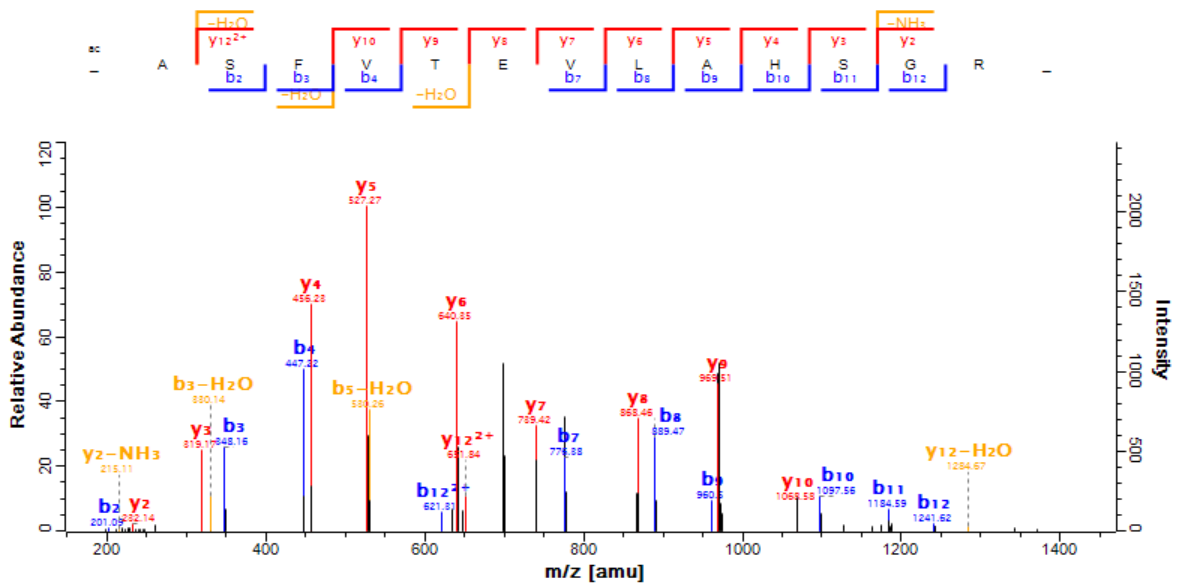


Supplemental Fig. 4. Annotated spectra for single peptide identifications in the in-solution protein IEF workflow in addition to those presented in supplemental Fig. 2. Where multiple spectra match the peptide sequence, the annotated spectrum corresponding to the best match is reported.

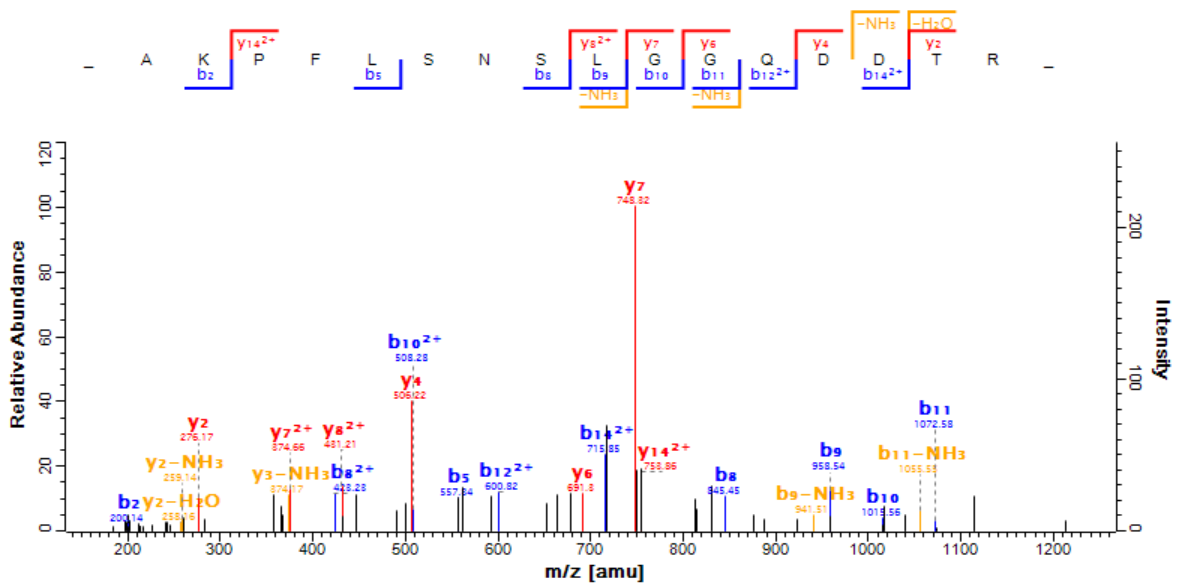
Protein Group ID: 4
Protein Accession Numbers: O43264; A1A528; F5H3C1
Gene Names: ZW10
Peptide Sequence: ASFVTEVLAHSGR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 113.35
Best Match Posterior Error Probability: 0.00016785
Best Match Spectrum:

Scan number 6789 **Raw file** Prt-OGE-Batch2-Mock-Frac12
Method ITMS; CID **Genenames** ZW10



Protein Group ID: 5
Protein Accession Numbers: A1X283
Gene Names: SH3PXD2B
Peptide Sequence: AKPFLNSLGGQDDTR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 87.447
Best Match Posterior Error Probability: 0.0016358
Best Match Spectrum:

Scan number 1418 **Raw file** Prt-OGE-Batch3--Mock-Frac19
Method ITMS; CID **Genenames** SH3PXD2B



Protein Group ID: 18

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

Gene Names: TSSC4

Peptide Sequence: VPPVPDYVAHPER

Total Number of Spectra: 1

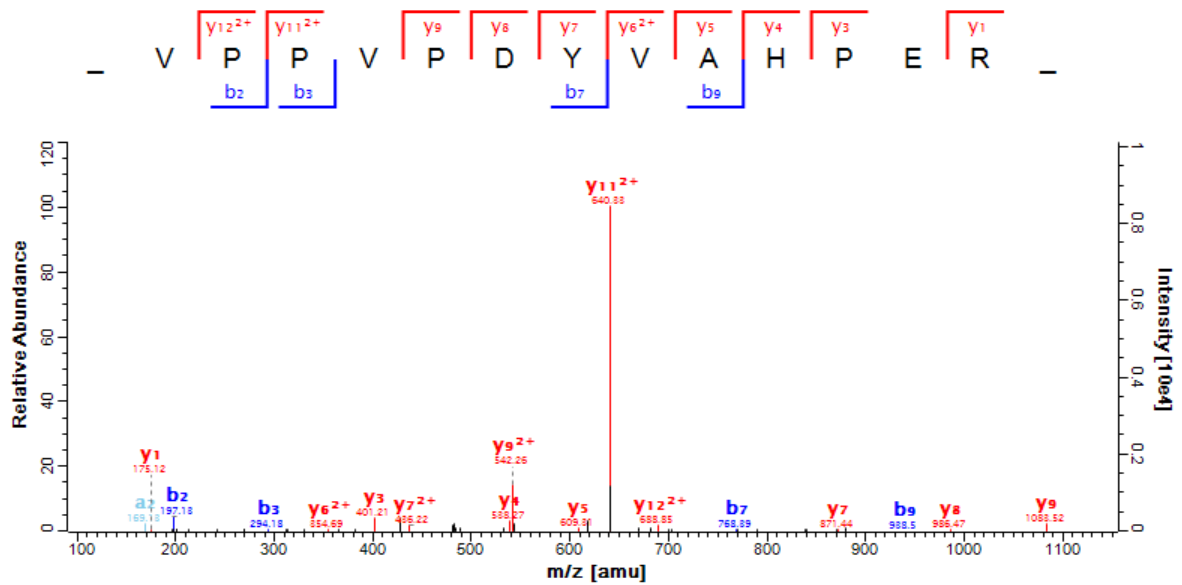
Number of Replicates (out of 10): 1

Best Match Score: 84.169

Best Match Posterior Error Probability: 0.0015703

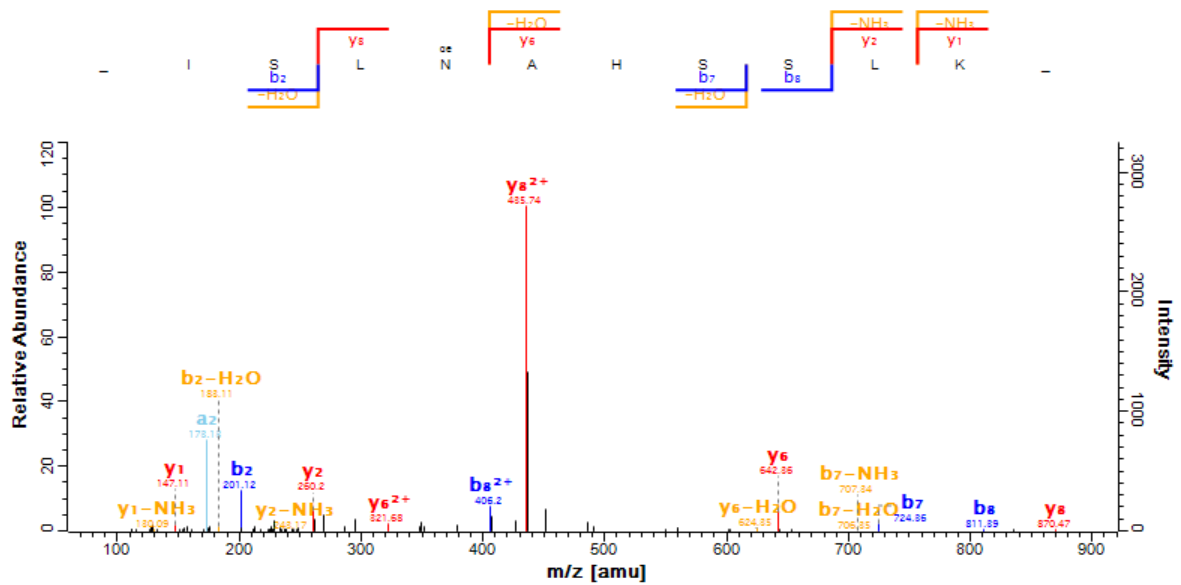
Best Match Spectrum:

Scan number	2817	Raw file	Prt-OGE-Batch3--Mock-Frac7
Method	ITMS; CID	Genenames	TSSC4



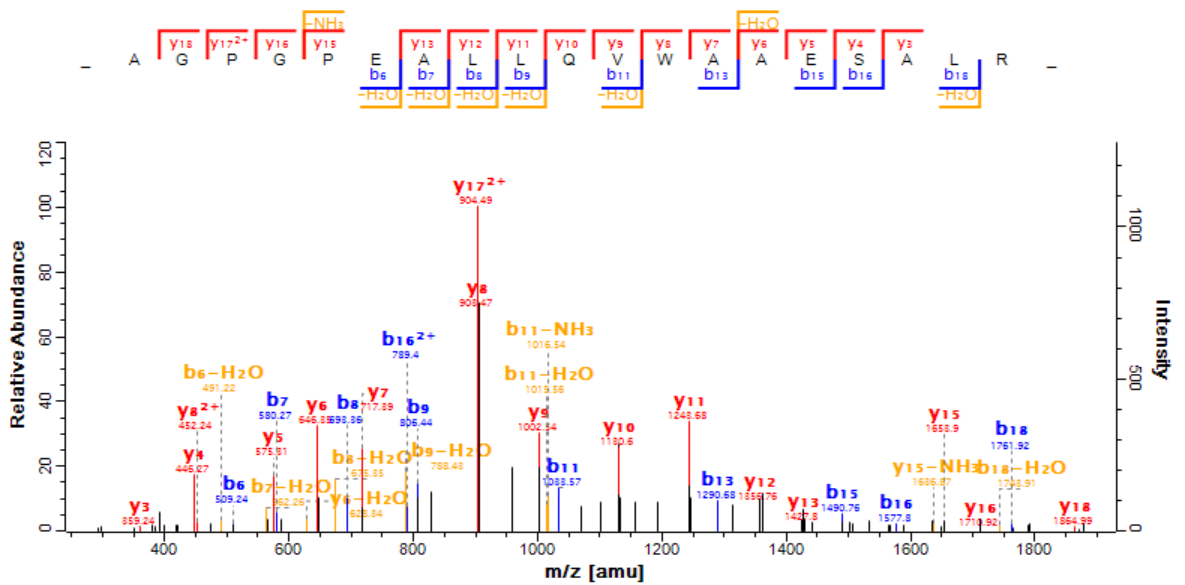
Protein Group ID: 23
Protein Accession Numbers: A6NDK8
Gene Names: FAM35B
Peptide Sequence: ISLNAHSSLK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 118.18
Best Match Posterior Error Probability: 0.0016756
Best Match Spectrum:

Scan number 2067 **Raw file** Prt-OGE-Batch2-Mock-Frac11
Method ITMS; CID **Genenames** FAM35B



Protein Group ID: 26
Protein Accession Numbers: A6NED2; G3V2I3
Gene Names: RCCD1
Peptide Sequence: AGPGPEALLQVWAAESALR
Total Number of Spectra: 7
Number of Replicates (out of 10): 5
Best Match Score: 174.65
Best Match Posterior Error Probability: 2.92E-23
Best Match Spectrum:

Scan number 7307 **Raw file** Prt-OGE-Batch2-Mock-Frac7
Method ITMS; CID **Genenames** RCCD1



Protein Group ID: 31

Protein Accession Numbers: P05026; P05026-2; A6NGH2; B7Z9S8

Gene Names: ATP1B1

Peptide Sequence: SYEAYVLNIVR

Total Number of Spectra: 1

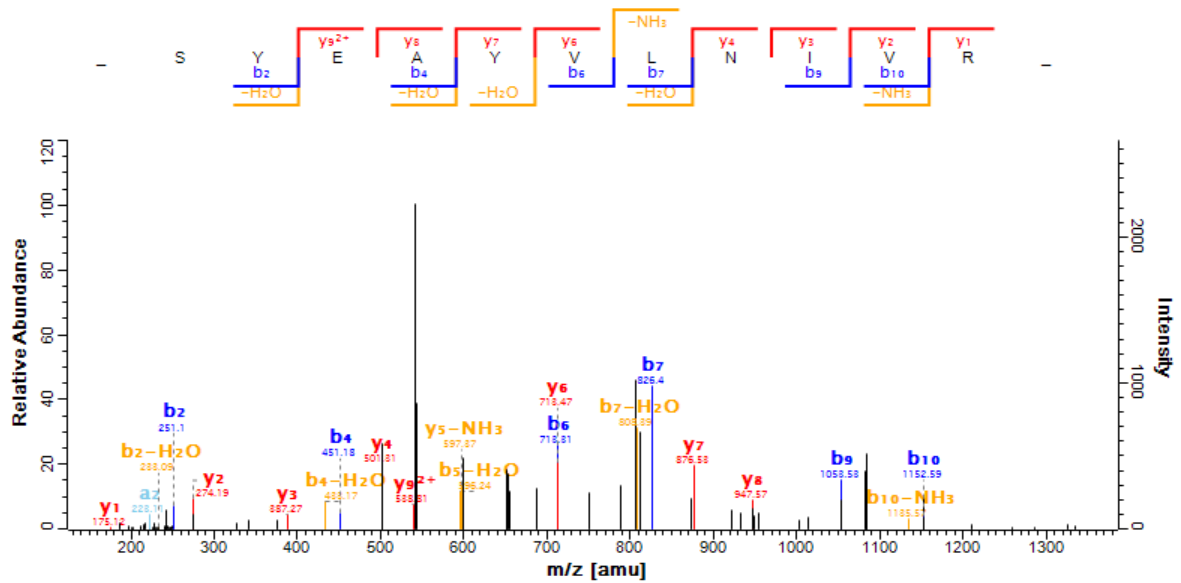
Number of Replicates (out of 10): 1

Best Match Score: 106.62

Best Match Posterior Error Probability: 0.00018257

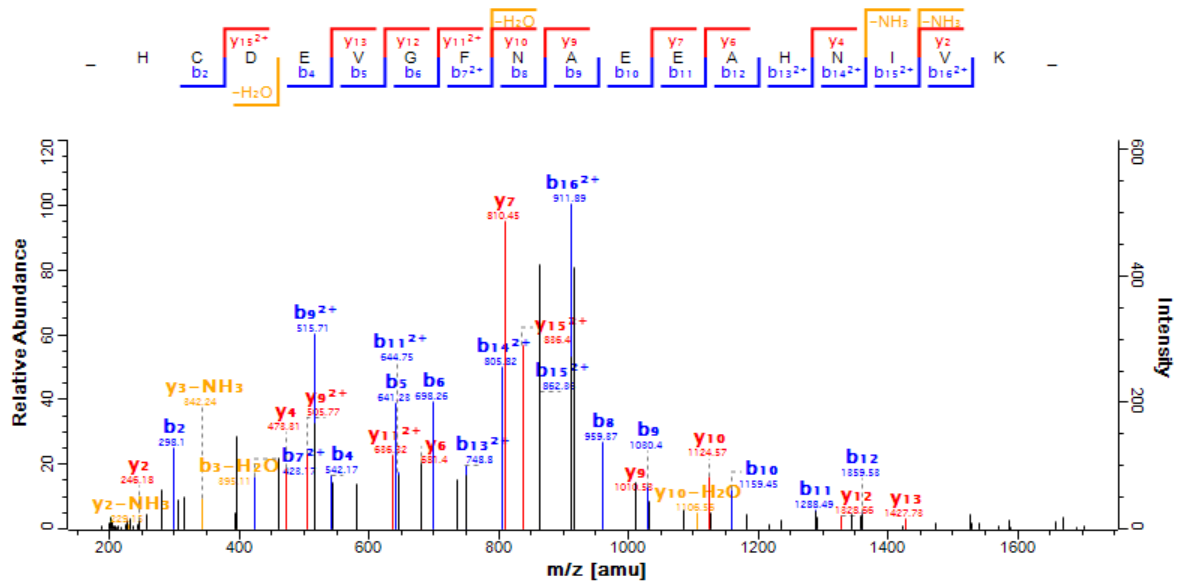
Best Match Spectrum:

Scan number 5035 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac12
Method ITMS; CID **Genenames** ATP1B1



Protein Group ID: 32
Protein Accession Numbers: A6NGJ0; P51808
Gene Names: DYNLT3
Peptide Sequence: HCDEVGFNAEEAHNIVK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 131.72
Best Match Posterior Error Probability: 2.29E-05
Best Match Spectrum:

Scan number 2591 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac7
Method ITMS; CID **Genenames** DYNLT3



Protein Group ID: 34

Protein Accession Numbers: O95825; A6NMA8; A6NHJ8; A6NND8; H7C3I5; B3KQ77; C9JZK8; F8WF64; C9JAL0; C9K0F7; H7C338; H7C3S0

Gene Names: CRYZL1

Peptide Sequence: SVLIMDGASAFGTIAIQLAHR

Total Number of Spectra: 2

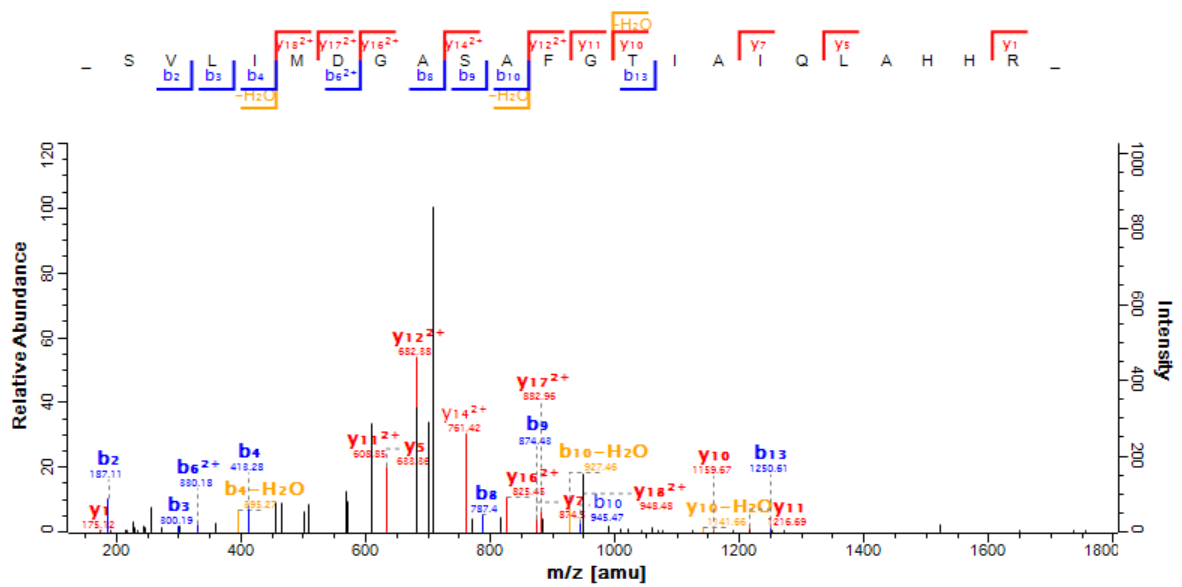
Number of Replicates (out of 10): 2

Best Match Score: 97.32

Best Match Posterior Error Probability: 8.89E-06

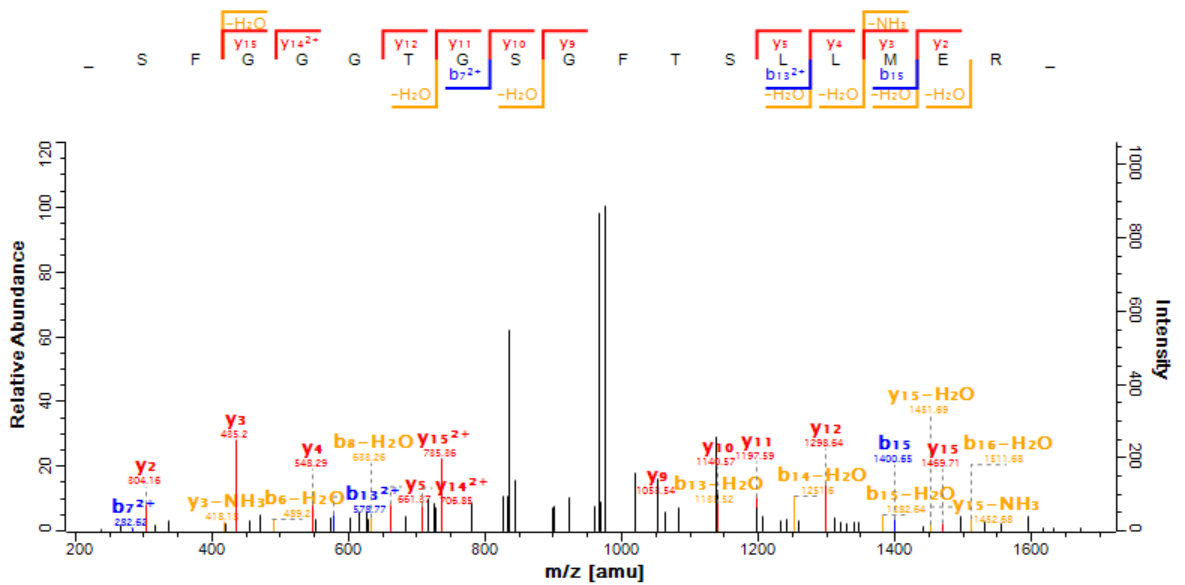
Best Match Spectrum:

Scan number	6469	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac10
Method	ITMS; CID	Genenames	CRYZL1



Protein Group ID: 35
Protein Accession Numbers: A6NHL2; A6NHL2-2
Gene Names: TUBAL3
Peptide Sequence: SFGGGTGS GFTS
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 78.326
Best Match Posterior Error Probability: 0.0013093
Best Match Spectrum:

Scan number 5282 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac11
Method ITMS; CID **Genenames** TUBAL3



Protein Group ID: 41

Protein Accession Numbers: A6NIZ1; P61224; P62834; P61224-3; P61224-4; P61224-2; F5GZG1; B7ZB78; F5H823

Gene Names: RAP1B;RAP1A

Peptide Sequence: INVNEIFYDLVR

Total Number of Spectra: 52

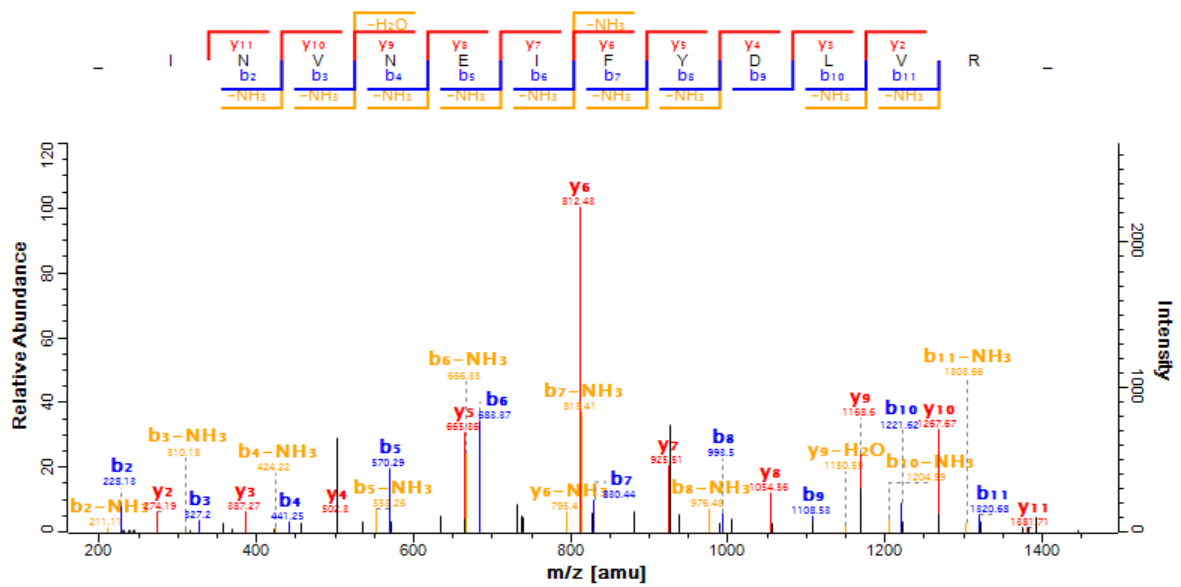
Number of Replicates (out of 10): 10

Best Match Score: 213.82

Best Match Posterior Error Probability: 8.36E-32

Best Match Spectrum:

Scan number	7087	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac14
Method	ITMS; CID	Genenames	RAP1B;RAP1A



Protein Group ID: 42

Protein Accession Numbers: P22310; P35503; P35504; P22309; P19224; O60656; Q9HAW7; Q9HAW8; Q9HAW9; B8K288; A6NJC3; Q7Z6H8; A6NKK6; B5MCT4

Gene Names:

UGT1A4;UGT1A3;UGT1A5;UGT1A1;UGT1A6;UGT1A9;UGT1A7;UGT1A10;UGT1A8;UGT1A4S

Peptide Sequence: GAGVTLNVLEMTS

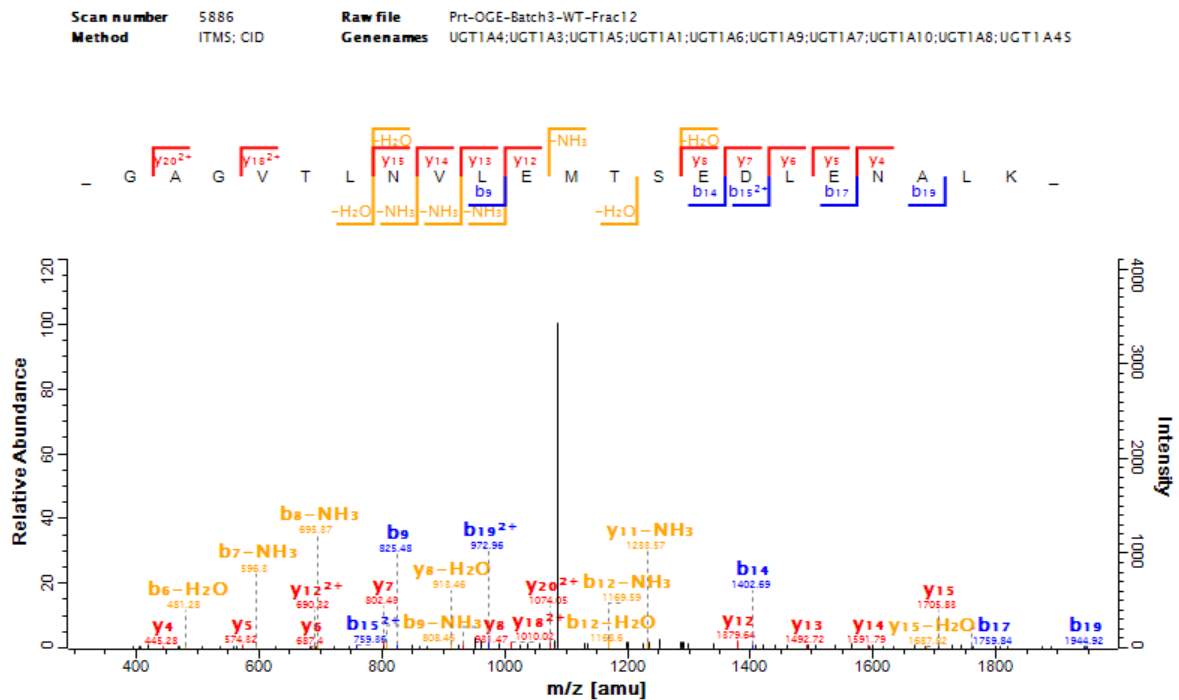
Total Number of Spectra: 1

Number of Replicates (out of 10): 1

Best Match Score: 67.579

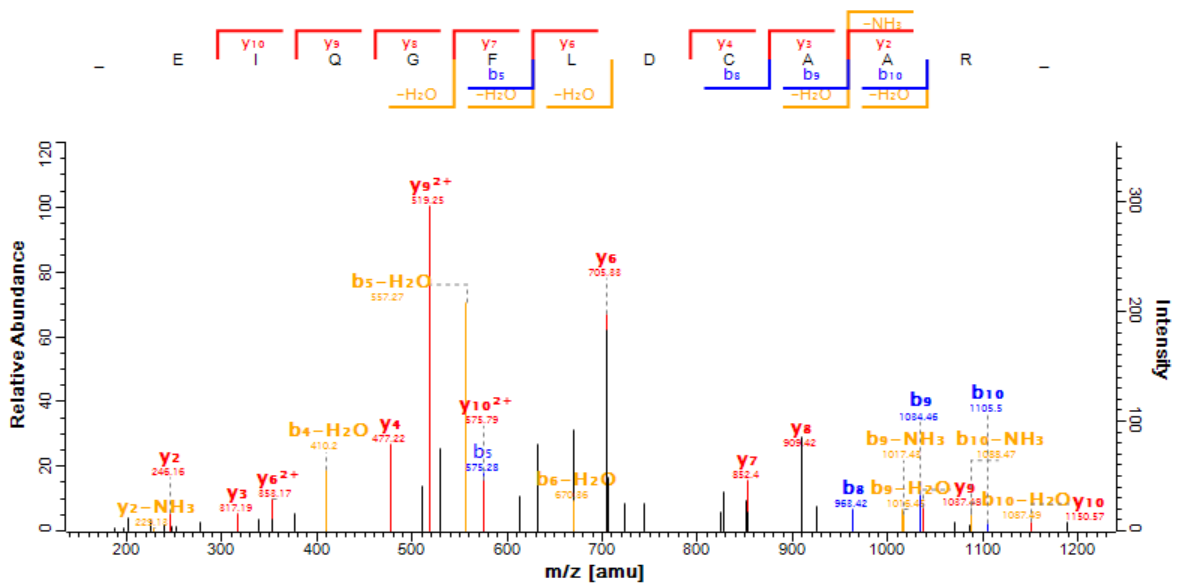
Best Match Posterior Error Probability: 0.0016236

Best Match Spectrum:



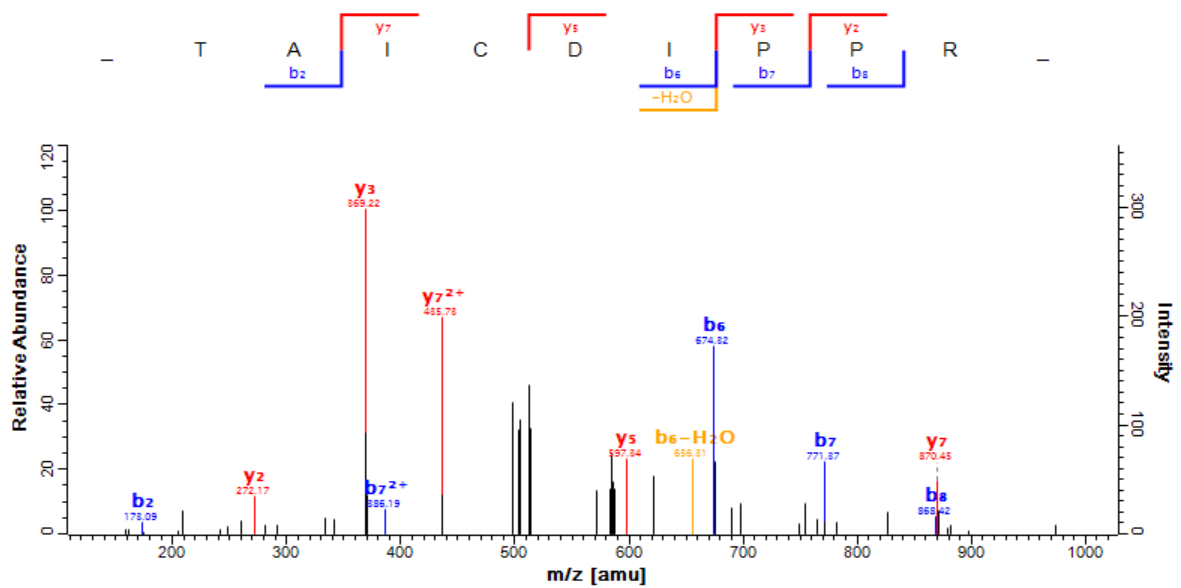
Protein Group ID: 43
Protein Accession Numbers: Q96BP2; A6NJX6
Gene Names: CHCHD1
Peptide Sequence: EIQGFLDCAAR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 134.13
Best Match Posterior Error Probability: 3.20E-05
Best Match Spectrum:

Scan number 2574 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac21
Method ITMS; CID **Genenames** CHCHD1



Protein Group ID: 45
Protein Accession Numbers: A6NKZ8
Gene Names:
Peptide Sequence: TAICDIPPR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 80.239
Best Match Posterior Error Probability: 0.0035877
Best Match Spectrum:

Scan number 1451 **Raw file** Prt-OGE-Batch3-WT-Frac5
Method ITMS; CID **Pepti...** 80.24



Protein Group ID: 46

Protein Accession Numbers: Q4V339; Q5JTY5; Q5RIA9; Q8IUF1; Q9BRT8; B4DNG9; F5H3X4; F8WEG4; Q4V338; Q5JTY2; Q5RIB3; Q9BRT8-2; A6NM15; H0Y857; E9PFE9

Gene Names: CBWD6;CBWD3;CBWD5;CBWD2;CBWD1;CBWD7

Peptide Sequence: VDLSNVLDLHAFDSLSGISLQK

Total Number of Spectra: 5

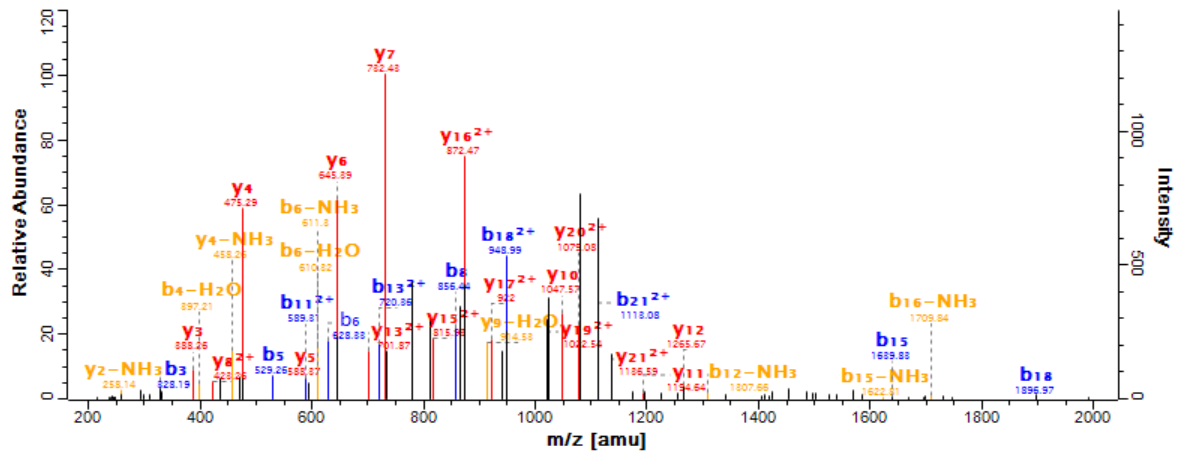
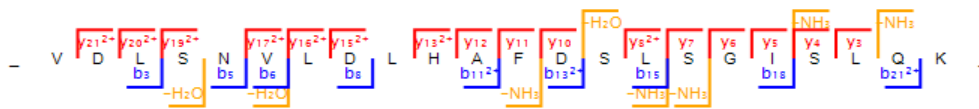
Number of Replicates (out of 10): 5

Best Match Score: 141.6

Best Match Posterior Error Probability: 1.47E-13

Best Match Spectrum:

Scan number 6749 Raw file Prt-OGE-Batch3-Mock-Frac5
Method ITMS: CID Genenames CBWD6;CBWD3;CBWD5;CBWD2;CBWD1;CBWD7



Protein Group ID: 58

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

Gene Names: ATPAF1

Peptide Sequence: YMSVIAELQSGALGK

Total Number of Spectra: 10

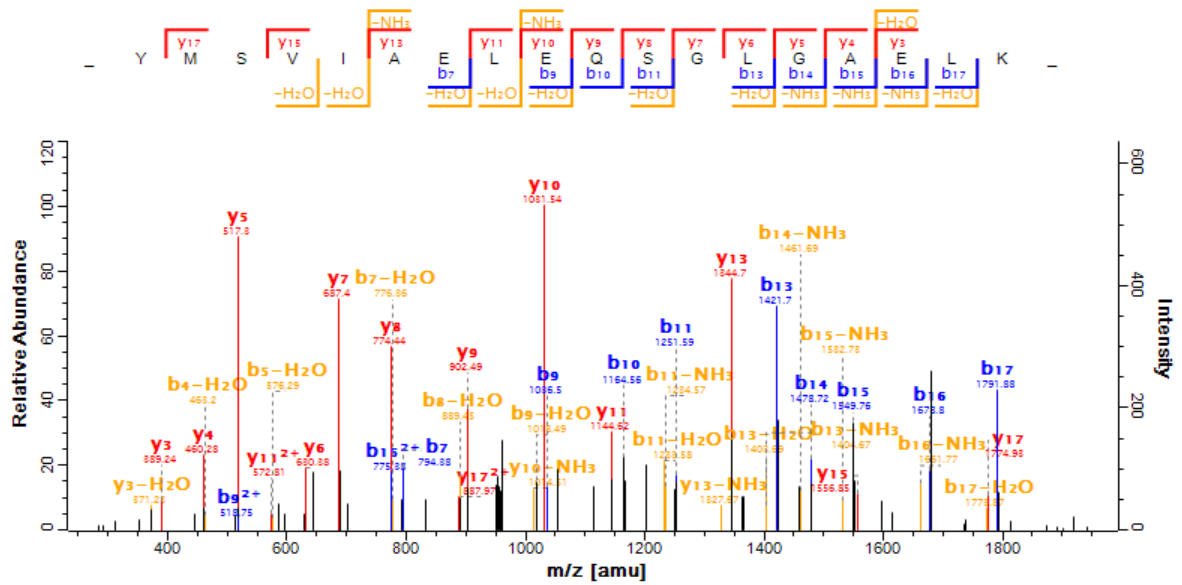
Number of Replicates (out of 10): 6

Best Match Score: 206.62

Best Match Posterior Error Probability: 7.02E-54

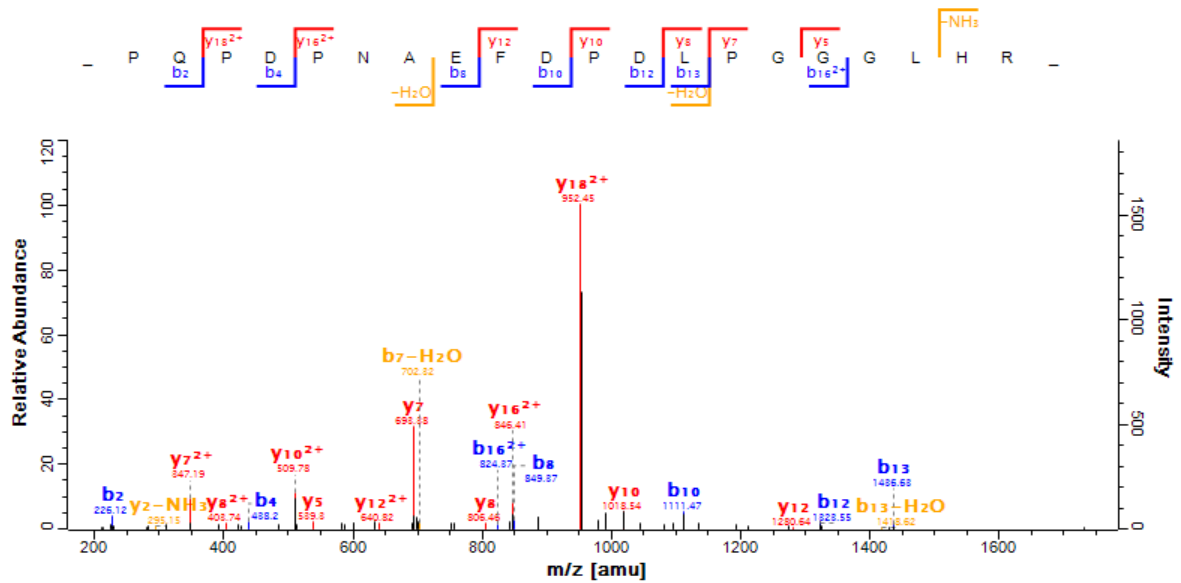
Best Match Spectrum:

Scan number	5695	Raw file	Prt-OGE-Batch2-WT-Frac1.2
Method	ITMS: CID	Genenames	ATPAF1



Protein Group ID: 78
Protein Accession Numbers: A9J4F5; O00488
Gene Names: ZNF593
Peptide Sequence: P Q P D P N A E F D P D L P G L H R
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 78.661
Best Match Posterior Error Probability: 0.0011133
Best Match Spectrum:

Scan number 3893 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac19
Method ITMS; CID **Genenames** ZNF593



Protein Group ID: 79

Protein Accession Numbers: Q5R3I4; E7ES35; A9UJP8; H7C2L7

Gene Names: TTC38

Peptide Sequence: LDKELDLAVK

Total Number of Spectra: 4

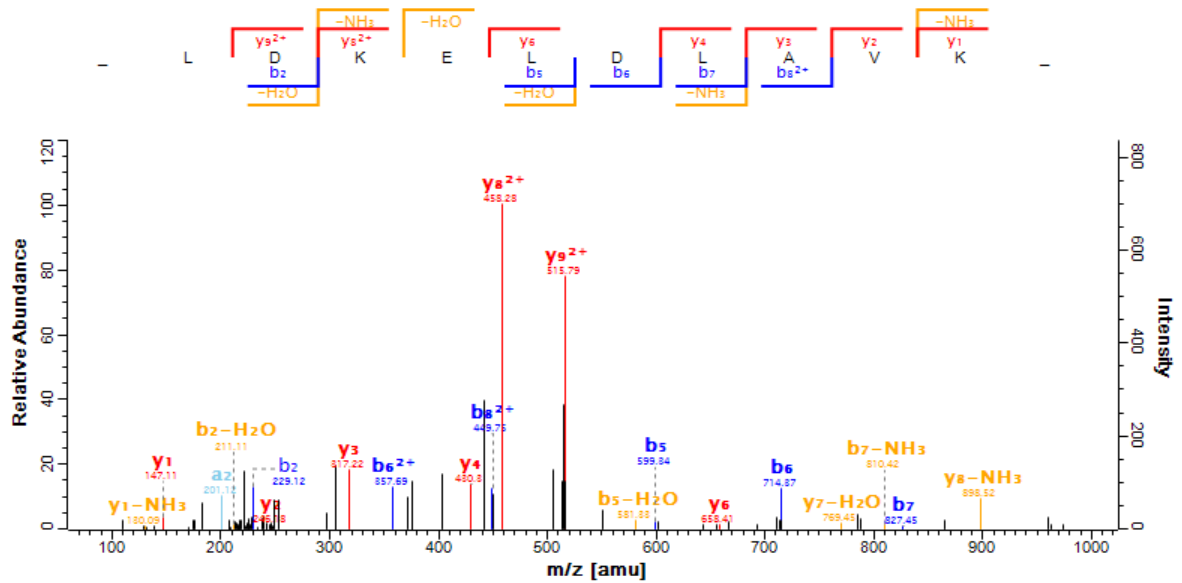
Number of Replicates (out of 10): 3

Best Match Score: 103.26

Best Match Posterior Error Probability: 0.001624

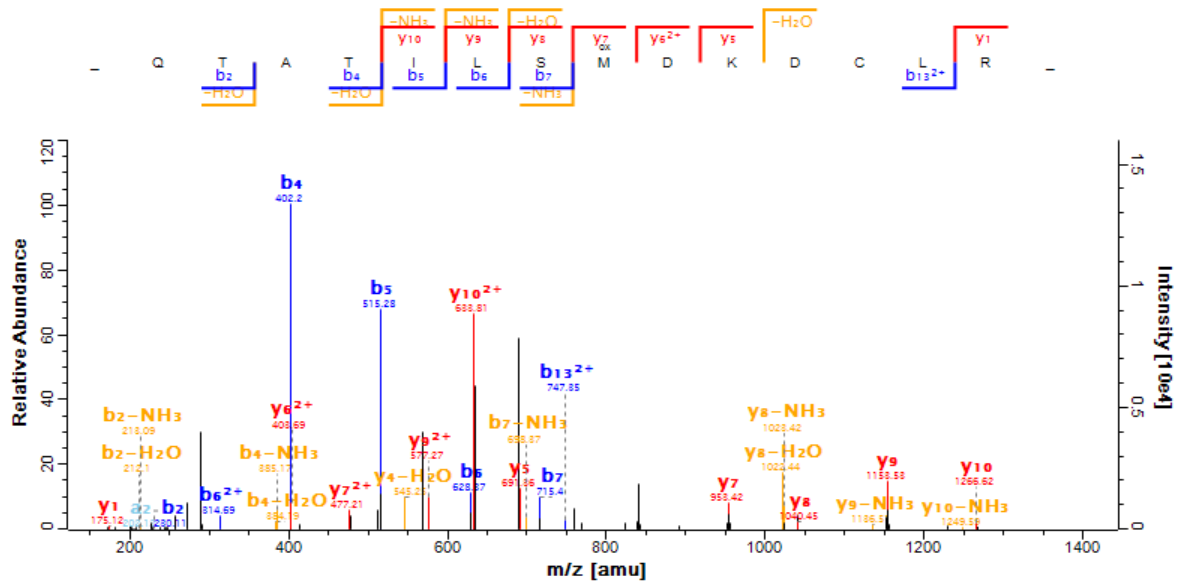
Best Match Spectrum:

Scan number 2743 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac11
Method ITMS; CID **Genenames** TTC38



Protein Group ID: 82
Protein Accession Numbers: O00178; B0QY59
Gene Names: GTPBP1
Peptide Sequence: QTATILSMDKDCLR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 127.71
Best Match Posterior Error Probability: 0.002904
Best Match Spectrum:

Scan number 6669 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac12
Method ITMS; CID **Genenames** GTPBP1



Protein Group ID: 84

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

Gene Names: MB

Peptide Sequence: HGATVLTALGGILK

Total Number of Spectra: 3

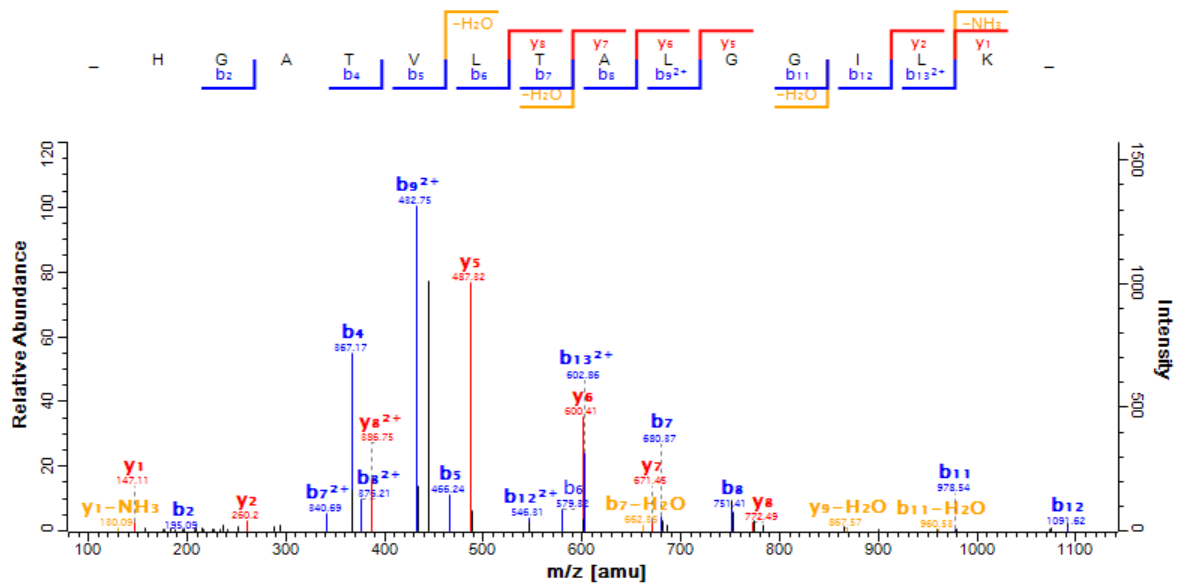
Number of Replicates (out of 10): 3

Best Match Score: 140.14

Best Match Posterior Error Probability: 2.81E-06

Best Match Spectrum:

Scan number	4527	Raw file	Prt-OGE-Batch3-Mock-Frac18
Method	ITMS; CID	Genenames	MB



Protein Group ID: 87

Protein Accession Numbers: Q5SSJ5; Q5SSJ5-2; Q5SSJ5-3; B0QZK4

Gene Names: HP1BP3

Peptide Sequence: SGEKPLLGGSLMEYAILSALISAIAMNEPK

Total Number of Spectra: 10

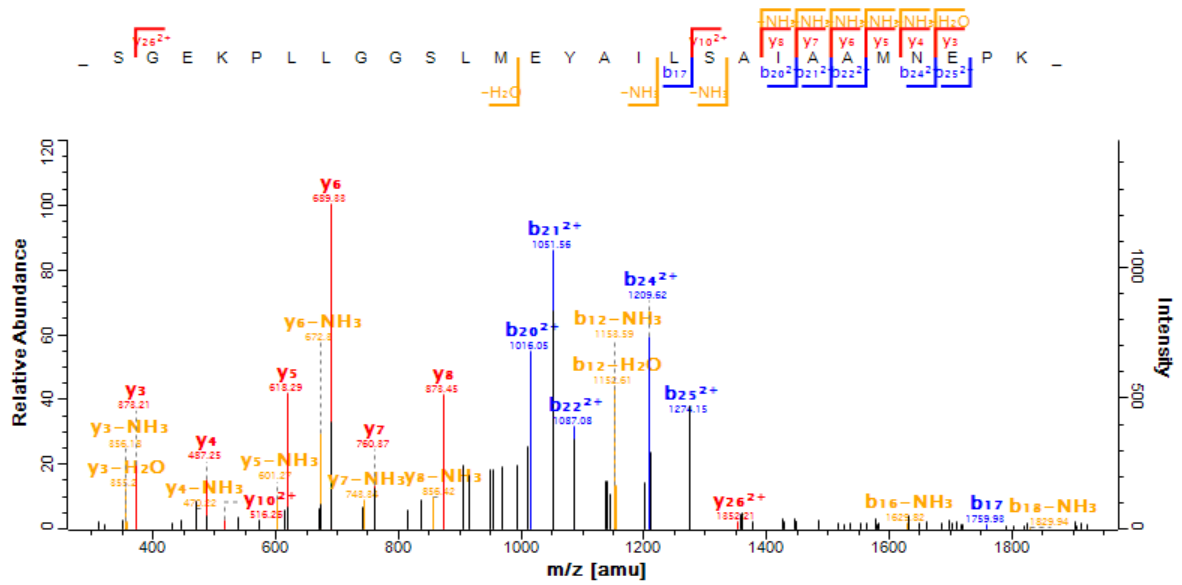
Number of Replicates (out of 10): 5

Best Match Score: 79.69

Best Match Posterior Error Probability: 1.23E-05

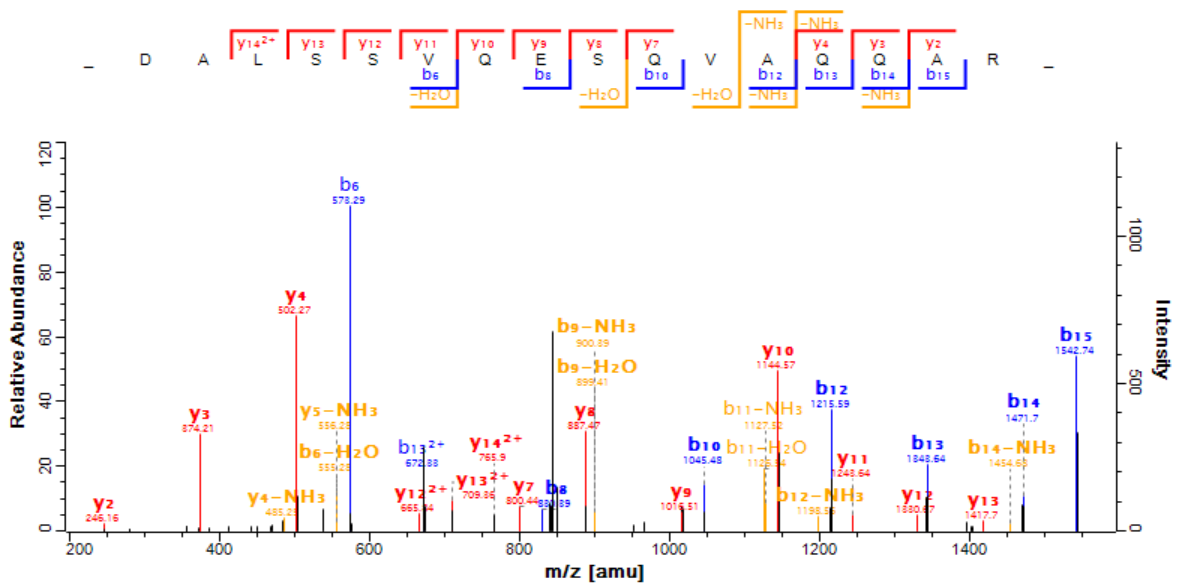
Best Match Spectrum:

Scan number 8534 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac15
Method ITMS; CID **Genenames** HP1BP3



Protein Group ID: 93
Protein Accession Numbers: B0YIW2; P02656
Gene Names: APOC3
Peptide Sequence: DALSSVQESQVAQQAR
Total Number of Spectra: 11
Number of Replicates (out of 10): 5
Best Match Score: 136.26
Best Match Posterior Error Probability: 1.09E-05
Best Match Spectrum:

Scan number 2364 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac2
Method ITMS; CID **Genenames** APOC3



Protein Group ID: 98

Protein Accession Numbers: REV__P82094-2; REV__P82094; Q9UIA0; B1AHH6; B1AHH5; B1AHH4

Gene Names: CYTH4

Peptide Sequence: QLLEDIQK

Total Number of Spectra: 2

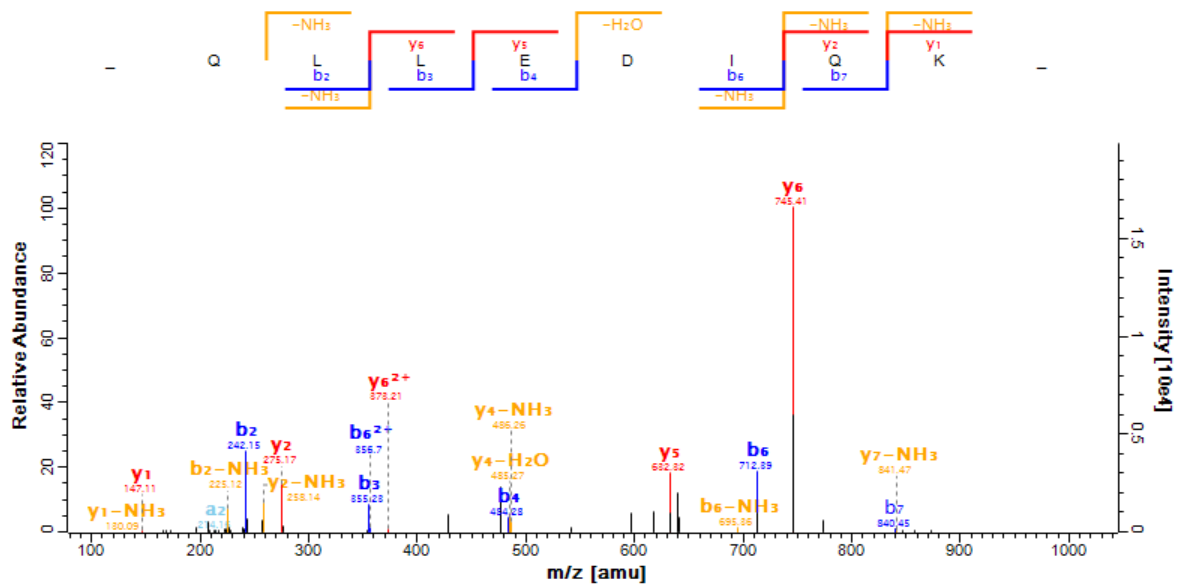
Number of Replicates (out of 10): 2

Best Match Score: 114.89

Best Match Posterior Error Probability: 0.0015884

Best Match Spectrum:

Scan number	3257	Raw file	OGE-Mock-Frac8
Method	ITMS; CID	Genenames	CYTH4



Protein Group ID: 101

Protein Accession Numbers: Q5TZA2; B1AKD8; Q5TZA2-2

Gene Names: CROCC

Peptide Sequence: LALLEEAR

Total Number of Spectra: 50

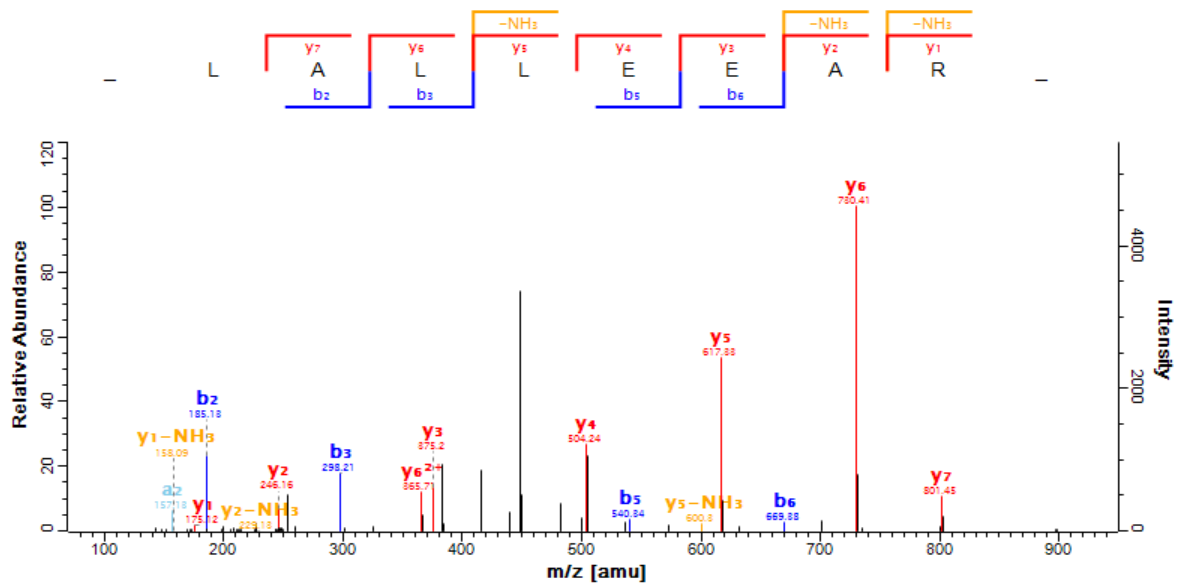
Number of Replicates (out of 10): 10

Best Match Score: 114.89

Best Match Posterior Error Probability: 0.0015884

Best Match Spectrum:

Scan number	3524	Raw file	Prt-OGE-Batch2-Mock-Frac20
Method	ITMS; CID	Genenames	CROCC



Protein Group ID: 102

Protein Accession Numbers: J3KPA3; Q96SU4-6; B1AKJ6; Q96SU4; Q96SU4-2; Q96SU4-7; E9PJW9; Q96SU4-3; H0YE19; E9PK98

Gene Names: OSBPL9

Peptide Sequence: LTEADAYLQILIEQLK

Total Number of Spectra: 4

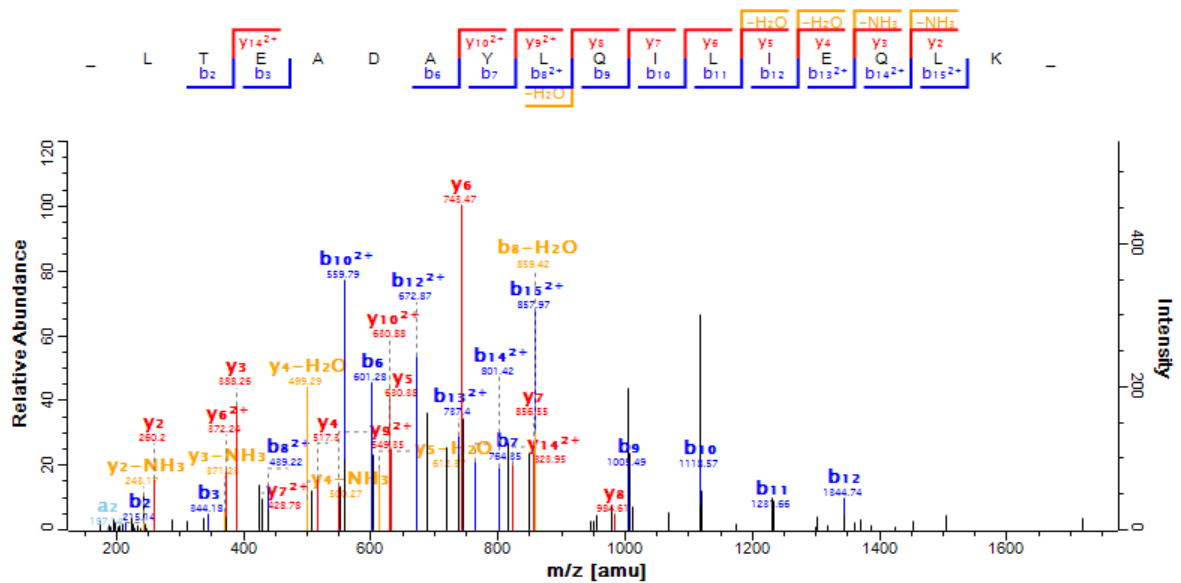
Number of Replicates (out of 10): 4

Best Match Score: 171.26

Best Match Posterior Error Probability: 1.44E-15

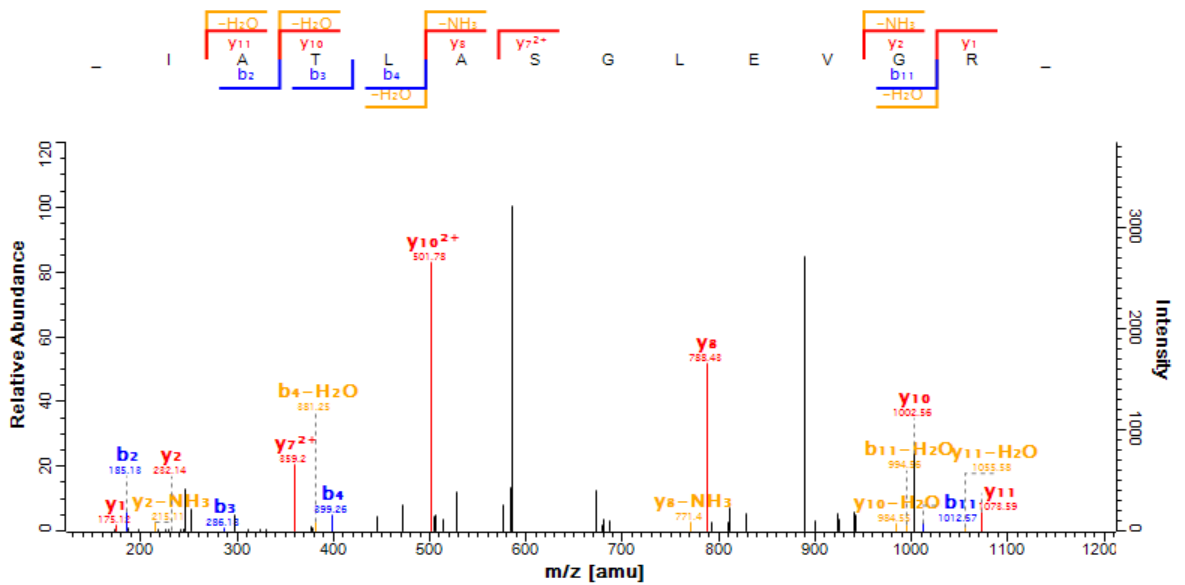
Best Match Spectrum:

Scan number	7873	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac13
Method	ITMS; CID	Genenames	OSBPL9



Protein Group ID: 103
Protein Accession Numbers: P50993; B1AKY9
Gene Names: ATP1A2
Peptide Sequence: IATLASGLEVGR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 84.687
Best Match Posterior Error Probability: 0.0013281
Best Match Spectrum:

Scan number 3343 **Raw file** OGE-WT-Frac3
Method ITMS; CID **Genenames** ATP1A2



Protein Group ID: 105

Protein Accession Numbers: Q14155-5; B7Z6G2; B1ALK7; Q14155-1

Gene Names: ARHGEF7

Peptide Sequence: SLVDTVYALKDEVQELR

Total Number of Spectra: 4

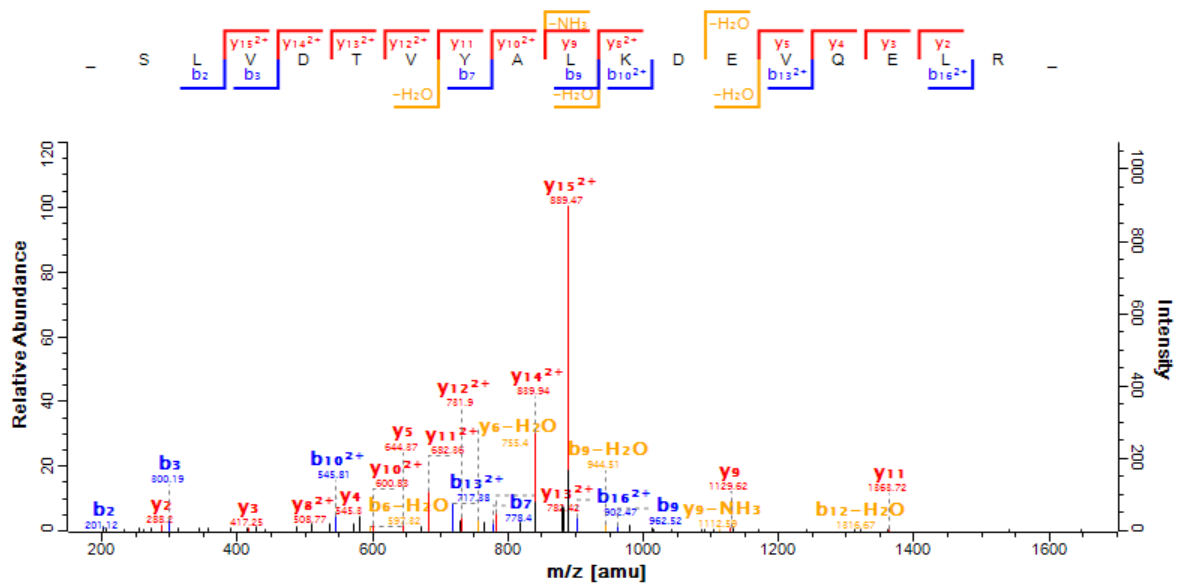
Number of Replicates (out of 10): 3

Best Match Score: 109.07

Best Match Posterior Error Probability: 0.00052743

Best Match Spectrum:

Scan number	6324	Raw file	20100914-KD-Batch4-Prt-OGE-Mock-Frac14
Method	ITMS; CID	Genenames	ARHGEF7



Protein Group ID: 106

Protein Accession Numbers: P29992; P50148; O95837; B1AM21

Gene Names: GNA11;GNAQ;GNA14

Peptide Sequence: LVYQNIFTAMQAMIR

Total Number of Spectra: 3

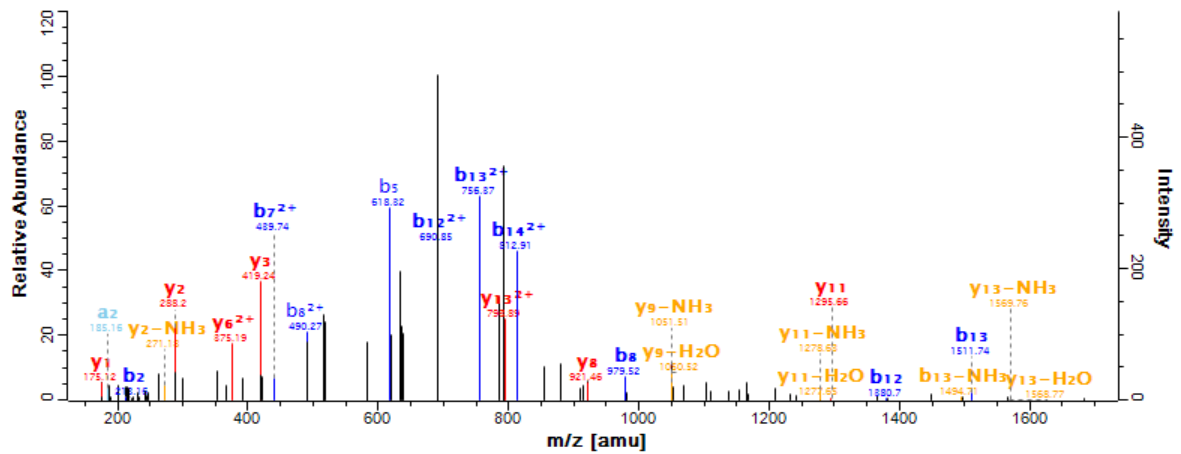
Number of Replicates (out of 10): 3

Best Match Score: 101.43

Best Match Posterior Error Probability: 0.00011006

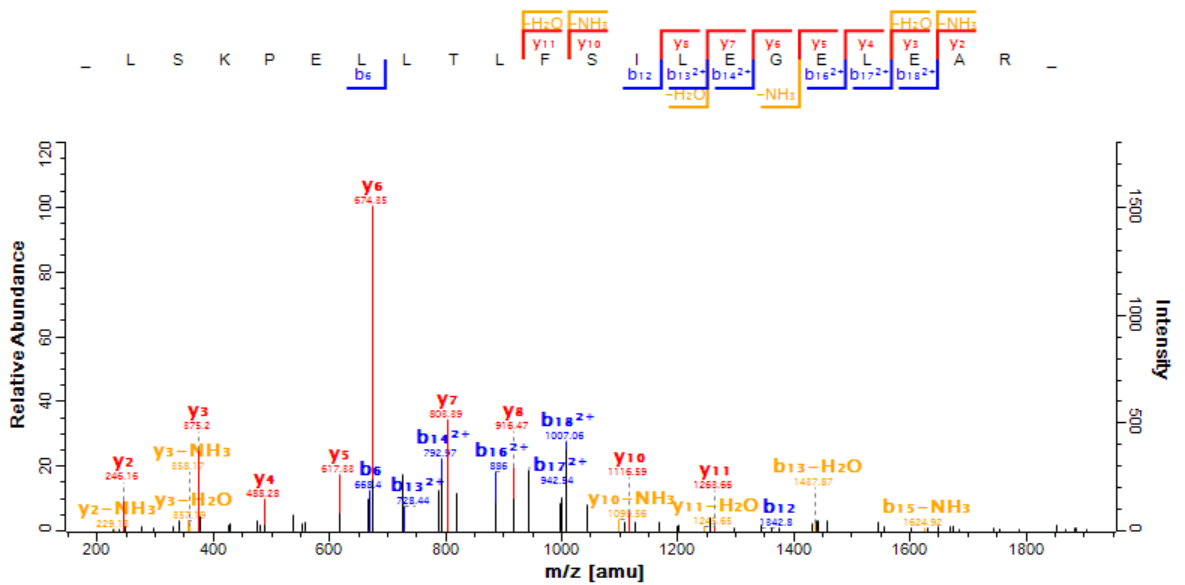
Best Match Spectrum:

Scan number 7541 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac10
Method ITMS; CID **Genenames** GNA11;GNAQ;GNA14



Protein Group ID: 107
Protein Accession Numbers: Q9P2B4; B1AMN7
Gene Names: CTTNBP2NL
Peptide Sequence: LSKPELLTLFSILEGELEAR
Total Number of Spectra: 7
Number of Replicates (out of 10): 5
Best Match Score: 88.565
Best Match Posterior Error Probability: 0.0007255
Best Match Spectrum:

Scan number 8303 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac14
Method ITMS; CID **Genenames** CTTNBP2NL



Protein Group ID: 108

Protein Accession Numbers: B1ANH2; B1ANH6; Q16774-2; B1ANH0; B1ANH5; Q16774

Gene Names: GUK1

Peptide Sequence: LAAQADMESSKEPGLFDVIVIIINDSLDQAAYAELEK

Total Number of Spectra: 2

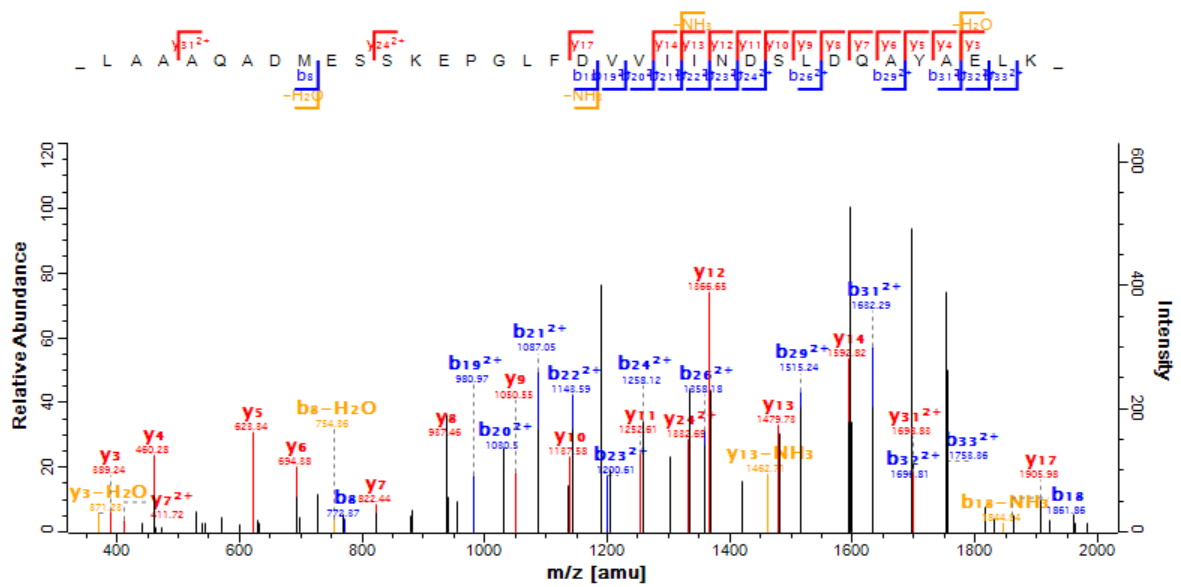
Number of Replicates (out of 10): 2

Best Match Score: 104.84

Best Match Posterior Error Probability: 8.79E-19

Best Match Spectrum:

Scan number	5719	Raw file	Prt-OGE-Batch3-WT-Frac12
Method	ITMS: CID	Genenames	GUK1



Protein Group ID: 112

Protein Accession Numbers: B1AZU4; Q5SPT7; E7EN49; E7EQP4; E7EWC3; F8W0J9; Q6ZUW0; D0EV57; B4DT81; F6R3U9; F6RUR5; B7Z760; F8VTQ8; H0Y4C2; H0Y5J2; H0Y5Q6; H0Y7Q7; H0Y7W0; H0Y805; P30511-3; P30511; E9PGX5; H0Y842

Gene Names: HLA-F

Peptide Sequence: WEQSPQPTIPIVGI VAGLVV LGA VV TGA VVA VMWR

Total Number of Spectra: 1

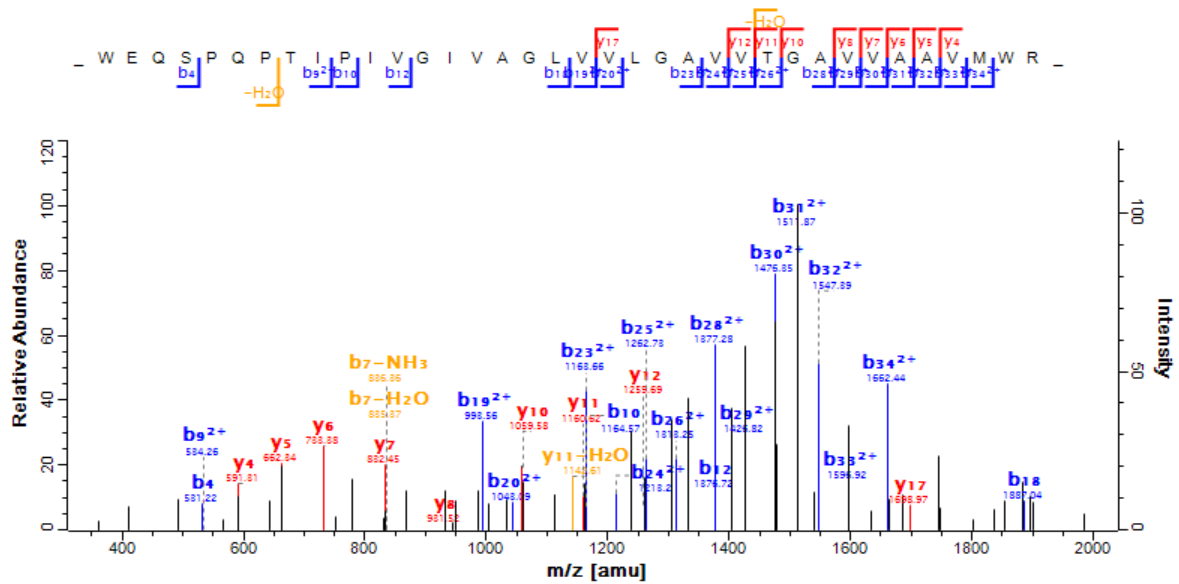
Number of Replicates (out of 10): 1

Best Match Score: 70.784

Best Match Posterior Error Probability: 2.41E-07

Best Match Spectrum:

Scan number	11393	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac10
Method	ITMS: CID	Genenames	HLA-F



Protein Group ID: 114

Protein Accession Numbers: Q9P0M9; H7C5U8; B3KN43; D6RE11

Gene Names: MRPL27

Peptide Sequence: KMEGHYVHAGNIATQR

Total Number of Spectra: 1

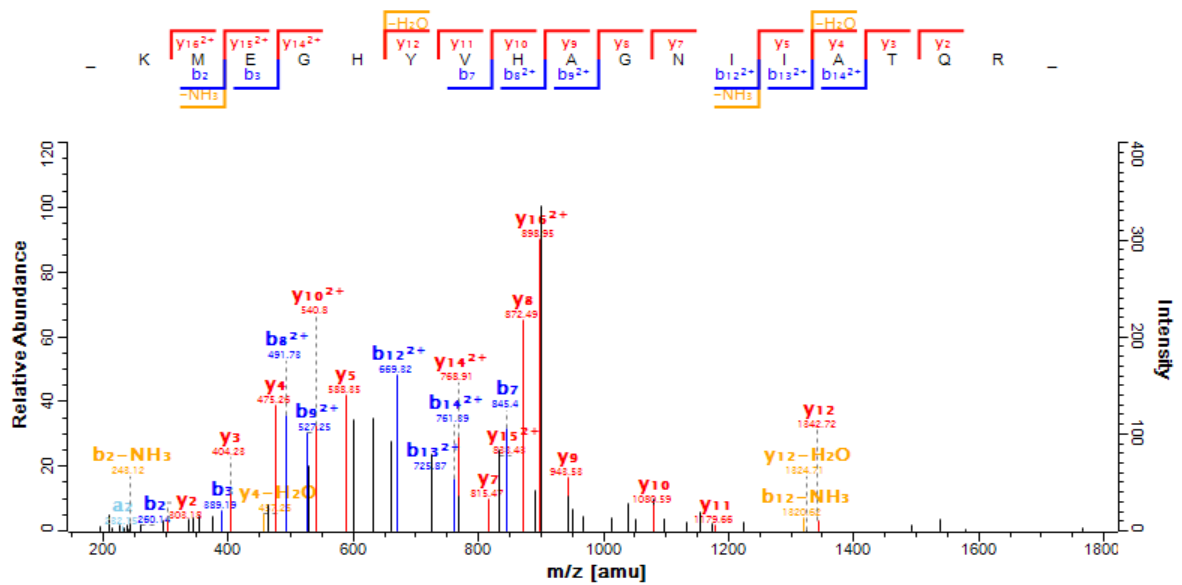
Number of Replicates (out of 10): 1

Best Match Score: 115.8

Best Match Posterior Error Probability: 0.00034213

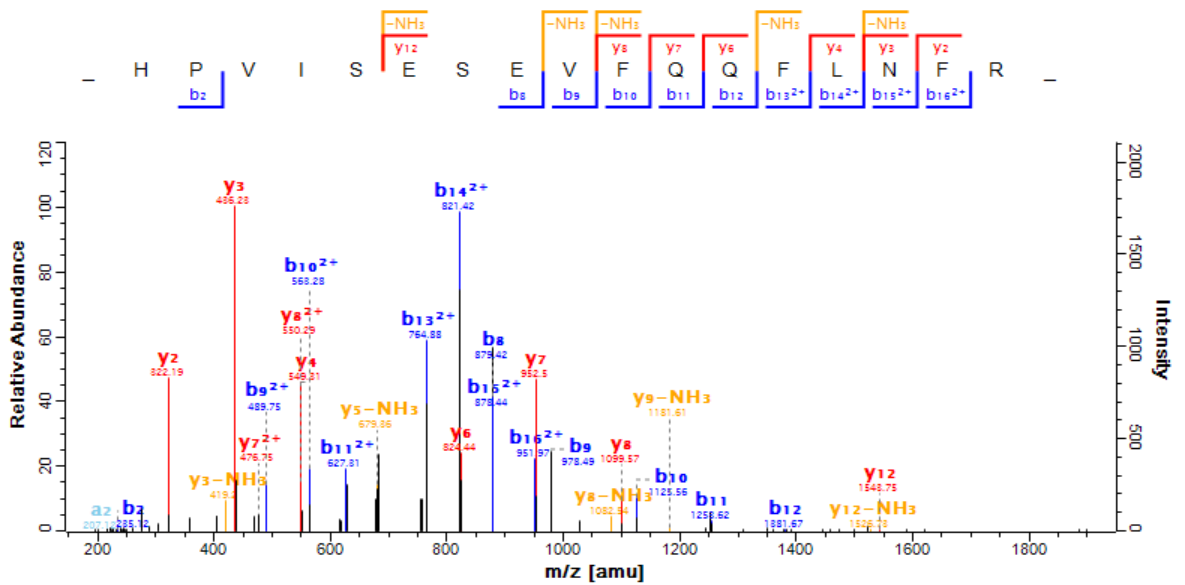
Best Match Spectrum:

Scan number 1542 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac19
Method ITMS; CID **Genenames** MRPL27



Protein Group ID: 127
Protein Accession Numbers: Q9Y5X1; B3KXH8
Gene Names: SNX9
Peptide Sequence: HPVISESEVFQQFLNFR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 128.96
Best Match Posterior Error Probability: 3.76E-05
Best Match Spectrum:

Scan number 5989 **Raw file** OGE-WT-Frac9
Method ITMS; CID **Genenames** SNX9



Protein Group ID: 129

Protein Accession Numbers: Q66PJ3; Q66PJ3-2; Q66PJ3-3; Q66PJ3-4; F5H7X4; F8WCT1; B3VOL1; H7BZV4; F5GYV5

Gene Names: ARL6IP4

Peptide Sequence: AEAQQVEALPGSLDQWHR

Total Number of Spectra: 4

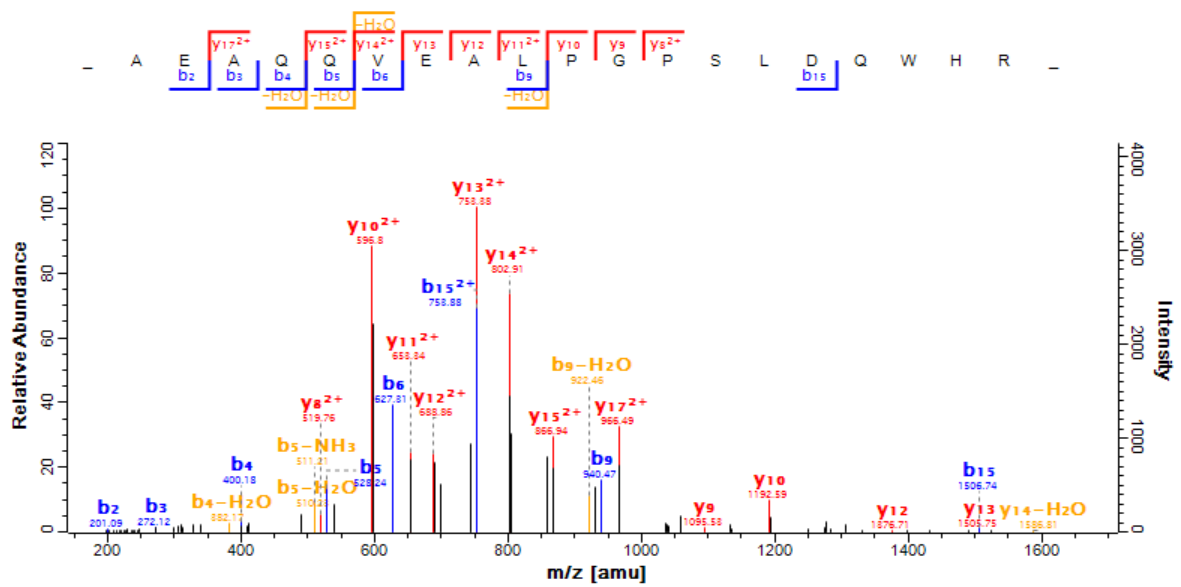
Number of Replicates (out of 10): 4

Best Match Score: 114.29

Best Match Posterior Error Probability: 3.23E-05

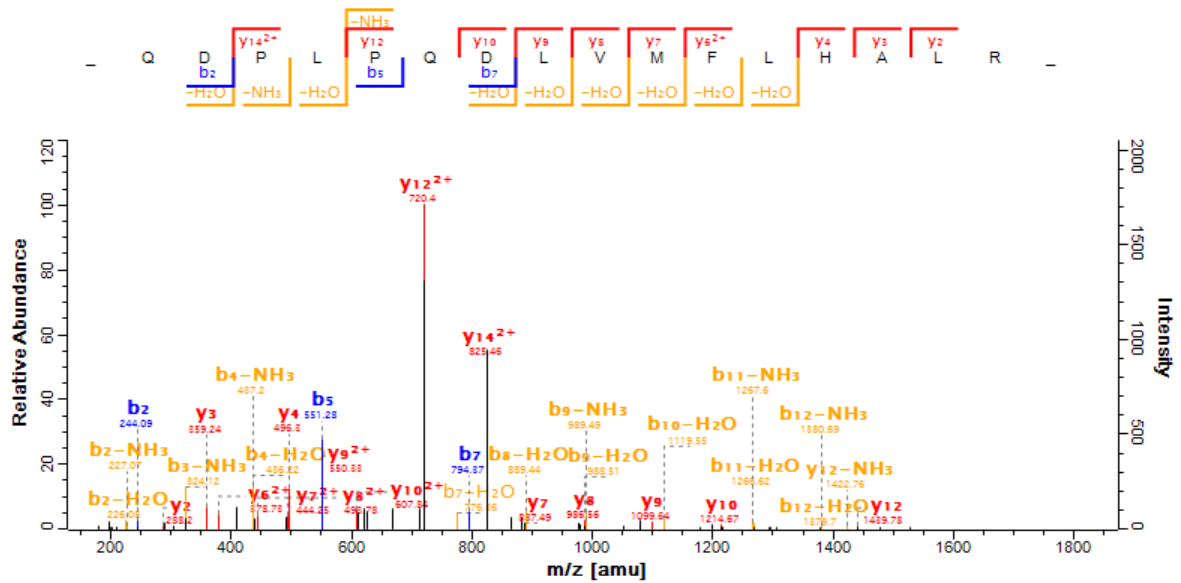
Best Match Spectrum:

Scan number 4533 Raw file Prt-OGE-Batch2-Mock-Frac17
Method ITMS: CID Genenames ARL6IP4



Protein Group ID: 130
Protein Accession Numbers: Q8IZ73; B4DDD1
Gene Names: RPUSD2
Peptide Sequence: QDPLPQDLVMFLHALR
Total Number of Spectra: 6
Number of Replicates (out of 10): 5
Best Match Score: 113.25
Best Match Posterior Error Probability: 0.000126
Best Match Spectrum:

Scan number 7444 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac14
Method ITMS; CID **Genenames** RPUSD2



Protein Group ID: 132

Protein Accession Numbers: O96005; F5H8J3; B4DDS3; K7EQQ1

Gene Names: CLPTM1

Peptide Sequence: NLLTGETEADPEMIK

Total Number of Spectra: 1

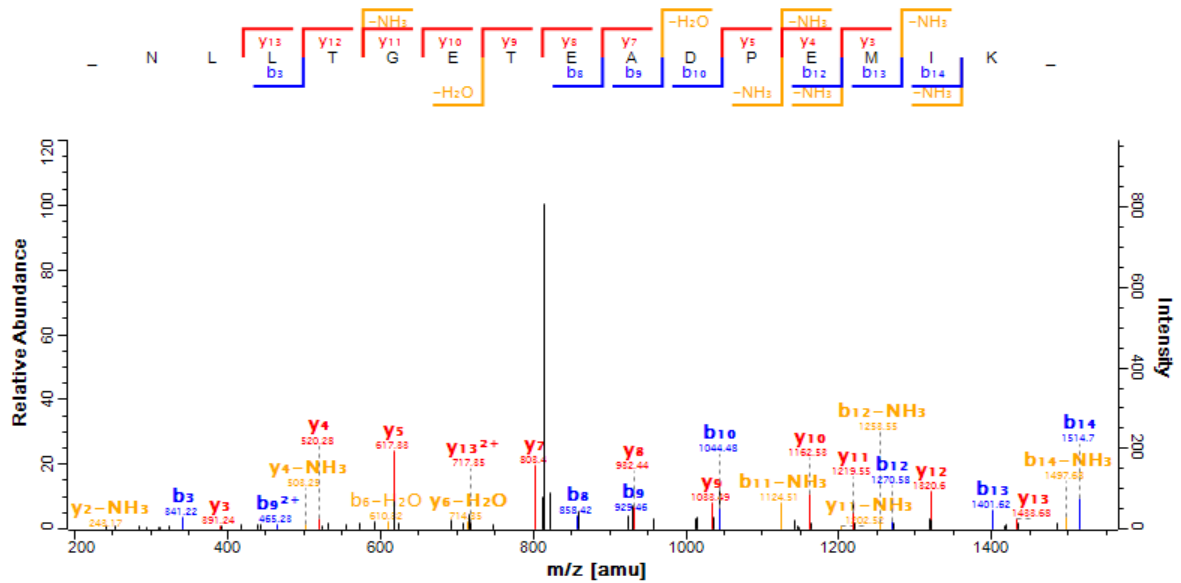
Number of Replicates (out of 10): 1

Best Match Score: 108.34

Best Match Posterior Error Probability: 5.86E-05

Best Match Spectrum:

Scan number 2974 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** CLPTM1



Protein Group ID: 133

Protein Accession Numbers: Q8N7V9; P54619; B4DDT7; F8VYY9; H0YIC9; F8W9D1

Gene Names: PRKAG1

Peptide Sequence: GIVSLSDILQALVLTGGEK

Total Number of Spectra: 9

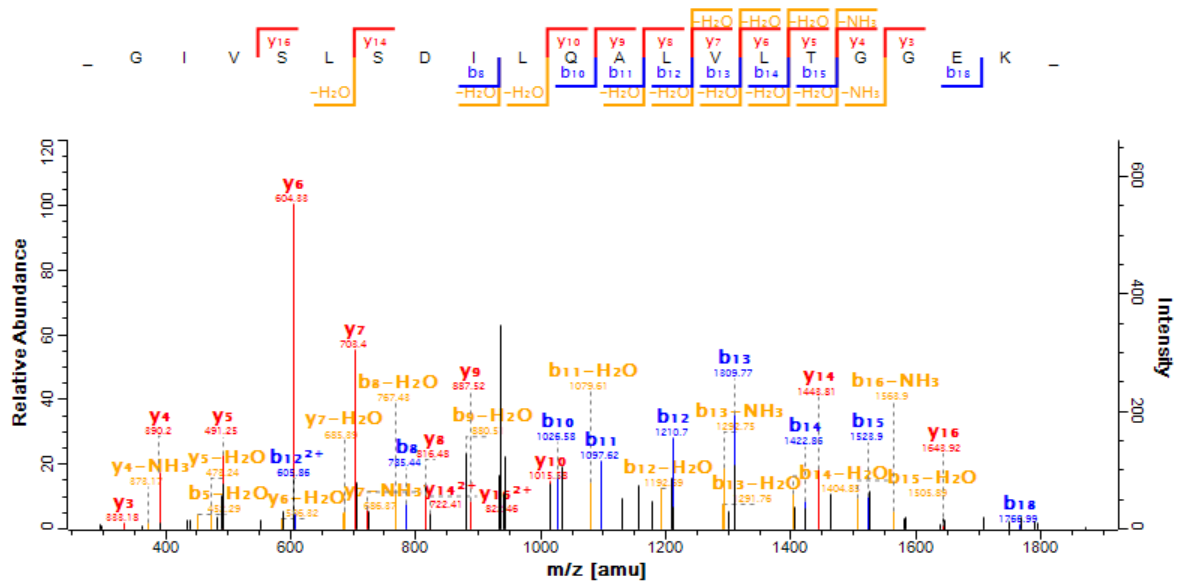
Number of Replicates (out of 10): 8

Best Match Score: 160.45

Best Match Posterior Error Probability: 6.53E-12

Best Match Spectrum:

Scan number 6619 **Raw file** Prt-OGE-Batch2-WT-Frac15
Method ITMS; CID **Genenames** PRKAG1



Protein Group ID: 138

Protein Accession Numbers: B4DFQ6; Q96CM8; B4DHT5; E9PF16; B4DUF5

Gene Names: ACSF2

Peptide Sequence: YIVFVTNYPLTISGK

Total Number of Spectra: 1

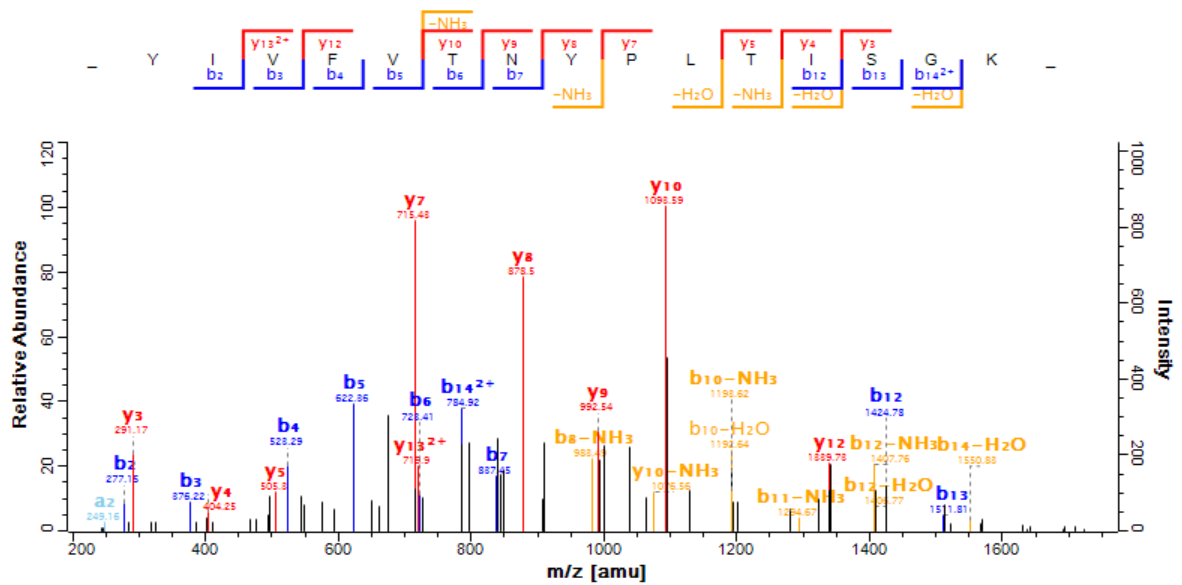
Number of Replicates (out of 10): 1

Best Match Score: 121.31

Best Match Posterior Error Probability: 4.44E-05

Best Match Spectrum:

Scan number	6162	Raw file	Prt-OGE-Batch2-Mock-Frac15
Method	ITMS; CID	Genenames	ACSF2



Protein Group ID: 139

Protein Accession Numbers: Q969G3; B4DGM3; C0IMW4; Q969G3-2; B4DFR4; C0IMW5; C0IMW7; J3QKS7; K7EMQ8; H7C048

Gene Names: SMARCE1

Peptide Sequence: IAAEIAQAEEQAR

Total Number of Spectra: 2

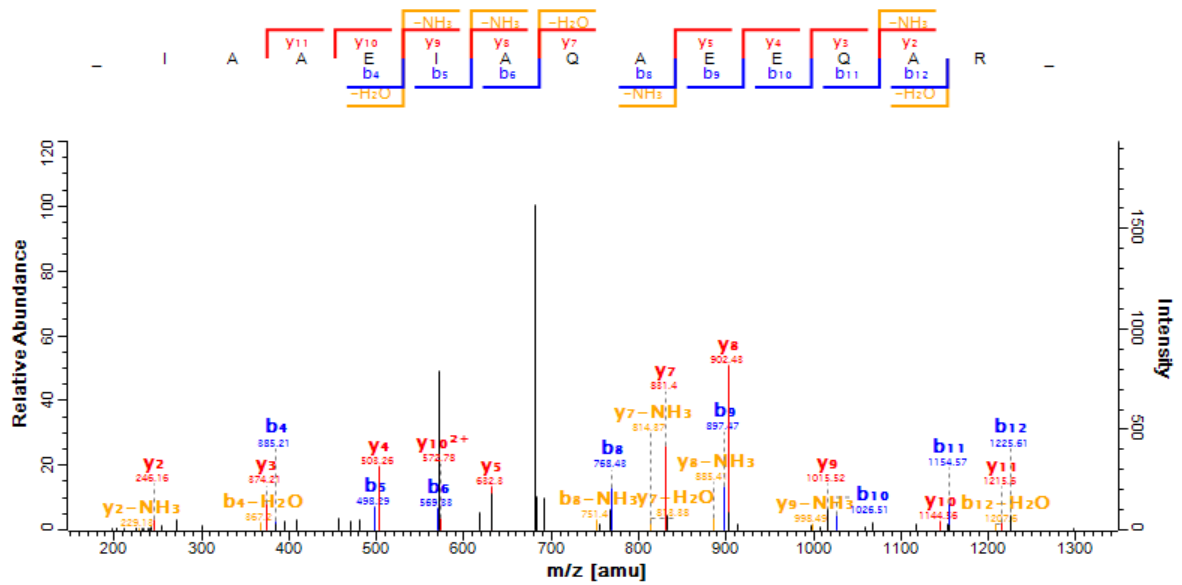
Number of Replicates (out of 10): 2

Best Match Score: 141.54

Best Match Posterior Error Probability: 1.67E-05

Best Match Spectrum:

Scan number 2118 Raw file 20100914-KD-Batch4-Prt-OGE-Mock-Frac16
Method ITMS: CID Genenames SMARCE1



Protein Group ID: 143

Protein Accession Numbers: O95273; O95273-2; O95273-3; O95273-4; B4DHB5

Gene Names: CCNDBP1

Peptide Sequence: AAALLMLTK

Total Number of Spectra: 1

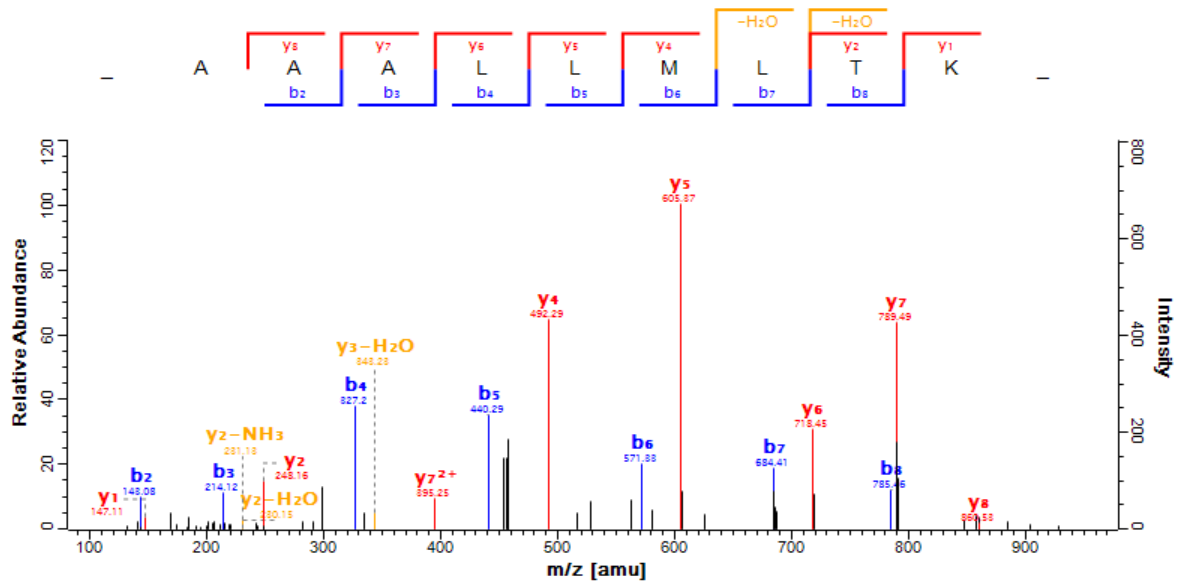
Number of Replicates (out of 10): 1

Best Match Score: 115.71

Best Match Posterior Error Probability: 0.00035571

Best Match Spectrum:

Scan number 3791 **Raw file** Prt-OGE-Batch3--Mock-Frac4
Method ITMS; CID **Genenames** CCNDBP1



Protein Group ID: 147

Protein Accession Numbers: B4DIY7; C9J2U4; Q96BW9

Gene Names: TAMM41

Peptide Sequence: SQGWLEIDKSPGQFTQLMTPK

Total Number of Spectra: 2

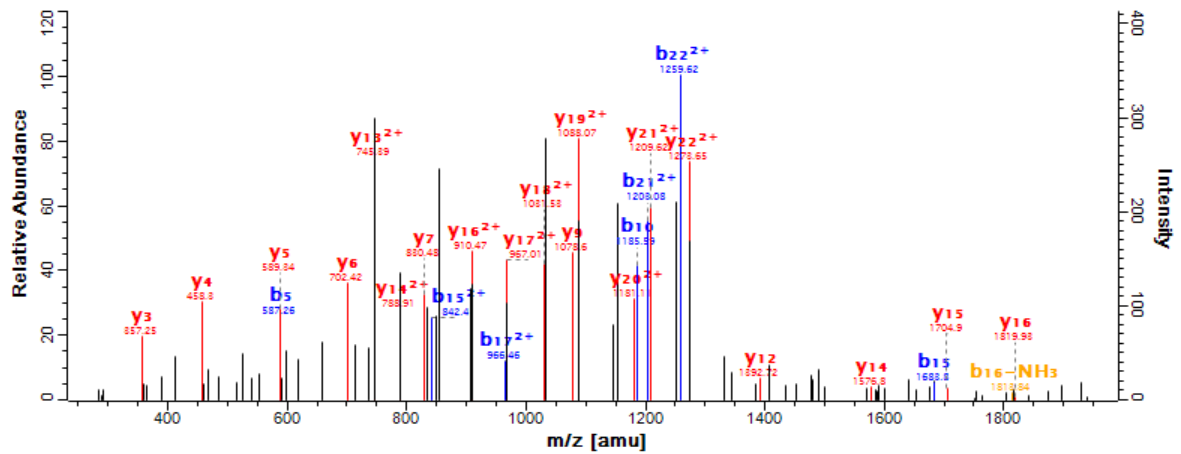
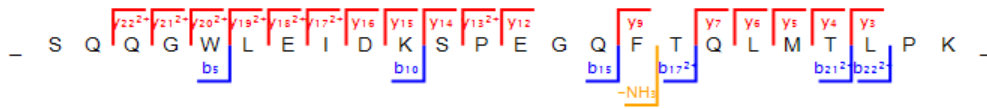
Number of Replicates (out of 10): 2

Best Match Score: 100.53

Best Match Posterior Error Probability: 1.26E-06

Best Match Spectrum:

Scan number	6065	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac21
Method	ITMS; CID	Genenames	TAMM41



Protein Group ID: 150

Protein Accession Numbers: B4DJK3; P01033; H0Y789; Q5H9A7

Gene Names: TIMP1

Peptide Sequence: LQDGLLHITTCSTFVAVPWNSLSLAQR

Total Number of Spectra: 1

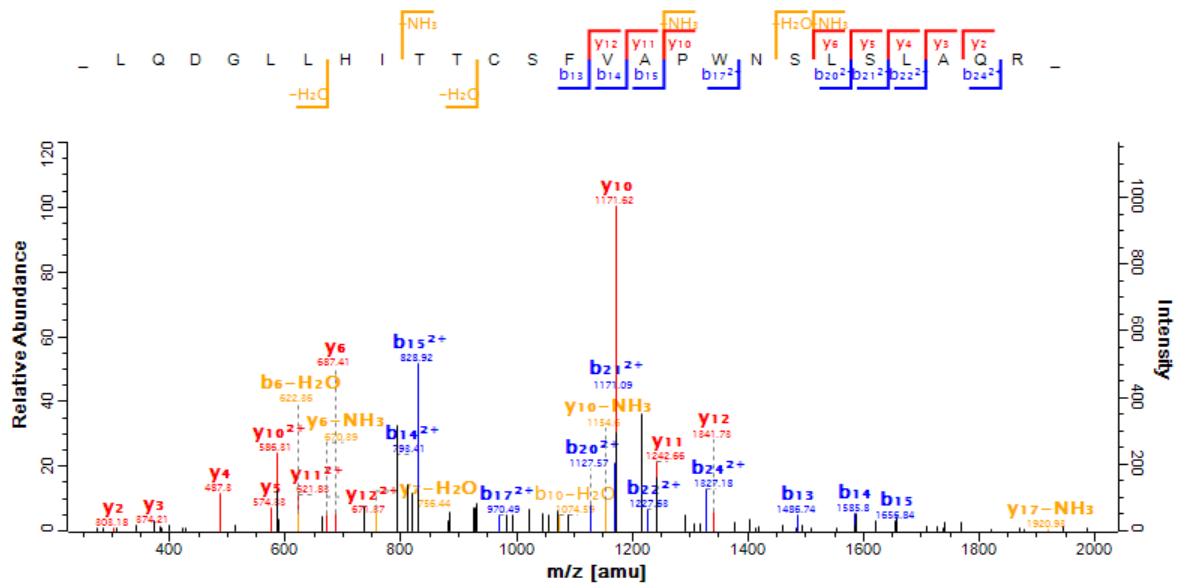
Number of Replicates (out of 10): 1

Best Match Score: 78.354

Best Match Posterior Error Probability: 1.54E-05

Best Match Spectrum:

Scan number 6414 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac20
Method ITMS; CID **Genenames** TIMP1



Protein Group ID: 156

Protein Accession Numbers: Q9BV36; Q9BV36-2; B4DKW7; Q9BV36-3; G5E9G5; C9JKV5; C9JI01

Gene Names: MLPH

Peptide Sequence: LTDEEAQHVLEVVQR

Total Number of Spectra: 2

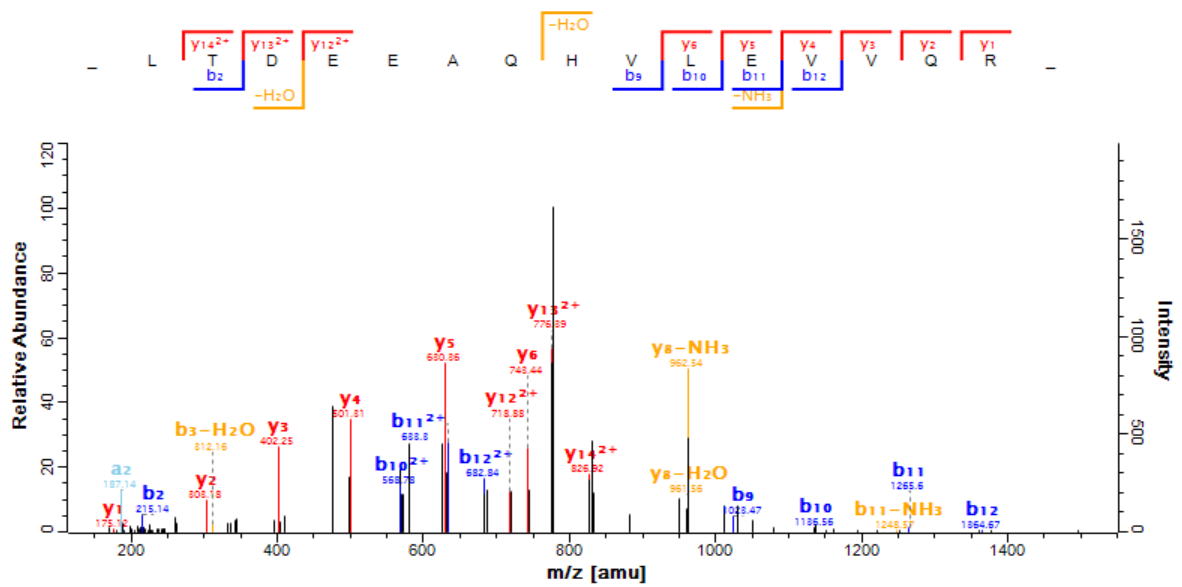
Number of Replicates (out of 10): 1

Best Match Score: 89.507

Best Match Posterior Error Probability: 0.00035733

Best Match Spectrum:

Scan number	3231	Raw file	Prt-OGE-Batch3-Mock-Frac15
Method	ITMS; CID	Genenames	MLPH



Protein Group ID: 160

Protein Accession Numbers: B4DLN1; Q9UBX3-2; Q9UBX3; B4E1E9; I3L1E8

Gene Names: SLC25A10

Peptide Sequence: VLLGSVSLAGGFVGTADLVNVR

Total Number of Spectra: 2

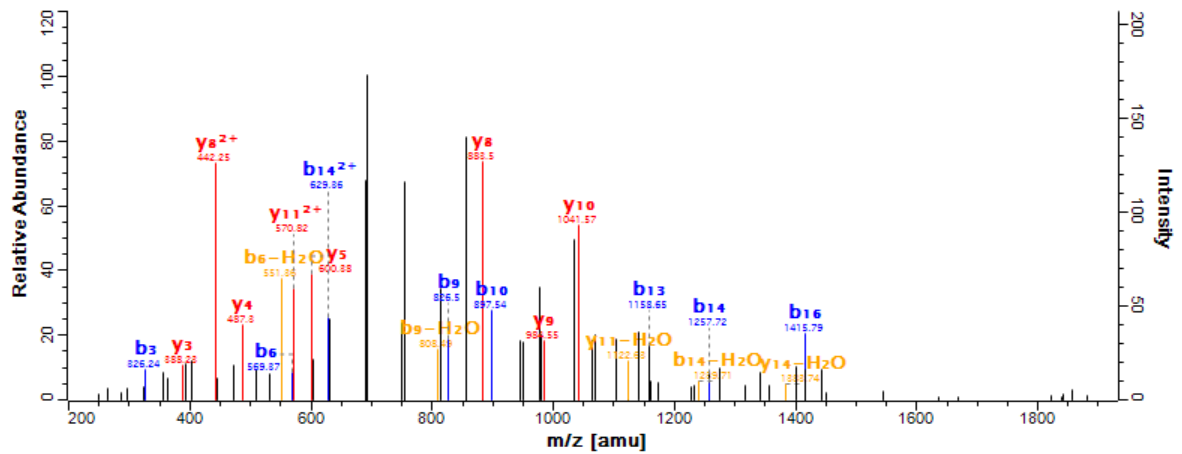
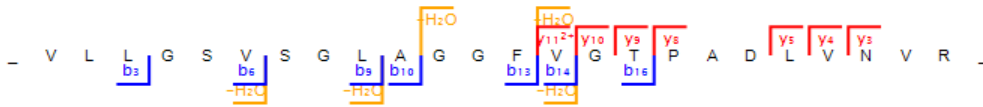
Number of Replicates (out of 10): 2

Best Match Score: 65.149

Best Match Posterior Error Probability: 0.00049514

Best Match Spectrum:

Scan number	5703	Raw file	20100914-KD-Batch4-Prt-OGE-Mock-Frac23
Method	ITMS; CID	Genenames	SLC25A10



Protein Group ID: 164

Protein Accession Numbers: Q9NSK0-3; Q9NSK0; B4DME9; Q9NSK0-4; C9J8T5

Gene Names: KLC4

Peptide Sequence: GHPDVATMLNLALVYR

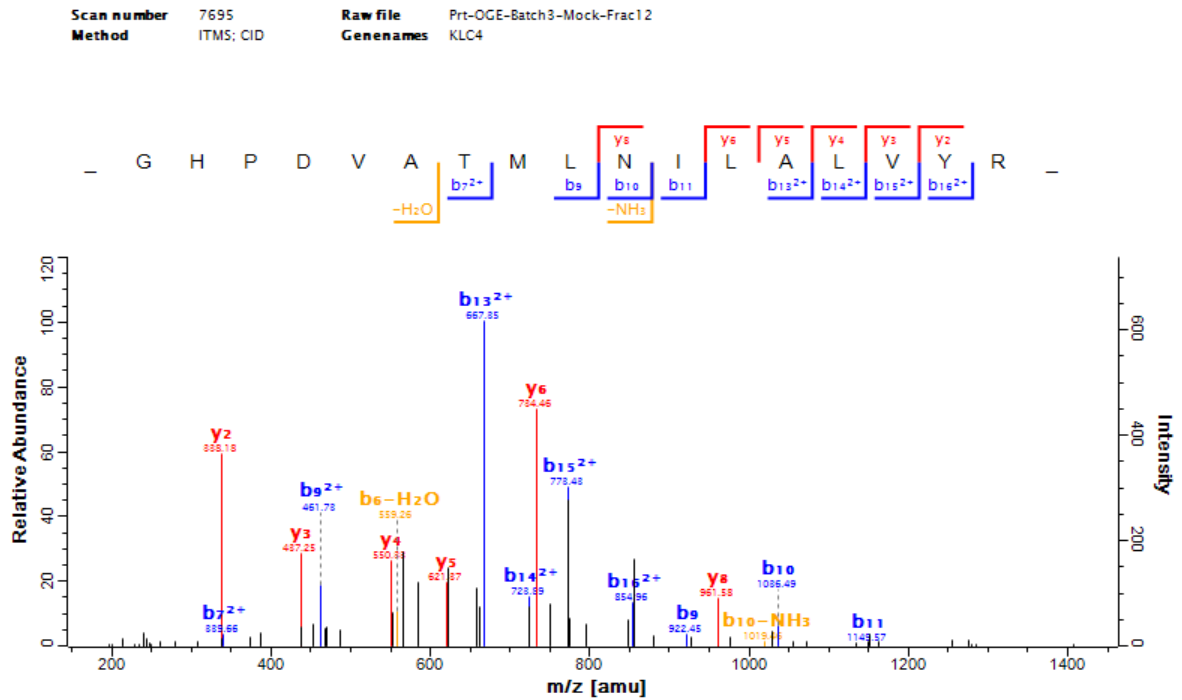
Total Number of Spectra: 9

Number of Replicates (out of 10): 5

Best Match Score: 83.692

Best Match Posterior Error Probability: 0.00083308

Best Match Spectrum:



Protein Group ID: 166

Protein Accession Numbers: P00750; P00750-3; E7ESF4; B4DN26; B4DNJ1; P00750-4; K4DI88; P00750-2

Gene Names: PLAT

Peptide Sequence: VYTAQNPSAQLGLGK

Total Number of Spectra: 1

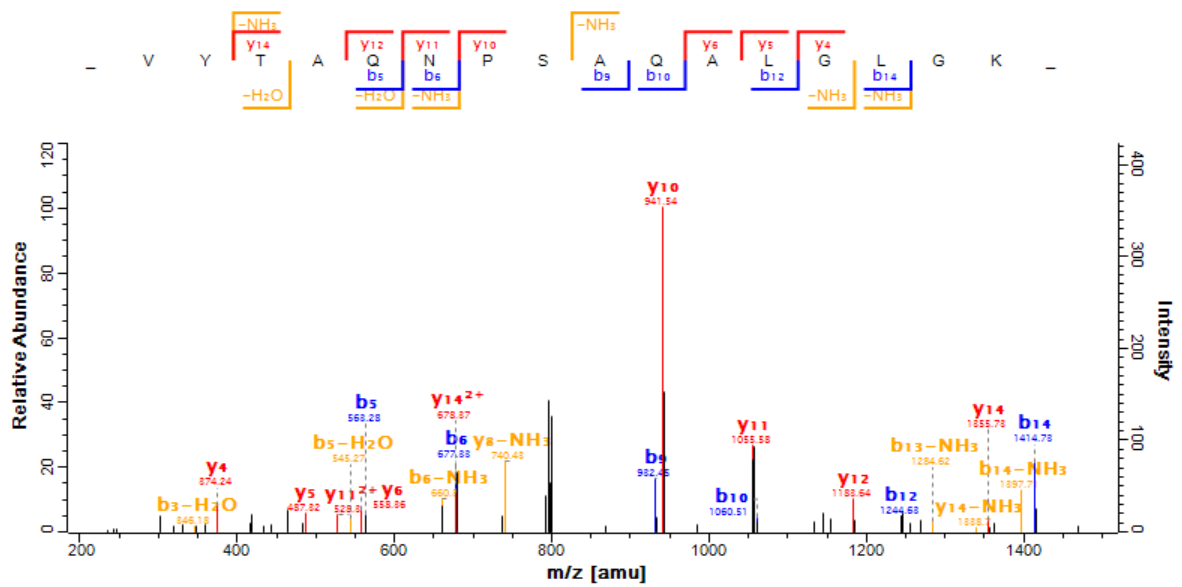
Number of Replicates (out of 10): 1

Best Match Score: 93.424

Best Match Posterior Error Probability: 0.00033096

Best Match Spectrum:

Scan number 2545 Raw file OGE-WT-Frac1
Method ITMS: CID Genenames PLAT



Protein Group ID: 172

Protein Accession Numbers: Q9NVM9; B4DNK1; H0YH12

Gene Names: Asun;ASUN

Peptide Sequence: GPVSLLSLWSNR

Total Number of Spectra: 3

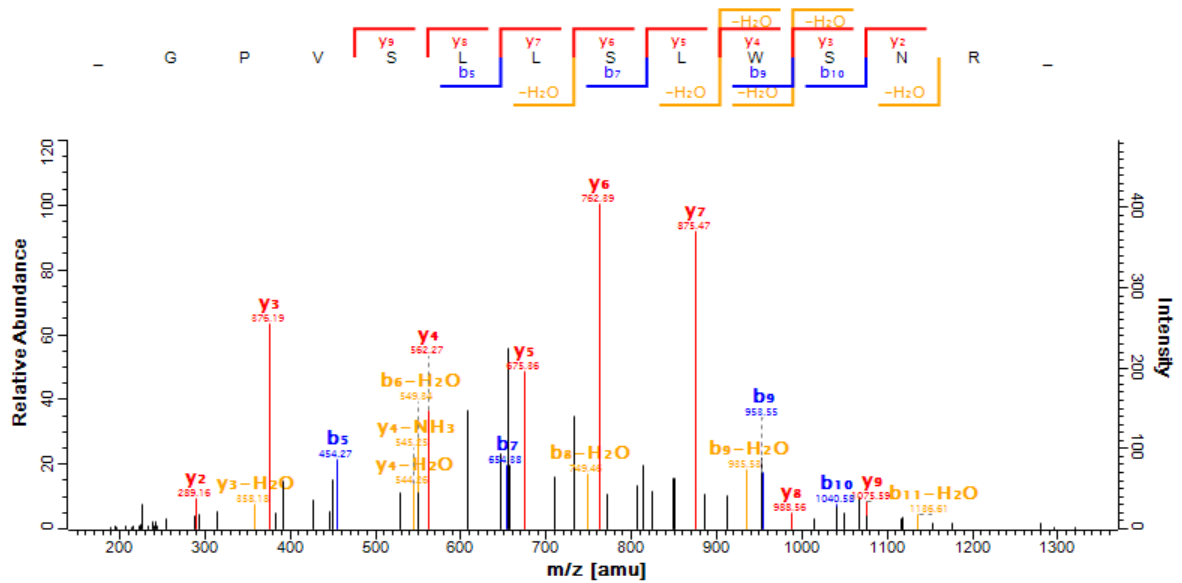
Number of Replicates (out of 10): 3

Best Match Score: 94.191

Best Match Posterior Error Probability: 0.00065178

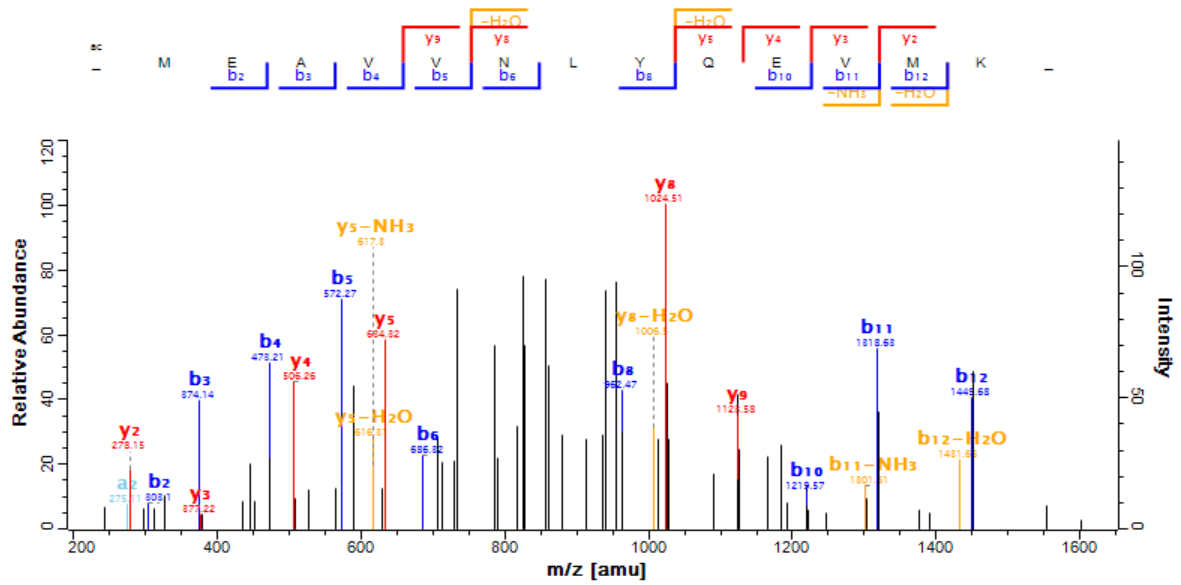
Best Match Spectrum:

Scan number	6562	Raw file	Prt-OGE-Batch2-Mock-Frac14
Method	ITMS; CID	Genenames	Asun;ASUN



Protein Group ID: 176
Protein Accession Numbers: Q9BW60; B4DP24
Gene Names: ELOVL1
Peptide Sequence: MEAVVNLYQEVMK
Total Number of Spectra: 17
Number of Replicates (out of 10): 7
Best Match Score: 119.25
Best Match Posterior Error Probability: 0.00010741
Best Match Spectrum:

Scan number 6776 **Raw file** Prt-OGE-Batch2-WT-Frac14
Method ITMS; CID **Genenames** ELOVL1



Protein Group ID: 179

Protein Accession Numbers: E7EQZ4; Q16637; Q16637-3; Q16637-2; Q16637-4; B4DP61; I3L4C1; H0YBZ9

Gene Names: SMN1

Peptide Sequence: SAPWNSFLPPPPMPGPR

Total Number of Spectra: 7

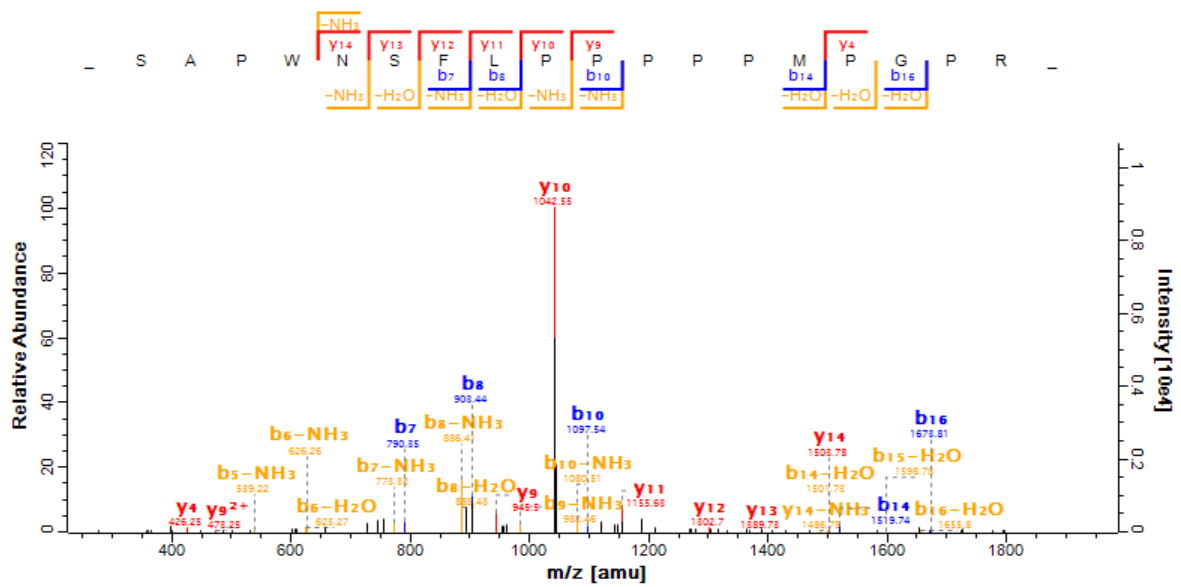
Number of Replicates (out of 10): 6

Best Match Score: 82.349

Best Match Posterior Error Probability: 0.0009698

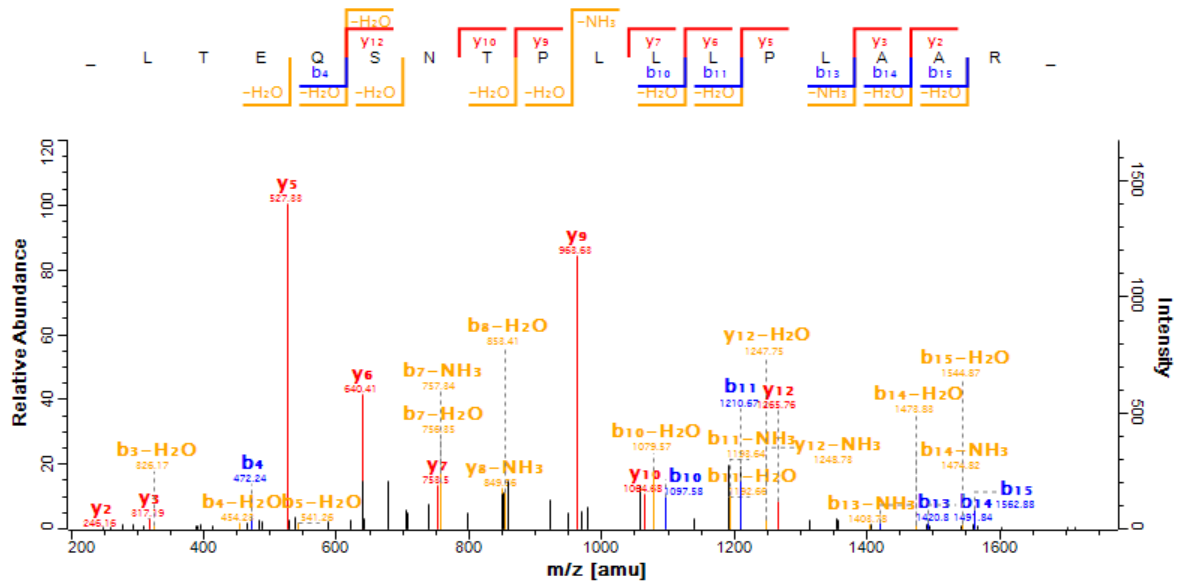
Best Match Spectrum:

Scan number 6373 Raw file Prt-OGE-Batch2-Mock-Frac13
Method ITMS: CID Genenames SMN1



Protein Group ID: 181
Protein Accession Numbers: Q9NYL2-2; B4DQ47
Gene Names: ZAK
Peptide Sequence: LTEQSNTPLLLPLAAR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 133.48
Best Match Posterior Error Probability: 1.72E-05
Best Match Spectrum:

Scan number 5491 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac12
Method ITMS; CID **Genenames** ZAK



Protein Group ID: 182

Protein Accession Numbers: G5E9T8; O95249; E9PCW1; K7EJC8; J3KST5; B4DQA8

Gene Names: GOSR1

Peptide Sequence: MFETMAIEIEQLLAR

Total Number of Spectra: 1

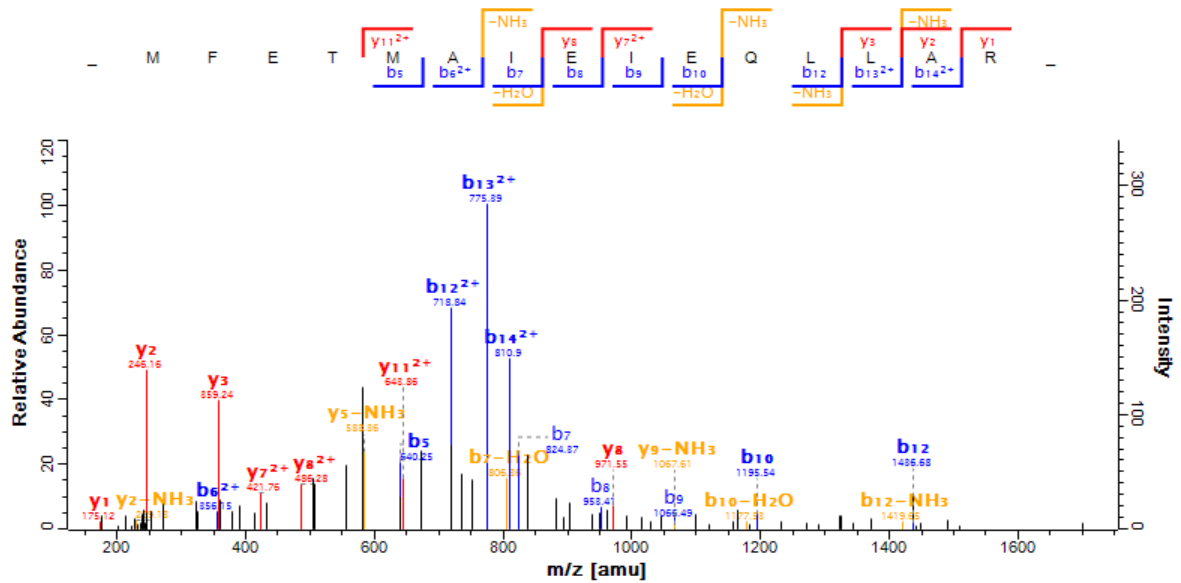
Number of Replicates (out of 10): 1

Best Match Score: 111.79

Best Match Posterior Error Probability: 5.63E-05

Best Match Spectrum:

Scan number	8211	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac11
Method	ITMS; CID	Genenames	GOSR1



Protein Group ID: 183

Protein Accession Numbers: Q9BW92; Q9H9V2; Q5T5F2; B4DQF3

Gene Names: TARS2

Peptide Sequence: LGLFEELWAAQVK

Total Number of Spectra: 1

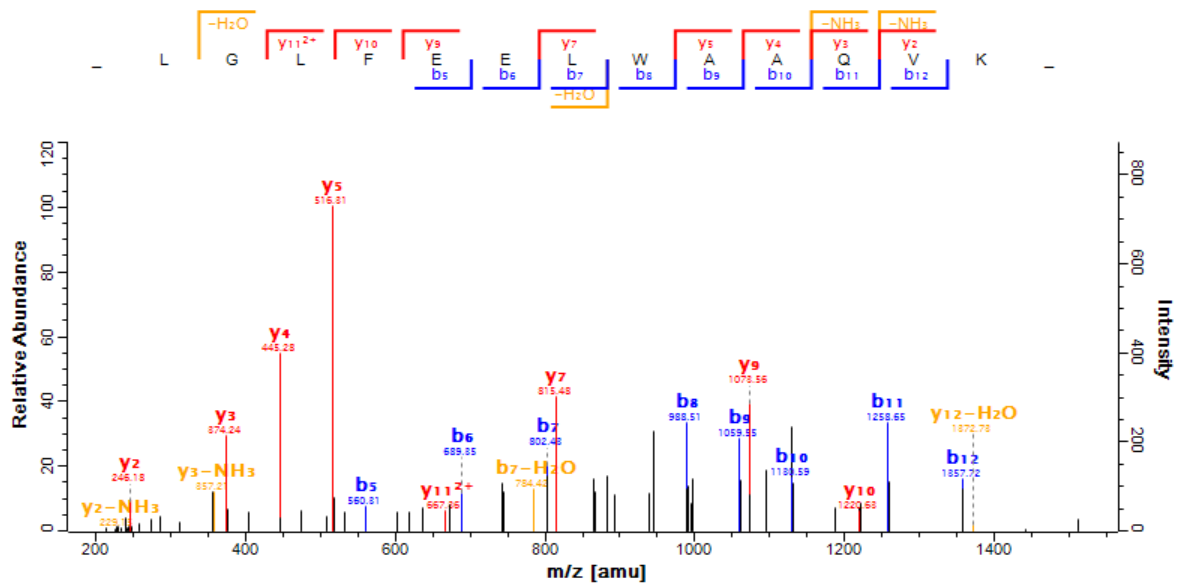
Number of Replicates (out of 10): 1

Best Match Score: 100.55

Best Match Posterior Error Probability: 0.0005437

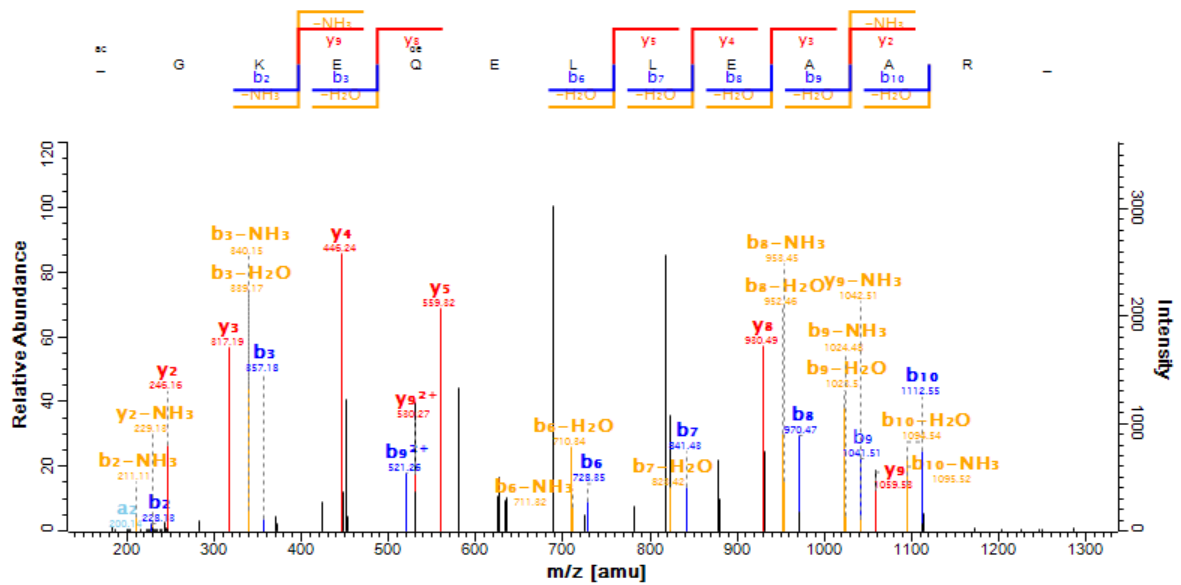
Best Match Spectrum:

Scan number 7037 **Raw file** Prt-OGE-Batch2-Mock-Frac15
Method ITMS; CID **Genenames** TARS2



Protein Group ID: 188
Protein Accession Numbers: Q92625; B4DQW8
Gene Names: ANKS1A
Peptide Sequence: GKEQELLEAAR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 211.64
Best Match Posterior Error Probability: 9.53E-29
Best Match Spectrum:

Scan number 2762 **Raw file** Prt-OGE-Batch3-WT-Frac13
Method ITMS; CID **Genenames** ANKS1A



Protein Group ID: 189

Protein Accession Numbers: Q86UY6; B4DR03; F5H2C9

Gene Names: NAA40

Peptide Sequence: LGDPLEAFPVK

Total Number of Spectra: 1

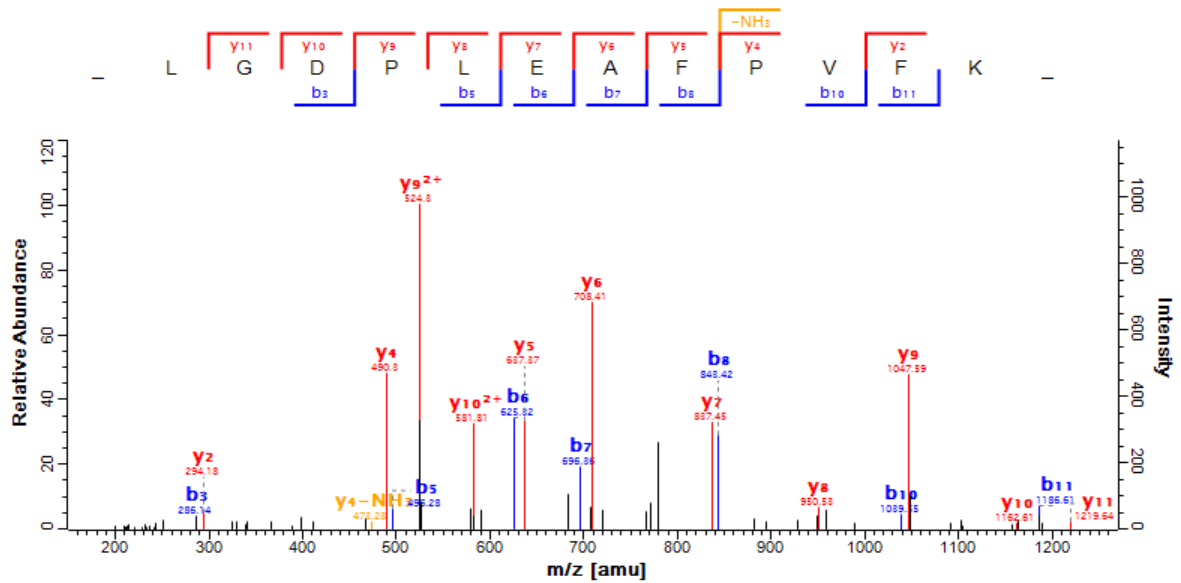
Number of Replicates (out of 10): 1

Best Match Score: 114.82

Best Match Posterior Error Probability: 0.00021262

Best Match Spectrum:

Scan number 6698 **Raw file** Prt-OGE-Batch2-Mock-Frac17
Method ITMS; CID **Genenames** NAA40



Protein Group ID: 196

Protein Accession Numbers: Q92973; Q92973-2; Q92973-3; E7EW37; B4DSC0; J3KPU5

Gene Names: TNPO1

Peptide Sequence: MEYEWKPDEQGLQQILQLLK

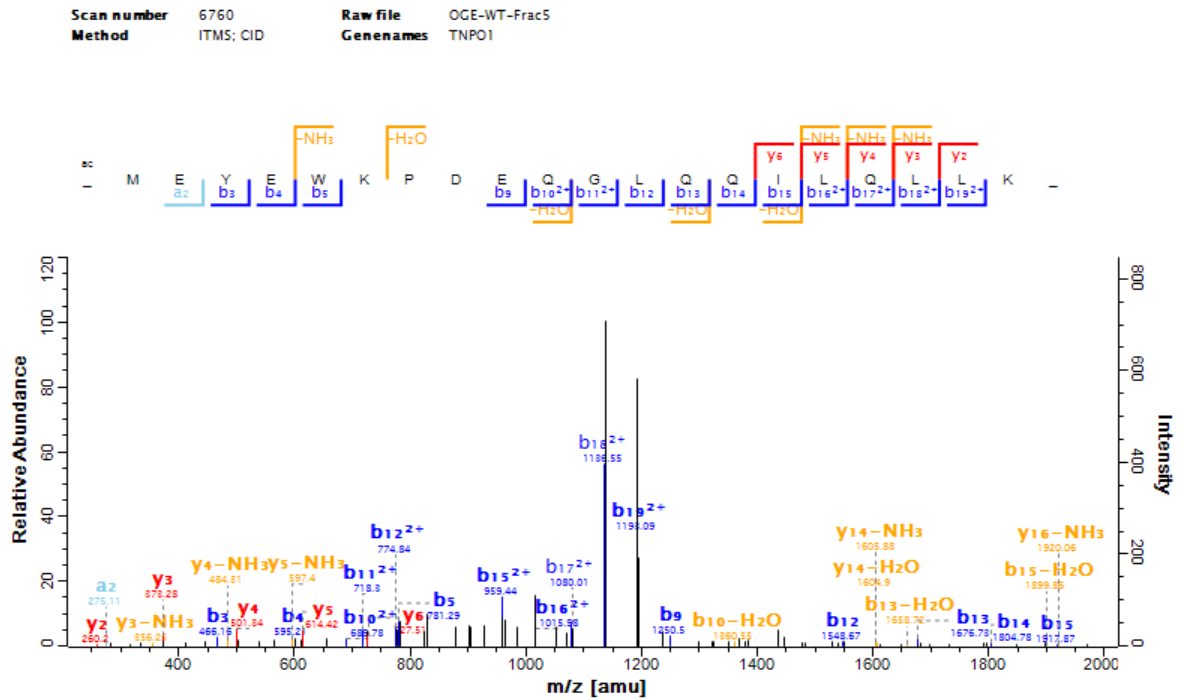
Total Number of Spectra: 26

Number of Replicates (out of 10): 9

Best Match Score: 147.64

Best Match Posterior Error Probability: 1.92E-09

Best Match Spectrum:



Protein Group ID: 200

Protein Accession Numbers: J3KMZ8; Q92785; B4DT58

Gene Names: DPF2

Peptide Sequence: EGLISQDGSSLEALLR

Total Number of Spectra: 2

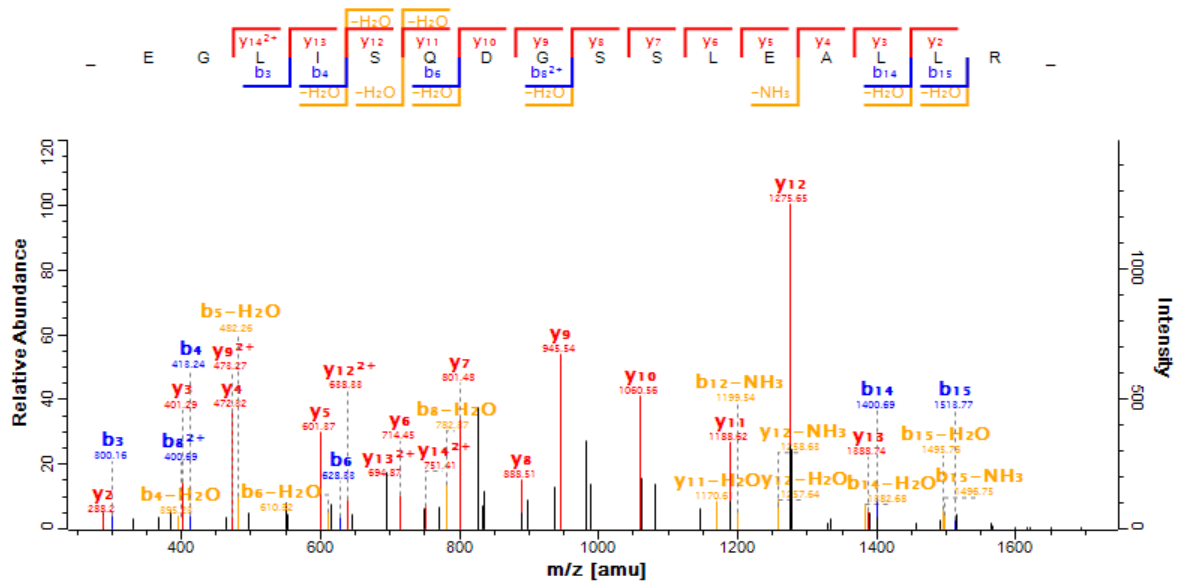
Number of Replicates (out of 10): 2

Best Match Score: 165.34

Best Match Posterior Error Probability: 5.83E-15

Best Match Spectrum:

Scan number 6167 **Raw file** Prt-OGE-Batch3-Mock-Frac12
Method ITMS; CID **Genenames** DPF2



Protein Group ID: 204

Protein Accession Numbers: Q8ND24; B4DTD1; E9PN76

Gene Names: RNF214

Peptide Sequence: TTMAGLTMEELIQLVAAR

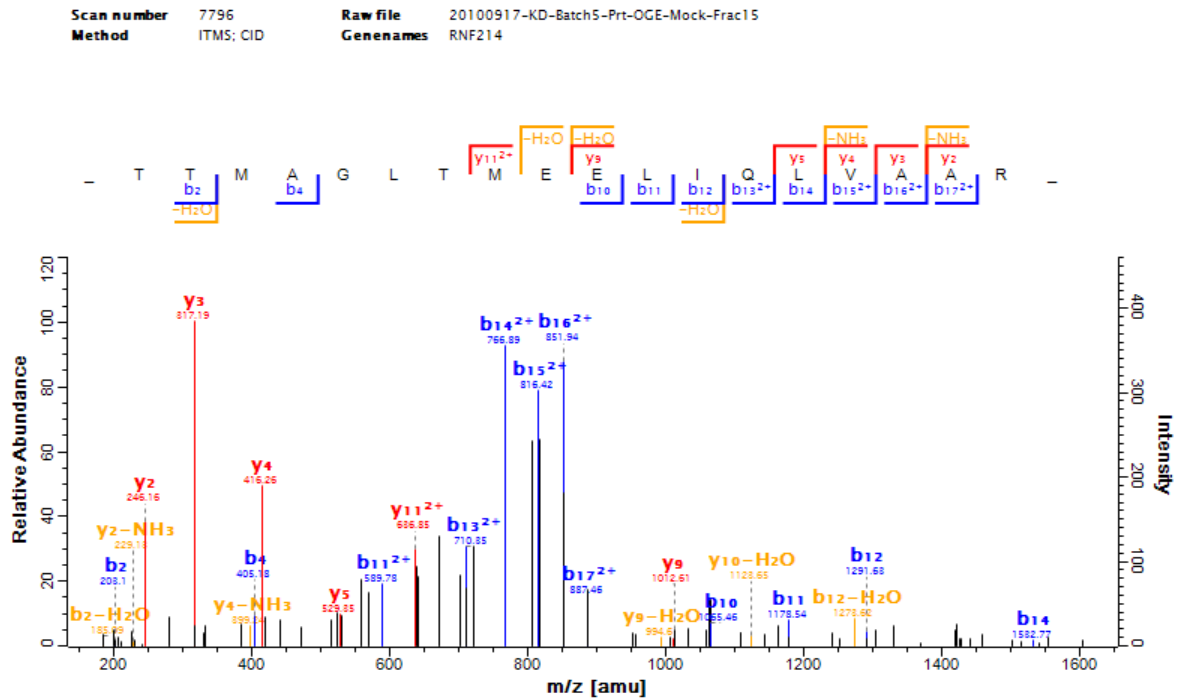
Total Number of Spectra: 5

Number of Replicates (out of 10): 3

Best Match Score: 95.57

Best Match Posterior Error Probability: 0.00031958

Best Match Spectrum:



Protein Group ID: 205

Protein Accession Numbers: O15162; C9J7K9; C9JE06; C9J9P4; B4DTE8; C9J0H3

Gene Names: PLSCR1

Peptide Sequence: IIDNMGQEVITLRLR

Total Number of Spectra: 1

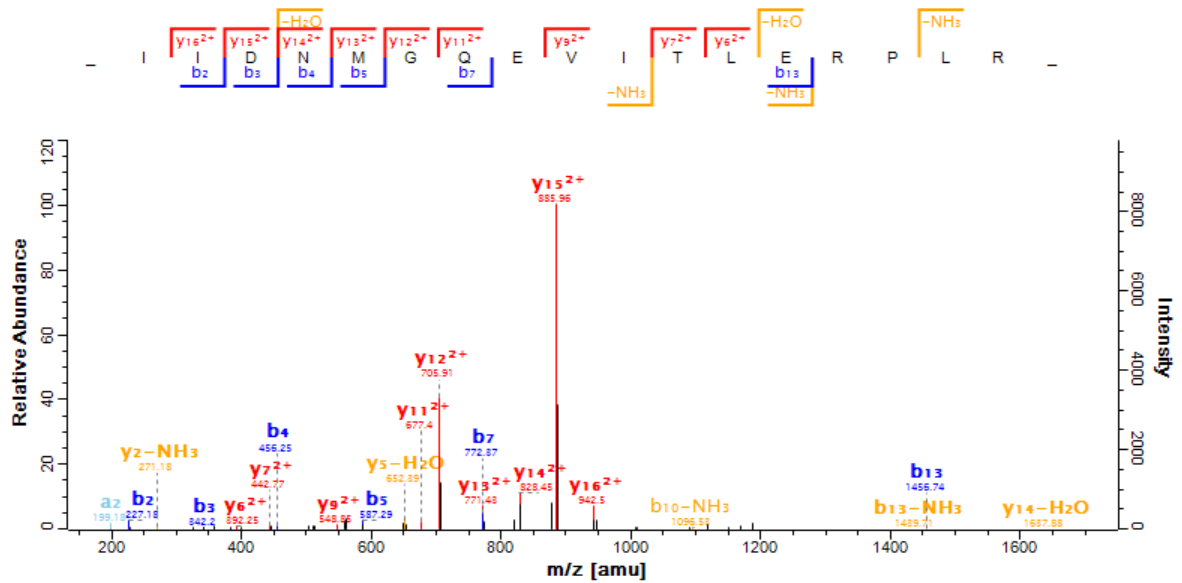
Number of Replicates (out of 10): 1

Best Match Score: 115.78

Best Match Posterior Error Probability: 0.0004844

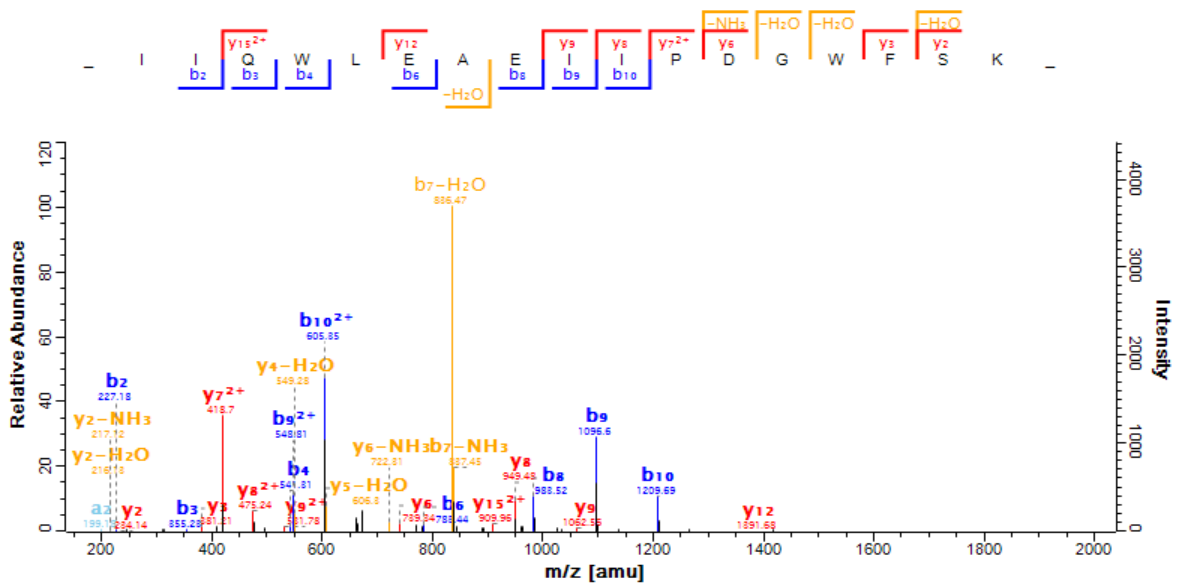
Best Match Spectrum:

Scan number 5132 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac12
Method ITMS; CID **Genenames** PLSCR1



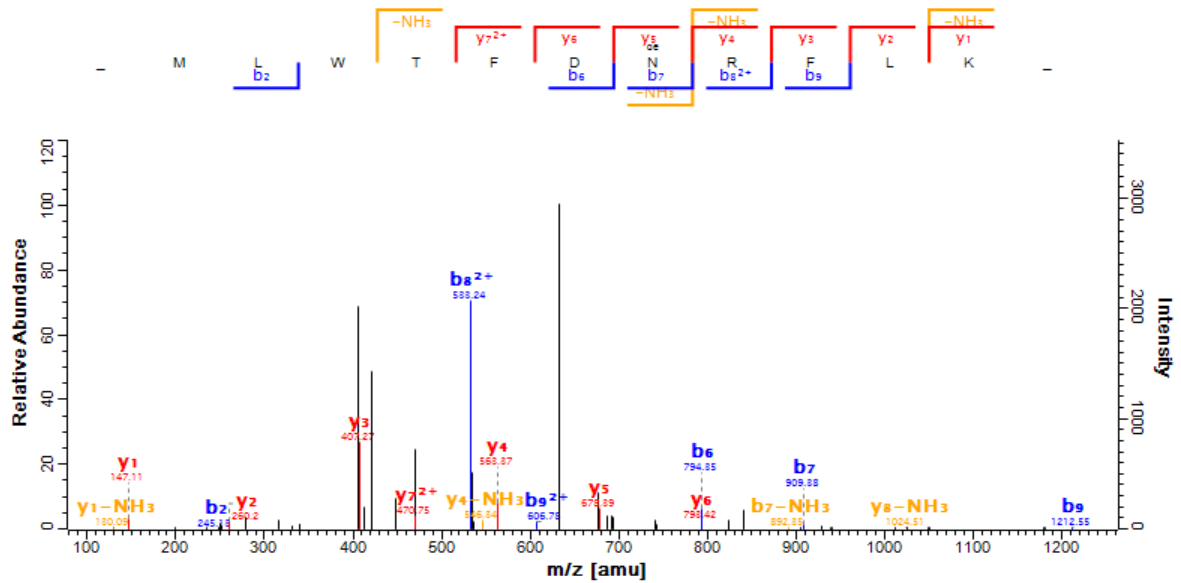
Protein Group ID: 207
Protein Accession Numbers: Q12841; B4DTT5
Gene Names: FSTL1
Peptide Sequence: IIQWLEAEIIPDGWFSK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 106.6
Best Match Posterior Error Probability: 0.00017919
Best Match Spectrum:

Scan number 6788 **Raw file** OGE-WT-Frac7
Method ITMS; CID **Genenames** FSTL1



Protein Group ID: 211
Protein Accession Numbers: Q9BRP7; B4DUU2
Gene Names: FDXACB1
Peptide Sequence: MLWTFDNRFLK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 104.22
Best Match Posterior Error Probability: 0.0080316
Best Match Spectrum:

Scan number 2226 **Raw file** Prt-OGE-Batch2-WT-Frac20
Method ITMS; CID **Genenames** FDXACB1



Protein Group ID: 214

Protein Accession Numbers: B4DW92; K7ES62; Q86WQ0

Gene Names: NR2C2AP

Peptide Sequence: VTFEDATDFFGR

Total Number of Spectra: 1

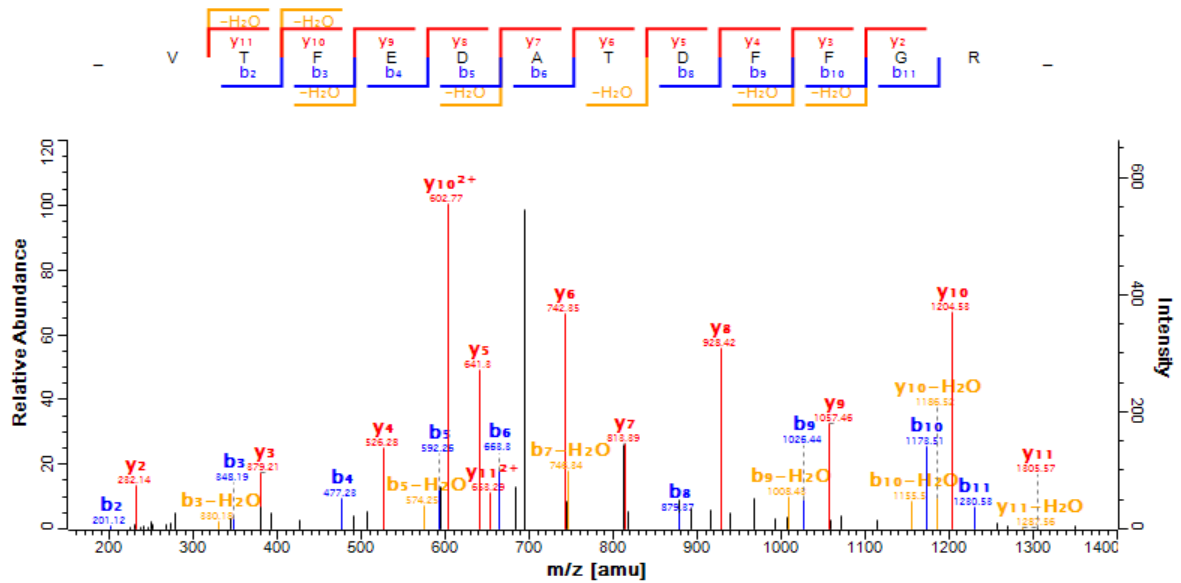
Number of Replicates (out of 10): 1

Best Match Score: 168.98

Best Match Posterior Error Probability: 3.29E-07

Best Match Spectrum:

Scan number 5487 **Raw file** Prt-OGE-Batch3--Mock-Frac10
Method ITMS; CID **Genenames** NR2C2AP



Protein Group ID: 215

Protein Accession Numbers: Q9Y6I4; H0YMI4; Q6JHV3; Q9Y6I4-2; H0YKU8; H0YLB7; B4DWJ6

Gene Names: USP3

Peptide Sequence: KFDPFLDLSLDIPSQFR

Total Number of Spectra: 4

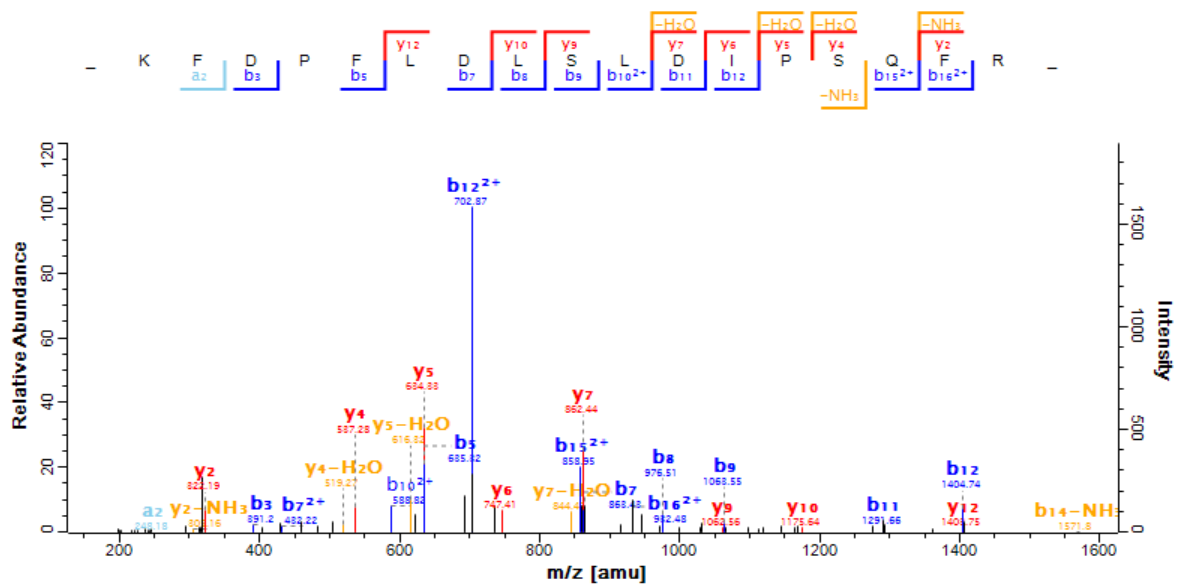
Number of Replicates (out of 10): 4

Best Match Score: 101.78

Best Match Posterior Error Probability: 0.00056212

Best Match Spectrum:

Scan number	6785	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac20
Method	ITMS; CID	Genenames	USP3



Protein Group ID: 216

Protein Accession Numbers: Q96F24; B4DWS0; Q96F24-2

Gene Names: NRBF2

Peptide Sequence: DIIPNLPLDFPSPLELPMLSEDLK

Total Number of Spectra: 4

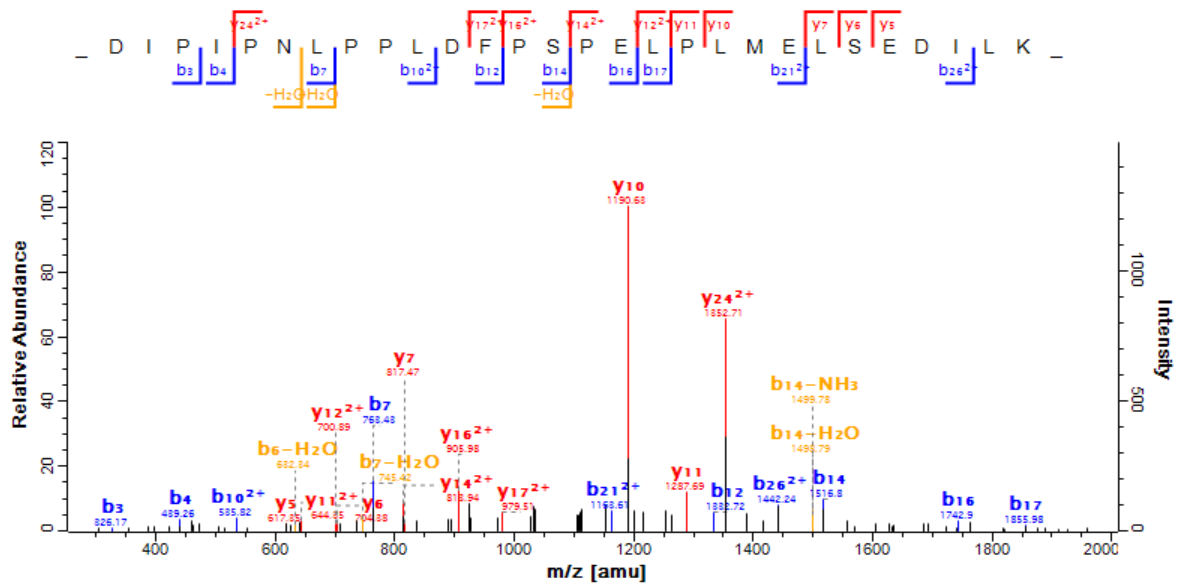
Number of Replicates (out of 10): 3

Best Match Score: 86.08

Best Match Posterior Error Probability: 2.11E-07

Best Match Spectrum:

Scan number 9732 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac10
Method ITMS; CID **Genenames** NRBF2



Protein Group ID: 217

Protein Accession Numbers: P40616; B4DWW1; B4DZG7; F8W1Z8

Gene Names: ARL1

Peptide Sequence: GTGLDEAMEWLVLK

Total Number of Spectra: 55

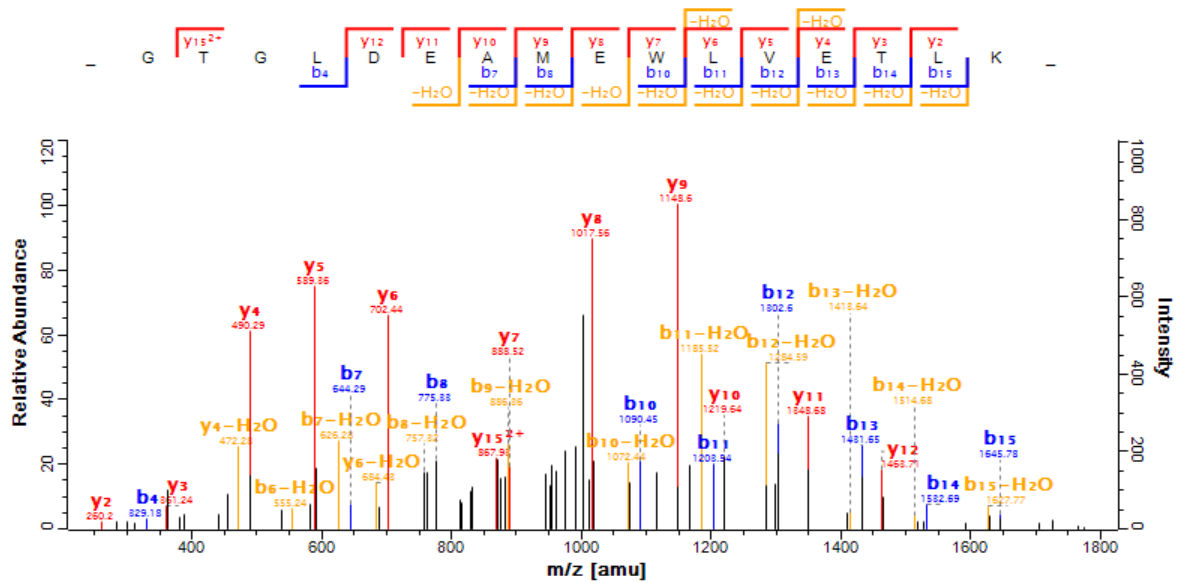
Number of Replicates (out of 10): 9

Best Match Score: 208.47

Best Match Posterior Error Probability: 9.46E-43

Best Match Spectrum:

Scan number 8553 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac9
Method ITMS; CID **Genenames** ARL1



Protein Group ID: 221

Protein Accession Numbers: O15523; B4DXX7; C9J081

Gene Names: DDX3Y

Peptide Sequence: TAAFLLPILSQIYTDGPGEALK

Total Number of Spectra: 7

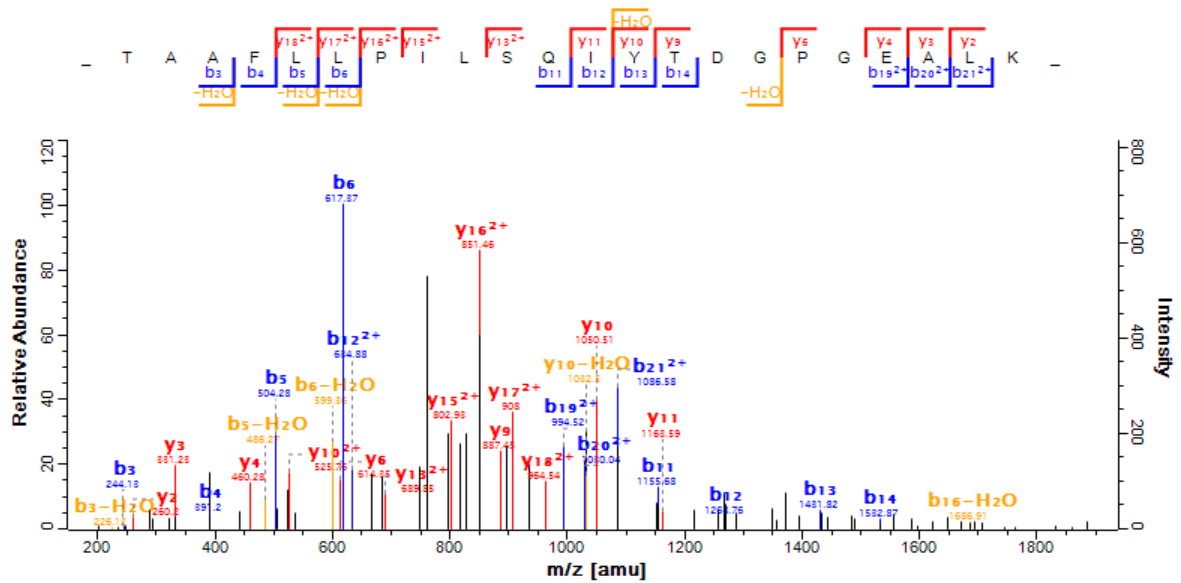
Number of Replicates (out of 10): 5

Best Match Score: 124.25

Best Match Posterior Error Probability: 2.81E-10

Best Match Spectrum:

Scan number	7978	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac17
Method	ITMS; CID	Genenames	DDX3Y



Protein Group ID: 227

Protein Accession Numbers: P04049-2; P04049; B4E0X2; H7C155; B4E1N6

Gene Names: RAF1

Peptide Sequence: PLFPQILSSIQLLQHS LPK

Total Number of Spectra: 1

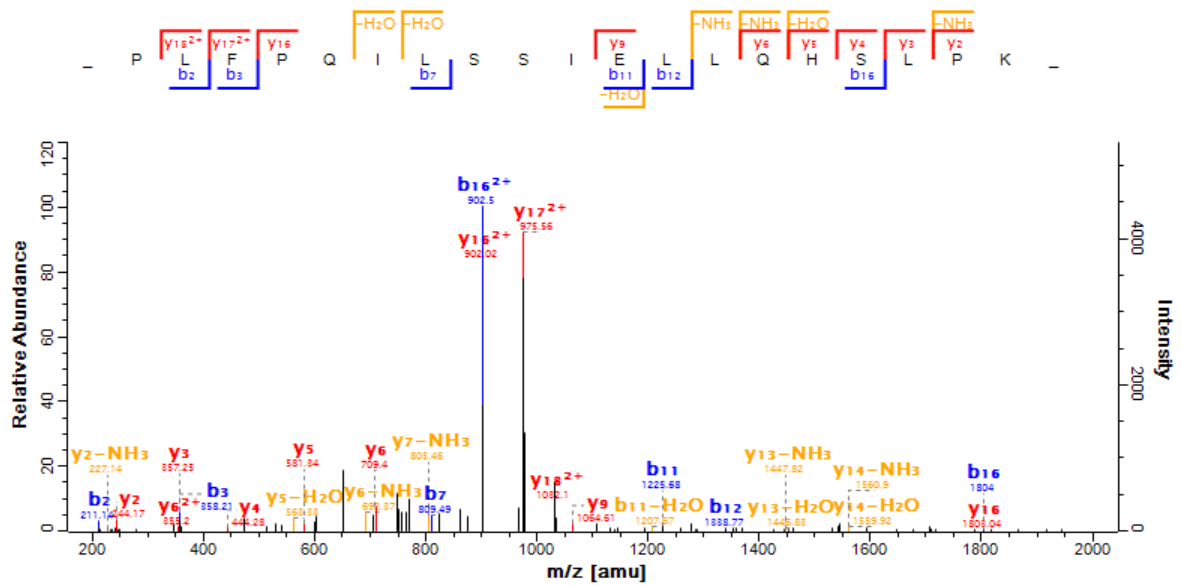
Number of Replicates (out of 10): 1

Best Match Score: 86.367

Best Match Posterior Error Probability: 0.00046082

Best Match Spectrum:

Scan number 8308 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac20
Method ITMS; CID **Genenames** RAF1



Protein Group ID: 233

Protein Accession Numbers: B4E2P2; Q9UNL2; C9JA28

Gene Names: SSR3

Peptide Sequence: QQSEEDLLLQDFSR

Total Number of Spectra: 1

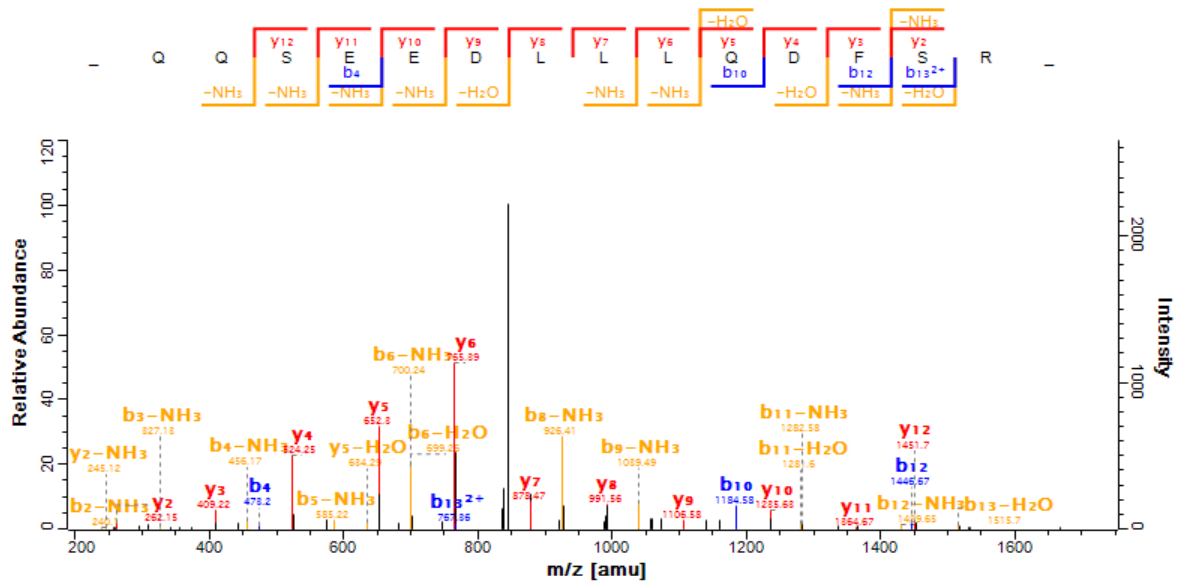
Number of Replicates (out of 10): 1

Best Match Score: 81.448

Best Match Posterior Error Probability: 0.0014743

Best Match Spectrum:

Scan number 3726 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** SSR3



Protein Group ID: 237

Protein Accession Numbers: Q8N6R0; B4E2X3; Q8N6R0-4; Q8N6R0-3; Q8N6R0-1

Gene Names: METTL13

Peptide Sequence: VMELAPAGMPTQQQVLPFSLVGGDVGVR

Total Number of Spectra: 2

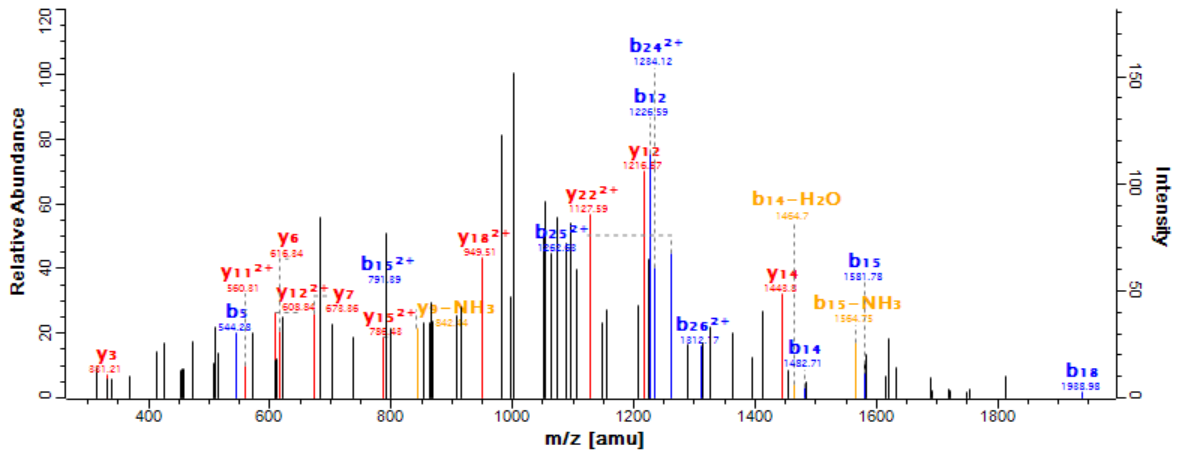
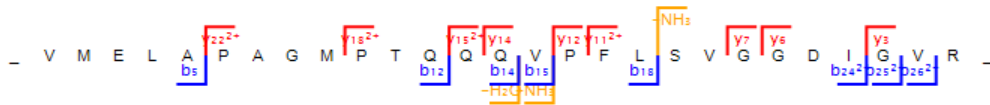
Number of Replicates (out of 10): 2

Best Match Score: 55.469

Best Match Posterior Error Probability: 0.00077373

Best Match Spectrum:

Scan number	6342	Raw file	20100914-KD-Batch4-Prt-OGE-Mock-Frac14
Method	ITMS; CID	Genenames	METTL13



Protein Group ID: 243

Protein Accession Numbers: B5MBZ0; Q9HC35; B5MCW9; F2Z2B5

Gene Names: EML4

Peptide Sequence: YSAHSSHTVNSFTHNSHLISTGGK

Total Number of Spectra: 1

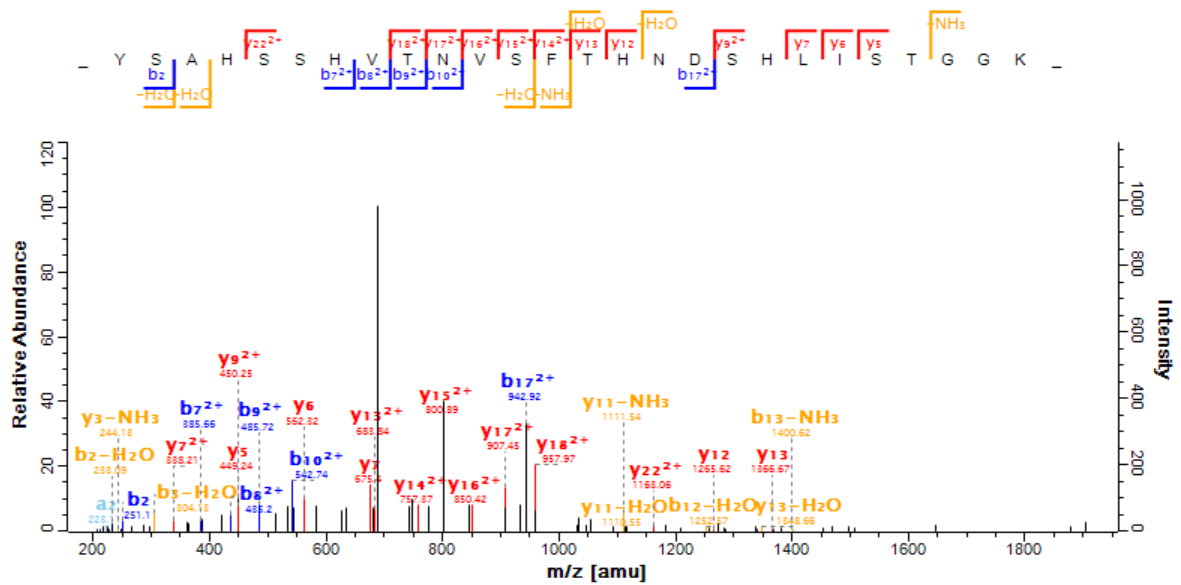
Number of Replicates (out of 10): 1

Best Match Score: 84.946

Best Match Posterior Error Probability: 2.17E-06

Best Match Spectrum:

Scan number	2698	Raw file	Prt-OGE-Batch2-Mock-Frac14
Method	ITMS; CID	Genenames	EML4



Protein Group ID: 246

Protein Accession Numbers: B5MCC9; B5MCP5; Q99674

Gene Names: CGREF1

Peptide Sequence: RESLDPVQEPGGQAEDGDVPGPR

Total Number of Spectra: 1

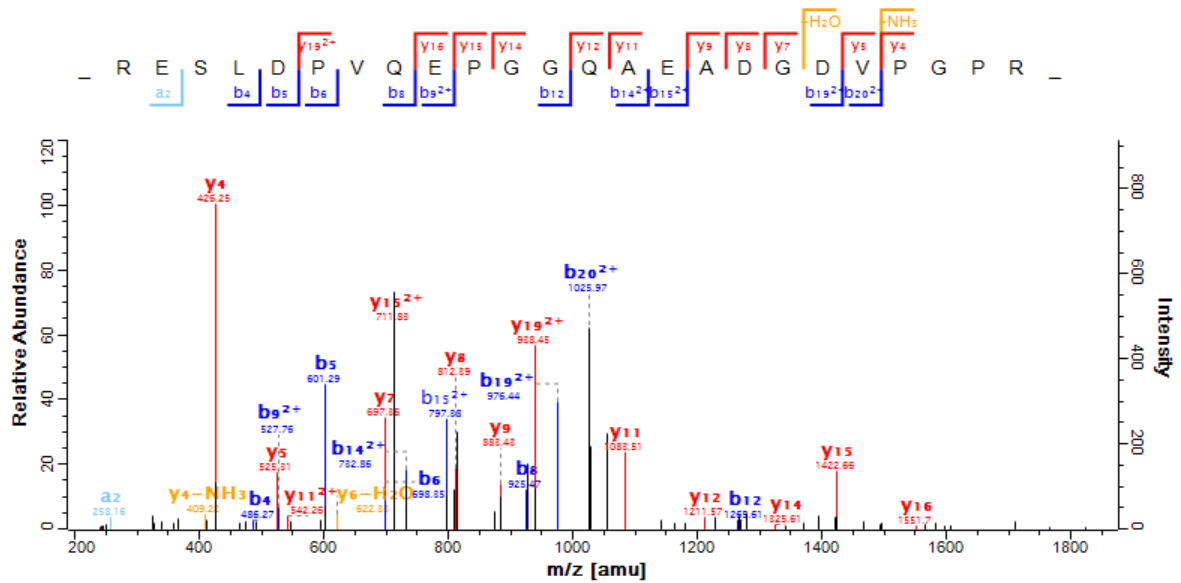
Number of Replicates (out of 10): 1

Best Match Score: 92.01

Best Match Posterior Error Probability: 8.93E-06

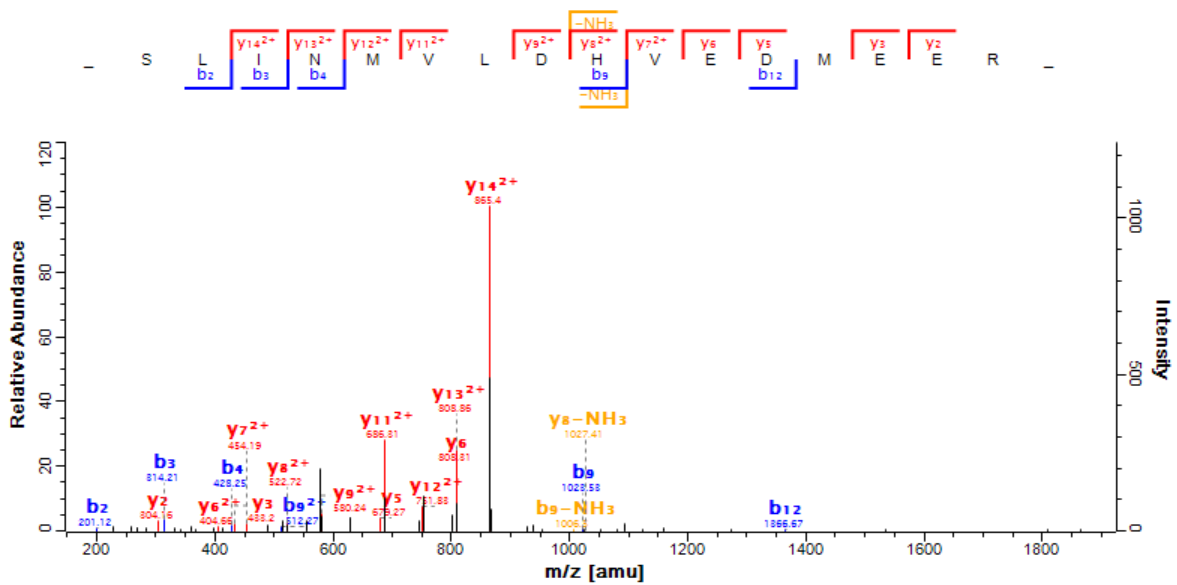
Best Match Spectrum:

Scan number	2606	Raw file	Prt-OGE-Batch3--Mock-Frac3
Method	ITMS; CID	Genenames	CGREF1



Protein Group ID: 249
Protein Accession Numbers: Q2NKX8; B5MDQ0
Gene Names: ERCC6L
Peptide Sequence: SLINMVLVDHVEDMEER
Total Number of Spectra: 9
Number of Replicates (out of 10): 6
Best Match Score: 110.98
Best Match Posterior Error Probability: 0.00012824
Best Match Spectrum:

Scan number 6519 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac4
Method ITMS; CID **Genenames** ERCC6L



Protein Group ID: 252

Protein Accession Numbers: D6W592; Q8WVV9; Q8WVV9-4; B7WPG3; Q5JB52; C9IYN3; Q8WVV9-2; Q8WVV9-3

Gene Names: HNRPLL

Peptide Sequence: LKTEEGEIDYSAEEGENR

Total Number of Spectra: 4

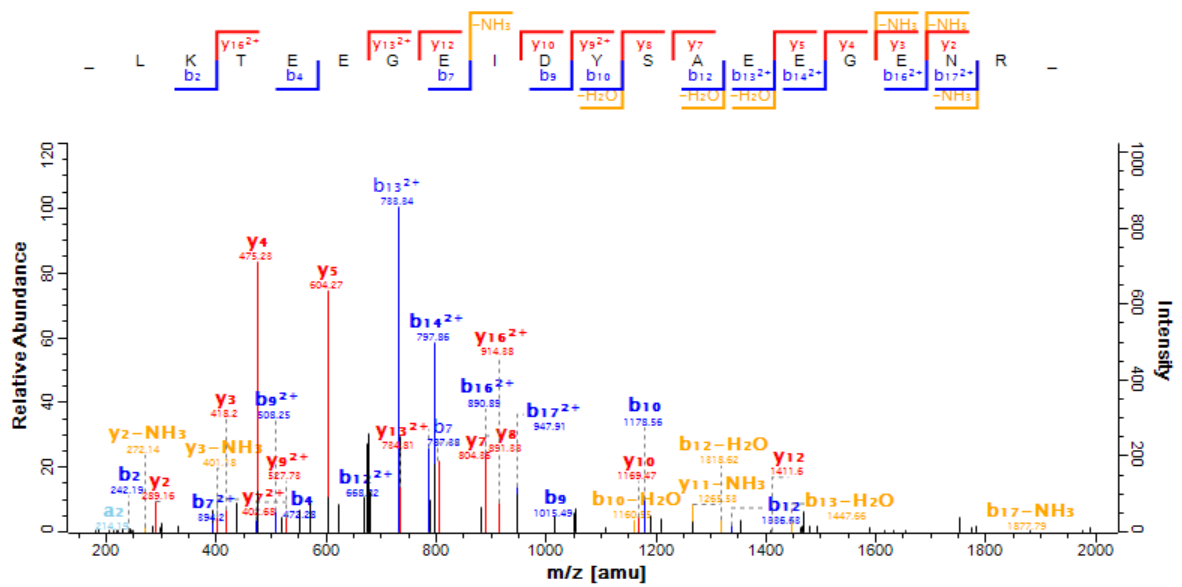
Number of Replicates (out of 10): 4

Best Match Score: 137.81

Best Match Posterior Error Probability: 1.72E-05

Best Match Spectrum:

Scan number	1386	Raw file	Prt-OGE-Batch3-WT-Frac17
Method	ITMS: CID	Genenames	HNRPLL



Protein Group ID: 253

Protein Accession Numbers: P40123; E9PDI2; B7Z1C4; B7Z385

Gene Names: CAP2

Peptide Sequence: SALFAQLNQGEAITK

Total Number of Spectra: 2

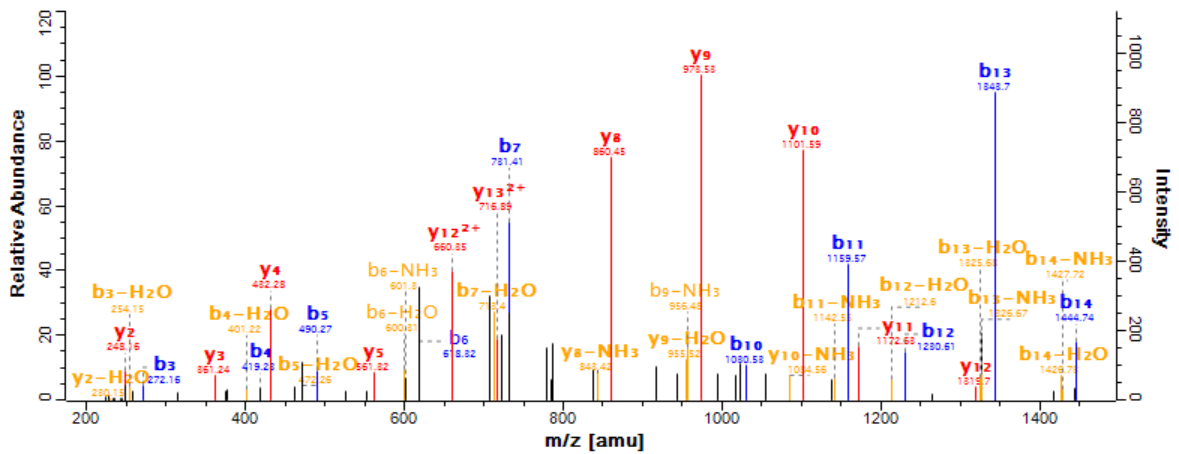
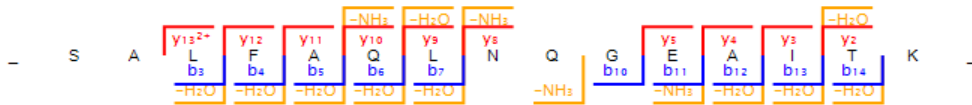
Number of Replicates (out of 10): 2

Best Match Score: 222.45

Best Match Posterior Error Probability: 4.79E-49

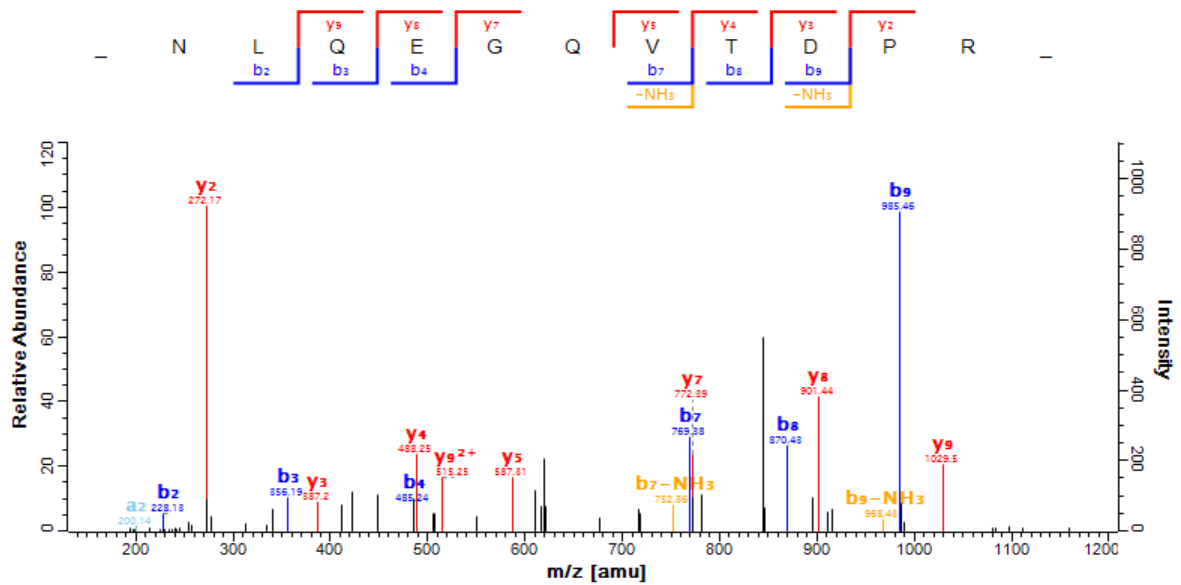
Best Match Spectrum:

Scan number 4205 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac12
Method ITMS; CID **Genenames** CAP2



Protein Group ID: 254
Protein Accession Numbers: B7Z1E5; Q92600
Gene Names: RQCD1
Peptide Sequence: NLQEGQVTDP
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 94.191
Best Match Posterior Error Probability: 0.00056414
Best Match Spectrum:

Scan number 1270 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac18
Method ITMS; CID **Genenames** RQCD1



Protein Group ID: 256

Protein Accession Numbers: Q8WZA2; E7EVE5; E9PB94; Q8WZA2-3; B7Z283; B7Z3T6; B7Z278; Q8WZA2-2

Gene Names: RAPGEF4

Peptide Sequence: ASNQNSQPQQK

Total Number of Spectra: 1

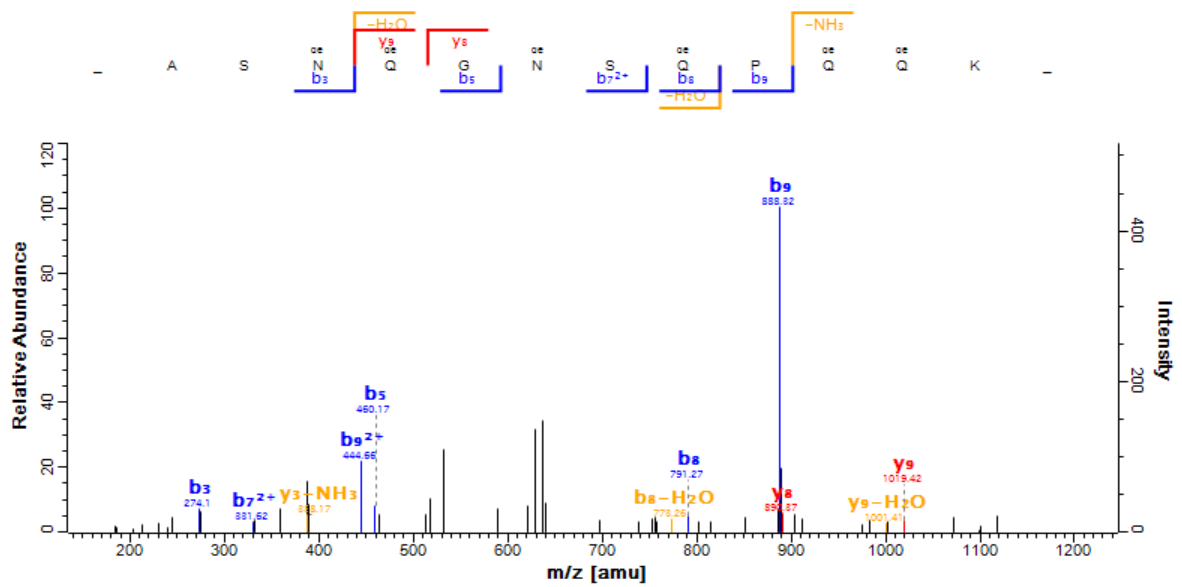
Number of Replicates (out of 10): 1

Best Match Score: 41.242

Best Match Posterior Error Probability: 0.049718

Best Match Spectrum:

Scan number 810 Raw file 20100927-KD-Batch4-Prt-OGE-WT-Frac3
Method ITMS; CID Genenames RAPGEF4



Protein Group ID: 258

Protein Accession Numbers: Q14746; Q14746-2; B7Z2Y2; F5H1E5; B7Z7N2

Gene Names: COG2

Peptide Sequence: SFSALAELVAAK

Total Number of Spectra: 1

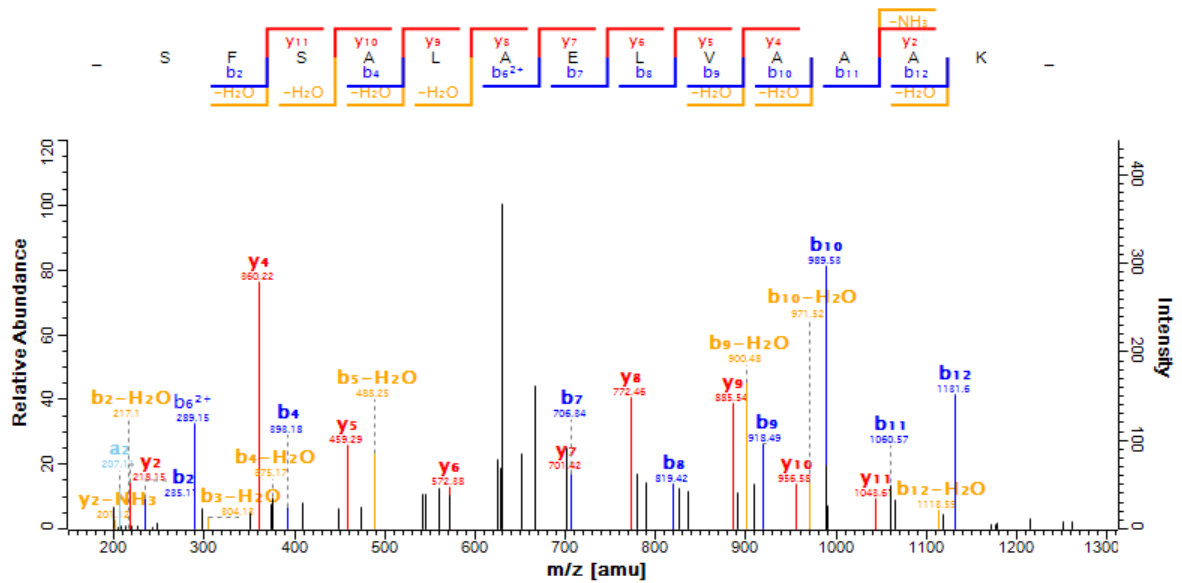
Number of Replicates (out of 10): 1

Best Match Score: 135.02

Best Match Posterior Error Probability: 3.27E-05

Best Match Spectrum:

Scan number 5064 **Raw file** Prt-OGE-Batch2-WT-Frac13
Method ITMS; CID **Genenames** COG2



Protein Group ID: 259

Protein Accession Numbers: Q14964; P20340; P20340-2; Q9NRW1; H0YGL6; B7Z337; F5H668; H7BYW1; F5GZB1; J3KR73; C9JU14; F5GXN4; C9JB90

Gene Names: RAB39A;RAB6A;RAB6B

Peptide Sequence: LQLWDTAGQER

Total Number of Spectra: 26

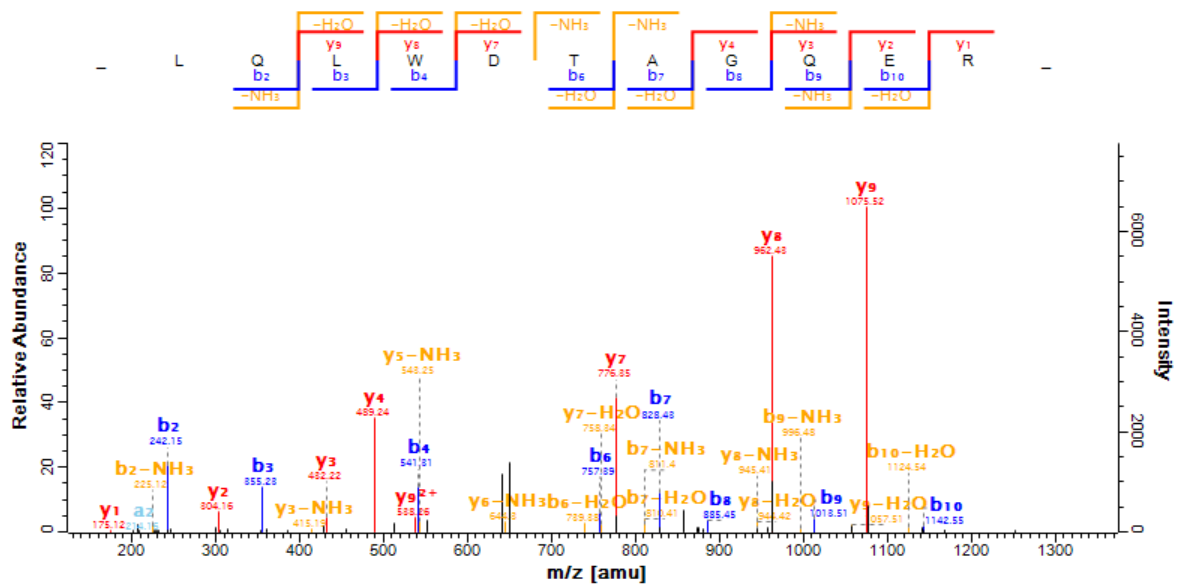
Number of Replicates (out of 10): 8

Best Match Score: 178.71

Best Match Posterior Error Probability: 8.12E-11

Best Match Spectrum:

Scan number 3216 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac13
Method ITMS: CID **Genenames** RAB39A;RAB6A;RAB6B



Protein Group ID: 260

Protein Accession Numbers: Q9NPH2; G5E9U0; Q9NPH2-2; G3V1R9; B7Z3K3; J3QRY8; J3KRC6

Gene Names: ISYNA1

Peptide Sequence: SVLVDFLIGSGLK

Total Number of Spectra: 6

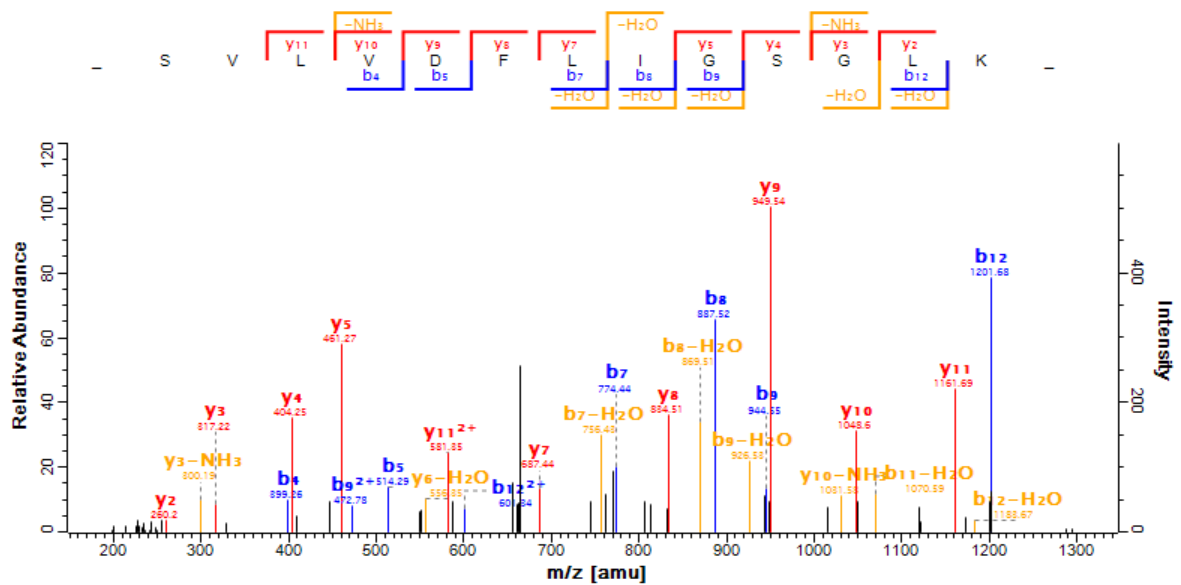
Number of Replicates (out of 10): 6

Best Match Score: 150.21

Best Match Posterior Error Probability: 1.01E-05

Best Match Spectrum:

Scan number	7277	Raw file	Prt-OGE-Batch2-Mock-Frac9
Method	ITMS; CID	Genenames	ISYNA1



Protein Group ID: 268

Protein Accession Numbers: O00115; B7Z4K6; K7ENE5

Gene Names: DNASE2

Peptide Sequence: ALINSPEGAVGR

Total Number of Spectra: 3

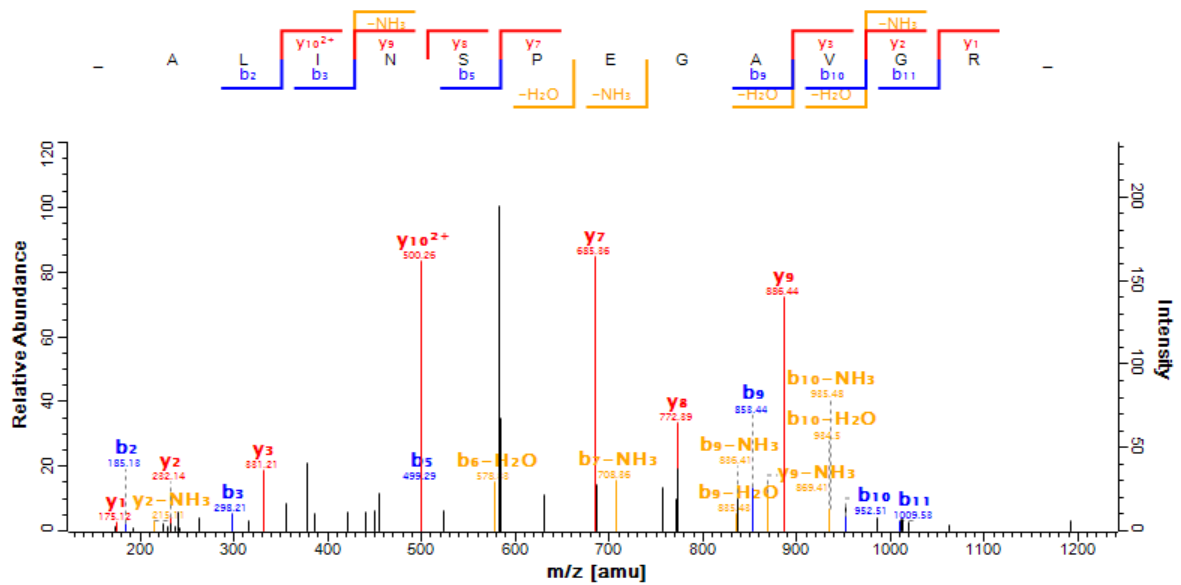
Number of Replicates (out of 10): 2

Best Match Score: 106.67

Best Match Posterior Error Probability: 0.00022814

Best Match Spectrum:

Scan number 2313 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac5
Method ITMS; CID **Genenames** DNASE2



Protein Group ID: 269

Protein Accession Numbers: B7Z4W5; Q16773; Q16773-2

Gene Names: CCBL1

Peptide Sequence: SLQSVGLKPIIPQGSYFLITDISDFK

Total Number of Spectra: 1

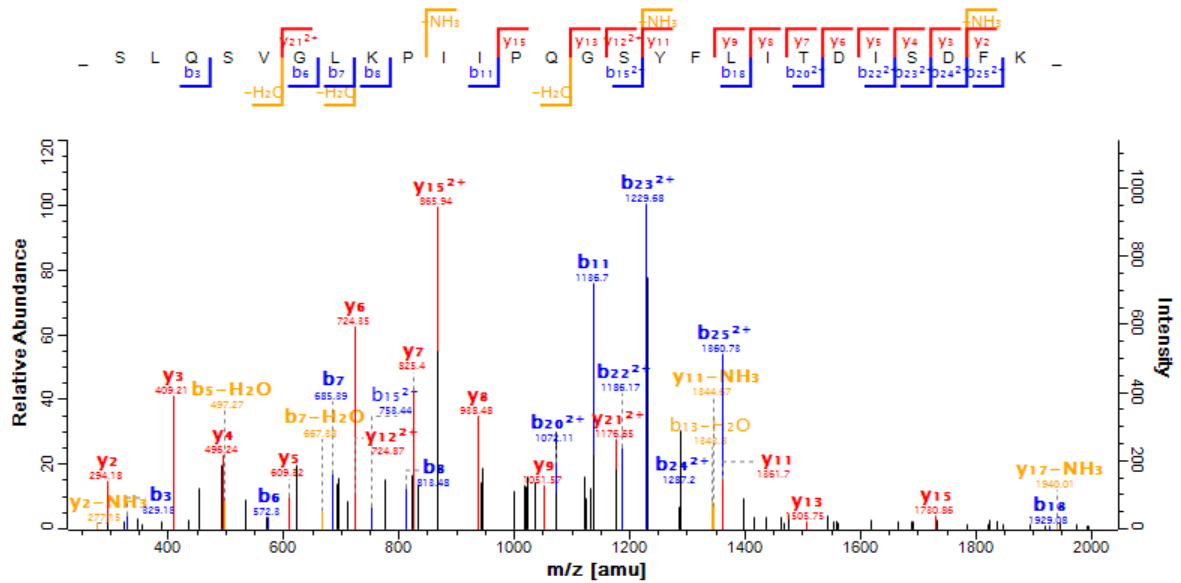
Number of Replicates (out of 10): 1

Best Match Score: 100.94

Best Match Posterior Error Probability: 2.86E-09

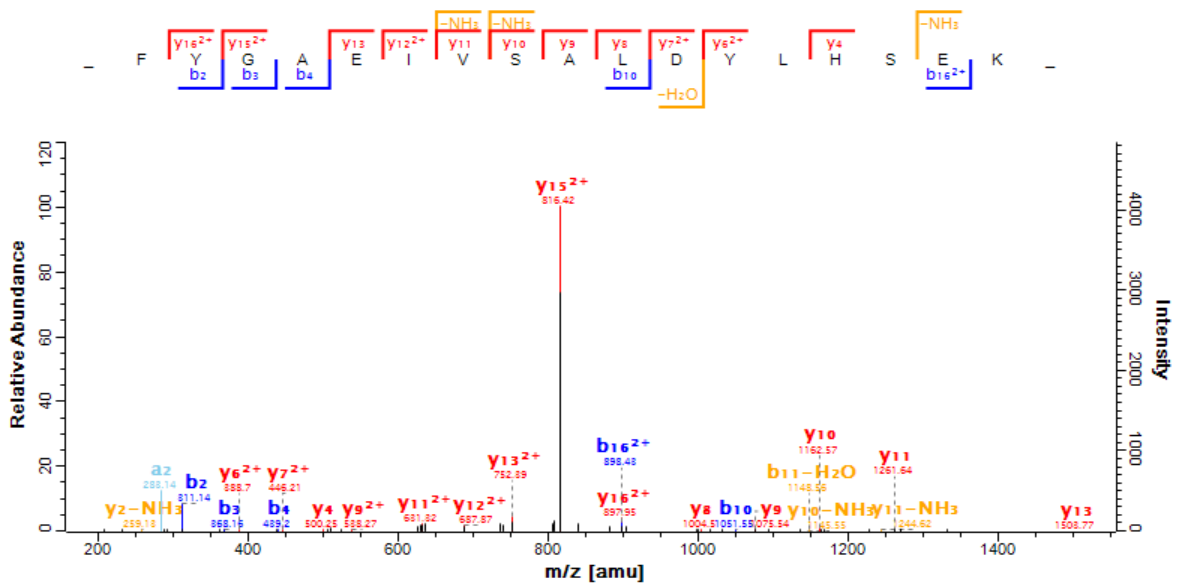
Best Match Spectrum:

Scan number 7499 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac13
Method ITMS; CID **Genenames** CCBL1



Protein Group ID: 271
Protein Accession Numbers: P31749; B7Z5R1
Gene Names: AKT1
Peptide Sequence: FYGAEIVSALDYLHSEK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 125.53
Best Match Posterior Error Probability: 7.27E-05
Best Match Spectrum:

Scan number 5124 **Raw file** Prt-OGE-Batch3-WT-Frac10
Method ITMS; CID **Genenames** AKT1



Protein Group ID: 272

Protein Accession Numbers: Q12979; Q12979-2; F5H8B3; B7Z683; I3L1U8

Gene Names: ABR

Peptide Sequence: ISQNFLSSINEDIDPR

Total Number of Spectra: 1

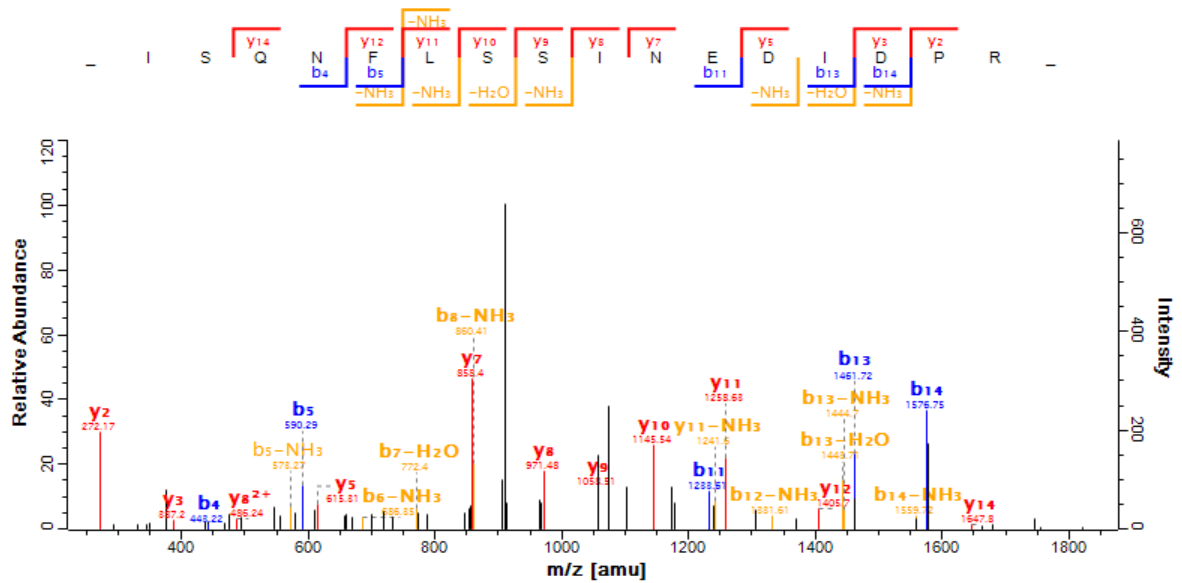
Number of Replicates (out of 10): 1

Best Match Score: 97.579

Best Match Posterior Error Probability: 0.00022337

Best Match Spectrum:

Scan number	4476	Raw file	Prt-OGE-Batch2-WT-Frac14
Method	ITMS; CID	Genenames	ABR



Protein Group ID: 273

Protein Accession Numbers: O15260; Q5T8U7; Q5T8U5; O15260-2; B7Z6A4

Gene Names: SURF4

Peptide Sequence: GQNLMGTAE D F A Q F L R

Total Number of Spectra: 18

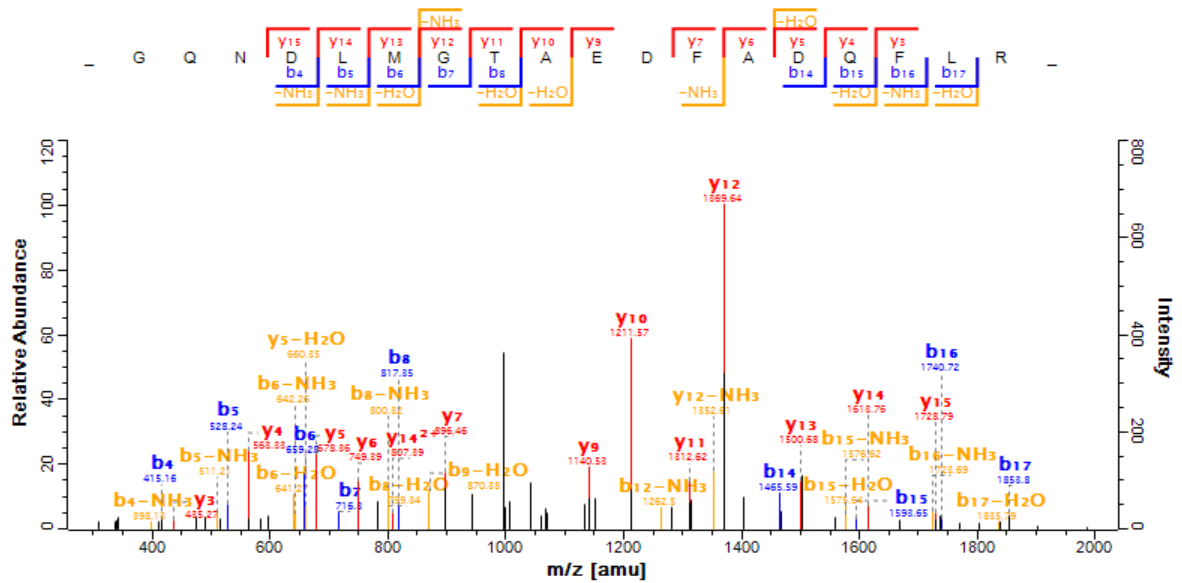
Number of Replicates (out of 10): 7

Best Match Score: 192.16

Best Match Posterior Error Probability: 7.15E-32

Best Match Spectrum:

Scan number 7466 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac9
Method ITMS; CID **Genenames** SURF4



Protein Group ID: 277

Protein Accession Numbers: B7Z713; D6RCM8; O95379; O95379-2; O95379-3; E5RIJ3

Gene Names: TNFAIP8

Peptide Sequence: SIATTLIDDTSSSEVLDELYR

Total Number of Spectra: 1

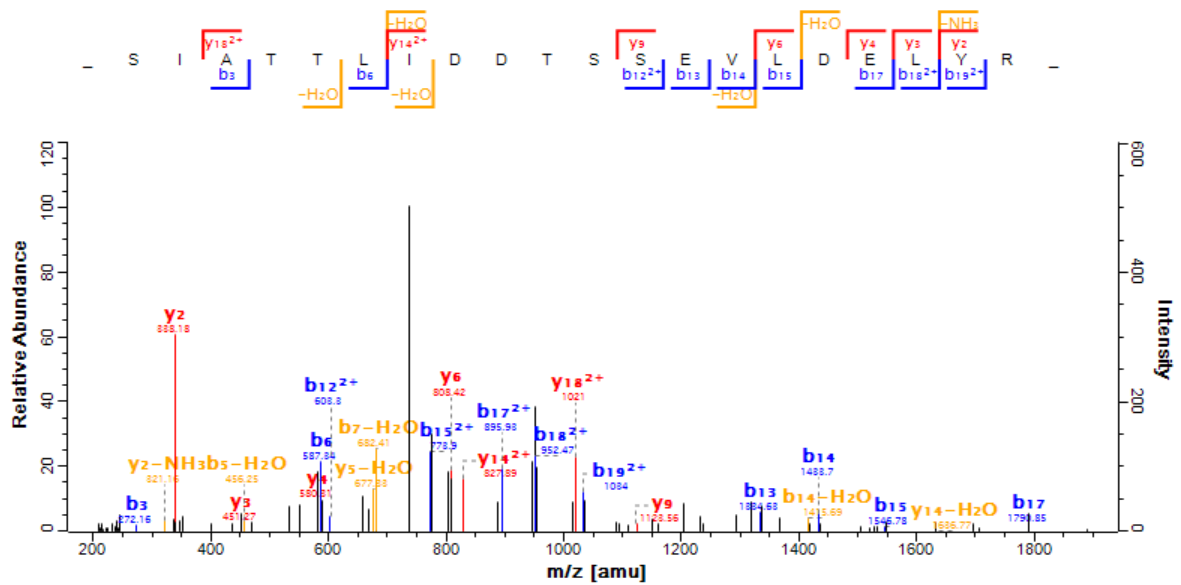
Number of Replicates (out of 10): 1

Best Match Score: 87.388

Best Match Posterior Error Probability: 0.00023534

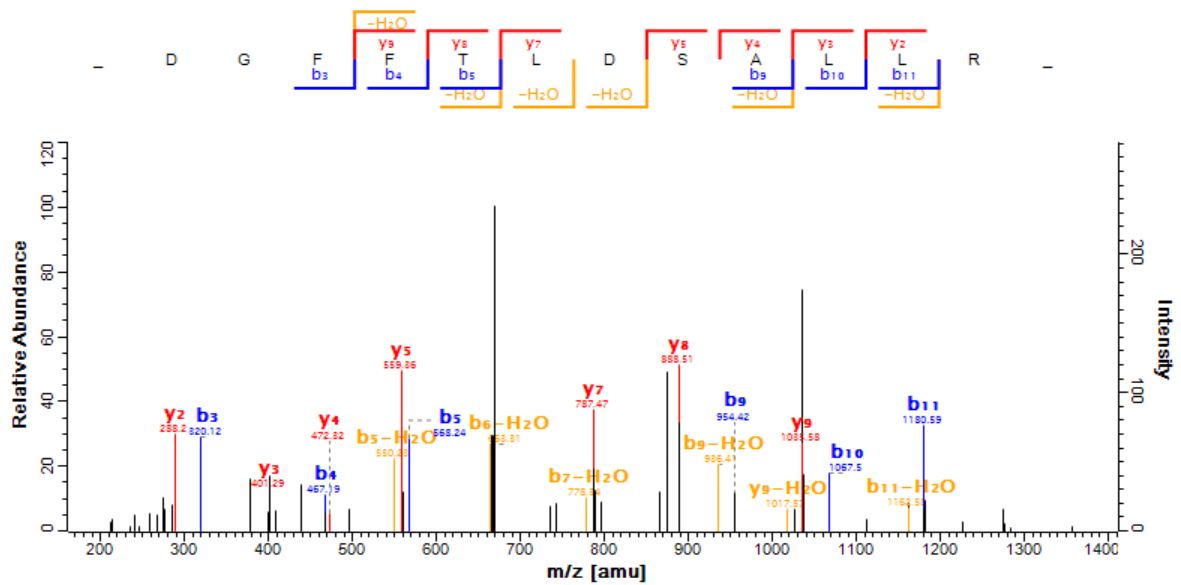
Best Match Spectrum:

Scan number	7966	Raw file	Prt-OGE-Batch2-Mock-Frac19
Method	ITMS; CID	Genenames	TNFAIP8



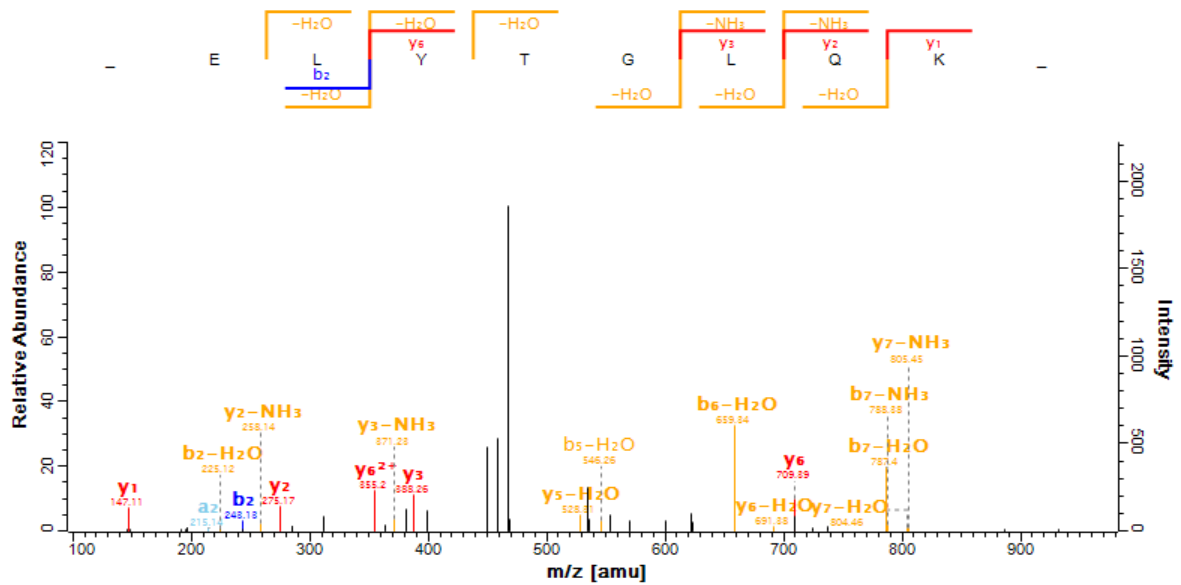
Protein Group ID: 279
Protein Accession Numbers: O95900; B7Z7G5
Gene Names: TRUB2
Peptide Sequence: DGFFTLDSALLR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 90.614
Best Match Posterior Error Probability: 0.00080802
Best Match Spectrum:

Scan number 5829 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac21
Method ITMS; CID **Genenames** TRUB2



Protein Group ID: 282
Protein Accession Numbers: B7Z7U4
Gene Names: NTRK3
Peptide Sequence: ELYTGLQK
Total Number of Spectra: 9
Number of Replicates (out of 10): 7
Best Match Score: 110.81
Best Match Posterior Error Probability: 0.0015946
Best Match Spectrum:

Scan number	2296	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac7
Method	ITMS; CID	Genenames	NTRK3



Protein Group ID: 283

Protein Accession Numbers: Q8NHH9; Q8NHH9-2; Q8NHH9-4; B7Z7X8; H7C3A2; C9JC25

Gene Names: ATL2

Peptide Sequence: SFLLDFMLR

Total Number of Spectra: 1

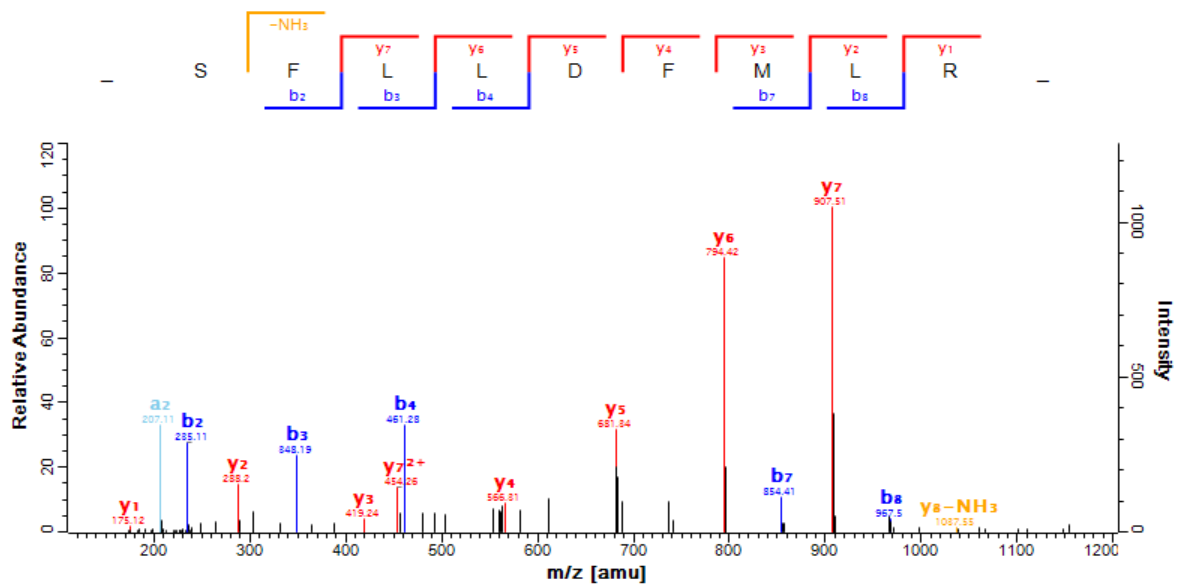
Number of Replicates (out of 10): 1

Best Match Score: 113.22

Best Match Posterior Error Probability: 0.00038882

Best Match Spectrum:

Scan number 7108 Raw file 20100927-KD-Batch4-Prt-OGE-WT-Frac11
Method ITMS: CID Genenames ATL2



Protein Group ID: 286

Protein Accession Numbers: P62820; B7Z8M7; E7END7; P62820-2; E7ETK2; P62820-3

Gene Names: RAB1A

Peptide Sequence: NATNVEQSFMTMAAEIK

Total Number of Spectra: 16

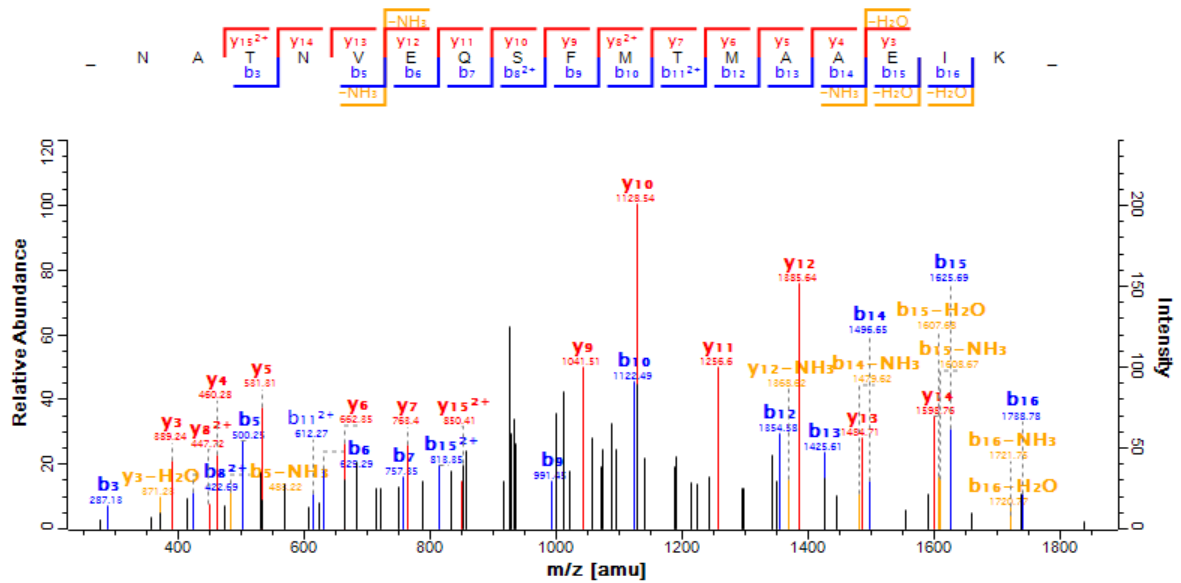
Number of Replicates (out of 10): 6

Best Match Score: 192.16

Best Match Posterior Error Probability: 9.39E-31

Best Match Spectrum:

Scan number 6645 **Raw file** Prt-OGE-Batch2-Mock-Frac11
Method ITMS; CID **Genenames** RAB1A



Protein Group ID: 287

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

Gene Names: NADKD1

Peptide Sequence: VATQAVEDVLNIAK

Total Number of Spectra: 1

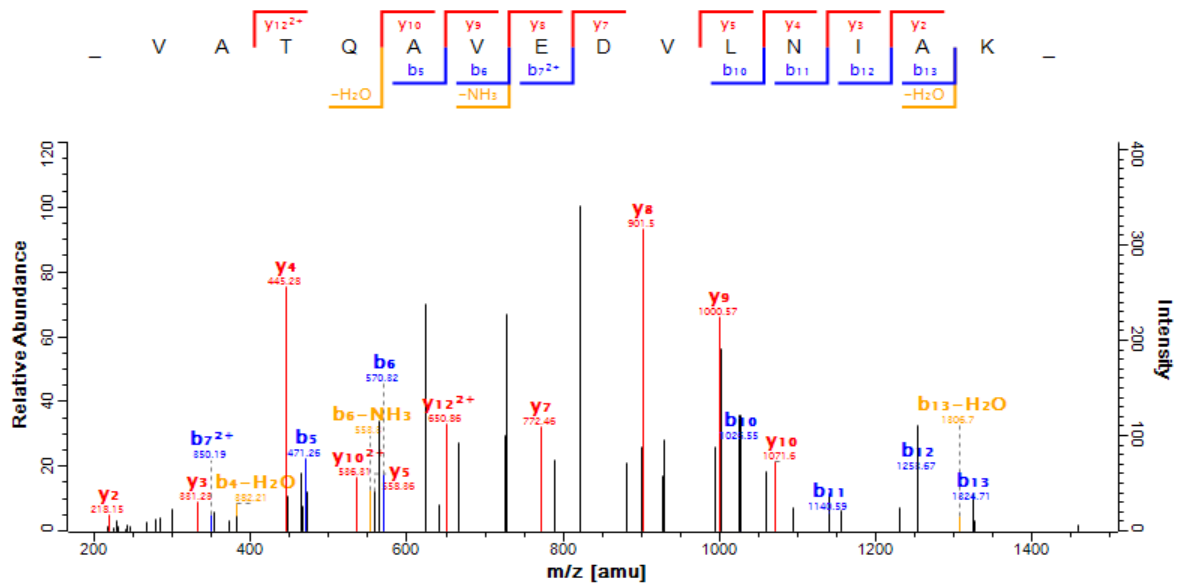
Number of Replicates (out of 10): 1

Best Match Score: 81.703

Best Match Posterior Error Probability: 0.0014407

Best Match Spectrum:

Scan number 5642 **Raw file** Prt-OGE-Batch2-Mock-Frac15
Method ITMS; CID **Genenames** NADKD1



Protein Group ID: 292

Protein Accession Numbers: P28332-2; P28332; E9PBI1; D6RH17; B7ZAL1

Gene Names: ADH6

Peptide Sequence: IIGVDVNKEK

Total Number of Spectra: 5

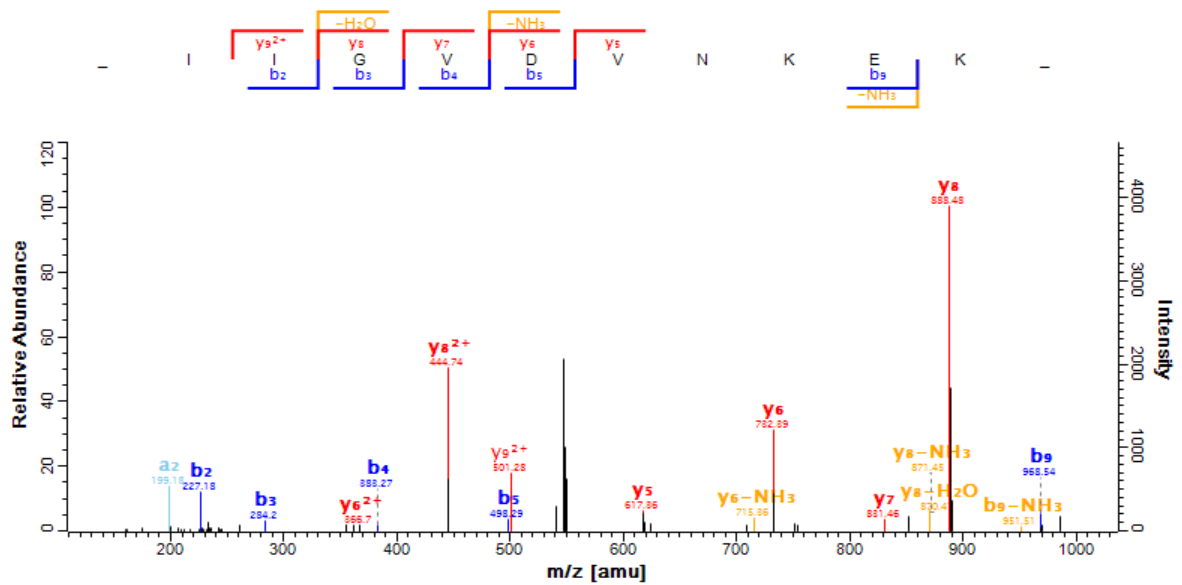
Number of Replicates (out of 10): 4

Best Match Score: 123.35

Best Match Posterior Error Probability: 0.00038

Best Match Spectrum:

Scan number 1832 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac17
Method ITMS; CID **Genenames** ADH6



Protein Group ID: 293

Protein Accession Numbers: Q01415; Q01415-2; B7ZAX5

Gene Names: GALK2

Peptide Sequence: QSLFATKPGGGALVLEA

Total Number of Spectra: 1

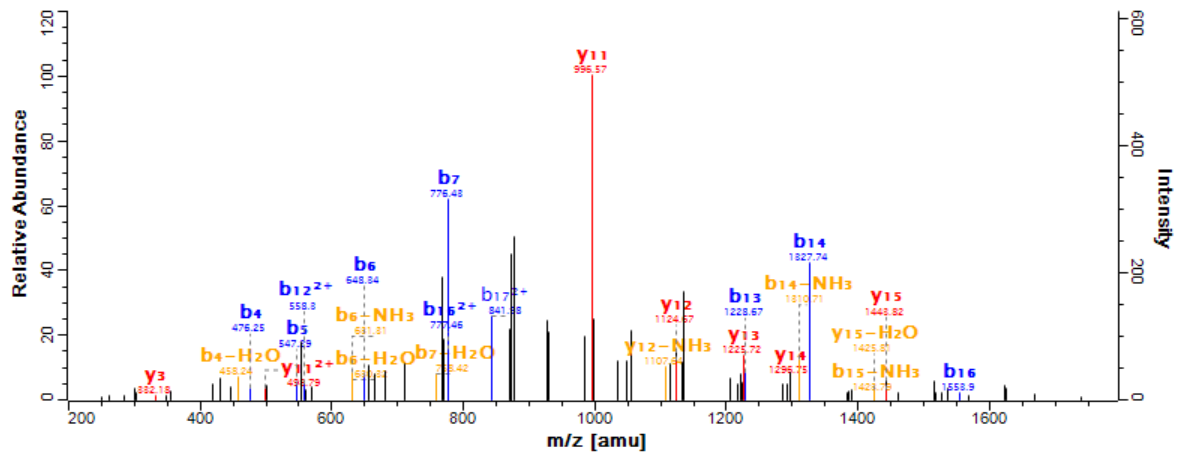
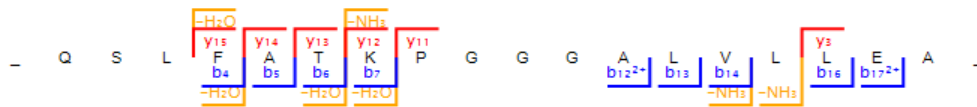
Number of Replicates (out of 10): 1

Best Match Score: 101.78

Best Match Posterior Error Probability: 0.00071735

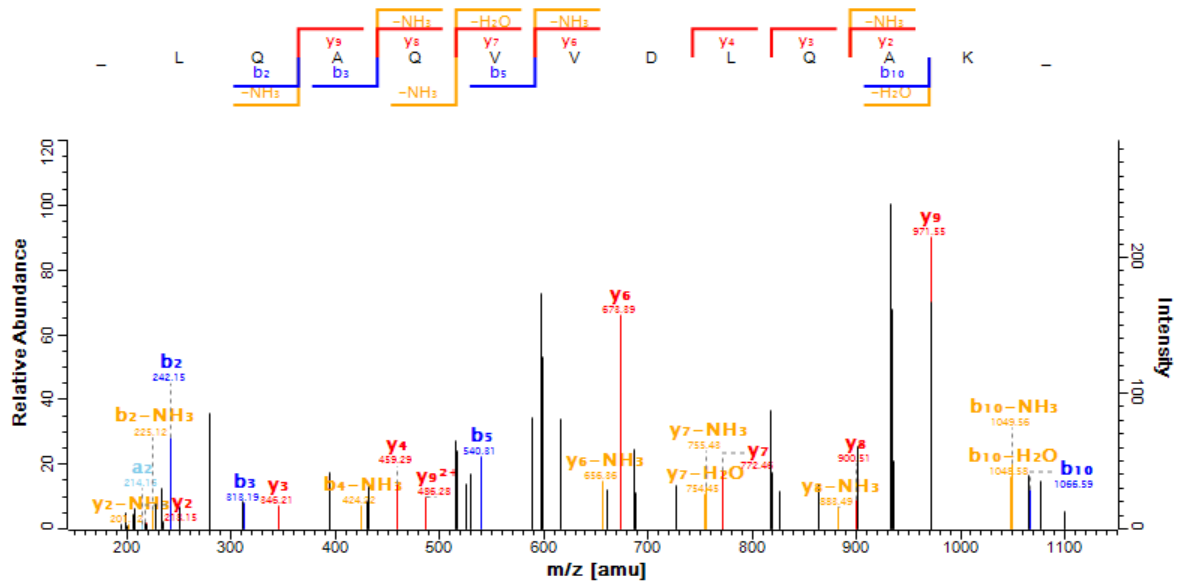
Best Match Spectrum:

Scan number 4949 **Raw file** Prt-OGE-Batch3-WT-Frac13
Method ITMS; CID **Genenames** GALK2



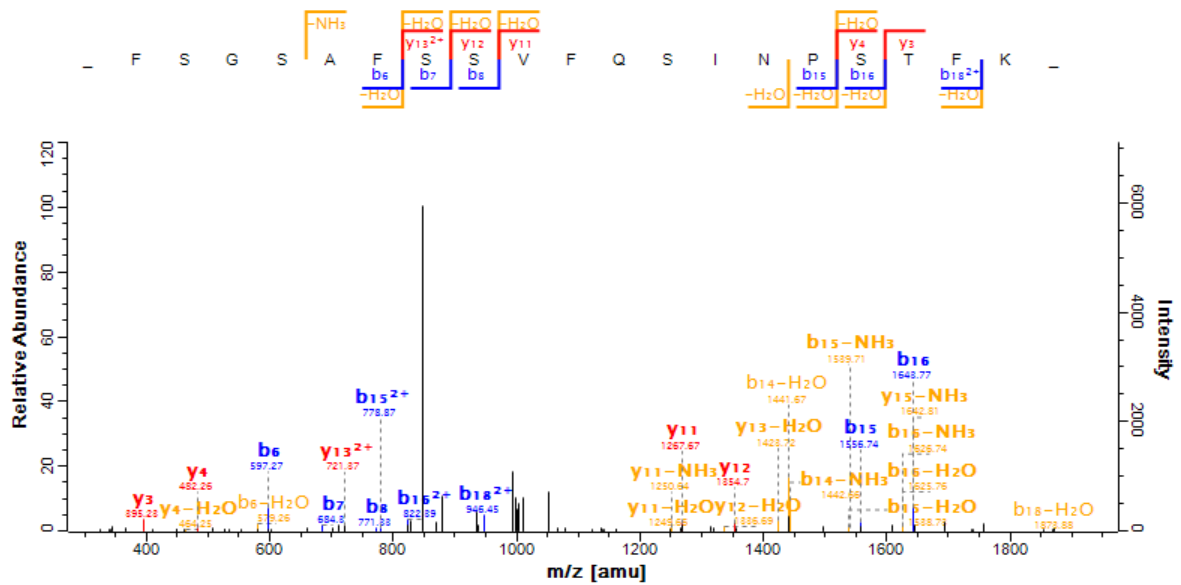
Protein Group ID: 297
Protein Accession Numbers: B7ZKT7; Q9BQS8
Gene Names: FYCO1
Peptide Sequence: LQAQVVDLQAK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 98.898
Best Match Posterior Error Probability: 0.00028209
Best Match Spectrum:

Scan number 3161 **Raw file** Prt-OGE-Batch2-Mock-Frac5
Method ITMS; CID **Genenames** FYCO1



Protein Group ID: 299
Protein Accession Numbers: Q6ZNL6; B7ZM68; Q6ZNL6-2
Gene Names: FGD5
Peptide Sequence: FSGSAFSSVFQSINPSTFK
Total Number of Spectra: 4
Number of Replicates (out of 10): 4
Best Match Score: 111.78
Best Match Posterior Error Probability: 3.53E-05
Best Match Spectrum:

Scan number 2099 **Raw file** Prt-OGE-Batch2-WT-Frac22
Method ITMS; CID **Genenames** FGD5



Protein Group ID: 301

Protein Accession Numbers: Q9UBP9; B8ZZ72; Q9UBP9-3; H7BZV7; H0Y6R1

Gene Names: GULP1

Peptide Sequence: SPSTDIFDMIPFSPISHQSSMPTR

Total Number of Spectra: 5

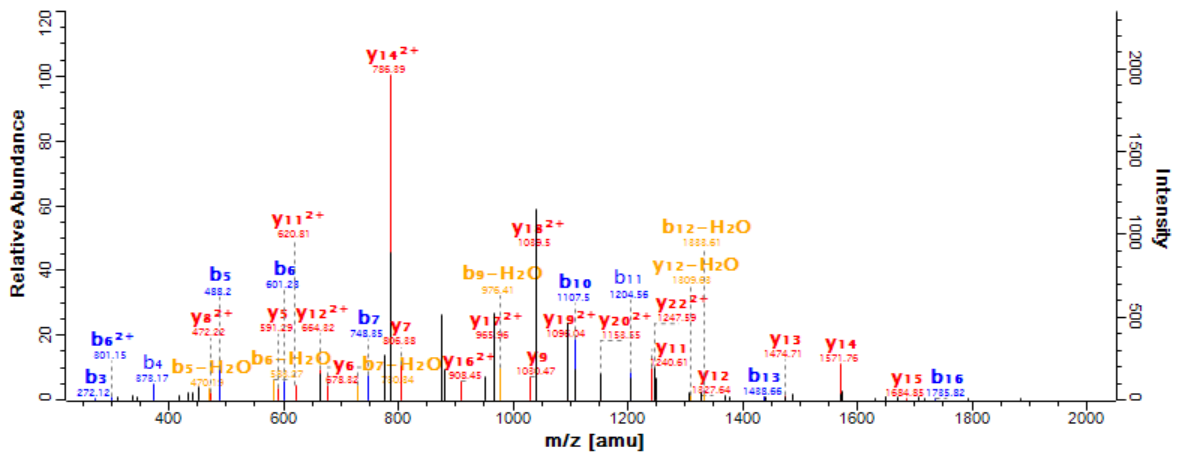
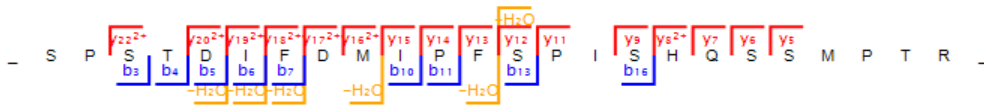
Number of Replicates (out of 10): 5

Best Match Score: 140.95

Best Match Posterior Error Probability: 3.81E-19

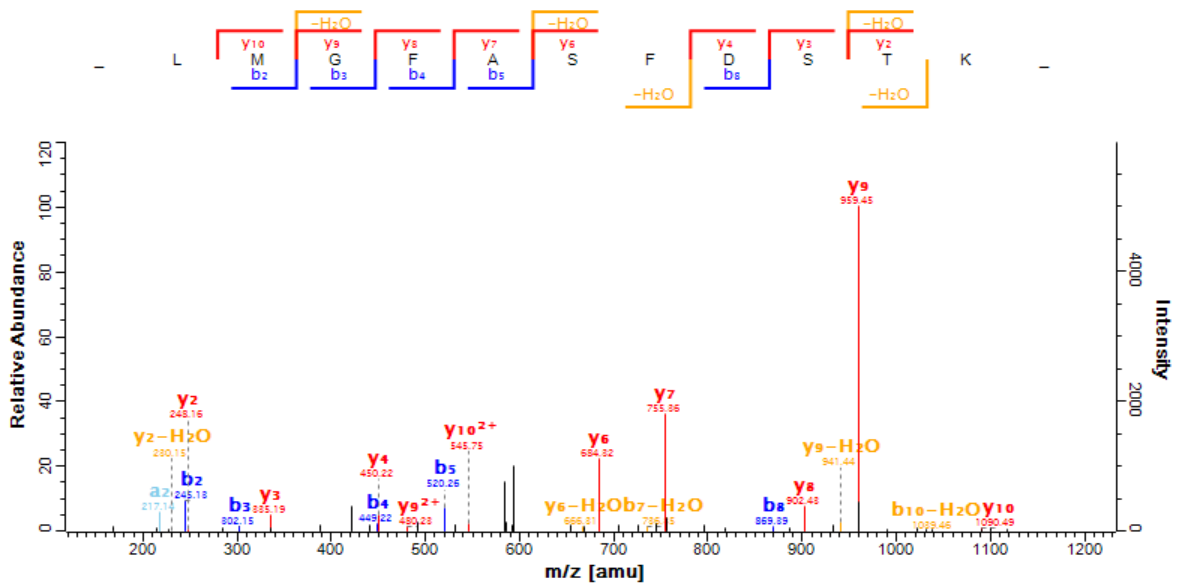
Best Match Spectrum:

Scan number 6353 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac18
Method ITMS; CID **Genenames** GULP1



Protein Group ID: 303
Protein Accession Numbers: B8ZZ98; Q8WVK2
Gene Names: SNRNP27
Peptide Sequence: LMGFASFDSTK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 100.69
Best Match Posterior Error Probability: 0.00025903
Best Match Spectrum:

Scan number 3249 **Raw file** Prt-OGE-Batch3-Mock-Frac15
Method ITMS; CID **Genenames** SNRNP27



Protein Group ID: 304

Protein Accession Numbers: B8ZZD4; Q86VP1; Q86VP1-2; E7ENV2; Q86VP1-3

Gene Names: TAX1BP1

Peptide Sequence: AHQLEEDIVSVTHK

Total Number of Spectra: 1

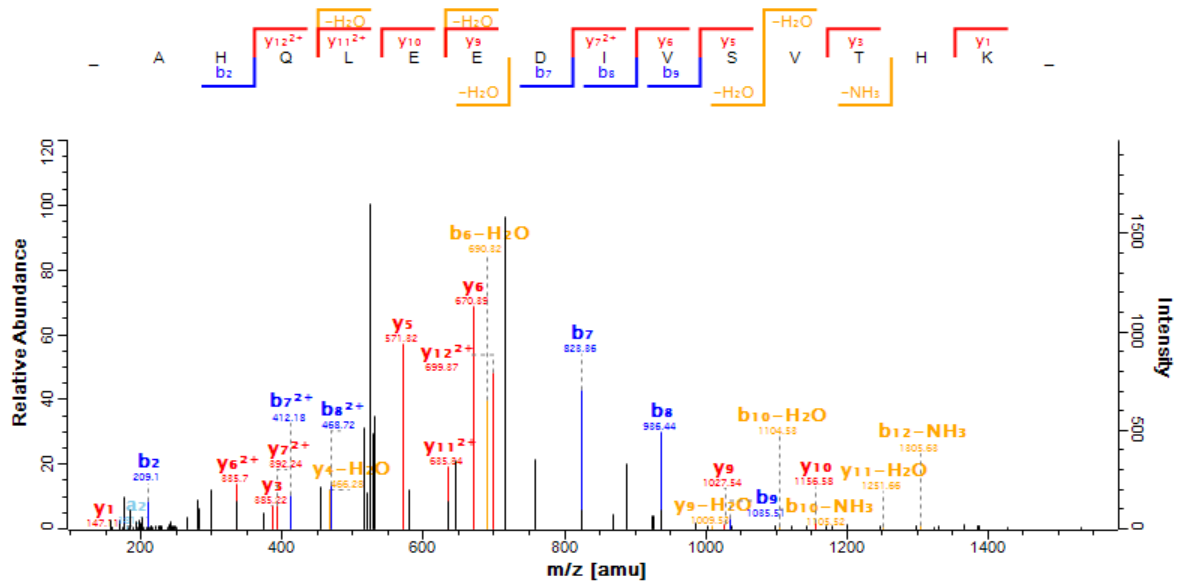
Number of Replicates (out of 10): 1

Best Match Score: 80.96

Best Match Posterior Error Probability: 0.0015384

Best Match Spectrum:

Scan number	2858	Raw file	Prt-OGE-Batch3-Mock-Frac7
Method	ITMS; CID	Genenames	TAX1BP1



Protein Group ID: 306

Protein Accession Numbers: O75688; O75688-2; O75688-4; C9JIR6; B8ZZF0; O75688-3

Gene Names: PPM1B

Peptide Sequence: NVIEAVYSR

Total Number of Spectra: 3

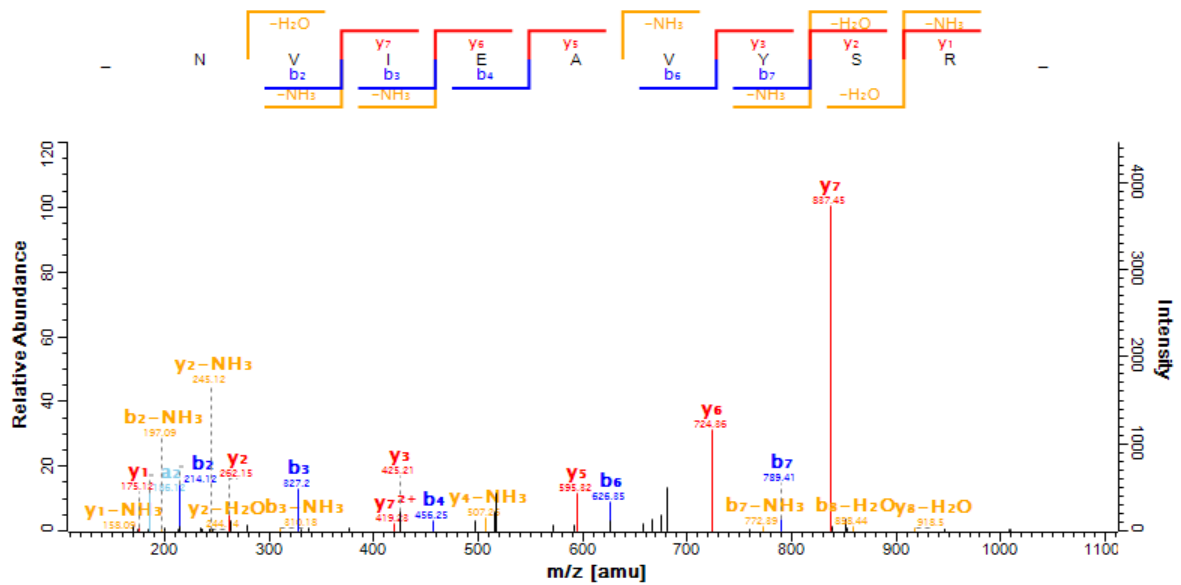
Number of Replicates (out of 10): 3

Best Match Score: 92.538

Best Match Posterior Error Probability: 0.0014964

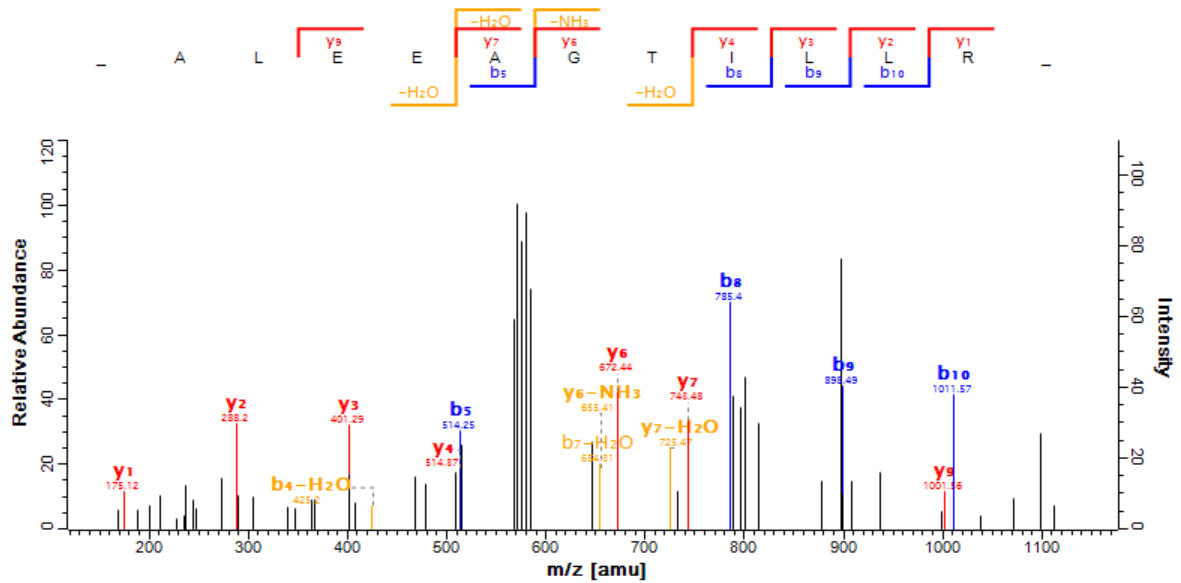
Best Match Spectrum:

Scan number	2886	Raw file	Prt-OGE-Batch3-Mock-Frac6
Method	ITMS; CID	Genenames	PPM1B



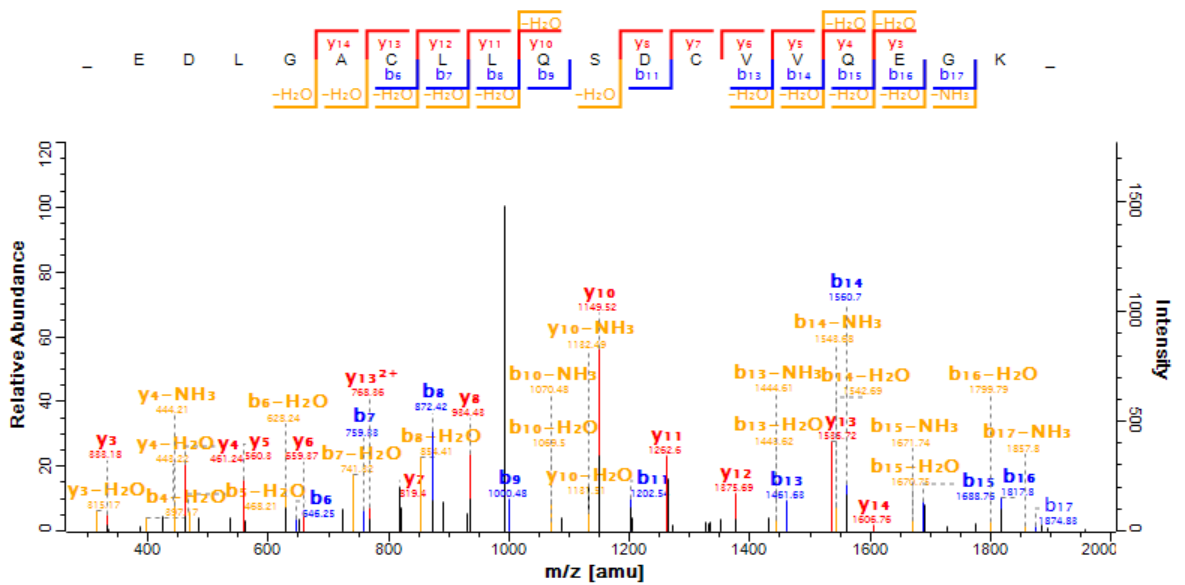
Protein Group ID: 311
Protein Accession Numbers: Q9H8Y5; B8ZZS4
Gene Names: ANKZF1
Peptide Sequence: ALEEAGTILLR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 93.258
Best Match Posterior Error Probability: 0.00063699
Best Match Spectrum:

Scan number 4717 **Raw file** Prt-OGE-Batch3-WT-Frac6
Method ITMS; CID **Genenames** ANKZF1



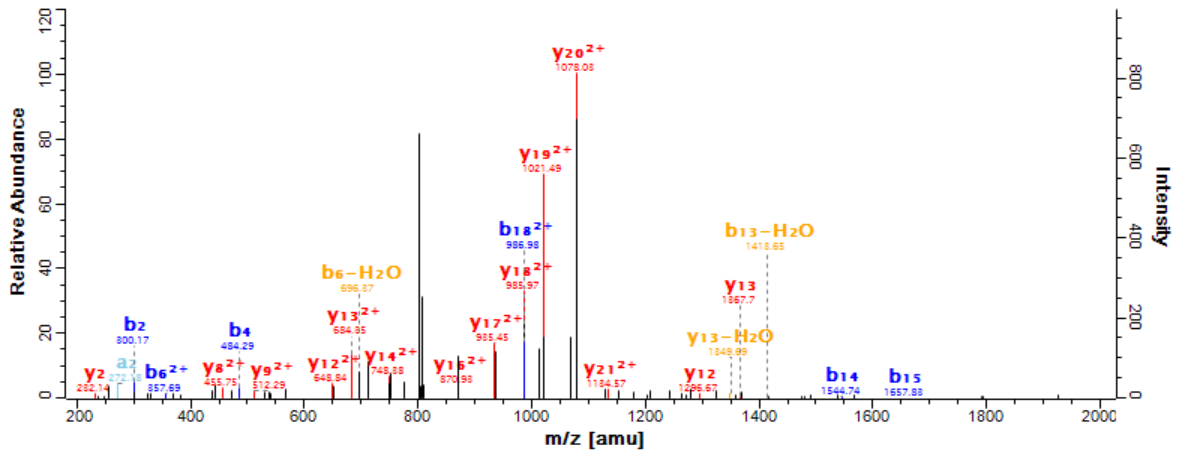
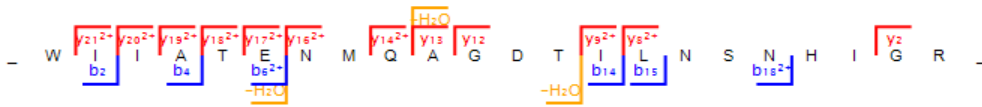
Protein Group ID: 314
Protein Accession Numbers: Q86WW8; B9A057
Gene Names: COA5
Peptide Sequence: EDLGACLLQSDCVVQEGK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 214.5
Best Match Posterior Error Probability: 1.37E-54
Best Match Spectrum:

Scan number 4239 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac22
Method ITMS; CID **Genenames** COA5



Protein Group ID: 317
Protein Accession Numbers: Q5T653; C9IY40
Gene Names: MRPL2
Peptide Sequence: WIATENMQAGDTILNSNHIGR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 113.29
Best Match Posterior Error Probability: 9.65E-08
Best Match Spectrum:

Scan number 4792 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac17
Method ITMS; CID **Genenames** MRPL2



Protein Group ID: 323

Protein Accession Numbers: Q9NSU2; Q9NSU2-3; Q9NSU2-2; C9J052

Gene Names: TREX1

Peptide Sequence: EGLLAPLGLLAILTLAVATLYGLSLATPGE

Total Number of Spectra: 1

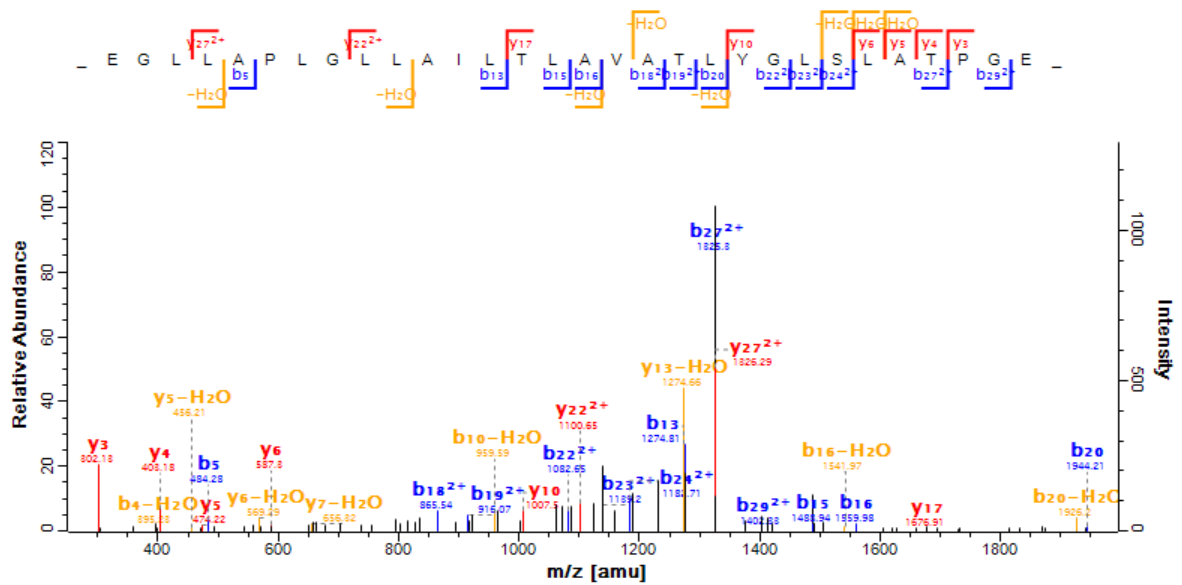
Number of Replicates (out of 10): 1

Best Match Score: 77.689

Best Match Posterior Error Probability: 2.94E-07

Best Match Spectrum:

Scan number 10544 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac18
Method ITMS; CID **Genenames** TREX1



Protein Group ID: 325

Protein Accession Numbers: Q96GG9; C9JVE2; C9J8R4; C9JUW4; C9J0B2; C9JRU6

Gene Names: DCUN1D1

Peptide Sequence: LDVATDNFFQNPELYIR

Total Number of Spectra: 8

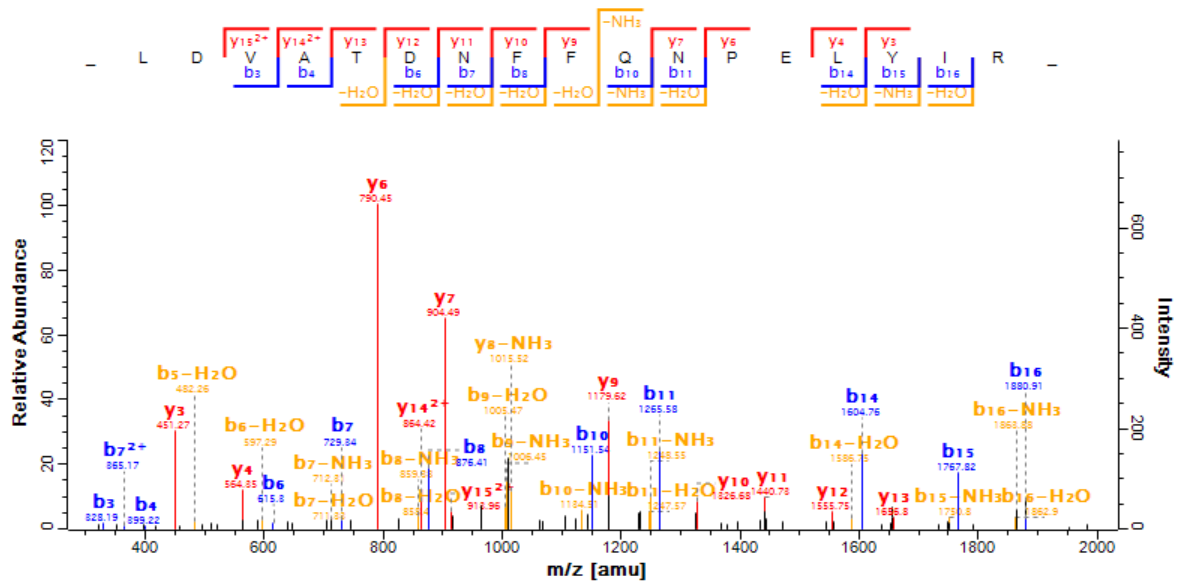
Number of Replicates (out of 10): 6

Best Match Score: 200.77

Best Match Posterior Error Probability: 5.58E-40

Best Match Spectrum:

Scan number	5959	Raw file	OGE-Mock-Frac6
Method	ITMS; CID	Genenames	DCUN1D1



Protein Group ID: 334

Protein Accession Numbers: P10145-2; P10145; C9J4T6

Gene Names: IL8

Peptide Sequence: VIESGPHCANTEIIVK

Total Number of Spectra: 1

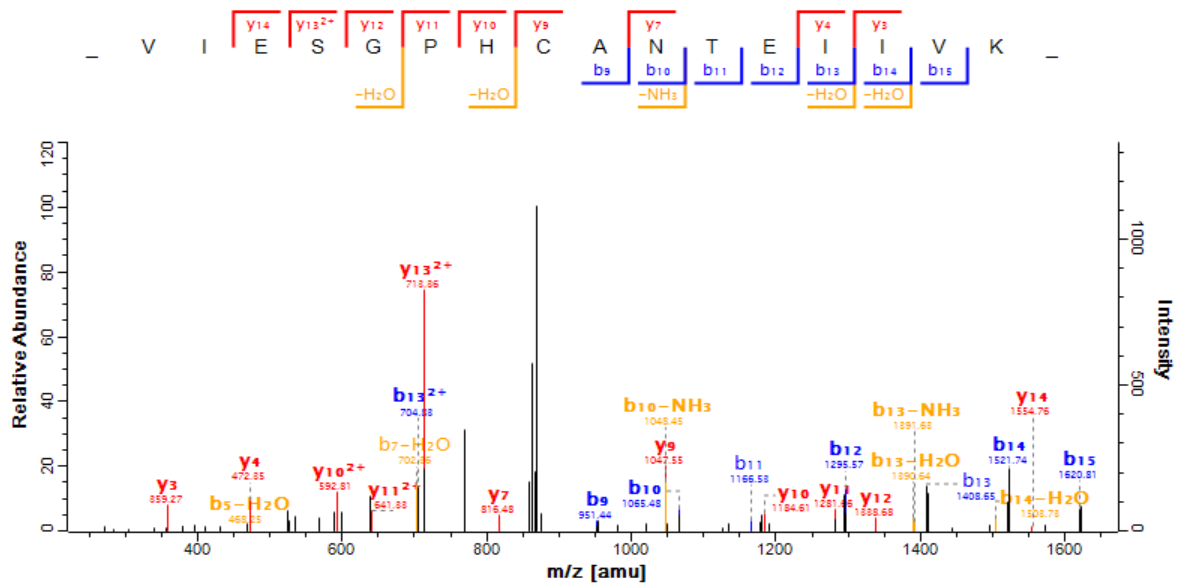
Number of Replicates (out of 10): 1

Best Match Score: 106.82

Best Match Posterior Error Probability: 0.00014423

Best Match Spectrum:

Scan number 2378 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac22
Method ITMS; CID **Genenames** IL8



Protein Group ID: 337

Protein Accession Numbers: P51149; C9J592

Gene Names: RAB7A

Peptide Sequence: TLDSWRDEFLIQASPR

Total Number of Spectra: 1

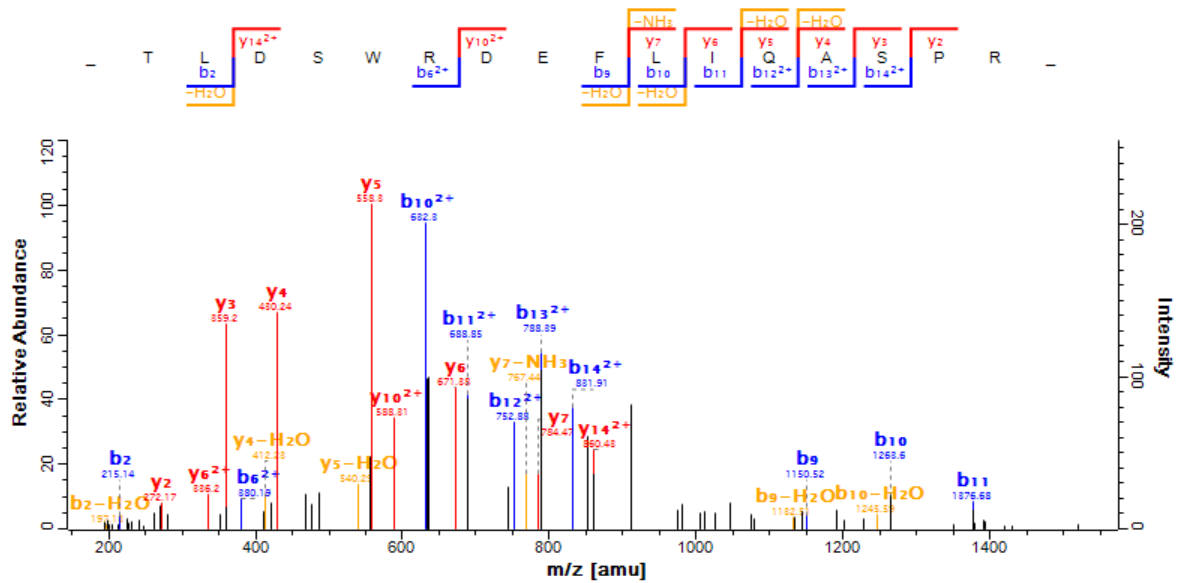
Number of Replicates (out of 10): 1

Best Match Score: 129.77

Best Match Posterior Error Probability: 9.12E-05

Best Match Spectrum:

Scan number	4242	Raw file	OGE-WT-Frac3
Method	ITMS; CID	Genenames	RAB7A



Protein Group ID: 339

Protein Accession Numbers: Q8N2F6; Q8N2F6-2; Q8N2F6-3; Q8N2F6-5; Q8N2F6-4; C9J5N7; F5GX65; H7BXQ8

Gene Names: ARMC10

Peptide Sequence: LLYLLESTEDPVIIER

Total Number of Spectra: 1

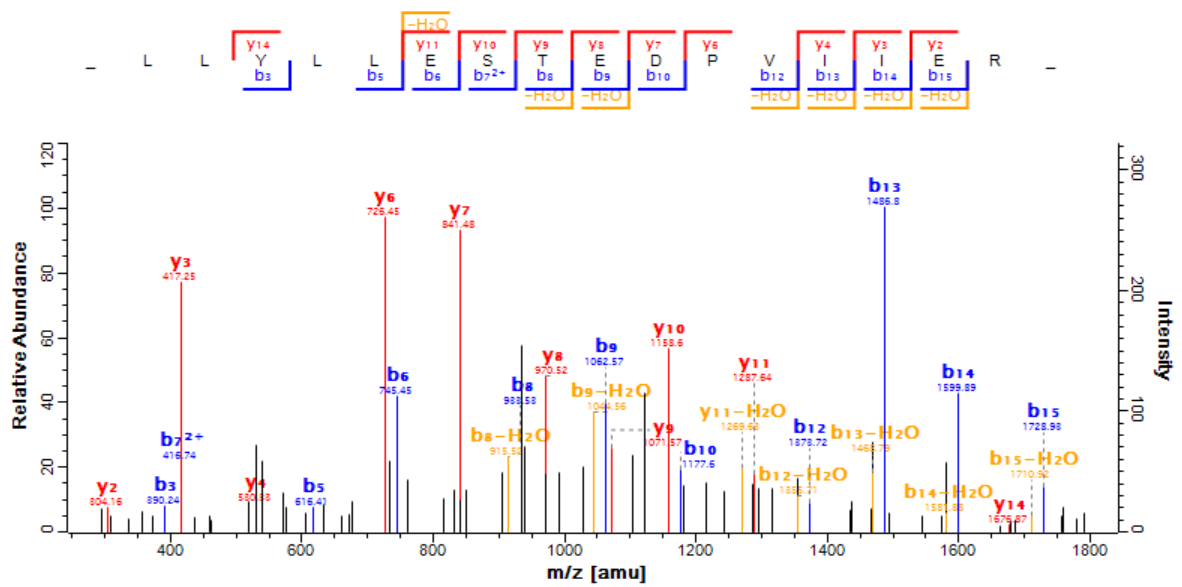
Number of Replicates (out of 10): 1

Best Match Score: 177.88

Best Match Posterior Error Probability: 8.61E-20

Best Match Spectrum:

Scan number	6561	Raw file	Prt-OGE-Batch2-Mock-Frac15
Method	ITMS: CID	Genenames	ARMC10



Protein Group ID: 340

Protein Accession Numbers: Q9UI15; C9J5W6; H7C5N2

Gene Names: TAGLN3

Peptide Sequence: TTDIFQTVDLWEGK

Total Number of Spectra: 1

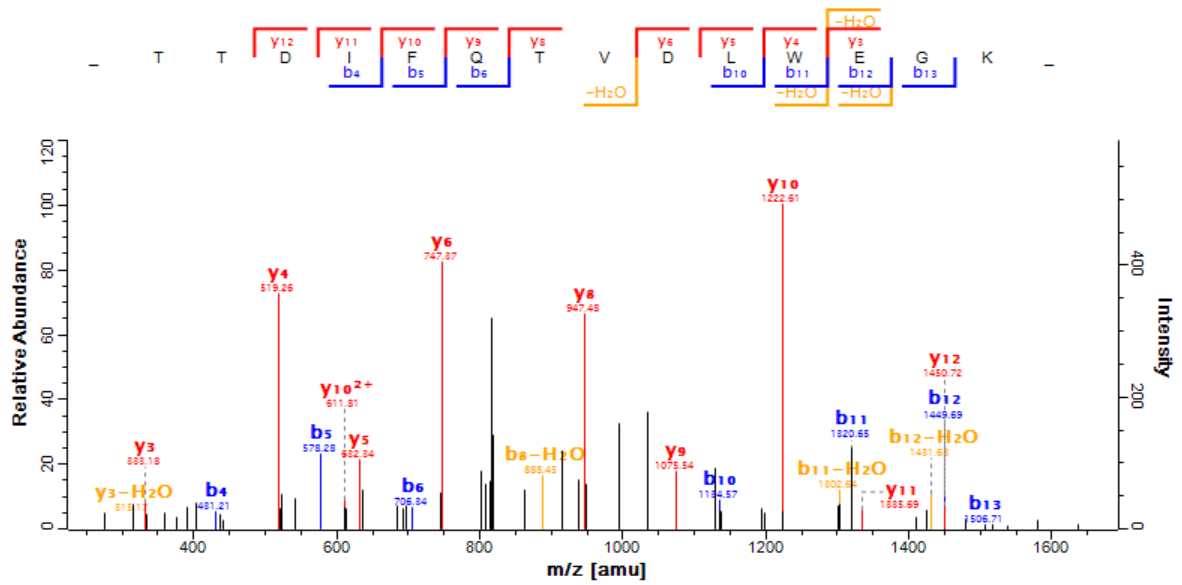
Number of Replicates (out of 10): 1

Best Match Score: 87.647

Best Match Posterior Error Probability: 0.00074256

Best Match Spectrum:

Scan number	5021	Raw file	Prt-OGE-Batch2-WT-Frac18
Method	ITMS; CID	Genenames	TAGLN3



Protein Group ID: 342

Protein Accession Numbers: Q6GPH4; Q6GPH4-5; C9J7Z8; Q6GPH4-3; I3L3D9

Gene Names: XAF1

Peptide Sequence: LEHQQVGC TMCQSMQK

Total Number of Spectra: 1

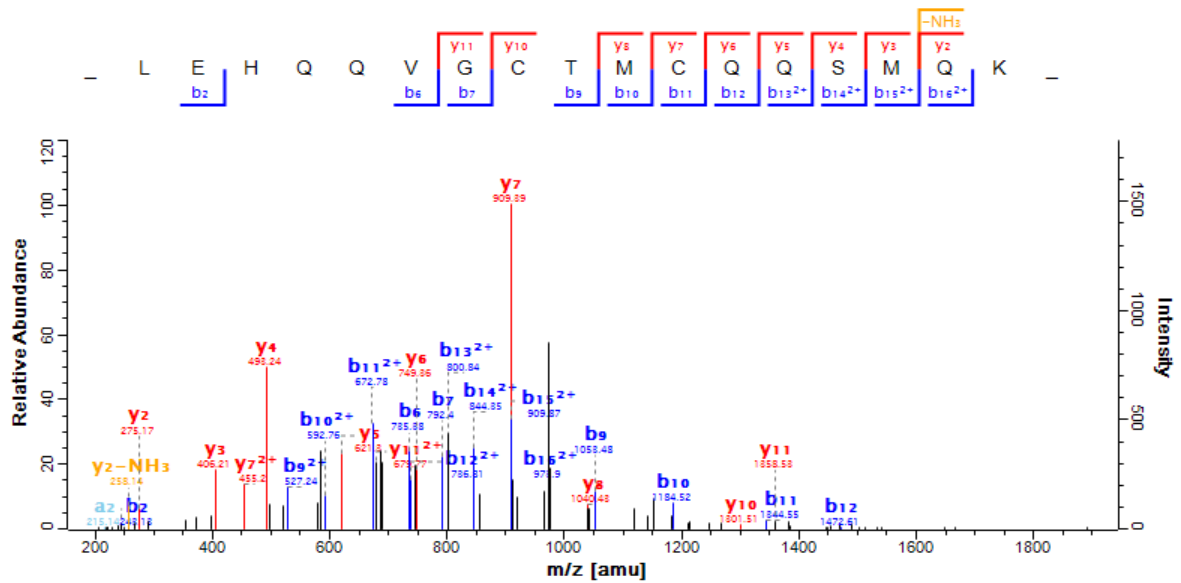
Number of Replicates (out of 10): 1

Best Match Score: 127.3

Best Match Posterior Error Probability: 5.46E-05

Best Match Spectrum:

Scan number	1298	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac20
Method	ITMS; CID	Genenames	XAF1



Protein Group ID: 343

Protein Accession Numbers: P16220; P16220-2; C9J896; C9JBT4; H7C1R5

Gene Names: CREB1

Peptide Sequence: TAPTSTIAPGVVMASSSPALP TQP AEEAAR

Total Number of Spectra: 1

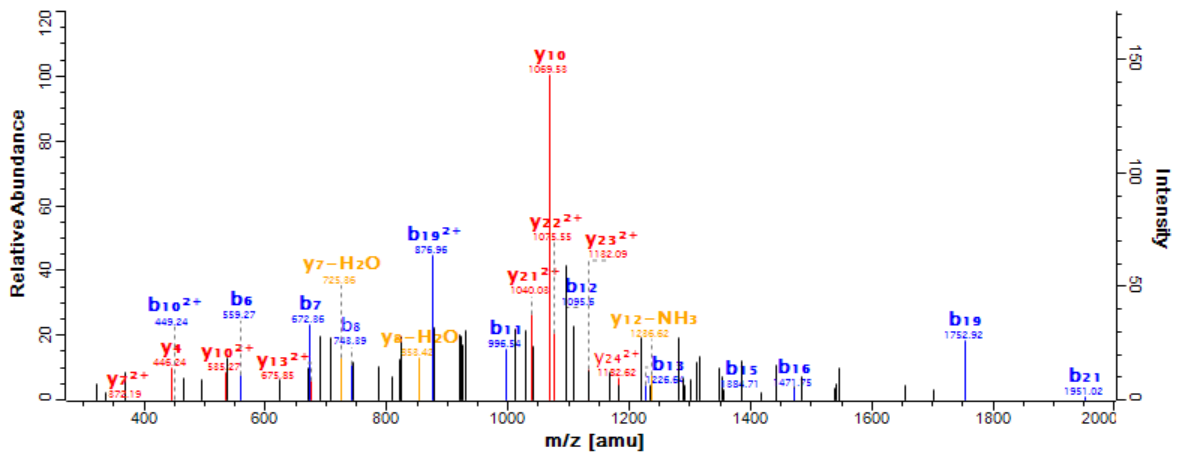
Number of Replicates (out of 10): 1

Best Match Score: 55.789

Best Match Posterior Error Probability: 0.00029257

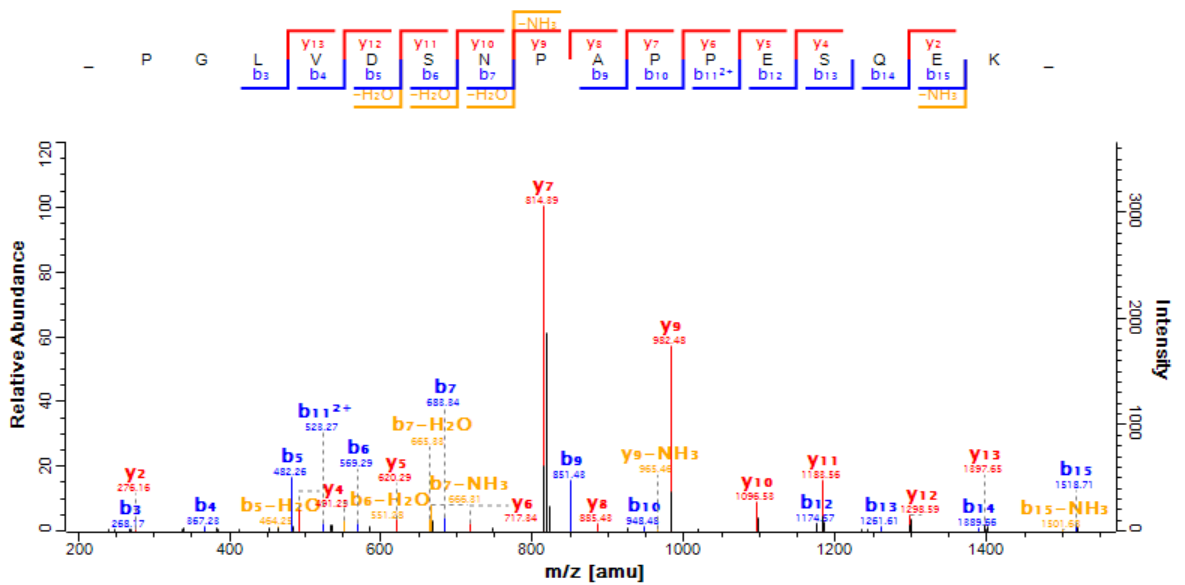
Best Match Spectrum:

Scan number 4647 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac7
Method ITMS; CID **Genenames** CREB1



Protein Group ID: 347
Protein Accession Numbers: C9J8T6; Q14061
Gene Names: COX17
Peptide Sequence: PGLVDSNPAPPESQEK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 148.52
Best Match Posterior Error Probability: 1.83E-07
Best Match Spectrum:

Scan number 1359 **Raw file** Prt-OGE-Batch3-WT-Frac17
Method ITMS; CID **Genenames** COX17



Protein Group ID: 350

Protein Accession Numbers: P18564; E9PEE8; C9JA97

Gene Names: ITGB6

Peptide Sequence: LGFGSFVEK

Total Number of Spectra: 22

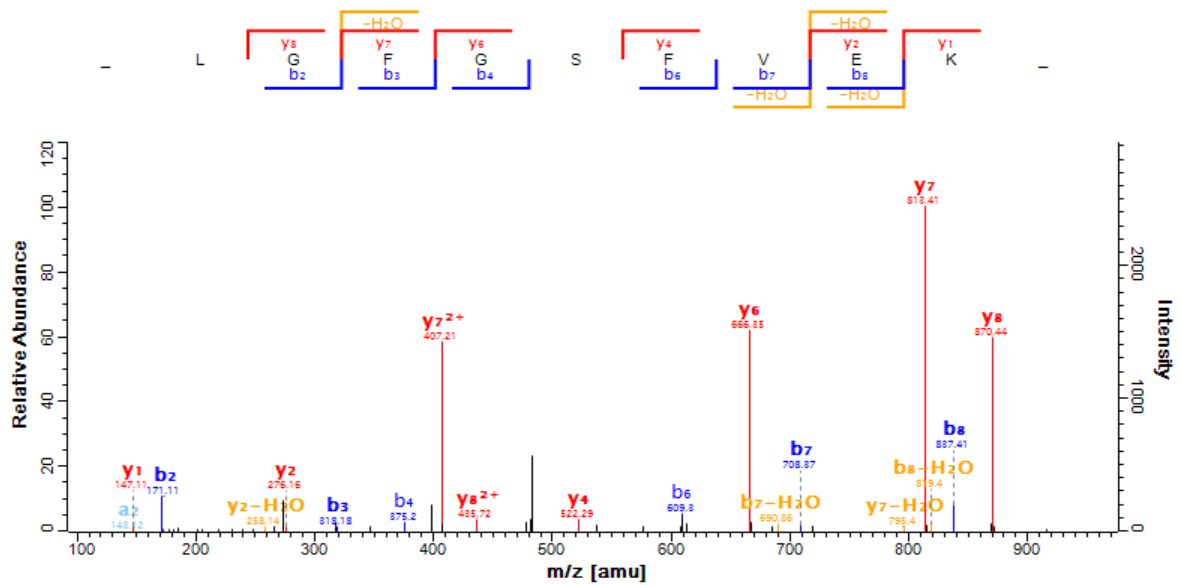
Number of Replicates (out of 10): 8

Best Match Score: 128.27

Best Match Posterior Error Probability: 0.00028966

Best Match Spectrum:

Scan number	3542	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac11
Method	ITMS; CID	Genenames	ITGB6



Protein Group ID: 356

Protein Accession Numbers: O15042; E7ET15; O15042-2; O15042-3; C9JB80; H7C4V2

Gene Names: U2SURP

Peptide Sequence: KPGQSFQEQVEHYR

Total Number of Spectra: 2

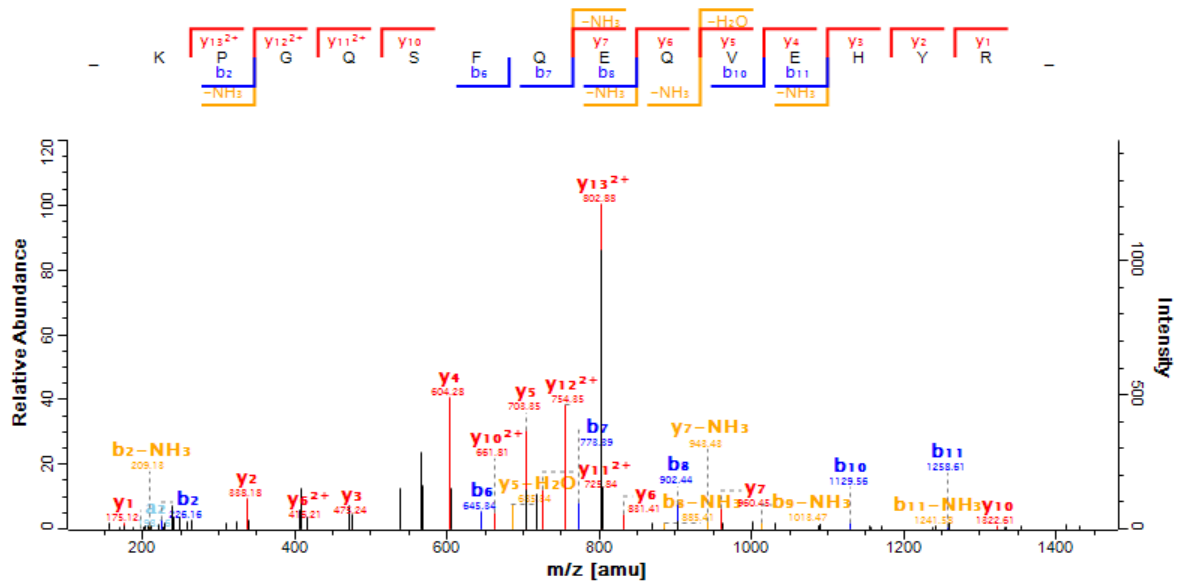
Number of Replicates (out of 10): 2

Best Match Score: 116.63

Best Match Posterior Error Probability: 0.0002432

Best Match Spectrum:

Scan number 1477 **Raw file** Prt-OGE-Batch3--Mock-Frac18
Method ITMS; CID **Genenames** U2SURP



Protein Group ID: 372

Protein Accession Numbers: Q9NSI2; Q9NSI2-2; C9JJU7

Gene Names: FAM207A

Peptide Sequence: DWAFINTNIFAR

Total Number of Spectra: 2

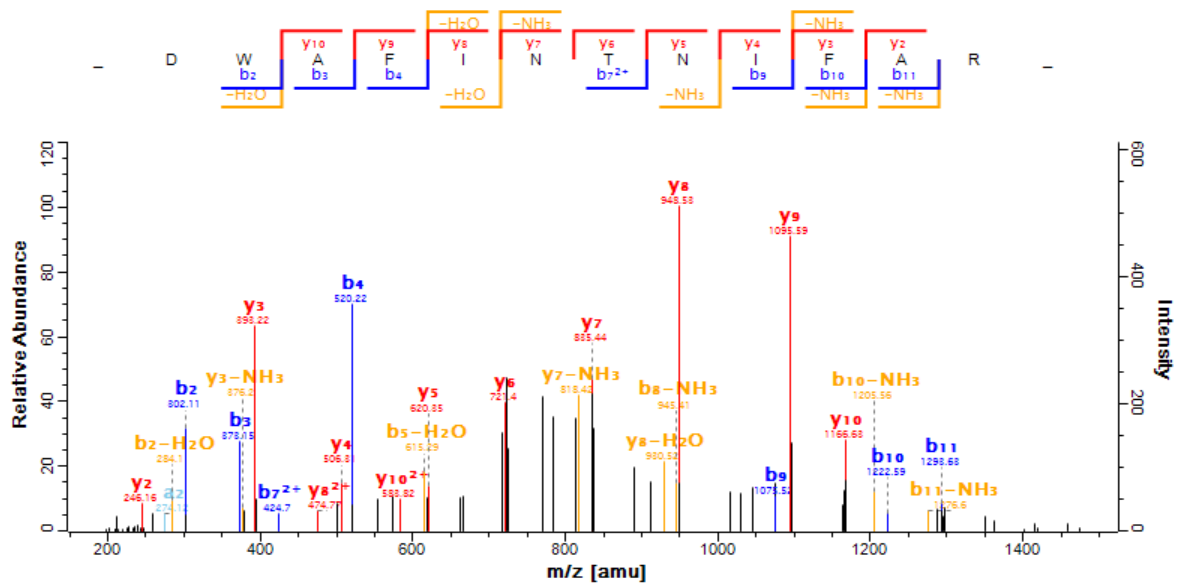
Number of Replicates (out of 10): 2

Best Match Score: 160.52

Best Match Posterior Error Probability: 8.83E-06

Best Match Spectrum:

Scan number	6060	Raw file	20100914-KD-Batch4-Prt-OGE-Mock-Frac18
Method	ITMS; CID	Genenames	FAM207A



Protein Group ID: 376

Protein Accession Numbers: Q6P087; Q6P087-2; H7C1H7; H7C454; C9JM75; H7C0K7; Q6P087-3

Gene Names: RPUSD3

Peptide Sequence: SGPLGDQPFAGLLPK

Total Number of Spectra: 1

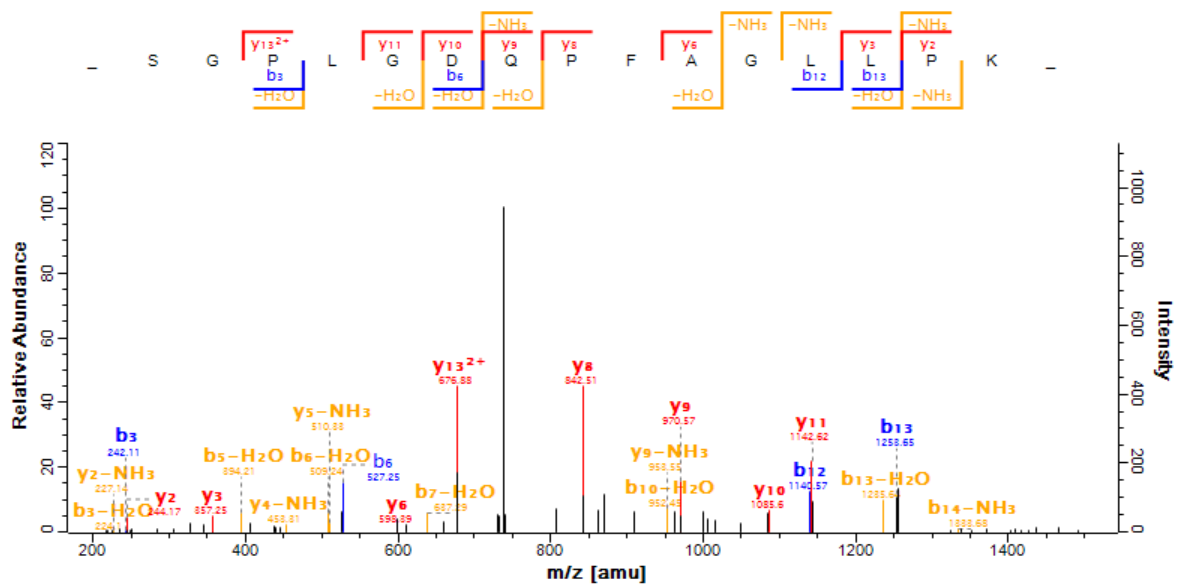
Number of Replicates (out of 10): 1

Best Match Score: 84.753

Best Match Posterior Error Probability: 0.000611

Best Match Spectrum:

Scan number 5301 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac23
Method ITMS; CID **Genenames** RPUSD3



Protein Group ID: 377

Protein Accession Numbers: P35520-2; P35520; C9JMA6

Gene Names: CBS

Peptide Sequence: PSETPQAEVGP TGCPHR

Total Number of Spectra: 2

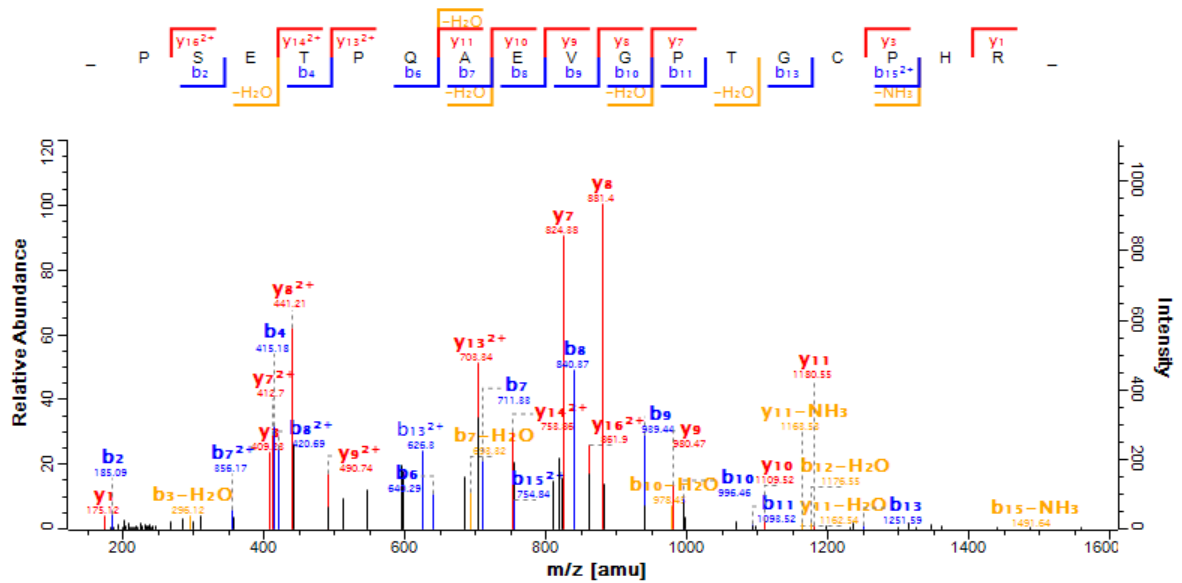
Number of Replicates (out of 10): 2

Best Match Score: 156

Best Match Posterior Error Probability: 2.51E-10

Best Match Spectrum:

Scan number	1118	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac14
Method	ITMS; CID	Genenames	CBS



Protein Group ID: 387

Protein Accession Numbers: P42575; P42575-2; C9JRR9; E9PDN0

Gene Names: CASP2

Peptide Sequence: VGSFSQNVLLPDK

Total Number of Spectra: 1

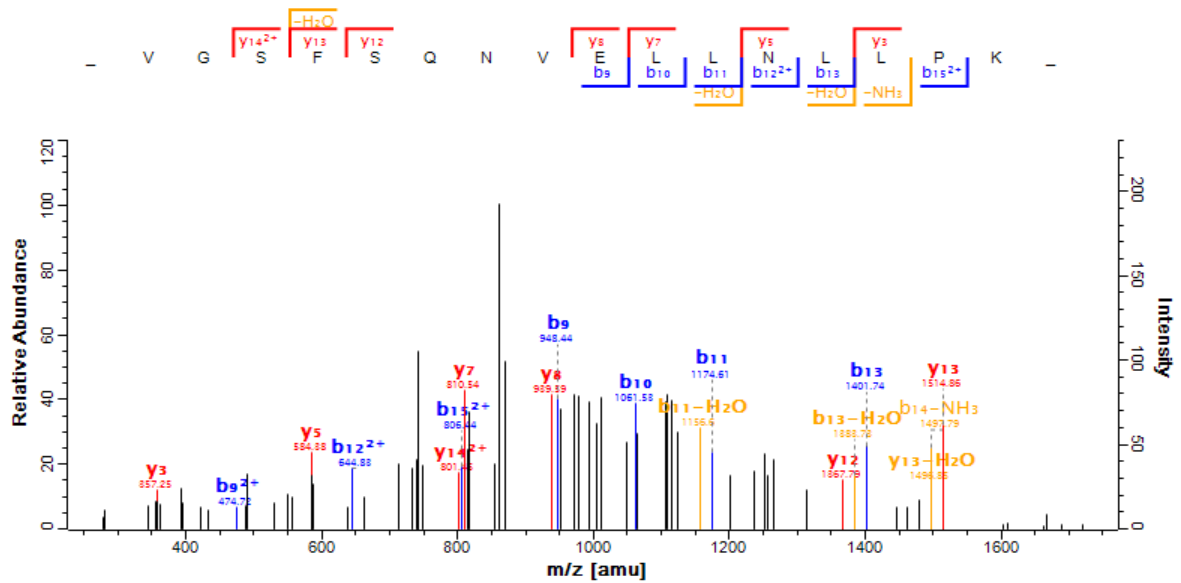
Number of Replicates (out of 10): 1

Best Match Score: 82.529

Best Match Posterior Error Probability: 0.00086683

Best Match Spectrum:

Scan number	6416	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac15
Method	ITMS; CID	Genenames	CASP2



Protein Group ID: 388

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

Gene Names: ZNF143

Peptide Sequence: LIDGQVIQLEDGSAAYVQHPK

Total Number of Spectra: 1

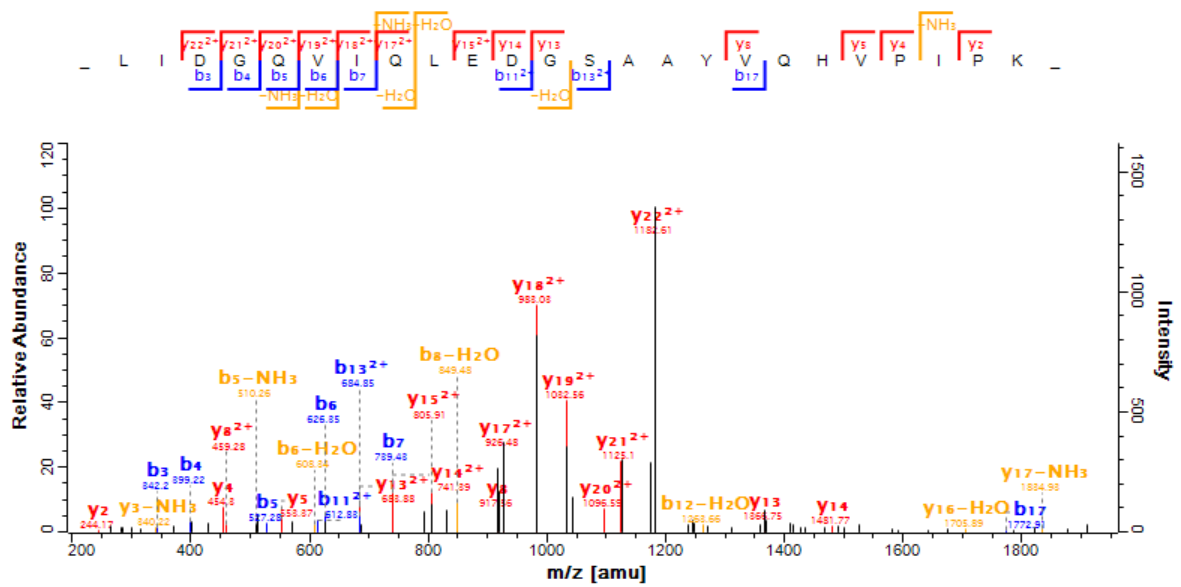
Number of Replicates (out of 10): 1

Best Match Score: 116.65

Best Match Posterior Error Probability: 4.84E-10

Best Match Spectrum:

Scan number	5891	Raw file	Prt-OGE-Batch3-Mock-Frac10
Method	ITMS: CID	Genenames	ZNF143



Protein Group ID: 389

Protein Accession Numbers: F5H189; C9JRX8; Q9HD34; H7C4Q5; C9JY28

Gene Names: LYRM4

Peptide Sequence: NVKDPVVEIQTLVNK

Total Number of Spectra: 2

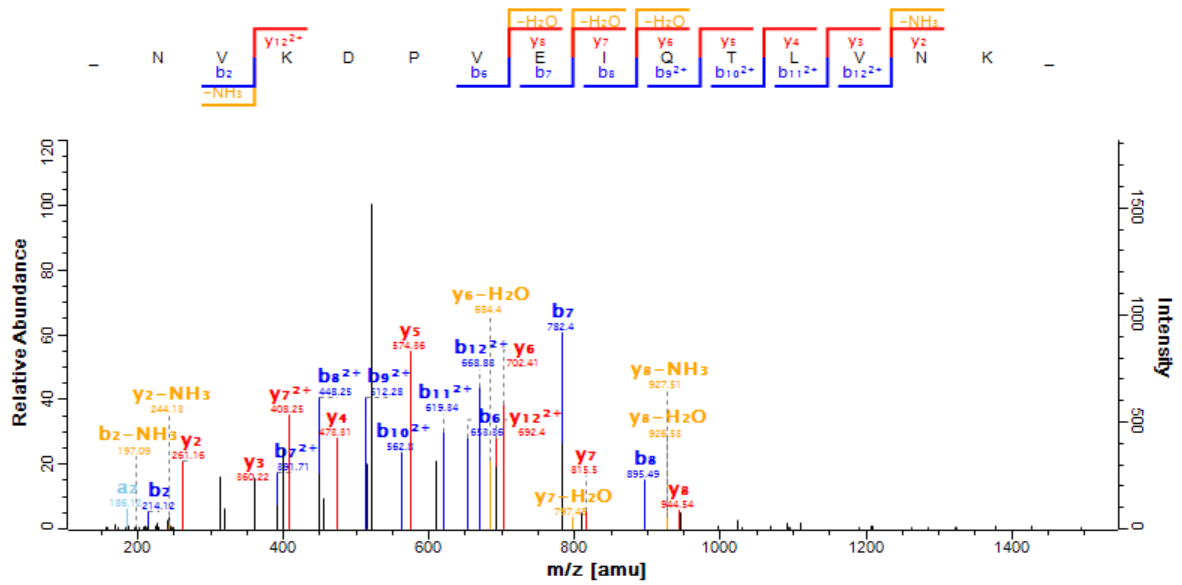
Number of Replicates (out of 10): 2

Best Match Score: 147.33

Best Match Posterior Error Probability: 1.43E-06

Best Match Spectrum:

Scan number	3080	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac21
Method	ITMS; CID	Genenames	LYRM4



Protein Group ID: 394

Protein Accession Numbers: Q96I51; F5H6C7; F5GX55; C9JWG9

Gene Names: WBSR16

Peptide Sequence: KVVENEIYSESHR

Total Number of Spectra: 2

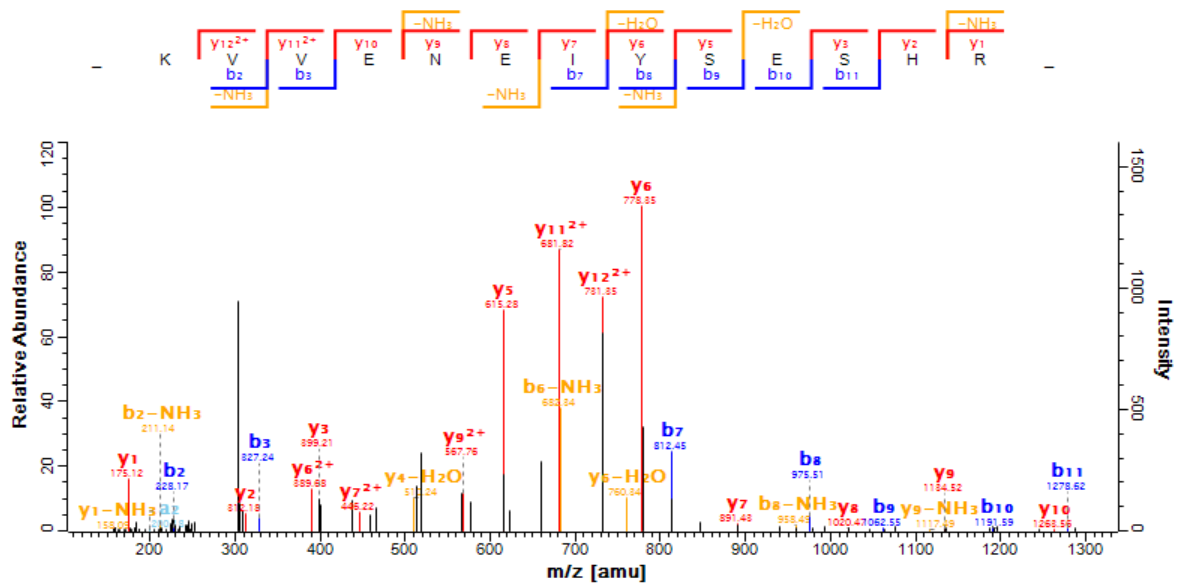
Number of Replicates (out of 10): 2

Best Match Score: 116.63

Best Match Posterior Error Probability: 0.00034469

Best Match Spectrum:

Scan number 1054 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac18
Method ITMS; CID **Genenames** WBSR16



Protein Group ID: 402

Protein Accession Numbers: C9K0X5; O95149; H3BRI5; H3BSK1; H3BTA6; H3BQR0

Gene Names: SNUPN

Peptide Sequence: MEELSQLASSFSVSQDLNSTAAPHPR

Total Number of Spectra: 16

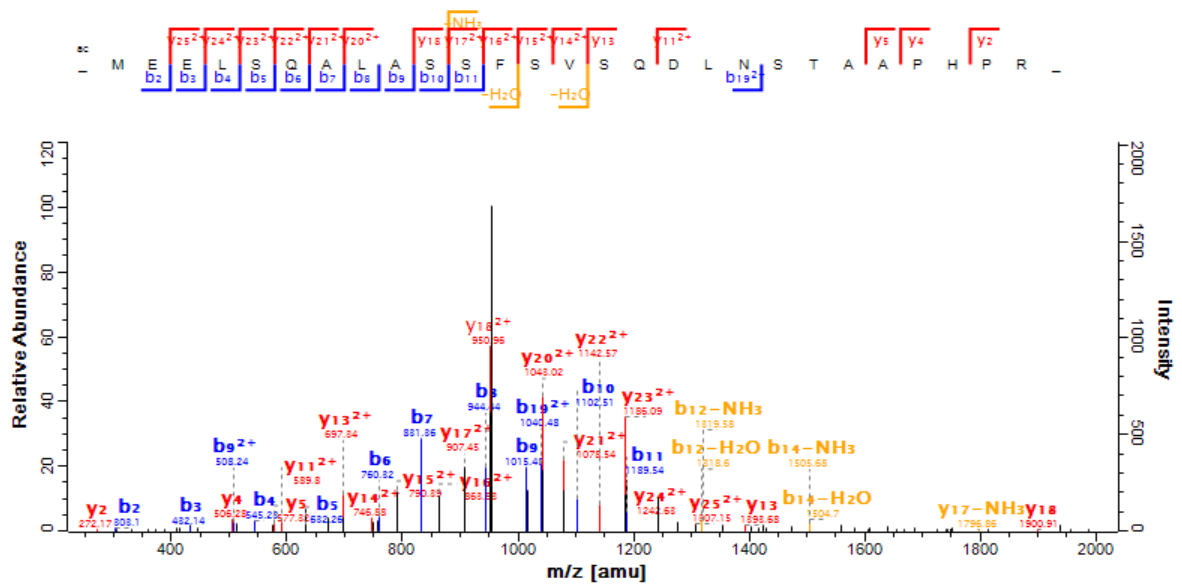
Number of Replicates (out of 10): 9

Best Match Score: 120.33

Best Match Posterior Error Probability: 3.02E-21

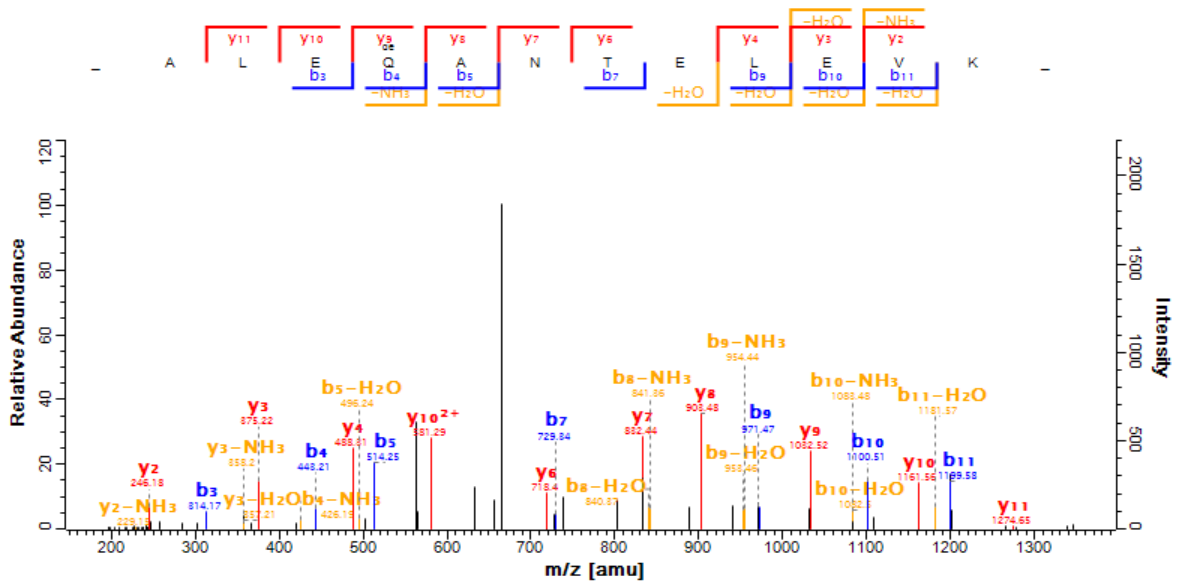
Best Match Spectrum:

Scan number 6176 **Raw file** Prt-OGE-Batch2-WT-Frac13
Method ITMS; CID **Genenames** SNUPN



Protein Group ID: 403
Protein Accession Numbers: CON__A2A4G1
Gene Names:
Peptide Sequence: ALEQANTELEVK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 157.56
Best Match Posterior Error Probability: 0.0026744
Best Match Spectrum:

Scan number 2164 **Raw file** Prt-OGE-Batch2-WT-Frac12
Method ITMS; CID **Pepti...** 157.56



Protein Group ID: 404

Protein Accession Numbers: CON__A2I7N0; CON__A2I7N1

Gene Names:

Peptide Sequence: VNRPFLLIYVVK

Total Number of Spectra: 2

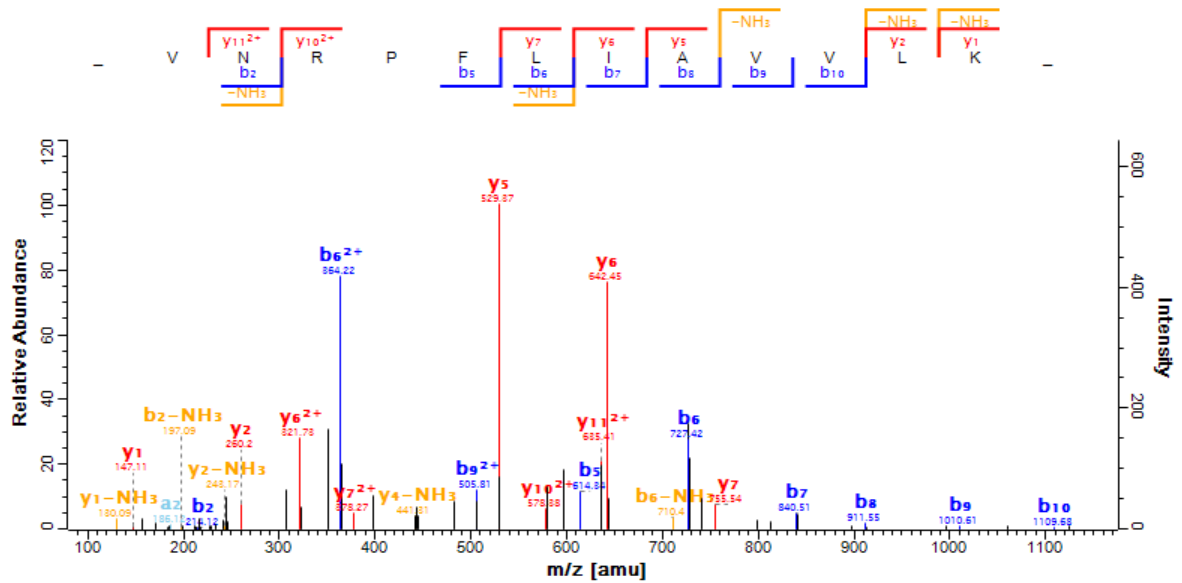
Number of Replicates (out of 10): 2

Best Match Score: 112.83

Best Match Posterior Error Probability: 0.00067781

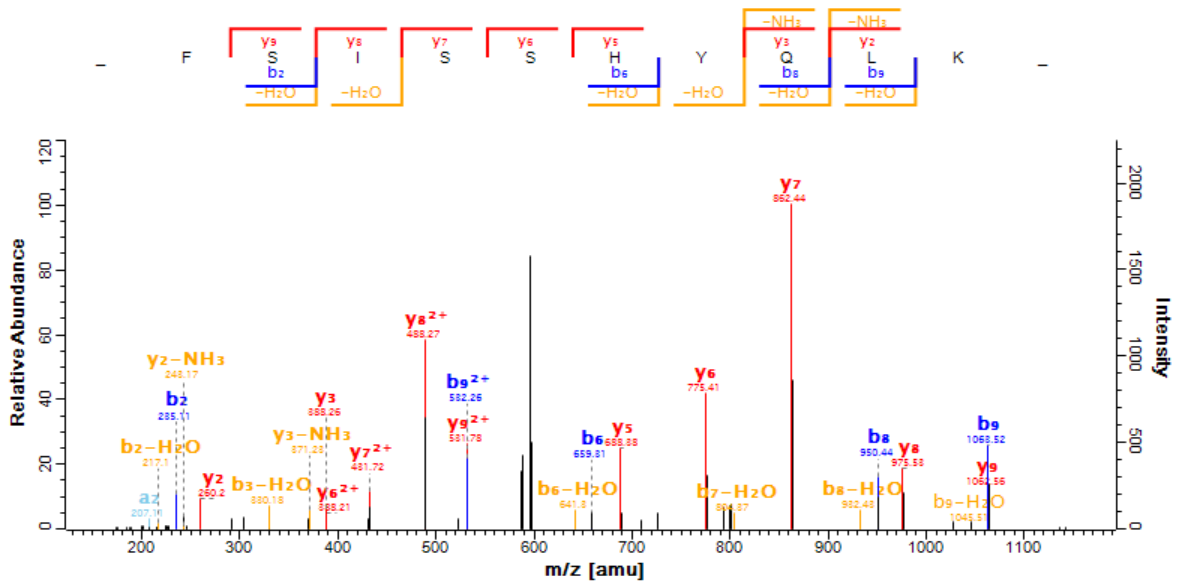
Best Match Spectrum:

Scan number 4660 **Raw file** OGE-WT-Frac3
Method ITMS; CID **Pepti...** 112.83



Protein Group ID: 405
Protein Accession Numbers: CON__A2I7N3
Gene Names:
Peptide Sequence: FSISSHYQLK
Total Number of Spectra: 21
Number of Replicates (out of 10): 10
Best Match Score: 170.47
Best Match Posterior Error Probability: 5.68E-07
Best Match Spectrum:

Scan number 2525 **Raw file** 201100930-KD-Batch5-Prt-OGE-WT-Frac5
Method ITMS; CID **Pepti...** 170.47



Protein Group ID: 410

Protein Accession Numbers: CON__ENSEMBL:ENSBTAP00000018574

Gene Names:

Peptide Sequence: VGAADNVFLAPVGVSAAMAMLSLGLAGDTHQEVHTALR

Total Number of Spectra: 3

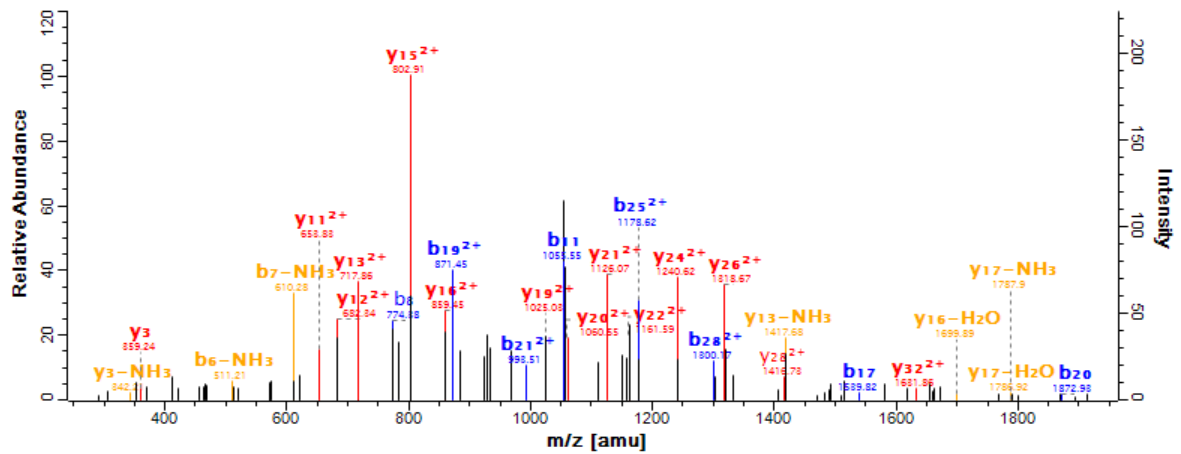
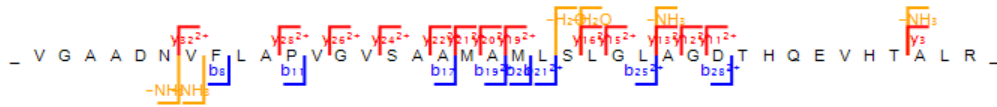
Number of Replicates (out of 10): 3

Best Match Score: 53.522

Best Match Posterior Error Probability: 0.00011249

Best Match Spectrum:

Scan number 7293 **Raw file** OGE-WT-Frac6
Method ITMS; CID **Pepti...** 53.52



Protein Group ID: 412

Protein Accession Numbers: CON__ENSEMBL:ENSBTAP00000038253

Gene Names:

Peptide Sequence: NTKVEISELNR

Total Number of Spectra: 1

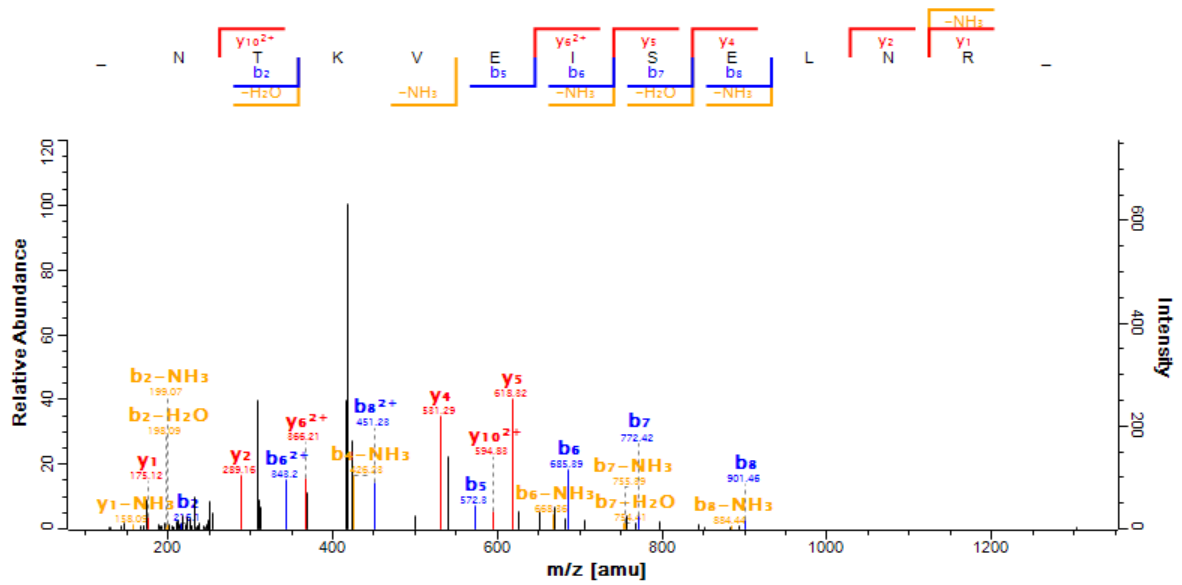
Number of Replicates (out of 10): 1

Best Match Score: 83.081

Best Match Posterior Error Probability: 0.0063805

Best Match Spectrum:

Scan number 1615 **Raw file** Prt-OGE-Batch2-WT-Frac3
Method ITMS; CID **Pepti...** 83.08



Protein Group ID: 413

Protein Accession Numbers: CON__ENSEMBL:ENSBTAP00000038329

Gene Names:

Peptide Sequence: LPENVTPPEEQHK

Total Number of Spectra: 13

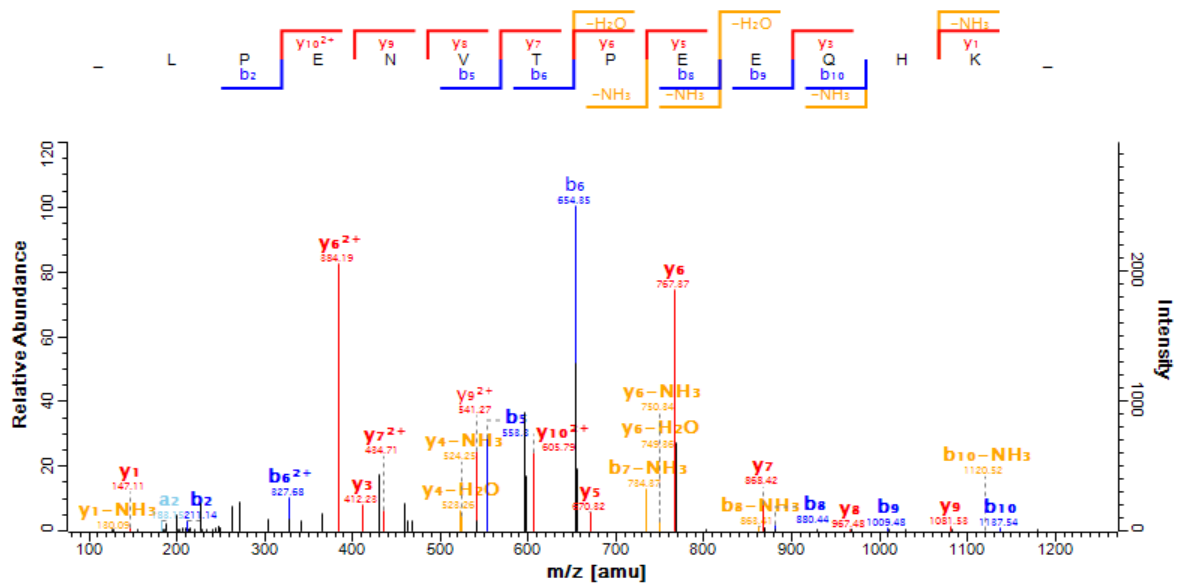
Number of Replicates (out of 10): 5

Best Match Score: 169.89

Best Match Posterior Error Probability: 2.58E-07

Best Match Spectrum:

Scan number	1303	Raw file	OGEWT-Frac4
Method	ITMS; CID	Pepti...	169.89



Protein Group ID: 414

Protein Accession Numbers: CON__H-INV:HIT000292931

Gene Names:

Peptide Sequence: LVSESSDILPK

Total Number of Spectra: 2

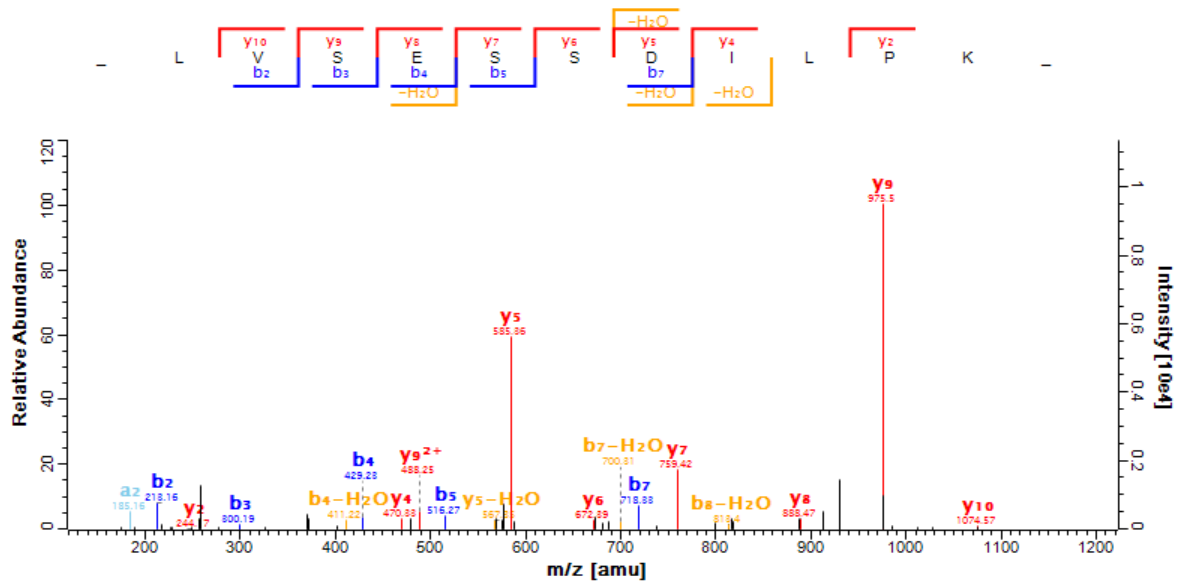
Number of Replicates (out of 10): 2

Best Match Score: 101.39

Best Match Posterior Error Probability: 0.00024992

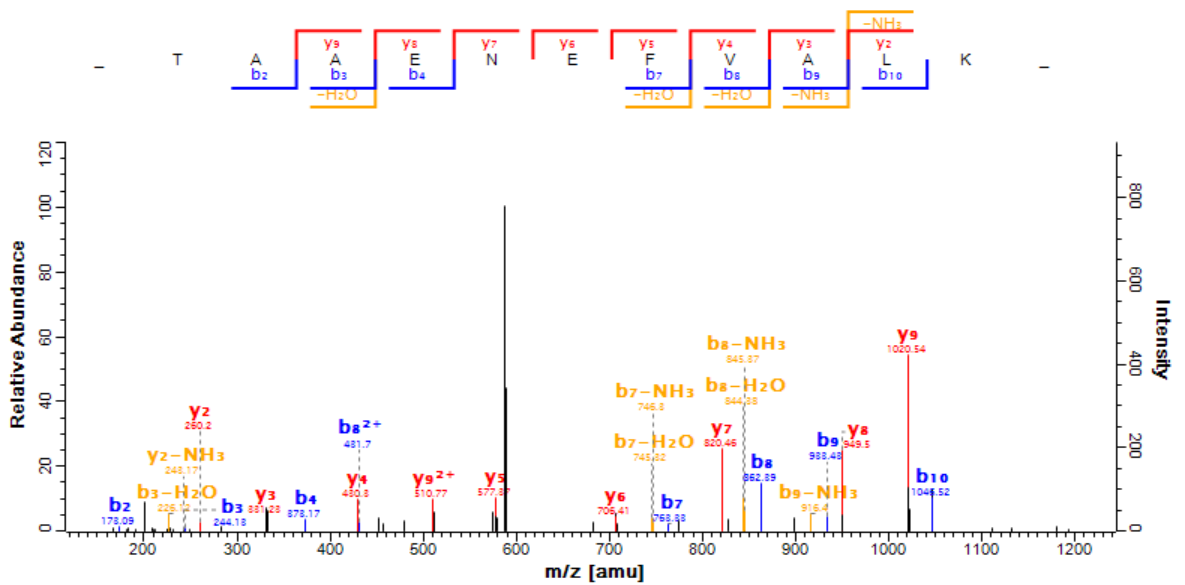
Best Match Spectrum:

Scan number 2920 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac12
Method ITMS; CID **Pepti...** 101.39



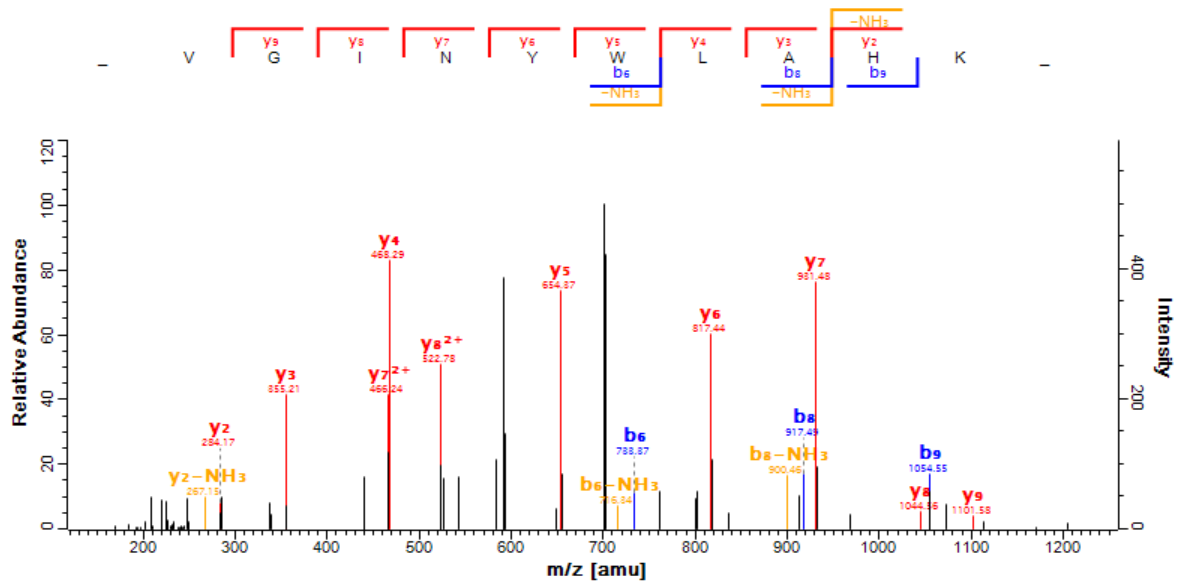
Protein Group ID: 417
Protein Accession Numbers: CON__O95678; O95678
Gene Names: KRT75
Peptide Sequence: TAAENEFVALK
Total Number of Spectra: 3
Number of Replicates (out of 10): 2
Best Match Score: 146.16
Best Match Posterior Error Probability: 1.39E-05
Best Match Spectrum:

Scan number 2640 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac2
Method ITMS; CID **Genenames** KRT75



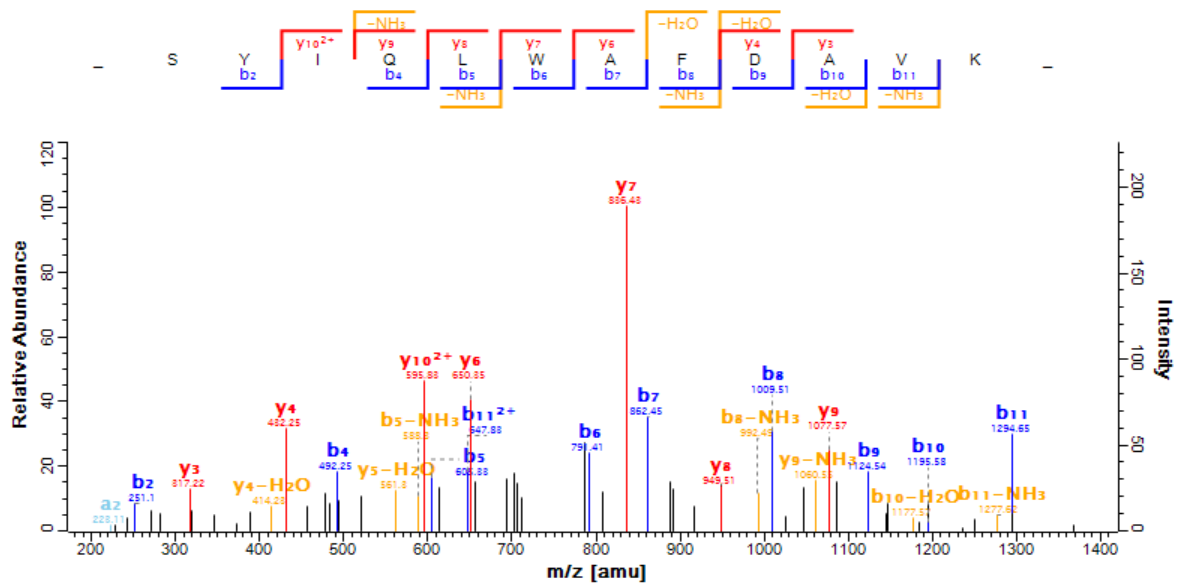
Protein Group ID: 418
Protein Accession Numbers: CON__P00711
Gene Names:
Peptide Sequence: VGINYWLAHK
Total Number of Spectra: 9
Number of Replicates (out of 10): 5
Best Match Score: 99.688
Best Match Posterior Error Probability: 0.00057515
Best Match Spectrum:

Scan number 3219 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac5
Method ITMS; CID **Pepti...** 99.69



Protein Group ID: 420
Protein Accession Numbers: CON_P00978
Gene Names:
Peptide Sequence: SYIQLWAFDAVK
Total Number of Spectra: 9
Number of Replicates (out of 10): 5
Best Match Score: 139.78
Best Match Posterior Error Probability: 6.76E-05
Best Match Spectrum:

Scan number 5662 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac4
Method ITMS; CID **Pepti...** 139.78



Protein Group ID: 424

Protein Accession Numbers: CON__P02070

Gene Names:

Peptide Sequence: EFTPVLQADFQK

Total Number of Spectra: 7

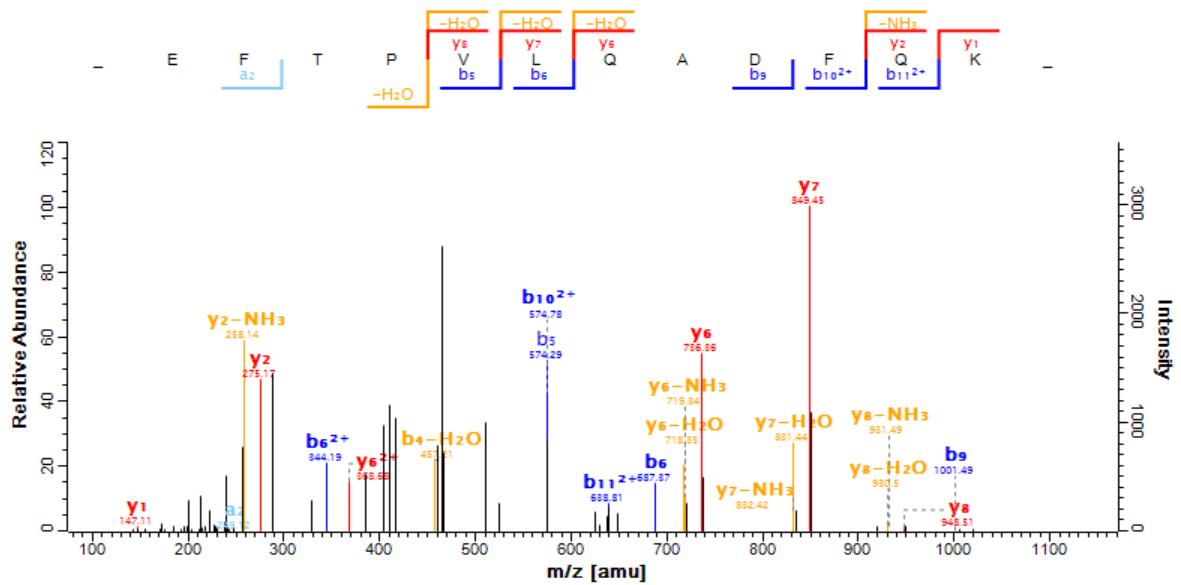
Number of Replicates (out of 10): 4

Best Match Score: 112.83

Best Match Posterior Error Probability: 0.00020126

Best Match Spectrum:

Scan number	1967	Raw file	OGE-Mock-Frac20
Method	ITMS; CID	Pepti...	112.83



Protein Group ID: 427

Protein Accession Numbers: CON__P02584

Gene Names:

Peptide Sequence: D S L L Q D G E F T M D L R

Total Number of Spectra: 1

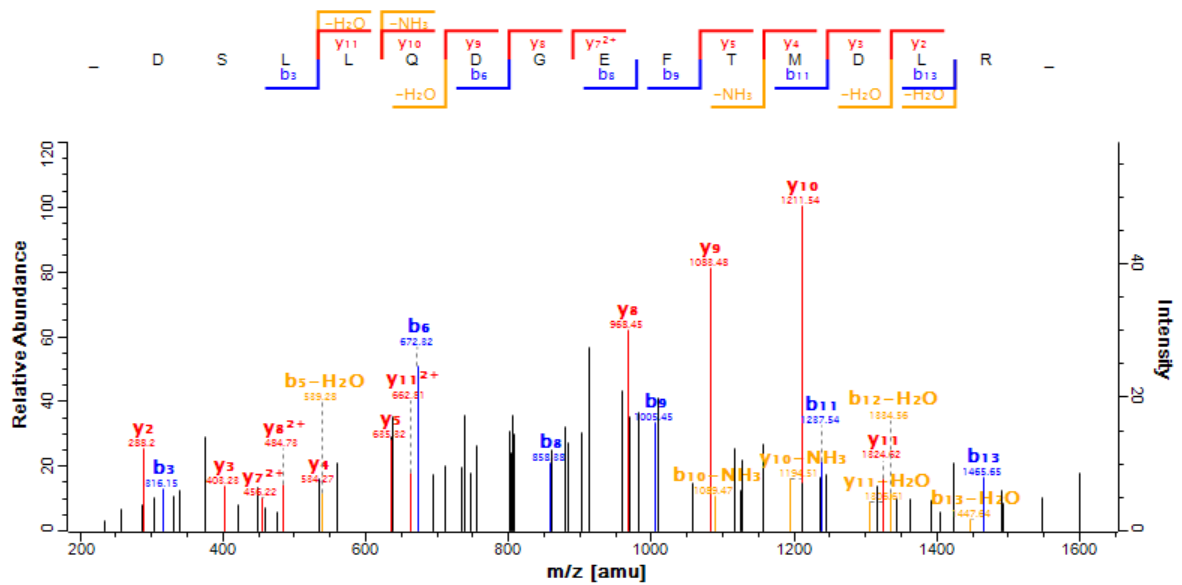
Number of Replicates (out of 10): 1

Best Match Score: 87.447

Best Match Posterior Error Probability: 0.00074949

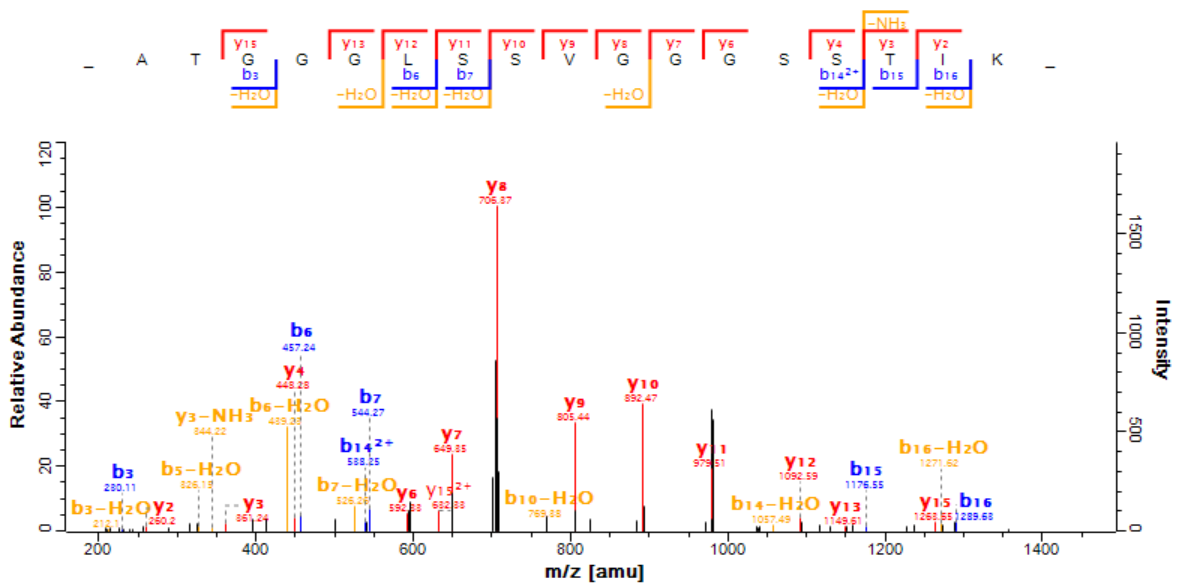
Best Match Spectrum:

Scan number 4642 **Raw file** OGE-WT-Frac3
Method ITMS; CID **Pepti...** 87.45



Protein Group ID: 435
Protein Accession Numbers: CON__P04259
Gene Names:
Peptide Sequence: ATGGGLSSVGGGSSTIK
Total Number of Spectra: 3
Number of Replicates (out of 10): 2
Best Match Score: 109.36
Best Match Posterior Error Probability: 0.00015606
Best Match Spectrum:

Scan number 1628 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac2
Method ITMS; CID **Pepti...** 109.36



Protein Group ID: 438

Protein Accession Numbers: E7EQ64; CON__P07477; P07477; H0Y8D1

Gene Names: PRSS1

Peptide Sequence: TLNNDIMLIK

Total Number of Spectra: 357

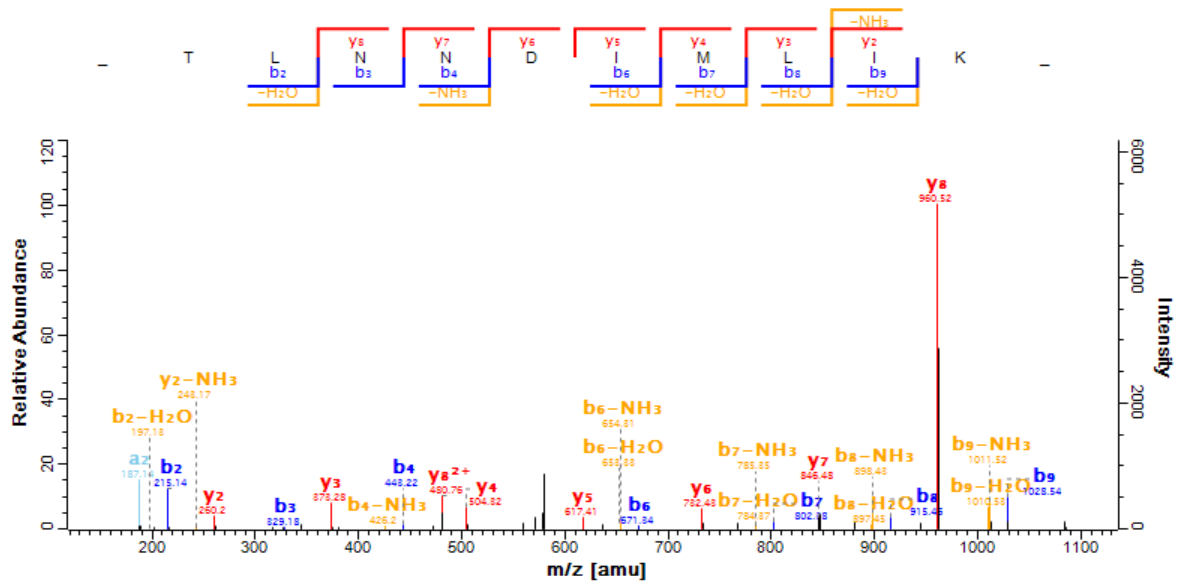
Number of Replicates (out of 10): 10

Best Match Score: 179.57

Best Match Posterior Error Probability: 1.46E-92

Best Match Spectrum:

Scan number 2955 **Raw file** Prt-OGE-Batch2-WT-Frac20
Method ITMS; CID **Genenames** PRSS1



Protein Group ID: 439

Protein Accession Numbers: CON__P07744

Gene Names:

Peptide Sequence: AQYEDIAR

Total Number of Spectra: 87

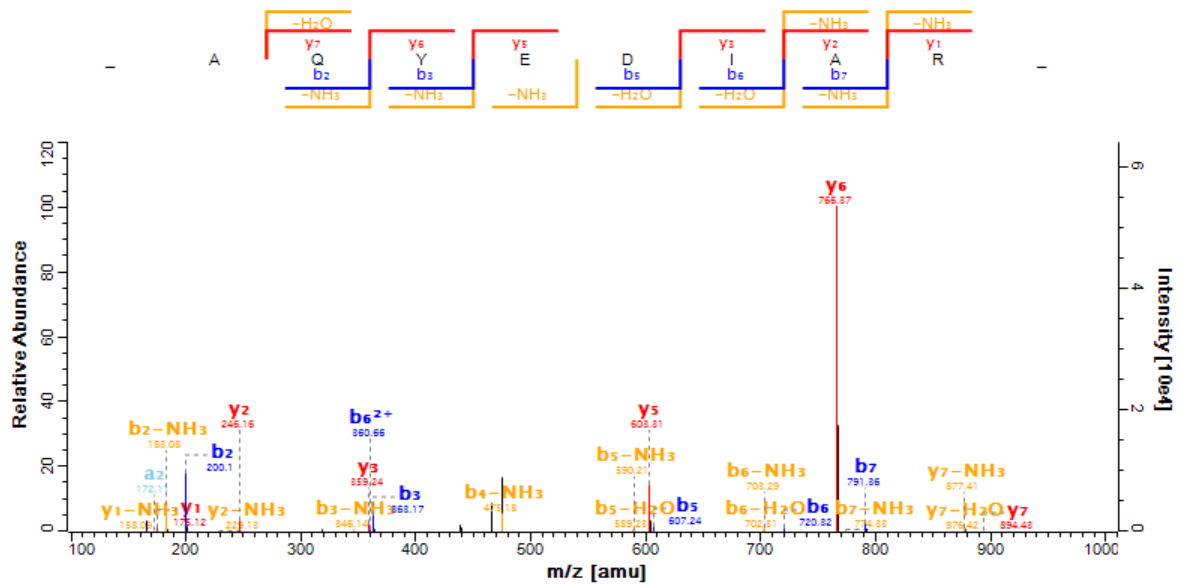
Number of Replicates (out of 10): 10

Best Match Score: 166.52

Best Match Posterior Error Probability: 0.00027213

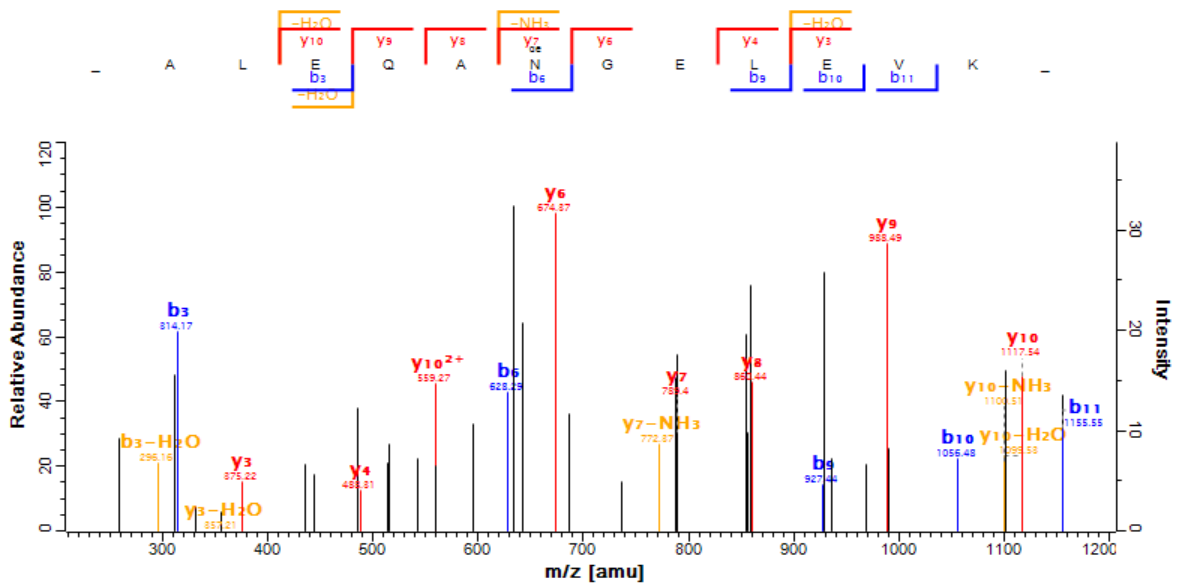
Best Match Spectrum:

Scan number 1157 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac9
Method ITMS; CID **Pepti...** 166.52



Protein Group ID: 447
Protein Accession Numbers: CON__P19001
Gene Names:
Peptide Sequence: ALEQANGELEVK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 84.892
Best Match Posterior Error Probability: 0.014453
Best Match Spectrum:

Scan number 1497 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac24
Method ITMS; CID **Pepti...** 84.89



Protein Group ID: 454

Protein Accession Numbers: CON__P60712; P60709; E7EVS6; G5E9R0; C9JZR7; C9JUM1; C9JTX5

Gene Names: ACTB

Peptide Sequence: DDDIAALVVDNGSGMCK

Total Number of Spectra: 181

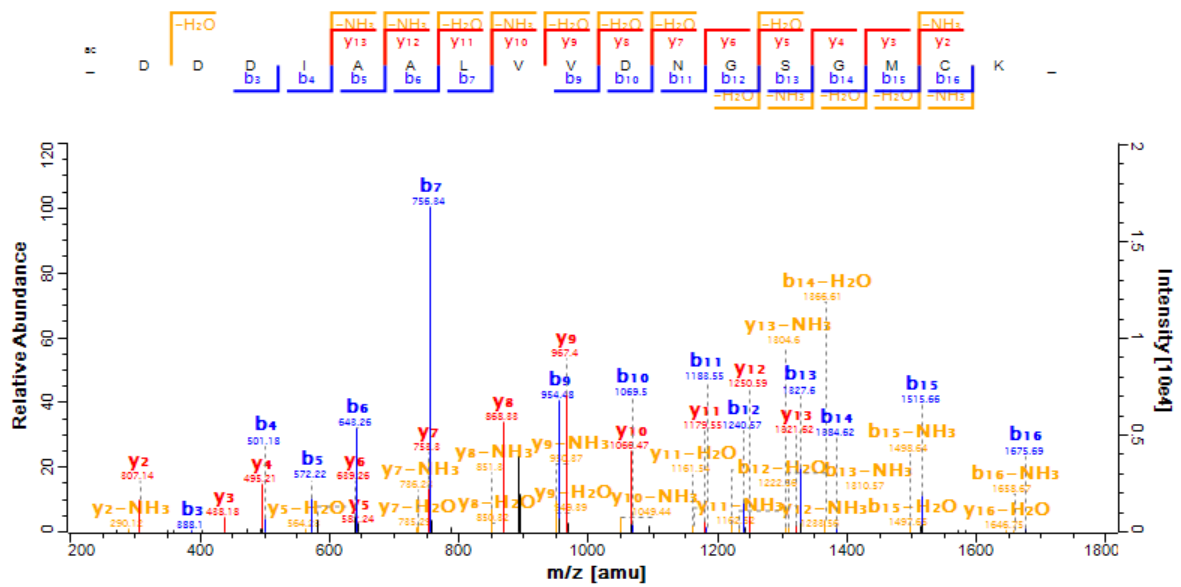
Number of Replicates (out of 10): 8

Best Match Score: 279.44

Best Match Posterior Error Probability: 1.18E-138

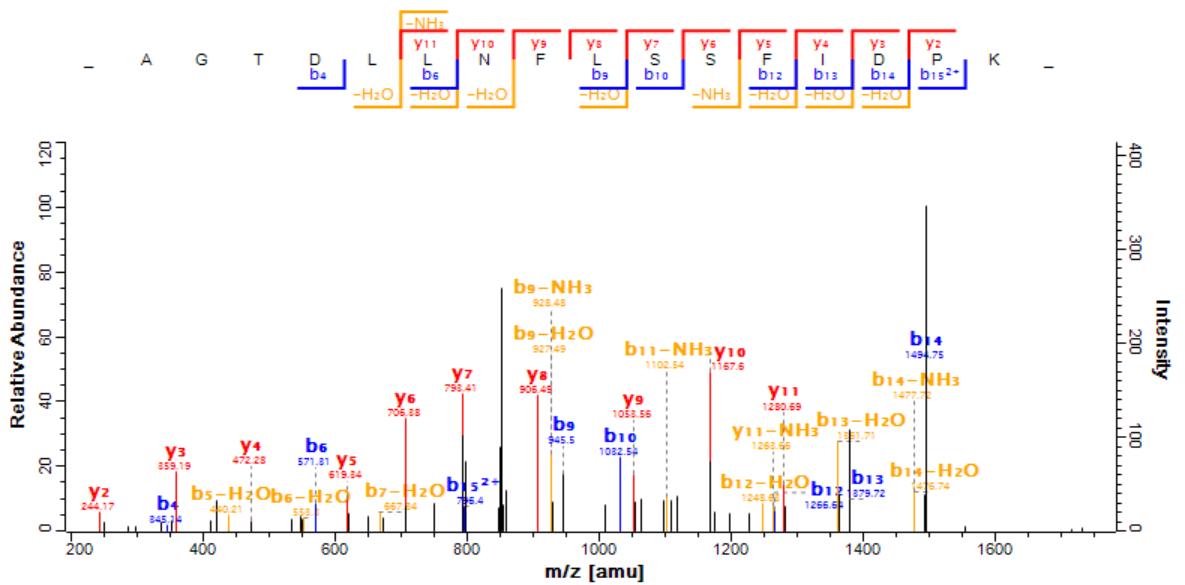
Best Match Spectrum:

Scan number	5130	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac8
Method	ITMS: CID	Genenames	ACTB



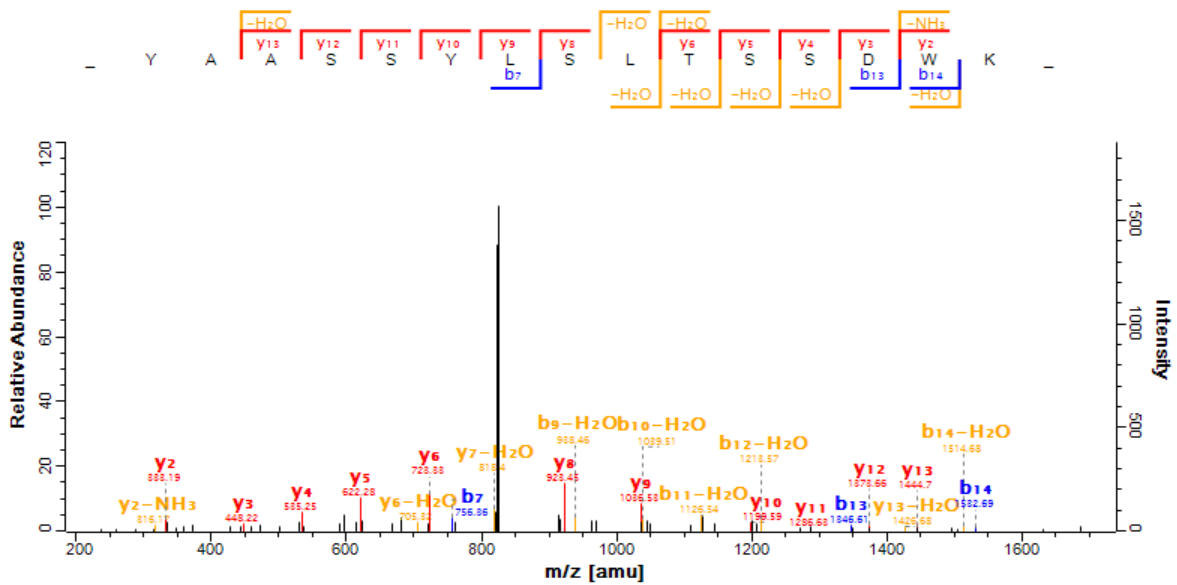
Protein Group ID: 456
Protein Accession Numbers: CON__P81644
Gene Names:
Peptide Sequence: AGTDLLNFLSSFIDPK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 121.32
Best Match Posterior Error Probability: 0.00010141
Best Match Spectrum:

Scan number 7773 **Raw file** OGE-Mock-Frac4
Method ITMS; CID **Pepti...** 121.32



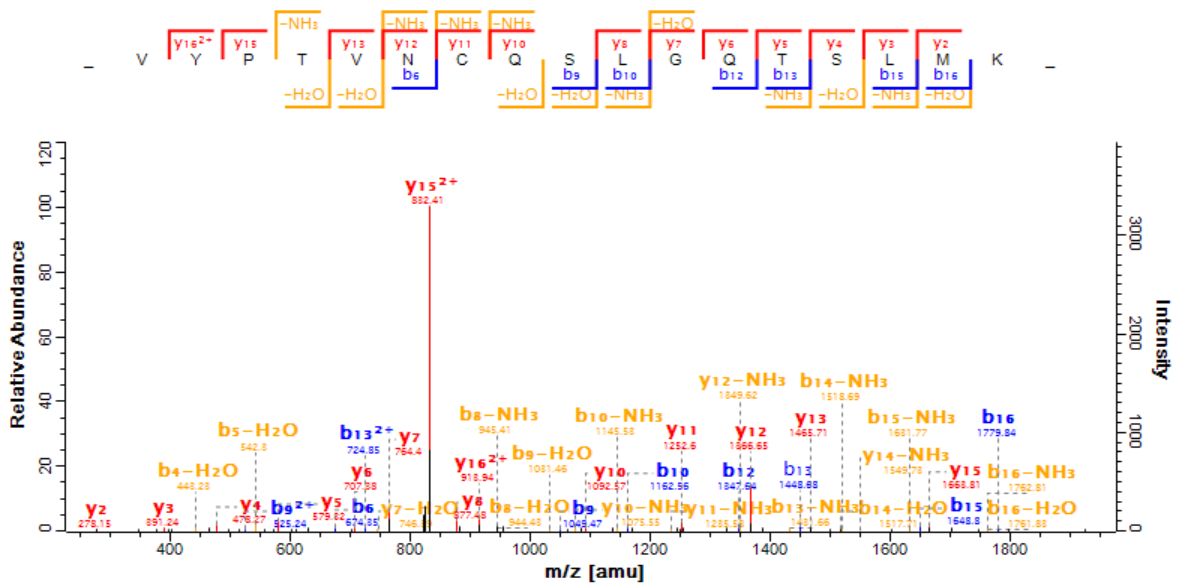
Protein Group ID: 463
Protein Accession Numbers: CON_Q1RMN8
Gene Names:
Peptide Sequence: YAASSYLSLTSSDWK
Total Number of Spectra: 3
Number of Replicates (out of 10): 1
Best Match Score: 96.673
Best Match Posterior Error Probability: 0.0001635
Best Match Spectrum:

Scan number 4338 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac5
Method ITMS; CID **Pepti...** 96.67



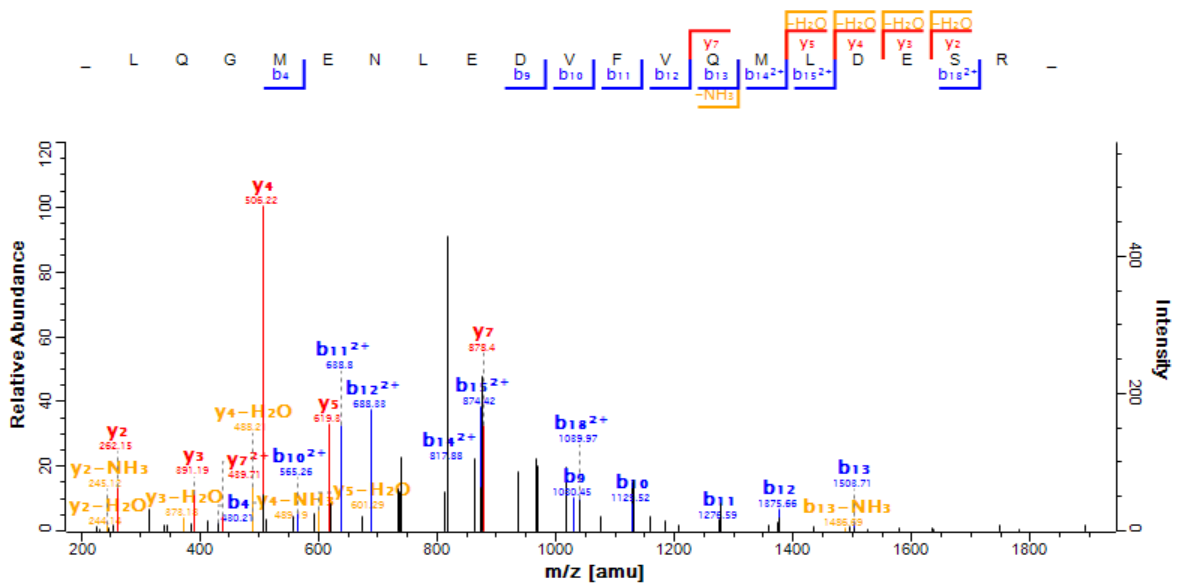
Protein Group ID: 466
Protein Accession Numbers: CON_Q2KJ62
Gene Names:
Peptide Sequence: VYPTVNCQLGQTSLMK
Total Number of Spectra: 3
Number of Replicates (out of 10): 2
Best Match Score: 171.78
Best Match Posterior Error Probability: 6.62E-16
Best Match Spectrum:

Scan number 3720 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac4
Method ITMS; CID **Pepti...** 171.78



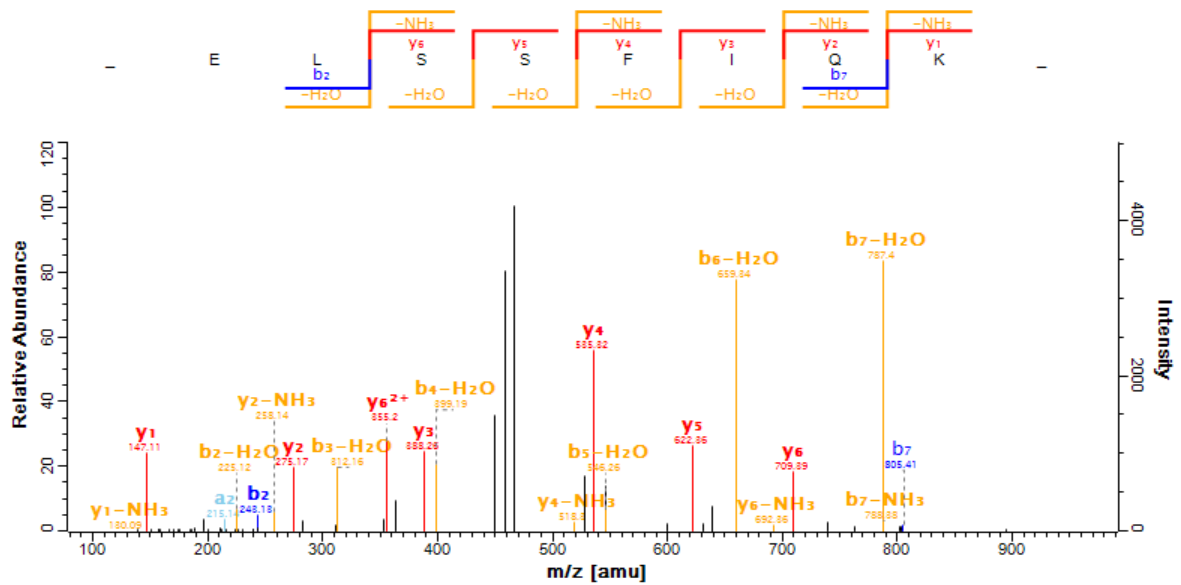
Protein Group ID: 470
Protein Accession Numbers: CON_Q3KUS7
Gene Names:
Peptide Sequence: LQGMENLEDVVFVQMLDESR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 129.05
Best Match Posterior Error Probability: 6.53E-06
Best Match Spectrum:

Scan number 6771 **Raw file** OGE-WT-Frac14
Method ITMS; CID **Pepti...** 129.05



Protein Group ID: 472
Protein Accession Numbers: CON_Q3MHN5
Gene Names:
Peptide Sequence: ELSSFIQK
Total Number of Spectra: 7
Number of Replicates (out of 10): 5
Best Match Score: 132.57
Best Match Posterior Error Probability: 0.001564
Best Match Spectrum:

Scan number 2699 **Raw file** OGE-WT-Frac6
Method ITMS; CID **Pepti...** 132.57



Protein Group ID: 482

Protein Accession Numbers: CON_Q5D862; Q5D862

Gene Names: FLG2

Peptide Sequence: SVVTVIDVFYK

Total Number of Spectra: 1

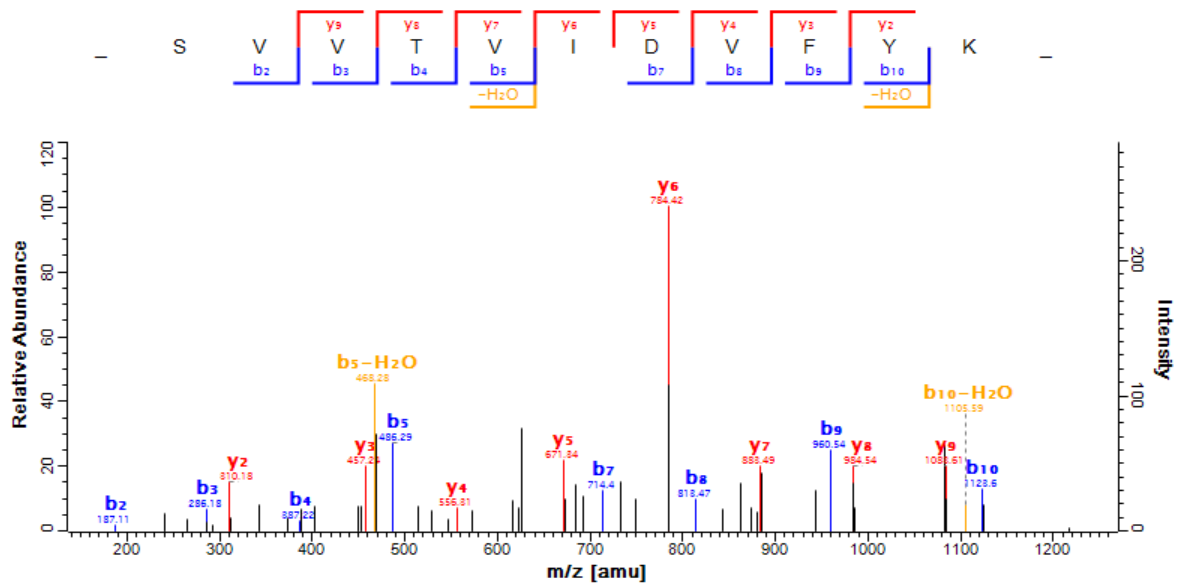
Number of Replicates (out of 10): 1

Best Match Score: 100.93

Best Match Posterior Error Probability: 0.00025588

Best Match Spectrum:

Scan number	4098	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac24
Method	ITMS; CID	Genenames	FLG2



Protein Group ID: 483

Protein Accession Numbers: CON_Q5XKE5; Q5XKE5

Gene Names: KRT79

Peptide Sequence: YEELQVTAGK

Total Number of Spectra: 103

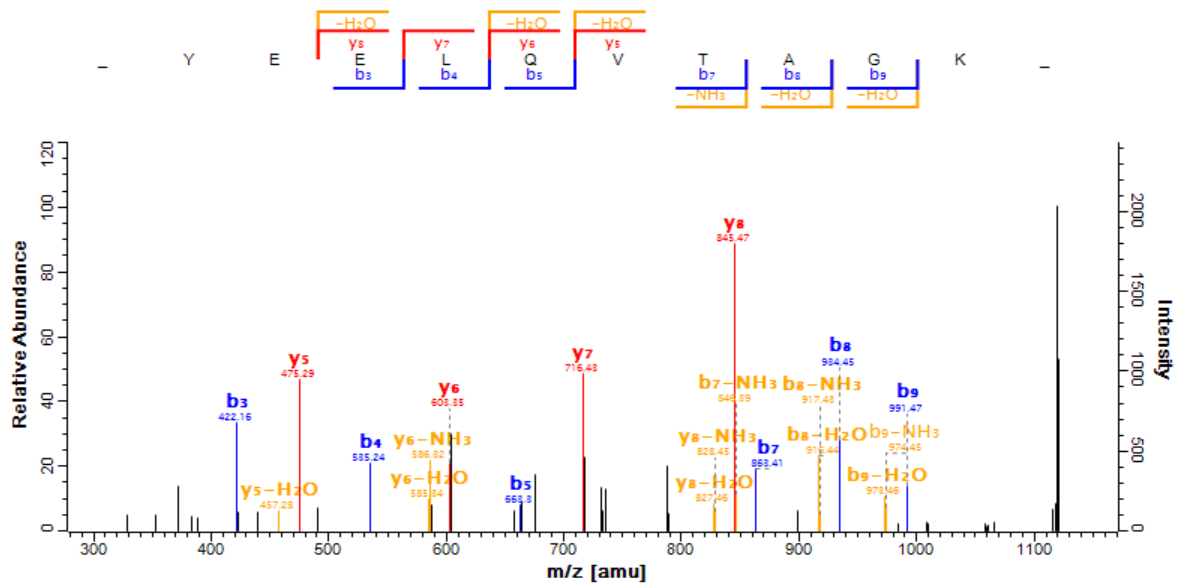
Number of Replicates (out of 10): 9

Best Match Score: 149.72

Best Match Posterior Error Probability: 5.81E-05

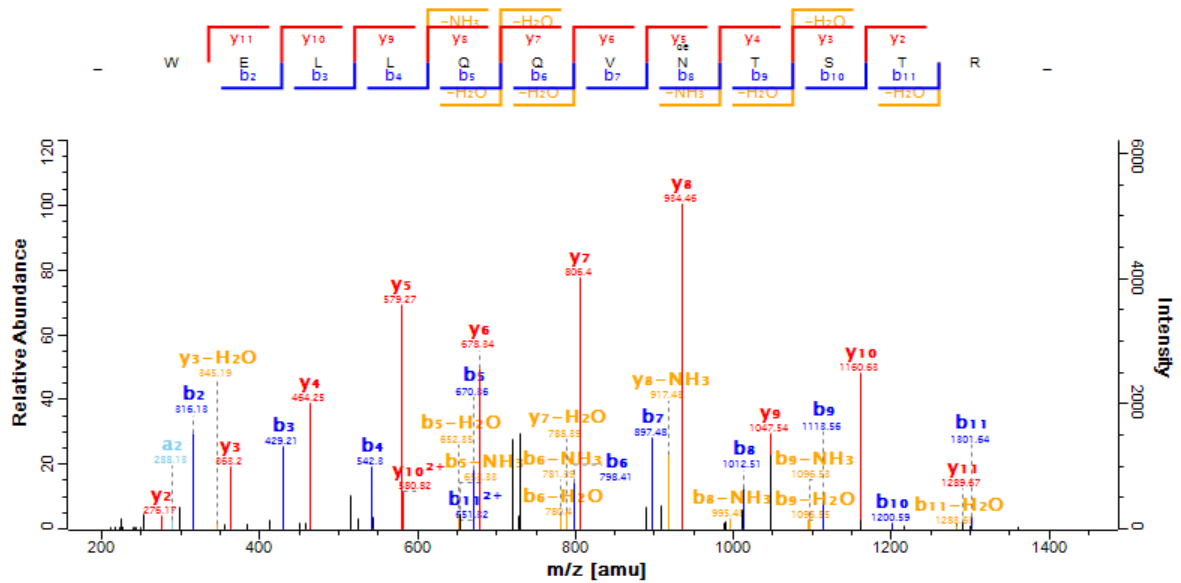
Best Match Spectrum:

Scan number 3076 **Raw file** OGE-Mock-Frac9
Method ITMS; CID **Genenames** KRT79



Protein Group ID: 484
Protein Accession Numbers: CON_Q6IFZ6
Gene Names:
Peptide Sequence: WELLQQVNTSTR
Total Number of Spectra: 116
Number of Replicates (out of 10): 10
Best Match Score: 234.82
Best Match Posterior Error Probability: 2.39E-53
Best Match Spectrum:

Scan number 4024 **Raw file** OGE-WT-Frac21
Method ITMS; CID **Pepti...** 234.82



Protein Group ID: 486

Protein Accession Numbers: CON_Q7RTT2; CON_Q8N1N4-2; Q8N1N4; Q8N1N4-2; F8VS93

Gene Names: KRT78

Peptide Sequence: YLDFSSIITEVR

Total Number of Spectra: 1

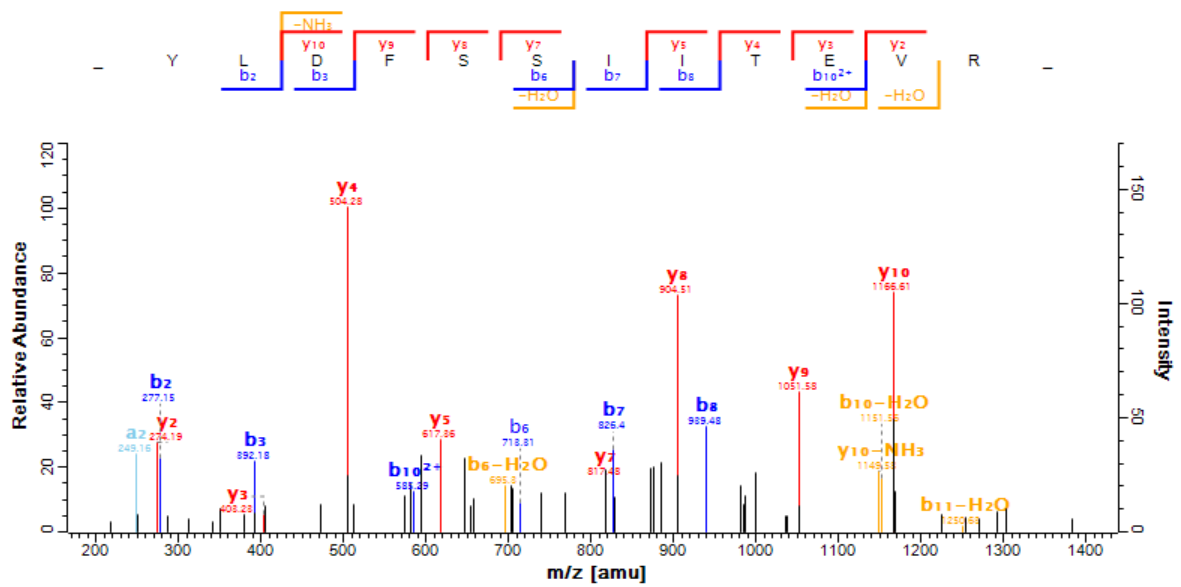
Number of Replicates (out of 10): 1

Best Match Score: 98.105

Best Match Posterior Error Probability: 0.00048775

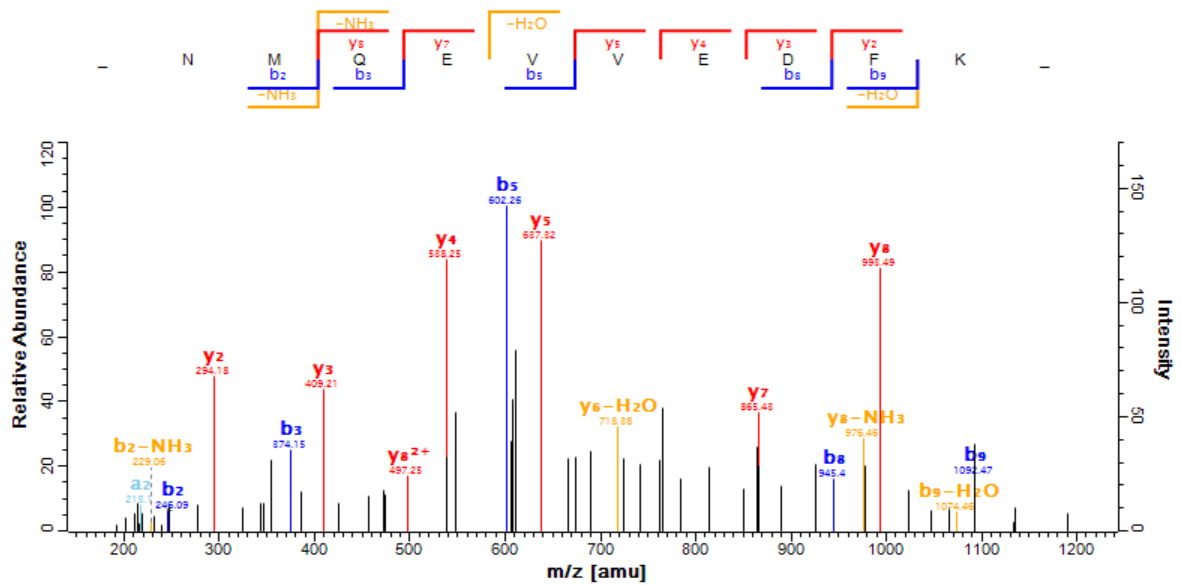
Best Match Spectrum:

Scan number 4383 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac24
Method ITMS: CID **Genenames** KRT78



Protein Group ID: 488
Protein Accession Numbers: CON_Q8BGZ7
Gene Names:
Peptide Sequence: NMQEVVEDFK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 77.64
Best Match Posterior Error Probability: 0.0034194
Best Match Spectrum:

Scan number 3927 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac2
Method ITMS; CID **Pepti...** 77.64



Protein Group ID: 489

Protein Accession Numbers: Q9BYR0; CON__Q9BYQ5; Q9BQ66; Q9BYQ5; I3L475; Q9BYR2

Gene Names: KRTAP4-7;KRTAP4-12;KRTAP4-6;KRTAP4-5

Peptide Sequence: PTCVISTCPR

Total Number of Spectra: 3

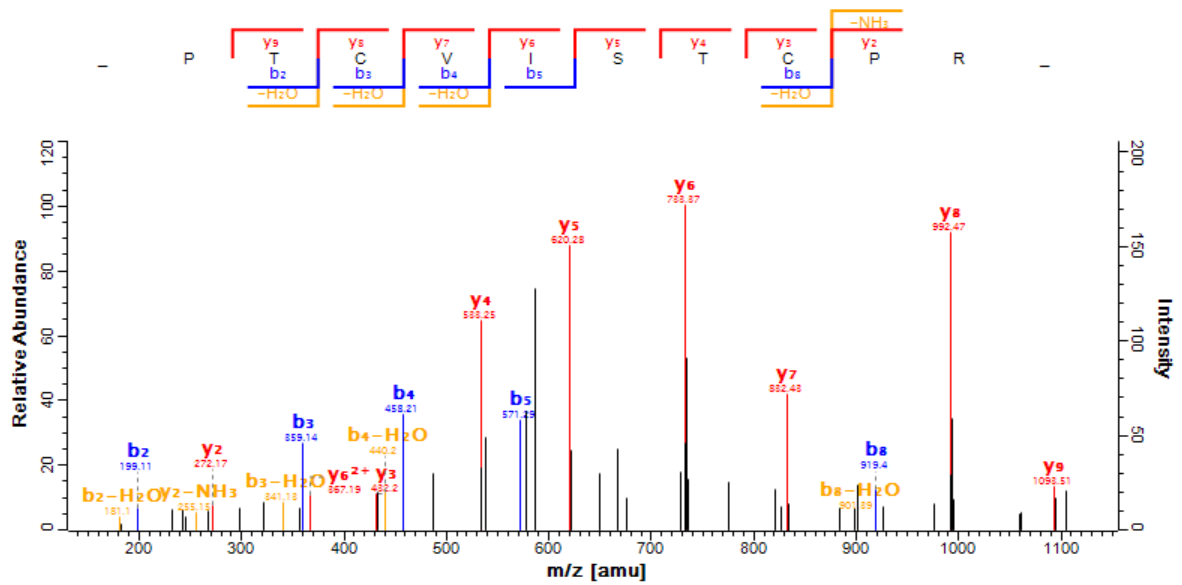
Number of Replicates (out of 10): 2

Best Match Score: 114.89

Best Match Posterior Error Probability: 0.00021656

Best Match Spectrum:

Scan number	1224	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac3
Method	ITMS: CID	Genenames	KRTAP4-7;KRTAP4-12;KRTAP4-6;KRTAP4-5



Protein Group ID: 490

Protein Accession Numbers: CON_Q9BYR8; Q9BYR8

Gene Names: KRTAP3-1

Peptide Sequence: SCSVPTGPATTFCSFDK

Total Number of Spectra: 6

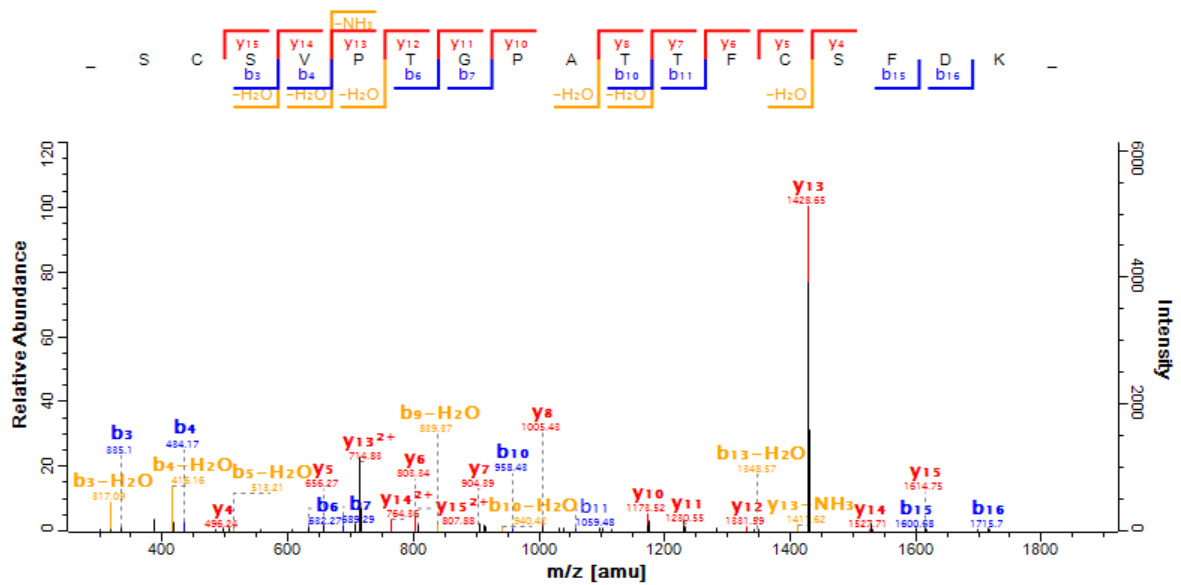
Number of Replicates (out of 10): 2

Best Match Score: 117.2

Best Match Posterior Error Probability: 0.00014114

Best Match Spectrum:

Scan number	3430	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac2
Method	ITMS; CID	Genenames	KRTAP3-1



Protein Group ID: 493

Protein Accession Numbers: CON_Q9QWL7; K7EPJ9

Gene Names:

Peptide Sequence: ALEEANTELEVK

Total Number of Spectra: 3

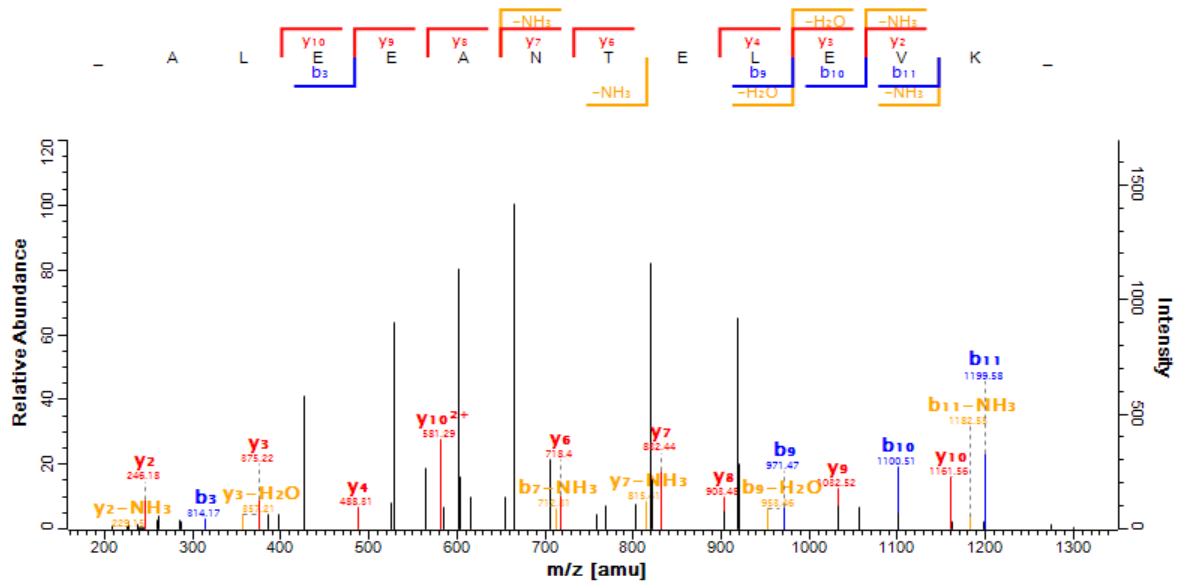
Number of Replicates (out of 10): 3

Best Match Score: 104.24

Best Match Posterior Error Probability: 0.00030161

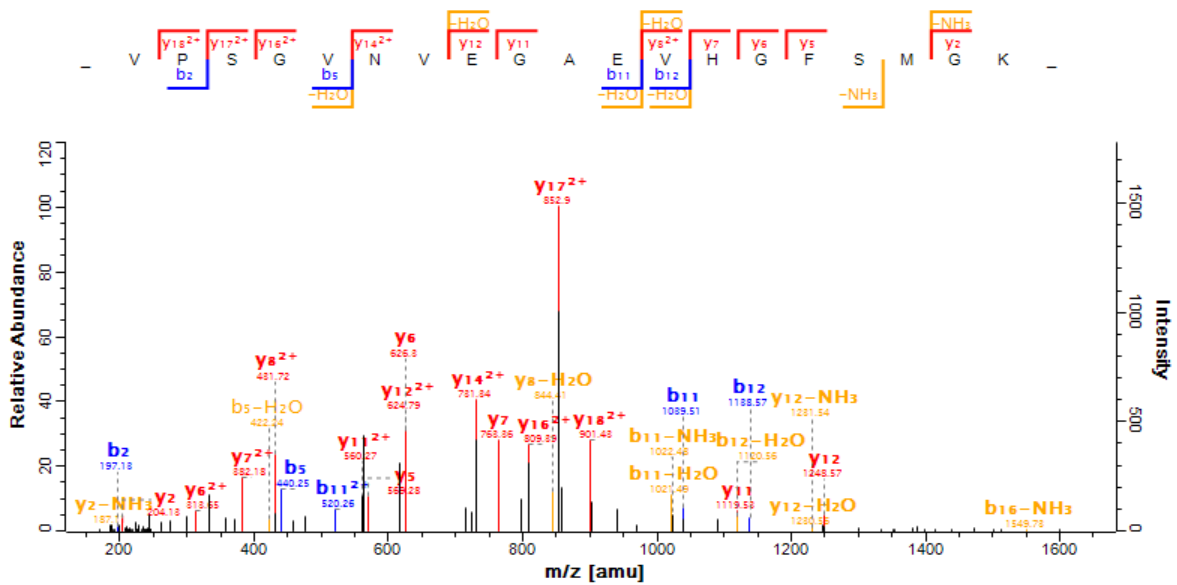
Best Match Spectrum:

Scan number 2079 **Raw file** Prt-OGE-Batch2-WT-Frac5
Method ITMS; CID **Pepti...** 104.24



Protein Group ID: 501
Protein Accession Numbers: Q8IVL5; D3DNV8
Gene Names: LEPREL1
Peptide Sequence: VPSGVNVEGAVGVHSGMK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 126.63
Best Match Posterior Error Probability: 1.14E-05
Best Match Spectrum:

Scan number 3185 **Raw file** Prt-OGE-Batch3-WT-Frac10
Method ITMS; CID **Genenames** LEPREL1



Protein Group ID: 508

Protein Accession Numbers: Q9BUT1; Q9BUT1-2; D6RIR6; D6R9U8; D6RFG2; D6RBF6

Gene Names: BDH2

Peptide Sequence: VIILTAAQGIGQAAALAFAR

Total Number of Spectra: 8

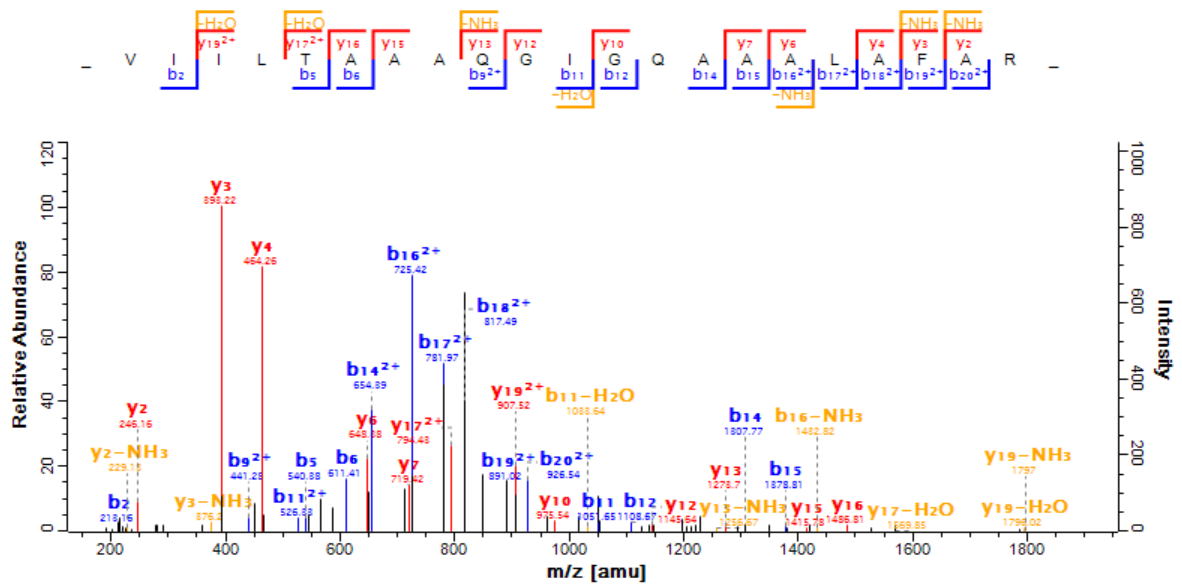
Number of Replicates (out of 10): 7

Best Match Score: 143.83

Best Match Posterior Error Probability: 2.66E-13

Best Match Spectrum:

Scan number 7026 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac18
Method ITMS; CID **Genenames** BDH2



Protein Group ID: 511

Protein Accession Numbers: Q8WUP2-2; Q8WUP2; Q8WUP2-3; E7EN81; E7EWE8; E7EPI5; D6RAI6

Gene Names: FBLIM1

Peptide Sequence: TPEAGLAGRSPWTTTTPGR

Total Number of Spectra: 5

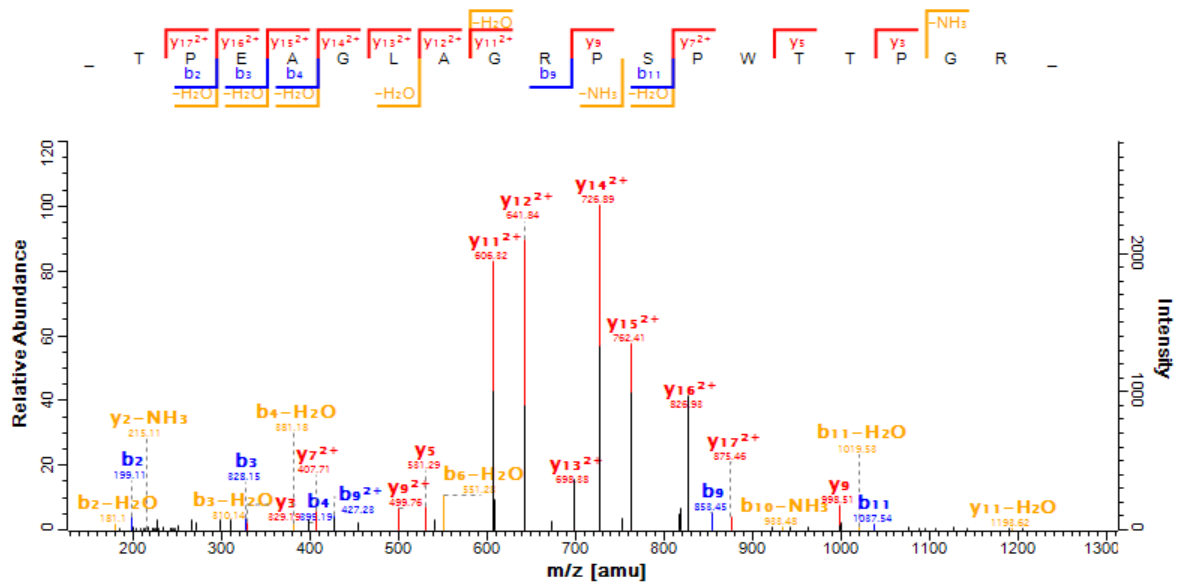
Number of Replicates (out of 10): 3

Best Match Score: 107.74

Best Match Posterior Error Probability: 0.00044295

Best Match Spectrum:

Scan number	2517	Raw file	Prt-OGE-Batch3-WT-Frac10
Method	ITMS; CID	Genenames	FBLIM1



Protein Group ID: 513

Protein Accession Numbers: Q9NVZ3-2; Q9NVZ3; F6SKB8; Q9NVZ3-3; D6RAN6; H0Y970

Gene Names: NECAP2

Peptide Sequence: AAEWQLDQPSWSGR

Total Number of Spectra: 2

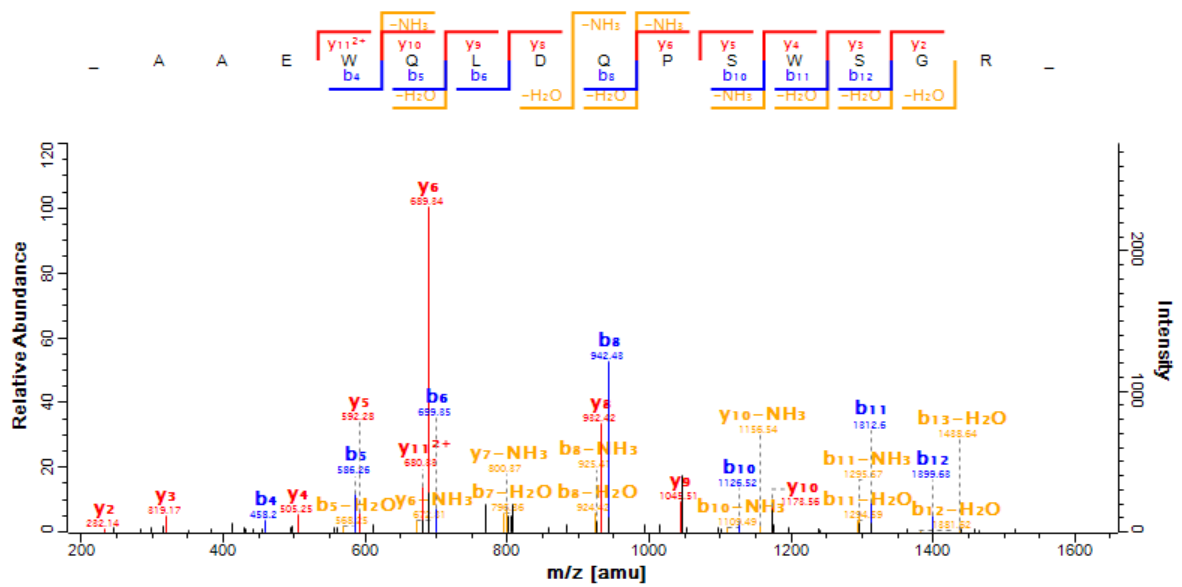
Number of Replicates (out of 10): 2

Best Match Score: 136.6

Best Match Posterior Error Probability: 1.25E-05

Best Match Spectrum:

Scan number 3307 **Raw file** Prt-OGE-Batch2-WT-Frac18
Method ITMS; CID **Genenames** NECAP2



Protein Group ID: 514

Protein Accession Numbers: Q9H819; D6RB03; D6RCS7

Gene Names: DNAJC18

Peptide Sequence: NYYEILGVSR

Total Number of Spectra: 2

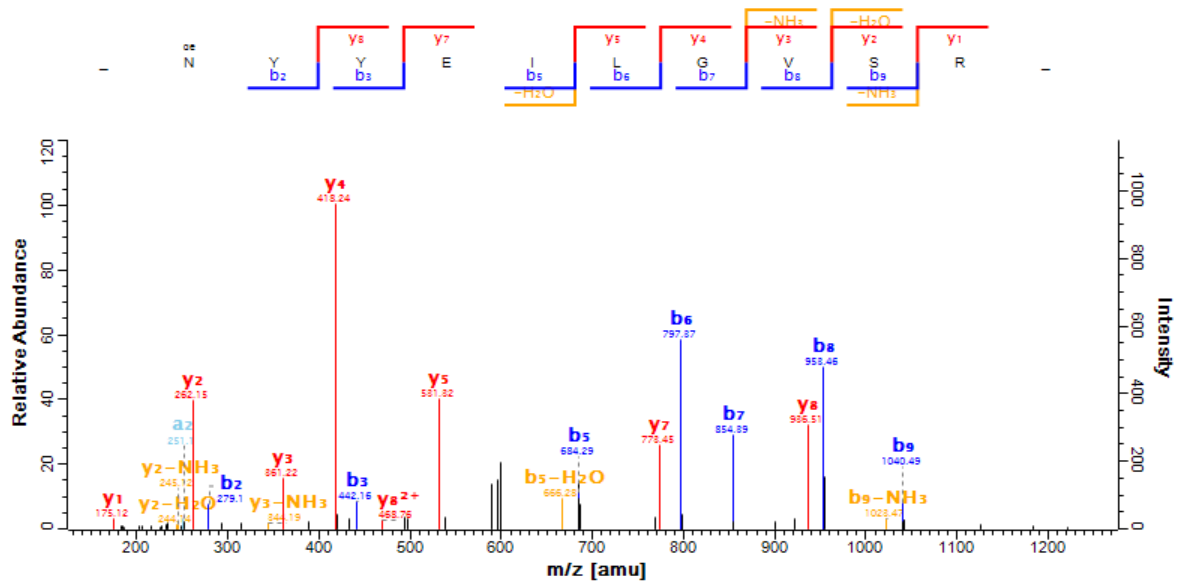
Number of Replicates (out of 10): 2

Best Match Score: 131.43

Best Match Posterior Error Probability: 0.00092552

Best Match Spectrum:

Scan number	3794	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac20
Method	ITMS; CID	Genenames	DNAJC18



Protein Group ID: 515

Protein Accession Numbers: Q96H20; Q96H20-2; D6RFY6; D6RJ86; D6RBI1; H0Y8S5

Gene Names: SNF8

Peptide Sequence: GTVLAEDQLAQMSK

Total Number of Spectra: 2

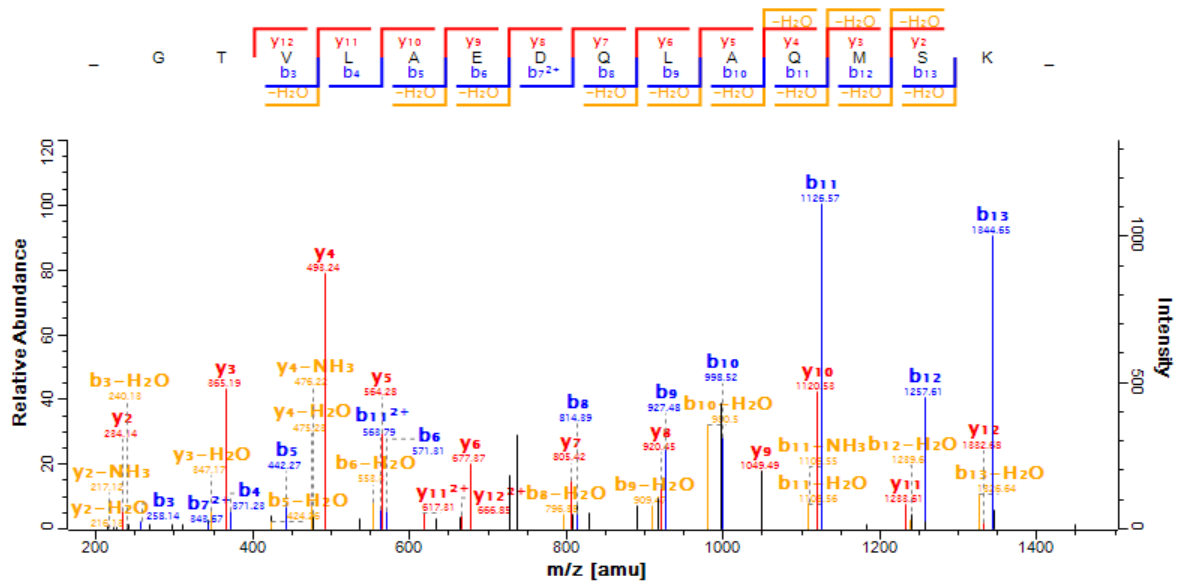
Number of Replicates (out of 10): 2

Best Match Score: 233.97

Best Match Posterior Error Probability: 7.30E-61

Best Match Spectrum:

Scan number	2991	Raw file	Prt-OGE-Batch2-WT-Frac13
Method	ITMS; CID	Genenames	SNF8



Protein Group ID: 521

Protein Accession Numbers: Q9Y6B6; D6RD69; Q9H029; D6R9R5

Gene Names: SAR1B;DKFZp434B2017

Peptide Sequence: EMFGLYGQTTGK

Total Number of Spectra: 1

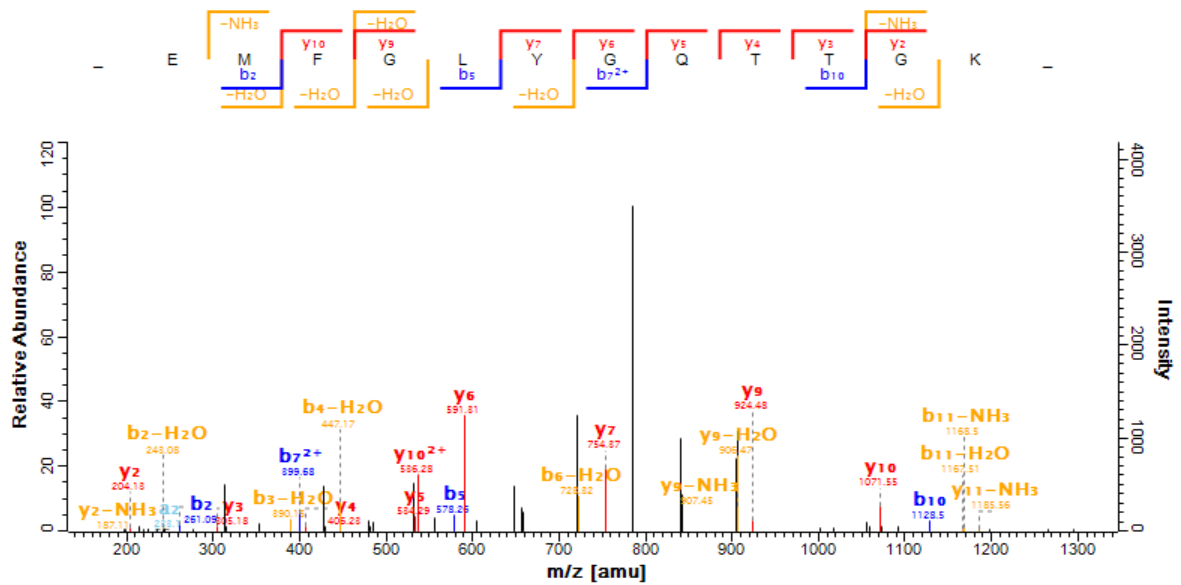
Number of Replicates (out of 10): 1

Best Match Score: 100.38

Best Match Posterior Error Probability: 0.00041889

Best Match Spectrum:

Scan number	3813	Raw file	Prt-OGE-Batch3-Mock-Frac11
Method	ITMS; CID	Genenames	SAR1B;DKFZp434B2017



Protein Group ID: 523

Protein Accession Numbers: F6VM53; Q96S19; F6TF62; H3BNB2; Q96S19-2; H3BRT2; D6REA6; Q96S19-3; H3BS73

Gene Names: C16orf13

Peptide Sequence: NKDPILHVLR

Total Number of Spectra: 3

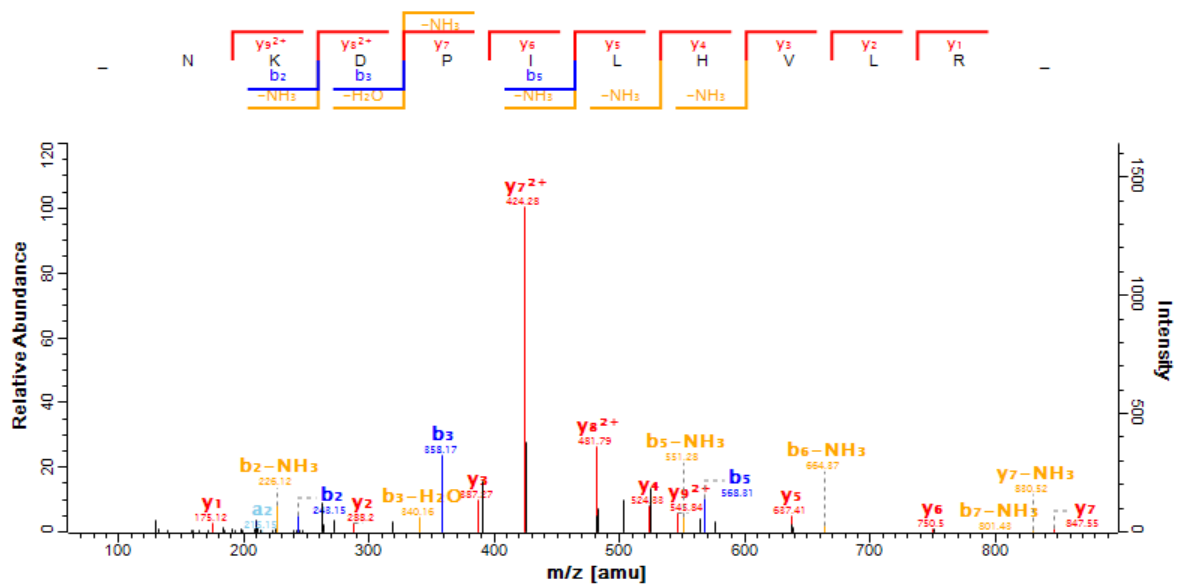
Number of Replicates (out of 10): 3

Best Match Score: 108.43

Best Match Posterior Error Probability: 0.0011706

Best Match Spectrum:

Scan number 1720 Raw file Prt-OGE-Batch3-Mock-Frac17
Method ITMS: CID Genenames C16orf13



Protein Group ID: 524

Protein Accession Numbers: Q6UX04; Q6UX04-2; D6REK3

Gene Names: CWC27

Peptide Sequence: NFSLLSFGEEAEVEEVEVNR

Total Number of Spectra: 1

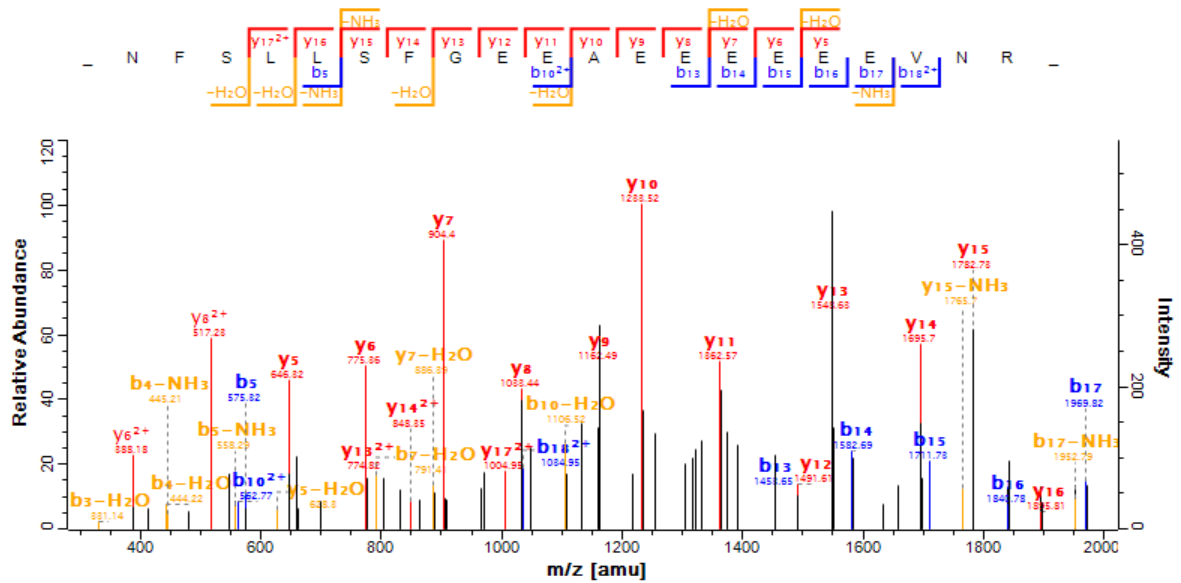
Number of Replicates (out of 10): 1

Best Match Score: 140.32

Best Match Posterior Error Probability: 7.93E-09

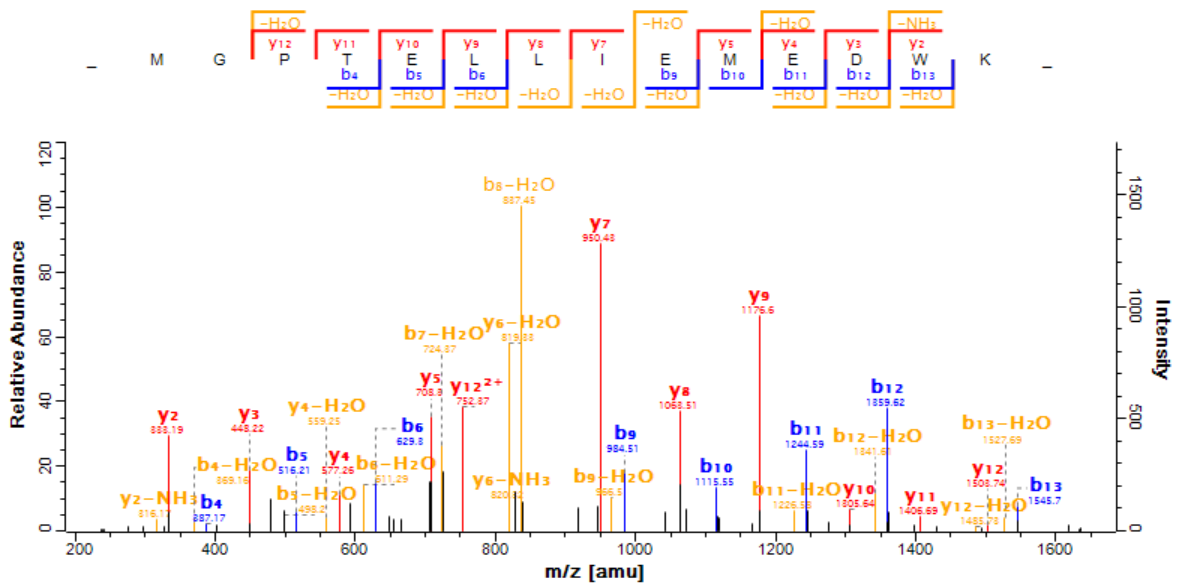
Best Match Spectrum:

Scan number 6528 **Raw file** Prt-OGE-Batch3--Mock-Frac11
Method ITMS; CID **Genenames** CWC27



Protein Group ID: 525
Protein Accession Numbers: P02675; D6REL8
Gene Names: FGB
Peptide Sequence: MGPTELLIEMEDWK
Total Number of Spectra: 5
Number of Replicates (out of 10): 4
Best Match Score: 210.91
Best Match Posterior Error Probability: 4.34E-37
Best Match Spectrum:

Scan number 5581 **Raw file** Prt-OGE-Batch3-Mock-Frac16
Method ITMS; CID **Genenames** FGB



Protein Group ID: 528

Protein Accession Numbers: P42702; D6RF33; D6RJ94

Gene Names: LIFR

Peptide Sequence: MMDIYVCLK

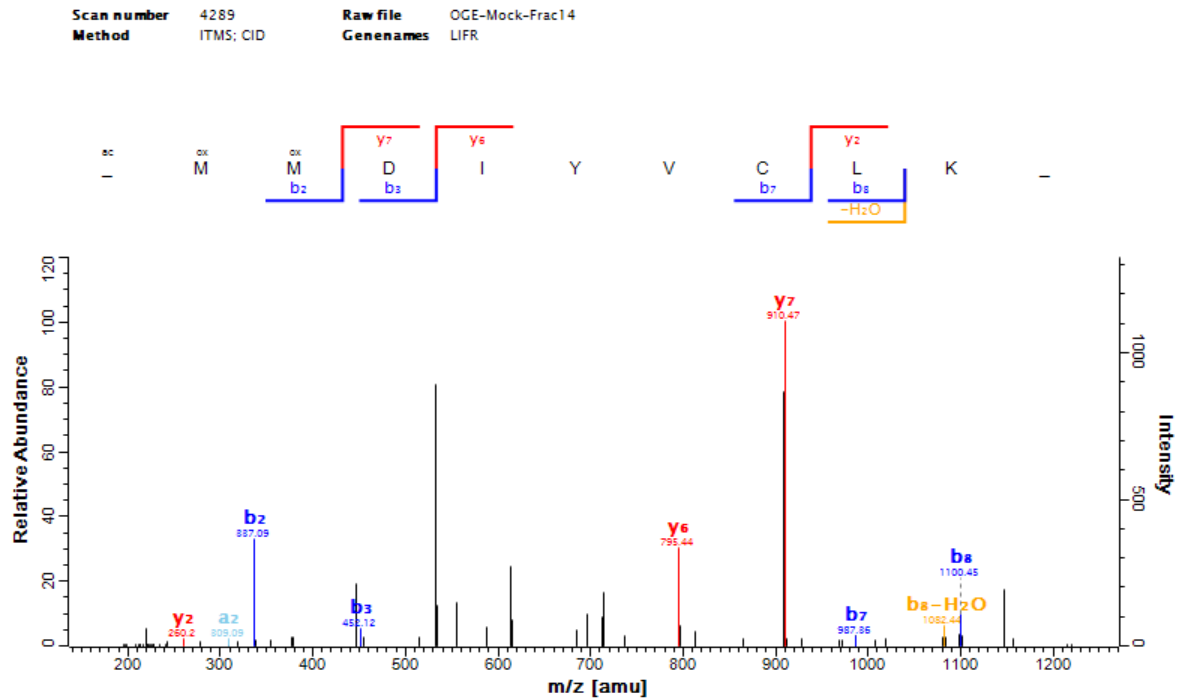
Total Number of Spectra: 4

Number of Replicates (out of 10): 4

Best Match Score: 71.223

Best Match Posterior Error Probability: 0.0091376

Best Match Spectrum:



Protein Group ID: 529

Protein Accession Numbers: P19838-2; P19838; P19838-3; D6RF93

Gene Names: NFKB1

Peptide Sequence: LMFTAFLPDSTGSFTR

Total Number of Spectra: 2

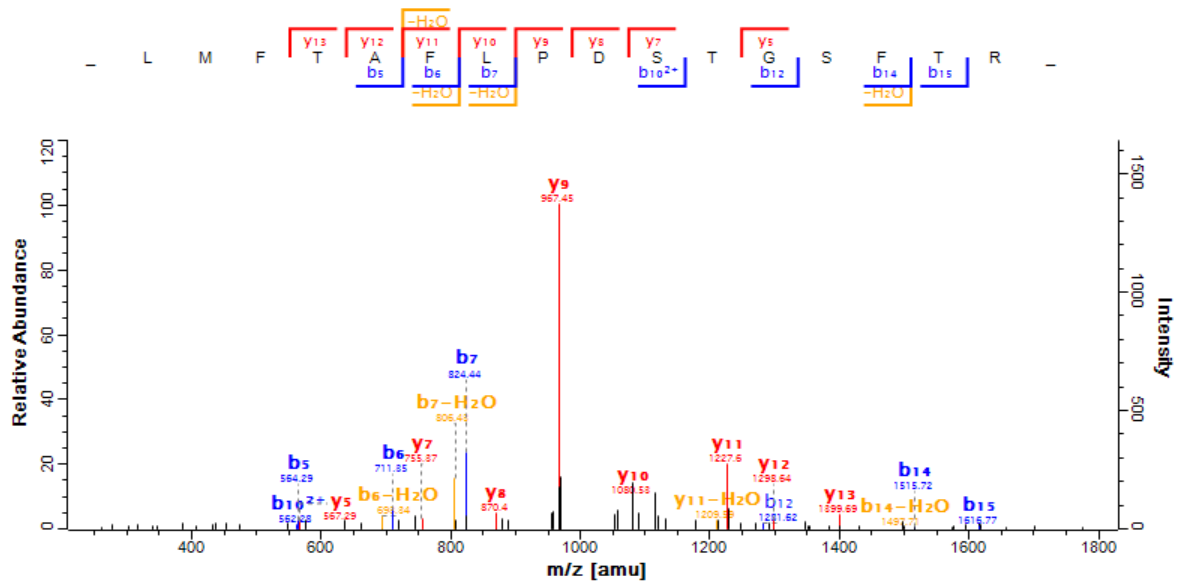
Number of Replicates (out of 10): 2

Best Match Score: 76.82

Best Match Posterior Error Probability: 0.0013548

Best Match Spectrum:

Scan number	5243	Raw file	Prt-OGE-Batch3-Mock-Frac16
Method	ITMS; CID	Genenames	NFKB1



Protein Group ID: 533

Protein Accession Numbers: Q96J01; Q6NZ53; D6RGZ2

Gene Names: THOC3

Peptide Sequence: YVLGMQELFR

Total Number of Spectra: 10

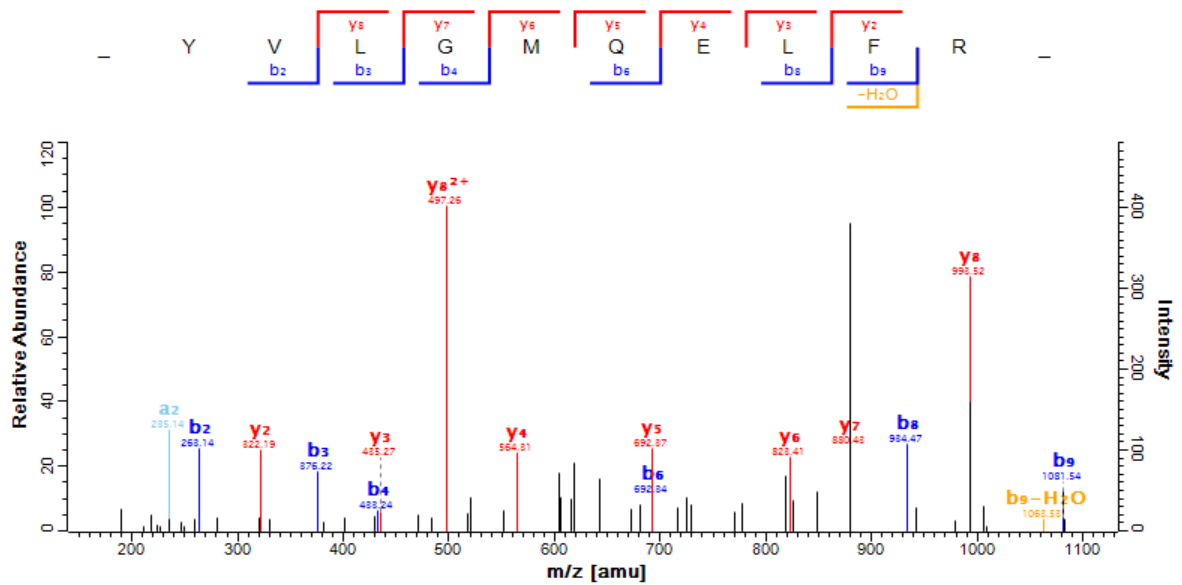
Number of Replicates (out of 10): 7

Best Match Score: 132.78

Best Match Posterior Error Probability: 7.94E-05

Best Match Spectrum:

Scan number	5806	Raw file	Prt-OGE-Batch3-Mock-Frac10
Method	ITMS; CID	Genenames	THOC3



Protein Group ID: 537

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

Gene Names: HNF1B

Peptide Sequence: L T S L Q Q E L S A L L S S G V T K

Total Number of Spectra: 2

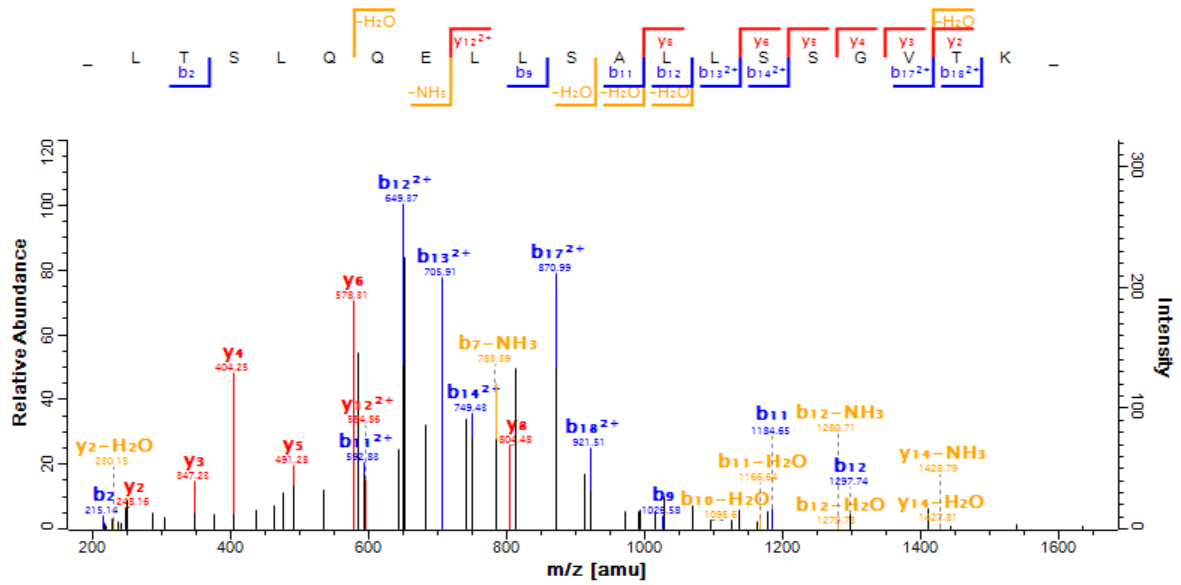
Number of Replicates (out of 10): 2

Best Match Score: 80.545

Best Match Posterior Error Probability: 0.0012609

Best Match Spectrum:

Scan number 7213 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac16
Method ITMS; CID **Genenames** HNF1B



Protein Group ID: 538

Protein Accession Numbers: Q7L4I2; Q7L4I2-2; E1B6W4; H0YGP9

Gene Names: RSRC2

Peptide Sequence: NTAMDAQEALAR

Total Number of Spectra: 4

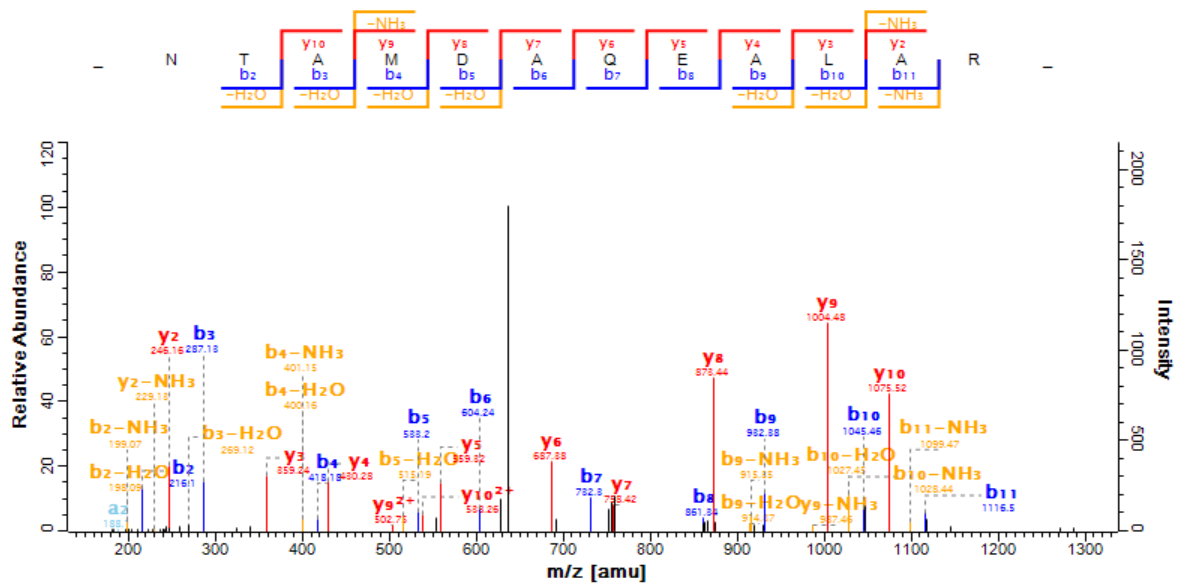
Number of Replicates (out of 10): 4

Best Match Score: 203.87

Best Match Posterior Error Probability: 2.83E-23

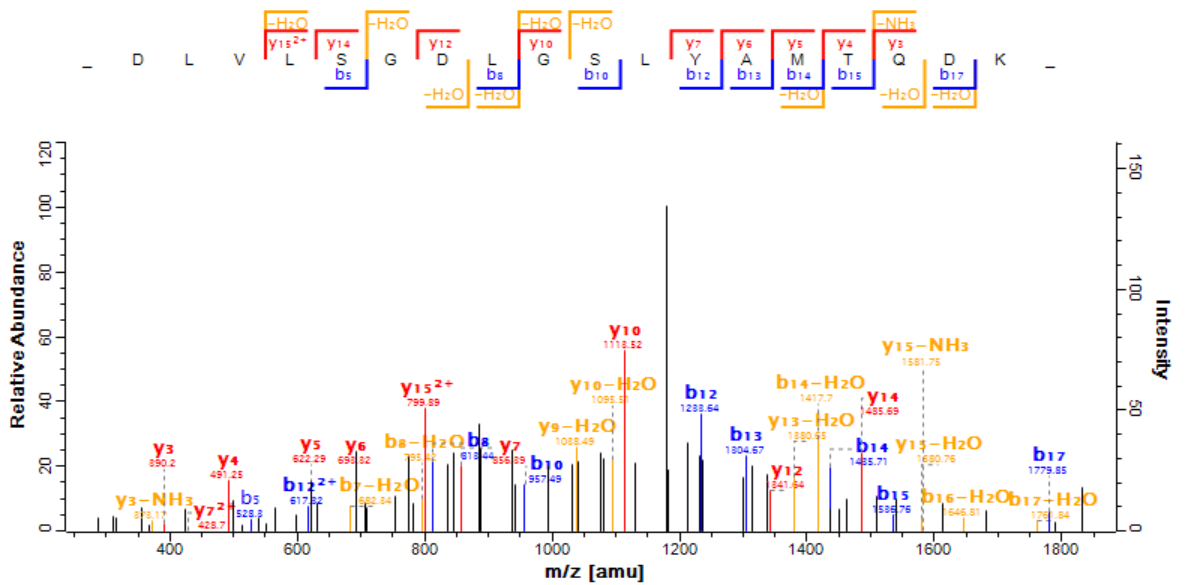
Best Match Spectrum:

Scan number 1777 **Raw file** Prt-OGE-Batch2-WT-Frac14
Method ITMS; CID **Genenames** RSRC2



Protein Group ID: 540
Protein Accession Numbers: O15031; E2PU09
Gene Names: PLXNB2
Peptide Sequence: DLVLSGDLGSLYAMTQDK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 101.78
Best Match Posterior Error Probability: 0.00021301
Best Match Spectrum:

Scan number 5862 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac10
Method ITMS; CID **Genenames** PLXNB2



Protein Group ID: 543

Protein Accession Numbers: P34913; E5RFU2; E5RFH6; H0YAW7; E5RI53

Gene Names: EPHX2

Peptide Sequence: AAVFDLDGVLALPAGVFLGR

Total Number of Spectra: 2

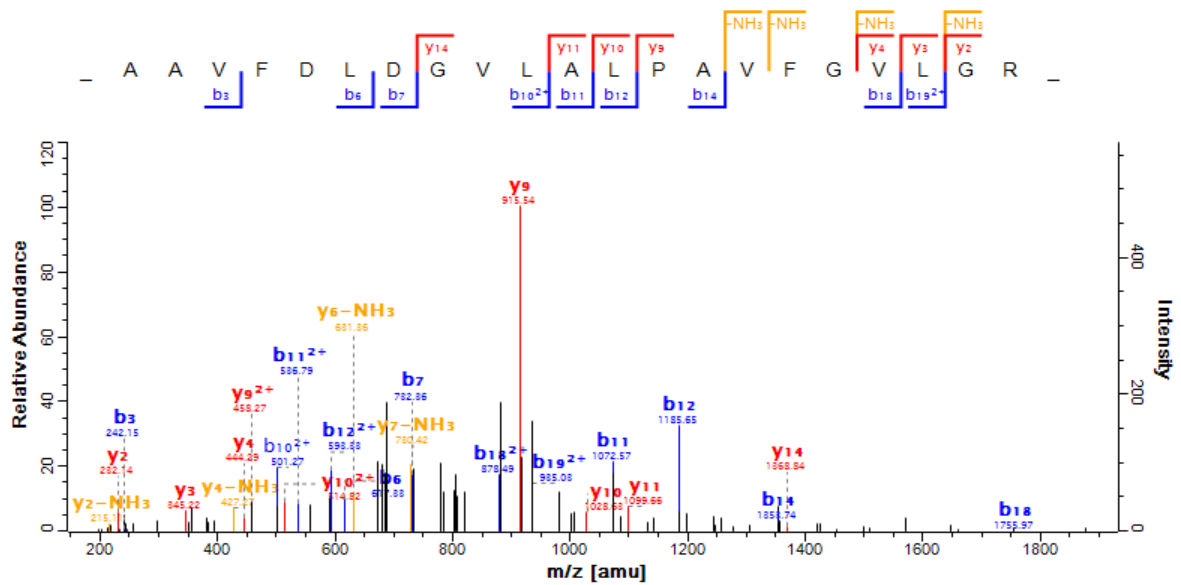
Number of Replicates (out of 10): 2

Best Match Score: 91.401

Best Match Posterior Error Probability: 5.22E-05

Best Match Spectrum:

Scan number 8668 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac12
Method ITMS; CID **Genenames** EPHX2



Protein Group ID: 545

Protein Accession Numbers: E7EV80; Q14168; Q14168-3; Q14168-2; E7EX01; E5RI47; E5RIU3; E5RI32; E5RK44; E5RJK0; E5RK50; E5RFN8

Gene Names: MPP2

Peptide Sequence: LEETKLEAVR

Total Number of Spectra: 17

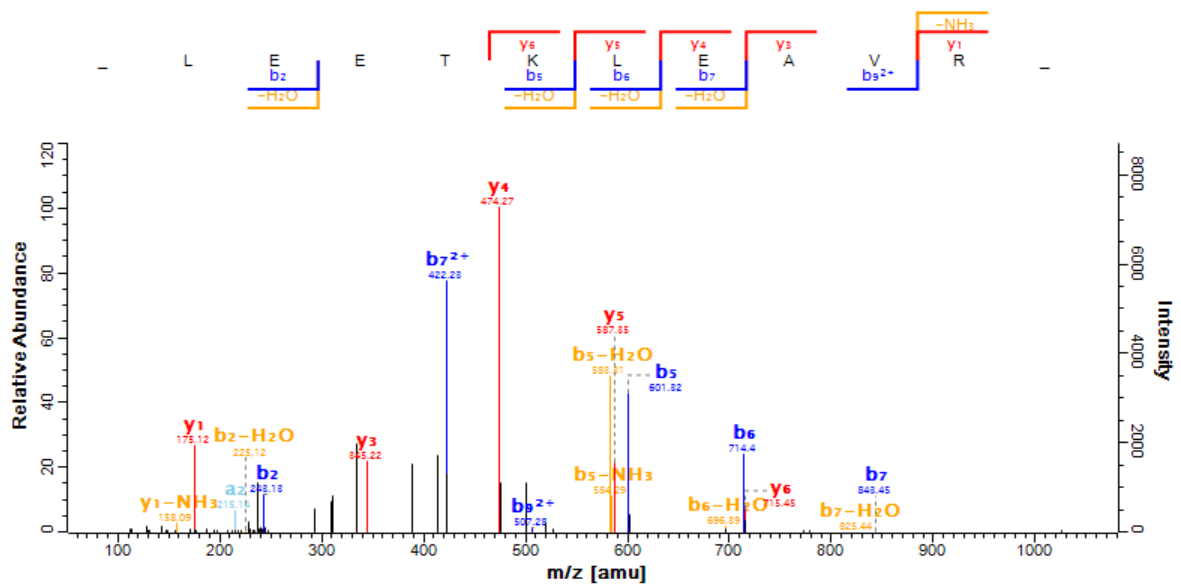
Number of Replicates (out of 10): 8

Best Match Score: 117.7

Best Match Posterior Error Probability: 0.00053782

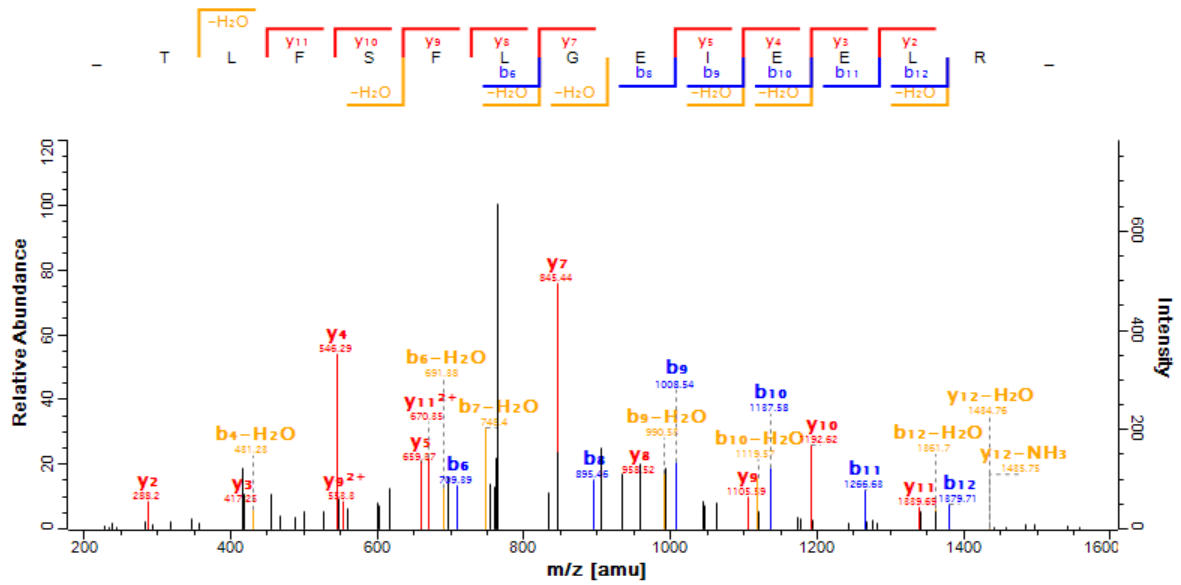
Best Match Spectrum:

Scan number	2488	Raw file	Prt-OGE-Batch3-WT-Frac7
Method	ITMS: CID	Genenames	MPP2



Protein Group ID: 546
Protein Accession Numbers: Q8WXA9-2; E5RFV3
Gene Names: SREK1
Peptide Sequence: TLFSFLGEIEELR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 105.95
Best Match Posterior Error Probability: 0.00033207
Best Match Spectrum:

Scan number 8105 **Raw file** Prt-OGE-Batch2-Mock-Frac16
Method ITMS; CID **Genenames** SREK1



Protein Group ID: 547

Protein Accession Numbers: Q8TCF1; E5RJ99; Q8TCF1-2; E5RI74; E5RGE5; E5RJ74; E5RK75

Gene Names: ZFAND1

Peptide Sequence: IYFQVFLPK

Total Number of Spectra: 3

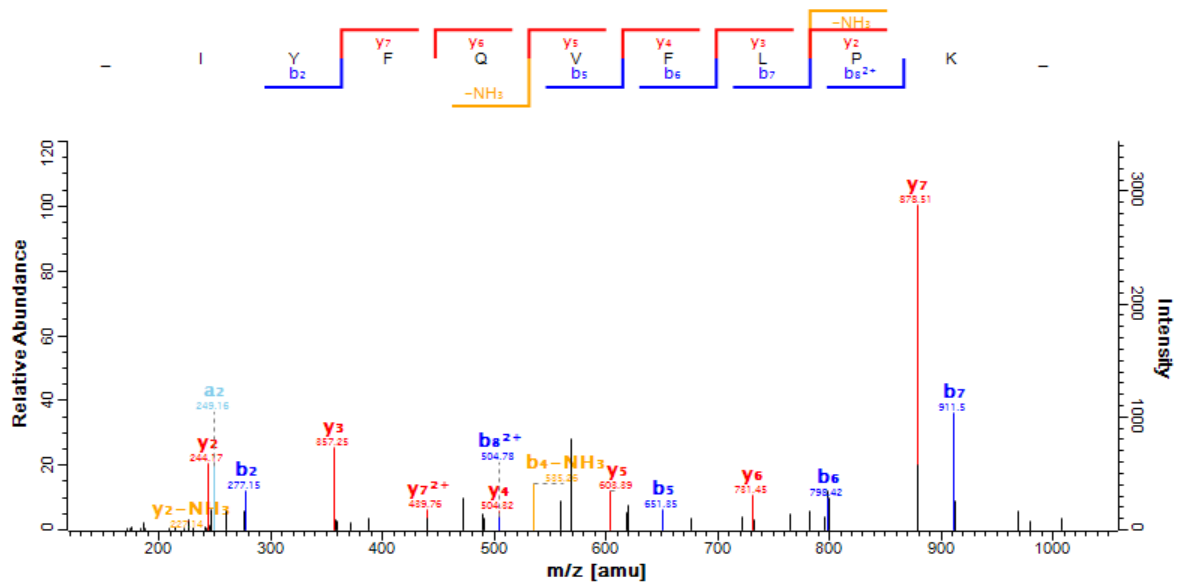
Number of Replicates (out of 10): 3

Best Match Score: 103.56

Best Match Posterior Error Probability: 0.00065663

Best Match Spectrum:

Scan number	4773	Raw file	Prt-OGE-Batch2-WT-Frac17
Method	ITMS: CID	Genenames	ZFAND1



Protein Group ID: 549

Protein Accession Numbers: O14920; O14920-2; O14920-4; G3V105; E5RGW5; O14920-3

Gene Names: IKBKB

Peptide Sequence: EGAILTLLSDIASALR

Total Number of Spectra: 4

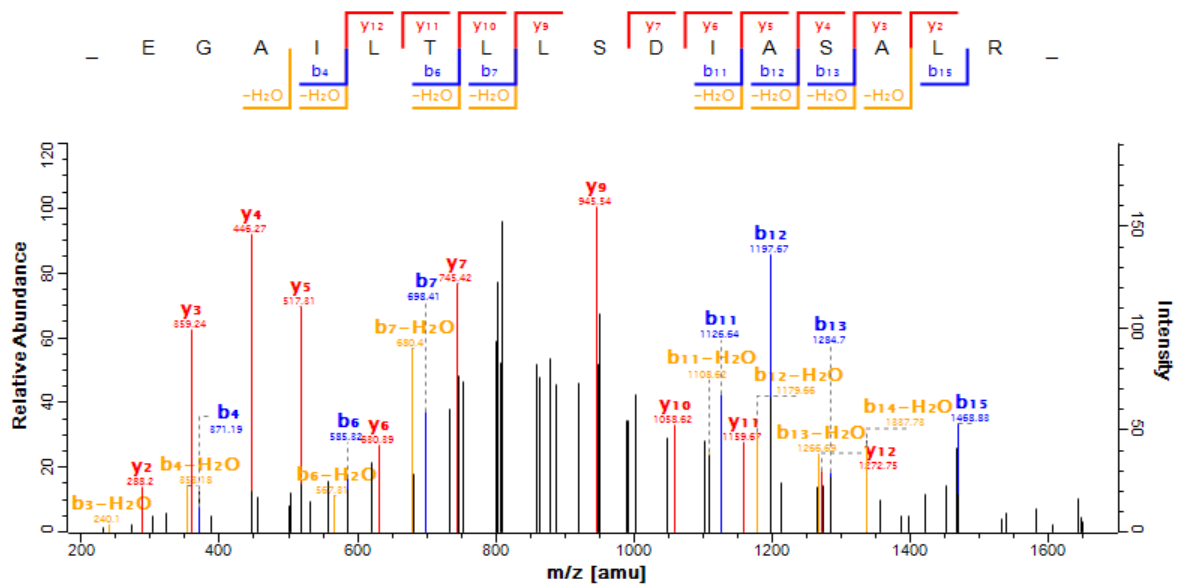
Number of Replicates (out of 10): 3

Best Match Score: 109.79

Best Match Posterior Error Probability: 0.00012942

Best Match Spectrum:

Scan number	8184	Raw file	OGE-WT-Frac10
Method	ITMS: CID	Genenames	IKBKB



Protein Group ID: 550

Protein Accession Numbers: Q93045-2; Q93045; E5RGX5

Gene Names: STMN2

Peptide Sequence: ALEENNNFSK

Total Number of Spectra: 8

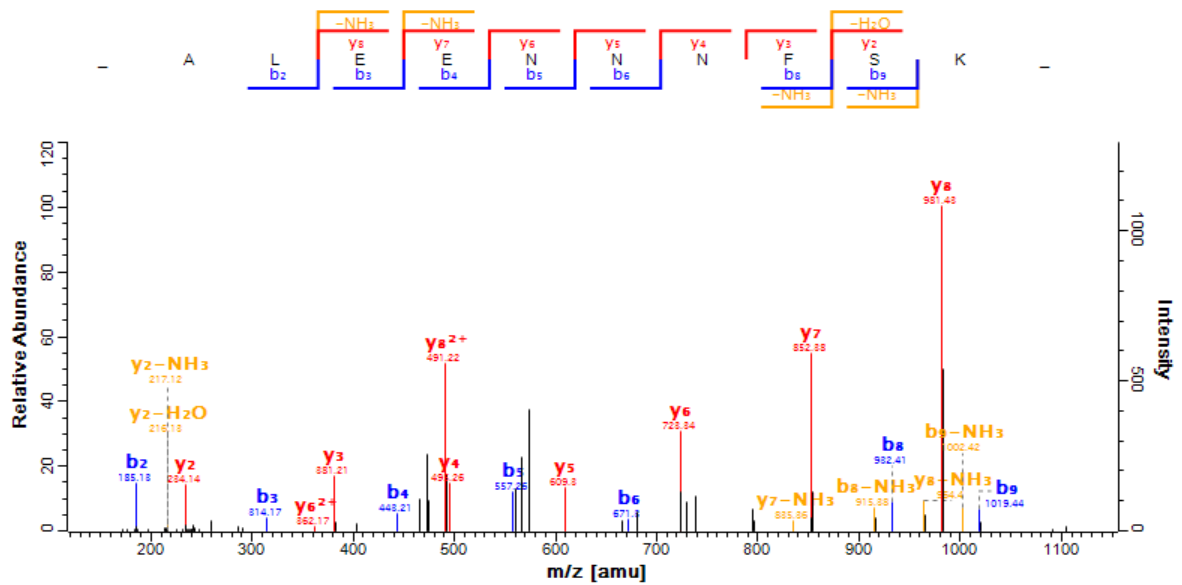
Number of Replicates (out of 10): 2

Best Match Score: 125.72

Best Match Posterior Error Probability: 0.00010344

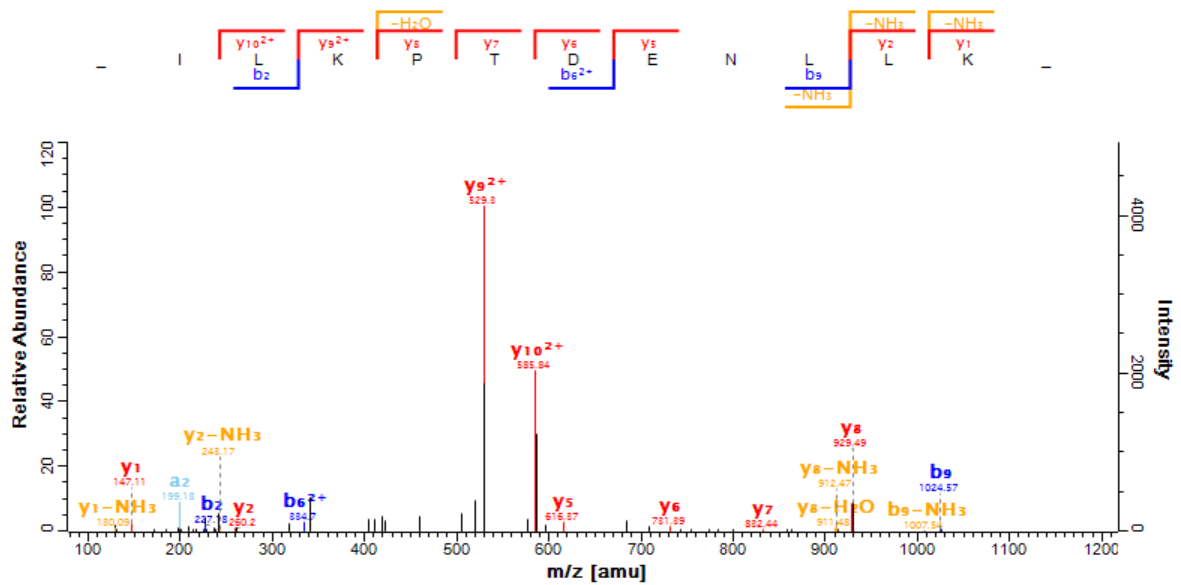
Best Match Spectrum:

Scan number 1536 **Raw file** OGE-WT-Frac8
Method ITMS; CID **Genenames** STMN2



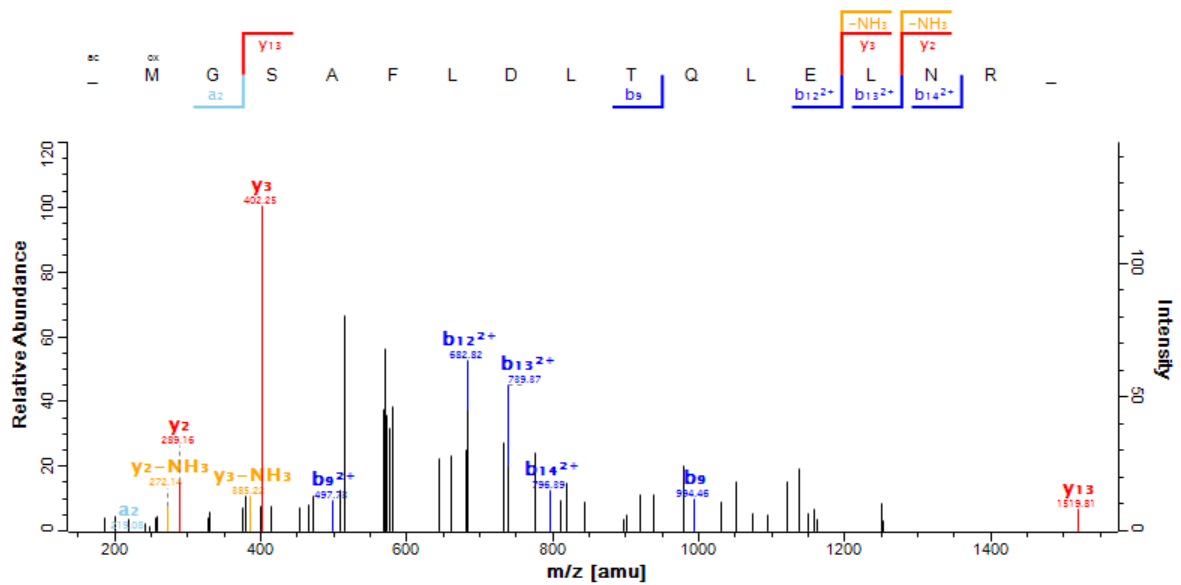
Protein Group ID: 557
Protein Accession Numbers: Q9P015; E5RIZ4
Gene Names: MRPL15
Peptide Sequence: ILKPTDENLLK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 97.813
Best Match Posterior Error Probability: 0.0009971
Best Match Spectrum:

Scan number 3396 **Raw file** Prt-OGE-Batch2-Mock-Frac17
Method ITMS; CID **Genenames** MRPL15



Protein Group ID: 560
Protein Accession Numbers: E5RJR1
Gene Names: MCTP1
Peptide Sequence: MGSAFLDLTQLELR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 47.189
Best Match Posterior Error Probability: 0.046843
Best Match Spectrum:

Scan number	6259	Raw file	OGE-Mock-Frac12
Method	ITMS; CID	Genenames	MCTP1



Protein Group ID: 568

Protein Accession Numbers: E9PJ55; Q9NUJ3; E7EN41

Gene Names: TCP11L1

Peptide Sequence: QPNSLDFVTQWLEEAASSEEDLMTQK

Total Number of Spectra: 1

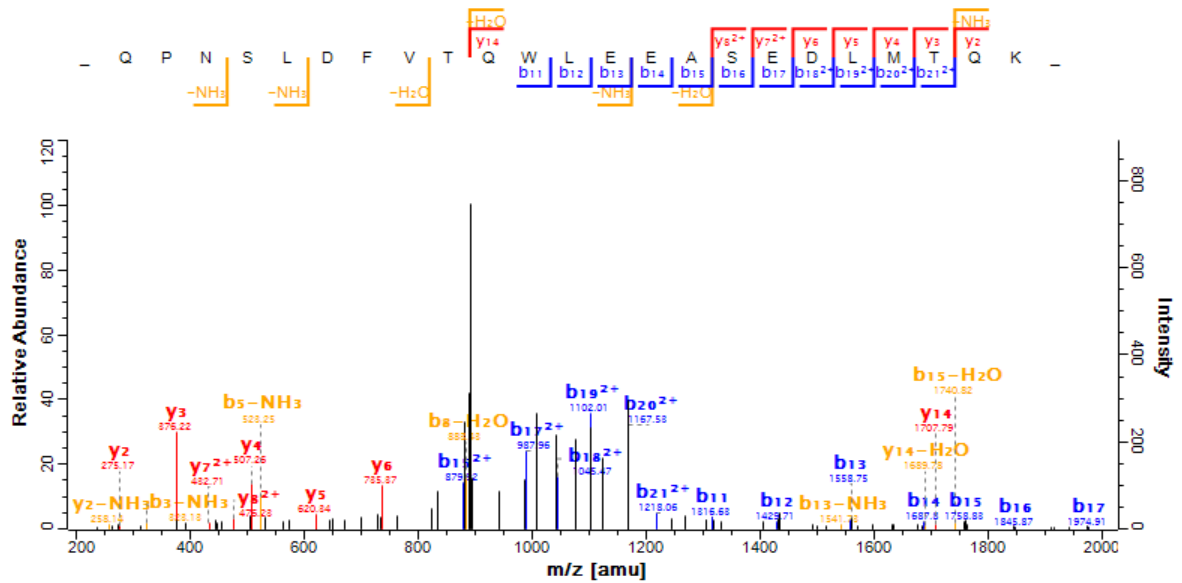
Number of Replicates (out of 10): 1

Best Match Score: 96.55

Best Match Posterior Error Probability: 2.66E-06

Best Match Spectrum:

Scan number 8241 **Raw file** OGE-Mock-Frac7
Method ITMS; CID **Genenames** TCP11L1



Protein Group ID: 570

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

Gene Names: SYNE1

Peptide Sequence: VLFTSLADNK

Total Number of Spectra: 5

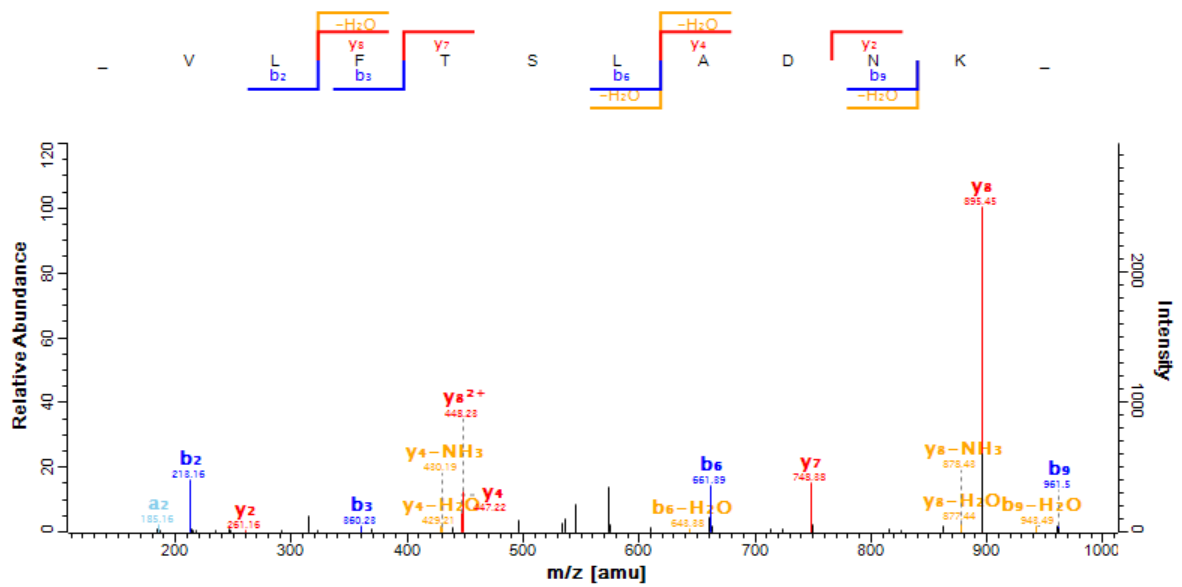
Number of Replicates (out of 10): 5

Best Match Score: 113.71

Best Match Posterior Error Probability: 0.00024064

Best Match Spectrum:

Scan number	2352	Raw file	20100914-KD-Batch4-Prt-OGE-Mock-Frac23
Method	ITMS; CID	Genenames	SYNE1



Protein Group ID: 574

Protein Accession Numbers: Q9UFG5-2; K7EK56; E7EP72; Q9UFG5; K7ELZ1; K7EQW1; K7ENK8

Gene Names: C19orf25

Peptide Sequence: VLLPTRPAPPTVEQILEDVR

Total Number of Spectra: 2

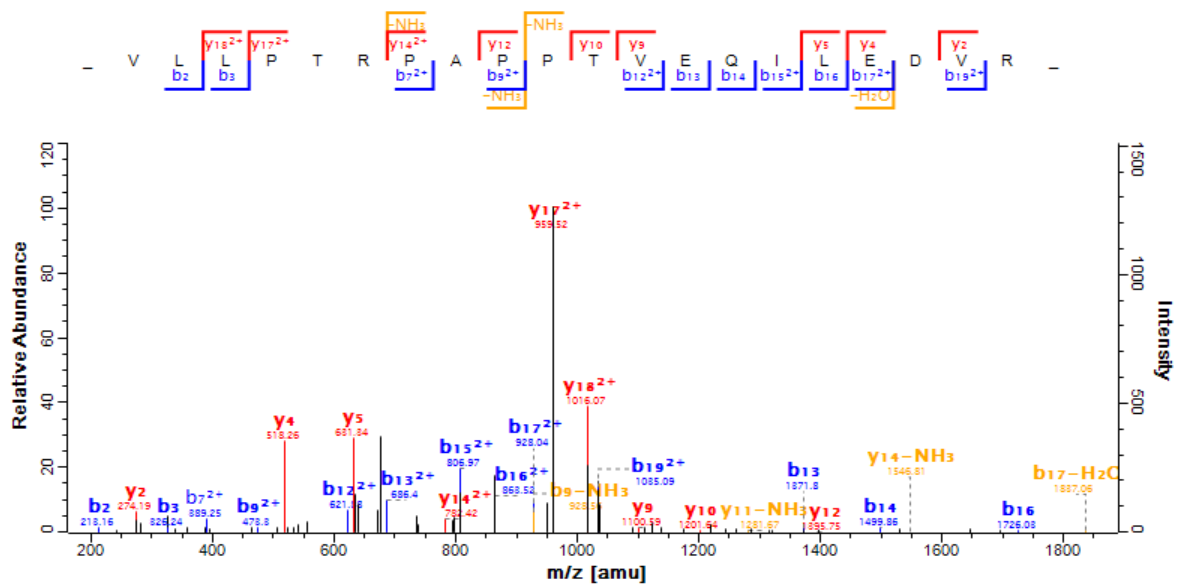
Number of Replicates (out of 10): 2

Best Match Score: 90.379

Best Match Posterior Error Probability: 0.00062212

Best Match Spectrum:

Scan number	5900	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac6
Method	ITMS; CID	Genenames	C19orf25



Protein Group ID: 581

Protein Accession Numbers: F5H160; F5H659; E7EPM3; J3KN18; Q7Z5Q1; Q7Z5Q1-3; Q7Z5Q1-6; Q7Z5Q1-4; Q7Z5Q1-5; Q7Z5Q1-7

Gene Names: CPEB2

Peptide Sequence: MYDSLNMHSLENSLIDIMR

Total Number of Spectra: 1

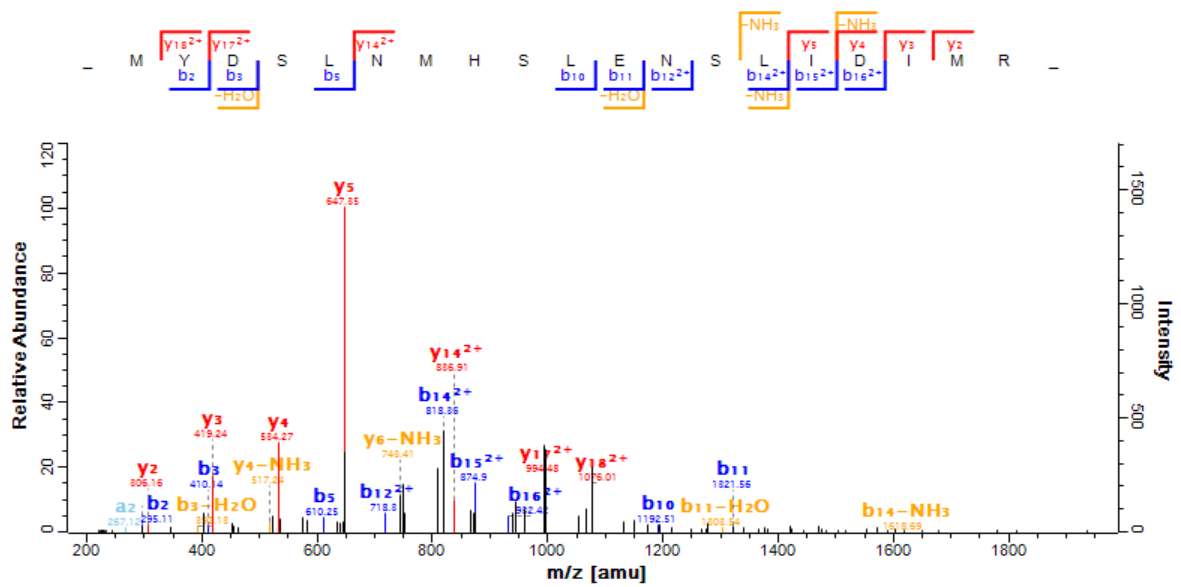
Number of Replicates (out of 10): 1

Best Match Score: 85.469

Best Match Posterior Error Probability: 0.00058421

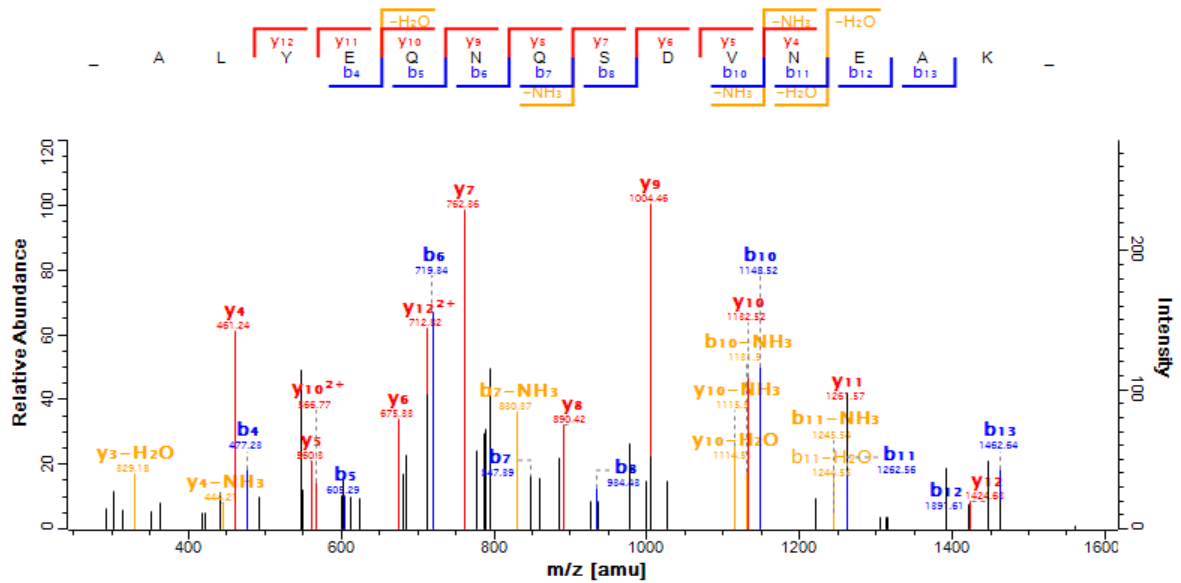
Best Match Spectrum:

Scan number	5903	Raw file	Prt-OGE-Batch2-WT-Frac14
Method	ITMS; CID	Genenames	CPEB2



Protein Group ID: 587
Protein Accession Numbers: Q14691; E7EQ95
Gene Names: GINS1
Peptide Sequence: ALYEQNQSDVNEAK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 136.39
Best Match Posterior Error Probability: 1.30E-05
Best Match Spectrum:

Scan number 1194 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac16
Method ITMS; CID **Genenames** GINS1



Protein Group ID: 590

Protein Accession Numbers: Q6P4F2; Q8N8B8; E7EQL1

Gene Names: FDX1L

Peptide Sequence: VGDNVLHLAQR

Total Number of Spectra: 5

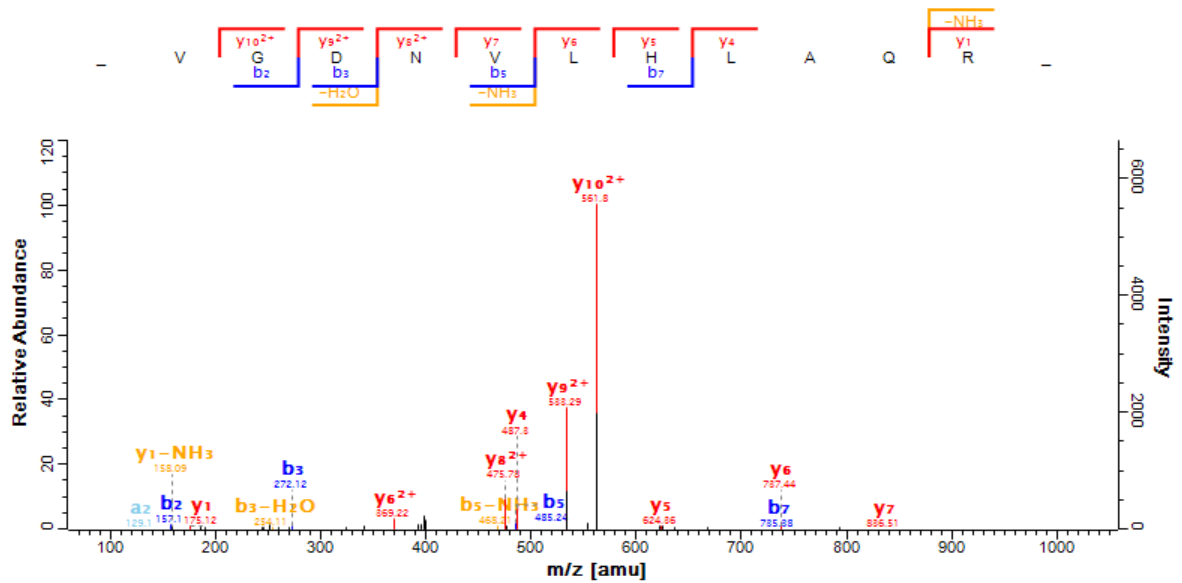
Number of Replicates (out of 10): 5

Best Match Score: 105.2

Best Match Posterior Error Probability: 0.00020091

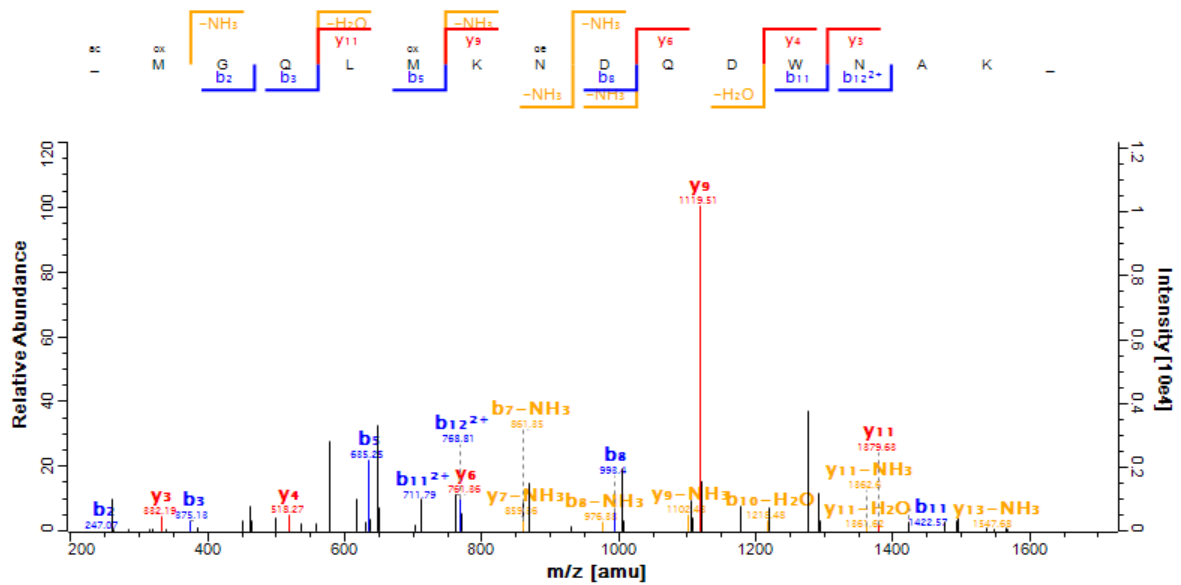
Best Match Spectrum:

Scan number 2243 **Raw file** Prt-OGE-Batch3-WT-Frac4
Method ITMS; CID **Genenames** FDX1L



Protein Group ID: 597
Protein Accession Numbers: E7ERX3
Gene Names: DST
Peptide Sequence: MGQLMKNDQDWNK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 80.312
Best Match Posterior Error Probability: 0.0028304
Best Match Spectrum:

Scan number 3371 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac16
Method ITMS; CID **Genenames** DST



Protein Group ID: 598

Protein Accession Numbers: Q9P2P6; H3BNE9; F8VPJ2; Q9NQT8; Q9H1H9; E9PDX3; Q9H1H9-2; Q9H1H9-4; Q9H1H9-3; Q96L93-2; Q96L93; Q96L93-4; Q96L93-6; Q96L93-5; O43896; E7ERX9; Q9P2P6-3

Gene Names: STARD9;KIF13A;KIF13B;KIF16B;KIF1C

Peptide Sequence: DSVLTWLLK

Total Number of Spectra: 12

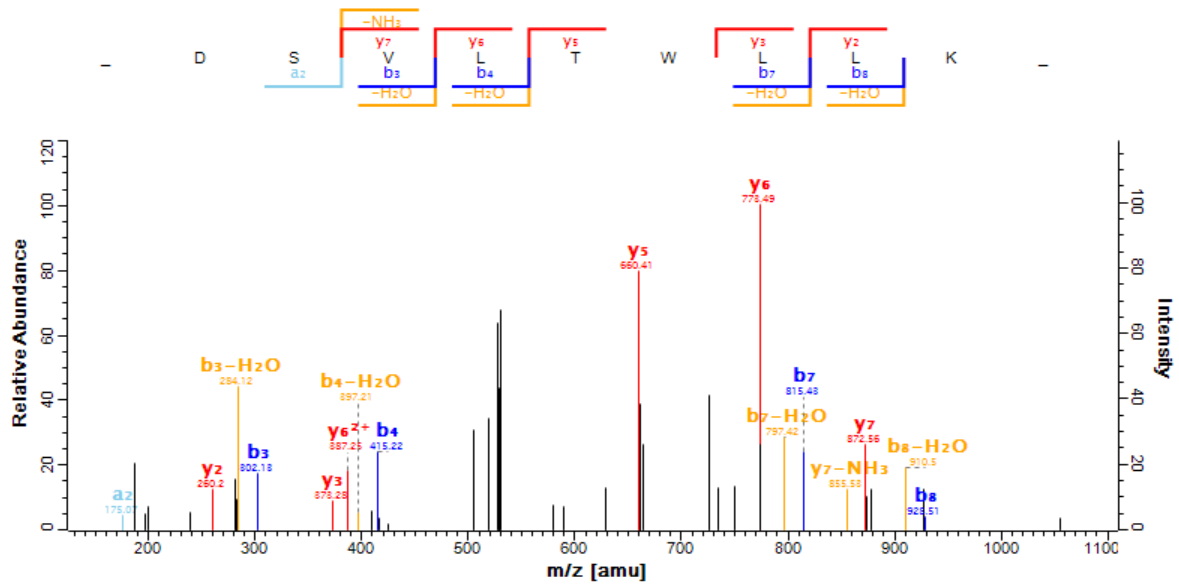
Number of Replicates (out of 10): 8

Best Match Score: 120.15

Best Match Posterior Error Probability: 0.00030744

Best Match Spectrum:

Scan number	5344	Raw file	Prt-OGE-Batch3-WT-Frac13
Method	ITMS: CID	Genenames	STARD9;KIF13A;KIF13B;KIF16B;KIF1C



Protein Group ID: 602

Protein Accession Numbers: Q92504; F5H0B5; E7ESG6

Gene Names: SLC39A7

Peptide Sequence: EASPLQSLLEVLGLLGGVIMMVLI AHLE

Total Number of Spectra: 2

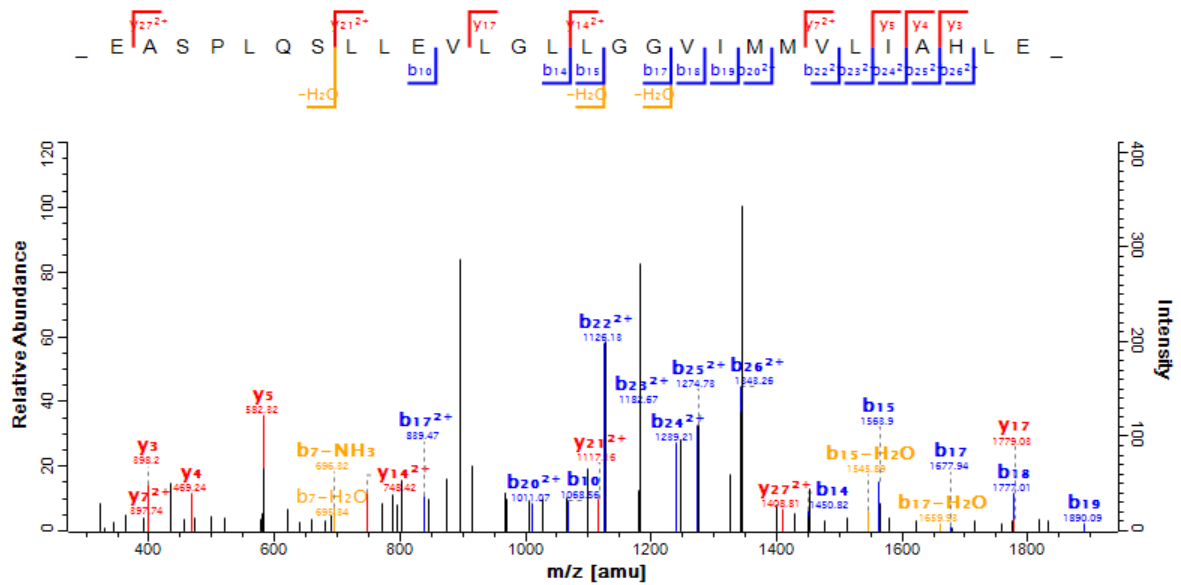
Number of Replicates (out of 10): 2

Best Match Score: 89.721

Best Match Posterior Error Probability: 3.12E-09

Best Match Spectrum:

Scan number	10967	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac11
Method	ITMS; CID	Genenames	SLC39A7



Protein Group ID: 606

Protein Accession Numbers: Q86UW9; E7ET89

Gene Names: DTX2

Peptide Sequence: VQQALAGMTSVLMSALIGLPLVCLSR

Total Number of Spectra: 1

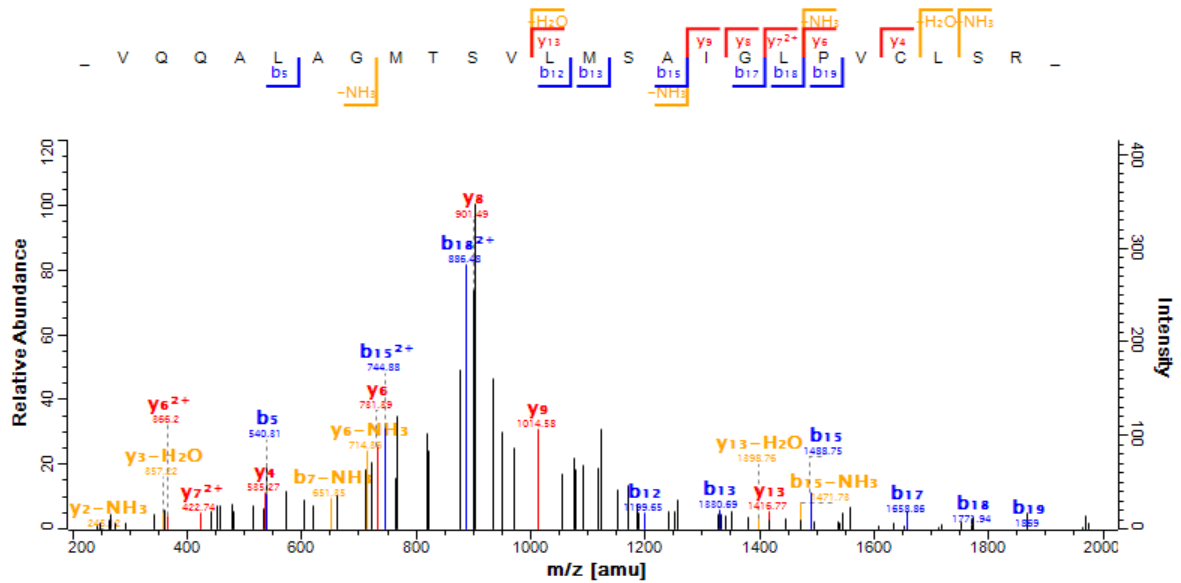
Number of Replicates (out of 10): 1

Best Match Score: 67.11

Best Match Posterior Error Probability: 0.00042002

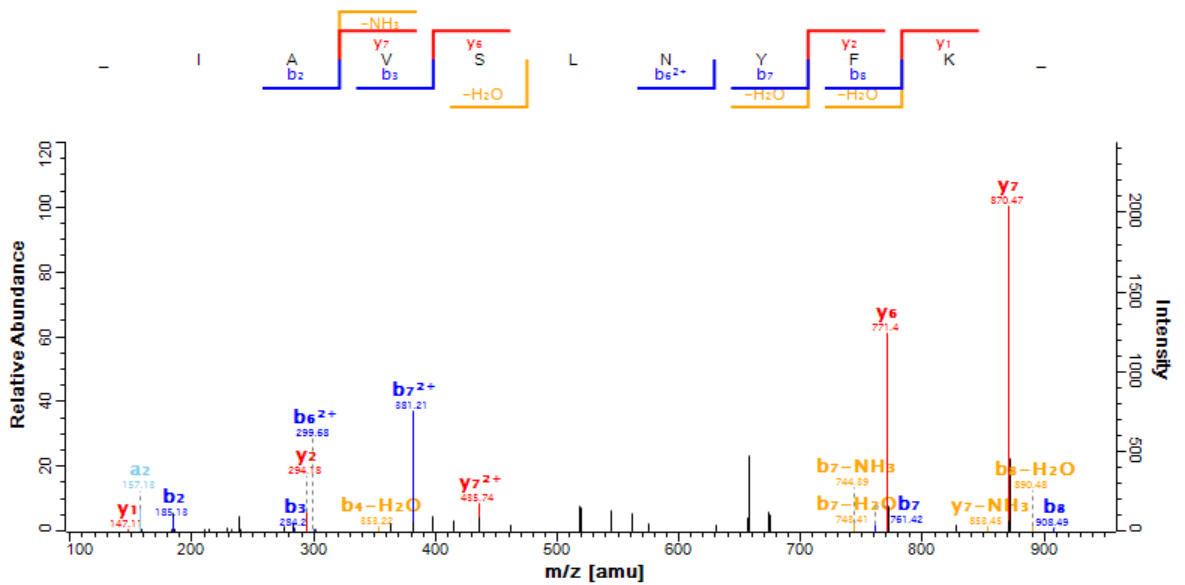
Best Match Spectrum:

Scan number 7927 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac20
Method ITMS; CID **Genenames** DTX2



Protein Group ID: 620
Protein Accession Numbers: E7EVQ5
Gene Names: CTHRC1
Peptide Sequence: IAVSLNYFK
Total Number of Spectra: 8
Number of Replicates (out of 10): 4
Best Match Score: 111.74
Best Match Posterior Error Probability: 0.00040846
Best Match Spectrum:

Scan number 4187 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac6
Method ITMS; CID **Genenames** CTHRC1



Protein Group ID: 625

Protein Accession Numbers: J3KNP0; Q6WKZ4; Q6WKZ4-3; Q6WKZ4-1; Q3I768; Q7L804; E7EX40

Gene Names: RAB11FIP1;RAB11FIP2

Peptide Sequence: ELEDYIDNLLVR

Total Number of Spectra: 1

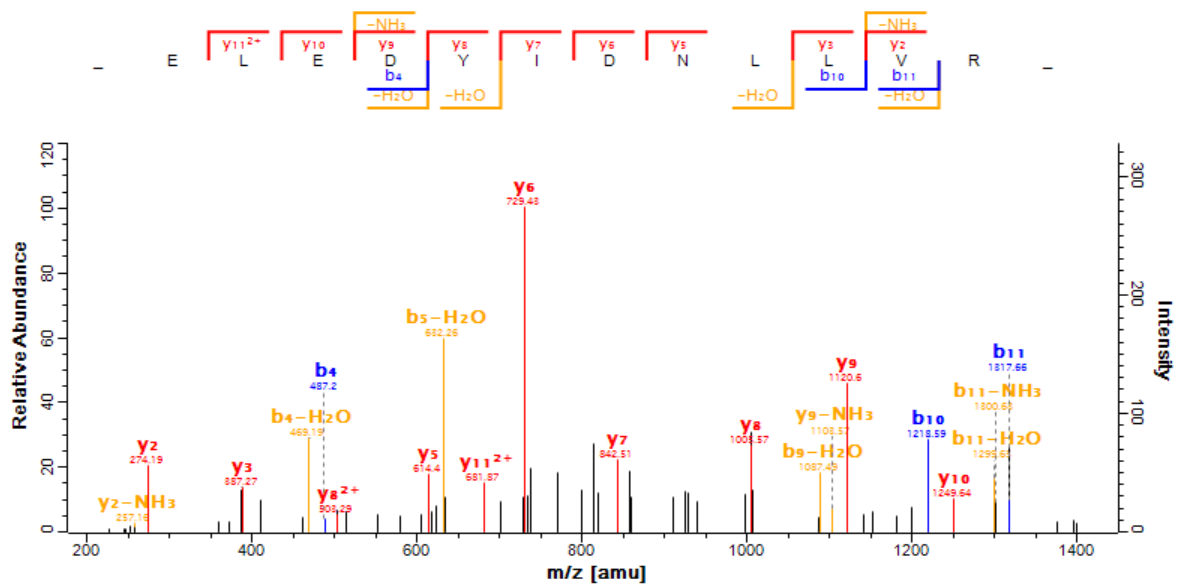
Number of Replicates (out of 10): 1

Best Match Score: 106.49

Best Match Posterior Error Probability: 0.00023346

Best Match Spectrum:

Scan number	5010	Raw file	Prt-OGE-Batch3-Mock-Frac18
Method	ITMS: CID	Genenames	RAB11FIP1;RAB11FIP2



Protein Group ID: 628

Protein Accession Numbers: P52298; E9PAR5; F8WE41

Gene Names: NCBP2

Peptide Sequence: SDSYVELSQYR

Total Number of Spectra: 5

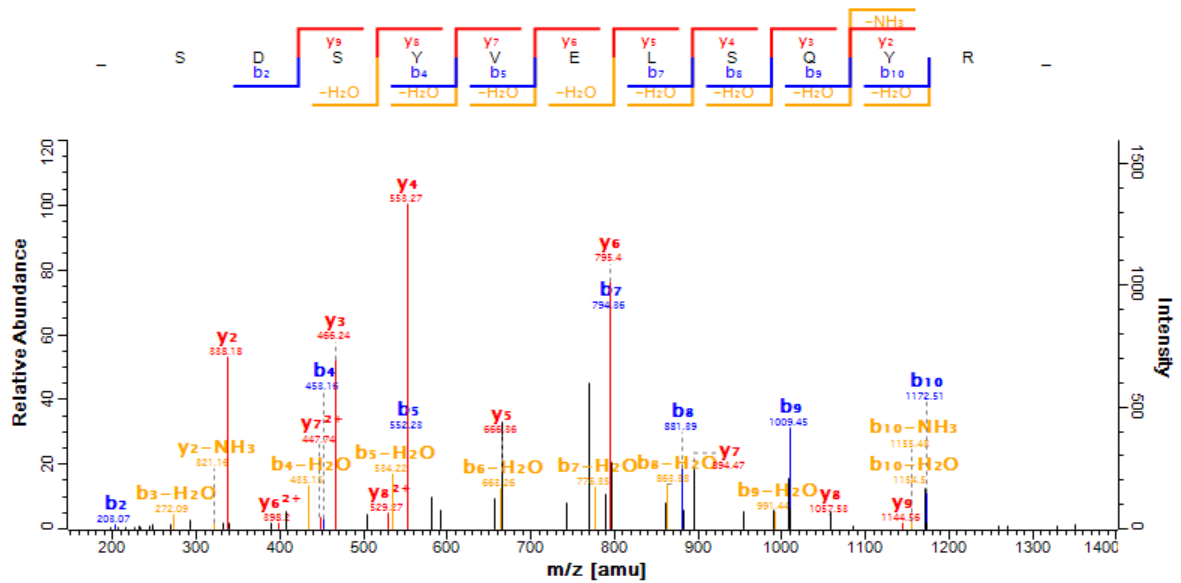
Number of Replicates (out of 10): 5

Best Match Score: 181.68

Best Match Posterior Error Probability: 3.56E-11

Best Match Spectrum:

Scan number	2246	Raw file	Prt-OGE-Batch3-Mock-Frac1 8
Method	ITMS; CID	Genenames	NCBP2



Protein Group ID: 636

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

Gene Names: WIPF1

Peptide Sequence: PSASSQAPPPPPPPSR

Total Number of Spectra: 1

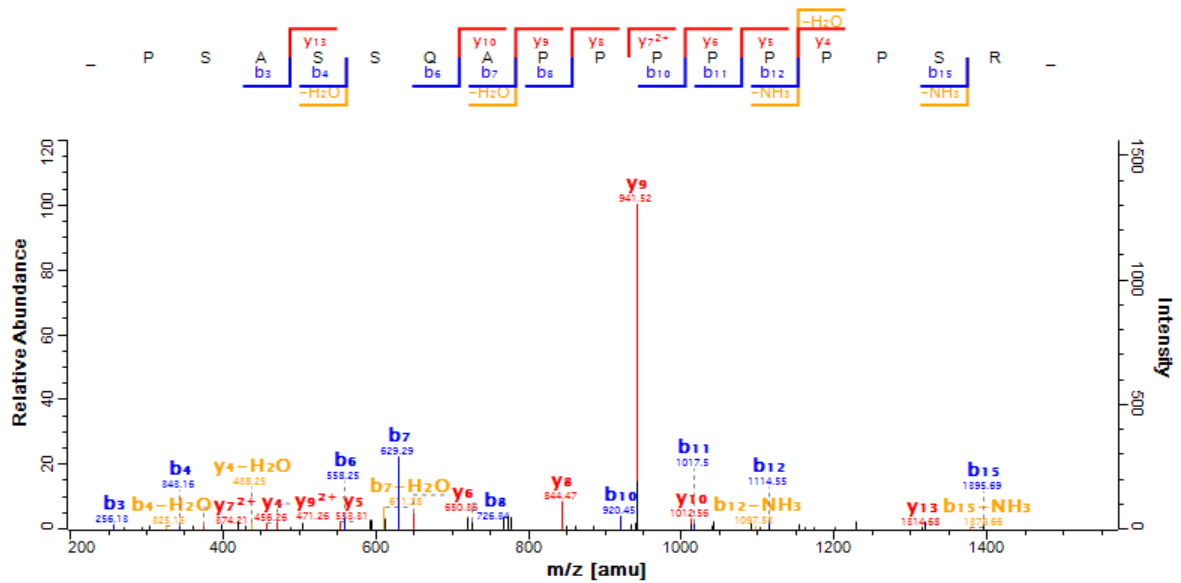
Number of Replicates (out of 10): 1

Best Match Score: 113.01

Best Match Posterior Error Probability: 0.00012623

Best Match Spectrum:

Scan number 1248 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac19
Method ITMS; CID **Genenames** WIPF1



Protein Group ID: 640

Protein Accession Numbers: Q53H12; E9PC15; E9PG39

Gene Names: AGK

Peptide Sequence: IPIGFILGETSSLSHTLFAESGNK

Total Number of Spectra: 14

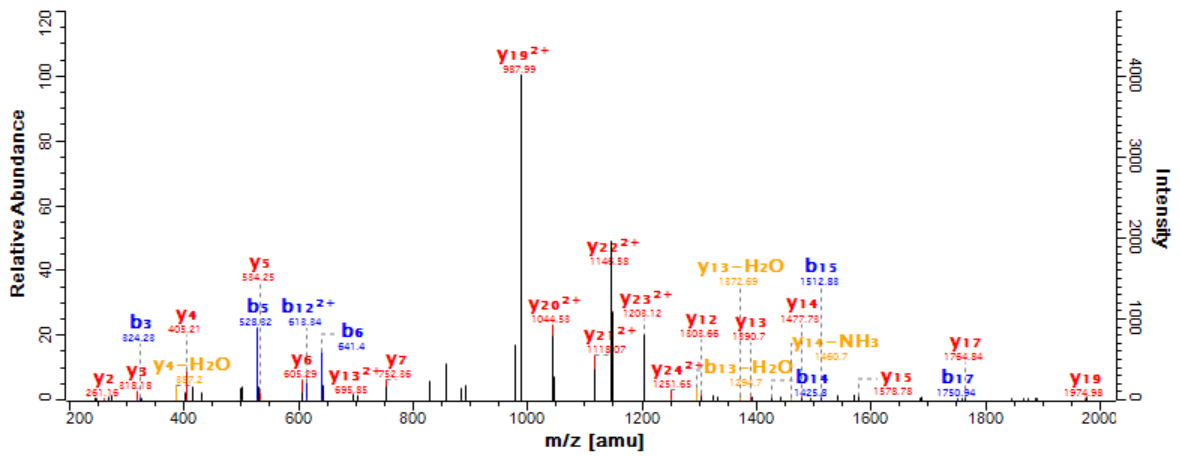
Number of Replicates (out of 10): 8

Best Match Score: 112.36

Best Match Posterior Error Probability: 3.91E-12

Best Match Spectrum:

Scan number	7283	Raw file	Prt-OGE-Batch2-Mock-Frac1 8
Method	ITMS; CID	Genenames	AGK



Protein Group ID: 641

Protein Accession Numbers: P24821; P24821-4; J3QSU6; E9PC84; F5H7V9; P24821-3; P24821-2; P24821-5; P24821-6

Gene Names: TNC

Peptide Sequence: LEELENLVSSLR

Total Number of Spectra: 1

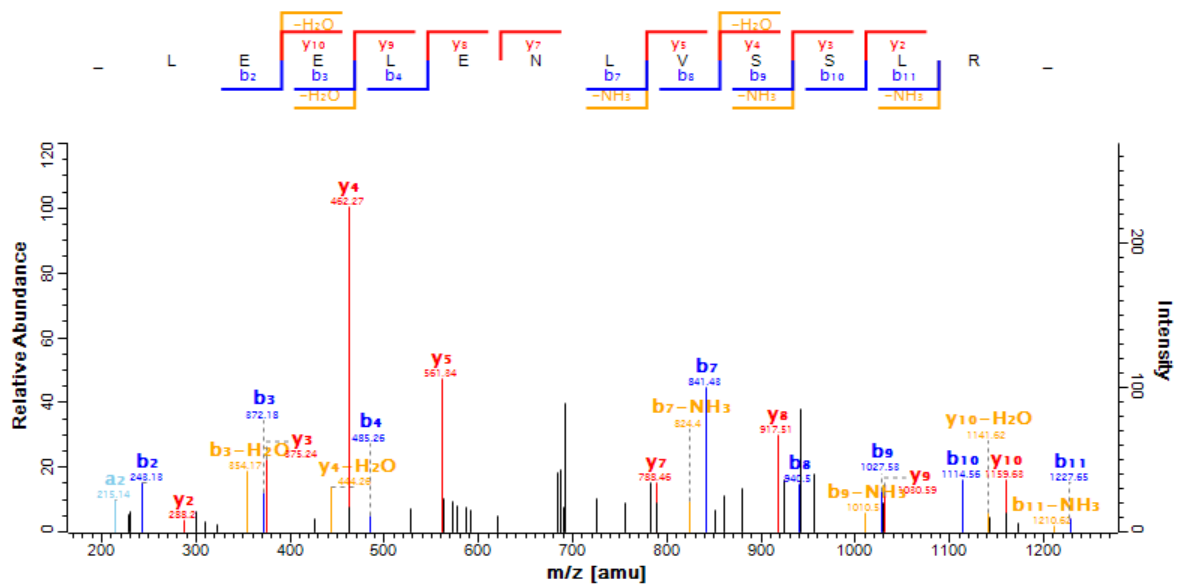
Number of Replicates (out of 10): 1

Best Match Score: 127.02

Best Match Posterior Error Probability: 0.00018061

Best Match Spectrum:

Scan number	5141	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac2
Method	ITMS: CID	Genenames	TNC



Protein Group ID: 653

Protein Accession Numbers: P32929; E9PDV0; P32929-2

Gene Names: CTH

Peptide Sequence: LSVGLEDEEDLLEDLDQALK

Total Number of Spectra: 1

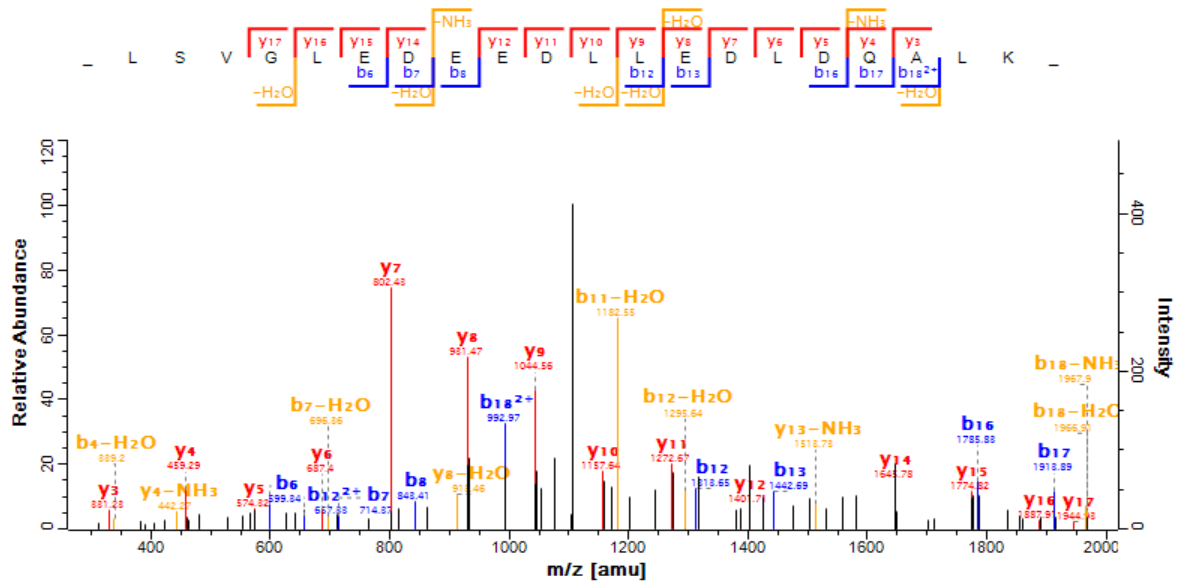
Number of Replicates (out of 10): 1

Best Match Score: 117.74

Best Match Posterior Error Probability: 1.77E-06

Best Match Spectrum:

Scan number 6361 **Raw file** Prt-OGE-Batch2-WT-Frac14
Method ITMS; CID **Genenames** CTH



Protein Group ID: 654

Protein Accession Numbers: P16219; E9PE82

Gene Names: ACADS

Peptide Sequence: IGIASQALGIAQTALDCAVNYAENR

Total Number of Spectra: 1

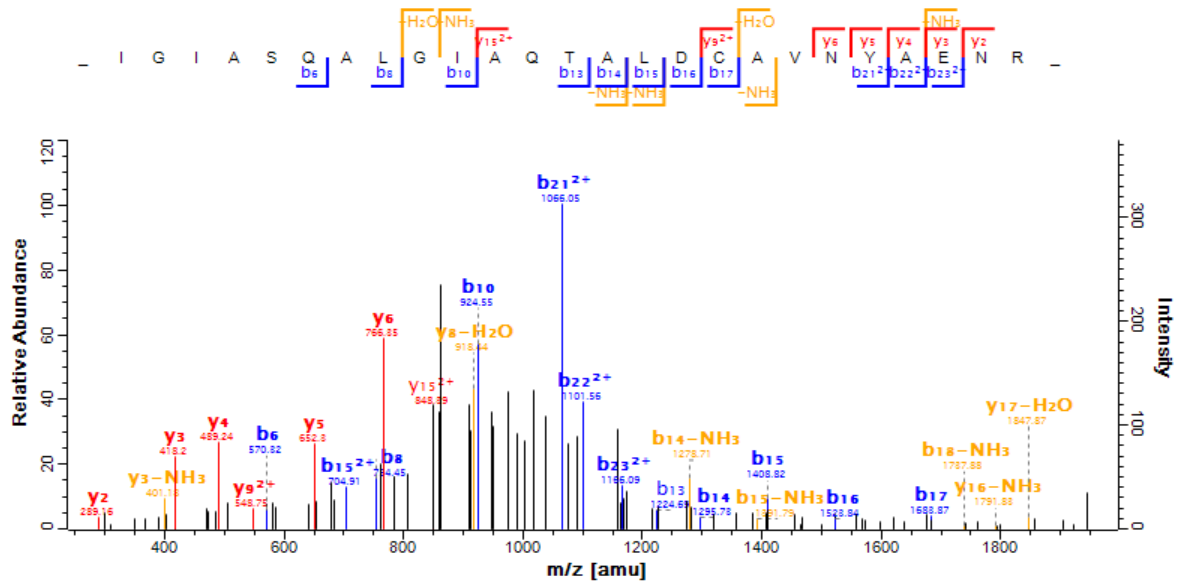
Number of Replicates (out of 10): 1

Best Match Score: 68.569

Best Match Posterior Error Probability: 0.00018505

Best Match Spectrum:

Scan number	8048	Raw file	20100914-KD-Batch4-Prt-OGE-Mock-Frac14
Method	ITMS; CID	Genenames	ACADS



Protein Group ID: 661

Protein Accession Numbers: Q5JPI3; Q5JPI3-2; E9PFZ1

Gene Names: C3orf38

Peptide Sequence: QDAVHAILAYSQSAEELLR

Total Number of Spectra: 8

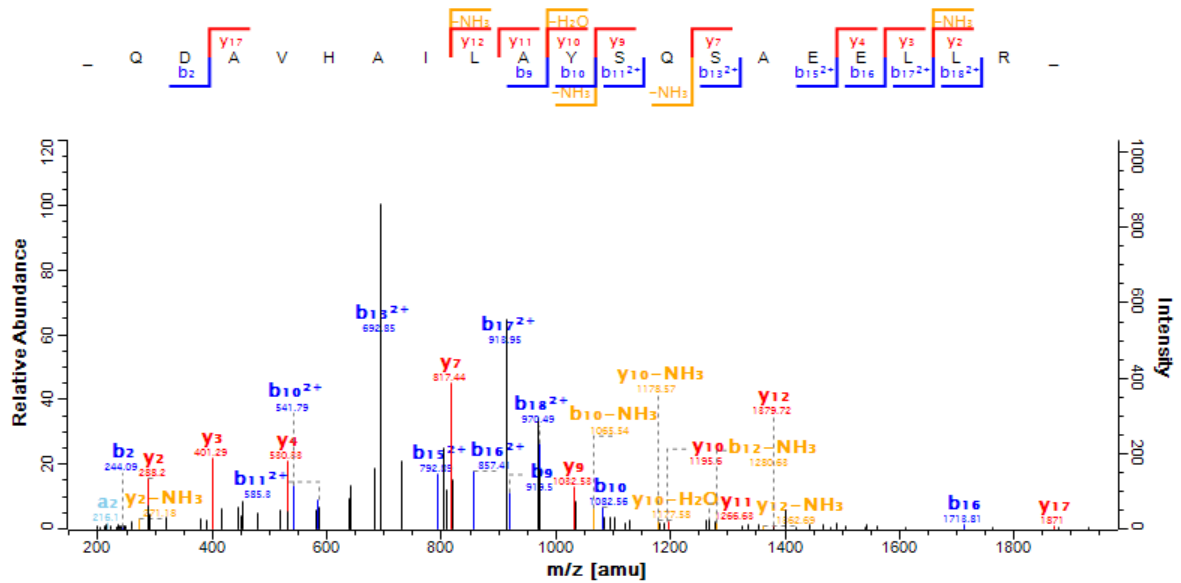
Number of Replicates (out of 10): 8

Best Match Score: 123.4

Best Match Posterior Error Probability: 1.80E-05

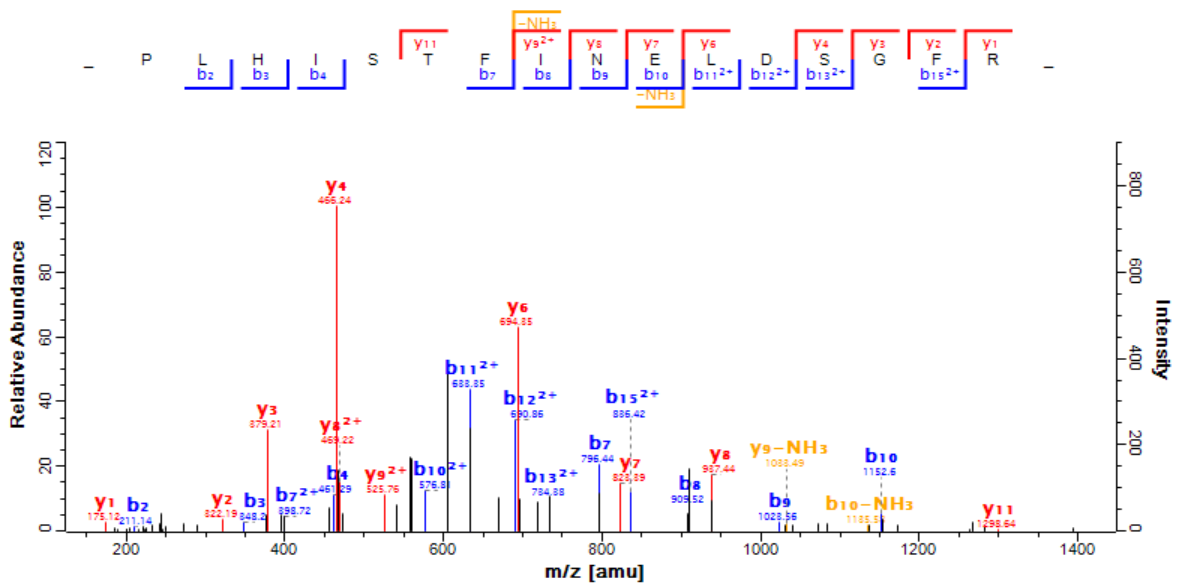
Best Match Spectrum:

Scan number 6661 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac13
Method ITMS; CID **Genenames** C3orf38



Protein Group ID: 662
Protein Accession Numbers: Q15631; E9PGT1
Gene Names: TSN
Peptide Sequence: PLHISTFINELDSGFR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 128.22
Best Match Posterior Error Probability: 4.07E-05
Best Match Spectrum:

Scan number 5454 **Raw file** Prt-OGE-Batch2-WTFrac11
Method ITMS; CID **Genenames** TSN



Protein Group ID: 669

Protein Accession Numbers: O43813; E9PHS0; F8WDS9

Gene Names: LANCL1

Peptide Sequence: SLAEGYFDAAGR

Total Number of Spectra: 1

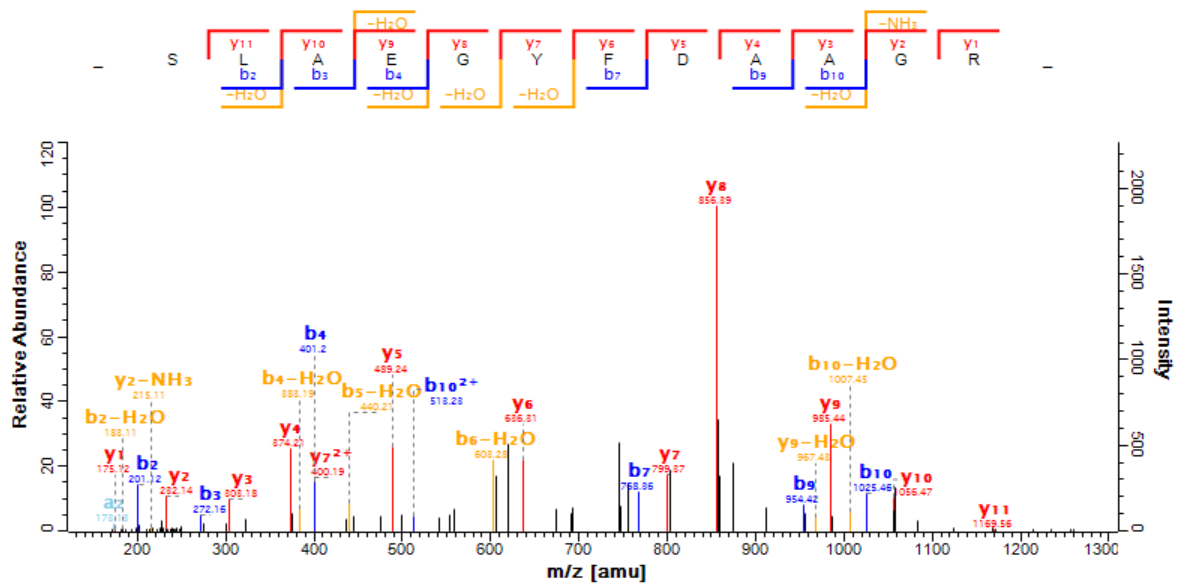
Number of Replicates (out of 10): 1

Best Match Score: 120.53

Best Match Posterior Error Probability: 0.00022794

Best Match Spectrum:

Scan number	2667	Raw file	Prt-OGE-Batch2-WT-Frac18
Method	ITMS; CID	Genenames	LANCL1



Protein Group ID: 672

Protein Accession Numbers: E9PI68; Q15005; E9PL01; E9PRB9

Gene Names: SPCS2

Peptide Sequence: FFDHSGTLVMDAYEPEISR

Total Number of Spectra: 1

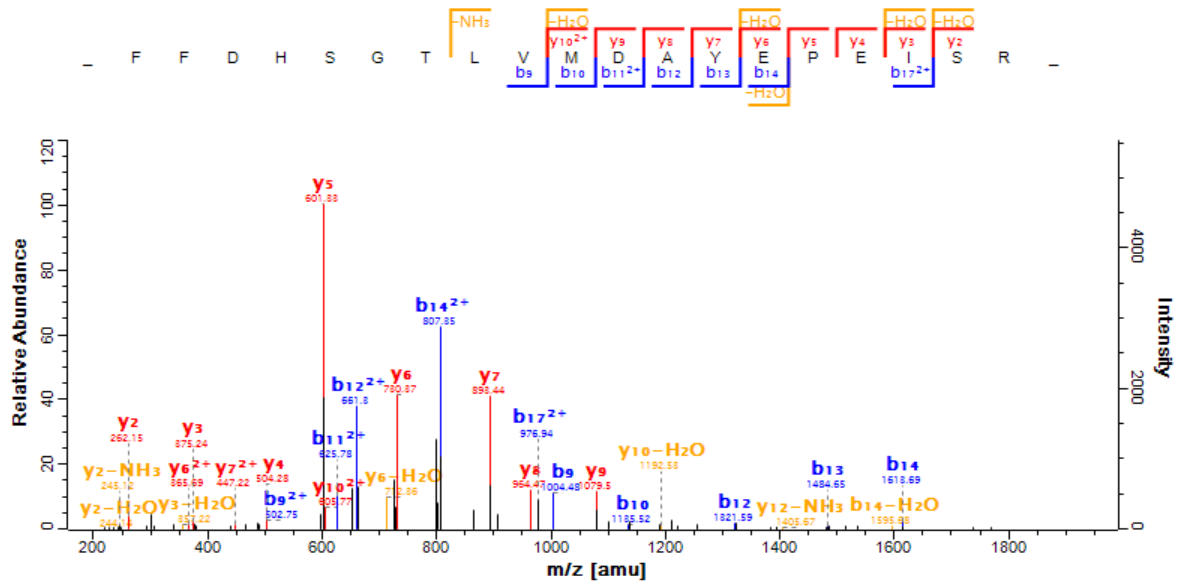
Number of Replicates (out of 10): 1

Best Match Score: 113.29

Best Match Posterior Error Probability: 3.35E-05

Best Match Spectrum:

Scan number 4948 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac13
Method ITMS; CID **Genenames** SPCS2



Protein Group ID: 673

Protein Accession Numbers: J3KNL3; Q9BWS9-2; Q9BWS9; Q9BWS9-3; E9PPA0; E9PPH0; E9PRL3; E9PIP0; E9PI70

Gene Names: CHID1

Peptide Sequence: FTQISPVWLQLK

Total Number of Spectra: 4

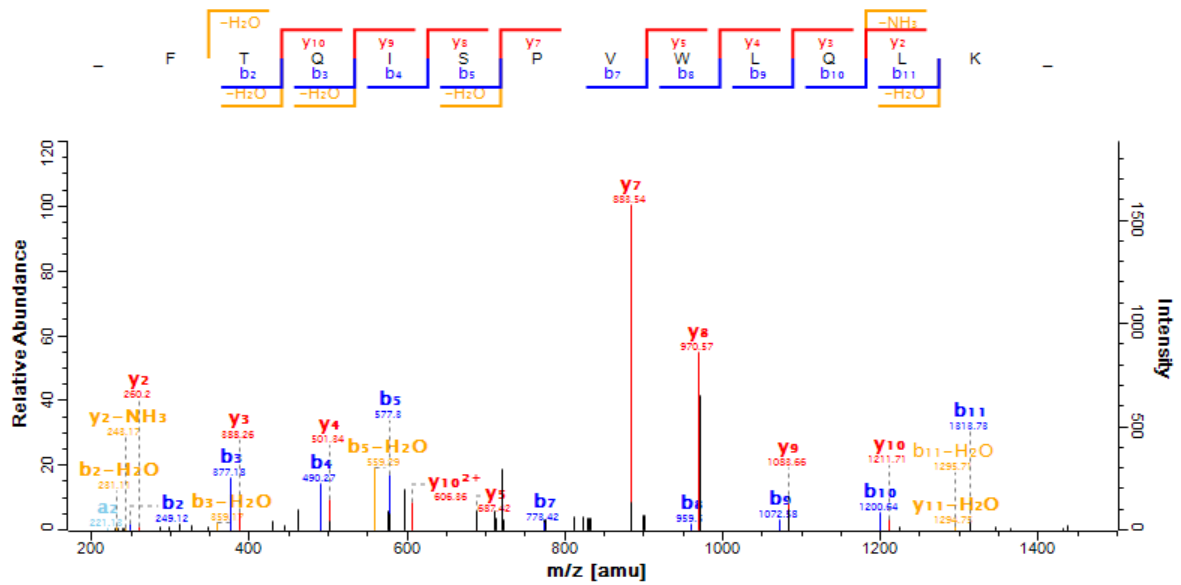
Number of Replicates (out of 10): 3

Best Match Score: 139.78

Best Match Posterior Error Probability: 6.76E-05

Best Match Spectrum:

Scan number	5674	Raw file	20100914-KD-Batch4-Prt-OGE-Mock-Frac19
Method	ITMS: CID	Genenames	CHID1



Protein Group ID: 676

Protein Accession Numbers: Q9Y6C9; E9PIE4

Gene Names: MTCH2

Peptide Sequence: ADAASQVLLGSLTILSQPLMYVK

Total Number of Spectra: 1

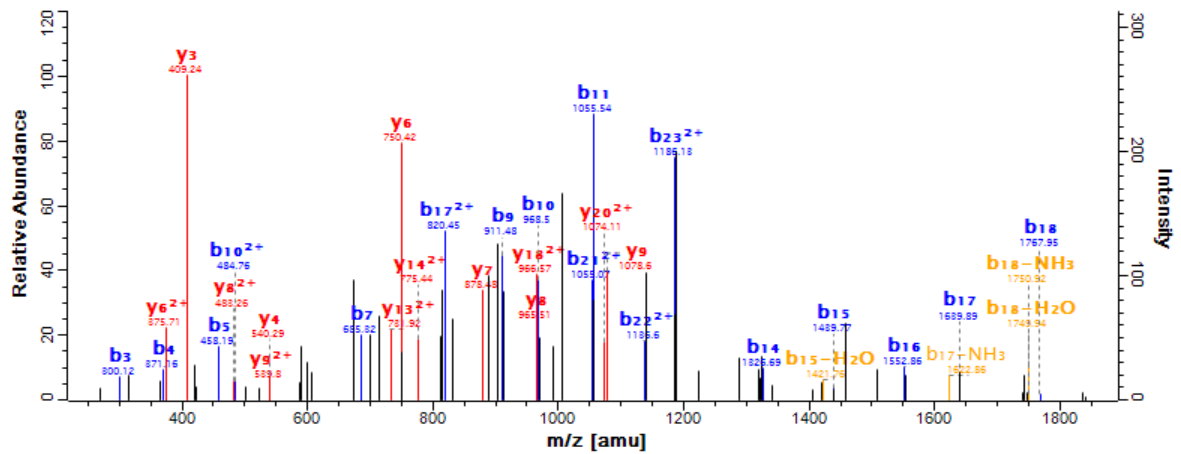
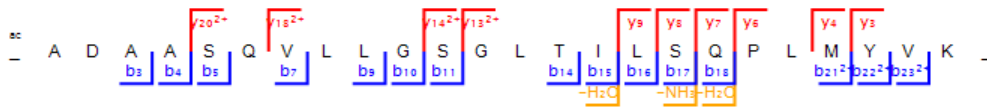
Number of Replicates (out of 10): 1

Best Match Score: 149.33

Best Match Posterior Error Probability: 7.52E-20

Best Match Spectrum:

Scan number 6834 **Raw file** Prt-OGE-Batch3--Mock-Frac1 8
Method ITMS; CID **Genenames** MTCH2



Protein Group ID: 681

Protein Accession Numbers: P08240; E9PJS4

Gene Names: SRPR

Peptide Sequence: LITVNTPLVLFVGEALVGN EAVDQLVK

Total Number of Spectra: 1

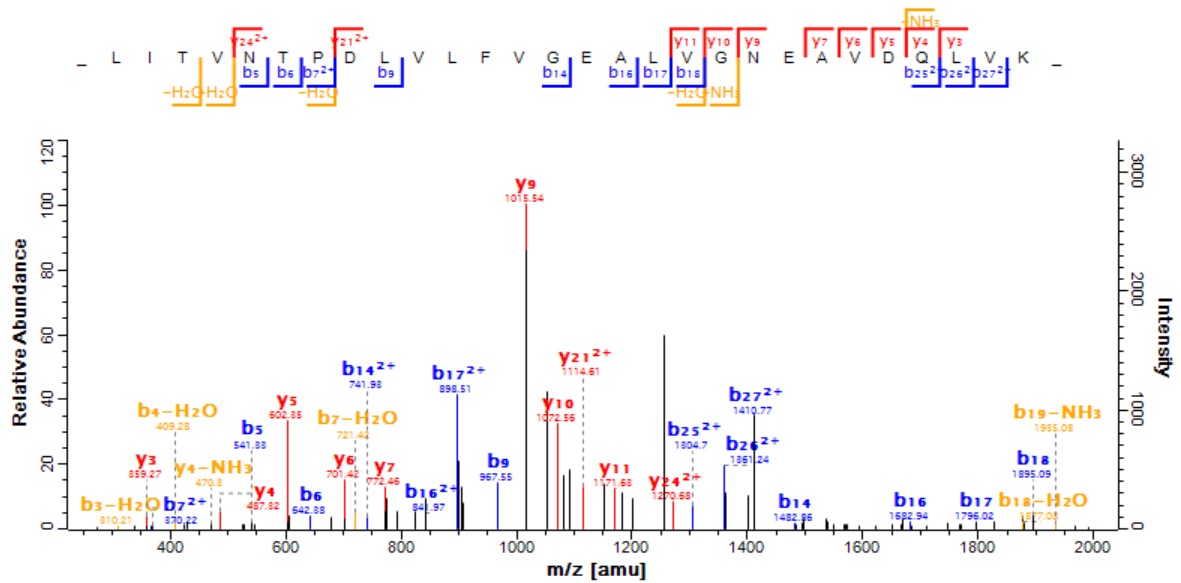
Number of Replicates (out of 10): 1

Best Match Score: 75.404

Best Match Posterior Error Probability: 6.32E-06

Best Match Spectrum:

Scan number 9187 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac19
Method ITMS; CID **Genenames** SRPR



Protein Group ID: 693

Protein Accession Numbers: Q9BTE7; E9PM04

Gene Names: DCUN1D5

Peptide Sequence: TVHADLSNYDEDGAWPVLLEDFVEWQK

Total Number of Spectra: 1

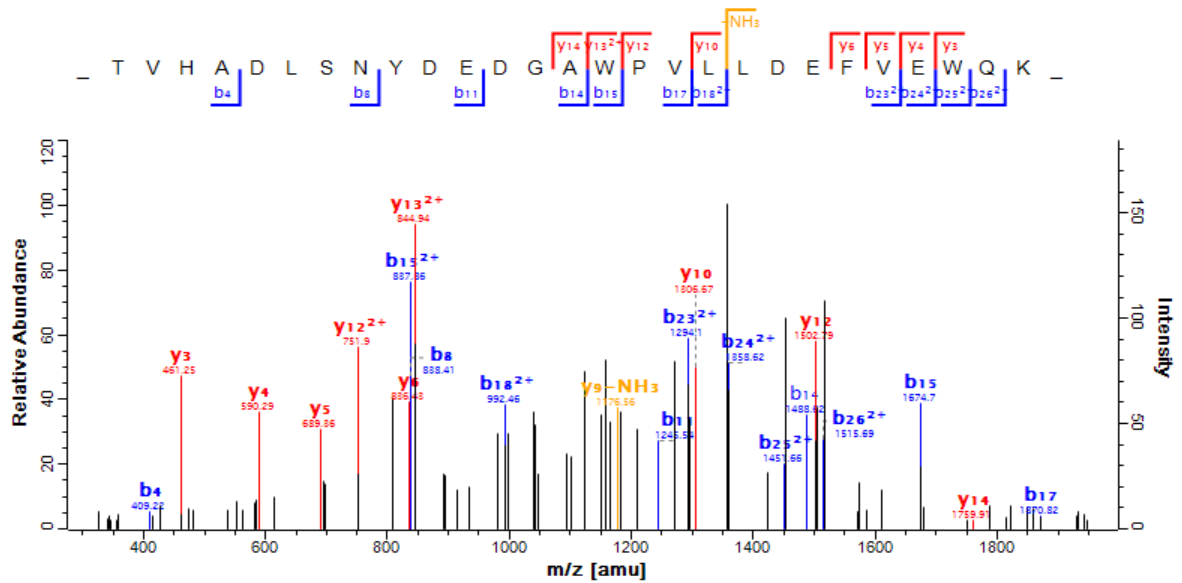
Number of Replicates (out of 10): 1

Best Match Score: 55.526

Best Match Posterior Error Probability: 0.00076982

Best Match Spectrum:

Scan number 7068 **Raw file** OGE-Mock-Frac9
Method ITMS; CID **Genenames** DCUN1D5



Protein Group ID: 694

Protein Accession Numbers: J3KPP7; P49407; P49407-2; E9PM35

Gene Names: ARRB1

Peptide Sequence: DFVDHIDLVDVDPVDGVVLVDPEYLK

Total Number of Spectra: 2

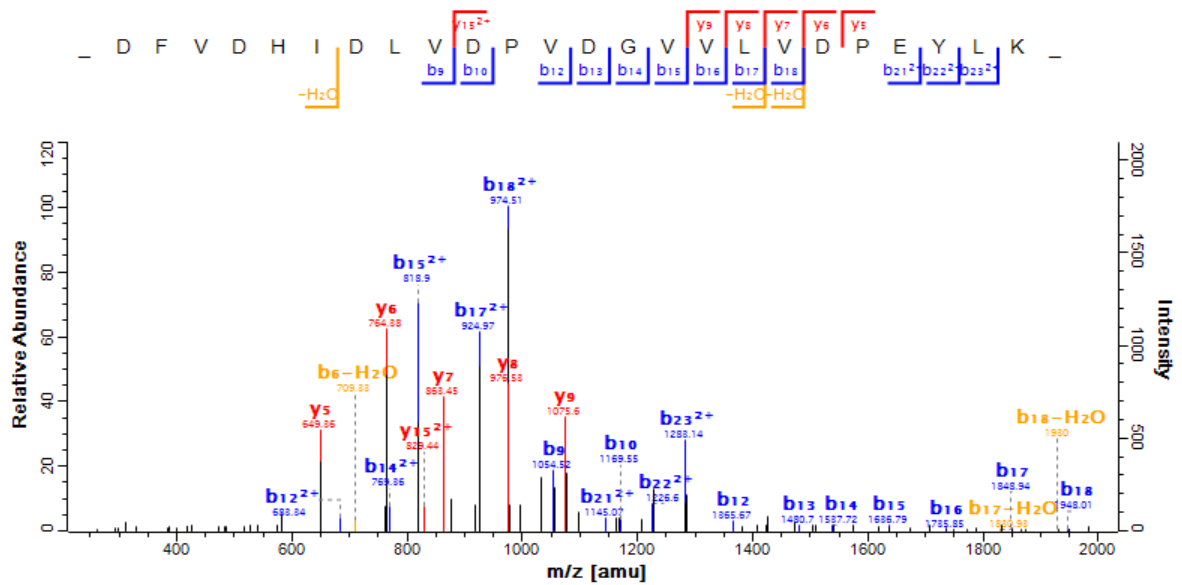
Number of Replicates (out of 10): 2

Best Match Score: 97.488

Best Match Posterior Error Probability: 5.73E-07

Best Match Spectrum:

Scan number	7620	Raw file	Prt-OGE-Batch3--Mock-Frac13
Method	ITMS; CID	Genenames	ARRB1



Protein Group ID: 698

Protein Accession Numbers: Q16798; E9PMB9

Gene Names: ME3

Peptide Sequence: HIPDEIFLLTAEQIAQEVSQHLSEGR

Total Number of Spectra: 1

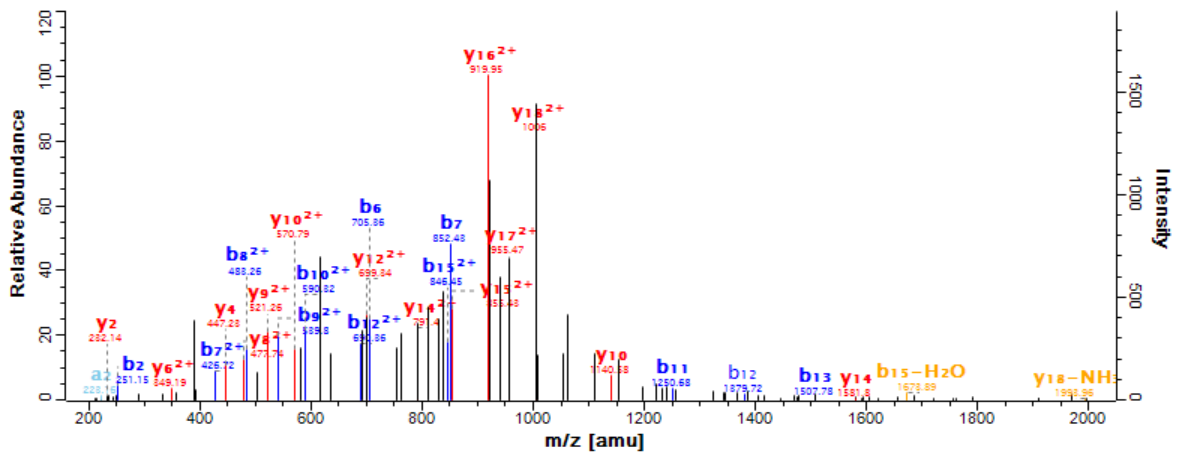
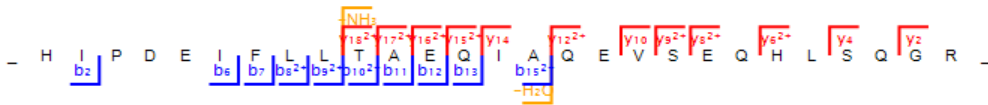
Number of Replicates (out of 10): 1

Best Match Score: 92.913

Best Match Posterior Error Probability: 3.37E-09

Best Match Spectrum:

Scan number 7382 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac17
Method ITMS; CID **Genenames** ME3



Protein Group ID: 703

Protein Accession Numbers: E9PN11; Q5JR05; P08134; Q5JR08; E9PQH6; Q5JR07; Q5JR06; E9PLA2

Gene Names: RHOC

Peptide Sequence: DQFPEVYVPTVFENYIADIEVDGK

Total Number of Spectra: 1

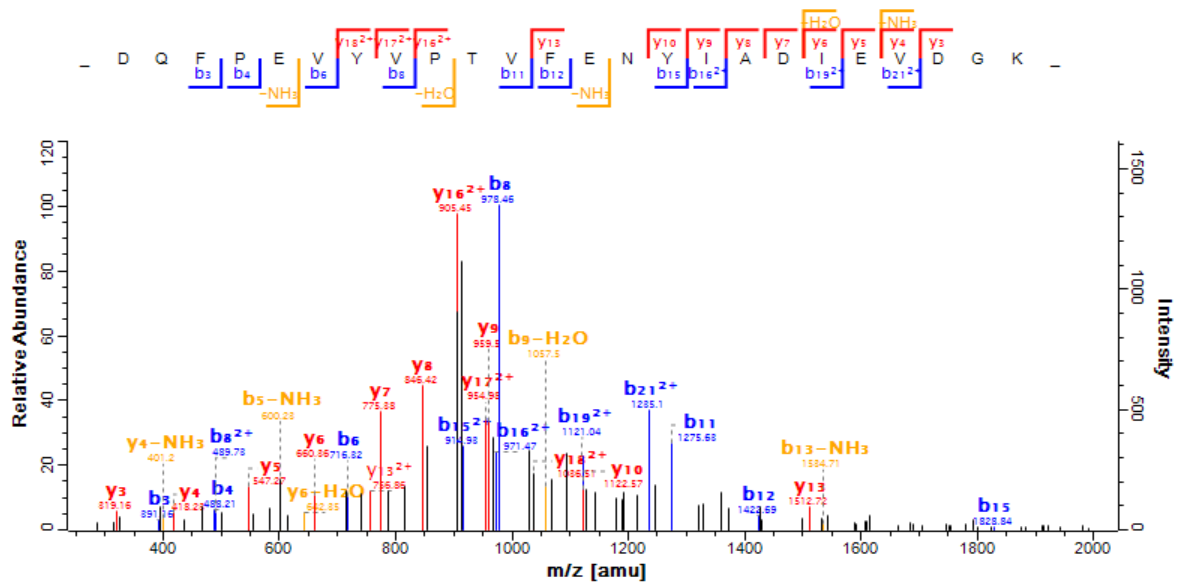
Number of Replicates (out of 10): 1

Best Match Score: 98.3

Best Match Posterior Error Probability: 4.80E-07

Best Match Spectrum:

Scan number	8315	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac11
Method	ITMS; CID	Genenames	RHOC



Protein Group ID: 707

Protein Accession Numbers: E9PR17; P13987; E9PNW4

Gene Names: CD59

Peptide Sequence: FEHCNFNDVTTR

Total Number of Spectra: 2

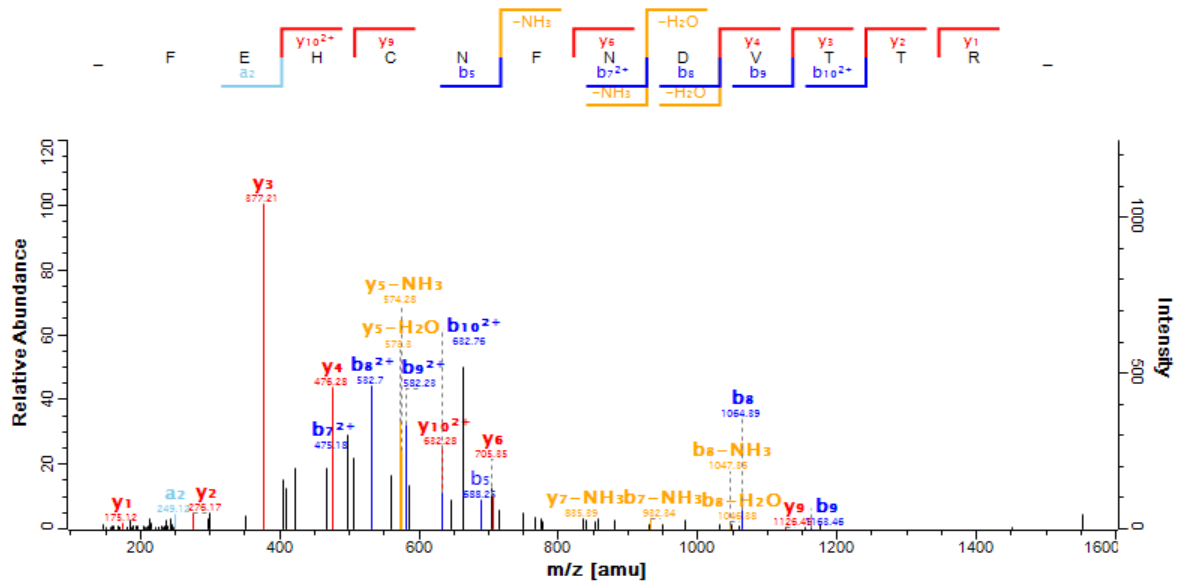
Number of Replicates (out of 10): 2

Best Match Score: 98.407

Best Match Posterior Error Probability: 0.00047859

Best Match Spectrum:

Scan number	1817	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac11
Method	ITMS; CID	Genenames	CD59



Protein Group ID: 708

Protein Accession Numbers: O00141-2; Q7Z3I4; E9PP33

Gene Names: DKFZp686H1615;SGK1

Peptide Sequence: MVNKDMNGFPVK

Total Number of Spectra: 1

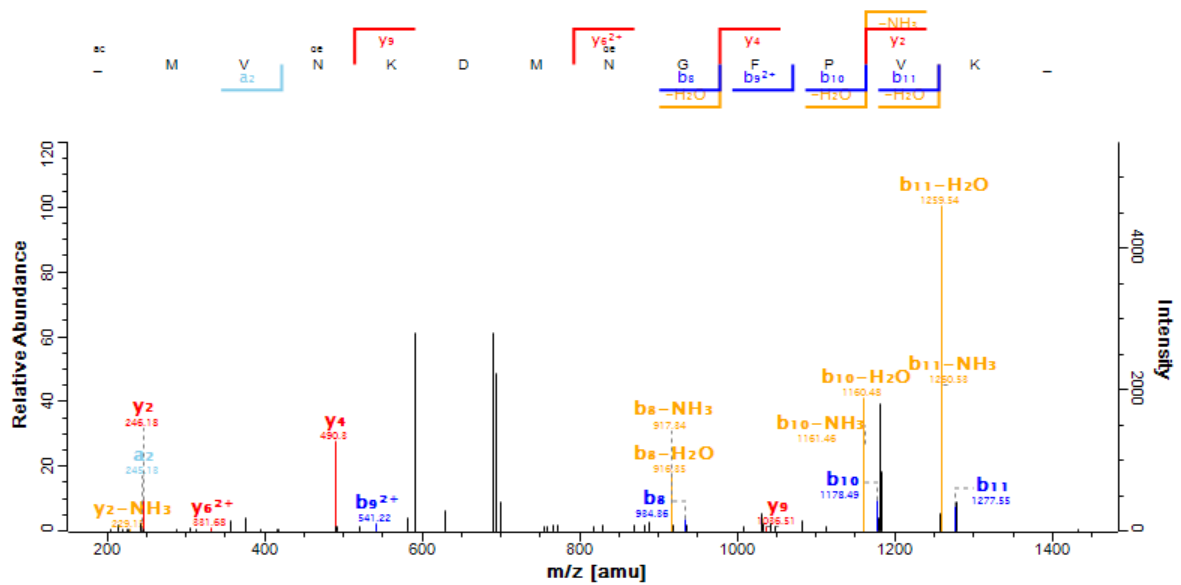
Number of Replicates (out of 10): 1

Best Match Score: 77.744

Best Match Posterior Error Probability: 0.011865

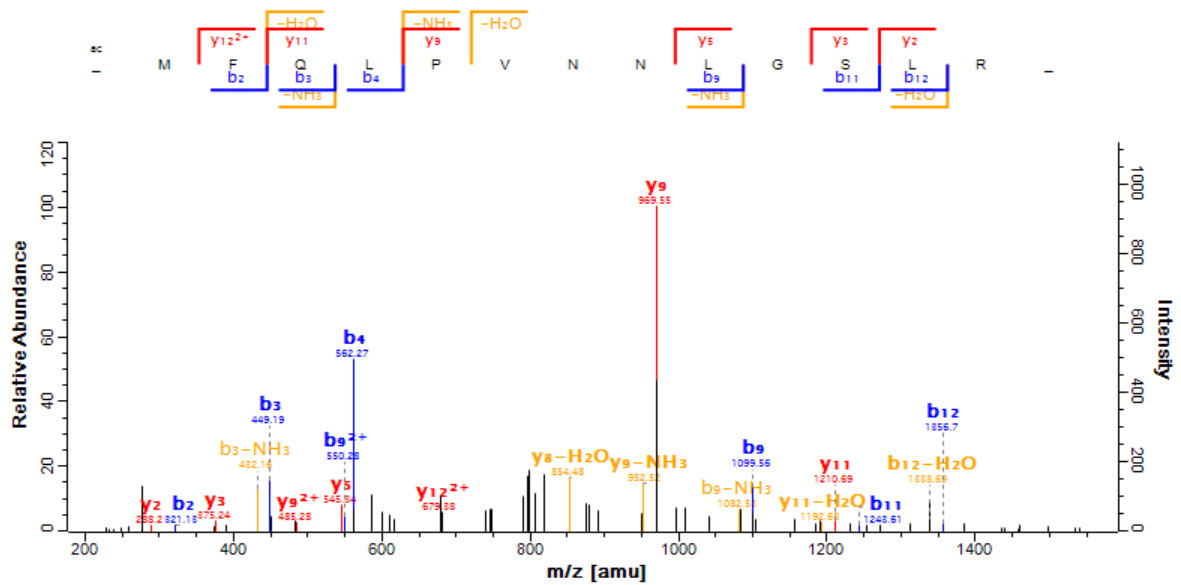
Best Match Spectrum:

Scan number 5612 **Raw file** OGE-Mock-Frac3
Method ITMS; CID **Genenames** DKFZp686H1615;SGK1



Protein Group ID: 711
Protein Accession Numbers: Q9H2P0; E9PQK8
Gene Names: ADNP
Peptide Sequence: MFQLPVNNLGLR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 101.53
Best Match Posterior Error Probability: 0.00046758
Best Match Spectrum:

Scan number 6247 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac21
Method ITMS; CID **Genenames** ADNP



Protein Group ID: 714

Protein Accession Numbers: O14497; O14497-2; O14497-3; E9PQW6

Gene Names: ARID1A

Peptide Sequence: P Q P Y G G T N P Y S Q Q C G P P S G P Q Q H G Y P G Q P Y G S Q T P Q R

Total Number of Spectra: 1

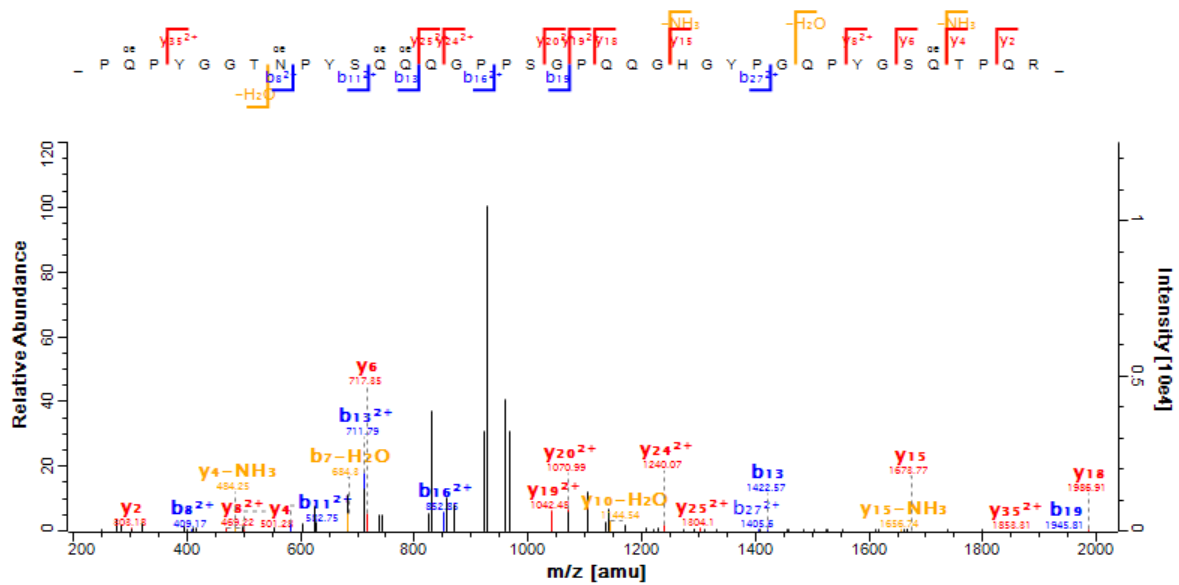
Number of Replicates (out of 10): 1

Best Match Score: 41.491

Best Match Posterior Error Probability: 0.0066044

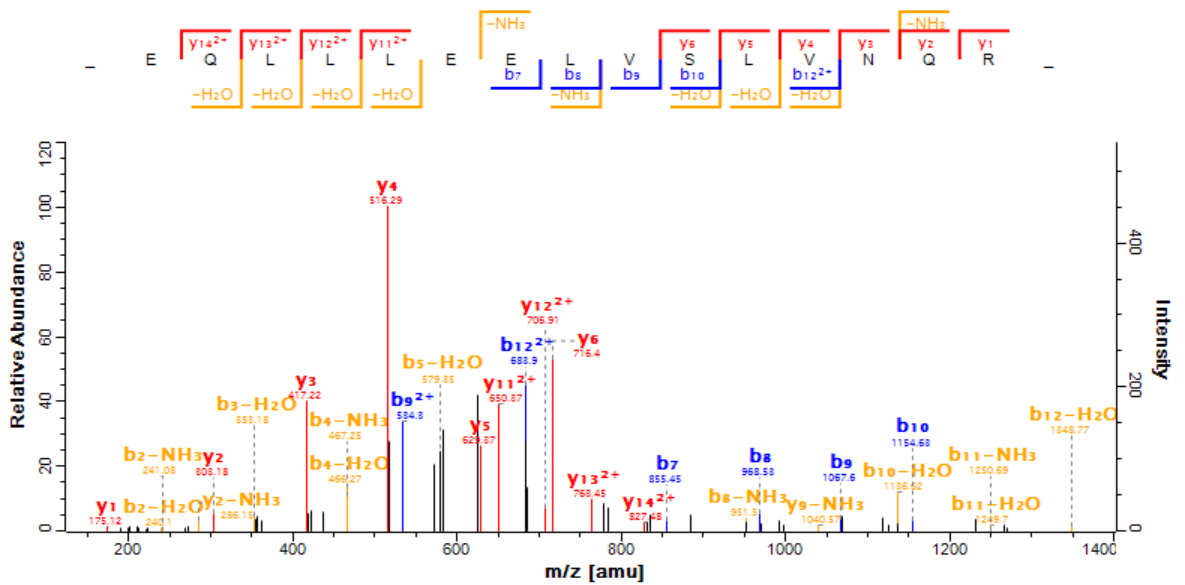
Best Match Spectrum:

Scan number 4718 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac21
Method ITMS; CID **Genenames** ARID1A



Protein Group ID: 719
Protein Accession Numbers: Q8N3D4; E9PSB0
Gene Names: EHBP1L1
Peptide Sequence: EQLLLEELVSLVNQR
Total Number of Spectra: 11
Number of Replicates (out of 10): 7
Best Match Score: 101.32
Best Match Posterior Error Probability: 0.00011088
Best Match Spectrum:

Scan number 6686 **Raw file** Prt-OGE-Batch3-WT-Frac7
Method ITMS; CID **Genenames** EHBP1L1



Protein Group ID: 720

Protein Accession Numbers: E9PSH4; Q9H063; H0YEV4

Gene Names: MAF1

Peptide Sequence: SISGSTYTPSEAGNELDMELGEEVVEEESR

Total Number of Spectra: 1

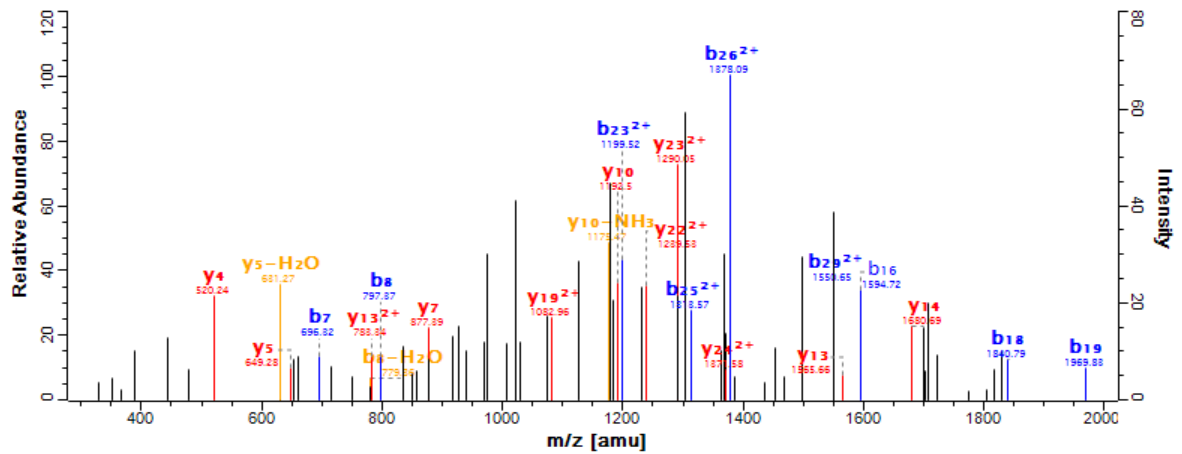
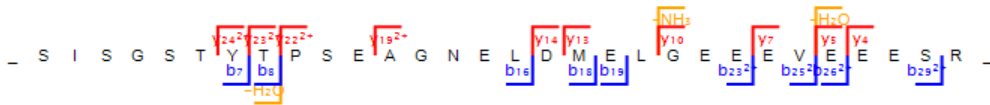
Number of Replicates (out of 10): 1

Best Match Score: 68.074

Best Match Posterior Error Probability: 7.59E-06

Best Match Spectrum:

Scan number	4345	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac3
Method	ITMS; CID	Genenames	MAF1



Protein Group ID: 721

Protein Accession Numbers: Q9Y2L1; Q9Y2L1-2; G3V1J5; F2Z2C0

Gene Names: DIS3

Peptide Sequence: AVHEDIVAVELLPK

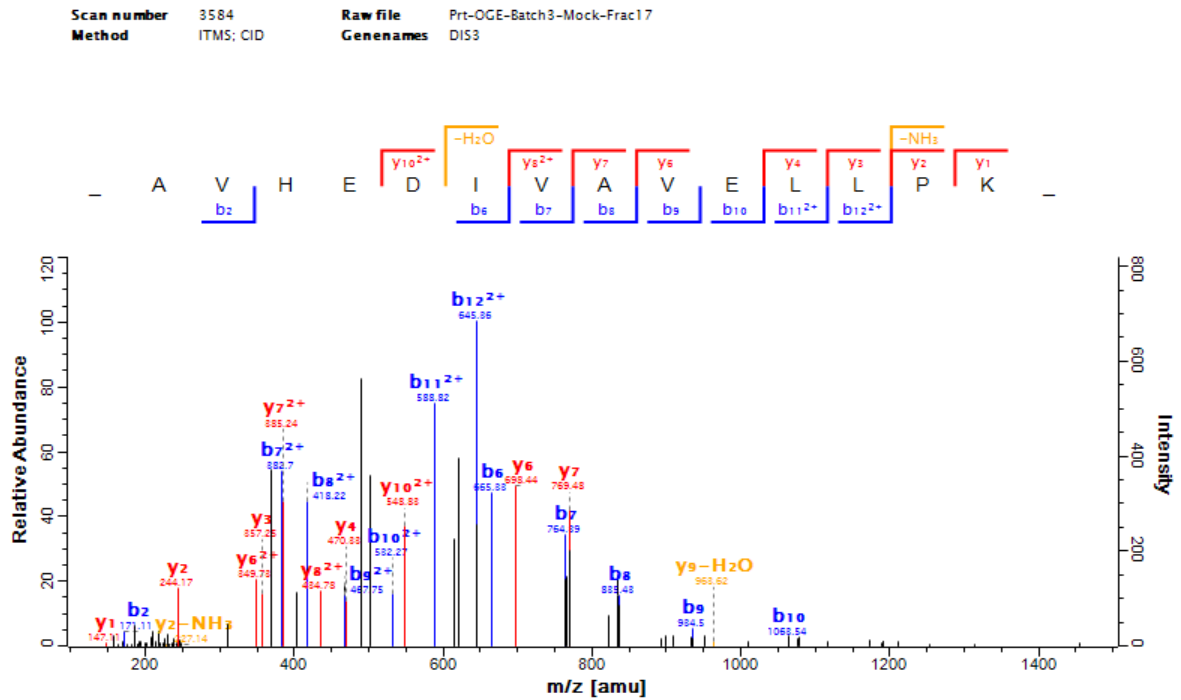
Total Number of Spectra: 3

Number of Replicates (out of 10): 3

Best Match Score: 116.03

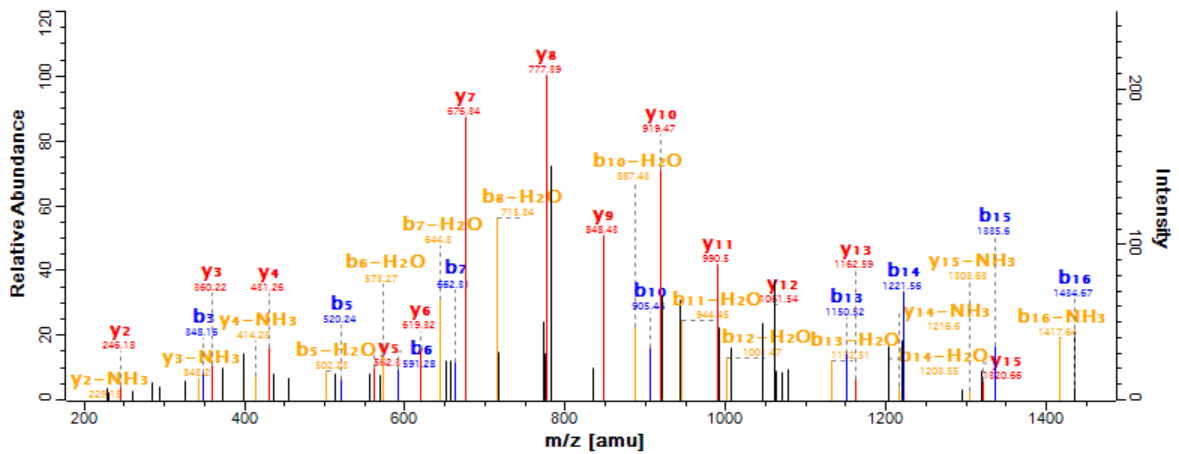
Best Match Posterior Error Probability: 0.00010693

Best Match Spectrum:



Protein Group ID: 722
Protein Accession Numbers: P23025; F2Z2T2
Gene Names: XPA
Peptide Sequence: PYSATAAAATGGMANVK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 180.7
Best Match Posterior Error Probability: 3.12E-22
Best Match Spectrum:

Scan number 2020 **Raw file** Prt-OGE-Batch3-WT-Frac14
Method ITMS; CID **Genenames** XPA



Protein Group ID: 731

Protein Accession Numbers: P10620; G5EA53; F5H6X2; F5H7F6; F5H613; F5GX73

Gene Names: MGST1

Peptide Sequence: VDLTQVMDDEVFMAFASYATIILSKMMLMSTATAFYR

Total Number of Spectra: 10

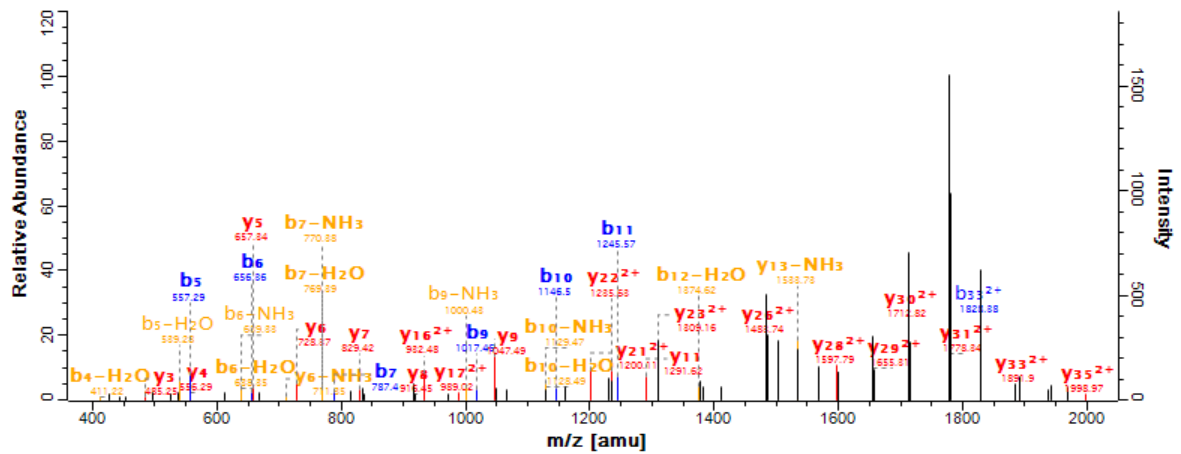
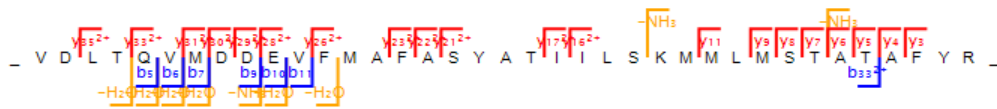
Number of Replicates (out of 10): 4

Best Match Score: 124.82

Best Match Posterior Error Probability: 4.36E-39

Best Match Spectrum:

Scan number	10017	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac13
Method	ITMS; CID	Genenames	MGST1



Protein Group ID: 732

Protein Accession Numbers: G5EA39; F5H6E4; P60006; F5H3R3; F8WDQ6; F5H2T3; F5GXB9

Gene Names: C11orf51;ANAPC15

Peptide Sequence: STLFP SLFPR

Total Number of Spectra: 7

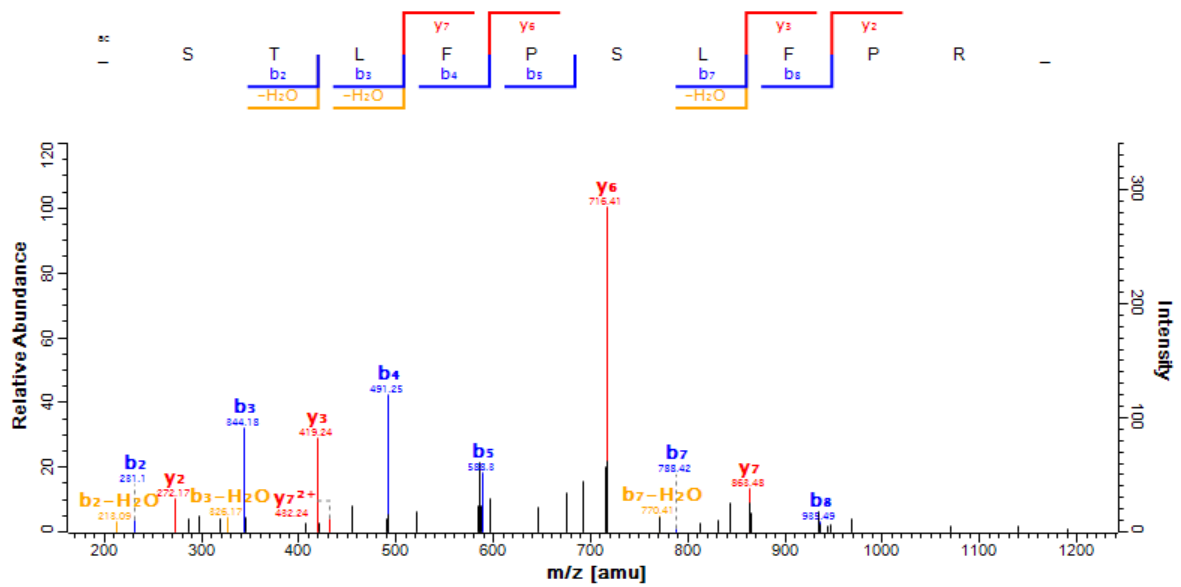
Number of Replicates (out of 10): 5

Best Match Score: 91.584

Best Match Posterior Error Probability: 0.00097898

Best Match Spectrum:

Scan number 6053 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac3
Method ITMS: CID **Genenames** C11orf51;ANAPC15



Protein Group ID: 736

Protein Accession Numbers: F5GXR3; P20962; F5H7R9

Gene Names: PTMS

Peptide Sequence: SVEAAAELSAK

Total Number of Spectra: 158

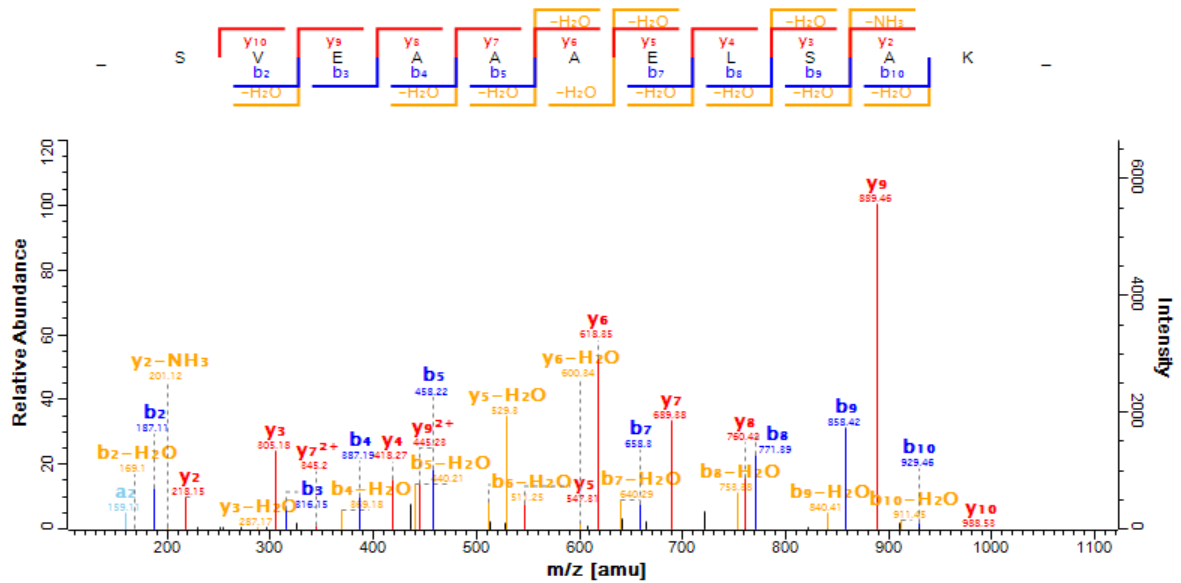
Number of Replicates (out of 10): 10

Best Match Score: 251.34

Best Match Posterior Error Probability: 1.44E-71

Best Match Spectrum:

Scan number 1745 **Raw file** OGEWT-Frac4
Method ITMS; CID **Genenames** PTMS



Protein Group ID: 737

Protein Accession Numbers: O14593; J3KPZ8; Q24JQ1; O14593-2; F5H1K6; F5GY33; H0YGQ6

Gene Names: RFXANK

Peptide Sequence: FLLEWGADPILAK

Total Number of Spectra: 2

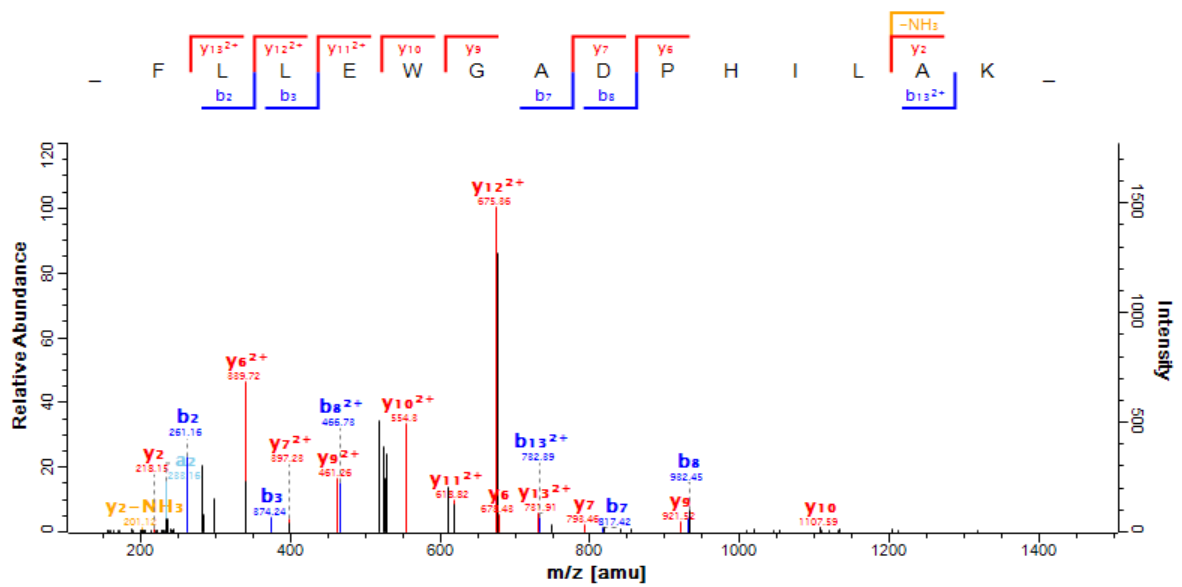
Number of Replicates (out of 10): 2

Best Match Score: 121.02

Best Match Posterior Error Probability: 7.37E-05

Best Match Spectrum:

Scan number	5530	Raw file	OGE-Mock-Frac3
Method	ITMS; CID	Genenames	RFXANK



Protein Group ID: 738

Protein Accession Numbers: Q02978; I3L1P8; F5GY65

Gene Names: SLC25A11

Peptide Sequence: AATASAGAGGIDGKPR

Total Number of Spectra: 2

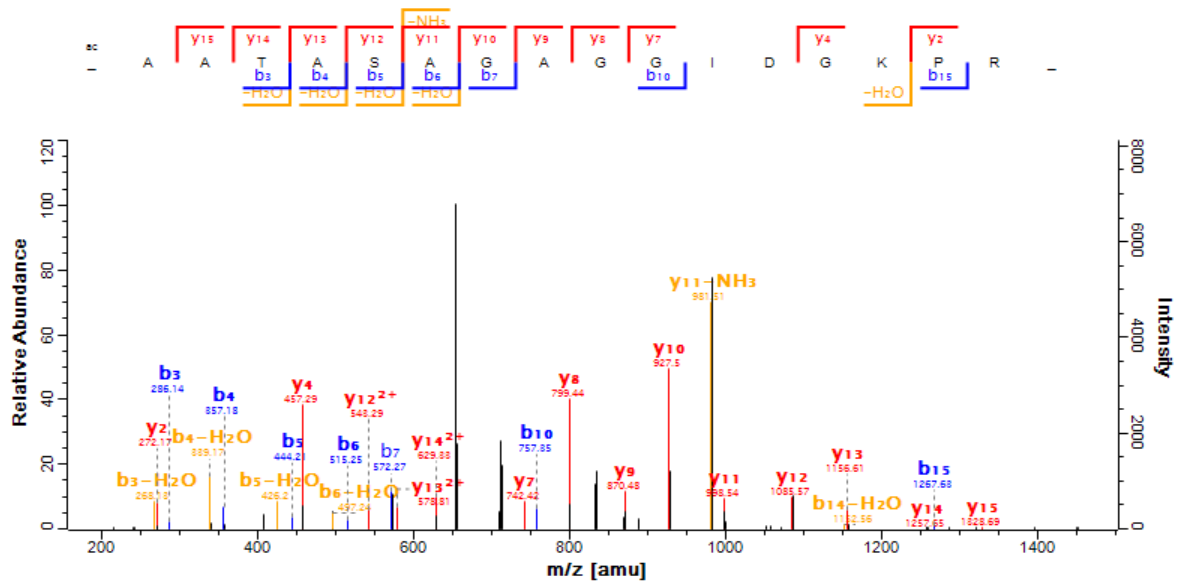
Number of Replicates (out of 10): 1

Best Match Score: 121.32

Best Match Posterior Error Probability: 0.00031605

Best Match Spectrum:

Scan number 1362 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac16
Method ITMS; CID **Genenames** SLC25A11



Protein Group ID: 739

Protein Accession Numbers: O14519; F5GYA4; F5GZF0

Gene Names: CDK2AP1

Peptide Sequence: YAELLAIEELGK

Total Number of Spectra: 18

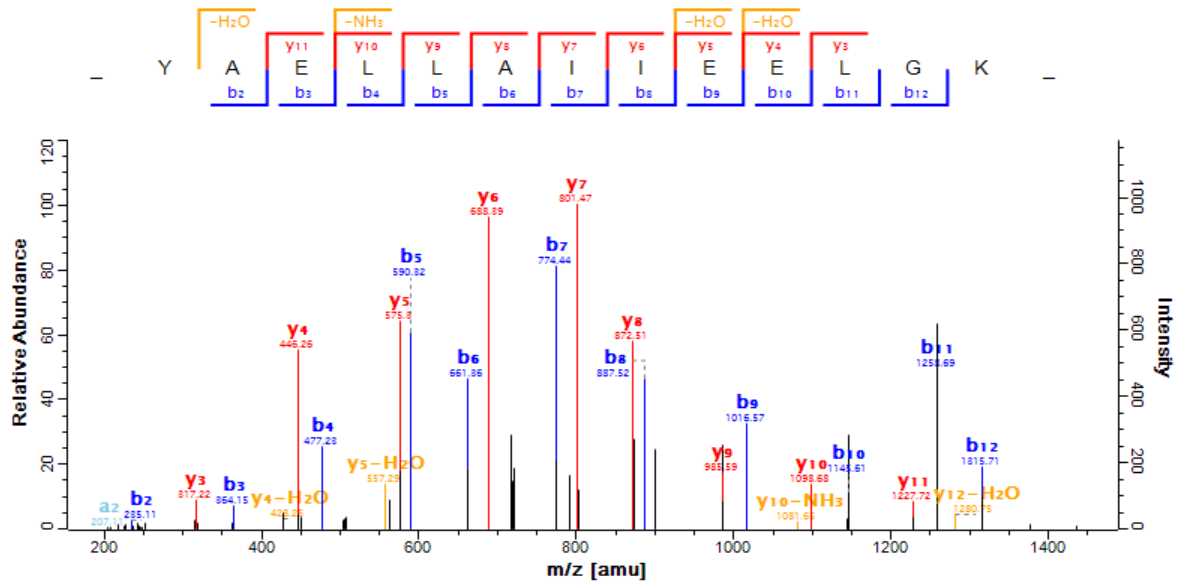
Number of Replicates (out of 10): 7

Best Match Score: 152.74

Best Match Posterior Error Probability: 8.12E-06

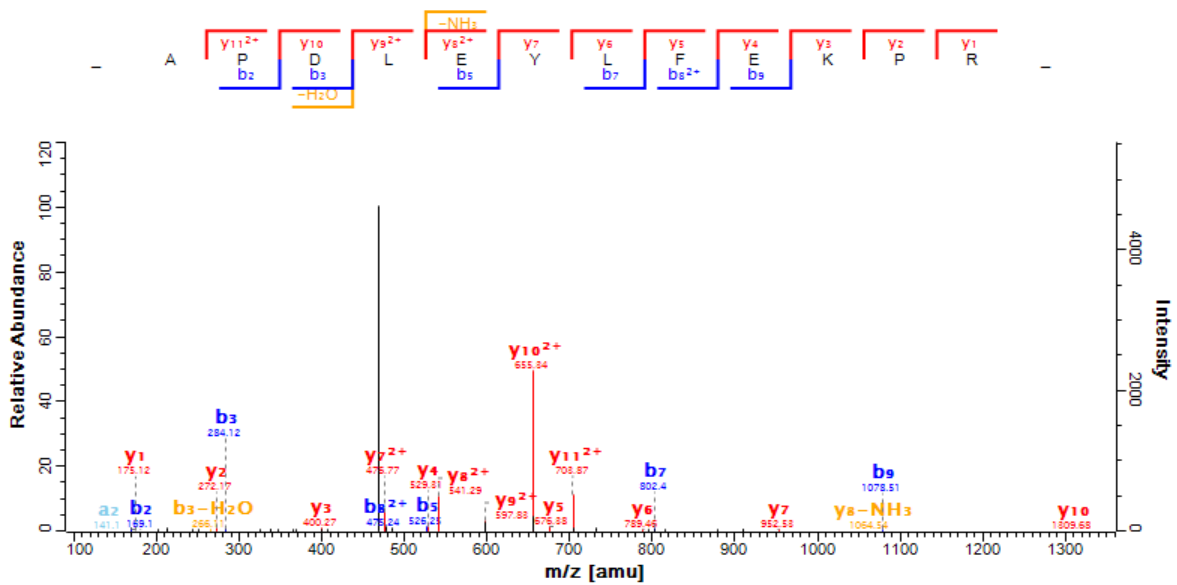
Best Match Spectrum:

Scan number 7468 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac22
Method ITMS; CID **Genenames** CDK2AP1



Protein Group ID: 740
Protein Accession Numbers: Q9NX18; F5GYJ5
Gene Names: SDHAF2
Peptide Sequence: APDLEYLF EKPR
Total Number of Spectra: 3
Number of Replicates (out of 10): 2
Best Match Score: 107.85
Best Match Posterior Error Probability: 0.0006479
Best Match Spectrum:

Scan number 4493 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac8
Method ITMS; CID **Genenames** SDHAF2



Protein Group ID: 744

Protein Accession Numbers: F5GZE1; Q8N4X5-4; Q8N4X5; Q8N4X5-2

Gene Names: AFAP1L2

Peptide Sequence: ALEQLLTELDDFLK

Total Number of Spectra: 4

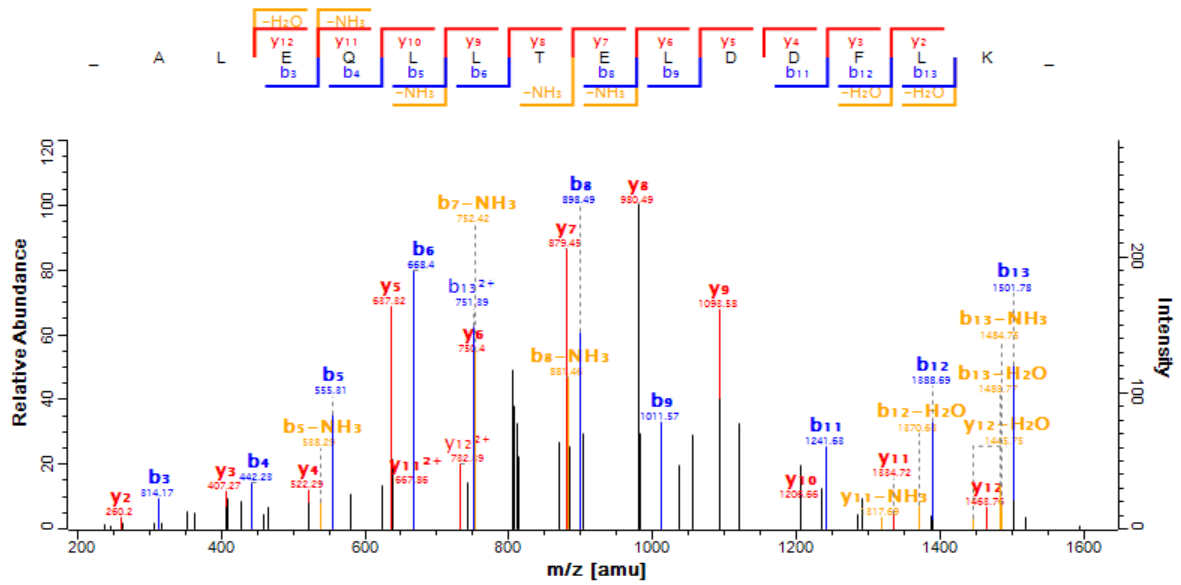
Number of Replicates (out of 10): 2

Best Match Score: 183.41

Best Match Posterior Error Probability: 1.11E-15

Best Match Spectrum:

Scan number 7583 **Raw file** OGE-WT-Frac9
Method ITMS; CID **Genenames** AFAP1L2



Protein Group ID: 745

Protein Accession Numbers: Q86YW0; F5H2Y6; Q86YW0-3; F5GZK3

Gene Names: PLCZ1

Peptide Sequence: AIAFEIIQK

Total Number of Spectra: 1

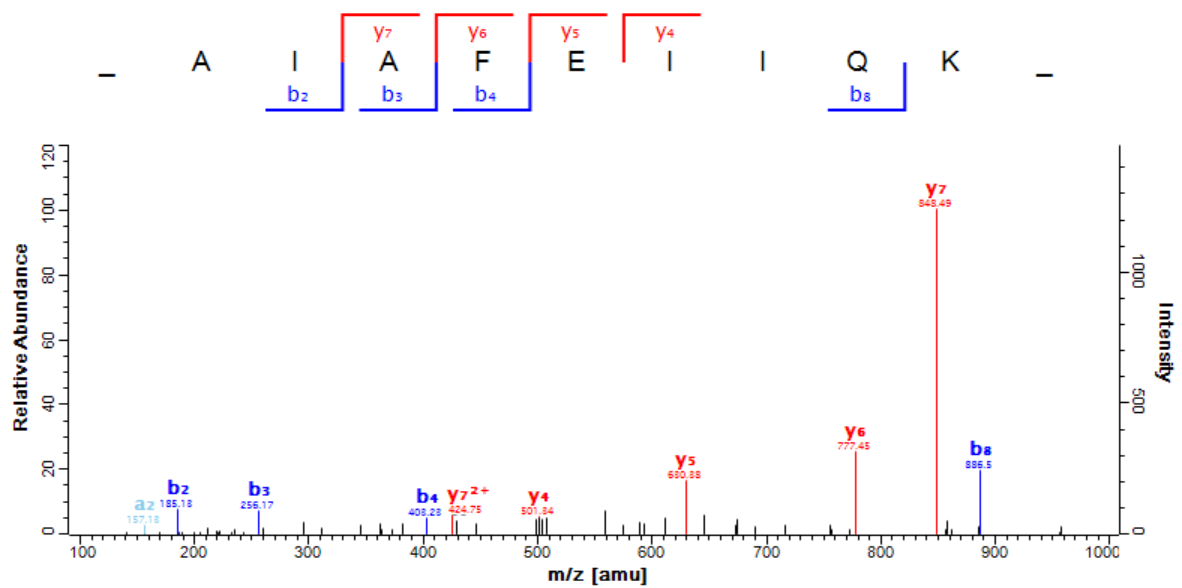
Number of Replicates (out of 10): 1

Best Match Score: 95.099

Best Match Posterior Error Probability: 0.0011986

Best Match Spectrum:

Scan number	5322	Raw file	Prt-OGE-Batch3-Mock-Frac7
Method	ITMS; CID	Genenames	PLCZ1



Protein Group ID: 747

Protein Accession Numbers: Q9H267; F5H008; G3V3F9

Gene Names: VPS33B

Peptide Sequence: AFPHRPDAPELPDFSMLK

Total Number of Spectra: 1

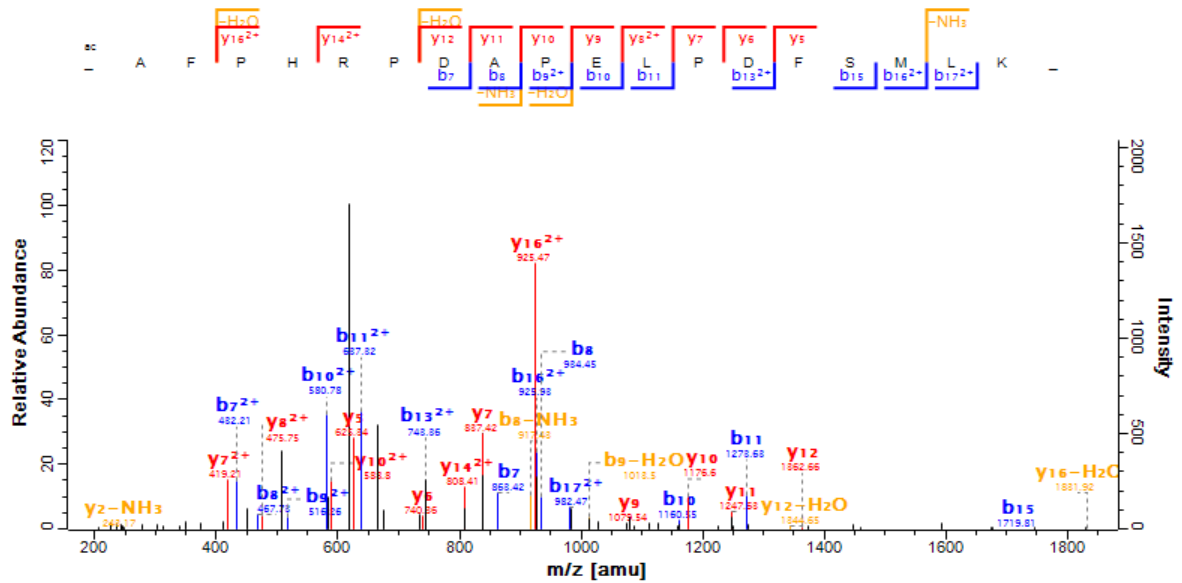
Number of Replicates (out of 10): 1

Best Match Score: 128.74

Best Match Posterior Error Probability: 8.49E-05

Best Match Spectrum:

Scan number 5636 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac14
Method ITMS; CID **Genenames** VPS33B



Protein Group ID: 750

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

Gene Names: DYNC111

Peptide Sequence: TPLSAAATHPVYCVNVVVG TQNAHNLITVSTDGK

Total Number of Spectra: 1

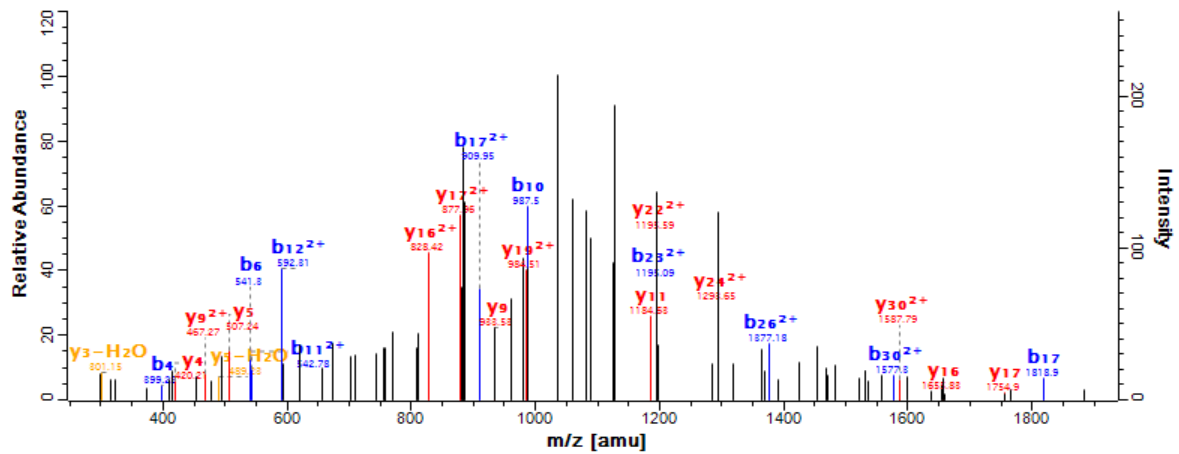
Number of Replicates (out of 10): 1

Best Match Score: 55.428

Best Match Posterior Error Probability: 8.38E-05

Best Match Spectrum:

Scan number	4030	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac9
Method	ITMS; CID	Genenames	DYNC111



Protein Group ID: 754

Protein Accession Numbers: Q9Y653; Q9Y653-2; F5H144; H3BRH0; H3BV52; H3BSJ6

Gene Names: GPR56

Peptide Sequence: DLQLLSQFLK

Total Number of Spectra: 5

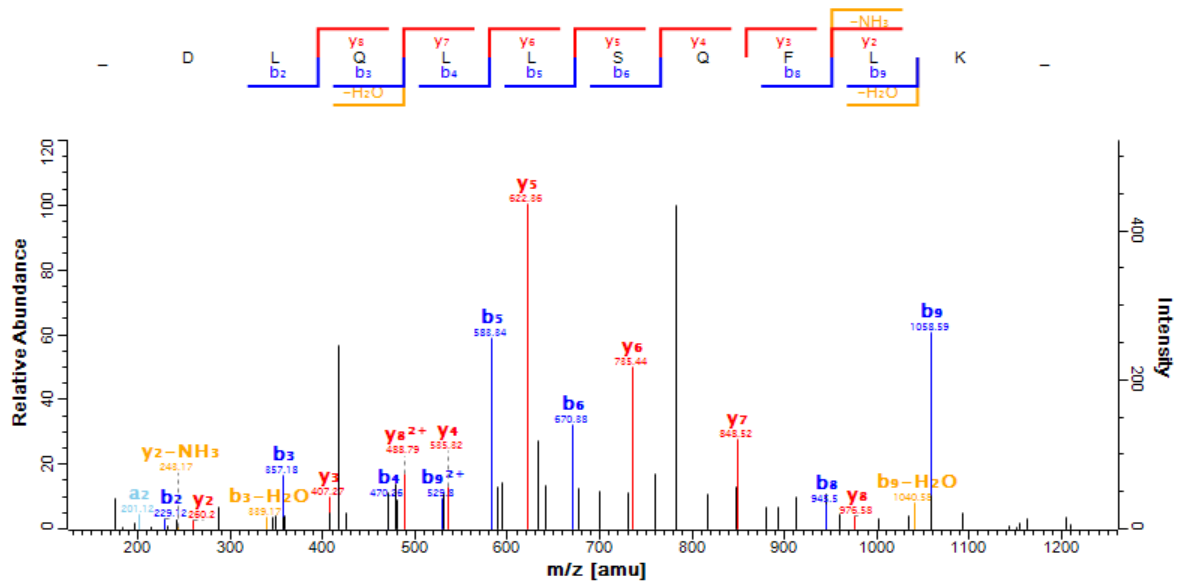
Number of Replicates (out of 10): 3

Best Match Score: 118.9

Best Match Posterior Error Probability: 0.00013522

Best Match Spectrum:

Scan number 6339 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac16
Method ITMS; CID **Genenames** GPR56



Protein Group ID: 755

Protein Accession Numbers: P07864; G3XAP5; F5H155; F5GZ11

Gene Names: LDHC

Peptide Sequence: IVIVTAGAR

Total Number of Spectra: 1

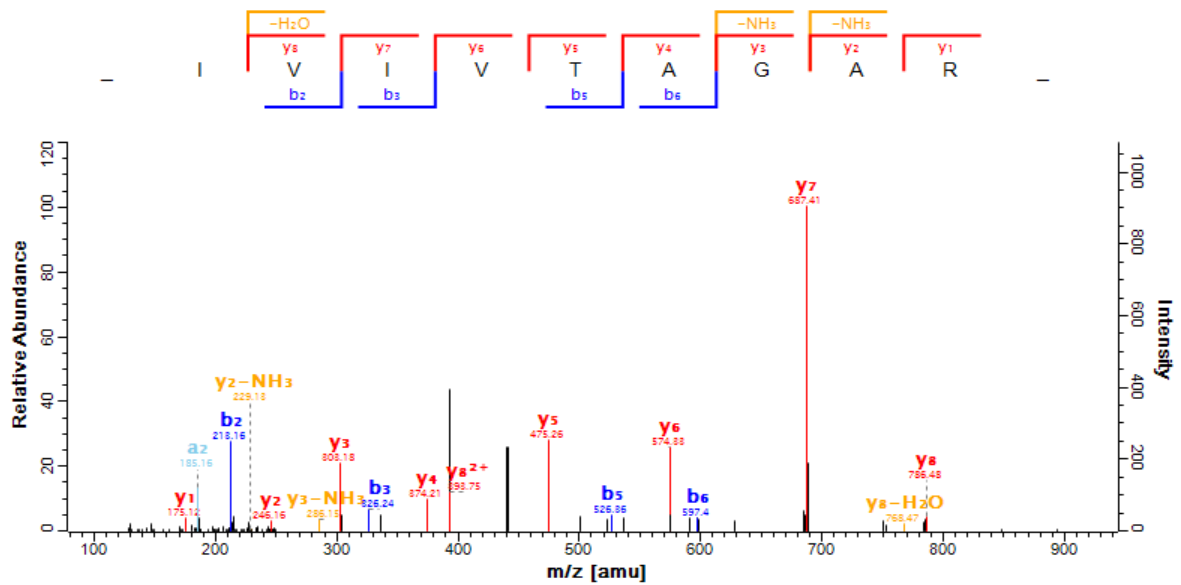
Number of Replicates (out of 10): 1

Best Match Score: 113.71

Best Match Posterior Error Probability: 0.00038235

Best Match Spectrum:

Scan number	2213	Raw file	OGE-WT-Frac3
Method	ITMS; CID	Genenames	LDHC



Protein Group ID: 759

Protein Accession Numbers: Q7LBC6; Q7LBC6-2; F5H275; Q7LBC6-3

Gene Names: KDM3B

Peptide Sequence: ASLPNFDLHILASVVENK

Total Number of Spectra: 11

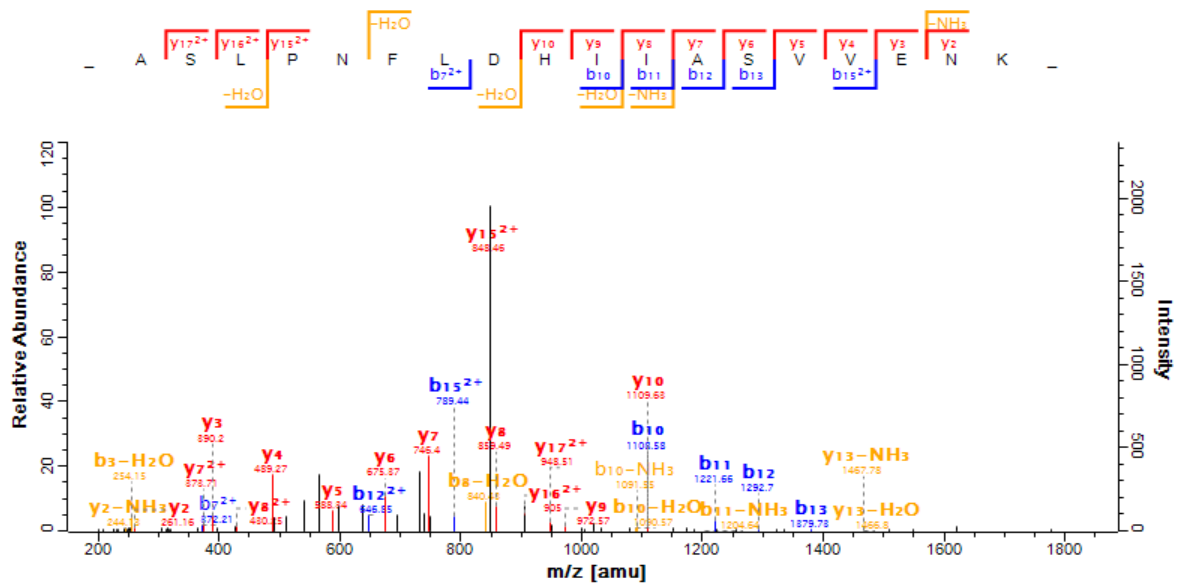
Number of Replicates (out of 10): 8

Best Match Score: 110.04

Best Match Posterior Error Probability: 0.00011908

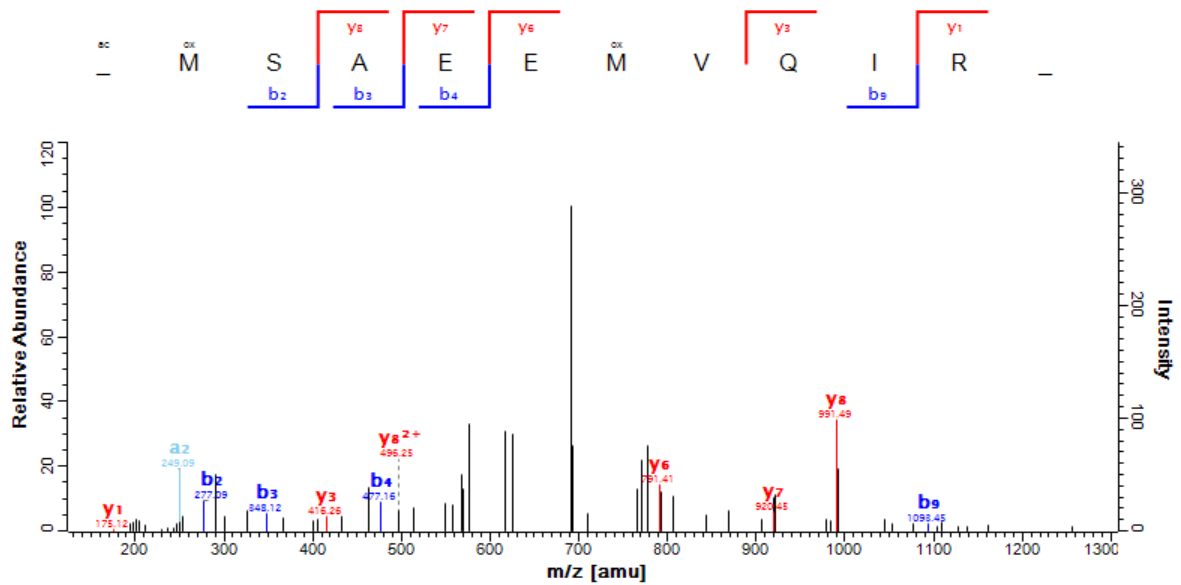
Best Match Spectrum:

Scan number 7918 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac16
Method ITMS; CID **Genenames** KDM3B



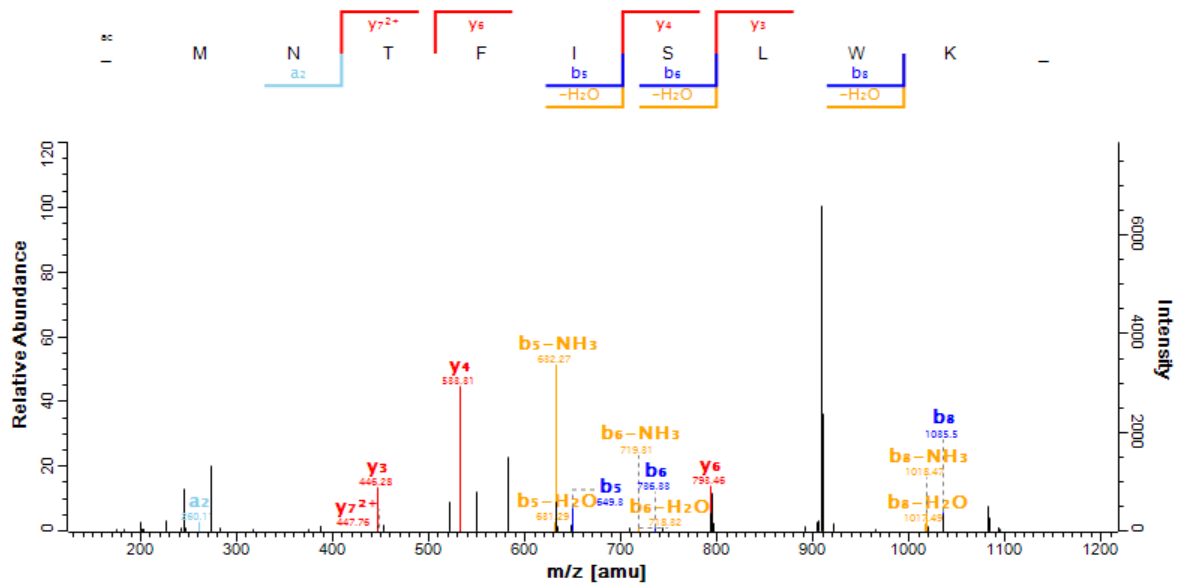
Protein Group ID: 771
Protein Accession Numbers: Q9P2K6; F5H523
Gene Names: KLHDC5
Peptide Sequence: MSAEEMVQIR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 57.348
Best Match Posterior Error Probability: 0.026632
Best Match Spectrum:

Scan number	2306	Raw file	OGEWT-Frac4
Method	ITMS; CID	Genenames	KLHDC5



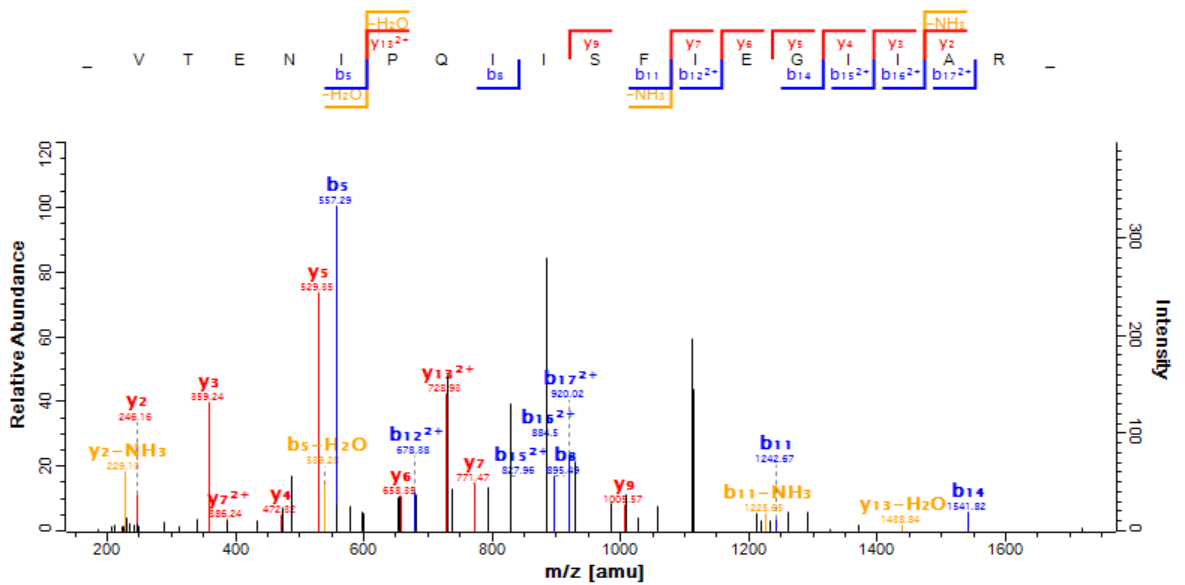
Protein Group ID: 772
Protein Accession Numbers: F5H555
Gene Names: CASC1
Peptide Sequence: MNTFISLWK
Total Number of Spectra: 16
Number of Replicates (out of 10): 6
Best Match Score: 96.948
Best Match Posterior Error Probability: 0.0009101
Best Match Spectrum:

Scan number	3511	Raw file	Prt-OGE-Batch3-WT-Frac16
Method	ITMS; CID	Genenames	CASC1



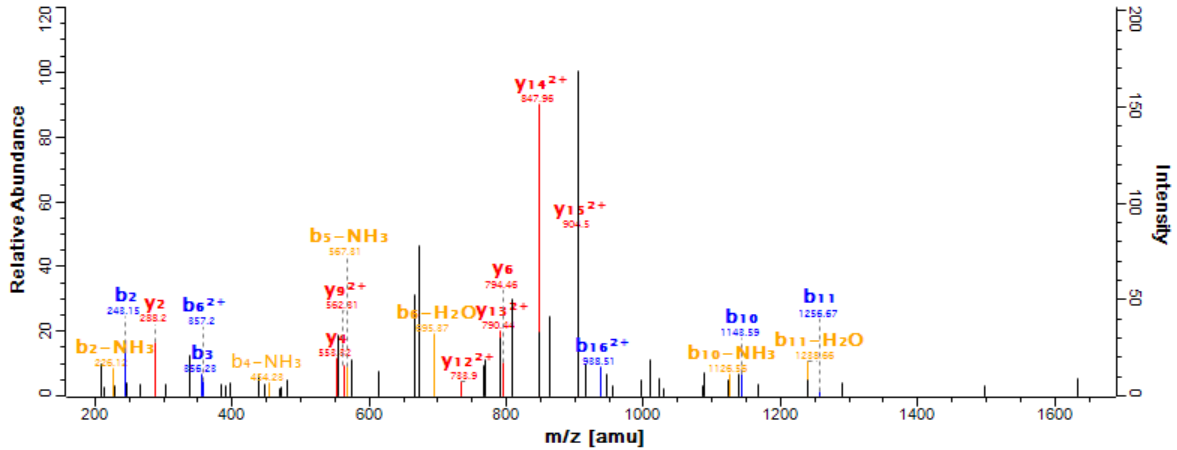
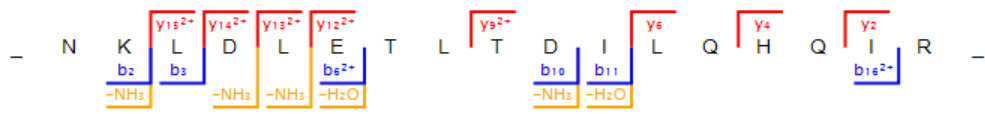
Protein Group ID: 773
Protein Accession Numbers: Q9HA77; F5H579
Gene Names: CARS2
Peptide Sequence: VTENIPQIISFIEGIGIYR
Total Number of Spectra: 7
Number of Replicates (out of 10): 6
Best Match Score: 91.657
Best Match Posterior Error Probability: 0.00041484
Best Match Spectrum:

Scan number 9363 **Raw file** Prt-OGE-Batch2-Mock-Frac18
Method ITMS; CID **Genenames** CARS2



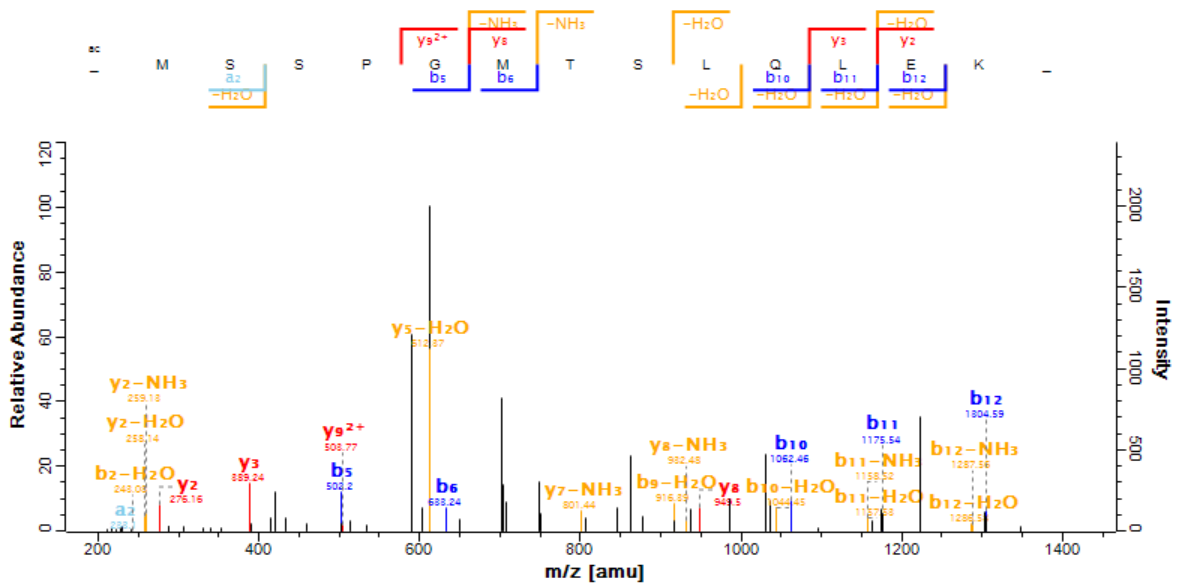
Protein Group ID: 779
Protein Accession Numbers: F5H5R8; P18440
Gene Names: NAT1
Peptide Sequence: NKLDLETLDILQHQR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 89.507
Best Match Posterior Error Probability: 0.0016492
Best Match Spectrum:

Scan number 6861 **Raw file** Prt-OGE-Batch2-Mock-Frac13
Method ITMS; CID **Genenames** NAT1



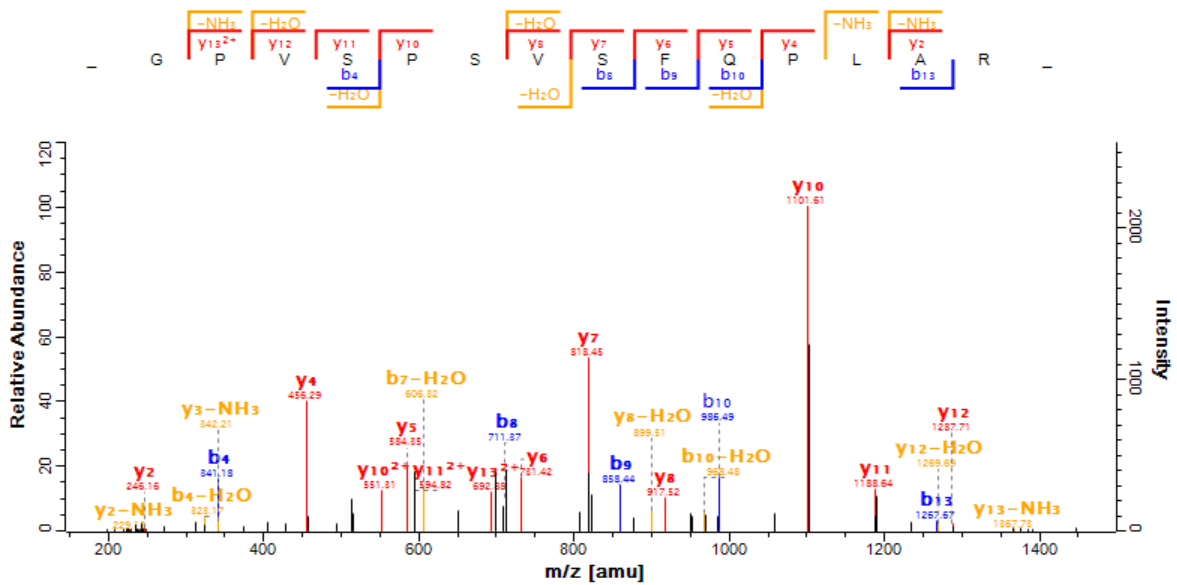
Protein Group ID: 780
Protein Accession Numbers: F5H607
Gene Names: TUFT1
Peptide Sequence: MSSPGMTSLQLEK
Total Number of Spectra: 5
Number of Replicates (out of 10): 3
Best Match Score: 83.137
Best Match Posterior Error Probability: 0.0016437
Best Match Spectrum:

Scan number 6498 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac4
Method ITMS; CID **Genenames** TUFT1



Protein Group ID: 782
Protein Accession Numbers: Q7Z434; F5H6C8
Gene Names: MAVS
Peptide Sequence: GPVSPSVSFQPLAR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 107.99
Best Match Posterior Error Probability: 0.00017449
Best Match Spectrum:

Scan number 4247 **Raw file** Prt-OGE-Batch3-Mock-Frac9
Method ITMS; CID **Genenames** MAVS



Protein Group ID: 786

Protein Accession Numbers: F5H7K4; J3KN69; Q6PIU2-2; Q6PIU2; Q6PIU2-3

Gene Names: NCEH1

Peptide Sequence: SAPLIADQAVLQLLPK

Total Number of Spectra: 4

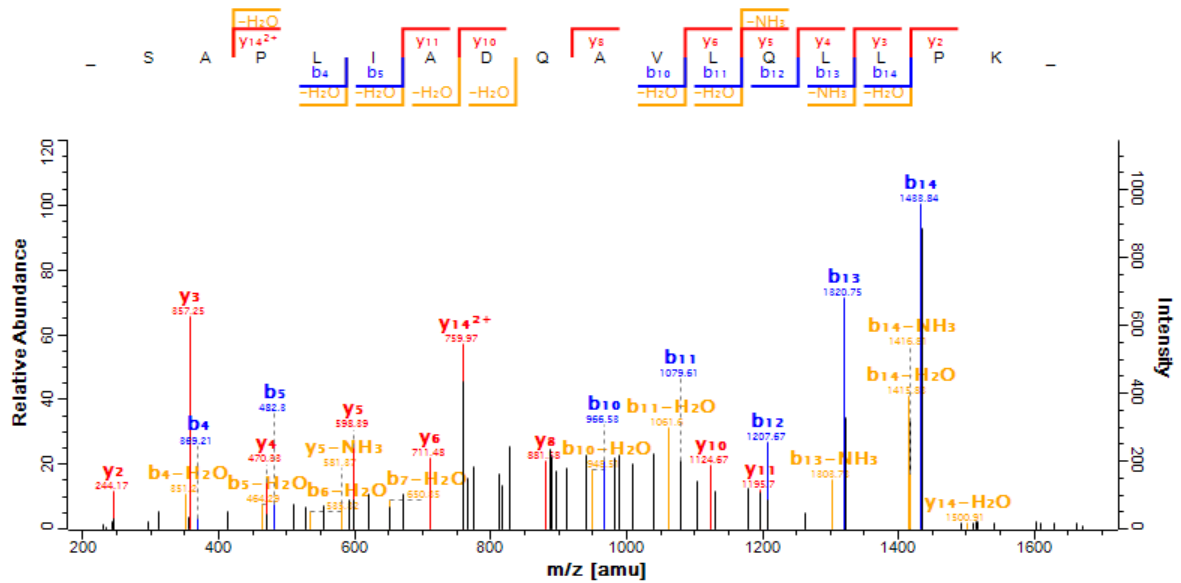
Number of Replicates (out of 10): 3

Best Match Score: 116.58

Best Match Posterior Error Probability: 0.00012272

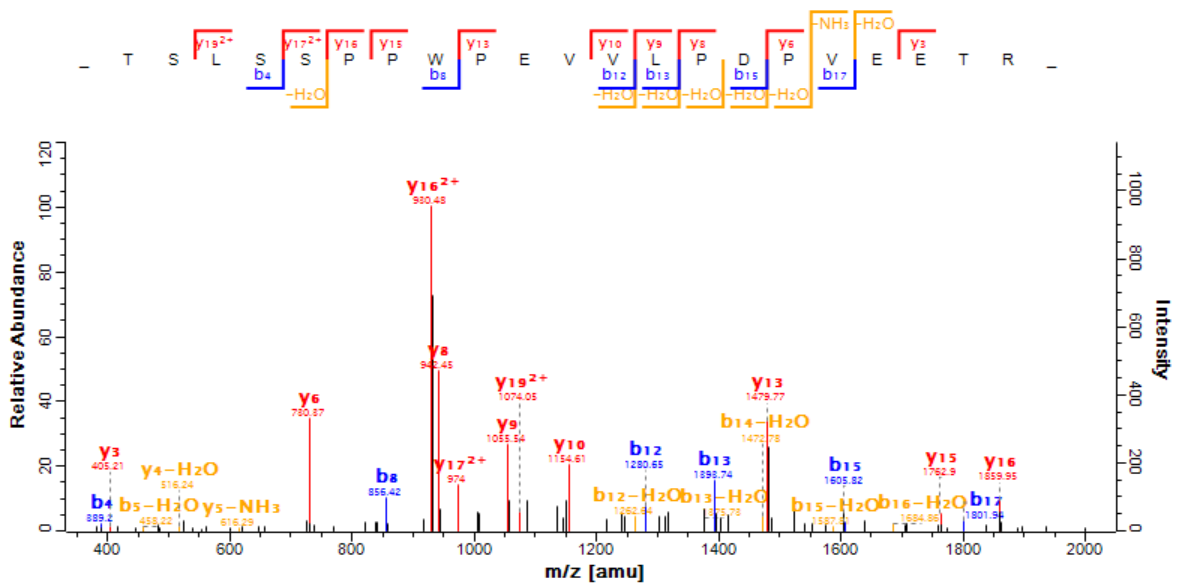
Best Match Spectrum:

Scan number 6567 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac15
Method ITMS; CID **Genenames** NCEH1



Protein Group ID: 787
Protein Accession Numbers: Q7Z2W9; F5H7V8
Gene Names: MRPL21
Peptide Sequence: TSLSSPPWPEVVLDPVEETR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 73.783
Best Match Posterior Error Probability: 0.00081878
Best Match Spectrum:

Scan number 6123 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac17
Method ITMS; CID **Genenames** MRPL21



Protein Group ID: 789

Protein Accession Numbers: F5H8A7; H0YN33; Q9BW66

Gene Names: CINP

Peptide Sequence: ELAHTGDPDLTSLYSMLWHLHQPVEESD^{-H₂O}SR

Total Number of Spectra: 1

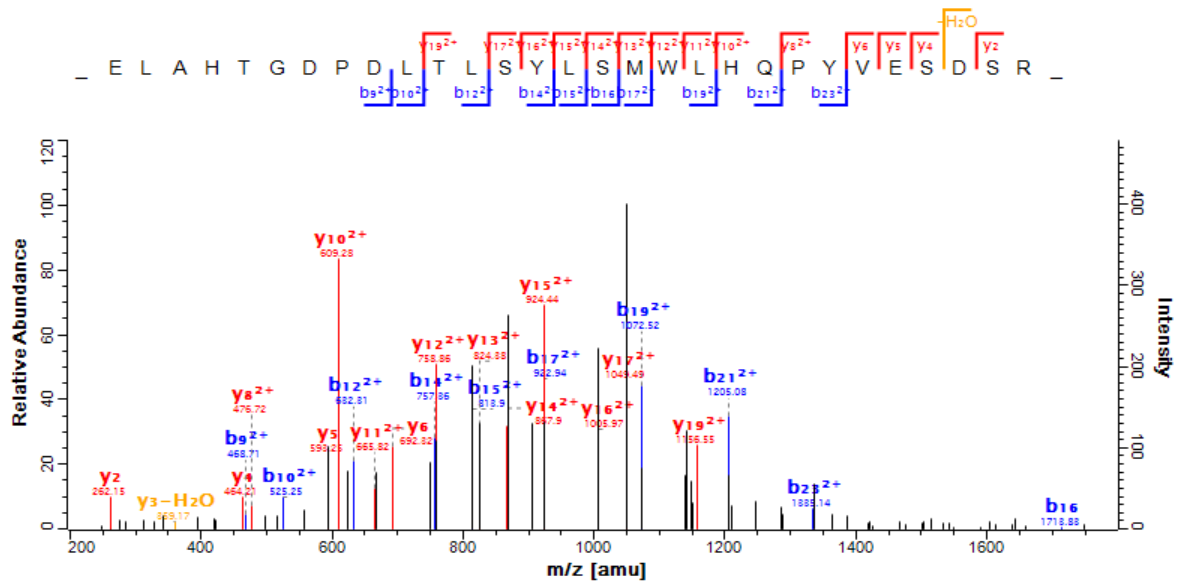
Number of Replicates (out of 10): 1

Best Match Score: 83.602

Best Match Posterior Error Probability: 2.44E-07

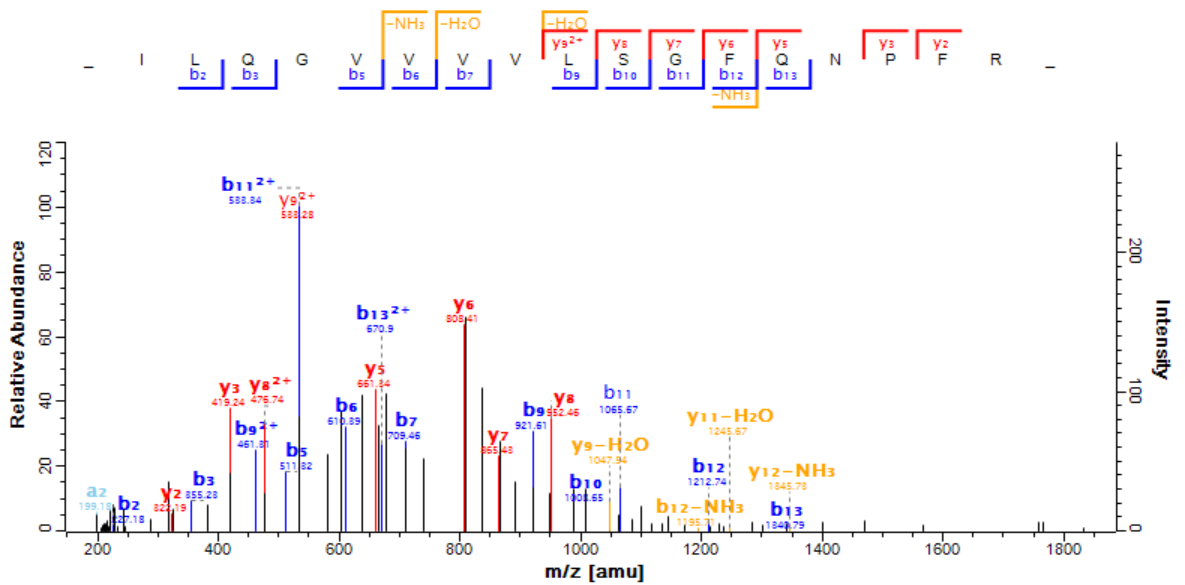
Best Match Spectrum:

Scan number 6669 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac13
Method ITMS; CID **Genenames** CINP



Protein Group ID: 790
Protein Accession Numbers: P18887; F5H8D7
Gene Names: XRCC1
Peptide Sequence: ILQGVVVVLSGFQNPFR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 99.747
Best Match Posterior Error Probability: 0.00026038
Best Match Spectrum:

Scan number 7112 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac17
Method ITMS; CID **Genenames** XRCC1



Protein Group ID: 791

Protein Accession Numbers: Q9UBL3; Q9UBL3-3; F5H8F7; H0YBF6; H0YAQ0

Gene Names: ASH2L

Peptide Sequence: DIFEGVYFPAISLYK

Total Number of Spectra: 2

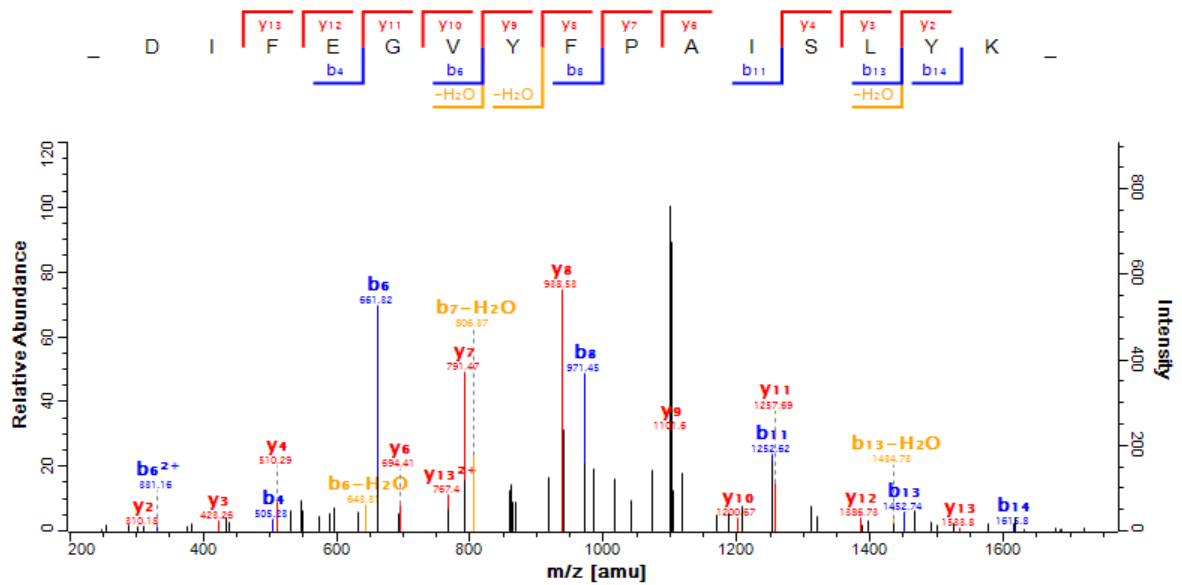
Number of Replicates (out of 10): 2

Best Match Score: 96.247

Best Match Posterior Error Probability: 0.00017502

Best Match Spectrum:

Scan number	6809	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac9
Method	ITMS; CID	Genenames	ASH2L



Protein Group ID: 794

Protein Accession Numbers: Q9H0Z9; Q9BX46; F6VZ39; Q9H0Z9-2; H0YA61

Gene Names: RBM38;RBM24

Peptide Sequence: GYGFVTMADR

Total Number of Spectra: 2

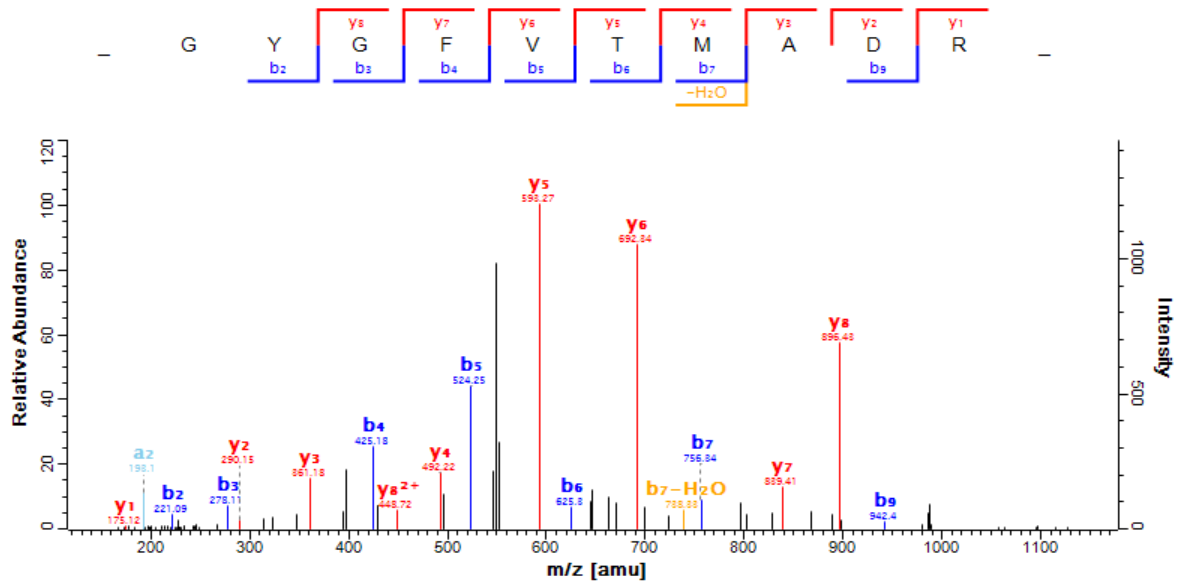
Number of Replicates (out of 10): 2

Best Match Score: 103.22

Best Match Posterior Error Probability: 0.00048312

Best Match Spectrum:

Scan number	3689	Raw file	Prt-OGE-Batch2-Mock-Frac18
Method	ITMS; CID	Genenames	RBM38;RBM24



Protein Group ID: 798

Protein Accession Numbers: Q5HYK3; F8V VX6; F8V VV7; F8V P53

Gene Names: COQ5

Peptide Sequence: FLNYVQSQHQR

Total Number of Spectra: 1

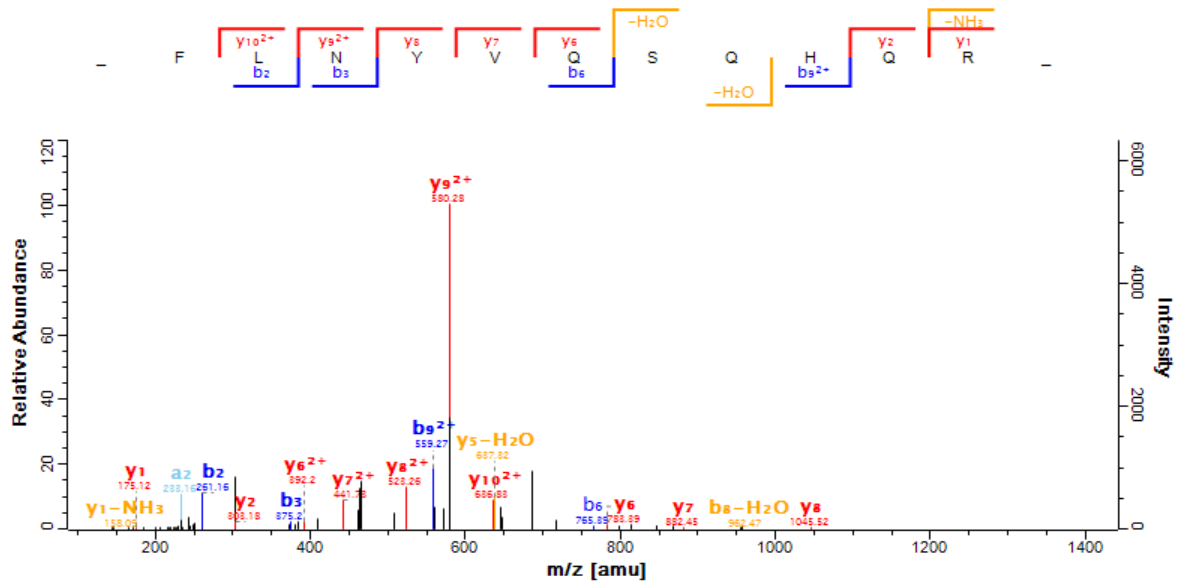
Number of Replicates (out of 10): 1

Best Match Score: 94.692

Best Match Posterior Error Probability: 0.00052508

Best Match Spectrum:

Scan number 1662 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac12
Method ITMS; CID **Genenames** COQ5



Protein Group ID: 799

Protein Accession Numbers: P78537; F8VP73; P78537-2; F8W036

Gene Names: BLOC1S1

Peptide Sequence: EAITAATCLTEALVDHLNVGVAQAYMNR

Total Number of Spectra: 1

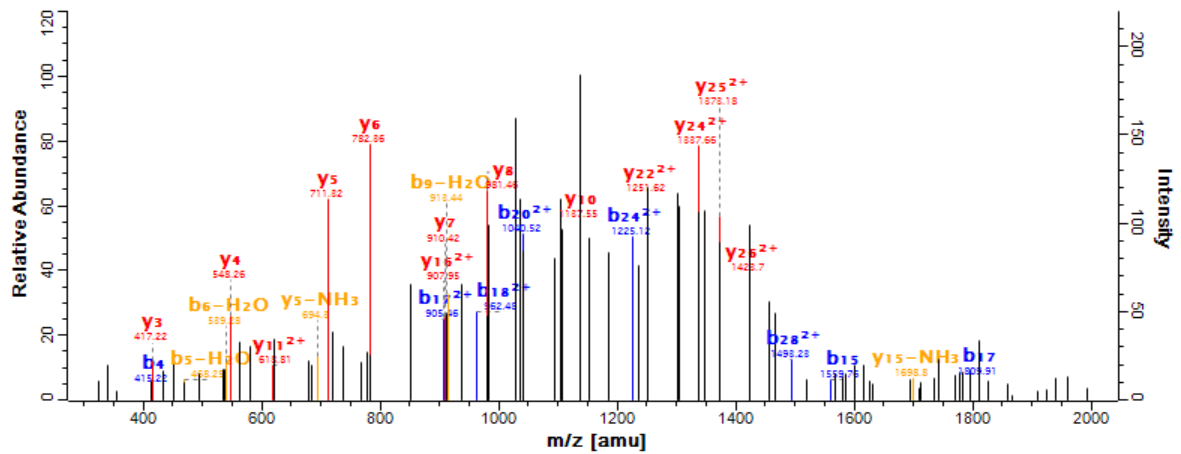
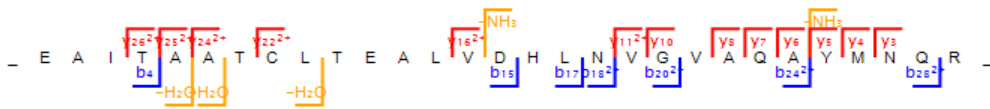
Number of Replicates (out of 10): 1

Best Match Score: 61.04

Best Match Posterior Error Probability: 0.00014064

Best Match Spectrum:

Scan number	7186	Raw file	20100914-KD-Batch4-Prt-OGE-Mock-Frac17
Method	ITMS; CID	Genenames	BLOC1S1



Protein Group ID: 802

Protein Accession Numbers: Q9BSB4; F8VQD9; F8VVA0; H3BMZ4

Gene Names: ATG101;C12orf44

Peptide Sequence: QVEEAMLAVLHTVLLHR

Total Number of Spectra: 4

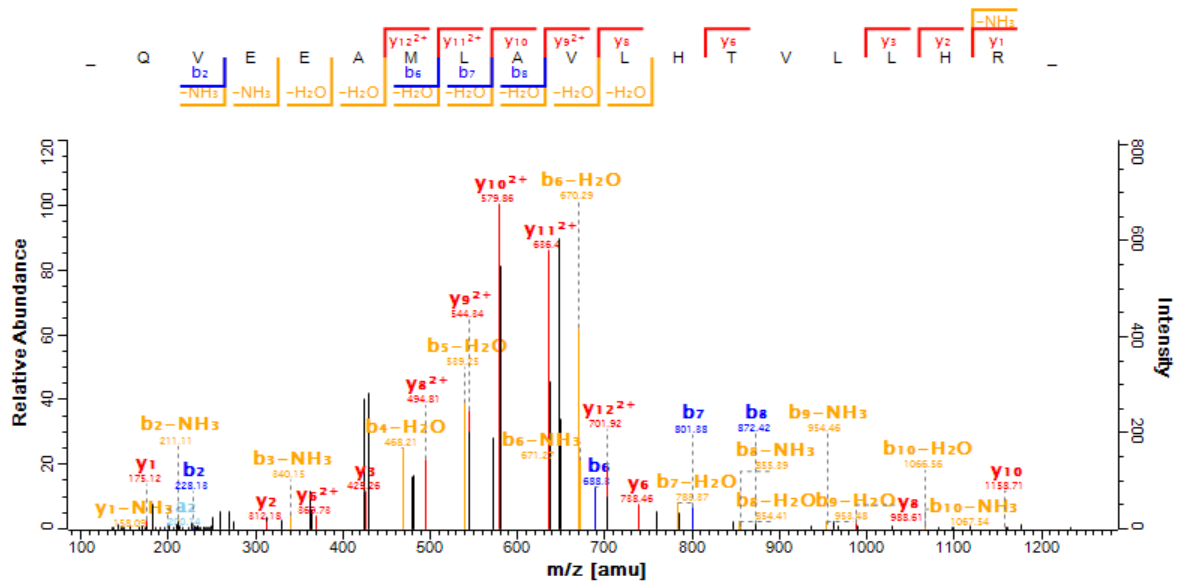
Number of Replicates (out of 10): 4

Best Match Score: 93.237

Best Match Posterior Error Probability: 0.00039566

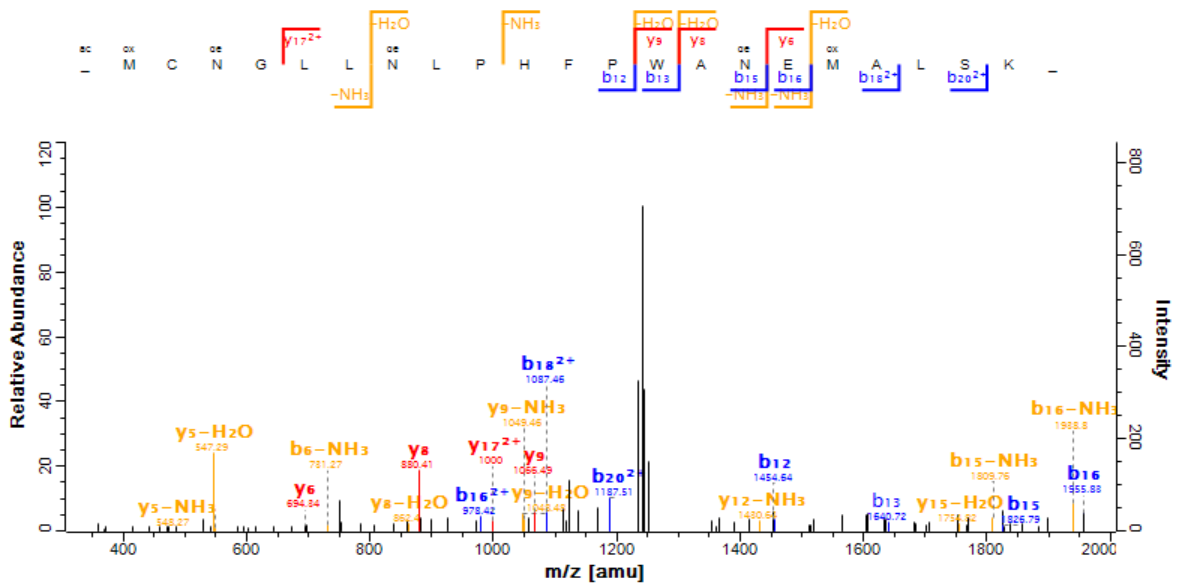
Best Match Spectrum:

Scan number	6605	Raw file	OGE-Mock-Frac10
Method	ITMS; CID	Genenames	ATG101;C12orf44



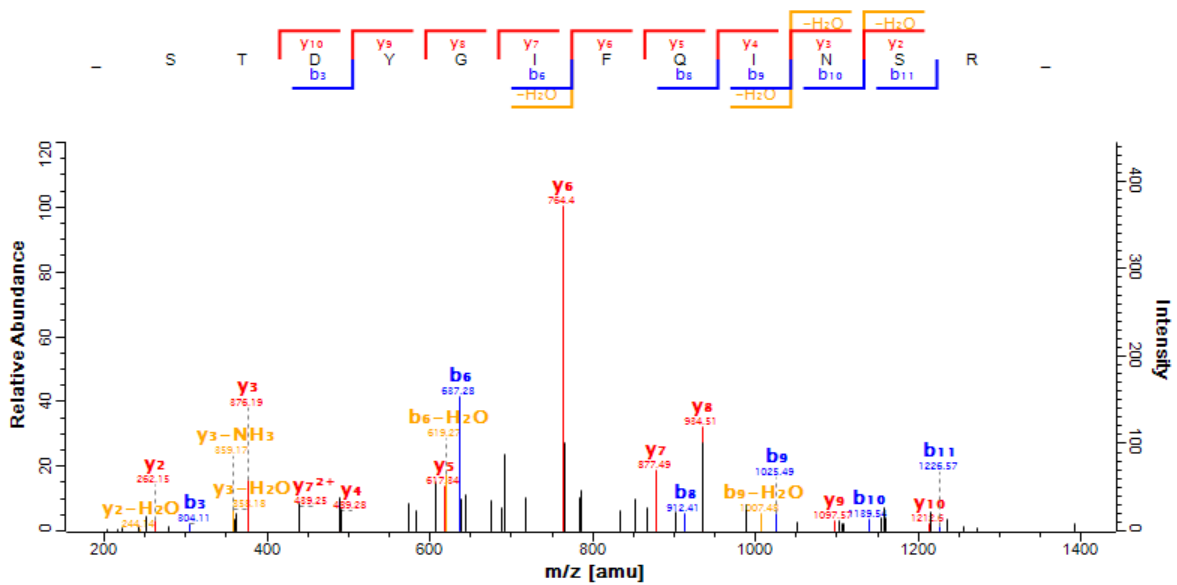
Protein Group ID: 805
Protein Accession Numbers: F8VRQ4
Gene Names: SMARCD1
Peptide Sequence: MCNGLLNLPHPWANEMALSK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 49.708
Best Match Posterior Error Probability: 0.00083528
Best Match Spectrum:

Scan number 4893 **Raw file** Prt-OGE-Batch3--Mock-Frac1 8
Method ITMS; CID **Genenames** SMARCD1



Protein Group ID: 808
Protein Accession Numbers: P61626; F8VV32
Gene Names: LYZ
Peptide Sequence: STDYGIFQINSR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 106.32
Best Match Posterior Error Probability: 0.00023858
Best Match Spectrum:

Scan number 2831 **Raw file** Prt-OGE-Batch2-WT-Frac20
Method ITMS; CID **Genenames** LYZ



Protein Group ID: 812

Protein Accession Numbers: P51687; F8VWV9

Gene Names: SUOX

Peptide Sequence: LMLAAGGLPEPFWALYAVHNQSHVR

Total Number of Spectra: 1

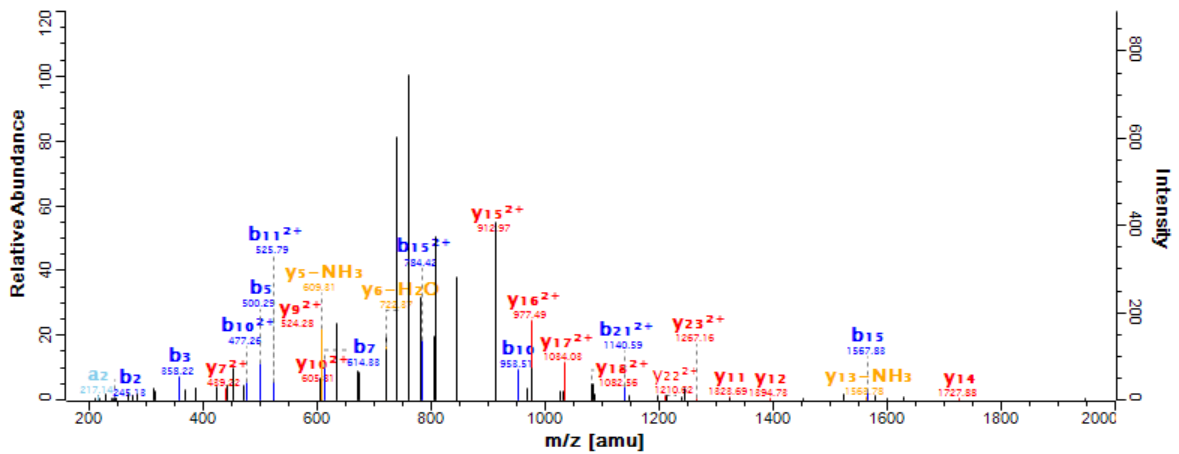
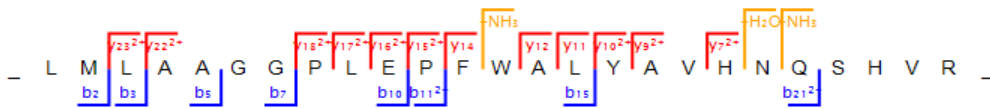
Number of Replicates (out of 10): 1

Best Match Score: 75.358

Best Match Posterior Error Probability: 3.36E-05

Best Match Spectrum:

Scan number	7040	Raw file	Prt-OGE-Batch3-Mock-Frac8
Method	ITMS; CID	Genenames	SUOX



Protein Group ID: 816

Protein Accession Numbers: Q12800; Q12800-4; Q12800-3; Q12800-2; F8VX55; F8VWL0

Gene Names: TFCP2

Peptide Sequence: ILDIDIPMSIVGIIIDPR

Total Number of Spectra: 4

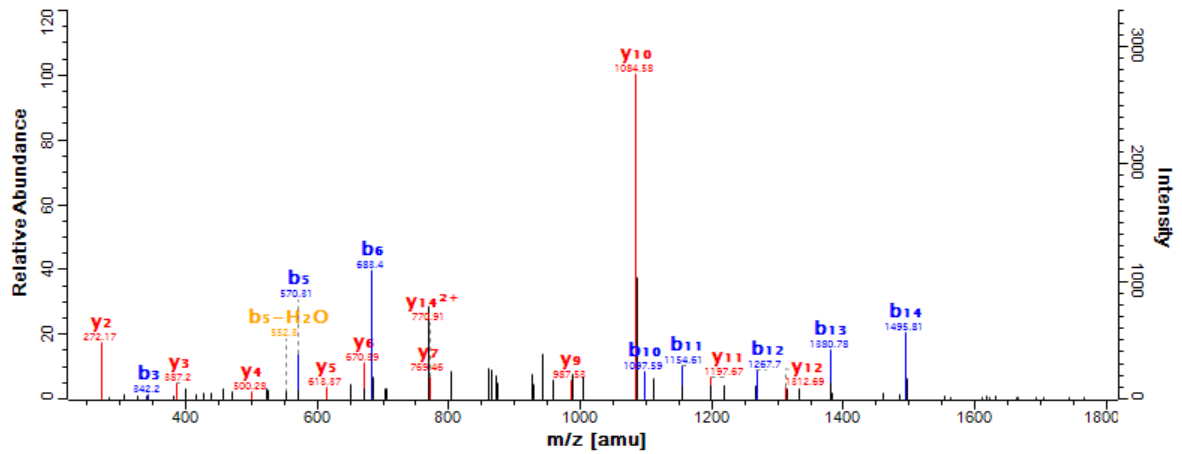
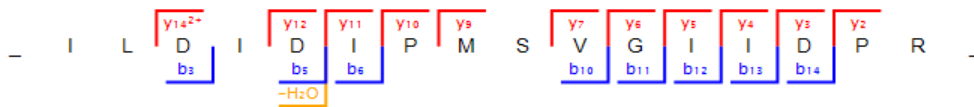
Number of Replicates (out of 10): 4

Best Match Score: 89.358

Best Match Posterior Error Probability: 0.00043624

Best Match Spectrum:

Scan number	7183	Raw file	Prt-OGE-Batch3-Mock-Frac8
Method	ITMS: CID	Genenames	TFCP2



Protein Group ID: 817

Protein Accession Numbers: Q14161; Q14161-3; Q14161-5; Q14161-4; F8VXI9; Q14161-8; F8WAK2; Q14161-10; Q14161-6; Q14161-7; Q14161-11; Q14161-2; F8W822

Gene Names: GIT2

Peptide Sequence: FNAHEFATLVIDILSDAK

Total Number of Spectra: 9

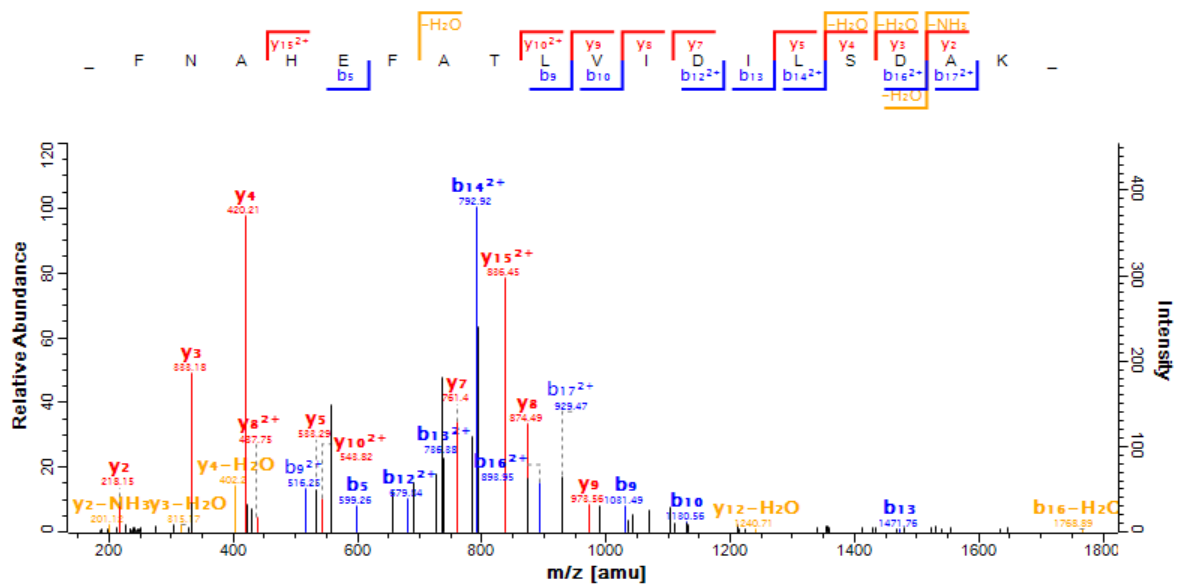
Number of Replicates (out of 10): 5

Best Match Score: 97.291

Best Match Posterior Error Probability: 0.00027768

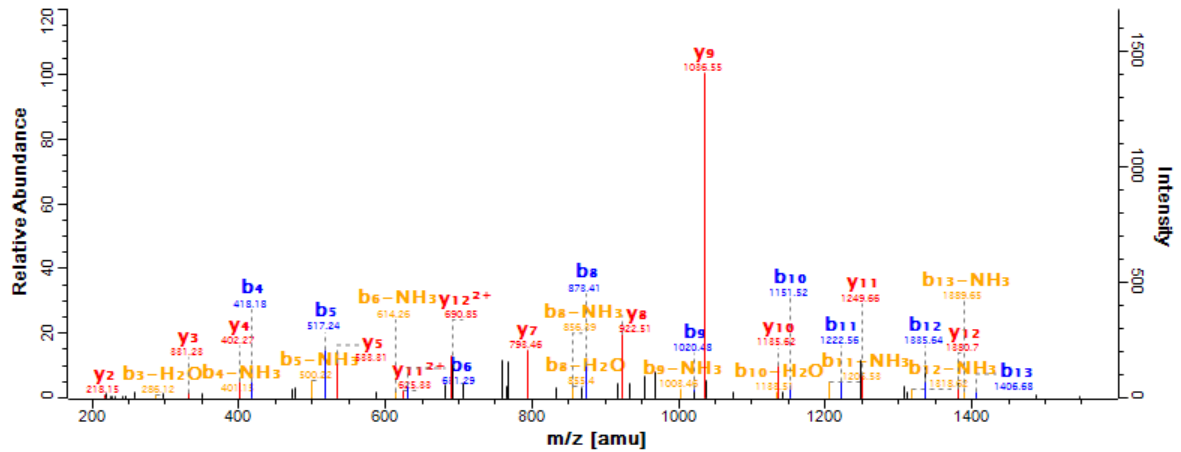
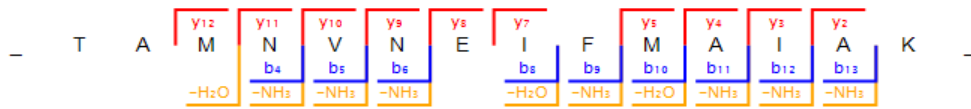
Best Match Spectrum:

Scan number	7335	Raw file	OGE-WT-Frac18
Method	ITMS: CID	Genenames	GIT2



Protein Group ID: 823
Protein Accession Numbers: F8W1H5; P51148
Gene Names: RAB5C
Peptide Sequence: TAMNVNEIFMAIAK
Total Number of Spectra: 30
Number of Replicates (out of 10): 9
Best Match Score: 194.48
Best Match Posterior Error Probability: 1.17E-21
Best Match Spectrum:

Scan number 5470 **Raw file** Prt-OGE-Batch2-WT-Frac12
Method ITMS; CID **Genenames** RAB5C



Protein Group ID: 825

Protein Accession Numbers: Q8WYA0; Q8WYA0-3; F8W1J4

Gene Names: IFT81

Peptide Sequence: NYNLITFDSLEPMQLQLVLSLVLAIEDPK

Total Number of Spectra: 1

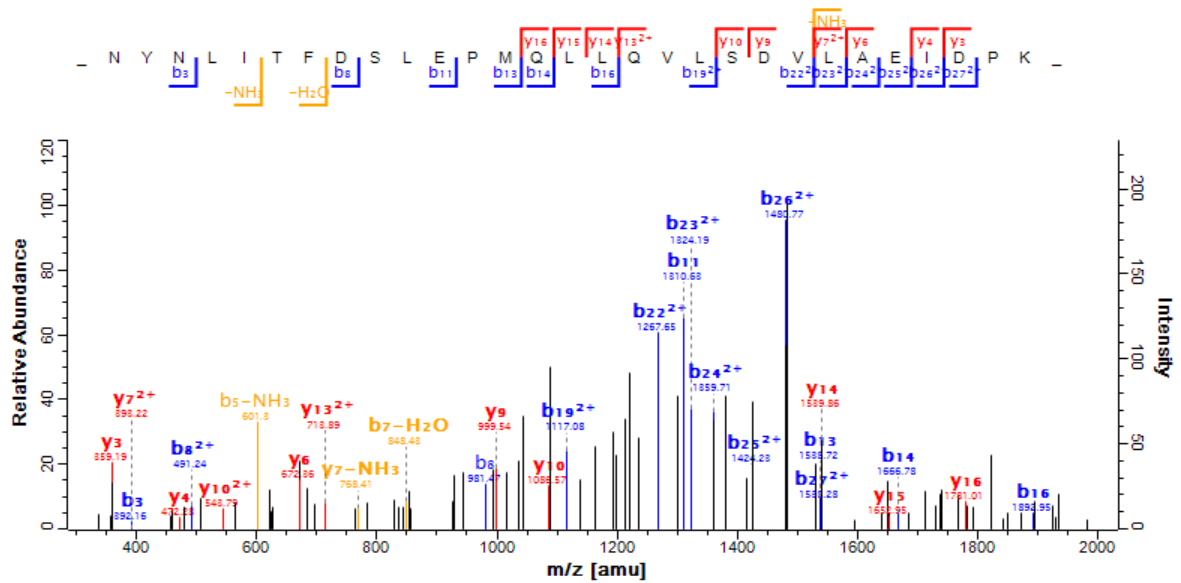
Number of Replicates (out of 10): 1

Best Match Score: 71.794

Best Match Posterior Error Probability: 8.52E-06

Best Match Spectrum:

Scan number 8889 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac21
Method ITMS; CID **Genenames** IFT81



Protein Group ID: 830

Protein Accession Numbers: Q9NXR7-1; Q9NXR7; Q9NXR7-3; Q9NXR7-4; F8W733

Gene Names: BRE

Peptide Sequence: LPVDFSNIPYTK

Total Number of Spectra: 3

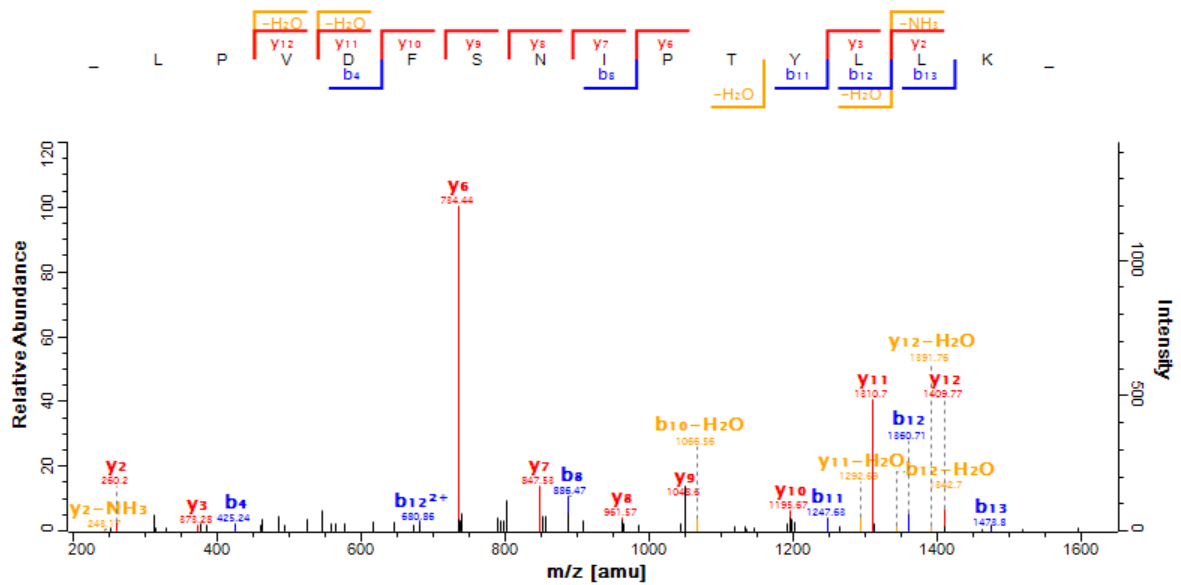
Number of Replicates (out of 10): 3

Best Match Score: 109.84

Best Match Posterior Error Probability: 0.00015476

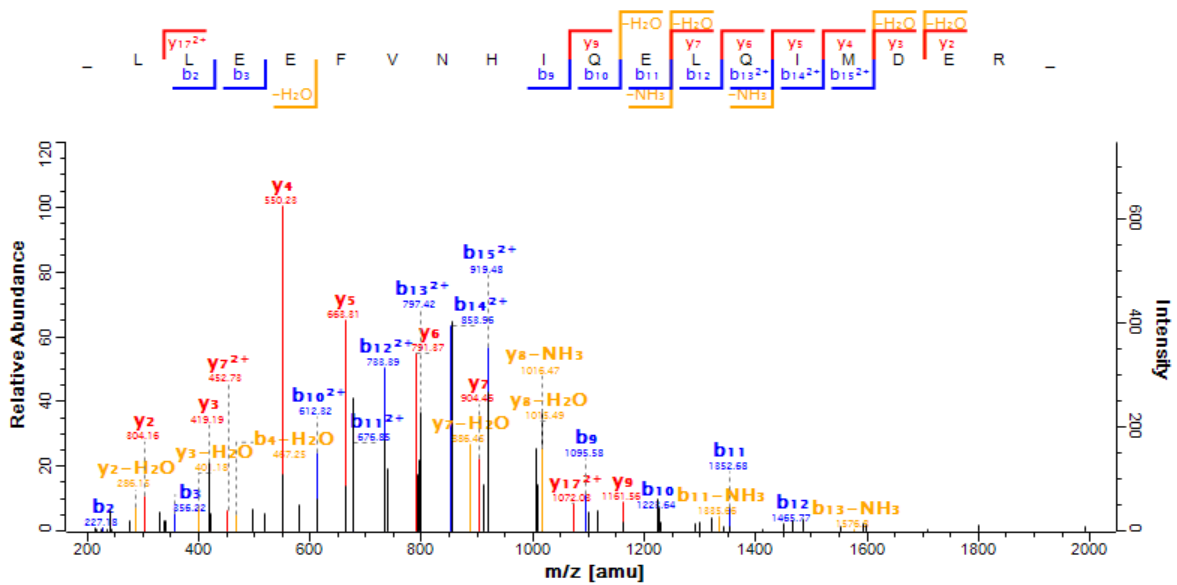
Best Match Spectrum:

Scan number 6786 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac10
Method ITMS; CID **Genenames** BRE



Protein Group ID: 837
Protein Accession Numbers: O00471; F8W9B8
Gene Names: EXOC5
Peptide Sequence: LLEEFVNHIQELQIMDER
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 141.55
Best Match Posterior Error Probability: 3.05E-07
Best Match Spectrum:

Scan number 5197 **Raw file** Prt-OGE-Batch2-WT-Frac15
Method ITMS; CID **Genenames** EXOC5



Protein Group ID: 838

Protein Accession Numbers: O94763; O94763-3; F8W9T0; O94763-2

Gene Names: URI1

Peptide Sequence: LLPLSVTPEAFSGTVIEK

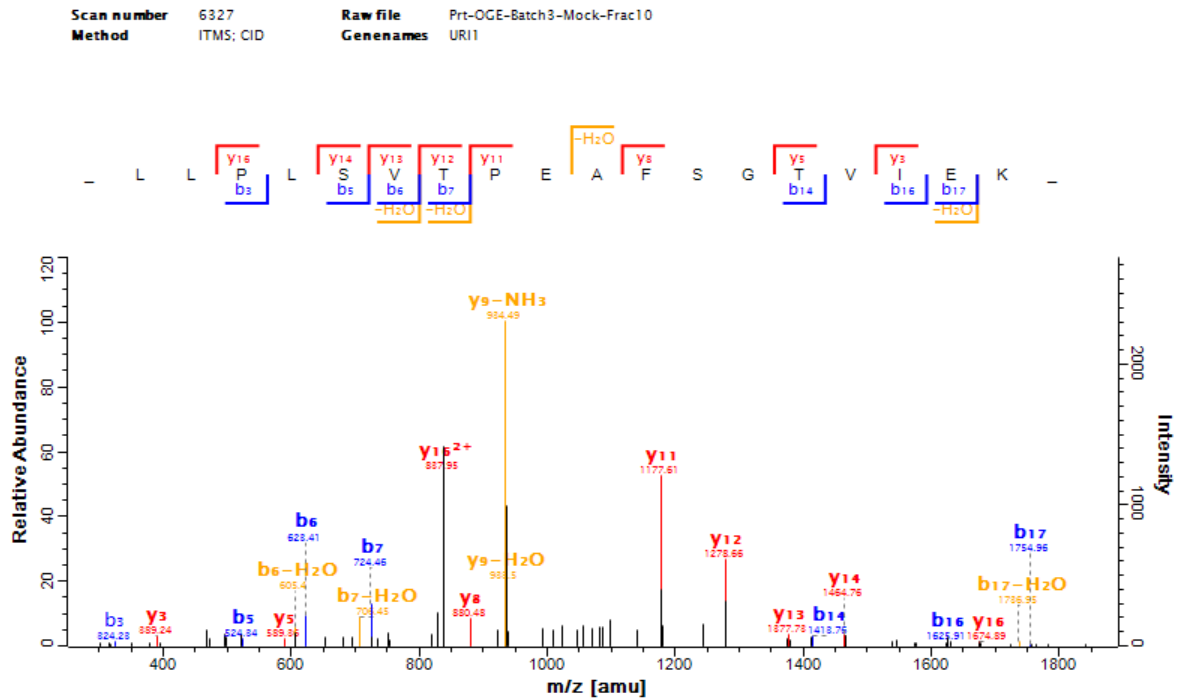
Total Number of Spectra: 1

Number of Replicates (out of 10): 1

Best Match Score: 81.317

Best Match Posterior Error Probability: 0.0010712

Best Match Spectrum:



Protein Group ID: 839

Protein Accession Numbers: O95456; O95456-2; F8WBH7

Gene Names: PSMG1

Peptide Sequence: AATFFGEVVK

Total Number of Spectra: 2

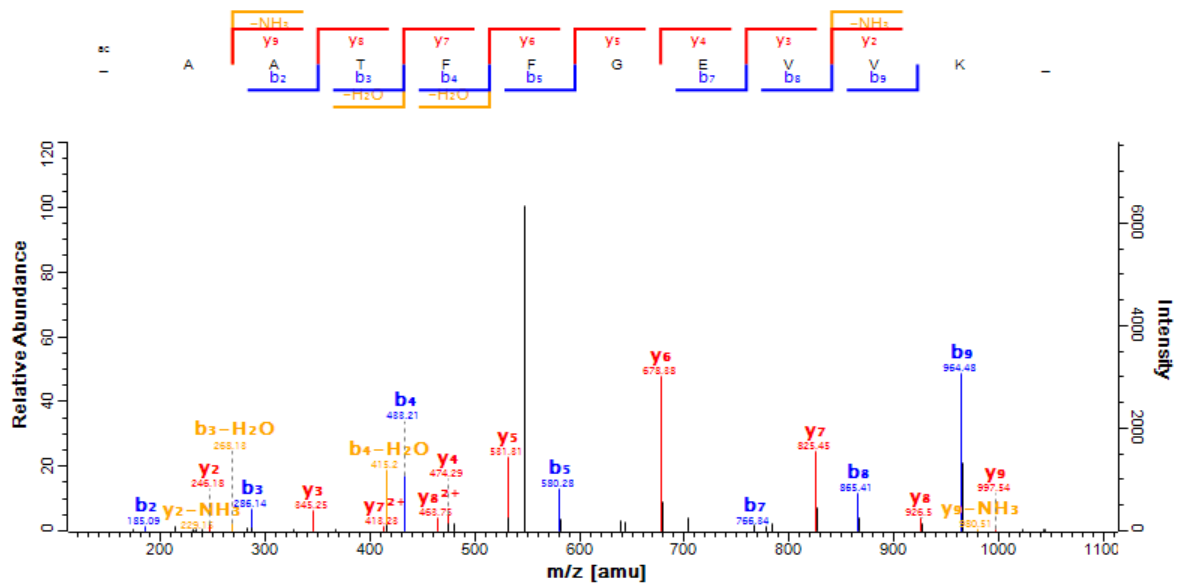
Number of Replicates (out of 10): 2

Best Match Score: 143.96

Best Match Posterior Error Probability: 5.38E-05

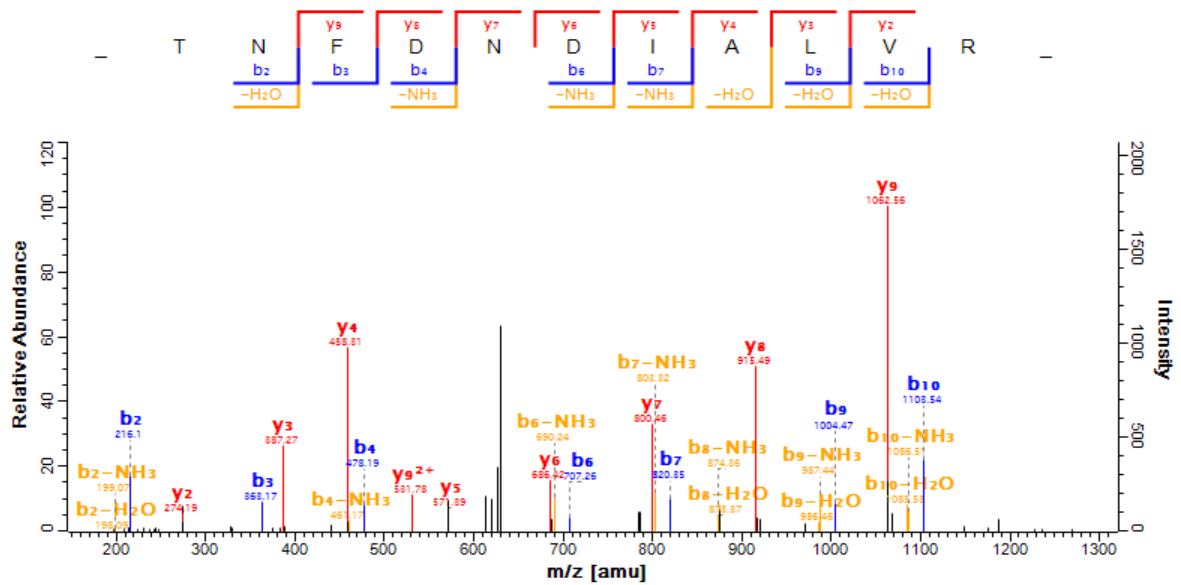
Best Match Spectrum:

Scan number 6201 **Raw file** Prt-OGE-Batch2-Mock-Frac15
Method ITMS; CID **Genenames** PSMG1



Protein Group ID: 844
Protein Accession Numbers: P09871; F8WCZ6
Gene Names: C1S
Peptide Sequence: TNFDNDIALVR
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 151.26
Best Match Posterior Error Probability: 1.37E-05
Best Match Spectrum:

Scan number 3253 **Raw file** Prt-OGE-Batch3-WT-Frac5
Method ITMS; CID **Genenames** C1S



Protein Group ID: 846

Protein Accession Numbers: Q9Y2H0; Q9Y2H0-1; Q9Y2H0-3; F8WF49

Gene Names: DLGAP4

Peptide Sequence: PTAQDLAGFWDLLQLSIEDISMK

Total Number of Spectra: 3

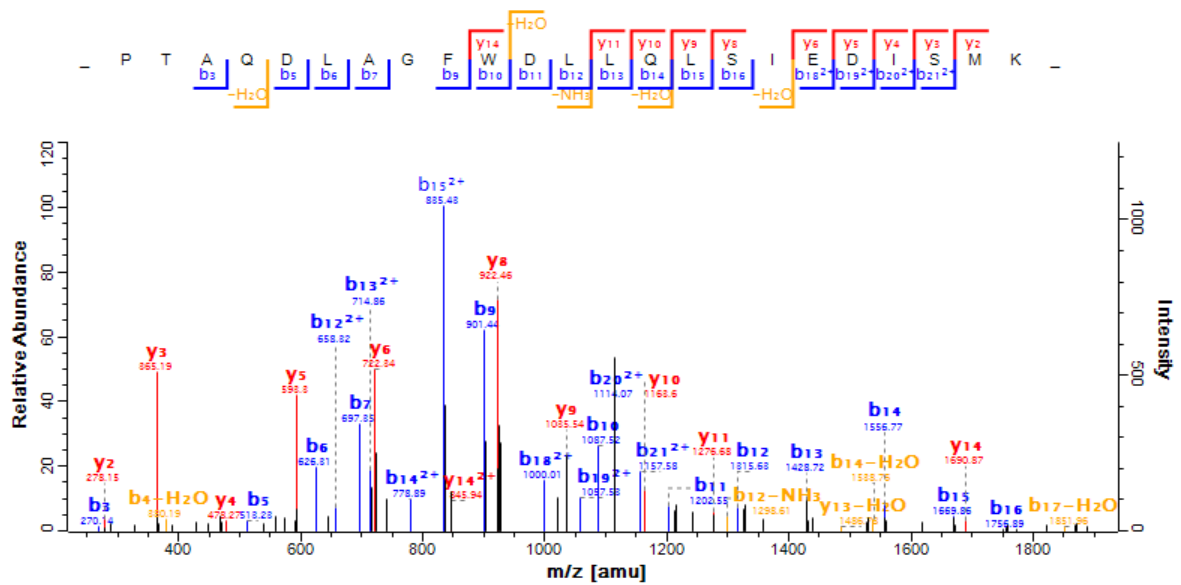
Number of Replicates (out of 10): 2

Best Match Score: 127.96

Best Match Posterior Error Probability: 1.25E-13

Best Match Spectrum:

Scan number 9700 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac10
Method ITMS; CID **Genenames** DLGAP4



Protein Group ID: 848

Protein Accession Numbers: Q9UHY8-2; Q9UHY8; G3V0F5

Gene Names: FEZ2

Peptide Sequence: AADGDWQDFYEFQEPAR

Total Number of Spectra: 2

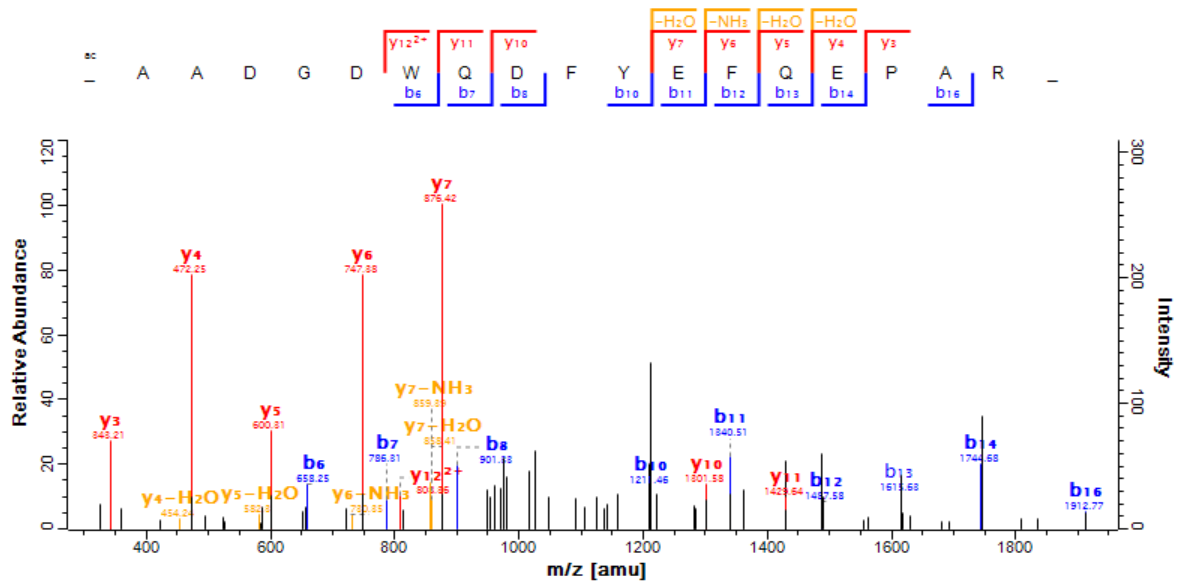
Number of Replicates (out of 10): 2

Best Match Score: 88.385

Best Match Posterior Error Probability: 0.00047933

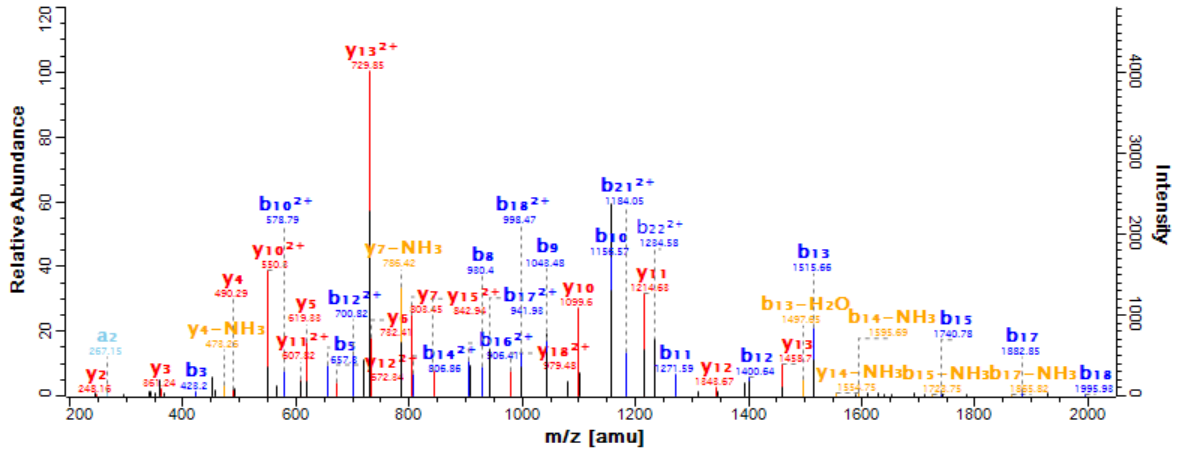
Best Match Spectrum:

Scan number 4022 **Raw file** Prt-OGE-Batch3-WT-Frac2
Method ITMS; CID **Genenames** FEZ2



Protein Group ID: 852
Protein Accession Numbers: G3V1B1
Gene Names: SUGT1P3
Peptide Sequence: FFQSFSDALIDQDPQAALEELTK
Total Number of Spectra: 33
Number of Replicates (out of 10): 10
Best Match Score: 208.92
Best Match Posterior Error Probability: 3.89E-67
Best Match Spectrum:

Scan number 7050 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac7
Method ITMS; CID **Genenames** SUGT1P3



Protein Group ID: 857

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

Gene Names: CHURC1;CHURC1-FNTB

Peptide Sequence: AEDTISILPDDPR

Total Number of Spectra: 9

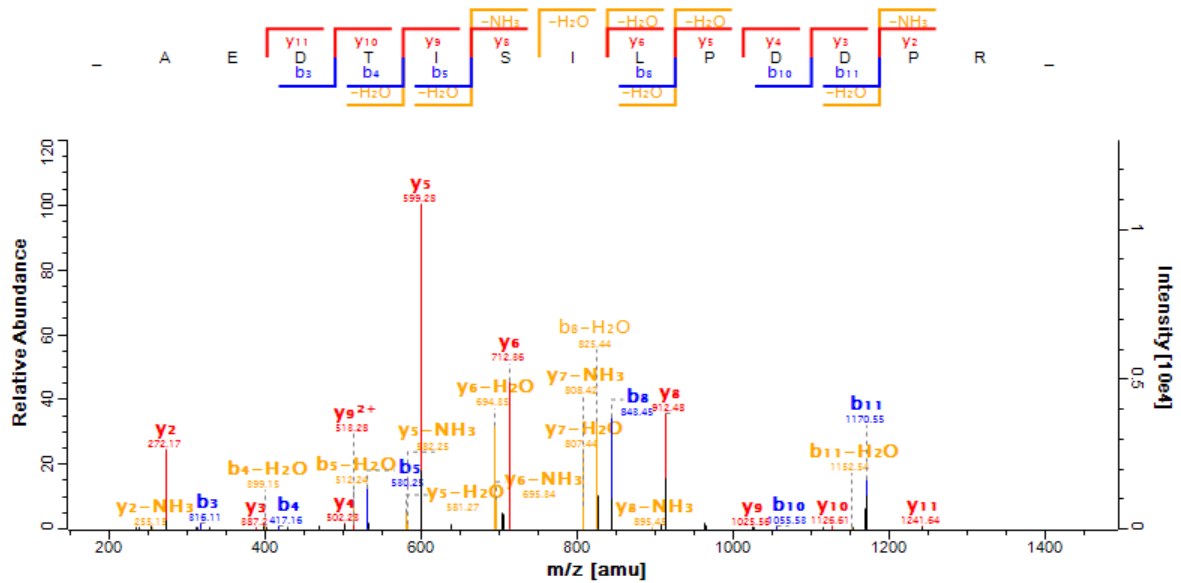
Number of Replicates (out of 10): 7

Best Match Score: 173.19

Best Match Posterior Error Probability: 1.38E-10

Best Match Spectrum:

Scan number	4241	Raw file	OGE-Mock-Frac4
Method	ITMS; CID	Genenames	CHURC1;CHURC1-FNTB



Protein Group ID: 859

Protein Accession Numbers: Q9UN36; Q9UN36-3; Q9UN36-2; G3V3N4; Q9UN36-5; Q9UN36-4; G3V4S9; G3V5H8; G3V2I9; G3V5G0; G3V392; G3V5S0; G3V383; G3V5B7; G3V2A6; G3V358; G3V271; G3V4S2; G3V285; G3V3X2; G3V3D5; G3V5V9; G3V3P1; G3V280; G3V5A6; G3V2T2; G3V4T9; G3V237; G3V3P6; G3V3X3; G3V552; G3V596; G3V5G7; G3V2Y3; G3V3C3; G3V2S0; G3V420; G3V5D7; G3V5P9; G3V239; G3V5B5; G3V4X3

Gene Names: NDRG2

Peptide Sequence: AELQEVQITEEKPLLPGQTPEAAK

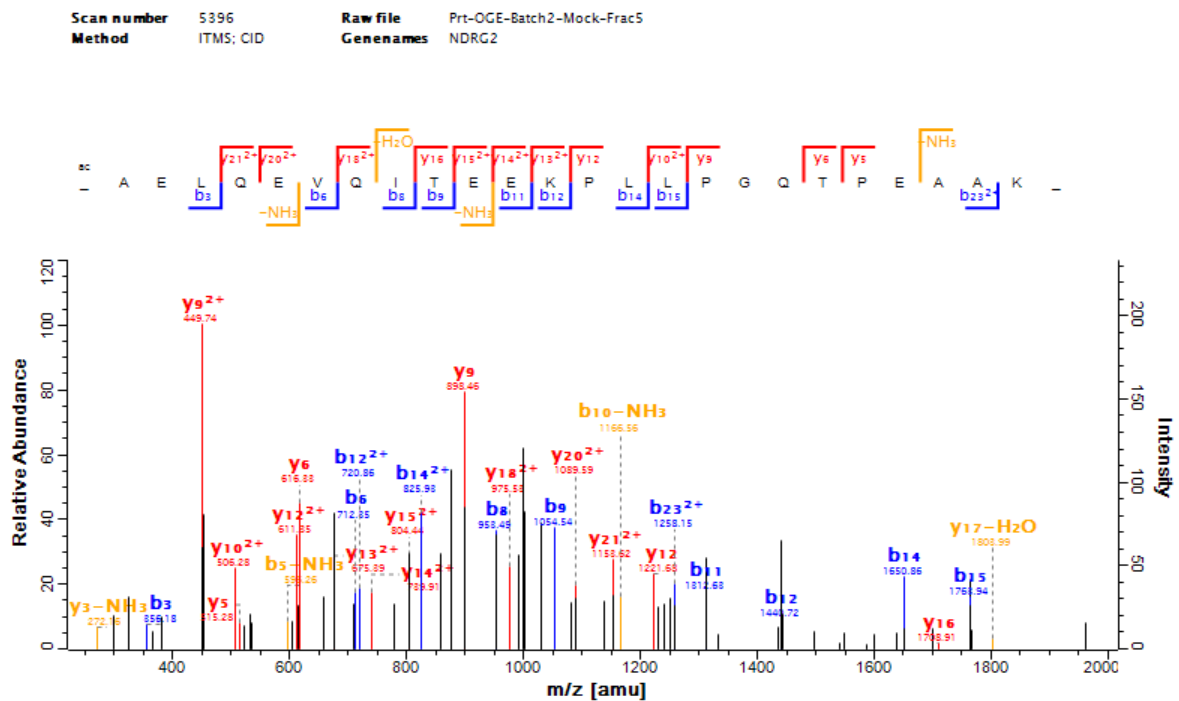
Total Number of Spectra: 2

Number of Replicates (out of 10): 2

Best Match Score: 110.67

Best Match Posterior Error Probability: 5.05E-09

Best Match Spectrum:



Protein Group ID: 863

Protein Accession Numbers: Q8N3R9; Q8N3R9-2; G3V2H1

Gene Names: MPP5

Peptide Sequence: ILEIEDLFSSLK

Total Number of Spectra: 12

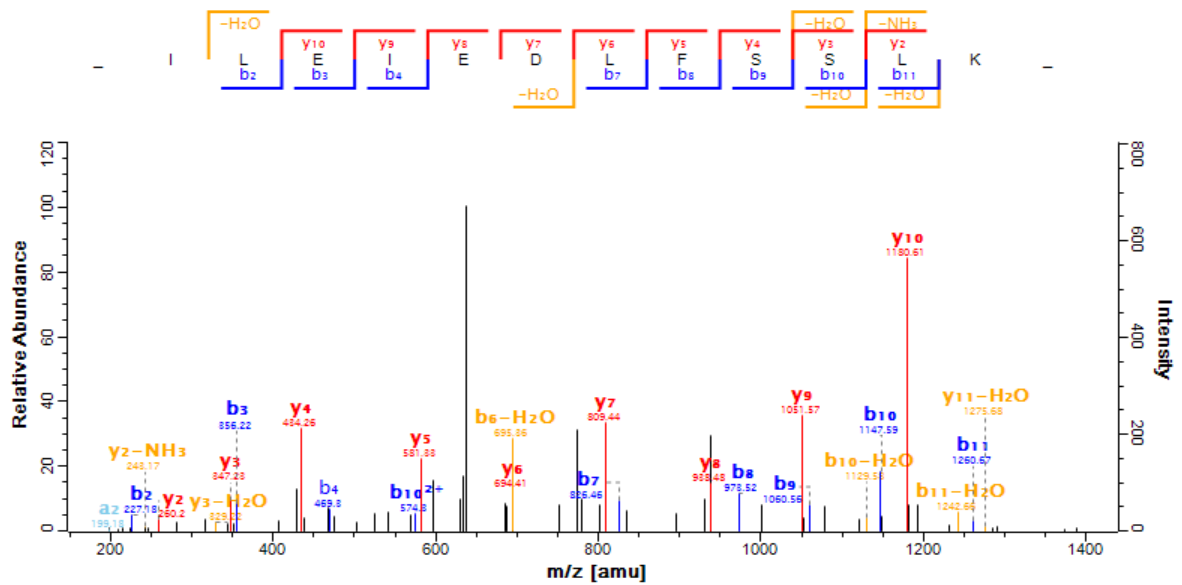
Number of Replicates (out of 10): 9

Best Match Score: 144.57

Best Match Posterior Error Probability: 5.41E-05

Best Match Spectrum:

Scan number 5535 **Raw file** Prt-OGE-Batch3-WT-Frac12
Method ITMS; CID **Genenames** MPP5



Protein Group ID: 868

Protein Accession Numbers: Q96FT9-2; Q96FT9; G3V385; Q96FT9-3; G3V4X2

Gene Names: IFT43

Peptide Sequence: MEDLLDLDEELR

Total Number of Spectra: 4

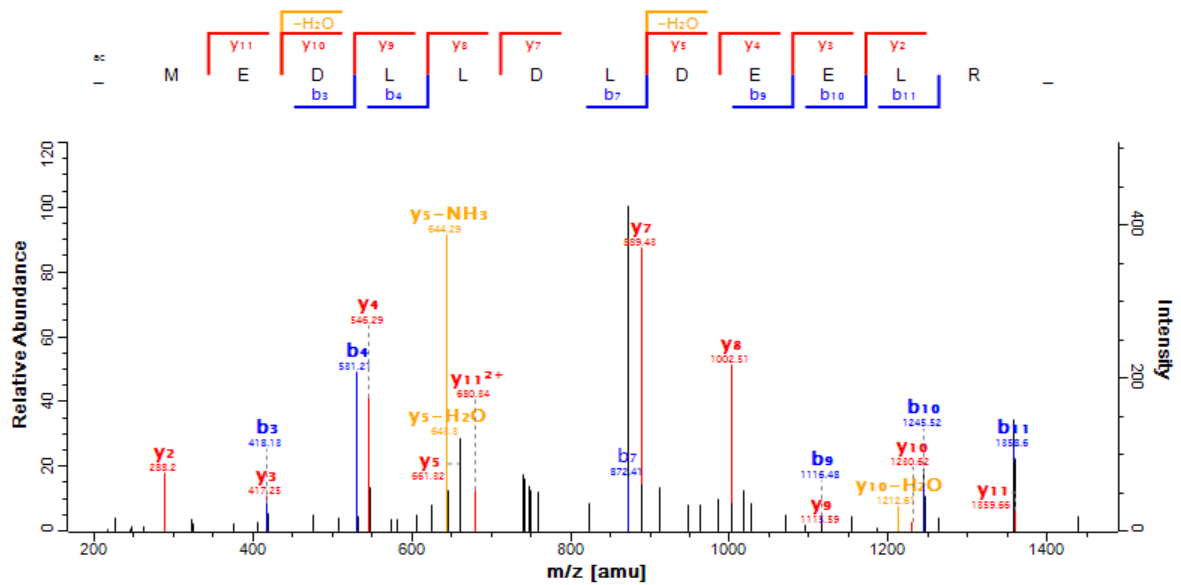
Number of Replicates (out of 10): 4

Best Match Score: 92.295

Best Match Posterior Error Probability: 0.00067979

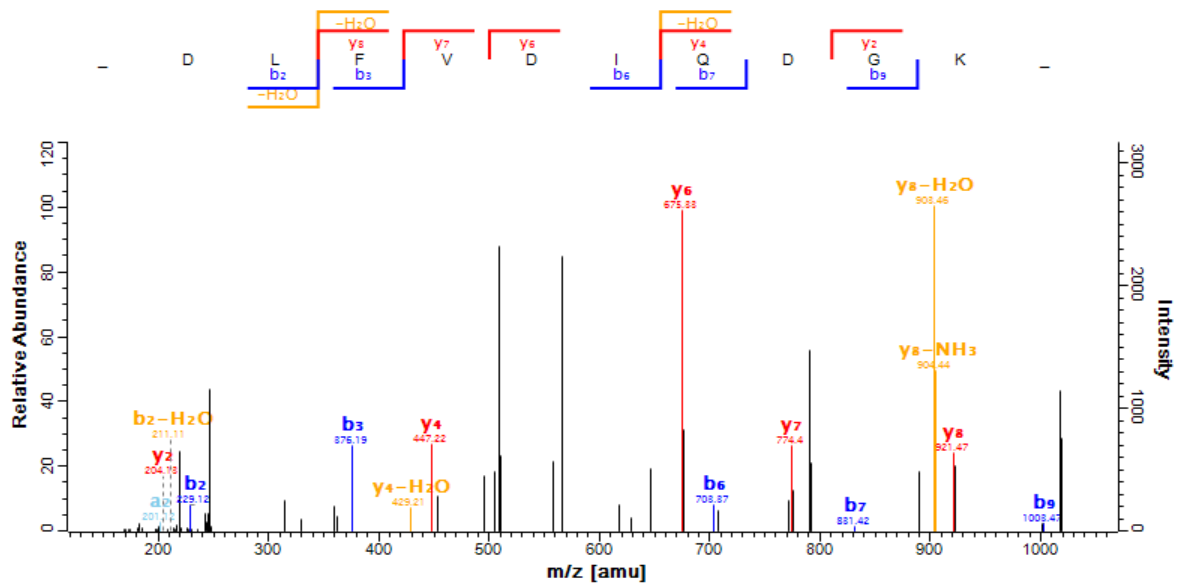
Best Match Spectrum:

Scan number 6704 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac4
Method ITMS; CID **Genenames** IFT43



Protein Group ID: 869
Protein Accession Numbers: Q96JQ2; G3V3D8
Gene Names: CLMN
Peptide Sequence: DLFVDIQDGK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 85.958
Best Match Posterior Error Probability: 0.0015831
Best Match Spectrum:

Scan number 3894 **Raw file** Prt-OGE-Batch3-Mock-Frac7
Method ITMS; CID **Genenames** CLMN



Protein Group ID: 870

Protein Accession Numbers: Q86TS9; Q86TS9-3; Q86TS9-2; G3V3U6

Gene Names: MRPL52

Peptide Sequence: VVLLSQEMDAGLQAWQLR

Total Number of Spectra: 2

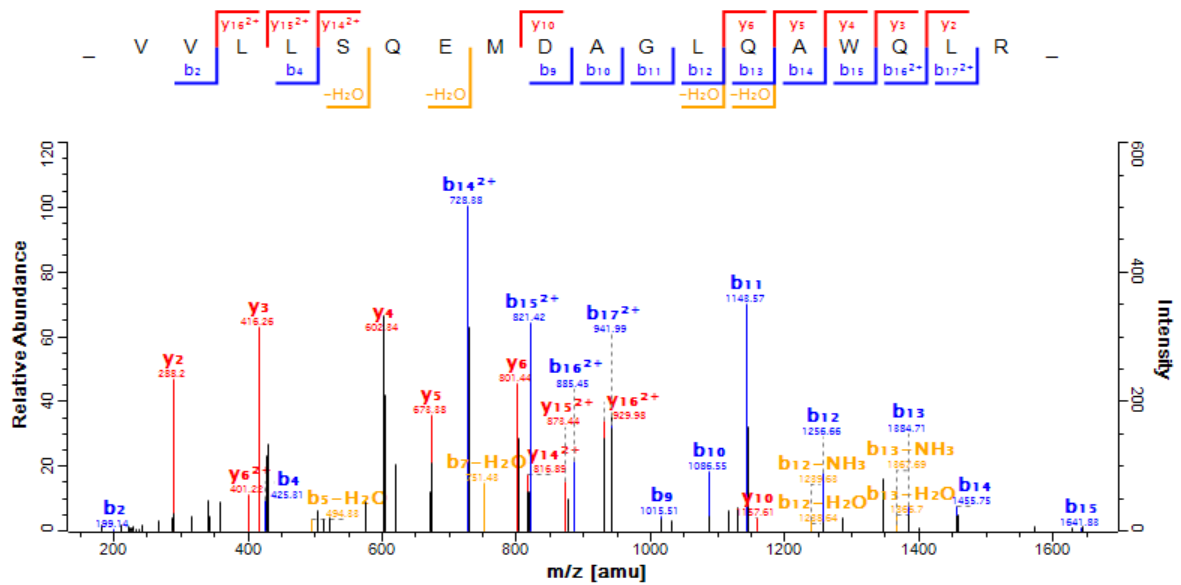
Number of Replicates (out of 10): 2

Best Match Score: 124.2

Best Match Posterior Error Probability: 6.19E-05

Best Match Spectrum:

Scan number 5094 **Raw file** Prt-OGE-Batch2-WT-Frac22
Method ITMS; CID **Genenames** MRPL52



Protein Group ID: 884

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

Gene Names: NFKB1B

Peptide Sequence: TPLGSAMLRPNPILAR

Total Number of Spectra: 4

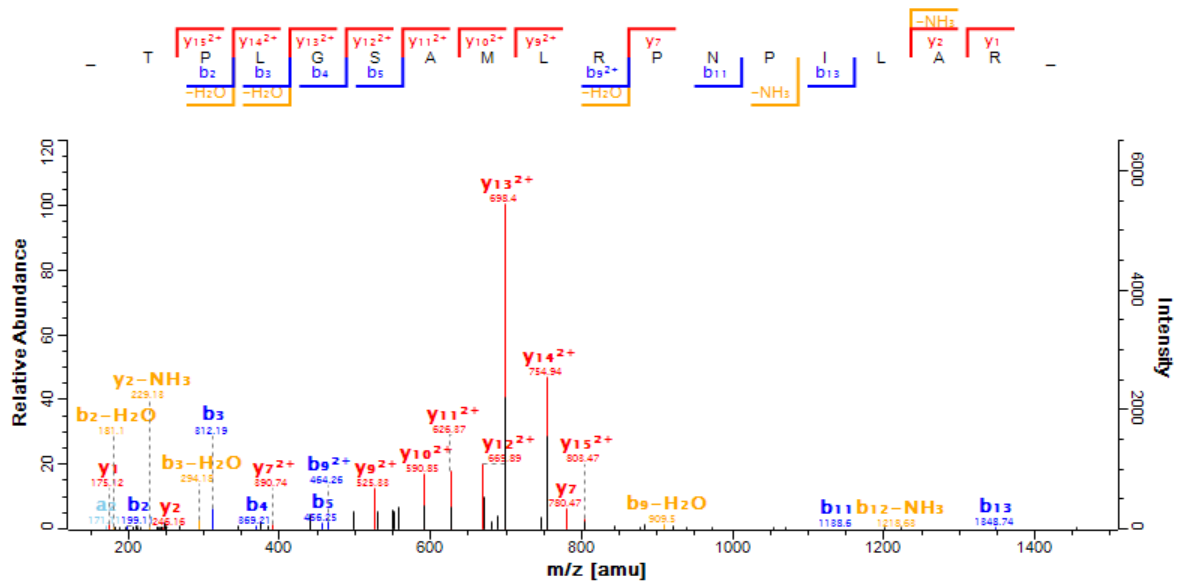
Number of Replicates (out of 10): 4

Best Match Score: 117.93

Best Match Posterior Error Probability: 0.00040876

Best Match Spectrum:

Scan number	3748	Raw file	Prt-OGE-Batch3-WT-Frac5
Method	ITMS; CID	Genenames	NFKB1B



Protein Group ID: 894

Protein Accession Numbers: O14791-2; O14791; O14791-3; G8JL88

Gene Names: APOL1

Peptide Sequence: VTEPISGERS

Total Number of Spectra: 1

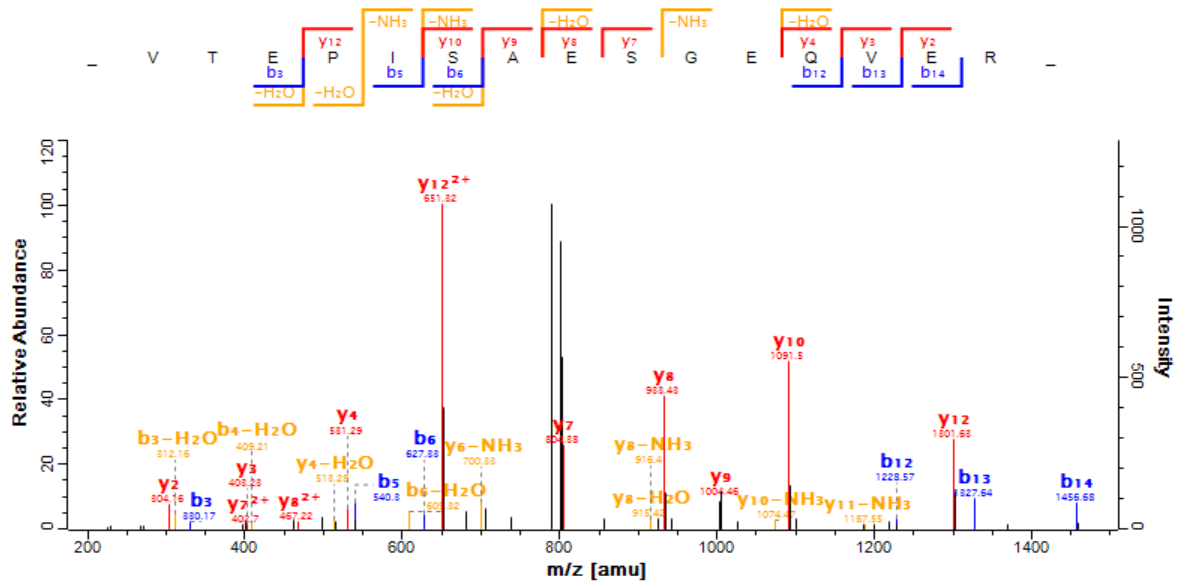
Number of Replicates (out of 10): 1

Best Match Score: 109.1

Best Match Posterior Error Probability: 5.78E-05

Best Match Spectrum:

Scan number	1416	Raw file	Prt-OGE-Batch3-WT-Frac11
Method	ITMS; CID	Genenames	APOL1



Protein Group ID: 897

Protein Accession Numbers: P51157; P51157-2; G8JLC5; Q8WVF3

Gene Names: RAB28

Peptide Sequence: IVVLGDGASGK

Total Number of Spectra: 1

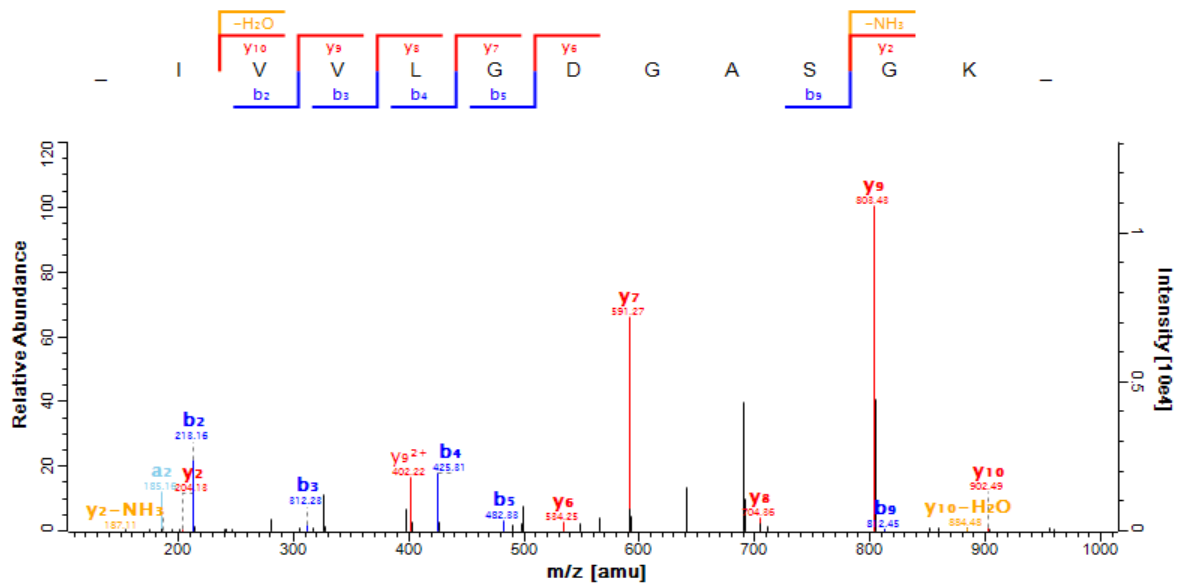
Number of Replicates (out of 10): 1

Best Match Score: 85.958

Best Match Posterior Error Probability: 0.0013104

Best Match Spectrum:

Scan number 2031 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac17
Method ITMS; CID **Genenames** RAB28



Protein Group ID: 898

Protein Accession Numbers: G8JLC6; Q5JRA6; Q5JRA6-2; H7BY50

Gene Names: MIA3

Peptide Sequence: EDLLISSFFK

Total Number of Spectra: 1

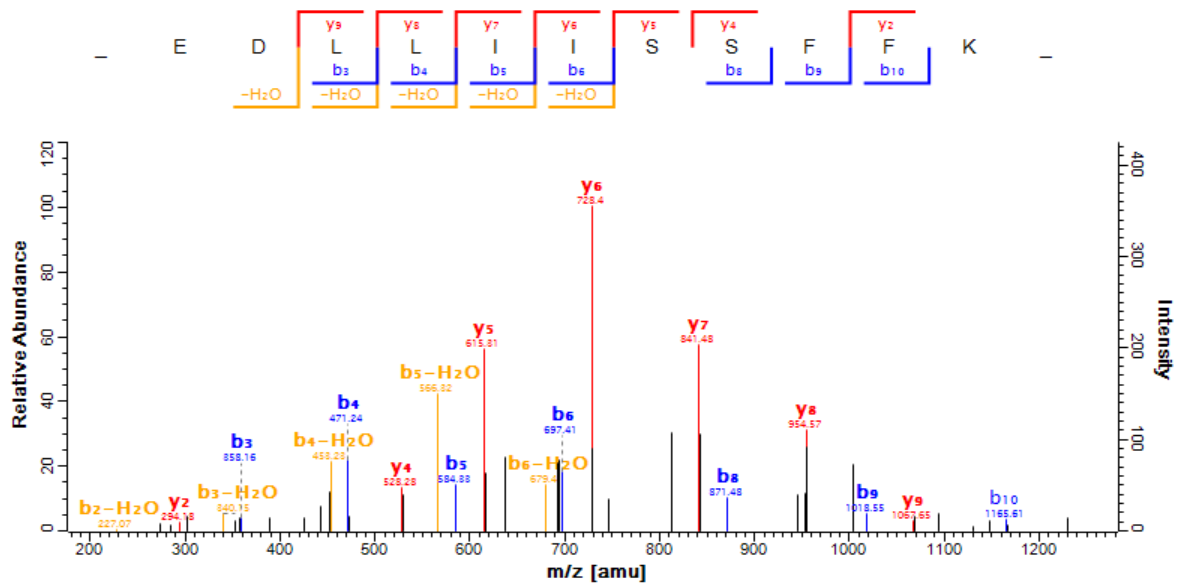
Number of Replicates (out of 10): 1

Best Match Score: 102.4

Best Match Posterior Error Probability: 0.00023694

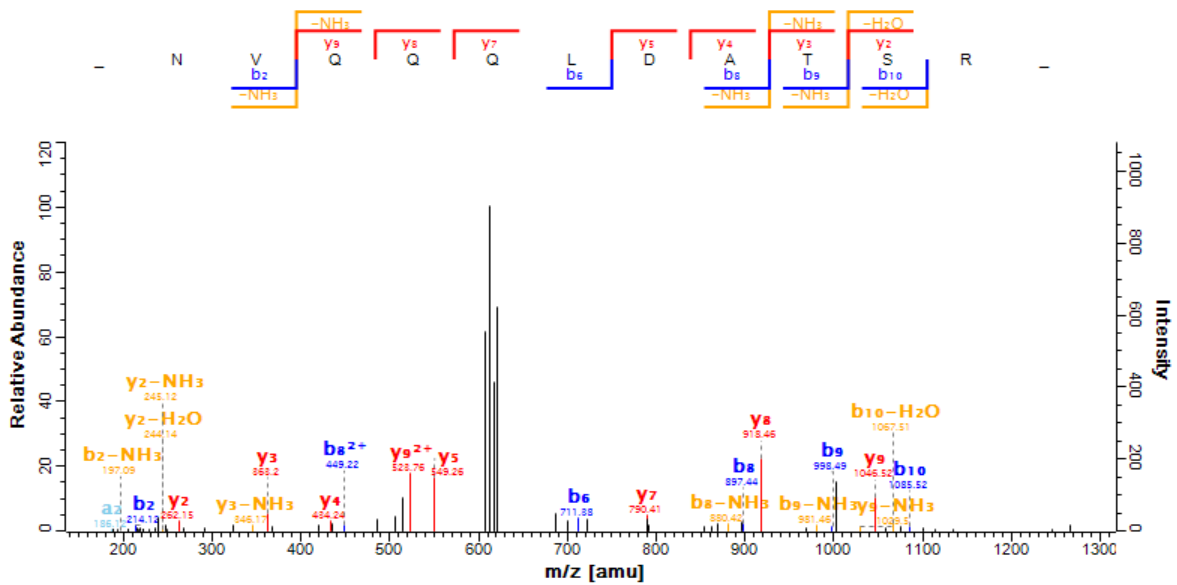
Best Match Spectrum:

Scan number	6554	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac4
Method	ITMS; CID	Genenames	MIA3



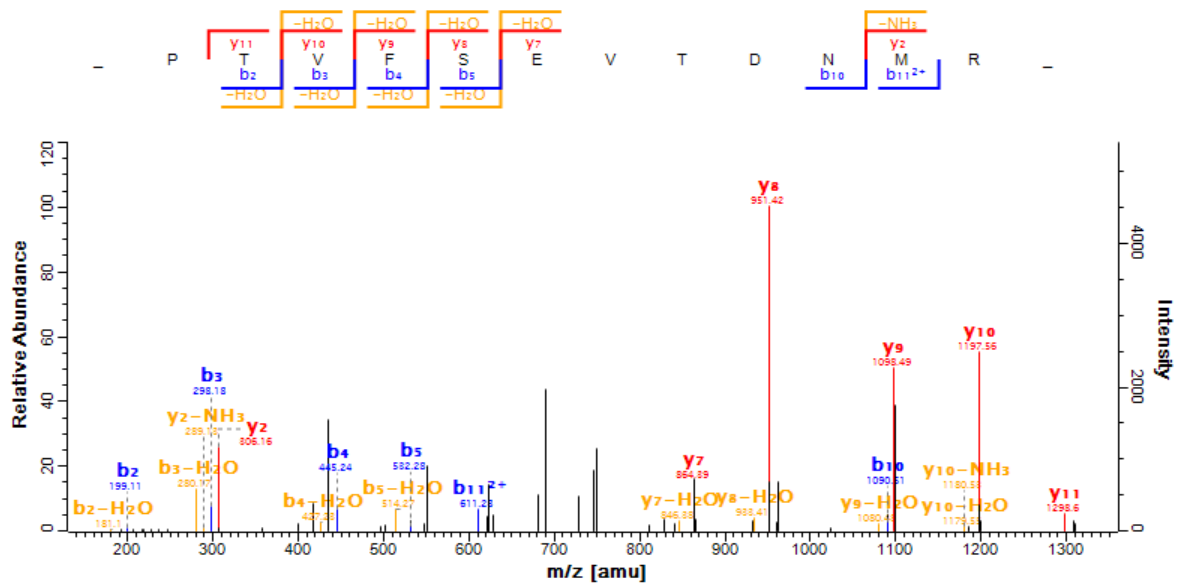
Protein Group ID: 901
Protein Accession Numbers: Q9BVW5; G8JLE5
Gene Names: TIPIN
Peptide Sequence: NVQQQLDATSR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 110.08
Best Match Posterior Error Probability: 0.00015077
Best Match Spectrum:

Scan number 2123 **Raw file** OGE-Mock-Frac4
Method ITMS; CID **Genenames** TIPIN



Protein Group ID: 904
Protein Accession Numbers: P47895; H0Y2X5
Gene Names: ALDH1A3
Peptide Sequence: PTVFSEVTDNMR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 123.67
Best Match Posterior Error Probability: 0.00020502
Best Match Spectrum:

Scan number 5127 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac14
Method ITMS; CID **Genenames** ALDH1A3



Protein Group ID: 906

Protein Accession Numbers: Q9NPB8; H0Y565

Gene Names: GPCPD1

Peptide Sequence: TTPIAMSFAQFENLLGLINVTHTEDLLR

Total Number of Spectra: 4

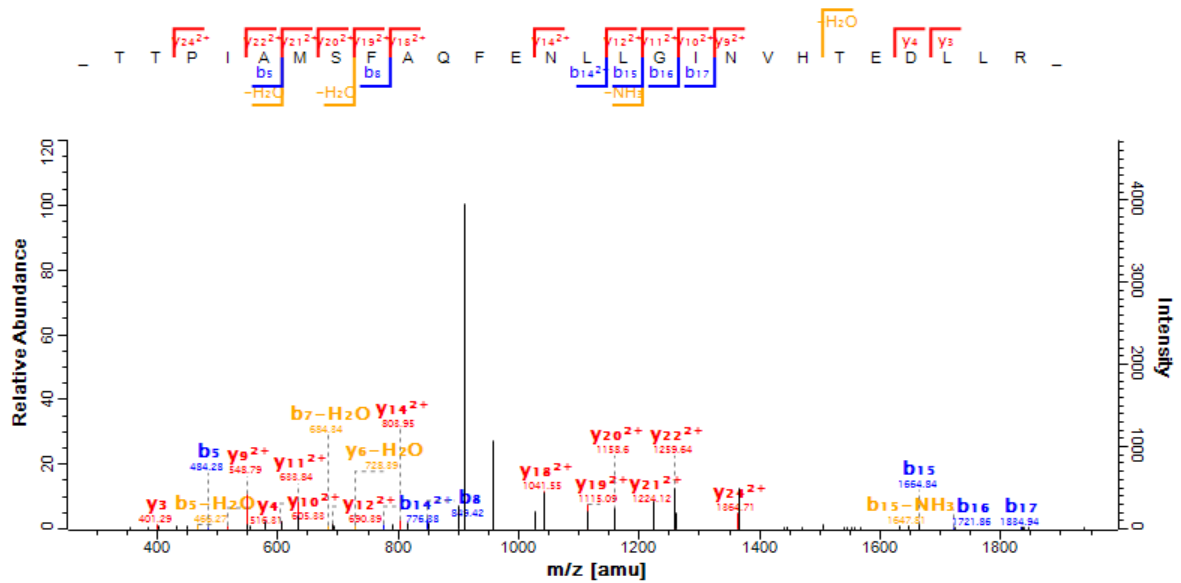
Number of Replicates (out of 10): 4

Best Match Score: 92.932

Best Match Posterior Error Probability: 6.01E-08

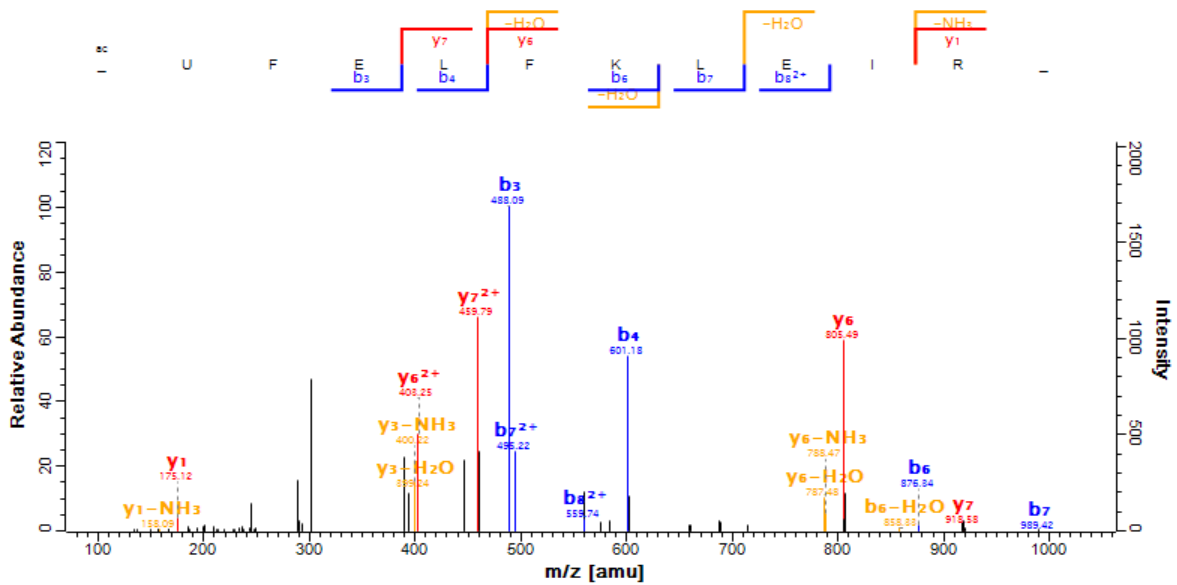
Best Match Spectrum:

Scan number 8365 **Raw file** Prt-OGE-Batch3-Mock-Frac8
Method ITMS; CID **Genenames** GPCPD1



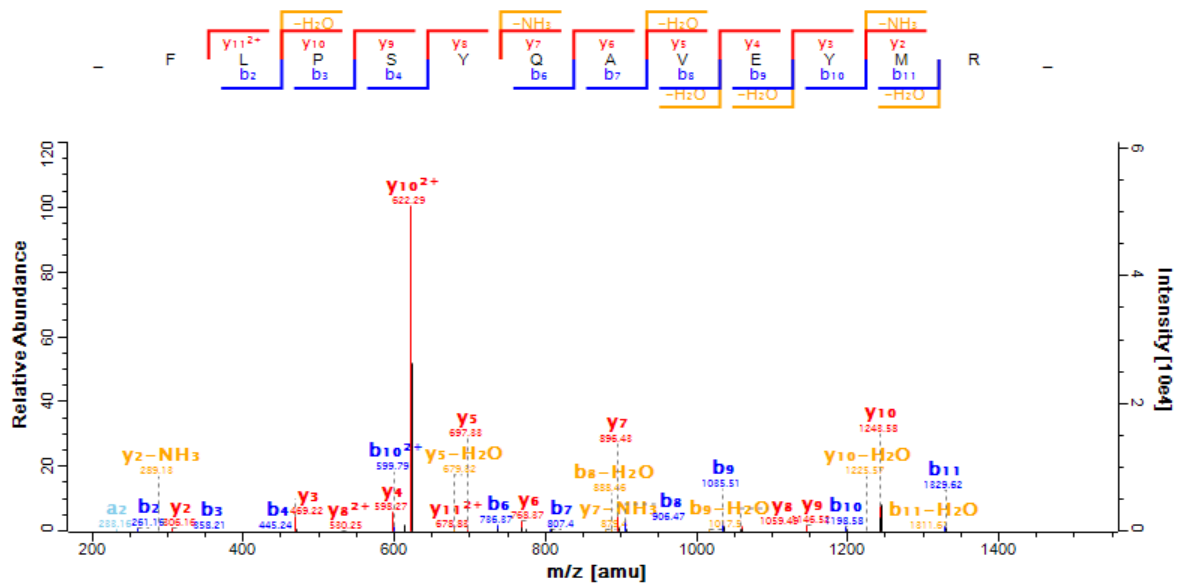
Protein Group ID: 911
Protein Accession Numbers: H0Y701
Gene Names: CCDC171
Peptide Sequence: UFELFKLEIR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 101.65
Best Match Posterior Error Probability: 0.0016335
Best Match Spectrum:

Scan number 1522 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac4
Method ITMS; CID **Genenames** CCDC171



Protein Group ID: 915
Protein Accession Numbers: P20933; H0Y9C7
Gene Names: AGA
Peptide Sequence: FLPSYQAVEYMR
Total Number of Spectra: 4
Number of Replicates (out of 10): 4
Best Match Score: 195.77
Best Match Posterior Error Probability: 1.60E-22
Best Match Spectrum:

Scan number 4005 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac20
Method ITMS; CID **Genenames** AGA



Protein Group ID: 916

Protein Accession Numbers: Q9H7D7; Q9H7D7-2; H0Y9R3

Gene Names: WDR26

Peptide Sequence: LALLNVATQGVHLWDLQDR

Total Number of Spectra: 1

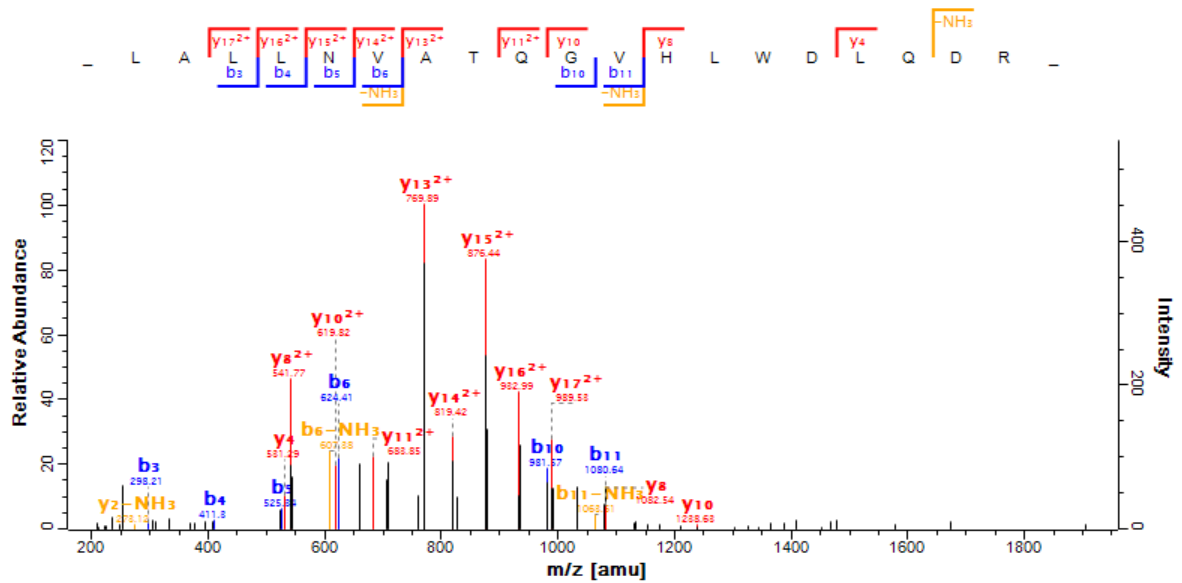
Number of Replicates (out of 10): 1

Best Match Score: 77.324

Best Match Posterior Error Probability: 0.0017036

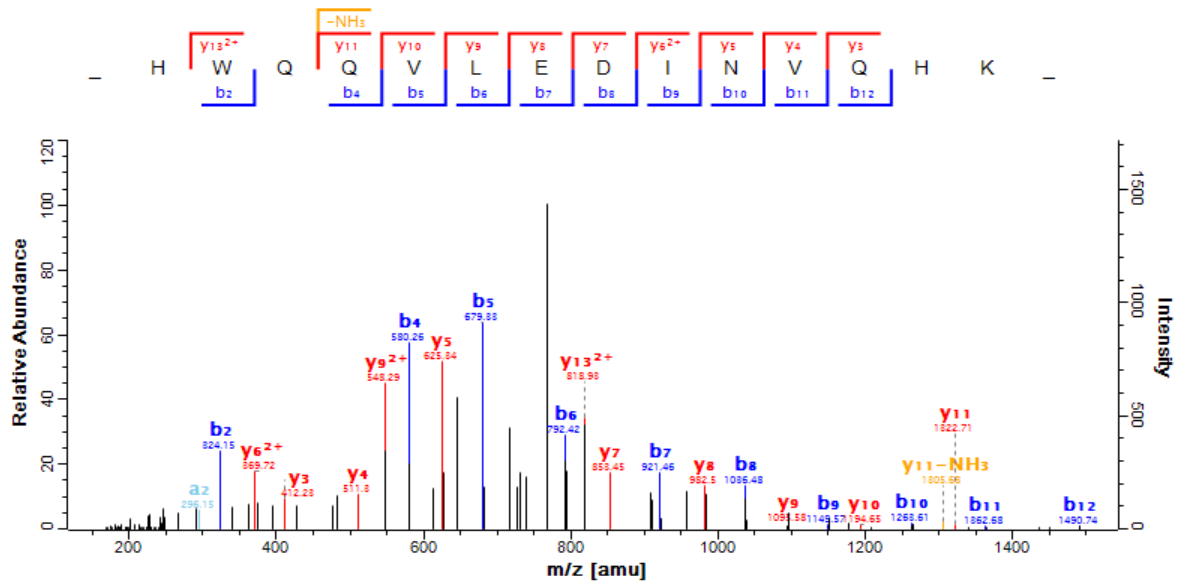
Best Match Spectrum:

Scan number 6297 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac12
Method ITMS; CID **Genenames** WDR26



Protein Group ID: 918
Protein Accession Numbers: H0YAA8; Q9H204
Gene Names: MED28
Peptide Sequence: HWQQVLEDINVQHK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 122.34
Best Match Posterior Error Probability: 6.73E-05
Best Match Spectrum:

Scan number 3868 **Raw file** Prt-OGE-Batch3-Mock-Frac7
Method ITMS; CID **Genenames** MED28



Protein Group ID: 923

Protein Accession Numbers: O14893; O14893-2; O14893-3; H0YEL0; H0YDP6

Gene Names: GEMIN2

Peptide Sequence: SSQLDSNVTMPK

Total Number of Spectra: 2

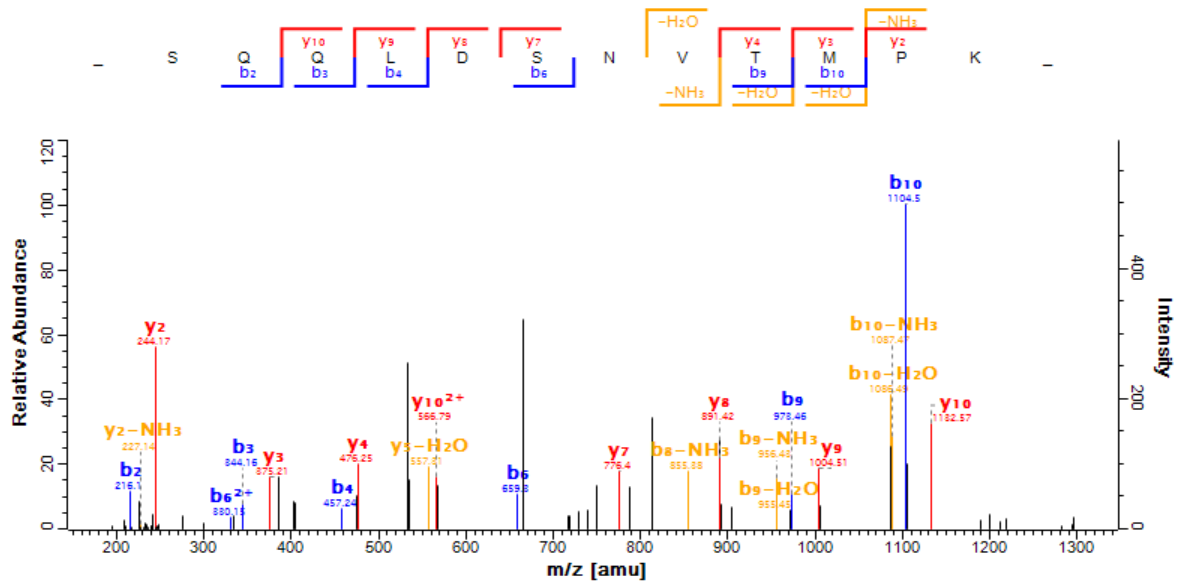
Number of Replicates (out of 10): 2

Best Match Score: 111.79

Best Match Posterior Error Probability: 0.00019531

Best Match Spectrum:

Scan number	2608	Raw file	Prt-OGE-Batch2-Mock-Frac6
Method	ITMS; CID	Genenames	GEMIN2



Protein Group ID: 929

Protein Accession Numbers: Q6P1R4; J3QLE4; H0YGW8; J3QKP9

Gene Names: DUS1L

Peptide Sequence: SPAVWELAAEEYLDIR

Total Number of Spectra: 2

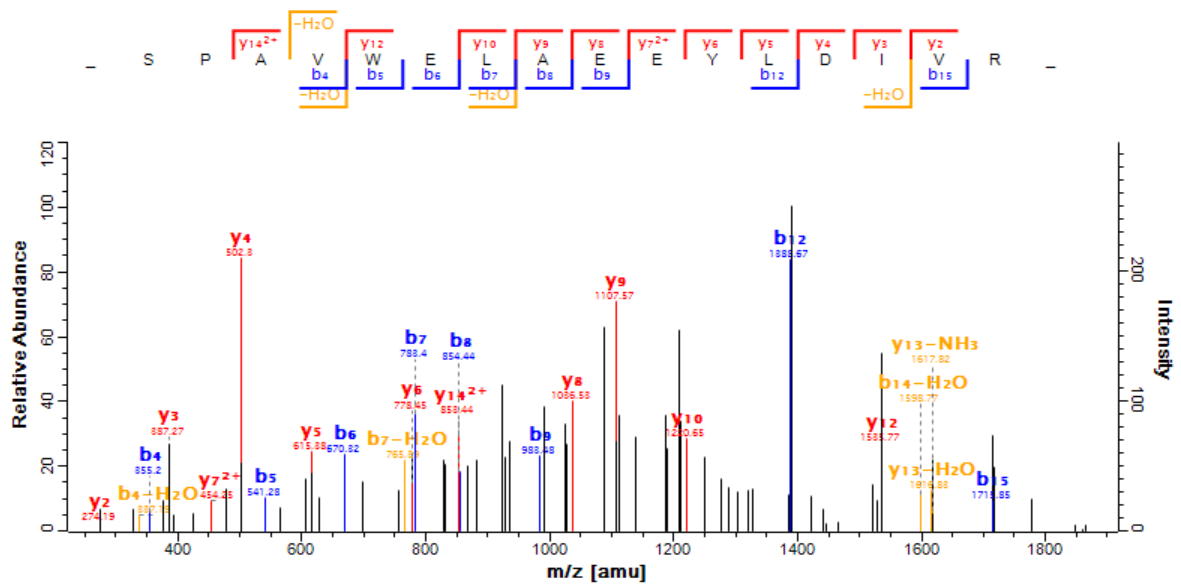
Number of Replicates (out of 10): 1

Best Match Score: 109.79

Best Match Posterior Error Probability: 0.00012942

Best Match Spectrum:

Scan number	7432	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac20
Method	ITMS; CID	Genenames	DUS1L



Protein Group ID: 934

Protein Accession Numbers: Q6FIF0; Q6FIF0-2; H0YK54; H0YK21; H0YME2; H0YLR2; H0YMR5

Gene Names: ZFAND6

Peptide Sequence: AVPETEDVQASVSDTAQQPSEEQSK

Total Number of Spectra: 2

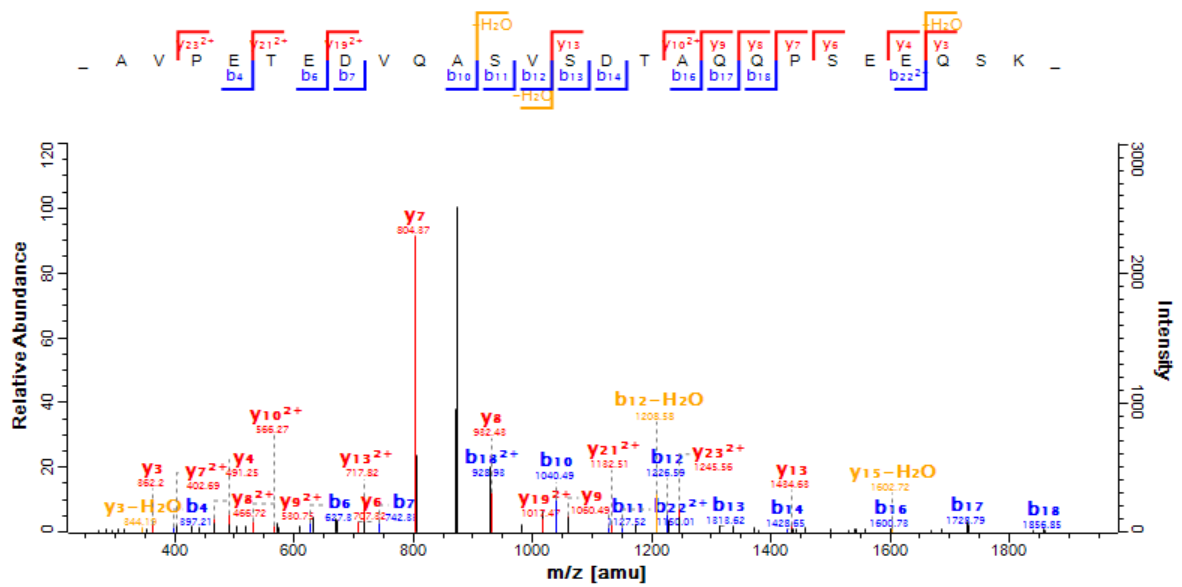
Number of Replicates (out of 10): 2

Best Match Score: 126.97

Best Match Posterior Error Probability: 7.24E-17

Best Match Spectrum:

Scan number	3134	Raw file	Prt-OGE-Batch2-Mock-Frac12
Method	ITMS: CID	Genenames	ZFAND6



Protein Group ID: 935

Protein Accession Numbers: H0YK83; P67812; H0YK72; H0YNG3; H0YKT4

Gene Names: SEC11A

Peptide Sequence: MLSLDFLDDVR

Total Number of Spectra: 2

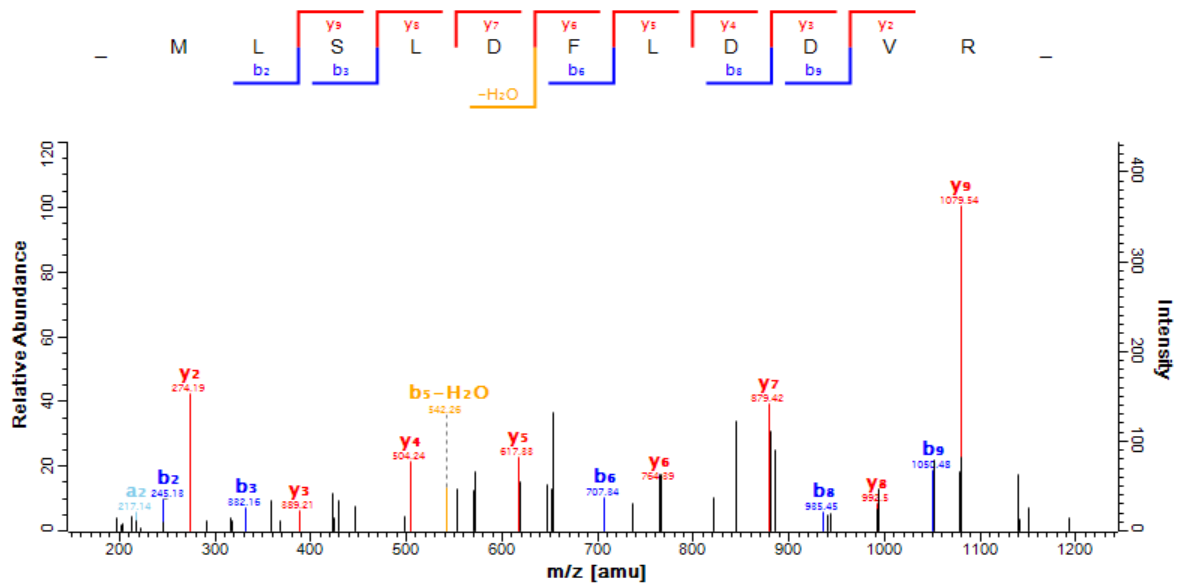
Number of Replicates (out of 10): 2

Best Match Score: 85.288

Best Match Posterior Error Probability: 0.0014464

Best Match Spectrum:

Scan number 4624 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** SEC11A



Protein Group ID: 936

Protein Accession Numbers: Q9NVM6; H0YK99; H0YLQ7

Gene Names: DNAJC17

Peptide Sequence: AAELFHQLSQALEVLTDAAR

Total Number of Spectra: 7

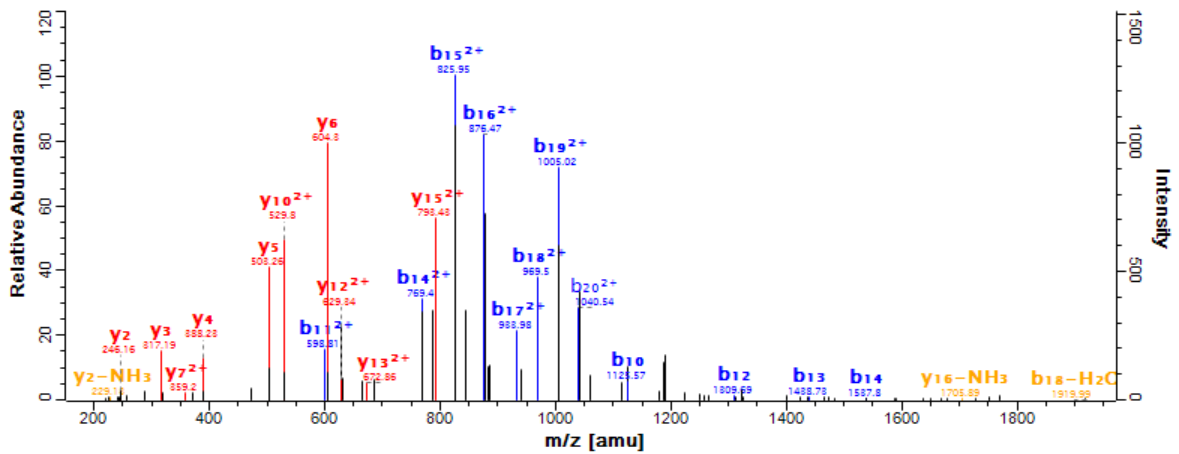
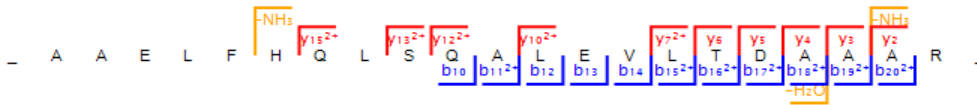
Number of Replicates (out of 10): 6

Best Match Score: 101.67

Best Match Posterior Error Probability: 1.05E-05

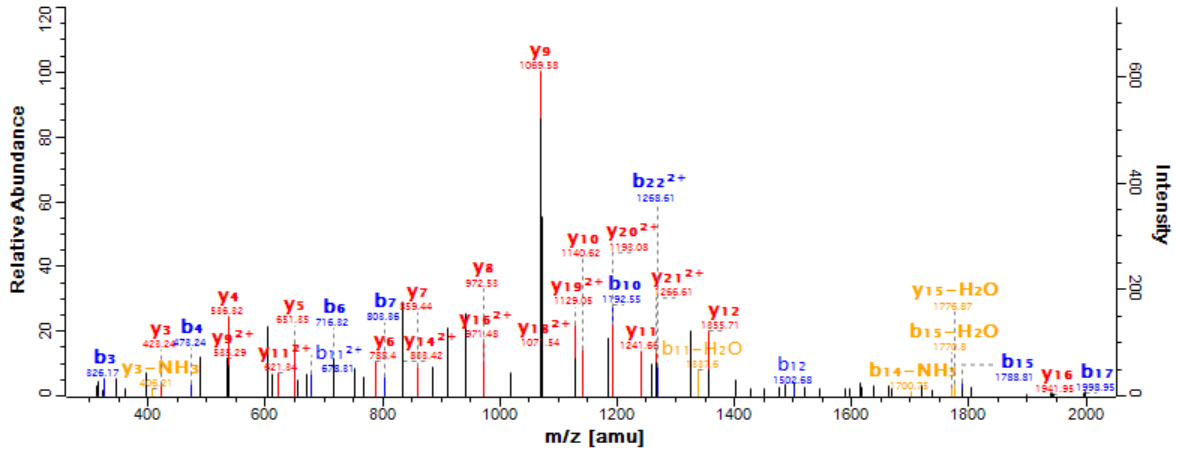
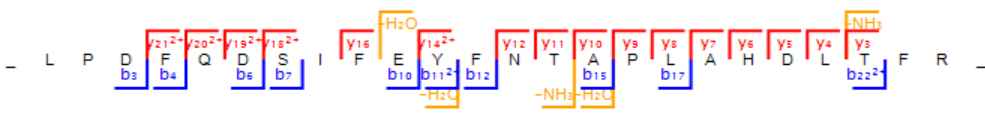
Best Match Spectrum:

Scan number	7815	Raw file	20100914-KD-Batch4-Prt-OGE-Mock-Frac17
Method	ITMS; CID	Genenames	DNAJC17



Protein Group ID: 939
Protein Accession Numbers: Q9Y5S2; H0YLY0
Gene Names: CDC42BPB
Peptide Sequence: LPDFQDSIFEYFNTAPLAHDLTFR
Total Number of Spectra: 7
Number of Replicates (out of 10): 7
Best Match Score: 133.41
Best Match Posterior Error Probability: 5.61E-17
Best Match Spectrum:

Scan number 6459 **Raw file** Prt-OGE-Batch2-WT-Frac13
Method ITMS; CID **Genenames** CDC42BPB



Protein Group ID: 940

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

Gene Names: ALDH1A2

Peptide Sequence: IFVEESIYEEFVR

Total Number of Spectra: 20

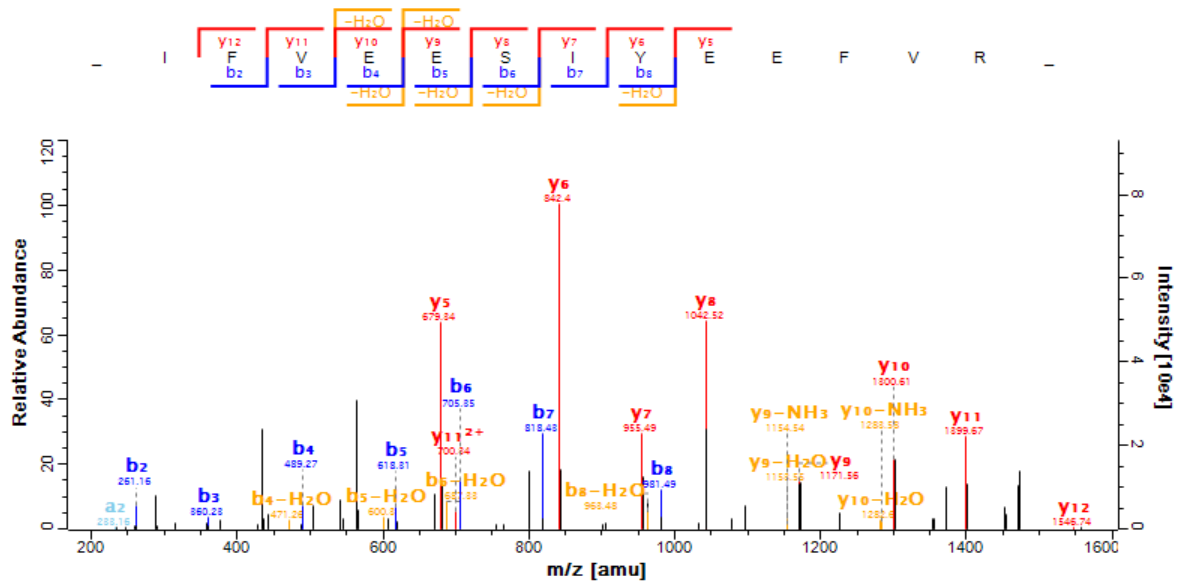
Number of Replicates (out of 10): 2

Best Match Score: 149.41

Best Match Posterior Error Probability: 1.07E-05

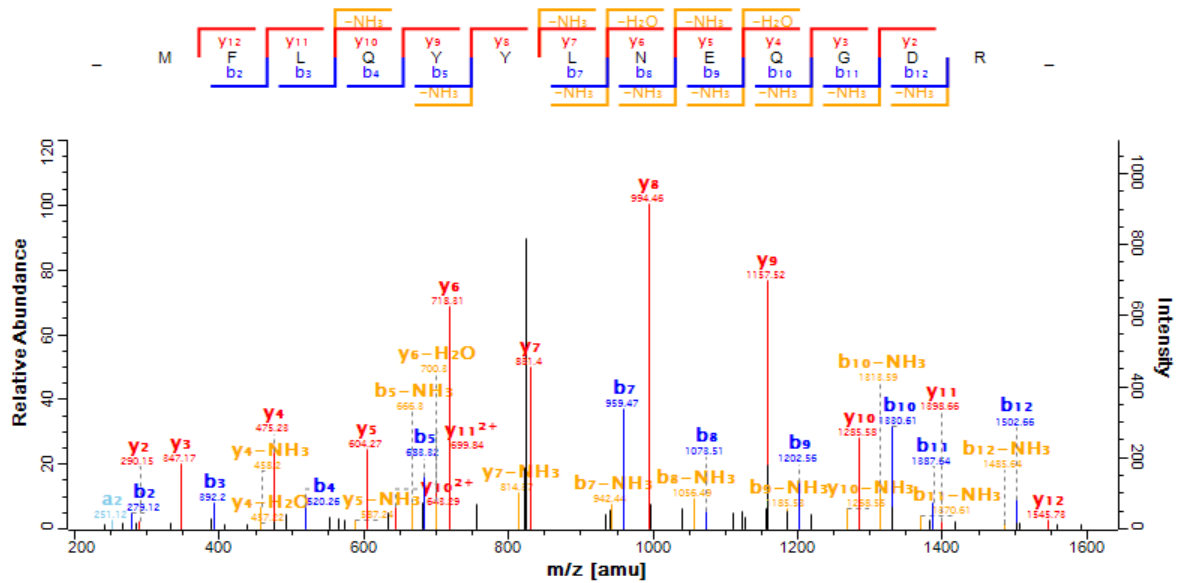
Best Match Spectrum:

Scan number 6020 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac14
Method ITMS; CID **Genenames** ALDH1A2



Protein Group ID: 941
Protein Accession Numbers: Q9NPE3; H0YM60
Gene Names: NOP10
Peptide Sequence: MFLQYYLNEQGDR
Total Number of Spectra: 3
Number of Replicates (out of 10): 2
Best Match Score: 254.89
Best Match Posterior Error Probability: 0
Best Match Spectrum:

Scan number 4033 **Raw file** Prt-OGE-Batch2-WT-Frac23
Method ITMS; CID **Genenames** NOP10



Protein Group ID: 943

Protein Accession Numbers: Q96TC7; Q96TC7-2; H0YMB1

Gene Names: FAM82A2

Peptide Sequence: TATALLESPLSATVEDALQSFLK

Total Number of Spectra: 6

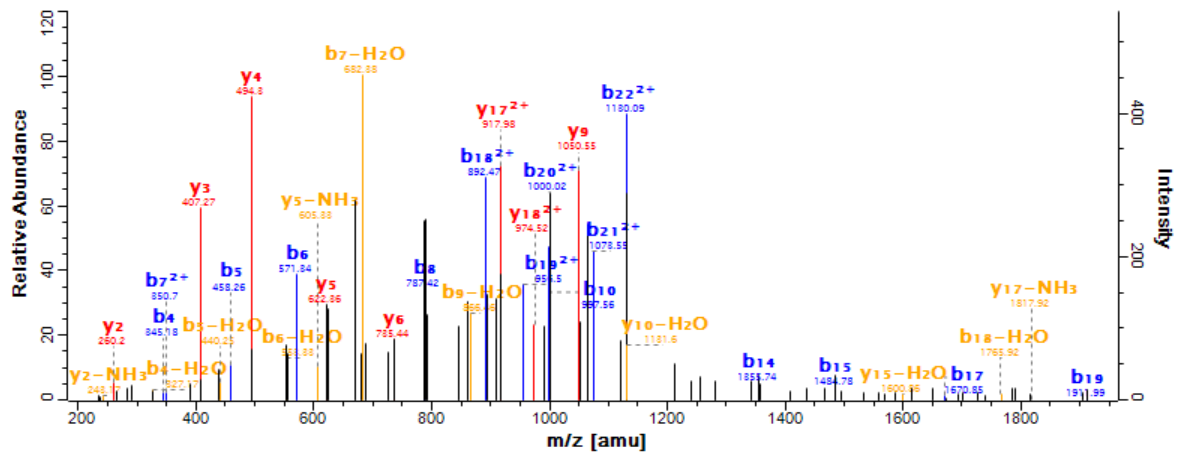
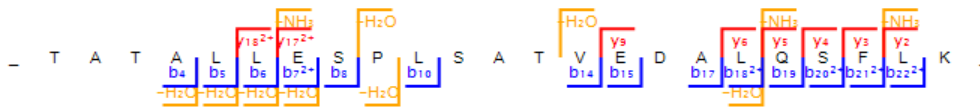
Number of Replicates (out of 10): 4

Best Match Score: 117.84

Best Match Posterior Error Probability: 6.23E-10

Best Match Spectrum:

Scan number	9152	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac8
Method	ITMS; CID	Genenames	FAM82A2



Protein Group ID: 944

Protein Accession Numbers: Q8TEX9-2; Q8TEX9; H0YMR4; H0YN07

Gene Names: IPO4

Peptide Sequence: LLGLLFLLAR

Total Number of Spectra: 13

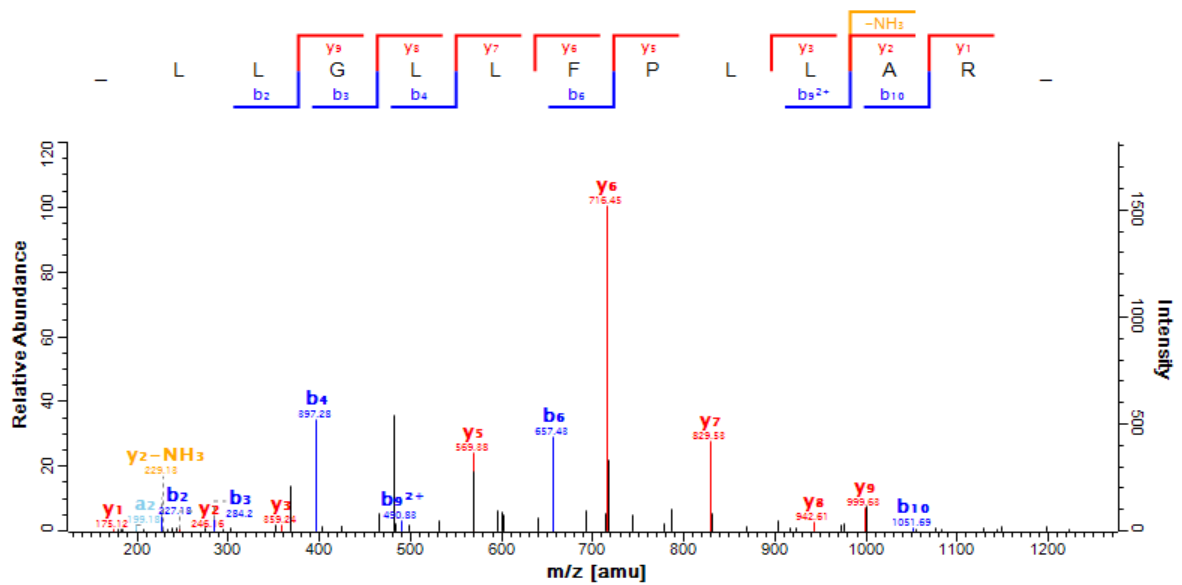
Number of Replicates (out of 10): 5

Best Match Score: 99.815

Best Match Posterior Error Probability: 0.00027027

Best Match Spectrum:

Scan number 7995 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac13
Method ITMS; CID **Genenames** IPO4



Protein Group ID: 954

Protein Accession Numbers: H3BM74; H3BM14; Q9Y5A7; Q9Y5A7-2; H7C5N1; H7C5E1

Gene Names: NUB1

Peptide Sequence: ACDGNVDHAATHITNR

Total Number of Spectra: 1

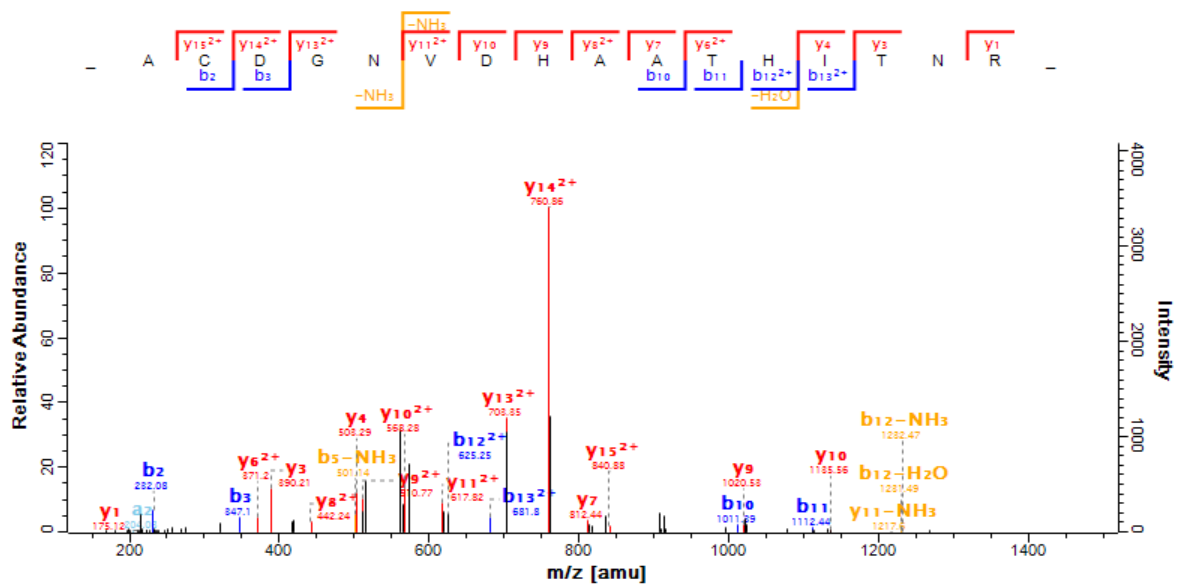
Number of Replicates (out of 10): 1

Best Match Score: 90.444

Best Match Posterior Error Probability: 0.00040812

Best Match Spectrum:

Scan number	922	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac18
Method	ITMS; CID	Genenames	NUB1



Protein Group ID: 955

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

Gene Names: MECR

Peptide Sequence: SLGAEHVITEELR

Total Number of Spectra: 5

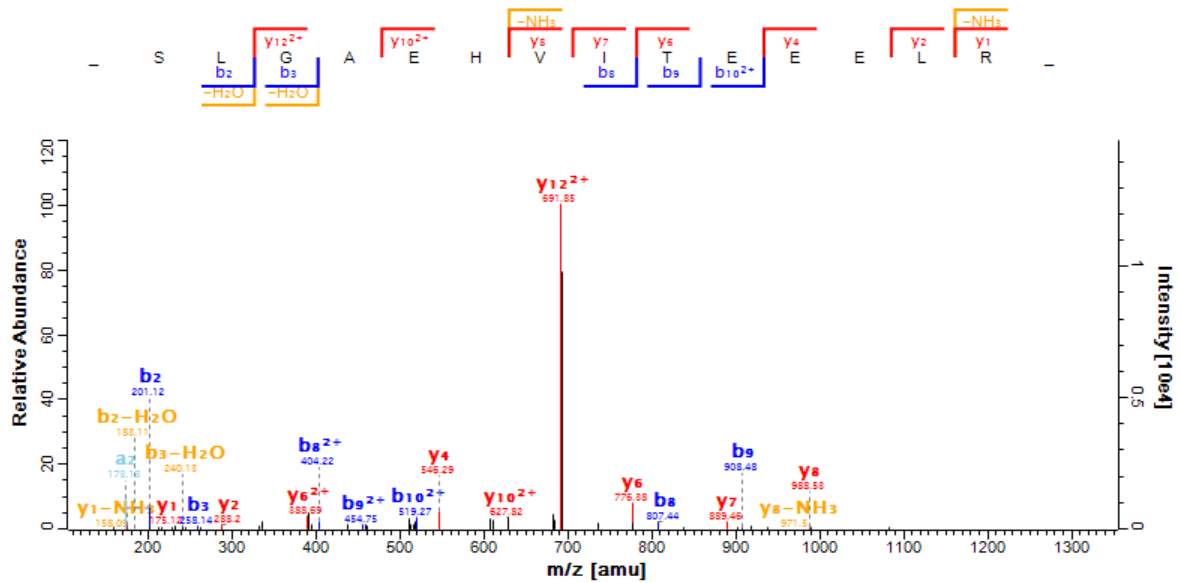
Number of Replicates (out of 10): 5

Best Match Score: 123.84

Best Match Posterior Error Probability: 6.01E-05

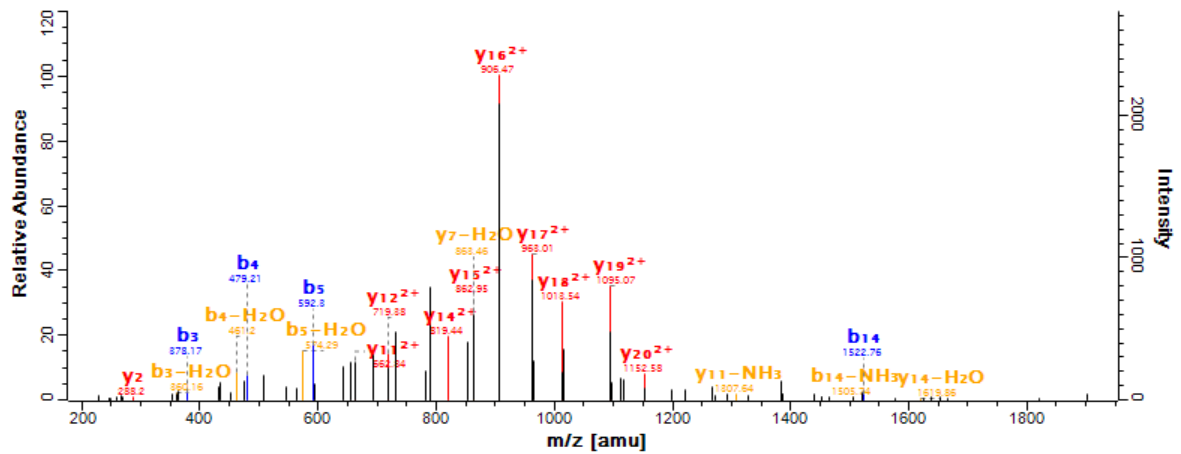
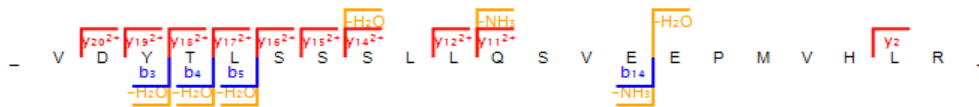
Best Match Spectrum:

Scan number 3638 **Raw file** Prt-OGE-Batch2-Mock-Frac1 8
Method ITMS; CID **Genenames** MECR



Protein Group ID: 956
Protein Accession Numbers: H3BM91; Q9H0A8
Gene Names: COMMD4
Peptide Sequence: VDYTLSSSLLQSVEEPMVHLR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 81.428
Best Match Posterior Error Probability: 0.00030407
Best Match Spectrum:

Scan number 6260 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac16
Method ITMS; CID **Genenames** COMMD4



Protein Group ID: 959

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

Gene Names: PRMT7

Peptide Sequence: ANILVTELFDEGLGEGALPSYEAHR

Total Number of Spectra: 6

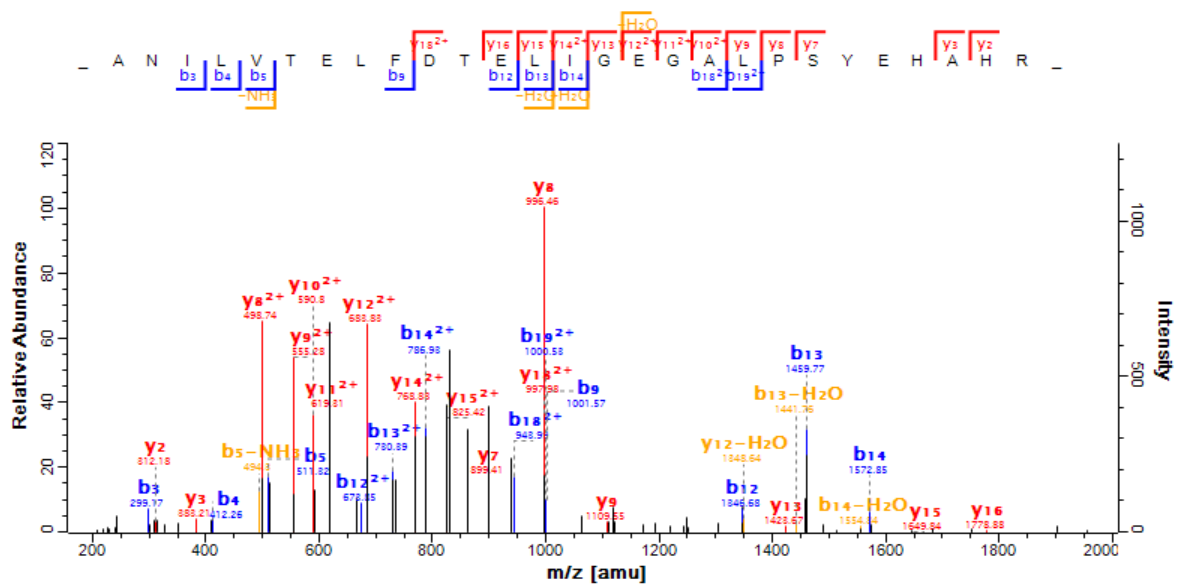
Number of Replicates (out of 10): 5

Best Match Score: 115.96

Best Match Posterior Error Probability: 4.26E-17

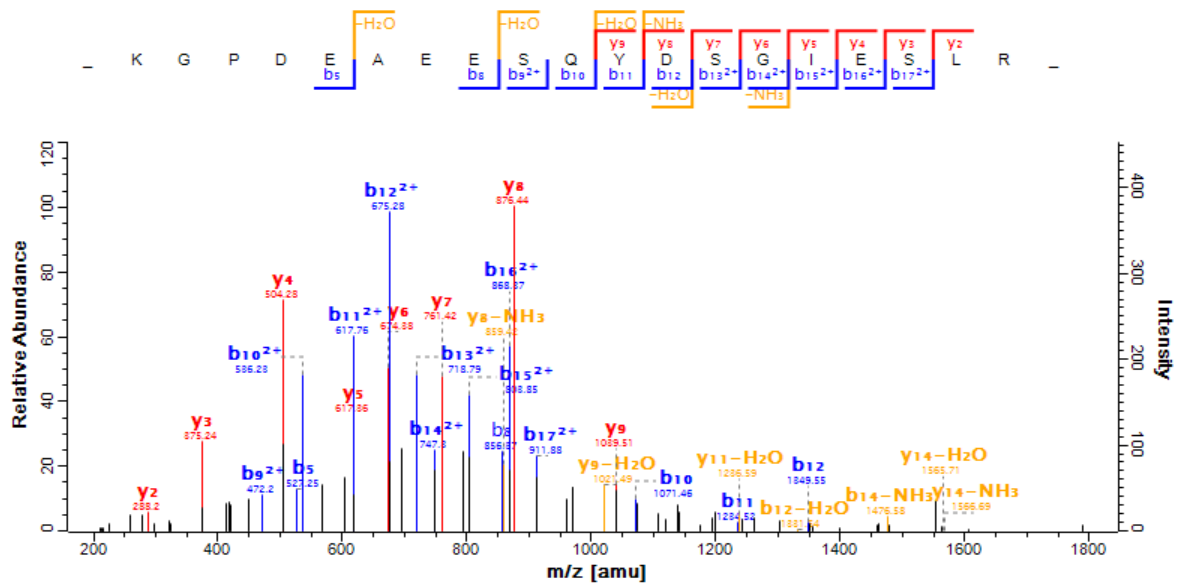
Best Match Spectrum:

Scan number	7339	Raw file	Prt-OGE-Batch3-Mock-Frac8
Method	ITMS; CID	Genenames	PRMT7



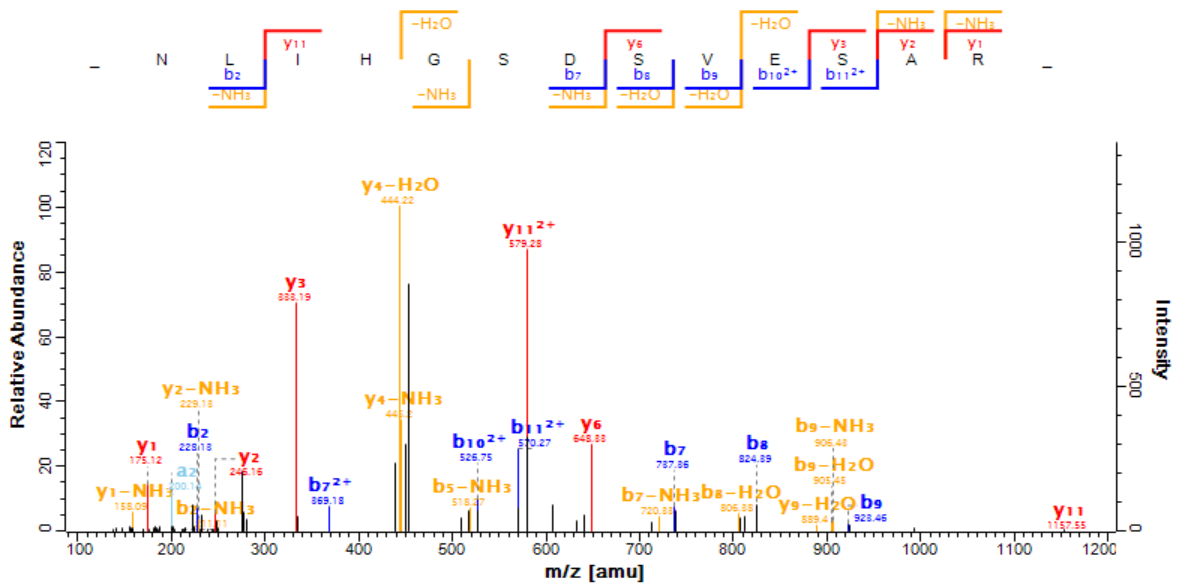
Protein Group ID: 960
Protein Accession Numbers: O00221; H3BNC2
Gene Names: NFKBIE
Peptide Sequence: KGPDEAESQYDSGIESLR
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 114.96
Best Match Posterior Error Probability: 7.49E-05
Best Match Spectrum:

Scan number	3141	Raw file	Prt-OGE-Batch2-Mock-Frac5
Method	ITMS; CID	Genenames	NFKBIE



Protein Group ID: 966
Protein Accession Numbers: Q13232; H3BPR2
Gene Names: NME3
Peptide Sequence: NLIHGSDSVESAR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 105.17
Best Match Posterior Error Probability: 0.00036267
Best Match Spectrum:

Scan number 1309 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac19
Method ITMS; CID **Genenames** NME3



Protein Group ID: 970

Protein Accession Numbers: Q15554; H3BR06; J3KSZ6

Gene Names: TERF2

Peptide Sequence: KDENESSAPADGEGGSELQPK

Total Number of Spectra: 1

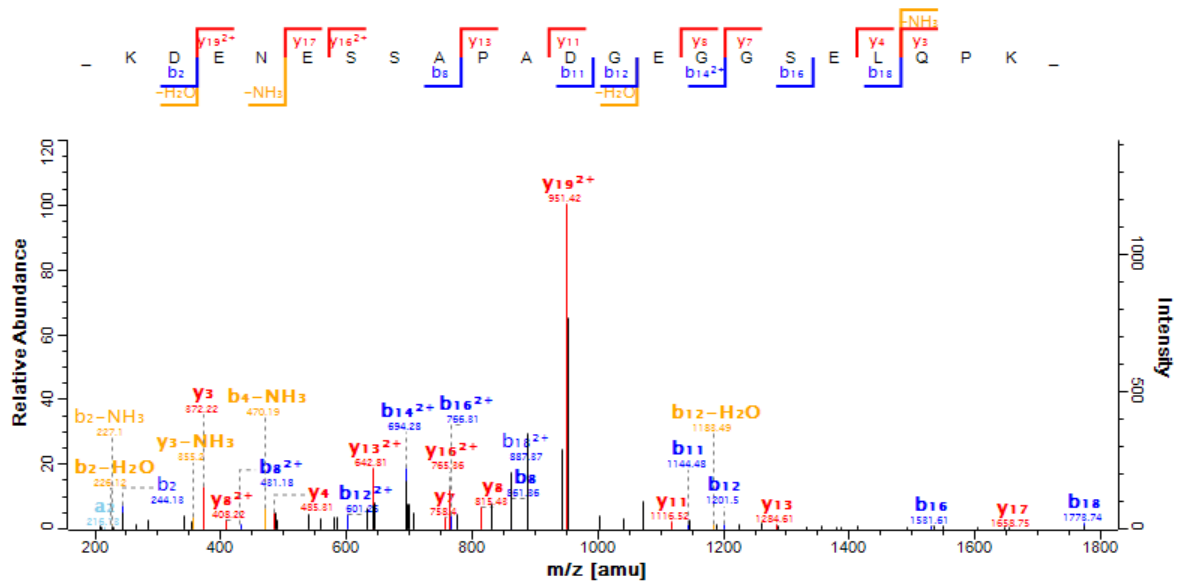
Number of Replicates (out of 10): 1

Best Match Score: 104.45

Best Match Posterior Error Probability: 1.51E-05

Best Match Spectrum:

Scan number	1056	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac20
Method	ITMS; CID	Genenames	TERF2



Protein Group ID: 971

Protein Accession Numbers: P55789; H3BRD2; H3BRW3

Gene Names: GFER

Peptide Sequence: SEMMDDLATDAR

Total Number of Spectra: 5

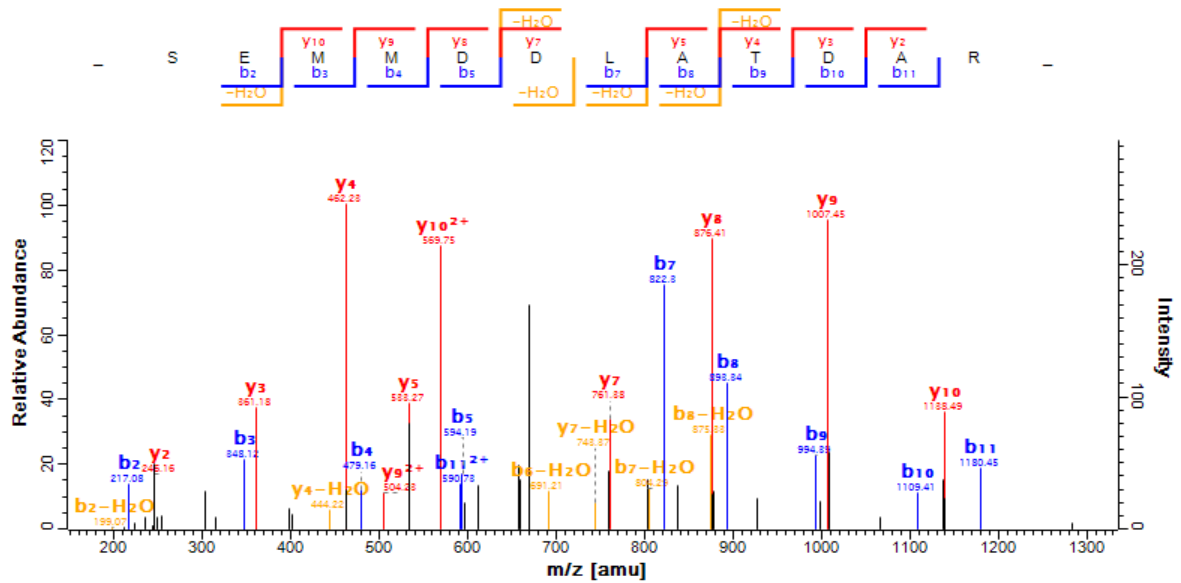
Number of Replicates (out of 10): 5

Best Match Score: 169.23

Best Match Posterior Error Probability: 3.10E-07

Best Match Spectrum:

Scan number 2651 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac17
Method ITMS; CID **Genenames** GFER



Protein Group ID: 973

Protein Accession Numbers: Q9NZD8; Q9NZD8-2; H3BRR0

Gene Names: SPG21

Peptide Sequence: DIPVTIMDVFDQSALSTEAK EEM YK

Total Number of Spectra: 1

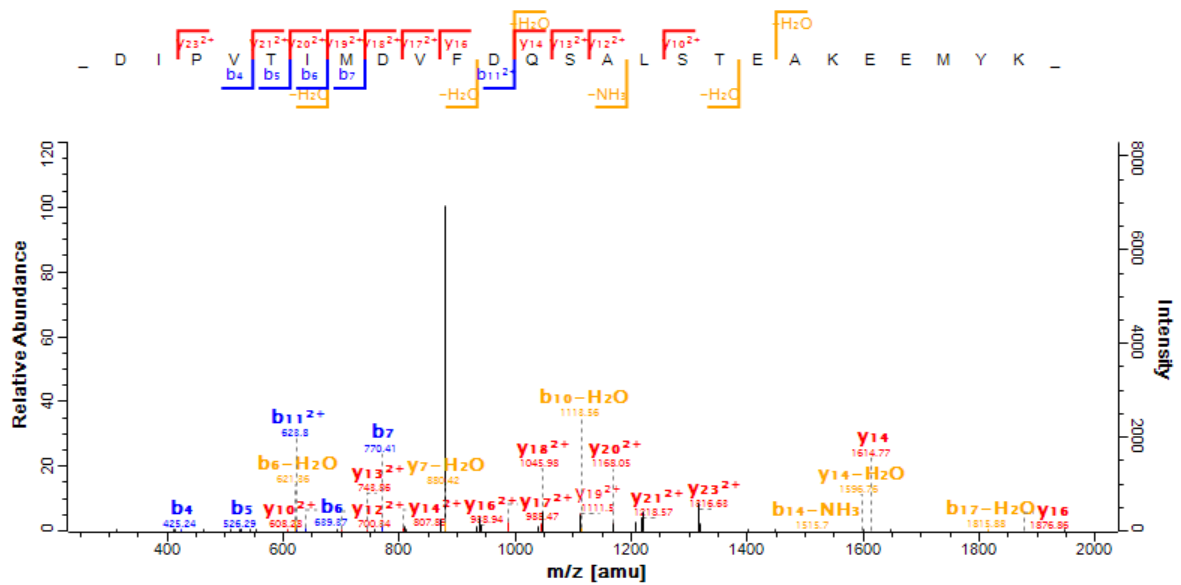
Number of Replicates (out of 10): 1

Best Match Score: 68.49

Best Match Posterior Error Probability: 0.00062917

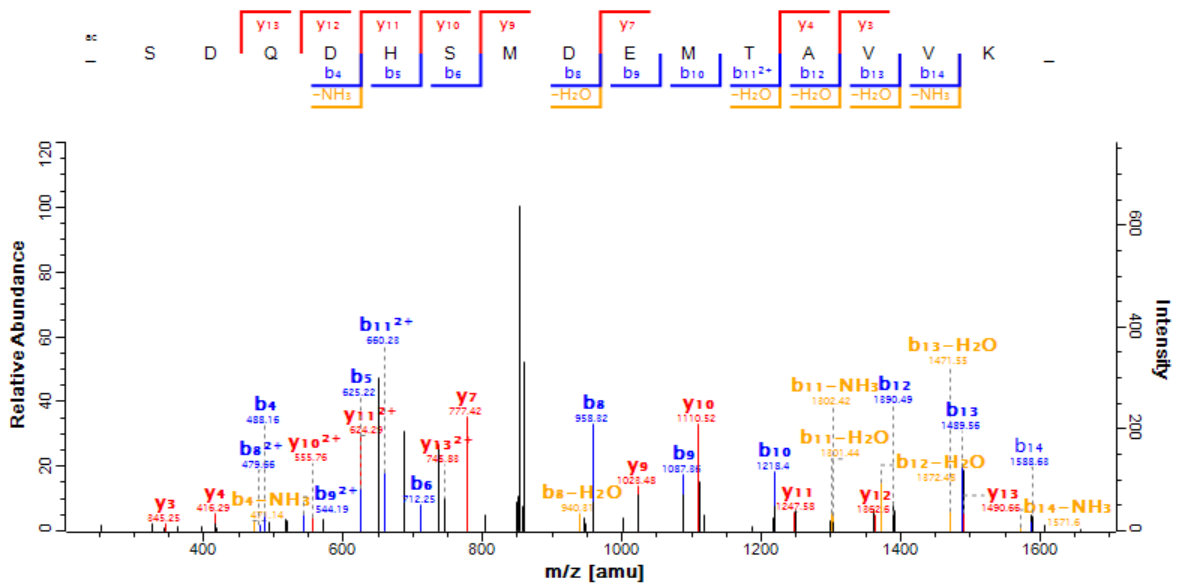
Best Match Spectrum:

Scan number 6524 **Raw file** OGE-Mock-Frac11
Method ITMS; CID **Genenames** SPG21



Protein Group ID: 976
Protein Accession Numbers: P08047; H3BUU5
Gene Names: SP1
Peptide Sequence: SDQDHSMDEMTAVVK
Total Number of Spectra: 20
Number of Replicates (out of 10): 10
Best Match Score: 144.18
Best Match Posterior Error Probability: 1.53E-07
Best Match Spectrum:

Scan number	2901	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac2
Method	ITMS; CID	Genenames	SP1



Protein Group ID: 977

Protein Accession Numbers: Q96S82; H3BUV9; H3BV23

Gene Names: UBL7

Peptide Sequence: SLSDWHLAVK

Total Number of Spectra: 1

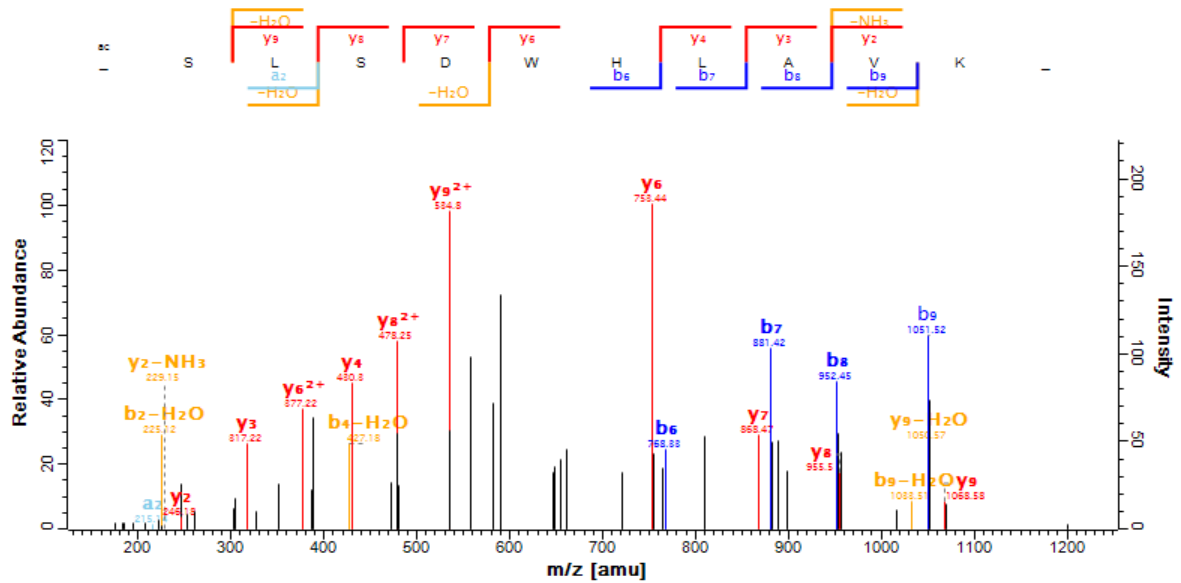
Number of Replicates (out of 10): 1

Best Match Score: 105.2

Best Match Posterior Error Probability: 0.00039948

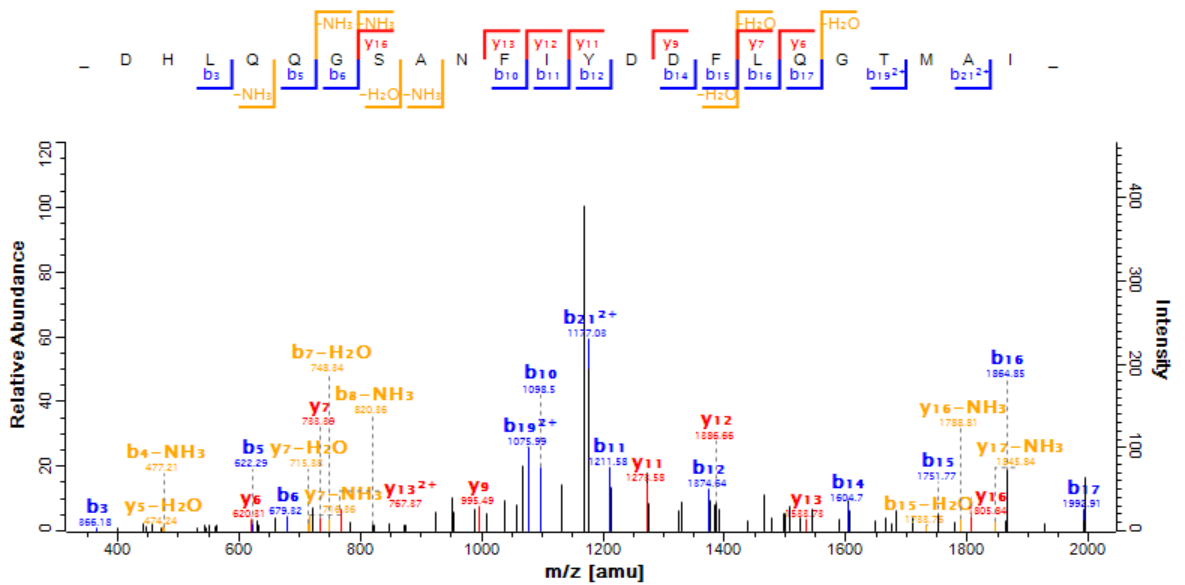
Best Match Spectrum:

Scan number 4391 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac5
Method ITMS; CID **Genenames** UBL7



Protein Group ID: 980
Protein Accession Numbers: P28676; H7BXD5
Gene Names: GCA
Peptide Sequence: DHLQQGSANFIYDDFLQGTMAI
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 77.53
Best Match Posterior Error Probability: 0.0003329
Best Match Spectrum:

Scan number 5884 **Raw file** Prt-OGE-Batch3-WT-Frac5
Method ITMS; CID **Genenames** GCA



Protein Group ID: 982

Protein Accession Numbers: Q9UNF1; H7BXW3; Q9UNF1-2; Q5H907

Gene Names: MAGED2

Peptide Sequence: DSSSMMQTLTQNVETPK

Total Number of Spectra: 3

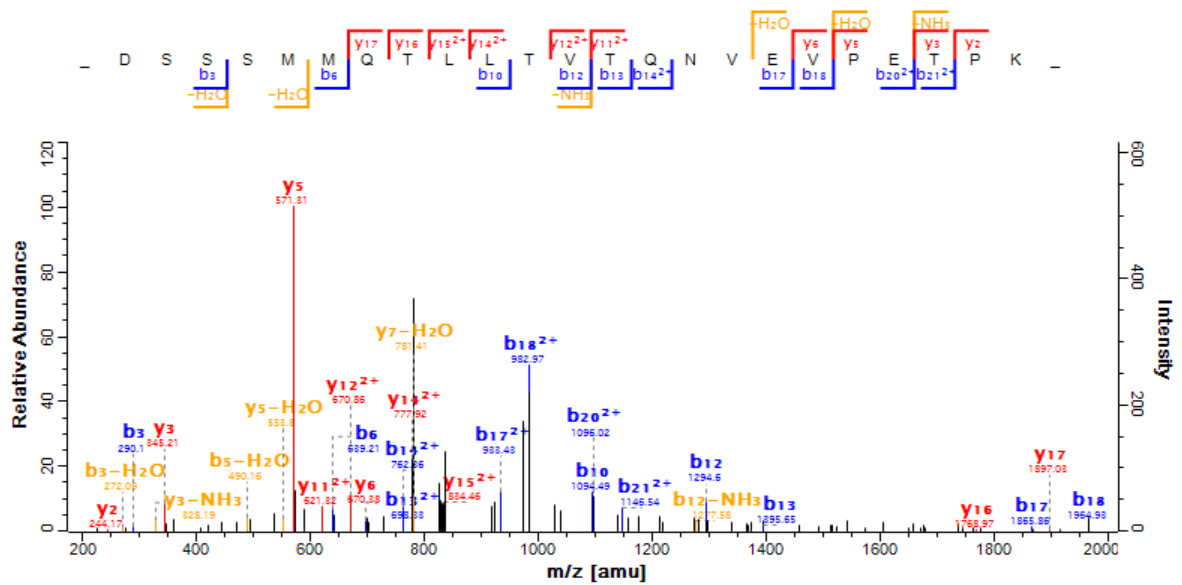
Number of Replicates (out of 10): 3

Best Match Score: 104.81

Best Match Posterior Error Probability: 4.14E-07

Best Match Spectrum:

Scan number 5792 **Raw file** OGEWT-Frac4
Method ITMS; CID **Genenames** MAGED2



Protein Group ID: 986

Protein Accession Numbers: Q9NQY0; H7BYV6; Q9NQY0-2

Gene Names: BIN3

Peptide Sequence: LDYFQPSFESLR

Total Number of Spectra: 1

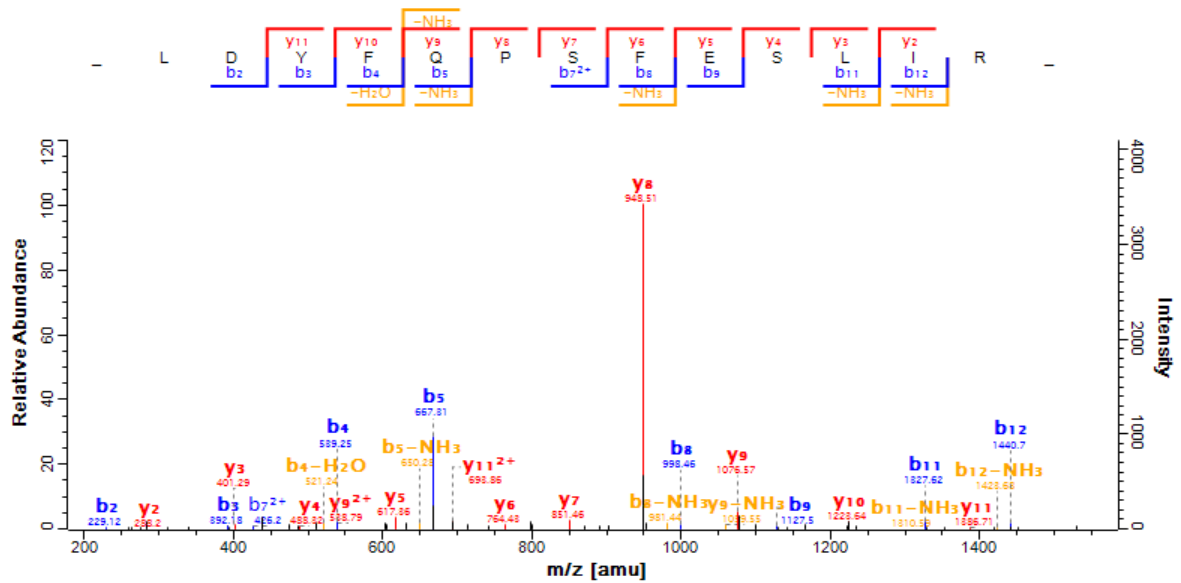
Number of Replicates (out of 10): 1

Best Match Score: 143.05

Best Match Posterior Error Probability: 1.55E-05

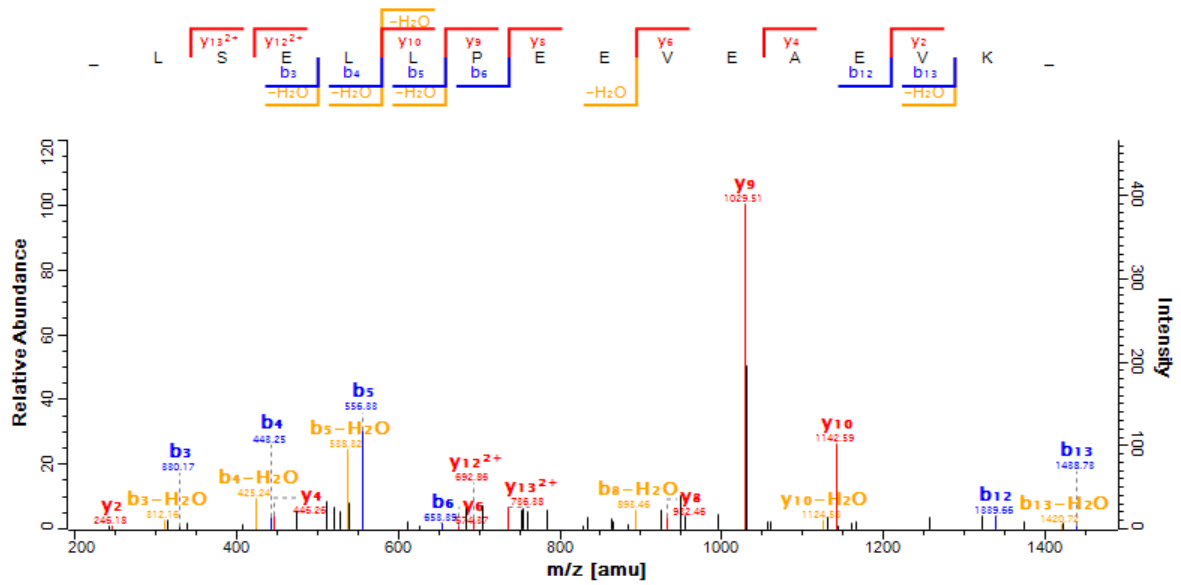
Best Match Spectrum:

Scan number 5051 **Raw file** Prt-OGE-Batch2-WT-Frac16
Method ITMS; CID **Genenames** BIN3



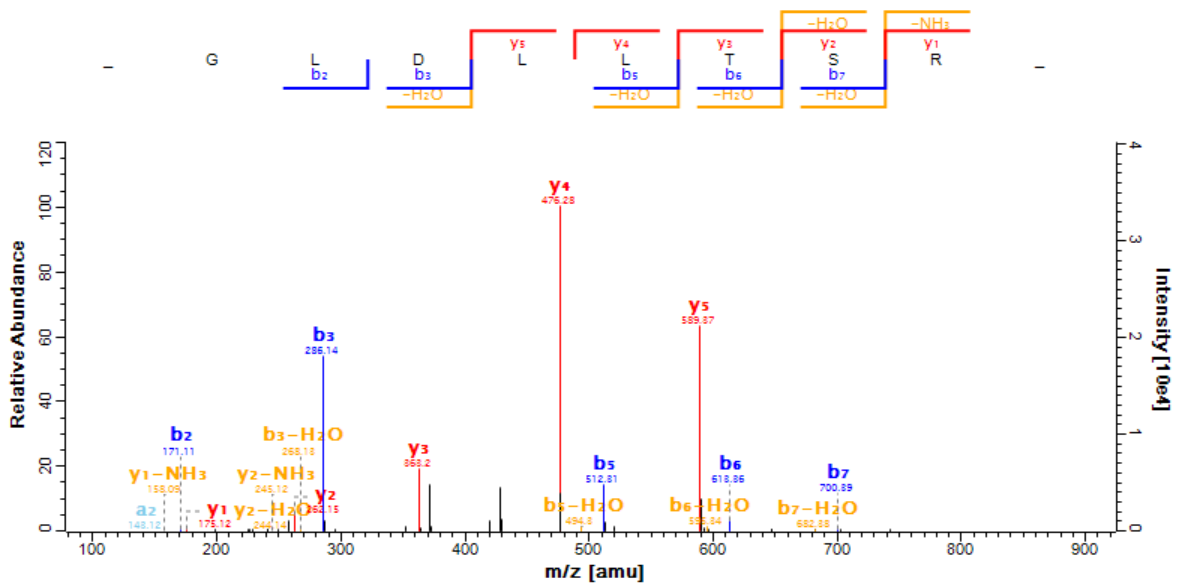
Protein Group ID: 988
Protein Accession Numbers: Q9Y2X3; H7BZ72
Gene Names: NOP58
Peptide Sequence: LSELLPEEVEAEVK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 104.17
Best Match Posterior Error Probability: 0.00025651
Best Match Spectrum:

Scan number	3410	Raw file	Prt-OGE-Batch3-WT-Frac20
Method	ITMS; CID	Genenames	NOP58



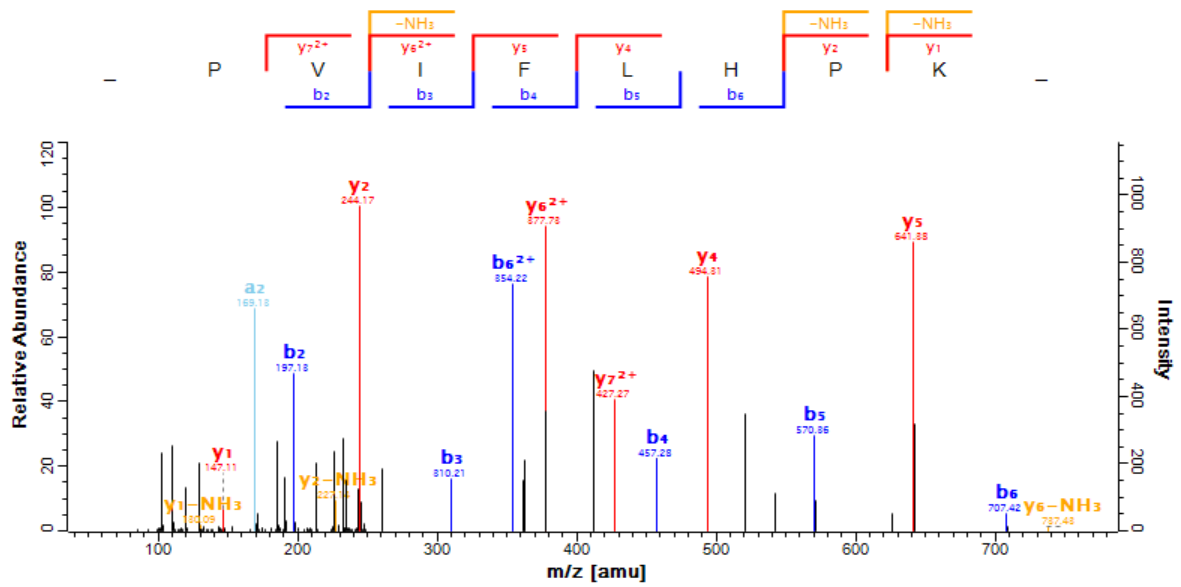
Protein Group ID: 989
Protein Accession Numbers: H7BZF5
Gene Names: C2orf80
Peptide Sequence: GLDLLTSR
Total Number of Spectra: 15
Number of Replicates (out of 10): 8
Best Match Score: 113.71
Best Match Posterior Error Probability: 0.0015902
Best Match Spectrum:

Scan number 1860 **Raw file** Prt-OGE-Batch3-WT-Frac12
Method ITMS; CID **Genenames** C2orf80



Protein Group ID: 991
Protein Accession Numbers: Q96PE7; H7BZS7
Gene Names: MCEE
Peptide Sequence: PVIFLHPK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 111.28
Best Match Posterior Error Probability: 0.0015939
Best Match Spectrum:

Scan number 2145 **Raw file** Prt-OGE-Batch2-WT-Frac17
Method ITMS; CID **Genenames** MCEE



Protein Group ID: 993

Protein Accession Numbers: Q99996-6; Q99996; Q99996-2; Q99996-3; Q99996-5; Q99996-4; Q6PJH3; H7BZV6

Gene Names: AKAP9

Peptide Sequence: VTYGTEGLQQLQEFEEAIK

Total Number of Spectra: 1

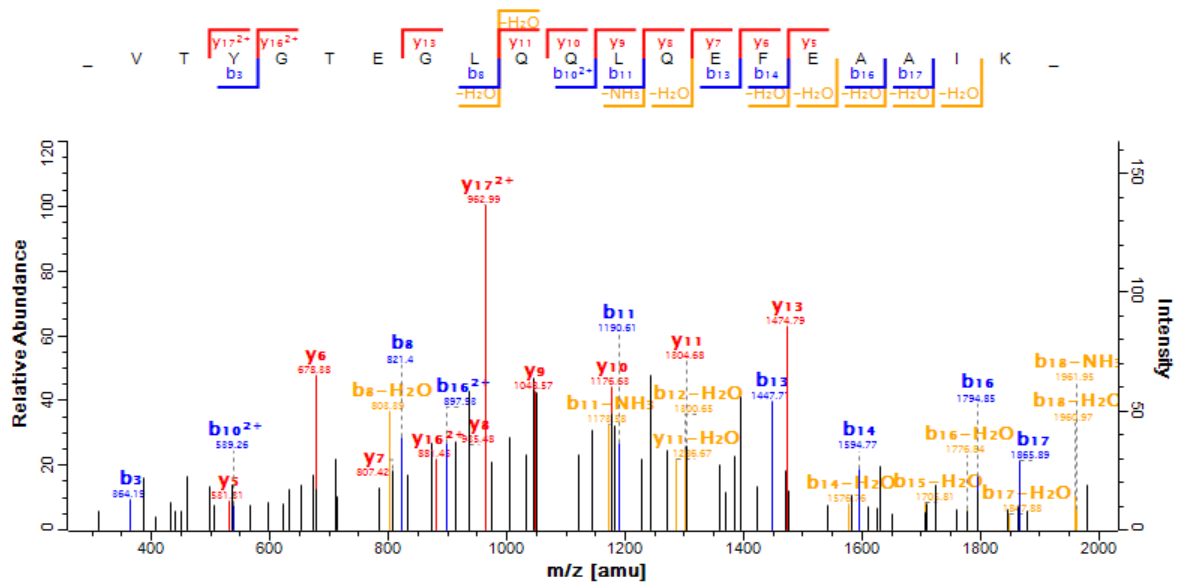
Number of Replicates (out of 10): 1

Best Match Score: 101.53

Best Match Posterior Error Probability: 0.00010224

Best Match Spectrum:

Scan number 5755 Raw file 20100930-KD-Batch5-Prt-OGE-WT-Frac6
Method ITMS: CID Genenames AKAP9



Protein Group ID: 996

Protein Accession Numbers: P61019; P61019-2; H7C125

Gene Names: RAB2A

Peptide Sequence: TASNVEEAFINTAK

Total Number of Spectra: 1

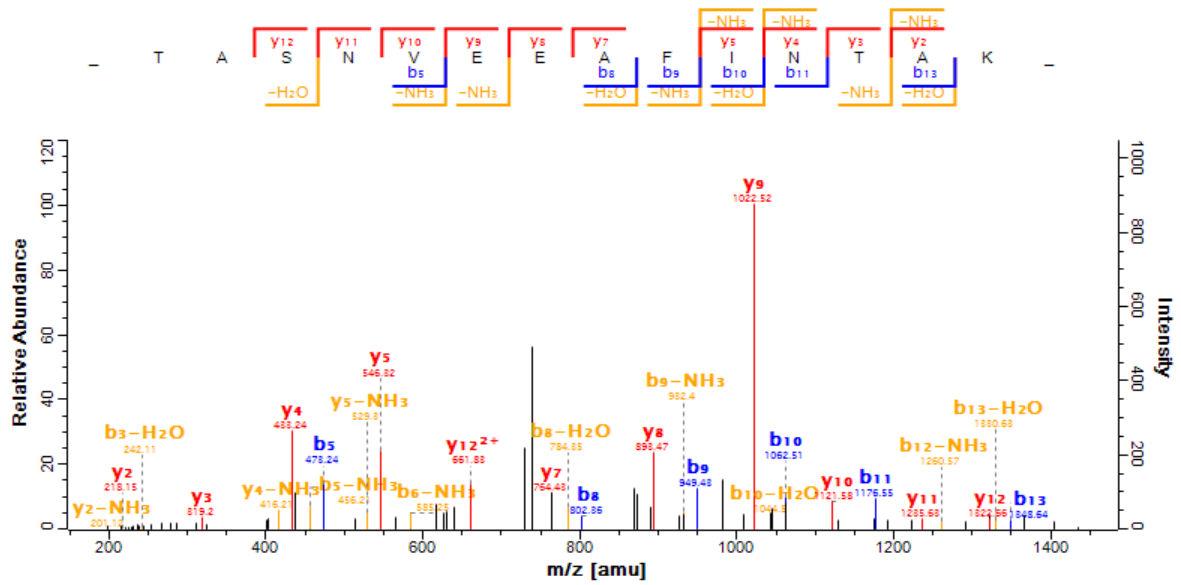
Number of Replicates (out of 10): 1

Best Match Score: 106.3

Best Match Posterior Error Probability: 0.00021087

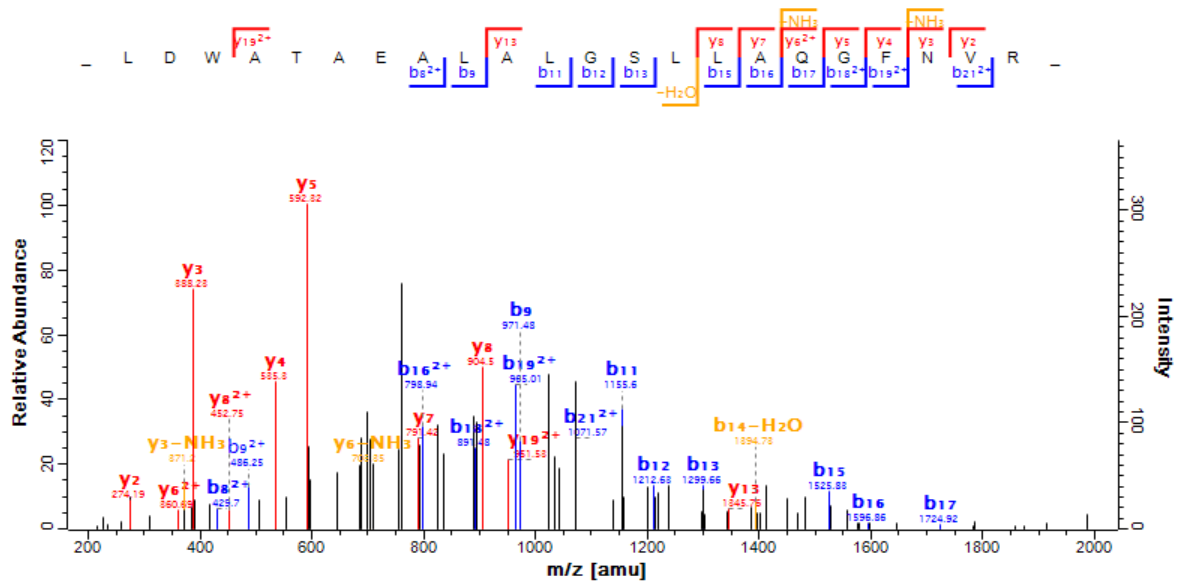
Best Match Spectrum:

Scan number	3998	Raw file	Prt-OGE-Batch3-Mock-Frac13
Method	ITMS; CID	Genenames	RAB2A



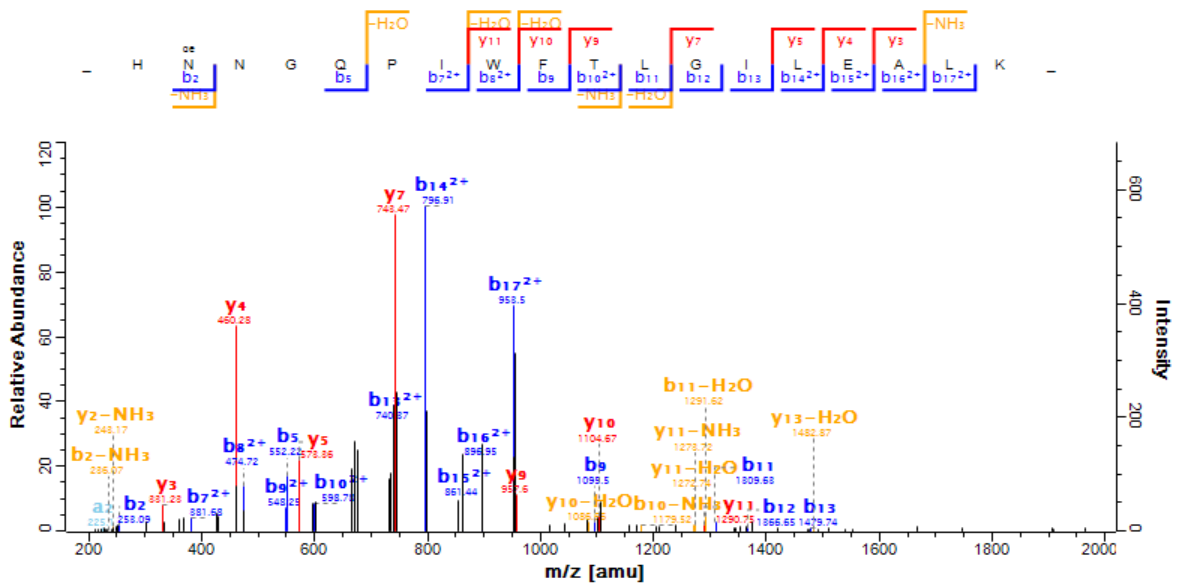
Protein Group ID: 998
Protein Accession Numbers: Q96HY7; H7C149
Gene Names: DHTKD1
Peptide Sequence: LDWATAEALALGSLLAQGFNVR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 100.45
Best Match Posterior Error Probability: 5.92E-06
Best Match Spectrum:

Scan number 8457 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac15
Method ITMS; CID **Genenames** DHTKD1



Protein Group ID: 1000
Protein Accession Numbers: Q9NWM8; H7C1Z9
Gene Names: FKBP14
Peptide Sequence: HNNGQPIWFTLGILEALK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 122.75
Best Match Posterior Error Probability: 0.00081448
Best Match Spectrum:

Scan number 7216 **Raw file** OGE-WT-Frac10
Method ITMS; CID **Genenames** FKBP14



Protein Group ID: 1001

Protein Accession Numbers: Q58EX2-4; Q58EX2; Q58EX2-3; Q58EX2-2; H7C2P2

Gene Names: SDK2

Peptide Sequence: GWGEAAEALVVVTTEK

Total Number of Spectra: 1

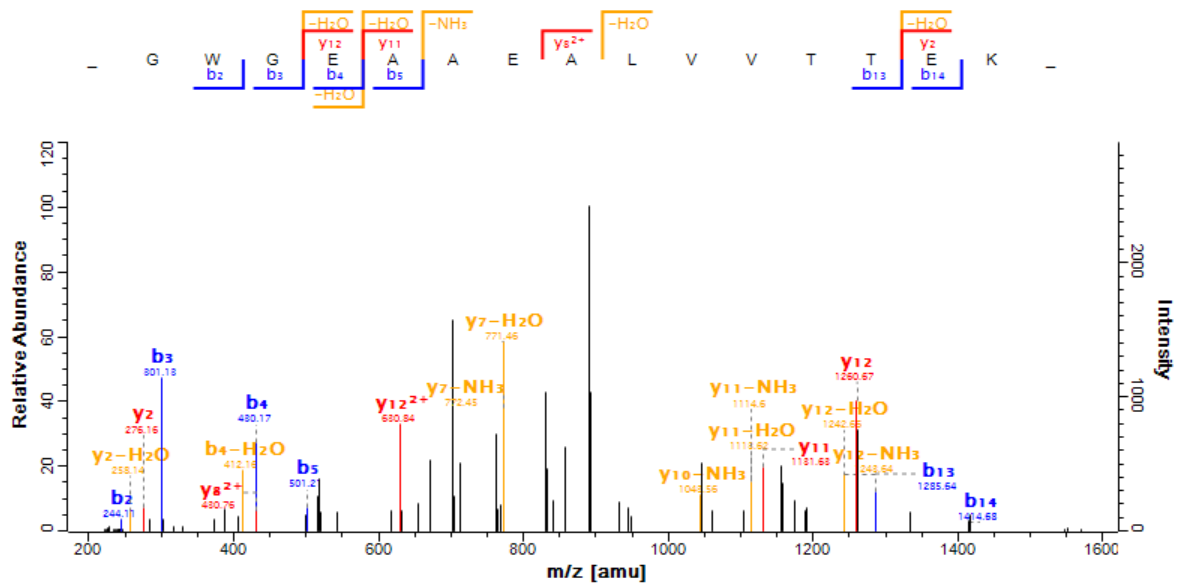
Number of Replicates (out of 10): 1

Best Match Score: 97.463

Best Match Posterior Error Probability: 0.00014213

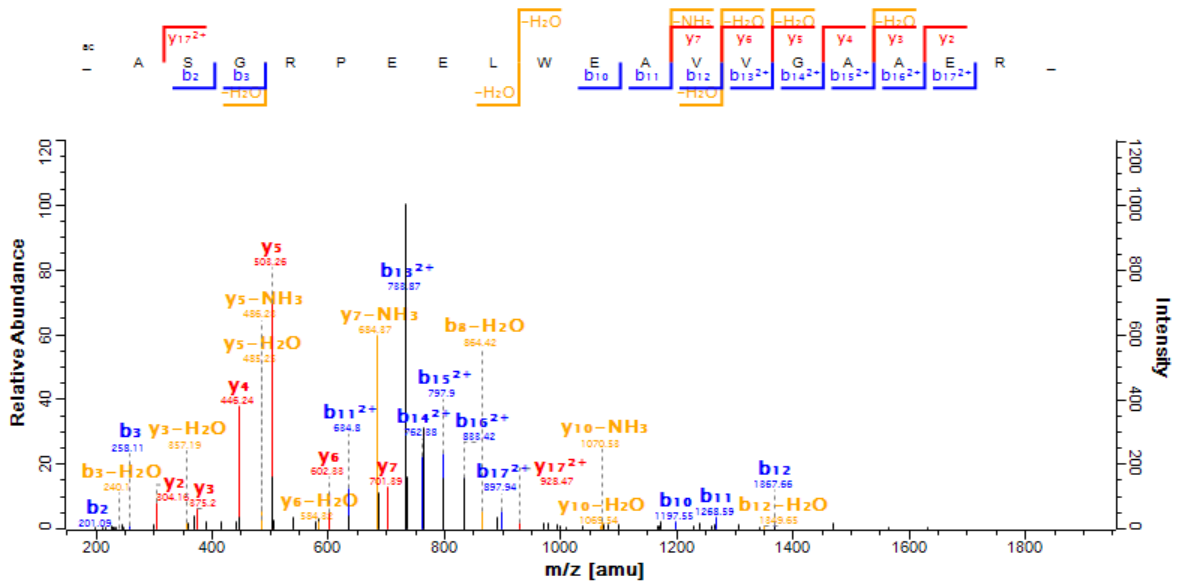
Best Match Spectrum:

Scan number	4151	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac7
Method	ITMS; CID	Genenames	SDK2



Protein Group ID: 1003
Protein Accession Numbers: Q96B36; H9KV91
Gene Names: AKT1S1
Peptide Sequence: ASGRPEELWEAVVGAAR
Total Number of Spectra: 10
Number of Replicates (out of 10): 5
Best Match Score: 106.6
Best Match Posterior Error Probability: 0.00045846
Best Match Spectrum:

Scan number 6094 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac15
Method ITMS; CID **Genenames** AKT1S1



Protein Group ID: 1008

Protein Accession Numbers: I3L416; I3L3T0; I3L0X9; I3L1U7; Q9Y3D7

Gene Names: PAM16

Peptide Sequence: SAAASNLSGLSLQEAQQILNVSK

Total Number of Spectra: 4

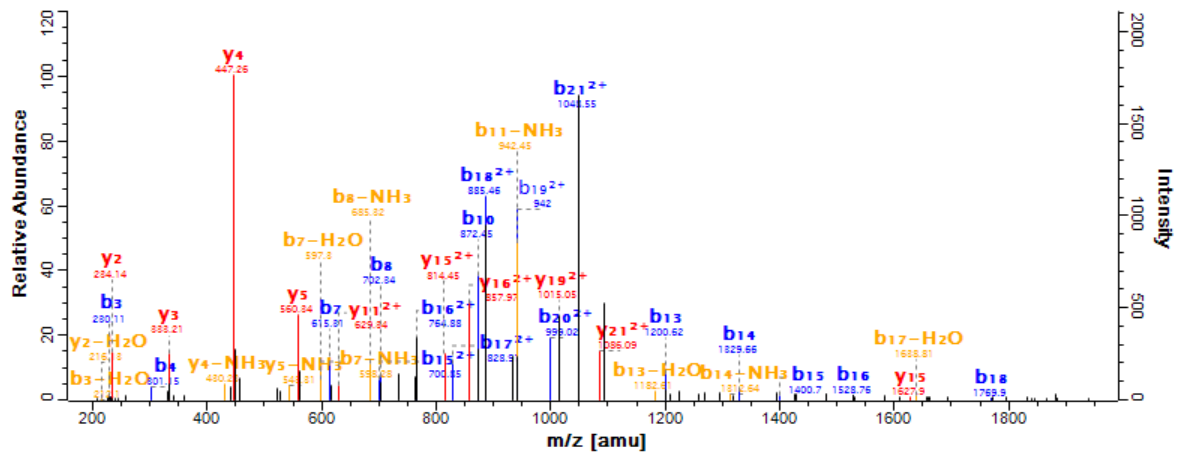
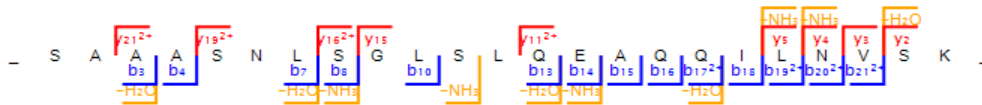
Number of Replicates (out of 10): 3

Best Match Score: 179.87

Best Match Posterior Error Probability: 1.77E-36

Best Match Spectrum:

Scan number 5976 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac22
Method ITMS; CID **Genenames** PAM16



Protein Group ID: 1021

Protein Accession Numbers: J3KN82; Q96GX9; Q96GX9-3

Gene Names: APIP

Peptide Sequence: YDDMLVVPIIENTPEEK

Total Number of Spectra: 1

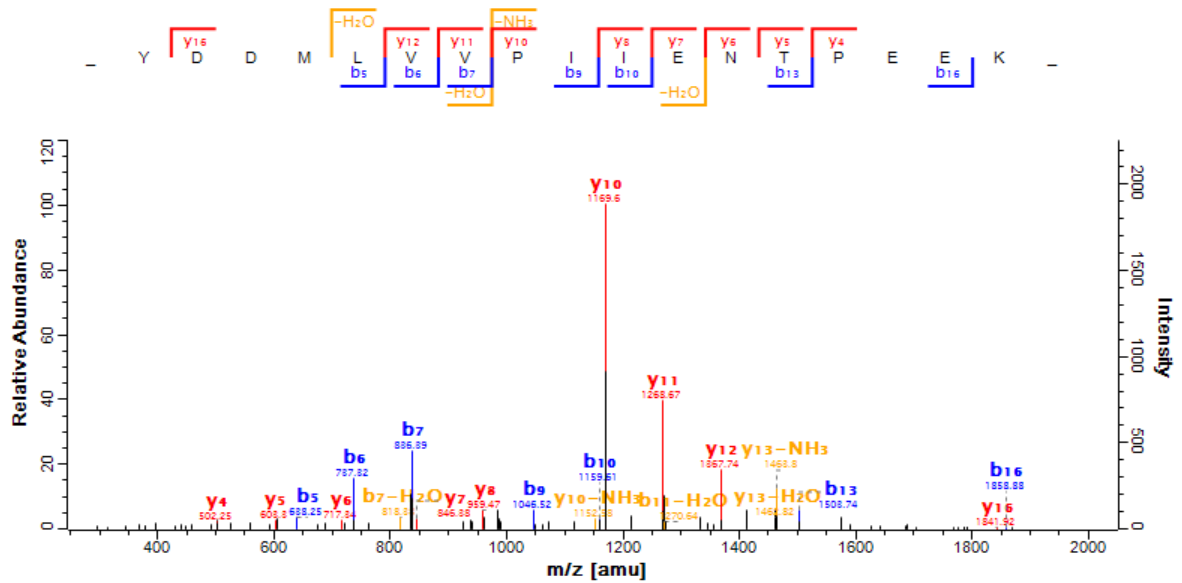
Number of Replicates (out of 10): 1

Best Match Score: 77.468

Best Match Posterior Error Probability: 0.0013854

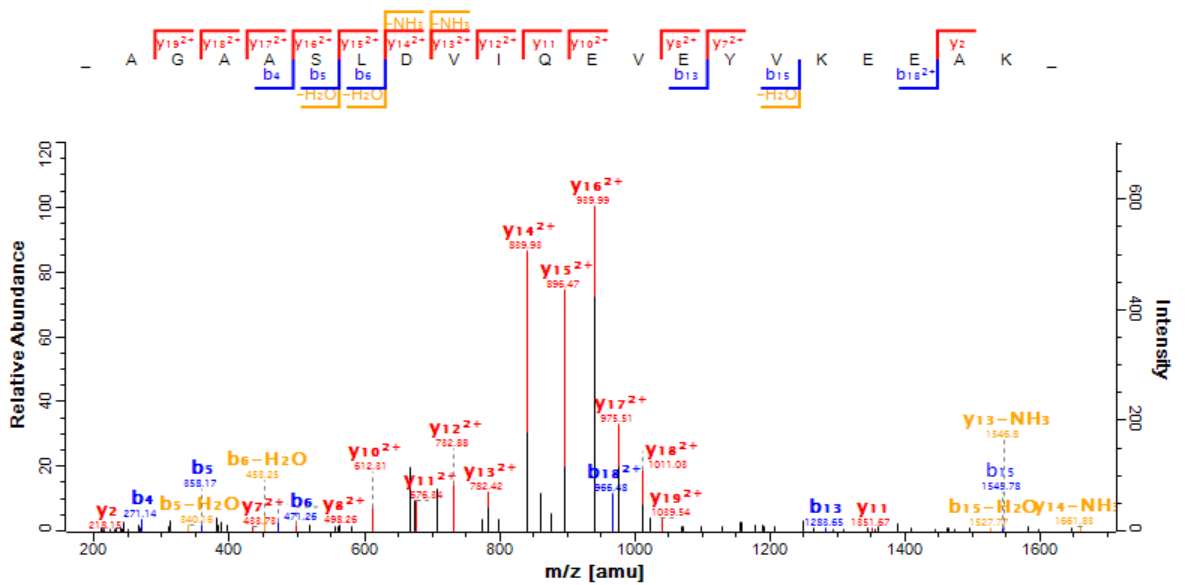
Best Match Spectrum:

Scan number 6320 **Raw file** Prt-OGE-Batch2-Mock-Frac16
Method ITMS; CID **Genenames** APIP



Protein Group ID: 1027
Protein Accession Numbers: J3KNN5; Q9UJV9
Gene Names: DDX41
Peptide Sequence: AGAASLDVIQEVEYVKEEK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 95.236
Best Match Posterior Error Probability: 0.00034531
Best Match Spectrum:

Scan number 4577 **Raw file** OGE-Mock-Frac14
Method ITMS; CID **Genenames** DDX41



Protein Group ID: 1047

Protein Accession Numbers: J3KQ73; Q14318-2; Q14318

Gene Names: FKBP8

Peptide Sequence: EFLAAMEPEPAPAPAEWLDILGNGLLR

Total Number of Spectra: 1

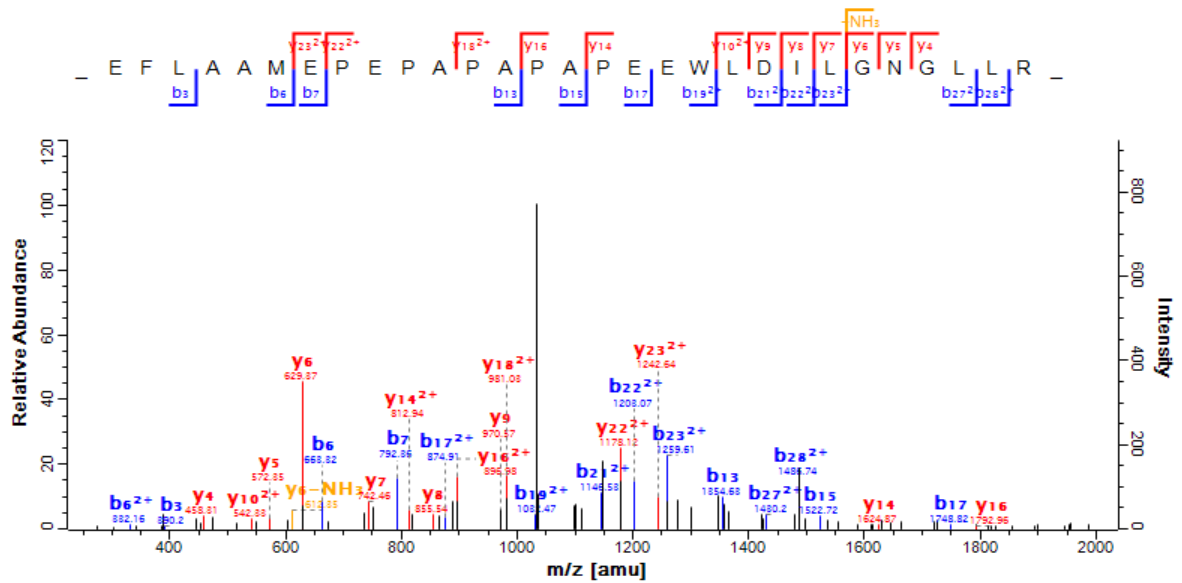
Number of Replicates (out of 10): 1

Best Match Score: 104.81

Best Match Posterior Error Probability: 9.10E-15

Best Match Spectrum:

Scan number	7828	Raw file	OGE-Mock-Frac9
Method	ITMS; CID	Genenames	FKBP8



Protein Group ID: 1052

Protein Accession Numbers: J3KQG9; Q9H3H3-3; Q9H3H3-2; Q9H3H3

Gene Names: C11orf68

Peptide Sequence: LGVLEADSAIR

Total Number of Spectra: 2

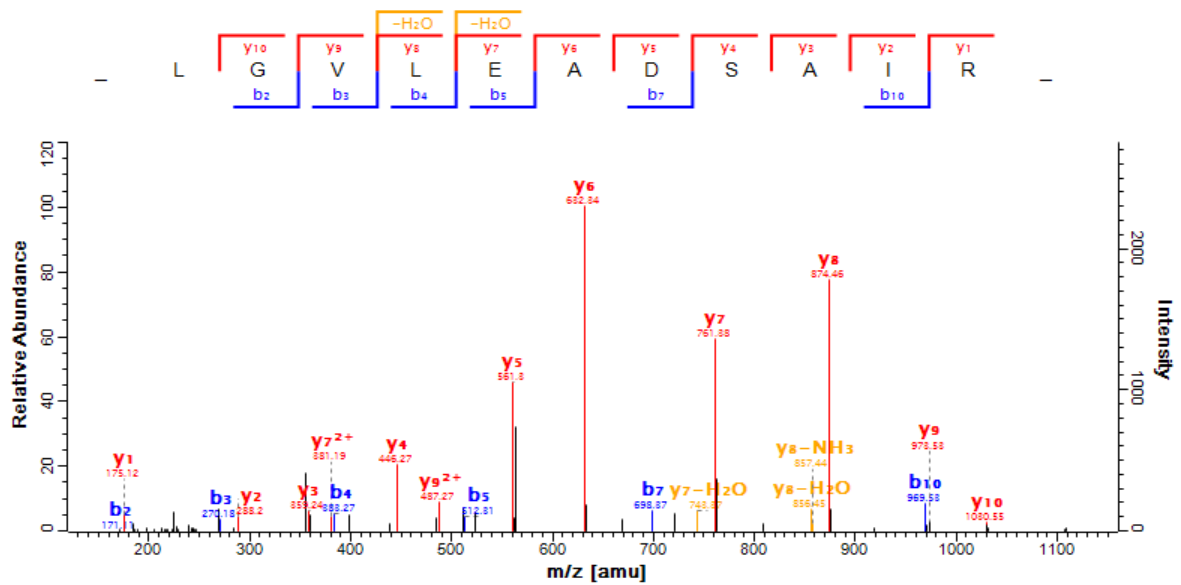
Number of Replicates (out of 10): 2

Best Match Score: 113.38

Best Match Posterior Error Probability: 0.00013328

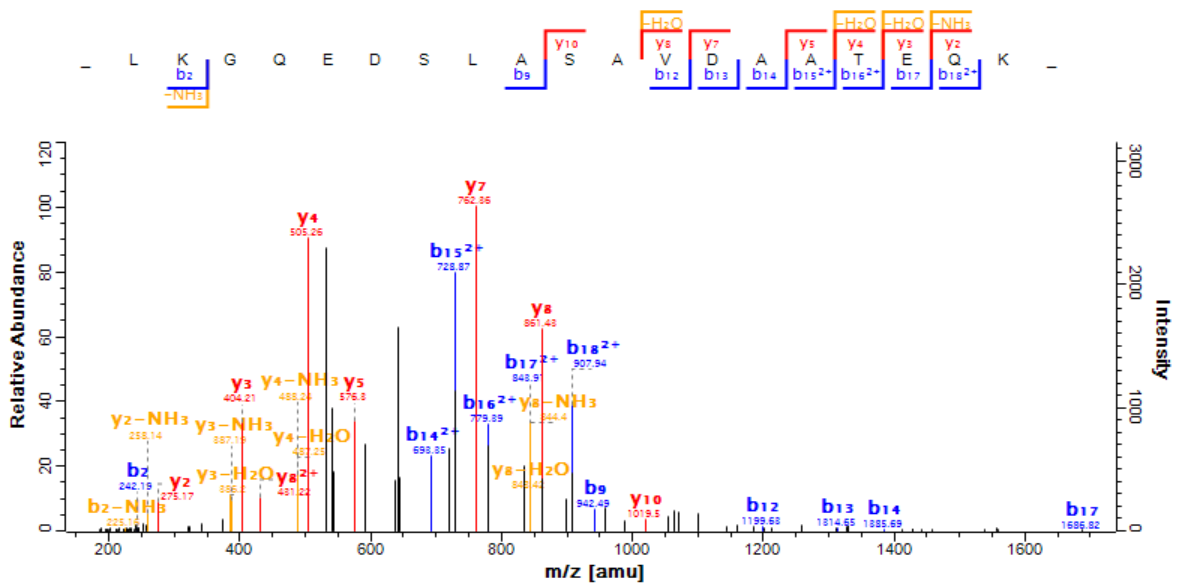
Best Match Spectrum:

Scan number	3403	Raw file	20100914-KD-Batch4-Prt-OGE-Mock-Frac13
Method	ITMS; CID	Genenames	C11orf68



Protein Group ID: 1057
Protein Accession Numbers: J3KR35; Q8WUD4
Gene Names: CCDC12
Peptide Sequence: LKGQEDSLASAVDAATEQK
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 106.93
Best Match Posterior Error Probability: 0.00017751
Best Match Spectrum:

Scan number 3728 **Raw file** Prt-OGE-Batch3-Mock-Frac12
Method ITMS; CID **Genenames** CCDC12



Protein Group ID: 1060

Protein Accession Numbers: Q9BT23; J3QQM5; J3KRR0

Gene Names: LIMD2

Peptide Sequence: MFQAAGAAQATPSHDAK

Total Number of Spectra: 1

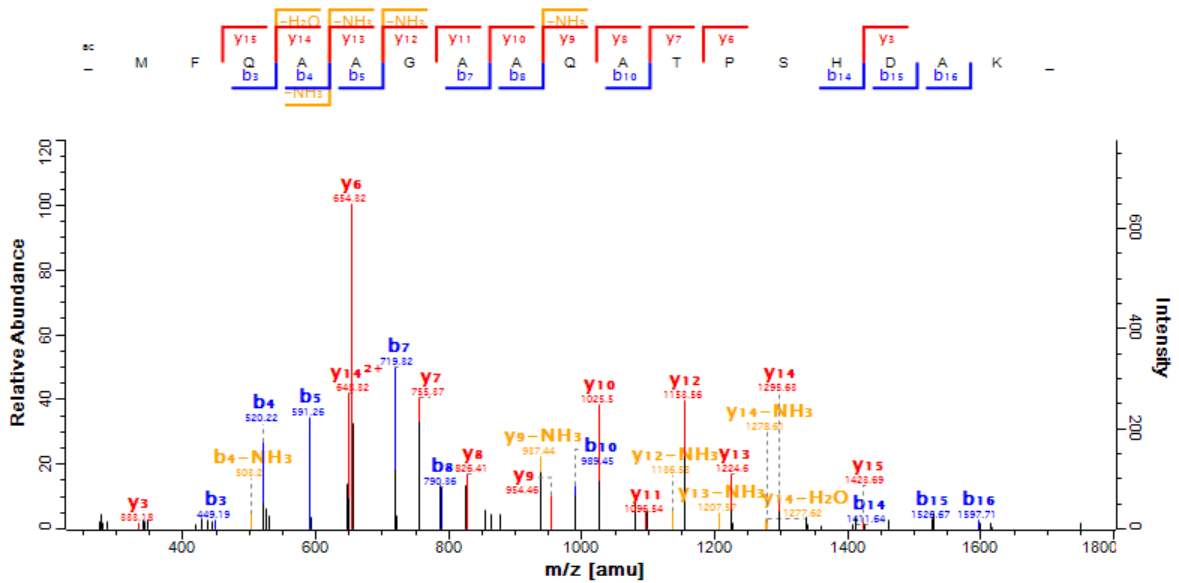
Number of Replicates (out of 10): 1

Best Match Score: 128.59

Best Match Posterior Error Probability: 3.84E-05

Best Match Spectrum:

Scan number 2863 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac22
Method ITMS; CID **Genenames** LIMD2



Protein Group ID: 1062

Protein Accession Numbers: P0CB44; Q8WVK7; J3KSP0; J3KRZ0; J3QS74

Gene Names: SKA2L;SKA2

Peptide Sequence: MEAEVDKLELMFQK

Total Number of Spectra: 1

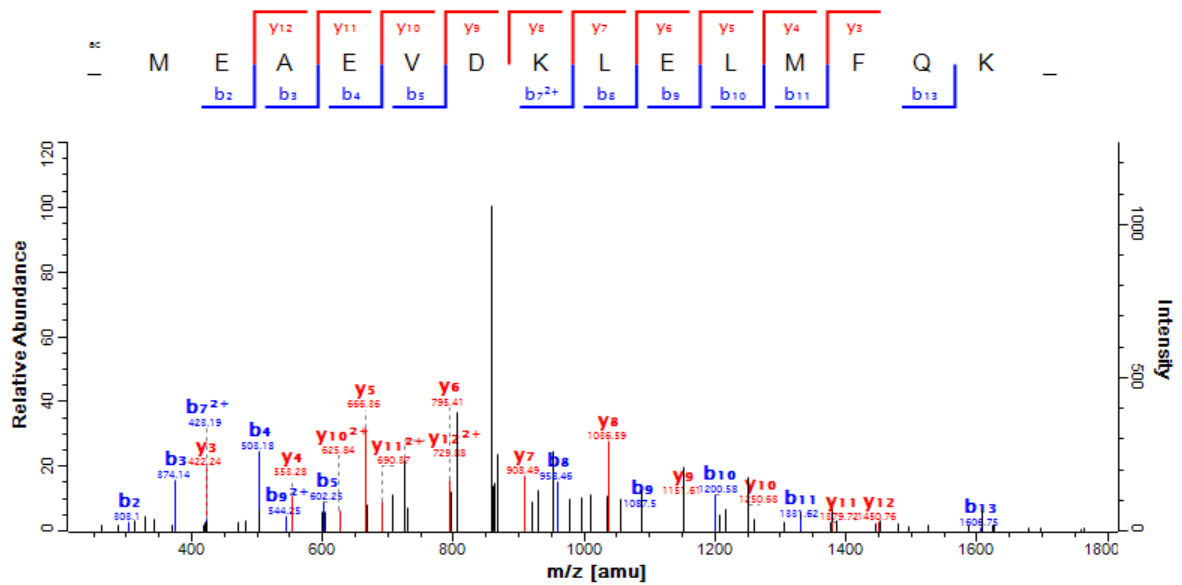
Number of Replicates (out of 10): 1

Best Match Score: 115.1

Best Match Posterior Error Probability: 0.00035553

Best Match Spectrum:

Scan number	7430	Raw file	Prt-OGE-Batch2-Mock-Frac14
Method	ITMS; CID	Genenames	SKA2L;SKA2



Protein Group ID: 1082

Protein Accession Numbers: J3QRS3; P19105; J3KTJ1

Gene Names: MYL12A

Peptide Sequence: NPTDEYLDAMMNEAPGPINFTMFLTMFGEK

Total Number of Spectra: 1

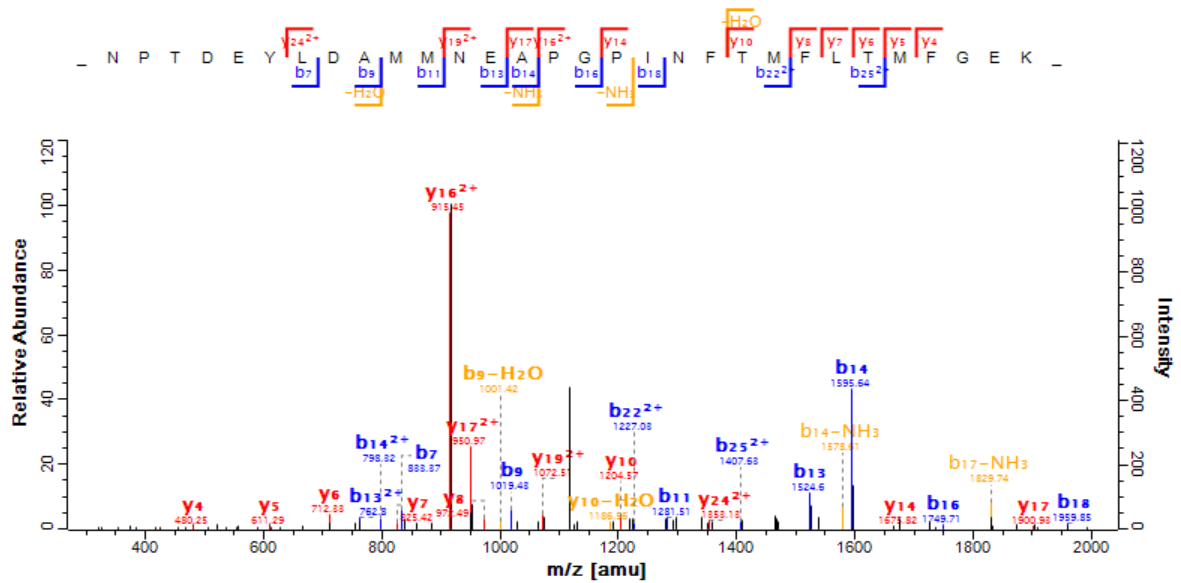
Number of Replicates (out of 10): 1

Best Match Score: 80.439

Best Match Posterior Error Probability: 2.05E-07

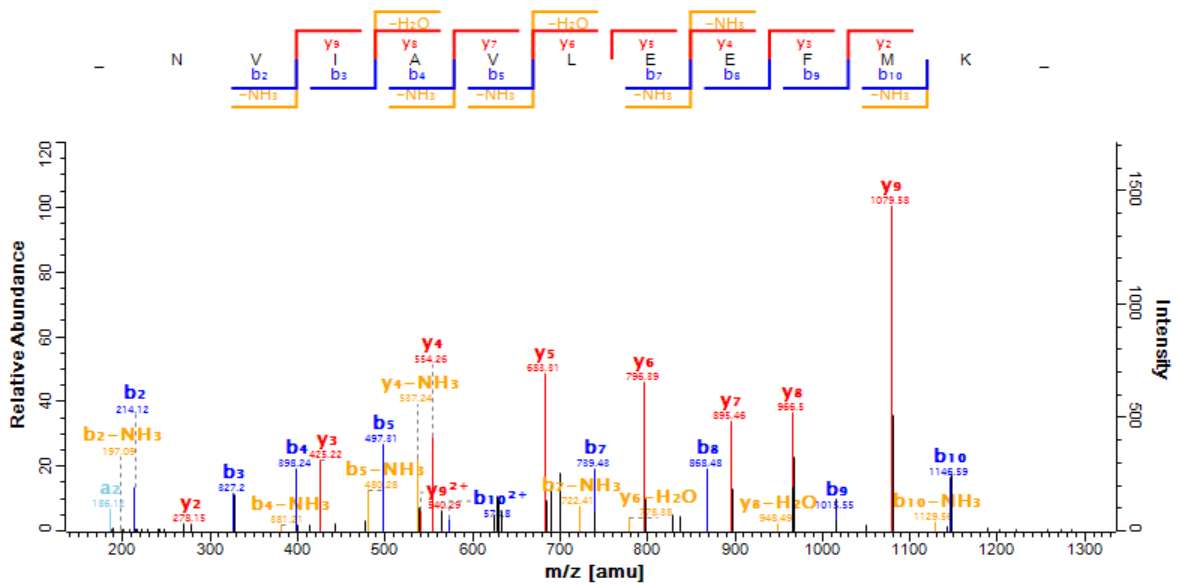
Best Match Spectrum:

Scan number 7202 **Raw file** OGEWT-Frac4
Method ITMS; CID **Genenames** MYL12A



Protein Group ID: 1090
Protein Accession Numbers: J9JIC5; Q9HAS0
Gene Names: C17orf75
Peptide Sequence: NVIAVLEEFMK
Total Number of Spectra: 22
Number of Replicates (out of 10): 10
Best Match Score: 178.71
Best Match Posterior Error Probability: 8.12E-11
Best Match Spectrum:

Scan number 6630 **Raw file** OGE-WT-Frac6
Method ITMS; CID **Genenames** C17orf75



Protein Group ID: 1094

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

Gene Names: KATNAL2

Peptide Sequence: GLLLYGPPGTGK

Total Number of Spectra: 72

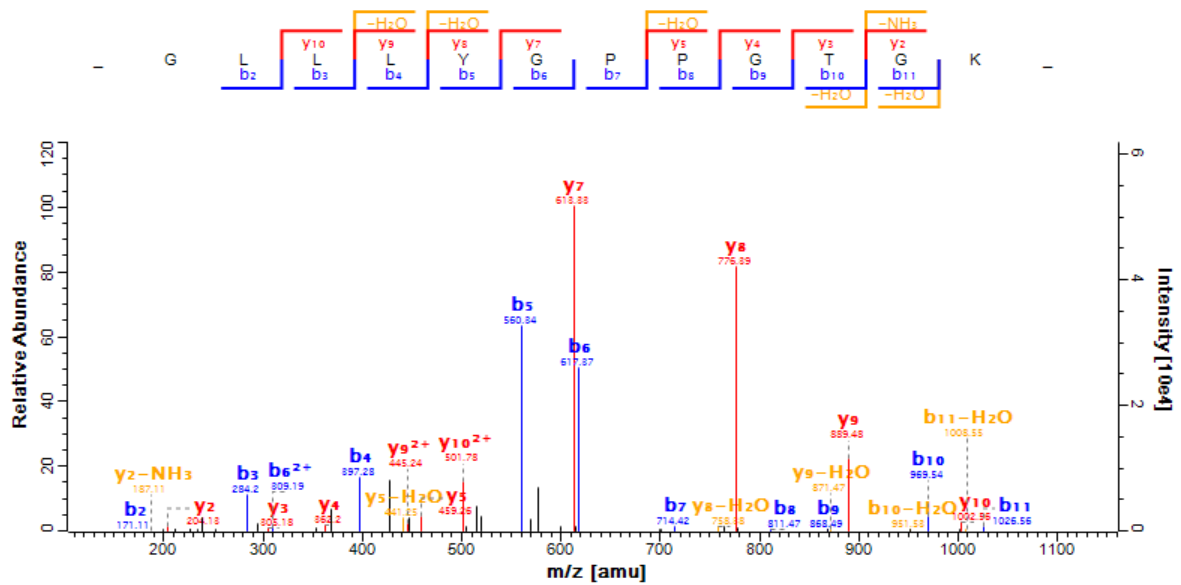
Number of Replicates (out of 10): 10

Best Match Score: 186.87

Best Match Posterior Error Probability: 1.19E-15

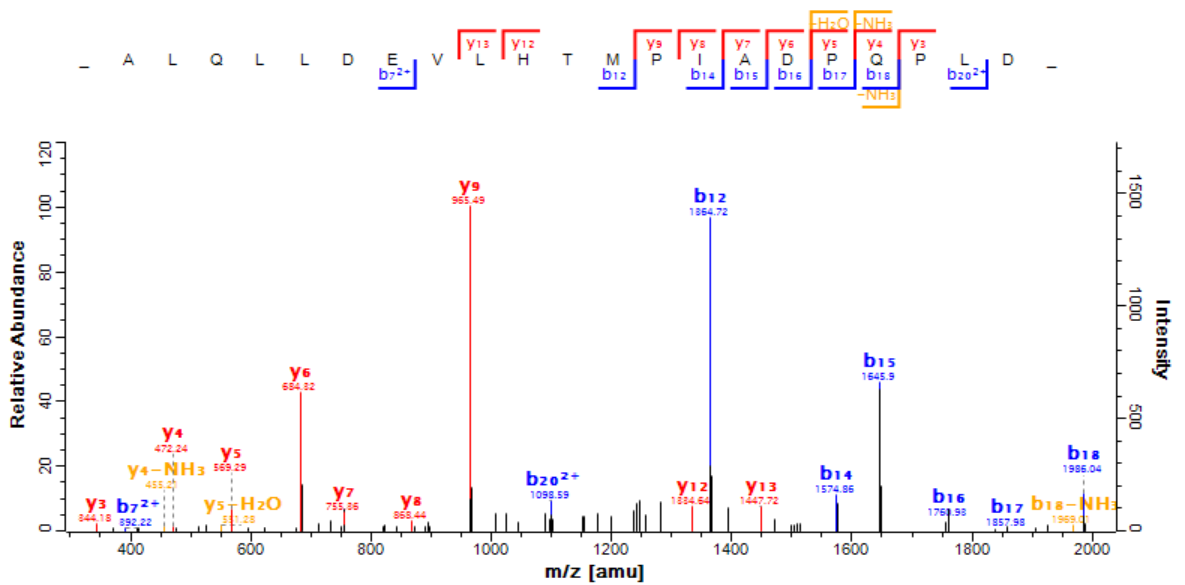
Best Match Spectrum:

Scan number 3726 **Raw file** OGE-WT-Frac7
Method ITMS; CID **Genenames** KATNAL2



Protein Group ID: 1097
Protein Accession Numbers: Q13485; K7EIU8
Gene Names: SMAD4
Peptide Sequence: ALQLLDEVLHTMPIADPQLD
Total Number of Spectra: 11
Number of Replicates (out of 10): 7
Best Match Score: 81.665
Best Match Posterior Error Probability: 0.00029407
Best Match Spectrum:

Scan number 7681 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac16
Method ITMS; CID **Genenames** SMAD4



Protein Group ID: 1098

Protein Accession Numbers: Q96ED9; Q96ED9-2; K7ENU5; K7EJ48; K7EJ65; K7EMR5; K7EMG7; K7EJA7; K7EQA2

Gene Names: HOOK2

Peptide Sequence: IMTLEESVQHVVMEAIQELMTK

Total Number of Spectra: 3

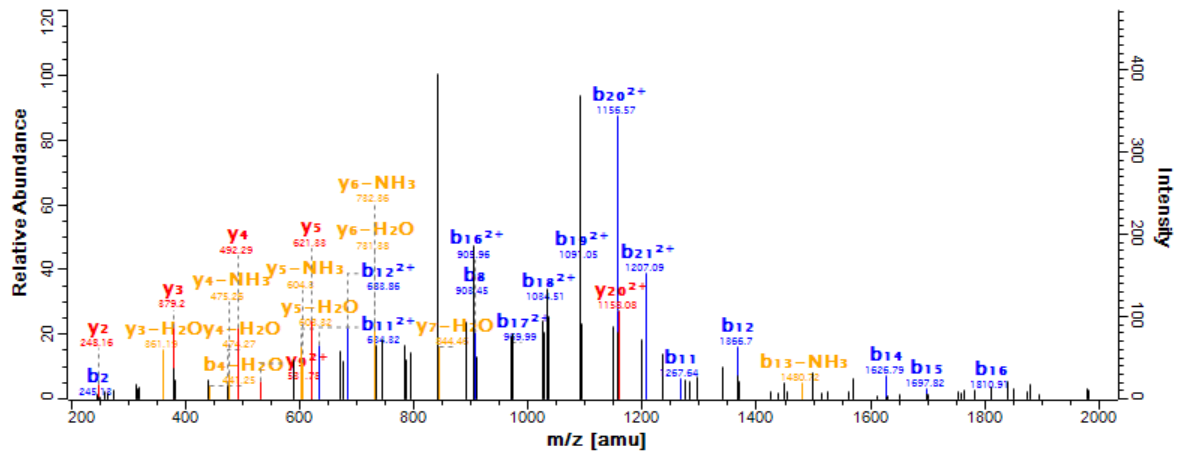
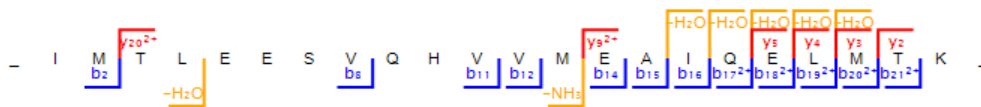
Number of Replicates (out of 10): 3

Best Match Score: 117.65

Best Match Posterior Error Probability: 2.55E-08

Best Match Spectrum:

Scan number	8973	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac9
Method	ITMS: CID	Genenames	HOOK2



Protein Group ID: 1102

Protein Accession Numbers: P84243; K7EK07

Gene Names: H3F3A

Peptide Sequence: FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK

Total Number of Spectra: 18

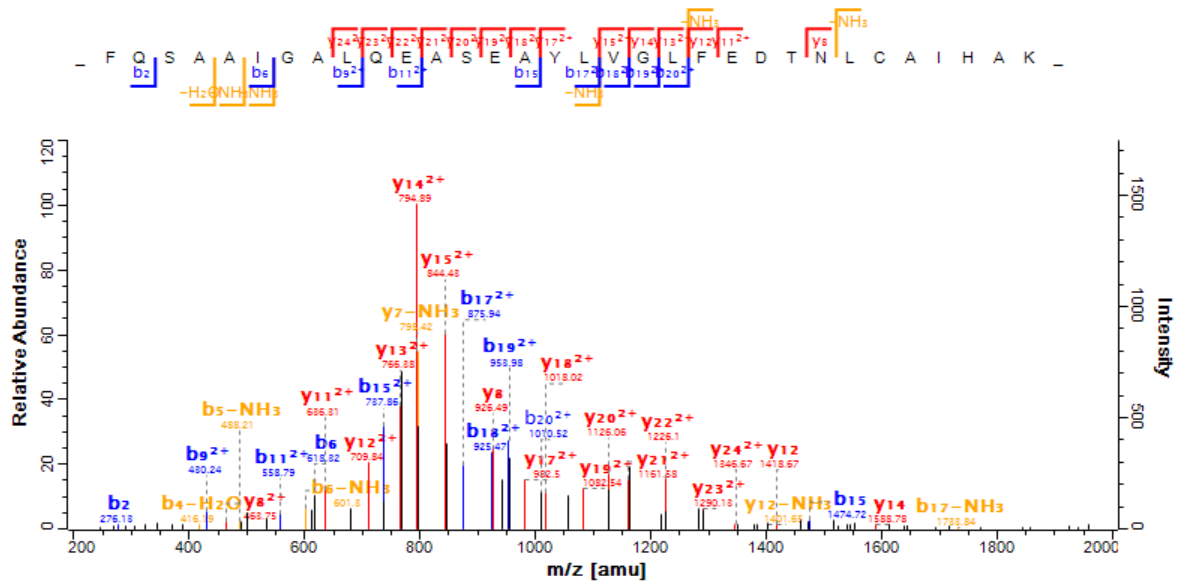
Number of Replicates (out of 10): 4

Best Match Score: 130.83

Best Match Posterior Error Probability: 1.15E-42

Best Match Spectrum:

Scan number 8309 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac14
Method ITMS; CID **Genenames** H3F3A



Protein Group ID: 1104

Protein Accession Numbers: Q96CS2; K7EKH4; Q96CS2-2

Gene Names: HAUS1

Peptide Sequence: DTSLASFIPAVNDLTSDLFR

Total Number of Spectra: 2

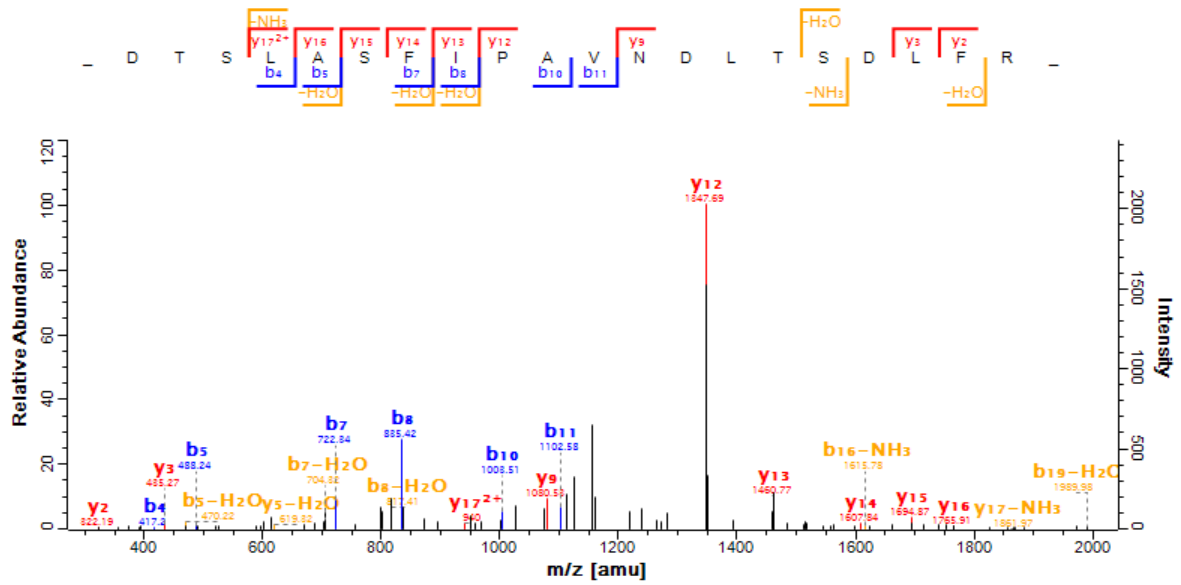
Number of Replicates (out of 10): 2

Best Match Score: 81.157

Best Match Posterior Error Probability: 0.00084689

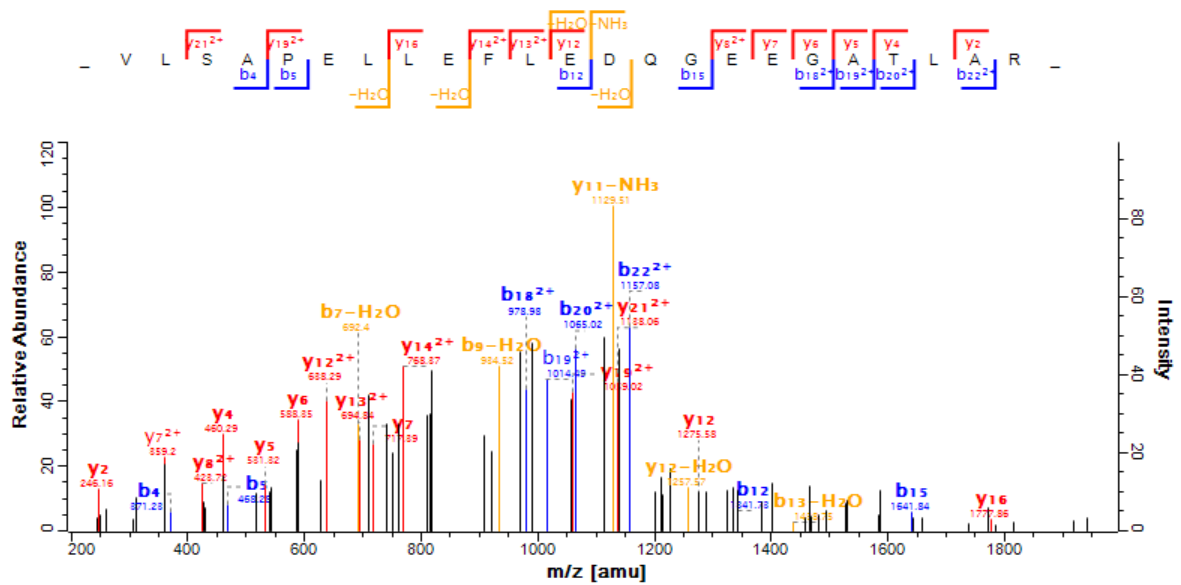
Best Match Spectrum:

Scan number 8042 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac8
Method ITMS; CID **Genenames** HAUS1



Protein Group ID: 1107
Protein Accession Numbers: Q8N3E9; K7EKJ1
Gene Names: PLCD3
Peptide Sequence: VLSAPLEFLQDQGGATLAR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 79.461
Best Match Posterior Error Probability: 0.00016693
Best Match Spectrum:

Scan number 6229 **Raw file** OGE-Mock-Frac16
Method ITMS; CID **Genenames** PLCD3



Protein Group ID: 1109

Protein Accession Numbers: O14732; O14732-2; K7ELF8; K7EL65; Q6PIP6

Gene Names: IMPA2

Peptide Sequence: TSAADLVTTEDHLVEDLIISELR

Total Number of Spectra: 13

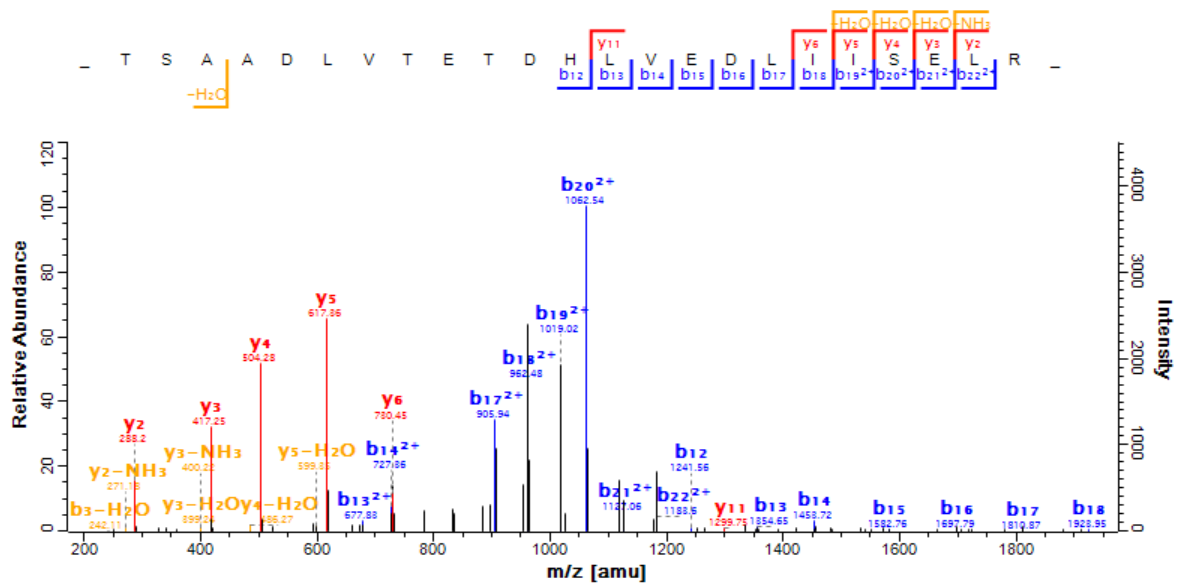
Number of Replicates (out of 10): 6

Best Match Score: 111.65

Best Match Posterior Error Probability: 3.46E-09

Best Match Spectrum:

Scan number 9400 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac13
Method ITMS; CID **Genenames** IMPA2



Protein Group ID: 1113

Protein Accession Numbers: Q6UW68; K7ELQ9; K7EPR0; K7EM09

Gene Names: TMEM205

Peptide Sequence: GLGGEVPGSHQGPDPYR

Total Number of Spectra: 14

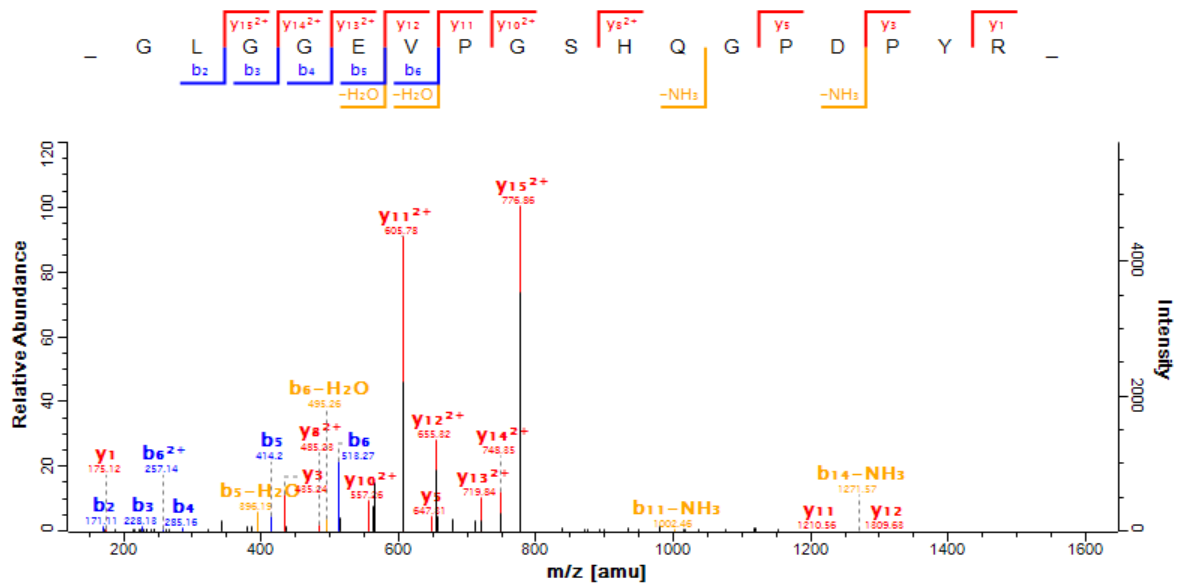
Number of Replicates (out of 10): 6

Best Match Score: 106.58

Best Match Posterior Error Probability: 0.00017942

Best Match Spectrum:

Scan number 1920 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac12
Method ITMS; CID **Genenames** TMEM205



Protein Group ID: 1114

Protein Accession Numbers: Q96EE3-1; Q96EE3; K7ELV2; K7EP88; K7ENI5

Gene Names: SEH1L

Peptide Sequence: DLIHDVSFDFHGR

Total Number of Spectra: 1

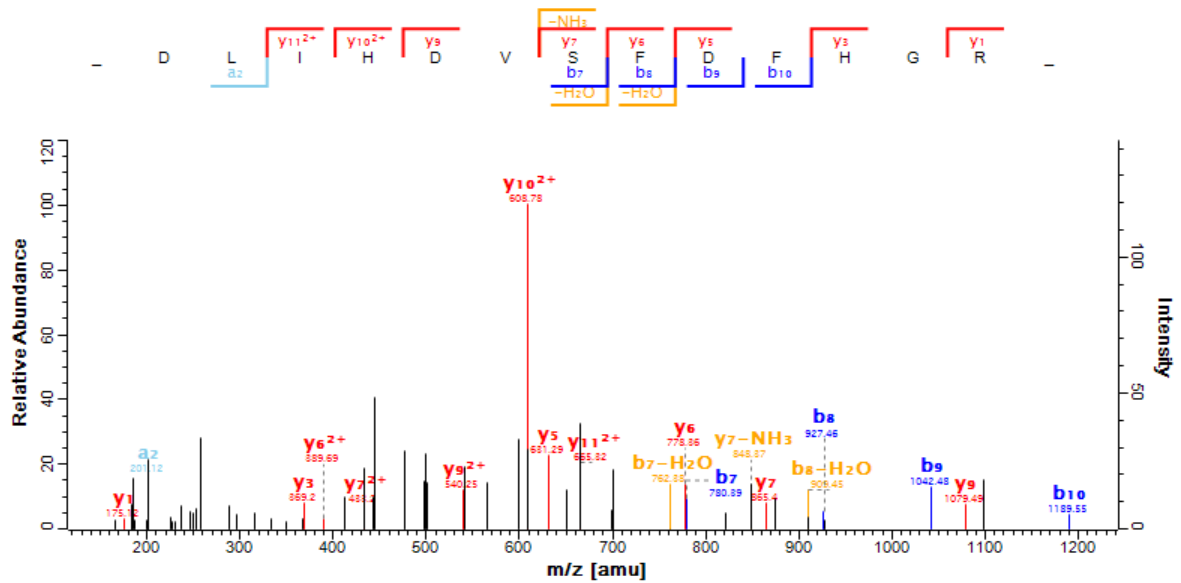
Number of Replicates (out of 10): 1

Best Match Score: 101.71

Best Match Posterior Error Probability: 0.00049825

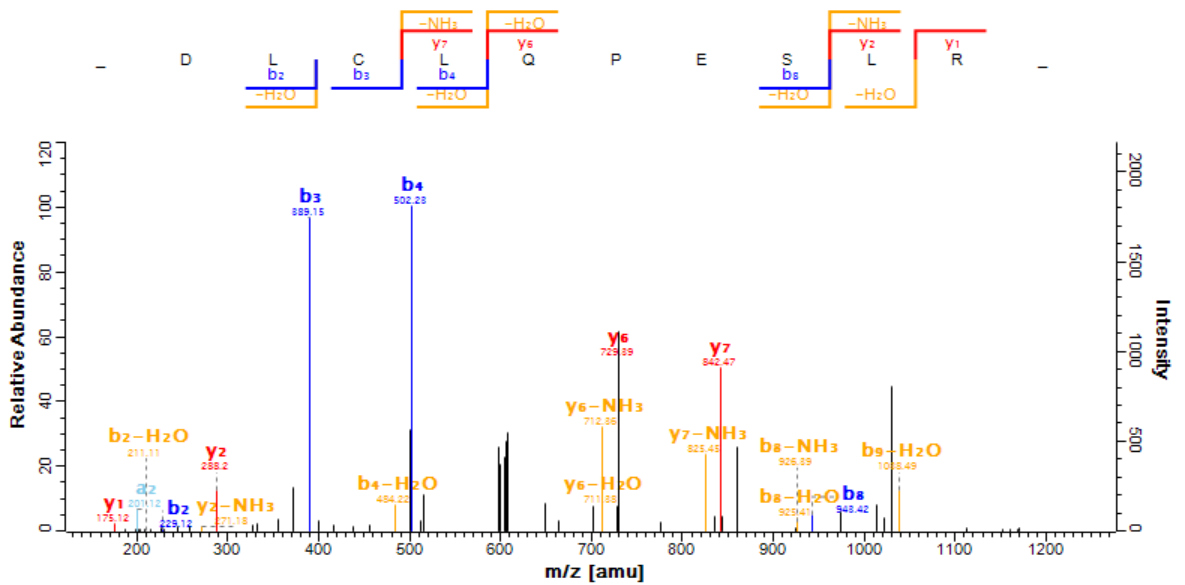
Best Match Spectrum:

Scan number 5306 **Raw file** Prt-OGE-Batch2-Mock-Frac18
Method ITMS; CID **Genenames** SEH1L



Protein Group ID: 1117
Protein Accession Numbers: K7EM50
Gene Names:
Peptide Sequence: DLCLQPESLR
Total Number of Spectra: 7
Number of Replicates (out of 10): 7
Best Match Score: 101.65
Best Match Posterior Error Probability: 0.00052413
Best Match Spectrum:

Scan number 3634 **Raw file** OGEWT-Frac4
Method ITMS; CID **Pepti...** 101.65



Protein Group ID: 1120

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

Gene Names: ELOF1

Peptide Sequence: MTGTLETQFTCPFNHEK

Total Number of Spectra: 1

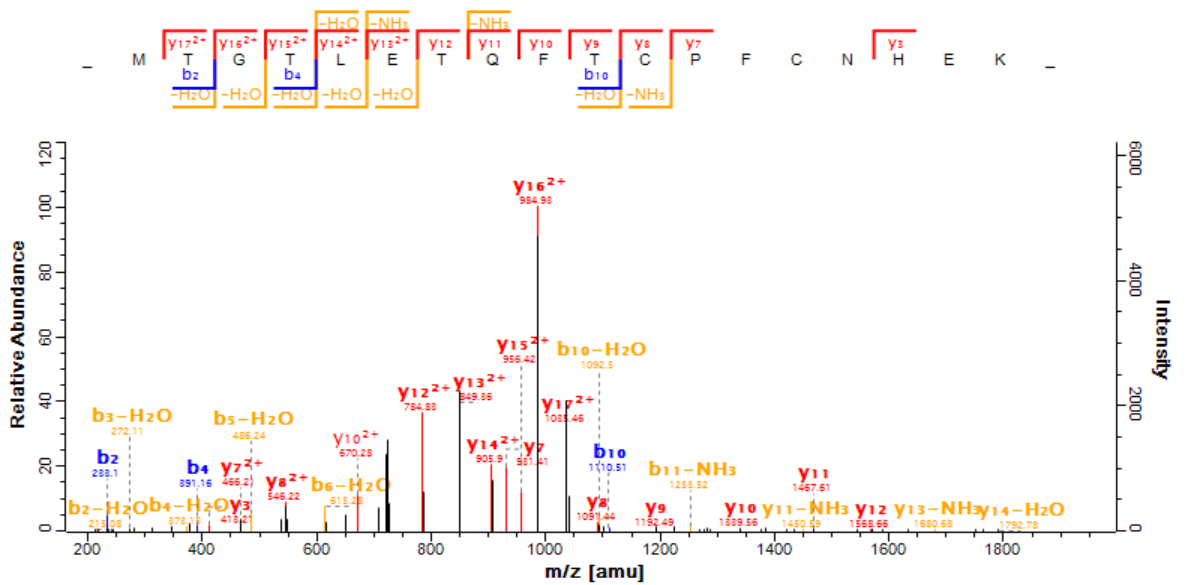
Number of Replicates (out of 10): 1

Best Match Score: 109.07

Best Match Posterior Error Probability: 0.00012111

Best Match Spectrum:

Scan number 4545 **Raw file** Prt-OGE-Batch2-Mock-Frac19
Method ITMS; CID **Genenames** ELOF1



Protein Group ID: 1121

Protein Accession Numbers: Q8N2U0; K7ERE1; K7ENI6

Gene Names: C17orf61

Peptide Sequence: AGPAAAFR

Total Number of Spectra: 2

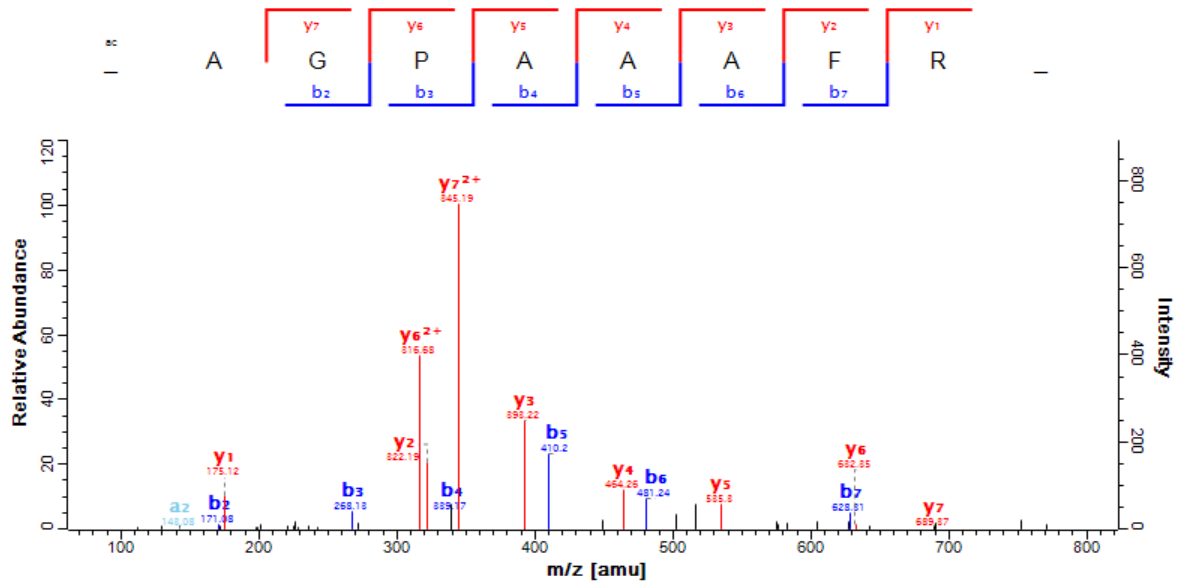
Number of Replicates (out of 10): 2

Best Match Score: 134.66

Best Match Posterior Error Probability: 0.0013815

Best Match Spectrum:

Scan number	2002	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac21
Method	ITMS; CID	Genenames	C17orf61



Protein Group ID: 1122

Protein Accession Numbers: Q9BTD8; K7EP90; Q9BTD8-3; Q9BTD8-2; Q9BTD8-4; K7EQ03

Gene Names: RBM42

Peptide Sequence: TAAGSSWEDPSLLEWDADDFR

Total Number of Spectra: 2

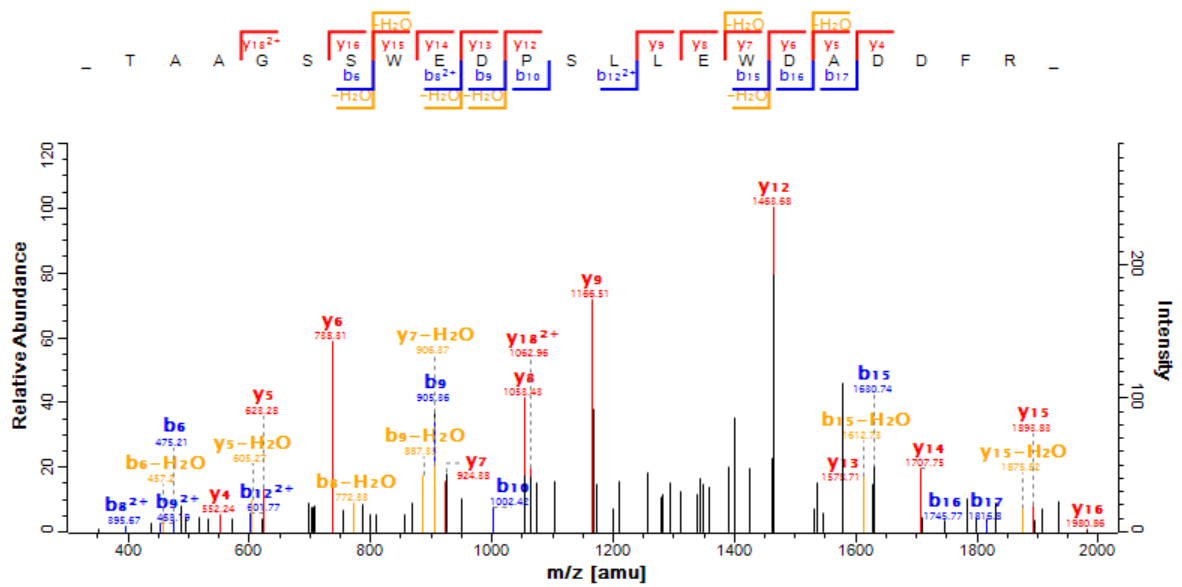
Number of Replicates (out of 10): 1

Best Match Score: 108.14

Best Match Posterior Error Probability: 7.79E-07

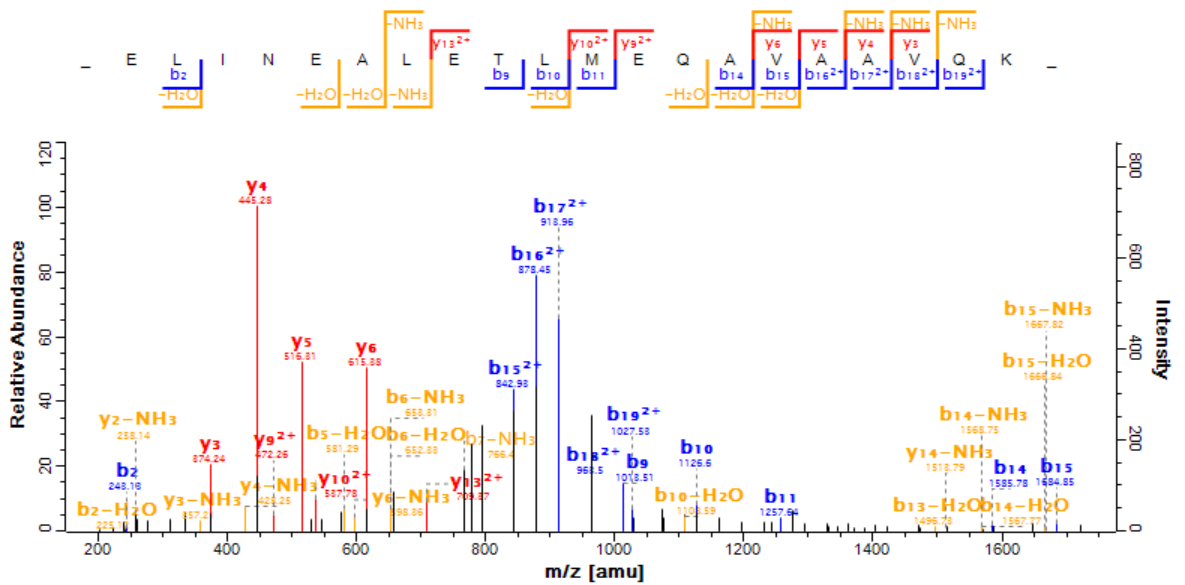
Best Match Spectrum:

Scan number 5086 **Raw file** Prt-OGE-Batch2-WT-Frac14
Method ITMS: CID **Genenames** RBM42



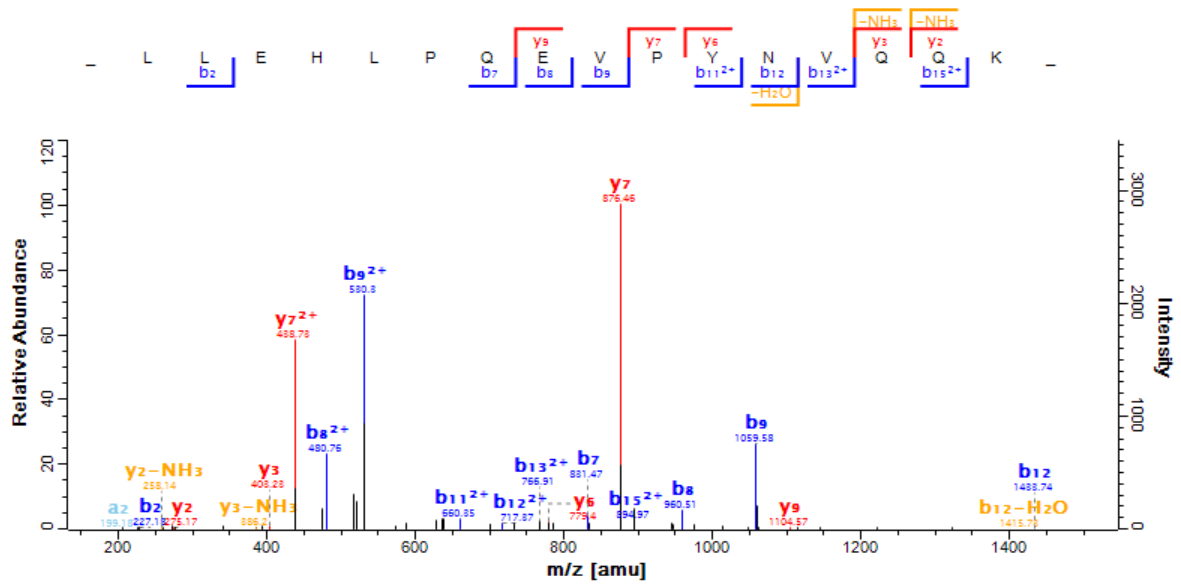
Protein Group ID: 1123
Protein Accession Numbers: Q96C10; K7EPP0
Gene Names: DHX58
Peptide Sequence: ELINEALETLMEQAVAAVQK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 130.21
Best Match Posterior Error Probability: 1.40E-07
Best Match Spectrum:

Scan number 6953 **Raw file** Prt-OGE-Batch2-WT-Frac17
Method ITMS; CID **Genenames** DHX58



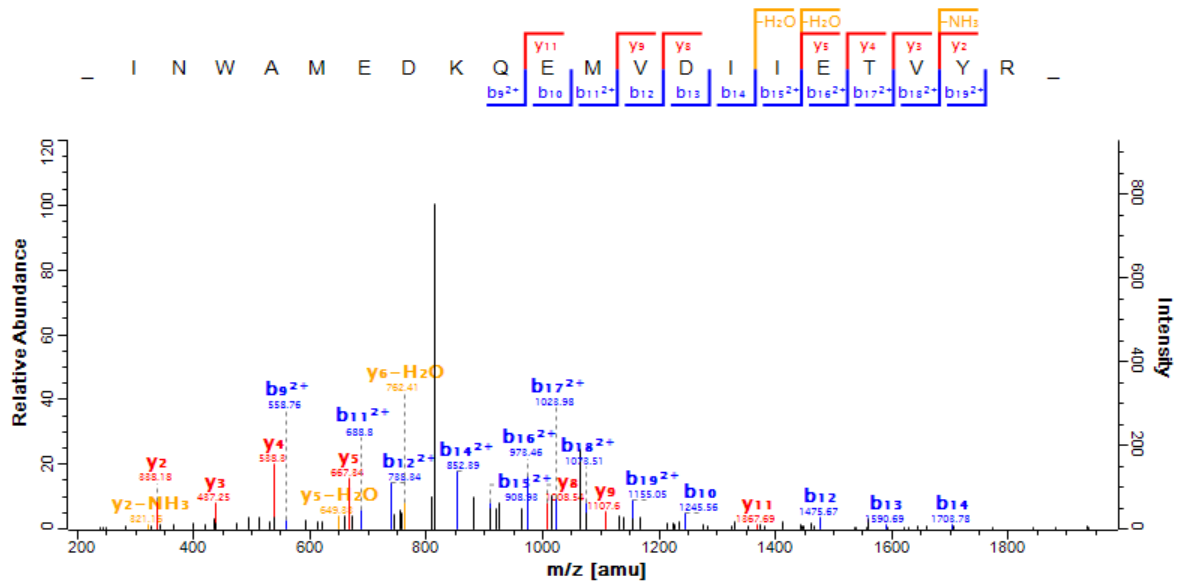
Protein Group ID: 1126
Protein Accession Numbers: O75616; K7EQJ8
Gene Names: ERAL1
Peptide Sequence: LLEHLPQEVYVNPVQK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 97.273
Best Match Posterior Error Probability: 0.0002313
Best Match Spectrum:

Scan number 3714 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac19
Method ITMS; CID **Genenames** ERAL1



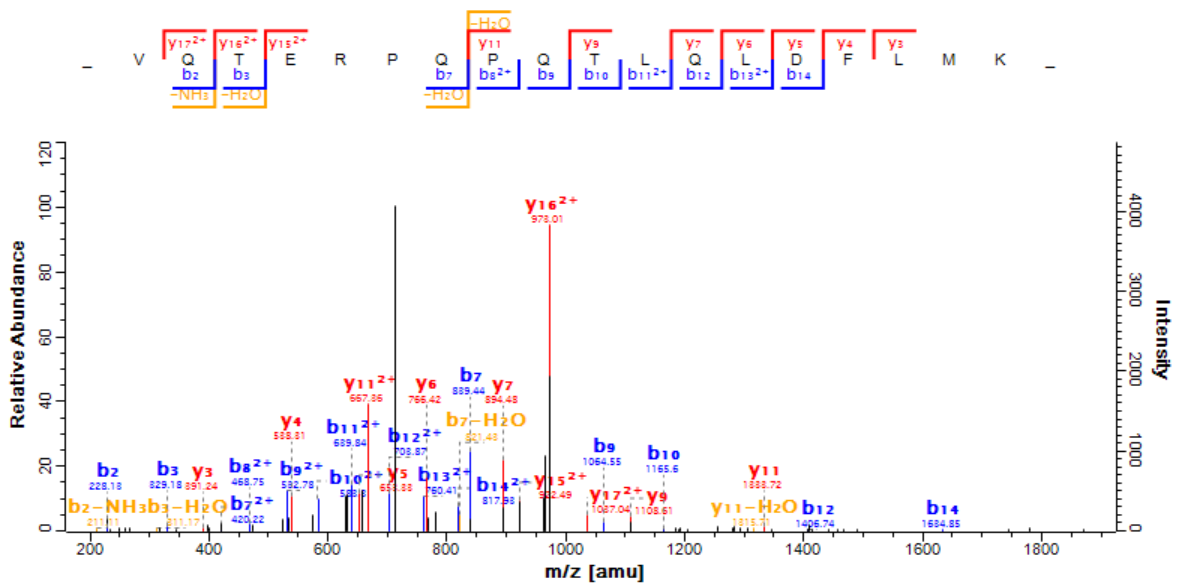
Protein Group ID: 1130
Protein Accession Numbers: P83876; K7ESL1
Gene Names: TXNL4A
Peptide Sequence: INWAMEDKQEMVDIIETVYR
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 91.475
Best Match Posterior Error Probability: 0.00055968
Best Match Spectrum:

Scan number 6531 **Raw file** OGE-Mock-Frac8
Method ITMS; CID **Genenames** TXNL4A



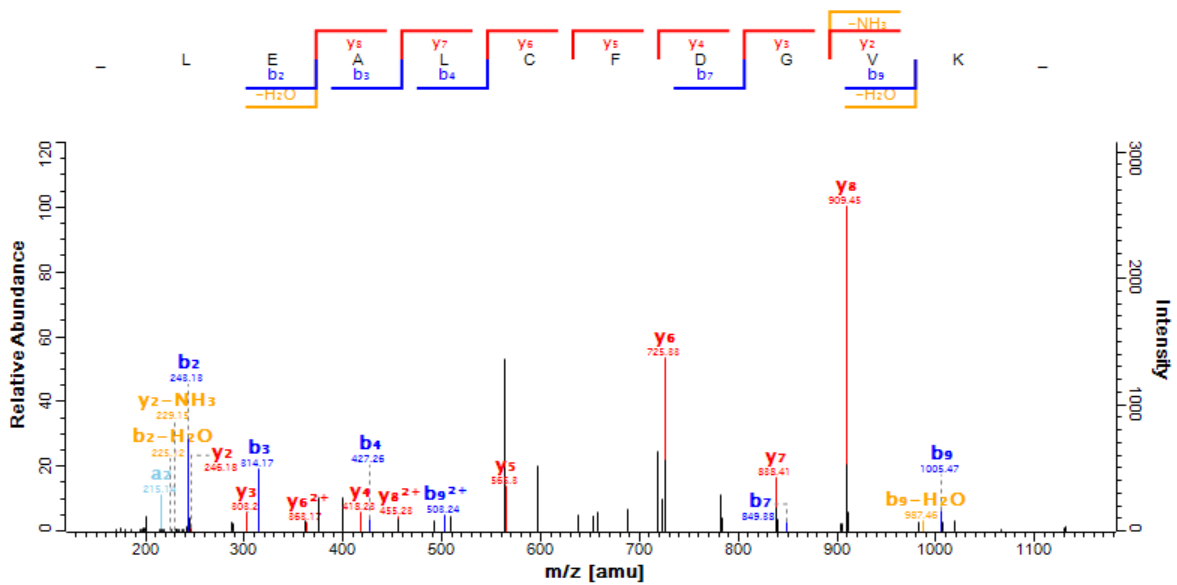
Protein Group ID: 1147
Protein Accession Numbers: O00399
Gene Names: DCTN6
Peptide Sequence: VQTERPQPQTLQLDFLMK
Total Number of Spectra: 10
Number of Replicates (out of 10): 7
Best Match Score: 166.04
Best Match Posterior Error Probability: 2.36E-15
Best Match Spectrum:

Scan number 4460 **Raw file** Prt-OGE-Batch3-WT-Frac10
Method ITMS; CID **Genenames** DCTN6



Protein Group ID: 1166
Protein Accession Numbers: O14602; A6NJH9
Gene Names: EIF1AY
Peptide Sequence: LEALCFDGVK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 89.171
Best Match Posterior Error Probability: 0.0012298
Best Match Spectrum:

Scan number 3752 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac7
Method ITMS; CID **Genenames** EIF1AY



Protein Group ID: 1167

Protein Accession Numbers: O14613

Gene Names: CDC42EP2

Peptide Sequence: FHLLPGTMVEGPEE^{-H₂O}DEE^{-H₂O}DGTFLDLPFQFTR

Total Number of Spectra: 1

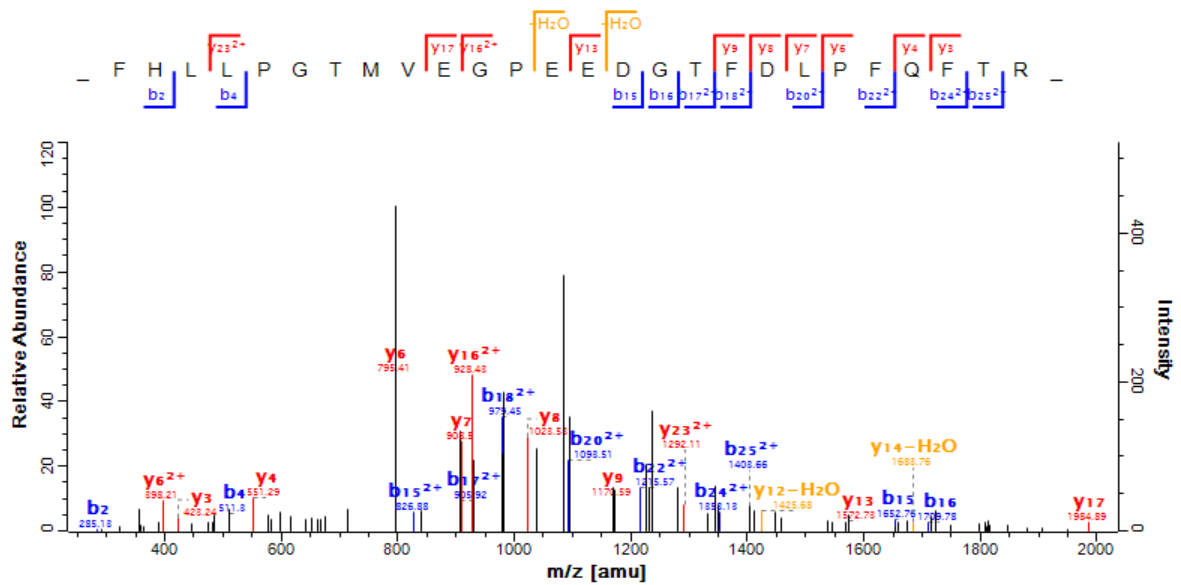
Number of Replicates (out of 10): 1

Best Match Score: 67.979

Best Match Posterior Error Probability: 0.00013526

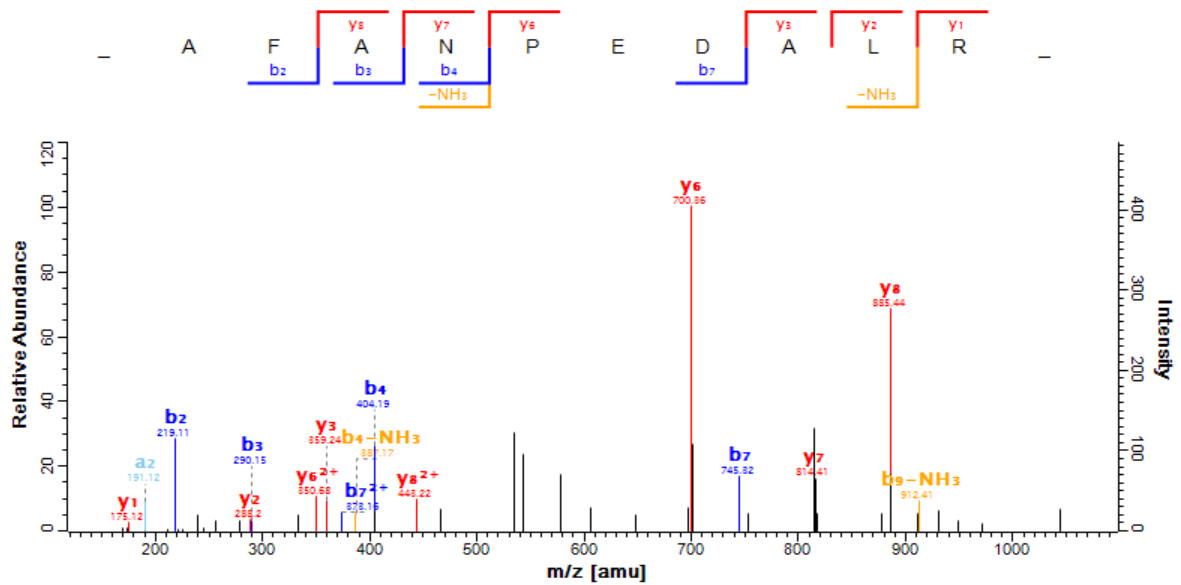
Best Match Spectrum:

Scan number	6547	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac4
Method	ITMS; CID	Genenames	CDC42EP2



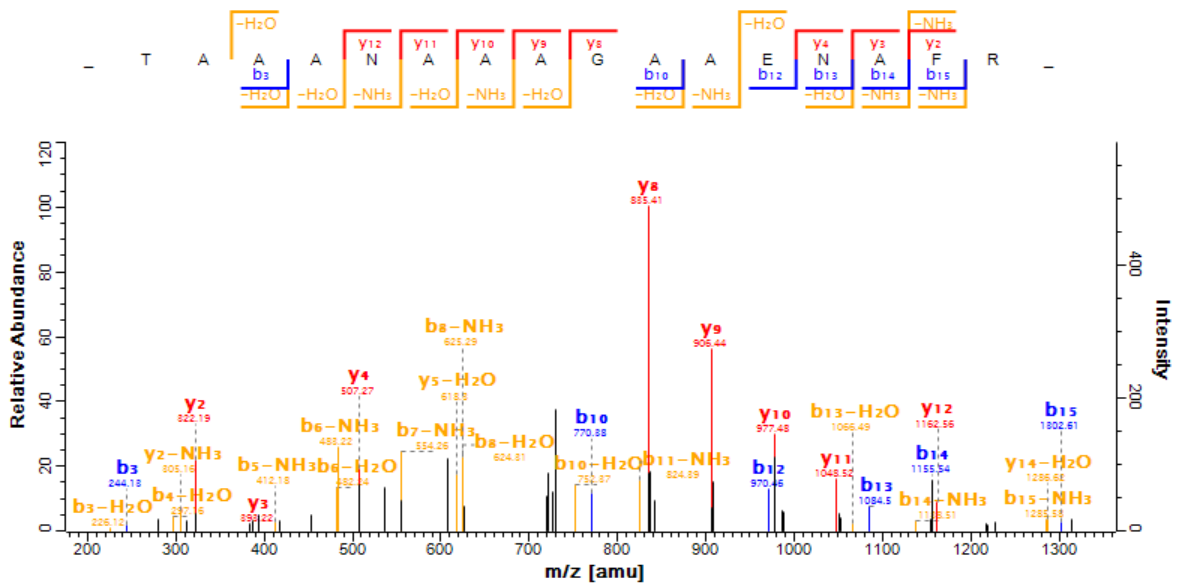
Protein Group ID: 1169
Protein Accession Numbers: O14684
Gene Names: PTGES
Peptide Sequence: AFANPEDALR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 91.584
Best Match Posterior Error Probability: 0.0010579
Best Match Spectrum:

Scan number 2189 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** PTGES



Protein Group ID: 1176
Protein Accession Numbers: O14828; O14828-2
Gene Names: SCAMP3
Peptide Sequence: TAAANAAAGAAENAFR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 85.469
Best Match Posterior Error Probability: 0.00061563
Best Match Spectrum:

Scan number 2115 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** SCAMP3



Protein Group ID: 1181

Protein Accession Numbers: O14950

Gene Names: MYL12B

Peptide Sequence: NPTDAYLDAMMNEAPGPINFTMFLTMFGEK

Total Number of Spectra: 2

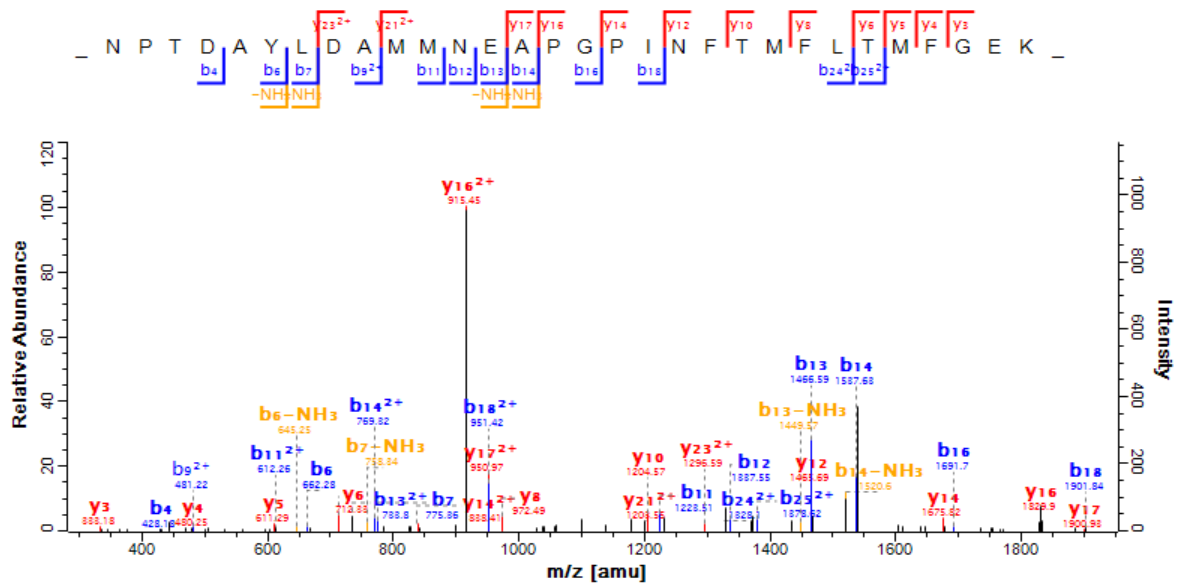
Number of Replicates (out of 10): 2

Best Match Score: 120.31

Best Match Posterior Error Probability: 6.27E-28

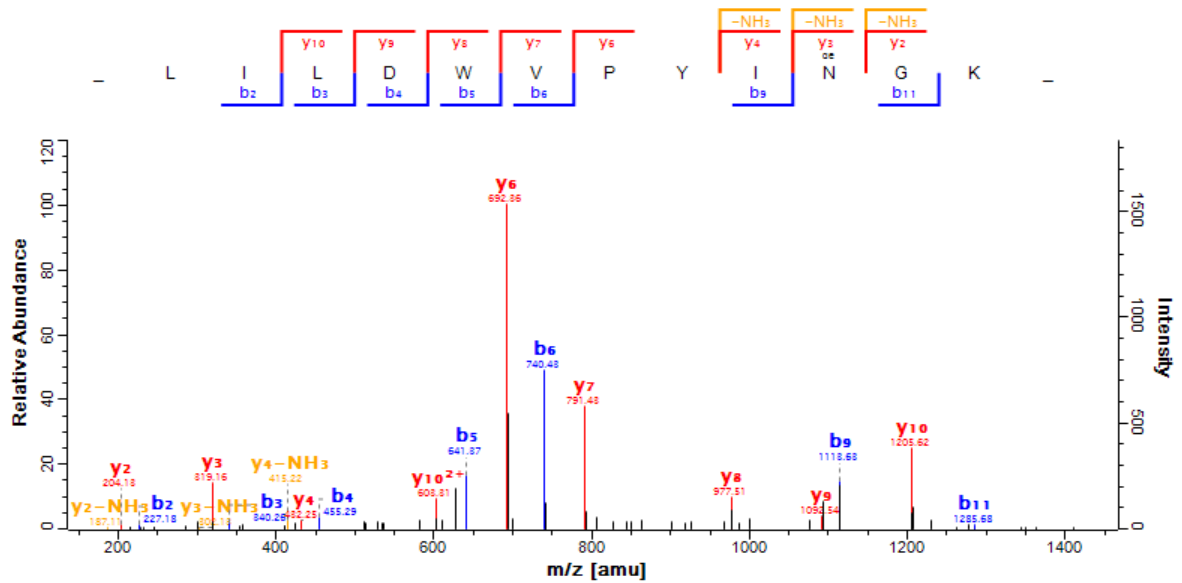
Best Match Spectrum:

Scan number 7205 **Raw file** OGEWT-Frac4
Method ITMS; CID **Genenames** MYL12B



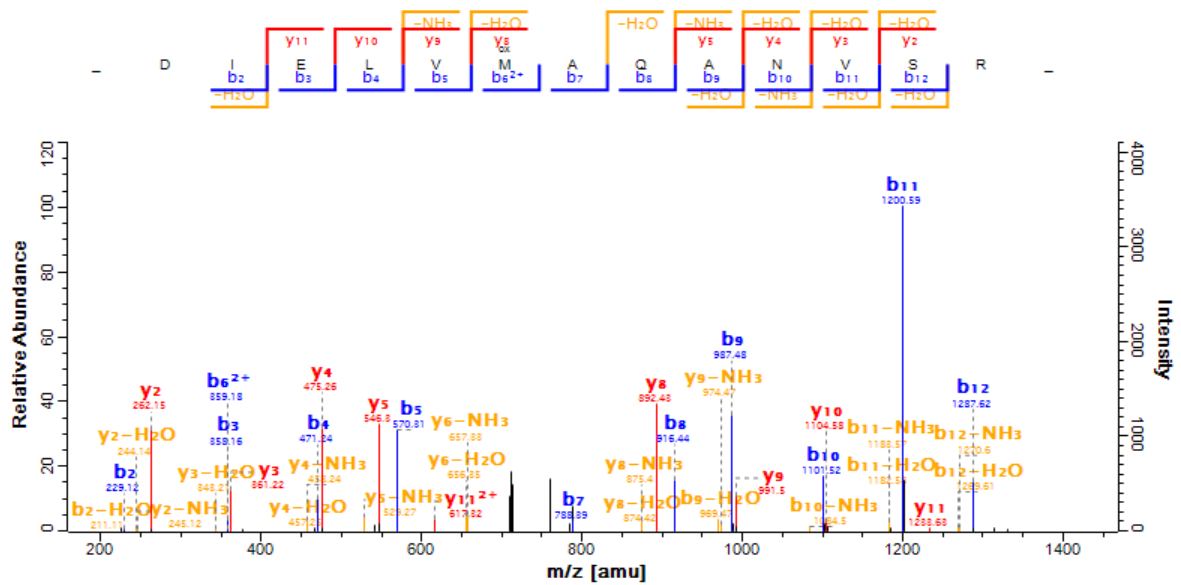
Protein Group ID: 1182
Protein Accession Numbers: O14957
Gene Names: UQCR11
Peptide Sequence: LILDWVPYINGK
Total Number of Spectra: 4
Number of Replicates (out of 10): 3
Best Match Score: 109.24
Best Match Posterior Error Probability: 0.0020184
Best Match Spectrum:

Scan number 5900 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac23
Method ITMS; CID **Genenames** UQCR11



Protein Group ID: 1188
Protein Accession Numbers: O15069
Gene Names: NACAD
Peptide Sequence: DIELVMAQANVSR
Total Number of Spectra: 13
Number of Replicates (out of 10): 8
Best Match Score: 239.03
Best Match Posterior Error Probability: 1.25E-68
Best Match Spectrum:

Scan number 4331 **Raw file** OGE-Mock-Frac5
Method ITMS; CID **Genenames** NACAD



Protein Group ID: 1202

Protein Accession Numbers: O15446-2; O15446

Gene Names: CD3EAP

Peptide Sequence: GHTVTEPIQLPEPELPGEGQPEAR

Total Number of Spectra: 1

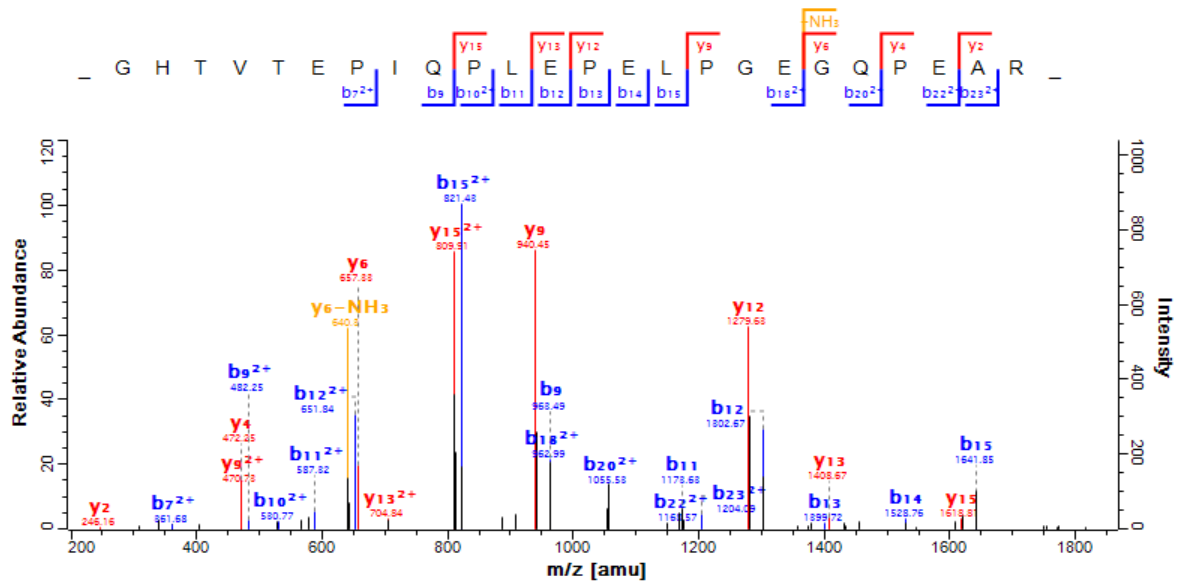
Number of Replicates (out of 10): 1

Best Match Score: 108.37

Best Match Posterior Error Probability: 2.93E-09

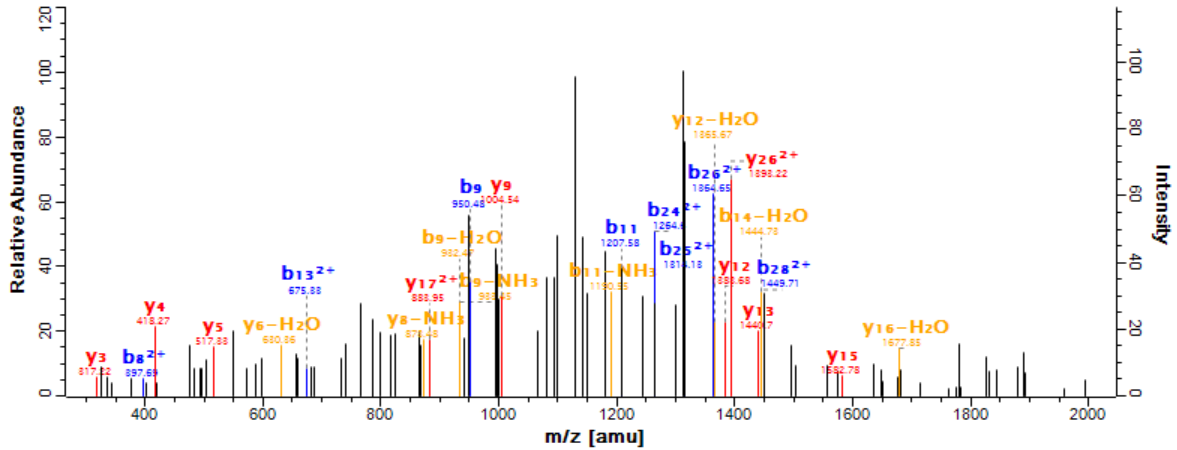
Best Match Spectrum:

Scan number 3043 **Raw file** Prt-OGE-Batch3-WT-Frac18
Method ITMS; CID **Genenames** CD3EAP



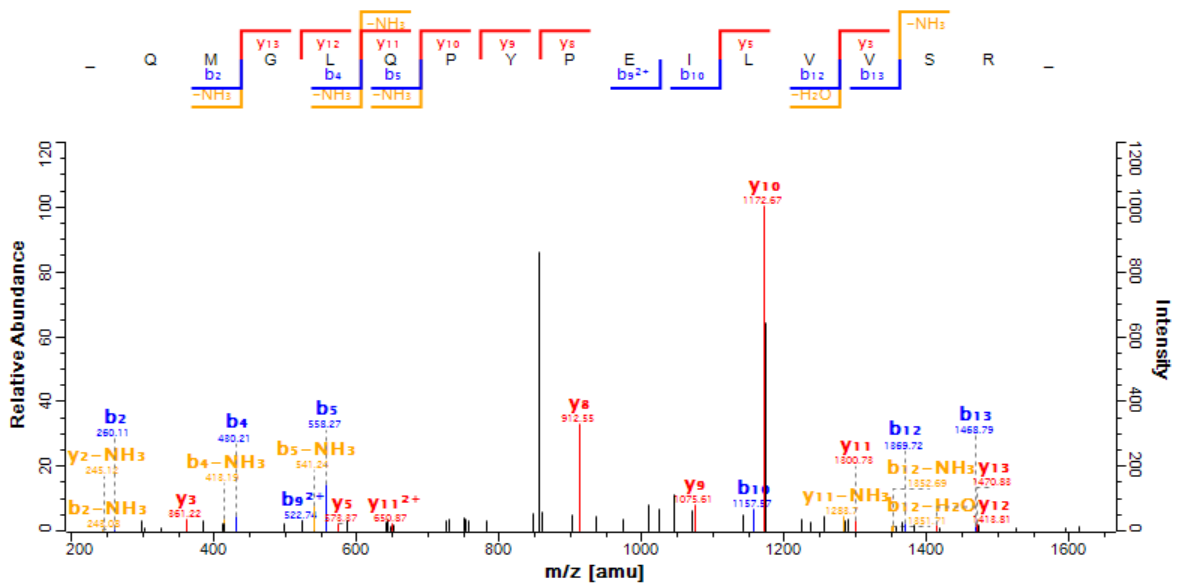
Protein Group ID: 1216
Protein Accession Numbers: O43298
Gene Names: ZBTB43
Peptide Sequence: SDGNLIGHRQEAAALAAAGYSENIEMVVTGK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 58.812
Best Match Posterior Error Probability: 0.00069073
Best Match Spectrum:

Scan number 6589 **Raw file** OGE-Mock-Frac7
Method ITMS; CID **Genenames** ZBTB43



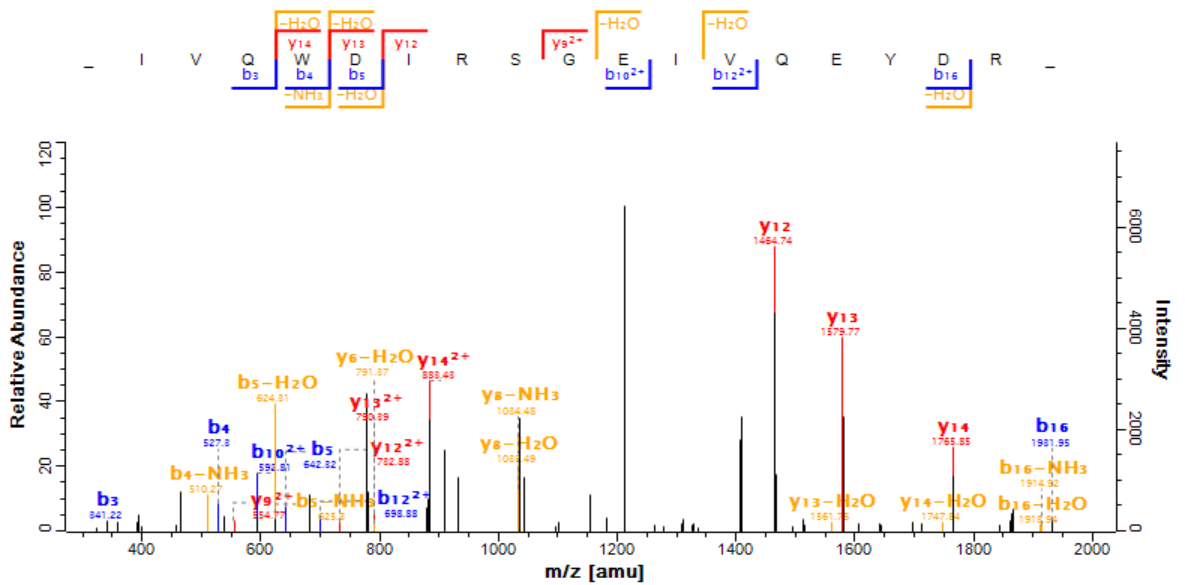
Protein Group ID: 1218
Protein Accession Numbers: O43353; O43353-2
Gene Names: RIPK2
Peptide Sequence: QMGLQPYPEILVVS
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 100.4
Best Match Posterior Error Probability: 0.00011776
Best Match Spectrum:

Scan number 4509 **Raw file** Prt-OGE-Batch2-WT-Frac15
Method ITMS; CID **Genenames** RIPK2



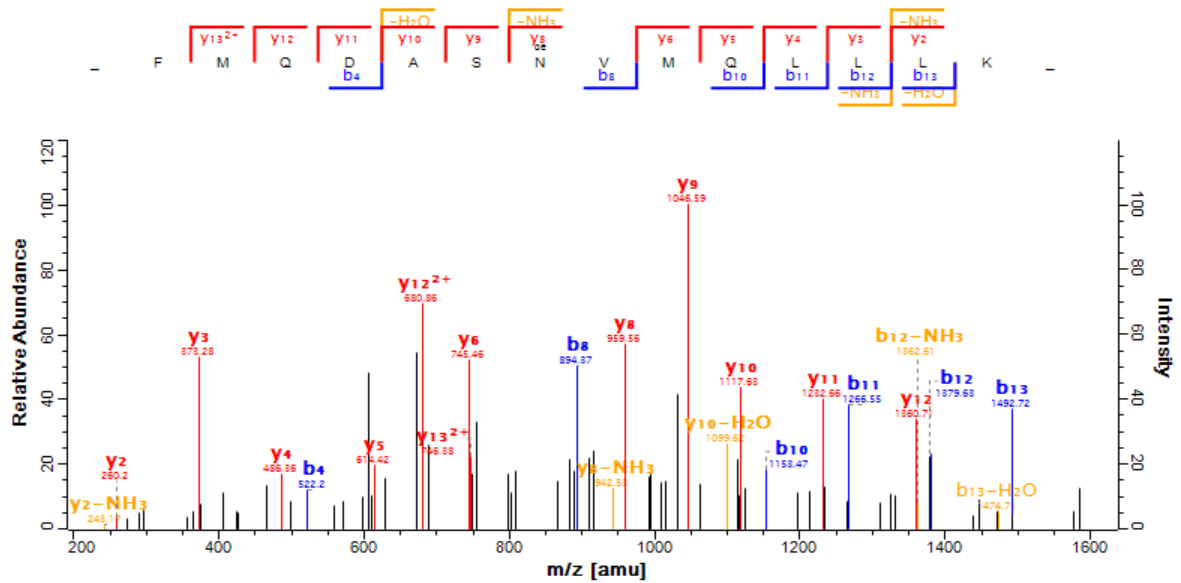
Protein Group ID: 1259
Protein Accession Numbers: O60508; Q5SRN1
Gene Names: CDC40
Peptide Sequence: IVQWDIRSGEIVQEYDR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 89.992
Best Match Posterior Error Probability: 0.0016079
Best Match Spectrum:

Scan number 6246 **Raw file** OGE-WT-Frac20
Method ITMS; CID **Genenames** CDC40



Protein Group ID: 1260
Protein Accession Numbers: O60518
Gene Names: RANBP6
Peptide Sequence: FMQDASNVMQLLLK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 130.24
Best Match Posterior Error Probability: 0.00033373
Best Match Spectrum:

Scan number 5637 **Raw file** OGE-WT-Frac3
Method ITMS; CID **Genenames** RANBP6



Protein Group ID: 1283

Protein Accession Numbers: O75155; O75155-2

Gene Names: CAND2

Peptide Sequence: SPIMADFSQIRSNPELAALFESI QK

Total Number of Spectra: 5

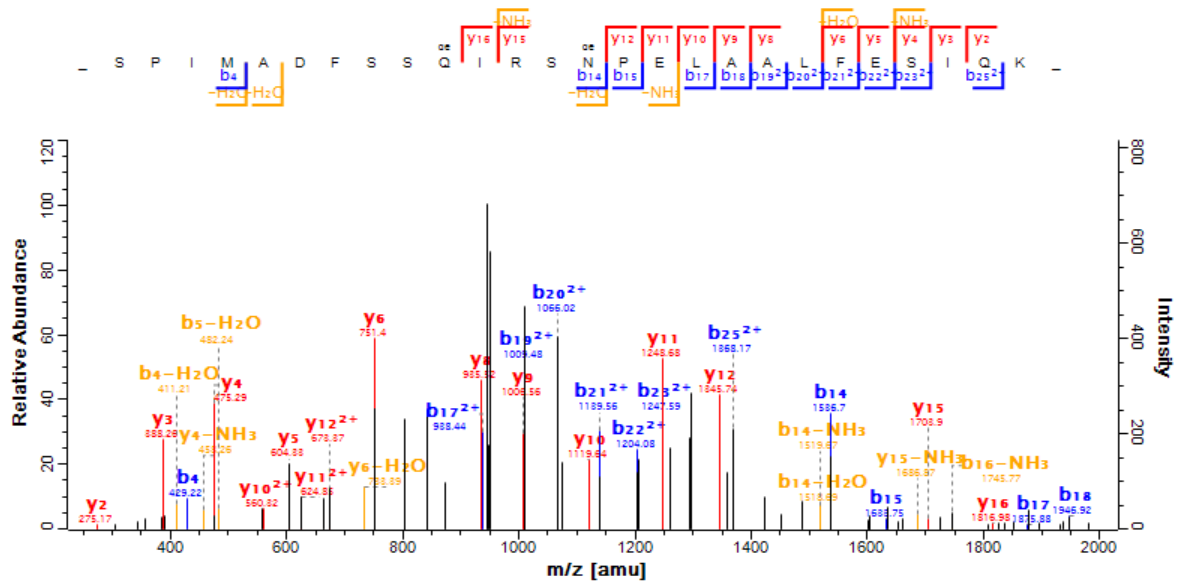
Number of Replicates (out of 10): 4

Best Match Score: 129.07

Best Match Posterior Error Probability: 1.54E-14

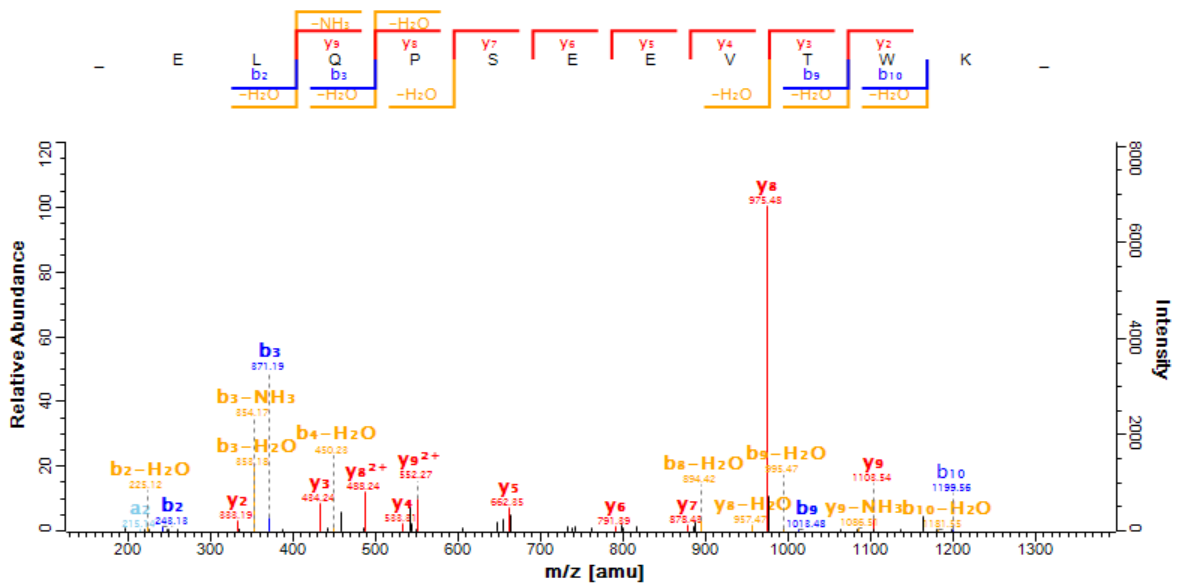
Best Match Spectrum:

Scan number 6450 **Raw file** Prt-OGE-Batch2-WT-Frac12
Method ITMS; CID **Genenames** CAND2



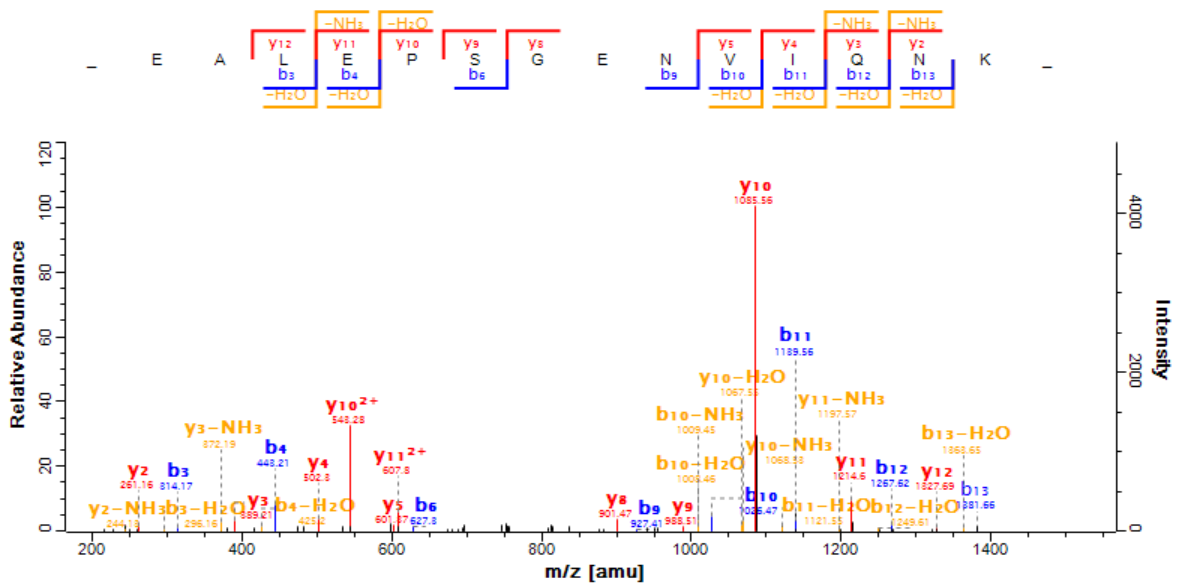
Protein Group ID: 1304
Protein Accession Numbers: O75438-2; O75438
Gene Names: NDUFB1
Peptide Sequence: ELQPSEEVTWK
Total Number of Spectra: 5
Number of Replicates (out of 10): 4
Best Match Score: 148.28
Best Match Posterior Error Probability: 1.38E-05
Best Match Spectrum:

Scan number 3481 **Raw file** Prt-OGE-Batch2-Mock-Frac20
Method ITMS; CID **Genenames** NDUFB1



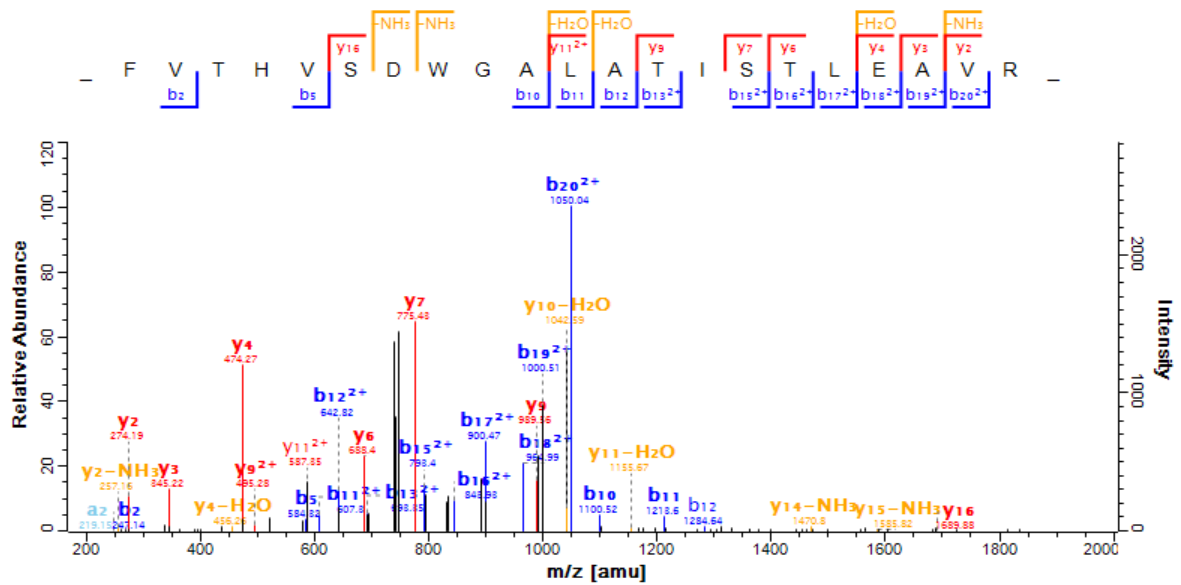
Protein Group ID: 1307
Protein Accession Numbers: O75477
Gene Names: ERLIN1
Peptide Sequence: EALEPSGENVIQNK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 181.67
Best Match Posterior Error Probability: 4.38E-15
Best Match Spectrum:

Scan number 2784 **Raw file** Prt-OGE-Batch2-Mock-Frac17
Method ITMS; CID **Genenames** ERLIN1



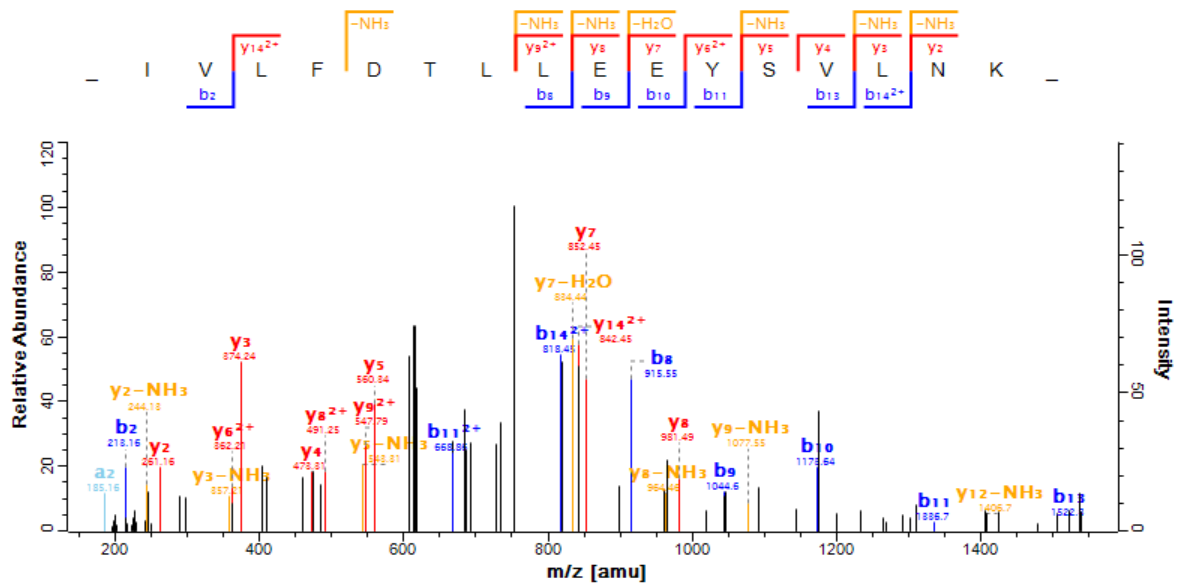
Protein Group ID: 1318
Protein Accession Numbers: O75629
Gene Names: CREG1
Peptide Sequence: FVTHVSDWGLATISLTLEAVR
Total Number of Spectra: 10
Number of Replicates (out of 10): 5
Best Match Score: 111.01
Best Match Posterior Error Probability: 3.04E-07
Best Match Spectrum:

Scan number 6340 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac11
Method ITMS; CID **Genenames** CREG1



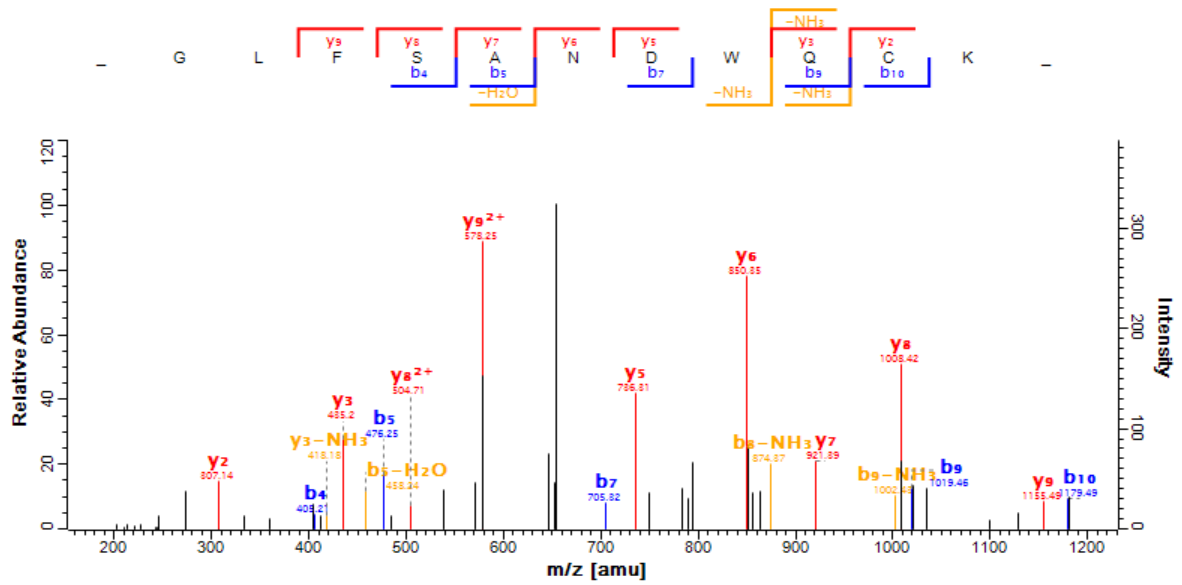
Protein Group ID: 1326
Protein Accession Numbers: O75844
Gene Names: ZMPSTE24
Peptide Sequence: IVLFDTLLLEEYSVLN K
Total Number of Spectra: 9
Number of Replicates (out of 10): 6
Best Match Score: 136.3
Best Match Posterior Error Probability: 1.08E-05
Best Match Spectrum:

Scan number 6780 **Raw file** OGE-WT-Frac11
Method ITMS; CID **Genenames** ZMPSTE24



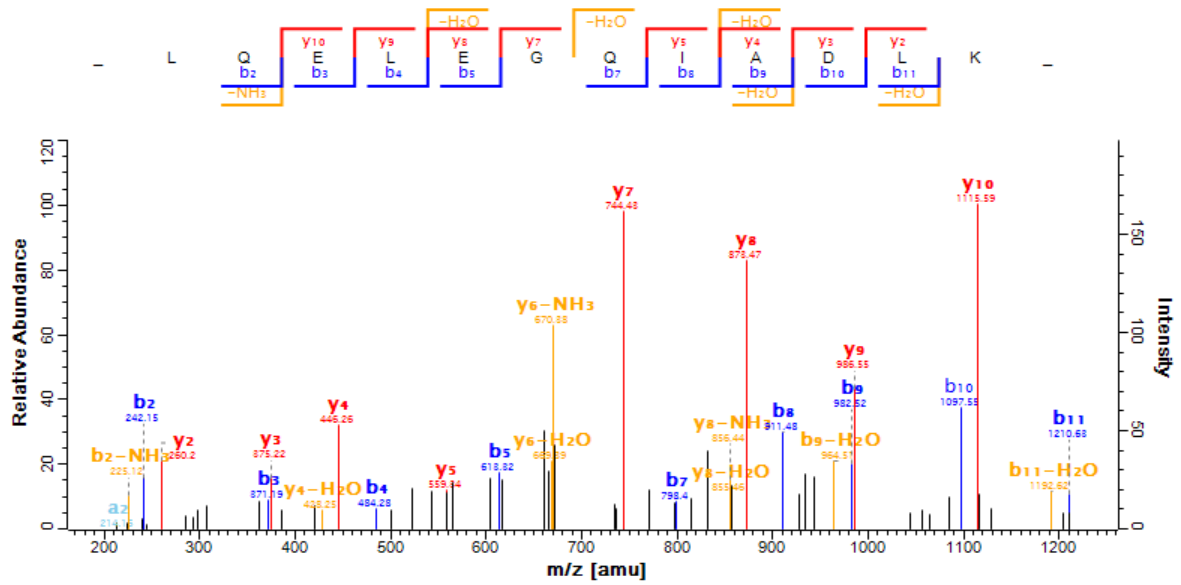
Protein Group ID: 1357
Protein Accession Numbers: O95218; O95218-2
Gene Names: ZRANB2
Peptide Sequence: GLFSANDWQCK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 87.001
Best Match Posterior Error Probability: 0.0011251
Best Match Spectrum:

Scan number 3232 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac17
Method ITMS; CID **Genenames** ZRANB2



Protein Group ID: 1360
Protein Accession Numbers: O95239; O95239-2
Gene Names: KIF4A
Peptide Sequence: LQELEGQIADLK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 150.11
Best Match Posterior Error Probability: 4.84E-05
Best Match Spectrum:

Scan number 4347 **Raw file** Prt-OGE-Batch2-Mock-Frac13
Method ITMS; CID **Genenames** KIF4A



Protein Group ID: 1370

Protein Accession Numbers: O95399-2; Q5H8X8; O95399

Gene Names: UTS2

Peptide Sequence: LTPEELER

Total Number of Spectra: 26

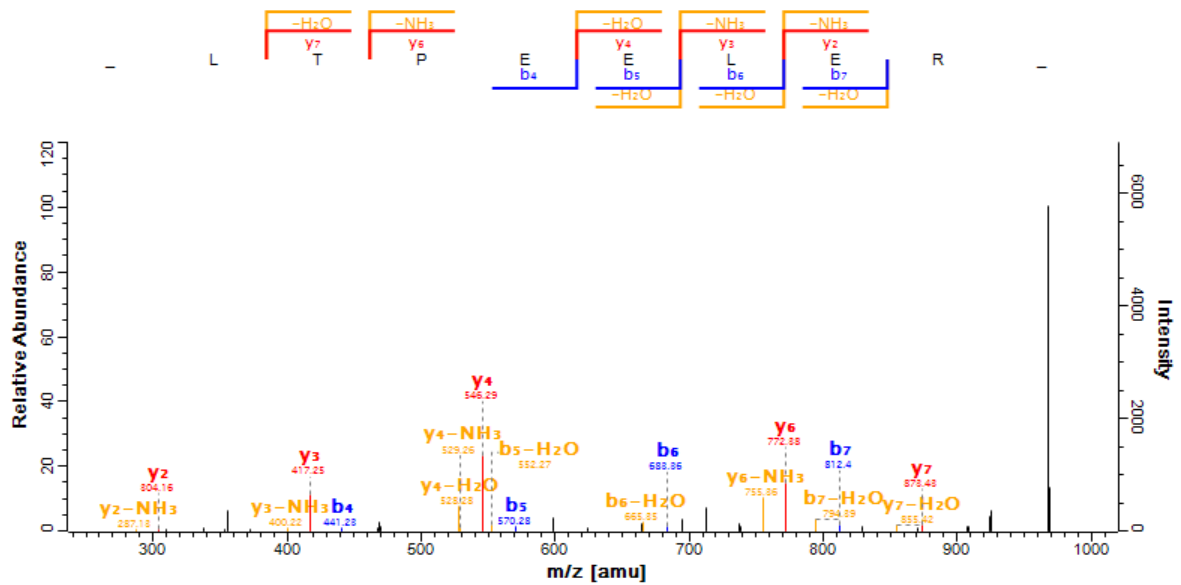
Number of Replicates (out of 10): 10

Best Match Score: 151.29

Best Match Posterior Error Probability: 0.0014204

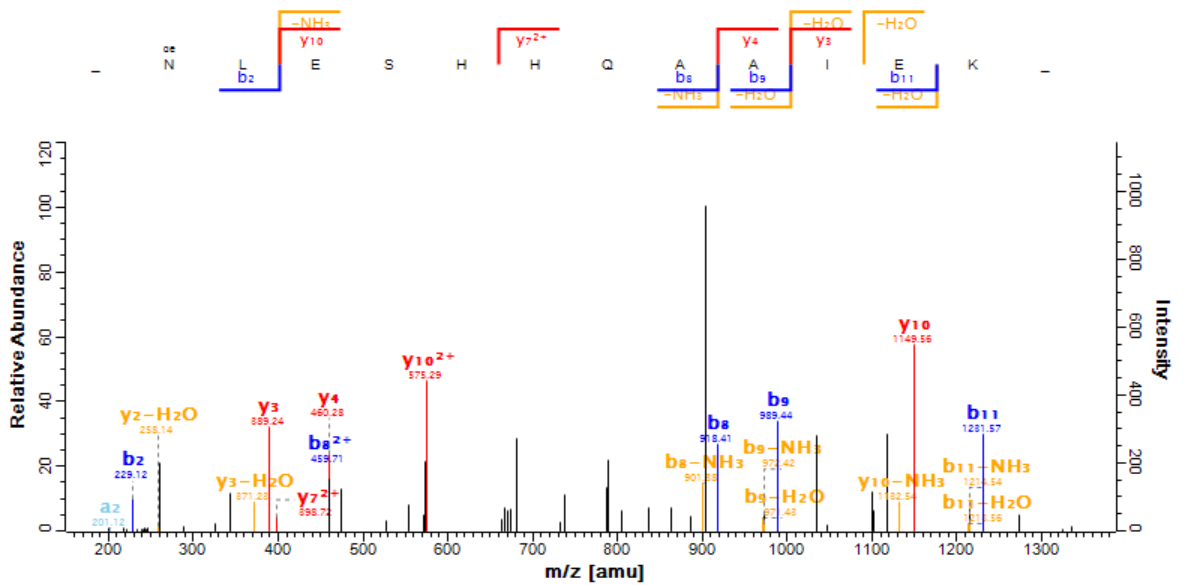
Best Match Spectrum:

Scan number 2512 **Raw file** OGE-Mock-Frac6
Method ITMS; CID **Genenames** UTS2



Protein Group ID: 1377
Protein Accession Numbers: O95613; O95613-2
Gene Names: PCNT
Peptide Sequence: NLESHHQA AIEK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 103.08
Best Match Posterior Error Probability: 0.0037629
Best Match Spectrum:

Scan number 6260 **Raw file** Prt-OGE-Batch3-Mock-Frac7
Method ITMS; CID **Genenames** PCNT



Protein Group ID: 1383

Protein Accession Numbers: O95782; O95782-2

Gene Names: AP2A1

Peptide Sequence: LLGFGSALLDNDNVDNPNPNFVVGAGIIQTK

Total Number of Spectra: 1

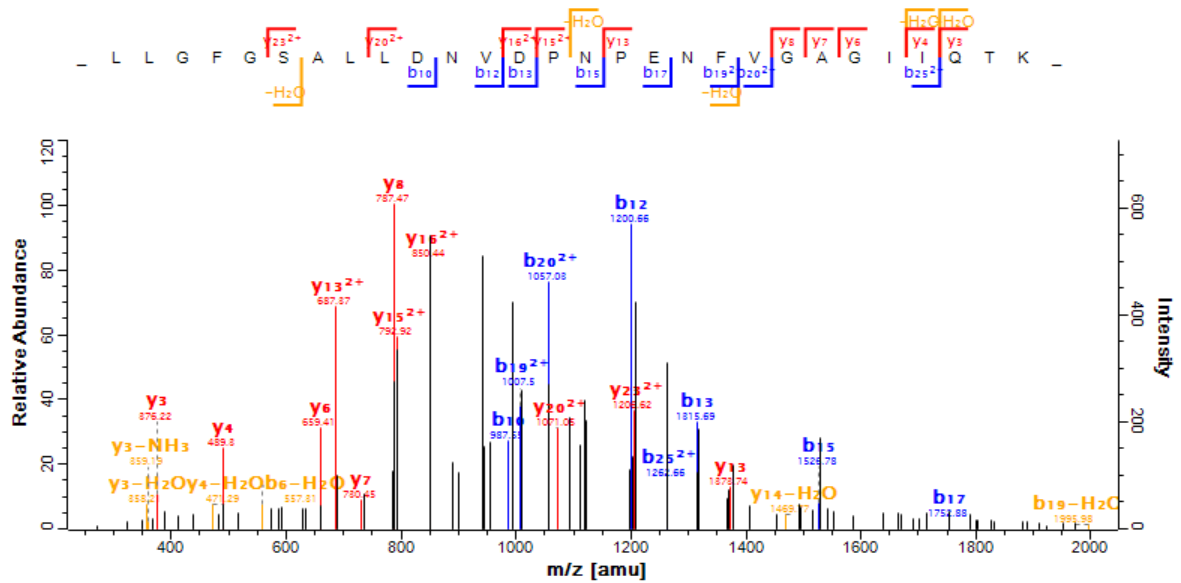
Number of Replicates (out of 10): 1

Best Match Score: 68.689

Best Match Posterior Error Probability: 4.28E-05

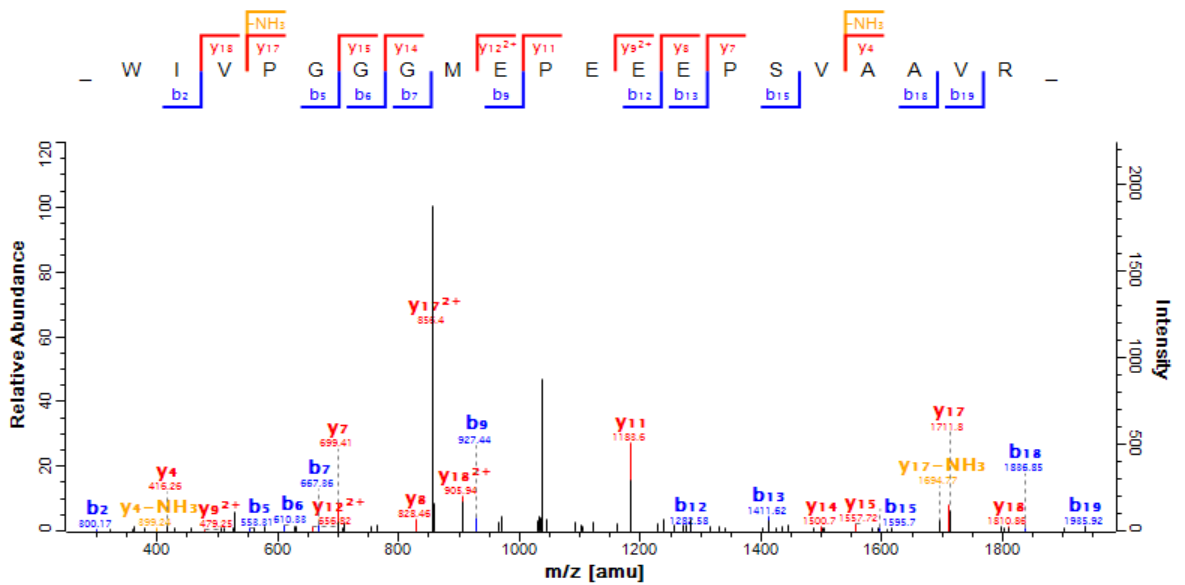
Best Match Spectrum:

Scan number 7679 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac12
Method ITMS; CID **Genenames** AP2A1



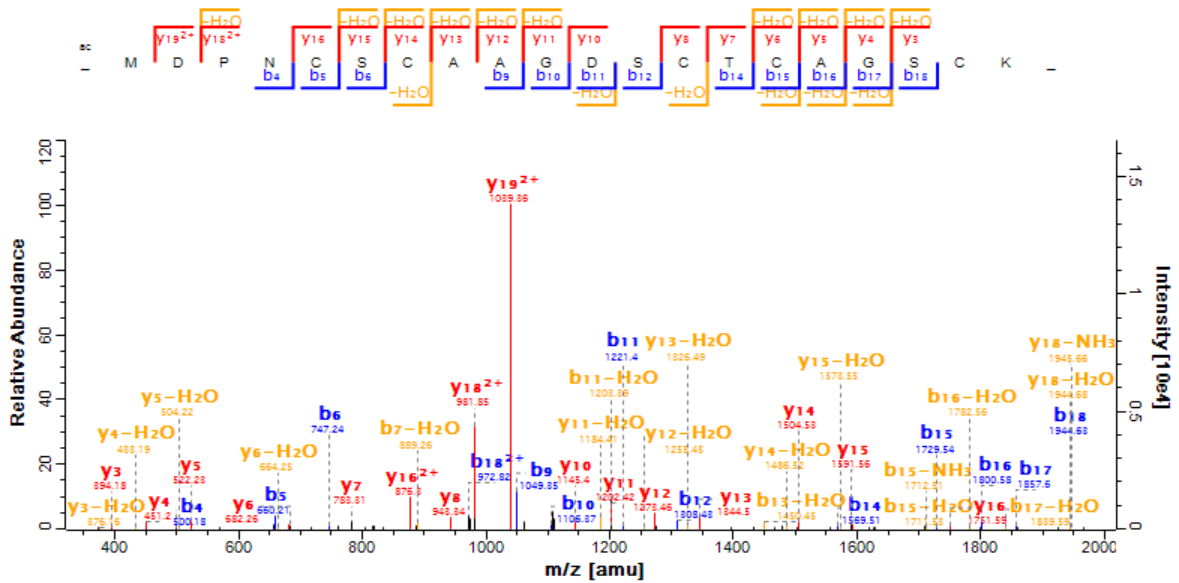
Protein Group ID: 1396
Protein Accession Numbers: O95989
Gene Names: NUDT3
Peptide Sequence: WIVPGGGMEPEEEPSVAAR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 95.954
Best Match Posterior Error Probability: 9.04E-05
Best Match Spectrum:

Scan number 3742 **Raw file** Prt-OGE-Batch3-WT-Frac12
Method ITMS; CID **Genenames** NUDT3



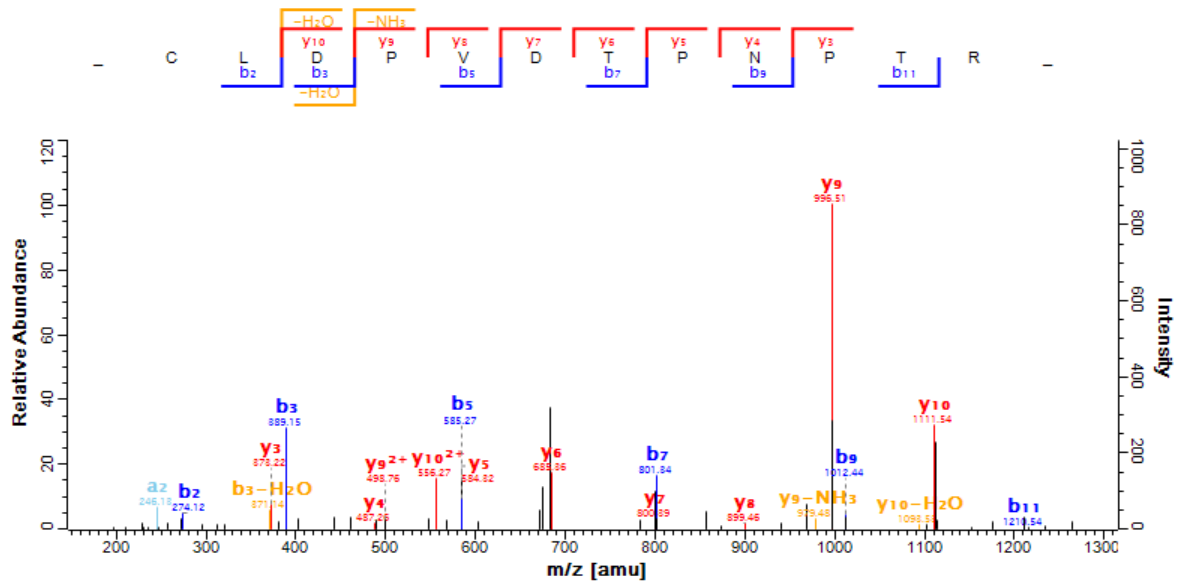
Protein Group ID: 1430
Protein Accession Numbers: P02795; H3BSP9
Gene Names: MT2A
Peptide Sequence: MDPNCSCAAGDSCTCAGSCK
Total Number of Spectra: 17
Number of Replicates (out of 10): 7
Best Match Score: 223.54
Best Match Posterior Error Probability: 1.29E-71
Best Match Spectrum:

Scan number 1589 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac19
Method ITMS; CID **Genenames** MT2A



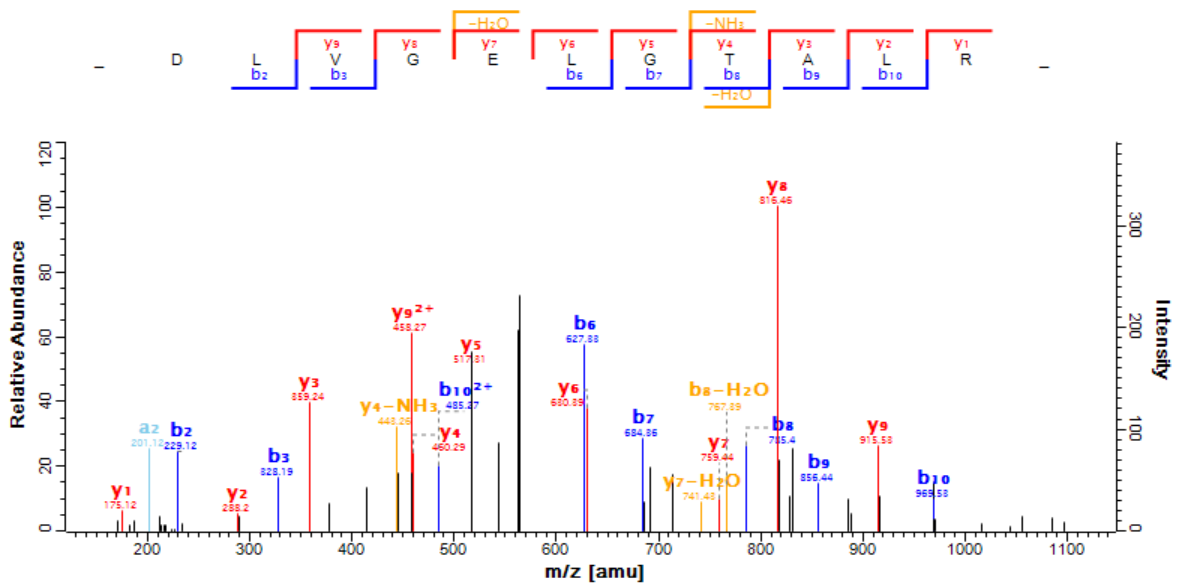
Protein Group ID: 1435
Protein Accession Numbers: P03973
Gene Names: SLPI
Peptide Sequence: CLDPVDTPNPTR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 102.97
Best Match Posterior Error Probability: 0.00034024
Best Match Spectrum:

Scan number 1911 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac22
Method ITMS; CID **Genenames** SLPI



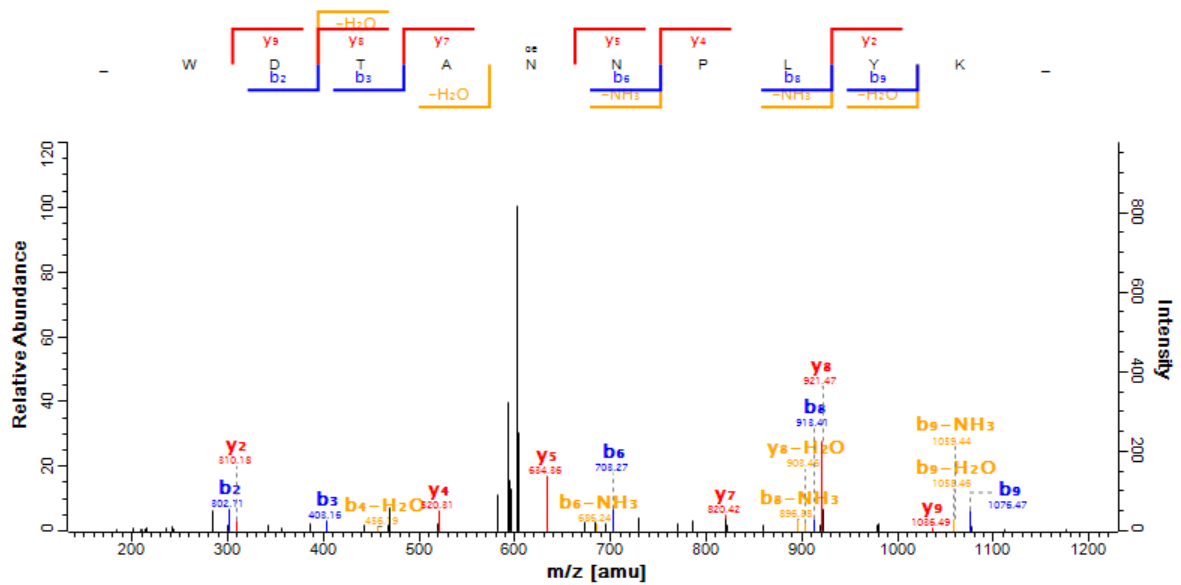
Protein Group ID: 1437
Protein Accession Numbers: P04066
Gene Names: FUCA1
Peptide Sequence: DLV⁹GELGTALR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 143.97
Best Match Posterior Error Probability: 1.41E-05
Best Match Spectrum:

Scan number 5595 **Raw file** Prt-OGE-Batch3--Mock-Frac12
Method ITMS; CID **Genenames** FUCA1



Protein Group ID: 1457
Protein Accession Numbers: P05106
Gene Names: ITGB3
Peptide Sequence: WDTANNPLYK
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 101.38
Best Match Posterior Error Probability: 0.0059329
Best Match Spectrum:

Scan number 3142 **Raw file** OGE-Mock-Frac11
Method ITMS; CID **Genenames** ITGB3



Protein Group ID: 1485

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: 4

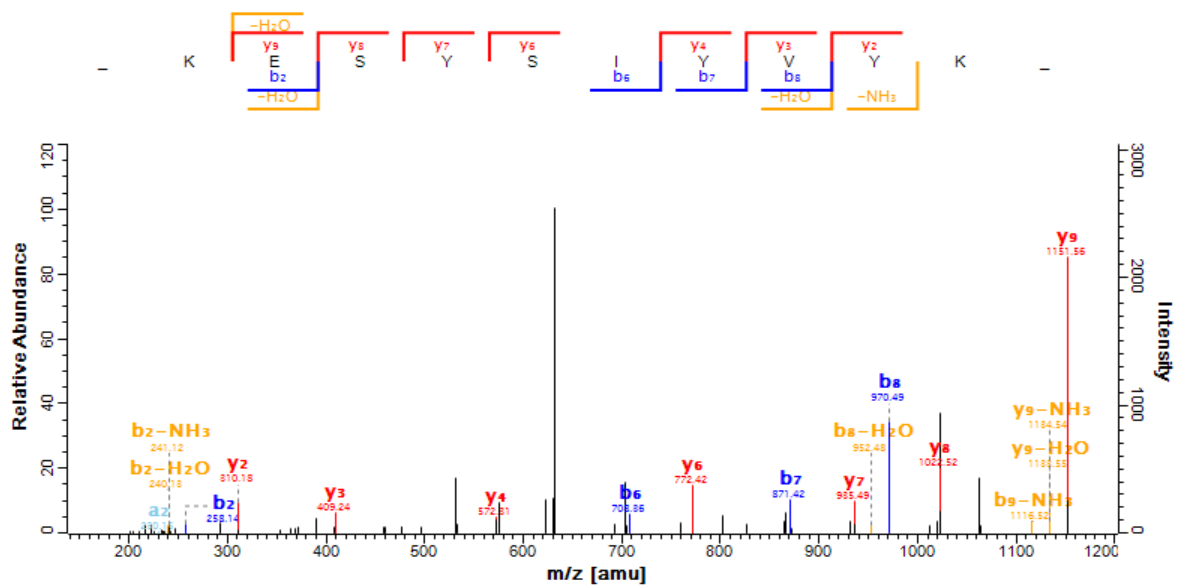
Number of Replicates (out of 10): 2

Best Match Score: 90.913

Best Match Posterior Error Probability: 0.0026308

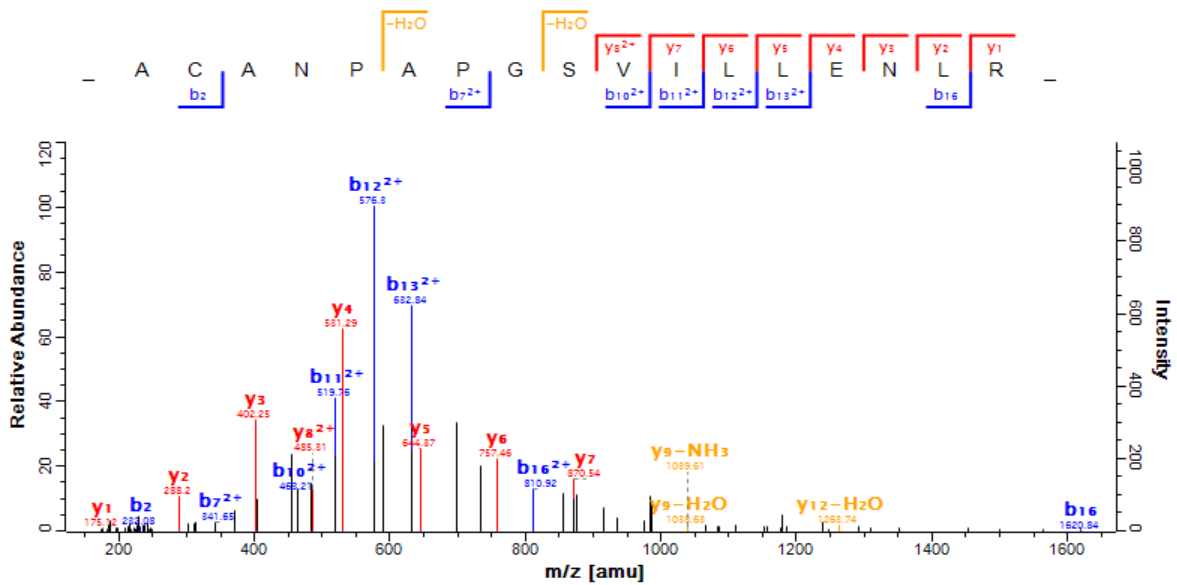
Best Match Spectrum:

Scan number 2137 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac18
Method ITMS: CID **Genenames** HIST1H2BJ; HIST1H2BO; HIST1H2BB; HIST2H2BE; HIST3H2BB; HIST2H2BC; HIST2H2BD



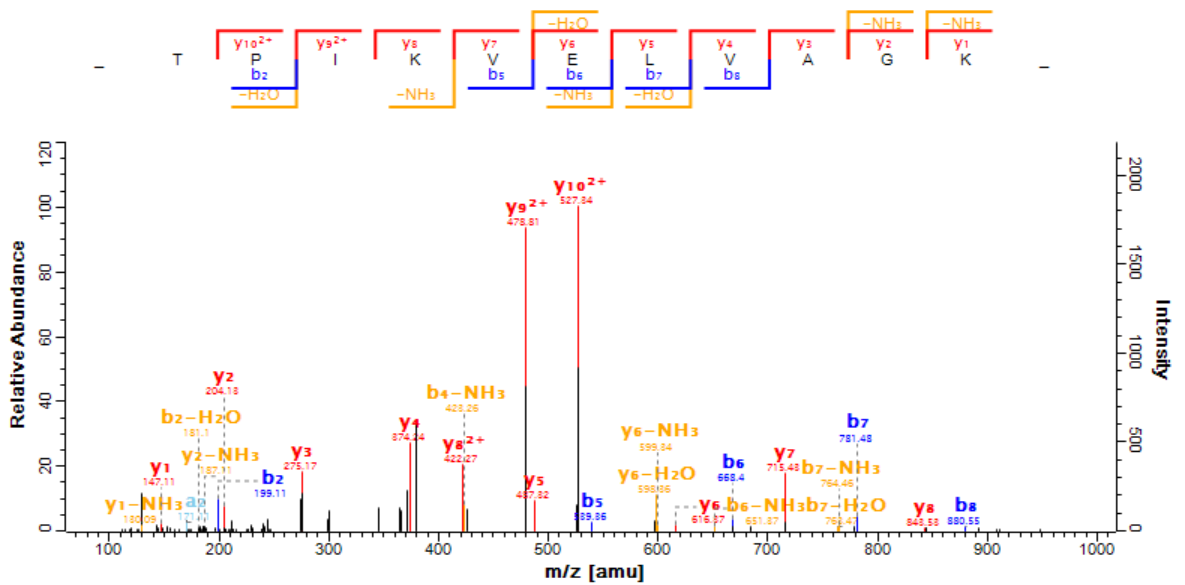
Protein Group ID: 1490
Protein Accession Numbers: P07205
Gene Names: PGK2
Peptide Sequence: ACANPAGSVILLLLENLR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 87.932
Best Match Posterior Error Probability: 0.00052937
Best Match Spectrum:

Scan number 6409 **Raw file** Prt-OGE-Batch2-Mock-Frac1 8
Method ITMS; CID **Genenames** PGK2



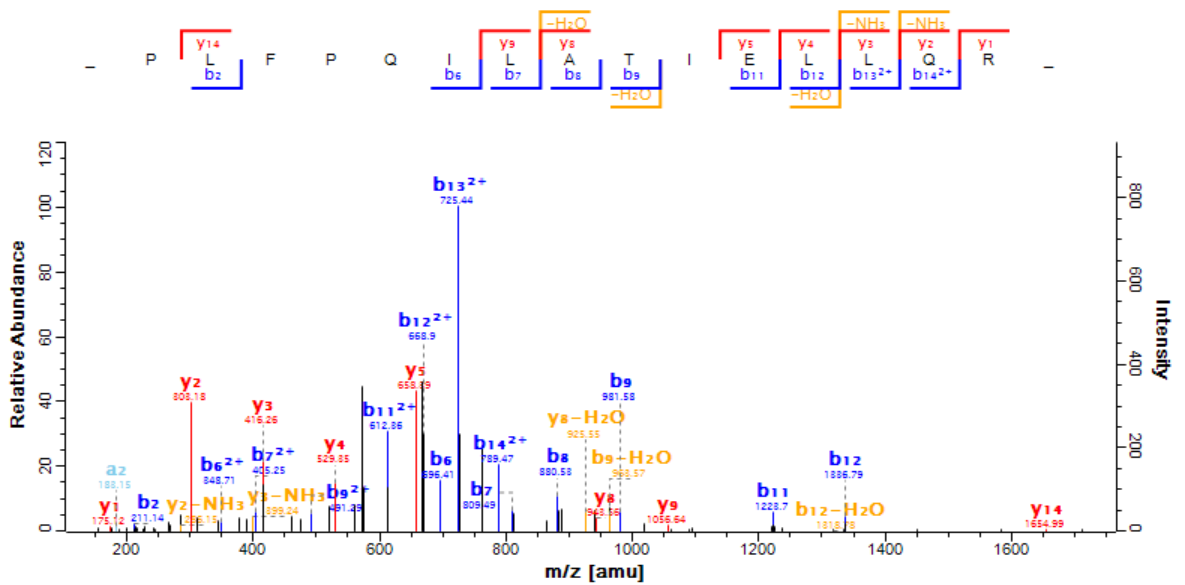
Protein Group ID: 1548
Protein Accession Numbers: P0C7P0
Gene Names: CISD3
Peptide Sequence: TPIKVELVAGK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 147.62
Best Match Posterior Error Probability: 4.67E-05
Best Match Spectrum:

Scan number 2519 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac23
Method ITMS; CID **Genenames** CISD3



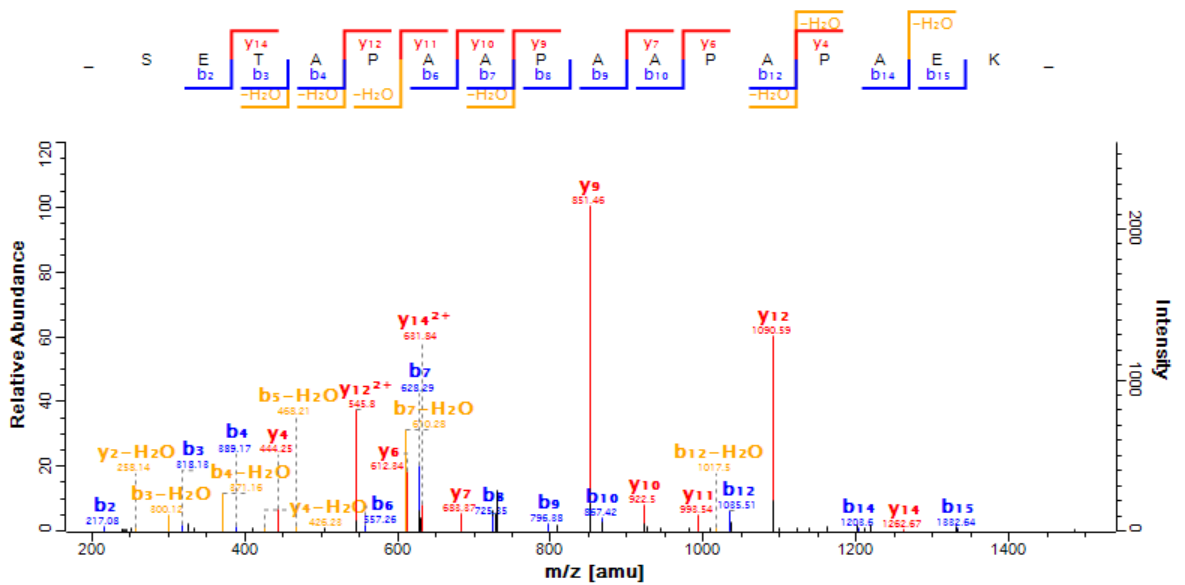
Protein Group ID: 1552
Protein Accession Numbers: P10398
Gene Names: ARAF
Peptide Sequence: PLFPQILATIELLQR
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 164.53
Best Match Posterior Error Probability: 1.80E-11
Best Match Spectrum:

Scan number 8490 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac20
Method ITMS; CID **Genenames** ARAF



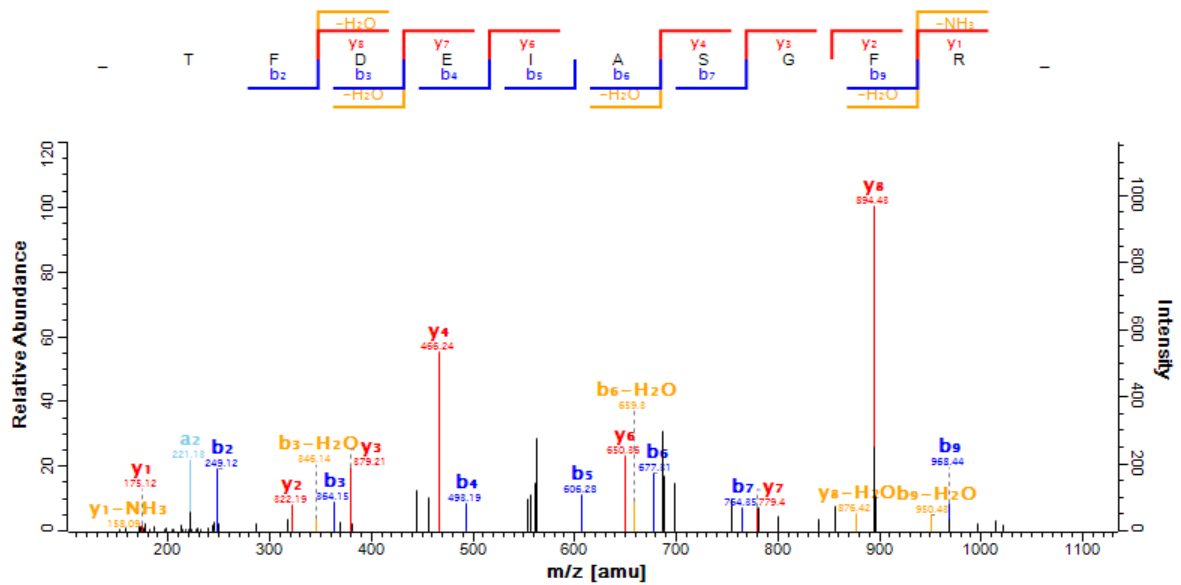
Protein Group ID: 1553
Protein Accession Numbers: P10412
Gene Names: HIST1H1E
Peptide Sequence: SETAPAAPAAPAEK
Total Number of Spectra: 28
Number of Replicates (out of 10): 9
Best Match Score: 147.12
Best Match Posterior Error Probability: 2.66E-07
Best Match Spectrum:

Scan number 1390 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac14
Method ITMS; CID **Genenames** HIST1H1E



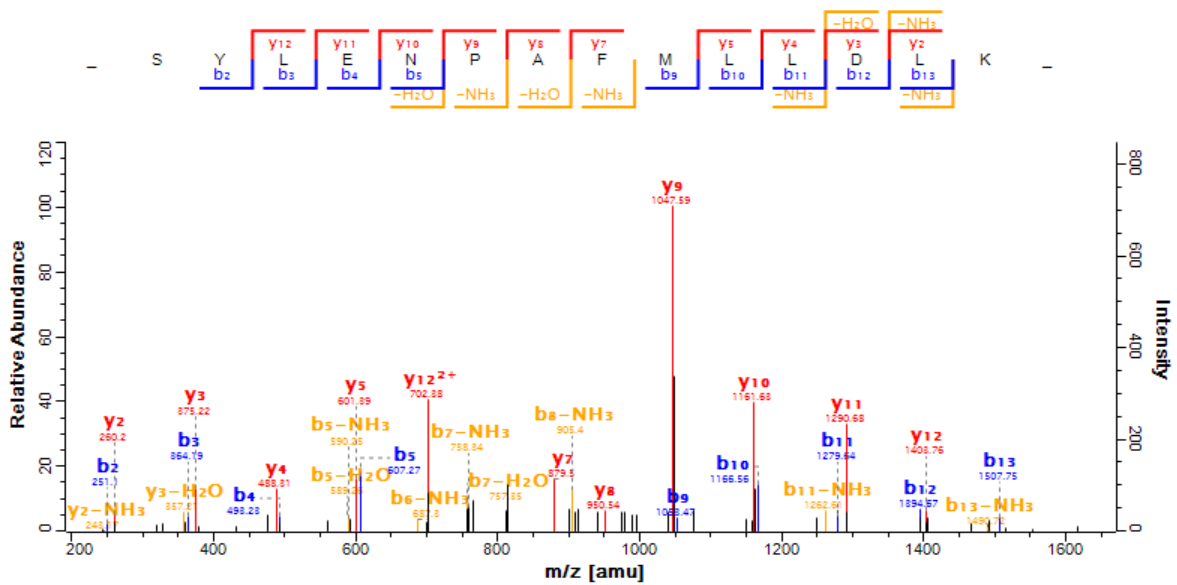
Protein Group ID: 1567
Protein Accession Numbers: P11166
Gene Names: SLC2A1
Peptide Sequence: TFDEIASGFR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 117.02
Best Match Posterior Error Probability: 0.0001734
Best Match Spectrum:

Scan number 2716 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** SLC2A1



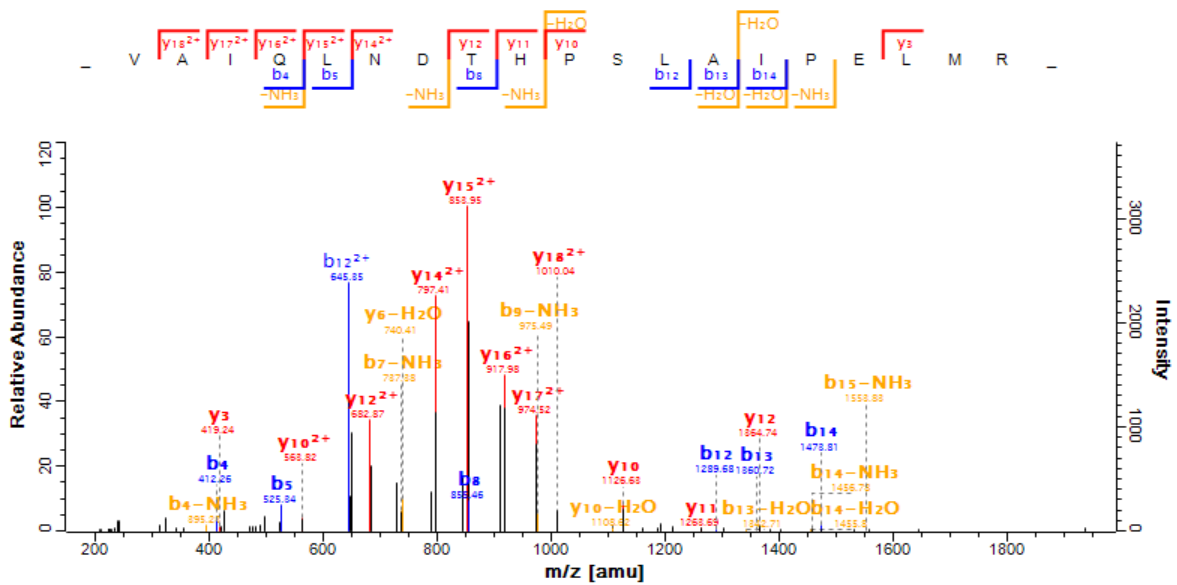
Protein Group ID: 1570
Protein Accession Numbers: P11182
Gene Names: DBT
Peptide Sequence: SYLENPAFMLLDLK
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 142.1
Best Match Posterior Error Probability: 9.04E-07
Best Match Spectrum:

Scan number 6435 **Raw file** OGE-Mock-Frac13
Method ITMS; CID **Genenames** DBT



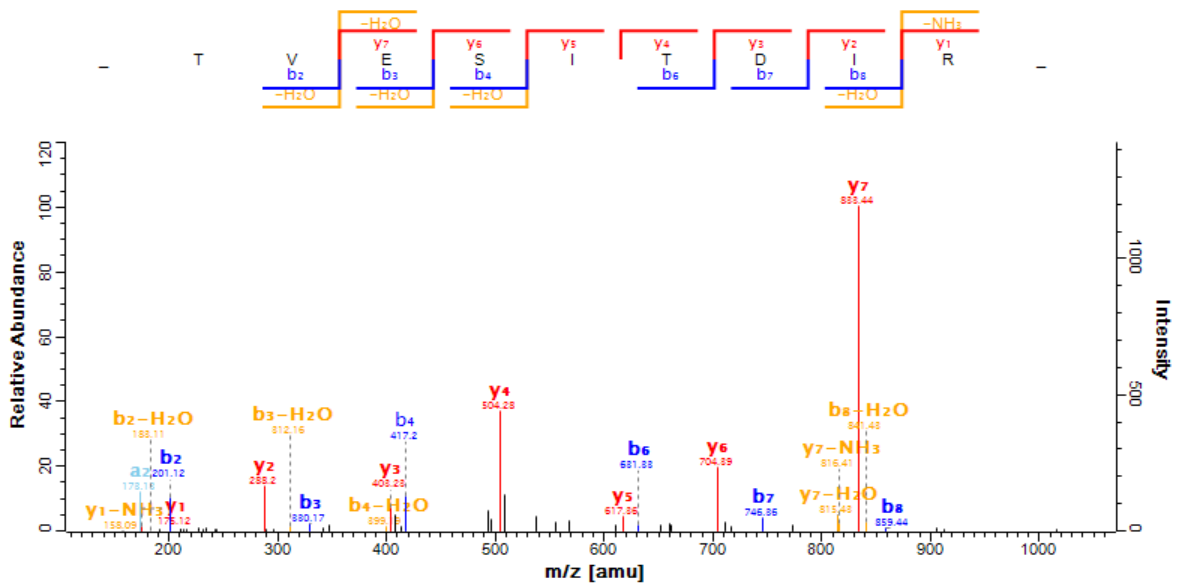
Protein Group ID: 1572
Protein Accession Numbers: P11217; P11217-2
Gene Names: PYGM
Peptide Sequence: VAIQLNDTHPSLAIPELMR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 121.82
Best Match Posterior Error Probability: 2.12E-05
Best Match Spectrum:

Scan number 4772 **Raw file** Prt-OGE-Batch2-WT-Frac15
Method ITMS; CID **Genenames** PYGM



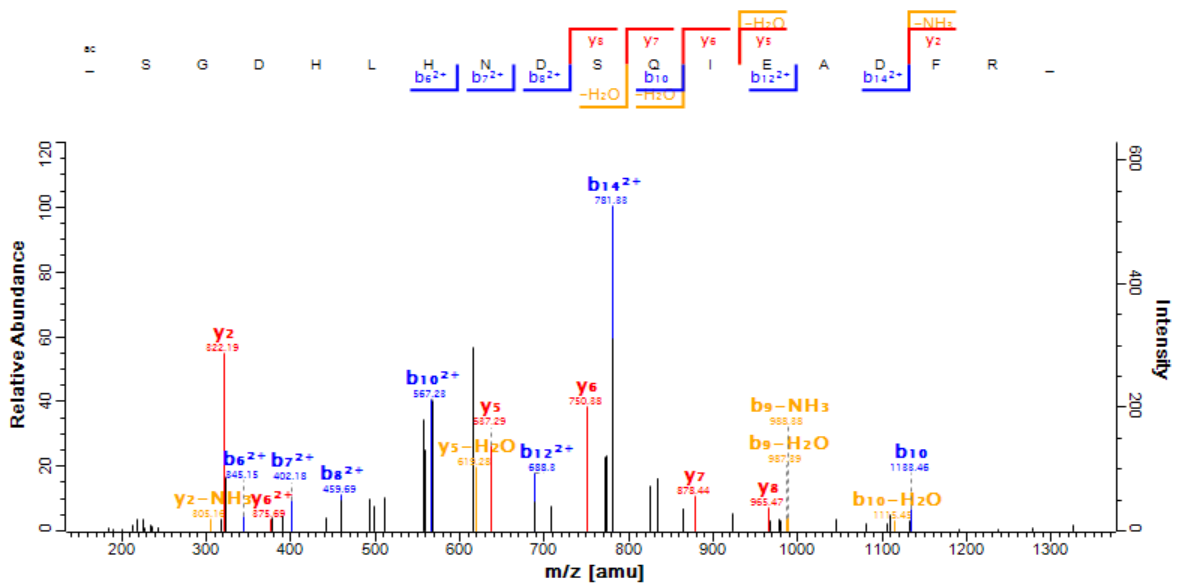
Protein Group ID: 1573
Protein Accession Numbers: P11279
Gene Names: LAMP1
Peptide Sequence: TVESITDIR
Total Number of Spectra: 7
Number of Replicates (out of 10): 5
Best Match Score: 126.31
Best Match Posterior Error Probability: 0.00029395
Best Match Spectrum:

Scan number 2385 **Raw file** OGE-Mock-Frac18
Method ITMS; CID **Genenames** LAMP1



Protein Group ID: 1574
Protein Accession Numbers: P11387
Gene Names: TOP1
Peptide Sequence: SGDHLHNSQIEADFR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 75.669
Best Match Posterior Error Probability: 0.0014047
Best Match Spectrum:

Scan number 2527 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac17
Method ITMS; CID **Genenames** TOP1



Protein Group ID: 1575

Protein Accession Numbers: P11388-4; P11388-3; P11388-2; P11388

Gene Names: TOP2A

Peptide Sequence: MEVSPLQPVNENMQVNEKIKK

Total Number of Spectra: 1

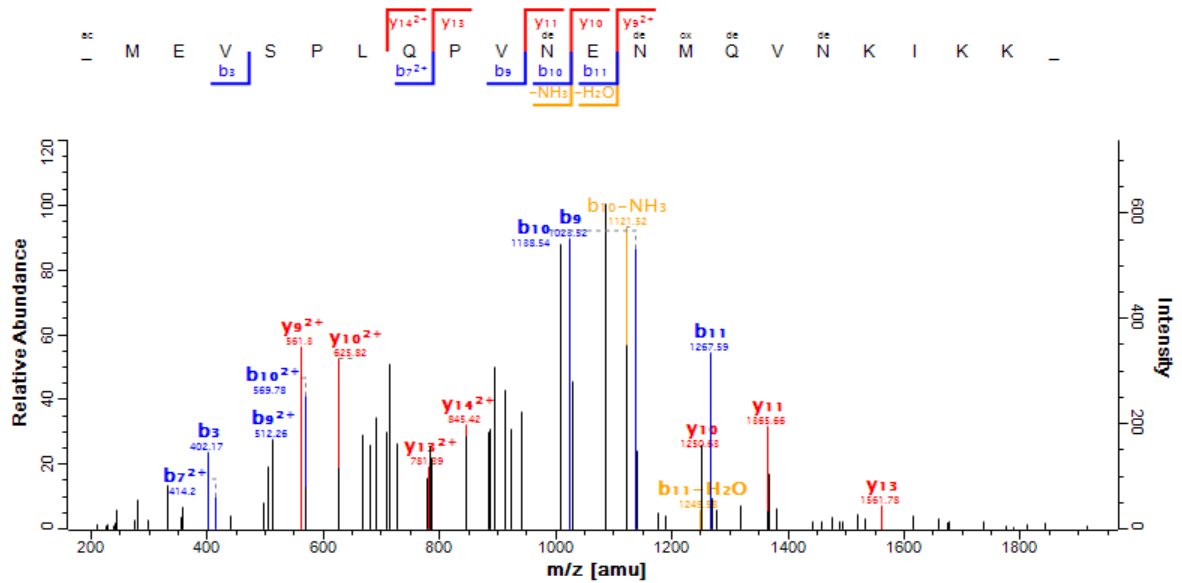
Number of Replicates (out of 10): 1

Best Match Score: 81.317

Best Match Posterior Error Probability: 0.00086178

Best Match Spectrum:

Scan number 5978 **Raw file** Prt-OGE-Batch2-WT-Frac21
Method ITMS; CID **Genenames** TOP2A



Protein Group ID: 1583

Protein Accession Numbers: P12074; Q5T8I0

Gene Names: COX6A1;COX6A1P2

Peptide Sequence: TKPFPWGDGNHTLFHNPHVNP LPTGYEDE

Total Number of Spectra: 13

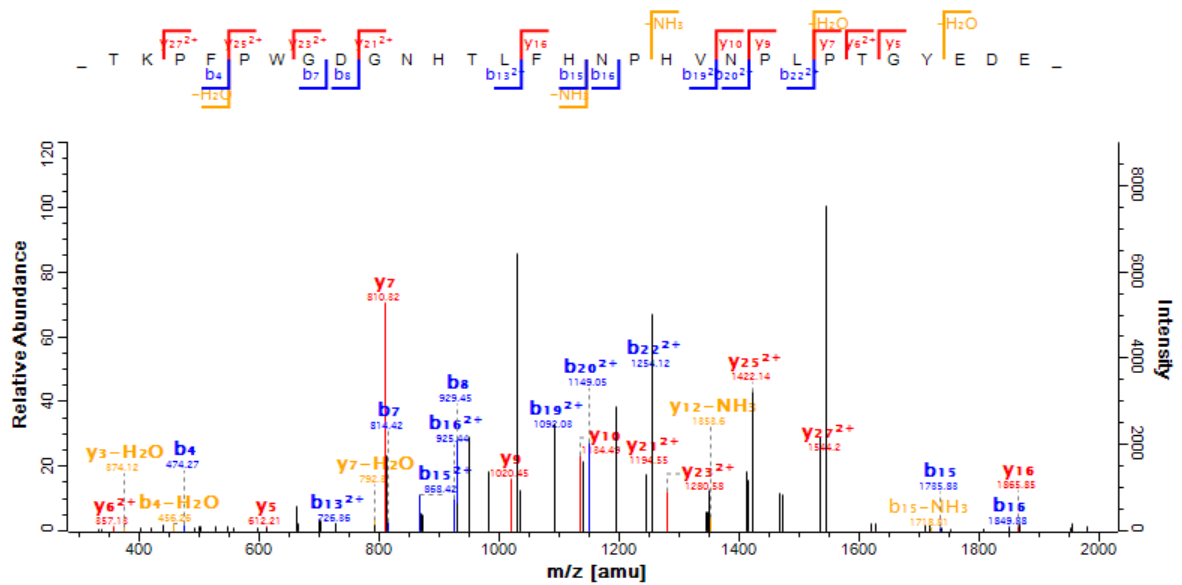
Number of Replicates (out of 10): 8

Best Match Score: 88.504

Best Match Posterior Error Probability: 2.52E-09

Best Match Spectrum:

Scan number 4659 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac16
Method ITMS; CID **Genenames** COX6A1;COX6A1P2



Protein Group ID: 1598

Protein Accession Numbers: P13498

Gene Names: CYBA

Peptide Sequence: KKPSEEEA VAAGPPGGPQVNPIPVTVDEVV

Total Number of Spectra: 1

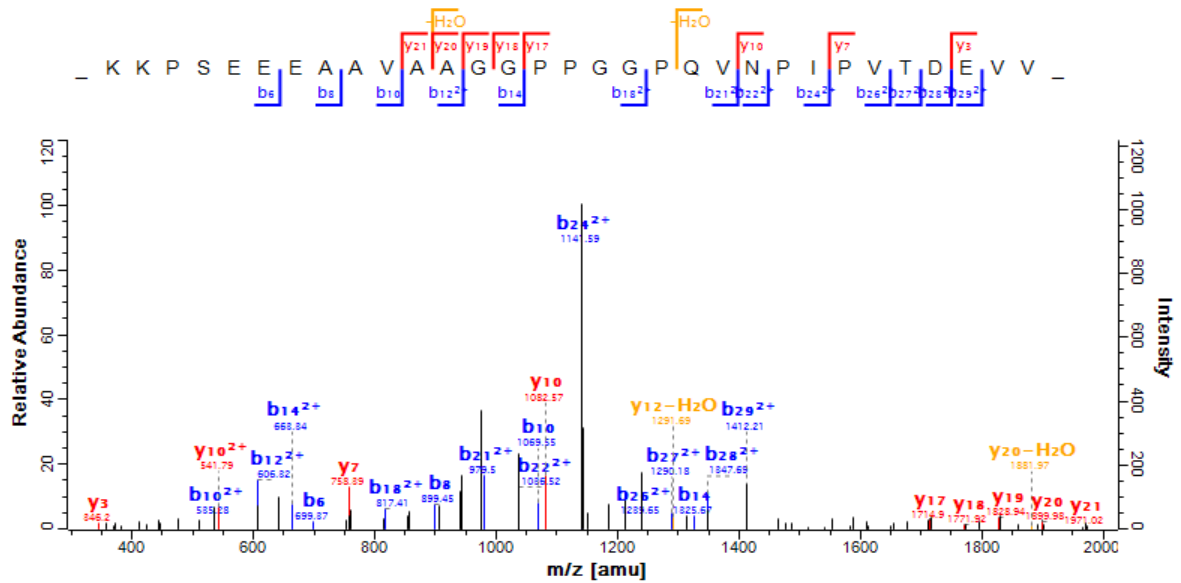
Number of Replicates (out of 10): 1

Best Match Score: 78.128

Best Match Posterior Error Probability: 1.43E-06

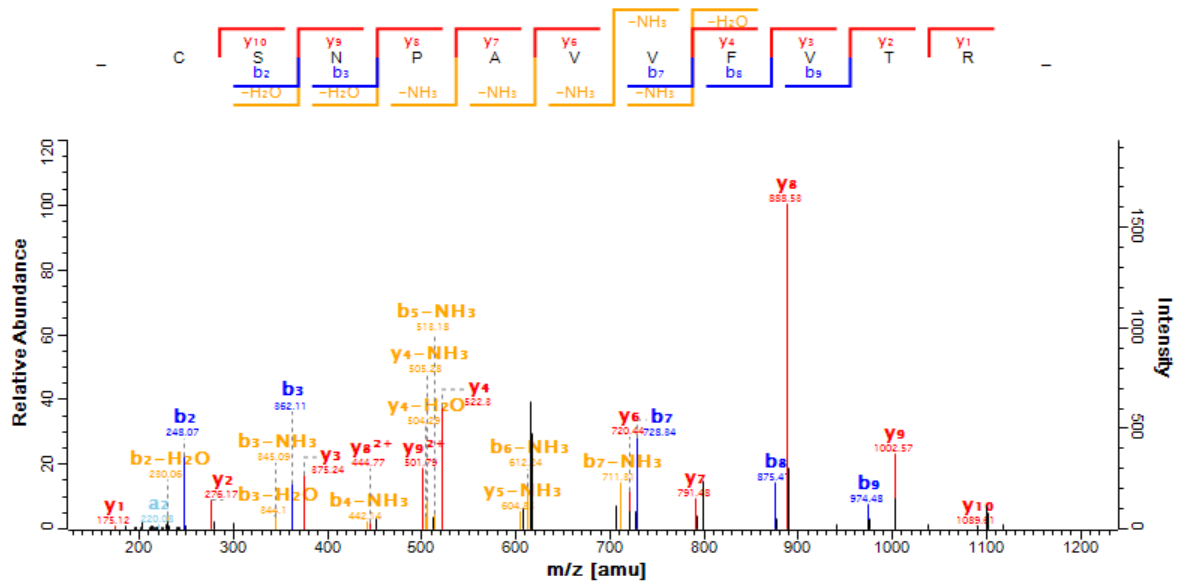
Best Match Spectrum:

Scan number 3441 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** CYBA



Protein Group ID: 1599
Protein Accession Numbers: P13501
Gene Names: CCL5
Peptide Sequence: CSNPAAVVFVTR
Total Number of Spectra: 5
Number of Replicates (out of 10): 3
Best Match Score: 134.49
Best Match Posterior Error Probability: 3.10E-05
Best Match Spectrum:

Scan number	2690	Raw file	Prt-OGE-Batch2-WT-Frac22
Method	ITMS; CID	Genenames	CCL5



Protein Group ID: 1608

Protein Accession Numbers: P13928; Q5T2P8; B4DKI1; Q5VTM3; Q5T2P7

Gene Names: ANXA8;ANXA8L1

Peptide Sequence: DDVSSFVDPGLALQDAQDLYAAGEK

Total Number of Spectra: 8

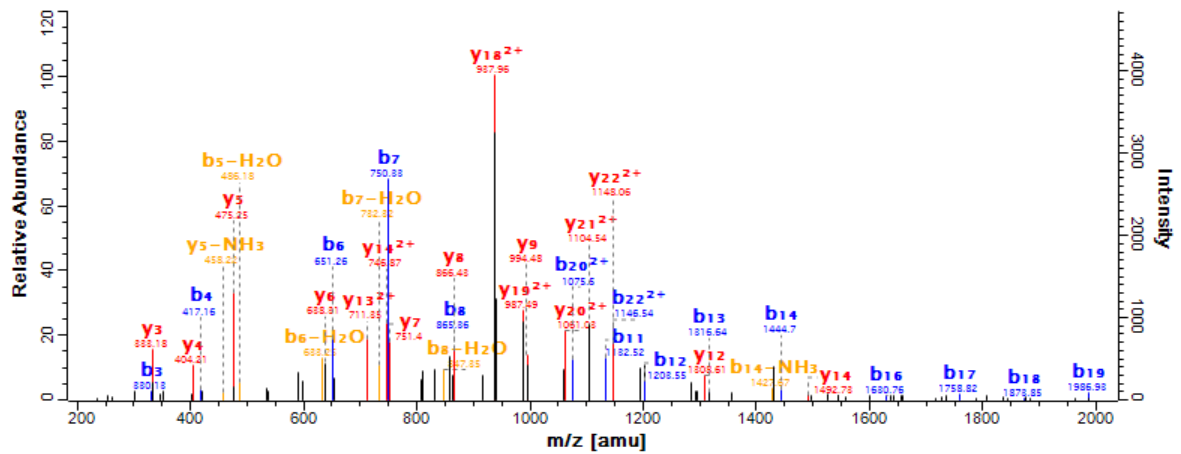
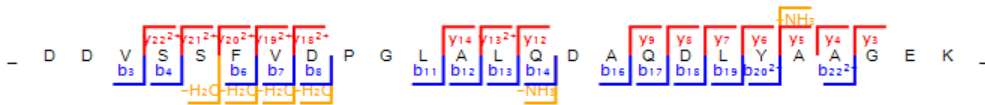
Number of Replicates (out of 10): 6

Best Match Score: 151.89

Best Match Posterior Error Probability: 3.09E-30

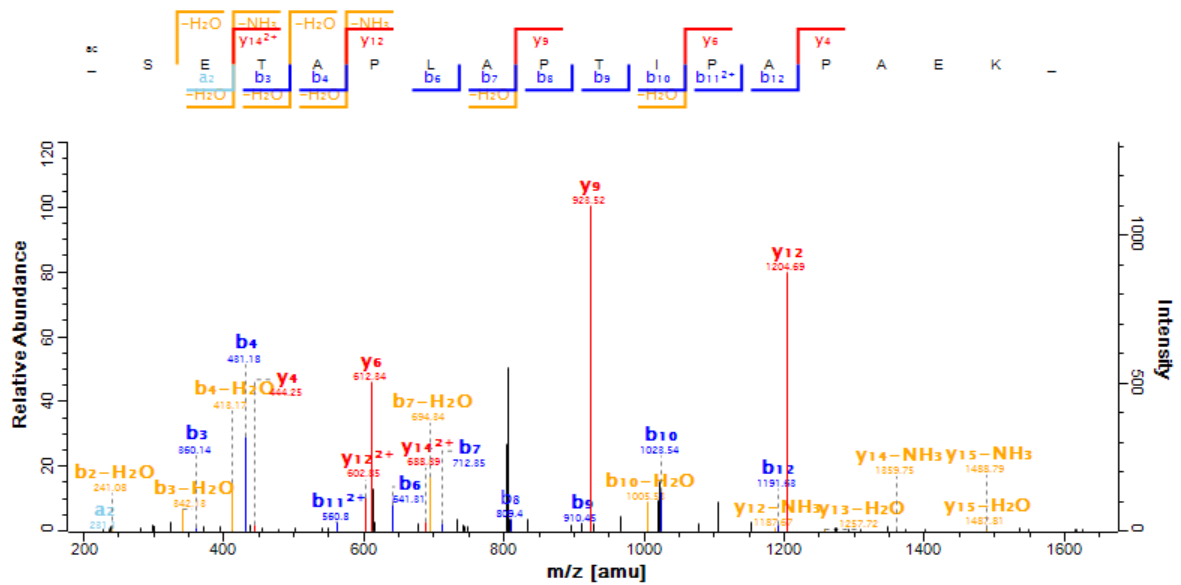
Best Match Spectrum:

Scan number 6849 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac10
Method ITMS; CID **Genenames** ANXA8;ANXA8L1



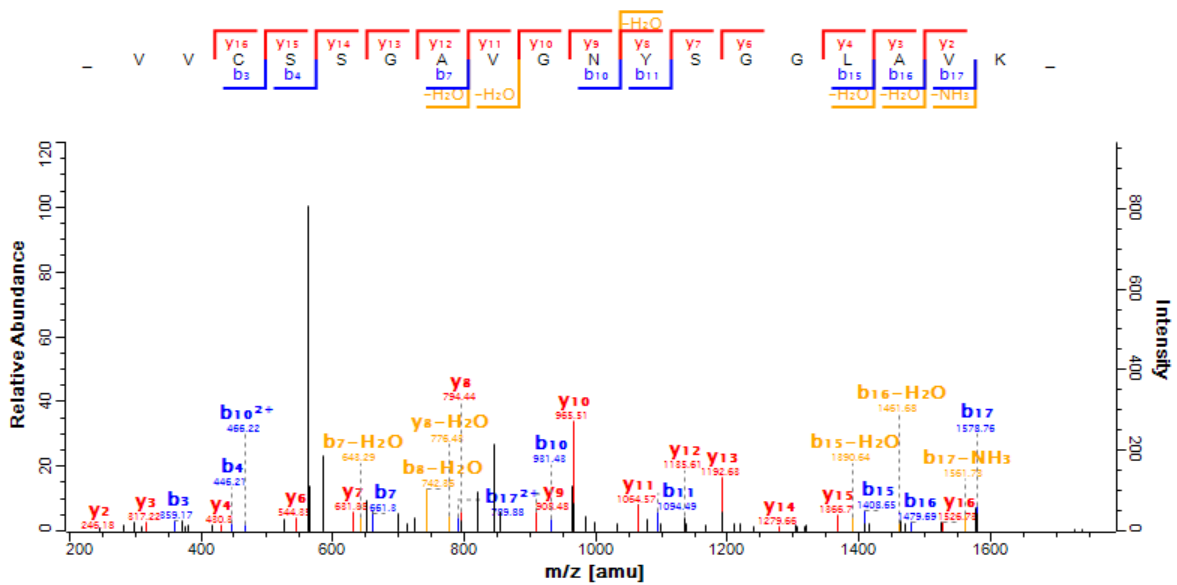
Protein Group ID: 1641
Protein Accession Numbers: P16402
Gene Names: HIST1H1D
Peptide Sequence: SETAPLAPTIPAPAEK
Total Number of Spectra: 15
Number of Replicates (out of 10): 5
Best Match Score: 119.96
Best Match Posterior Error Probability: 0.0001049
Best Match Spectrum:

Scan number 4523 **Raw file** Prt-OGE-Batch2-Mock-Frac23
Method ITMS; CID **Genenames** HIST1H1D



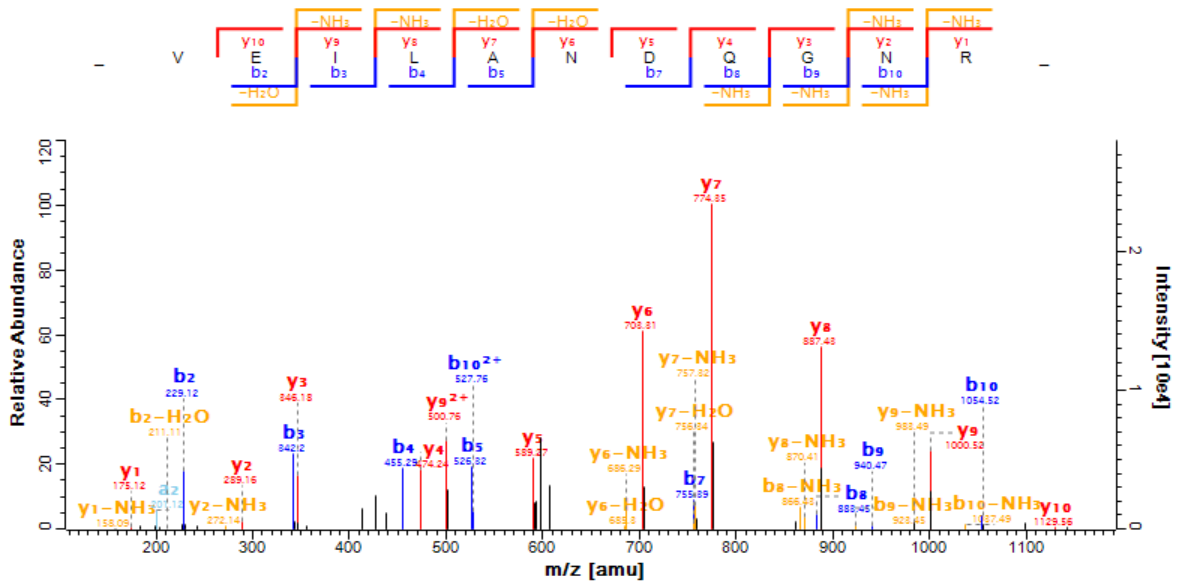
Protein Group ID: 1643
Protein Accession Numbers: P16455
Gene Names: MGMT
Peptide Sequence: VVCSSGAVGNYSGGLAVK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 131.25
Best Match Posterior Error Probability: 1.56E-05
Best Match Spectrum:

Scan number 2820 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac19
Method ITMS; CID **Genenames** MGMT



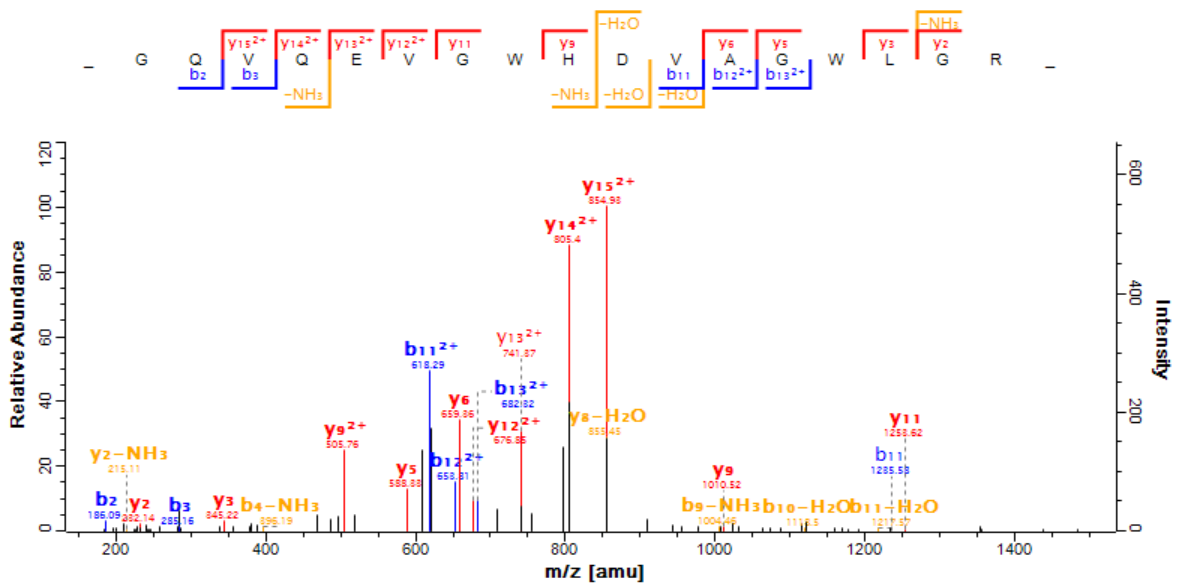
Protein Group ID: 1648
Protein Accession Numbers: P17066; P48741
Gene Names: HSPA6;HSPA7
Peptide Sequence: VEILANDQGNR
Total Number of Spectra: 257
Number of Replicates (out of 10): 10
Best Match Score: 231.7
Best Match Posterior Error Probability: 2.94E-225
Best Match Spectrum:

Scan number 2018 **Raw file** OGE-WT-Frac8
Method ITMS; CID **Genenames** HSPA6;HSPA7



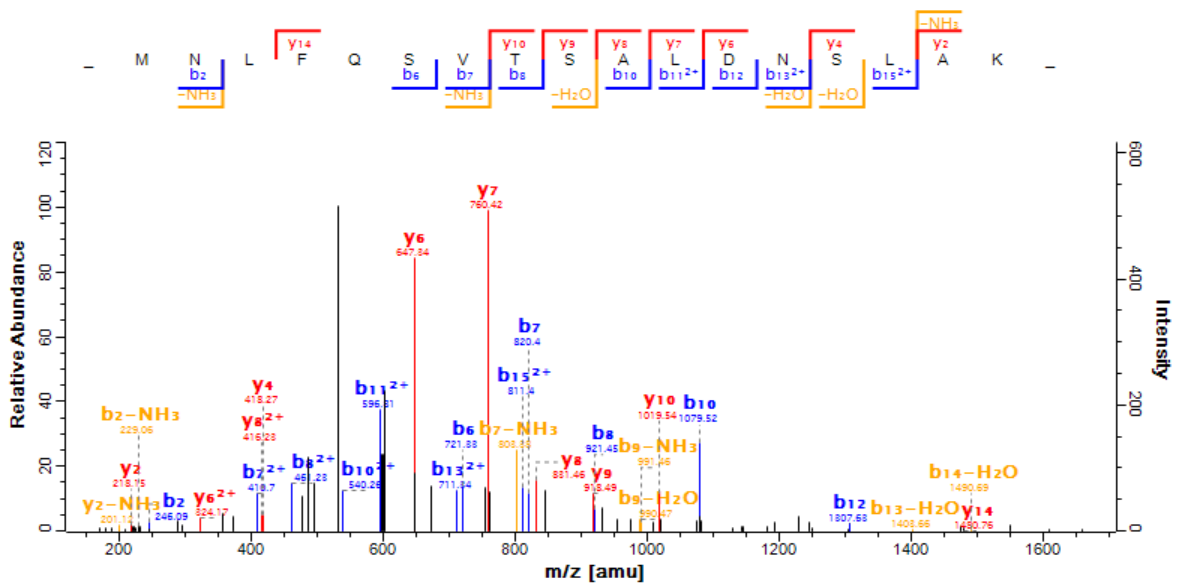
Protein Group ID: 1655
Protein Accession Numbers: P17858; P17858-2
Gene Names: PFKL
Peptide Sequence: GQVQVEVGVWHDVAVGLGR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 77.42
Best Match Posterior Error Probability: 0.0013896
Best Match Spectrum:

Scan number 4401 **Raw file** OGE-WT-Frac3
Method ITMS; CID **Genenames** PFKL



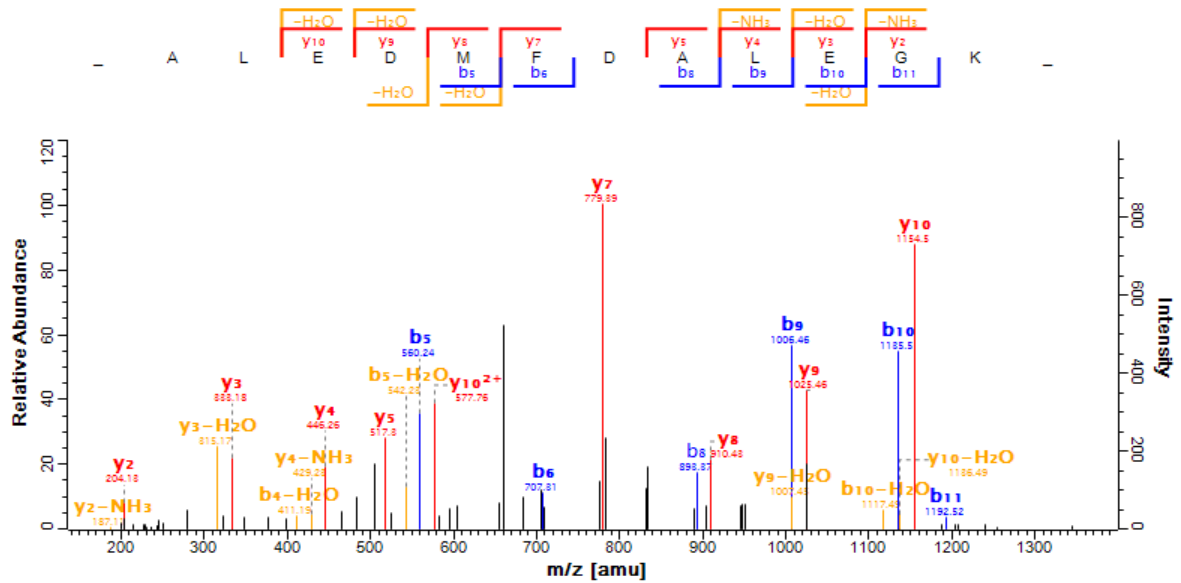
Protein Group ID: 1689
Protein Accession Numbers: P21953; Q5T2J3
Gene Names: BCKDHB
Peptide Sequence: MNLFQSVTSALDNSLAK
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 122.08
Best Match Posterior Error Probability: 0.00010788
Best Match Spectrum:

Scan number 7543 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac8
Method ITMS; CID **Genenames** BCKDHB



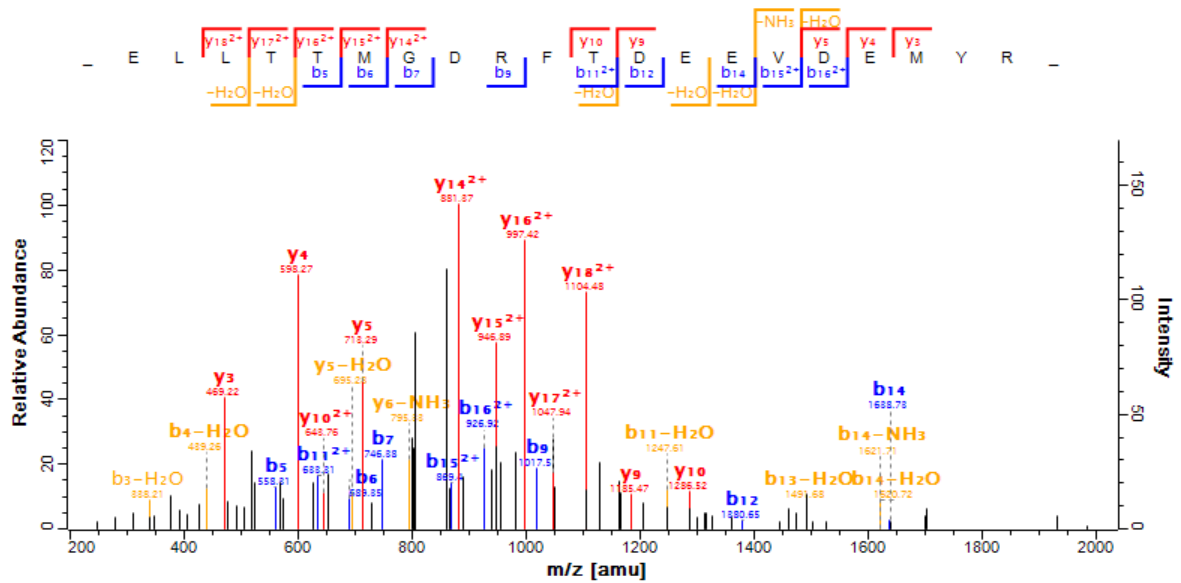
Protein Group ID: 1713
Protein Accession Numbers: P23786
Gene Names: CPT2
Peptide Sequence: ALEDMFDALGK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 140.14
Best Match Posterior Error Probability: 6.42E-05
Best Match Spectrum:

Scan number 4822 **Raw file** Prt-OGE-Batch2-WT-Frac17
Method ITMS; CID **Genenames** CPT2



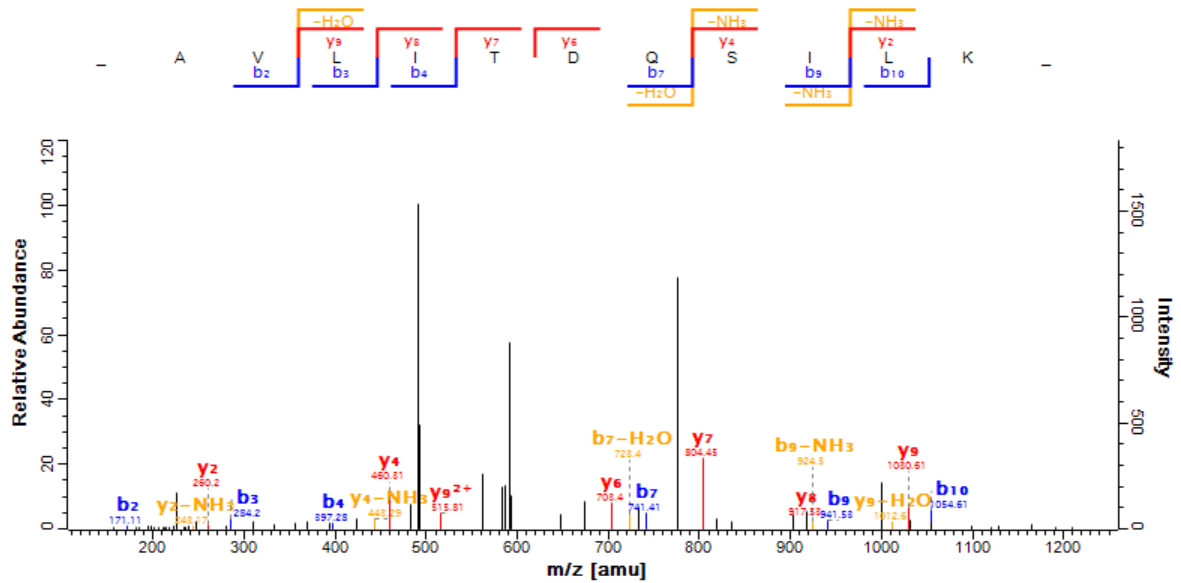
Protein Group ID: 1720
Protein Accession Numbers: P24844; P24844-2
Gene Names: MYL9
Peptide Sequence: ELLTTMGDRFTDEEVDEMYR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 124.68
Best Match Posterior Error Probability: 1.88E-06
Best Match Spectrum:

Scan number 4362 **Raw file** OGE-WT-Frac5
Method ITMS; CID **Genenames** MYL9



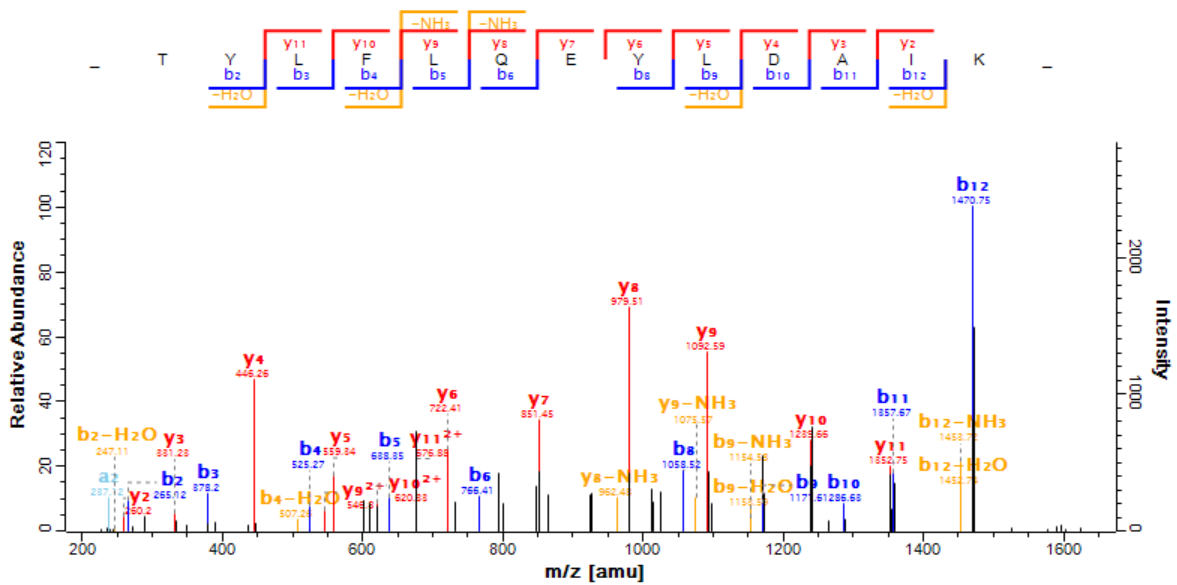
Protein Group ID: 1738
Protein Accession Numbers: P26374
Gene Names: CHML
Peptide Sequence: AVLITDQSILK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 90.913
Best Match Posterior Error Probability: 0.00081989
Best Match Spectrum:

Scan number 3607 **Raw file** Prt-OGE-Batch3-WT-Frac5
Method ITMS; CID **Genenames** CHML



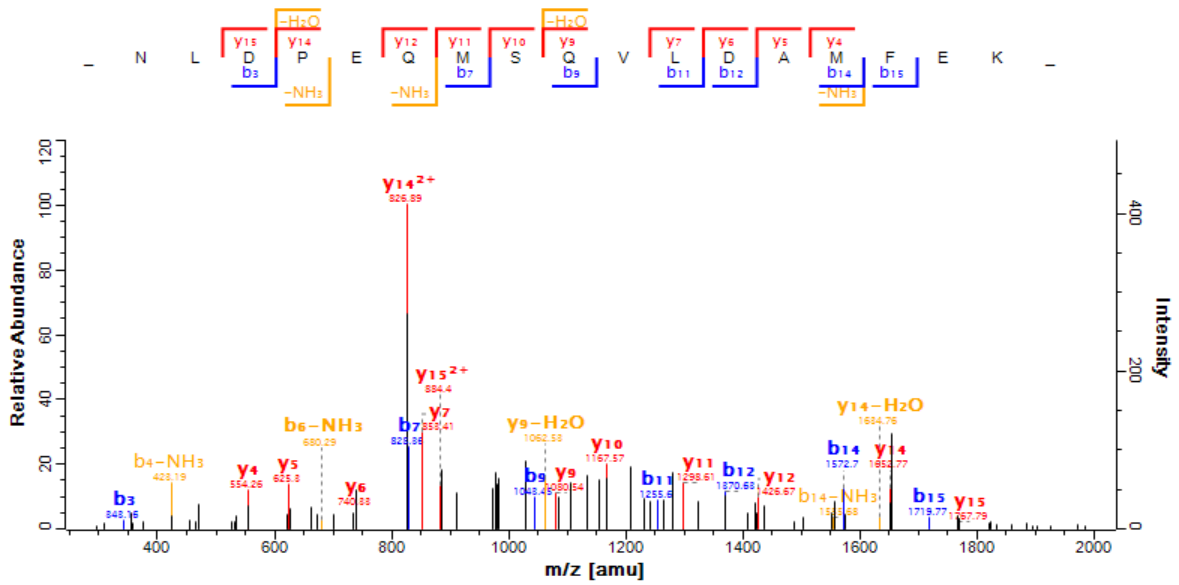
Protein Group ID: 1766
Protein Accession Numbers: P29508; P29508-2
Gene Names: SERPINB3
Peptide Sequence: TYLFLQEYLDAIK
Total Number of Spectra: 5
Number of Replicates (out of 10): 4
Best Match Score: 200.16
Best Match Posterior Error Probability: 1.82E-24
Best Match Spectrum:

Scan number 6933 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac14
Method ITMS; CID **Genenames** SERPINB3



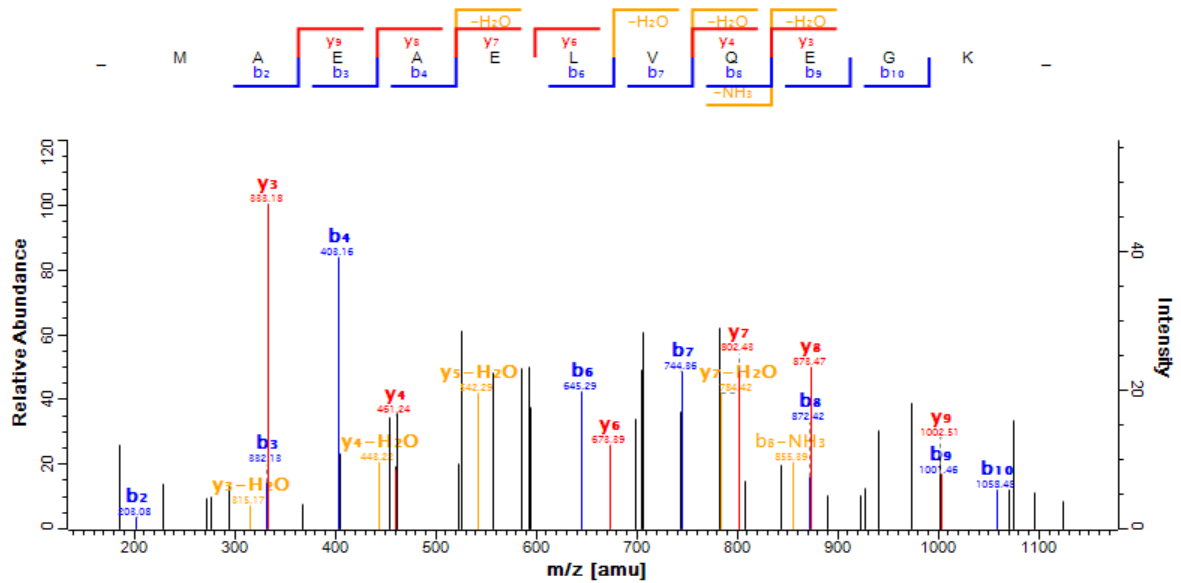
Protein Group ID: 1798
Protein Accession Numbers: P31323
Gene Names: PRKAR2B
Peptide Sequence: NLDPEQMSQVLDAMFEK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 84.208
Best Match Posterior Error Probability: 0.00078724
Best Match Spectrum:

Scan number 6362 **Raw file** OGE-WT-Frac6
Method ITMS; CID **Genenames** PRKAR2B



Protein Group ID: 1805
Protein Accession Numbers: P31944
Gene Names: CASP14
Peptide Sequence: MAEAELVQEGK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 95.094
Best Match Posterior Error Probability: 0.00049374
Best Match Spectrum:

Scan number 1358 **Raw file** Prt-OGE-Batch2-WT-Frac20
Method ITMS; CID **Genenames** CASP14



Protein Group ID: 1811

Protein Accession Numbers: P32320

Gene Names: CDA

Peptide Sequence: EFGTNWPVYMTKPDGTYIVMTVQELLPSFSGPEDLQK

Total Number of Spectra: 6

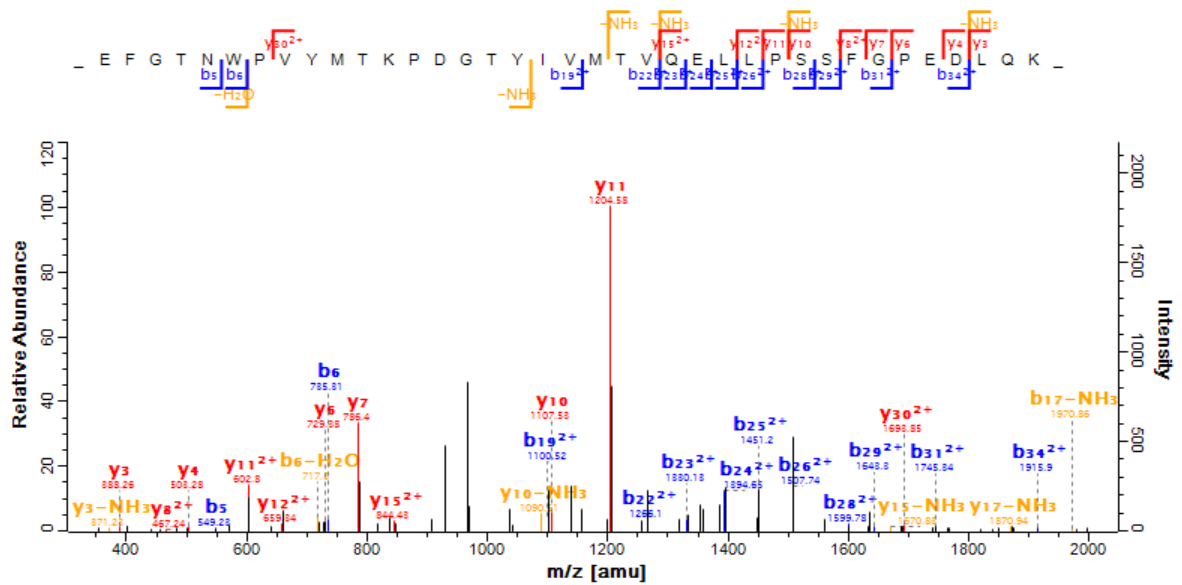
Number of Replicates (out of 10): 4

Best Match Score: 69.523

Best Match Posterior Error Probability: 5.27E-07

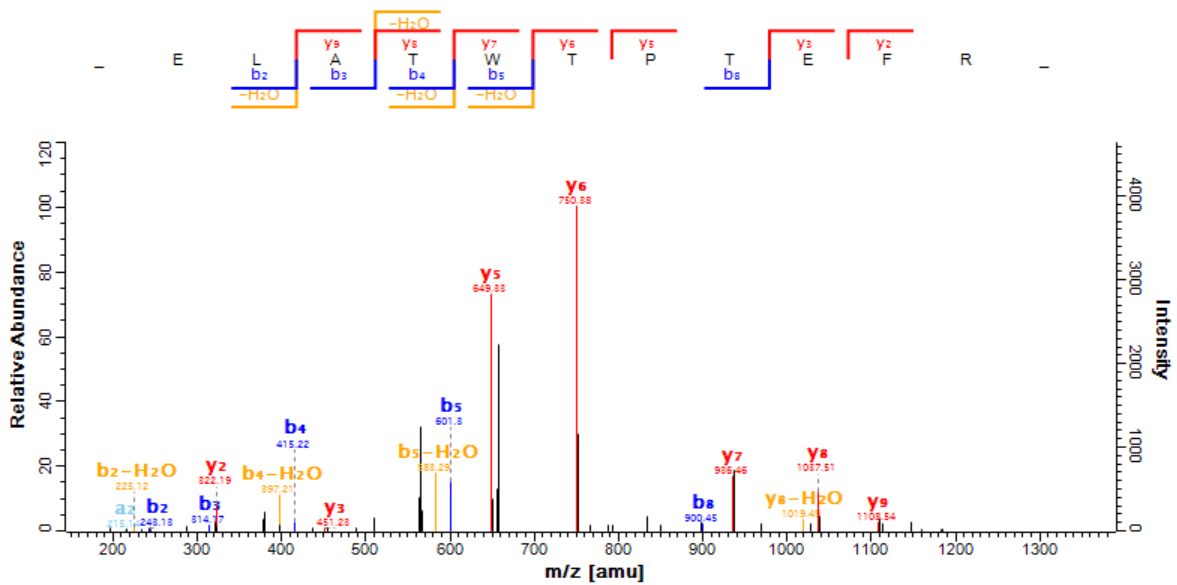
Best Match Spectrum:

Scan number 6872 **Raw file** Prt-OGE-Batch2-WT-Frac8
Method ITMS; CID **Genenames** CDA



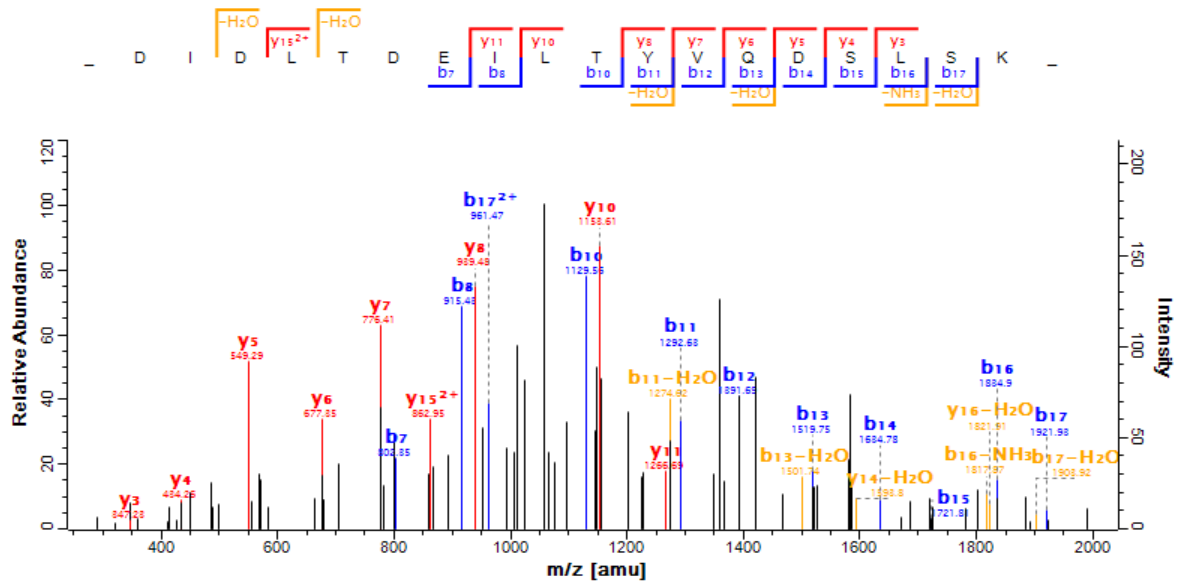
Protein Group ID: 1819
Protein Accession Numbers: P33764
Gene Names: S100A3
Peptide Sequence: ELATWTPTEFR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 101.39
Best Match Posterior Error Probability: 0.00024992
Best Match Spectrum:

Scan number 4493 **Raw file** OGE-Mock-Frac3
Method ITMS; CID **Genenames** S100A3



Protein Group ID: 1843
Protein Accession Numbers: P35869
Gene Names: AHR
Peptide Sequence: DIDLTDEILTYVQDSLK
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 127.22
Best Match Posterior Error Probability: 3.88E-05
Best Match Spectrum:

Scan number 8365 **Raw file** Prt-OGE-Batch3--Mock-Frac12
Method ITMS; CID **Genenames** AHR



Protein Group ID: 1848

Protein Accession Numbers: P36406; P36406-2; P36406-3

Gene Names: TRIM23

Peptide Sequence: DALLLIFANK

Total Number of Spectra: 1

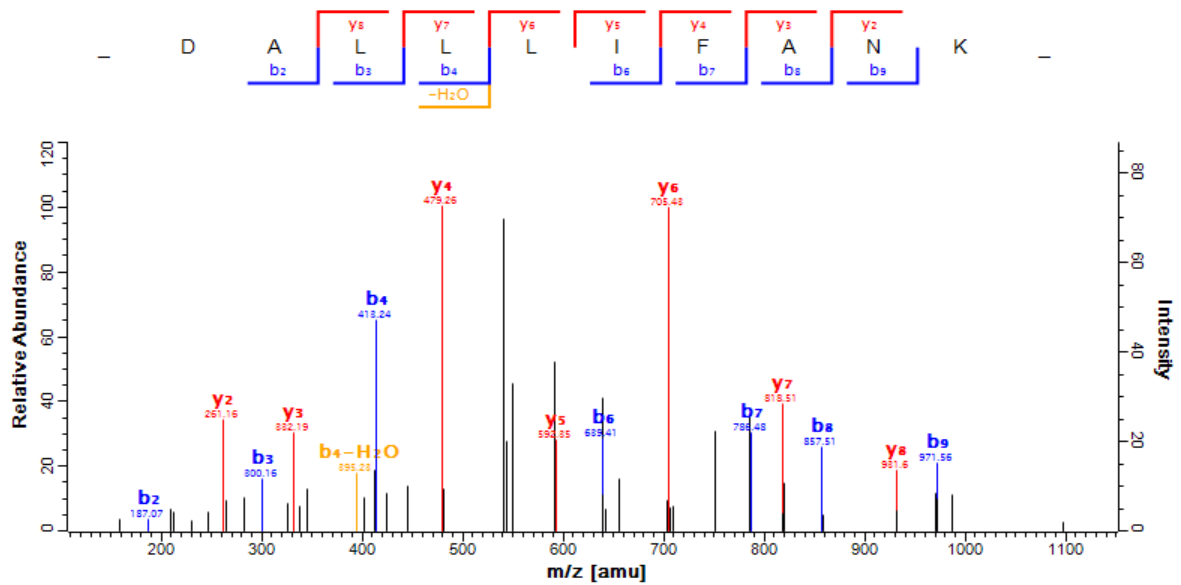
Number of Replicates (out of 10): 1

Best Match Score: 98.943

Best Match Posterior Error Probability: 0.00059455

Best Match Spectrum:

Scan number 4010 **Raw file** Prt-OGE-Batch2-WT-Frac19
Method ITMS; CID **Genenames** TRIM23



Protein Group ID: 1894

Protein Accession Numbers: P42226; P42226-3; P42226-2

Gene Names: STAT6

Peptide Sequence: LLLEGQGESGGSLGAQPLLQPSHYGQSGISM^{-H₂O}SHMDLR

Total Number of Spectra: 1

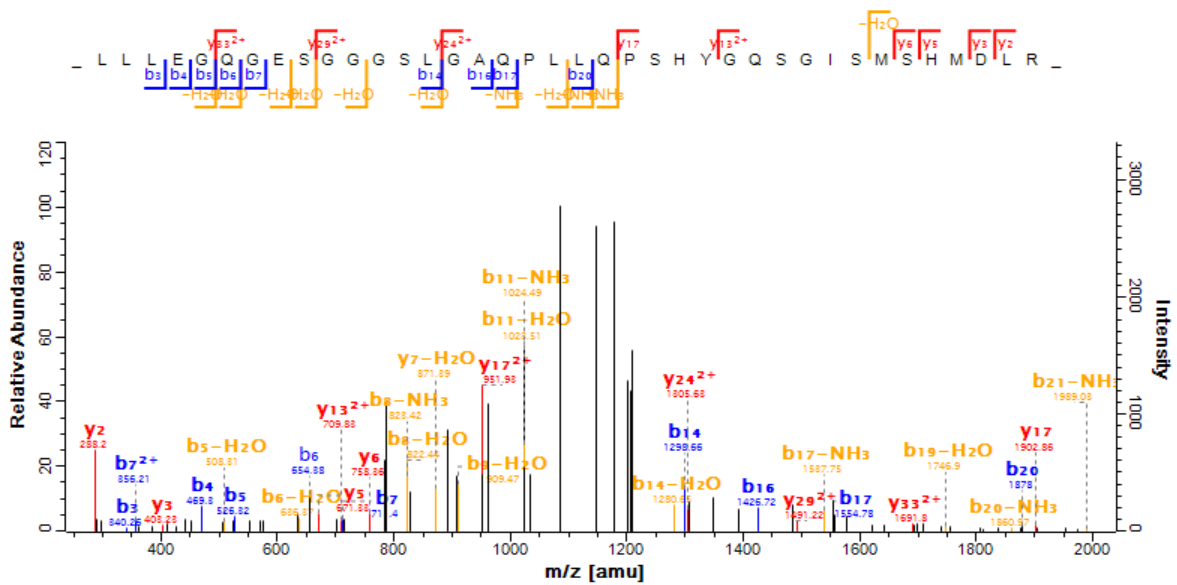
Number of Replicates (out of 10): 1

Best Match Score: 49.025

Best Match Posterior Error Probability: 0.00051341

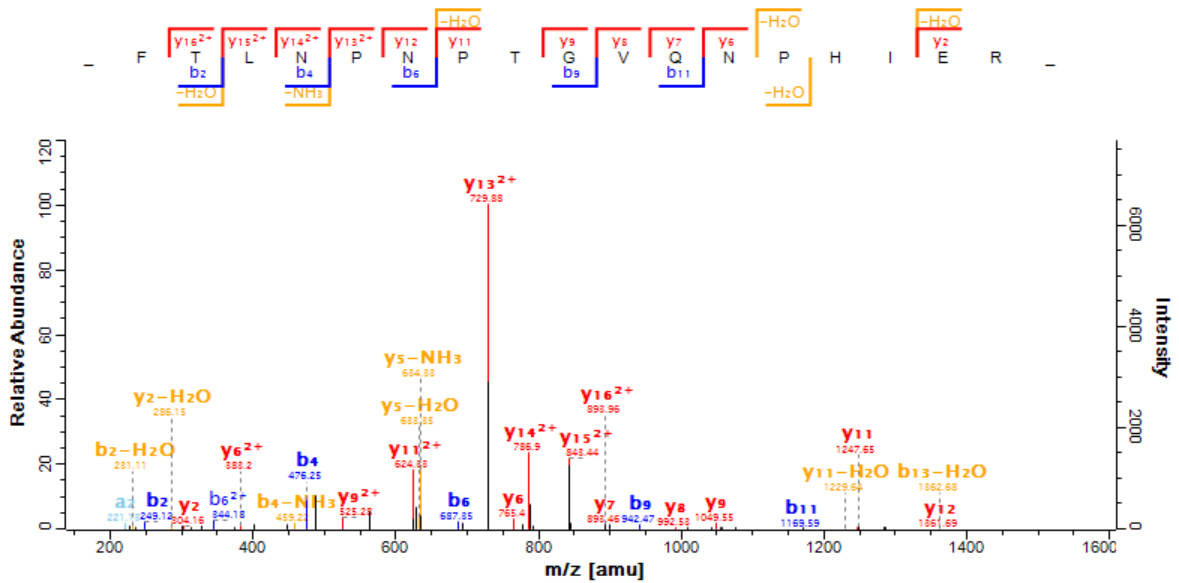
Best Match Spectrum:

Scan number	4234	Raw file	Prt-OGE-Batch3-WT-Frac12
Method	ITMS; CID	Genenames	STAT6



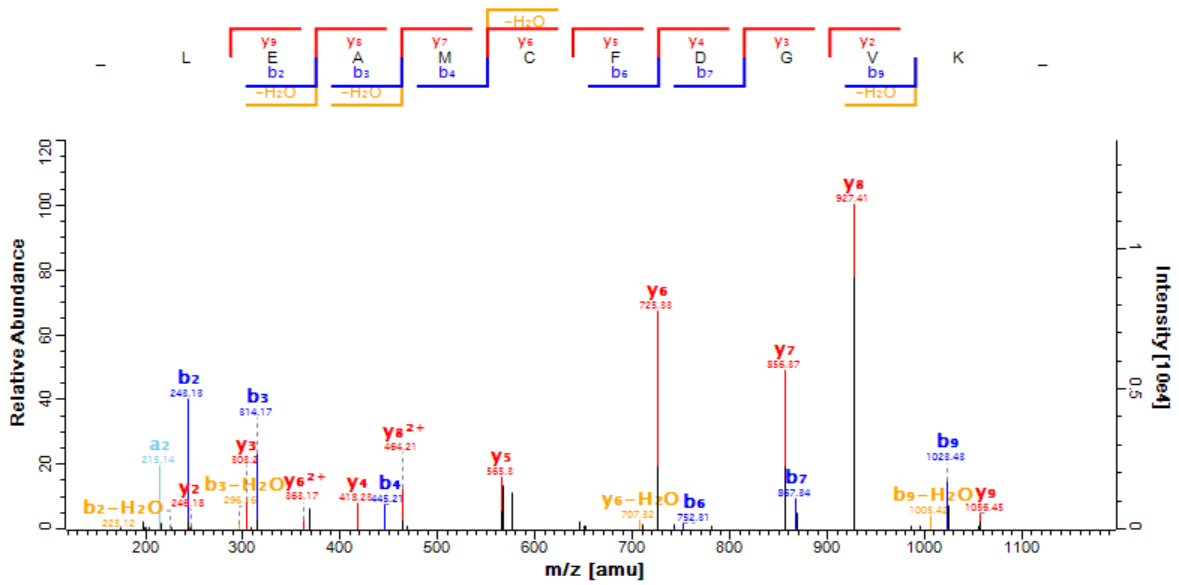
Protein Group ID: 1912
Protein Accession Numbers: P45985-2; P45985
Gene Names: MAP2K4
Peptide Sequence: FTLNPNPTGVQNPHIER
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 118.2
Best Match Posterior Error Probability: 0.00013922
Best Match Spectrum:

Scan number 2751 **Raw file** Prt-OGE-Batch3--Mock-Frac1 8
Method ITMS; CID **Genenames** MAP2K4



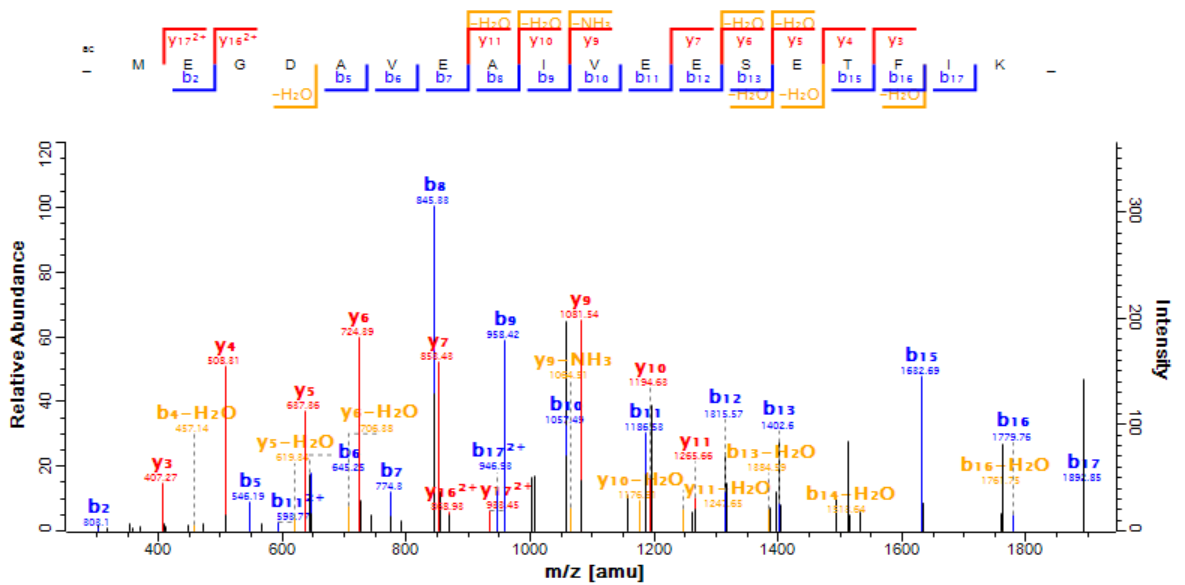
Protein Group ID: 1934
Protein Accession Numbers: P47813
Gene Names: EIF1AX
Peptide Sequence: LEAMCFDGVK
Total Number of Spectra: 12
Number of Replicates (out of 10): 7
Best Match Score: 143.96
Best Match Posterior Error Probability: 5.81E-05
Best Match Spectrum:

Scan number 3527 **Raw file** OGE-WT-Frac7
Method ITMS; CID **Genenames** EIF1AX



Protein Group ID: 1969
Protein Accession Numbers: P49711
Gene Names: CTCF
Peptide Sequence: MEGDAVEAIVEESETFIK
Total Number of Spectra: 5
Number of Replicates (out of 10): 5
Best Match Score: 169.02
Best Match Posterior Error Probability: 3.78E-16
Best Match Spectrum:

Scan number 7476 **Raw file** OGE-Mock-Frac2
Method ITMS; CID **Genenames** CTCF



Protein Group ID: 1974

Protein Accession Numbers: P49753; P49753-2; B3KSA0

Gene Names: ACOT2

Peptide Sequence: TMETLHLEYFEEAMNYLLSHPEVK

Total Number of Spectra: 12

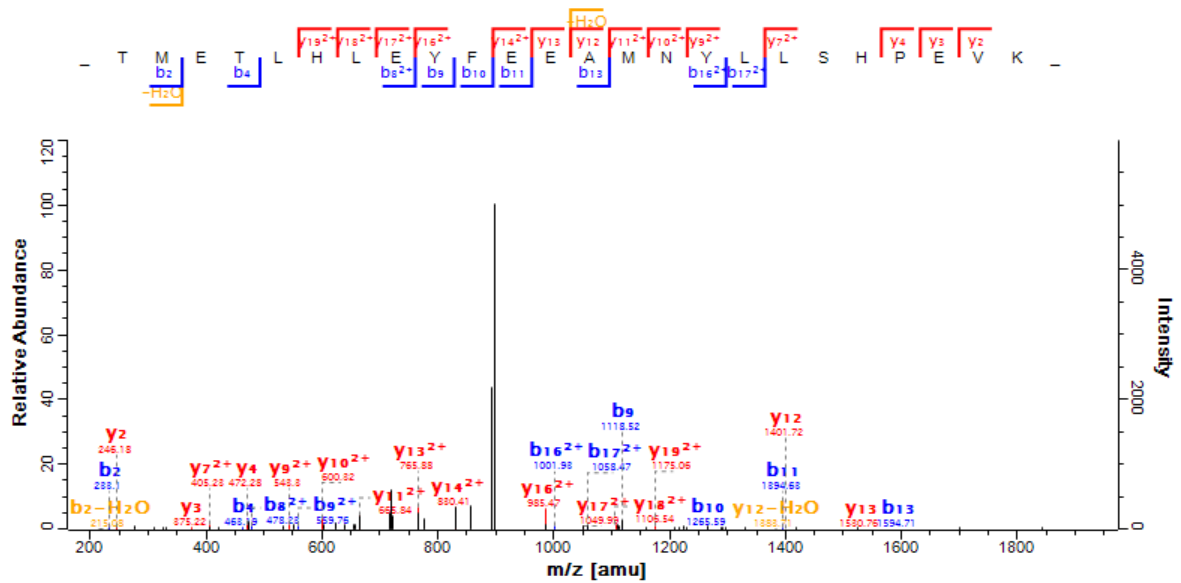
Number of Replicates (out of 10): 8

Best Match Score: 118.96

Best Match Posterior Error Probability: 4.39E-11

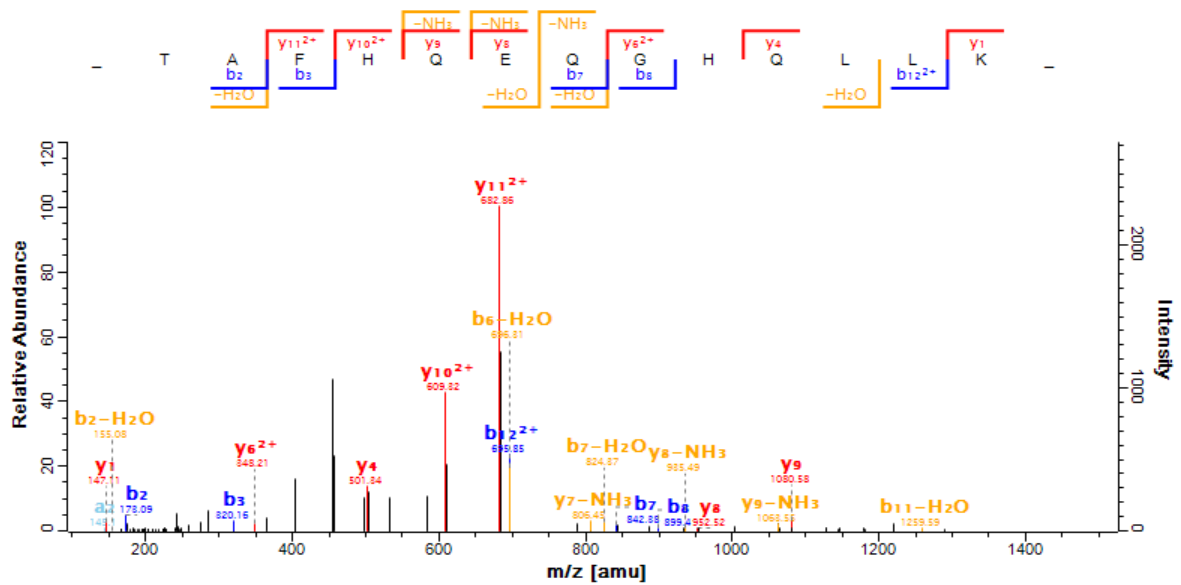
Best Match Spectrum:

Scan number 6617 **Raw file** OGE-WT-Frac19
Method ITMS; CID **Genenames** ACOT2



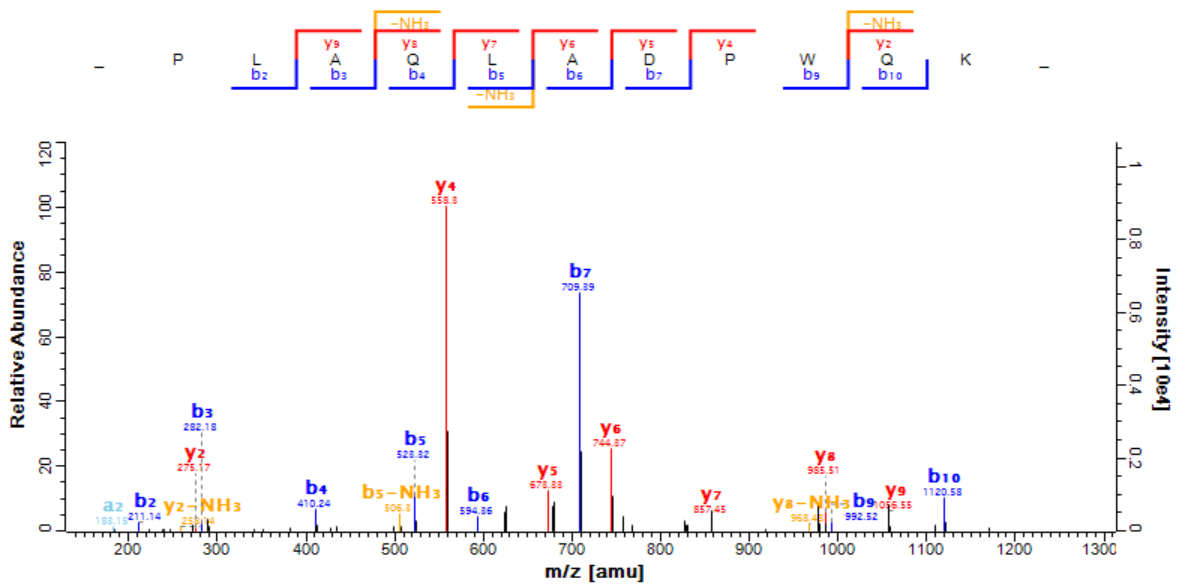
Protein Group ID: 2007
Protein Accession Numbers: P51580
Gene Names: TPMT
Peptide Sequence: TAFHQEQGHQLLK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 91.961
Best Match Posterior Error Probability: 0.00086156
Best Match Spectrum:

Scan number	1350	Raw file	20100914-KD-Batch4-Prt-OGE-Mock-Frac12
Method	ITMS; CID	Genenames	TPMT



Protein Group ID: 2011
Protein Accession Numbers: P51812
Gene Names: RPS6KA3
Peptide Sequence: PLAQLADPWQK
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 107.85
Best Match Posterior Error Probability: 0.00016673
Best Match Spectrum:

Scan number 4484 **Raw file** Prt-OGE-Batch3--Mock-Frac14
Method ITMS; CID **Genenames** RPS6KA3



Protein Group ID: 2027

Protein Accession Numbers: P52740; P52740-2

Gene Names: ZNF132

Peptide Sequence: AFNNNSNLAQHQK

Total Number of Spectra: 1

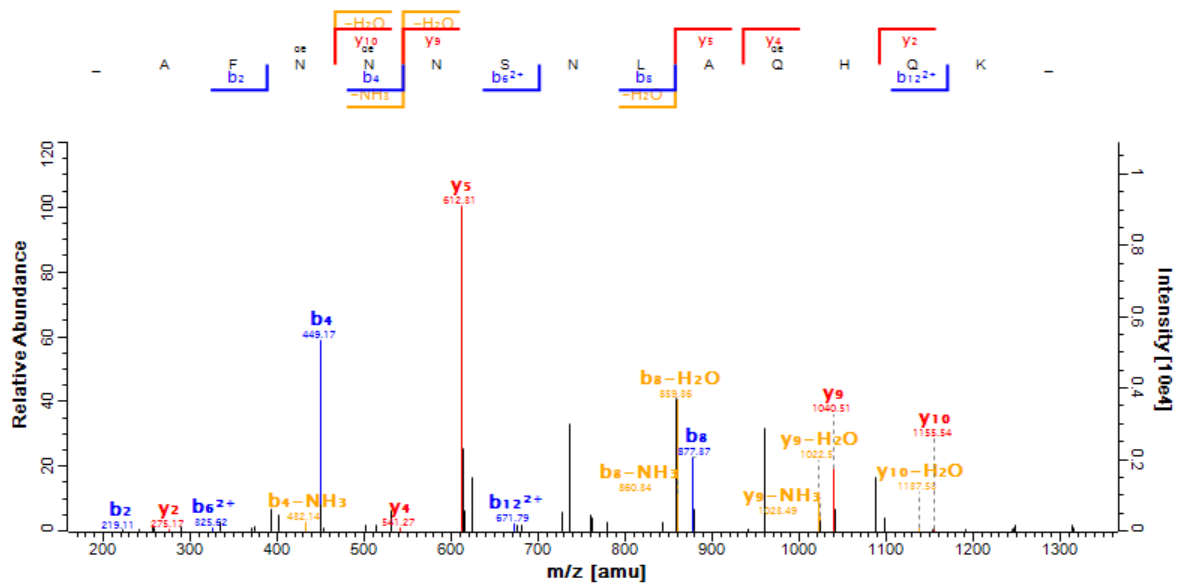
Number of Replicates (out of 10): 1

Best Match Score: 81.625

Best Match Posterior Error Probability: 0.021486

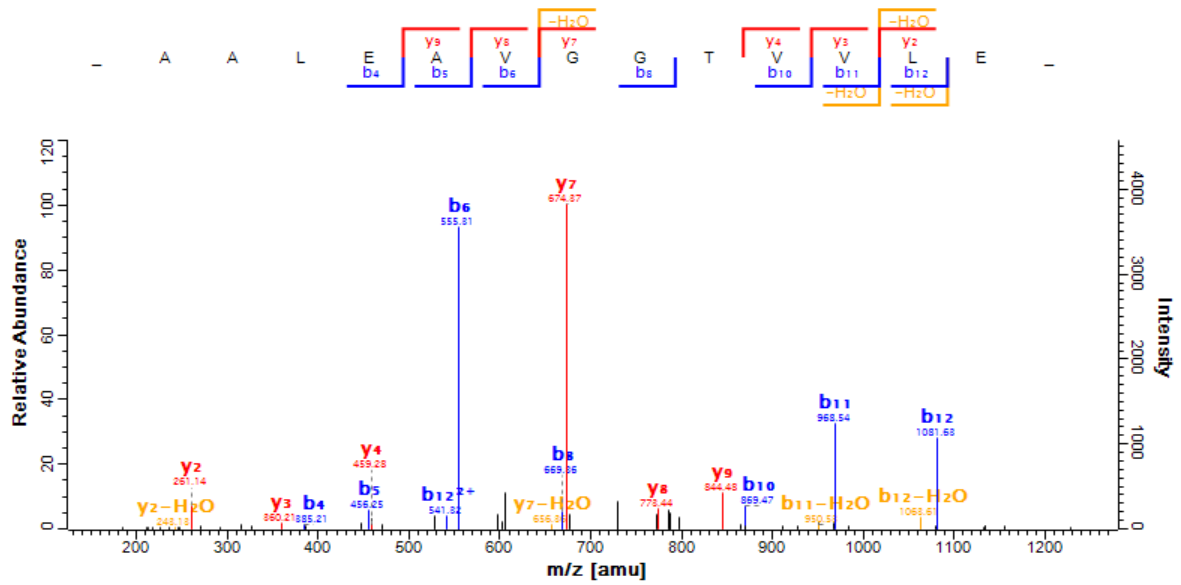
Best Match Spectrum:

Scan number 2701 **Raw file** Prt-OGE-Batch2-WT-Frac22
Method ITMS; CID **Genenames** ZNF132



Protein Group ID: 2030
Protein Accession Numbers: P52815
Gene Names: MRPL12
Peptide Sequence: AALEAVGGTVVLE
Total Number of Spectra: 12
Number of Replicates (out of 10): 9
Best Match Score: 122.7
Best Match Posterior Error Probability: 9.36E-05
Best Match Spectrum:

Scan number 4594 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac7
Method ITMS; CID **Genenames** MRPL12



Protein Group ID: 2049

Protein Accession Numbers: Q13131-2; Q13131; P54646; Q96E92

Gene Names: PRKAA1;PRKAA2

Peptide Sequence: IADFGLSNMMSDGEFLR

Total Number of Spectra: 3

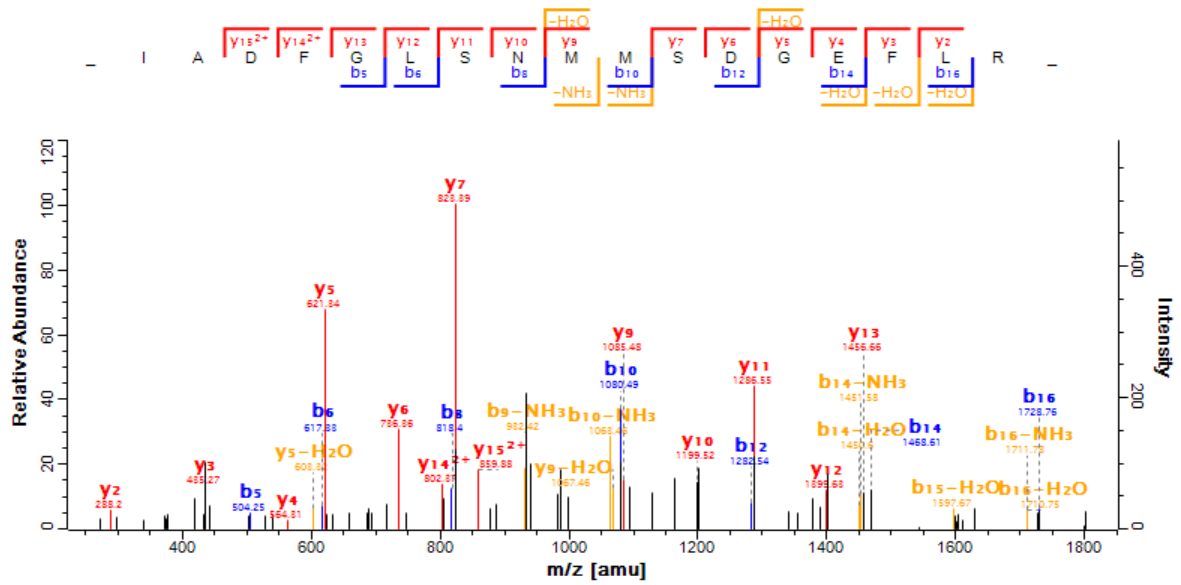
Number of Replicates (out of 10): 3

Best Match Score: 123.08

Best Match Posterior Error Probability: 9.77E-05

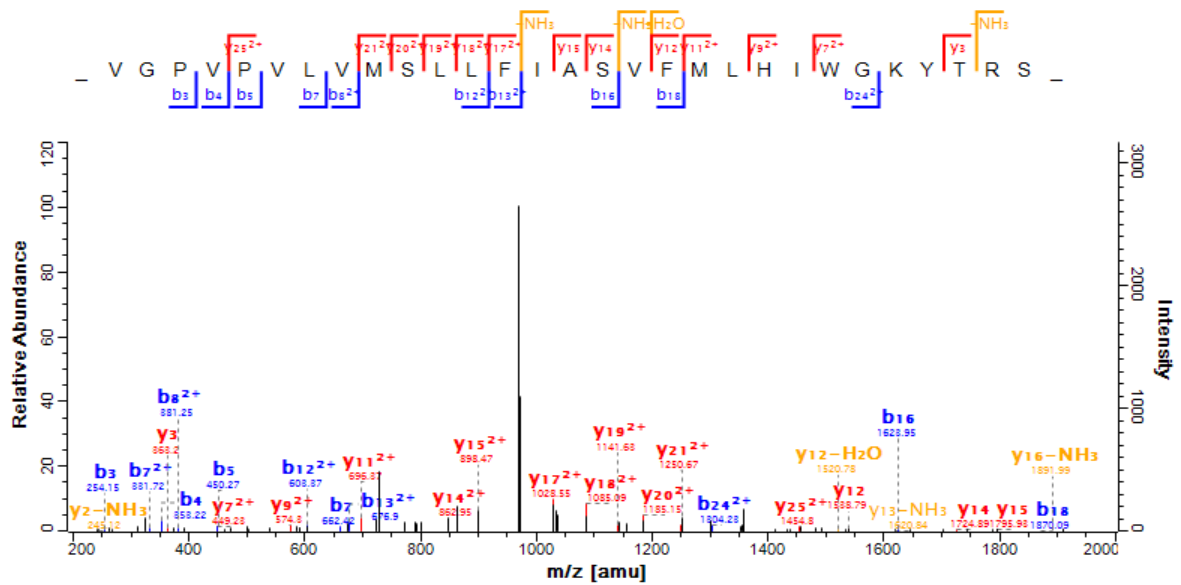
Best Match Spectrum:

Scan number 6097 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac17
Method ITMS; CID **Genenames** PRKAA1;PRKAA2



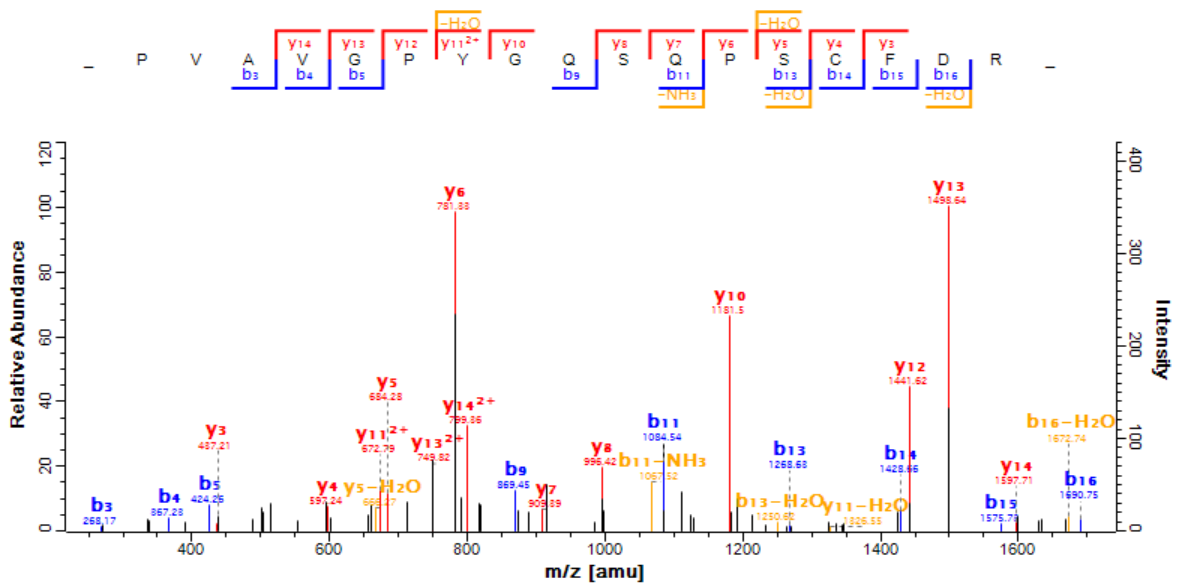
Protein Group ID: 2081
Protein Accession Numbers: P60468
Gene Names: SEC61B
Peptide Sequence: VGPVPLVMSLLFIASVFM LHIWGKYTRS
Total Number of Spectra: 7
Number of Replicates (out of 10): 5
Best Match Score: 93.729
Best Match Posterior Error Probability: 4.37E-09
Best Match Spectrum:

Scan number 10358 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac11
Method ITMS; CID **Genenames** SEC61B



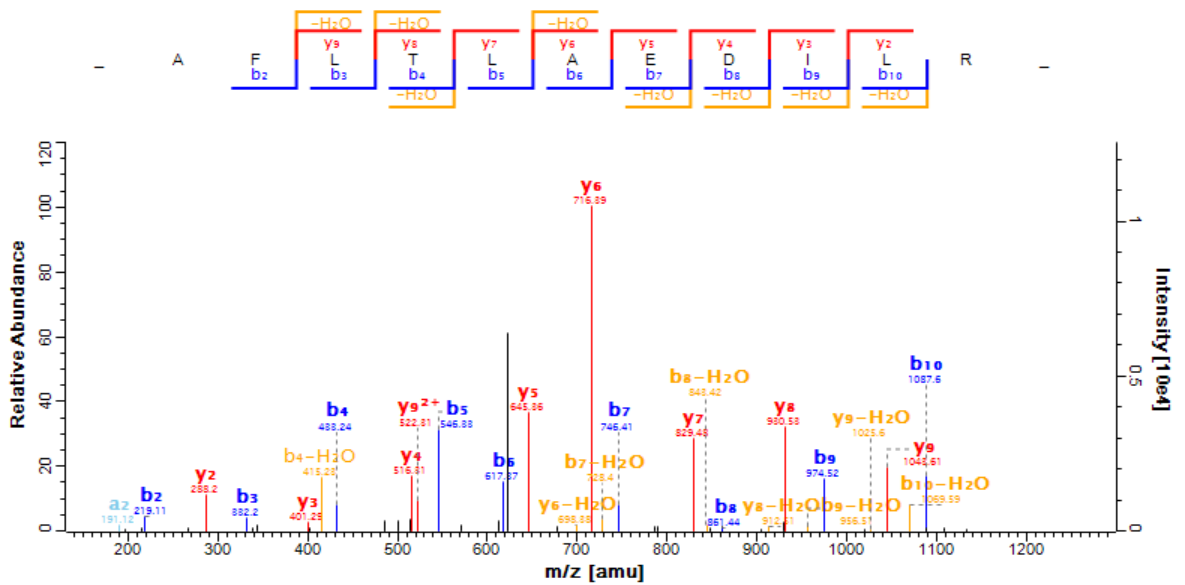
Protein Group ID: 2083
Protein Accession Numbers: P60602; P60602-2
Gene Names: ROMO1
Peptide Sequence: PVAVGPGYSQPSCFDR
Total Number of Spectra: 5
Number of Replicates (out of 10): 3
Best Match Score: 131.18
Best Match Posterior Error Probability: 2.42E-05
Best Match Spectrum:

Scan number 2814 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac21
Method ITMS; CID **Genenames** ROMO1



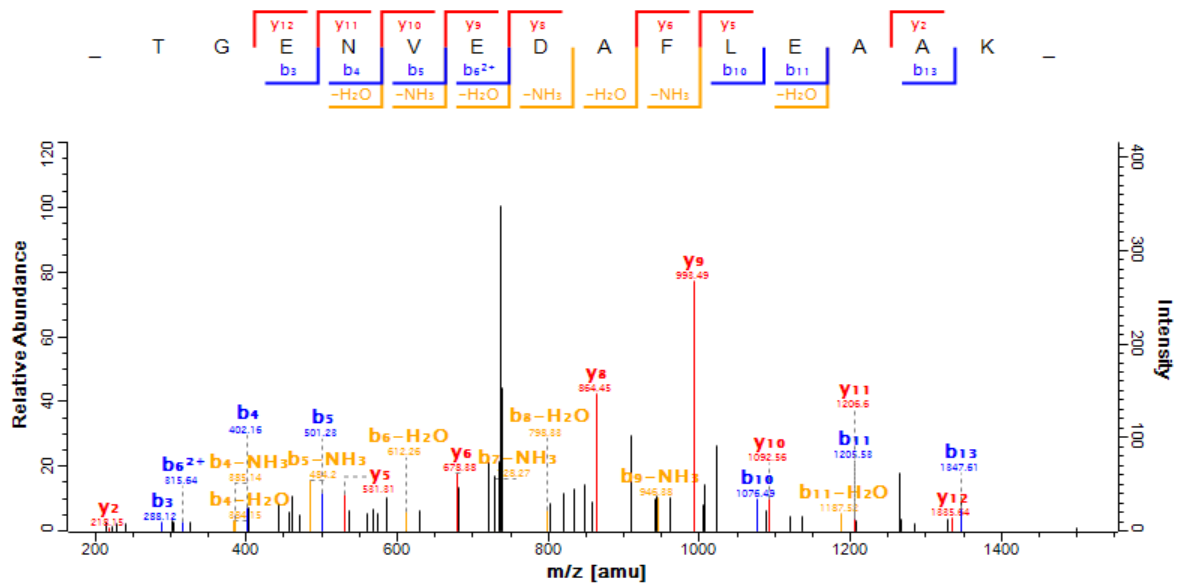
Protein Group ID: 2095
Protein Accession Numbers: P61026
Gene Names: RAB10
Peptide Sequence: AFLTLAEDILR
Total Number of Spectra: 83
Number of Replicates (out of 10): 10
Best Match Score: 212.82
Best Match Posterior Error Probability: 2.89E-31
Best Match Spectrum:

Scan number 6978 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac11
Method ITMS; CID **Genenames** RAB10



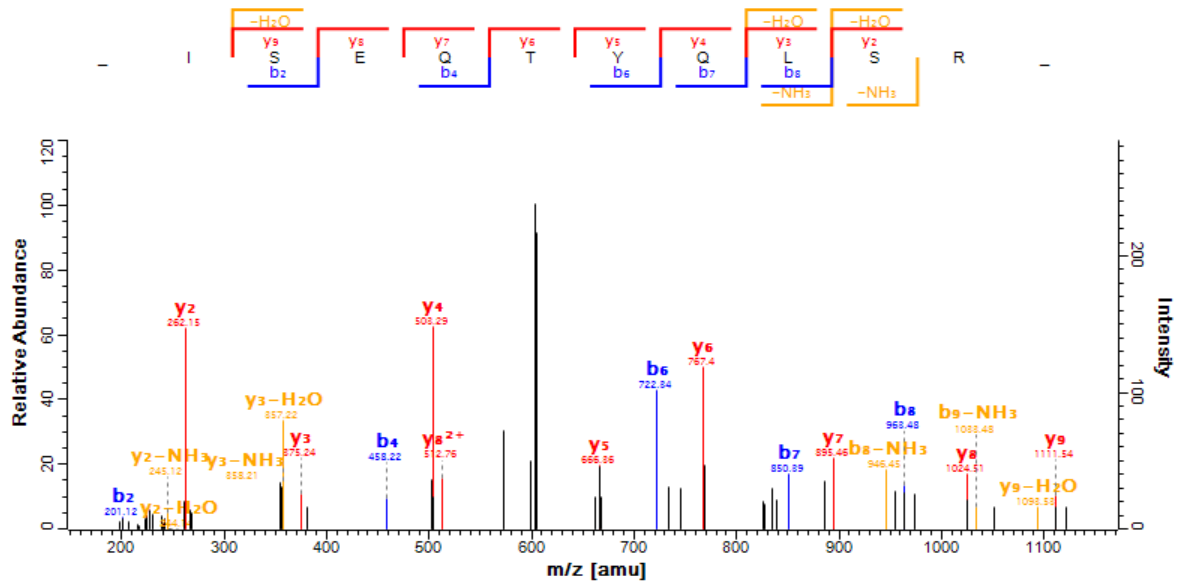
Protein Group ID: 2099
Protein Accession Numbers: P61106
Gene Names: RAB14
Peptide Sequence: TGENVEDAFLEAAK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 92.265
Best Match Posterior Error Probability: 0.00058249
Best Match Spectrum:

Scan number 4843 **Raw file** Prt-OGE-Batch2-Mock-Frac13
Method ITMS; CID **Genenames** RAB14



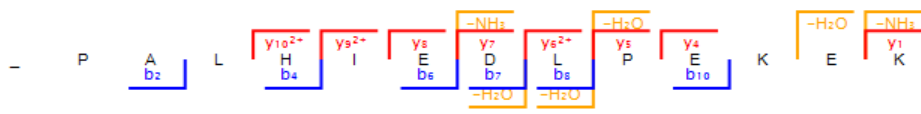
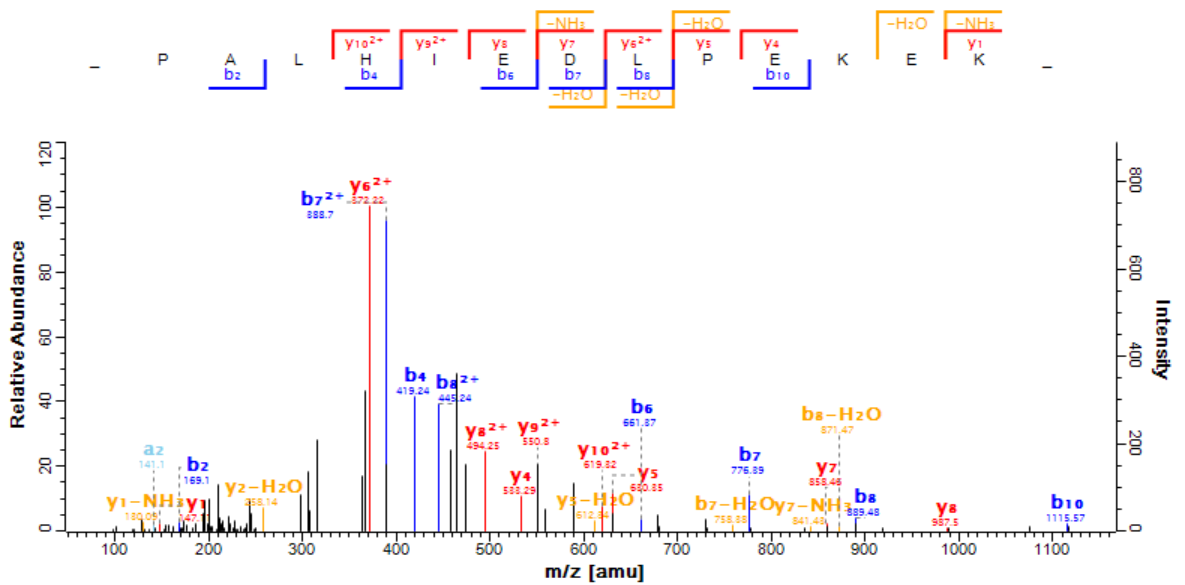
Protein Group ID: 2114
Protein Accession Numbers: P61764-2; P61764
Gene Names: STXBP1
Peptide Sequence: ISEQTYQLSR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 107.18
Best Match Posterior Error Probability: 0.0003801
Best Match Spectrum:

Scan number 1492 **Raw file** Prt-OGE-Batch3-Mock-Frac16
Method ITMS; CID **Genenames** STXBP1



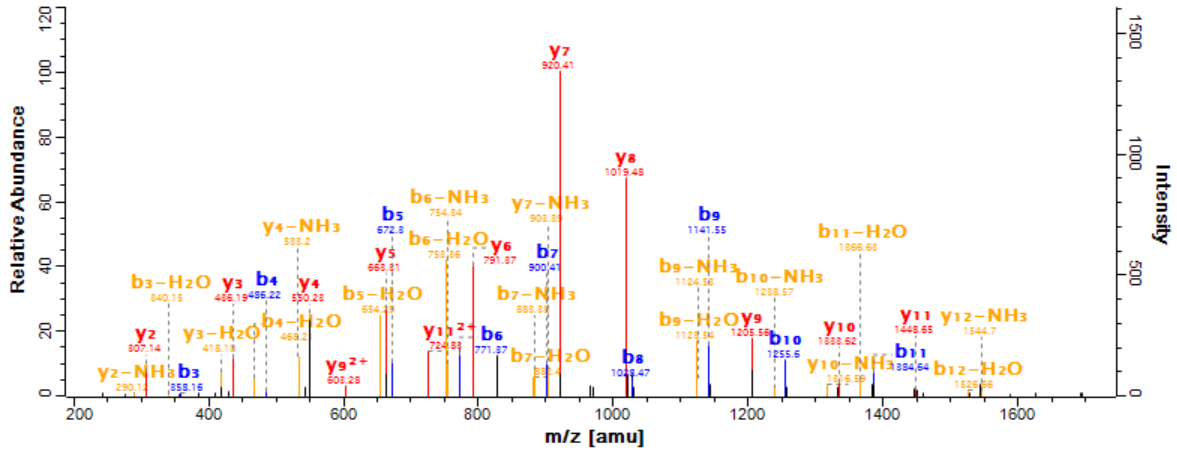
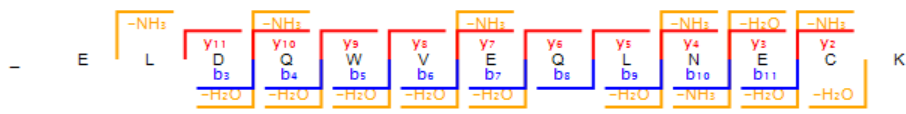
Protein Group ID: 2115
Protein Accession Numbers: P61952
Gene Names: GNG11
Peptide Sequence: PALHIEDLPEKEK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 113.38
Best Match Posterior Error Probability: 0.00060963
Best Match Spectrum:

Scan number 2837 **Raw file** Prt-OGE-Batch3--Mock-Frac13
Method ITMS; CID **Genenames** GNG11



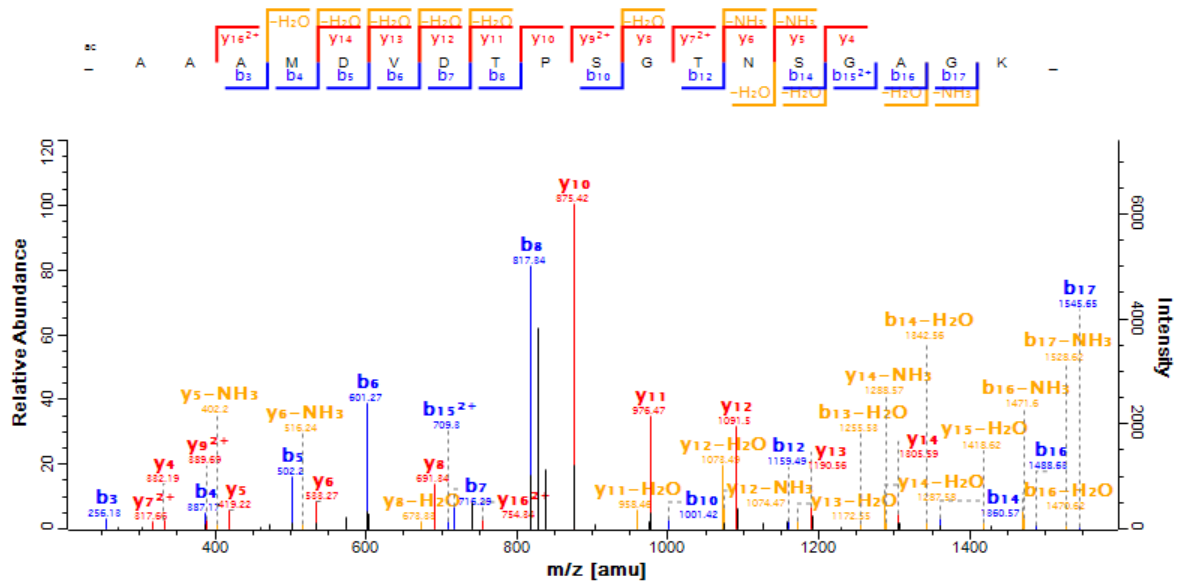
Protein Group ID: 2151
Protein Accession Numbers: P62714; E5RJX4
Gene Names: PPP2CB
Peptide Sequence: ELDQWVEQLNECK
Total Number of Spectra: 10
Number of Replicates (out of 10): 7
Best Match Score: 267.93
Best Match Posterior Error Probability: 0
Best Match Spectrum:

Scan number 4243 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac7
Method ITMS; CID **Genenames** PPP2CB



Protein Group ID: 2160
Protein Accession Numbers: P62877
Gene Names: RBX1
Peptide Sequence: AAAMDVDTPSGTNSGAGK
Total Number of Spectra: 11
Number of Replicates (out of 10): 7
Best Match Score: 222.57
Best Match Posterior Error Probability: 8.49E-68
Best Match Spectrum:

Scan number 2443 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac15
Method ITMS; CID **Genenames** RBX1



Protein Group ID: 2181

Protein Accession Numbers: P63261; I3L3I4; I3L1U9; I3L3I0; I3L4N8; I3L3R2; J3KT65; K7EM38

Gene Names: ACTG1

Peptide Sequence: EEEIAALVIDNGSGMCK

Total Number of Spectra: 210

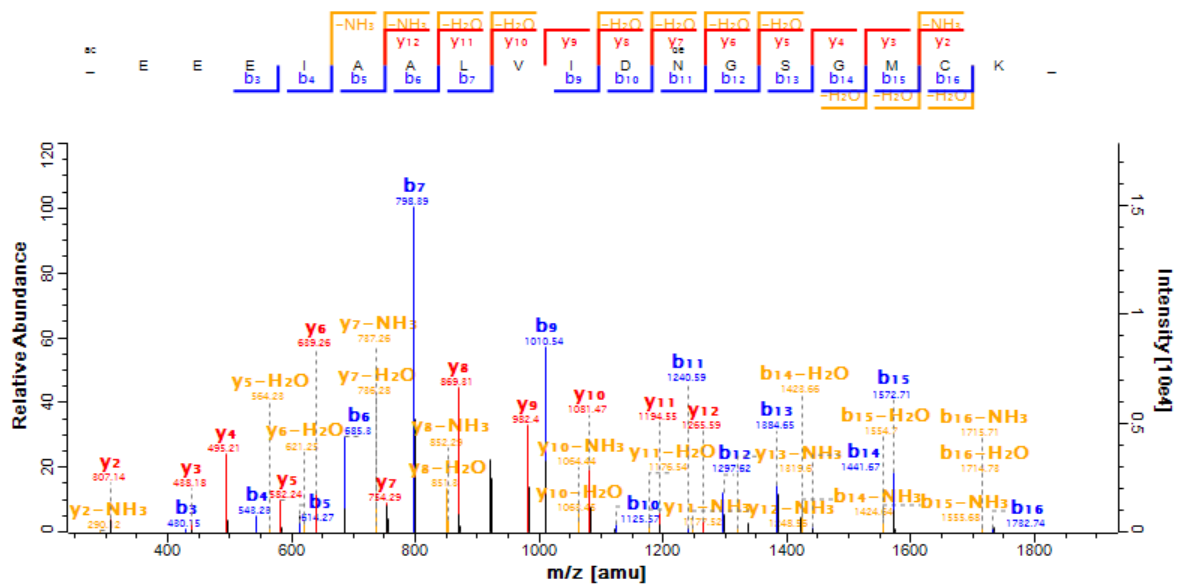
Number of Replicates (out of 10): 8

Best Match Score: 268.93

Best Match Posterior Error Probability: 1.26E-119

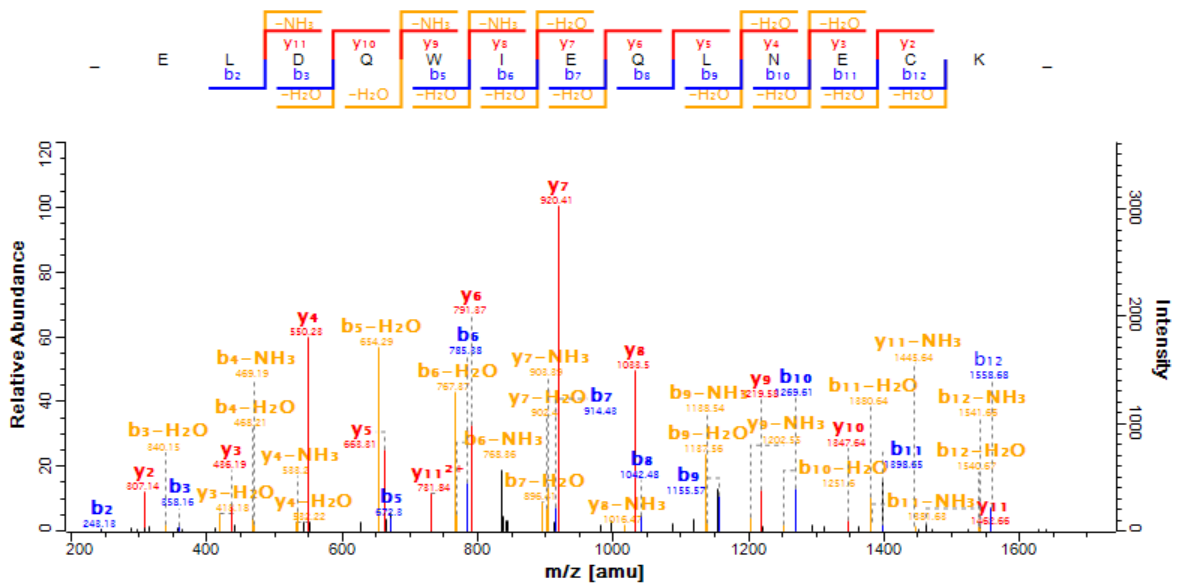
Best Match Spectrum:

Scan number	5924	Raw file	OGE-WT-Frac7
Method	ITMS: CID	Genenames	ACTG1



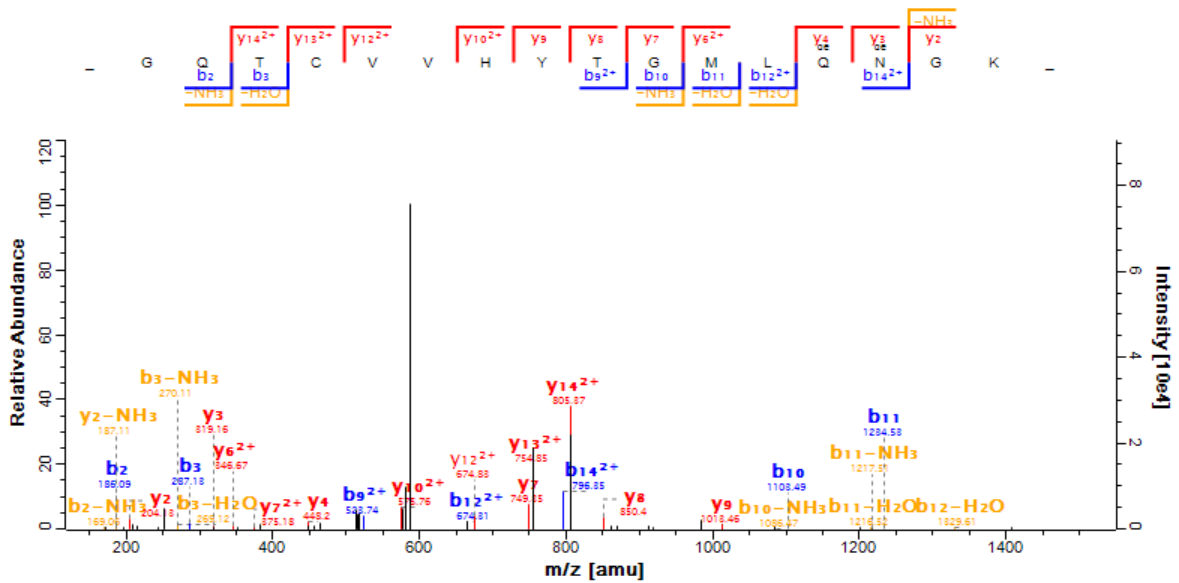
Protein Group ID: 2185
Protein Accession Numbers: P67775; P67775-2
Gene Names: PPP2CA
Peptide Sequence: ELDQWIEQLNECK
Total Number of Spectra: 14
Number of Replicates (out of 10): 7
Best Match Score: 295.86
Best Match Posterior Error Probability: 1.67E-156
Best Match Spectrum:

Scan number 4948 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac8
Method ITMS; CID **Genenames** PPP2CA



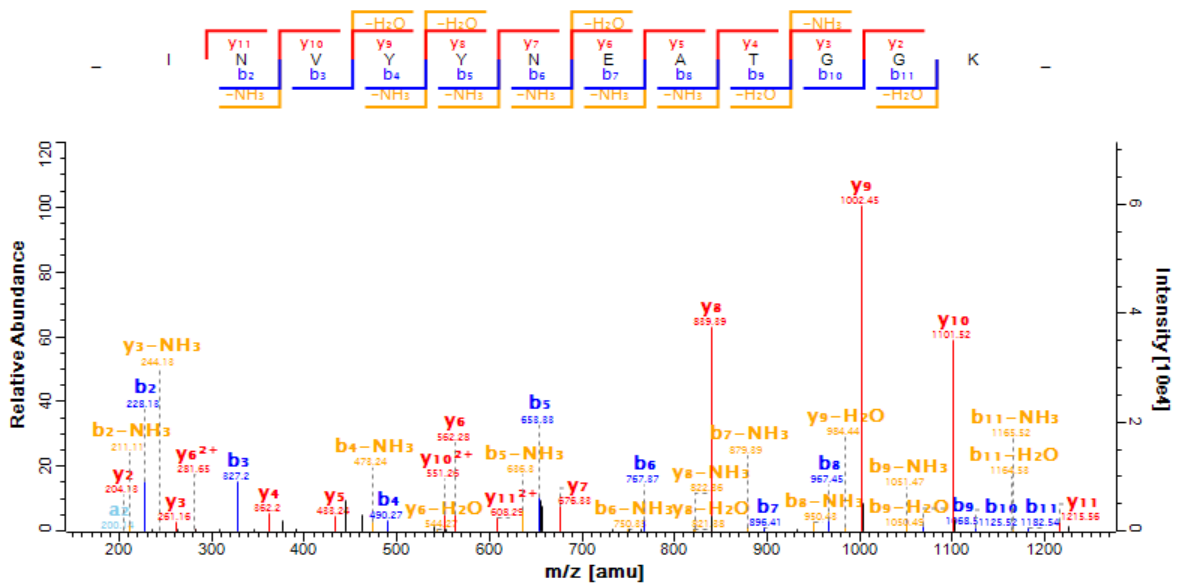
Protein Group ID: 2192
Protein Accession Numbers: P68106; P68106-2
Gene Names: FKBP1B
Peptide Sequence: GQTCVVHYTGMLQNGK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 145
Best Match Posterior Error Probability: 0.0001804
Best Match Spectrum:

Scan number 2756 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac19
Method ITMS; CID **Genenames** FKBP1B



Protein Group ID: 2195
Protein Accession Numbers: P68371
Gene Names: TUBB4B
Peptide Sequence: INVYYNEATGGK
Total Number of Spectra: 137
Number of Replicates (out of 10): 10
Best Match Score: 269.93
Best Match Posterior Error Probability: 6.74E-98
Best Match Spectrum:

Scan number 2749 **Raw file** OGE-Mock-Frac7
Method ITMS; CID **Genenames** TUBB4B



Protein Group ID: 2197

Protein Accession Numbers: P68431

Gene Names: HIST1H3A

Peptide Sequence: FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK

Total Number of Spectra: 2

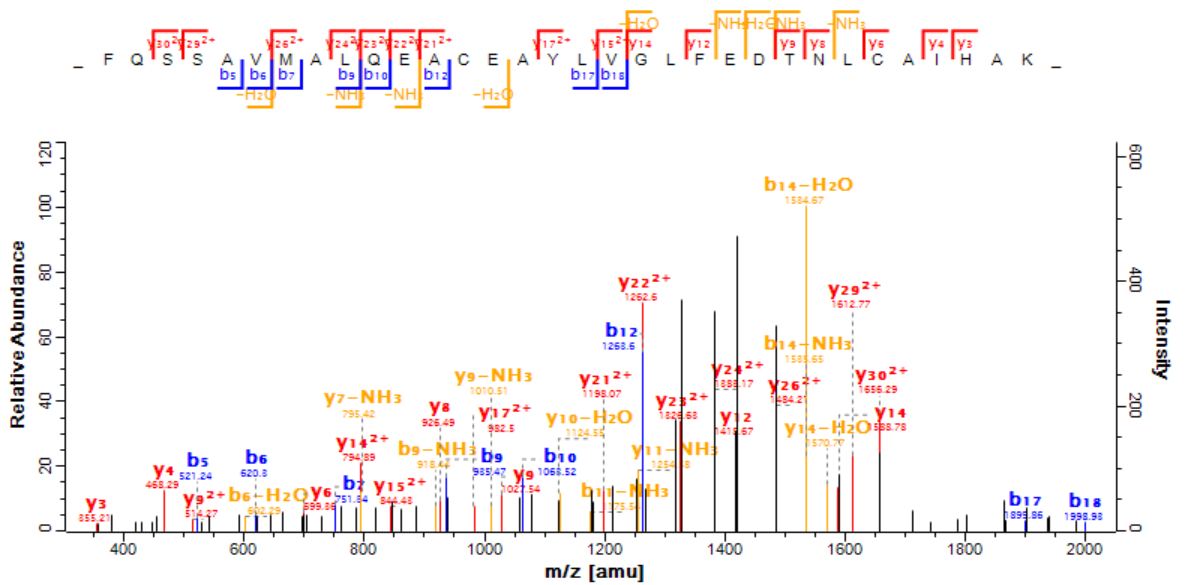
Number of Replicates (out of 10): 1

Best Match Score: 94.767

Best Match Posterior Error Probability: 1.64E-13

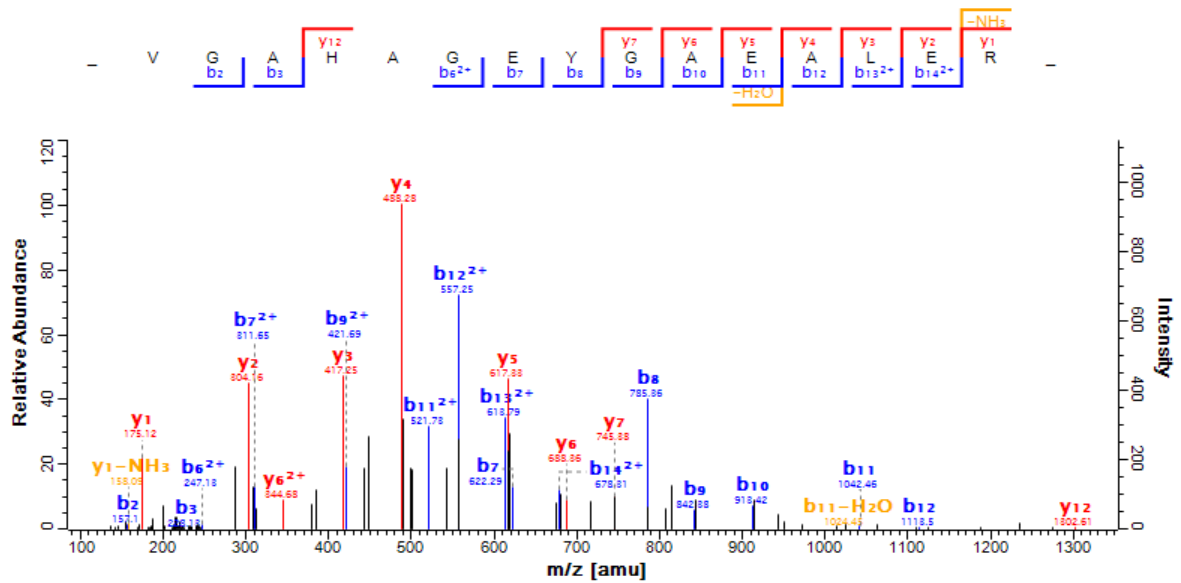
Best Match Spectrum:

Scan number 7757 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac22
Method ITMS; CID **Genenames** HIST1H3A



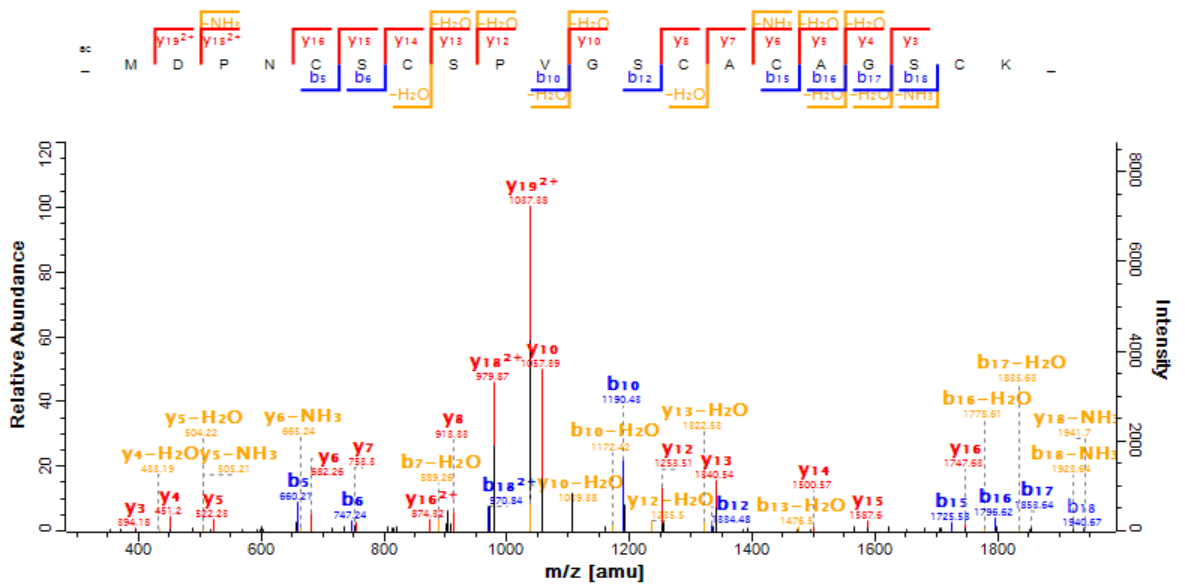
Protein Group ID: 2198
Protein Accession Numbers: P69905
Gene Names: HBA1
Peptide Sequence: VGAHAGEYGAEALER
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 131.35
Best Match Posterior Error Probability: 1.11E-05
Best Match Spectrum:

Scan number 1562 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac19
Method ITMS; CID **Genenames** HBA1



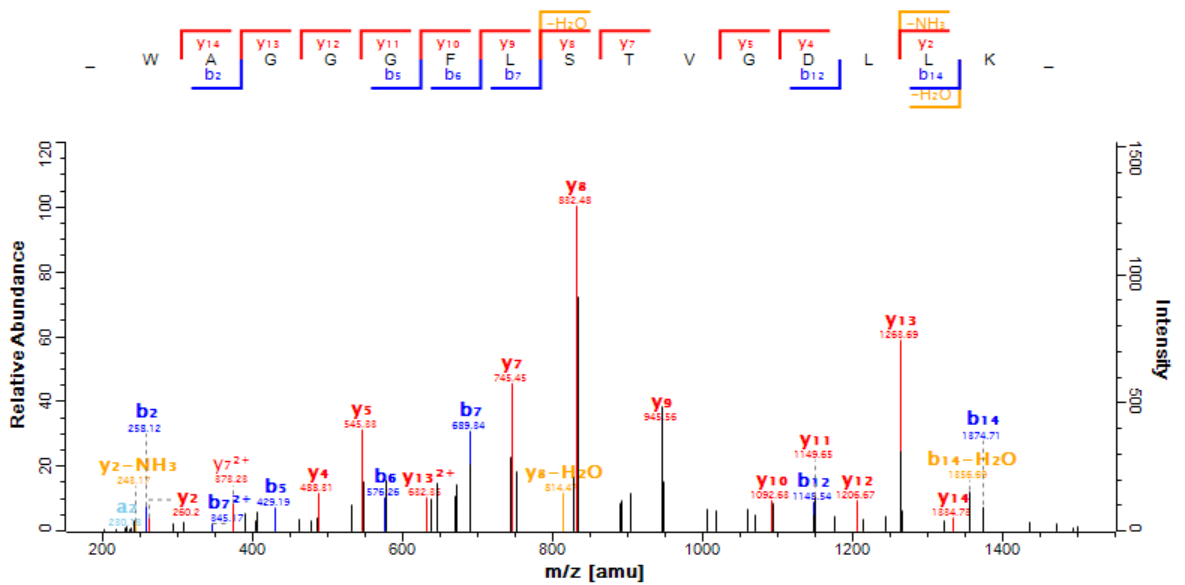
Protein Group ID: 2208
Protein Accession Numbers: P80297; H3BT50
Gene Names: MT1X
Peptide Sequence: MDPNCSCSPVGSCACAGSCK
Total Number of Spectra: 11
Number of Replicates (out of 10): 5
Best Match Score: 189.55
Best Match Posterior Error Probability: 8.42E-35
Best Match Spectrum:

Scan number 2637 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac19
Method ITMS; CID **Genenames** MT1X



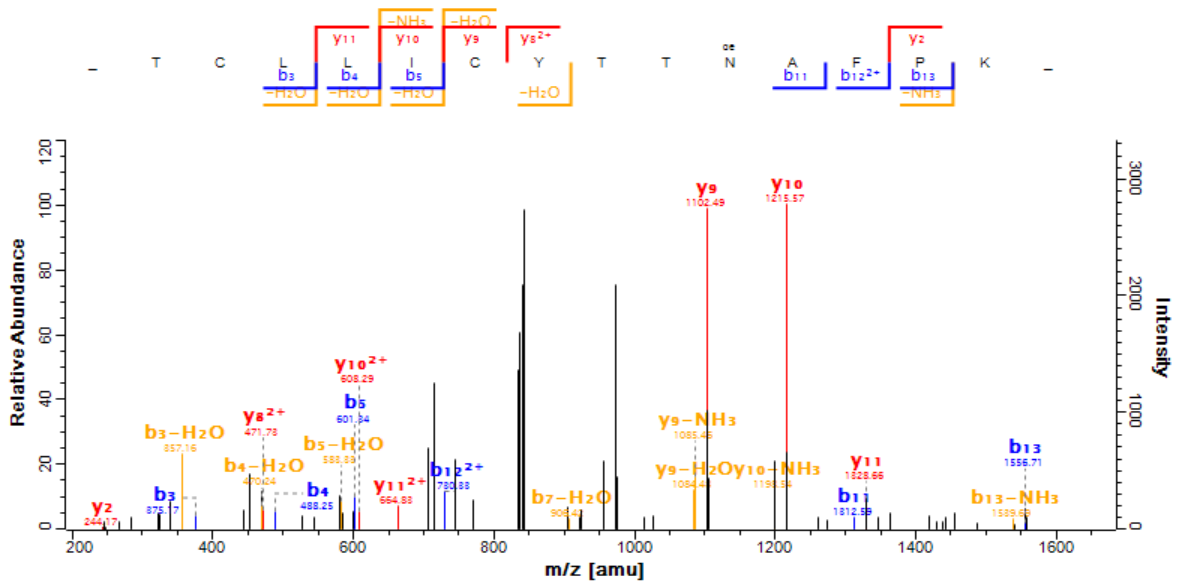
Protein Group ID: 2223
Protein Accession Numbers: P83111
Gene Names: LACTB
Peptide Sequence: WAGGGFLSTVGDLLK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 117.08
Best Match Posterior Error Probability: 5.33E-05
Best Match Spectrum:

Scan number 6990 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac17
Method ITMS; CID **Genenames** LACTB



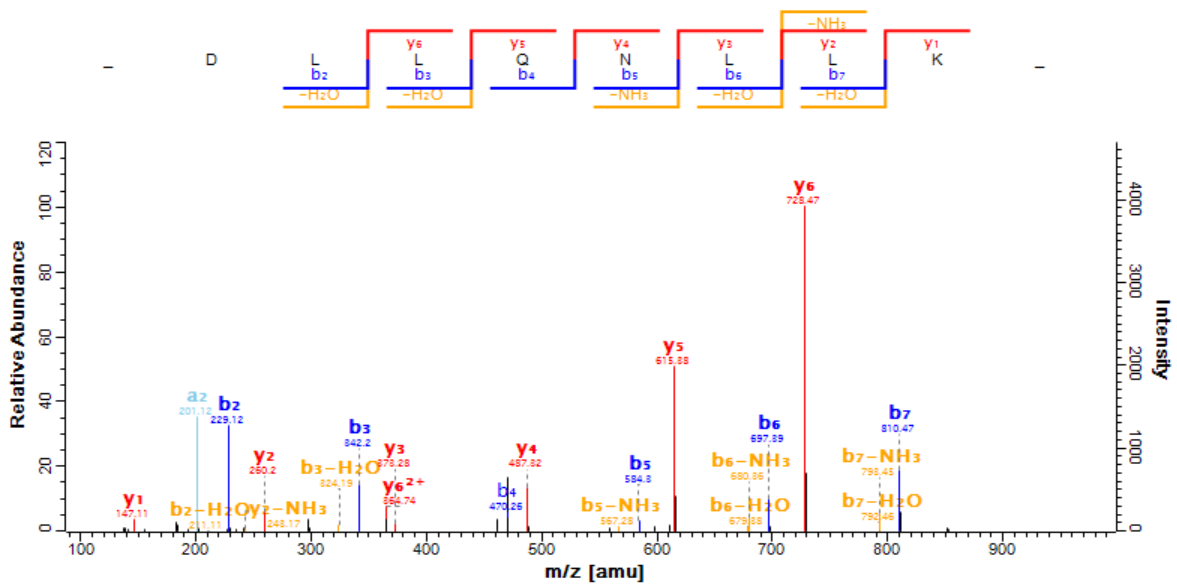
Protein Group ID: 2225
Protein Accession Numbers: P84095
Gene Names: RHOG
Peptide Sequence: TCLLIC^YTTNAFPK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 104.59
Best Match Posterior Error Probability: 0.0027654
Best Match Spectrum:

Scan number 3421 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac13
Method ITMS; CID **Genenames** RHOG



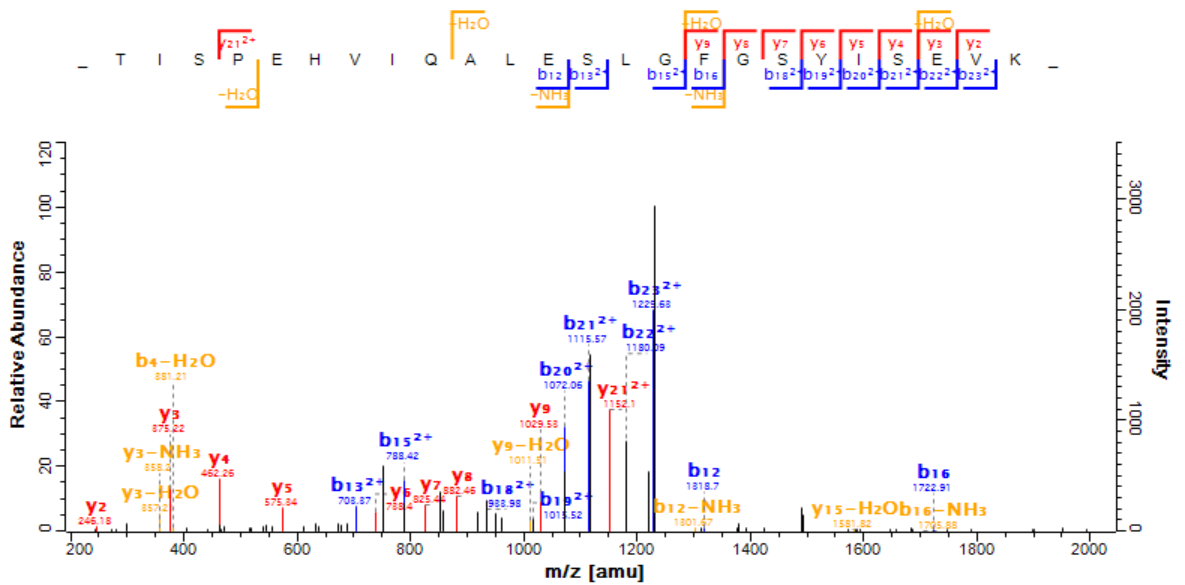
Protein Group ID: 2234
Protein Accession Numbers: Q00535; Q00535-2
Gene Names: CDK5
Peptide Sequence: DLLQNLLK
Total Number of Spectra: 11
Number of Replicates (out of 10): 10
Best Match Score: 156.51
Best Match Posterior Error Probability: 0.00055176
Best Match Spectrum:

Scan number 4794 **Raw file** Prt-OGE-Batch2-WT-Frac17
Method ITMS; CID **Genenames** CDK5



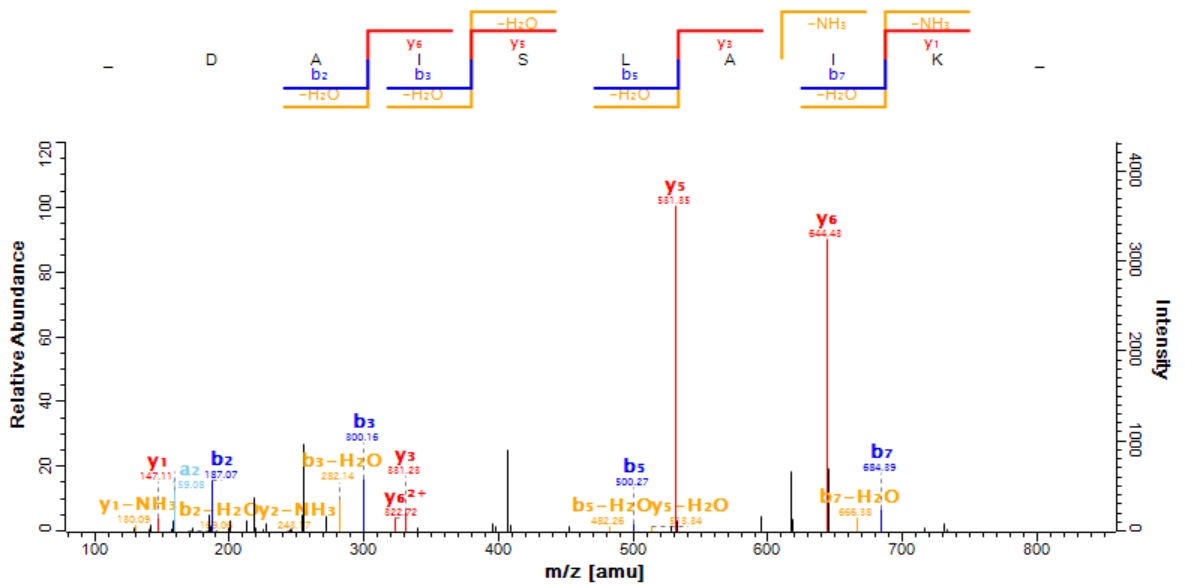
Protein Group ID: 2252
Protein Accession Numbers: Q01658
Gene Names: DR1
Peptide Sequence: TISPEHVIQALESLGFGSYISEVK
Total Number of Spectra: 14
Number of Replicates (out of 10): 6
Best Match Score: 92.932
Best Match Posterior Error Probability: 3.22E-06
Best Match Spectrum:

Scan number 6844 **Raw file** Prt-OGE-Batch2-WT-Frac9
Method ITMS; CID **Genenames** DR1



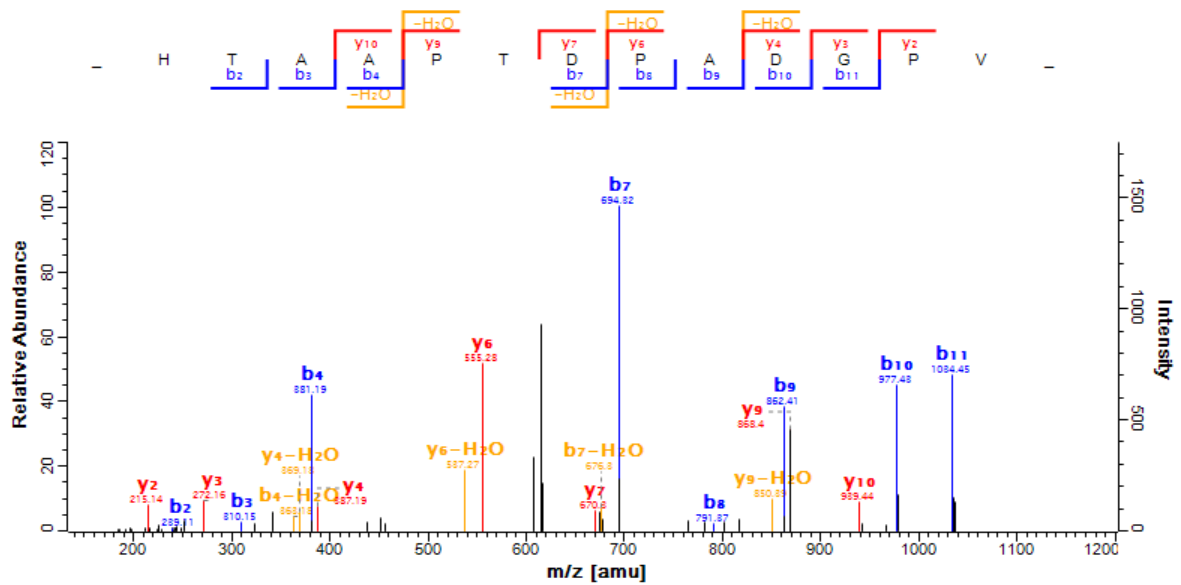
Protein Group ID: 2257
Protein Accession Numbers: Q02410
Gene Names: APBA1
Peptide Sequence: DAISLAIK
Total Number of Spectra: 6
Number of Replicates (out of 10): 6
Best Match Score: 110.81
Best Match Posterior Error Probability: 0.0015946
Best Match Spectrum:

Scan number 3722 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac14
Method ITMS; CID **Genenames** APBA1



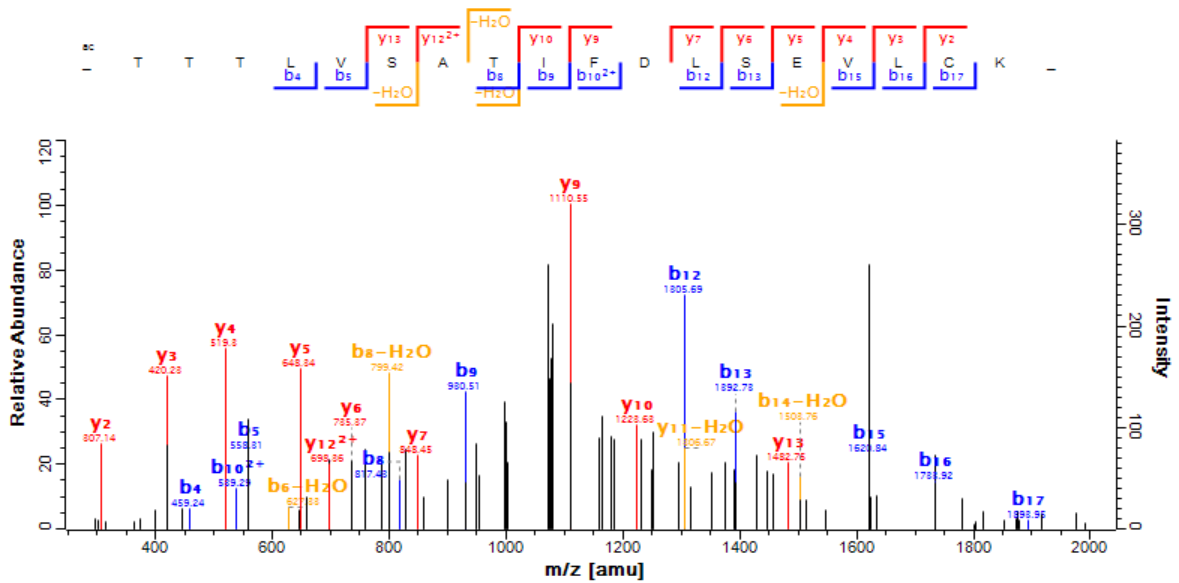
Protein Group ID: 2268
Protein Accession Numbers: Q04941
Gene Names: PLP2
Peptide Sequence: HTAAPTDPADGPV
Total Number of Spectra: 10
Number of Replicates (out of 10): 4
Best Match Score: 117.09
Best Match Posterior Error Probability: 0.0001398
Best Match Spectrum:

Scan number 1414 **Raw file** Prt-OGE-Batch2-WT-Frac9
Method ITMS; CID **Genenames** PLP2



Protein Group ID: 2281
Protein Accession Numbers: Q07352
Gene Names: ZFP36L1
Peptide Sequence: TTTLVSATIFDLSEVLCK
Total Number of Spectra: 2
Number of Replicates (out of 10): 1
Best Match Score: 79.514
Best Match Posterior Error Probability: 0.0011553
Best Match Spectrum:

Scan number 8905 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac22
Method ITMS; CID **Genenames** ZFP36L1



Protein Group ID: 2293

Protein Accession Numbers: Q08499; Q08499-11; Q08499-6; Q08499-9; Q08499-10; Q08499-2; Q08499-3; Q08499-12; Q08499-7

Gene Names: PDE4D

Peptide Sequence: NSSIASDIHGDDLIVTPFAQLV

Total Number of Spectra: 15

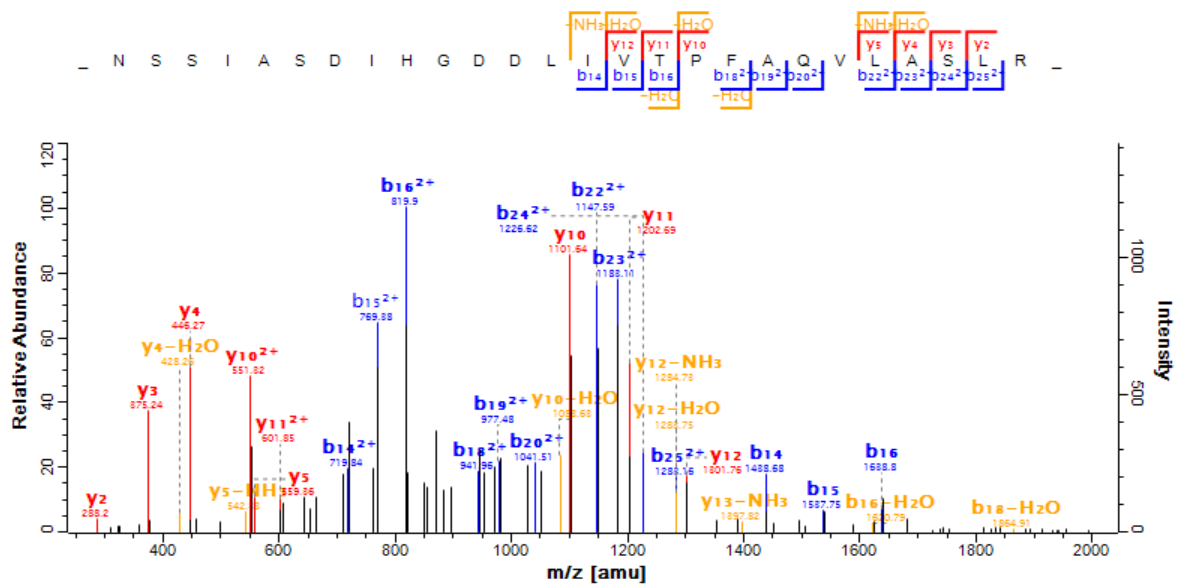
Number of Replicates (out of 10): 7

Best Match Score: 119.27

Best Match Posterior Error Probability: 1.15E-16

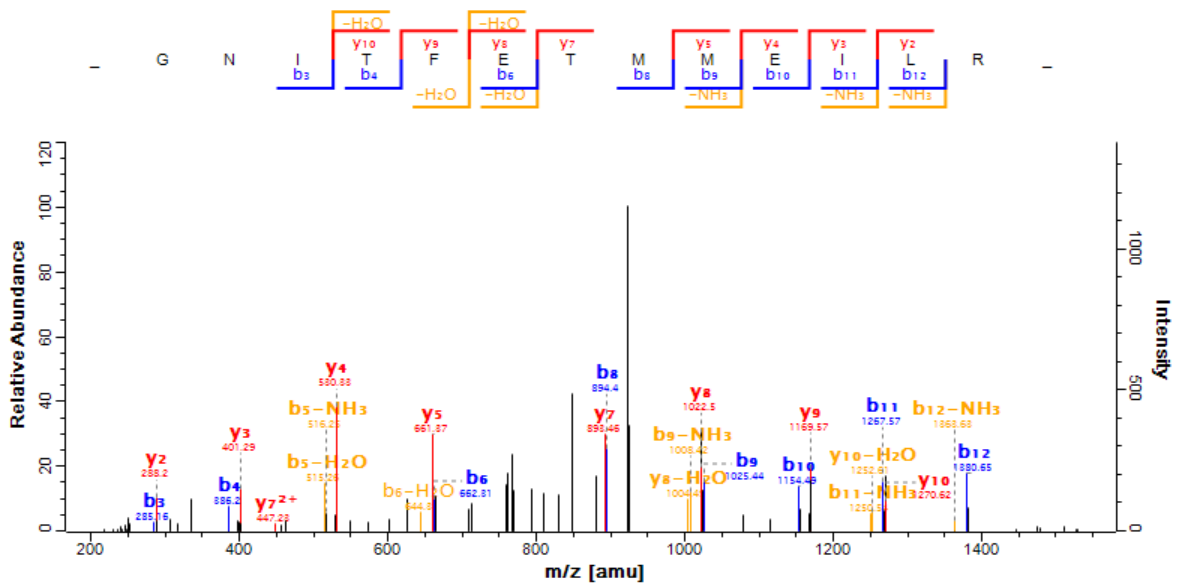
Best Match Spectrum:

Scan number	7899	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac15
Method	ITMS: CID	Genenames	PDE4D



Protein Group ID: 2302
Protein Accession Numbers: Q0VVDG4; Q0VVDG4-2
Gene Names: SCR3
Peptide Sequence: GNITFETMMEILR
Total Number of Spectra: 8
Number of Replicates (out of 10): 7
Best Match Score: 115.06
Best Match Posterior Error Probability: 0.0001623
Best Match Spectrum:

Scan number 6974 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac10
Method ITMS; CID **Genenames** SCR3



Protein Group ID: 2306

Protein Accession Numbers: Q12834

Gene Names: CDC20

Peptide Sequence: AQFAFESDLHSLQLDAPLNAPPAR

Total Number of Spectra: 1

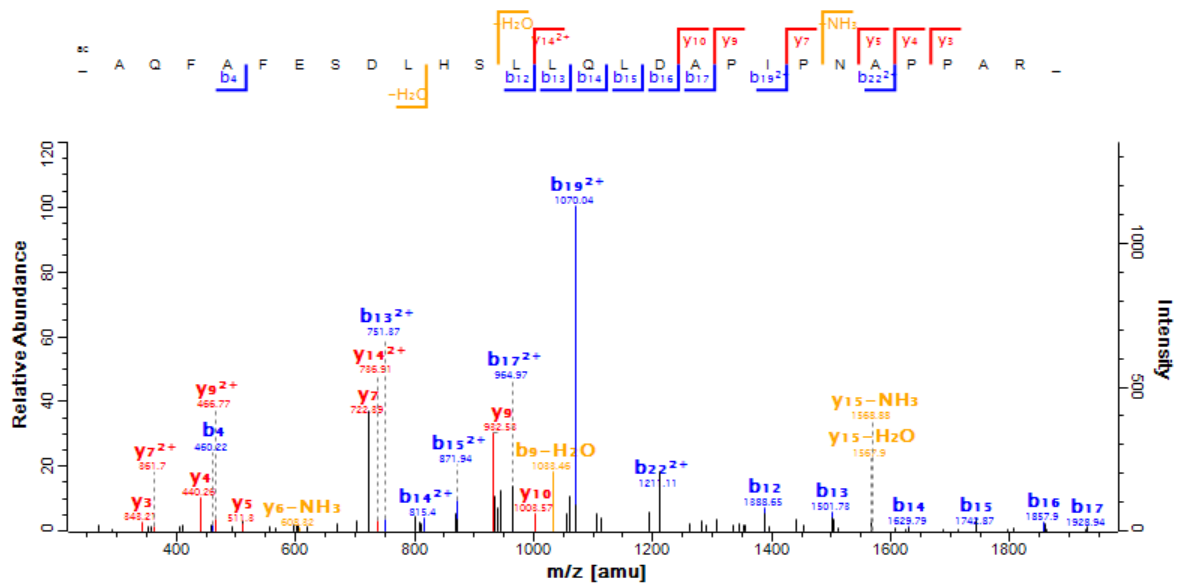
Number of Replicates (out of 10): 1

Best Match Score: 73.546

Best Match Posterior Error Probability: 4.59E-05

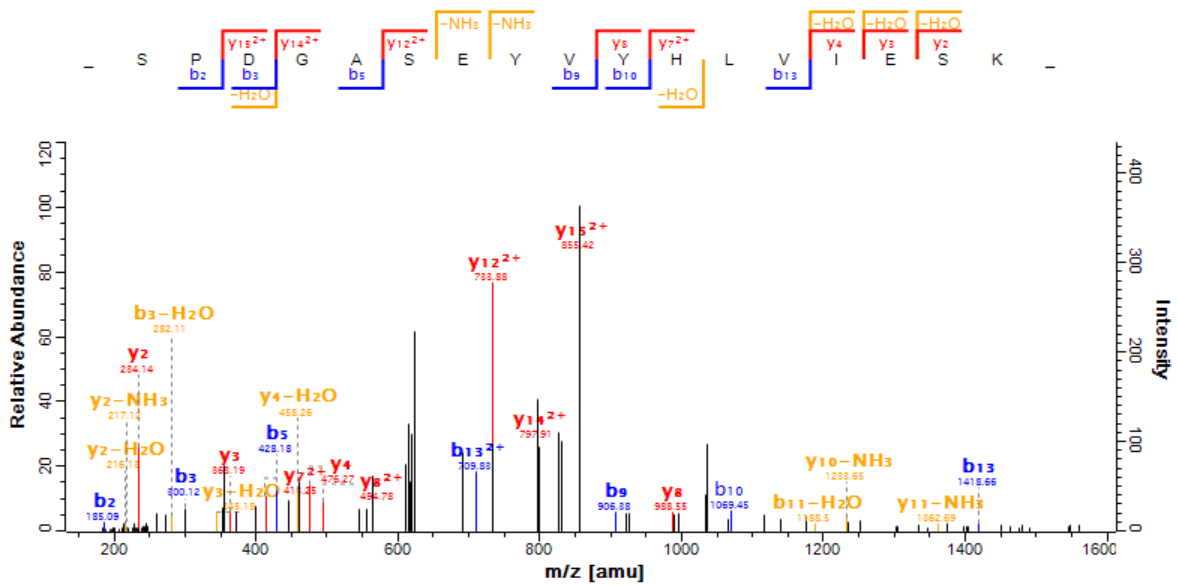
Best Match Spectrum:

Scan number 6509 **Raw file** Prt-OGE-Batch2-WT-Frac21
Method ITMS; CID **Genenames** CDC20



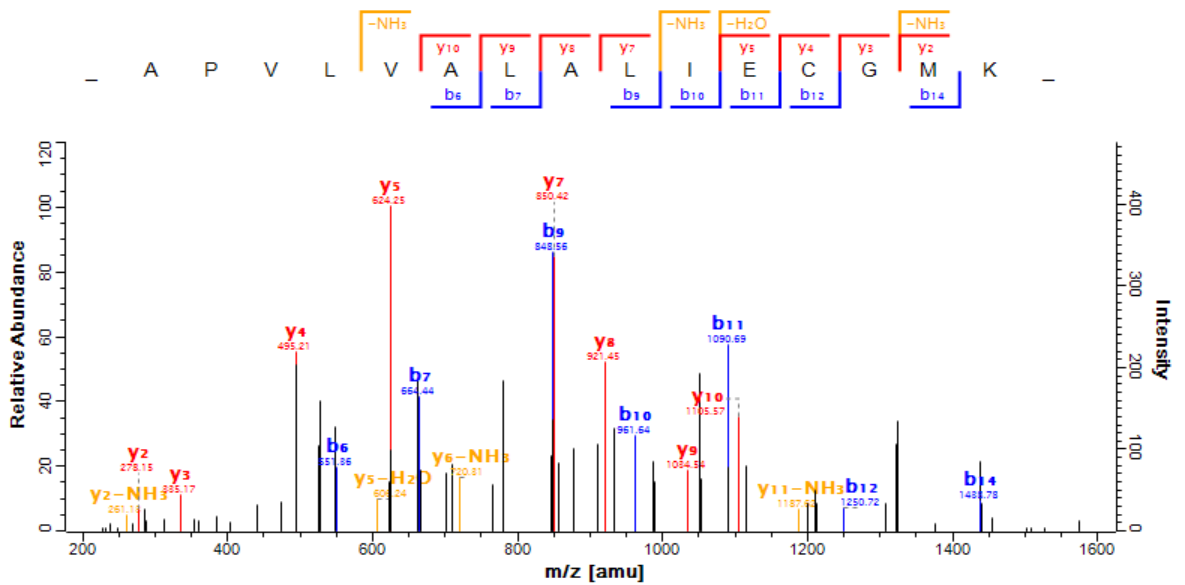
Protein Group ID: 2312
Protein Accession Numbers: Q12913
Gene Names: PTPRJ
Peptide Sequence: SPDGASEYVYHLVIESK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 79.337
Best Match Posterior Error Probability: 0.0012195
Best Match Spectrum:

Scan number 4180 **Raw file** OGE-WT-Frac3
Method ITMS; CID **Genenames** PTPRJ



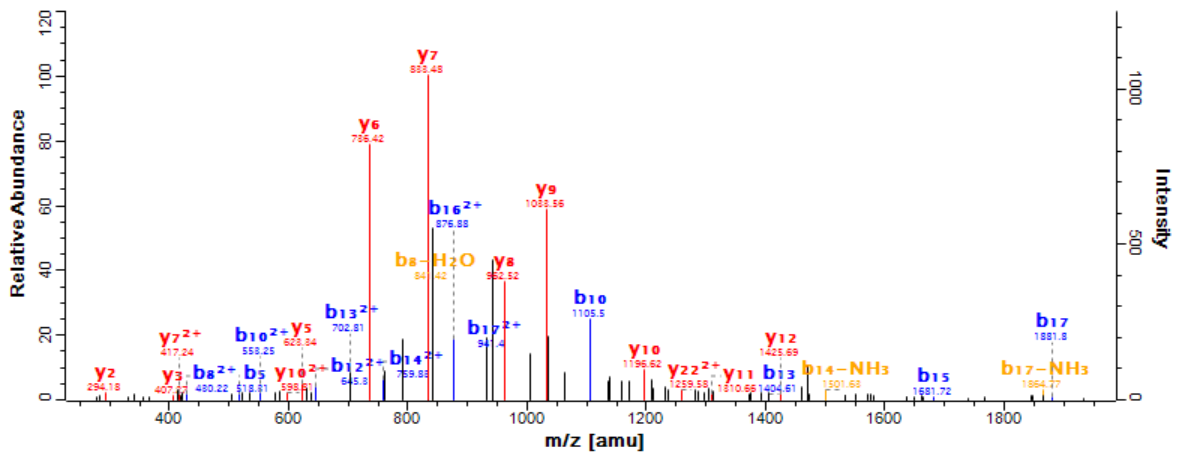
Protein Group ID: 2314
Protein Accession Numbers: Q12974; Q12974-3
Gene Names: PTP4A2
Peptide Sequence: APVLVALIECGMK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 94.551
Best Match Posterior Error Probability: 0.00022088
Best Match Spectrum:

Scan number 7078 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac20
Method ITMS; CID **Genenames** PTP4A2



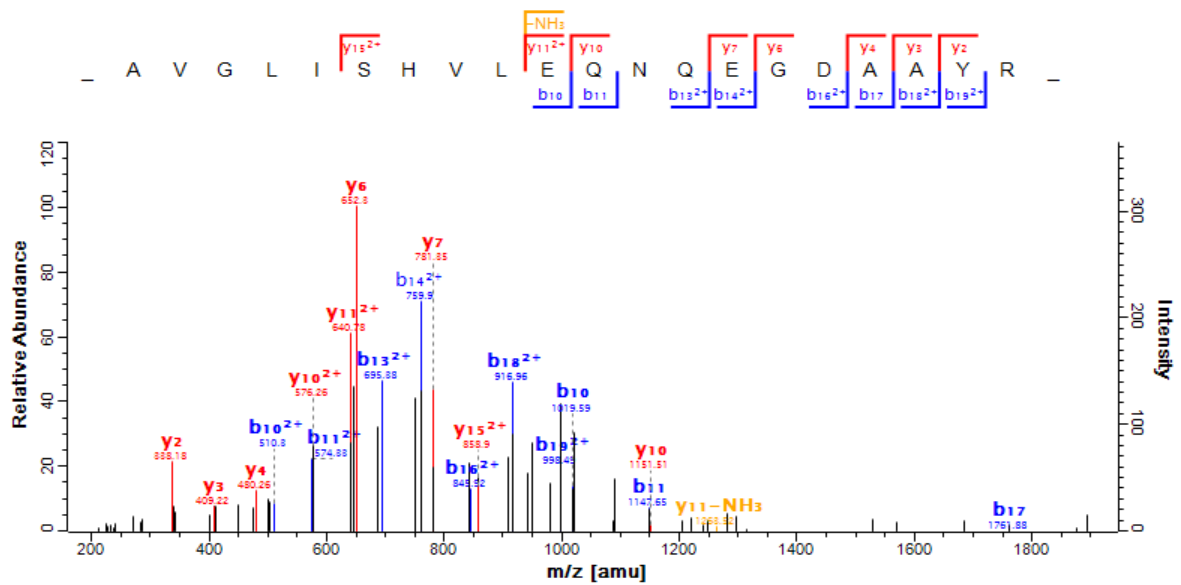
Protein Group ID: 2318
Protein Accession Numbers: Q13017; Q13017-2
Gene Names: ARHGAP5
Peptide Sequence: VPLAHPEDMDPSDNYAEPIIDTIFFK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 99.569
Best Match Posterior Error Probability: 4.20E-07
Best Match Spectrum:

Scan number 4654 **Raw file** Prt-OGE-Batch2-WT-Frac13
Method ITMS; CID **Genenames** ARHGAP5



Protein Group ID: 2365
Protein Accession Numbers: Q13825; Q13825-2
Gene Names: AUH
Peptide Sequence: AVGLISHVLEQNQEGDAAYR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 79.393
Best Match Posterior Error Probability: 0.0010352
Best Match Spectrum:

Scan number 3296 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac21
Method ITMS; CID **Genenames** AUH



Protein Group ID: 2368

Protein Accession Numbers: Q13901

Gene Names: CID

Peptide Sequence: AGEEINEDYPVEIHEYLSAFENSIGAVDEMLLK

Total Number of Spectra: 1

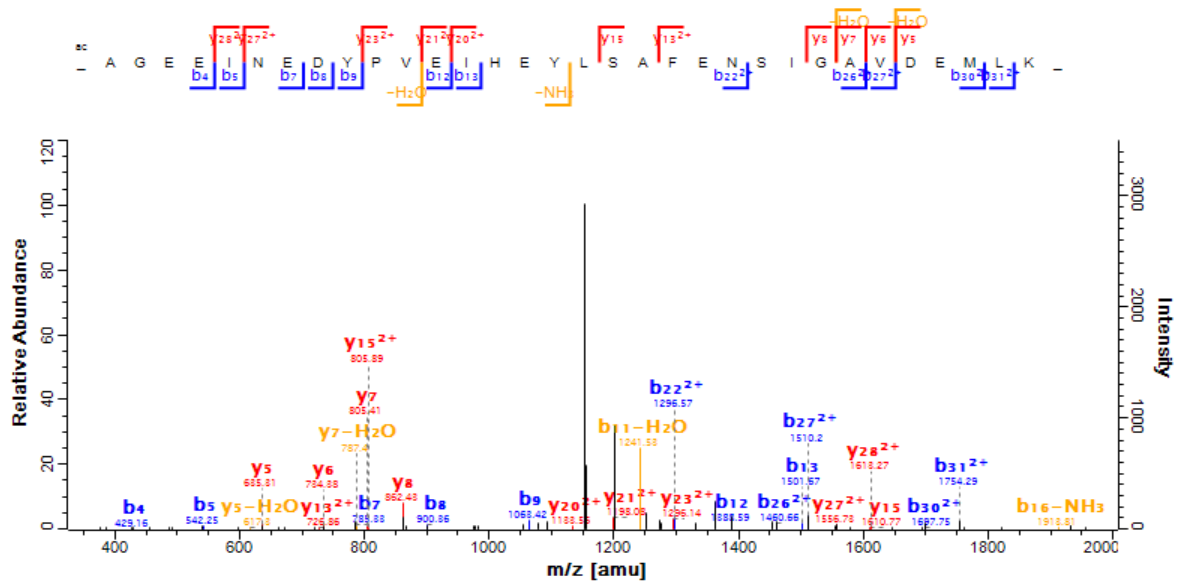
Number of Replicates (out of 10): 1

Best Match Score: 68.386

Best Match Posterior Error Probability: 4.65E-07

Best Match Spectrum:

Scan number 7315 **Raw file** Prt-OGE-Batch2-WT-Frac21
Method ITMS; CID **Genenames** CID



Protein Group ID: 2378

Protein Accession Numbers: Q14137; Q96Q25

Gene Names: BOP1;KM-PA-2

Peptide Sequence: DLGVLDFVIFHP TQPWPVFS SGA DGT V R

Total Number of Spectra: 2

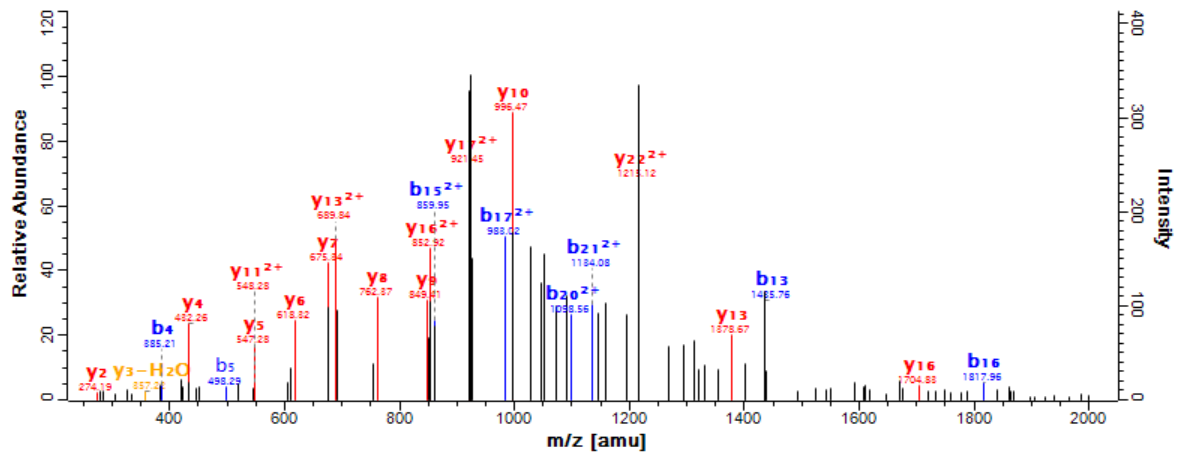
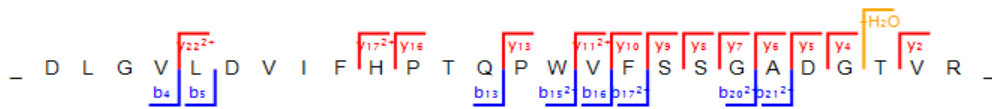
Number of Replicates (out of 10): 2

Best Match Score: 95.835

Best Match Posterior Error Probability: 2.34E-08

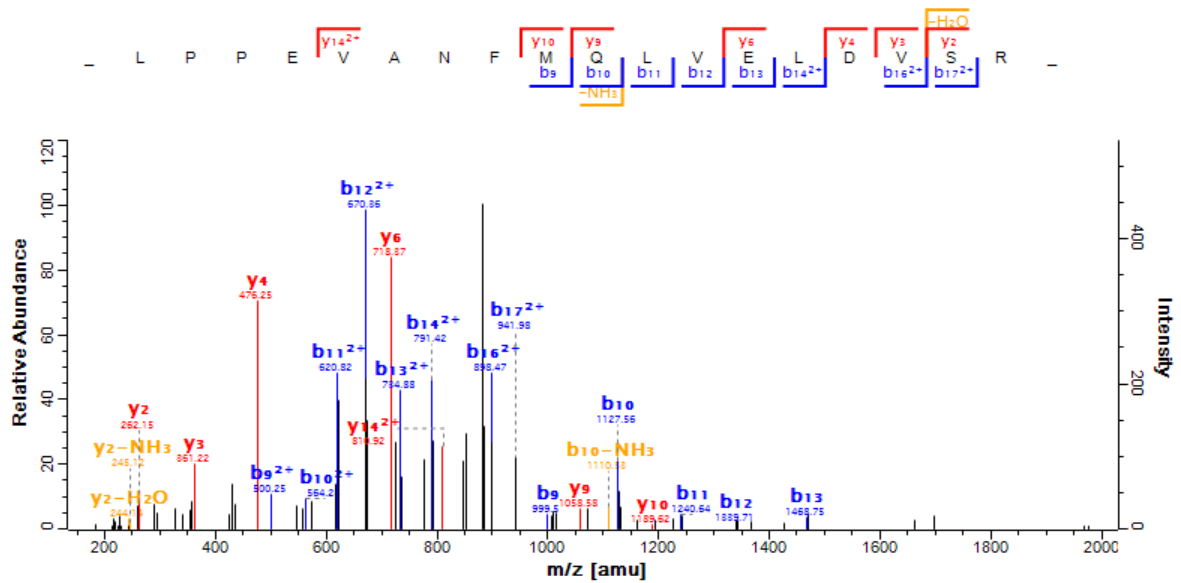
Best Match Spectrum:

Scan number	6864	Raw file	OGE-WT-Frac16
Method	ITMS; CID	Genenames	BOP1;KM-PA-2



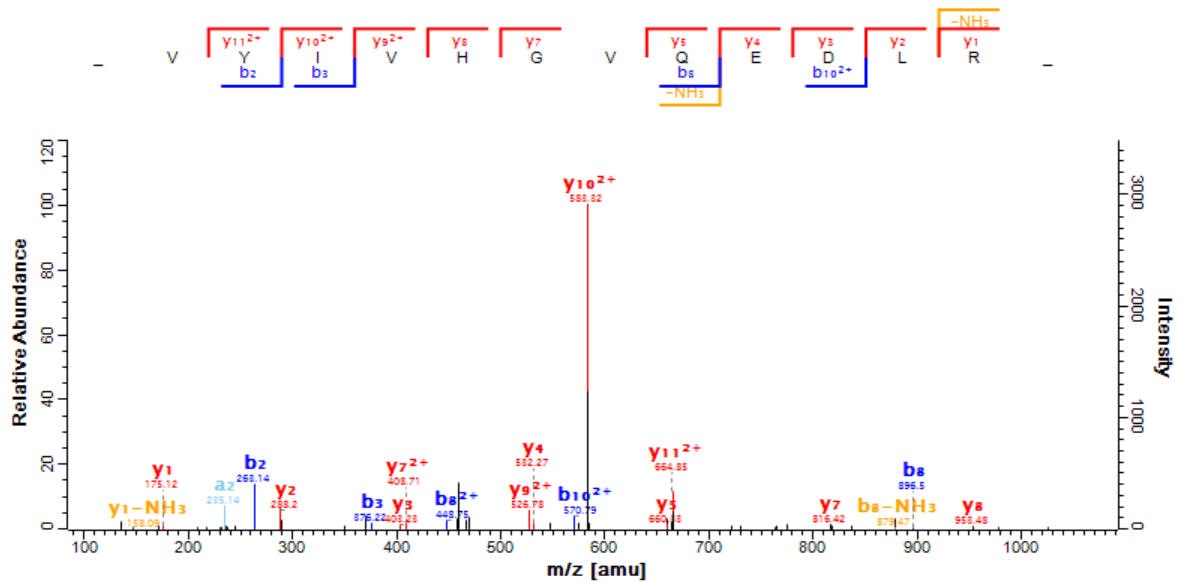
Protein Group ID: 2380
Protein Accession Numbers: Q14160-3; Q14160
Gene Names: SCRIB
Peptide Sequence: LPPEVANFMQLVELDVSR
Total Number of Spectra: 8
Number of Replicates (out of 10): 6
Best Match Score: 104.2
Best Match Posterior Error Probability: 0.00017998
Best Match Spectrum:

Scan number 7682 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac7
Method ITMS; CID **Genenames** SCRIB



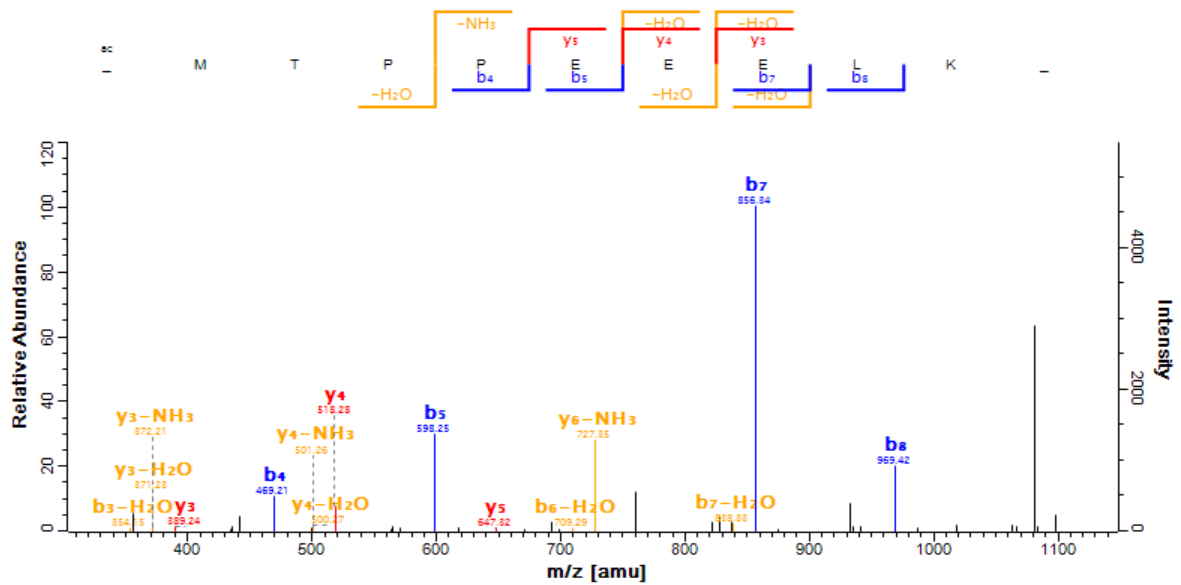
Protein Group ID: 2417
Protein Accession Numbers: Q15024
Gene Names: EXOSC7
Peptide Sequence: VYIVHGVQEDLR
Total Number of Spectra: 4
Number of Replicates (out of 10): 4
Best Match Score: 113.69
Best Match Posterior Error Probability: 0.00020615
Best Match Spectrum:

Scan number 2443 **Raw file** Prt-OGE-Batch2-WT-Frac6
Method ITMS; CID **Genenames** EXOSC7



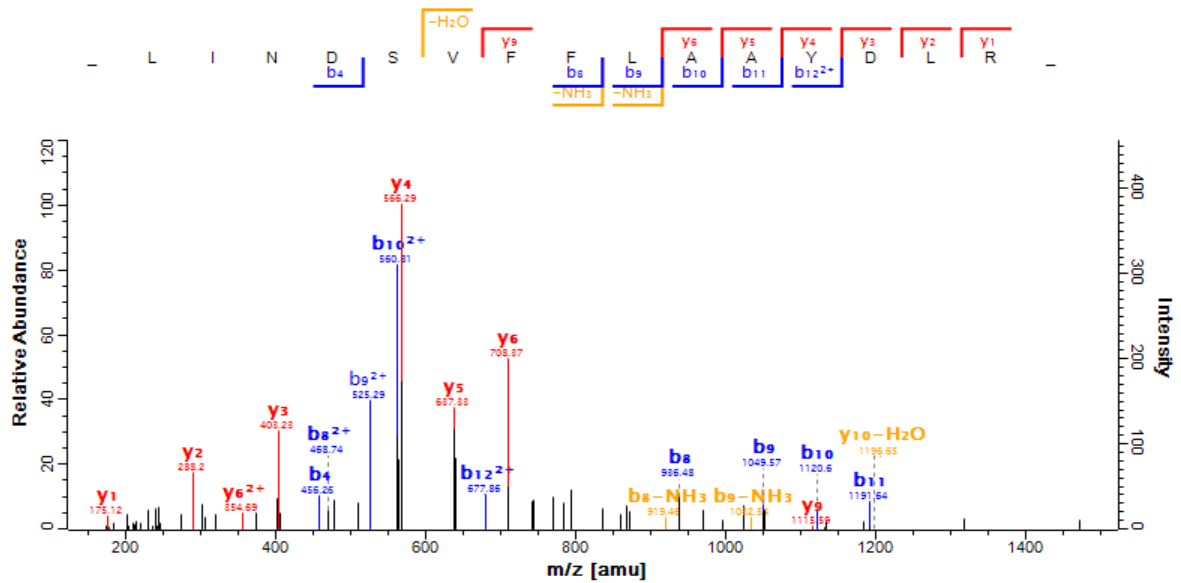
Protein Group ID: 2418
Protein Accession Numbers: Q15042-2
Gene Names:
Peptide Sequence: MTPPEEELK
Total Number of Spectra: 11
Number of Replicates (out of 10): 8
Best Match Score: 122.13
Best Match Posterior Error Probability: 0.00049598
Best Match Spectrum:

Scan number 5105 **Raw file** Prt-OGE-Batch3-Mock-Frac4
Method ITMS; CID **Pepti...** 122.13



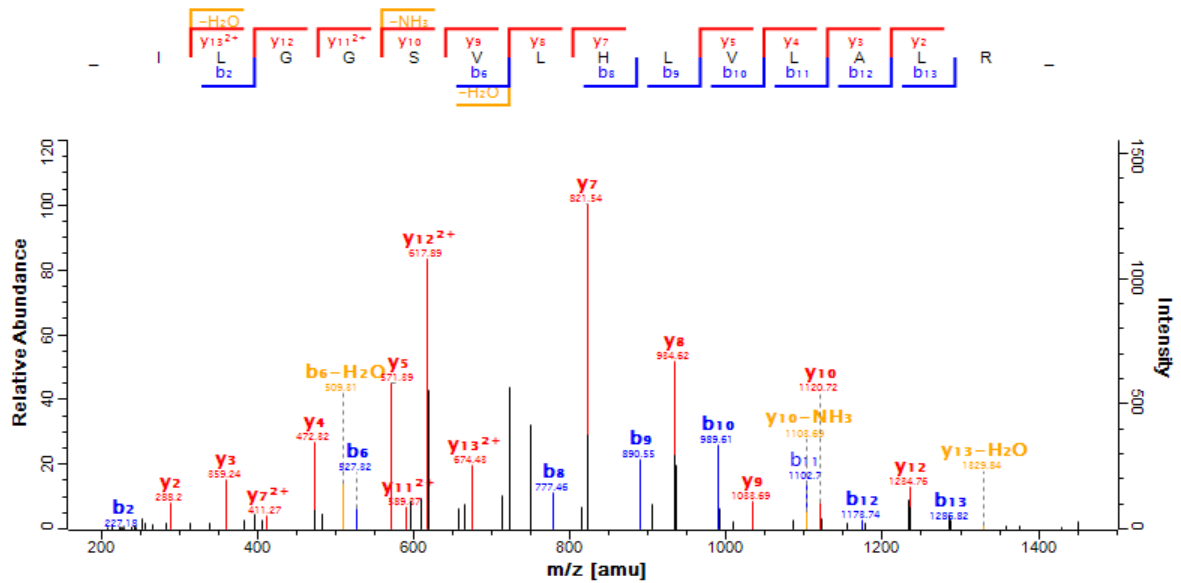
Protein Group ID: 2461
Protein Accession Numbers: Q15814
Gene Names: TBCC
Peptide Sequence: LINDSVFFLAAYDLR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 79.771
Best Match Posterior Error Probability: 0.0010519
Best Match Spectrum:

Scan number 7029 **Raw file** Prt-OGE-Batch3-Mock-Frac9
Method ITMS; CID **Genenames** TBCC



Protein Group ID: 2463
Protein Accession Numbers: Q15843
Gene Names: NEDD8
Peptide Sequence: ILGGSVLHLVLALR
Total Number of Spectra: 15
Number of Replicates (out of 10): 5
Best Match Score: 141.38
Best Match Posterior Error Probability: 2.11E-17
Best Match Spectrum:

Scan number 6712 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac16
Method ITMS; CID **Genenames** NEDD8



Protein Group ID: 2464

Protein Accession Numbers: Q15853; Q15853-2; Q15853-3; Q6YI47

Gene Names: USF2

Peptide Sequence: AQLQQHNL**EMV**GEGTR

Total Number of Spectra: 7

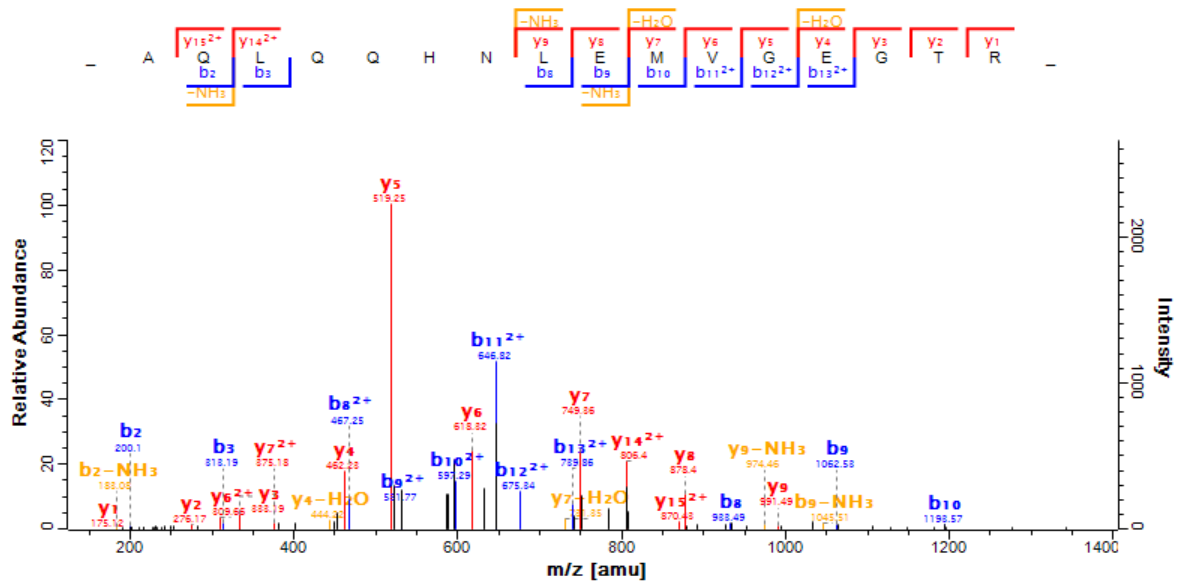
Number of Replicates (out of 10): 7

Best Match Score: 171.21

Best Match Posterior Error Probability: 1.48E-15

Best Match Spectrum:

Scan number	2037	Raw file	Prt-OGE-Batch3-WT-Frac5
Method	ITMS; CID	Genenames	USF2



Protein Group ID: 2468

Protein Accession Numbers: Q16222; Q16222-3; Q16222-2

Gene Names: UAP1

Peptide Sequence: FVFDIFQFAK

Total Number of Spectra: 14

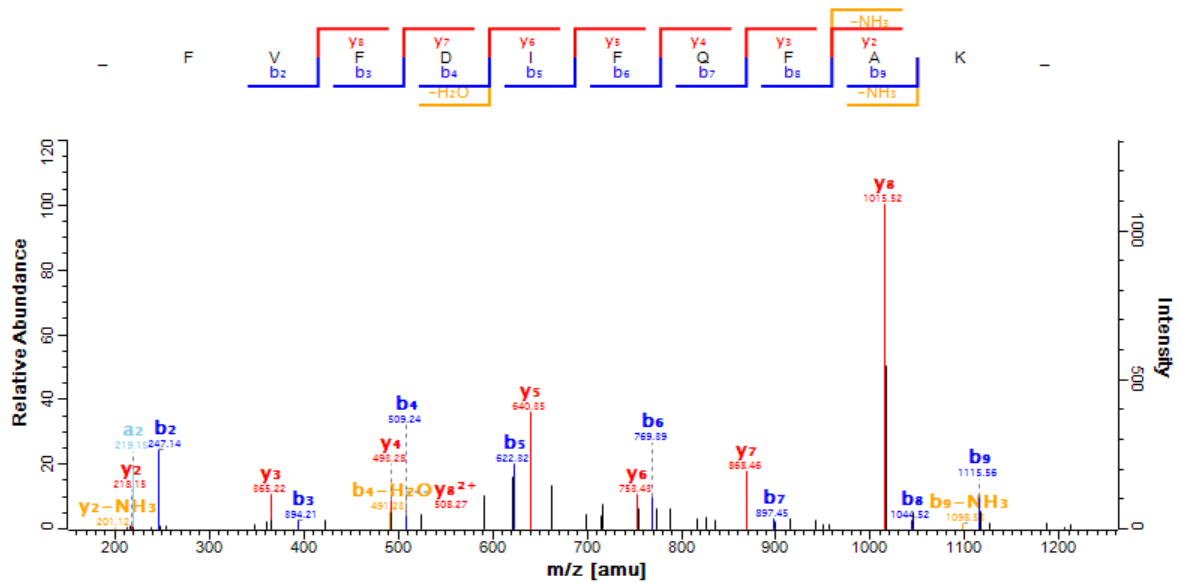
Number of Replicates (out of 10): 9

Best Match Score: 129.7

Best Match Posterior Error Probability: 8.76E-05

Best Match Spectrum:

Scan number	5463	Raw file	Prt-OGE-Batch3-WT-Frac12
Method	ITMS; CID	Genenames	UAP1



Protein Group ID: 2483

Protein Accession Numbers: Q16763

Gene Names: UBE2S

Peptide Sequence: ALASGTEASSTDPGAPGGPGGAEGPMAK

Total Number of Spectra: 4

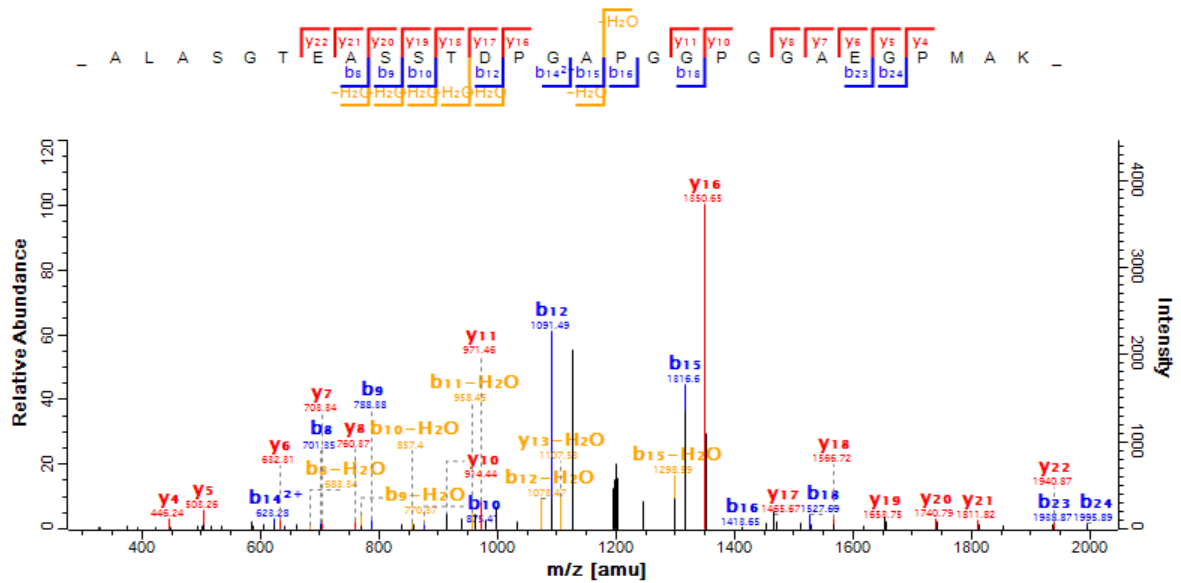
Number of Replicates (out of 10): 4

Best Match Score: 134.76

Best Match Posterior Error Probability: 4.91E-28

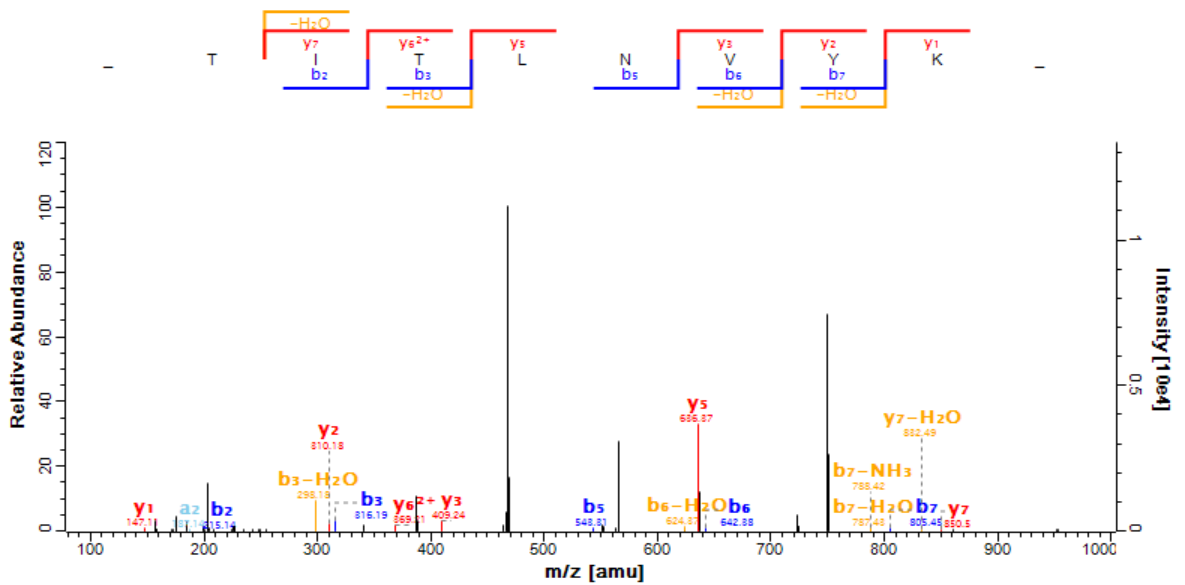
Best Match Spectrum:

Scan number 2534 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac18
Method ITMS; CID **Genenames** UBE2S



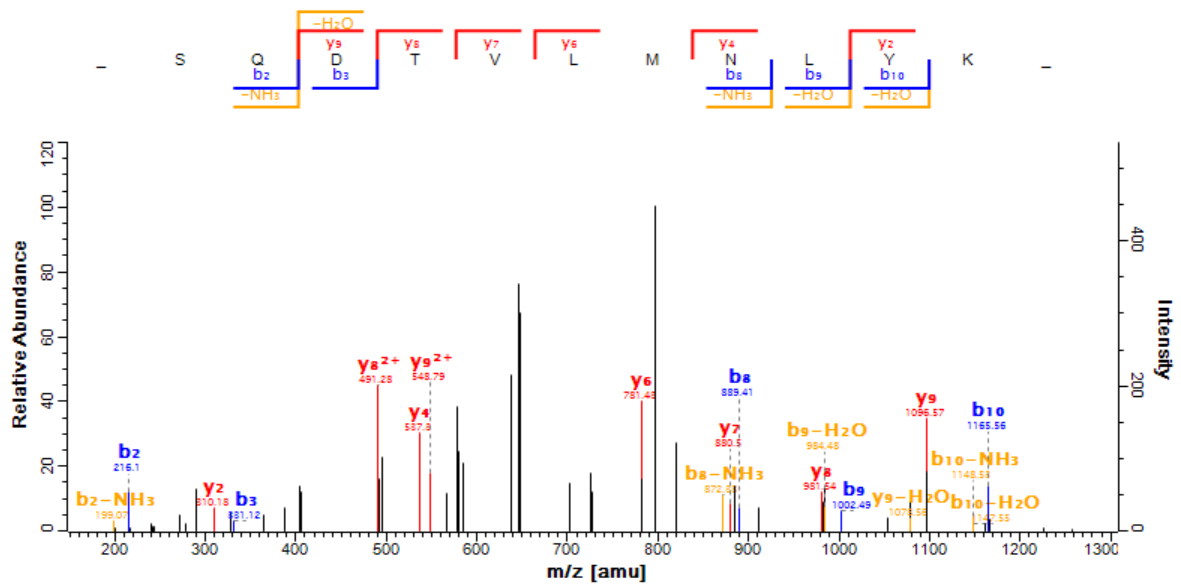
Protein Group ID: 2492
Protein Accession Numbers: Q2KHT3; Q2KHT3-2
Gene Names: CLEC16A
Peptide Sequence: TITLNVYK
Total Number of Spectra: 10
Number of Replicates (out of 10): 6
Best Match Score: 111.17
Best Match Posterior Error Probability: 0.0015941
Best Match Spectrum:

Scan number 2231 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac12
Method ITMS; CID **Genenames** CLEC16A



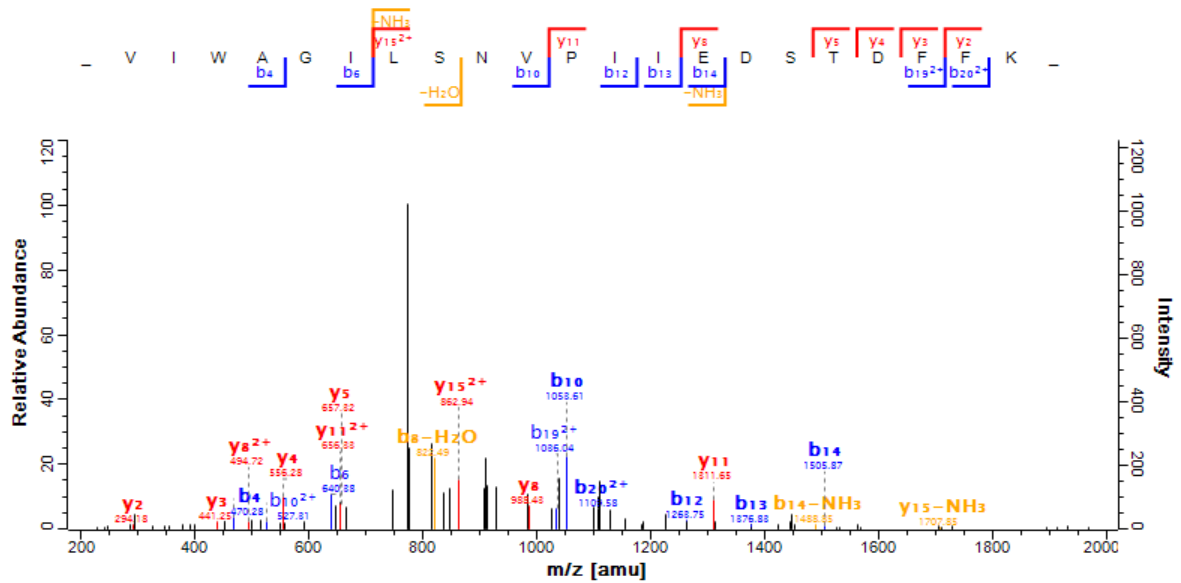
Protein Group ID: 2493
Protein Accession Numbers: Q2NL82
Gene Names: TSR1
Peptide Sequence: SQDTVLMNLYK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 111.86
Best Match Posterior Error Probability: 0.001508
Best Match Spectrum:

Scan number 3911 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac17
Method ITMS; CID **Genenames** TSR1



Protein Group ID: 2500
Protein Accession Numbers: Q3SY69; Q3SY69-3
Gene Names: ALDH1L2
Peptide Sequence: VIWAGILSNVPIIEDSTDFK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 77.899
Best Match Posterior Error Probability: 0.00045243
Best Match Spectrum:

Scan number 8293 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac11
Method ITMS; CID **Genenames** ALDH1L2



Protein Group ID: 2507

Protein Accession Numbers: Q4KWH8; Q4KWH8-2; Q4KWH8-4; Q4KWH8-3

Gene Names: PLCH1

Peptide Sequence: ILIDSIYK

Total Number of Spectra: 11

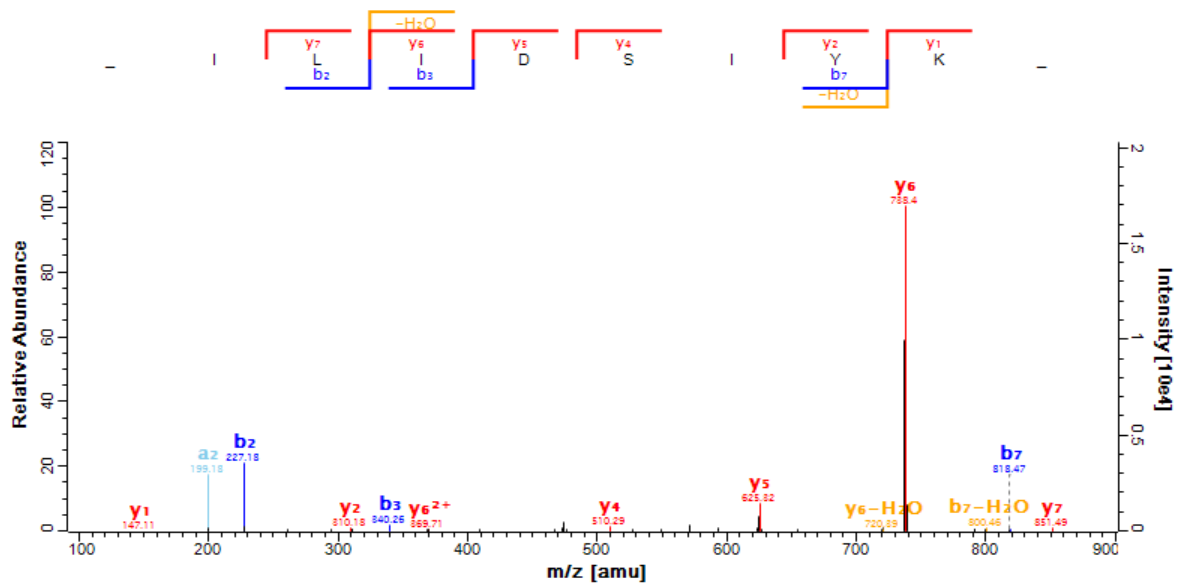
Number of Replicates (out of 10): 7

Best Match Score: 107.66

Best Match Posterior Error Probability: 0.0016793

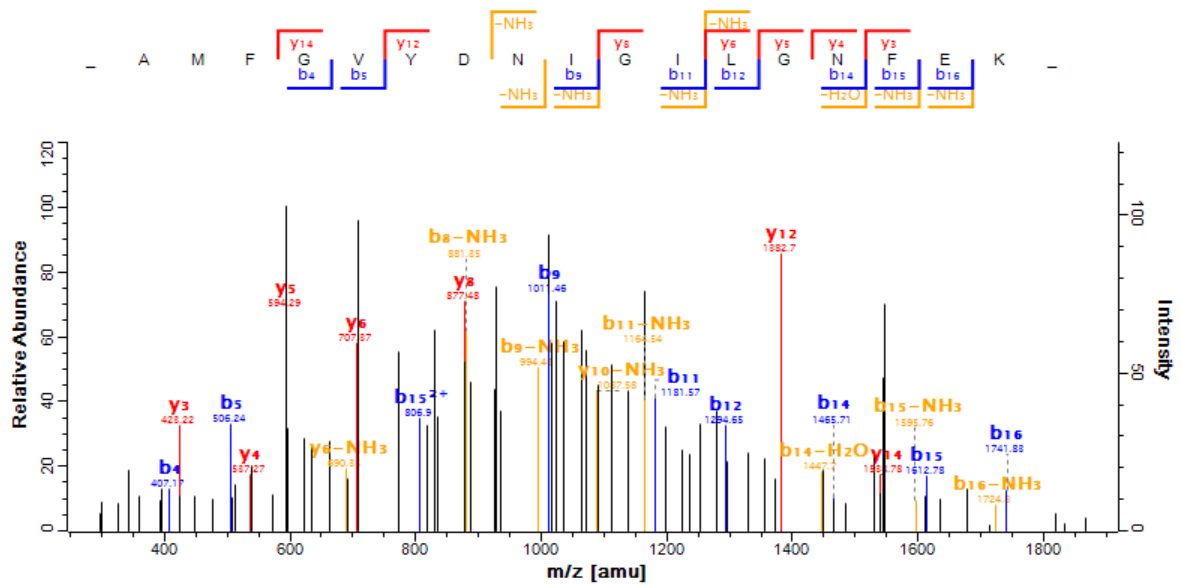
Best Match Spectrum:

Scan number	3554	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac4
Method	ITMS; CID	Genenames	PLCH1



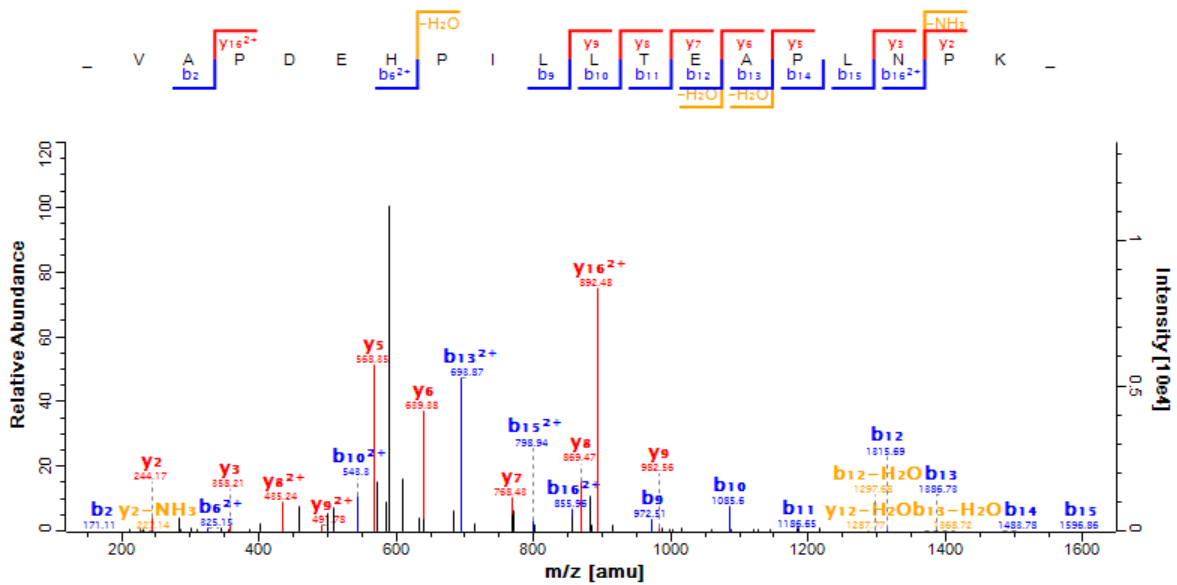
Protein Group ID: 2508
Protein Accession Numbers: Q4U2R6
Gene Names: MRPL51
Peptide Sequence: AMFGVYDNI⁸LG⁸NFEK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 89.311
Best Match Posterior Error Probability: 0.00049461
Best Match Spectrum:

Scan number 6580 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac18
Method ITMS; CID **Genenames** MRPL51



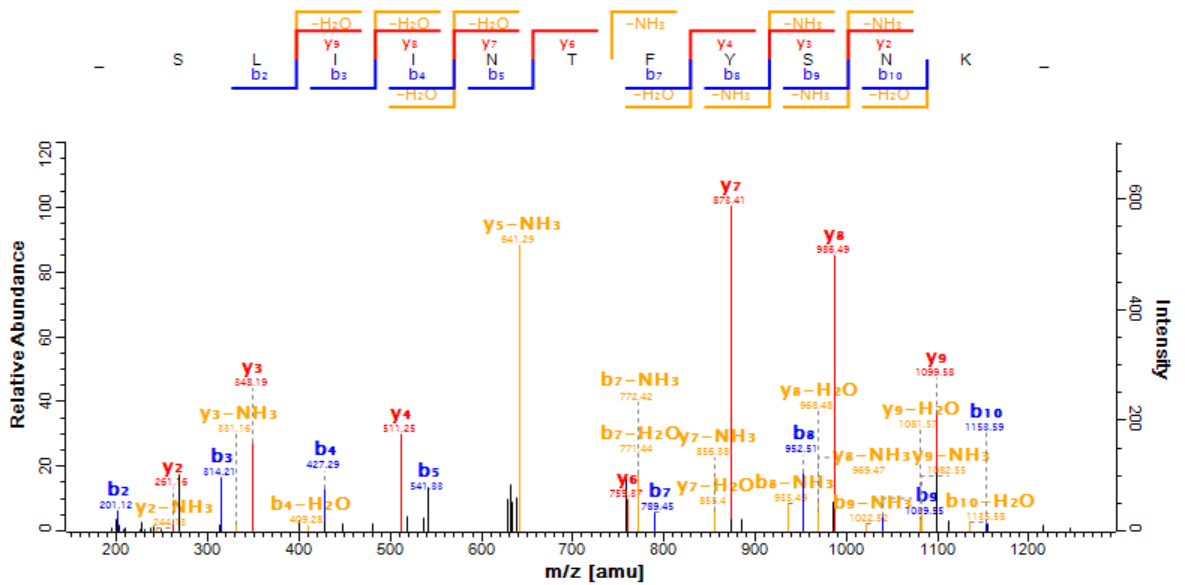
Protein Group ID: 2521
Protein Accession Numbers: Q562R1
Gene Names: ACTBL2
Peptide Sequence: VAPDEHPILLTEAPLNPK
Total Number of Spectra: 72
Number of Replicates (out of 10): 10
Best Match Score: 129.38
Best Match Posterior Error Probability: 2.24E-05
Best Match Spectrum:

Scan number 4168 **Raw file** OGE-Mock-Frac10
Method ITMS; CID **Genenames** ACTBL2



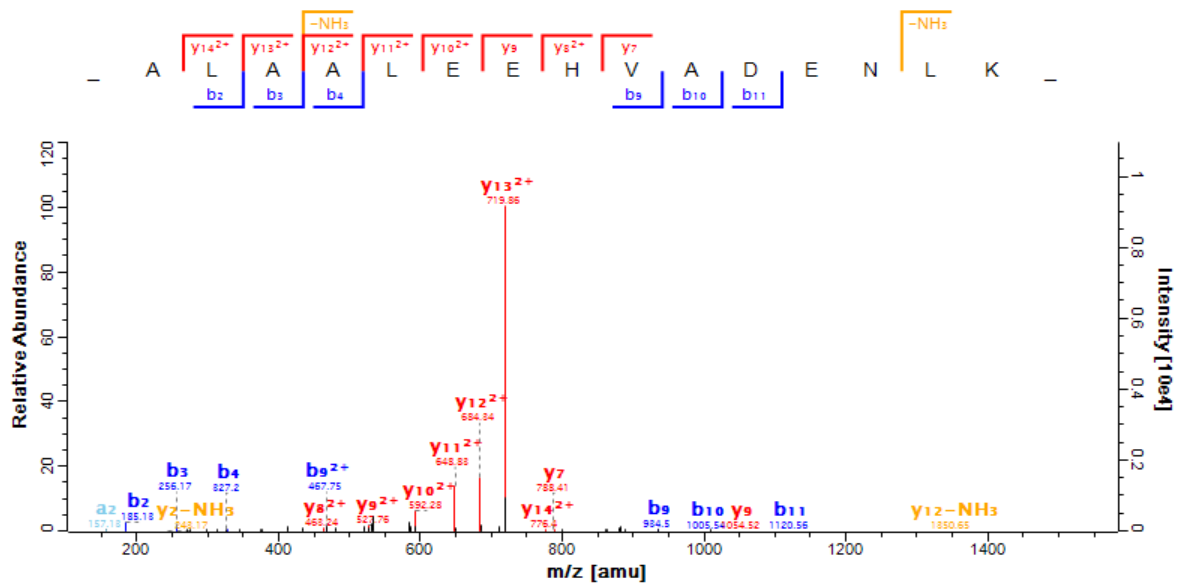
Protein Group ID: 2523
Protein Accession Numbers: Q58FF6
Gene Names: HSP90AB4P
Peptide Sequence: SLINTFYSNK
Total Number of Spectra: 3
Number of Replicates (out of 10): 2
Best Match Score: 190.53
Best Match Posterior Error Probability: 5.90E-16
Best Match Spectrum:

Scan number 4098 **Raw file** OGE-WT-Frac6
Method ITMS; CID **Genenames** HSP90AB4P



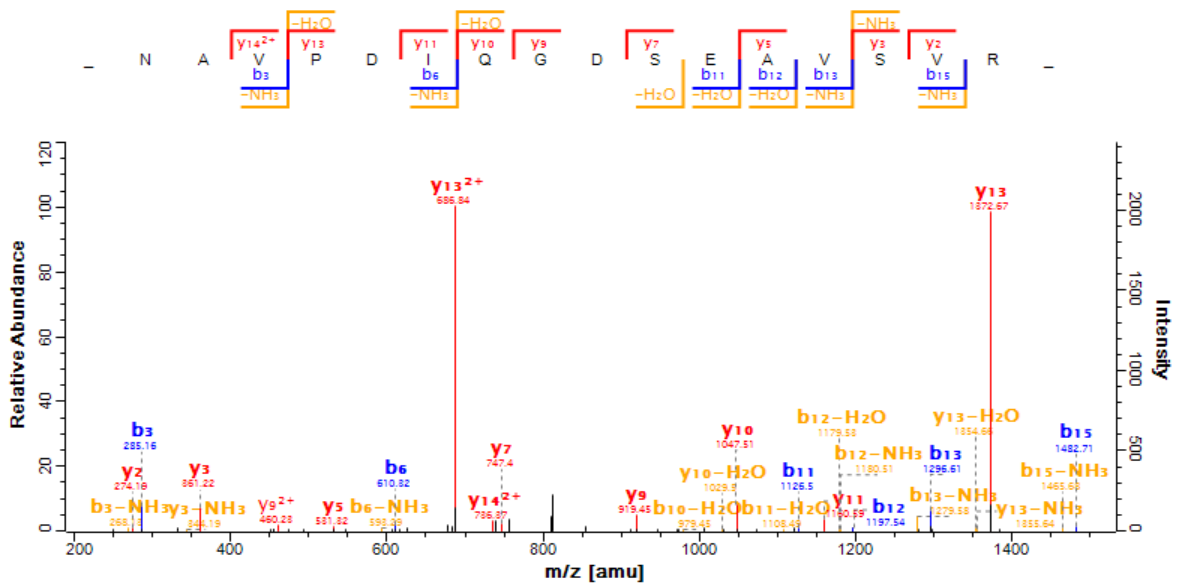
Protein Group ID: 2525
Protein Accession Numbers: Q5BKU9
Gene Names: C17orf90
Peptide Sequence: ALAALEEHVADENLK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 94.191
Best Match Posterior Error Probability: 0.00023062
Best Match Spectrum:

Scan number	3600	Raw file	Prt-OGE-Batch3--Mock-Frac7
Method	ITMS; CID	Genenames	C17orf90



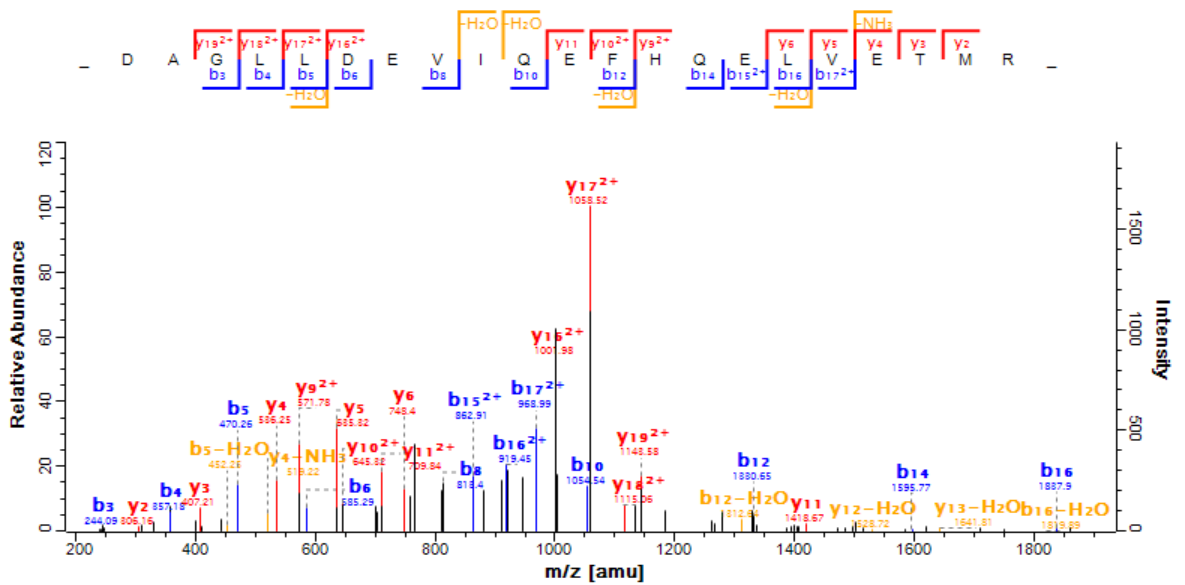
Protein Group ID: 2529
Protein Accession Numbers: Q9Y2B9; Q5H937
Gene Names: PKIG
Peptide Sequence: NAVPDIQGDSEAVSVR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 164.15
Best Match Posterior Error Probability: 6.72E-15
Best Match Spectrum:

Scan number 3668 **Raw file** OGE-Mock-Frac1
Method ITMS; CID **Genenames** PKIG



Protein Group ID: 2534
Protein Accession Numbers: Q9UKD1; Q5JTV1
Gene Names: GMEB2
Peptide Sequence: DAGLLDEVIQEFHQELVETMR
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 149.52
Best Match Posterior Error Probability: 7.11E-14
Best Match Spectrum:

Scan number 9065 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac9
Method ITMS; CID **Genenames** GMEB2



Protein Group ID: 2542

Protein Accession Numbers: Q9HB21; Q5RGS4; Q9HB21-2

Gene Names: PLEKHA1

Peptide Sequence: DNLFEIVTTSR

Total Number of Spectra: 1

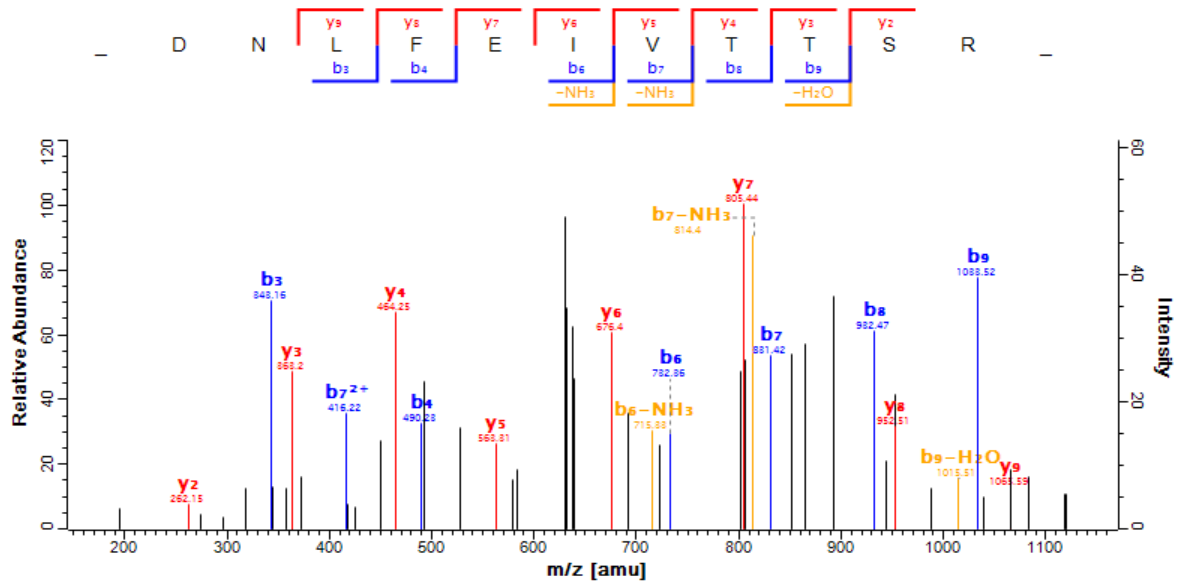
Number of Replicates (out of 10): 1

Best Match Score: 101.53

Best Match Posterior Error Probability: 0.00024813

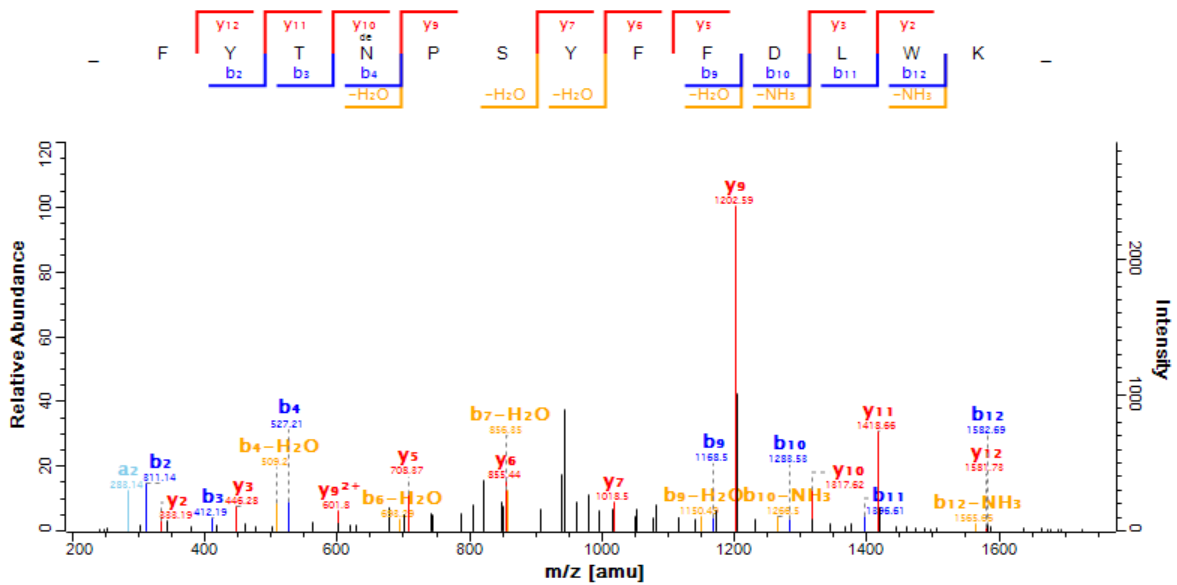
Best Match Spectrum:

Scan number 4688 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac21
Method ITMS; CID **Genenames** PLEKHA1



Protein Group ID: 2546
Protein Accession Numbers: Q92558; Q5SZK5
Gene Names: WASF1
Peptide Sequence: FYTNPSYFFDLWK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 140.08
Best Match Posterior Error Probability: 0.0002139
Best Match Spectrum:

Scan number 7340 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac13
Method ITMS; CID **Genenames** WASF1



Protein Group ID: 2550

Protein Accession Numbers: Q5T6J7-2; Q5T6J7; Q5T6J8

Gene Names: IDNK;C9orf103

Peptide Sequence: STVGALLASELGWK

Total Number of Spectra: 1

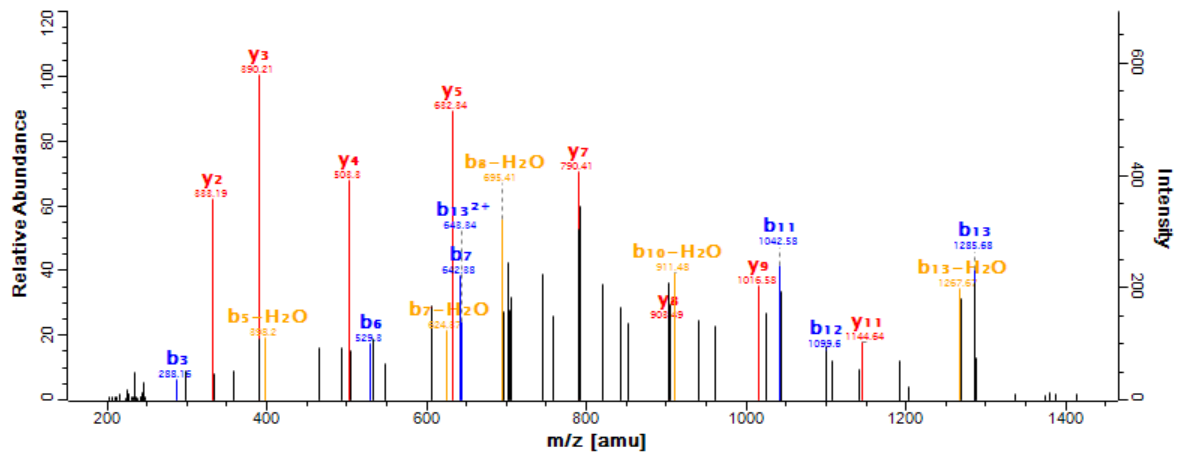
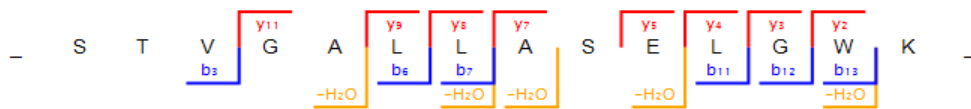
Number of Replicates (out of 10): 1

Best Match Score: 83.087

Best Match Posterior Error Probability: 0.0012588

Best Match Spectrum:

Scan number	6616	Raw file	Prt-OGE-Batch3-Mock-Frac11
Method	ITMS; CID	Genenames	IDNK;C9orf103



Protein Group ID: 2552

Protein Accession Numbers: Q9HD45; Q5TB53

Gene Names: TM9SF3;RP11-34E5.1

Peptide Sequence: SISYHETLGEALQGV E A L Q G V E L E F S G L D I K

Total Number of Spectra: 4

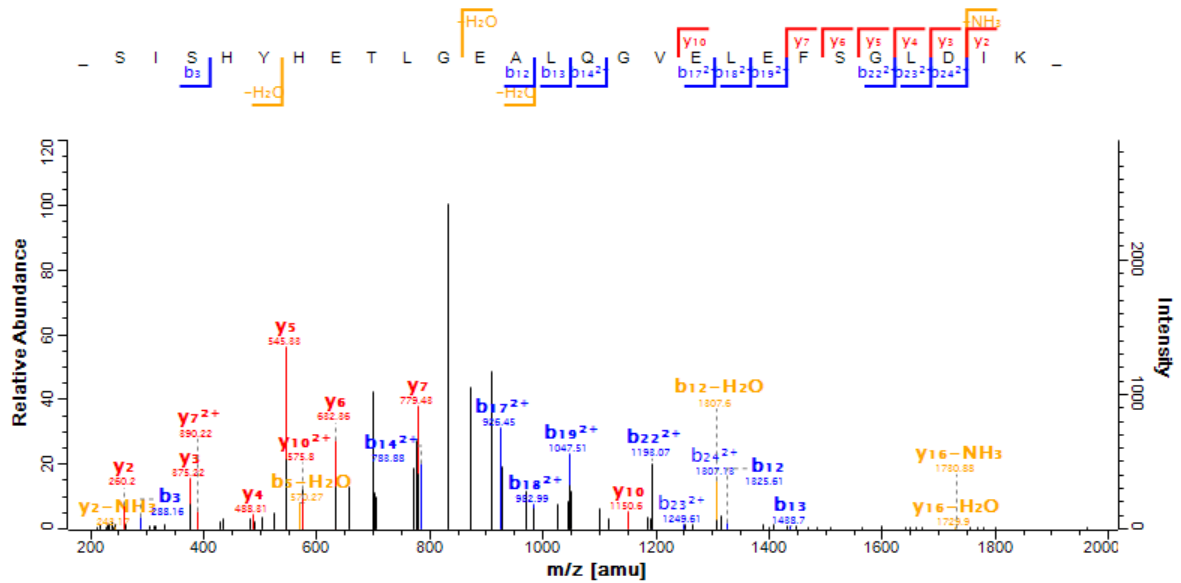
Number of Replicates (out of 10): 2

Best Match Score: 64.488

Best Match Posterior Error Probability: 0.00024663

Best Match Spectrum:

Scan number 7119 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac11
Method ITMS; CID **Genenames** TM9SF3;RP11-34E5.1



Protein Group ID: 2556

Protein Accession Numbers: Q9NWM0-6; Q9NWM0; Q9NWM0-4; Q9NWM0-2; Q5TE25; Q9NWM0-5

Gene Names: SMOX

Peptide Sequence: VVELLAEGIPAHVIQLGKPV R

Total Number of Spectra: 1

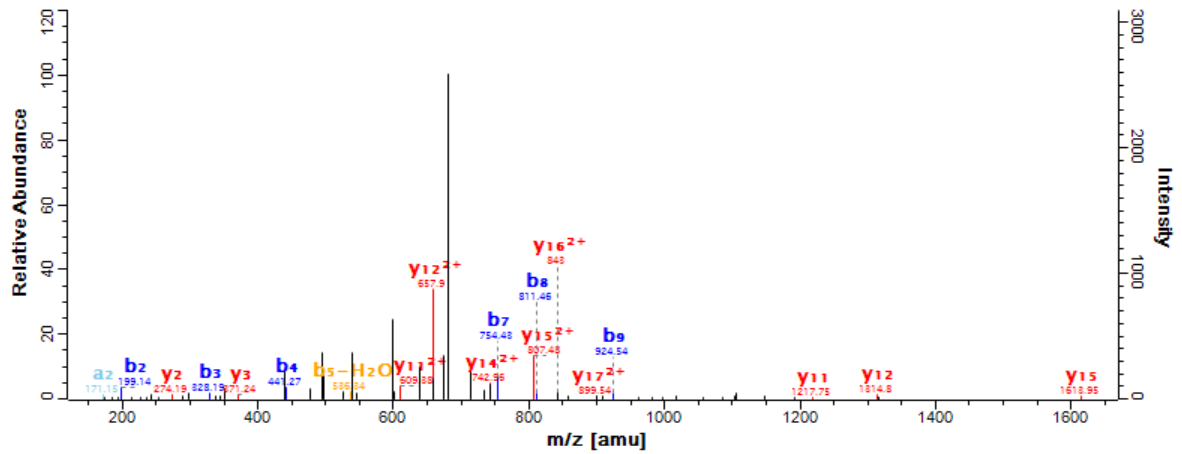
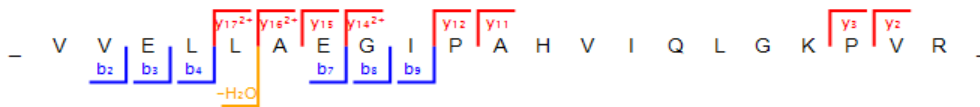
Number of Replicates (out of 10): 1

Best Match Score: 95.767

Best Match Posterior Error Probability: 9.15E-05

Best Match Spectrum:

Scan number	5803	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac9
Method	ITMS; CID	Genenames	SMOX



Protein Group ID: 2561

Protein Accession Numbers: Q5VT79; Q5VT79-2; E7EVD9

Gene Names: ANXA8L2

Peptide Sequence: AWIEQEGVTVK

Total Number of Spectra: 20

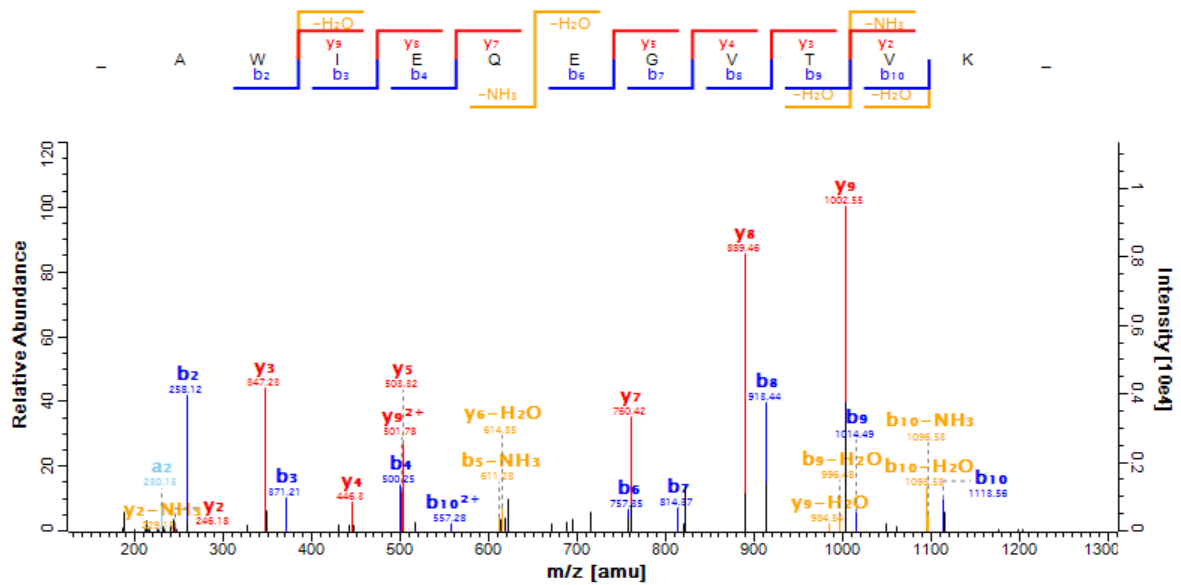
Number of Replicates (out of 10): 10

Best Match Score: 140.24

Best Match Posterior Error Probability: 2.15E-15

Best Match Spectrum:

Scan number	2891	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac11
Method	ITMS; CID	Genenames	ANXA8L2



Protein Group ID: 2567

Protein Accession Numbers: Q9H497; Q9H497-2; Q9H497-3; Q5W0C6

Gene Names: TOR3A

Peptide Sequence: AESPWTIFLFLSNLR

Total Number of Spectra: 1

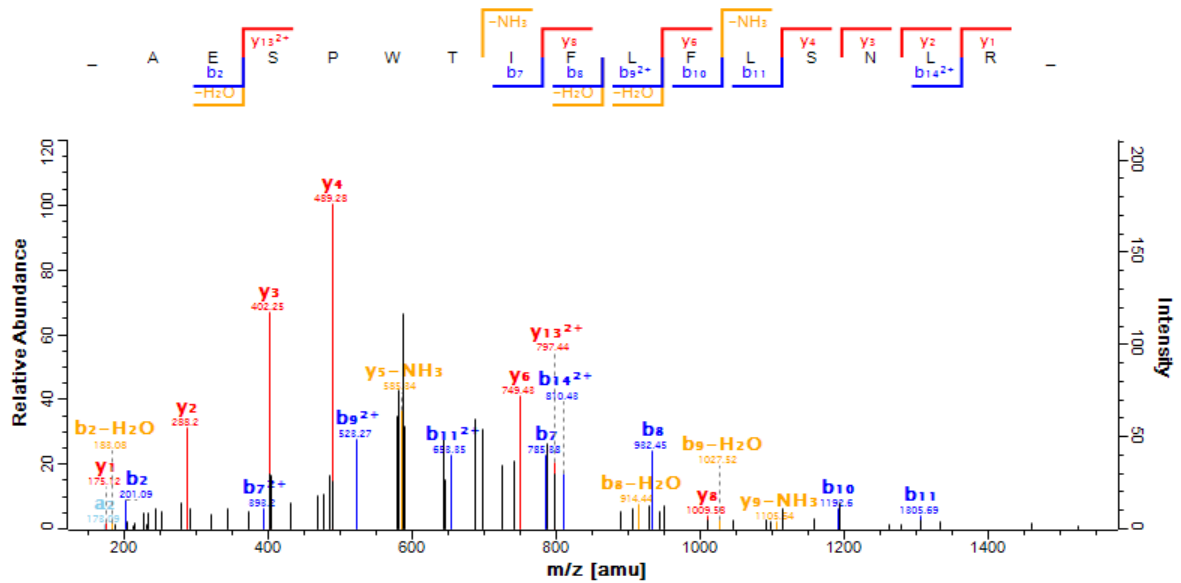
Number of Replicates (out of 10): 1

Best Match Score: 92.039

Best Match Posterior Error Probability: 0.00028884

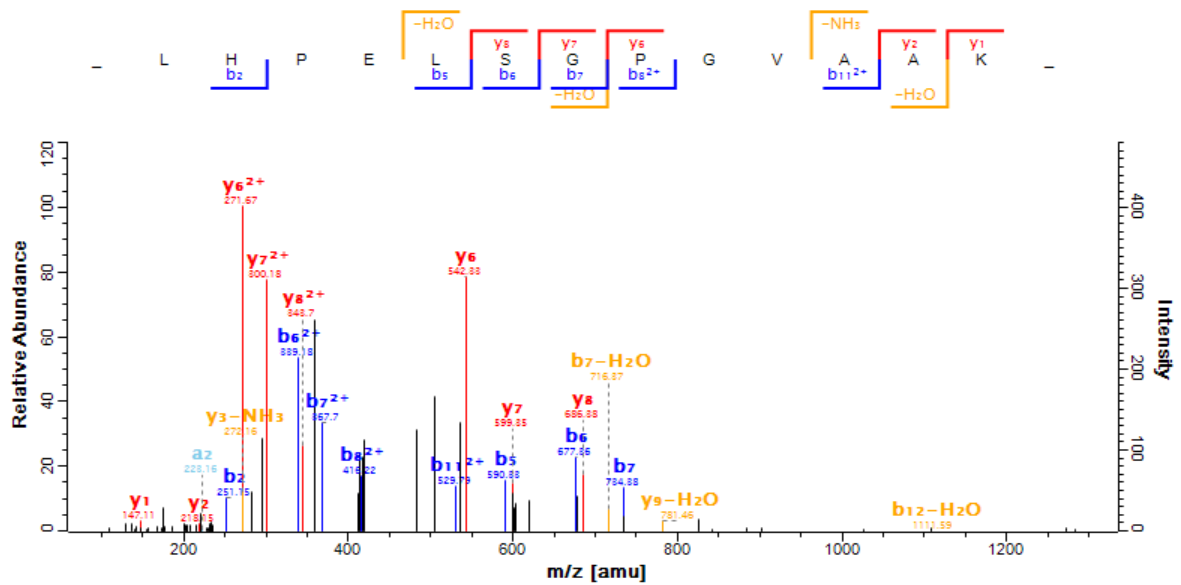
Best Match Spectrum:

Scan number	7766	Raw file	OGE-WT-Frac10
Method	ITMS; CID	Genenames	TOR3A



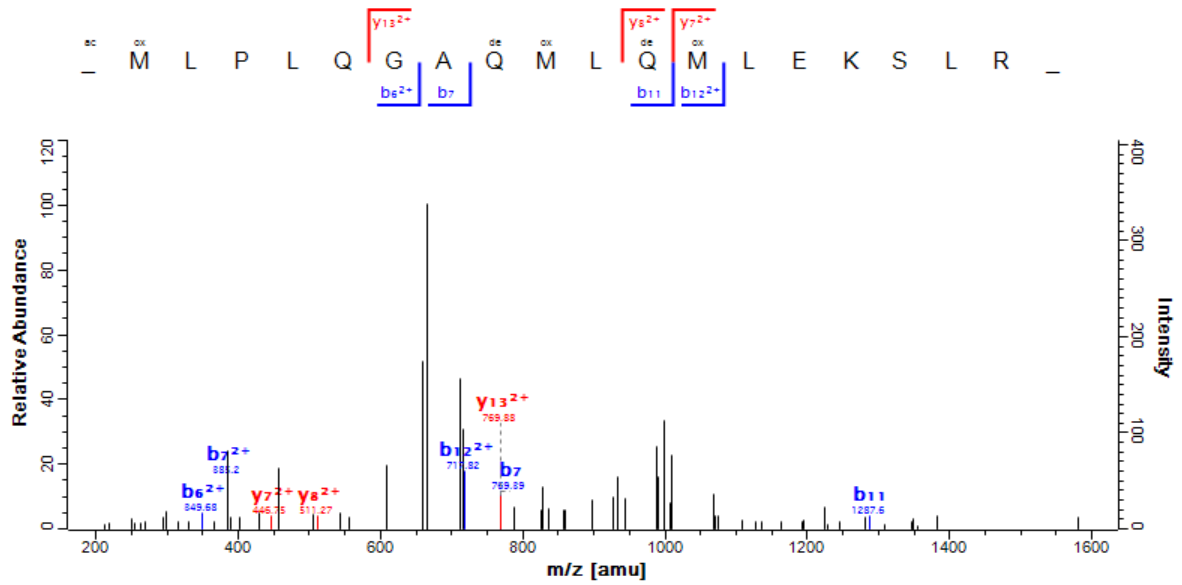
Protein Group ID: 2571
Protein Accession Numbers: Q6DD87
Gene Names: ZNF787
Peptide Sequence: LHPELSGPGVAAK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 90.913
Best Match Posterior Error Probability: 0.00089914
Best Match Spectrum:

Scan number 1650 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac18
Method ITMS; CID **Genenames** ZNF787



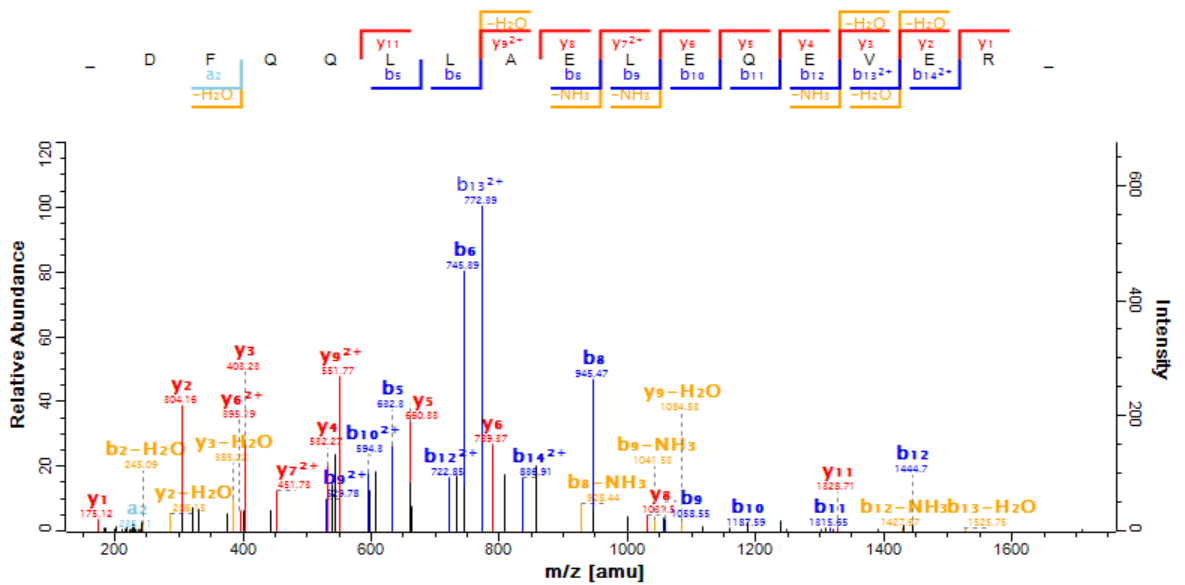
Protein Group ID: 2576
Protein Accession Numbers: Q6IB77; Q6IB77-2
Gene Names: GLYAT
Peptide Sequence: MLPLQGAQLQMLEKSLR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 33.796
Best Match Posterior Error Probability: 0.014525
Best Match Spectrum:

Scan number 4769 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac9
Method ITMS; CID **Genenames** GLYAT



Protein Group ID: 2580
Protein Accession Numbers: Q6N063
Gene Names: OGFOD2
Peptide Sequence: DFQQLLAELEQEVER
Total Number of Spectra: 11
Number of Replicates (out of 10): 8
Best Match Score: 149.3
Best Match Posterior Error Probability: 5.39E-08
Best Match Spectrum:

Scan number 7288 **Raw file** OGE-WT-Frac9
Method ITMS; CID **Genenames** OGFOD2



Protein Group ID: 2584

Protein Accession Numbers: Q6NXT1-2

Gene Names:

Peptide Sequence: MVLILTSEM^{ox}GWGT^{-H₂O}R

Total Number of Spectra: 3

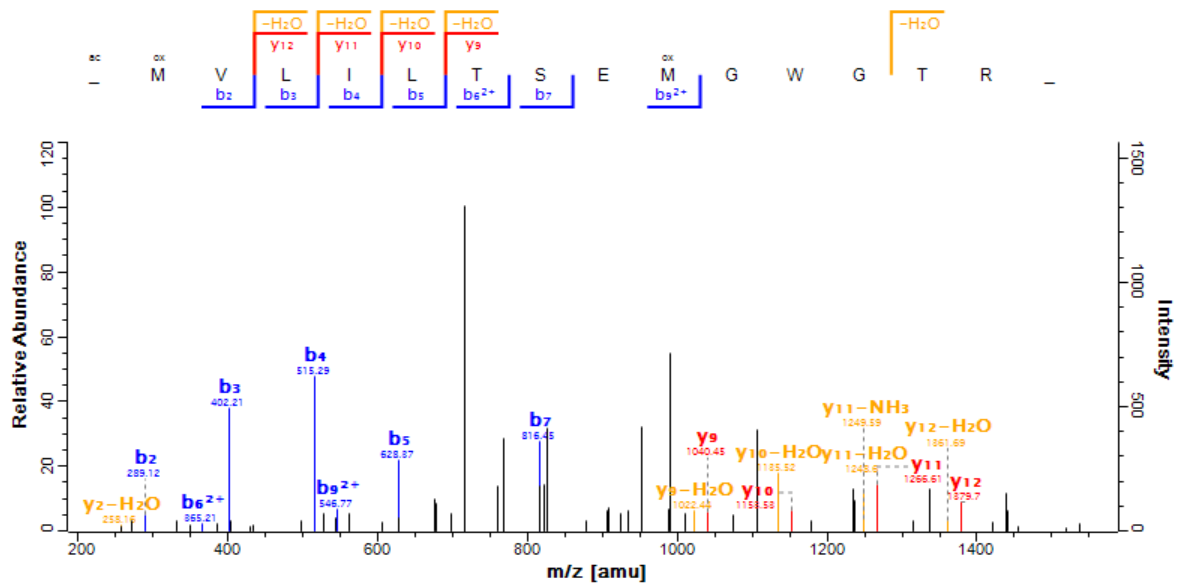
Number of Replicates (out of 10): 2

Best Match Score: 80.69

Best Match Posterior Error Probability: 0.0080769

Best Match Spectrum:

Scan number 6404 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac14
Method ITMS; CID **Pepti...** 80.69



Protein Group ID: 2589

Protein Accession Numbers: Q6P1K2-5; Q6P1K2-2; Q6P1K2; Q6P1K2-6; Q6P1K2-3

Gene Names: PMF1

Peptide Sequence: LLDTMVDTFLLQK

Total Number of Spectra: 1

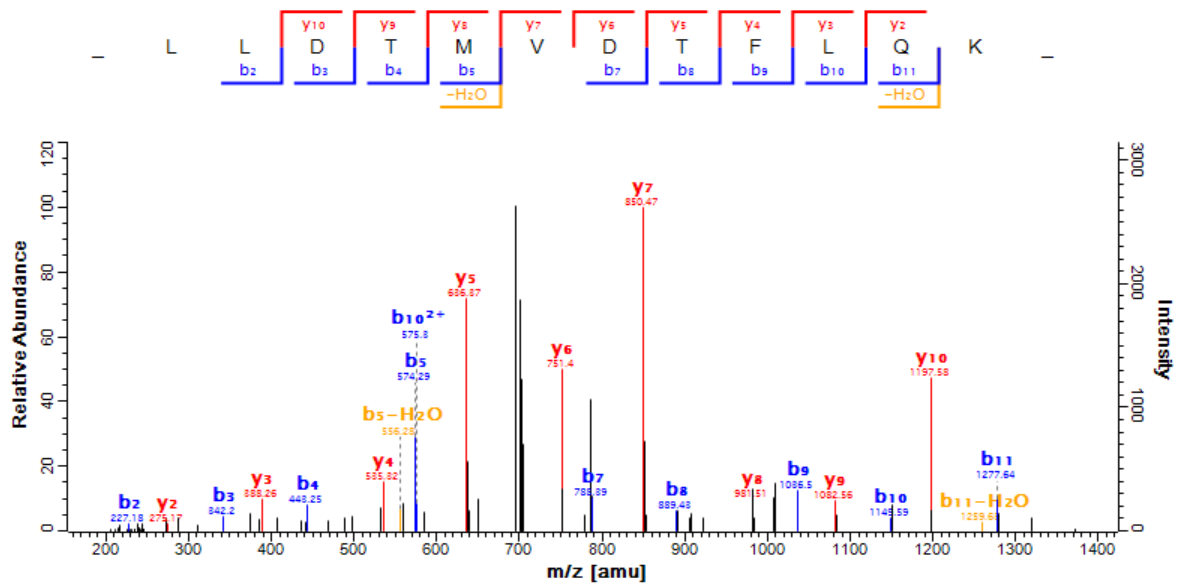
Number of Replicates (out of 10): 1

Best Match Score: 110.8

Best Match Posterior Error Probability: 0.00018963

Best Match Spectrum:

Scan number 6173 **Raw file** Prt-OGE-Batch3-Mock-Frac8
Method ITMS; CID **Genenames** PMF1



Protein Group ID: 2596

Protein Accession Numbers: Q6P461-3; Q6P461; Q6P461-2

Gene Names: ACSM6

Peptide Sequence: MSKAQCIVANEAMAPVVNSAVSDCPY3LTK

Total Number of Spectra: 3

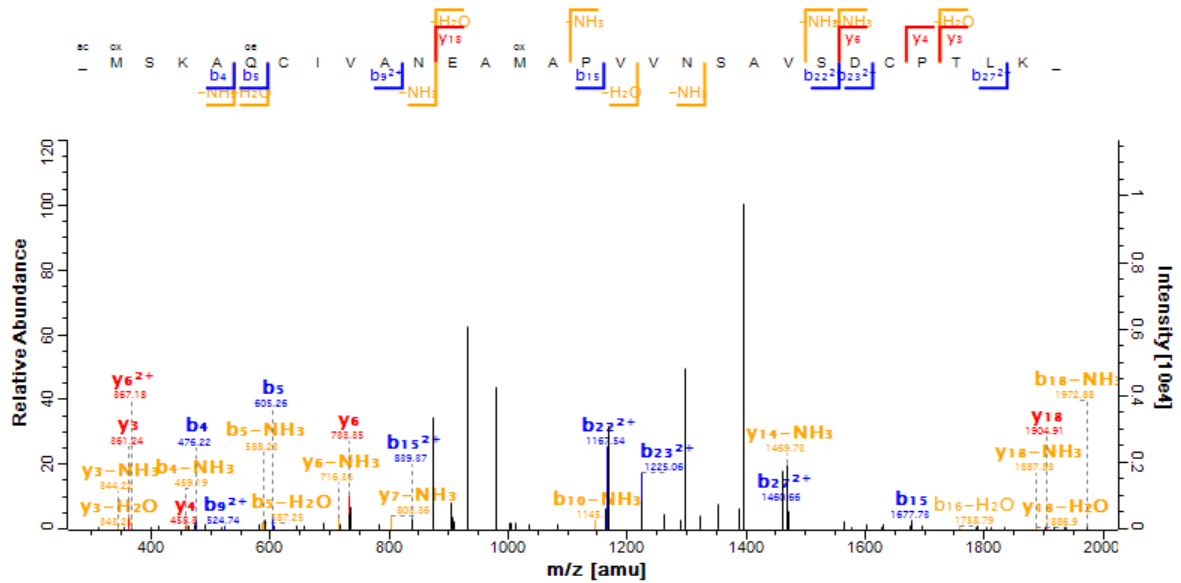
Number of Replicates (out of 10): 3

Best Match Score: 61.437

Best Match Posterior Error Probability: 0.00083447

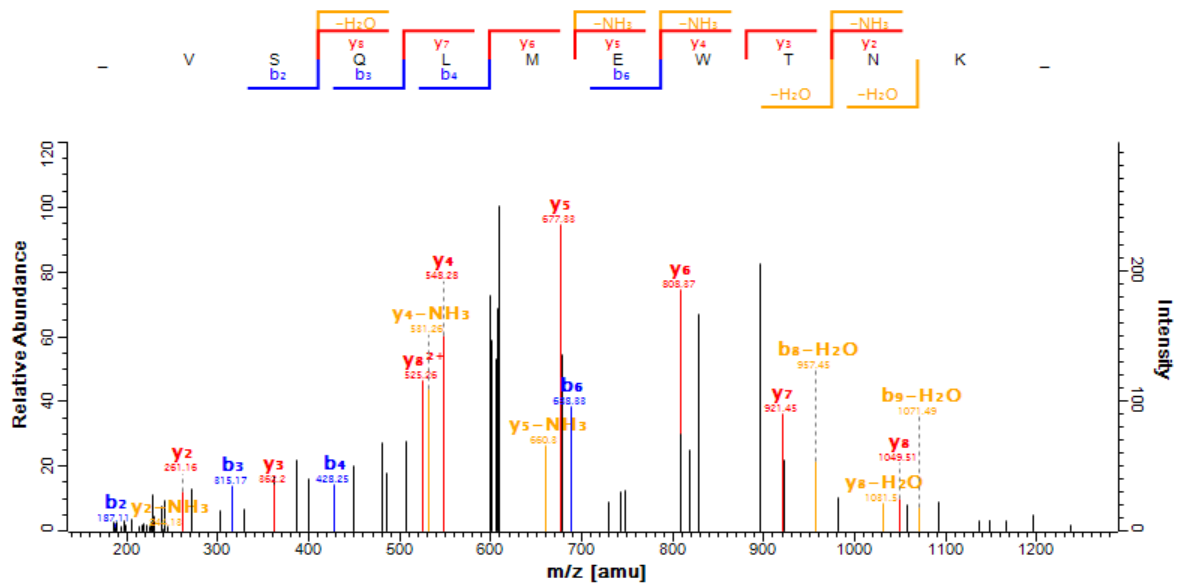
Best Match Spectrum:

Scan number 3765 **Raw file** Prt-OGE-Batch3-WT-Frac15
Method ITMS; CID **Genenames** ACSM6



Protein Group ID: 2597
Protein Accession Numbers: Q9H0U3; Q6P577
Gene Names: MAGT1
Peptide Sequence: VSQLMWNTNK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 87.184
Best Match Posterior Error Probability: 0.0013714
Best Match Spectrum:

Scan number 2407 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** MAGT1



Protein Group ID: 2609

Protein Accession Numbers: Q6S8J3; P0CG38; Q9BYX7; P0CG39

Gene Names: POTEE;POTEI;POTEKP;POTEJ

Peptide Sequence: VAPEEHPILLETAPLNPK

Total Number of Spectra: 2

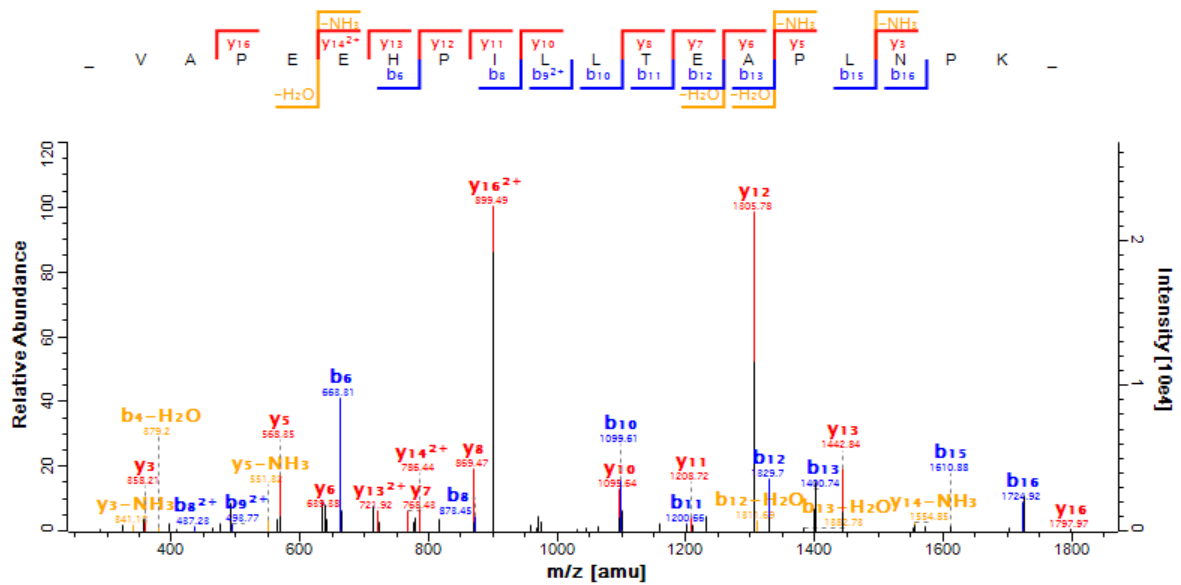
Number of Replicates (out of 10): 1

Best Match Score: 137.61

Best Match Posterior Error Probability: 5.43E-06

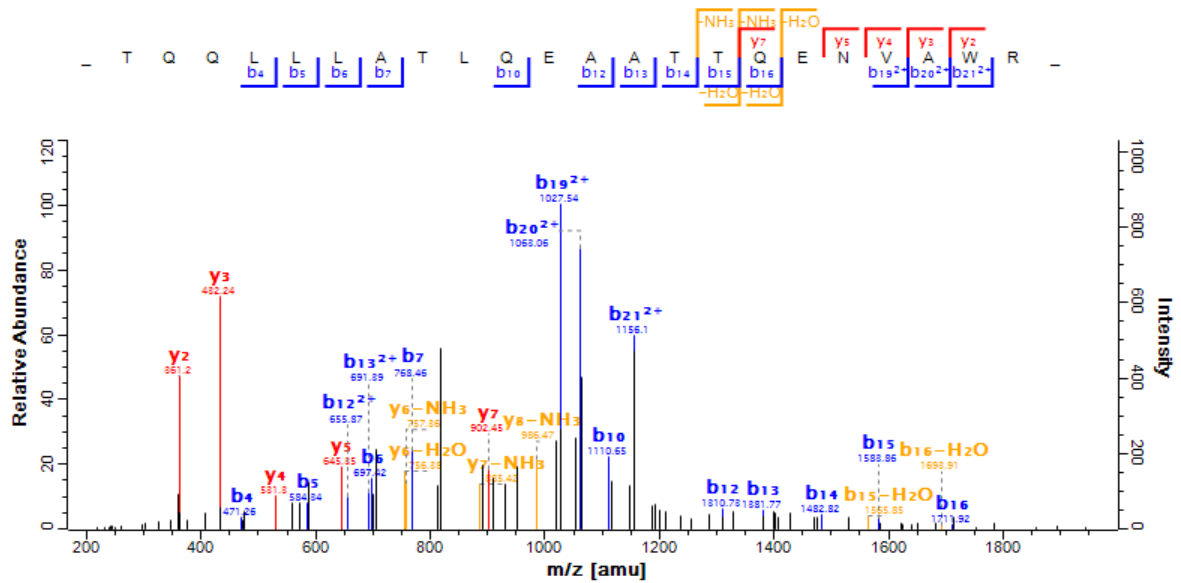
Best Match Spectrum:

Scan number 3928 **Raw file** OGE-WT-Frac22
Method ITMS; CID **Genenames** POTEE;POTEI;POTEKP;POTEJ



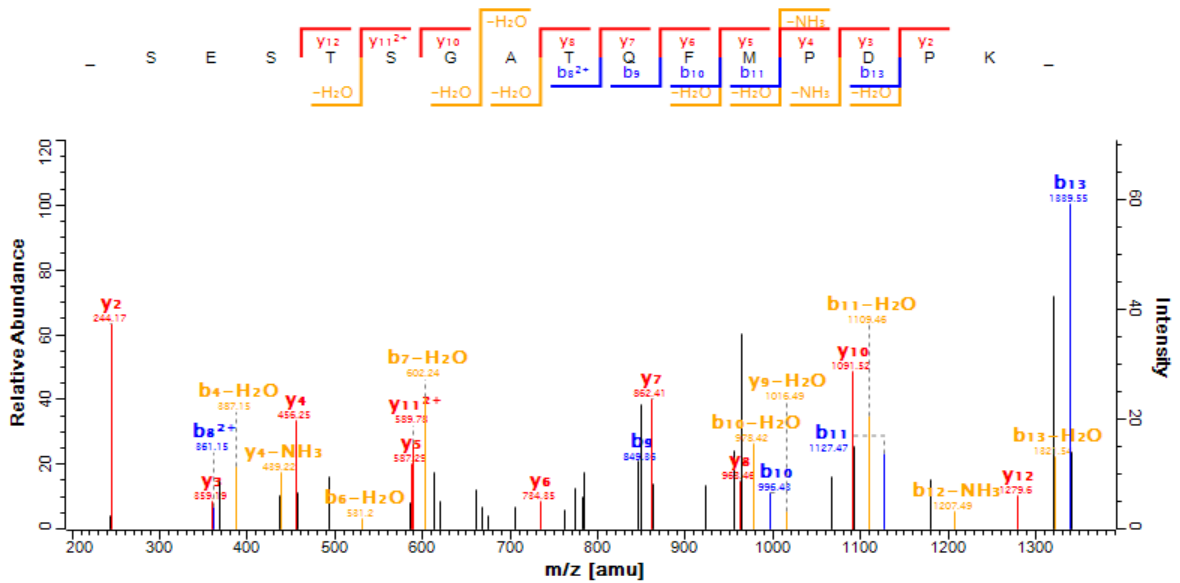
Protein Group ID: 2611
Protein Accession Numbers: Q6UW78
Gene Names: C11orf83
Peptide Sequence: TQQLLATLQEAATTQENVAWR
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 84.107
Best Match Posterior Error Probability: 0.00012775
Best Match Spectrum:

Scan number 6490 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac19
Method ITMS; CID **Genenames** C11orf83



Protein Group ID: 2613
Protein Accession Numbers: Q6UXV4
Gene Names: APOOL
Peptide Sequence: SESTSGATQFMPPK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 80.387
Best Match Posterior Error Probability: 0.0009974
Best Match Spectrum:

Scan number 1773 **Raw file** Prt-OGE-Batch3-WT-Frac21
Method ITMS; CID **Genenames** APOOL



Protein Group ID: 2616

Protein Accession Numbers: Q6ZSZ5; Q6ZSZ5-2

Gene Names: ARHGEF18

Peptide Sequence: IQTLSQLLLNLQAVIAHQDSYVETQR

Total Number of Spectra: 1

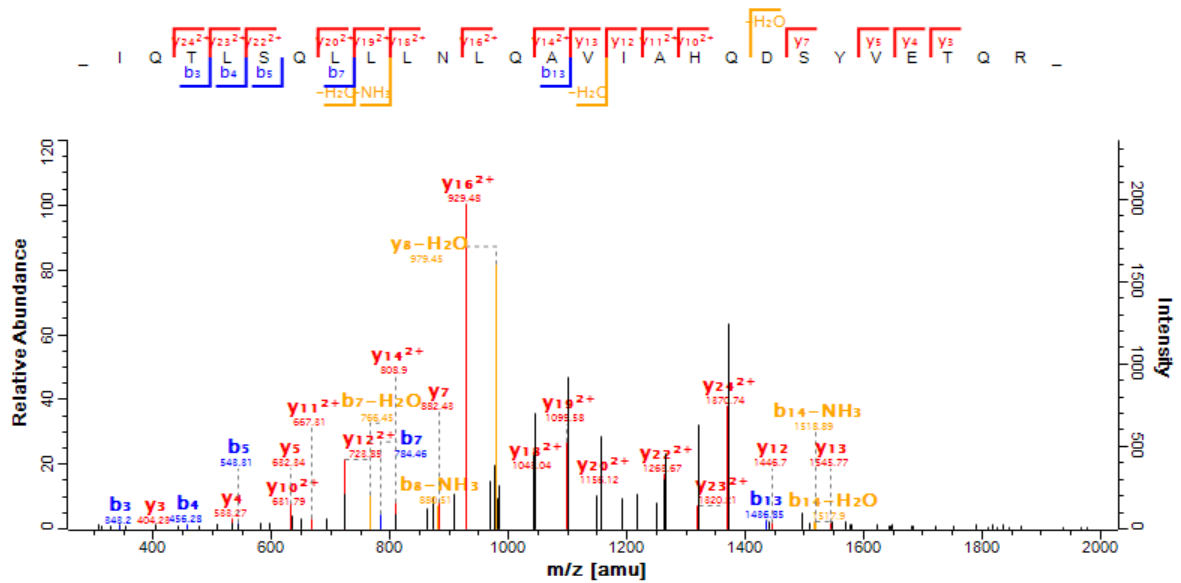
Number of Replicates (out of 10): 1

Best Match Score: 81.312

Best Match Posterior Error Probability: 6.17E-06

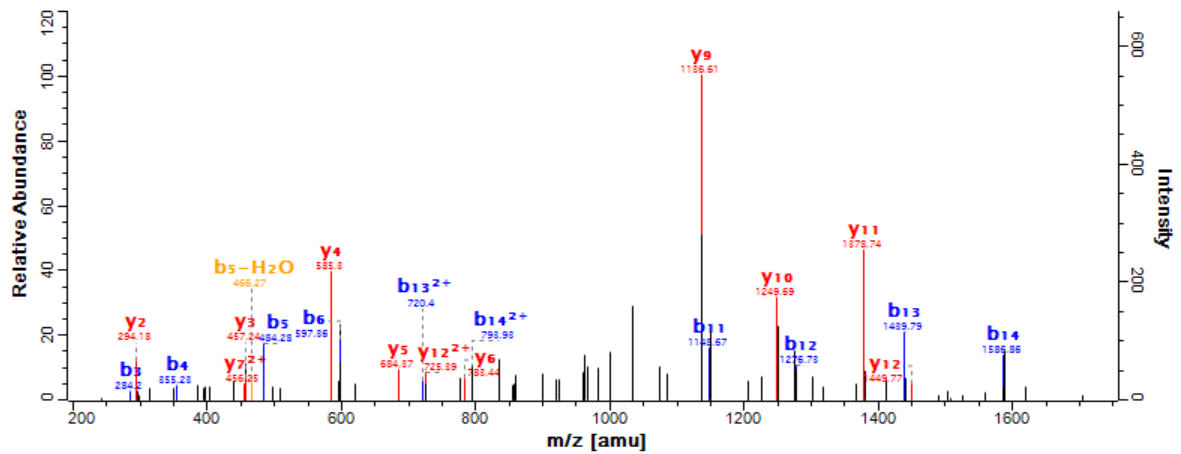
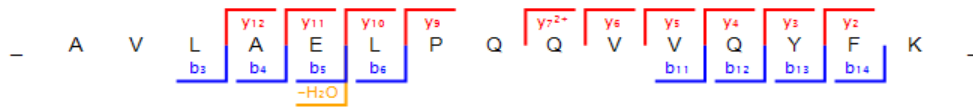
Best Match Spectrum:

Scan number 8552 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac12
Method ITMS; CID **Genenames** ARHGEF18



Protein Group ID: 2621
Protein Accession Numbers: Q96FN4; Q719H8
Gene Names: CPNE2
Peptide Sequence: AVLAE L P Q V V Q Y F K
Total Number of Spectra: 5
Number of Replicates (out of 10): 5
Best Match Score: 109.83
Best Match Posterior Error Probability: 5.74E-05
Best Match Spectrum:

Scan number 5490 **Raw file** Prt-OGE-Batch2-WT-Frac12
Method ITMS; CID **Genenames** CPNE2



Protein Group ID: 2622

Protein Accession Numbers: Q71DI3

Gene Names: HIST2H3A

Peptide Sequence: FQSSAVMLQEASEAYLVGLFEDTNLC A I H A K

Total Number of Spectra: 22

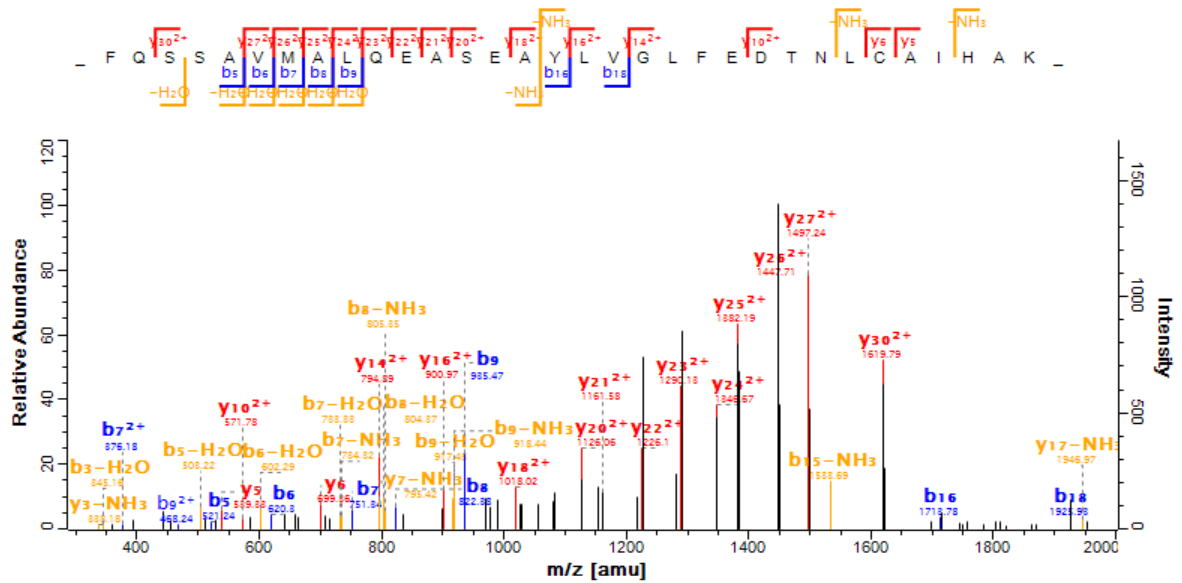
Number of Replicates (out of 10): 3

Best Match Score: 124.39

Best Match Posterior Error Probability: 1.92E-33

Best Match Spectrum:

Scan number 8772 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac13
Method ITMS; CID **Genenames** HIST2H3A



Protein Group ID: 2623

Protein Accession Numbers: Q71U36; G3V1U9; Q13748; F8VXZ4; Q6PEY2; Q13748-2; F8VQQ4

Gene Names: TUBA1A;TUBA3C;TUBA3E

Peptide Sequence: LIGQIVSSITASLR

Total Number of Spectra: 53

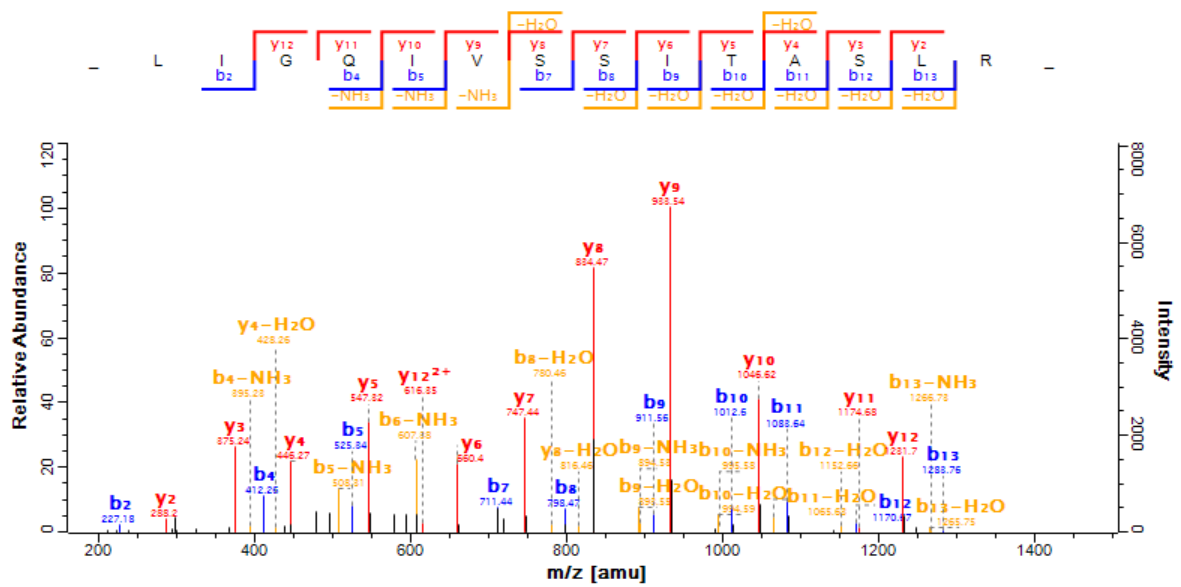
Number of Replicates (out of 10): 10

Best Match Score: 213.99

Best Match Posterior Error Probability: 1.91E-37

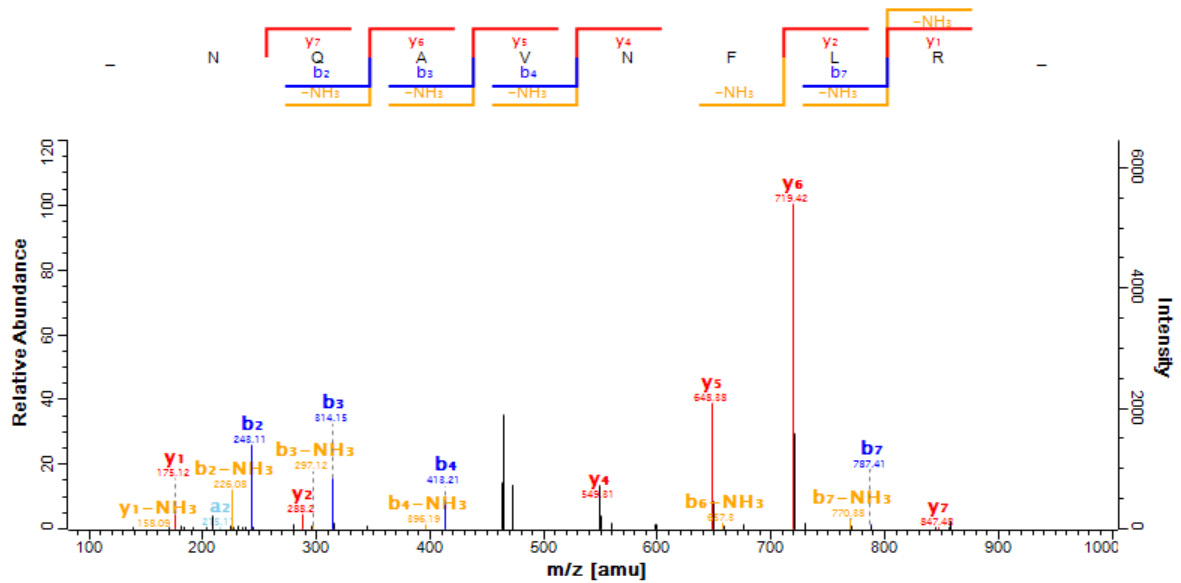
Best Match Spectrum:

Scan number	6073	Raw file	OGE-WT-Frac11
Method	ITMS: CID	Genenames	TUBA1A;TUBA3C;TUBA3E



Protein Group ID: 2631
Protein Accession Numbers: Q7LBR1
Gene Names: CHMP1B
Peptide Sequence: NQAVNFLR
Total Number of Spectra: 9
Number of Replicates (out of 10): 9
Best Match Score: 114.93
Best Match Posterior Error Probability: 0.0015884
Best Match Spectrum:

Scan number	1836	Raw file	Prt-OGE-Batch3-WT-Frac17
Method	ITMS; CID	Genenames	CHMP1B



Protein Group ID: 2636

Protein Accession Numbers: Q7Z309-3; Q7Z309-2; Q7Z309; Q7Z309-4

Gene Names: FAM122B

Peptide Sequence: MELDLEPDTSYGGTLR

Total Number of Spectra: 2

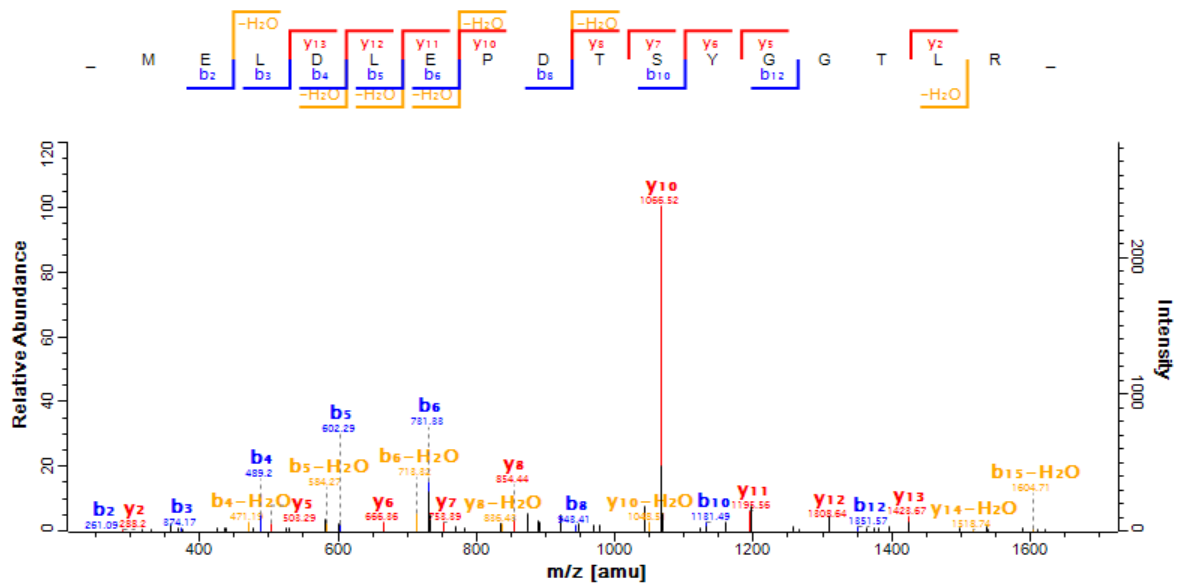
Number of Replicates (out of 10): 2

Best Match Score: 100.43

Best Match Posterior Error Probability: 0.00019885

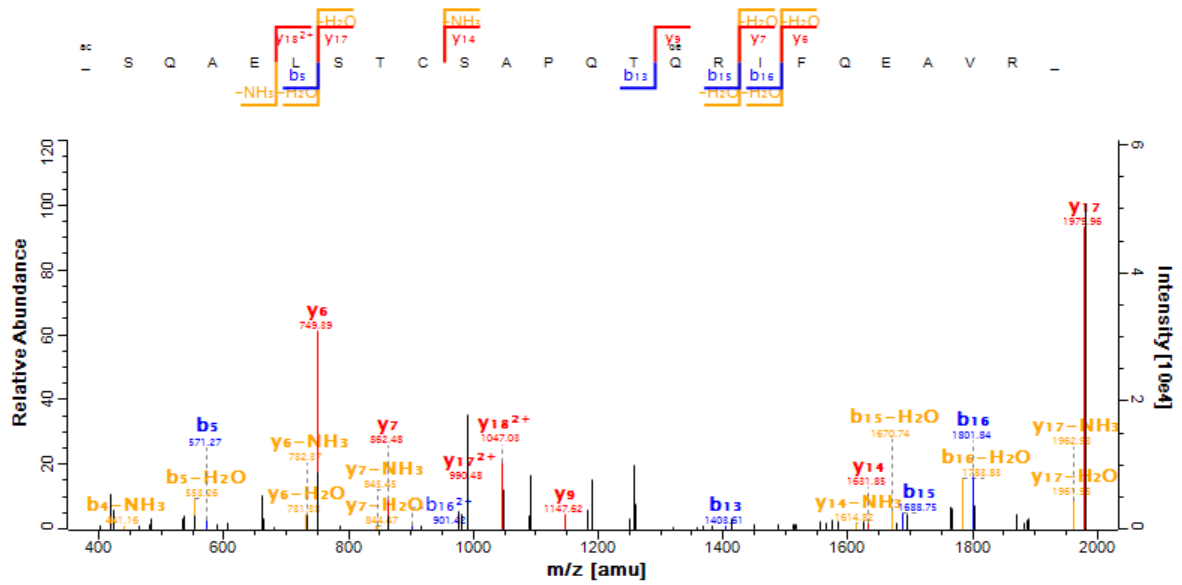
Best Match Spectrum:

Scan number 4377 **Raw file** Prt-OGE-Batch3-Mock-Frac4
Method ITMS; CID **Genenames** FAM122B



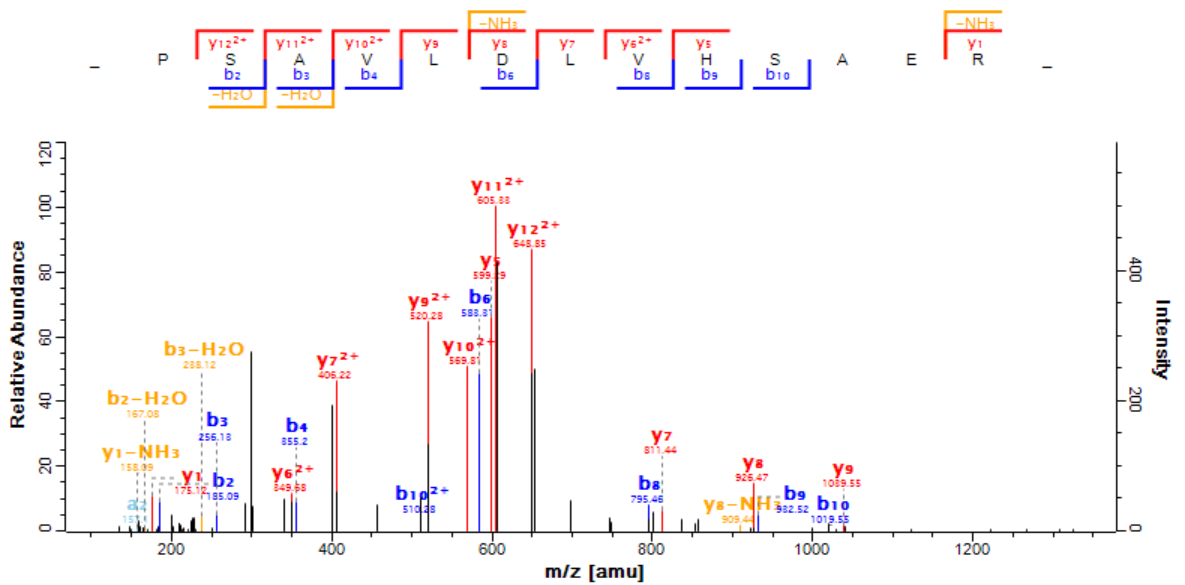
Protein Group ID: 2643
Protein Accession Numbers: Q7Z6K4
Gene Names: NRARP
Peptide Sequence: SQAELSTCSAPQTQRIFQEAVR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 91.414
Best Match Posterior Error Probability: 0.0071265
Best Match Spectrum:

Scan number 5122 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac3
Method ITMS; CID **Genenames** NRARP



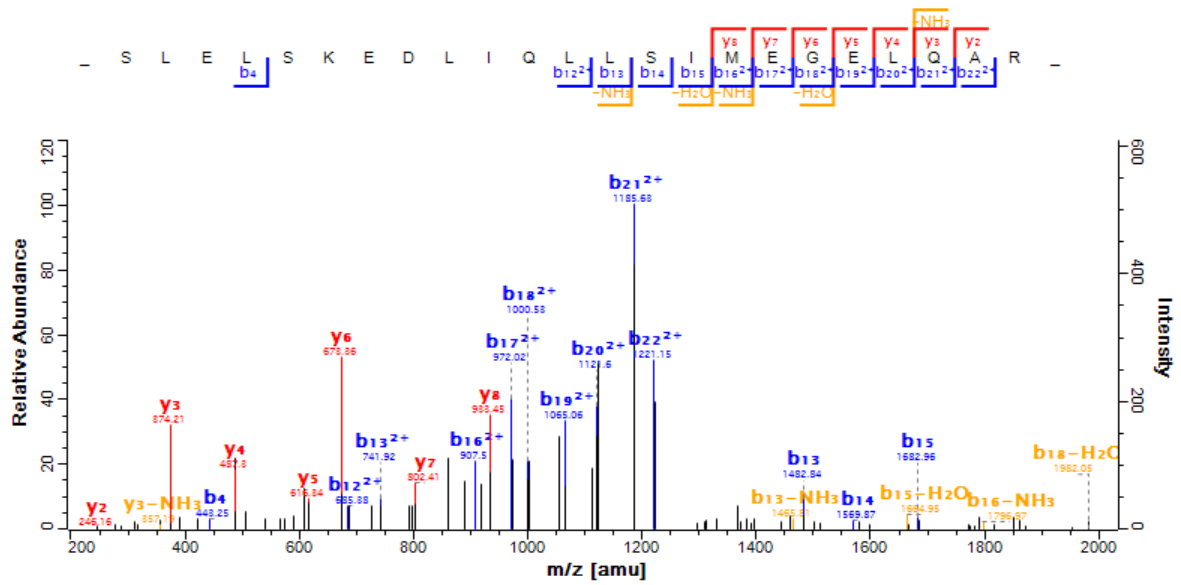
Protein Group ID: 2645
Protein Accession Numbers: Q7Z7A3
Gene Names: CTU1
Peptide Sequence: PSAVLDLVHSAER
Total Number of Spectra: 5
Number of Replicates (out of 10): 3
Best Match Score: 133.05
Best Match Posterior Error Probability: 3.80E-05
Best Match Spectrum:

Scan number 3009 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac23
Method ITMS; CID **Genenames** CTU1



Protein Group ID: 2646
Protein Accession Numbers: Q7Z7B0; Q7Z7B0-2
Gene Names: FILIP1
Peptide Sequence: SLESKEDLIQLLSIMEGELQAR
Total Number of Spectra: 4
Number of Replicates (out of 10): 3
Best Match Score: 92.492
Best Match Posterior Error Probability: 2.76E-05
Best Match Spectrum:

Scan number 8539 **Raw file** Prt-OGE-Batch2-Mock-Frac1 8
Method ITMS; CID **Genenames** FILIP1



Protein Group ID: 2648

Protein Accession Numbers: Q7Z7G8; Q7Z7G8-6; Q7Z7G8-2

Gene Names: VPS13B

Peptide Sequence: SILCDINEFSLK

Total Number of Spectra: 5

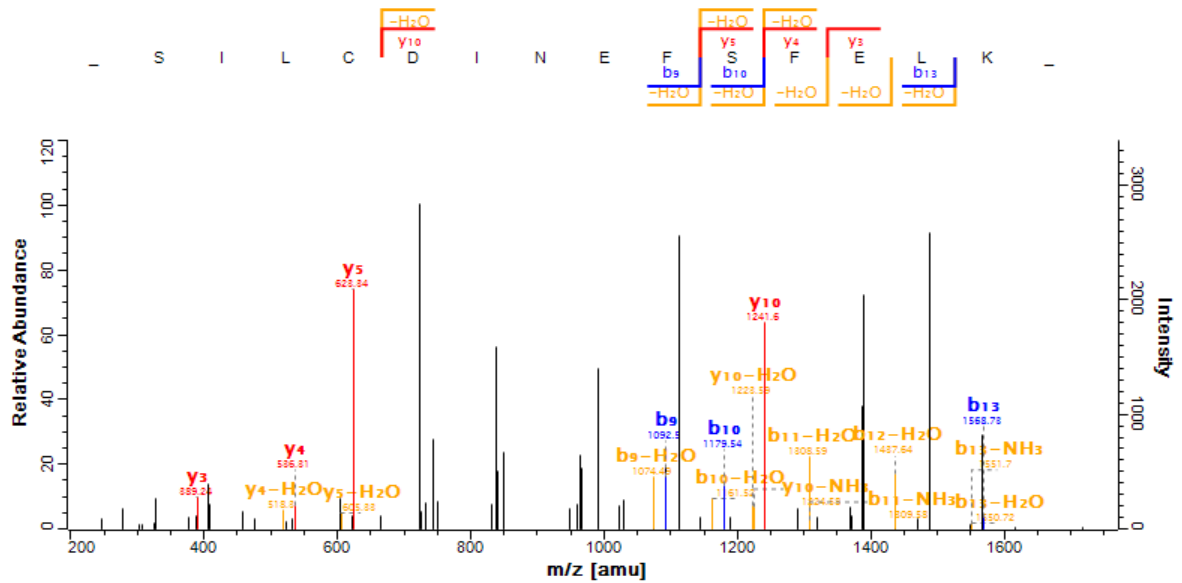
Number of Replicates (out of 10): 3

Best Match Score: 84.365

Best Match Posterior Error Probability: 0.0010909

Best Match Spectrum:

Scan number	5036	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac19
Method	ITMS; CID	Genenames	VPS13B



Protein Group ID: 2652

Protein Accession Numbers: Q86SQ4-3; Q86SQ4-4; Q86SQ4; Q86SQ4-2

Gene Names: GPR126

Peptide Sequence: TGLFQDVGPQR

Total Number of Spectra: 3

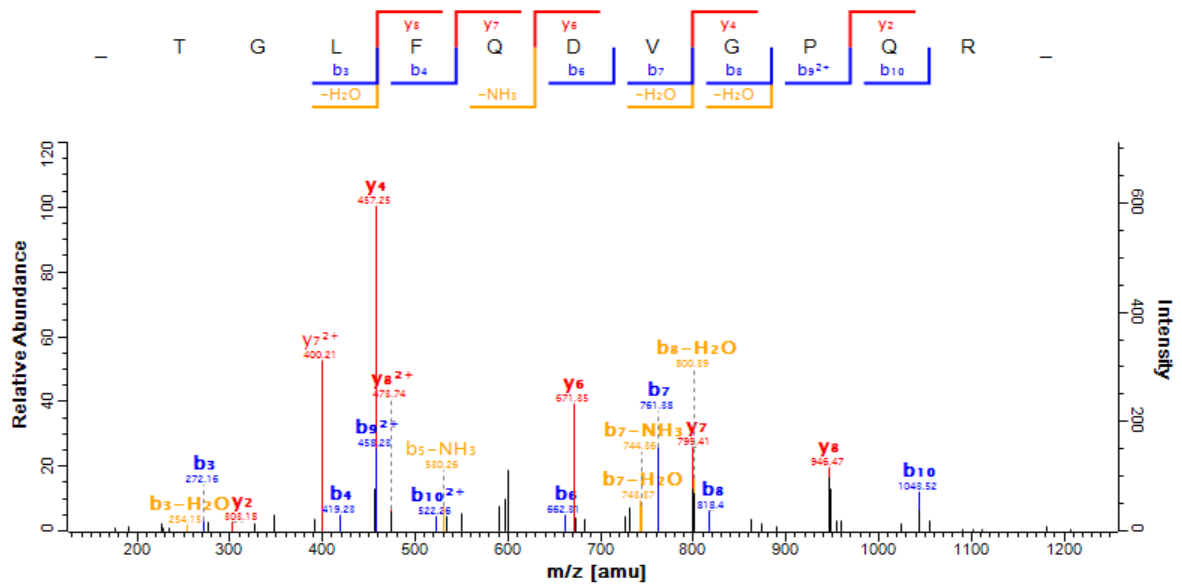
Number of Replicates (out of 10): 2

Best Match Score: 120.77

Best Match Posterior Error Probability: 9.38E-05

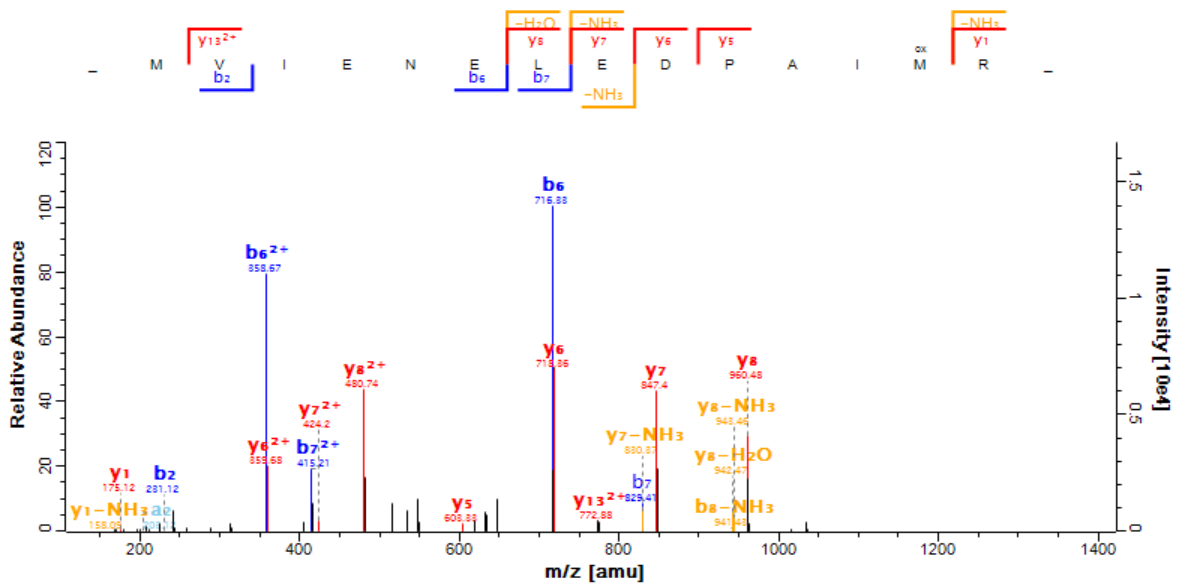
Best Match Spectrum:

Scan number	2815	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac2
Method	ITMS; CID	Genenames	GPR126



Protein Group ID: 2654
Protein Accession Numbers: Q86TB9; Q86TB9-4
Gene Names: PATL1
Peptide Sequence: MVIENELEDPAIMR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 86.772
Best Match Posterior Error Probability: 0.016099
Best Match Spectrum:

Scan number 4545 **Raw file** OGE-WT-Frac14
Method ITMS; CID **Genenames** PATL1



Protein Group ID: 2655

Protein Accession Numbers: Q86TI2-2; Q86TI2; Q86TI2-4

Gene Names: DPP9

Peptide Sequence: LAEFQTDSQGK

Total Number of Spectra: 3

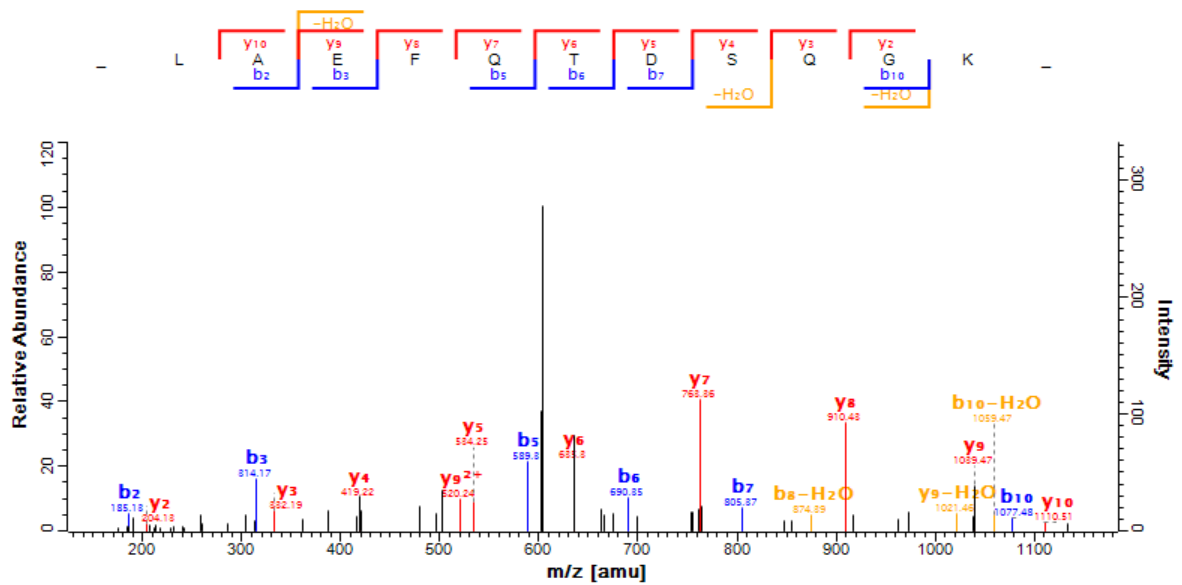
Number of Replicates (out of 10): 3

Best Match Score: 90.793

Best Match Posterior Error Probability: 0.00082927

Best Match Spectrum:

Scan number 1687 **Raw file** OGE-WT-Frac15
Method ITMS; CID **Genenames** DPP9



Protein Group ID: 2664

Protein Accession Numbers: Q86V88; Q86V88-2; Q86V88-3

Gene Names: MDP1

Peptide Sequence: LAVFDLDYTLWPFVVDTHVDPFPFHK

Total Number of Spectra: 3

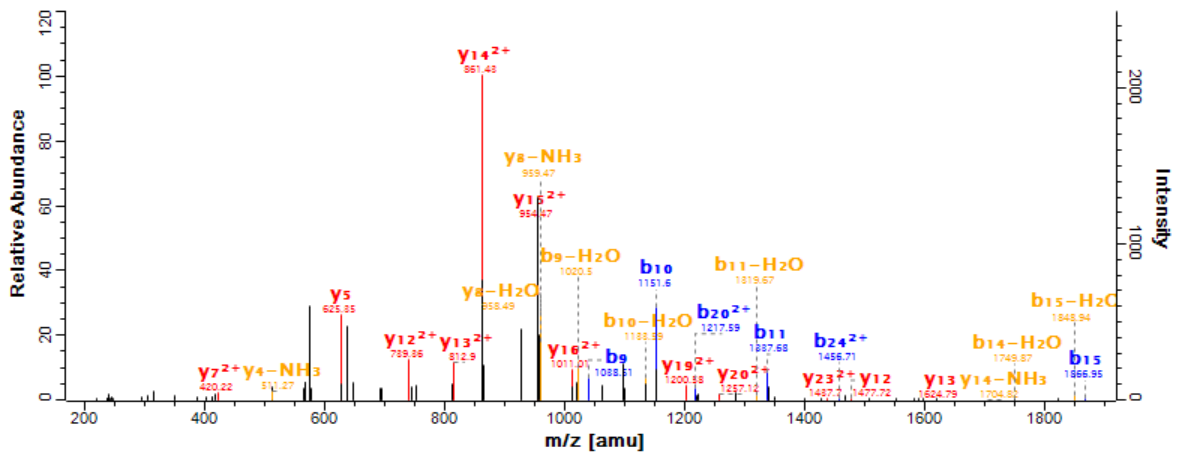
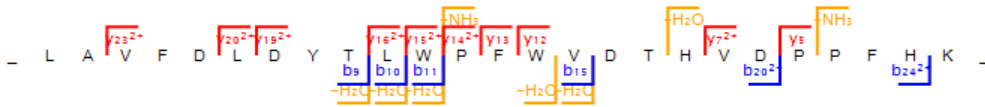
Number of Replicates (out of 10): 3

Best Match Score: 76.027

Best Match Posterior Error Probability: 1.95E-05

Best Match Spectrum:

Scan number 8231 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac13
Method ITMS; CID **Genenames** MDP1



Protein Group ID: 2667

Protein Accession Numbers: Q9UPY6; Q86VQ2; Q9Y6W5; Q9Y6W5-2

Gene Names: WASF3;WASF2

Peptide Sequence: FYTDPSYFFDLWK

Total Number of Spectra: 2

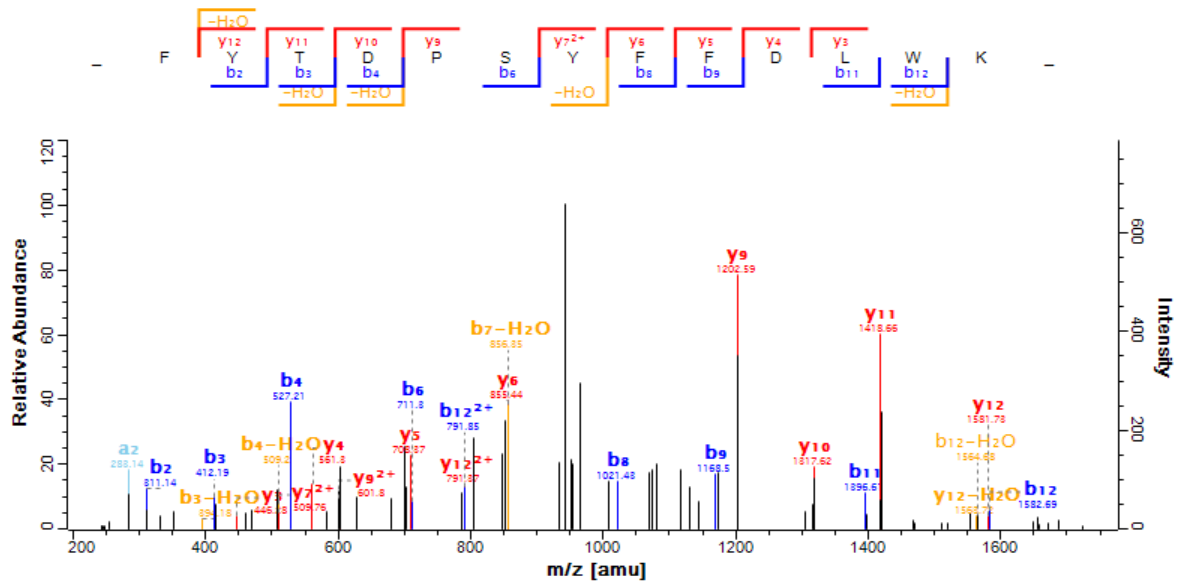
Number of Replicates (out of 10): 2

Best Match Score: 147.33

Best Match Posterior Error Probability: 1.23E-05

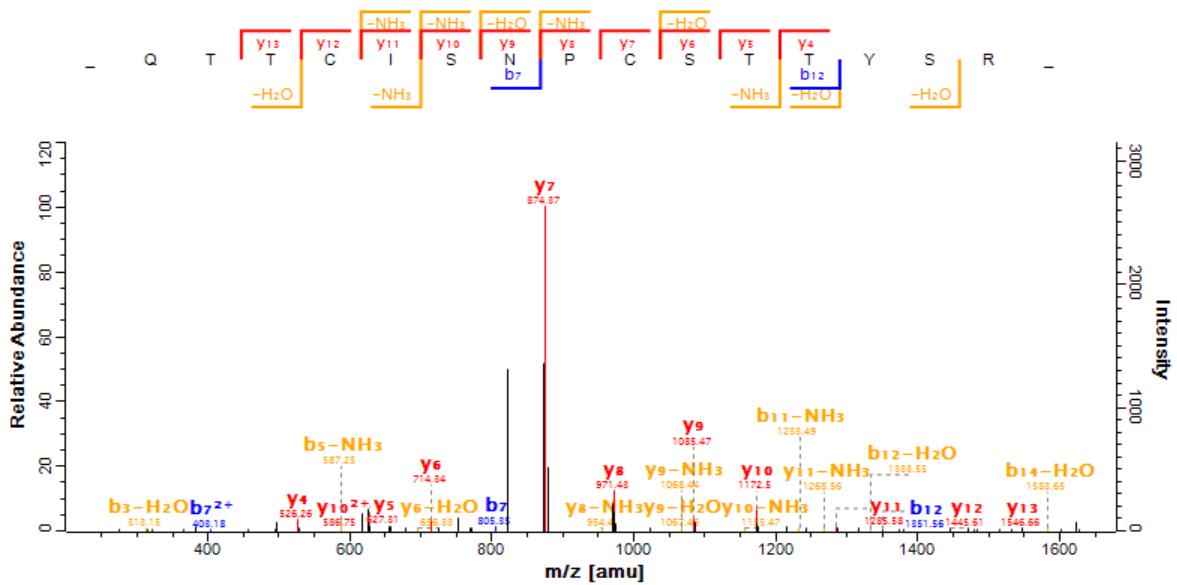
Best Match Spectrum:

Scan number	7373	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac13
Method	ITMS; CID	Genenames	WASF3;WASF2



Protein Group ID: 2681
Protein Accession Numbers: Q8IUC1
Gene Names: KRTAP11-1
Peptide Sequence: QTTCISNPCSTTYSR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 93.237
Best Match Posterior Error Probability: 0.00025643
Best Match Spectrum:

Scan number 1408 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac2
Method ITMS; CID **Genenames** KRTAP11-1



Protein Group ID: 2687

Protein Accession Numbers: Q8IVB5

Gene Names: LIX1L

Peptide Sequence: VNVVEALQEFWQMK

Total Number of Spectra: 2

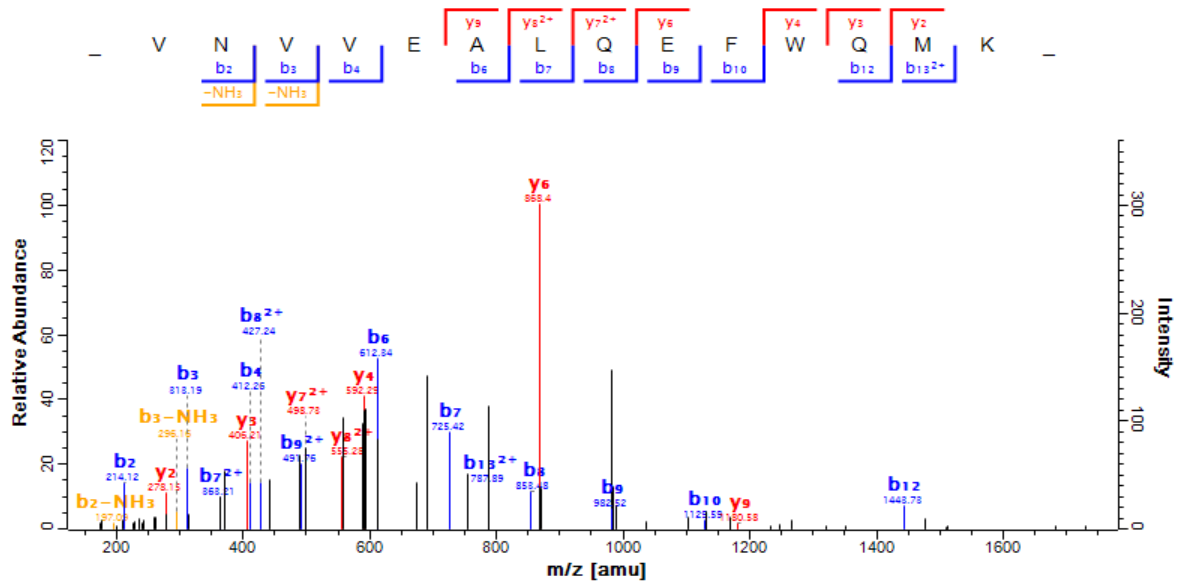
Number of Replicates (out of 10): 2

Best Match Score: 101.43

Best Match Posterior Error Probability: 0.00031543

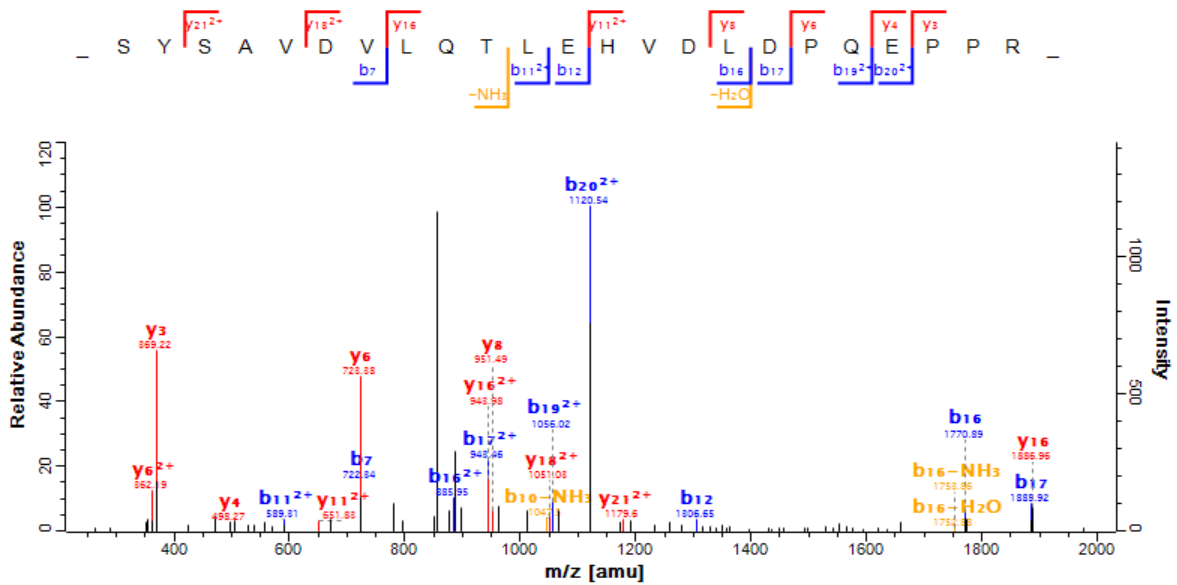
Best Match Spectrum:

Scan number	7345	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac20
Method	ITMS; CID	Genenames	LIX1L



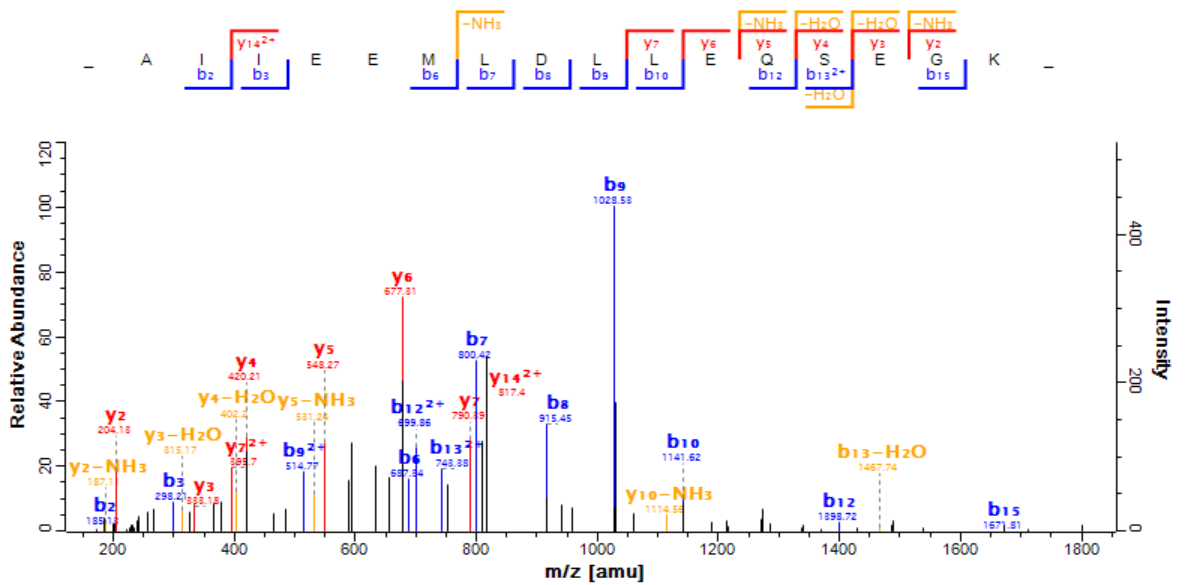
Protein Group ID: 2691
Protein Accession Numbers: Q8IVS2
Gene Names: MCAT
Peptide Sequence: SYSAVDVLQTLQLEHVDLDPQEP
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 74.776
Best Match Posterior Error Probability: 0.00029886
Best Match Spectrum:

Scan number 5570 **Raw file** Prt-OGE-Batch2-WT-Frac18
Method ITMS; CID **Genenames** MCAT



Protein Group ID: 2692
Protein Accession Numbers: Q9NXJ5; Q8IVT1
Gene Names: PGPEP1
Peptide Sequence: AIIEMLDLLEQSEGK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 117.08
Best Match Posterior Error Probability: 0.00012222
Best Match Spectrum:

Scan number 8175 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac10
Method ITMS; CID **Genenames** PGPEP1



Protein Group ID: 2694

Protein Accession Numbers: Q8IVU3; Q8IVU3-2; Q8IVU3-3

Gene Names: HERC6

Peptide Sequence: GELPEPIQALETLVSDLVSYCGK

Total Number of Spectra: 1

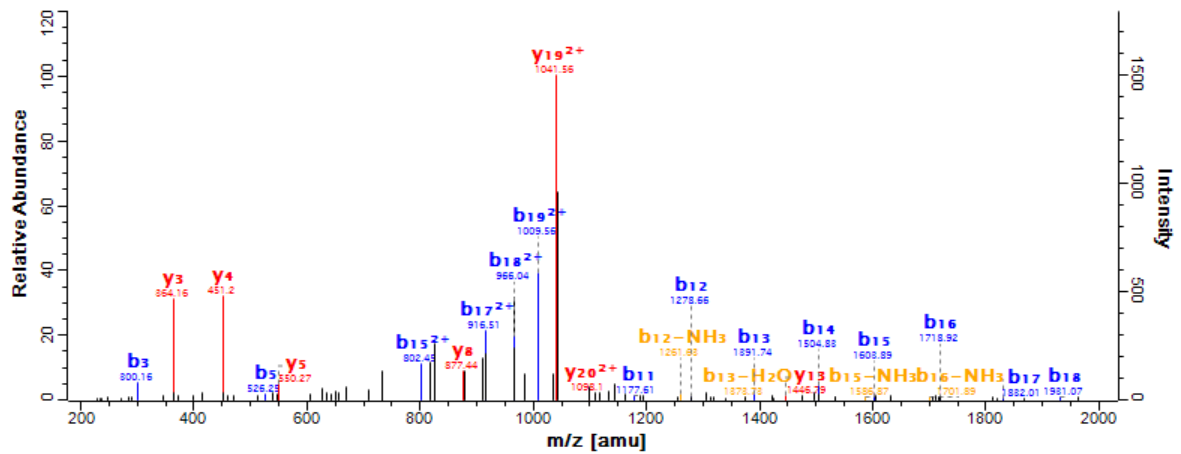
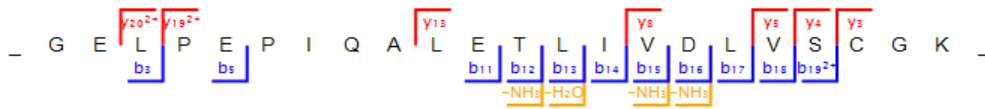
Number of Replicates (out of 10): 1

Best Match Score: 101.17

Best Match Posterior Error Probability: 5.40E-06

Best Match Spectrum:

Scan number	9945	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac19
Method	ITMS; CID	Genenames	HERC6



Protein Group ID: 2700

Protein Accession Numbers: Q8IXQ3

Gene Names: C9orf40

Peptide Sequence: EDHGLETGDPPPLPPPPVLPGPGEELPGAR

Total Number of Spectra: 4

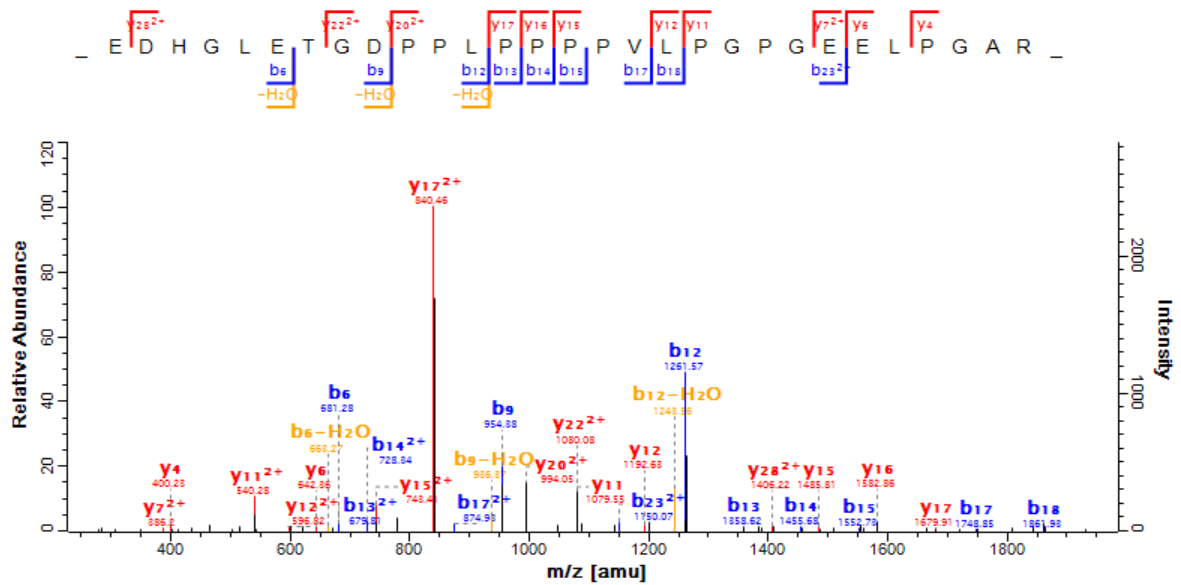
Number of Replicates (out of 10): 4

Best Match Score: 115.88

Best Match Posterior Error Probability: 2.44E-18

Best Match Spectrum:

Scan number 3882 **Raw file** Prt-OGE-Batch3-WT-Frac2
Method ITMS; CID **Genenames** C9orf40



Protein Group ID: 2712

Protein Accession Numbers: Q8N1A6

Gene Names: C4orf33

Peptide Sequence: SFNFNTLLGEEWKLWLIK

Total Number of Spectra: 1

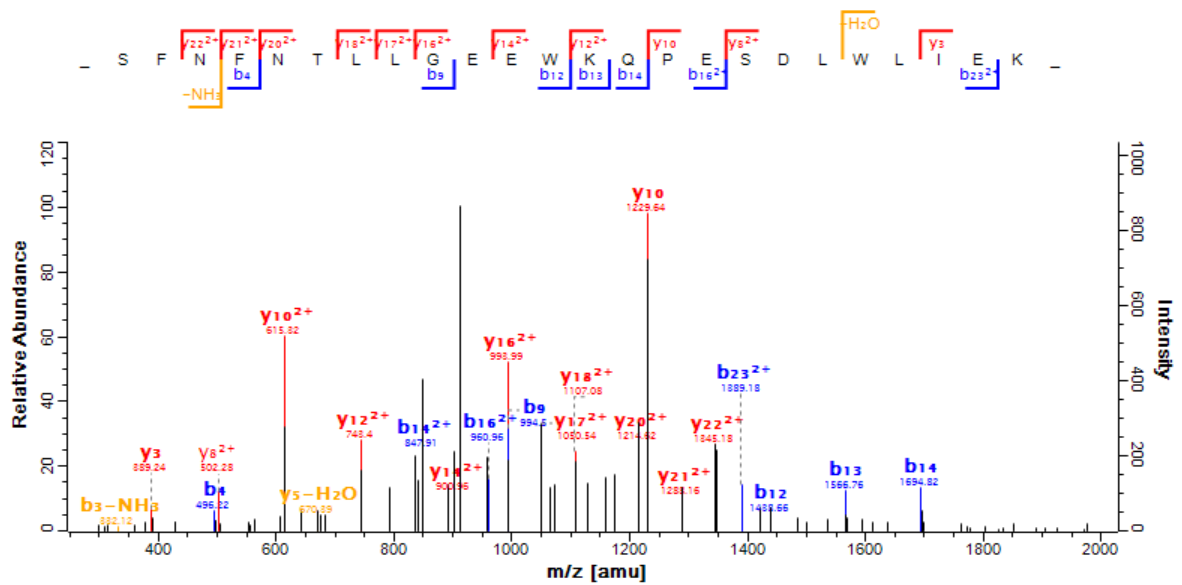
Number of Replicates (out of 10): 1

Best Match Score: 89.028

Best Match Posterior Error Probability: 1.85E-05

Best Match Spectrum:

Scan number 6114 **Raw file** Prt-OGE-Batch3-WT-Frac7
Method ITMS; CID **Genenames** C4orf33



Protein Group ID: 2715

Protein Accession Numbers: Q8N3V7; Q8N3V7-2; Q8N3V7-3

Gene Names: SYNPO

Peptide Sequence: VTPNPDLLDLVQTAEK

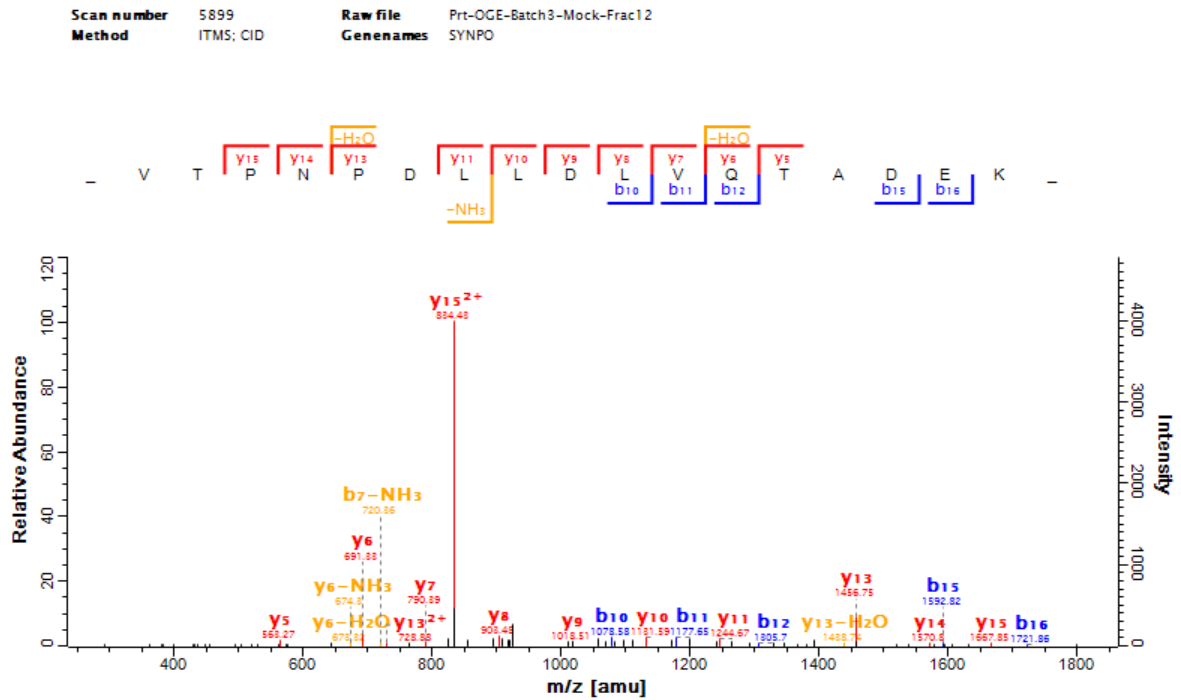
Total Number of Spectra: 1

Number of Replicates (out of 10): 1

Best Match Score: 98.796

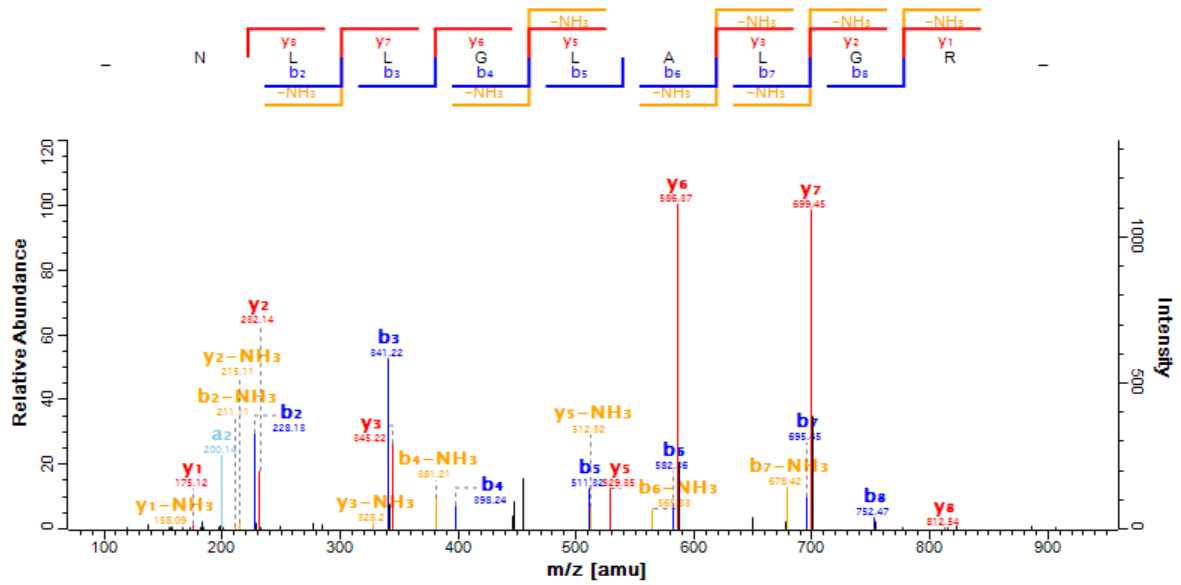
Best Match Posterior Error Probability: 0.00027165

Best Match Spectrum:



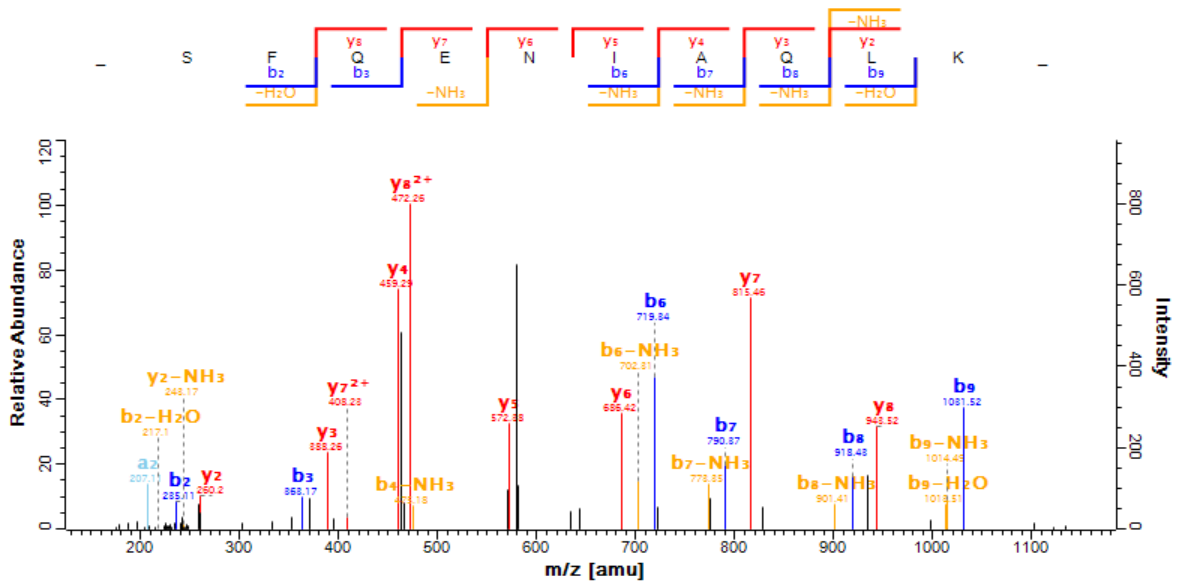
Protein Group ID: 2721
Protein Accession Numbers: Q8N5L8
Gene Names: RPP25L
Peptide Sequence: NLLGLALGR
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 176.6
Best Match Posterior Error Probability: 3.36E-07
Best Match Spectrum:

Scan number 4102 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac23
Method ITMS; CID **Genenames** RPP25L



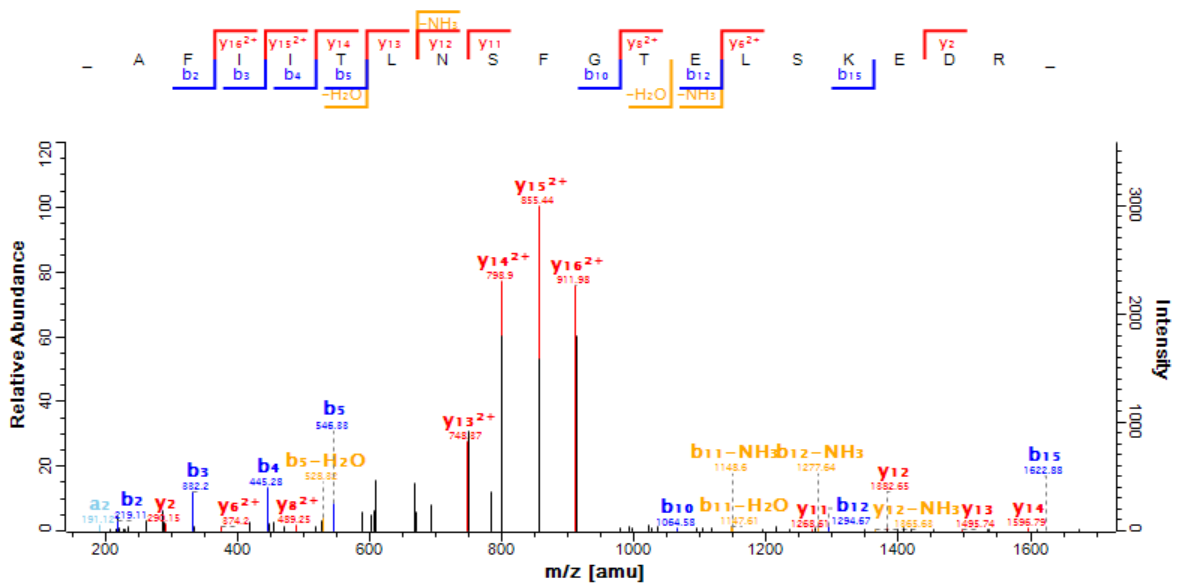
Protein Group ID: 2733
Protein Accession Numbers: Q8N8V2
Gene Names: GBP7
Peptide Sequence: SFQENIAQLK
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 156.48
Best Match Posterior Error Probability: 3.14E-05
Best Match Spectrum:

Scan number 3072 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac13
Method ITMS; CID **Genenames** GBP7



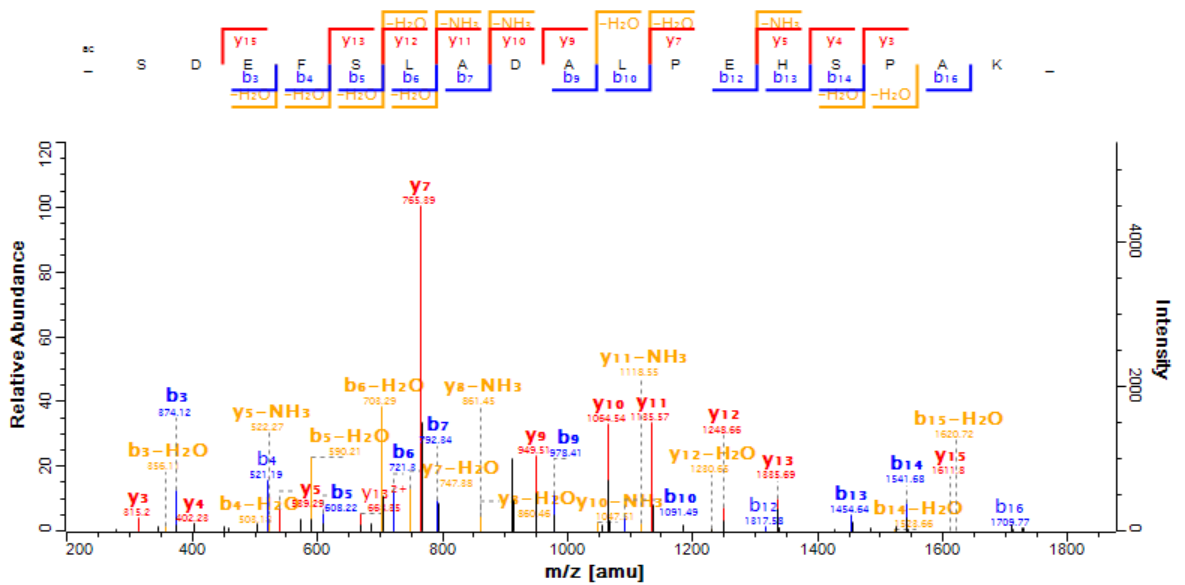
Protein Group ID: 2734
Protein Accession Numbers: Q8N8Y2
Gene Names: ATP6V0D2
Peptide Sequence: AFITLNSFGTELSKEDR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 101.42
Best Match Posterior Error Probability: 0.00073403
Best Match Spectrum:

Scan number 5410 **Raw file** Prt-OGE-Batch3--Mock-Frac5
Method ITMS; CID **Genenames** ATP6V0D2



Protein Group ID: 2749
Protein Accession Numbers: Q8NDC0
Gene Names: MAPK1IP1L
Peptide Sequence: SDEFSLADALPEHSPAK
Total Number of Spectra: 4
Number of Replicates (out of 10): 3
Best Match Score: 169.02
Best Match Posterior Error Probability: 1.81E-15
Best Match Spectrum:

Scan number 4929 **Raw file** OGE-Mock-Frac6
Method ITMS; CID **Genenames** MAPK1IP1L



Protein Group ID: 2751

Protein Accession Numbers: Q8NDI1; Q8NDI1-2; Q8NDI1-3

Gene Names: EHBP1

Peptide Sequence: EQLLLDELVALVNK

Total Number of Spectra: 22

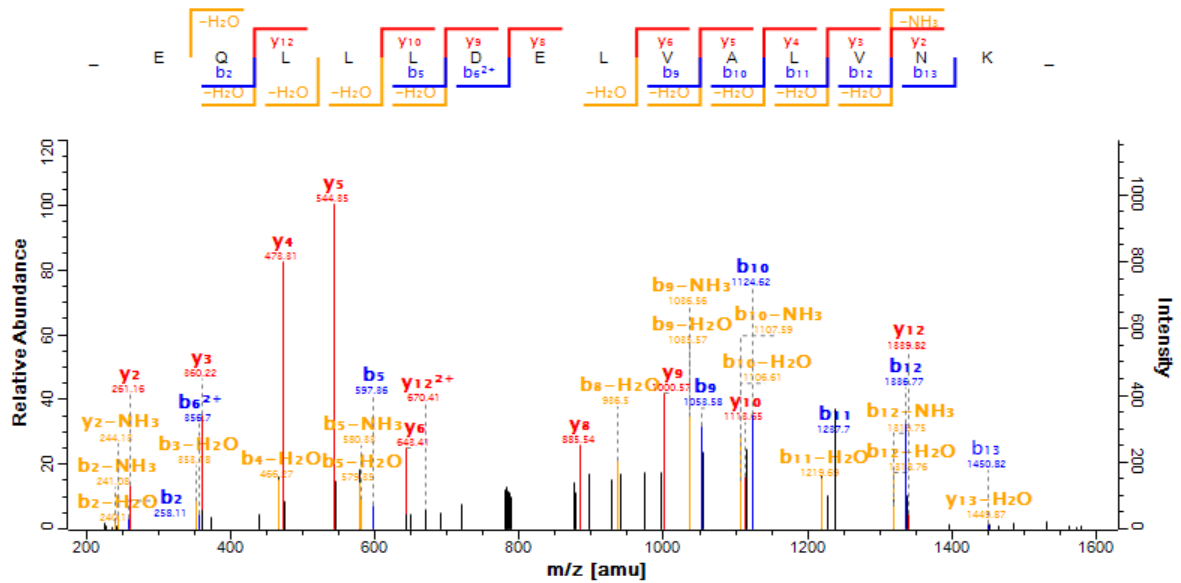
Number of Replicates (out of 10): 7

Best Match Score: 181.67

Best Match Posterior Error Probability: 4.38E-15

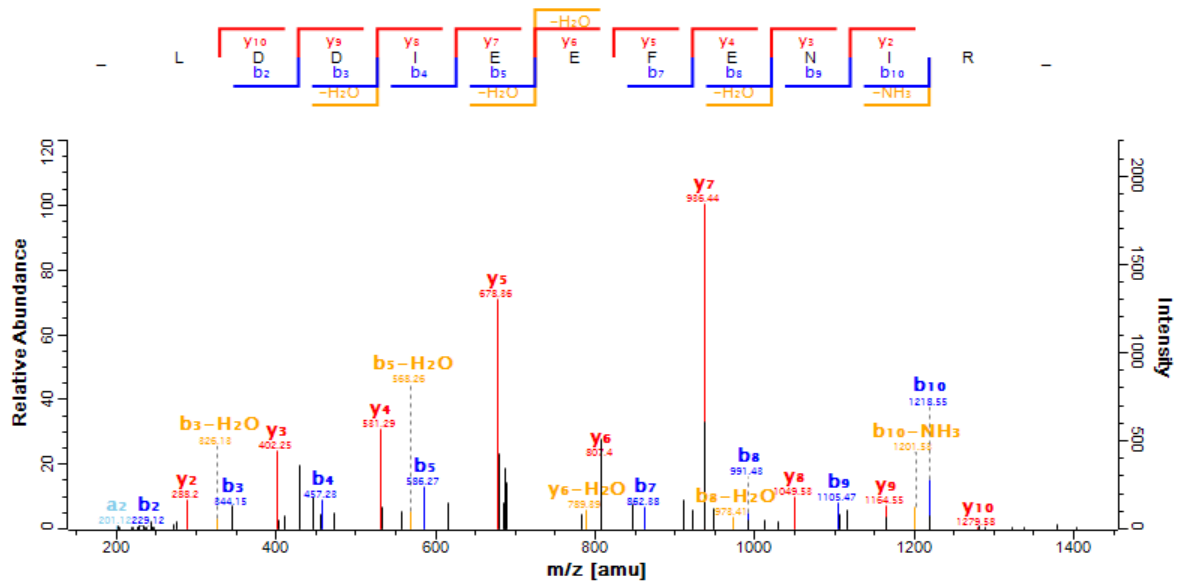
Best Match Spectrum:

Scan number 7952 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac8
Method ITMS; CID **Genenames** EHBP1



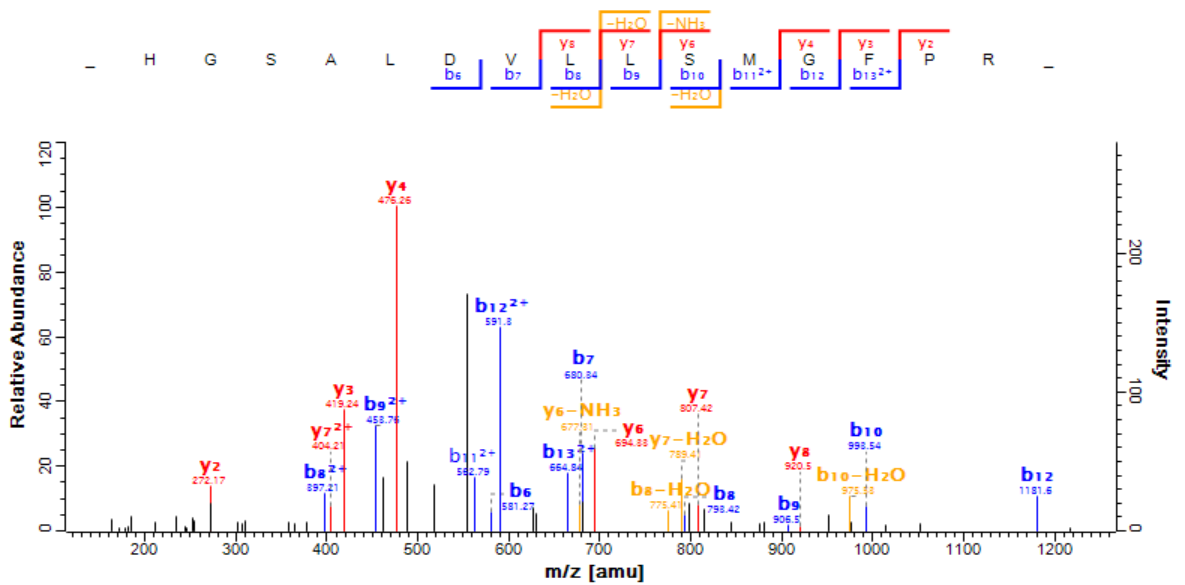
Protein Group ID: 2763
Protein Accession Numbers: Q8NHZ8
Gene Names: CDC26
Peptide Sequence: LDDIEEFENIR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 140.14
Best Match Posterior Error Probability: 1.60E-05
Best Match Spectrum:

Scan number 4186 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac11
Method ITMS; CID **Genenames** CDC26



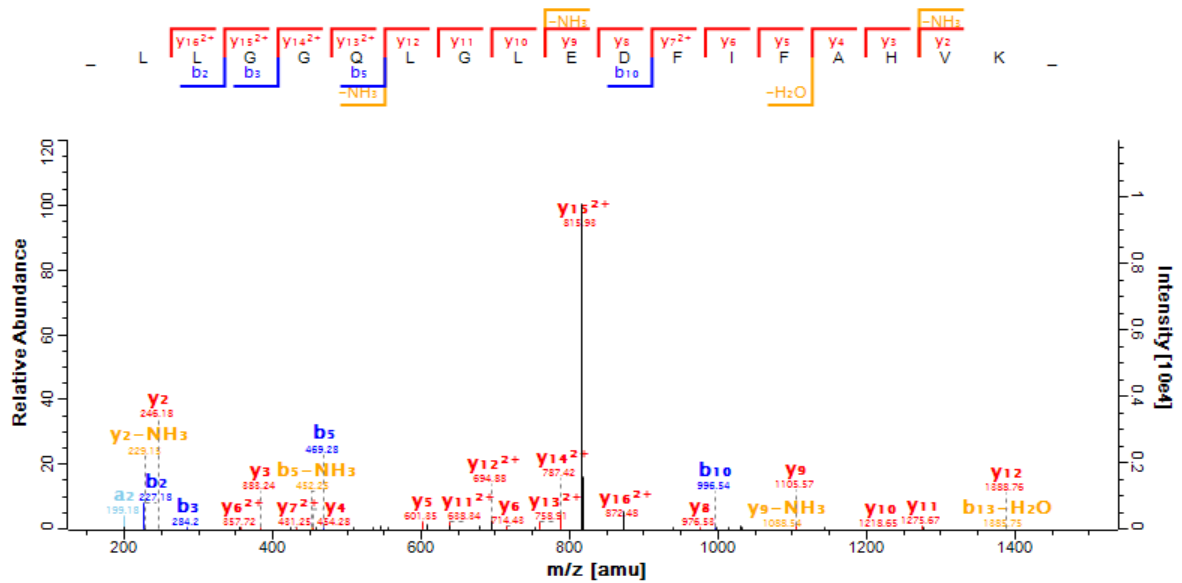
Protein Group ID: 2782
Protein Accession Numbers: Q8TF42
Gene Names: UBASH3B
Peptide Sequence: HGSALDVLLSMGFPR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 115.34
Best Match Posterior Error Probability: 5.43E-05
Best Match Spectrum:

Scan number 7160 **Raw file** Prt-OGE-Batch2-Mock-Frac15
Method ITMS; CID **Genenames** UBASH3B



Protein Group ID: 2783
Protein Accession Numbers: Q8TF65
Gene Names: GIPC2
Peptide Sequence: LLGGQLGLEDFIFAHVK
Total Number of Spectra: 8
Number of Replicates (out of 10): 8
Best Match Score: 123.76
Best Match Posterior Error Probability: 9.08E-05
Best Match Spectrum:

Scan number 6382 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac13
Method ITMS; CID **Genenames** GIPC2



Protein Group ID: 2786

Protein Accession Numbers: Q8WUA8

Gene Names: TSKU

Peptide Sequence: YLSLDGNPLAVIGPGAFAGLGGGLTHLSLASLQR

Total Number of Spectra: 1

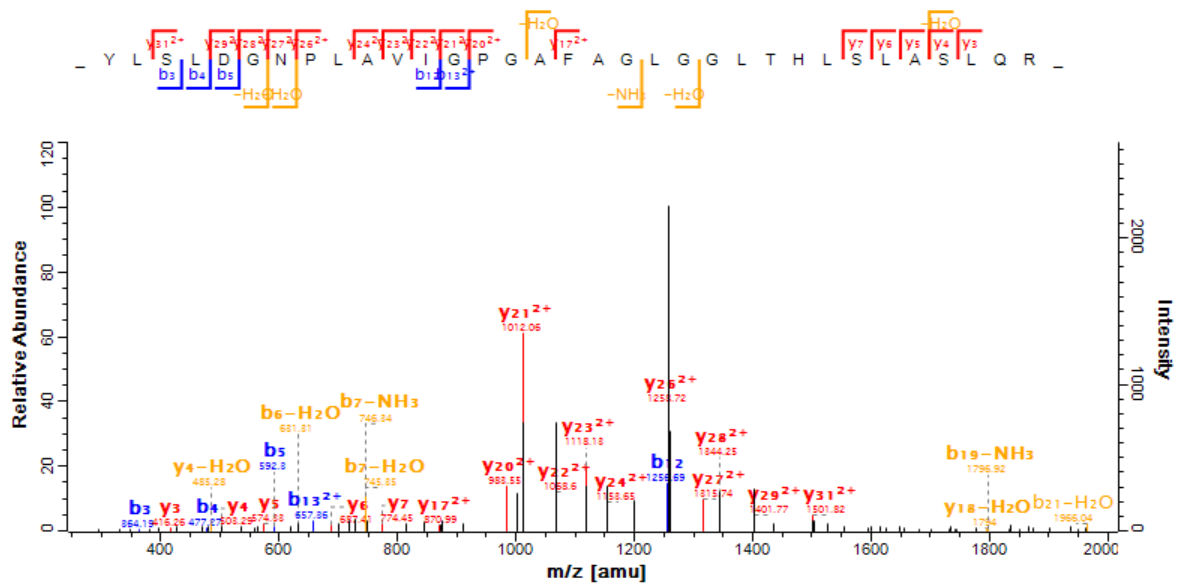
Number of Replicates (out of 10): 1

Best Match Score: 52.96

Best Match Posterior Error Probability: 0.00032262

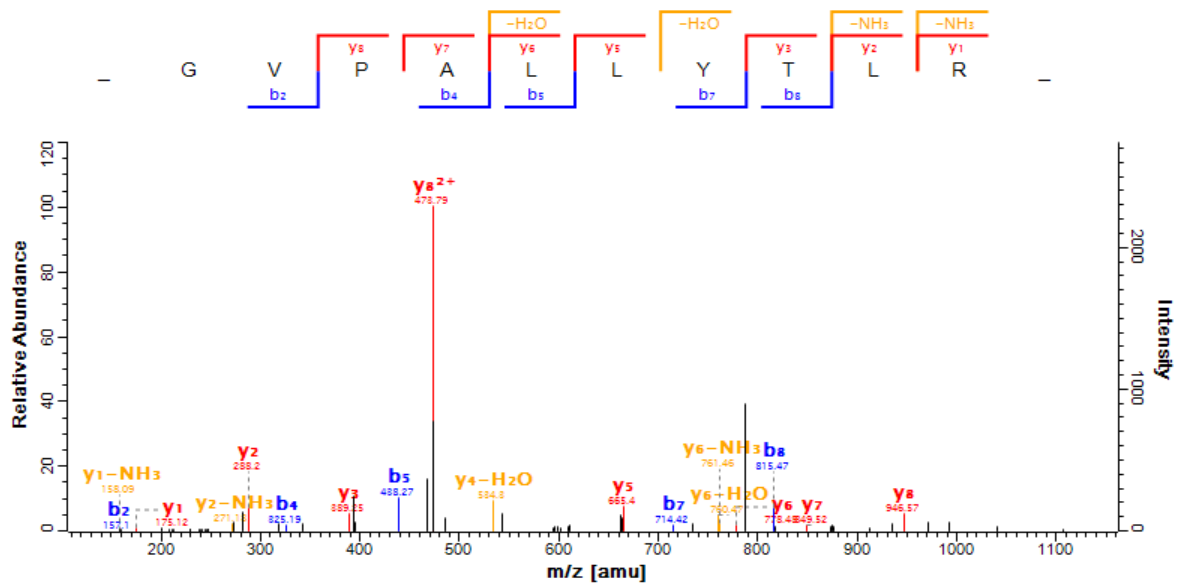
Best Match Spectrum:

Scan number 8484 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac15
Method ITMS; CID **Genenames** TSKU



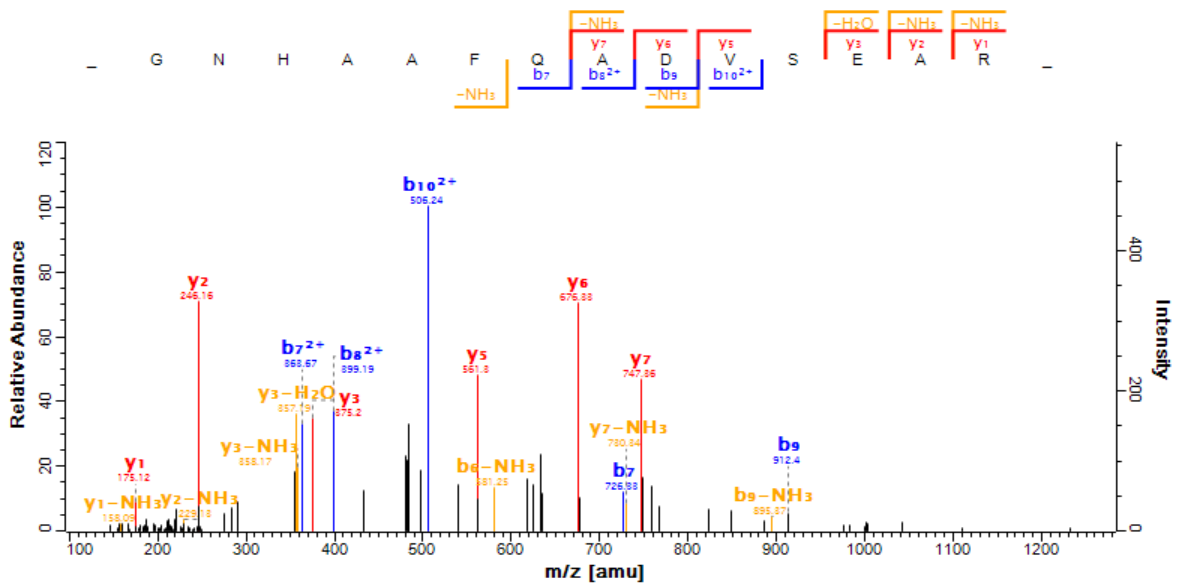
Protein Group ID: 2790
Protein Accession Numbers: Q8WV74; Q8WV74-2
Gene Names: NUDT8
Peptide Sequence: GVPALLYLTYLR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 85.533
Best Match Posterior Error Probability: 0.001677
Best Match Spectrum:

Scan number 4701 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac20
Method ITMS; CID **Genenames** NUDT8



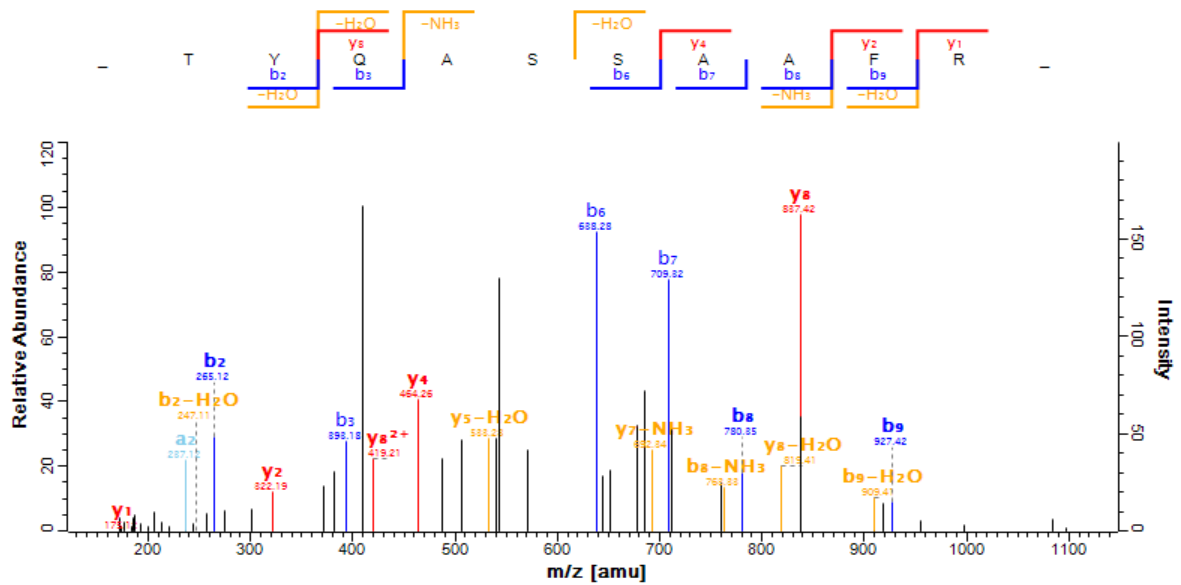
Protein Group ID: 2808
Protein Accession Numbers: Q92506
Gene Names: HSD17B8
Peptide Sequence: GNHAAFQADVSEAR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 81.565
Best Match Posterior Error Probability: 0.0014588
Best Match Spectrum:

Scan number 1378 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac13
Method ITMS; CID **Genenames** HSD17B8



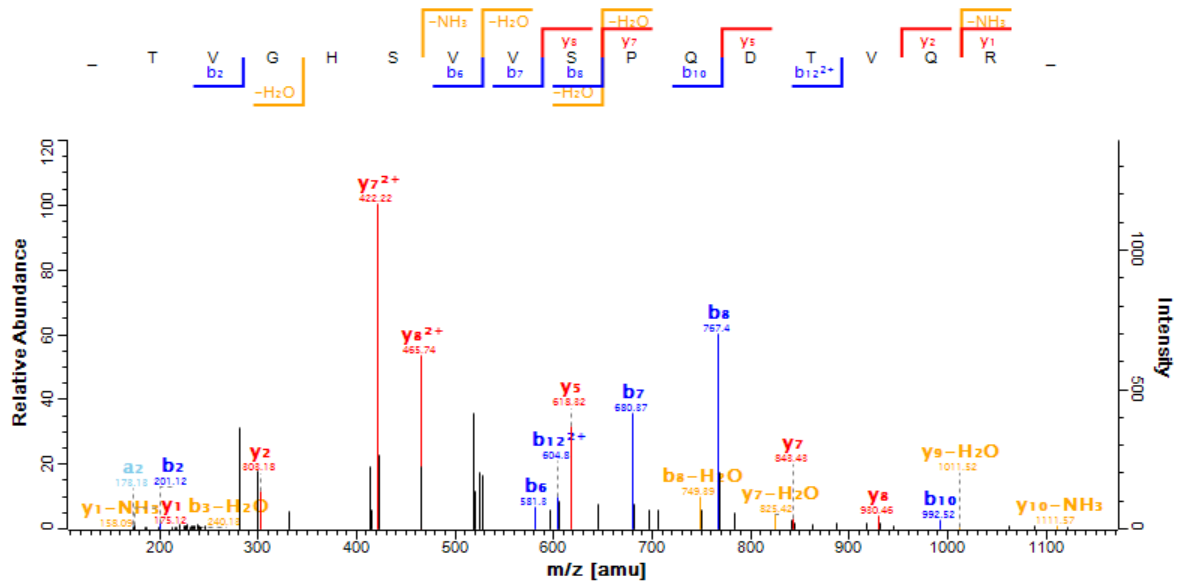
Protein Group ID: 2811
Protein Accession Numbers: Q92567; Q92567-2
Gene Names: FAM168A
Peptide Sequence: TYQASSAAFR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 85.288
Best Match Posterior Error Probability: 0.001731
Best Match Spectrum:

Scan number	1740	Raw file	Prt-OGE-Batch2-Mock-Frac20
Method	ITMS; CID	Genenames	FAM168A



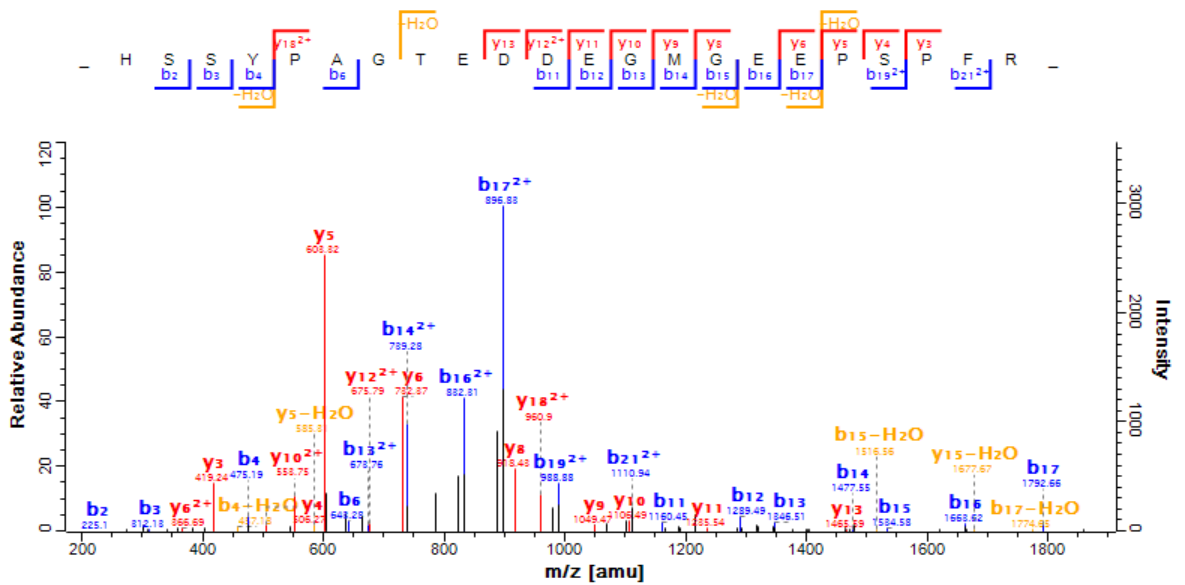
Protein Group ID: 2825
Protein Accession Numbers: Q92871
Gene Names: PMM1
Peptide Sequence: TVGHSVSPQDTVQR
Total Number of Spectra: 3
Number of Replicates (out of 10): 2
Best Match Score: 89.231
Best Match Posterior Error Probability: 0.0003648
Best Match Spectrum:

Scan number 1558 **Raw file** Prt-OGE-Batch3--Mock-Frac9
Method ITMS; CID **Genenames** PMM1



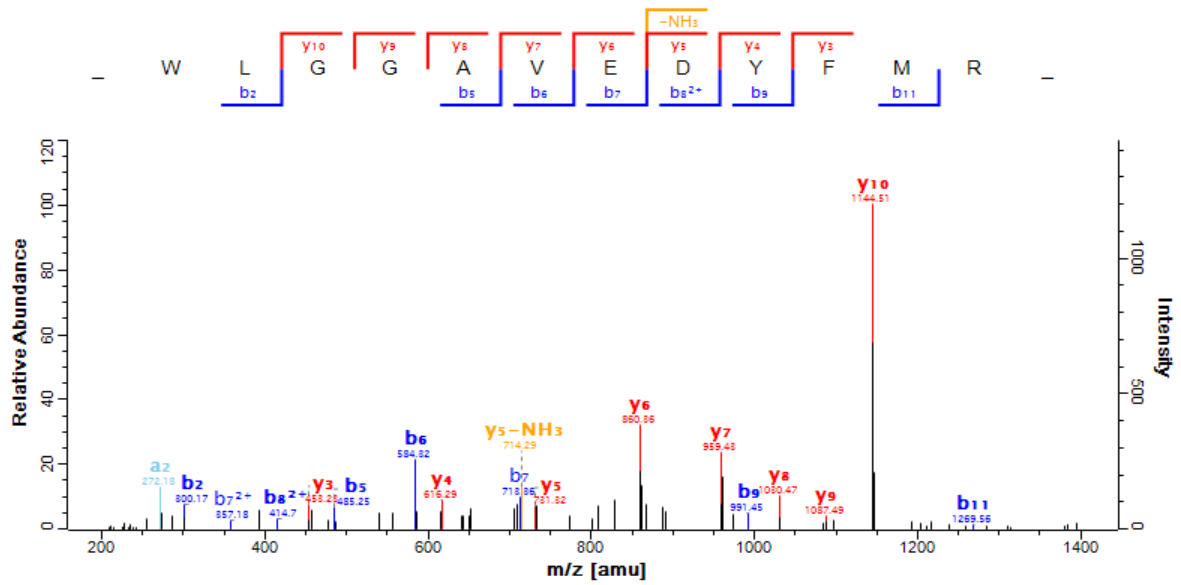
Protein Group ID: 2833
Protein Accession Numbers: Q92934
Gene Names: BAD
Peptide Sequence: HSSYPAGTEDDEGMGEEPSFR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 185.85
Best Match Posterior Error Probability: 2.32E-39
Best Match Spectrum:

Scan number 3358 **Raw file** Prt-OGE-Batch3--Mock-Frac13
Method ITMS; CID **Genenames** BAD



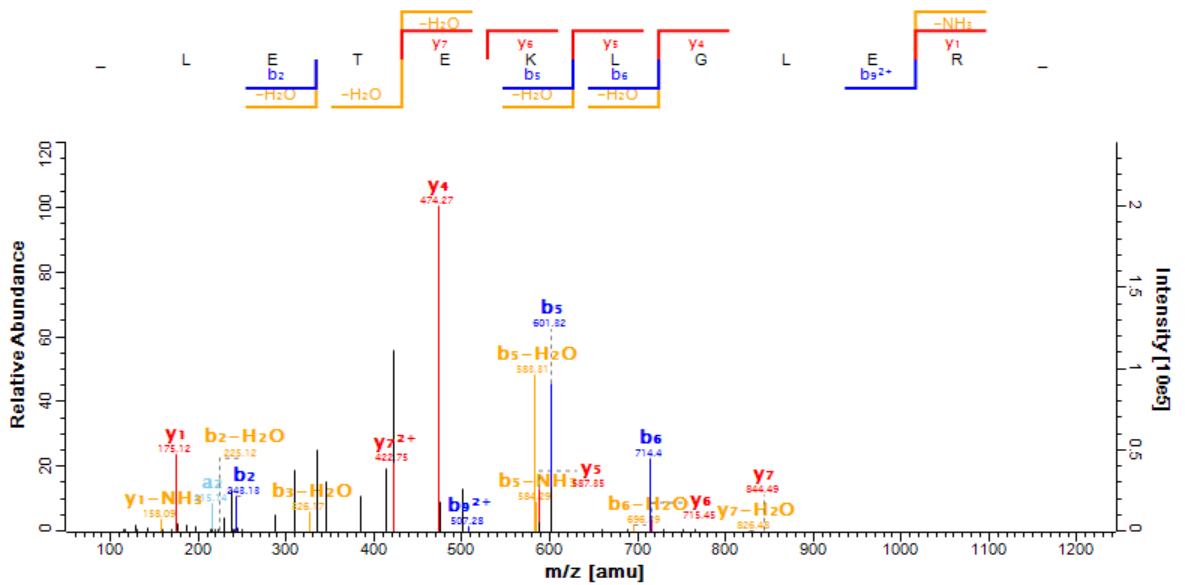
Protein Group ID: 2839
Protein Accession Numbers: Q969E8
Gene Names: TSR2
Peptide Sequence: WLGGAVEDYFM R
Total Number of Spectra: 15
Number of Replicates (out of 10): 8
Best Match Score: 132.76
Best Match Posterior Error Probability: 0.00013304
Best Match Spectrum:

Scan number 5908 **Raw file** Prt-OGE-Batch2-Mock-Frac5
Method ITMS; CID **Genenames** TSR2



Protein Group ID: 2846
Protein Accession Numbers: Q96A19
Gene Names: CCDC102A
Peptide Sequence: LETEKLGLER
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 105.2
Best Match Posterior Error Probability: 0.0014538
Best Match Spectrum:

Scan number 2656 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac9
Method ITMS; CID **Genenames** CCDC102A



Protein Group ID: 2862

Protein Accession Numbers: Q96BN8

Gene Names: FAM105B

Peptide Sequence: ATLFQAMSQAVGLPPWLQDPELMLLPK

Total Number of Spectra: 5

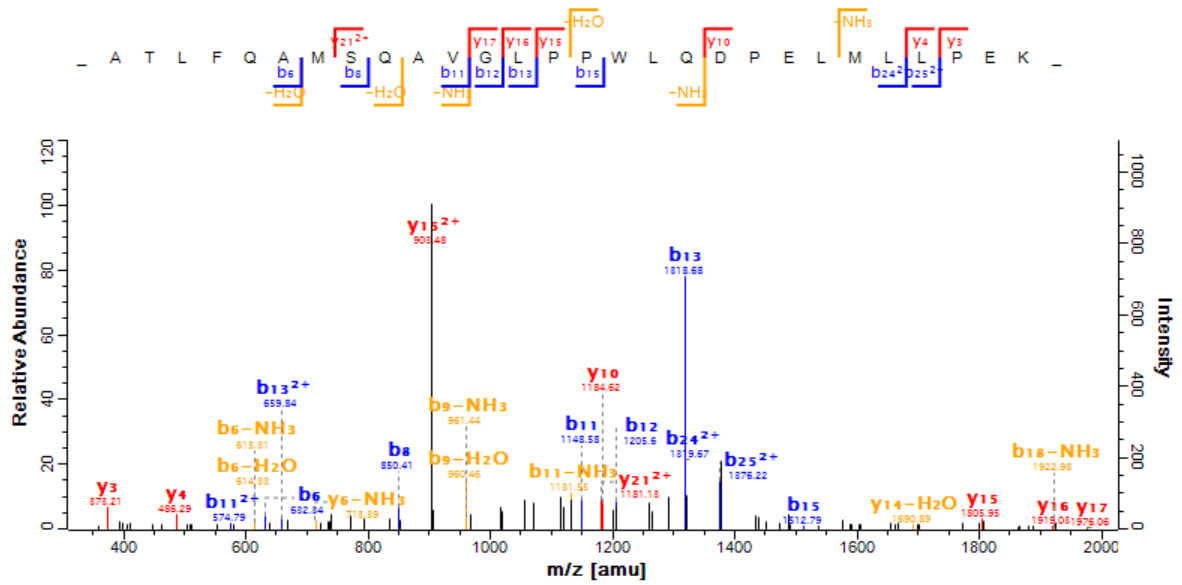
Number of Replicates (out of 10): 4

Best Match Score: 84.404

Best Match Posterior Error Probability: 6.98E-07

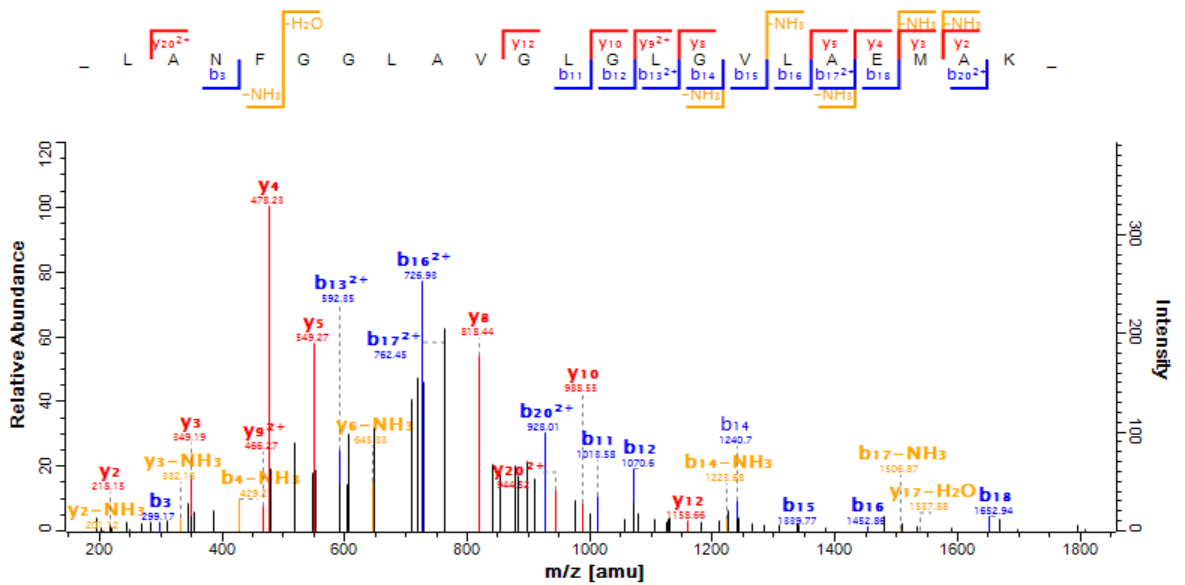
Best Match Spectrum:

Scan number 8735 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac9
Method ITMS; CID **Genenames** FAM105B



Protein Group ID: 2878
Protein Accession Numbers: Q96D53; Q96D53-2
Gene Names: ADCK4
Peptide Sequence: LANFGGLAVGLGLGVLAEMAK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 93.381
Best Match Posterior Error Probability: 4.08E-05
Best Match Spectrum:

Scan number 8418 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac14
Method ITMS; CID **Genenames** ADCK4



Protein Group ID: 2895

Protein Accession Numbers: Q96EM0

Gene Names: C14orf149

Peptide Sequence: LPPHDPGTPVLSVVDMMHTGGEPLR

Total Number of Spectra: 1

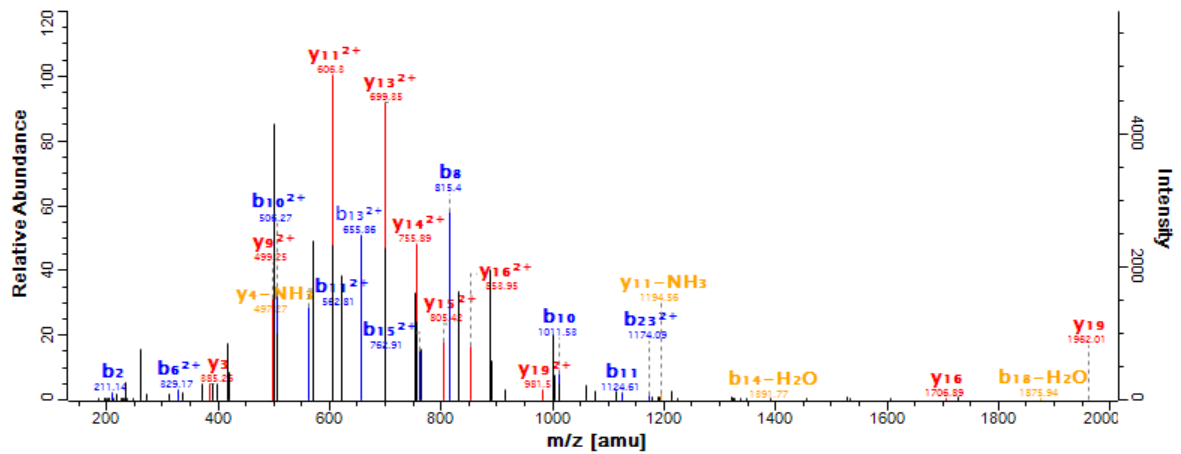
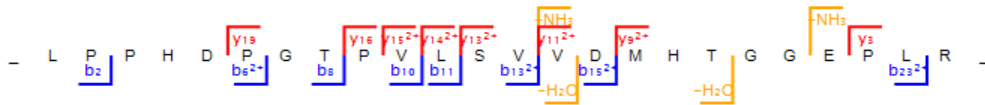
Number of Replicates (out of 10): 1

Best Match Score: 65.085

Best Match Posterior Error Probability: 0.00050949

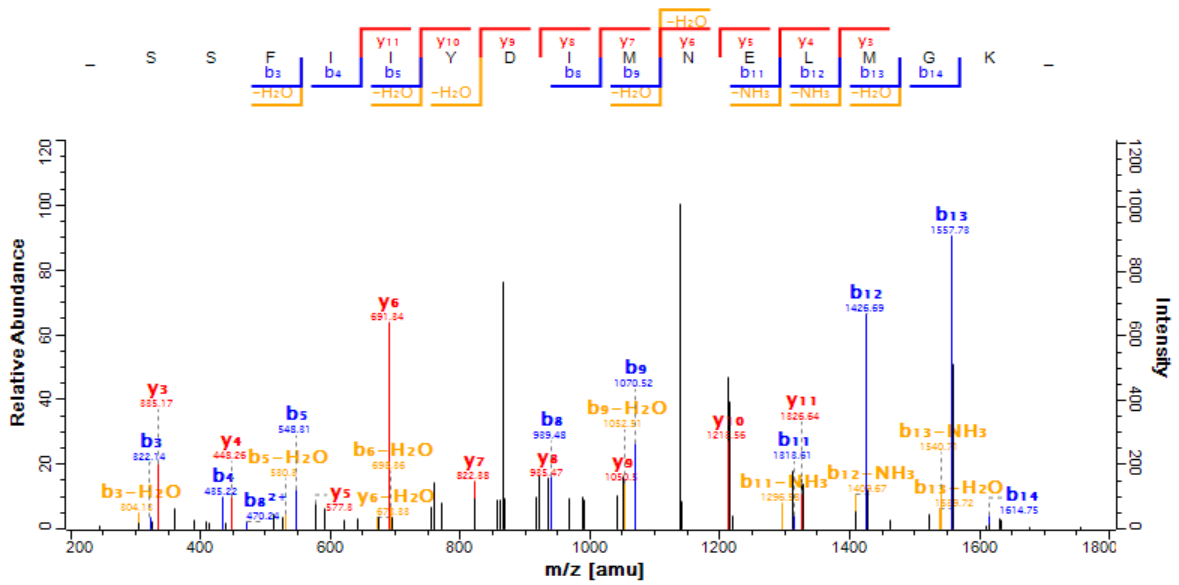
Best Match Spectrum:

Scan number	4572	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac14
Method	ITMS; CID	Genenames	C14orf149



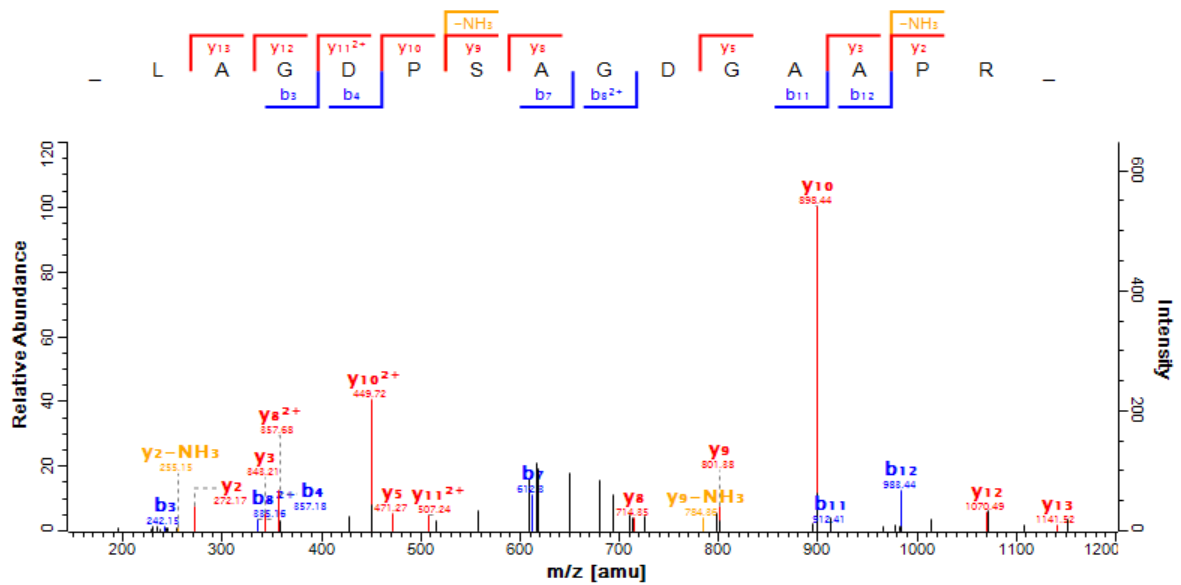
Protein Group ID: 2899
Protein Accession Numbers: Q96EY7
Gene Names: PTCD3
Peptide Sequence: SSFIIYDIMNELMGK
Total Number of Spectra: 9
Number of Replicates (out of 10): 7
Best Match Score: 139.66
Best Match Posterior Error Probability: 1.55E-06
Best Match Spectrum:

Scan number 8904 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac13
Method ITMS; CID **Genenames** PTCD3



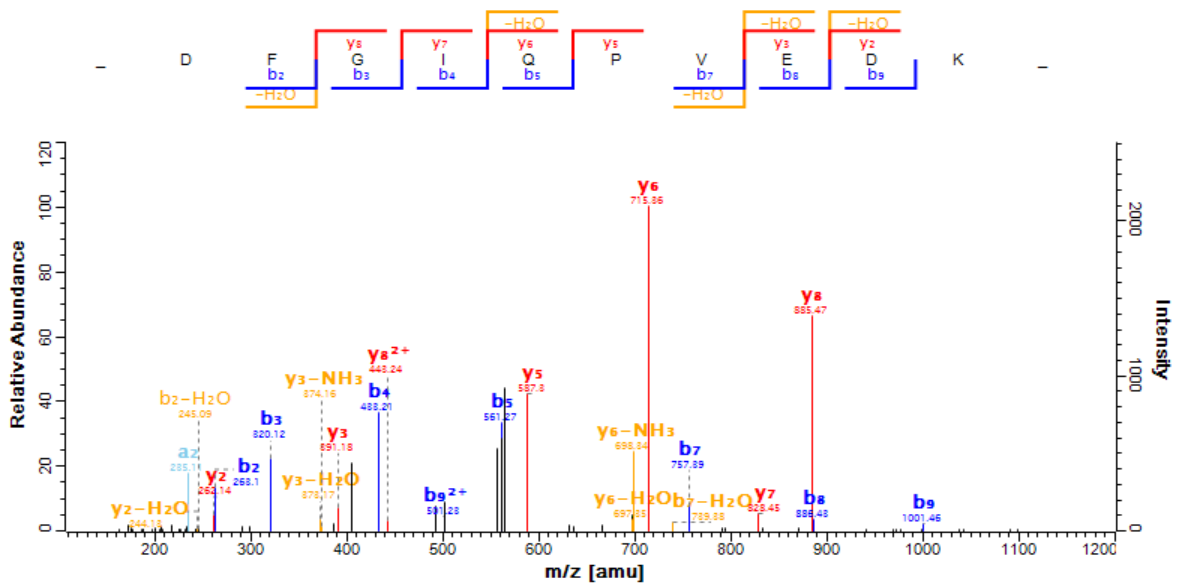
Protein Group ID: 2908
Protein Accession Numbers: Q96GD0
Gene Names: PDXP
Peptide Sequence: LAGDPSAGDGAAPR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 89.46
Best Match Posterior Error Probability: 0.00067972
Best Match Spectrum:

Scan number 801 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac14
Method ITMS; CID **Genenames** PDXP



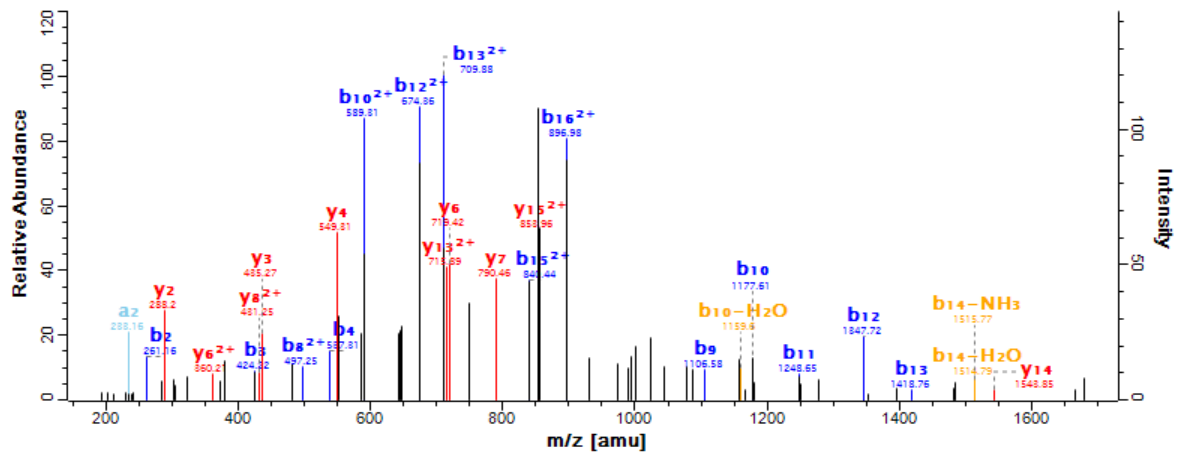
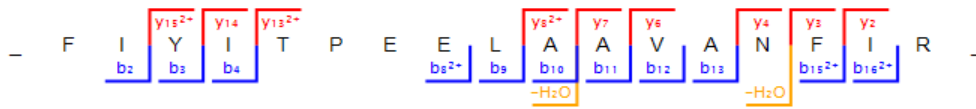
Protein Group ID: 2910
Protein Accession Numbers: Q96GX2
Gene Names: ATXN7L3B
Peptide Sequence: DFGIQPVEDK
Total Number of Spectra: 7
Number of Replicates (out of 10): 7
Best Match Score: 137.89
Best Match Posterior Error Probability: 6.66E-05
Best Match Spectrum:

Scan number 3494 **Raw file** OGE-Mock-Frac2
Method ITMS; CID **Genenames** ATXN7L3B



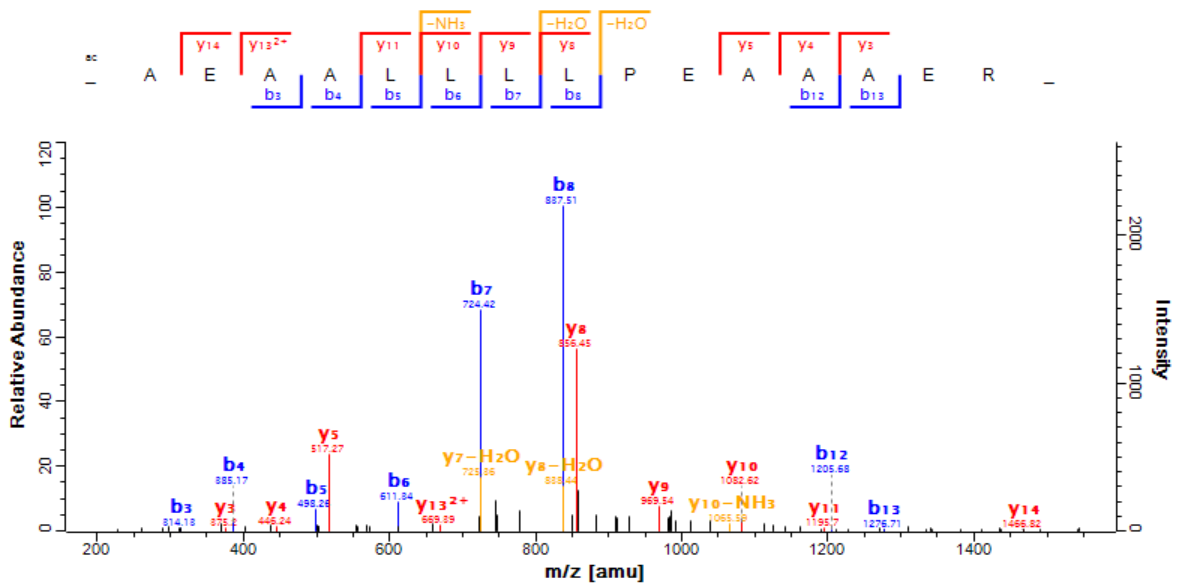
Protein Group ID: 2916
Protein Accession Numbers: Q96HY6
Gene Names: DDRGK1
Peptide Sequence: FIYTPEELAAVAVANFIR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 145.81
Best Match Posterior Error Probability: 3.59E-07
Best Match Spectrum:

Scan number 6626 **Raw file** OGE-WT-Frac5
Method ITMS; CID **Genenames** DDRGK1



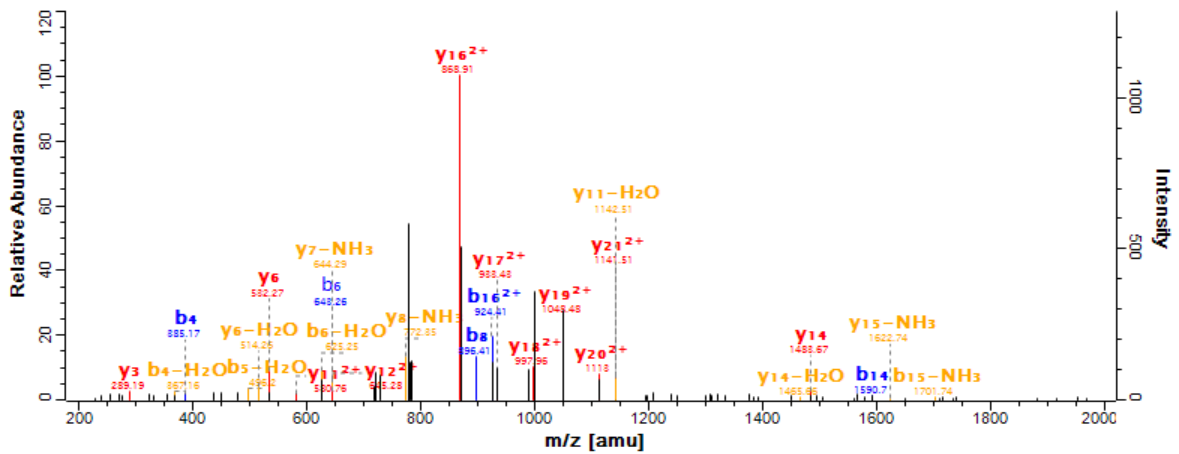
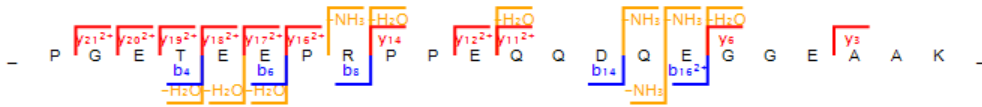
Protein Group ID: 2924
Protein Accession Numbers: Q96JB2; Q96JB2-2
Gene Names: COG3
Peptide Sequence: AEAALLLLPEAAAER
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 89.911
Best Match Posterior Error Probability: 0.00032056
Best Match Spectrum:

Scan number 5880 **Raw file** Prt-OGE-Batch3-WT-Frac9
Method ITMS; CID **Genenames** COG3



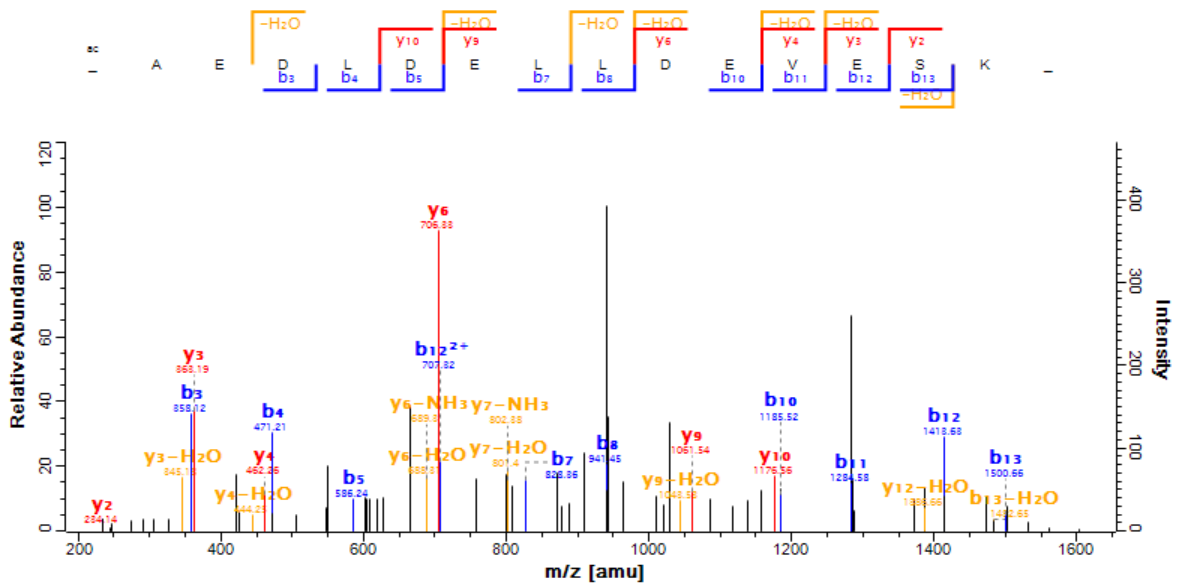
Protein Group ID: 2926
Protein Accession Numbers: Q96JP5; Q96JP5-2
Gene Names: ZFP91
Peptide Sequence: PGETEERPRPEQQDQEGGEEAAK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 75.564
Best Match Posterior Error Probability: 0.0014059
Best Match Spectrum:

Scan number 851 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac15
Method ITMS; CID **Genenames** ZFP91



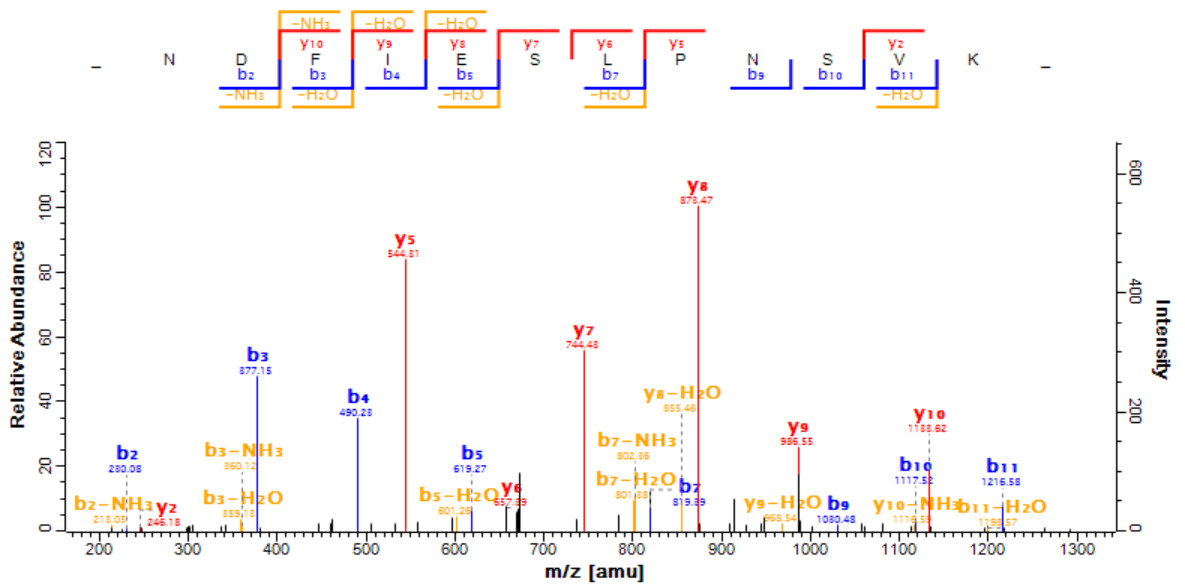
Protein Group ID: 2934
Protein Accession Numbers: Q96NL8
Gene Names: C8orf37
Peptide Sequence: AEDLDELLDEVESK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 112.08
Best Match Posterior Error Probability: 0.00012715
Best Match Spectrum:

Scan number 5918 **Raw file** Prt-OGE-Batch2-WT-Frac15
Method ITMS; CID **Genenames** C8orf37



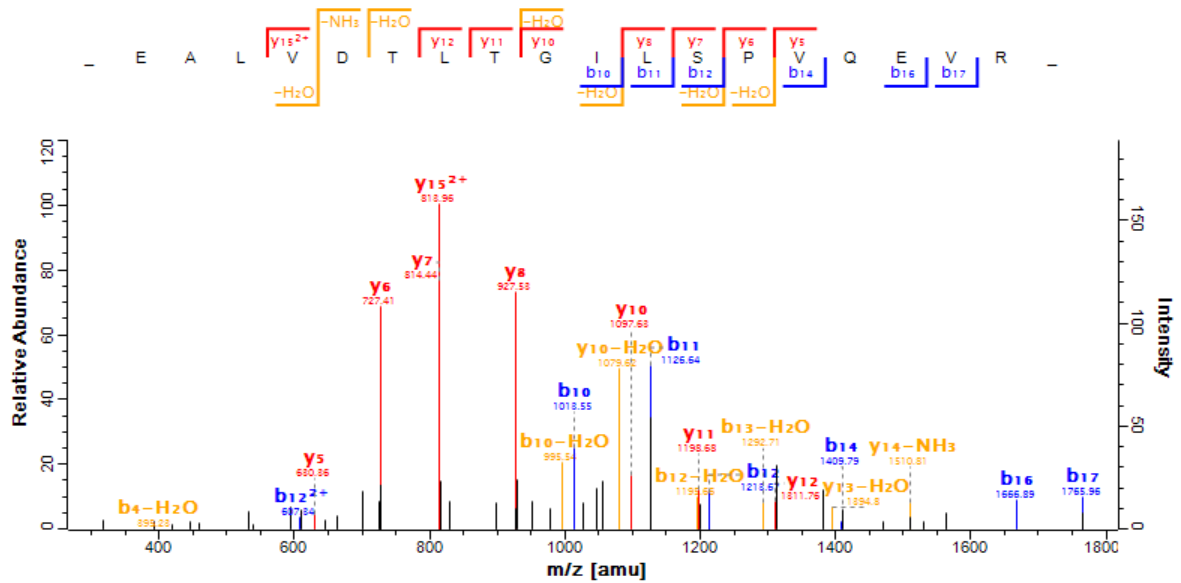
Protein Group ID: 2935
Protein Accession Numbers: Q96NT1
Gene Names: NAP1L5
Peptide Sequence: NDFIESLPNSVK
Total Number of Spectra: 6
Number of Replicates (out of 10): 6
Best Match Score: 138.02
Best Match Posterior Error Probability: 8.40E-05
Best Match Spectrum:

Scan number 3277 **Raw file** OGE-WT-Frac2
Method ITMS; CID **Genenames** NAP1L5



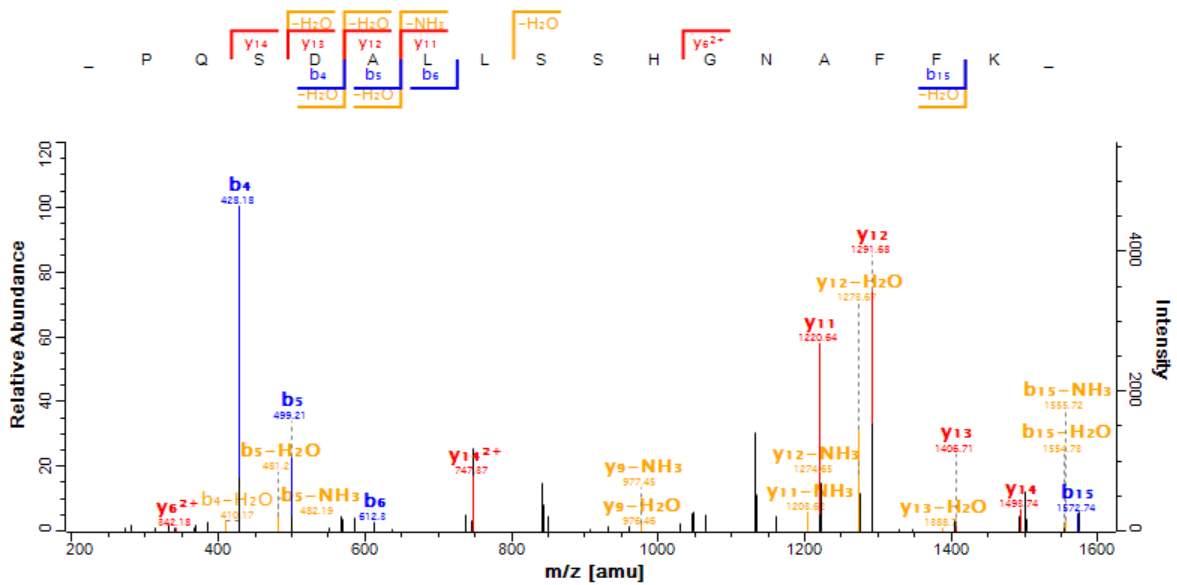
Protein Group ID: 2937
Protein Accession Numbers: Q96P70
Gene Names: IPO9
Peptide Sequence: EALVDTLTGILSPVQEV
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 81.317
Best Match Posterior Error Probability: 0.0010712
Best Match Spectrum:

Scan number 4956 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** IPO9



Protein Group ID: 2942
Protein Accession Numbers: Q96PX9
Gene Names: PLEKHG4B
Peptide Sequence: PQSDALLSSHGNAFFK
Total Number of Spectra: 3
Number of Replicates (out of 10): 1
Best Match Score: 91.812
Best Match Posterior Error Probability: 0.0003727
Best Match Spectrum:

Scan number 3307 **Raw file** OGE-Mock-Frac19
Method ITMS; CID **Genenames** PLEKHG4B



Protein Group ID: 2950

Protein Accession Numbers: Q96SI9; Q96SI9-2; Q5JPA5; E9PKQ0

Gene Names: STRBP;DKFZp434P151

Peptide Sequence: HSTIYPSPEELEAVQNMVSTVECALK

Total Number of Spectra: 2

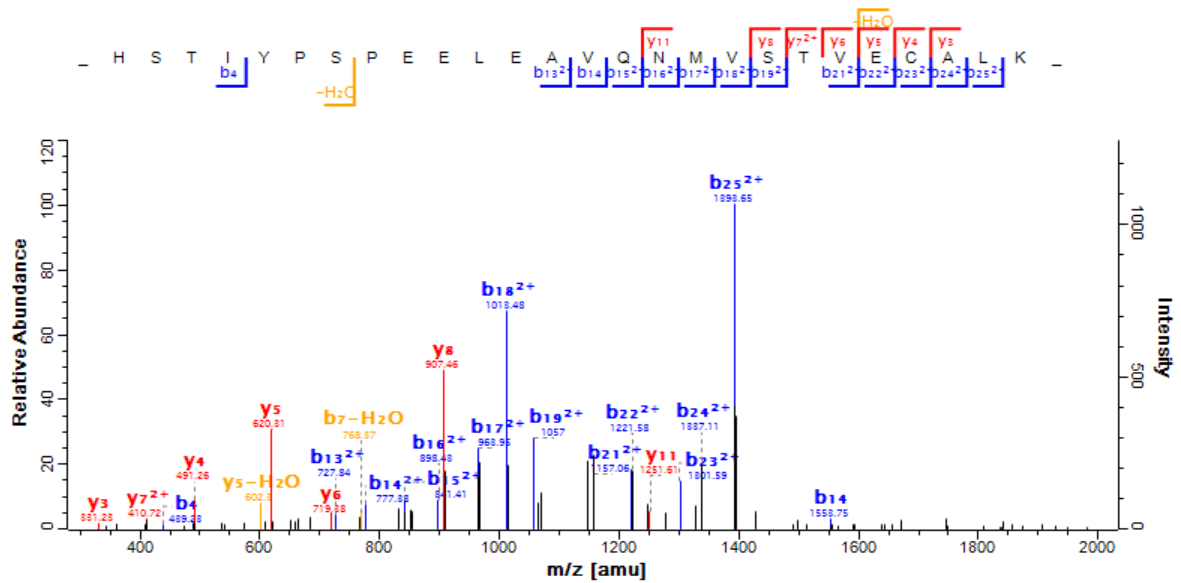
Number of Replicates (out of 10): 2

Best Match Score: 87.326

Best Match Posterior Error Probability: 1.31E-07

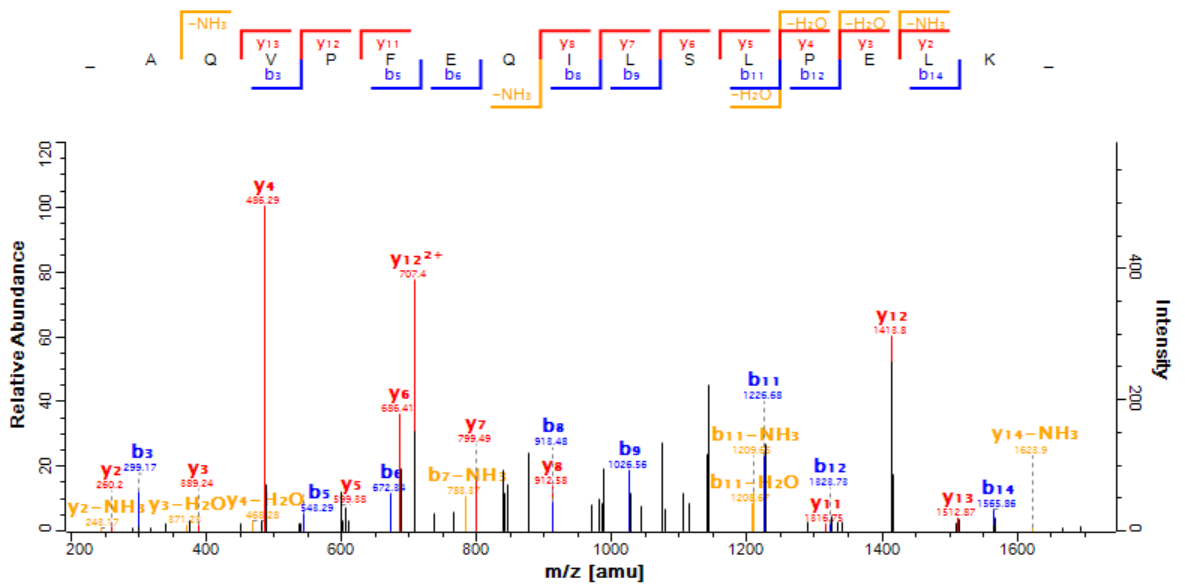
Best Match Spectrum:

Scan number	7402	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac20
Method	ITMS; CID	Genenames	STRBP;DKFZp434P151



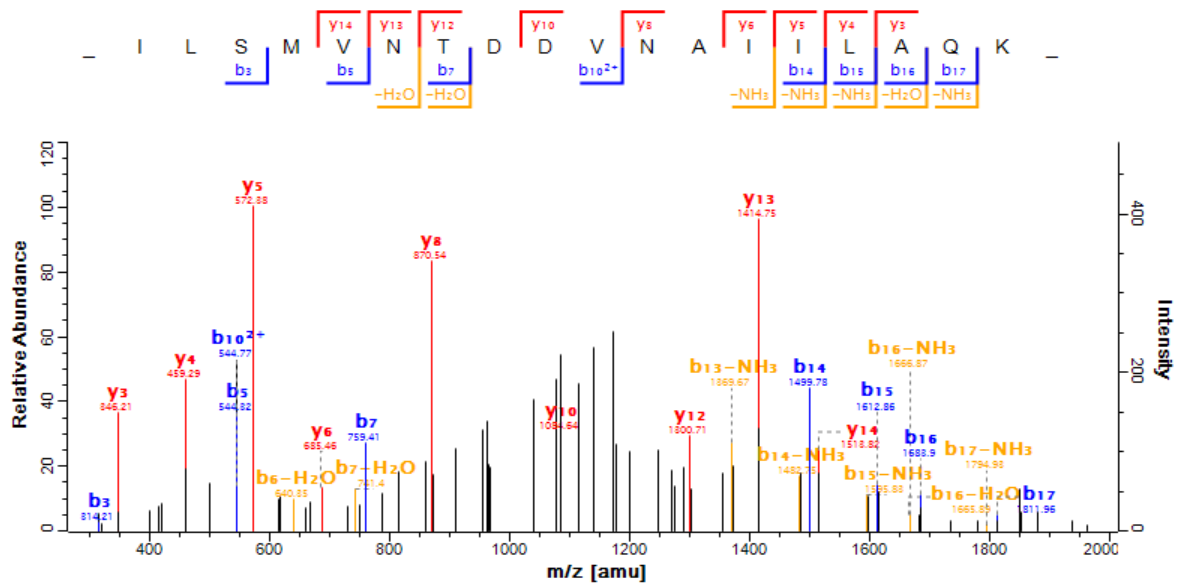
Protein Group ID: 2980
Protein Accession Numbers: Q99828
Gene Names: CIB1
Peptide Sequence: AQVPFEQILSLPELK
Total Number of Spectra: 6
Number of Replicates (out of 10): 6
Best Match Score: 115.38
Best Match Posterior Error Probability: 5.43E-05
Best Match Spectrum:

Scan number 5783 **Raw file** OGEWT-Frac4
Method ITMS; CID **Genenames** CIB1



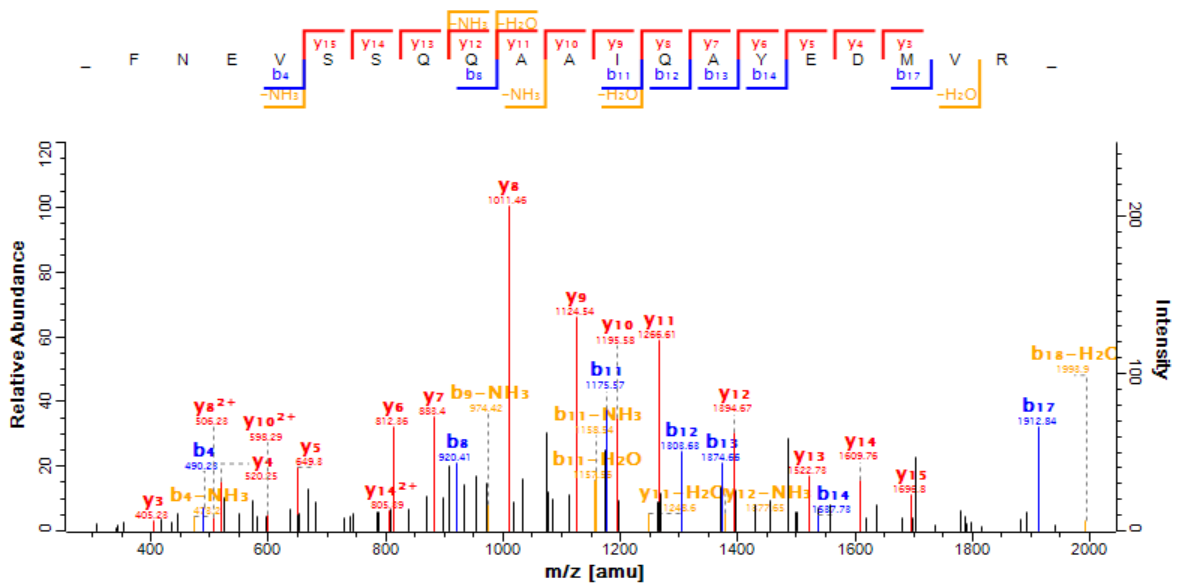
Protein Group ID: 2993
Protein Accession Numbers: Q9BQD3
Gene Names: KXD1
Peptide Sequence: ILSMVNTDDVNAILILAK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 100.77
Best Match Posterior Error Probability: 0.00022686
Best Match Spectrum:

Scan number 5466 **Raw file** Prt-OGE-Batch3-Mock-Frac4
Method ITMS; CID **Genenames** KXD1



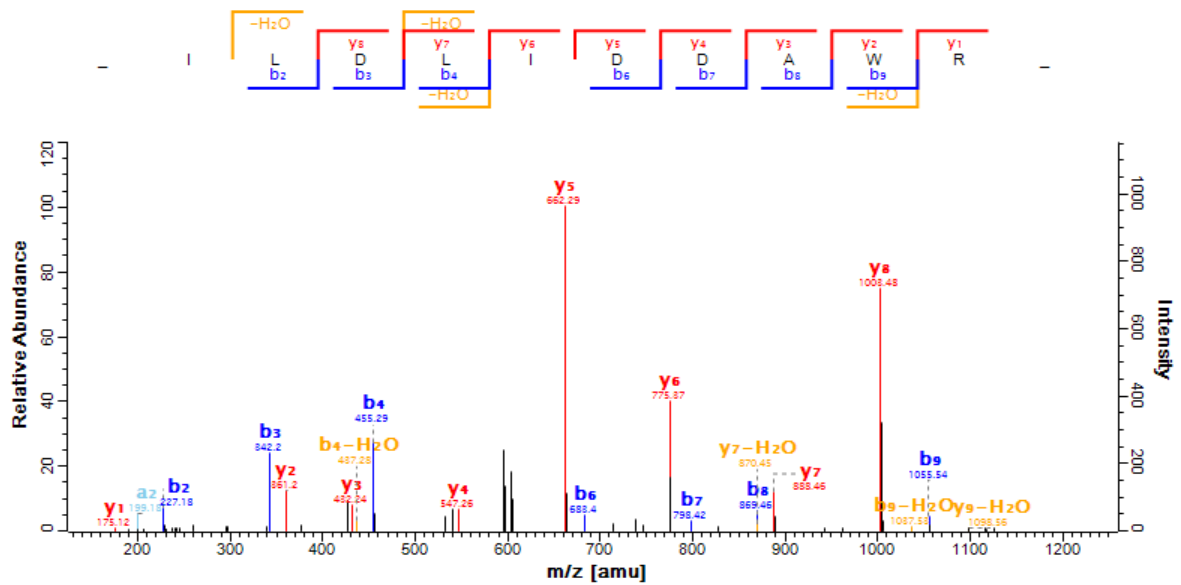
Protein Group ID: 3007
Protein Accession Numbers: Q9BRQ8
Gene Names: AIFM2
Peptide Sequence: FNEVSSSQAAIQAYEDMVR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 112.58
Best Match Posterior Error Probability: 3.43E-05
Best Match Spectrum:

Scan number 4706 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac21
Method ITMS; CID **Genenames** AIFM2



Protein Group ID: 3011
Protein Accession Numbers: Q9BS18
Gene Names: ANAPC13
Peptide Sequence: ILDLIDDAWR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 114.89
Best Match Posterior Error Probability: 0.00021656
Best Match Spectrum:

Scan number 5518 **Raw file** OGE-Mock-Frac1
Method ITMS; CID **Genenames** ANAPC13



Protein Group ID: 3015

Protein Accession Numbers: Q9BSE5

Gene Names: AGMAT

Peptide Sequence: LPVQTSPEGLDAAAFIVIGVPLDTGTSNRPGAR

Total Number of Spectra: 2

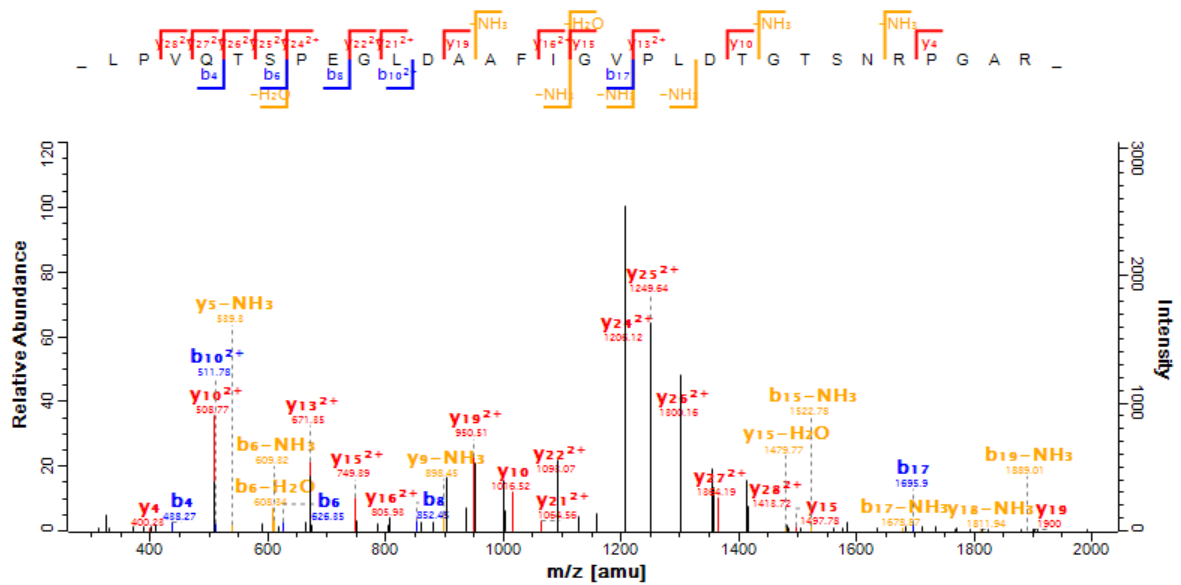
Number of Replicates (out of 10): 2

Best Match Score: 78.451

Best Match Posterior Error Probability: 9.07E-07

Best Match Spectrum:

Scan number	6191	Raw file	Prt-OGE-Batch3--Mock-Frac13
Method	ITMS; CID	Genenames	AGMAT



Protein Group ID: 3022

Protein Accession Numbers: Q9BTA9; Q9BTA9-2; Q9BTA9-5

Gene Names: WAC

Peptide Sequence: QGPVQSATQQPVTK

Total Number of Spectra: 2

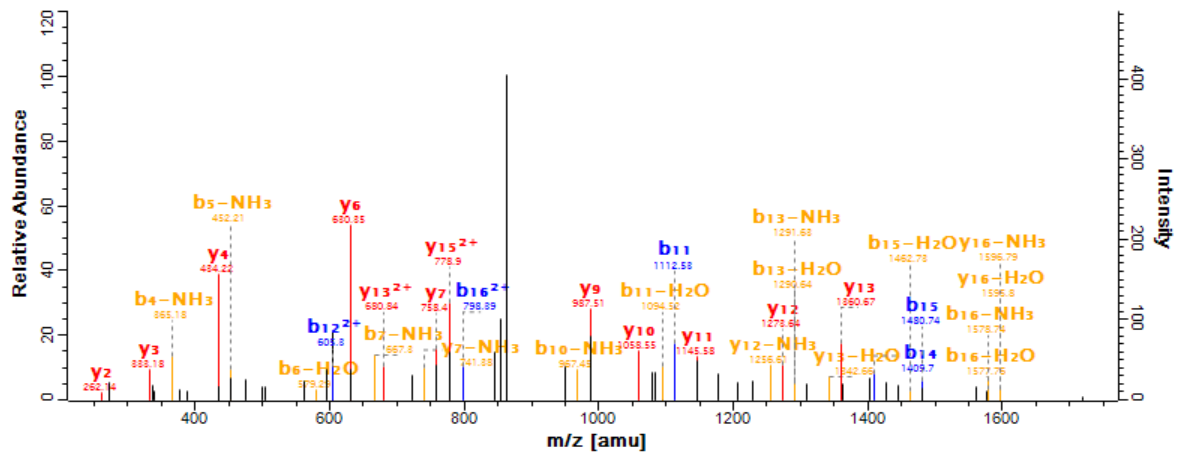
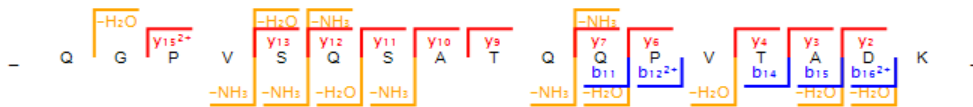
Number of Replicates (out of 10): 1

Best Match Score: 122.1

Best Match Posterior Error Probability: 0.00010766

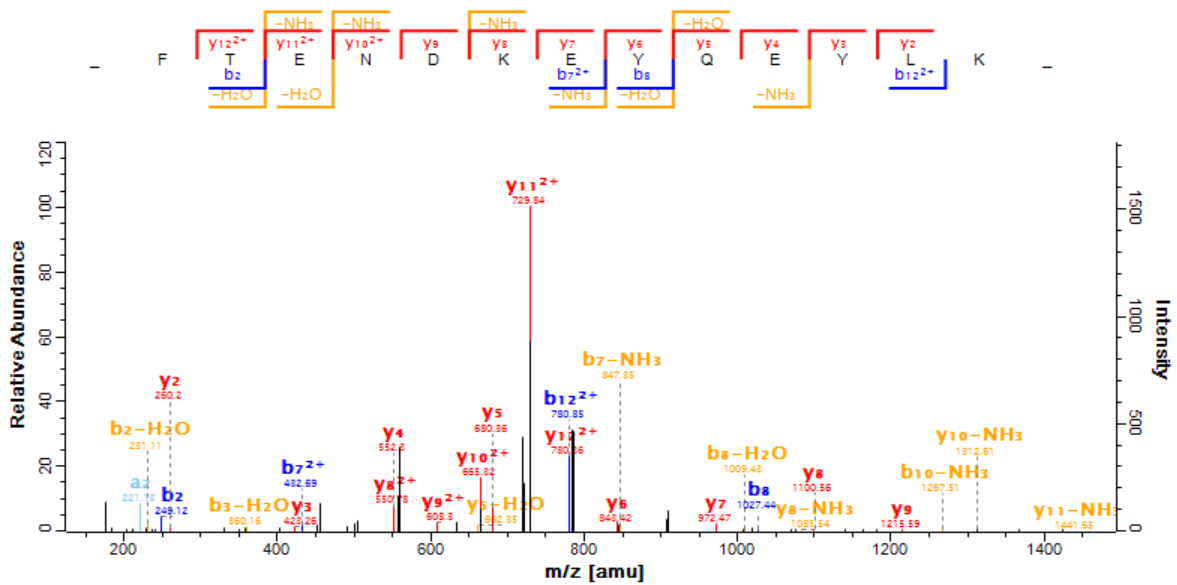
Best Match Spectrum:

Scan number 1263 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac20
Method ITMS; CID **Genenames** WAC



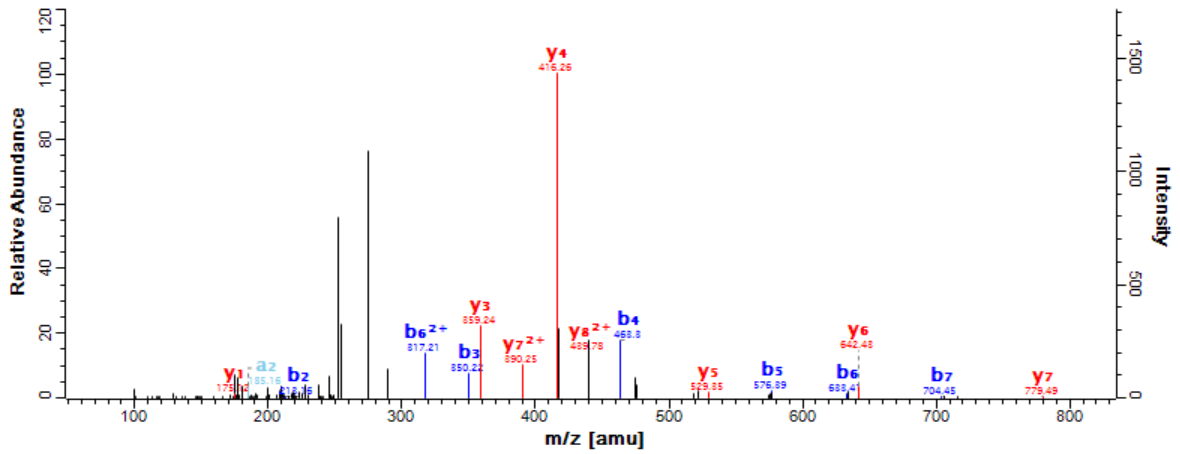
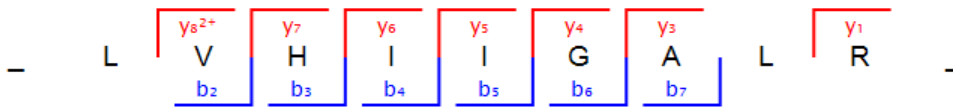
Protein Group ID: 3024
Protein Accession Numbers: Q9BTL3
Gene Names: FAM103A1
Peptide Sequence: FTENDKEYQEYLK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 126.12
Best Match Posterior Error Probability: 0.00024041
Best Match Spectrum:

Scan number 2627 **Raw file** OGE-Mock-Frac19
Method ITMS; CID **Genenames** FAM103A1



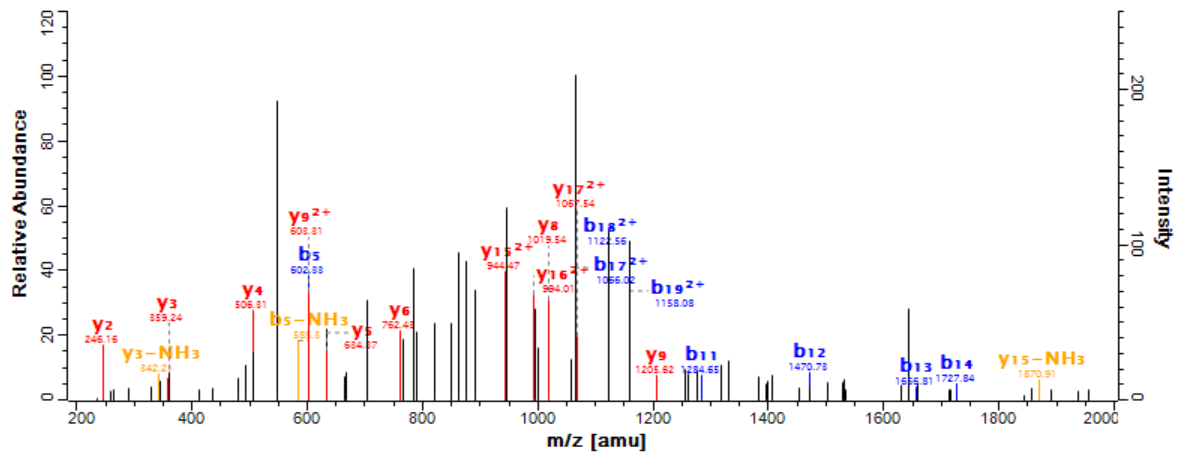
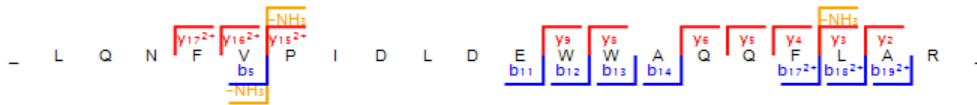
Protein Group ID: 3026
Protein Accession Numbers: Q9BTV4
Gene Names: TMEM43
Peptide Sequence: LVHIIGALR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 98.523
Best Match Posterior Error Probability: 0.00086929
Best Match Spectrum:

Scan number 2364 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** TMEM43



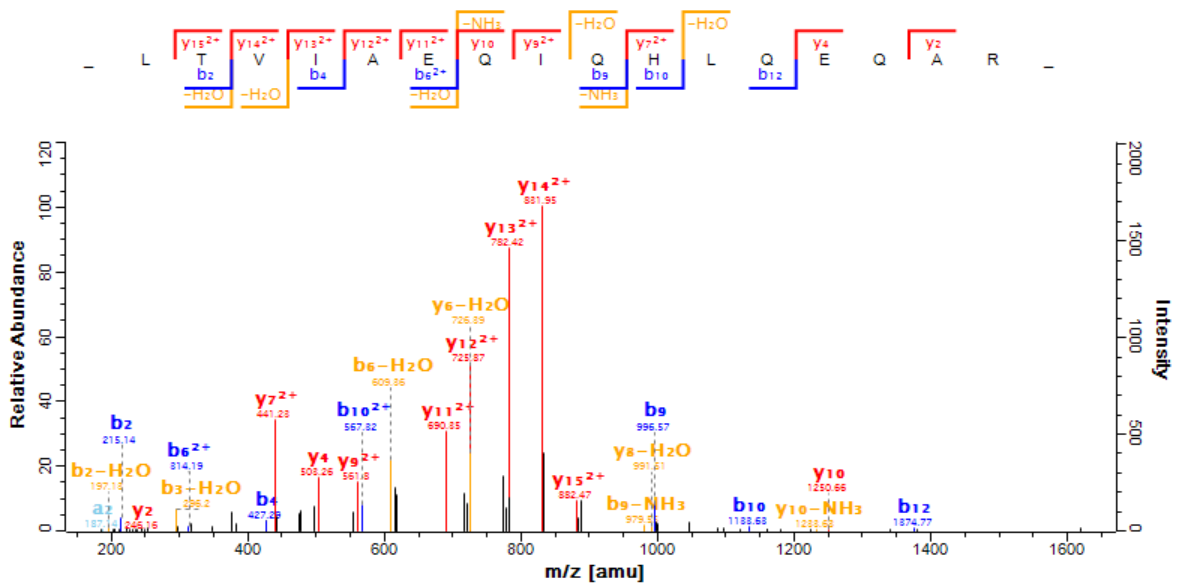
Protein Group ID: 3039
Protein Accession Numbers: Q9BUT9
Gene Names: FAM195A
Peptide Sequence: LQNFVPIDLD EEWAWAQQLAR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 79.514
Best Match Posterior Error Probability: 0.0010223
Best Match Spectrum:

Scan number	8138	Raw file	Prt-OGE-Batch2-Mock-Frac20
Method	ITMS; CID	Genenames	FAM195A



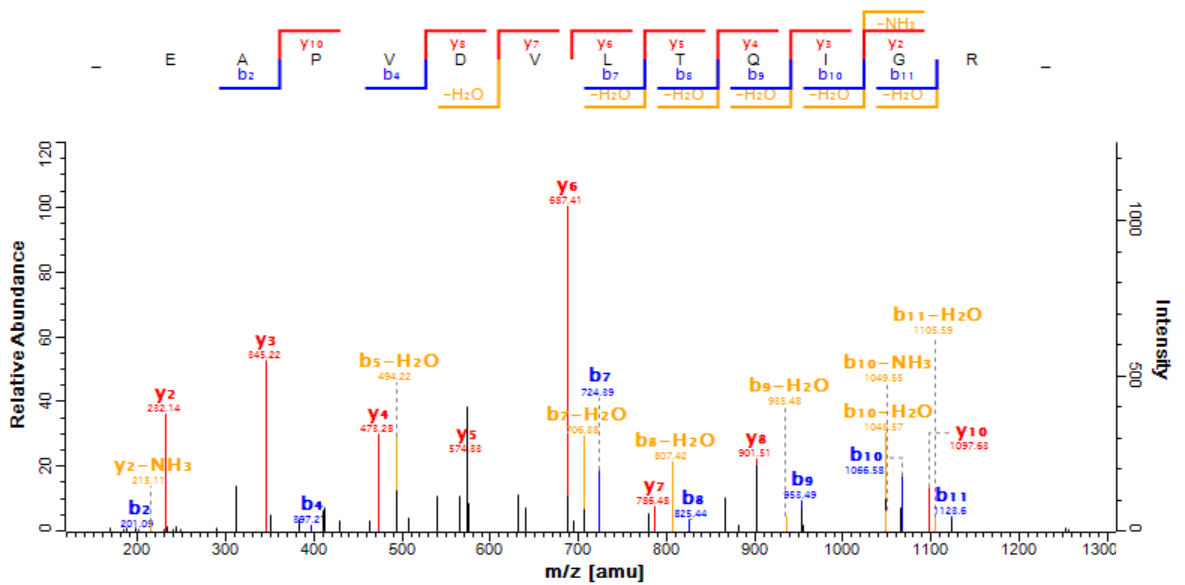
Protein Group ID: 3041
Protein Accession Numbers: Q9BV19
Gene Names: C1orf50
Peptide Sequence: LTVIAEQIQLQEQR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 105.03
Best Match Posterior Error Probability: 0.00015953
Best Match Spectrum:

Scan number 4789 **Raw file** Prt-OGE-Batch3-Mock-Frac9
Method ITMS; CID **Genenames** C1orf50



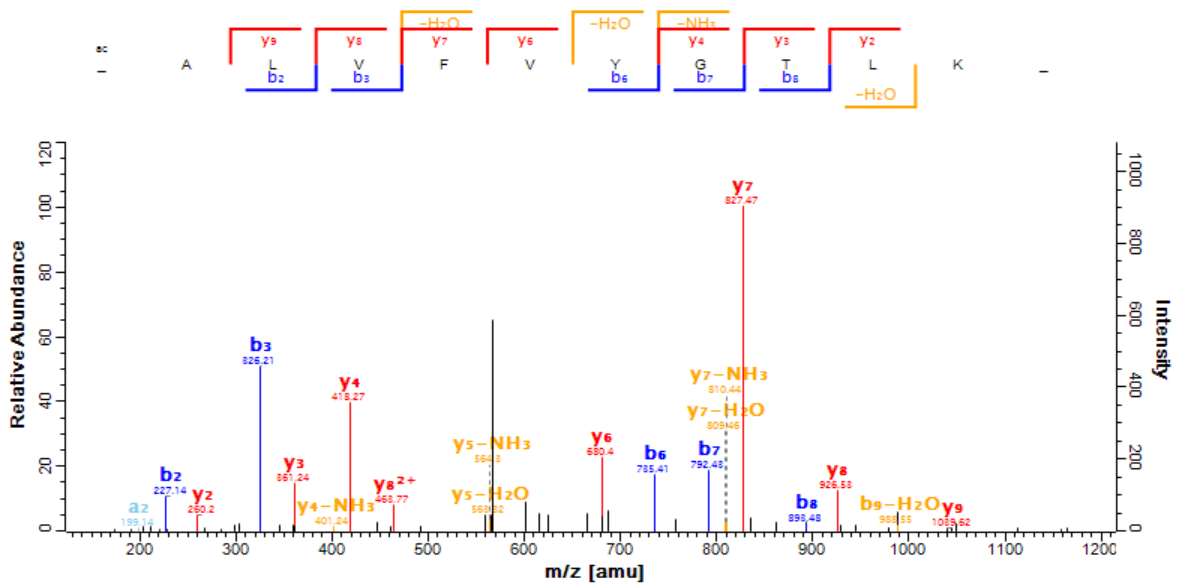
Protein Group ID: 3046
Protein Accession Numbers: Q9BVC6
Gene Names: TMEM109
Peptide Sequence: EAPVDVLTQIGR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 112.51
Best Match Posterior Error Probability: 0.00019939
Best Match Spectrum:

Scan number 3514 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** TMEM109



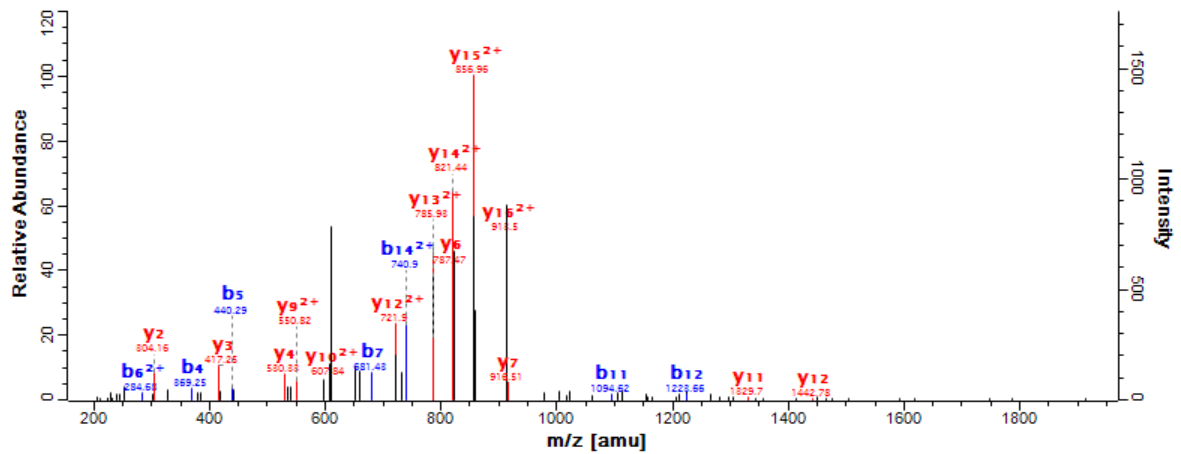
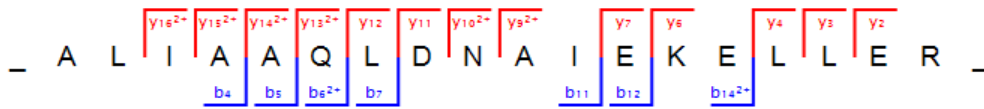
Protein Group ID: 3051
Protein Accession Numbers: Q9BVM4
Gene Names: A2LD1
Peptide Sequence: ALVFVYGTK
Total Number of Spectra: 4
Number of Replicates (out of 10): 4
Best Match Score: 116.52
Best Match Posterior Error Probability: 0.00016993
Best Match Spectrum:

Scan number 6653 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac15
Method ITMS; CID **Genenames** A2LD1



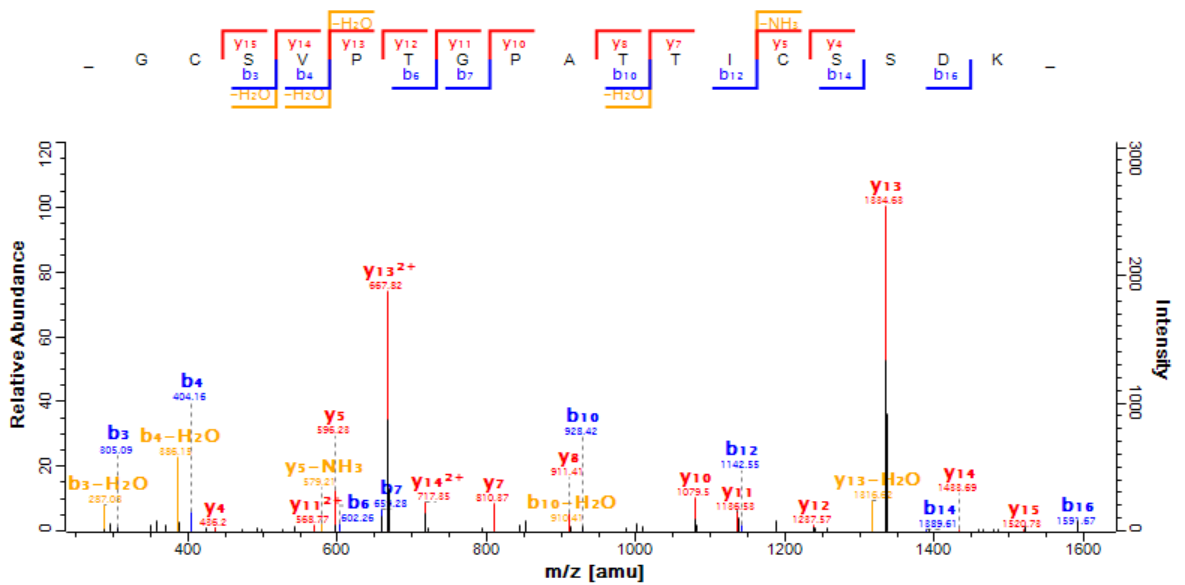
Protein Group ID: 3064
Protein Accession Numbers: Q9BXY0
Gene Names: MAK16
Peptide Sequence: ALIAAQLDNAIEKELELER
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 89.358
Best Match Posterior Error Probability: 0.0015855
Best Match Spectrum:

Scan number 4964 **Raw file** Prt-OGE-Batch3-WT-Frac17
Method ITMS; CID **Genenames** MAK16



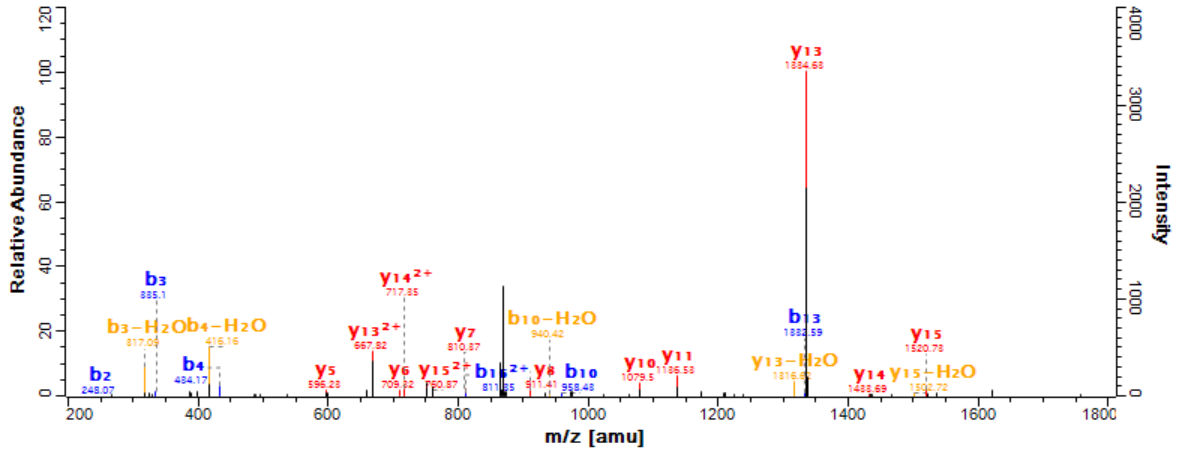
Protein Group ID: 3075
Protein Accession Numbers: Q9BYR6
Gene Names: KRTAP3-3
Peptide Sequence: GCSVPTGPATTICSSDK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 120.63
Best Match Posterior Error Probability: 0.0001227
Best Match Spectrum:

Scan number 2011 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac2
Method ITMS; CID **Genenames** KRTAP3-3



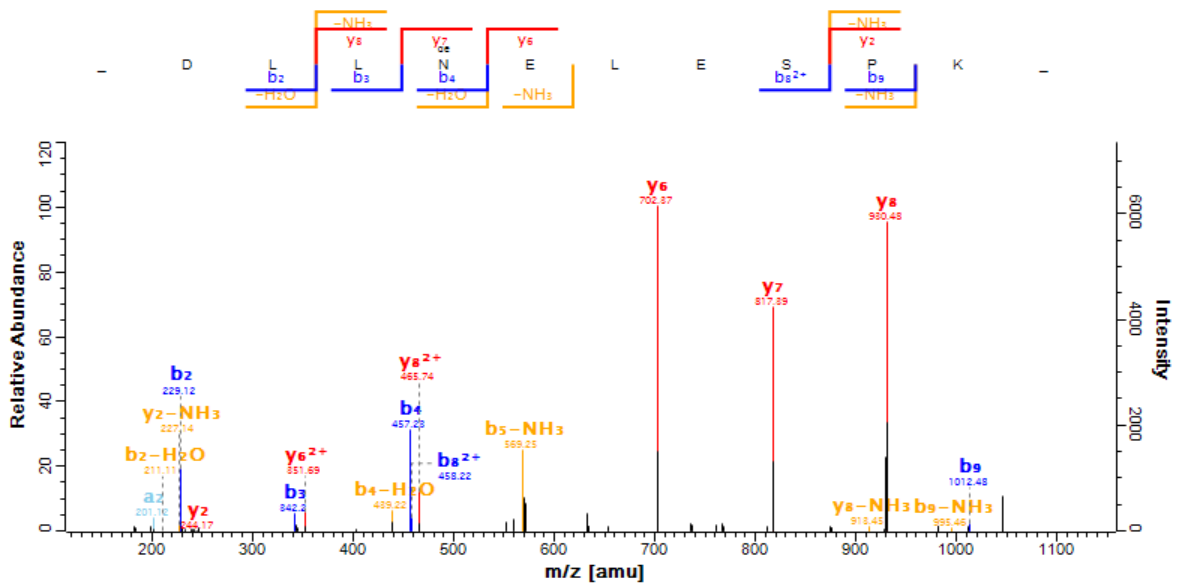
Protein Group ID: 3076
Protein Accession Numbers: Q9BYR7
Gene Names: KRTAP3-2
Peptide Sequence: SCSVPTGPATTICSSDK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 101.01
Best Match Posterior Error Probability: 0.00024543
Best Match Spectrum:

Scan number 2010 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac2
Method ITMS; CID **Genenames** KRTAP3-2



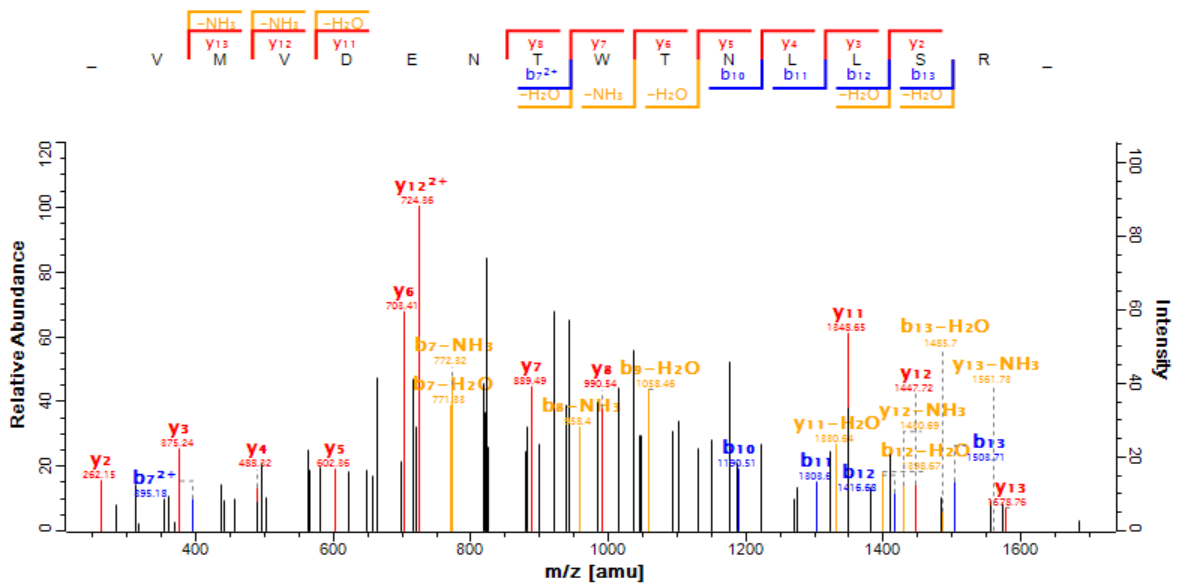
Protein Group ID: 3081
Protein Accession Numbers: Q9BZH6
Gene Names: WDR11
Peptide Sequence: DLLNELESPK
Total Number of Spectra: 3
Number of Replicates (out of 10): 2
Best Match Score: 98.048
Best Match Posterior Error Probability: 0.0069027
Best Match Spectrum:

Scan number 3348 **Raw file** Prt-OGE-Batch2-Mock-Frac6
Method ITMS; CID **Genenames** WDR11



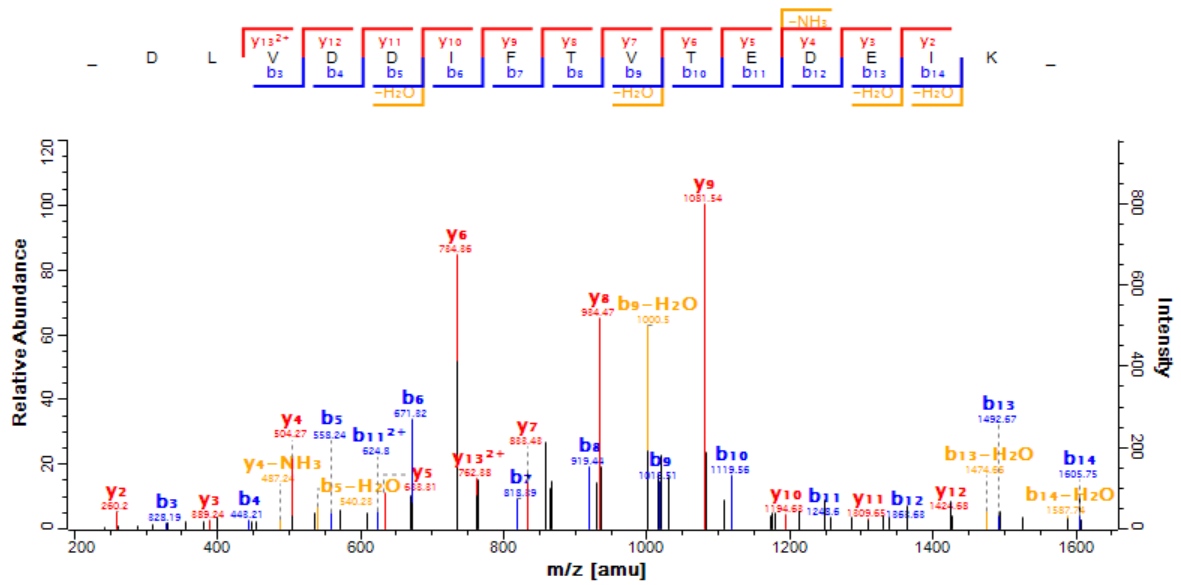
Protein Group ID: 3090
Protein Accession Numbers: Q9C0F1-2; Q9C0F1
Gene Names: CEP44
Peptide Sequence: VMVDENTWTNLLSR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 98.676
Best Match Posterior Error Probability: 0.00037458
Best Match Spectrum:

Scan number 5105 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac7
Method ITMS; CID **Genenames** CEP44



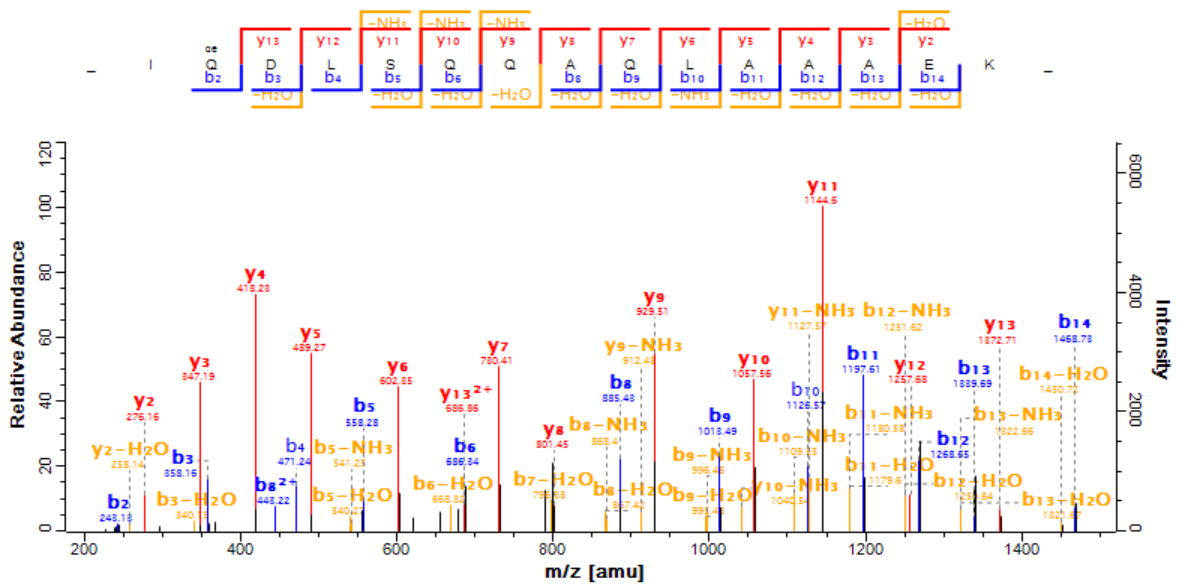
Protein Group ID: 3097
Protein Accession Numbers: Q9GZT4
Gene Names: SRR
Peptide Sequence: DLVDDIFTVTEDEIK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 165.34
Best Match Posterior Error Probability: 1.63E-11
Best Match Spectrum:

Scan number 7052 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac13
Method ITMS; CID **Genenames** SRR



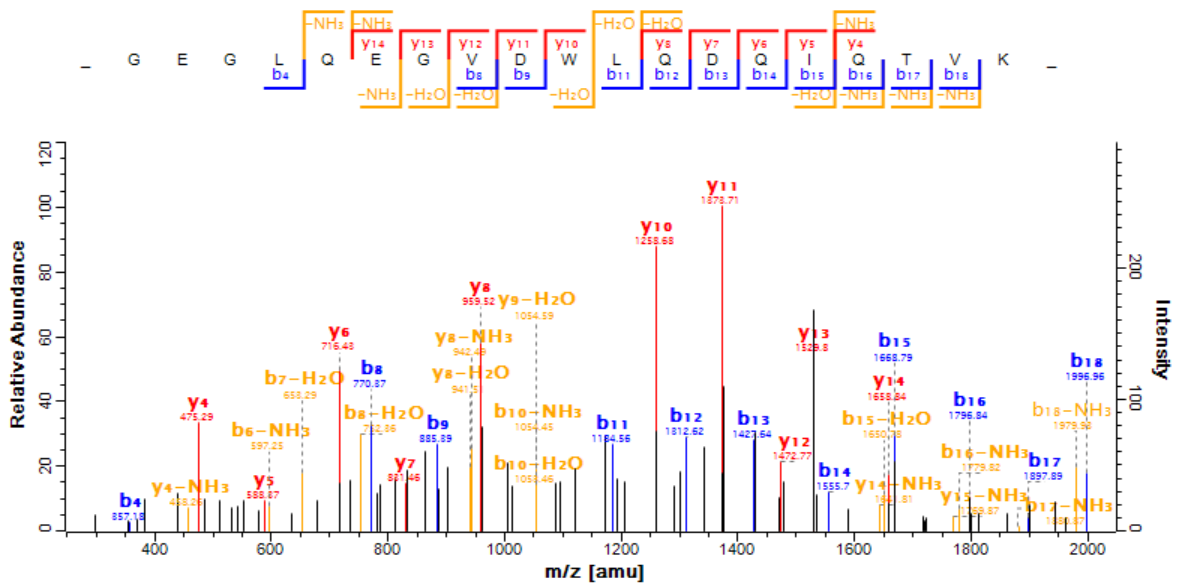
Protein Group ID: 3102
Protein Accession Numbers: Q9H009
Gene Names: NACA2
Peptide Sequence: IQDLSQQAQLAAAEK
Total Number of Spectra: 5
Number of Replicates (out of 10): 3
Best Match Score: 305.29
Best Match Posterior Error Probability: 3.64E-186
Best Match Spectrum:

Scan number 3164 **Raw file** Prt-OGE-Batch3-Mock-Frac6
Method ITMS; CID **Genenames** NACA2



Protein Group ID: 3106
Protein Accession Numbers: Q9H0F7
Gene Names: ARL6
Peptide Sequence: GEGLQEGVDWLQDQIQTVK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 126.25
Best Match Posterior Error Probability: 1.22E-05
Best Match Spectrum:

Scan number 5826 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac20
Method ITMS; CID **Genenames** ARL6



Protein Group ID: 3108

Protein Accession Numbers: Q9H0L4

Gene Names: CSTF2T

Peptide Sequence: SVFVGNIPYEATEEQLKDI FSEVGSVVSVFR

Total Number of Spectra: 3

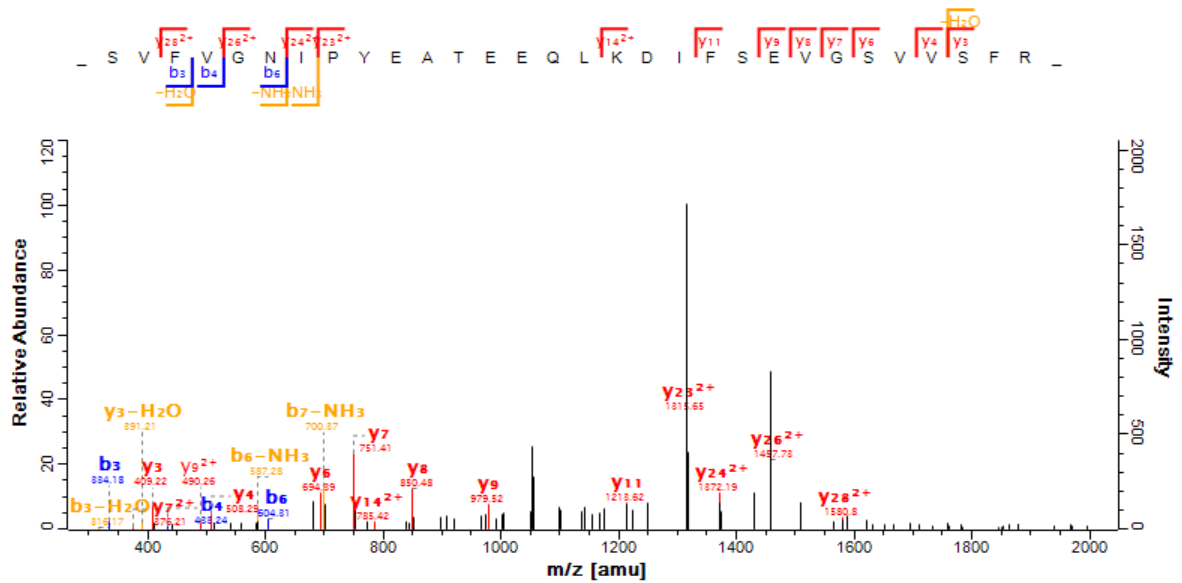
Number of Replicates (out of 10): 3

Best Match Score: 74.274

Best Match Posterior Error Probability: 6.46E-06

Best Match Spectrum:

Scan number	8429	Raw file	20100927-KD-Batch4-Prt-OGE-WT-Frac15
Method	ITMS; CID	Genenames	CSTF2T



Protein Group ID: 3118

Protein Accession Numbers: Q9H2A2; Q9H2A2-4; Q9H2A2-2

Gene Names: ALDH8A1

Peptide Sequence: LSLELGGK

Total Number of Spectra: 7

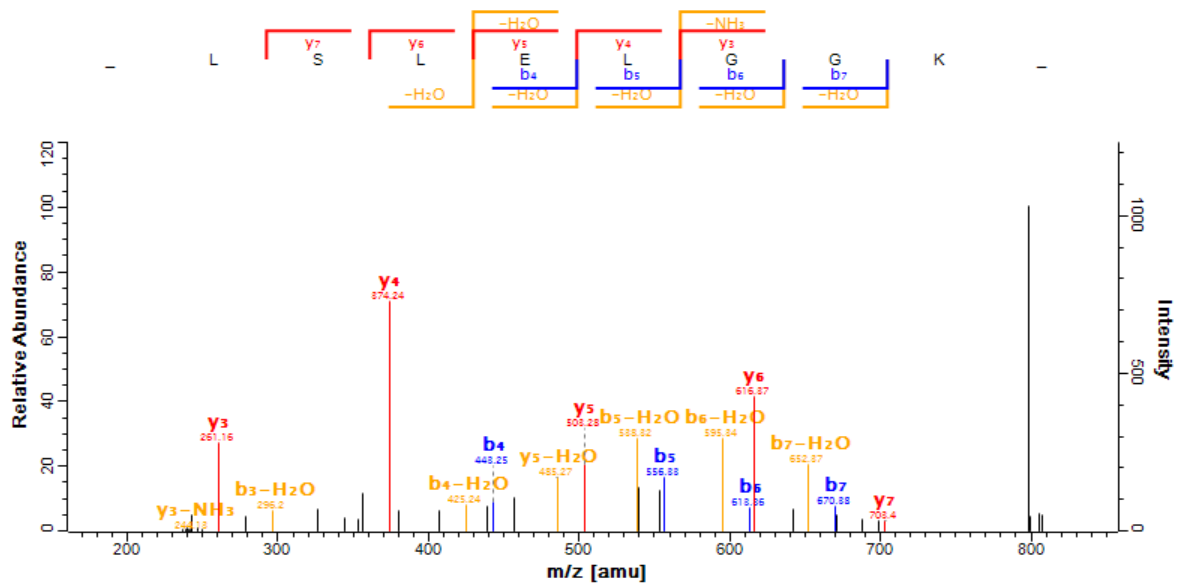
Number of Replicates (out of 10): 6

Best Match Score: 127.84

Best Match Posterior Error Probability: 0.0015856

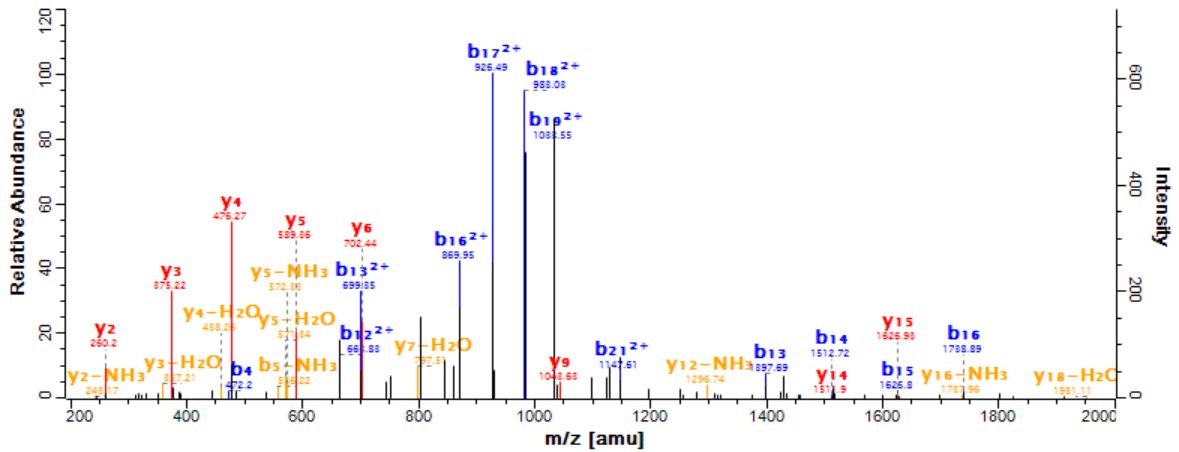
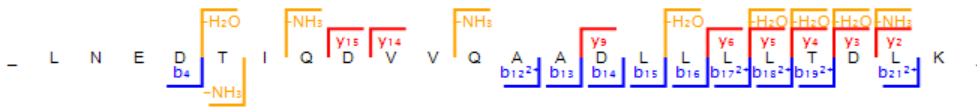
Best Match Spectrum:

Scan number	2558	Raw file	OGE-WT-Frac15
Method	ITMS; CID	Genenames	ALDH8A1



Protein Group ID: 3119
Protein Accession Numbers: Q9H2C0
Gene Names: GAN
Peptide Sequence: LNEDTIQDVVQAADLLLLTDLK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 98.443
Best Match Posterior Error Probability: 7.37E-06
Best Match Spectrum:

Scan number 8115 **Raw file** OGE-Mock-Frac10
Method ITMS; CID **Genenames** GAN



Protein Group ID: 3123

Protein Accession Numbers: Q9H2P9-5; Q9H2P9; Q9H2P9-4; Q9H2P9-6; Q9H2P9-2; Q9H2P9-3

Gene Names: DPH5

Peptide Sequence: YMSVNQAAQQLLEIVQNQR

Total Number of Spectra: 7

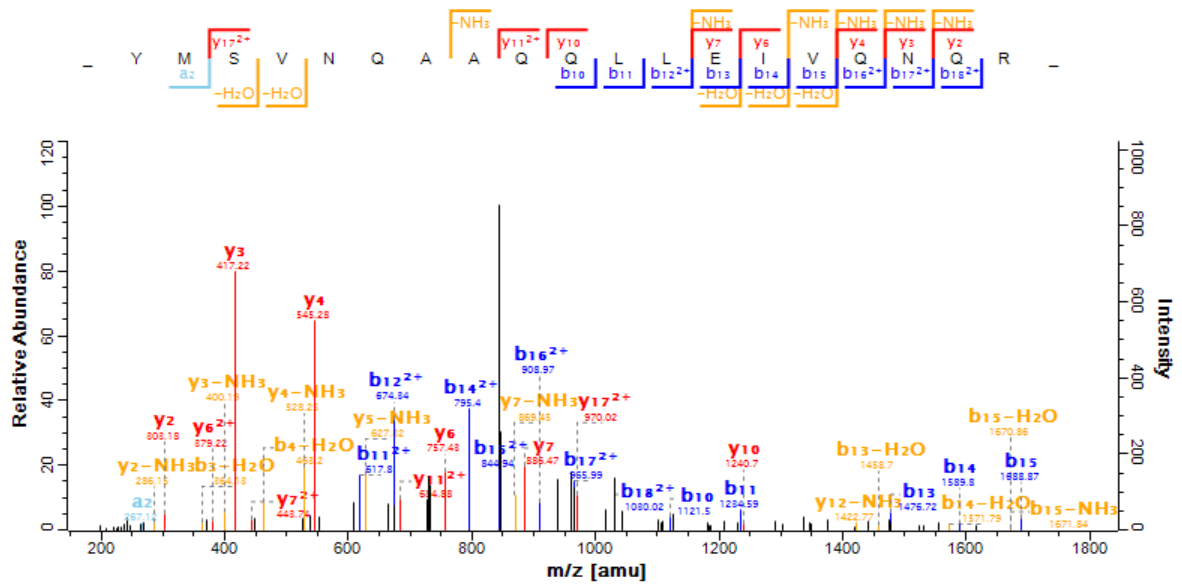
Number of Replicates (out of 10): 7

Best Match Score: 169.94

Best Match Posterior Error Probability: 8.10E-17

Best Match Spectrum:

Scan number	7370	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac8
Method	ITMS; CID	Genenames	DPH5



Protein Group ID: 3126

Protein Accession Numbers: Q9H361; H3BNY3; H3BPI5

Gene Names: PABPC3

Peptide Sequence: SGVGNIFVK

Total Number of Spectra: 1

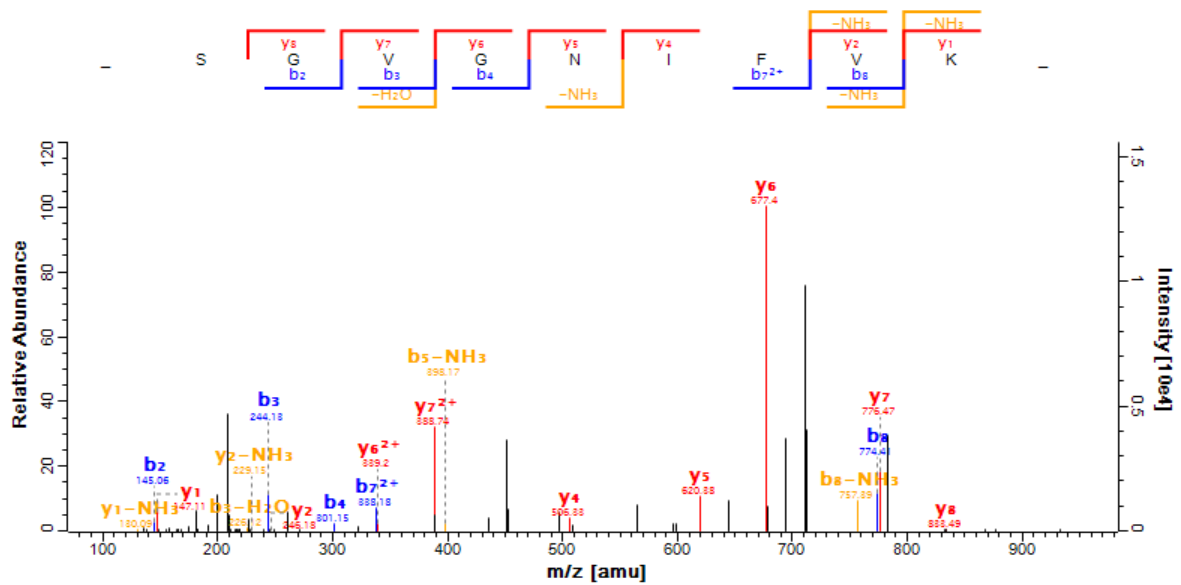
Number of Replicates (out of 10): 1

Best Match Score: 98.033

Best Match Posterior Error Probability: 0.00088997

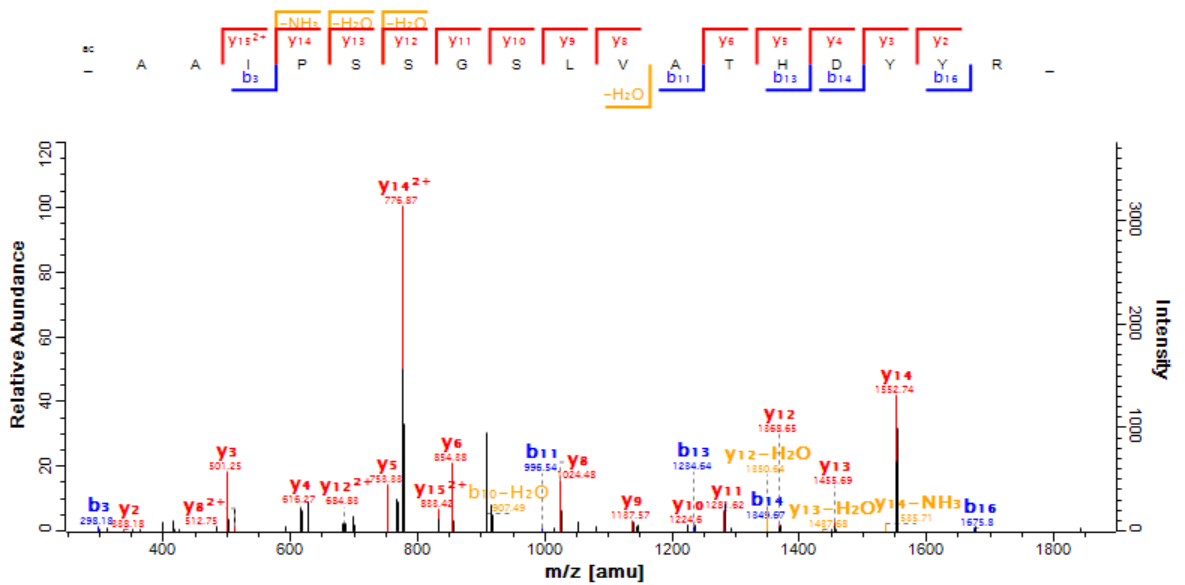
Best Match Spectrum:

Scan number 2441 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac20
Method ITMS; CID **Genenames** PABPC3



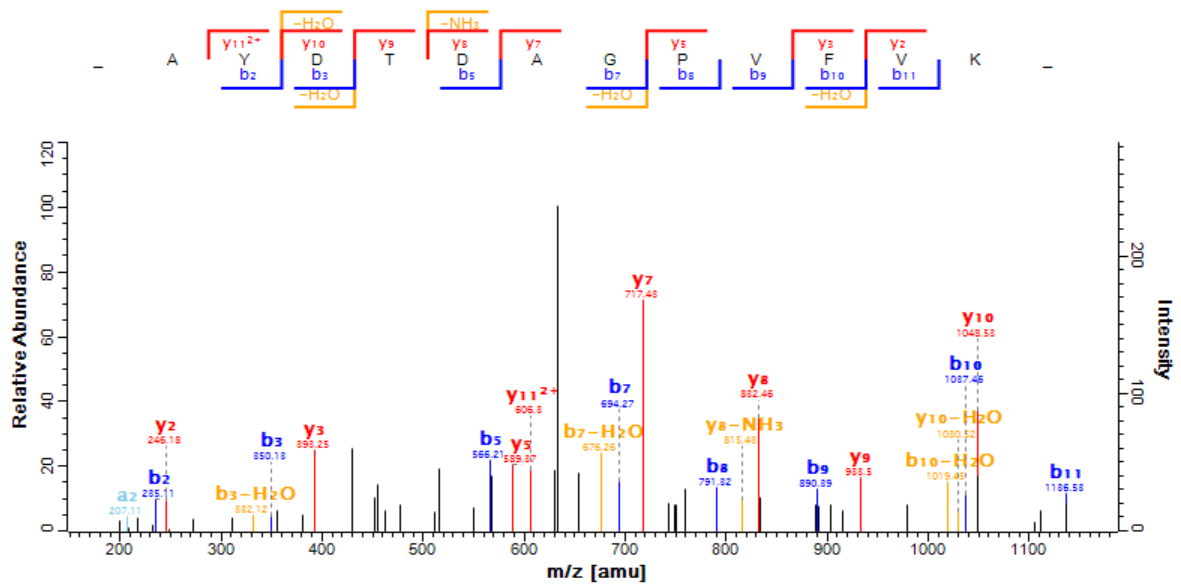
Protein Group ID: 3132
Protein Accession Numbers: Q9H3Y8; Q9H3Y8-2
Gene Names: PDPDF
Peptide Sequence: AAIPSSGSLVATHDYR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 105.53
Best Match Posterior Error Probability: 0.00017756
Best Match Spectrum:

Scan number 3382 **Raw file** Prt-OGE-Batch3-Mock-Frac16
Method ITMS; CID **Genenames** PDPDF



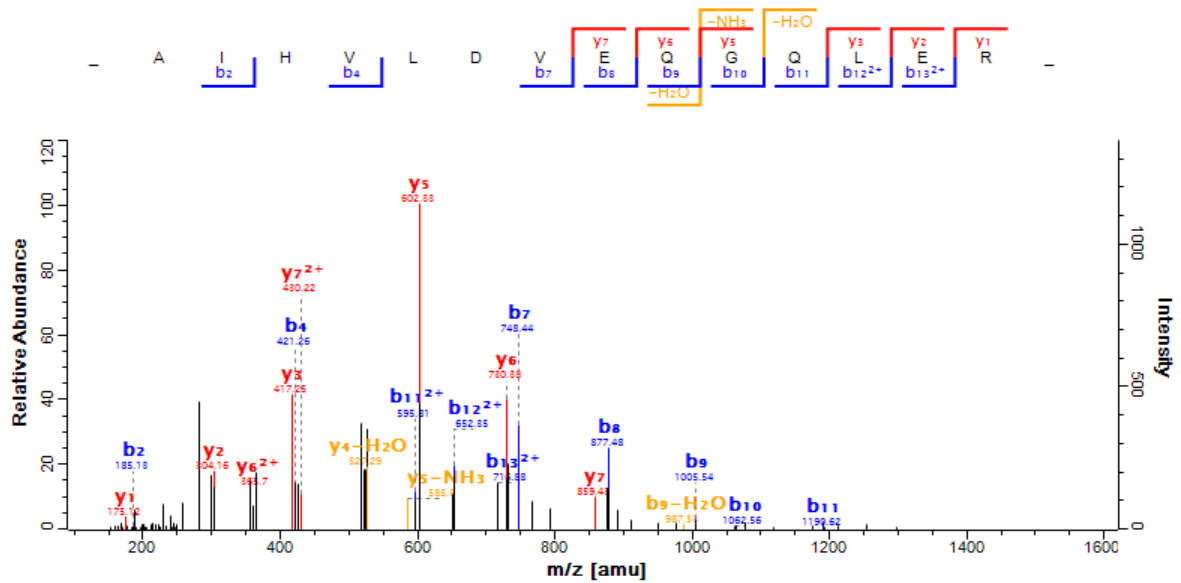
Protein Group ID: 3135
Protein Accession Numbers: Q9H479
Gene Names: FN3K
Peptide Sequence: AYDTDAGPVFVK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 138.99
Best Match Posterior Error Probability: 7.49E-05
Best Match Spectrum:

Scan number 2480 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac17
Method ITMS; CID **Genenames** FN3K



Protein Group ID: 3147
Protein Accession Numbers: Q9H6Y2
Gene Names: WDR55
Peptide Sequence: AIHVLDVEQGQLER
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 92.039
Best Match Posterior Error Probability: 0.00059034
Best Match Spectrum:

Scan number	3294	Raw file	Prt-OGE-Batch3--Mock-Frac4
Method	ITMS; CID	Genenames	WDR55



Protein Group ID: 3150

Protein Accession Numbers: Q9H7E2-3; Q9H7E2; Q9H7E2-2

Gene Names: TDRD3

Peptide Sequence: PSAPSTLFDLFLESK

Total Number of Spectra: 1

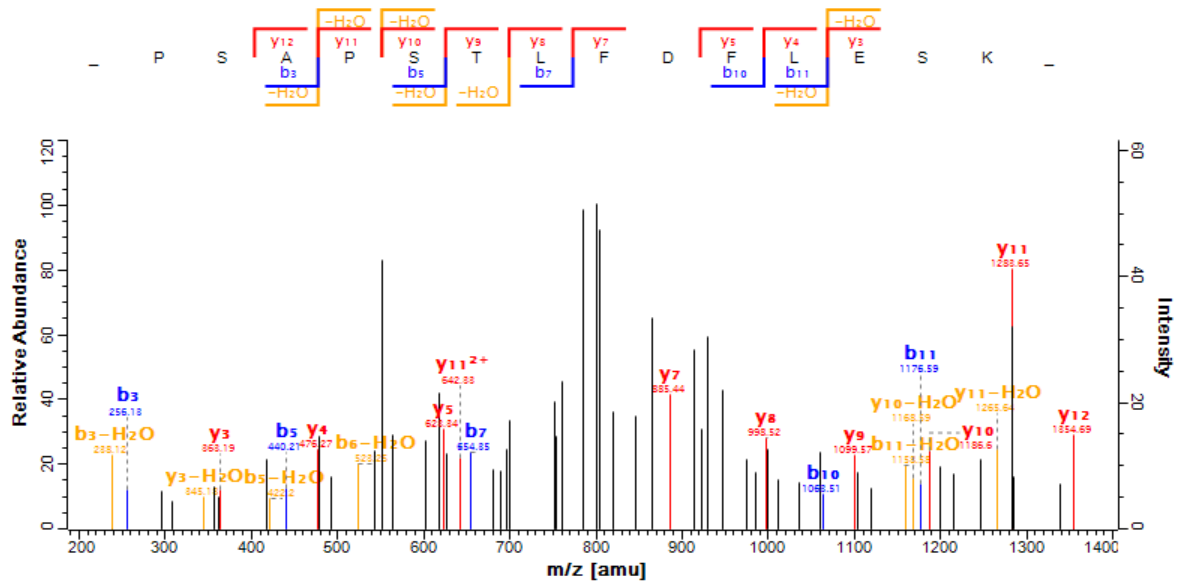
Number of Replicates (out of 10): 1

Best Match Score: 99.991

Best Match Posterior Error Probability: 0.00034635

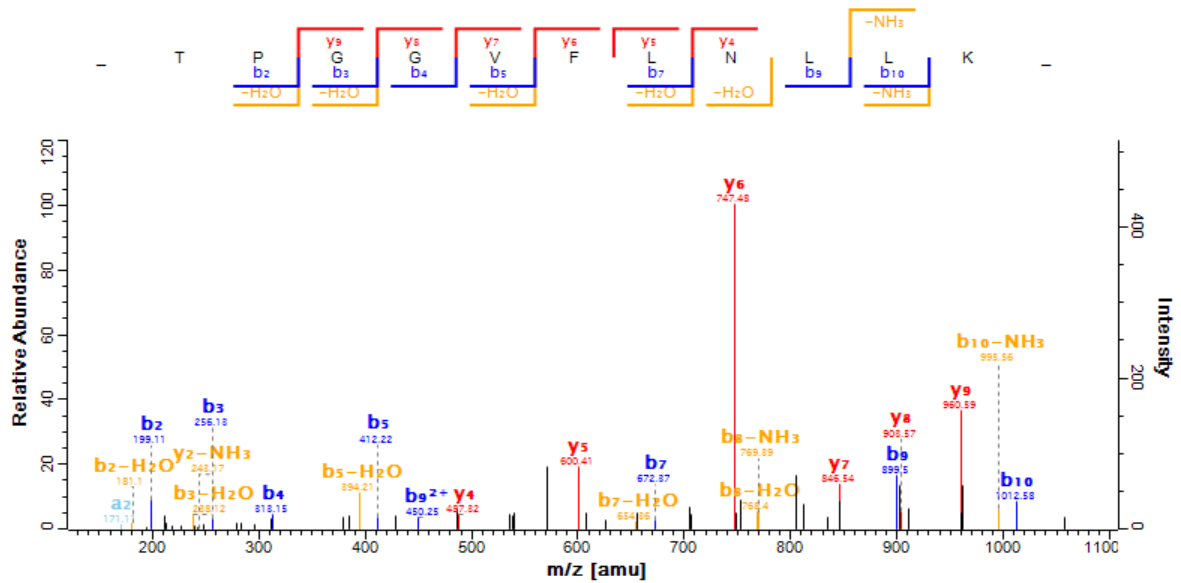
Best Match Spectrum:

Scan number	6467	Raw file	20100930-KD-Batch5-Prt-OGE-WT-Frac20
Method	ITMS; CID	Genenames	TDRD3



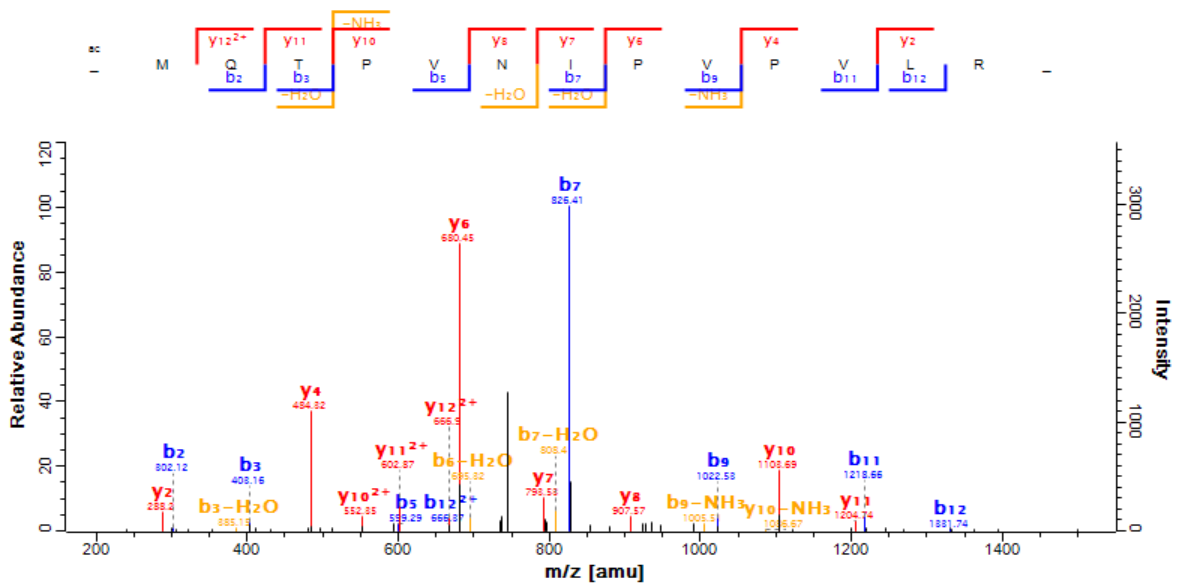
Protein Group ID: 3153
Protein Accession Numbers: Q9H814
Gene Names: PHAX
Peptide Sequence: TPGGVFLNLLK
Total Number of Spectra: 6
Number of Replicates (out of 10): 3
Best Match Score: 140.49
Best Match Posterior Error Probability: 1.51E-05
Best Match Spectrum:

Scan number 6364 **Raw file** Prt-OGE-Batch2-Mock-Frac14
Method ITMS; CID **Genenames** PHAX



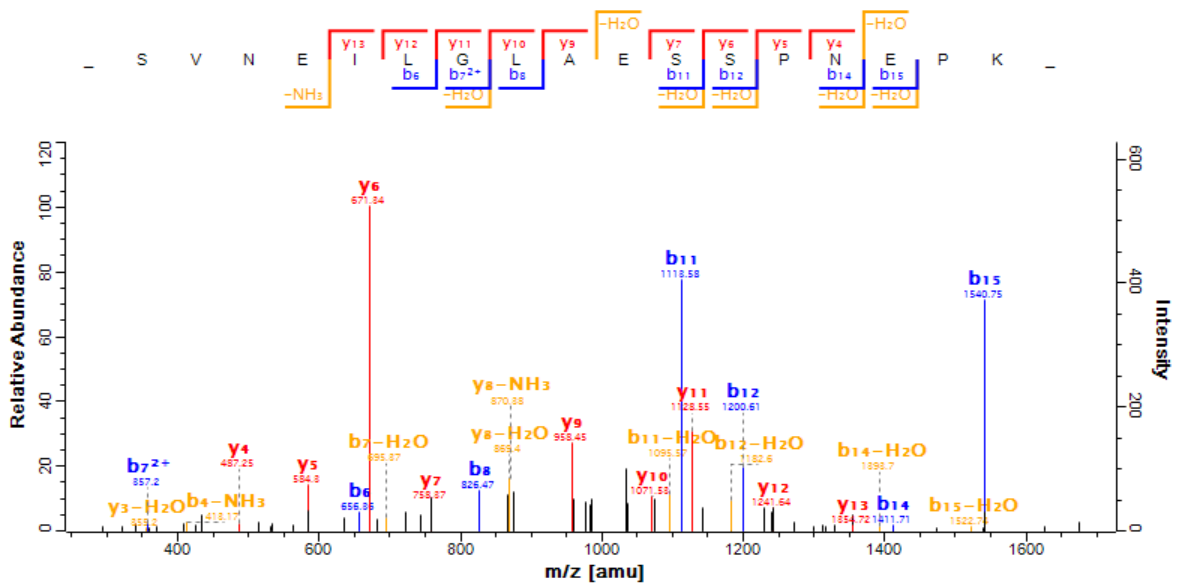
Protein Group ID: 3155
Protein Accession Numbers: Q9H840
Gene Names: GEMIN7
Peptide Sequence: MQTPVNIPVPVLR
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 142.83
Best Match Posterior Error Probability: 1.45E-05
Best Match Spectrum:

Scan number 5020 **Raw file** Prt-OGE-Batch3--Mock-Frac15
Method ITMS; CID **Genenames** GEMIN7



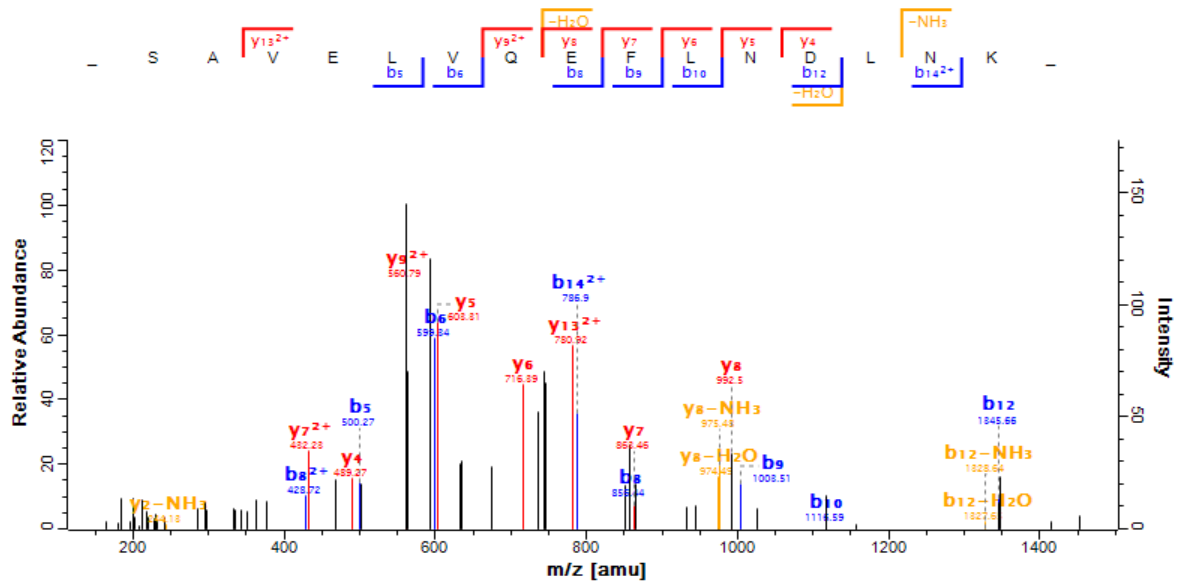
Protein Group ID: 3156
Protein Accession Numbers: Q9H8G2; Q9H8G2-2
Gene Names: CAAP1
Peptide Sequence: SVNEILGLAESSNEPK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 109.04
Best Match Posterior Error Probability: 0.00015667
Best Match Spectrum:

Scan number 3431 **Raw file** Prt-OGE-Batch3-WT-Frac3
Method ITMS; CID **Genenames** CAAP1



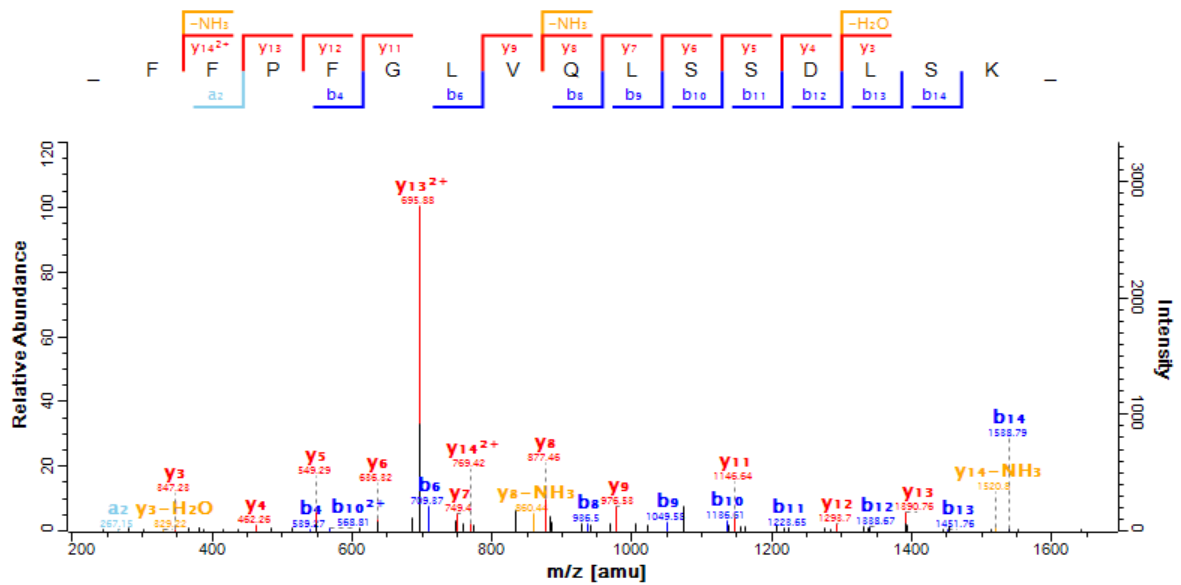
Protein Group ID: 3158
Protein Accession Numbers: Q9H900; Q9H900-2
Gene Names: ZWILCH
Peptide Sequence: SAVELVQEFLNDLNK
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 89.992
Best Match Posterior Error Probability: 0.00034419
Best Match Spectrum:

Scan number 8320 **Raw file** Prt-OGE-Batch2-Mock-Frac12
Method ITMS; CID **Genenames** ZWILCH



Protein Group ID: 3167
Protein Accession Numbers: Q9HAT2; Q9HAT2-2
Gene Names: SIAE
Peptide Sequence: FPFGLVQLSSDLISK
Total Number of Spectra: 4
Number of Replicates (out of 10): 3
Best Match Score: 156.17
Best Match Posterior Error Probability: 2.21E-09
Best Match Spectrum:

Scan number 7150 **Raw file** 20100927-KD-Batch4-Prt-OGE-WT-Frac16
Method ITMS; CID **Genenames** SIAE



Protein Group ID: 3181

Protein Accession Numbers: Q9NP74; Q9NP74-2; Q9NP74-3

Gene Names: PALMD

Peptide Sequence: TGESTVLSSIPLPSDDFK

Total Number of Spectra: 2

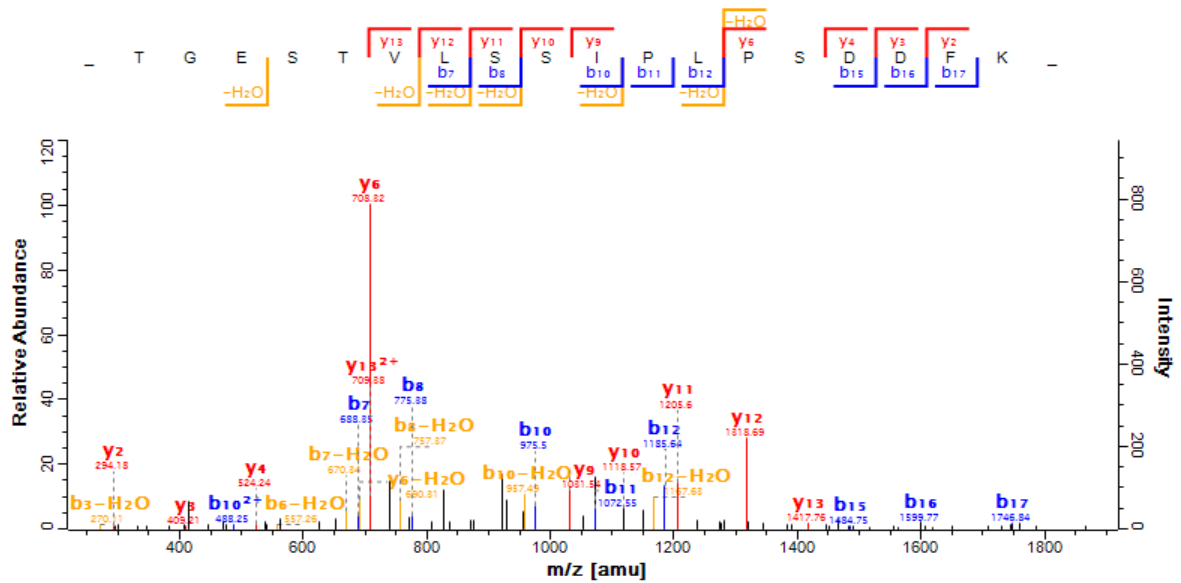
Number of Replicates (out of 10): 2

Best Match Score: 109.36

Best Match Posterior Error Probability: 0.00012051

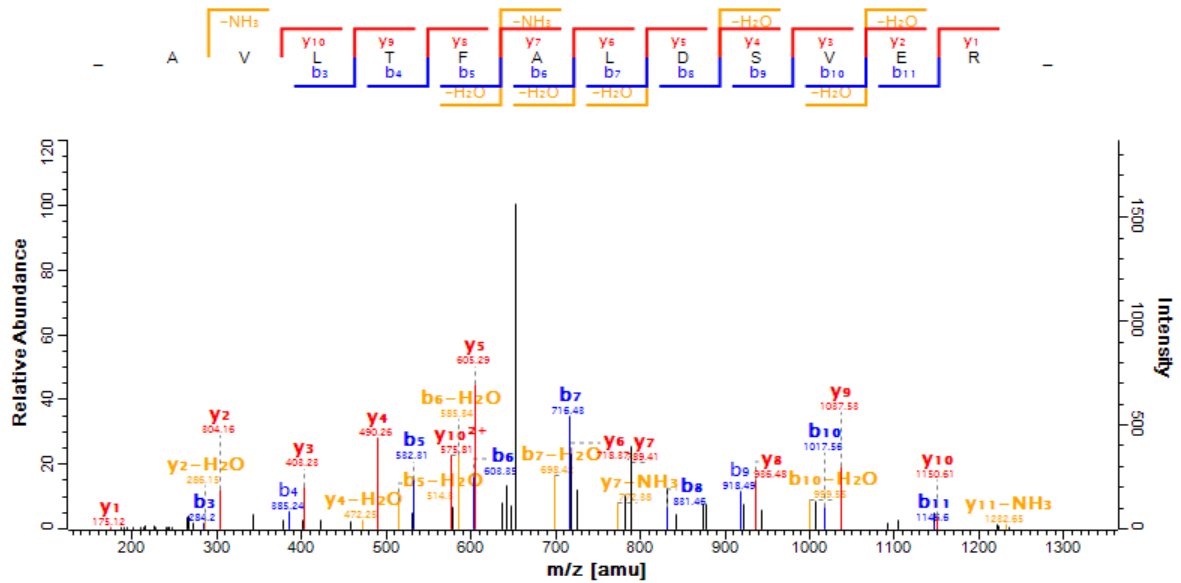
Best Match Spectrum:

Scan number	5596	Raw file	OGE-Mock-Frac8
Method	ITMS; CID	Genenames	PALMD



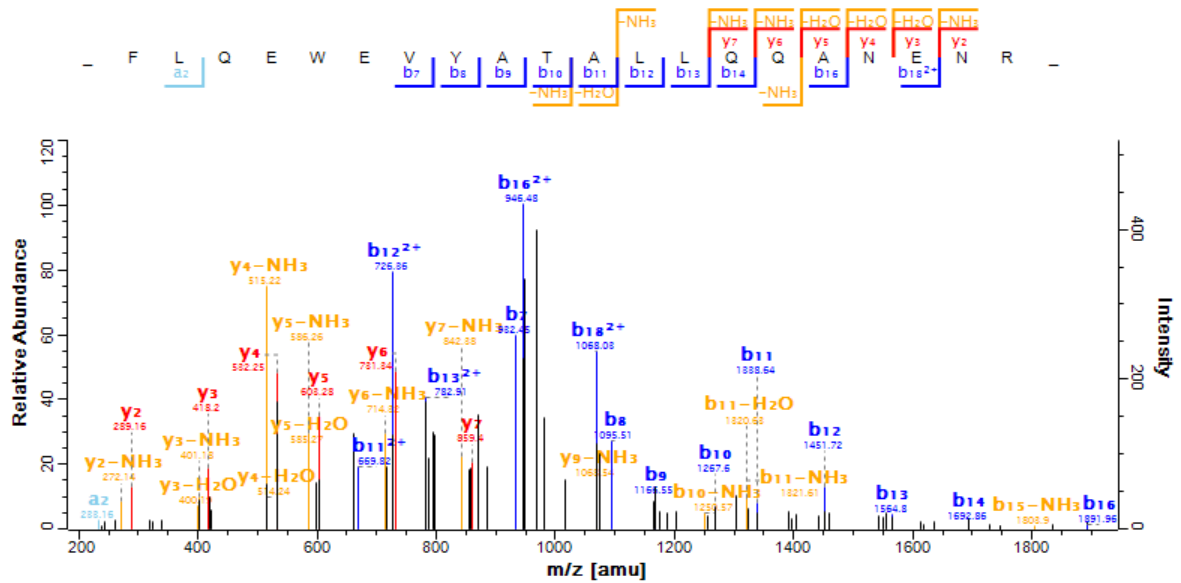
Protein Group ID: 3205
Protein Accession Numbers: Q9NQ4
Gene Names: EXOSC5
Peptide Sequence: AVLTFALDSVER
Total Number of Spectra: 4
Number of Replicates (out of 10): 4
Best Match Score: 166.7
Best Match Posterior Error Probability: 5.07E-07
Best Match Spectrum:

Scan number 4311 **Raw file** Prt-OGE-Batch2-WT-Frac17
Method ITMS; CID **Genenames** EXOSC5



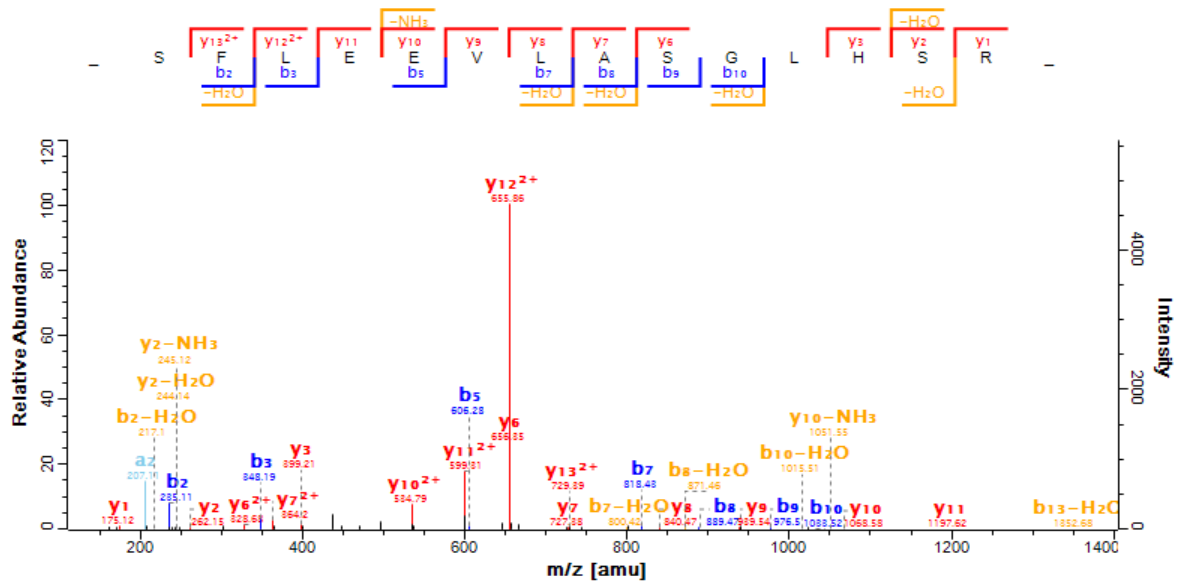
Protein Group ID: 3220
Protein Accession Numbers: Q9NRP4
Gene Names: ACN9
Peptide Sequence: FLQEWVYATALLQQANENR
Total Number of Spectra: 2
Number of Replicates (out of 10): 2
Best Match Score: 186.94
Best Match Posterior Error Probability: 1.36E-34
Best Match Spectrum:

Scan number 7706 **Raw file** Prt-OGE-Batch2-Mock-Frac20
Method ITMS; CID **Genenames** ACN9



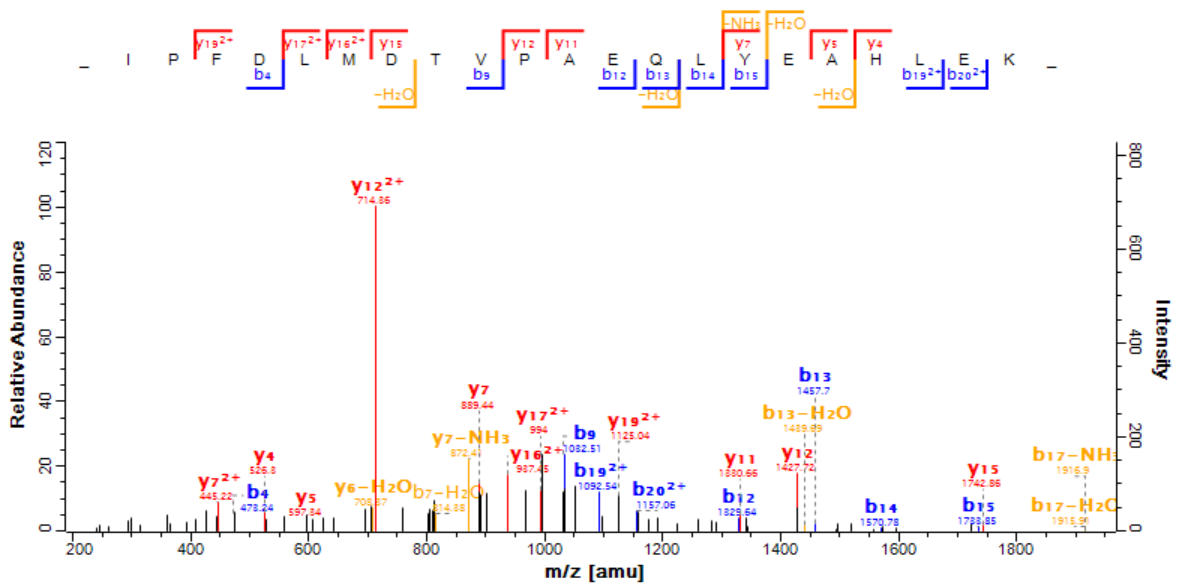
Protein Group ID: 3223
Protein Accession Numbers: Q9NRW7
Gene Names: VPS45
Peptide Sequence: SFLEEVLASGLHSR
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 156.08
Best Match Posterior Error Probability: 1.84E-08
Best Match Spectrum:

Scan number 6006 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac19
Method ITMS; CID **Genenames** VPS45



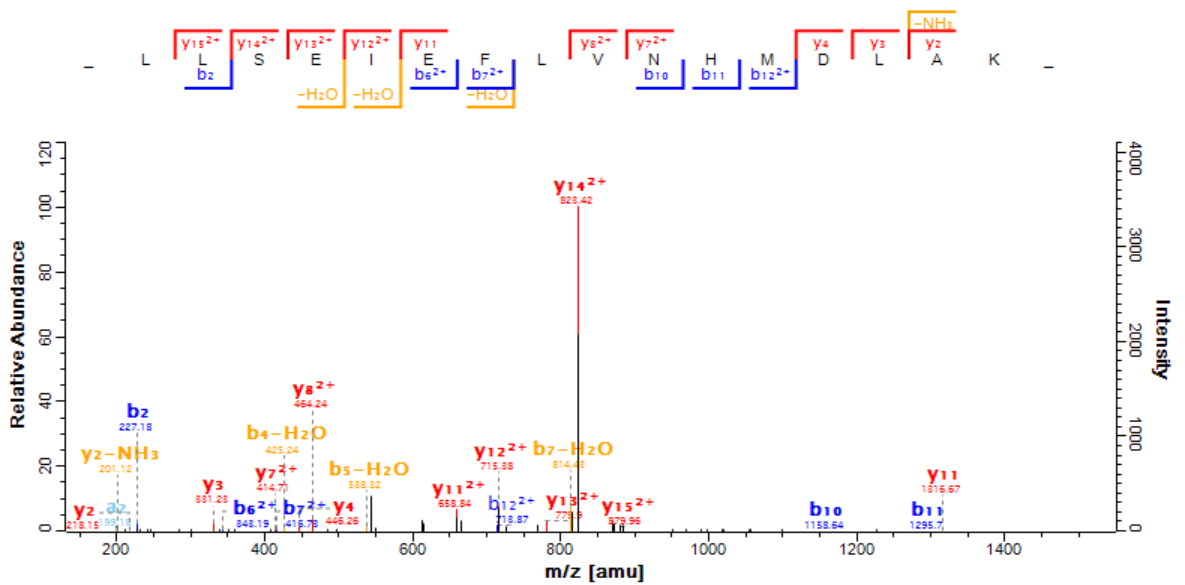
Protein Group ID: 3227
Protein Accession Numbers: Q9NRY4
Gene Names: ARHGAP35
Peptide Sequence: IPFDLMDTVPAEQLYEAHLEK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 87.49
Best Match Posterior Error Probability: 7.46E-05
Best Match Spectrum:

Scan number 6714 **Raw file** Prt-OGE-Batch3--Mock-Frac13
Method ITMS; CID **Genenames** ARHGAP35



Protein Group ID: 3245
Protein Accession Numbers: Q9NV70; Q9NV70-2
Gene Names: EXOC1
Peptide Sequence: LLSEIEFLVNHMDLAK
Total Number of Spectra: 5
Number of Replicates (out of 10): 3
Best Match Score: 81.904
Best Match Posterior Error Probability: 0.00092031
Best Match Spectrum:

Scan number 6220 **Raw file** OGE-WT-Frac16
Method ITMS; CID **Genenames** EXOC1



Protein Group ID: 3251

Protein Accession Numbers: Q9NVX0; Q9NVX0-3; Q9NVX0-2

Gene Names: HAUS2

Peptide Sequence: MDILVTETEELAENLK

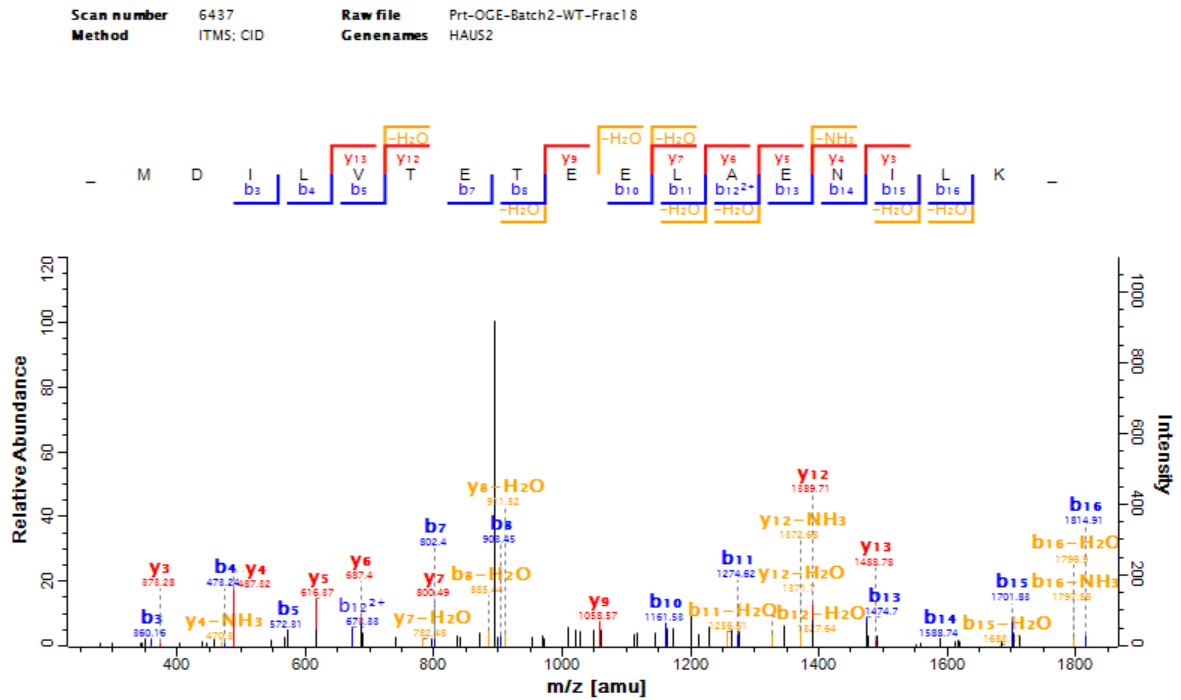
Total Number of Spectra: 2

Number of Replicates (out of 10): 2

Best Match Score: 146.2

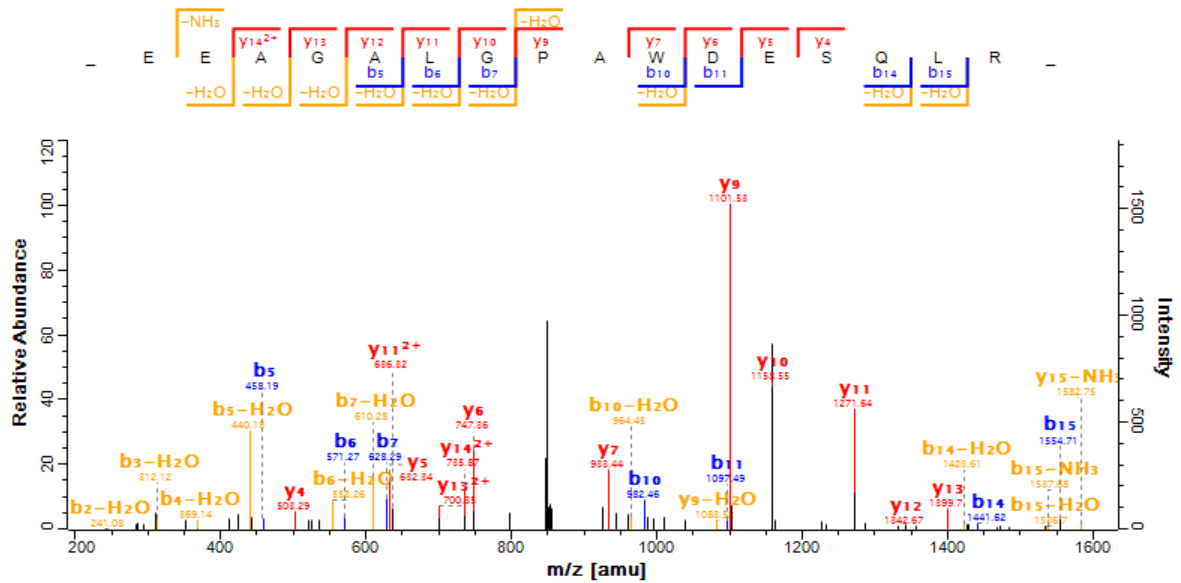
Best Match Posterior Error Probability: 3.35E-07

Best Match Spectrum:



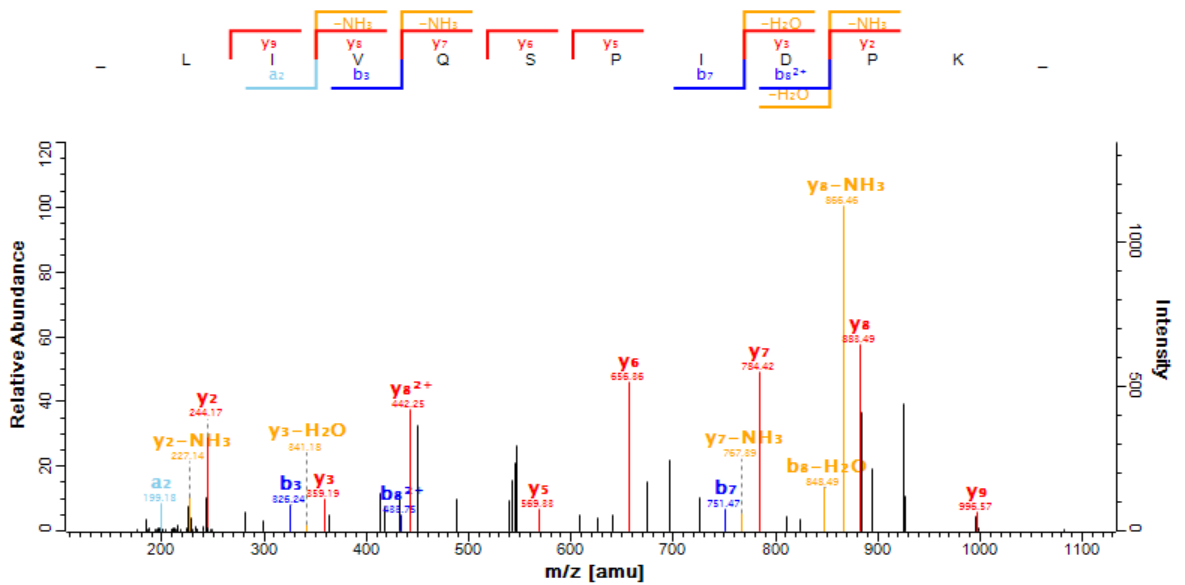
Protein Group ID: 3254
Protein Accession Numbers: Q9NWT6
Gene Names: HIF1AN
Peptide Sequence: EEAGALGPAWDESQR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 136.39
Best Match Posterior Error Probability: 1.06E-05
Best Match Spectrum:

Scan number 4209 **Raw file** Prt-OGE-Batch3-Mock-Frac8
Method ITMS; CID **Genenames** HIF1AN



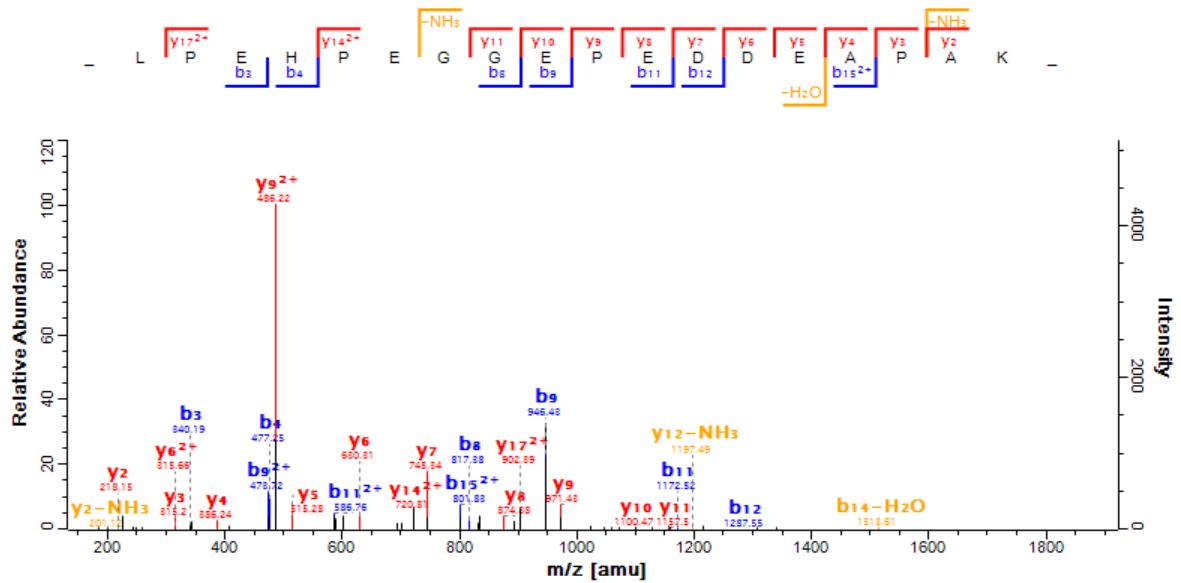
Protein Group ID: 3258
Protein Accession Numbers: Q9NX01
Gene Names: TXNL4B
Peptide Sequence: LIVQSPIDPK
Total Number of Spectra: 3
Number of Replicates (out of 10): 3
Best Match Score: 98.04
Best Match Posterior Error Probability: 0.00061806
Best Match Spectrum:

Scan number 3261 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac8
Method ITMS; CID **Genenames** TXNL4B



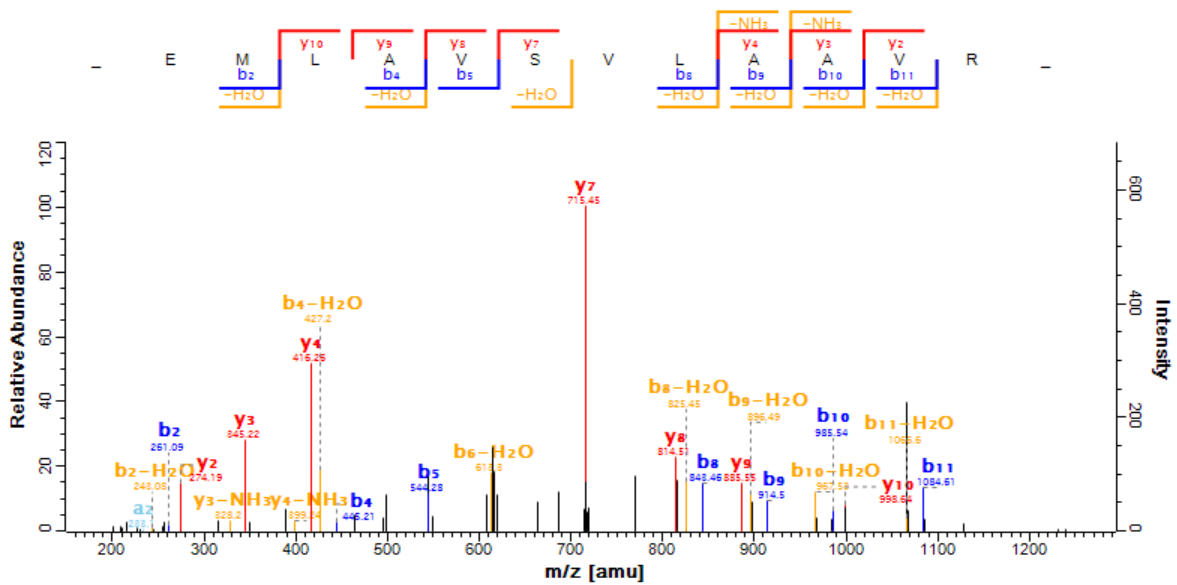
Protein Group ID: 3264
Protein Accession Numbers: Q9NX58
Gene Names: LYAR
Peptide Sequence: LPEHPEGGEPEDDEAPAK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 88.19
Best Match Posterior Error Probability: 0.00049923
Best Match Spectrum:

Scan number 1289 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac18
Method ITMS; CID **Genenames** LYAR



Protein Group ID: 3265
Protein Accession Numbers: Q9NX62
Gene Names: IMPAD1
Peptide Sequence: EMLAVSVLAAVR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 125.97
Best Match Posterior Error Probability: 0.00018825
Best Match Spectrum:

Scan number 6160 **Raw file** Prt-OGE-Batch3-Mock-Frac8
Method ITMS; CID **Genenames** IMPAD1



Protein Group ID: 3268

Protein Accession Numbers: Q9NXX6; Q9NXX6-2

Gene Names: NSMCE4A

Peptide Sequence: EDILNAGDKLTEVLEEANNTLTFNENR

Total Number of Spectra: 6

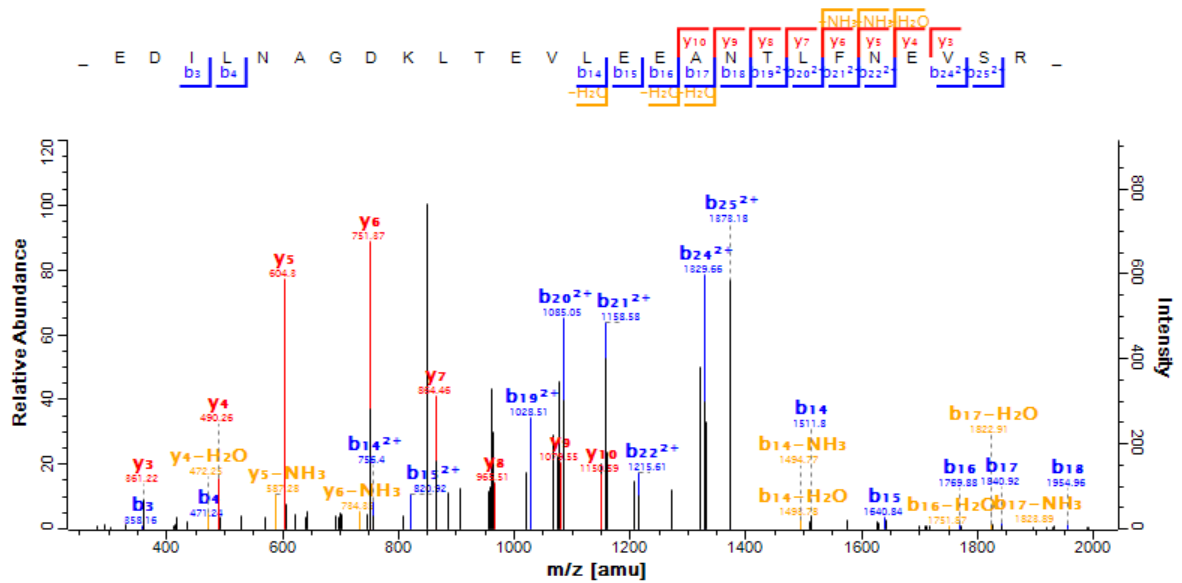
Number of Replicates (out of 10): 5

Best Match Score: 121.33

Best Match Posterior Error Probability: 3.12E-16

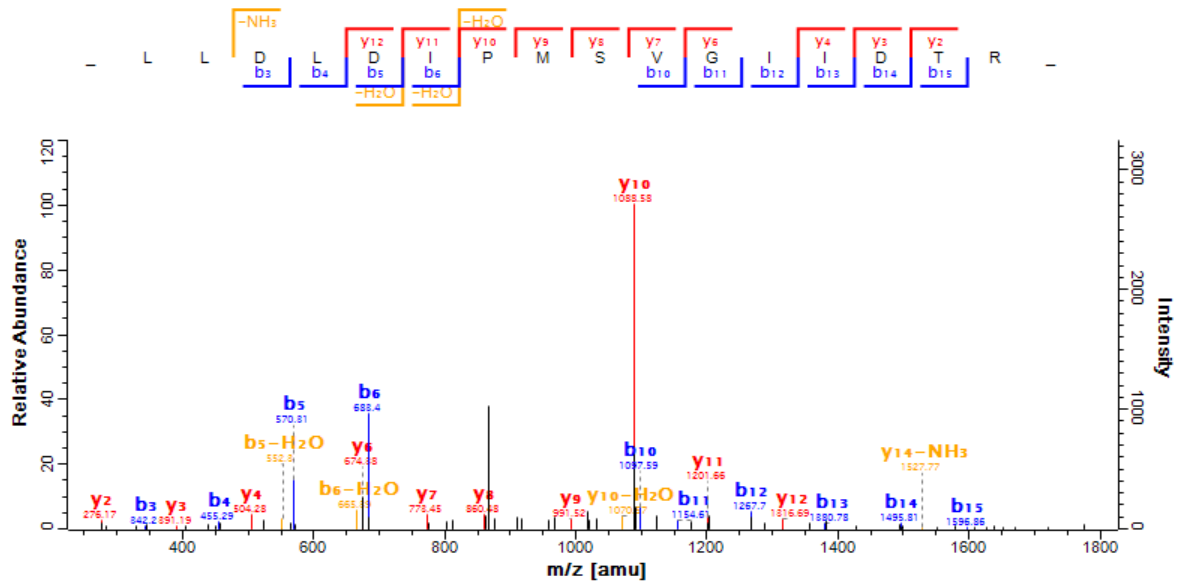
Best Match Spectrum:

Scan number 7602 **Raw file** OGE-WT-Frac6
Method ITMS; CID **Genenames** NSMCE4A



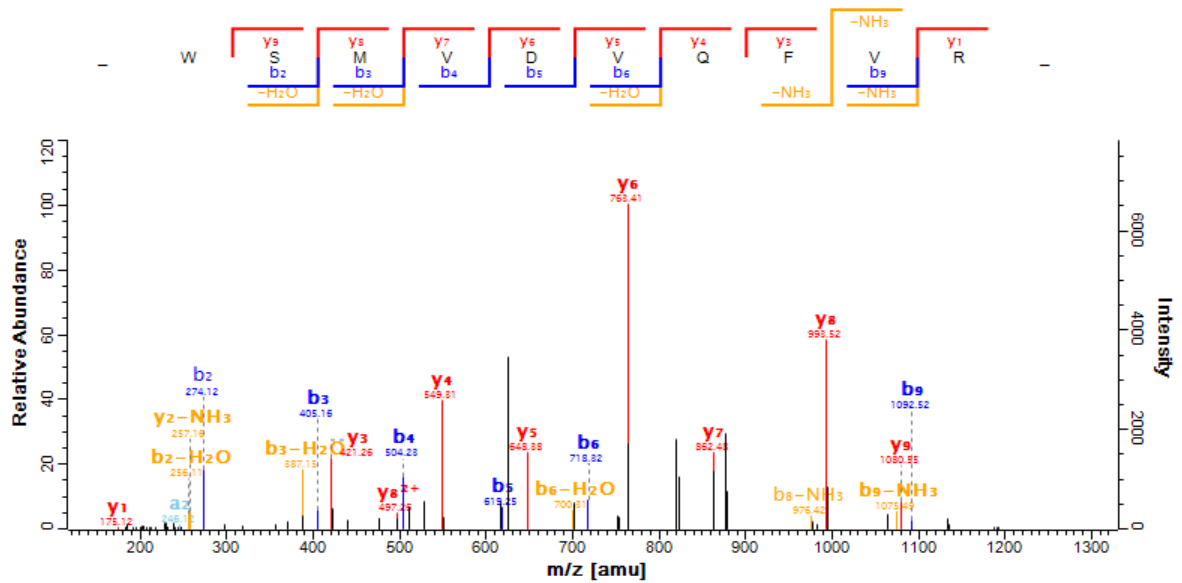
Protein Group ID: 3277
Protein Accession Numbers: Q9NZI7; Q9NZI7-4
Gene Names: UBPI
Peptide Sequence: LLDLDIPMSVGIIDTR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 123.02
Best Match Posterior Error Probability: 8.64E-05
Best Match Spectrum:

Scan number 5819 **Raw file** Prt-OGE-Batch2-WT-Frac12
Method ITMS; CID **Genenames** UBPI



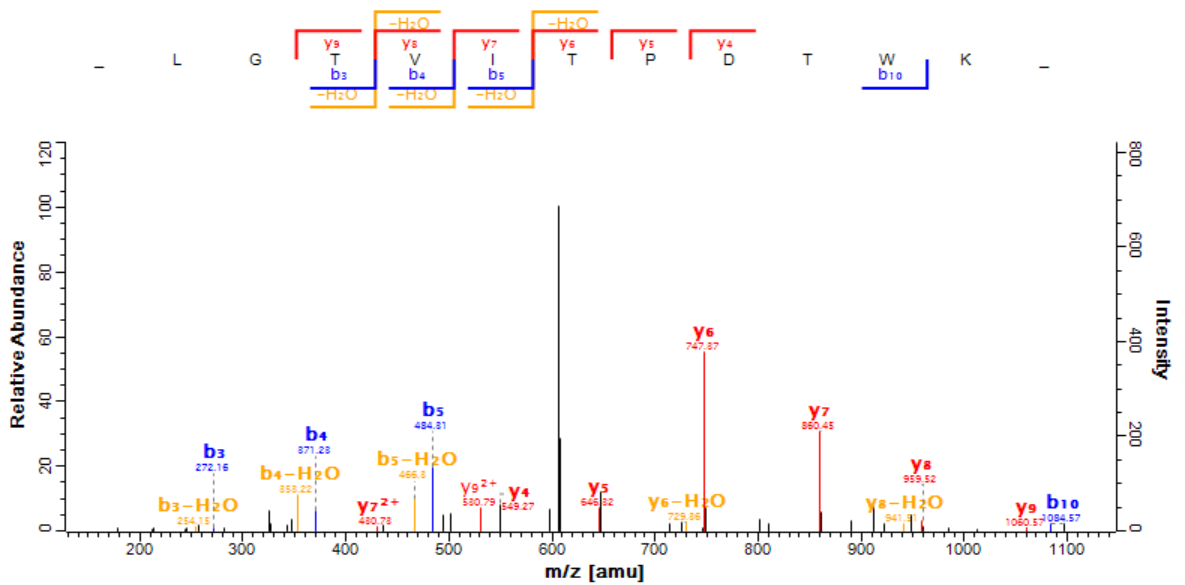
Protein Group ID: 3288
Protein Accession Numbers: Q9P016
Gene Names: THYN1
Peptide Sequence: WSMVDVQFVR
Total Number of Spectra: 6
Number of Replicates (out of 10): 5
Best Match Score: 128.01
Best Match Posterior Error Probability: 9.43E-05
Best Match Spectrum:

Scan number 4868 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac22
Method ITMS; CID **Genenames** THYN1



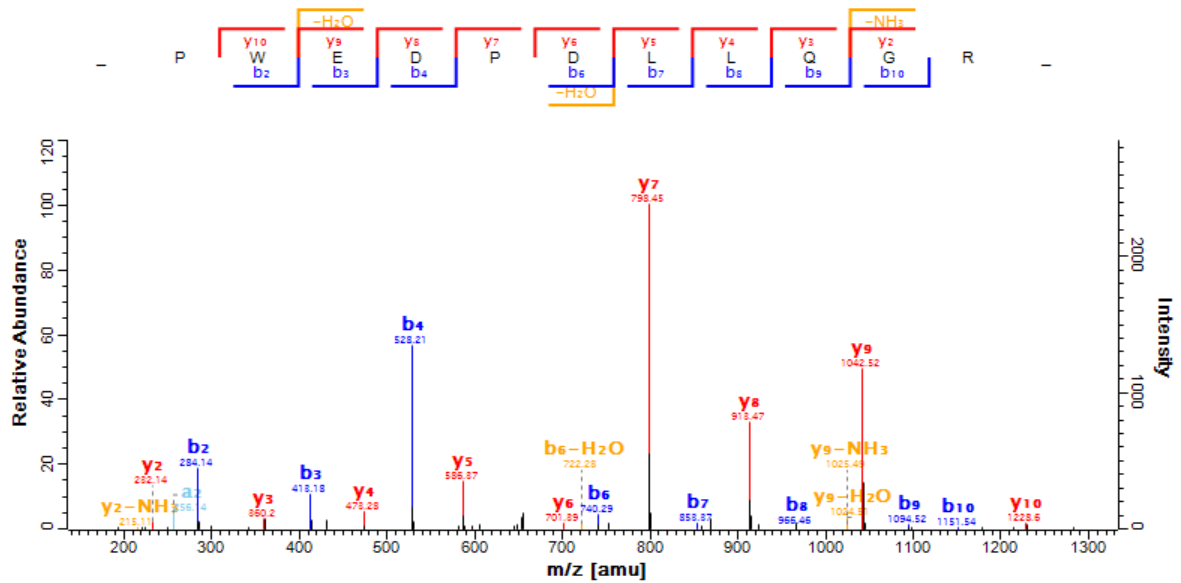
Protein Group ID: 3289
Protein Accession Numbers: Q9P021
Gene Names: CRIPT
Peptide Sequence: LGTVITPDTWK
Total Number of Spectra: 6
Number of Replicates (out of 10): 3
Best Match Score: 108.7
Best Match Posterior Error Probability: 0.00015808
Best Match Spectrum:

Scan number 2574 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac22
Method ITMS; CID **Genenames** CRIPT



Protein Group ID: 3296
Protein Accession Numbers: Q9P0S2
Gene Names: COX16
Peptide Sequence: PWEDPDLLQGR
Total Number of Spectra: 4
Number of Replicates (out of 10): 3
Best Match Score: 130.56
Best Match Posterior Error Probability: 4.15E-05
Best Match Spectrum:

Scan number 3243 **Raw file** OGE-WT-Frac23
Method ITMS; CID **Genenames** COX16



Protein Group ID: 3298

Protein Accession Numbers: Q9P1Z9-2; Q9P1Z9

Gene Names: C9orf174

Peptide Sequence: CQVAKSNSQTNGLNFSLQQLQNKIK

Total Number of Spectra: 1

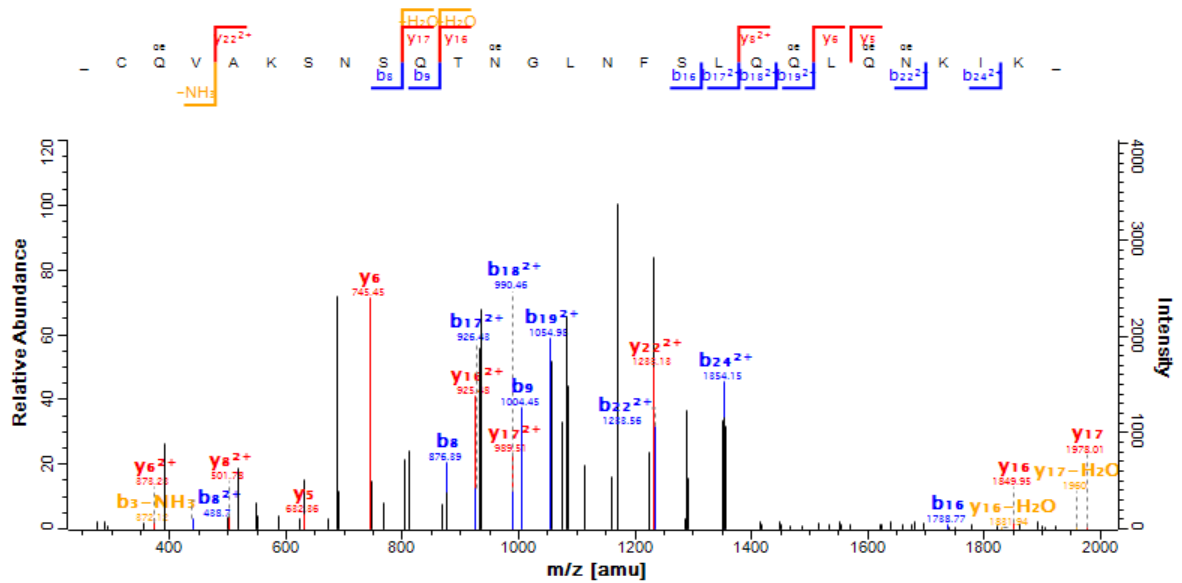
Number of Replicates (out of 10): 1

Best Match Score: 74.048

Best Match Posterior Error Probability: 0.0031304

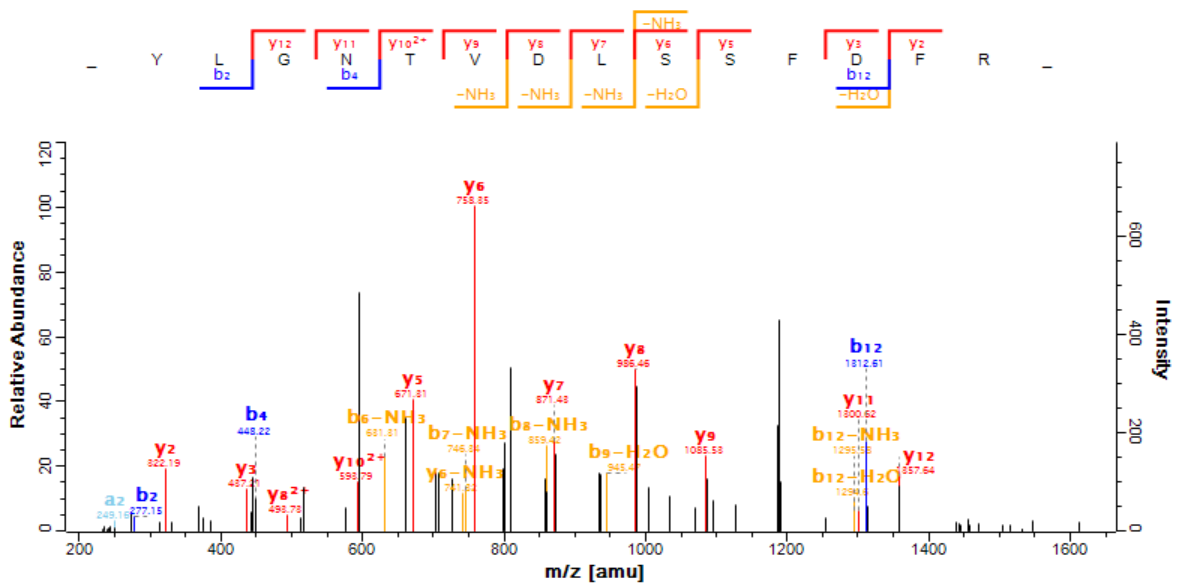
Best Match Spectrum:

Scan number 4998 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac10
Method ITMS; CID **Genenames** C9orf174



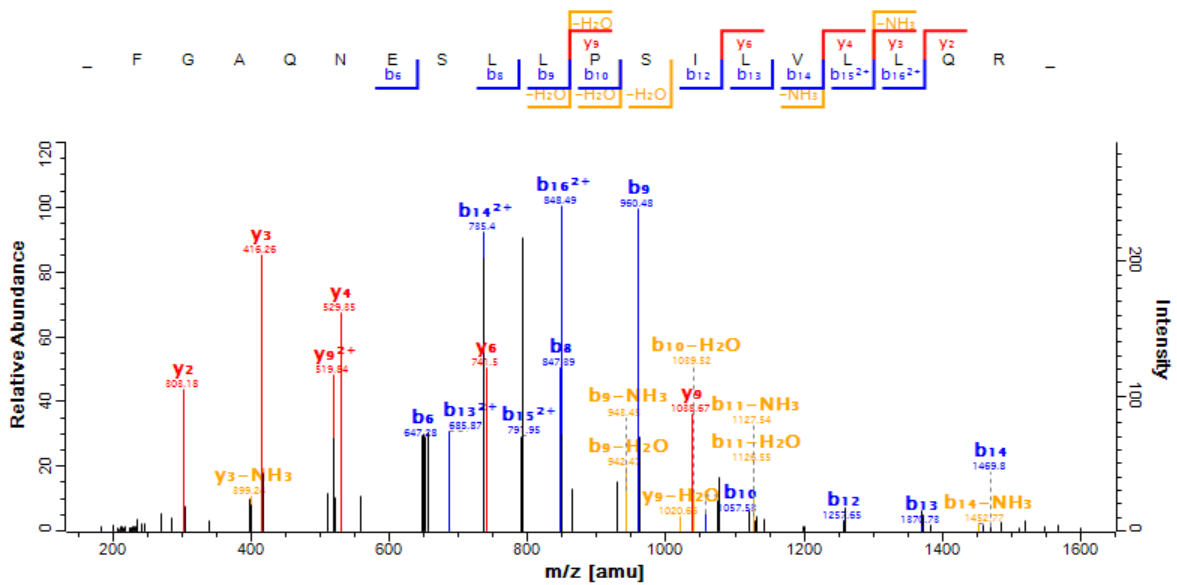
Protein Group ID: 3307
Protein Accession Numbers: Q9UBB5; Q9UBB5-3
Gene Names: MBD2
Peptide Sequence: YLGNTVDLSSFDFR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 86.944
Best Match Posterior Error Probability: 0.00076693
Best Match Spectrum:

Scan number 4656 **Raw file** Prt-OGE-Batch2-WT-Frac21
Method ITMS; CID **Genenames** MBD2



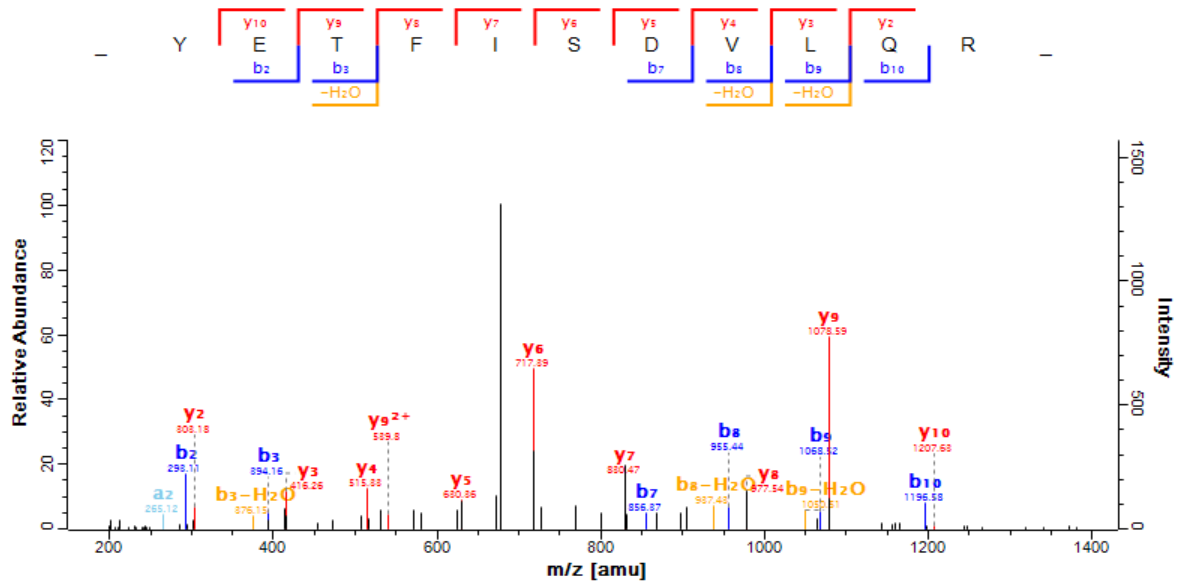
Protein Group ID: 3309
Protein Accession Numbers: Q9UBF2
Gene Names: COPG2
Peptide Sequence: FGAQNESLLPSILVLLQR
Total Number of Spectra: 3
Number of Replicates (out of 10): 2
Best Match Score: 106.6
Best Match Posterior Error Probability: 0.0001471
Best Match Spectrum:

Scan number 7227 **Raw file** OGE-Mock-Frac11
Method ITMS; CID **Genenames** COPG2



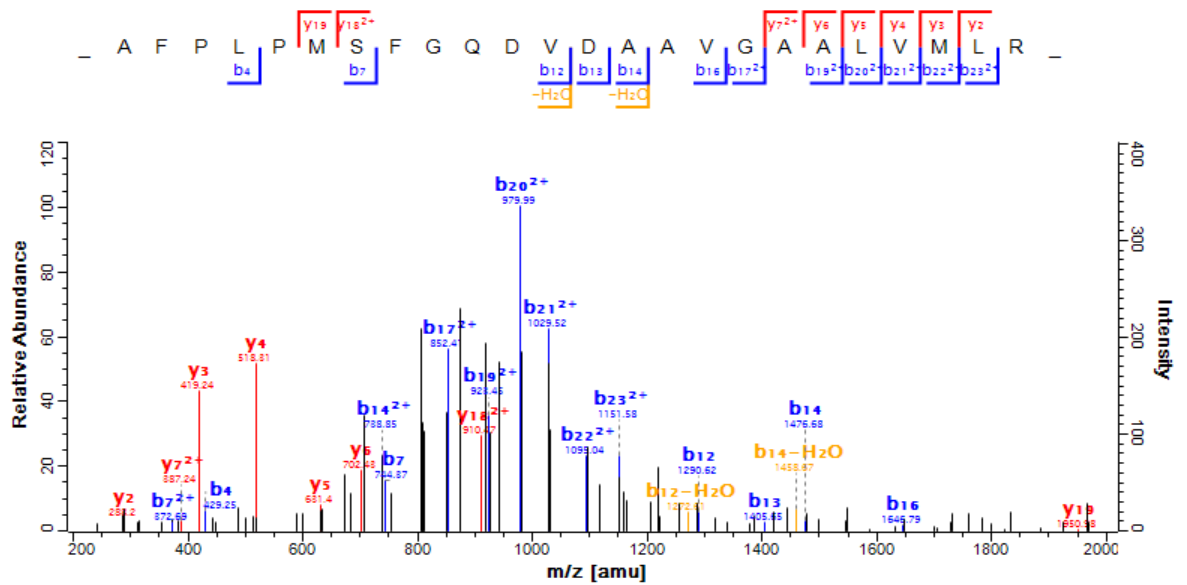
Protein Group ID: 3312
Protein Accession Numbers: Q9UBK9
Gene Names: UXT
Peptide Sequence: YETFISDVLQR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 125.97
Best Match Posterior Error Probability: 1.82E-06
Best Match Spectrum:

Scan number 4928 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac17
Method ITMS; CID **Genenames** UXT



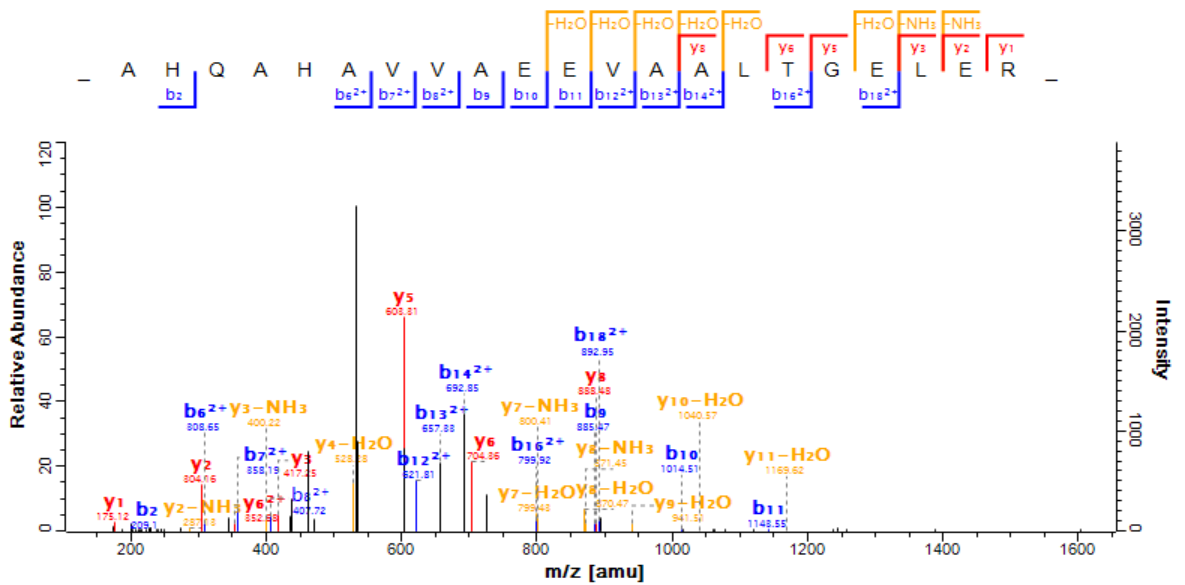
Protein Group ID: 3335
Protein Accession Numbers: Q9UHI6
Gene Names: SHPK
Peptide Sequence: AFPLPMSFGQDVDAAVGAALVMLR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 93.5
Best Match Posterior Error Probability: 2.89E-06
Best Match Spectrum:

Scan number 8880 **Raw file** 20100914-KD-Batch4-Prt-OGE-Mock-Frac16
Method ITMS; CID **Genenames** SHPK



Protein Group ID: 3338
Protein Accession Numbers: Q9UHR6
Gene Names: ZNHIT2
Peptide Sequence: AHQAHAVVAEEVAALTEGELER
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 81.854
Best Match Posterior Error Probability: 0.00028614
Best Match Spectrum:

Scan number 5735 **Raw file** Prt-OGE-Batch3--Mock-Frac11
Method ITMS; CID **Genenames** ZNHIT2



Protein Group ID: 3365

Protein Accession Numbers: Q9UKT9; Q9UKT9-7; Q9UKT9-3; Q9UKT9-4; Q9UKT9-15; Q9UKT9-2; Q9UKT9-8; Q9UKT9-6; Q9UKT9-5; Q9UKT9-13; Q9UKT9-14

Gene Names: IKZF3

Peptide Sequence: EYNEYENIK

Total Number of Spectra: 23

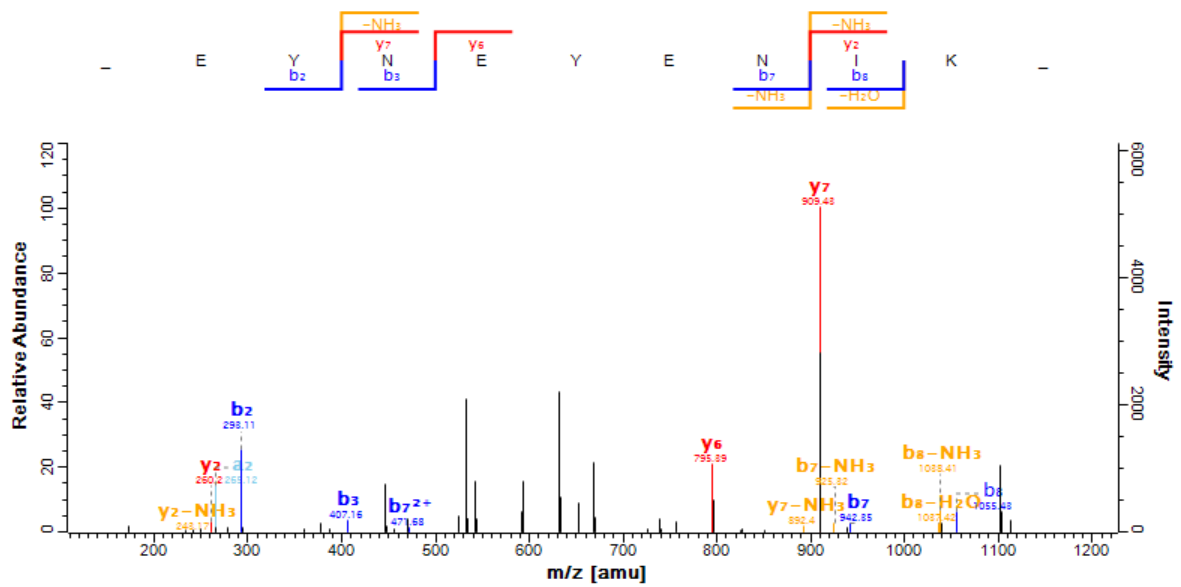
Number of Replicates (out of 10): 7

Best Match Score: 95.502

Best Match Posterior Error Probability: 0.0011517

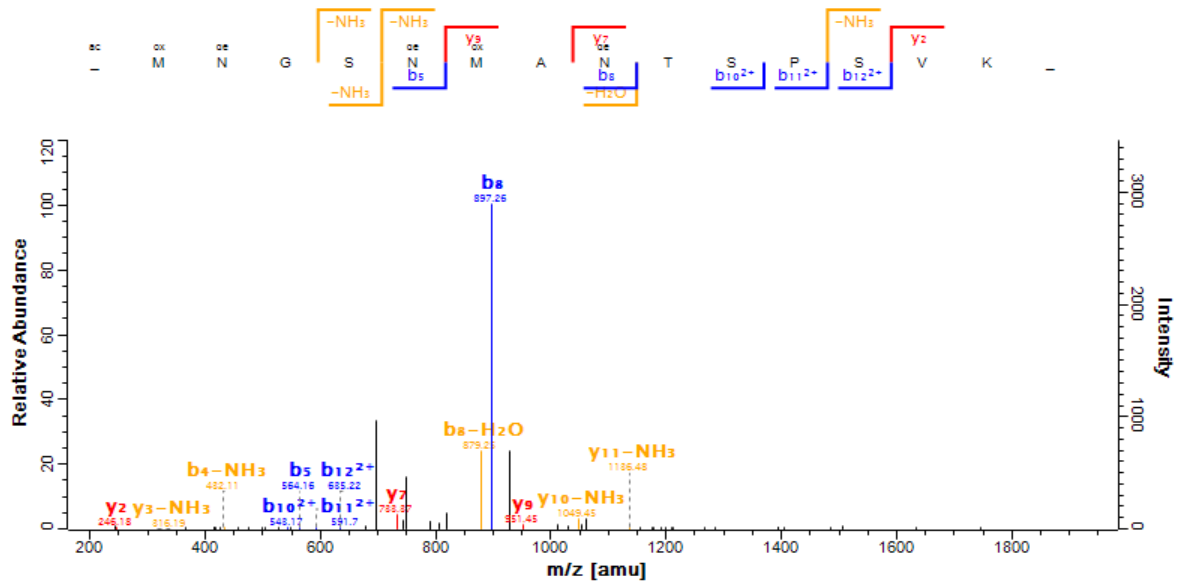
Best Match Spectrum:

Scan number	3916	Raw file	20100917-KD-Batch5-Prt-OGE-Mock-Frac21
Method	ITMS; CID	Genenames	IKZF3



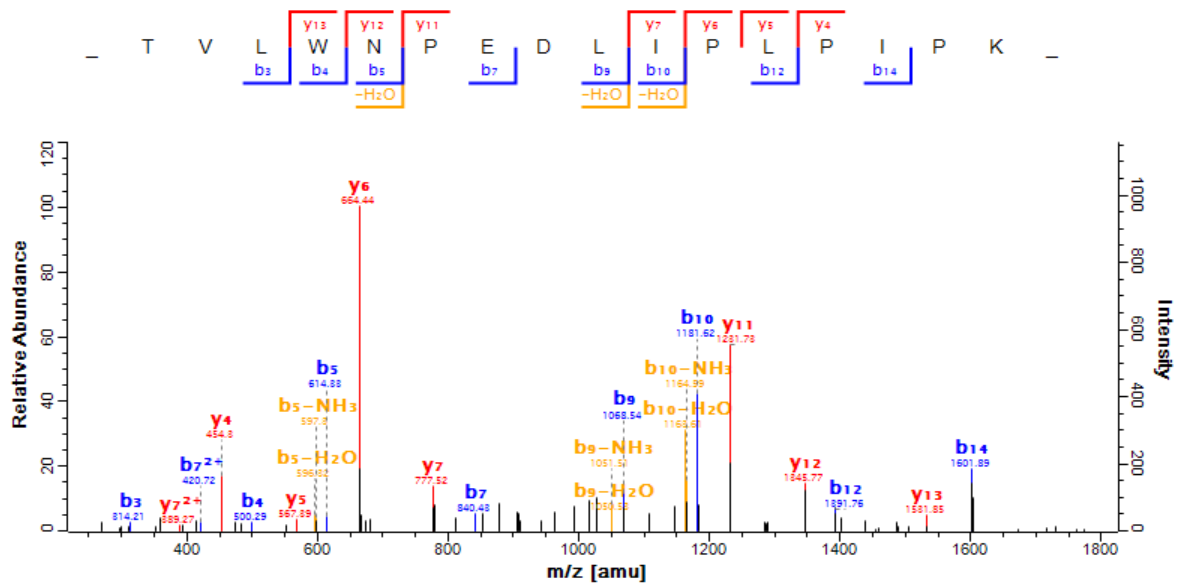
Protein Group ID: 3374
Protein Accession Numbers: Q9ULR5
Gene Names: PAIP2B
Peptide Sequence: MNGSNMANTSPSVK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 30.567
Best Match Posterior Error Probability: 0.0072043
Best Match Spectrum:

Scan number 7868 **Raw file** OGE-Mock-Frac11
Method ITMS; CID **Genenames** PAIP2B



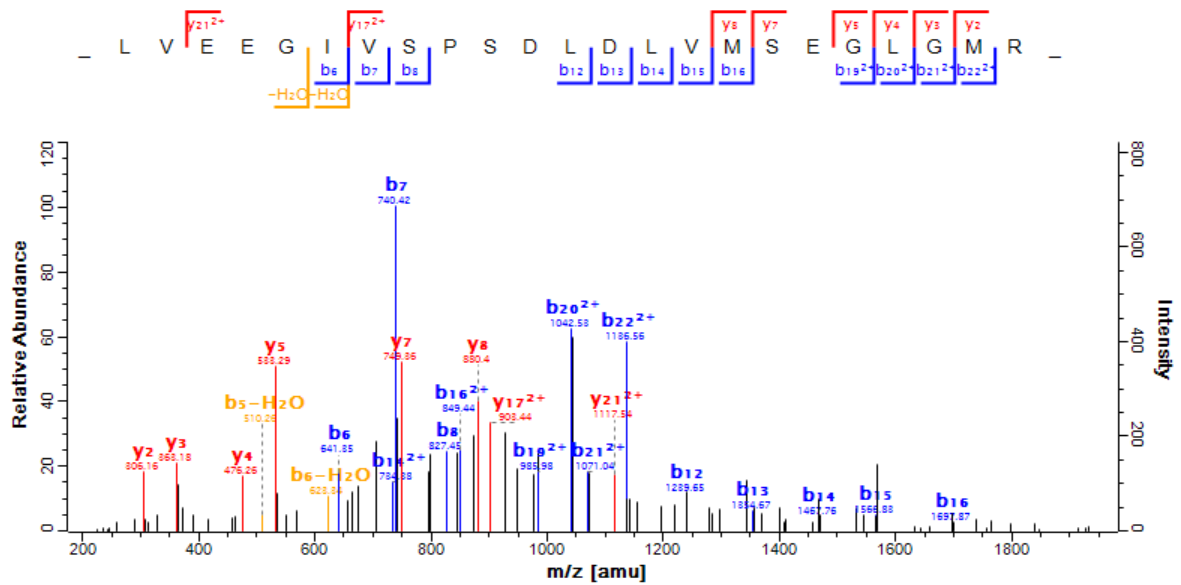
Protein Group ID: 3396
Protein Accession Numbers: Q9UPT8
Gene Names: ZC3H4
Peptide Sequence: TVLWNPEDLIPLIPK
Total Number of Spectra: 17
Number of Replicates (out of 10): 7
Best Match Score: 120.7
Best Match Posterior Error Probability: 0.00010684
Best Match Spectrum:

Scan number 6300 **Raw file** Prt-OGE-Batch2-WT-Frac14
Method ITMS; CID **Genenames** ZC3H4



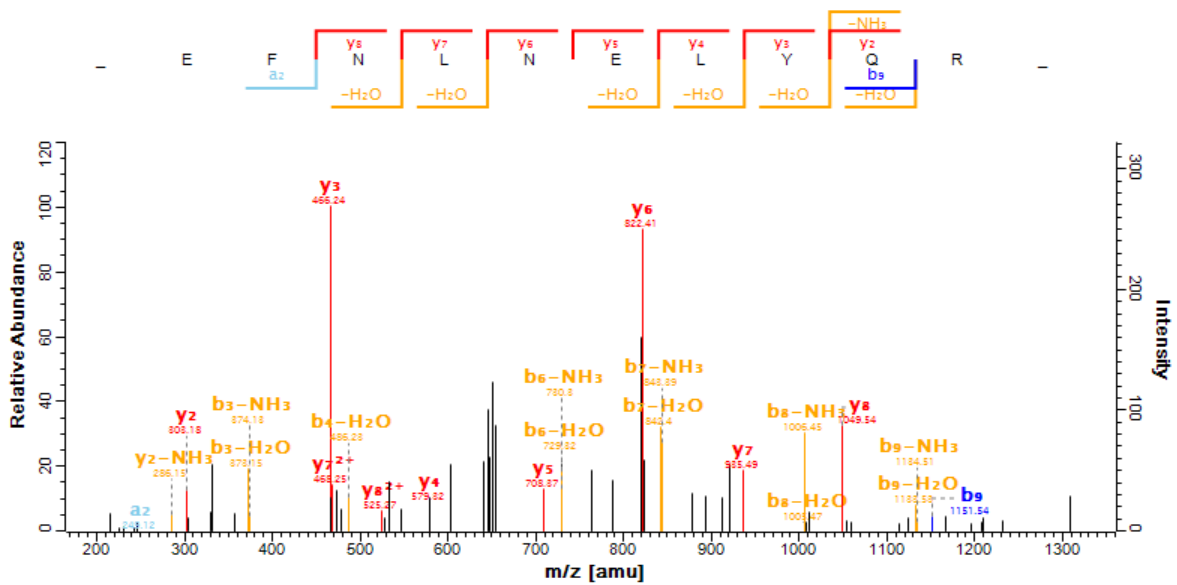
Protein Group ID: 3419
Protein Accession Numbers: Q9Y2S2; Q9Y2S2-2
Gene Names: CRYL1
Peptide Sequence: LVEEGIVSPSDLVMS EGLGM R
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 107.72
Best Match Posterior Error Probability: 8.14E-08
Best Match Spectrum:

Scan number 6785 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac12
Method ITMS; CID **Genenames** CRYL1



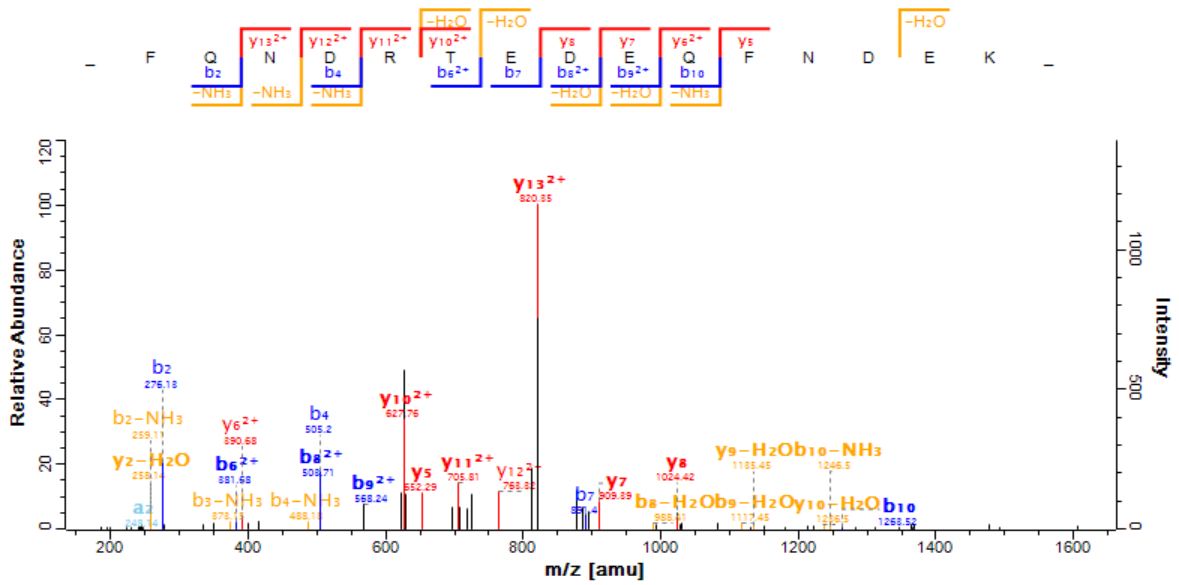
Protein Group ID: 3431
Protein Accession Numbers: Q9Y320; Q9Y320-2
Gene Names: TMX2
Peptide Sequence: EFNLNELYQR
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 85.533
Best Match Posterior Error Probability: 0.001677
Best Match Spectrum:

Scan number 3327 **Raw file** Prt-OGE-Batch3-WT-Frac1
Method ITMS; CID **Genenames** TMX2



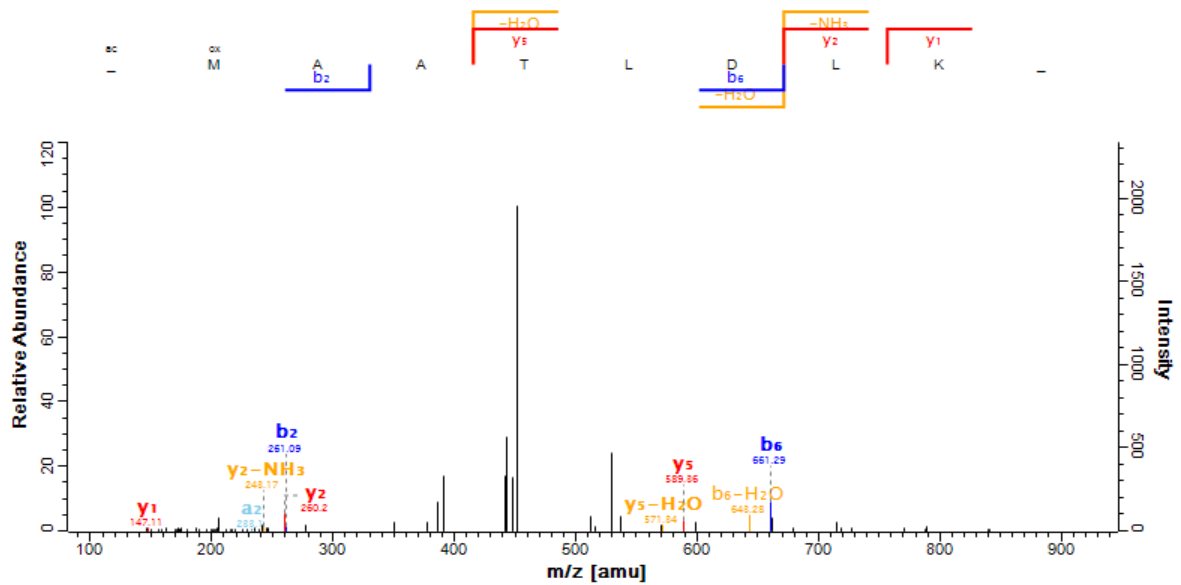
Protein Group ID: 3434
Protein Accession Numbers: Q9Y376
Gene Names: CAB39
Peptide Sequence: FQNDRTED EQFNDEK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 111.83
Best Match Posterior Error Probability: 0.00018948
Best Match Spectrum:

Scan number 890 **Raw file** 20100930-KD-Batch5-Prt-OGE-WT-Frac15
Method ITMS; CID **Genenames** CAB39



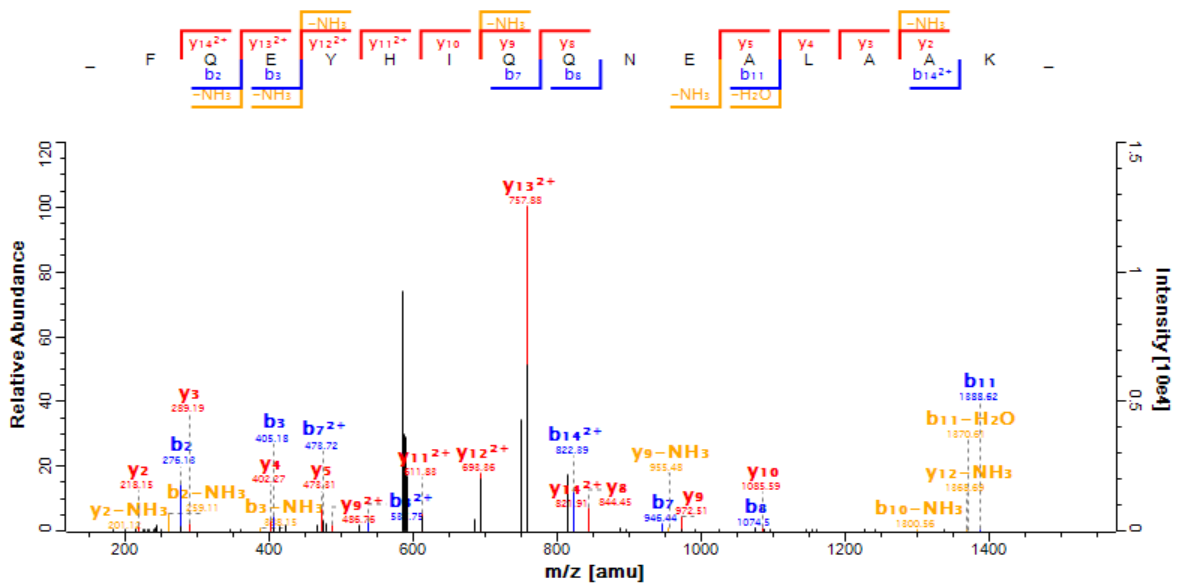
Protein Group ID: 3459
Protein Accession Numbers: Q9Y3X0
Gene Names: CCDC9
Peptide Sequence: MAATLDLK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 50.127
Best Match Posterior Error Probability: 0.044436
Best Match Spectrum:

Scan number 5300 **Raw file** OGE-Mock-Frac4
Method ITMS; CID **Genenames** CCDC9



Protein Group ID: 3473
Protein Accession Numbers: Q9Y5J7
Gene Names: TIMM9
Peptide Sequence: FQEYHIQQNEALAAK
Total Number of Spectra: 7
Number of Replicates (out of 10): 6
Best Match Score: 134.61
Best Match Posterior Error Probability: 7.38E-06
Best Match Spectrum:

Scan number 2100 **Raw file** Prt-OGE-Batch3-WT-Frac14
Method ITMS; CID **Genenames** TIMM9



Protein Group ID: 3479

Protein Accession Numbers: Q9Y5U8

Gene Names: BRP44L

Peptide Sequence: DYLMSTHFWGPVANWGLPIAAAI⁺NDMK

Total Number of Spectra: 2

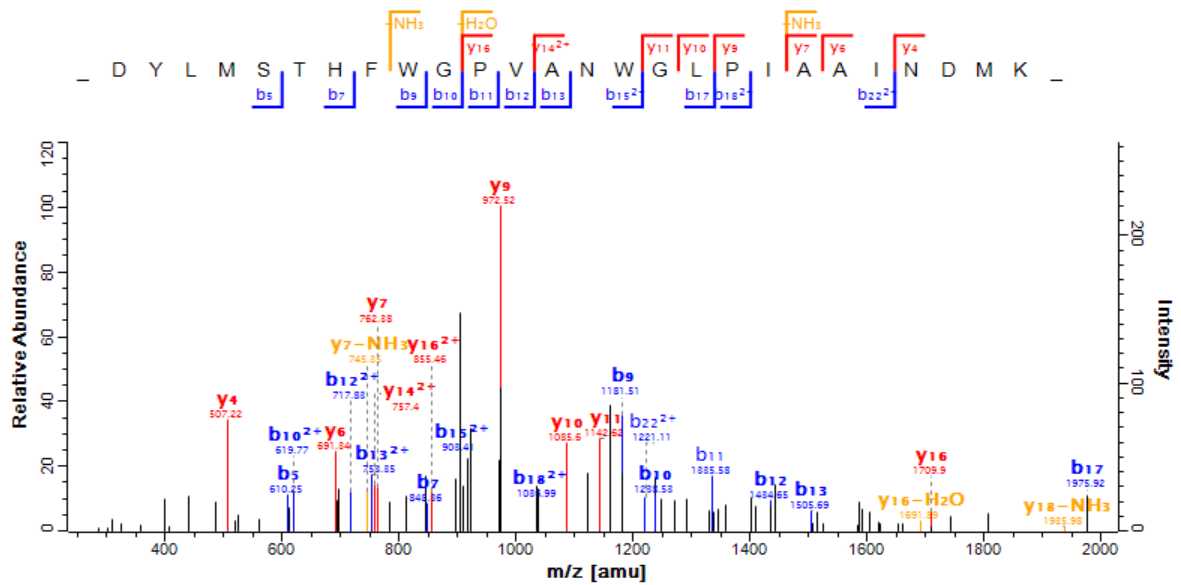
Number of Replicates (out of 10): 2

Best Match Score: 80.702

Best Match Posterior Error Probability: 6.85E-06

Best Match Spectrum:

Scan number 7059 **Raw file** 20100917-KD-Batch5-Prt-OGE-Mock-Frac23
Method ITMS; CID **Genenames** BRP44L



Protein Group ID: 3499
Protein Accession Numbers: Q9Y6R6
Gene Names: ZNF780B
Peptide Sequence: ISPENDIFEINLPK
Total Number of Spectra: 1
Number of Replicates (out of 10): 1
Best Match Score: 86.803
Best Match Posterior Error Probability: 0.0086229
Best Match Spectrum:

Scan number 3984 **Raw file** OGE-WT-Frac10
Method ITMS; CID **Genenames** ZNF780B

