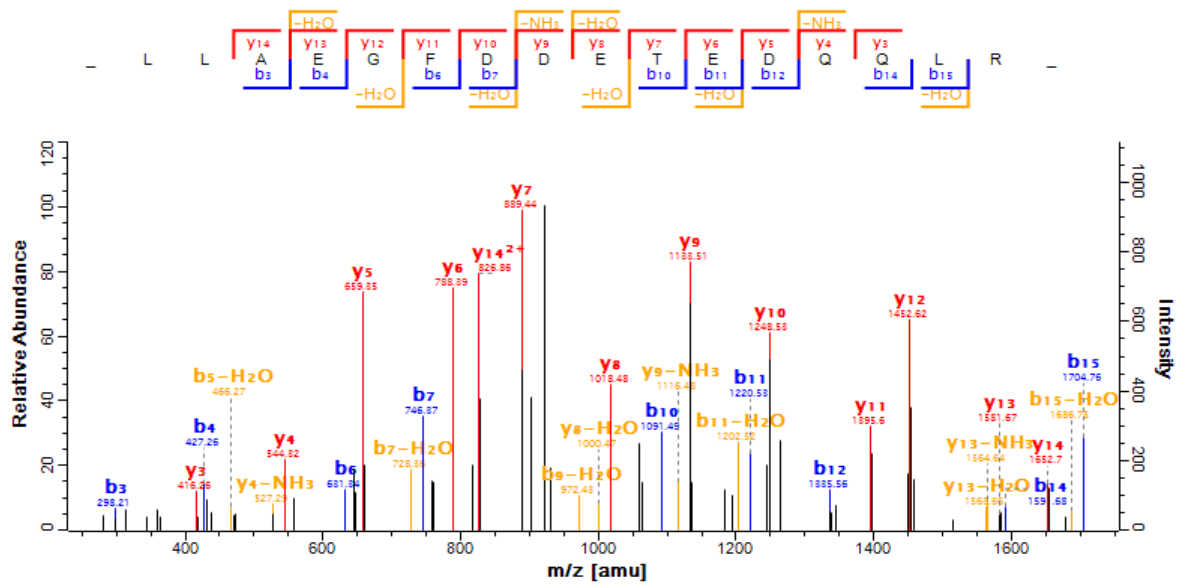
Best Match Spectrum:

Scan number	8237	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	HDDC3



Protein Group ID: 1372
Protein Accession Numbers: Q9UPM8; H0YKX4
Gene Names: AP4E1
Peptide Sequence: LLAEGFDDETEDQQLR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 178.03
Best Match Posterior Error Probability: 1.01E-14
Best Match Spectrum:

Scan number 42455 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** AP4E1



Protein Group ID: 1378

Protein Accession Numbers: O94788; O94788-3; H0YMG7; O94788-2; H0YM00

Gene Names: ALDH1A2

Peptide Sequence: IFVEESIYEEFVR

Total Number of Spectra: 1

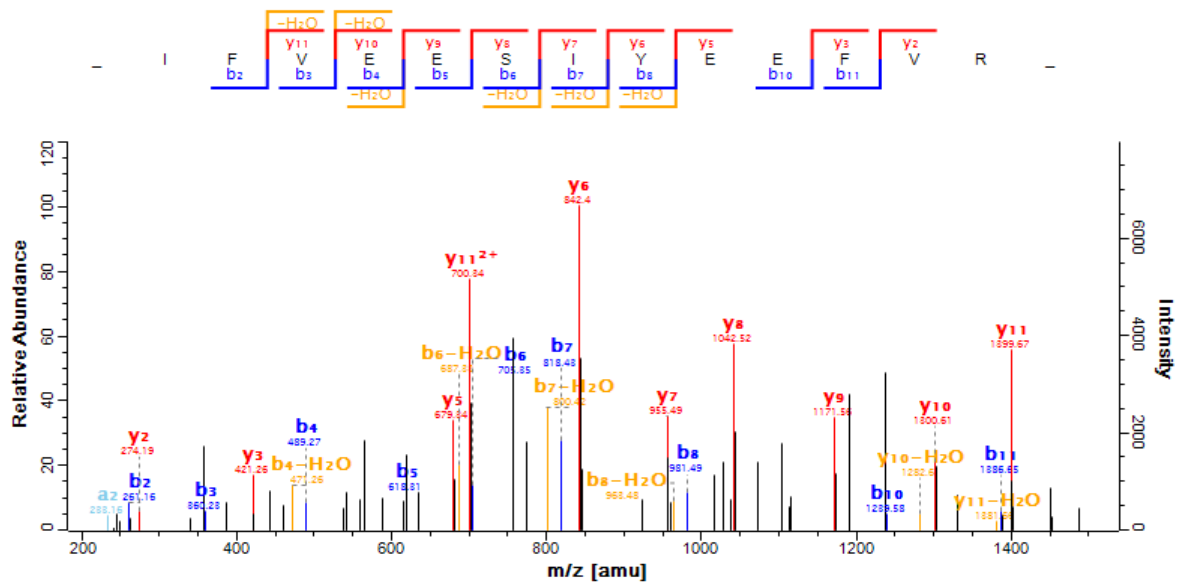
Number of Replicates (out of 8): 1

Best Match Score: 155.86

Best Match Posterior Error Probability: 1.99E-07

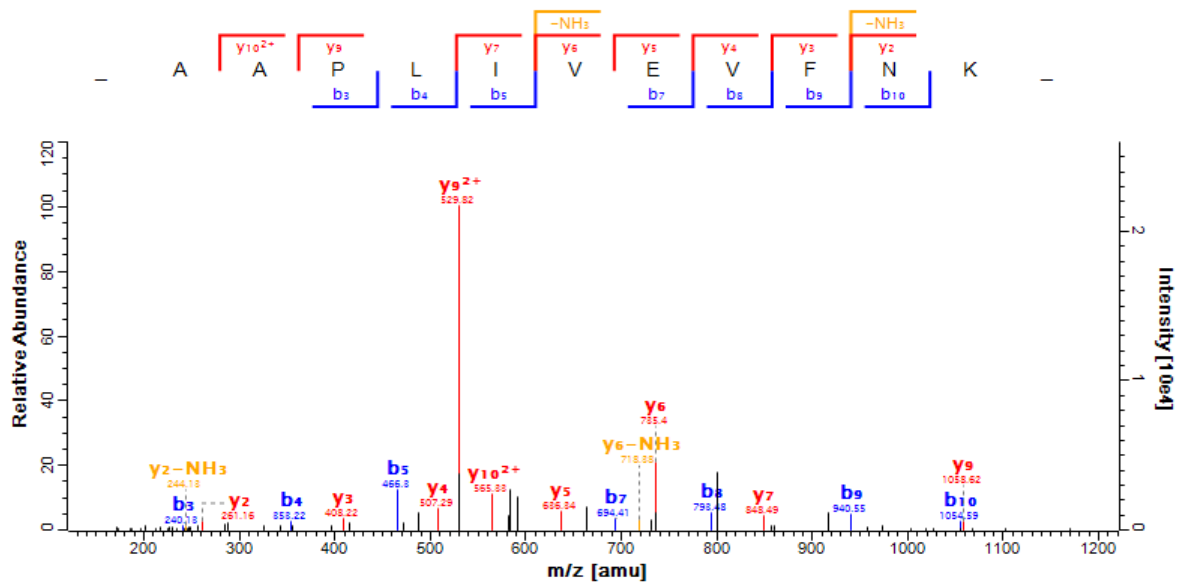
Best Match Spectrum:

Scan number	80074	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	ALDH1A2



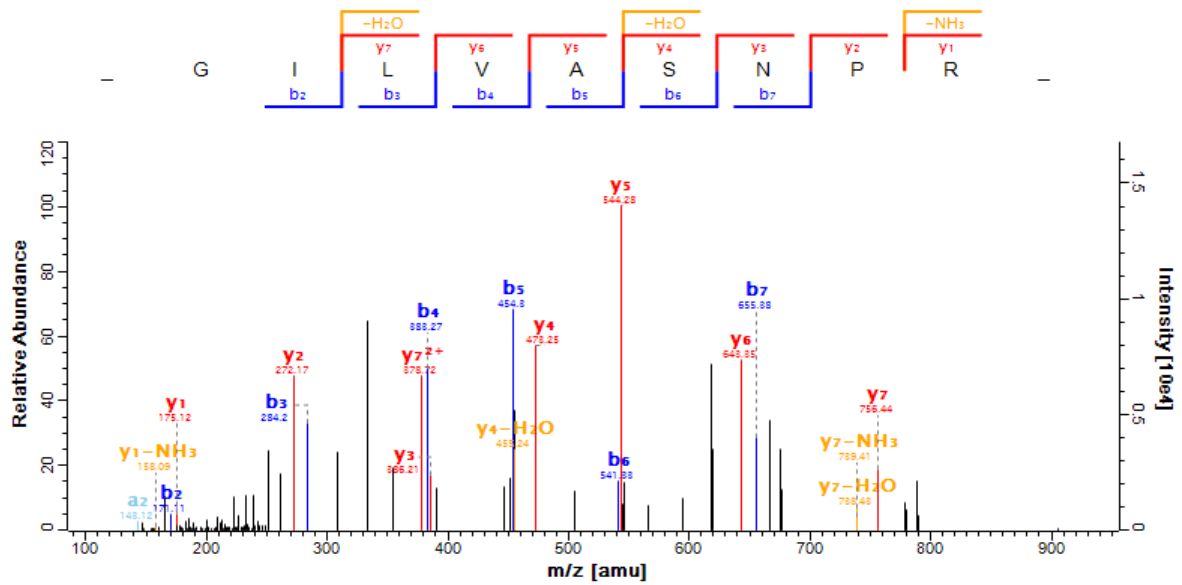
Protein Group ID: 1379
Protein Accession Numbers: Q92610; H0YM74
Gene Names: ZNF592
Peptide Sequence: AAPLIVEVFNK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 104.82
Best Match Posterior Error Probability: 0.00034383
Best Match Spectrum:

Scan number 62255 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ZNF592



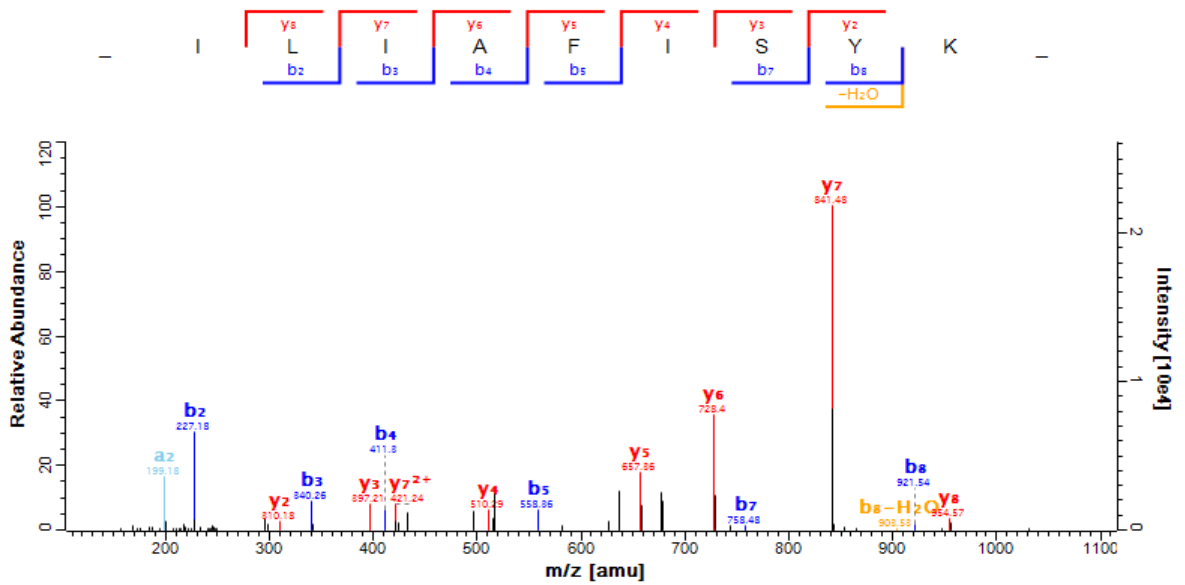
Protein Group ID: 1380
Protein Accession Numbers: Q00978; H0YMB0
Gene Names: IRF9
Peptide Sequence: GILVASNP
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 128.36
Best Match Posterior Error Probability: 0.00017413
Best Match Spectrum:

Scan number 17763 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** IRF9



Protein Group ID: 1384
Protein Accession Numbers: Q8TCT8; H0YNA7
Gene Names: SPPL2A
Peptide Sequence: ILIAFISYK
Total Number of Spectra: 8
Number of Replicates (out of 8): 8
Best Match Score: 131.44
Best Match Posterior Error Probability: 0.00010739
Best Match Spectrum:

Scan number 62448 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SPPL2A



Protein Group ID: 1391

Protein Accession Numbers: Q9BV79; Q9BV79-2; H3BM30; Q5SYU3

Gene Names: MECR

Peptide Sequence: SLGAEHVITEELR

Total Number of Spectra: 1

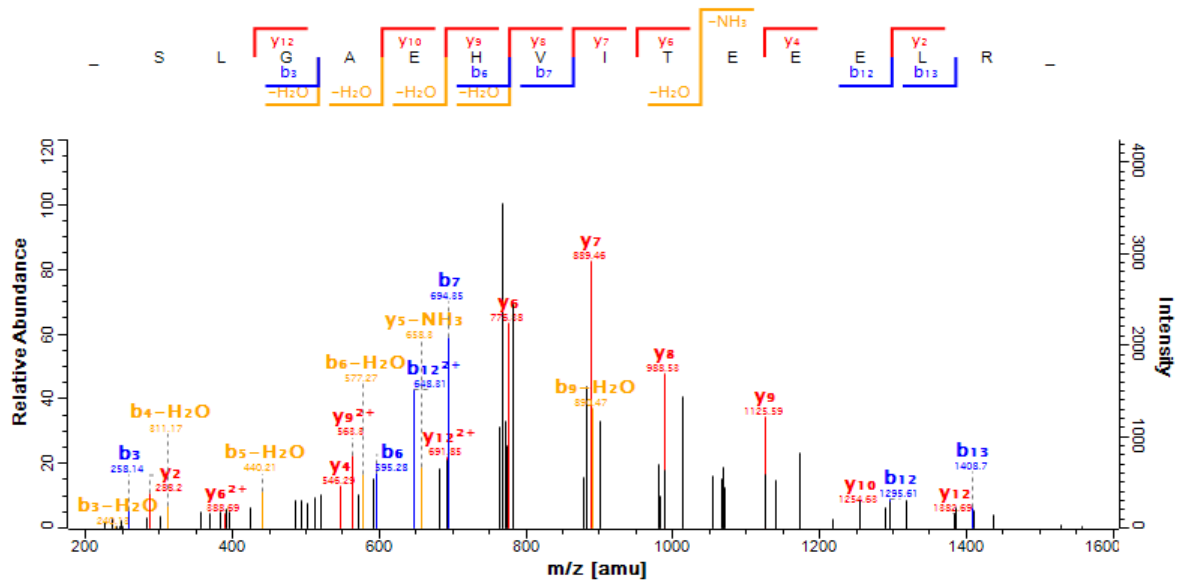
Number of Replicates (out of 8): 1

Best Match Score: 84.468

Best Match Posterior Error Probability: 0.0021471

Best Match Spectrum:

Scan number	34249	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	MECR



Protein Group ID: 1393

Protein Accession Numbers: Q9BVC4; H3BSZ4; Q9BVC4-4; H3BN58; H3BPT1; H3BR25; H3BPU5; H3BM50; H3BR38

Gene Names: MLST8

Peptide Sequence: TVQHQSQVNALEVT PDR

Total Number of Spectra: 3

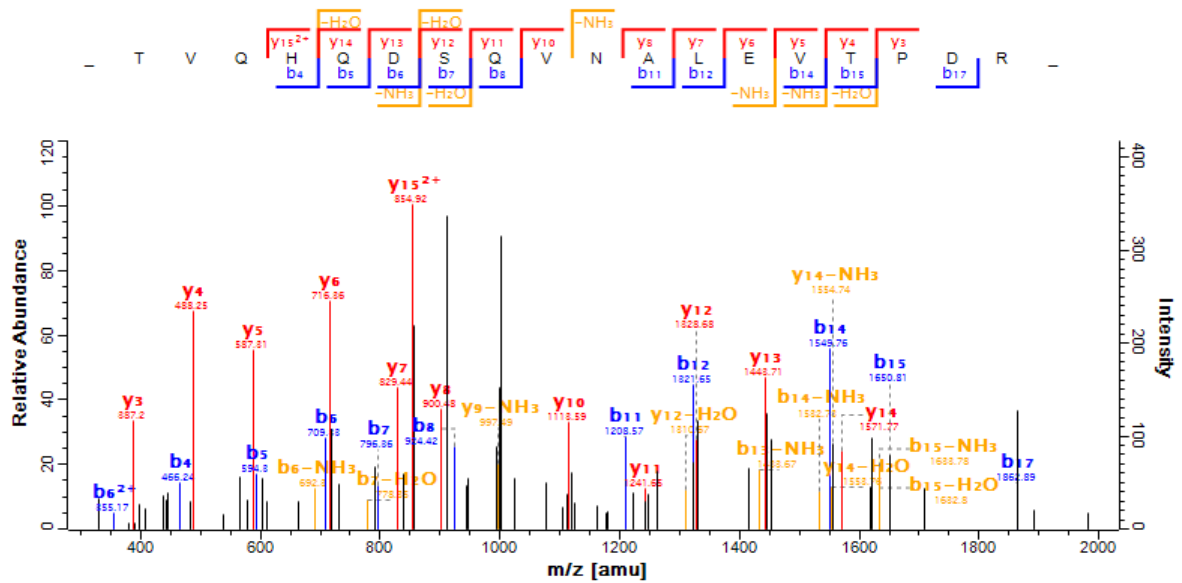
Number of Replicates (out of 8): 2

Best Match Score: 138.46

Best Match Posterior Error Probability: 4.48E-11

Best Match Spectrum:

Scan number 24803 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS: CID **Genenames** MLST8



Protein Group ID: 1397

Protein Accession Numbers: Q9BTX3; H3BMW4; J3KRY7

Gene Names: TMEM208

Peptide Sequence: AAFSEDGALMDGGMDLNMEQGM AEHLK

Total Number of Spectra: 2

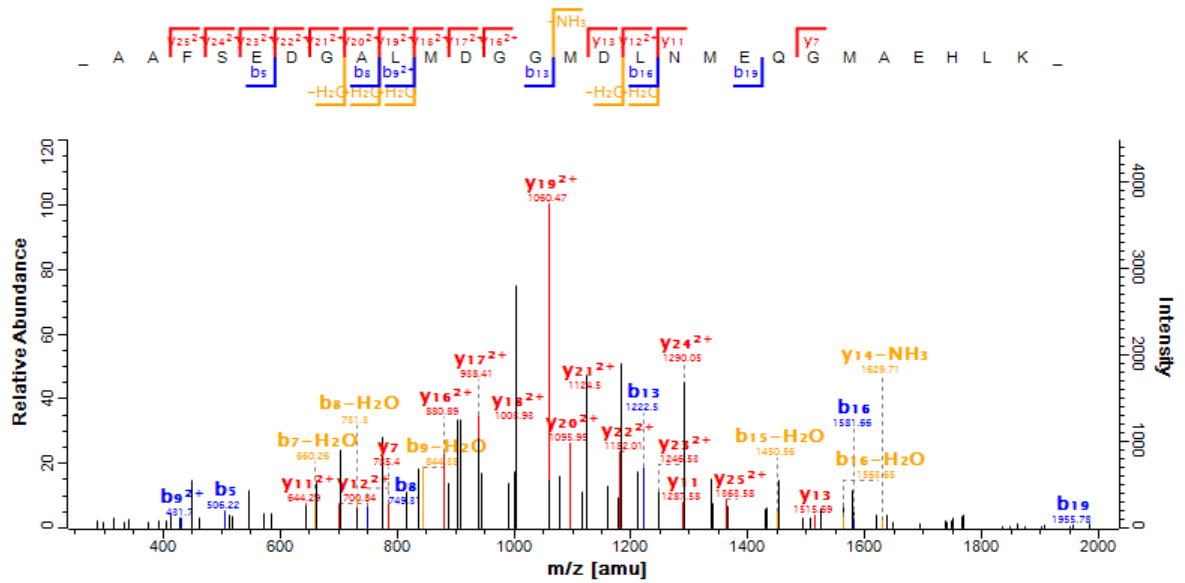
Number of Replicates (out of 8): 2

Best Match Score: 71.756

Best Match Posterior Error Probability: 0.00017176

Best Match Spectrum:

Scan number 67134 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TMEM208



Protein Group ID: 1398

Protein Accession Numbers: H3BUT6; Q9NTJ4; H3BQY8; H3BMX2

Gene Names: MAN2C1

Peptide Sequence: QFLQGQNFFLQEFQK

Total Number of Spectra: 2

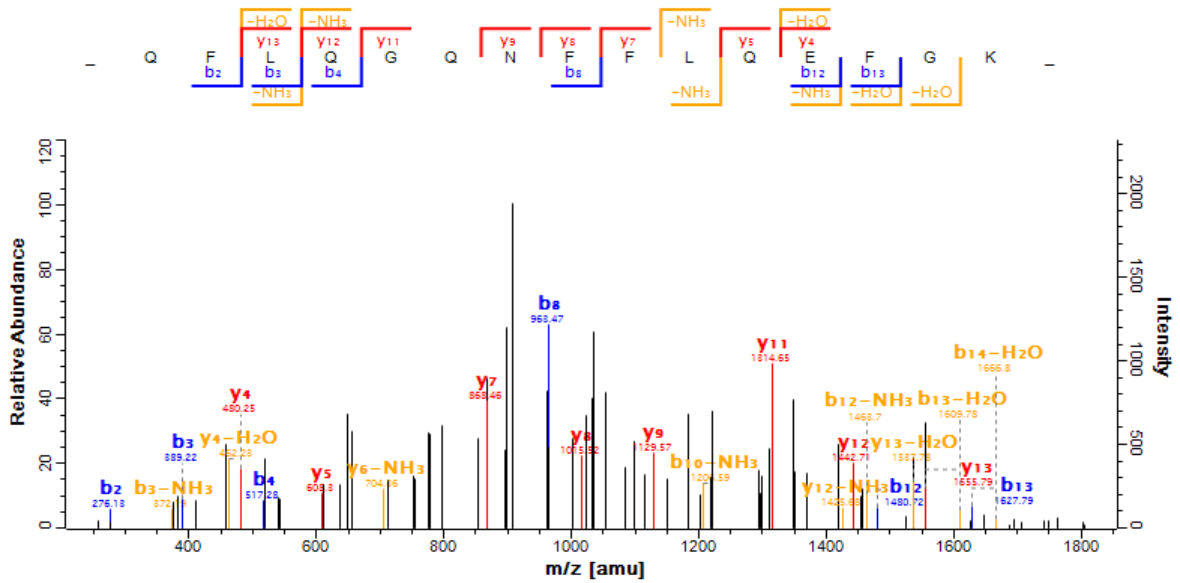
Number of Replicates (out of 8): 2

Best Match Score: 85.006

Best Match Posterior Error Probability: 0.0015016

Best Match Spectrum:

Scan number	74936	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	MAN2C1



Protein Group ID: 1399

Protein Accession Numbers: Q9GZU8; H3BU93; H3BMX9; H3BUL4; H3BP64; H3BSY6; H3BTP8; H3BTI2; H3BQQ6

Gene Names: FAM192A

Peptide Sequence: GLDEDETNFLDEVSR

Total Number of Spectra: 8

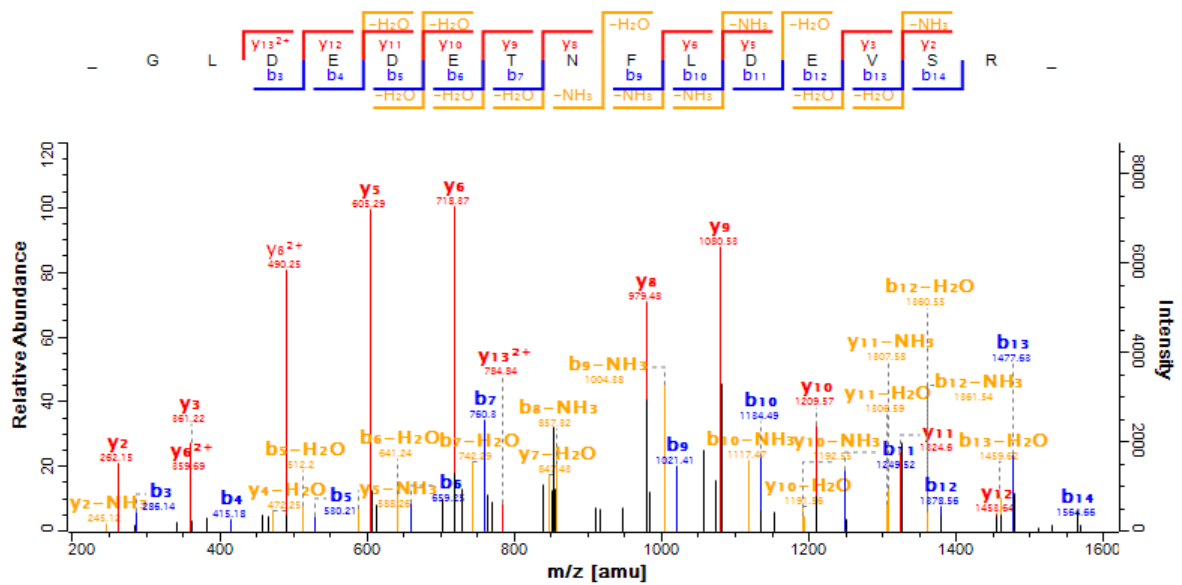
Number of Replicates (out of 8): 7

Best Match Score: 266.15

Best Match Posterior Error Probability: 3.73E-105

Best Match Spectrum:

Scan number 57927 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS: CID **Genenames** FAM192A



Protein Group ID: 1401

Protein Accession Numbers: Q9NVM4; Q9NVM4-3; H3BNC0; Q9NVM4-4; H3BPZ8; H3BSS9

Gene Names: PRMT7

Peptide Sequence: ANILVTELFDTLELILIGEGALPSYEHAHR

Total Number of Spectra: 1

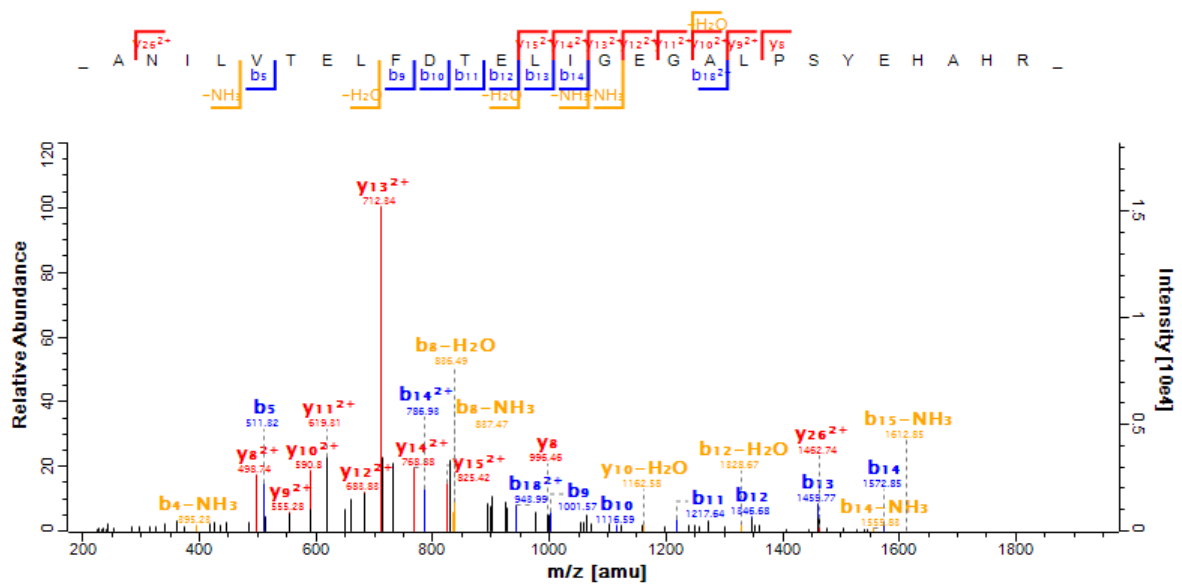
Number of Replicates (out of 8): 1

Best Match Score: 63.398

Best Match Posterior Error Probability: 0.00041501

Best Match Spectrum:

Scan number	88728	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	PRMT7



Protein Group ID: 1403

Protein Accession Numbers: Q9NWW5; H3BUT1; H3BUV4; H3BTY4; H3BNF1; H3BRN7

Gene Names: CLN6

Peptide Sequence: QHLGATGGPGAQLGASFLQAR

Total Number of Spectra: 6

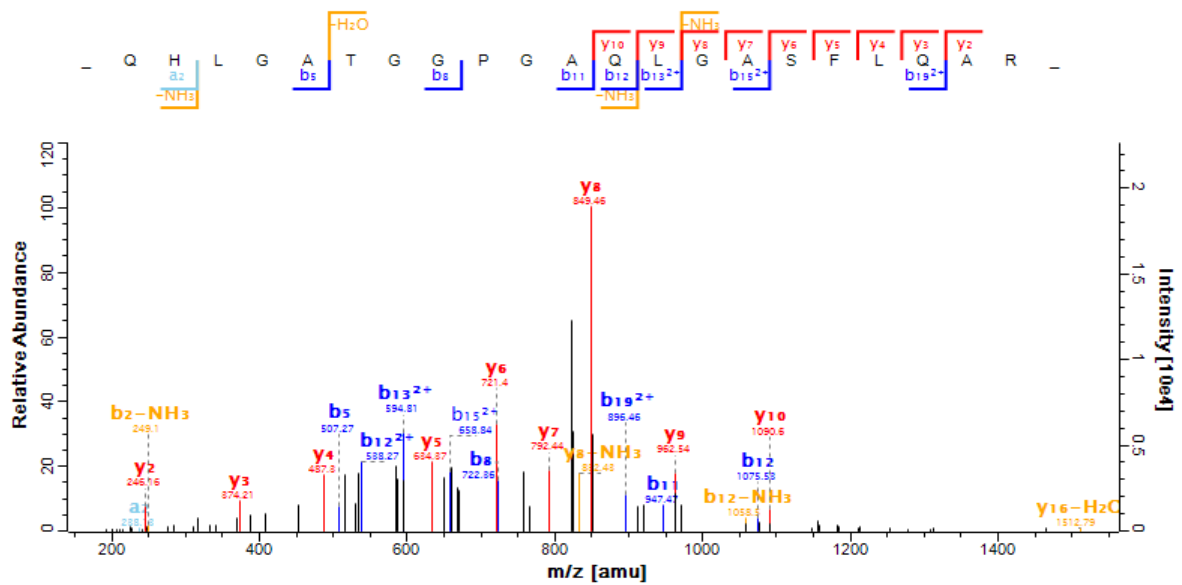
Number of Replicates (out of 8): 6

Best Match Score: 87.49

Best Match Posterior Error Probability: 0.00010132

Best Match Spectrum:

Scan number 48202 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CLN6



Protein Group ID: 1409

Protein Accession Numbers: Q8TBB5; Q8TBB5-3; H3BQ90; H3BQL0; H3BP99

Gene Names: KLHDC4

Peptide Sequence: KEEEDLEALIAHFQTLDAK

Total Number of Spectra: 7

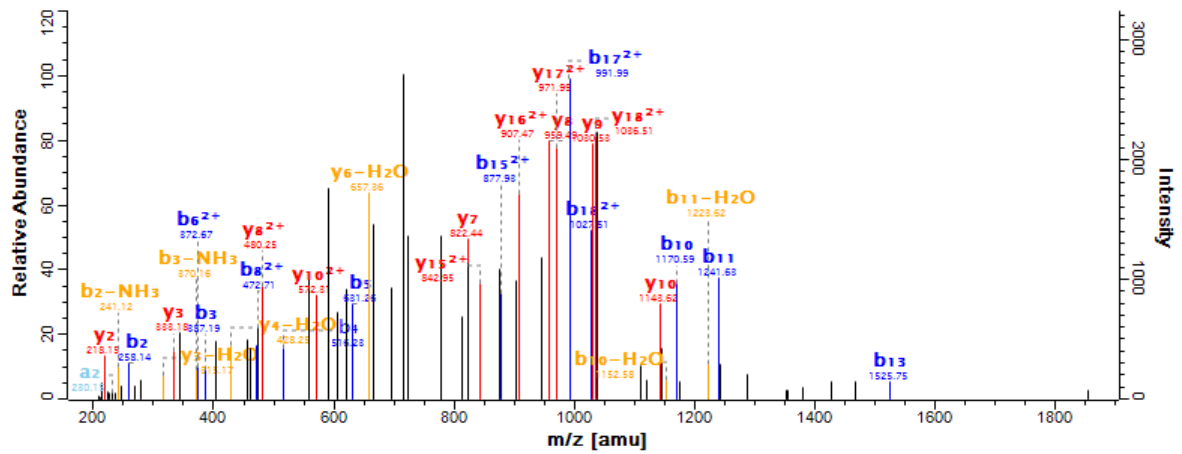
Number of Replicates (out of 8): 4

Best Match Score: 149.97

Best Match Posterior Error Probability: 2.75E-07

Best Match Spectrum:

Scan number 74241 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** KLHDC4



Protein Group ID: 1414

Protein Accession Numbers: Q96CD2; H3BRQ0; H3BQB0; H3BSE3; Q96CD2-2; H3BU63; H3BPW5

Gene Names: PPCDC

Peptide Sequence: PLLFCPAMNTAMWEHPITAAQQVDQLK

Total Number of Spectra: 1

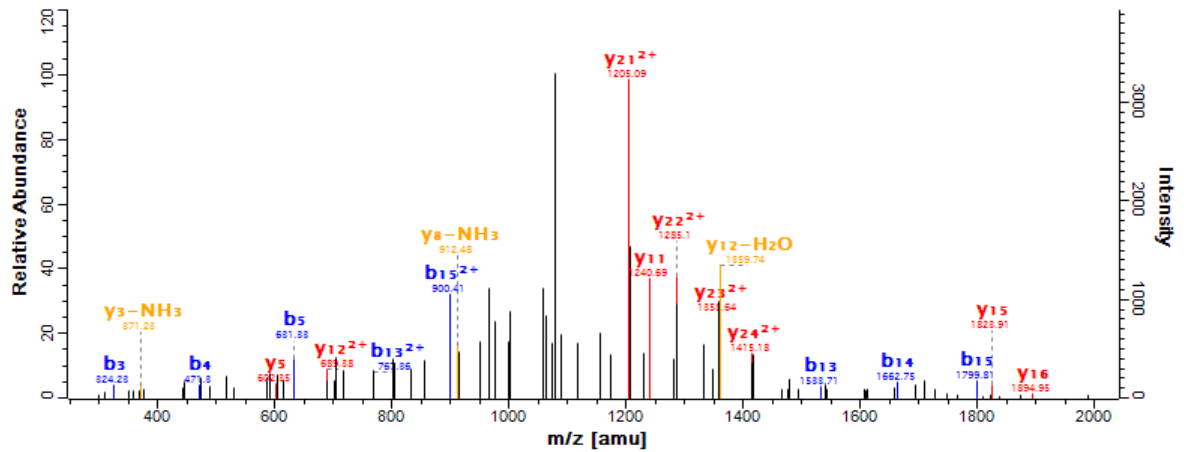
Number of Replicates (out of 8): 1

Best Match Score: 55.228

Best Match Posterior Error Probability: 0.0022872

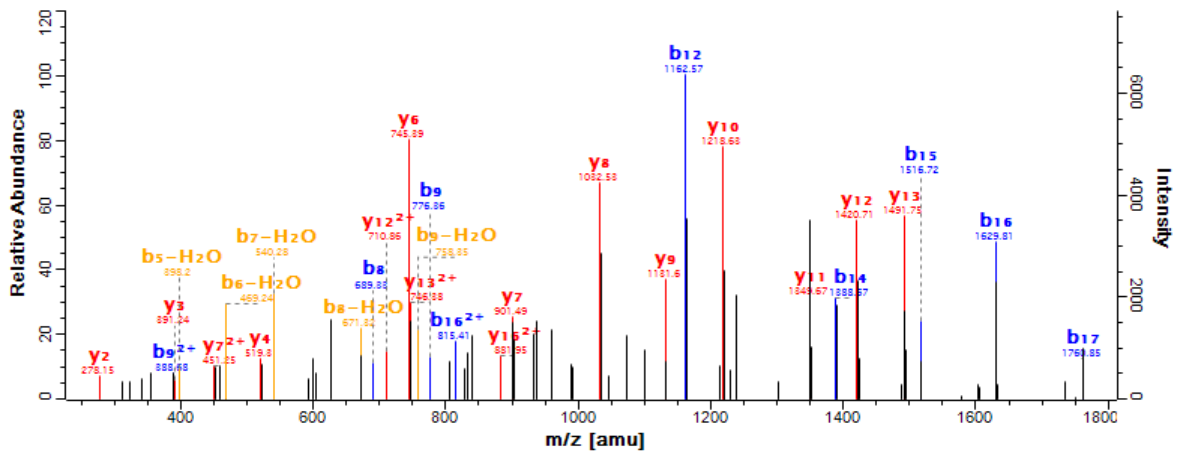
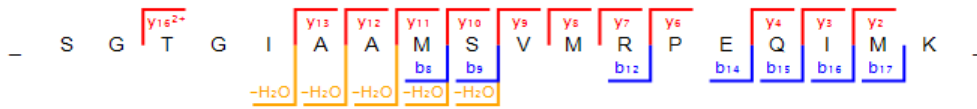
Best Match Spectrum:

Scan number	78528	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS: CID	Genenames	PPCDC



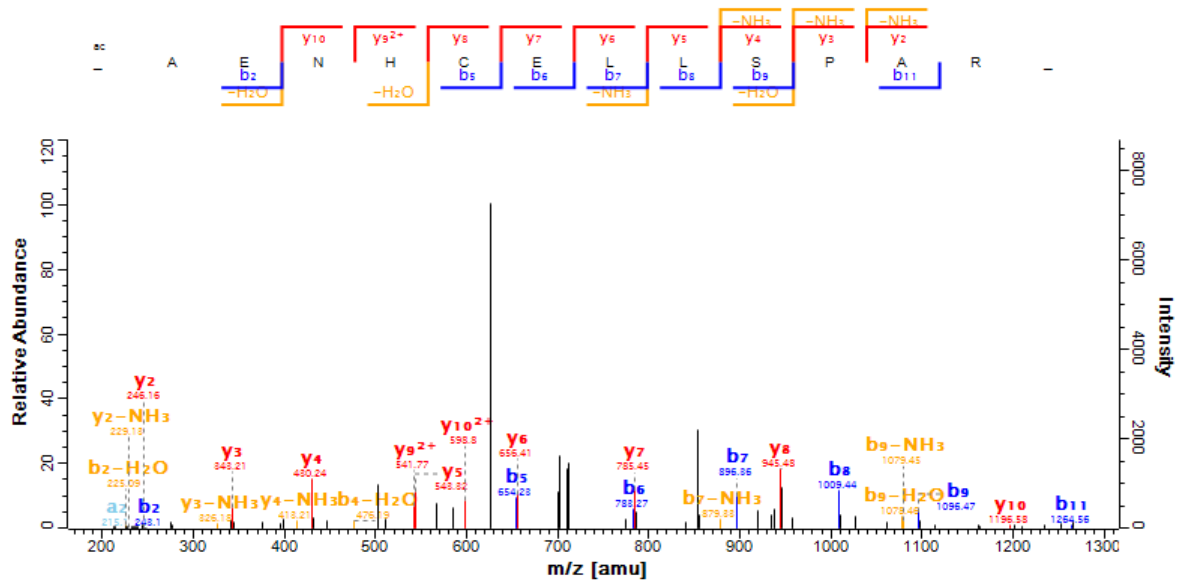
Protein Group ID: 1419
Protein Accession Numbers: P27449; H3BR50
Gene Names: ATP6V0C
Peptide Sequence: SGTGIAAMSVMRP EQIMK
Total Number of Spectra: 3
Number of Replicates (out of 8): 2
Best Match Score: 110.77
Best Match Posterior Error Probability: 0.00025064
Best Match Spectrum:

Scan number 52855 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ATP6V0C



Protein Group ID: 1427
Protein Accession Numbers: H3BSS5; Q9NXV2
Gene Names: KCTD5
Peptide Sequence: AENHCELLSPAR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 120.84
Best Match Posterior Error Probability: 0.00017059
Best Match Spectrum:

Scan number 26713 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** KCTD5



Protein Group ID: 1428

Protein Accession Numbers: H3BSW6; Q2VPK5; Q2VPK5-5; Q2VPK5-3

Gene Names: CTU2

Peptide Sequence: LFSVPSVFTPAVDTK

Total Number of Spectra: 1

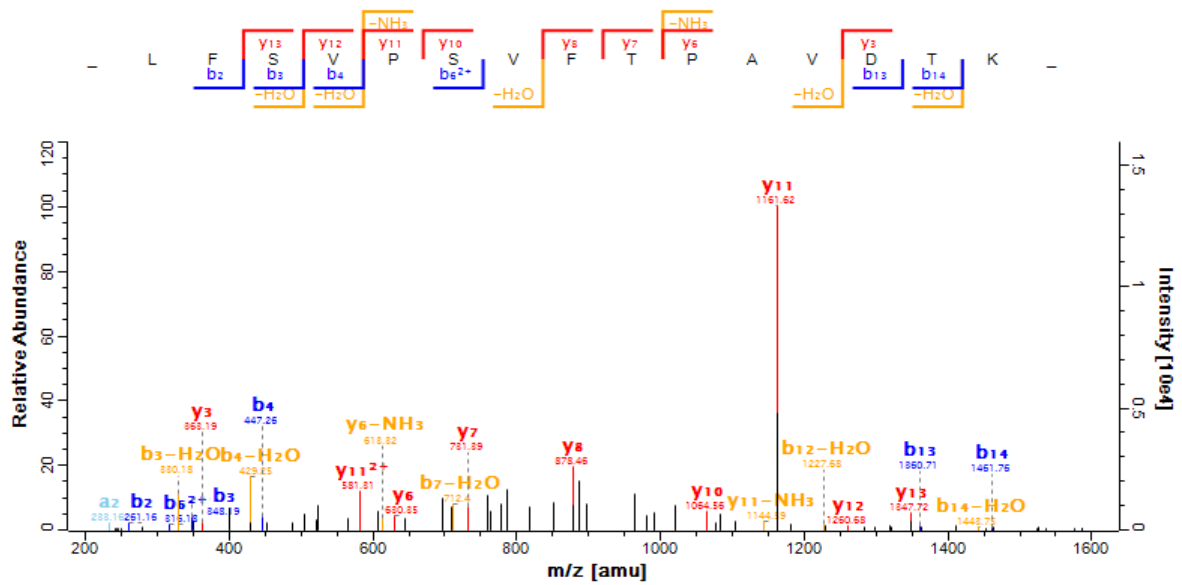
Number of Replicates (out of 8): 1

Best Match Score: 113.25

Best Match Posterior Error Probability: 0.00010472

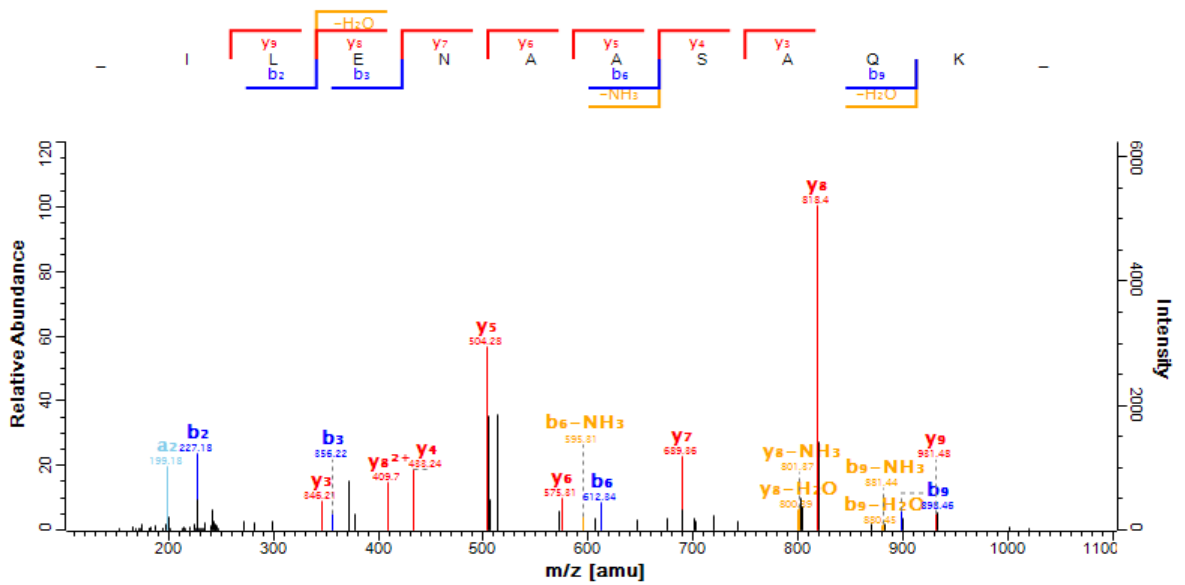
Best Match Spectrum:

Scan number	67188	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	CTU2



Protein Group ID: 1429
Protein Accession Numbers: Q9Y5N6; H3BT22
Gene Names: ORC6
Peptide Sequence: ILENAASAQK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 106.4
Best Match Posterior Error Probability: 0.00050108
Best Match Spectrum:

Scan number 6847 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ORC6



Protein Group ID: 1432

Protein Accession Numbers: Q9NXD2; Q9NXD2-3; H3BUS9

Gene Names: MTMR10

Peptide Sequence: KLEPVLLPGEIVVNEVNFVR

Total Number of Spectra: 3

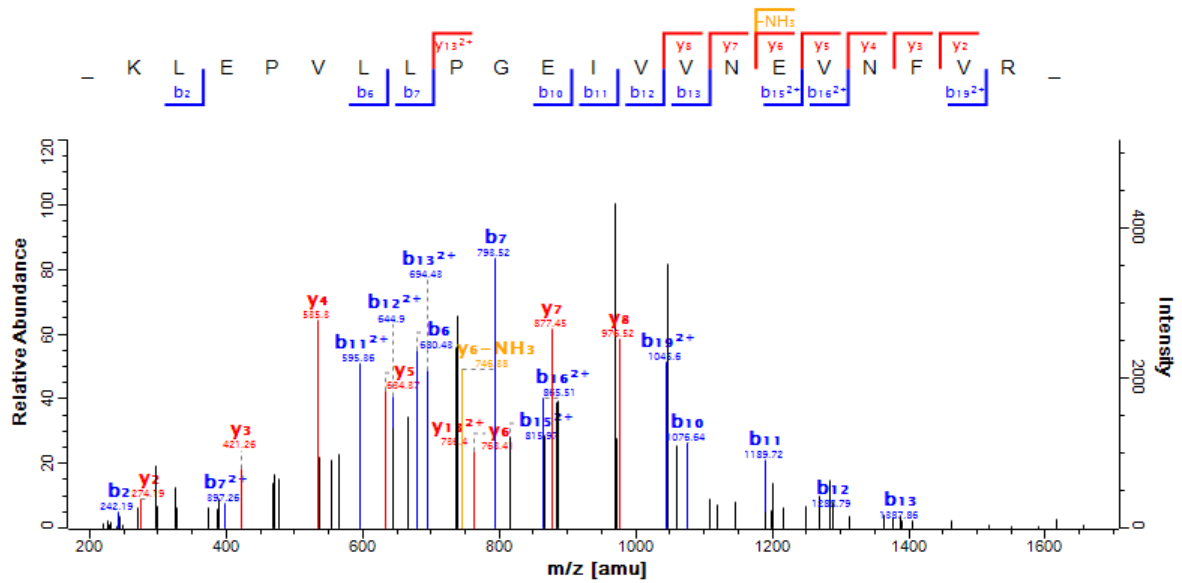
Number of Replicates (out of 8): 3

Best Match Score: 87.24

Best Match Posterior Error Probability: 0.00045104

Best Match Spectrum:

Scan number	83854	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	MTMR10



Protein Group ID: 1433

Protein Accession Numbers: Q8WV22; I3L1I3; H3BV05

Gene Names: NSMCE1

Peptide Sequence: AILEMEQYIR

Total Number of Spectra: 4

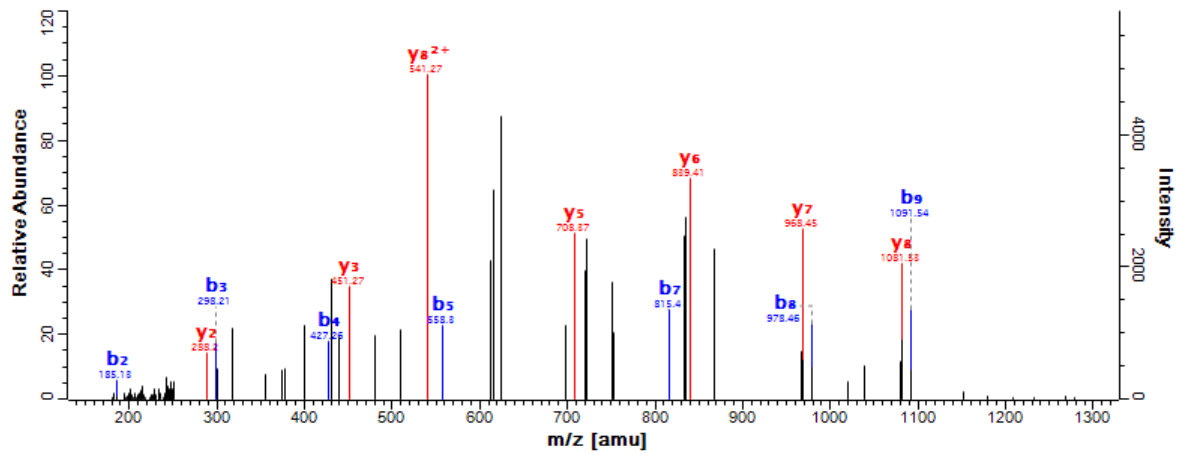
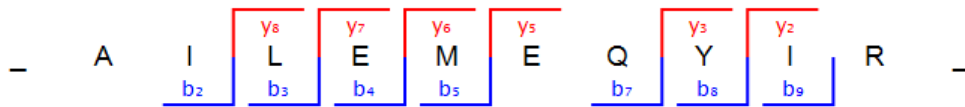
Number of Replicates (out of 8): 3

Best Match Score: 90.685

Best Match Posterior Error Probability: 0.0018902

Best Match Spectrum:

Scan number	53776	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	NSMCE1



Protein Group ID: 1439

Protein Accession Numbers: P39060; P39060-1; P39060-2; H7BXV5; H7C457

Gene Names: COL18A1

Peptide Sequence: DFQPVLHLVALNSPLSGGMR

Total Number of Spectra: 6

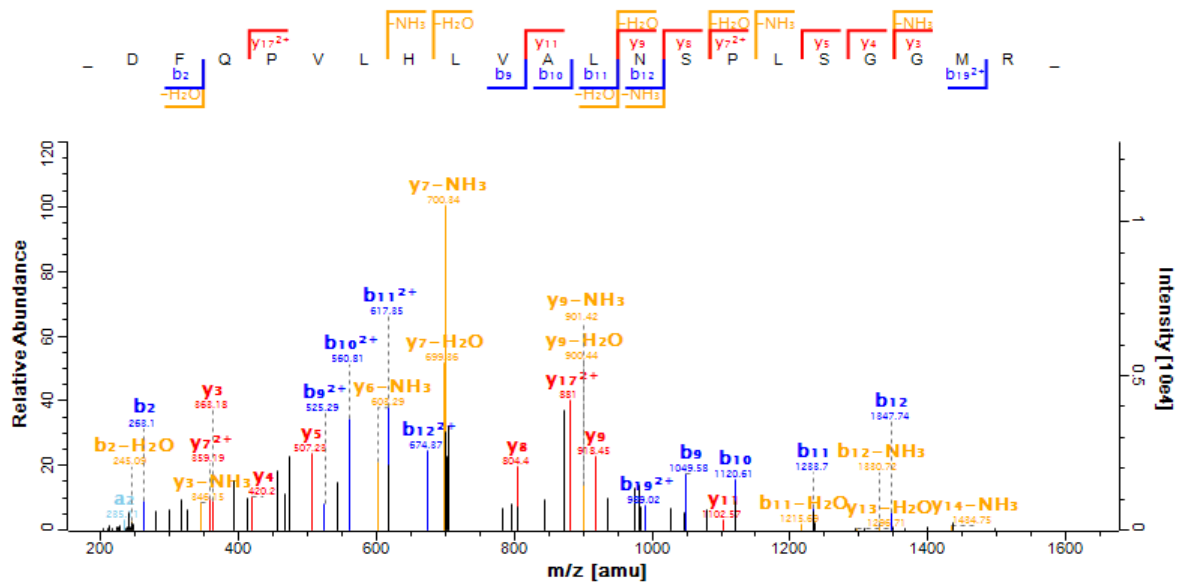
Number of Replicates (out of 8): 5

Best Match Score: 128.59

Best Match Posterior Error Probability: 2.18E-06

Best Match Spectrum:

Scan number 78108 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** COL18A1



Protein Group ID: 1442

Protein Accession Numbers: Q8IXI2-3; J9JIH9; Q8IXI2-2; Q8IXI2-5; Q8IXI2; H7BXZ6; Q8IXI2-4; J3KXS7

Gene Names: RHOT1

Peptide Sequence: ICFNTPLAPQALEDVK

Total Number of Spectra: 2

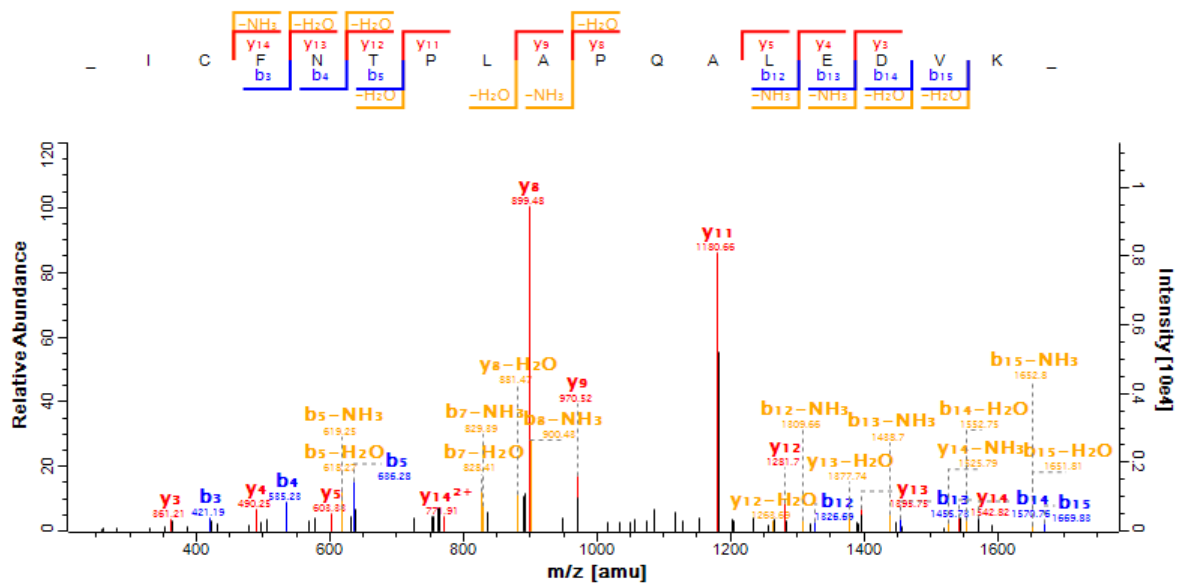
Number of Replicates (out of 8): 2

Best Match Score: 144.29

Best Match Posterior Error Probability: 6.07E-06

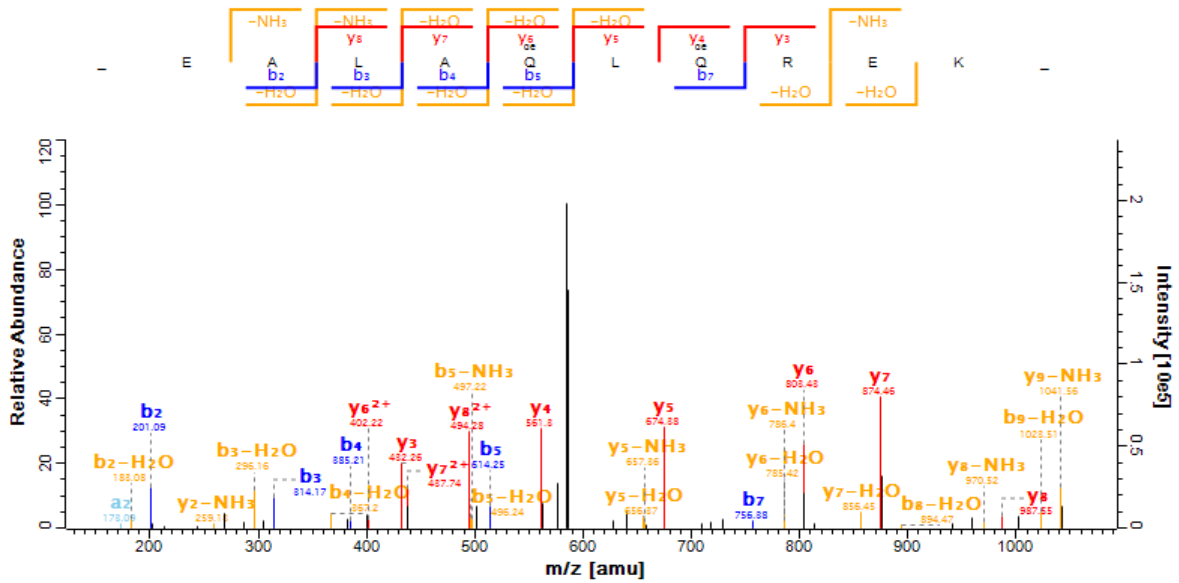
Best Match Spectrum:

Scan number 63765 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS: CID **Genenames** RHOT1



Protein Group ID: 1450
Protein Accession Numbers: H7BZ55; H7BZ68
Gene Names:
Peptide Sequence: EALAQLQREK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 218.6
Best Match Posterior Error Probability: 4.38E-25
Best Match Spectrum:

Scan number 18373 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Pepti...** 218.6



Protein Group ID: 1454

Protein Accession Numbers: J3KN59; Q12982-2; Q12982; H7C096

Gene Names: BNIP2

Peptide Sequence: MP^{SL}GWLR

Total Number of Spectra: 5

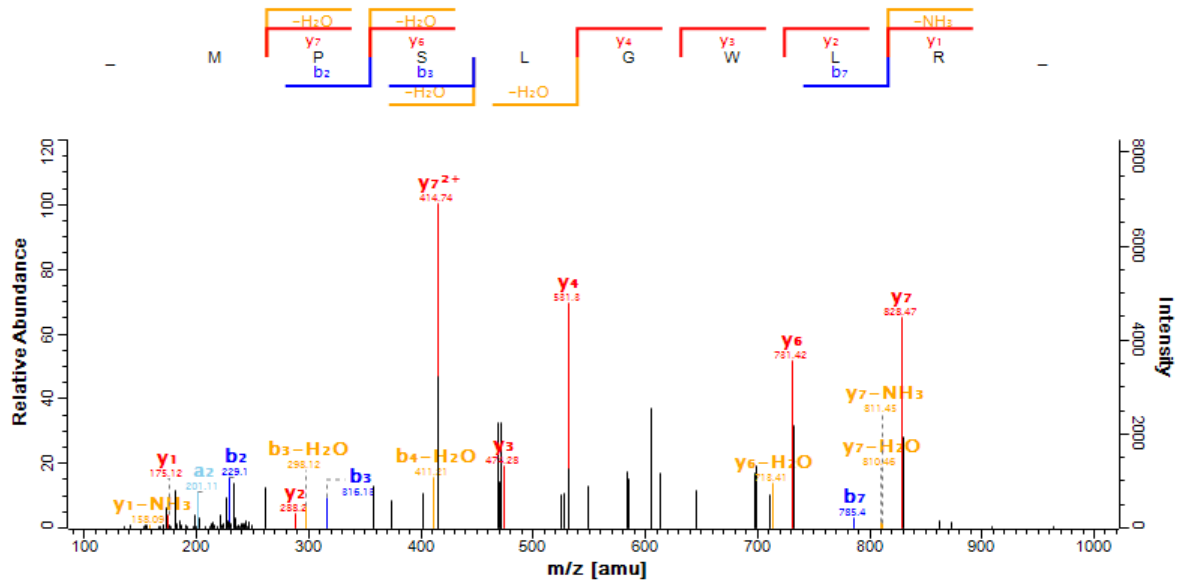
Number of Replicates (out of 8): 5

Best Match Score: 122.13

Best Match Posterior Error Probability: 0.0018606

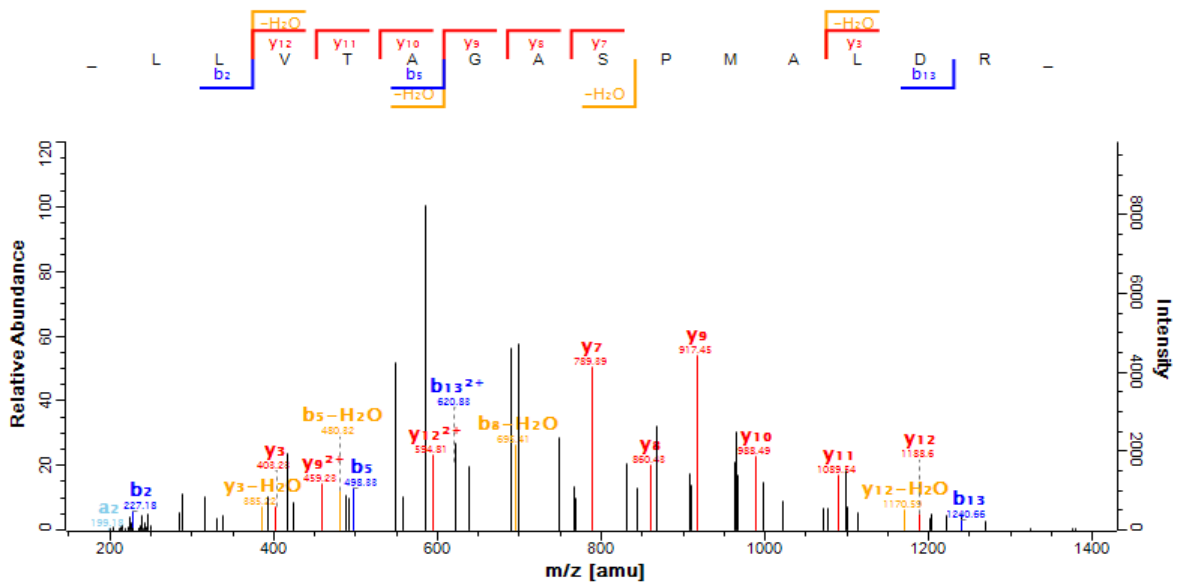
Best Match Spectrum:

Scan number 57314 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** BNIP2



Protein Group ID: 1455
Protein Accession Numbers: P20749; H7C0A2
Gene Names: BCL3
Peptide Sequence: LLVTAGASPMALDR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 77.894
Best Match Posterior Error Probability: 0.0037663
Best Match Spectrum:

Scan number 47929 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** BCL3



Protein Group ID: 1457

Protein Accession Numbers: Q9H330; Q9H330-2; H7C0G1; Q9H330-3

Gene Names: TMEM245

Peptide Sequence: ALNSAANNVYQYGR

Total Number of Spectra: 1

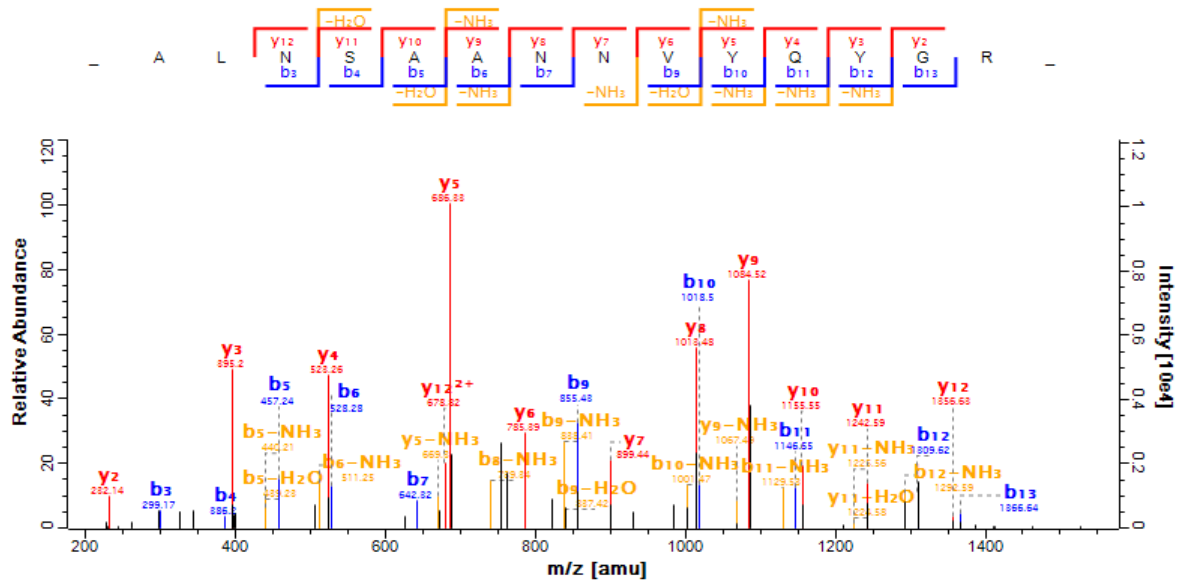
Number of Replicates (out of 8): 1

Best Match Score: 220.21

Best Match Posterior Error Probability: 1.05E-41

Best Match Spectrum:

Scan number 28342 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TMEM245



Protein Group ID: 1459

Protein Accession Numbers: Q9Y6W3; H7C1B7

Gene Names: CAPN7

Peptide Sequence: VMGGYDFPGSNSNSNIDLHALTGWIPER

Total Number of Spectra: 2

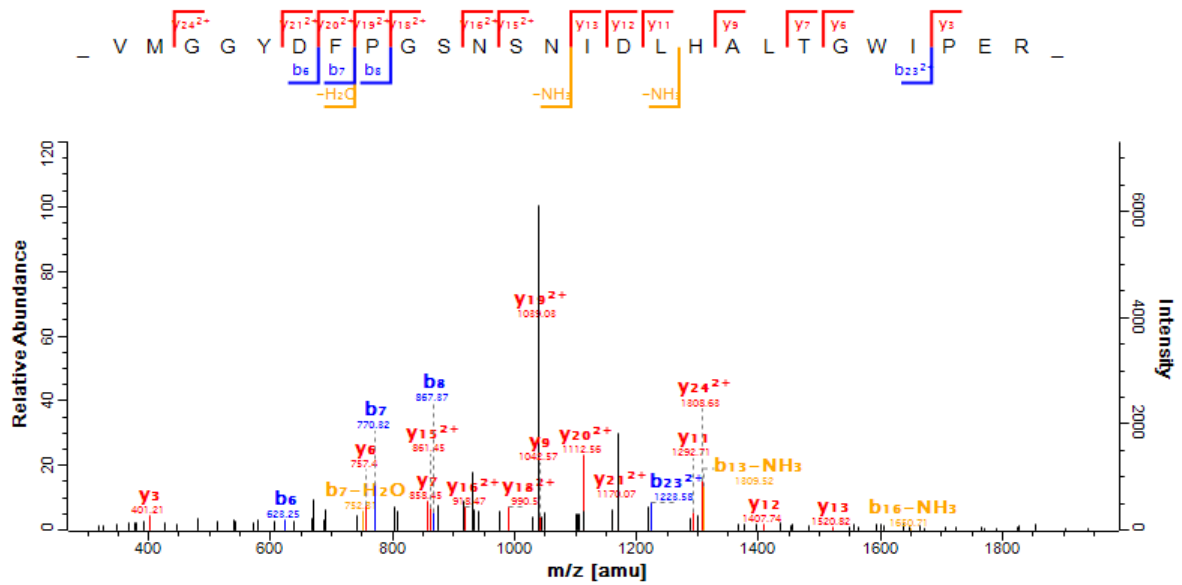
Number of Replicates (out of 8): 2

Best Match Score: 68.552

Best Match Posterior Error Probability: 0.0003327

Best Match Spectrum:

Scan number 82085 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CAPN7



Protein Group ID: 1462

Protein Accession Numbers: Q5VZL5; Q5VZL5-4; Q5VZL5-2; Q5VZL5-3; H7C1I7

Gene Names: ZMYM4

Peptide Sequence: IIGDASTQTDALK

Total Number of Spectra: 2

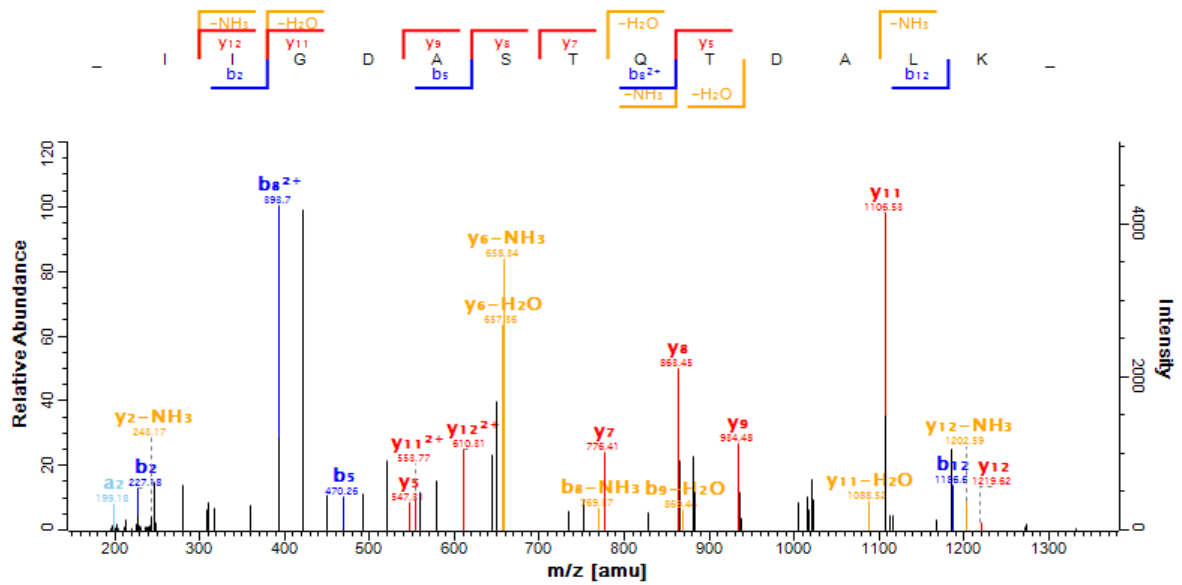
Number of Replicates (out of 8): 2

Best Match Score: 82.85

Best Match Posterior Error Probability: 0.0026669

Best Match Spectrum:

Scan number 23204 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ZMYM4



Protein Group ID: 1463

Protein Accession Numbers: Q9H147; H7C1M5; H7C1J2

Gene Names: DNTTIP1

Peptide Sequence: SFVLPSWMVEK

Total Number of Spectra: 2

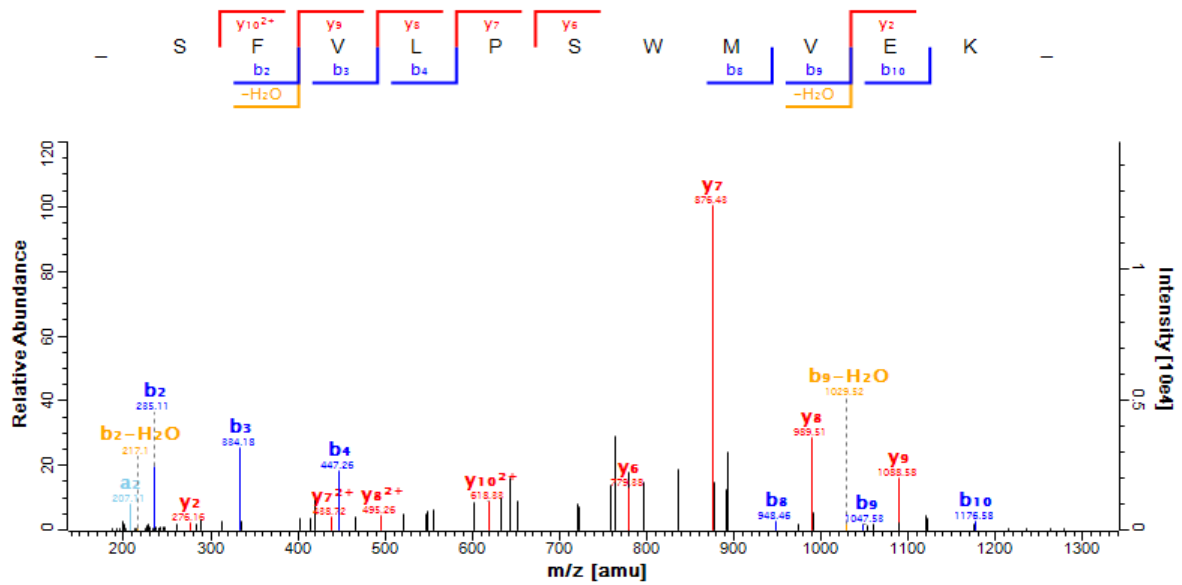
Number of Replicates (out of 8): 2

Best Match Score: 94.465

Best Match Posterior Error Probability: 0.0010138

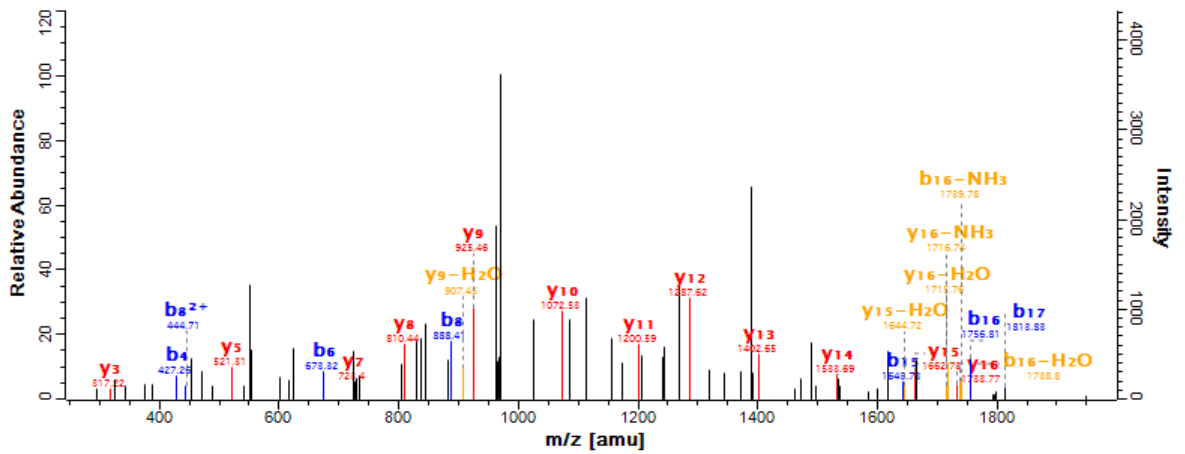
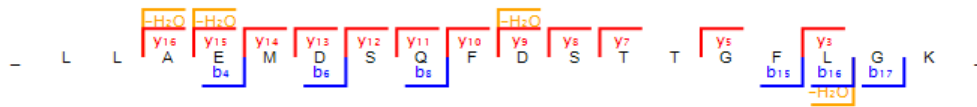
Best Match Spectrum:

Scan number 68810 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** DNTTIP1



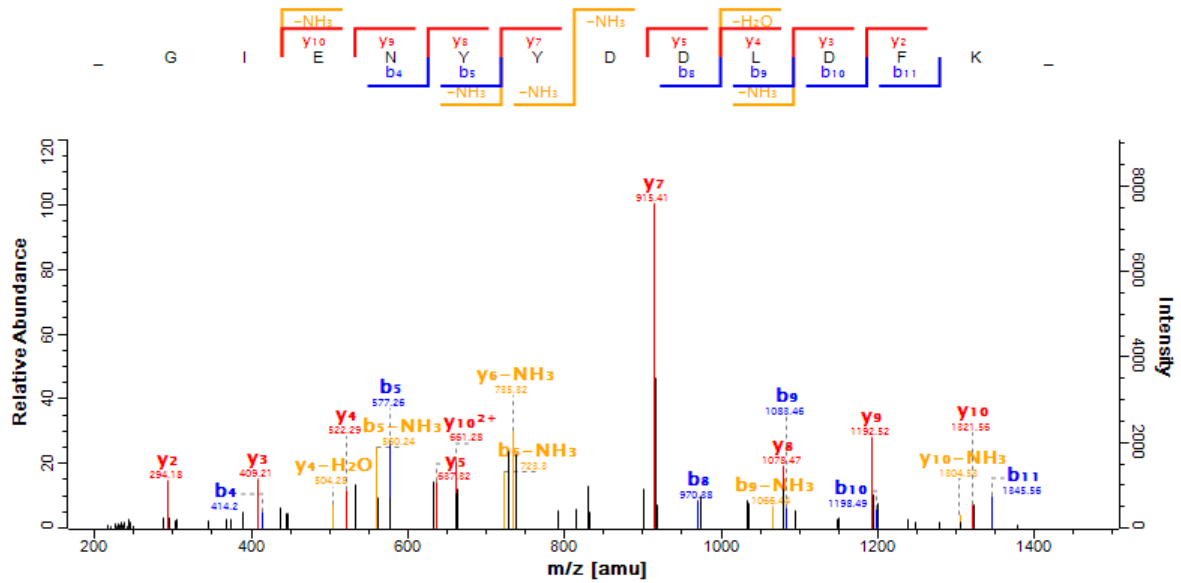
Protein Group ID: 1464
Protein Accession Numbers: H7C1N3; O15155
Gene Names: BET1
Peptide Sequence: LLAEMDSQFDSTTGFLGK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 101.53
Best Match Posterior Error Probability: 0.00015183
Best Match Spectrum:

Scan number 64822 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** BET1



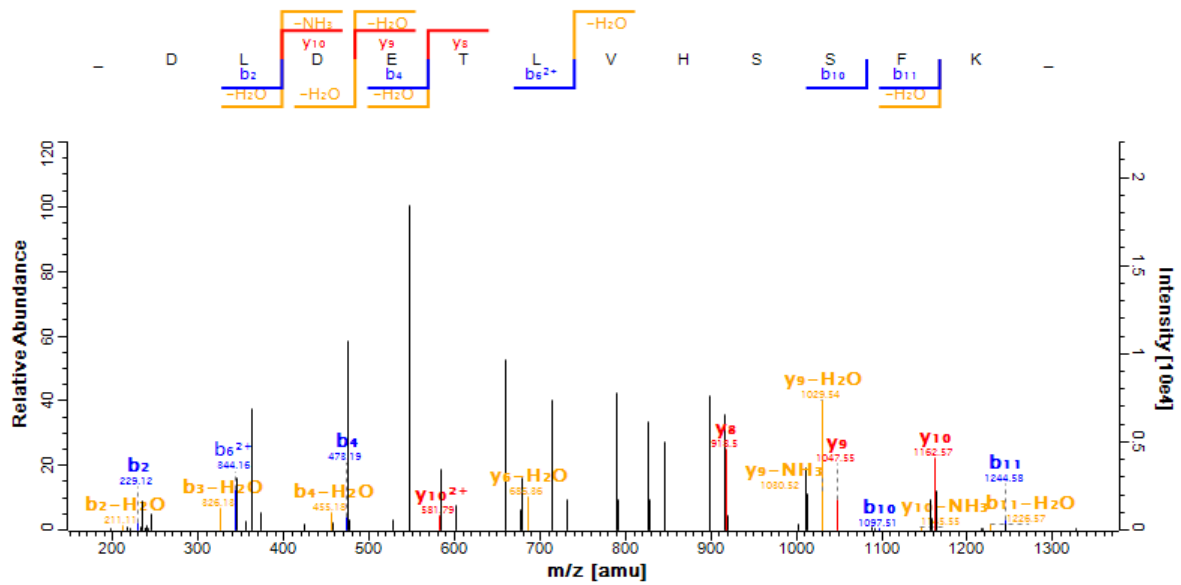
Protein Group ID: 1468
Protein Accession Numbers: O95858; H7C285
Gene Names: TSPAN15
Peptide Sequence: GIENYYDDLDFK
Total Number of Spectra: 4
Number of Replicates (out of 8): 3
Best Match Score: 101.32
Best Match Posterior Error Probability: 0.00047971
Best Match Spectrum:

Scan number 56188 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TSPAN15



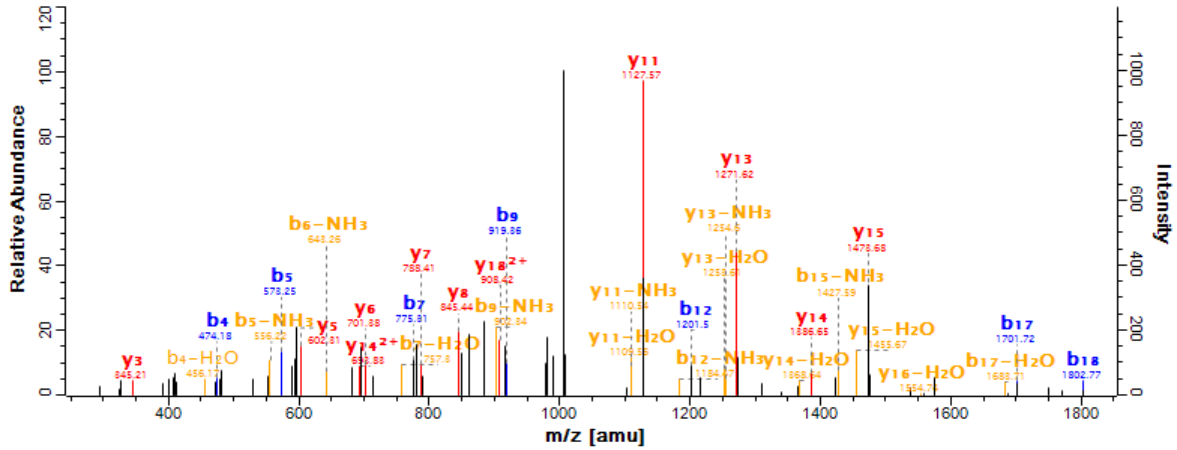
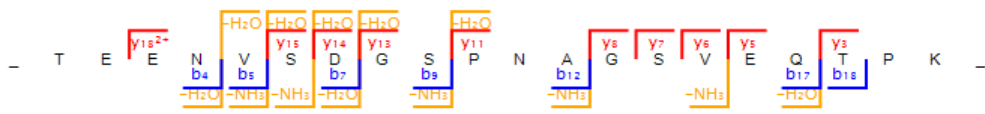
Protein Group ID: 1471
Protein Accession Numbers: H7C2S4
Gene Names: CTDSPL
Peptide Sequence: DLDETLVHSSFK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 96.113
Best Match Posterior Error Probability: 0.00081657
Best Match Spectrum:

Scan number 33160 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CTDSPL



Protein Group ID: 1472
Protein Accession Numbers: P46527; H7C2T1
Gene Names: CDKN1B
Peptide Sequence: TEENVSDGSPNAGSVEQTPK
Total Number of Spectra: 5
Number of Replicates (out of 8): 4
Best Match Score: 153.36
Best Match Posterior Error Probability: 2.37E-21
Best Match Spectrum:

Scan number 16965 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CDKN1B



Protein Group ID: 1474

Protein Accession Numbers: J3KPZ3; O75592; O75592-2; H7C3U4

Gene Names: MYCBP2

Peptide Sequence: LISGDAEPTPEEK

Total Number of Spectra: 2

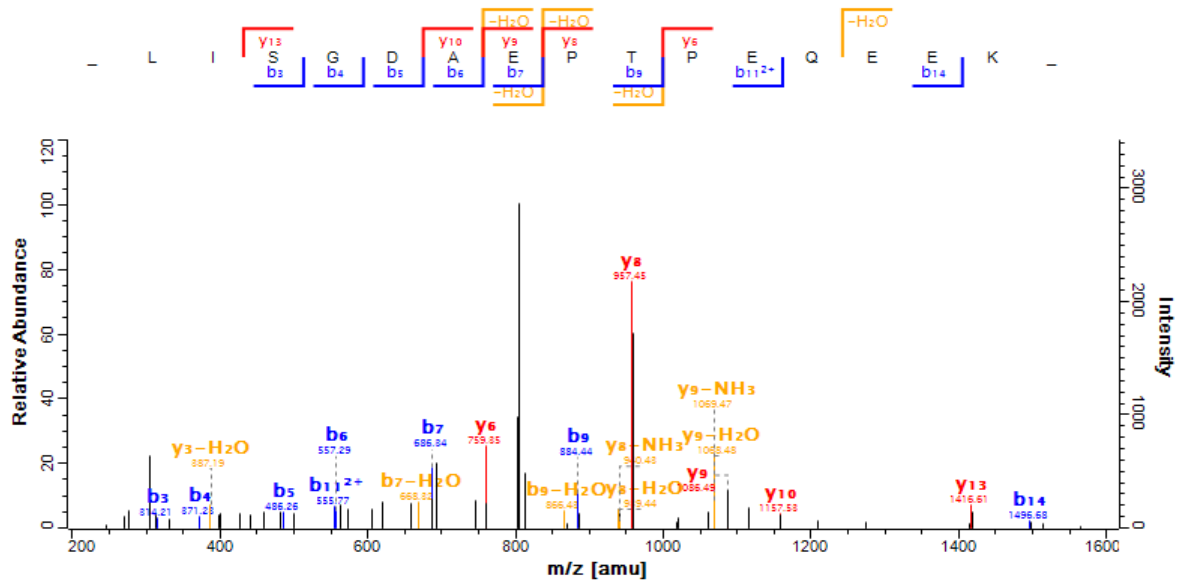
Number of Replicates (out of 8): 1

Best Match Score: 88.282

Best Match Posterior Error Probability: 0.00093743

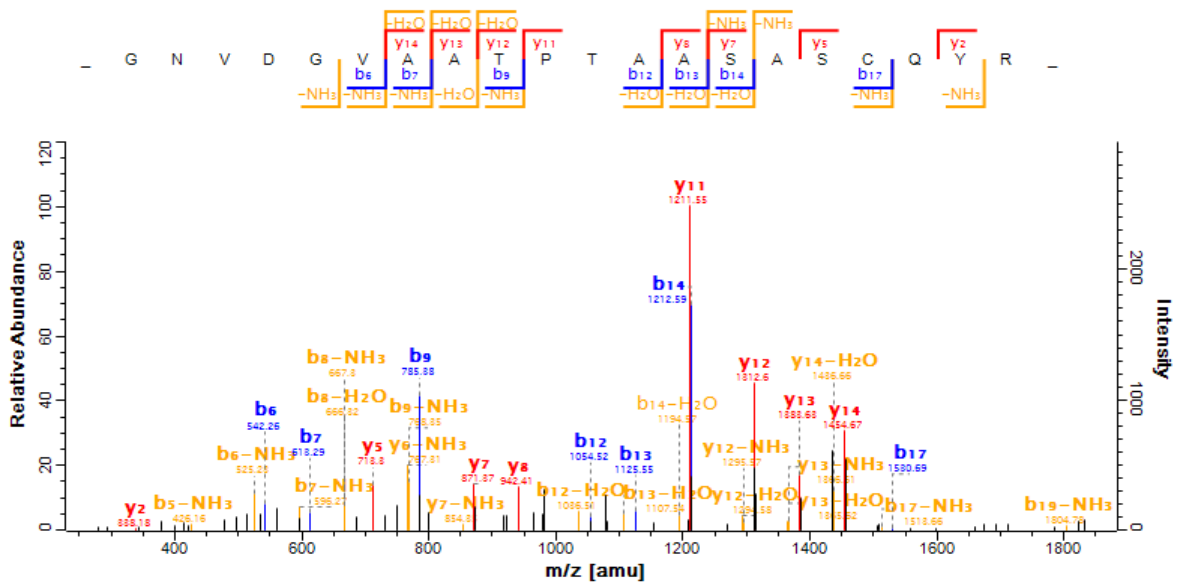
Best Match Spectrum:

Scan number 17838 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MYCBP2



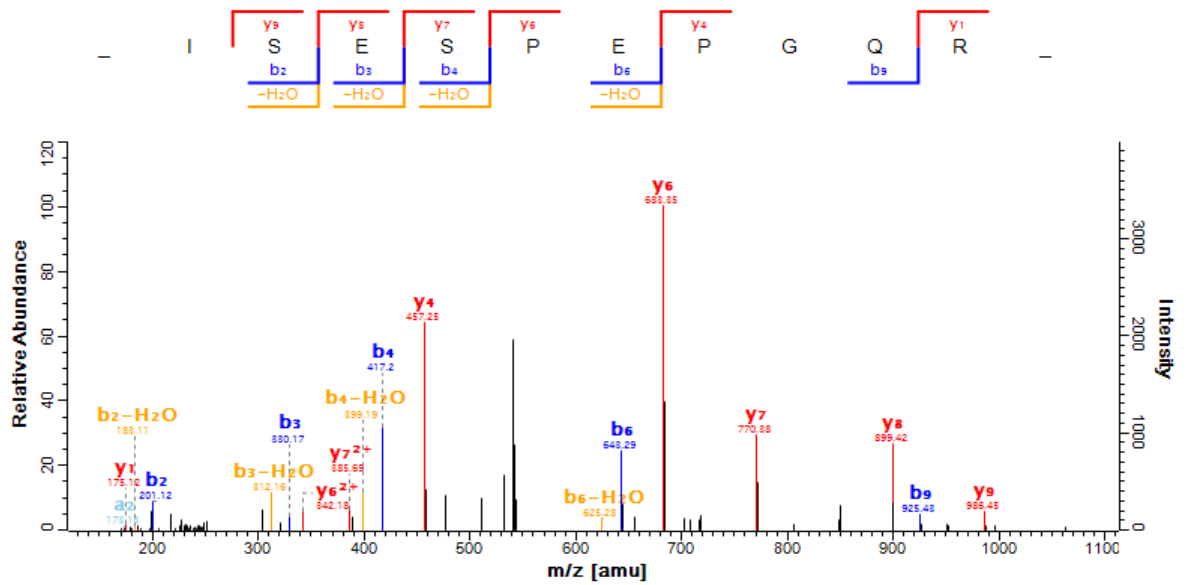
Protein Group ID: 1475
Protein Accession Numbers: Q9H2C2; H7C484
Gene Names: ARV1
Peptide Sequence: GNVDGVAATPTAASASCQYR
Total Number of Spectra: 7
Number of Replicates (out of 8): 5
Best Match Score: 153.21
Best Match Posterior Error Probability: 1.03E-08
Best Match Spectrum:

Scan number 25486 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ARV1



Protein Group ID: 1476
Protein Accession Numbers: O14867; H7C4B6
Gene Names: BACH1
Peptide Sequence: ISESPEPGQR
Total Number of Spectra: 4
Number of Replicates (out of 8): 3
Best Match Score: 115.78
Best Match Posterior Error Probability: 0.00021181
Best Match Spectrum:

Scan number 5371 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** BACH1



Protein Group ID: 1480

Protein Accession Numbers: H9KV90; Q9Y566; Q9Y566-3; Q9Y566-2

Gene Names: SHANK1

Peptide Sequence: AGLGSQEK

Total Number of Spectra: 1

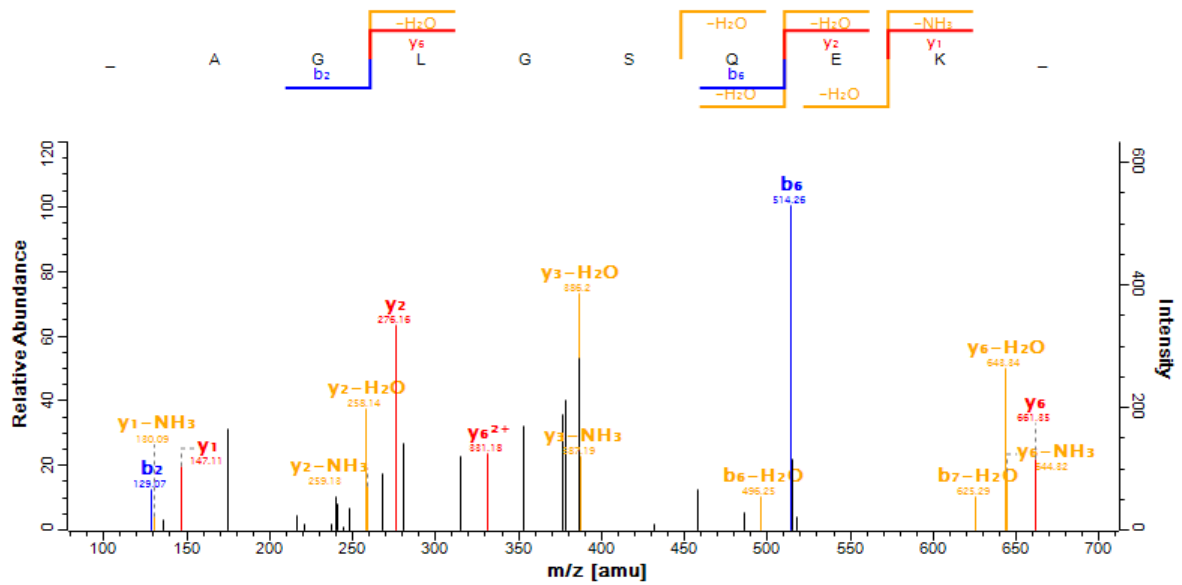
Number of Replicates (out of 8): 1

Best Match Score: 109.01

Best Match Posterior Error Probability: 0.0032088

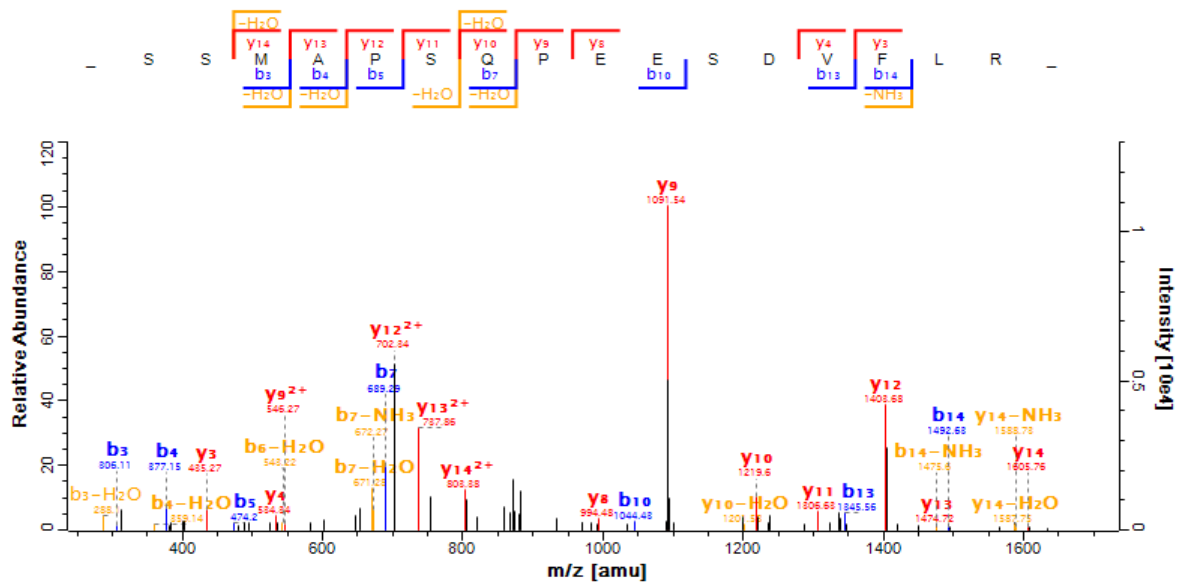
Best Match Spectrum:

Scan number	1025	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	SHANK1



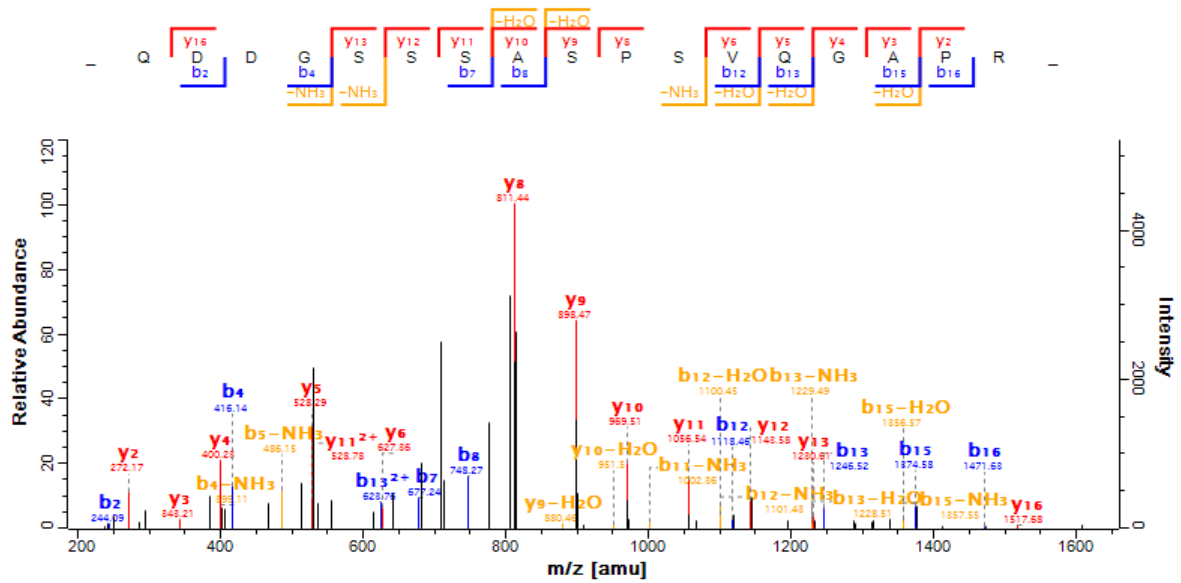
Protein Group ID: 1483
Protein Accession Numbers: I3L097; Q6ZSR9
Gene Names:
Peptide Sequence: SSMAPSQPEESDVFLR
Total Number of Spectra: 11
Number of Replicates (out of 8): 7
Best Match Score: 140.93
Best Match Posterior Error Probability: 1.99E-05
Best Match Spectrum:

Scan number 42326 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Pepti...** 140.93



Protein Group ID: 1484
Protein Accession Numbers: I3L0A4; Q9NQA3
Gene Names: WASH6P
Peptide Sequence: QDDGSSASPSVQGAPR
Total Number of Spectra: 6
Number of Replicates (out of 8): 5
Best Match Score: 154.51
Best Match Posterior Error Probability: 6.67E-07
Best Match Spectrum:

Scan number 9532 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** WASH6P



Protein Group ID: 1489

Protein Accession Numbers: I3L156; Q9BSJ6; I3L419; I3L1U3; Q9BSJ6-2; I3L476; I3L427

Gene Names: FAM64A

Peptide Sequence: SLQHQEQLDSK

Total Number of Spectra: 2

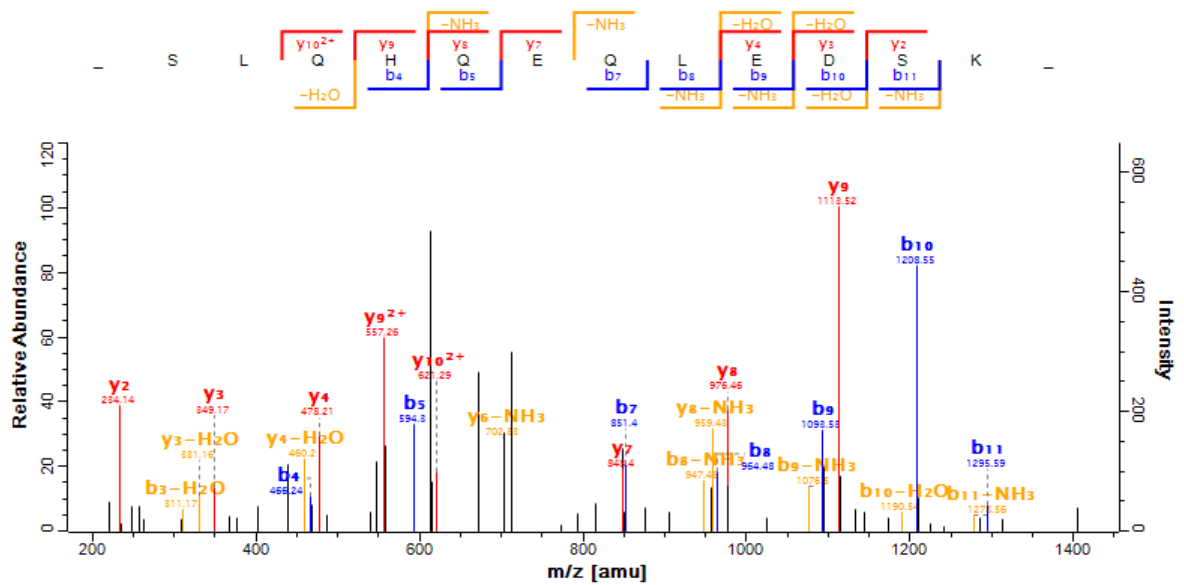
Number of Replicates (out of 8): 2

Best Match Score: 141.13

Best Match Posterior Error Probability: 1.17E-06

Best Match Spectrum:

Scan number 6046 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** FAM64A



Protein Group ID: 1490

Protein Accession Numbers: Q9GZP9; I3L1T3

Gene Names: DERL2

Peptide Sequence: AIFDTPDEDPNYNPLPEERPGGFAGWGEGR

Total Number of Spectra: 12

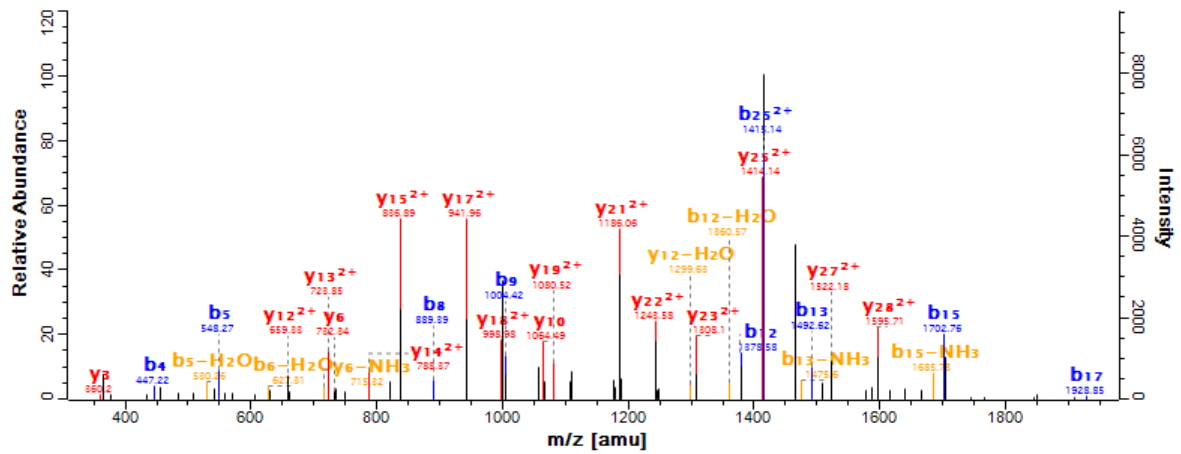
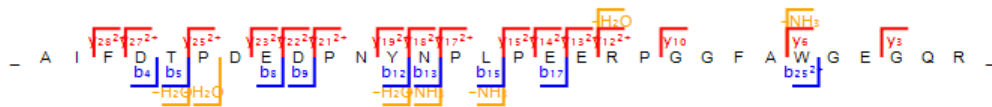
Number of Replicates (out of 8): 7

Best Match Score: 133.95

Best Match Posterior Error Probability: 1.09E-27

Best Match Spectrum:

Scan number 65217 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** DERL2



Protein Group ID: 1491

Protein Accession Numbers: I3L291; Q16625; Q16625-3; Q16625-2; Q16625-4; Q16625-5

Gene Names: OCLN

Peptide Sequence: YSSGGNFETPSK

Total Number of Spectra: 2

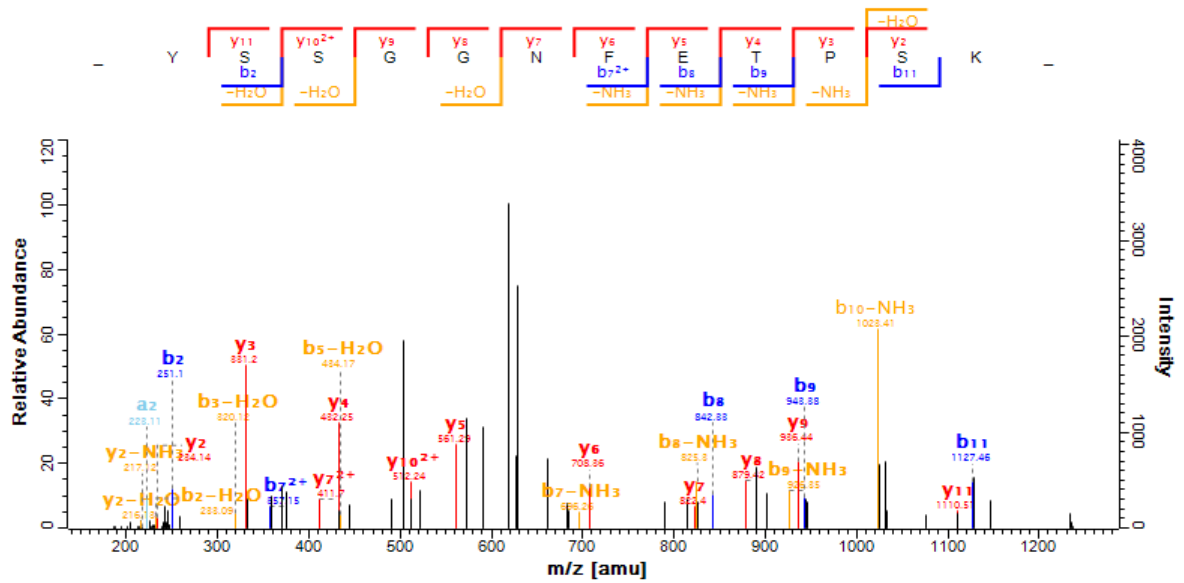
Number of Replicates (out of 8): 2

Best Match Score: 96.866

Best Match Posterior Error Probability: 0.00074086

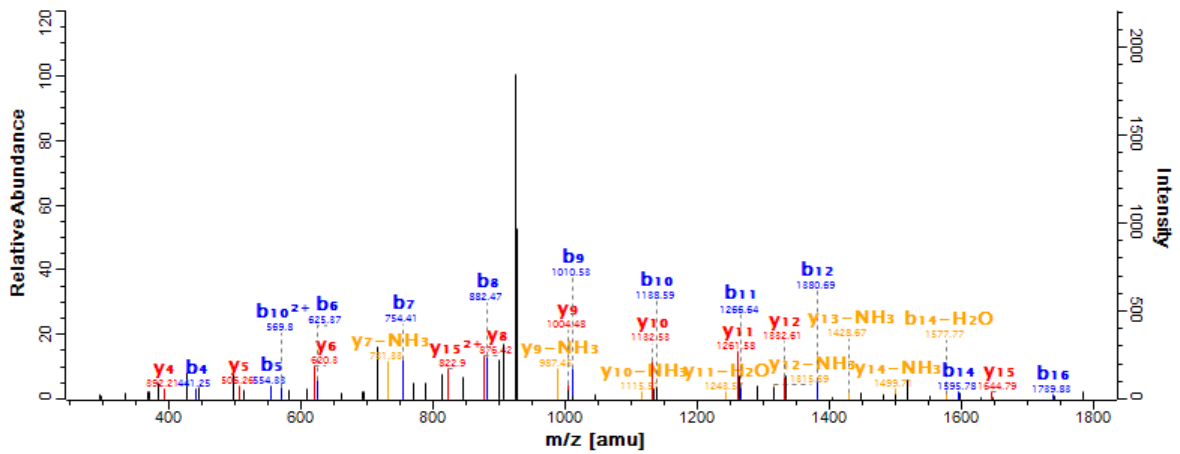
Best Match Spectrum:

Scan number	12826	Raw file	A549-US-WT-top20CID-Elite-2ug-814
Method	ITMS; CID	Genenames	OCLN



Protein Group ID: 1494
Protein Accession Numbers: Q9Y3C7; I3L2J1
Gene Names: MED31
Peptide Sequence: LQQALAEQQQNNTSGK
Total Number of Spectra: 2
Number of Replicates (out of 8): 1
Best Match Score: 135.08
Best Match Posterior Error Probability: 6.84E-05
Best Match Spectrum:

Scan number 9049 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MED31



Protein Group ID: 1496

Protein Accession Numbers: I3L4A1; Q96FZ7; I3L4G8; I3L3E4

Gene Names: CHMP6

Peptide Sequence: ILDETQEAVEYQR

Total Number of Spectra: 4

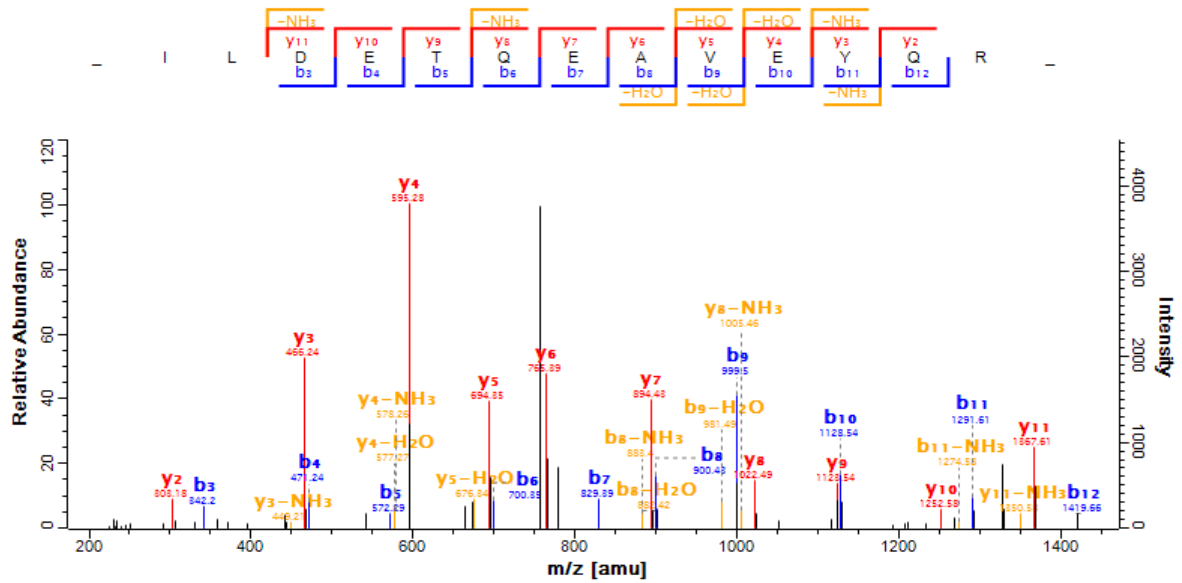
Number of Replicates (out of 8): 4

Best Match Score: 173.25

Best Match Posterior Error Probability: 1.15E-13

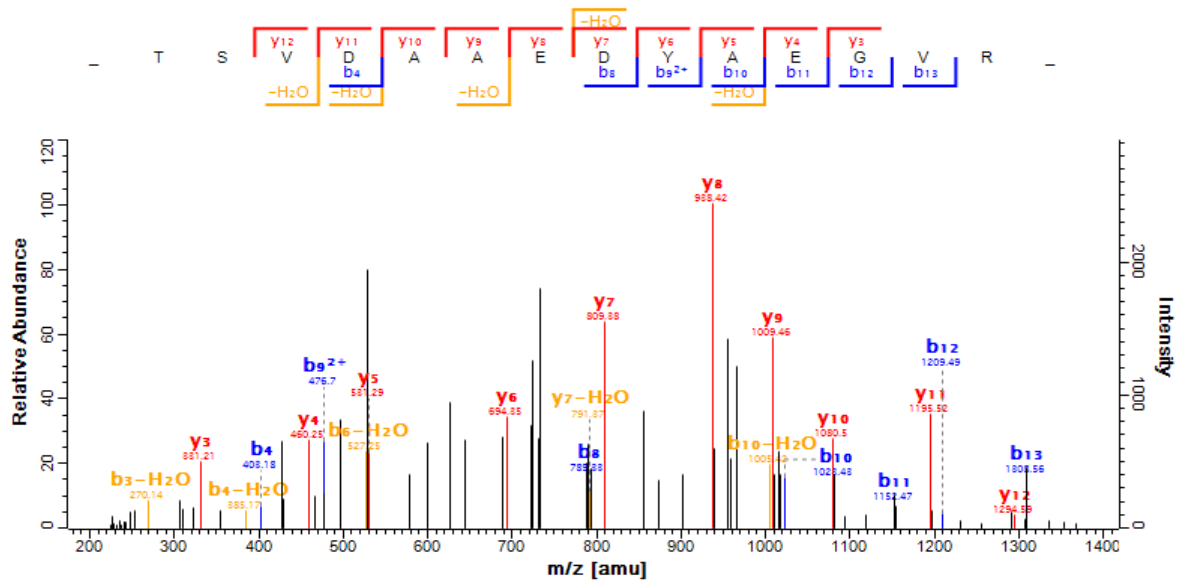
Best Match Spectrum:

Scan number 29513 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CHMP6



Protein Group ID: 1501
Protein Accession Numbers: Q02127; I3NI32
Gene Names: DHODH
Peptide Sequence: TSVDAEDYAEGVR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 88.706
Best Match Posterior Error Probability: 0.0013205
Best Match Spectrum:

Scan number 32047 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** DHODH



Protein Group ID: 1510

Protein Accession Numbers: J3KN36; Q5JPE7; P69849; Q5JPE7-2; F5H826; Q4G177

Gene Names: NOMO2;NOMO3

Peptide Sequence: LQGVGALGQAASDNSGPEDAK

Total Number of Spectra: 9

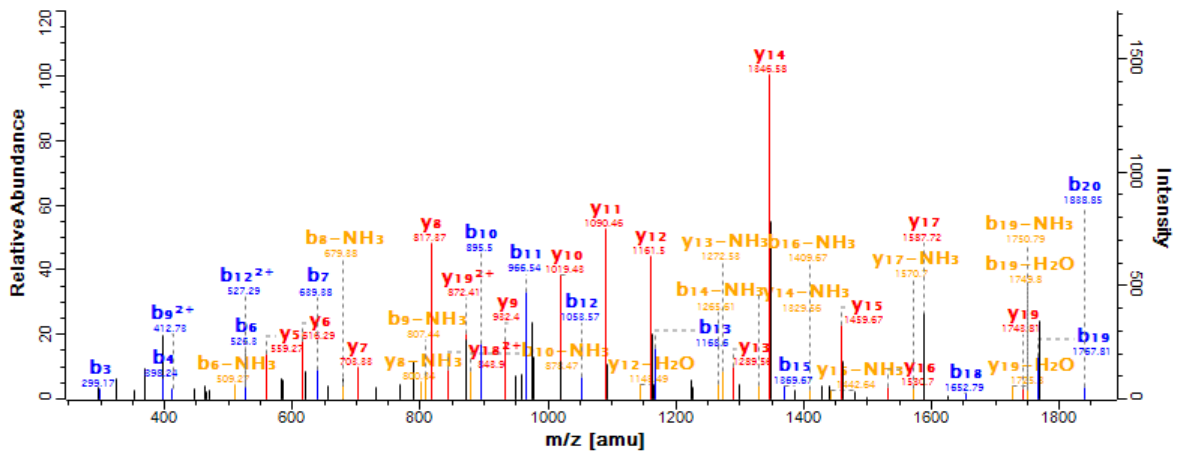
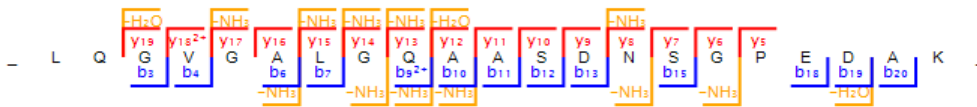
Number of Replicates (out of 8): 6

Best Match Score: 223.46

Best Match Posterior Error Probability: 3.15E-60

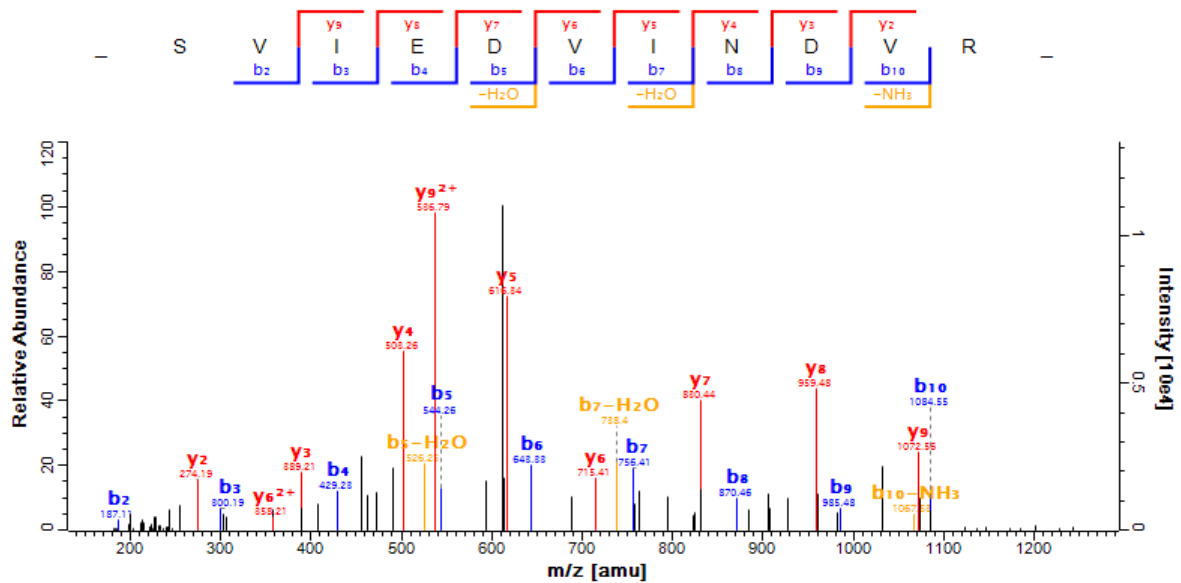
Best Match Spectrum:

Scan number	31468	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	NOMO2;NOMO3



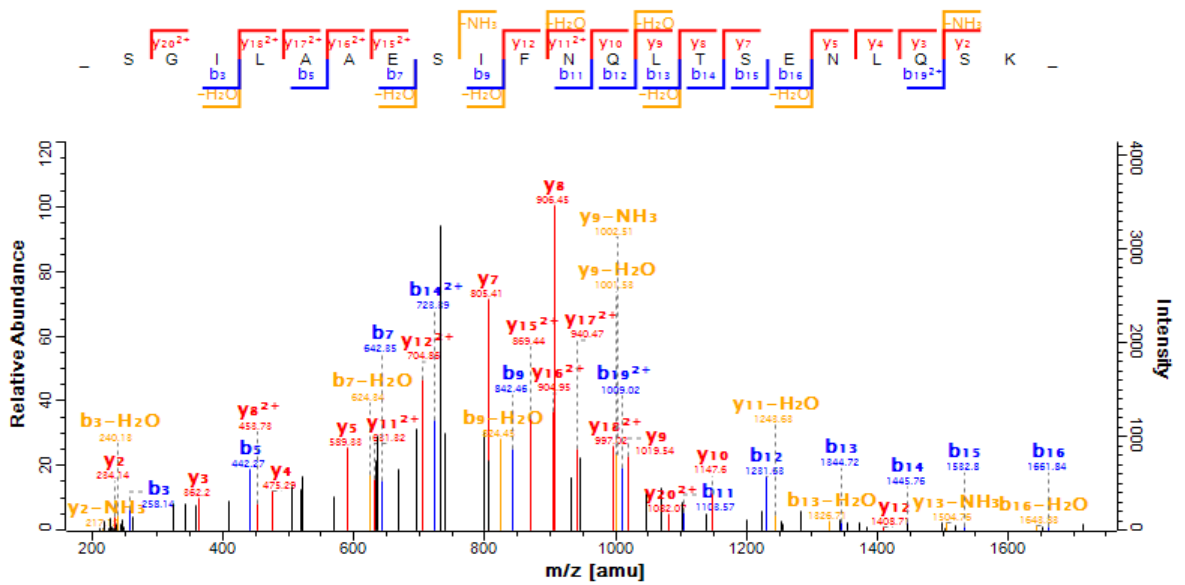
Protein Group ID: 1515
Protein Accession Numbers: P52655; J3KNC0
Gene Names: GTF2A1
Peptide Sequence: SVIEDVINDV R
Total Number of Spectra: 9
Number of Replicates (out of 8): 8
Best Match Score: 134.99
Best Match Posterior Error Probability: 3.77E-05
Best Match Spectrum:

Scan number 62766 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** GTF2A1



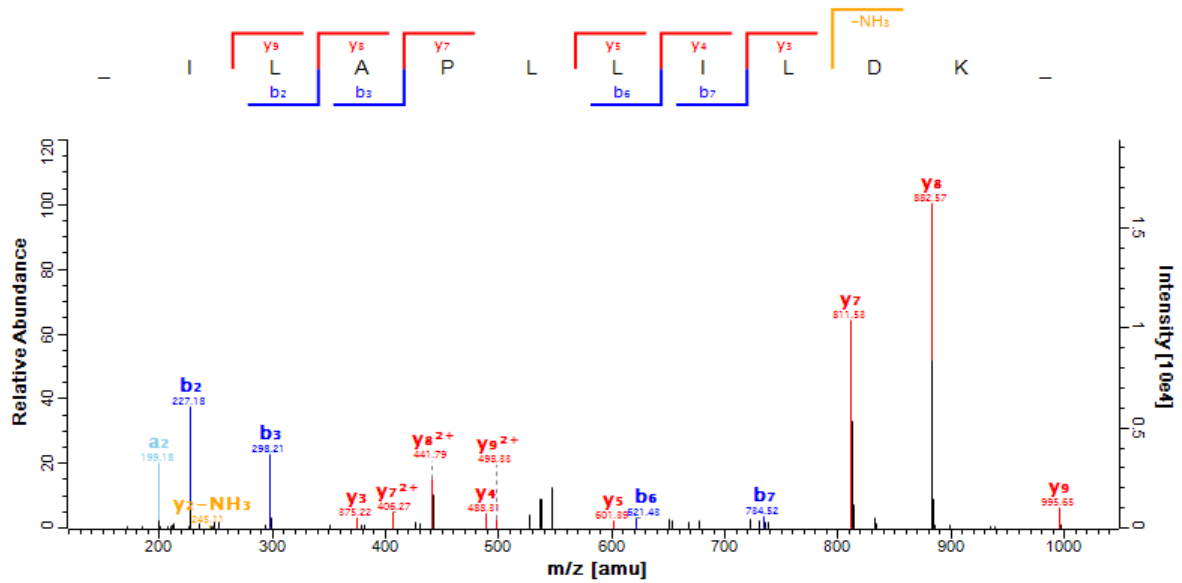
Protein Group ID: 1516
Protein Accession Numbers: Q16134; J3KND9
Gene Names: ETFDH
Peptide Sequence: SGILAAESIFNQLTSENLSK
Total Number of Spectra: 7
Number of Replicates (out of 8): 6
Best Match Score: 182.82
Best Match Posterior Error Probability: 5.43E-27
Best Match Spectrum:

Scan number 84173 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ETFDH



Protein Group ID: 1523
Protein Accession Numbers: J3KNK4; Q9Y587
Gene Names: AP4S1
Peptide Sequence: ILAPLLILDK
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 98.249
Best Match Posterior Error Probability: 0.00091571
Best Match Spectrum:

Scan number 72627 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** AP4S1



Protein Group ID: 1525

Protein Accession Numbers: J3KNM0; P35813; P35813-2

Gene Names: PPM1A

Peptide Sequence: VCNEVVDTCLYK

Total Number of Spectra: 1

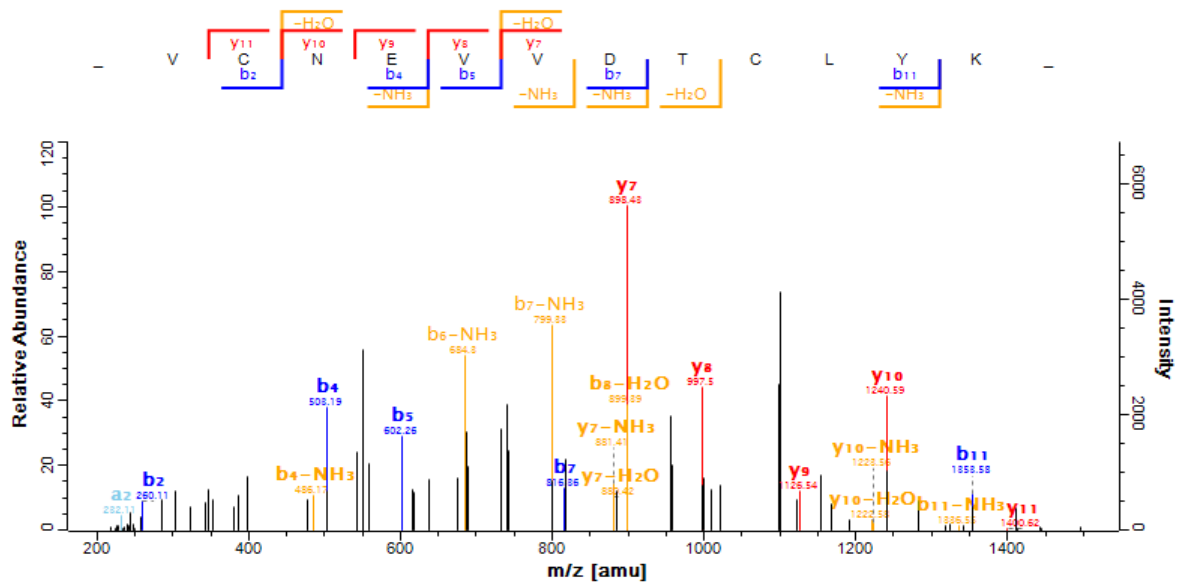
Number of Replicates (out of 8): 1

Best Match Score: 108.72

Best Match Posterior Error Probability: 0.00029906

Best Match Spectrum:

Scan number 33294 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PPM1A



Protein Group ID: 1529

Protein Accession Numbers: P32856; P32856-2; P32856-3; J3KNU7

Gene Names: STX2

Peptide Sequence: DHFMDDFFHQVEEIR

Total Number of Spectra: 2

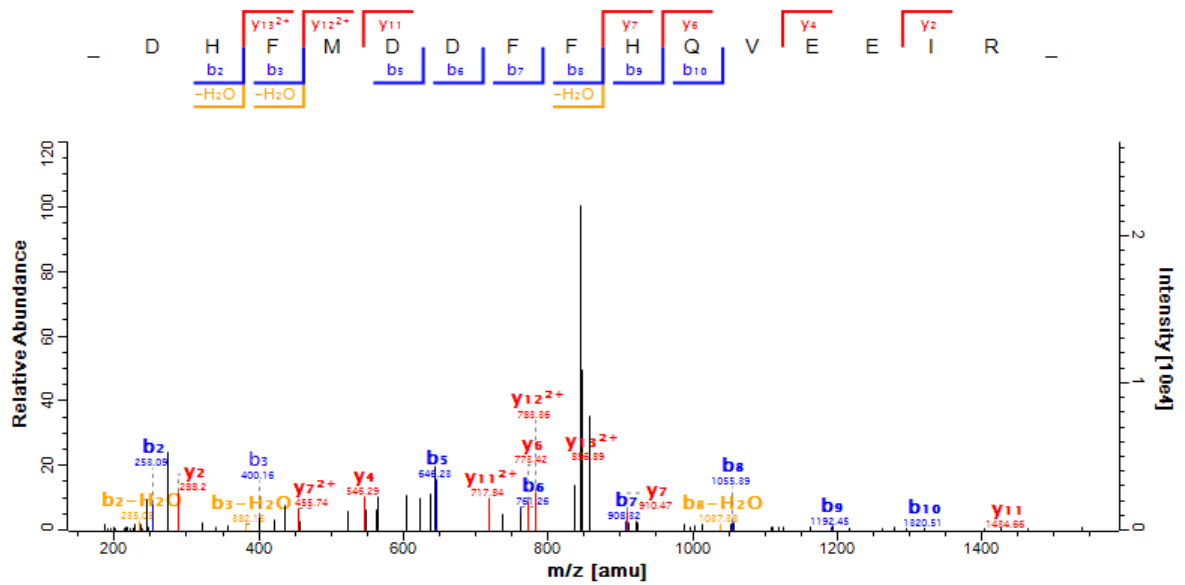
Number of Replicates (out of 8): 2

Best Match Score: 106.58

Best Match Posterior Error Probability: 0.00015487

Best Match Spectrum:

Scan number	74554	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	STX2



Protein Group ID: 1539

Protein Accession Numbers: J3KPT4; Q9H4I3; Q9H4I3-2

Gene Names: TRABD

Peptide Sequence: MDGEEQPPHEANVEPVPSEASEPVPR

Total Number of Spectra: 3

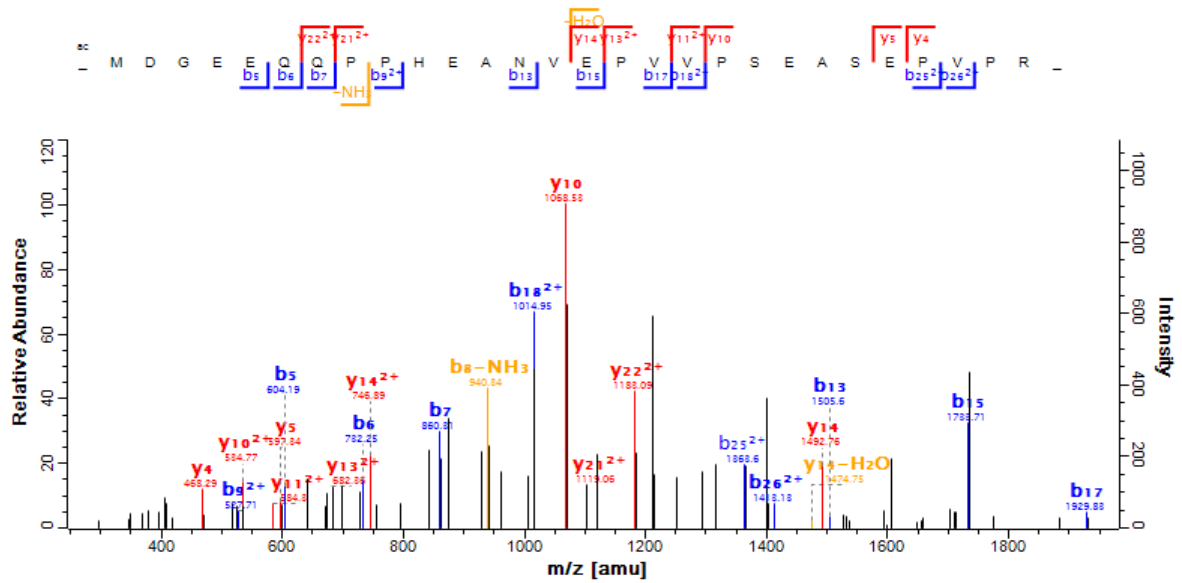
Number of Replicates (out of 8): 3

Best Match Score: 69.981

Best Match Posterior Error Probability: 0.00017647

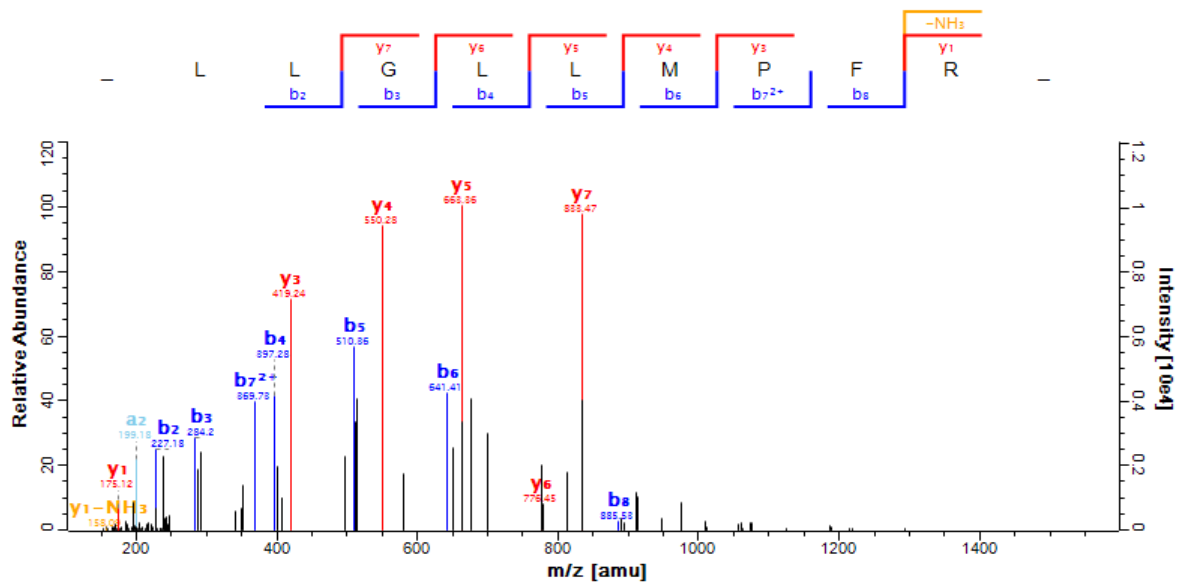
Best Match Spectrum:

Scan number 44305 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TRABD



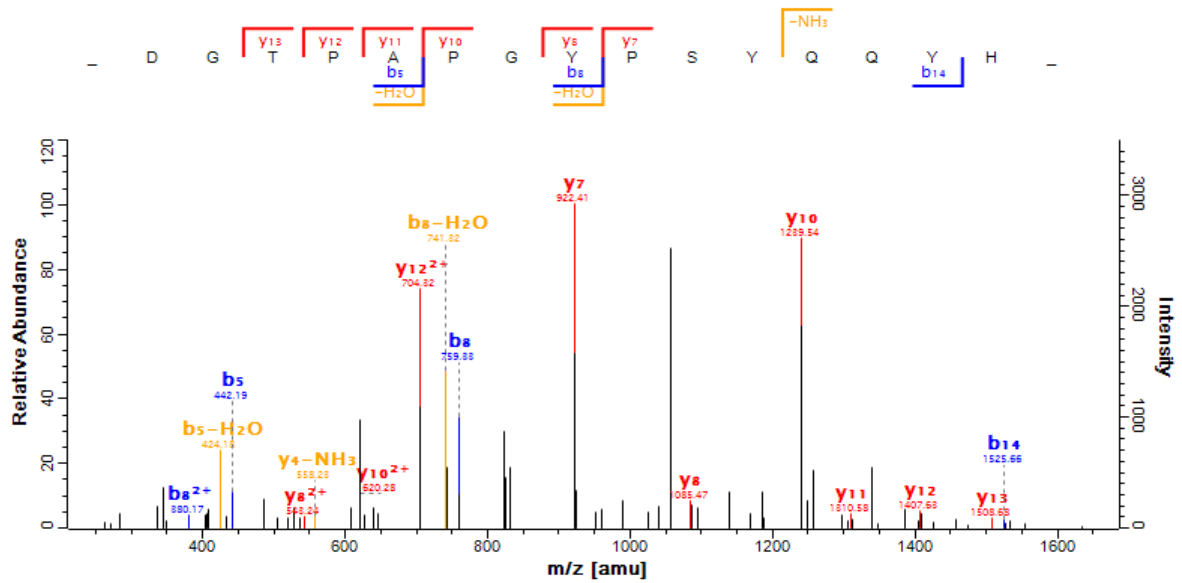
Protein Group ID: 1540
Protein Accession Numbers: J3KPU0; Q9P0J1
Gene Names: PDP1
Peptide Sequence: LLGLLMPFR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 109.86
Best Match Posterior Error Probability: 0.00099556
Best Match Spectrum:

Scan number	79018	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	PDP1



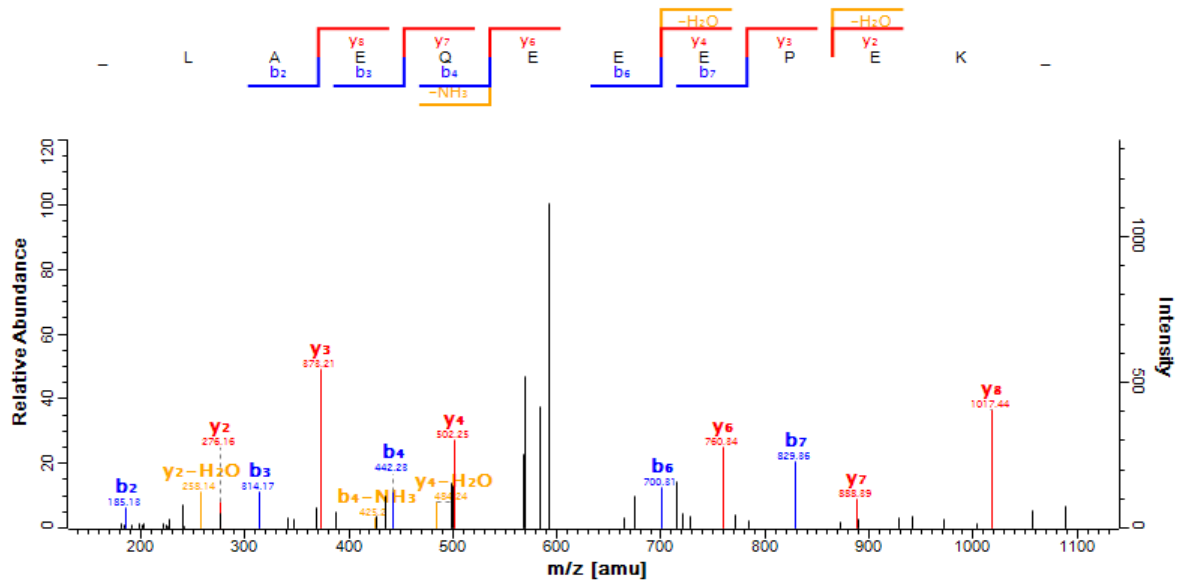
Protein Group ID: 1541
Protein Accession Numbers: J3KPV3; O60830
Gene Names: TIMM17B
Peptide Sequence: DGTPAPGYPSYQYH
Total Number of Spectra: 6
Number of Replicates (out of 8): 5
Best Match Score: 107.14
Best Match Posterior Error Probability: 0.00015065
Best Match Spectrum:

Scan number 29091 **Raw file** A549-US-WT-top20CID-Elite-2ug-814
Method ITMS; CID **Genenames** TIMM17B



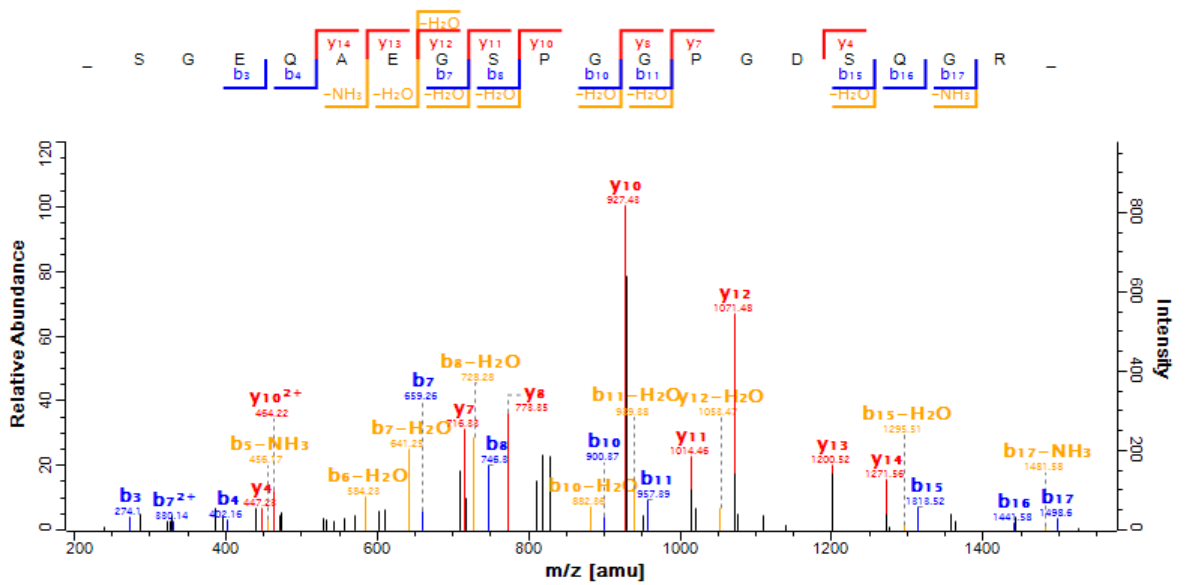
Protein Group ID: 1548
Protein Accession Numbers: J3KQ40; O95759
Gene Names: TBC1D8
Peptide Sequence: LAEQEEEPEK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 89.548
Best Match Posterior Error Probability: 0.0020368
Best Match Spectrum:

Scan number	5414	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	TBC1D8



Protein Group ID: 1559
Protein Accession Numbers: J3KQV0; P38936
Gene Names: CDKN1A
Peptide Sequence: SGEQAEGSPGGPGDSQGR
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 117.3
Best Match Posterior Error Probability: 5.52E-05
Best Match Spectrum:

Scan number 3148 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CDKN1A



Protein Group ID: 1567

Protein Accession Numbers: P02686; J3QQK6; P02686-2; J3KS94

Gene Names: MBP

Peptide Sequence: DRPSEDELQTIQEDSAATSESLDVMASQK

Total Number of Spectra: 1

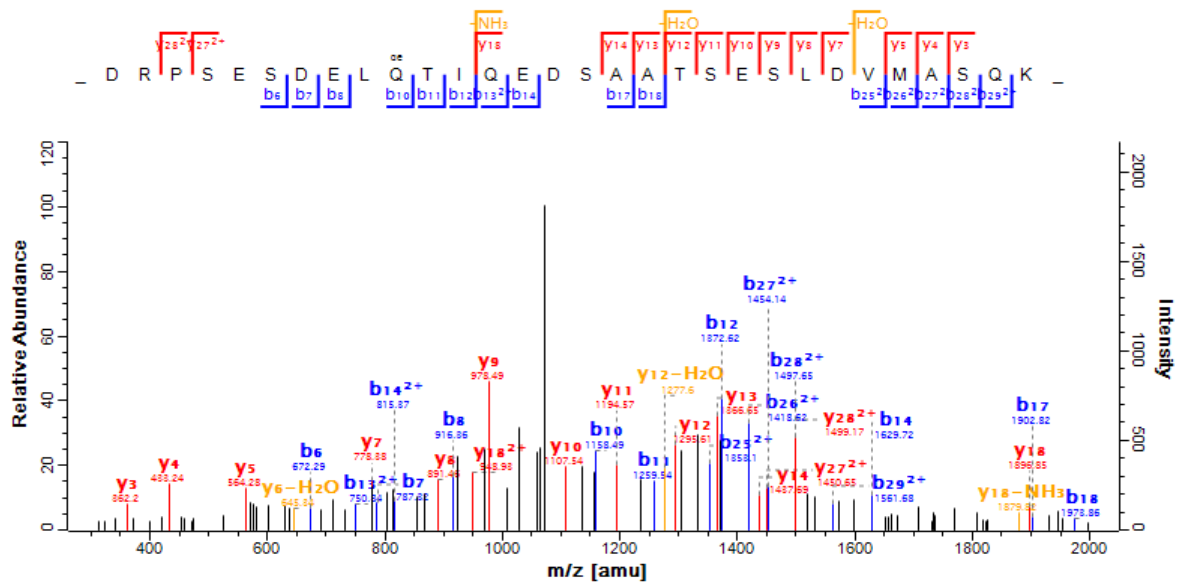
Number of Replicates (out of 8): 1

Best Match Score: 103.04

Best Match Posterior Error Probability: 2.32E-06

Best Match Spectrum:

Scan number	65618	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	MBP



Protein Group ID: 1569

Protein Accession Numbers: Q8WYR1; J3KSW1; Q8WYR1-2

Gene Names: PIK3R5

Peptide Sequence: ILQSVVRCEVPYK

Total Number of Spectra: 1

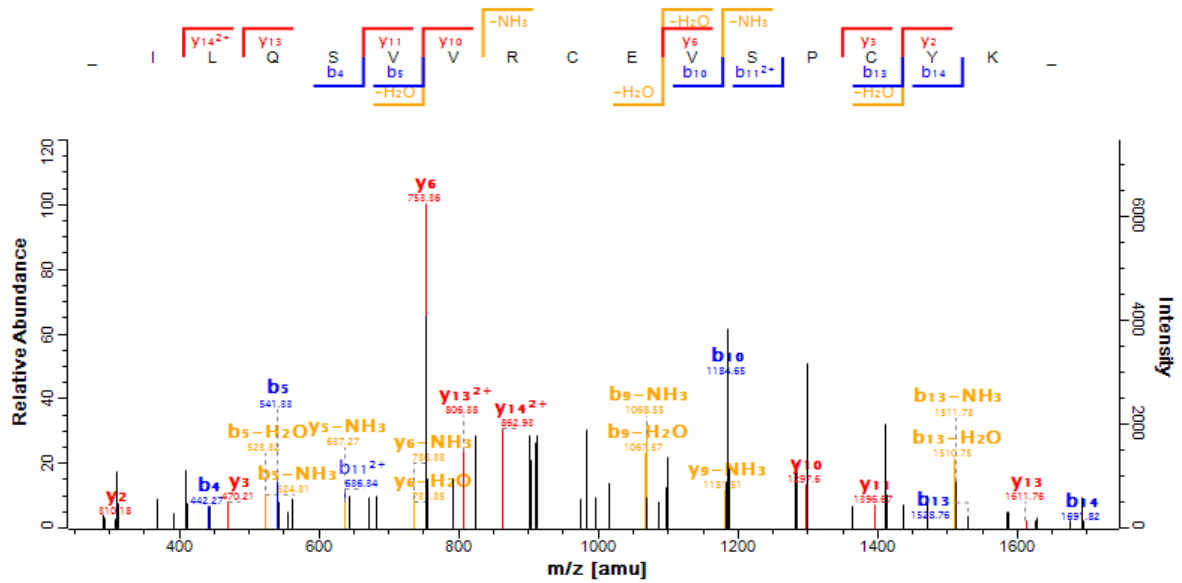
Number of Replicates (out of 8): 1

Best Match Score: 94.717

Best Match Posterior Error Probability: 0.002263

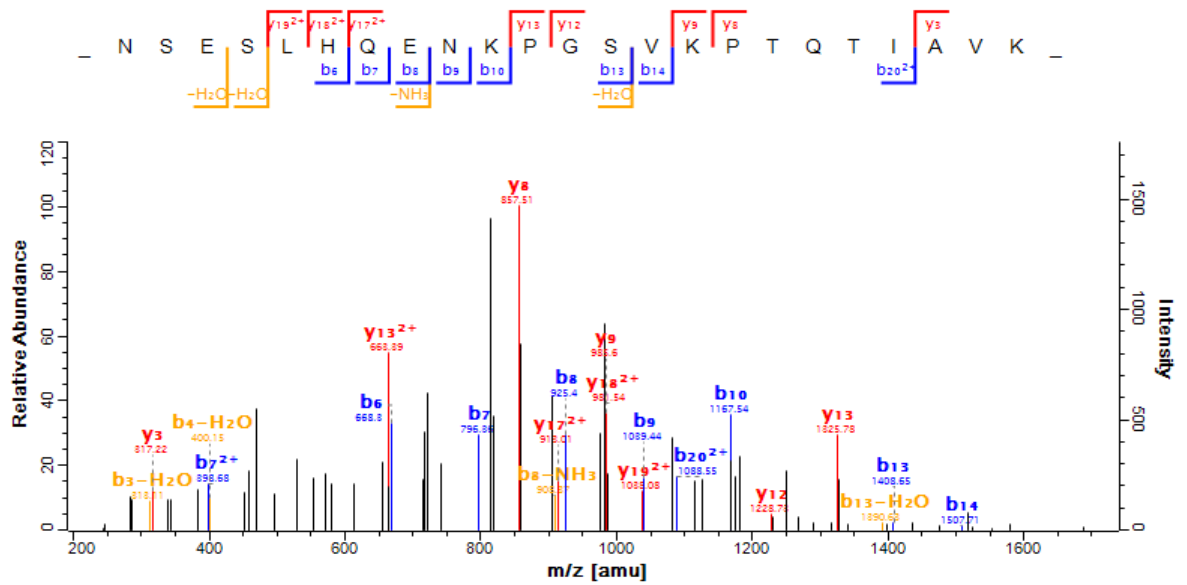
Best Match Spectrum:

Scan number 42384 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** PIK3R5



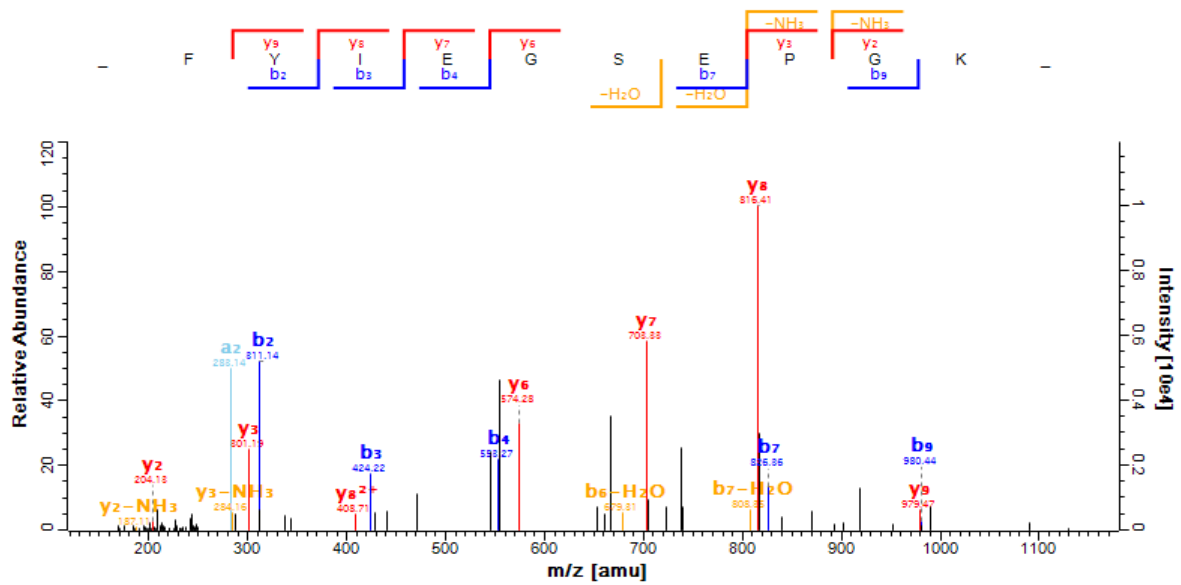
Protein Group ID: 1583
Protein Accession Numbers: Q15022; J3QQW9
Gene Names: SUZ12
Peptide Sequence: NSESLHQENKPGSVKPTQTIAVK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 80.303
Best Match Posterior Error Probability: 0.0022941
Best Match Spectrum:

Scan number 16615 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SUZ12



Protein Group ID: 1587
Protein Accession Numbers: Q9BVV7; J3QRI1
Gene Names: TIMM21
Peptide Sequence: FYIEGSEPGK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 96.143
Best Match Posterior Error Probability: 0.001187
Best Match Spectrum:

Scan number	24298	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	TIMM21



Protein Group ID: 1589

Protein Accession Numbers: J3QRS3; P19105; J3KTJ1

Gene Names: MYL12A

Peptide Sequence: NPTDEYLDAMMNEAPGPINFTMFLTMFGEK

Total Number of Spectra: 7

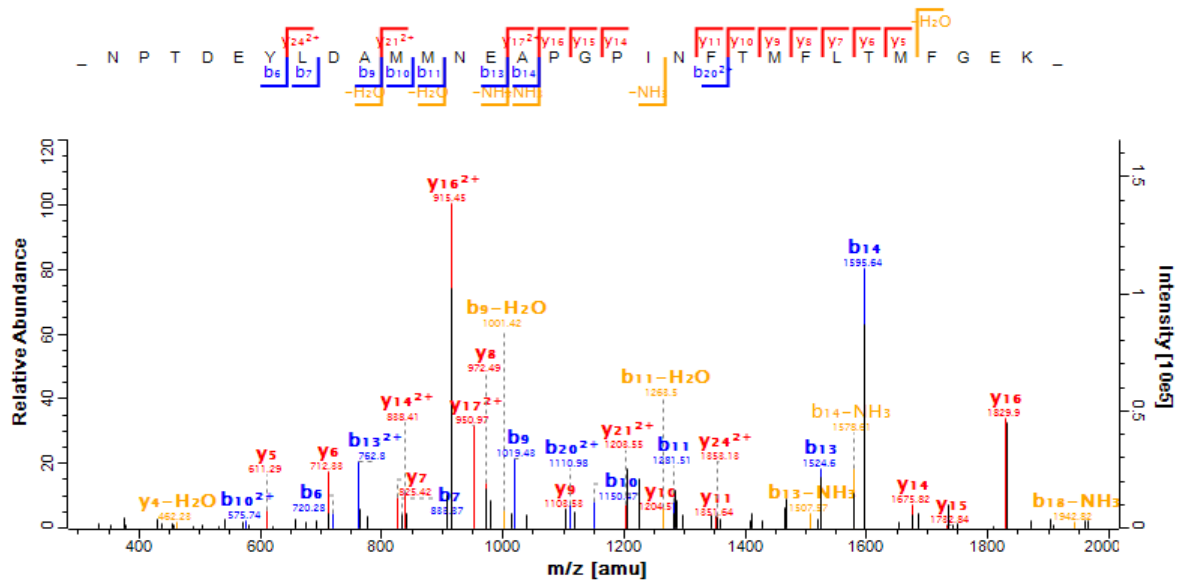
Number of Replicates (out of 8): 7

Best Match Score: 100.17

Best Match Posterior Error Probability: 9.42E-10

Best Match Spectrum:

Scan number 97392 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MYL12A



Protein Group ID: 1592

Protein Accession Numbers: Q8N9M1; Q8N9M1-2; Q8N9M1-3; J3QS80

Gene Names: C19orf47

Peptide Sequence: ATSSATTAAPTLR

Total Number of Spectra: 4

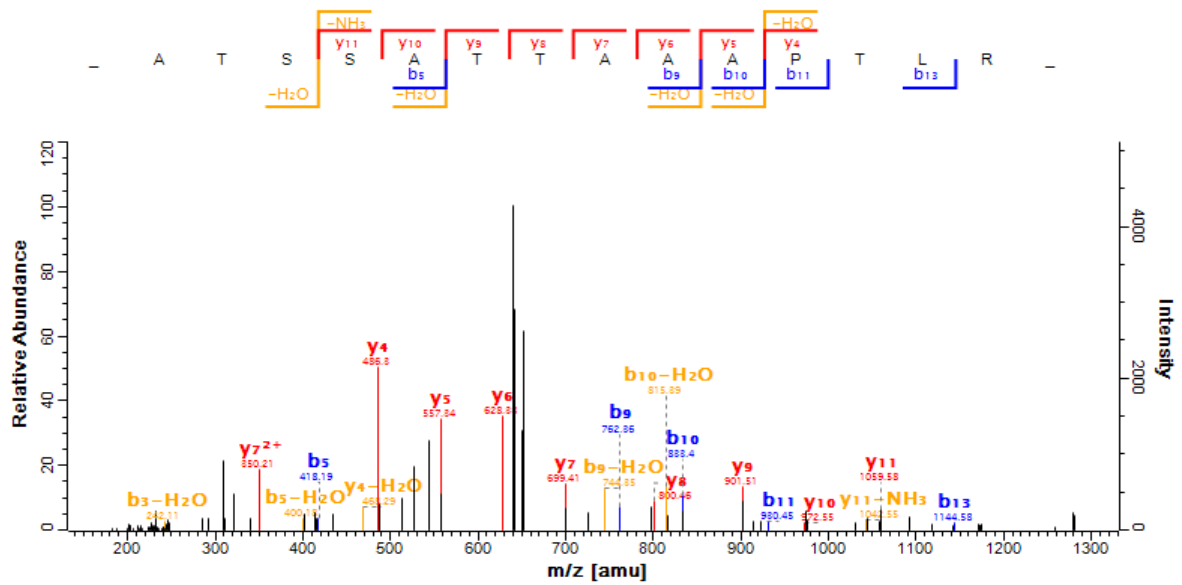
Number of Replicates (out of 8): 4

Best Match Score: 89.507

Best Match Posterior Error Probability: 0.0012443

Best Match Spectrum:

Scan number 15159 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** C19orf47



Protein Group ID: 1600

Protein Accession Numbers: J3QTI6; Q5CZC0; Q5CZC0-2

Gene Names: FSIP2

Peptide Sequence: EKEILLSNAHIPSVASEIENMLEK

Total Number of Spectra: 1

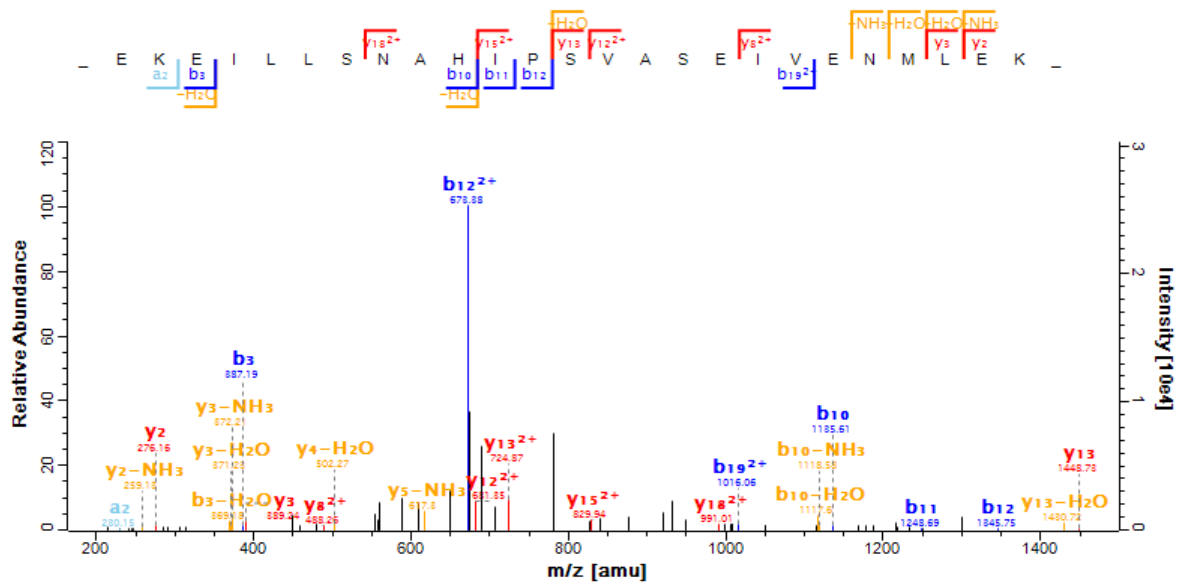
Number of Replicates (out of 8): 1

Best Match Score: 70.072

Best Match Posterior Error Probability: 0.0017736

Best Match Spectrum:

Scan number	74012	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	FSIP2



Protein Group ID: 1605

Protein Accession Numbers: Q96SI1; Q96SI1-2; K7EN63; K7EM48; K7EQS3; K7EPF0; K7EIF1

Gene Names: KCTD15

Peptide Sequence: SPVSPLAAQGIPLPAQLTK

Total Number of Spectra: 1

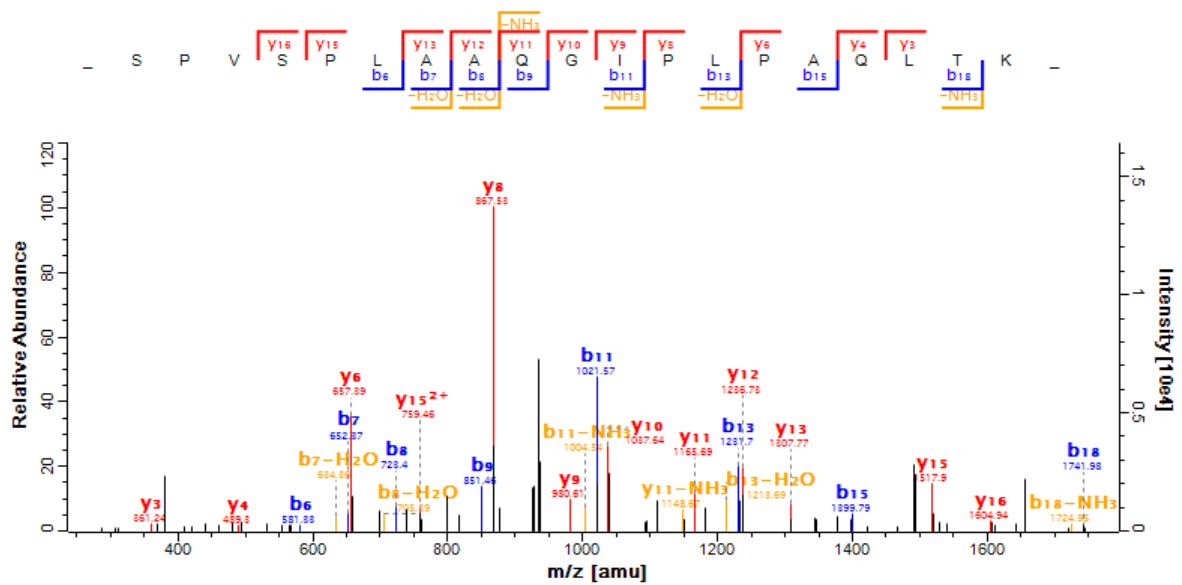
Number of Replicates (out of 8): 1

Best Match Score: 101.49

Best Match Posterior Error Probability: 0.00012862

Best Match Spectrum:

Scan number 64085 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** KCTD15



Protein Group ID: 1606

Protein Accession Numbers: Q8IYT4; Q8IYT4-2; K7EIJ8; K7EM02

Gene Names: KATNAL2

Peptide Sequence: GLLLYGPPGTGK

Total Number of Spectra: 8

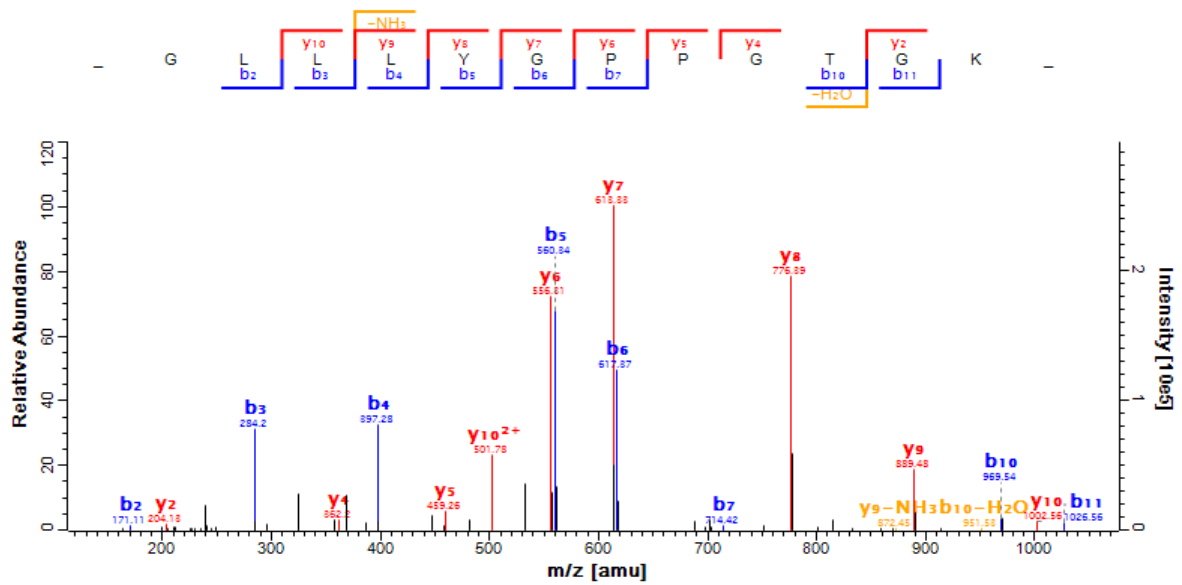
Number of Replicates (out of 8): 8

Best Match Score: 122.7

Best Match Posterior Error Probability: 0.00010371

Best Match Spectrum:

Scan number 42255 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** KATNAL2



Protein Group ID: 1612

Protein Accession Numbers: Q6AI08; K7EIX2; K7ELR8

Gene Names: HEATR6

Peptide Sequence: ESSGEIEAAPVTGTGR

Total Number of Spectra: 2

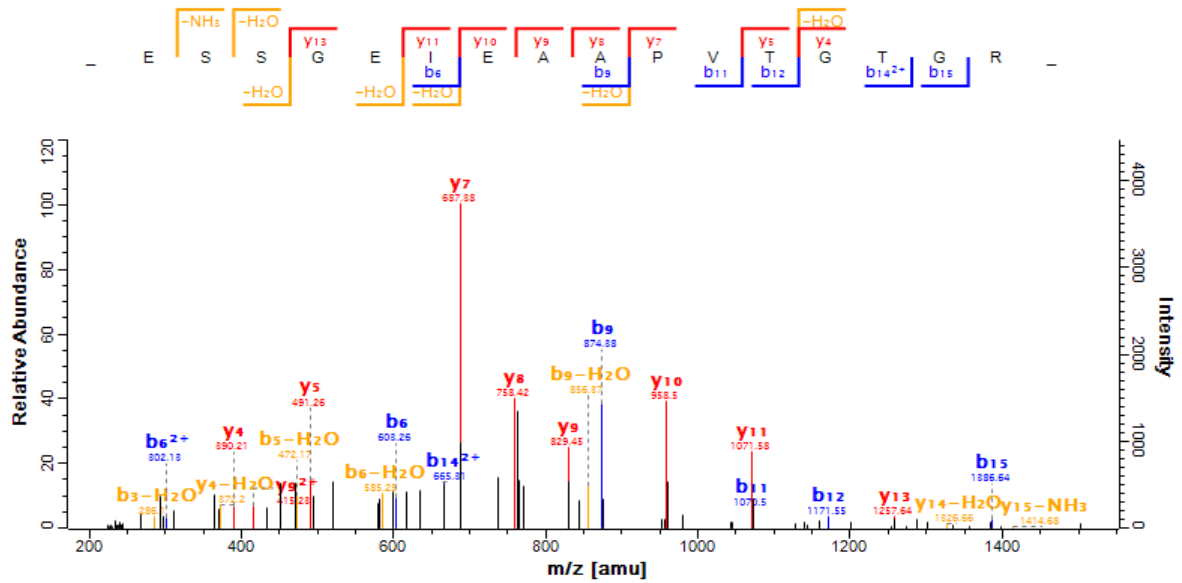
Number of Replicates (out of 8): 2

Best Match Score: 86.497

Best Match Posterior Error Probability: 0.00084114

Best Match Spectrum:

Scan number 18914 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** HEATR6



Protein Group ID: 1613

Protein Accession Numbers: Q6PJF5; Q6PJF5-2; K7EPV3; K7EKI1; K7EQ53; K7EIY3; K7EKA3; K7EQT5; K7EJ10; K7ELA9

Gene Names: RHBDF2

Peptide Sequence: NGGSVSSVSSSR

Total Number of Spectra: 1

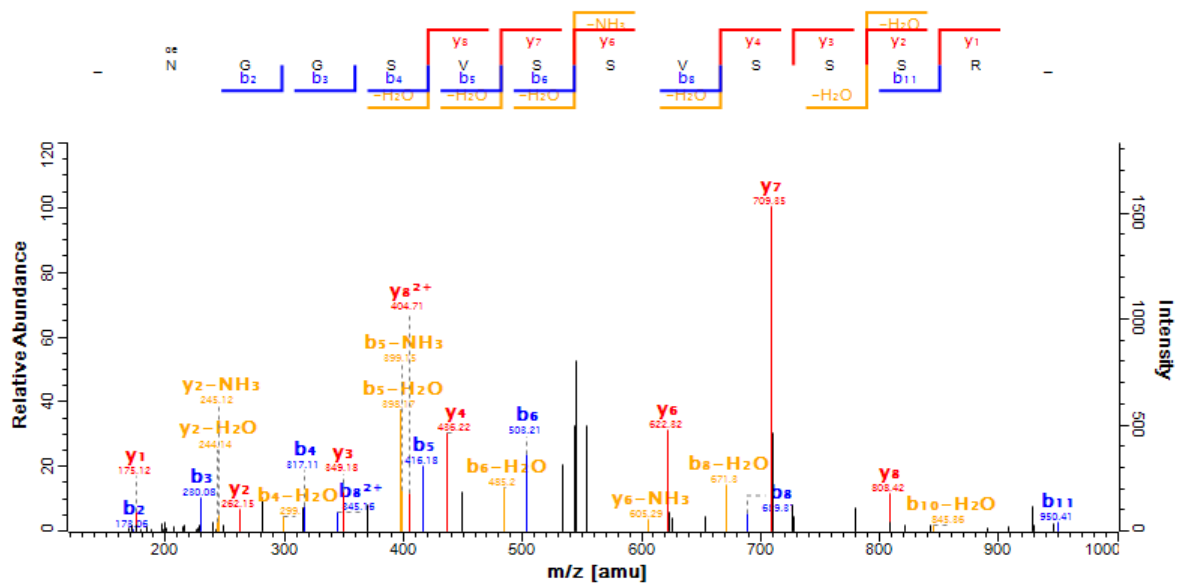
Number of Replicates (out of 8): 1

Best Match Score: 118.76

Best Match Posterior Error Probability: 0.00073596

Best Match Spectrum:

Scan number 4263 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS: CID **Genenames** RHBDF2



Protein Group ID: 1614

Protein Accession Numbers: K7EJ20; P36969; K7EKX7; P36969-2; K7ENB4; K7ERP4

Gene Names: GPX4

Peptide Sequence: DIDGHMVNLDK

Total Number of Spectra: 1

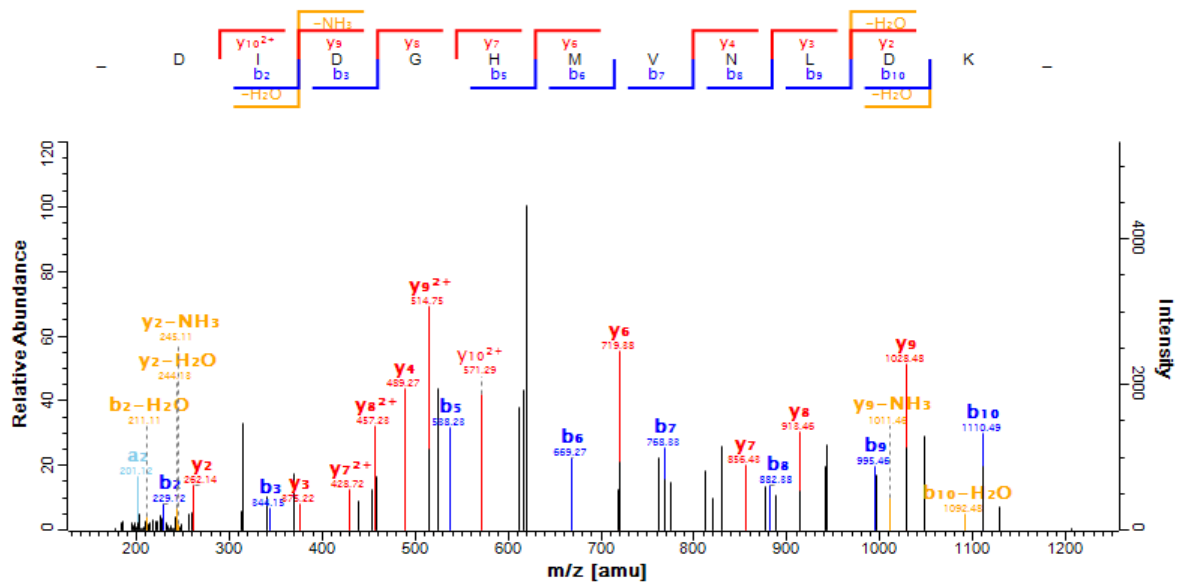
Number of Replicates (out of 8): 1

Best Match Score: 136.53

Best Match Posterior Error Probability: 3.36E-05

Best Match Spectrum:

Scan number 26623 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** GPX4



Protein Group ID: 1615

Protein Accession Numbers: Q86VR2; K7EQI9; K7EJ42; K7EPD0

Gene Names: FAM134C

Peptide Sequence: VPRPDALDNESWGFVHPR

Total Number of Spectra: 7

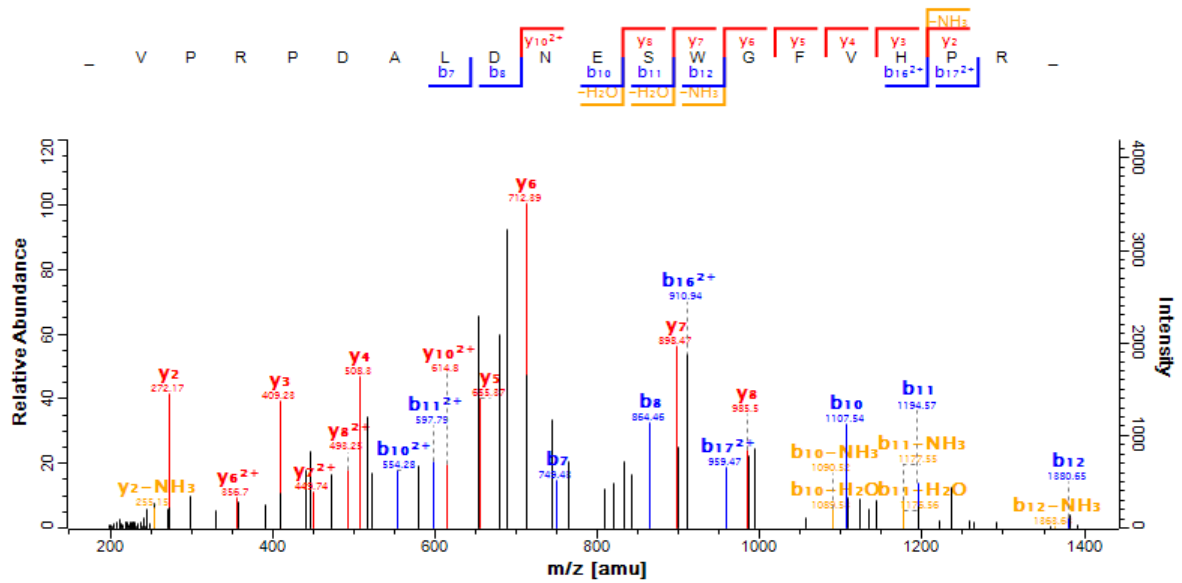
Number of Replicates (out of 8): 6

Best Match Score: 128.71

Best Match Posterior Error Probability: 0.00019335

Best Match Spectrum:

Scan number	48627	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	FAM134C



Protein Group ID: 1617

Protein Accession Numbers: Q13111; Q13111-3; Q13111-2; K7EJF1

Gene Names: CHAF1A

Peptide Sequence: GKADDMSDDQGTSVQSK

Total Number of Spectra: 1

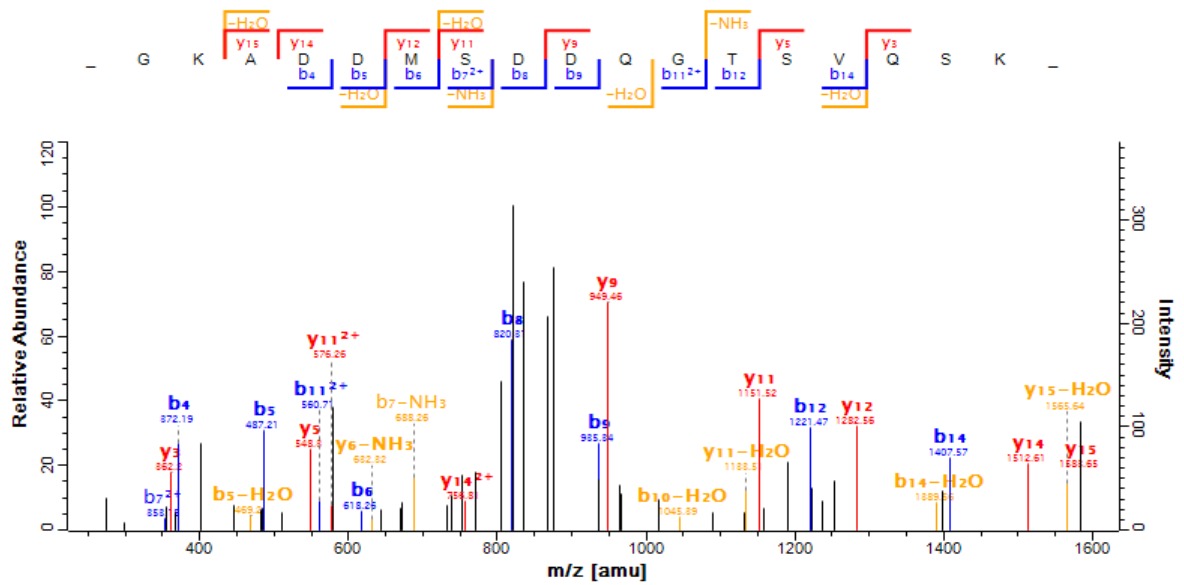
Number of Replicates (out of 8): 1

Best Match Score: 93.226

Best Match Posterior Error Probability: 0.0015502

Best Match Spectrum:

Scan number	4281	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	CHAF1A



Protein Group ID: 1619

Protein Accession Numbers: Q6P1N0; Q6P1N0-2; K7EJY5

Gene Names: CC2D1A

Peptide Sequence: GPASTPTYSPAPTQPAPR

Total Number of Spectra: 1

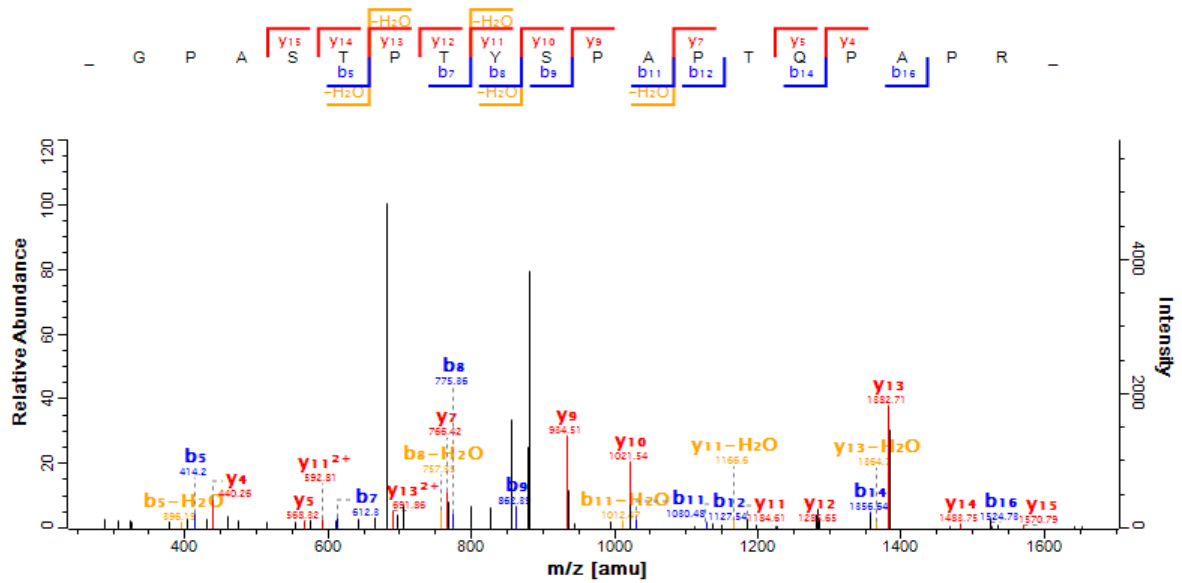
Number of Replicates (out of 8): 1

Best Match Score: 106.28

Best Match Posterior Error Probability: 0.00010039

Best Match Spectrum:

Scan number 20645 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CC2D1A



Protein Group ID: 1620

Protein Accession Numbers: Q96ND0; K7EK00; K7ERQ2

Gene Names: FAM210A

Peptide Sequence: KEEPDPPLQDK

Total Number of Spectra: 4

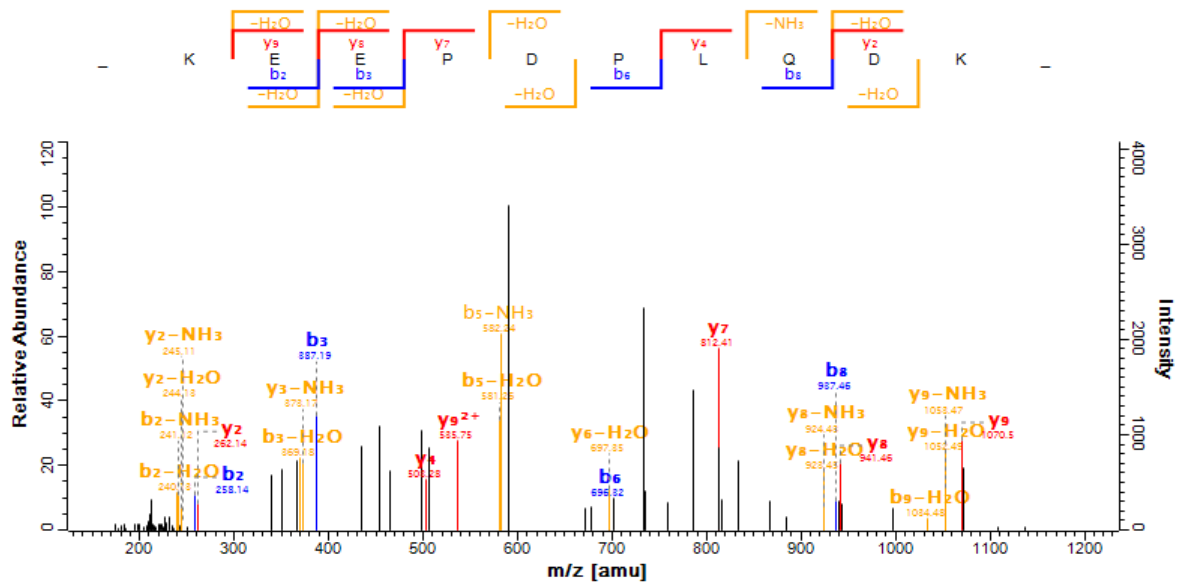
Number of Replicates (out of 8): 4

Best Match Score: 112.83

Best Match Posterior Error Probability: 0.00063548

Best Match Spectrum:

Scan number 10056 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** FAM210A



Protein Group ID: 1621

Protein Accession Numbers: P84243; K7EK07

Gene Names: H3F3A

Peptide Sequence: FQSAAAGALQEASYLEVGLFEDTNLC A I H A K

Total Number of Spectra: 18

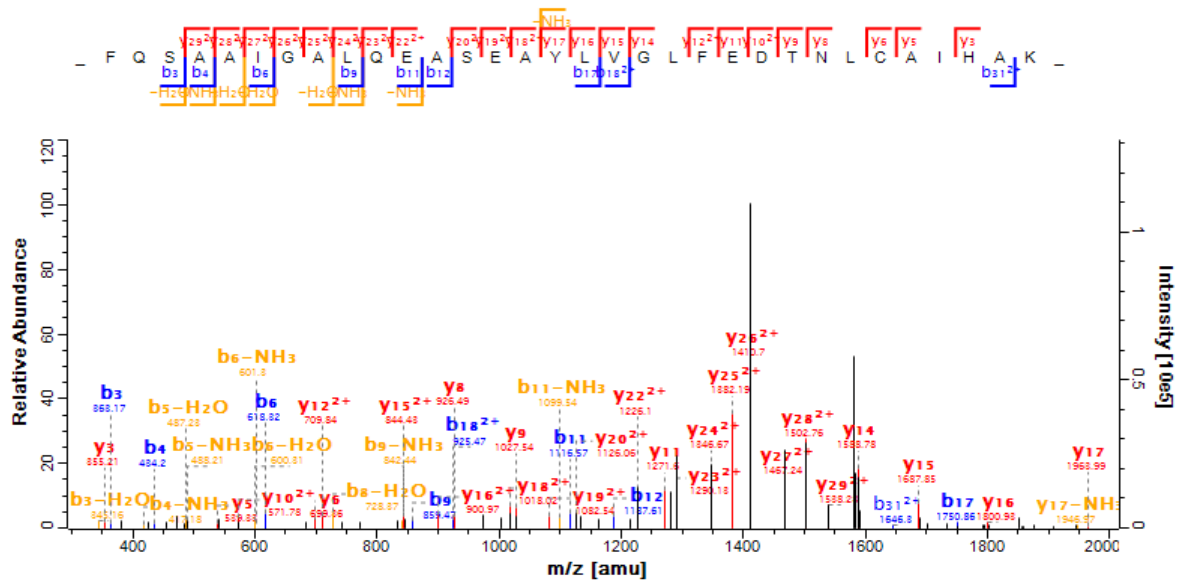
Number of Replicates (out of 8): 8

Best Match Score: 167.67

Best Match Posterior Error Probability: 1.25E-55

Best Match Spectrum:

Scan number 92614 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** H3F3A



Protein Group ID: 1624

Protein Accession Numbers: Q92947; Q92947-2; K7ERX1; K7EKH1; K7ES74

Gene Names: GCDH

Peptide Sequence: SSRPEFDWQDPLVLEEQLTTEILIR

Total Number of Spectra: 3

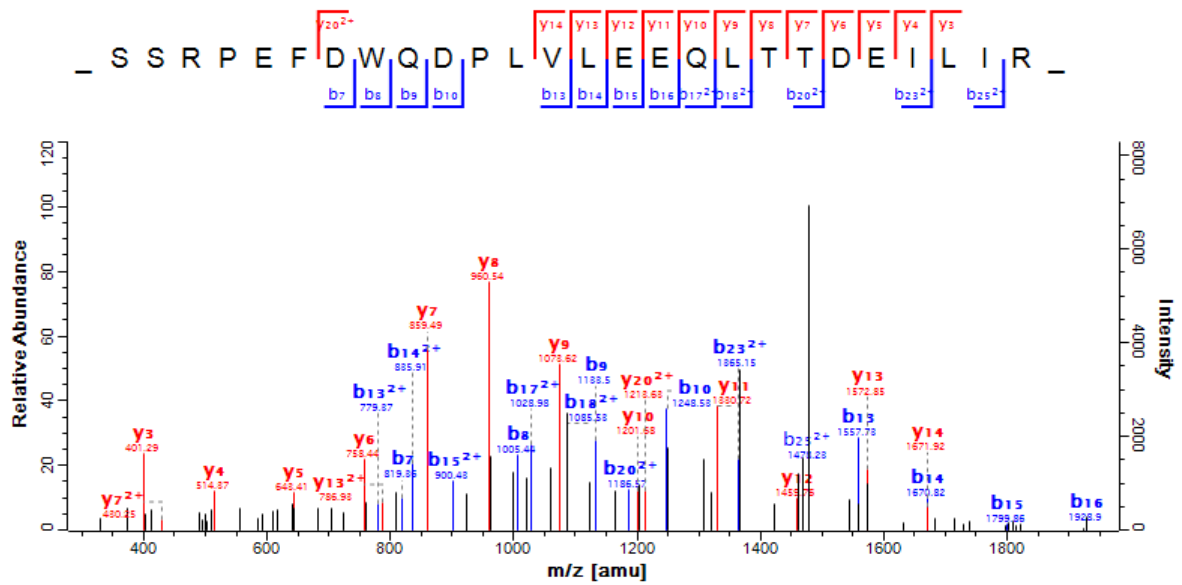
Number of Replicates (out of 8): 3

Best Match Score: 107.03

Best Match Posterior Error Probability: 1.35E-07

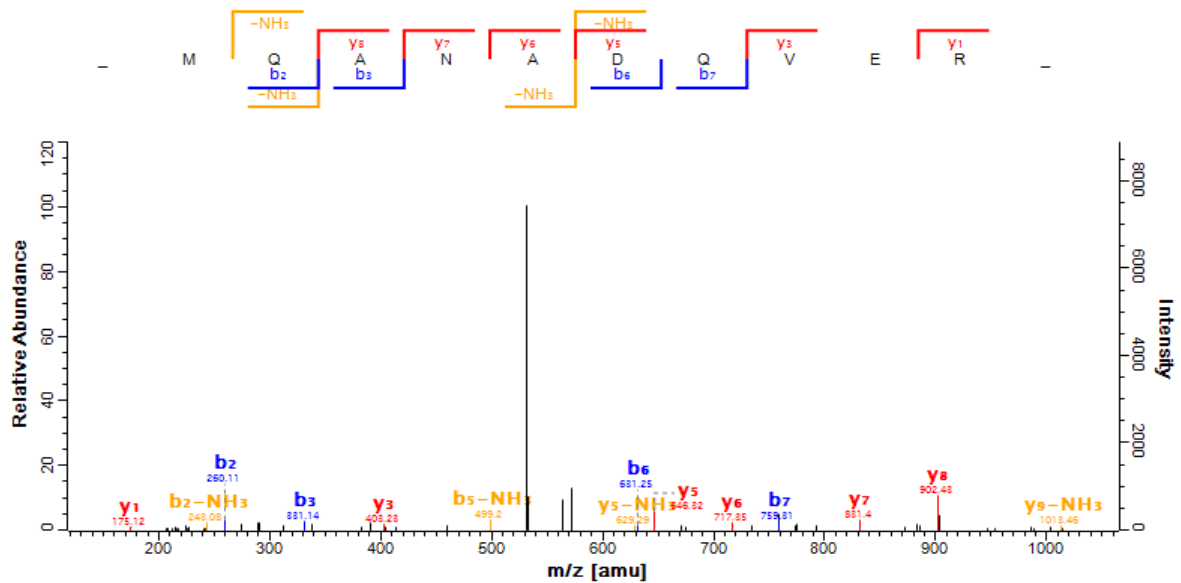
Best Match Spectrum:

Scan number 88016 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** GCDH



Protein Group ID: 1625
Protein Accession Numbers: K7EKI0; Q92817
Gene Names: EVPL
Peptide Sequence: MQANADQVER
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 84.658
Best Match Posterior Error Probability: 0.003286
Best Match Spectrum:

Scan number 6992 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** EVPL



Protein Group ID: 1626

Protein Accession Numbers: O60437; K7EKI8; K7EQ71

Gene Names: PPL

Peptide Sequence: VVLQQDPQAR

Total Number of Spectra: 2

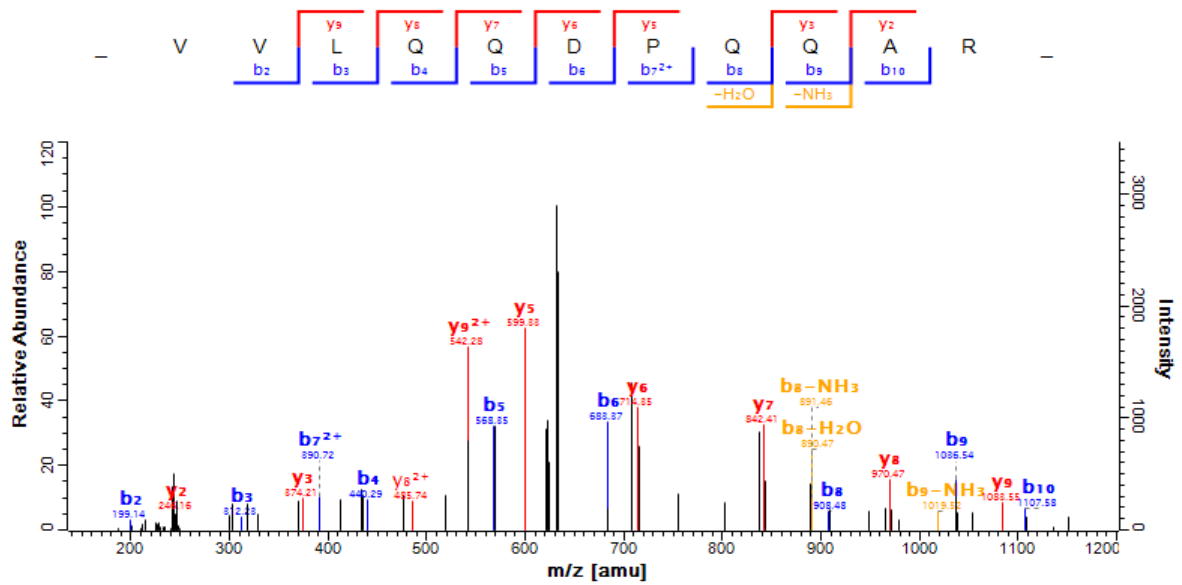
Number of Replicates (out of 8): 2

Best Match Score: 127.87

Best Match Posterior Error Probability: 4.28E-05

Best Match Spectrum:

Scan number	11888	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	PPL



Protein Group ID: 1632

Protein Accession Numbers: Q53F19; Q53F19-2; K7ELP6

Gene Names: C17orf85

Peptide Sequence: APGAEEDDSELQR

Total Number of Spectra: 9

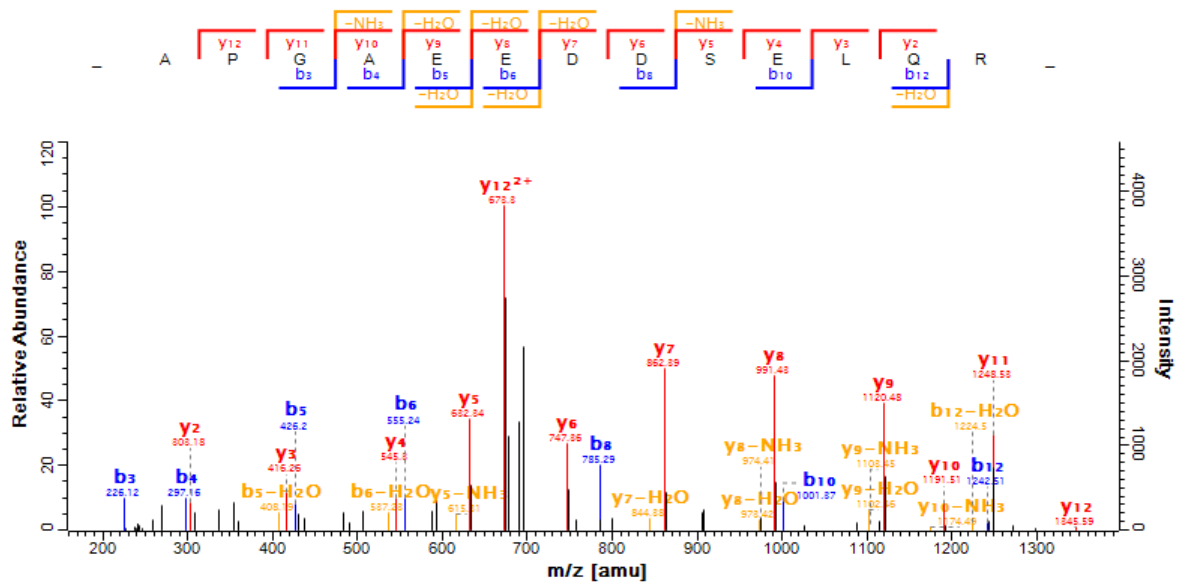
Number of Replicates (out of 8): 7

Best Match Score: 181.98

Best Match Posterior Error Probability: 9.81E-18

Best Match Spectrum:

Scan number 11084 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** C17orf85



Protein Group ID: 1636

Protein Accession Numbers: Q14457; K7ER46; K7EMA2

Gene Names: BECN1

Peptide Sequence: TQFNSEEQWTK

Total Number of Spectra: 1

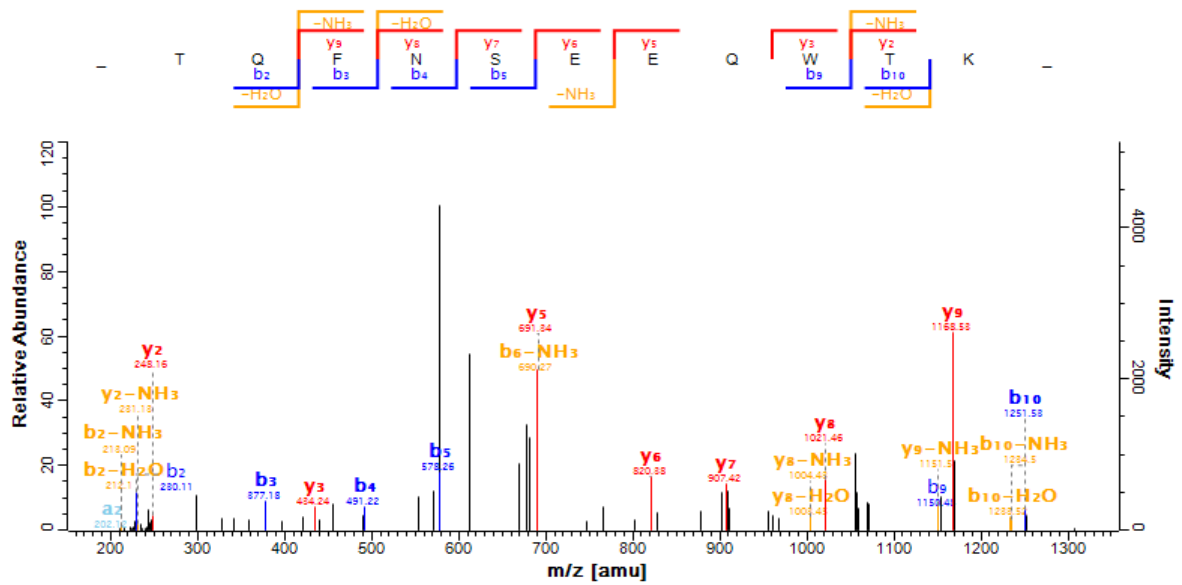
Number of Replicates (out of 8): 1

Best Match Score: 89.43

Best Match Posterior Error Probability: 0.0015369

Best Match Spectrum:

Scan number 25533 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** BECN1



Protein Group ID: 1638

Protein Accession Numbers: O75298; Q7RTN0; K7EMR7

Gene Names: RTN2

Peptide Sequence: TSLLAVYK

Total Number of Spectra: 5

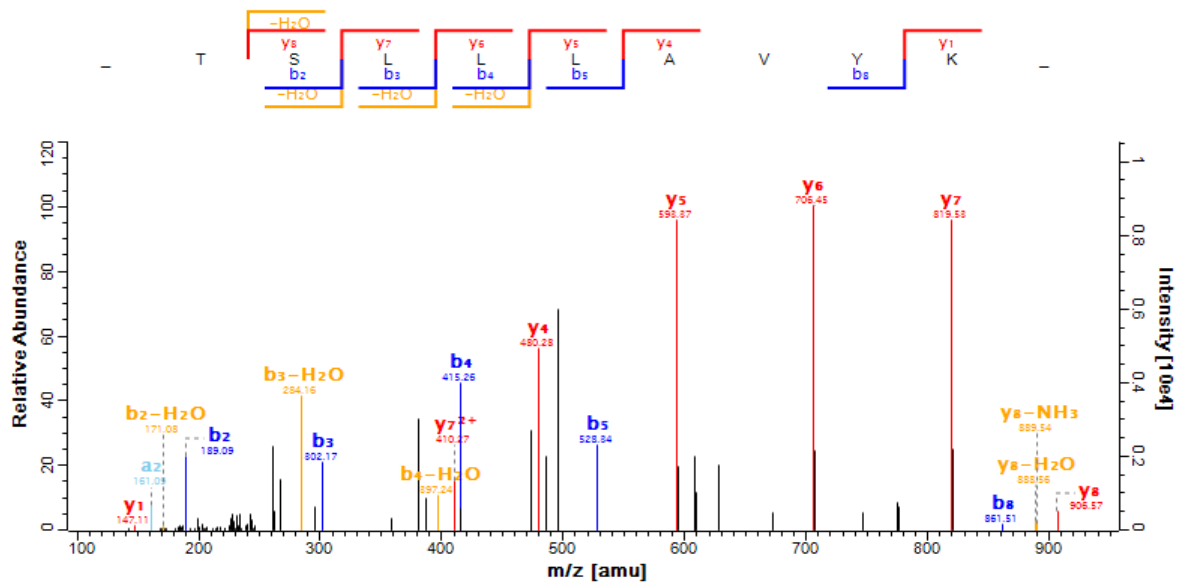
Number of Replicates (out of 8): 5

Best Match Score: 120.15

Best Match Posterior Error Probability: 0.00041533

Best Match Spectrum:

Scan number	58542	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	RTN2



Protein Group ID: 1640

Protein Accession Numbers: K7EMV4; K7EQ44; K7EPC8; P60002; K7EN05

Gene Names: ELOF1

Peptide Sequence: MTGTLETQFTCPFNHEK

Total Number of Spectra: 1

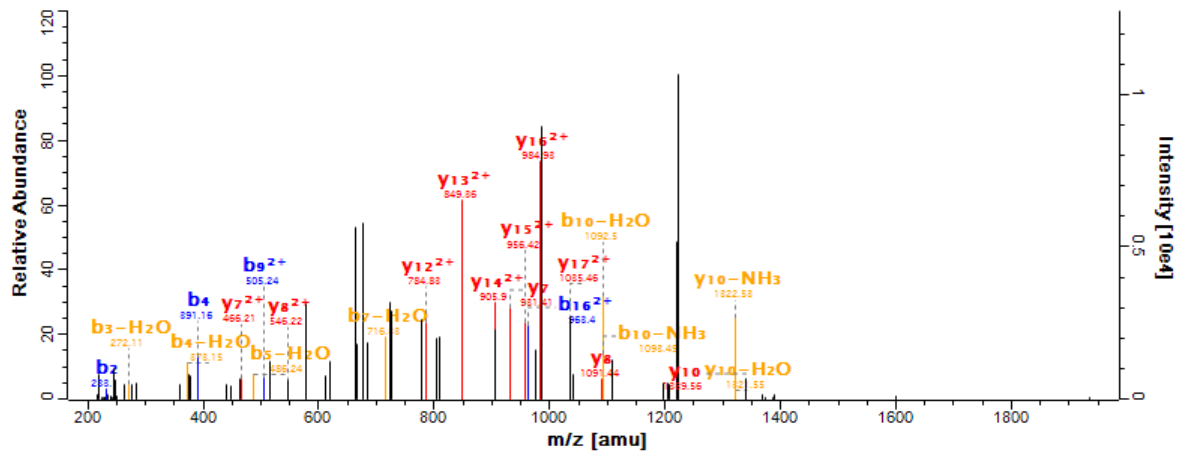
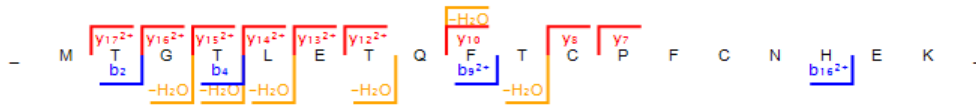
Number of Replicates (out of 8): 1

Best Match Score: 77.42

Best Match Posterior Error Probability: 0.0015252

Best Match Spectrum:

Scan number 46924 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ELOF1



Protein Group ID: 1642

Protein Accession Numbers: Q8N2U0; K7ERE1; K7ENI6

Gene Names: C17orf61

Peptide Sequence: LGALSGAAALGFASYGAHGAQFPDAGYK

Total Number of Spectra: 14

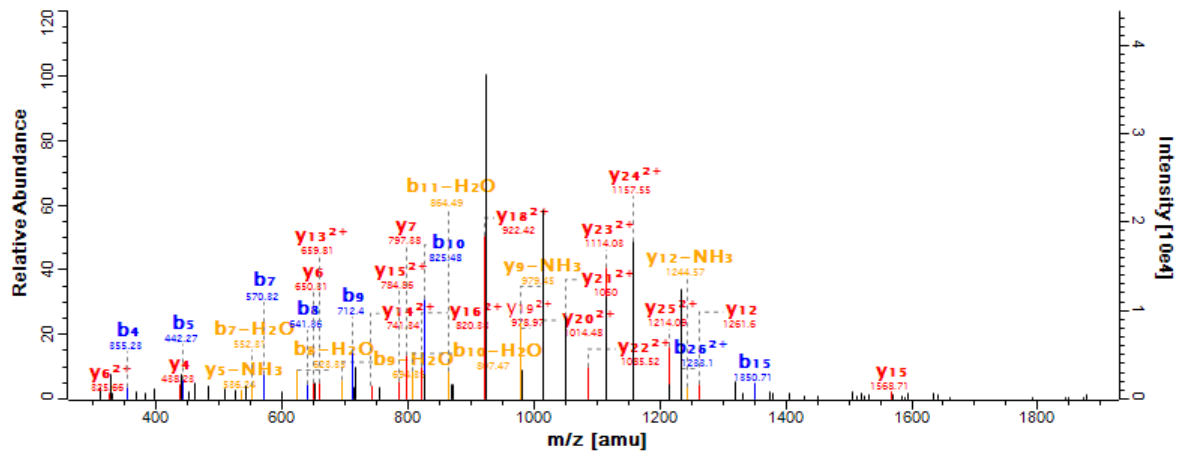
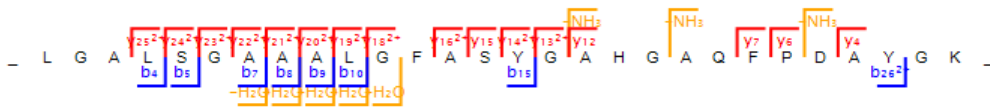
Number of Replicates (out of 8): 8

Best Match Score: 122.47

Best Match Posterior Error Probability: 3.97E-18

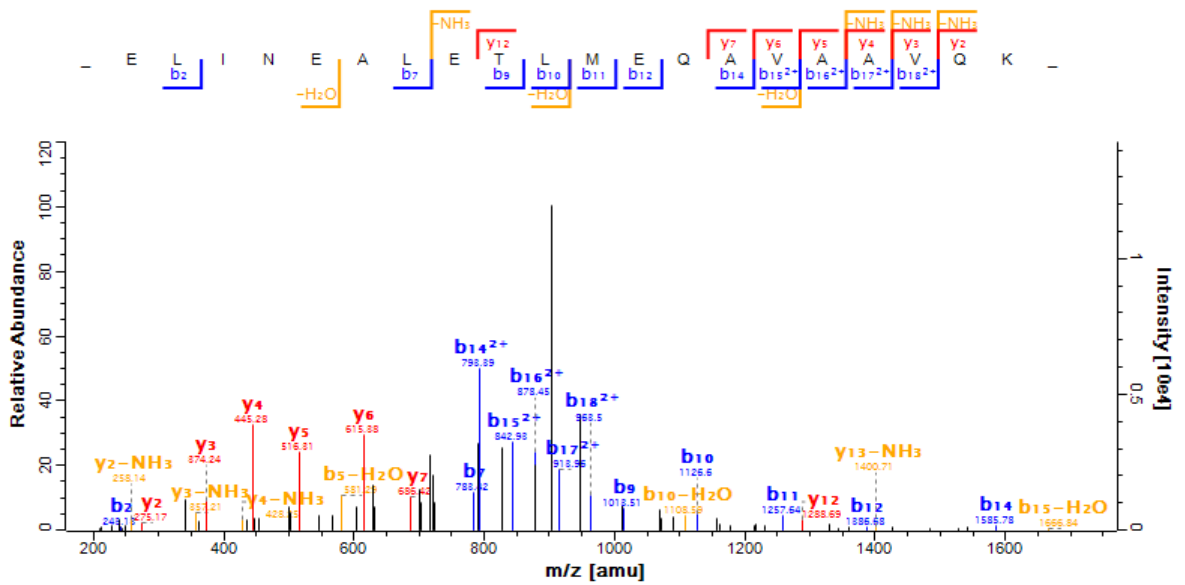
Best Match Spectrum:

Scan number 66603 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** C17orf61



Protein Group ID: 1647
Protein Accession Numbers: Q96C10; K7EPP0
Gene Names: DHX58
Peptide Sequence: ELINEALETLMEQAVAAVQK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 105.9
Best Match Posterior Error Probability: 5.30E-05
Best Match Spectrum:

Scan number 95695 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** DHX58



Protein Group ID: 1650

Protein Accession Numbers: Q17RN3; Q17RN3-2; K7EQT7; K7EQL1

Gene Names: FAM98C

Peptide Sequence: EAGAEVLSAGDGPGAEEDFLR

Total Number of Spectra: 4

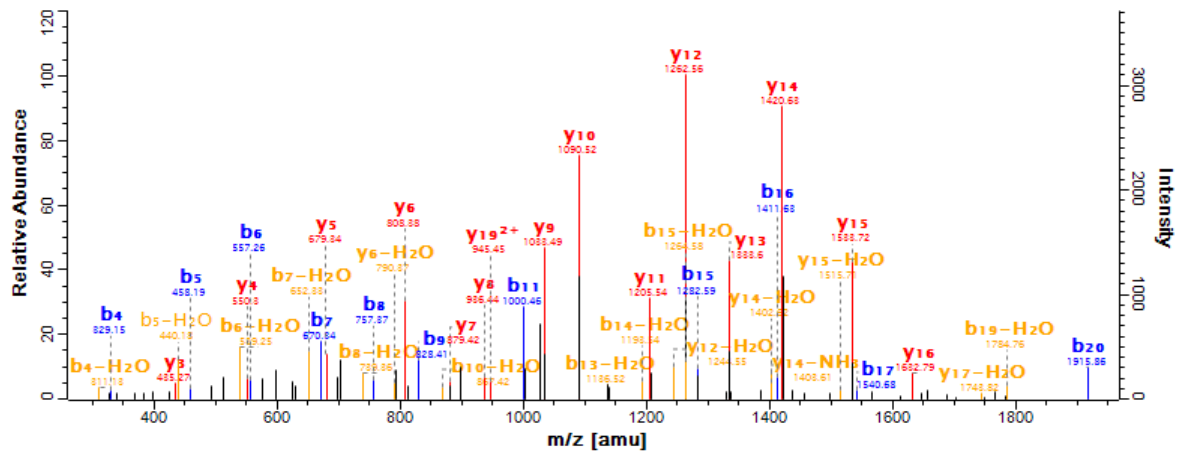
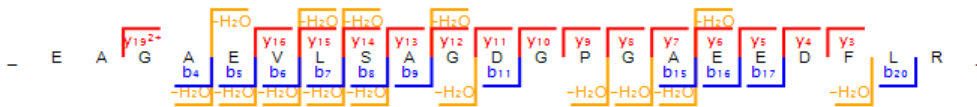
Number of Replicates (out of 8): 4

Best Match Score: 196.3

Best Match Posterior Error Probability: 3.29E-36

Best Match Spectrum:

Scan number	53577	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	FAM98C



Protein Group ID: 1654

Protein Accession Numbers: O95633; O95633-2; K7ES54

Gene Names: FSTL3

Peptide Sequence: DSCDGVCEGPGK

Total Number of Spectra: 1

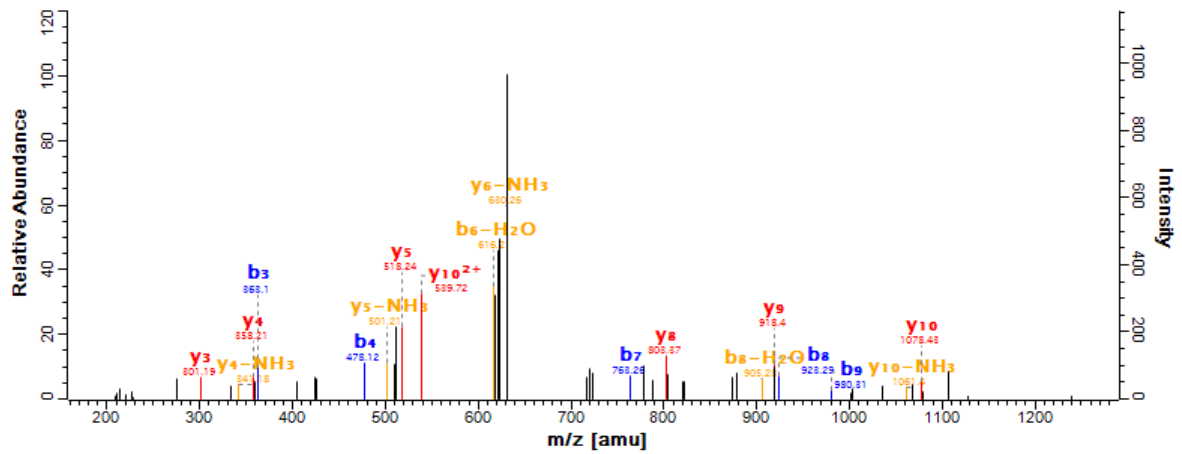
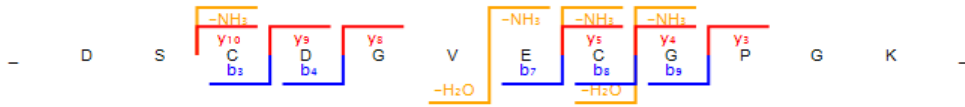
Number of Replicates (out of 8): 1

Best Match Score: 80.014

Best Match Posterior Error Probability: 0.0033637

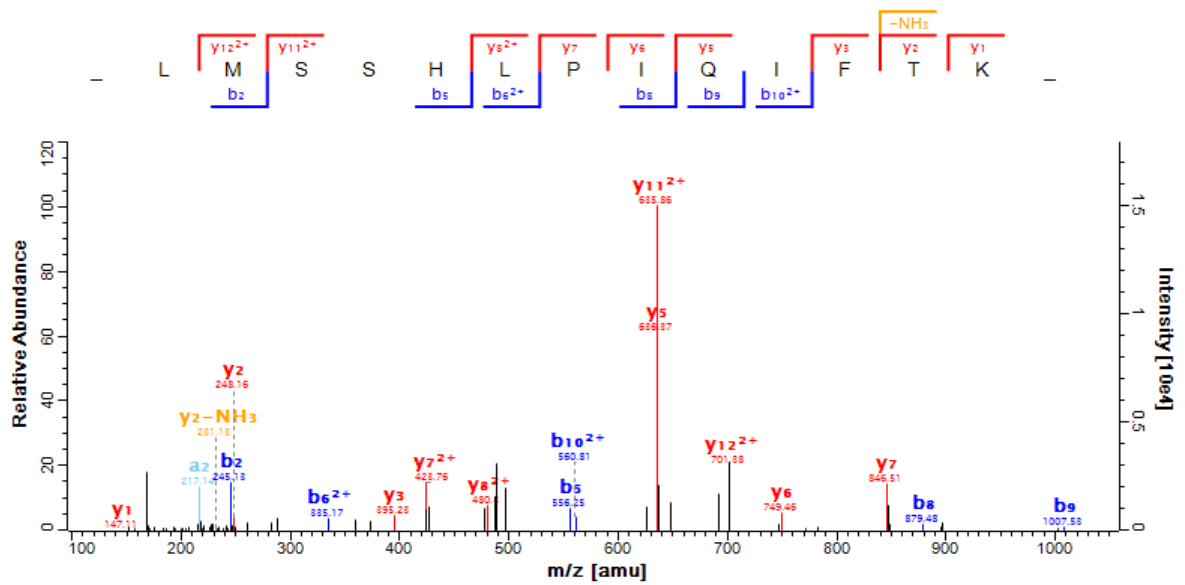
Best Match Spectrum:

Scan number 4391 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** FSTL3



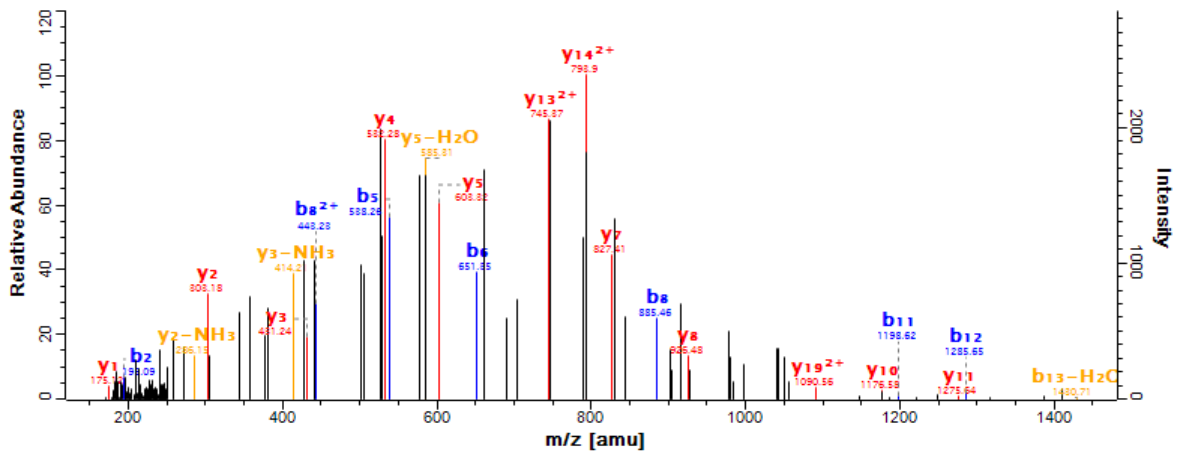
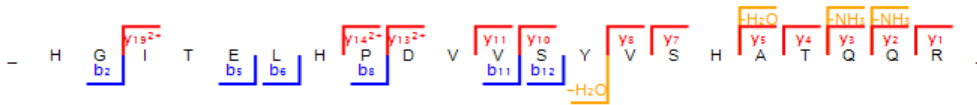
Protein Group ID: 1667
Protein Accession Numbers: O00204; O00204-2
Gene Names: SULT2B1
Peptide Sequence: LMSSHLPIQIFTK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 88.021
Best Match Posterior Error Probability: 0.0015942
Best Match Spectrum:

Scan number 57675 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** SULT2B1



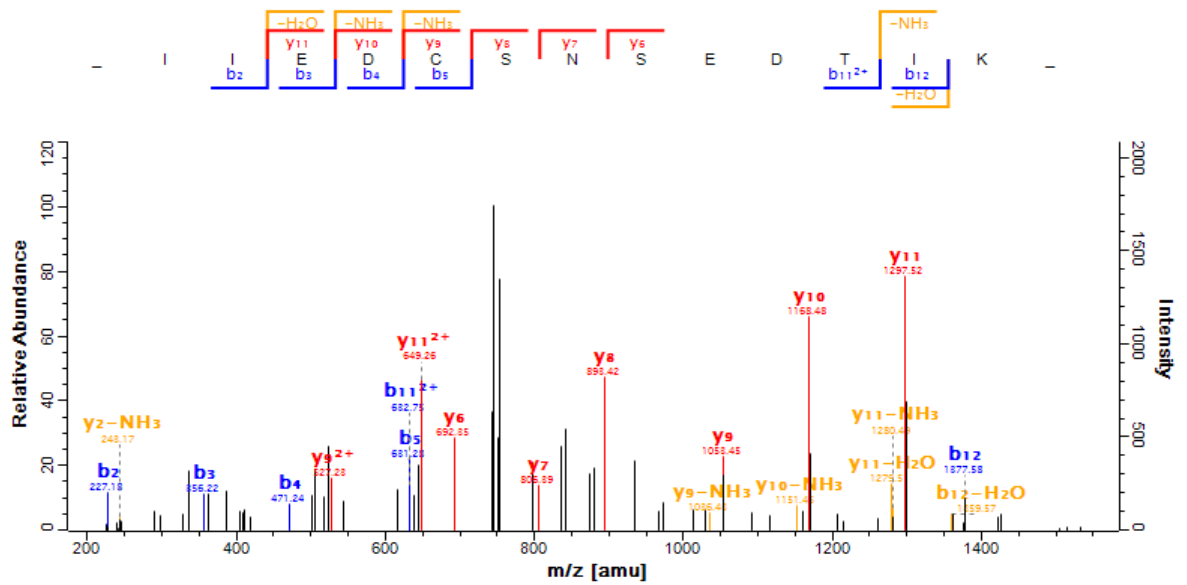
Protein Group ID: 1674
Protein Accession Numbers: O00268; Q5TBP5
Gene Names: TAF4
Peptide Sequence: HGITELHPDVVSYVSHATQQR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 71.872
Best Match Posterior Error Probability: 0.0010618
Best Match Spectrum:

Scan number 45222 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** TAF4



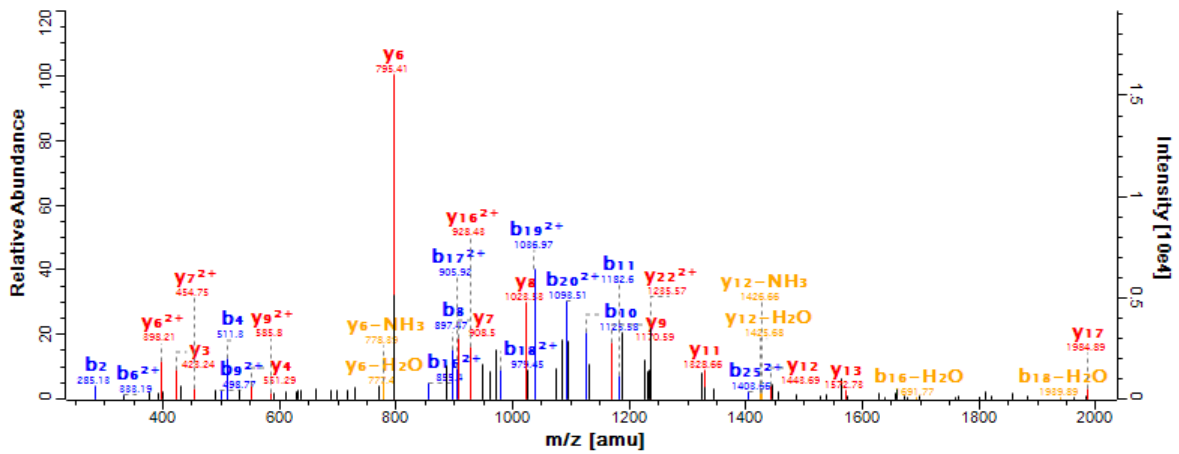
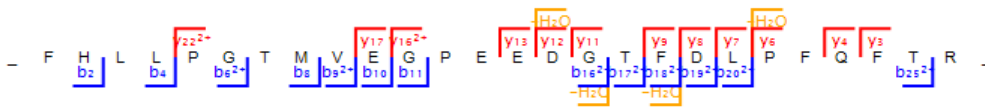
Protein Group ID: 1695
Protein Accession Numbers: O00507
Gene Names: USP9Y
Peptide Sequence: IEDCSNSEDTIK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 116.24
Best Match Posterior Error Probability: 0.00021059
Best Match Spectrum:

Scan number 12547 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** USP9Y



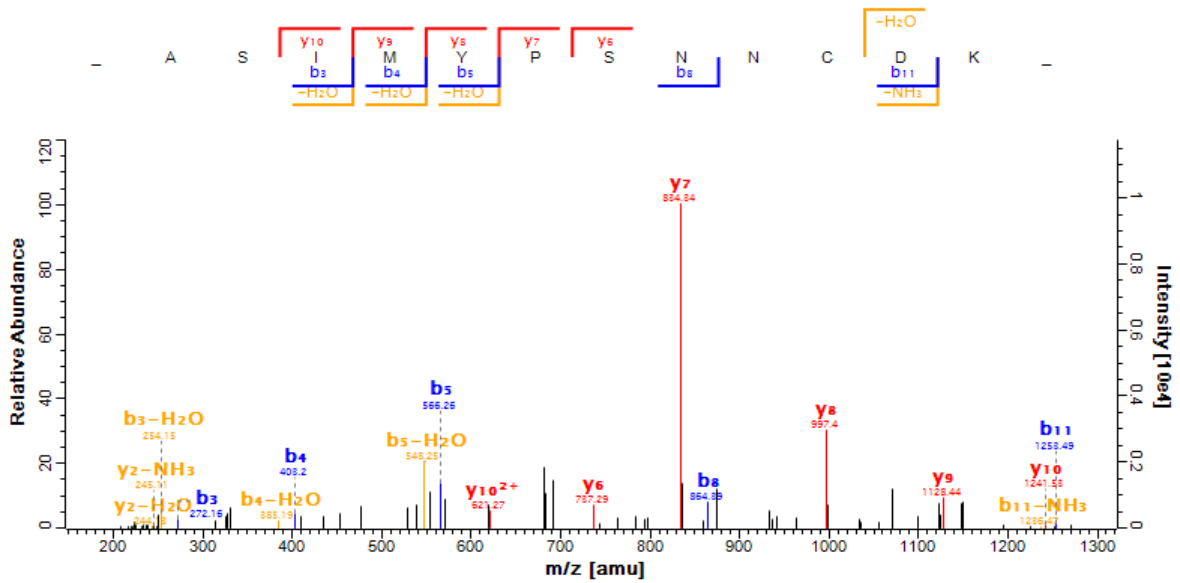
Protein Group ID: 1711
Protein Accession Numbers: O14613
Gene Names: CDC42EP2
Peptide Sequence: FHLLPGTMVEGPEEDGTDFDLPFQFTR
Total Number of Spectra: 3
Number of Replicates (out of 8): 2
Best Match Score: 130.37
Best Match Posterior Error Probability: 2.23E-16
Best Match Spectrum:

Scan number 88510 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CDC42EP2



Protein Group ID: 1713
Protein Accession Numbers: O14625
Gene Names: CXCL11
Peptide Sequence: ASIMYPSNNCDK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 80.69
Best Match Posterior Error Probability: 0.0032094
Best Match Spectrum:

Scan number 17619 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CXCL11



Protein Group ID: 1715

Protein Accession Numbers: O14647; O14647-2; B7Z3I4; O14647-3; G3V4S8

Gene Names: CHD2

Peptide Sequence: MWEEYDPVYGVGR

Total Number of Spectra: 3

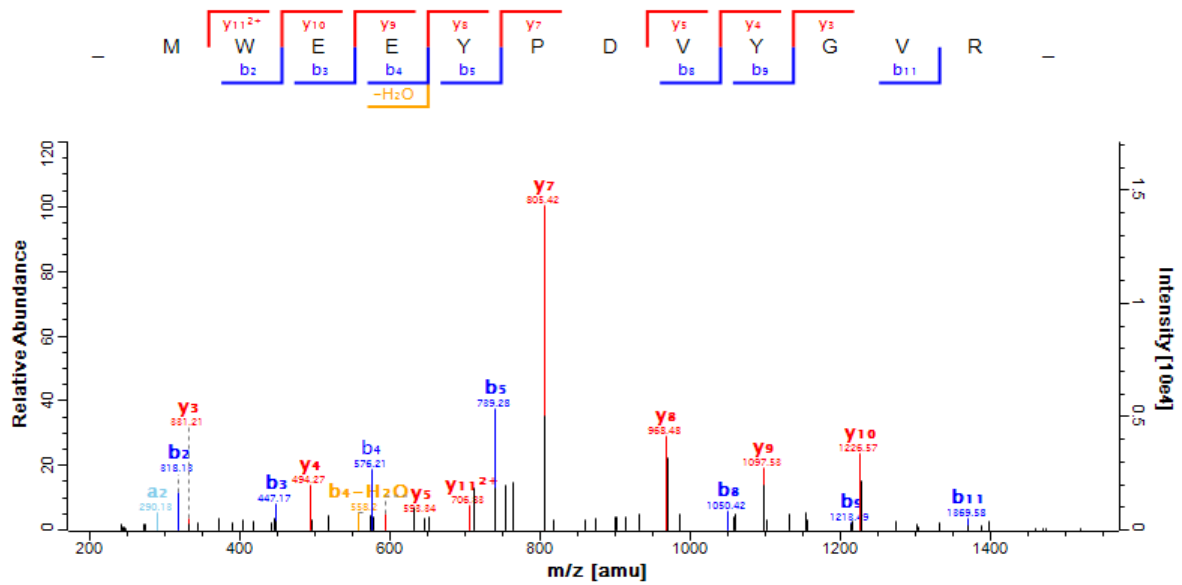
Number of Replicates (out of 8): 3

Best Match Score: 96.604

Best Match Posterior Error Probability: 0.00076716

Best Match Spectrum:

Scan number	51070	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	CHD2



Protein Group ID: 1718

Protein Accession Numbers: O14684

Gene Names: PTGES

Peptide Sequence: SVTYTLAQLPCASMLQILWVWELAAAR

Total Number of Spectra: 1

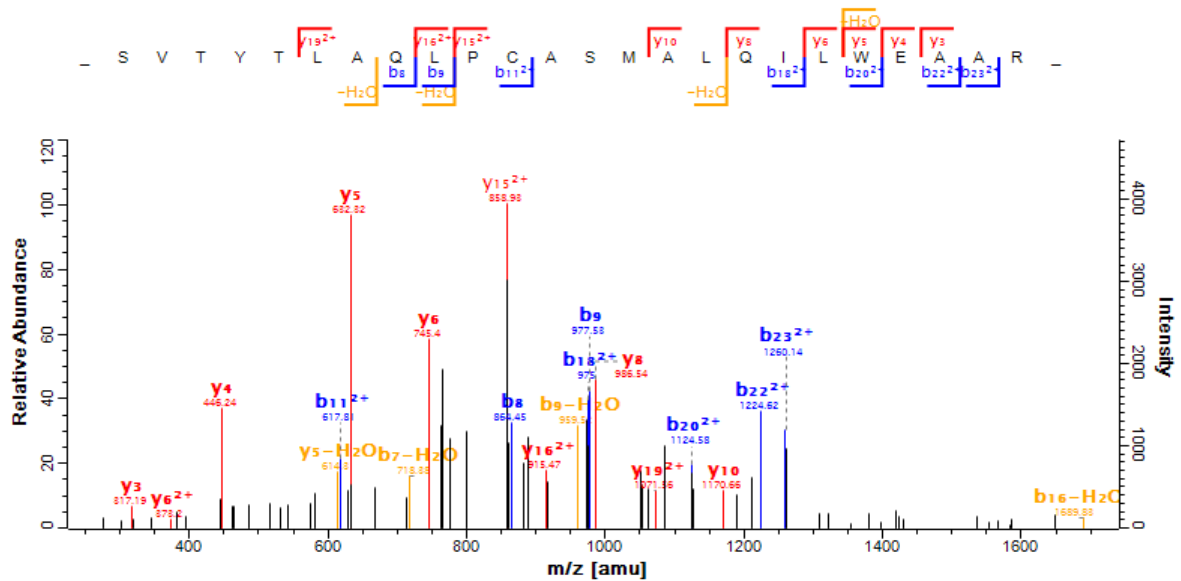
Number of Replicates (out of 8): 1

Best Match Score: 63.706

Best Match Posterior Error Probability: 0.0010064

Best Match Spectrum:

Scan number 94637 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PTGES



Protein Group ID: 1719

Protein Accession Numbers: O14715; Q99666; J3KQ37; F8W705; Q99666-2

Gene Names: RGP8;RGP5

Peptide Sequence: QMLNSVMQELEDYSEGGPLYK

Total Number of Spectra: 2

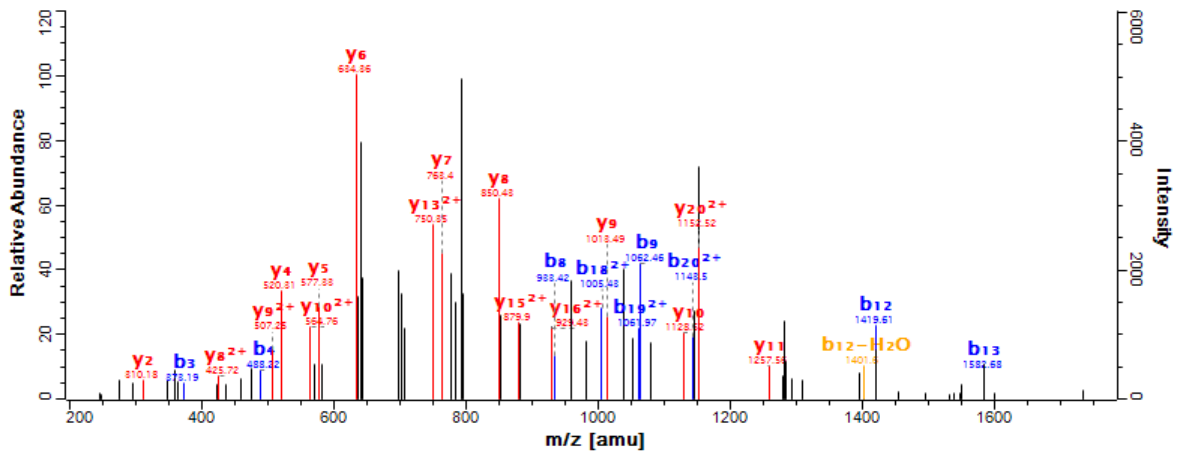
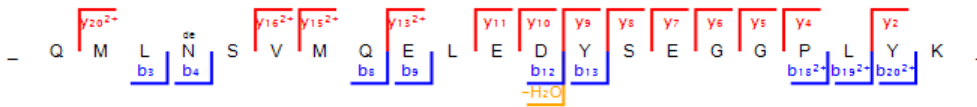
Number of Replicates (out of 8): 2

Best Match Score: 122.44

Best Match Posterior Error Probability: 4.23E-07

Best Match Spectrum:

Scan number 86298 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** RGP8;RGP5



Protein Group ID: 1720

Protein Accession Numbers: O14727; O14727-2; O14727-4; O14727-3

Gene Names: APAF1

Peptide Sequence: IWSFDLLLPLHELRL

Total Number of Spectra: 1

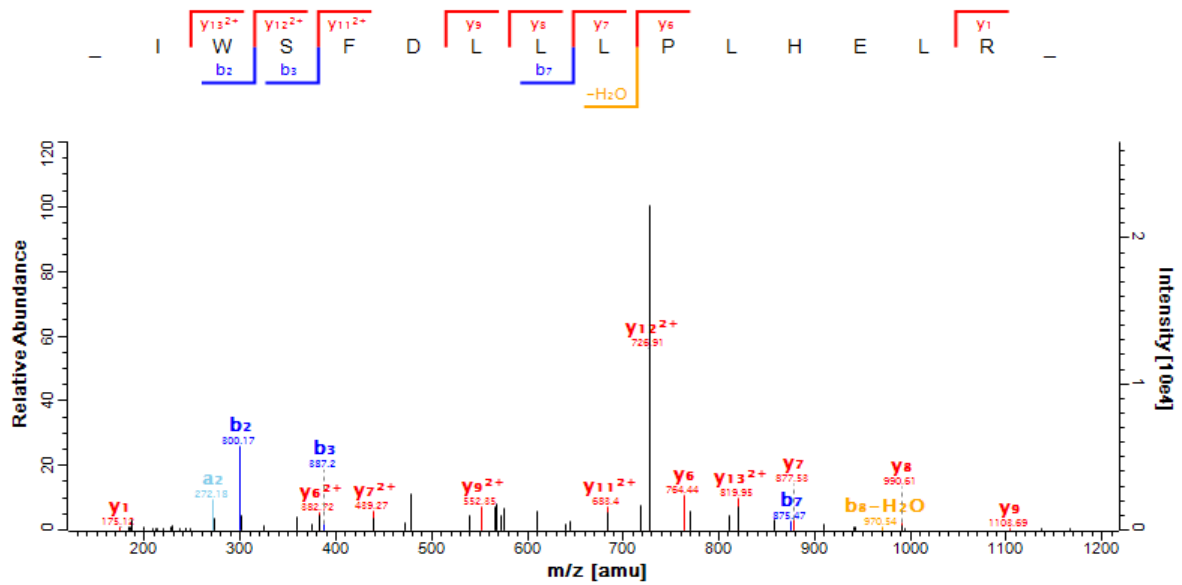
Number of Replicates (out of 8): 1

Best Match Score: 78.324

Best Match Posterior Error Probability: 0.0036605

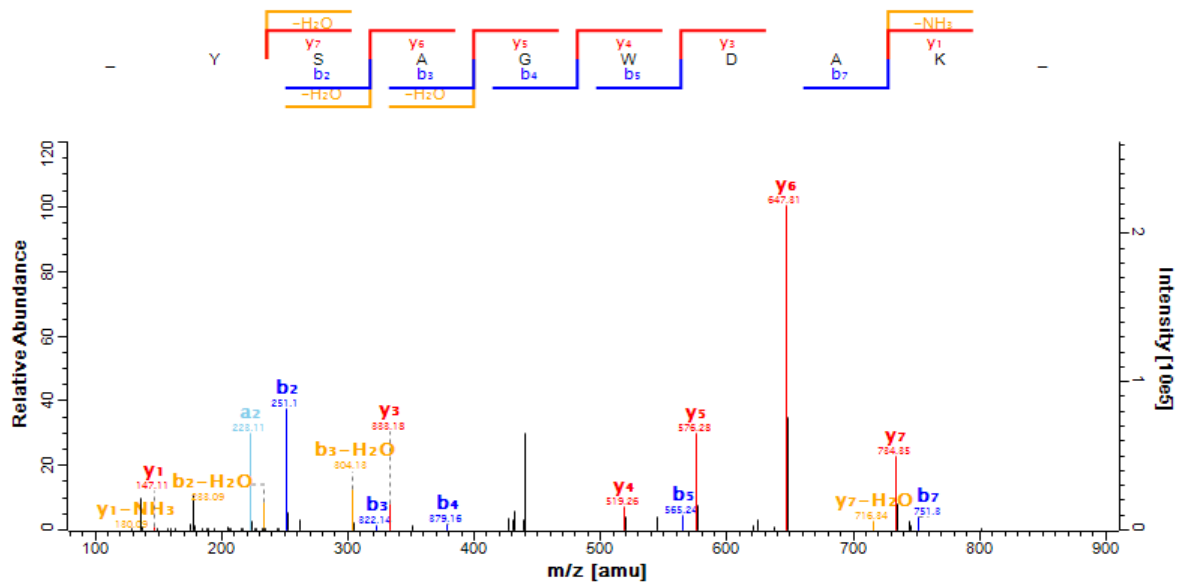
Best Match Spectrum:

Scan number 90371 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** APAF1



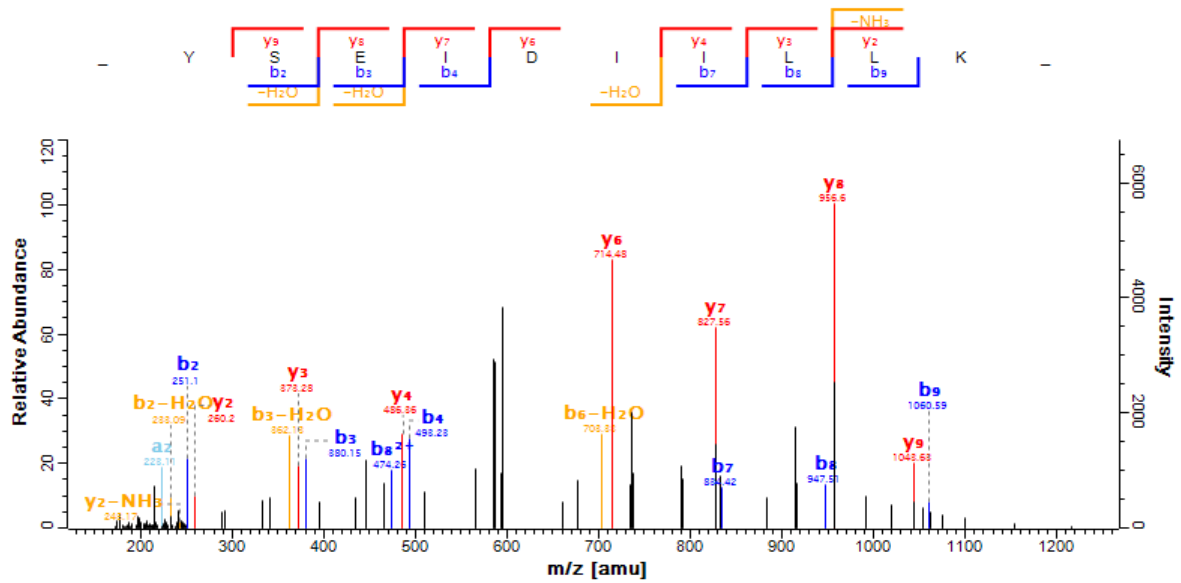
Protein Group ID: 1724
Protein Accession Numbers: O14756; O75452
Gene Names: HSD17B6;RDH16
Peptide Sequence: YSAGWDAK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 106.42
Best Match Posterior Error Probability: 0.0037968
Best Match Spectrum:

Scan number	13353	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	HSD17B6;RDH16



Protein Group ID: 1729
Protein Accession Numbers: O14787-2; O14787
Gene Names: TNPO2
Peptide Sequence: YSEIDIILLK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 99.568
Best Match Posterior Error Probability: 0.00080511
Best Match Spectrum:

Scan number	65543	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	TNPO2



Protein Group ID: 1743

Protein Accession Numbers: O14950

Gene Names: MYL12B

Peptide Sequence: NPTDAYLDAMMNEAPGPI N F T M F L T M F G E K

Total Number of Spectra: 12

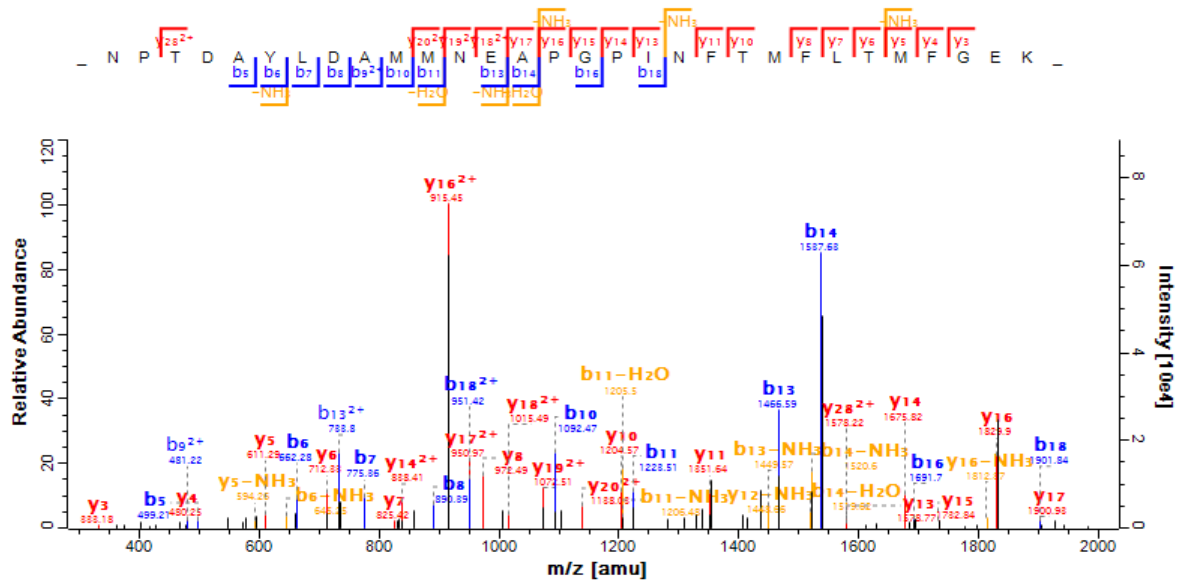
Number of Replicates (out of 8): 8

Best Match Score: 175.59

Best Match Posterior Error Probability: 1.30E-50

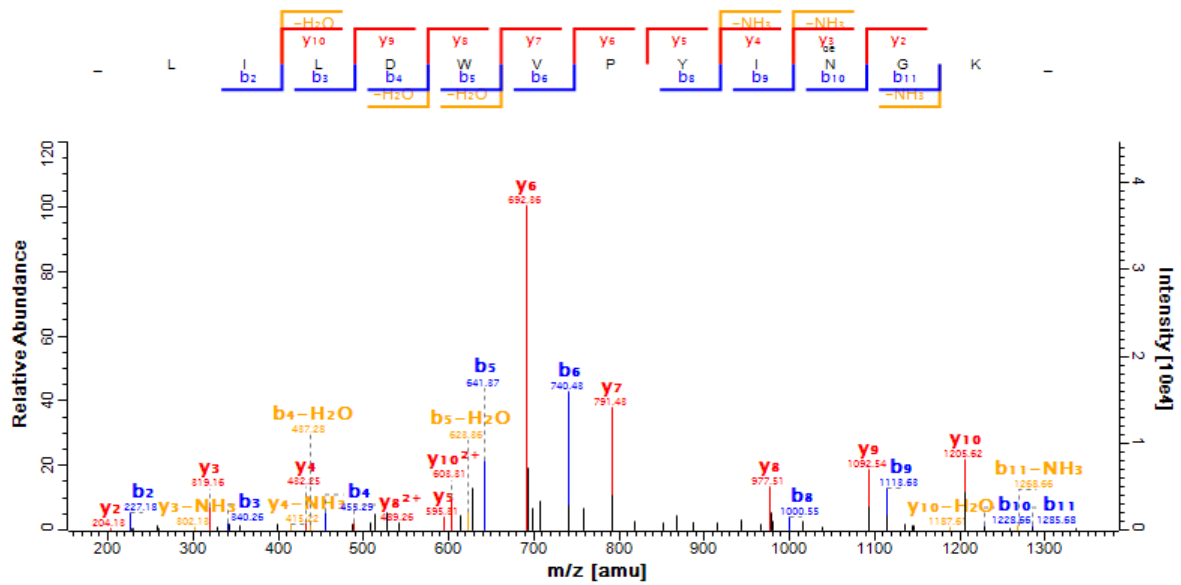
Best Match Spectrum:

Scan number 97395 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MYL12B



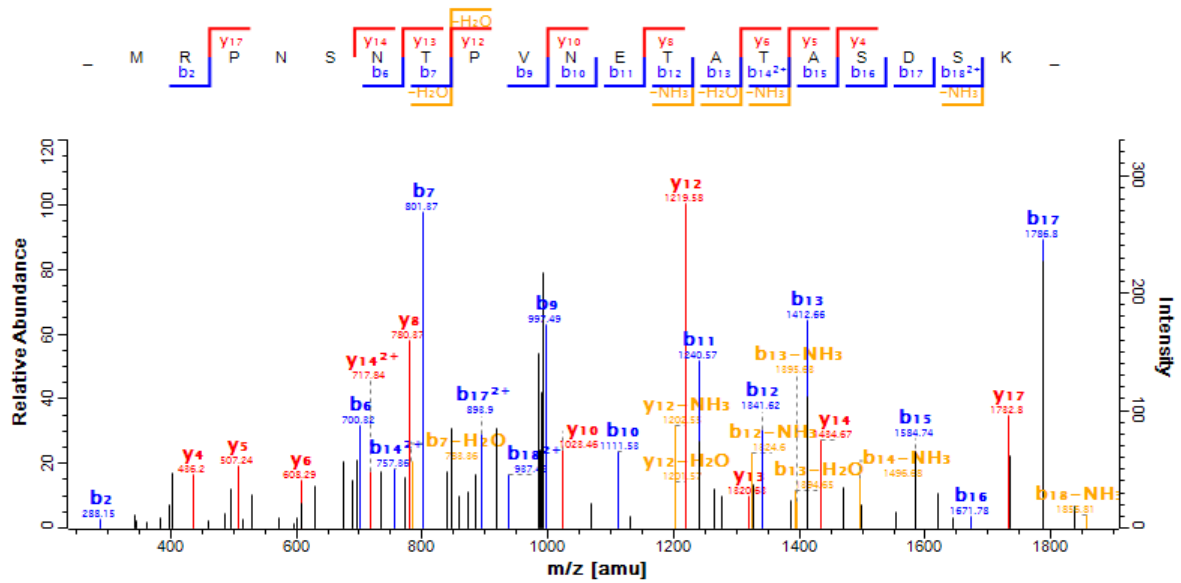
Protein Group ID: 1744
Protein Accession Numbers: O14957
Gene Names: UQCR11
Peptide Sequence: LILDWVPYINGK
Total Number of Spectra: 7
Number of Replicates (out of 8): 6
Best Match Score: 172.17
Best Match Posterior Error Probability: 6.82E-09
Best Match Spectrum:

Scan number 79450 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** UQCR11



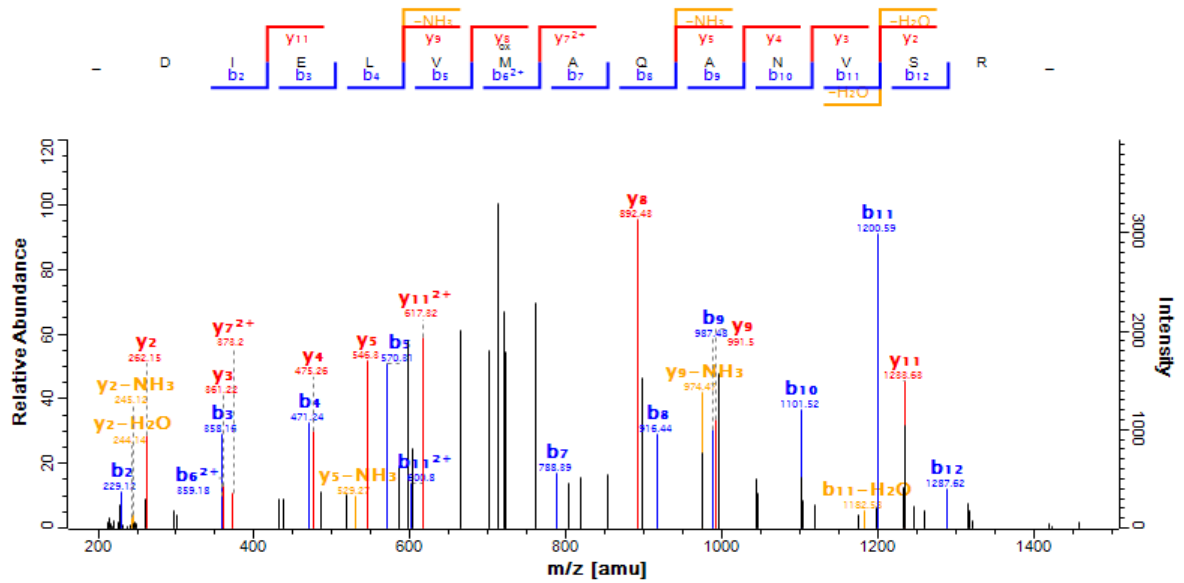
Protein Group ID: 1753
Protein Accession Numbers: O15014
Gene Names: ZNF609
Peptide Sequence: MRPNSNTPVNETATASDSK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 128.74
Best Match Posterior Error Probability: 5.81E-05
Best Match Spectrum:

Scan number 10830 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ZNF609



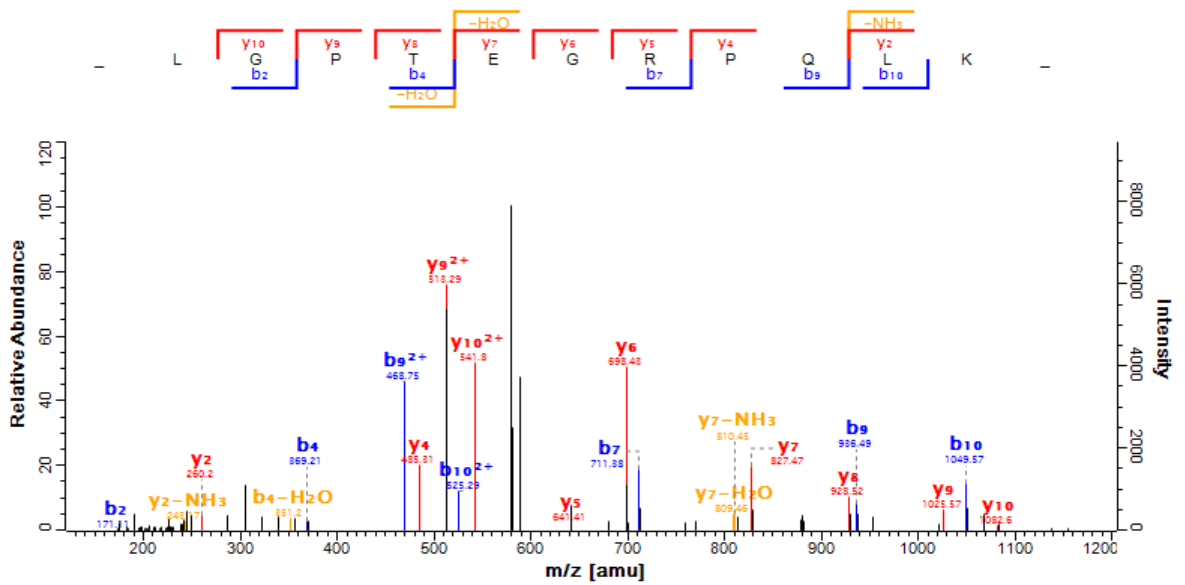
Protein Group ID: 1758
Protein Accession Numbers: O15069
Gene Names: NACAD
Peptide Sequence: DIELVMAQANVSR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 134.04
Best Match Posterior Error Probability: 0.0022958
Best Match Spectrum:

Scan number 46085 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** NACAD



Protein Group ID: 1776
Protein Accession Numbers: O15235
Gene Names: MRPS12
Peptide Sequence: LGPTEGRPQLK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 110.08
Best Match Posterior Error Probability: 0.00071137
Best Match Spectrum:

Scan number 14797 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** MRPS12



Protein Group ID: 1787

Protein Accession Numbers: O15379-2; O15379; E7EWI8

Gene Names: HDAC3

Peptide Sequence: PYQASQHDMCR

Total Number of Spectra: 10

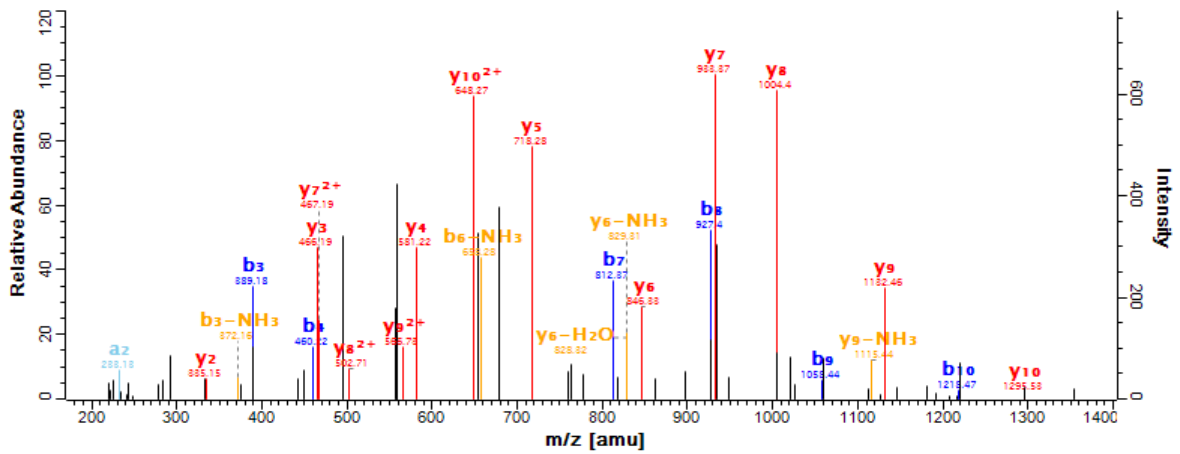
Number of Replicates (out of 8): 8

Best Match Score: 162.68

Best Match Posterior Error Probability: 1.13E-05

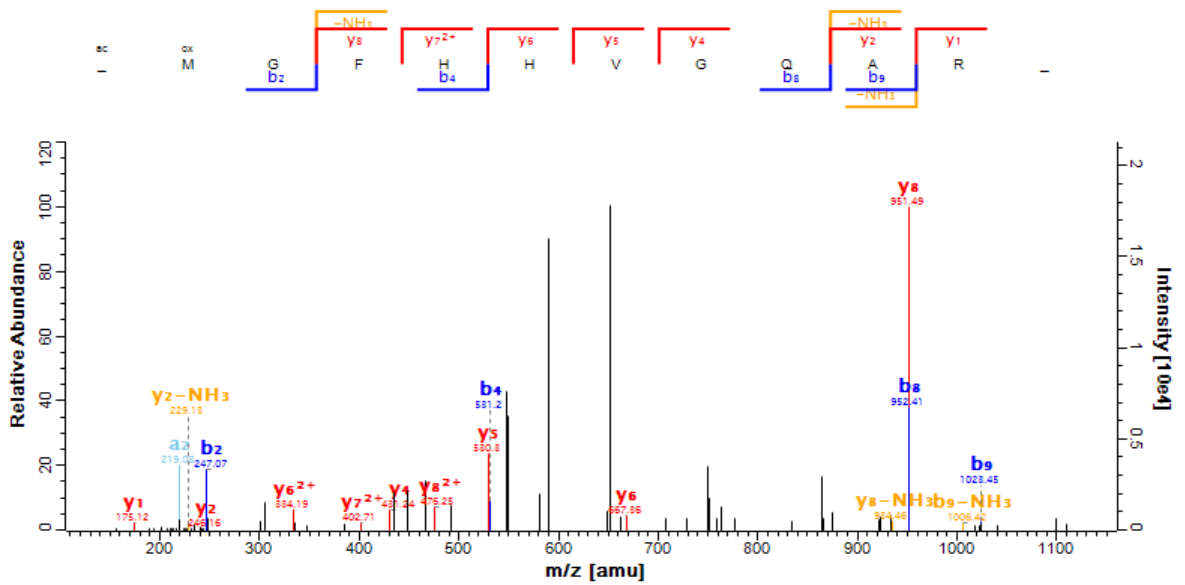
Best Match Spectrum:

Scan number 5144 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** HDAC3



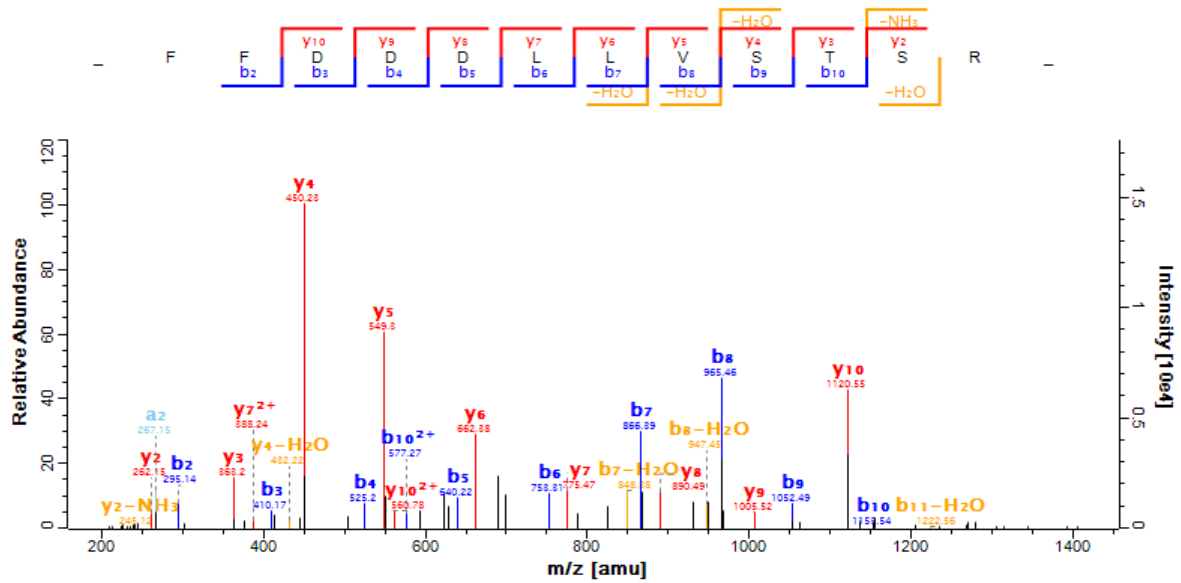
Protein Group ID: 1827
Protein Accession Numbers: O43439-4
Gene Names:
Peptide Sequence: MGFHHVGQAR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 106.6
Best Match Posterior Error Probability: 0.0025465
Best Match Spectrum:

Scan number 29791 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Pepti...** 106.6



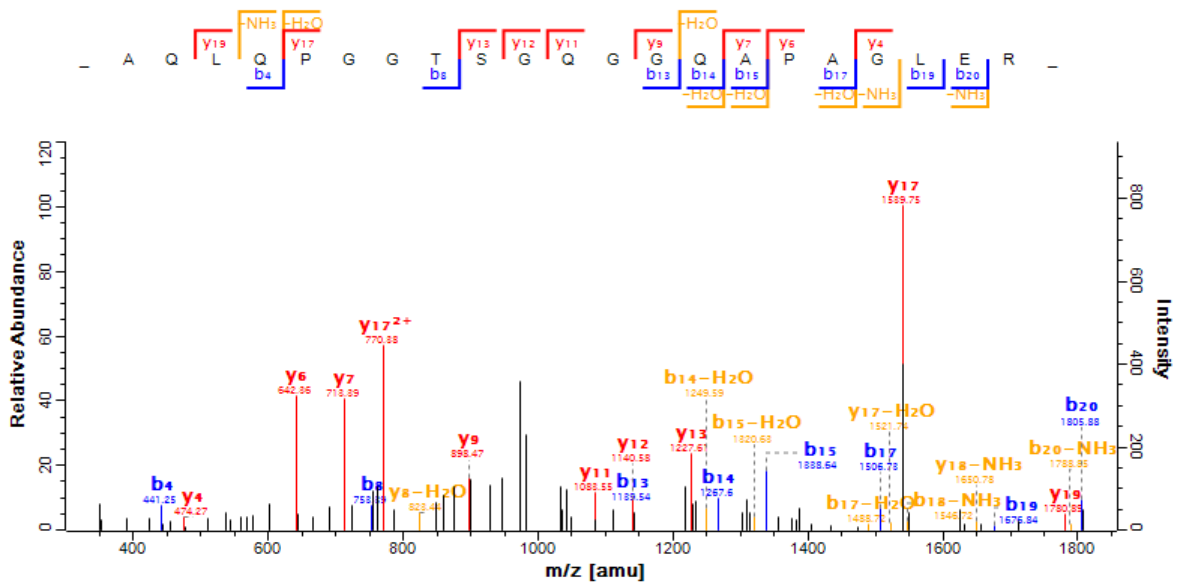
Protein Group ID: 1863
Protein Accession Numbers: O43924
Gene Names: PDE6D
Peptide Sequence: FD²⁺DDLLVSTSR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 147.33
Best Match Posterior Error Probability: 5.50E-06
Best Match Spectrum:

Scan number 56072 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PDE6D



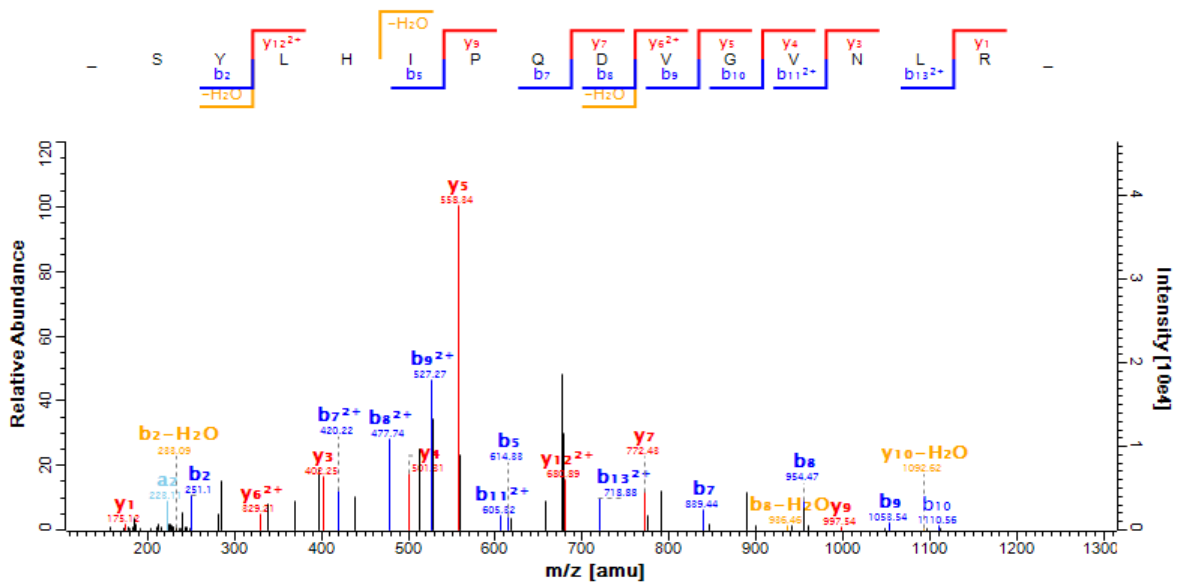
Protein Group ID: 1871
Protein Accession Numbers: O60269
Gene Names: GPRIN2
Peptide Sequence: AQLQPGGTSGQGQAPAGLER
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 78.975
Best Match Posterior Error Probability: 0.00034979
Best Match Spectrum:

Scan number 22169 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** GPRIN2



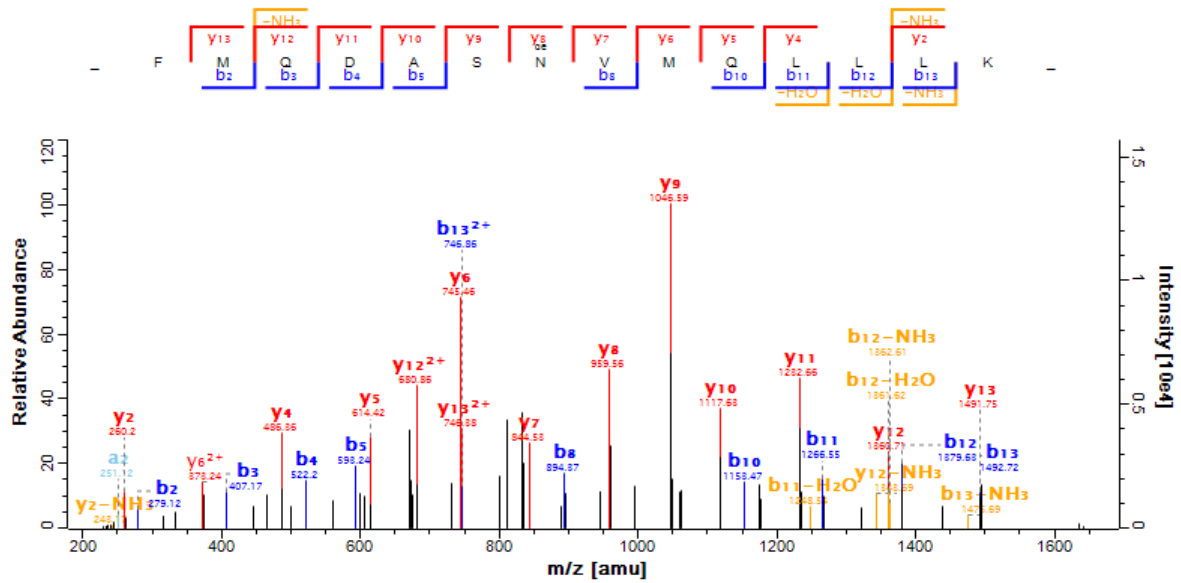
Protein Group ID: 1887
Protein Accession Numbers: O60508; Q5SRN1
Gene Names: CDC40
Peptide Sequence: SYLHIPQDVGVNLR
Total Number of Spectra: 7
Number of Replicates (out of 8): 6
Best Match Score: 112.08
Best Match Posterior Error Probability: 0.00014601
Best Match Spectrum:

Scan number 51407 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CDC40



Protein Group ID: 1888
Protein Accession Numbers: O60518
Gene Names: RANBP6
Peptide Sequence: FMQDASNVMQLLLK
Total Number of Spectra: 9
Number of Replicates (out of 8): 6
Best Match Score: 181.71
Best Match Posterior Error Probability: 2.60E-18
Best Match Spectrum:

Scan number 84147 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** RANBP6



Protein Group ID: 1913

Protein Accession Numbers: O60942; O60942-2; O60942-4; Q5TCW7; O60942-3

Gene Names: RNGTT

Peptide Sequence: YDSQVAEENR

Total Number of Spectra: 3

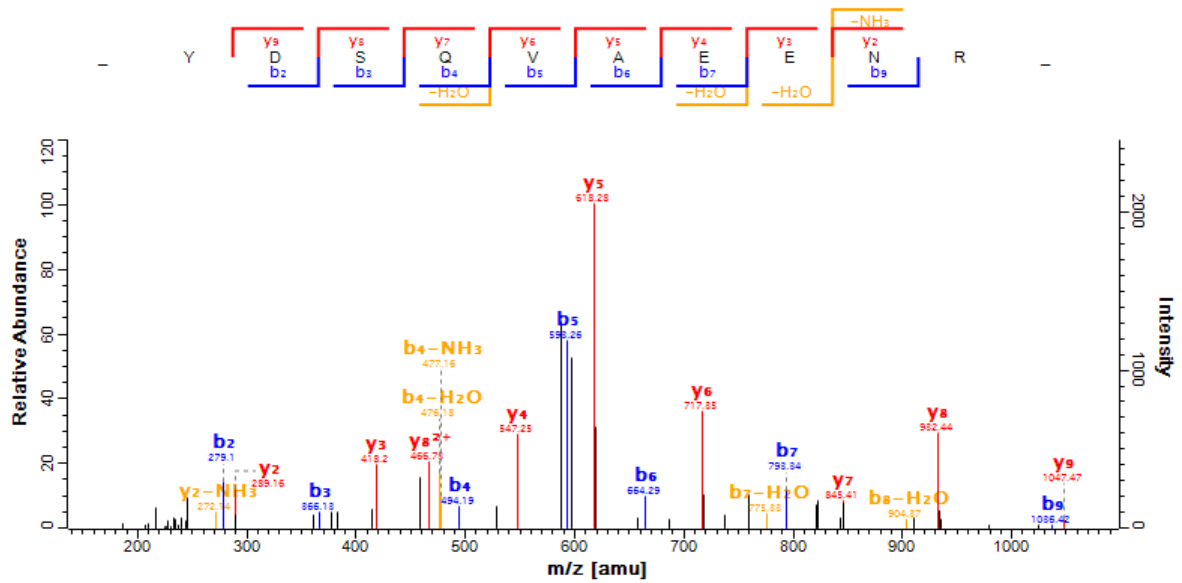
Number of Replicates (out of 8): 3

Best Match Score: 119.39

Best Match Posterior Error Probability: 0.00023613

Best Match Spectrum:

Scan number 5862 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** RNGTT



Protein Group ID: 1919

Protein Accession Numbers: O75151

Gene Names: PHF2

Peptide Sequence: VPGSQLTGLGYMEEELHGGFTPEILVPK

Total Number of Spectra: 1

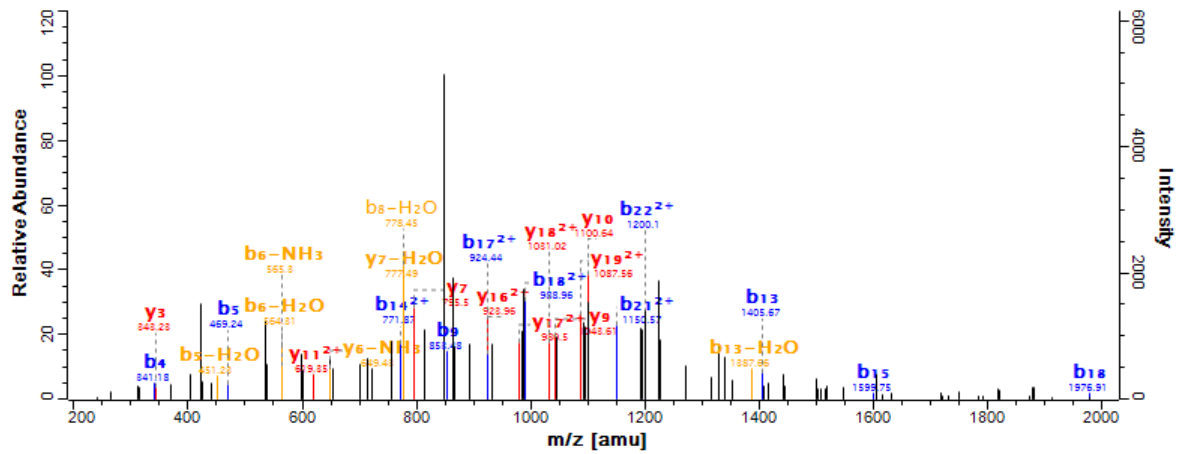
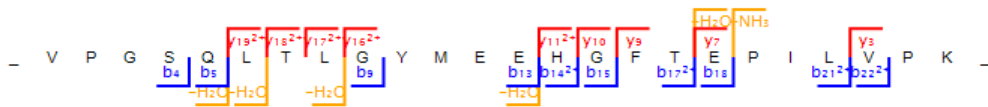
Number of Replicates (out of 8): 1

Best Match Score: 83.723

Best Match Posterior Error Probability: 5.33E-05

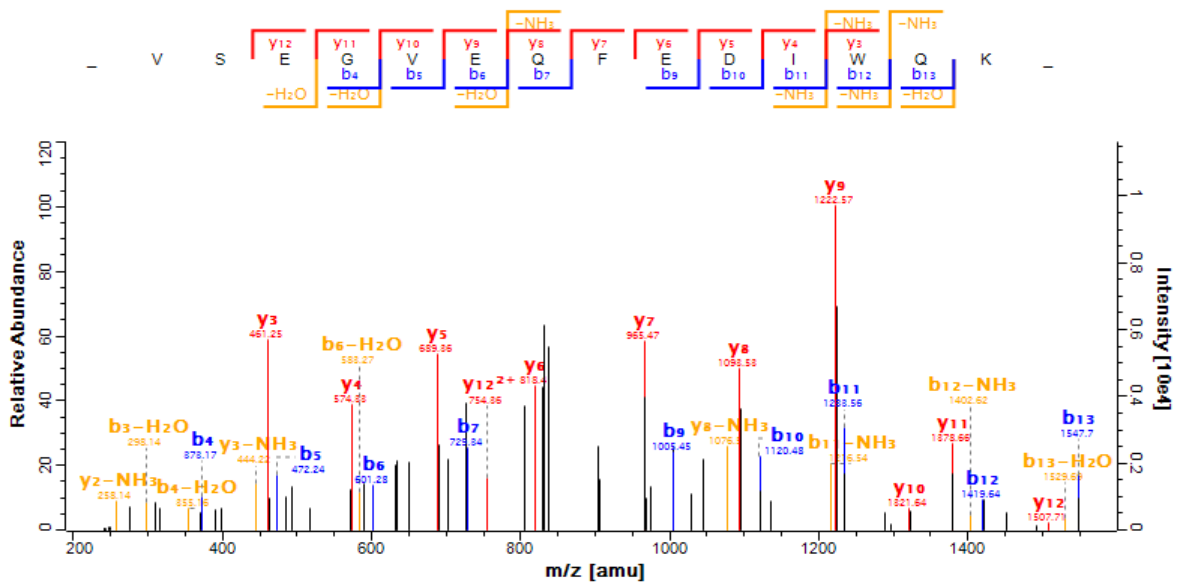
Best Match Spectrum:

Scan number	72836	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	PHF2



Protein Group ID: 1924
Protein Accession Numbers: O75175; O75175-2
Gene Names: CNOT3
Peptide Sequence: VSEGVEQFEDIWQK
Total Number of Spectra: 4
Number of Replicates (out of 8): 3
Best Match Score: 150.05
Best Match Posterior Error Probability: 1.48E-06
Best Match Spectrum:

Scan number 62090 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CNOT3



Protein Group ID: 1938

Protein Accession Numbers: O75381; O75381-2

Gene Names: PEX14

Peptide Sequence: ASSEQAEQSPQSSTPGSENVLP

Total Number of Spectra: 3

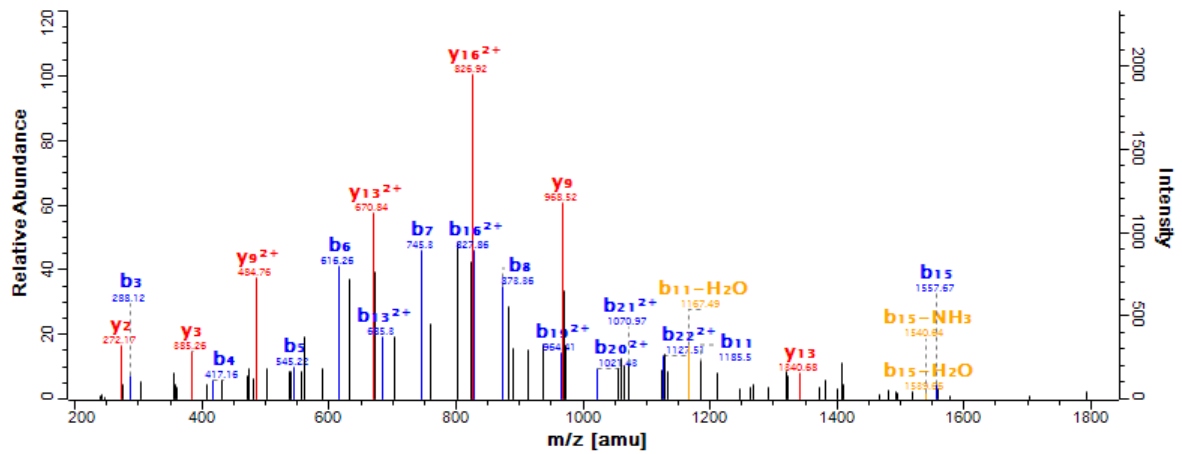
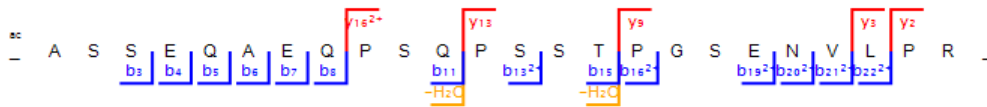
Number of Replicates (out of 8): 3

Best Match Score: 96.718

Best Match Posterior Error Probability: 4.13E-06

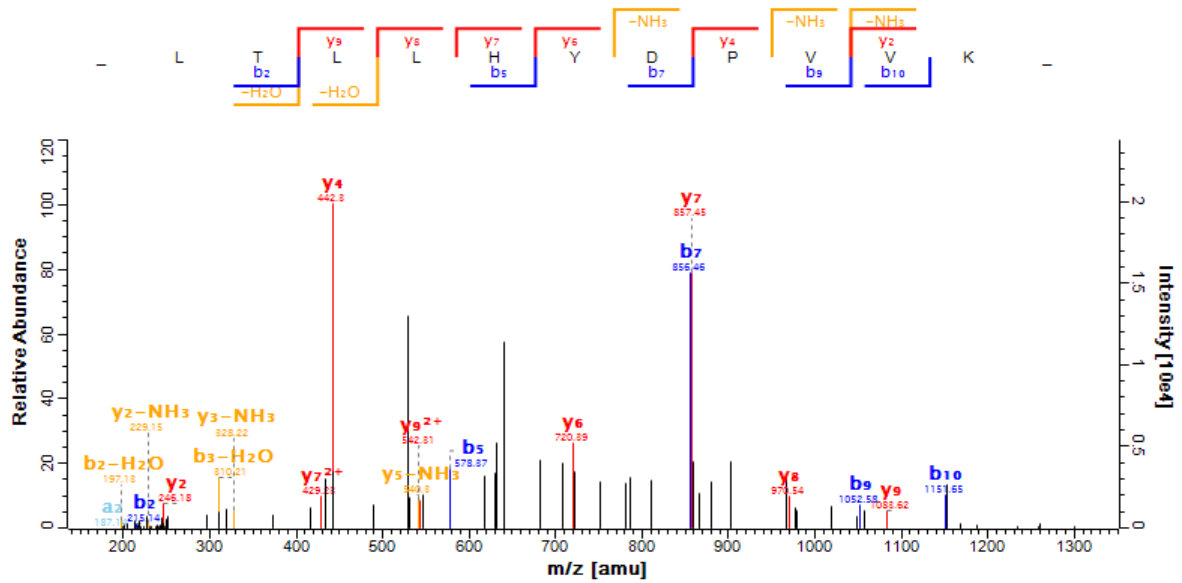
Best Match Spectrum:

Scan number	34177	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	PEX14



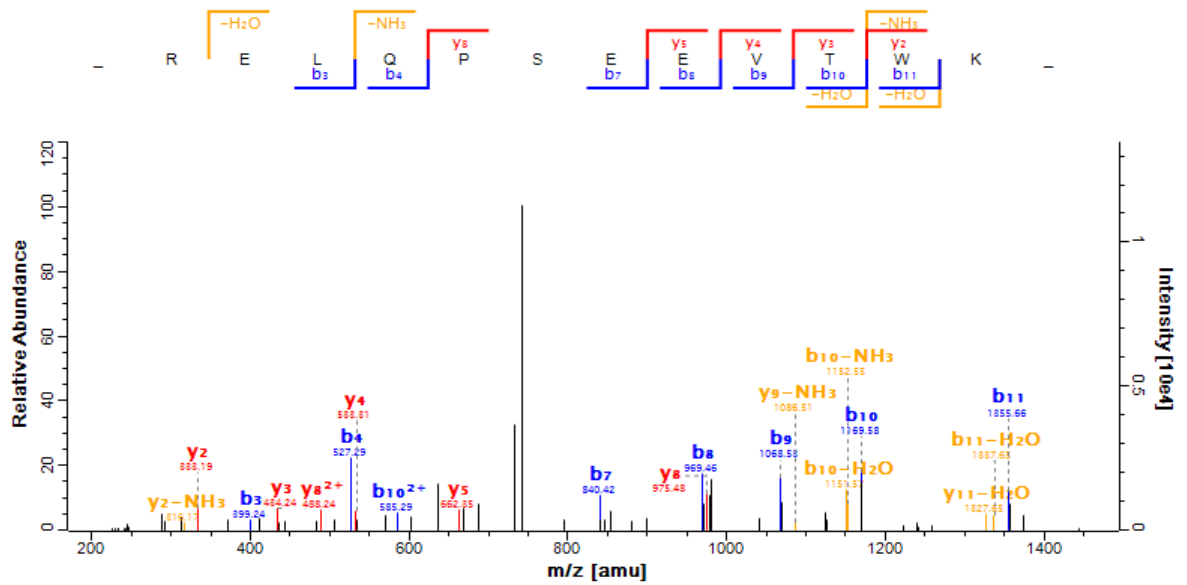
Protein Group ID: 1940
Protein Accession Numbers: O75394
Gene Names: MRPL33
Peptide Sequence: LTLHYDPVVK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 87.184
Best Match Posterior Error Probability: 0.0017866
Best Match Spectrum:

Scan number 45928 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** MRPL33



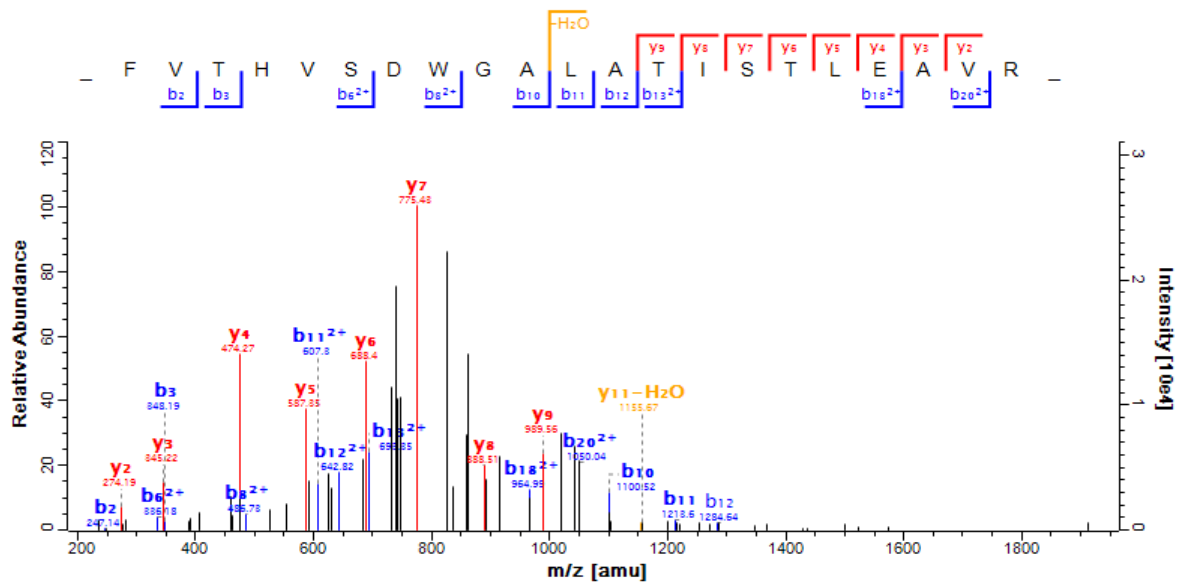
Protein Group ID: 1945
Protein Accession Numbers: O75438-2; O75438
Gene Names: NDUFB1
Peptide Sequence: RELQPSEEVTK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 102.87
Best Match Posterior Error Probability: 0.0010323
Best Match Spectrum:

Scan number 27567 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** NDUFB1



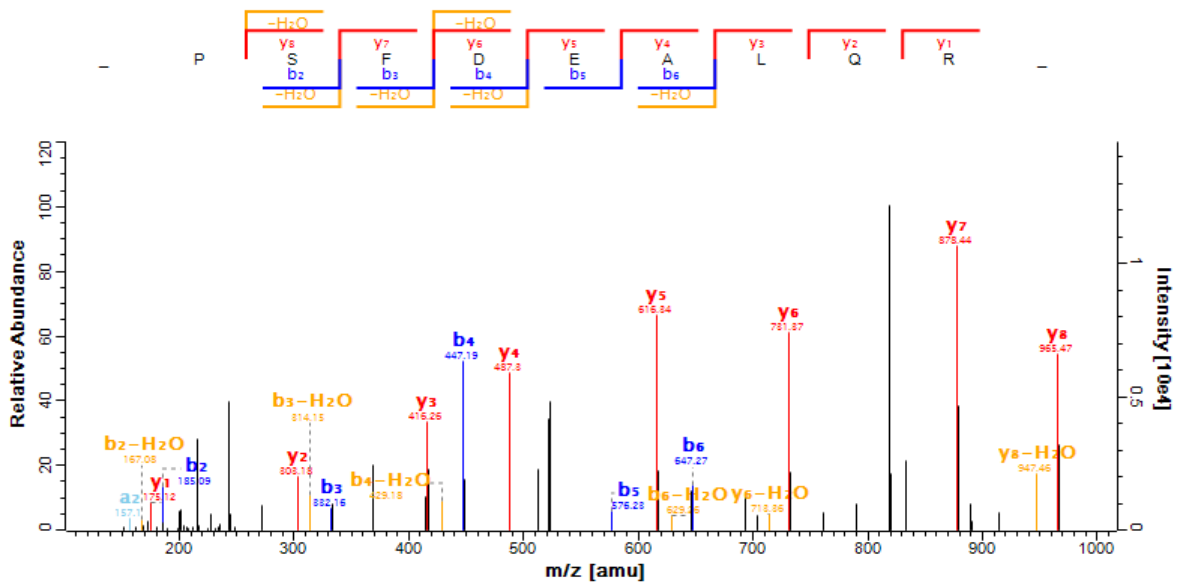
Protein Group ID: 1959
Protein Accession Numbers: O75629
Gene Names: CREG1
Peptide Sequence: FVTHVSDWGLALATISLTLEAVR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 79.676
Best Match Posterior Error Probability: 0.00032886
Best Match Spectrum:

Scan number 79059 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CREG1



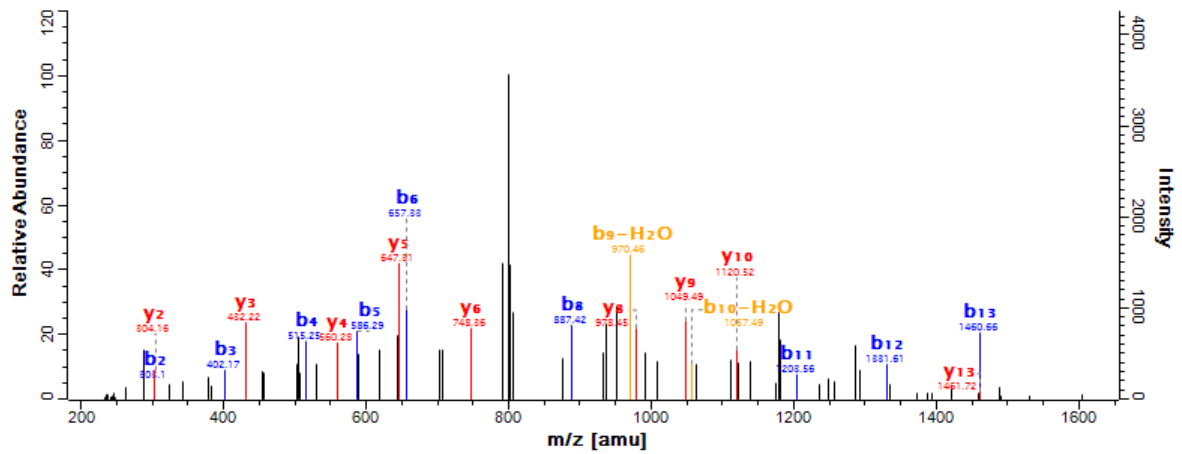
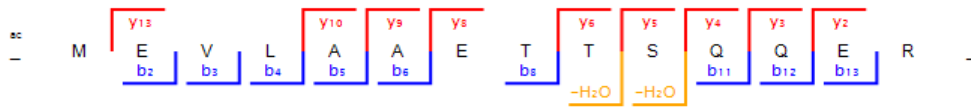
Protein Group ID: 1970
Protein Accession Numbers: Q96KH7; O75751
Gene Names: SLC22A3
Peptide Sequence: PSFDEALQR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 130.66
Best Match Posterior Error Probability: 0.00029753
Best Match Spectrum:

Scan number 27162 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SLC22A3



Protein Group ID: 1971
Protein Accession Numbers: O75781; O75781-2
Gene Names: PALM
Peptide Sequence: MEVLAAETTSQQER
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 94.487
Best Match Posterior Error Probability: 0.0010948
Best Match Spectrum:

Scan number	54721	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	PALM



Protein Group ID: 1981

Protein Accession Numbers: O75882; O75882-2; O75882-3

Gene Names: ATRN

Peptide Sequence: LTGSSGFVTDGPGNYK

Total Number of Spectra: 2

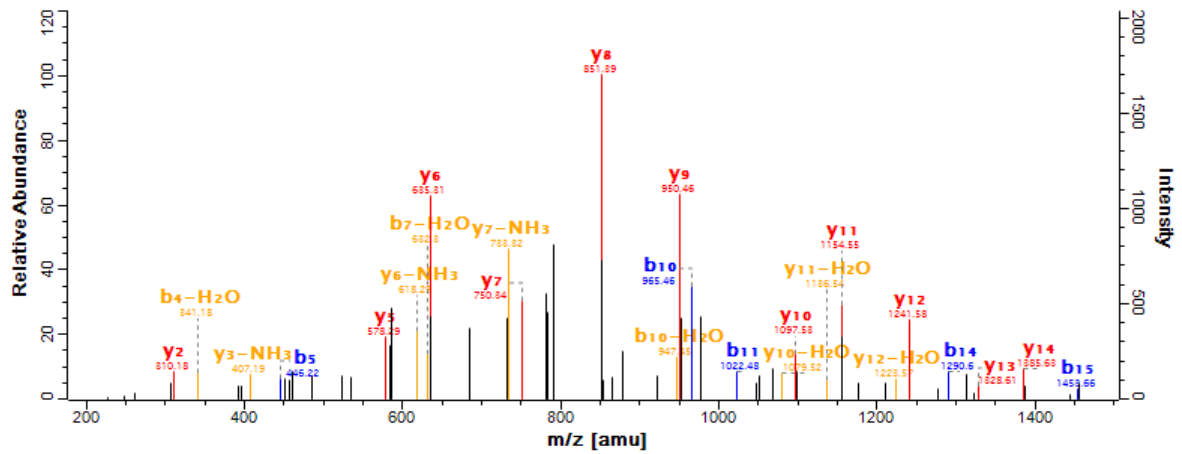
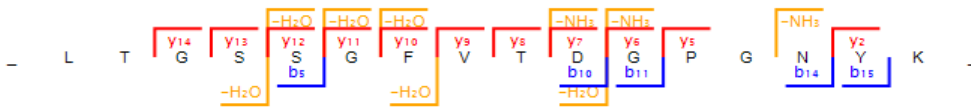
Number of Replicates (out of 8): 2

Best Match Score: 100.23

Best Match Posterior Error Probability: 0.0020664

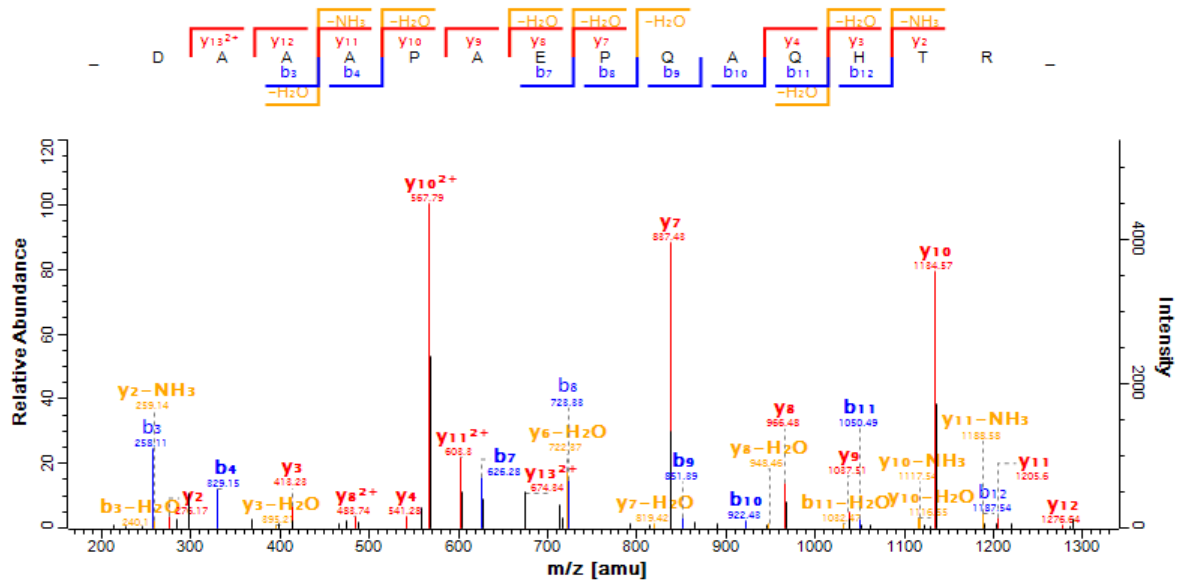
Best Match Spectrum:

Scan number 30735 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ATRN



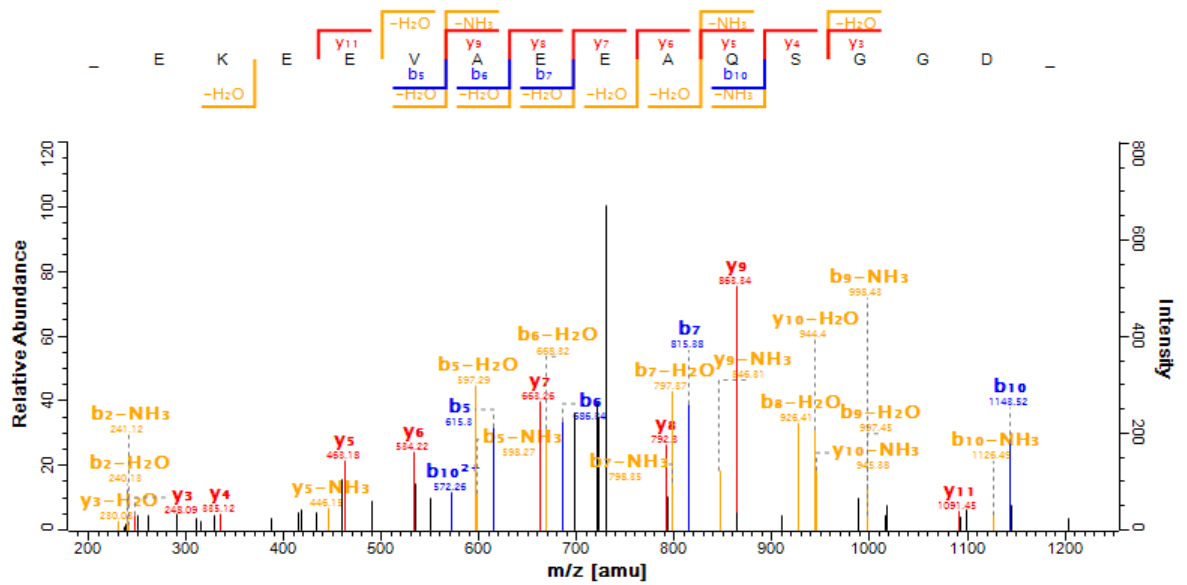
Protein Group ID: 1993
Protein Accession Numbers: O76024
Gene Names: WFS1
Peptide Sequence: DAAAPAEPQAQHTR
Total Number of Spectra: 7
Number of Replicates (out of 8): 7
Best Match Score: 185.95
Best Match Posterior Error Probability: 2.98E-19
Best Match Spectrum:

Scan number 4469 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** WFS1



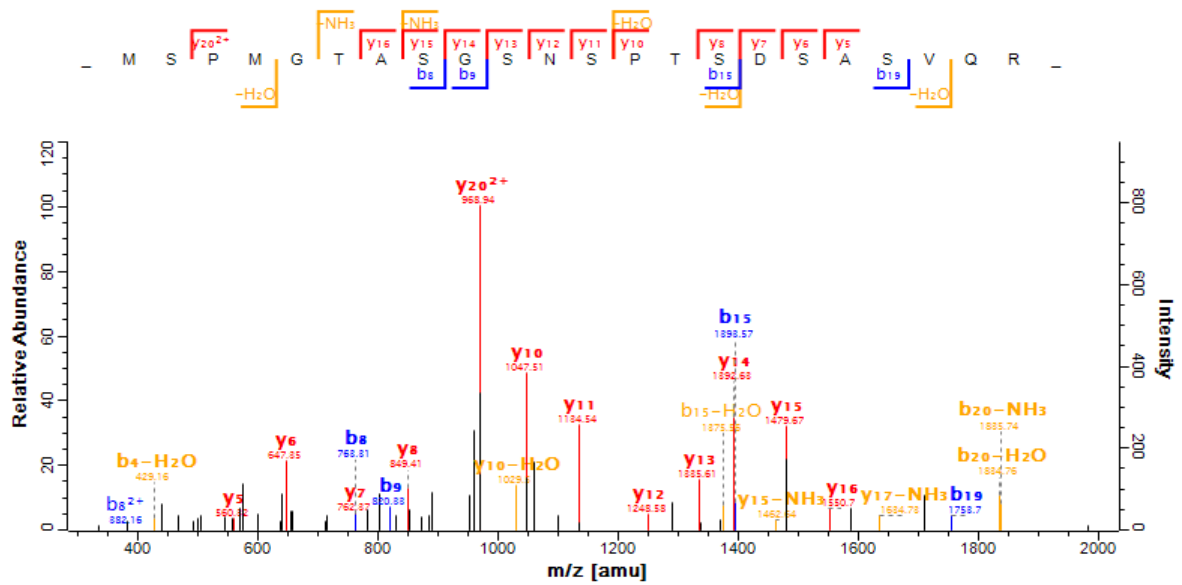
Protein Group ID: 1996
Protein Accession Numbers: O76070
Gene Names: SNCG
Peptide Sequence: EKEEVAEEAQSGGD
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 132.97
Best Match Posterior Error Probability: 0.00019455
Best Match Spectrum:

Scan number 6101 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** SNCG



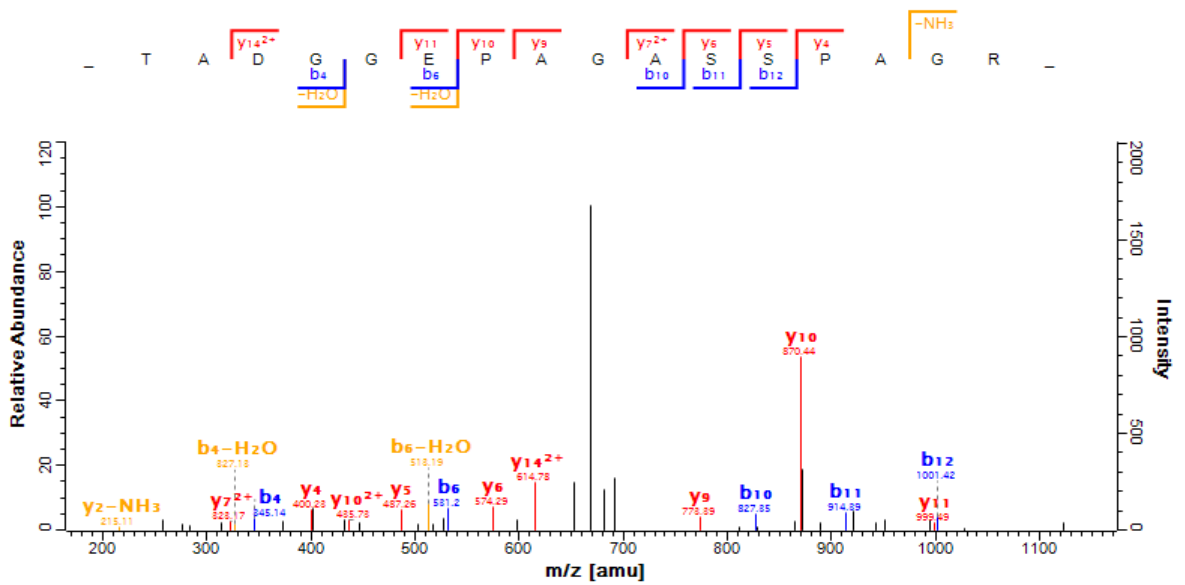
Protein Group ID: 1998
Protein Accession Numbers: O76080; Q5QPB1
Gene Names: ZFAND5
Peptide Sequence: MSPMGTASGSNSPTSDSASVQR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 76.492
Best Match Posterior Error Probability: 0.00018973
Best Match Spectrum:

Scan number 21151 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ZFAND5



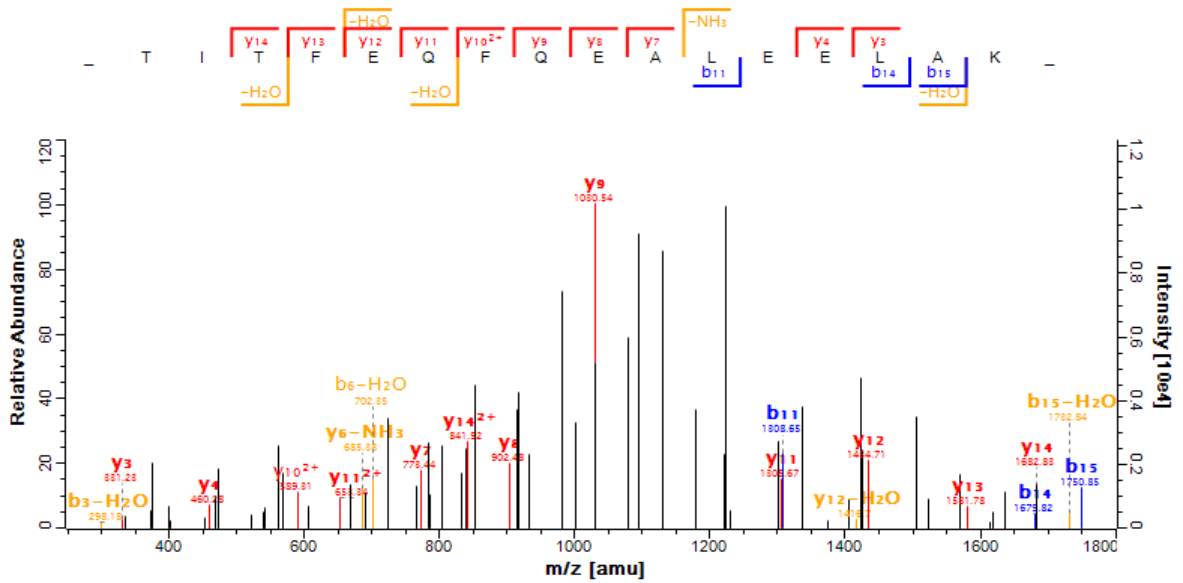
Protein Group ID: 1999
Protein Accession Numbers: O76081-6
Gene Names:
Peptide Sequence: TADGGEPAGASSPAGR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 73.834
Best Match Posterior Error Probability: 0.0037142
Best Match Spectrum:

Scan number 4367 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Pepti...** 73.83



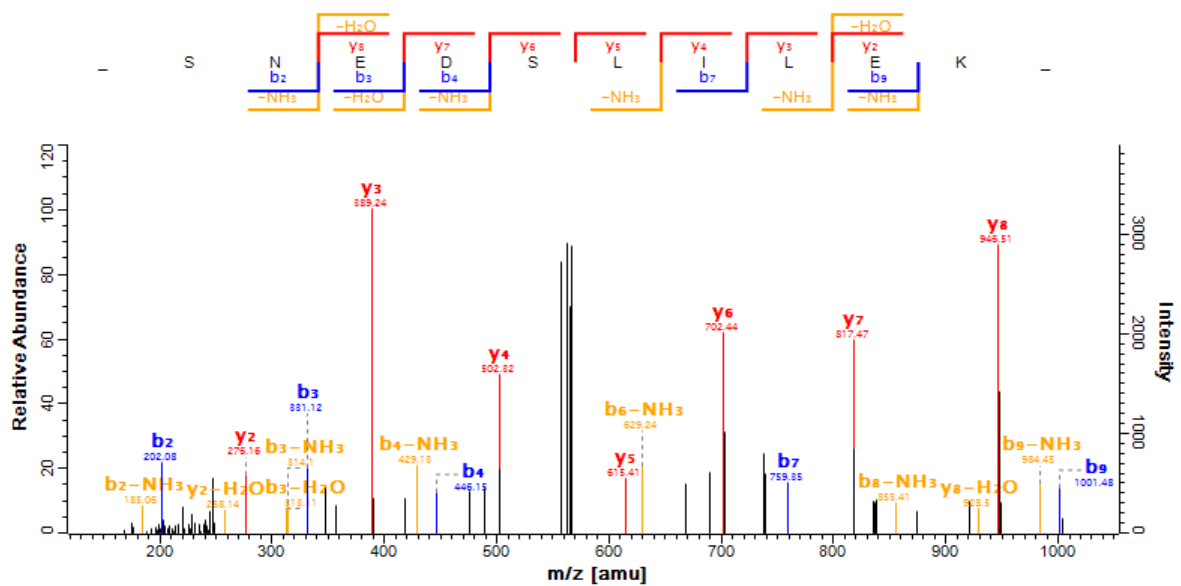
Protein Group ID: 2004
Protein Accession Numbers: O94811
Gene Names: TPPP
Peptide Sequence: TITFEQFQEALAK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 74.428
Best Match Posterior Error Probability: 0.0034311
Best Match Spectrum:

Scan number 90834 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TPPP



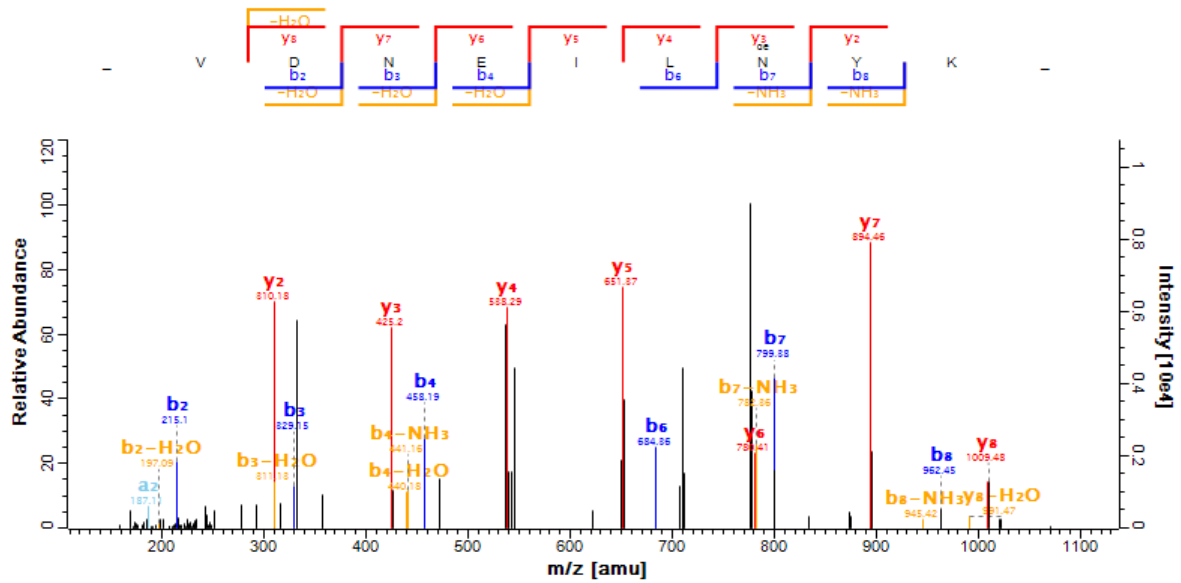
Protein Group ID: 2010
Protein Accession Numbers: O94880
Gene Names: PHF14
Peptide Sequence: SNEDSLILEK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 113.22
Best Match Posterior Error Probability: 0.000264
Best Match Spectrum:

Scan number 26542 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PHF14



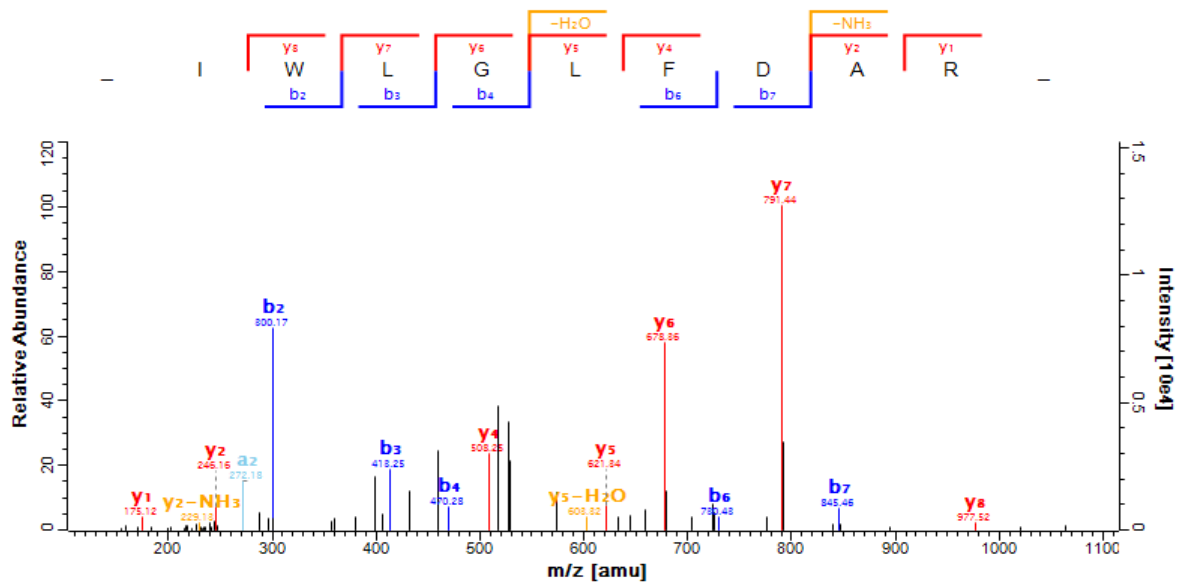
Protein Group ID: 2017
Protein Accession Numbers: O94929
Gene Names: ABLIM3
Peptide Sequence: VDNEILNYK
Total Number of Spectra: 4
Number of Replicates (out of 8): 3
Best Match Score: 133.23
Best Match Posterior Error Probability: 0.0002056
Best Match Spectrum:

Scan number 30812 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ABLIM3



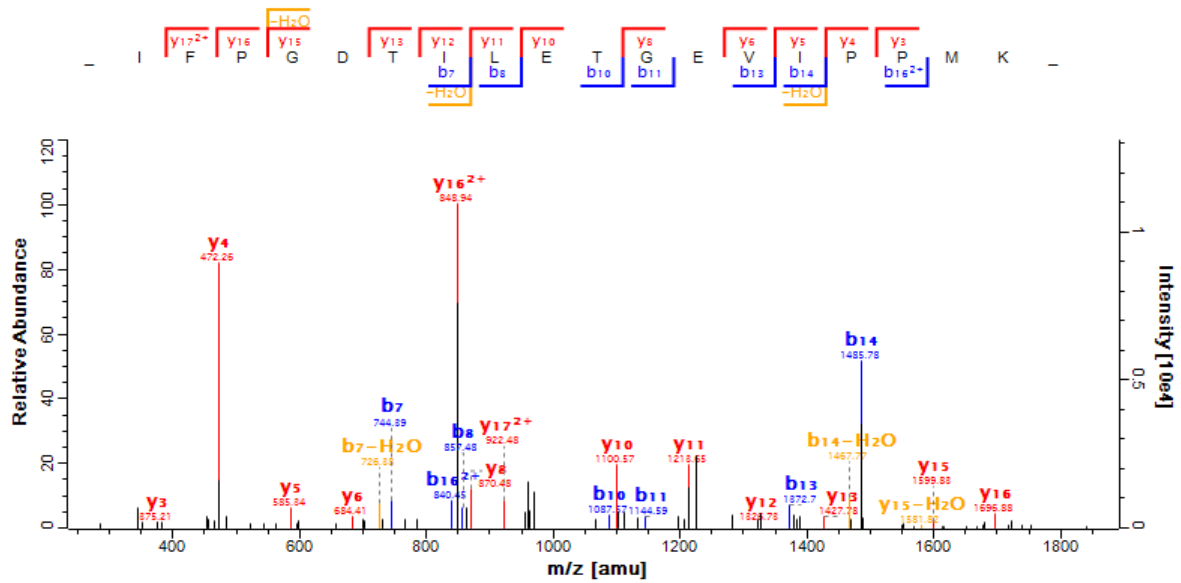
Protein Group ID: 2020
Protein Accession Numbers: O95081; O95081-2
Gene Names: AGFG2
Peptide Sequence: IWLGLFDAR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 104.2
Best Match Posterior Error Probability: 0.0014418
Best Match Spectrum:

Scan number	72951	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	AGFG2



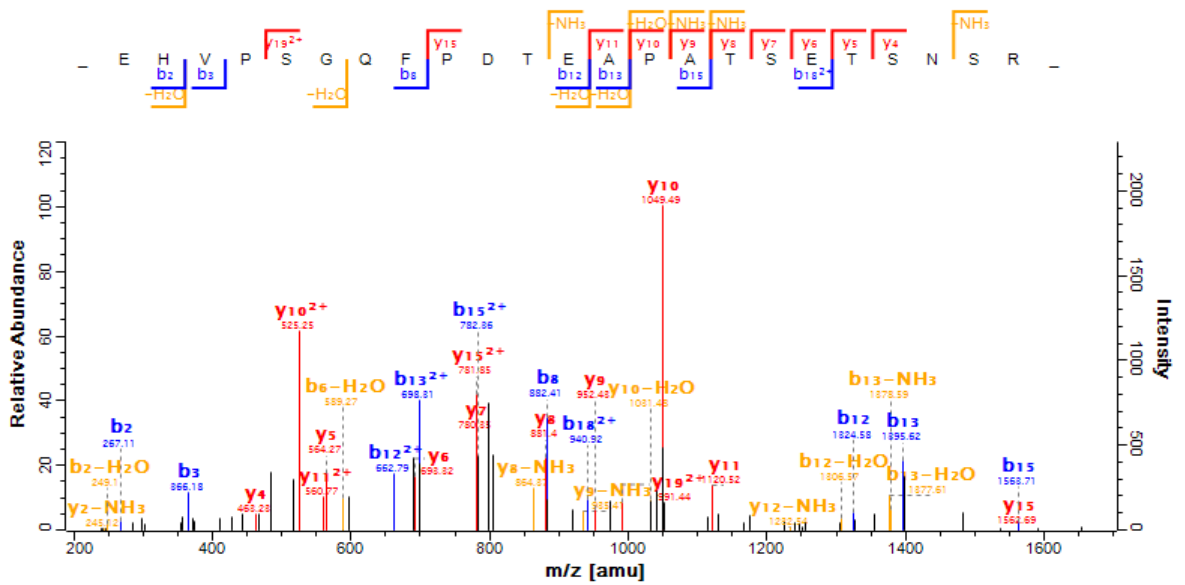
Protein Group ID: 2021
Protein Accession Numbers: O95139
Gene Names: NDUFB6
Peptide Sequence: IFPGDTILETGEVIPPVK
Total Number of Spectra: 17
Number of Replicates (out of 8): 8
Best Match Score: 111.22
Best Match Posterior Error Probability: 5.50E-05
Best Match Spectrum:

Scan number 74383 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** NDUFB6



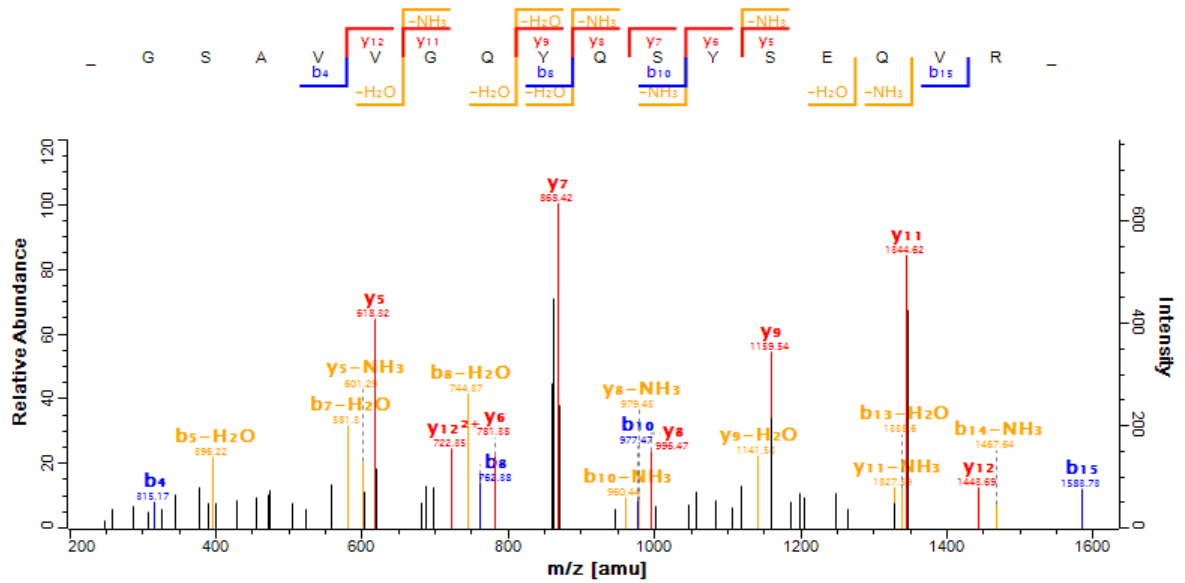
Protein Group ID: 2029
Protein Accession Numbers: O95210
Gene Names: STBD1
Peptide Sequence: EHVPSGQFPDTEAPATSETSNSR
Total Number of Spectra: 12
Number of Replicates (out of 8): 7
Best Match Score: 124.69
Best Match Posterior Error Probability: 2.97E-11
Best Match Spectrum:

Scan number 25804 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** STBD1



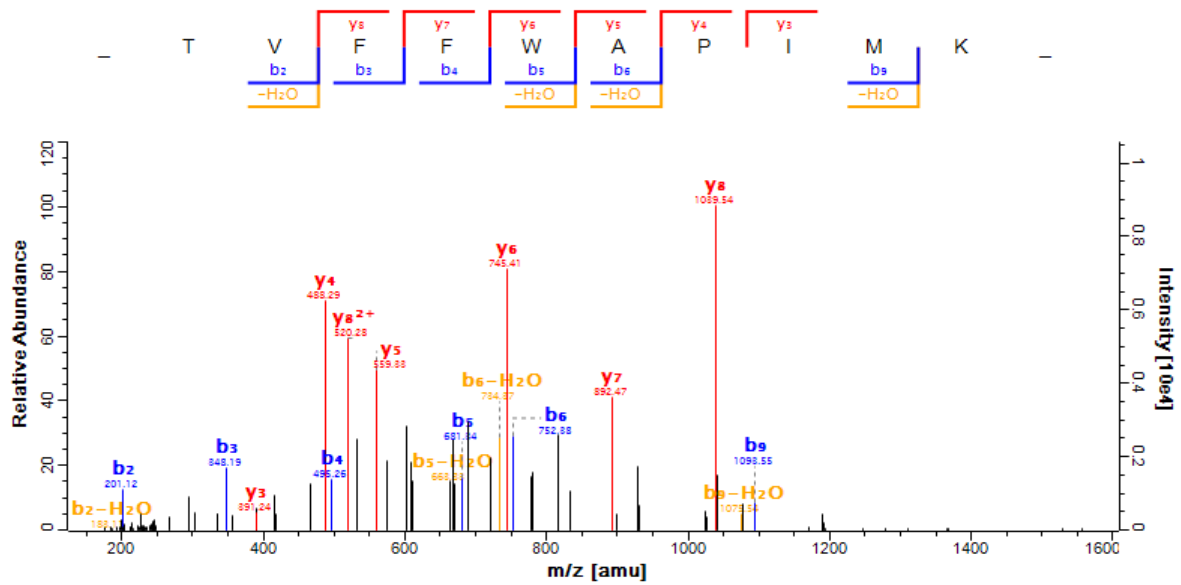
Protein Group ID: 2055
Protein Accession Numbers: O95479
Gene Names: H6PD
Peptide Sequence: GSAVVGQYQSYSEQR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 95.428
Best Match Posterior Error Probability: 0.0030653
Best Match Spectrum:

Scan number 30552 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** H6PD



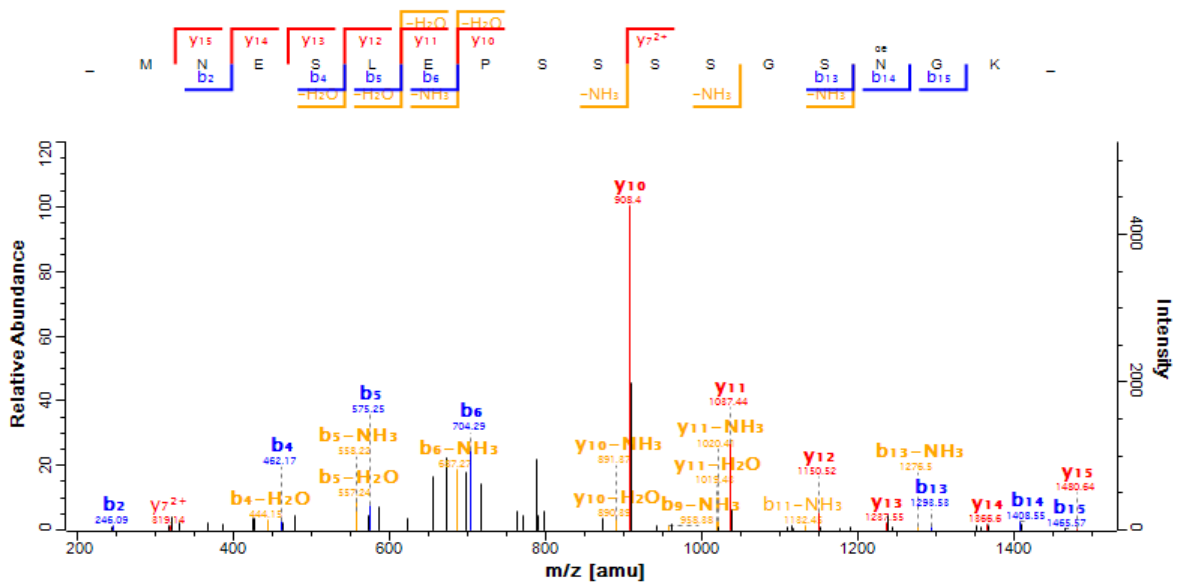
Protein Group ID: 2058
Protein Accession Numbers: O95563; Q5R3B4
Gene Names: BRP44
Peptide Sequence: TVFFWAPIMK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 109.29
Best Match Posterior Error Probability: 0.00037245
Best Match Spectrum:

Scan number	78725	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	BRP44



Protein Group ID: 2067
Protein Accession Numbers: O95716
Gene Names: RAB3D
Peptide Sequence: MNESLEPSSSSGSNGK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 118.21
Best Match Posterior Error Probability: 0.00045235
Best Match Spectrum:

Scan number 11473 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** RAB3D



Protein Group ID: 2082

Protein Accession Numbers: O95926

Gene Names: SYF2

Peptide Sequence: AAIAASEVLVDSAEEGSLAAAELAAQK

Total Number of Spectra: 2

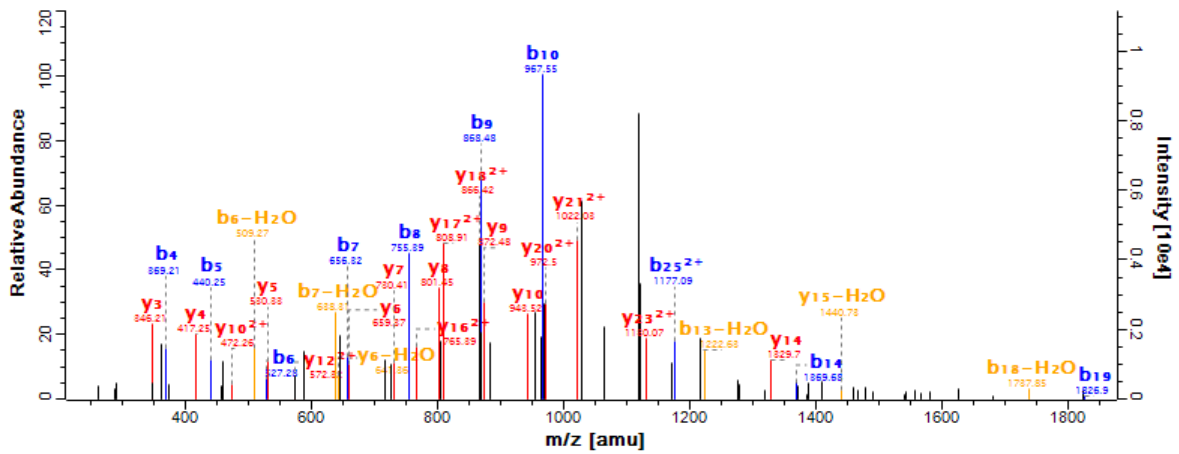
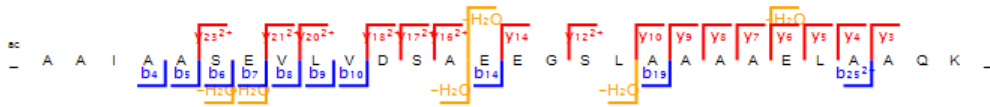
Number of Replicates (out of 8): 2

Best Match Score: 119.34

Best Match Posterior Error Probability: 1.05E-12

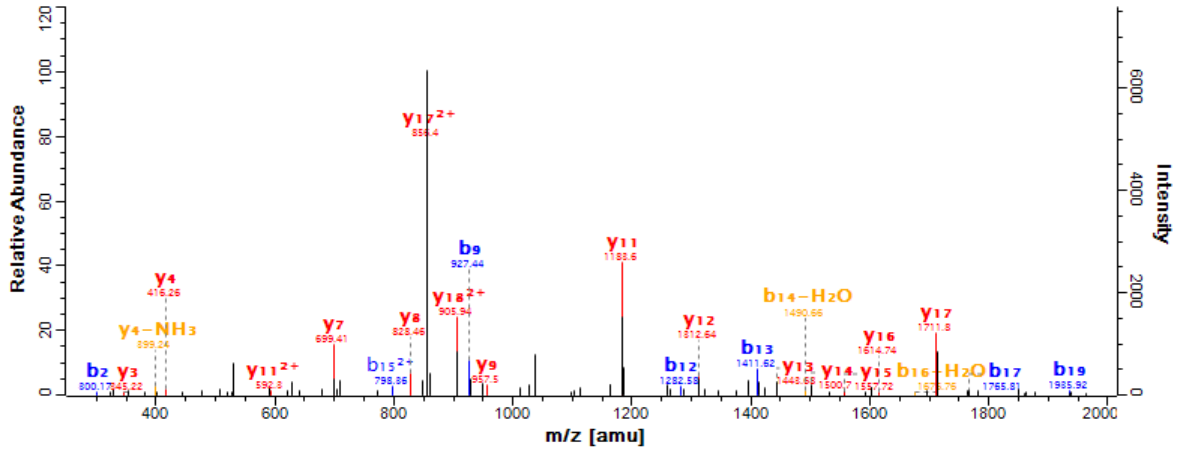
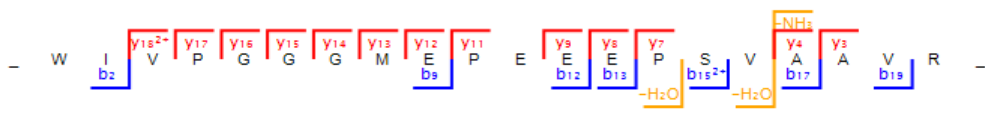
Best Match Spectrum:

Scan number 93179 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SYF2



Protein Group ID: 2083
Protein Accession Numbers: O95989
Gene Names: NUDT3
Peptide Sequence: WIVPGGMEPEEEPSVAAVR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 83.423
Best Match Posterior Error Probability: 0.00037585
Best Match Spectrum:

Scan number 56506 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** NUDT3



Protein Group ID: 2098

Protein Accession Numbers: P00395

Gene Names: MT-CO1

Peptide Sequence: VLMVEEPPSMNLEWLYGCPPPYHTFEPEPVMK

Total Number of Spectra: 10

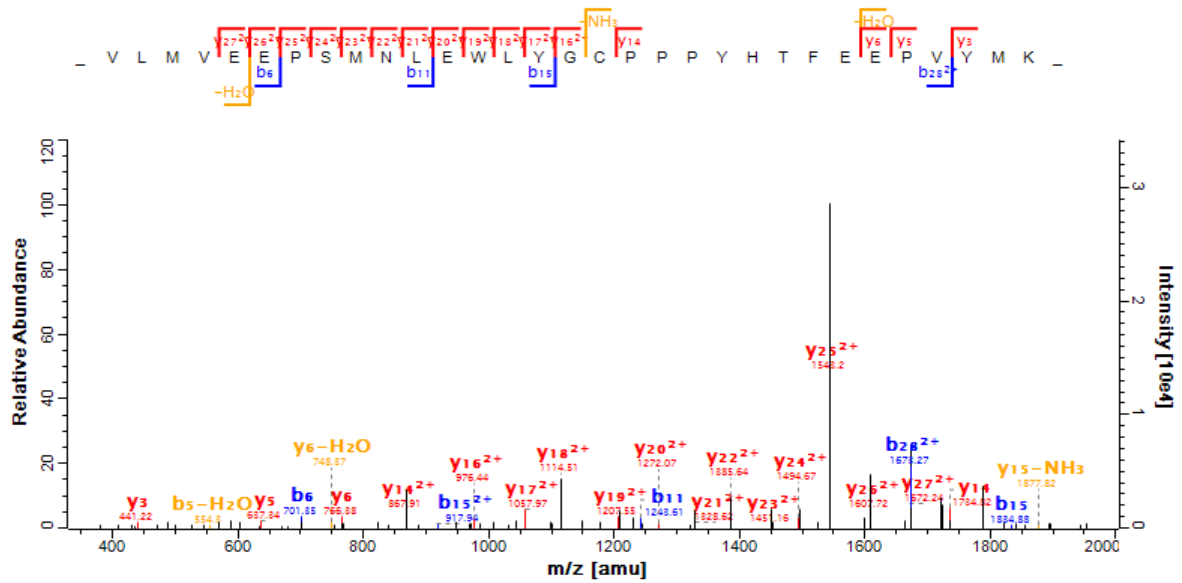
Number of Replicates (out of 8): 5

Best Match Score: 76.799

Best Match Posterior Error Probability: 2.91E-06

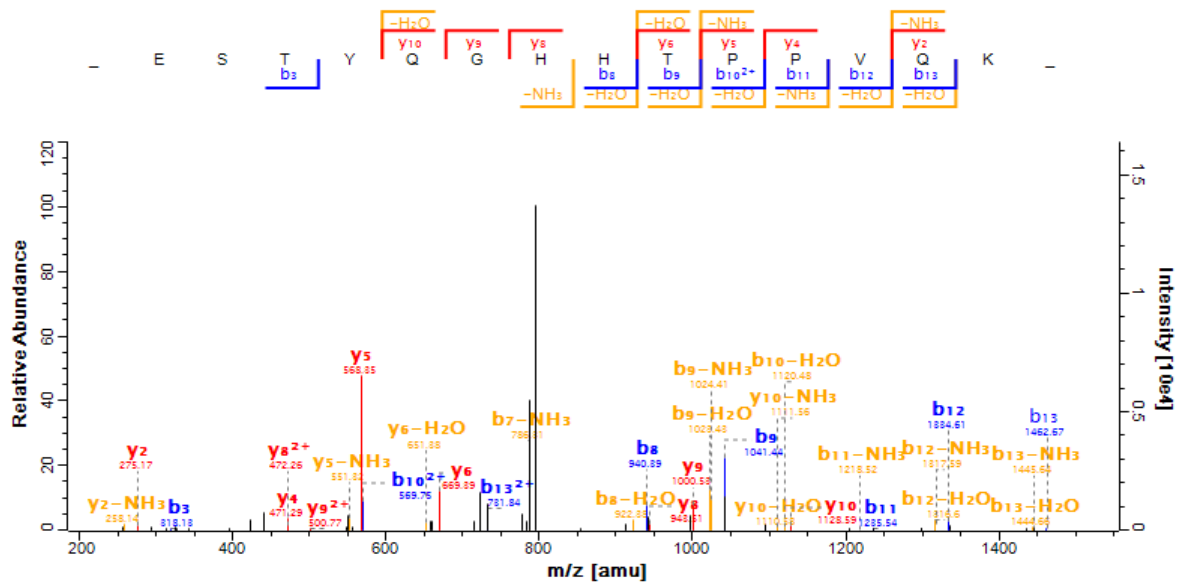
Best Match Spectrum:

Scan number 87483 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** MT-CO1



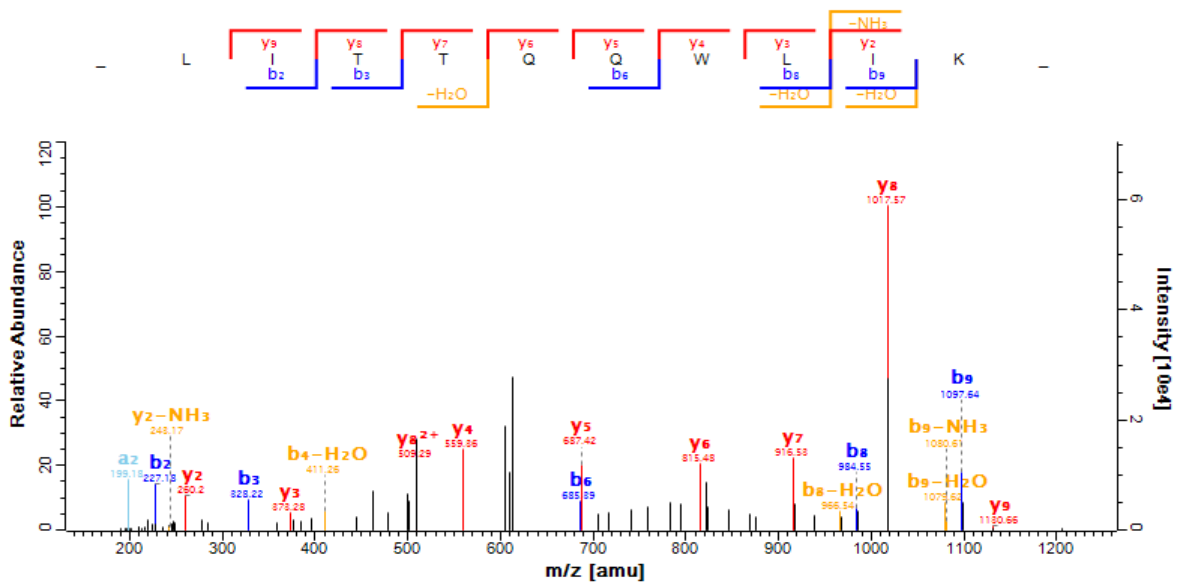
Protein Group ID: 2100
Protein Accession Numbers: P00414
Gene Names: MT-CO3
Peptide Sequence: ESTYQGHHTPPVQK
Total Number of Spectra: 8
Number of Replicates (out of 8): 8
Best Match Score: 193.28
Best Match Posterior Error Probability: 1.03E-24
Best Match Spectrum:

Scan number 4423 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** MT-CO3



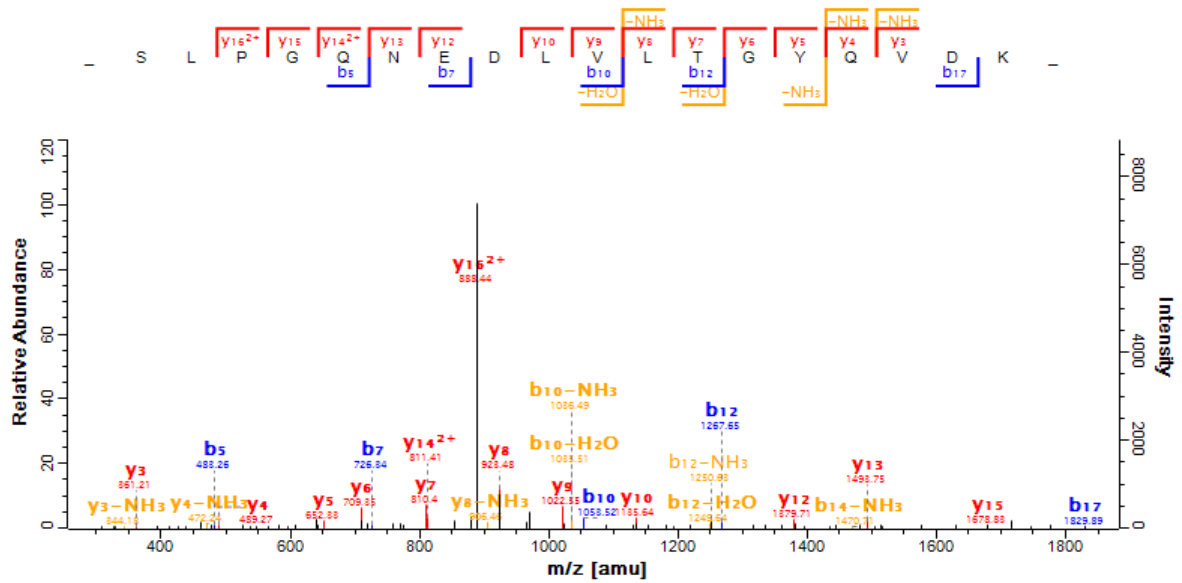
Protein Group ID: 2109
Protein Accession Numbers: P00846
Gene Names: MT-ATP6
Peptide Sequence: LITTQQWLIK
Total Number of Spectra: 7
Number of Replicates (out of 8): 7
Best Match Score: 135.86
Best Match Posterior Error Probability: 8.77E-06
Best Match Spectrum:

Scan number 53666 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MT-ATP6



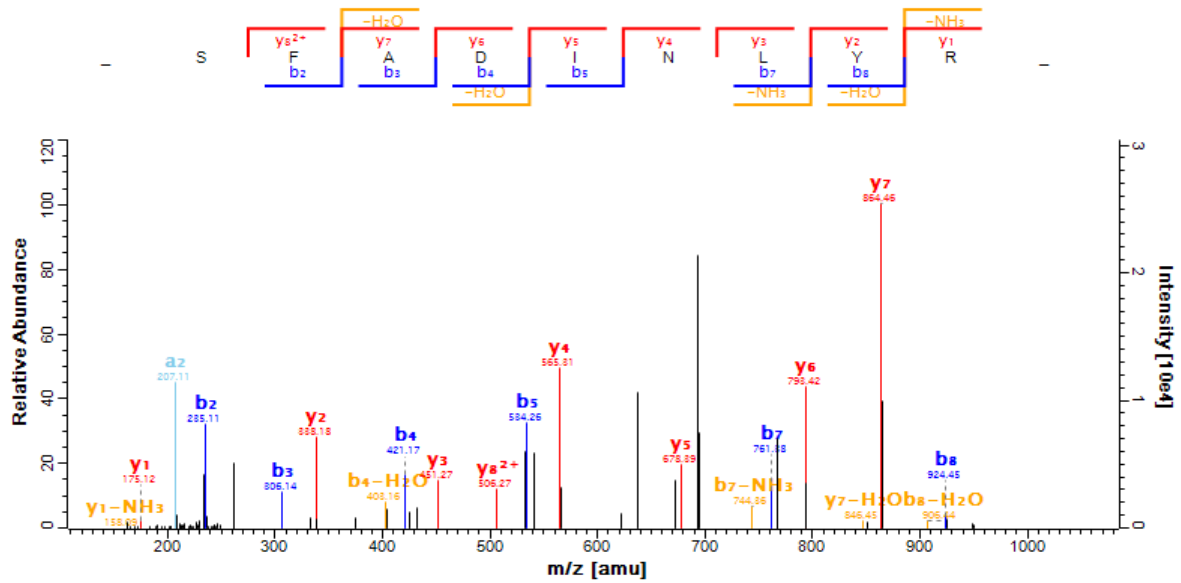
Protein Group ID: 2114
Protein Accession Numbers: P01040
Gene Names: CSTA
Peptide Sequence: SLPGQNEDLVLTGYQVDK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 104.89
Best Match Posterior Error Probability: 0.00011537
Best Match Spectrum:

Scan number 50500 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CSTA



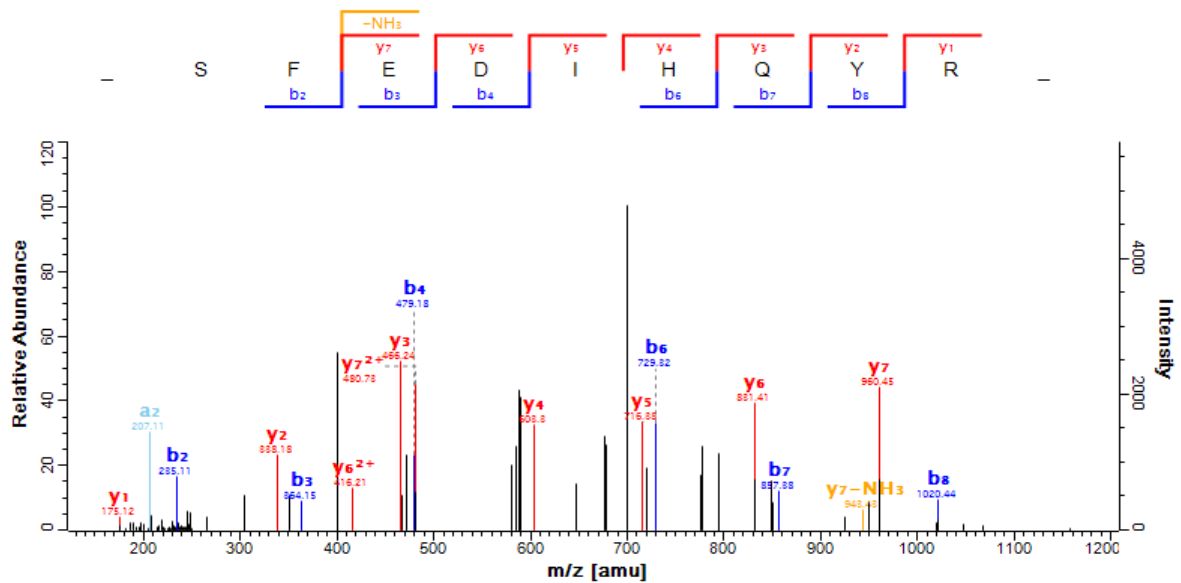
Protein Group ID: 2115
Protein Accession Numbers: P01111
Gene Names: NRAS
Peptide Sequence: SFADINLYR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 128.86
Best Match Posterior Error Probability: 0.00016337
Best Match Spectrum:

Scan number 45925 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** NRAS



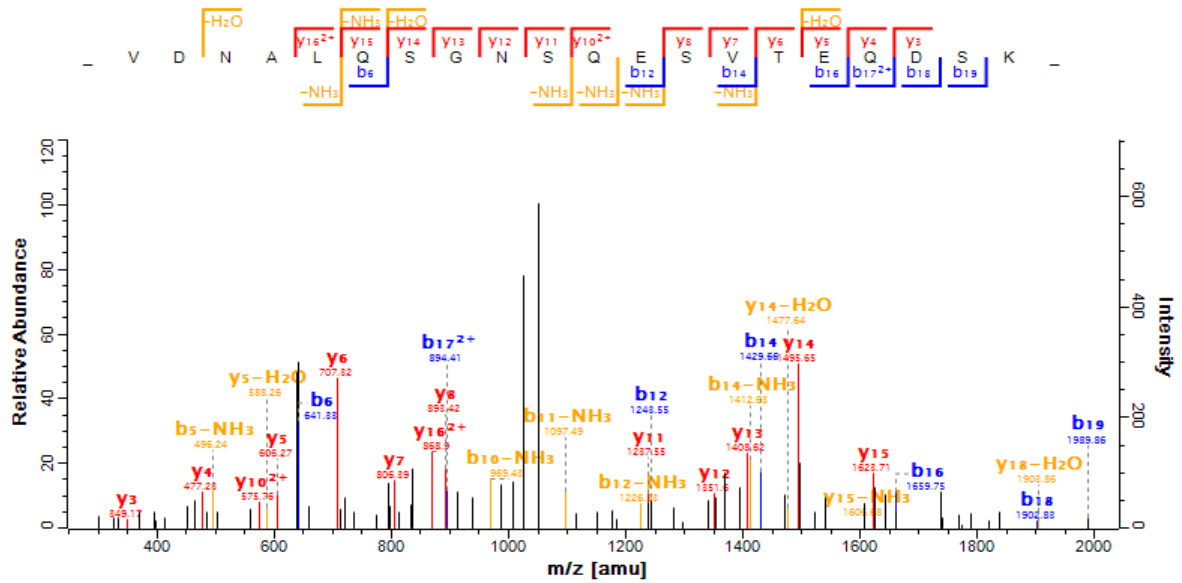
Protein Group ID: 2116
Protein Accession Numbers: P01112; P01112-2
Gene Names: HRAS
Peptide Sequence: SFEDIHQYR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 121.73
Best Match Posterior Error Probability: 0.00032853
Best Match Spectrum:

Scan number 19705 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** HRAS



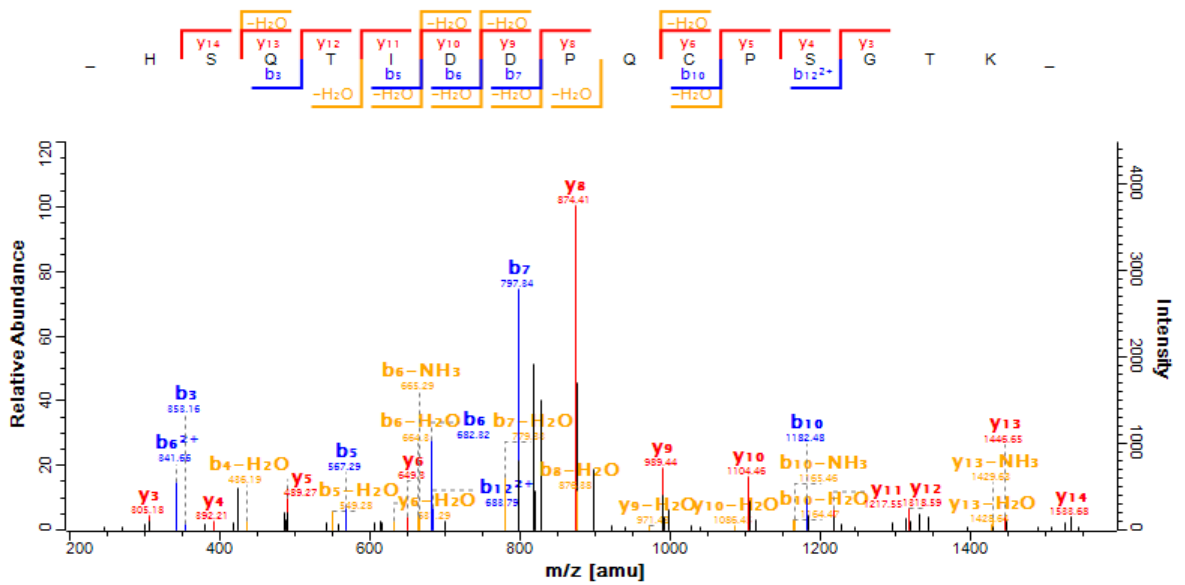
Protein Group ID: 2118
Protein Accession Numbers: P01834
Gene Names: IGKC
Peptide Sequence: VDNALQSGNSQESVTEQDSK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 99.409
Best Match Posterior Error Probability: 0.00011482
Best Match Spectrum:

Scan number 15624 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** IGKC



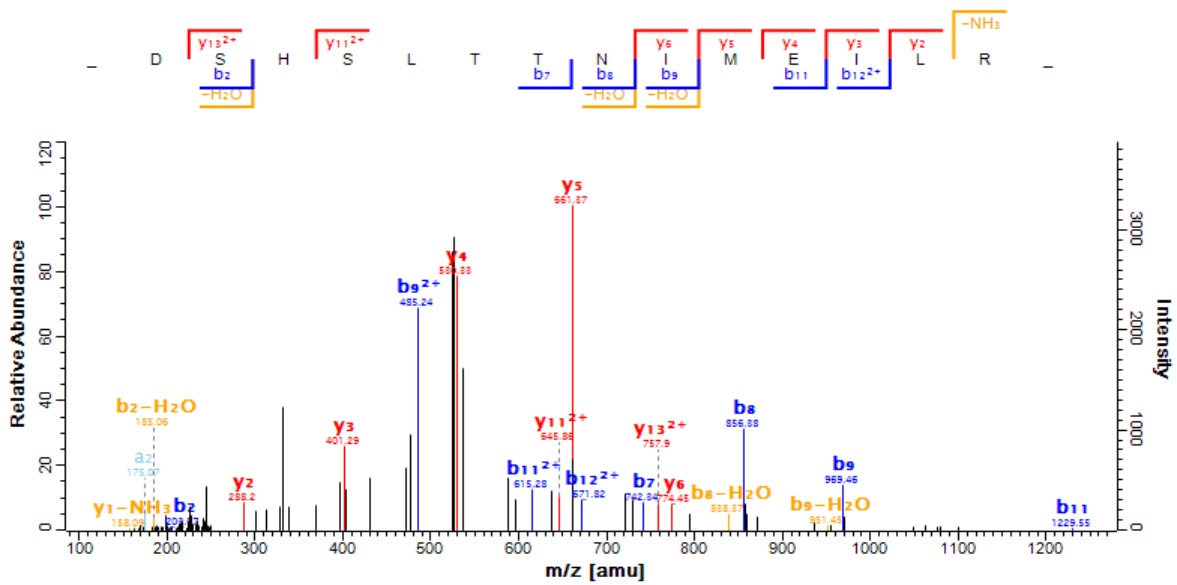
Protein Group ID: 2119
Protein Accession Numbers: P02462; P02462-2
Gene Names: COL4A1
Peptide Sequence: HSQTIDDPQCPSGTK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 174.59
Best Match Posterior Error Probability: 2.68E-14
Best Match Spectrum:

Scan number 7577 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** COL4A1



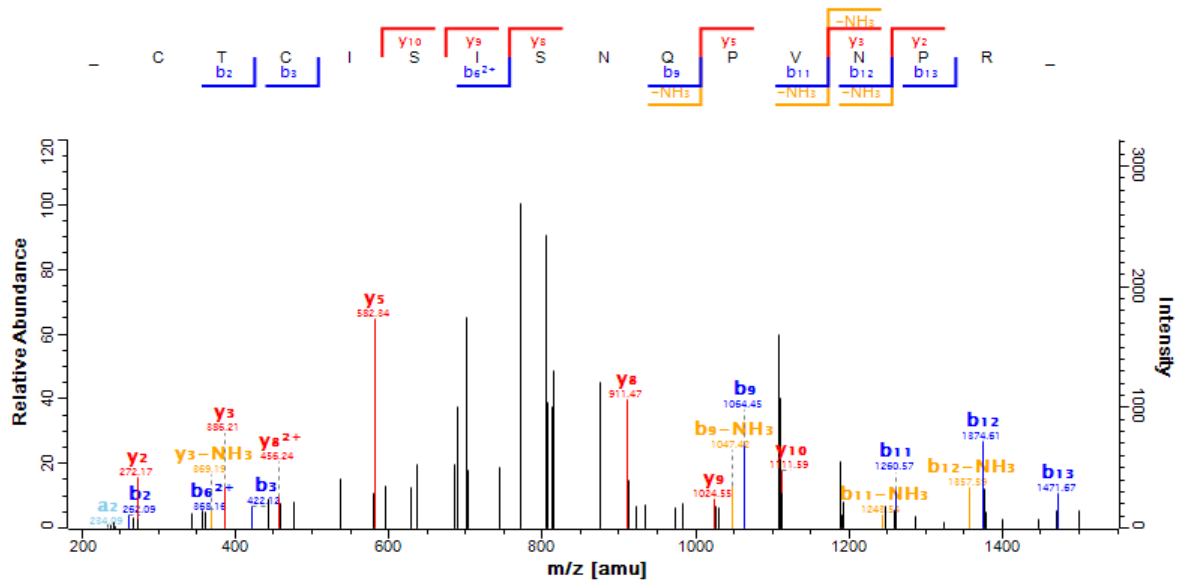
Protein Group ID: 2122
Protein Accession Numbers: P02671; P02671-2
Gene Names: FGA
Peptide Sequence: DSHSLTTNIMEILR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 82.202
Best Match Posterior Error Probability: 0.0027053
Best Match Spectrum:

Scan number 68997 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** FGA



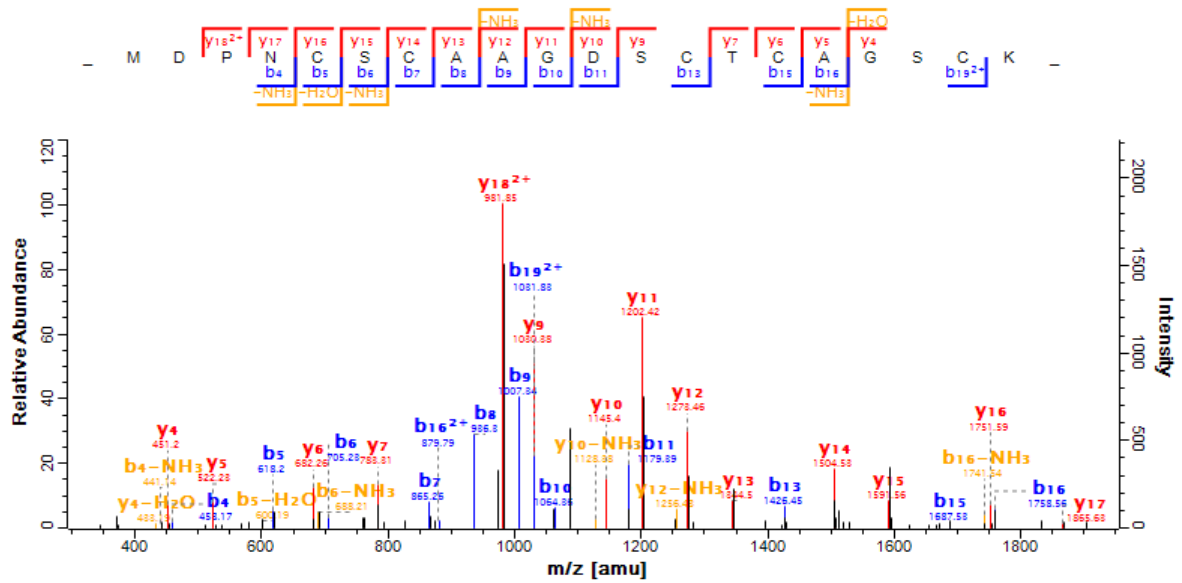
Protein Group ID: 2123
Protein Accession Numbers: P02778
Gene Names: CXCL10
Peptide Sequence: CTCISISNQVPNQR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 92.039
Best Match Posterior Error Probability: 0.0010033
Best Match Spectrum:

Scan number 28139 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CXCL10



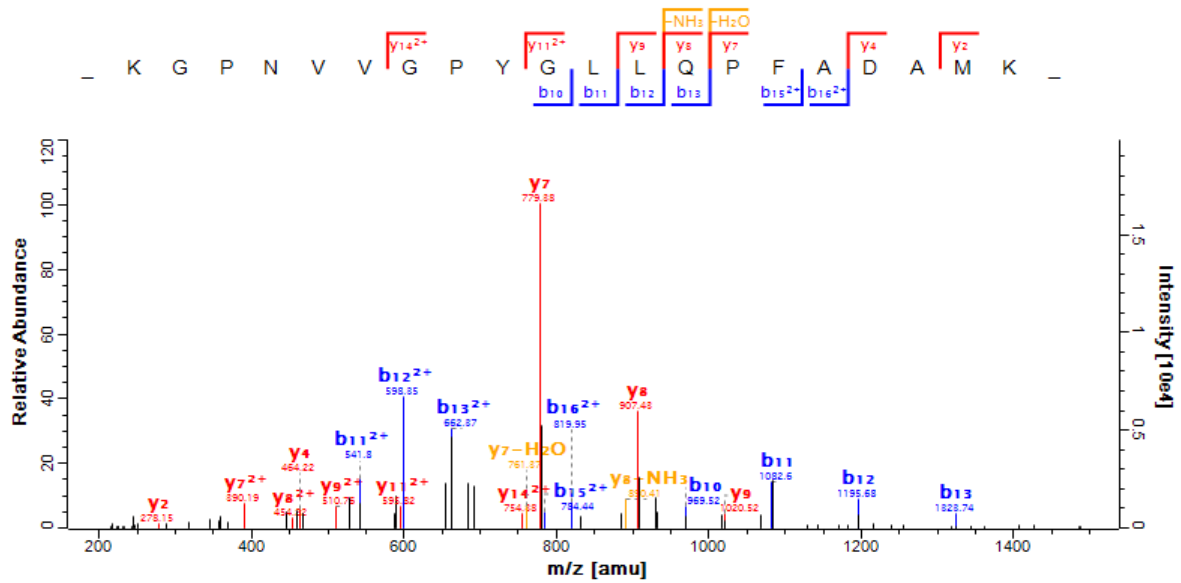
Protein Group ID: 2128
Protein Accession Numbers: P02795; H3BSP9
Gene Names: MT2A
Peptide Sequence: MDPNCSCAAGDSCTCAGSCK
Total Number of Spectra: 28
Number of Replicates (out of 8): 8
Best Match Score: 168.64
Best Match Posterior Error Probability: 8.69E-17
Best Match Spectrum:

Scan number 9607 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** MT2A



Protein Group ID: 2134
Protein Accession Numbers: P03886
Gene Names: MT-ND1
Peptide Sequence: KGPNVVGPLYGLLQPLFADAMK
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 81.594
Best Match Posterior Error Probability: 0.0010829
Best Match Spectrum:

Scan number 78094 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MT-ND1



Protein Group ID: 2155

Protein Accession Numbers: P04908; Q7L7L0; Q93077

Gene Names: HIST1H2AB;HIST3H2A;HIST1H2AC

Peptide Sequence: LLGRVTIAQGGVLPNIQAVLLLPK

Total Number of Spectra: 4

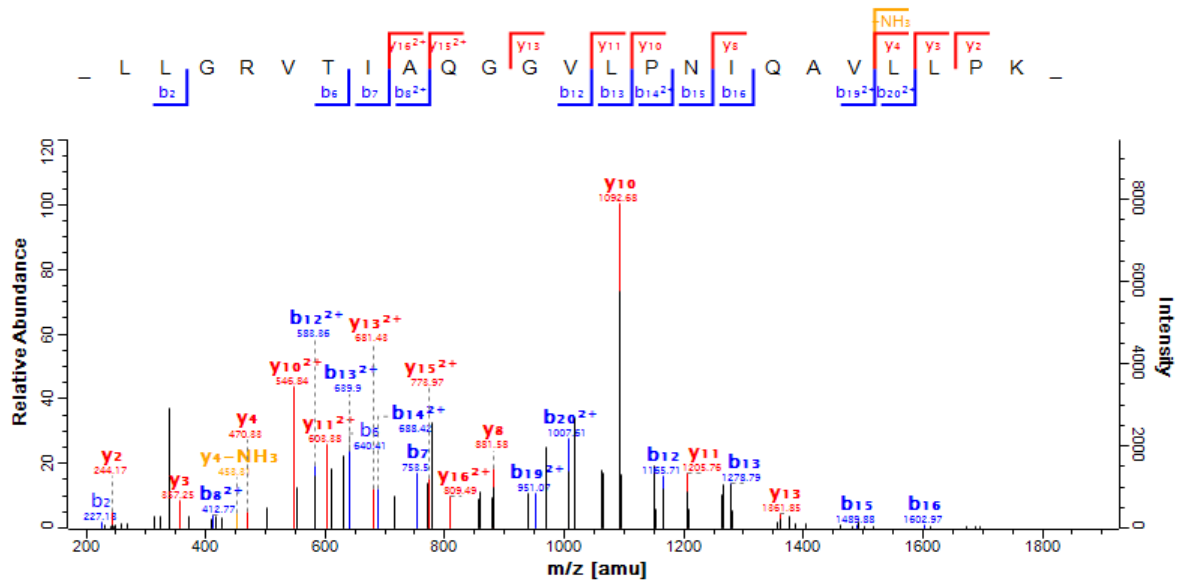
Number of Replicates (out of 8): 4

Best Match Score: 130.56

Best Match Posterior Error Probability: 5.23E-11

Best Match Spectrum:

Scan number	81528	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	HIST1H2AB;HIST3H2A;HIST1H2AC



Protein Group ID: 2167

Protein Accession Numbers: P05423

Gene Names: POLR3D

Peptide Sequence: EEELLFLQLPDTLPGQPPTQDIKPIK

Total Number of Spectra: 3

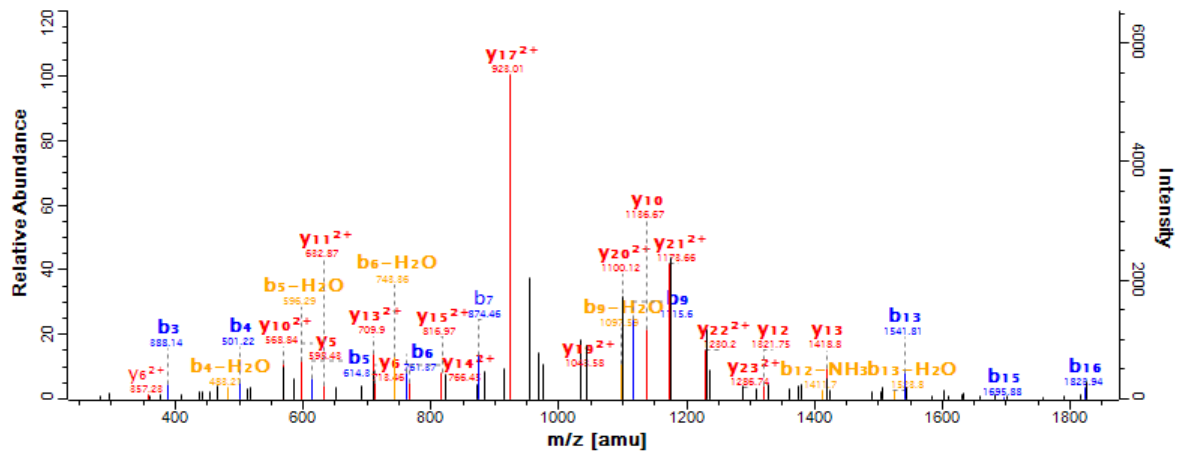
Number of Replicates (out of 8): 3

Best Match Score: 134.86

Best Match Posterior Error Probability: 4.55E-18

Best Match Spectrum:

Scan number	83749	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	POLR3D



Protein Group ID: 2170

Protein Accession Numbers: P08590; P05976; P05976-2

Gene Names: MYL3;MYL1

Peptide Sequence: EGNGTVMGAELR

Total Number of Spectra: 3

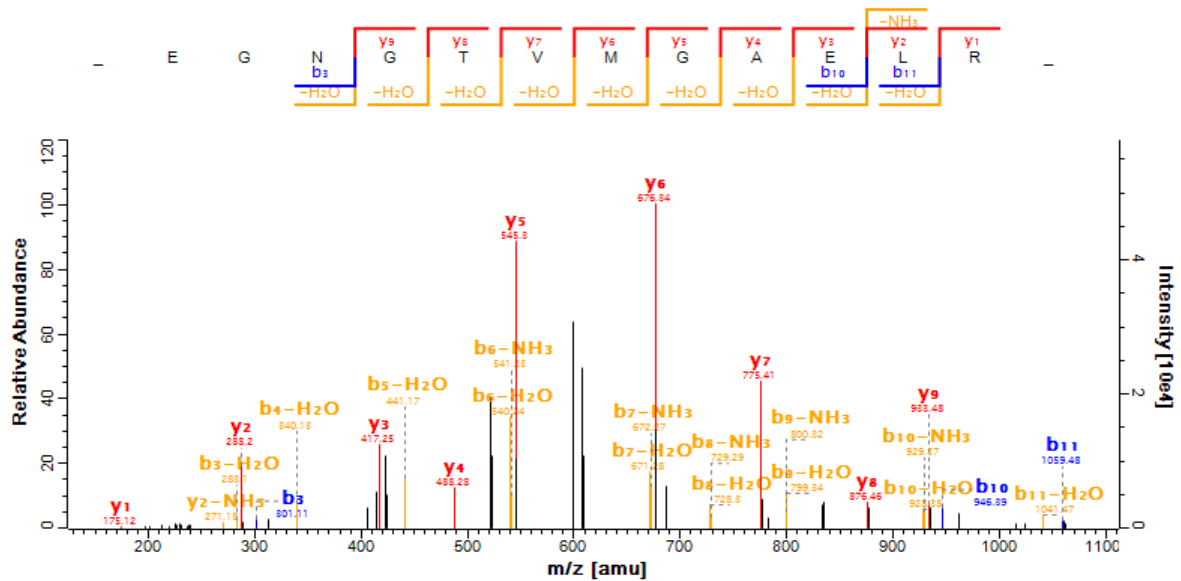
Number of Replicates (out of 8): 3

Best Match Score: 84.365

Best Match Posterior Error Probability: 0.0023701

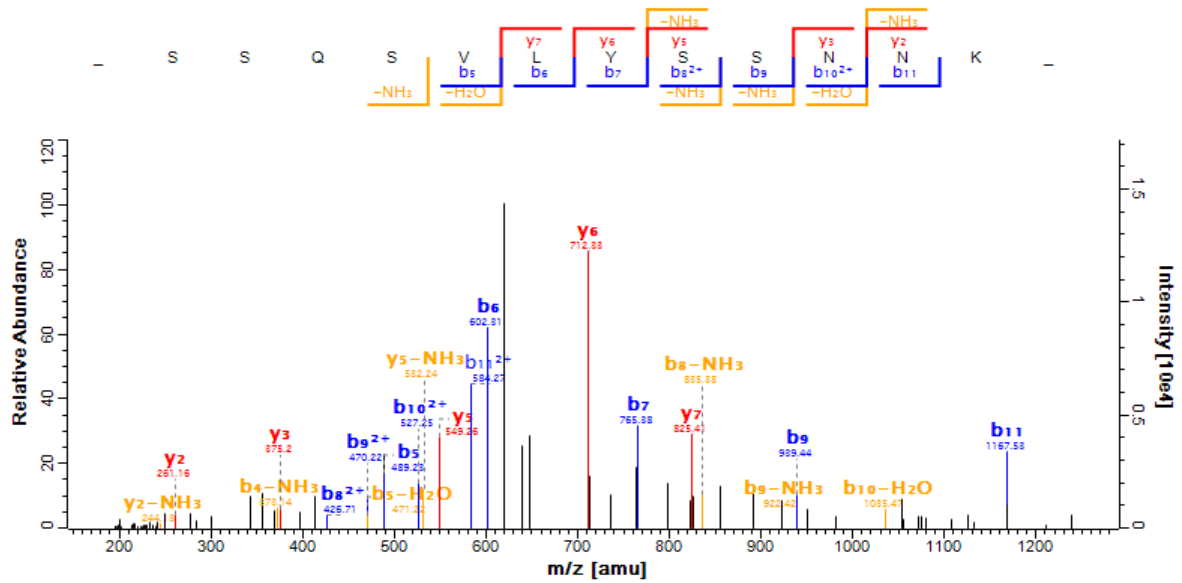
Best Match Spectrum:

Scan number	21880	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	MYL3;MYL1



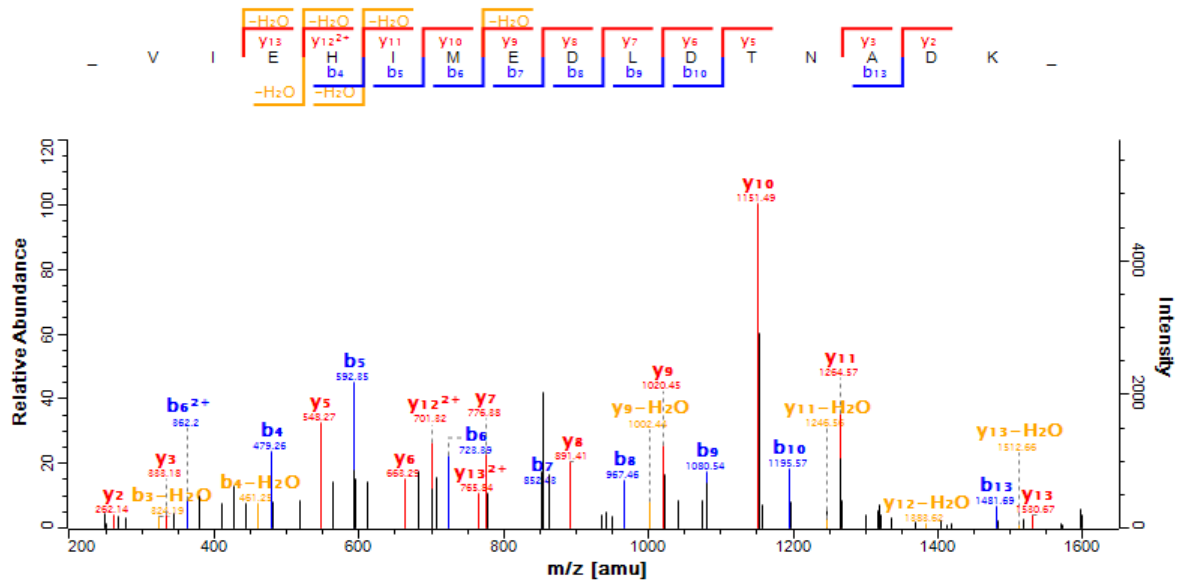
Protein Group ID: 2174
Protein Accession Numbers: P06313; P06312; P83593
Gene Names: IGKV4-1
Peptide Sequence: SSQSVLYSSNNK
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 95.094
Best Match Posterior Error Probability: 0.0009192
Best Match Spectrum:

Scan number 54345 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** IGKV4-1



Protein Group ID: 2178
Protein Accession Numbers: P06702
Gene Names: S100A9
Peptide Sequence: VIEHIMEDLDTNADK
Total Number of Spectra: 2
Number of Replicates (out of 8): 1
Best Match Score: 138.73
Best Match Posterior Error Probability: 1.70E-05
Best Match Spectrum:

Scan number 41571 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** S100A9



Protein Group ID: 2188

Protein Accession Numbers: P06899; P23527; P33778; Q16778; Q8N257; Q6DN03; Q6DRA6

Gene Names:

HIST1H2BJ; HIST1H2BO; HIST1H2BB; HIST2H2BE; HIST3H2BB; HIST2H2BC; HIST2H2BD

Peptide Sequence: KESYSIYVYK

Total Number of Spectra: 3

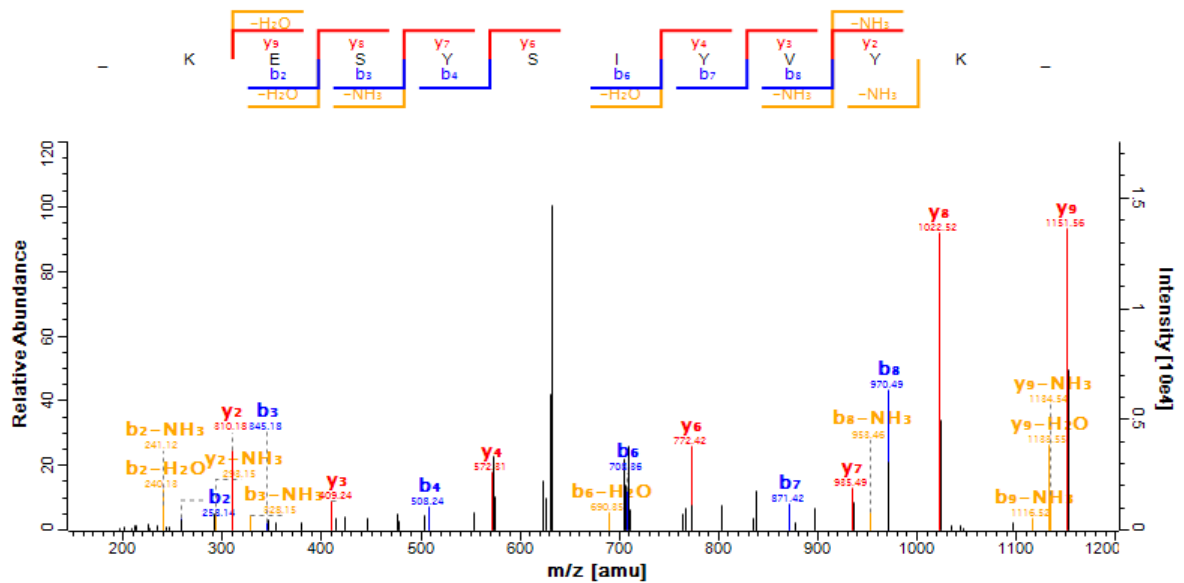
Number of Replicates (out of 8): 3

Best Match Score: 134.3

Best Match Posterior Error Probability: 1.72E-05

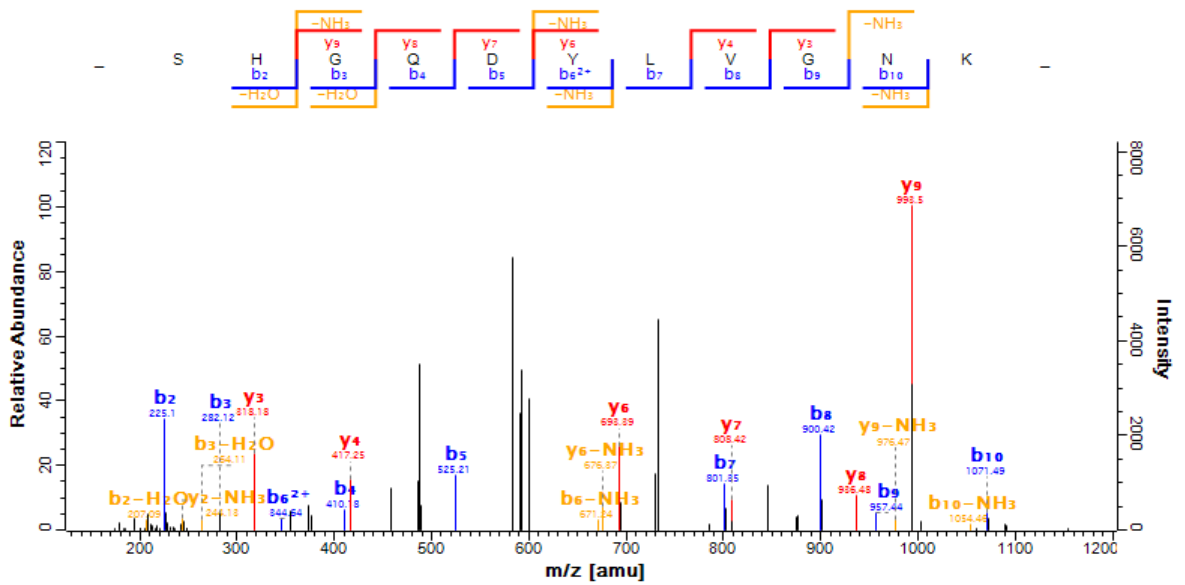
Best Match Spectrum:

Scan number 28164 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS: CID **Genenames** HIST1H2BJ; HIST1H2BO; HIST1H2BB; HIST2H2BE; HIST3H2BB; HIST2H2BC; HIST2H2BD



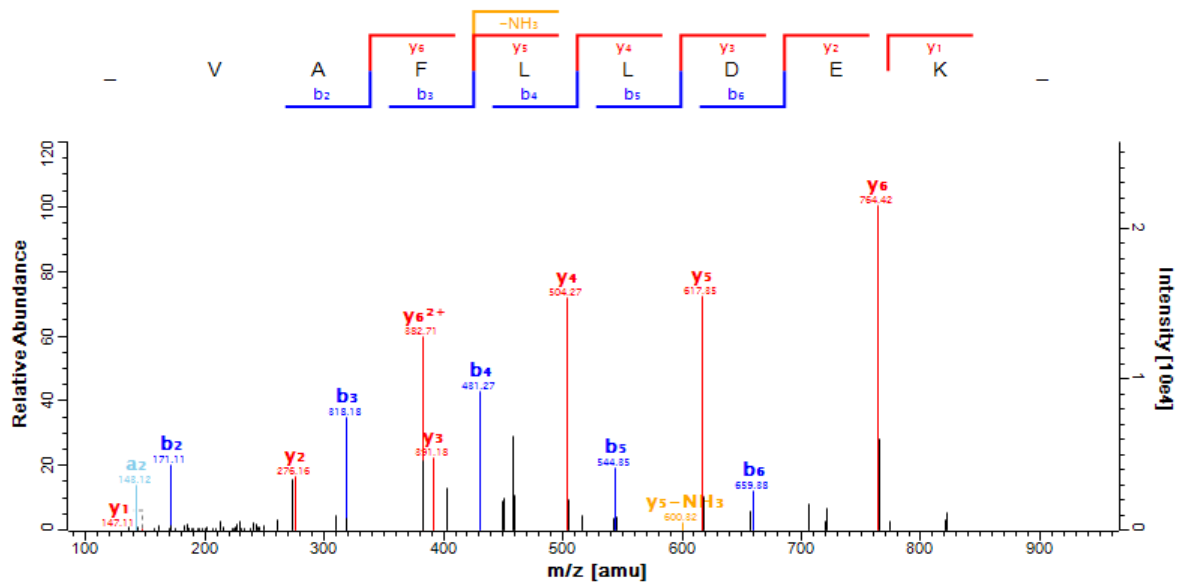
Protein Group ID: 2219
Protein Accession Numbers: P08263; P09210
Gene Names: GSTA1;GSTA2
Peptide Sequence: SHGQDYLVGNK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 109.72
Best Match Posterior Error Probability: 0.00016885
Best Match Spectrum:

Scan number 9782 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** GSTA1;GSTA2



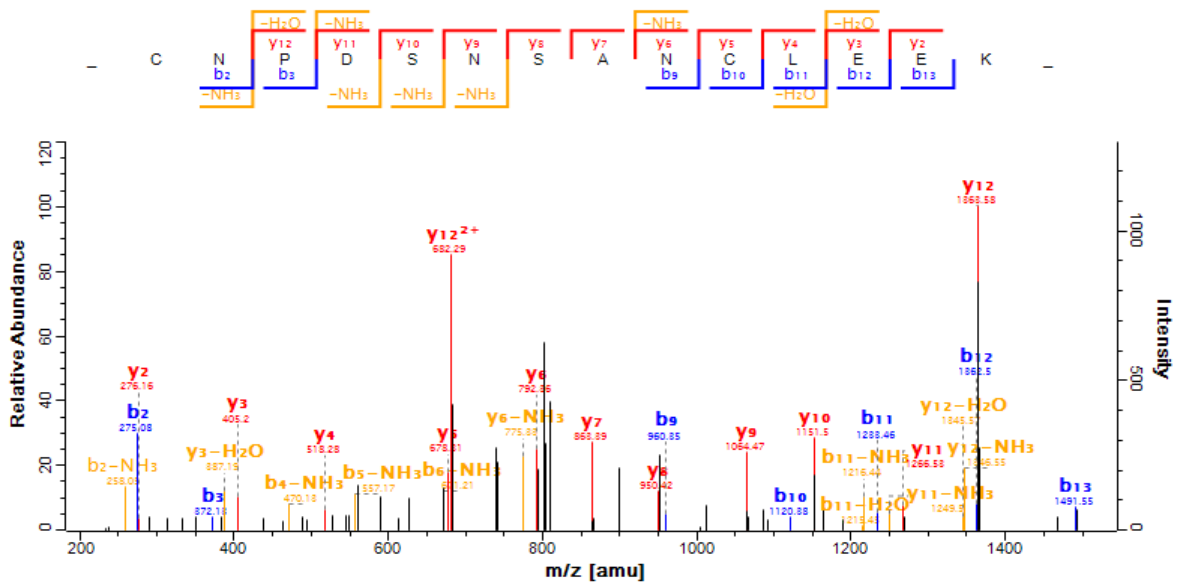
Protein Group ID: 2261
Protein Accession Numbers: P0C2Y1
Gene Names: NBPF7
Peptide Sequence: VAFLLEK
Total Number of Spectra: 6
Number of Replicates (out of 8): 5
Best Match Score: 111.04
Best Match Posterior Error Probability: 0.0028296
Best Match Spectrum:

Scan number 52409 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** NBPF7



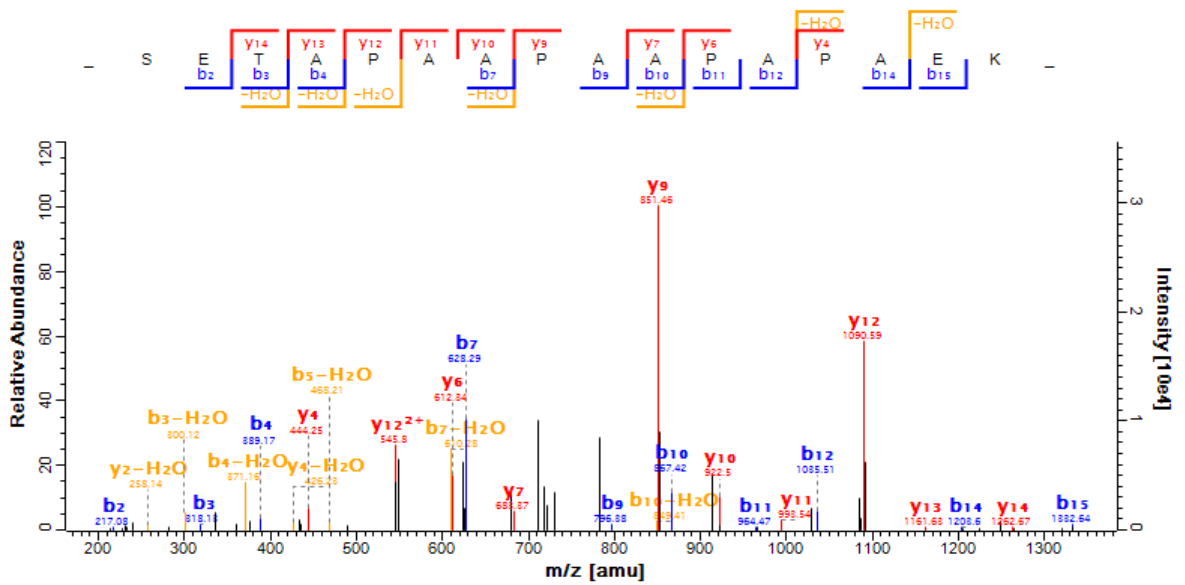
Protein Group ID: 2265
Protein Accession Numbers: P10124
Gene Names: SRGN
Peptide Sequence: CNPDSNSANCLEEK
Total Number of Spectra: 2
Number of Replicates (out of 8): 1
Best Match Score: 134.81
Best Match Posterior Error Probability: 3.93E-05
Best Match Spectrum:

Scan number 10204 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** SRGN



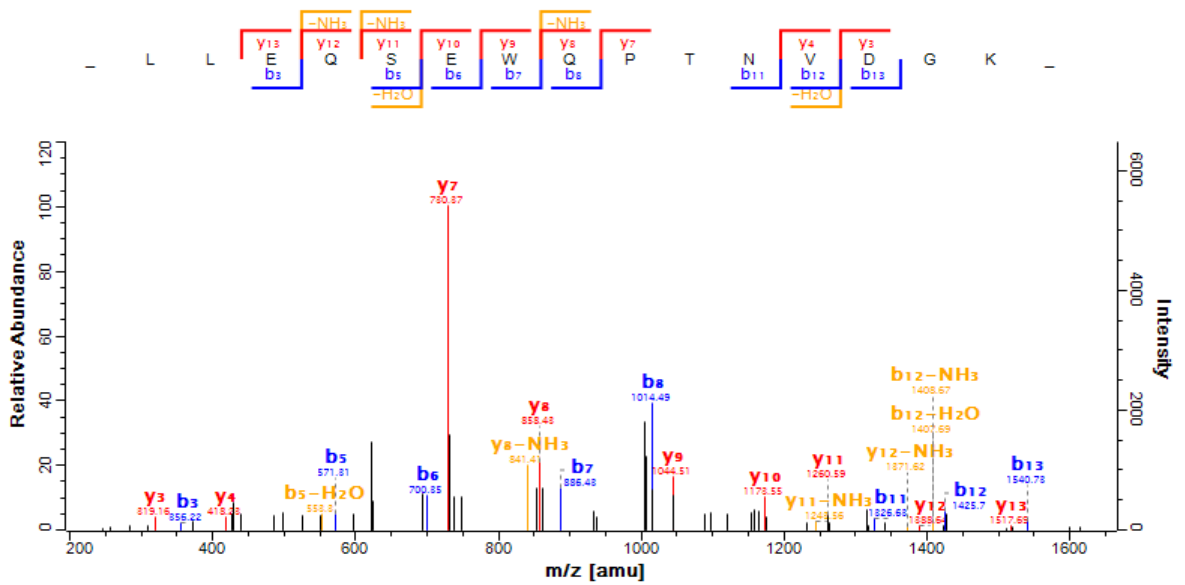
Protein Group ID: 2270
Protein Accession Numbers: P10412
Gene Names: HIST1H1E
Peptide Sequence: SETAPAAPAAPAEK
Total Number of Spectra: 9
Number of Replicates (out of 8): 7
Best Match Score: 145.69
Best Match Posterior Error Probability: 2.07E-06
Best Match Spectrum:

Scan number 15243 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** HIST1H1E



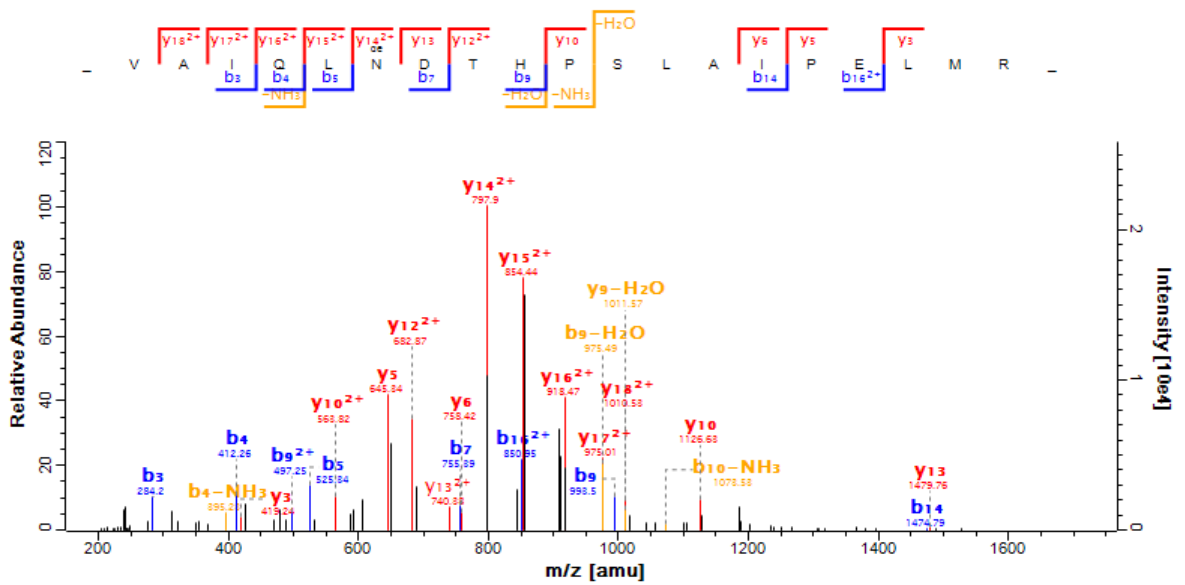
Protein Group ID: 2281
Protein Accession Numbers: P10914
Gene Names: IRF1
Peptide Sequence: LLEQSEWQPTNVGDK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 105.28
Best Match Posterior Error Probability: 0.00016463
Best Match Spectrum:

Scan number 39181 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** IRF1



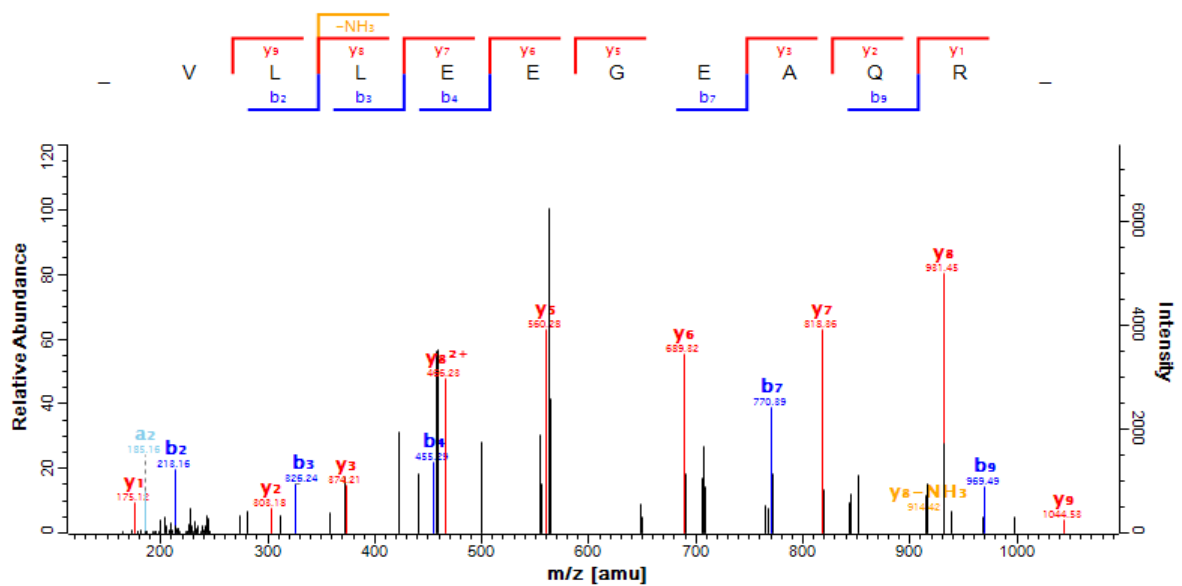
Protein Group ID: 2292
Protein Accession Numbers: P11217; P11217-2
Gene Names: PYGM
Peptide Sequence: VAIQLNDTHPSLAIPELMR
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 127.75
Best Match Posterior Error Probability: 6.73E-05
Best Match Spectrum:

Scan number 71836 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PYGM



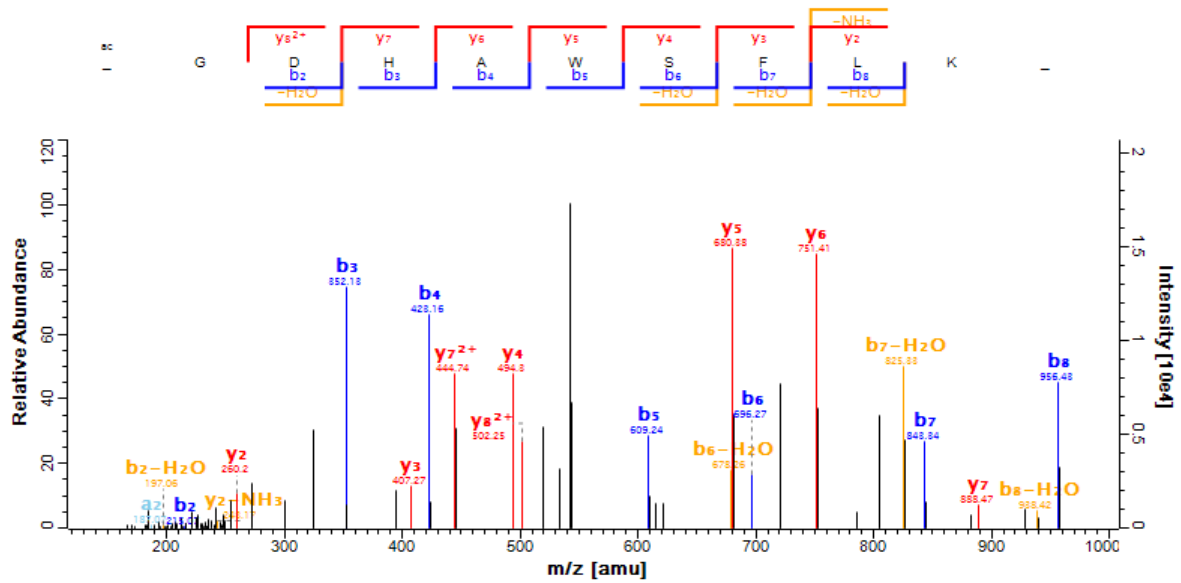
Protein Group ID: 2299
Protein Accession Numbers: Q5HY81; P11441
Gene Names: UBL4A
Peptide Sequence: VLLEEGEAQR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 96.015
Best Match Posterior Error Probability: 0.0012035
Best Match Spectrum:

Scan number 17371 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** UBL4A



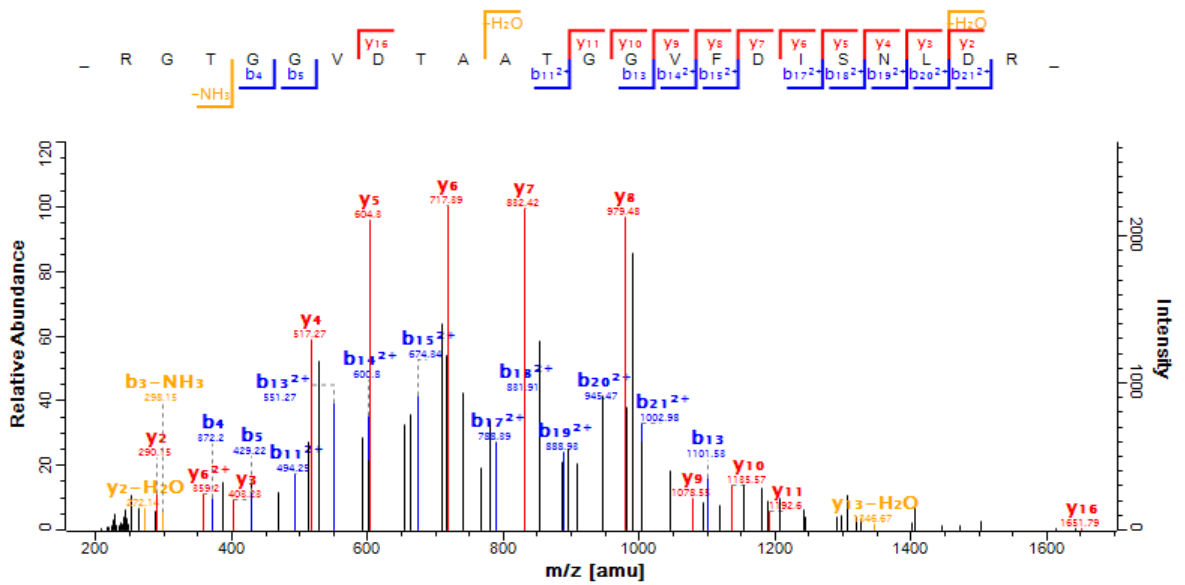
Protein Group ID: 2308
Protein Accession Numbers: P12235
Gene Names: SLC25A4
Peptide Sequence: GDHAWSFLK
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 118.71
Best Match Posterior Error Probability: 0.00070316
Best Match Spectrum:

Scan number 50371 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SLC25A4



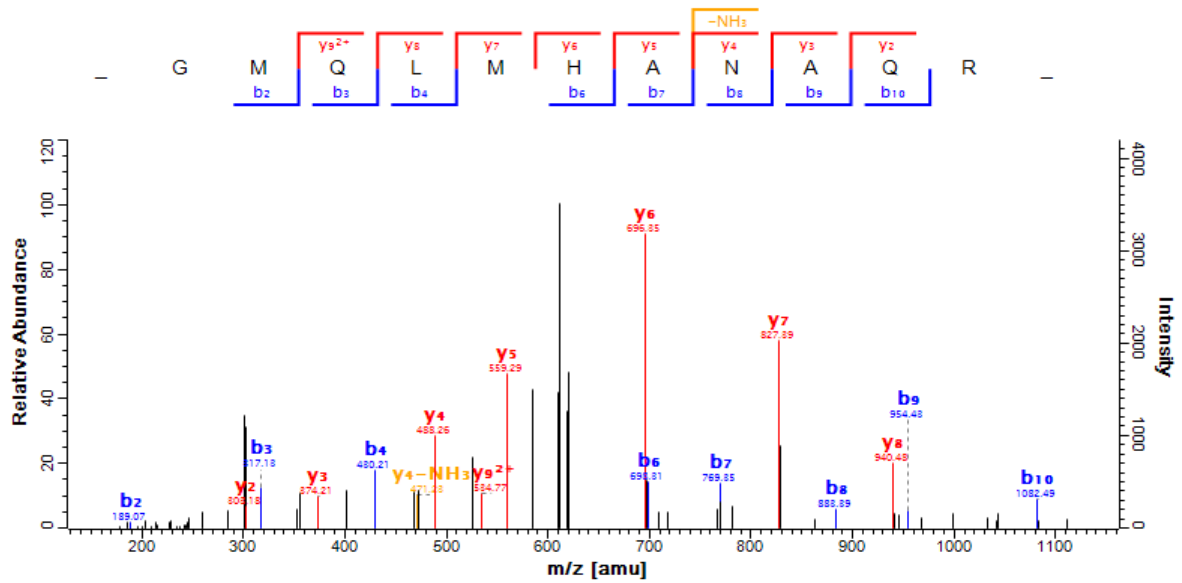
Protein Group ID: 2313
Protein Accession Numbers: P12532-2; P12532
Gene Names: CKMT1A
Peptide Sequence: RGTGGVDTAATAAGVFDISNLR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 88.951
Best Match Posterior Error Probability: 5.57E-05
Best Match Spectrum:

Scan number 52344 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CKMT1A



Protein Group ID: 2322
Protein Accession Numbers: P13284
Gene Names: IFI30
Peptide Sequence: GMQLMHANAQR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 108.47
Best Match Posterior Error Probability: 0.00021357
Best Match Spectrum:

Scan number 14165 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** IFI30



Protein Group ID: 2341

Protein Accession Numbers: P14316; P14316-2

Gene Names: IRF2

Peptide Sequence: GSYLLPGMASFVTSNKPDLQVTIK

Total Number of Spectra: 1

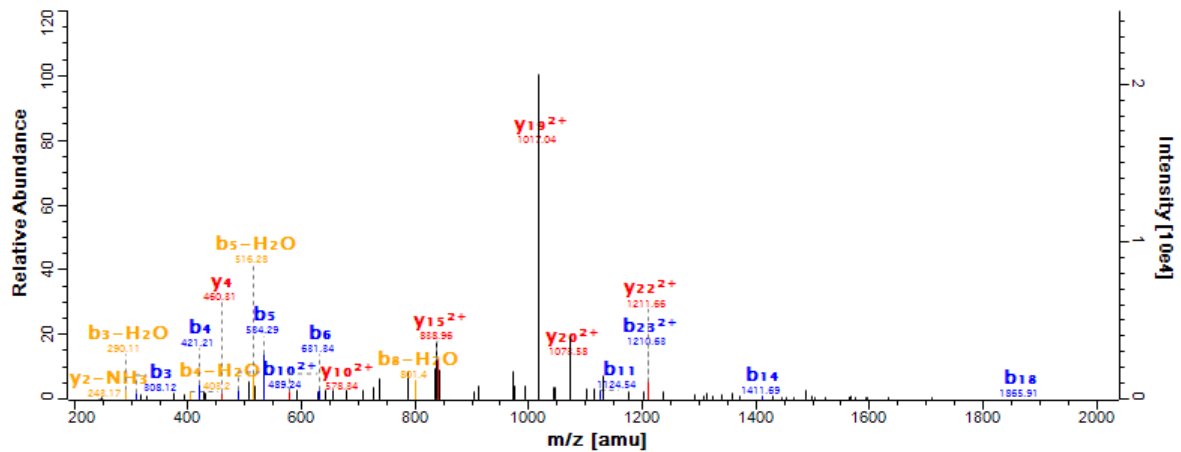
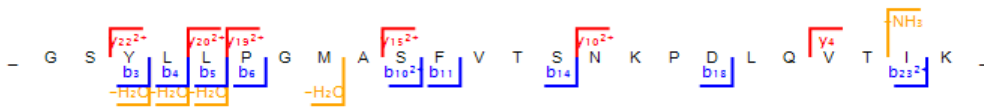
Number of Replicates (out of 8): 1

Best Match Score: 73.783

Best Match Posterior Error Probability: 0.0012123

Best Match Spectrum:

Scan number 77154 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** IRF2



Protein Group ID: 2370

Protein Accession Numbers: P16104; Q96QV6; Q8IUE6

Gene Names: H2AFX;HIST1H2AA;HIST2H2AB

Peptide Sequence: LLGGVTIAQGGVLPNIQAVLLPK

Total Number of Spectra: 14

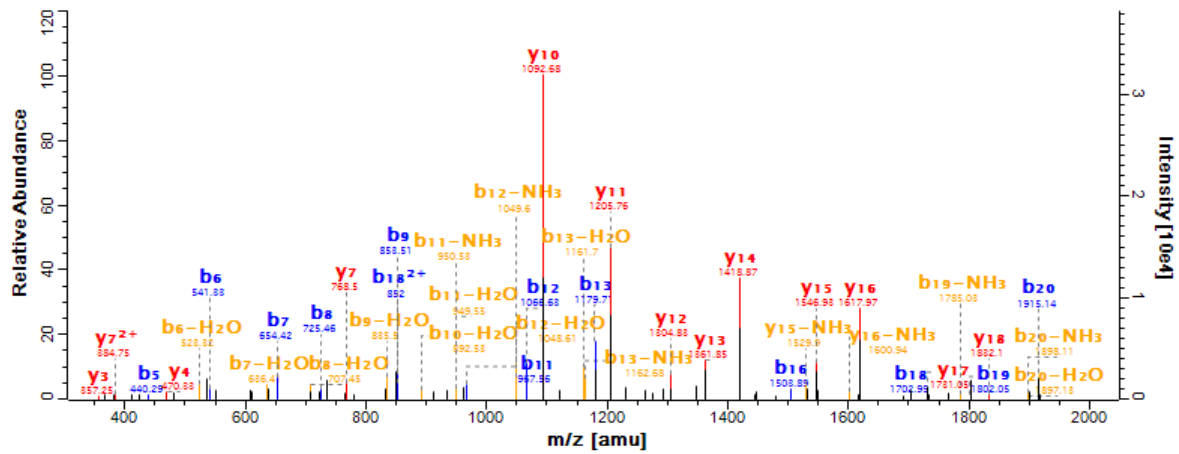
Number of Replicates (out of 8): 7

Best Match Score: 214.59

Best Match Posterior Error Probability: 9.50E-55

Best Match Spectrum:

Scan number 89153 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** H2AFX;HIST1H2AA;HIST2H2AB



Protein Group ID: 2374

Protein Accession Numbers: P16298-4; P16298; P16298-3; P16298-2; Q5F2F8

Gene Names: PPP3CB

Peptide Sequence: IINEGAILR

Total Number of Spectra: 1

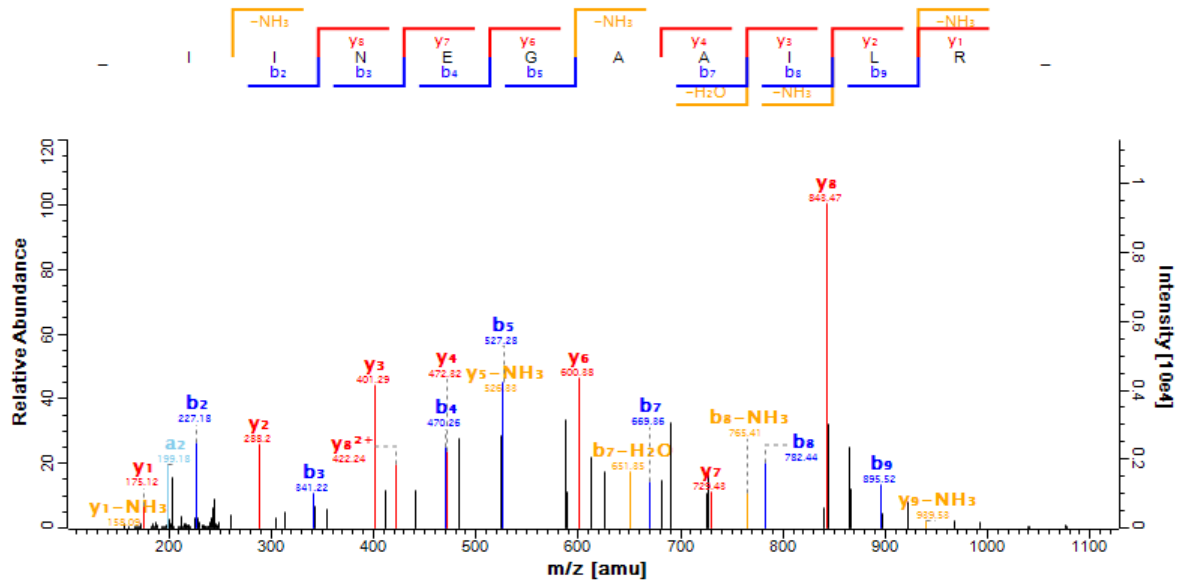
Number of Replicates (out of 8): 1

Best Match Score: 120.06

Best Match Posterior Error Probability: 0.00012445

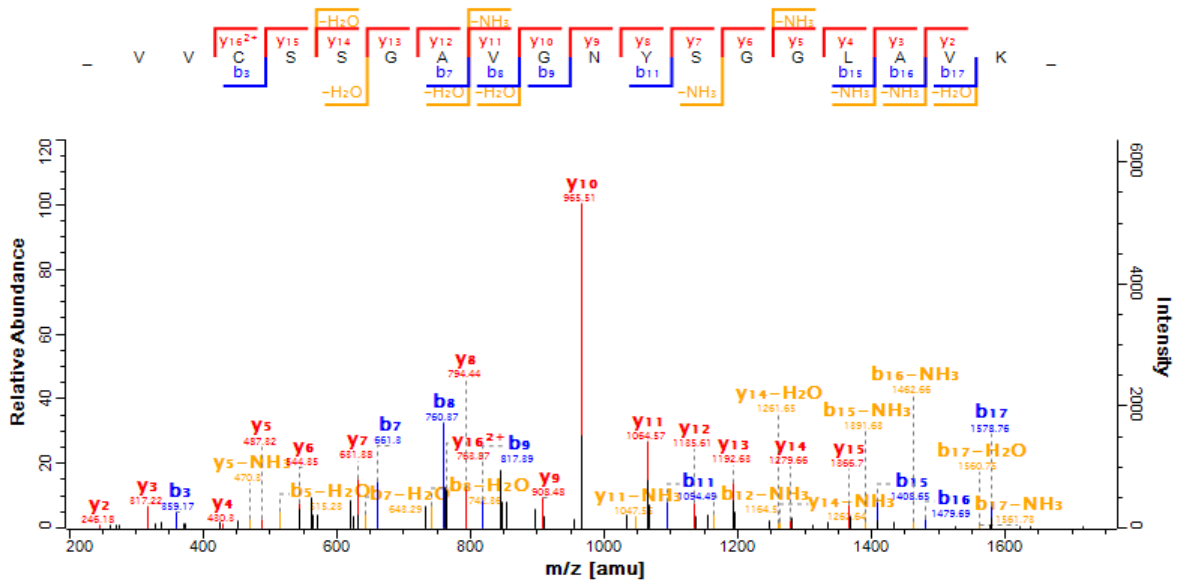
Best Match Spectrum:

Scan number	32896	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	PPP3CB



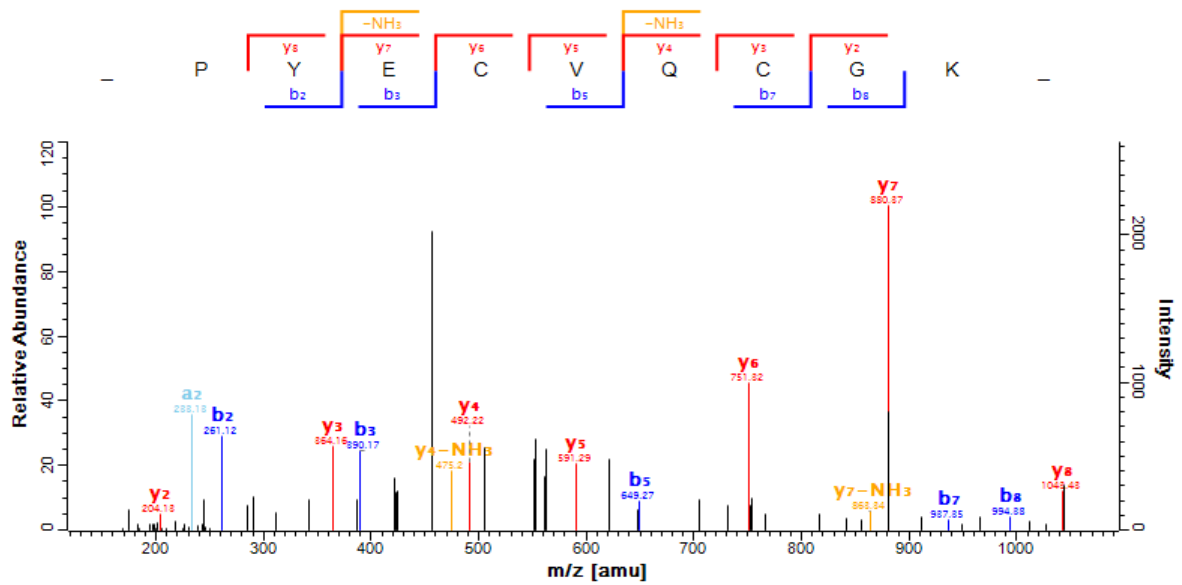
Protein Group ID: 2379
Protein Accession Numbers: P16455
Gene Names: MGMT
Peptide Sequence: VVCSSGAVGNYSGGLAVK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 168.42
Best Match Posterior Error Probability: 6.14E-32
Best Match Spectrum:

Scan number 32483 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MGMT



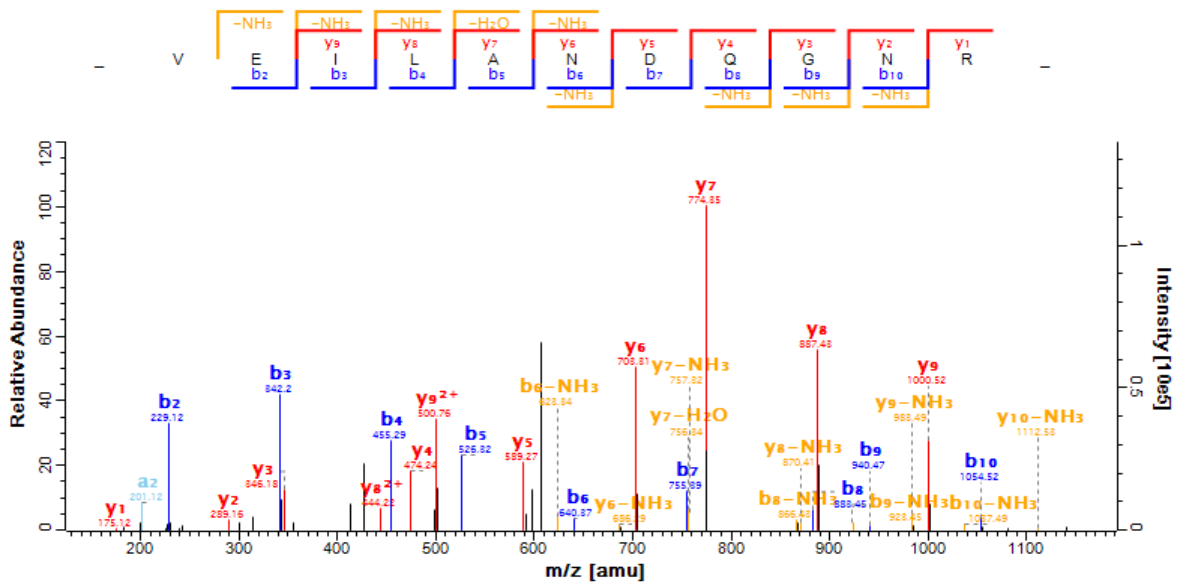
Protein Group ID: 2383
Protein Accession Numbers: Q9C0F3; P17028
Gene Names: ZNF436;ZNF24
Peptide Sequence: PYECVQCGK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 100.02
Best Match Posterior Error Probability: 0.0017716
Best Match Spectrum:

Scan number	5554	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	ZNF436;ZNF24



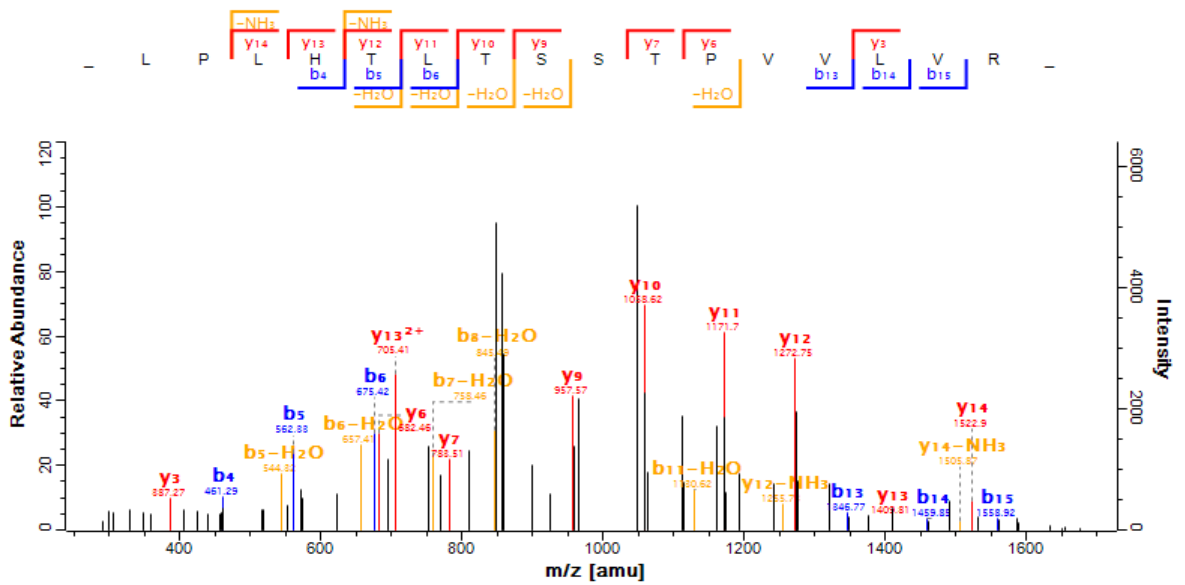
Protein Group ID: 2385
Protein Accession Numbers: P17066; P48741
Gene Names: HSPA6;HSPA7
Peptide Sequence: VEILANDQGNR
Total Number of Spectra: 18
Number of Replicates (out of 8): 7
Best Match Score: 209.19
Best Match Posterior Error Probability: 1.10E-21
Best Match Spectrum:

Scan number 15118 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** HSPA6;HSPA7



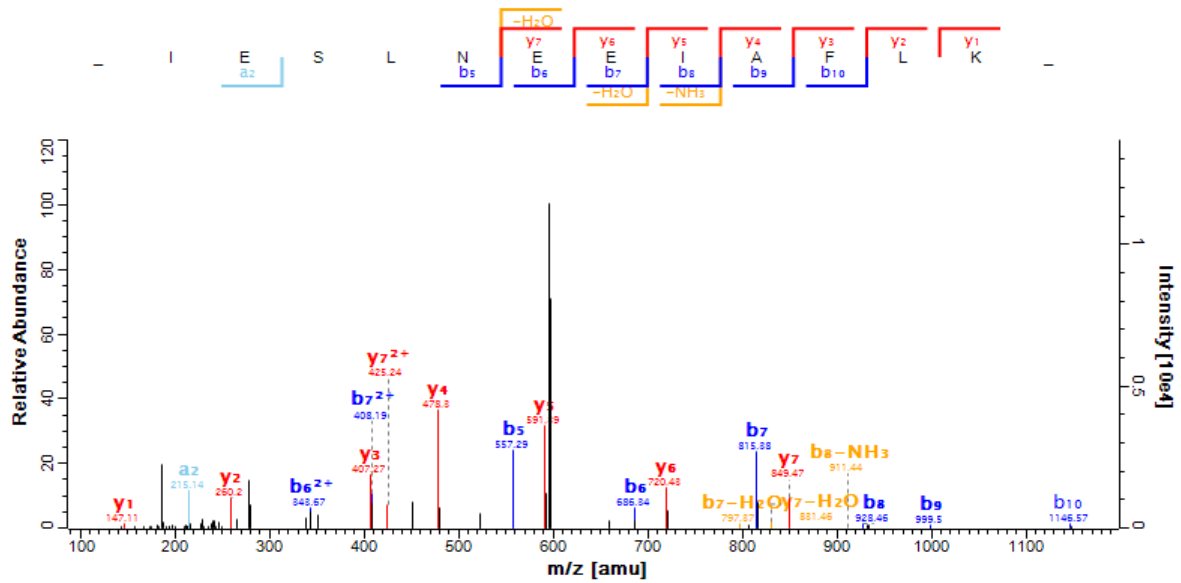
Protein Group ID: 2386
Protein Accession Numbers: P17152
Gene Names: TMEM11
Peptide Sequence: LPLHTLTSSTPVVLVR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 88.768
Best Match Posterior Error Probability: 0.00063028
Best Match Spectrum:

Scan number 53133 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TMEM11



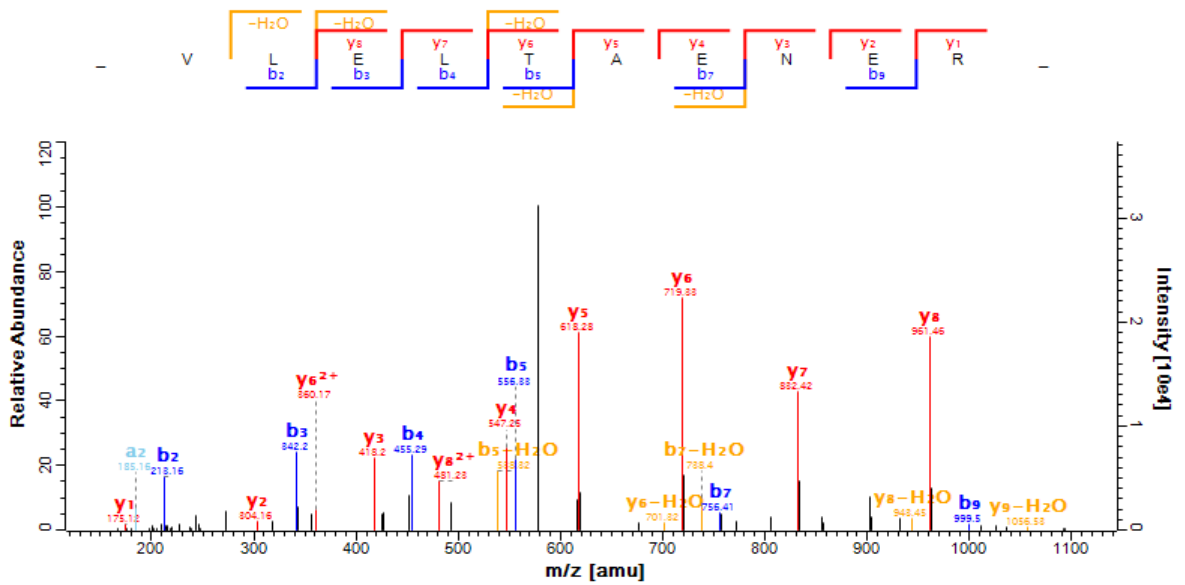
Protein Group ID: 2397
Protein Accession Numbers: P17661
Gene Names: DES
Peptide Sequence: IESLN^{EEIA}FLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 127.17
Best Match Posterior Error Probability: 0.00010154
Best Match Spectrum:

Scan number 62777 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** DES



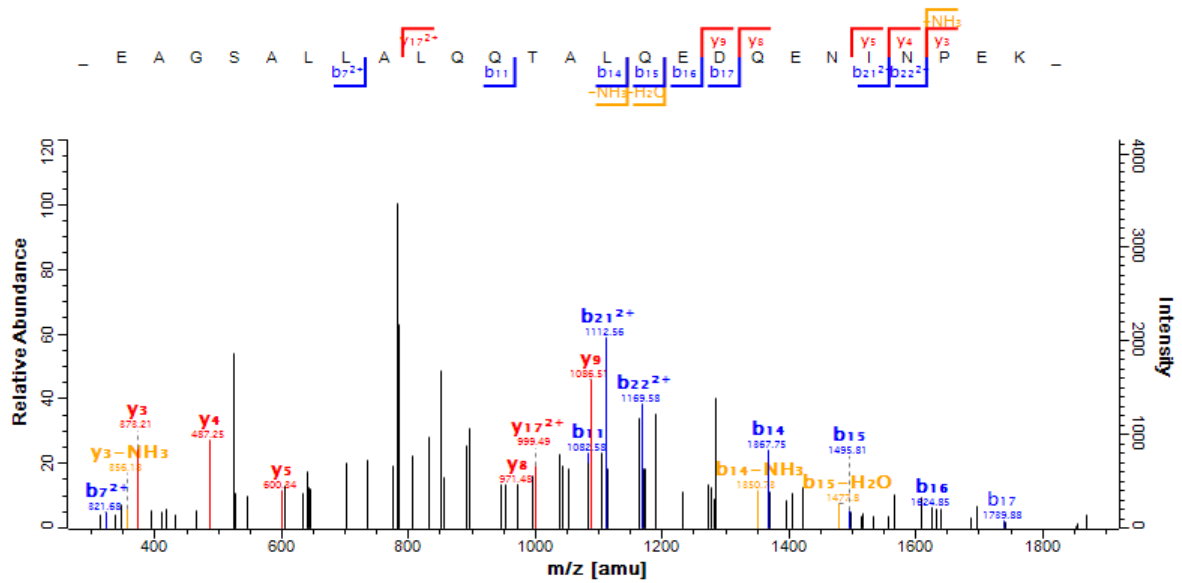
Protein Group ID: 2398
Protein Accession Numbers: P17676
Gene Names: CEBPB
Peptide Sequence: VLELTAENER
Total Number of Spectra: 9
Number of Replicates (out of 8): 8
Best Match Score: 136.02
Best Match Posterior Error Probability: 8.91E-06
Best Match Spectrum:

Scan number 23914 **Raw file** A549-US-WT-top20CID-Elite-2ug-811
Method ITMS; CID **Genenames** CEBPB



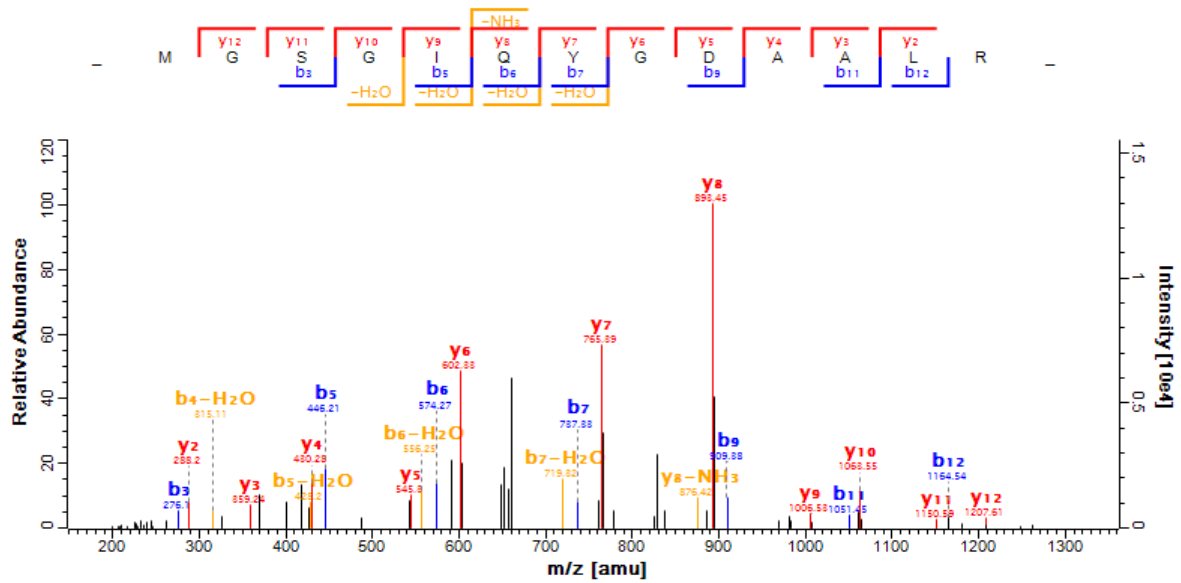
Protein Group ID: 2432
Protein Accession Numbers: P20248
Gene Names: CCNA2
Peptide Sequence: EAGSALLQQTALQEDQENINPEK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 61.524
Best Match Posterior Error Probability: 0.0013223
Best Match Spectrum:

Scan number 64188 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CCNA2



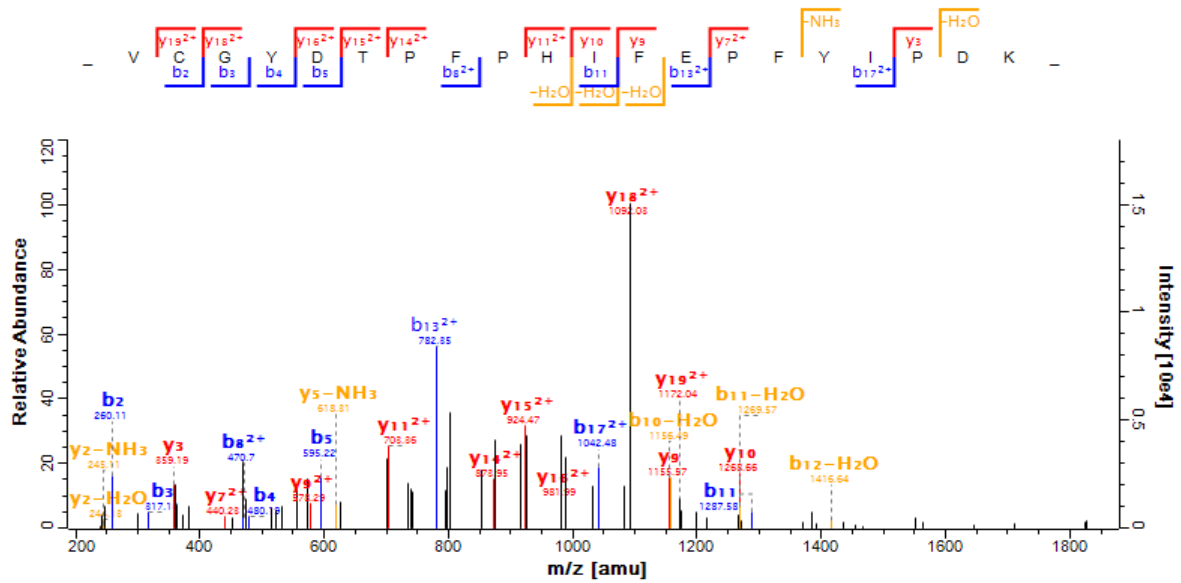
Protein Group ID: 2437
Protein Accession Numbers: P20338
Gene Names: RAB4A
Peptide Sequence: MGSGIQYGDAALR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 118.51
Best Match Posterior Error Probability: 0.00016997
Best Match Spectrum:

Scan number 32024 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** RAB4A



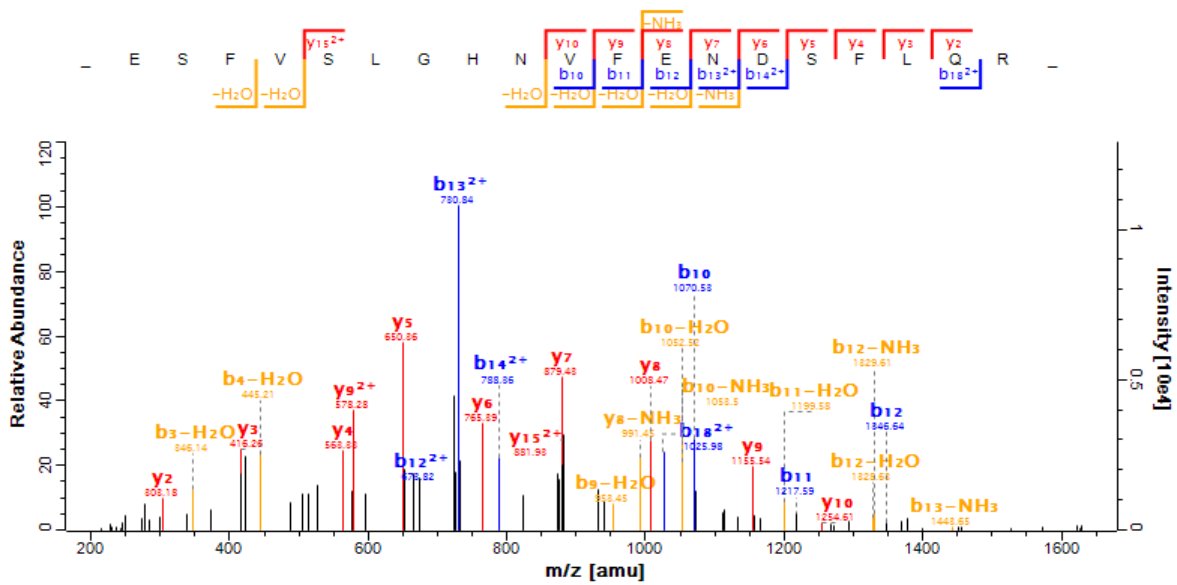
Protein Group ID: 2455
Protein Accession Numbers: P21953
Gene Names: BCKDHB
Peptide Sequence: VCGYDTPFPFHIFEPFYIPDK
Total Number of Spectra: 7
Number of Replicates (out of 8): 7
Best Match Score: 83.37
Best Match Posterior Error Probability: 0.0003784
Best Match Spectrum:

Scan number	83127	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	BCKDHB



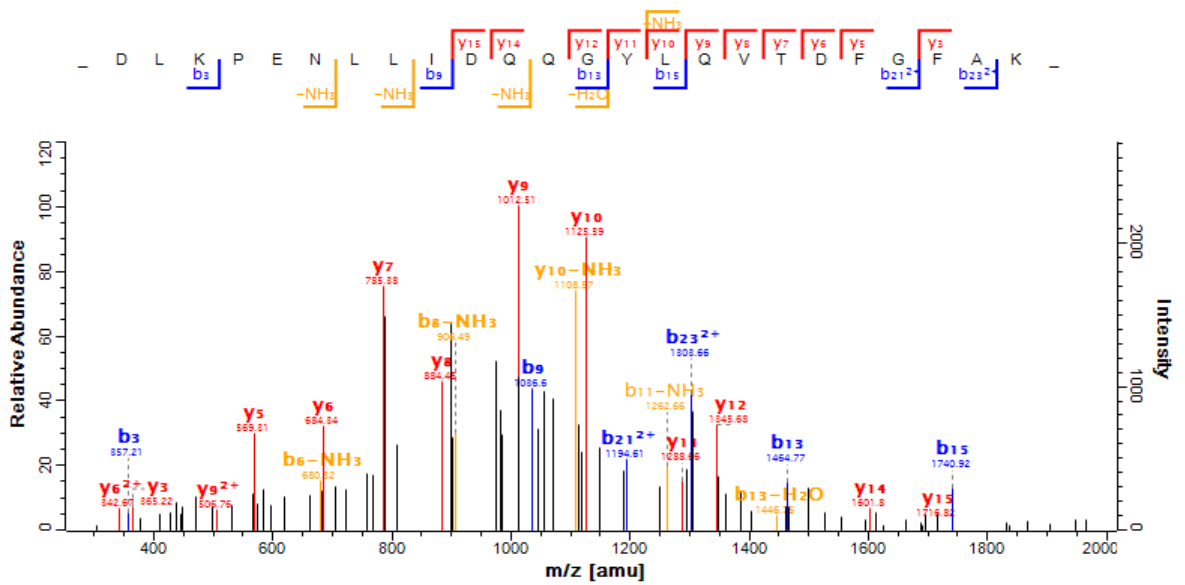
Protein Group ID: 2463
Protein Accession Numbers: P22309; A6NJC3
Gene Names: UGT1A1
Peptide Sequence: ESFVSLGHN**Y**₁₀V**Y**₉F**Y**₈E**Y**₇N**D**₁₃²⁺**D**₁₄²⁺**Y**₅S**Y**₄F**Y**₃L**Y**₂Q**D**₁₆²⁺R

Scan number 67878 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** UGT1A1



Protein Group ID: 2466
Protein Accession Numbers: P22612
Gene Names: PRKACG
Peptide Sequence: DLKPENLLIDQQGYLQVTDFGFAK
Total Number of Spectra: 6
Number of Replicates (out of 8): 3
Best Match Score: 82.593
Best Match Posterior Error Probability: 0.00030165
Best Match Spectrum:

Scan number 82235 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** PRKACG



Protein Group ID: 2477

Protein Accession Numbers: P23378

Gene Names: GLDC

Peptide Sequence: DVSGVLFQYPDTEGKVELVER

Total Number of Spectra: 2

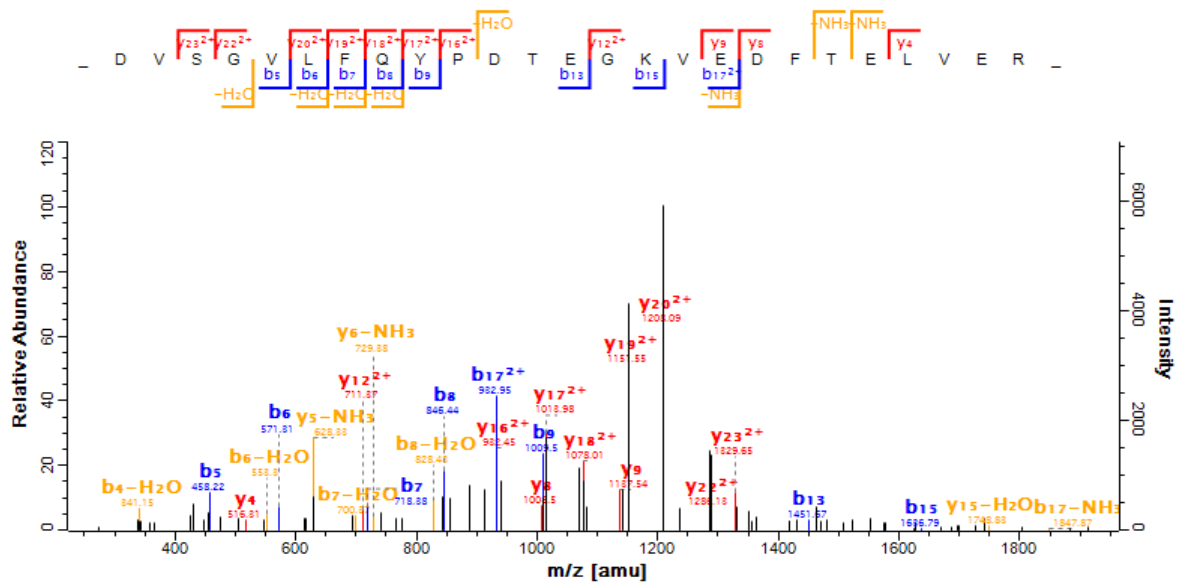
Number of Replicates (out of 8): 2

Best Match Score: 75.773

Best Match Posterior Error Probability: 0.0006188

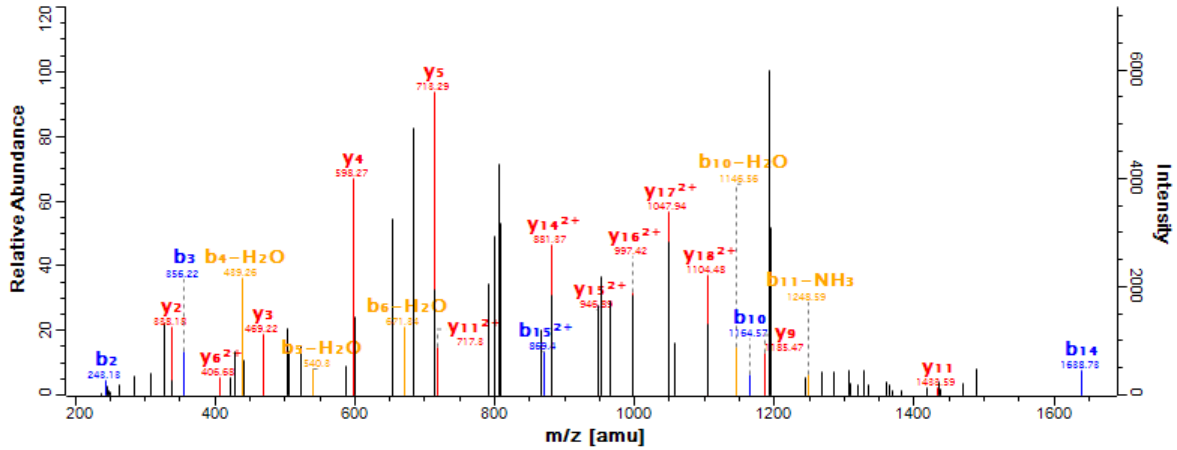
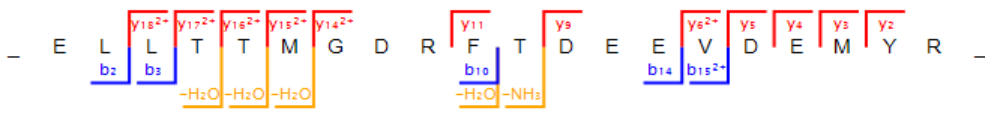
Best Match Spectrum:

Scan number 78968 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** GLDC



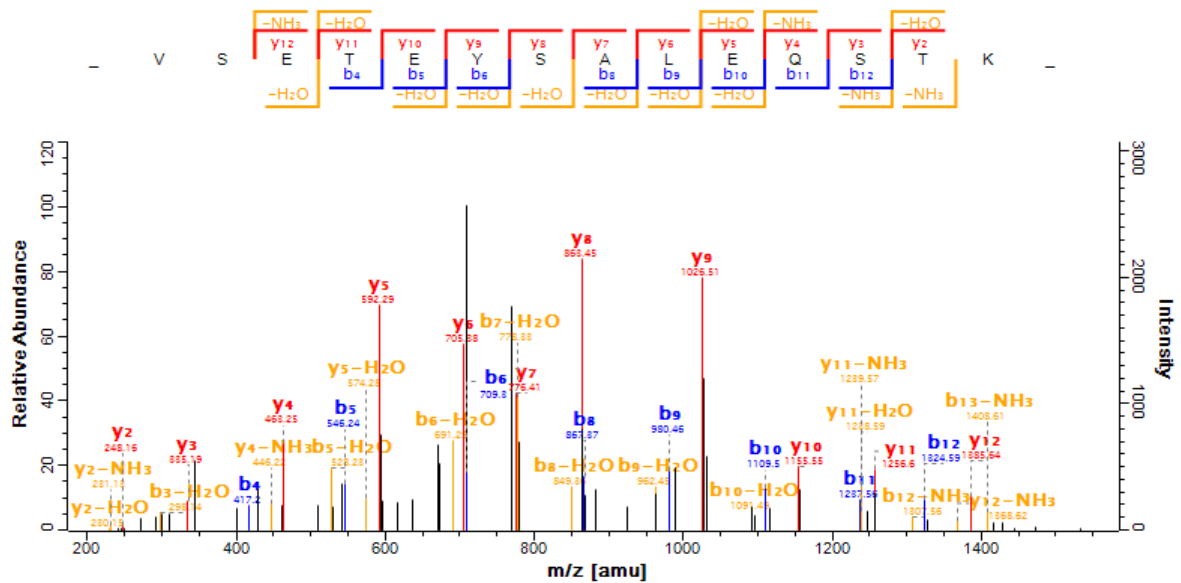
Protein Group ID: 2494
Protein Accession Numbers: P24844; P24844-2
Gene Names: MYL9
Peptide Sequence: ELLTTMGDRFTDEEVDEMYR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 69.935
Best Match Posterior Error Probability: 0.0088815
Best Match Spectrum:

Scan number 60562 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MYL9



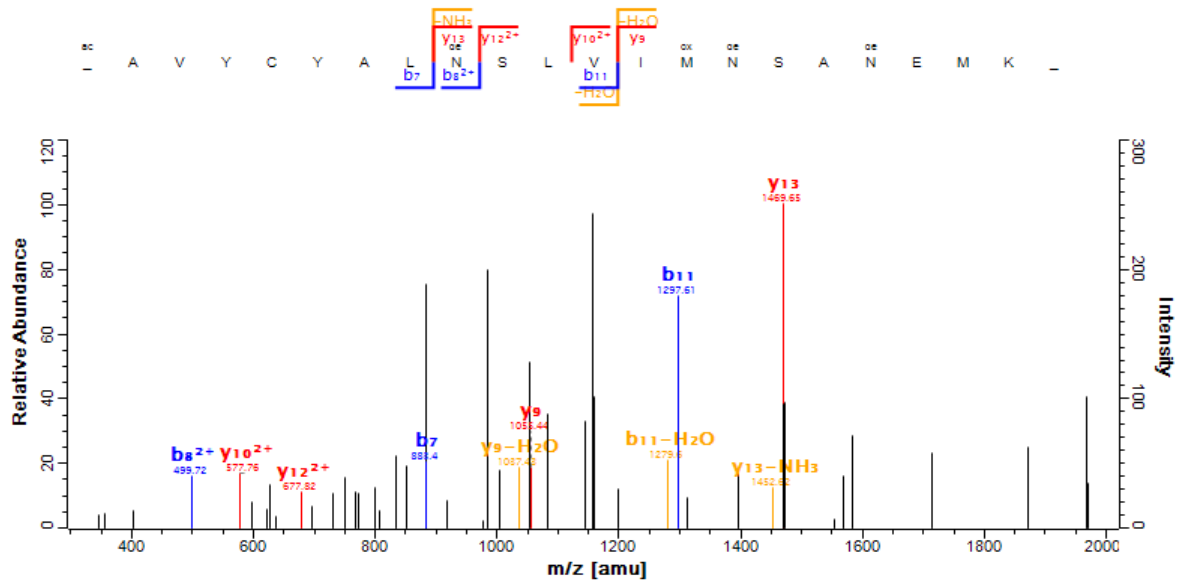
Protein Group ID: 2497
Protein Accession Numbers: P25106
Gene Names: CXCR7
Peptide Sequence: VSETEYSALEQSTK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 192.39
Best Match Posterior Error Probability: 1.12E-24
Best Match Spectrum:

Scan number 26019 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CXCR7



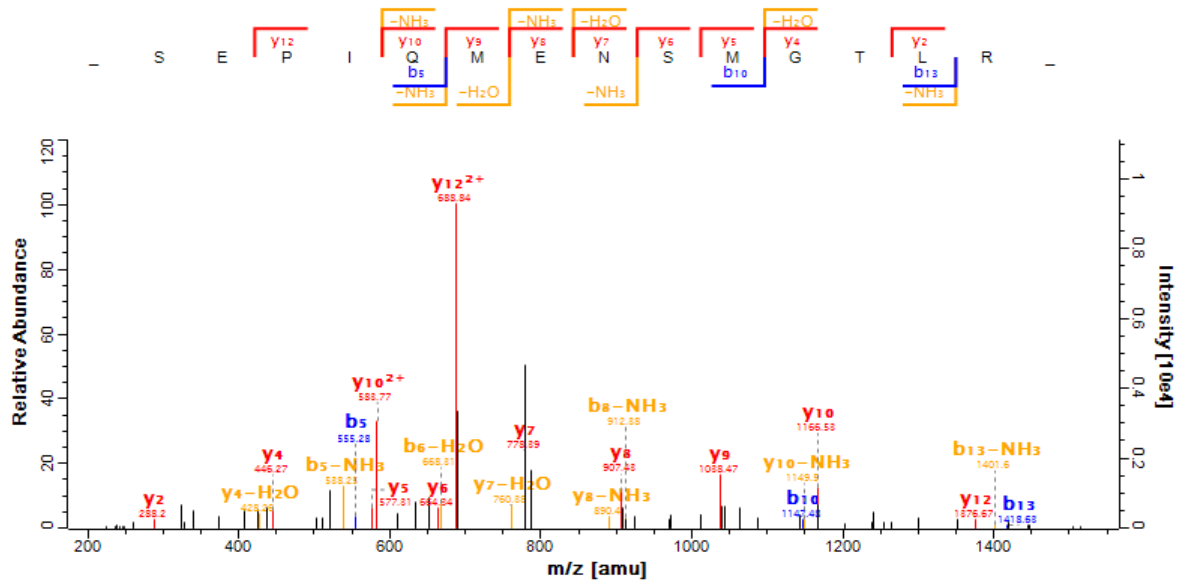
Protein Group ID: 2531
Protein Accession Numbers: P27987; P27987-2
Gene Names: ITPKB
Peptide Sequence: AVYCYALNSLVIMNSANEMK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 32.366
Best Match Posterior Error Probability: 0.026495
Best Match Spectrum:

Scan number 14714 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ITPKB



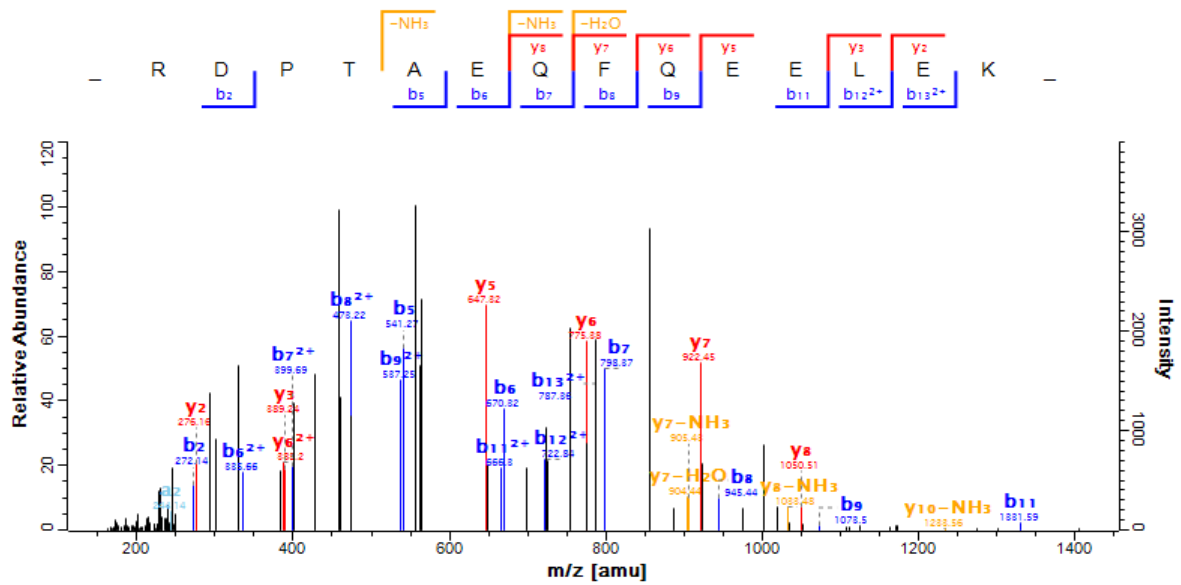
Protein Group ID: 2572
Protein Accession Numbers: P30411; P30411-2
Gene Names: BDKRB2
Peptide Sequence: SEPIQMENSMGTLR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 91.307
Best Match Posterior Error Probability: 0.001073
Best Match Spectrum:

Scan number 39749 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** BDKRB2



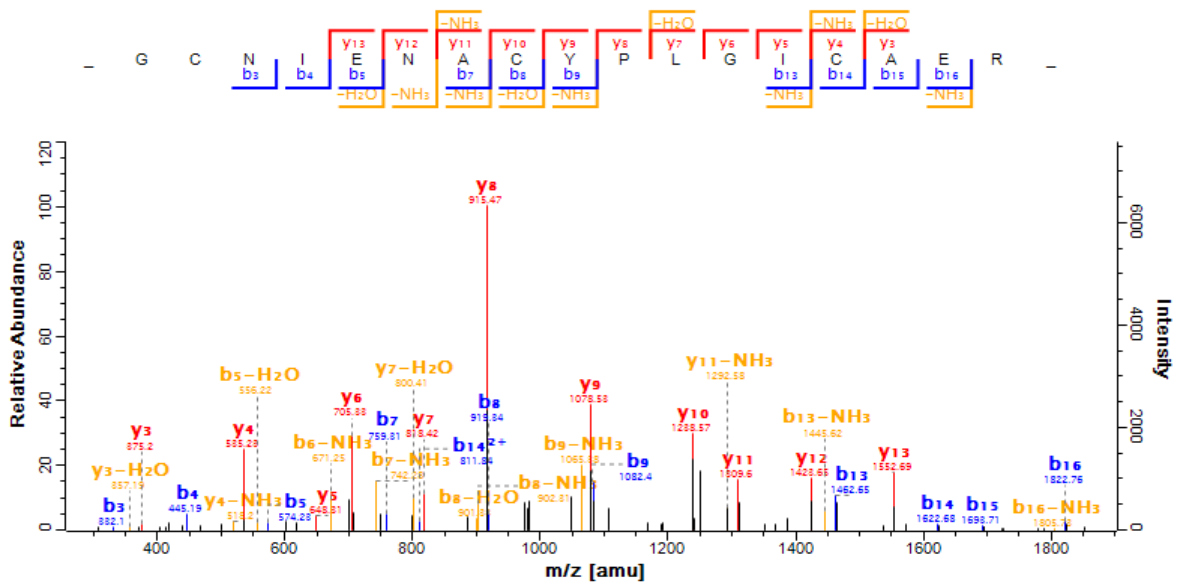
Protein Group ID: 2595
Protein Accession Numbers: P31944
Gene Names: CASP14
Peptide Sequence: RDPTAEQFQEELK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 129.77
Best Match Posterior Error Probability: 9.27E-05
Best Match Spectrum:

Scan number 34296 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CASP14



Protein Group ID: 2600
Protein Accession Numbers: P32320
Gene Names: CDA
Peptide Sequence: GCNIENACYPLGICAER
Total Number of Spectra: 6
Number of Replicates (out of 8): 4
Best Match Score: 161.99
Best Match Posterior Error Probability: 1.66E-09
Best Match Spectrum:

Scan number 46025 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CDA



Protein Group ID: 2641

Protein Accession Numbers: P35869

Gene Names: AHR

Peptide Sequence: LPFMFTTGEAVLYEATNPFPAIMDPLPLR

Total Number of Spectra: 1

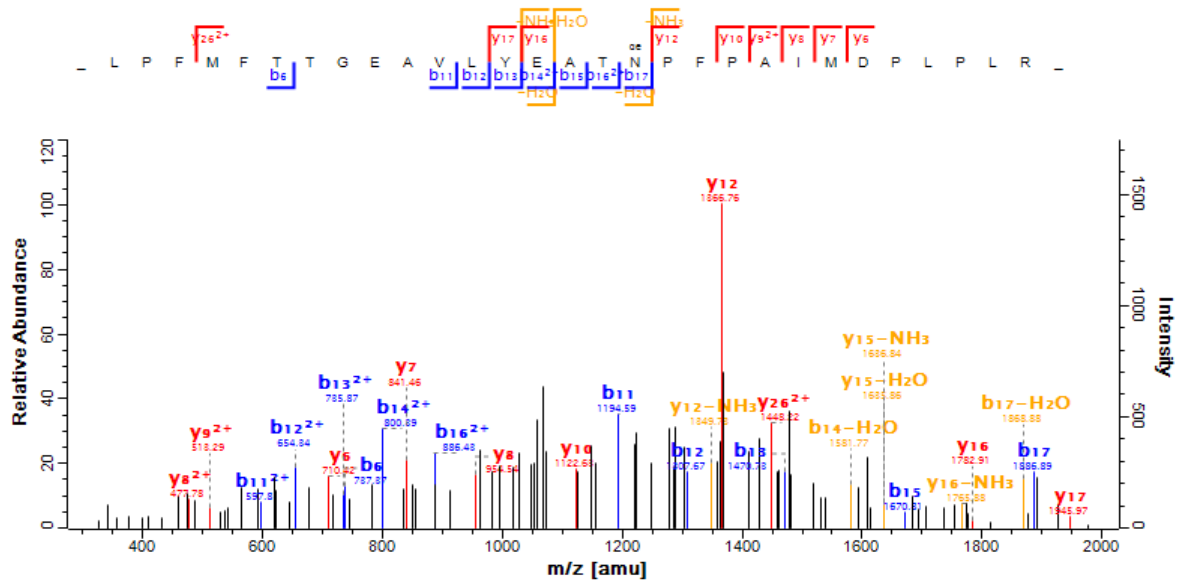
Number of Replicates (out of 8): 1

Best Match Score: 65.387

Best Match Posterior Error Probability: 0.012243

Best Match Spectrum:

Scan number 96263 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** AHR



Protein Group ID: 2642

Protein Accession Numbers: P35908

Gene Names: KRT2

Peptide Sequence: GGGFGGSSFGGGSGFSGGGFGGGGFGGGR

Total Number of Spectra: 16

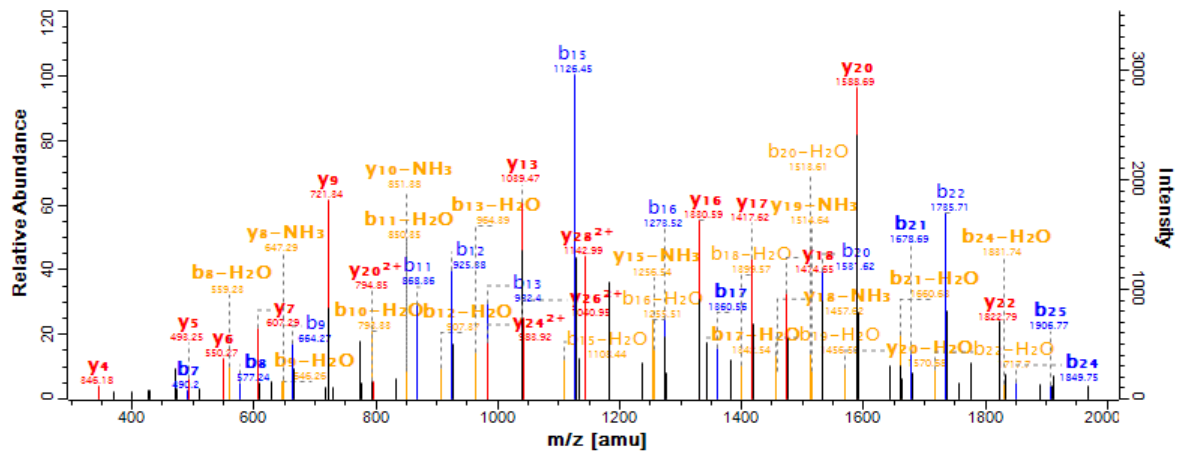
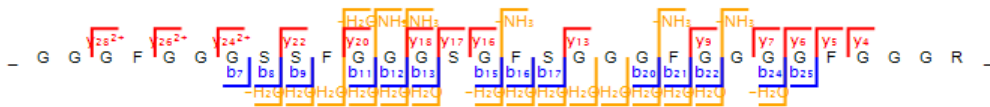
Number of Replicates (out of 8): 7

Best Match Score: 226.72

Best Match Posterior Error Probability: 2.19E-111

Best Match Spectrum:

Scan number	56027	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	KRT2



Protein Group ID: 2646

Protein Accession Numbers: P36406; P36406-2; P36406-3

Gene Names: TRIM23

Peptide Sequence: DALLLIFANK

Total Number of Spectra: 7

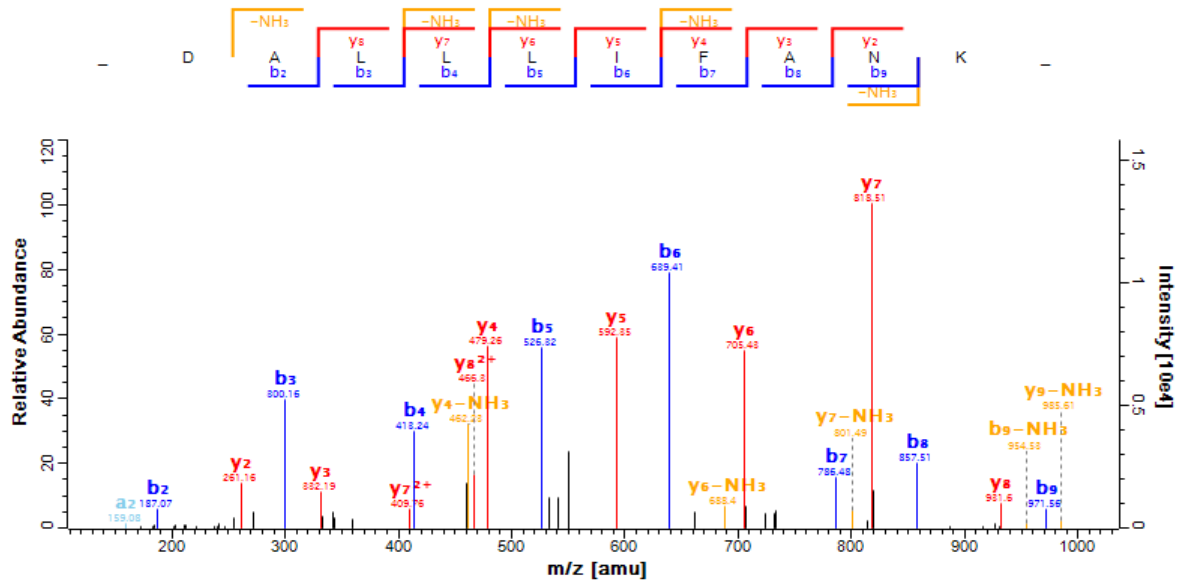
Number of Replicates (out of 8): 7

Best Match Score: 192.32

Best Match Posterior Error Probability: 8.24E-13

Best Match Spectrum:

Scan number 65447 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TRIM23



Protein Group ID: 2652

Protein Accession Numbers: P36639; P36639-2; P36639-3; P36639-4

Gene Names: NUDT1

Peptide Sequence: DMWPDDSYWFPDLLQK

Total Number of Spectra: 10

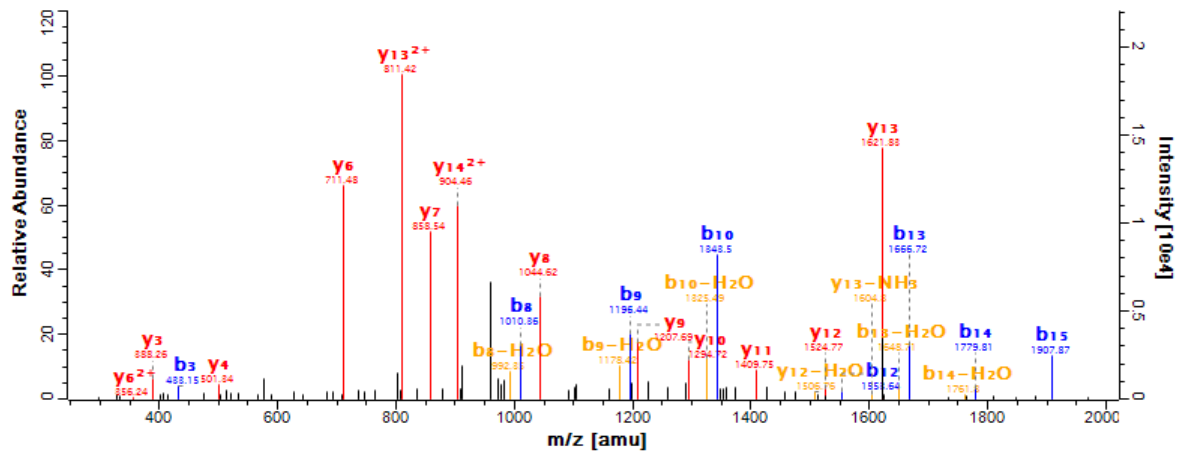
Number of Replicates (out of 8): 8

Best Match Score: 193.16

Best Match Posterior Error Probability: 2.01E-28

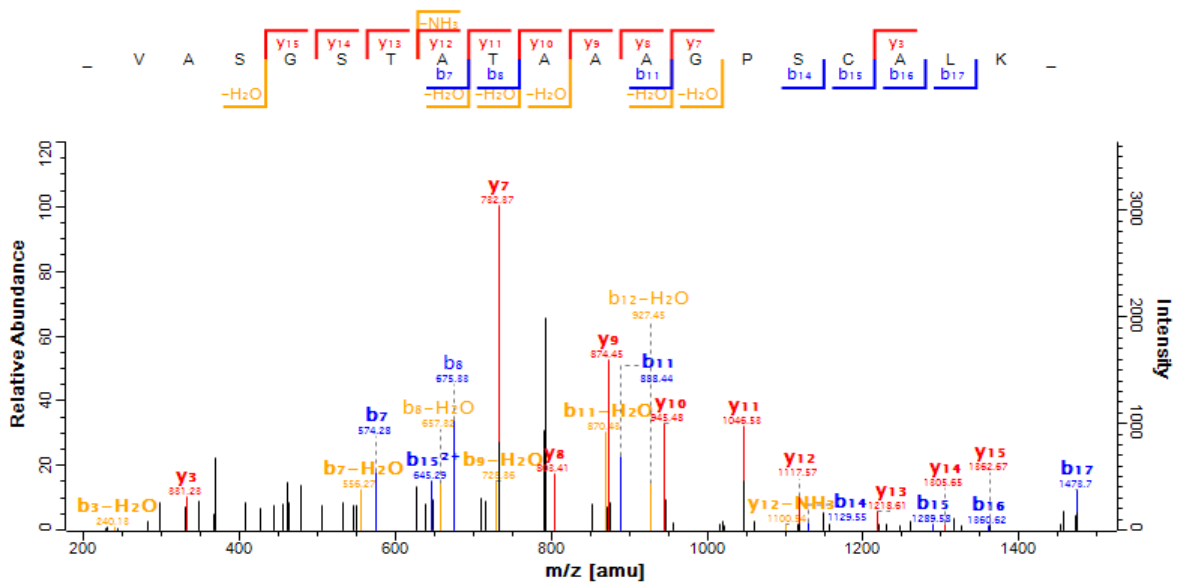
Best Match Spectrum:

Scan number 93657 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** NUDT1



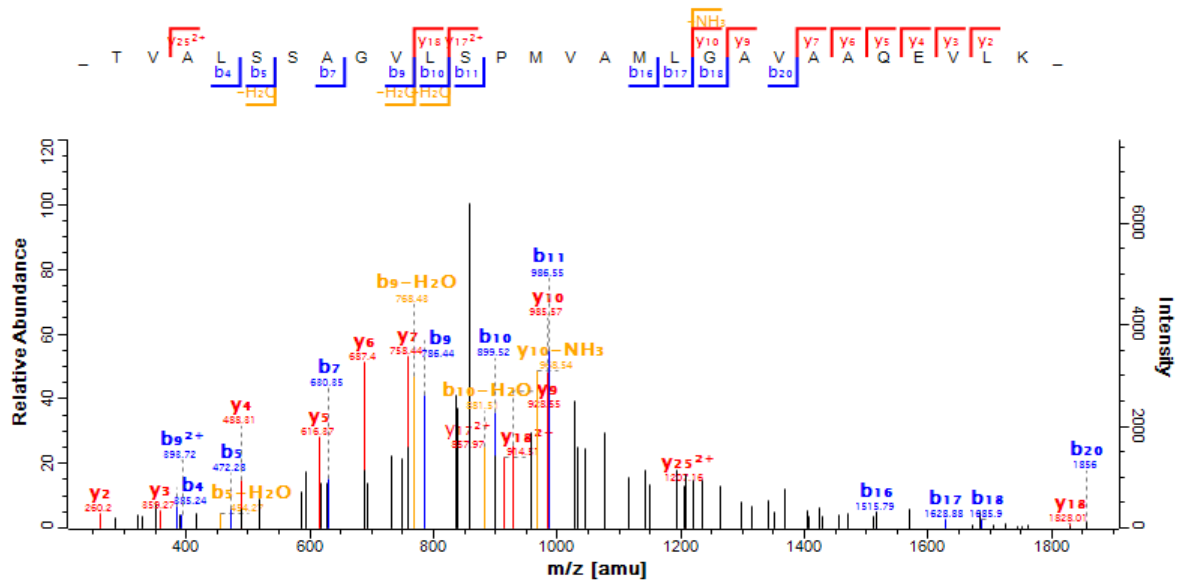
Protein Group ID: 2686
Protein Accession Numbers: P41134; P41134-2
Gene Names: ID1
Peptide Sequence: VASGSTATAAAGPSCALK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 109.42
Best Match Posterior Error Probability: 3.53E-05
Best Match Spectrum:

Scan number 16816 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ID1



Protein Group ID: 2691
Protein Accession Numbers: P41226
Gene Names: UBA7
Peptide Sequence: TVALSSAGVLSPLMVAAMLGAVAAQEVLK
Total Number of Spectra: 2
Number of Replicates (out of 8): 1
Best Match Score: 84.127
Best Match Posterior Error Probability: 4.00E-05
Best Match Spectrum:

Scan number 96777 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** UBA7



Protein Group ID: 2693

Protein Accession Numbers: P41235-4; P41235; P41235-2; P41235-5; P41235-6; P41235-3; P41235-7

Gene Names: HNF4A

Peptide Sequence: DVLLLGNDYIVPR

Total Number of Spectra: 1

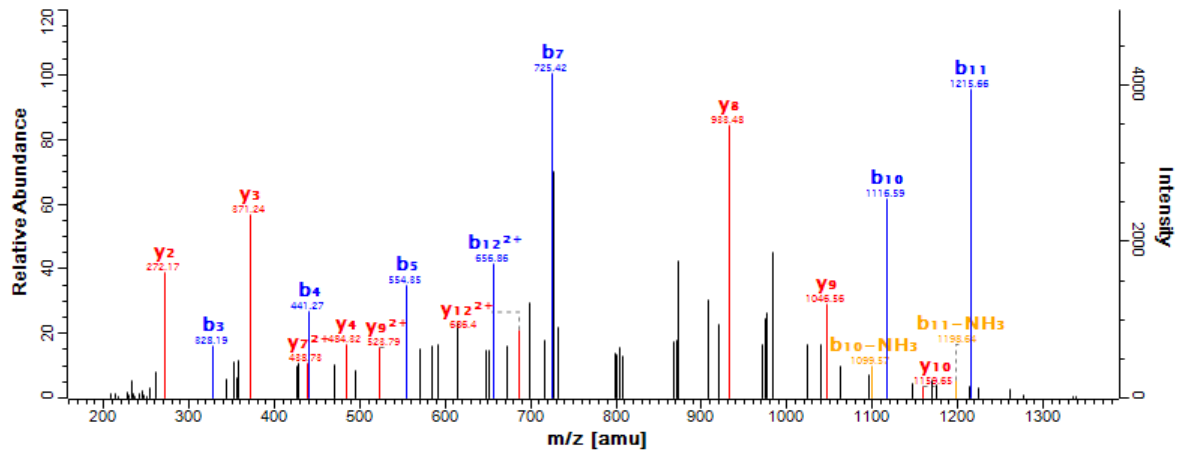
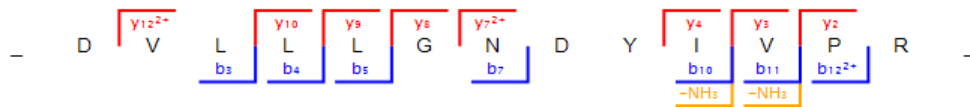
Number of Replicates (out of 8): 1

Best Match Score: 112.43

Best Match Posterior Error Probability: 0.00027875

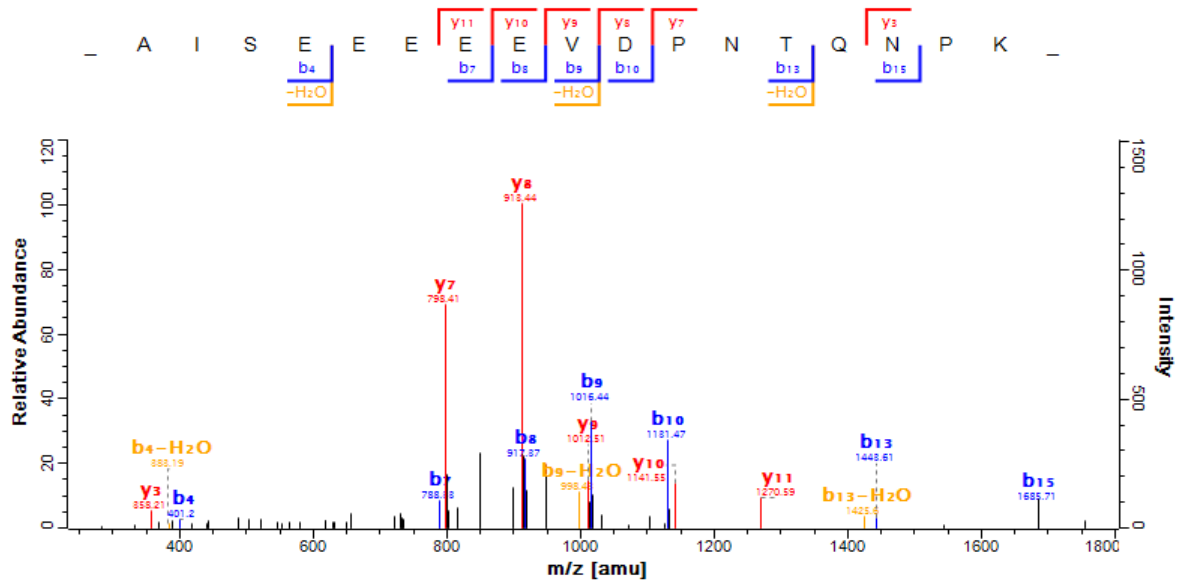
Best Match Spectrum:

Scan number 65947 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS: CID **Genenames** HNF4A



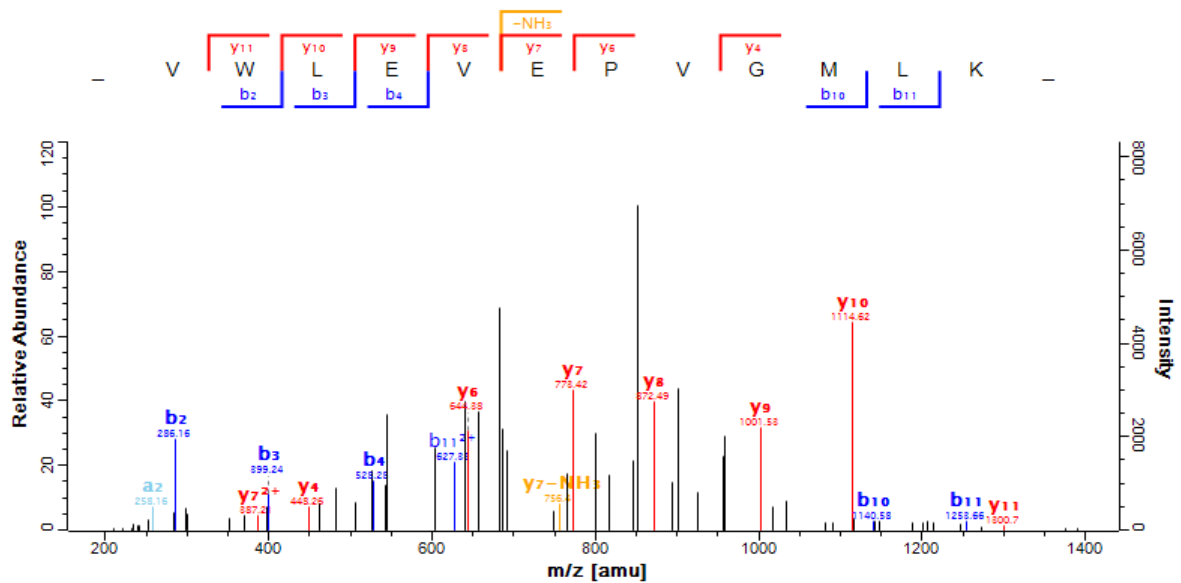
Protein Group ID: 2712
Protein Accession Numbers: P42858
Gene Names: HTT
Peptide Sequence: AISEEEEEVDPNTQNP K
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 83.106
Best Match Posterior Error Probability: 0.0011246
Best Match Spectrum:

Scan number 19712 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** HTT



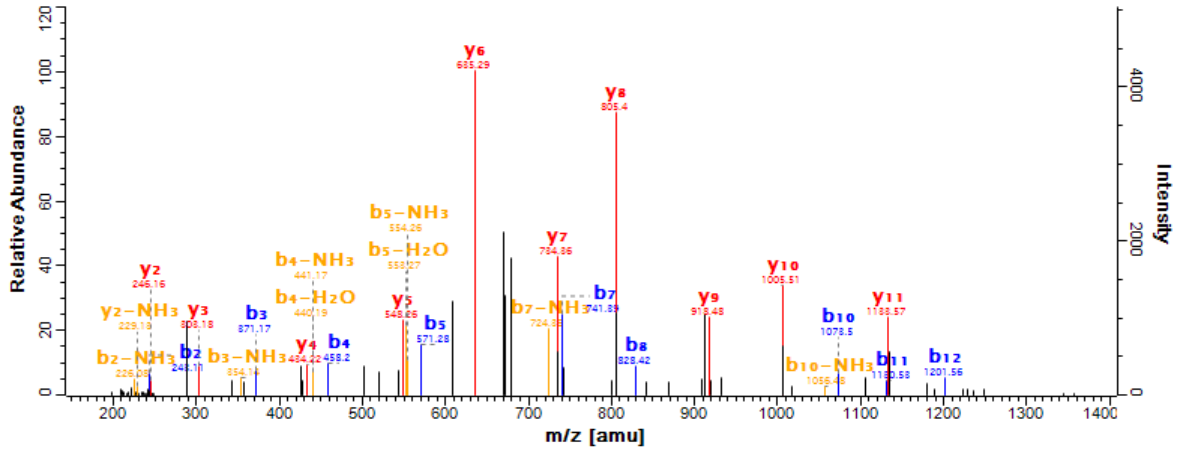
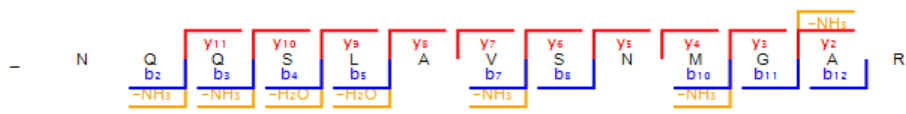
Protein Group ID: 2715
Protein Accession Numbers: P43121; P43121-2
Gene Names: MCAM
Peptide Sequence: VWLEVEPVGM LK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 77.597
Best Match Posterior Error Probability: 0.0039159
Best Match Spectrum:

Scan number	68746	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	MCAM



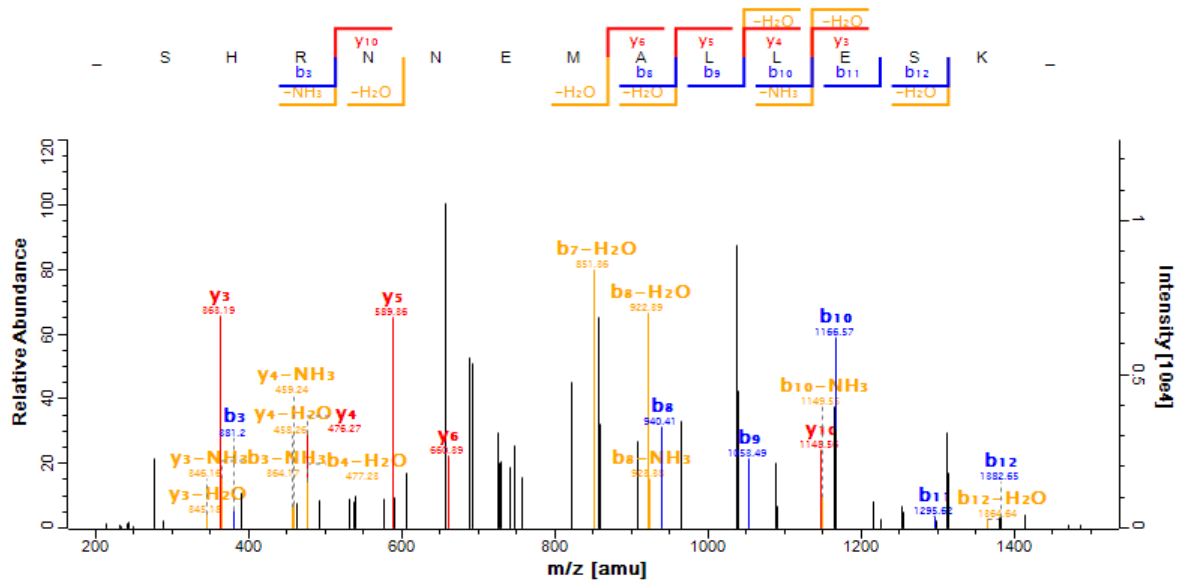
Protein Group ID: 2722
Protein Accession Numbers: P43378
Gene Names: PTPN9
Peptide Sequence: NQQLAVSNMGAR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 178.84
Best Match Posterior Error Probability: 2.02E-14
Best Match Spectrum:

Scan number 20145 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PTPN9



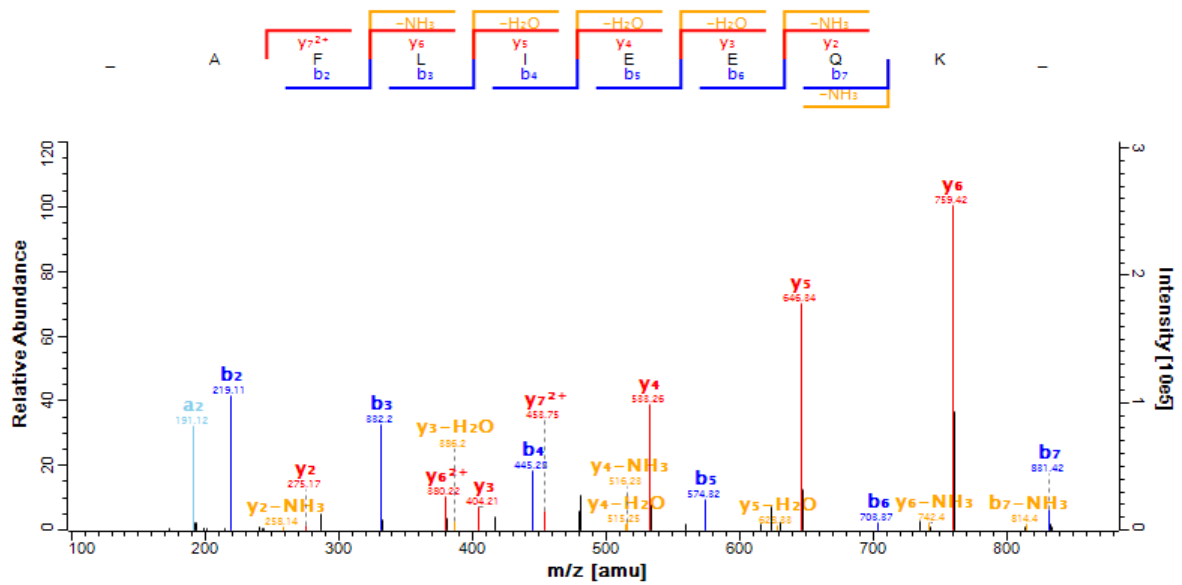
Protein Group ID: 2769
Protein Accession Numbers: P48552
Gene Names: NR1P1
Peptide Sequence: SHRNNEMALLESK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 98.337
Best Match Posterior Error Probability: 0.0026583
Best Match Spectrum:

Scan number 59686 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** NR1P1



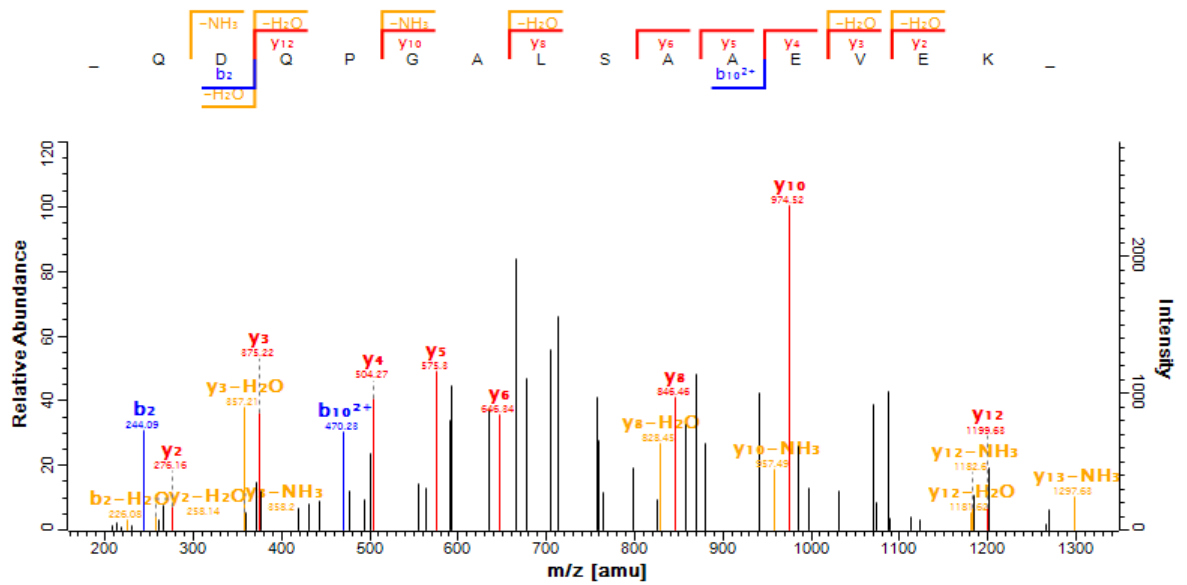
Protein Group ID: 2780
Protein Accession Numbers: P49207
Gene Names: RPL34
Peptide Sequence: AFLIEEQK
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 182.68
Best Match Posterior Error Probability: 1.10E-08
Best Match Spectrum:

Scan number 29190 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** RPL34



Protein Group ID: 2799
Protein Accession Numbers: P49703
Gene Names: ARL4D
Peptide Sequence: QDQPGALSAAEVEK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 80.905
Best Match Posterior Error Probability: 0.0030248
Best Match Spectrum:

Scan number 22516 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ARL4D



Protein Group ID: 2805

Protein Accession Numbers: P49753; P49753-2; B3KSA0

Gene Names: ACOT2

Peptide Sequence: TMETLHLEYFEEAMNYLLSHPEVK

Total Number of Spectra: 8

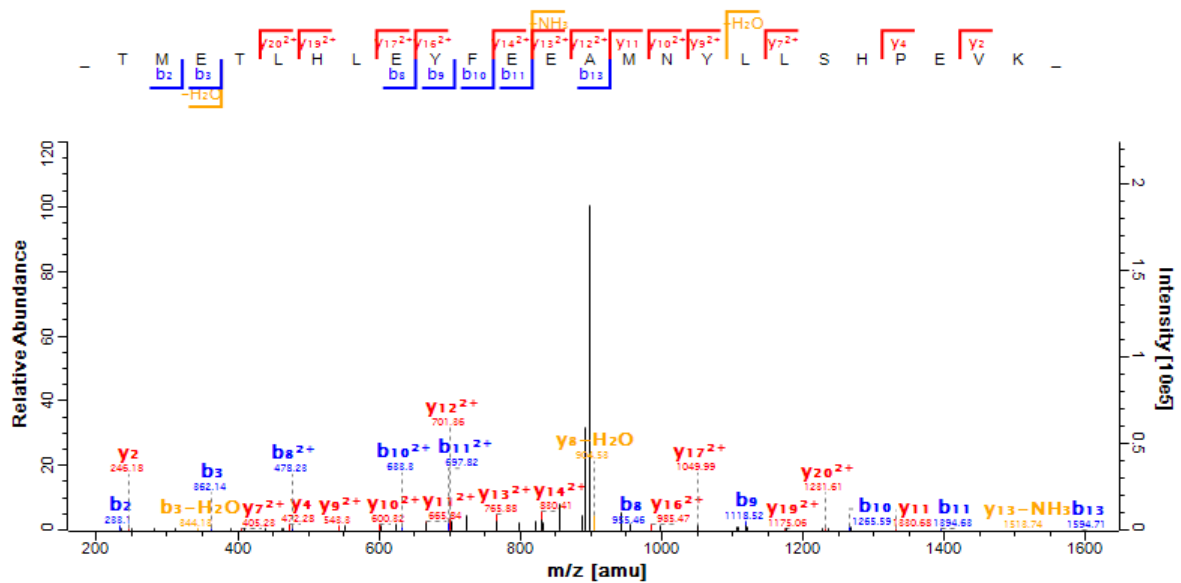
Number of Replicates (out of 8): 8

Best Match Score: 111.95

Best Match Posterior Error Probability: 5.42E-09

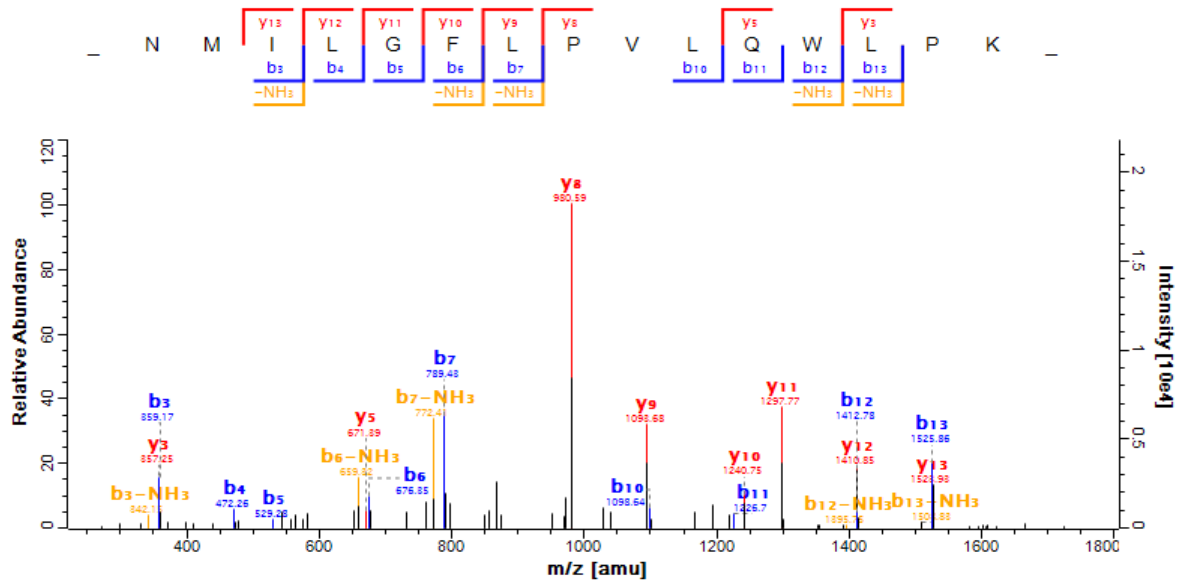
Best Match Spectrum:

Scan number 91959 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ACOT2



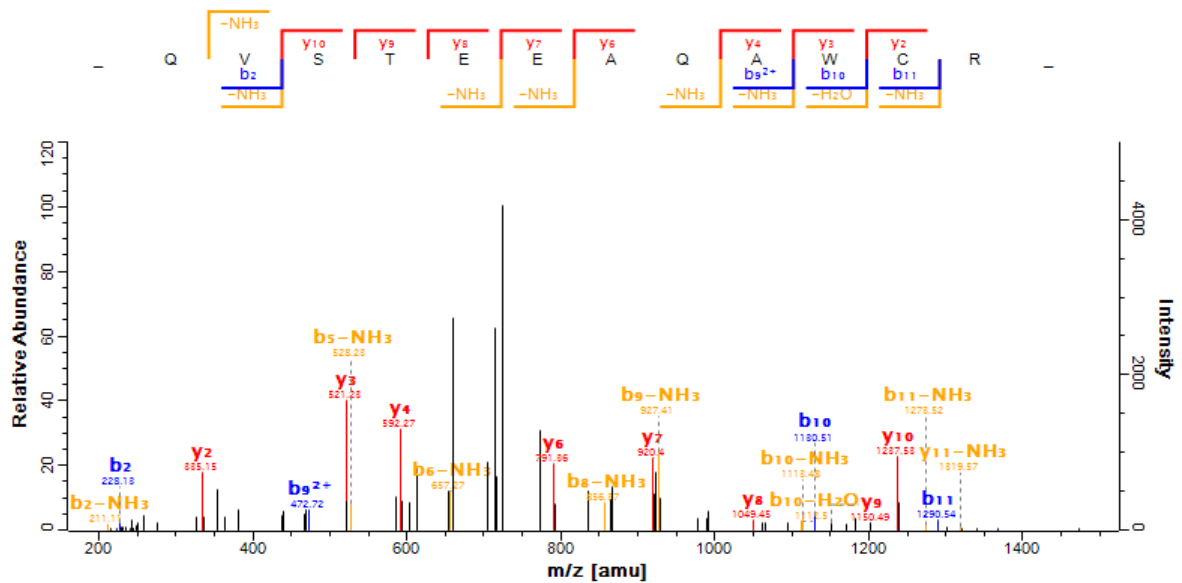
Protein Group ID: 2824
Protein Accession Numbers: P50443
Gene Names: SLC26A2
Peptide Sequence: NMILGFLPVLQWLPLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 125.53
Best Match Posterior Error Probability: 3.57E-05
Best Match Spectrum:

Scan number 97178 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SLC26A2



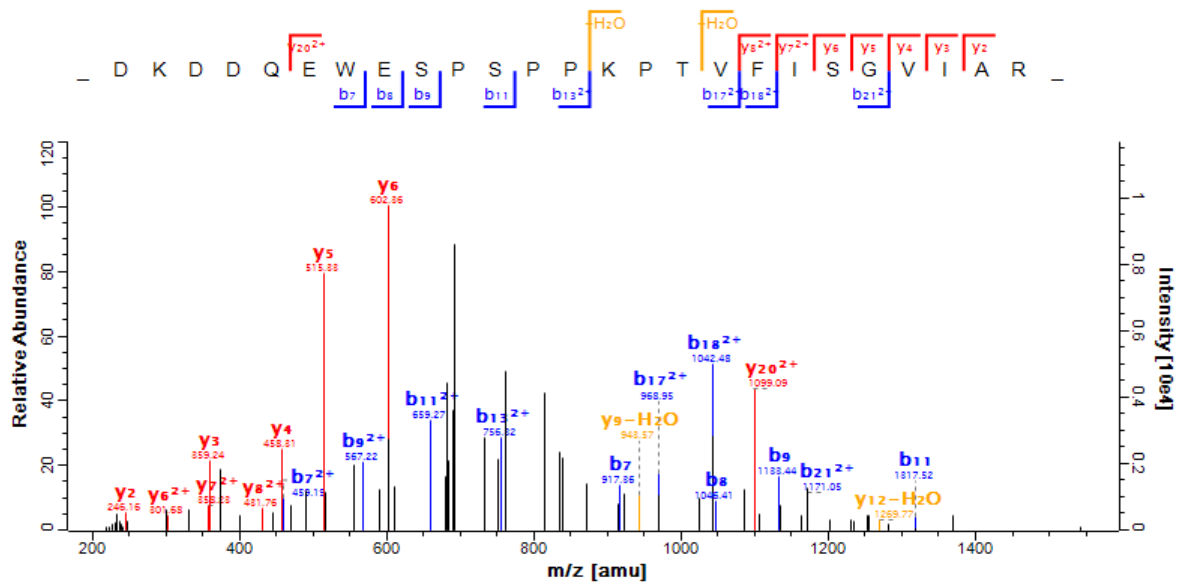
Protein Group ID: 2843
Protein Accession Numbers: P51151
Gene Names: RAB9A
Peptide Sequence: QVSTEEAQWCR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 86.911
Best Match Posterior Error Probability: 0.0017887
Best Match Spectrum:

Scan number 24038 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** RAB9A



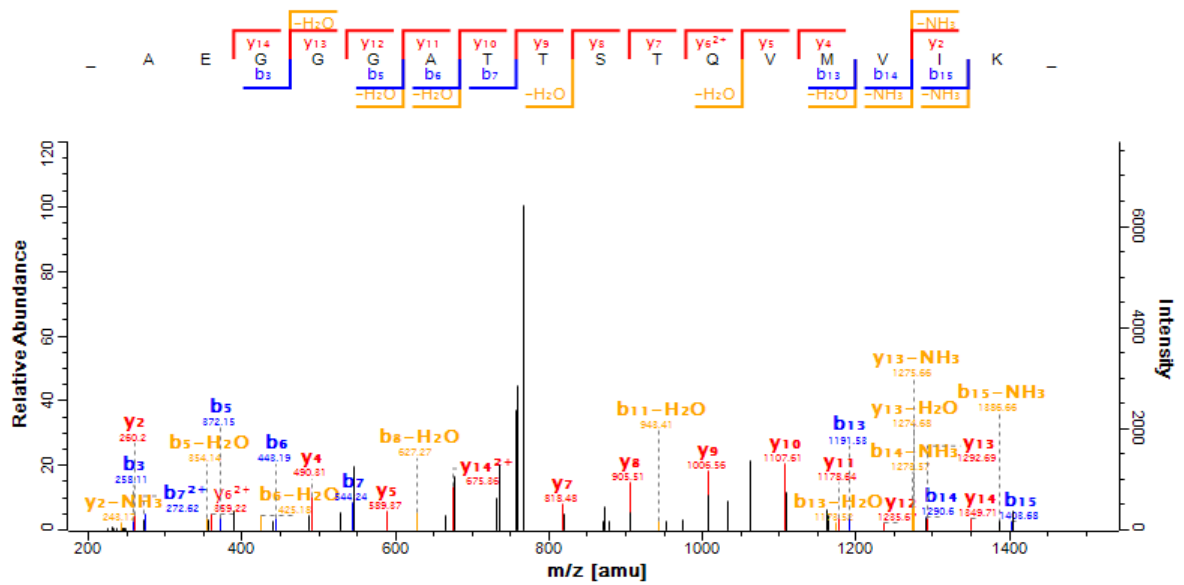
Protein Group ID: 2845
Protein Accession Numbers: P51397
Gene Names: DAP
Peptide Sequence: DKDDQEWESPPPKPTVFISGVIA R
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 78.324
Best Match Posterior Error Probability: 0.0024478
Best Match Spectrum:

Scan number 62887 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** DAP



Protein Group ID: 2853
Protein Accession Numbers: P51608-2; P51608
Gene Names: MECP2
Peptide Sequence: AEGGGATTSTQVMVIK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 160.8
Best Match Posterior Error Probability: 1.63E-09
Best Match Spectrum:

Scan number 27992 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** MECP2



Protein Group ID: 2858

Protein Accession Numbers: P51809-2; P51809; P51809-3

Gene Names: VAMP7

Peptide Sequence: AFNFLNEIK

Total Number of Spectra: 8

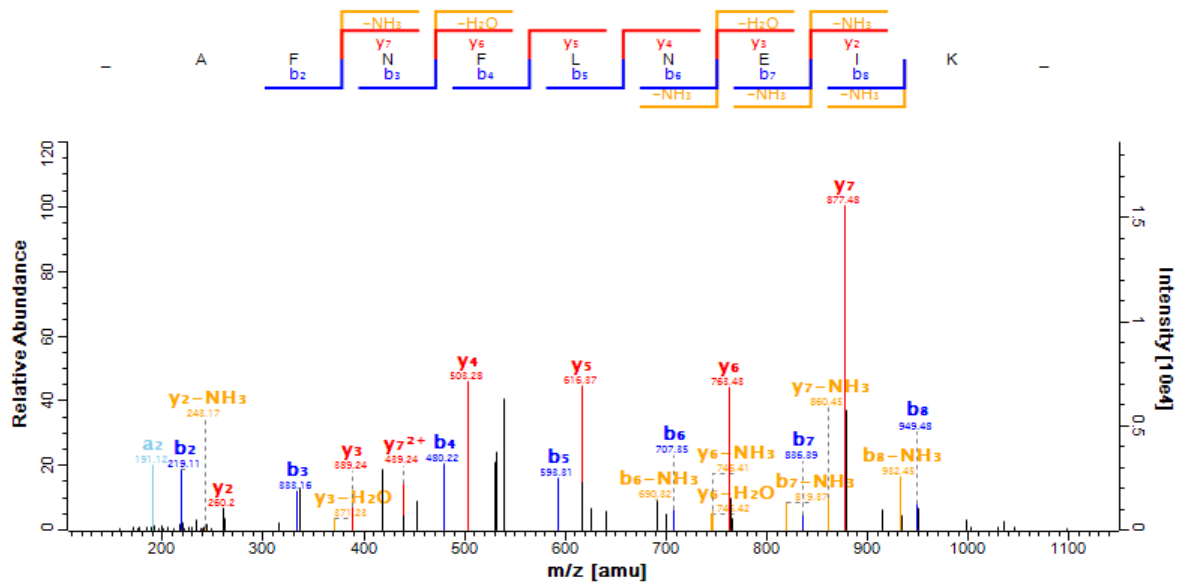
Number of Replicates (out of 8): 8

Best Match Score: 163.94

Best Match Posterior Error Probability: 1.31E-05

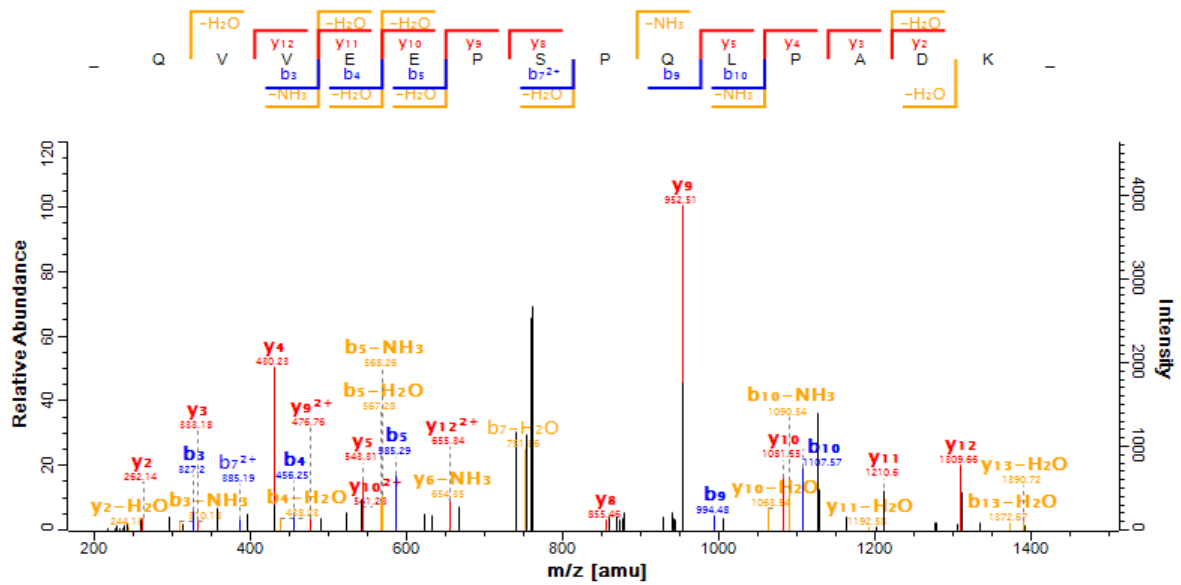
Best Match Spectrum:

Scan number	59891	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	VAMP7



Protein Group ID: 2867
Protein Accession Numbers: P52564; P52564-2
Gene Names: MAP2K6
Peptide Sequence: QVVEEPSQLPADK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 156.6
Best Match Posterior Error Probability: 5.42E-08
Best Match Spectrum:

Scan number 28328 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** MAP2K6



Protein Group ID: 2886

Protein Accession Numbers: P53567

Gene Names: CEBPG

Peptide Sequence: DLFLEHAHNLDNVQSISTENTTADGDNAGQ

Total Number of Spectra: 1

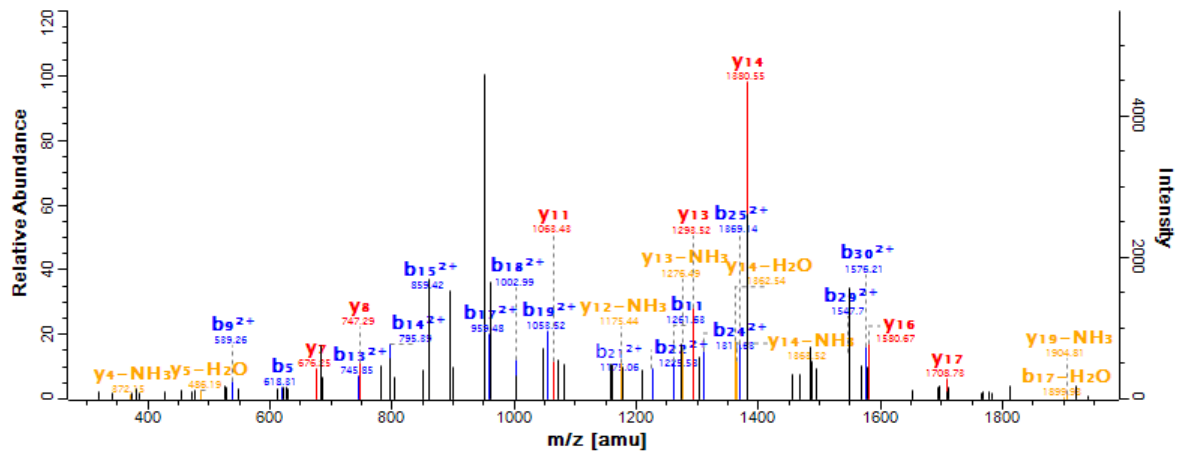
Number of Replicates (out of 8): 1

Best Match Score: 74.287

Best Match Posterior Error Probability: 7.90E-06

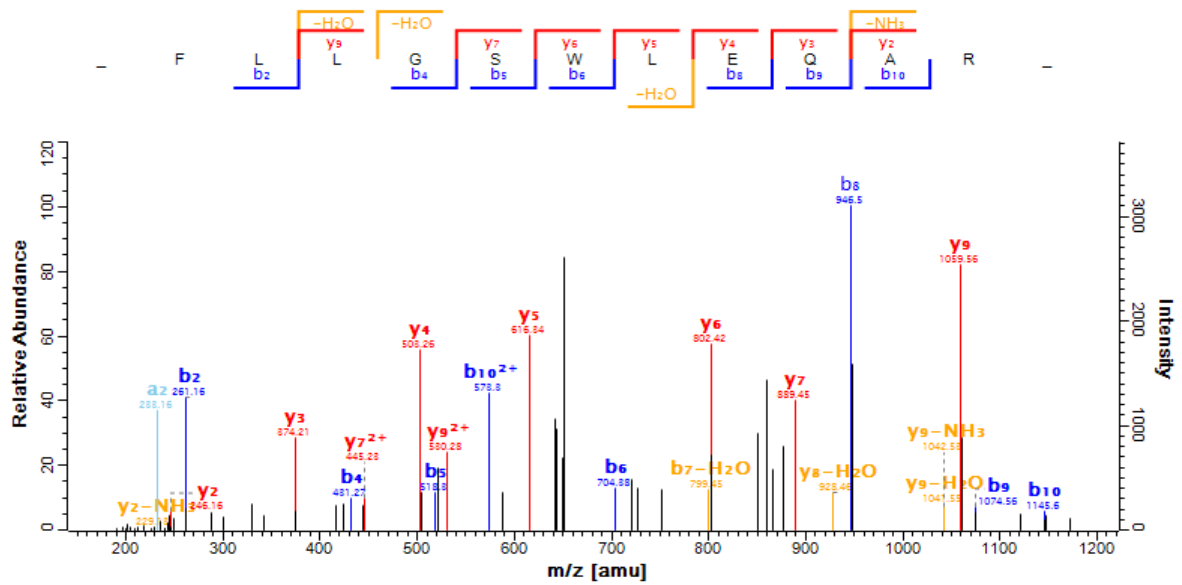
Best Match Spectrum:

Scan number	59264	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	CEBPG



Protein Group ID: 2907
Protein Accession Numbers: P54802
Gene Names: NAGLU
Peptide Sequence: FLLGSWLEQAR
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 145.91
Best Match Posterior Error Probability: 1.12E-05
Best Match Spectrum:

Scan number 72062 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** NAGLU



Protein Group ID: 2932

Protein Accession Numbers: P56962

Gene Names: STX17

Peptide Sequence: LAALPVAGALIGGMVGGPIGLLAGFK

Total Number of Spectra: 1

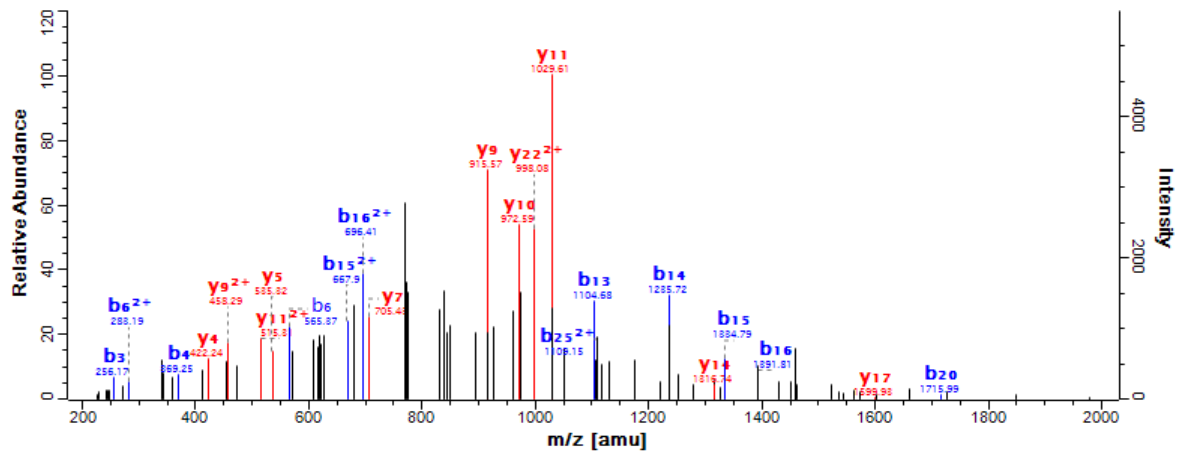
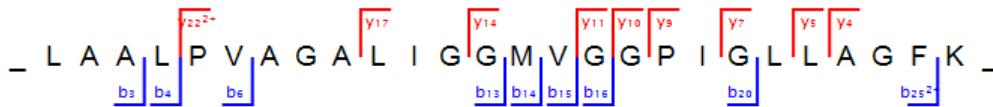
Number of Replicates (out of 8): 1

Best Match Score: 112.55

Best Match Posterior Error Probability: 1.23E-11

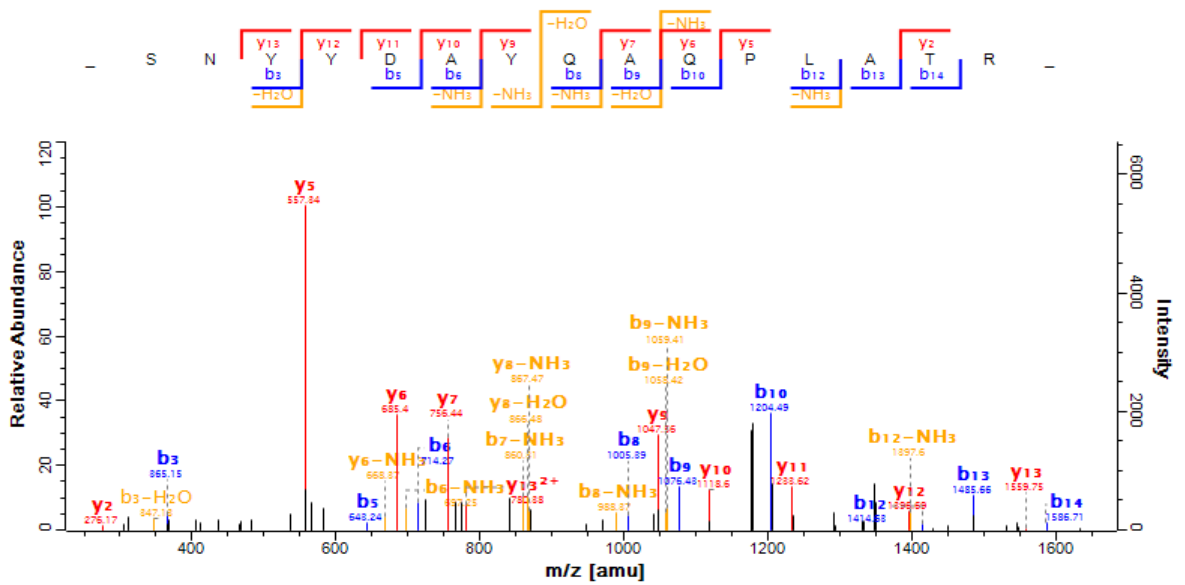
Best Match Spectrum:

Scan number	93648	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	STX17



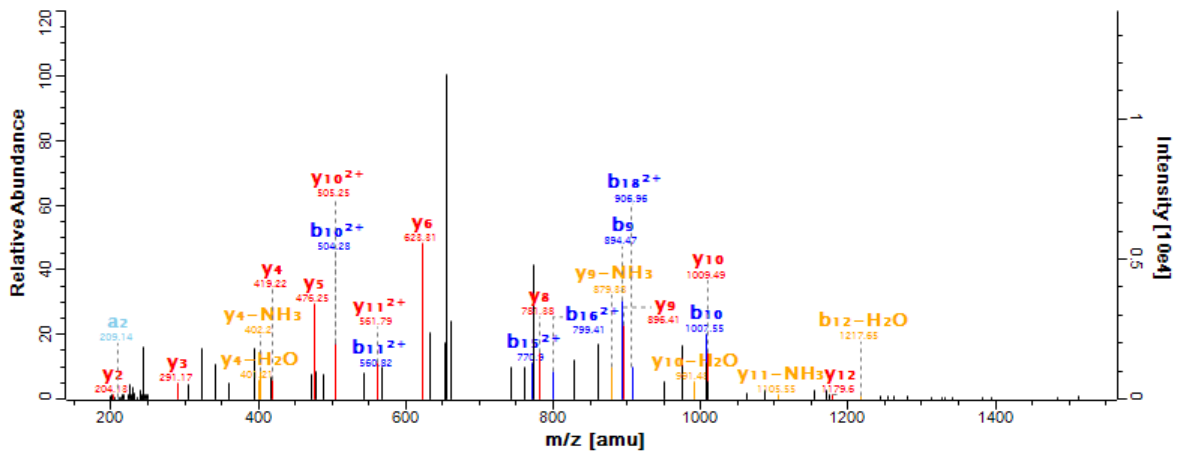
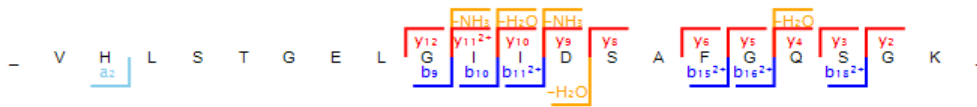
Protein Group ID: 2937
Protein Accession Numbers: P57739
Gene Names: CLDN2
Peptide Sequence: SNYYDAYQAQPLATR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 135.23
Best Match Posterior Error Probability: 2.54E-05
Best Match Spectrum:

Scan number 34861 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CLDN2



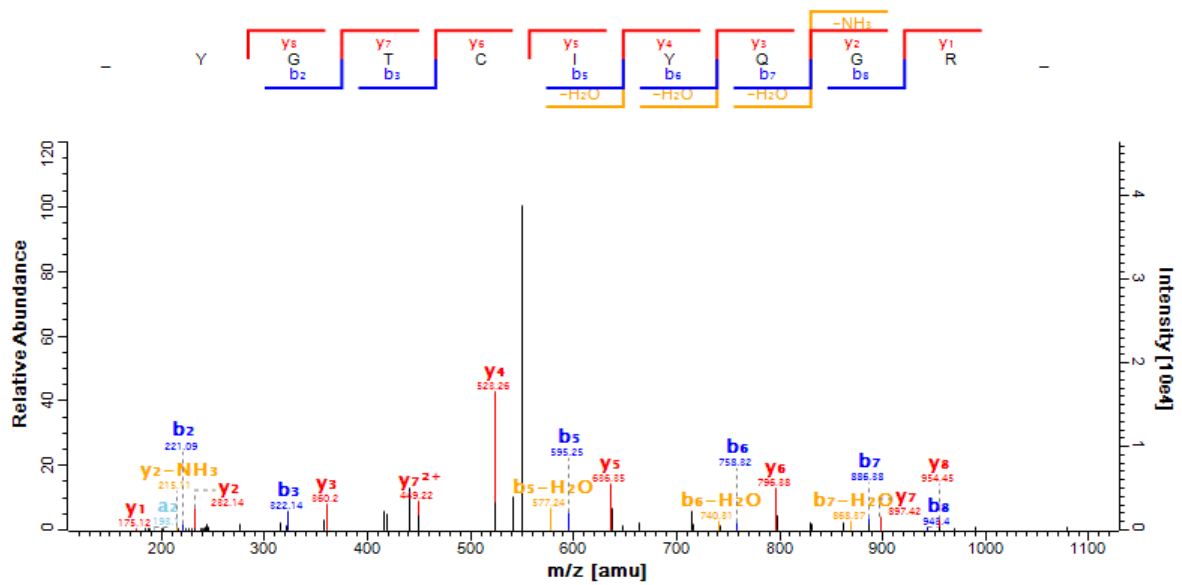
Protein Group ID: 2939
Protein Accession Numbers: P57772
Gene Names: EEFSEC
Peptide Sequence: VHLSTGELGIIDSAFGQSGK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 82.449
Best Match Posterior Error Probability: 0.00042249
Best Match Spectrum:

Scan number 61537 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** EEFSEC



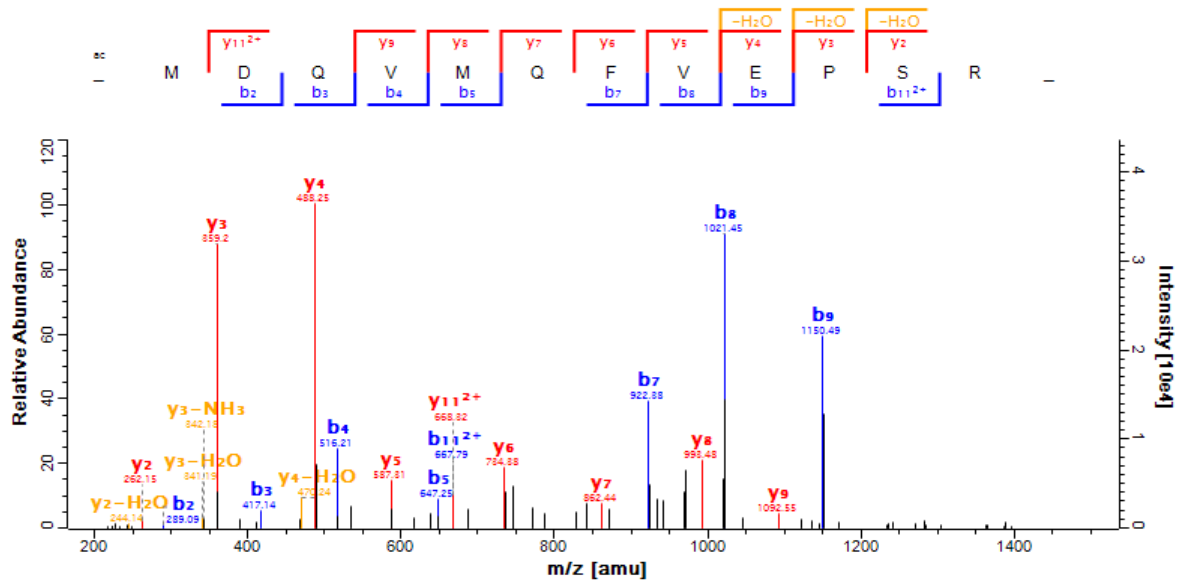
Protein Group ID: 2943
Protein Accession Numbers: P59665; P59666
Gene Names: DEFA1;DEFA3
Peptide Sequence: YGTCIYQGR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 130.66
Best Match Posterior Error Probability: 0.00012438
Best Match Spectrum:

Scan number 16643 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** DEFA1;DEFA3



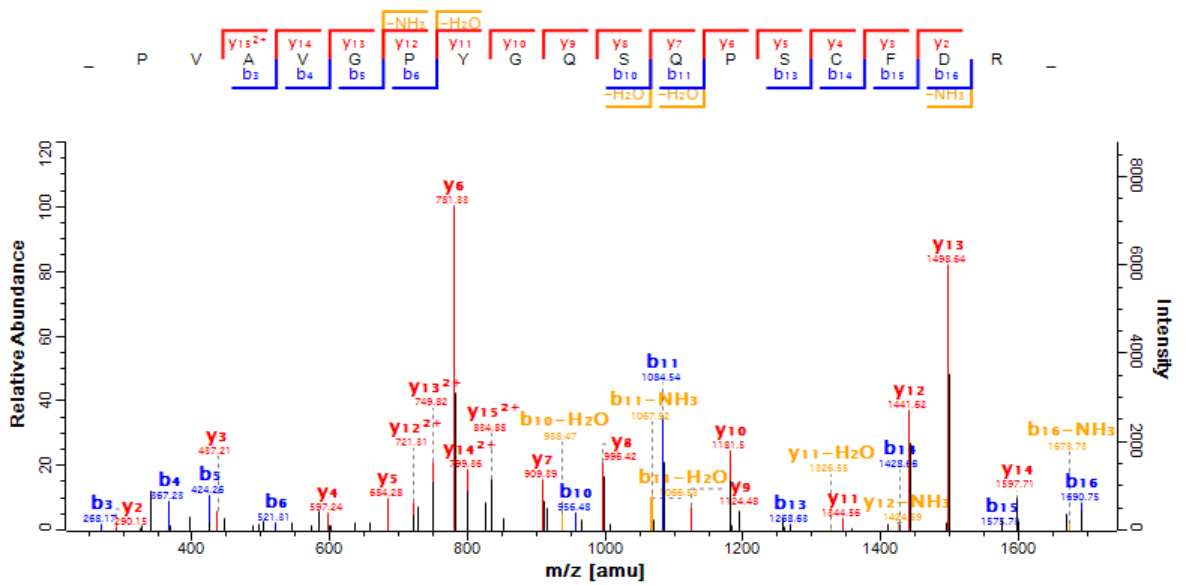
Protein Group ID: 2944
Protein Accession Numbers: P60059
Gene Names: SEC61G
Peptide Sequence: MDQVMQFVEPSR
Total Number of Spectra: 8
Number of Replicates (out of 8): 8
Best Match Score: 125.61
Best Match Posterior Error Probability: 0.00014541
Best Match Spectrum:

Scan number 78066 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SEC61G



Protein Group ID: 2949
Protein Accession Numbers: P60602; P60602-2
Gene Names: ROMO1
Peptide Sequence: PVAVGPYGQSQPSCFDR
Total Number of Spectra: 7
Number of Replicates (out of 8): 7
Best Match Score: 168.64
Best Match Posterior Error Probability: 4.54E-14
Best Match Spectrum:

Scan number 34003 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ROMO1



Protein Group ID: 2963

Protein Accession Numbers: P61020; P61020-2; H0YHA1

Gene Names: RAB5B

Peptide Sequence: TAMNVNDLFLAIK

Total Number of Spectra: 7

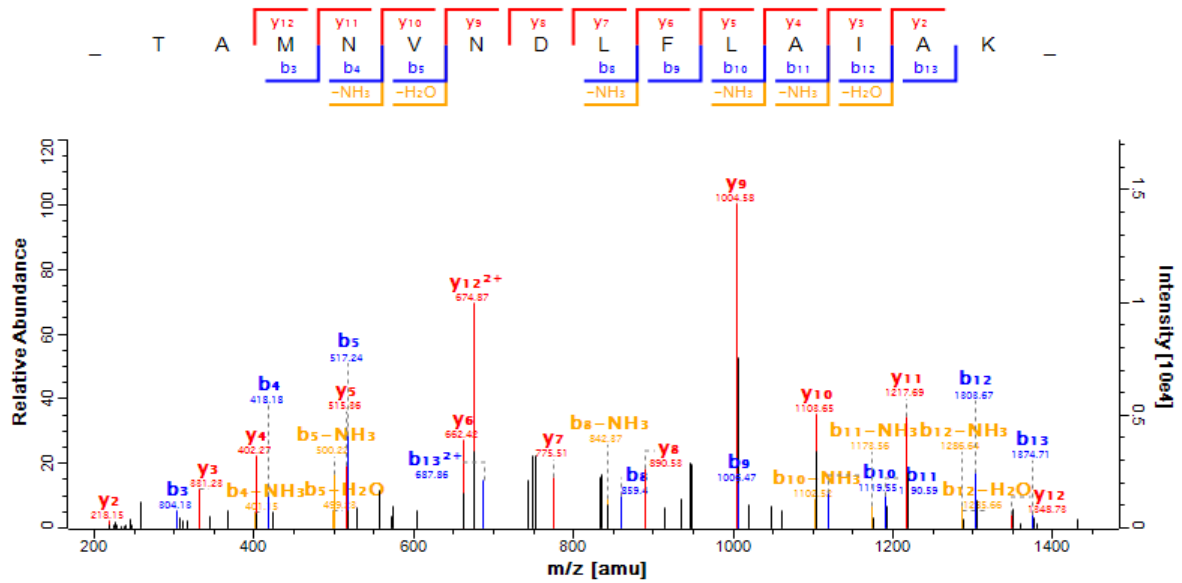
Number of Replicates (out of 8): 7

Best Match Score: 194.48

Best Match Posterior Error Probability: 9.05E-25

Best Match Spectrum:

Scan number	78517	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	RAB5B



Protein Group ID: 2974

Protein Accession Numbers: P61204; B7ZB63; H0YGG7

Gene Names: ARF3

Peptide Sequence: N W Y I Q A T C A T S G D G L Y L Y E G L W Y L A N Q L K

Total Number of Spectra: 9

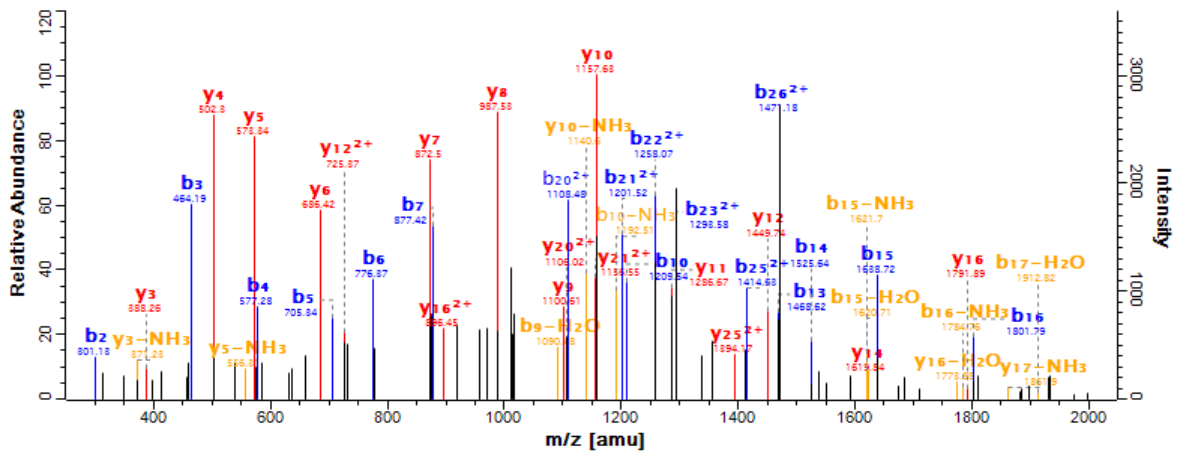
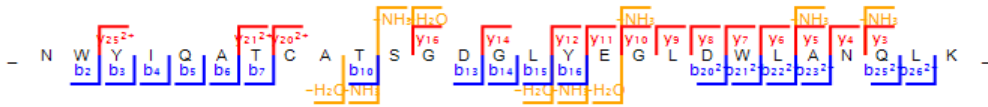
Number of Replicates (out of 8): 8

Best Match Score: 198.22

Best Match Posterior Error Probability: 1.33E-58

Best Match Spectrum:

Scan number 92832 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ARF3



Protein Group ID: 2984

Protein Accession Numbers: P61601; E5RGA9; E5RIZ1

Gene Names: NCALD

Peptide Sequence: AEMLEIVQAIYK

Total Number of Spectra: 2

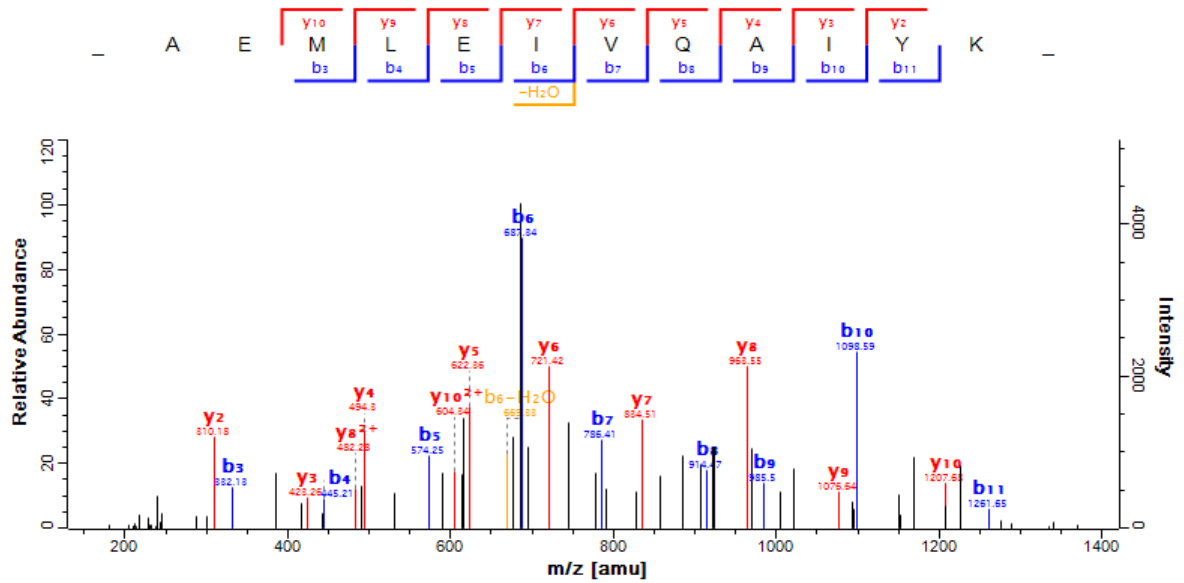
Number of Replicates (out of 8): 1

Best Match Score: 110.38

Best Match Posterior Error Probability: 0.00025844

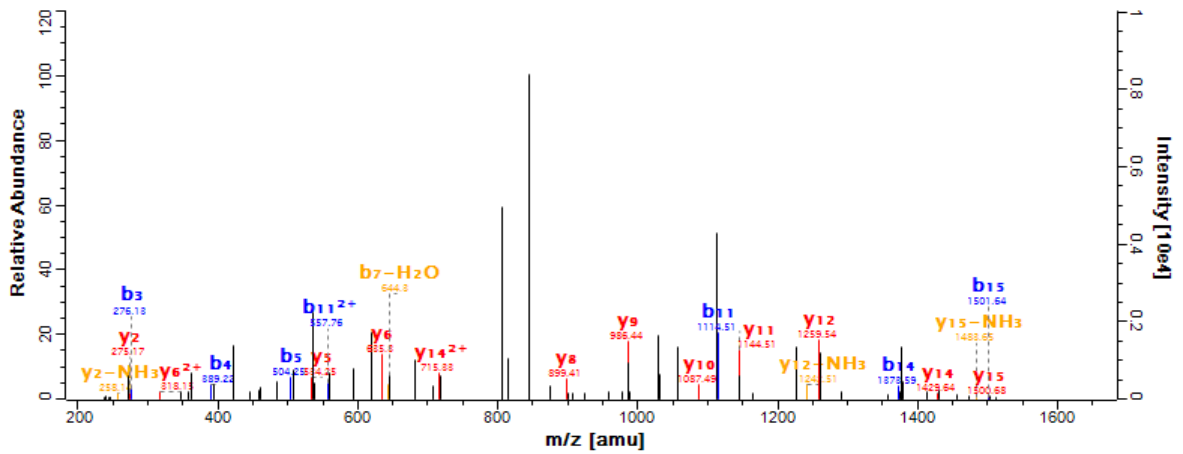
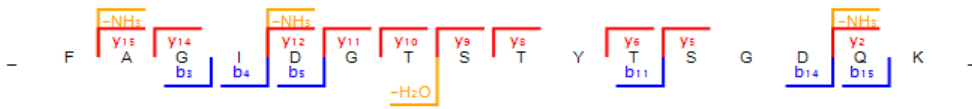
Best Match Spectrum:

Scan number	72368	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	NCALD



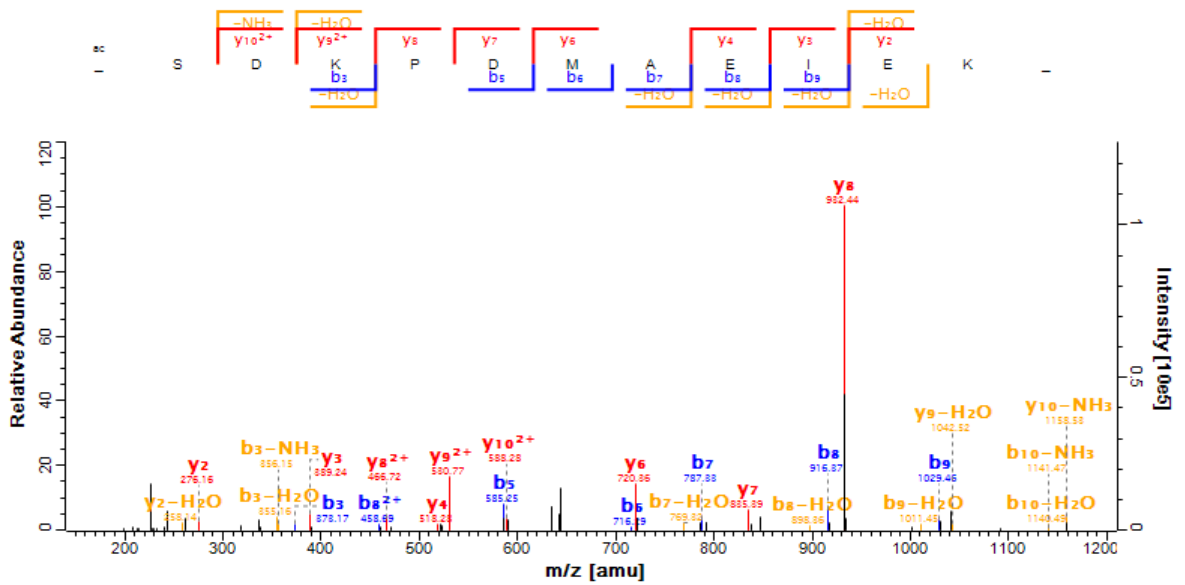
Protein Group ID: 2988
Protein Accession Numbers: P61812-2; P61812
Gene Names: TGFB2
Peptide Sequence: FAGIDGTSTYTSGDQK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 96.489
Best Match Posterior Error Probability: 0.00027832
Best Match Spectrum:

Scan number 29361 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TGFB2



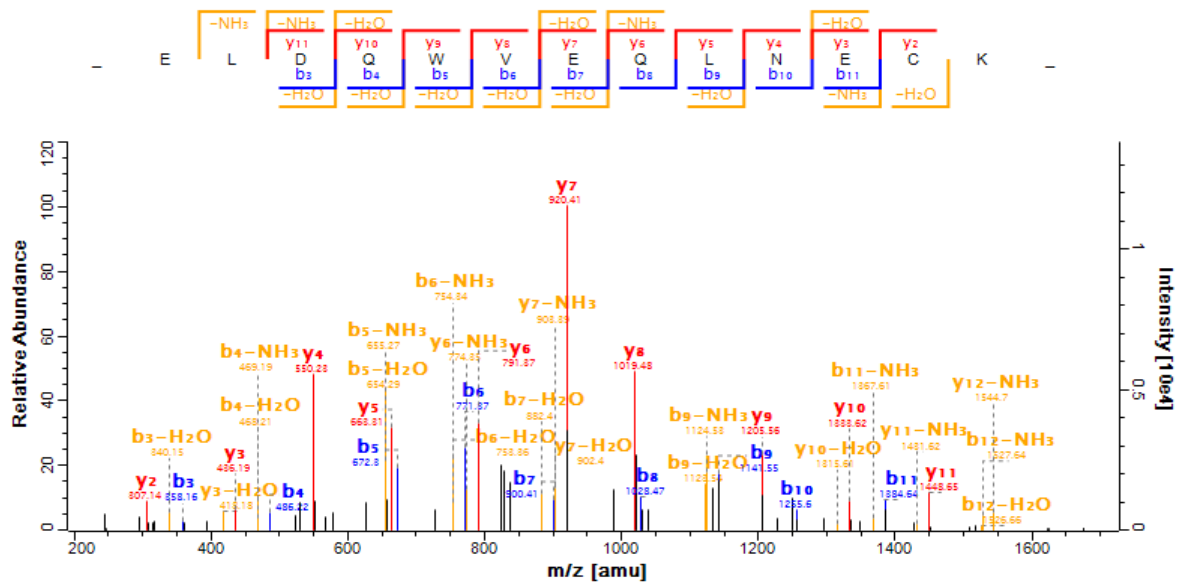
Protein Group ID: 3018
Protein Accession Numbers: P62328; Q5T4B6
Gene Names: TMSB4X;TMSL4
Peptide Sequence: SDKPDMAEIEK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 155.99
Best Match Posterior Error Probability: 0.00013559
Best Match Spectrum:

Scan number 22596 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TMSB4X;TMSL4



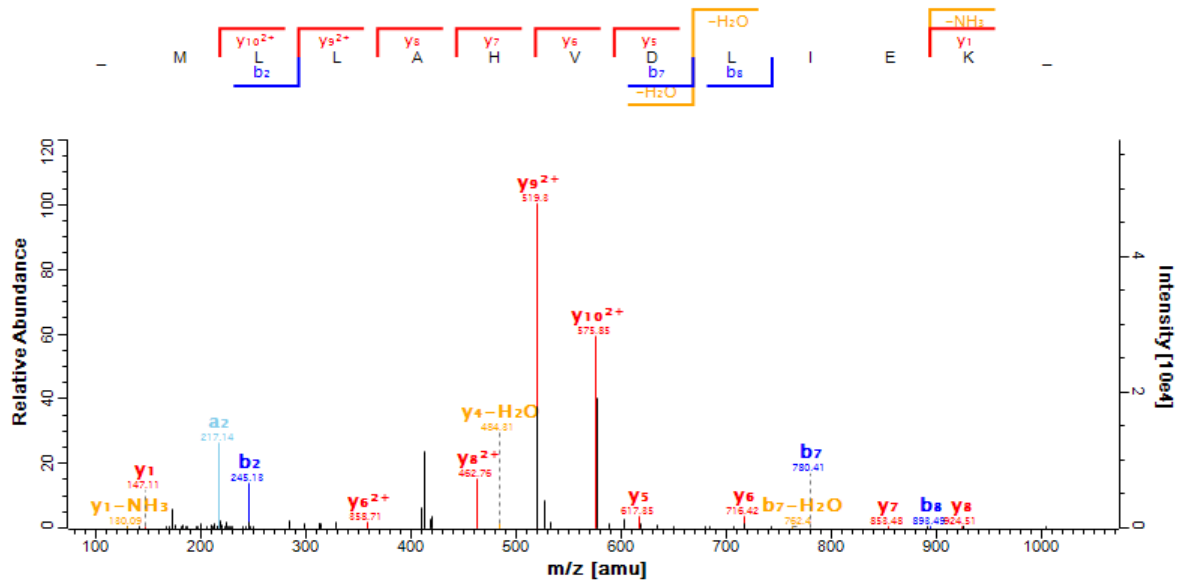
Protein Group ID: 3027
Protein Accession Numbers: P62714; E5RJX4
Gene Names: PPP2CB
Peptide Sequence: ELDQWVEQLNECK
Total Number of Spectra: 7
Number of Replicates (out of 8): 7
Best Match Score: 284.24
Best Match Posterior Error Probability: 2.15E-115
Best Match Spectrum:

Scan number 55308 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PPP2CB



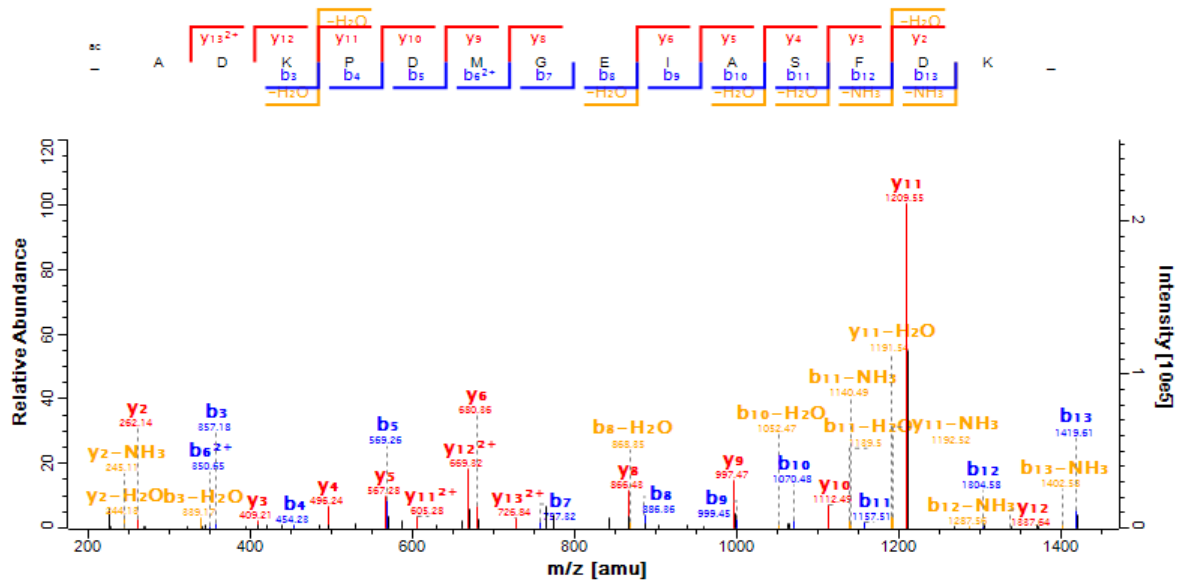
Protein Group ID: 3037
Protein Accession Numbers: P62875
Gene Names: POLR2L
Peptide Sequence: MLLAHVDLIEK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 87.298
Best Match Posterior Error Probability: 0.0017584
Best Match Spectrum:

Scan number 48288 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** POLR2L



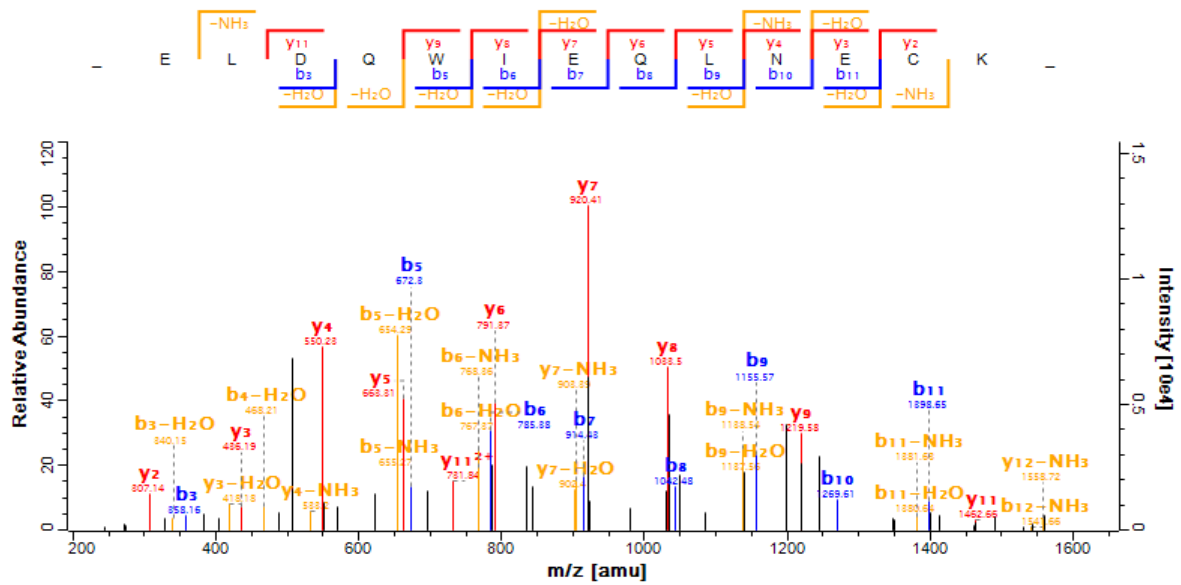
Protein Group ID: 3064
Protein Accession Numbers: P63313
Gene Names: TMSB10
Peptide Sequence: ADKPDMGELIASFDK
Total Number of Spectra: 8
Number of Replicates (out of 8): 8
Best Match Score: 199.37
Best Match Posterior Error Probability: 2.58E-24
Best Match Spectrum:

Scan number 44116 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TMSB10



Protein Group ID: 3065
Protein Accession Numbers: P67775; P67775-2
Gene Names: PPP2CA
Peptide Sequence: ELDQWIEQLNECK
Total Number of Spectra: 8
Number of Replicates (out of 8): 6
Best Match Score: 208.68
Best Match Posterior Error Probability: 4.10E-31
Best Match Spectrum:

Scan number 60713 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** PPP2CA



Protein Group ID: 3069

Protein Accession Numbers: P68032; P62736; P63267; P68133; A6NL76; Q5T8M8; F6QUT6; F6UVQ4; C9JFL5; B8ZZJ2; F8WB63

Gene Names: ACTC1;ACTA2;ACTG2;ACTA1

Peptide Sequence: YPIEHGIITNWDDMEK

Total Number of Spectra: 38

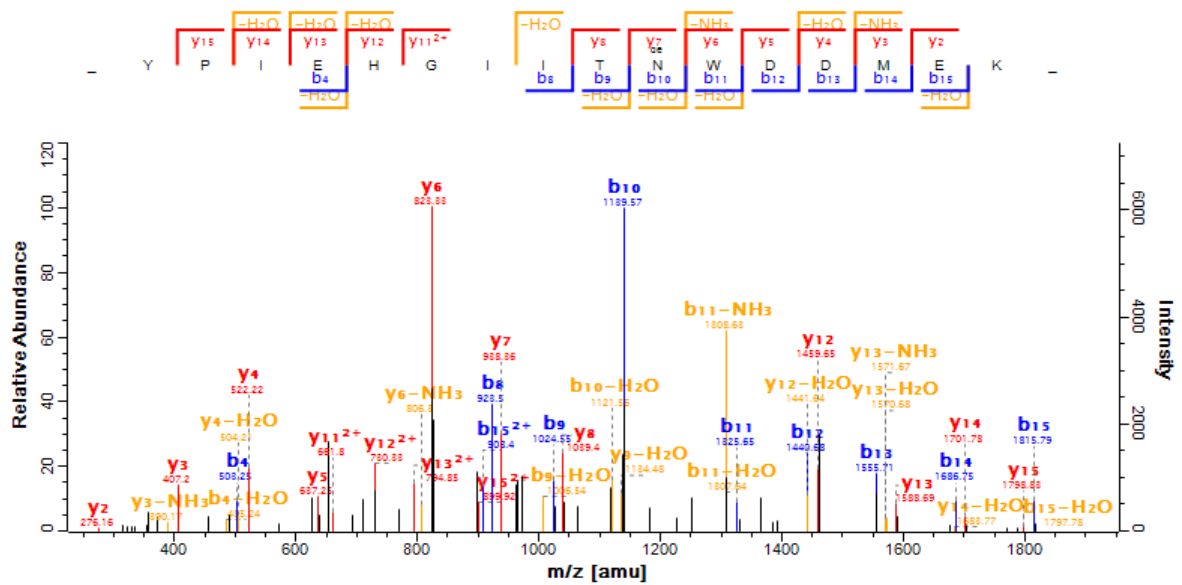
Number of Replicates (out of 8): 8

Best Match Score: 228.9

Best Match Posterior Error Probability: 1.04E-62

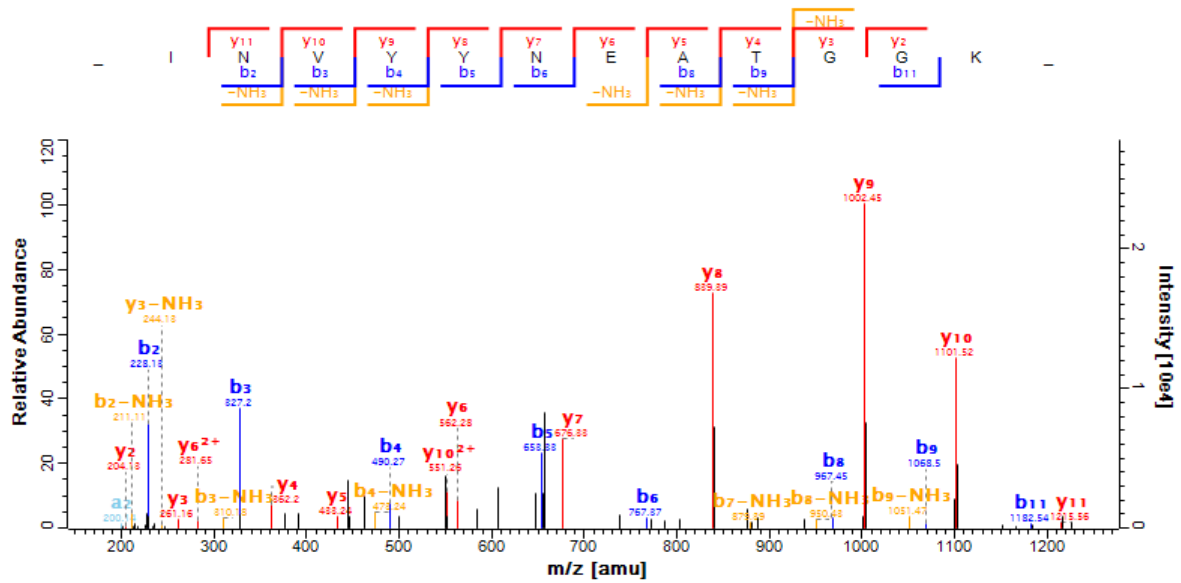
Best Match Spectrum:

Scan number 51439 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS: CID **Genenames** ACTC1;ACTA2;ACTG2;ACTA1



Protein Group ID: 3073
Protein Accession Numbers: P68371
Gene Names: TUBB4B
Peptide Sequence: INVYYNEATGGK
Total Number of Spectra: 10
Number of Replicates (out of 8): 5
Best Match Score: 148.62
Best Match Posterior Error Probability: 4.77E-06
Best Match Spectrum:

Scan number 24730 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TUBB4B



Protein Group ID: 3075

Protein Accession Numbers: P68431

Gene Names: HIST1H3A

Peptide Sequence: FQSSAVMALQEACEAYLVGLFEDTNLCAIHK

Total Number of Spectra: 14

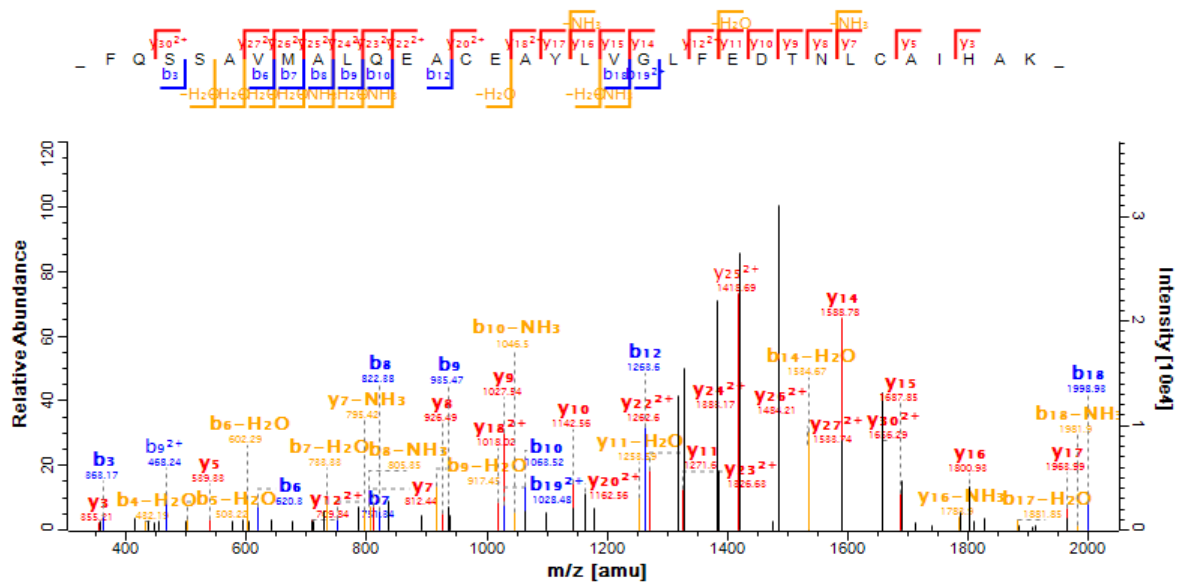
Number of Replicates (out of 8): 8

Best Match Score: 149.97

Best Match Posterior Error Probability: 4.77E-43

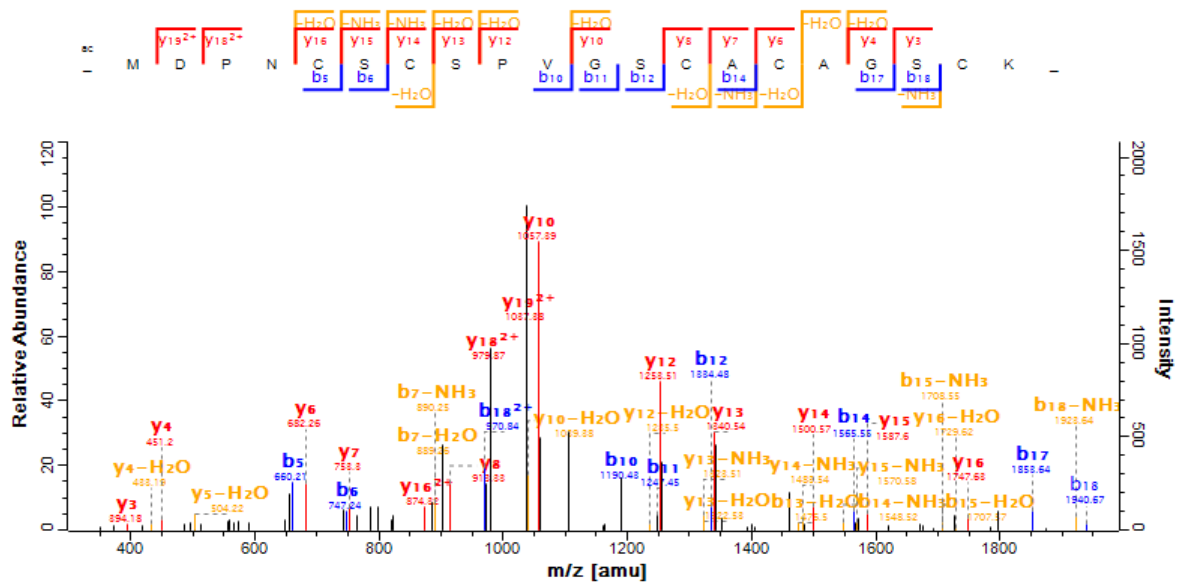
Best Match Spectrum:

Scan number	90404	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	HIST1H3A



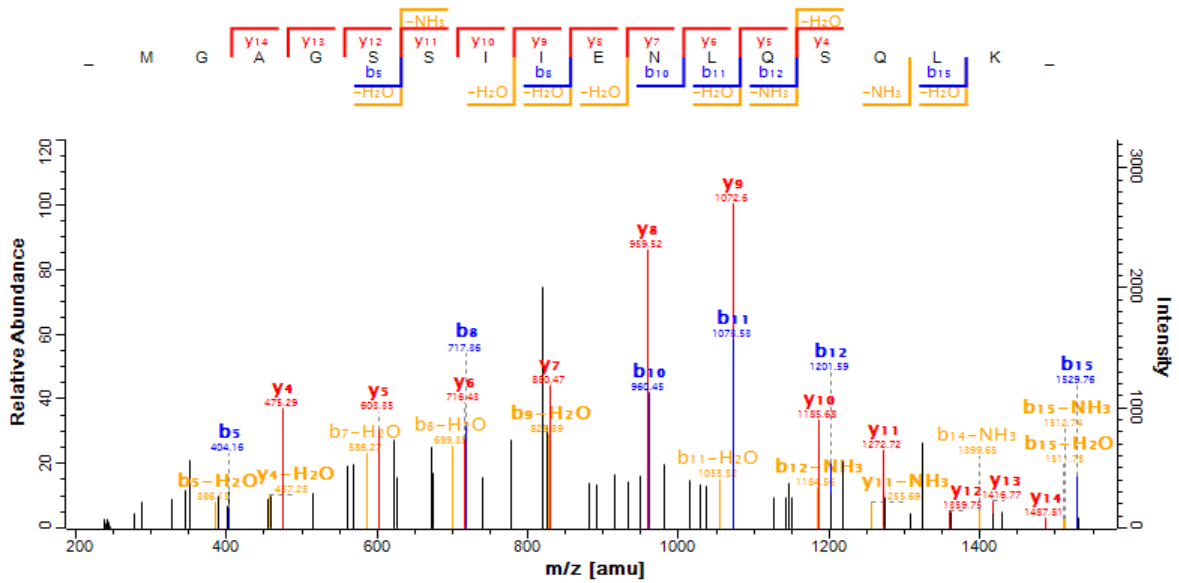
Protein Group ID: 3091
Protein Accession Numbers: P80297; H3BT50
Gene Names: MT1X
Peptide Sequence: MDPNCSCSPVGVSCACAGSCK
Total Number of Spectra: 3
Number of Replicates (out of 8): 2
Best Match Score: 150.23
Best Match Posterior Error Probability: 2.66E-08
Best Match Spectrum:

Scan number 28132 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MT1X



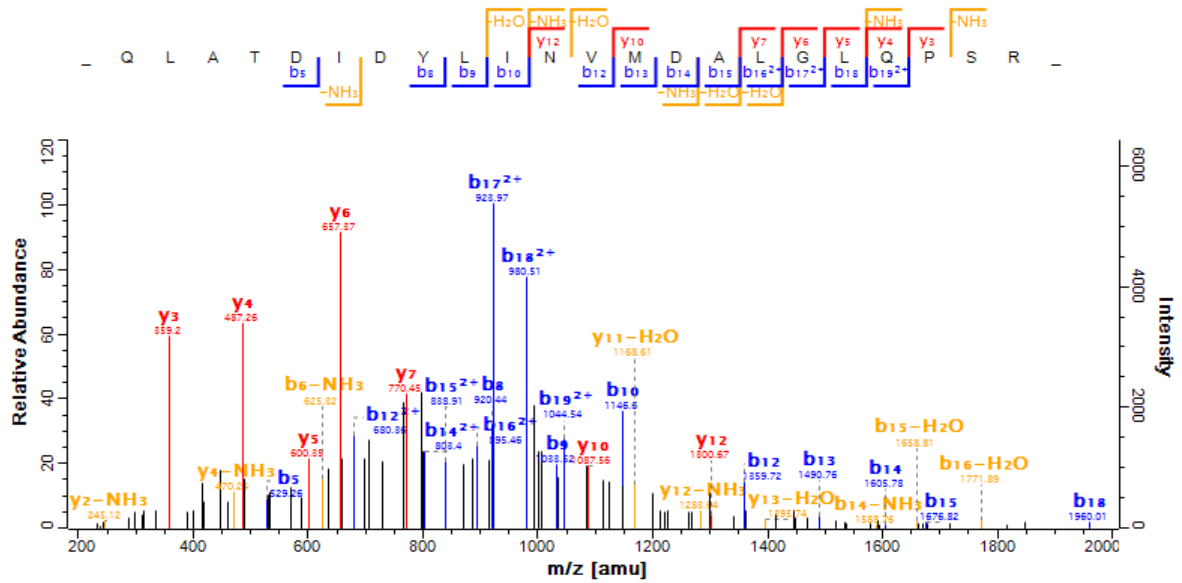
Protein Group ID: 3095
Protein Accession Numbers: P82094-2; P82094
Gene Names: TMF1
Peptide Sequence: MGAGSSIENLQSQLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 135.23
Best Match Posterior Error Probability: 6.33E-08
Best Match Spectrum:

Scan number 62336 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TMF1



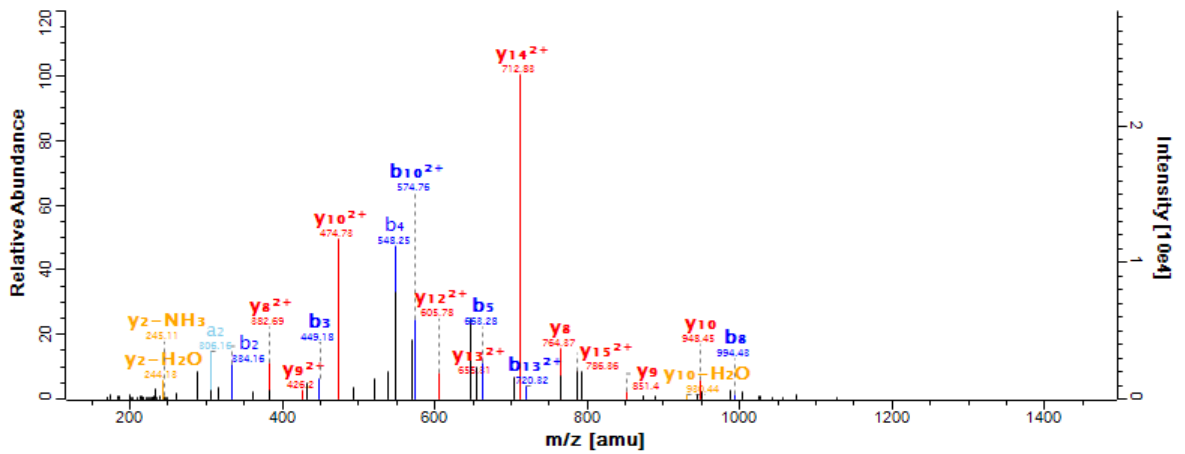
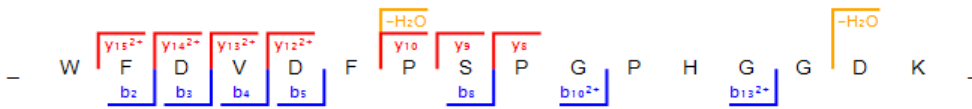
Protein Group ID: 3109
Protein Accession Numbers: P83436
Gene Names: COG7
Peptide Sequence: QLATDIDYLVNMDALGLQPSR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 113.26
Best Match Posterior Error Probability: 3.19E-07
Best Match Spectrum:

Scan number 96422 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** COG7



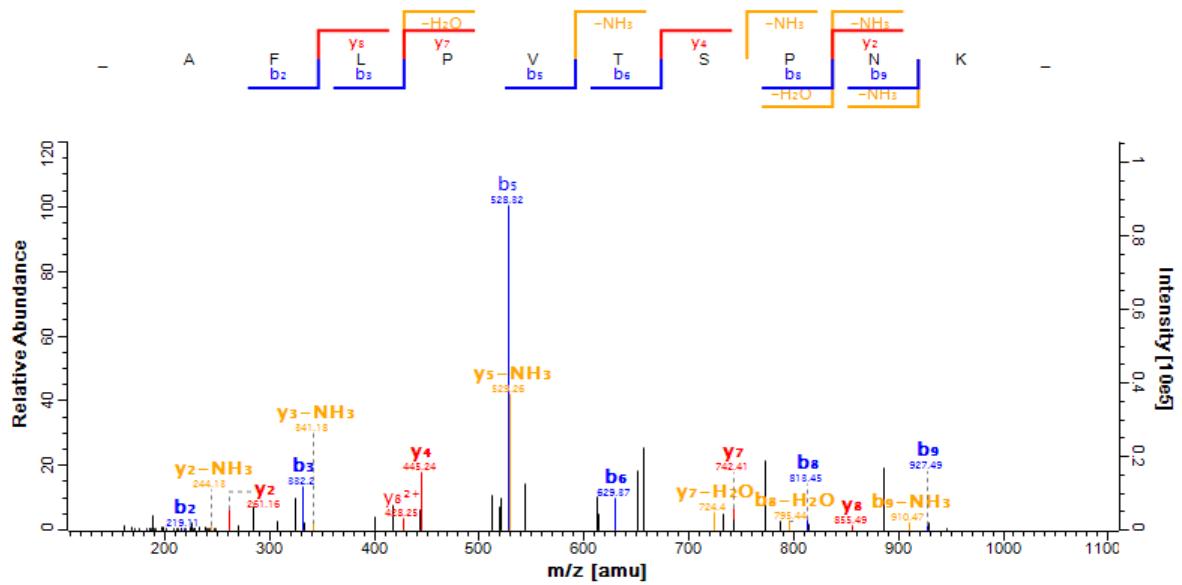
Protein Group ID: 3120
Protein Accession Numbers: P98088
Gene Names: MUC5AC
Peptide Sequence: WFDVDFPSPGPHGGDK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 102.73
Best Match Posterior Error Probability: 0.00014957
Best Match Spectrum:

Scan number 55949 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MUC5AC



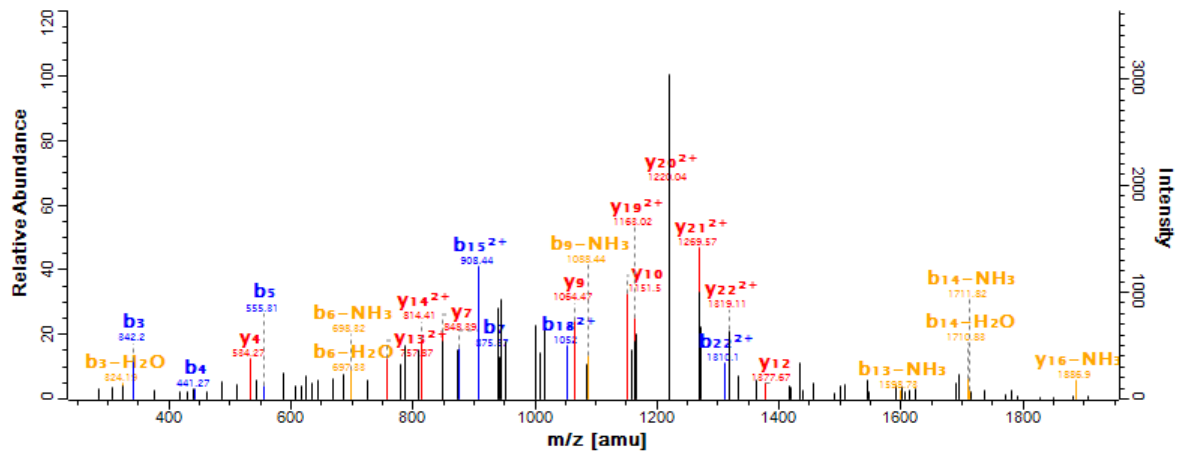
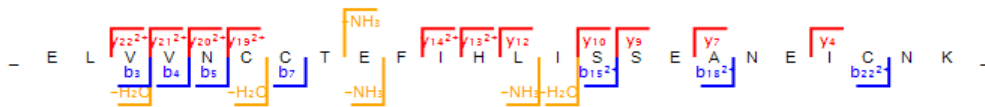
Protein Group ID: 3147
Protein Accession Numbers: Q01151
Gene Names: CD83
Peptide Sequence: AFLPVTSPNK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 89.047
Best Match Posterior Error Probability: 0.0021013
Best Match Spectrum:

Scan number 41233 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CD83



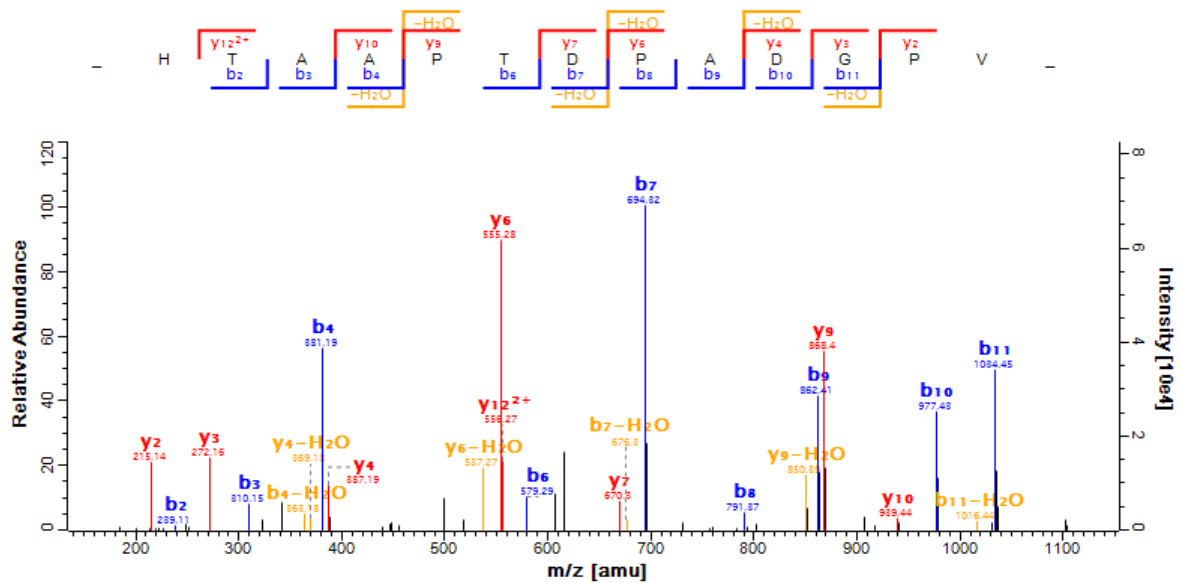
Protein Group ID: 3153
Protein Accession Numbers: Q01658
Gene Names: DR1
Peptide Sequence: ELVVNCCTEFIHLISSEANEICK
Total Number of Spectra: 3
Number of Replicates (out of 8): 2
Best Match Score: 66.644
Best Match Posterior Error Probability: 0.0007223
Best Match Spectrum:

Scan number 81904 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** DR1



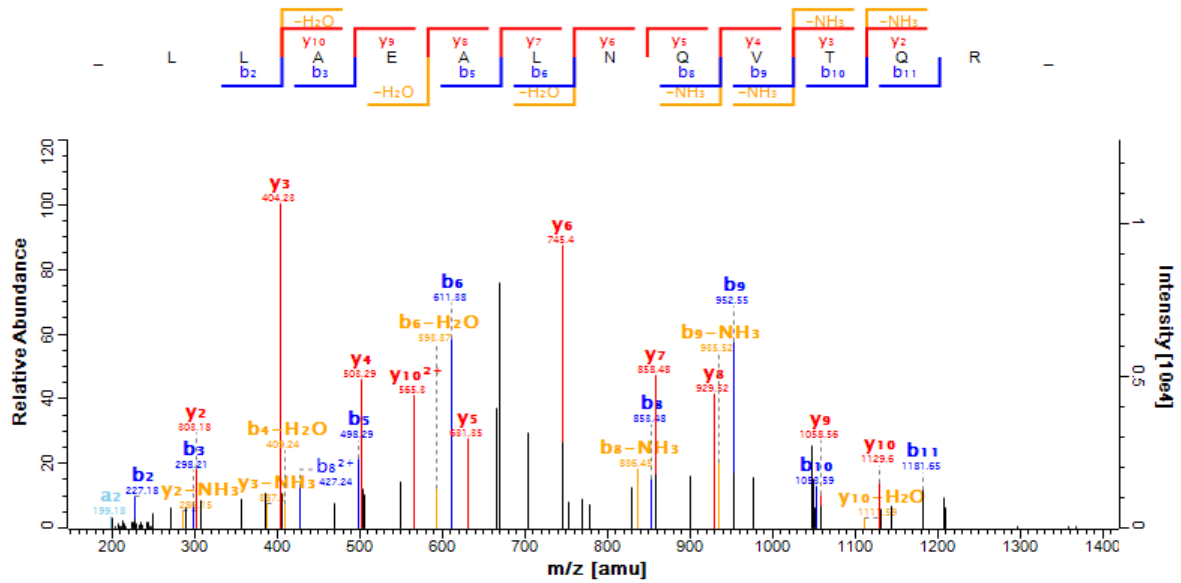
Protein Group ID: 3176
Protein Accession Numbers: Q04941
Gene Names: PLP2
Peptide Sequence: HTAAPTDPADGPV
Total Number of Spectra: 7
Number of Replicates (out of 8): 7
Best Match Score: 143
Best Match Posterior Error Probability: 1.79E-13
Best Match Spectrum:

Scan number 16248 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** PLP2



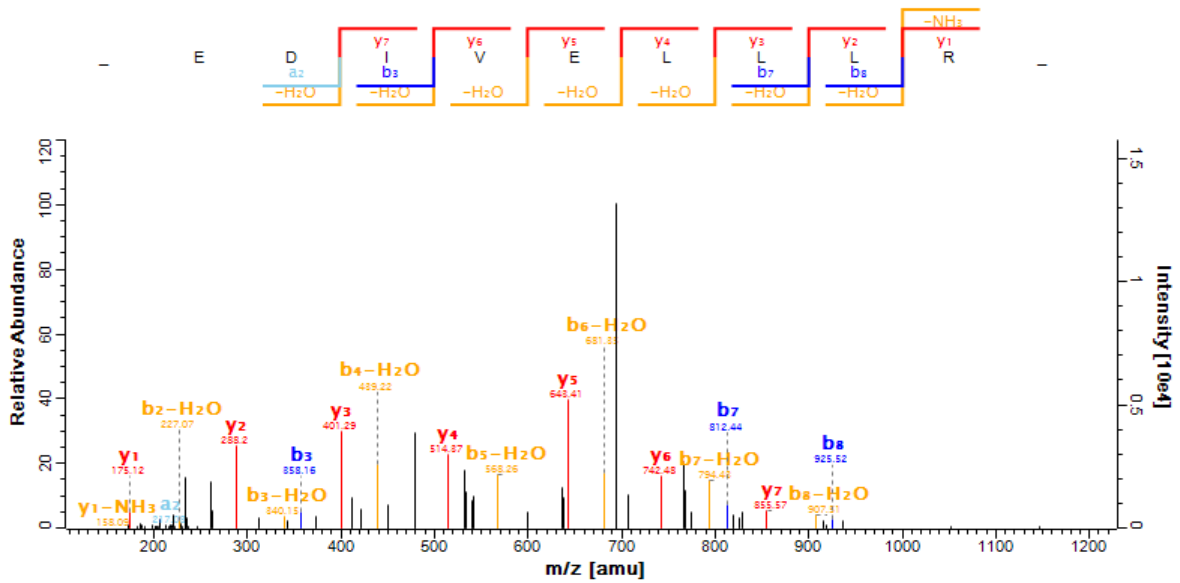
Protein Group ID: 3183
Protein Accession Numbers: Q05655-2; Q05655
Gene Names: PRKCD
Peptide Sequence: LLAEALNQVTQR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 164.48
Best Match Posterior Error Probability: 3.90E-08
Best Match Spectrum:

Scan number 44965 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PRKCD



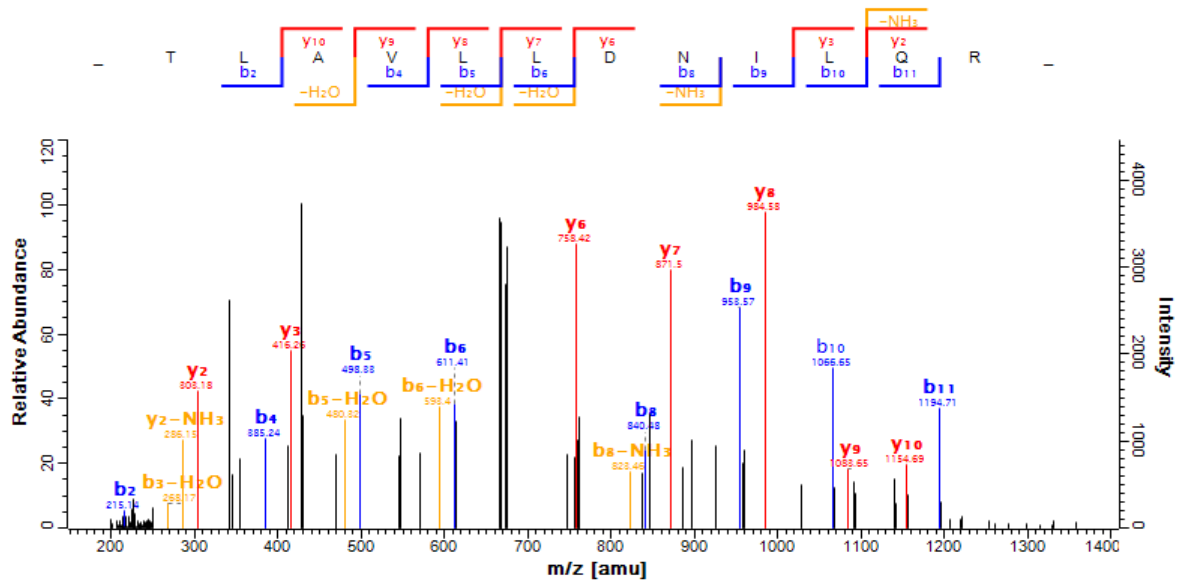
Protein Group ID: 3186
Protein Accession Numbers: Q05823; Q6AI46
Gene Names: RNASEL;DKFZp781D08126
Peptide Sequence: EDIVELLR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 93.649
Best Match Posterior Error Probability: 0.0028963
Best Match Spectrum:

Scan number	79735	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	RNASEL;DKFZp781D08126



Protein Group ID: 3226
Protein Accession Numbers: Q09328
Gene Names: MGAT5
Peptide Sequence: TLAVLLDNILQR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 122.45
Best Match Posterior Error Probability: 0.00010384
Best Match Spectrum:

Scan number 84148 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** MGAT5



Protein Group ID: 3257

Protein Accession Numbers: Q12962

Gene Names: TAF10

Peptide Sequence: ASPAGTAGGPGAGAAAGGTGPLAAR

Total Number of Spectra: 10

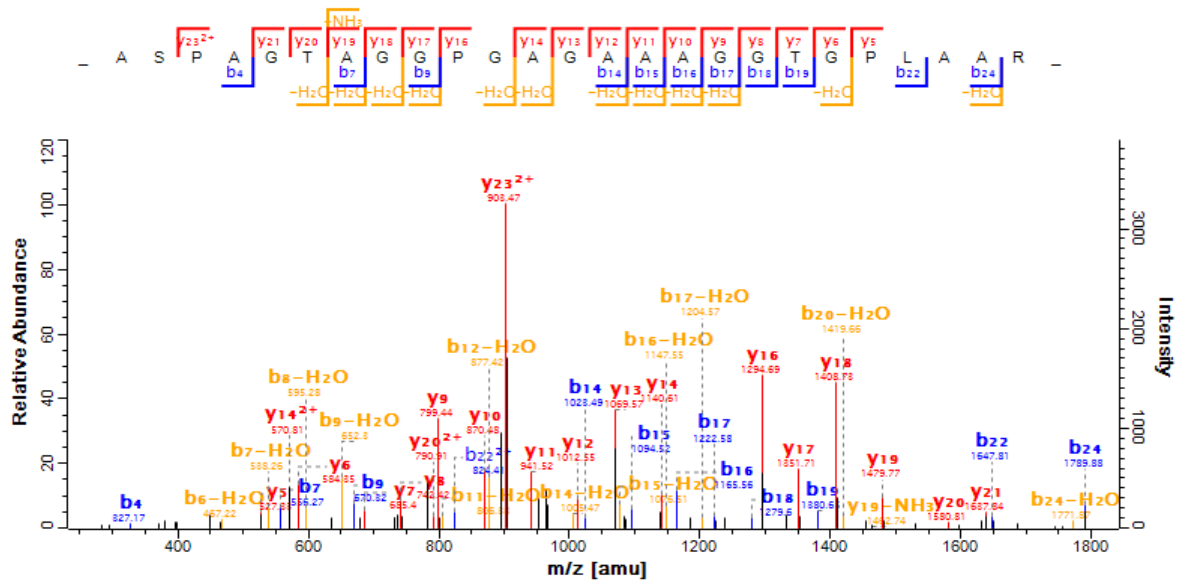
Number of Replicates (out of 8): 8

Best Match Score: 177.91

Best Match Posterior Error Probability: 3.90E-32

Best Match Spectrum:

Scan number 25168 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TAF10



Protein Group ID: 3262

Protein Accession Numbers: Q12986; Q12986-2; Q12986-3

Gene Names: NFX1

Peptide Sequence: SPASQADGQSGWR

Total Number of Spectra: 4

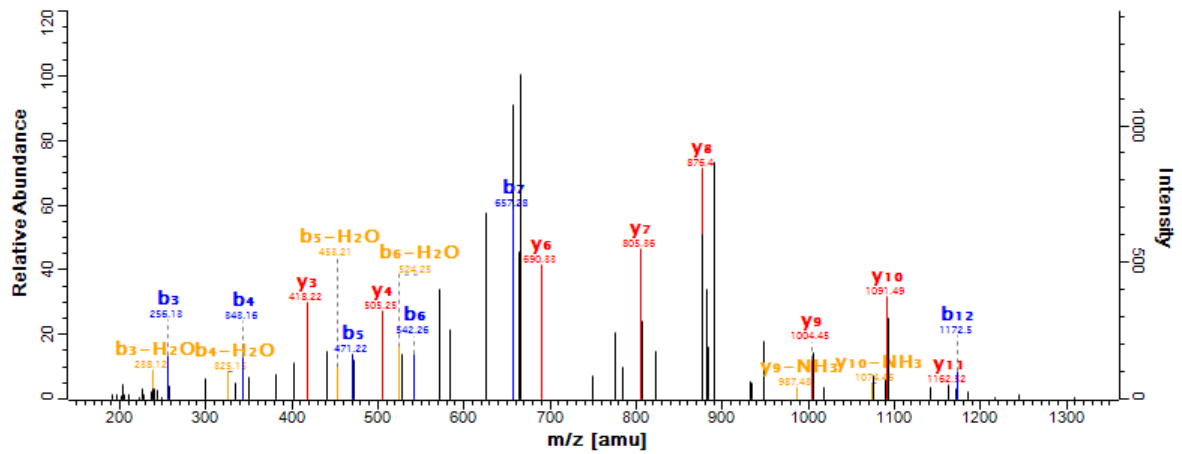
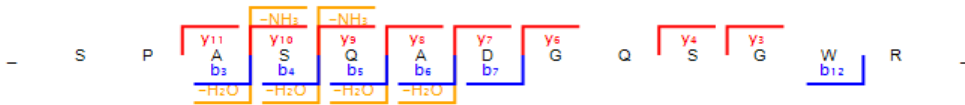
Number of Replicates (out of 8): 3

Best Match Score: 94.023

Best Match Posterior Error Probability: 0.0010062

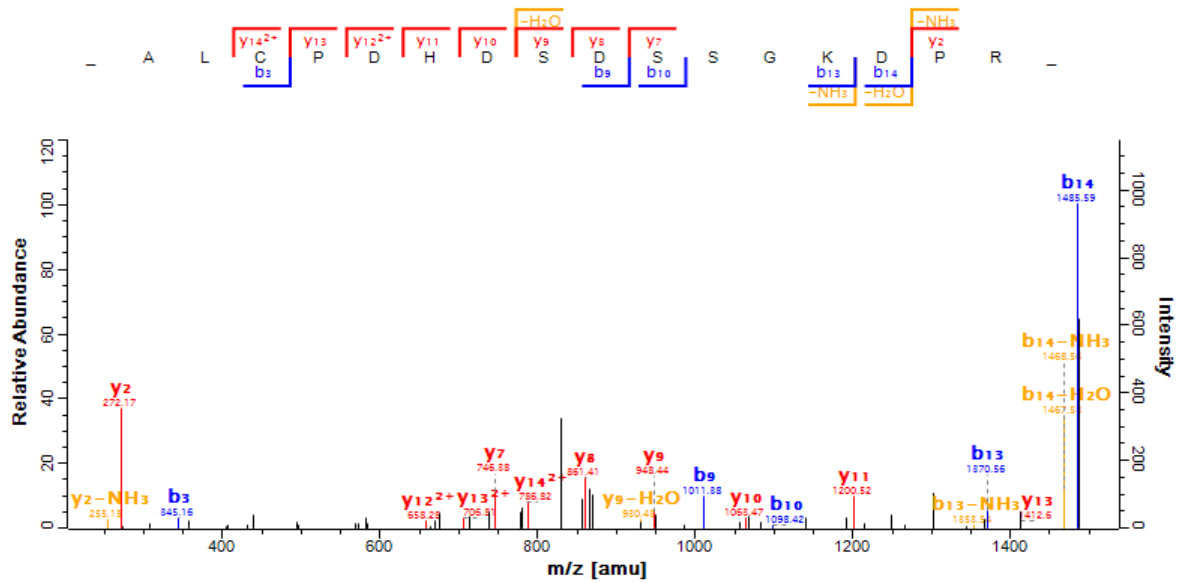
Best Match Spectrum:

Scan number	11905	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	NFX1



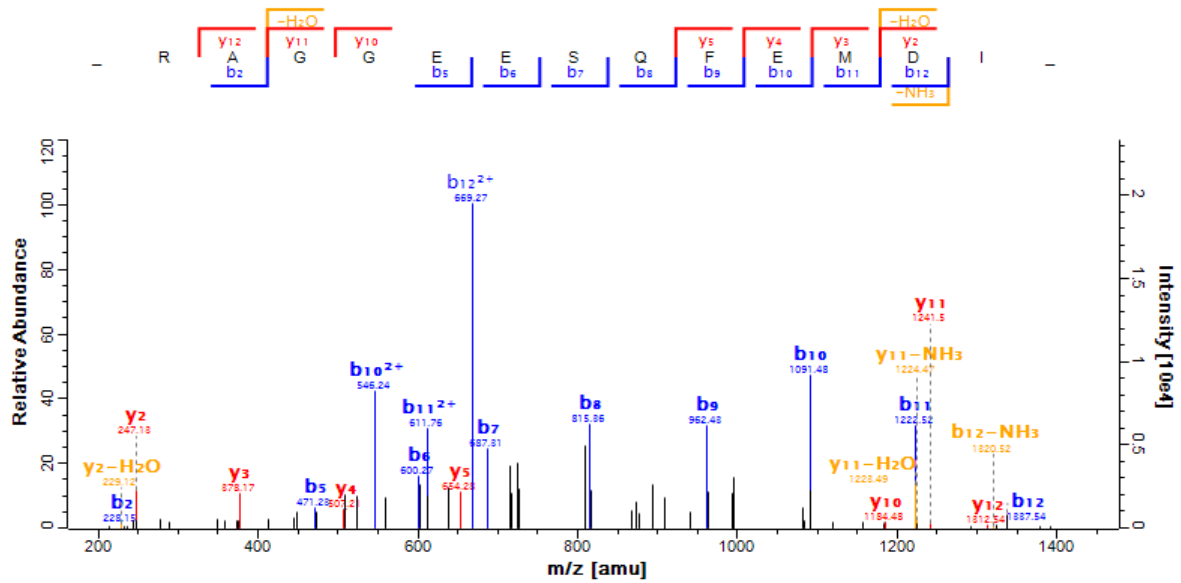
Protein Group ID: 3309
Protein Accession Numbers: Q13433
Gene Names: SLC39A6
Peptide Sequence: ALCPDHDS DSSGKDPR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 97.797
Best Match Posterior Error Probability: 0.00099632
Best Match Spectrum:

Scan number 3800 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** SLC39A6



Protein Group ID: 3323
Protein Accession Numbers: Q13541
Gene Names: EIF4EBP1
Peptide Sequence: RAGGEESQFEMDI
Total Number of Spectra: 7
Number of Replicates (out of 8): 6
Best Match Score: 118.24
Best Match Posterior Error Probability: 0.00040834
Best Match Spectrum:

Scan number 45306 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** EIF4EBP1



Protein Group ID: 3327

Protein Accession Numbers: Q13563; Q13563-3; Q13563-5; Q13563-4; Q13563-2

Gene Names: PKD2

Peptide Sequence: FTEGSLLDGLYWK

Total Number of Spectra: 1

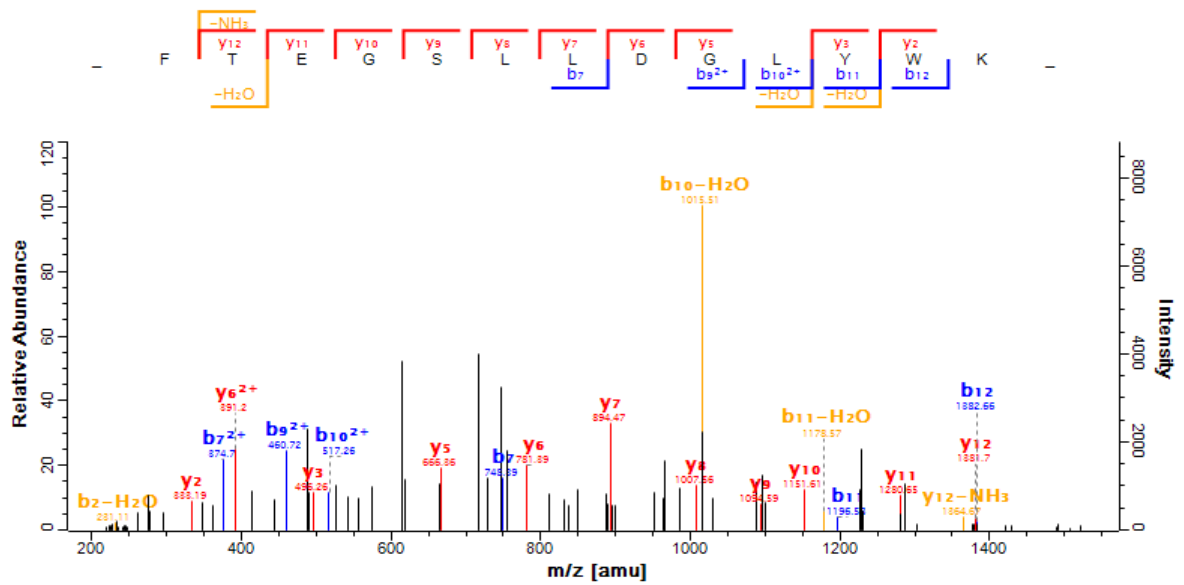
Number of Replicates (out of 8): 1

Best Match Score: 92.295

Best Match Posterior Error Probability: 0.0011754

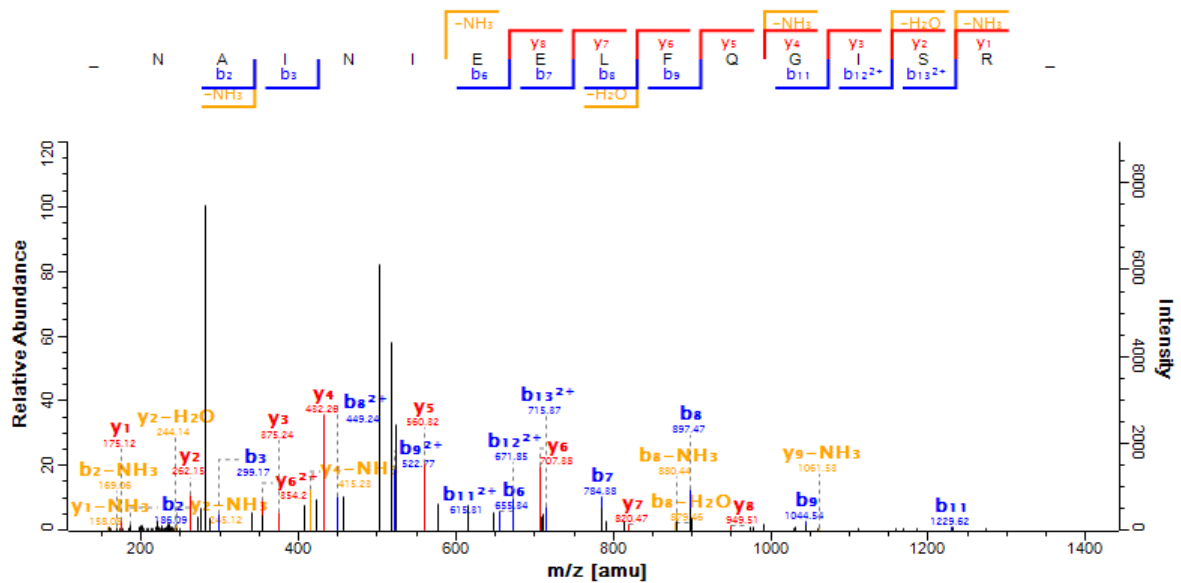
Best Match Spectrum:

Scan number 72717 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PKD2



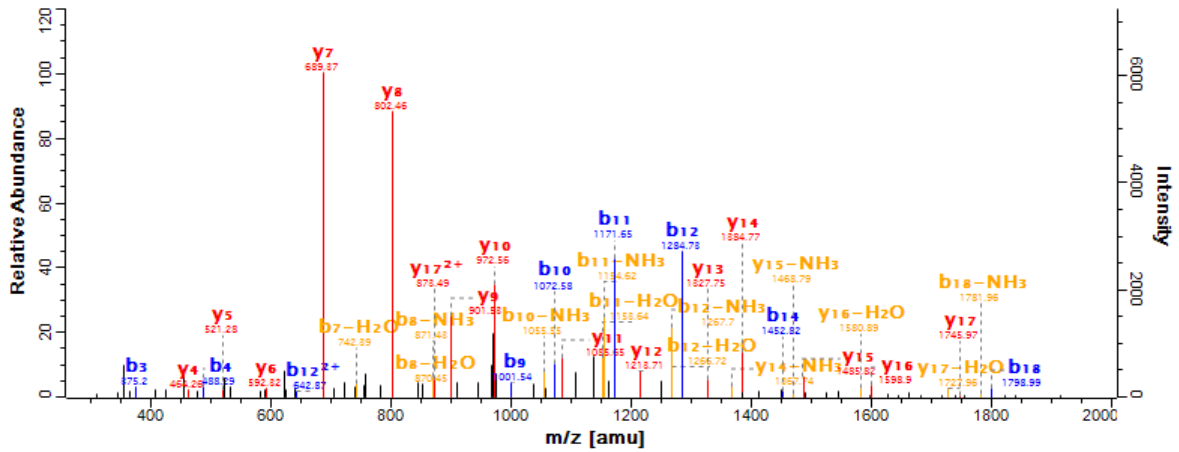
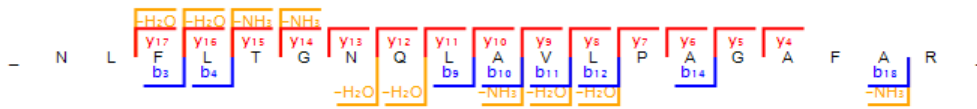
Protein Group ID: 3340
Protein Accession Numbers: Q13636
Gene Names: RAB31
Peptide Sequence: NAINIEELFQGISR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 121.18
Best Match Posterior Error Probability: 4.23E-05
Best Match Spectrum:

Scan number	81732	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	RAB31



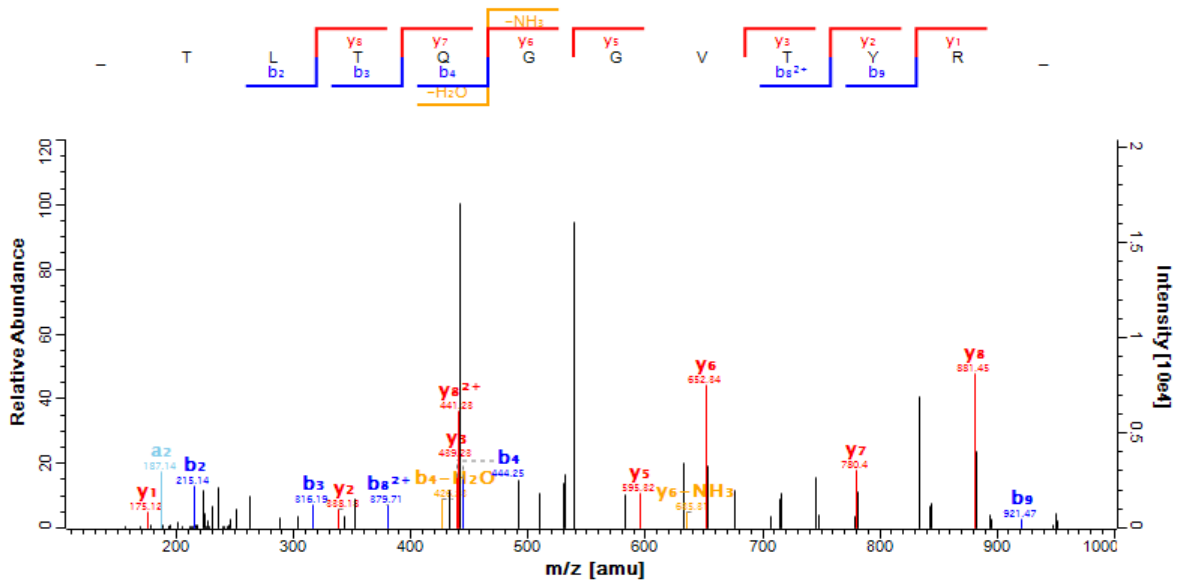
Protein Group ID: 3342
Protein Accession Numbers: Q13641
Gene Names: TPBG
Peptide Sequence: NLFLTGNQLAVLPAGAFAR
Total Number of Spectra: 12
Number of Replicates (out of 8): 6
Best Match Score: 193.8
Best Match Posterior Error Probability: 7.95E-32
Best Match Spectrum:

Scan number 80120 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** TPBG



Protein Group ID: 3343
Protein Accession Numbers: Q13643
Gene Names: FHL3
Peptide Sequence: TLTQGGVTYR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 86.344
Best Match Posterior Error Probability: 0.0026689
Best Match Spectrum:

Scan number 14813 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** FHL3



Protein Group ID: 3354

Protein Accession Numbers: Q13901

Gene Names: CID

Peptide Sequence: AGEEINEDYPVEIHEYLSAFENSI GAVDEMLK

Total Number of Spectra: 2

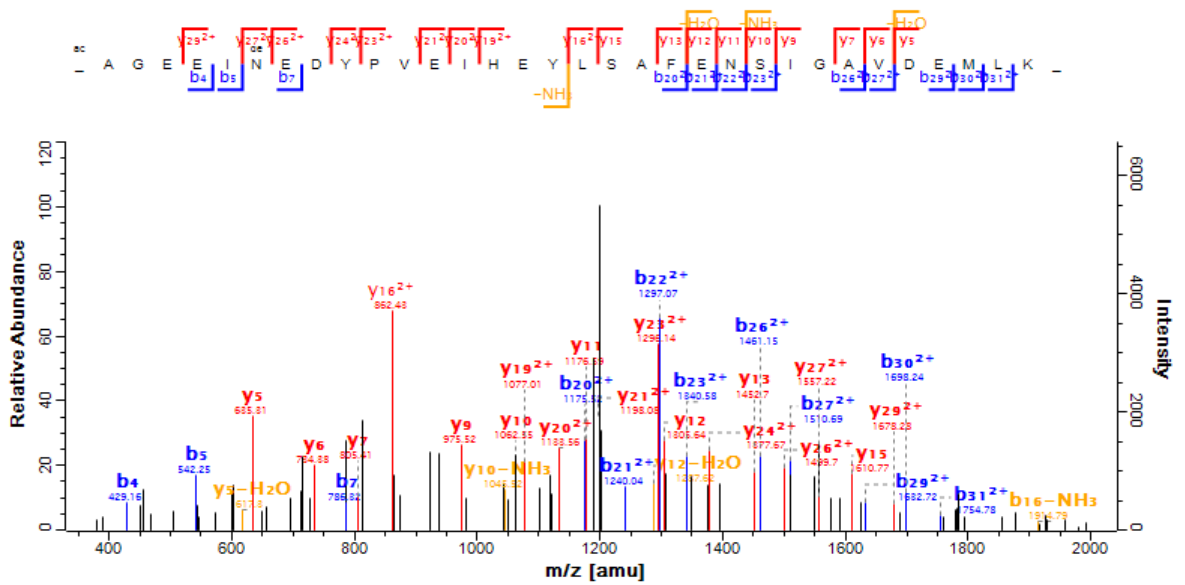
Number of Replicates (out of 8): 2

Best Match Score: 117.96

Best Match Posterior Error Probability: 3.49E-16

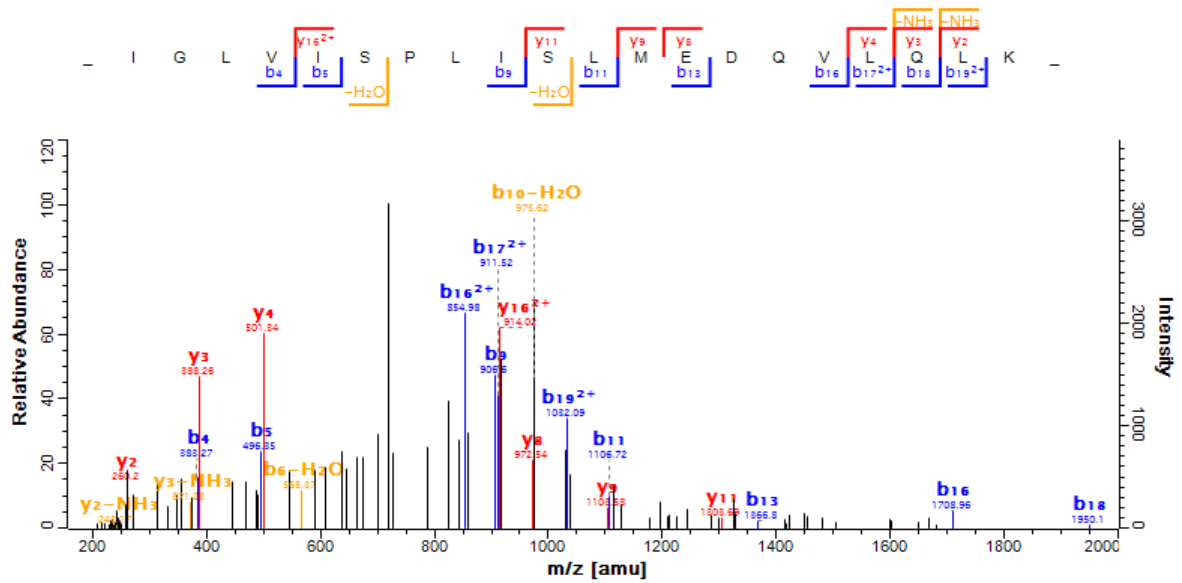
Best Match Spectrum:

Scan number 95536 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CID



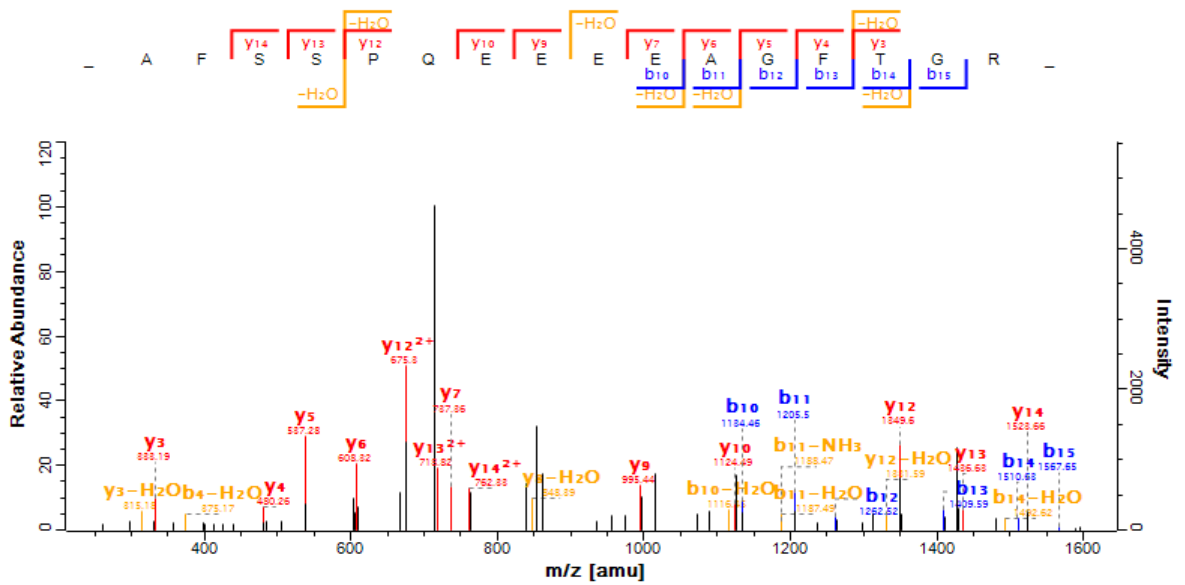
Protein Group ID: 3379
Protein Accession Numbers: Q14191
Gene Names: WRN
Peptide Sequence: IGLVISPLISLMEDQVLQLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 69.935
Best Match Posterior Error Probability: 0.0019496
Best Match Spectrum:

Scan number 95303 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** WRN



Protein Group ID: 3382
Protein Accession Numbers: Q14241
Gene Names: TCEB3
Peptide Sequence: AFSSPQEEEEAGFTGR
Total Number of Spectra: 4
Number of Replicates (out of 8): 3
Best Match Score: 128.64
Best Match Posterior Error Probability: 6.35E-05
Best Match Spectrum:

Scan number 31860 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TCEB3



Protein Group ID: 3392

Protein Accession Numbers: Q14451-3; Q14451; Q14451-4

Gene Names: GRB7

Peptide Sequence: FTDLLQLVEFHQLNR

Total Number of Spectra: 1

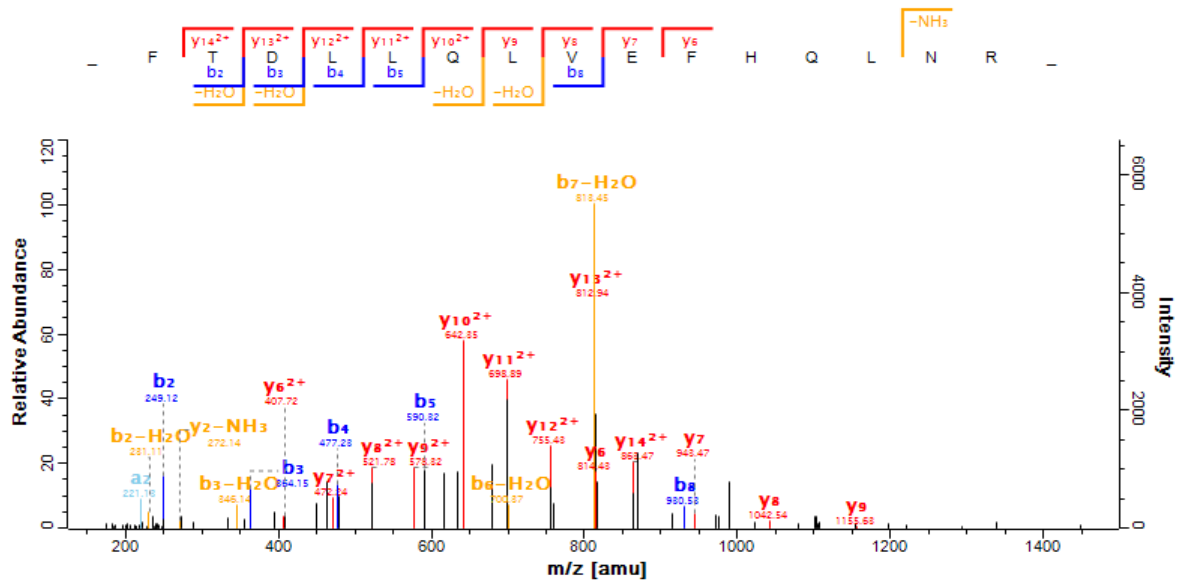
Number of Replicates (out of 8): 1

Best Match Score: 124.12

Best Match Posterior Error Probability: 3.69E-05

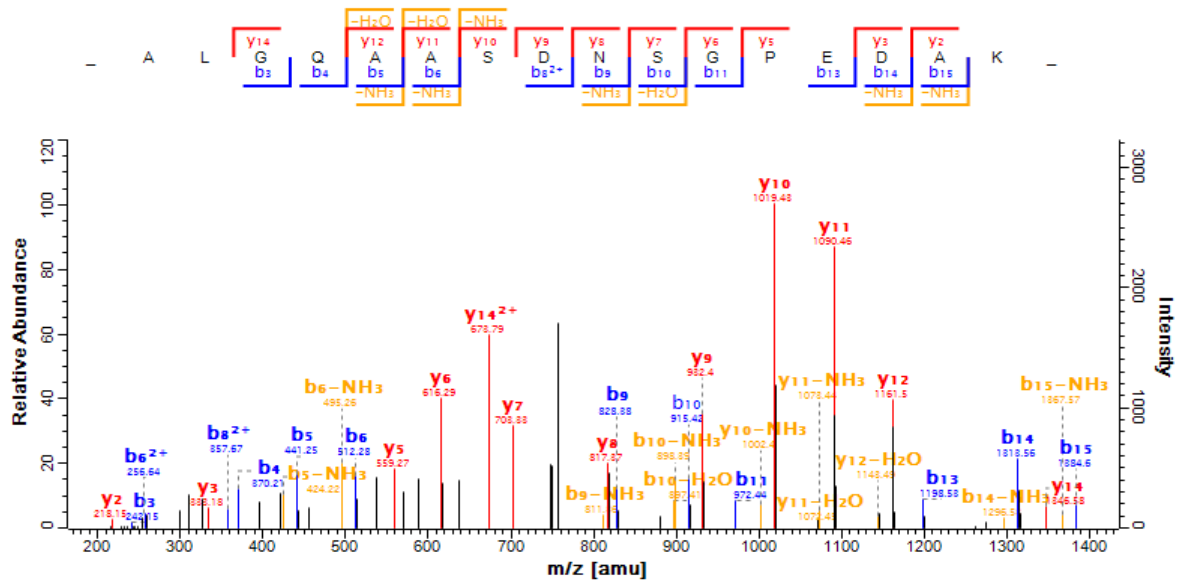
Best Match Spectrum:

Scan number	77441	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	GRB7



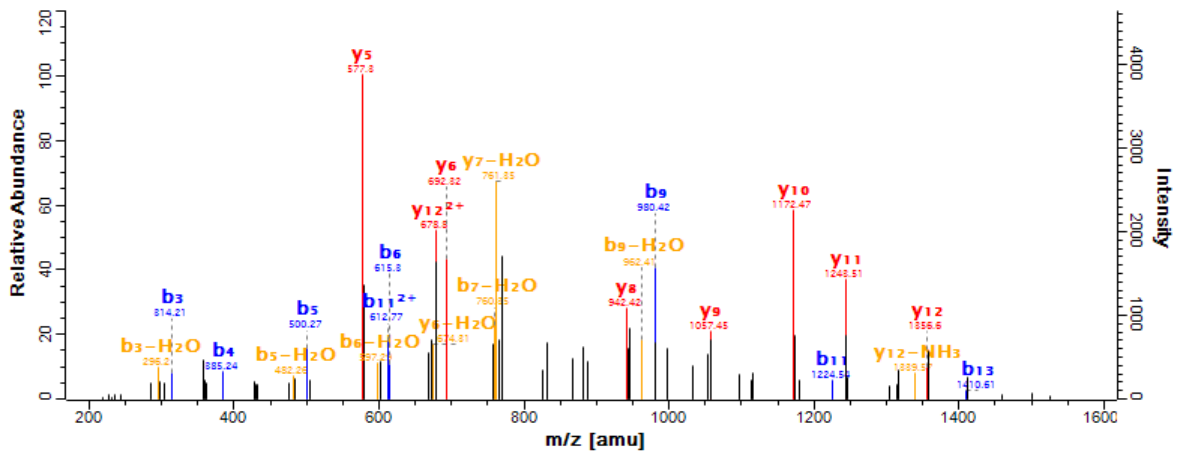
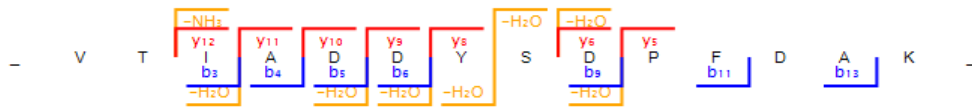
Protein Group ID: 3458
Protein Accession Numbers: Q15155; H3BUC9
Gene Names: NOMO1
Peptide Sequence: ALGQAASDNSGPEDAK
Total Number of Spectra: 9
Number of Replicates (out of 8): 8
Best Match Score: 199.15
Best Match Posterior Error Probability: 8.11E-29
Best Match Spectrum:

Scan number 7997 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** NOMO1



Protein Group ID: 3488
Protein Accession Numbers: Q15464; Q15464-2
Gene Names: SHB
Peptide Sequence: VTIADDYSDPFDAK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 110.51
Best Match Posterior Error Probability: 0.00016395
Best Match Spectrum:

Scan number 48093 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** SHB



Protein Group ID: 3491

Protein Accession Numbers: Q15545

Gene Names: TAF7

Peptide Sequence: LNESDEQHQENQLVMIQK

Total Number of Spectra: 4

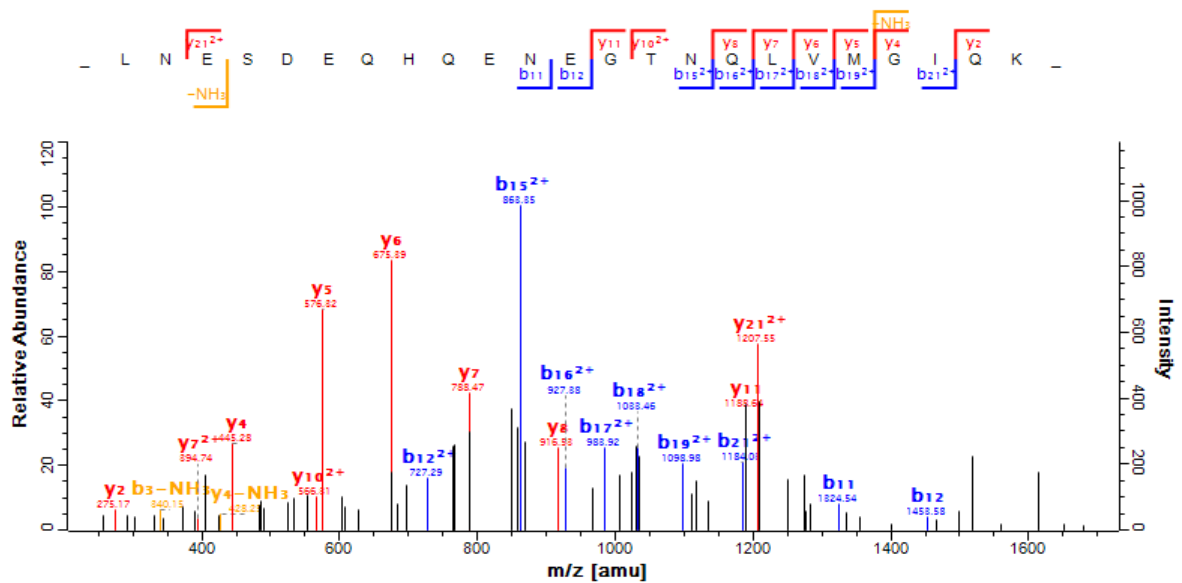
Number of Replicates (out of 8): 4

Best Match Score: 77.871

Best Match Posterior Error Probability: 0.00013261

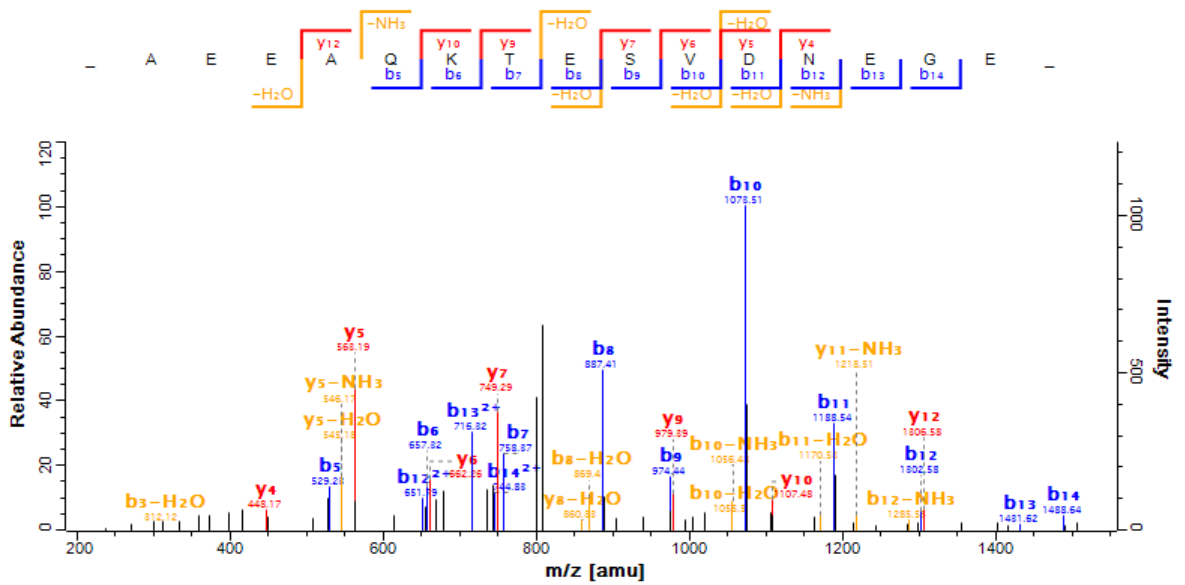
Best Match Spectrum:

Scan number 33871 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** TAF7



Protein Group ID: 3501
Protein Accession Numbers: Q15651
Gene Names: HMGN3
Peptide Sequence: AEEAQKTESVDNEGE
Total Number of Spectra: 7
Number of Replicates (out of 8): 5
Best Match Score: 142.91
Best Match Posterior Error Probability: 3.21E-05
Best Match Spectrum:

Scan number 5054 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** HMGN3



Protein Group ID: 3504

Protein Accession Numbers: Q15714; Q15714-3; Q15714-2

Gene Names: TSC22D1

Peptide Sequence: NSQLEQENLLK

Total Number of Spectra: 8

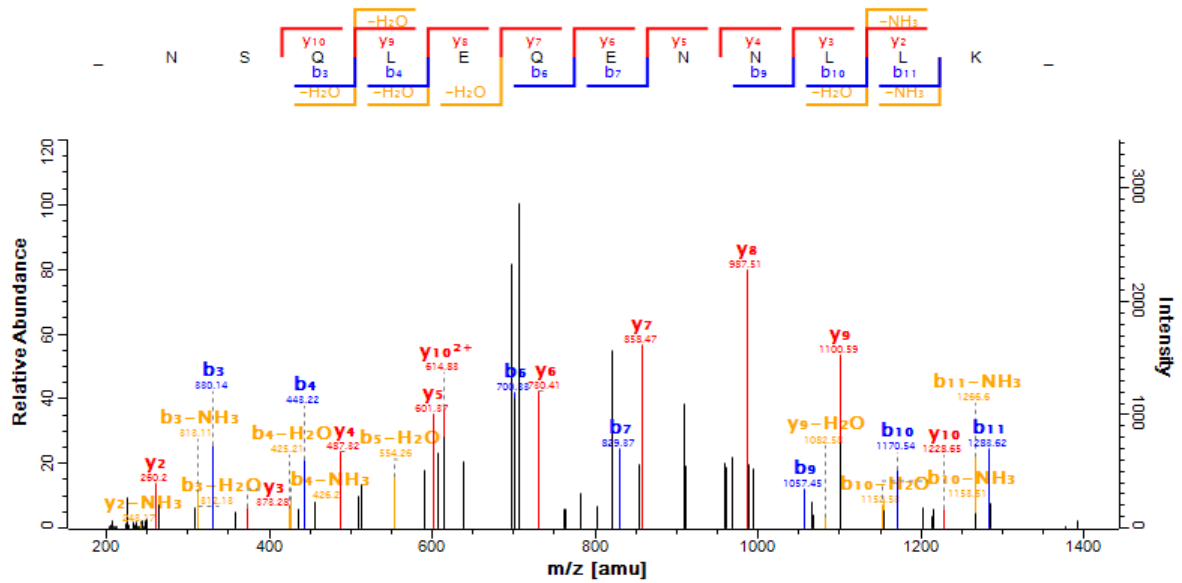
Number of Replicates (out of 8): 6

Best Match Score: 160.38

Best Match Posterior Error Probability: 7.73E-08

Best Match Spectrum:

Scan number	28760	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	TSC22D1



Protein Group ID: 3507

Protein Accession Numbers: Q15750; Q15750-2

Gene Names: TAB1

Peptide Sequence: ALEAAHGPGQANQEIAMIDTEFAK

Total Number of Spectra: 5

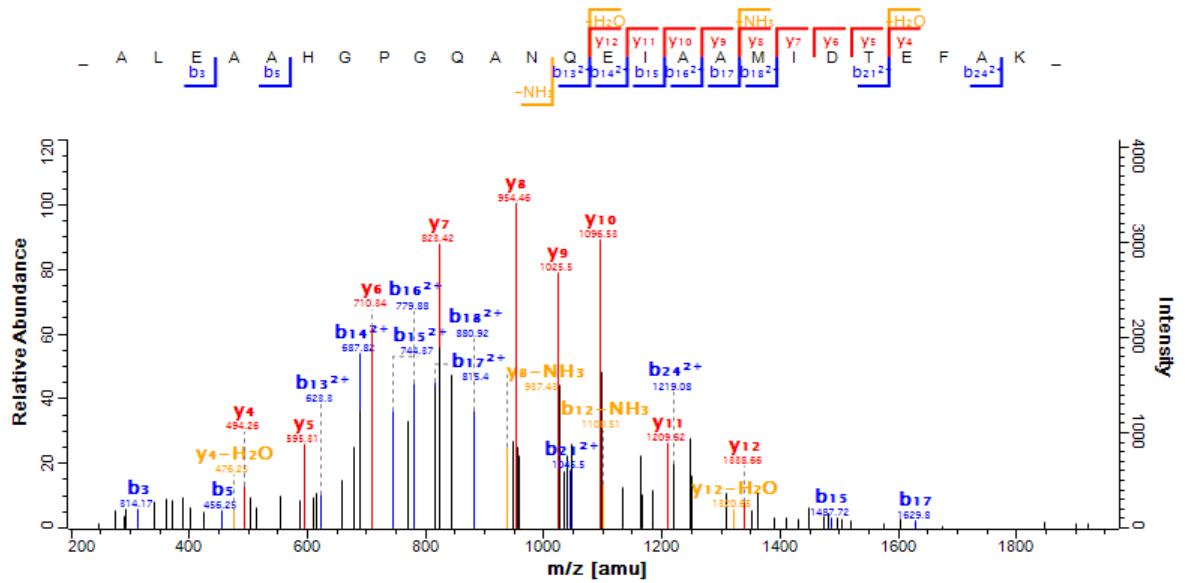
Number of Replicates (out of 8): 3

Best Match Score: 90.308

Best Match Posterior Error Probability: 1.11E-05

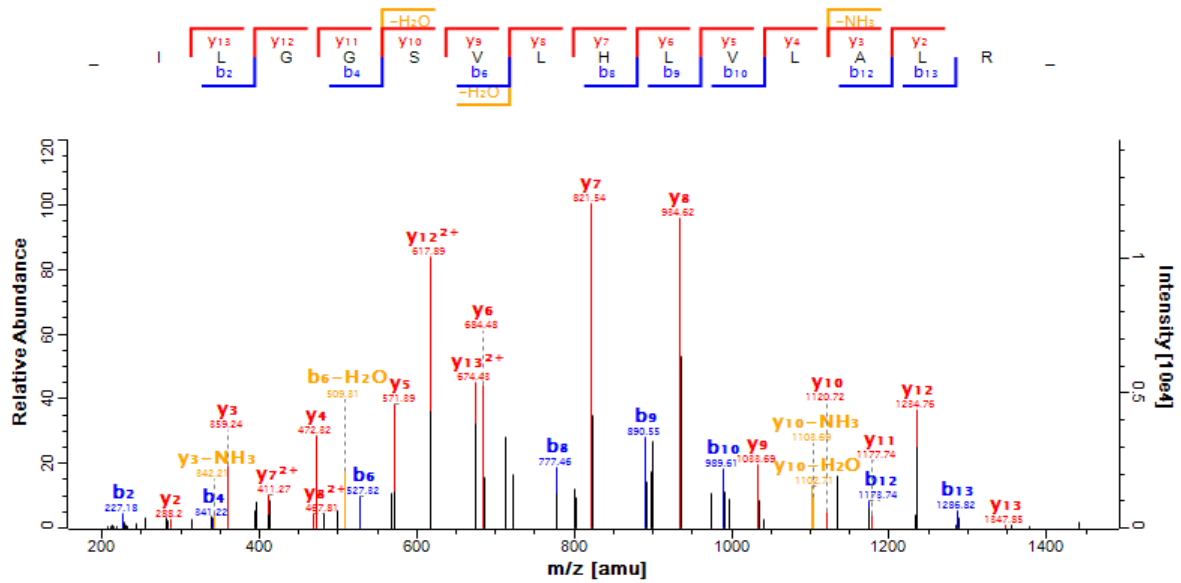
Best Match Spectrum:

Scan number 65991 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TAB1



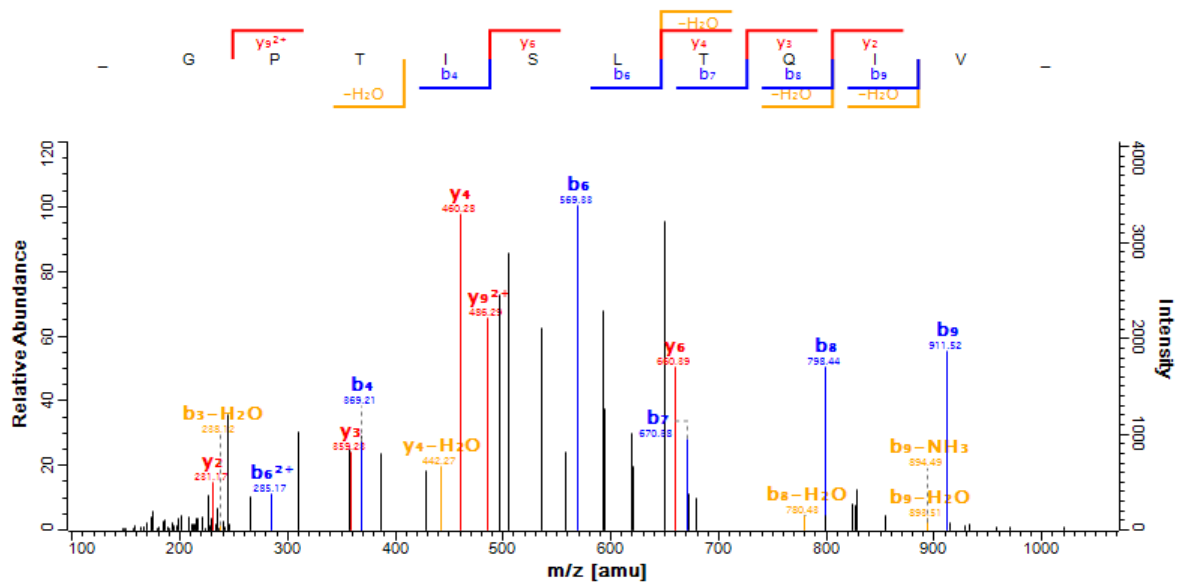
Protein Group ID: 3514
Protein Accession Numbers: Q15843
Gene Names: NEDD8
Peptide Sequence: ILGGSVLHLVLALR
Total Number of Spectra: 10
Number of Replicates (out of 8): 6
Best Match Score: 189.3
Best Match Posterior Error Probability: 1.22E-19
Best Match Spectrum:

Scan number 84559 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** NEDD8



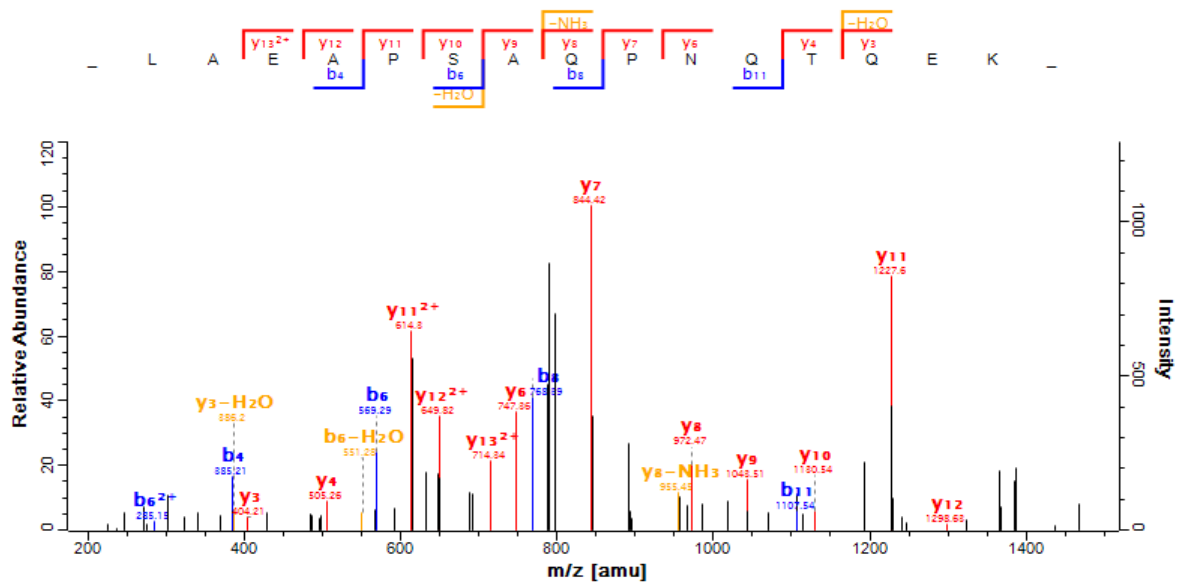
Protein Group ID: 3515
Protein Accession Numbers: Q15904
Gene Names: ATP6AP1
Peptide Sequence: GPTISLTQIV
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 98.044
Best Match Posterior Error Probability: 0.00094211
Best Match Spectrum:

Scan number 64547 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ATP6AP1



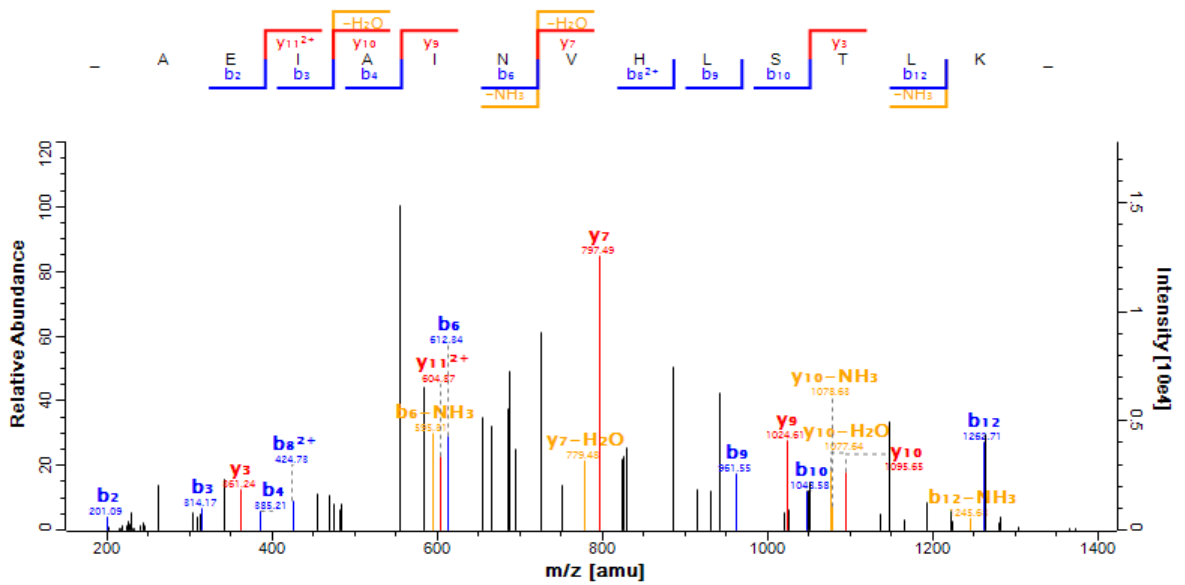
Protein Group ID: 3518
Protein Accession Numbers: Q15911; Q15911-2
Gene Names: ZFH3
Peptide Sequence: LAEAPSAQPNQTQEK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 85.006
Best Match Posterior Error Probability: 0.0015016
Best Match Spectrum:

Scan number 8720 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ZFH3



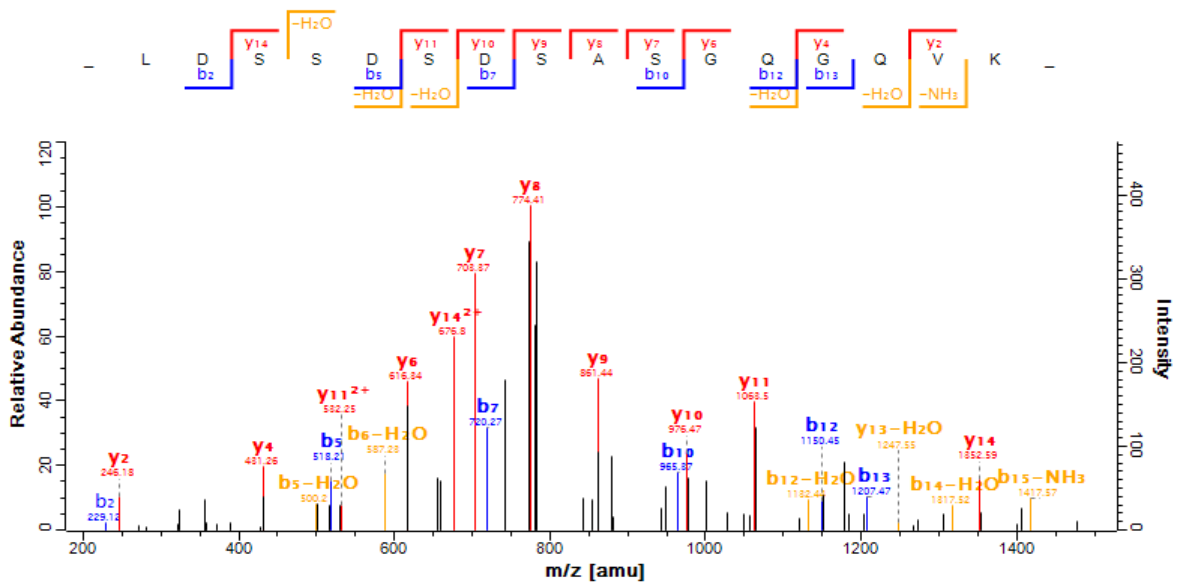
Protein Group ID: 3525
Protein Accession Numbers: Q16280
Gene Names: CNGA2
Peptide Sequence: AEIAINVHLSTLK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 84.892
Best Match Posterior Error Probability: 0.0022053
Best Match Spectrum:

Scan number 48801 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CNGA2



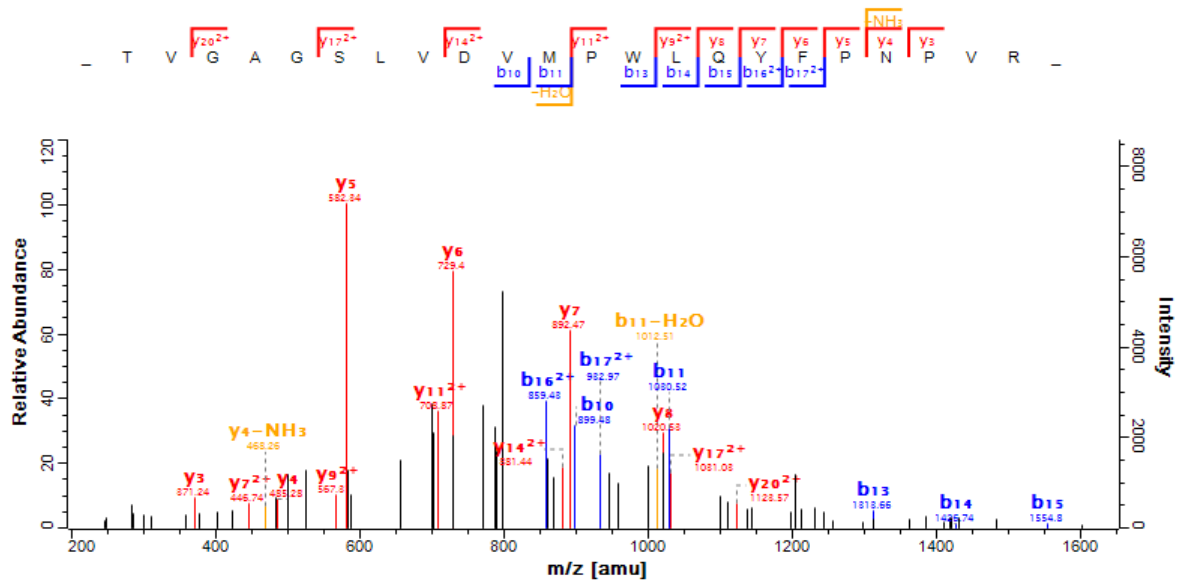
Protein Group ID: 3531
Protein Accession Numbers: Q16533
Gene Names: SNAPC1
Peptide Sequence: LDSSSDSASGQGQVK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 107.98
Best Match Posterior Error Probability: 0.00012175
Best Match Spectrum:

Scan number 4488 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** SNAPC1



Protein Group ID: 3540
Protein Accession Numbers: Q16678
Gene Names: CYP1B1
Peptide Sequence: TVGAGSLVDVMPWLQYFNPVR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 75.564
Best Match Posterior Error Probability: 0.0002151
Best Match Spectrum:

Scan number 93865 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CYP1B1



Protein Group ID: 3544

Protein Accession Numbers: Q16720; Q16720-4; Q16720-2; Q16720-5; Q16720-3;
Q16720-6; Q16720-7; Q16720-8

Gene Names: ATP2B3

Peptide Sequence: GEIEQERL D

Total Number of Spectra: 2

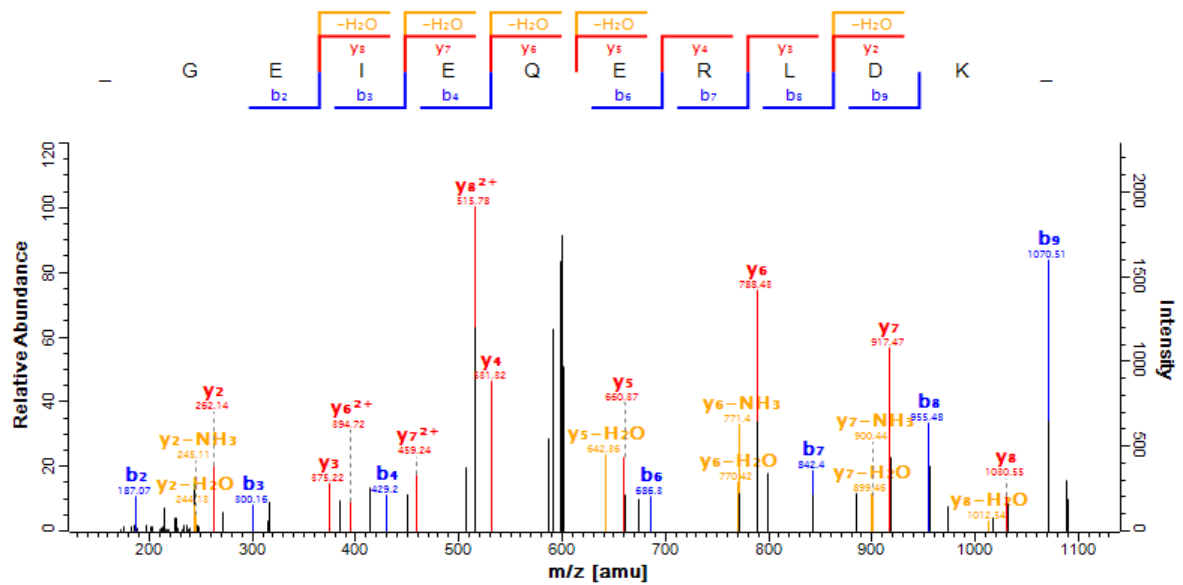
Number of Replicates (out of 8): 2

Best Match Score: 174.4

Best Match Posterior Error Probability: 2.96E-05

Best Match Spectrum:

Scan number 7708 Raw file A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS: CID Genenames ATP2B3



Protein Group ID: 3548

Protein Accession Numbers: Q6FI13; Q16777

Gene Names: HIST2H2AA3; HIST2H2AC

Peptide Sequence: VGAGAPVYMAAVLEYLELAGNAAR

Total Number of Spectra: 14

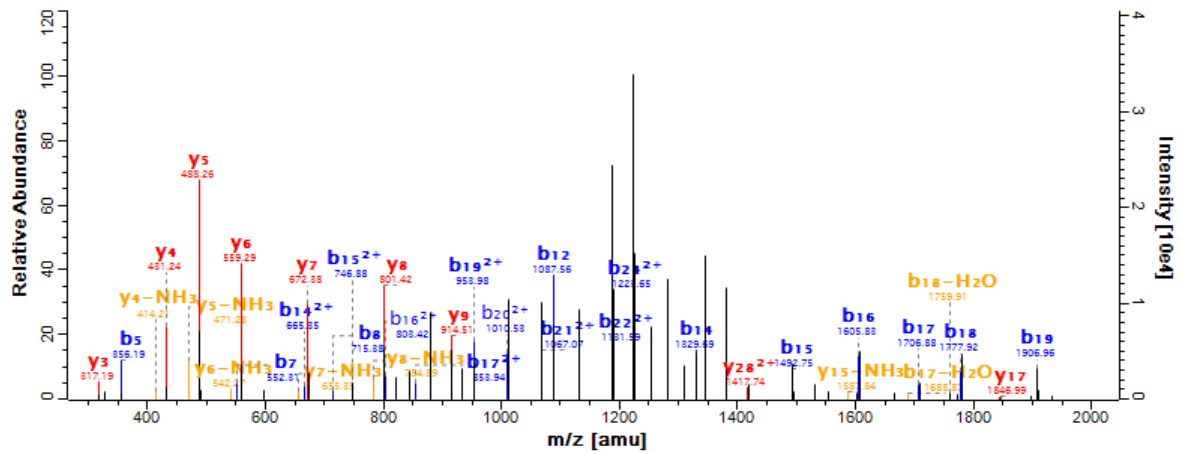
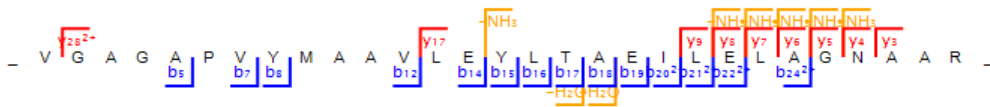
Number of Replicates (out of 8): 7

Best Match Score: 171.39

Best Match Posterior Error Probability: 1.05E-41

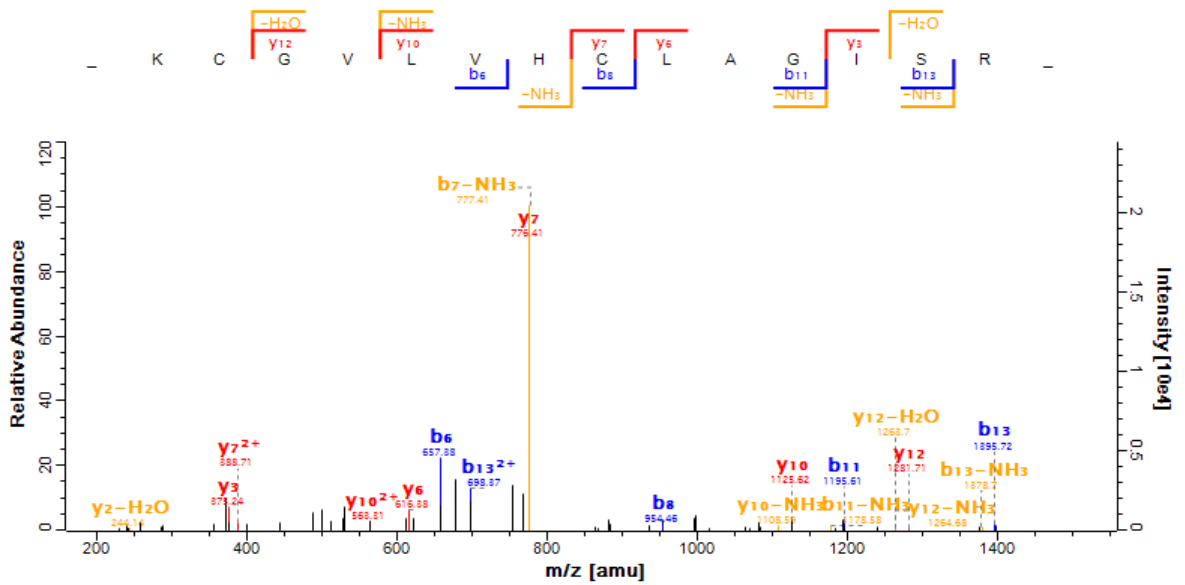
Best Match Spectrum:

Scan number	96235	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	HIST2H2AA3; HIST2H2AC



Protein Group ID: 3551
Protein Accession Numbers: Q16829; Q16829-2
Gene Names: DUSP7
Peptide Sequence: KCGVLVHCLAGISR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 88.101
Best Match Posterior Error Probability: 0.0032201
Best Match Spectrum:

Scan number 16119 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** DUSP7



Protein Group ID: 3555

Protein Accession Numbers: Q16854; Q16854-2

Gene Names: DGUOK

Peptide Sequence: TYPEWHVATEPVATWQNIQAAGTQK

Total Number of Spectra: 11

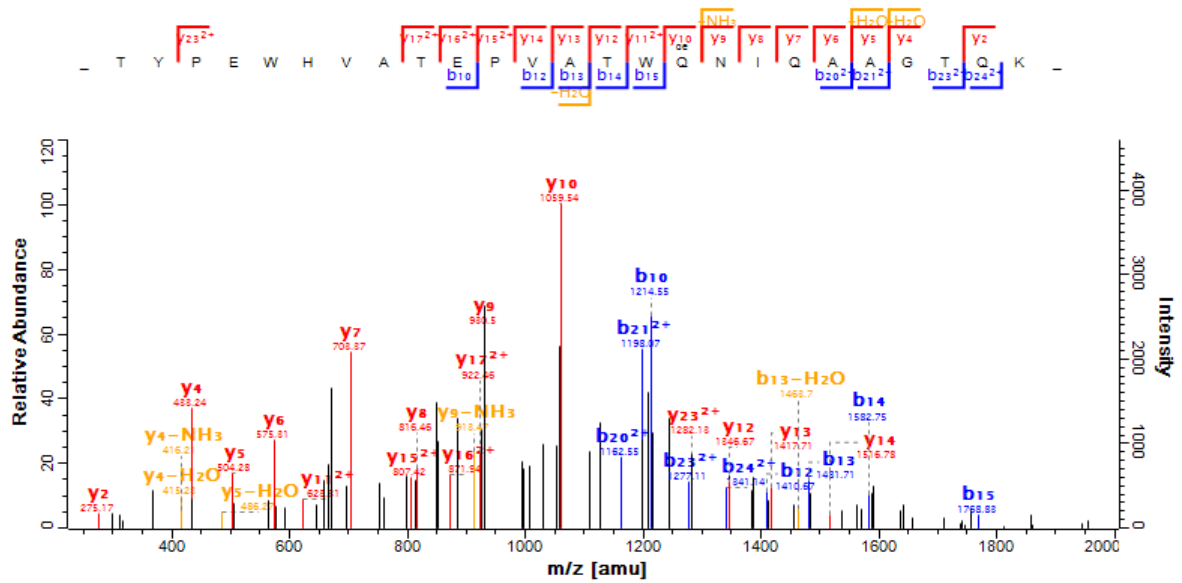
Number of Replicates (out of 8): 8

Best Match Score: 118.36

Best Match Posterior Error Probability: 7.22E-10

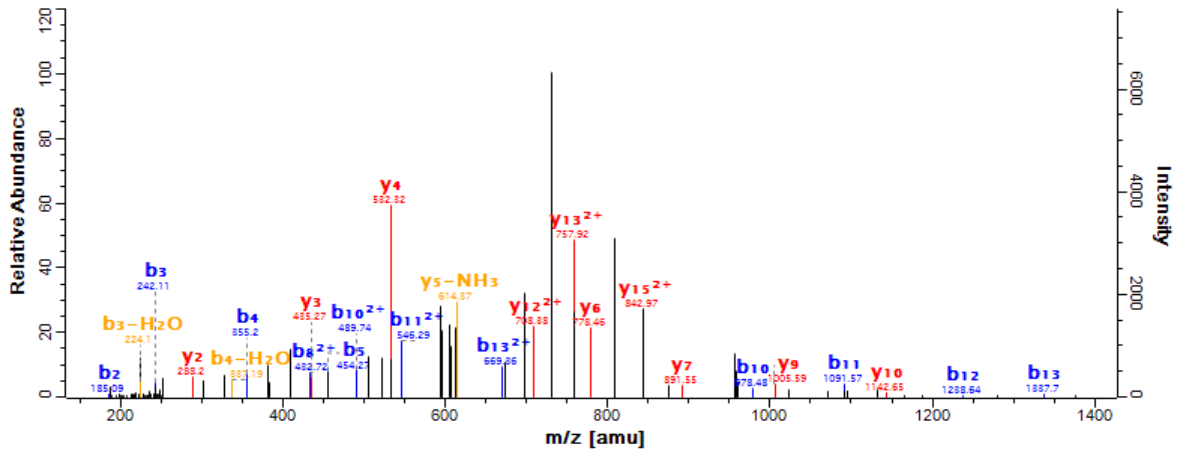
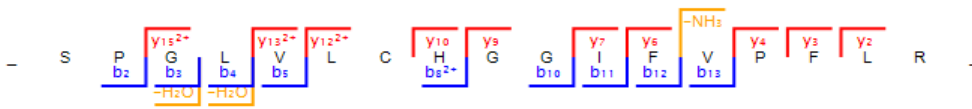
Best Match Spectrum:

Scan number 62273 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** DGUOK



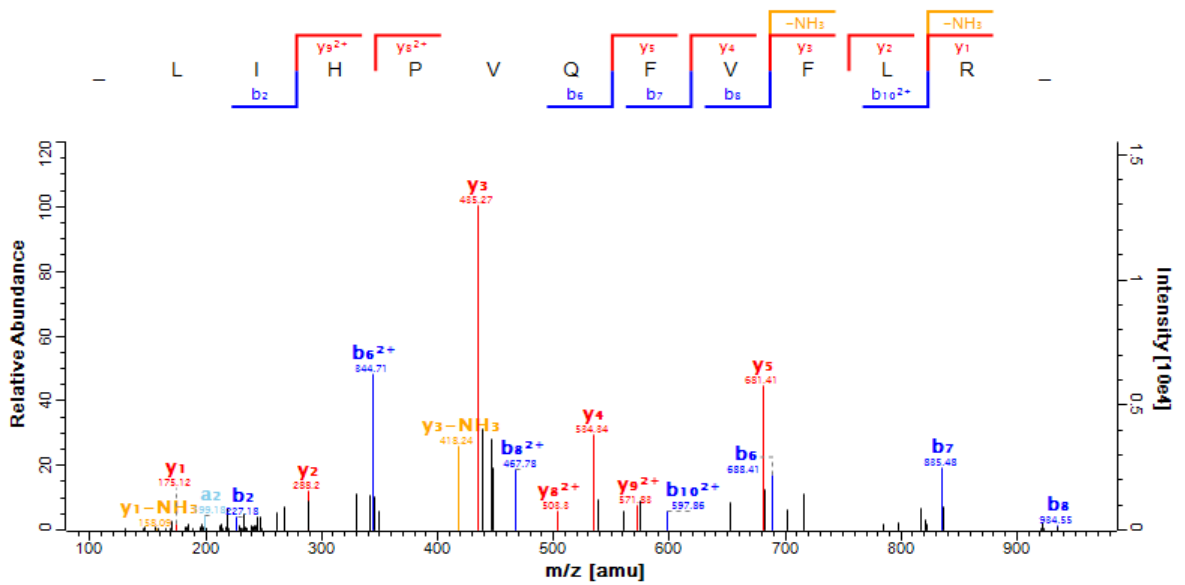
Protein Group ID: 3567
Protein Accession Numbers: Q2T9J0; Q2T9J0-2
Gene Names: TYSND1
Peptide Sequence: SPGLVLCHGGIFVPFLR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 112.02
Best Match Posterior Error Probability: 9.94E-05
Best Match Spectrum:

Scan number 78609 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** TYSND1



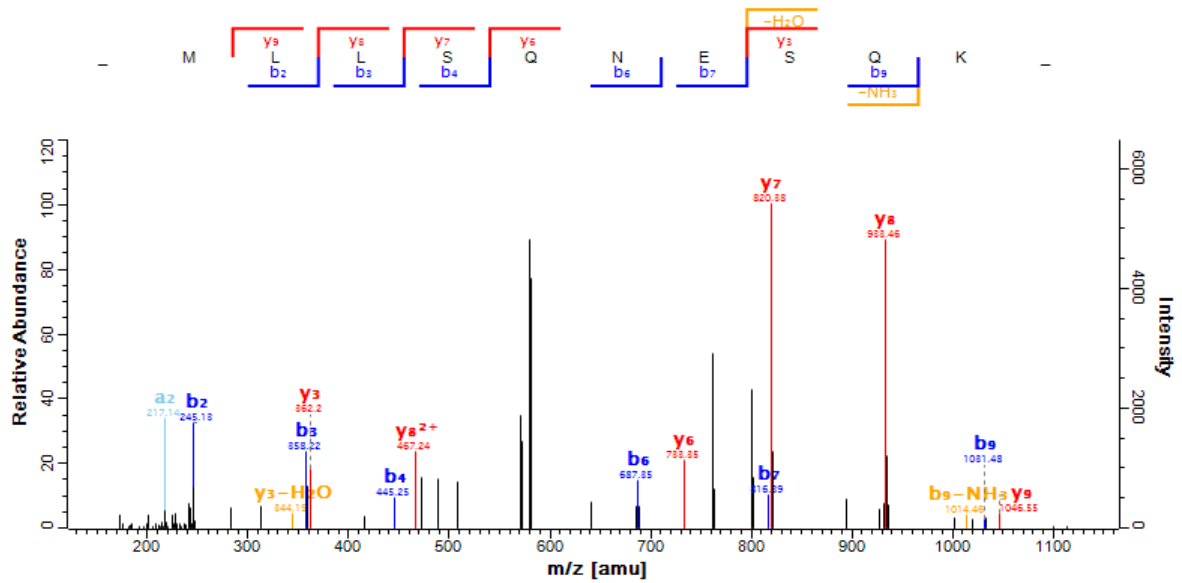
Protein Group ID: 3568
Protein Accession Numbers: Q2TAA5
Gene Names: ALG11
Peptide Sequence: LIHPVQFVFLR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 88.495
Best Match Posterior Error Probability: 0.001634
Best Match Spectrum:

Scan number 63728 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ALG11



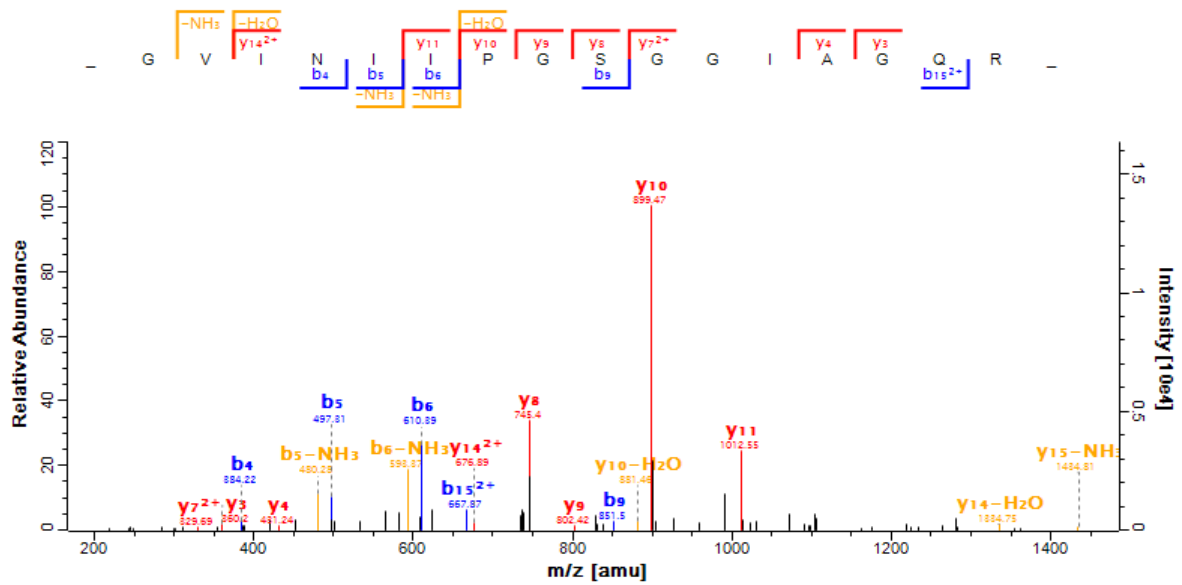
Protein Group ID: 3573
Protein Accession Numbers: Q32NC0
Gene Names: C18orf21
Peptide Sequence: MLLSQNESQK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 89.171
Best Match Posterior Error Probability: 0.0020853
Best Match Spectrum:

Scan number	14054	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	C18orf21



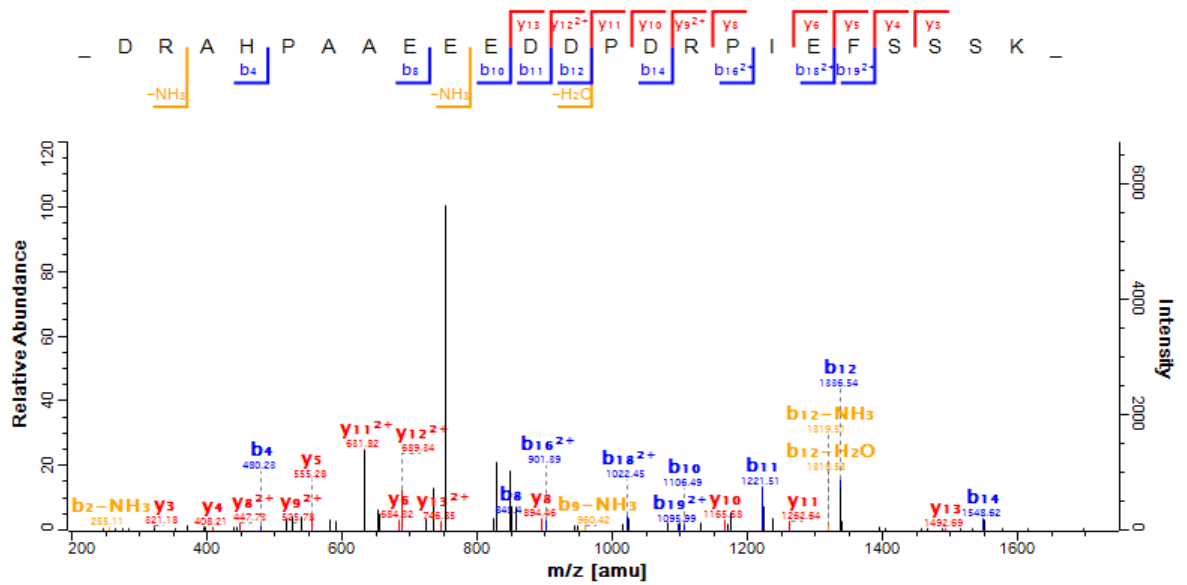
Protein Group ID: 3579
Protein Accession Numbers: Q3SY69
Gene Names: ALDH1L2
Peptide Sequence: GVINIIPGSGGIAGQR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 80.534
Best Match Posterior Error Probability: 0.0019411
Best Match Spectrum:

Scan number 51769 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ALDH1L2



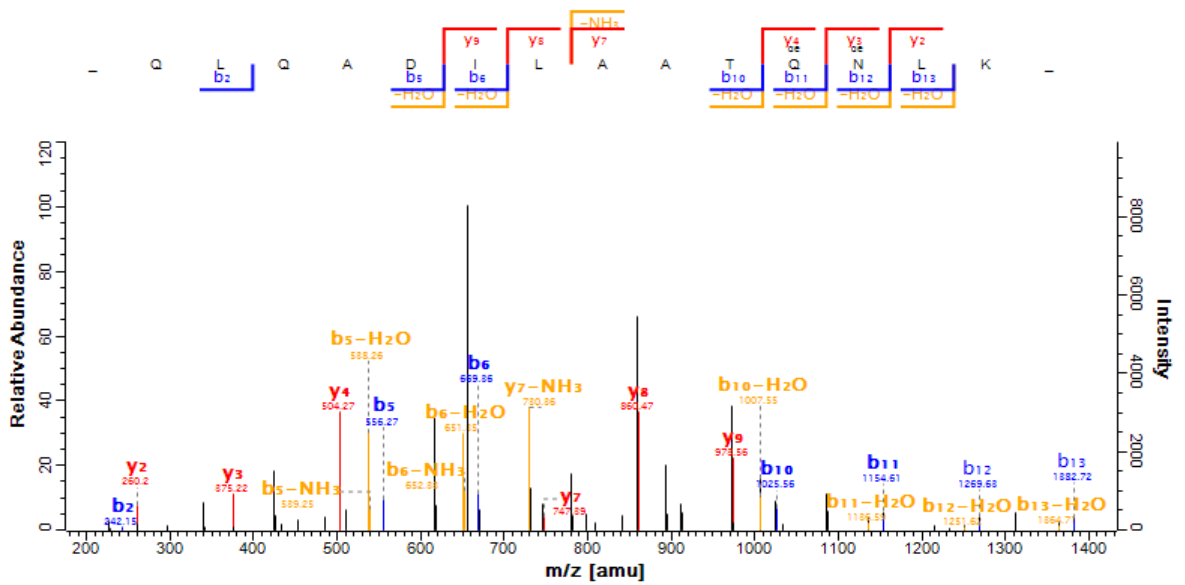
Protein Group ID: 3587
Protein Accession Numbers: Q4G0I0
Gene Names: CCSMST1
Peptide Sequence: DRAHPAAEEEDDPDRPIEFSSSK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 86.357
Best Match Posterior Error Probability: 0.0005932
Best Match Spectrum:

Scan number 22218 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CCSMST1



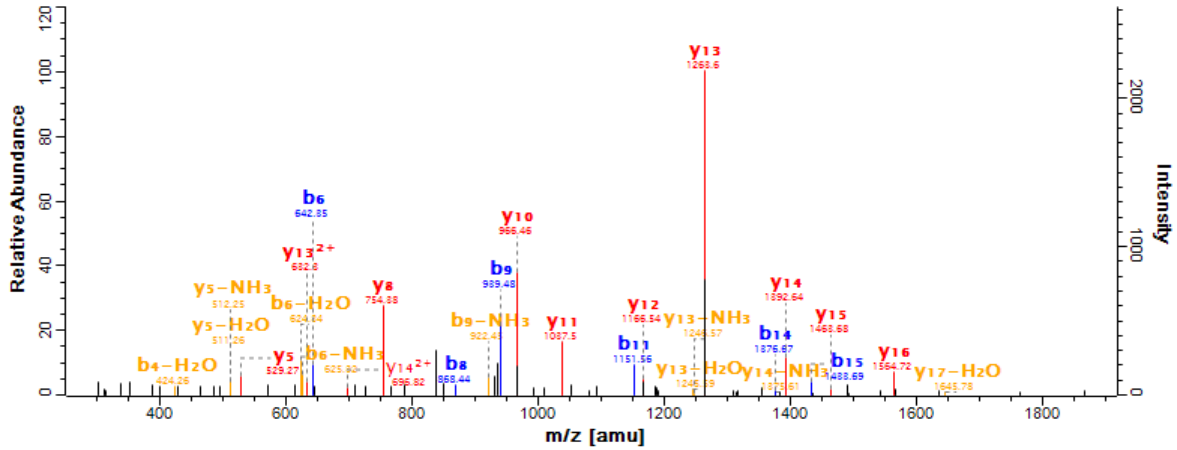
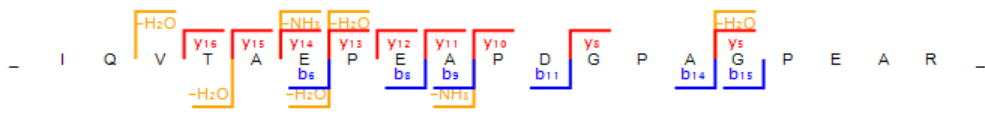
Protein Group ID: 3596
Protein Accession Numbers: Q4V9L6
Gene Names: TMEM119
Peptide Sequence: QLQADILAATQNLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 116.19
Best Match Posterior Error Probability: 0.009967
Best Match Spectrum:

Scan number 88035 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** TMEM119



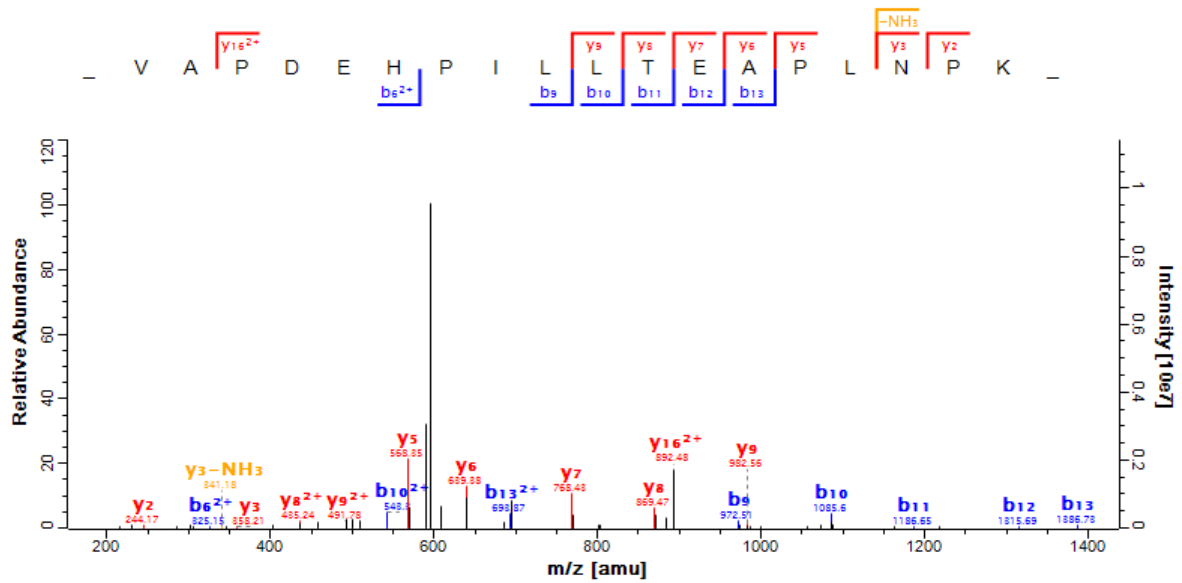
Protein Group ID: 3608
Protein Accession Numbers: Q53LP3
Gene Names: SOWAHC
Peptide Sequence: IQVTAEPEAPDGPAGPEAR
Total Number of Spectra: 7
Number of Replicates (out of 8): 4
Best Match Score: 116.6
Best Match Posterior Error Probability: 2.22E-05
Best Match Spectrum:

Scan number 29832 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** SOWAHC



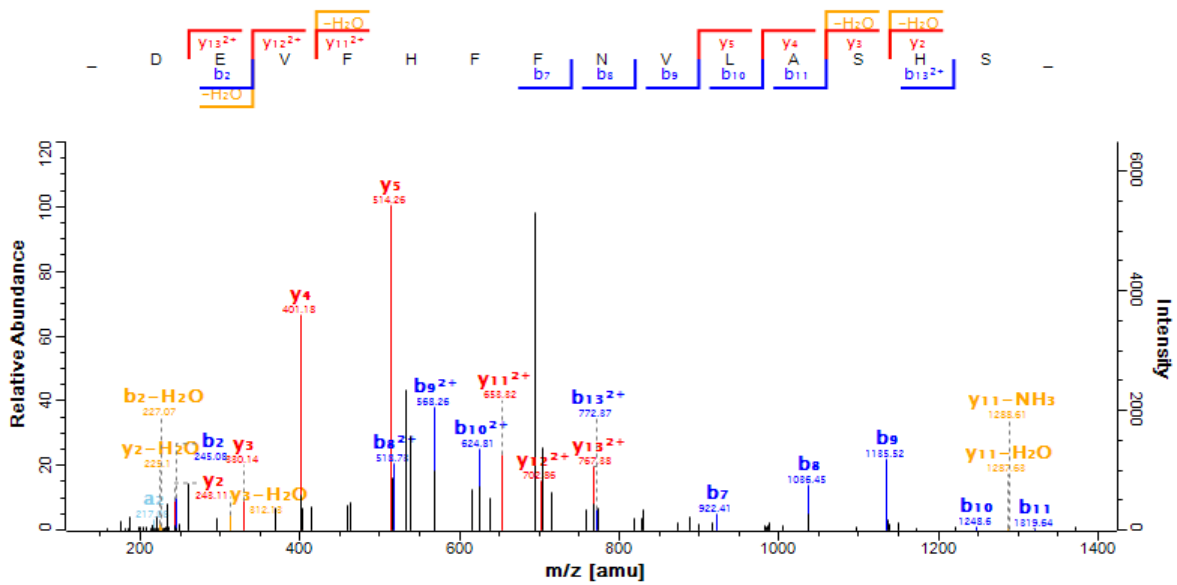
Protein Group ID: 3612
Protein Accession Numbers: Q562R1
Gene Names: ACTBL2
Peptide Sequence: VAPDEHPILTLTETAPLNPK
Total Number of Spectra: 4
Number of Replicates (out of 8): 3
Best Match Score: 93.51
Best Match Posterior Error Probability: 0.00029775
Best Match Spectrum:

Scan number 44473 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ACTBL2



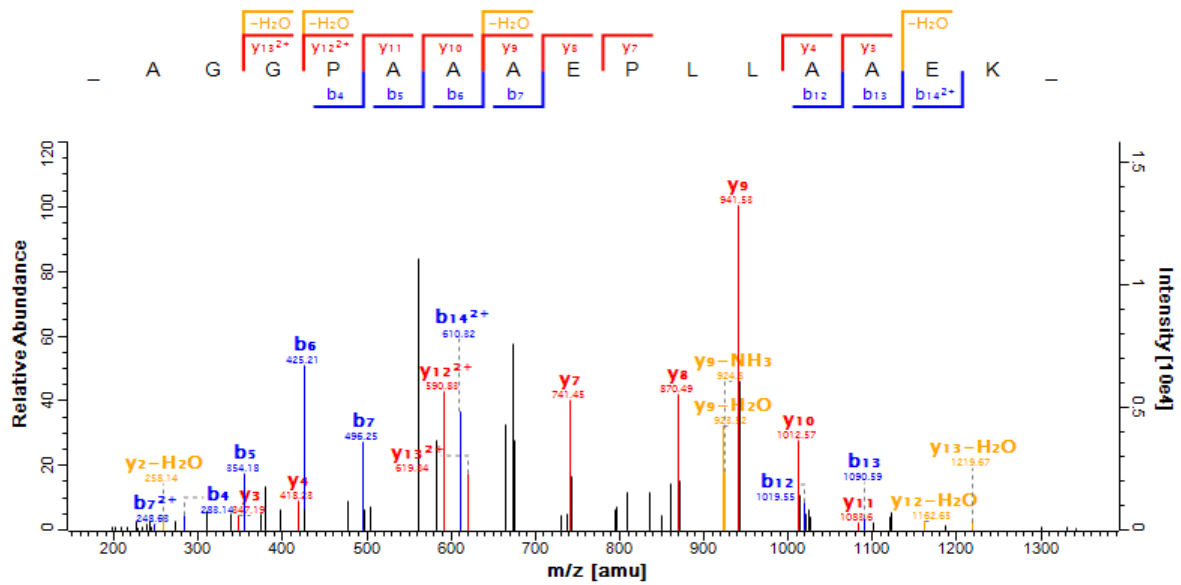
Protein Group ID: 3613
Protein Accession Numbers: Q56P03
Gene Names: EAPP
Peptide Sequence: DEVFHFFNVLASHS
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 101.6
Best Match Posterior Error Probability: 0.00030903
Best Match Spectrum:

Scan number 75027 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** EAPP



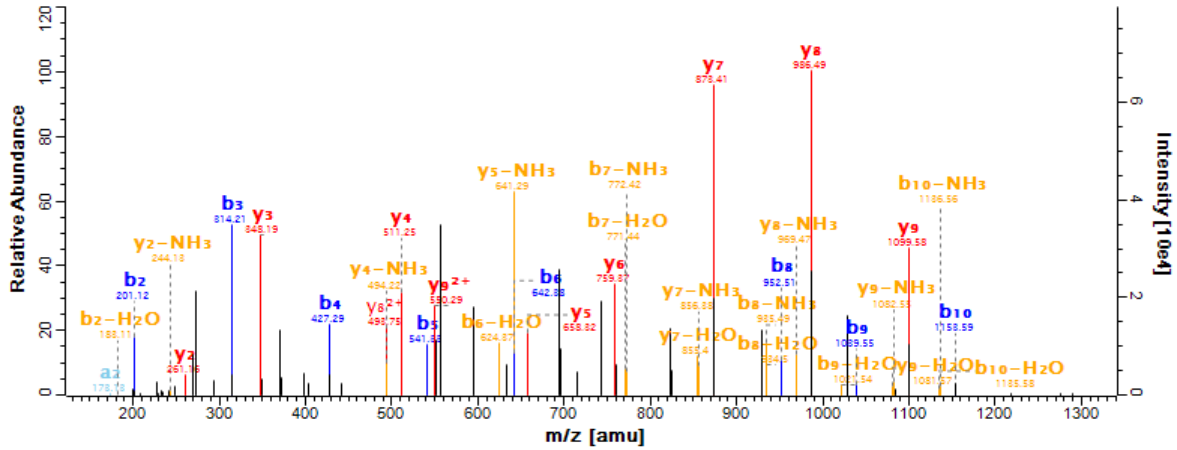
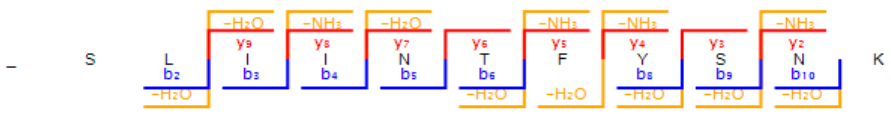
Protein Group ID: 3615
Protein Accession Numbers: Q587I9
Gene Names: SFT2D3
Peptide Sequence: AGGPAAAEPLLAELLAELAEK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 95.264
Best Match Posterior Error Probability: 0.00045926
Best Match Spectrum:

Scan number 34862 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** SFT2D3



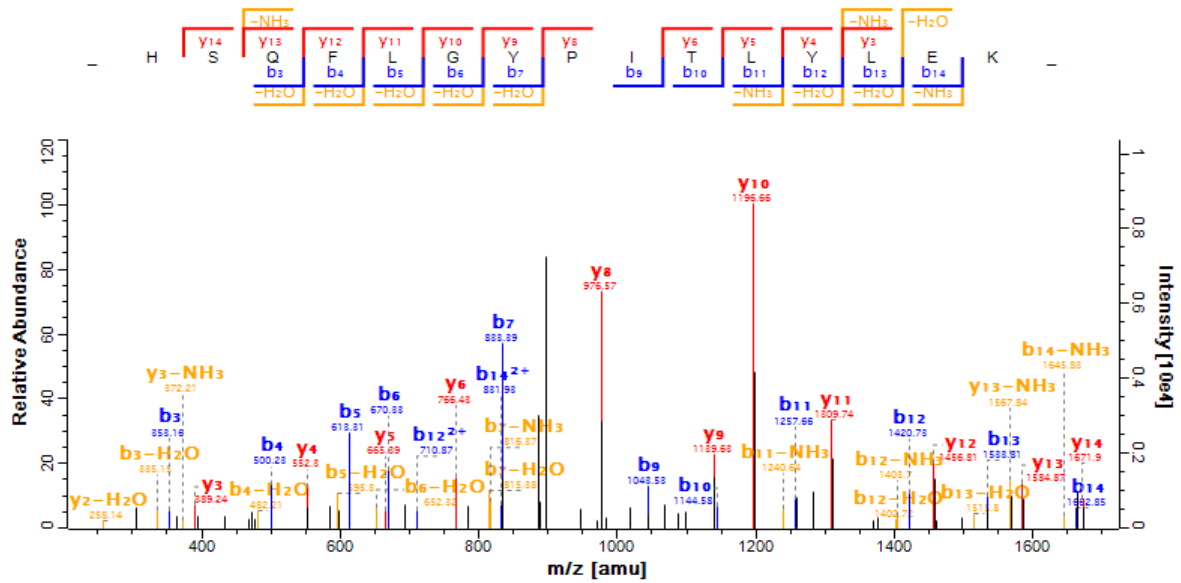
Protein Group ID: 3616
Protein Accession Numbers: Q58FF6
Gene Names: HSP90AB4P
Peptide Sequence: SLINTFYSNK
Total Number of Spectra: 16
Number of Replicates (out of 8): 8
Best Match Score: 234.3
Best Match Posterior Error Probability: 1.18E-40
Best Match Spectrum:

Scan number 49181 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** HSP90AB4P



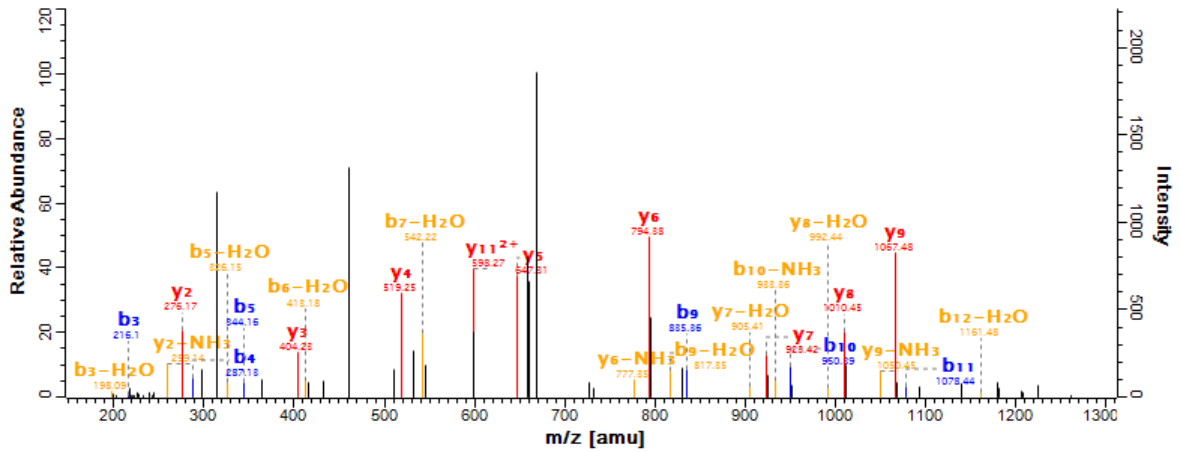
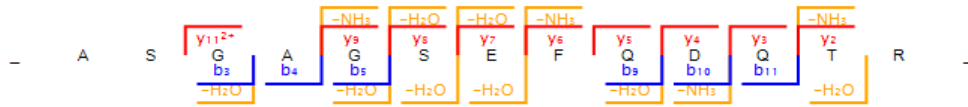
Protein Group ID: 3617
Protein Accession Numbers: Q58FF8
Gene Names: HSP90AB2P
Peptide Sequence: HSQFLGYPITLYLEK
Total Number of Spectra: 19
Number of Replicates (out of 8): 8
Best Match Score: 216.71
Best Match Posterior Error Probability: 2.63E-48
Best Match Spectrum:

Scan number 67895 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** HSP90AB2P



Protein Group ID: 3619
Protein Accession Numbers: Q5C9Z4
Gene Names: NOM1
Peptide Sequence: ASGAGSEFQDQTR
Total Number of Spectra: 8
Number of Replicates (out of 8): 5
Best Match Score: 121.56
Best Match Posterior Error Probability: 0.00011536
Best Match Spectrum:

Scan number 9504 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** NOM1



Protein Group ID: 3624

Protein Accession Numbers: Q8N8Z6; Q5H993

Gene Names: DCBLD1

Peptide Sequence: HSLSSGGFSPVAGVGAQDGDYQRPHSAQPADR

Total Number of Spectra: 1

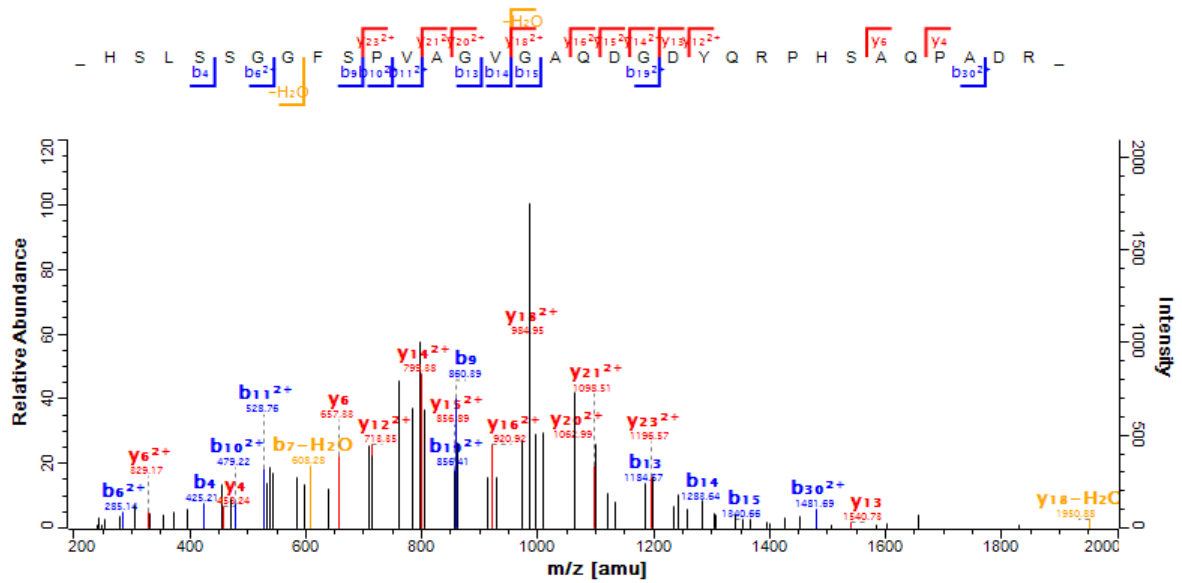
Number of Replicates (out of 8): 1

Best Match Score: 66.282

Best Match Posterior Error Probability: 9.35E-05

Best Match Spectrum:

Scan number 31162 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** DCBLD1



Protein Group ID: 3625

Protein Accession Numbers: Q5H9L2; Q6IPX3; Q969E4; Q6IPX3-2

Gene Names: TCEAL5;TCEAL6;TCEAL3

Peptide Sequence: DSQEDLQER

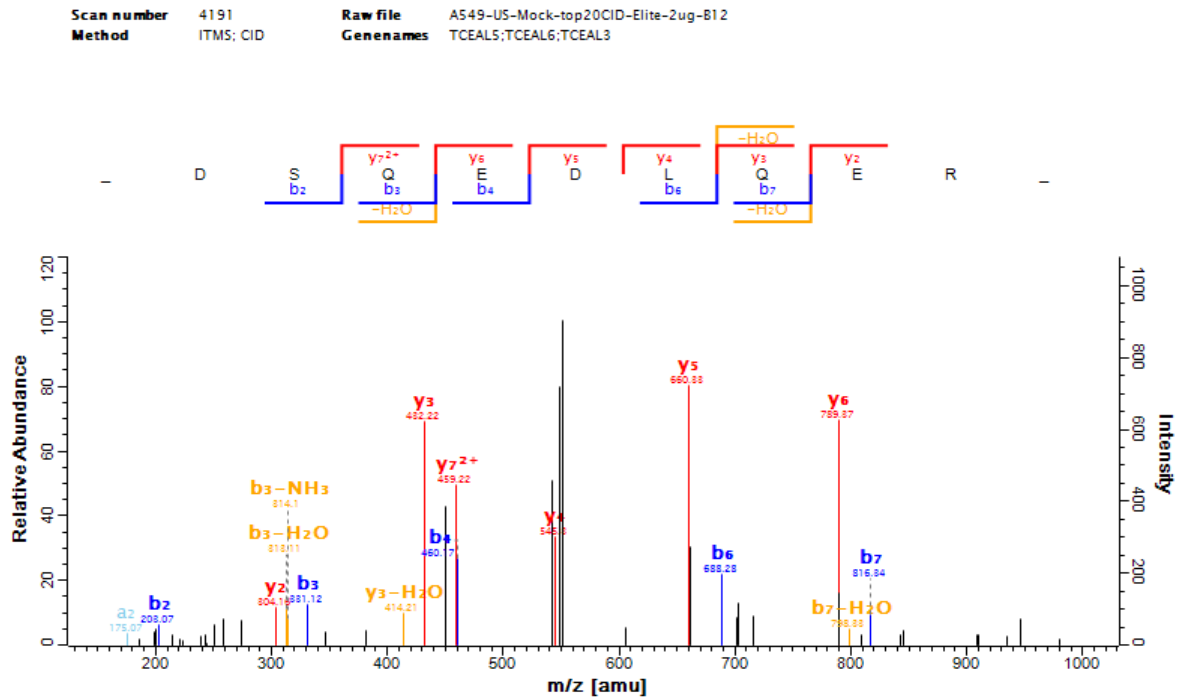
Total Number of Spectra: 2

Number of Replicates (out of 8): 2

Best Match Score: 93.096

Best Match Posterior Error Probability: 0.003006

Best Match Spectrum:



Protein Group ID: 3627

Protein Accession Numbers: Q5HYI7; Q5HYI7-4; Q5HYI7-2

Gene Names: MTX3

Peptide Sequence: GDVPILTTEDDMVSQPAK

Total Number of Spectra: 2

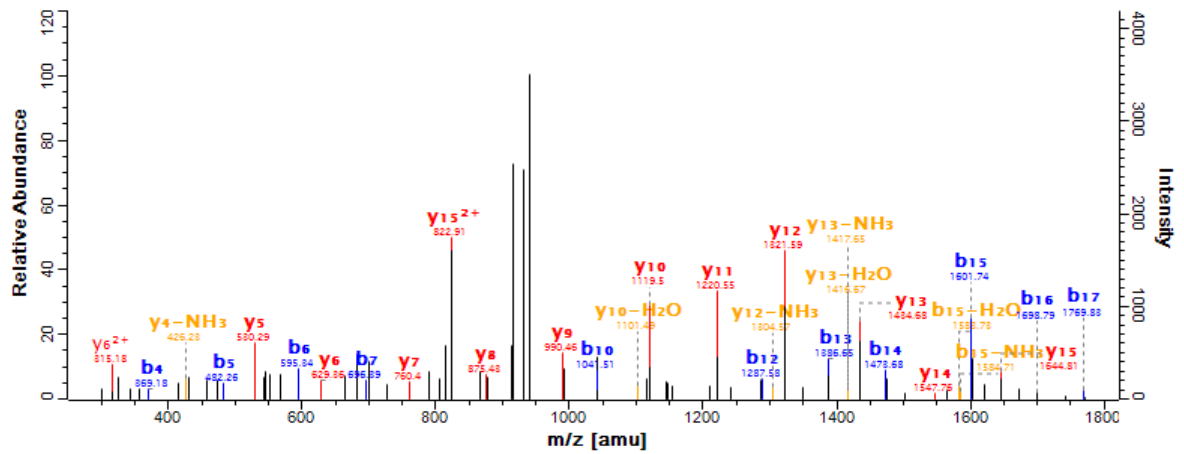
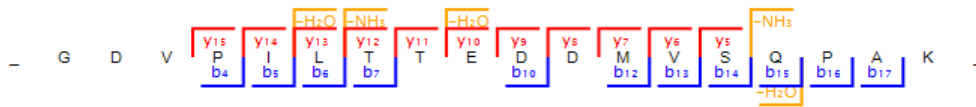
Number of Replicates (out of 8): 2

Best Match Score: 136.66

Best Match Posterior Error Probability: 2.47E-05

Best Match Spectrum:

Scan number 48209 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MTX3



Protein Group ID: 3628

Protein Accession Numbers: Q5HYK7; Q5HYK7-2; Q5HYK7-3

Gene Names: SH3D19

Peptide Sequence: VFEGQTNIETSLGPK

Total Number of Spectra: 1

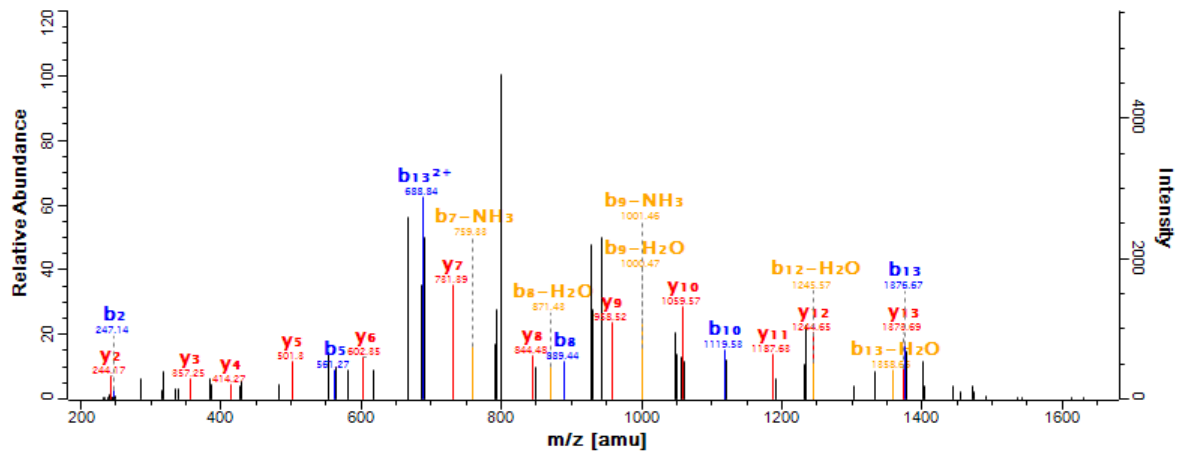
Number of Replicates (out of 8): 1

Best Match Score: 92.773

Best Match Posterior Error Probability: 0.00062991

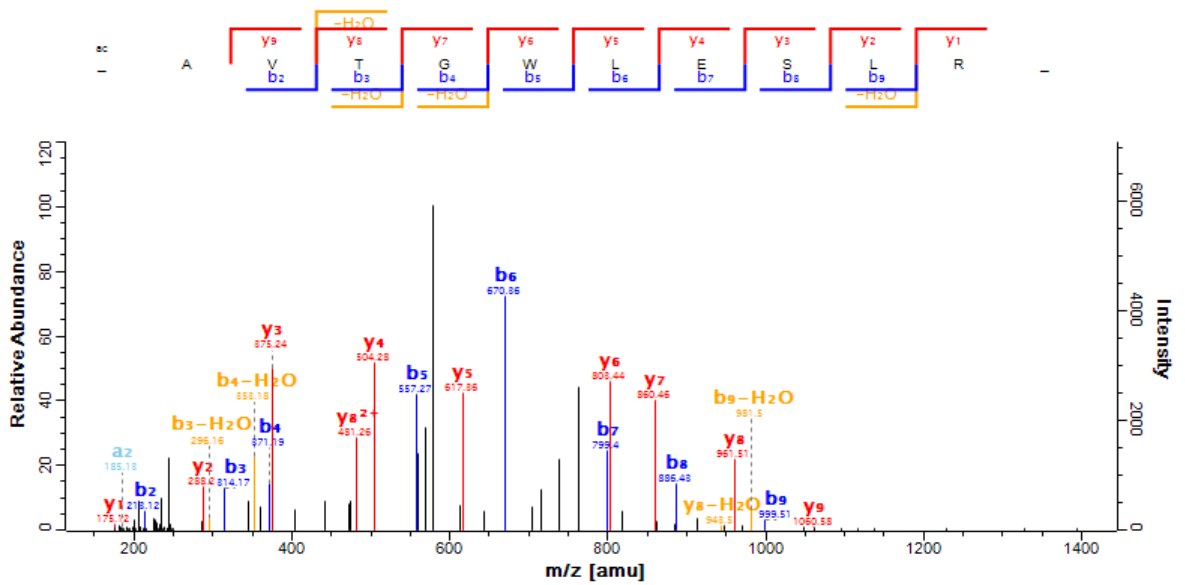
Best Match Spectrum:

Scan number	36852	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	SH3D19



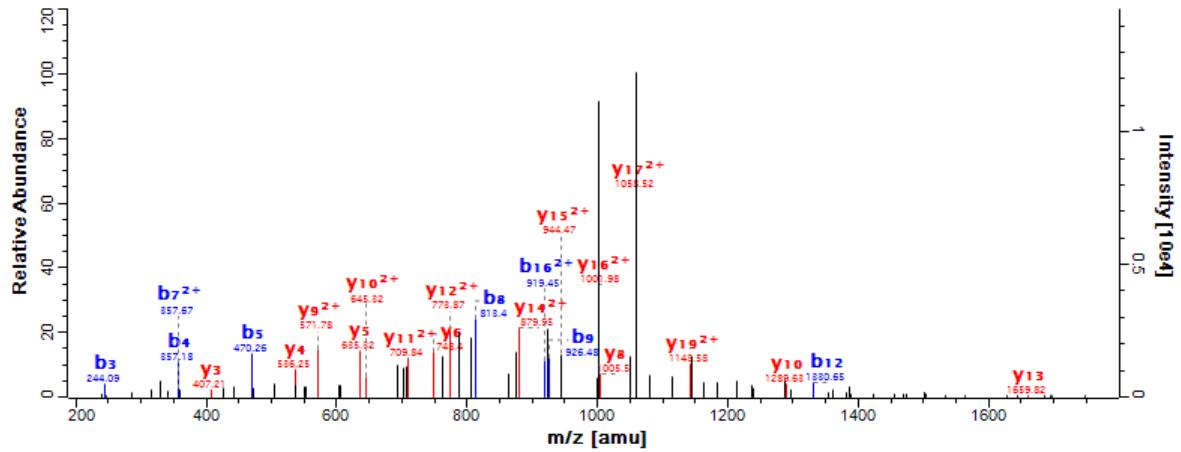
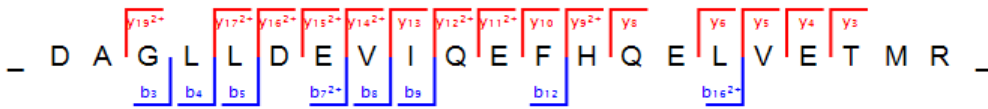
Protein Group ID: 3631
Protein Accession Numbers: Q9BVM2; Q5JQQ4
Gene Names: DPCD;RP11-529I10.4
Peptide Sequence: AVTGWLESLR
Total Number of Spectra: 7
Number of Replicates (out of 8): 7
Best Match Score: 175.15
Best Match Posterior Error Probability: 8.00E-06
Best Match Spectrum:

Scan number 84256 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** DPCD;RP11-529I10.4



Protein Group ID: 3637
Protein Accession Numbers: Q9UKD1; Q5JTV1
Gene Names: GMEB2
Peptide Sequence: DAGLLDEVIQEFHQELVETMR
Total Number of Spectra: 5
Number of Replicates (out of 8): 4
Best Match Score: 110.74
Best Match Posterior Error Probability: 3.42E-06
Best Match Spectrum:

Scan number 93122 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** GMEB2



Protein Group ID: 3646

Protein Accession Numbers: Q5MIZ7; Q5MIZ7-2; Q5MIZ7-3

Gene Names: SMEK2

Peptide Sequence: LGILPALEIVMGMGMDDDLQVR

Total Number of Spectra: 9

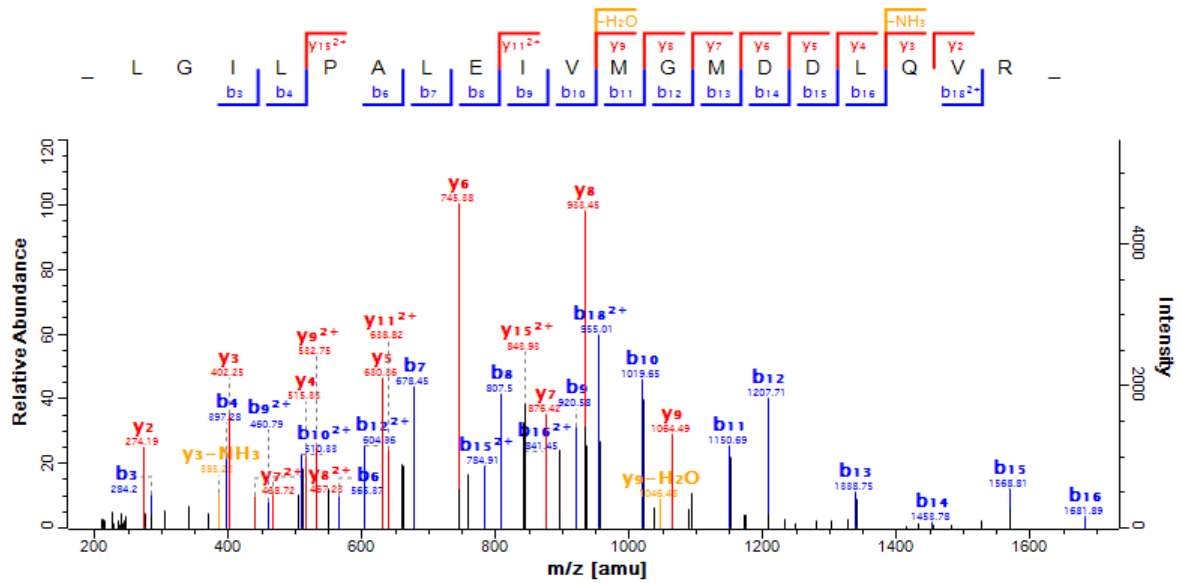
Number of Replicates (out of 8): 8

Best Match Score: 206.43

Best Match Posterior Error Probability: 1.90E-42

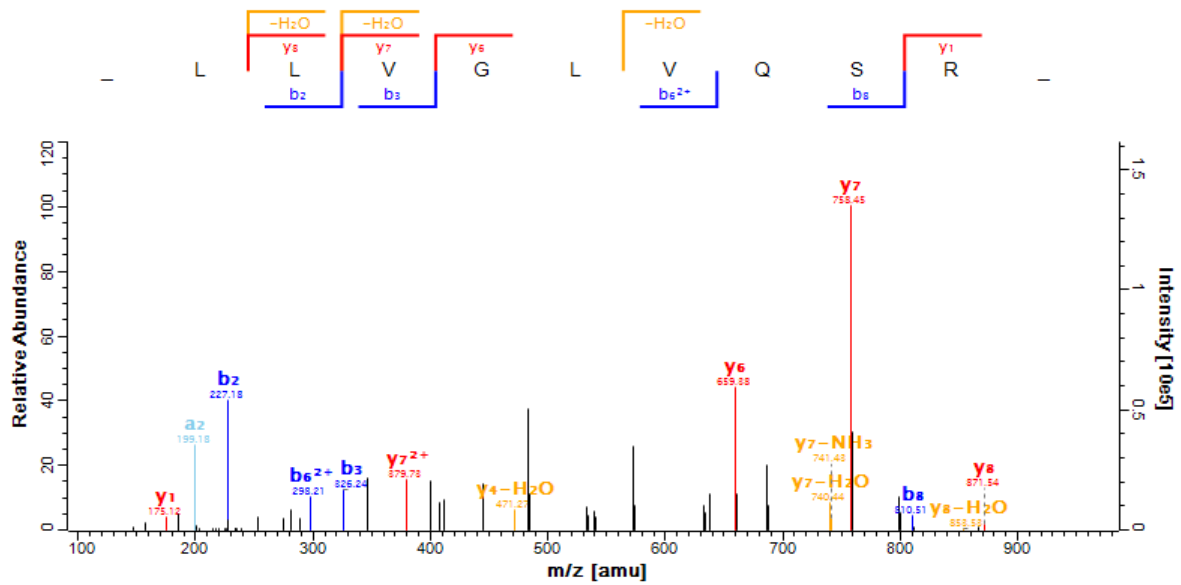
Best Match Spectrum:

Scan number 94767 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** SMEK2



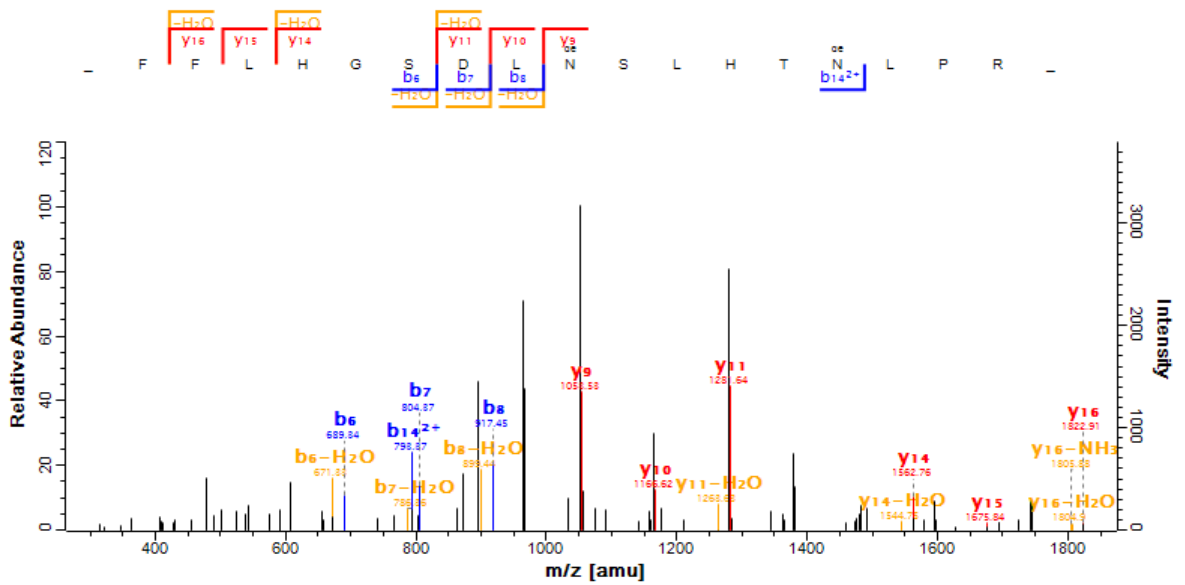
Protein Group ID: 3647
Protein Accession Numbers: Q5MY95; Q5MY95-2
Gene Names: ENTPD8
Peptide Sequence: LLVGLVQSR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 90.657
Best Match Posterior Error Probability: 0.0034895
Best Match Spectrum:

Scan number 36733 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ENTPD8



Protein Group ID: 3651
Protein Accession Numbers: Q9BTX7; Q5QPC2
Gene Names: TTPAL
Peptide Sequence: FFLHGSDLNSLHTNLPR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 88.561
Best Match Posterior Error Probability: 0.012905
Best Match Spectrum:

Scan number 84095 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TTPAL



Protein Group ID: 3652

Protein Accession Numbers: Q5QPG6; Q9BUV8; Q9BUV8-2; Q9BUV8-3; Q9BUV8-4

Gene Names: C20orf24

Peptide Sequence: RKEEPQPQLANGALK

Total Number of Spectra: 1

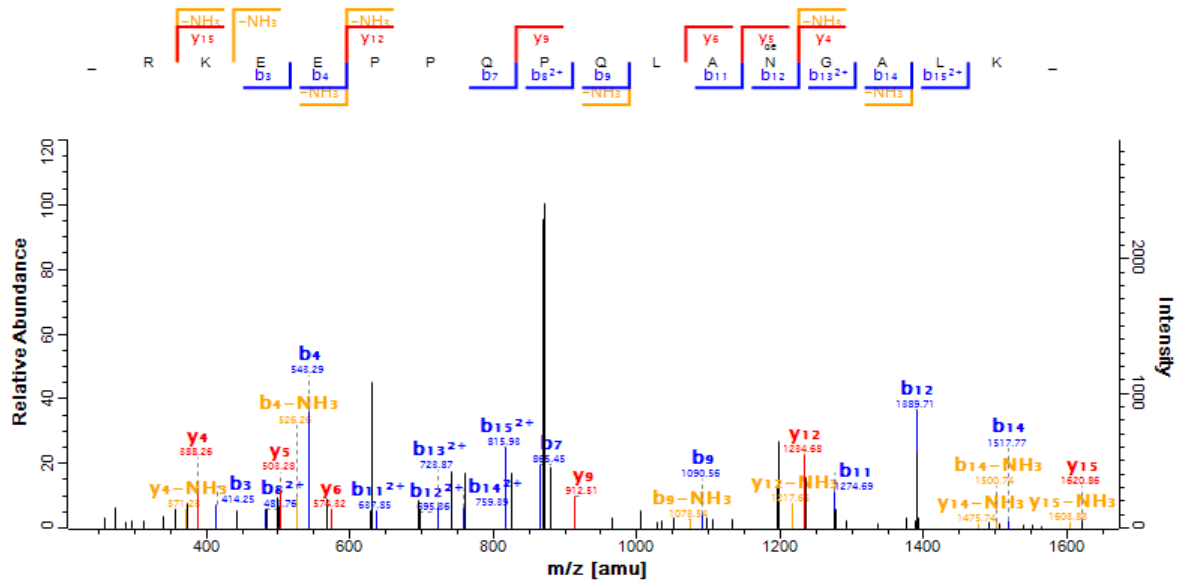
Number of Replicates (out of 8): 1

Best Match Score: 127.32

Best Match Posterior Error Probability: 0.0075267

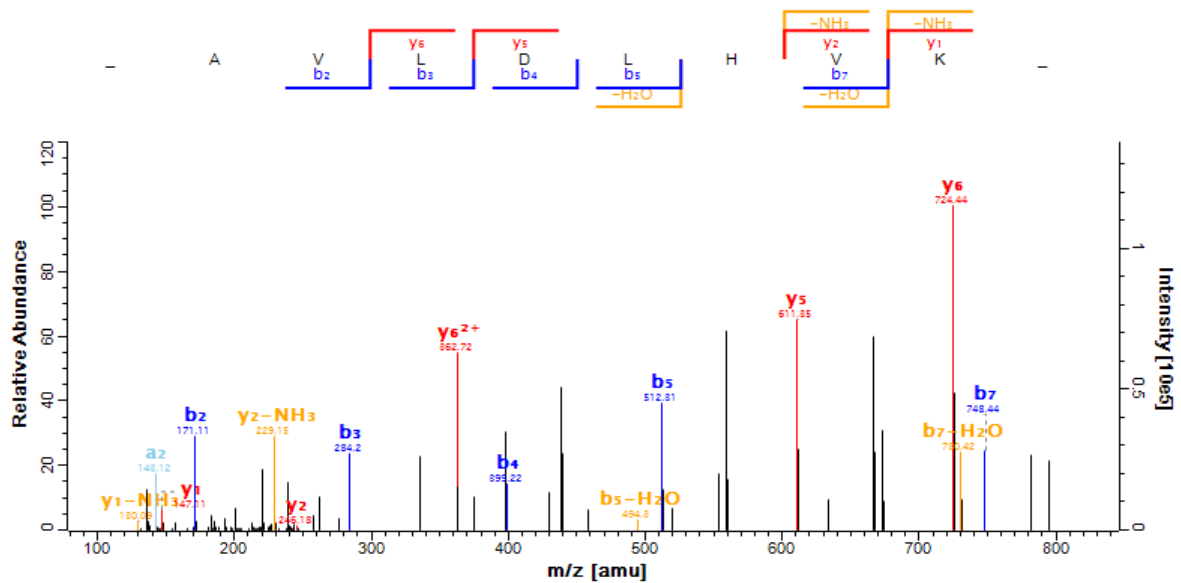
Best Match Spectrum:

Scan number 20032 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** C20orf24



Protein Group ID: 3654
Protein Accession Numbers: Q5R3K3
Gene Names: FAM26F
Peptide Sequence: AVLDLHVK
Total Number of Spectra: 8
Number of Replicates (out of 8): 8
Best Match Score: 111.82
Best Match Posterior Error Probability: 0.0027613
Best Match Spectrum:

Scan number 18293 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** FAM26F



Protein Group ID: 3655

Protein Accession Numbers: Q9HB21; Q5RGS4; Q9HB21-2

Gene Names: PLEKHA1

Peptide Sequence: TDIVGGVPIITPTQK

Total Number of Spectra: 3

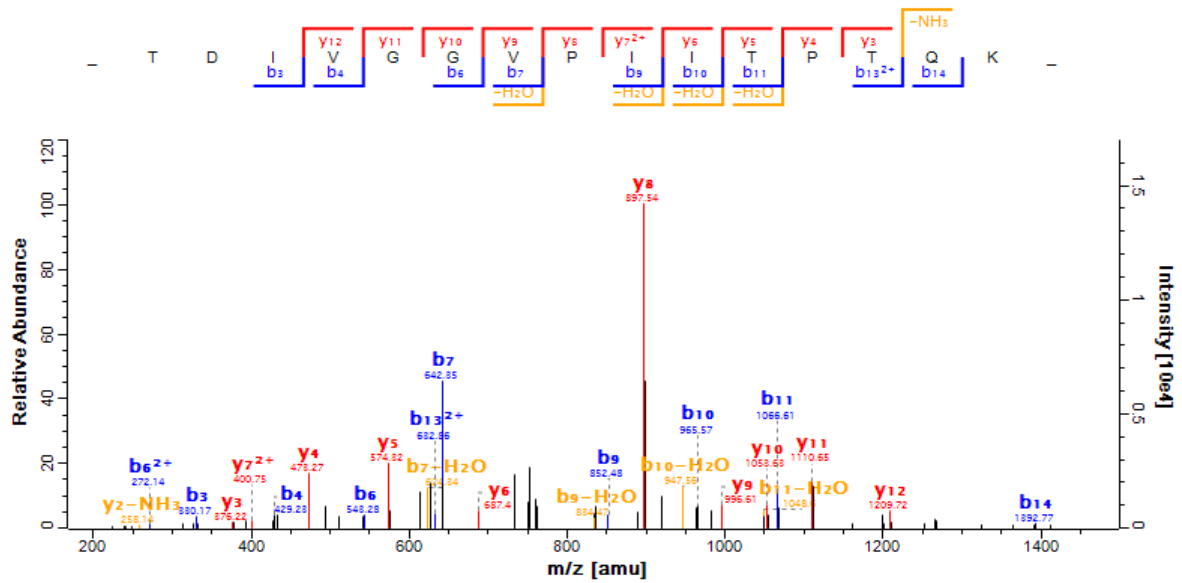
Number of Replicates (out of 8): 2

Best Match Score: 115.1

Best Match Posterior Error Probability: 9.08E-05

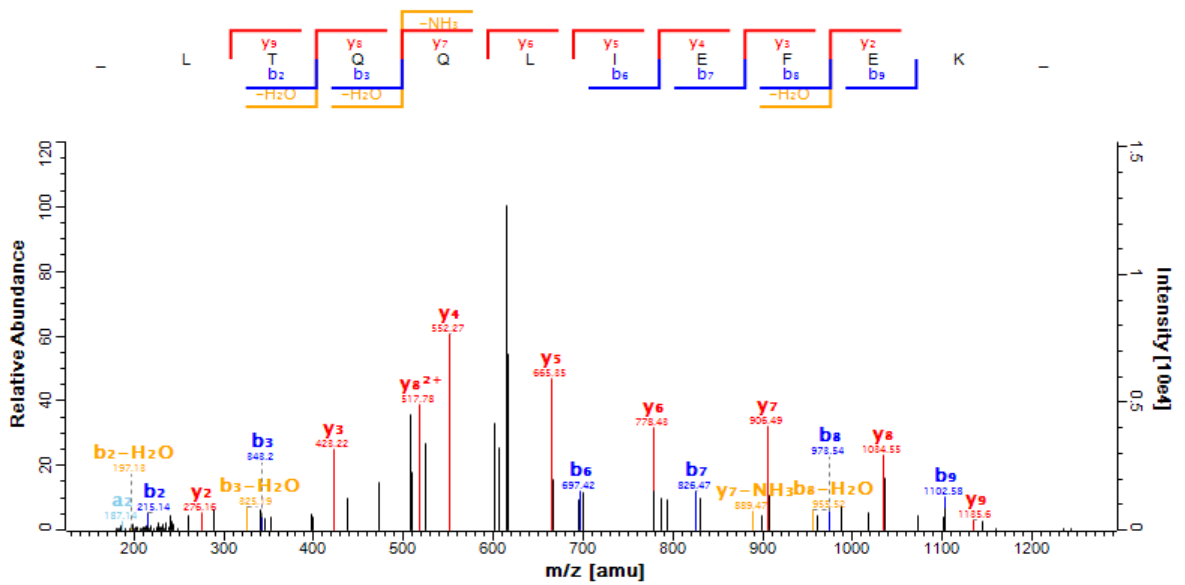
Best Match Spectrum:

Scan number 50571 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PLEKHA1



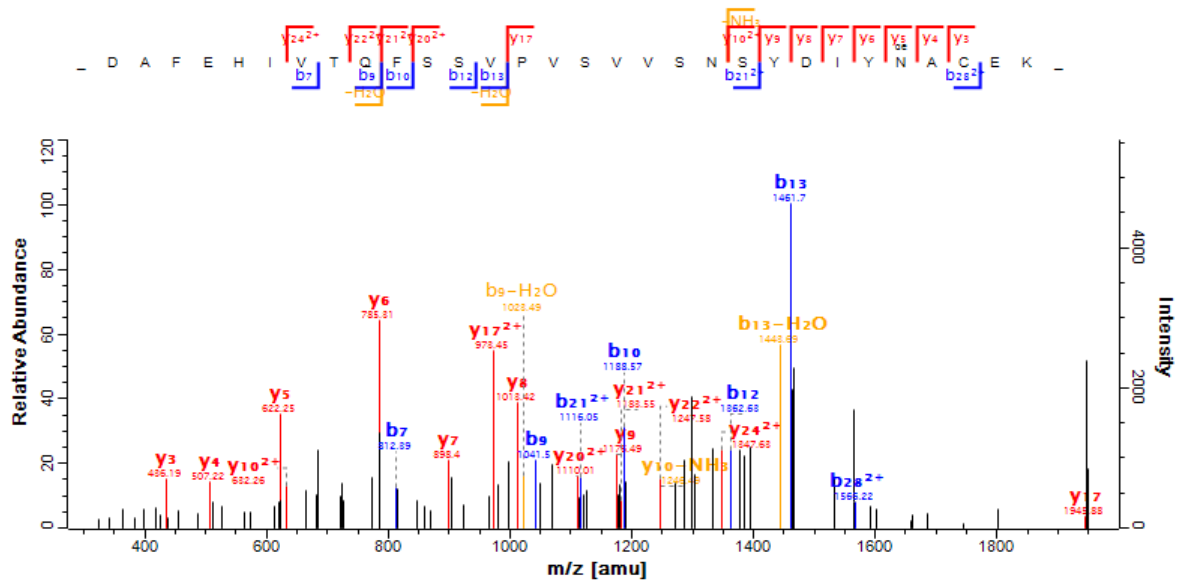
Protein Group ID: 3660
Protein Accession Numbers: Q5SVK8; Q6XZF7
Gene Names: RP11-114F7.3;DNMBP
Peptide Sequence: LTQQLIEFEK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 130.56
Best Match Posterior Error Probability: 2.73E-05
Best Match Spectrum:

Scan number 43445 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** RP11-114F7.3;DNMBP



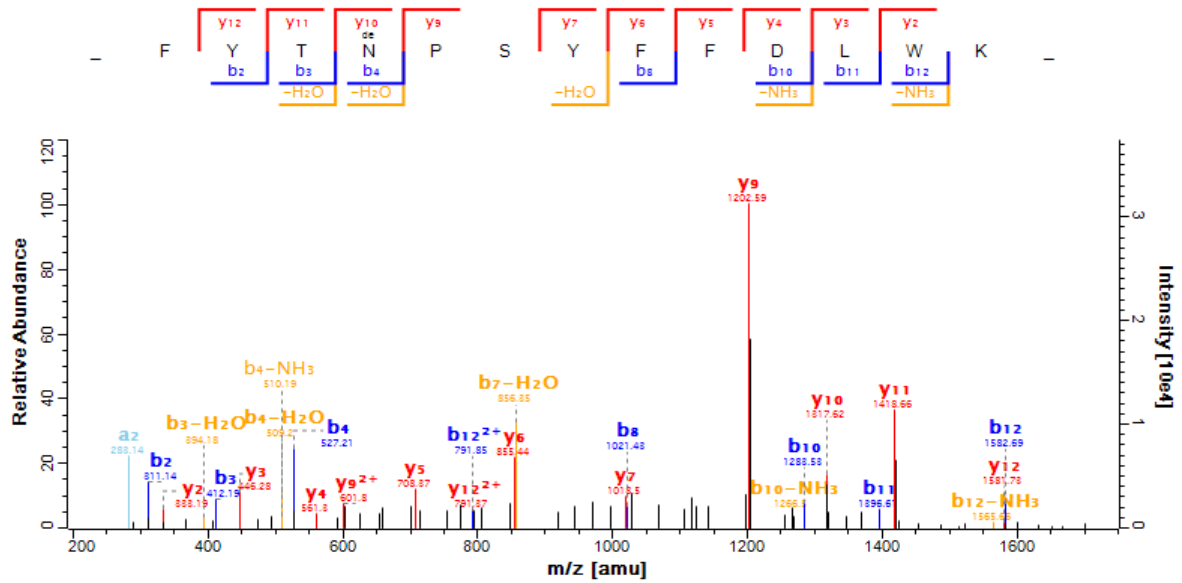
Protein Group ID: 3666
Protein Accession Numbers: Q5SYT8
Gene Names: RP11-92J19.4
Peptide Sequence: DAFEHIVTQFSSVPVSVVSN SYDIYNACEK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 71.528
Best Match Posterior Error Probability: 0.00013461
Best Match Spectrum:

Scan number 88724 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** RP11-92J19.4



Protein Group ID: 3667
Protein Accession Numbers: Q92558; Q5SZK5
Gene Names: WASF1
Peptide Sequence: FYTNPSYFFDLWK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 166.38
Best Match Posterior Error Probability: 3.00E-09
Best Match Spectrum:

Scan number 89497 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** WASF1



Protein Group ID: 3669

Protein Accession Numbers: Q9P2S5; Q5T0D5; Q5TBW1

Gene Names: WRAP73;WDR8

Peptide Sequence: MNFSEVFK

Total Number of Spectra: 3

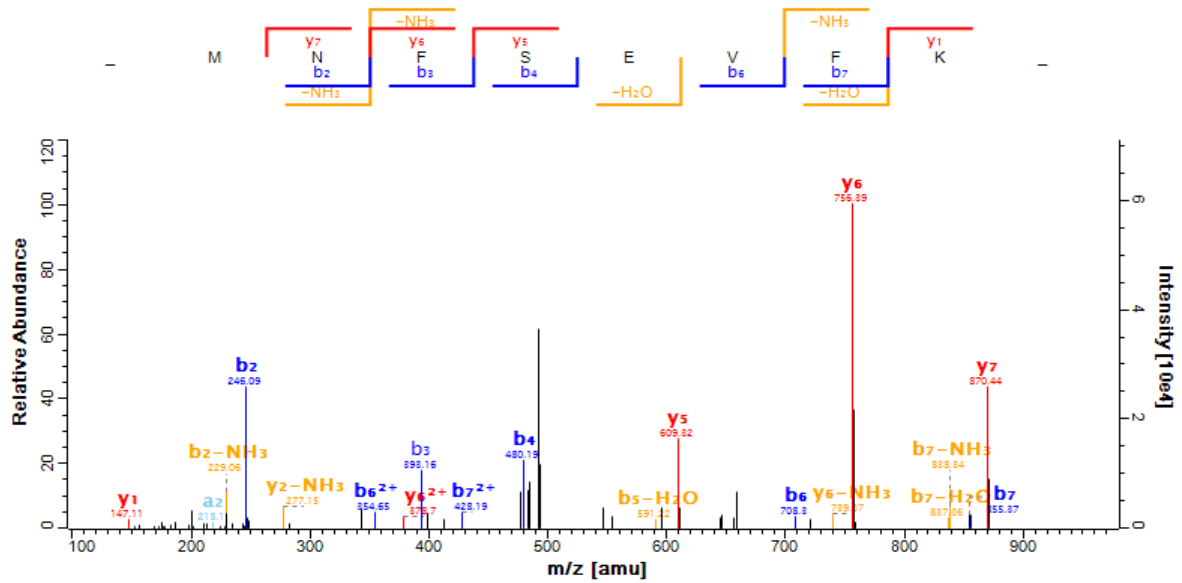
Number of Replicates (out of 8): 3

Best Match Score: 113.18

Best Match Posterior Error Probability: 0.0026419

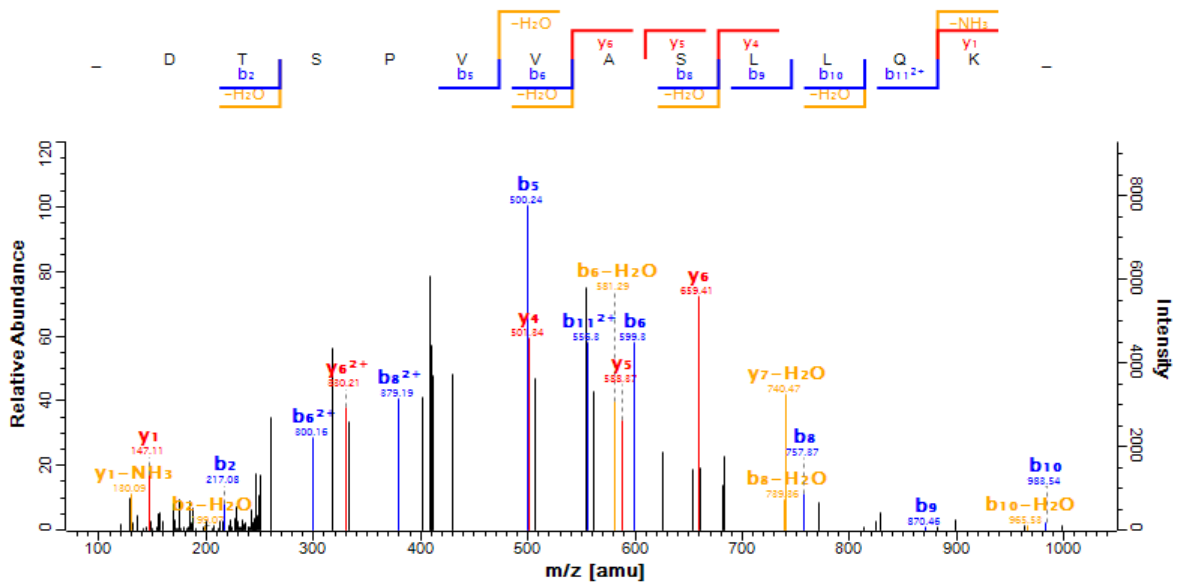
Best Match Spectrum:

Scan number 46998 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** WRAP73;WDR8



Protein Group ID: 3677
Protein Accession Numbers: Q8N5I2; Q5T370
Gene Names: ARRDC1
Peptide Sequence: DTSPVVASLLQK
Total Number of Spectra: 4
Number of Replicates (out of 8): 3
Best Match Score: 92.611
Best Match Posterior Error Probability: 0.0011691
Best Match Spectrum:

Scan number 21692 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ARRDC1



Protein Group ID: 3684

Protein Accession Numbers: Q5T6J7-2; Q5T6J7; Q5T6J7-3

Gene Names: IDNK

Peptide Sequence: NVSEIIATIMETLK

Total Number of Spectra: 1

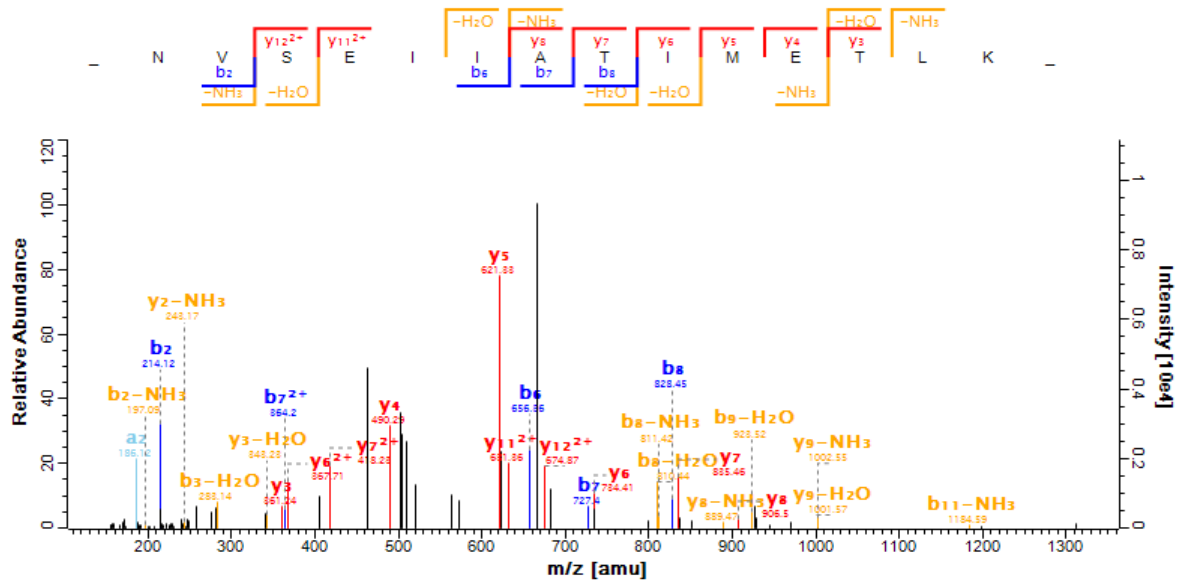
Number of Replicates (out of 8): 1

Best Match Score: 96.866

Best Match Posterior Error Probability: 0.00054379

Best Match Spectrum:

Scan number 96302 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** IDNK



Protein Group ID: 3686

Protein Accession Numbers: Q8NI60; Q8NI60-3; Q5T7A4; Q5T7A2

Gene Names: ADCK3;CABC1

Peptide Sequence: LGQMLSIQDDAFINPHLAK

Total Number of Spectra: 1

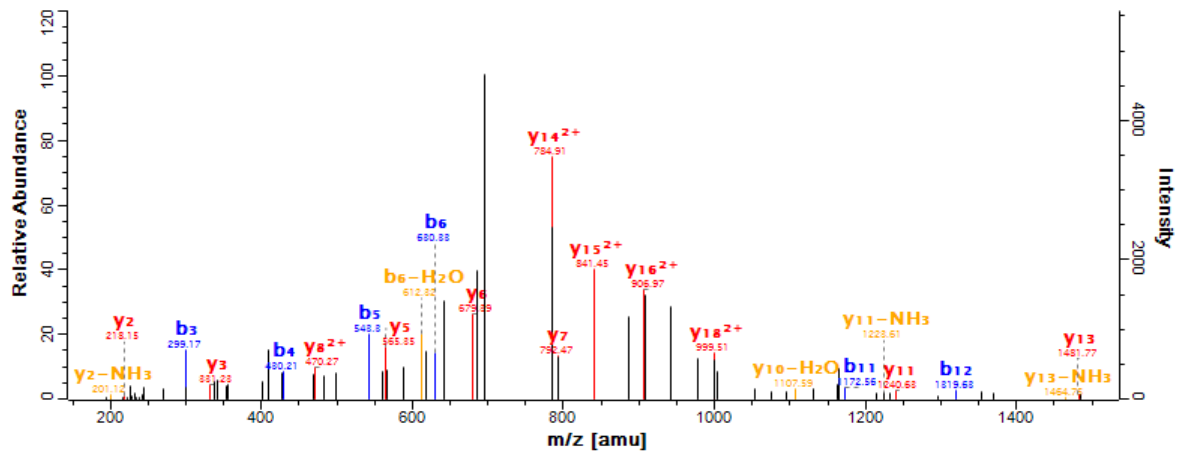
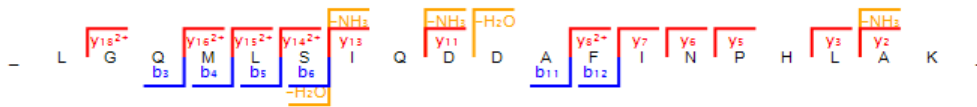
Number of Replicates (out of 8): 1

Best Match Score: 87.388

Best Match Posterior Error Probability: 0.00032391

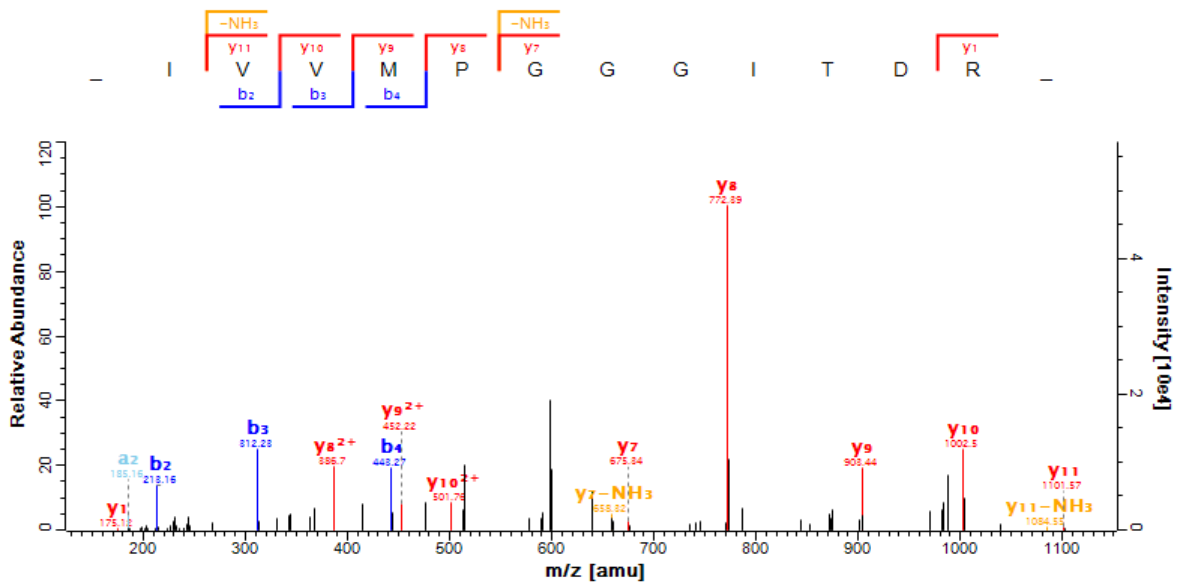
Best Match Spectrum:

Scan number	62282	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	ADCK3;CABC1



Protein Group ID: 3692
Protein Accession Numbers: Q9NTM9; Q5TCZ7
Gene Names: CUTC;RP11-483F11.3
Peptide Sequence: IVVMPGGGITDR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 89.548
Best Match Posterior Error Probability: 0.0014774
Best Match Spectrum:

Scan number 36087 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CUTC;RP11-483F11.3



Protein Group ID: 3693

Protein Accession Numbers: Q9Y2G8; Q5TDH4; Q5TDG9

Gene Names: DNAJC16

Peptide Sequence: AYEILSNEEK

Total Number of Spectra: 2

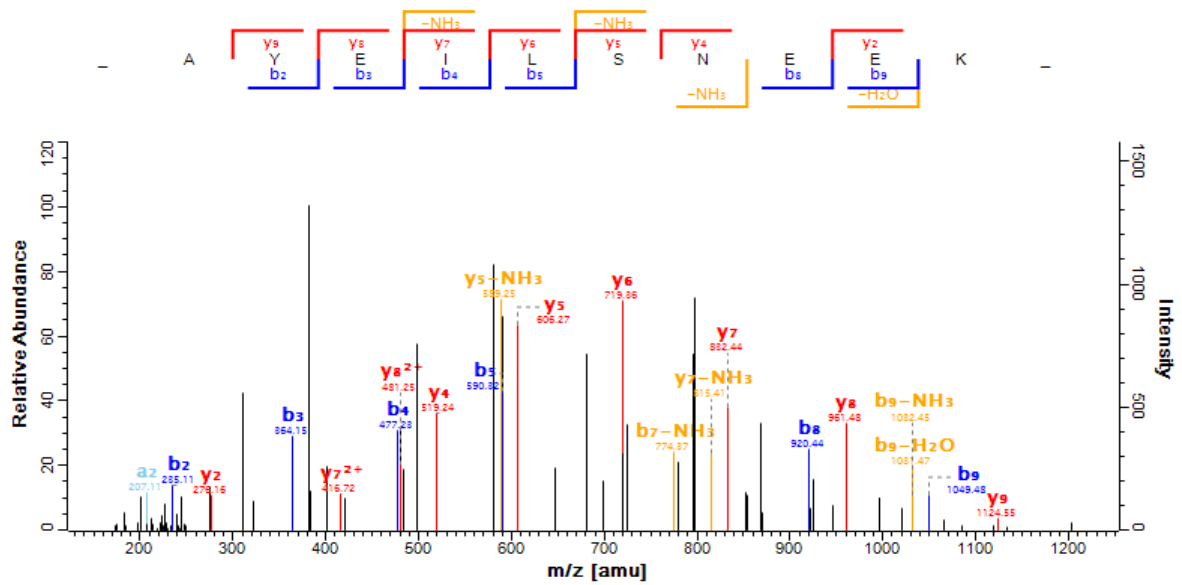
Number of Replicates (out of 8): 2

Best Match Score: 121.36

Best Match Posterior Error Probability: 9.79E-05

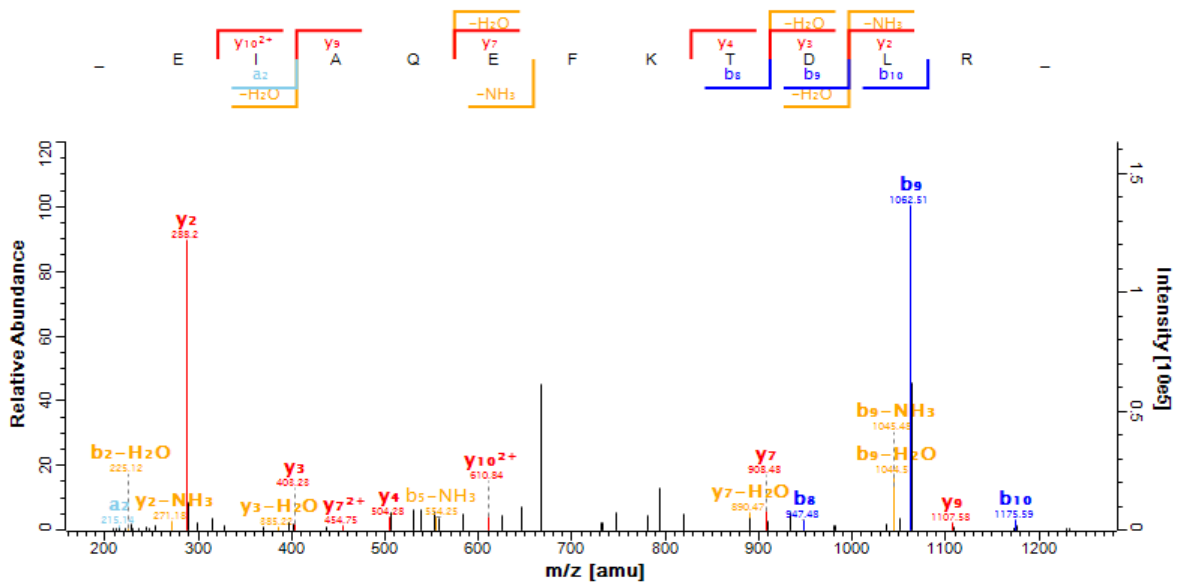
Best Match Spectrum:

Scan number 24474 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** DNAJC16



Protein Group ID: 3696
Protein Accession Numbers: Q5TEC6
Gene Names: HIST2H3PS2
Peptide Sequence: EIAQEFKTDLR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 96.113
Best Match Posterior Error Probability: 0.0038382
Best Match Spectrum:

Scan number 30852 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** HIST2H3PS2



Protein Group ID: 3700

Protein Accession Numbers: Q5TGZ0

Gene Names: MINOS1

Peptide Sequence: MWPLAFGSGMGLGMAYSNQCQHDFFQAPLYLLHGK

Total Number of Spectra: 1

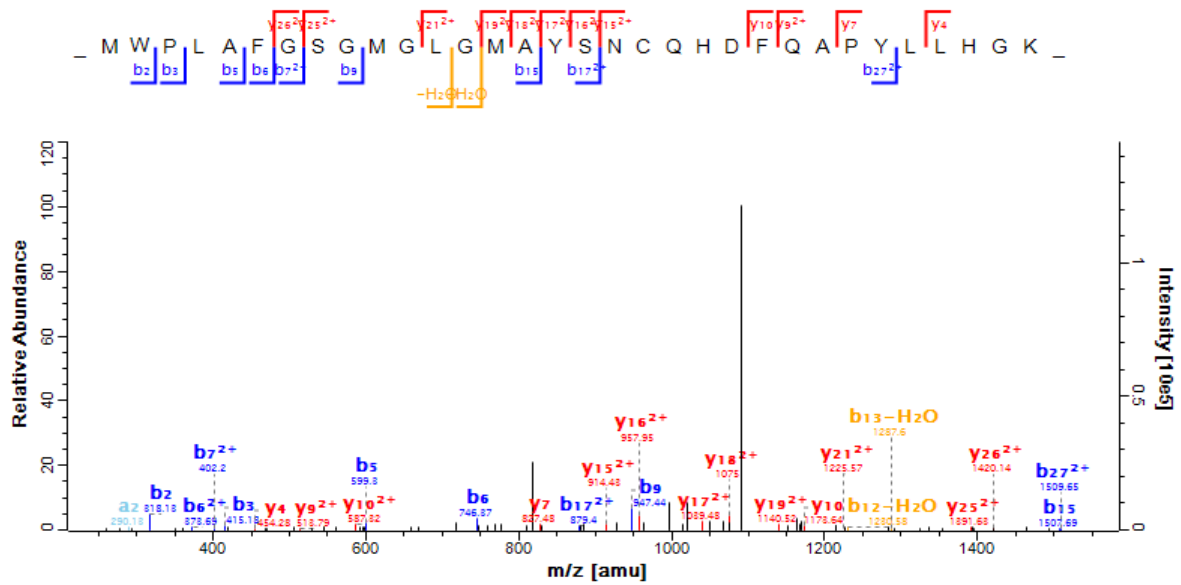
Number of Replicates (out of 8): 1

Best Match Score: 68.192

Best Match Posterior Error Probability: 1.64E-05

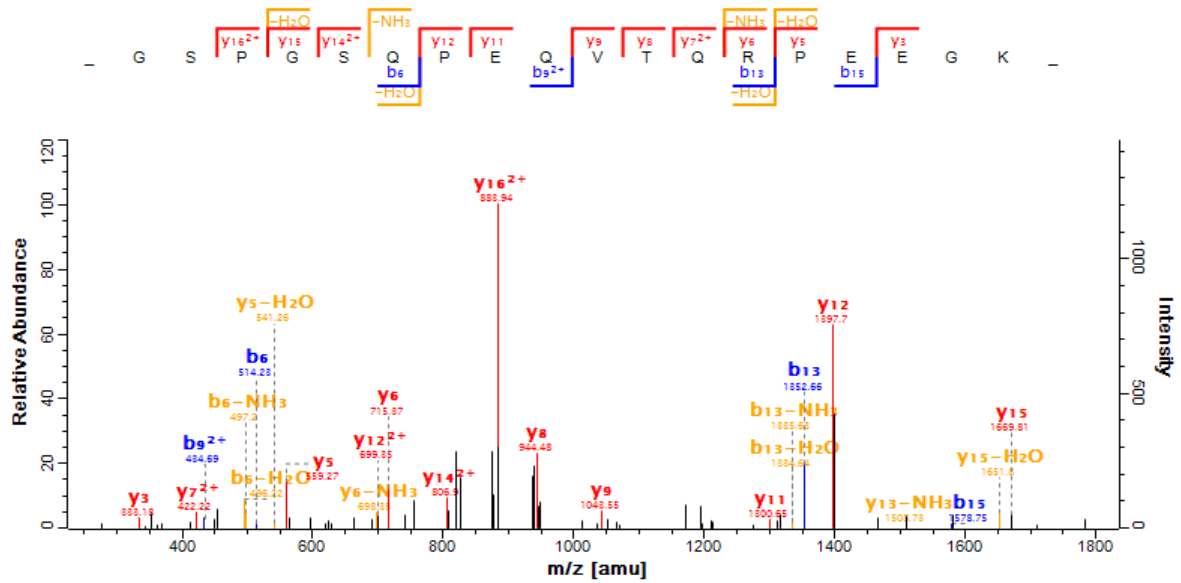
Best Match Spectrum:

Scan number 83946 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MINOS1



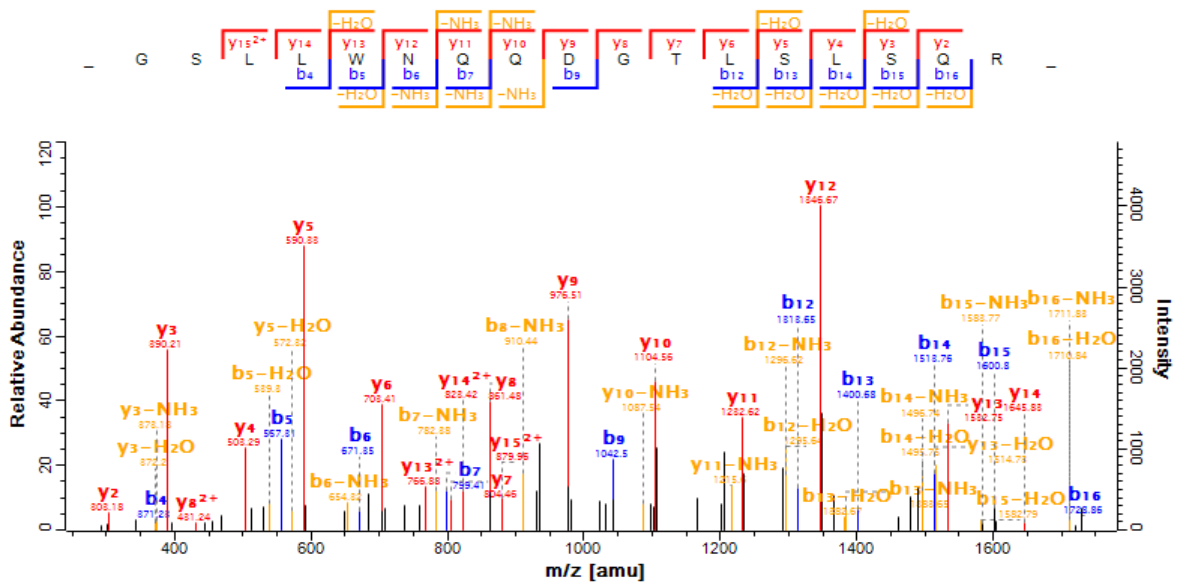
Protein Group ID: 3701
Protein Accession Numbers: Q5U3C3; Q9H617
Gene Names: TMEM164;RP13-360B22.2
Peptide Sequence: GSPGSQPEQVTQRPEEGK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 97.291
Best Match Posterior Error Probability: 0.00098005
Best Match Spectrum:

Scan number 8715 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TMEM164;RP13-360B22.2



Protein Group ID: 3703
Protein Accession Numbers: Q5UCC4; Q5UCC4-2
Gene Names: C19orf63
Peptide Sequence: GSLLWNQQDGTLSLSQR
Total Number of Spectra: 8
Number of Replicates (out of 8): 7
Best Match Score: 294.93
Best Match Posterior Error Probability: 2.89E-162
Best Match Spectrum:

Scan number 56048 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** C19orf63



Protein Group ID: 3720

Protein Accession Numbers: Q5VZM2; Q5VZM2-2; Q7L523; Q5VZM0

Gene Names: RRAGB;RRAGA

Peptide Sequence: MDLVQEDQR

Total Number of Spectra: 3

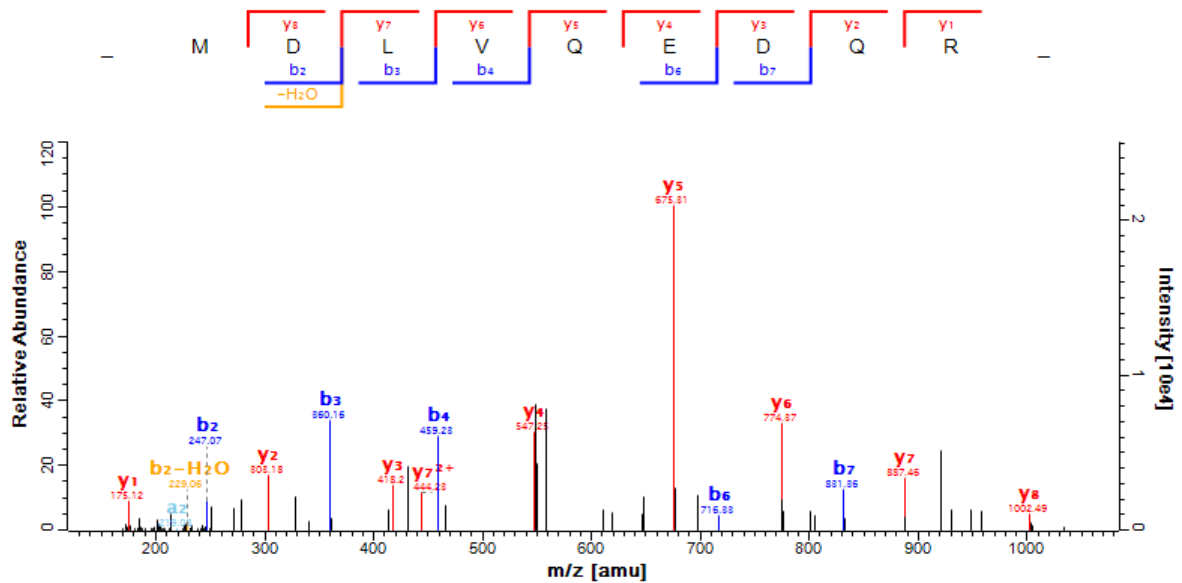
Number of Replicates (out of 8): 3

Best Match Score: 91.549

Best Match Posterior Error Probability: 0.0035899

Best Match Spectrum:

Scan number	17489	Raw file	A549-US-WT-top20CID-Elite-2ug-811
Method	ITMS; CID	Genenames	RRAGB;RRAGA



Protein Group ID: 3721

Protein Accession Numbers: Q9H497; Q9H497-2; Q9H497-3; Q5W0C6

Gene Names: TOR3A

Peptide Sequence: AESPWTIFLFLSNLR

Total Number of Spectra: 1

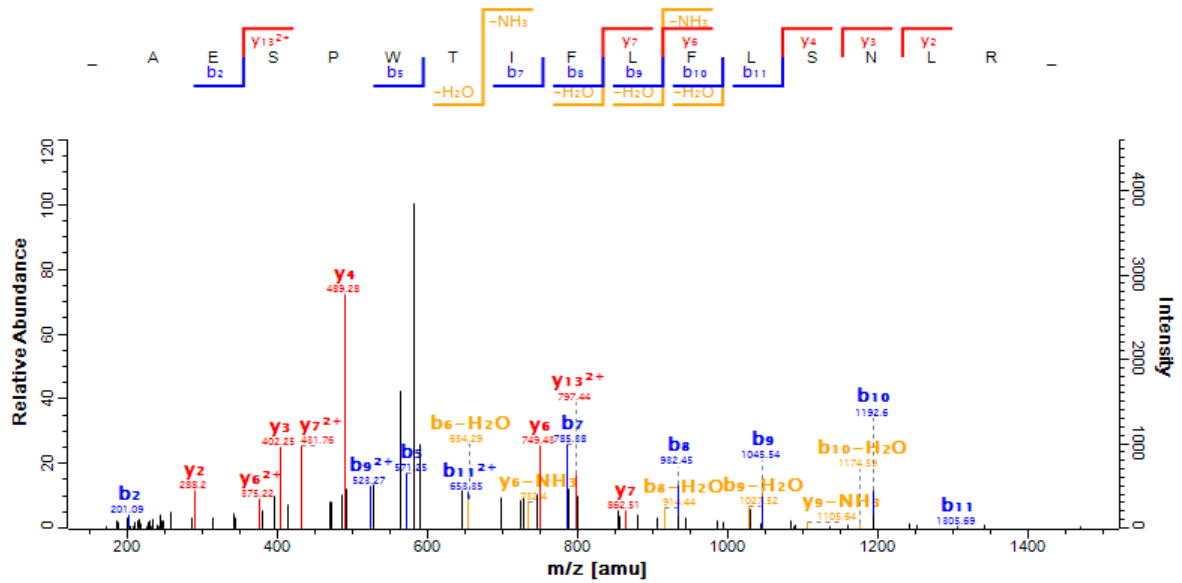
Number of Replicates (out of 8): 1

Best Match Score: 126.95

Best Match Posterior Error Probability: 7.84E-05

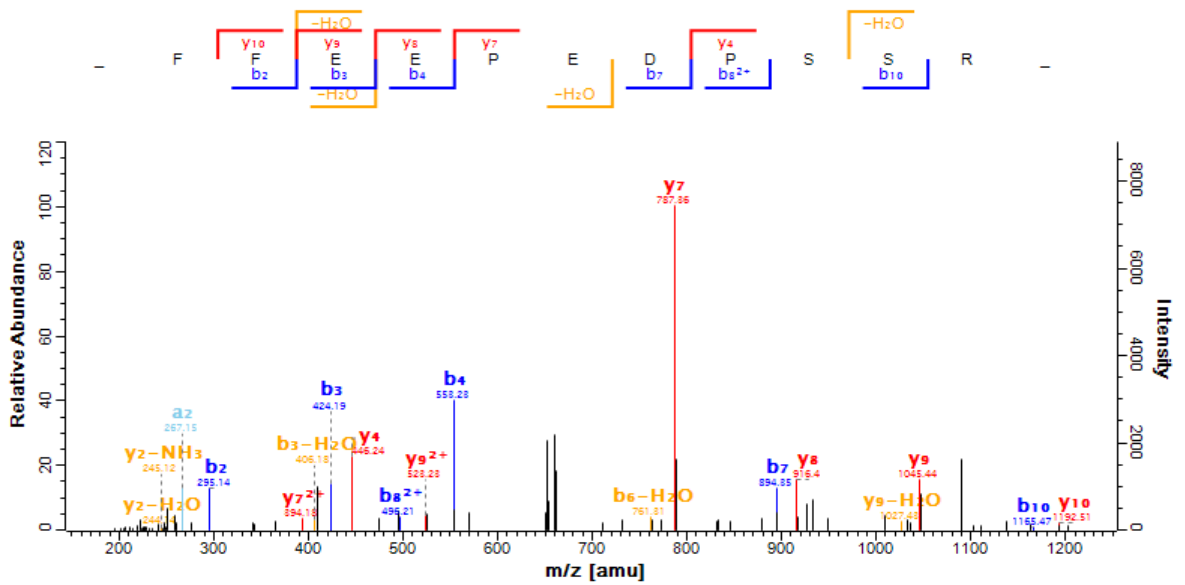
Best Match Spectrum:

Scan number	94435	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	TOR3A



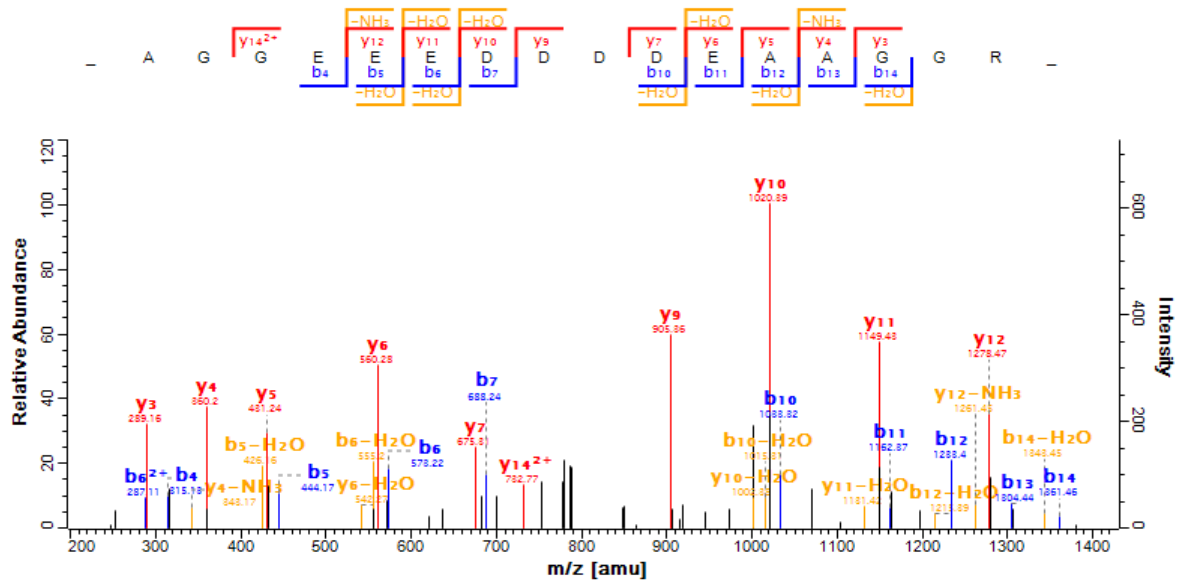
Protein Group ID: 3729
Protein Accession Numbers: Q66LE6; F5GXJ6
Gene Names: PPP2R2D
Peptide Sequence: FFEEPEDPSSR
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 86.344
Best Match Posterior Error Probability: 0.0020358
Best Match Spectrum:

Scan number 26747 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PPP2R2D



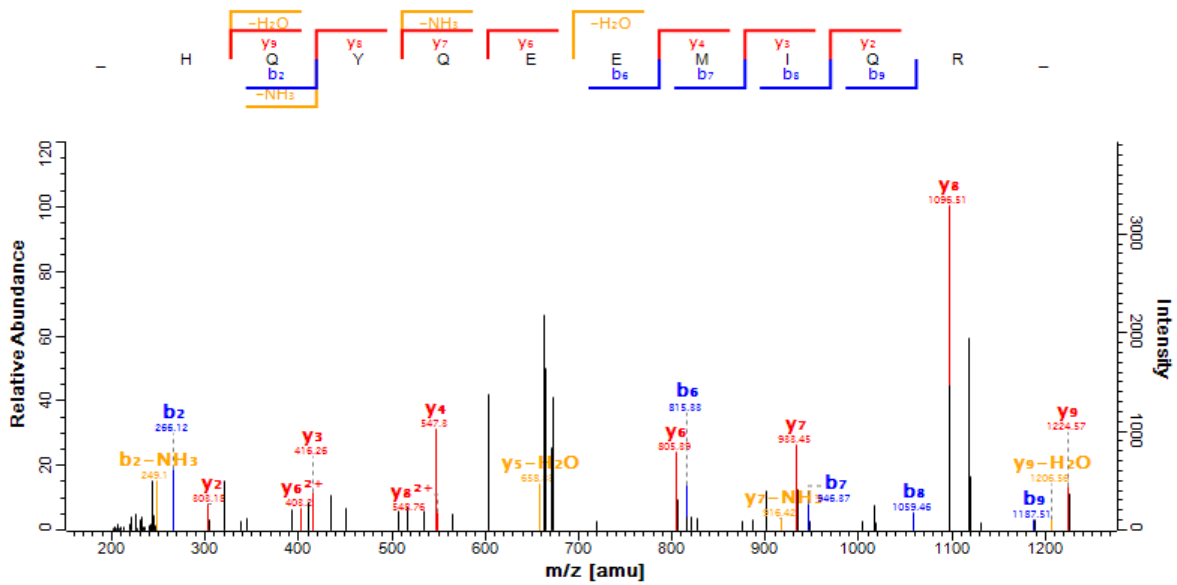
Protein Group ID: 3737
Protein Accession Numbers: Q6DD87
Gene Names: ZNF787
Peptide Sequence: AGGEEEDDDDEAAGGR
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 171.26
Best Match Posterior Error Probability: 4.44E-14
Best Match Spectrum:

Scan number 2953 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ZNF787



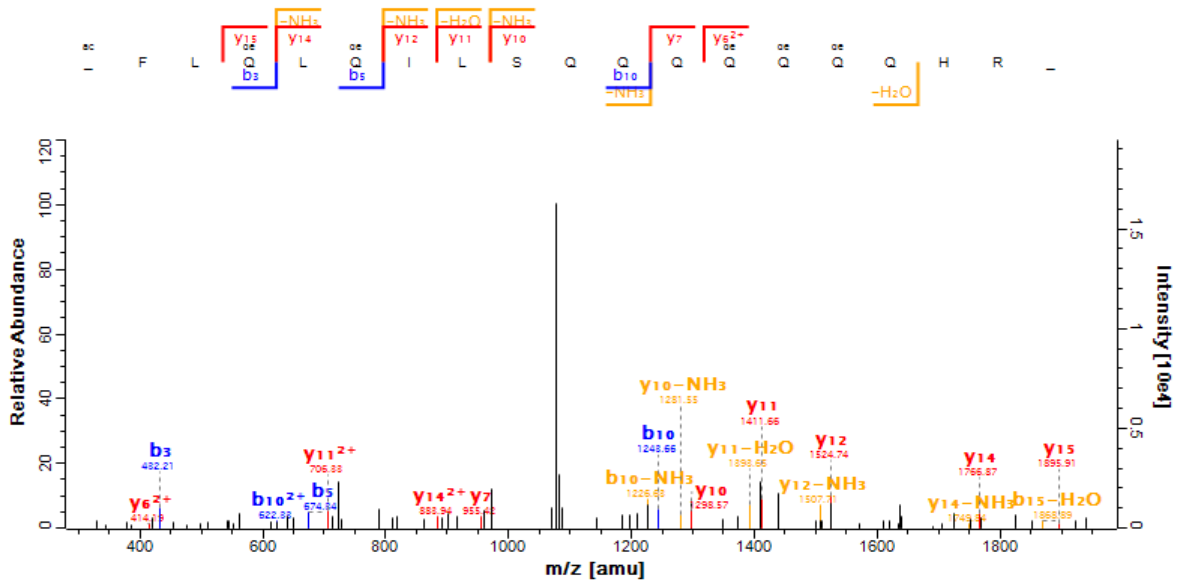
Protein Group ID: 3745
Protein Accession Numbers: Q6GQQ9
Gene Names: OTUD7B
Peptide Sequence: HQYQEEMIQR
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 104.82
Best Match Posterior Error Probability: 0.00057121
Best Match Spectrum:

Scan number 13076 **Raw file** A549-US-WT-top20CID-Elite-2ug-814
Method ITMS; CID **Genenames** OTUD7B



Protein Group ID: 3754
Protein Accession Numbers: Q6N065
Gene Names: DKFZp686O15128
Peptide Sequence: FLQLQILSQQQQQQHR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 74.296
Best Match Posterior Error Probability: 0.00036652
Best Match Spectrum:

Scan number 69332 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** DKFZp686O15128



Protein Group ID: 3757

Protein Accession Numbers: Q6NUK4

Gene Names: REEP3

Peptide Sequence: SFSMHDLTITQGDPEVGRPYQLPEAK

Total Number of Spectra: 1

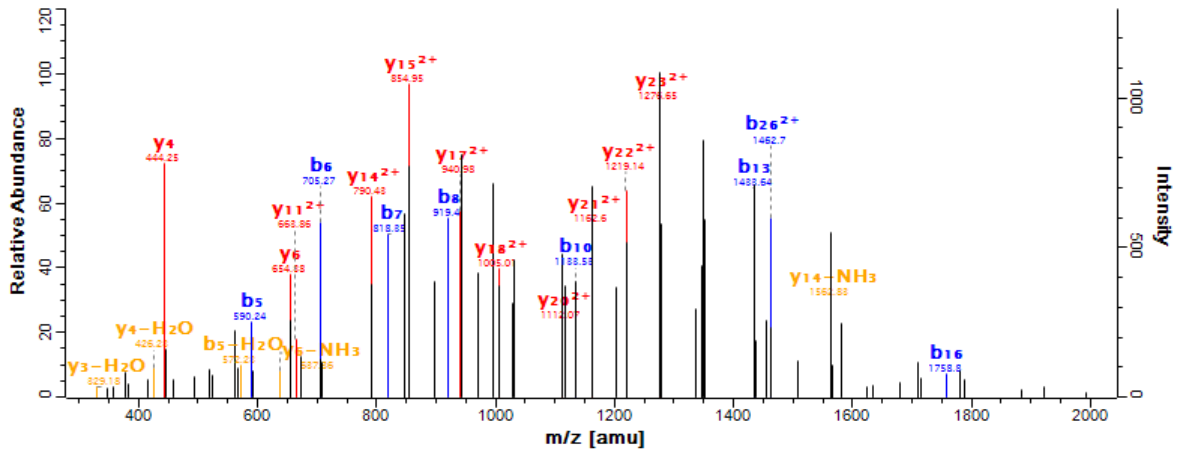
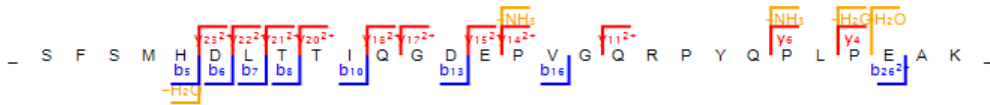
Number of Replicates (out of 8): 1

Best Match Score: 73.831

Best Match Posterior Error Probability: 0.00036063

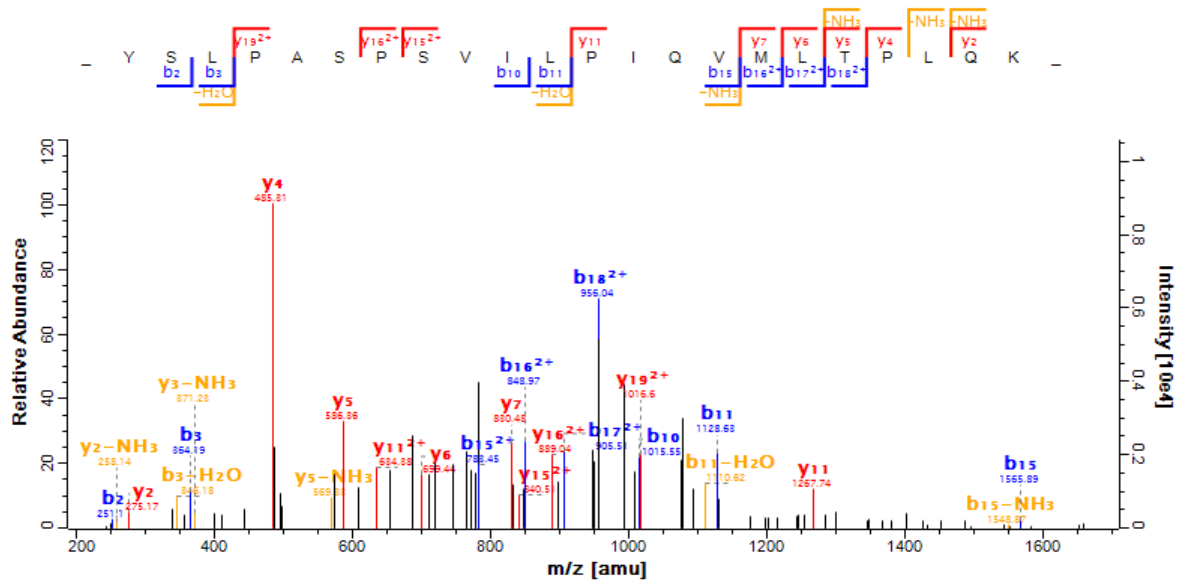
Best Match Spectrum:

Scan number 54342 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** REEP3



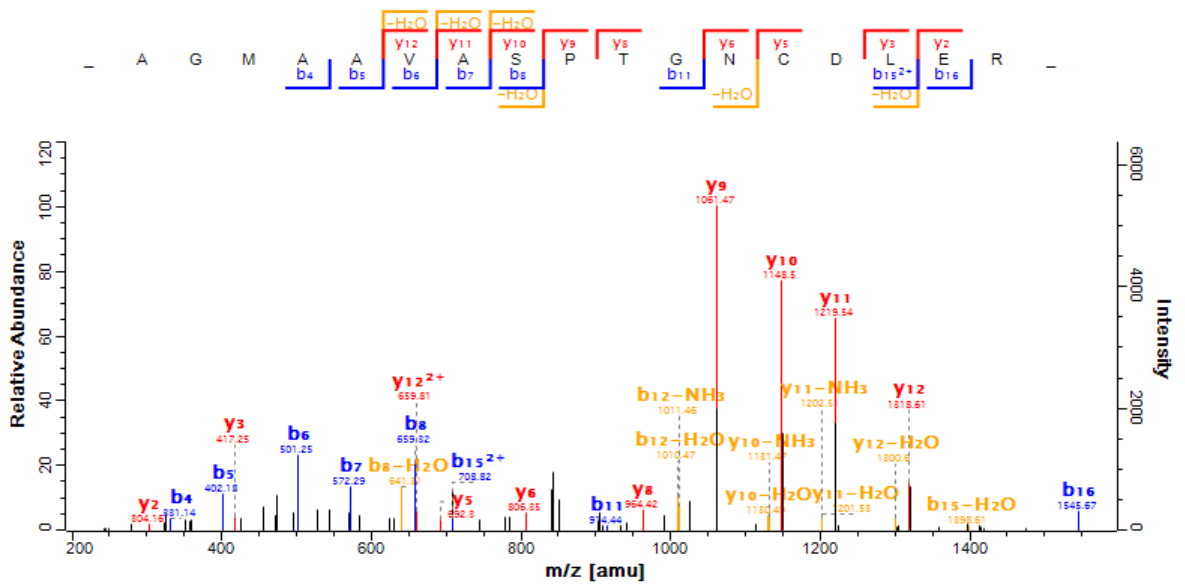
Protein Group ID: 3758
Protein Accession Numbers: Q6NUQ1
Gene Names: RINT1
Peptide Sequence: YSLPASPSVILPIQVMLTPLQK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 106.67
Best Match Posterior Error Probability: 4.19E-06
Best Match Spectrum:

Scan number 91875 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** RINT1



Protein Group ID: 3768
Protein Accession Numbers: Q6P1M0; Q96G53
Gene Names: SLC27A4
Peptide Sequence: AGMAAVASPTGNCDLER
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 110.84
Best Match Posterior Error Probability: 9.66E-05
Best Match Spectrum:

Scan number 28996 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** SLC27A4



Protein Group ID: 3774

Protein Accession Numbers: Q6P4E1-4; Q6P4E1; Q6P4E1-2

Gene Names: CASC4

Peptide Sequence: RGGDAGMPGIEENDLAK

Total Number of Spectra: 1

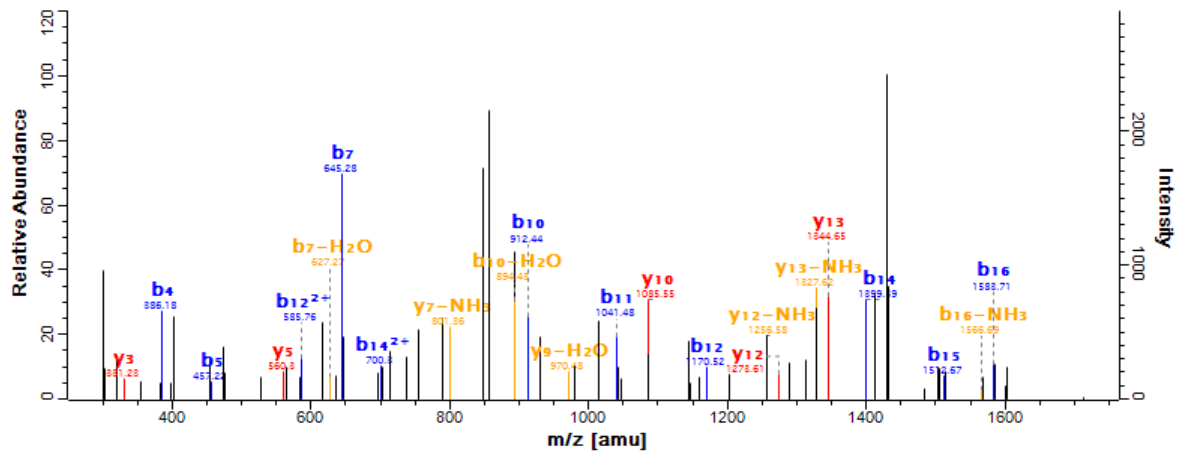
Number of Replicates (out of 8): 1

Best Match Score: 80.545

Best Match Posterior Error Probability: 0.0035143

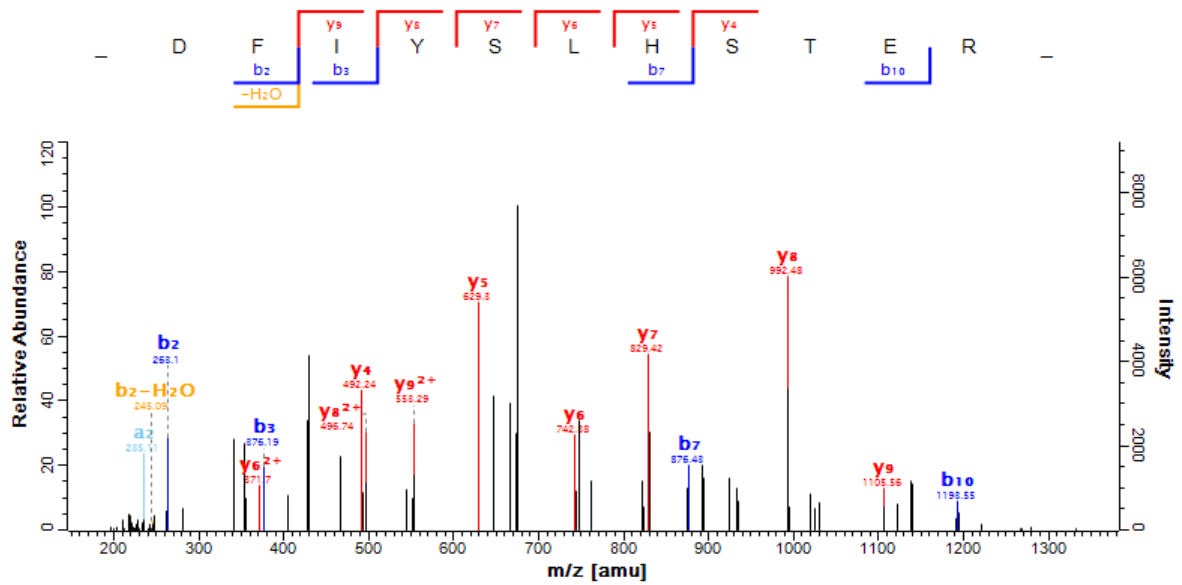
Best Match Spectrum:

Scan number	29318	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	CASC4



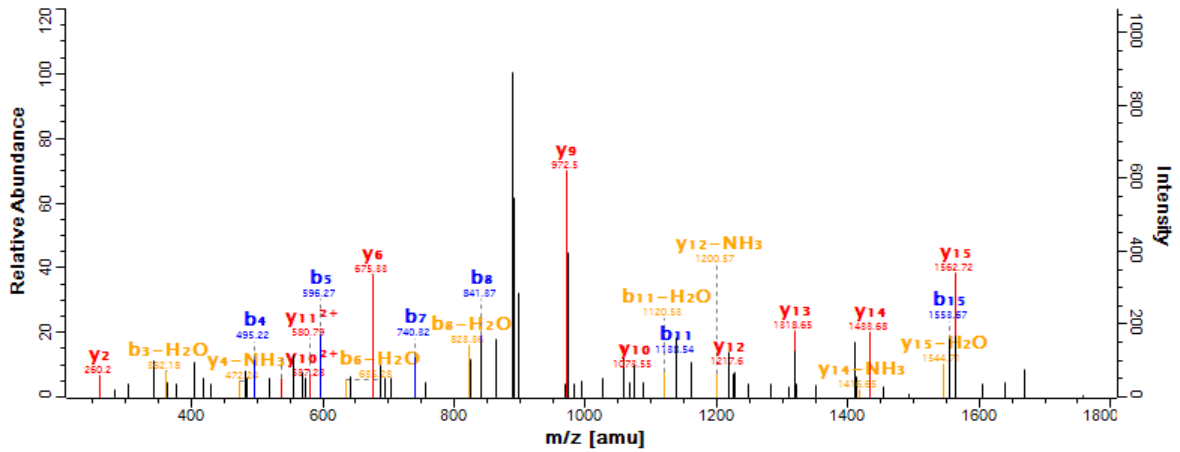
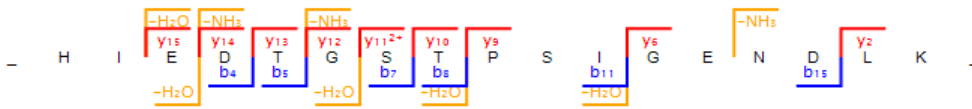
Protein Group ID: 3783
Protein Accession Numbers: Q6PI78
Gene Names: TMEM65
Peptide Sequence: DFIYSLHSTER
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 91.937
Best Match Posterior Error Probability: 0.0012764
Best Match Spectrum:

Scan number	35571	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	TMEM65



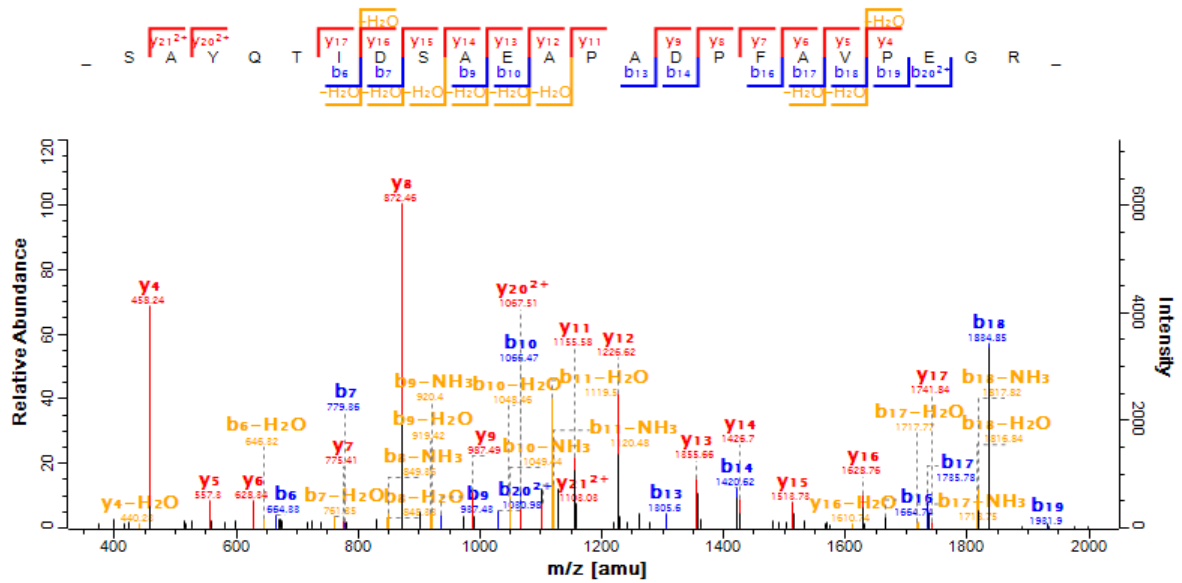
Protein Group ID: 3791
Protein Accession Numbers: Q6R327-3; Q6R327
Gene Names: RICTOR
Peptide Sequence: HIEDTGSTPSIGENDLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 85.988
Best Match Posterior Error Probability: 0.00069742
Best Match Spectrum:

Scan number	26988	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	RICTOR



Protein Group ID: 3792
Protein Accession Numbers: Q6RW13; Q6RW13-2
Gene Names: AGTRAP
Peptide Sequence: SAYQTIDSAEAPADPFAVPEGR
Total Number of Spectra: 14
Number of Replicates (out of 8): 8
Best Match Score: 171.42
Best Match Posterior Error Probability: 1.15E-20
Best Match Spectrum:

Scan number 54412 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** AGTRAP



Protein Group ID: 3796

Protein Accession Numbers: Q6UWJ1; Q6UWJ1-2; Q6UWJ1-3

Gene Names: TMCO3

Peptide Sequence: LFQVHTFEIFQK

Total Number of Spectra: 2

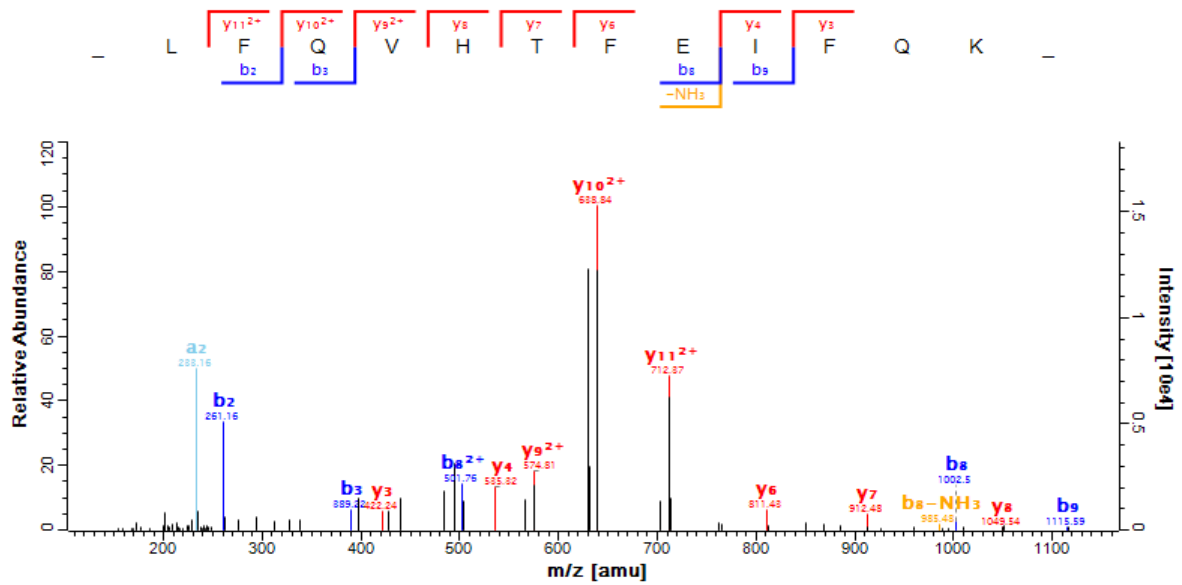
Number of Replicates (out of 8): 2

Best Match Score: 99.522

Best Match Posterior Error Probability: 0.00052363

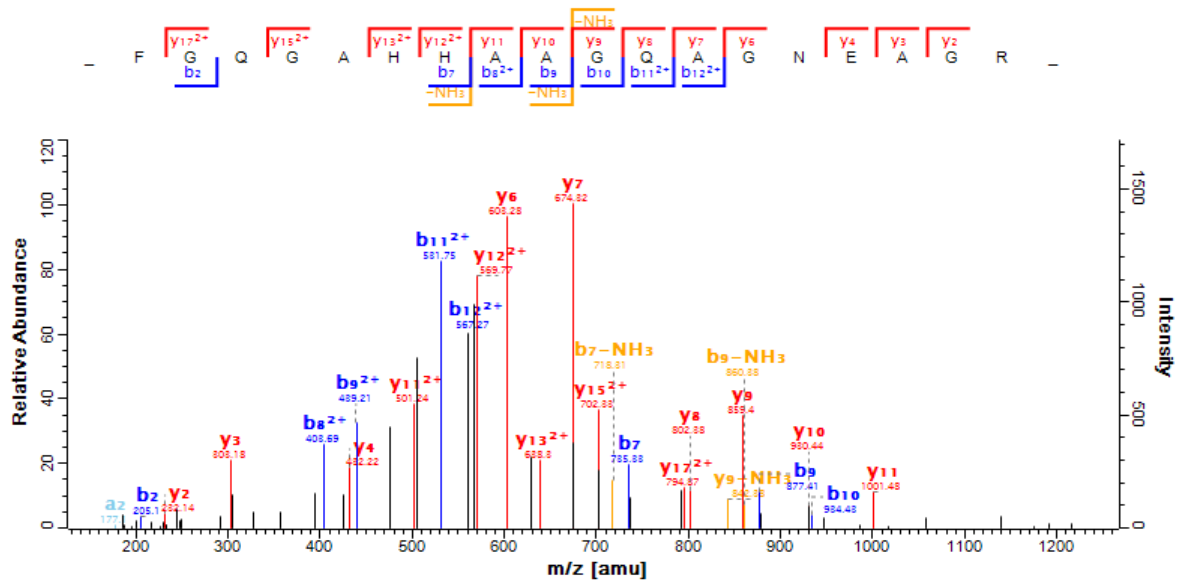
Best Match Spectrum:

Scan number 61413 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TMCO3



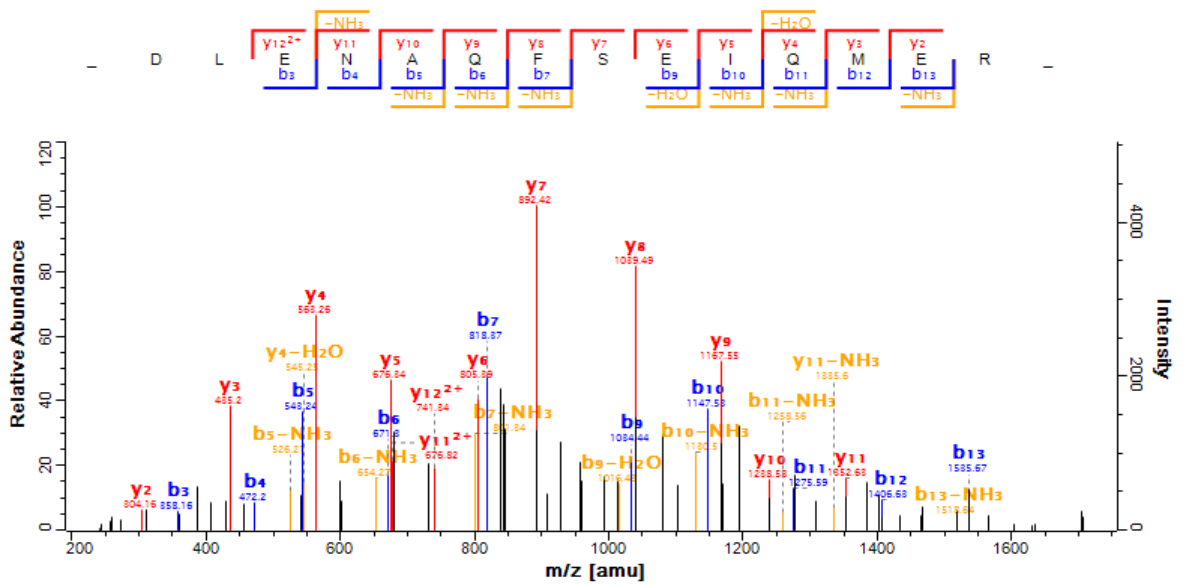
Protein Group ID: 3798
Protein Accession Numbers: Q6UWP8
Gene Names: SBSN
Peptide Sequence: FGQGAHHAAGQAGNEAGR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 127.18
Best Match Posterior Error Probability: 4.54E-05
Best Match Spectrum:

Scan number 3383 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** SBSN



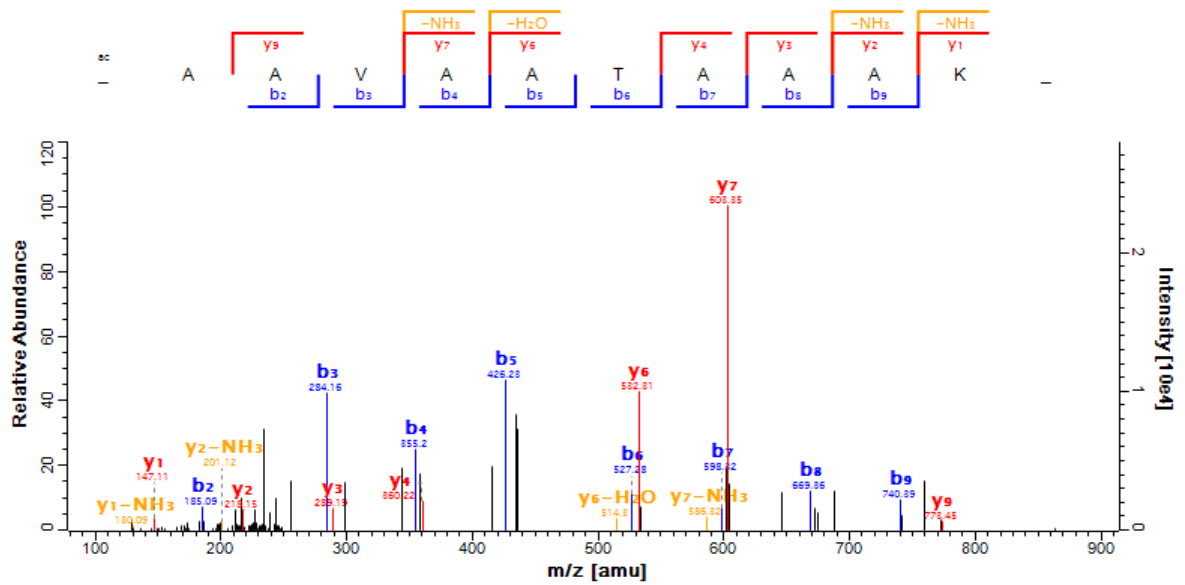
Protein Group ID: 3800
Protein Accession Numbers: Q6UX53
Gene Names: METTL7B
Peptide Sequence: DLENAQFSEIQMER
Total Number of Spectra: 10
Number of Replicates (out of 8): 7
Best Match Score: 168.1
Best Match Posterior Error Probability: 7.09E-11
Best Match Spectrum:

Scan number 47249 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** METTL7B



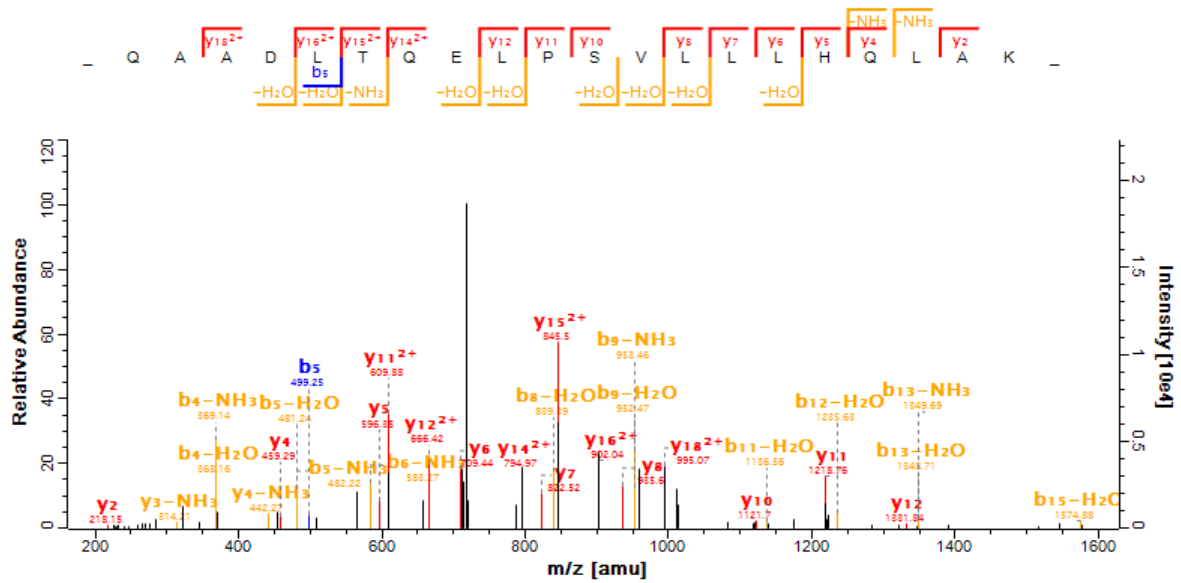
Protein Group ID: 3805
Protein Accession Numbers: Q6Y1H2
Gene Names: PTPLB
Peptide Sequence: AAVAATAAAK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 116.52
Best Match Posterior Error Probability: 0.00027971
Best Match Spectrum:

Scan number 18257 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** PTPLB



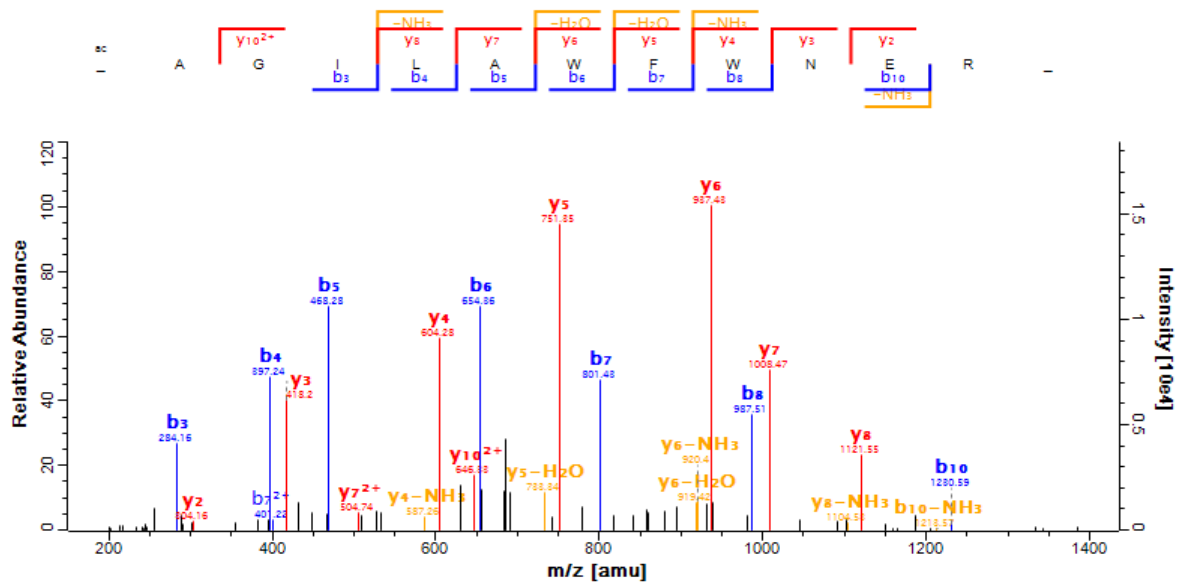
Protein Group ID: 3806
Protein Accession Numbers: Q6Y288
Gene Names: B3GALTL
Peptide Sequence: QAADLTQELPSVLLQLAK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 69.522
Best Match Posterior Error Probability: 0.0020361
Best Match Spectrum:

Scan number 79939 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** B3GALTL



Protein Group ID: 3812
Protein Accession Numbers: Q6ZMG9-2; Q6ZMG9
Gene Names: CERS6
Peptide Sequence: AGILAWFWNER
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 174.98
Best Match Posterior Error Probability: 3.84E-23
Best Match Spectrum:

Scan number 95859 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** CERS6



Protein Group ID: 3813

Protein Accession Numbers: Q6ZMI0; Q6ZMI0-2; Q6ZMI0-5; Q6ZMI0-3; Q6ZMI0-4

Gene Names: PPP1R21

Peptide Sequence: LATLETEAAQHQA VVDGLTR

Total Number of Spectra: 1

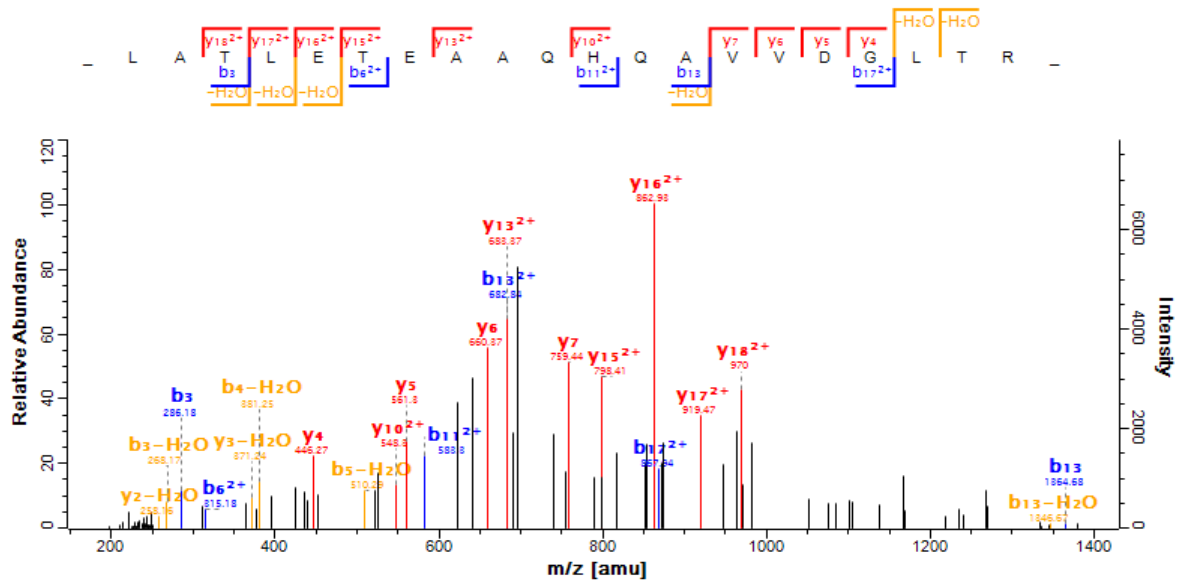
Number of Replicates (out of 8): 1

Best Match Score: 71.697

Best Match Posterior Error Probability: 0.0015803

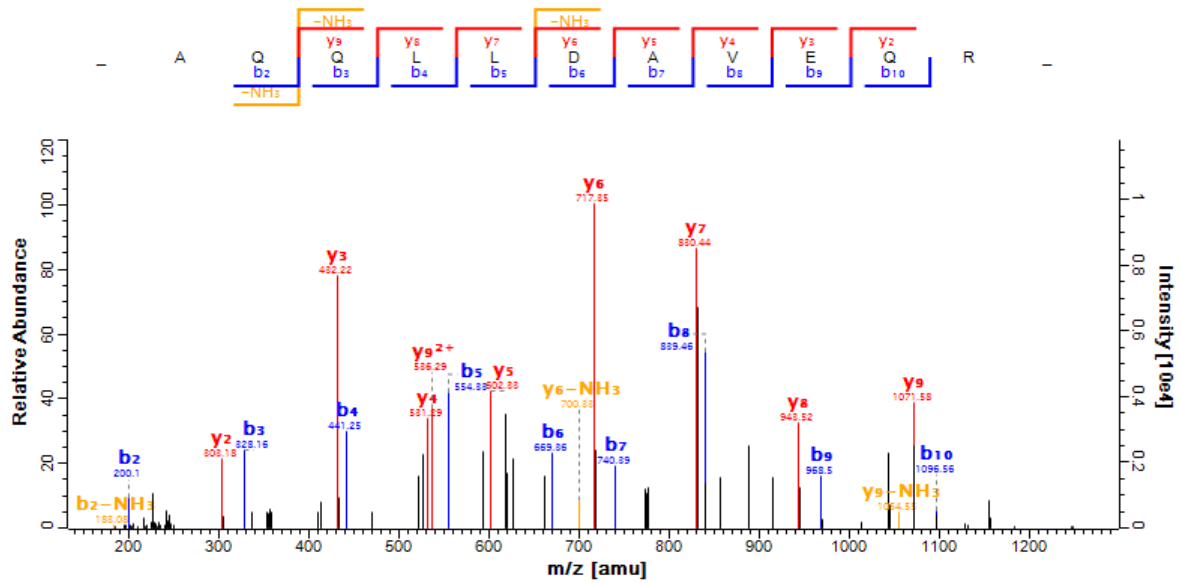
Best Match Spectrum:

Scan number	44933	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	PPP1R21



Protein Group ID: 3817
Protein Accession Numbers: Q6ZSJ8
Gene Names: Clorf122
Peptide Sequence: AQQLLDAVEQR
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 131.13
Best Match Posterior Error Probability: 4.19E-05
Best Match Spectrum:

Scan number 34388 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** Clorf122



Protein Group ID: 3819

Protein Accession Numbers: Q6ZT12-4; Q6ZT12

Gene Names: UBR3

Peptide Sequence: AAAAAAVGGQQPSQPELPAPGLALDK

Total Number of Spectra: 2

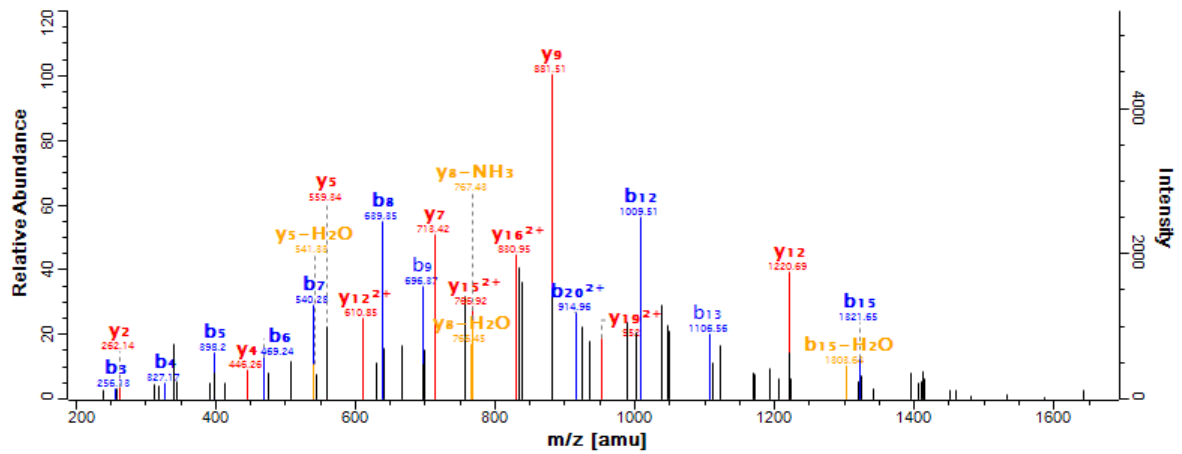
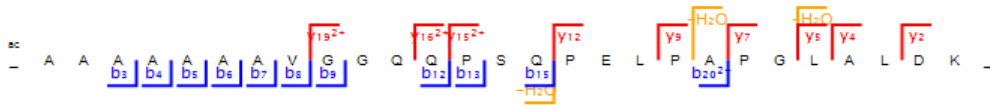
Number of Replicates (out of 8): 2

Best Match Score: 100.76

Best Match Posterior Error Probability: 9.22E-08

Best Match Spectrum:

Scan number 64893 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** UBR3



Protein Group ID: 3820

Protein Accession Numbers: Q6ZUT1-2; Q6ZUT1; Q6ZUT1-3

Gene Names: C11orf57

Peptide Sequence: AHTSVANNEIQER

Total Number of Spectra: 1

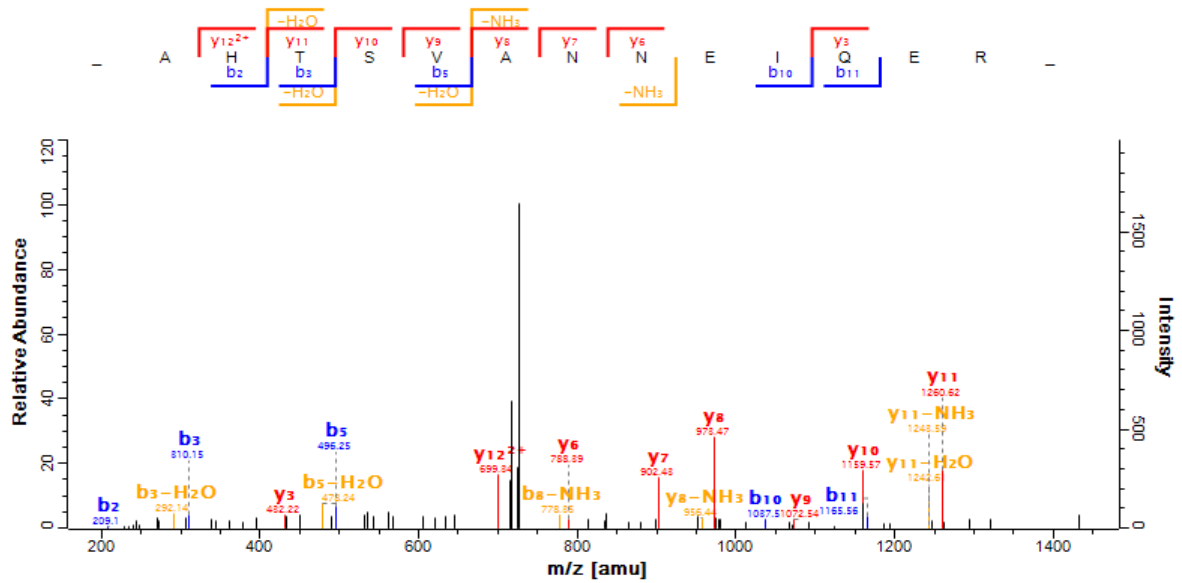
Number of Replicates (out of 8): 1

Best Match Score: 88.552

Best Match Posterior Error Probability: 0.0015422

Best Match Spectrum:

Scan number 6828 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** C11orf57



Protein Group ID: 3831

Protein Accession Numbers: Q71DI3

Gene Names: HIST2H3A

Peptide Sequence: FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK

Total Number of Spectra: 22

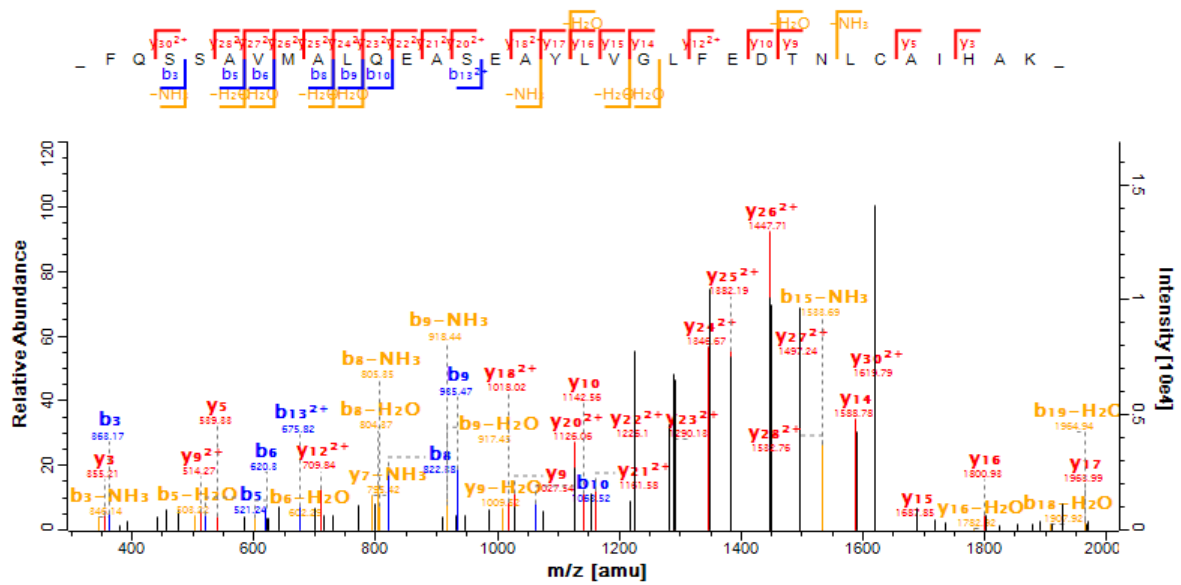
Number of Replicates (out of 8): 7

Best Match Score: 149.99

Best Match Posterior Error Probability: 4.76E-43

Best Match Spectrum:

Scan number 94242 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** HIST2H3A



Protein Group ID: 3833

Protein Accession Numbers: Q71U36; G3V1U9; Q13748; F8VXZ4; Q6PEY2; Q13748-2; F8VQQ4

Gene Names: TUBA1A;TUBA3C;TUBA3E

Peptide Sequence: LIGQIVSSITASLR

Total Number of Spectra: 16

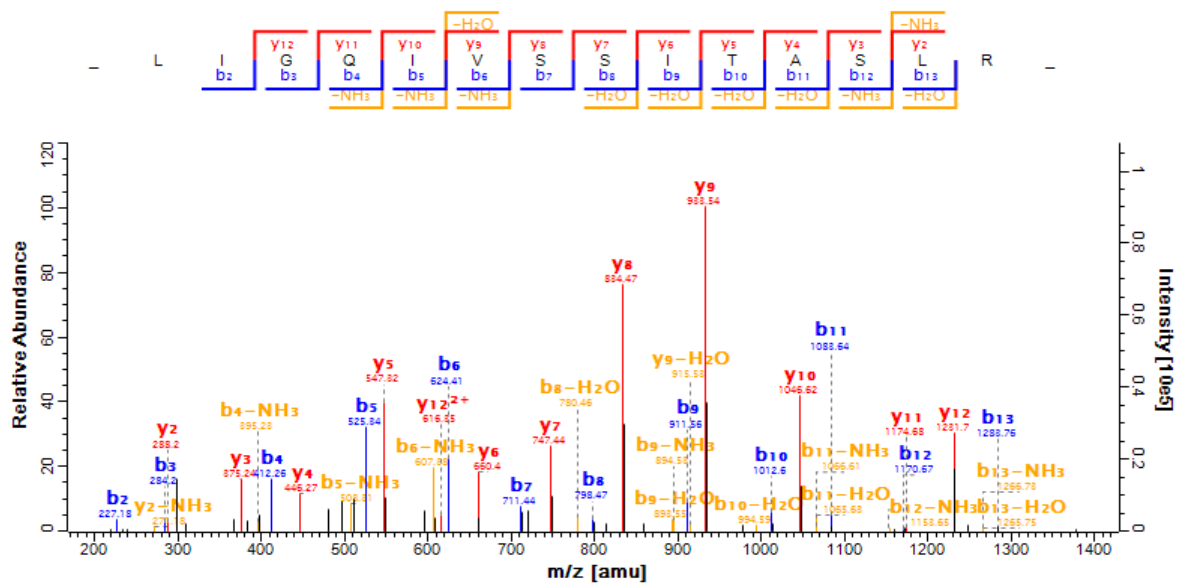
Number of Replicates (out of 8): 8

Best Match Score: 245.4

Best Match Posterior Error Probability: 7.58E-66

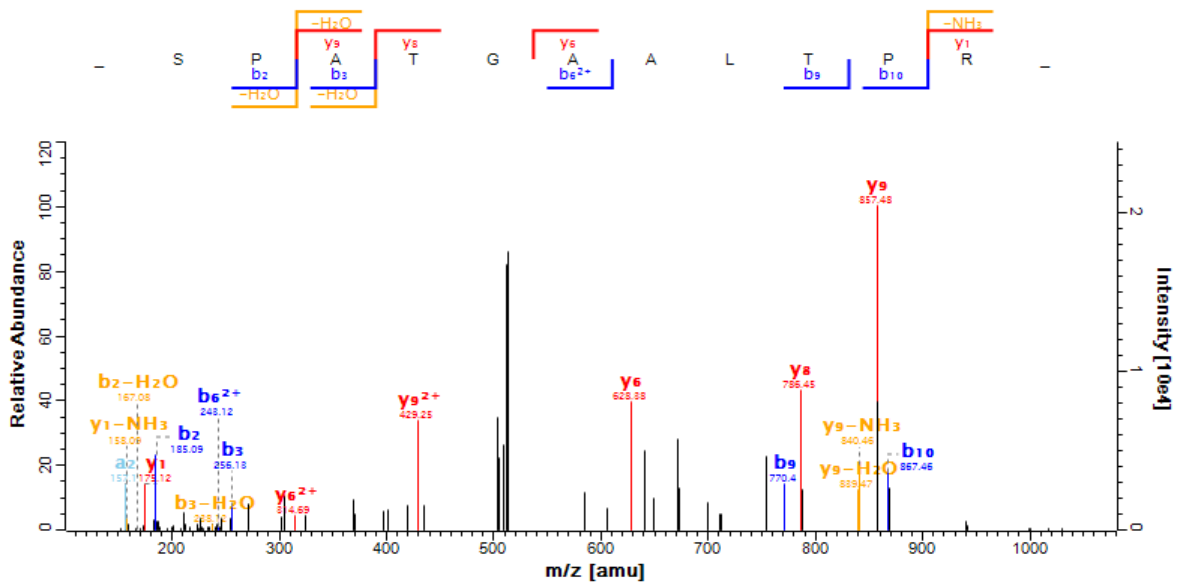
Best Match Spectrum:

Scan number	81769	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS: CID	Genenames	TUBA1A;TUBA3C;TUBA3E



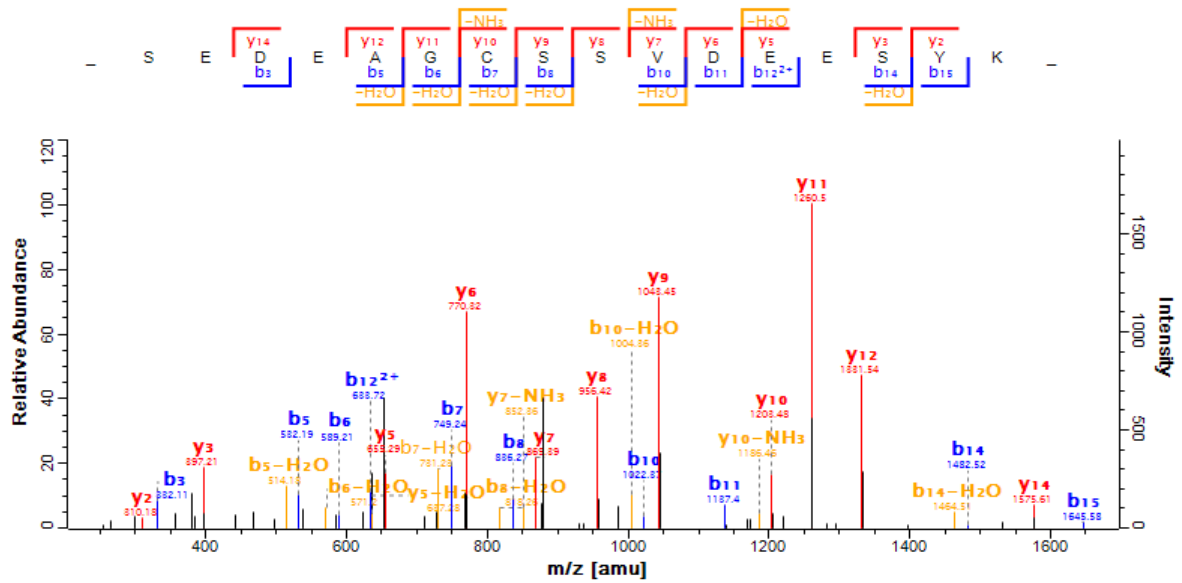
Protein Group ID: 3835
Protein Accession Numbers: Q75MW2
Gene Names: ZNF767
Peptide Sequence: SPATGALTPR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 83.862
Best Match Posterior Error Probability: 0.0027723
Best Match Spectrum:

Scan number 17873 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ZNF767



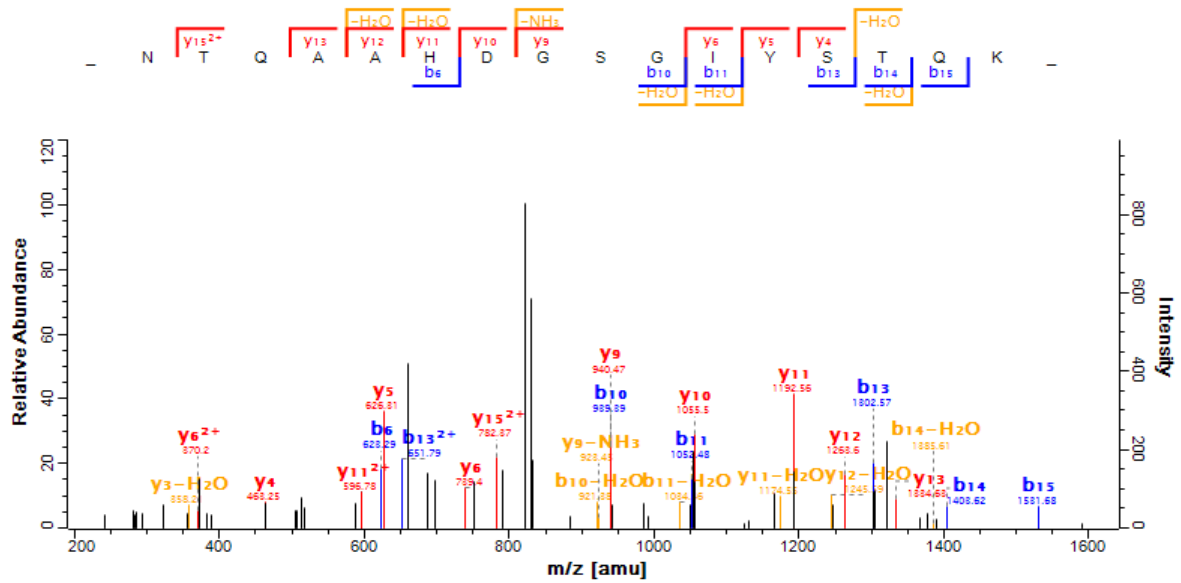
Protein Group ID: 3846
Protein Accession Numbers: Q7L4I2; Q7L4I2-2
Gene Names: RSRC2
Peptide Sequence: SEDEAGCSSVDEESYK
Total Number of Spectra: 9
Number of Replicates (out of 8): 5
Best Match Score: 160.8
Best Match Posterior Error Probability: 1.63E-09
Best Match Spectrum:

Scan number 13108 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** RSRC2



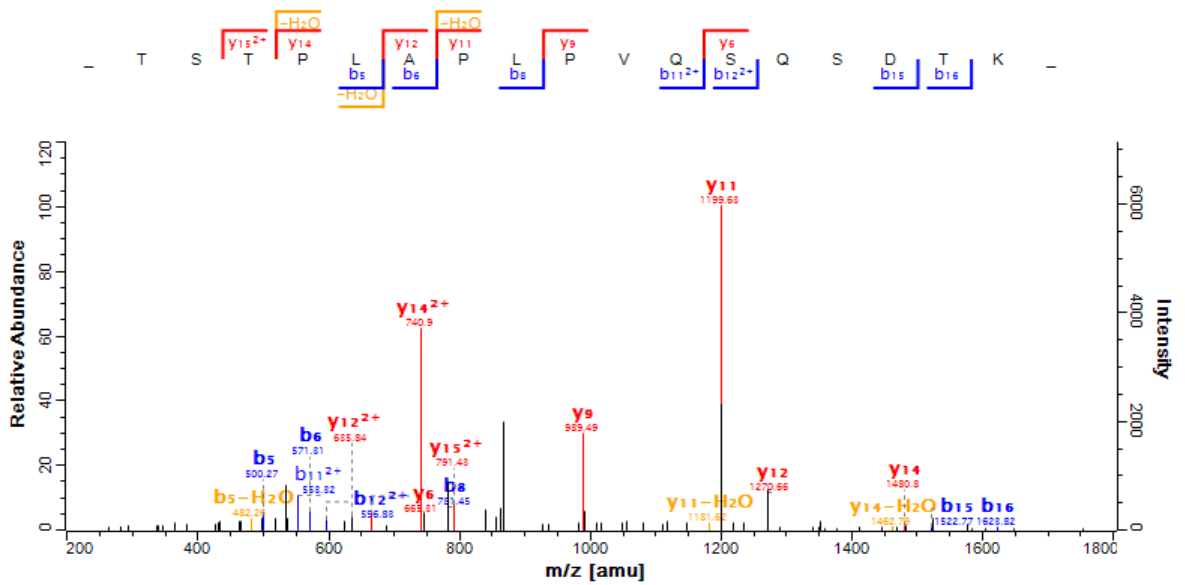
Protein Group ID: 3856
Protein Accession Numbers: Q7LGC8
Gene Names: CHST3
Peptide Sequence: NTQAAHDGSGIYSTQK
Total Number of Spectra: 6
Number of Replicates (out of 8): 5
Best Match Score: 115.56
Best Match Posterior Error Probability: 9.67E-05
Best Match Spectrum:

Scan number 6415 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CHST3



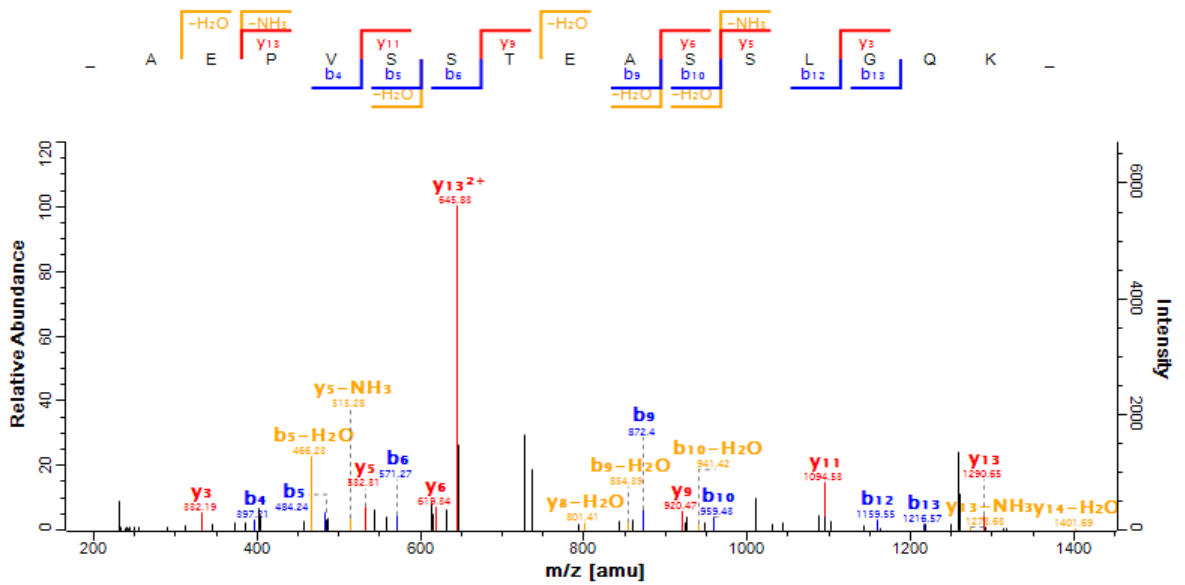
Protein Group ID: 3857
Protein Accession Numbers: Q7RTP6
Gene Names: MICAL3
Peptide Sequence: TSTPLAPLVQSQSDTK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 77.746
Best Match Posterior Error Probability: 0.0019188
Best Match Spectrum:

Scan number 36048 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MICAL3



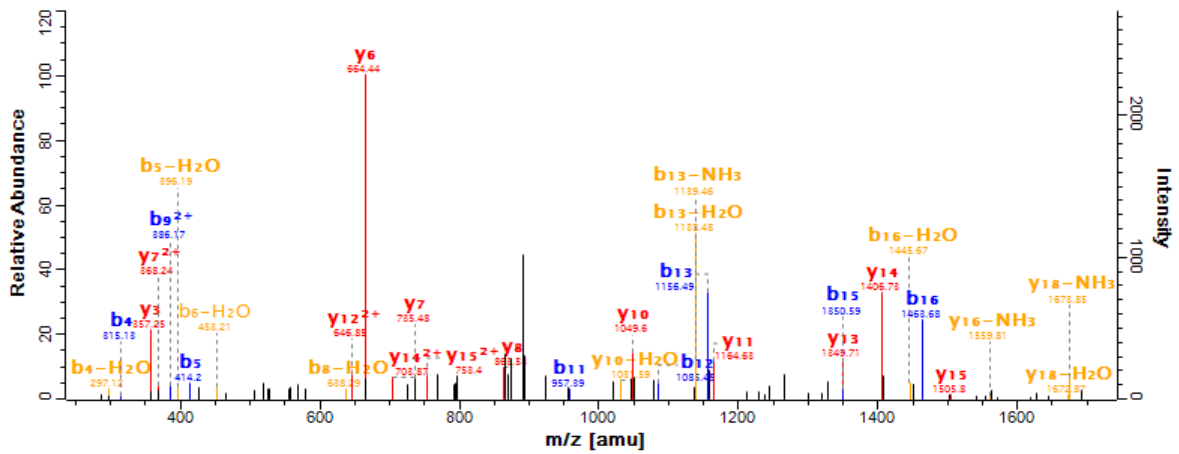
Protein Group ID: 3859
Protein Accession Numbers: Q7Z2K8
Gene Names: GPRIN1
Peptide Sequence: AEPVSSTEASSLGQK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 91.307
Best Match Posterior Error Probability: 0.0007303
Best Match Spectrum:

Scan number 16896 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** GPRIN1



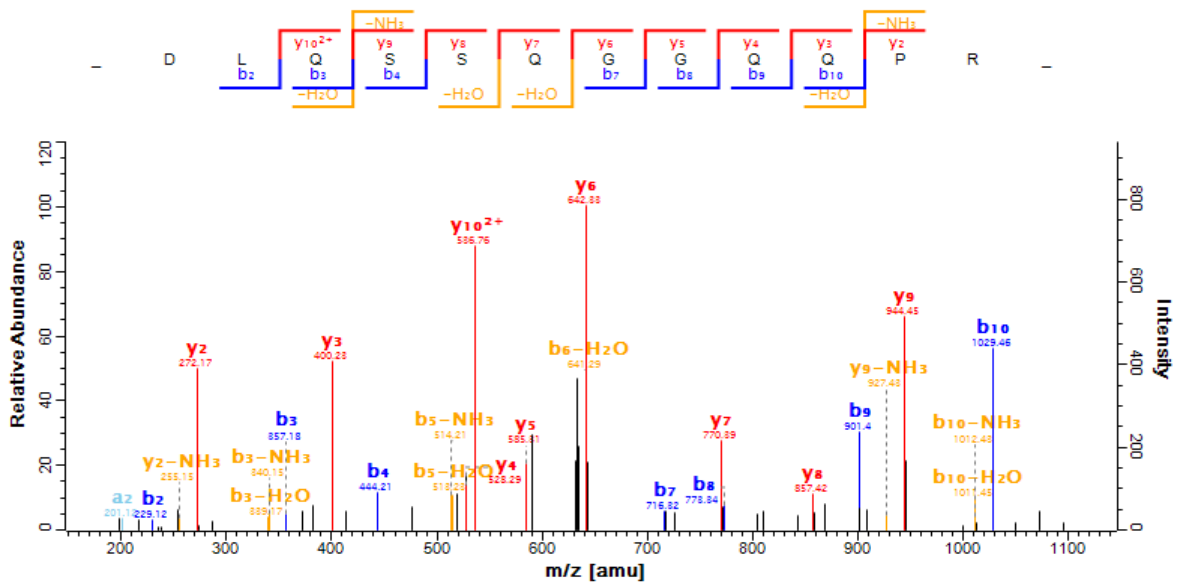
Protein Group ID: 3871
Protein Accession Numbers: Q7Z4F1
Gene Names: LRP10
Peptide Sequence: EGGAVGGQDGEQAPPLIK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 136.39
Best Match Posterior Error Probability: 2.17E-11
Best Match Spectrum:

Scan number 36550 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** LRP10



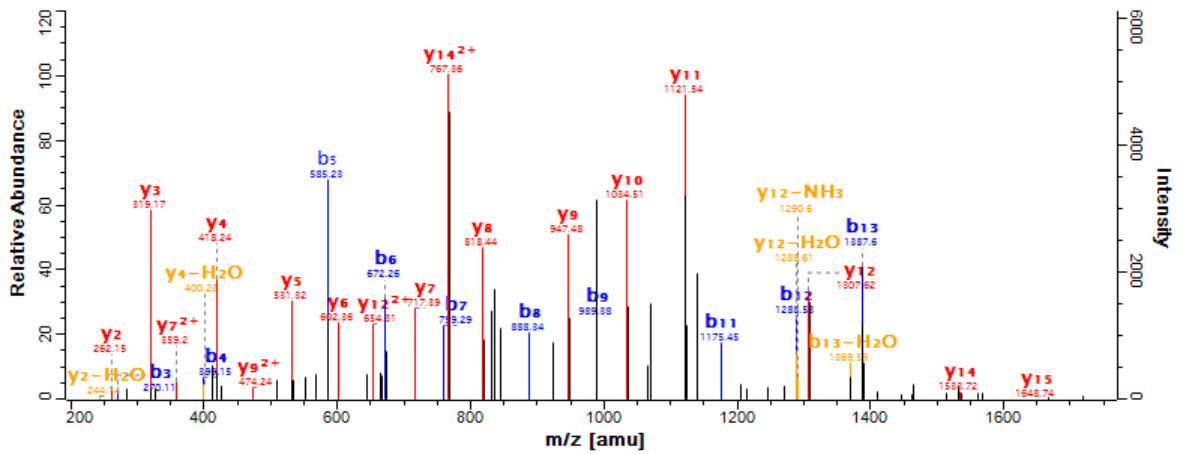
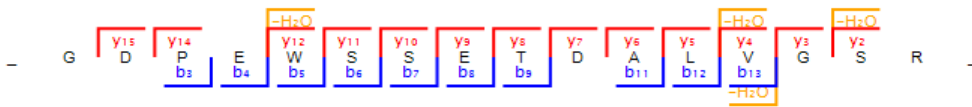
Protein Group ID: 3878
Protein Accession Numbers: Q7Z6J0; Q7Z6J0-3
Gene Names: SH3RF1
Peptide Sequence: DLQSSQGGQQPR
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 132.5
Best Match Posterior Error Probability: 9.89E-05
Best Match Spectrum:

Scan number 3616 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** SH3RF1



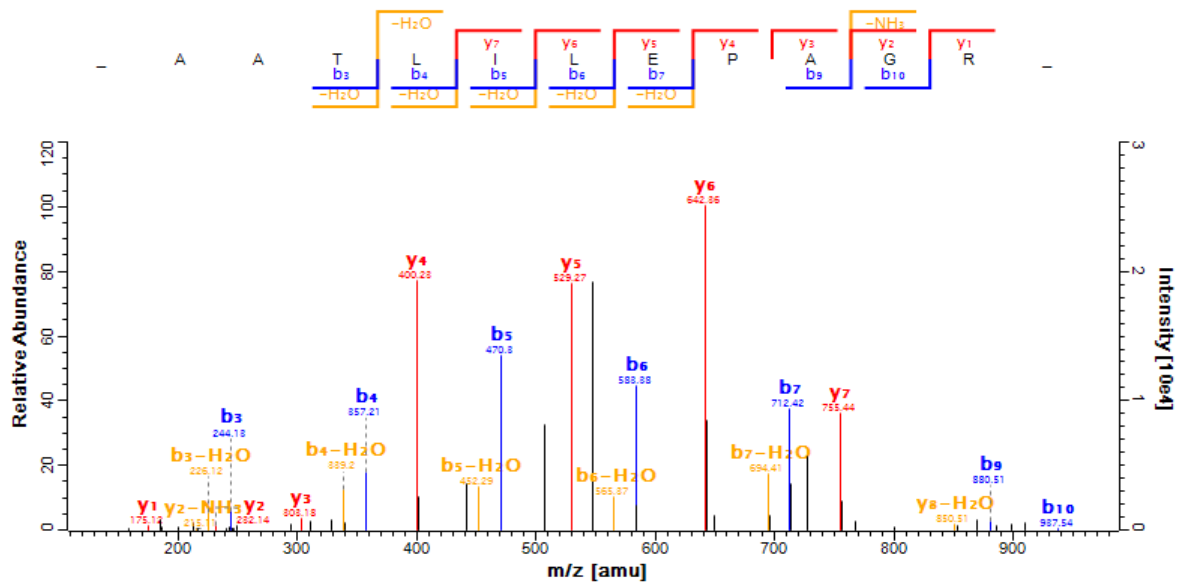
Protein Group ID: 3889
Protein Accession Numbers: Q7Z7N9
Gene Names: TMEM179B
Peptide Sequence: GDPEWSSETDALVGSR
Total Number of Spectra: 9
Number of Replicates (out of 8): 8
Best Match Score: 181.51
Best Match Posterior Error Probability: 2.43E-20
Best Match Spectrum:

Scan number 43647 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TMEM179B



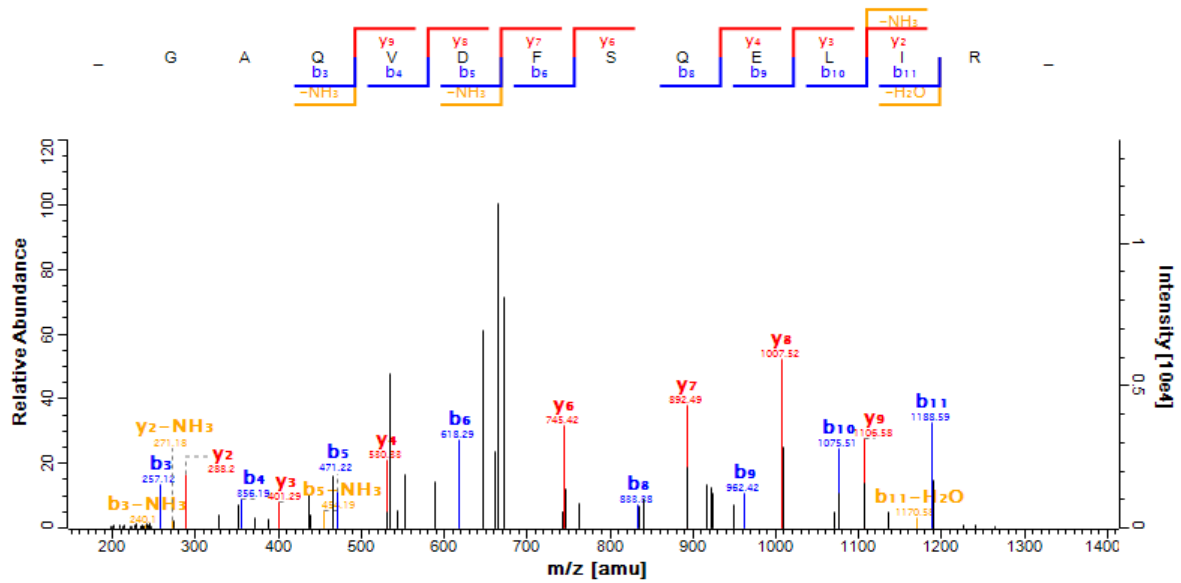
Protein Group ID: 3902
Protein Accession Numbers: Q86TX2; G3V4F2
Gene Names: ACOT1
Peptide Sequence: AATLILEPAGR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 138.25
Best Match Posterior Error Probability: 2.90E-05
Best Match Spectrum:

Scan number 33652 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ACOT1



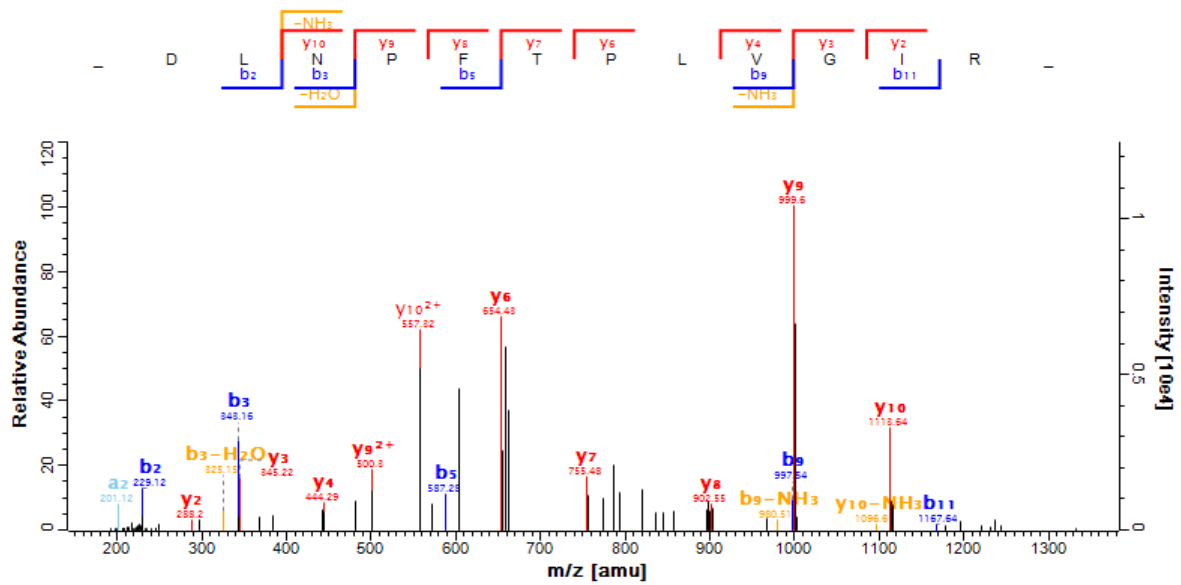
Protein Group ID: 3903
Protein Accession Numbers: Q86U28
Gene Names: ISCA2
Peptide Sequence: GAQVDFSQELIR
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 98.942
Best Match Posterior Error Probability: 0.0005378
Best Match Spectrum:

Scan number	46133	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	ISCA2



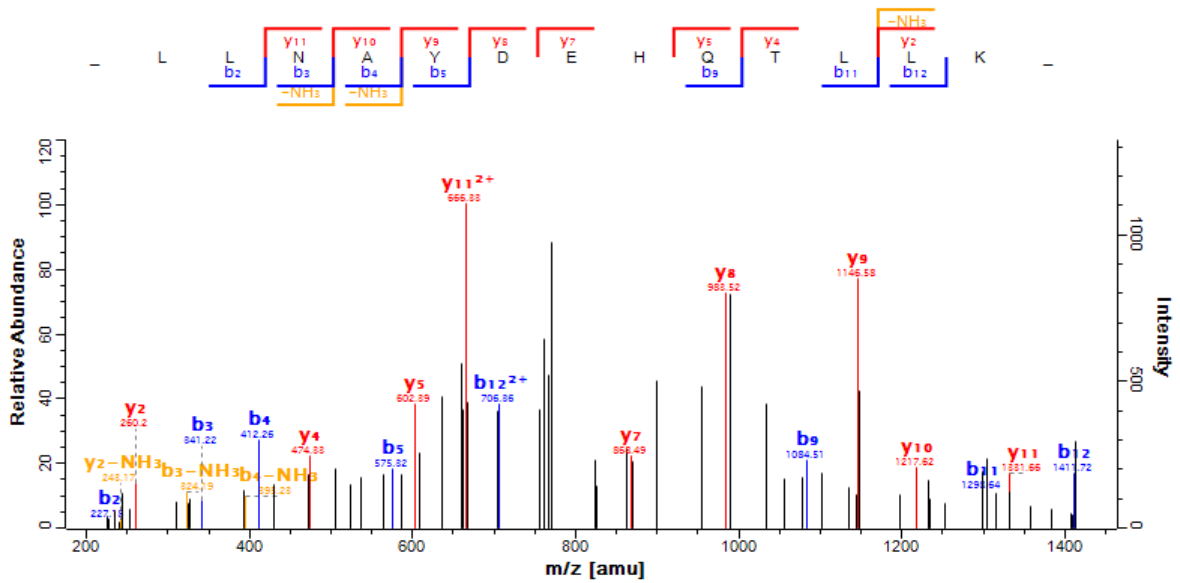
Protein Group ID: 3907
Protein Accession Numbers: Q86U90
Gene Names: YRDC
Peptide Sequence: DLNPFTPLVGIR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 112.43
Best Match Posterior Error Probability: 0.00023058
Best Match Spectrum:

Scan number 72157 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** YRDC



Protein Group ID: 3908
Protein Accession Numbers: Q86UA1; Q86UA1-2
Gene Names: PRPF39
Peptide Sequence: LLNAYDEHQTLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 106.32
Best Match Posterior Error Probability: 0.0024998
Best Match Spectrum:

Scan number 36132 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PRPF39



Protein Group ID: 3910

Protein Accession Numbers: Q86UF2; P0CG41; Q8IX94

Gene Names: CTAGE6P;CTAGE8;CTAGE4

Peptide Sequence: HSQQDELMADISK

Total Number of Spectra: 3

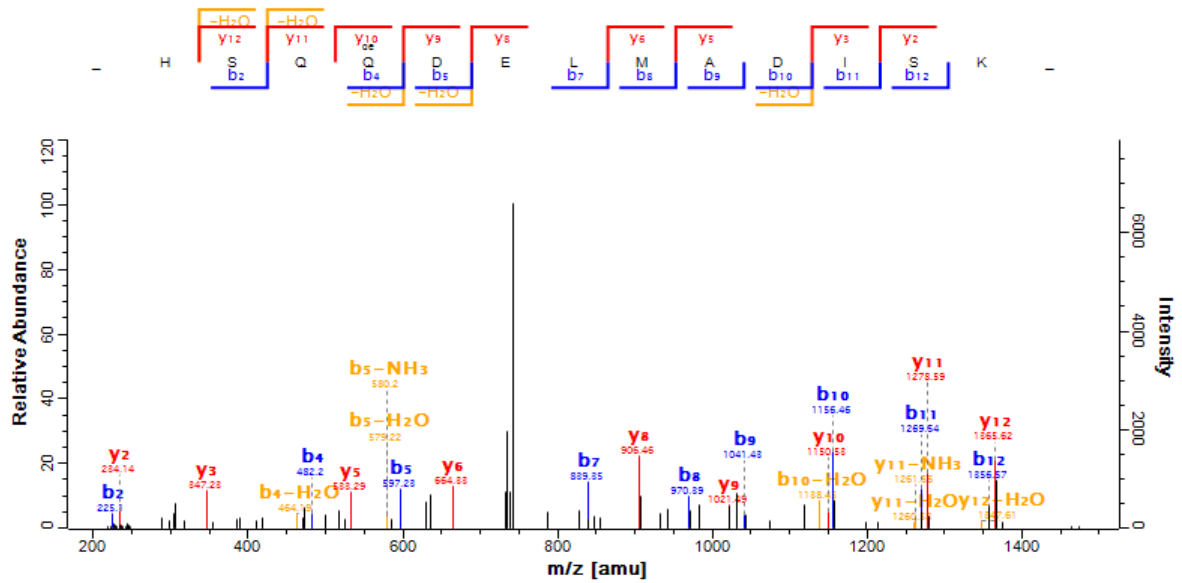
Number of Replicates (out of 8): 3

Best Match Score: 131.96

Best Match Posterior Error Probability: 4.57E-05

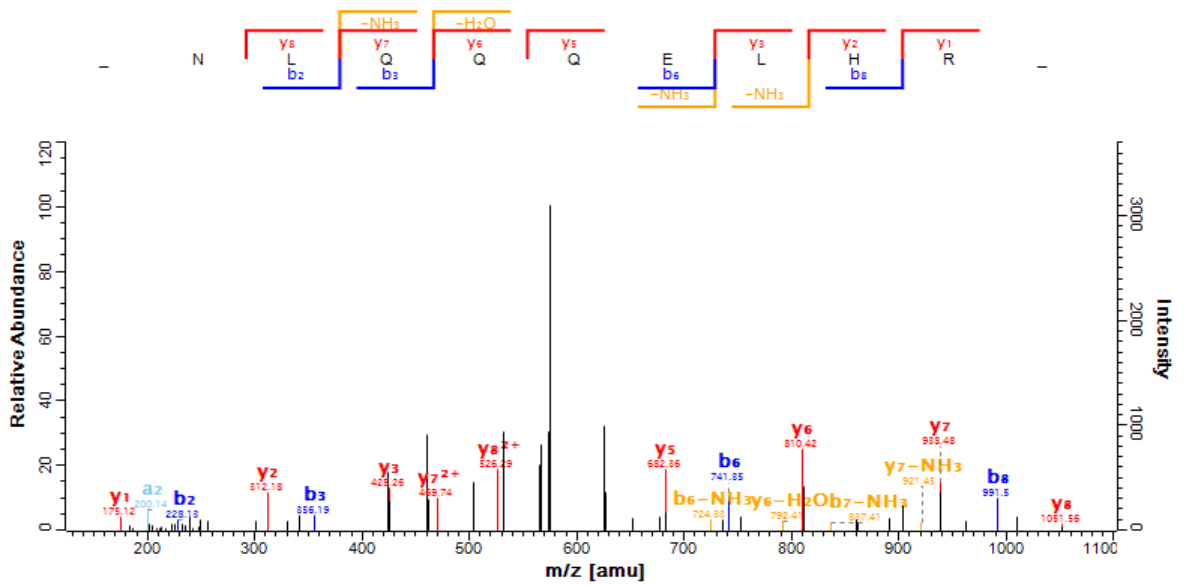
Best Match Spectrum:

Scan number 34950 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CTAGE6P;CTAGE8;CTAGE4



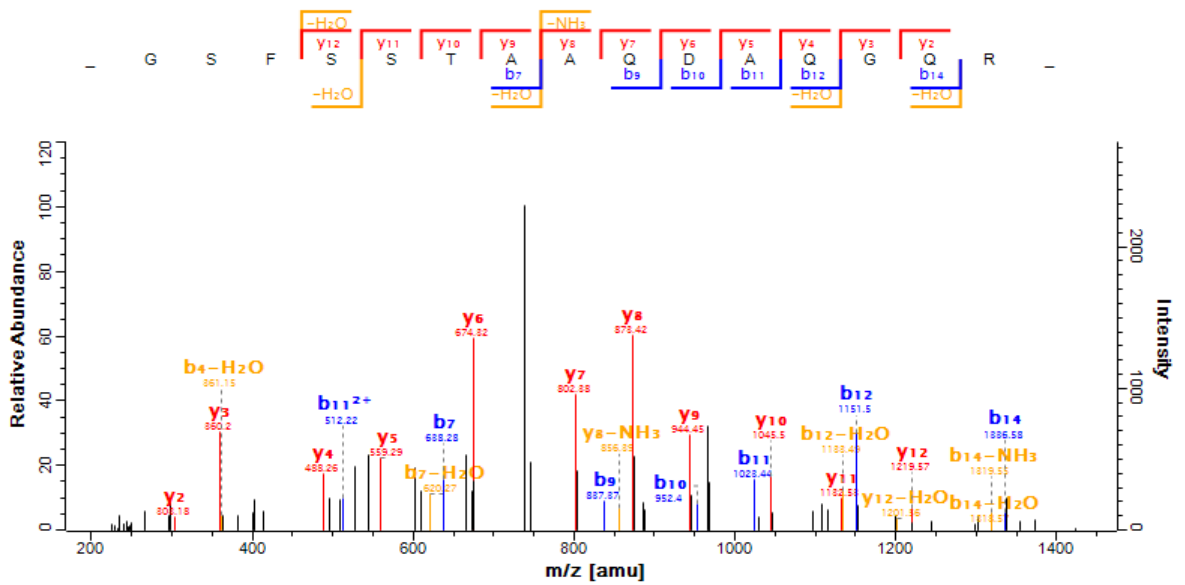
Protein Group ID: 3913
Protein Accession Numbers: Q86US8
Gene Names: SMG6
Peptide Sequence: NLQQQELHR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 106.2
Best Match Posterior Error Probability: 0.0012843
Best Match Spectrum:

Scan number 7061 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SMG6



Protein Group ID: 3920
Protein Accession Numbers: Q86V85
Gene Names: GPR180
Peptide Sequence: GSFSSSTAAQDAQGQR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 112.24
Best Match Posterior Error Probability: 0.00011237
Best Match Spectrum:

Scan number 13821 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** GPR180



Protein Group ID: 3921

Protein Accession Numbers: Q86VF7-2; Q86VF7; Q86VF7-3; Q86VF7-4

Gene Names: NRAP

Peptide Sequence: GMGWVATGSLNVEQAKK

Total Number of Spectra: 1

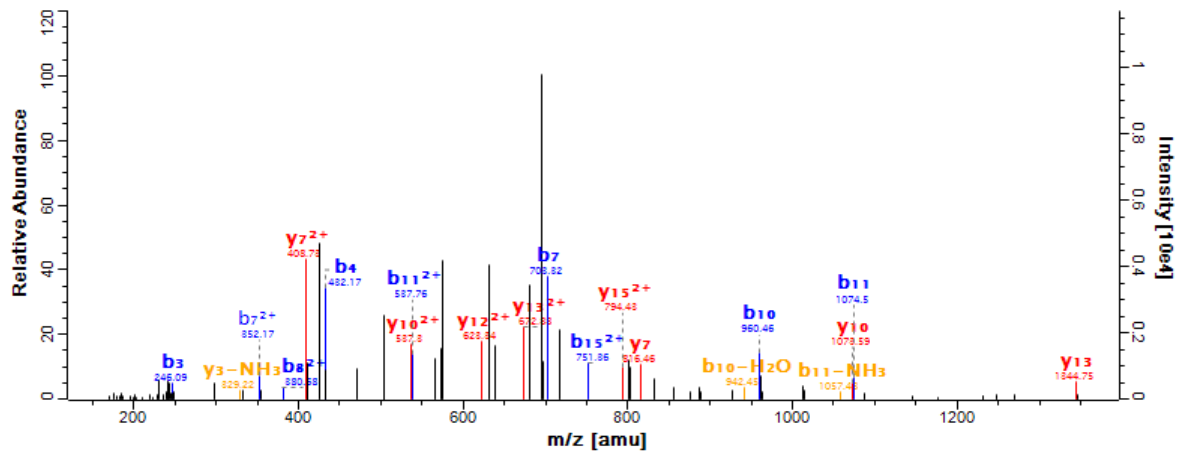
Number of Replicates (out of 8): 1

Best Match Score: 88.282

Best Match Posterior Error Probability: 0.0011195

Best Match Spectrum:

Scan number	69091	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	NRAP



Protein Group ID: 3936

Protein Accession Numbers: Q92574; Q92574-2; Q86WV8

Gene Names: TSC1

Peptide Sequence: MAQQANVGELLAMLDSPLGVR

Total Number of Spectra: 1

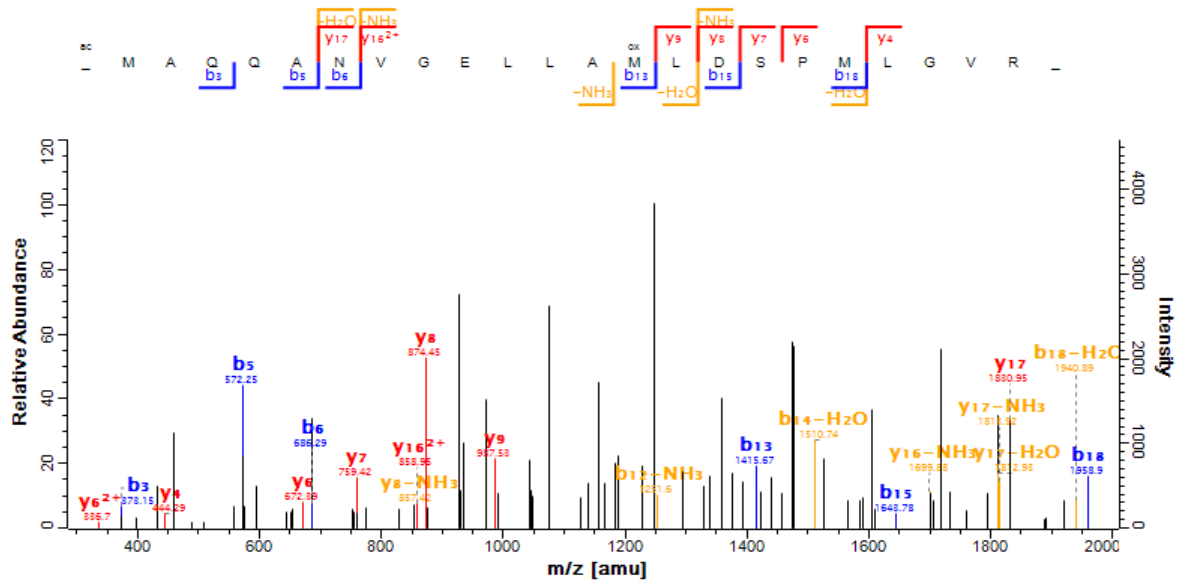
Number of Replicates (out of 8): 1

Best Match Score: 69.122

Best Match Posterior Error Probability: 0.0050181

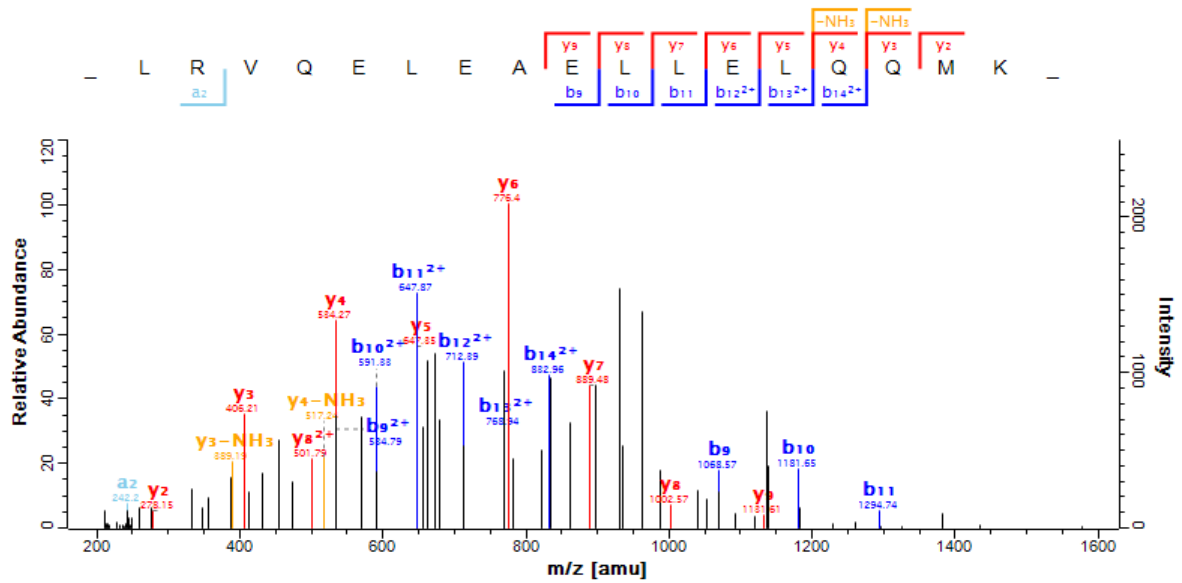
Best Match Spectrum:

Scan number	95803	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	TSC1



Protein Group ID: 3937
Protein Accession Numbers: Q86X02
Gene Names: CDR2L
Peptide Sequence: LRVQELEELLEQAELQLQMK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 103.79
Best Match Posterior Error Probability: 0.00066185
Best Match Spectrum:

Scan number 78136 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CDR2L



Protein Group ID: 3940

Protein Accession Numbers: Q86XK3-2; Q86XK3; Q86XK3-3

Gene Names: SFR1

Peptide Sequence: VESEENDQTFSEK

Total Number of Spectra: 1

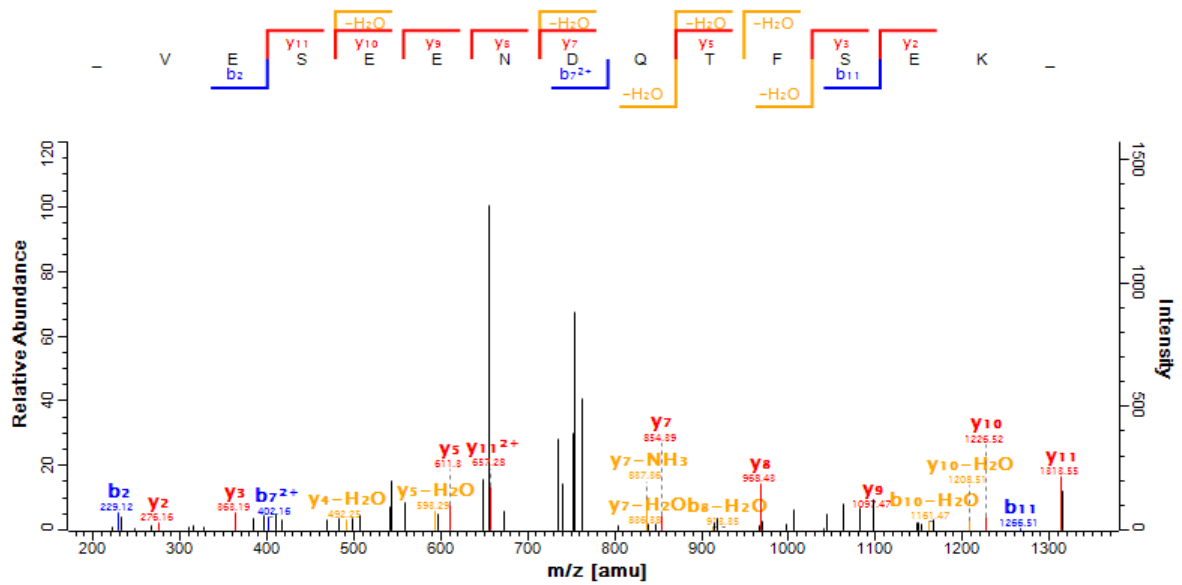
Number of Replicates (out of 8): 1

Best Match Score: 83.204

Best Match Posterior Error Probability: 0.0025871

Best Match Spectrum:

Scan number 9832 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SFR1



Protein Group ID: 3948

Protein Accession Numbers: Q86YL5-2; Q86YL5

Gene Names: C8orf42

Peptide Sequence: LALEDISADPEDTVGGHPSWSGWEDEDAK

Total Number of Spectra: 1

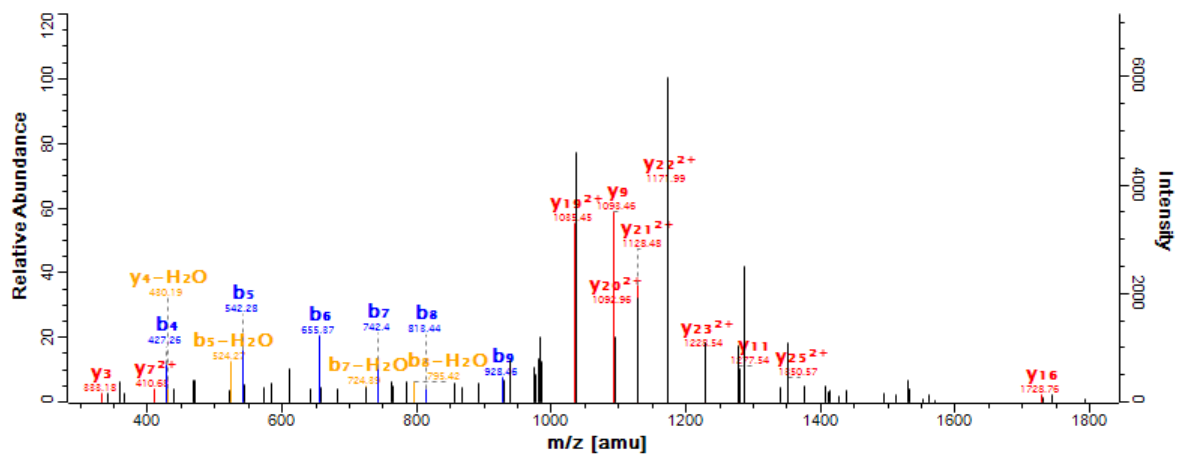
Number of Replicates (out of 8): 1

Best Match Score: 56.131

Best Match Posterior Error Probability: 0.001201

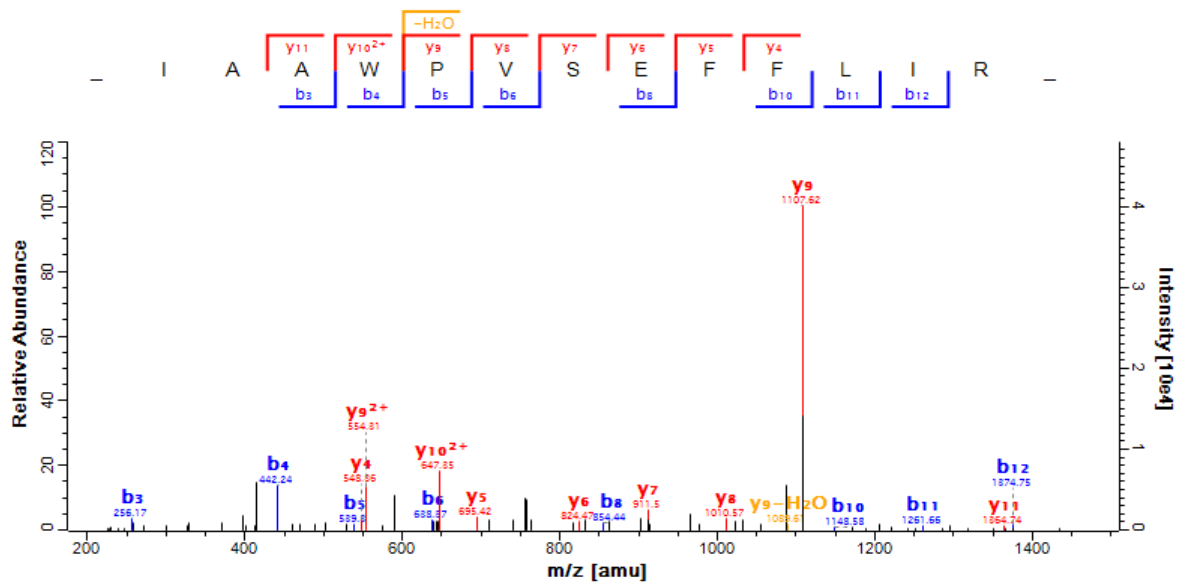
Best Match Spectrum:

Scan number	64116	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	C8orf42



Protein Group ID: 3949
Protein Accession Numbers: Q86YN1
Gene Names: DOLPP1
Peptide Sequence: IAAWPVSEFFLIR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 103.88
Best Match Posterior Error Probability: 0.00043764
Best Match Spectrum:

Scan number 91594 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** DOLPP1



Protein Group ID: 3951

Protein Accession Numbers: Q86YV9

Gene Names: HPS6

Peptide Sequence: TYLPDEVGPPTPFPEPGAEPPLTVGLLK

Total Number of Spectra: 3

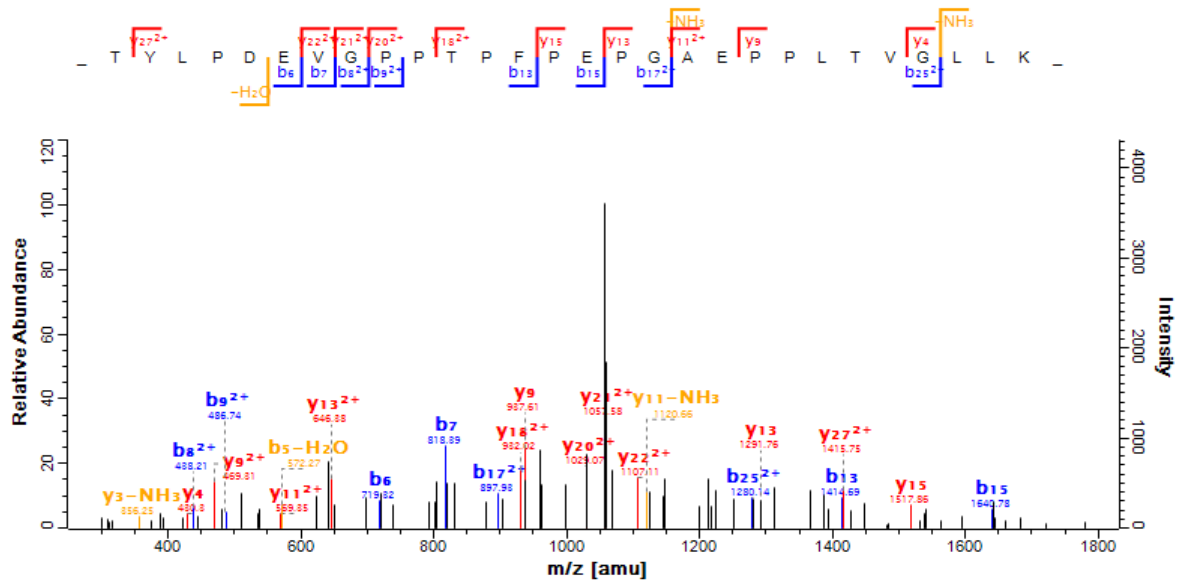
Number of Replicates (out of 8): 2

Best Match Score: 57.802

Best Match Posterior Error Probability: 0.0009891

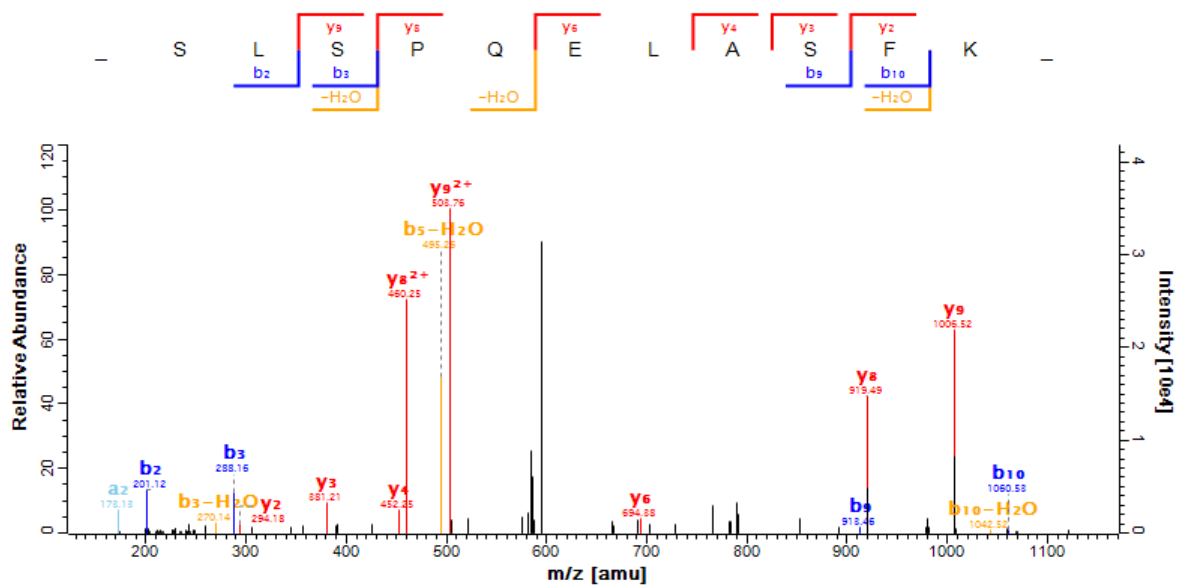
Best Match Spectrum:

Scan number 84145 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** HPS6



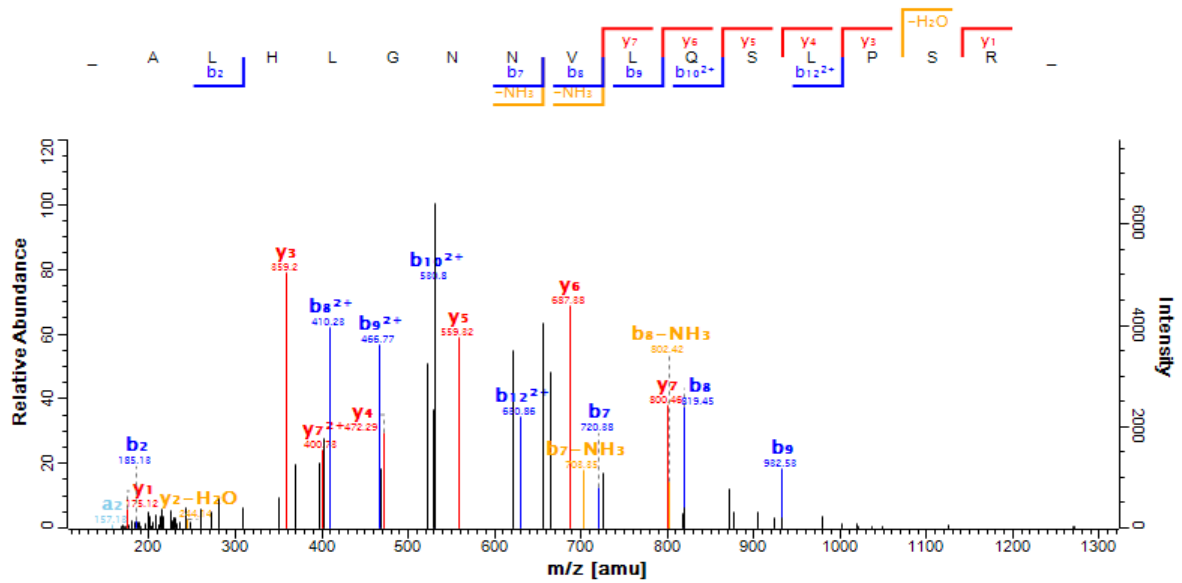
Protein Group ID: 3952
Protein Accession Numbers: Q8IU54
Gene Names: IL29
Peptide Sequence: SLSPQELASFSFK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 101.93
Best Match Posterior Error Probability: 0.00044728
Best Match Spectrum:

Scan number 44548 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** IL29



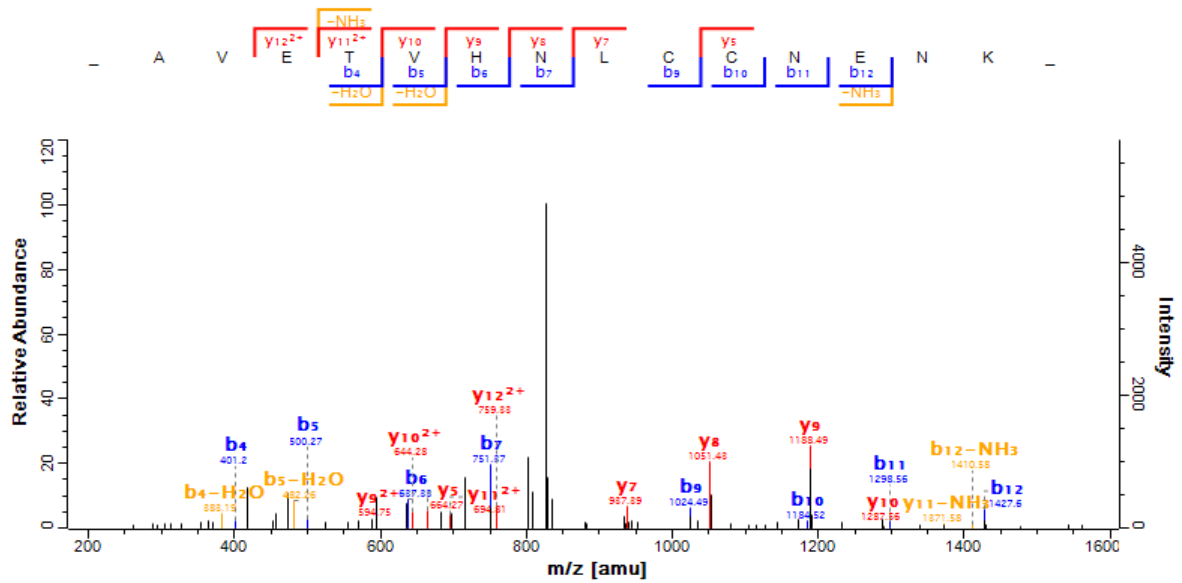
Protein Group ID: 3973
Protein Accession Numbers: Q8IWT6
Gene Names: LRRC8A
Peptide Sequence: ALHLGNNVLQSLPSR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 89.231
Best Match Posterior Error Probability: 0.00087245
Best Match Spectrum:

Scan number 47631 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** LRRC8A



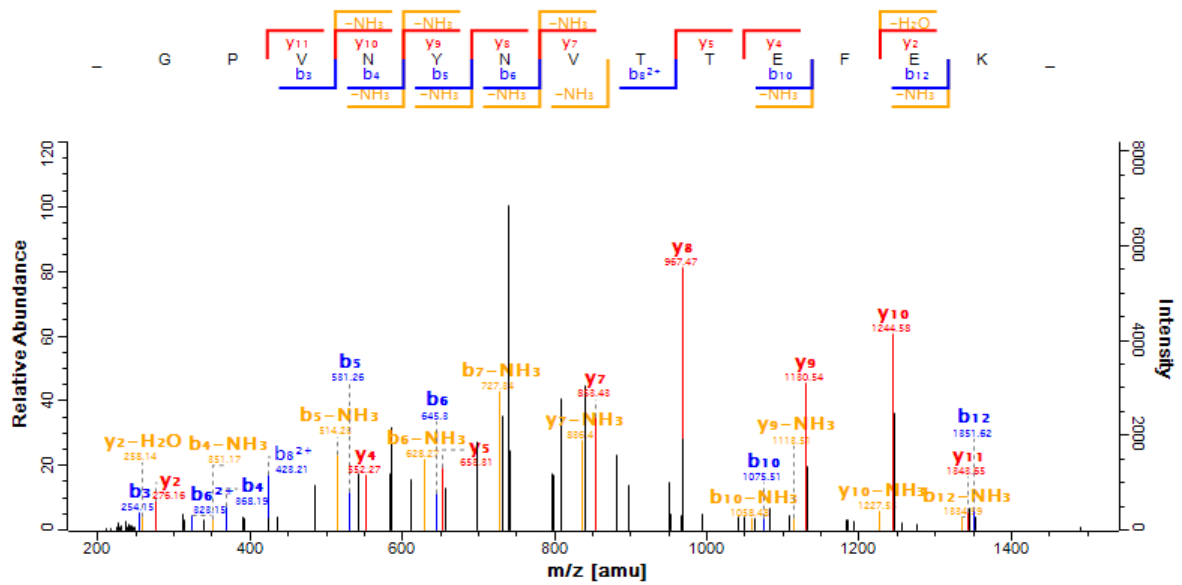
Protein Group ID: 3979
Protein Accession Numbers: Q8IXH7; Q8IXH7-4
Gene Names: TH1L
Peptide Sequence: AVETVHNLCCNENK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 91.307
Best Match Posterior Error Probability: 0.001073
Best Match Spectrum:

Scan number 12209 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TH1L



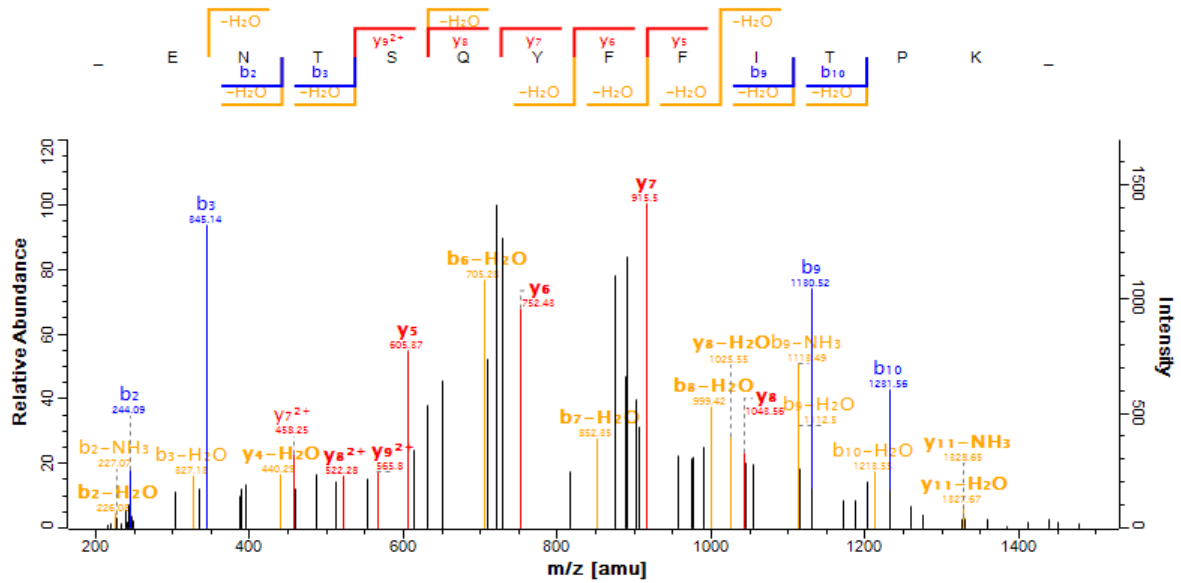
Protein Group ID: 3984
Protein Accession Numbers: Q8IXQ4; Q8IXQ4-2
Gene Names: KIAA1704
Peptide Sequence: GPVNYNVTTTEFEK
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 141.37
Best Match Posterior Error Probability: 1.64E-05
Best Match Spectrum:

Scan number 40036 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** KIAA1704



Protein Group ID: 3985
Protein Accession Numbers: Q8IY18
Gene Names: SMC5
Peptide Sequence: ENTSQYFFITPK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 117.07
Best Match Posterior Error Probability: 0.00016953
Best Match Spectrum:

Scan number 49951 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SMC5



Protein Group ID: 3991

Protein Accession Numbers: Q8IYB5; Q8IYB5-2; Q8IYB5-3

Gene Names: SMAP1

Peptide Sequence: RPQTDQAVEFFIR

Total Number of Spectra: 8

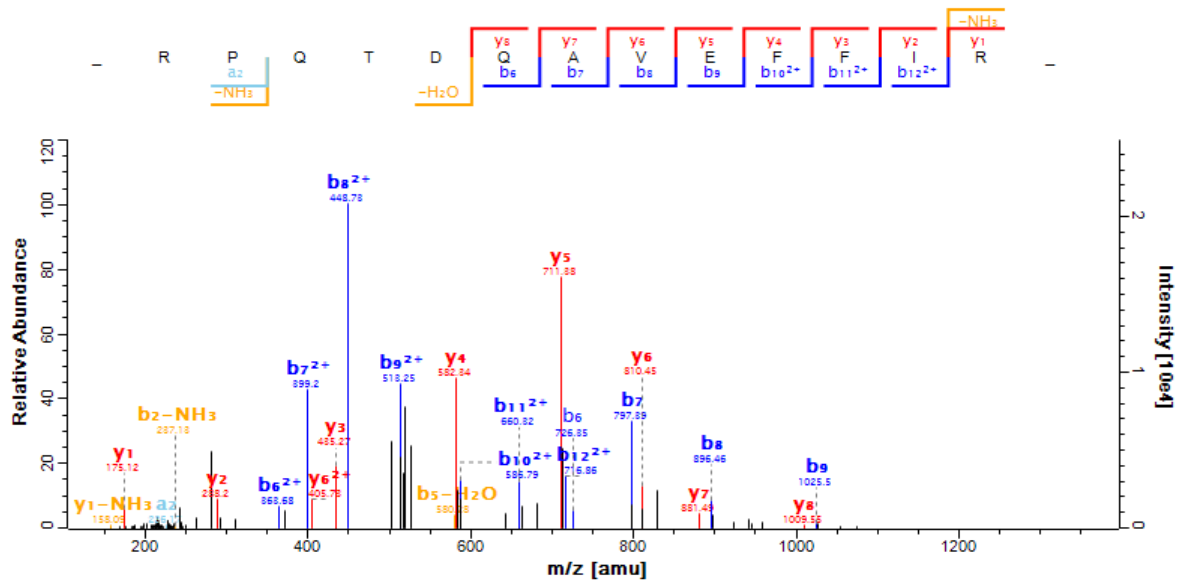
Number of Replicates (out of 8): 7

Best Match Score: 133.32

Best Match Posterior Error Probability: 0.00010771

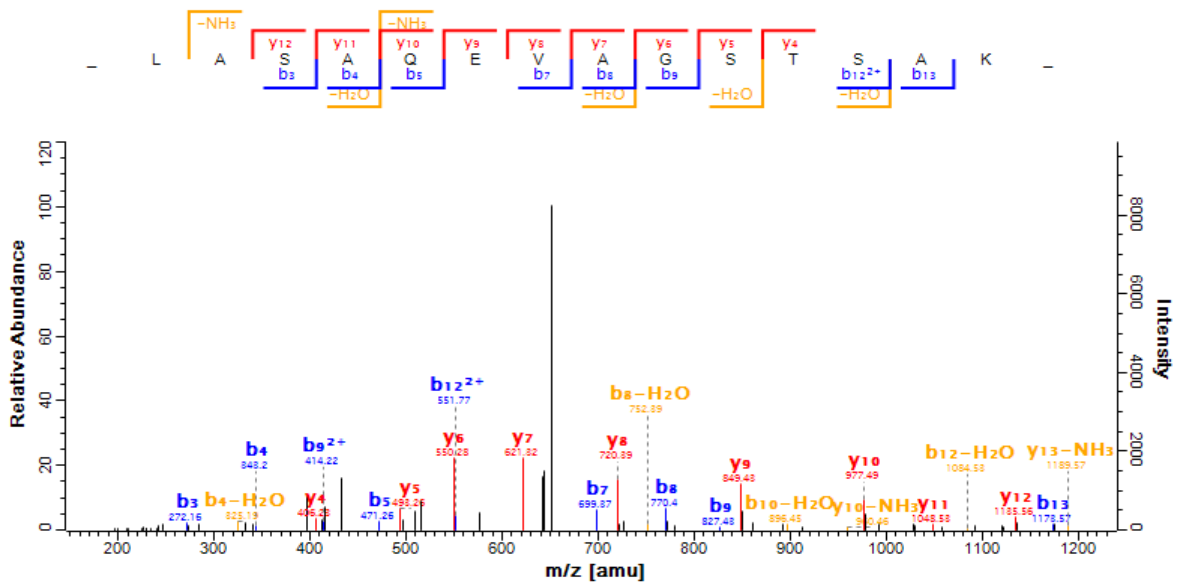
Best Match Spectrum:

Scan number	49095	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	SMAP1



Protein Group ID: 3995
Protein Accession Numbers: Q8IYL3
Gene Names: Clorf174
Peptide Sequence: LASAQEVAGSTSAK
Total Number of Spectra: 4
Number of Replicates (out of 8): 3
Best Match Score: 90.725
Best Match Posterior Error Probability: 0.0011283
Best Match Spectrum:

Scan number 11899 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** Clorf174



Protein Group ID: 3997

Protein Accession Numbers: Q8IYS1

Gene Names: PM20D2

Peptide Sequence: ASHSASYPWEGLNALDAAVLAYNNLSVFR

Total Number of Spectra: 2

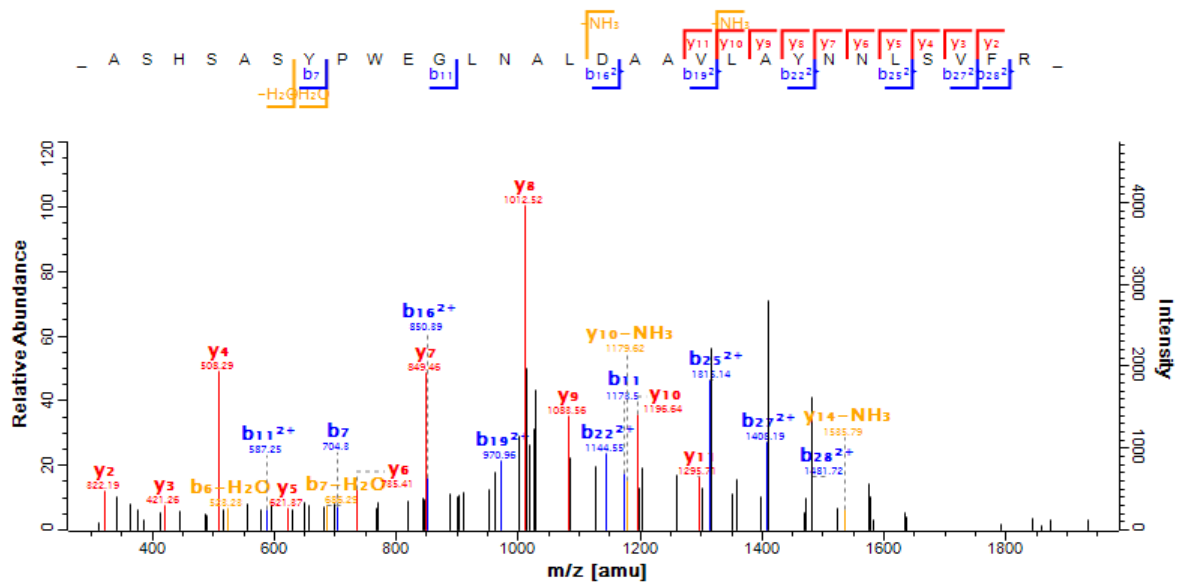
Number of Replicates (out of 8): 2

Best Match Score: 61.417

Best Match Posterior Error Probability: 0.00033224

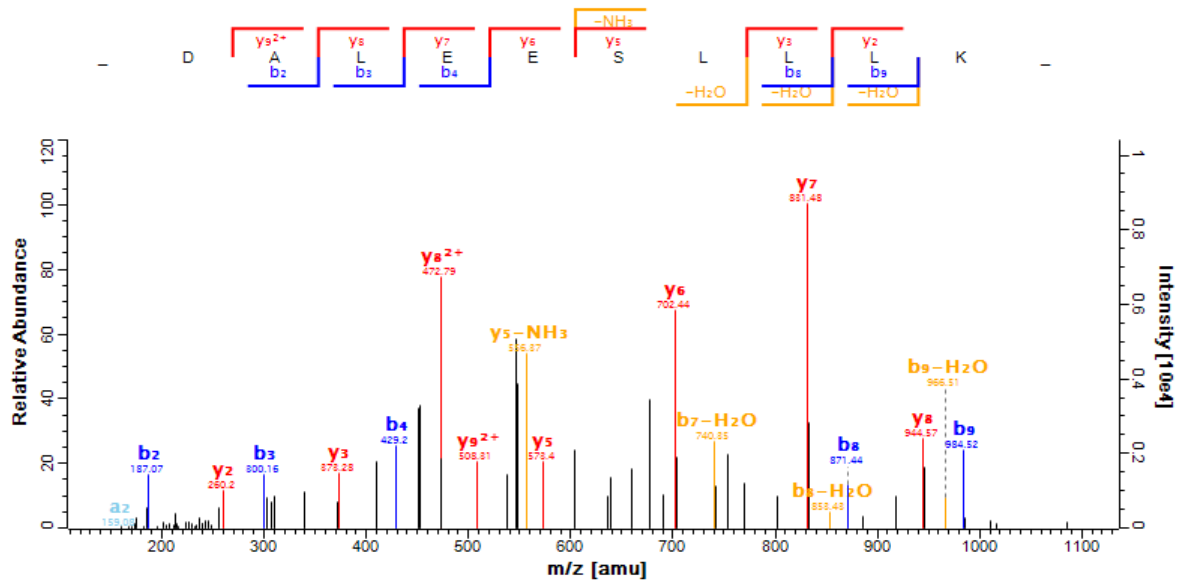
Best Match Spectrum:

Scan number	92597	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	PM20D2



Protein Group ID: 4001
Protein Accession Numbers: Q8IZJ0; Q8IZI9
Gene Names: IL28A;IL28B
Peptide Sequence: DALEESLLLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 92.538
Best Match Posterior Error Probability: 0.0016515
Best Match Spectrum:

Scan number 52811 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** IL28A;IL28B



Protein Group ID: 4006

Protein Accession Numbers: Q8N108-12; Q8N108-13; Q8N108; Q8N108-15; Q8N108-17; Q8N108-18; Q8N108-14; Q8N108-16; Q8N108-19

Gene Names: MIER1

Peptide Sequence: DNEQALYELVK

Total Number of Spectra: 1

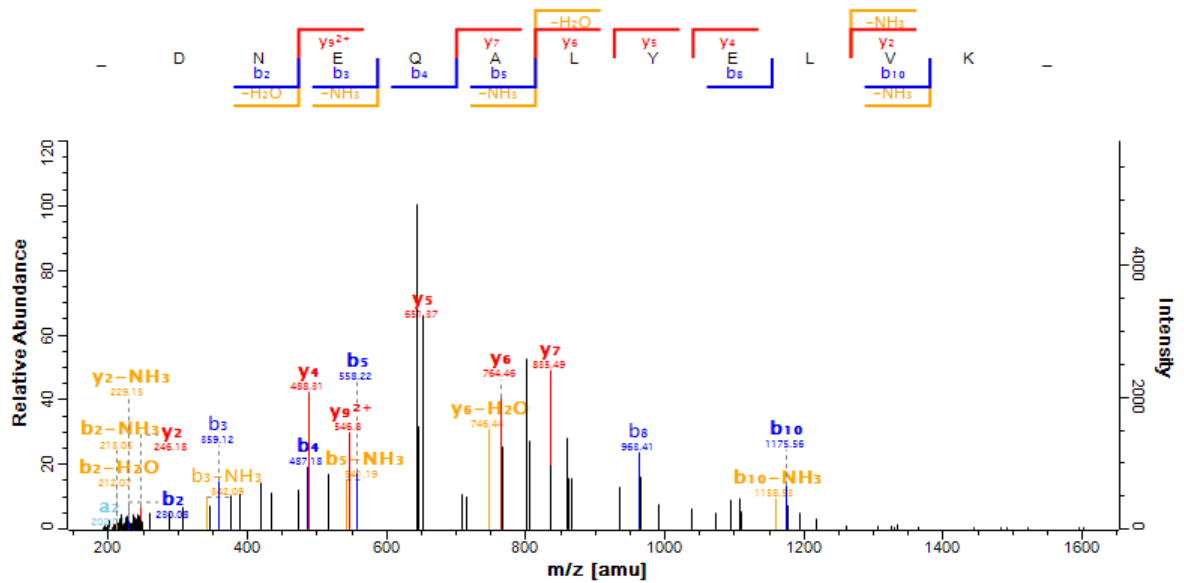
Number of Replicates (out of 8): 1

Best Match Score: 86.772

Best Match Posterior Error Probability: 0.0019088

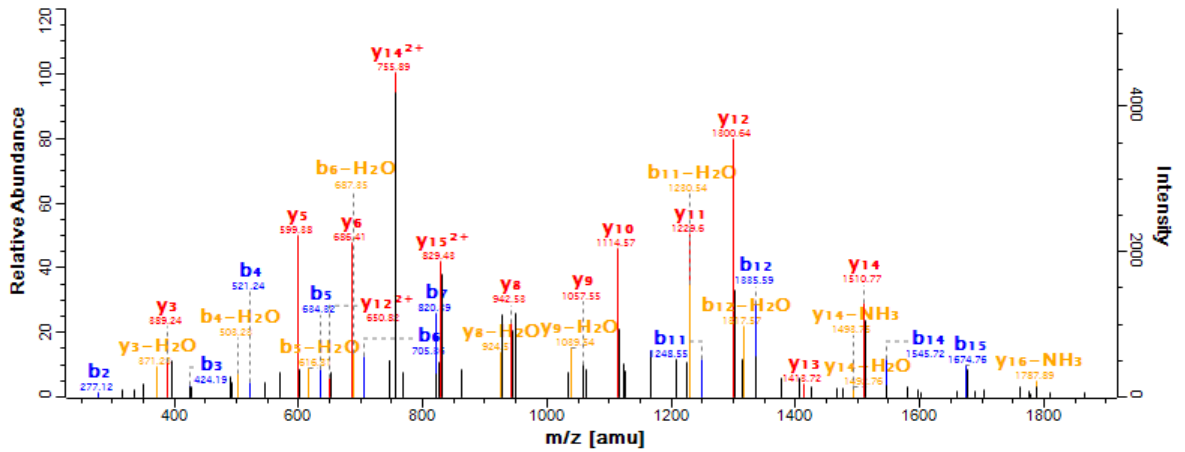
Best Match Spectrum:

Scan number 50004 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** MIER1



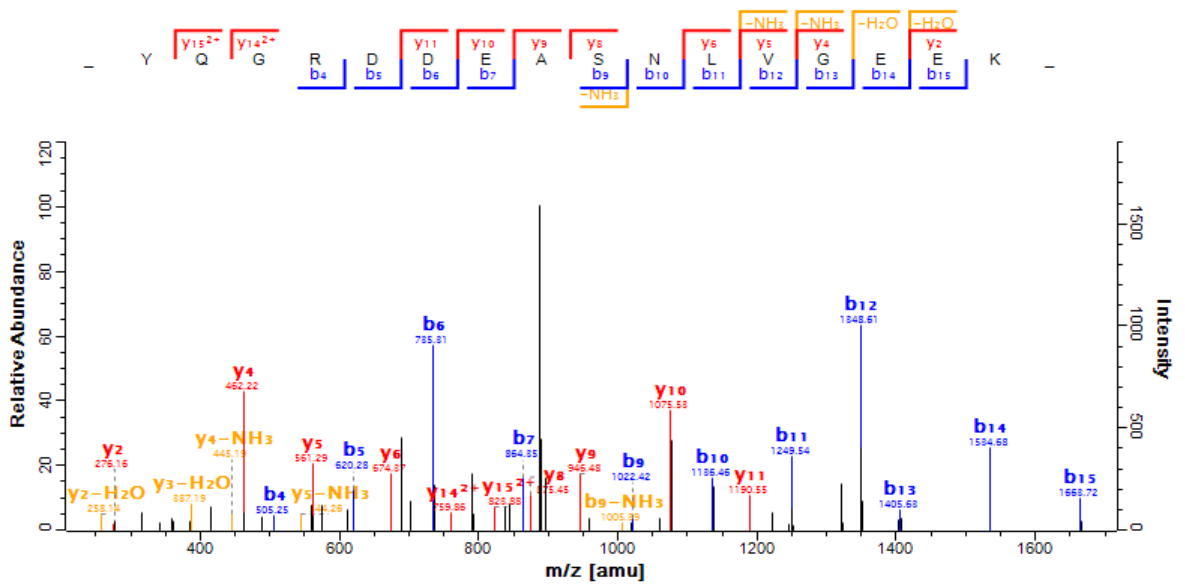
Protein Group ID: 4011
Protein Accession Numbers: Q8N1Q1
Gene Names: CA13
Peptide Sequence: EFFPIADGDQQSPIEIK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 202.41
Best Match Posterior Error Probability: 3.20E-30
Best Match Spectrum:

Scan number 64703 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CA13



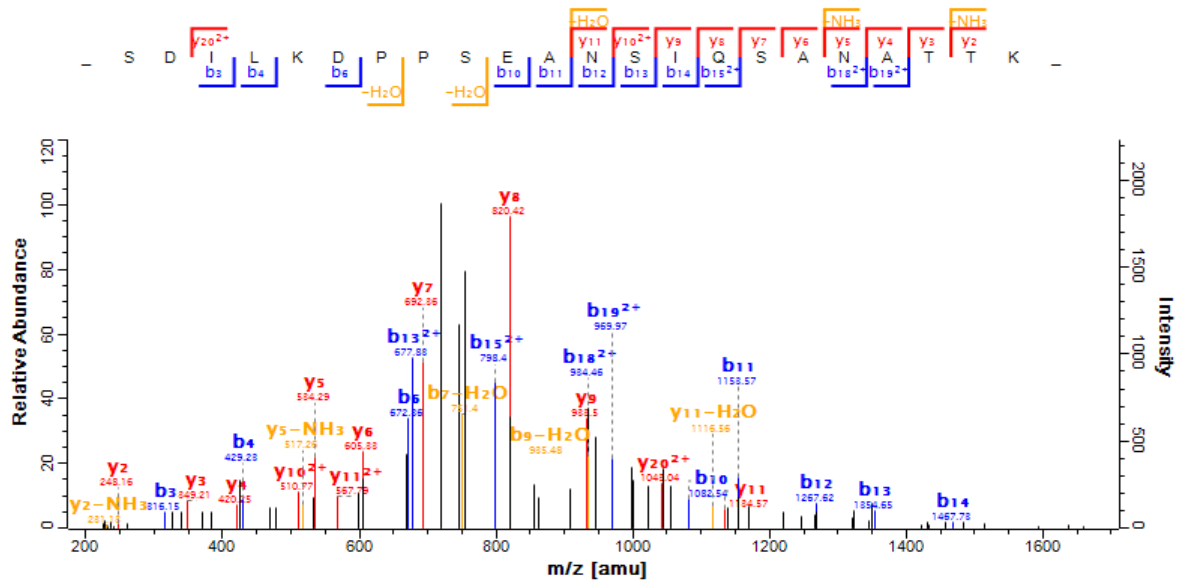
Protein Group ID: 4016
Protein Accession Numbers: Q8N392; Q8N392-2
Gene Names: ARHGAP18
Peptide Sequence: YQGRDDEASNLVGEEK
Total Number of Spectra: 5
Number of Replicates (out of 8): 4
Best Match Score: 133.86
Best Match Posterior Error Probability: 0.00022249
Best Match Spectrum:

Scan number 17381 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ARHGAP18



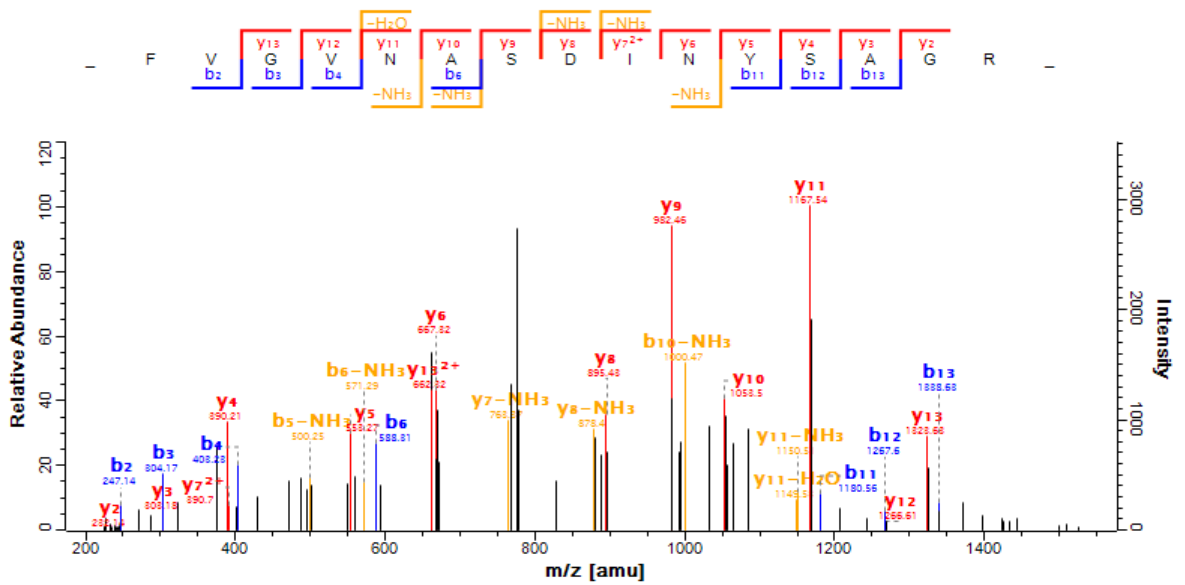
Protein Group ID: 4023
Protein Accession Numbers: Q8N488
Gene Names: RYBP
Peptide Sequence: SDILKDPPEANSIQSANATTK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 99.569
Best Match Posterior Error Probability: 5.12E-05
Best Match Spectrum:

Scan number 31582 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** RYBP



Protein Group ID: 4027
Protein Accession Numbers: Q8N4Q0
Gene Names: ZADH2
Peptide Sequence: FVGVNASDINYSAGR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 112.96
Best Match Posterior Error Probability: 0.00010689
Best Match Spectrum:

Scan number 38888 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ZADH2



Protein Group ID: 4029

Protein Accession Numbers: Q8N4V1-2; Q8N4V1

Gene Names: MMGT1

Peptide Sequence: VLFRPSDTANSSNQDALSSLK

Total Number of Spectra: 10

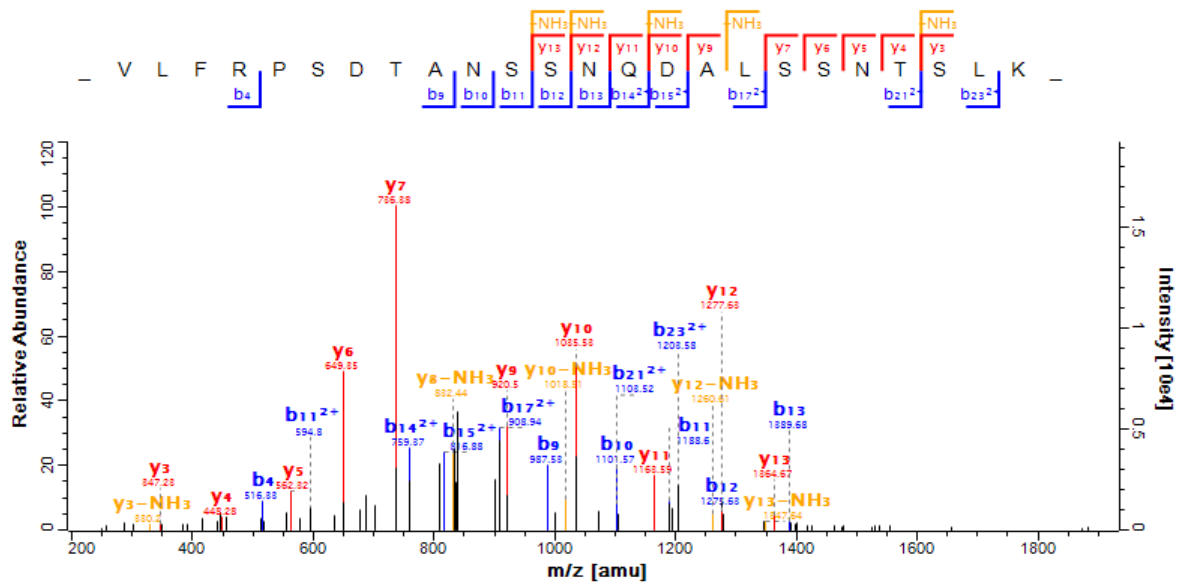
Number of Replicates (out of 8): 8

Best Match Score: 124.08

Best Match Posterior Error Probability: 2.53E-11

Best Match Spectrum:

Scan number 36423 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MMGT1



Protein Group ID: 4031

Protein Accession Numbers: Q8N5A5; Q8N5A5-2; Q8N5A5-3

Gene Names: ZGPAT

Peptide Sequence: EAITEAVEAPAAAR

Total Number of Spectra: 3

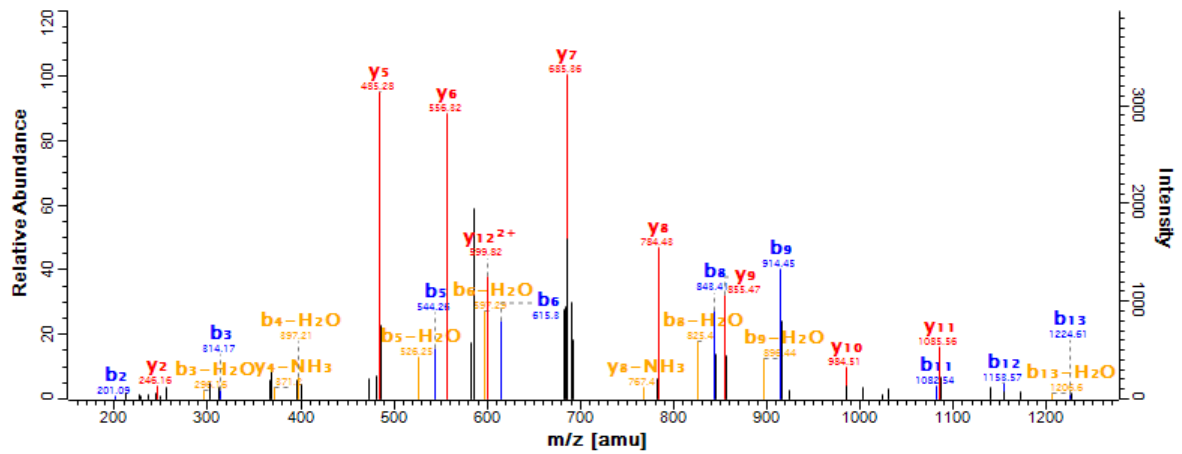
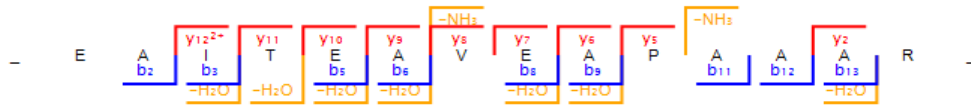
Number of Replicates (out of 8): 3

Best Match Score: 146.79

Best Match Posterior Error Probability: 2.19E-06

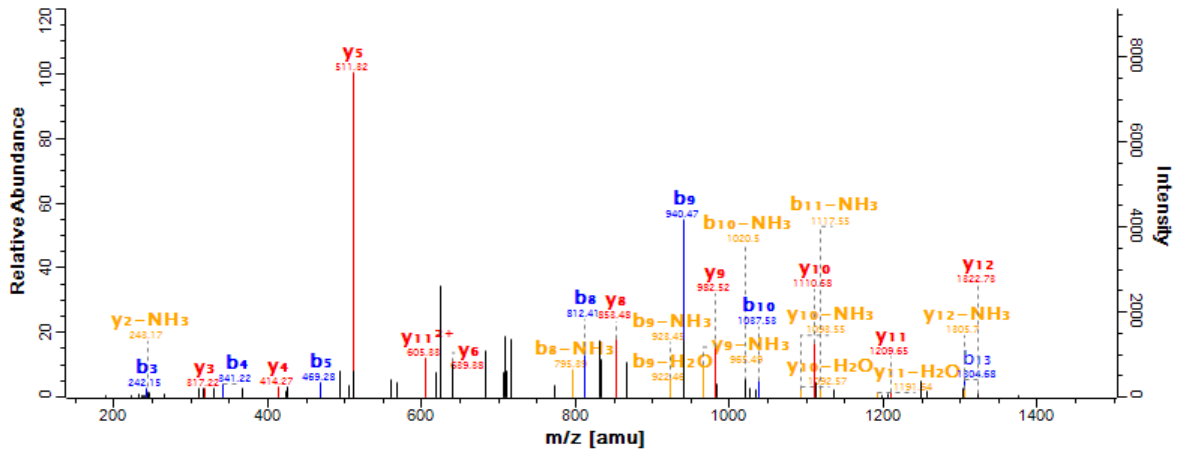
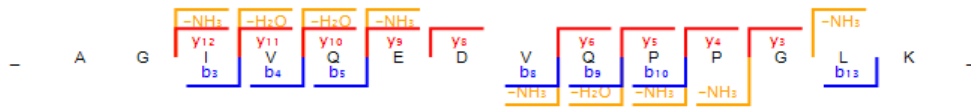
Best Match Spectrum:

Scan number 30143 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ZGPAT



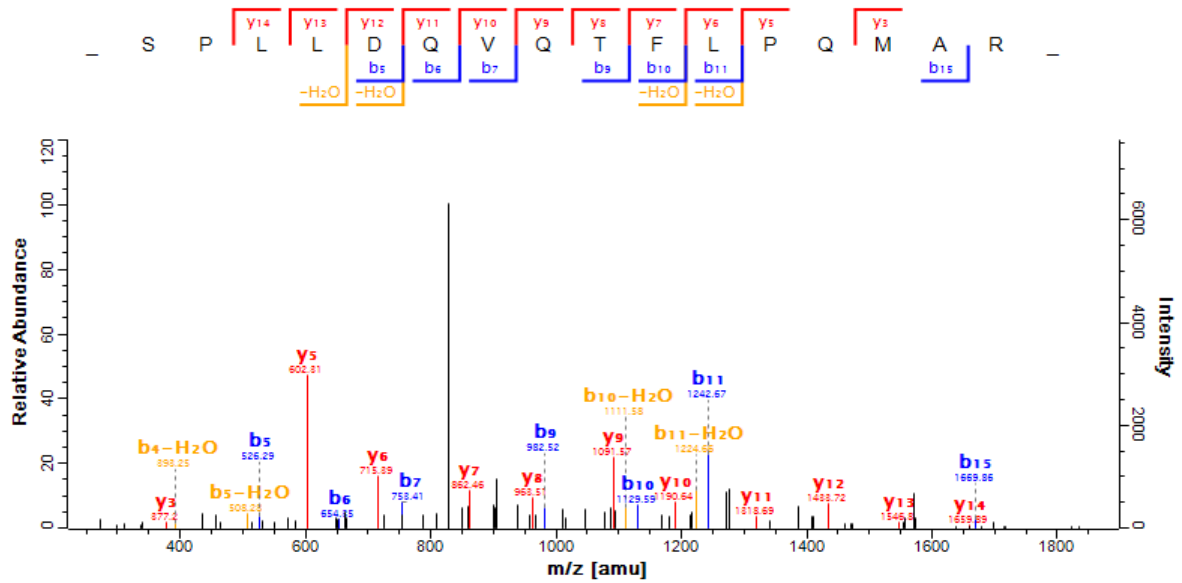
Protein Group ID: 4034
Protein Accession Numbers: Q8N5G0; Q8N5G0-2
Gene Names: C4orf52
Peptide Sequence: AGIVQEDVQPPGLK
Total Number of Spectra: 5
Number of Replicates (out of 8): 4
Best Match Score: 143.94
Best Match Posterior Error Probability: 7.11E-06
Best Match Spectrum:

Scan number 37720 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** C4orf52



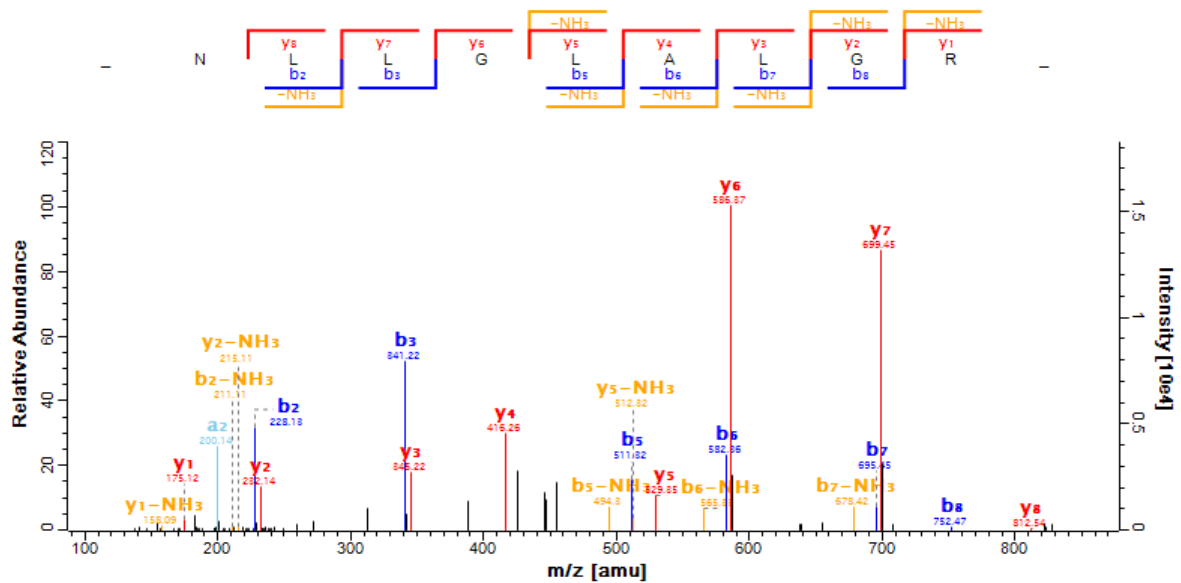
Protein Group ID: 4035
Protein Accession Numbers: Q8N5I9
Gene Names: C12orf45
Peptide Sequence: SPLLDQVQTFLPQMAR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 95.767
Best Match Posterior Error Probability: 0.00031126
Best Match Spectrum:

Scan number 78421 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** C12orf45



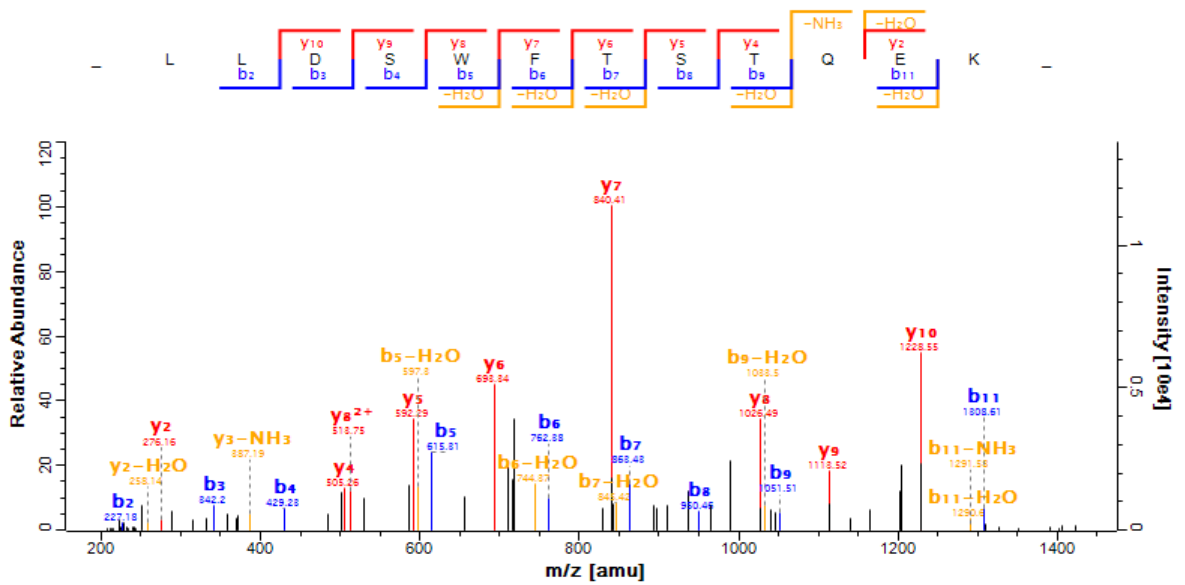
Protein Group ID: 4036
Protein Accession Numbers: Q8N5L8
Gene Names: RPP25L
Peptide Sequence: NLLGLALGR
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 149.82
Best Match Posterior Error Probability: 1.93E-05
Best Match Spectrum:

Scan number 57615 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** RPP25L



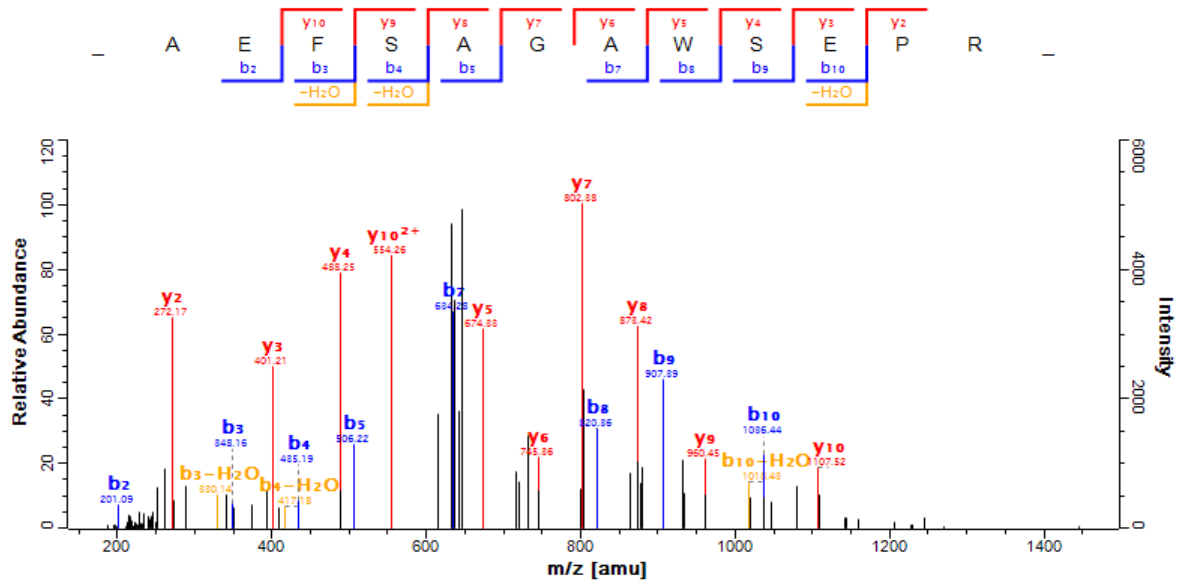
Protein Group ID: 4037
Protein Accession Numbers: Q8N5M9
Gene Names: JAGN1
Peptide Sequence: LLDSWFTSTQEK
Total Number of Spectra: 8
Number of Replicates (out of 8): 8
Best Match Score: 156.36
Best Match Posterior Error Probability: 3.80E-07
Best Match Spectrum:

Scan number 56051 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** JAGN1



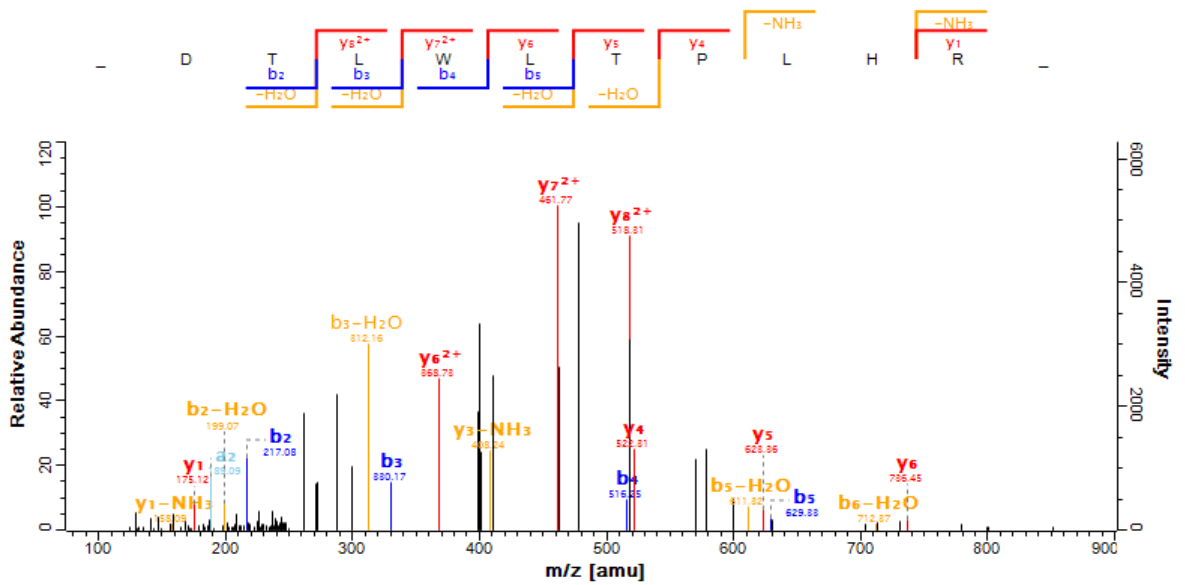
Protein Group ID: 4044
Protein Accession Numbers: Q8N6S5
Gene Names: ARL6IP6
Peptide Sequence: AEFSAGAWSEPR
Total Number of Spectra: 5
Number of Replicates (out of 8): 3
Best Match Score: 124.12
Best Match Posterior Error Probability: 0.00010302
Best Match Spectrum:

Scan number 35999 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ARL6IP6



Protein Group ID: 4055
Protein Accession Numbers: Q8NB46
Gene Names: ANKRD52
Peptide Sequence: DTLWLTP LHR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 100.02
Best Match Posterior Error Probability: 0.00078513
Best Match Spectrum:

Scan number 51132 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ANKRD52



Protein Group ID: 4061

Protein Accession Numbers: Q8NBM4; Q8NBM4-2; Q8NBM4-3; Q8NBM4-4

Gene Names: UBAC2

Peptide Sequence: QSEPAAPPLEVSEEQVAR

Total Number of Spectra: 6

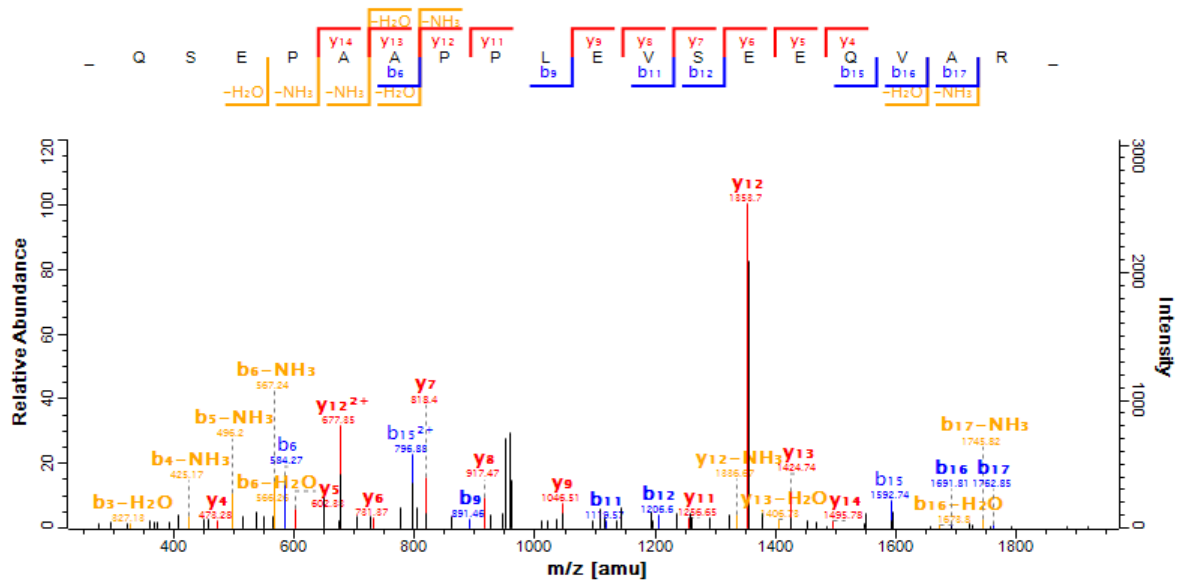
Number of Replicates (out of 8): 4

Best Match Score: 98.169

Best Match Posterior Error Probability: 0.00019595

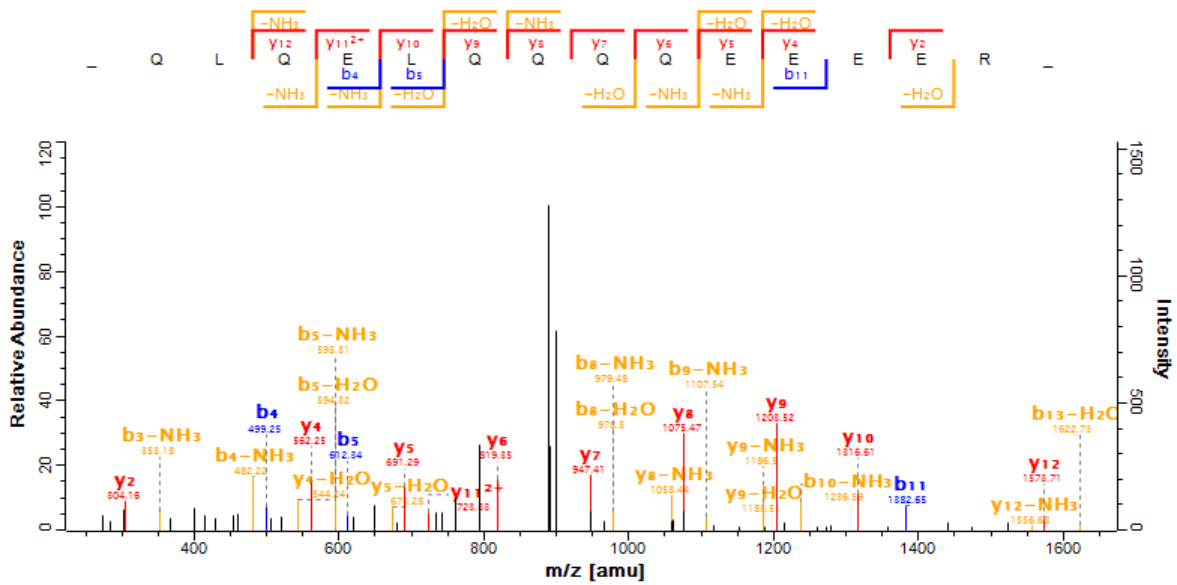
Best Match Spectrum:

Scan number 37912 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** UBAC2



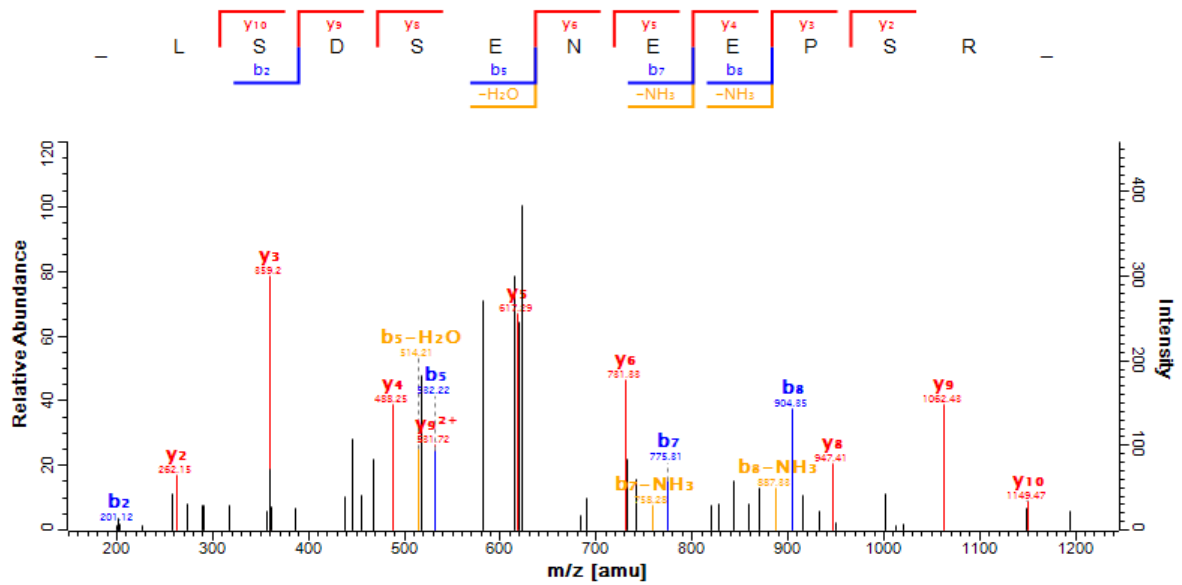
Protein Group ID: 4071
Protein Accession Numbers: Q8NC60
Gene Names: NOA1
Peptide Sequence: QLQELQQQEEEEER
Total Number of Spectra: 3
Number of Replicates (out of 8): 2
Best Match Score: 144.27
Best Match Posterior Error Probability: 5.96E-06
Best Match Spectrum:

Scan number 18130 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** NOA1



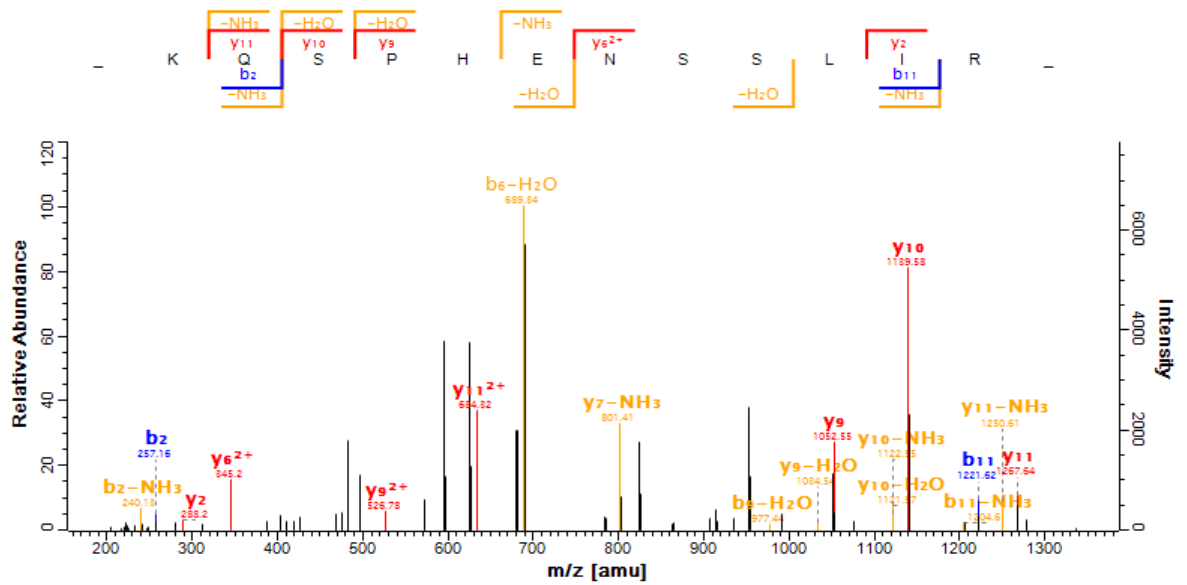
Protein Group ID: 4074
Protein Accession Numbers: Q8NCN4
Gene Names: RNF169
Peptide Sequence: LSDSENEEPSR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 85.522
Best Match Posterior Error Probability: 0.0022799
Best Match Spectrum:

Scan number 4393 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** RNF169



Protein Group ID: 4079
Protein Accession Numbers: Q8NDH2
Gene Names: CCDC168
Peptide Sequence: KQSPHENSILR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 87.184
Best Match Posterior Error Probability: 0.0040334
Best Match Spectrum:

Scan number 15047 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CCDC168



Protein Group ID: 4082

Protein Accession Numbers: Q8NDV7; Q8NDV7-5; Q8NDV7-6; Q8NDV7-2

Gene Names: TNRC6A

Peptide Sequence: TGGTVESDGSTESTGR

Total Number of Spectra: 2

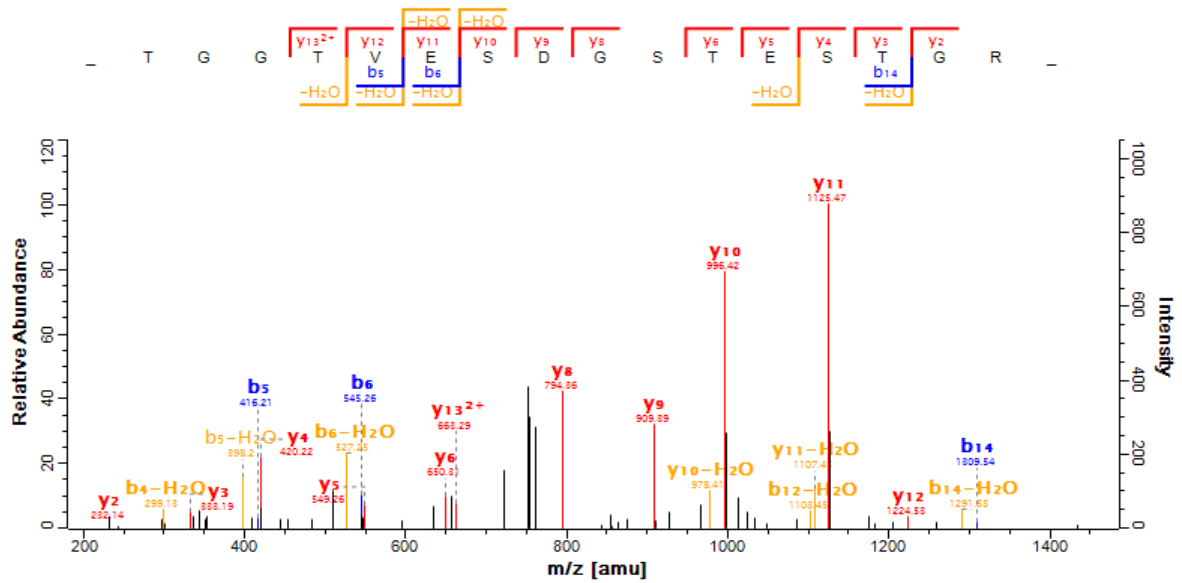
Number of Replicates (out of 8): 2

Best Match Score: 104.41

Best Match Posterior Error Probability: 0.00014064

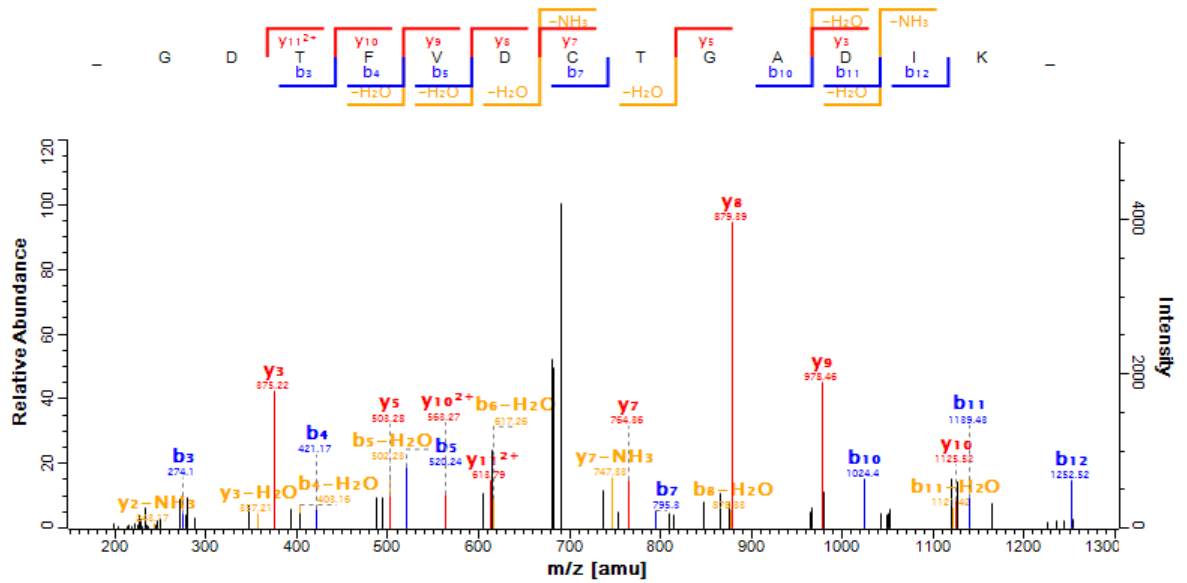
Best Match Spectrum:

Scan number 2860 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TNRC6A



Protein Group ID: 4087
Protein Accession Numbers: Q8NEM2
Gene Names: SHCBP1
Peptide Sequence: GDTFVDCTGADIK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 113.24
Best Match Posterior Error Probability: 0.00026425
Best Match Spectrum:

Scan number 30302 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** SHCBP1



Protein Group ID: 4095

Protein Accession Numbers: Q8NFJ5

Gene Names: GPRC5A

Peptide Sequence: AYSQEEITQGFEETGDTLYAPYSTHFQLQNQPQK

Total Number of Spectra: 12

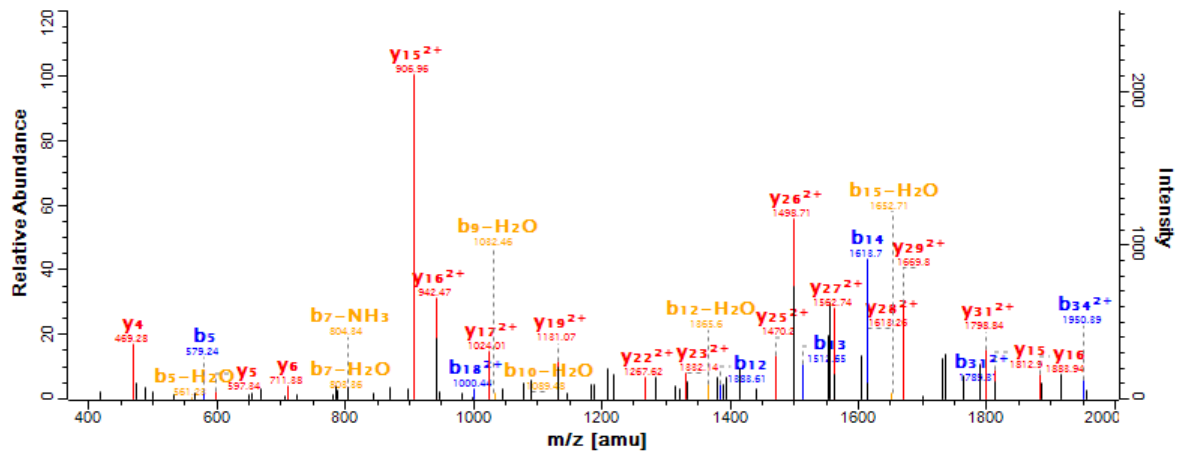
Number of Replicates (out of 8): 7

Best Match Score: 100.95

Best Match Posterior Error Probability: 4.28E-18

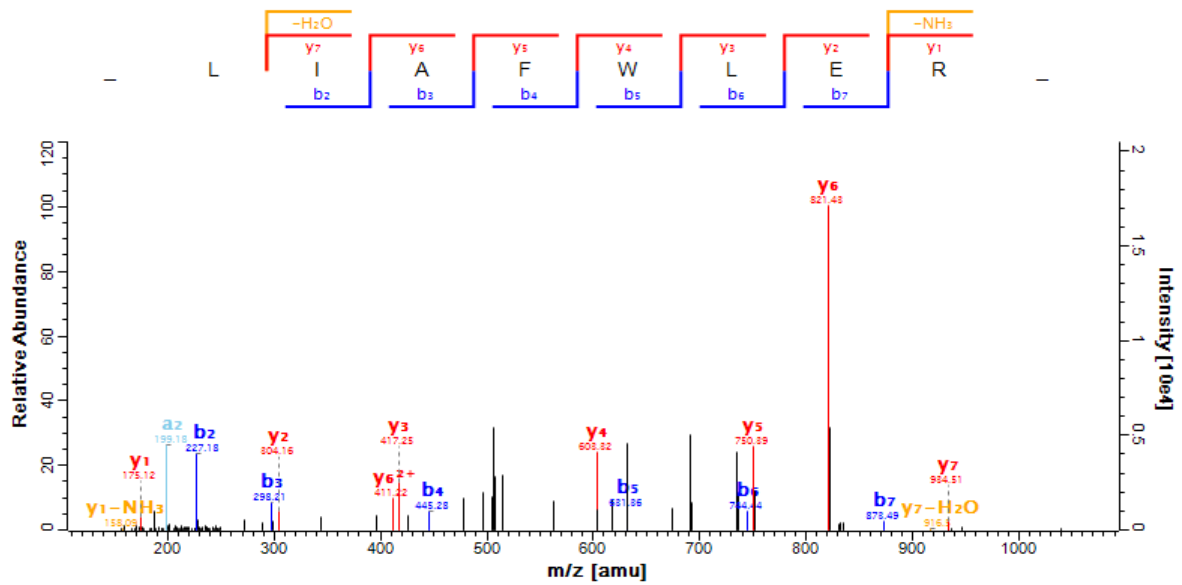
Best Match Spectrum:

Scan number 68303 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** GPRC5A



Protein Group ID: 4099
Protein Accession Numbers: Q8NHP6; Q8NHP6-2
Gene Names: MOSPD2
Peptide Sequence: LIAFWLER
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 111.95
Best Match Posterior Error Probability: 0.0027497
Best Match Spectrum:

Scan number	68101	Raw file	A549-US-WT-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	MOSPD2



Protein Group ID: 4107

Protein Accession Numbers: Q8TAD4; Q8TAD4-2

Gene Names: SLC30A5

Peptide Sequence: GTLIGYSPEGTPLYNFMGDAFQHSQSIPR

Total Number of Spectra: 1

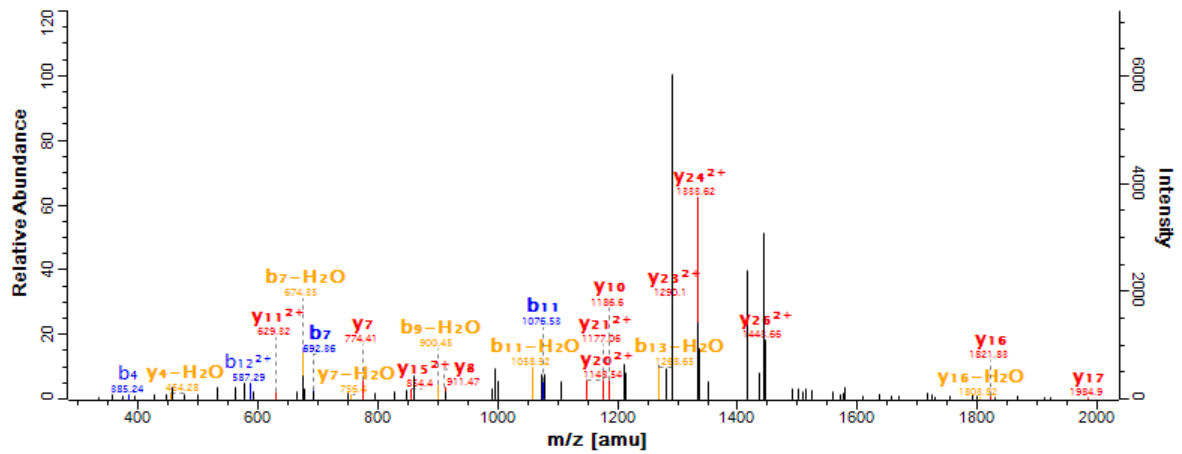
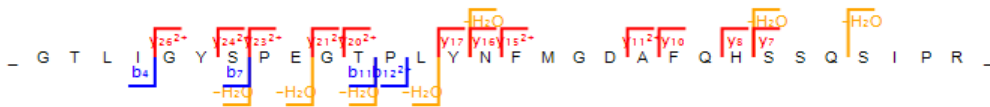
Number of Replicates (out of 8): 1

Best Match Score: 58.272

Best Match Posterior Error Probability: 0.00052967

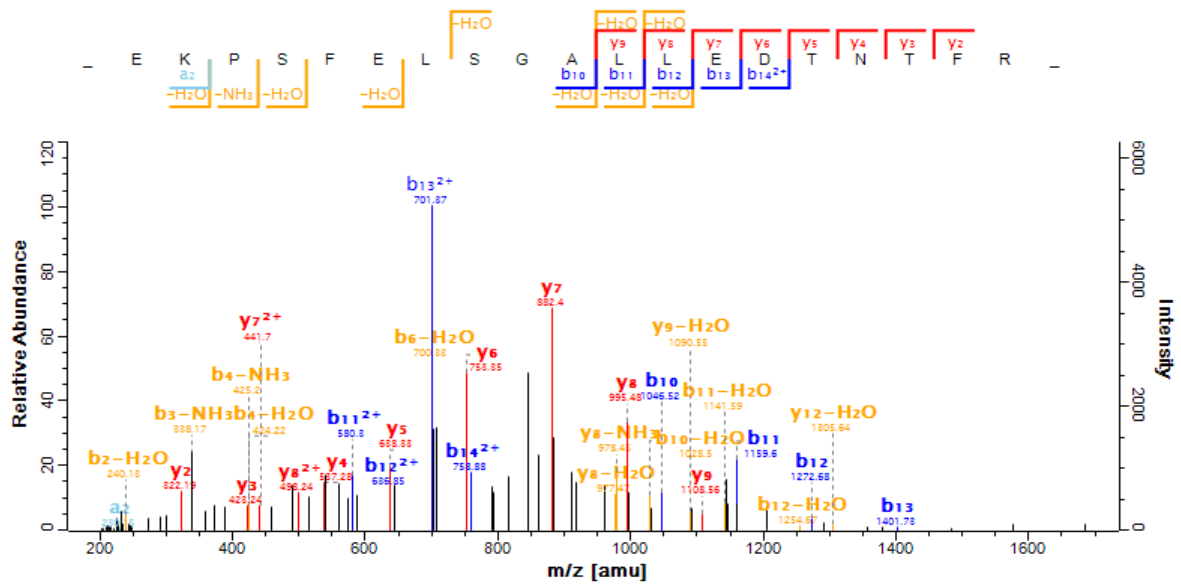
Best Match Spectrum:

Scan number 83432 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** SLC30A5



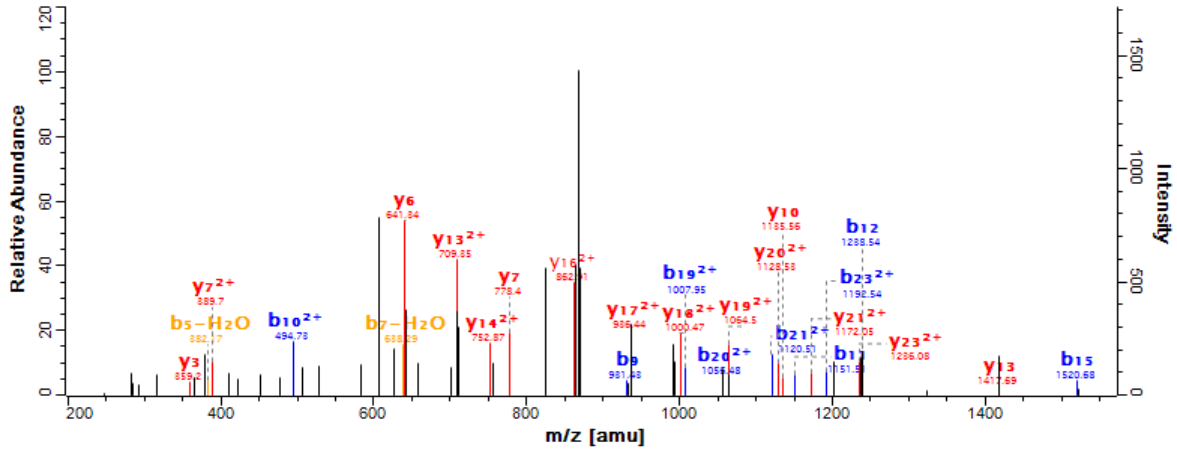
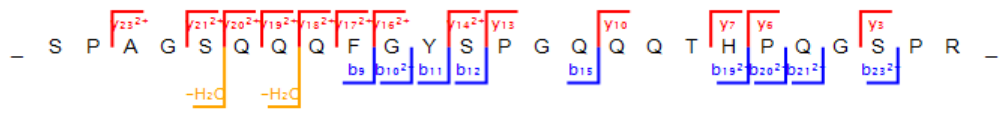
Protein Group ID: 4108
Protein Accession Numbers: Q8TAD8
Gene Names: SNIP1
Peptide Sequence: EKPSFELSGALSLR
Total Number of Spectra: 5
Number of Replicates (out of 8): 4
Best Match Score: 117.18
Best Match Posterior Error Probability: 9.88E-05
Best Match Spectrum:

Scan number 64570 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** SNIP1



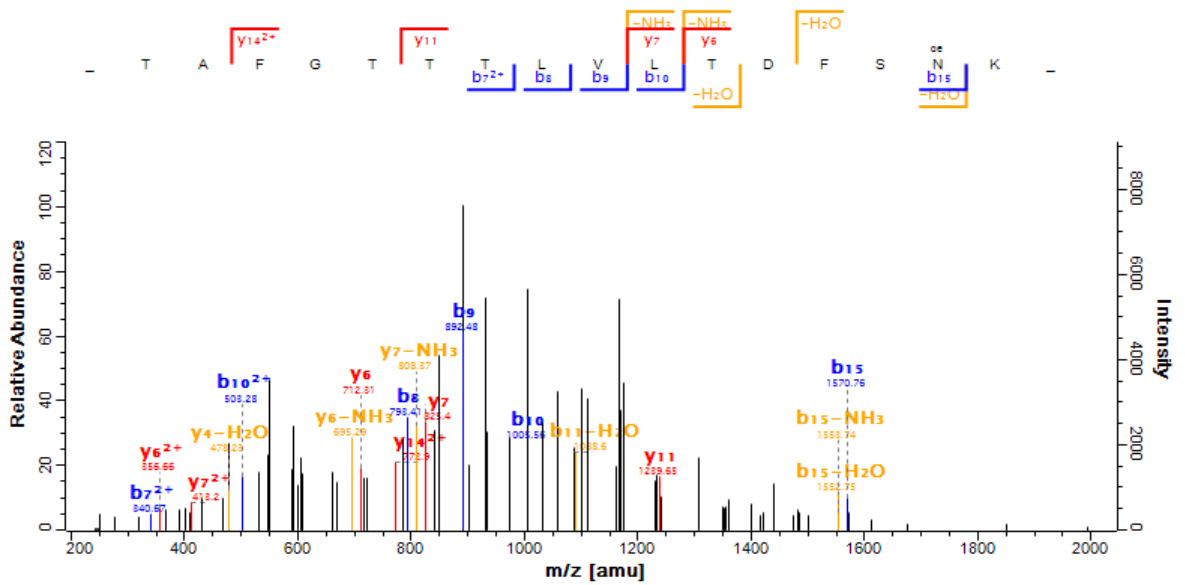
Protein Group ID: 4111
Protein Accession Numbers: Q8TAP9
Gene Names: MPLKIP
Peptide Sequence: SPAGSQQFGYSPGQQTHPQGS
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 80.109
Best Match Posterior Error Probability: 9.03E-05
Best Match Spectrum:

Scan number 19427 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MPLKIP



Protein Group ID: 4113
Protein Accession Numbers: Q8TAT5
Gene Names: NEIL3
Peptide Sequence: TAFGTTTLVLTFDSNK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 81.904
Best Match Posterior Error Probability: 0.0084319
Best Match Spectrum:

Scan number 64962 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** NEIL3



Protein Group ID: 4115

Protein Accession Numbers: Q8TB22-2; Q8TB22; Q8TB22-4

Gene Names: SPATA20

Peptide Sequence: SATVSSVPMAGGK

Total Number of Spectra: 2

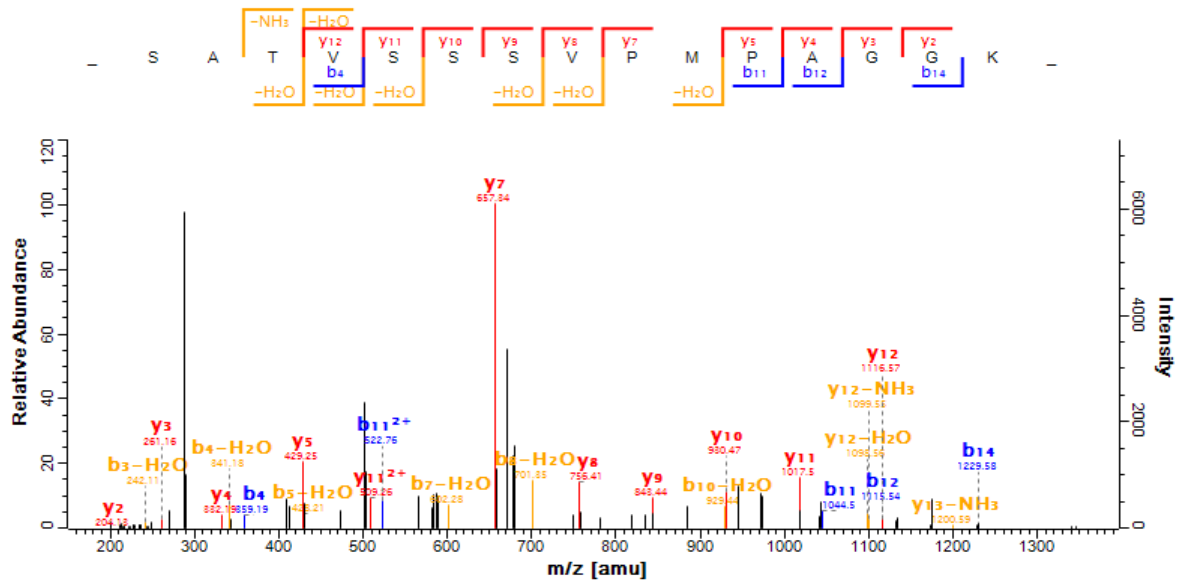
Number of Replicates (out of 8): 2

Best Match Score: 76.01

Best Match Posterior Error Probability: 0.0034692

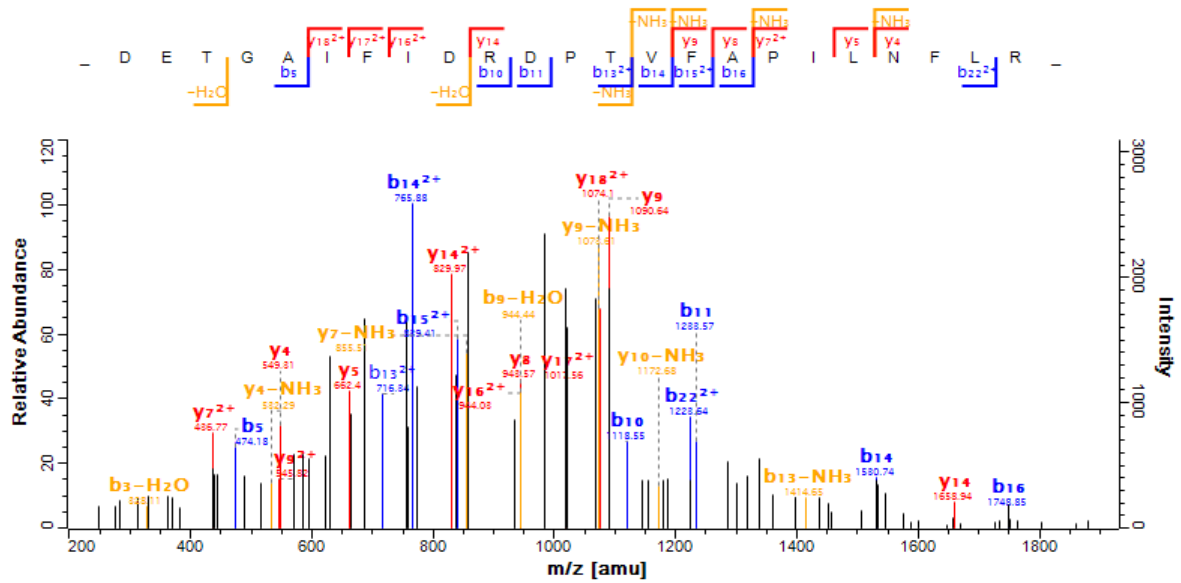
Best Match Spectrum:

Scan number	22806	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	SPATA20



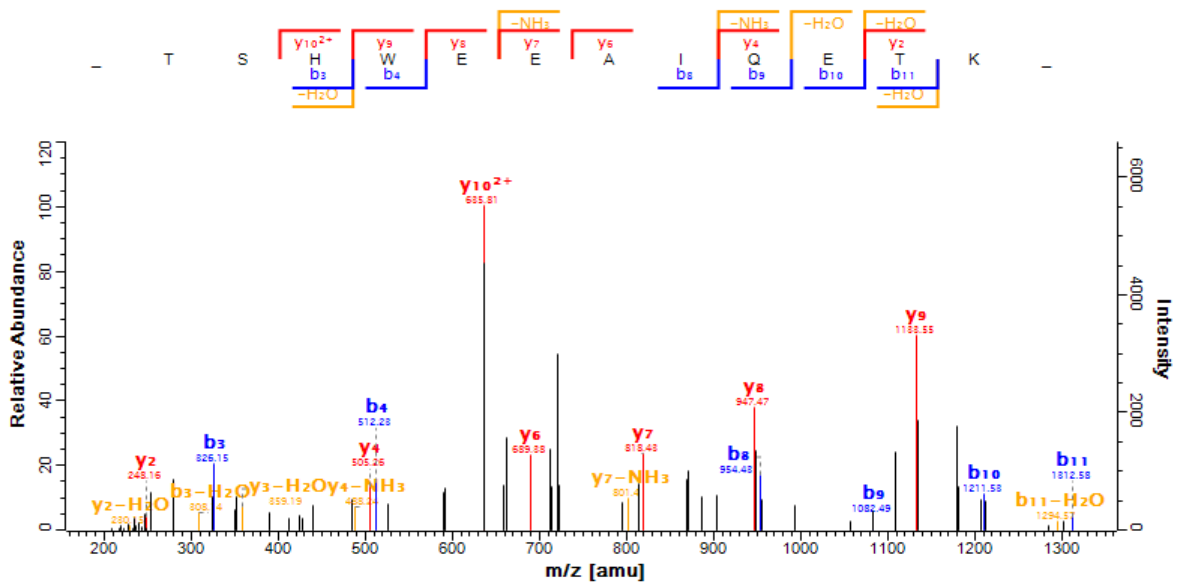
Protein Group ID: 4118
Protein Accession Numbers: Q8TBC3; Q8TBC3-2
Gene Names: SHKBP1
Peptide Sequence: DETGAIFIDRDPTVFAPILNFLR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 90.453
Best Match Posterior Error Probability: 5.36E-05
Best Match Spectrum:

Scan number 92671 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** SHKBP1



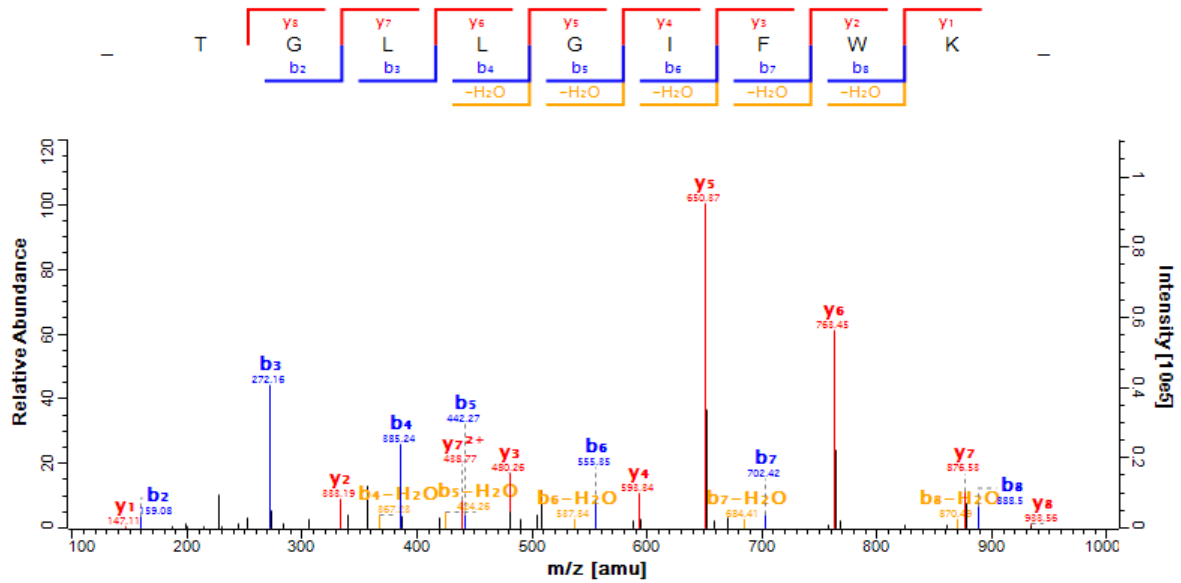
Protein Group ID: 4120
Protein Accession Numbers: Q8TBE9
Gene Names: NANP
Peptide Sequence: TSHWEEAIQETK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 78.964
Best Match Posterior Error Probability: 0.0036036
Best Match Spectrum:

Scan number 24826 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** NANP



Protein Group ID: 4122
Protein Accession Numbers: Q8TBQ9
Gene Names: TMEM167A
Peptide Sequence: TGLLGIFWK
Total Number of Spectra: 8
Number of Replicates (out of 8): 8
Best Match Score: 175.51
Best Match Posterior Error Probability: 2.23E-06
Best Match Spectrum:

Scan number 77772 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TMEM167A



Protein Group ID: 4132

Protein Accession Numbers: Q8TD08; Q8TD08-3; Q8TD08-2

Gene Names: MAPK15

Peptide Sequence: LCDDFGLAR

Total Number of Spectra: 7

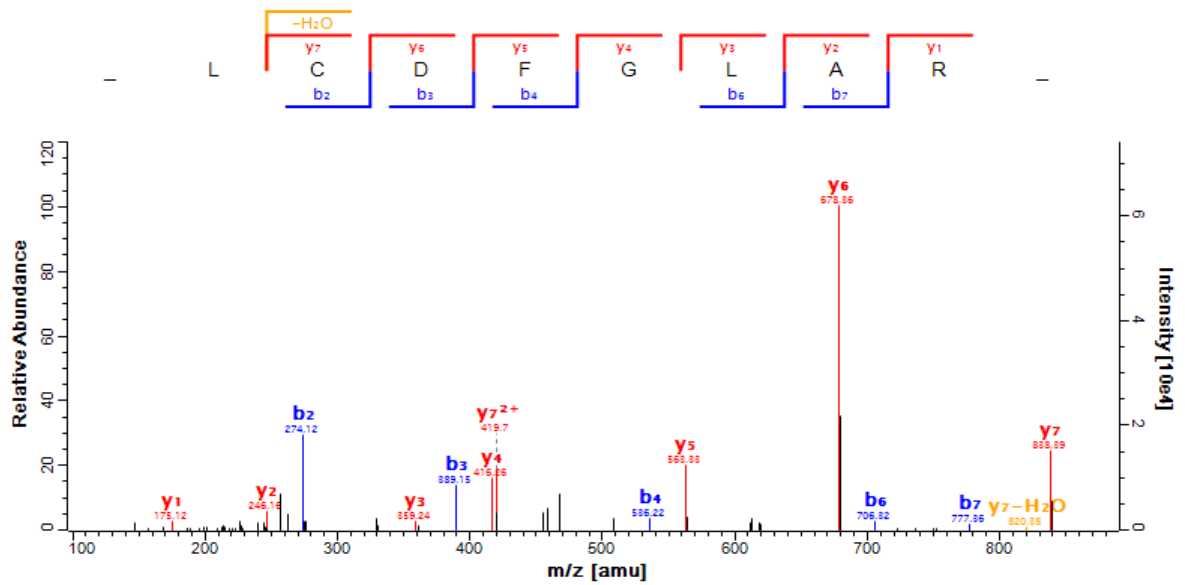
Number of Replicates (out of 8): 7

Best Match Score: 117.04

Best Match Posterior Error Probability: 0.002303

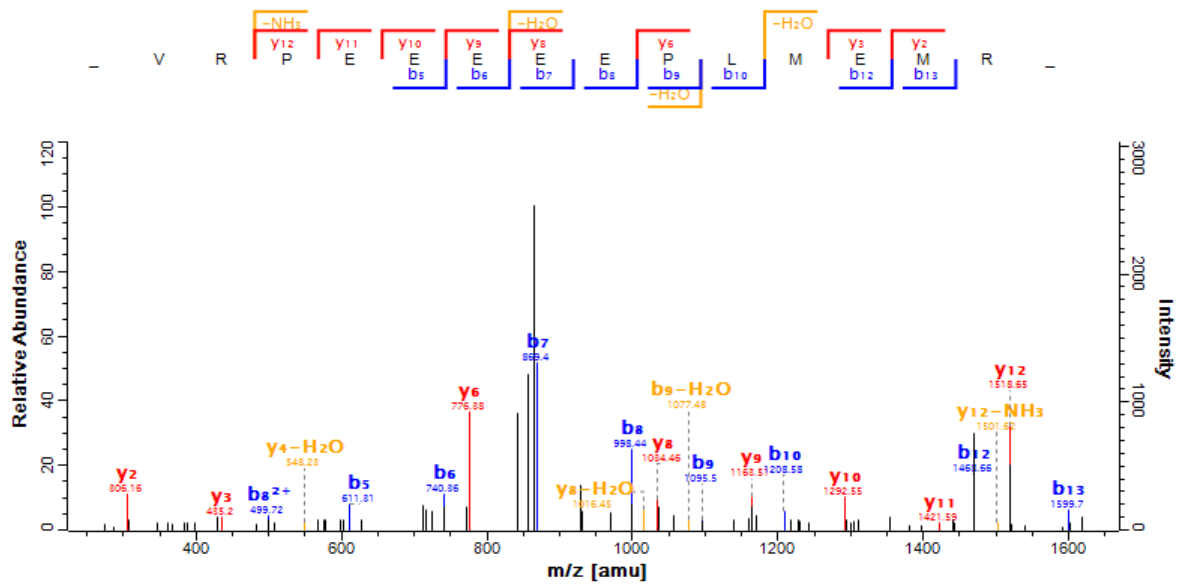
Best Match Spectrum:

Scan number	32624	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	MAPK15



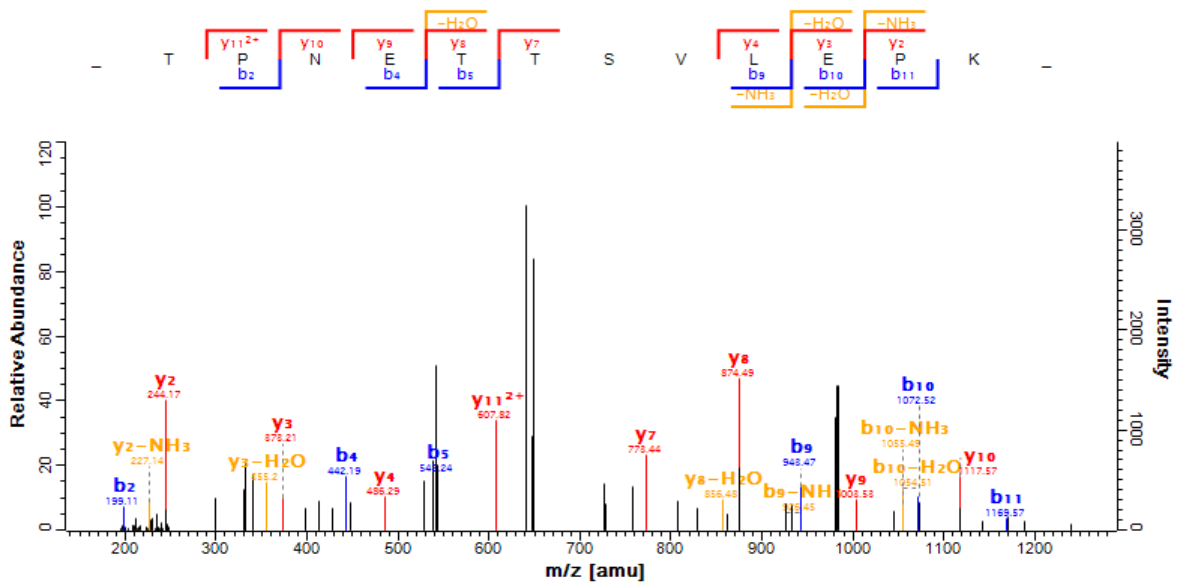
Protein Group ID: 4146
Protein Accession Numbers: Q8TEQ8; Q8TEQ8-2
Gene Names: PIGO
Peptide Sequence: VRPEEEEEPLMEMR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 95.067
Best Match Posterior Error Probability: 0.0032572
Best Match Spectrum:

Scan number 35508 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PIGO



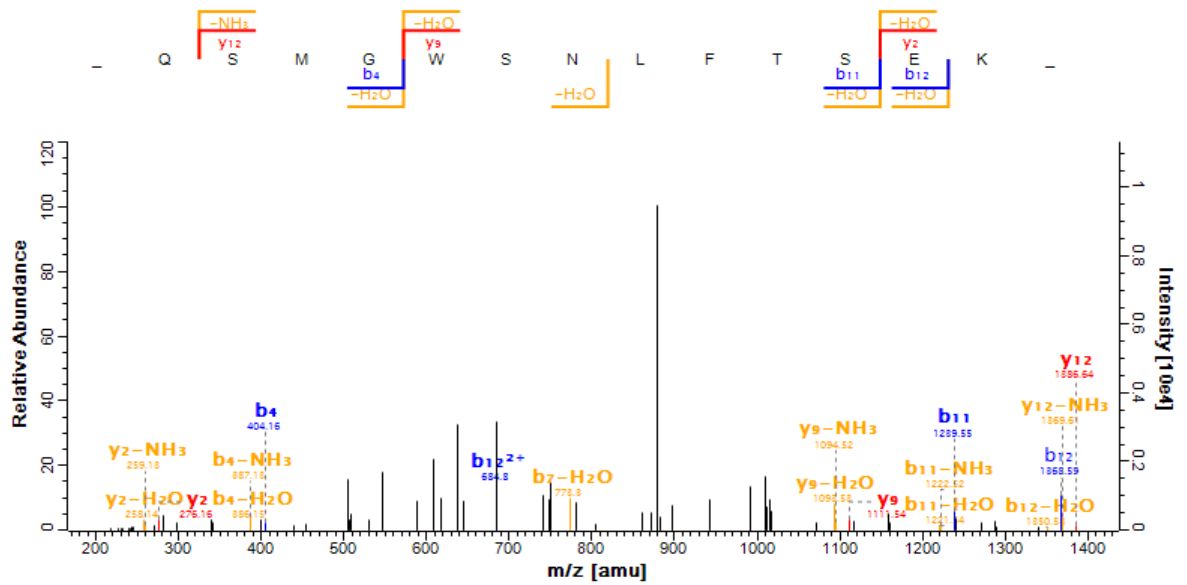
Protein Group ID: 4150
Protein Accession Numbers: Q8TF01
Gene Names: PNISR
Peptide Sequence: TPNETTSVLEPK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 111.79
Best Match Posterior Error Probability: 0.00023896
Best Match Spectrum:

Scan number 20844 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PNISR



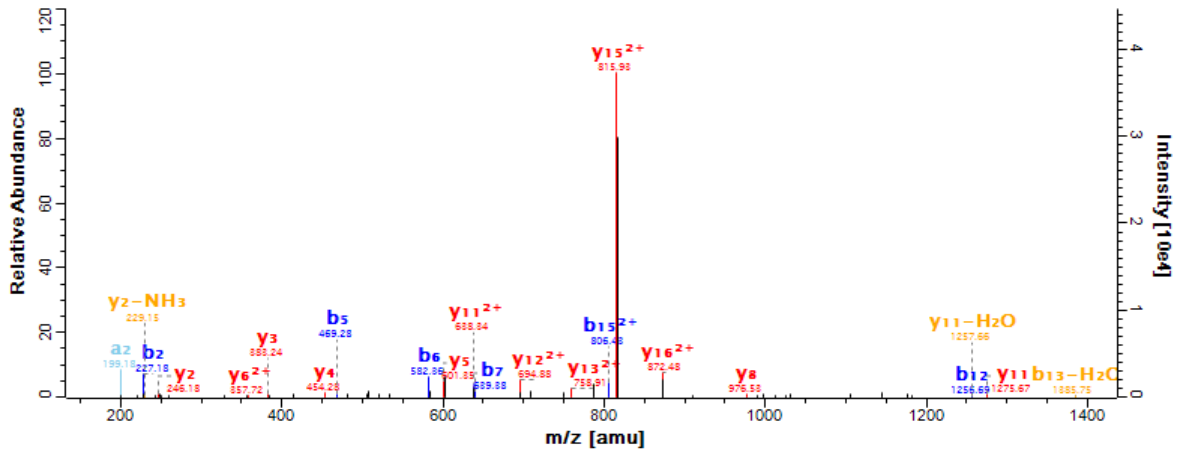
Protein Group ID: 4152
Protein Accession Numbers: Q8TF27
Gene Names: AGAP11
Peptide Sequence: QSMGWSNLFTSEK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 98.156
Best Match Posterior Error Probability: 0.00060124
Best Match Spectrum:

Scan number 24634 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** AGAP11



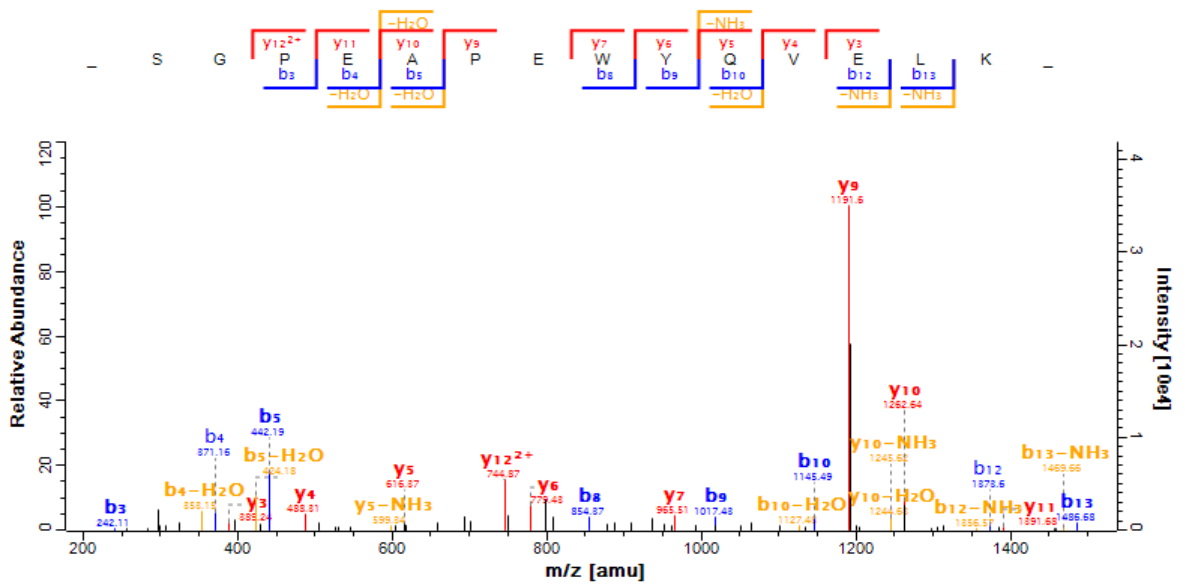
Protein Group ID: 4154
Protein Accession Numbers: Q8TF65
Gene Names: GIPC2
Peptide Sequence: LLGGQLGLEDFIFAHVK
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 102.5
Best Match Posterior Error Probability: 0.00015486
Best Match Spectrum:

Scan number 81711 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** GIPC2



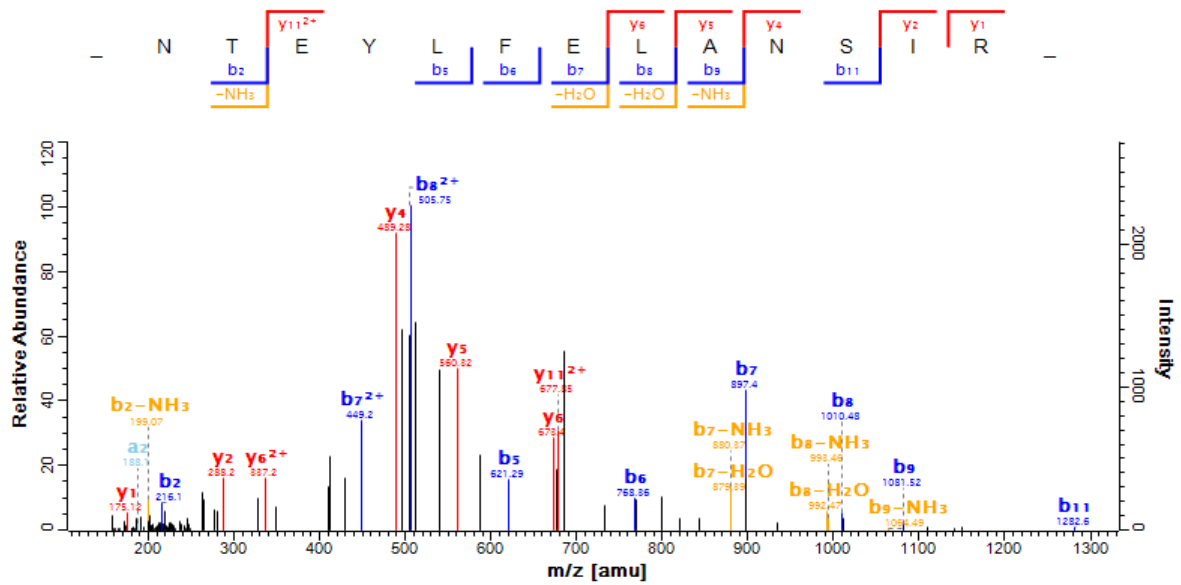
Protein Group ID: 4155
Protein Accession Numbers: Q8WTS6
Gene Names: SETD7
Peptide Sequence: SGPEAPEWYQVELK
Total Number of Spectra: 7
Number of Replicates (out of 8): 5
Best Match Score: 148.72
Best Match Posterior Error Probability: 1.77E-06
Best Match Spectrum:

Scan number 52730 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** SETD7



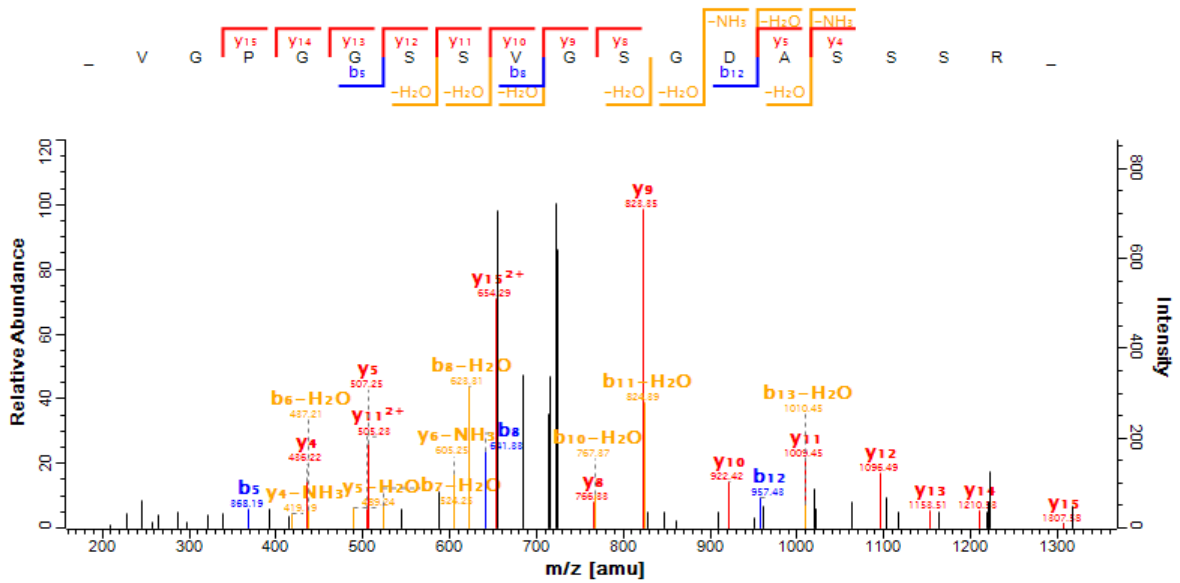
Protein Group ID: 4167
Protein Accession Numbers: Q8WUX2
Gene Names: CHAC2
Peptide Sequence: NTEYLFELANSIR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 152.47
Best Match Posterior Error Probability: 8.74E-07
Best Match Spectrum:

Scan number 73384 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CHAC2



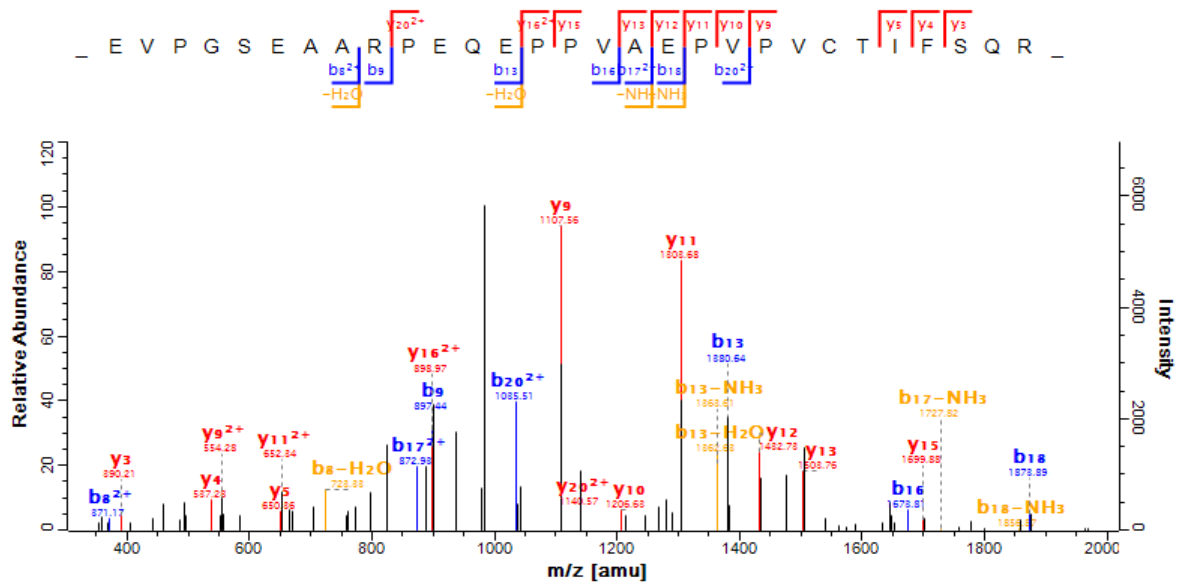
Protein Group ID: 4169
Protein Accession Numbers: Q8WV44; Q8WV44-3
Gene Names: TRIM41
Peptide Sequence: VGPGSSVGS GDASSSR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 75.376
Best Match Posterior Error Probability: 0.0023392
Best Match Spectrum:

Scan number 6229 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** TRIM41



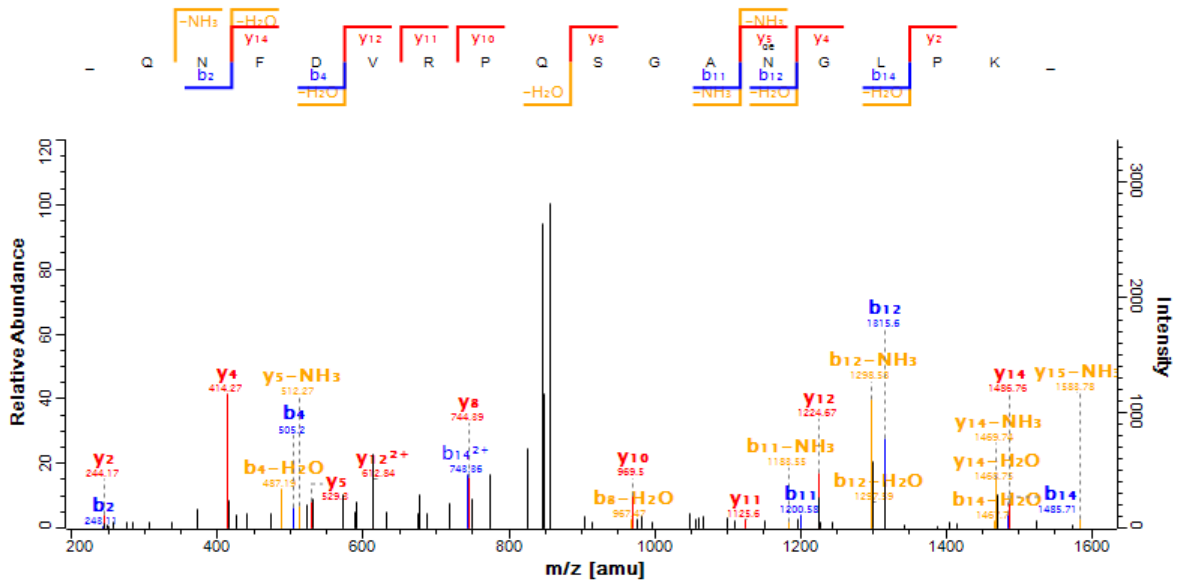
Protein Group ID: 4175
Protein Accession Numbers: Q8WVT3
Gene Names: TRAPPC12
Peptide Sequence: EVPGSEARPEQEPVVAEPVPVCTIFSQR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 66.925
Best Match Posterior Error Probability: 0.00030917
Best Match Spectrum:

Scan number 58658 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TRAPPC12



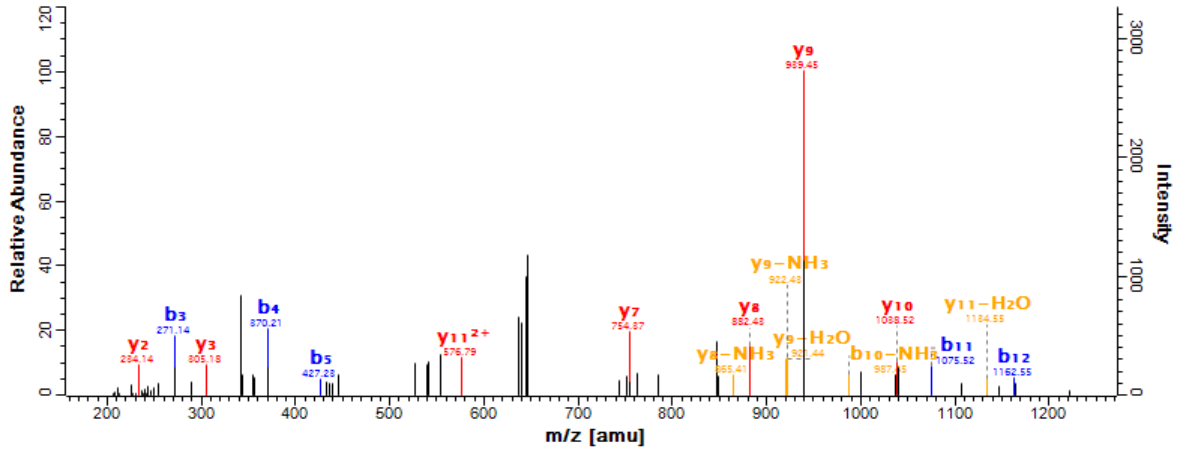
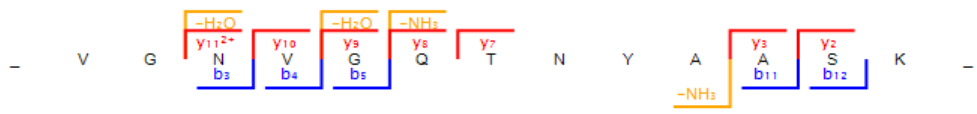
Protein Group ID: 4177
Protein Accession Numbers: Q8WVX3-2; Q8WVX3
Gene Names: C4orf3
Peptide Sequence: QNF DV RP QS GANGLPK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 99.069
Best Match Posterior Error Probability: 0.0038443
Best Match Spectrum:

Scan number 28264 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** C4orf3



Protein Group ID: 4201
Protein Accession Numbers: Q92506
Gene Names: HSD17B8
Peptide Sequence: VGNVGQTNYAASK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 79.466
Best Match Posterior Error Probability: 0.003432
Best Match Spectrum:

Scan number 9171 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** HSD17B8



Protein Group ID: 4209

Protein Accession Numbers: Q92567; Q92567-2; Q92567-3

Gene Names: FAM168A

Peptide Sequence: MNPVYSPVQPGAPYGNPK

Total Number of Spectra: 1

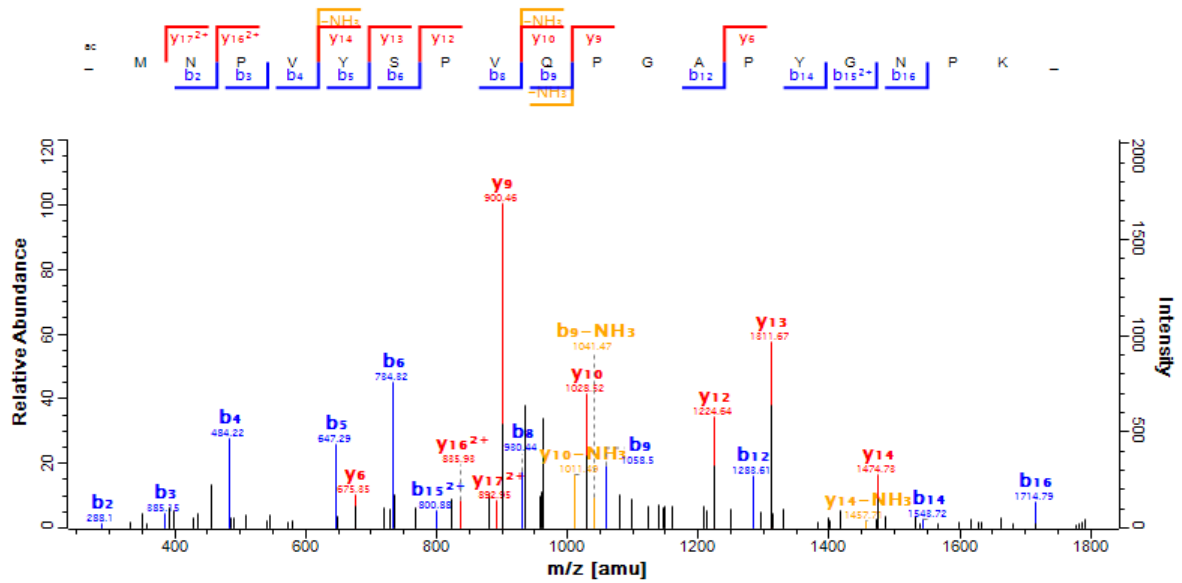
Number of Replicates (out of 8): 1

Best Match Score: 87.088

Best Match Posterior Error Probability: 0.00064564

Best Match Spectrum:

Scan number 48860 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** FAM168A



Protein Group ID: 4230

Protein Accession Numbers: Q92766-2; Q92766; Q92766-4

Gene Names: RREB1

Peptide Sequence: LAEGDGEAGAGGAASQEQK

Total Number of Spectra: 2

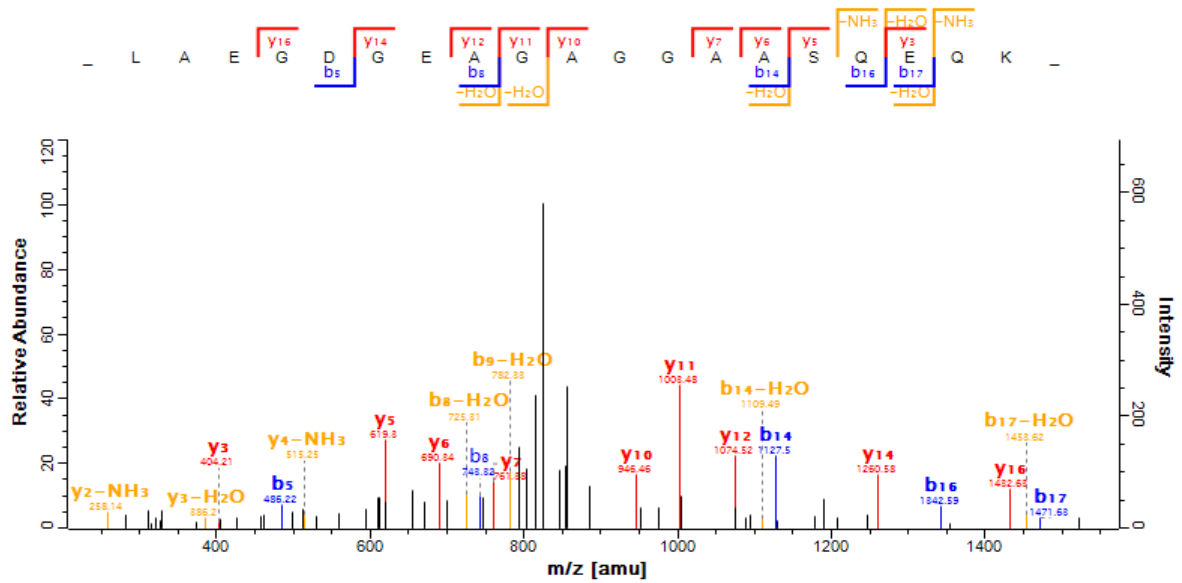
Number of Replicates (out of 8): 1

Best Match Score: 67.43

Best Match Posterior Error Probability: 0.0034351

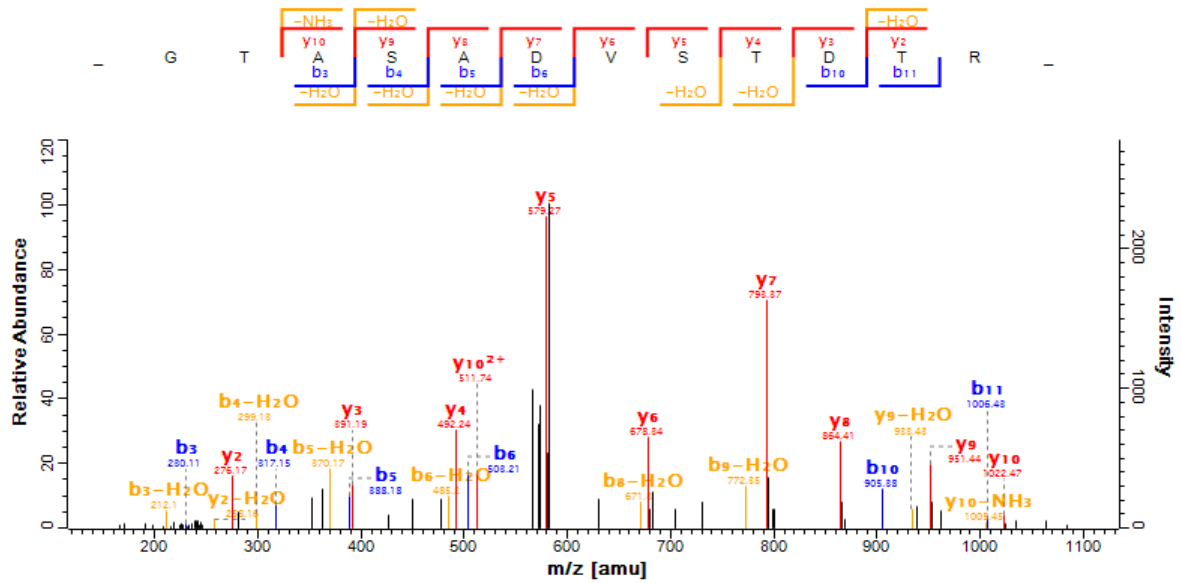
Best Match Spectrum:

Scan number	7629	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	RREB1



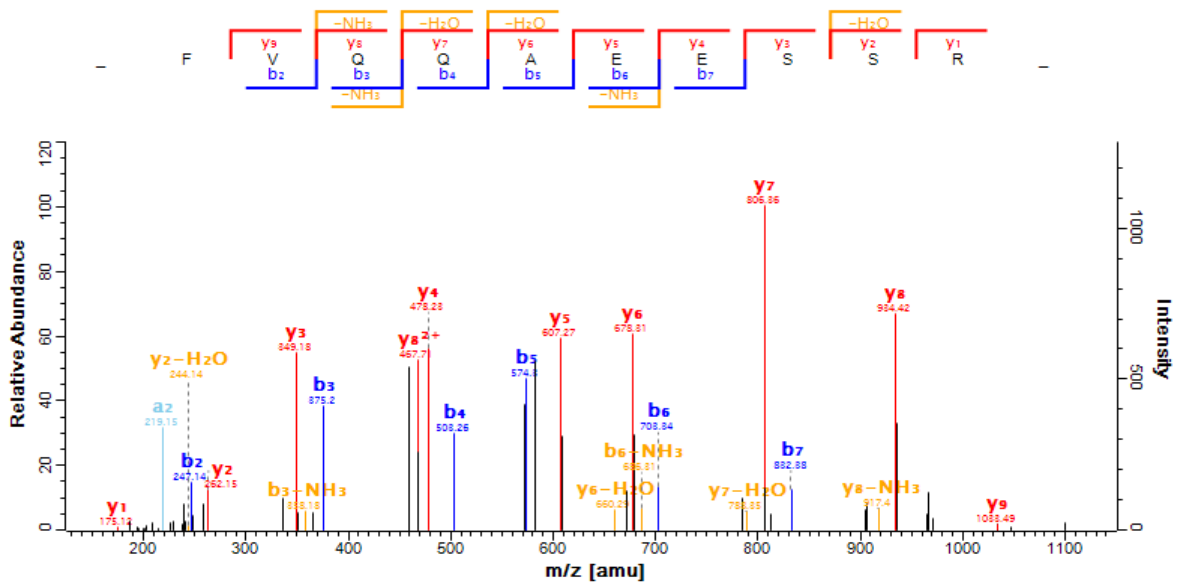
Protein Group ID: 4242
Protein Accession Numbers: Q92889
Gene Names: ERCC4
Peptide Sequence: GTASADVSTDTR
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 136.38
Best Match Posterior Error Probability: 7.68E-05
Best Match Spectrum:

Scan number 4865 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ERCC4



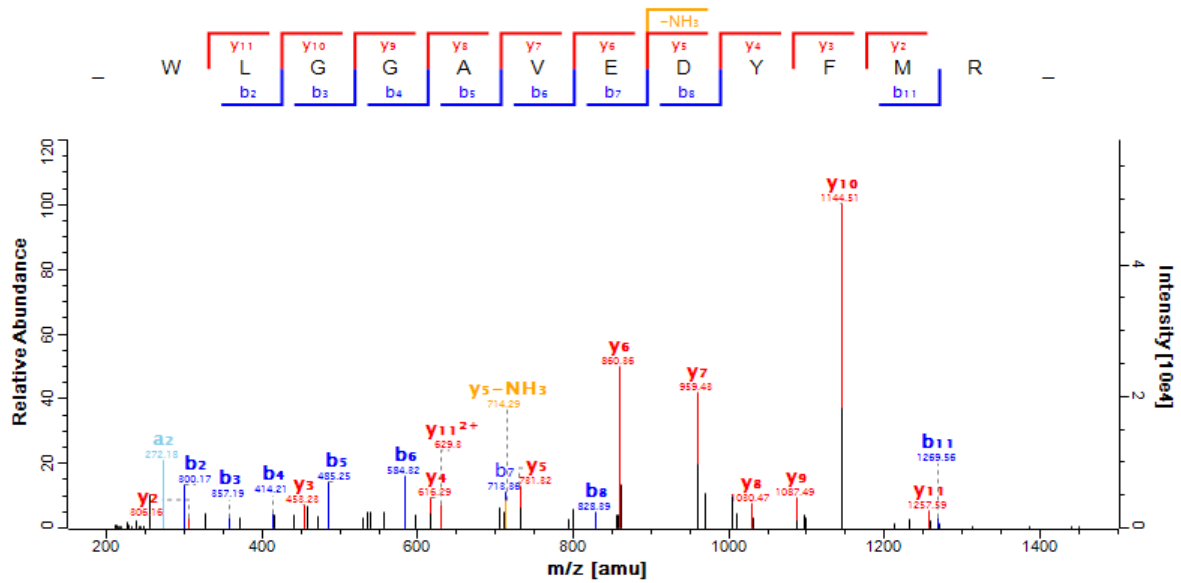
Protein Group ID: 4250
Protein Accession Numbers: Q92968
Gene Names: PEX13
Peptide Sequence: FVQQAEESSR
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 136.5
Best Match Posterior Error Probability: 9.35E-06
Best Match Spectrum:

Scan number 5538 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PEX13



Protein Group ID: 4261
Protein Accession Numbers: Q969E8
Gene Names: TSR2
Peptide Sequence: WLGGAVEDYFM
Total Number of Spectra: 9
Number of Replicates (out of 8): 8
Best Match Score: 151.98
Best Match Posterior Error Probability: 2.86E-06
Best Match Spectrum:

Scan number 73197 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TSR2



Protein Group ID: 4269

Protein Accession Numbers: Q969S2; Q969S2-2; Q969S2-3; Q969S2-4

Gene Names: NEIL2

Peptide Sequence: EVLVDHVVVEFSTAWLQGK

Total Number of Spectra: 1

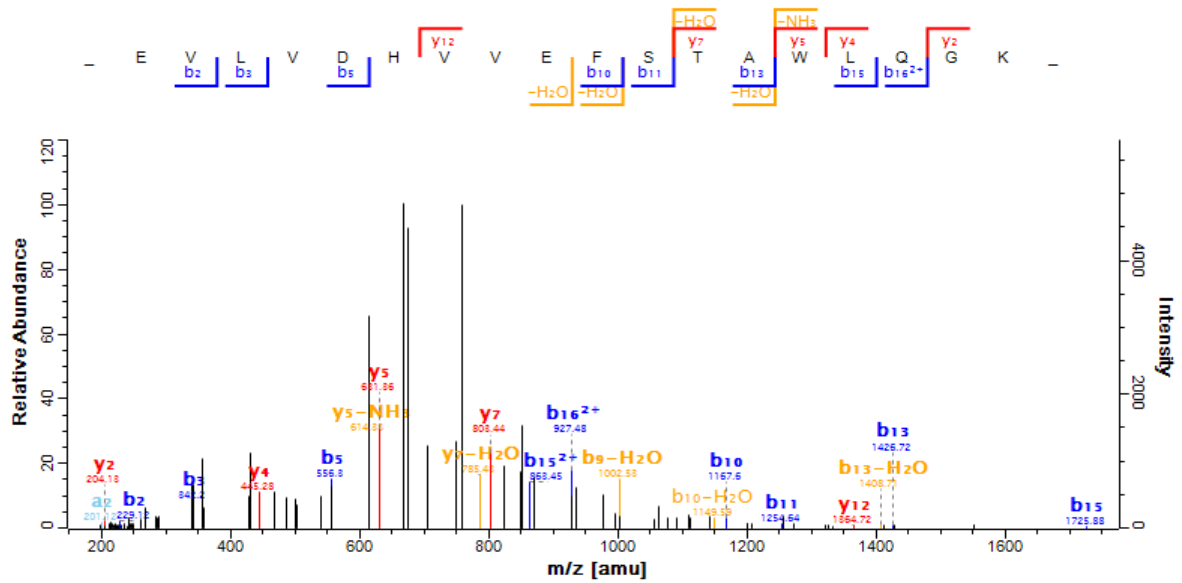
Number of Replicates (out of 8): 1

Best Match Score: 74.89

Best Match Posterior Error Probability: 0.0019736

Best Match Spectrum:

Scan number	84201	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	NEIL2



Protein Group ID: 4273

Protein Accession Numbers: Q969W9; Q969W9-2; Q969W9-3

Gene Names: PMEPA1

Peptide Sequence: MEGPPPTYSEVIGHYPGSSFQHQSSGPPSLLEGTR

Total Number of Spectra: 2

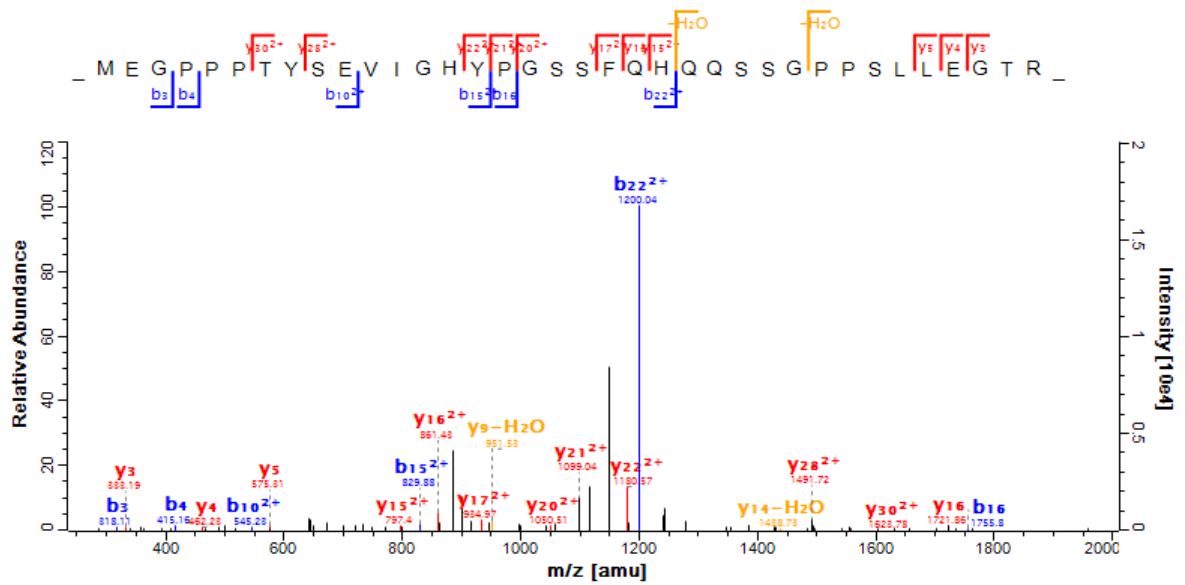
Number of Replicates (out of 8): 2

Best Match Score: 48.226

Best Match Posterior Error Probability: 0.001218

Best Match Spectrum:

Scan number	58039	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	PMEPA1



Protein Group ID: 4281

Protein Accession Numbers: Q96A73; Q96A73-2; Q96A73-3

Gene Names: KIAA1191

Peptide Sequence: YDSGSFATQAYR

Total Number of Spectra: 1

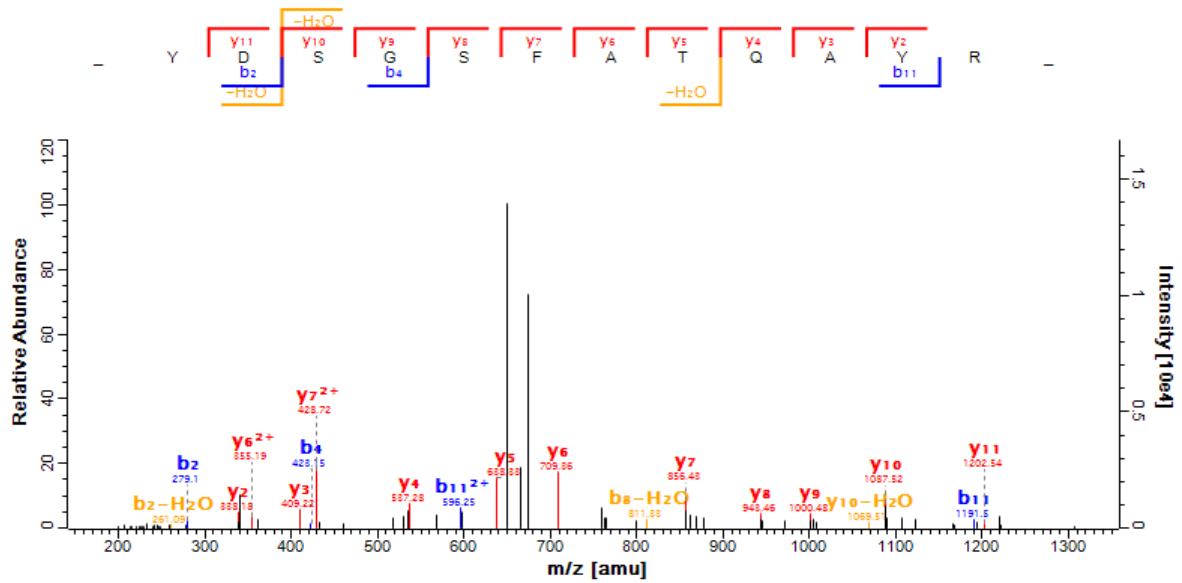
Number of Replicates (out of 8): 1

Best Match Score: 87.719

Best Match Posterior Error Probability: 0.0016615

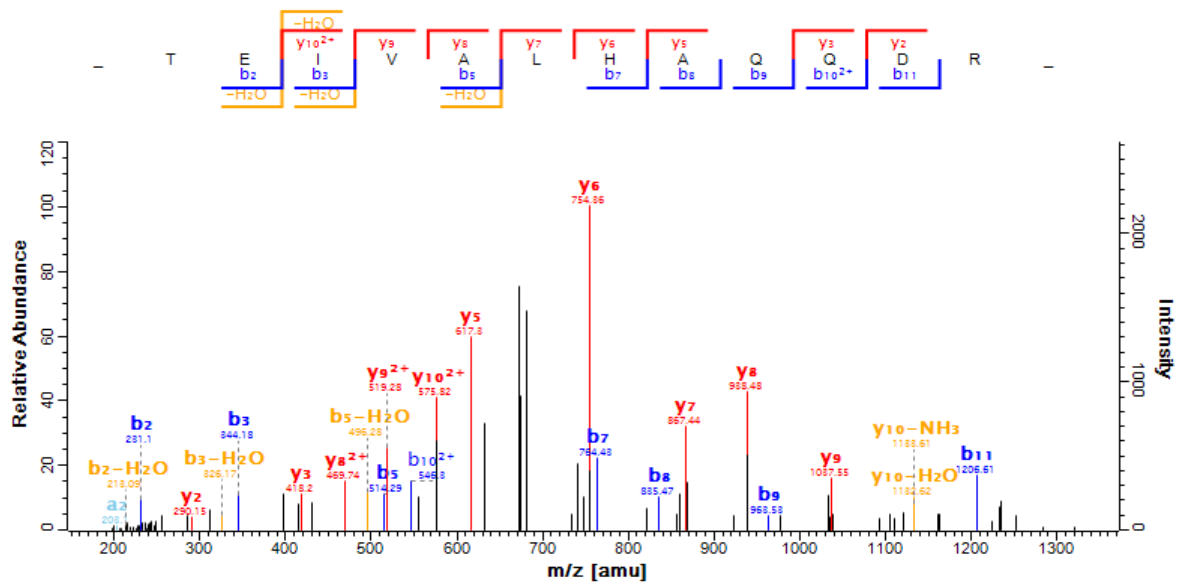
Best Match Spectrum:

Scan number 26190 **Raw file** A549-US-WT-top20CID-Elite-2ug-812
Method ITMS; CID **Genenames** KIAA1191



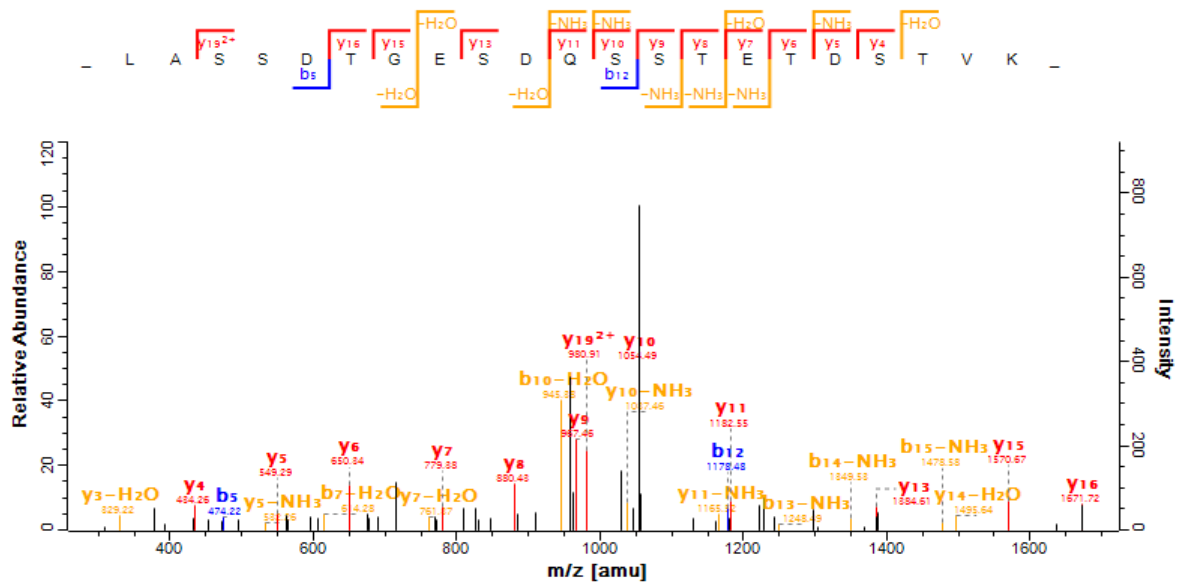
Protein Group ID: 4287
Protein Accession Numbers: Q96AQ8
Gene Names: CCDC90A
Peptide Sequence: TEIVALHAQQDR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 113.99
Best Match Posterior Error Probability: 0.0002101
Best Match Spectrum:

Scan number 18164 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CCDC90A



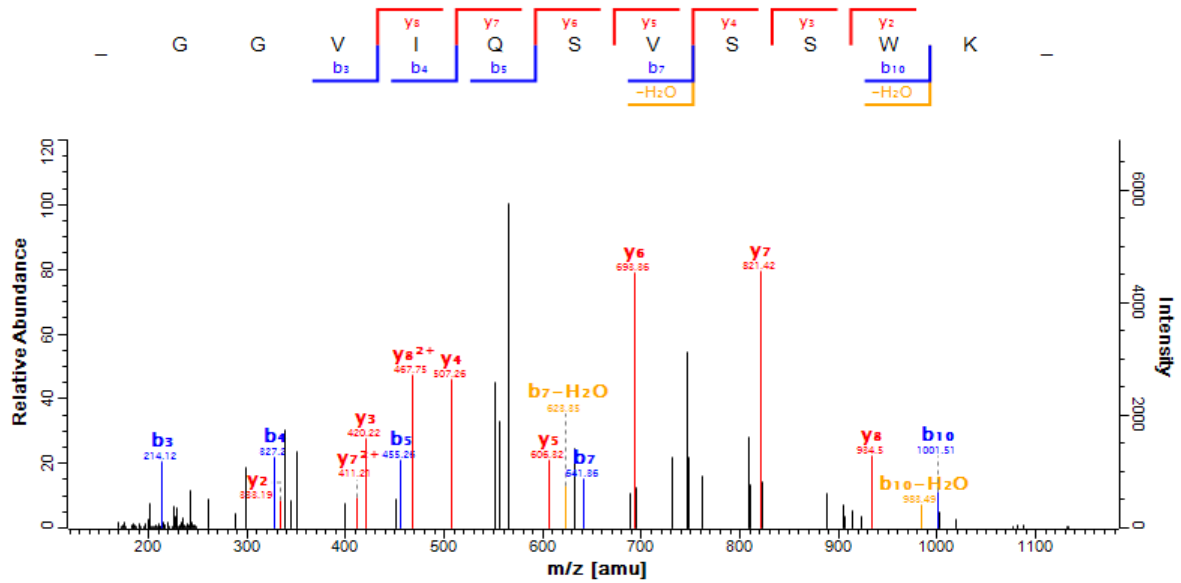
Protein Group ID: 4291
Protein Accession Numbers: Q96AY4
Gene Names: TTC28
Peptide Sequence: LASSDTGESDQSSTETDSTVK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 74.048
Best Match Posterior Error Probability: 0.00071085
Best Match Spectrum:

Scan number 9099 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TTC28



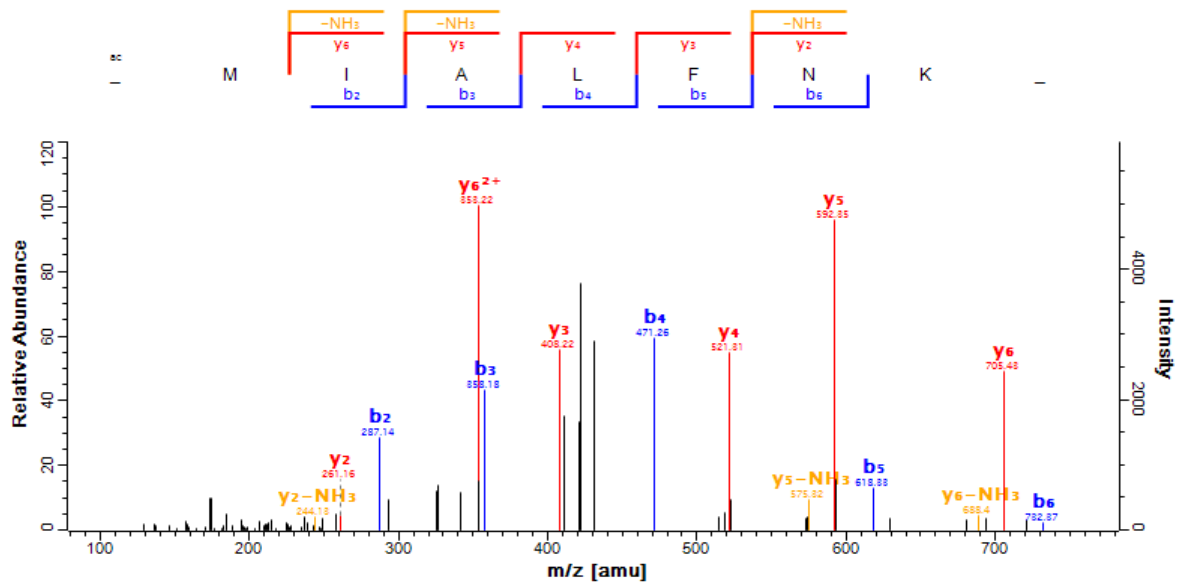
Protein Group ID: 4293
Protein Accession Numbers: Q96B23; Q96B23-2
Gene Names: C18orf25
Peptide Sequence: GGVIQSVSSWK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 94.767
Best Match Posterior Error Probability: 0.00098239
Best Match Spectrum:

Scan number 38292 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** C18orf25



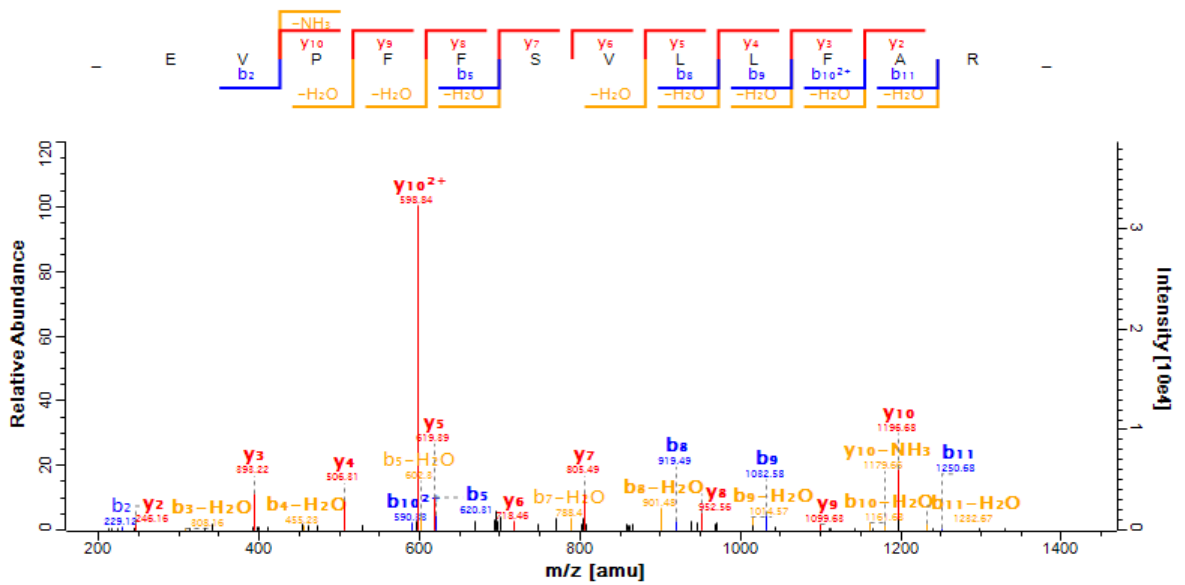
Protein Group ID: 4299
Protein Accession Numbers: Q96BM9
Gene Names: ARL8A
Peptide Sequence: MIALFNK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 126.68
Best Match Posterior Error Probability: 0.0014942
Best Match Spectrum:

Scan number 70938 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ARL8A



Protein Group ID: 4300
Protein Accession Numbers: Q96BN8
Gene Names: FAM105B
Peptide Sequence: EVPFFSVLLFAR
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 153.95
Best Match Posterior Error Probability: 1.75E-06
Best Match Spectrum:

Scan number 89912 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** FAM105B



Protein Group ID: 4303

Protein Accession Numbers: Q96BW5; Q96BW5-2

Gene Names: PTER

Peptide Sequence: AMSVEQLTDVLMNEILHGADGTSIK

Total Number of Spectra: 5

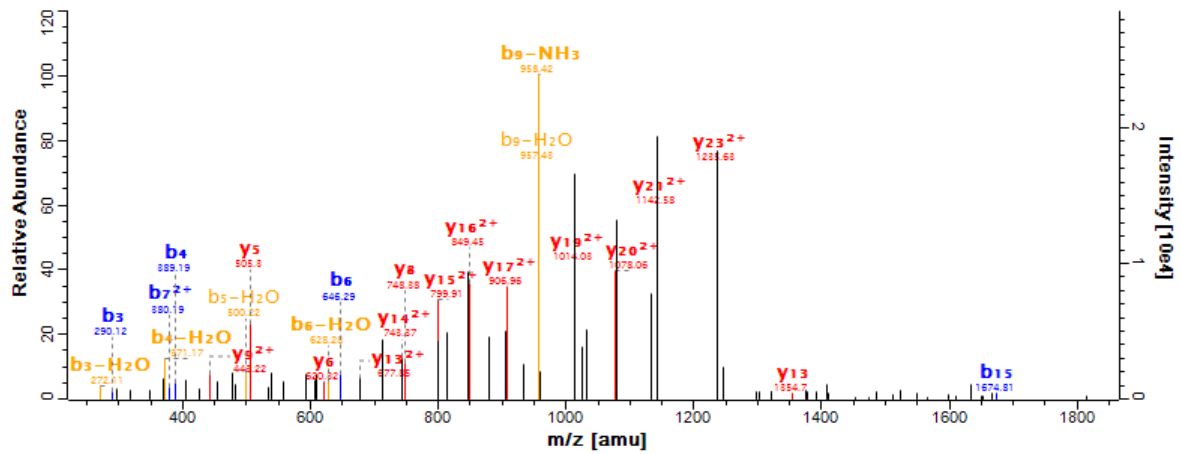
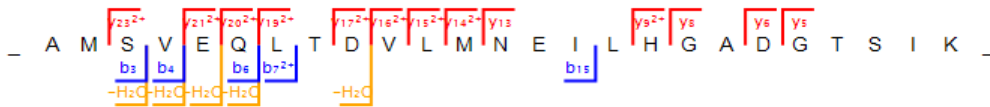
Number of Replicates (out of 8): 5

Best Match Score: 97.457

Best Match Posterior Error Probability: 1.91E-06

Best Match Spectrum:

Scan number	95442	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	PTER



Protein Group ID: 4310

Protein Accession Numbers: Q96CB9; Q96CB9-4; Q96CB9-3

Gene Names: NSUN4

Peptide Sequence: VLVDVPCTTDR

Total Number of Spectra: 1

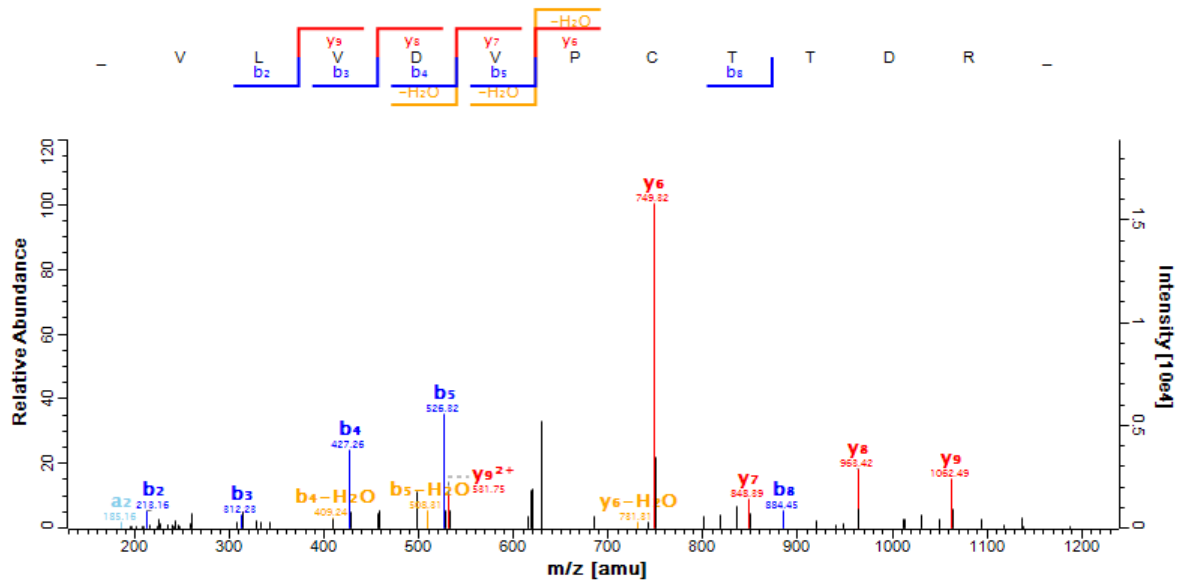
Number of Replicates (out of 8): 1

Best Match Score: 82.261

Best Match Posterior Error Probability: 0.0032473

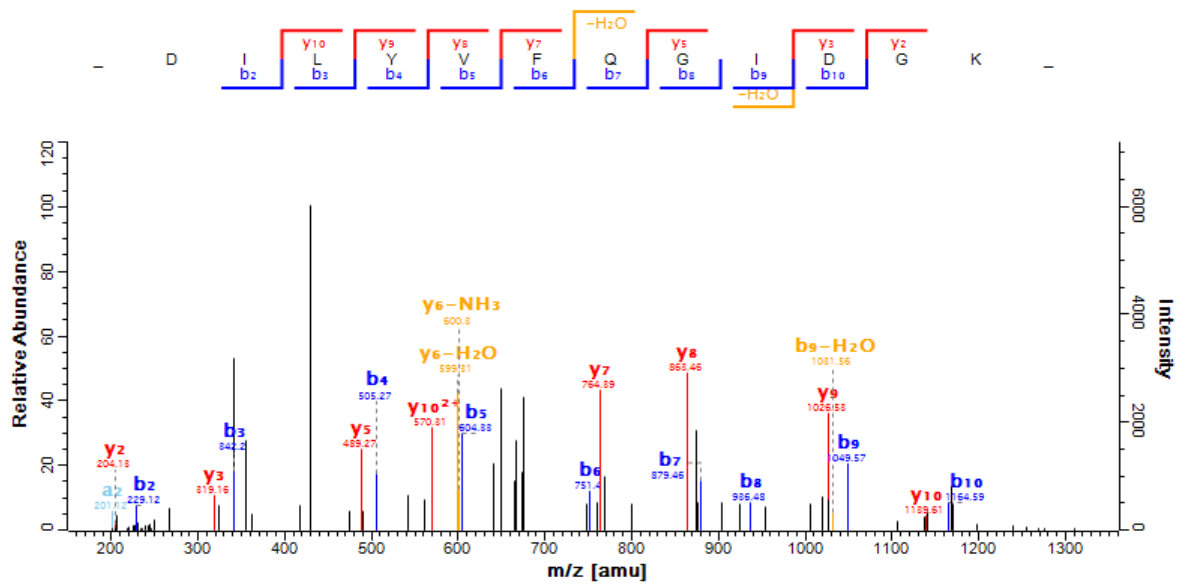
Best Match Spectrum:

Scan number 30992 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** NSUN4



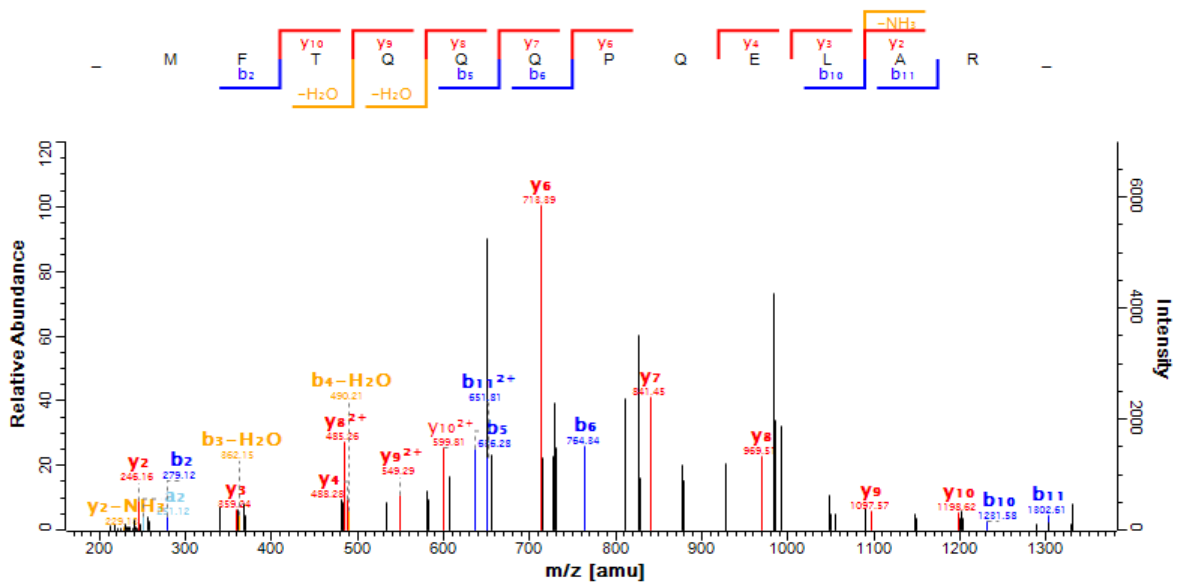
Protein Group ID: 4316
Protein Accession Numbers: Q96CW5; Q96CW5-2; Q96CW5-3
Gene Names: TUBGCP3
Peptide Sequence: DILYVFQIDGK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 89.46
Best Match Posterior Error Probability: 0.0014863
Best Match Spectrum:

Scan number 68824 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** TUBGCP3



Protein Group ID: 4317
Protein Accession Numbers: Q96CX2
Gene Names: KCTD12
Peptide Sequence: MFTQQQPQELAR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 94.122
Best Match Posterior Error Probability: 0.0010171
Best Match Spectrum:

Scan number 27106 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** KCTD12



Protein Group ID: 4324

Protein Accession Numbers: Q96DX5; Q96DX5-2; Q96DX5-3

Gene Names: ASB9

Peptide Sequence: RPVELVPPESPLAQLFLER

Total Number of Spectra: 8

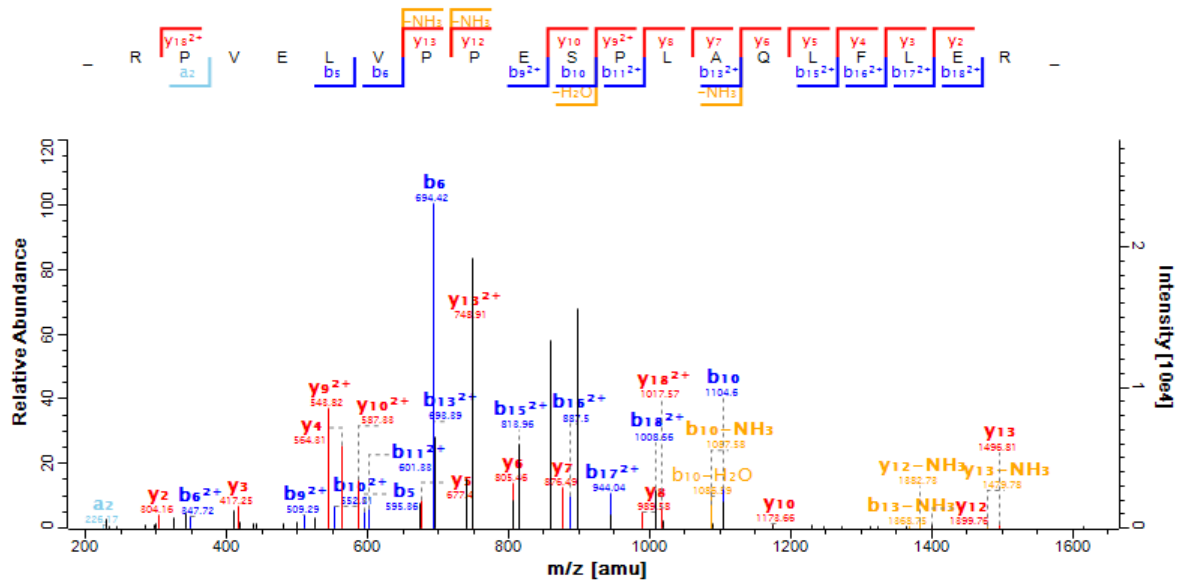
Number of Replicates (out of 8): 8

Best Match Score: 167.28

Best Match Posterior Error Probability: 1.85E-11

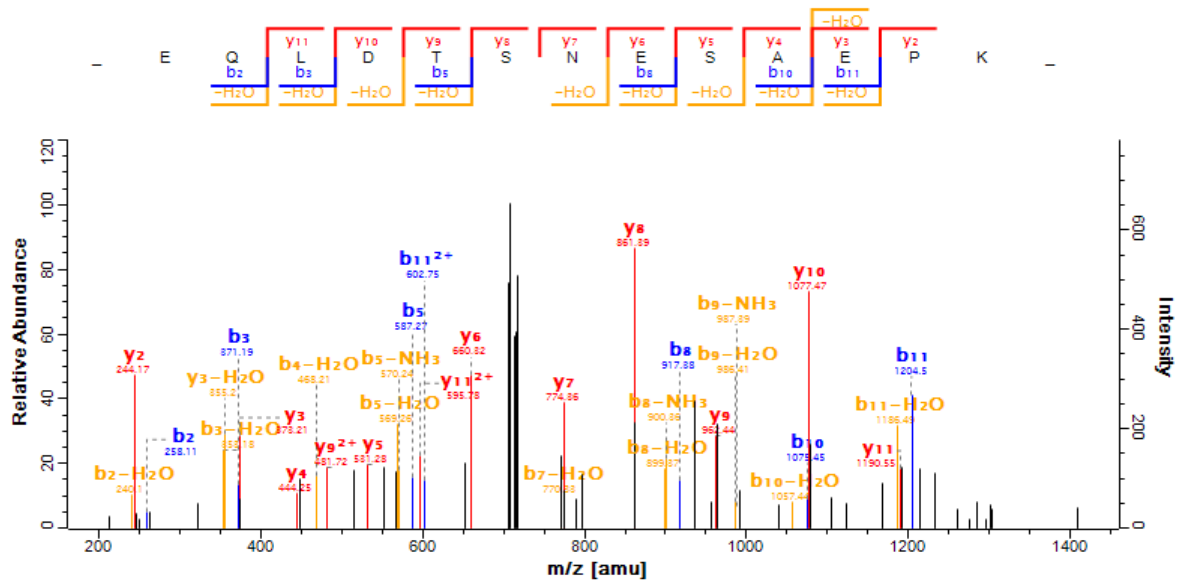
Best Match Spectrum:

Scan number 84417 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ASB9



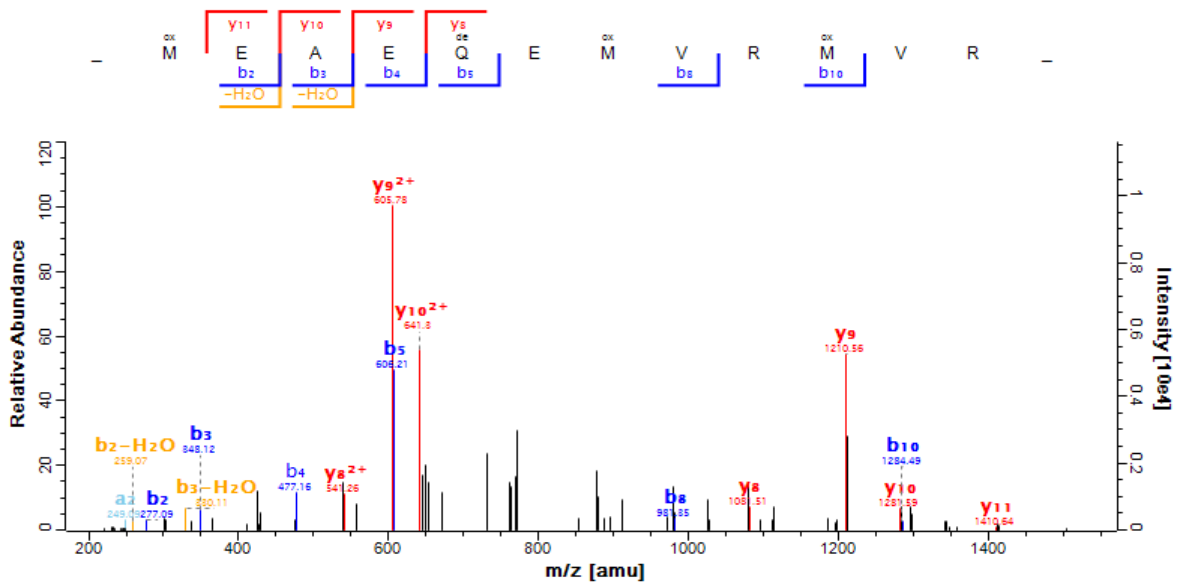
Protein Group ID: 4325
Protein Accession Numbers: Q96DX7
Gene Names: TRIM44
Peptide Sequence: EQLDTSNESAEPK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 160.48
Best Match Posterior Error Probability: 2.33E-09
Best Match Spectrum:

Scan number 8419 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TRIM44



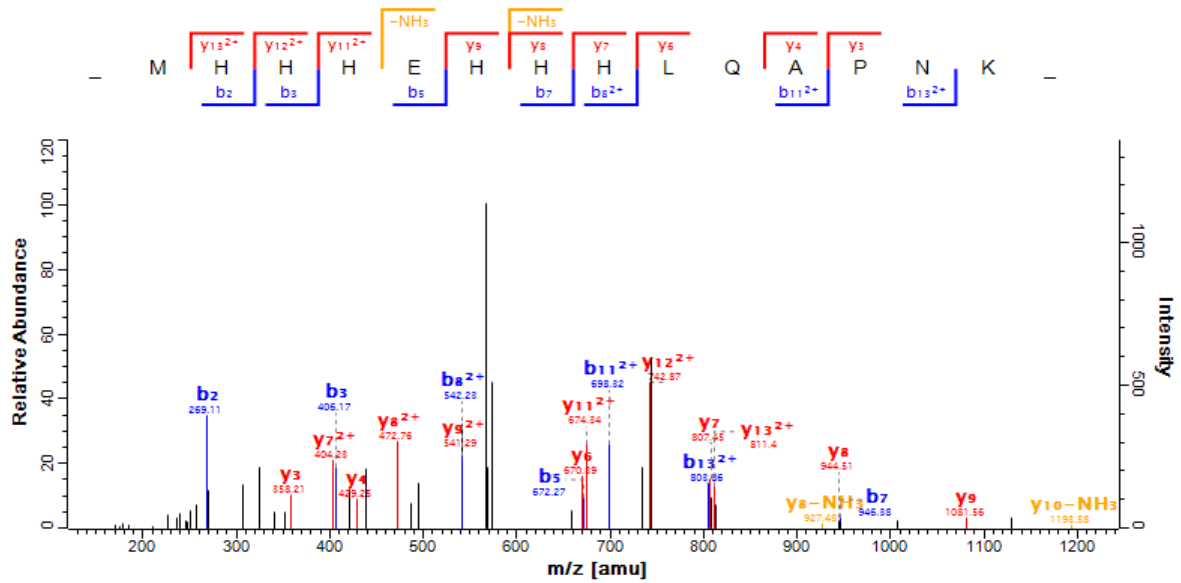
Protein Group ID: 4326
Protein Accession Numbers: Q96DY2; Q96DY2-2
Gene Names: IQCD
Peptide Sequence: MEAEQEMVRMVR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 86.911
Best Match Posterior Error Probability: 0.0095023
Best Match Spectrum:

Scan number 37589 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** IQCD



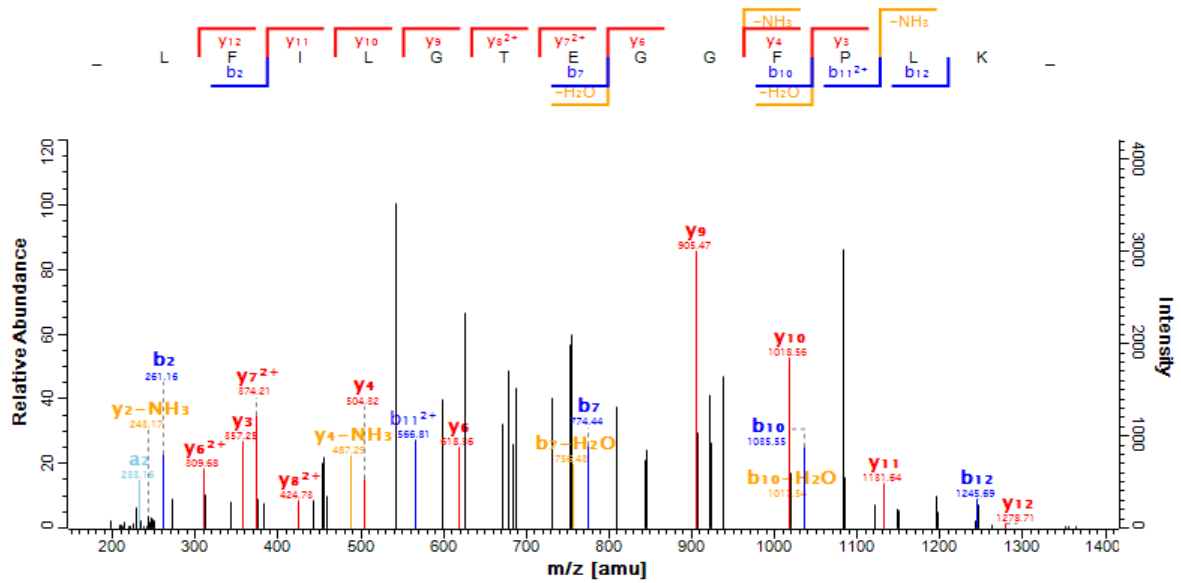
Protein Group ID: 4342
Protein Accession Numbers: Q96EU7
Gene Names: CIGALT1C1
Peptide Sequence: MHHHEHHHLQAPNK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 118.9
Best Match Posterior Error Probability: 6.83E-05
Best Match Spectrum:

Scan number 1679 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CIGALT1C1



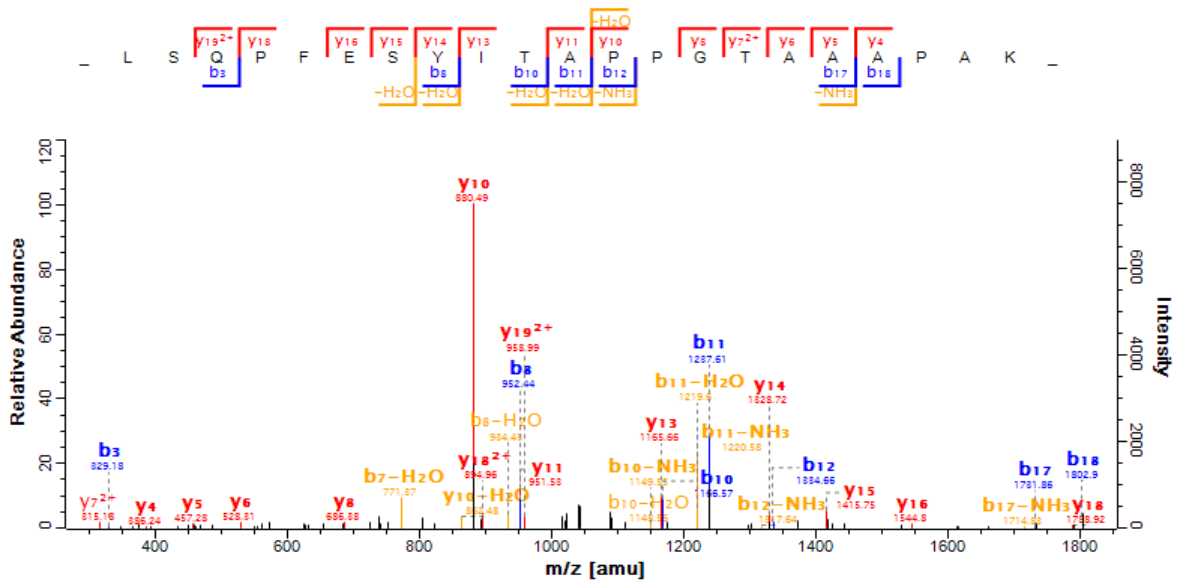
Protein Group ID: 4344
Protein Accession Numbers: Q96EX3
Gene Names: WDR34
Peptide Sequence: LFILGTEGGFPLK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 115.33
Best Match Posterior Error Probability: 0.0002269
Best Match Spectrum:

Scan number 73118 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** WDR34



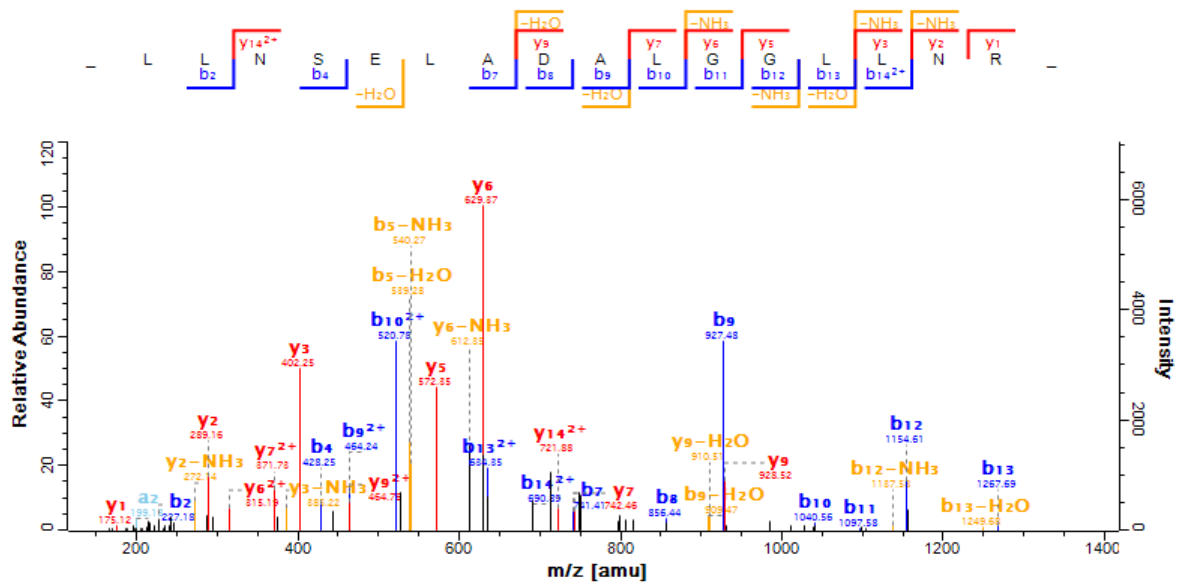
Protein Group ID: 4361
Protein Accession Numbers: Q96GE9; Q96GE9-2
Gene Names: C9orf123
Peptide Sequence: LSQPFESYITAPPGTAAAPAK
Total Number of Spectra: 7
Number of Replicates (out of 8): 4
Best Match Score: 133.21
Best Match Posterior Error Probability: 2.85E-08
Best Match Spectrum:

Scan number 53273 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** C9orf123



Protein Group ID: 4365
Protein Accession Numbers: Q96GW9
Gene Names: MARS2
Peptide Sequence: LLNSELADALGGLNR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 192.39
Best Match Posterior Error Probability: 2.16E-28
Best Match Spectrum:

Scan number 85086 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** MARS2



Protein Group ID: 4368

Protein Accession Numbers: Q96H55; Q96H55-4; Q96H55-3

Gene Names: MYO19

Peptide Sequence: TAASLLGLPEDVLLLEMVQIR

Total Number of Spectra: 8

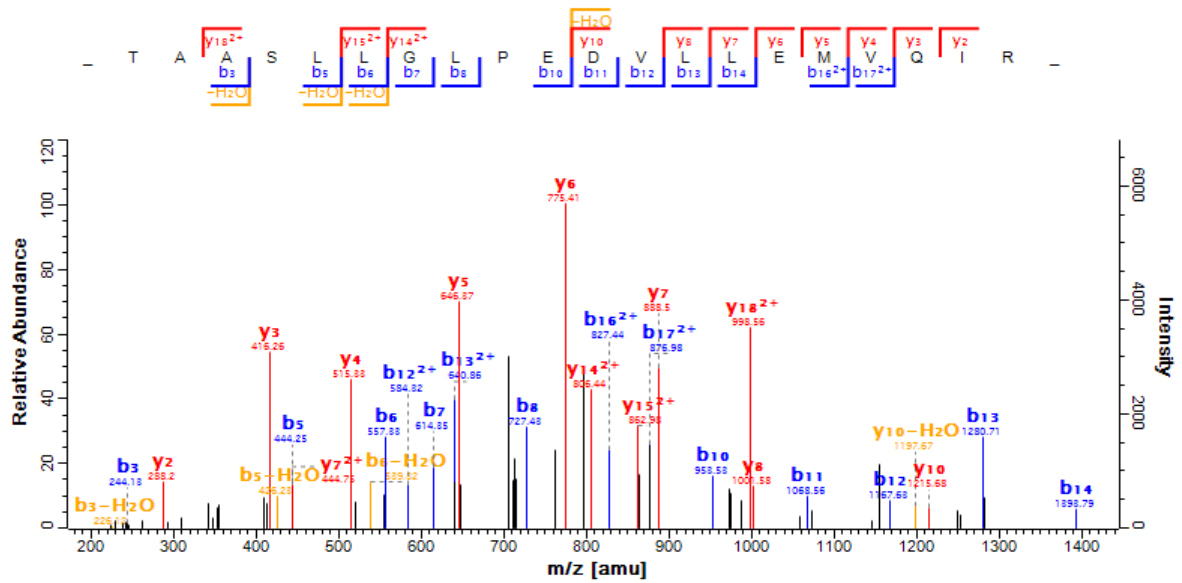
Number of Replicates (out of 8): 8

Best Match Score: 170.91

Best Match Posterior Error Probability: 6.96E-17

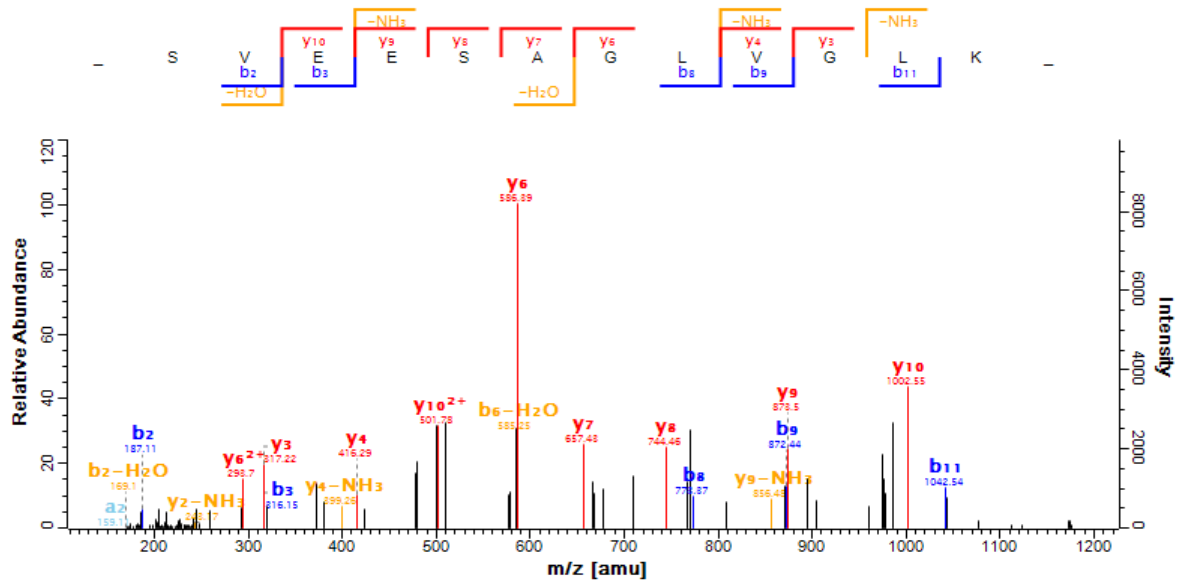
Best Match Spectrum:

Scan number 96377 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** MYO19



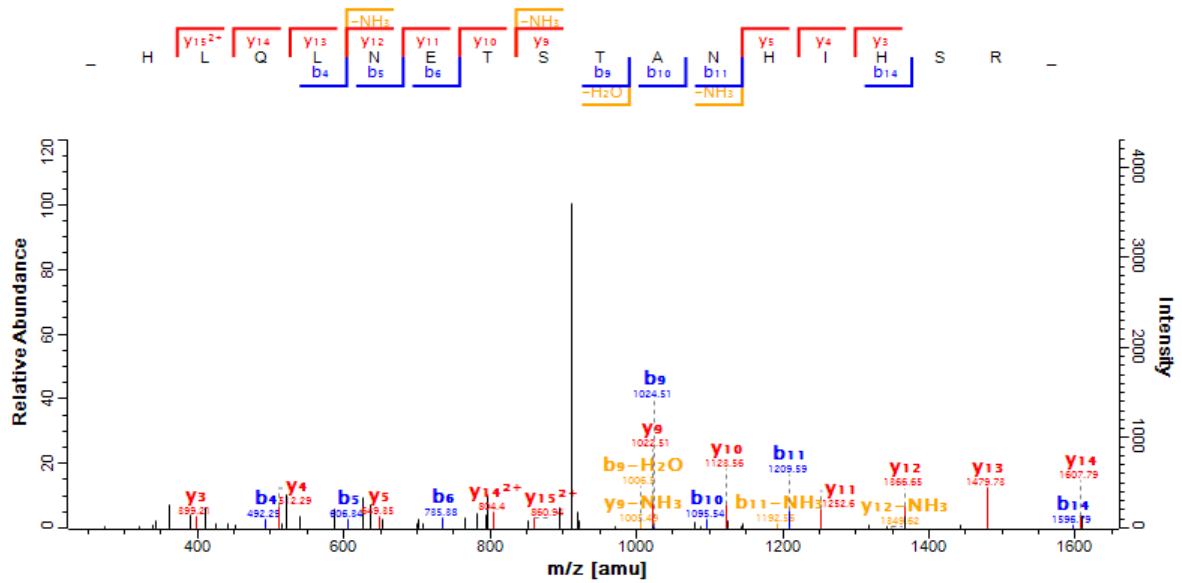
Protein Group ID: 4373
Protein Accession Numbers: Q96HJ9
Gene Names: C7orf55
Peptide Sequence: SVEESAGLVGLK
Total Number of Spectra: 5
Number of Replicates (out of 8): 4
Best Match Score: 89.805
Best Match Posterior Error Probability: 0.0014516
Best Match Spectrum:

Scan number 33644 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** C7orf55



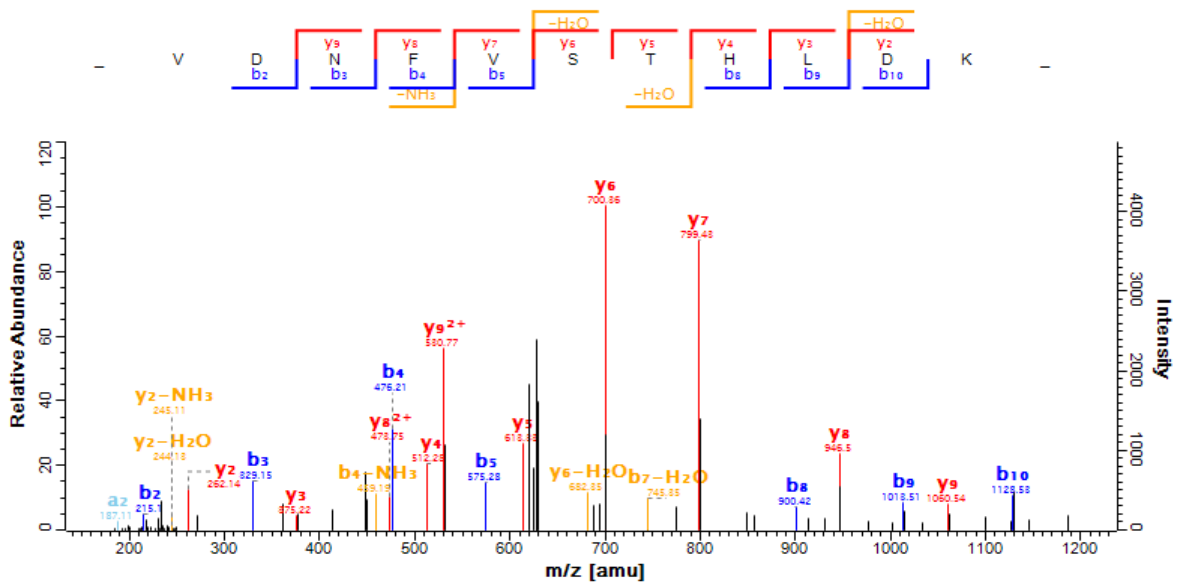
Protein Group ID: 4376
Protein Accession Numbers: Q96HV5
Gene Names: TMEM41A
Peptide Sequence: HLQLNETSTANHHISR
Total Number of Spectra: 3
Number of Replicates (out of 8): 2
Best Match Score: 104.21
Best Match Posterior Error Probability: 0.00014174
Best Match Spectrum:

Scan number 13462 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TMEM41A



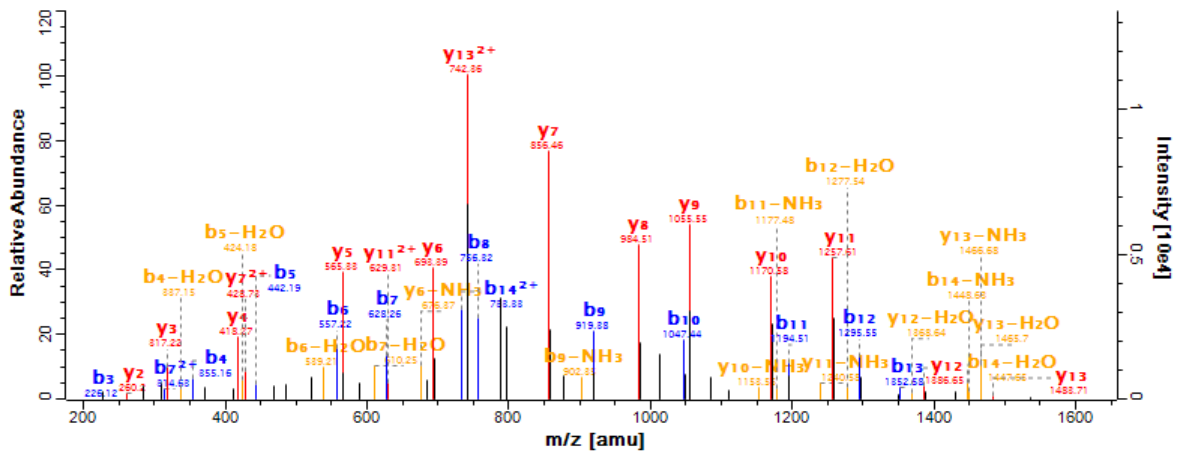
Protein Group ID: 4385
Protein Accession Numbers: Q96IK1; Q96IK1-2
Gene Names: BOD1
Peptide Sequence: VDNFVSTHLDK
Total Number of Spectra: 6
Number of Replicates (out of 8): 5
Best Match Score: 124.12
Best Match Posterior Error Probability: 4.39E-05
Best Match Spectrum:

Scan number 25286 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** BOD1



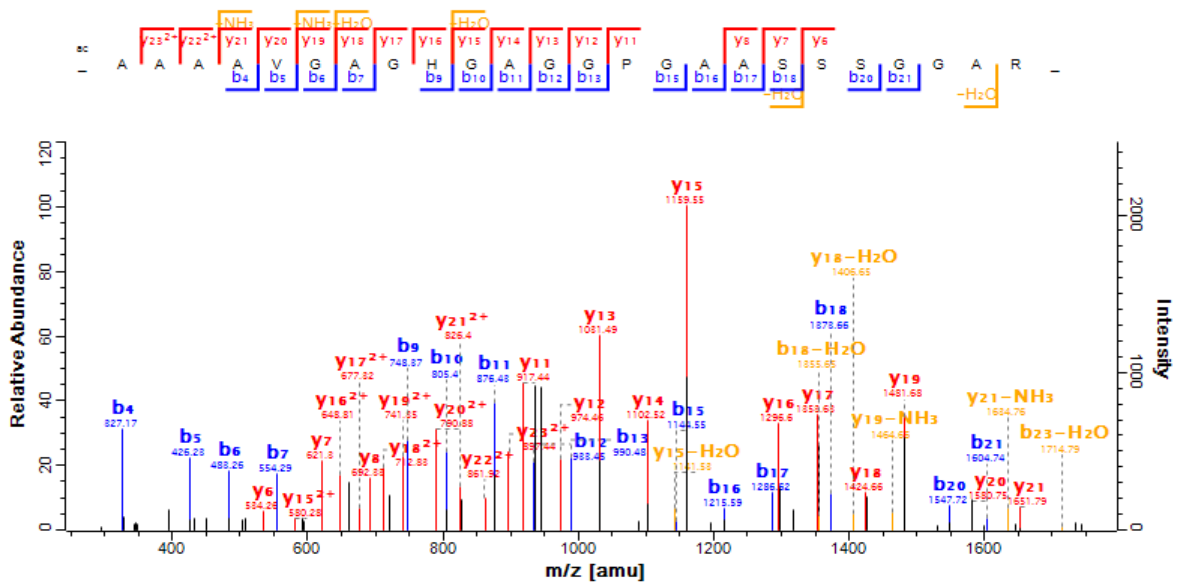
Protein Group ID: 4386
Protein Accession Numbers: Q96IX5
Gene Names: USMG5
Peptide Sequence: AGPESDAQYQFTGIK
Total Number of Spectra: 10
Number of Replicates (out of 8): 7
Best Match Score: 288.45
Best Match Posterior Error Probability: 3.27E-144
Best Match Spectrum:

Scan number 36773 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** USMG5



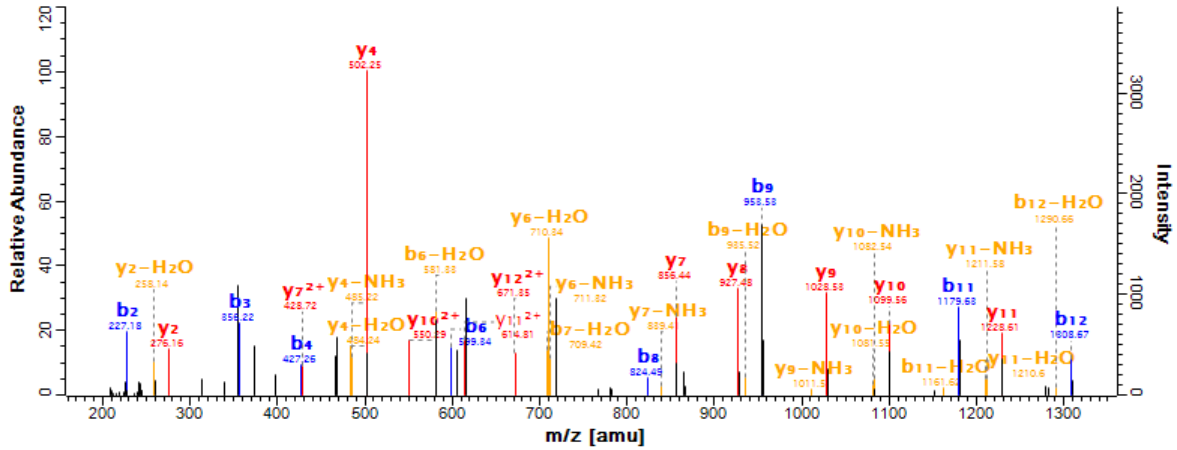
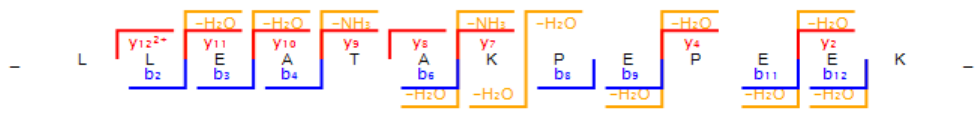
Protein Group ID: 4399
Protein Accession Numbers: Q96K37
Gene Names: SLC35E1
Peptide Sequence: AAAAVGAGHGAGGPGAASSSGGAR
Total Number of Spectra: 13
Number of Replicates (out of 8): 7
Best Match Score: 228.85
Best Match Posterior Error Probability: 1.24E-81
Best Match Spectrum:

Scan number 15639 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** SLC35E1



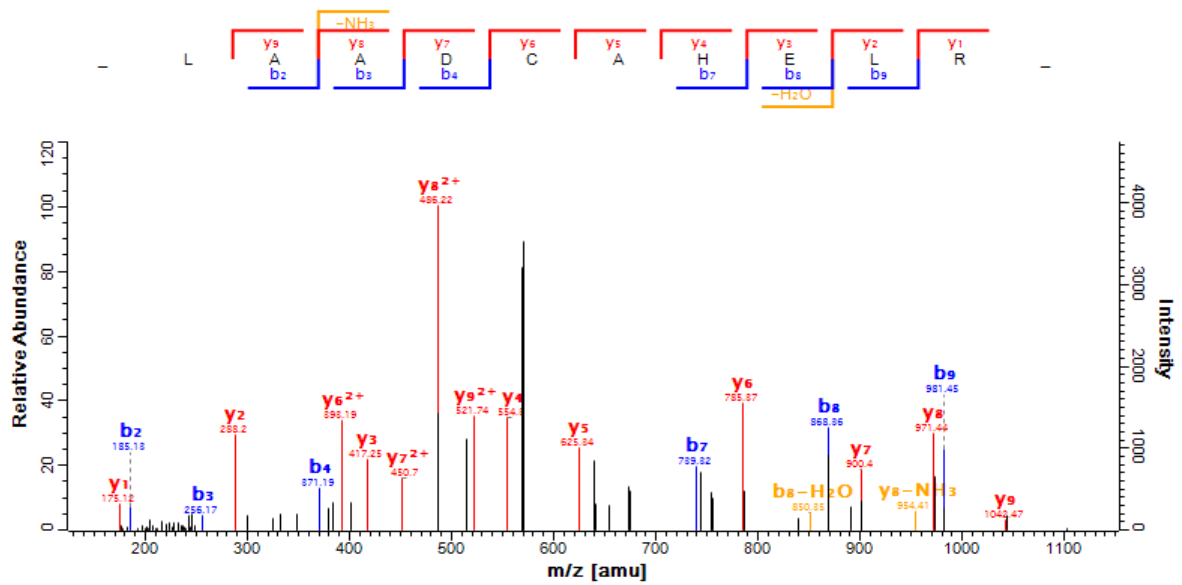
Protein Group ID: 4402
Protein Accession Numbers: Q96KC8
Gene Names: DNAJC1
Peptide Sequence: LEATAKPEPEEK
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 219.43
Best Match Posterior Error Probability: 1.06E-39
Best Match Spectrum:

Scan number 13475 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** DNAJC1



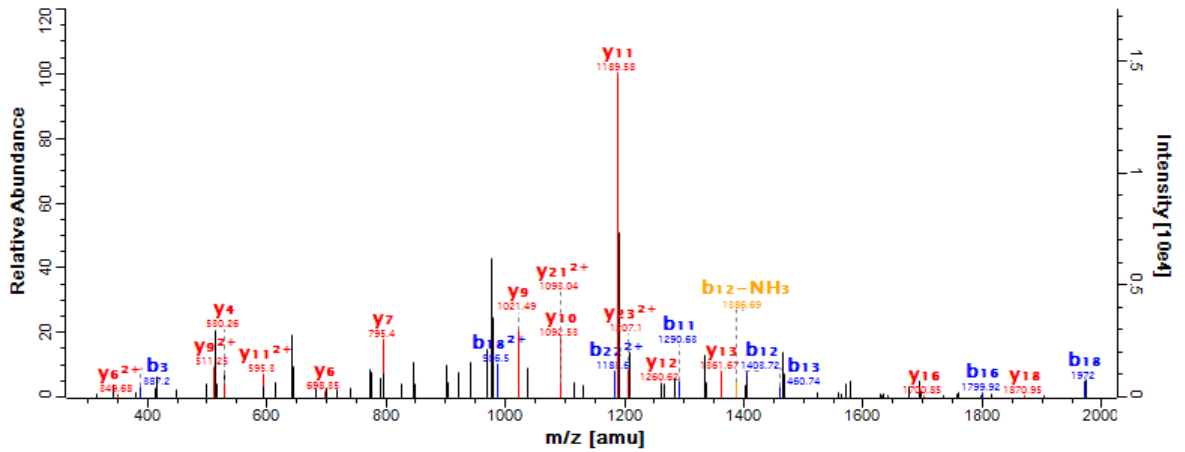
Protein Group ID: 4410
Protein Accession Numbers: Q96LJ7
Gene Names: DHRS1
Peptide Sequence: LAADCAHELK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 138.22
Best Match Posterior Error Probability: 1.09E-05
Best Match Spectrum:

Scan number 10145 **Raw file** A549-US-WT-top20CID-Elite-2ug-813
Method ITMS; CID **Genenames** DHRS1



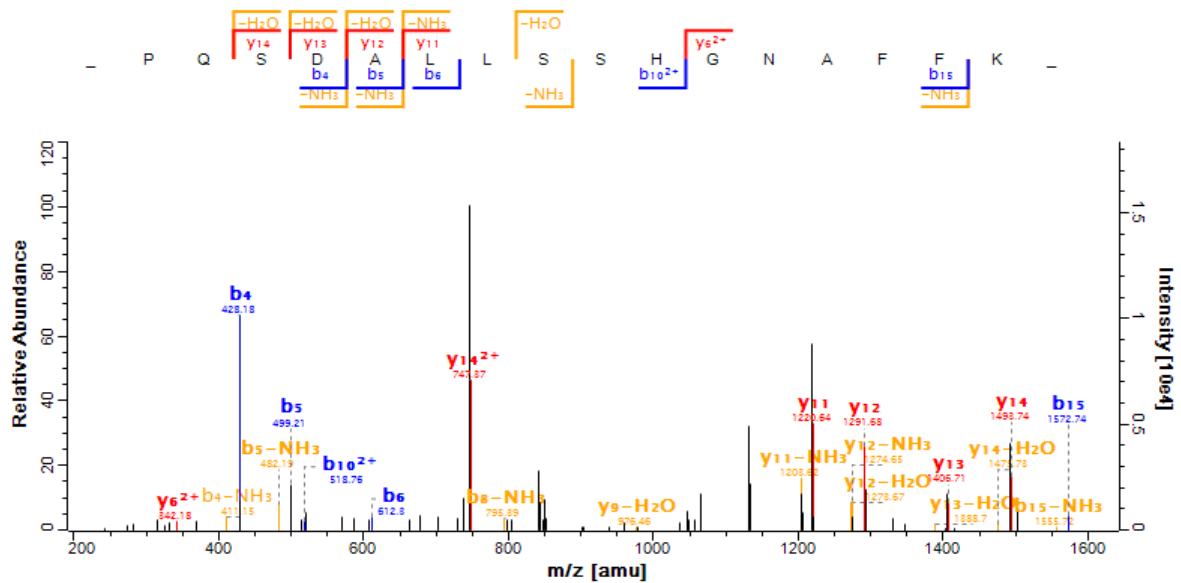
Protein Group ID: 4414
Protein Accession Numbers: Q96MW5
Gene Names: COG8
Peptide Sequence: RETLFTLDDQALGPLTAPPEPPAEEPR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 60.382
Best Match Posterior Error Probability: 0.0010003
Best Match Spectrum:

Scan number 67403 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** COG8



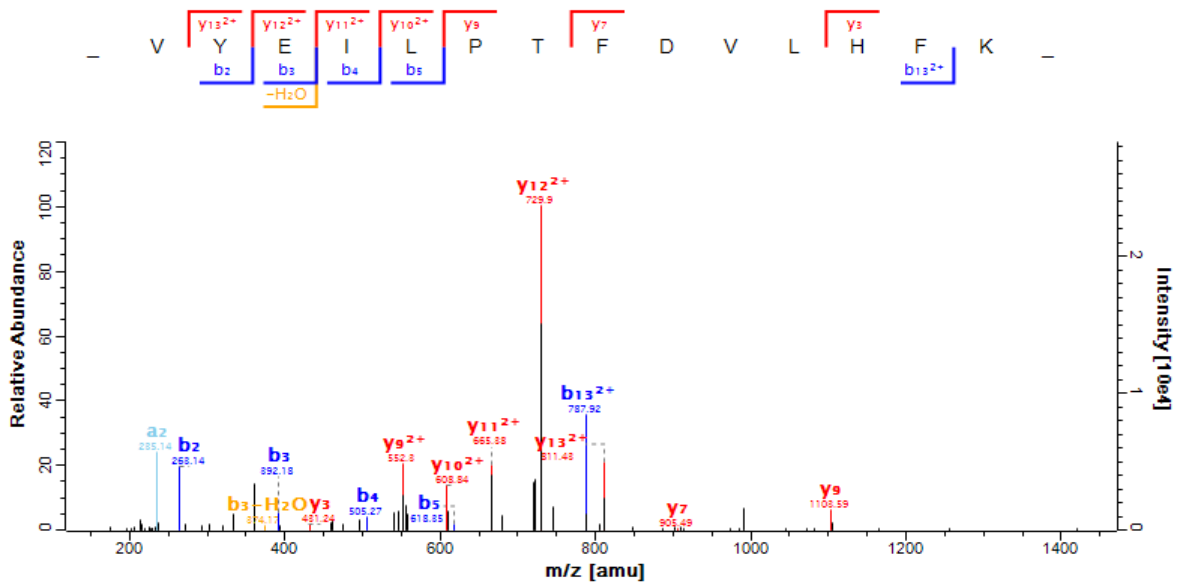
Protein Group ID: 4429
Protein Accession Numbers: Q96PX9
Gene Names: PLEKHG4B
Peptide Sequence: PQSDALLSSHGNAFFK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 90.444
Best Match Posterior Error Probability: 0.00055388
Best Match Spectrum:

Scan number 42956 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PLEKHG4B



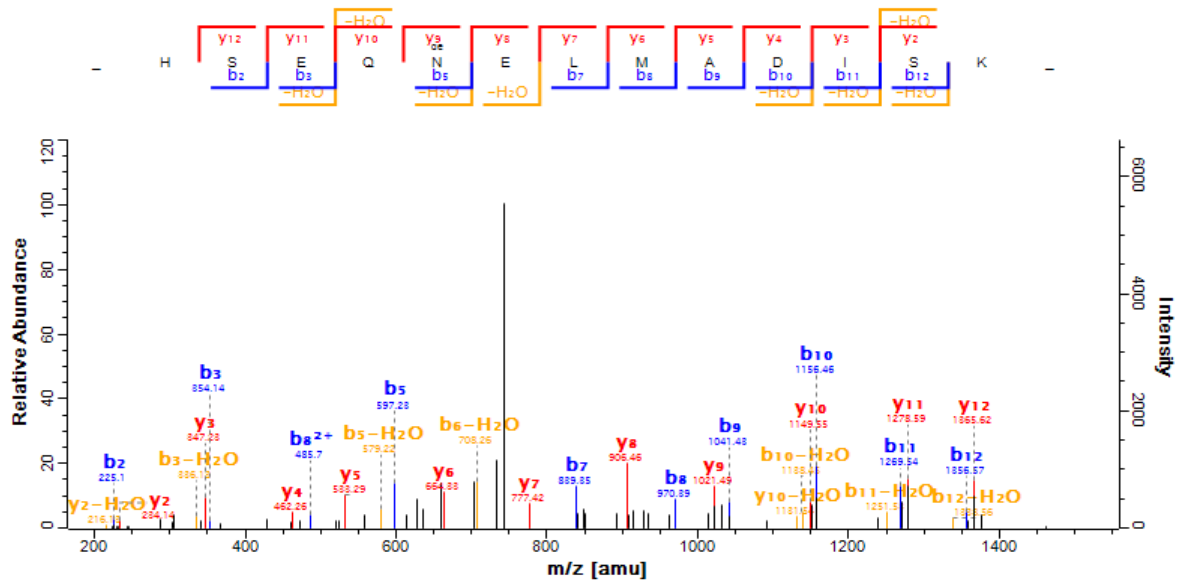
Protein Group ID: 4439
Protein Accession Numbers: Q96RD7; Q96RD7-2
Gene Names: PANX1
Peptide Sequence: VYEILPFDVLHFYK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 78.903
Best Match Posterior Error Probability: 0.003518
Best Match Spectrum:

Scan number 80186 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PANX1



Protein Group ID: 4444
Protein Accession Numbers: Q96RT6
Gene Names: CTAGE1
Peptide Sequence: HSEQNELMADISK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 157.23
Best Match Posterior Error Probability: 1.64E-08
Best Match Spectrum:

Scan number 34415 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CTAGE1



Protein Group ID: 4448

Protein Accession Numbers: Q96S55; Q96S55-2; Q96S55-3

Gene Names: WRNIP1

Peptide Sequence: TTLAHIIASNSK

Total Number of Spectra: 1

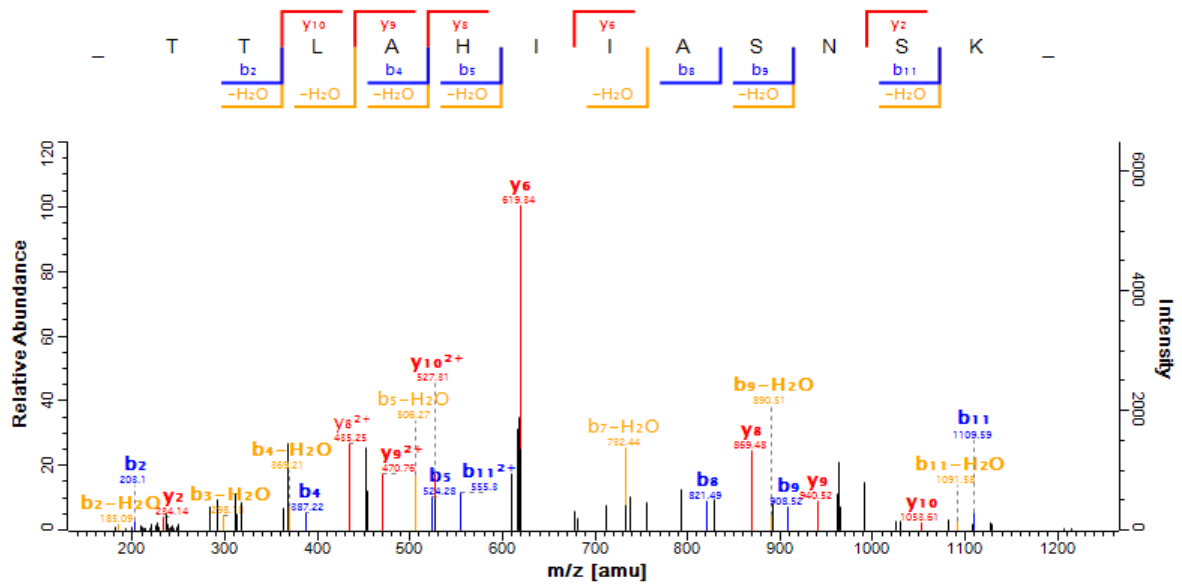
Number of Replicates (out of 8): 1

Best Match Score: 127.56

Best Match Posterior Error Probability: 0.00010135

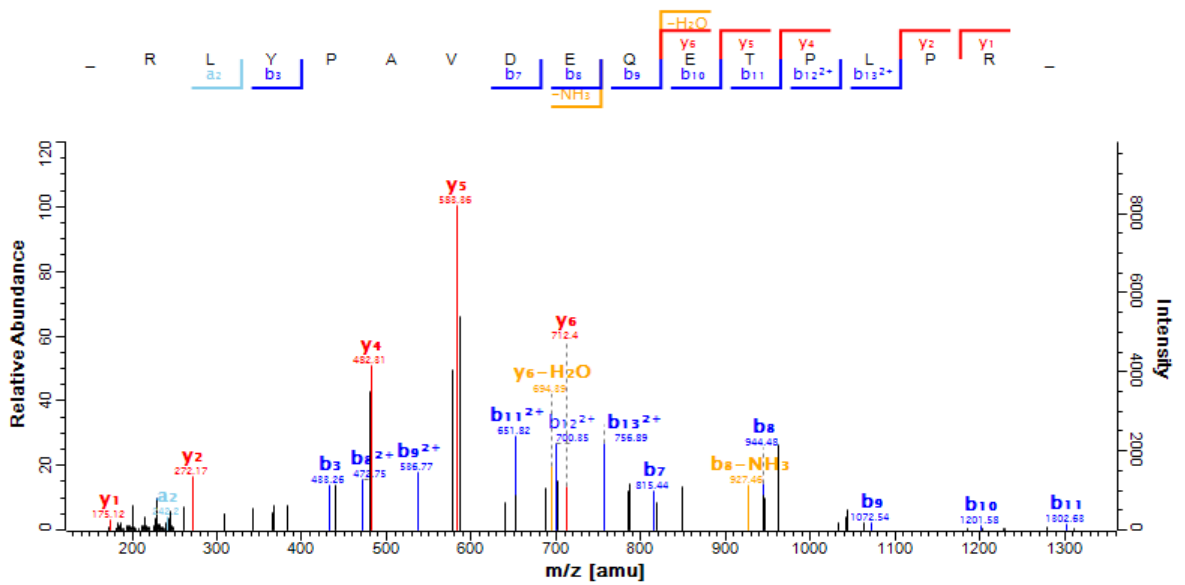
Best Match Spectrum:

Scan number	26061	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	WRNIP1



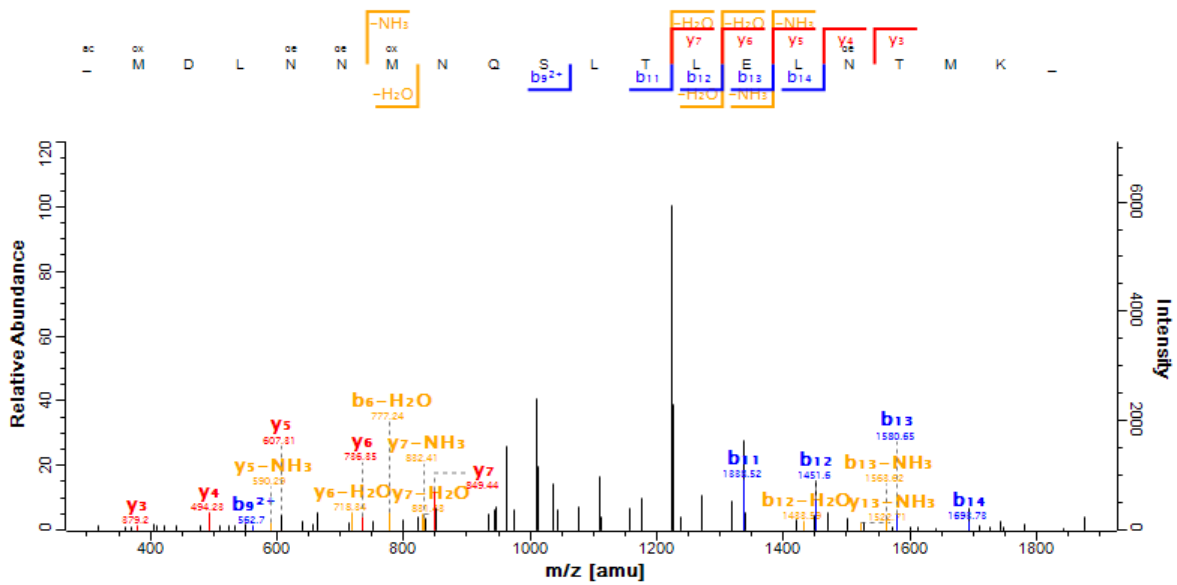
Protein Group ID: 4449
Protein Accession Numbers: Q96S59
Gene Names: RANBP9
Peptide Sequence: RLYPAVDEQETPLPR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 87.083
Best Match Posterior Error Probability: 0.0024477
Best Match Spectrum:

Scan number 37170 **Raw file** A549-US-WT-top20CID-Elite-2ug-811
Method ITMS; CID **Genenames** RANBP9



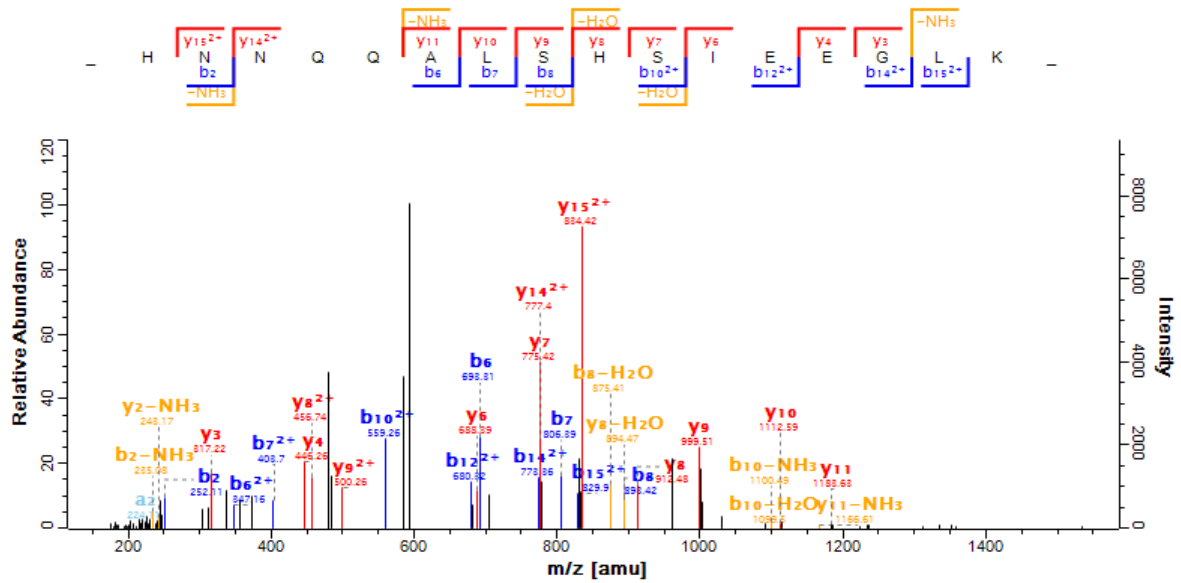
Protein Group ID: 4457
Protein Accession Numbers: Q96ST8-2
Gene Names:
Peptide Sequence: MDLNNMNQSLTLELNTMK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 63.827
Best Match Posterior Error Probability: 0.00015283
Best Match Spectrum:

Scan number 72292 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Pepti...** 63.83



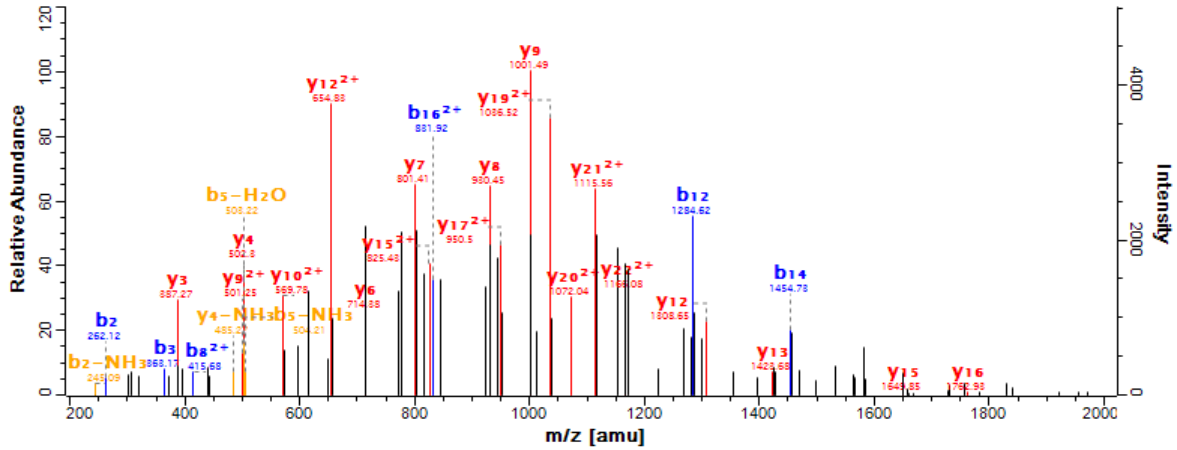
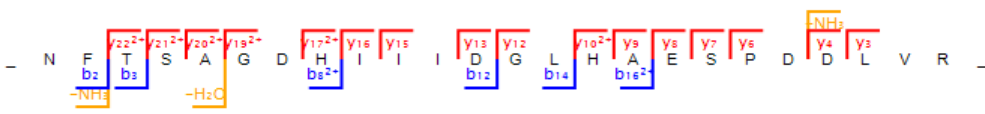
Protein Group ID: 4475
Protein Accession Numbers: Q99496
Gene Names: RNF2
Peptide Sequence: HNNQQALSHSIEEGLK
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 138.55
Best Match Posterior Error Probability: 2.96E-05
Best Match Spectrum:

Scan number 24540 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** RNF2



Protein Group ID: 4497
Protein Accession Numbers: Q99797
Gene Names: MIPEP
Peptide Sequence: NFTSAGDHHIIDGLHAESPDDLVR
Total Number of Spectra: 8
Number of Replicates (out of 8): 6
Best Match Score: 99.603
Best Match Posterior Error Probability: 6.18E-07
Best Match Spectrum:

Scan number 60109 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** MIPEP



Protein Group ID: 4501

Protein Accession Numbers: Q99871-2; Q99871; Q99871-3

Gene Names: HAUS7

Peptide Sequence: QLHFMDQLLDTIR

Total Number of Spectra: 3

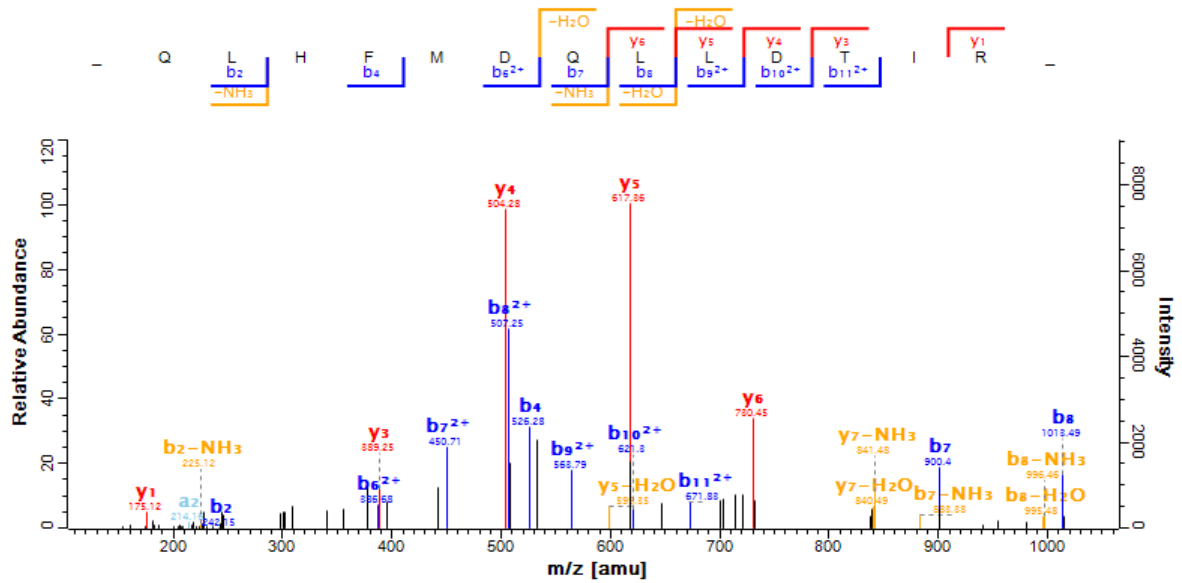
Number of Replicates (out of 8): 3

Best Match Score: 100.04

Best Match Posterior Error Probability: 0.00050986

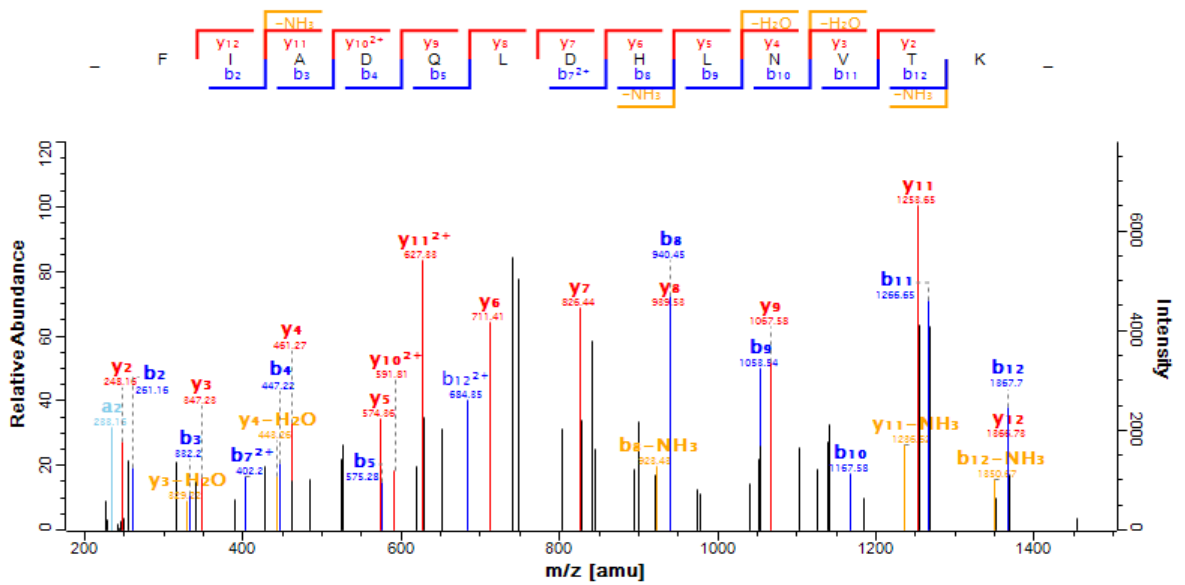
Best Match Spectrum:

Scan number 74135 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** HAUS7



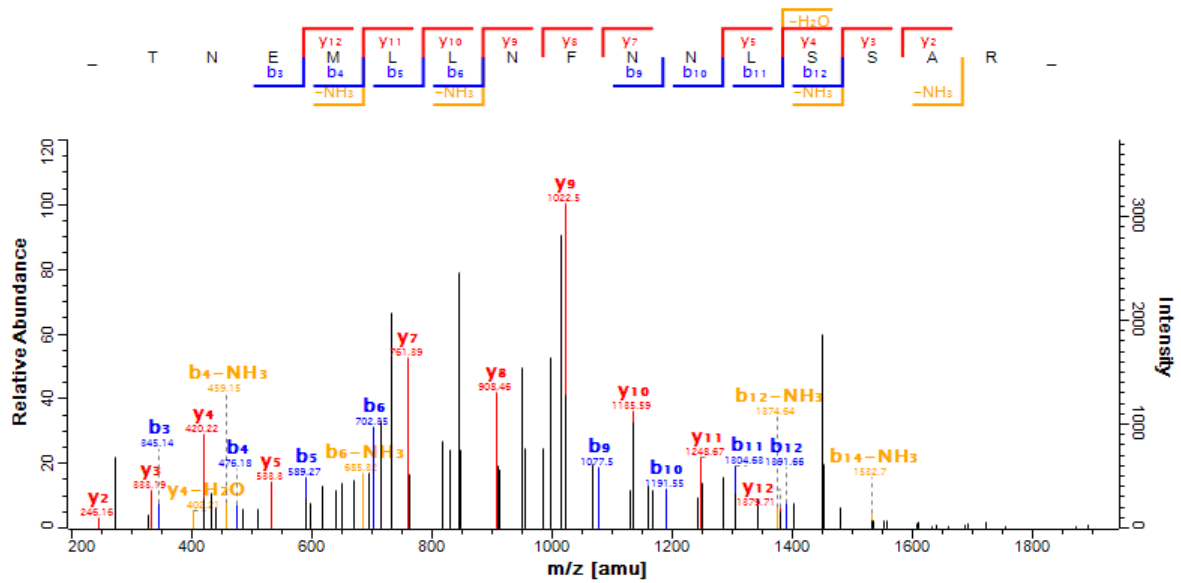
Protein Group ID: 4516
Protein Accession Numbers: Q9BQC6
Gene Names: MRP63
Peptide Sequence: FIADQLDHLNVTK
Total Number of Spectra: 5
Number of Replicates (out of 8): 4
Best Match Score: 176.87
Best Match Posterior Error Probability: 5.35E-14
Best Match Spectrum:

Scan number 46220 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** MRP63



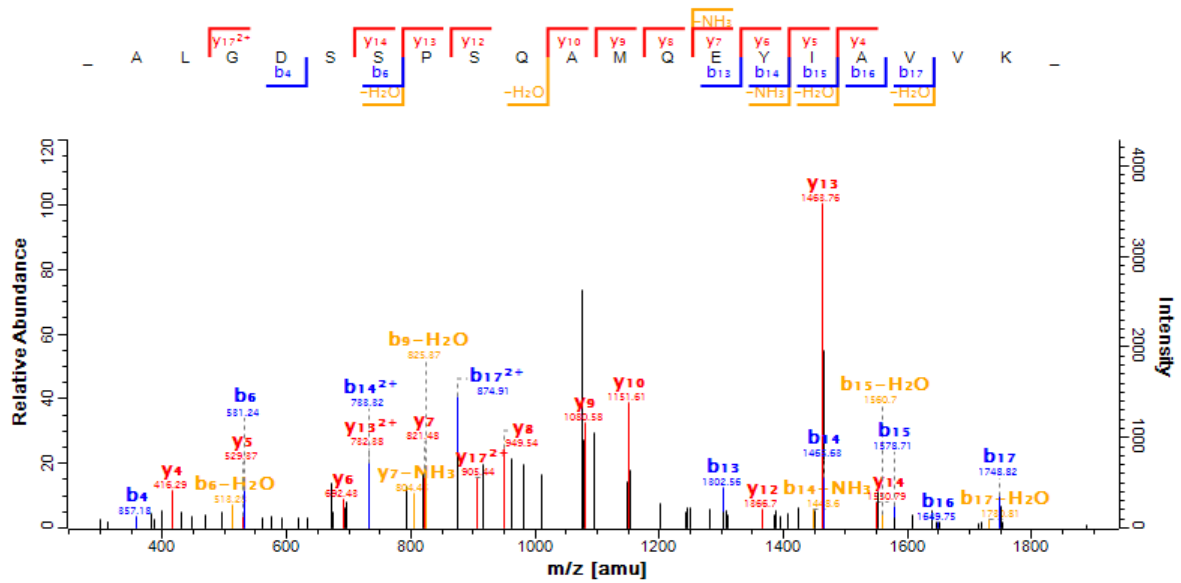
Protein Group ID: 4517
Protein Accession Numbers: Q9BQD3
Gene Names: KXD1
Peptide Sequence: TNEMLLNFNNLSSAR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 103.04
Best Match Posterior Error Probability: 0.00018141
Best Match Spectrum:

Scan number 59435 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** KXD1



Protein Group ID: 4523
Protein Accession Numbers: Q9BR61
Gene Names: ACBD6
Peptide Sequence: ALGDSSPSQAMQEYIAVVK
Total Number of Spectra: 4
Number of Replicates (out of 8): 3
Best Match Score: 135.08
Best Match Posterior Error Probability: 8.10E-06
Best Match Spectrum:

Scan number 63201 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ACBD6



Protein Group ID: 4543

Protein Accession Numbers: Q9BSE5

Gene Names: AGMAT

Peptide Sequence: LPVQTSPEGLDAAFVIGVPLDGTGTSNRPGAR

Total Number of Spectra: 3

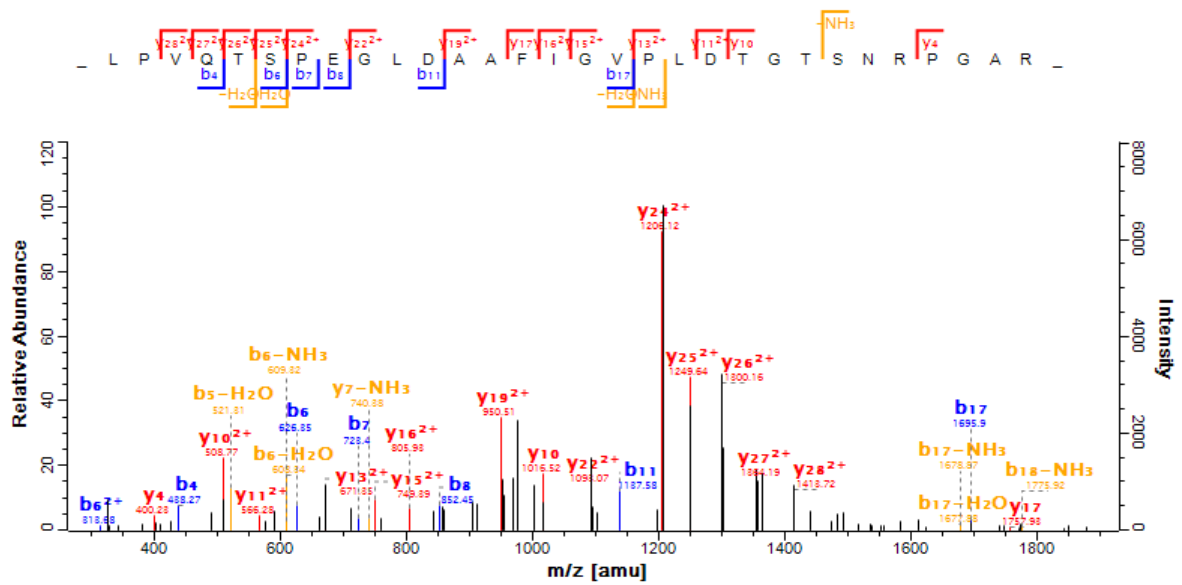
Number of Replicates (out of 8): 3

Best Match Score: 87.72

Best Match Posterior Error Probability: 2.05E-06

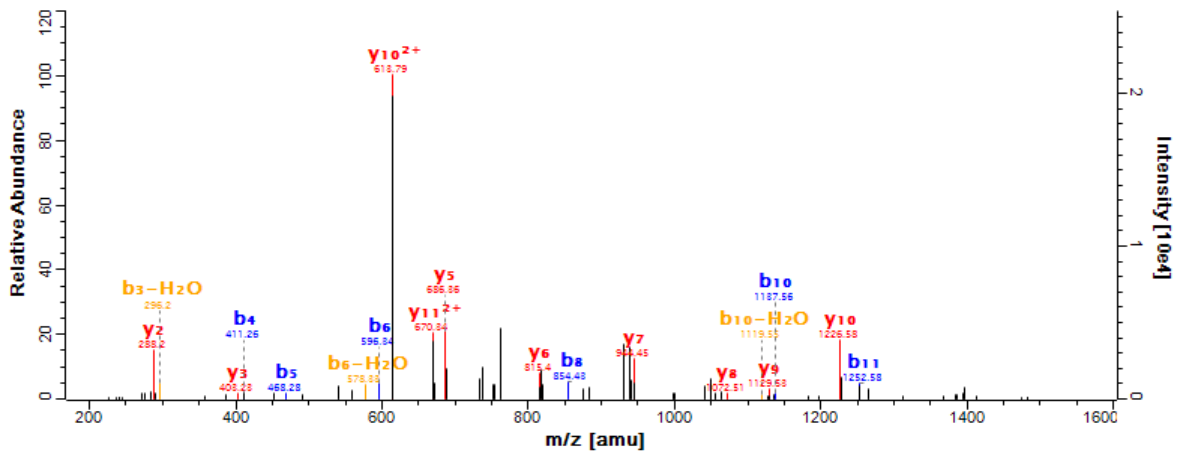
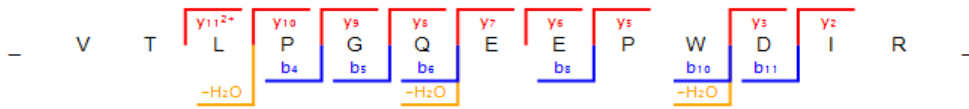
Best Match Spectrum:

Scan number	66522	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	AGMAT



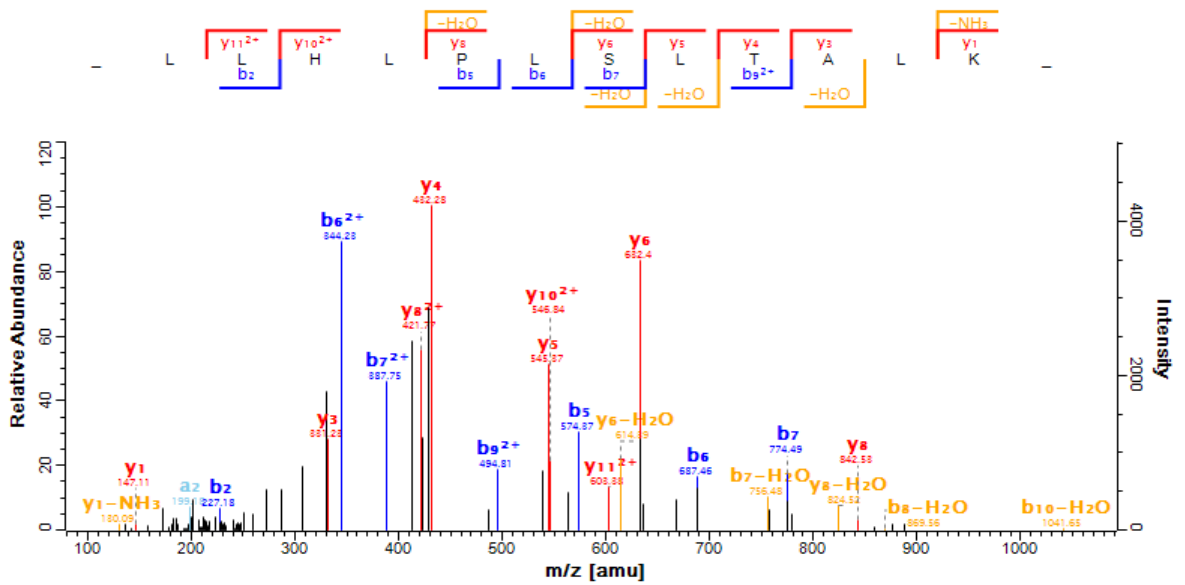
Protein Group ID: 4556
Protein Accession Numbers: Q9BTM9-2; Q9BTM9
Gene Names: URM1
Peptide Sequence: VTLPGQEEPWDI R
Total Number of Spectra: 3
Number of Replicates (out of 8): 2
Best Match Score: 95.264
Best Match Posterior Error Probability: 0.00088456
Best Match Spectrum:

Scan number 51777 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** URM1



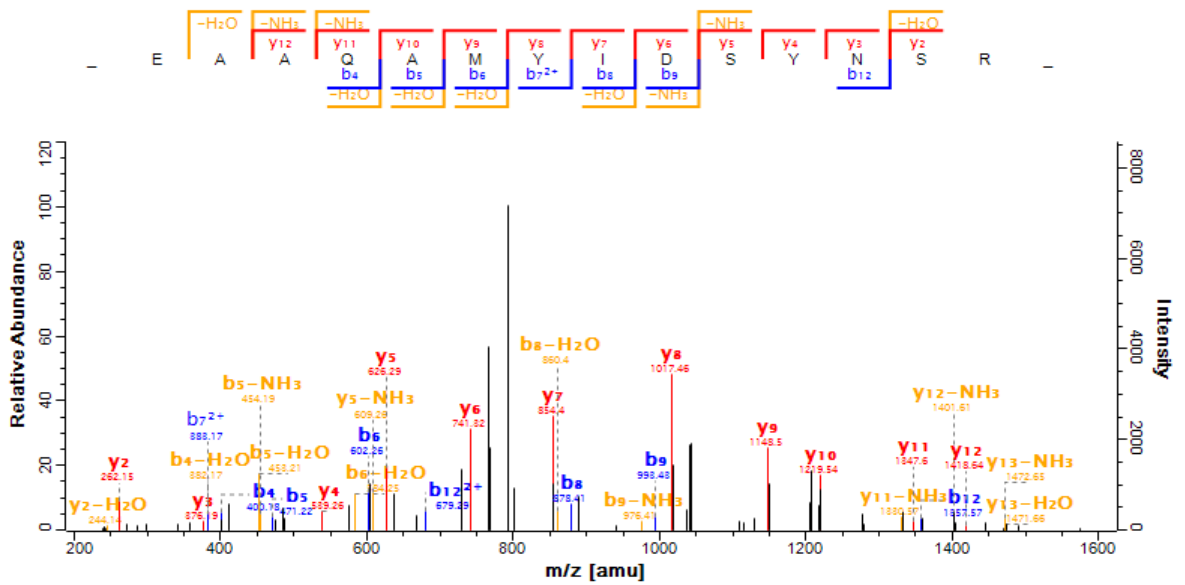
Protein Group ID: 4558
Protein Accession Numbers: Q9BTT6
Gene Names: LRRC1
Peptide Sequence: LLHLPLSLTALK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 136.96
Best Match Posterior Error Probability: 7.22E-05
Best Match Spectrum:

Scan number 68486 **Raw file** A549-US-WT-top20CID-Elite-2ug-811
Method ITMS; CID **Genenames** LRRC1



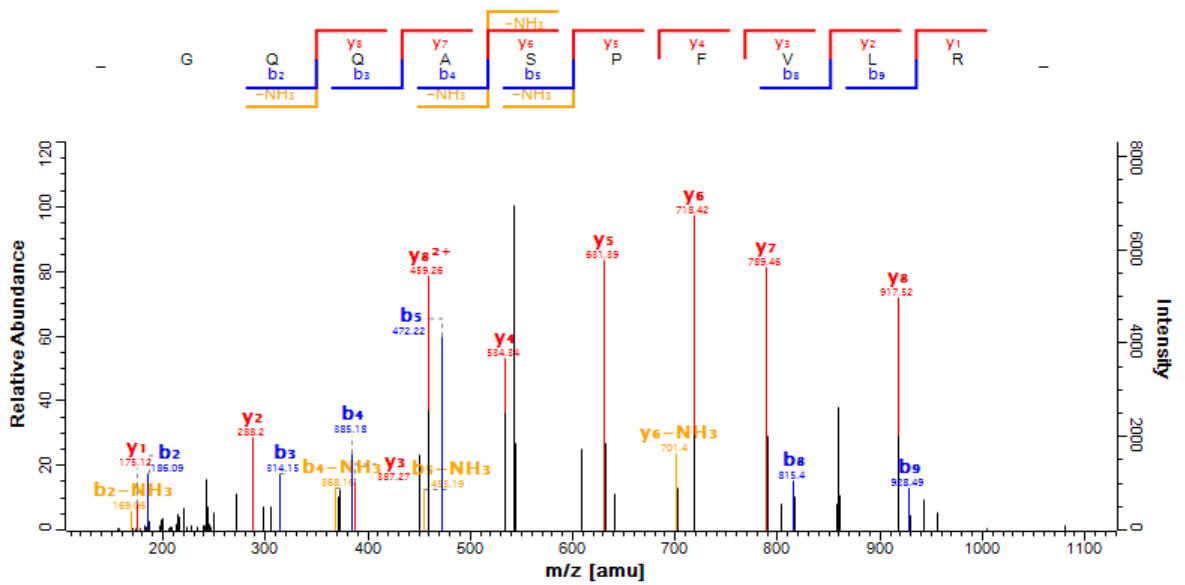
Protein Group ID: 4563
Protein Accession Numbers: Q9BU61
Gene Names: NDUFAF3
Peptide Sequence: EAAQAMYIDSYNSR
Total Number of Spectra: 6
Number of Replicates (out of 8): 3
Best Match Score: 157.35
Best Match Posterior Error Probability: 2.39E-09
Best Match Spectrum:

Scan number 31685 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** NDUFAF3



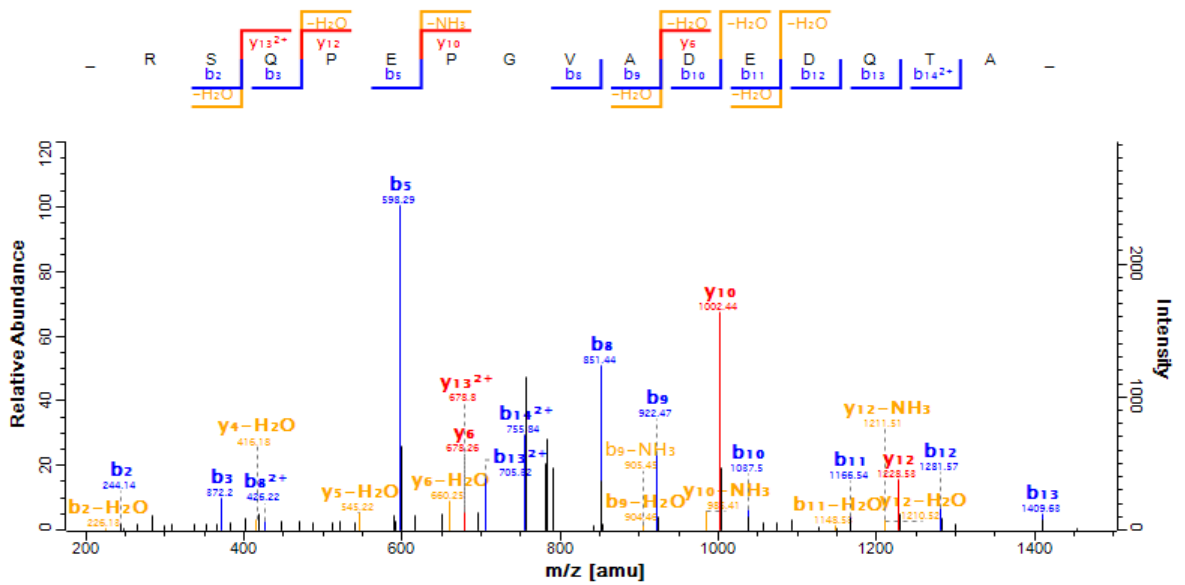
Protein Group ID: 4566
Protein Accession Numbers: Q9BUE0
Gene Names: MED18
Peptide Sequence: GQQASPFVLR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 140.07
Best Match Posterior Error Probability: 1.26E-05
Best Match Spectrum:

Scan number 32948 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MED18



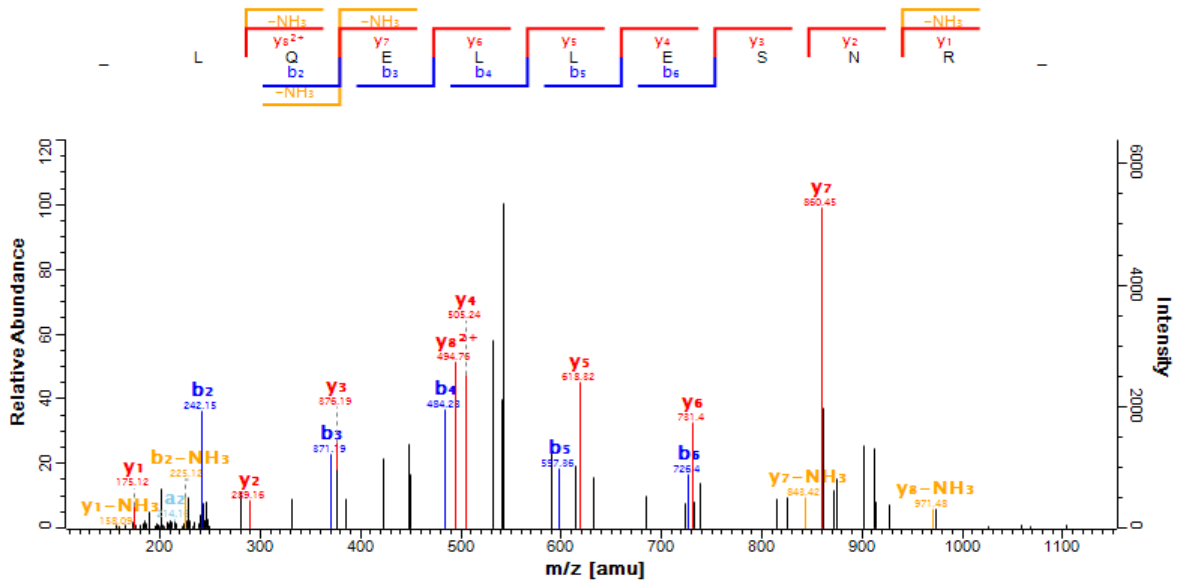
Protein Group ID: 4571
Protein Accession Numbers: Q9BUL9
Gene Names: RPP25
Peptide Sequence: RSQPEPGVADEDQTA
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 123.76
Best Match Posterior Error Probability: 8.68E-05
Best Match Spectrum:

Scan number 10753 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** RPP25



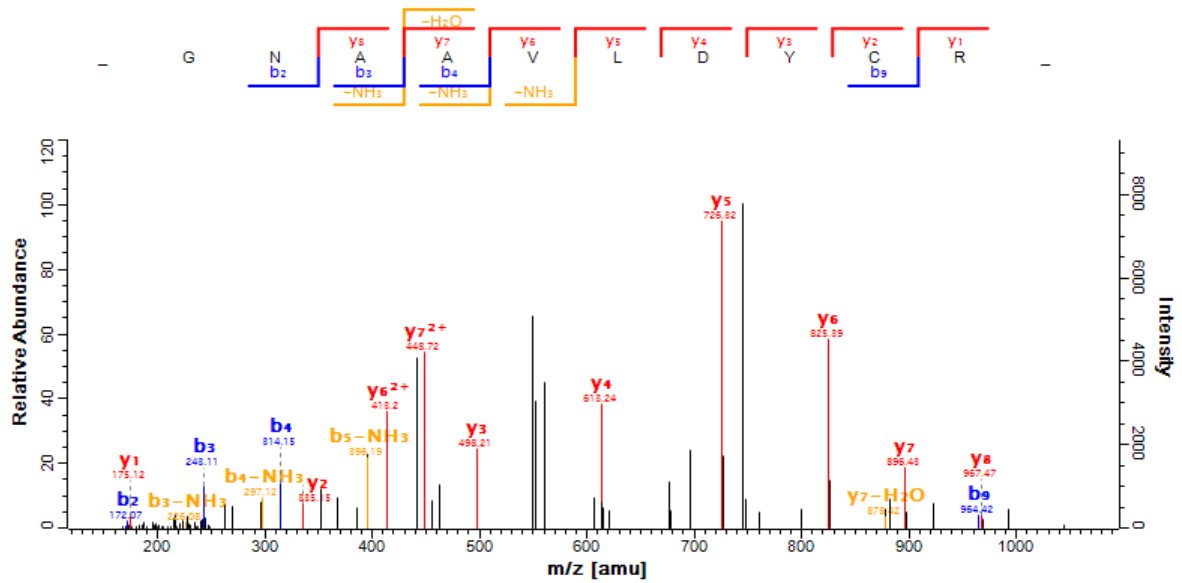
Protein Group ID: 4576
Protein Accession Numbers: Q9BUW7
Gene Names: C9orf16
Peptide Sequence: LQELLESNR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 89.171
Best Match Posterior Error Probability: 0.003784
Best Match Spectrum:

Scan number 23105 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** C9orf16



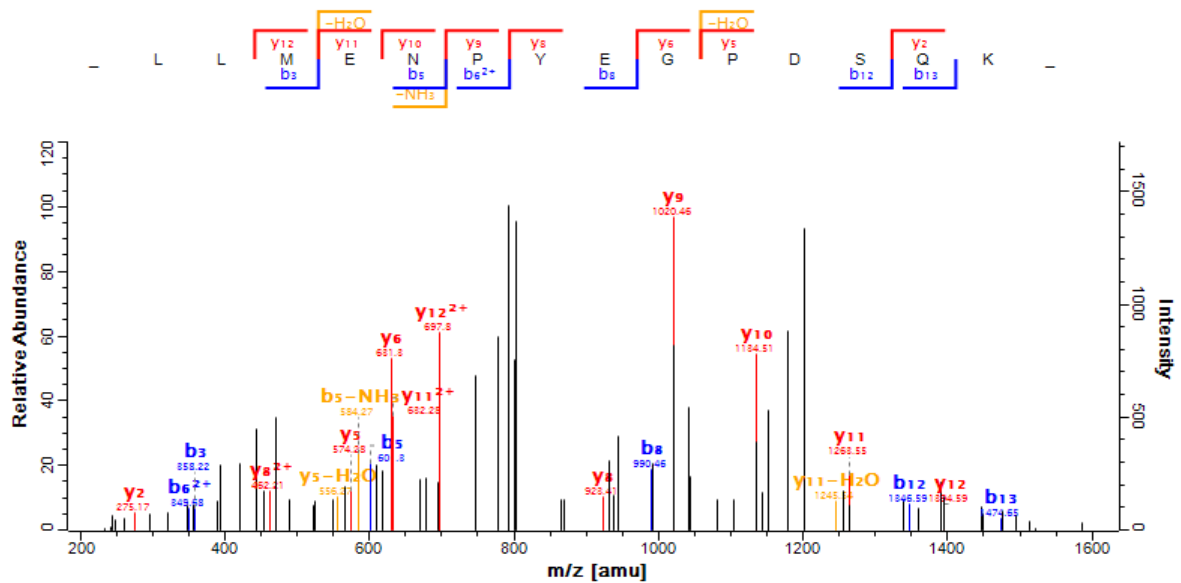
Protein Group ID: 4582
Protein Accession Numbers: Q9BV81
Gene Names: TMEM93
Peptide Sequence: GNAAVLDYCR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 99.283
Best Match Posterior Error Probability: 0.00081781
Best Match Spectrum:

Scan number 21799 **Raw file** A549-US-WT-top20CID-Elite-2ug-814
Method ITMS; CID **Genenames** TMEM93



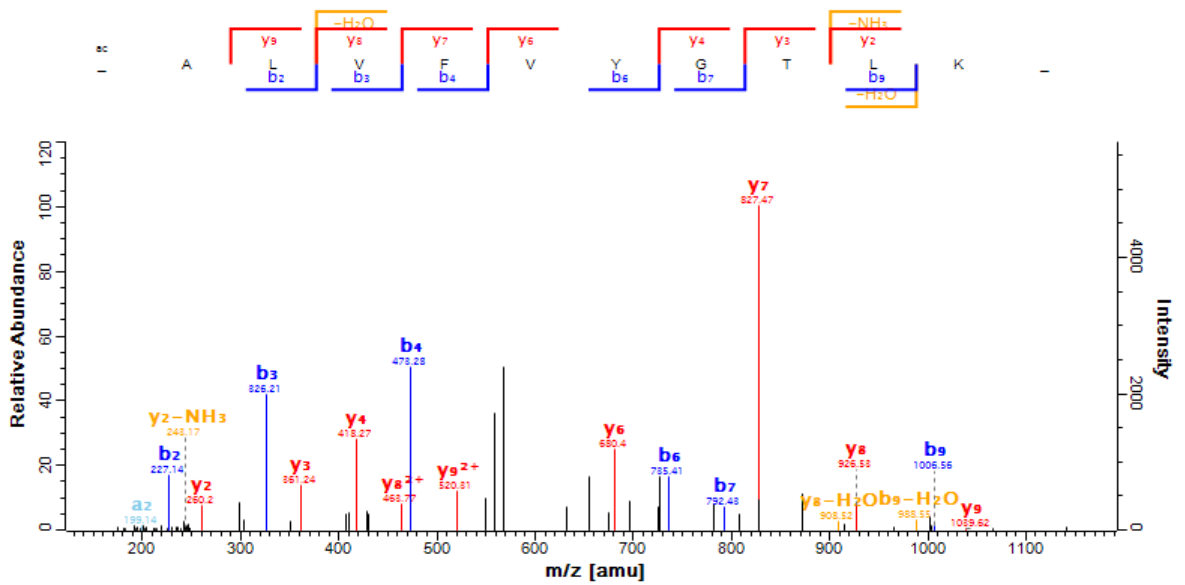
Protein Group ID: 4584
Protein Accession Numbers: Q9BVC3
Gene Names: DSCC1
Peptide Sequence: LLMENPYEGPDSQK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 91.307
Best Match Posterior Error Probability: 0.001073
Best Match Spectrum:

Scan number 34925 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** DSCC1



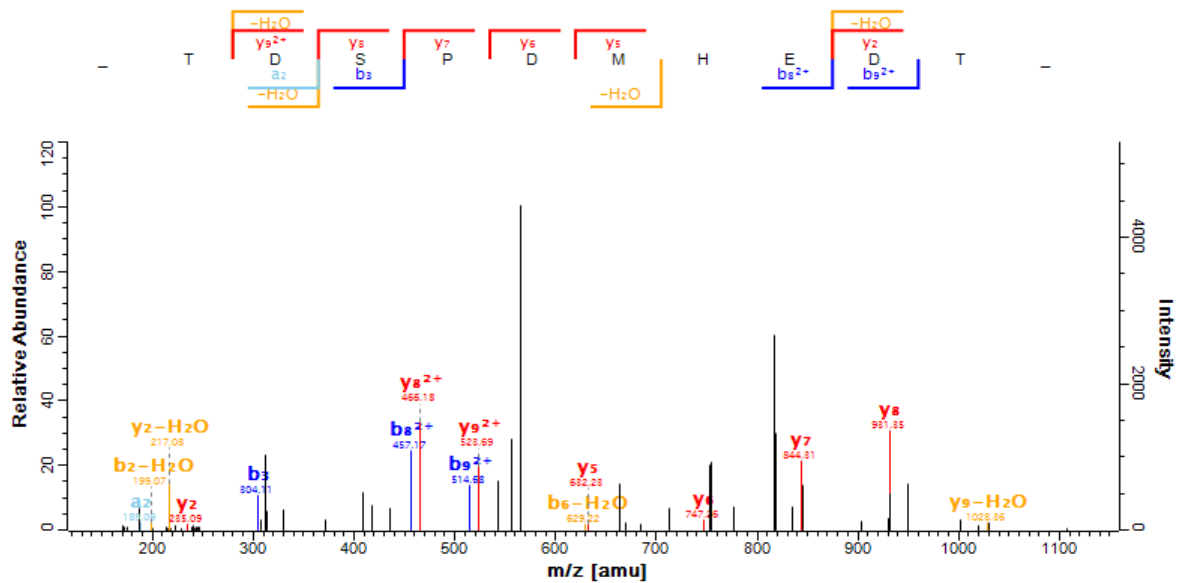
Protein Group ID: 4591
Protein Accession Numbers: Q9BVM4
Gene Names: A2LD1
Peptide Sequence: ALVFVYGTK
Total Number of Spectra: 5
Number of Replicates (out of 8): 4
Best Match Score: 128.27
Best Match Posterior Error Probability: 6.04E-05
Best Match Spectrum:

Scan number 84899 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** A2LD1



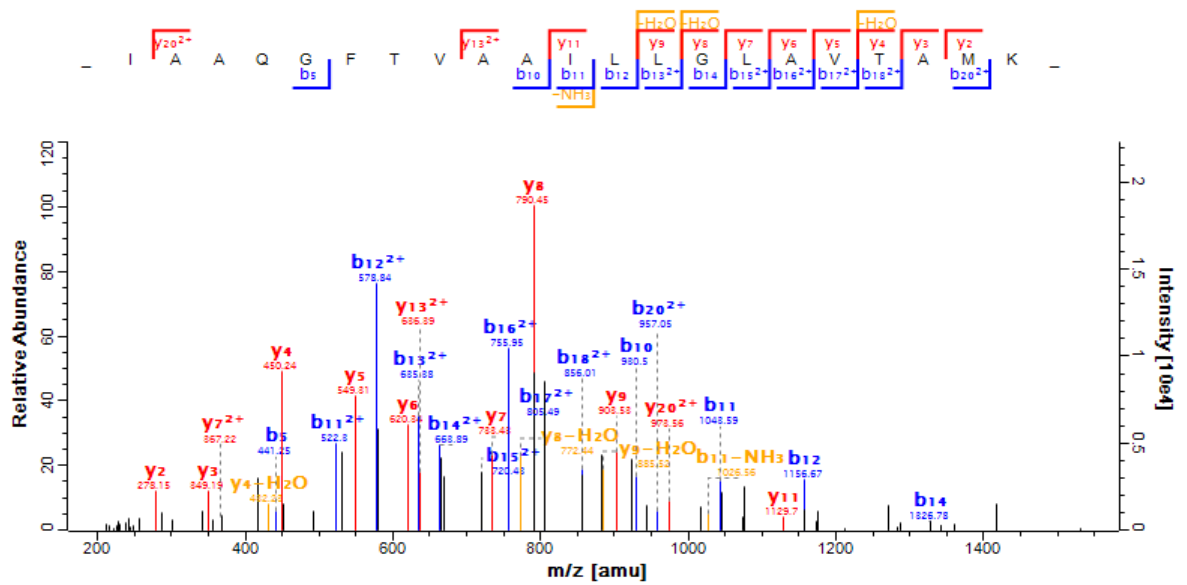
Protein Group ID: 4595
Protein Accession Numbers: Q9BW61
Gene Names: DDA1
Peptide Sequence: TDSPDMHEDT
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 84.615
Best Match Posterior Error Probability: 0.003302
Best Match Spectrum:

Scan number 5700 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** DDA1



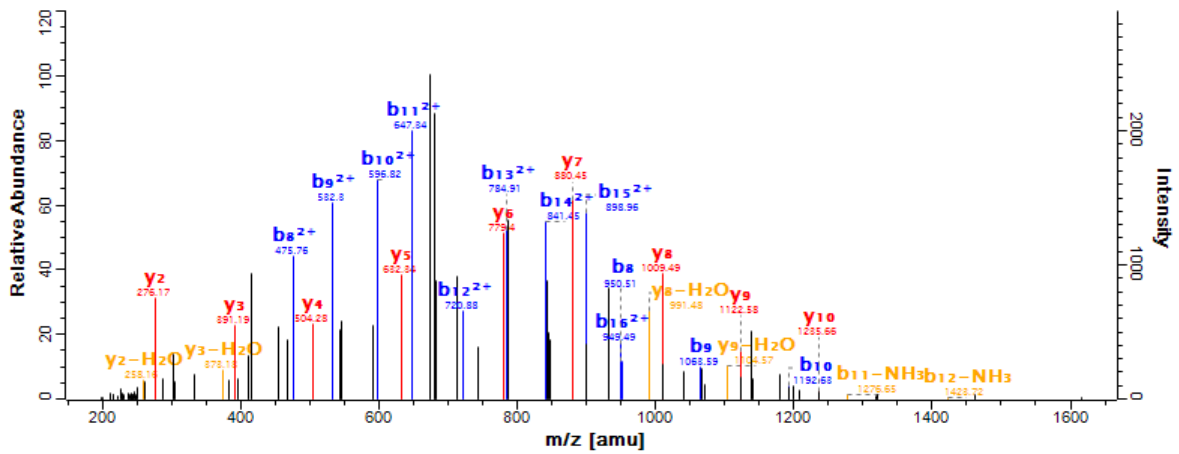
Protein Group ID: 4596
Protein Accession Numbers: Q9BW72
Gene Names: HIGD2A
Peptide Sequence: IAAQGFTVAAILLGLAVTAMK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 136.66
Best Match Posterior Error Probability: 2.83E-14
Best Match Spectrum:

Scan number 96196 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** HIGD2A



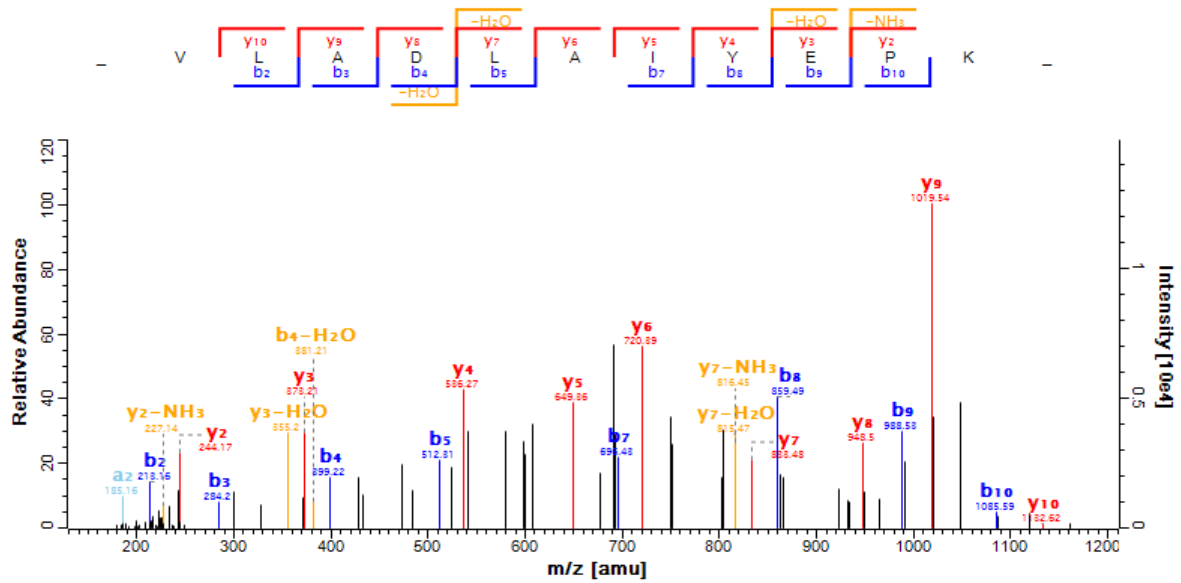
Protein Group ID: 4618
Protein Accession Numbers: Q9BXW9; Q9BXW9-2
Gene Names: FANCD2
Peptide Sequence: HREDVLSLETFLDTR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 134.25
Best Match Posterior Error Probability: 0.00033567
Best Match Spectrum:

Scan number 80956 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** FANCD2



Protein Group ID: 4625
Protein Accession Numbers: Q9BYC9
Gene Names: MRPL20
Peptide Sequence: VLADLAIYEPK
Total Number of Spectra: 11
Number of Replicates (out of 8): 8
Best Match Score: 140.78
Best Match Posterior Error Probability: 2.23E-05
Best Match Spectrum:

Scan number 51373 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** MRPL20



Protein Group ID: 4636

Protein Accession Numbers: Q9BYV8; Q9BYV8-2; Q9BYV8-5; Q9BYV8-3

Gene Names: CEP41

Peptide Sequence: SAQNLPGGGPASHSNPR

Total Number of Spectra: 2

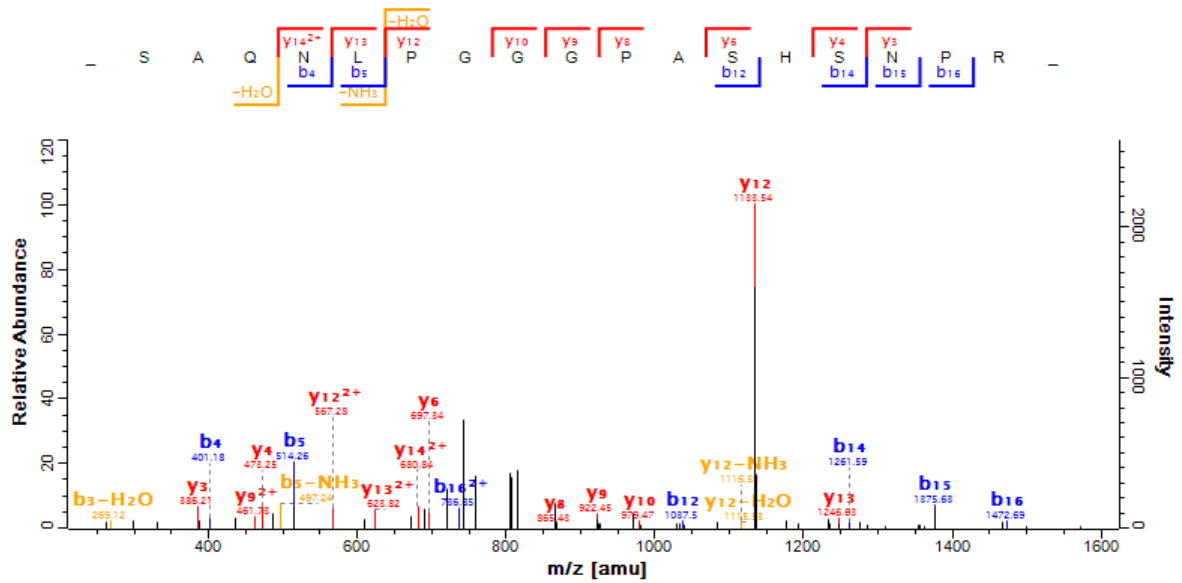
Number of Replicates (out of 8): 2

Best Match Score: 103.13

Best Match Posterior Error Probability: 0.0001502

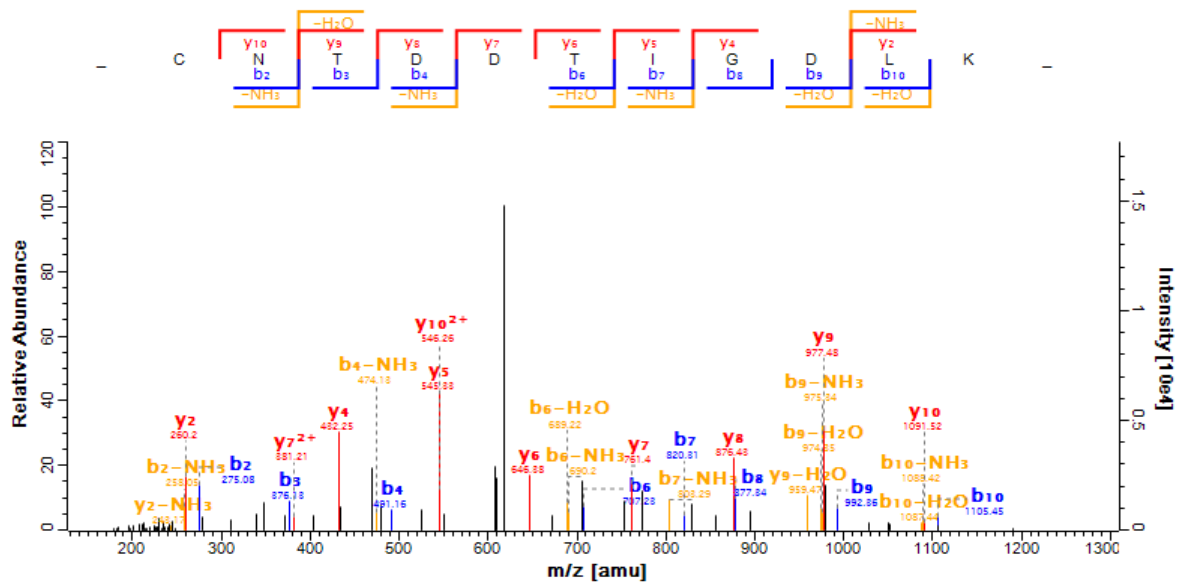
Best Match Spectrum:

Scan number 8499 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CEP41



Protein Group ID: 4646
Protein Accession Numbers: Q9BZL1
Gene Names: UBL5
Peptide Sequence: CNTDDTIGDLK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 180.24
Best Match Posterior Error Probability: 8.26E-10
Best Match Spectrum:

Scan number 20178 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** UBL5



Protein Group ID: 4660

Protein Accession Numbers: Q9C0F1-2; Q9C0F1

Gene Names: CEP44

Peptide Sequence: SEVERPASIPLSSGYSTASSTPR

Total Number of Spectra: 8

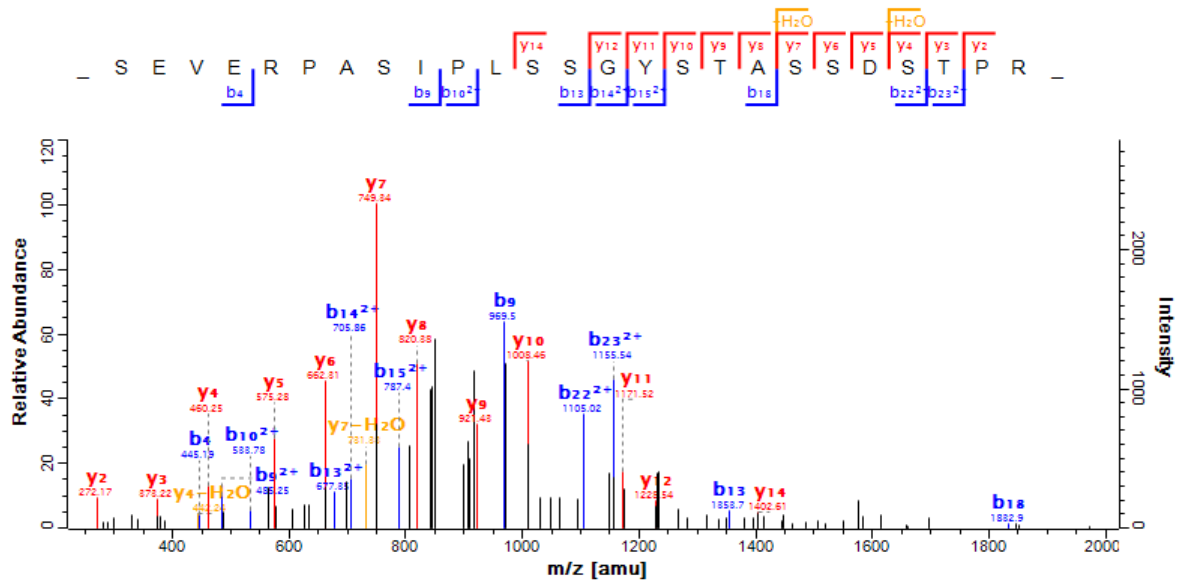
Number of Replicates (out of 8): 5

Best Match Score: 87.659

Best Match Posterior Error Probability: 6.61E-05

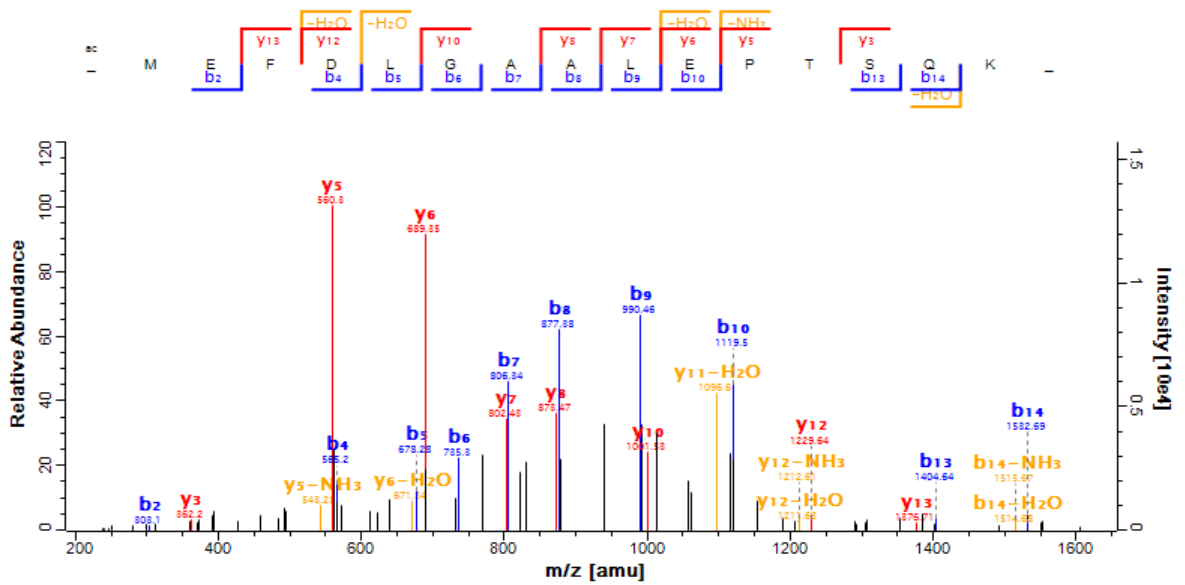
Best Match Spectrum:

Scan number	34854	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	CEP44



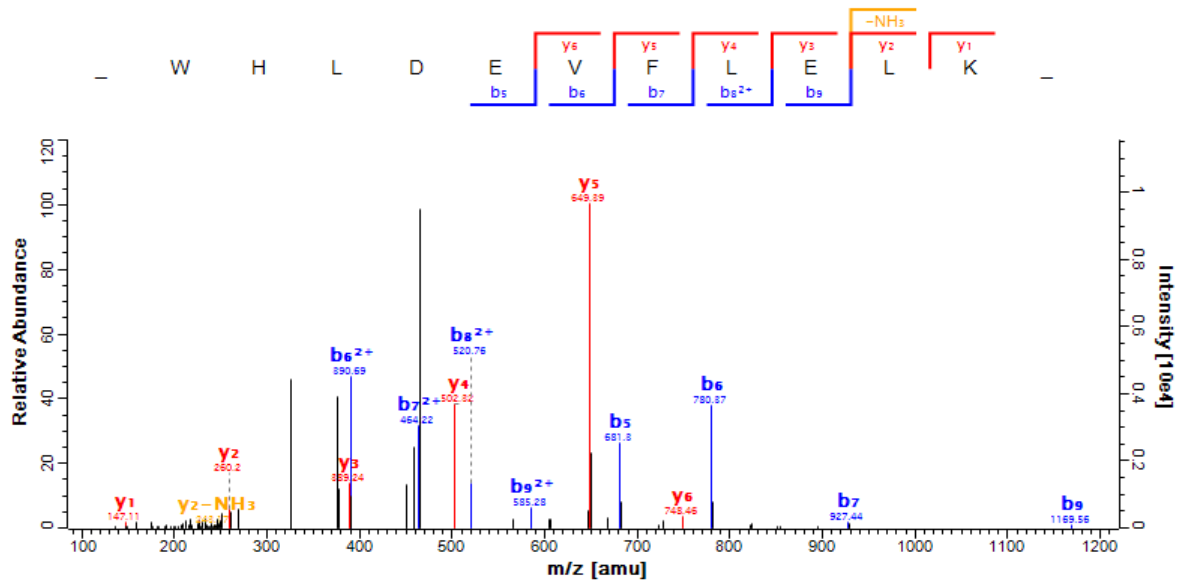
Protein Group ID: 4665
Protein Accession Numbers: Q9GZP8; Q9GZP8-2
Gene Names: IMUP
Peptide Sequence: MEFDLGAALEPTSQK
Total Number of Spectra: 7
Number of Replicates (out of 8): 7
Best Match Score: 115.1
Best Match Posterior Error Probability: 0.0001291
Best Match Spectrum:

Scan number 76448 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** IMUP



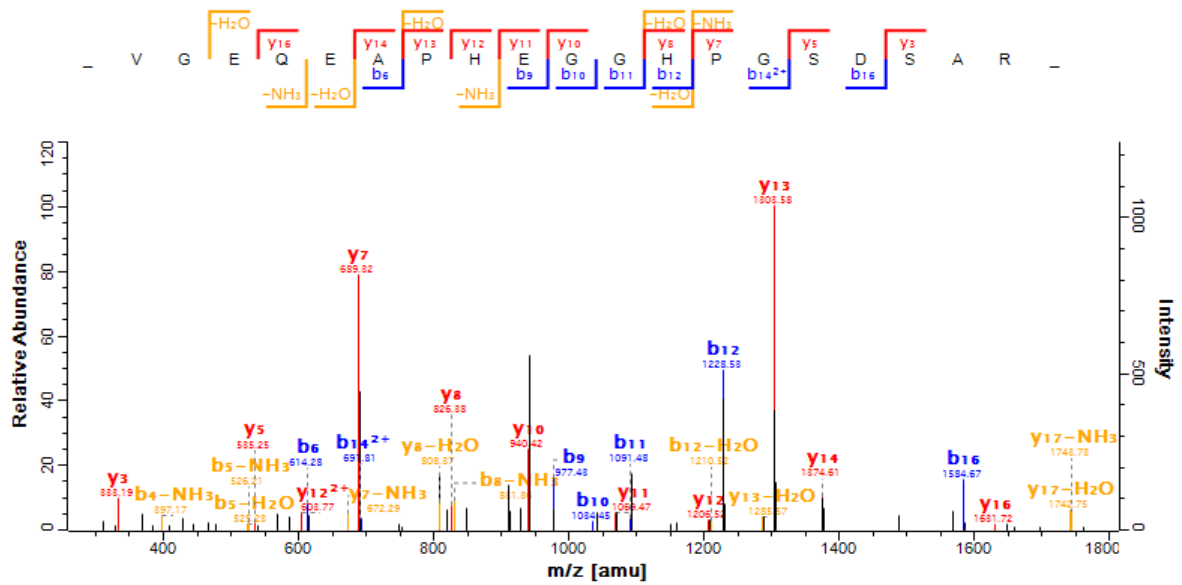
Protein Group ID: 4671
Protein Accession Numbers: Q9GZY4
Gene Names: C7orf44
Peptide Sequence: WHLDEVFLK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 106.29
Best Match Posterior Error Probability: 0.00029143
Best Match Spectrum:

Scan number	72852	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	C7orf44



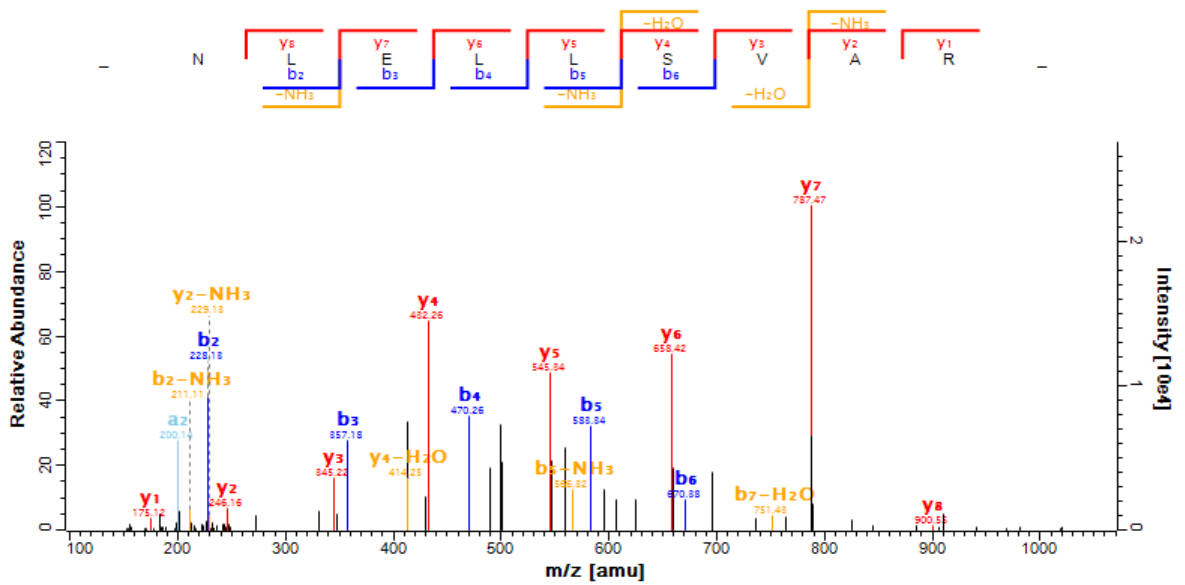
Protein Group ID: 4678
Protein Accession Numbers: Q9H093
Gene Names: NUAK2
Peptide Sequence: VGEQAEPAHGEGHPGSDSAR
Total Number of Spectra: 3
Number of Replicates (out of 8): 2
Best Match Score: 81.016
Best Match Posterior Error Probability: 0.00081093
Best Match Spectrum:

Scan number 3544 **Raw file** A549-US-WT-top20CID-Elite-2ug-811
Method ITMS; CID **Genenames** NUAK2



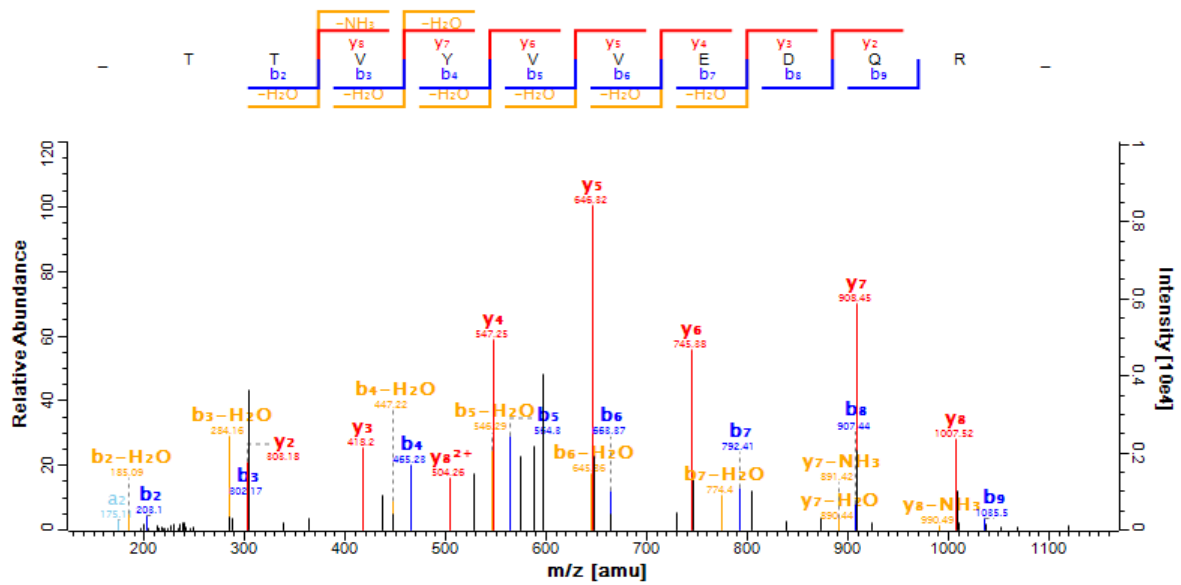
Protein Group ID: 4695
Protein Accession Numbers: Q9H0U6
Gene Names: MRPL18
Peptide Sequence: NLELLSVAR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 97.813
Best Match Posterior Error Probability: 0.0020707
Best Match Spectrum:

Scan number 46707 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** MRPL18



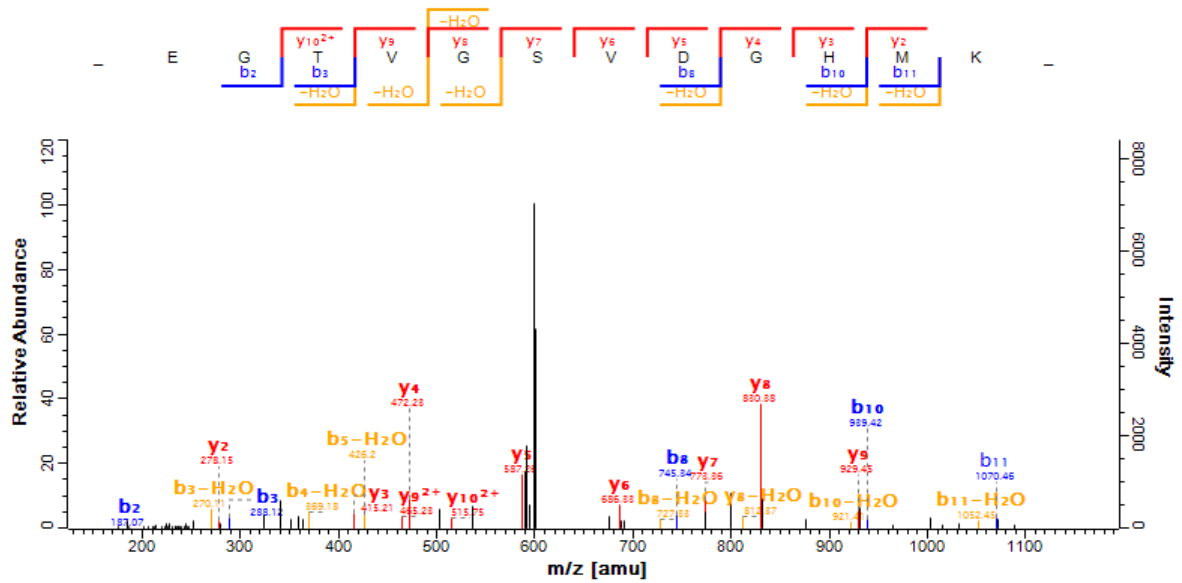
Protein Group ID: 4703
Protein Accession Numbers: Q9H1C7
Gene Names: CYSTM1
Peptide Sequence: TTVYVVEDQR
Total Number of Spectra: 5
Number of Replicates (out of 8): 4
Best Match Score: 185.96
Best Match Posterior Error Probability: 1.24E-08
Best Match Spectrum:

Scan number 19226 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CYSTM1



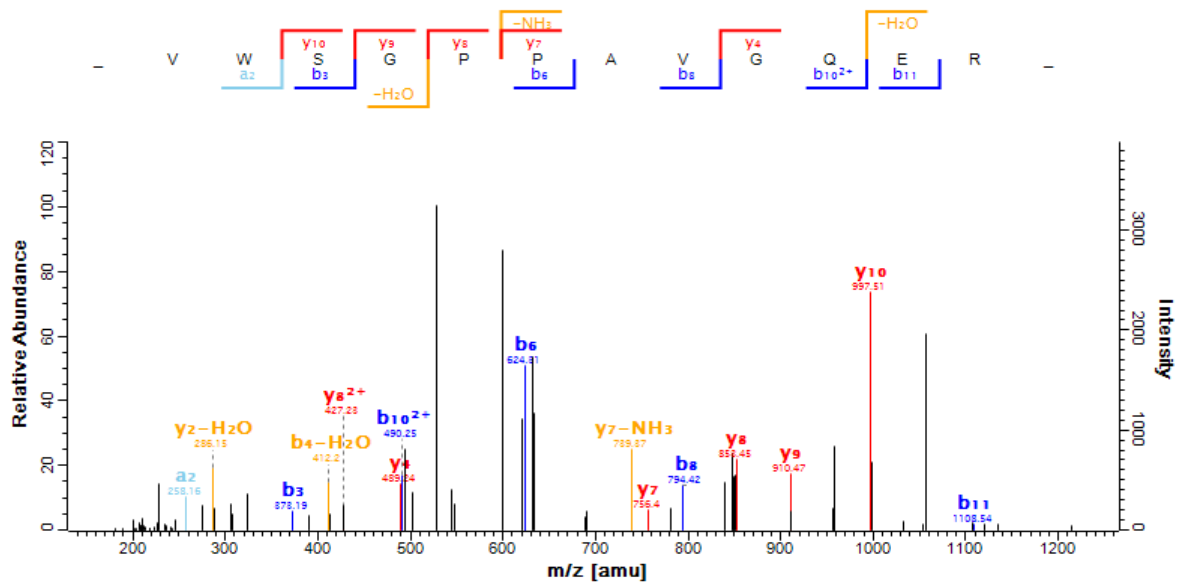
Protein Group ID: 4704
Protein Accession Numbers: Q9H1D9
Gene Names: POLR3F
Peptide Sequence: EGTVGSVVDGHMK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 105.03
Best Match Posterior Error Probability: 0.0020341
Best Match Spectrum:

Scan number 7940 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** POLR3F



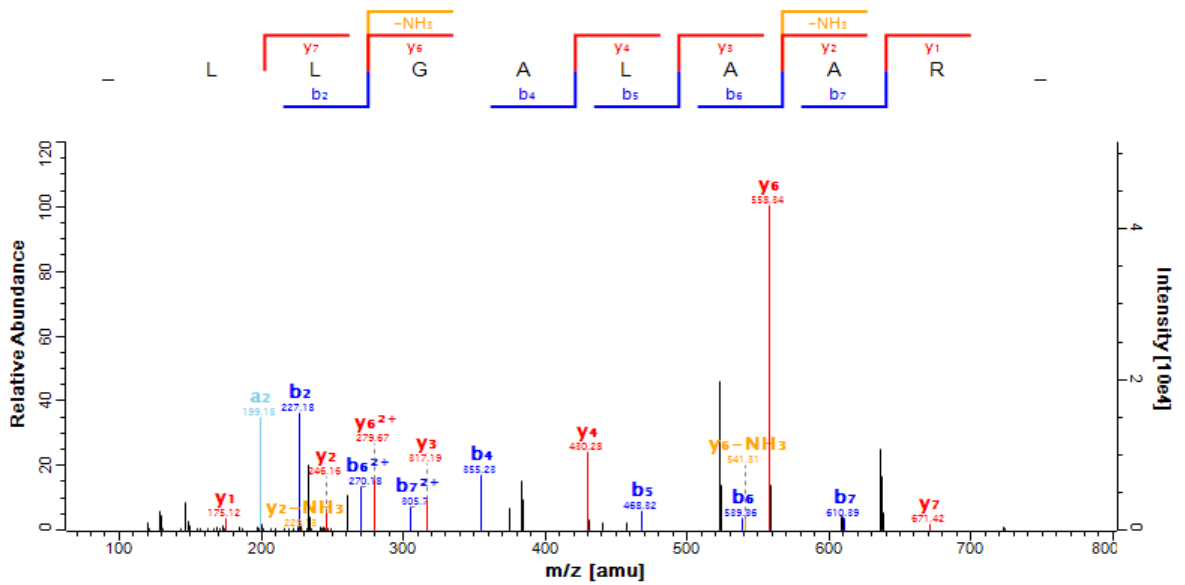
Protein Group ID: 4708
Protein Accession Numbers: Q9H1K0
Gene Names: ZFYVE20
Peptide Sequence: VWSGPPAVGQER
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 83.182
Best Match Posterior Error Probability: 0.0026403
Best Match Spectrum:

Scan number 26833 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ZFYVE20



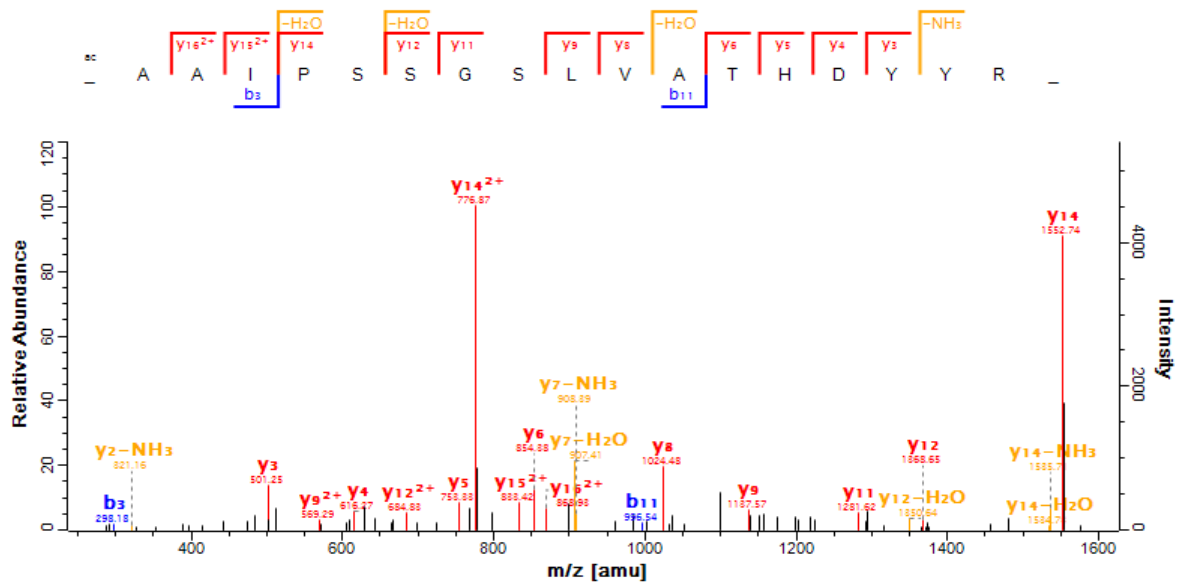
Protein Group ID: 4711
Protein Accession Numbers: Q9H1Z9
Gene Names: TSPAN10
Peptide Sequence: LLGALAAR
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 124.37
Best Match Posterior Error Probability: 0.0018004
Best Match Spectrum:

Scan number 21218 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** TSPAN10



Protein Group ID: 4736
Protein Accession Numbers: Q9H3Y8; Q9H3Y8-2
Gene Names: PPDPF
Peptide Sequence: AAIPSSGSLVATHDYR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 93.51
Best Match Posterior Error Probability: 0.00047234
Best Match Spectrum:

Scan number 46649 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** PPDPF



Protein Group ID: 4740

Protein Accession Numbers: Q9H467

Gene Names: CUEDC2

Peptide Sequence: ENLQPSSGVQGQVPISPEPLQRP EMLK

Total Number of Spectra: 4

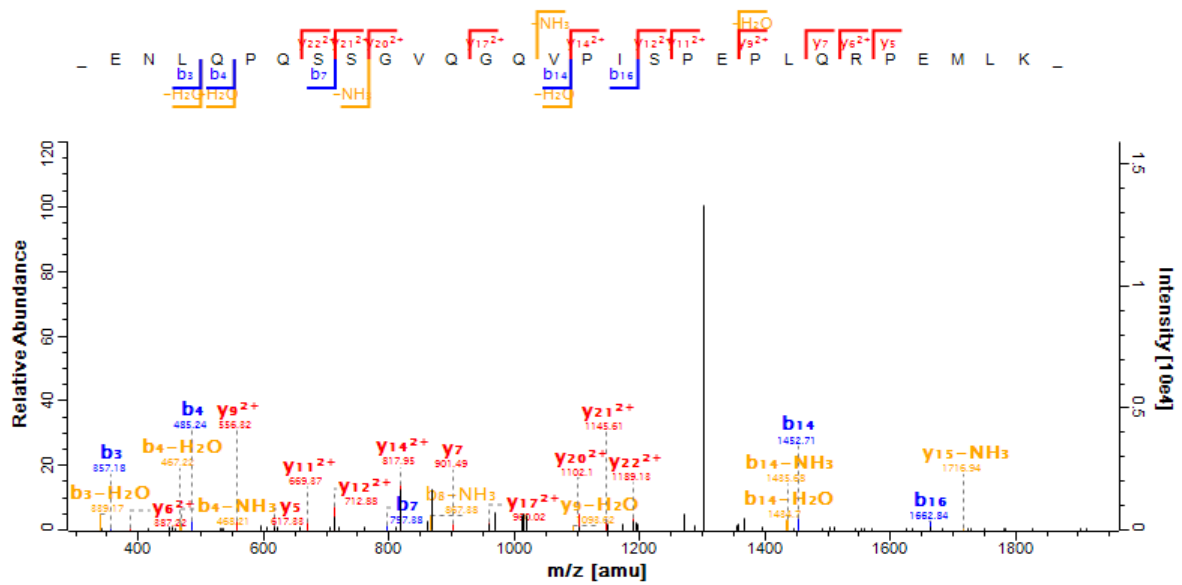
Number of Replicates (out of 8): 3

Best Match Score: 92.01

Best Match Posterior Error Probability: 2.28E-05

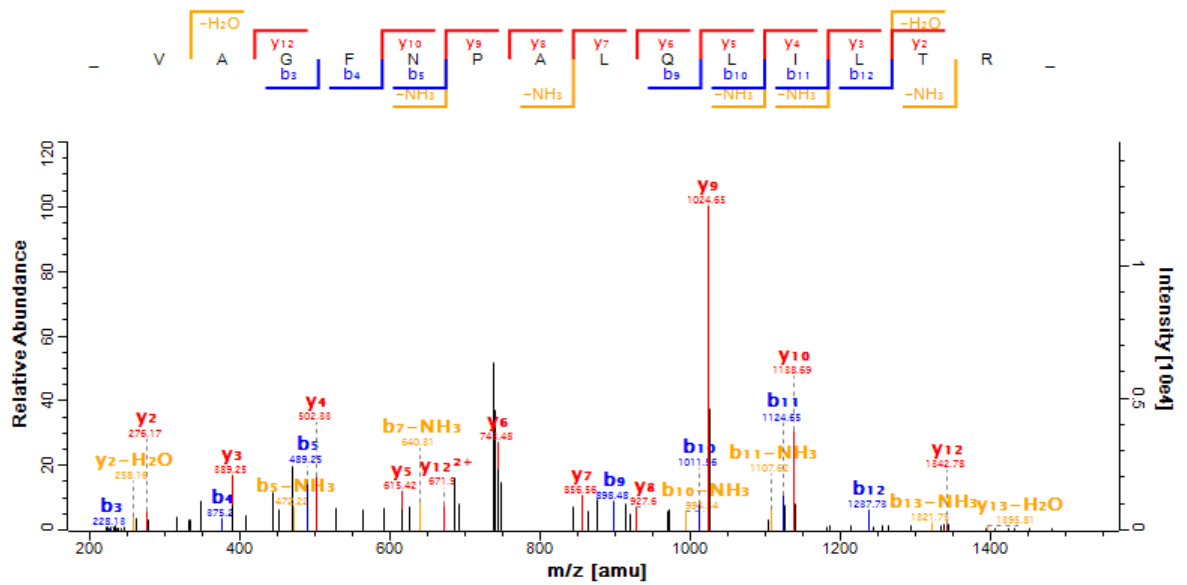
Best Match Spectrum:

Scan number 51310 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CUEDC2



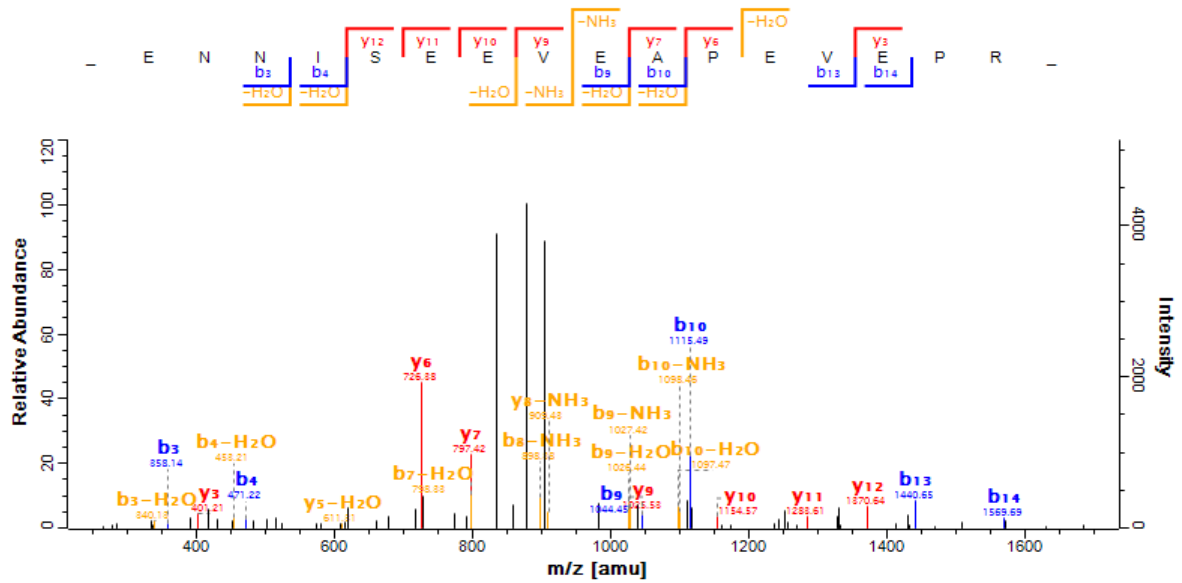
Protein Group ID: 4742
Protein Accession Numbers: Q9H496
Gene Names: IFRG15
Peptide Sequence: VAGFNPALQLILTR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 102.5
Best Match Posterior Error Probability: 0.0002942
Best Match Spectrum:

Scan number 75222 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** IFRG15



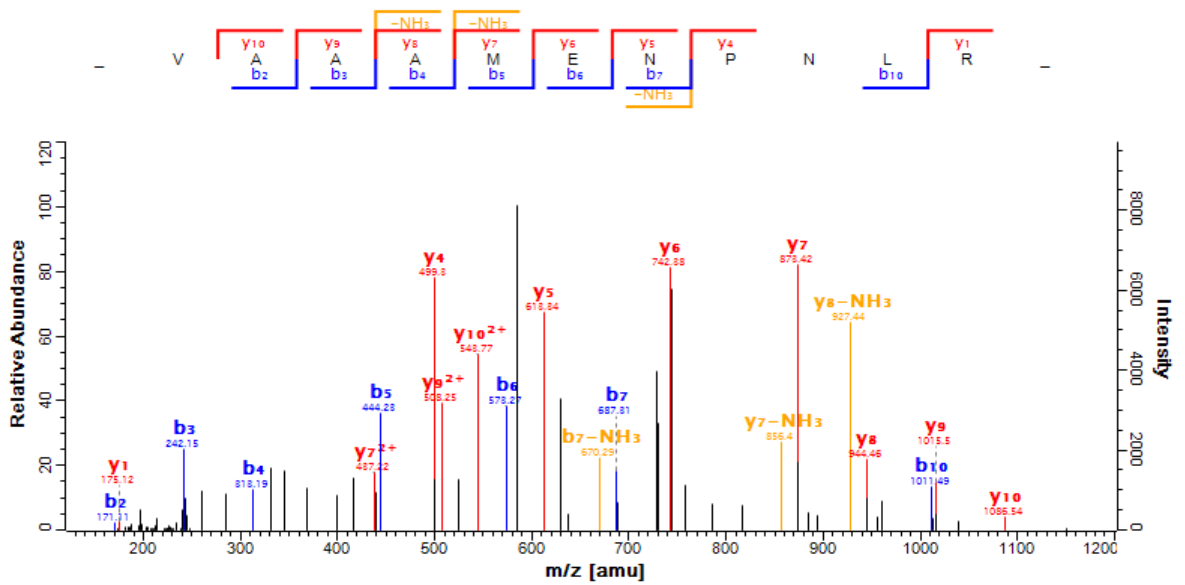
Protein Group ID: 4752
Protein Accession Numbers: Q9H4Z3
Gene Names: PCIF1
Peptide Sequence: ENNISEEVEAPEVEPR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 83.37
Best Match Posterior Error Probability: 0.001418
Best Match Spectrum:

Scan number 35016 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PCIF1



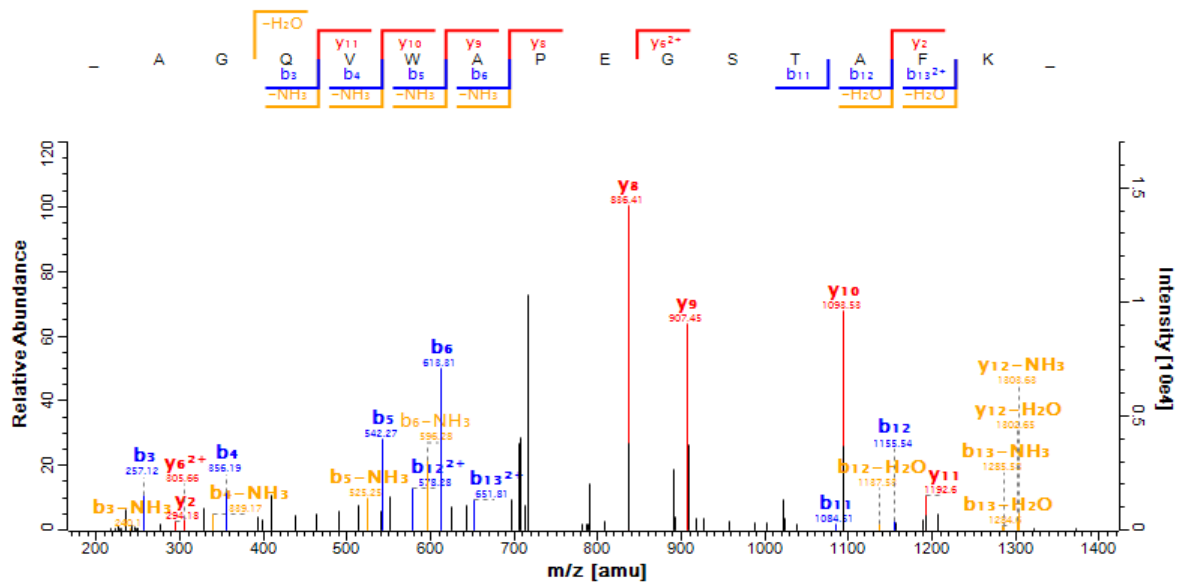
Protein Group ID: 4759
Protein Accession Numbers: Q9H5X1
Gene Names: FAM96A
Peptide Sequence: VAAAMENPNLR
Total Number of Spectra: 5
Number of Replicates (out of 8): 4
Best Match Score: 152.07
Best Match Posterior Error Probability: 1.71E-05
Best Match Spectrum:

Scan number 19335 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** FAM96A



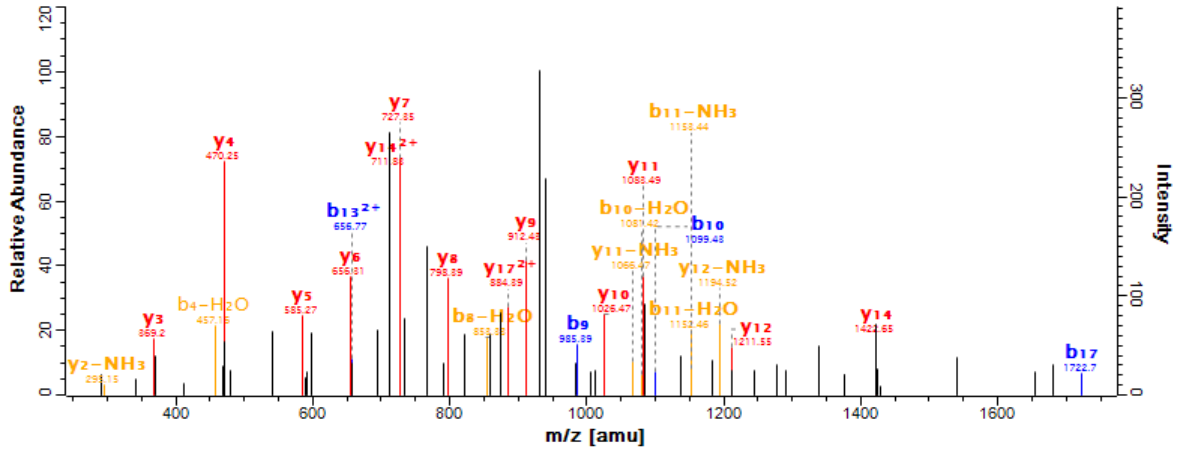
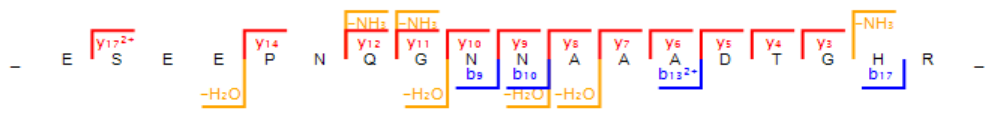
Protein Group ID: 4765
Protein Accession Numbers: Q9H6U8-3; Q9H6U8
Gene Names: ALG9
Peptide Sequence: AGQVWAPEGSTAK
Total Number of Spectra: 6
Number of Replicates (out of 8): 5
Best Match Score: 120.84
Best Match Posterior Error Probability: 4.62E-05
Best Match Spectrum:

Scan number 38930 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ALG9



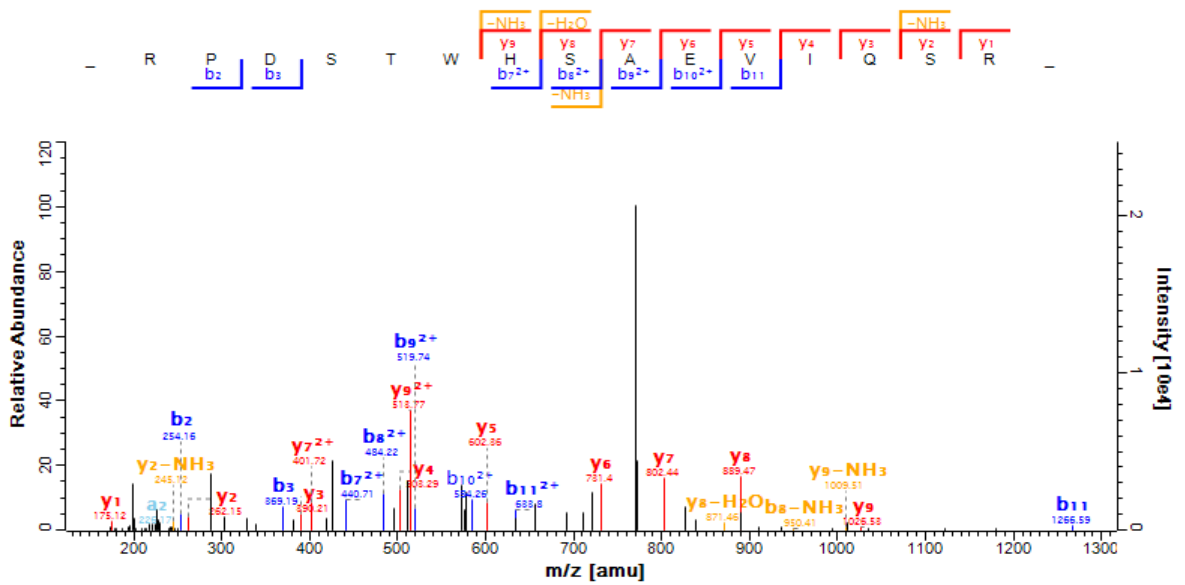
Protein Group ID: 4776
Protein Accession Numbers: Q9H7Z3
Gene Names: C14orf102
Peptide Sequence: ESEEPNQGNGNANAAADTGHR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 90.379
Best Match Posterior Error Probability: 0.00036615
Best Match Spectrum:

Scan number 3160 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** C14orf102



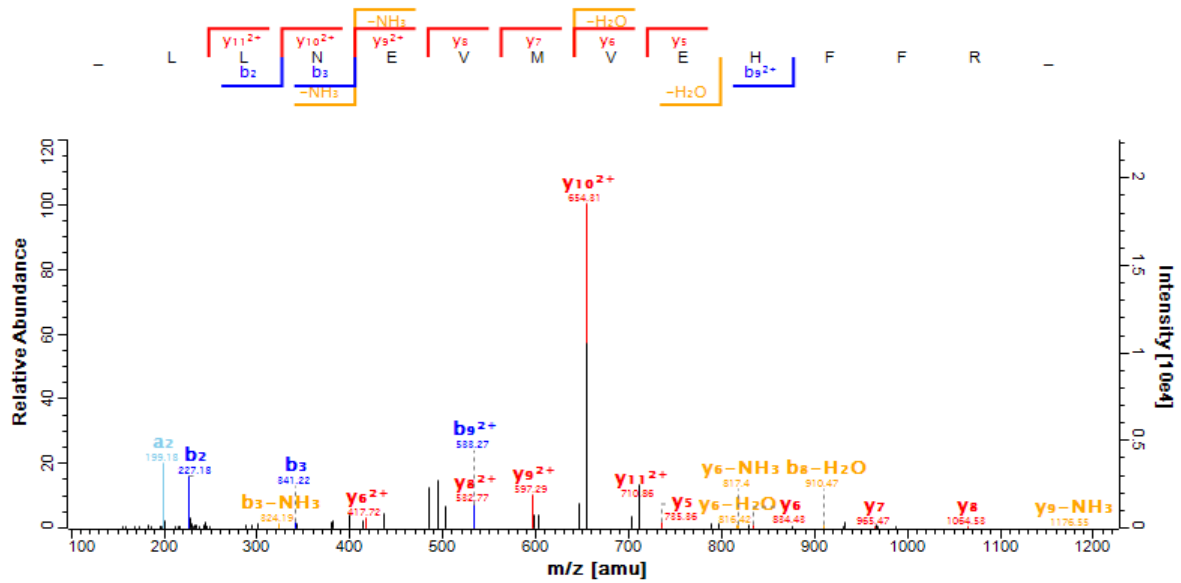
Protein Group ID: 4777
Protein Accession Numbers: Q9H7Z6-2; Q9H7Z6
Gene Names: KAT8
Peptide Sequence: RPDSTWHSAEVIQSR
Total Number of Spectra: 2
Number of Replicates (out of 8): 1
Best Match Score: 110.44
Best Match Posterior Error Probability: 0.00029415
Best Match Spectrum:

Scan number 20792 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** KAT8



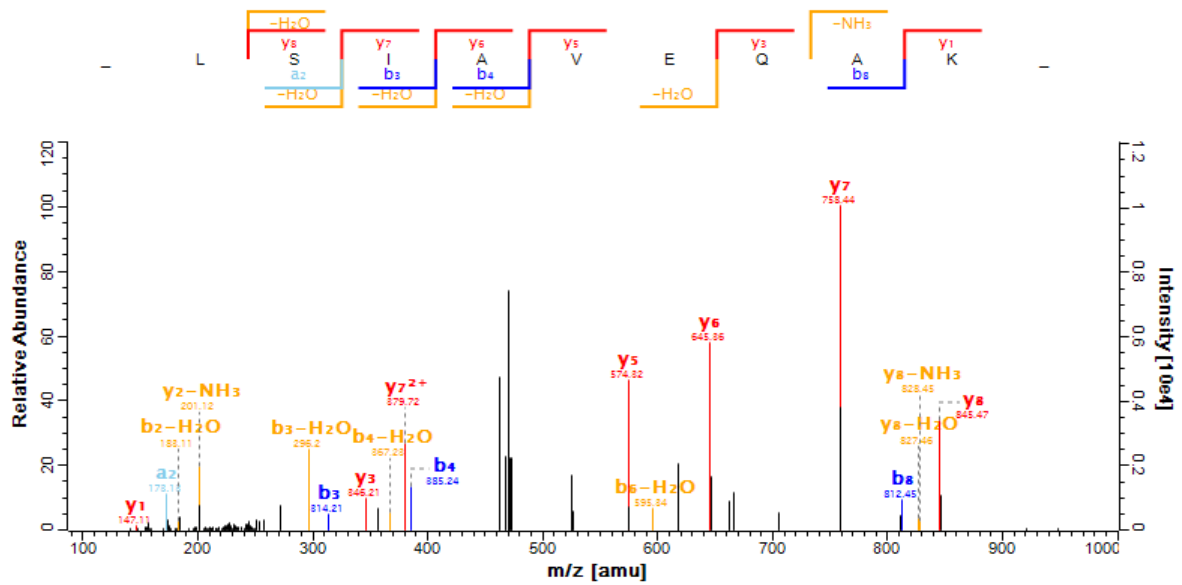
Protein Group ID: 4782
Protein Accession Numbers: Q9H871
Gene Names: RMND5A
Peptide Sequence: LLNEVMVEHFFR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 99.568
Best Match Posterior Error Probability: 0.00052251
Best Match Spectrum:

Scan number 65904 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** RMND5A



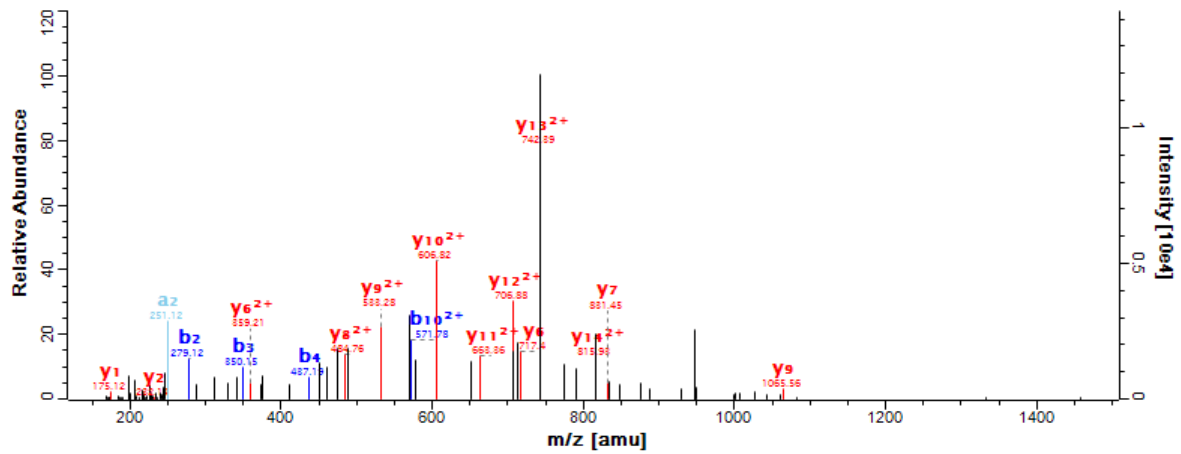
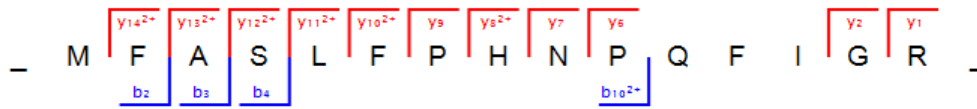
Protein Group ID: 4793
Protein Accession Numbers: Q9H9F9
Gene Names: ACTR5
Peptide Sequence: LSIAVEQAK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 99.688
Best Match Posterior Error Probability: 0.0017975
Best Match Spectrum:

Scan number 36833 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** ACTR5



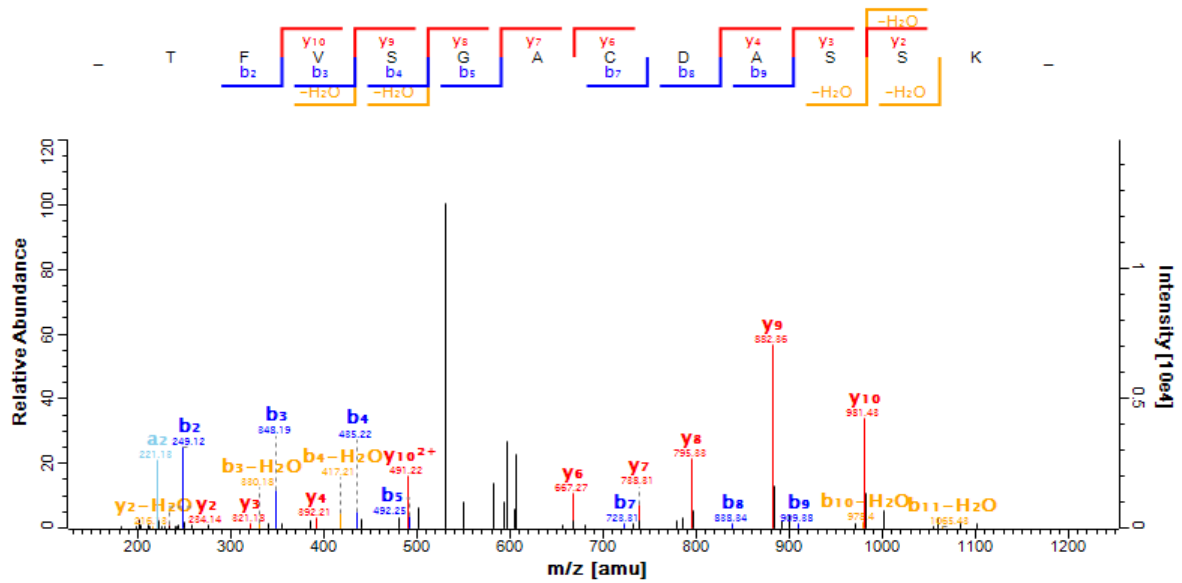
Protein Group ID: 4799
Protein Accession Numbers: Q9H9Y2
Gene Names: RPF1
Peptide Sequence: MFASLFPHNPQFI⁺GR
Total Number of Spectra: 2
Number of Replicates (out of 8): 1
Best Match Score: 95.094
Best Match Posterior Error Probability: 0.00047094
Best Match Spectrum:

Scan number 62045 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** RPF1



Protein Group ID: 4805
Protein Accession Numbers: Q9HAV0; H7C5J5
Gene Names: GNB4
Peptide Sequence: TFVSGACDASSK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 97.463
Best Match Posterior Error Probability: 0.00068072
Best Match Spectrum:

Scan number 10853 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** GNB4



Protein Group ID: 4808

Protein Accession Numbers: Q9HAW7; Q9HAW9; Q9HAW8; Q7Z6H8

Gene Names: UGT1A7;UGT1A8;UGT1A10

Peptide Sequence: LLVVPMDGSHWFTMQSVVEK

Total Number of Spectra: 2

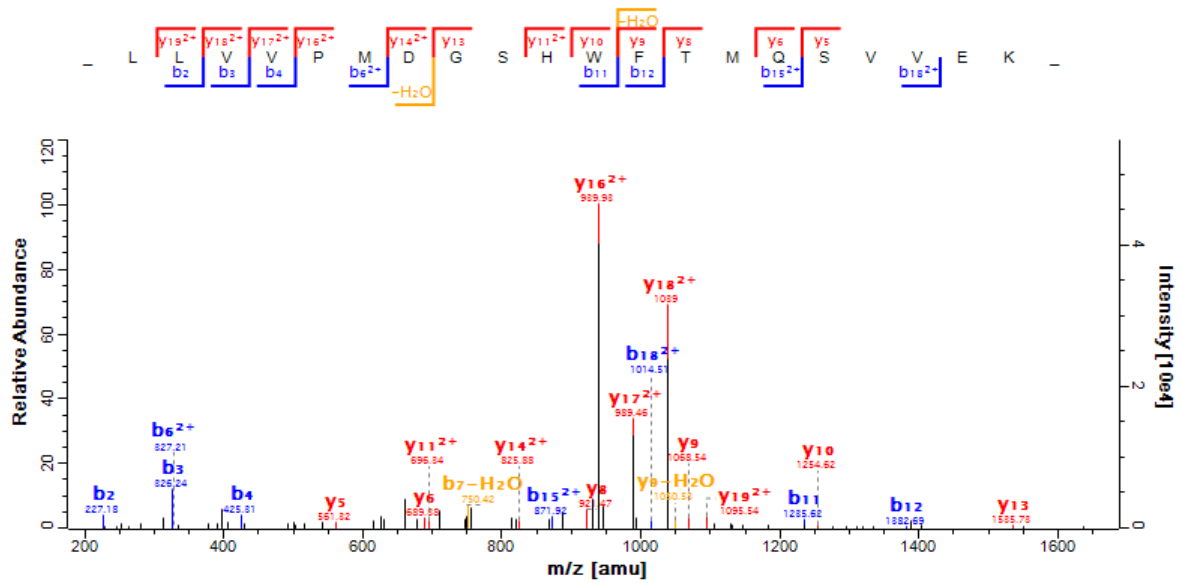
Number of Replicates (out of 8): 2

Best Match Score: 80.545

Best Match Posterior Error Probability: 0.00051372

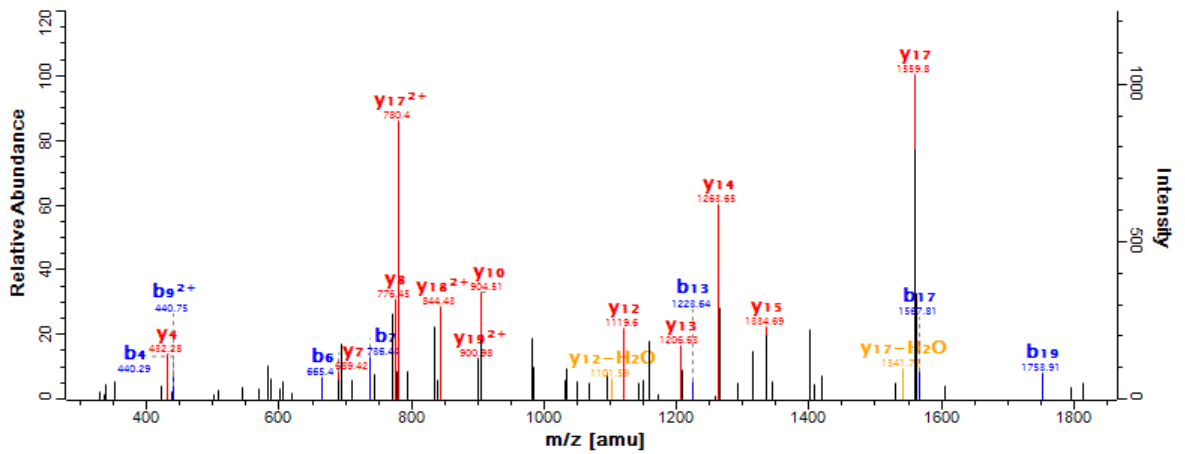
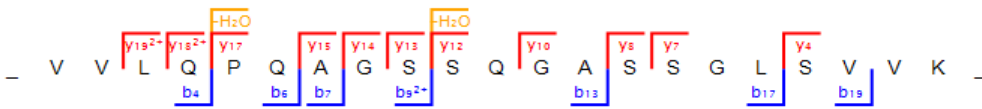
Best Match Spectrum:

Scan number 76330 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** UGT1A7;UGT1A8;UGT1A10



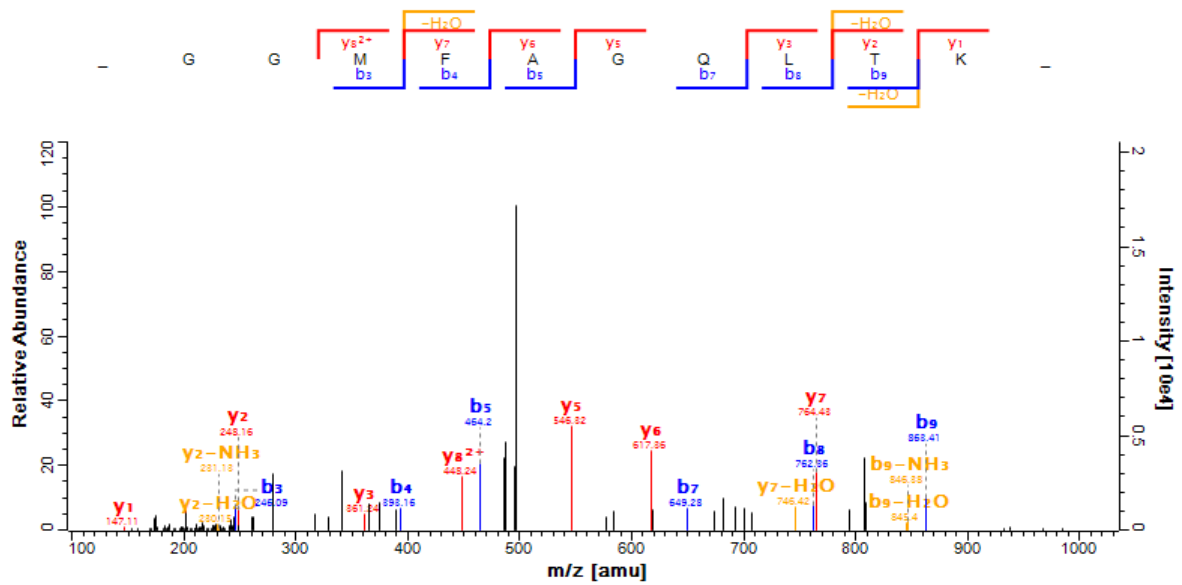
Protein Group ID: 4823
Protein Accession Numbers: Q9HCK8; Q9HCK8-2
Gene Names: CHD8
Peptide Sequence: VVLQPQAGSSQGASSGLSVVK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 79.293
Best Match Posterior Error Probability: 0.00034031
Best Match Spectrum:

Scan number 37172 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CHD8



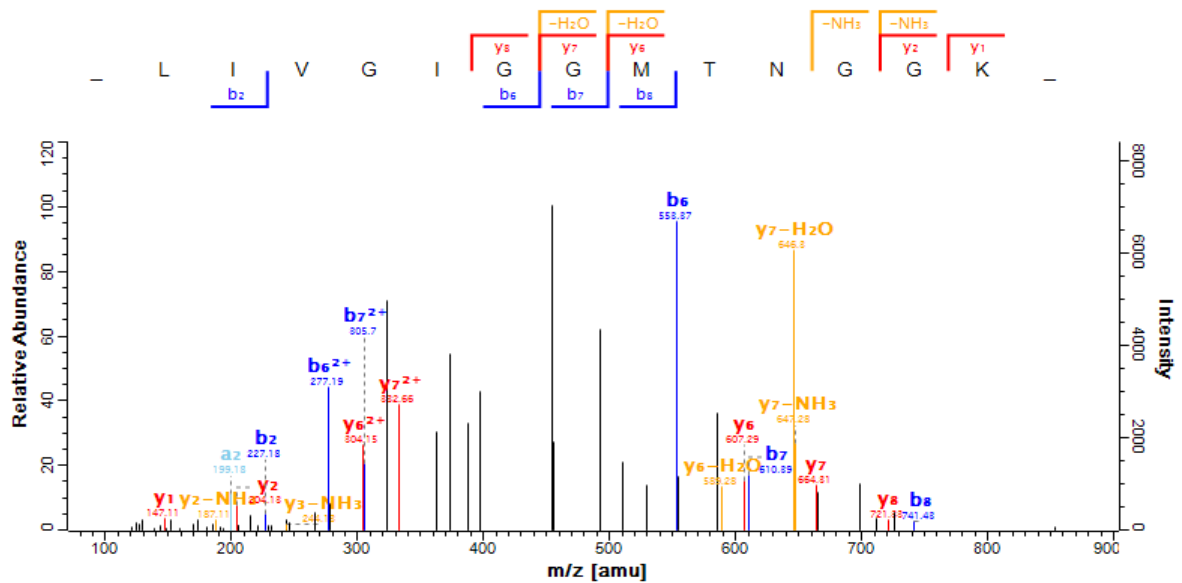
Protein Group ID: 4843
Protein Accession Numbers: Q9NPH0; Q9NPH0-2
Gene Names: ACP6
Peptide Sequence: GGMFAGQLTK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 91.658
Best Match Posterior Error Probability: 0.0017649
Best Match Spectrum:

Scan number 28928 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ACP6



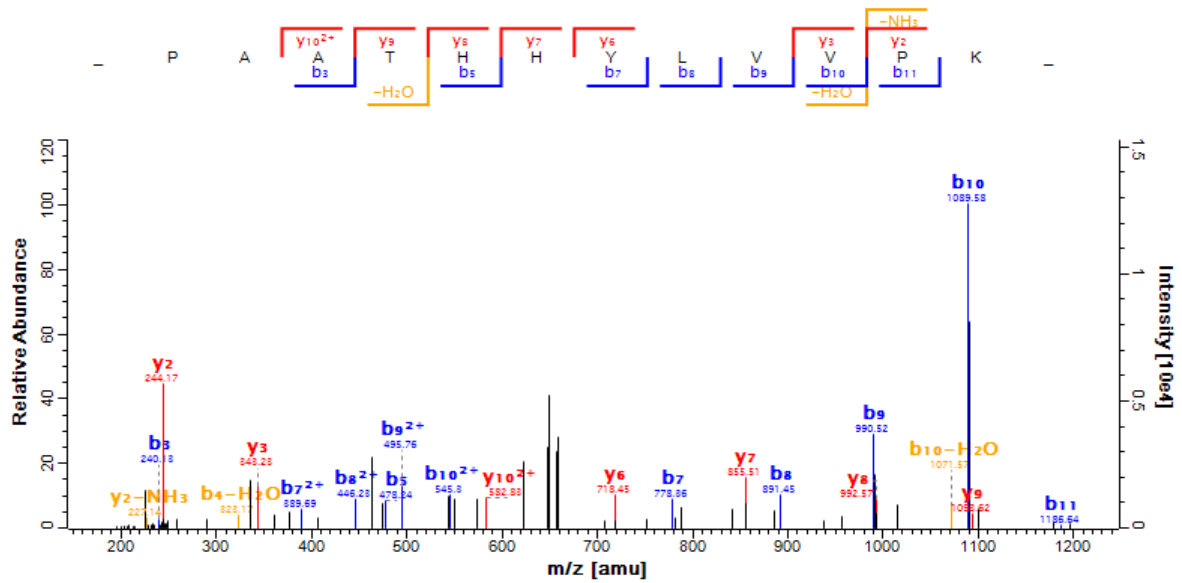
Protein Group ID: 4844
Protein Accession Numbers: Q9NPI5
Gene Names: ITGB1BP3
Peptide Sequence: LIVIGGMTNGK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 102.53
Best Match Posterior Error Probability: 0.000463
Best Match Spectrum:

Scan number 17779 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** ITGB1BP3



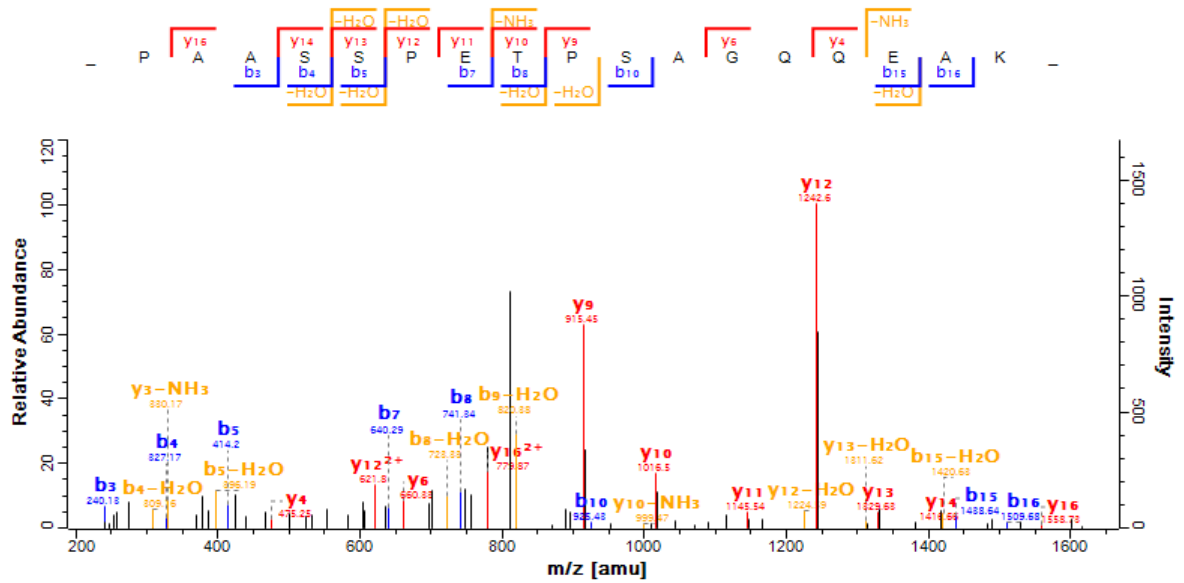
Protein Group ID: 4852
Protein Accession Numbers: Q9NQE9
Gene Names: HINT3
Peptide Sequence: PAATHHYLVVPK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 141.88
Best Match Posterior Error Probability: 3.33E-05
Best Match Spectrum:

Scan number 17014 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** HINT3



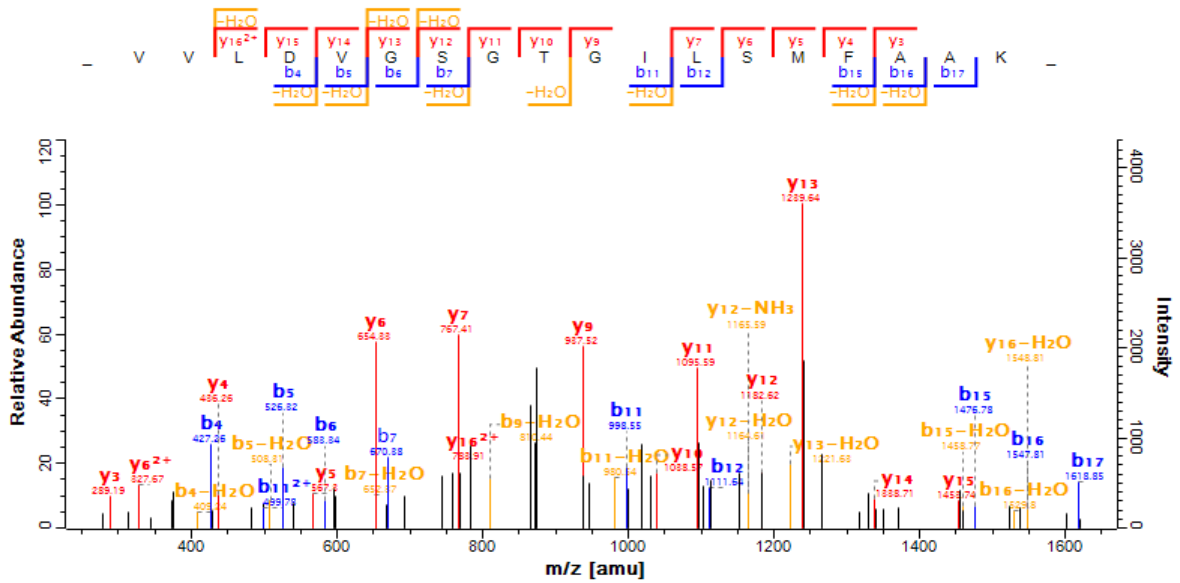
Protein Group ID: 4857
Protein Accession Numbers: Q9NQS7; Q9NQS7-2
Gene Names: INCENP
Peptide Sequence: PAASSPETPSAGQEQEAK
Total Number of Spectra: 6
Number of Replicates (out of 8): 5
Best Match Score: 130.01
Best Match Posterior Error Probability: 9.19E-05
Best Match Spectrum:

Scan number 6737 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** INCENP



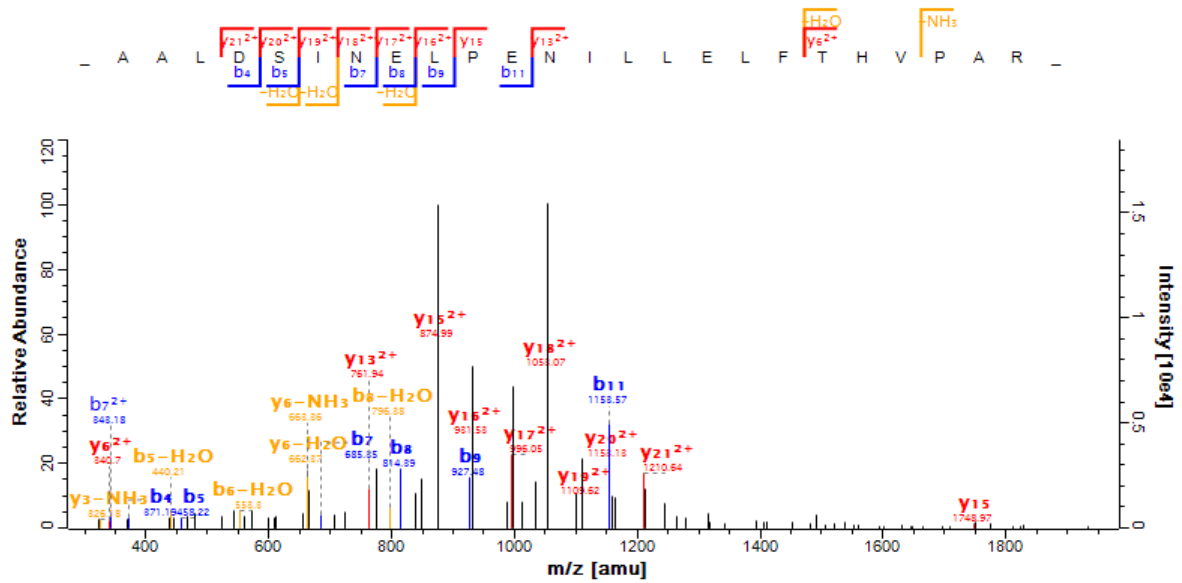
Protein Group ID: 4865
Protein Accession Numbers: Q9NR22; Q9NR22-2
Gene Names: PRMT8
Peptide Sequence: VVLDVGS GTGILSMFAAK
Total Number of Spectra: 11
Number of Replicates (out of 8): 6
Best Match Score: 188.44
Best Match Posterior Error Probability: 9.91E-22
Best Match Spectrum:

Scan number 82692 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** PRMT8



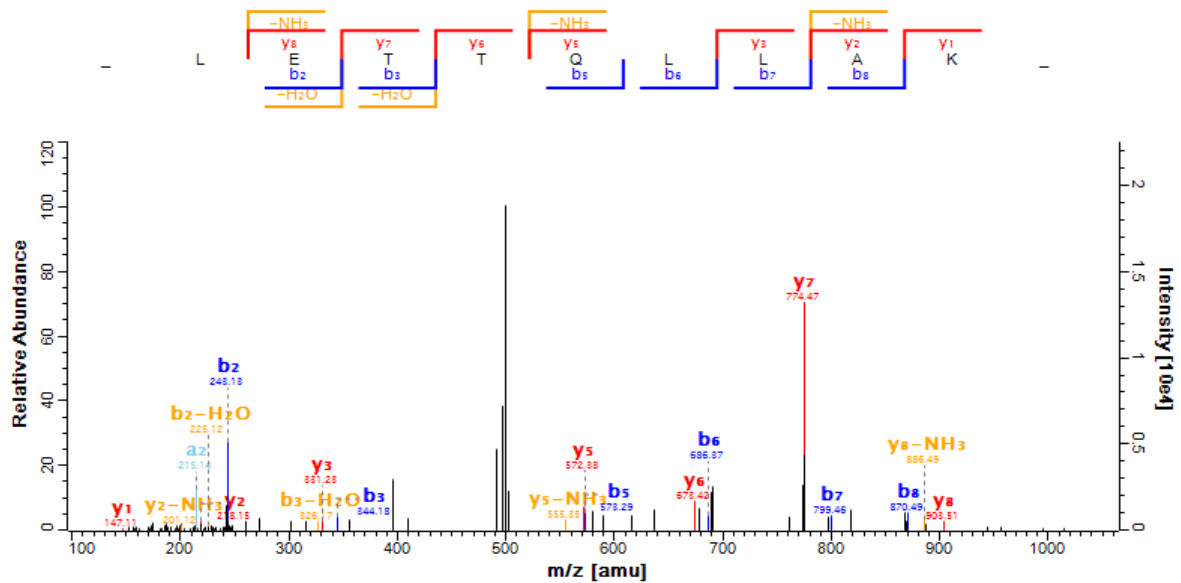
Protein Group ID: 4873
Protein Accession Numbers: Q9NRD1
Gene Names: FBXO6
Peptide Sequence: AALDSINELP E N I L L E L F T H V P A R
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 61.087
Best Match Posterior Error Probability: 0.0018476
Best Match Spectrum:

Scan number	96143	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	FBXO6



Protein Group ID: 4876
Protein Accession Numbers: Q9NRG7; Q9NRG7-2
Gene Names: SDR39U1
Peptide Sequence: LETTQLLAK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 89.827
Best Match Posterior Error Probability: 0.0036541
Best Match Spectrum:

Scan number 28996 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** SDR39U1



Protein Group ID: 4883

Protein Accession Numbers: Q9NRR8

Gene Names: CDC42SE1

Peptide Sequence: TMIGEPMNFVHLTHIGSGEMGAGDGLAMTGA VQE QMR

Total Number of Spectra: 1

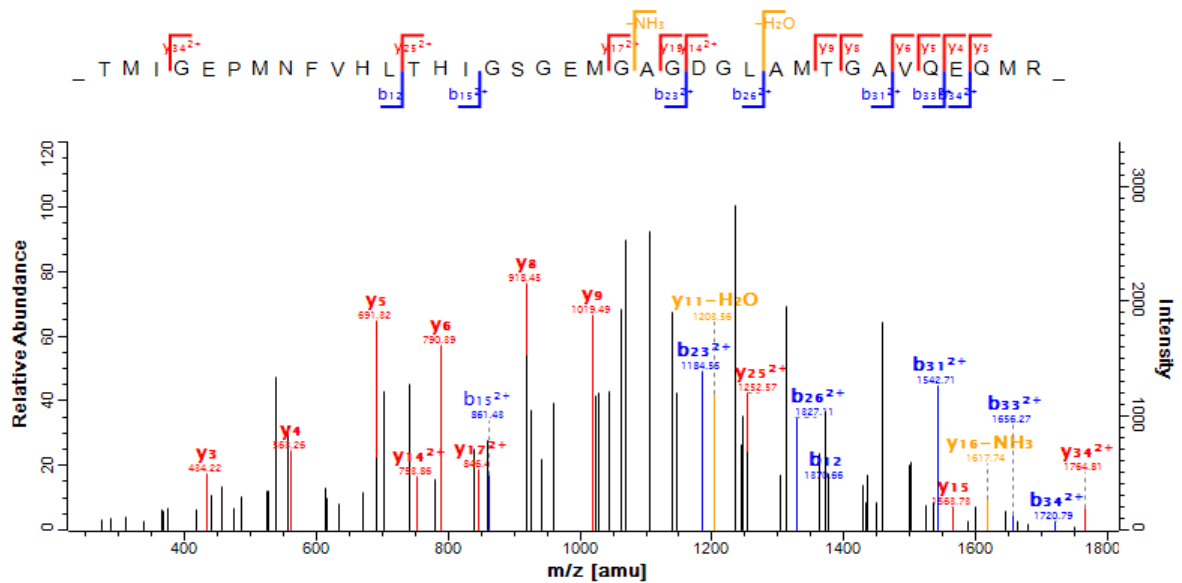
Number of Replicates (out of 8): 1

Best Match Score: 42.571

Best Match Posterior Error Probability: 0.0022742

Best Match Spectrum:

Scan number	75235	Raw file	A549-US-WT-top20CID-Elite-2ug-811
Method	ITMS; CID	Genenames	CDC42SE1



Protein Group ID: 4896

Protein Accession Numbers: Q9NS87; Q9NS87-4

Gene Names: KIF15

Peptide Sequence: TTFD¹³HVADVDTTQESVFA¹⁶TVAK

Total Number of Spectra: 1

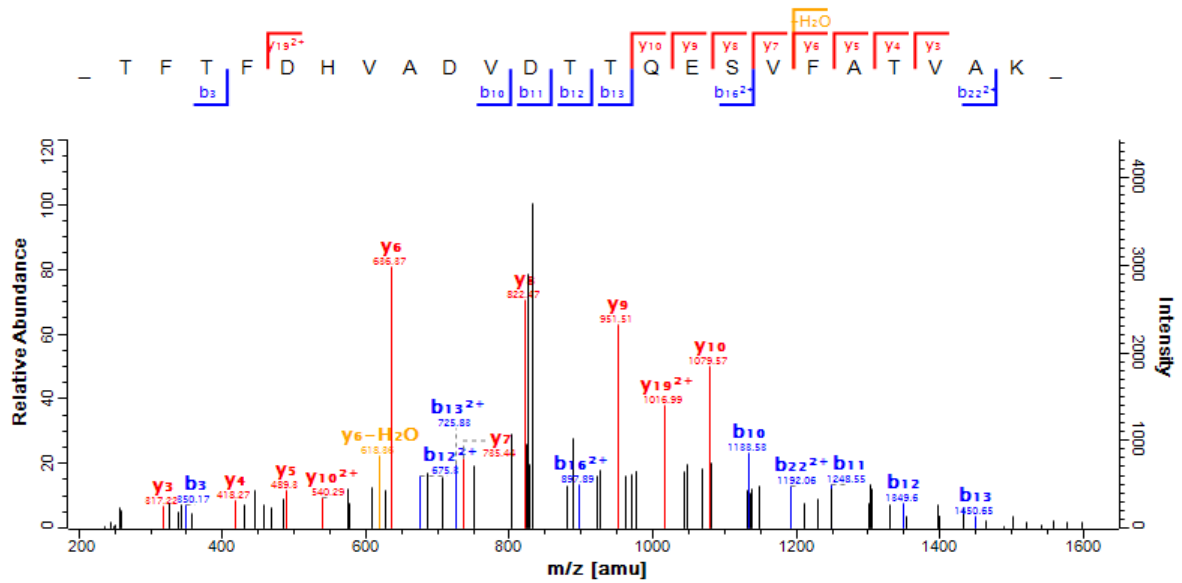
Number of Replicates (out of 8): 1

Best Match Score: 87.352

Best Match Posterior Error Probability: 1.49E-05

Best Match Spectrum:

Scan number	64814	Raw file	A549-US-Mock-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	KIF15



Protein Group ID: 4899

Protein Accession Numbers: Q9NSG2; Q9NSG2-2; Q9NSG2-3

Gene Names: Clorf112

Peptide Sequence: SALHTIAGLEATSESLQLK

Total Number of Spectra: 3

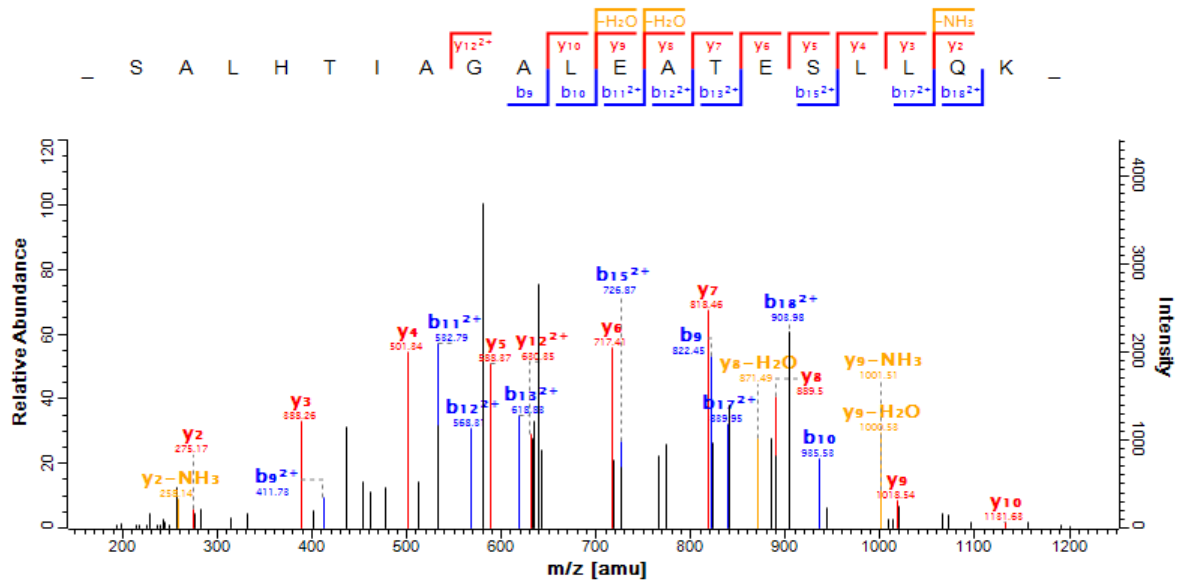
Number of Replicates (out of 8): 3

Best Match Score: 98.508

Best Match Posterior Error Probability: 0.00016345

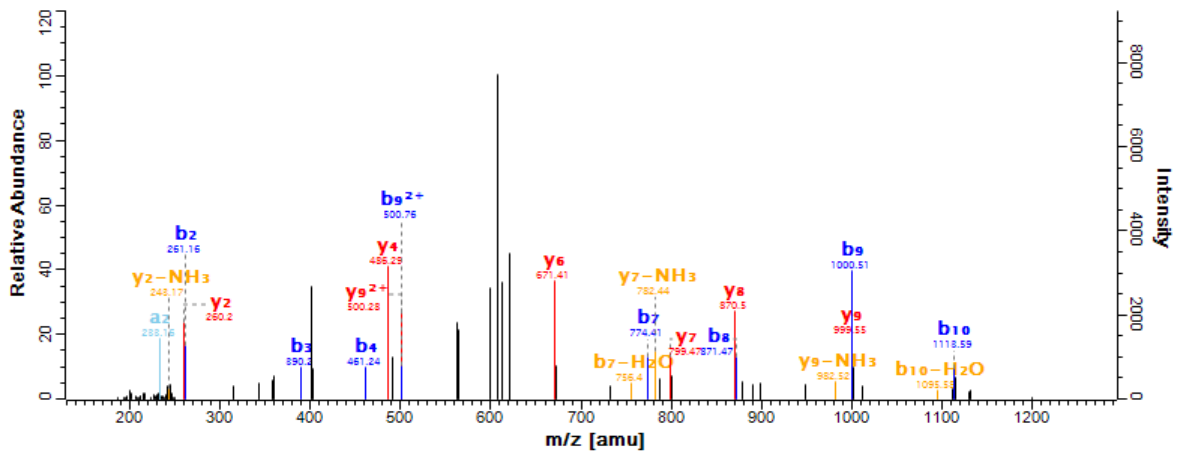
Best Match Spectrum:

Scan number 81367 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** Clorf112



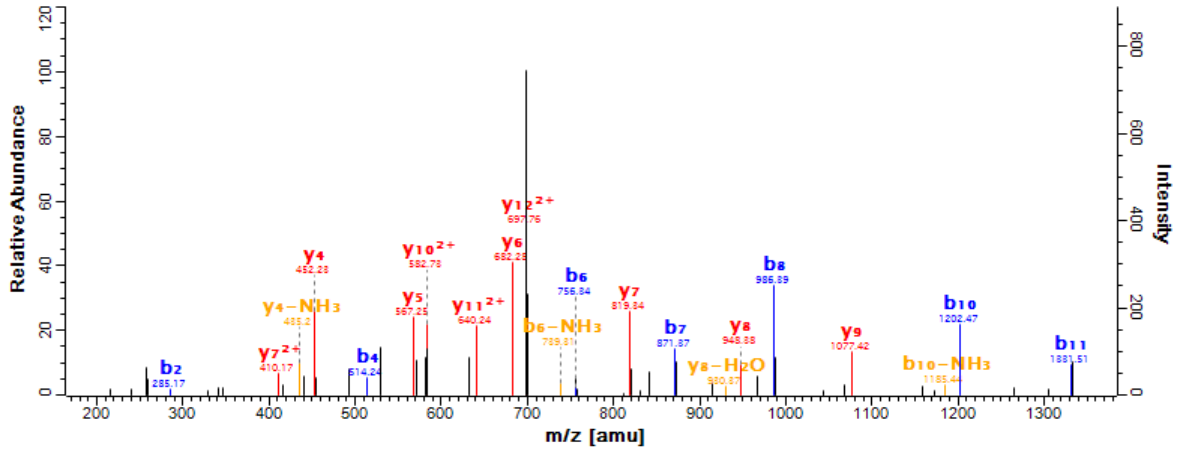
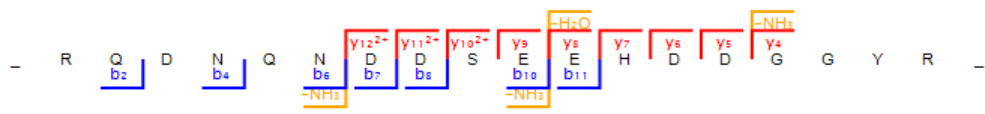
Protein Group ID: 4909
Protein Accession Numbers: Q9NUG6
Gene Names: PDRG1
Peptide Sequence: LFEAQGKPELK
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 123.67
Best Match Posterior Error Probability: 0.00020036
Best Match Spectrum:

Scan number 22865 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** PDRG1



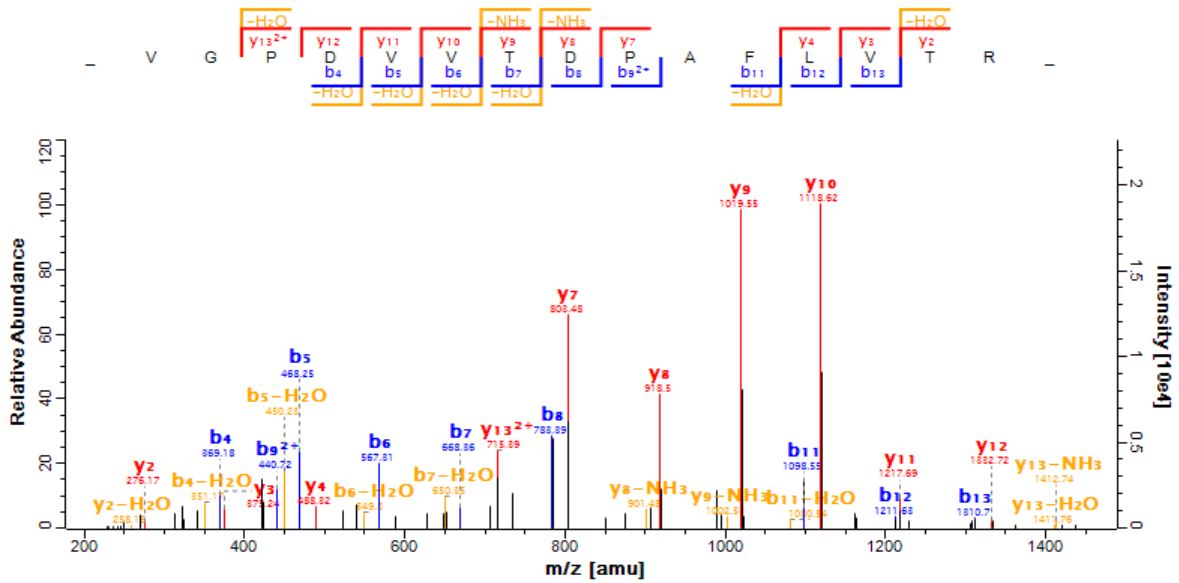
Protein Group ID: 4912
Protein Accession Numbers: Q9NUP7
Gene Names: CCDC76
Peptide Sequence: RQDNQNDDSEEHDDGGYR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 102.08
Best Match Posterior Error Probability: 0.00034075
Best Match Spectrum:

Scan number 2744 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CCDC76



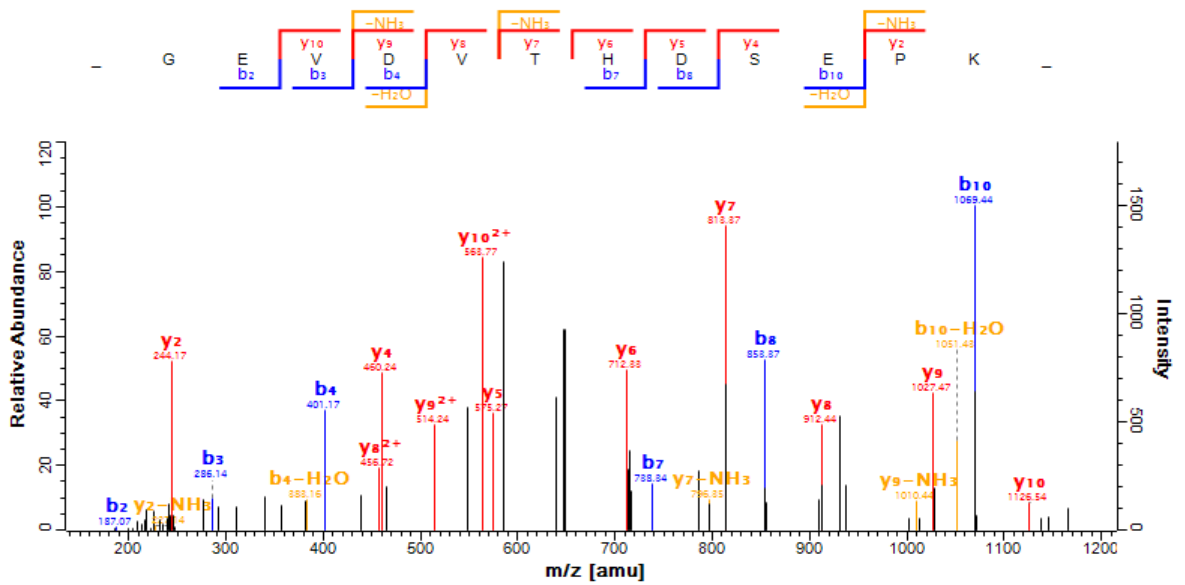
Protein Group ID: 4920
Protein Accession Numbers: Q9NV31
Gene Names: IMP3
Peptide Sequence: VGPDVVTDPAFLVTR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 162.41
Best Match Posterior Error Probability: 1.05E-09
Best Match Spectrum:

Scan number 59685 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** IMP3



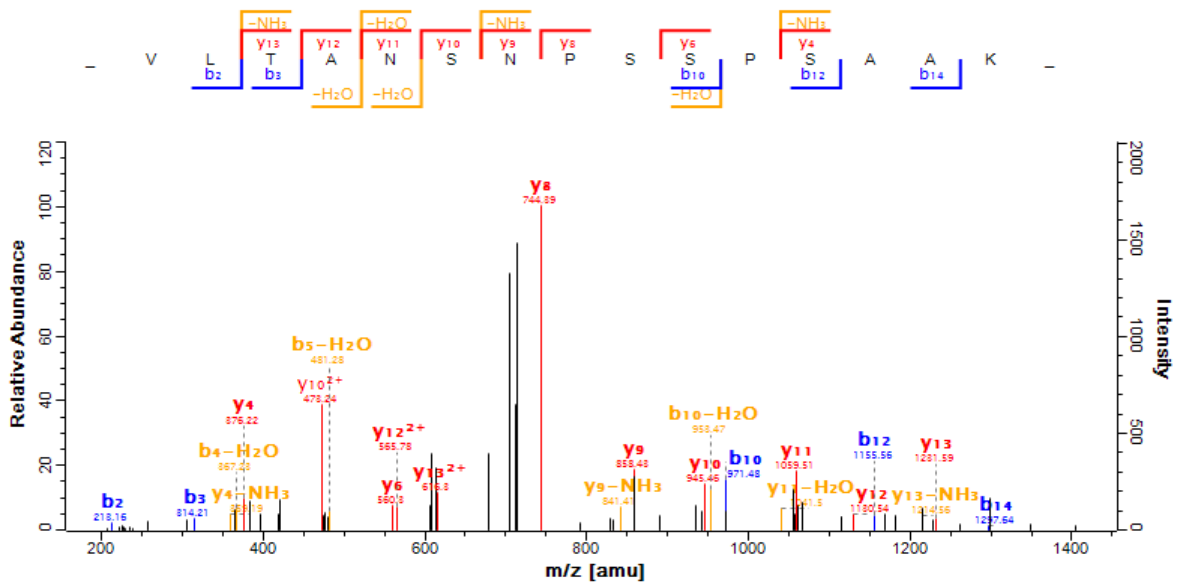
Protein Group ID: 4921
Protein Accession Numbers: Q9NV35
Gene Names: NUDT15
Peptide Sequence: GEVDVTHDSEPK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 120.57
Best Match Posterior Error Probability: 0.00012349
Best Match Spectrum:

Scan number 6552 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** NUDT15



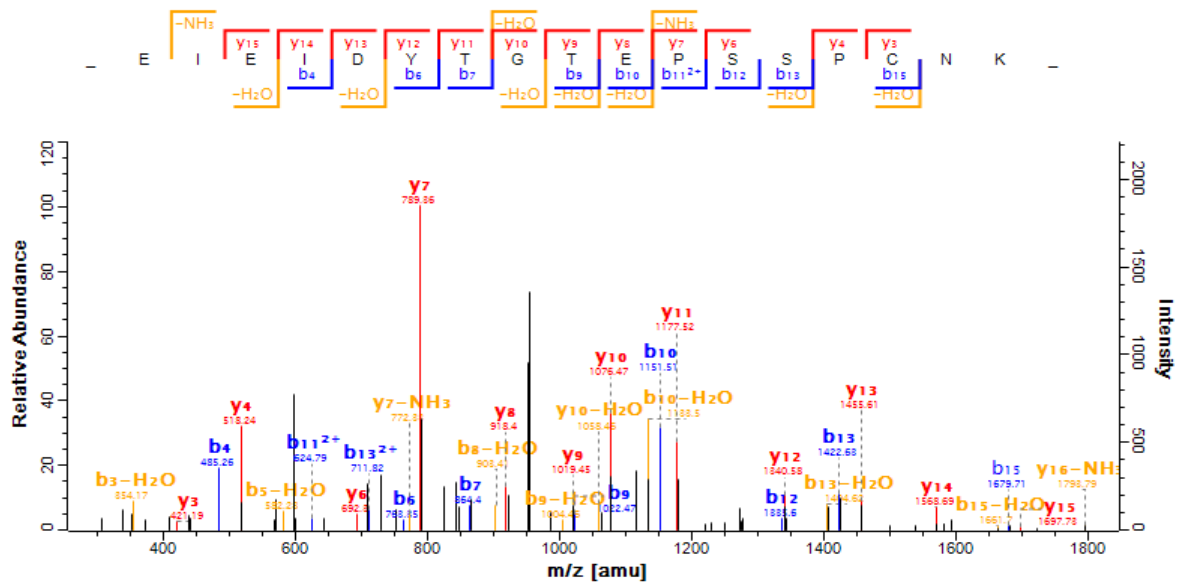
Protein Group ID: 4922
Protein Accession Numbers: Q9NV56
Gene Names: MRGBP
Peptide Sequence: VLTANSNPSSPSAAK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 105.46
Best Match Posterior Error Probability: 0.00016325
Best Match Spectrum:

Scan number 9540 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** MRGBP



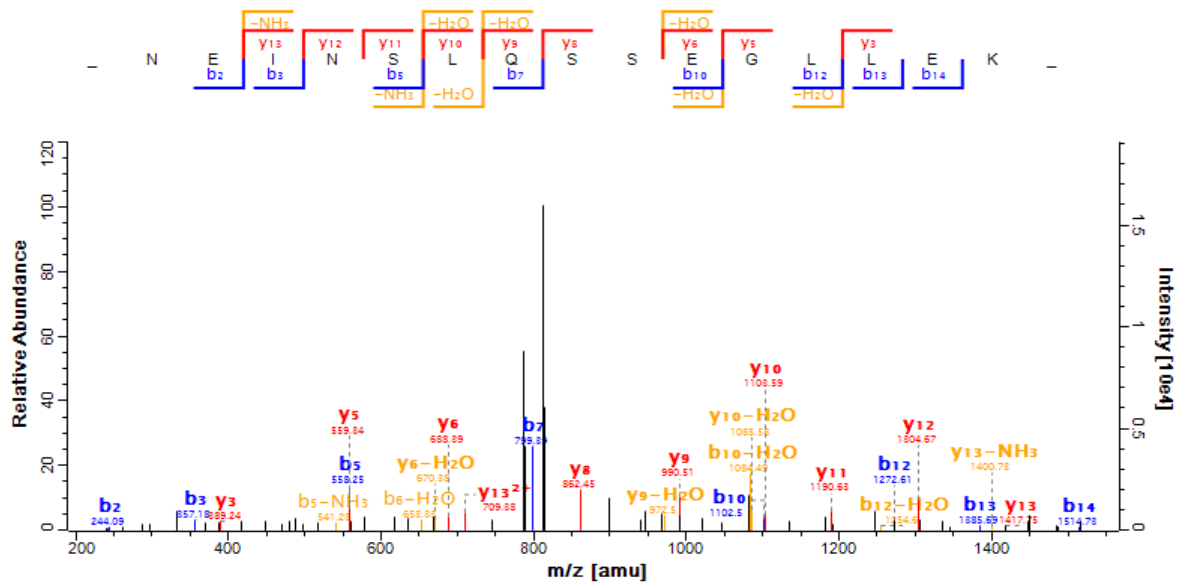
Protein Group ID: 4924
Protein Accession Numbers: Q9NV96
Gene Names: TMEM30A
Peptide Sequence: EIEIDYTGTEPSSPCNK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 141.86
Best Match Posterior Error Probability: 2.50E-05
Best Match Spectrum:

Scan number 34476 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TMEM30A



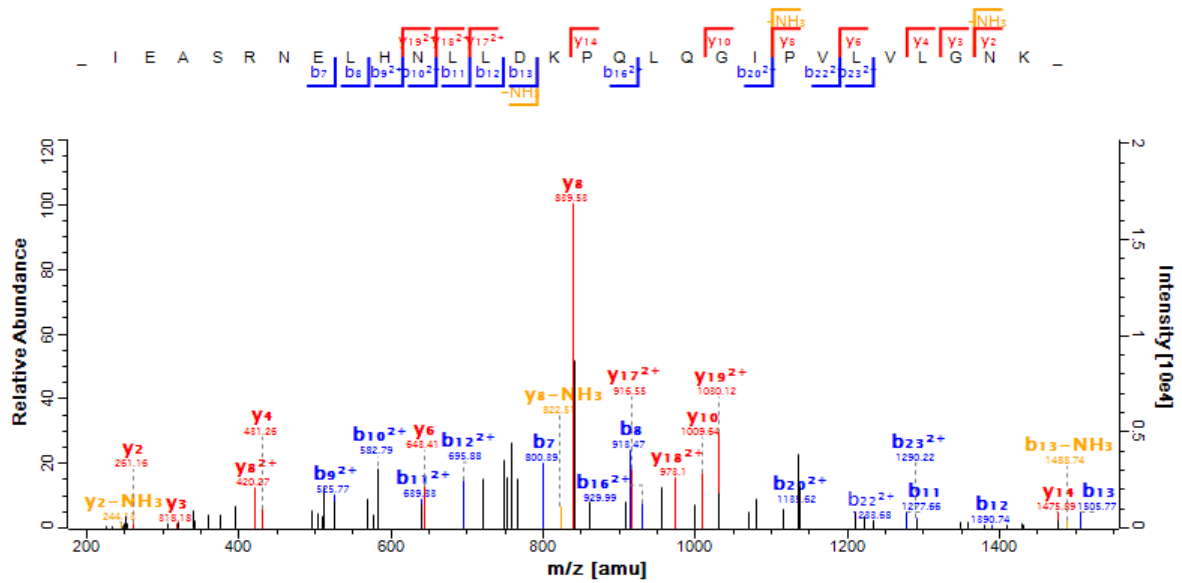
Protein Group ID: 4925
Protein Accession Numbers: Q9NVC6
Gene Names: MED17
Peptide Sequence: NEINSLQSSEGLLEK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 122.75
Best Match Posterior Error Probability: 0.00014665
Best Match Spectrum:

Scan number	45018	Raw file	A549-US-WT-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	MED17



Protein Group ID: 4930
Protein Accession Numbers: Q9NVJ2
Gene Names: ARL8B
Peptide Sequence: IEASRNELHNLNLLDKPQLQGIPVLVGLGNK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 97.509
Best Match Posterior Error Probability: 2.29E-05
Best Match Spectrum:

Scan number 70069 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ARL8B



Protein Group ID: 4938

Protein Accession Numbers: Q9NVX0; Q9NVX0-3; Q9NVX0-2

Gene Names: HAUS2

Peptide Sequence: ILAEESYLYK

Total Number of Spectra: 1

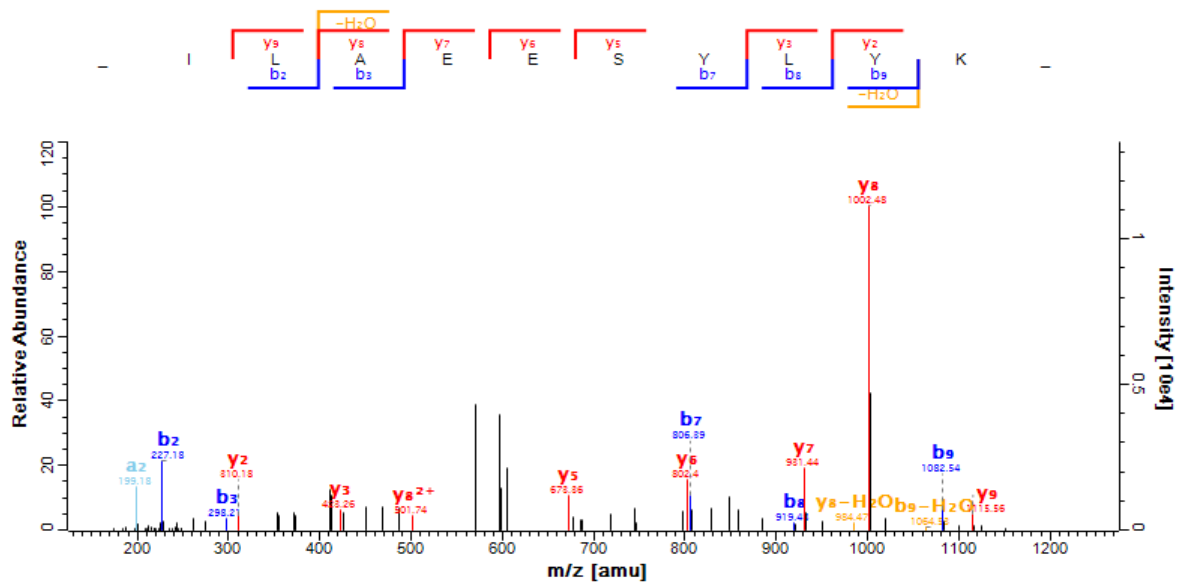
Number of Replicates (out of 8): 1

Best Match Score: 92.538

Best Match Posterior Error Probability: 0.0016515

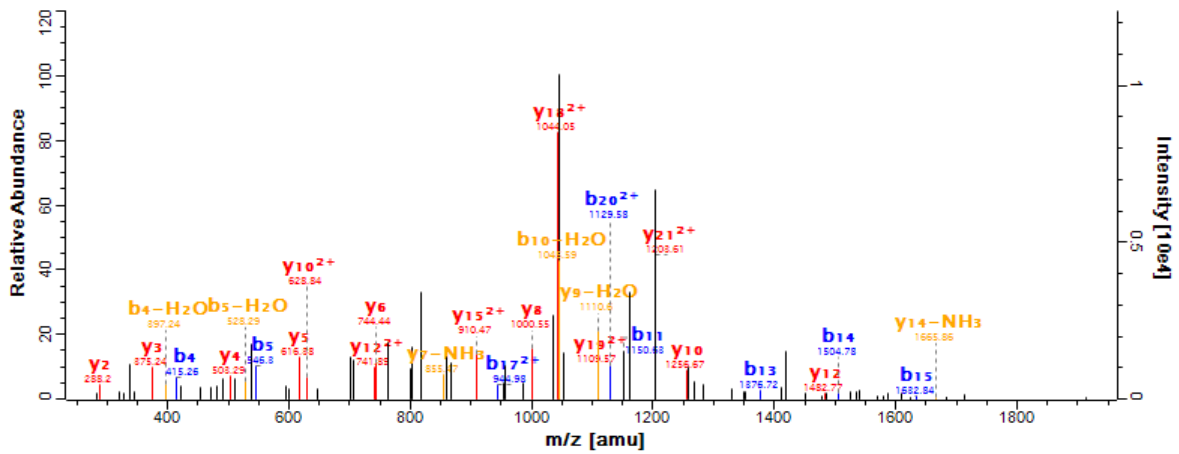
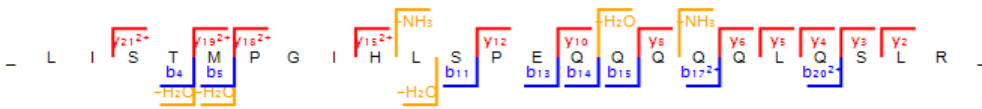
Best Match Spectrum:

Scan number 36812 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** HAUS2



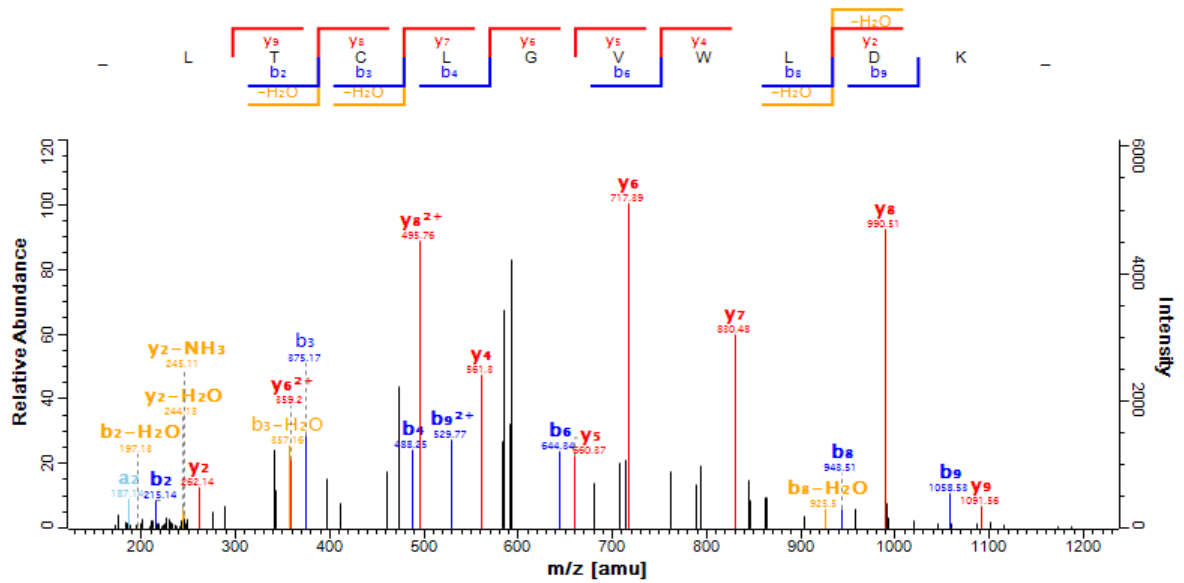
Protein Group ID: 4943
Protein Accession Numbers: Q9NWA0
Gene Names: MED9
Peptide Sequence: LISTMPGIHLSPEQQQQQLQLSLR
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 82.8
Best Match Posterior Error Probability: 7.09E-05
Best Match Spectrum:

Scan number 53973 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MED9



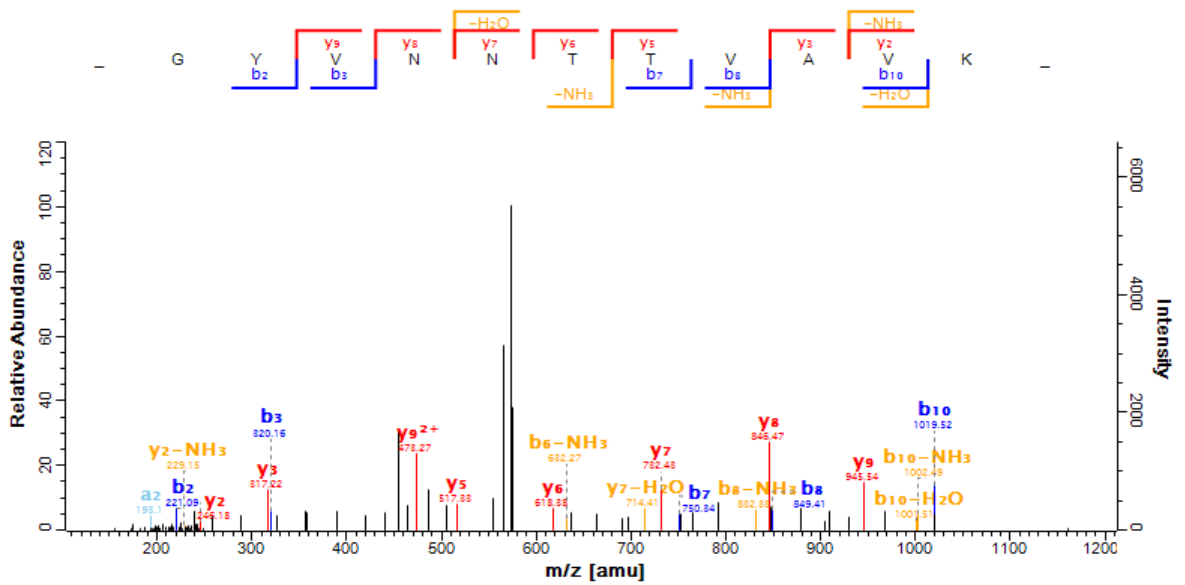
Protein Group ID: 4946
Protein Accession Numbers: Q9NWT1
Gene Names: PAK1IP1
Peptide Sequence: LTCLGVWLDK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 137.89
Best Match Posterior Error Probability: 1.06E-05
Best Match Spectrum:

Scan number 57527 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** PAK1IP1



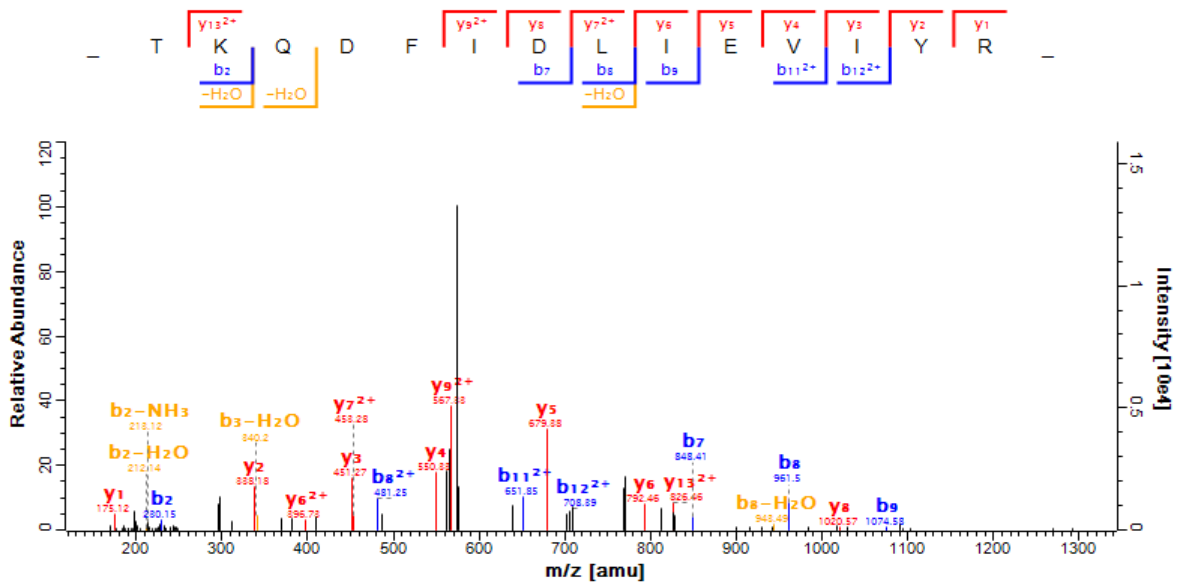
Protein Group ID: 4953
Protein Accession Numbers: Q9NWZ3; Q9NWZ3-2
Gene Names: IRAK4
Peptide Sequence: GYVNNTTVAVK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 98.898
Best Match Posterior Error Probability: 0.00055555
Best Match Spectrum:

Scan number 17819 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** IRAK4



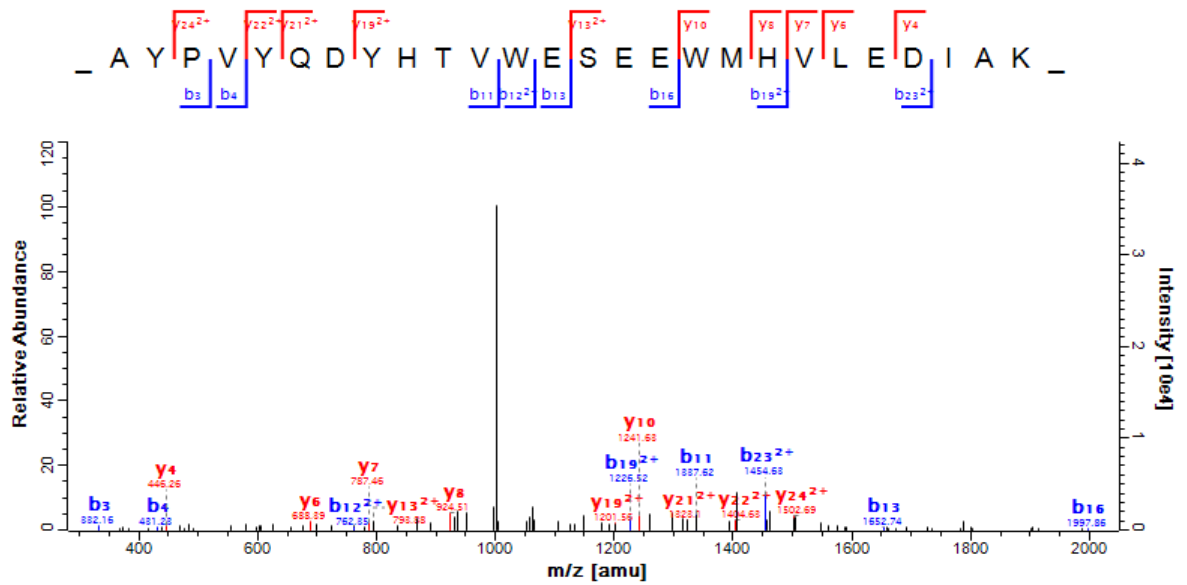
Protein Group ID: 4954
Protein Accession Numbers: Q9NX01
Gene Names: TXNL4B
Peptide Sequence: TKQDFIDLIEVILYR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 102.73
Best Match Posterior Error Probability: 0.0013234
Best Match Spectrum:

Scan number 83929 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TXNL4B



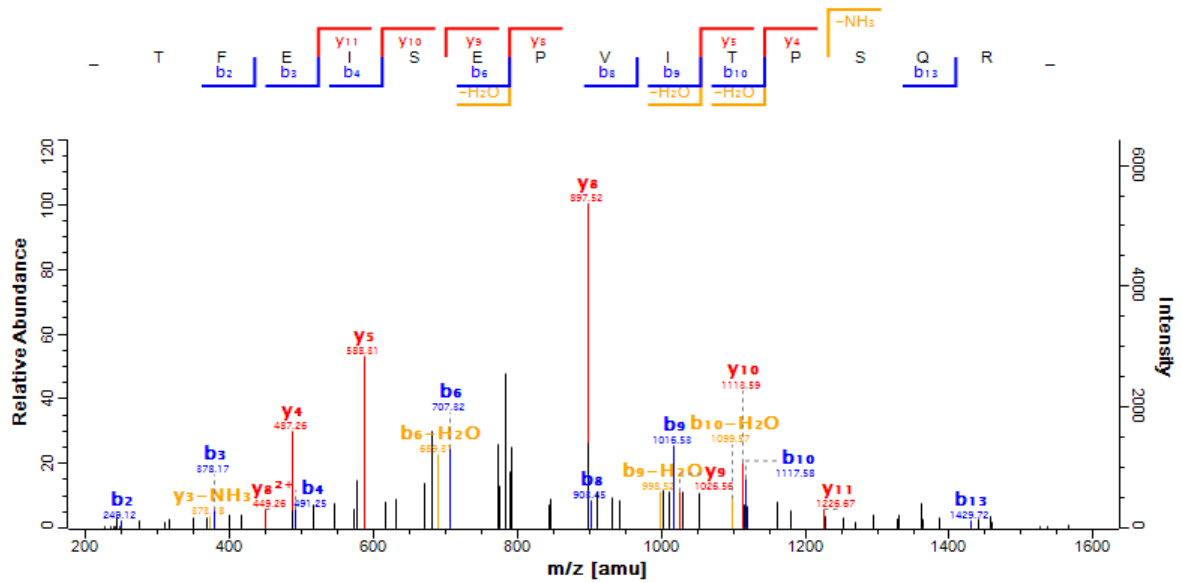
Protein Group ID: 4956
Protein Accession Numbers: Q9NX08
Gene Names: COMMD8
Peptide Sequence: AYPVYQDYHTVWESEEWMLHVLEDIAK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 54.235
Best Match Posterior Error Probability: 0.0024923
Best Match Spectrum:

Scan number 89125 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** COMMD8



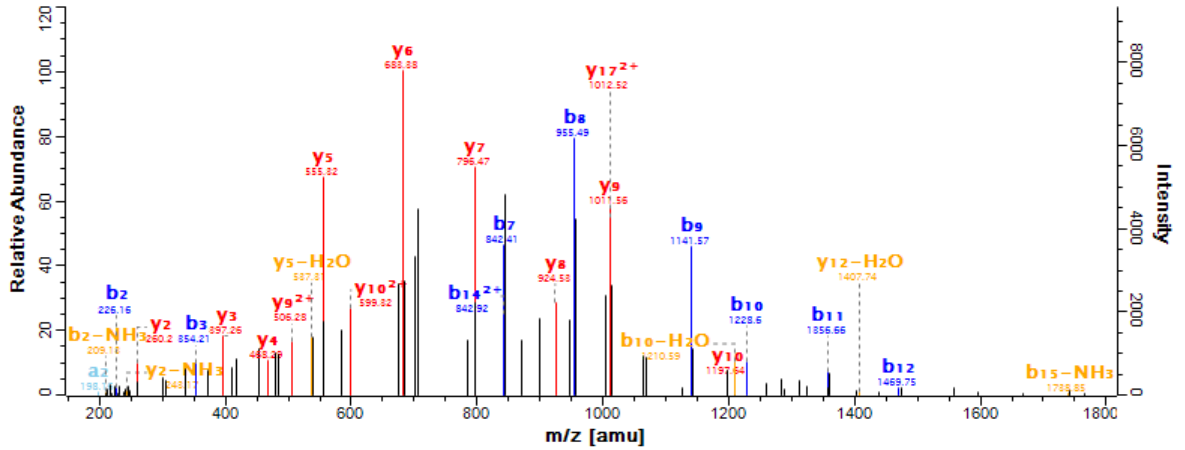
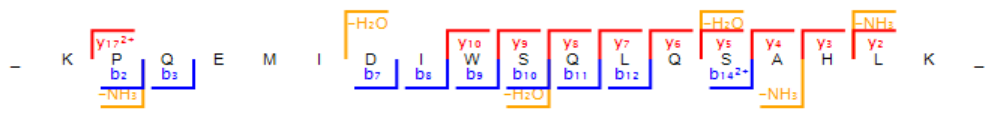
Protein Group ID: 4972
Protein Accession Numbers: Q9NXX6
Gene Names: NSMCE4A
Peptide Sequence: TFEISEPVITPSQR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 83.499
Best Match Posterior Error Probability: 0.0023858
Best Match Spectrum:

Scan number 46509 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** NSMCE4A



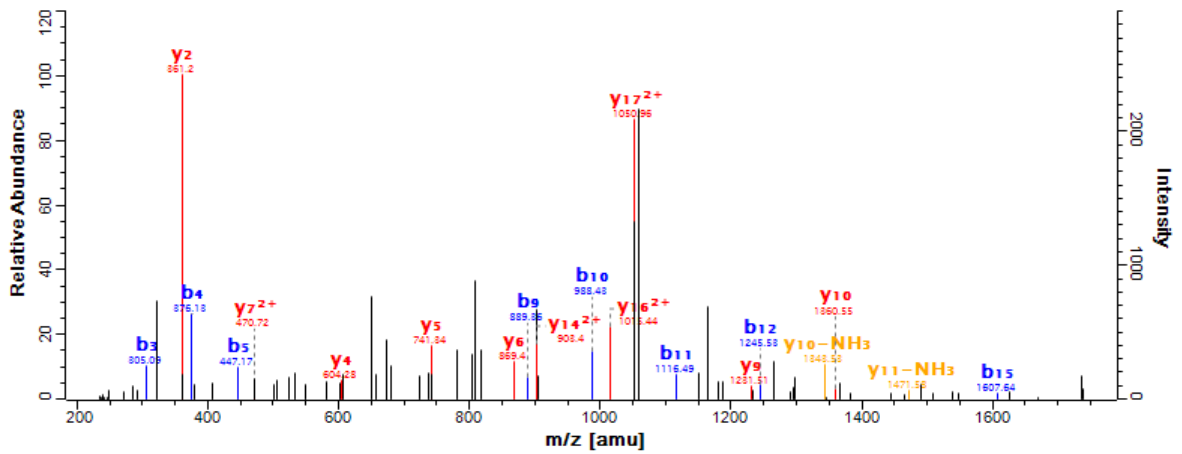
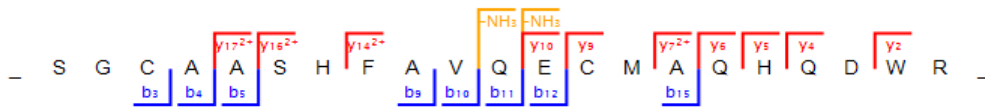
Protein Group ID: 4977
Protein Accession Numbers: Q9NY97; Q9NY97-2
Gene Names: B3GNT2
Peptide Sequence: KPQEMIDIWSQLQSAHLK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 97.095
Best Match Posterior Error Probability: 0.00051267
Best Match Spectrum:

Scan number 66512 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** B3GNT2



Protein Group ID: 4981
Protein Accession Numbers: Q9NYJ1-2; Q9NYJ1
Gene Names: CHCHD8
Peptide Sequence: SGCAASHFAVQEQCM AQHQDWR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 68.639
Best Match Posterior Error Probability: 0.0015832
Best Match Spectrum:

Scan number 35092 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** CHCHD8



Protein Group ID: 4985

Protein Accession Numbers: Q9NYQ6

Gene Names: CELSR1

Peptide Sequence: SLDLTGPLLLGGVPNLPEDFPVHNR

Total Number of Spectra: 1

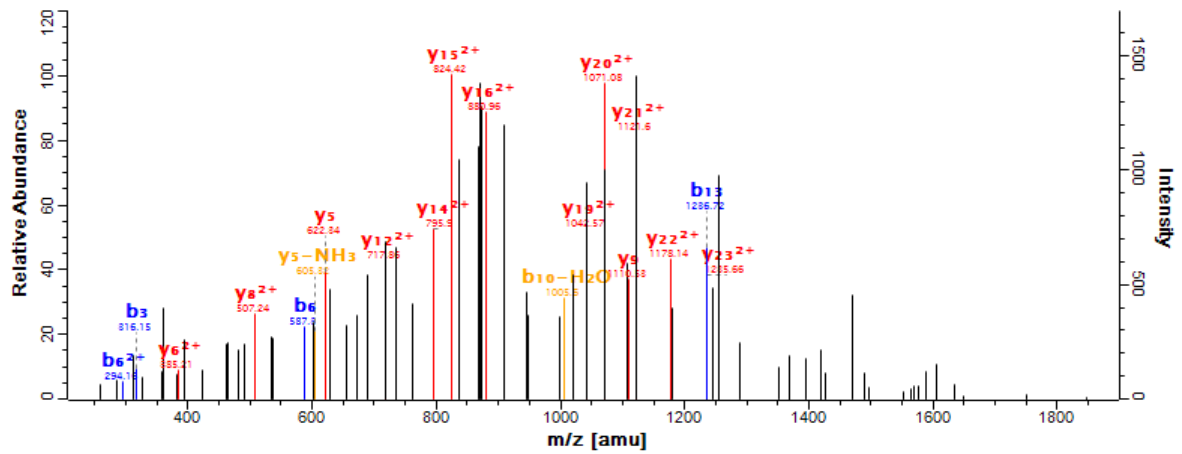
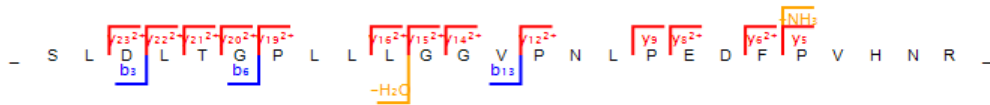
Number of Replicates (out of 8): 1

Best Match Score: 55.337

Best Match Posterior Error Probability: 0.0029273

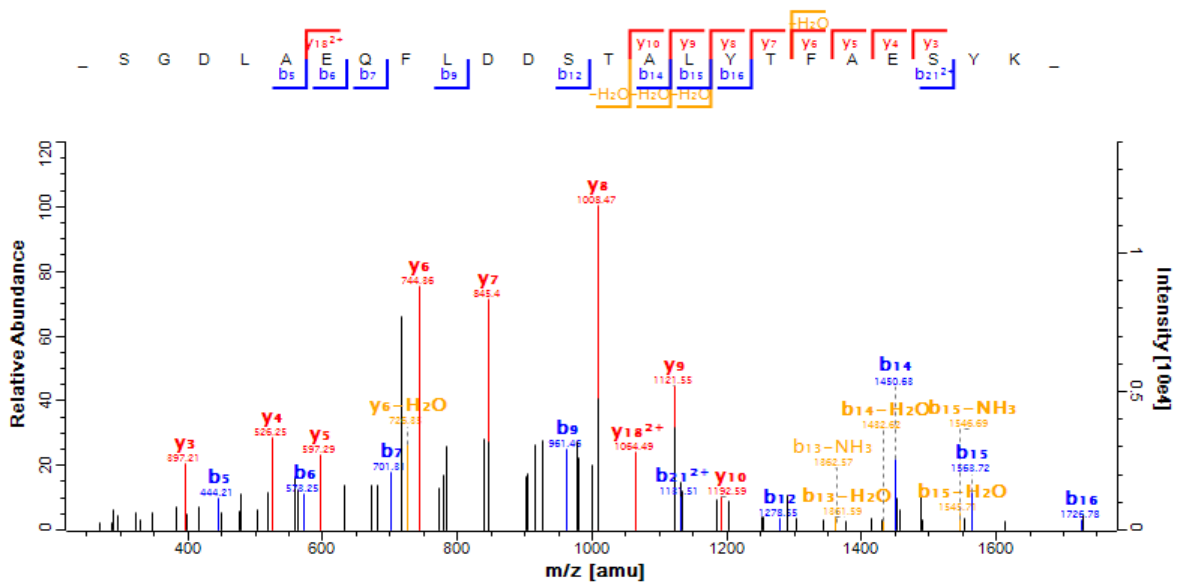
Best Match Spectrum:

Scan number	84678	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	CELSR1



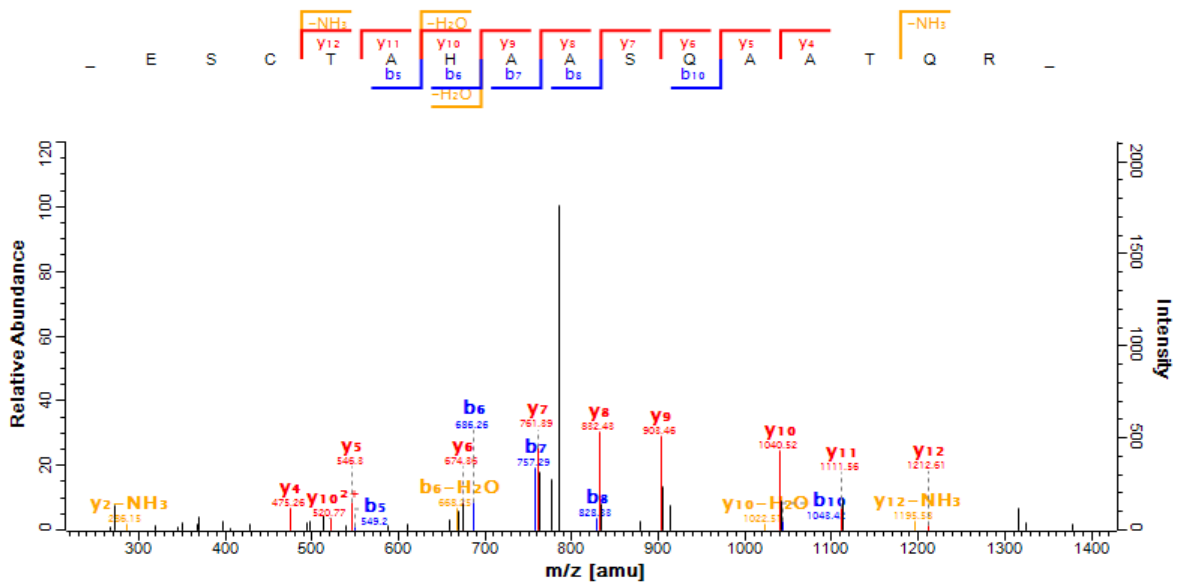
Protein Group ID: 4986
Protein Accession Numbers: Q9NYT0
Gene Names: PLEK2
Peptide Sequence: SGDLAEQFLDDSTALYTFAESYK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 65.425
Best Match Posterior Error Probability: 0.0010724
Best Match Spectrum:

Scan number 93865 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** PLEK2



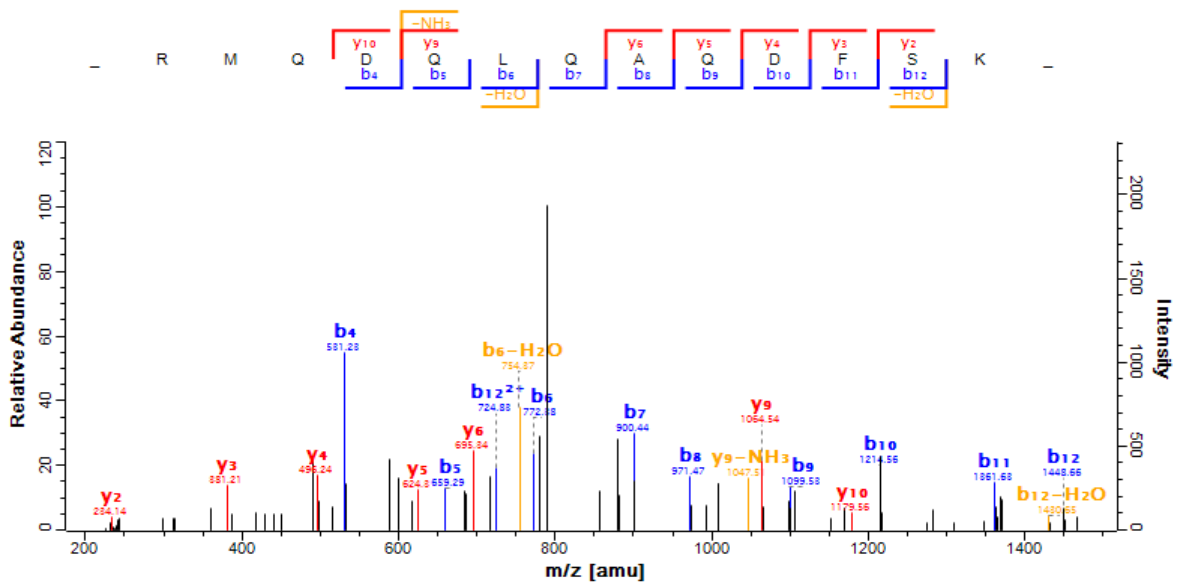
Protein Group ID: 4990
Protein Accession Numbers: Q9NYZ3
Gene Names: GTSE1
Peptide Sequence: ESCTAHAASQAATQR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 78.69
Best Match Posterior Error Probability: 0.002883
Best Match Spectrum:

Scan number 4179 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** GTSE1



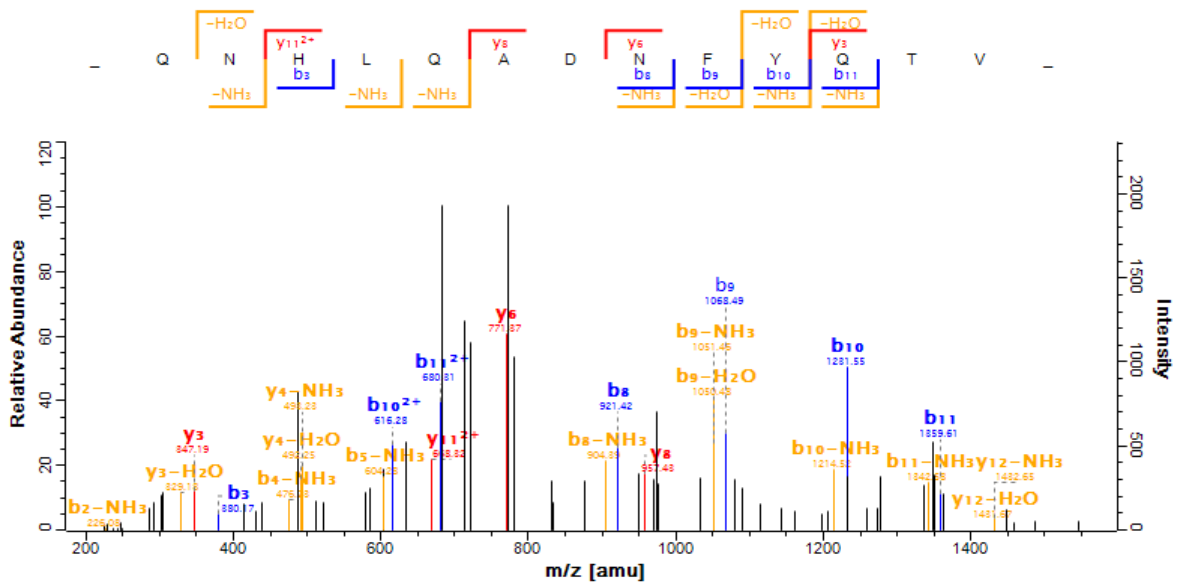
Protein Group ID: 5005
Protein Accession Numbers: Q9NZN3
Gene Names: EHD3
Peptide Sequence: RMQDQLQAQDFSK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 96.673
Best Match Posterior Error Probability: 0.0055343
Best Match Spectrum:

Scan number 23228 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** EHD3



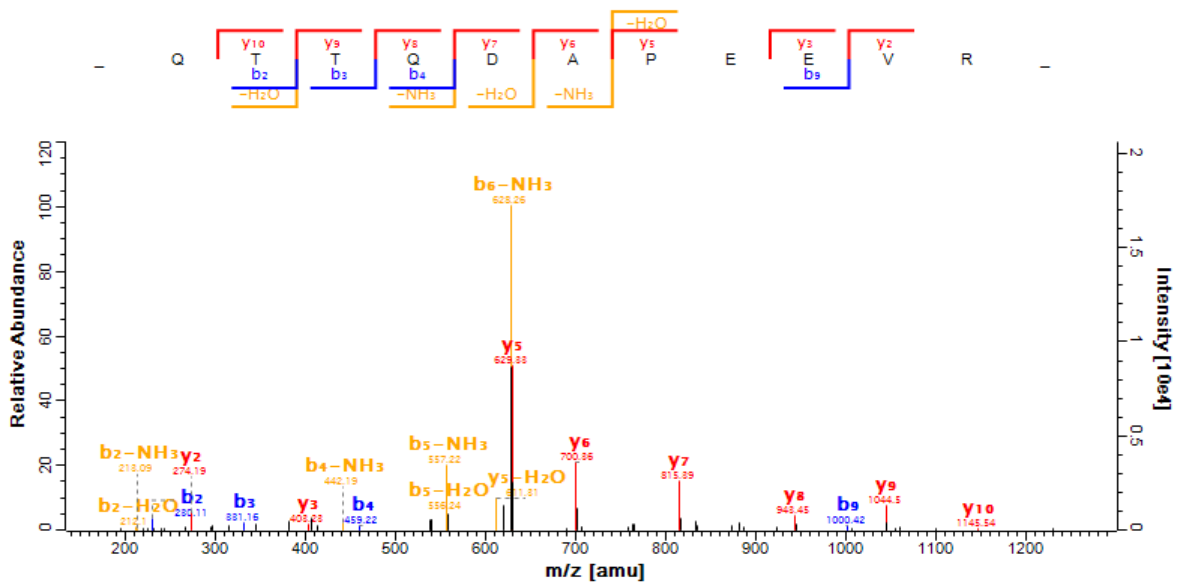
Protein Group ID: 5009
Protein Accession Numbers: Q9NZV1
Gene Names: CRIM1
Peptide Sequence: QNHLQADNFYQTV
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 107.09
Best Match Posterior Error Probability: 0.00037736
Best Match Spectrum:

Scan number 39495 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CRIM1



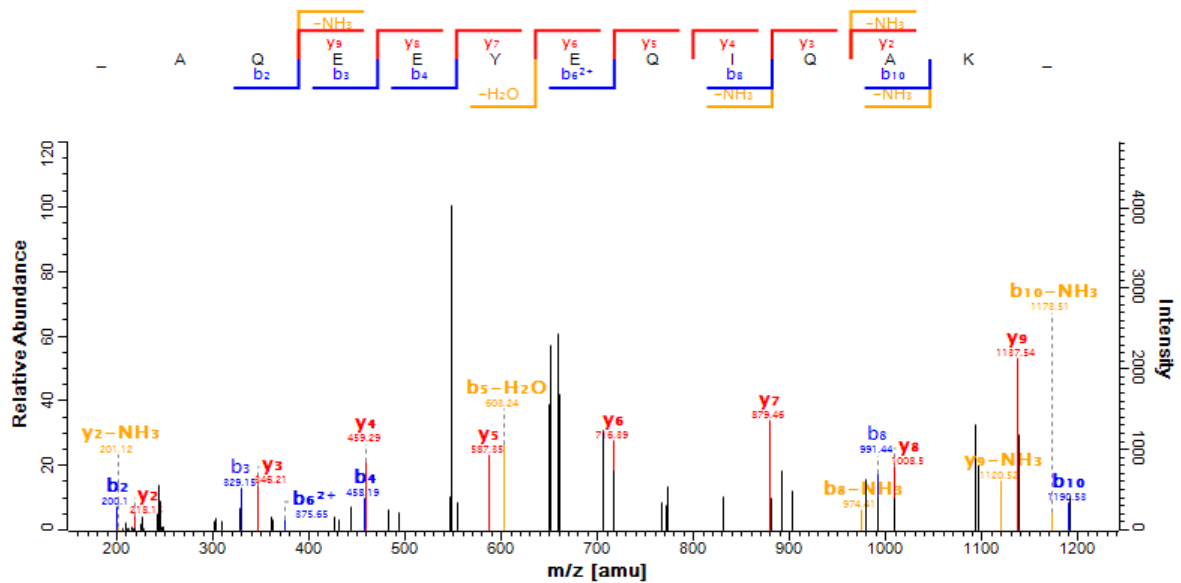
Protein Group ID: 5012
Protein Accession Numbers: Q9P013
Gene Names: CWC15
Peptide Sequence: QTTQDAPEEVR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 94.191
Best Match Posterior Error Probability: 0.0010422
Best Match Spectrum:

Scan number 6762 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CWC15



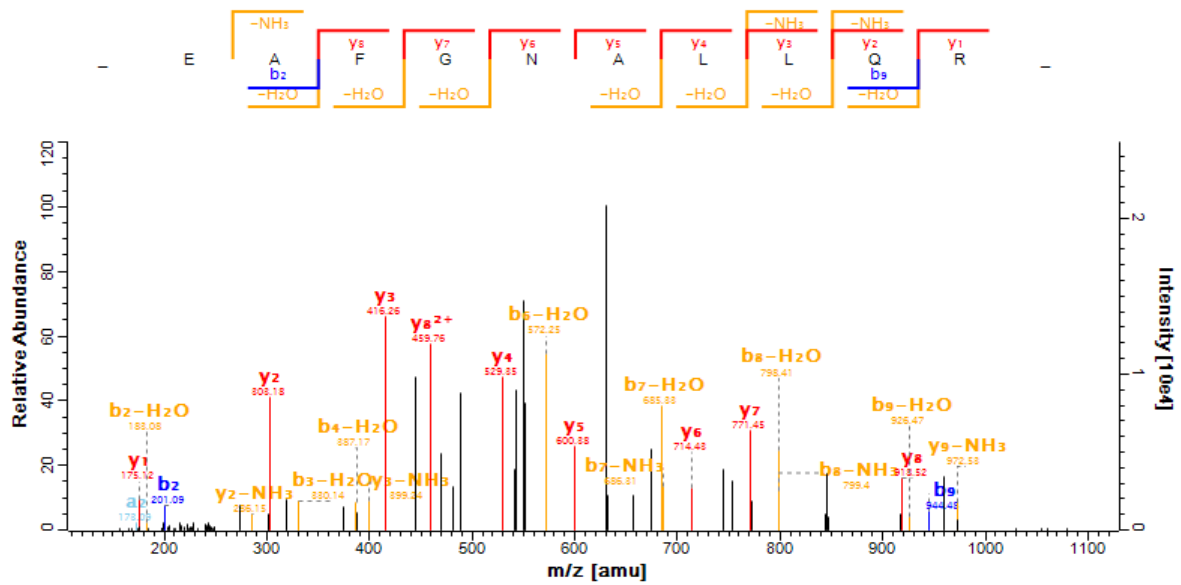
Protein Group ID: 5016
Protein Accession Numbers: Q9P031
Gene Names: CCDC59
Peptide Sequence: AQEYEYEQIAK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 84.605
Best Match Posterior Error Probability: 0.0025518
Best Match Spectrum:

Scan number 14200 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** CCDC59



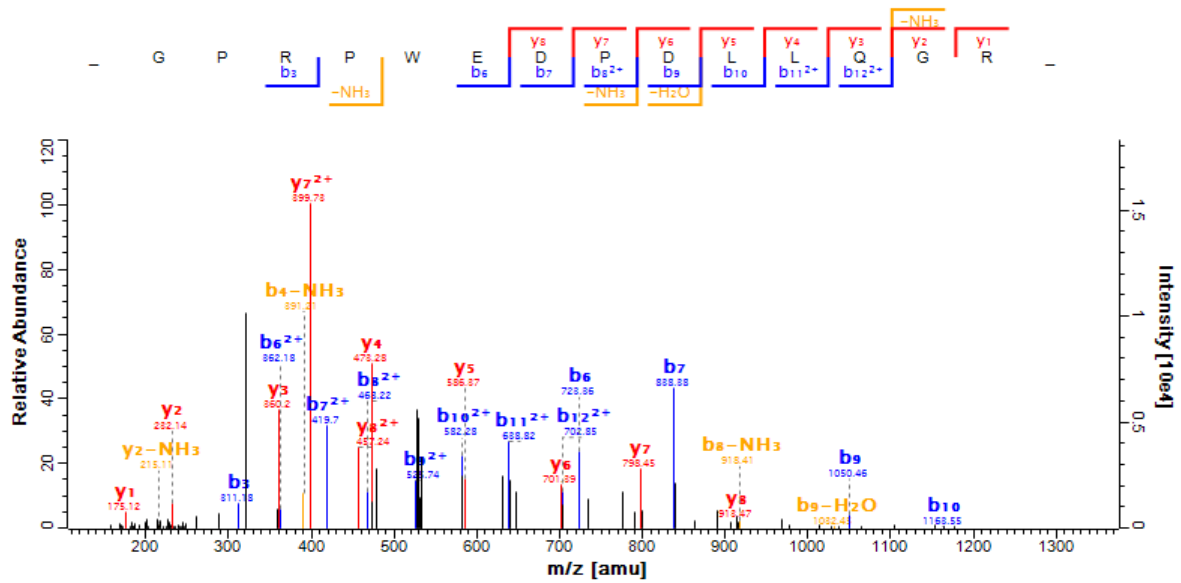
Protein Group ID: 5023
Protein Accession Numbers: Q9P0R6
Gene Names: GSKIP
Peptide Sequence: EAFGNALLQR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 89.08
Best Match Posterior Error Probability: 0.0020971
Best Match Spectrum:

Scan number	38925	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	GSKIP



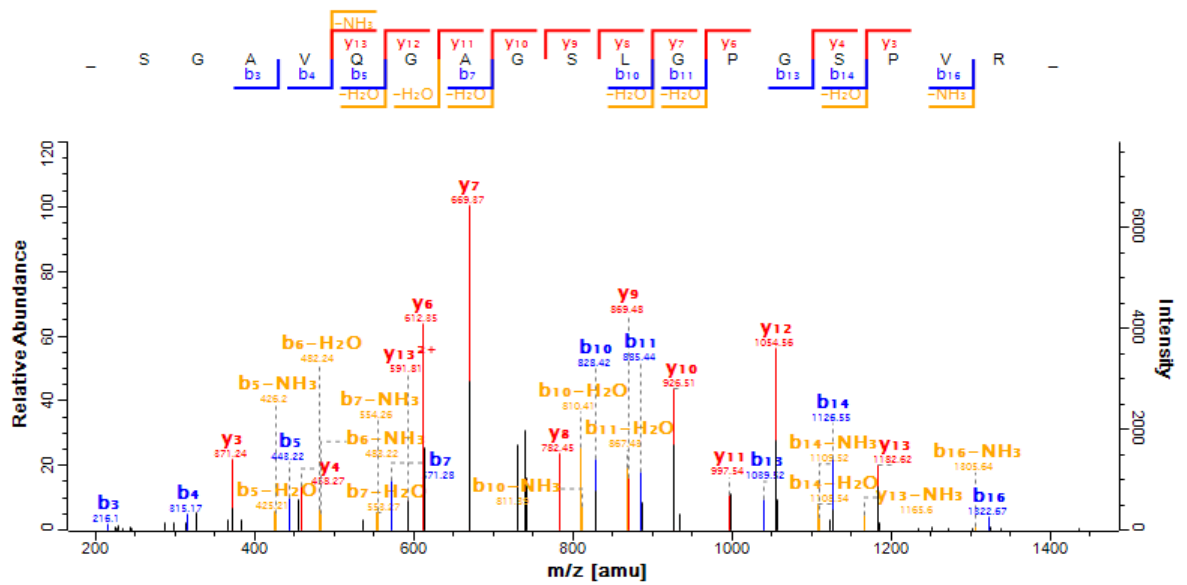
Protein Group ID: 5024
Protein Accession Numbers: Q9P0S2
Gene Names: COX16
Peptide Sequence: GPRPWEDPDLQGR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 126.95
Best Match Posterior Error Probability: 0.0001686
Best Match Spectrum:

Scan number 44922 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** COX16



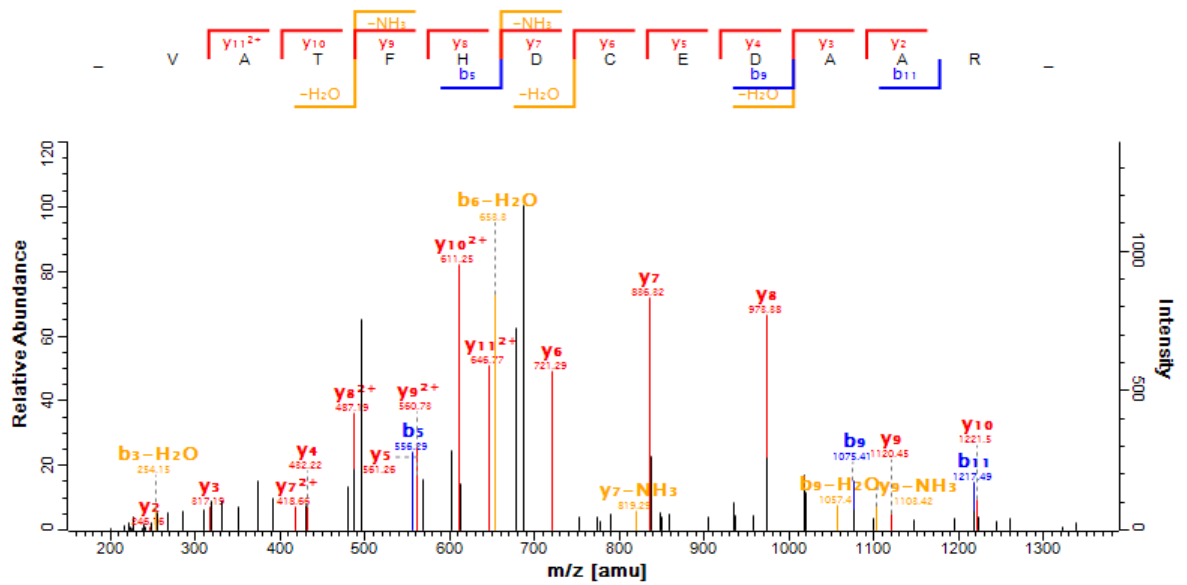
Protein Group ID: 5032
Protein Accession Numbers: Q9P270
Gene Names: SLAIN2
Peptide Sequence: SGAVQGAGSLGPGSPVR
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 166.48
Best Match Posterior Error Probability: 5.05E-10
Best Match Spectrum:

Scan number 23654 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** SLAIN2



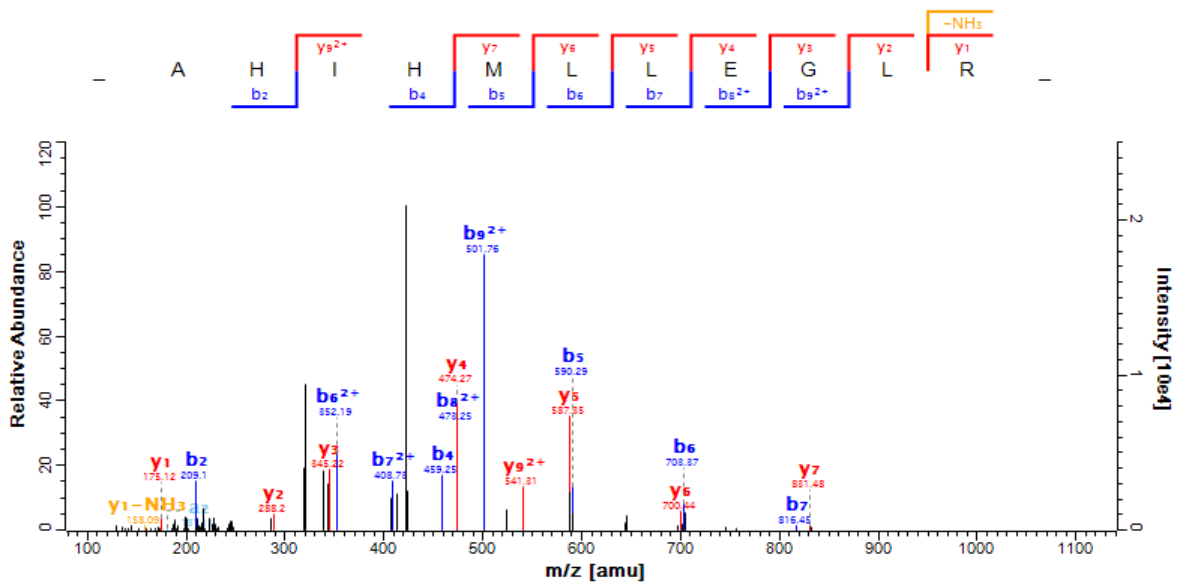
Protein Group ID: 5044
Protein Accession Numbers: Q9P2X0-2; Q9P2X0
Gene Names: DPM3
Peptide Sequence: VATFHDCEDAAR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 113.61
Best Match Posterior Error Probability: 0.00021508
Best Match Spectrum:

Scan number 10216 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** DPM3



Protein Group ID: 5056
Protein Accession Numbers: Q9UBK9
Gene Names: UXT
Peptide Sequence: AHIHMLLEGLR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 105.98
Best Match Posterior Error Probability: 0.00030271
Best Match Spectrum:

Scan number 40053 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** UXT



Protein Group ID: 5090

Protein Accession Numbers: Q9UHA4

Gene Names: LAMTOR3

Peptide Sequence: VANDNAP EHLRLP GFLSTFALATDQGSK

Total Number of Spectra: 5

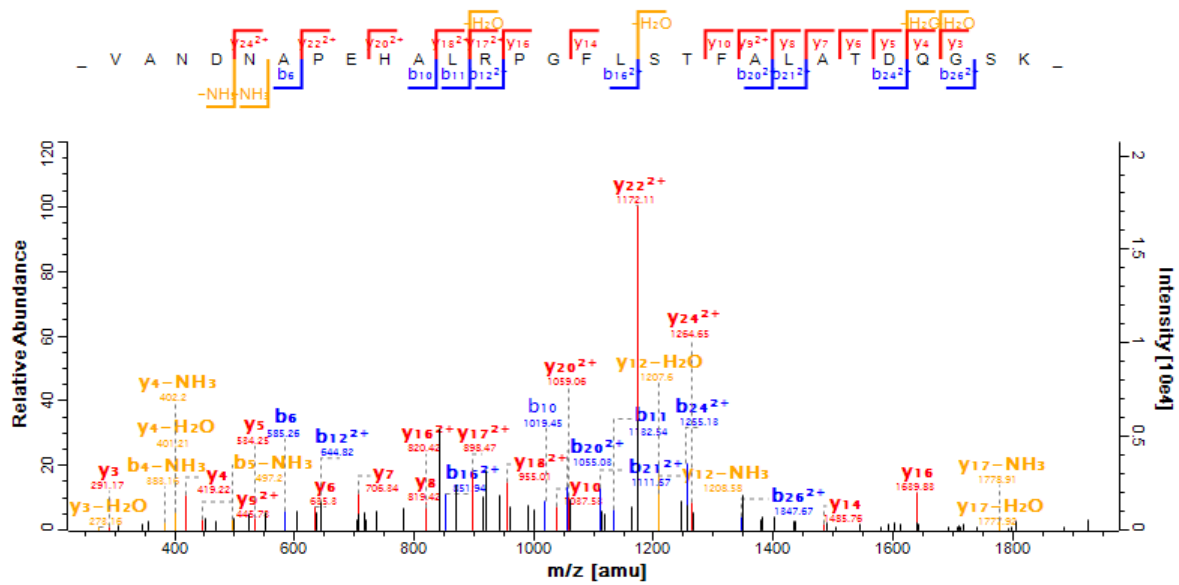
Number of Replicates (out of 8): 5

Best Match Score: 107.75

Best Match Posterior Error Probability: 4.22E-08

Best Match Spectrum:

Scan number 62019 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** LAMTOR3



Protein Group ID: 5097

Protein Accession Numbers: Q9UHG0; Q9UHG0-2

Gene Names: DCDC2

Peptide Sequence: ITSPEENENNQQNK

Total Number of Spectra: 2

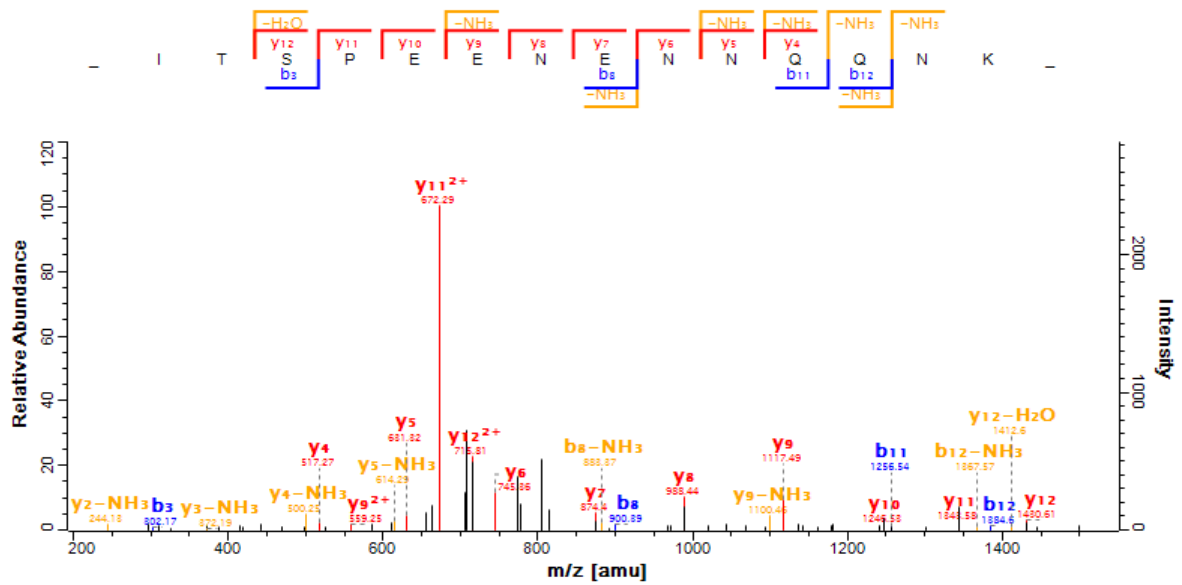
Number of Replicates (out of 8): 2

Best Match Score: 110.51

Best Match Posterior Error Probability: 0.00016395

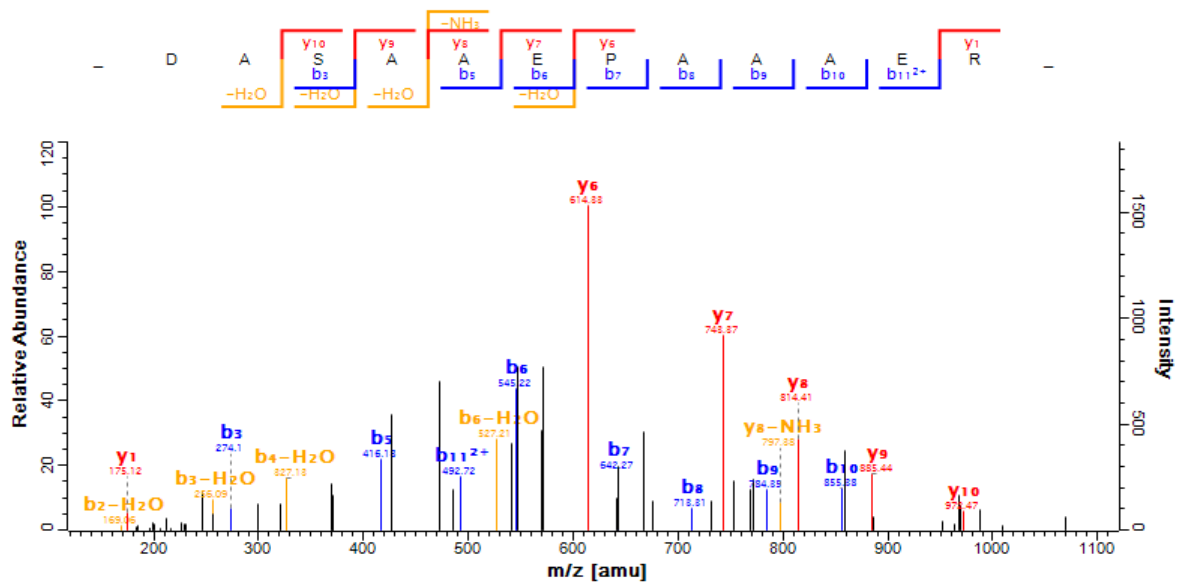
Best Match Spectrum:

Scan number 3714 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** DCDC2



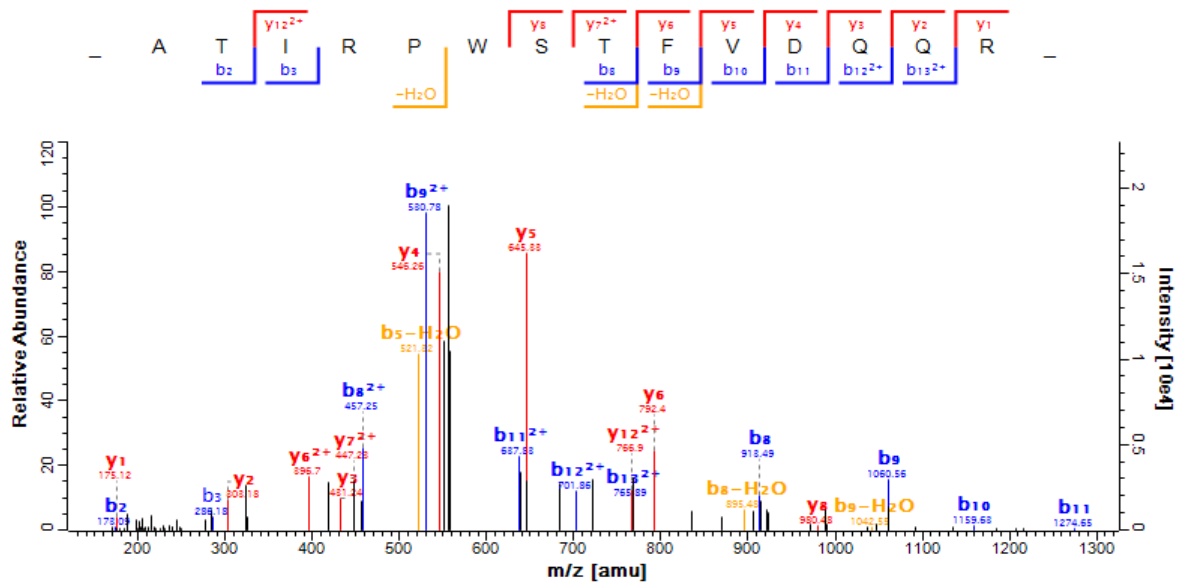
Protein Group ID: 5106
Protein Accession Numbers: Q9UHR6
Gene Names: ZNHIT2
Peptide Sequence: DASAAEPAAAER
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 83.137
Best Match Posterior Error Probability: 0.0026505
Best Match Spectrum:

Scan number 4982 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ZNHIT2



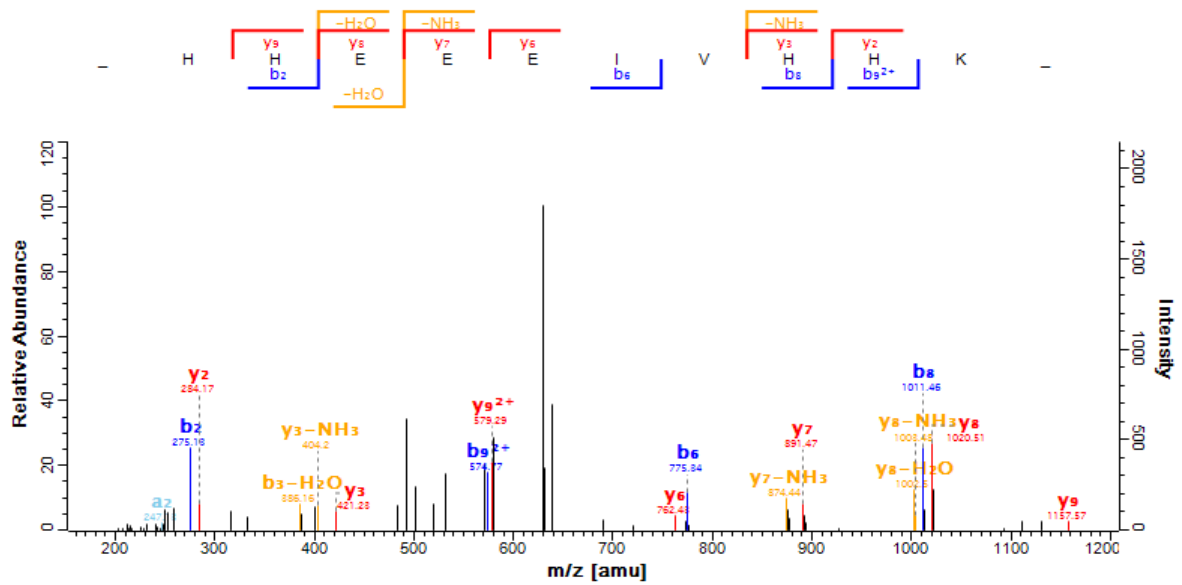
Protein Group ID: 5115
Protein Accession Numbers: Q9UI14
Gene Names: RABAC1
Peptide Sequence: ATIRPWSTFVDQQR
Total Number of Spectra: 6
Number of Replicates (out of 8): 5
Best Match Score: 115.12
Best Match Posterior Error Probability: 0.00050755
Best Match Spectrum:

Scan number 46683 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** RABAC1



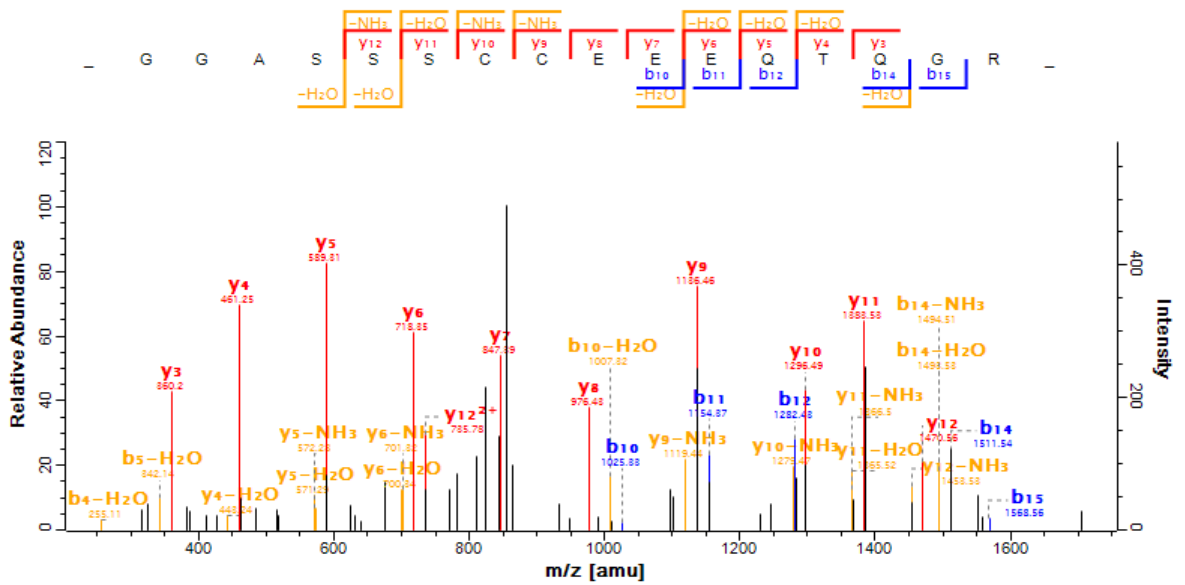
Protein Group ID: 5120
Protein Accession Numbers: Q9UII2
Gene Names: ATP1F1
Peptide Sequence: HHEEEIVHHK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 108.67
Best Match Posterior Error Probability: 0.0013835
Best Match Spectrum:

Scan number 1629 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** ATP1F1



Protein Group ID: 5127
Protein Accession Numbers: Q9UJK0
Gene Names: C16orf42
Peptide Sequence: GGASSSCCEEEQTQGR
Total Number of Spectra: 6
Number of Replicates (out of 8): 6
Best Match Score: 160.04
Best Match Posterior Error Probability: 1.79E-09
Best Match Spectrum:

Scan number 2642 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** C16orf42



Protein Group ID: 5138

Protein Accession Numbers: Q9UK45

Gene Names: LSM7

Peptide Sequence: GFDPLLNLVLDGTIEYMRDPDDQYK

Total Number of Spectra: 4

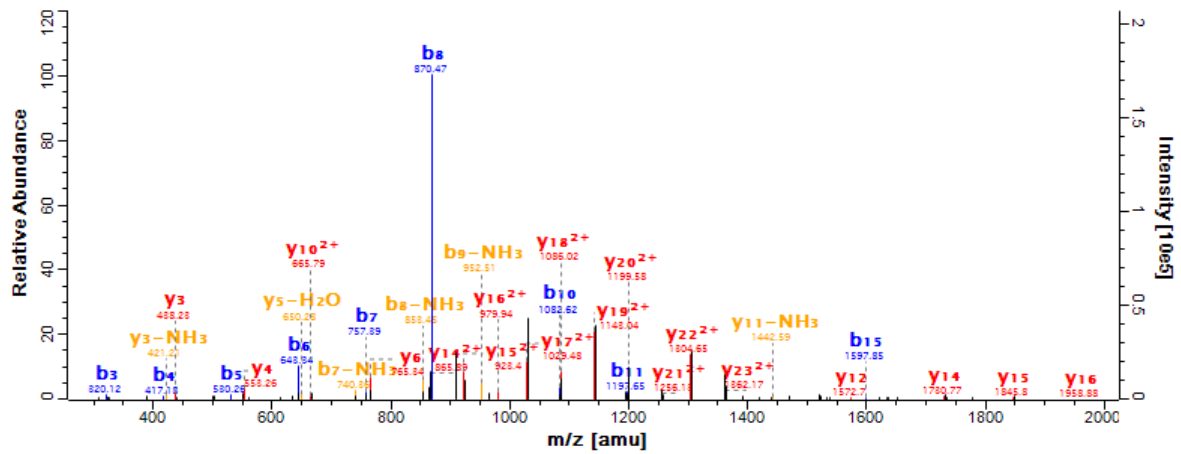
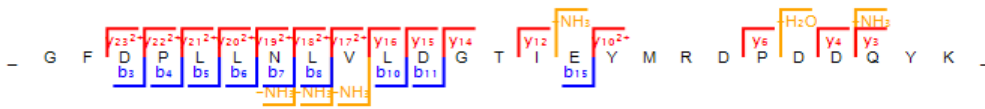
Number of Replicates (out of 8): 4

Best Match Score: 134.86

Best Match Posterior Error Probability: 1.36E-17

Best Match Spectrum:

Scan number 92241 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** LSM7



Protein Group ID: 5158

Protein Accession Numbers: Q9UL54; Q9UL54-4; Q9UL54-3; Q9UL54-2

Gene Names: TAOK2

Peptide Sequence: EELQENPSTPK

Total Number of Spectra: 2

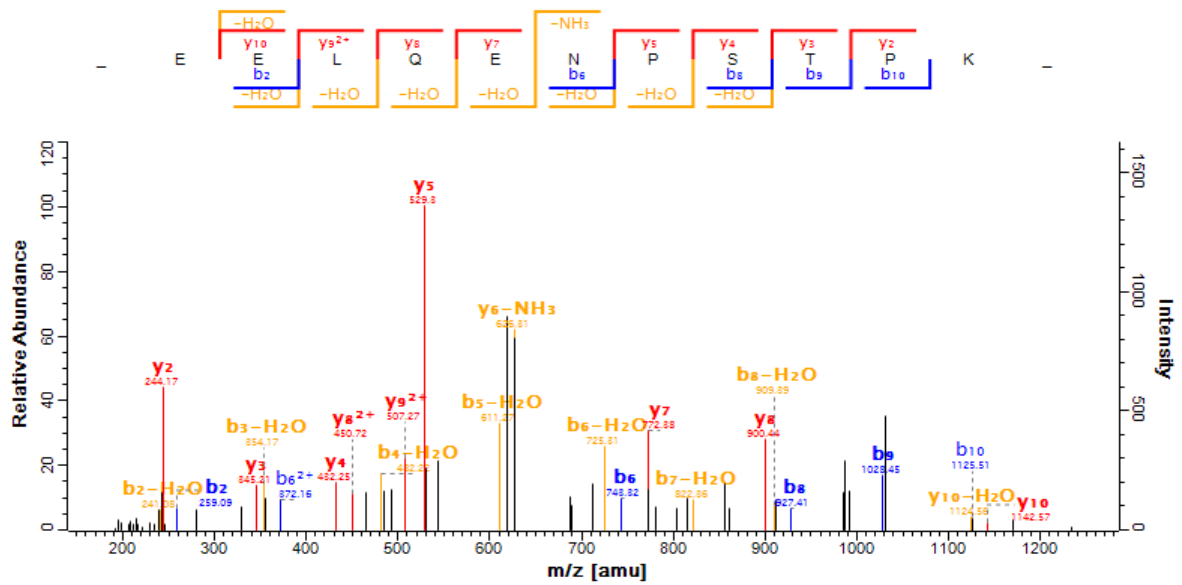
Number of Replicates (out of 8): 2

Best Match Score: 113.61

Best Match Posterior Error Probability: 0.00011586

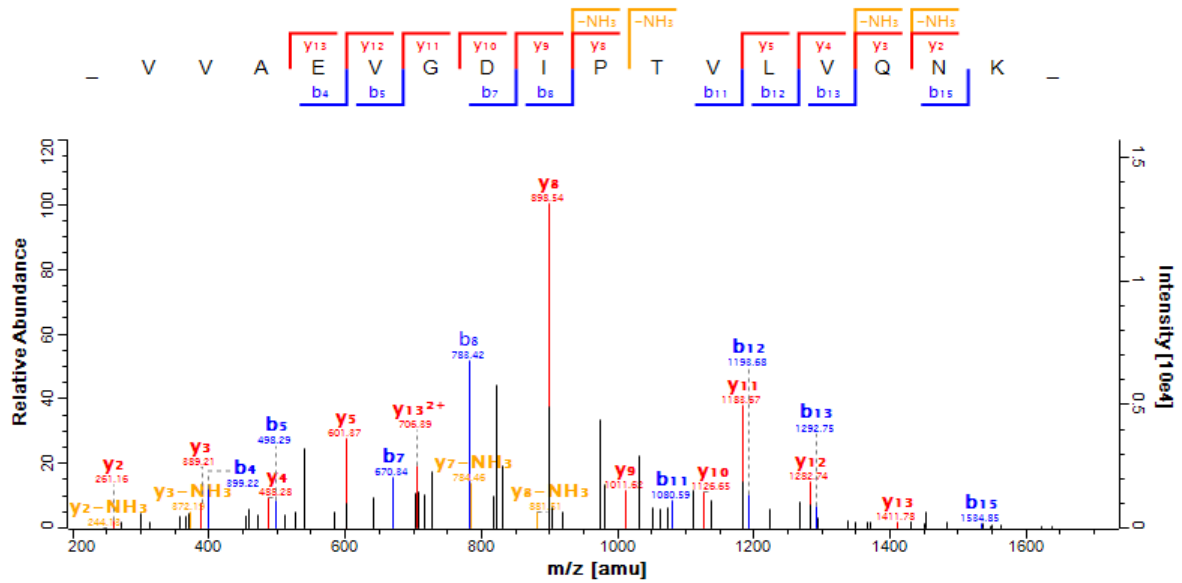
Best Match Spectrum:

Scan number	9472	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	TAOK2



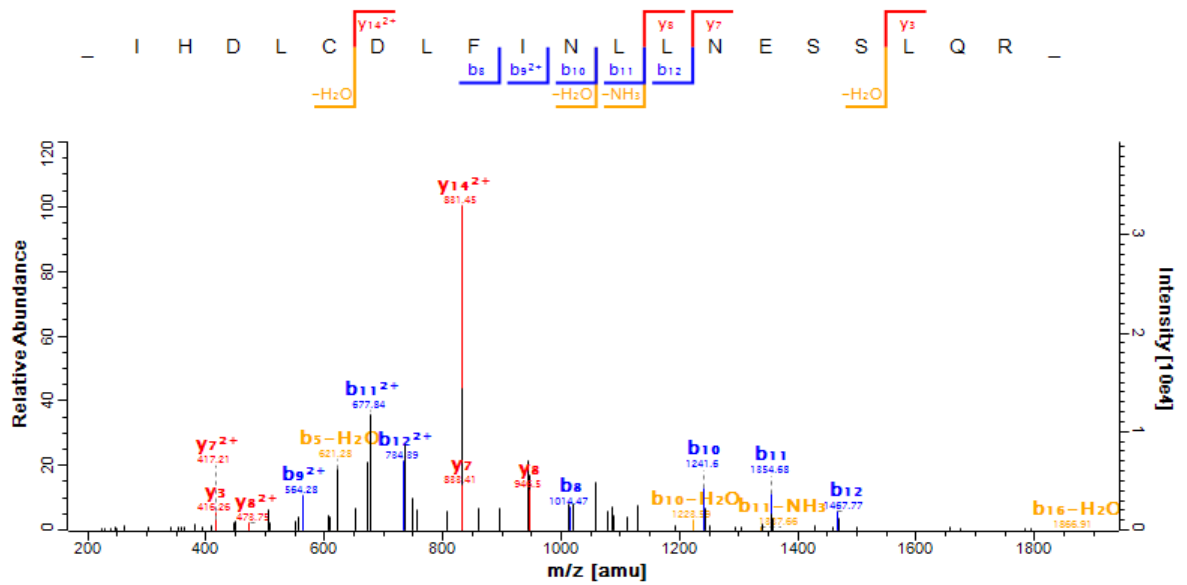
Protein Group ID: 5159
Protein Accession Numbers: Q9ULC3
Gene Names: RAB23
Peptide Sequence: VVAEVDIPTVLVQNK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 110.35
Best Match Posterior Error Probability: 0.00010918
Best Match Spectrum:

Scan number 56374 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** RAB23



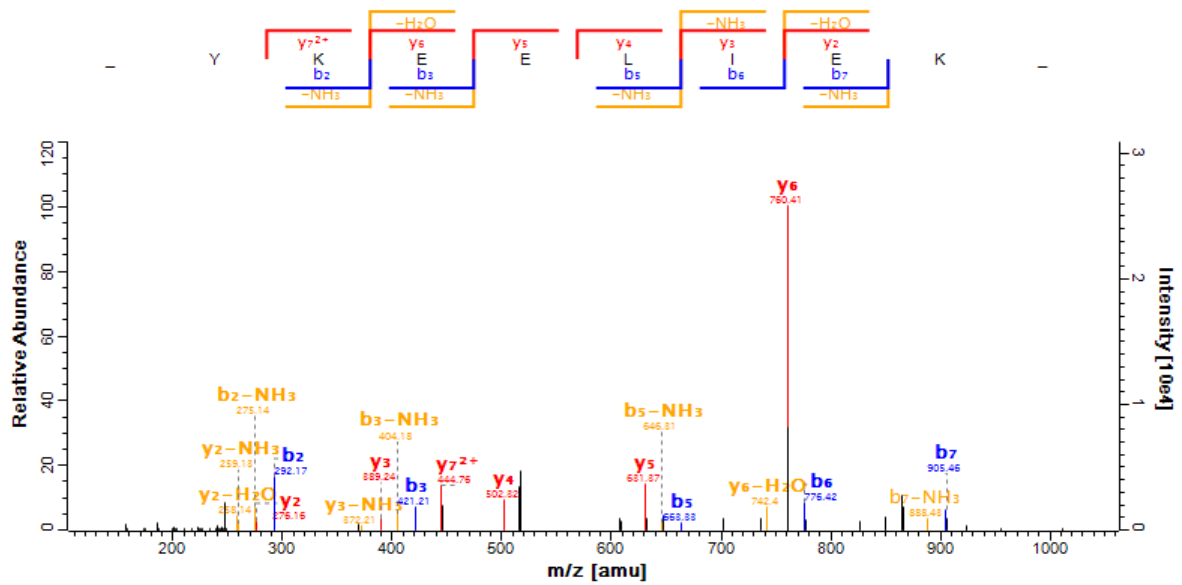
Protein Group ID: 5165
Protein Accession Numbers: Q9ULI1
Gene Names: KIAA1239
Peptide Sequence: IHDLDLFINLLNESSLR
Total Number of Spectra: 2
Number of Replicates (out of 8): 1
Best Match Score: 73.983
Best Match Posterior Error Probability: 0.0016788
Best Match Spectrum:

Scan number 88077 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** KIAA1239



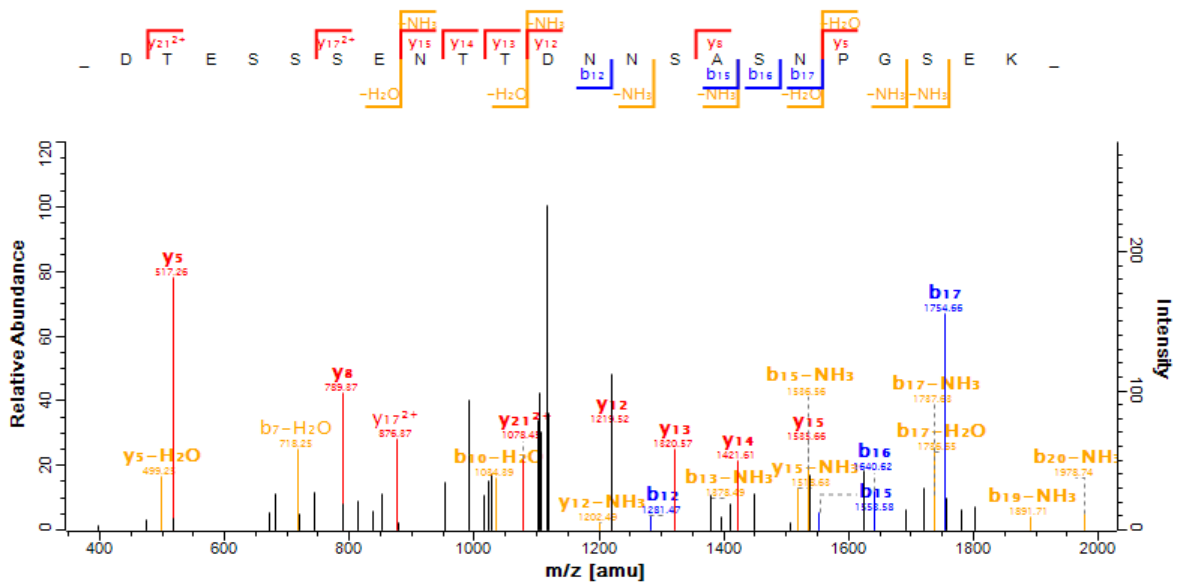
Protein Group ID: 5191
Protein Accession Numbers: Q9UNX3
Gene Names: RPL26L1
Peptide Sequence: YKEELIEK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 128.86
Best Match Posterior Error Probability: 0.0076547
Best Match Spectrum:

Scan number	12061	Raw file	A549-US-Mock-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	RPL26L1



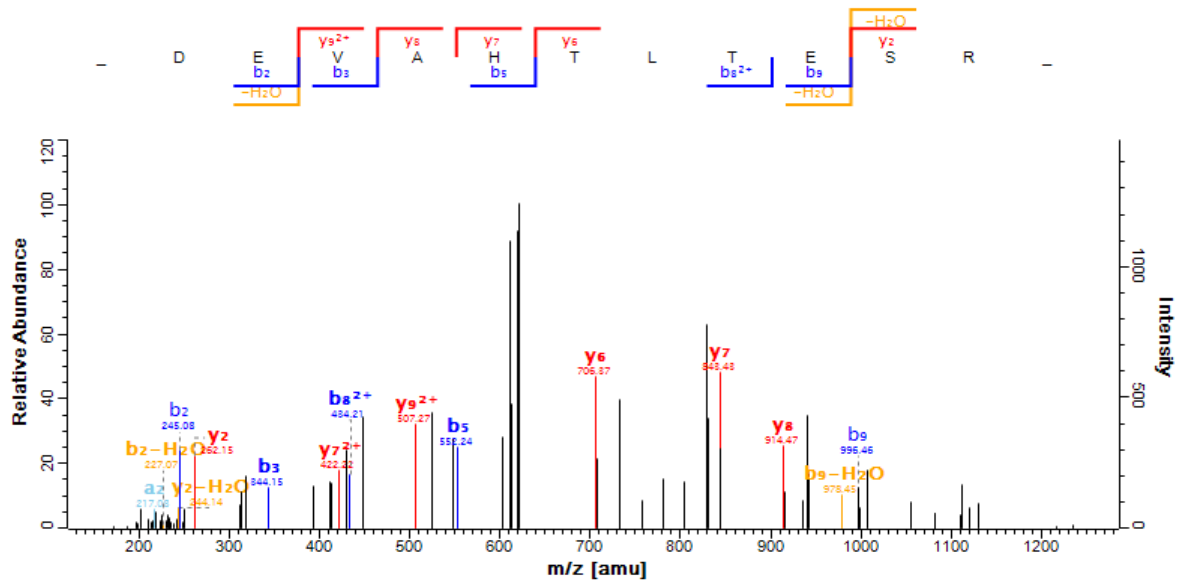
Protein Group ID: 5195
Protein Accession Numbers: Q9UPQ9; Q9UPQ9-1
Gene Names: TNRC6B
Peptide Sequence: DTESSSENTTDNNSASNPGSEK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 70.453
Best Match Posterior Error Probability: 0.00081396
Best Match Spectrum:

Scan number 3808 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TNRC6B



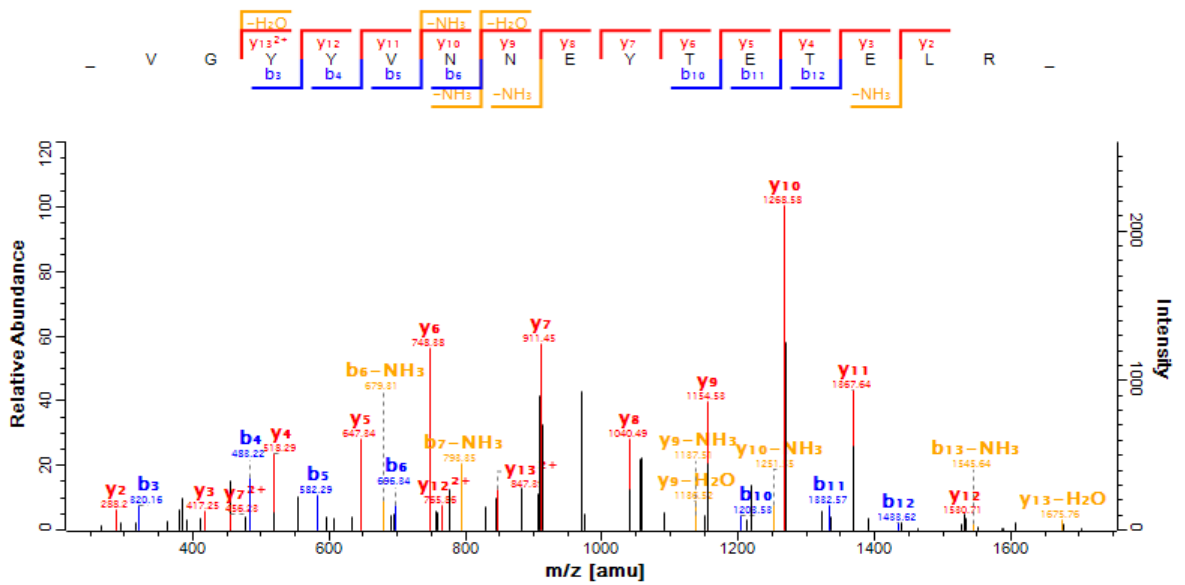
Protein Group ID: 5209
Protein Accession Numbers: Q9Y243; Q9Y243-2
Gene Names: AKT3
Peptide Sequence: DEVAHTLTESR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 82.417
Best Match Posterior Error Probability: 0.003201
Best Match Spectrum:

Scan number 12187 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** AKT3



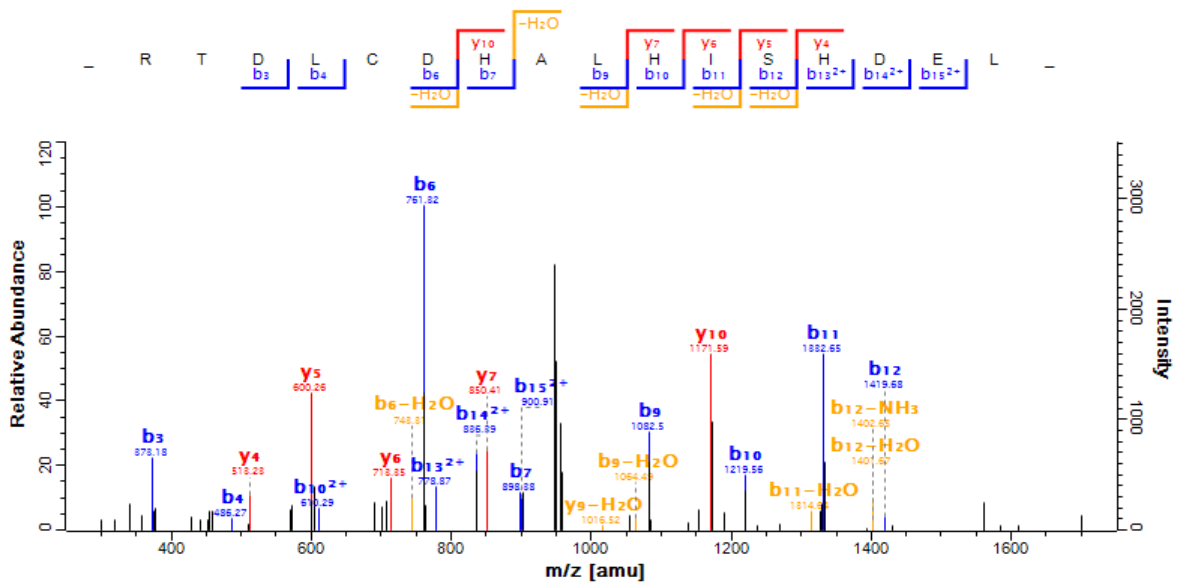
Protein Group ID: 5222
Protein Accession Numbers: Q9Y294
Gene Names: ASF1A
Peptide Sequence: VGYYYVNNNEYTETELR
Total Number of Spectra: 6
Number of Replicates (out of 8): 5
Best Match Score: 148.57
Best Match Posterior Error Probability: 1.04E-06
Best Match Spectrum:

Scan number 40587 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** ASF1A



Protein Group ID: 5225
Protein Accession Numbers: Q9Y2B0; H0YI18
Gene Names: CNPY2
Peptide Sequence: RTDLCDHALHISHDEL
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 115.68
Best Match Posterior Error Probability: 0.00022537
Best Match Spectrum:

Scan number 33365 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CNPY2



Protein Group ID: 5228

Protein Accession Numbers: Q9Y2J4-4; Q9Y2J4-2; Q9Y2J4; Q9Y2J4-3

Gene Names: AMOTL2

Peptide Sequence: TQEAQAGSQDMVAK

Total Number of Spectra: 7

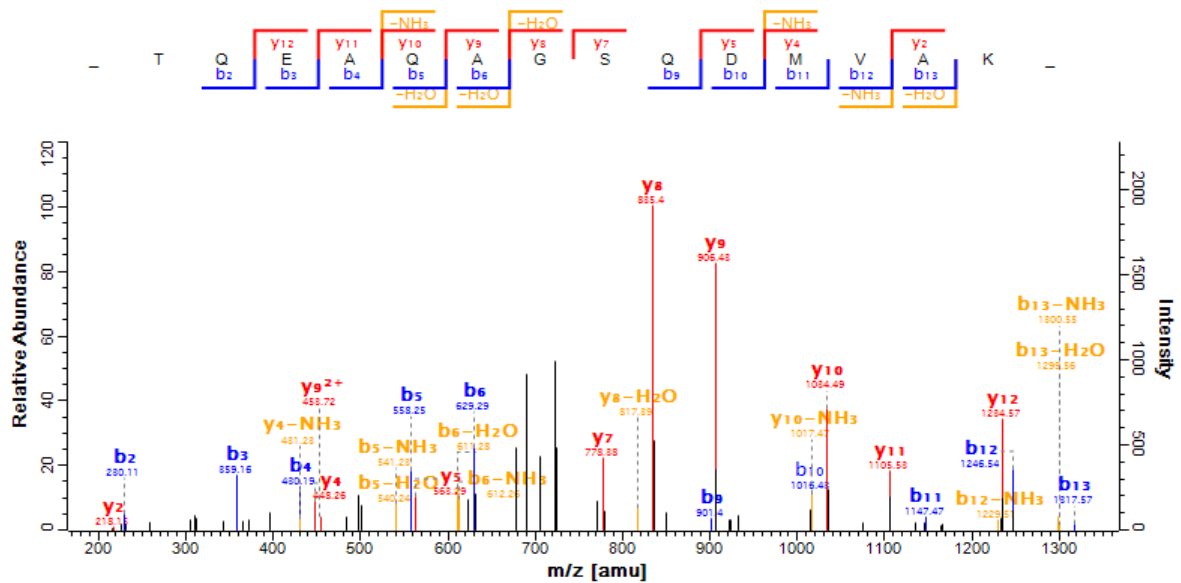
Number of Replicates (out of 8): 6

Best Match Score: 163.64

Best Match Posterior Error Probability: 1.03E-09

Best Match Spectrum:

Scan number 8360 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** AMOTL2



Protein Group ID: 5230

Protein Accession Numbers: Q9Y2L9-3; Q9Y2L9; Q9Y2L9-2

Gene Names: LRCH1

Peptide Sequence: NLESIDPQFTIR

Total Number of Spectra: 2

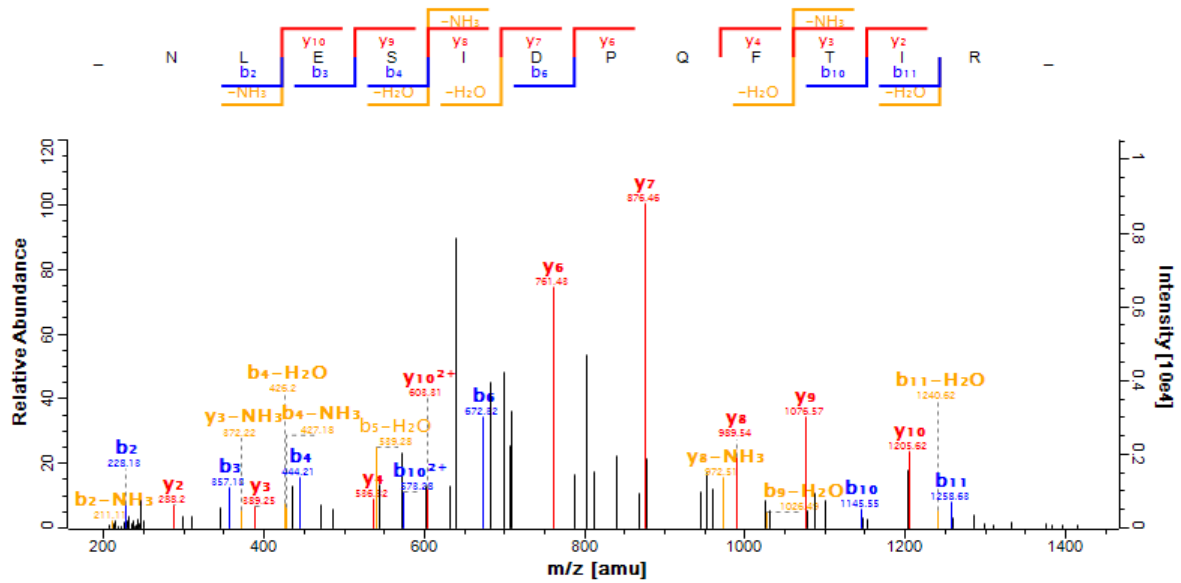
Number of Replicates (out of 8): 2

Best Match Score: 117.03

Best Match Posterior Error Probability: 0.0001701

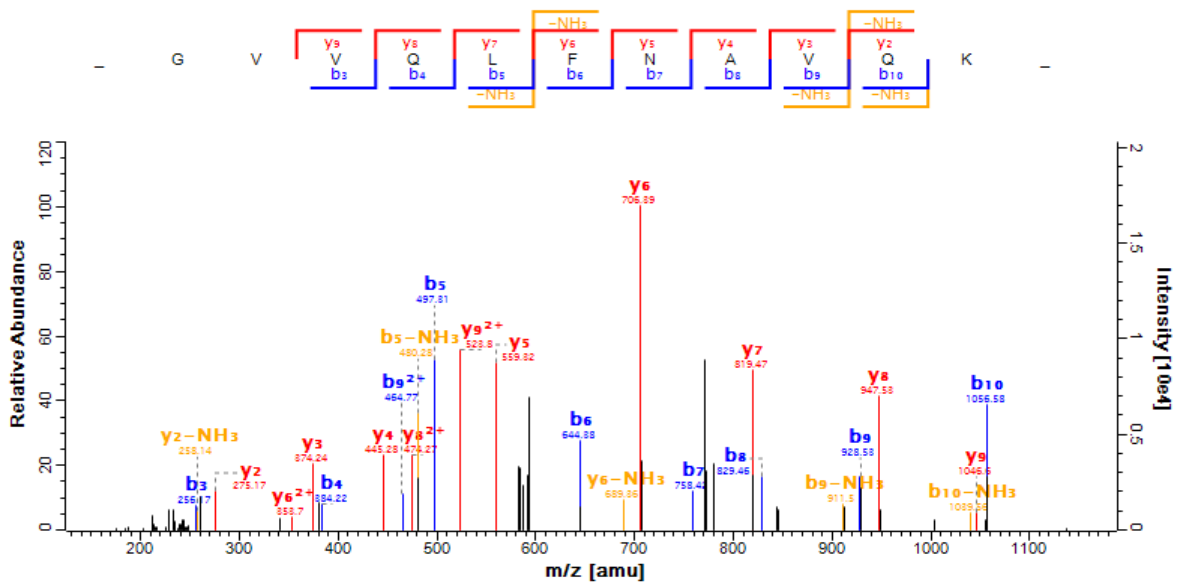
Best Match Spectrum:

Scan number	53849	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	LRCH1



Protein Group ID: 5264
Protein Accession Numbers: Q9Y3B9
Gene Names: RRP15
Peptide Sequence: GVVQLFNAVQK
Total Number of Spectra: 7
Number of Replicates (out of 8): 7
Best Match Score: 185.61
Best Match Posterior Error Probability: 4.37E-10
Best Match Spectrum:

Scan number 50417 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** RRP15



Protein Group ID: 5270

Protein Accession Numbers: Q9Y3D2

Gene Names: MSRB2

Peptide Sequence: GQAGGGGPGTGPGLGEAGSLATCELPLAK

Total Number of Spectra: 3

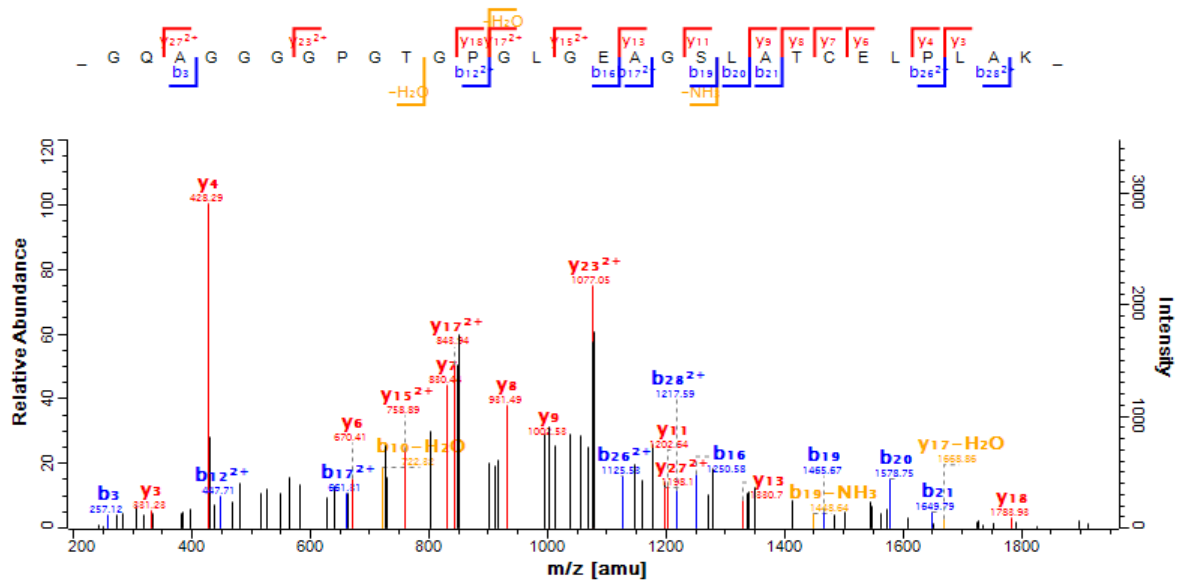
Number of Replicates (out of 8): 3

Best Match Score: 63.893

Best Match Posterior Error Probability: 0.00010306

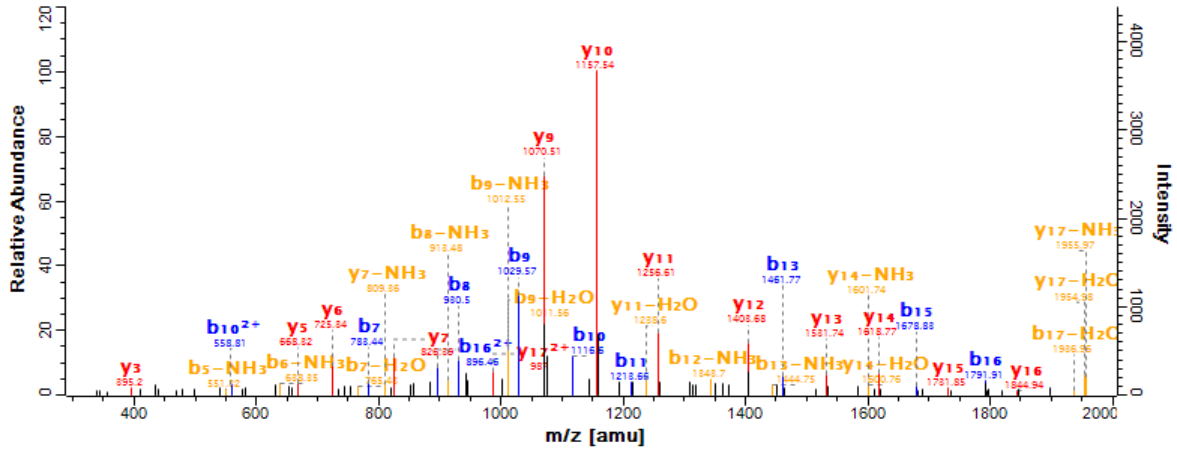
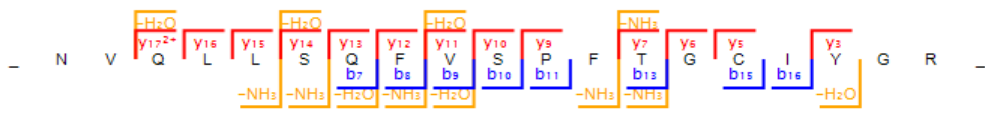
Best Match Spectrum:

Scan number 58996 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MSRB2



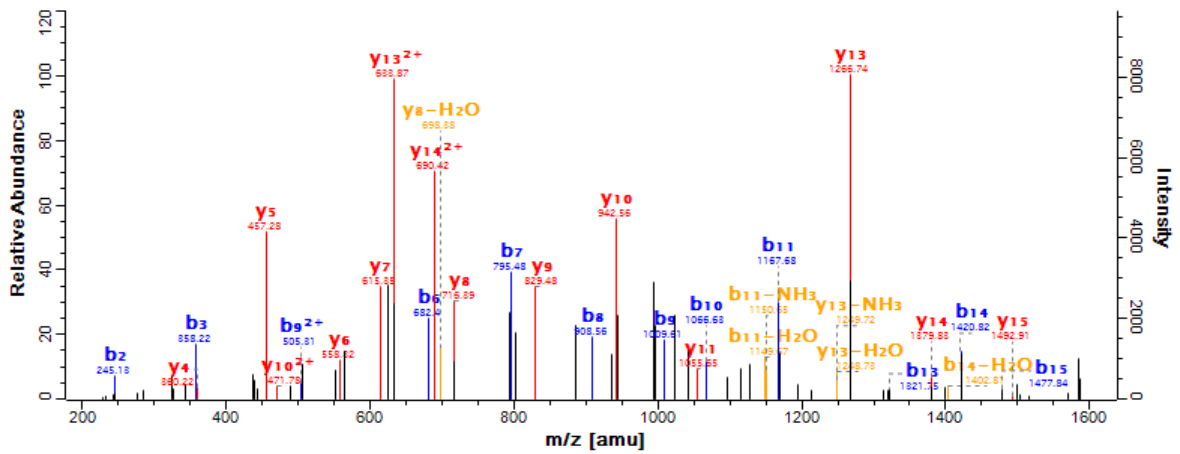
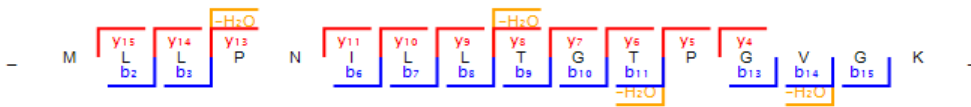
Protein Group ID: 5272
Protein Accession Numbers: Q9Y3D5
Gene Names: MRPS18C
Peptide Sequence: NVQLLSQFVSPFTGCIYGR
Total Number of Spectra: 18
Number of Replicates (out of 8): 8
Best Match Score: 187.39
Best Match Posterior Error Probability: 2.14E-23
Best Match Spectrum:

Scan number 84928 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** MRPS18C



Protein Group ID: 5274
Protein Accession Numbers: Q9Y3D8
Gene Names: TAF9
Peptide Sequence: MLLPNILLTGTPGVGK
Total Number of Spectra: 10
Number of Replicates (out of 8): 8
Best Match Score: 170.78
Best Match Posterior Error Probability: 4.68E-14
Best Match Spectrum:

Scan number 76968 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TAF9



Protein Group ID: 5276

Protein Accession Numbers: Q9Y3E1; H3BTV7; H3BPM9

Gene Names: HDGFRP3

Peptide Sequence: GFNEGLWEINNPVG

Total Number of Spectra: 1

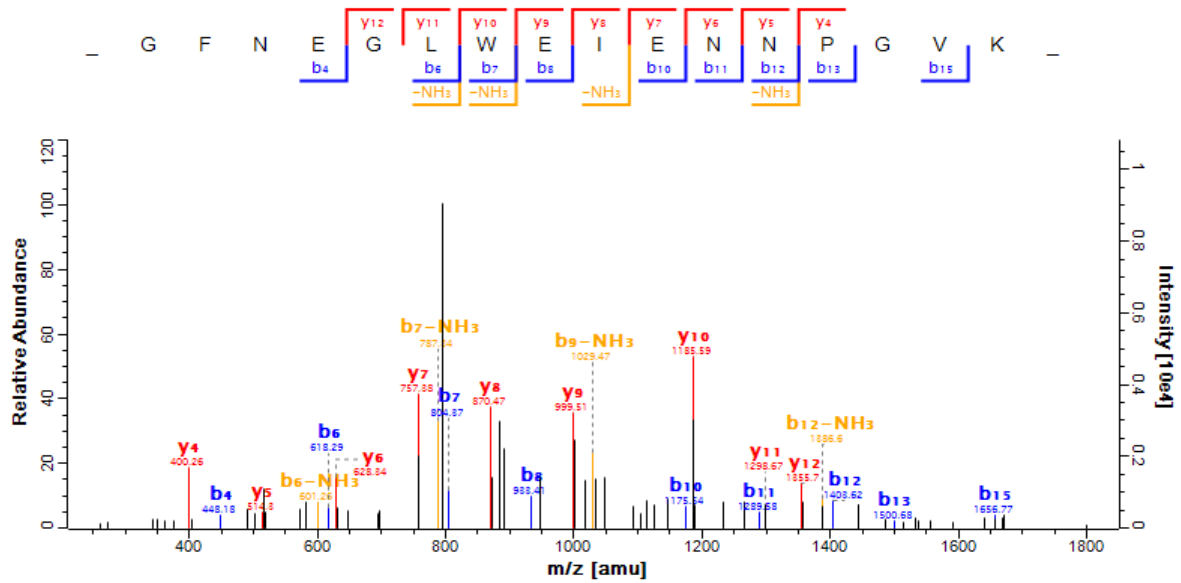
Number of Replicates (out of 8): 1

Best Match Score: 83.758

Best Match Posterior Error Probability: 0.0013463

Best Match Spectrum:

Scan number	57352	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	HDGFRP3



Protein Group ID: 5280

Protein Accession Numbers: Q9Y3I1; Q9Y3I1-2; Q9Y3I1-3

Gene Names: FBX07

Peptide Sequence: FDPVGPLPGNPILPGR

Total Number of Spectra: 4

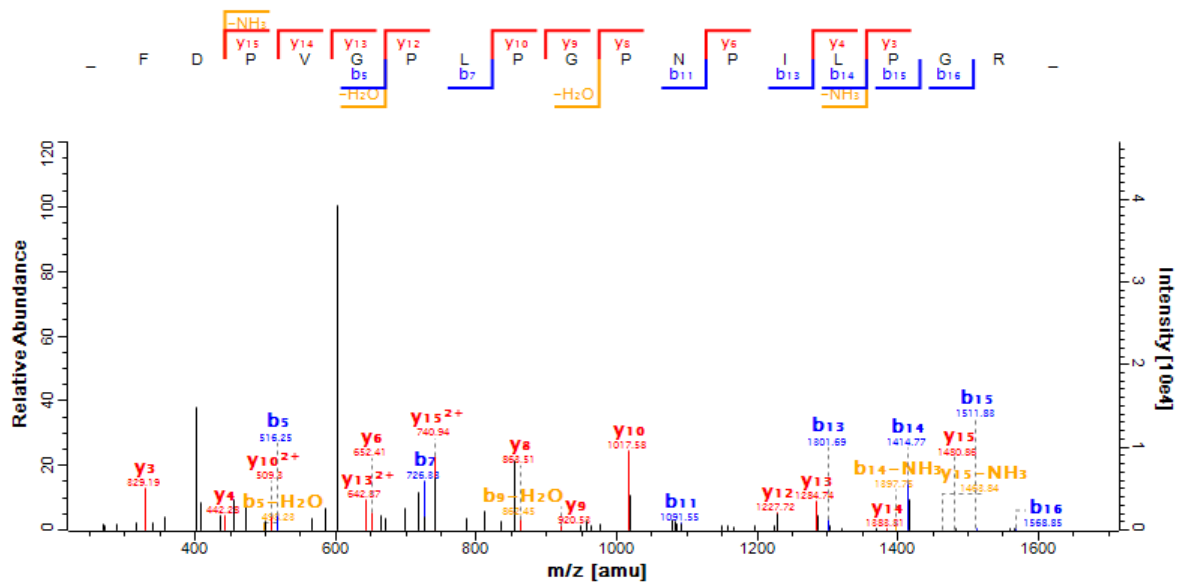
Number of Replicates (out of 8): 4

Best Match Score: 109.07

Best Match Posterior Error Probability: 0.00010596

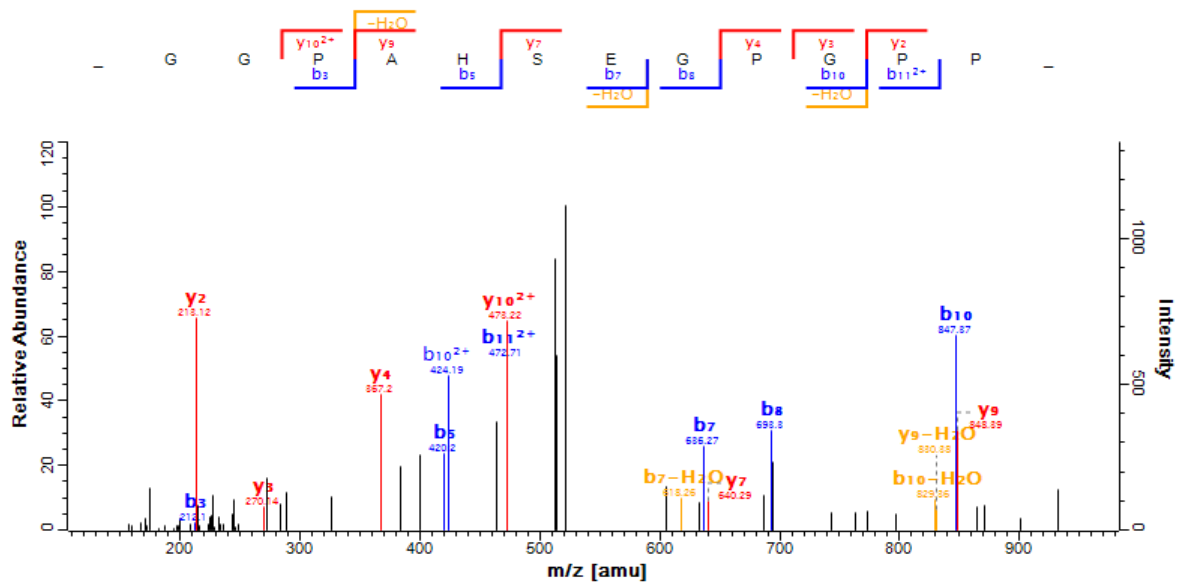
Best Match Spectrum:

Scan number	63859	Raw file	A549-US-WT-top20CID-Elite-2ug-B11
Method	ITMS; CID	Genenames	FBX07



Protein Group ID: 5282
Protein Accession Numbers: Q9Y3P4
Gene Names: RHBDD3
Peptide Sequence: GGPAHSEGPGPP
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 85.29
Best Match Posterior Error Probability: 0.0021588
Best Match Spectrum:

Scan number	6484	Raw file	A549-US-WT-top20CID-Elite-2ug-B14
Method	ITMS; CID	Genenames	RHBDD3



Protein Group ID: 5291

Protein Accession Numbers: Q9Y448; Q9Y448-2

Gene Names: SKAP

Peptide Sequence: QESTTDHMDSMMLLETLQEELK

Total Number of Spectra: 1

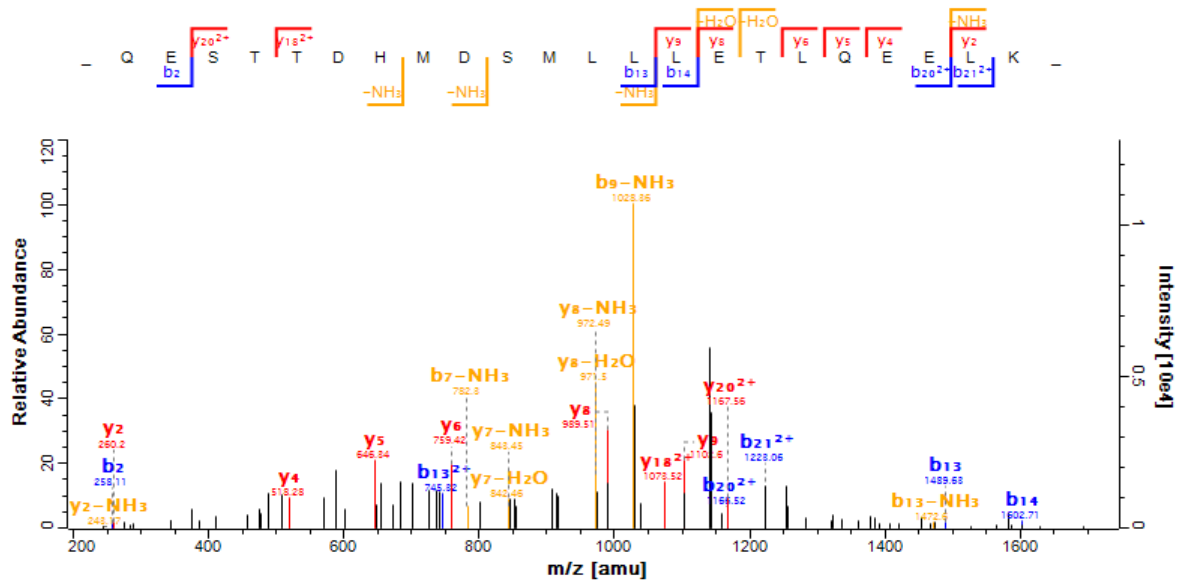
Number of Replicates (out of 8): 1

Best Match Score: 61.942

Best Match Posterior Error Probability: 0.0026576

Best Match Spectrum:

Scan number	84824	Raw file	A549-US-Mock-top20CID-Elite-2ug-B13
Method	ITMS; CID	Genenames	SKAP



Protein Group ID: 5300

Protein Accession Numbers: Q9Y4H2

Gene Names: IRS2

Peptide Sequence: AAAAAAAAAVPSAGPAGPAP TSAAGR

Total Number of Spectra: 1

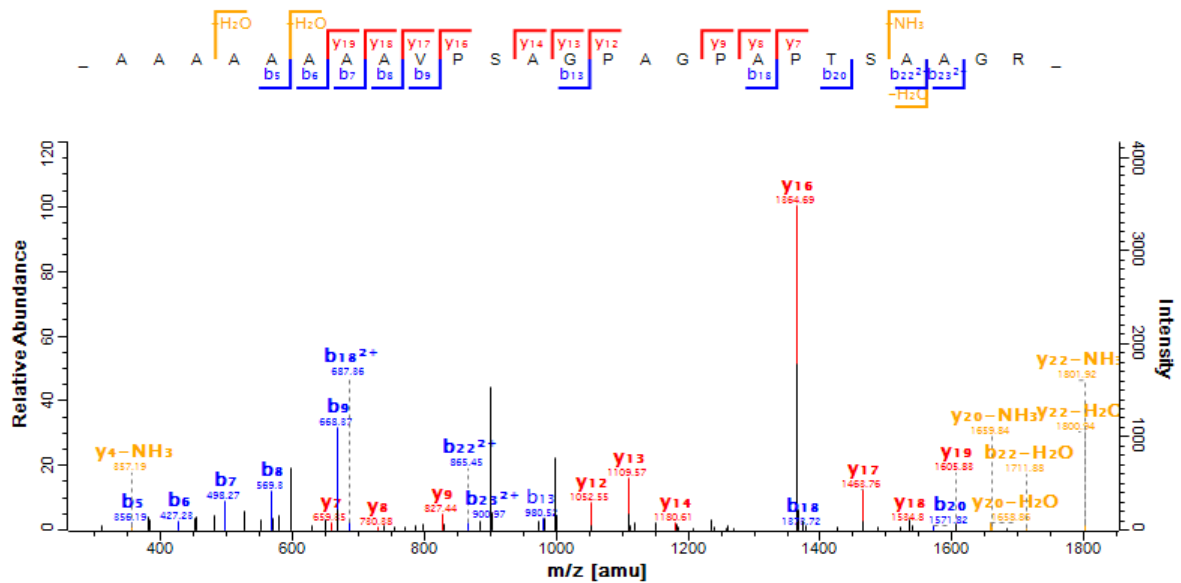
Number of Replicates (out of 8): 1

Best Match Score: 67.88

Best Match Posterior Error Probability: 0.00048812

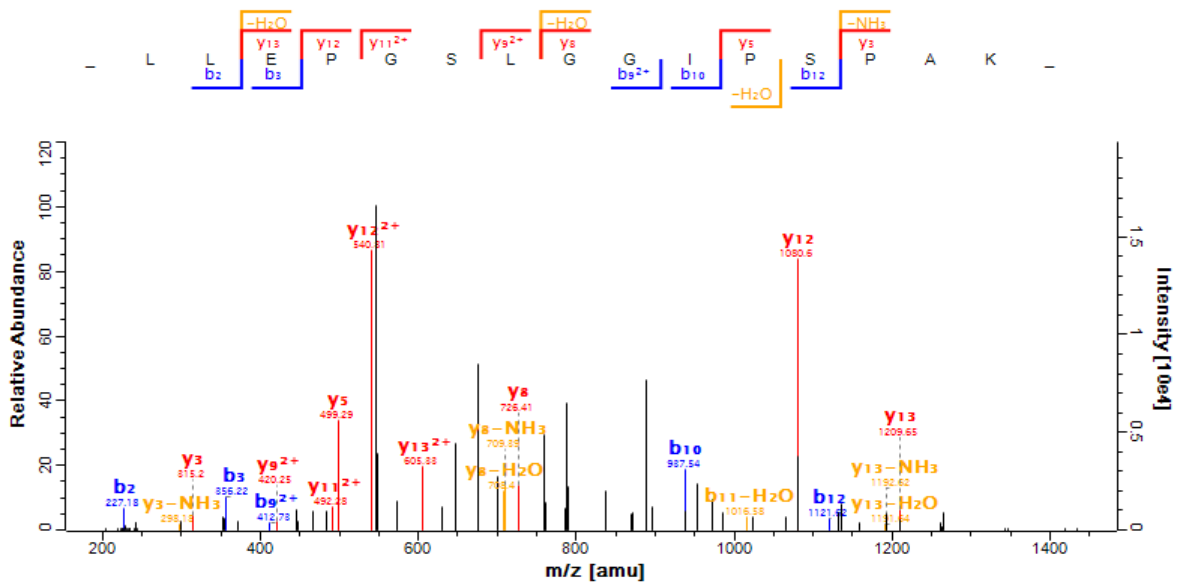
Best Match Spectrum:

Scan number 26169 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** IRS2



Protein Group ID: 5312
Protein Accession Numbers: Q9Y584
Gene Names: TIMM22
Peptide Sequence: LLEPGSLGGIPSPAK
Total Number of Spectra: 7
Number of Replicates (out of 8): 7
Best Match Score: 92.295
Best Match Posterior Error Probability: 0.00066259
Best Match Spectrum:

Scan number 48342 **Raw file** A549-US-WT-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** TIMM22



Protein Group ID: 5313

Protein Accession Numbers: Q9Y597; Q9Y597-2; Q9Y597-3

Gene Names: KCTD3

Peptide Sequence: GATGECNISR

Total Number of Spectra: 2

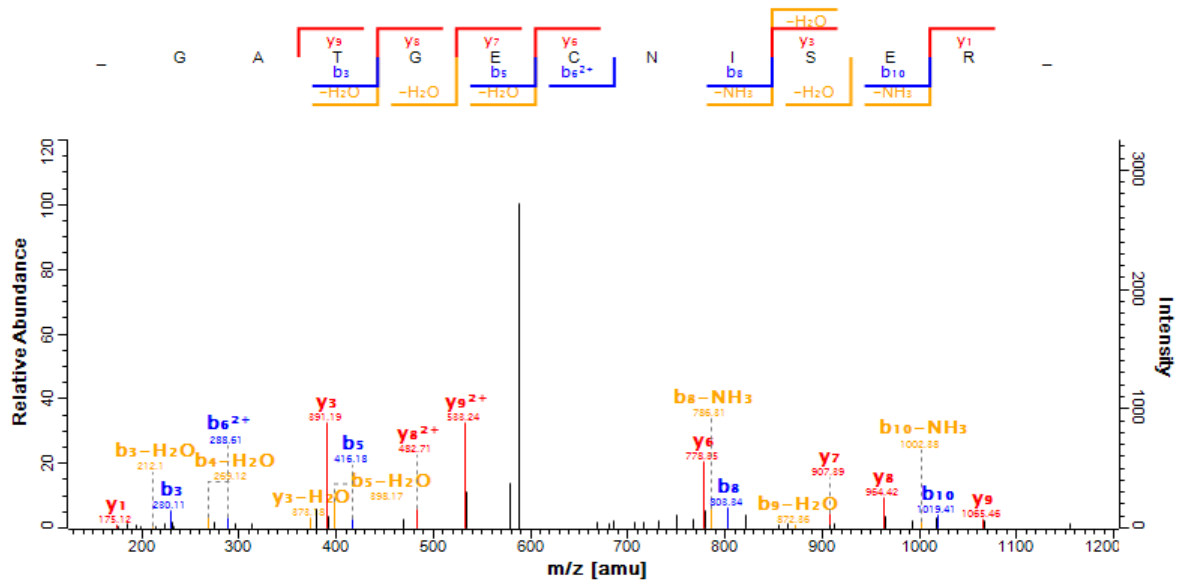
Number of Replicates (out of 8): 2

Best Match Score: 90.913

Best Match Posterior Error Probability: 0.0013828

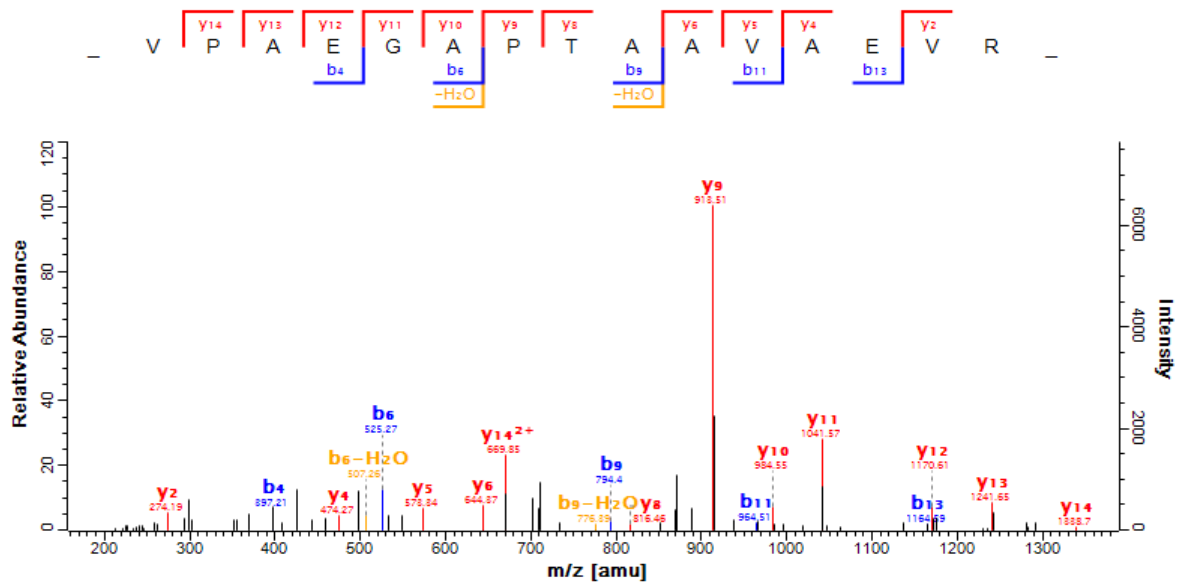
Best Match Spectrum:

Scan number 4693 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** KCTD3



Protein Group ID: 5315
Protein Accession Numbers: Q9Y5B0; Q9Y5B0-4
Gene Names: CTDPI
Peptide Sequence: VPAEGAPTAAVAEVR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 94.487
Best Match Posterior Error Probability: 0.00051249
Best Match Spectrum:

Scan number 28196 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CTDPI



Protein Group ID: 5316

Protein Accession Numbers: Q9Y5B6; Q9Y5B6-2; Q9Y5B6-4; Q9Y5B6-3

Gene Names: GCFC1

Peptide Sequence: TGGAFSNALSSLNVLRLPGELIPDAAFIHAAR

Total Number of Spectra: 1

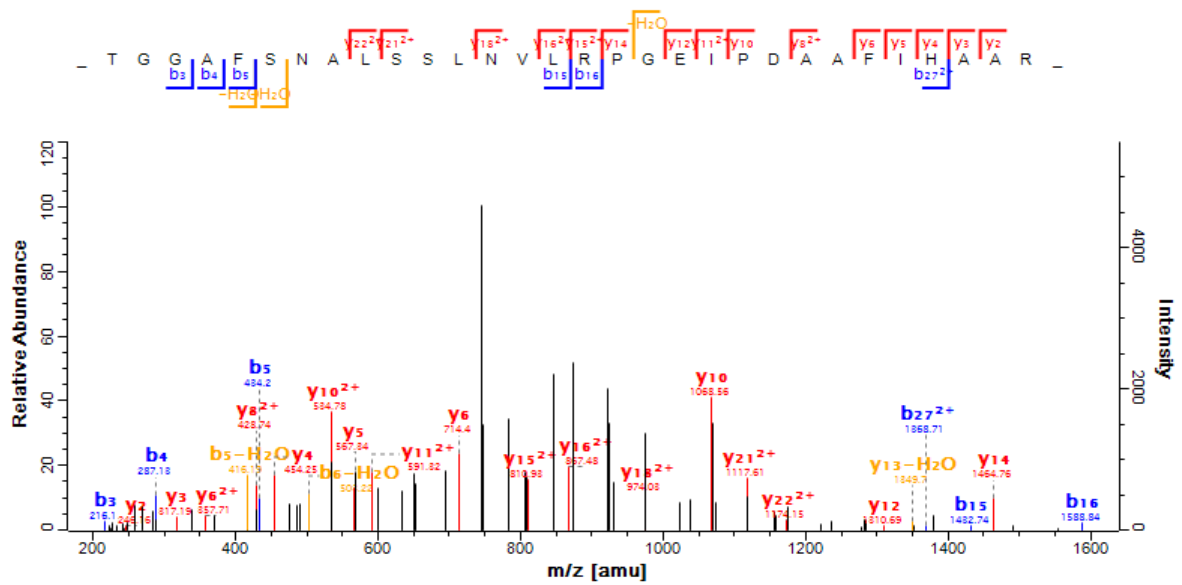
Number of Replicates (out of 8): 1

Best Match Score: 66.372

Best Match Posterior Error Probability: 0.0002344

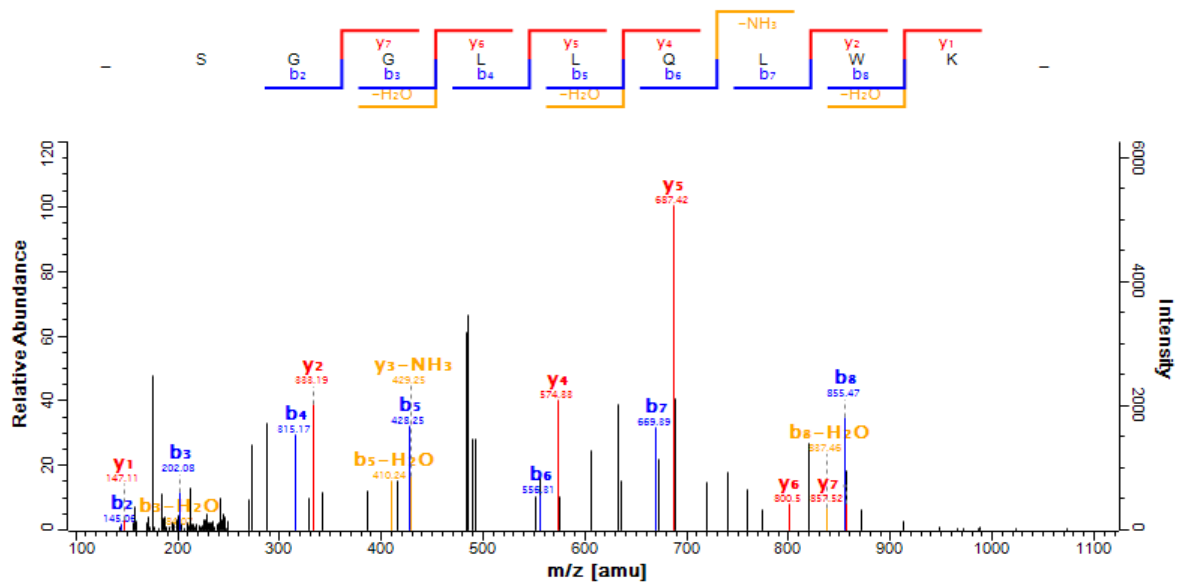
Best Match Spectrum:

Scan number 81417 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** GCFC1



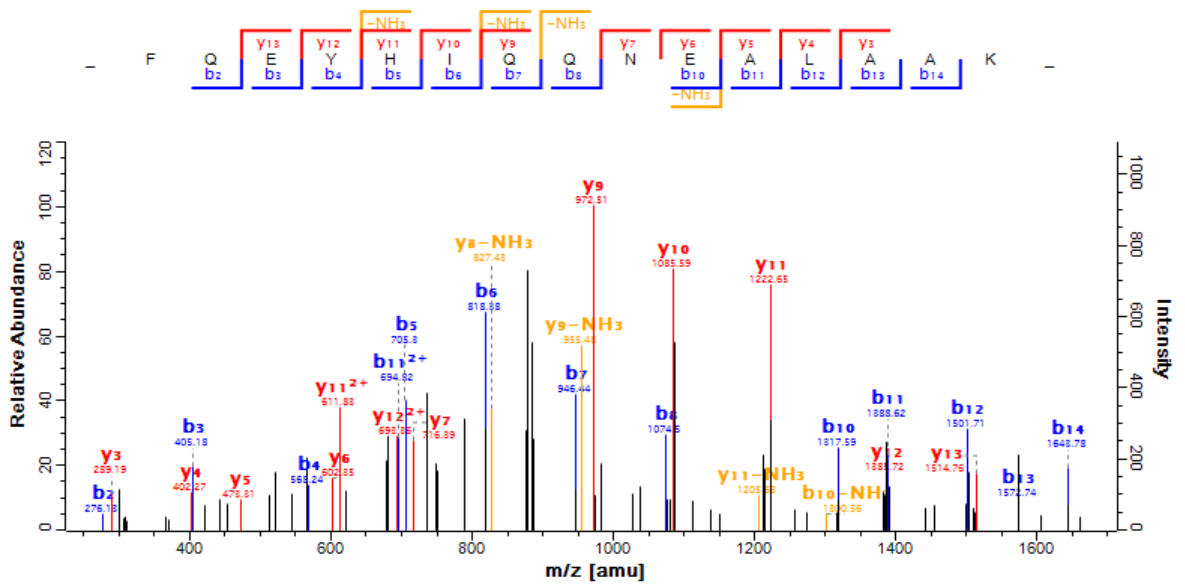
Protein Group ID: 5319
Protein Accession Numbers: Q9Y5J5
Gene Names: PHLDA3
Peptide Sequence: SGGLQLWK
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 88.495
Best Match Posterior Error Probability: 0.0039179
Best Match Spectrum:

Scan number	59752	Raw file	A549-US-Mock-top20CID-Elite-2ug-B12
Method	ITMS; CID	Genenames	PHLDA3



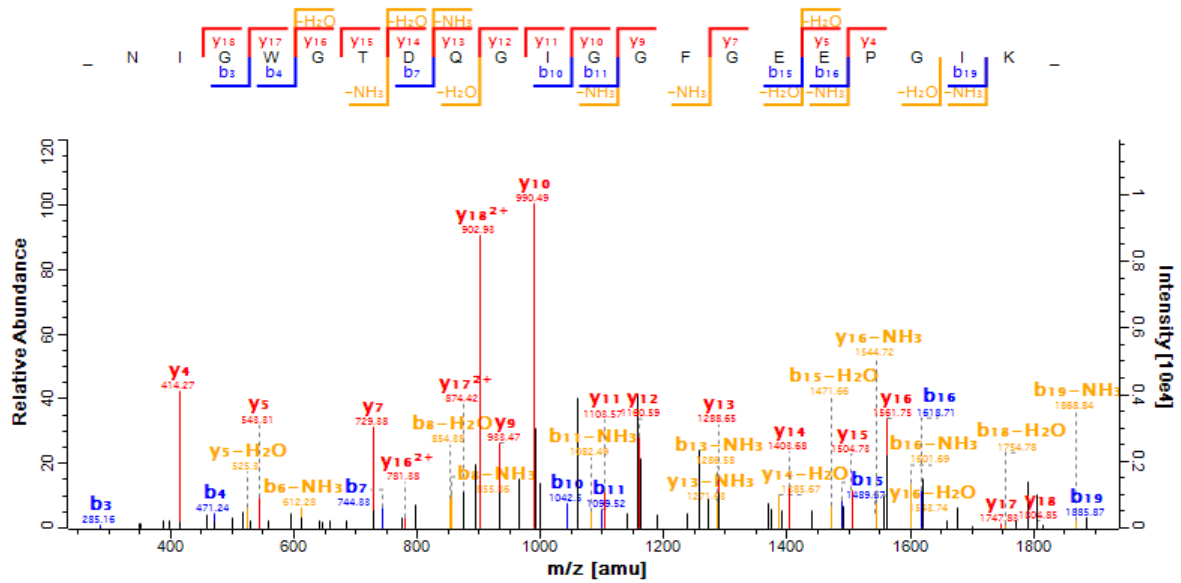
Protein Group ID: 5320
Protein Accession Numbers: Q9Y5J7
Gene Names: TIMM9
Peptide Sequence: FQEYHIQQNEALAAK
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 132.51
Best Match Posterior Error Probability: 3.01E-05
Best Match Spectrum:

Scan number 29432 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** TIMM9



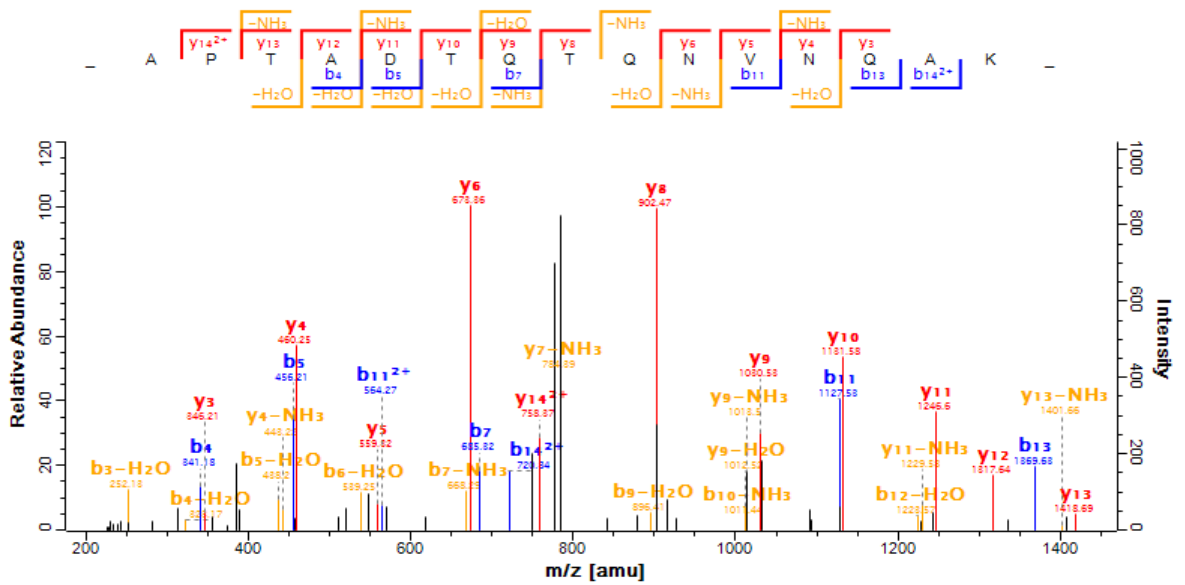
Protein Group ID: 5332
Protein Accession Numbers: Q9Y5U9
Gene Names: IER3IP1
Peptide Sequence: NIGWGTDQGIGGGFGEEPGIK
Total Number of Spectra: 3
Number of Replicates (out of 8): 3
Best Match Score: 162.42
Best Match Posterior Error Probability: 6.77E-12
Best Match Spectrum:

Scan number 59493 **Raw file** A549-US-WT-top20CID-Elite-2ug-B14
Method ITMS; CID **Genenames** IER3IP1



Protein Group ID: 5333
Protein Accession Numbers: Q9Y5V3-2; Q9Y5V3
Gene Names: MAGED1
Peptide Sequence: APTADTQTQNVNQAK
Total Number of Spectra: 7
Number of Replicates (out of 8): 7
Best Match Score: 157.2
Best Match Posterior Error Probability: 1.96E-09
Best Match Spectrum:

Scan number 4590 **Raw file** A549-US-WT-top20CID-Elite-2ug-B11
Method ITMS; CID **Genenames** MAGED1



Protein Group ID: 5335

Protein Accession Numbers: Q9Y5X2

Gene Names: SNX8

Peptide Sequence: ELSAIGSDTTPLPSWAALNSSTWGLK

Total Number of Spectra: 1

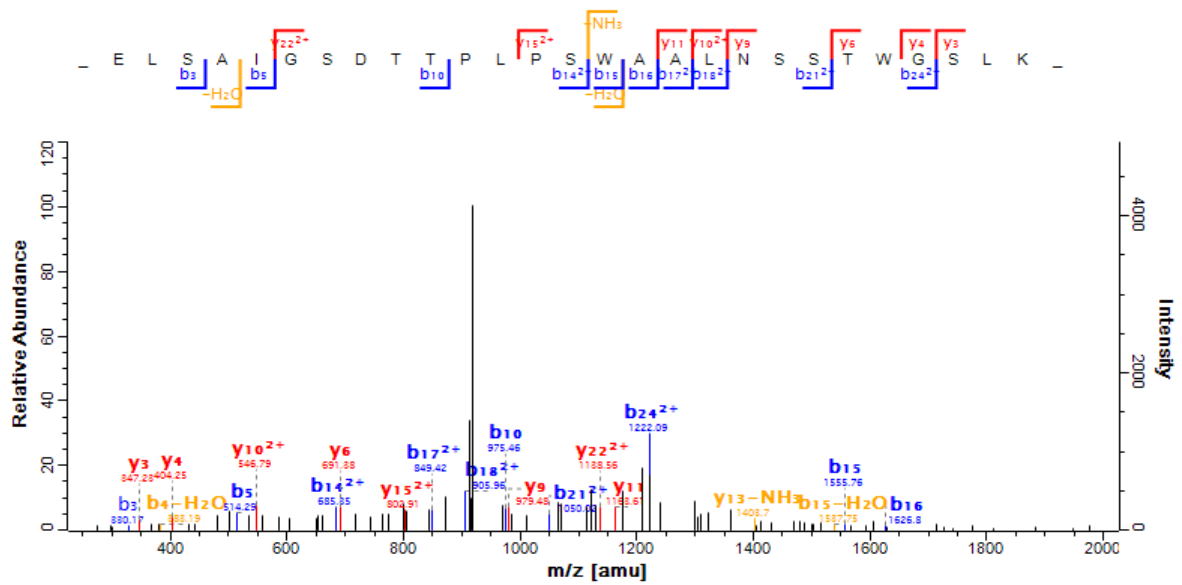
Number of Replicates (out of 8): 1

Best Match Score: 57.802

Best Match Posterior Error Probability: 0.001323

Best Match Spectrum:

Scan number 84265 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** SNX8



Protein Group ID: 5341
Protein Accession Numbers: Q9Y619
Gene Names: SLC25A15
Peptide Sequence: LQTMYESGK
Total Number of Spectra: 5
Number of Replicates (out of 8): 5
Best Match Score: 113.61
Best Match Posterior Error Probability: 0.00021508
Best Match Spectrum:

Scan number 28630 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** SLC25A15

