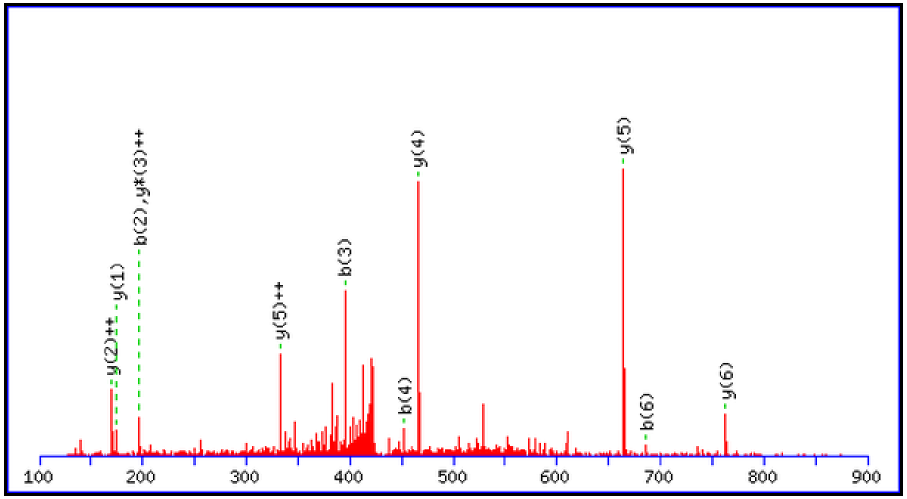
Supplementary Figure S3

a.

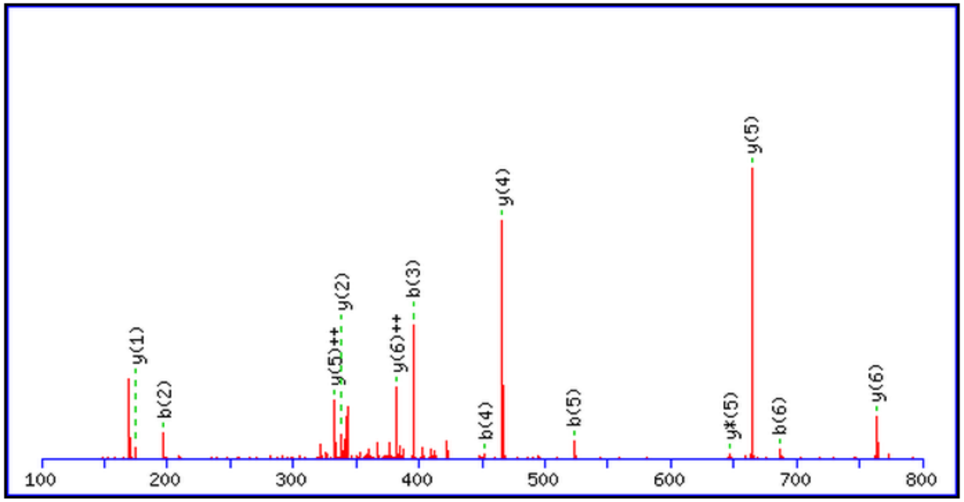
MS/MS Fragmentation of **PVKGAYR**
Found in **Q07666**, KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1

Match to Query 1018: 859.491428 from(430.752990,2+) intensity(111006.5938)
Title: File1319 Spectrum5739 scans: 6249
Data file I:\2013-9-13-Hela-Prometh-Fr2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 859.4916
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termi
Variable modifications:
K3     : Propionyl-Methylation (K)
Ions Score: 20  Expect: 4.6
Matches : 11/44 fragment ions using 24 most intense peaks   (help)
```

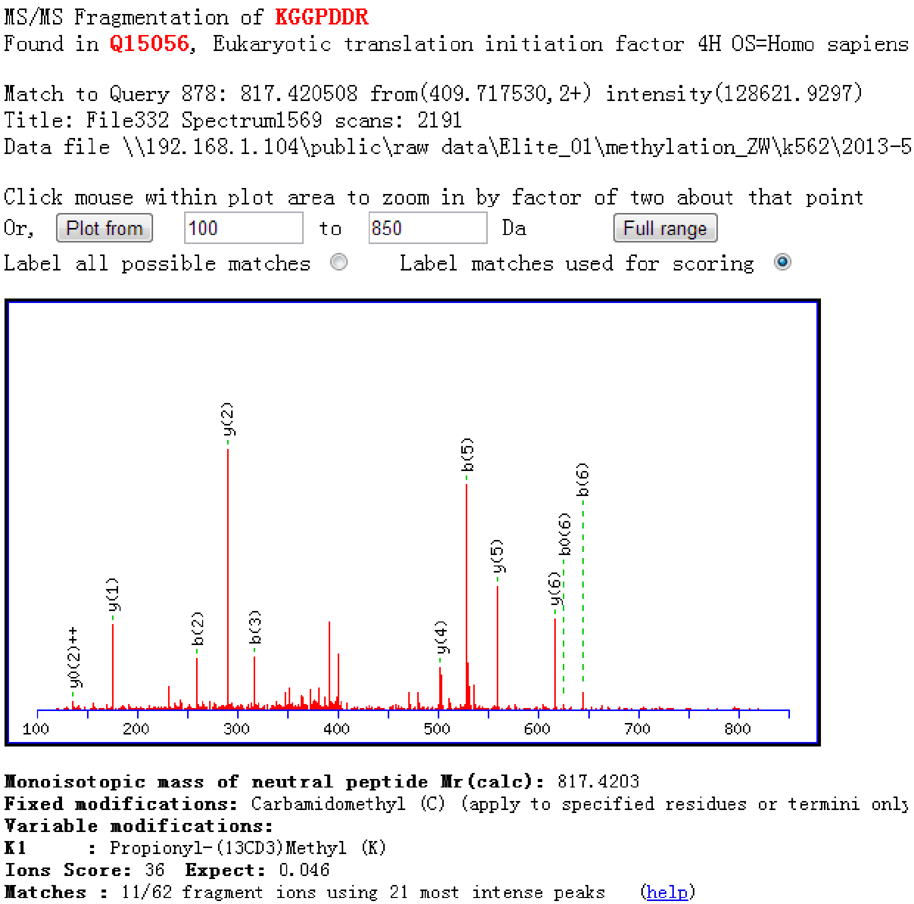


```
Monoisotopic mass of neutral peptide Mr(calc): 859.4916
Variable modifications:
K3     : Propionyl-Methylation (K)
Ions Score: 31  Expect: 0.26
Matches : 13/44 fragment ions using 28 most intense peaks    (help)
```

MS/MS spectrum of HeLa cell derived peptide PVK$_{pr+me1}$GAYR from protein KHDRBS1

Corresponding synthetic peptide

b.

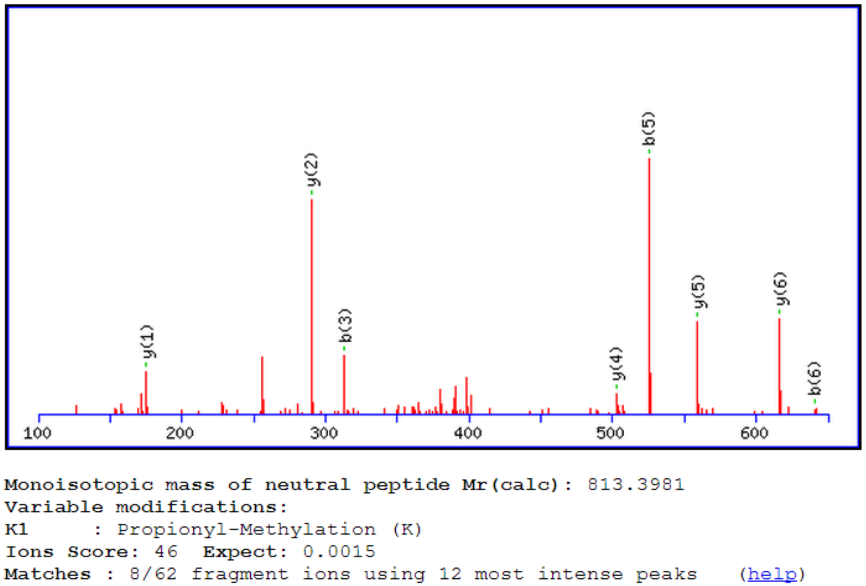


MS/MS Fragmentation of **KGGPDDR**
Found in **Q15056**, Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5

Match to Query 878: 817.420508 from(409.717530,2+) intensity(128621.9297)
Title: File332 Spectrum1569 scans: 2191
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr10-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 817.4203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 36 **Expect:** 0.046
Matches : 11/62 fragment ions using 21 most intense peaks (help)



Monoisotopic mass of neutral peptide Mr(calc): 813.3981
Variable modifications:
K1 : Propionyl-Methylation (K)
Ions Score: 46 **Expect:** 0.0015
Matches : 8/62 fragment ions using 12 most intense peaks (help)

MS/MS spectrum of K562 cell derived peptide K_{pr+me1}GGPDDR from protein EIF4H

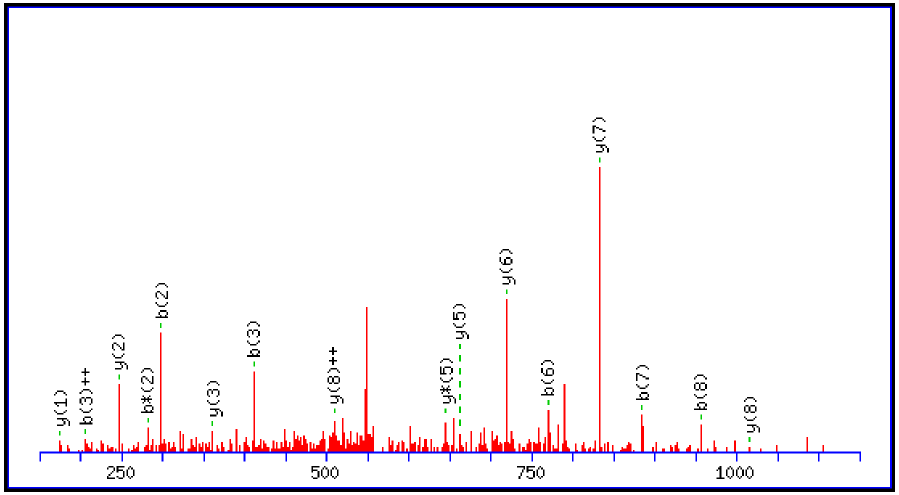
Corresponding synthetic peptide

C.

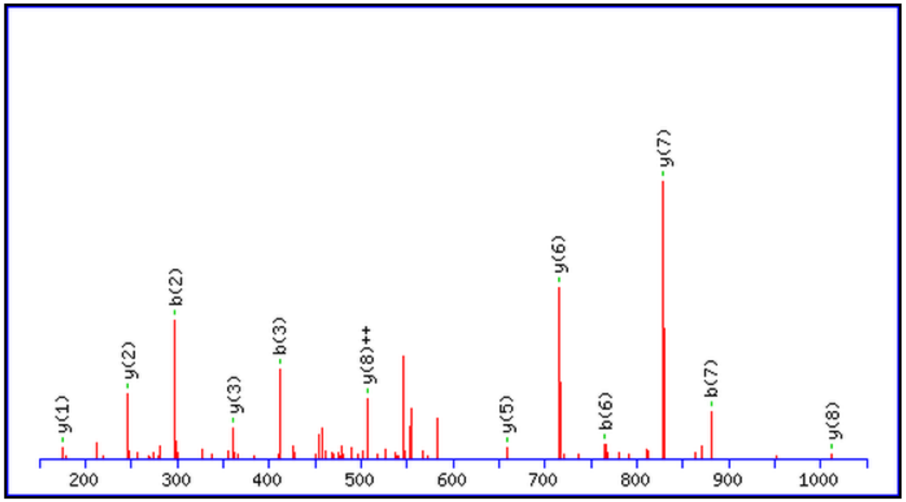
MS/MS Fragmentation of **LKLGVKDAR**
Found in **F8WCX5**, Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3 PE=2 SV=1

Match to Query 2801: 1128.713848 from(565.364200,2+) intensity(20450.9316)
Title: File365 Spectrum9513 scans: 11035
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-6-3-K562-Kpropio-methyl-IP-Fr20-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1128.7139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini (
Variable modifications:
K2 : Propionyl (K)
K6 : Propionyl-(13CD3)Methyl (K)
Ions Score: 28 **Expect:** 0.27
Matches : 16/78 fragment ions using 47 most intense peaks (help)

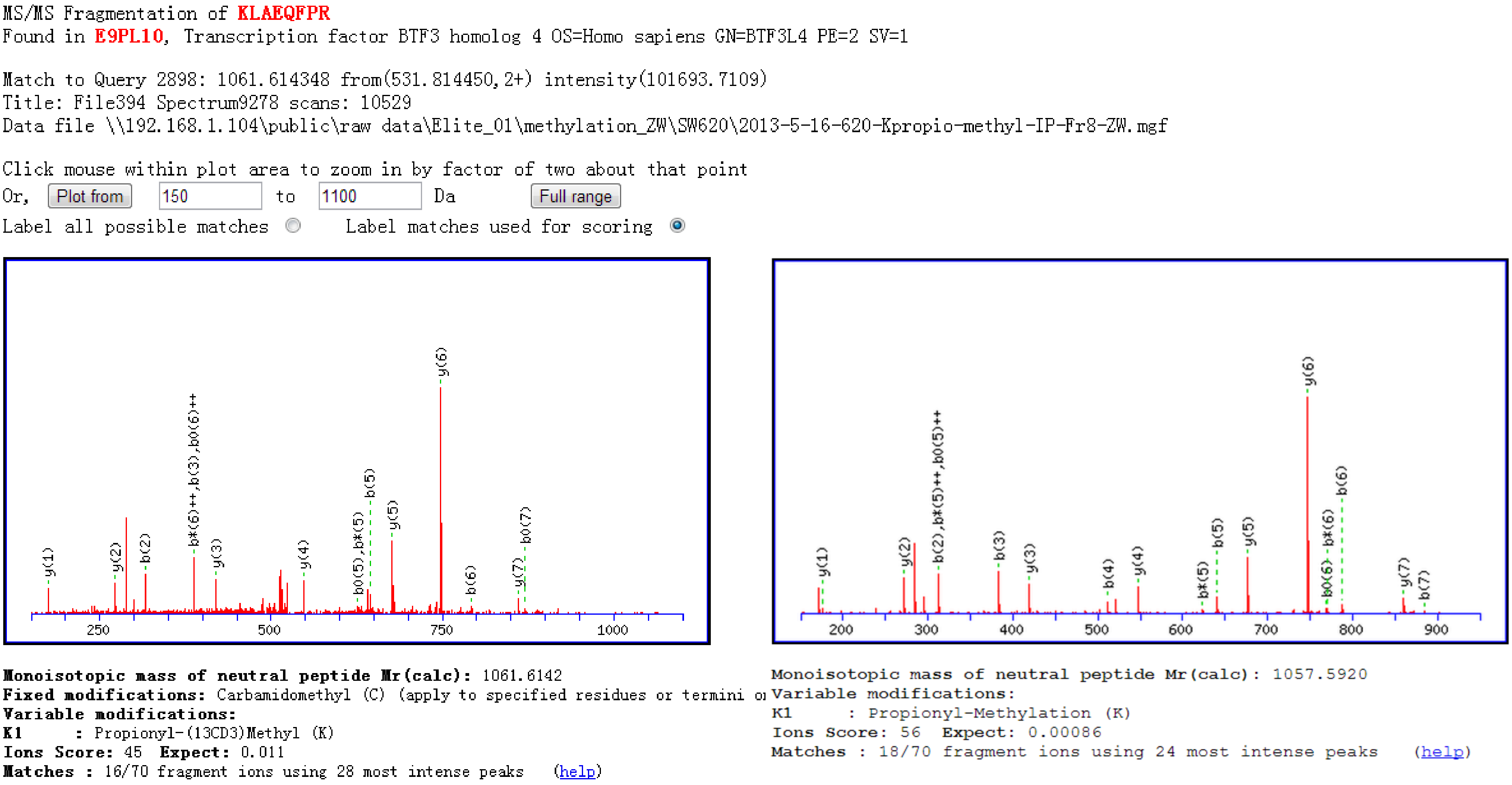


Monoisotopic mass of neutral peptide Mr(calc): 1124.6917
Variable modifications:
K2 : Propionyl (K)
K6 : Propionyl-Methylation (K)
Ions Score: 46 Expect: 0.0028
Matches : 12/78 fragment ions using 24 most intense peaks (help)

MS/MS spectrum of K562 cell derived peptide LK$_{pr}$ LGVK$_{pr+me1}$DAR from protein POLDIP3

Corresponding synthetic peptide

d.



MS/MS Fragmentation of **KLAEQFPR**
Found in **E9PL10**, Transcription factor BTF3 homolog 4 OS=Homo sapiens GN=BTF3L4 PE=2 SV=1

Match to Query 2898: 1061.614348 from(531.814450,2+) intensity(101693.7109)
Title: File394 Spectrum9278 scans: 10529
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

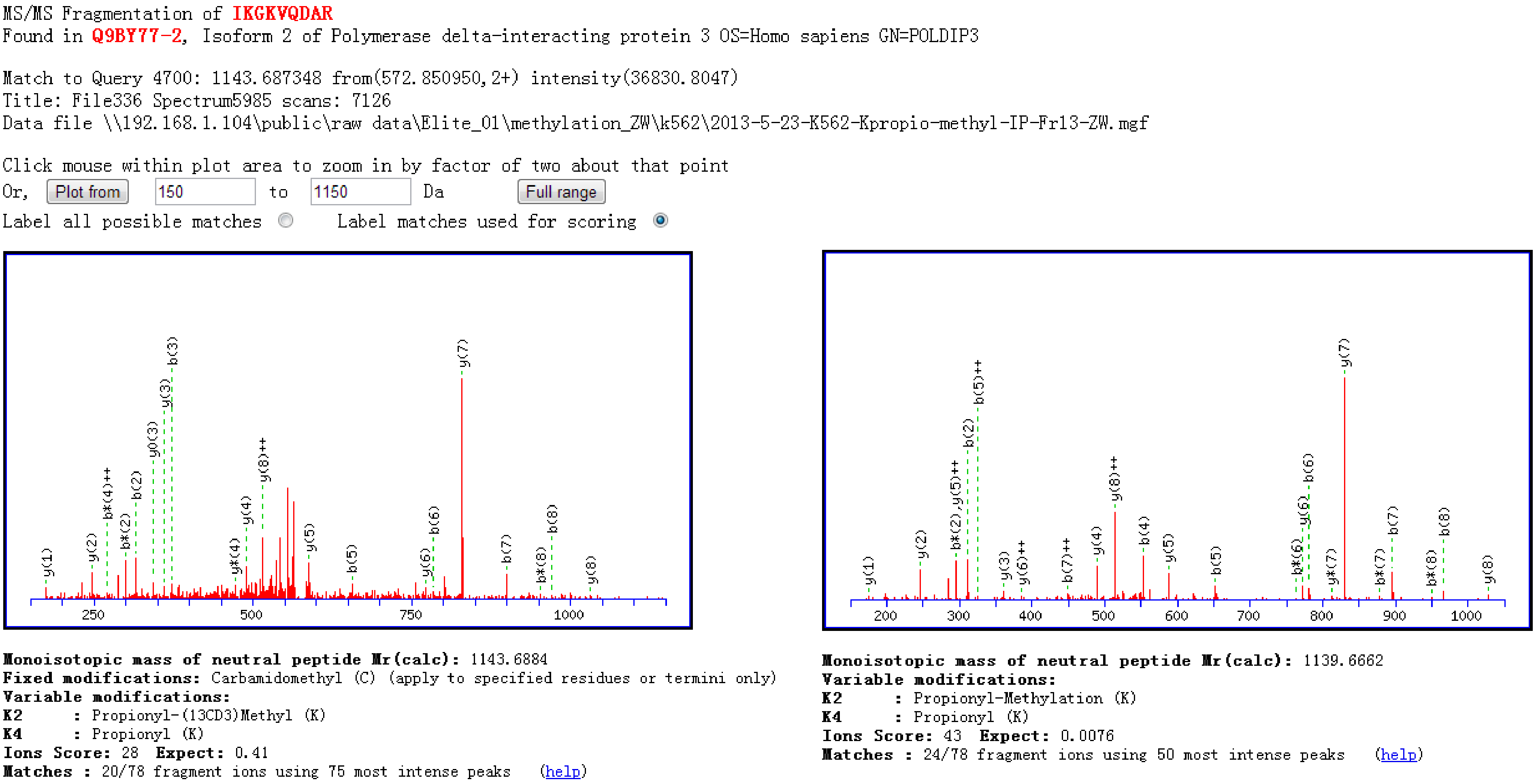
Monoisotopic mass of neutral peptide Mr(calc): 1061.6142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini o
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 45 **Expect:** 0.011
Matches : 16/70 fragment ions using 28 most intense peaks (help)

Monoisotopic mass of neutral peptide Mr(calc): 1057.5920
Variable modifications:
K1 : Propionyl-Methylation (K)
Ions Score: 56 **Expect:** 0.00086
Matches : 18/70 fragment ions using 24 most intense peaks (help)

MS/MS spectrum of SW620 cell derived peptide K_{pr+me1}LAEQFPR from protein BTF3L4

Corresponding synthetic peptide

e.



MS/MS Fragmentation of **IKGKVQDAR**
Found in **Q9BY77-2**, Isoform 2 of Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3

Match to Query 4700: 1143.687348 from(572.850950,2+) intensity(36830.8047)
Title: File336 Spectrum5985 scans: 7126
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1143.6884
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K4 : Propionyl (K)
Ions Score: 28 **Expect:** 0.41
Matches : 20/78 fragment ions using 75 most intense peaks (help)

Monoisotopic mass of neutral peptide Mr(calc): 1139.6662
Variable modifications:
K2 : Propionyl-Methylation (K)
K4 : Propionyl (K)
Ions Score: 43 **Expect:** 0.0076
Matches : 24/78 fragment ions using 50 most intense peaks (help)

MS/MS spectrum of K562 cell derived peptide IK$_{pr+me1}$GK$_{pr}$VQDAR from protein POLDIP3

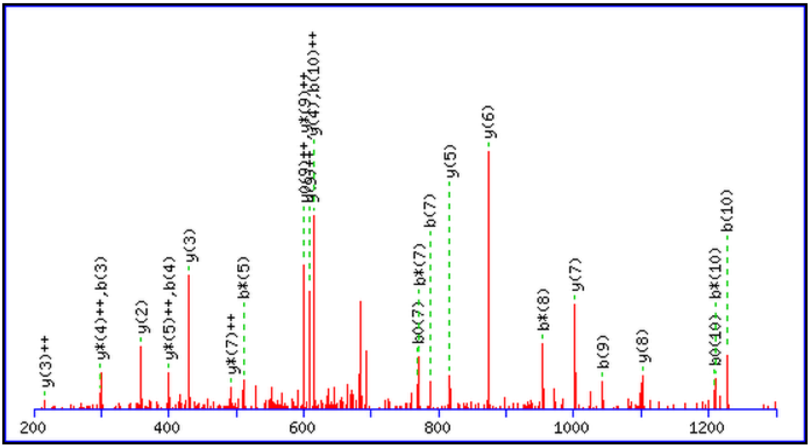
Corresponding synthetic peptide

f.

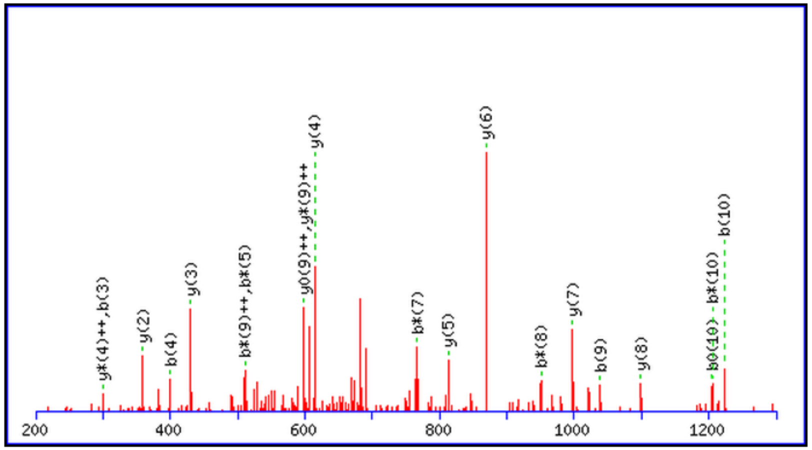
MS/MS Fragmentation of **LANTQGKKAKR**
Found in **Q99459**, Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2

Match to Query 8167: 1399.843368 from(700.928960,2+) intensity(262291.8750)
Title: File359 Spectrum6057 scans: 7190
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-6-3-K562-Kpropio-methyl-IP-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1399.8419
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini onl
Variable modifications:
K7 : Propionyl-(13CD3)Methyl (K)
K8 : Propionyl (K)
K10 : Propionyl (K)
Ions Score: 48 **Expect:** 0.0035
Matches : 26/96 fragment ions using 33 most intense peaks (help)

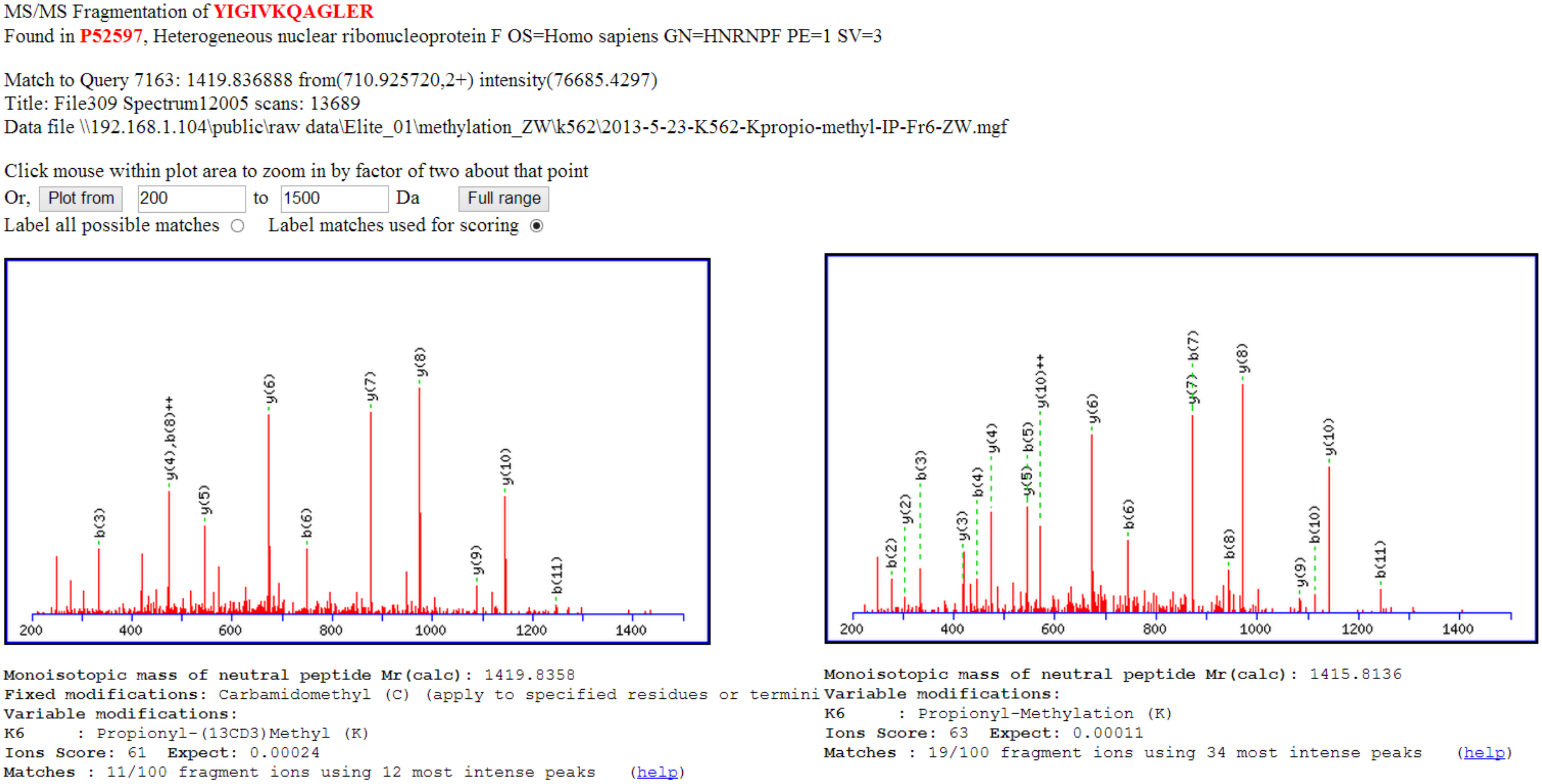


Monoisotopic mass of neutral peptide Mr(calc): 1395.8198
Variable modifications:
K7 : Propionyl-Methylation (K)
K8 : Propionyl (K)
K10 : Propionyl (K)
Ions Score: 60 **Expect:** 0.00023
Matches : 20/96 fragment ions using 22 most intense peaks (help)

MS/MS spectrum of K562 cell derived peptide LANTQGK$_{\mathrm{pr+me1}}$K$_{\mathrm{pr}}$AK$_{\mathrm{pr}}$R from protein CDC5L

Corresponding synthetic peptide

g.



MS/MS Fragmentation of **YIGIVKQAGLER**
Found in **P52597**, Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3

Match to Query 7163: 1419.836888 from(710.925720,2+) intensity(76685.4297)
Title: File309 Spectrum12005 scans: 13689
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

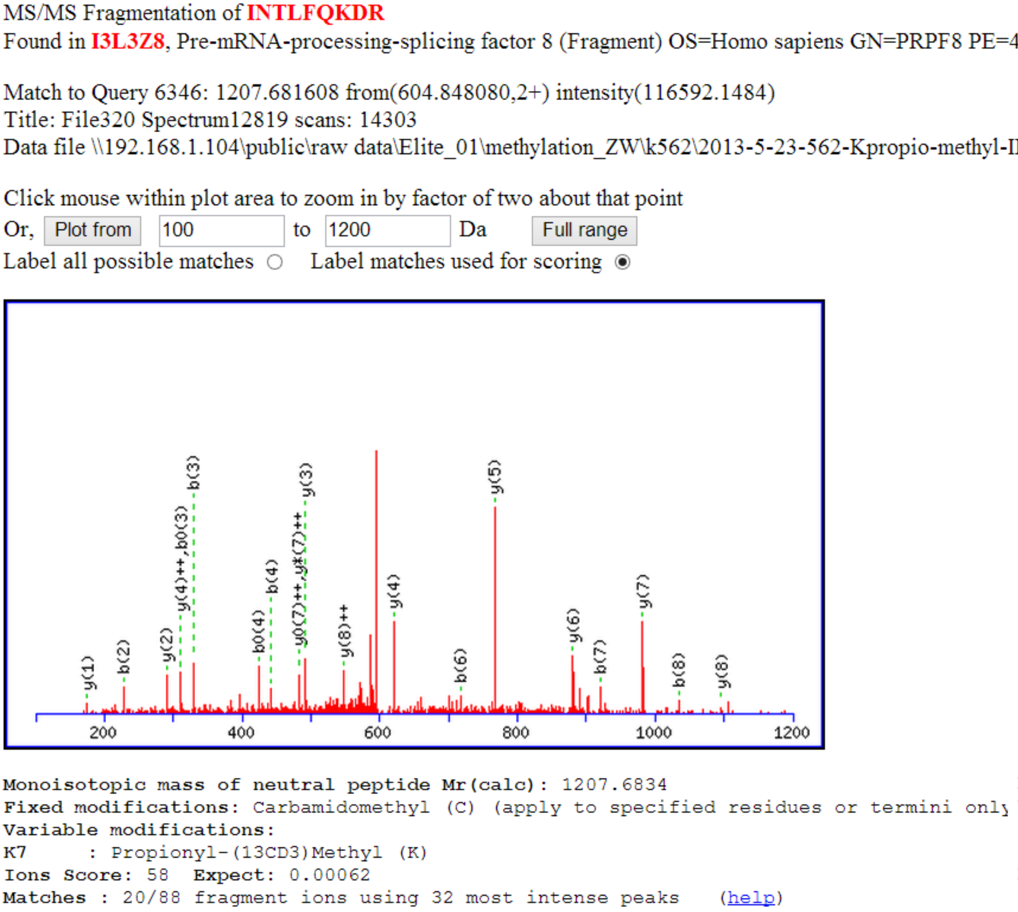
```
Monoisotopic mass of neutral peptide Mr(calc): 1419.8358
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini
Variable modifications:
K6      : Propionyl-(13CD3)Methyl (K)
Ions Score: 61  Expect: 0.00024
Matches : 11/100 fragment ions using 12 most intense peaks   (help)
```

```
Monoisotopic mass of neutral peptide Mr(calc): 1415.8136
Variable modifications:
K6      : Propionyl-Methylation (K)
Ions Score: 63  Expect: 0.00011
Matches : 19/100 fragment ions using 34 most intense peaks   (help)
```

MS/MS spectrum of K562 cell derived peptide YIGIVK$_{pr+me1}$ QAGLER from protein HNRNPF

Corresponding synthetic peptide

h.

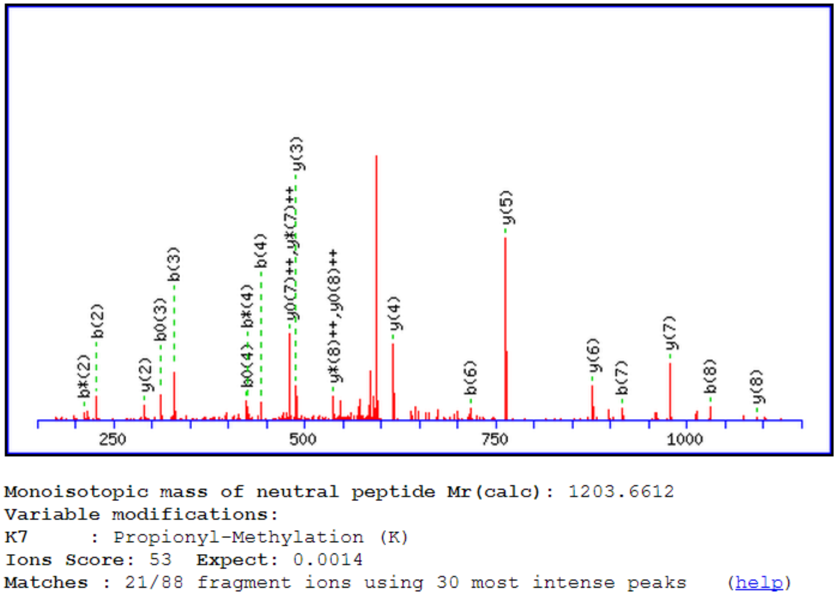


MS/MS Fragmentation of **INTLFQKDR**
Found in **I3L3Z8**, Pre-mRNA-processing-splicing factor 8 (Fragment) OS=Homo sapiens GN=PRPF8 PE=4 SV=1

Match to Query 6346: 1207.681608 from(604.848080,2+) intensity(116592.1484)
Title: File320 Spectrum12819 scans: 14303
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1207.6834
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini onl
Variable modifications:
K7      : Propionyl-(13CD3)Methyl (K)
Ions Score: 58  Expect: 0.00062
Matches : 20/88 fragment ions using 32 most intense peaks   (help)
```

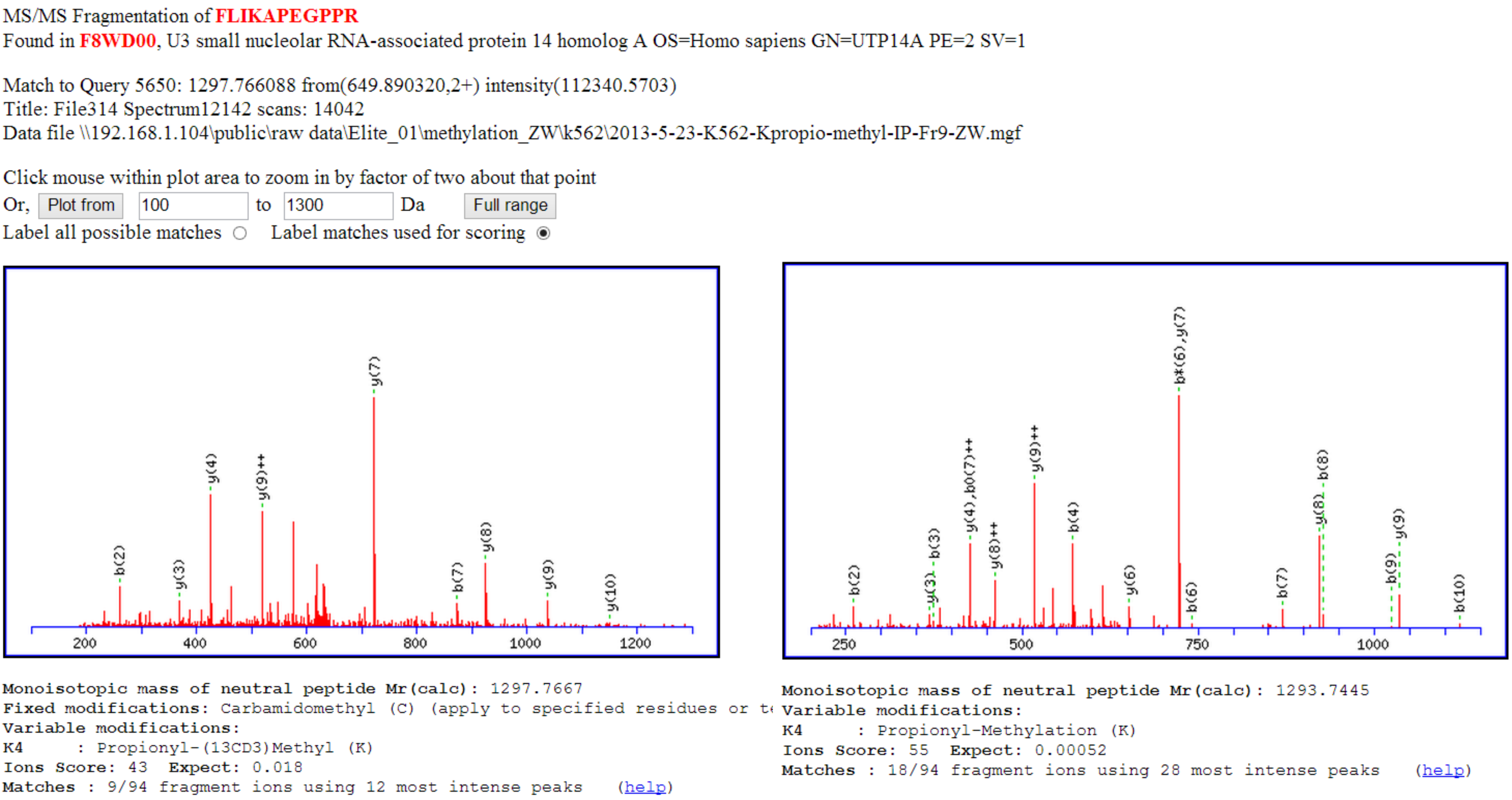


```
Monoisotopic mass of neutral peptide Mr(calc): 1203.6612
Variable modifications:
K7      : Propionyl-Methylation (K)
Ions Score: 53  Expect: 0.0014
Matches : 21/88 fragment ions using 30 most intense peaks   (help)
```

MS/MS spectrum of K562 cell derived peptide INTLFQK$_{pr+me1}$ DR from protein PRPF8

Corresponding synthetic peptide

i.



MS/MS Fragmentation of **FLIKAPEGPPR**
Found in **F8WD00**, U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=2 SV=1

Match to Query 5650: 1297.766088 from(649.890320,2+) intensity(112340.5703)
Title: File314 Spectrum12142 scans: 14042
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr9-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●

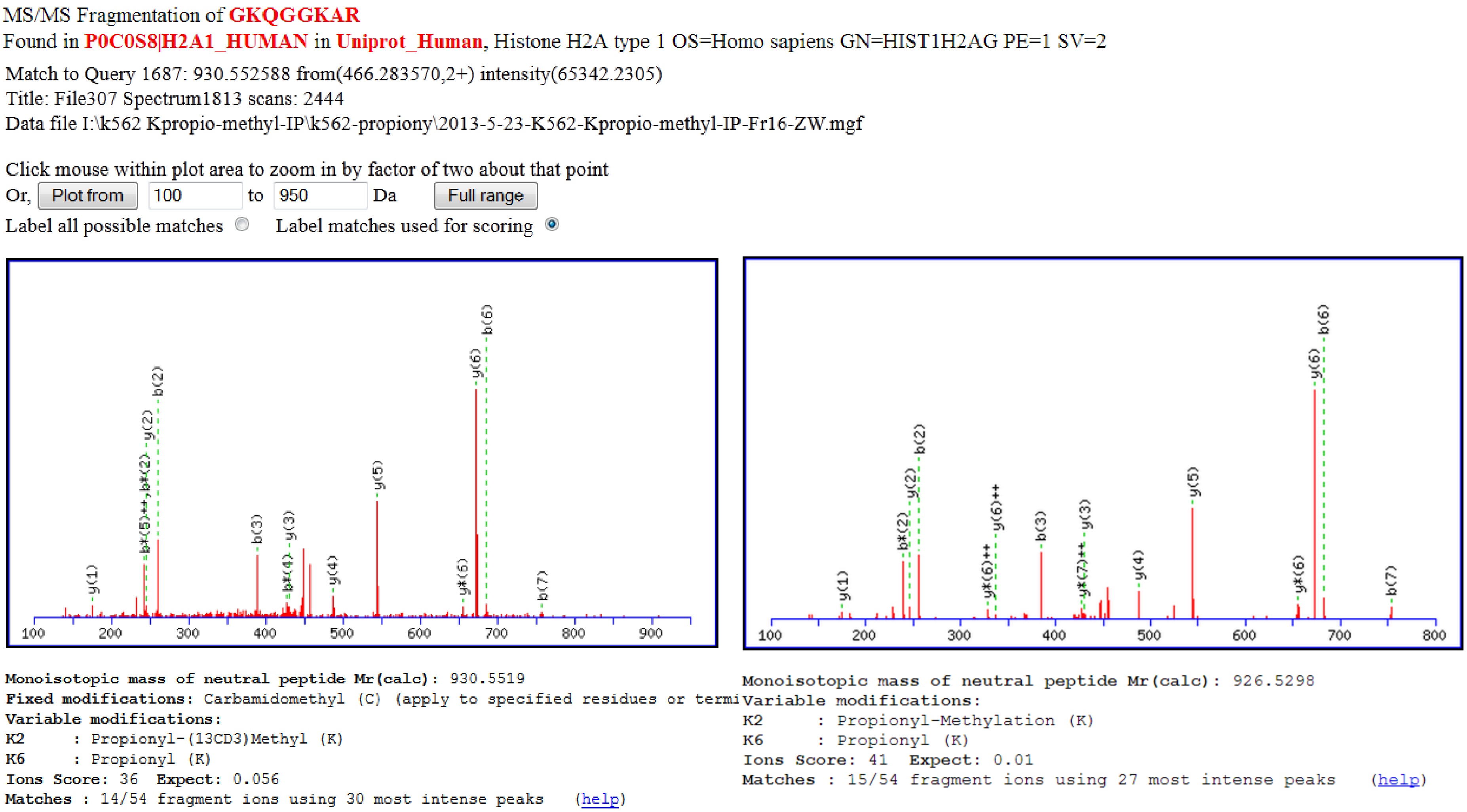
```
Monoisotopic mass of neutral peptide Mr(calc): 1297.7667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or t
Variable modifications:
K4      : Propionyl-(13CD3)Methyl (K)
Ions Score: 43  Expect: 0.018
Matches : 9/94 fragment ions using 12 most intense peaks   (help)
```

```
Monoisotopic mass of neutral peptide Mr(calc): 1293.7445
Variable modifications:
K4      : Propionyl-Methylation (K)
Ions Score: 55  Expect: 0.00052
Matches : 18/94 fragment ions using 28 most intense peaks   (help)
```

MS/MS spectrum of K562 cell derived peptide FLIK$_{pr+me1}$ APEGPPR from protein UTP14A

Corresponding synthetic peptide

j.



MS/MS Fragmentation of **GKQGGKAR**

Found in **P0C0S8|H2A1_HUMAN** in **Uniprot_Human**, Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2

Match to Query 1687: 930.552588 from(466.283570,2+) intensity(65342.2305)
Title: File307 Spectrum1813 scans: 2444
Data file I:\k562 Kpropio-methyl-IP\k562-propiony\2013-5-23-K562-Kpropio-methyl-IP-Fr16-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

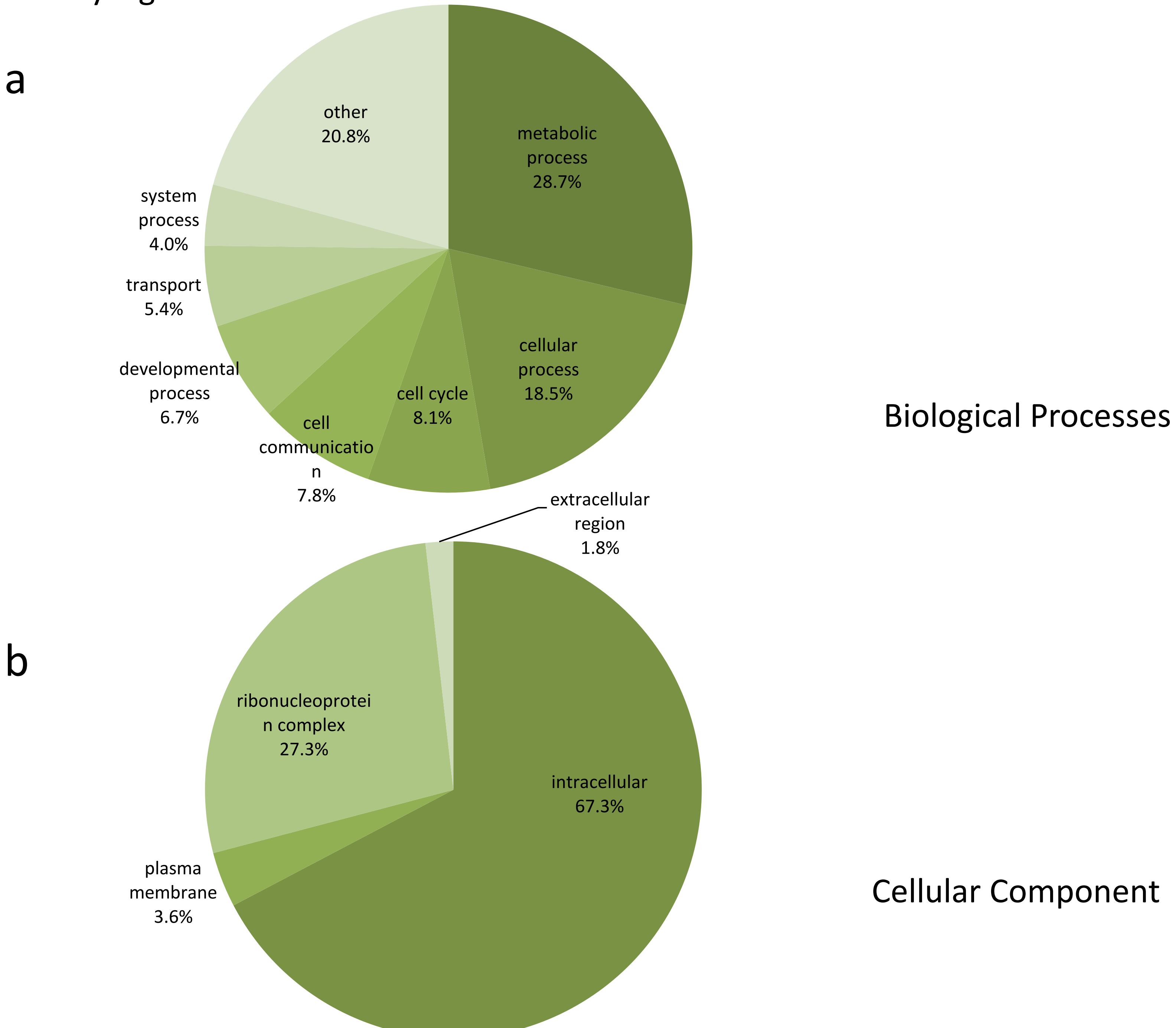
```
Monoisotopic mass of neutral peptide Mr(calc): 930.5519
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termi
Variable modifications:
K2      : Propionyl-(13CD3)Methyl (K)
K6      : Propionyl (K)
Ions Score: 36  Expect: 0.056
Matches : 14/54 fragment ions using 30 most intense peaks    (help)
```

```
Monoisotopic mass of neutral peptide Mr(calc): 926.5298
Variable modifications:
K2      : Propionyl-Methylation (K)
K6      : Propionyl (K)
Ions Score: 41  Expect: 0.01
Matches : 15/54 fragment ions using 27 most intense peaks    (help)
```

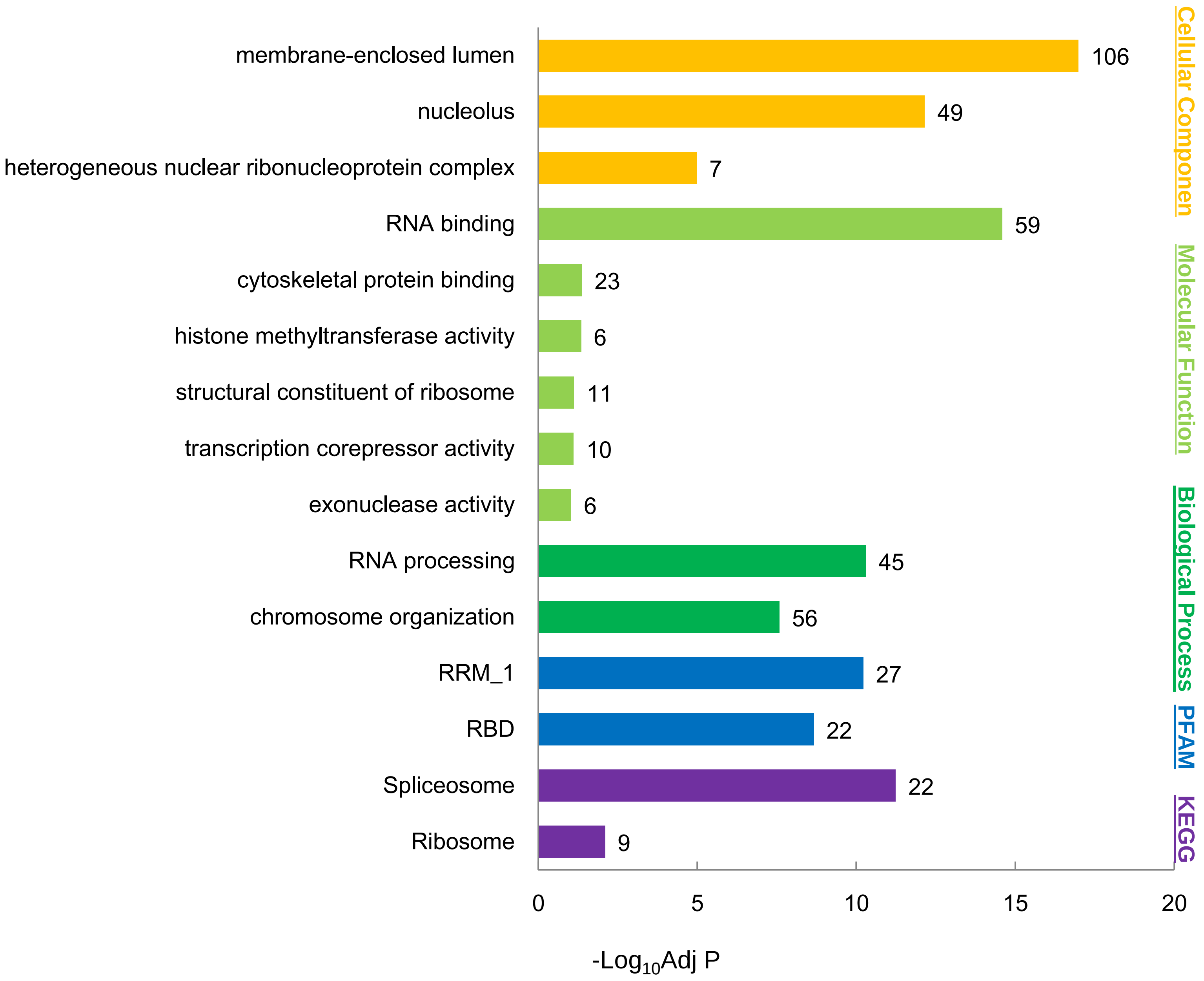
MS/MS spectrum of K562 cell derived peptide GK_{pr+me1} $QGGK_{pr}AR$ from protein H2A

Corresponding synthetic peptide

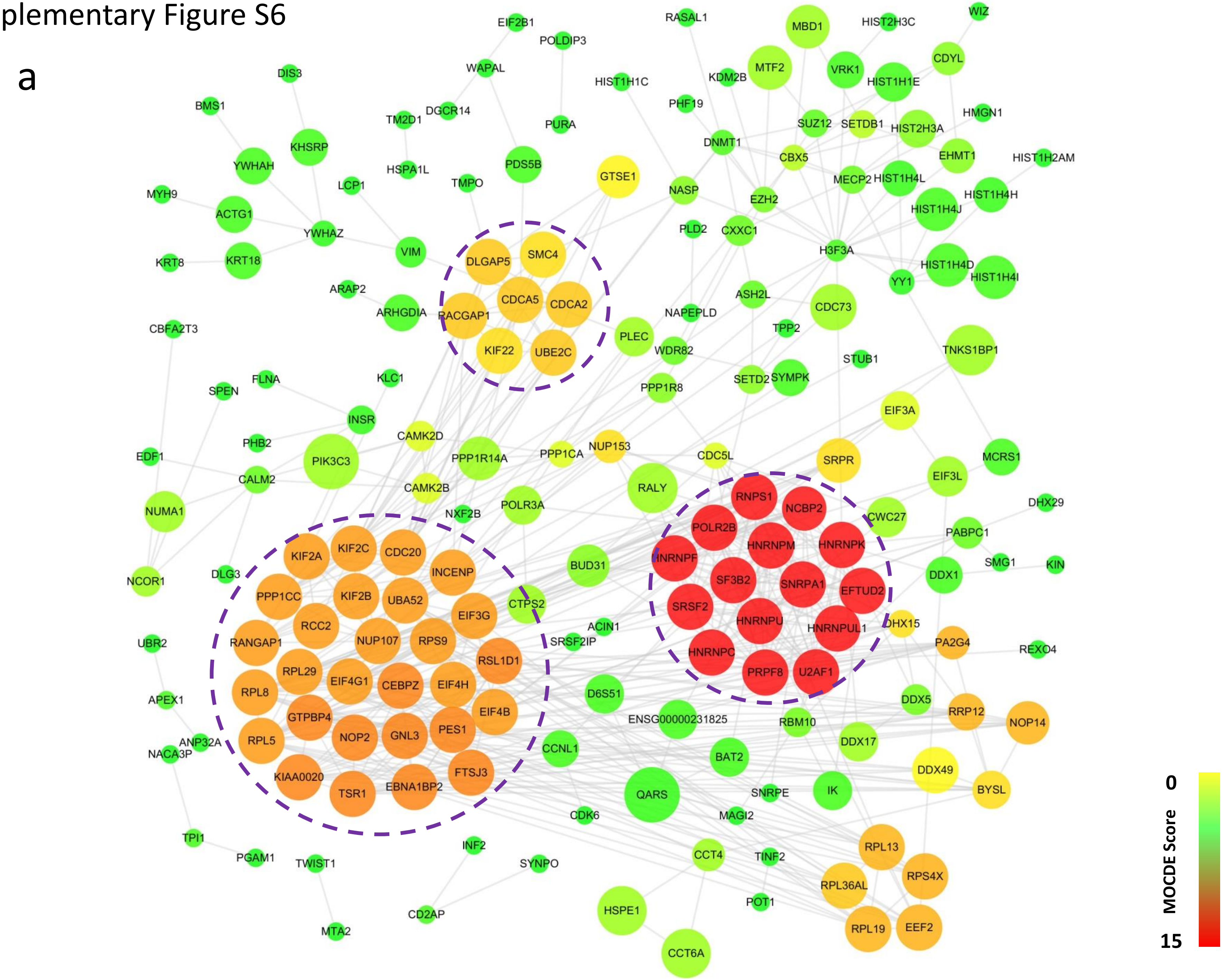
Supplementary Figure S4

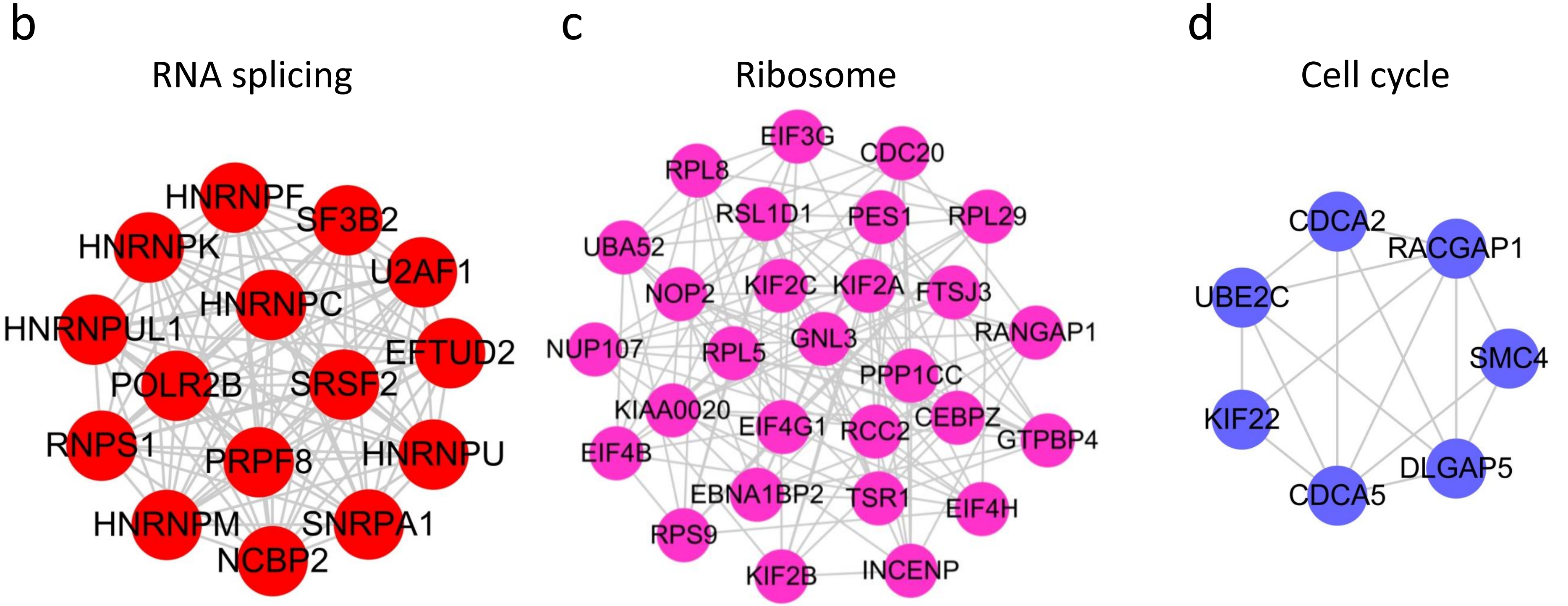


Supplementary Figure S5



Supplementary Figure S6





RNA splicing

Ribosome

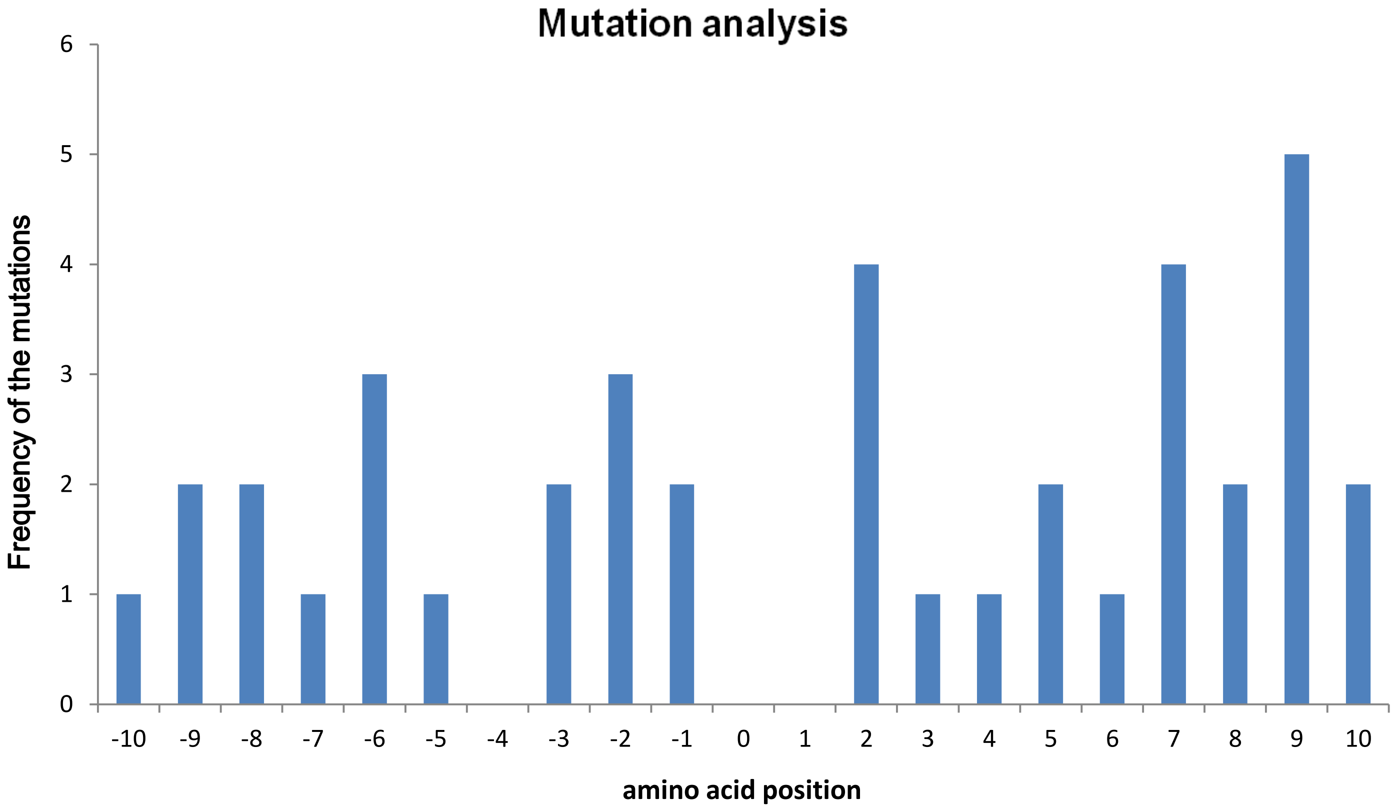
Cell cycle

Cluster 1 (Cluster score = 15)
nodes = 15 , edges = 105

Cluster 2 (Cluster score = 8.96)
nodes = 28 , edges = 121

Cluster 3 (Cluster score = 5.33)
nodes = 7 , edges = 16

Supplementary Figure S7



Supplementary Figure S8