

- M S M y13
ac y12 y11 y10 y9 y8²⁺ y7 y6 y5 y4 y3
 - M S M K E V D E Q M L N V Q N K -
b4 b5 b6 b7 b9 b10 b11 b12 b13 b14 b15

062513_SCW_II_53_4_Vargas_Enriched

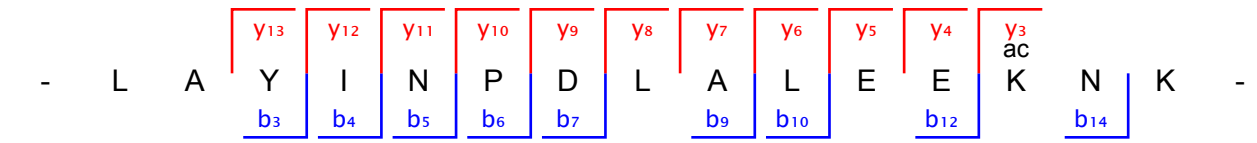
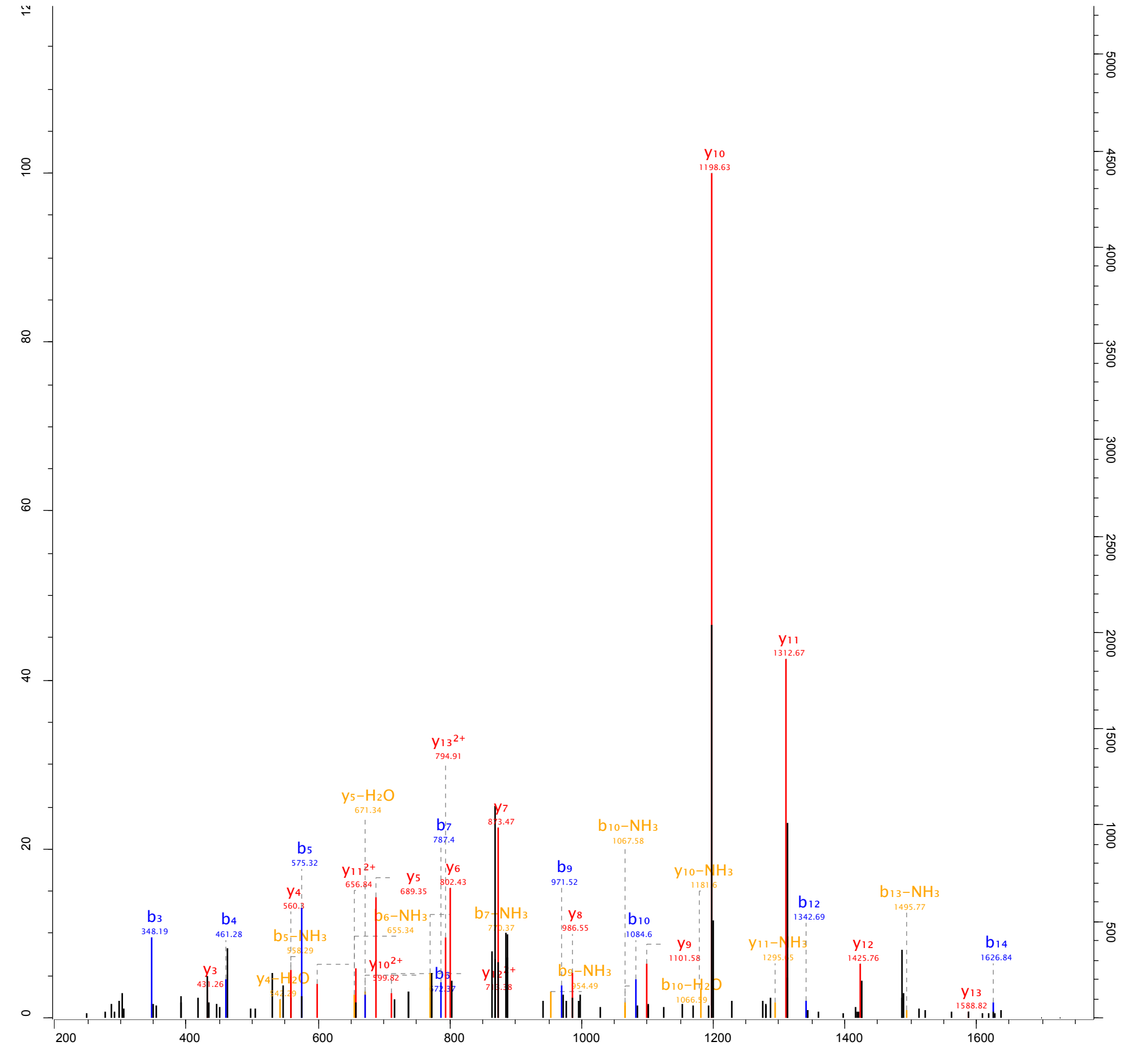
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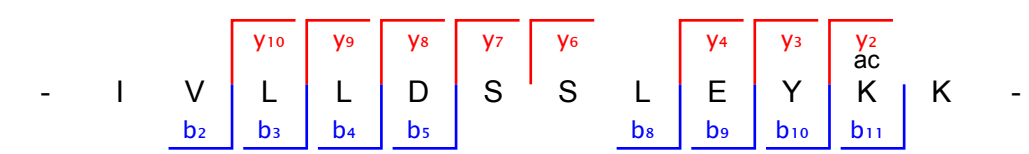
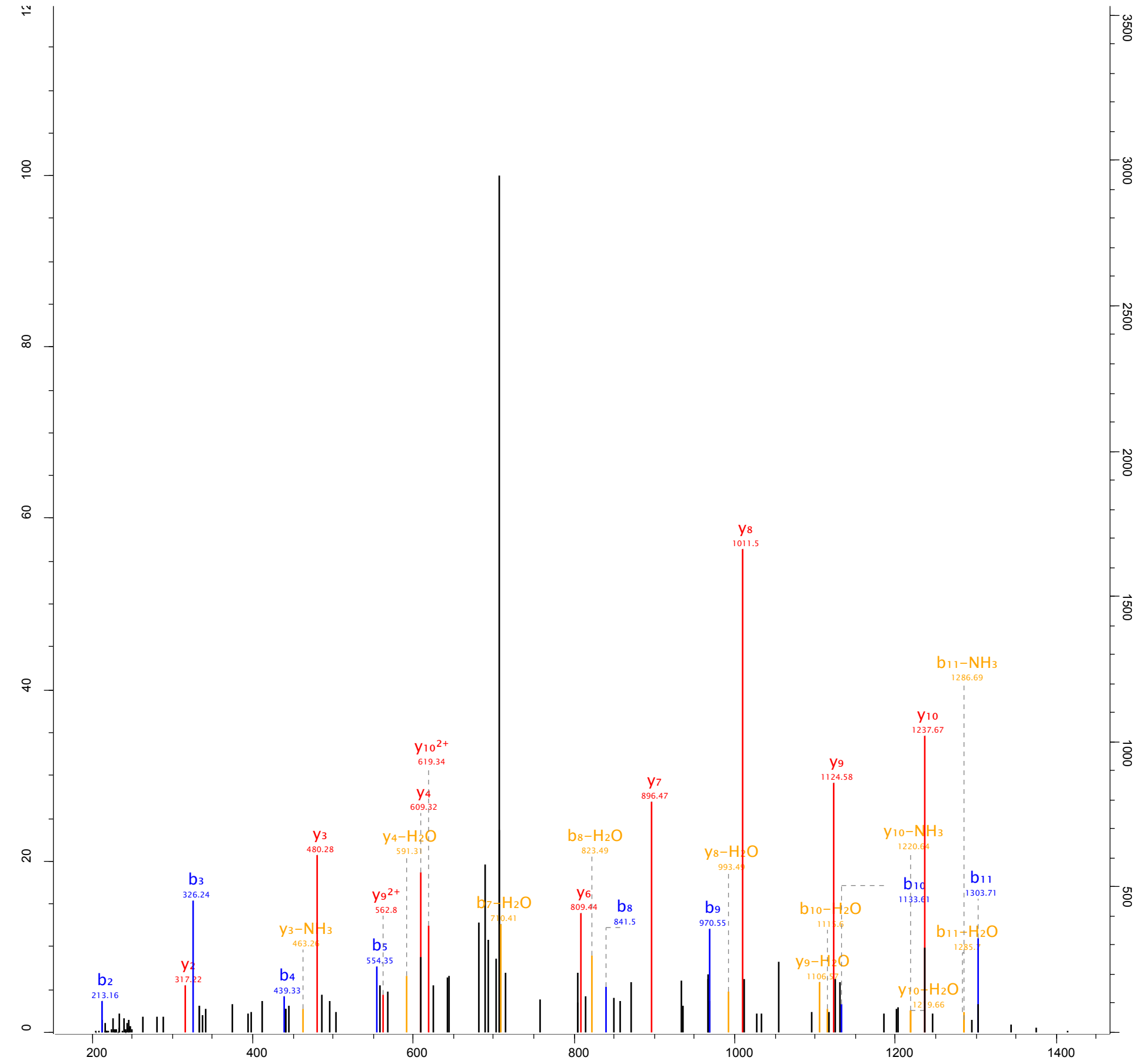
ITMS; CID

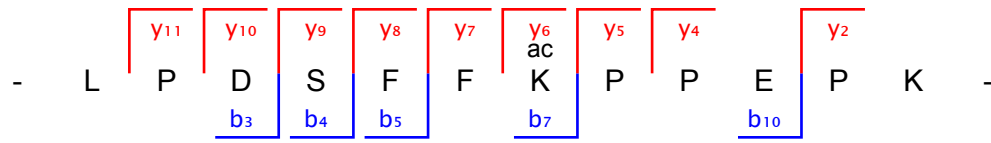
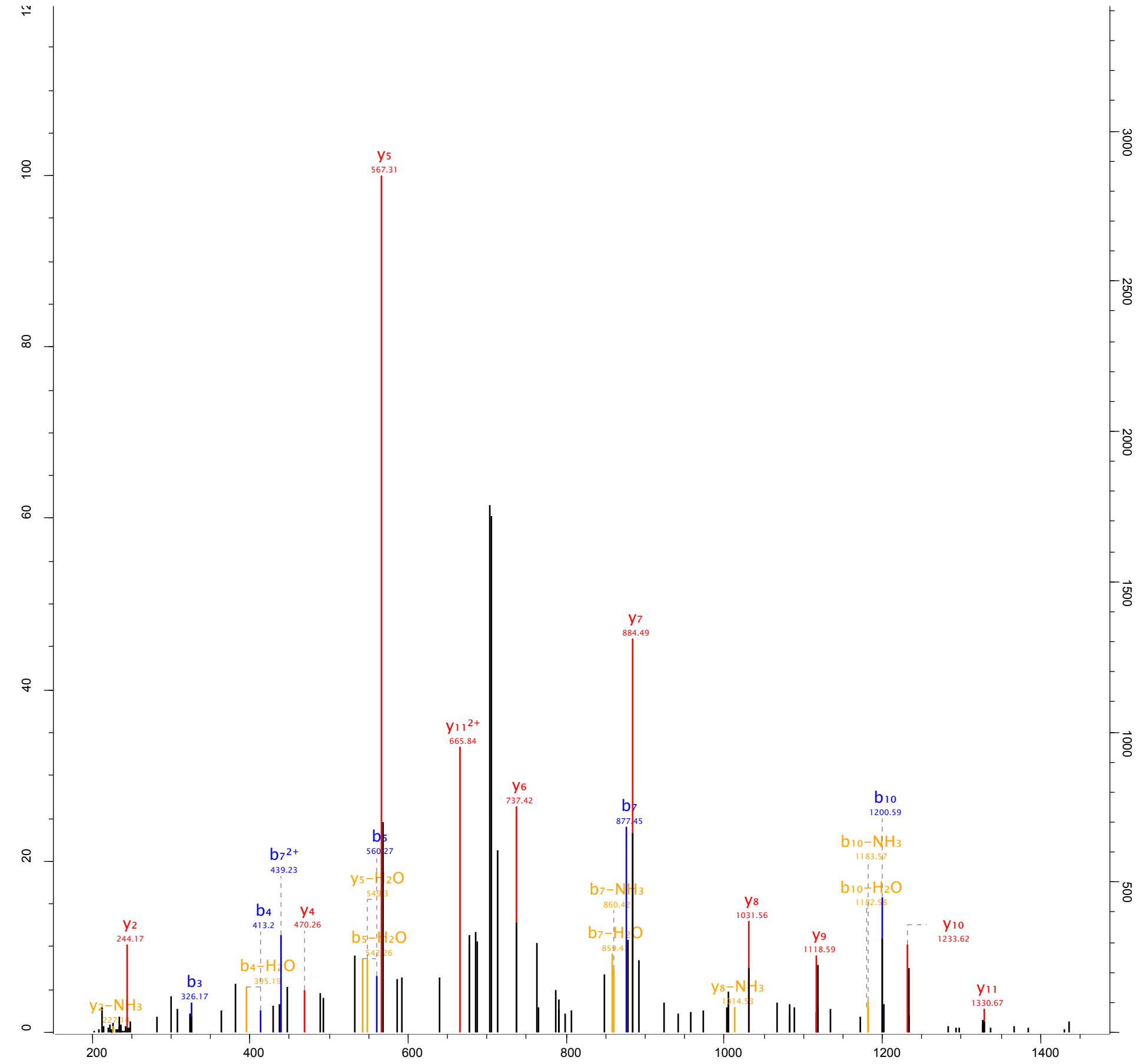
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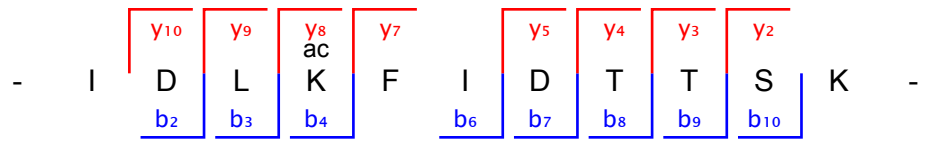
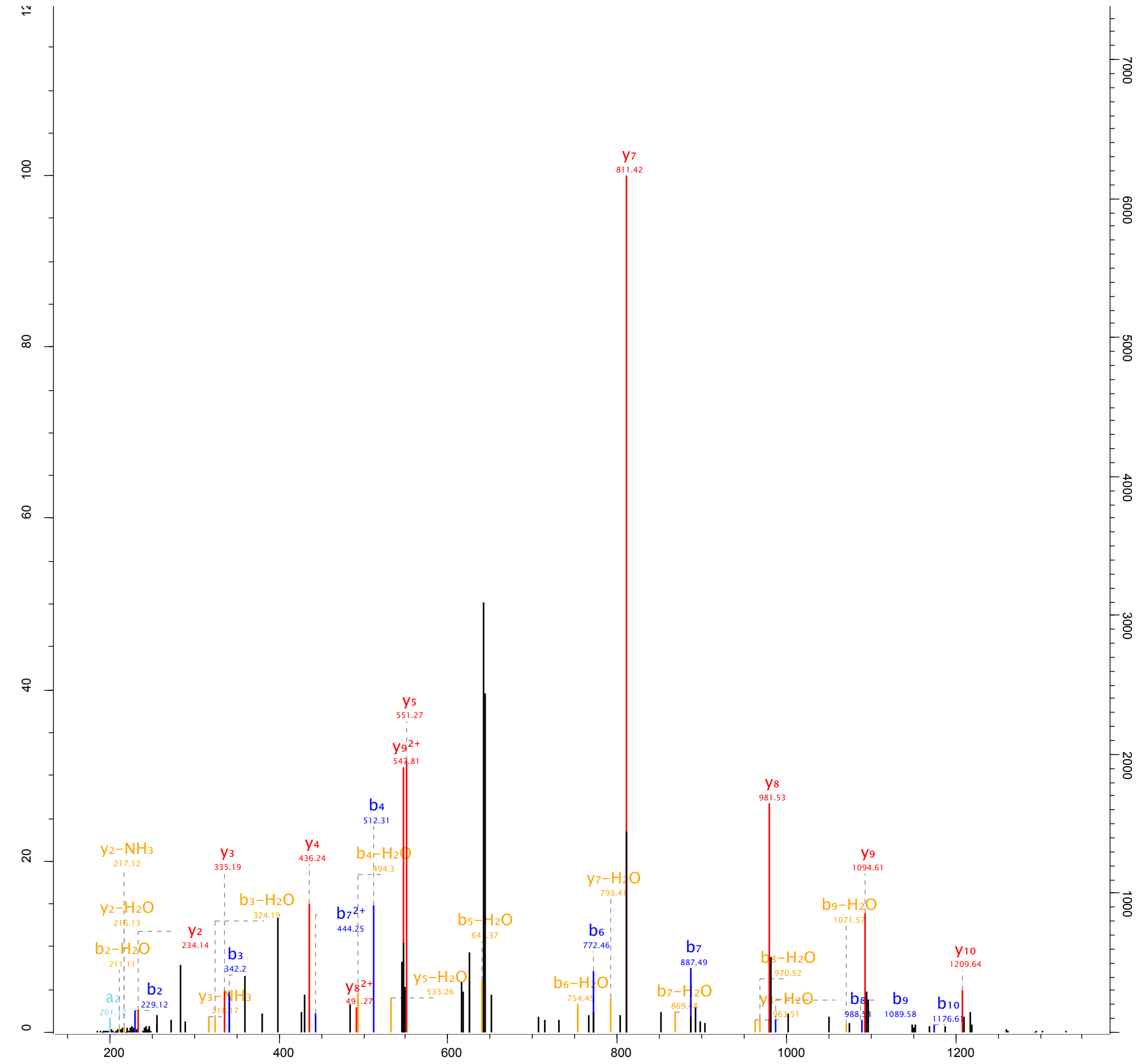
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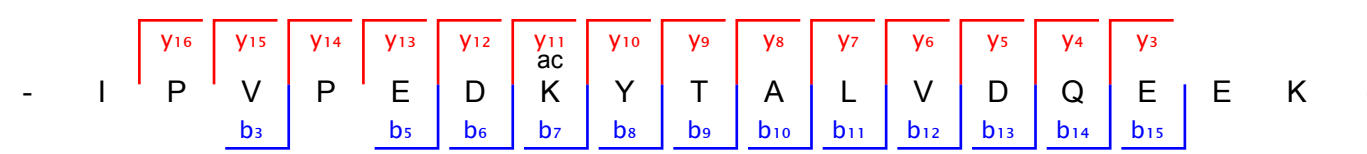
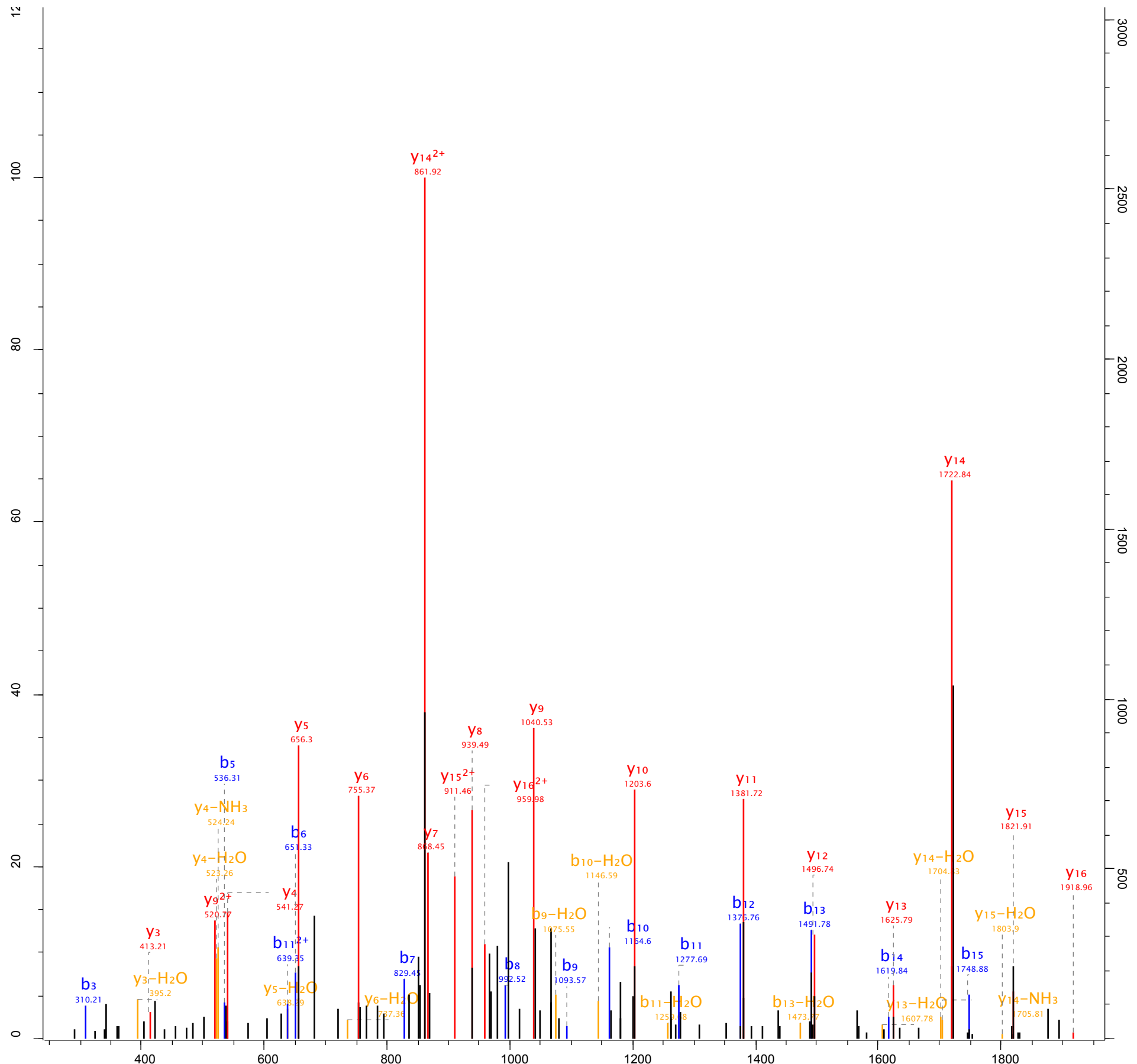
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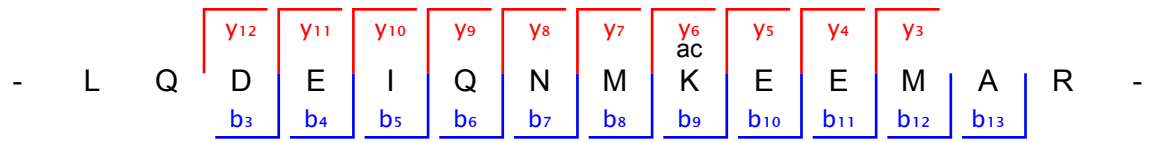
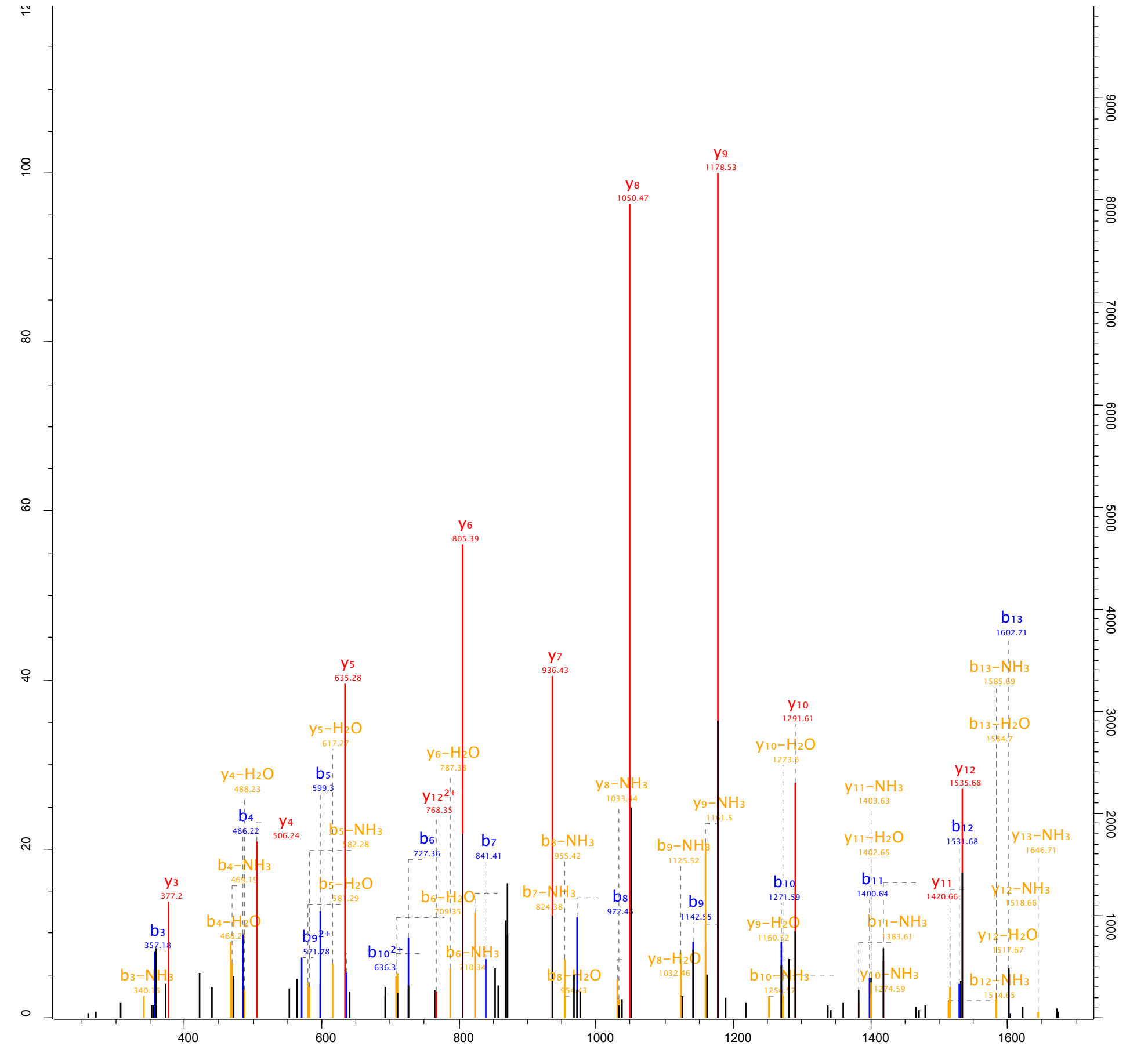


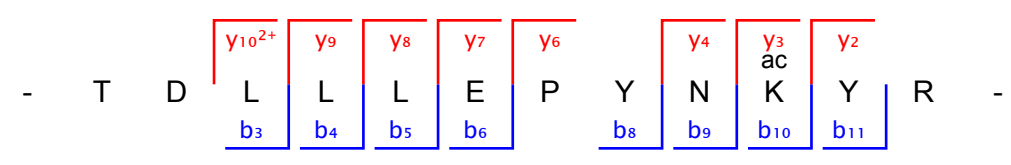
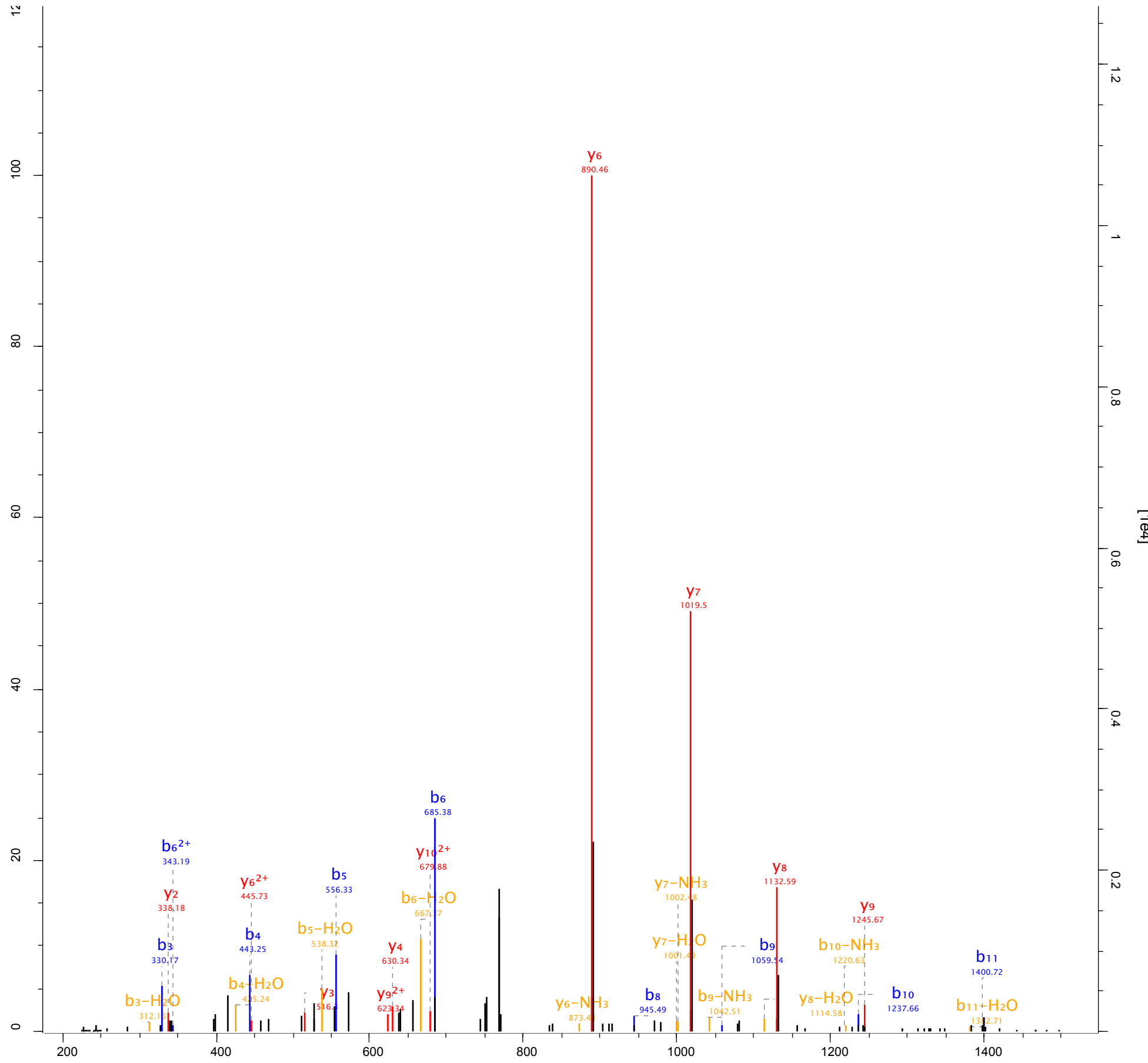


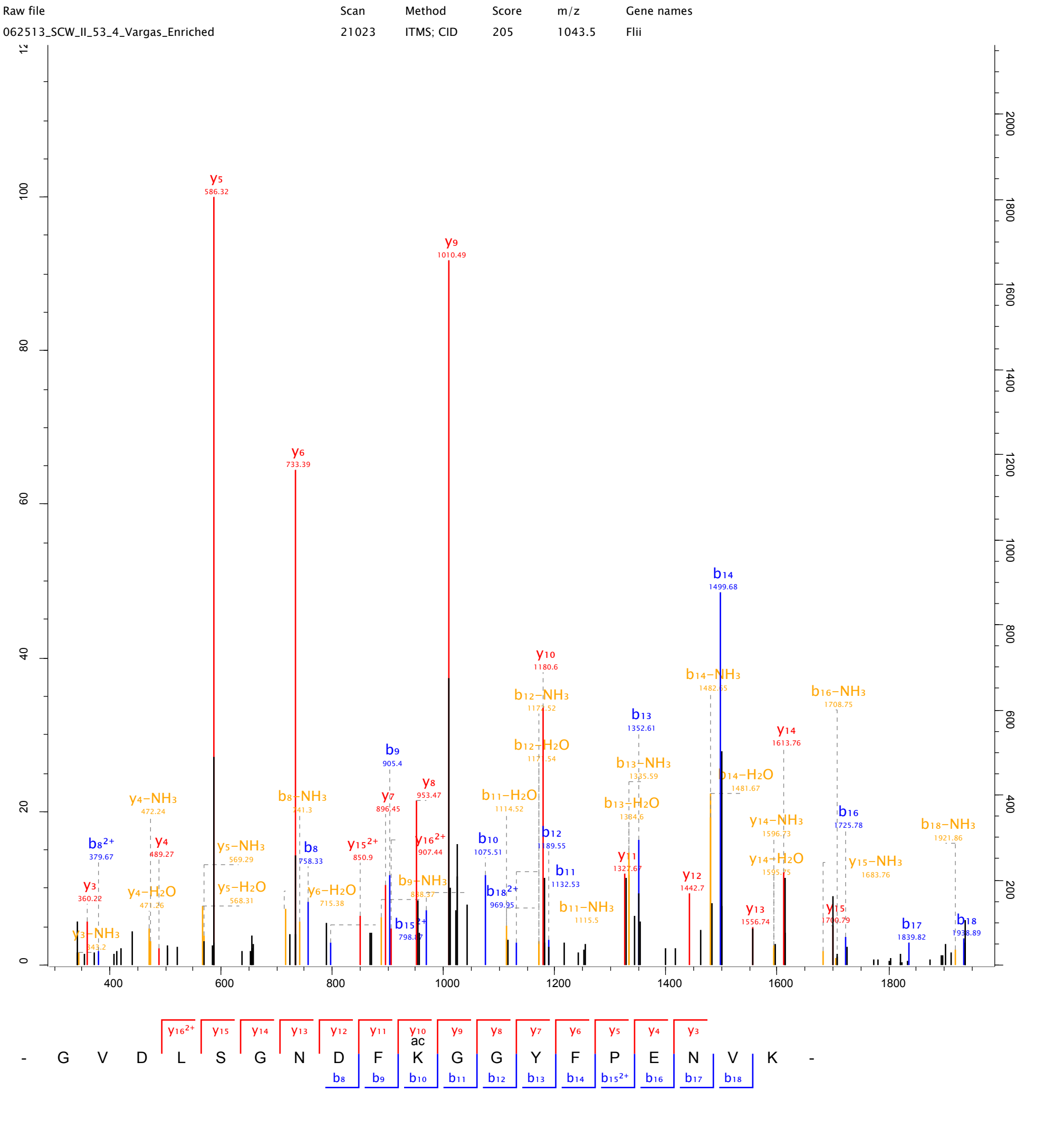


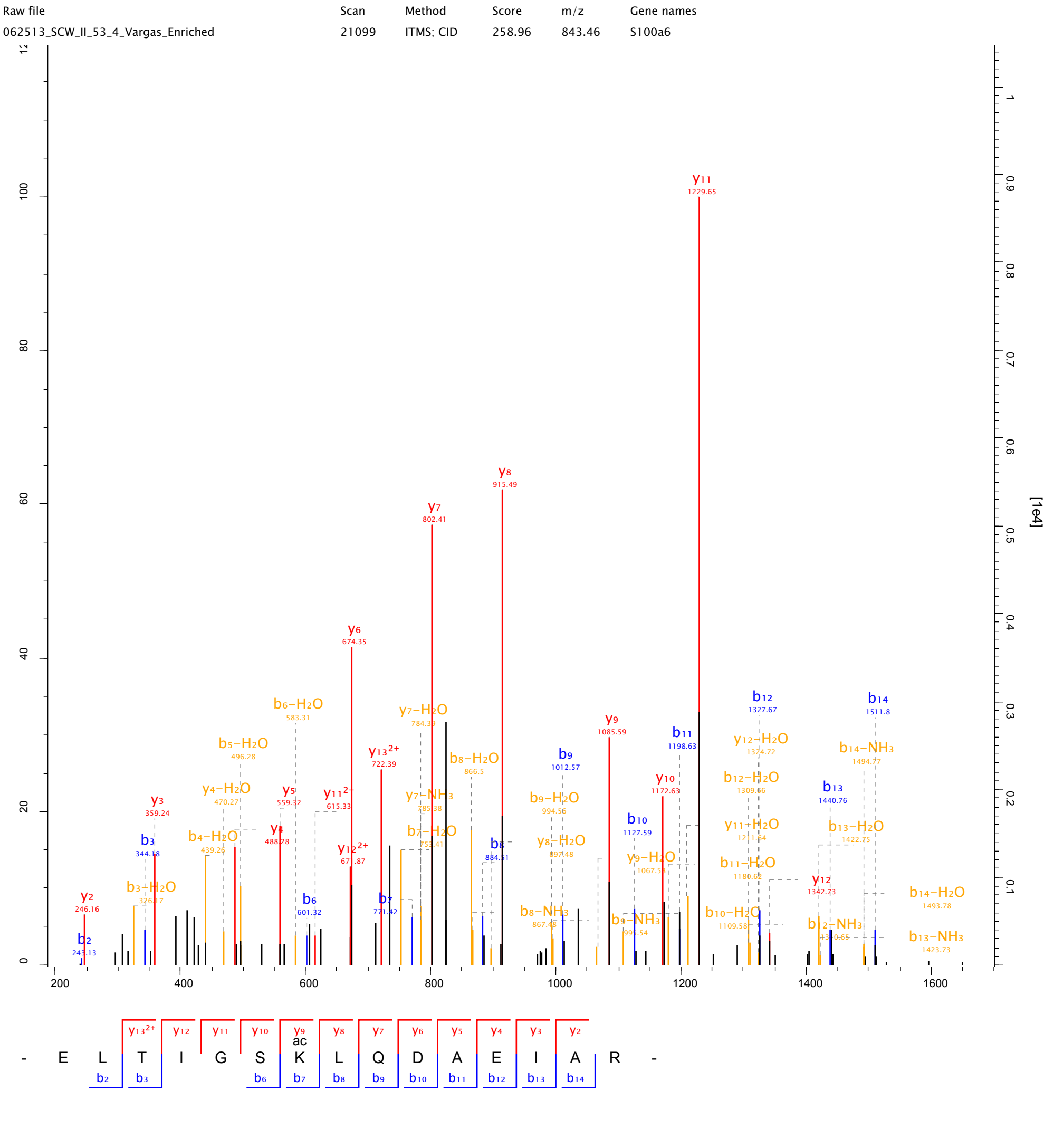


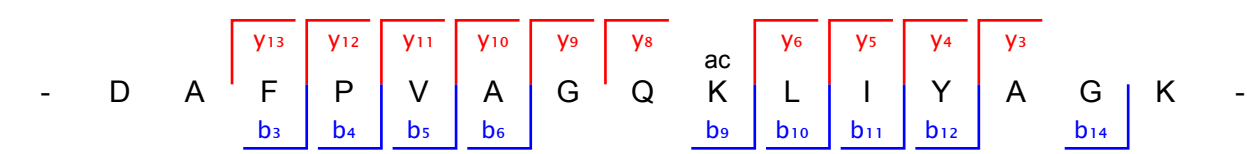
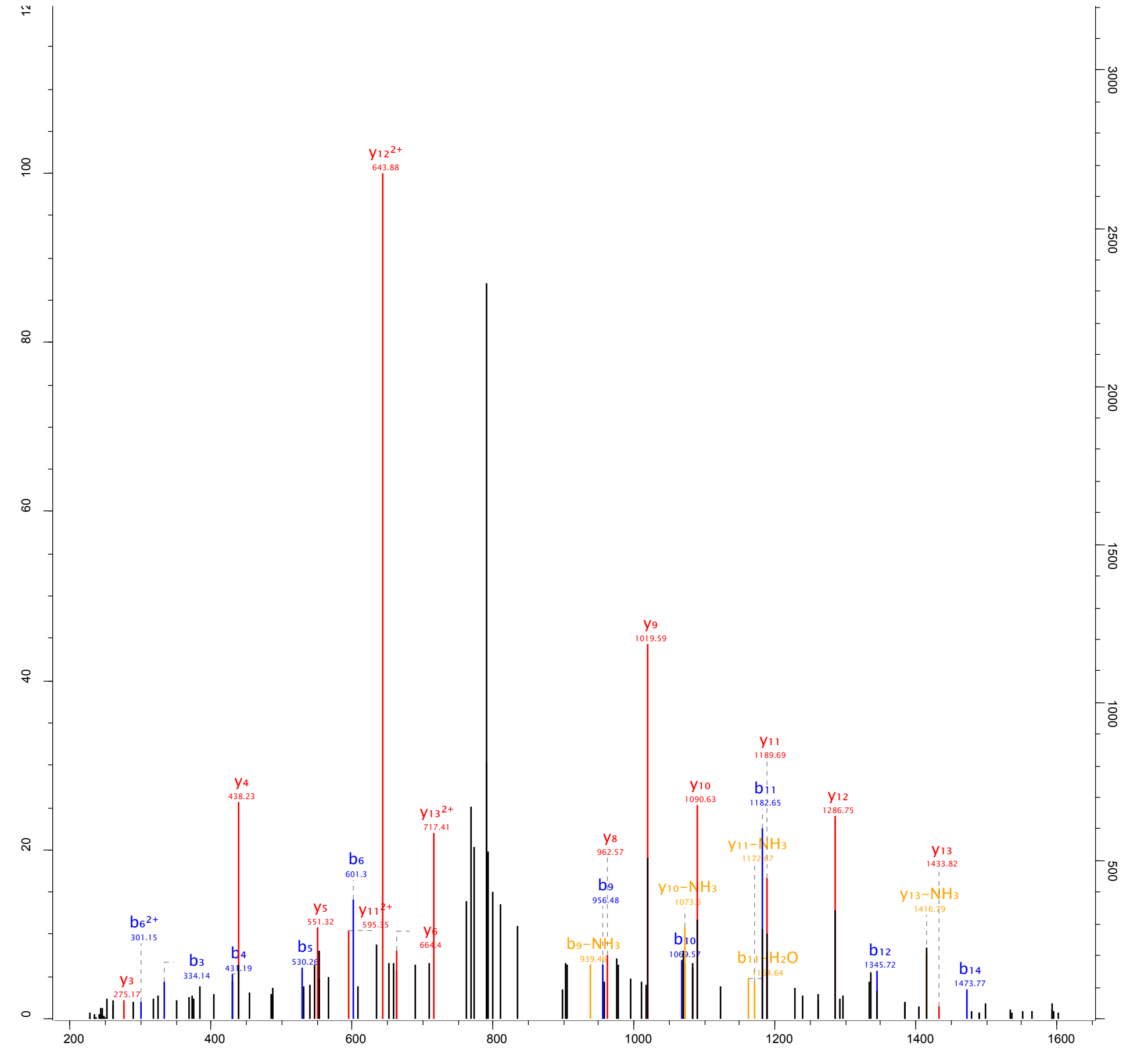


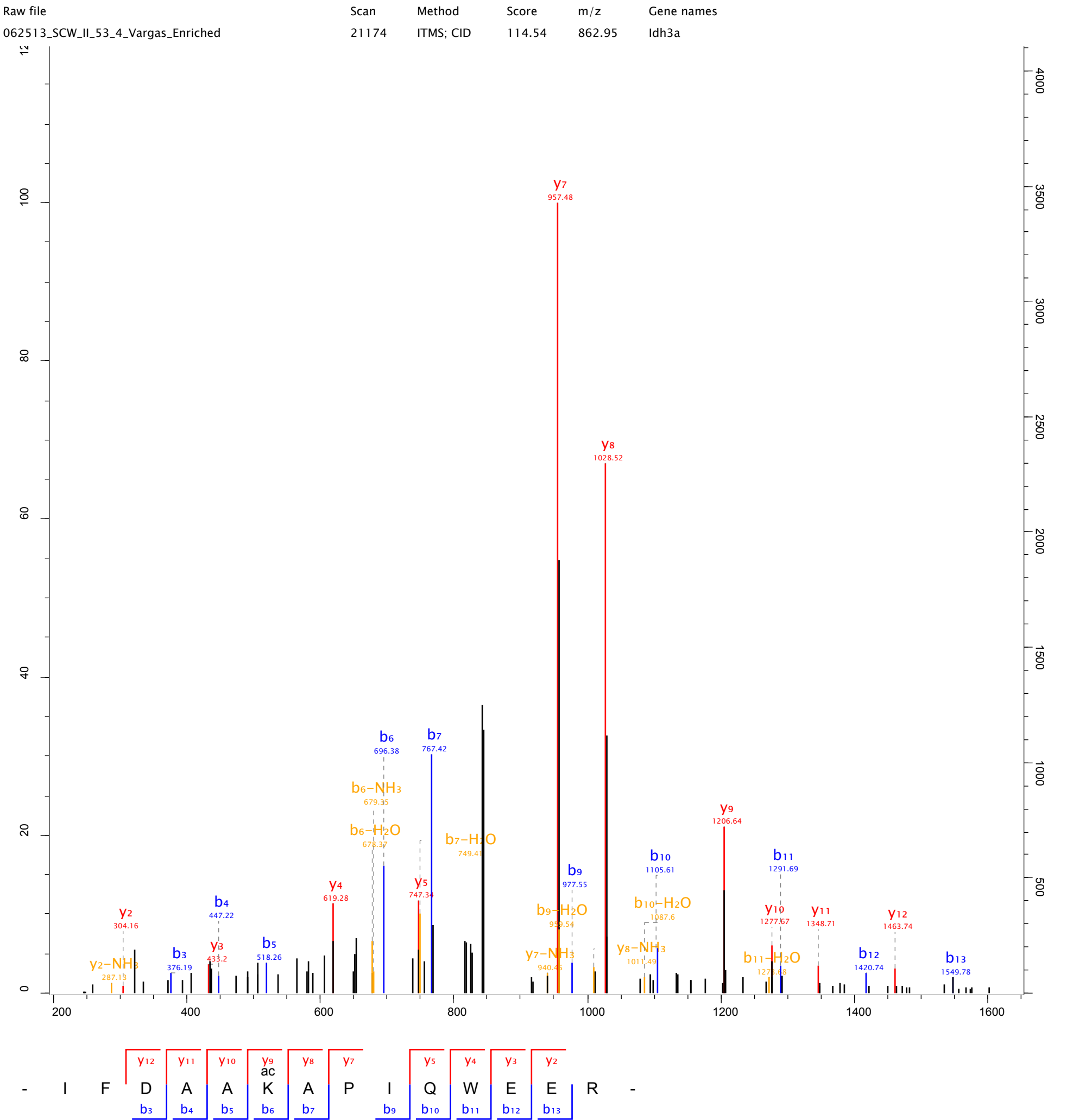


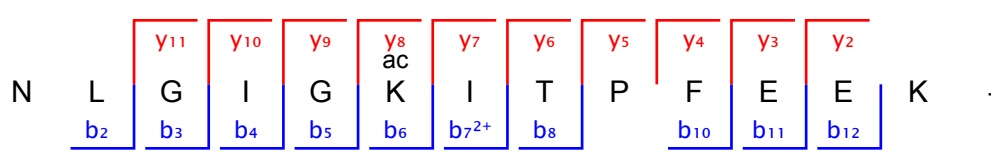
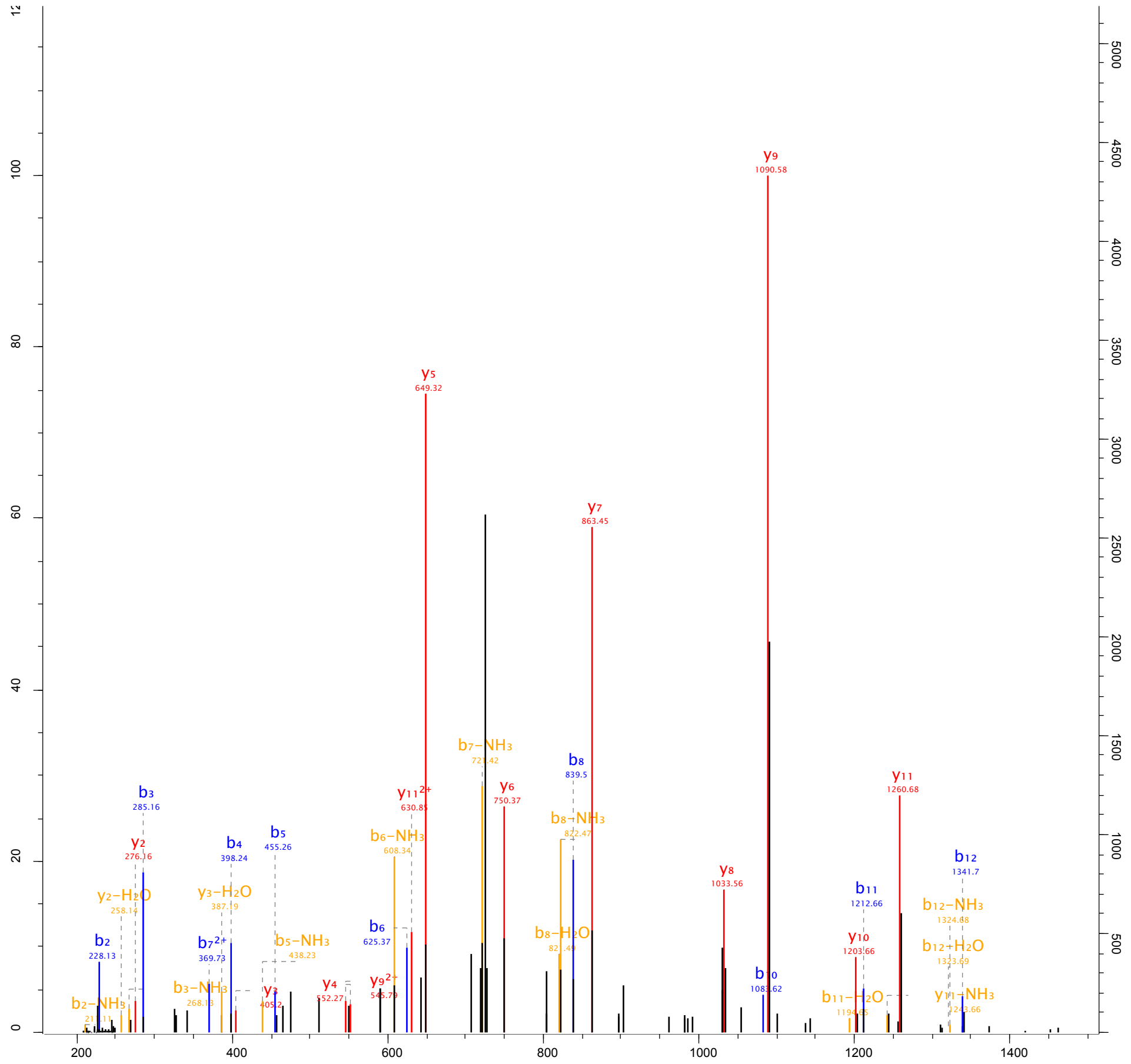


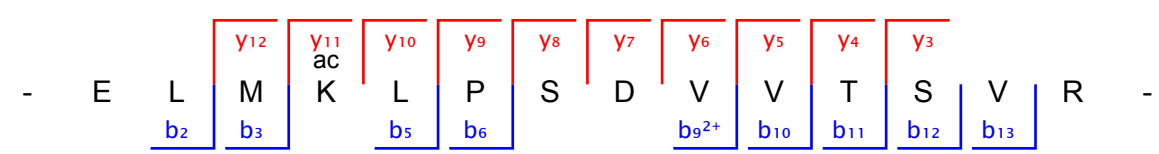
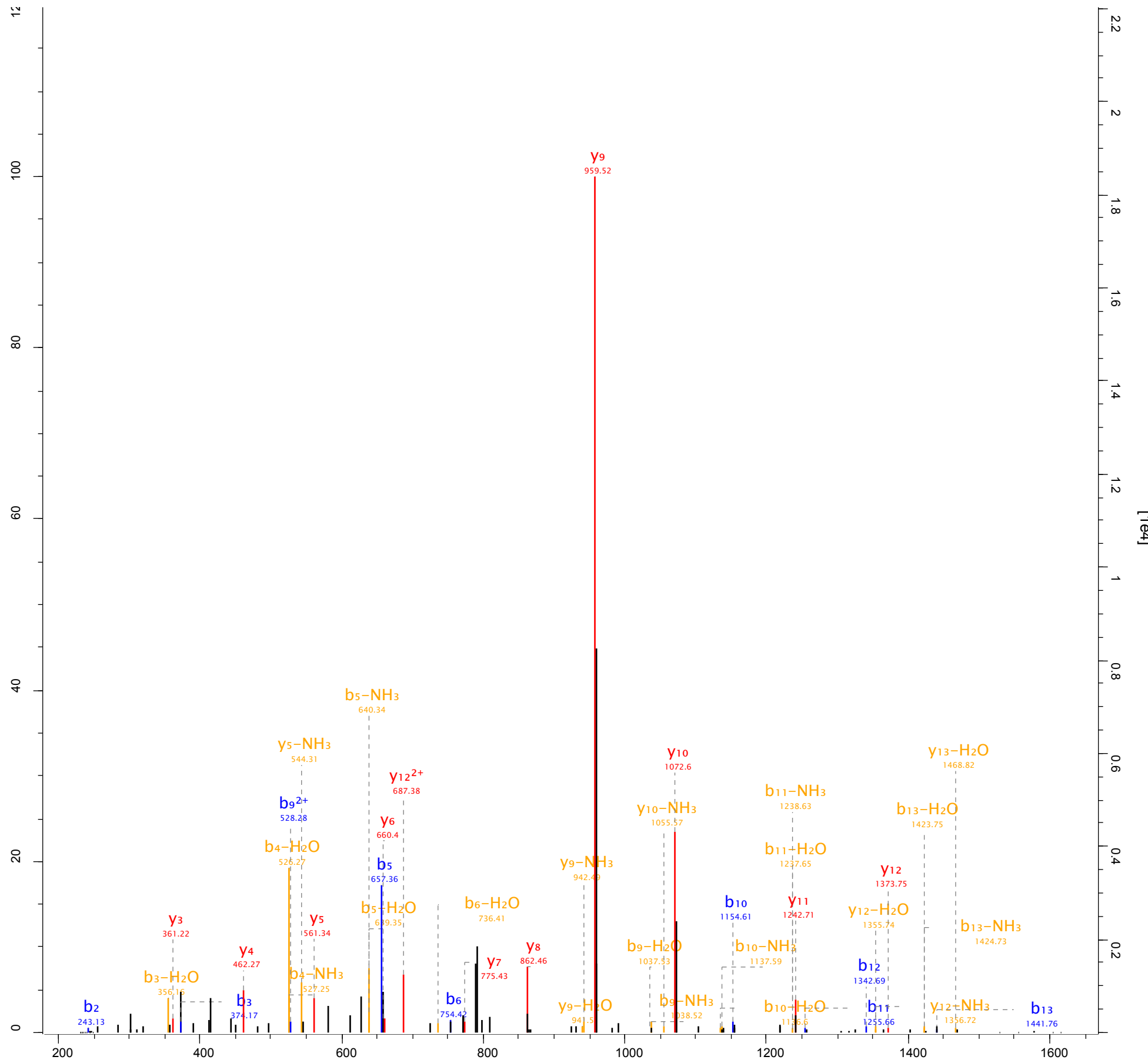


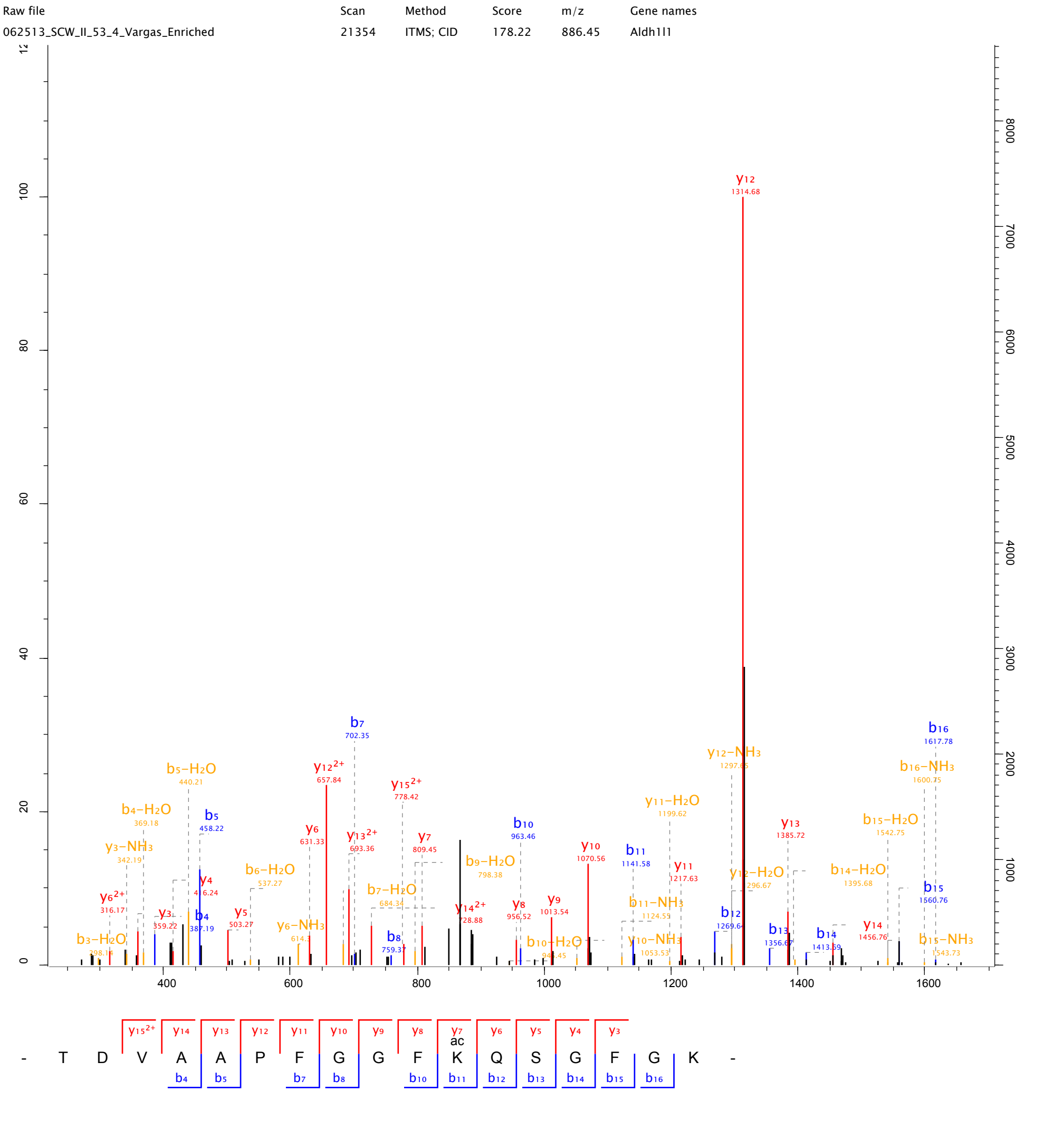


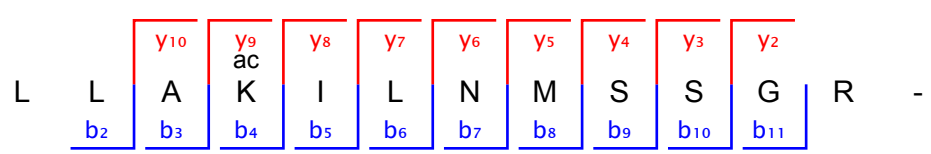
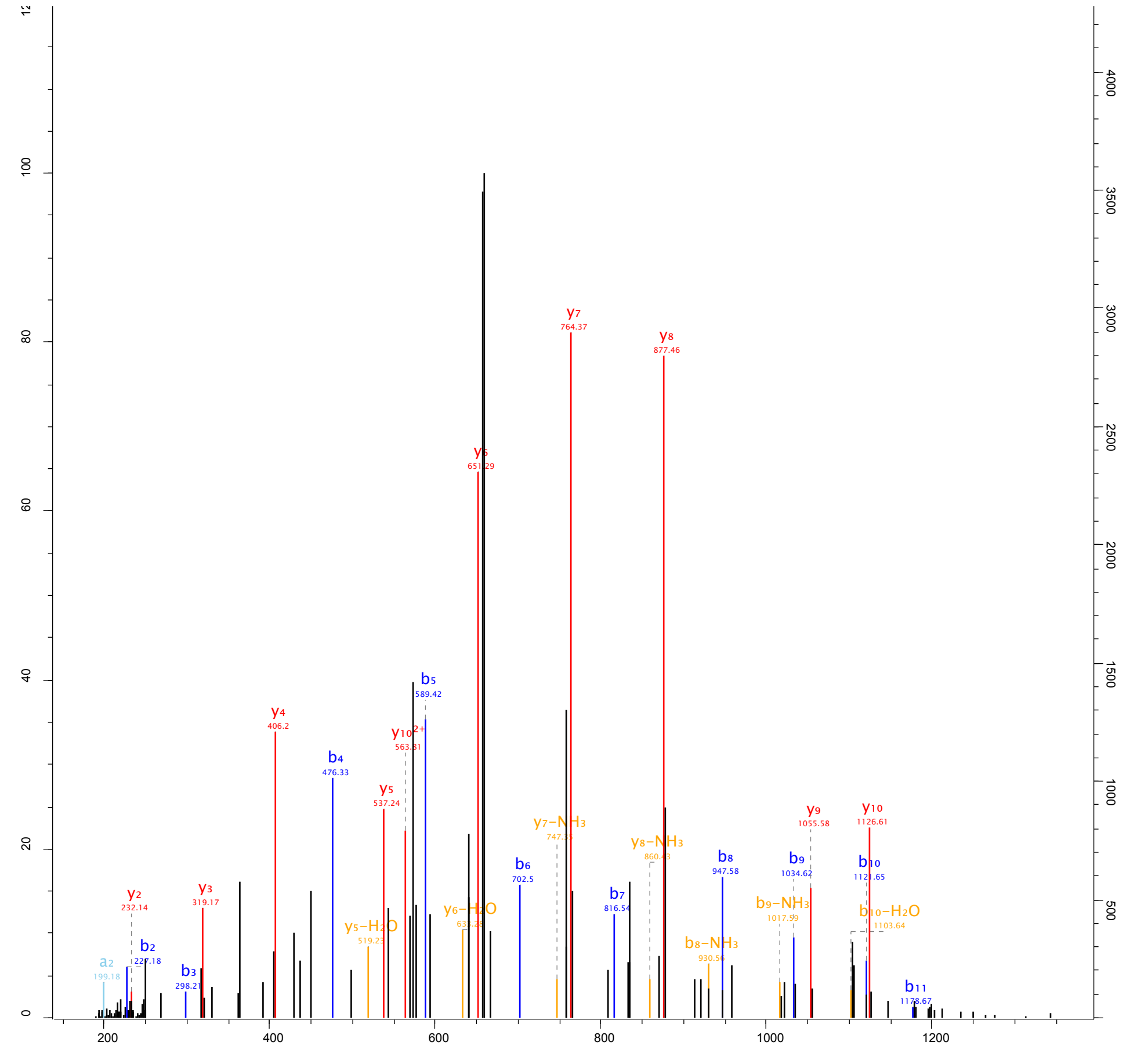


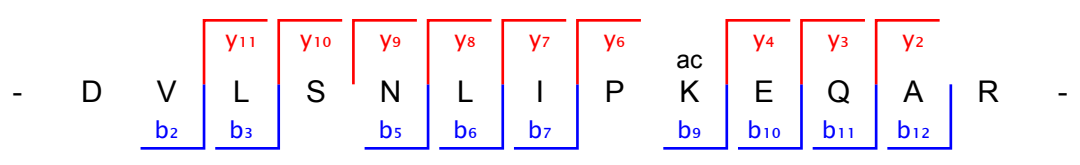
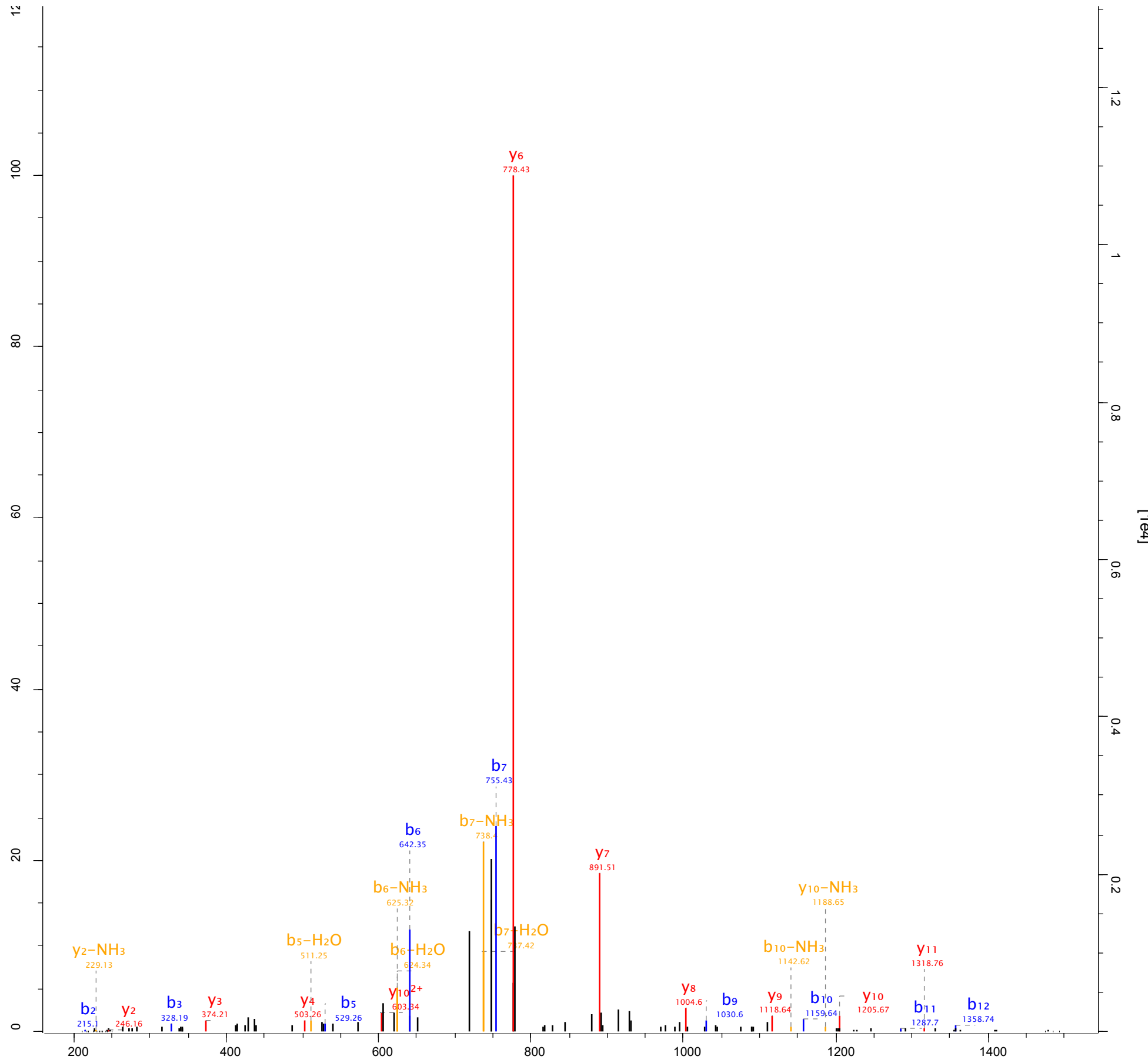


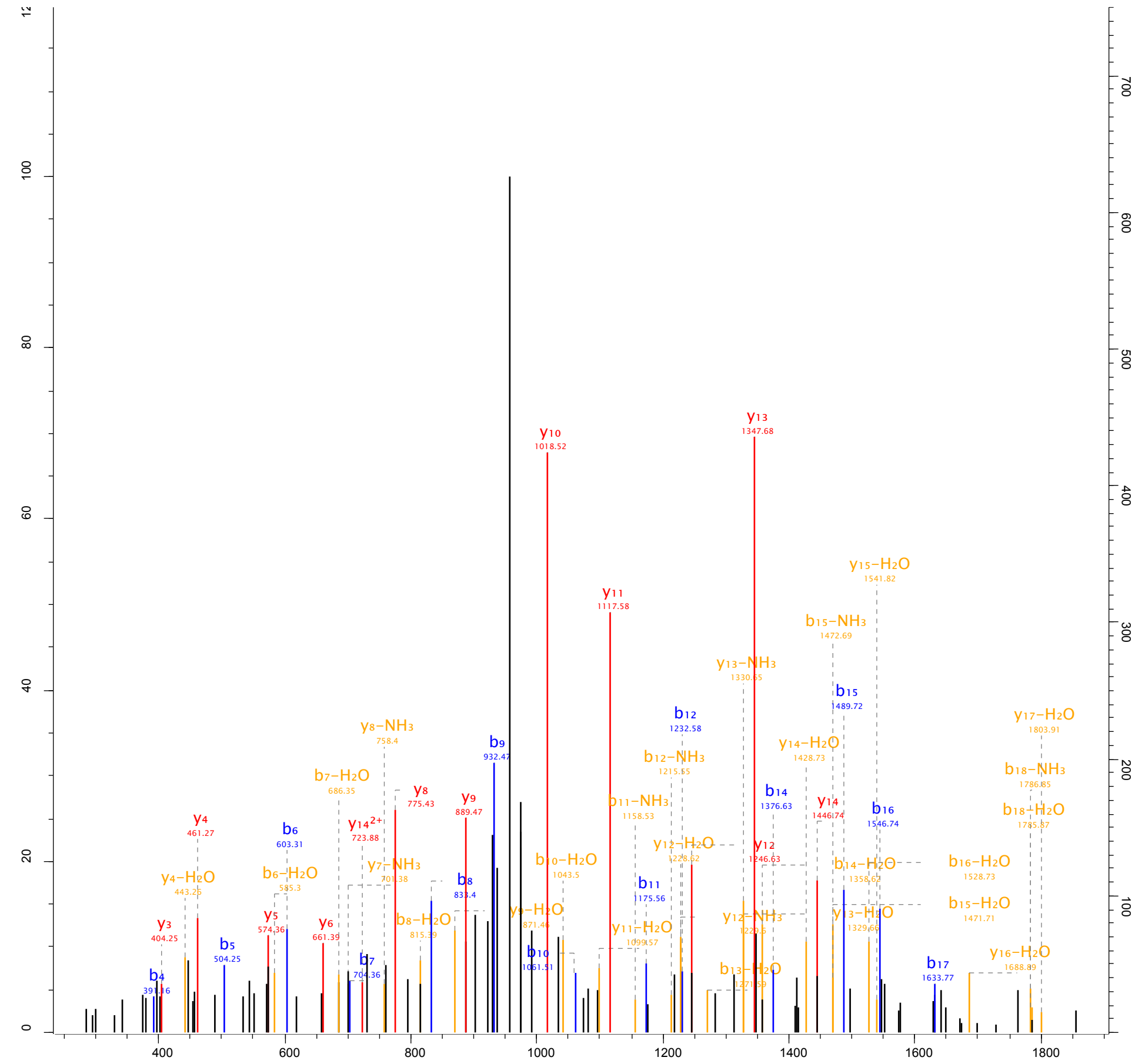






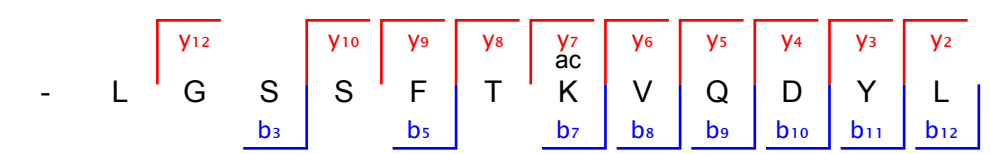
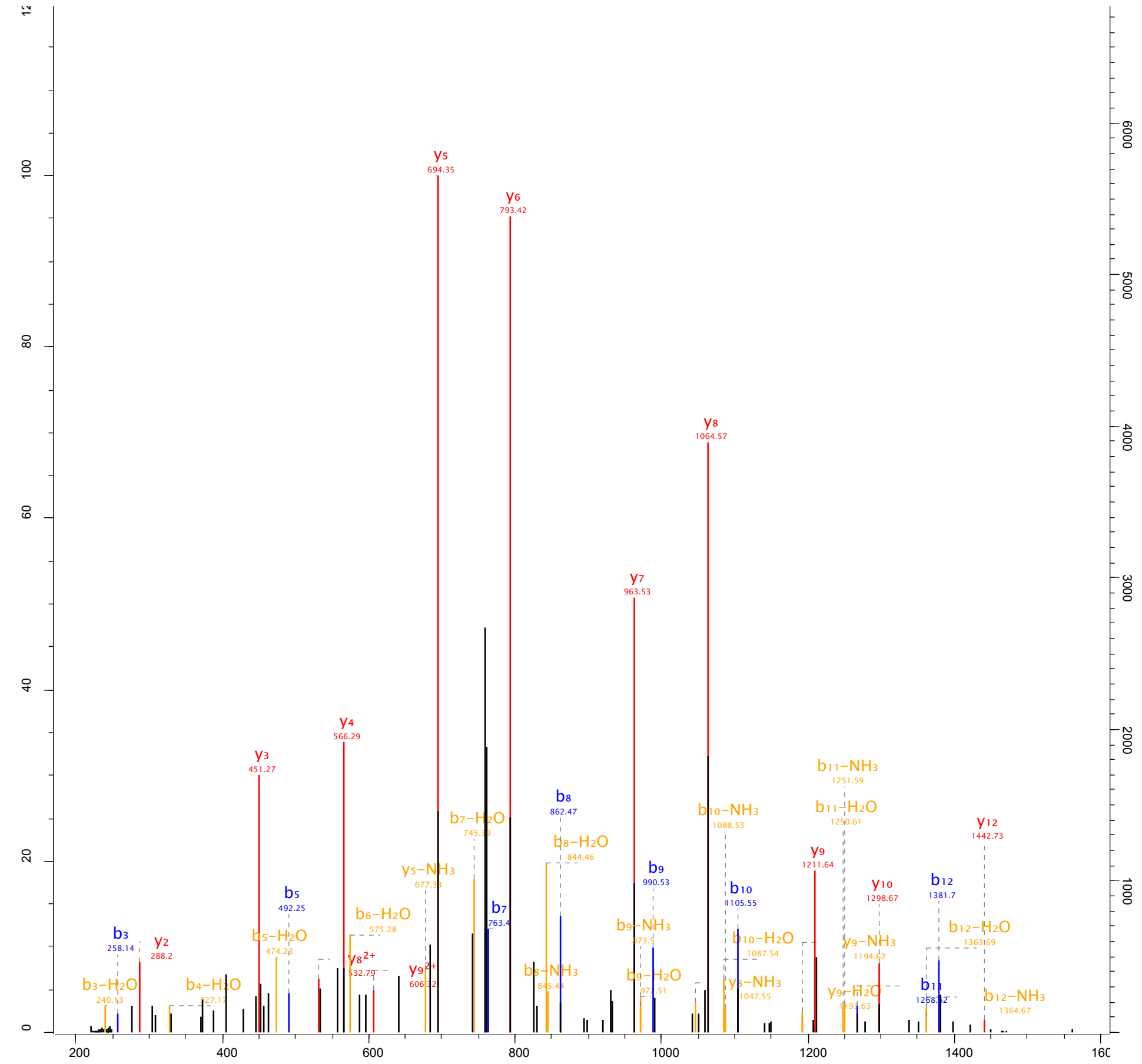


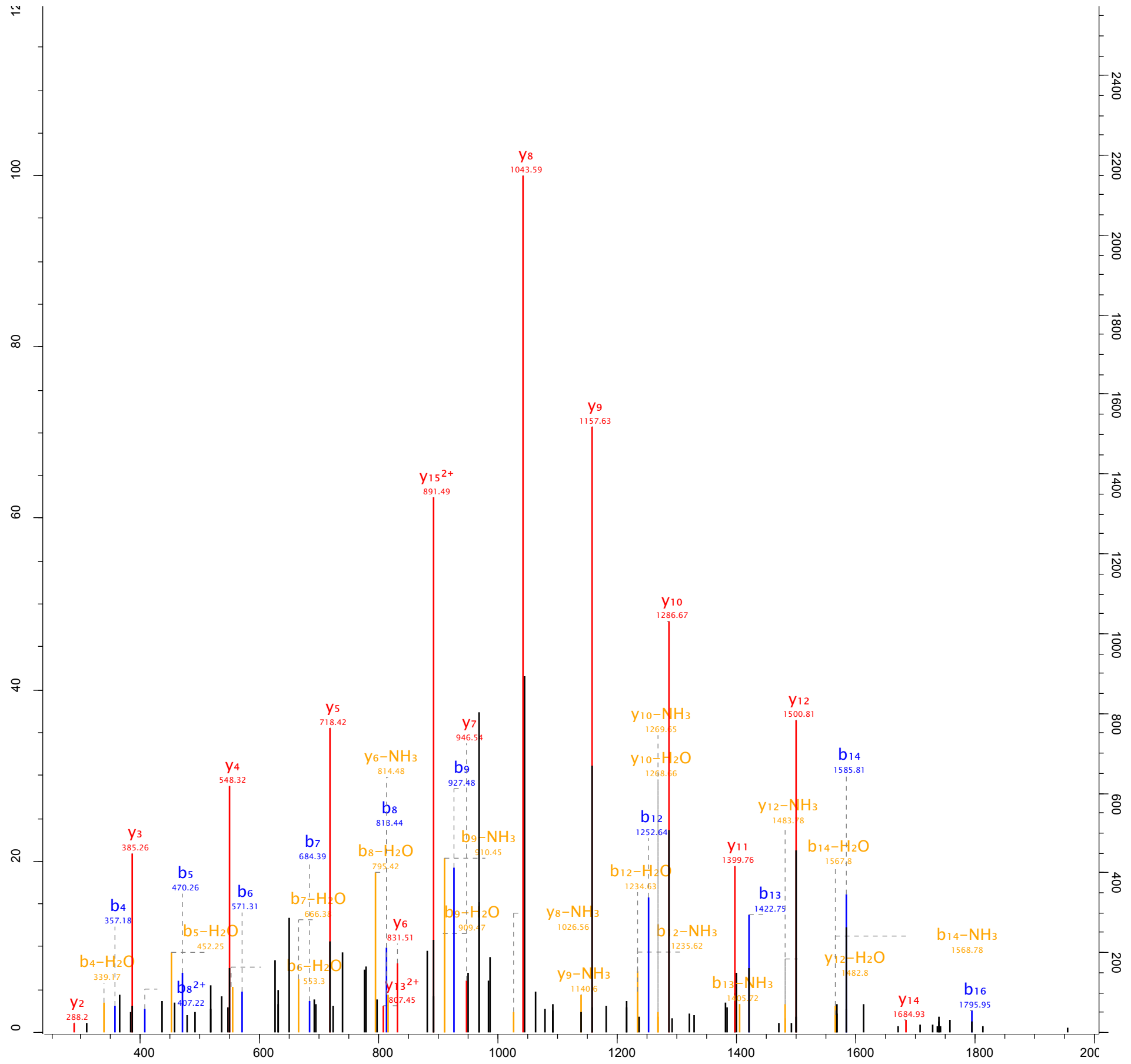




- G A D F L V T E V E N G G S L G S ac K K -

b4 b5 b6 b7 b8 b9 b10 b11 b12 b14 b15 b16 b17

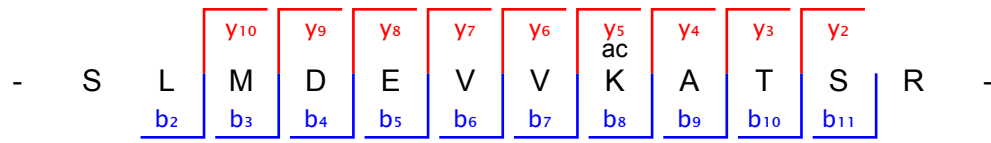
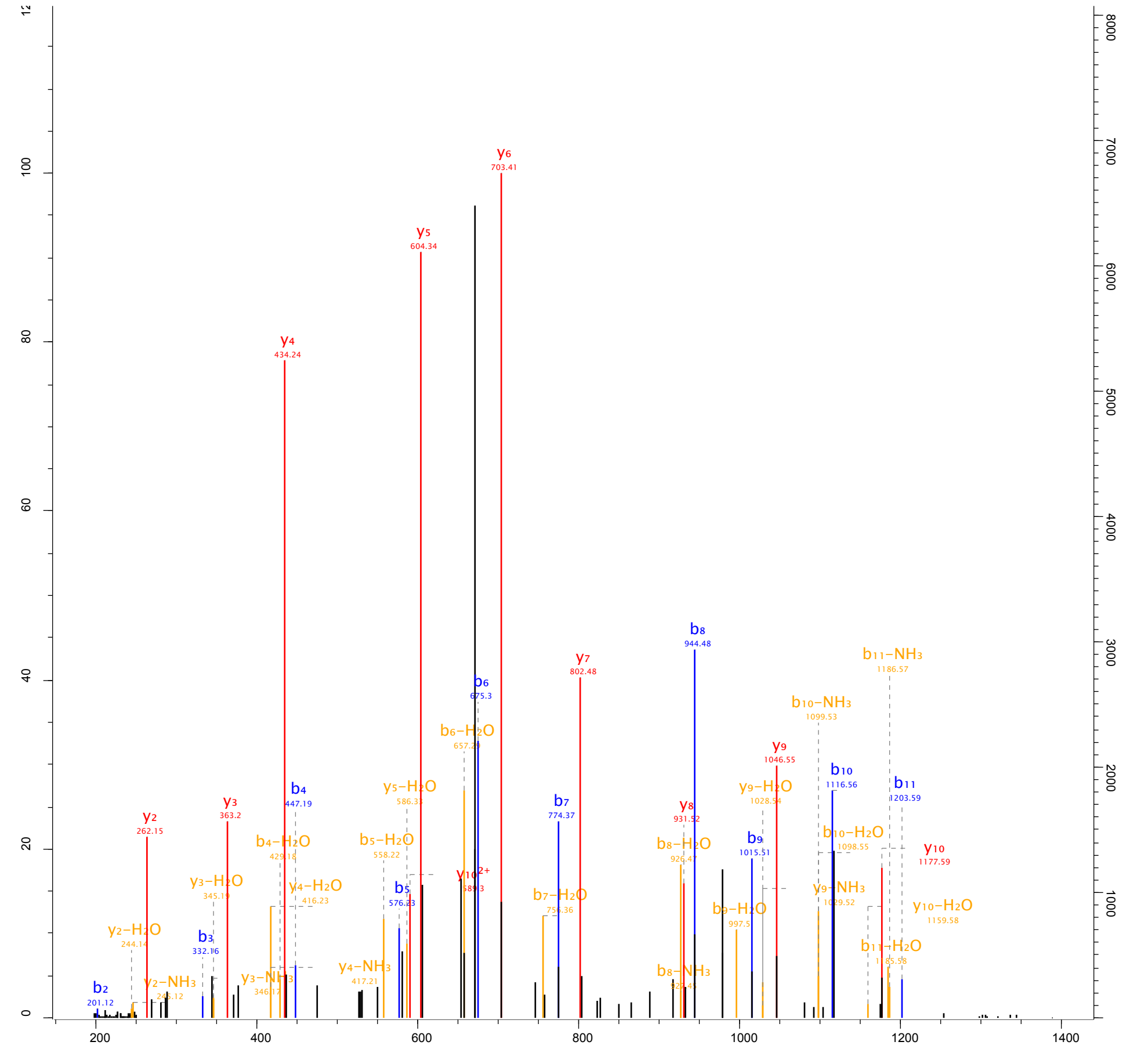


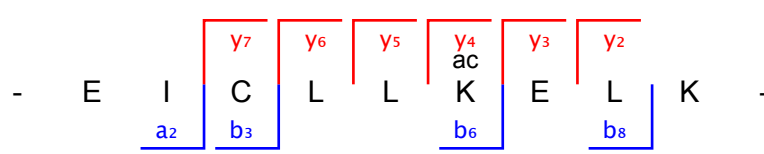
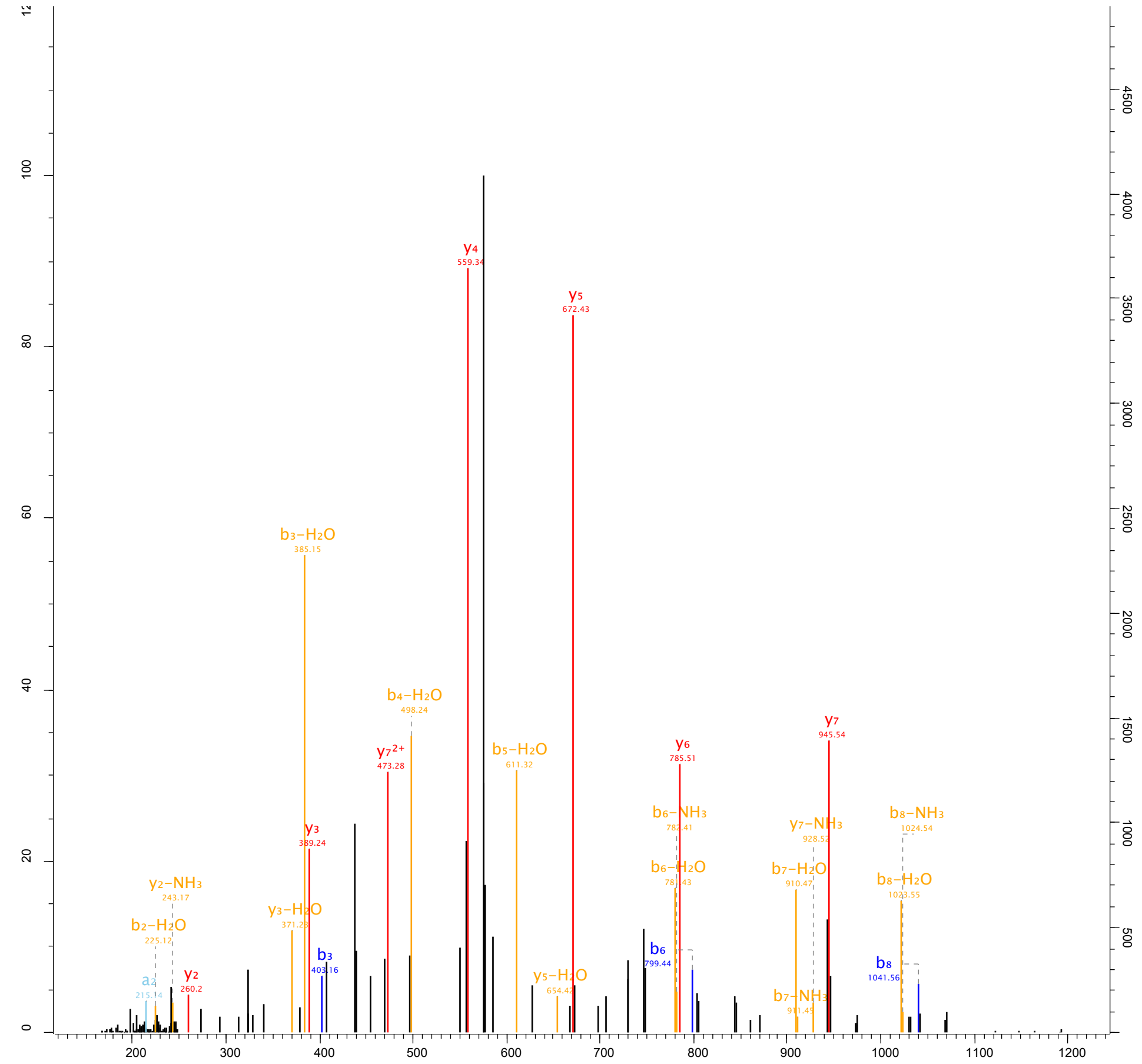


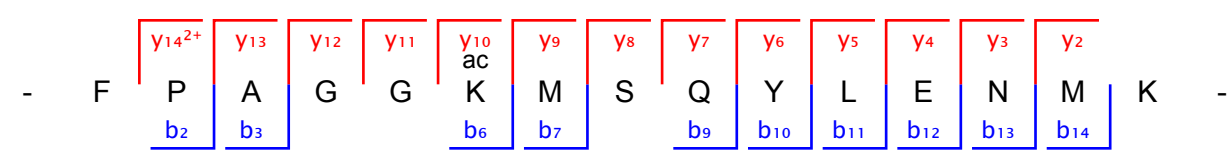
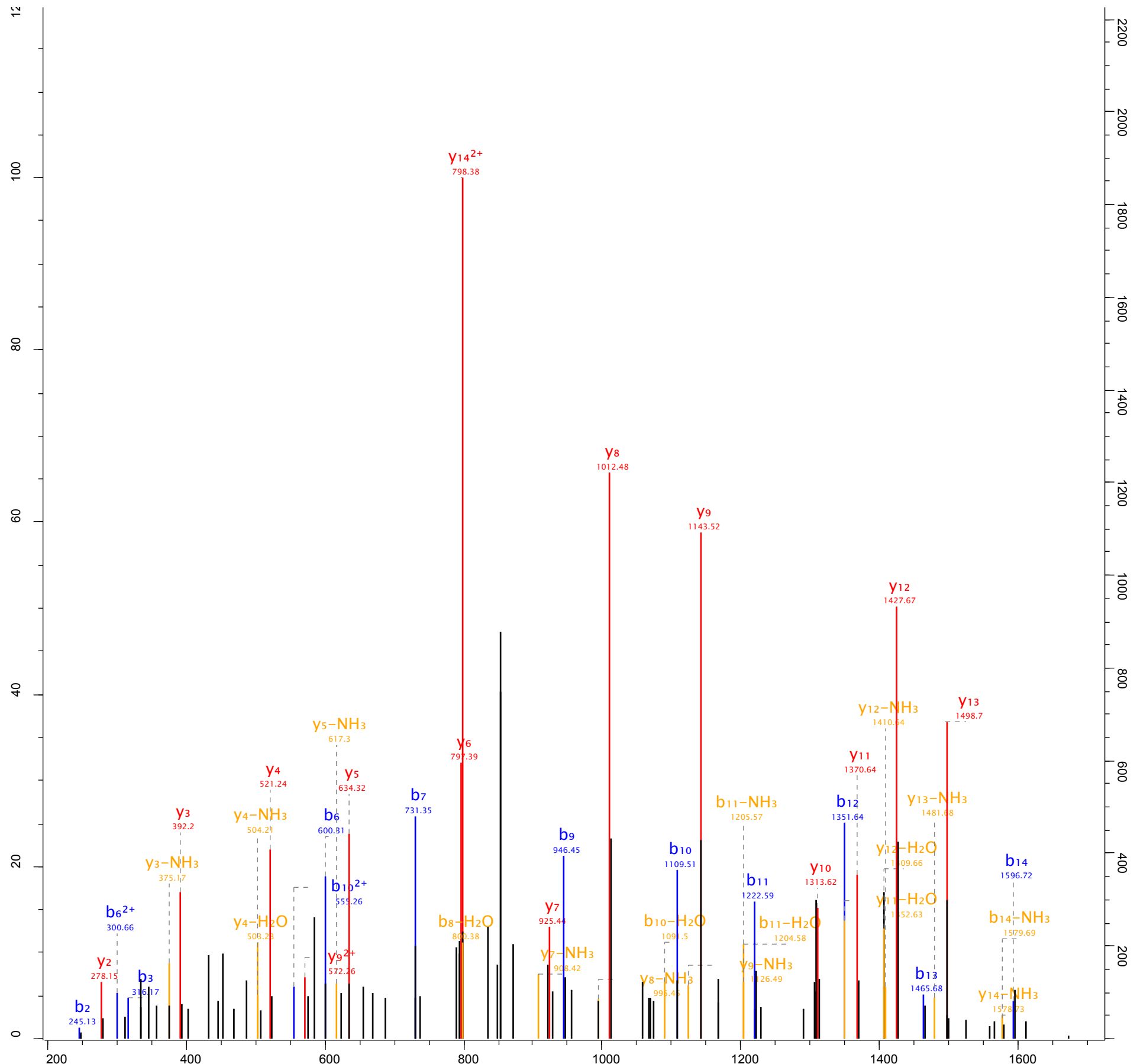
- S T P A I T L E N P D I K Y P L R -

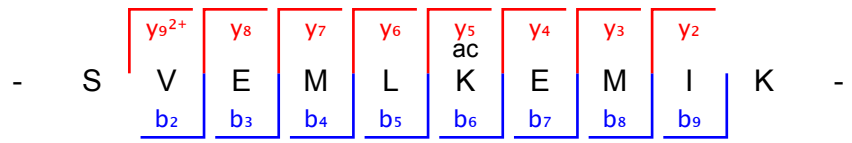
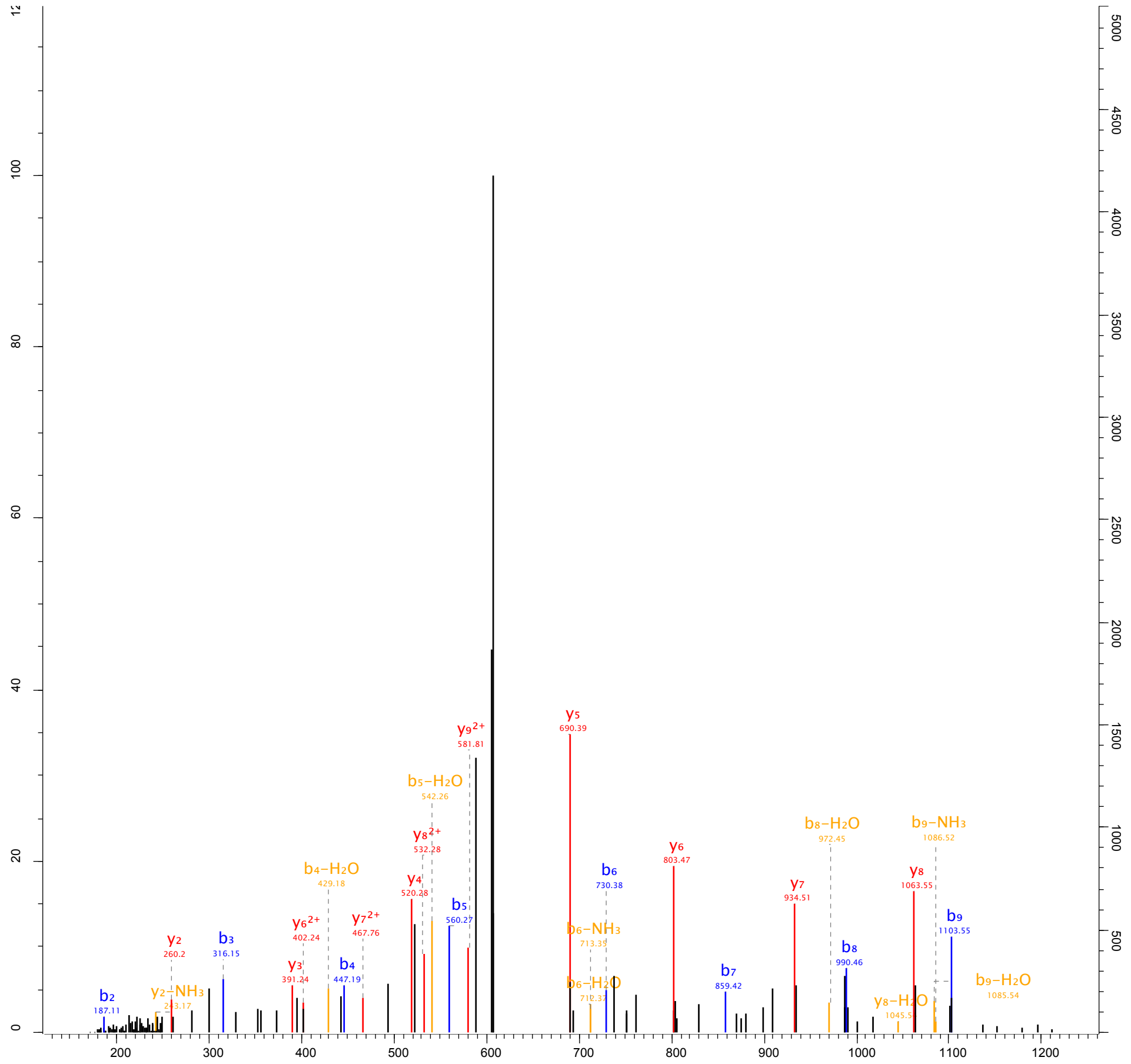
y15²⁺
y14
y13²⁺
y12
y11
y10
y9
y8
y7
y6
y5
y4
y3
y2

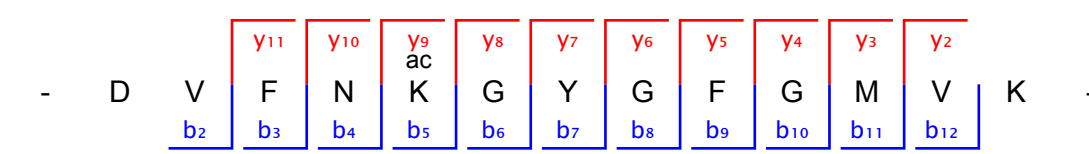
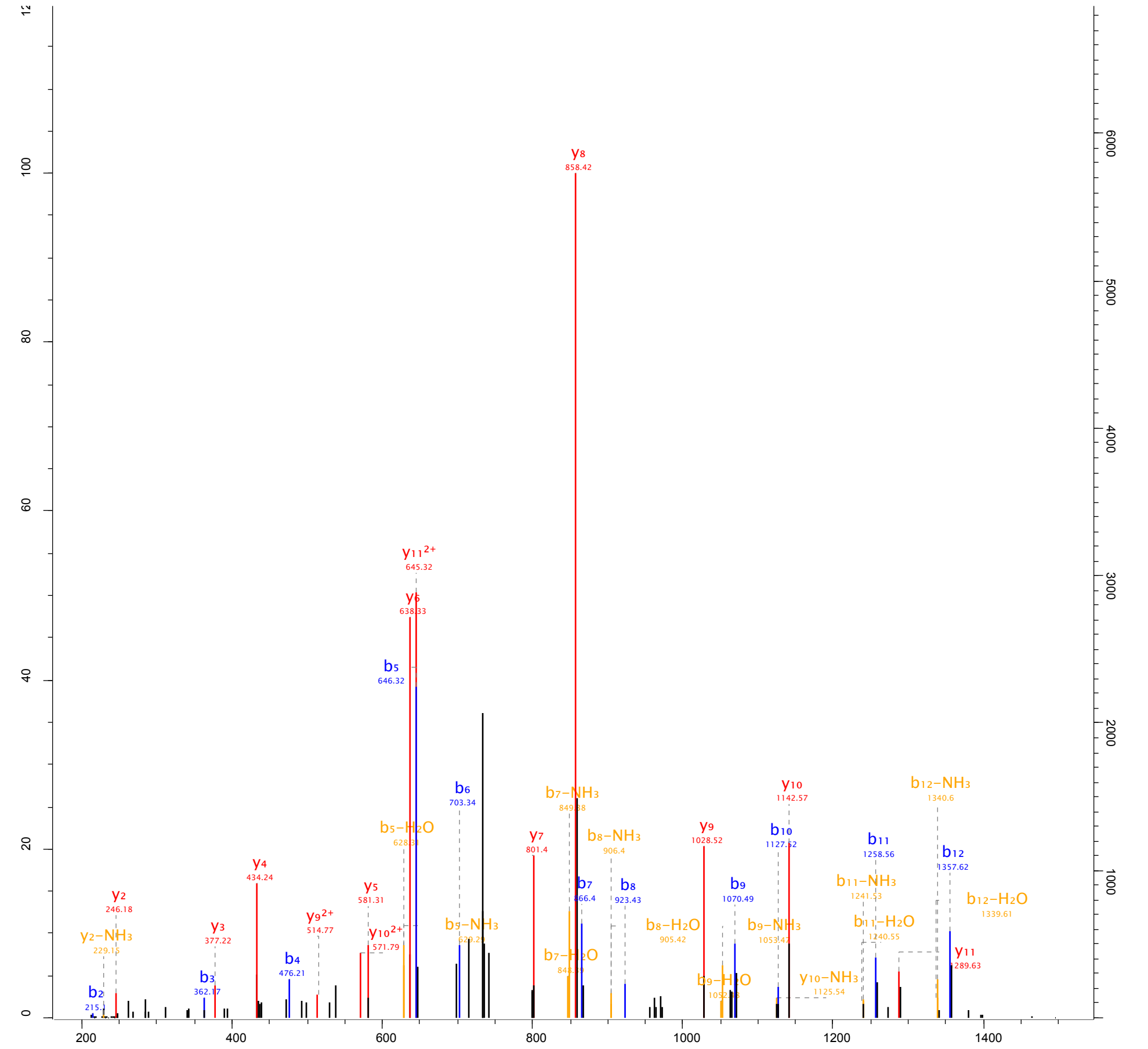
b4
b5
b6
b7
b8
b9
b12
b13
b14
b16

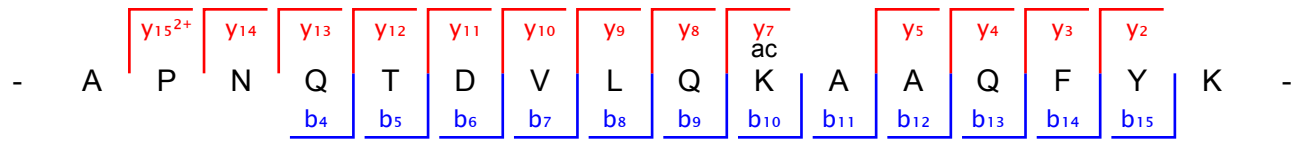
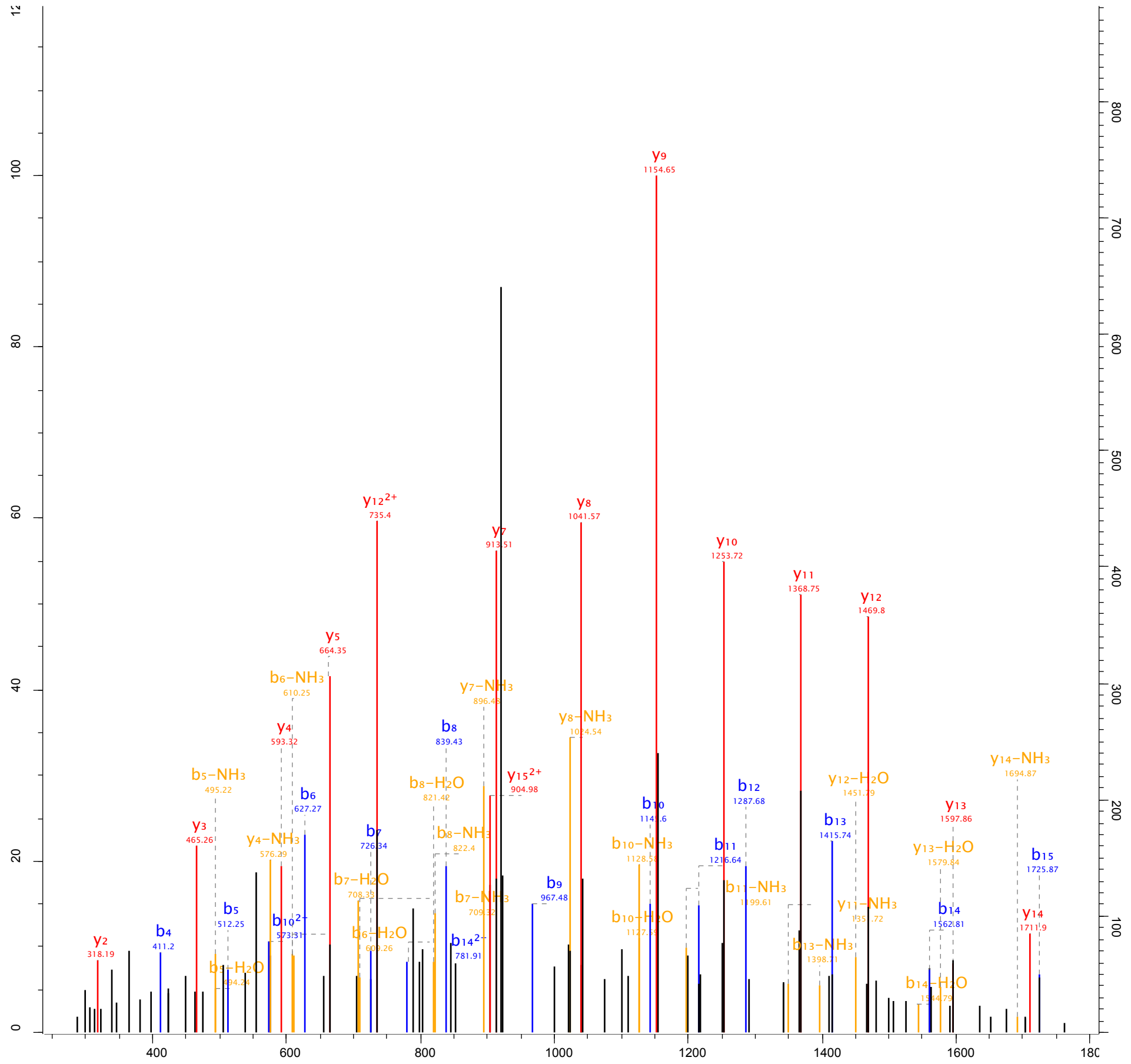


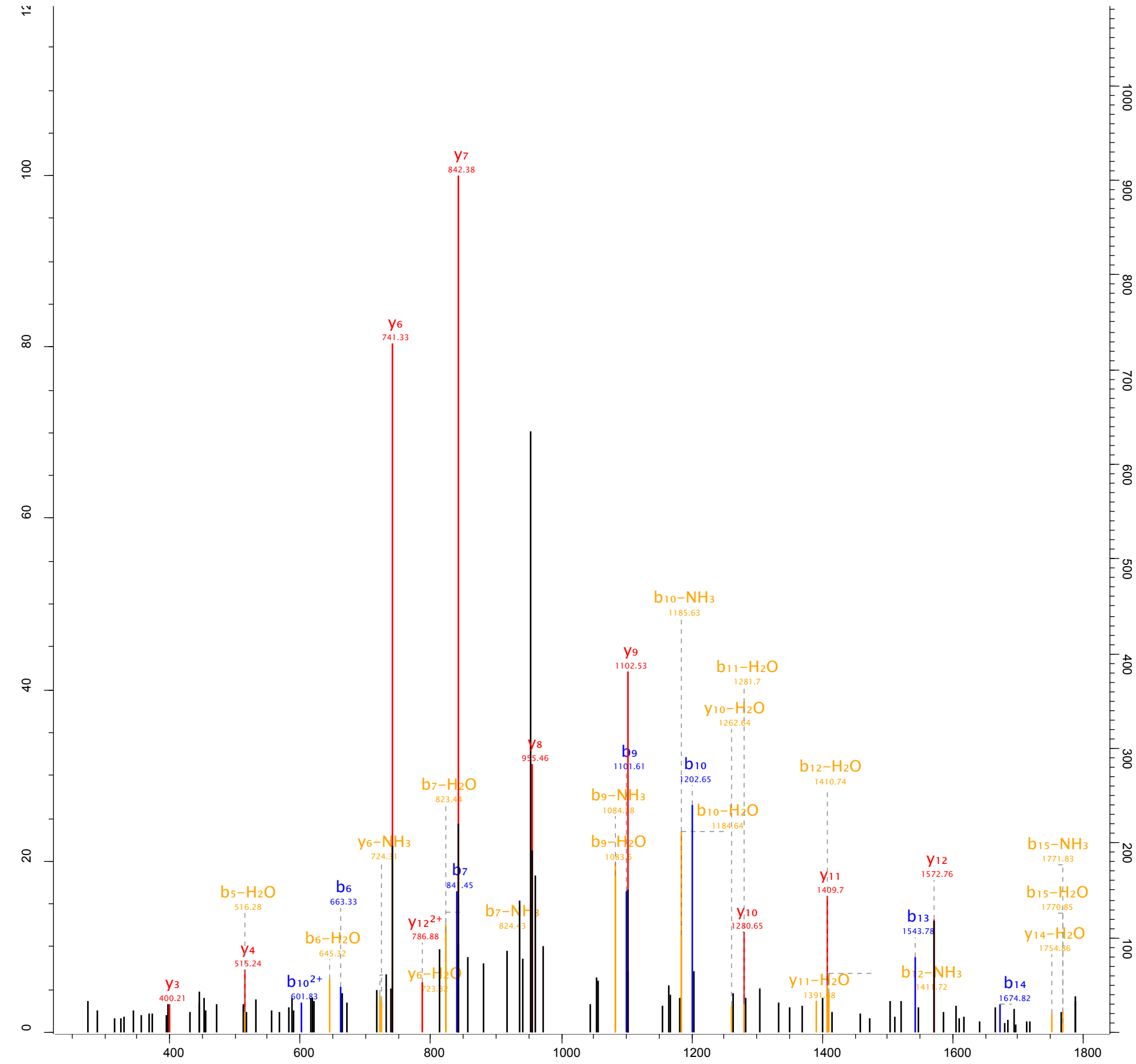






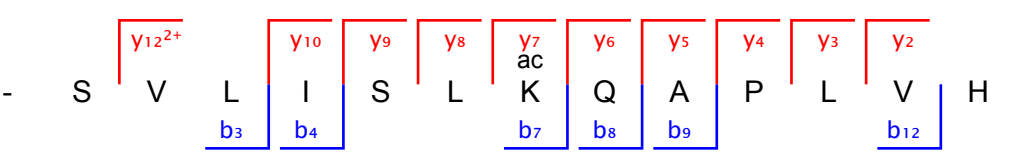
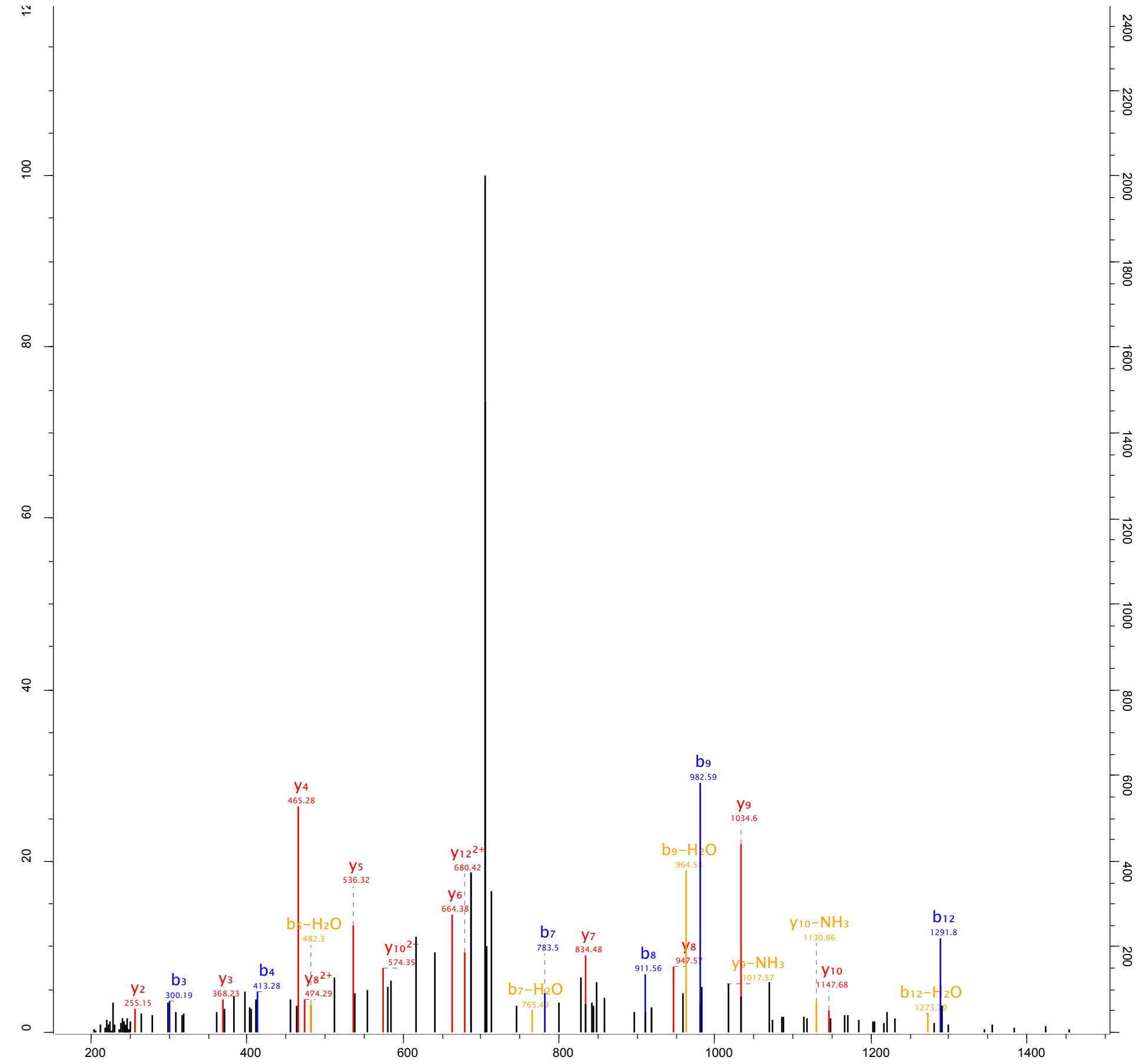


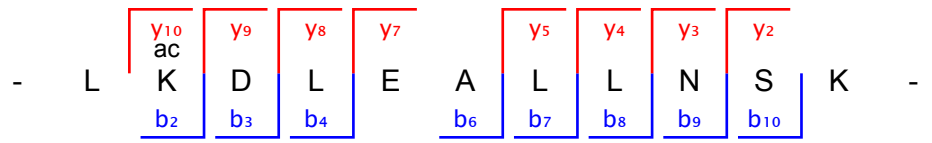
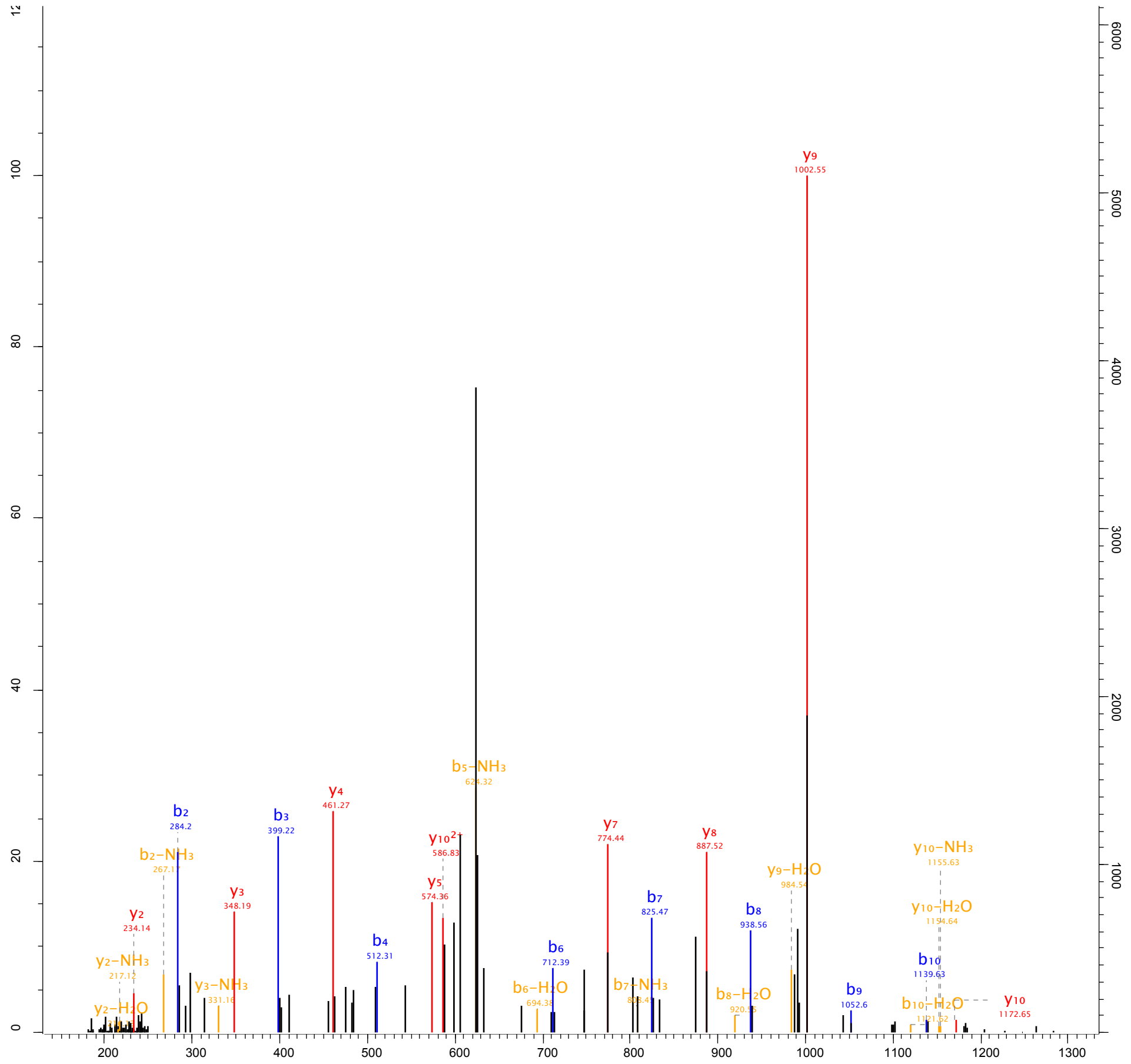


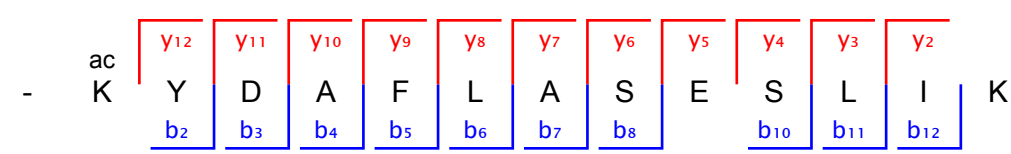
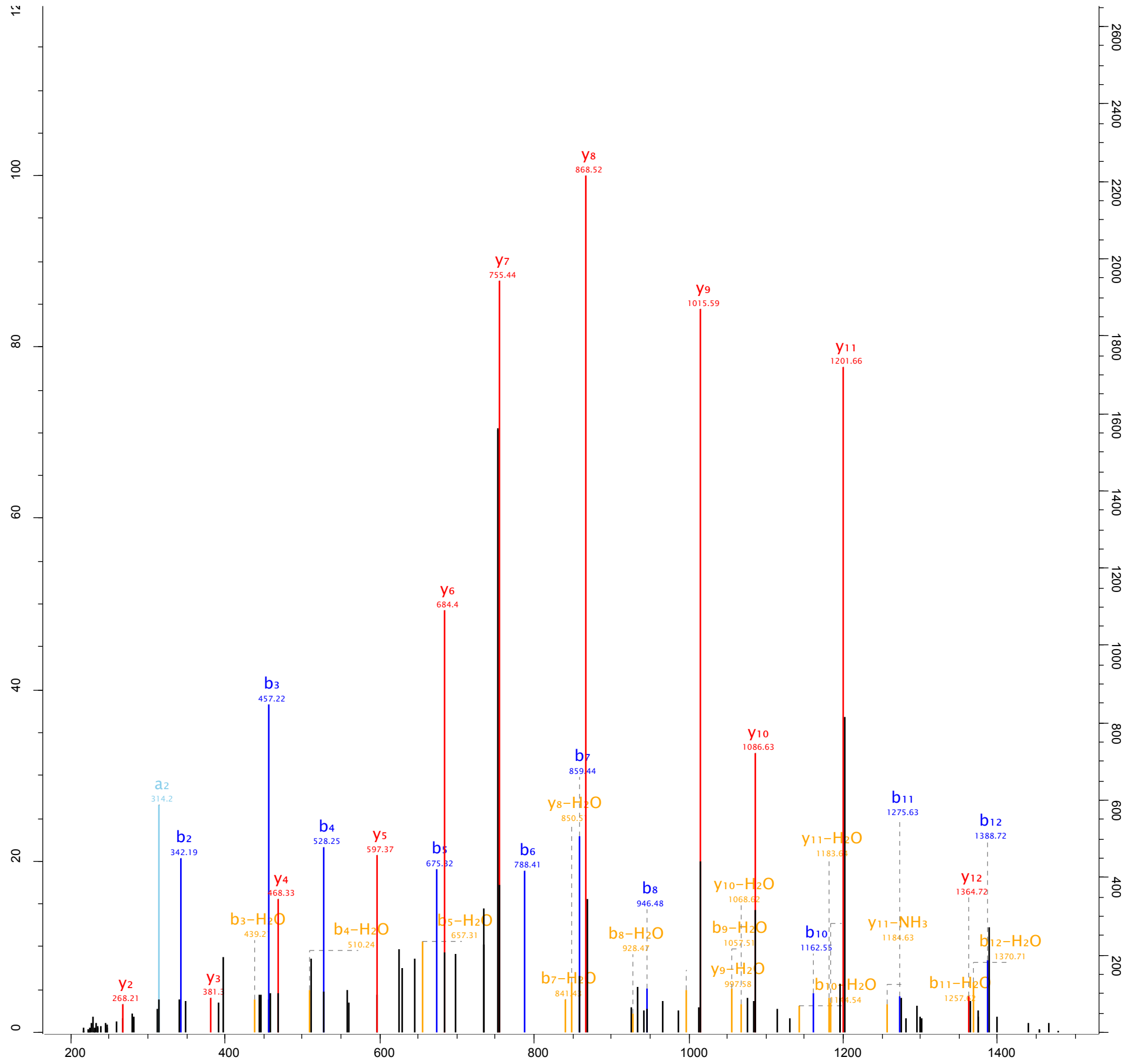


- L G T V **Y** **E** **K** F **I** **T** P E **D** **M** N K -

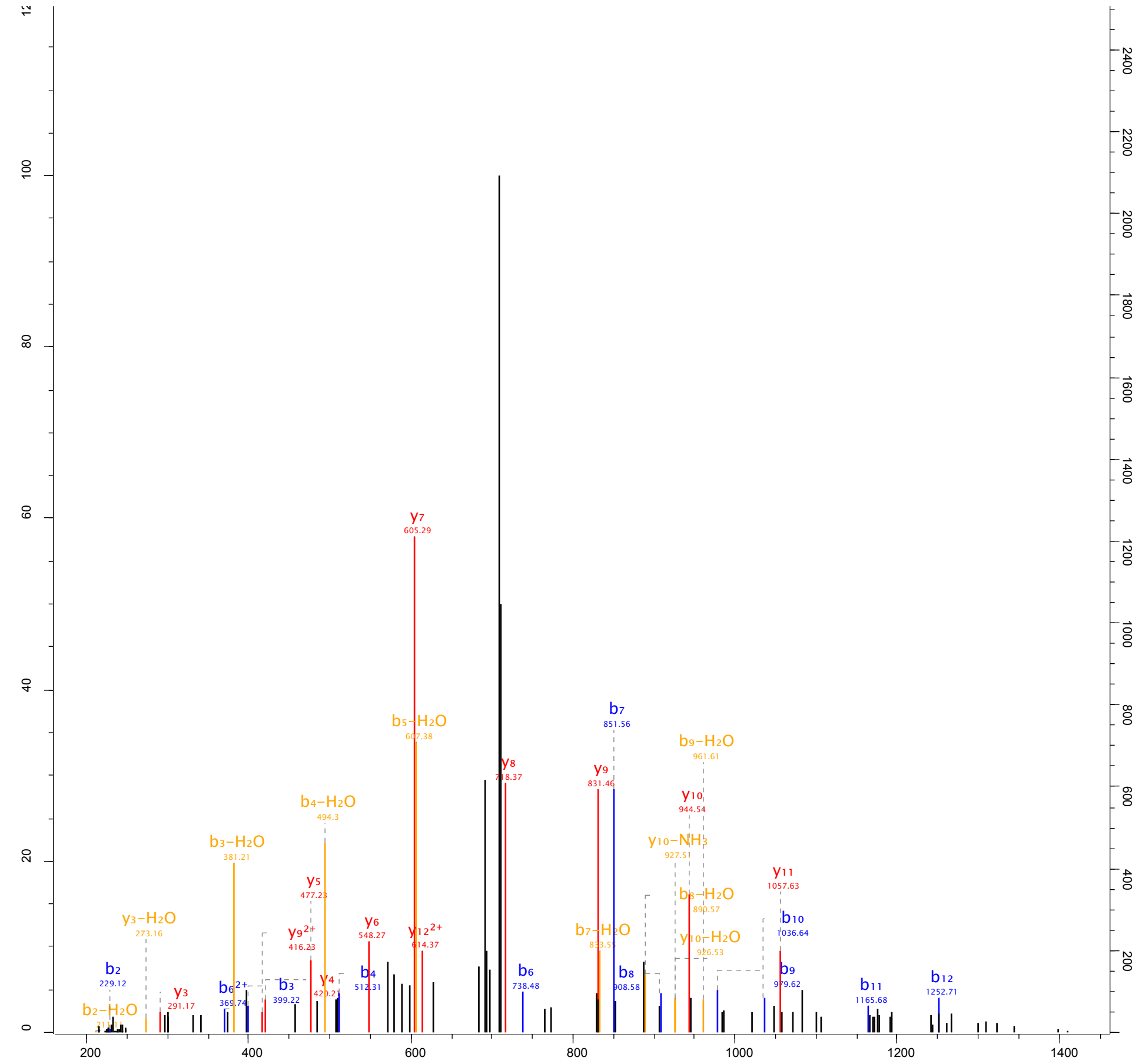
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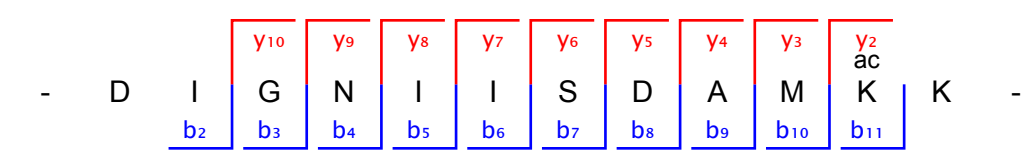
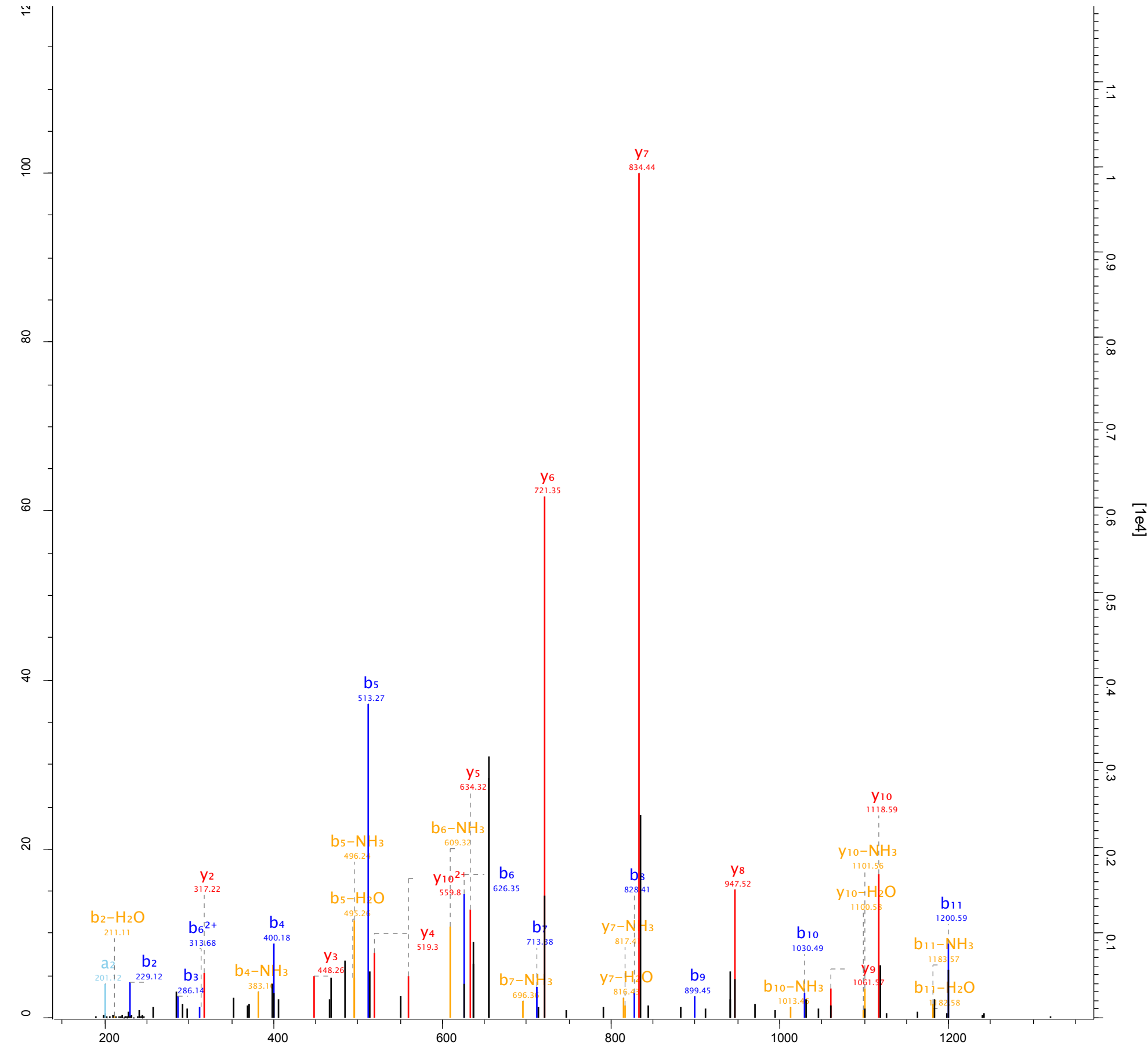


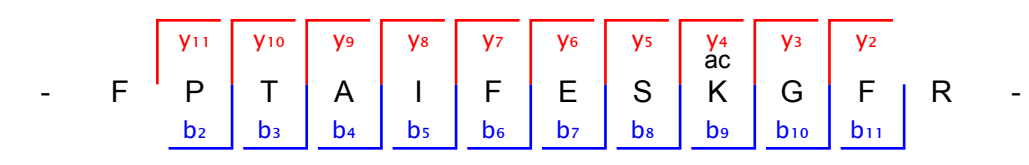
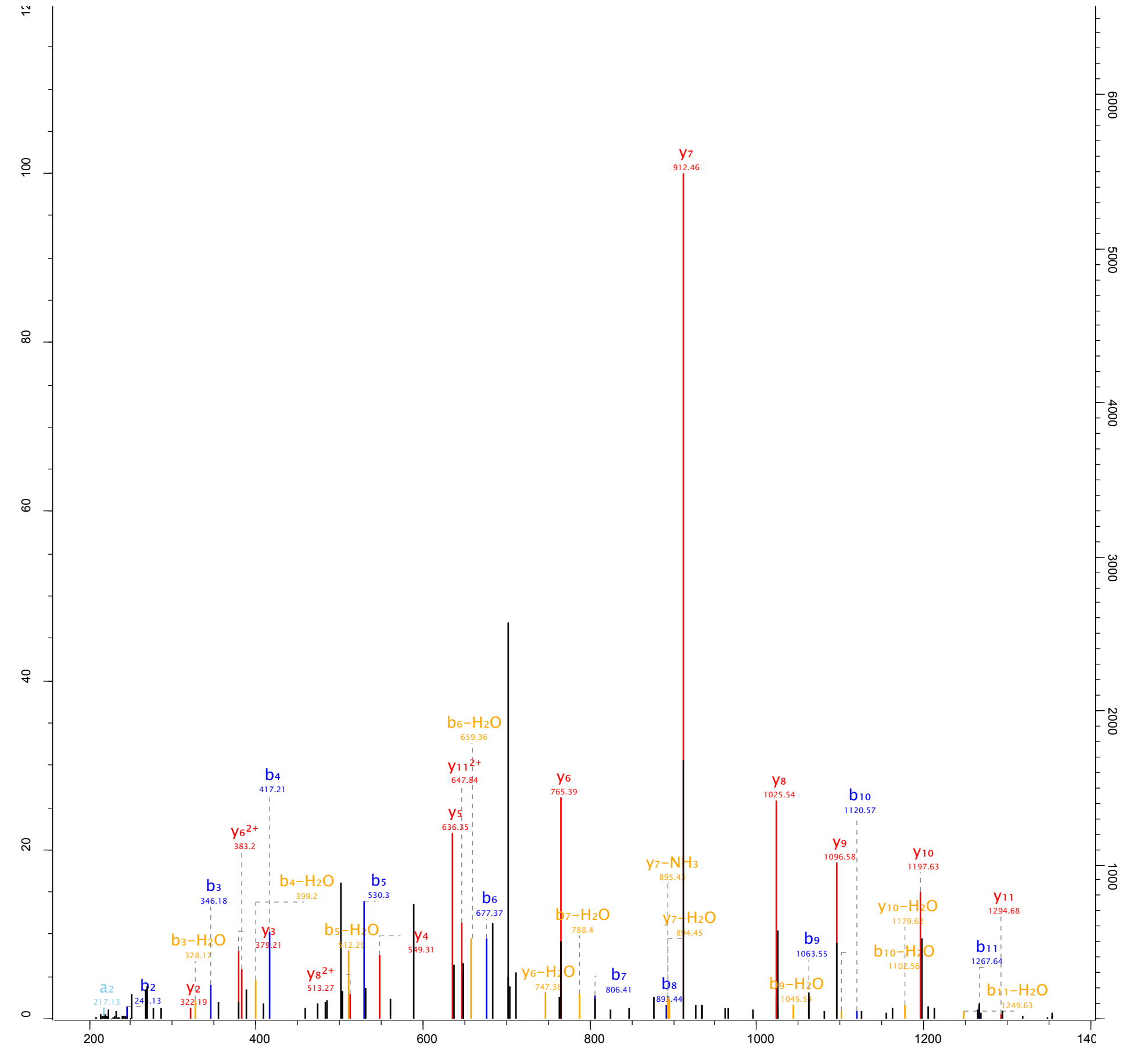
Raw file: 062513_SCW_II_53_4_Vargas_Enriched
 Scan: 22415 Method: ITMS; CID Score: 114.54 m/z: 728.43 Gene names: Gnai2;Gnai1;Gnai3

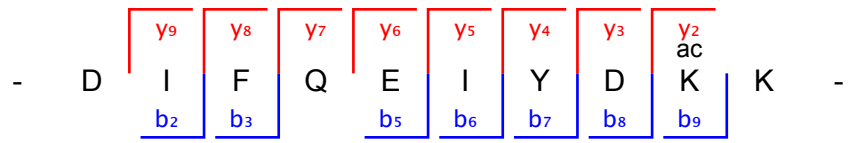
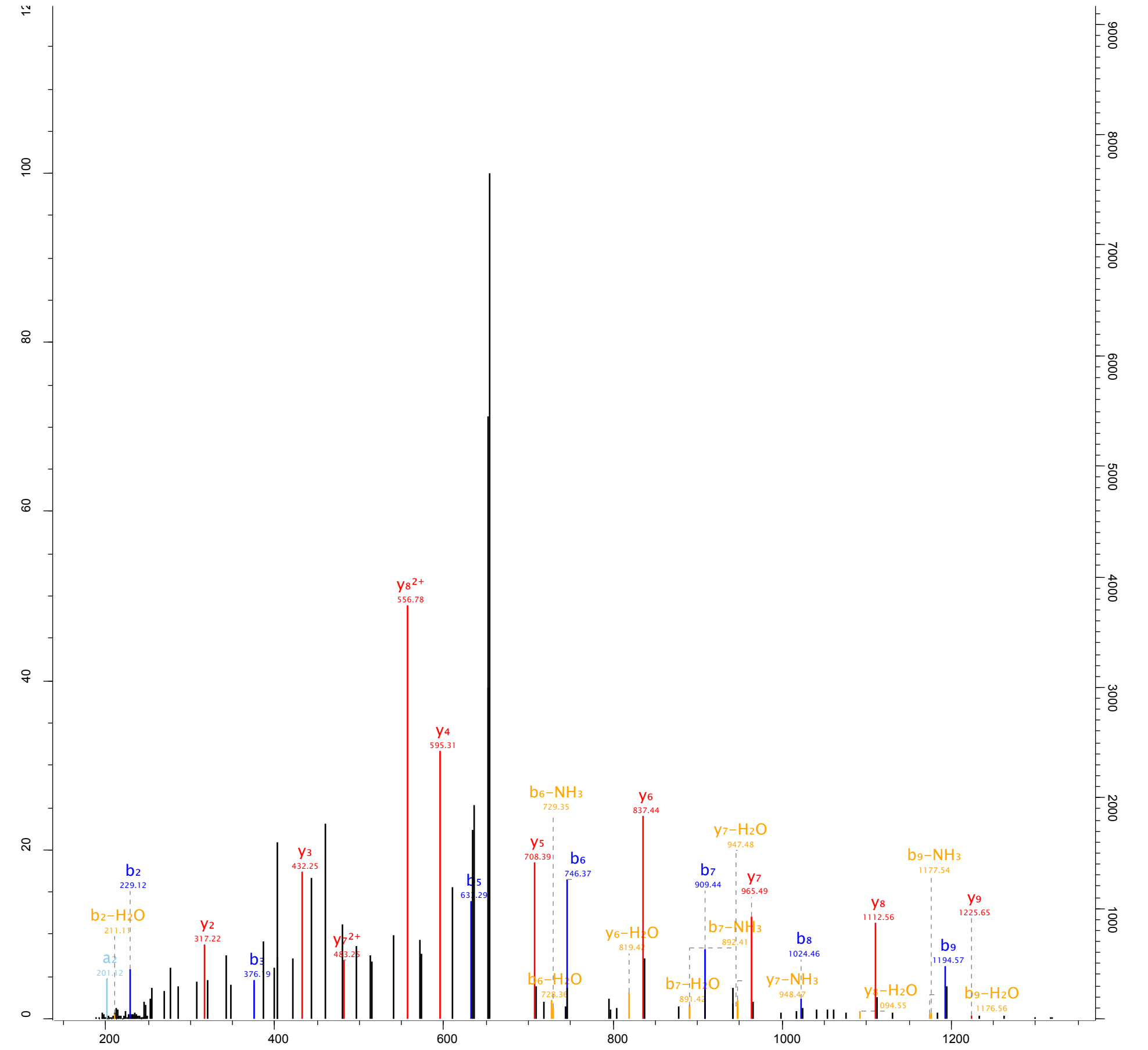


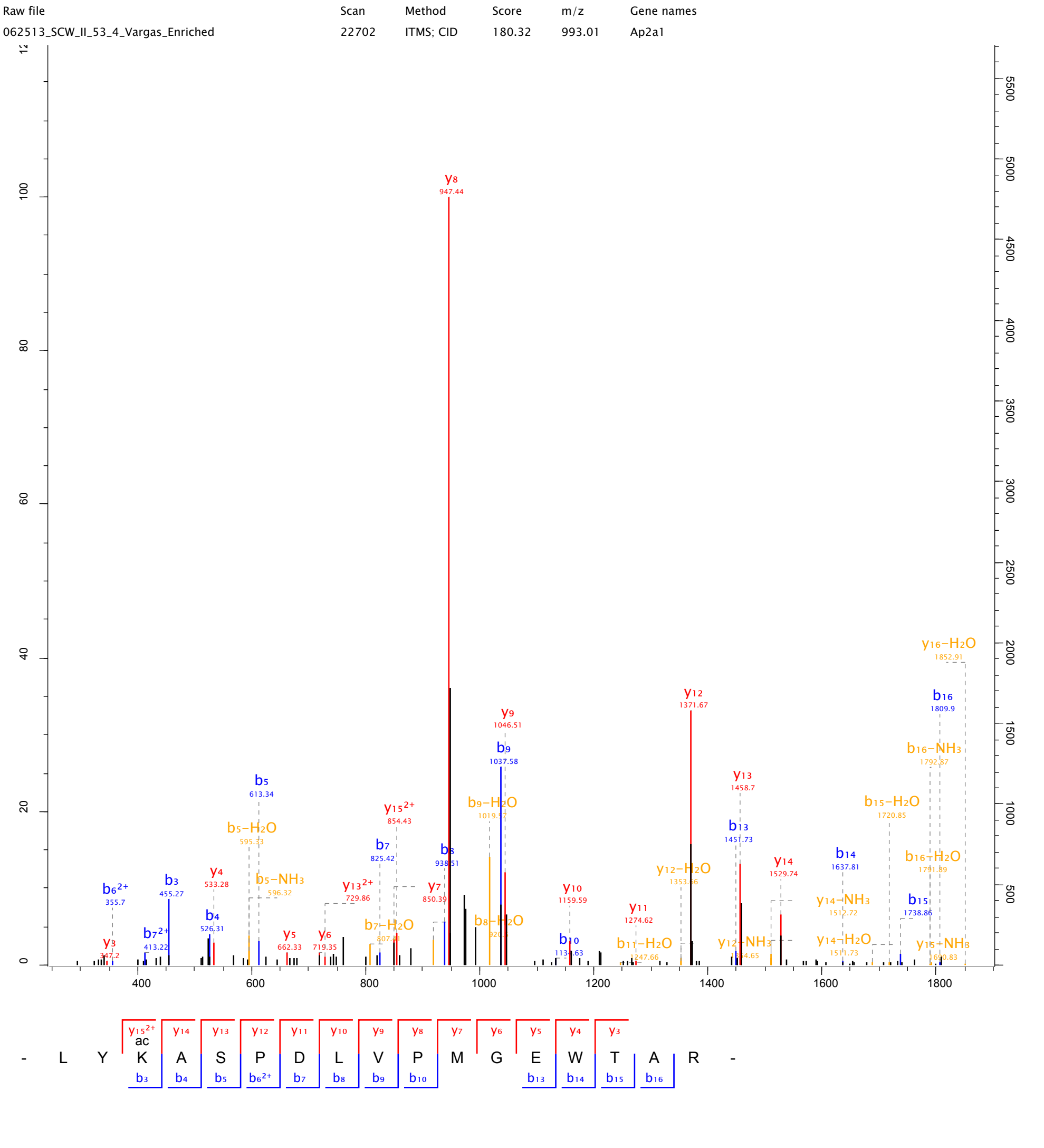
- E V y₁₂2⁺
ac
K y₁₁
L y₁₀
L y₉
L y₈
L y₇
G y₆
A y₅
G y₄
E y₃
S G K -

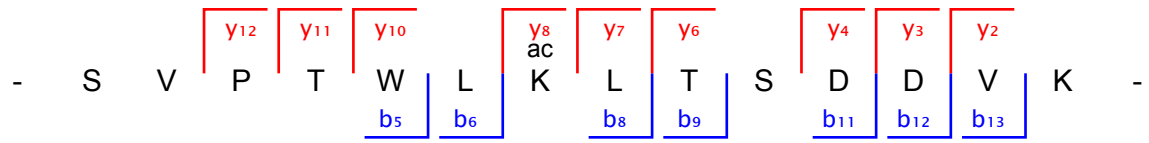
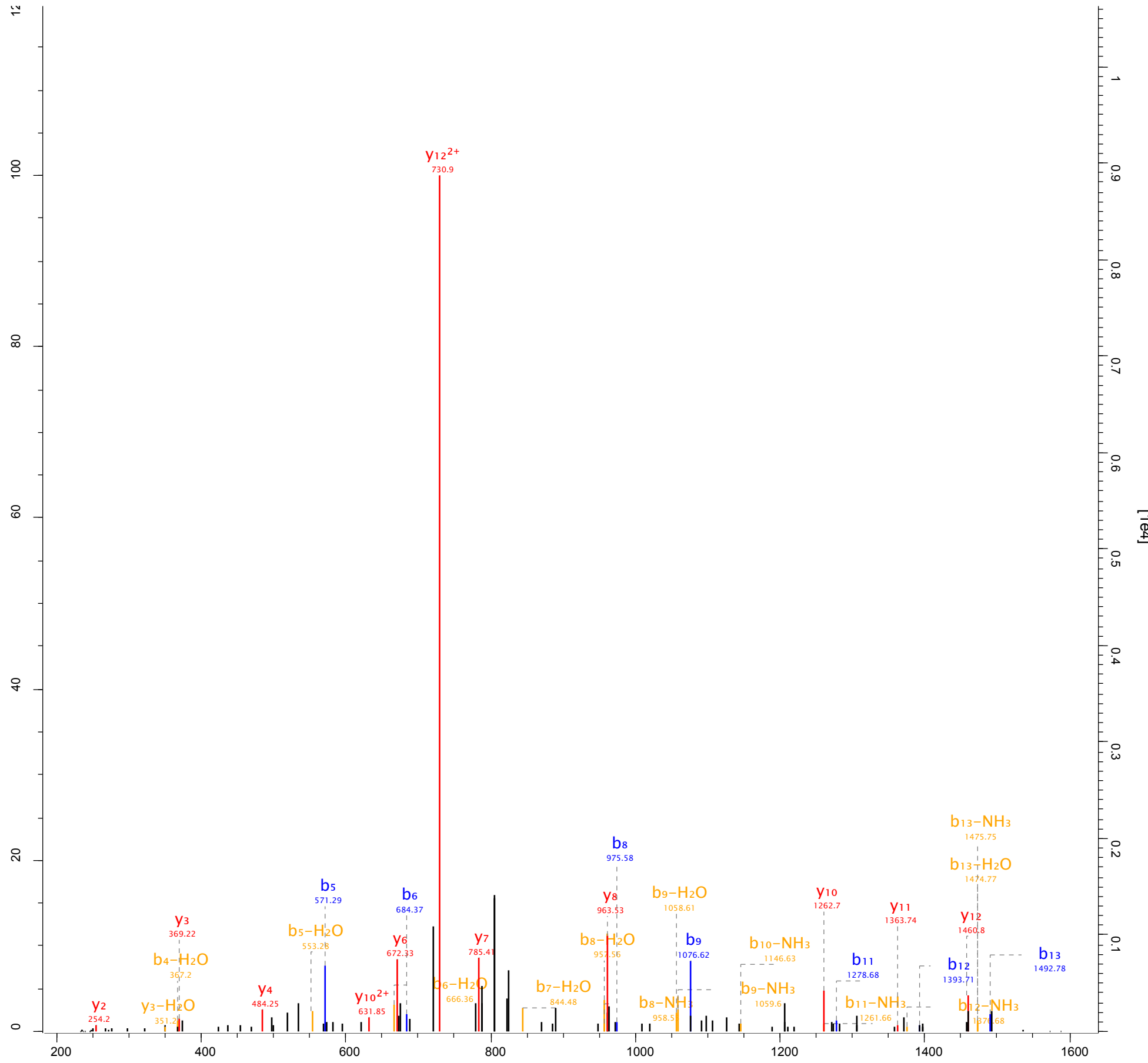
b₂ b₃ b₄ b₆ b₇ b₈ b₉ b₁₀ b₁₁ b₁₂

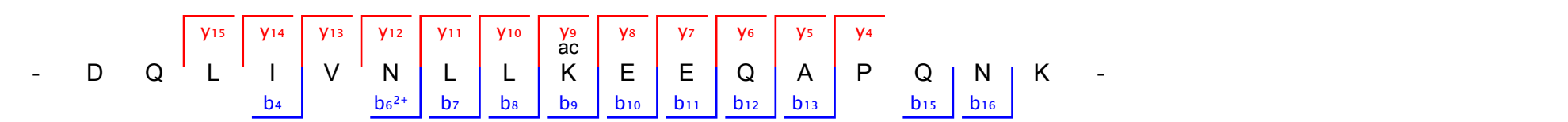
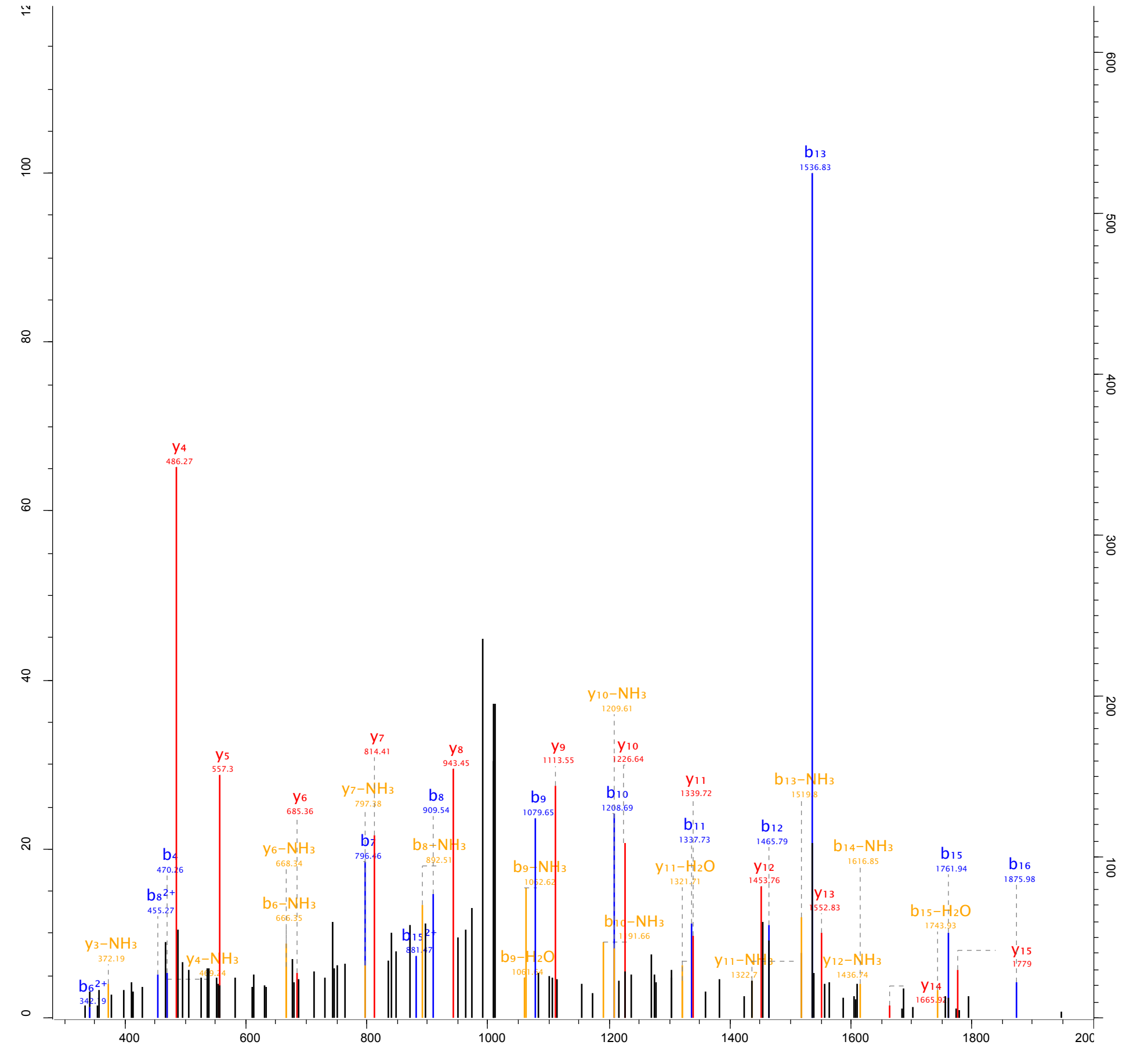


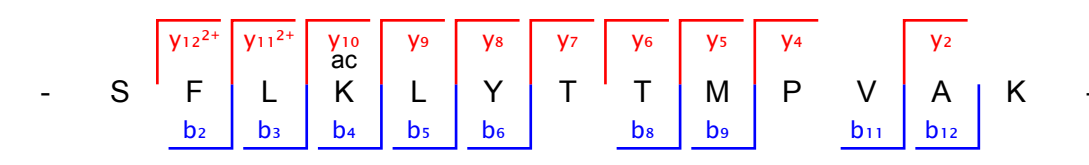
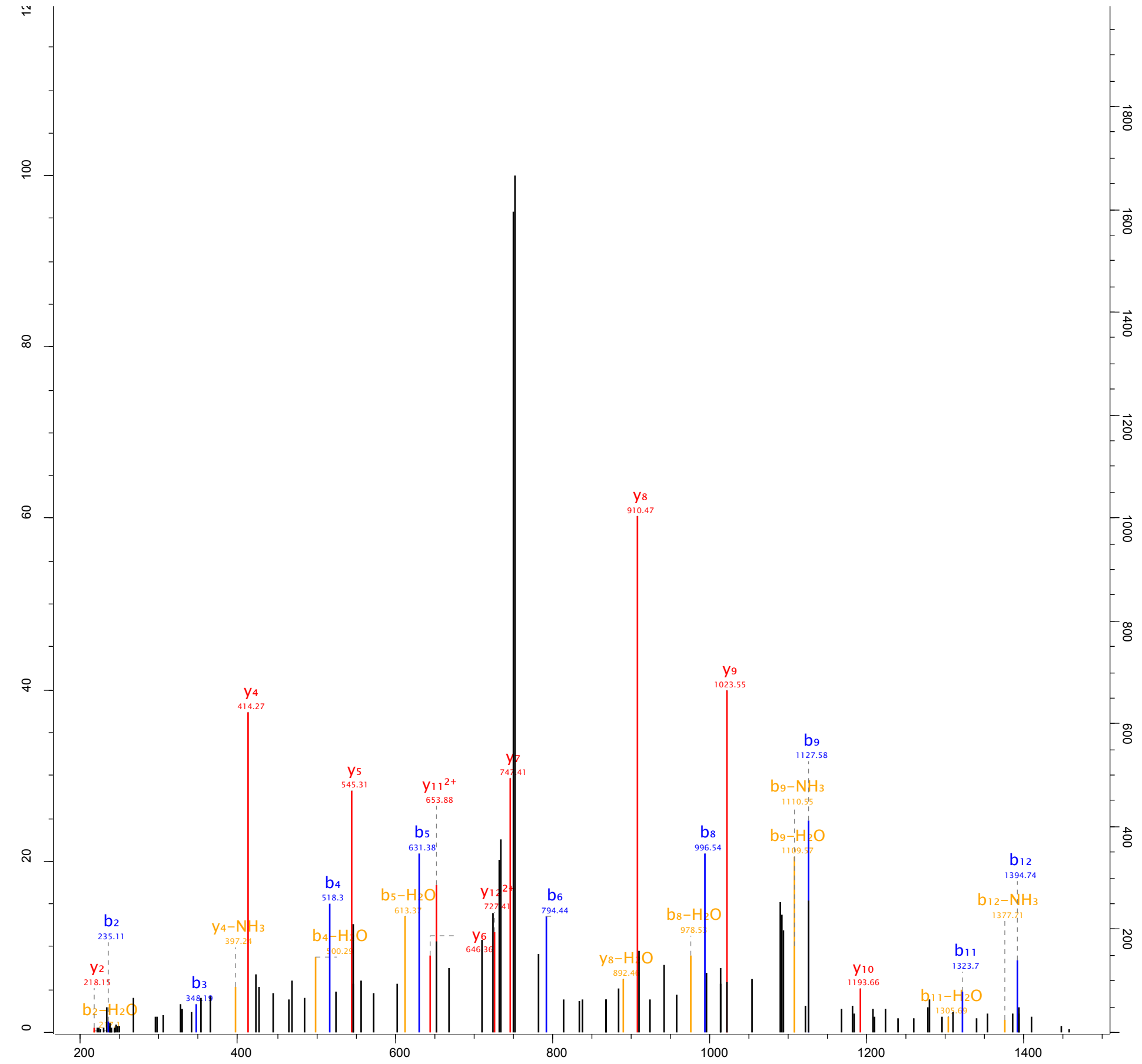


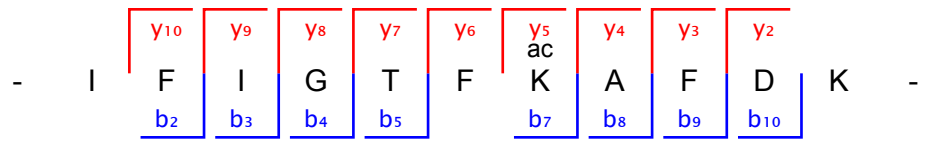
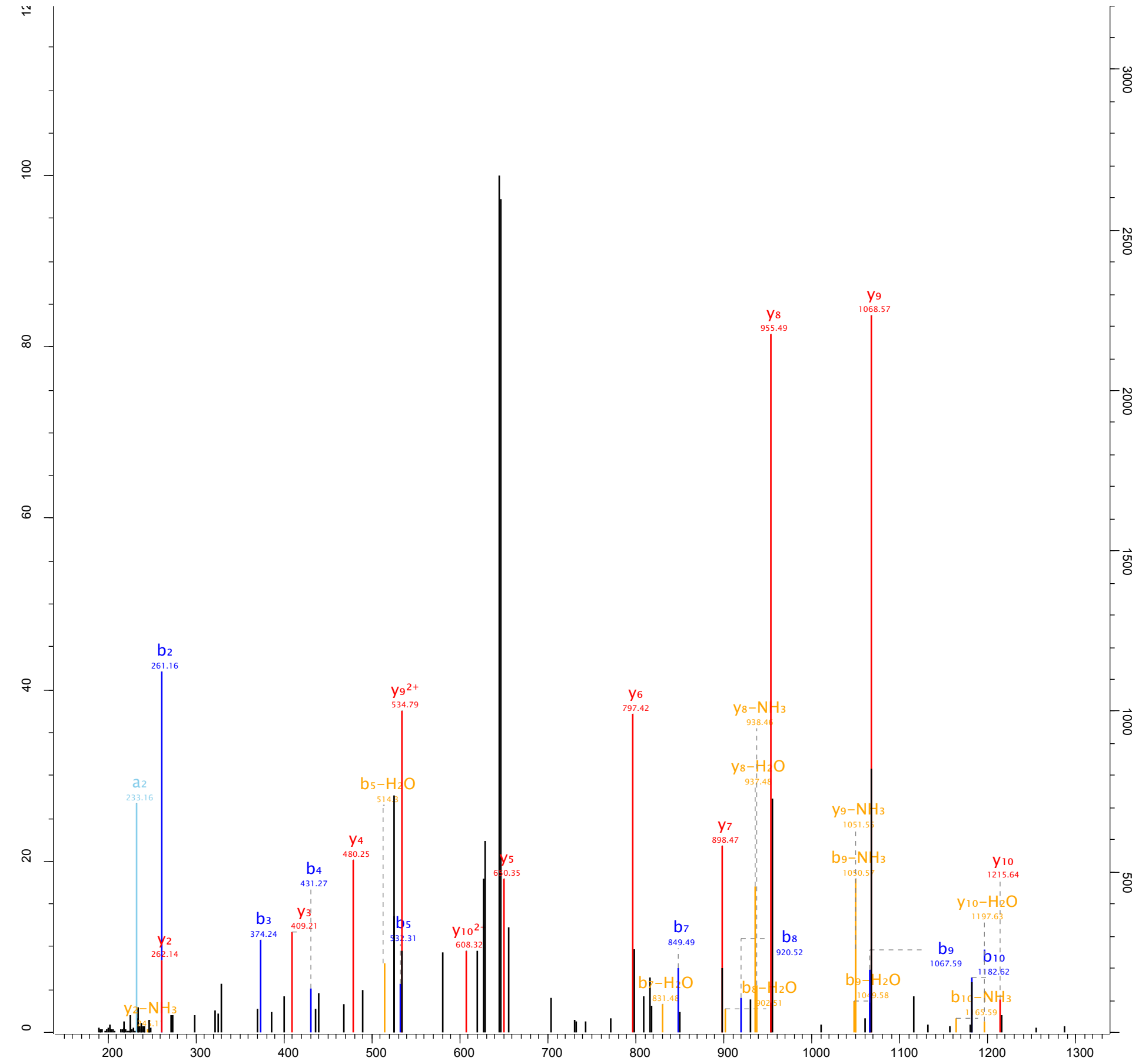






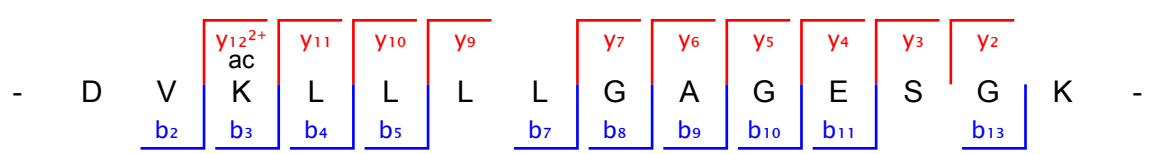
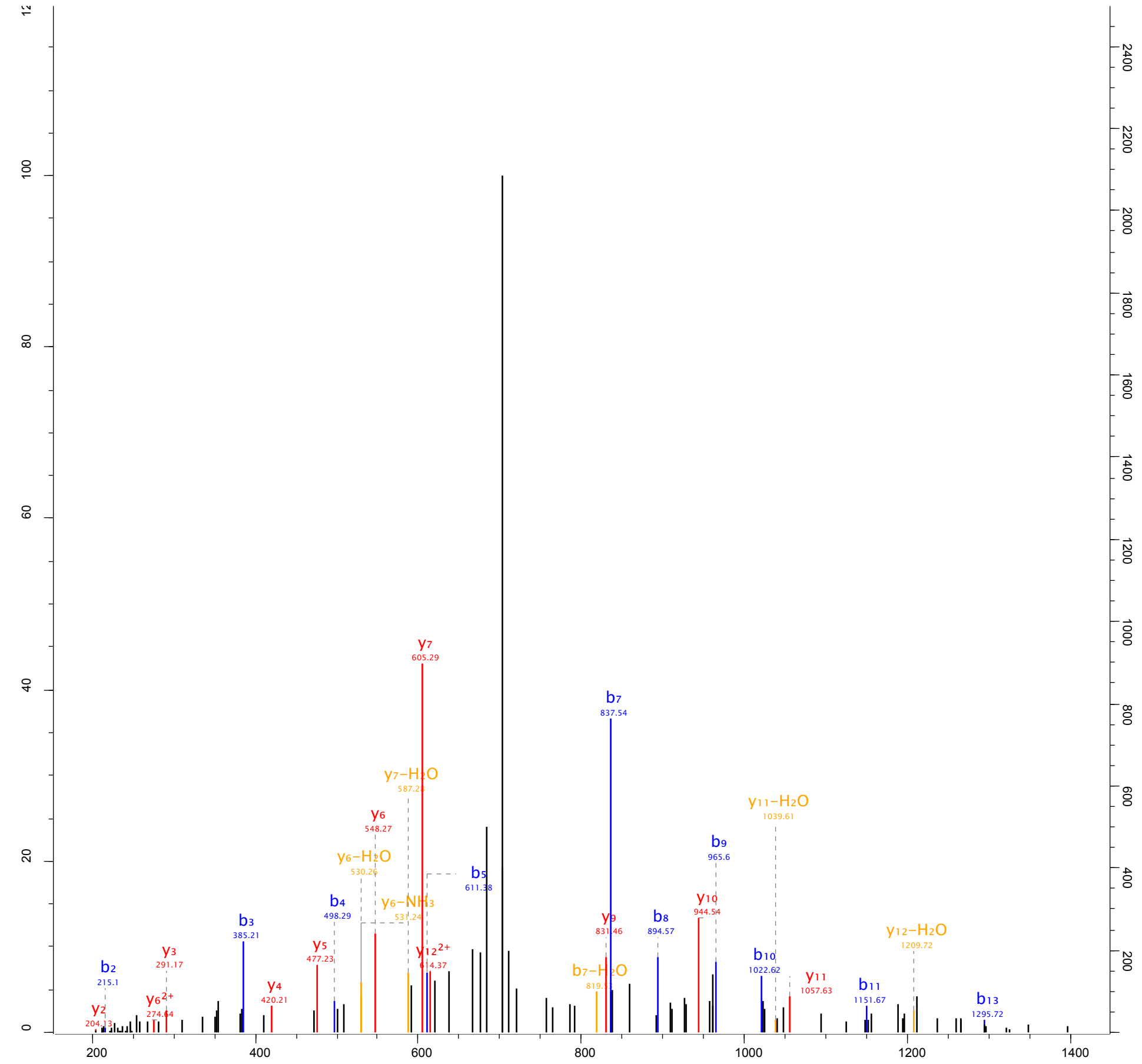


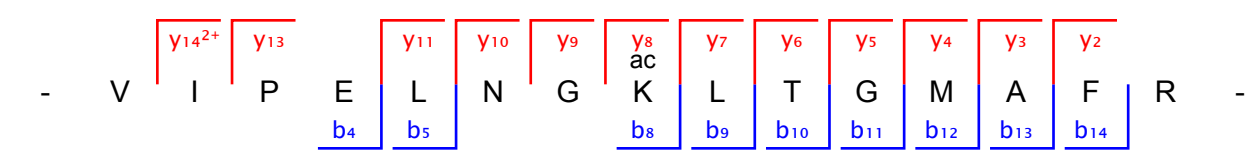
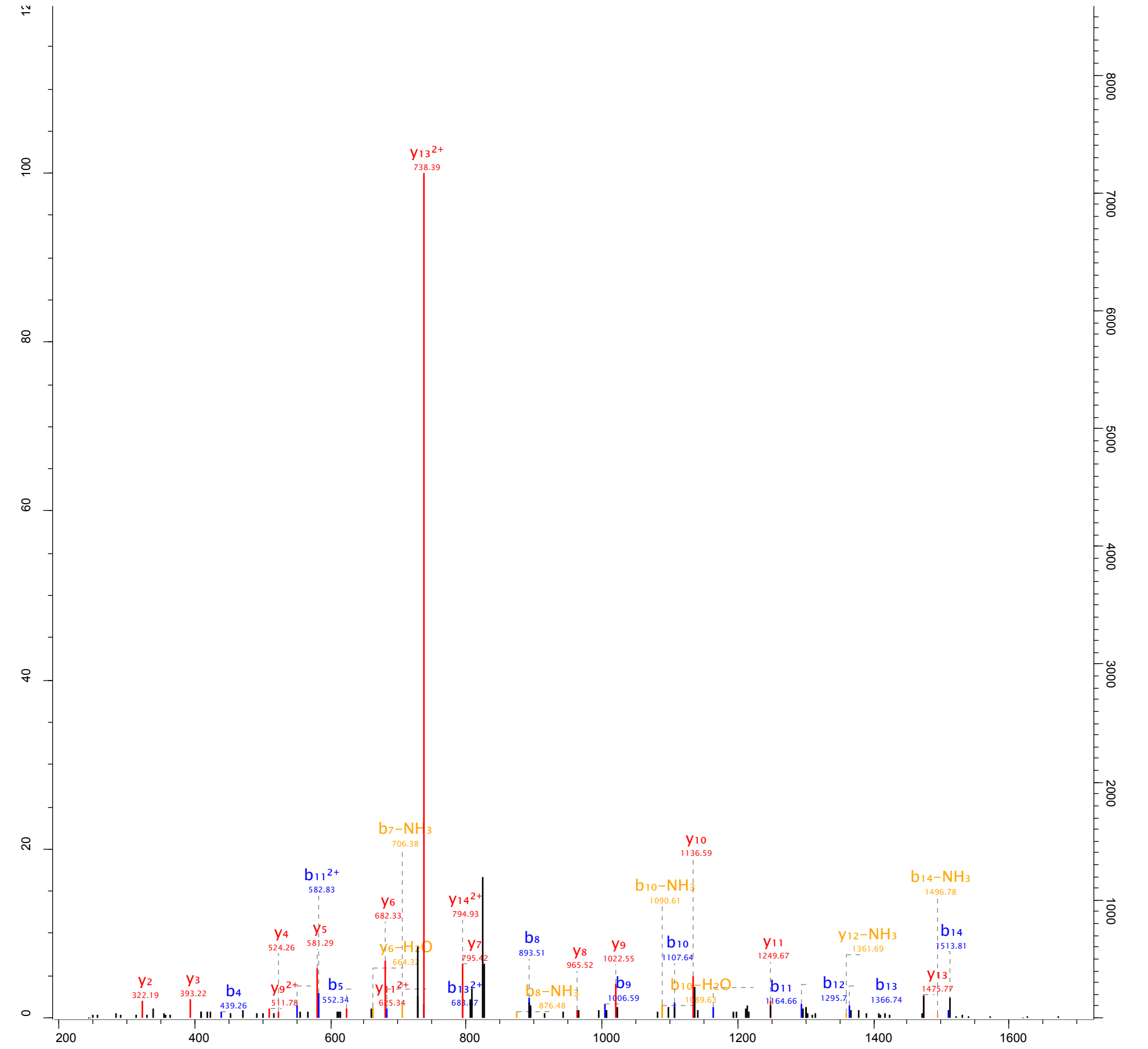


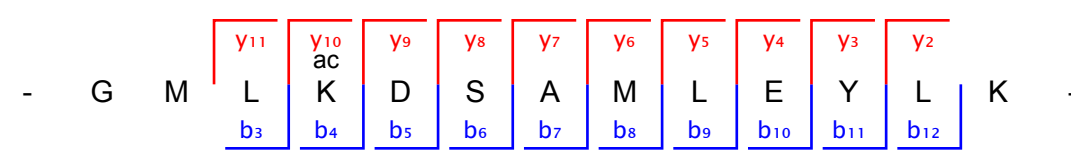
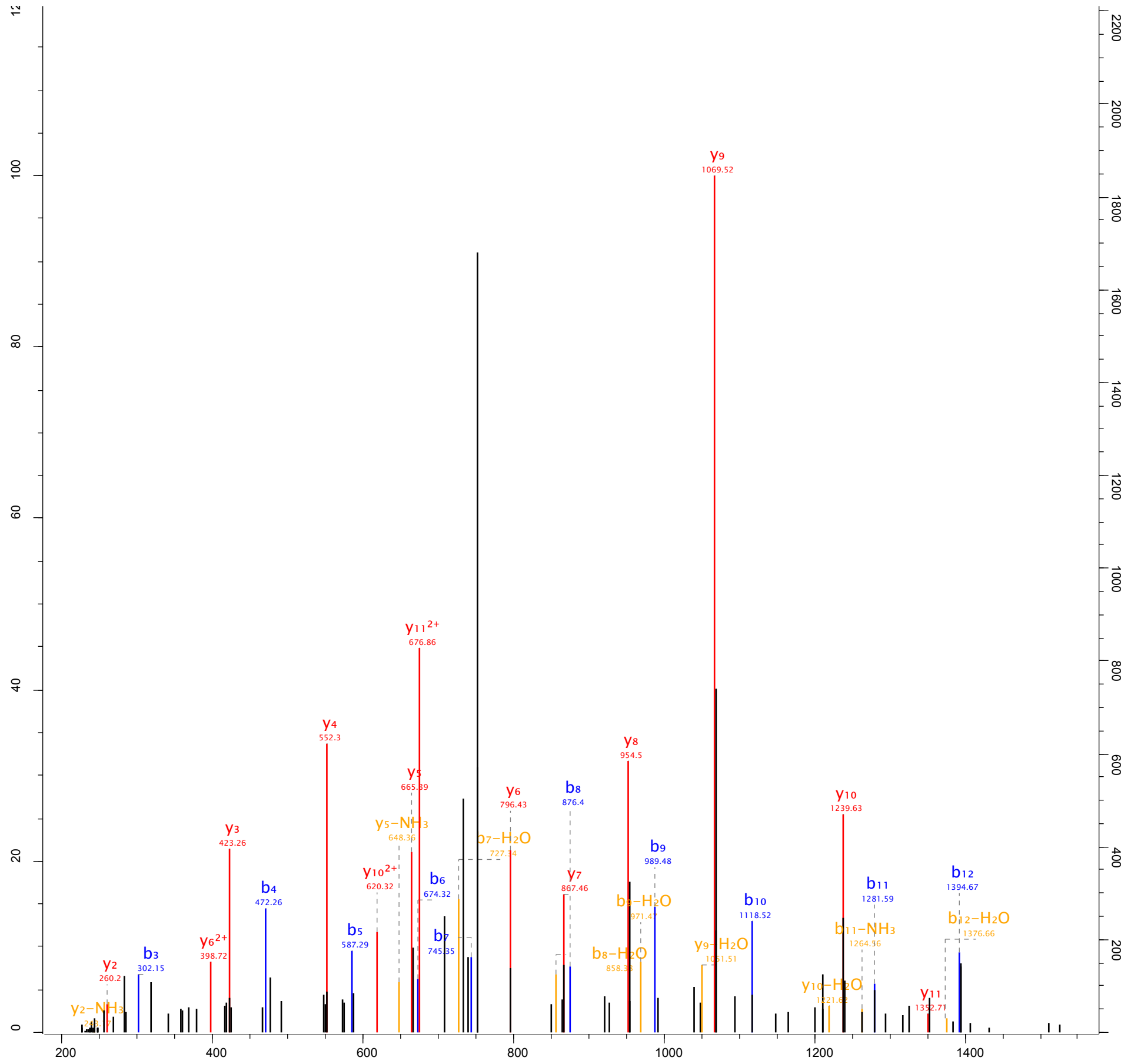


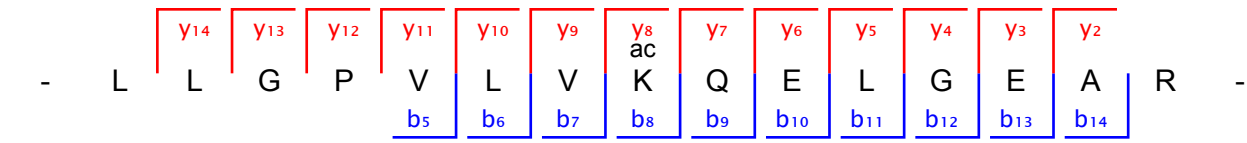
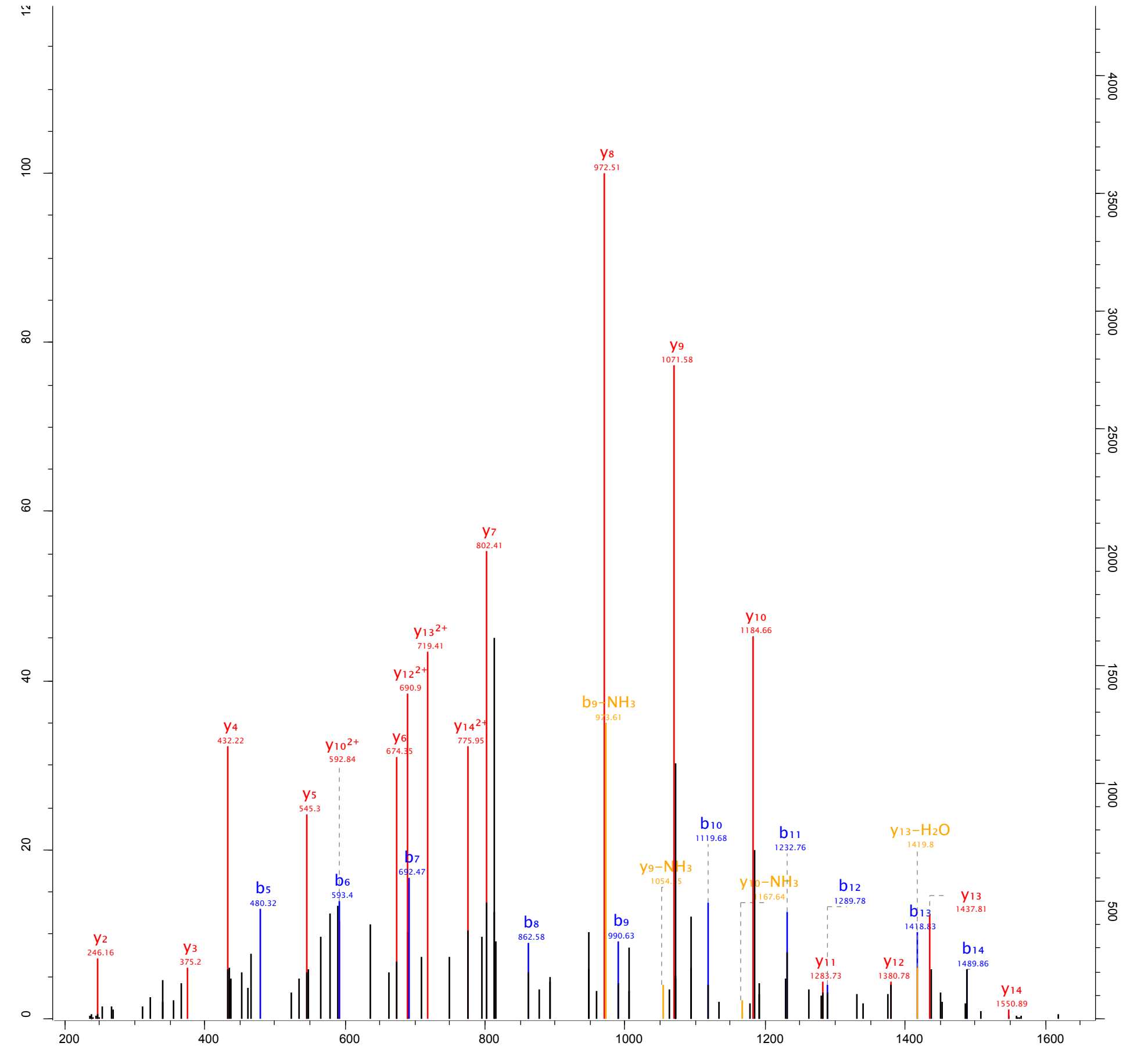
062513_SCW_II_53_4_Vargas_Enriched

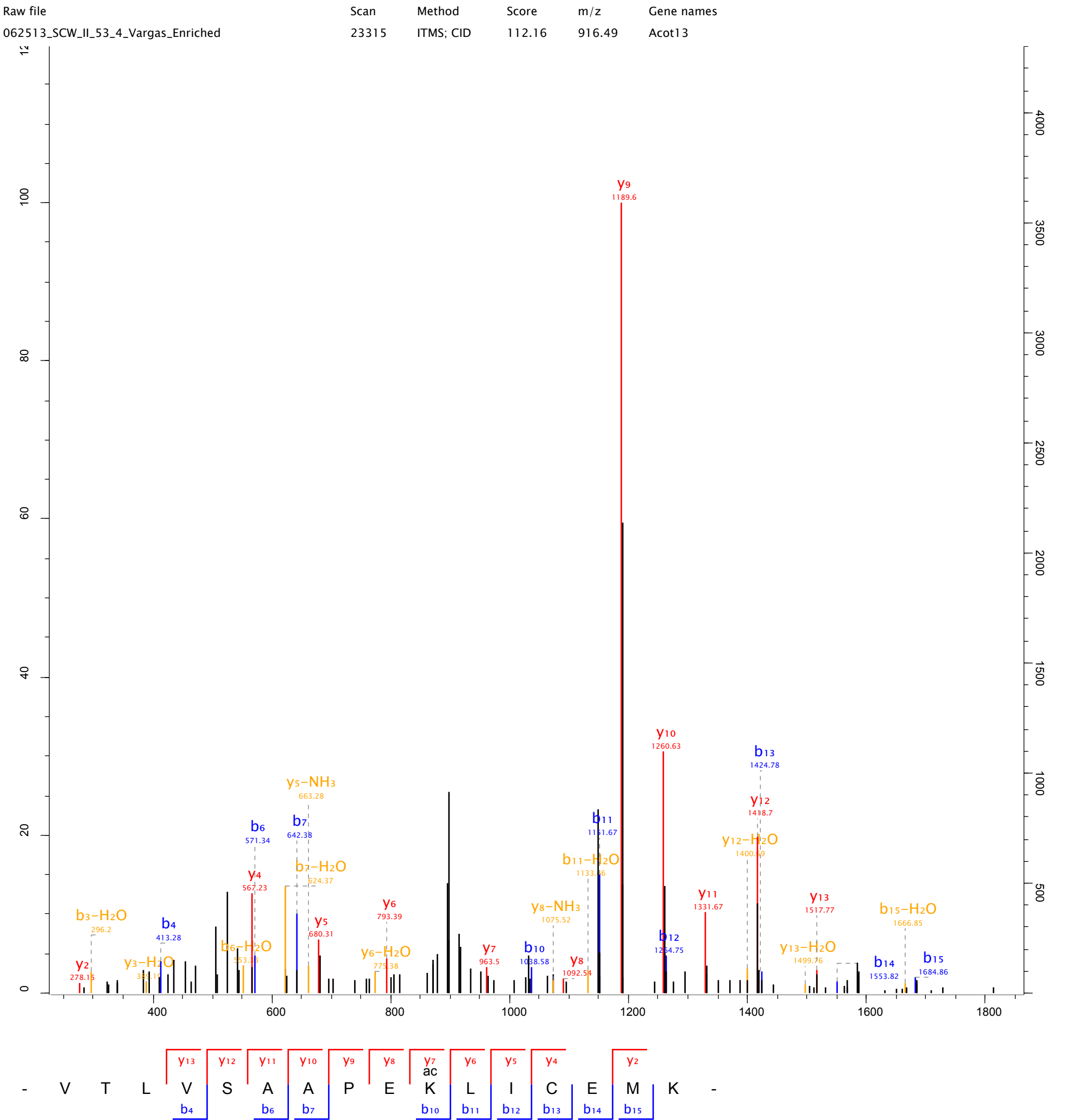
23158 ITMS; CID 95.2 721.42 Gnao1

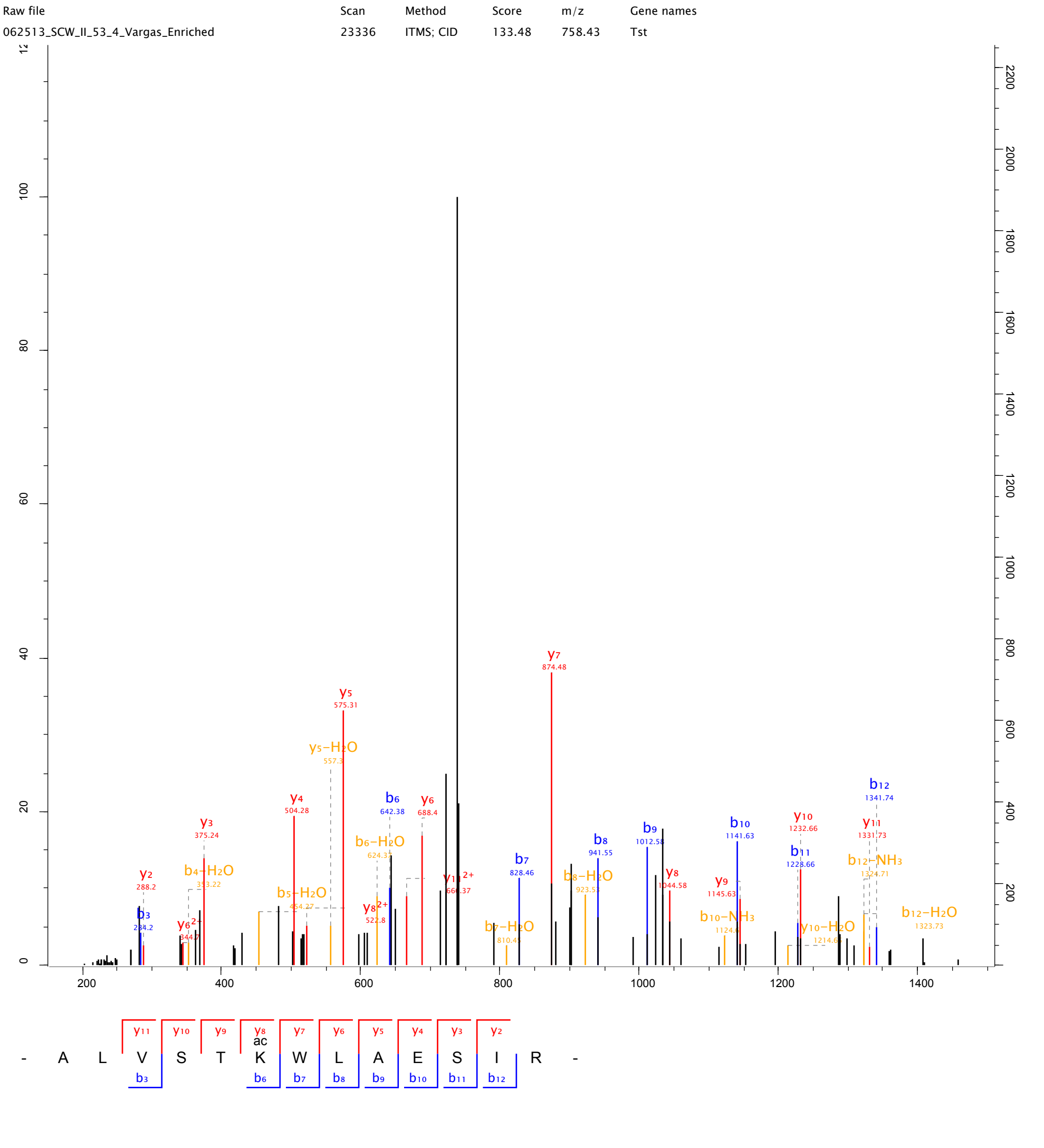


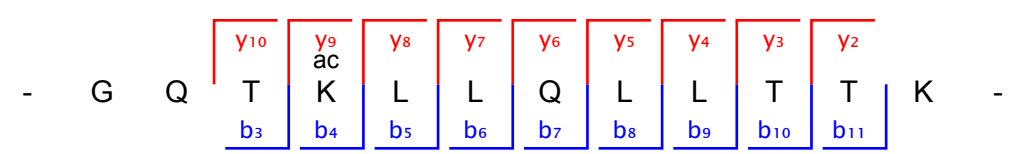
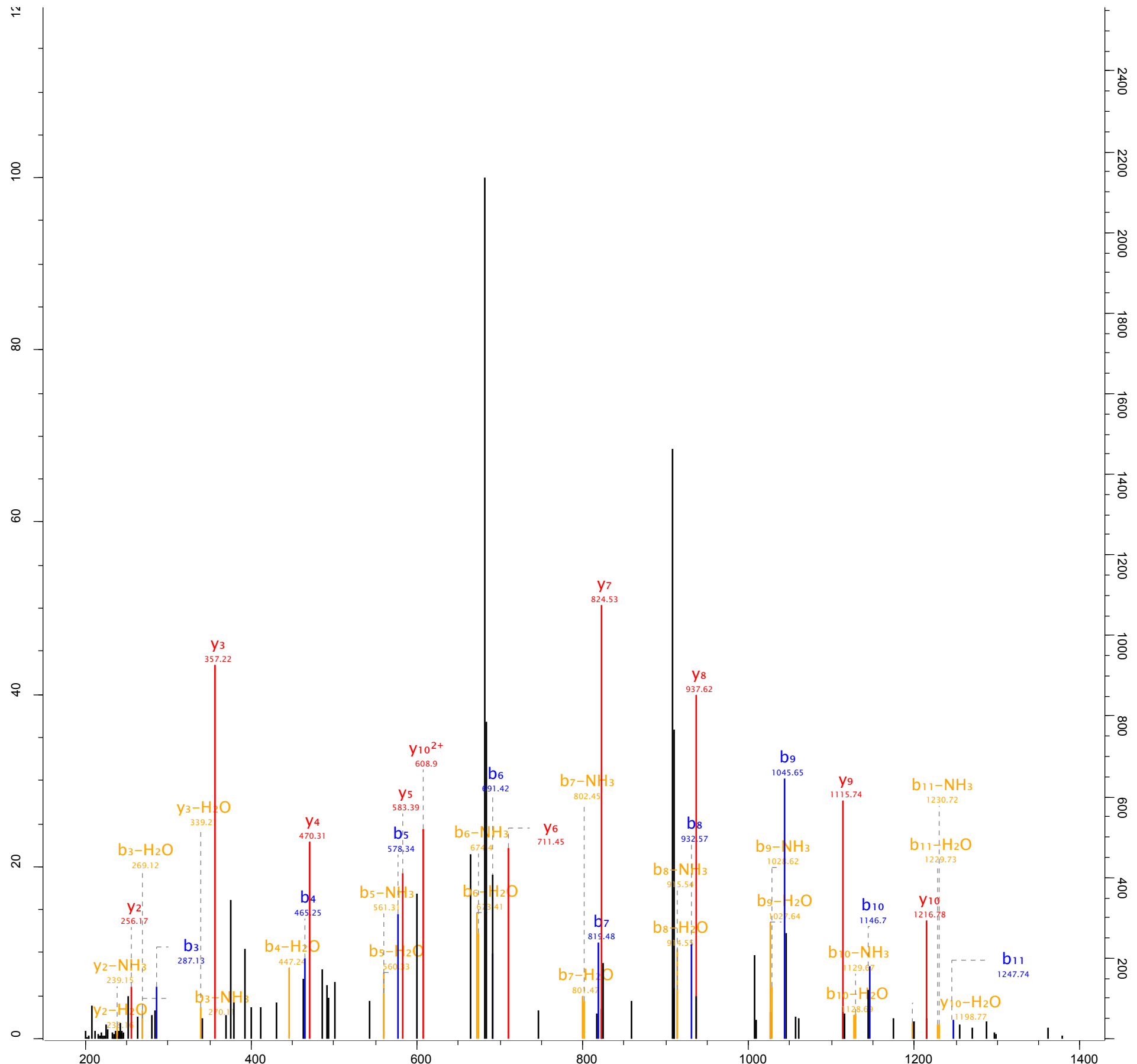


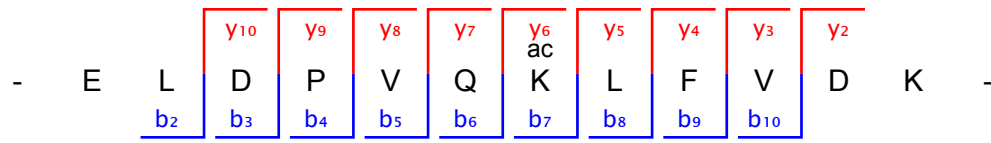
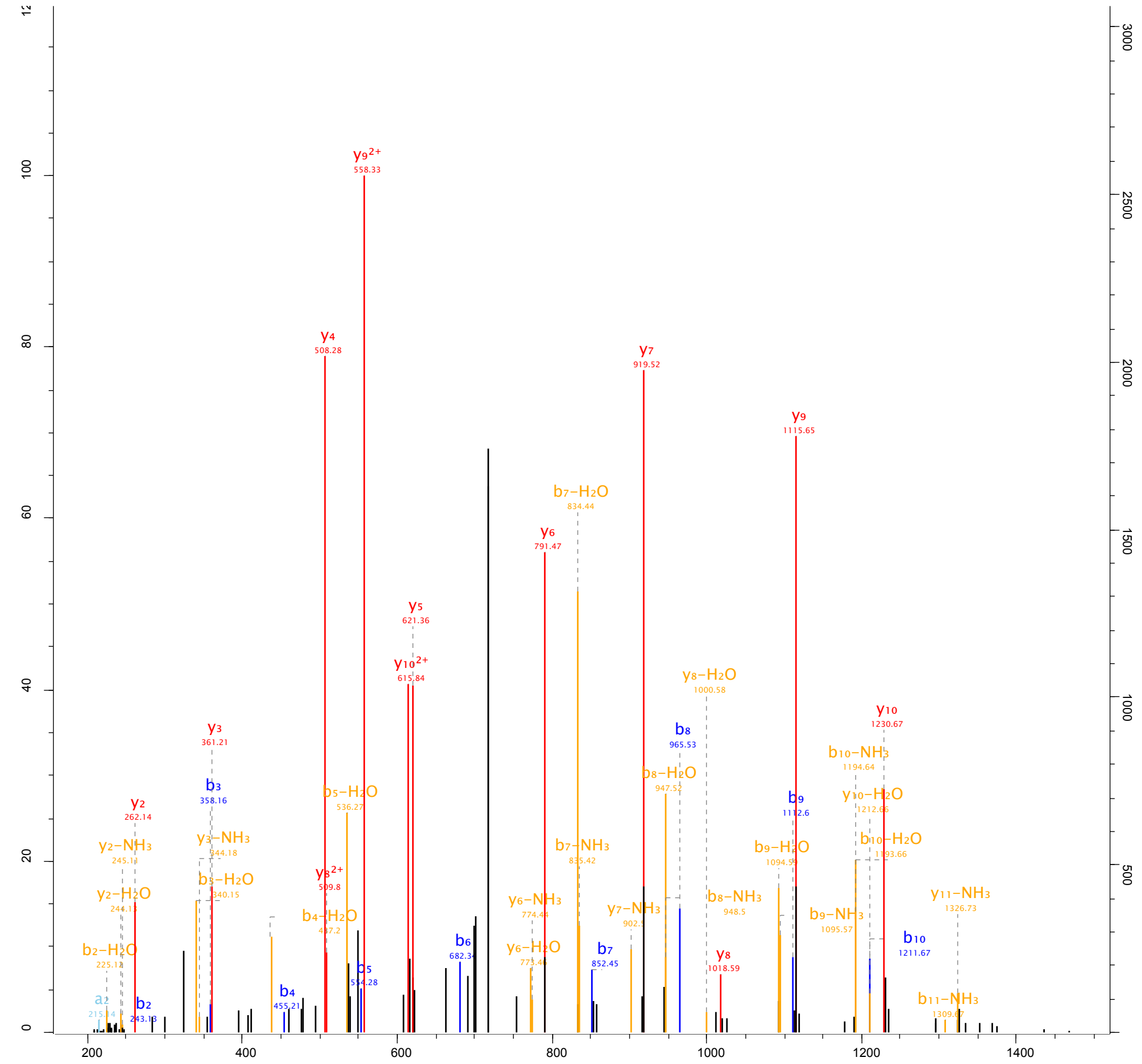


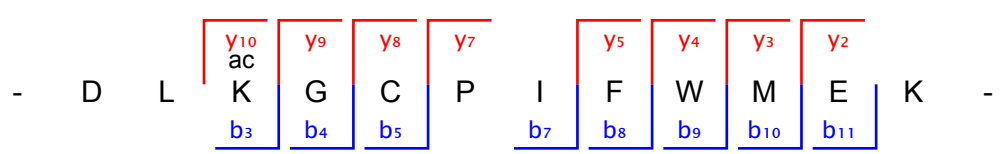
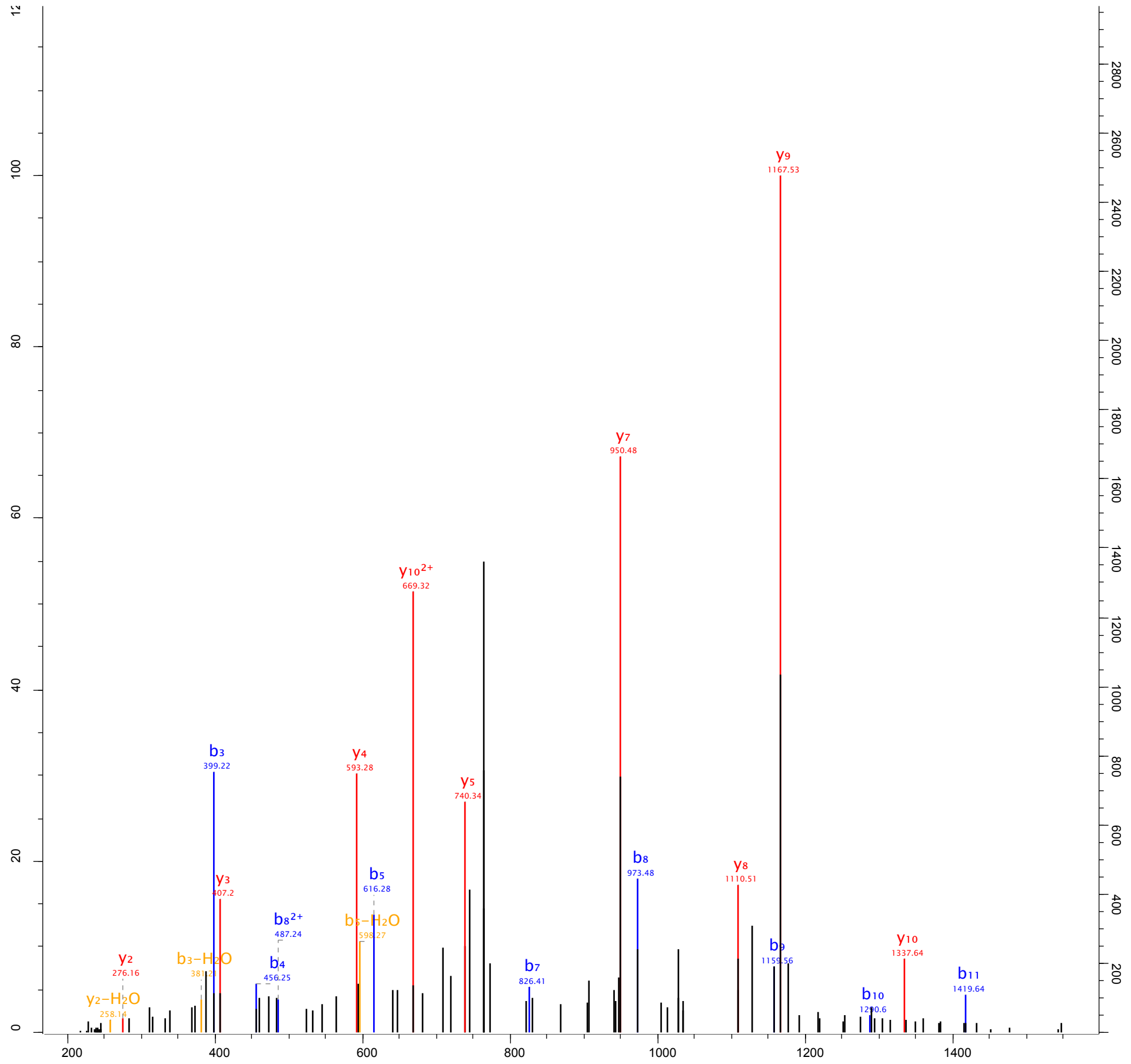


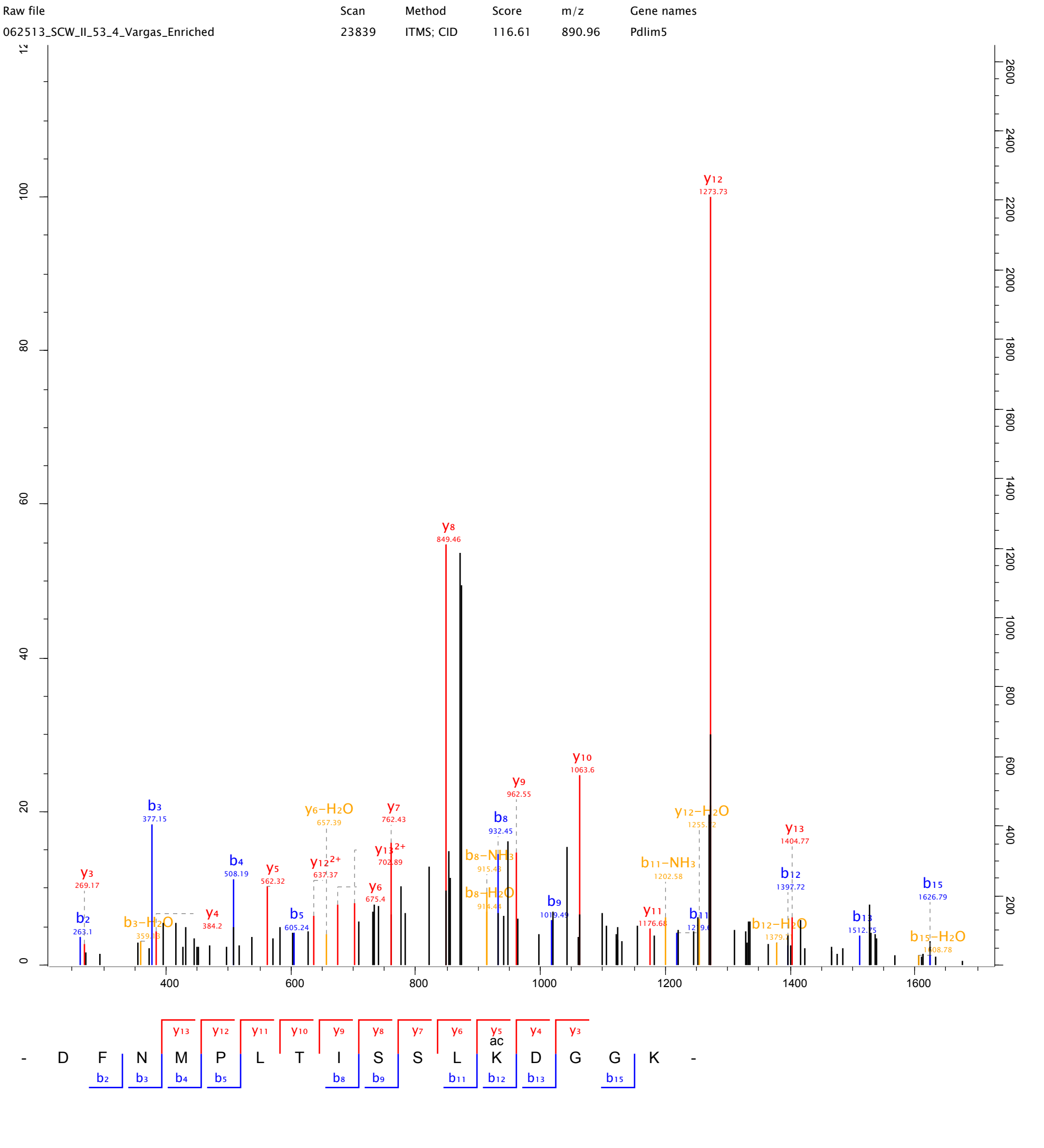


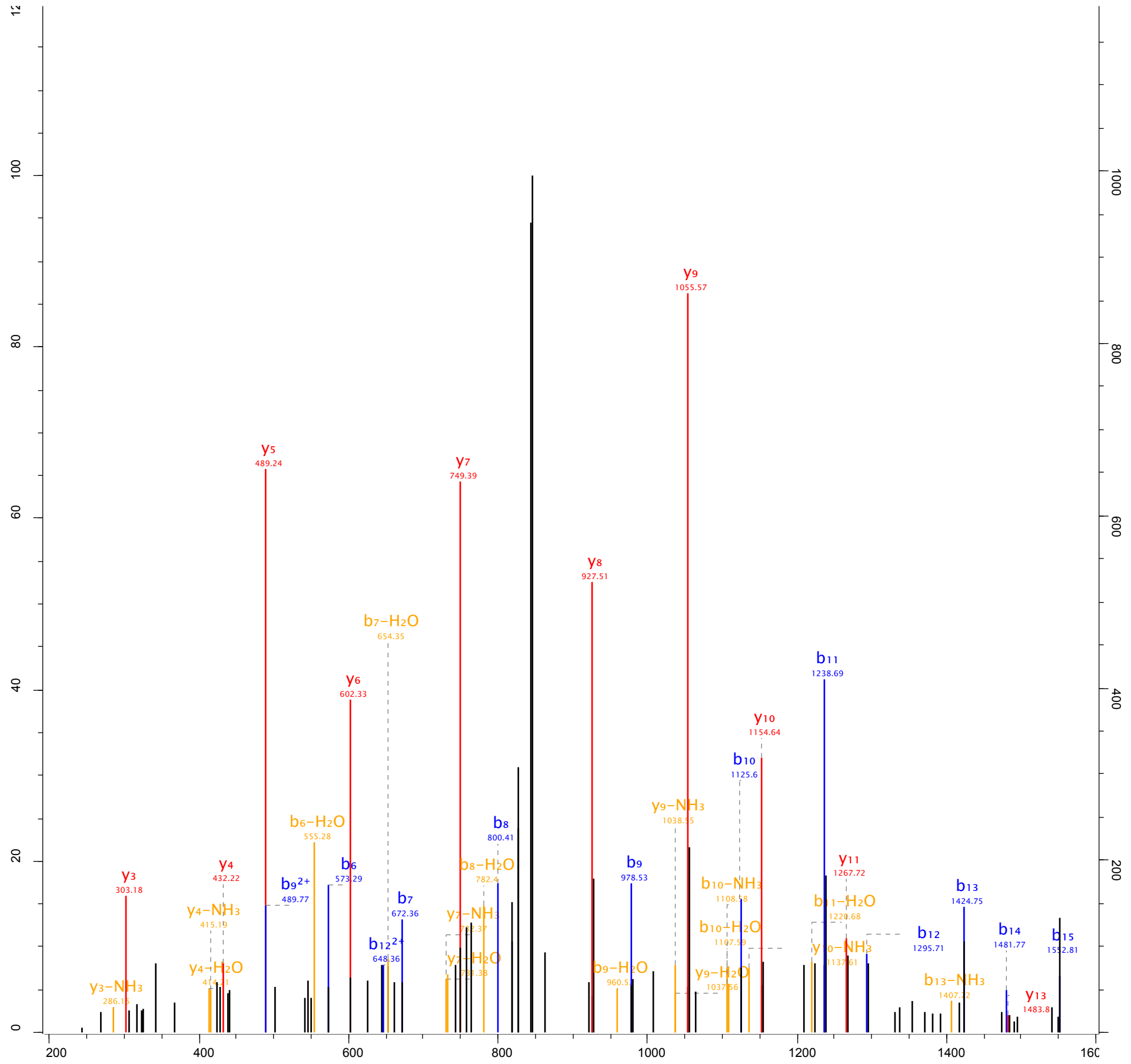








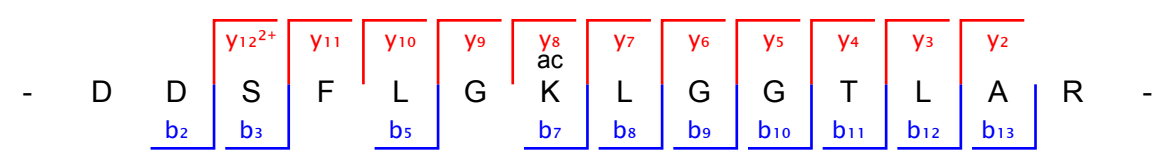
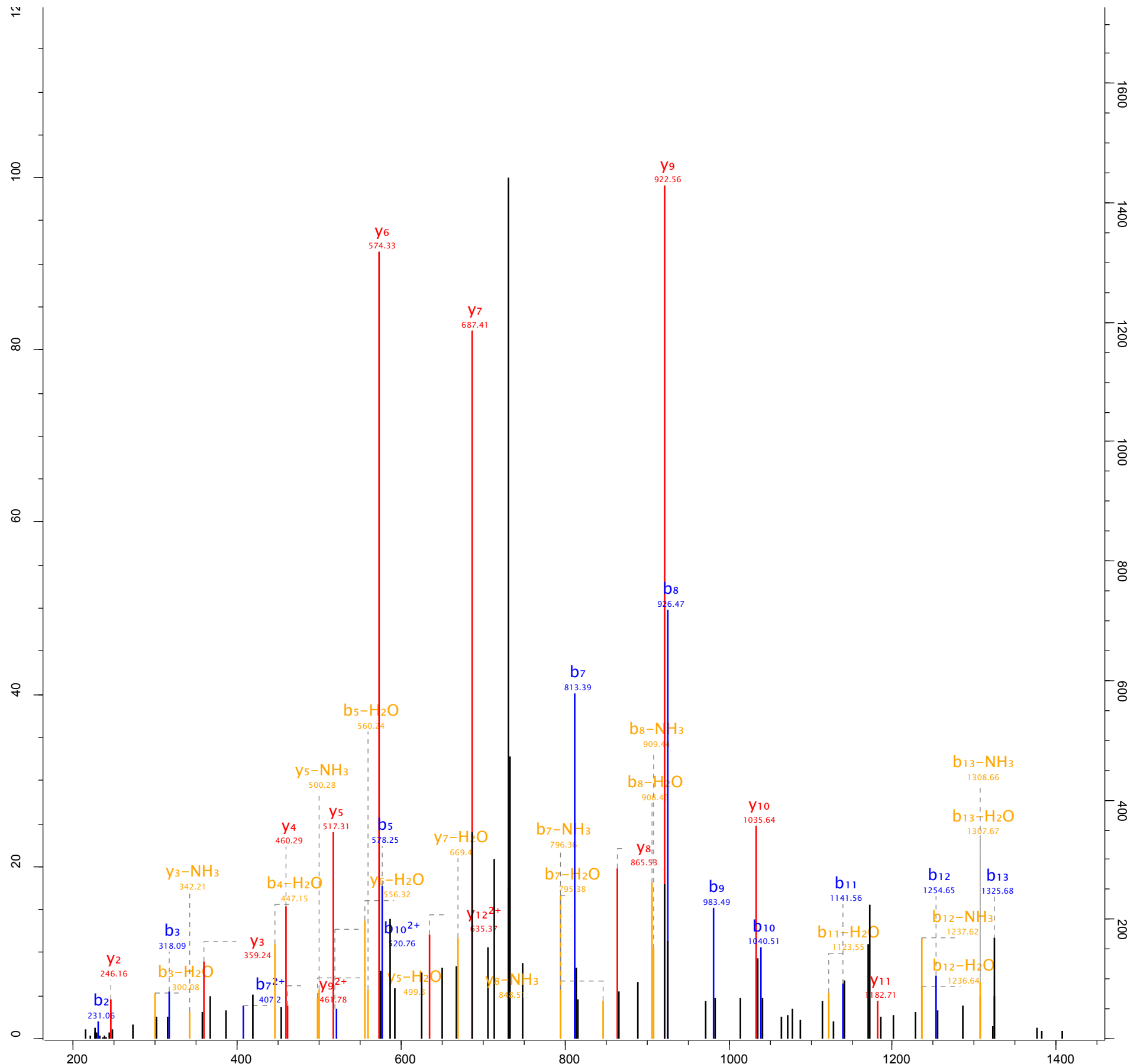


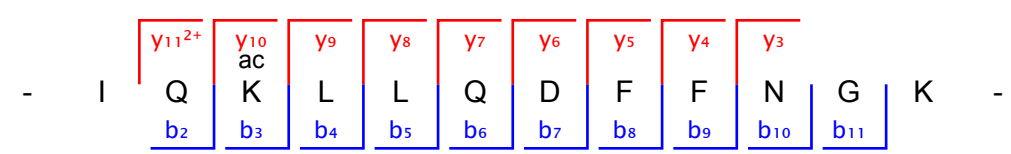
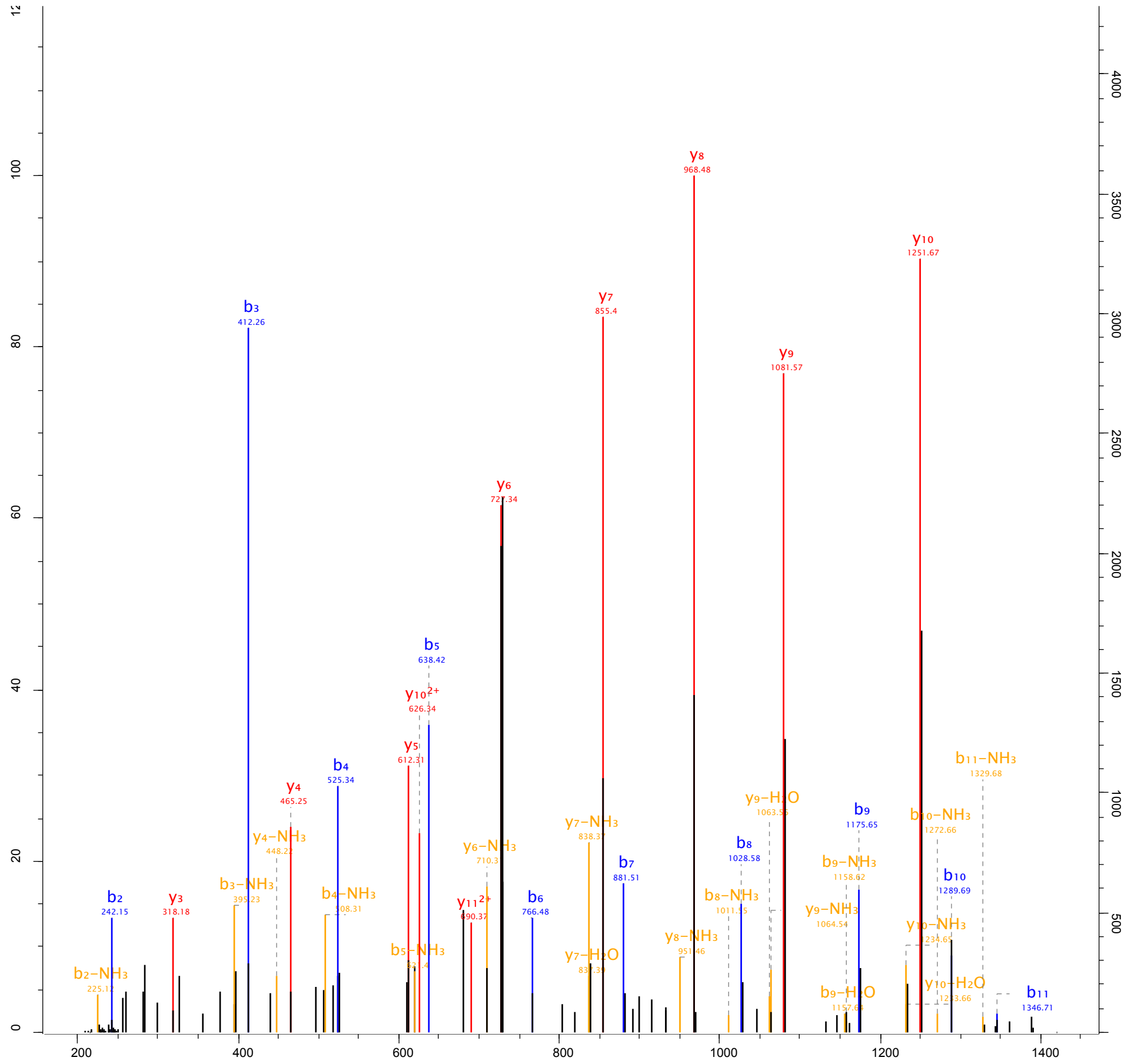


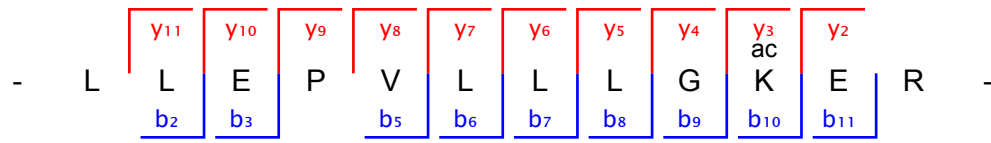
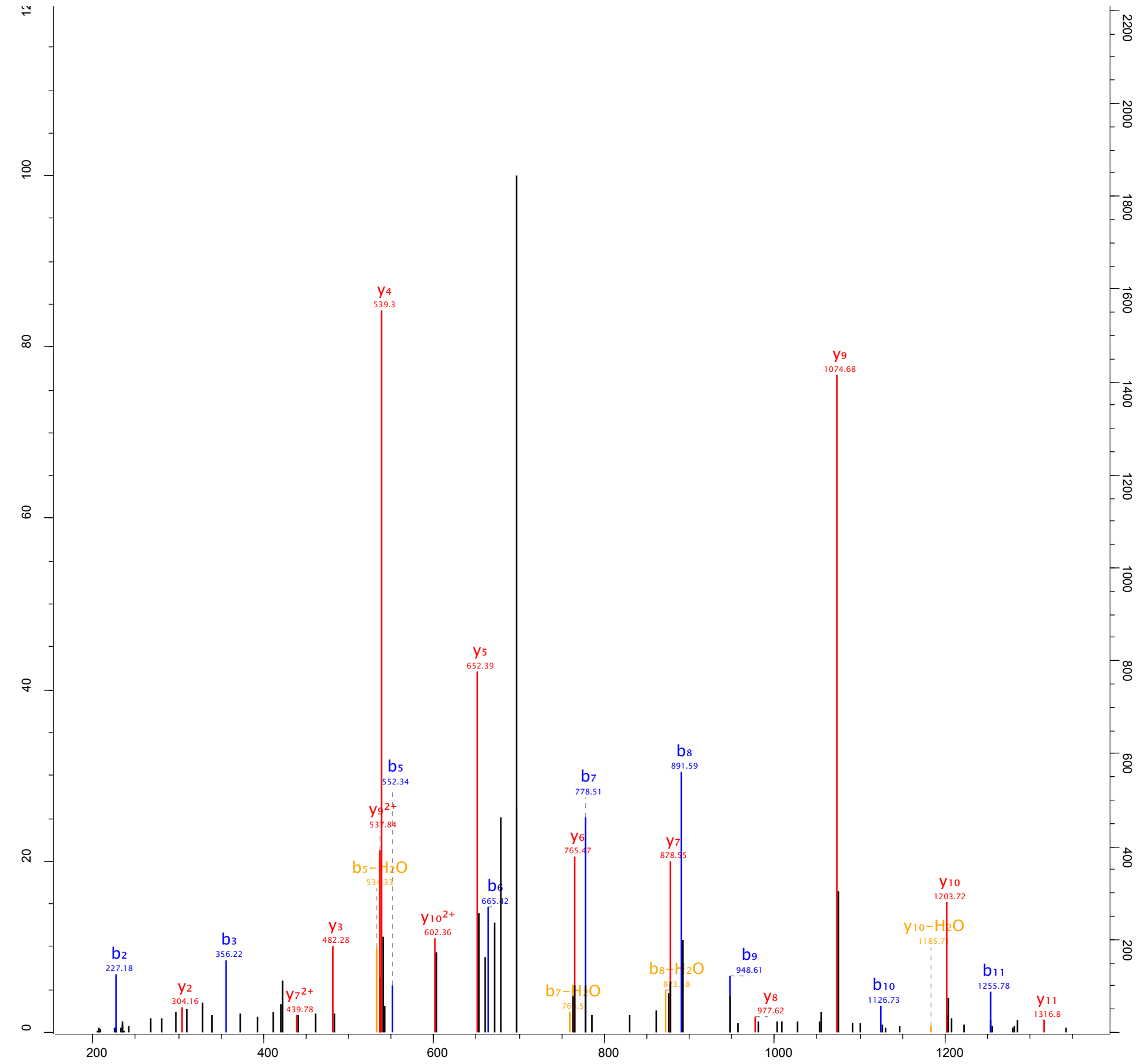
- V S G S E L V Q K F I G E G A R -

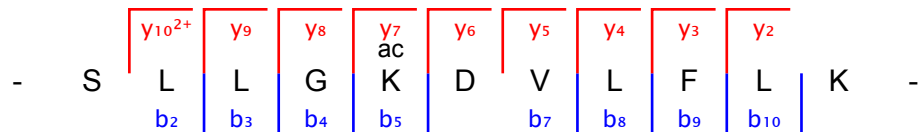
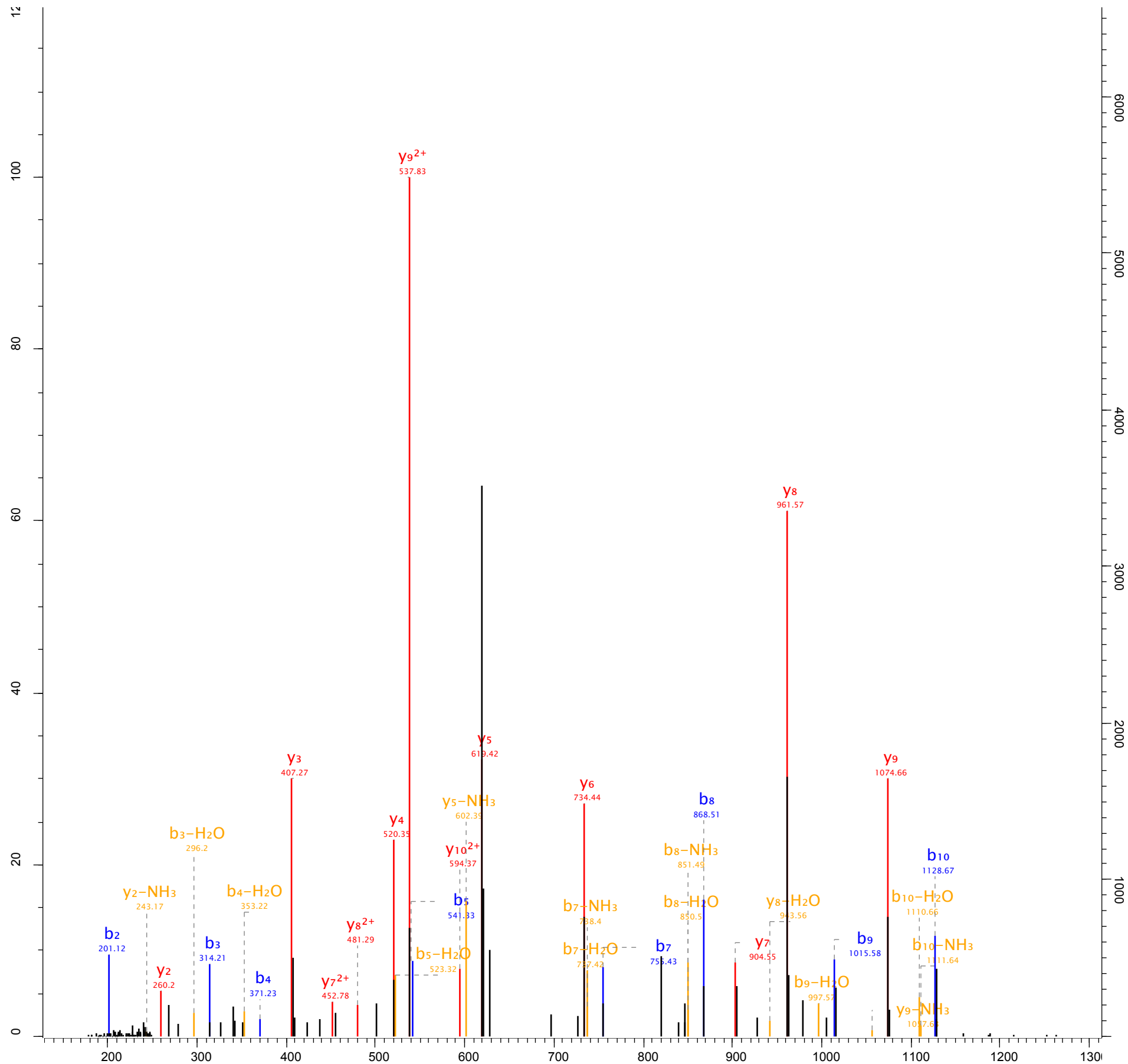
y13
y11
y10
y9
y8 ac
y7
y6
y5
y4
y3

b6
b7
b8
b9
b10
b11
b12
b13
b14
b15









062513_SCW_II_53_4_Vargas_Enriched

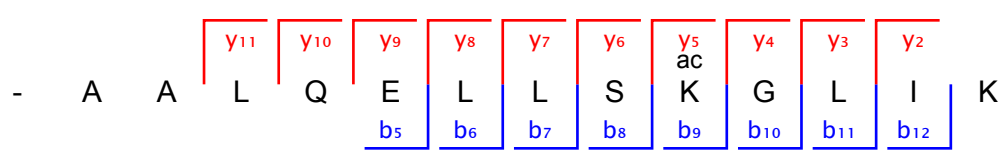
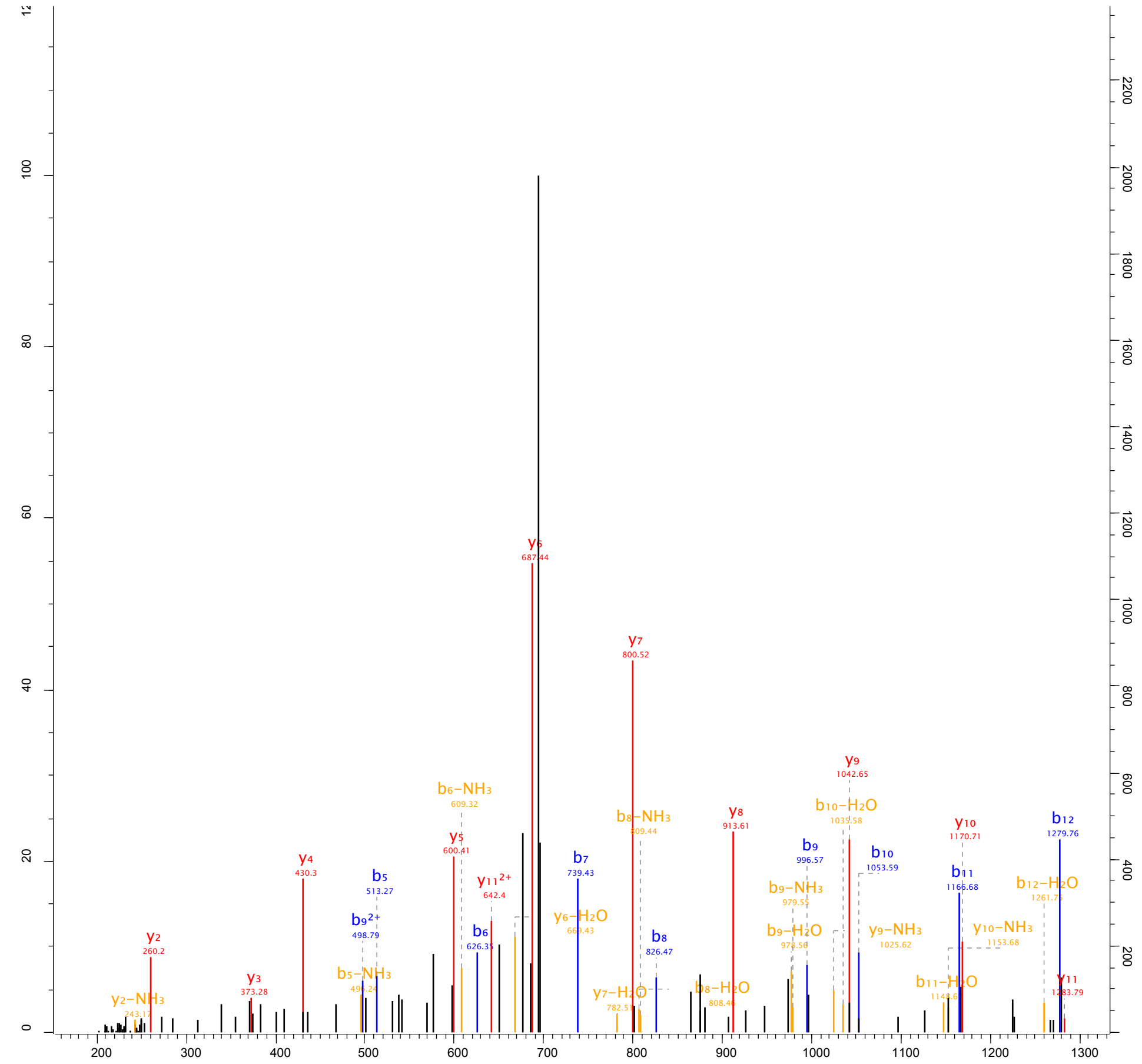
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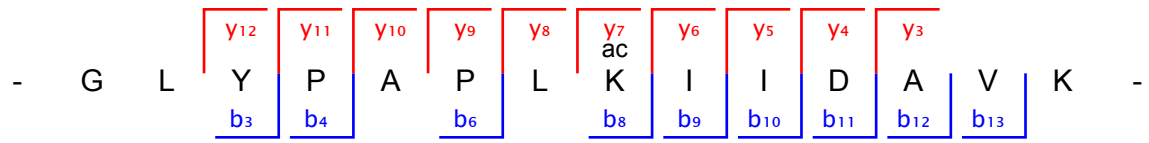
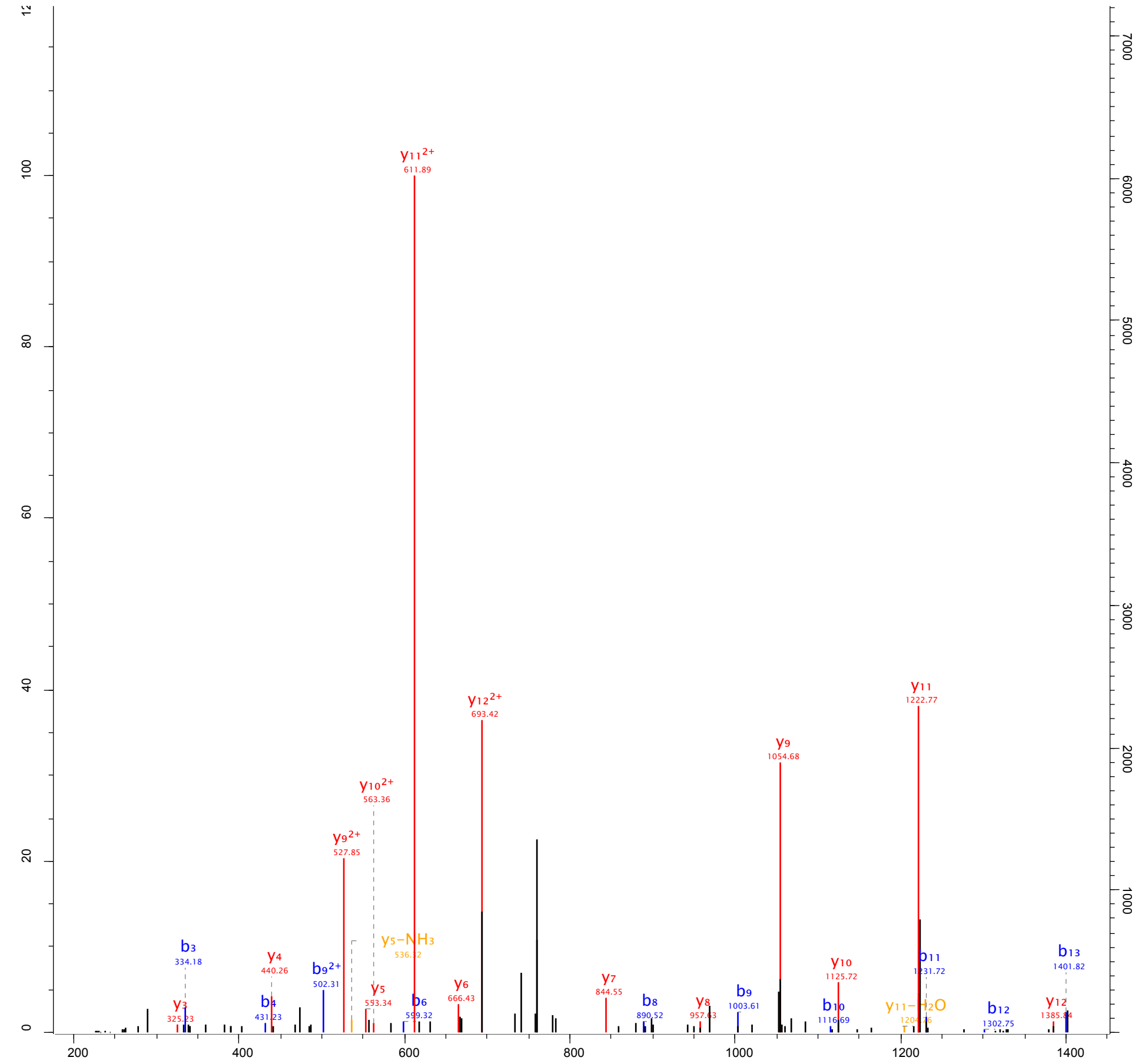
ITMS; CID

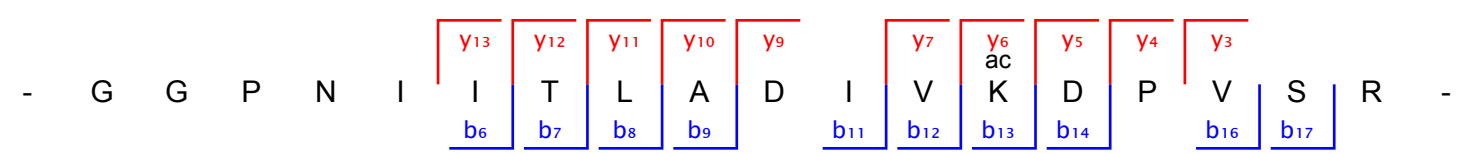
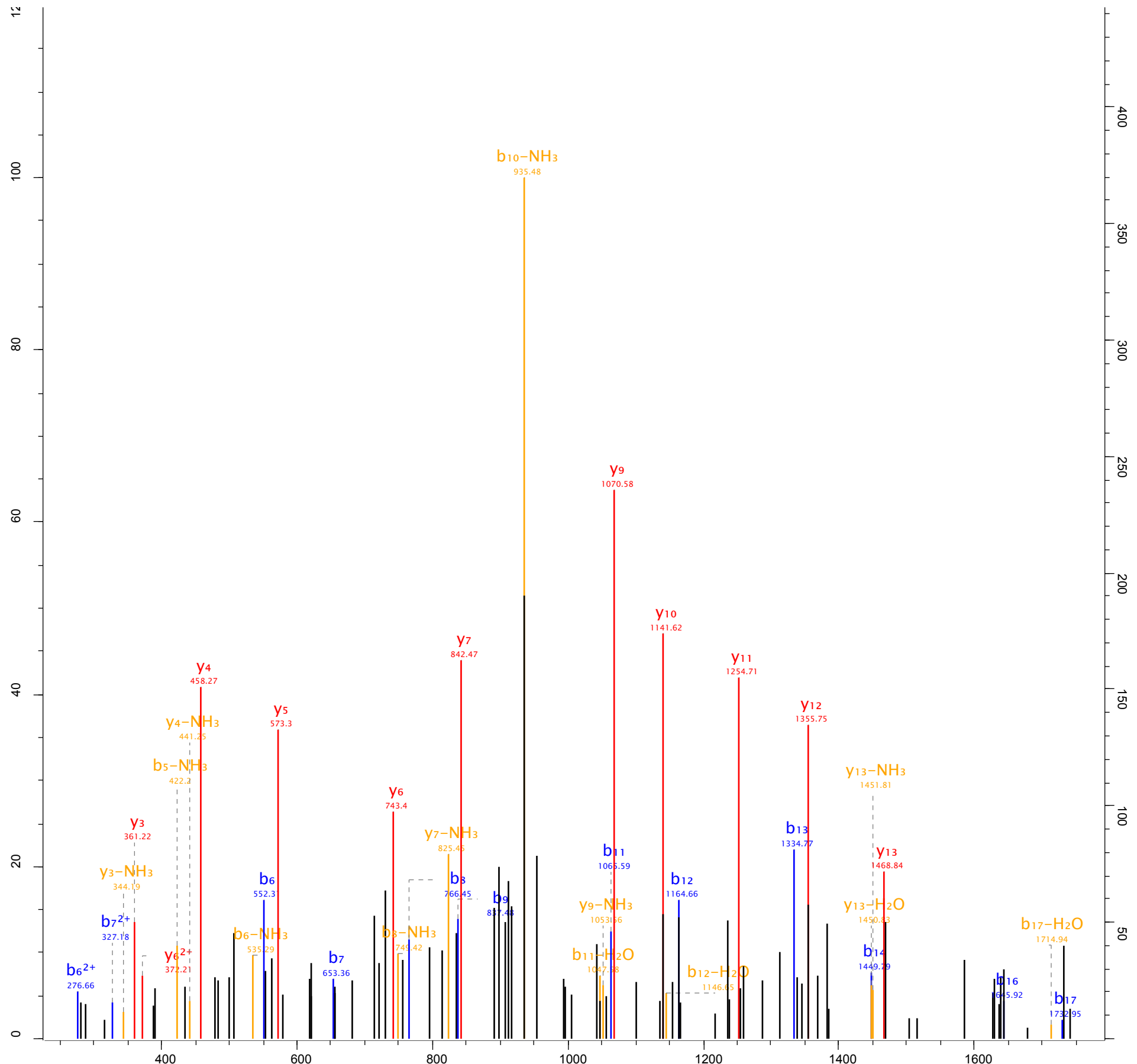
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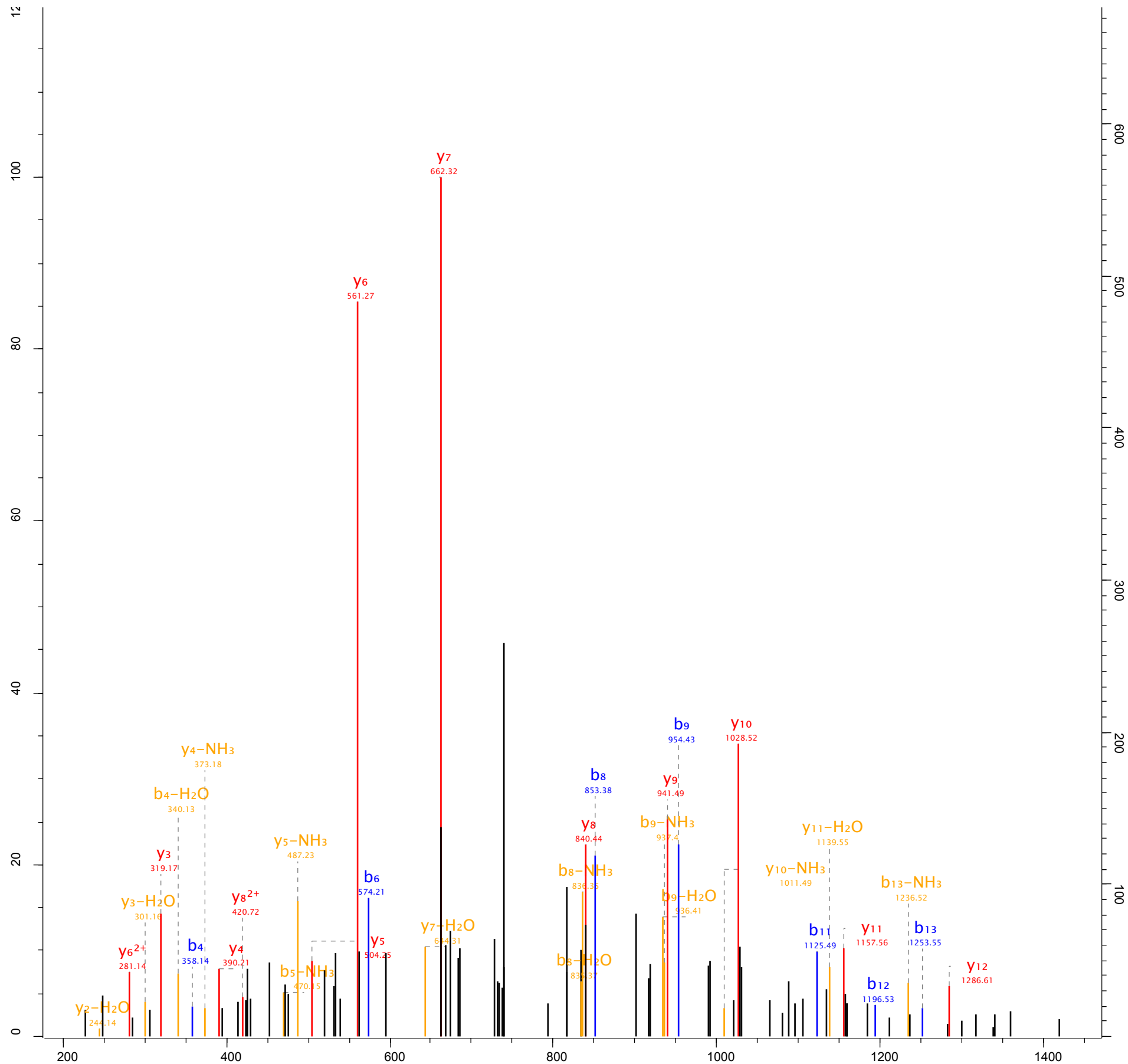
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Rps25



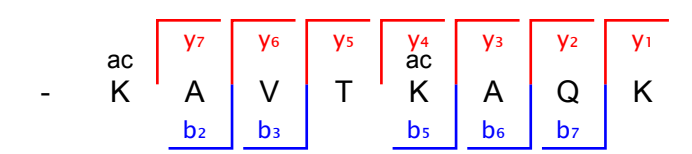
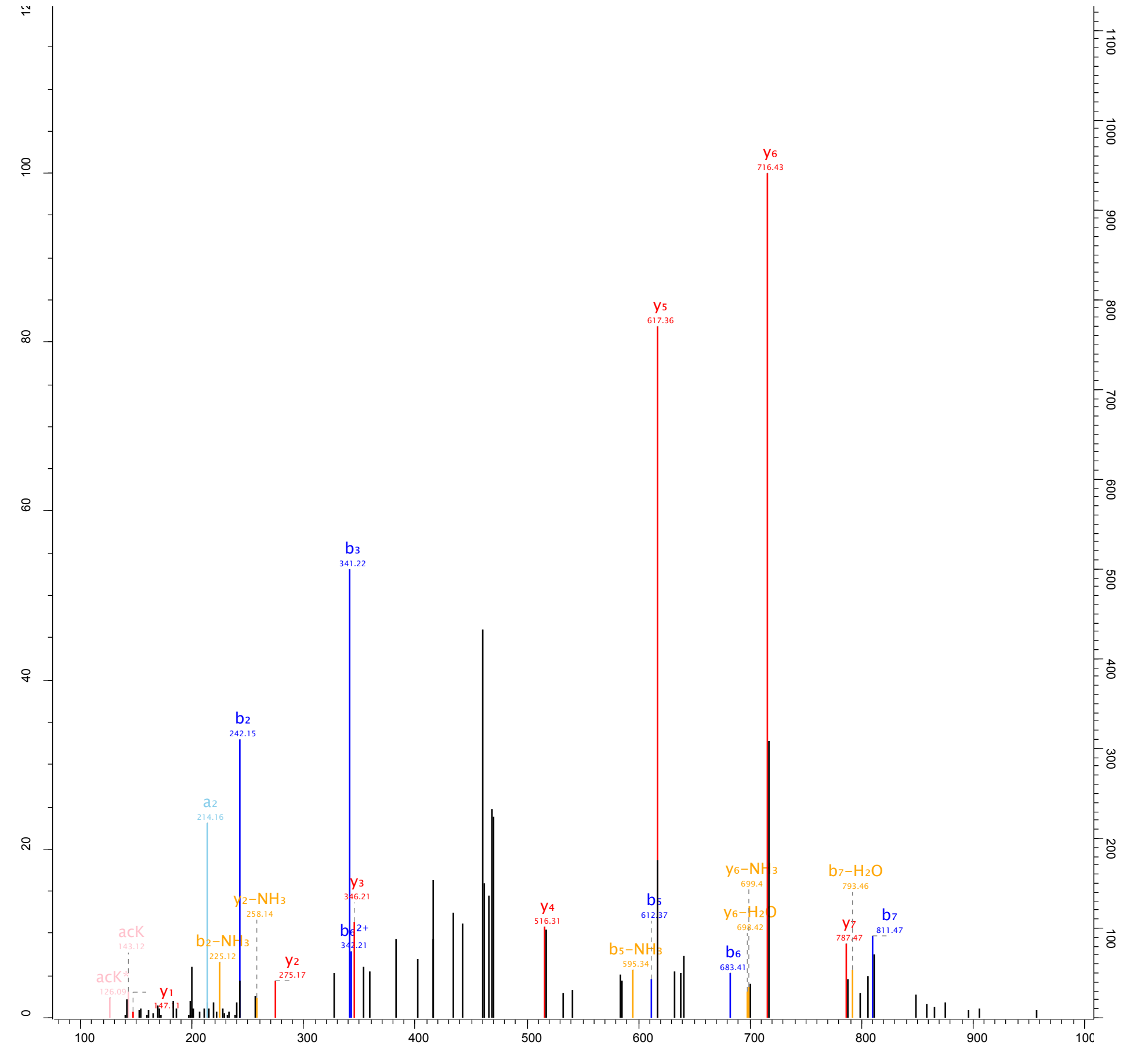


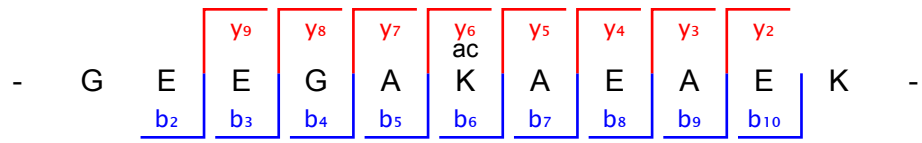
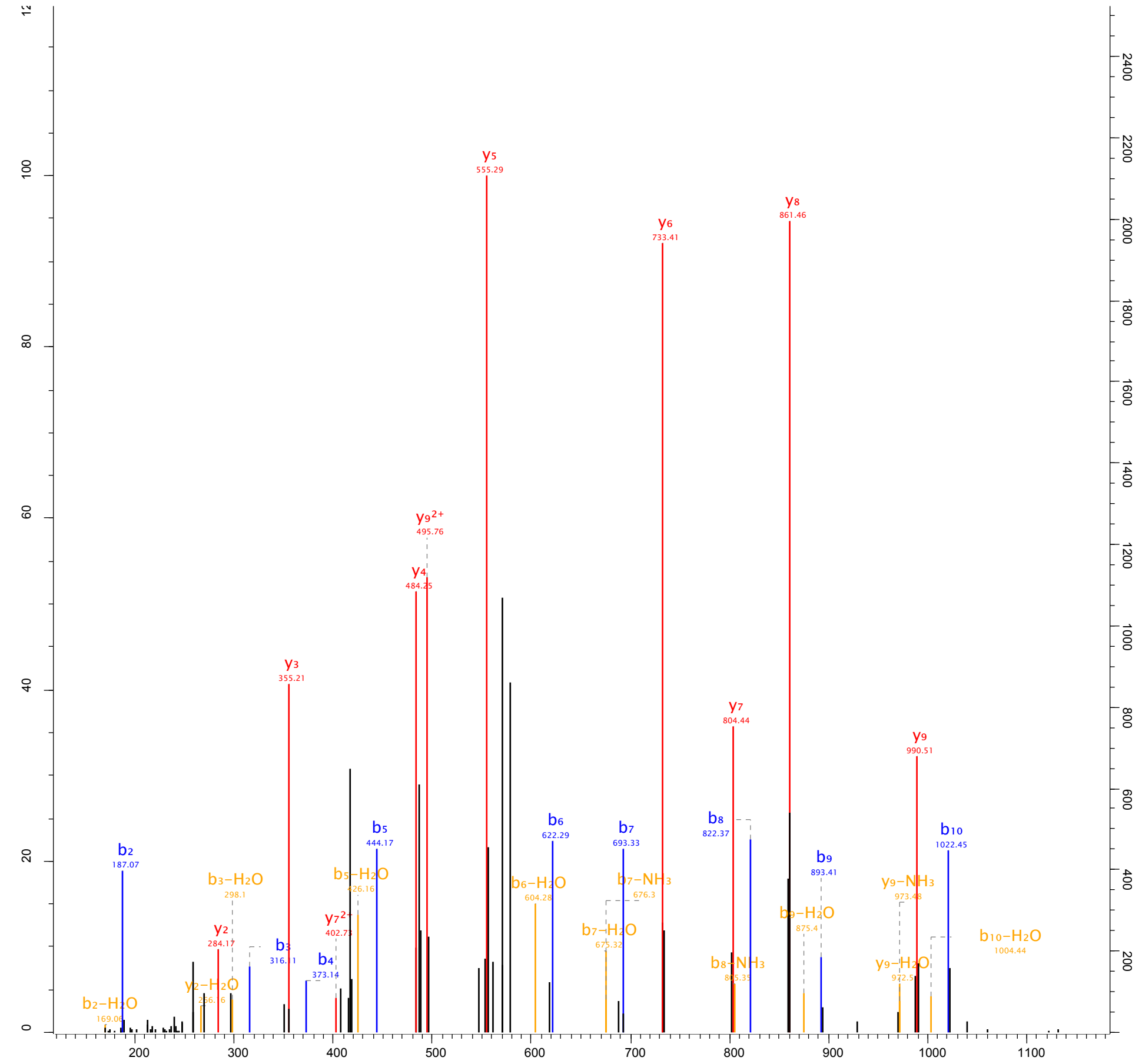


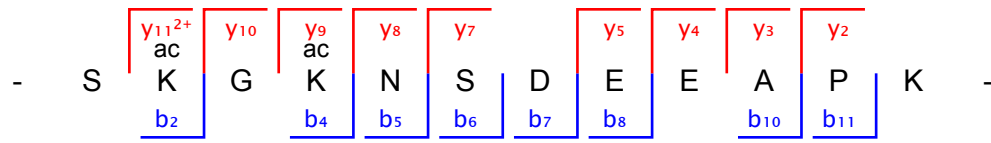
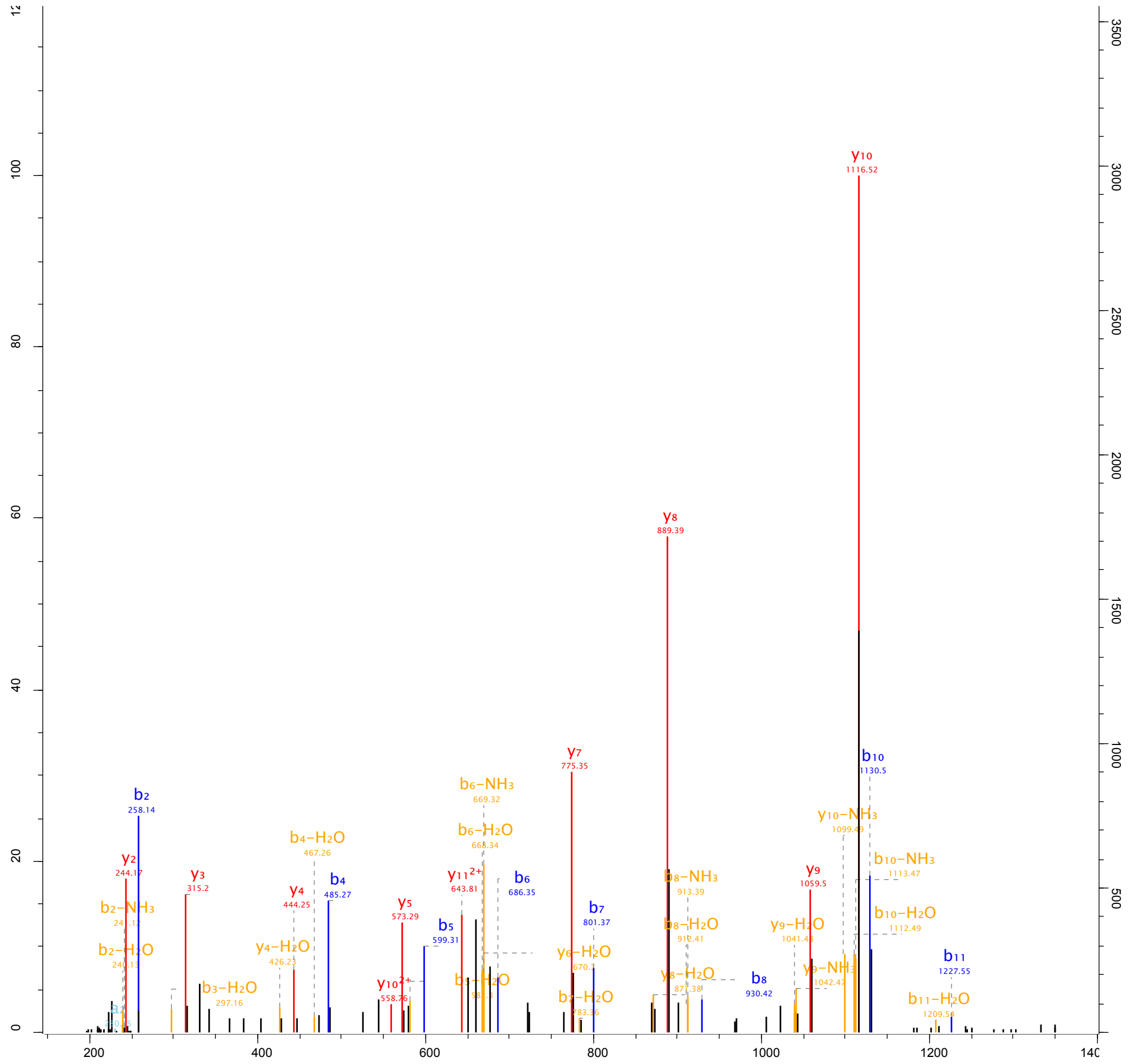


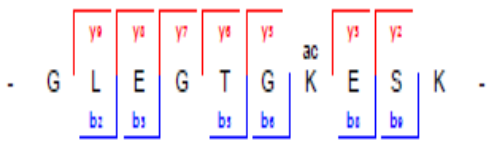
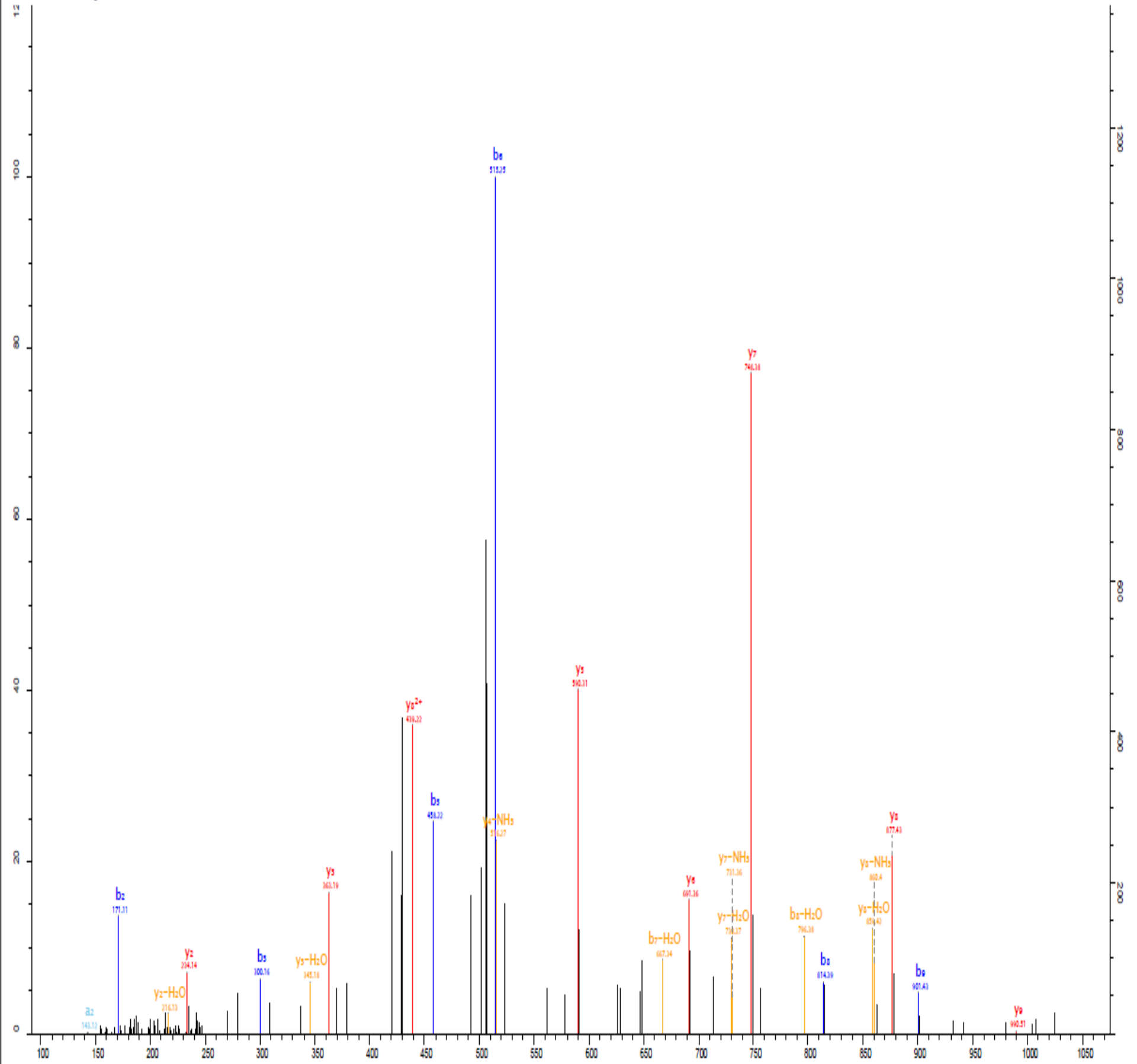
- G G N E E S T K T G N A G S R -

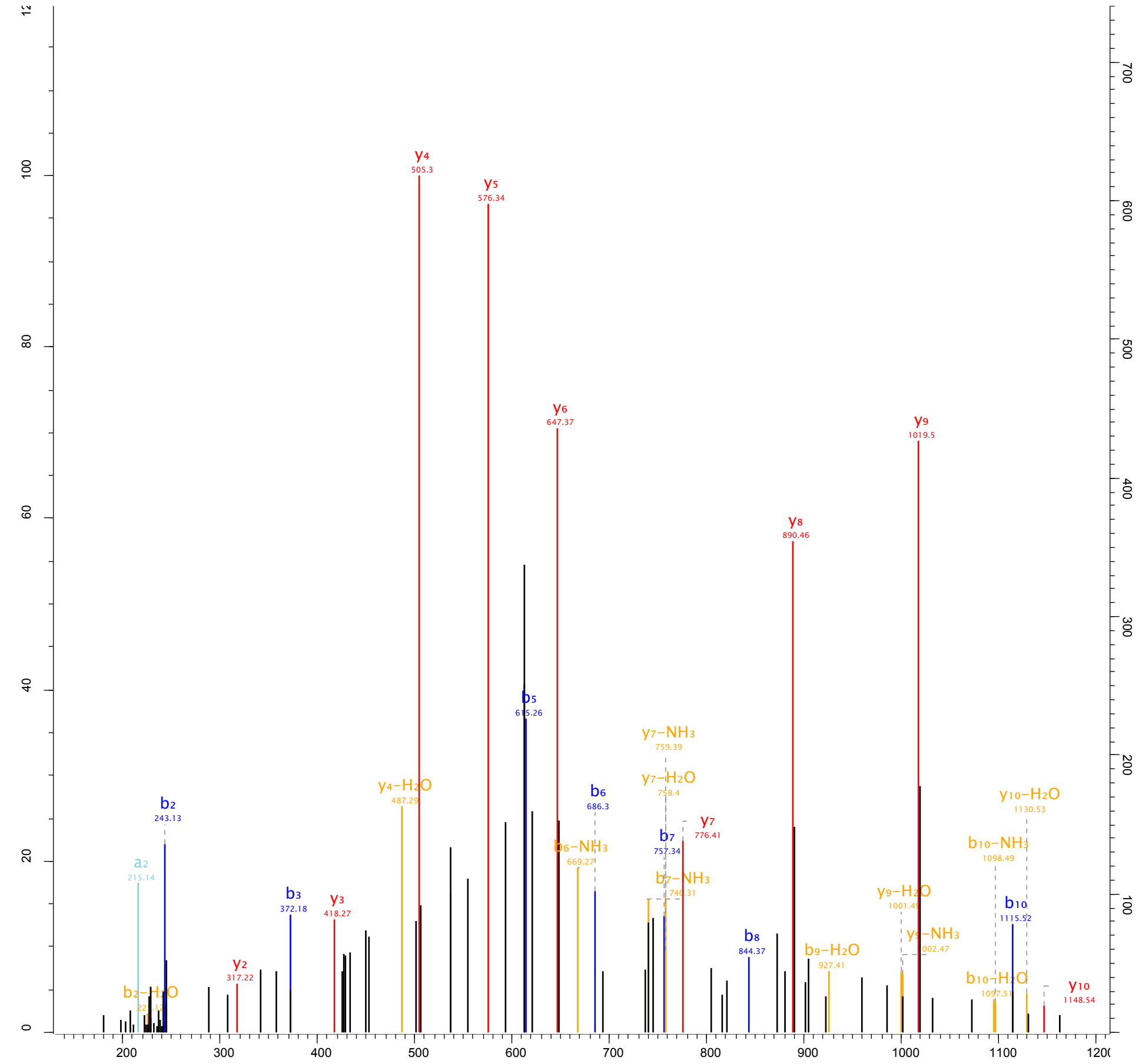
Fragmentation mapping: Red boxes above the sequence indicate y ions (y3 to y12) and blue boxes below indicate b ions (b4 to b13). Vertical dashed lines connect the b and y ions to their corresponding amino acid residues.





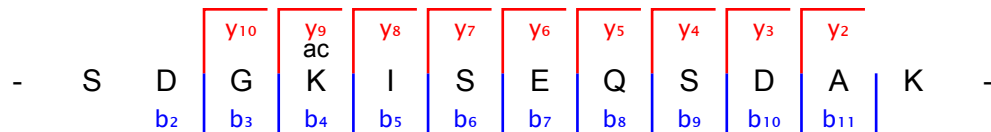
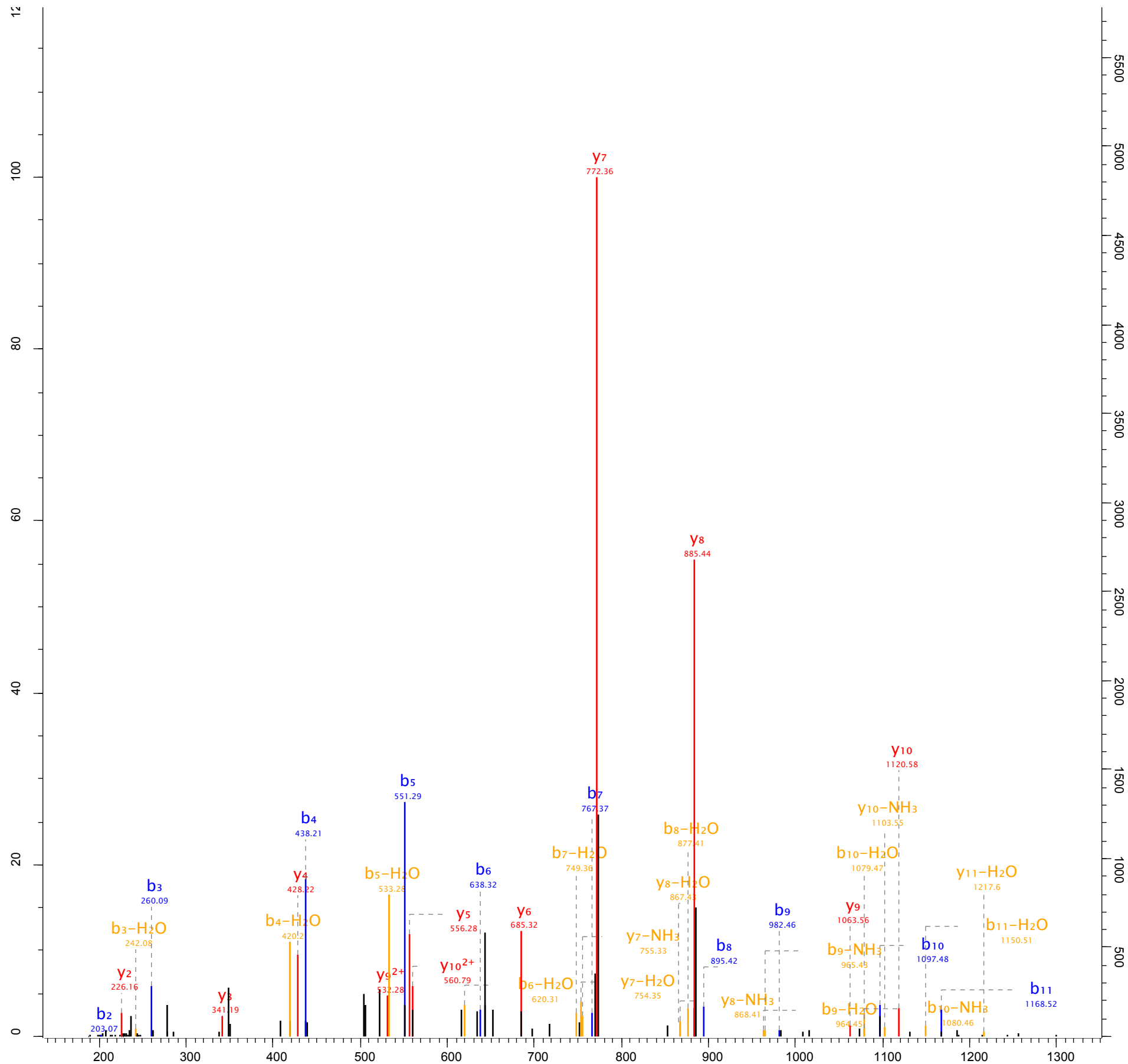


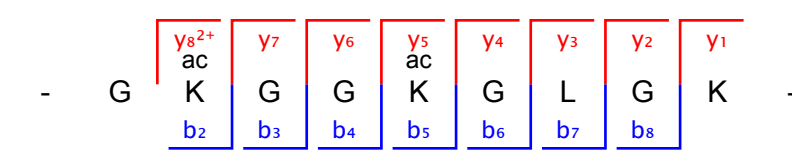
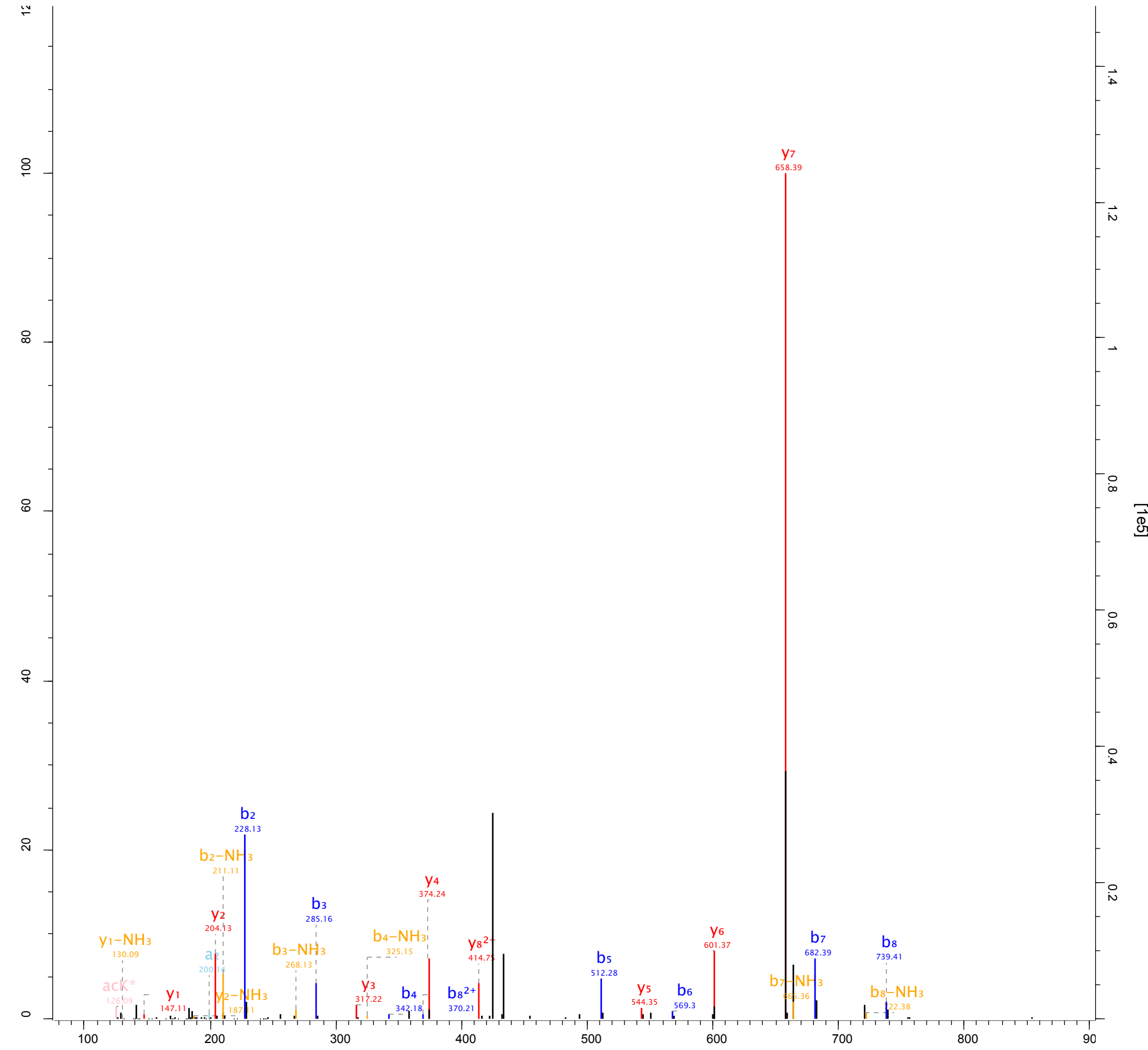


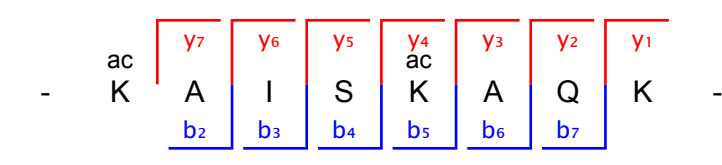
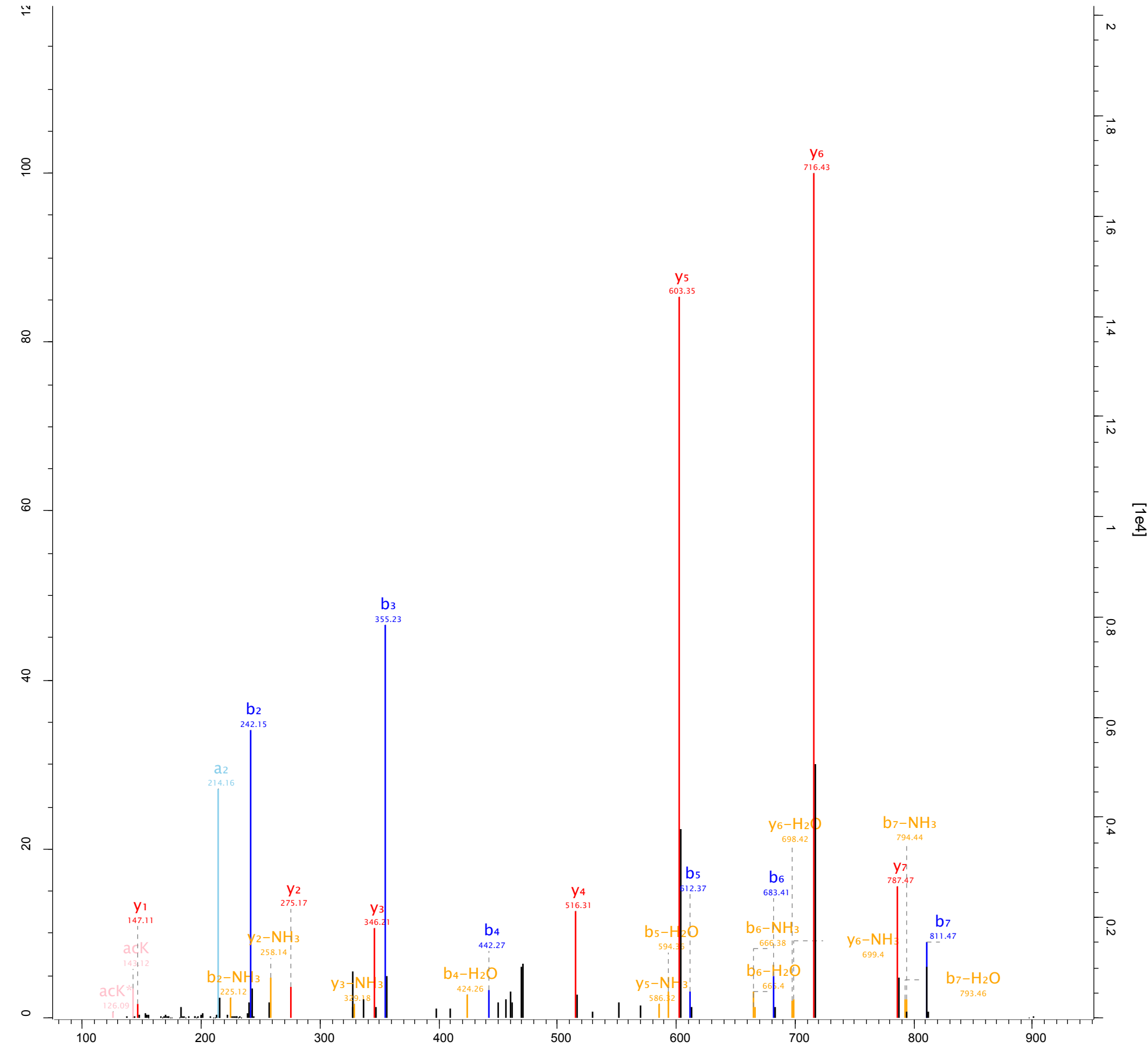


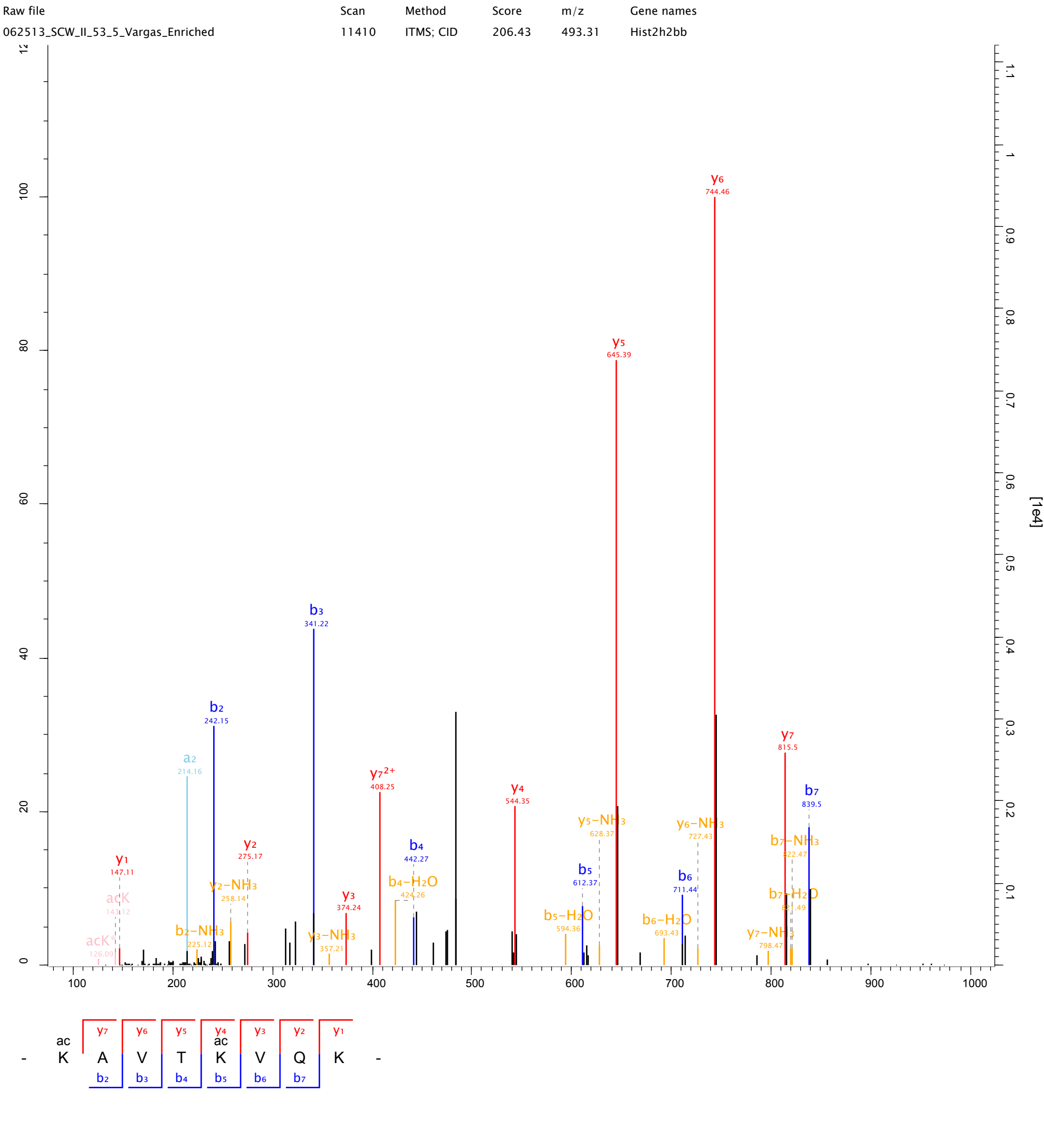
- L E E N E A A S T K -

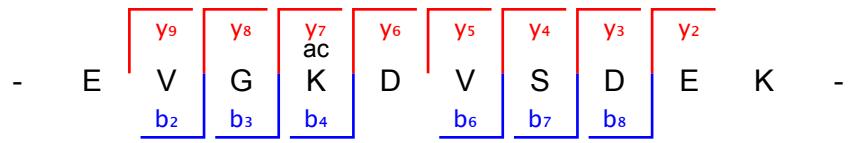
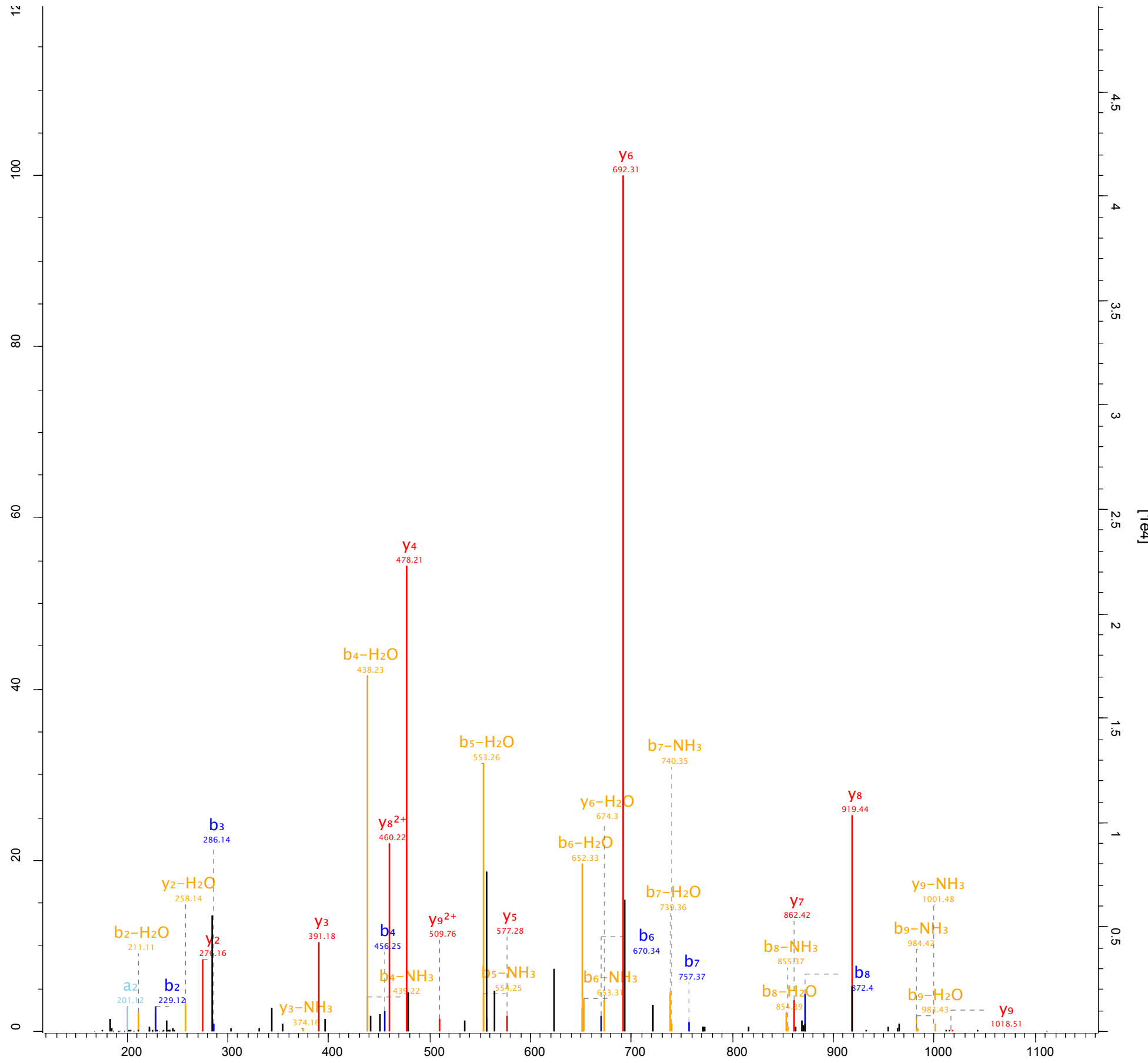
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b2 b3 b5 b6 b7 b8 b10

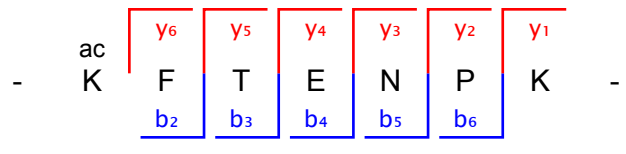
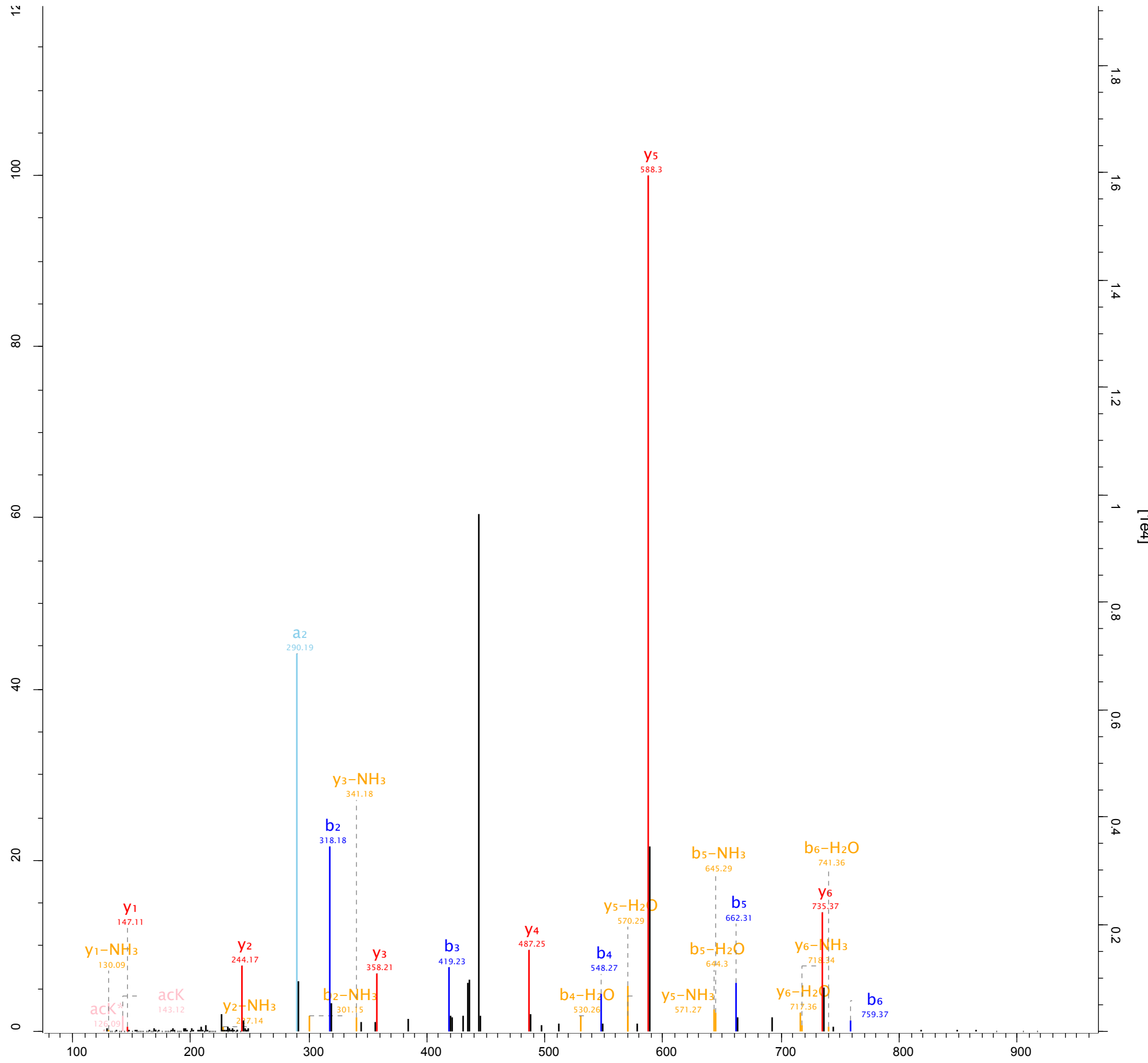


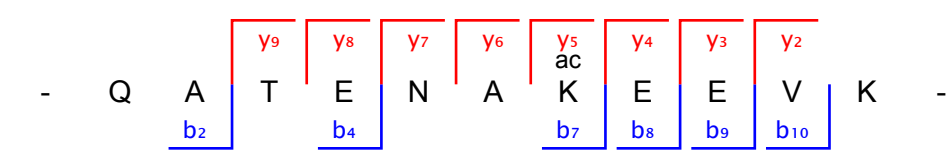
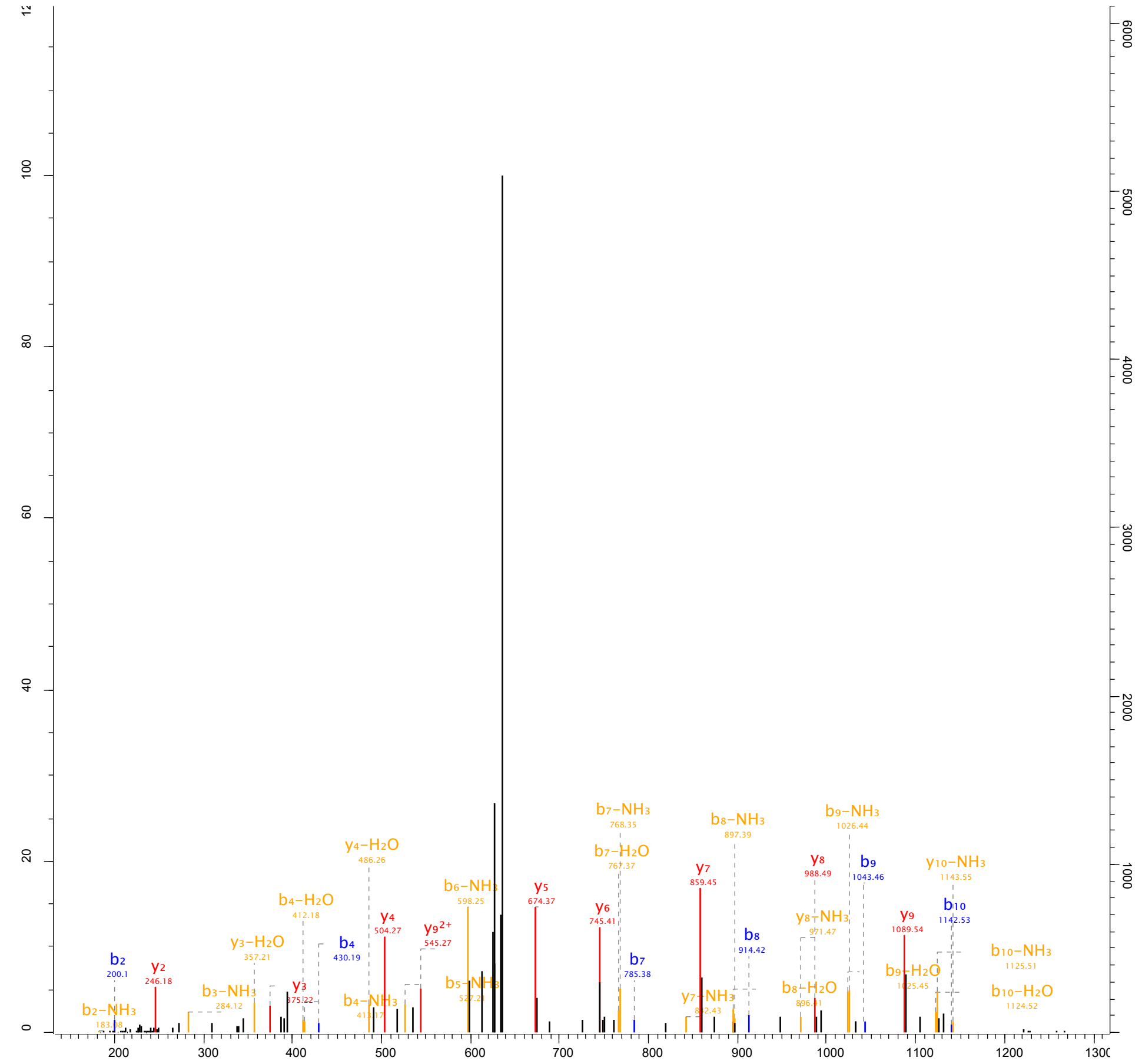


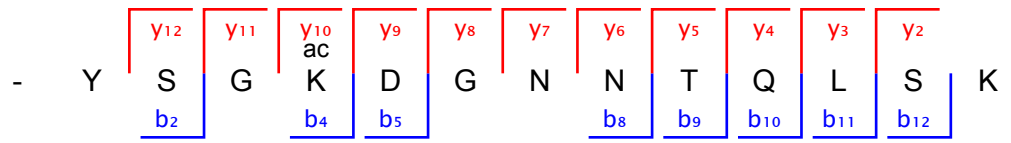
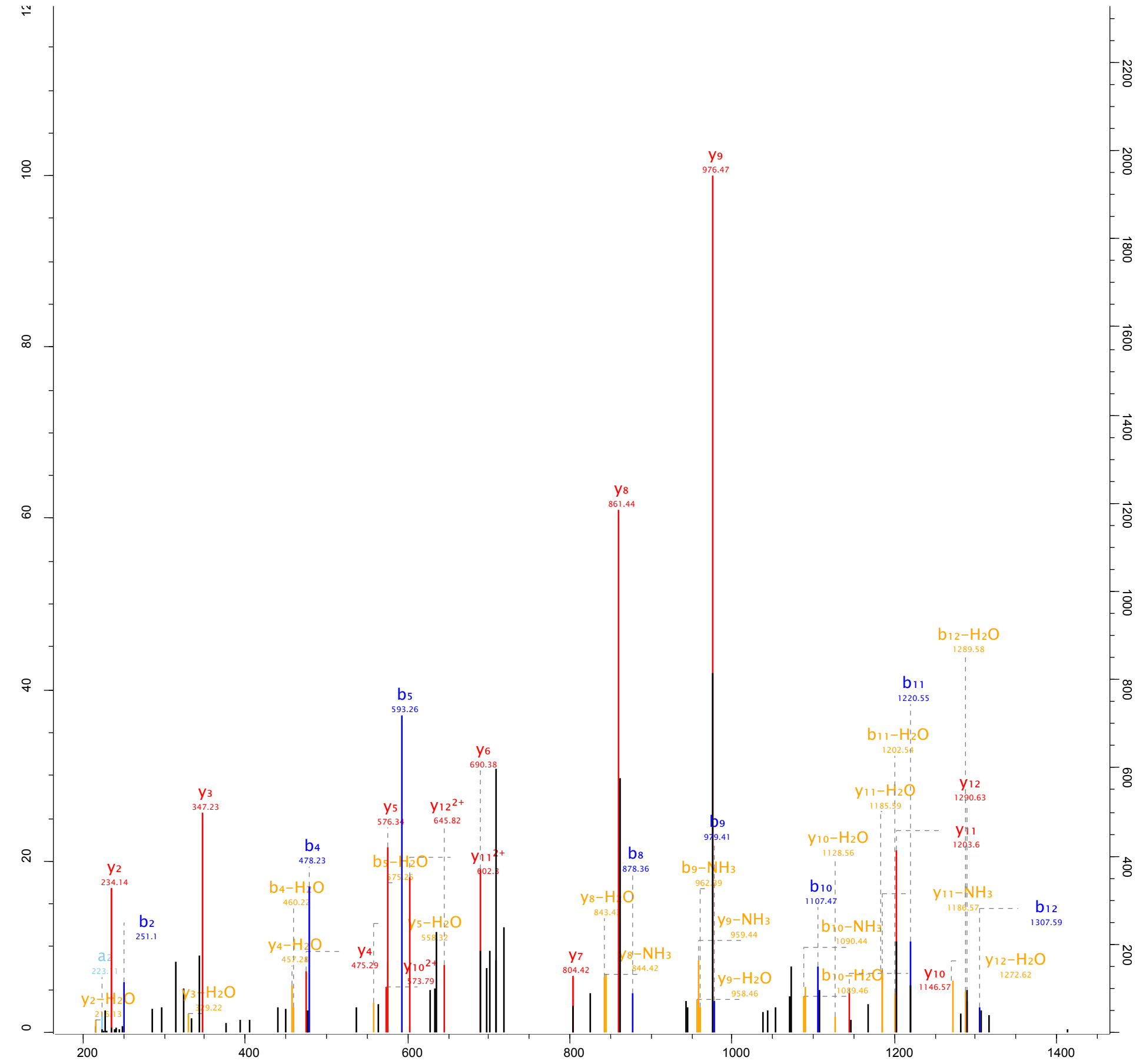


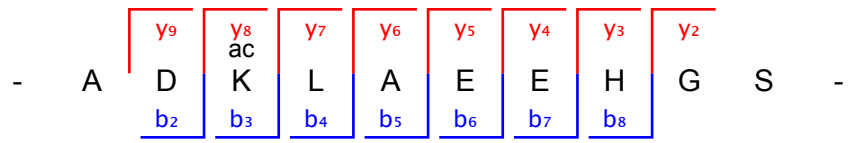
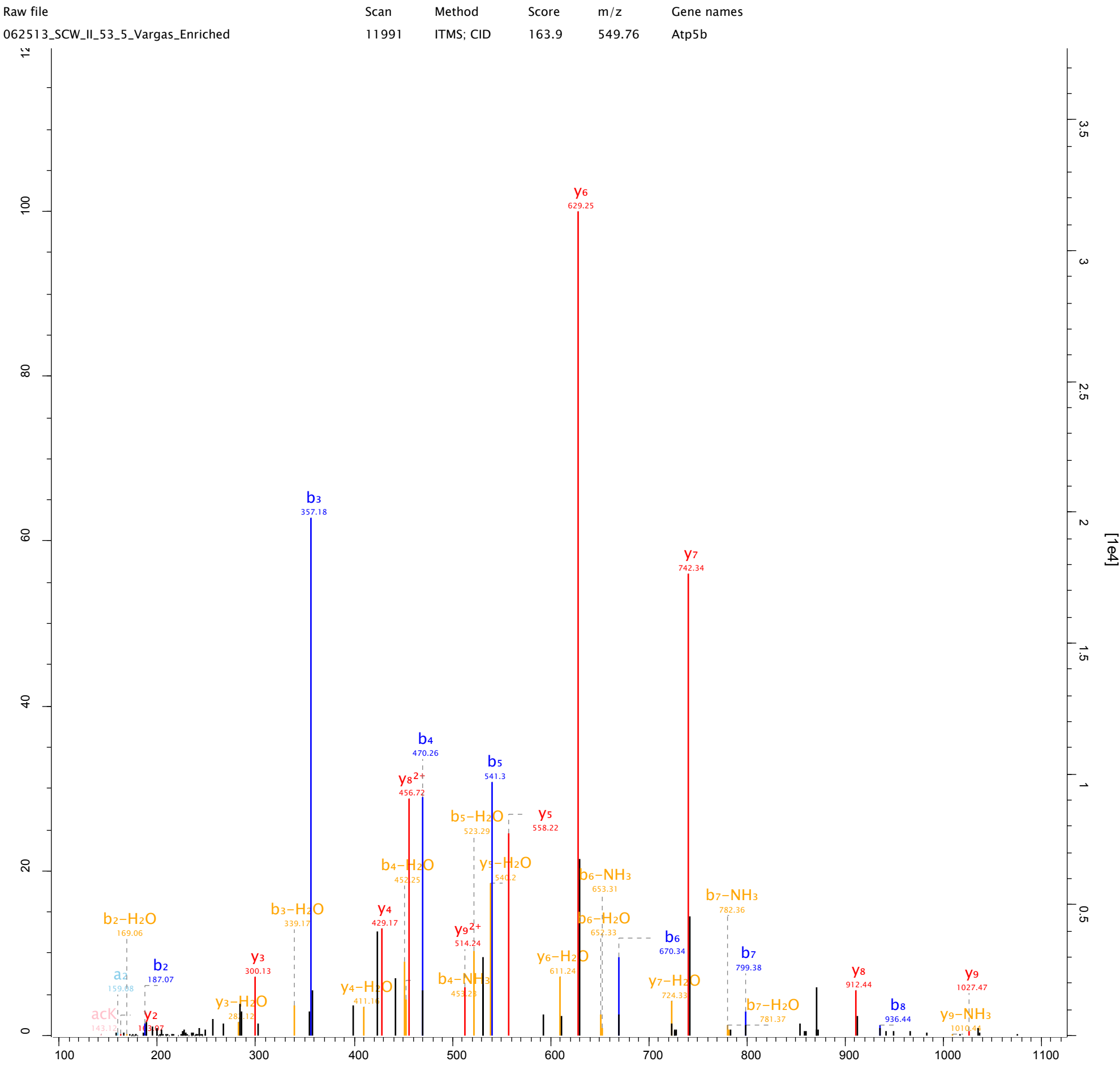


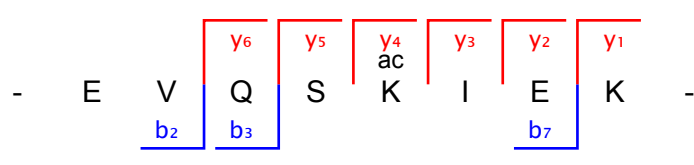
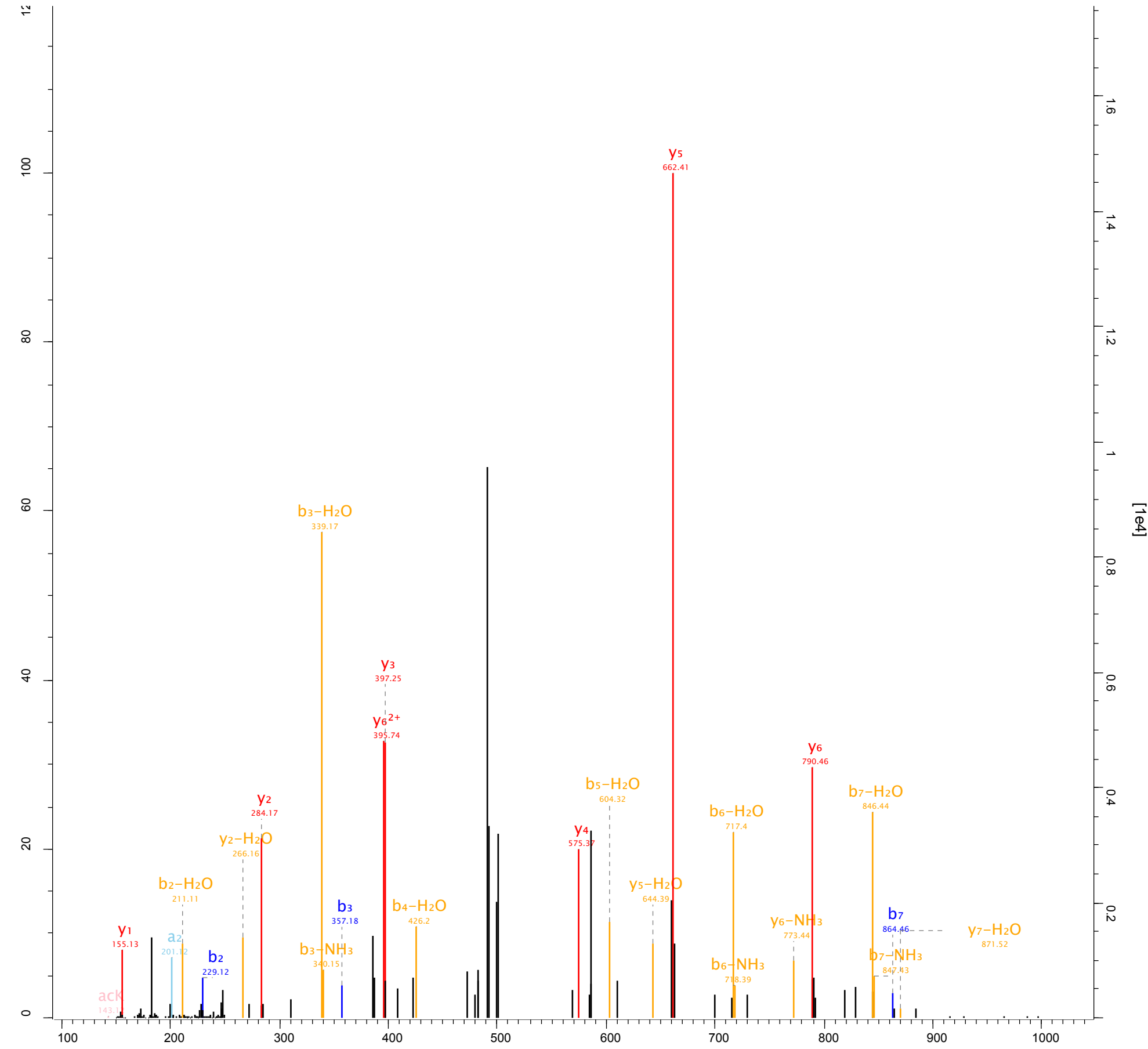


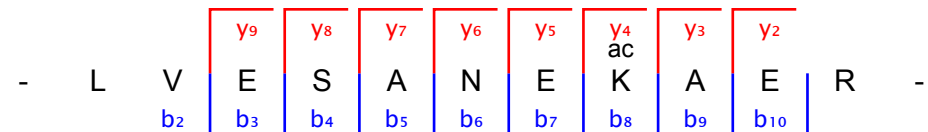
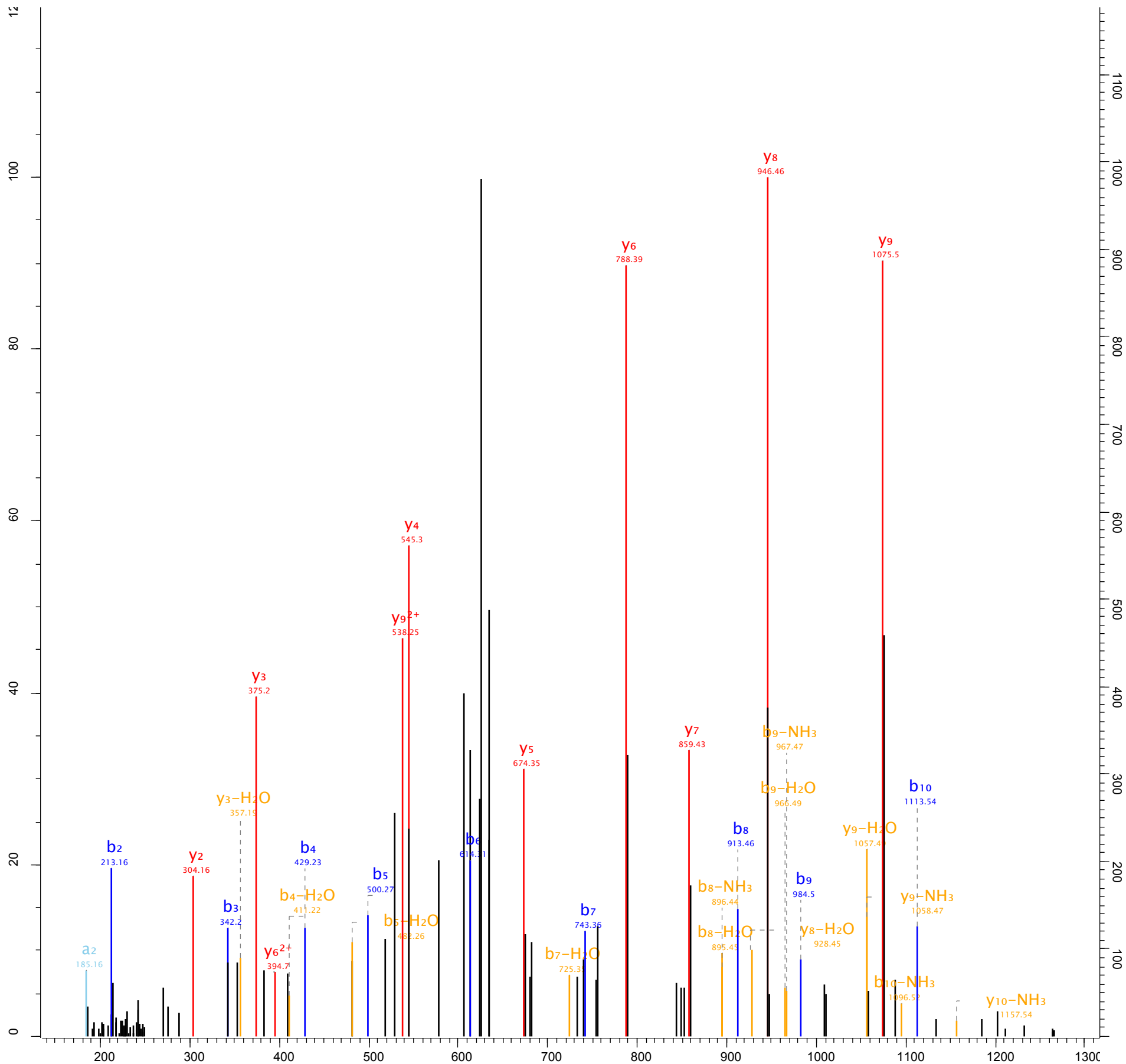


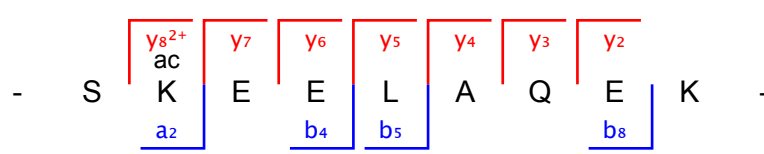
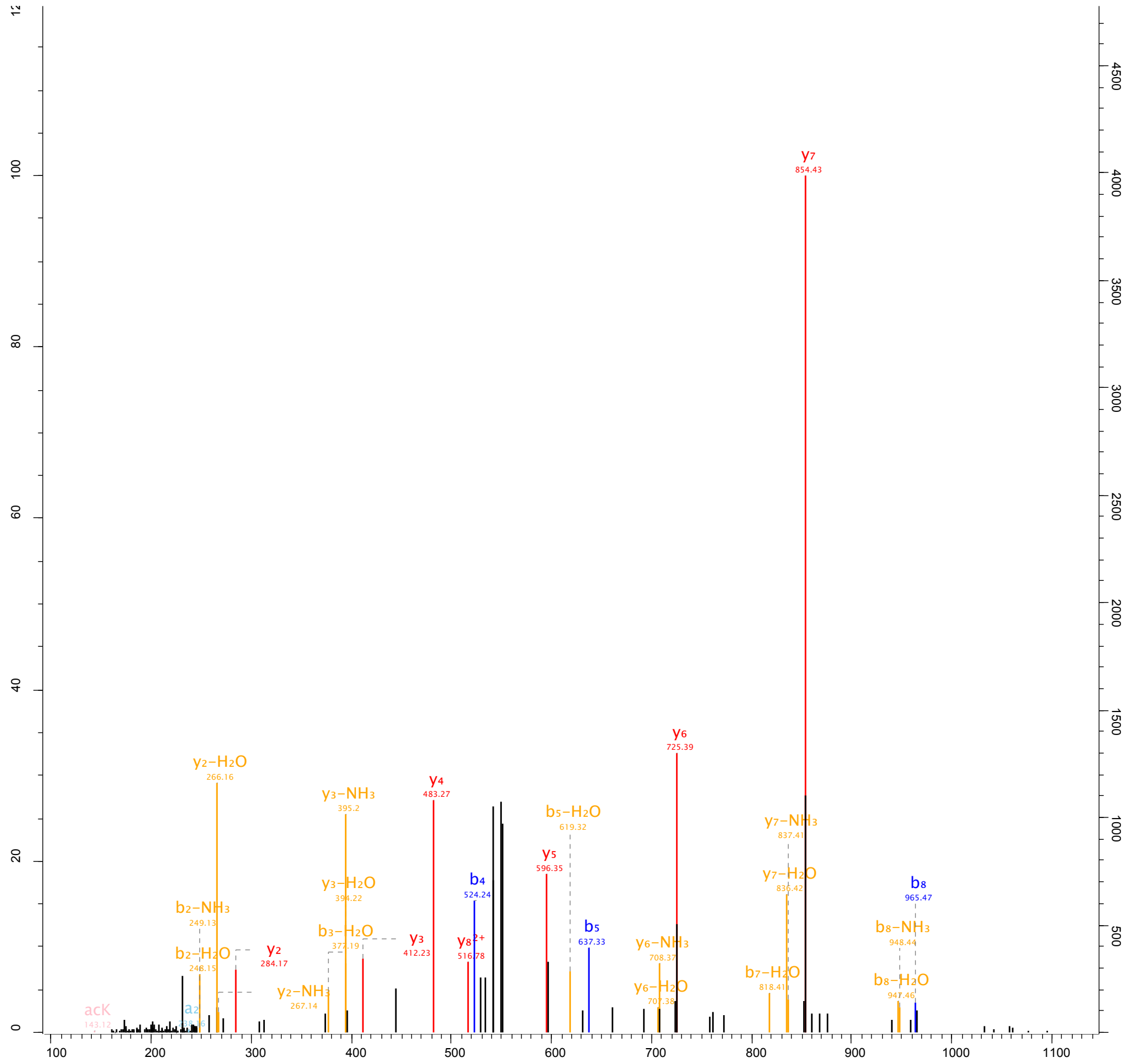




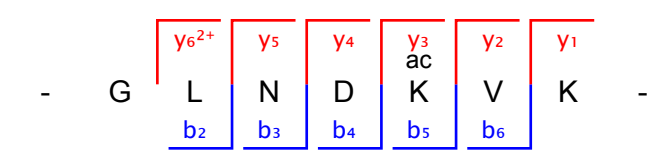
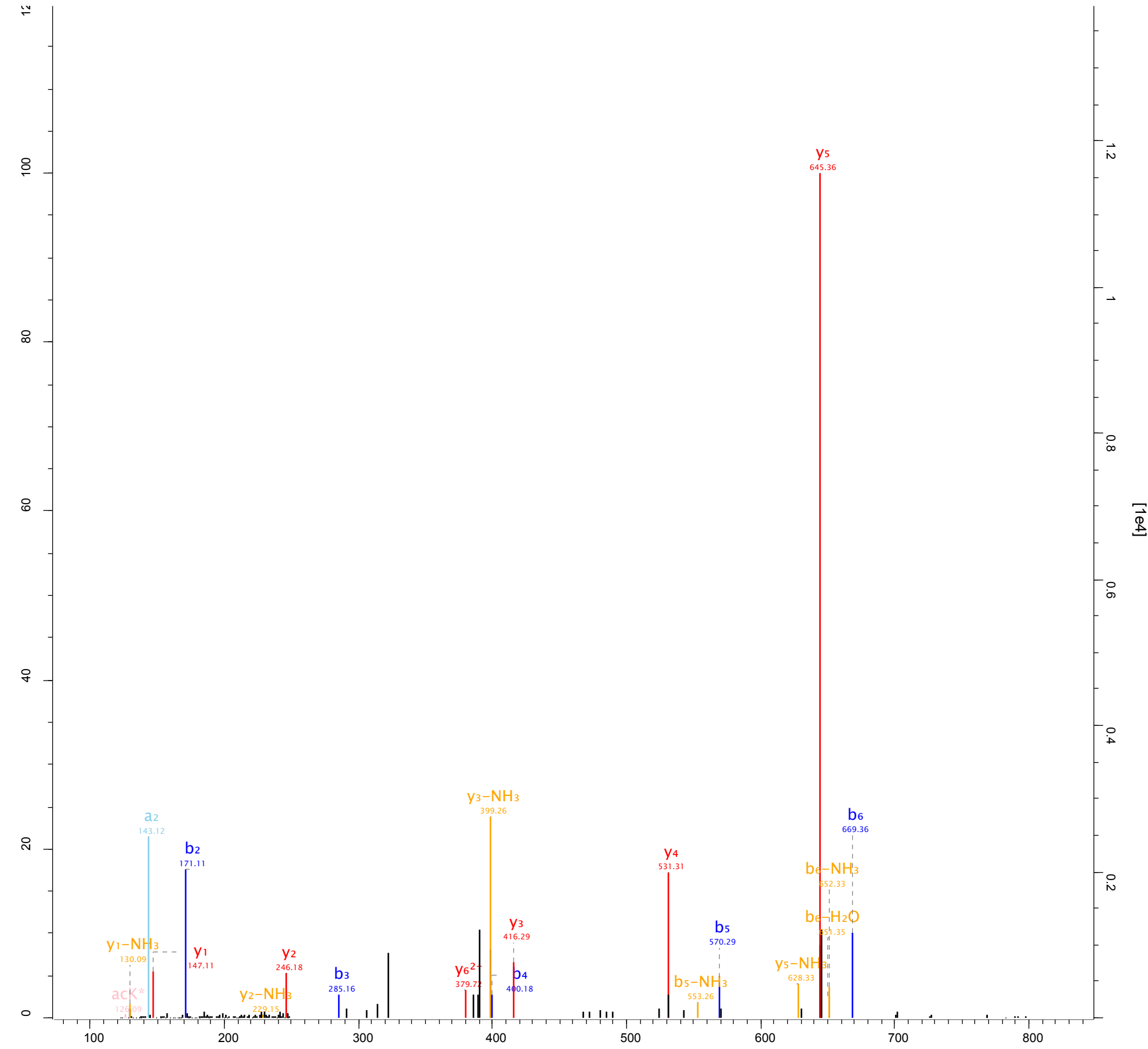


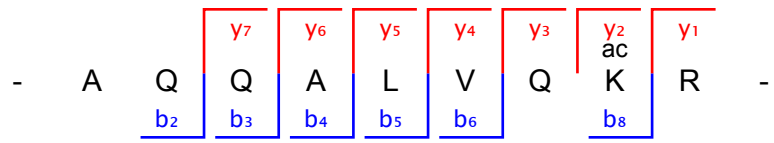
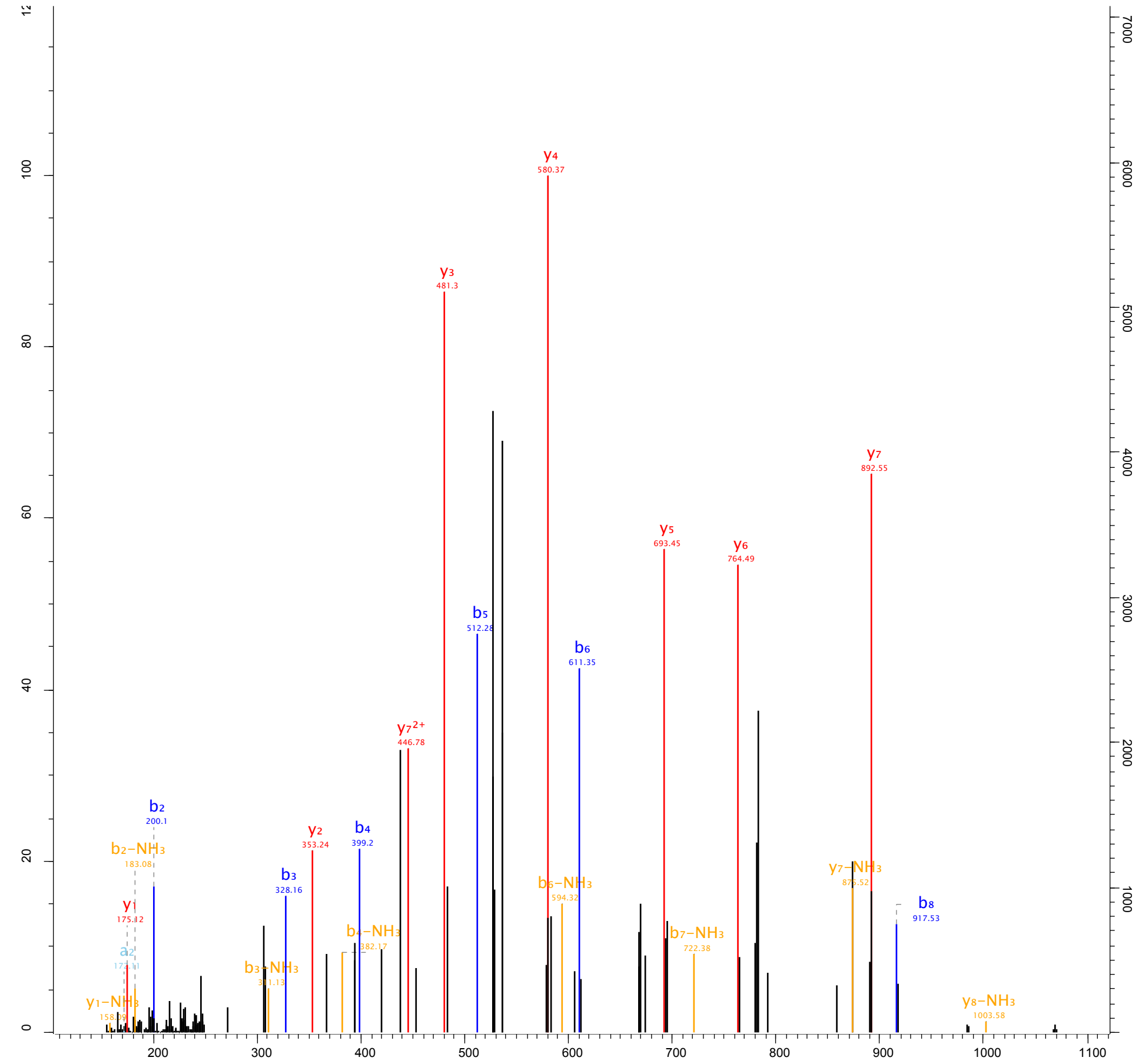


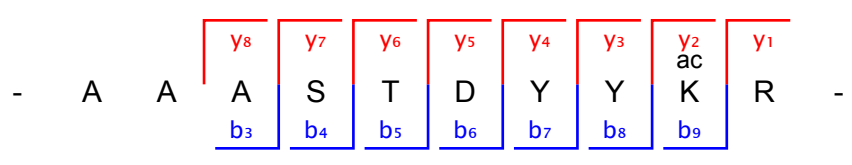
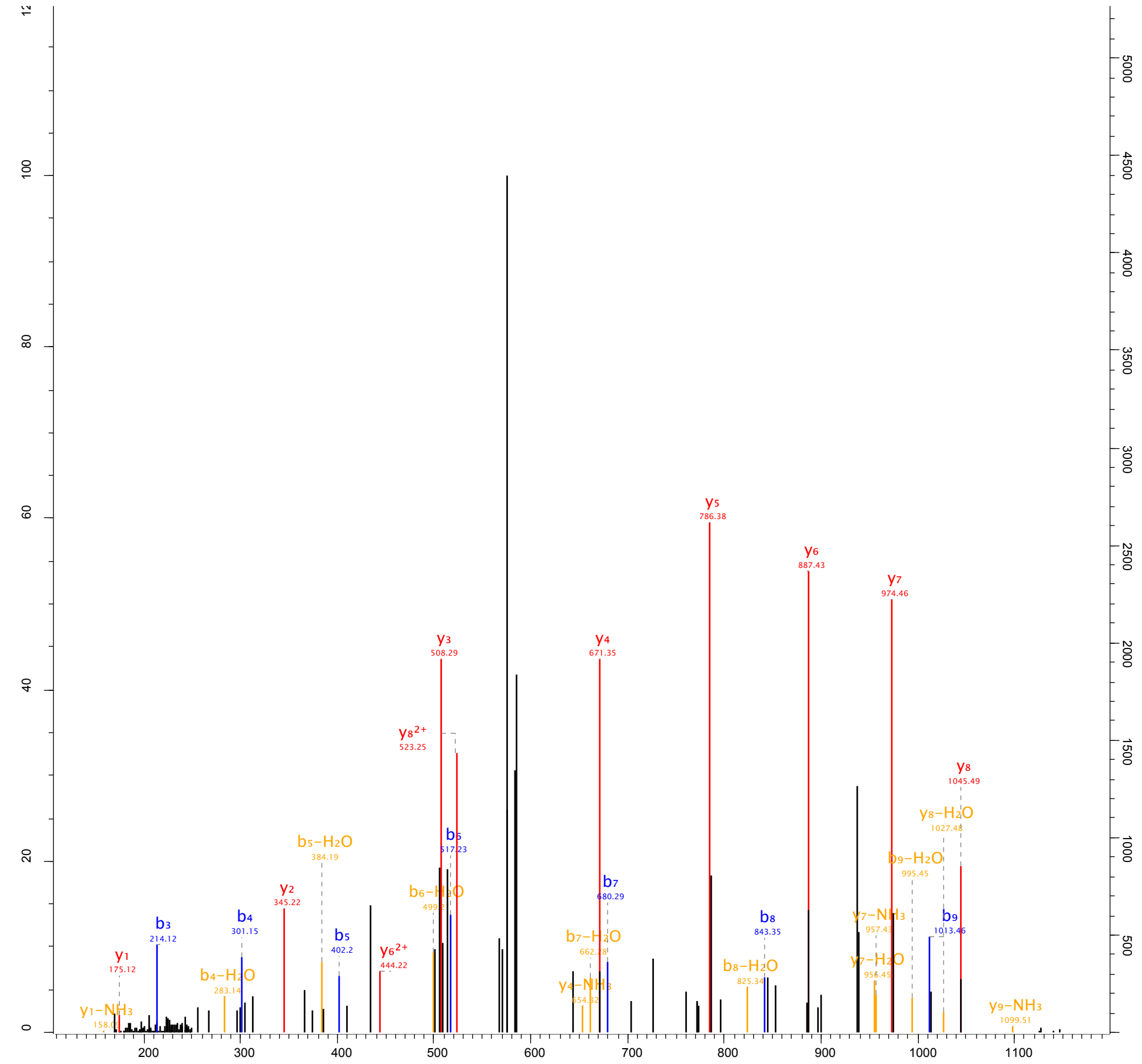


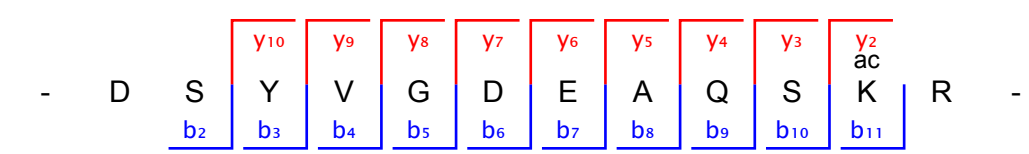
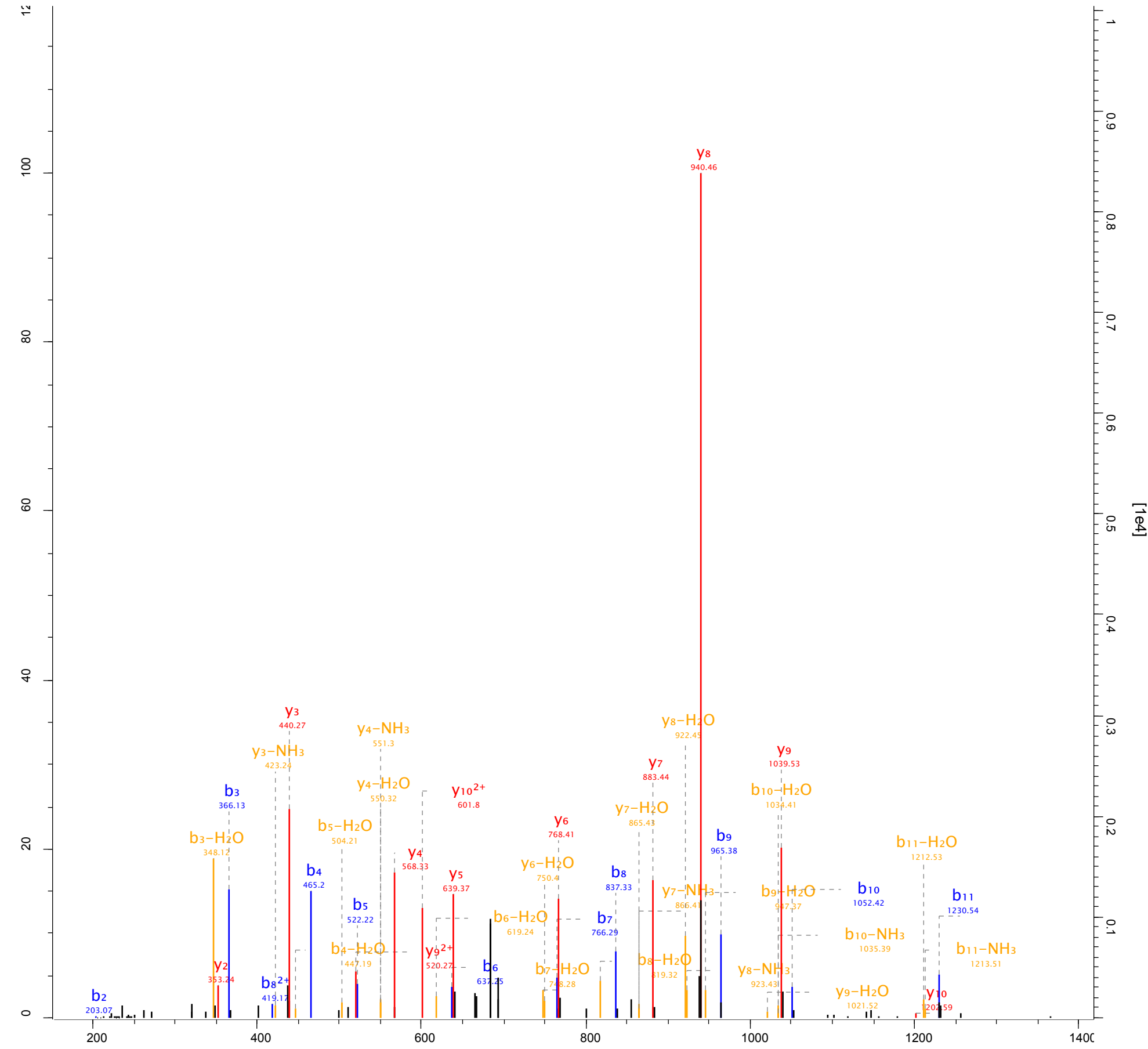


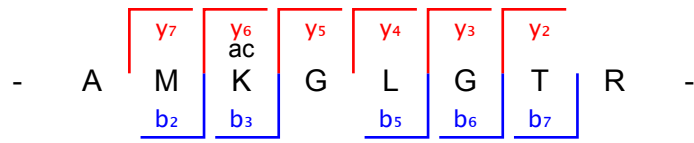
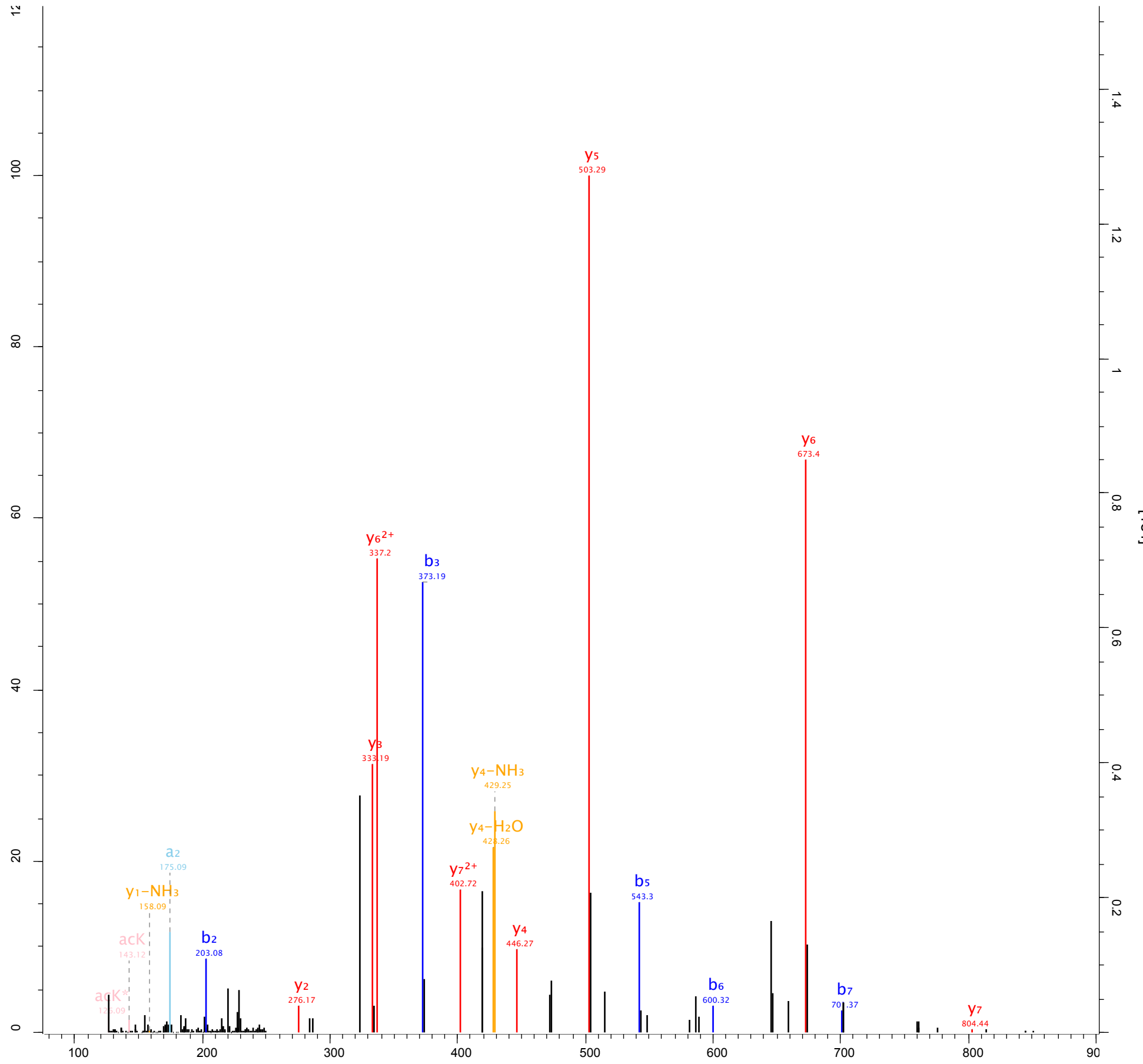
Raw file 062513_SCW_II_53_5_Vargas_Enriched Scan 12584 Method ITMS; CID Score 143.61 m/z 408.23 Gene names Hadha











062513_SCW_II_53_5_Vargas_Enriched

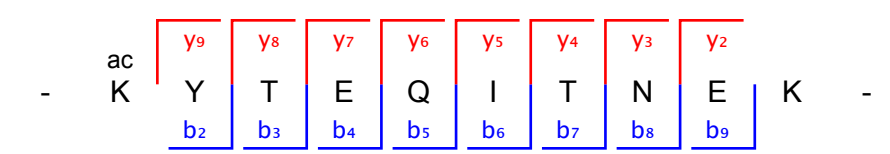
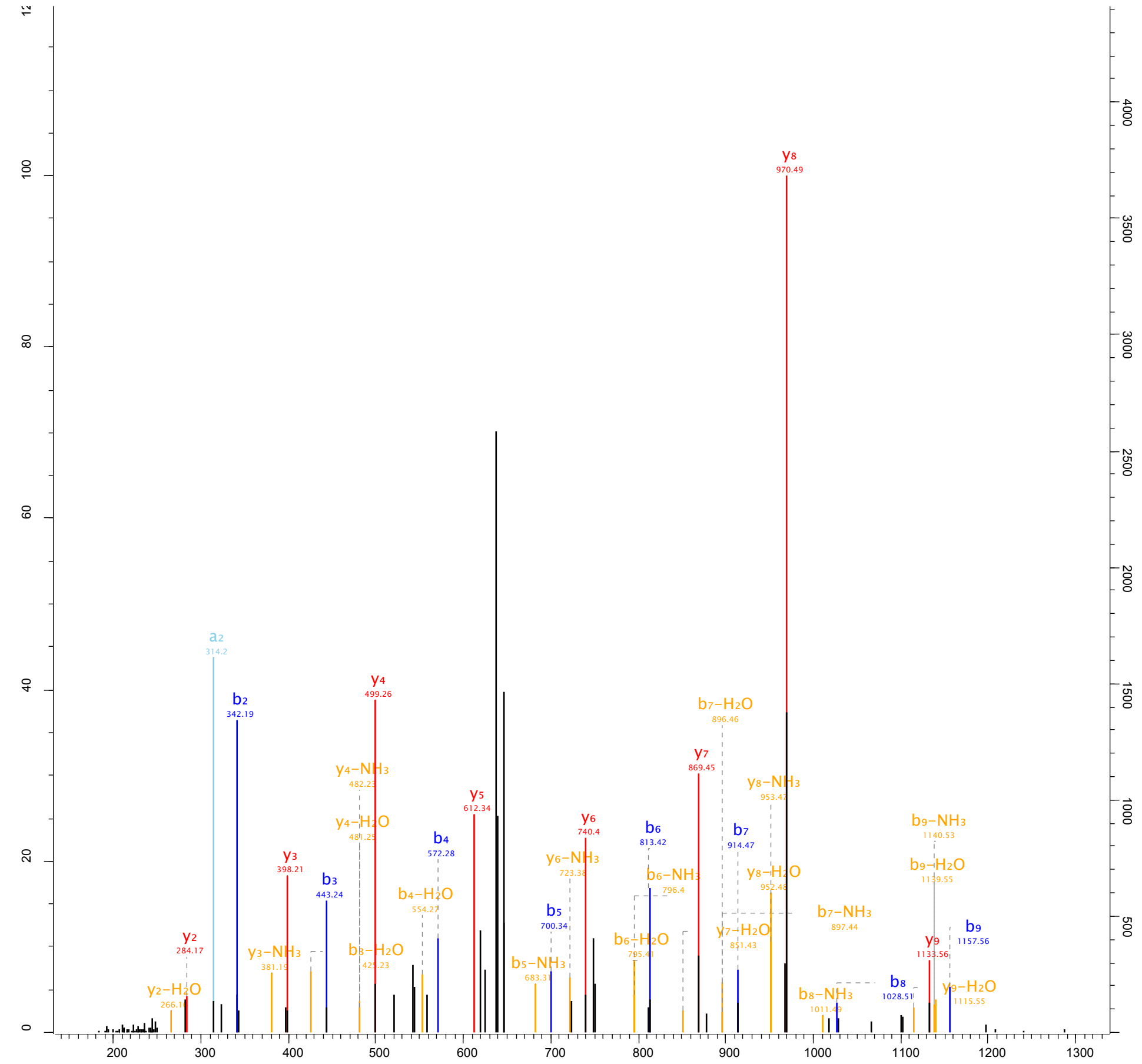
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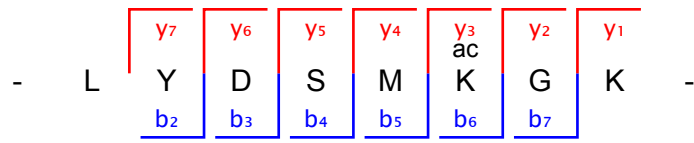
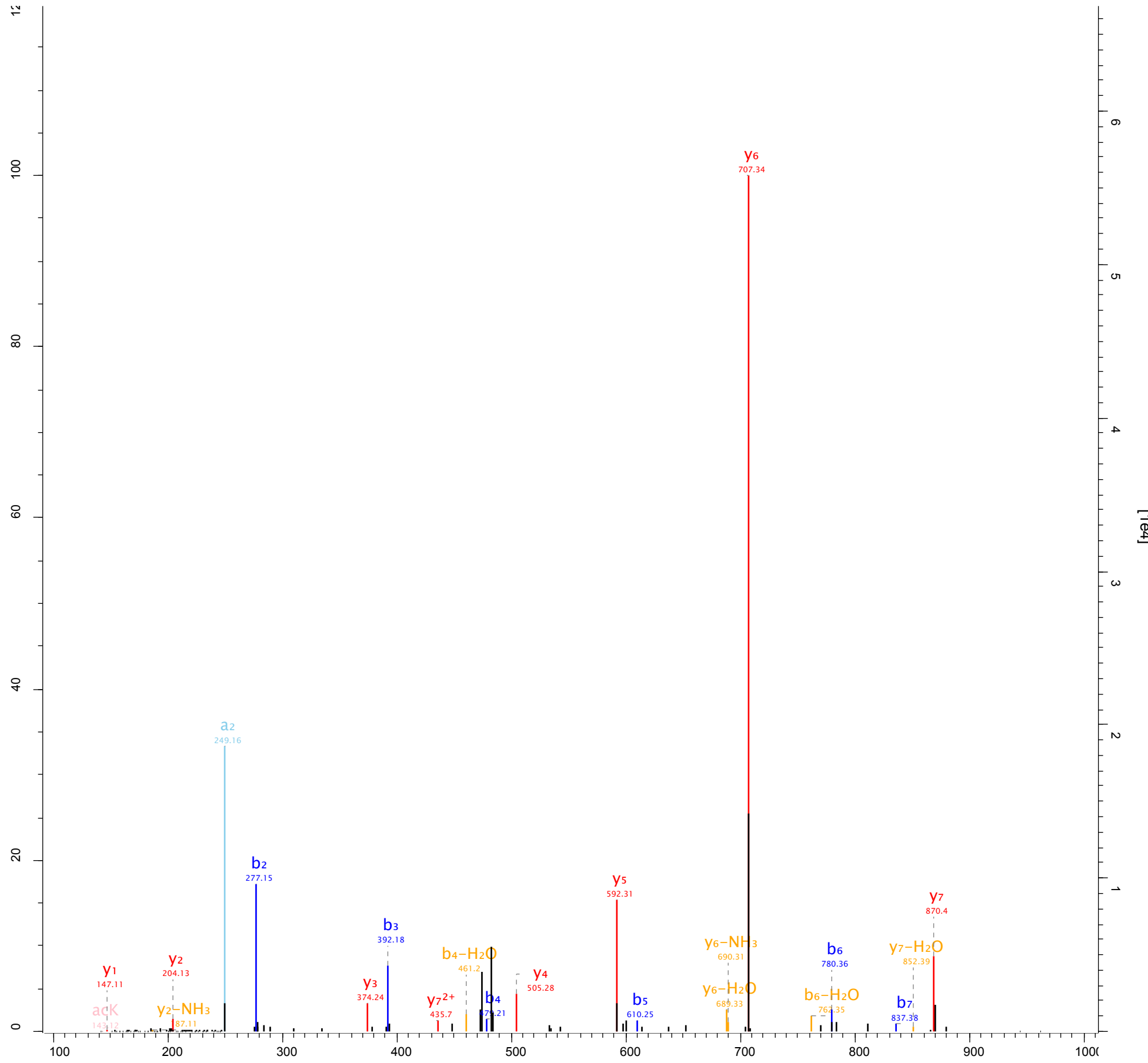
ITMS; CID

216.91

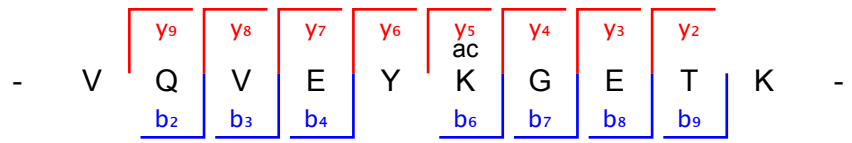
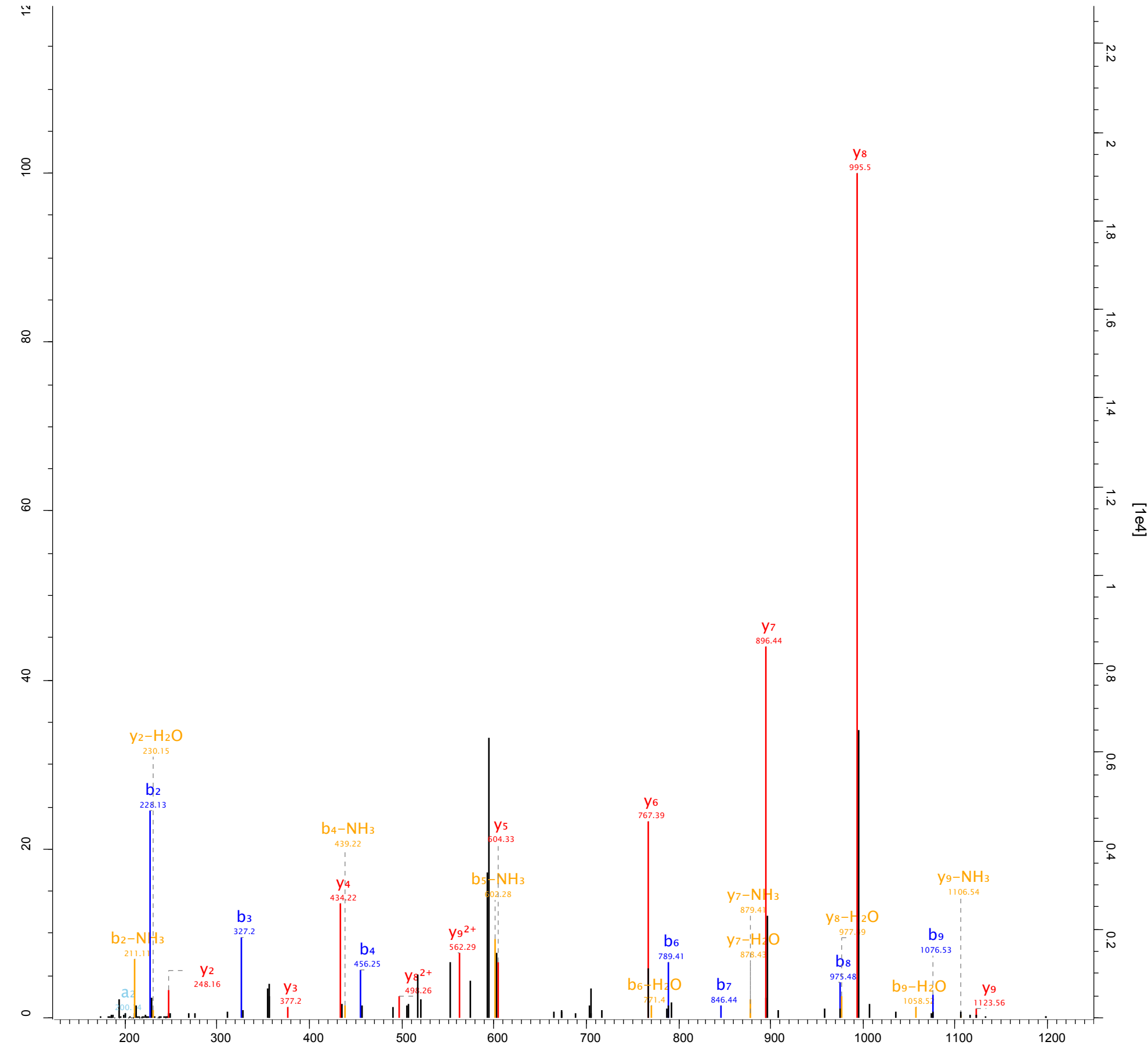
656.34

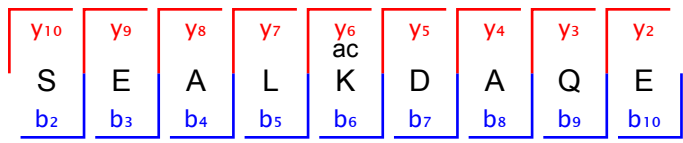
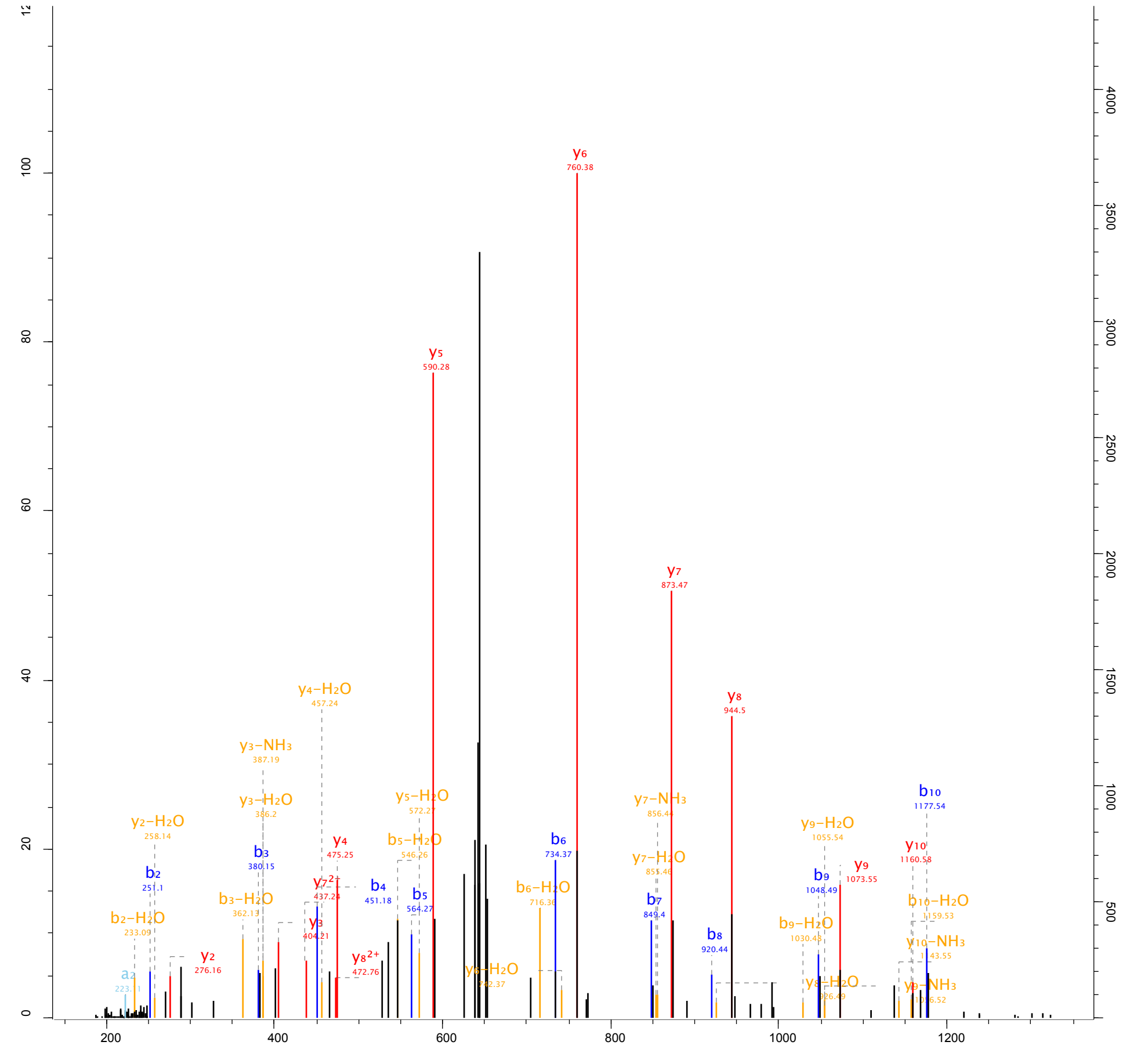
Ndufa5

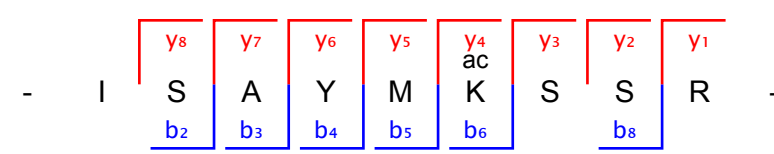
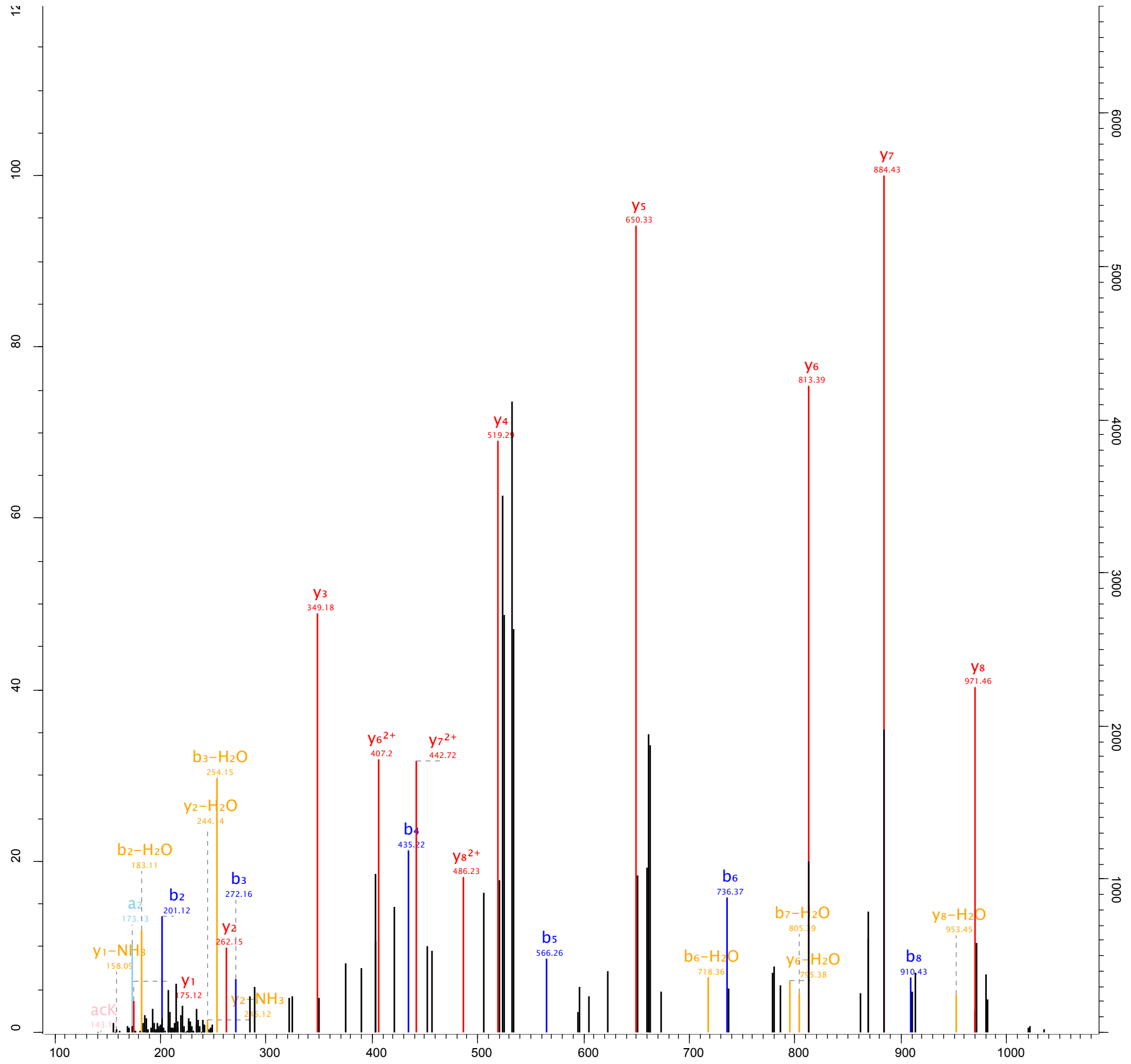


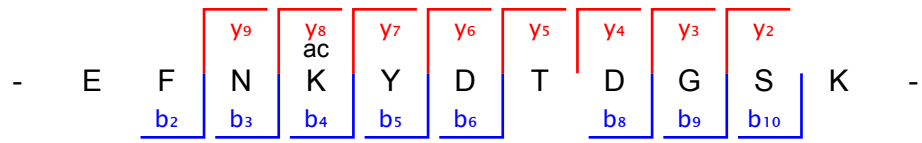
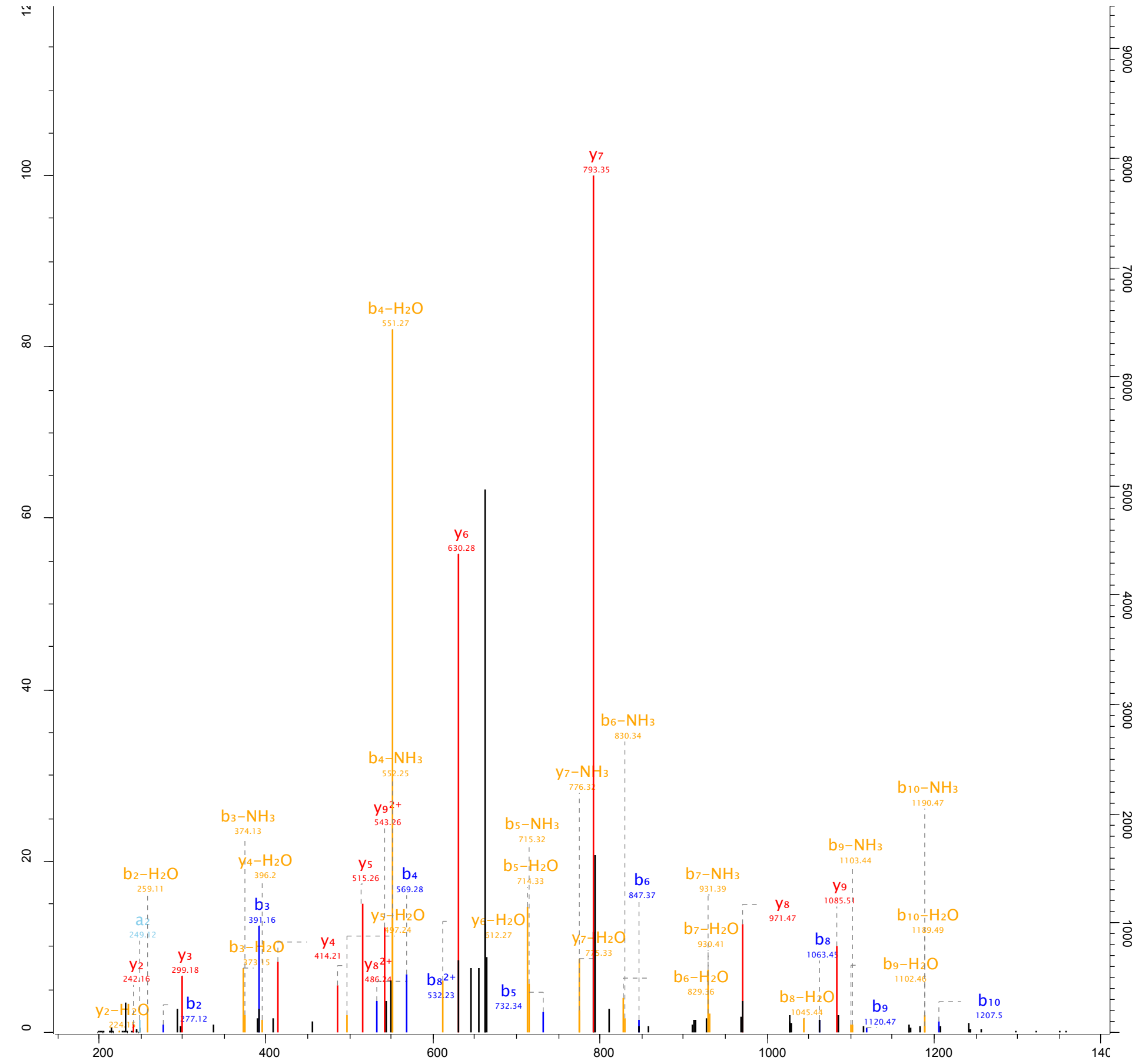


Raw file 062513_SCW_II_53_5_Vargas_Enriched Scan 13848 Method ITMS; CID Score 137.4 m/z 611.82 Gene names Hspa8









062513_SCW_II_53_5_Vargas_Enriched

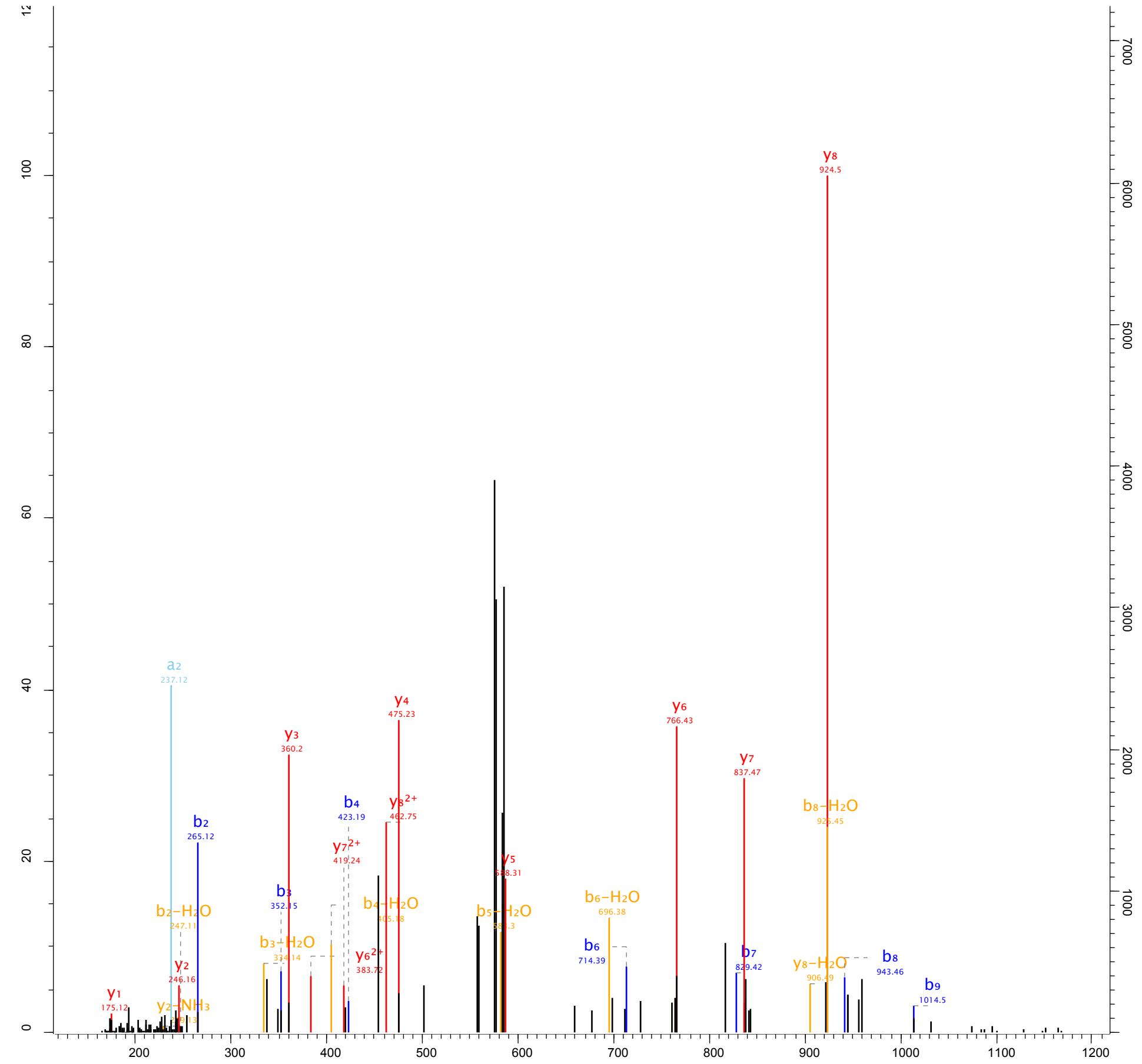
14459

ITMS; CID

116.84

594.81

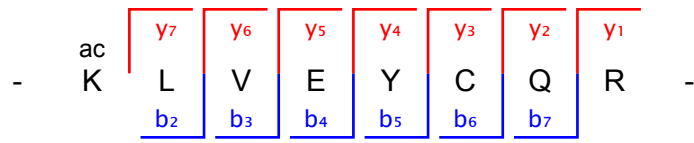
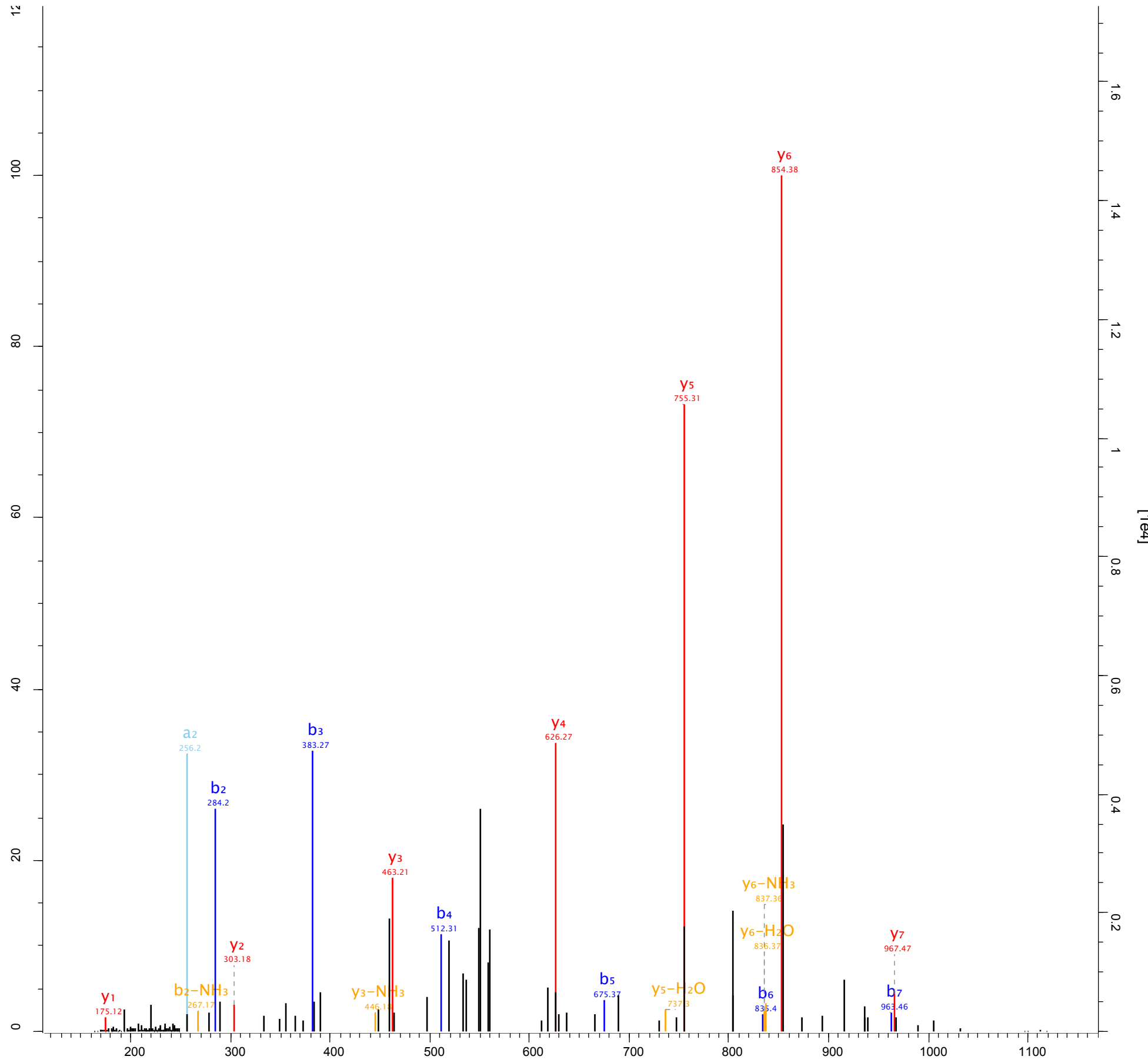
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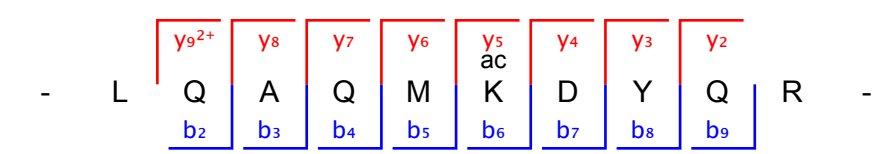
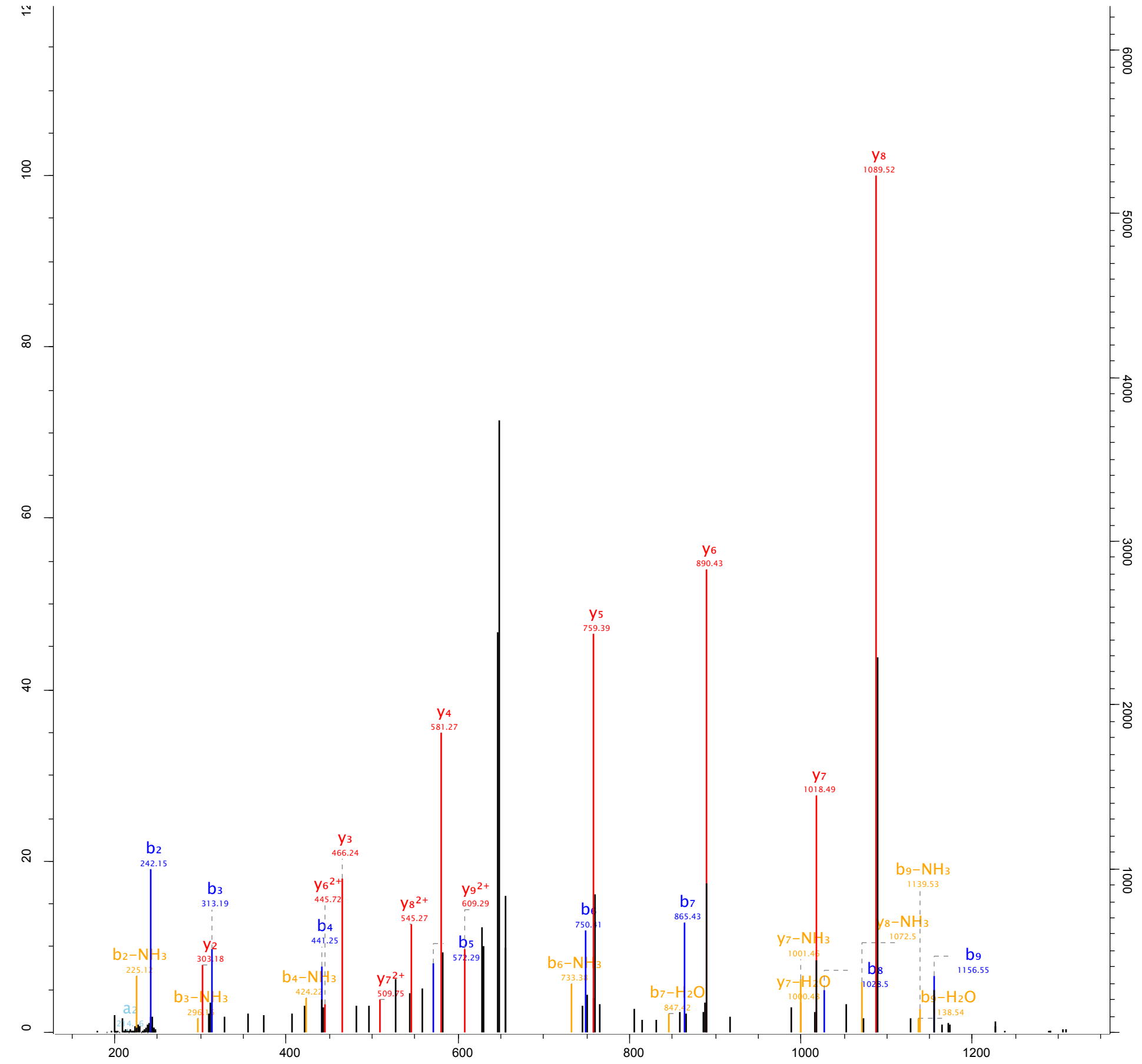


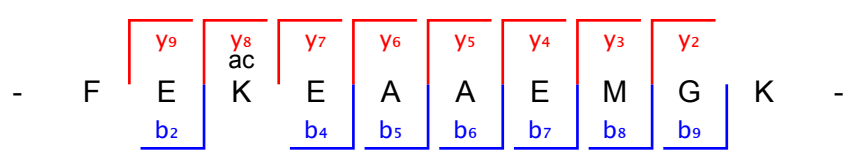
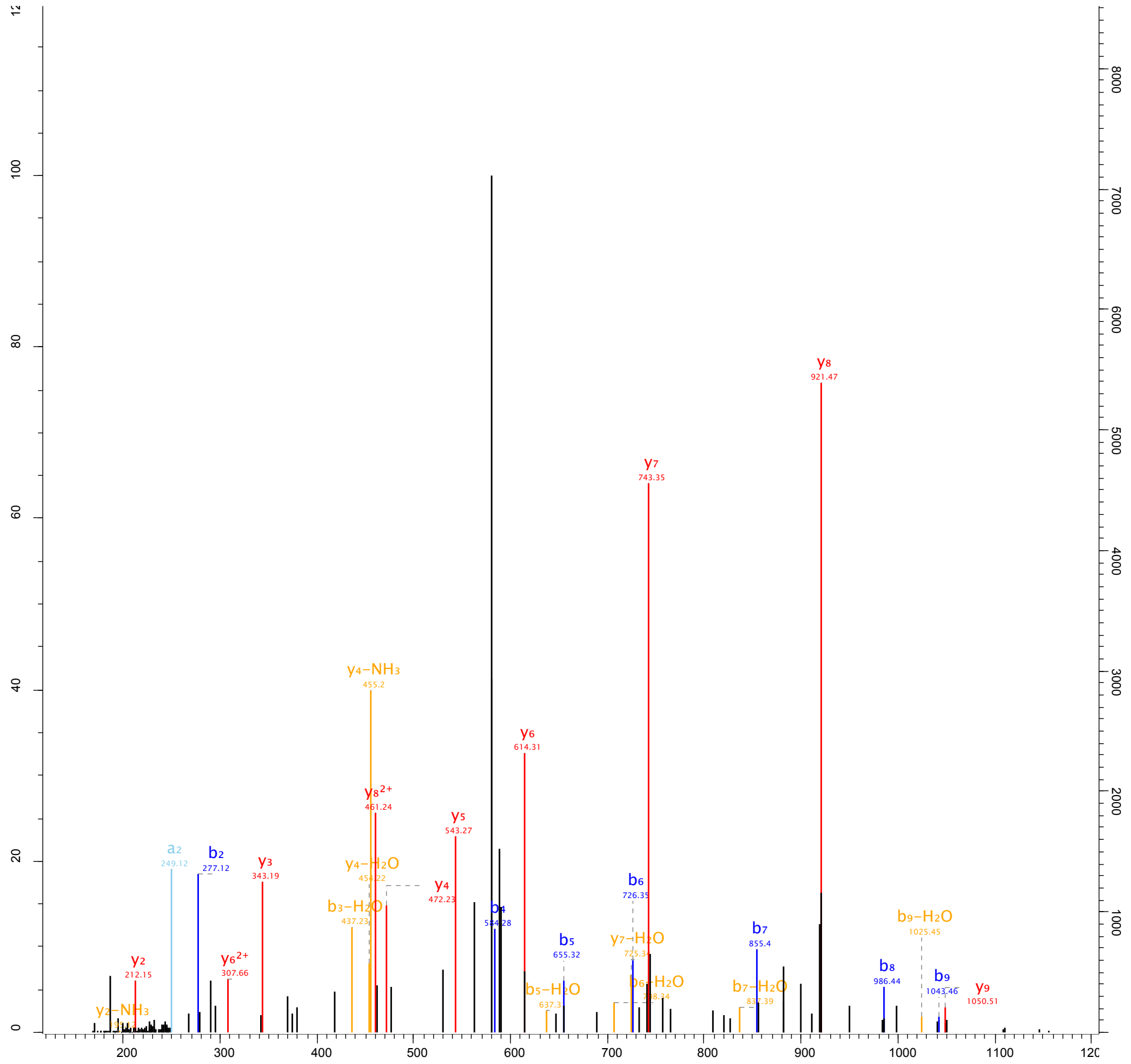
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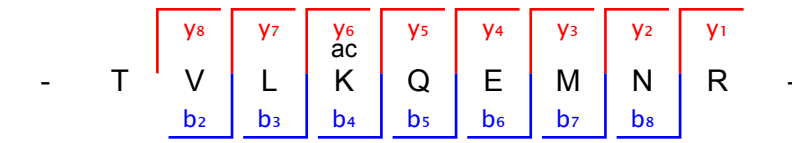
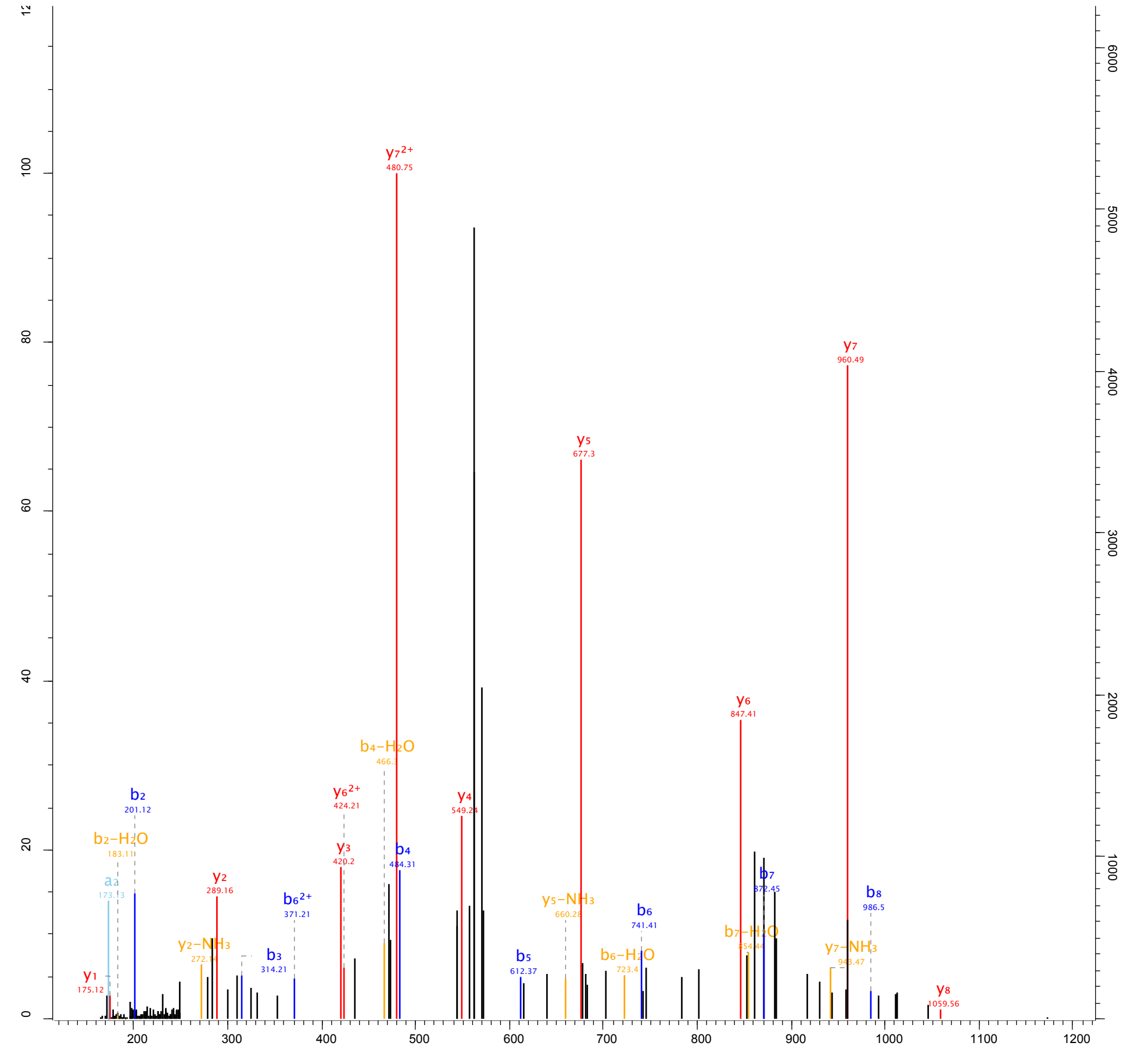
y8
y7
y6
ac
y5
y4
y3
y2
y1

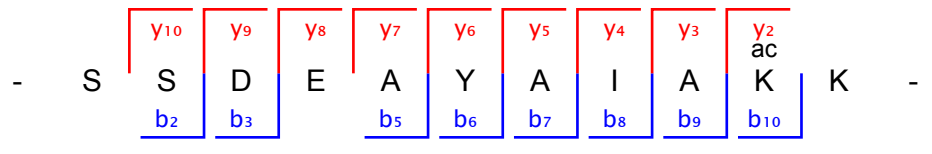
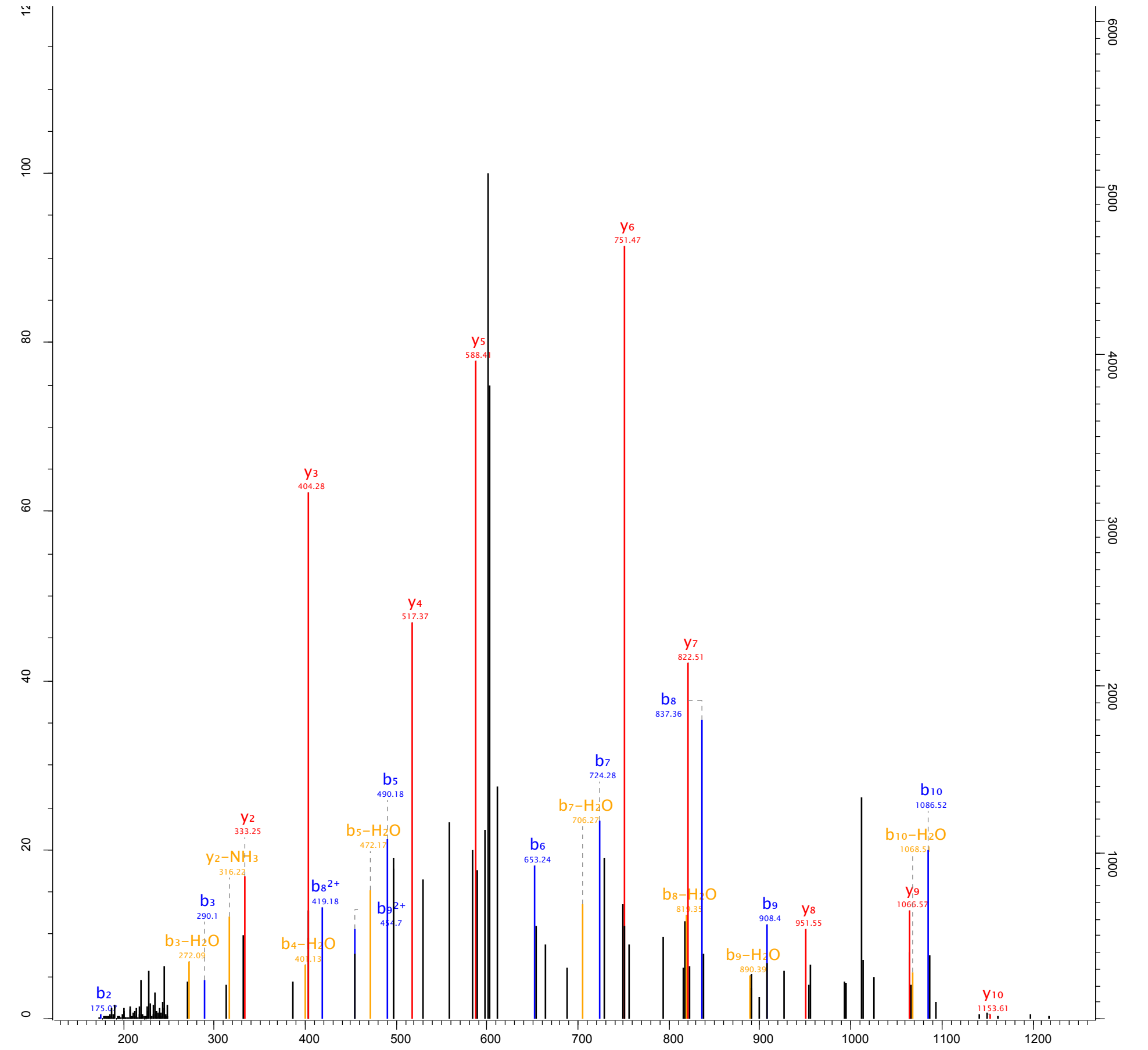
b2
b3
b4
b6
b7
b8
b9

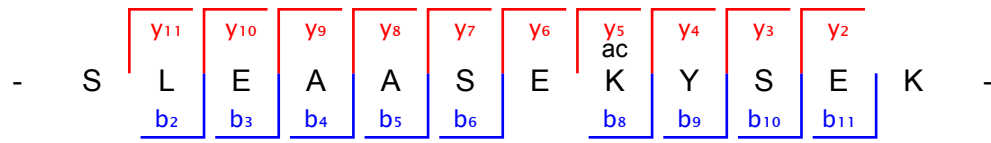
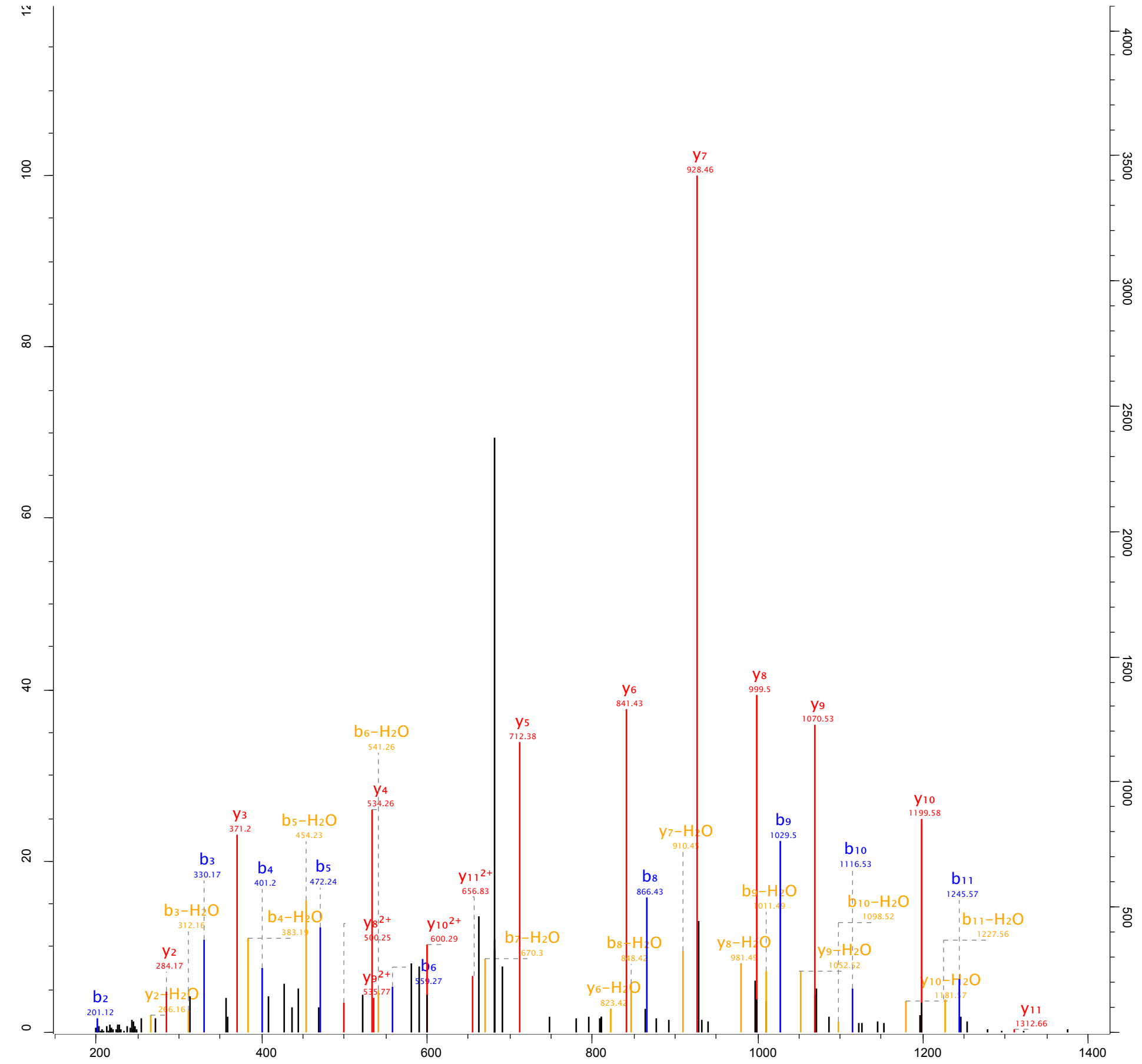


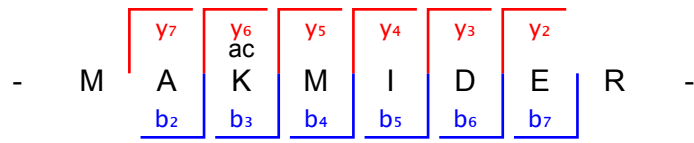
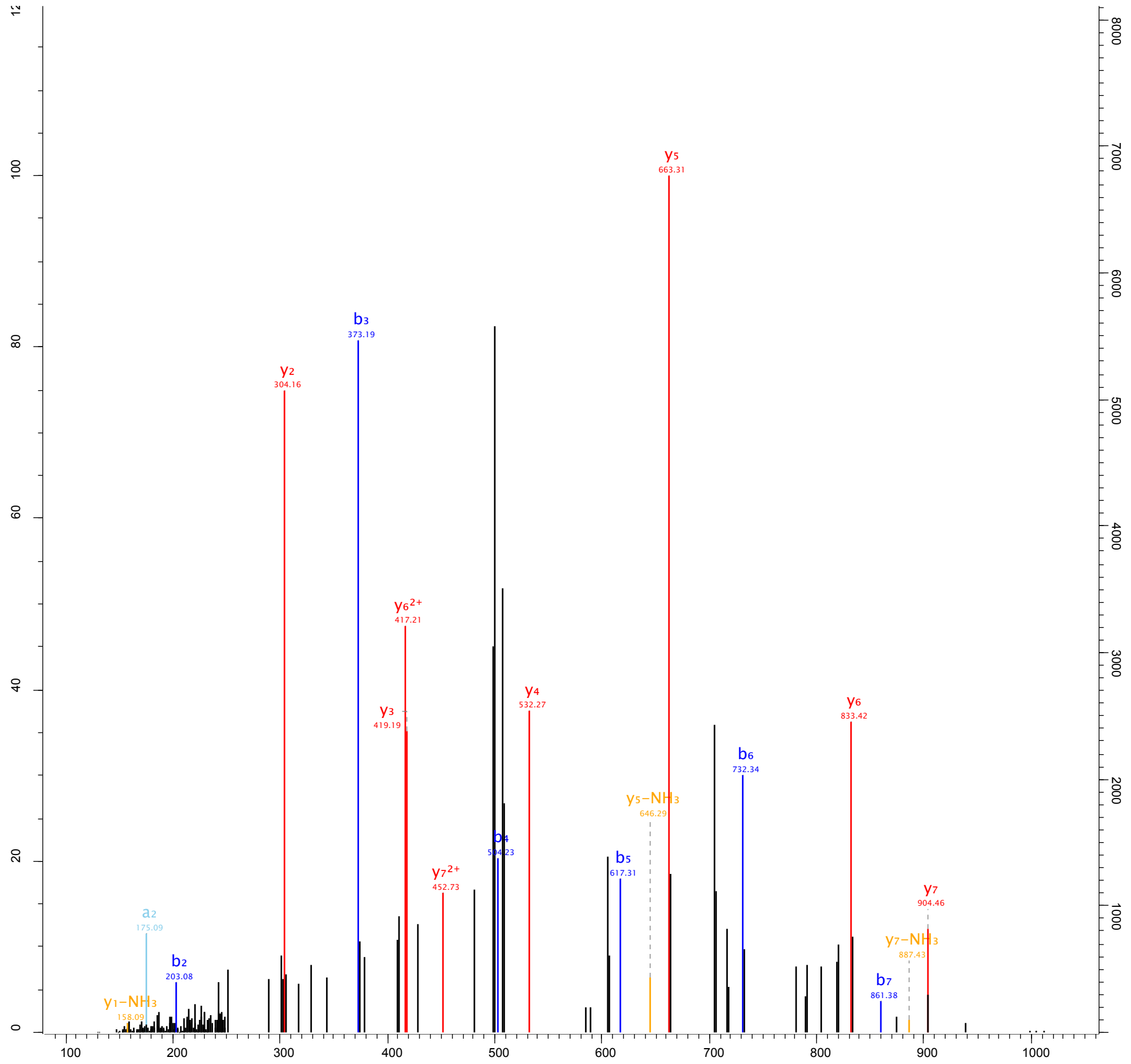


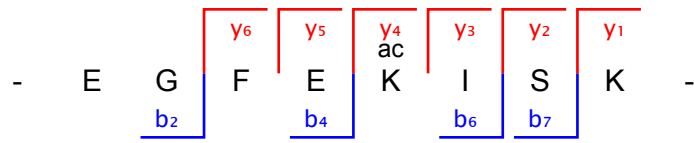
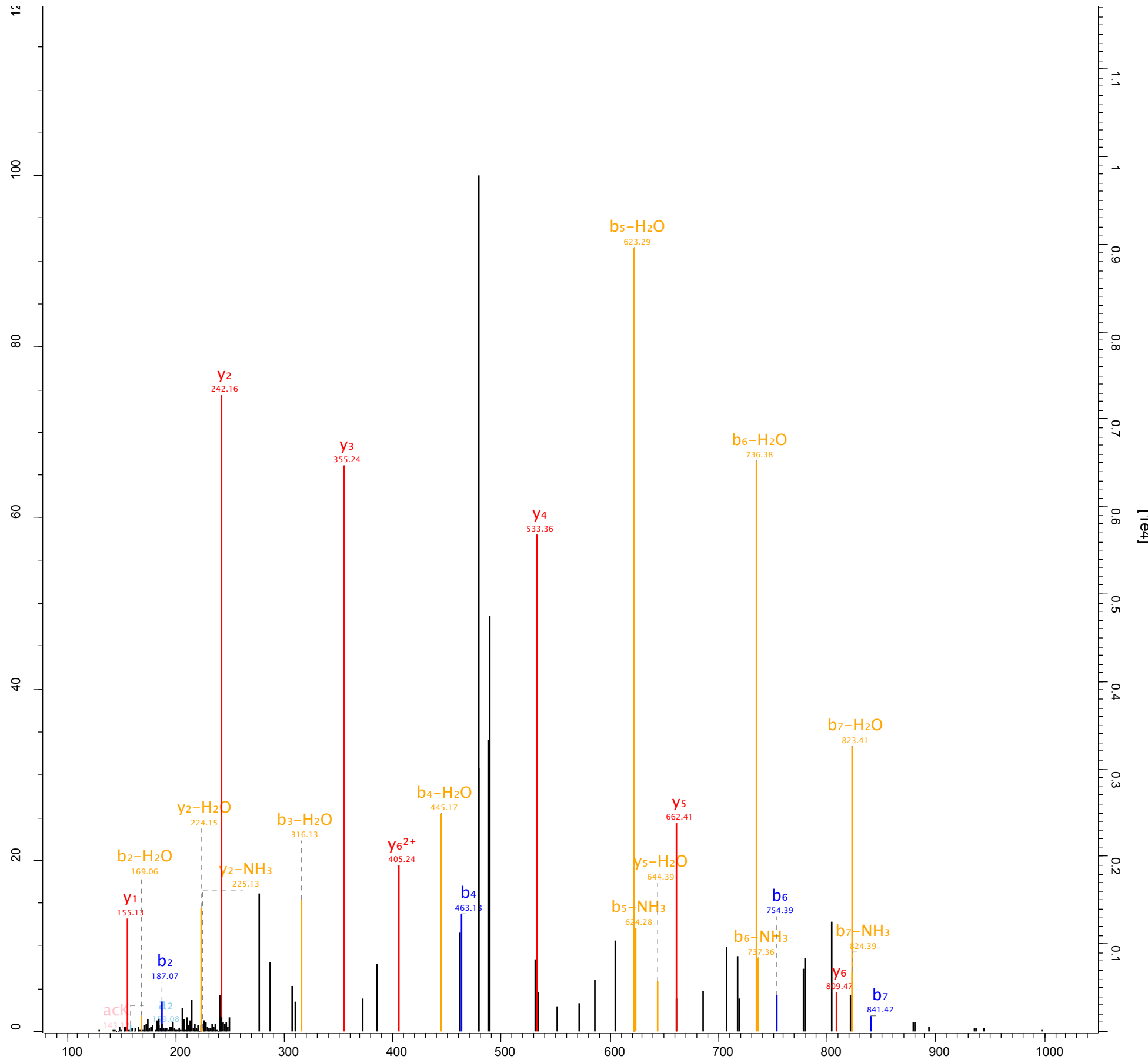




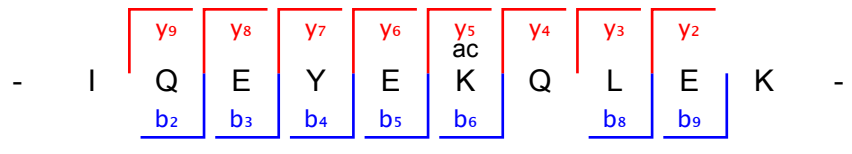
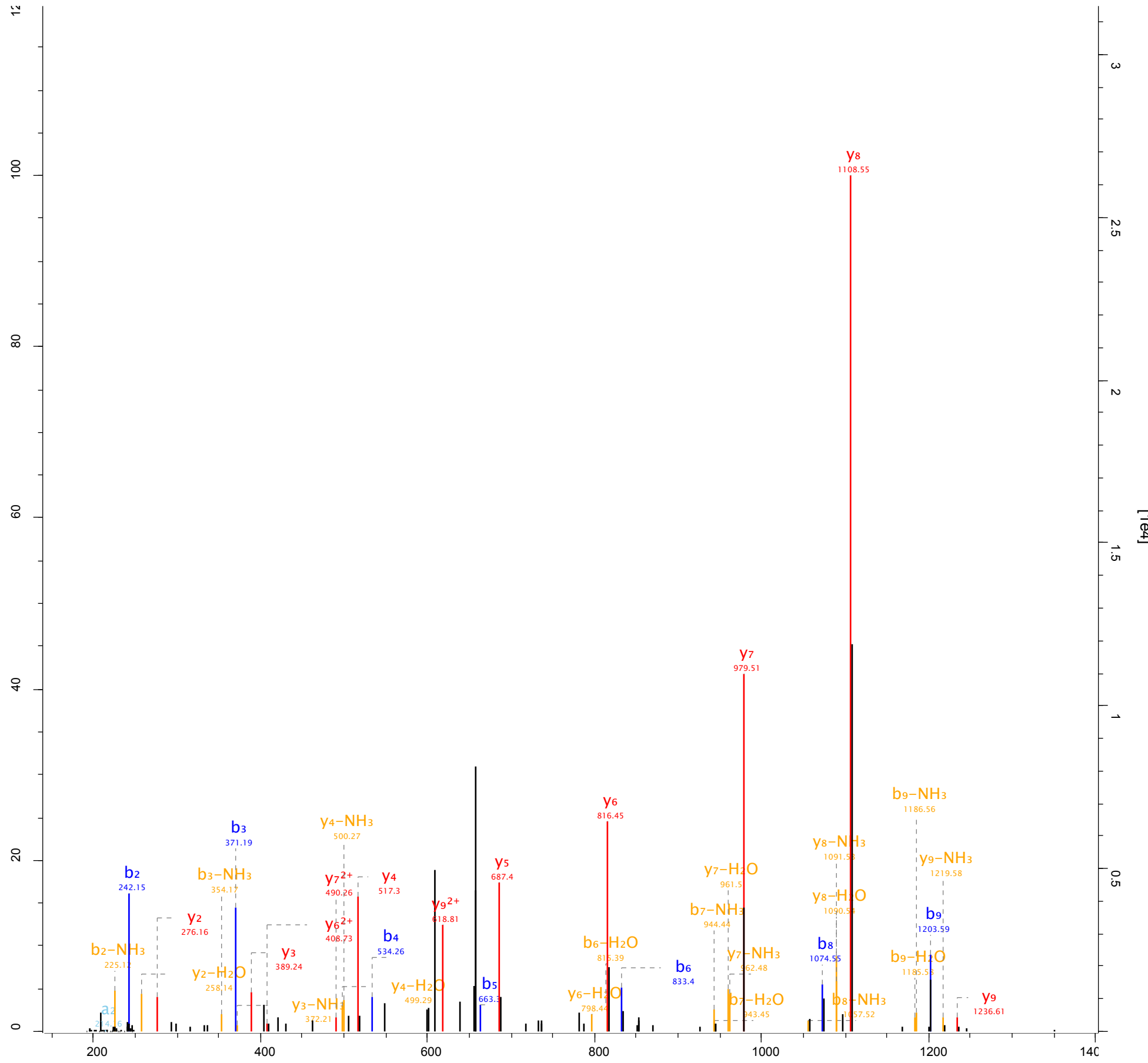


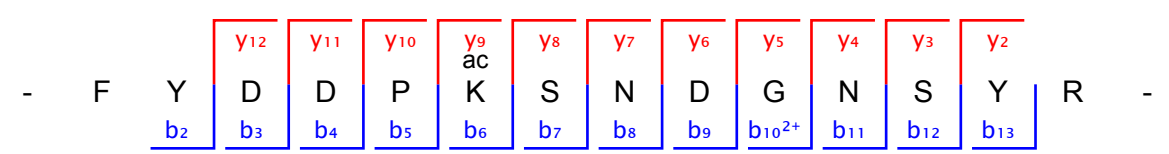
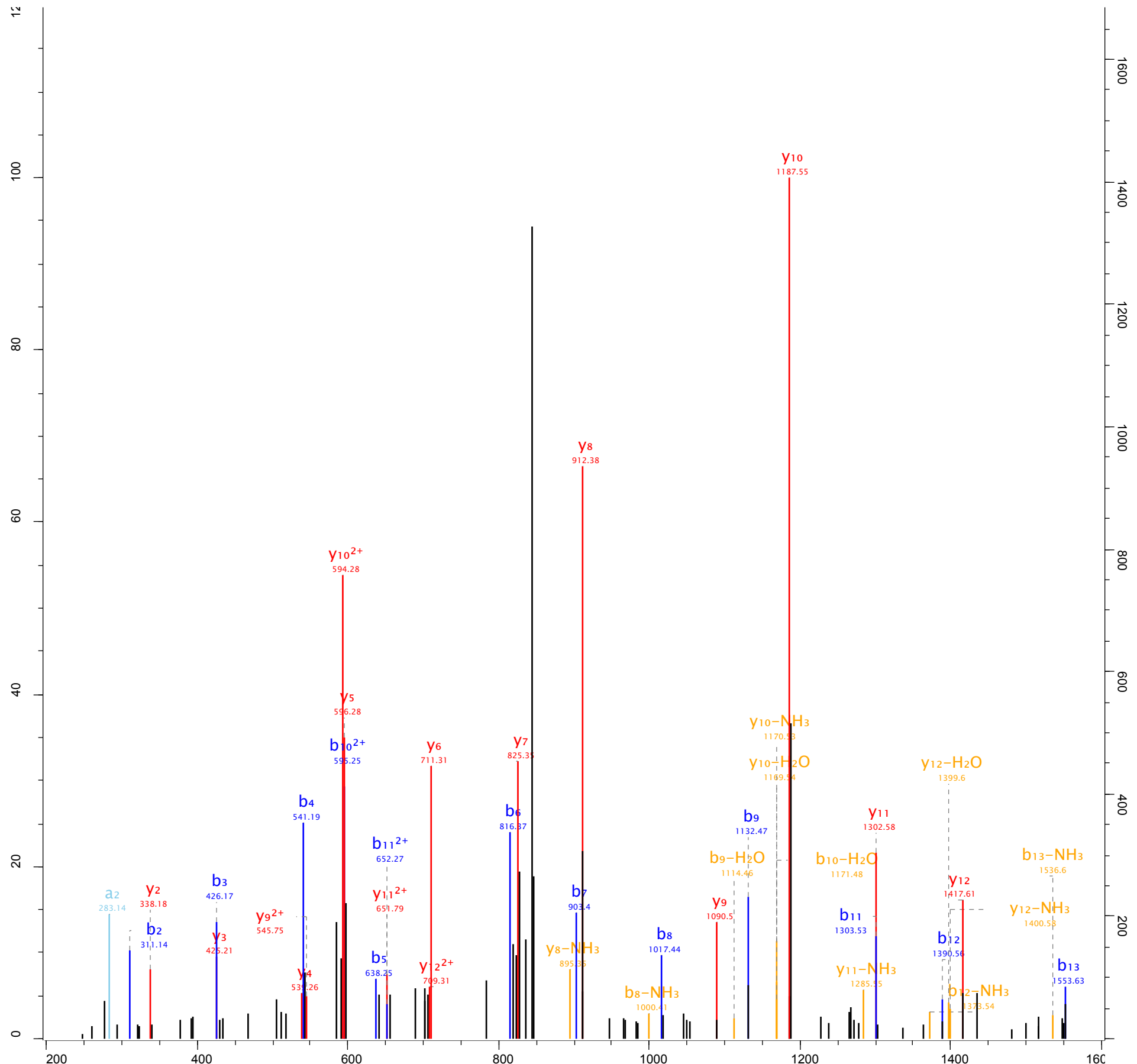






Raw file 062513_SCW_II_53_5_Vargas_Enriched Scan 15649 Method ITMS; CID Score 248.21 m/z 675.35 Gene names Gm10250;Atp5h





062513_SCW_II_53_5_Vargas_Enriched

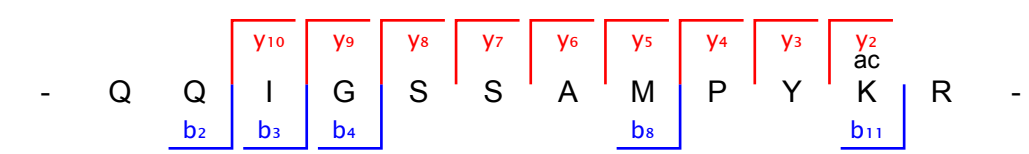
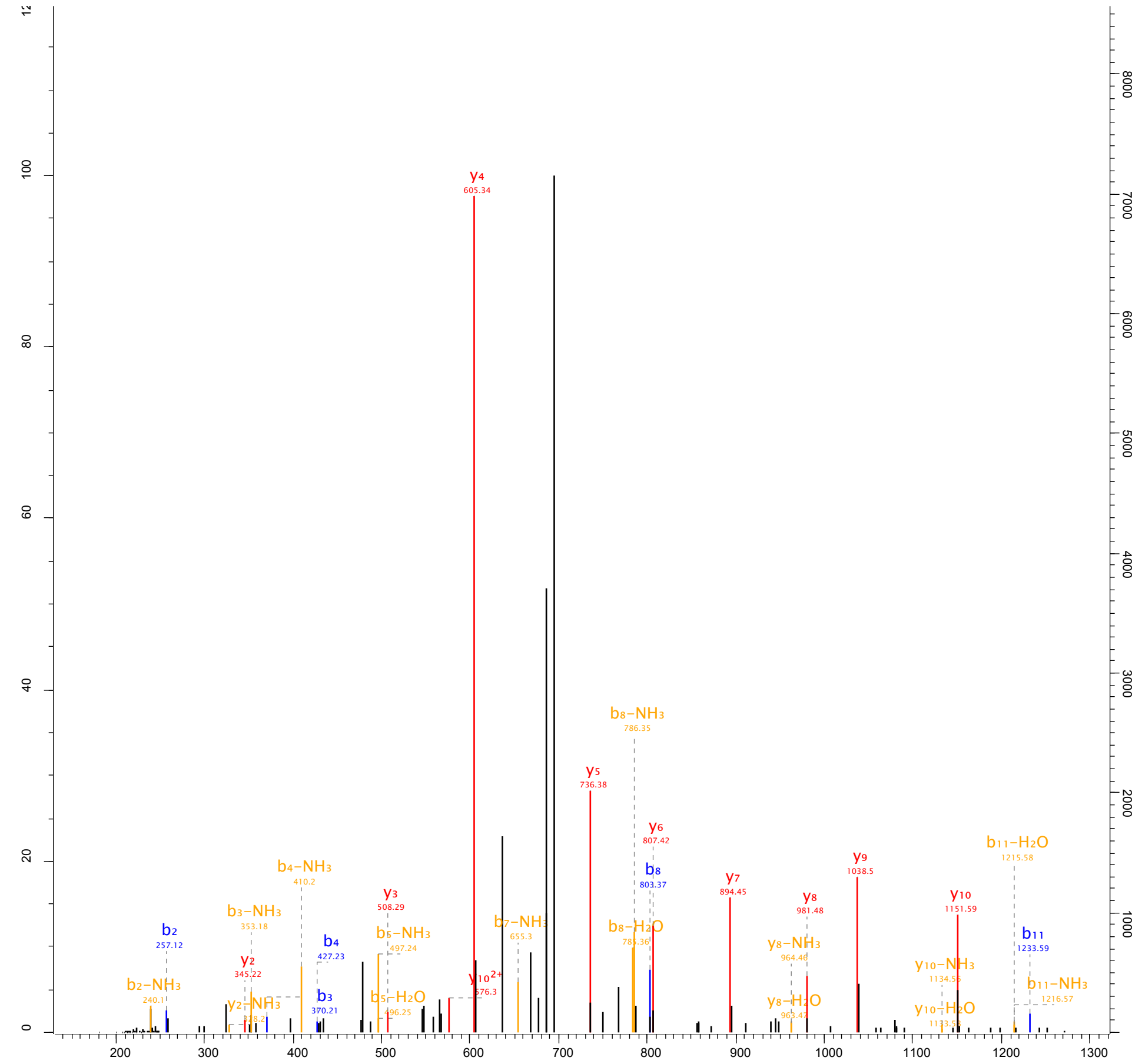
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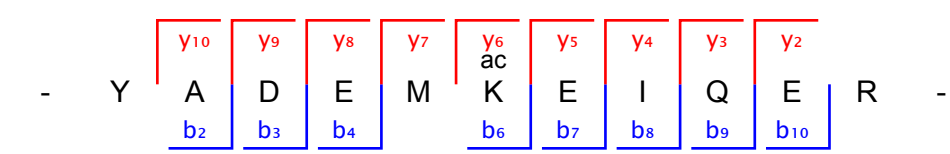
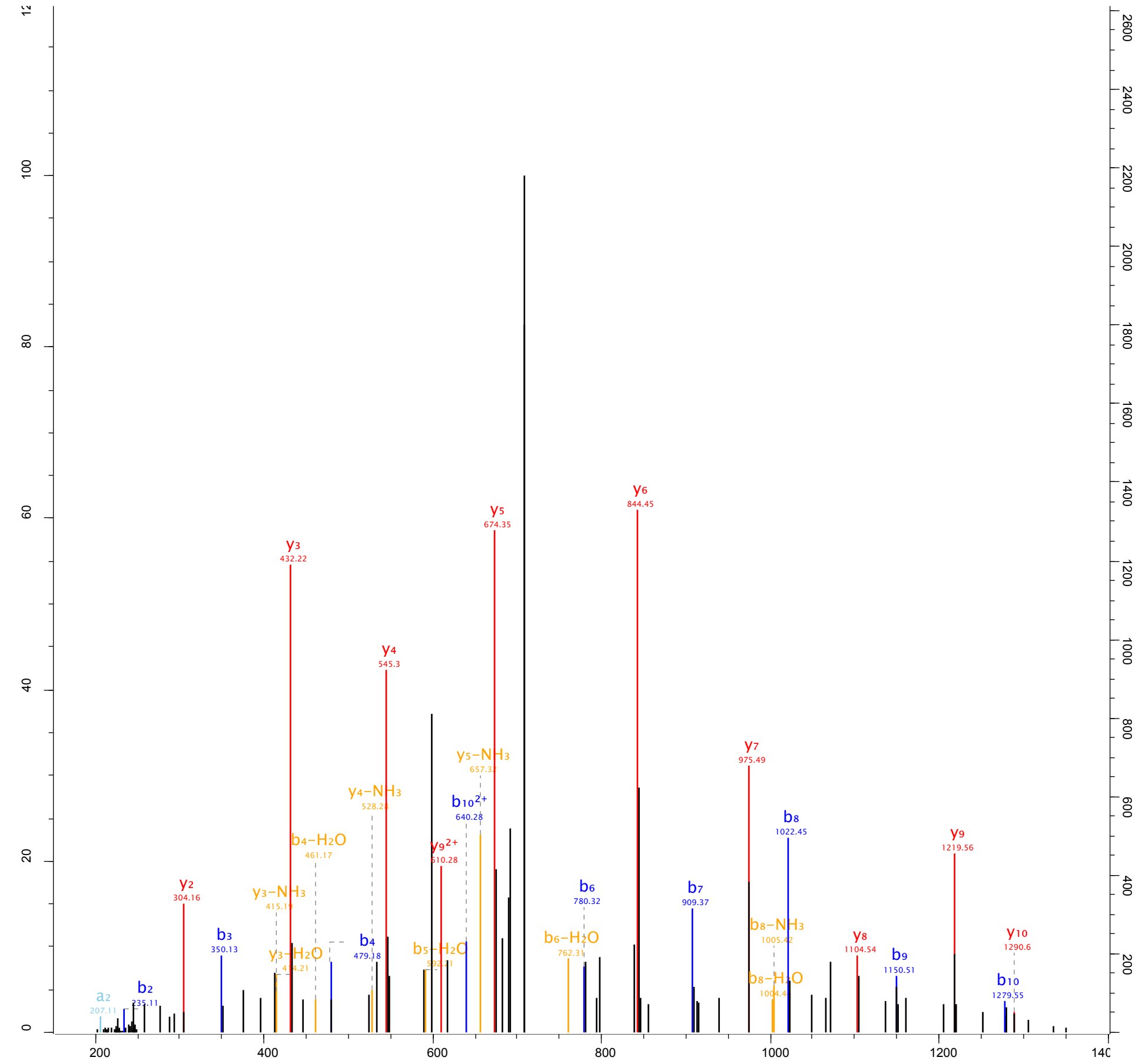
ITMS; CID

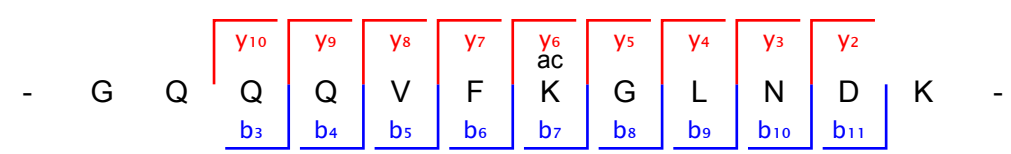
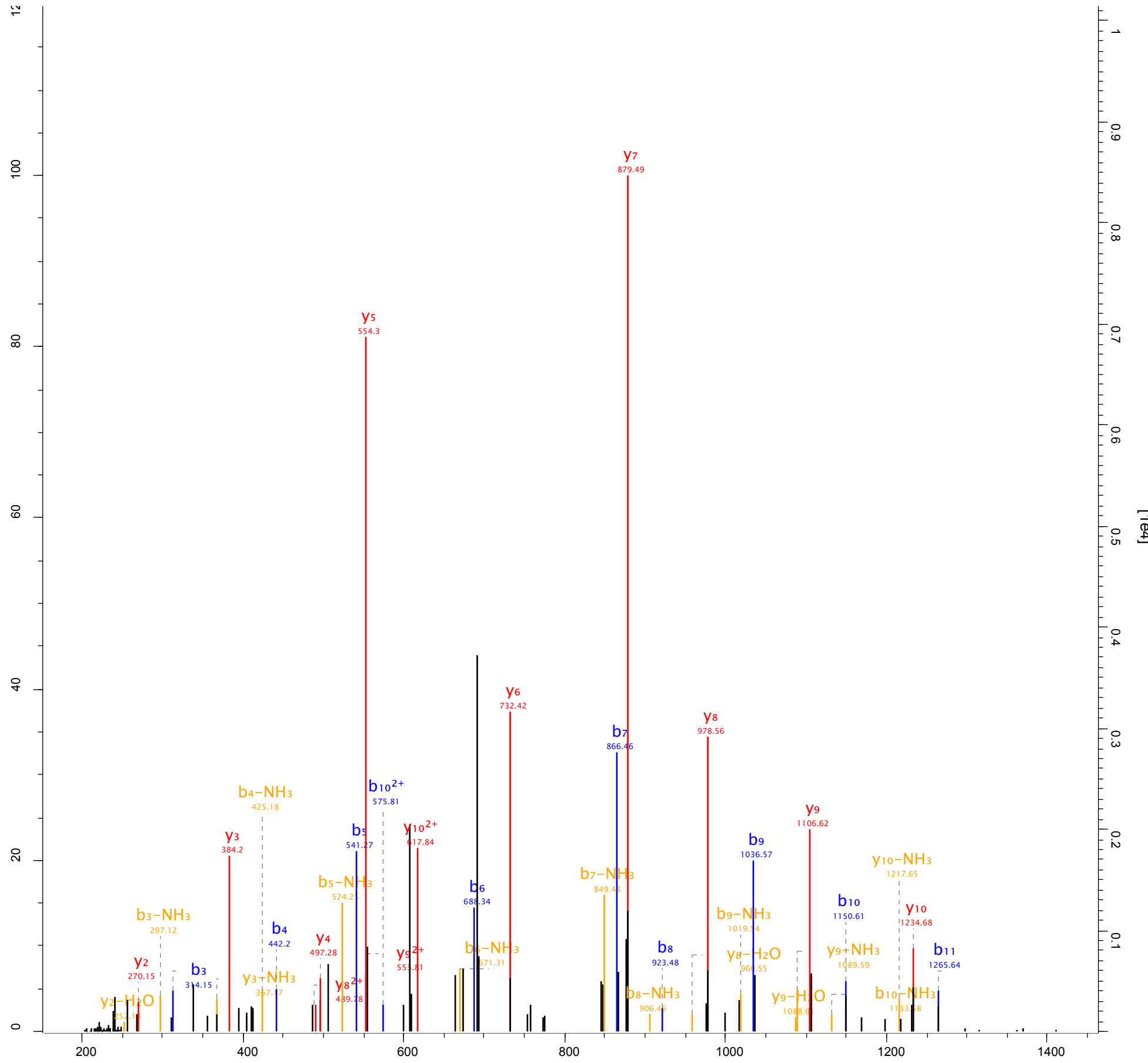
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704.36

Adsl

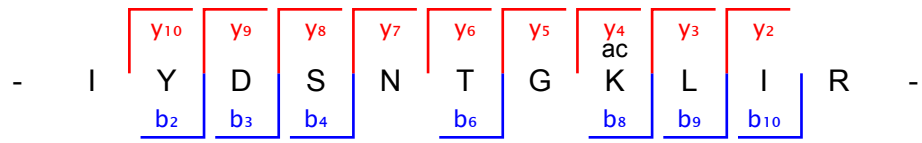
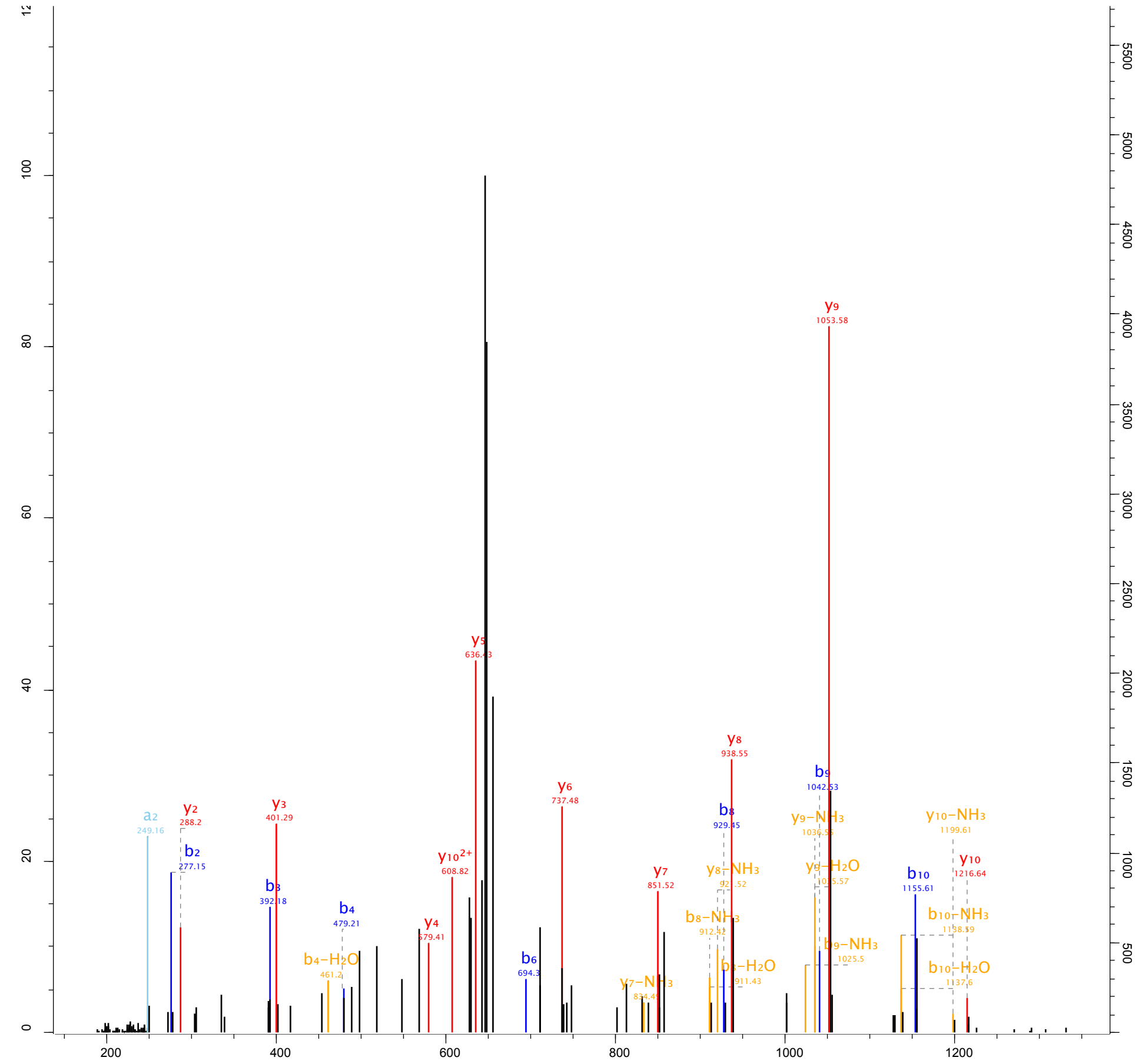


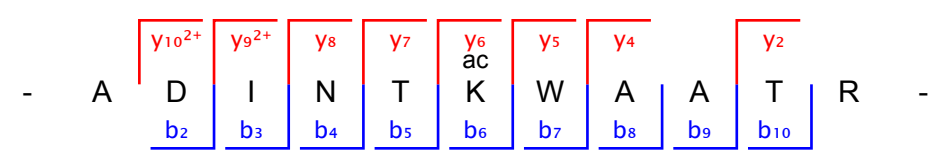
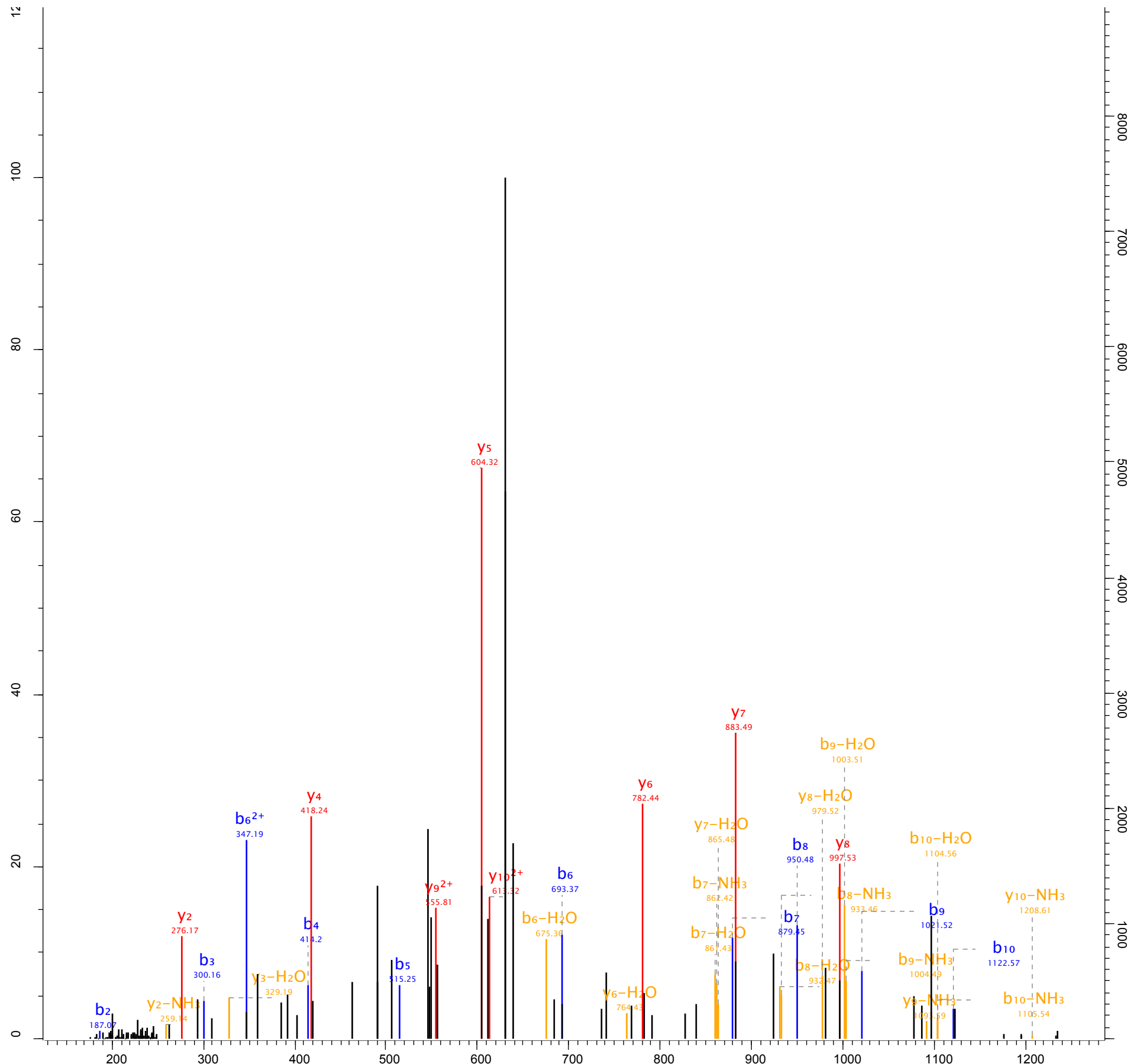




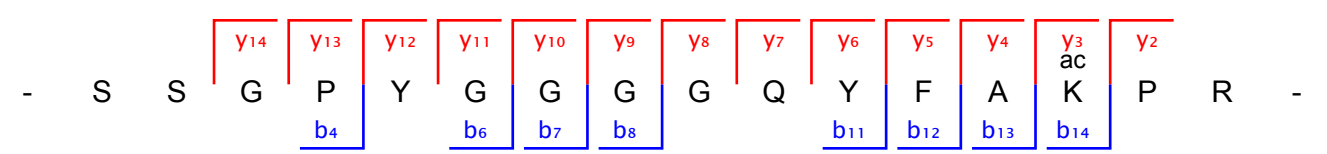
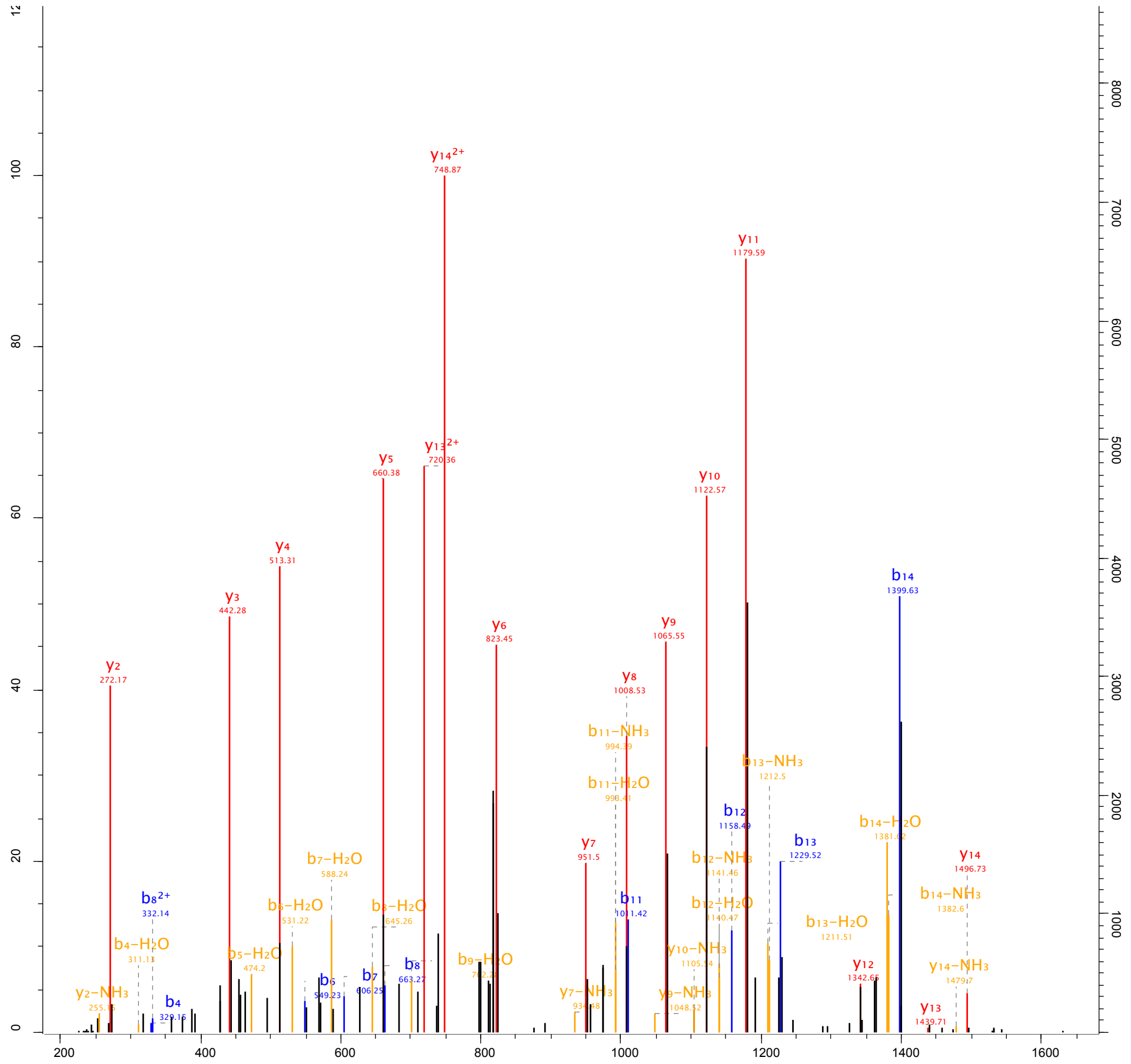
Raw file
062513_SCW_II_53_5_Vargas_Enriched

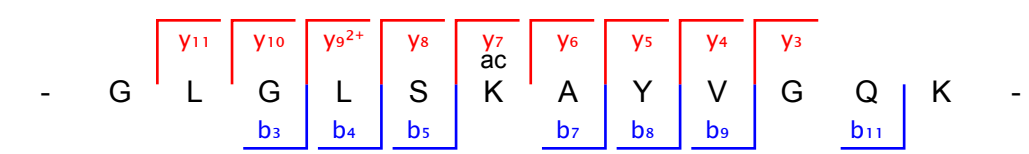
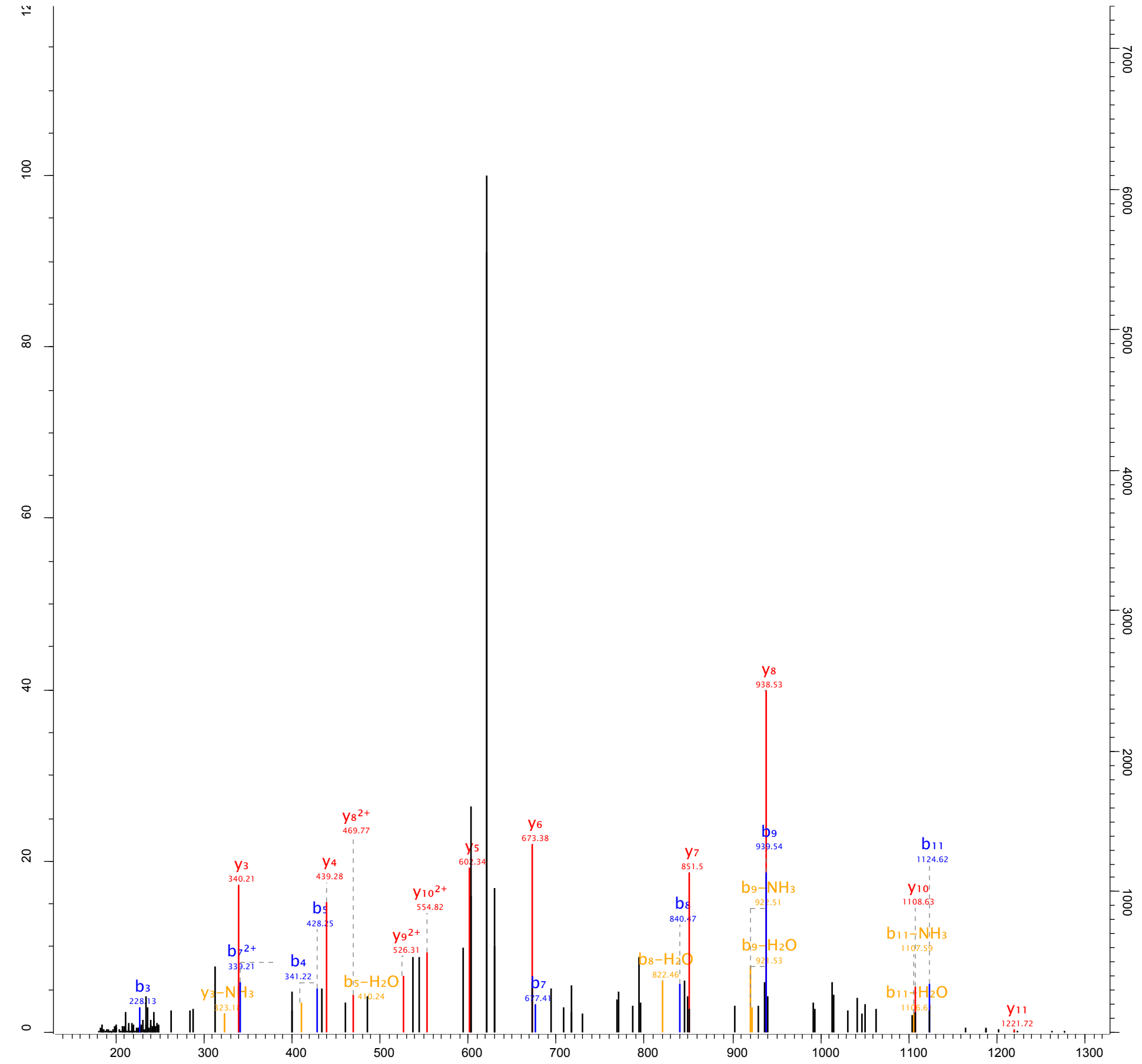
Scan 17173 Method ITMS; CID Score 151.26 m/z 665.87 Gene names Ctdp1

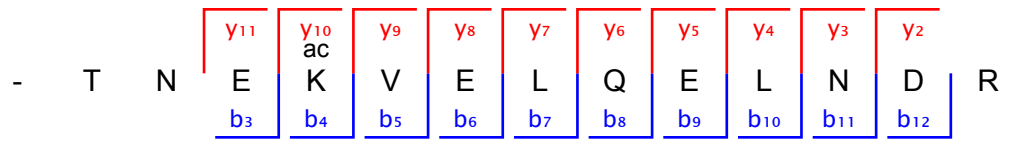
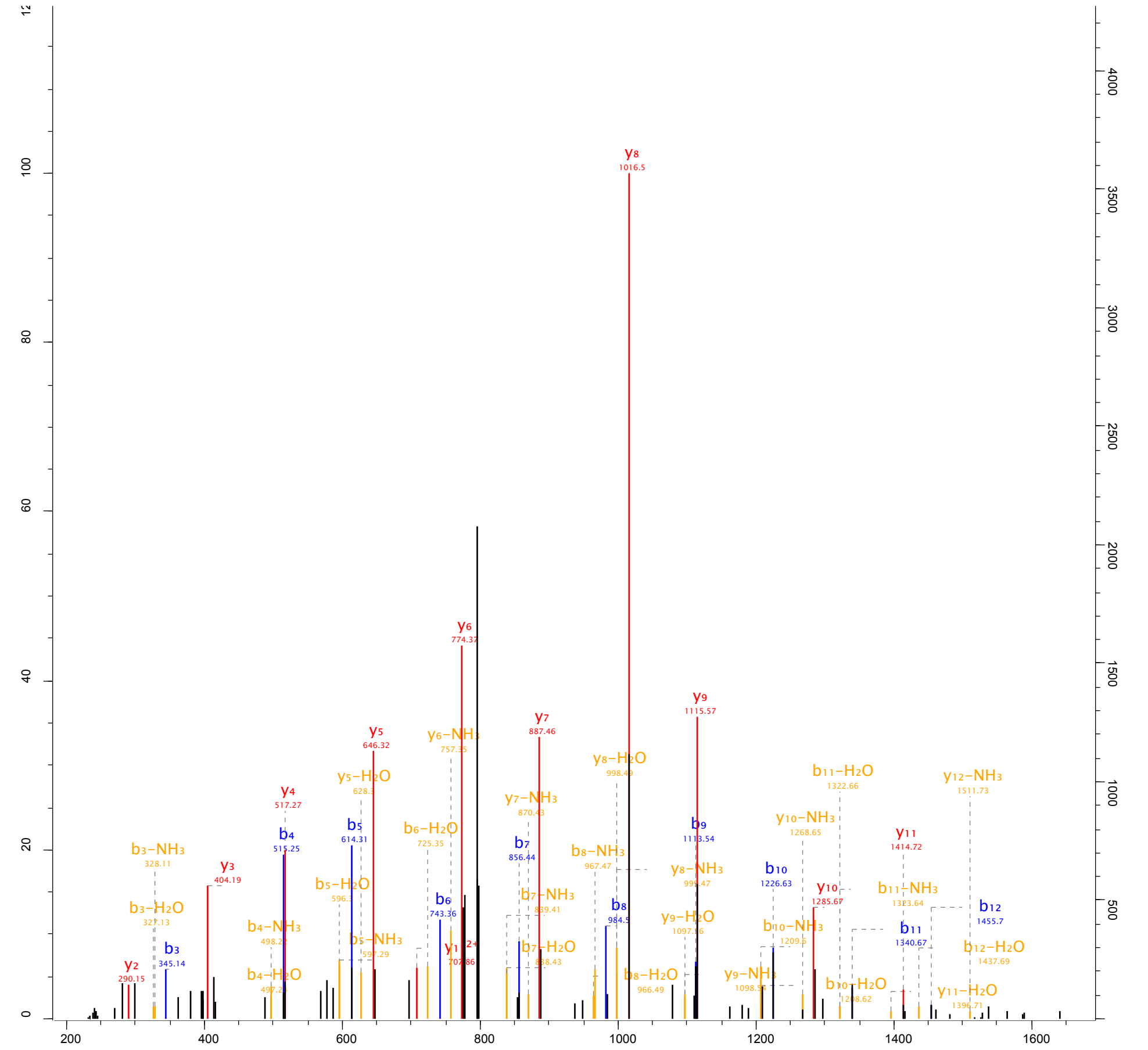




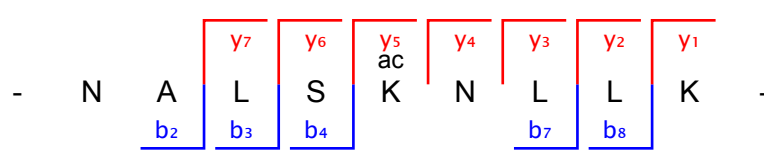
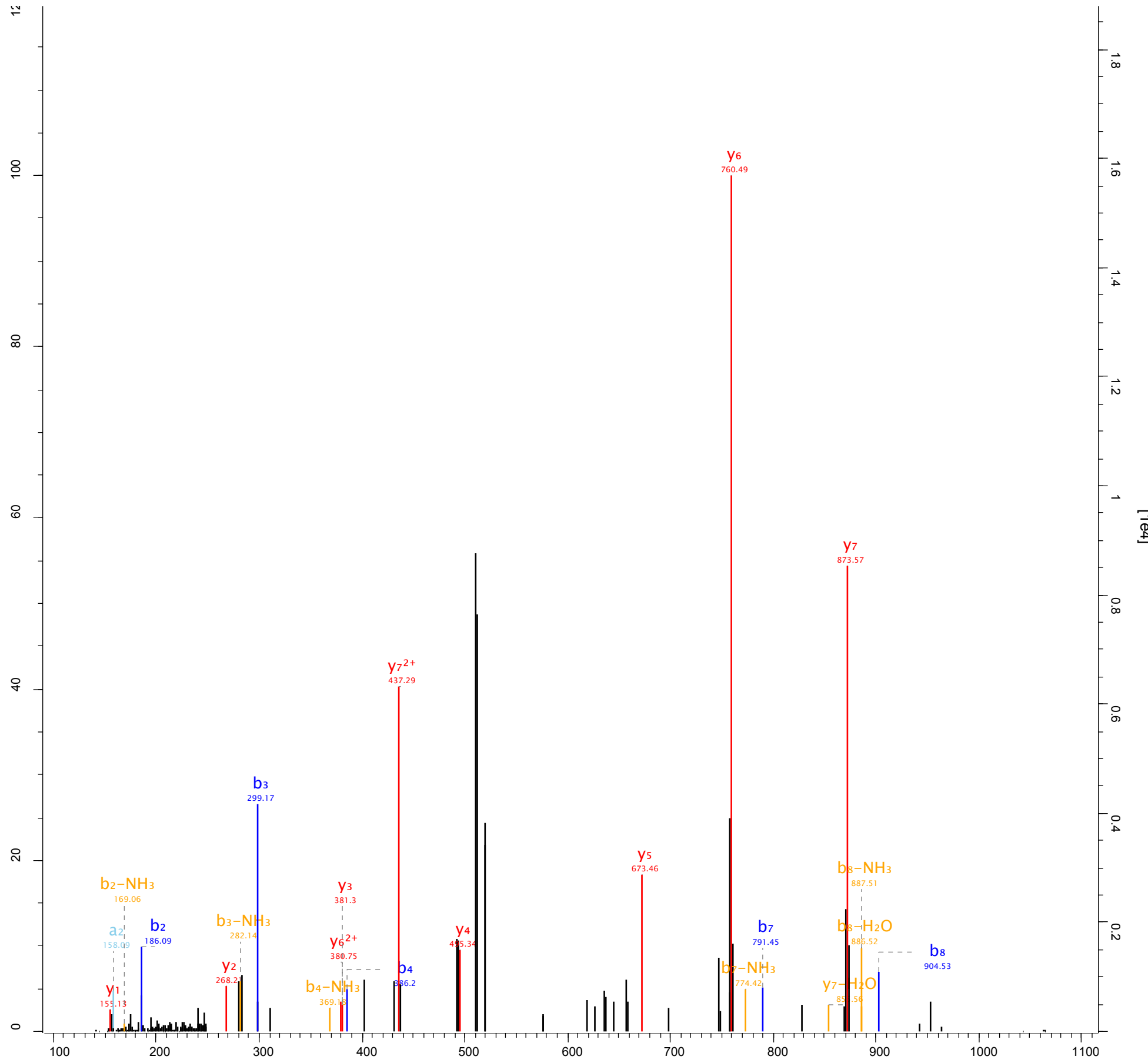
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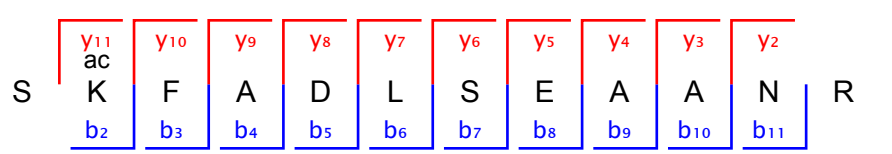
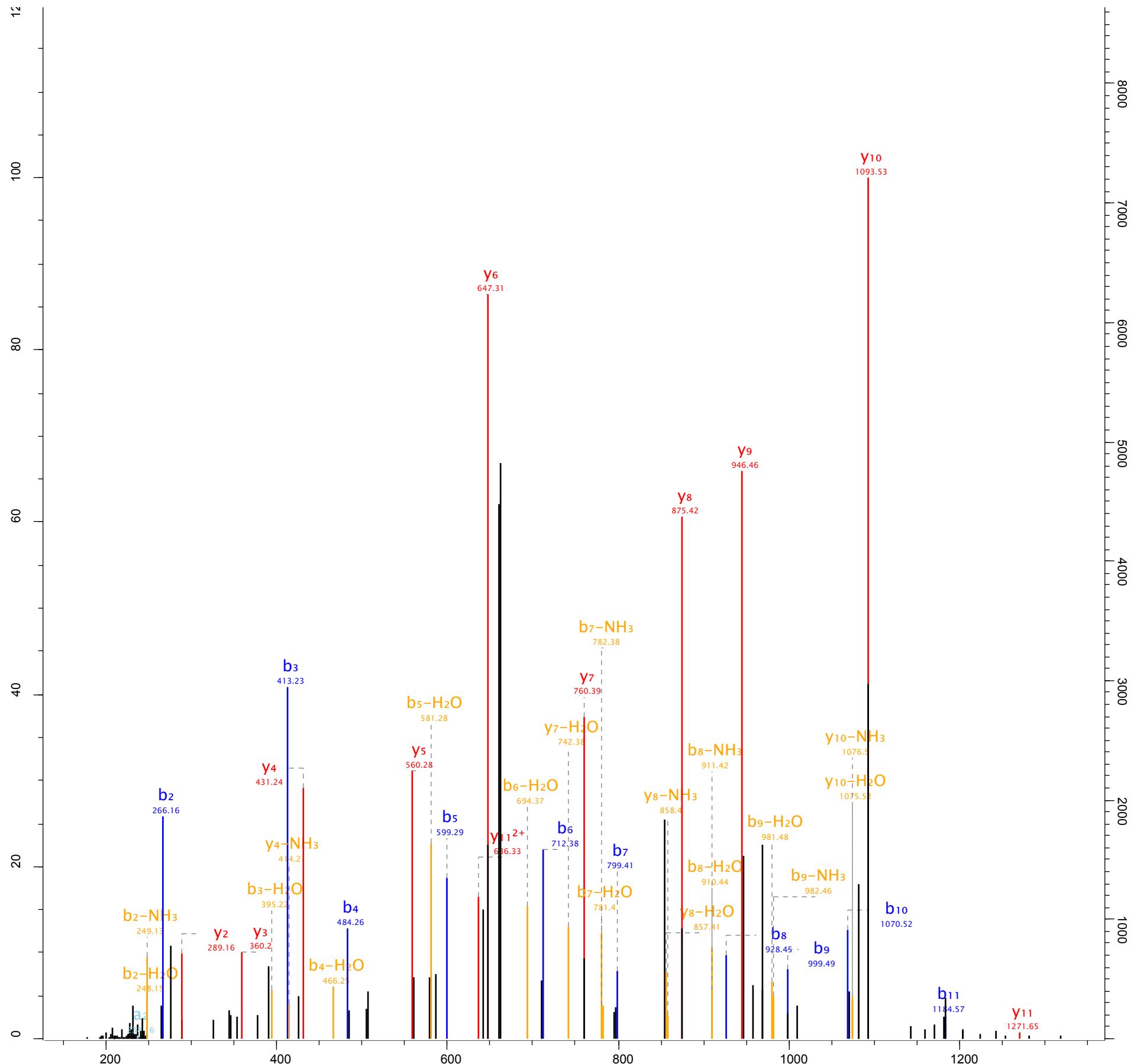


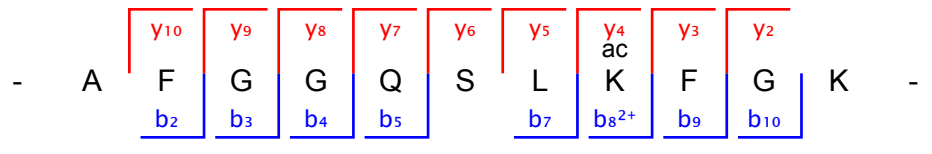
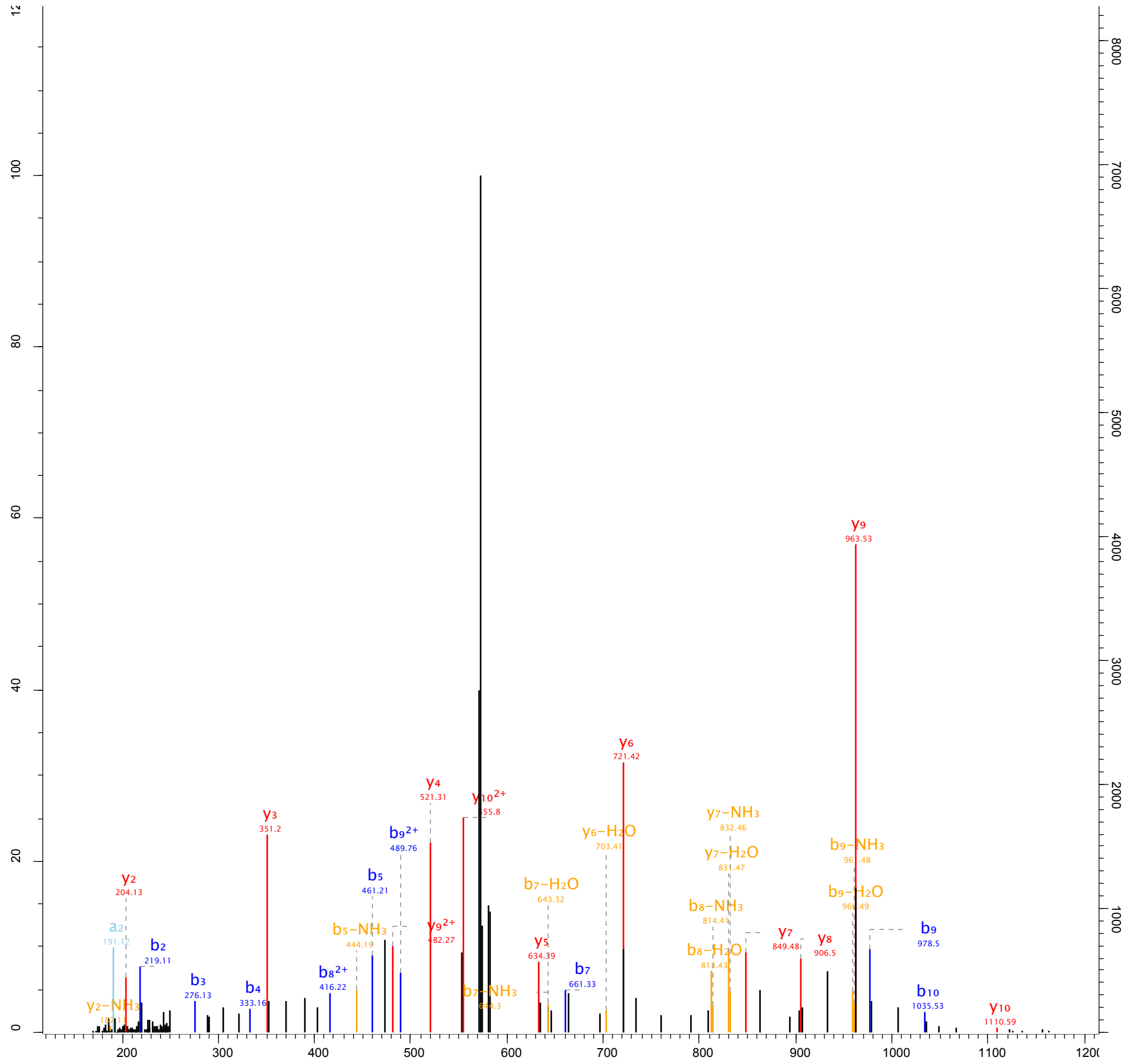


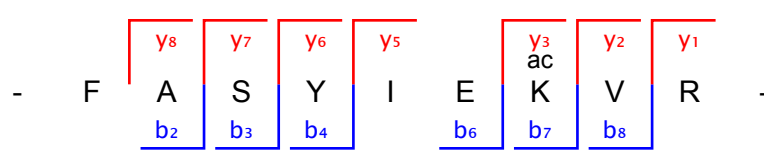
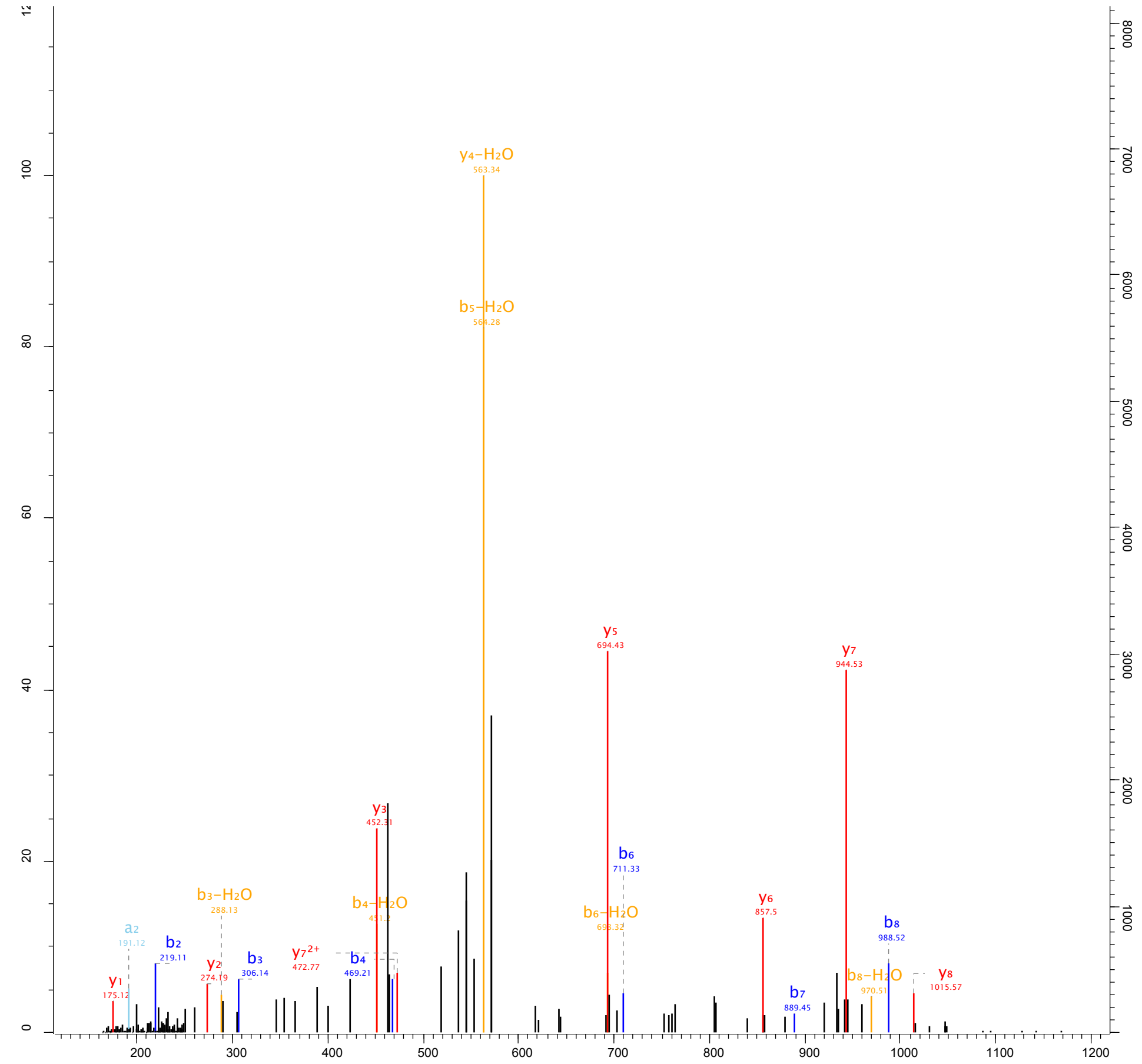


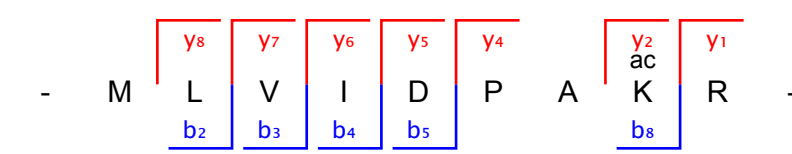
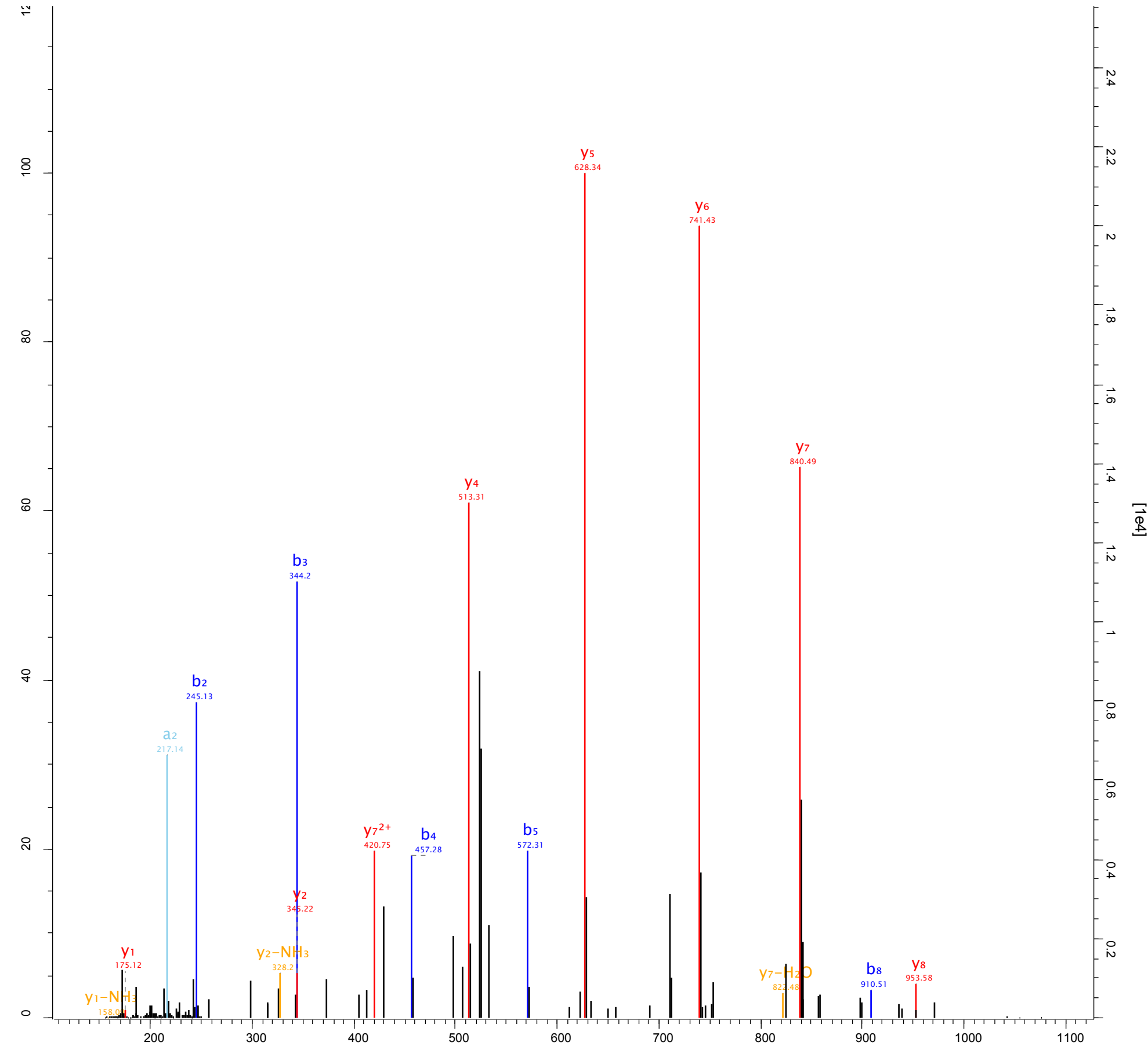
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 Scan: 18674 Method: ITMS; CID Score: 122.94 m/z: 529.83 Gene names: Auh

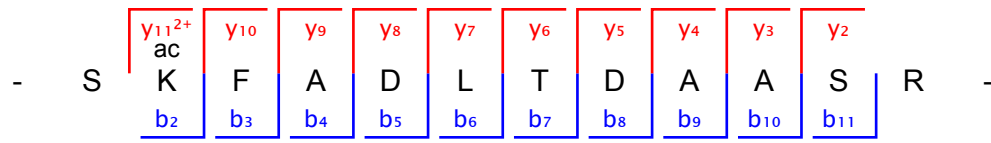
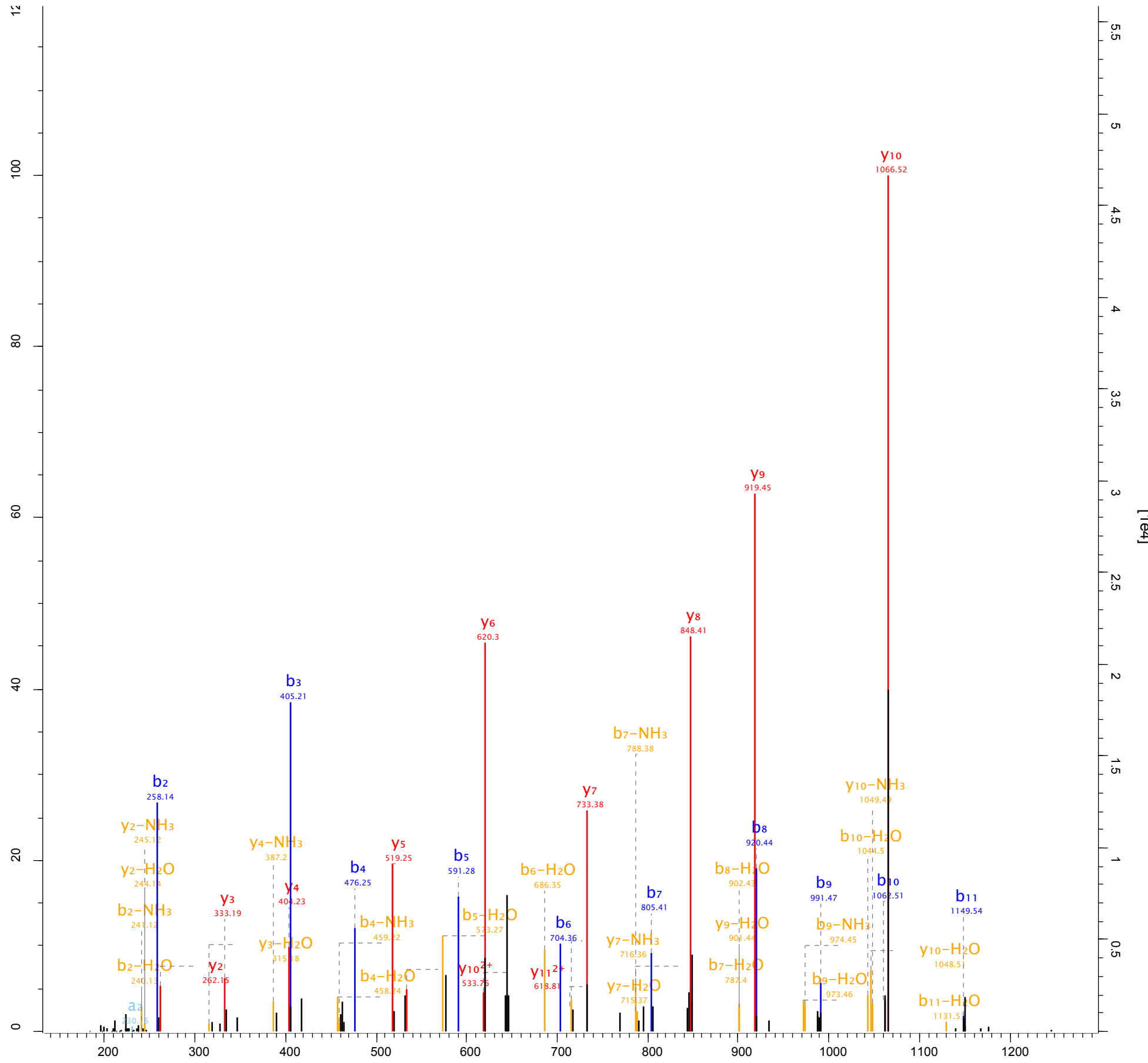


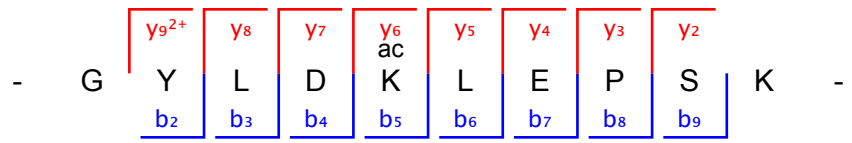
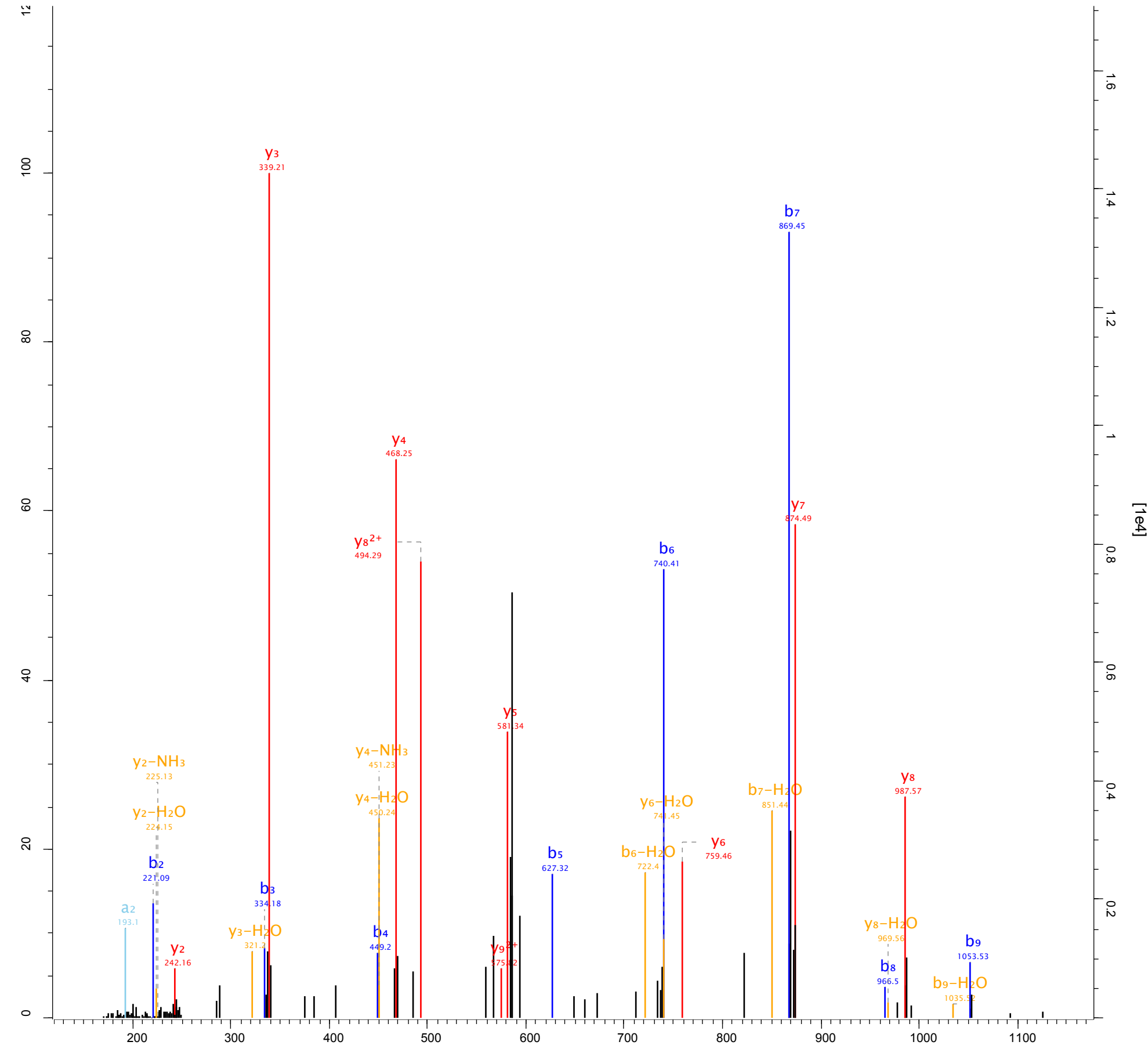


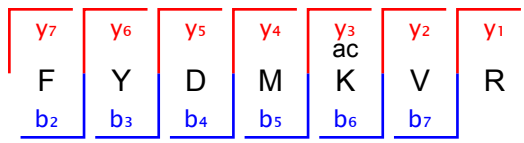
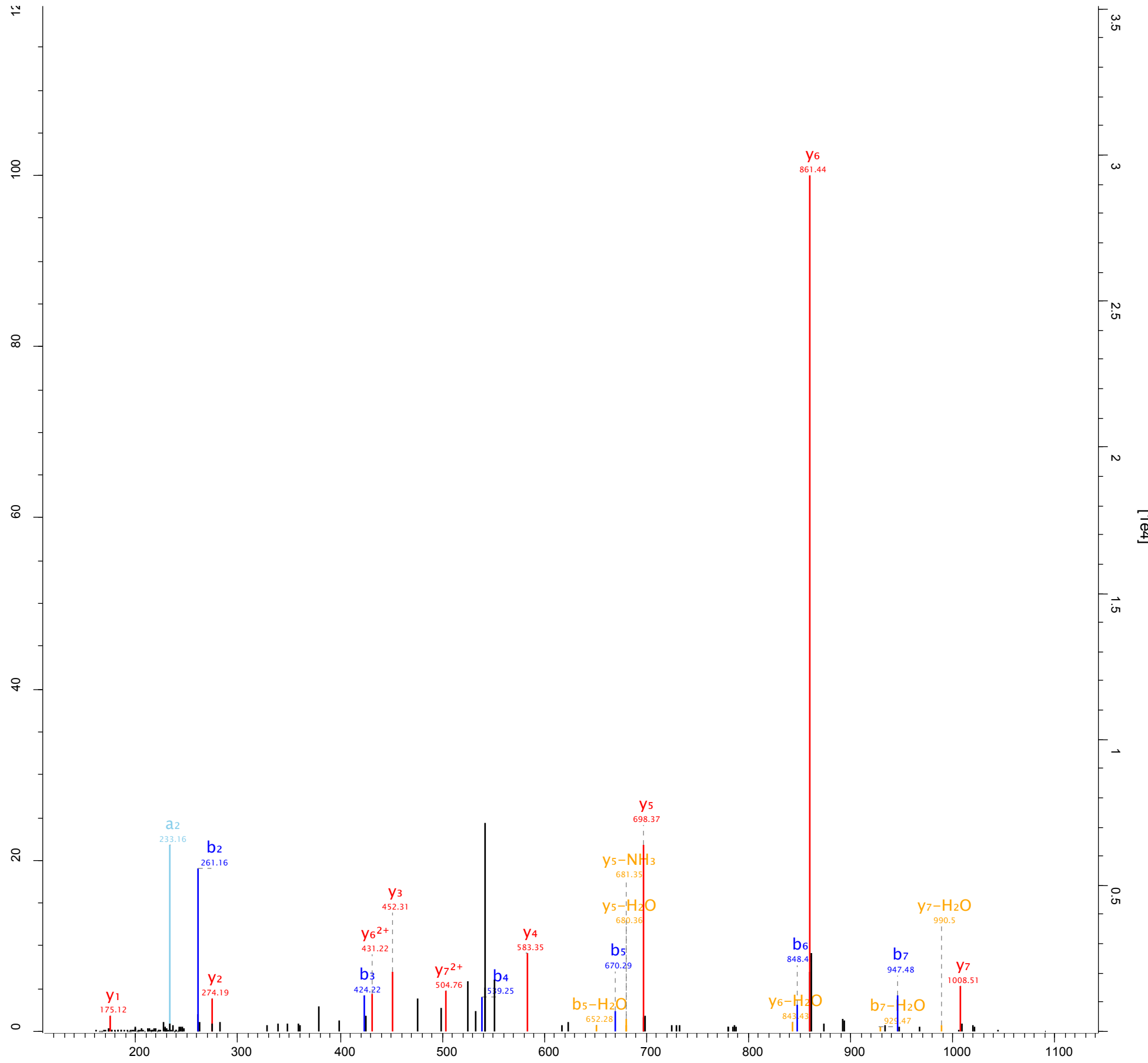


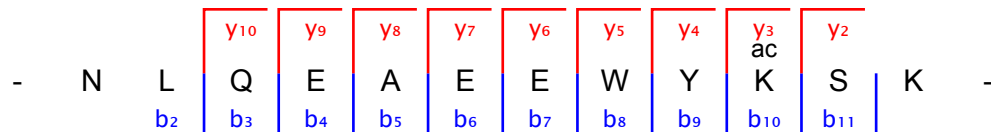
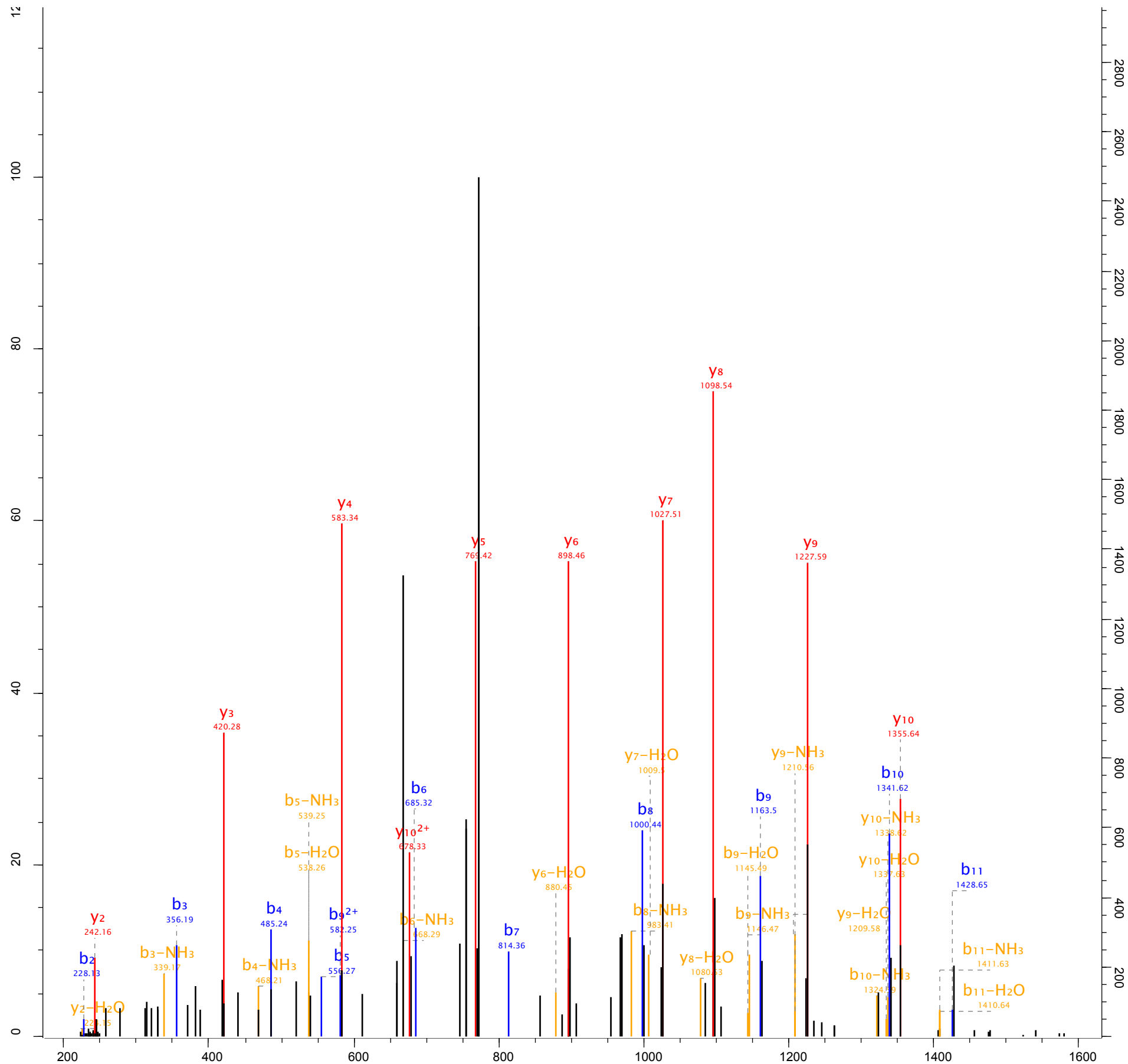


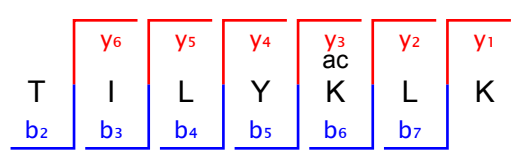
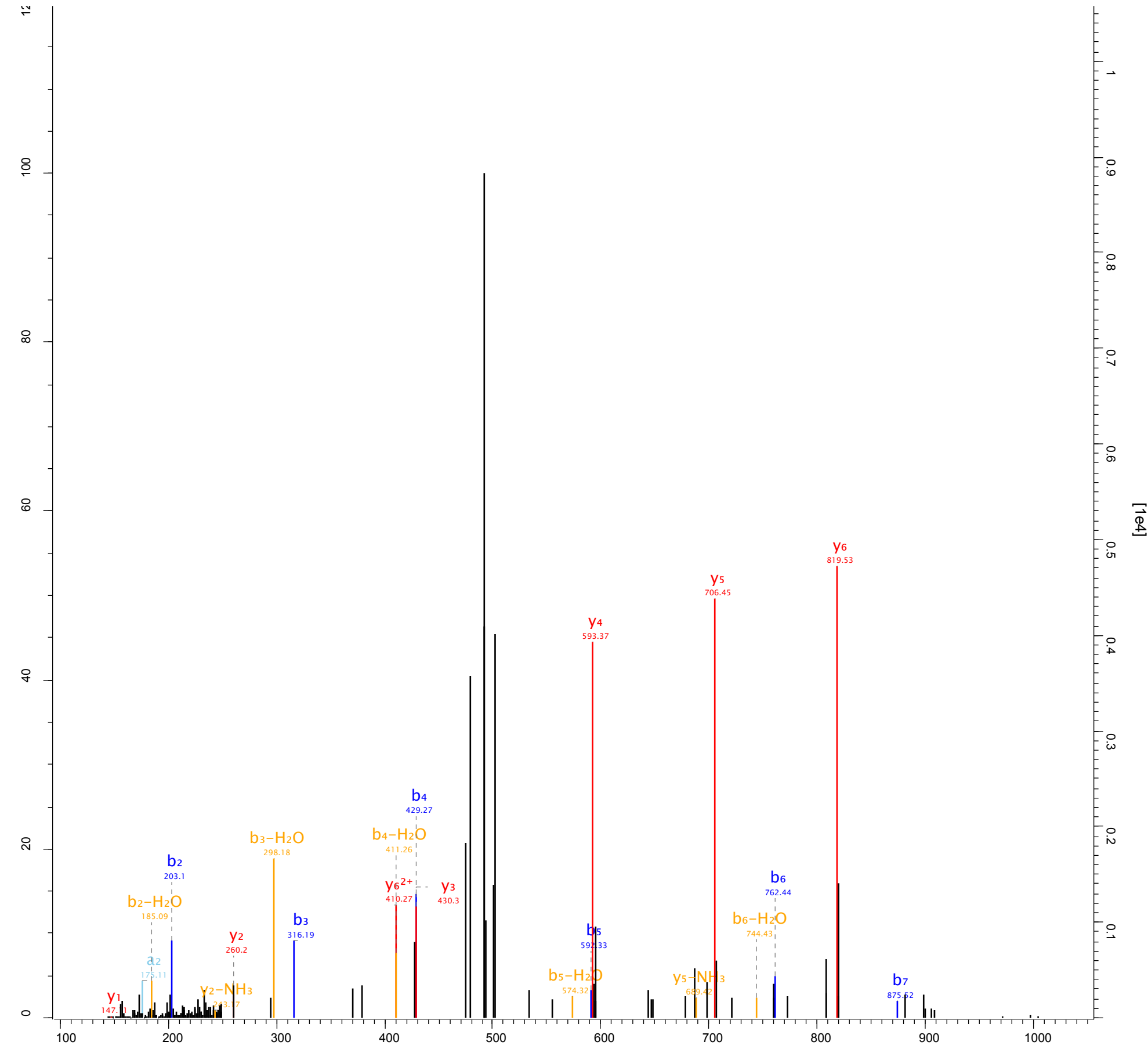












062513_SCW_II_53_5_Vargas_Enriched

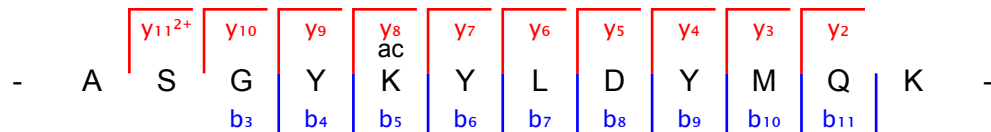
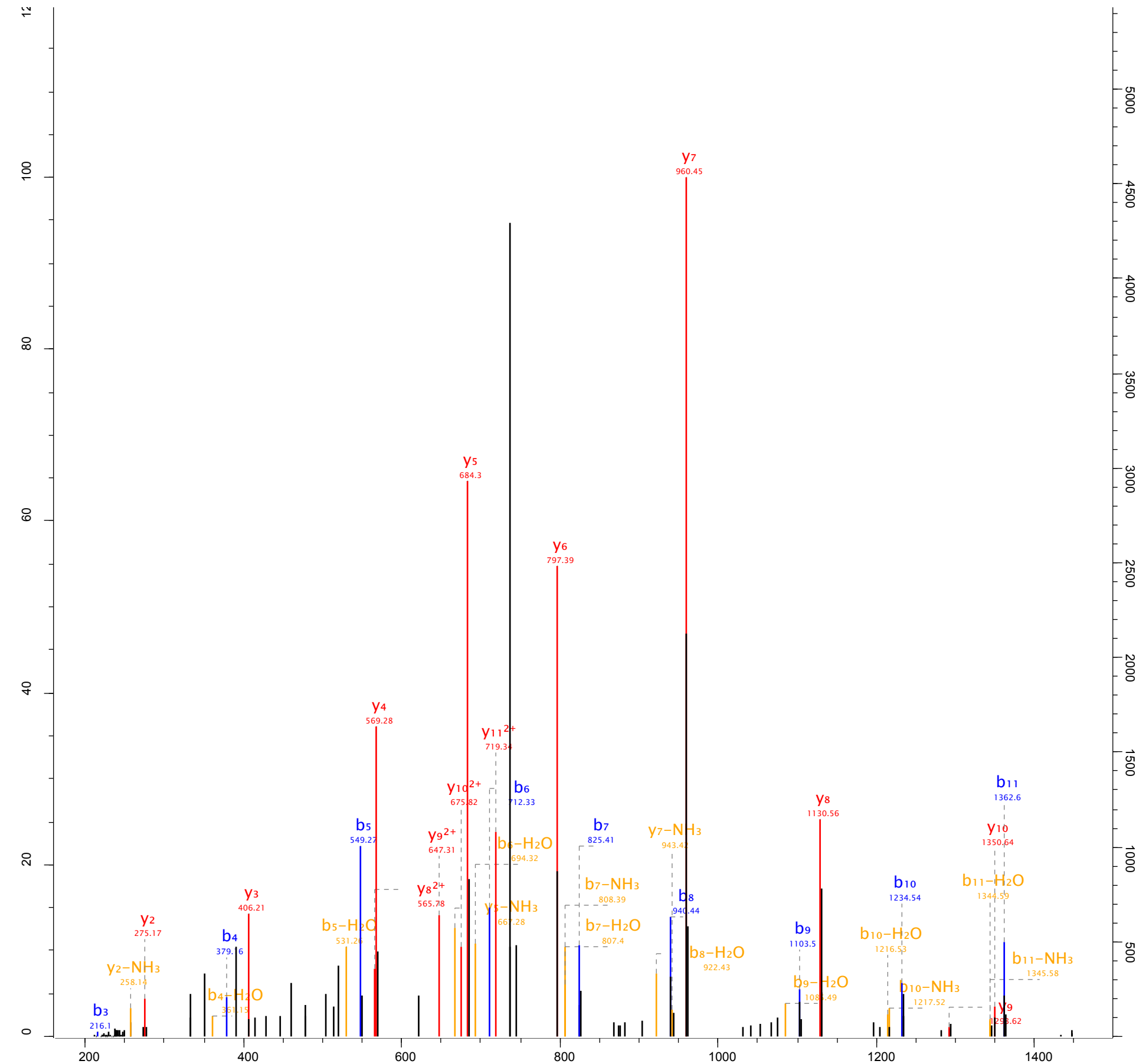
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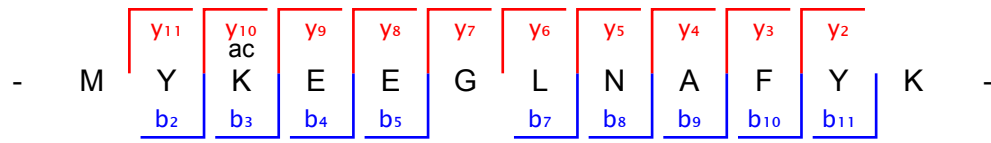
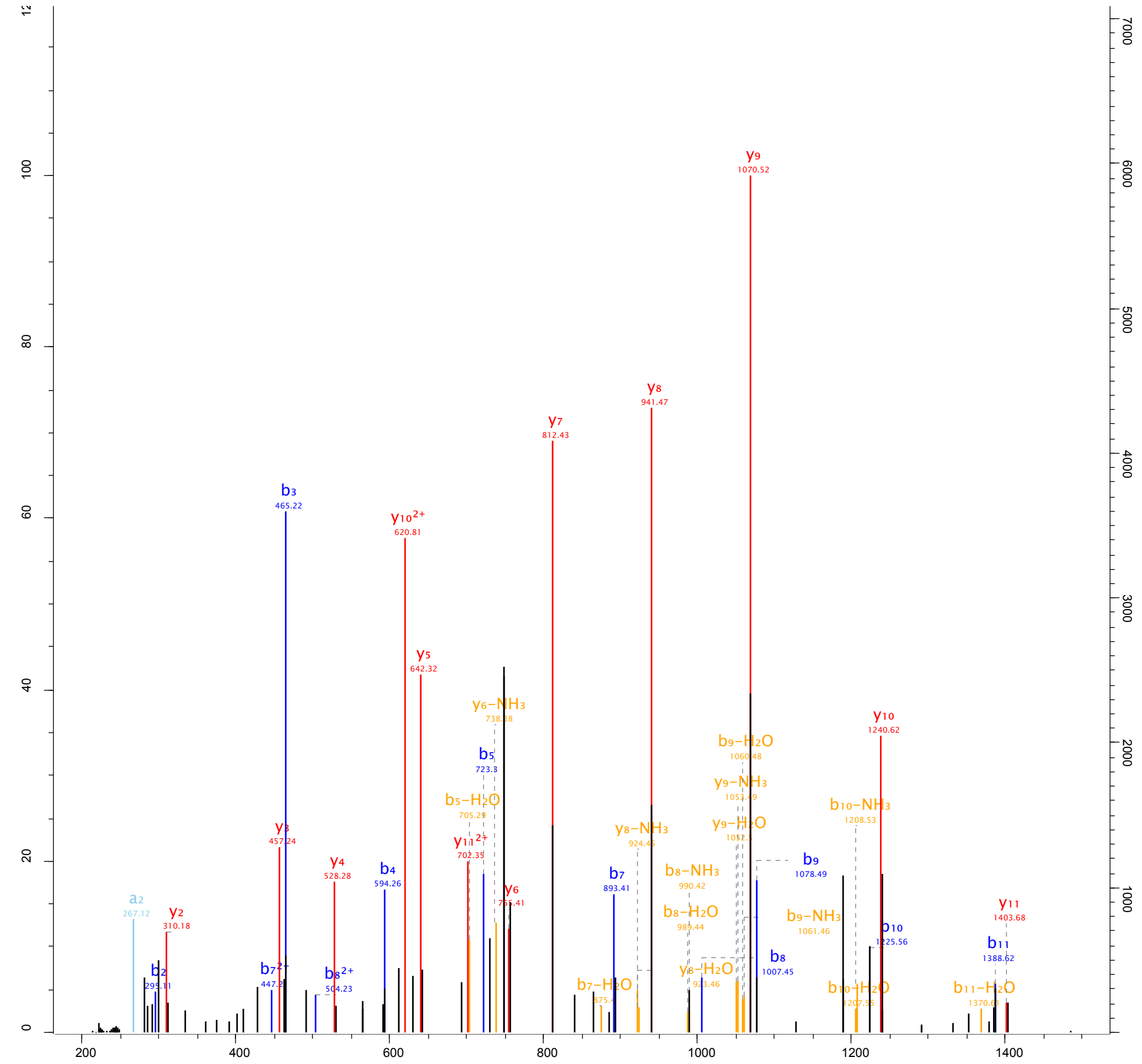
ITMS; CID

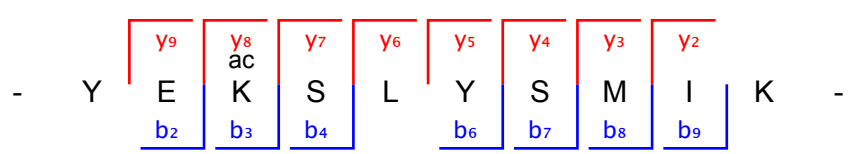
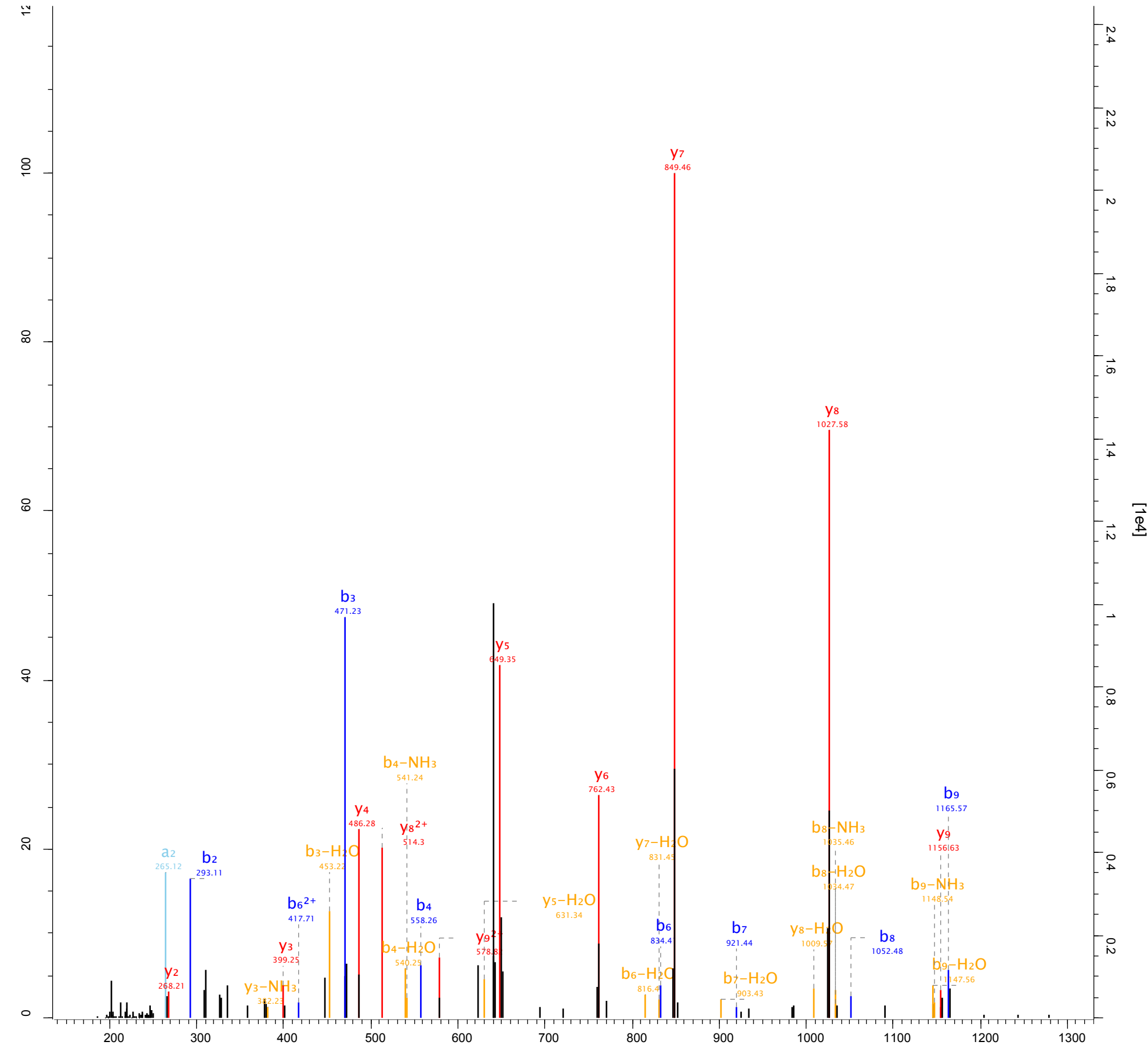
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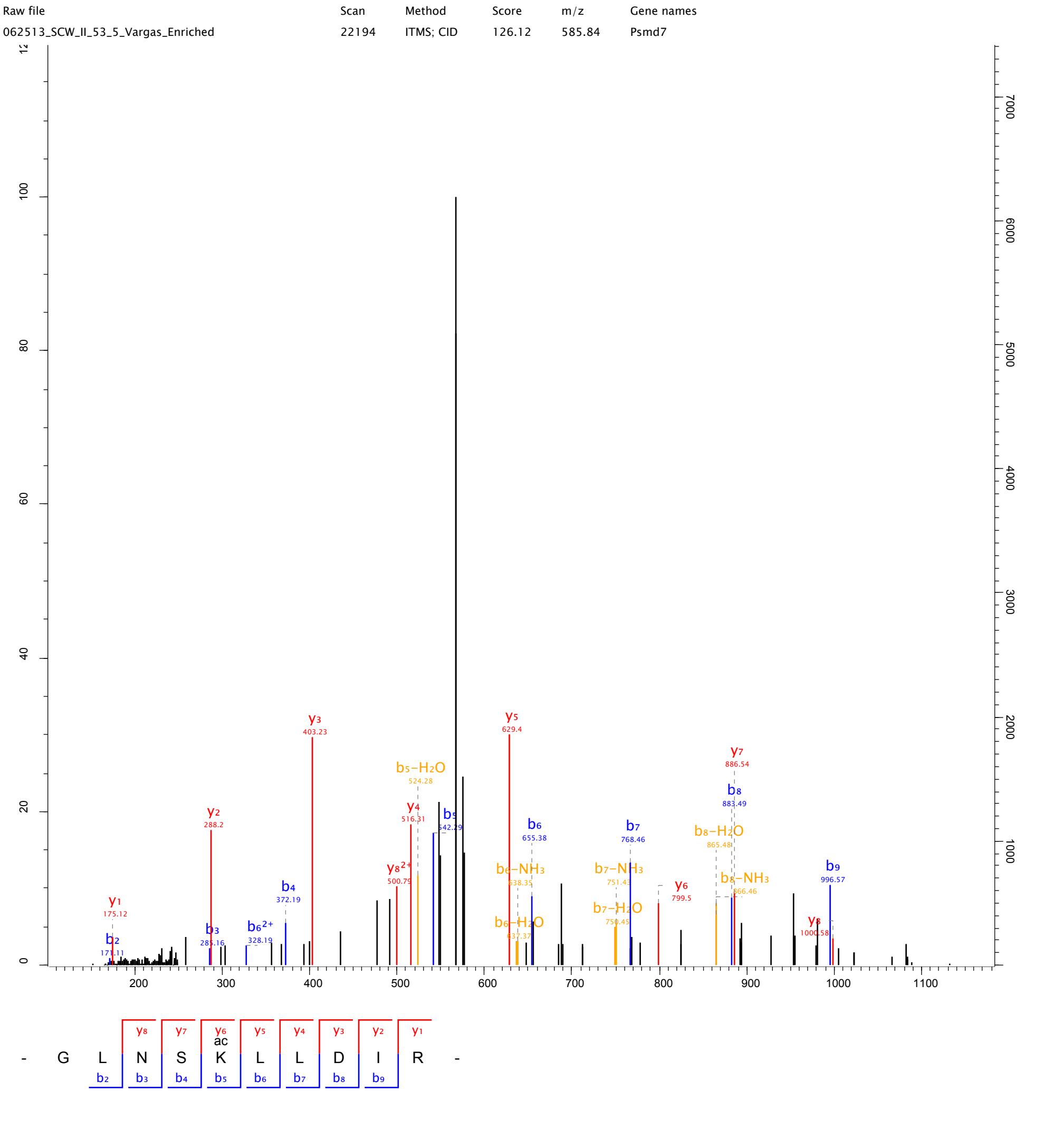
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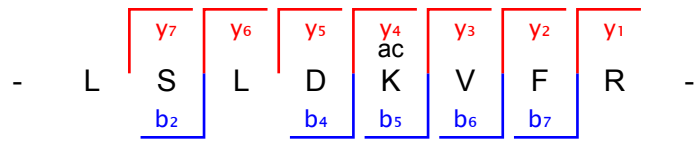
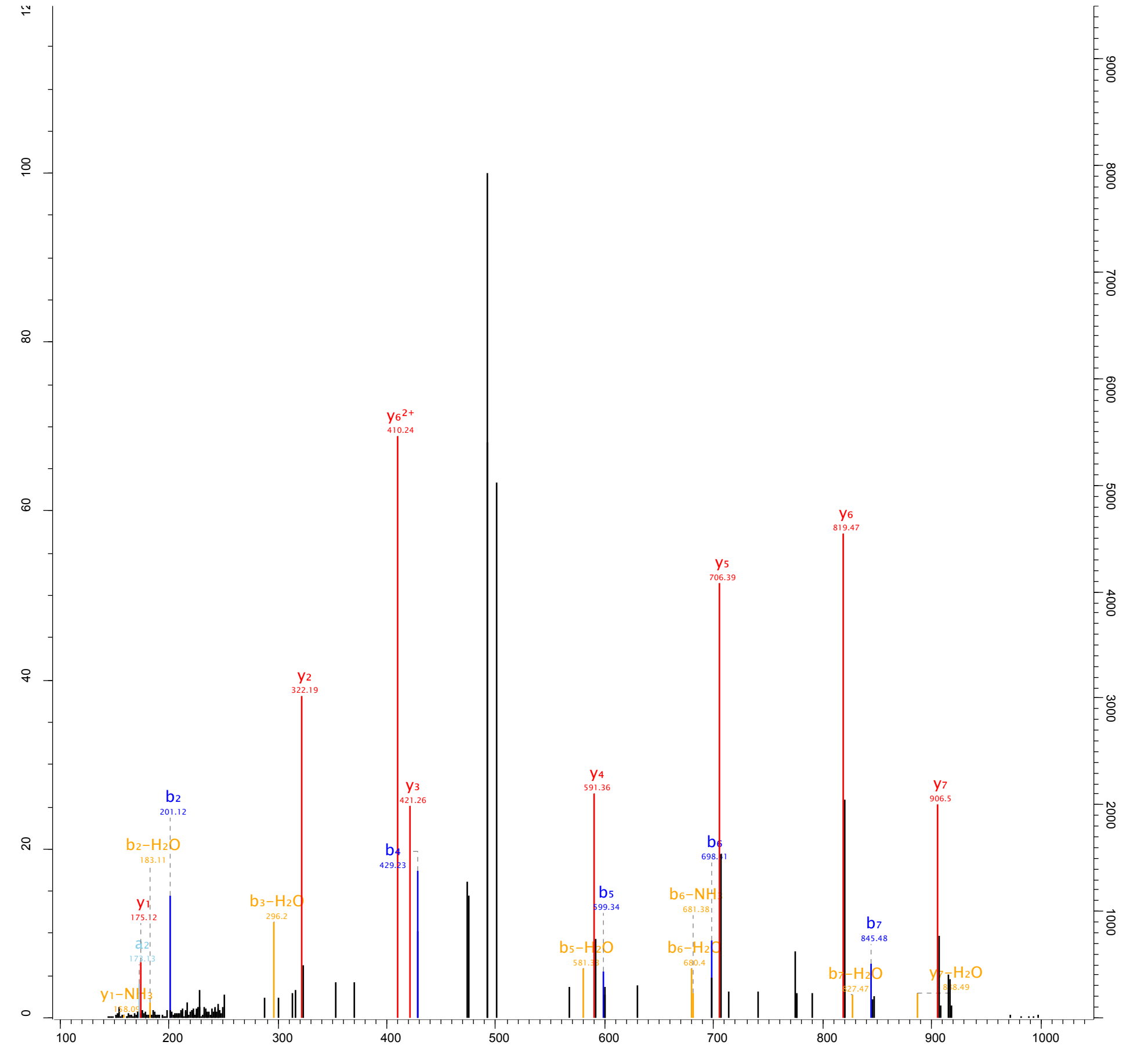
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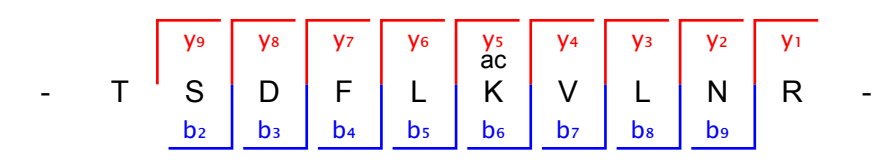
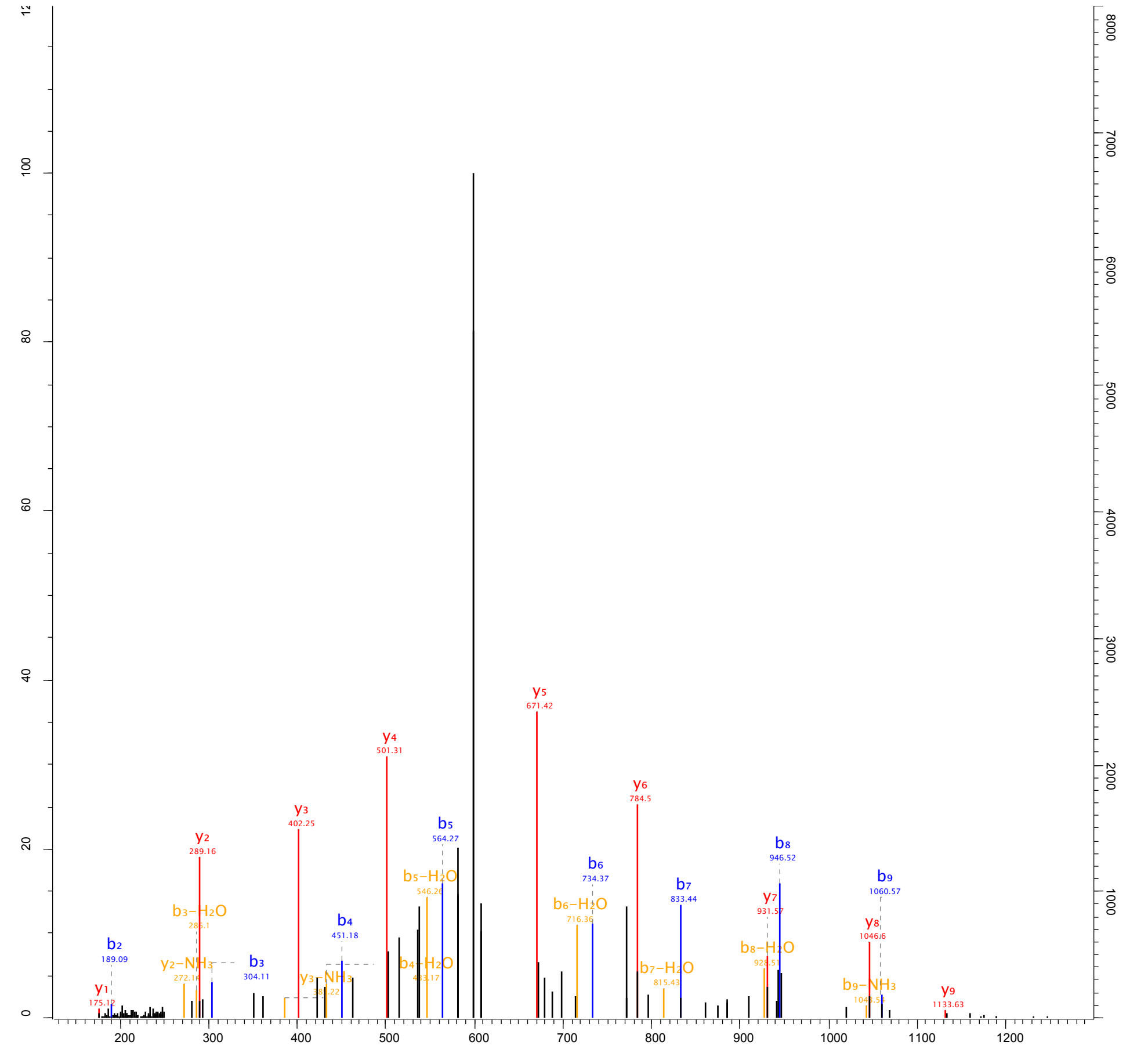


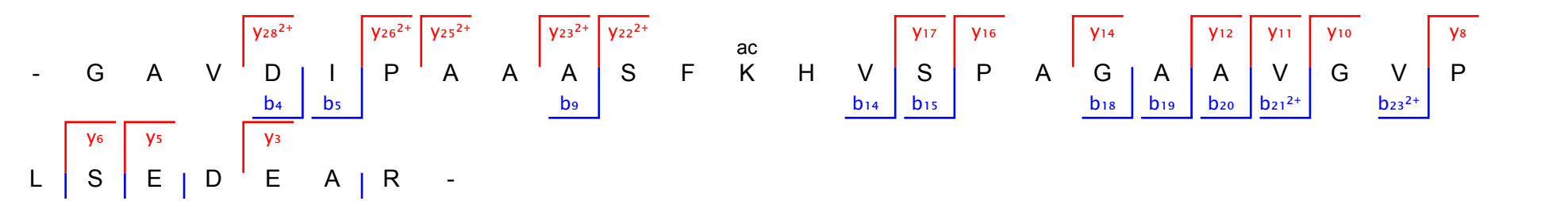
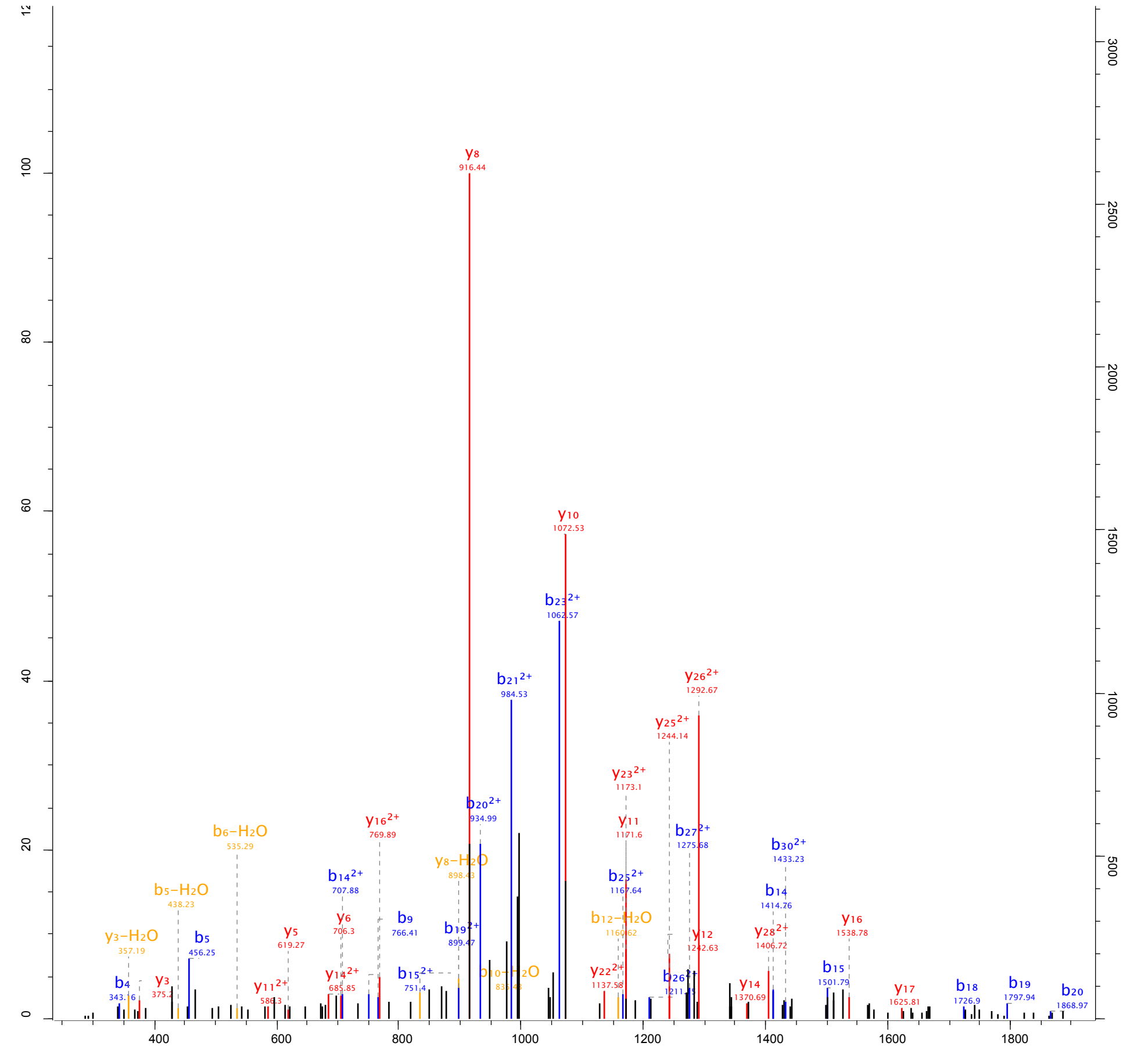




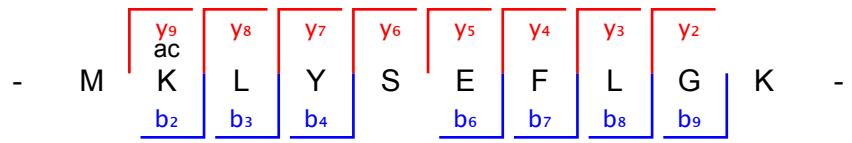
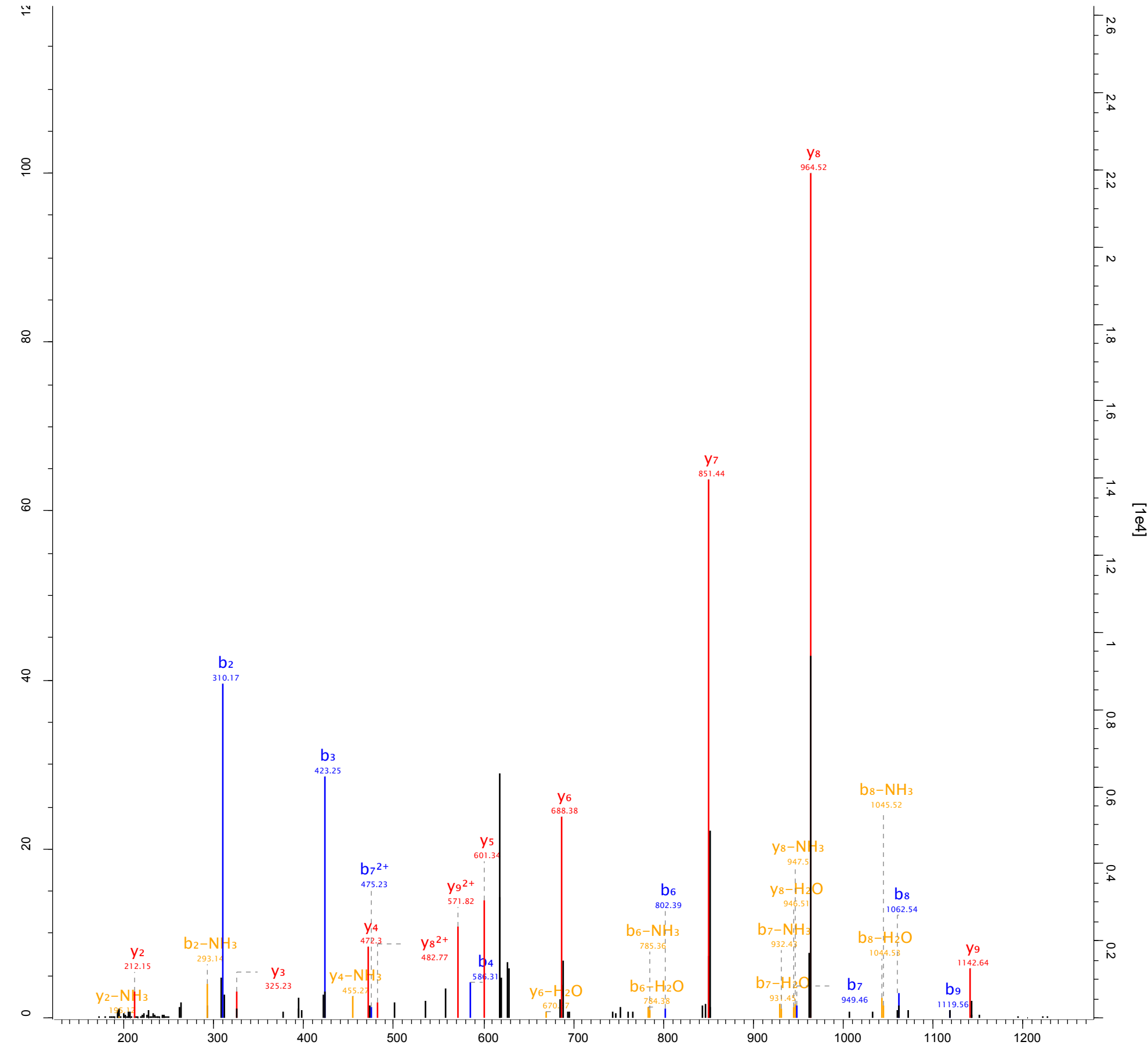


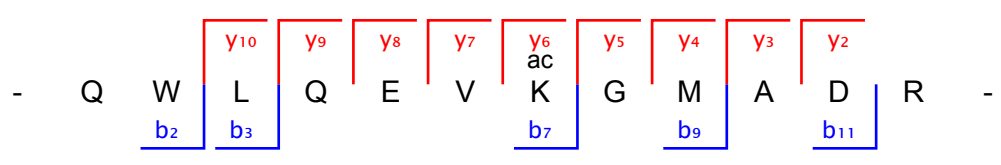
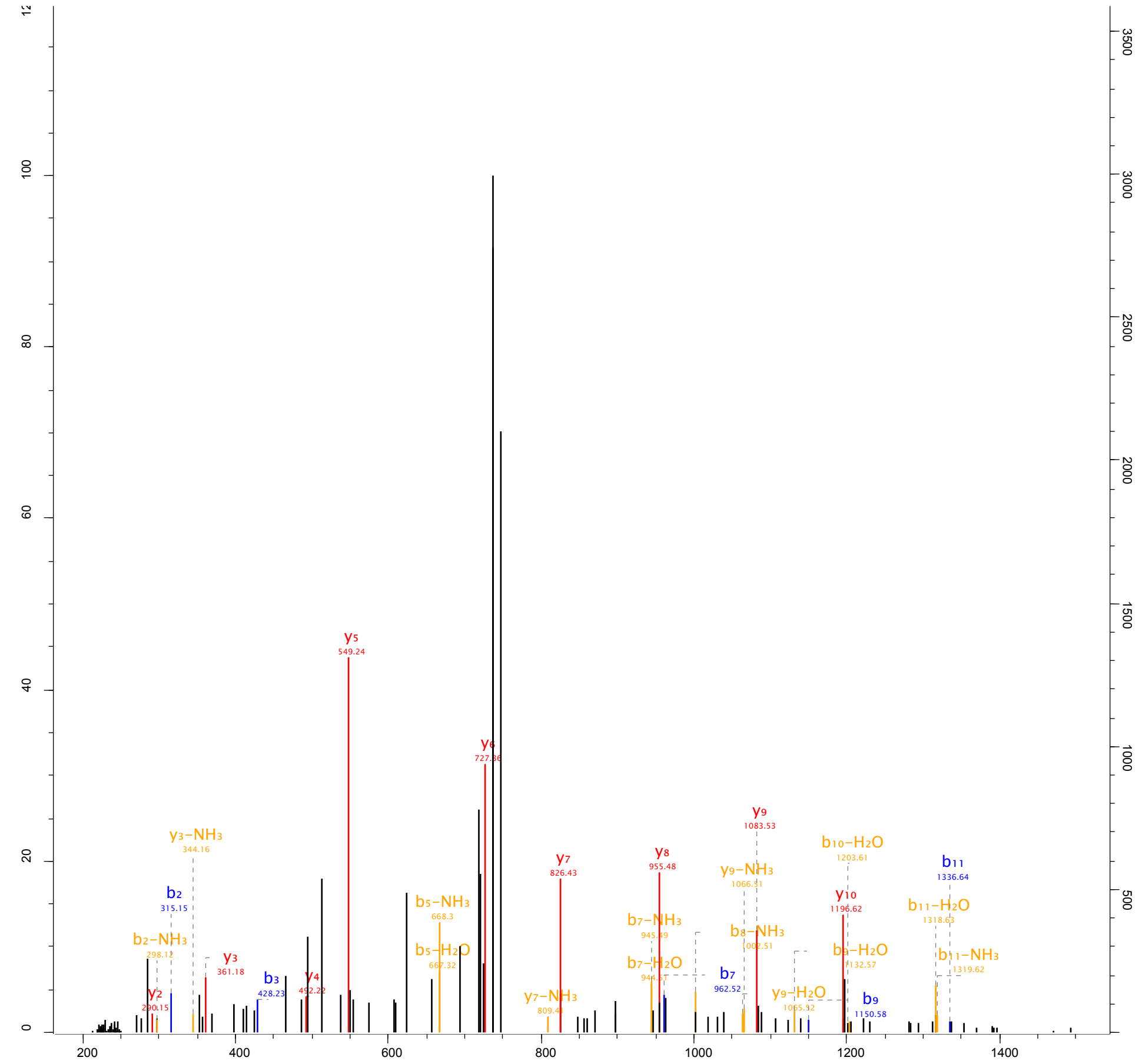


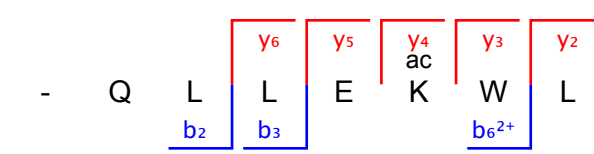
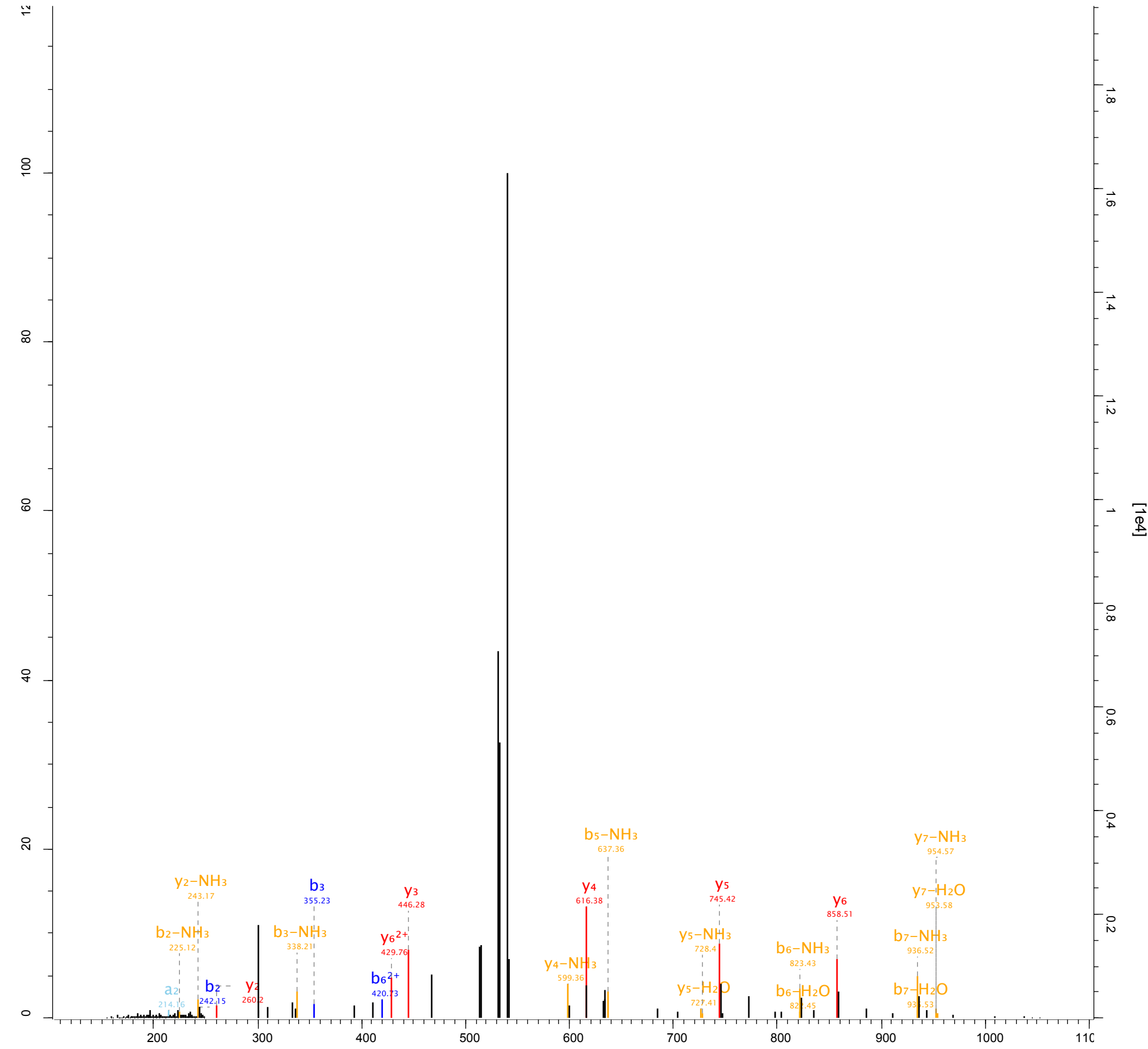


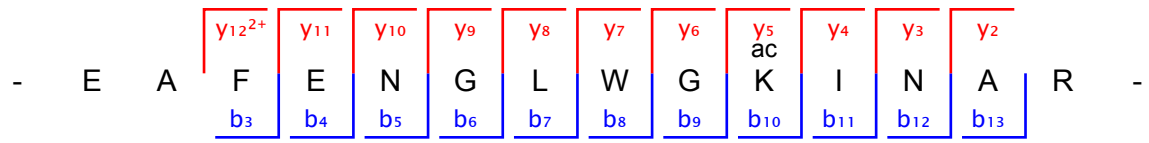
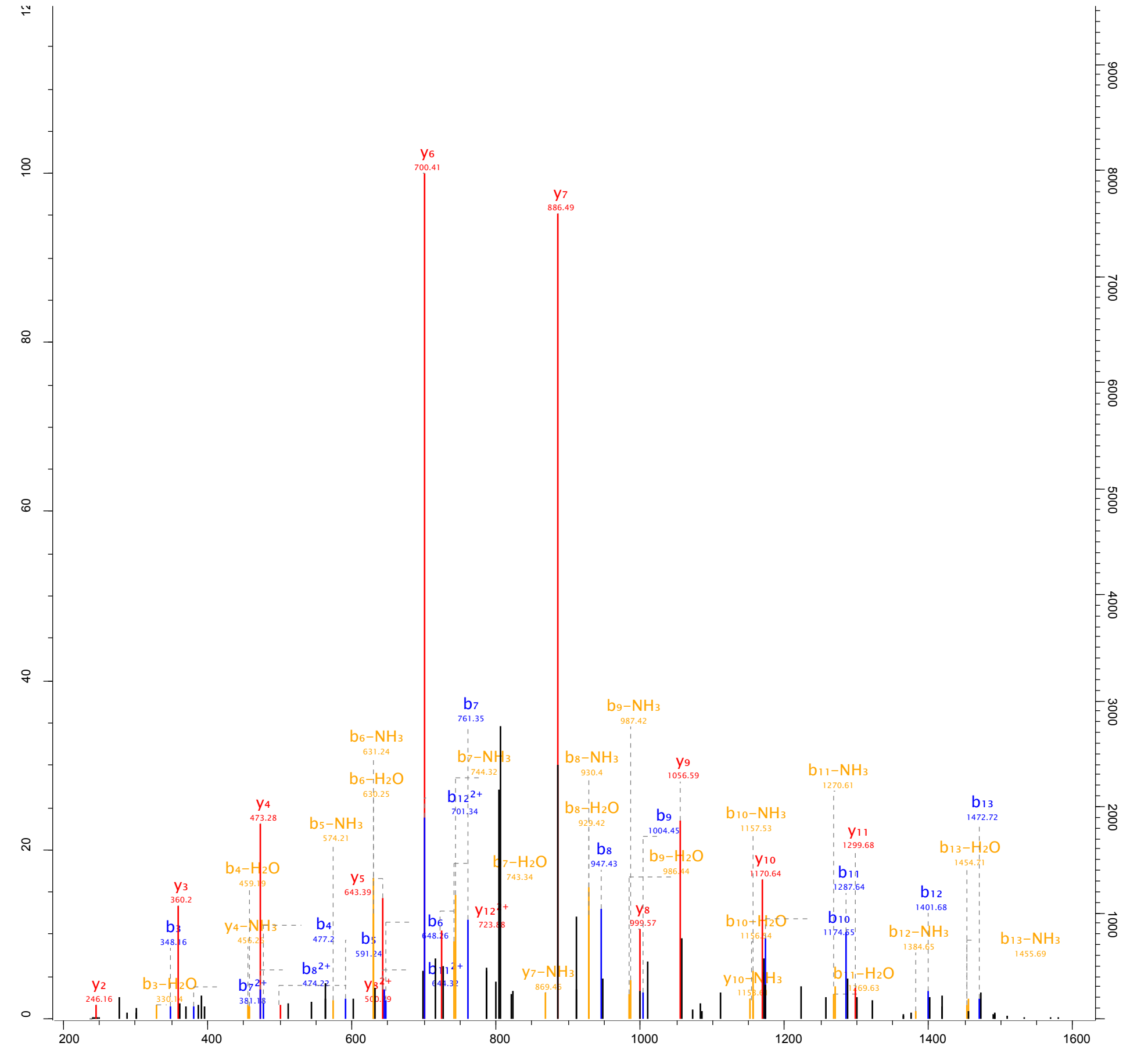


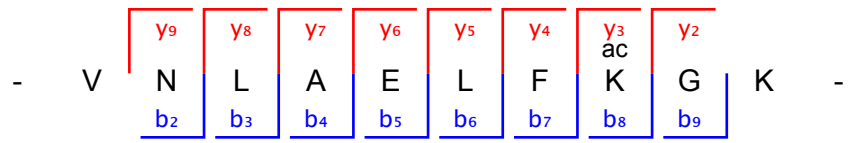
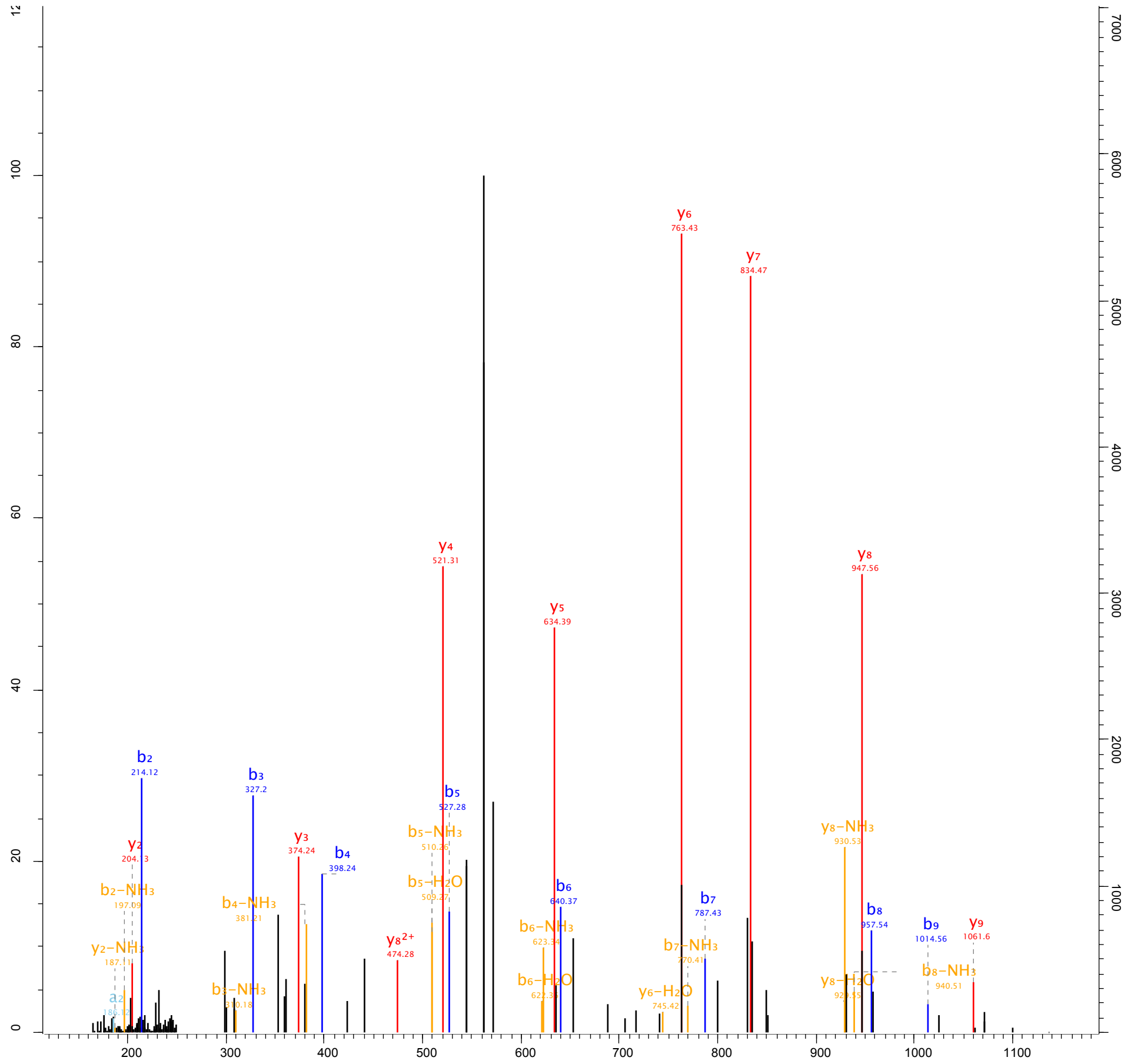
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062513_SCW_II_53_5_Vargas_Enriched

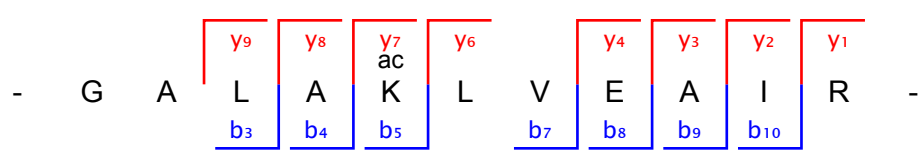
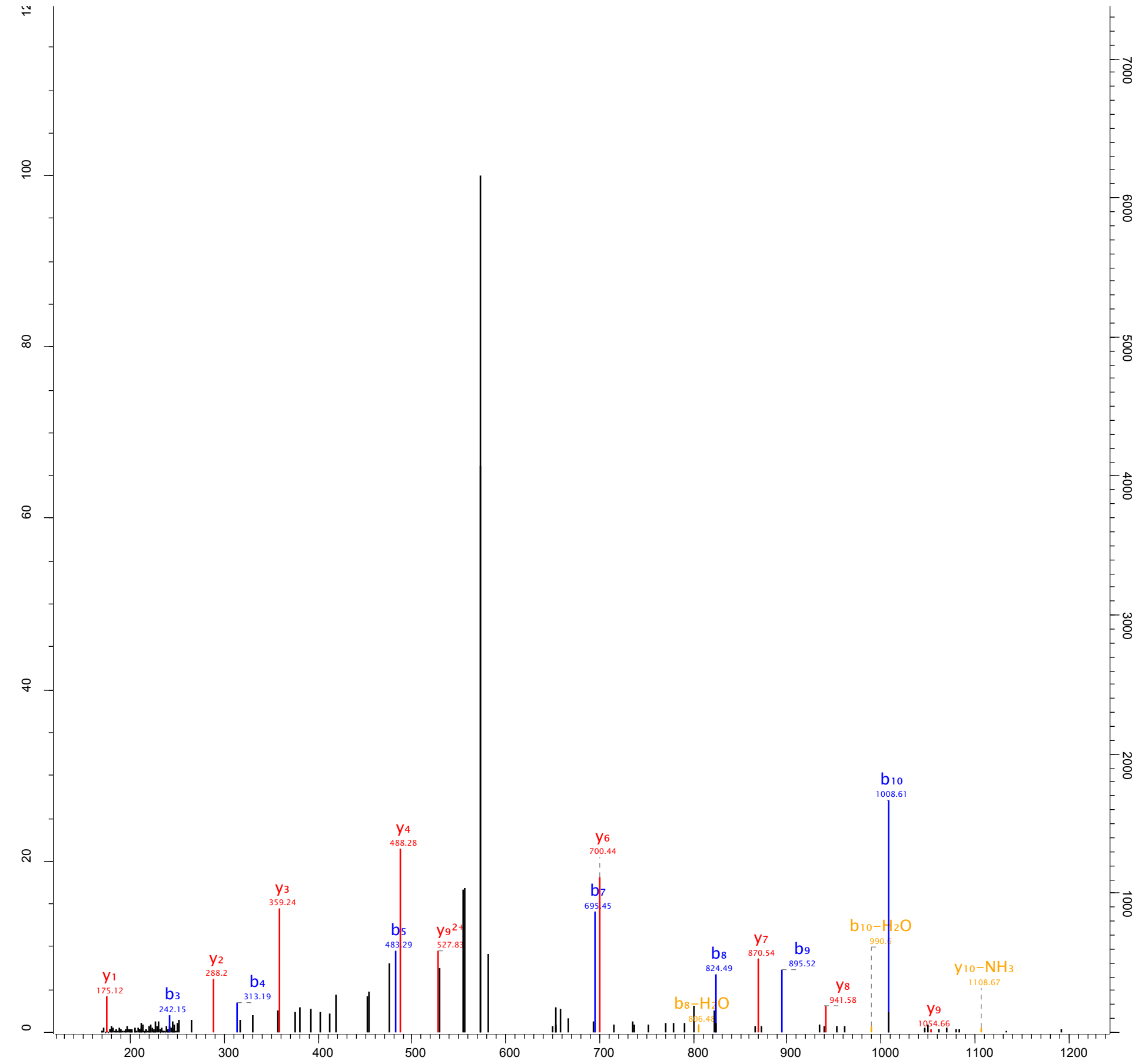
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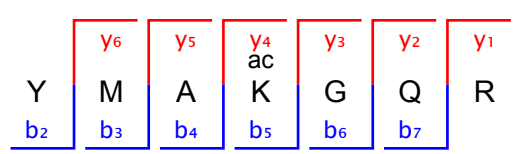
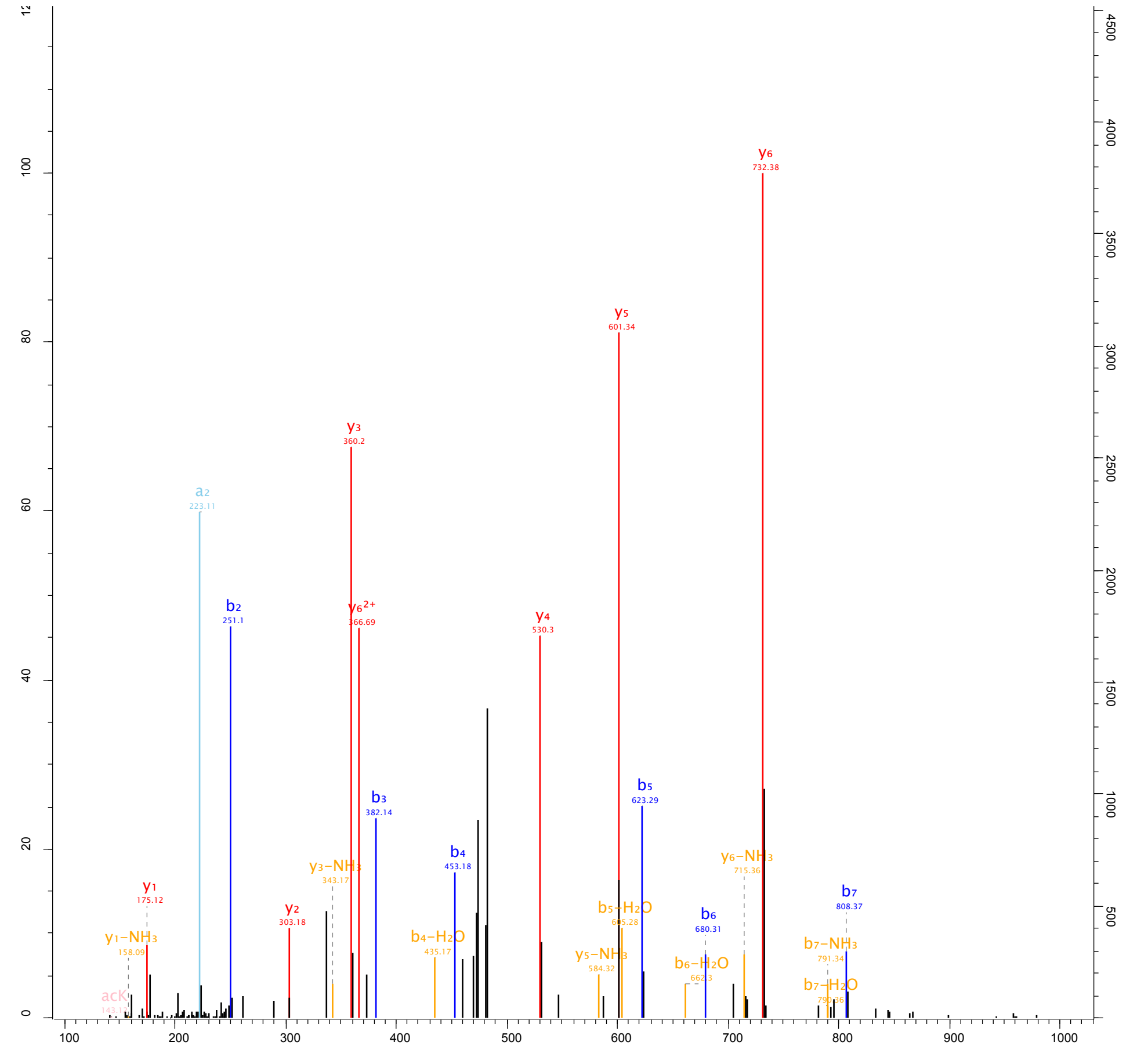
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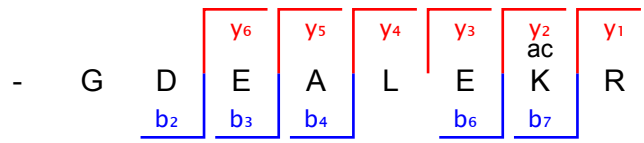
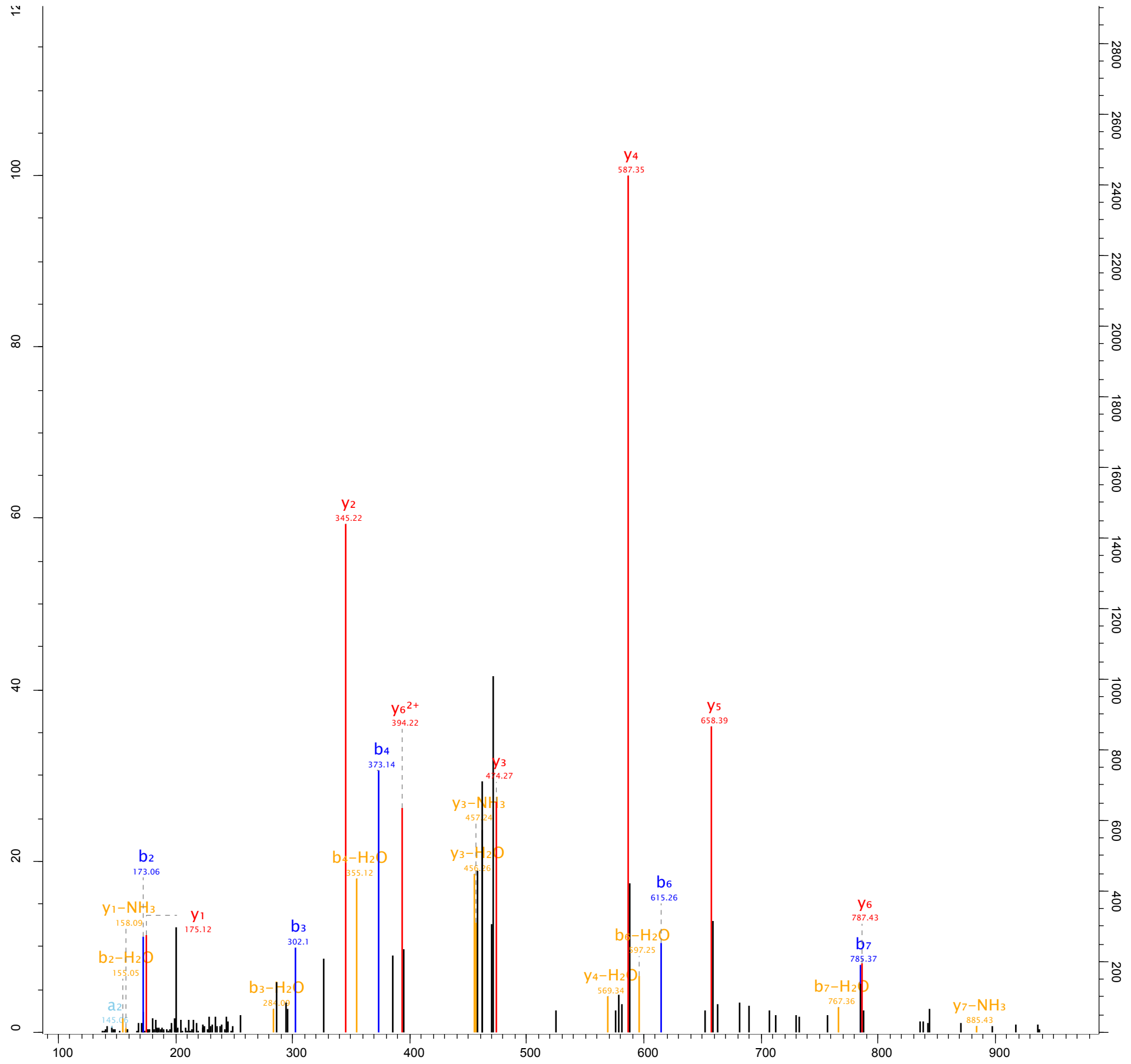
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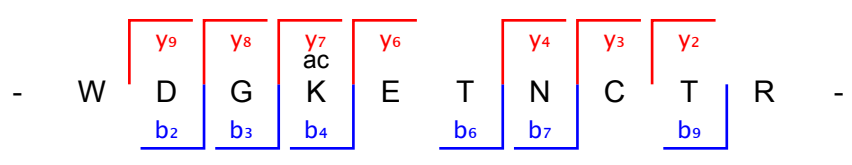
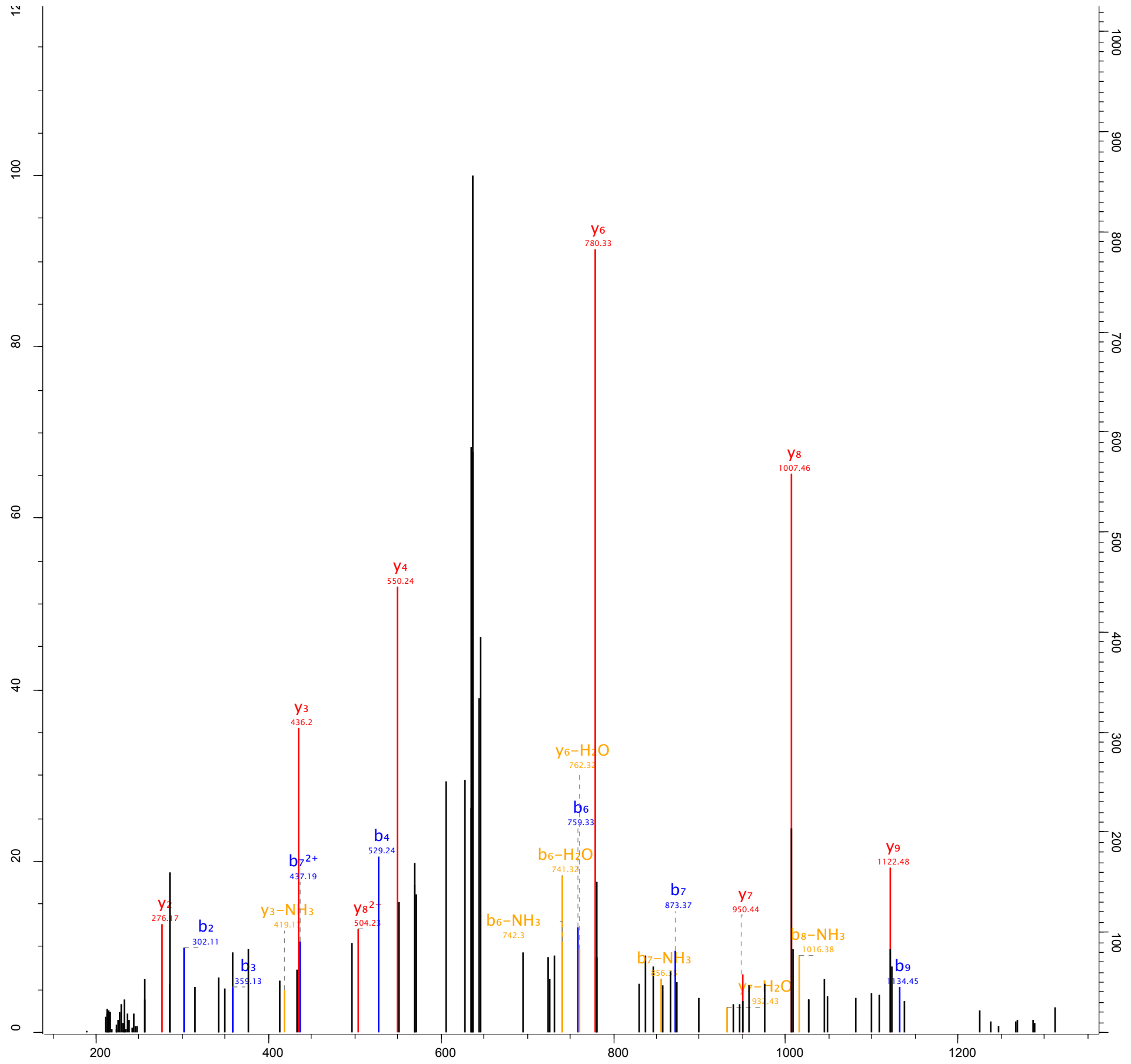
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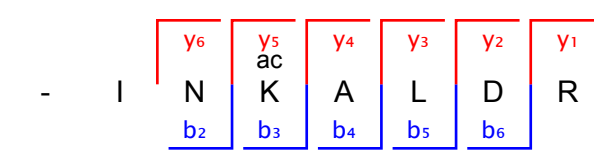
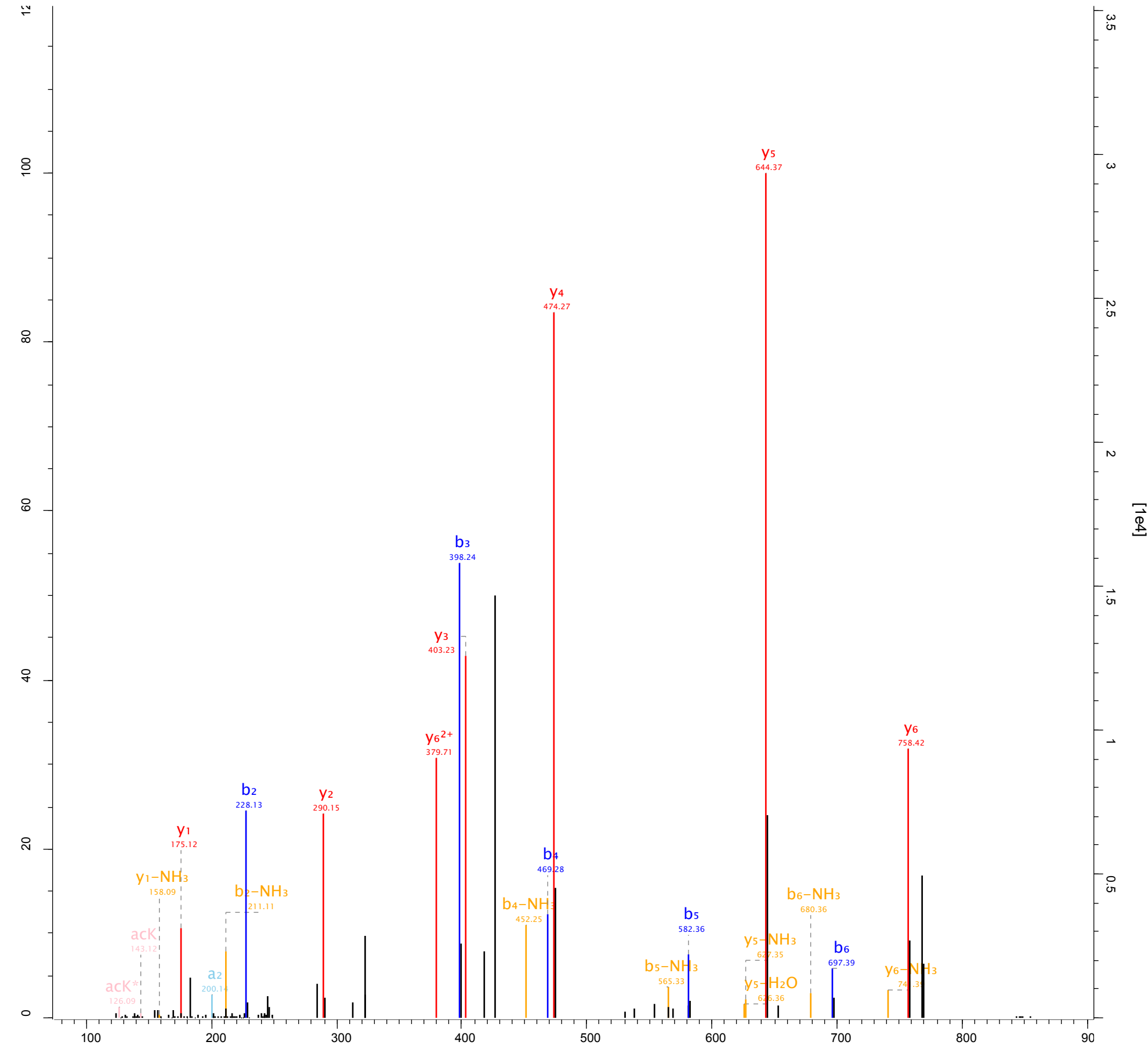
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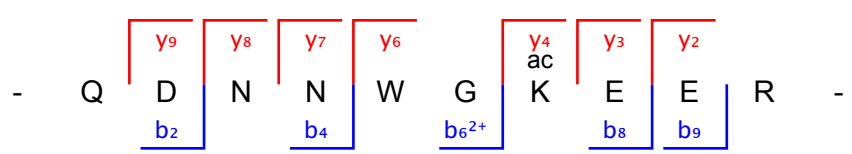
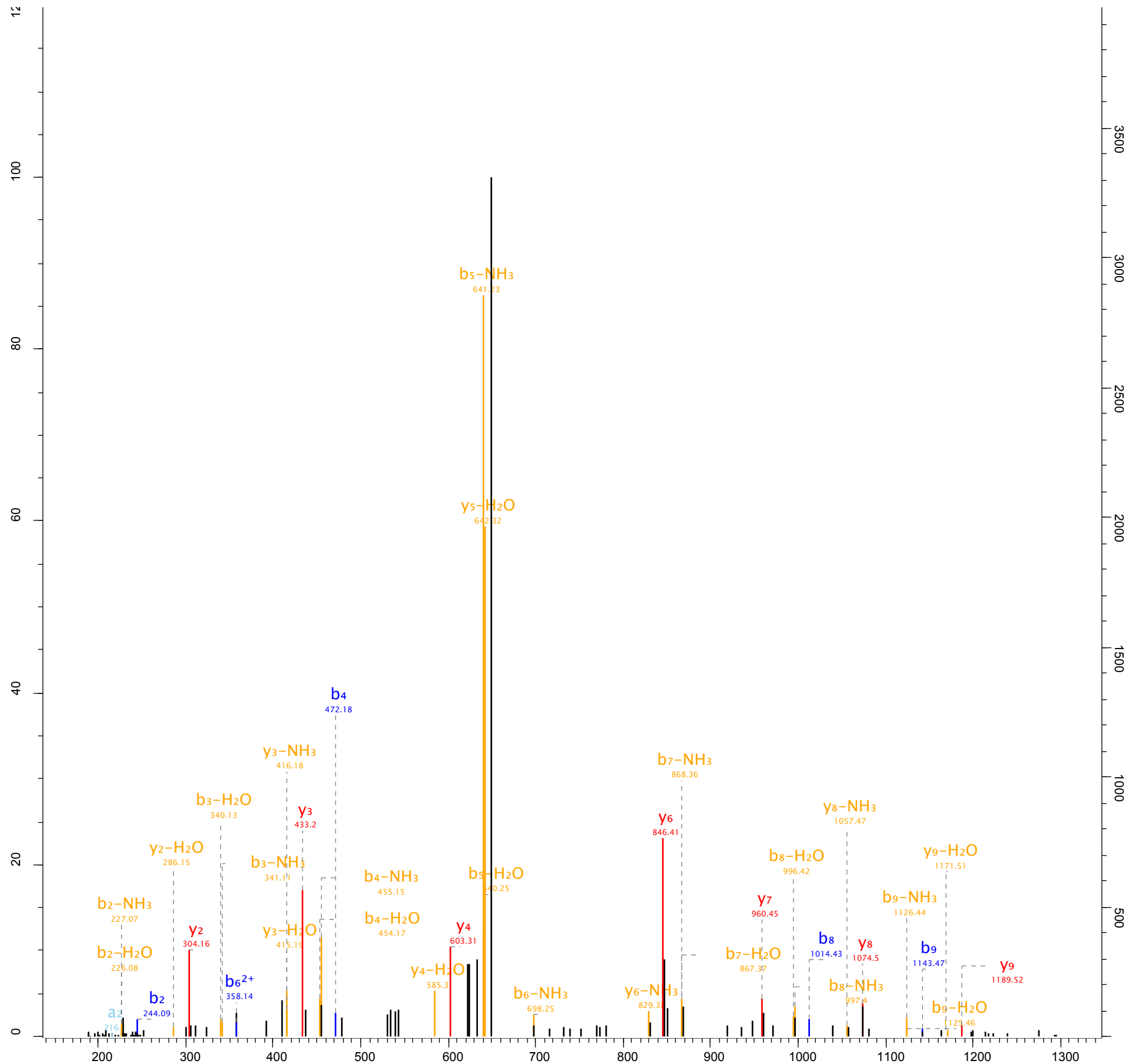


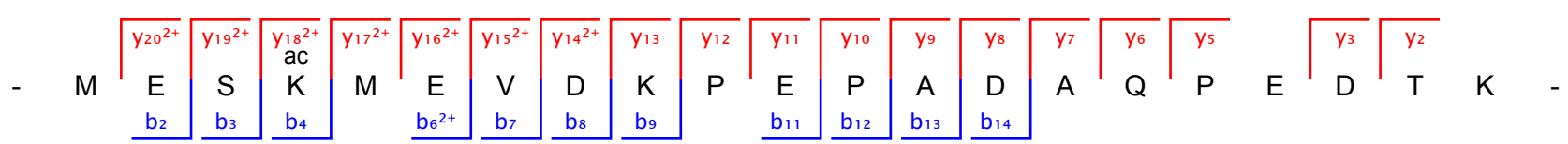
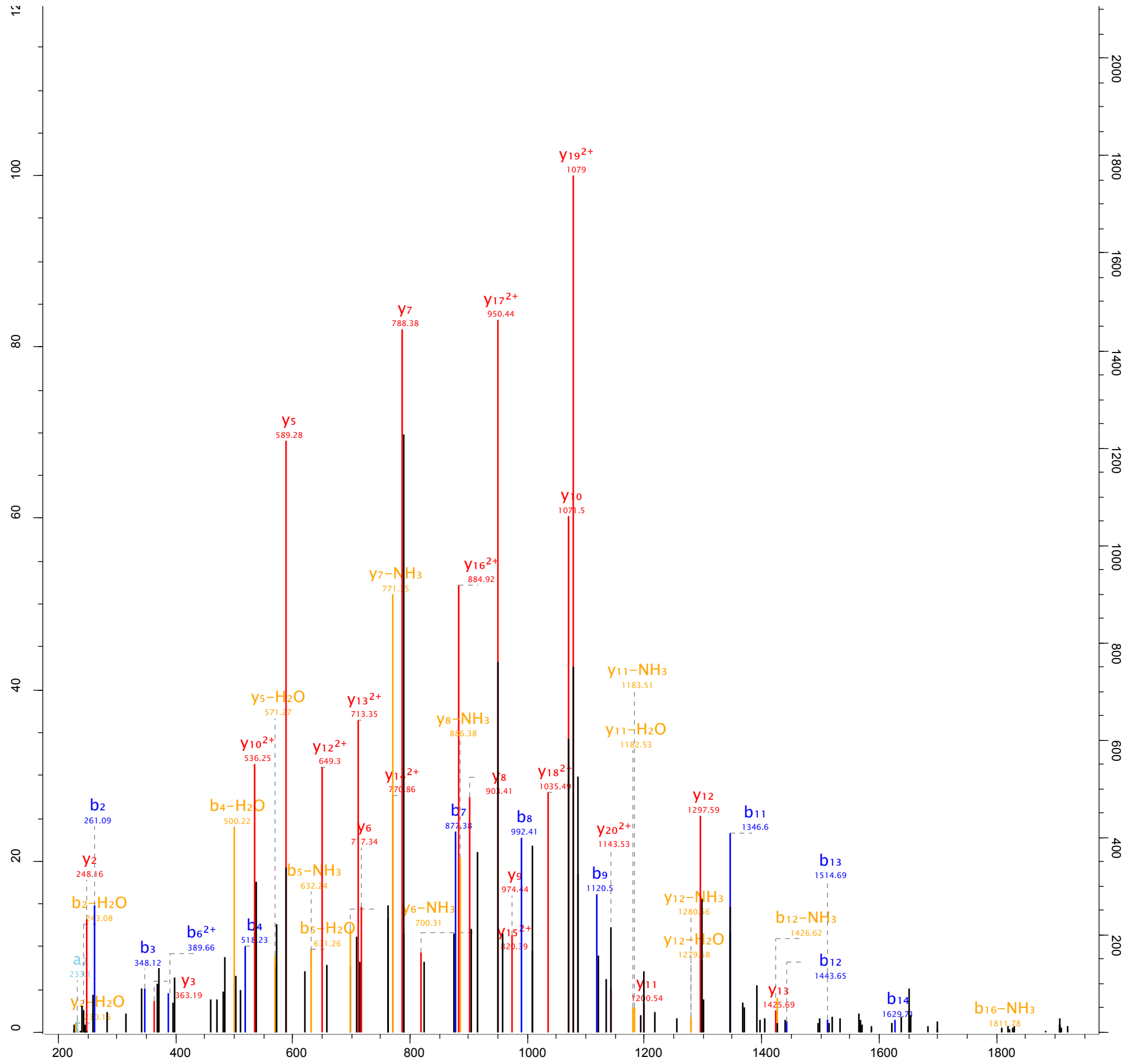


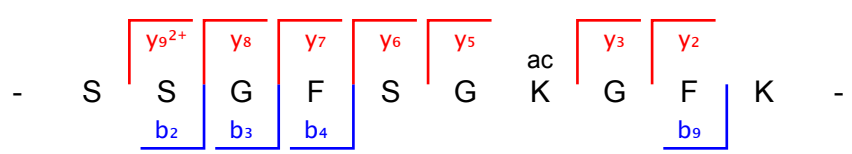
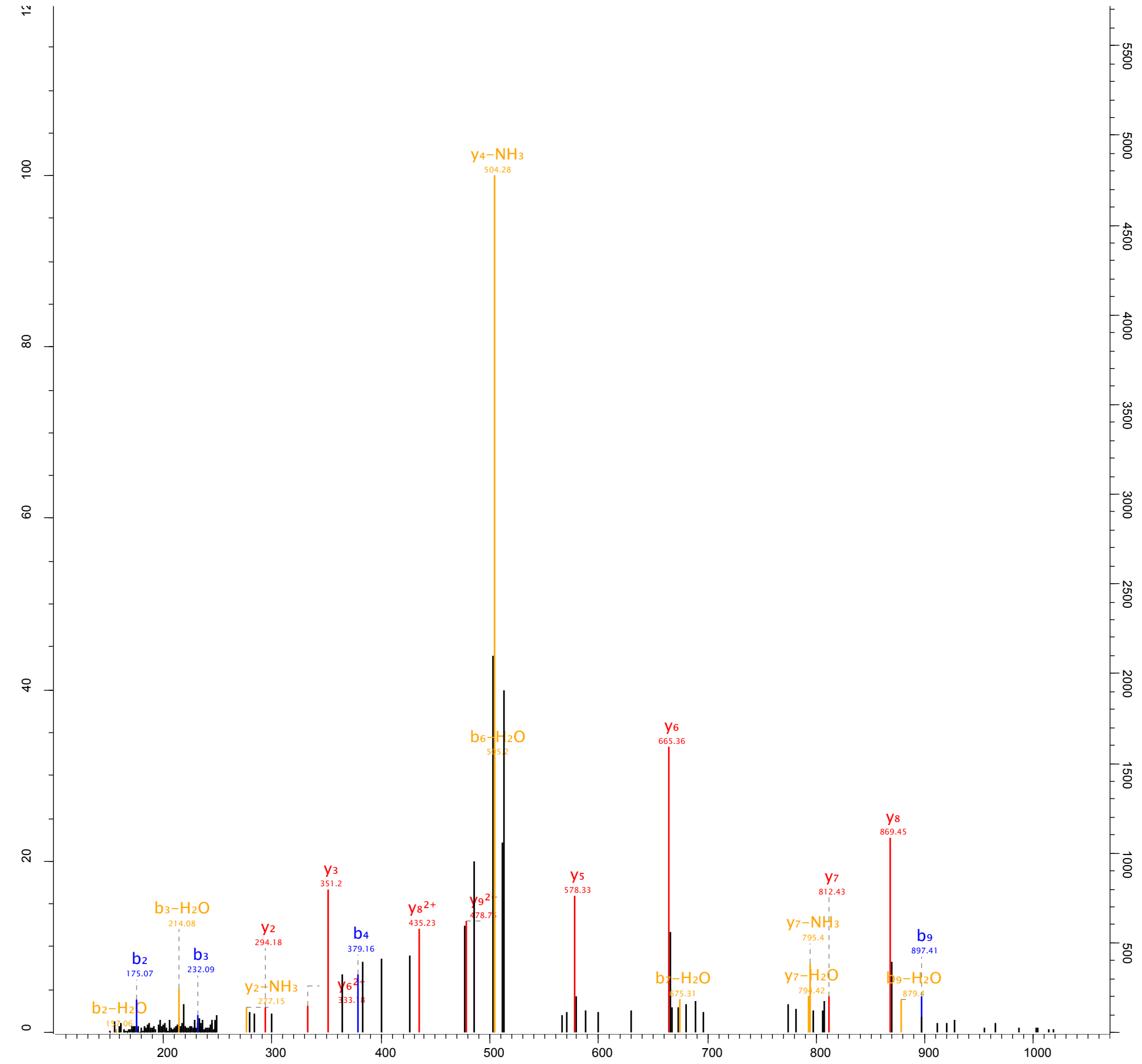


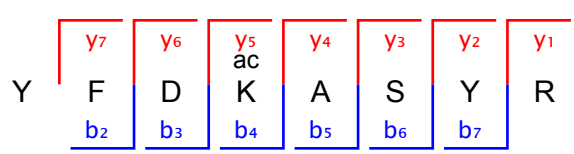
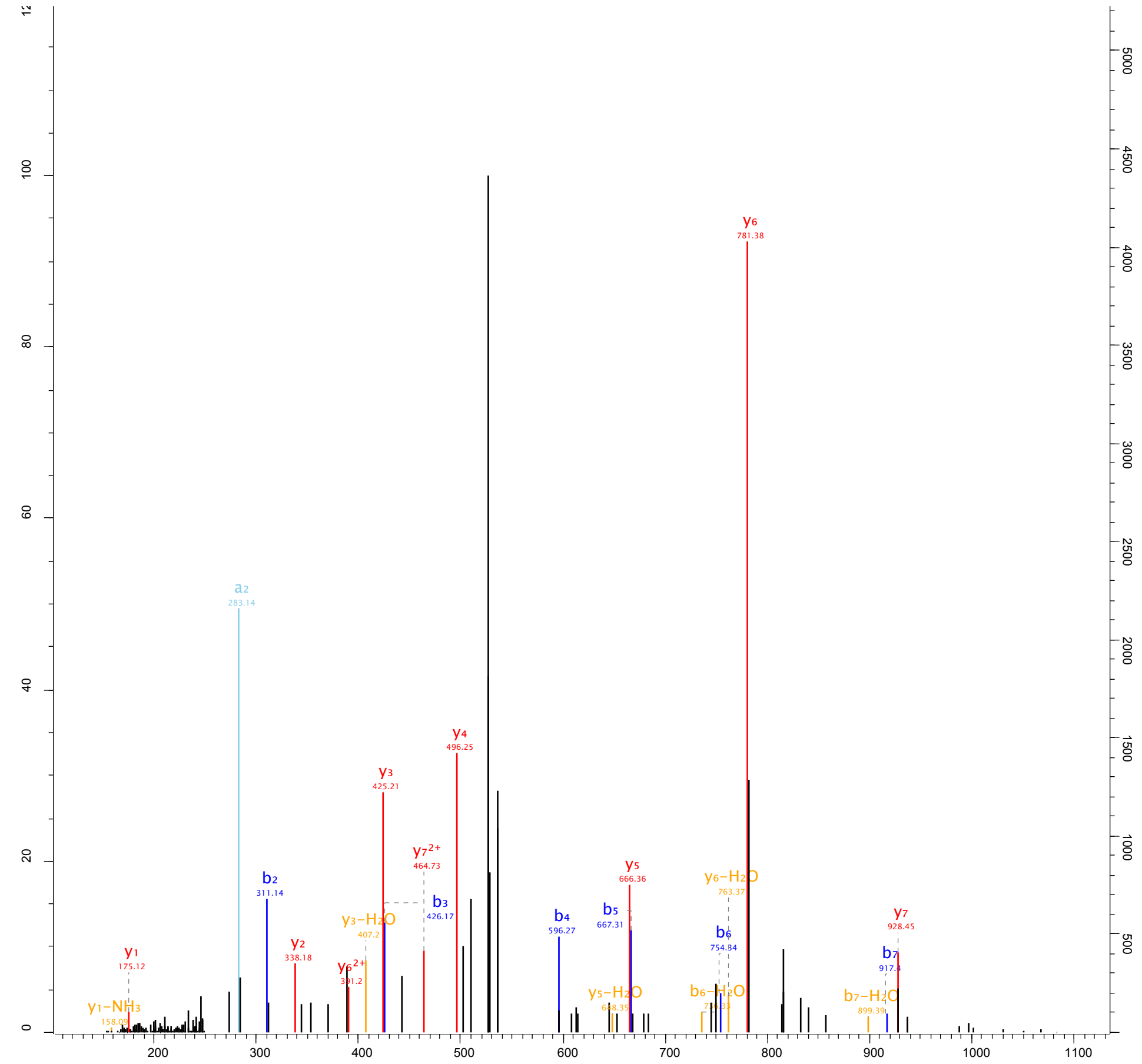


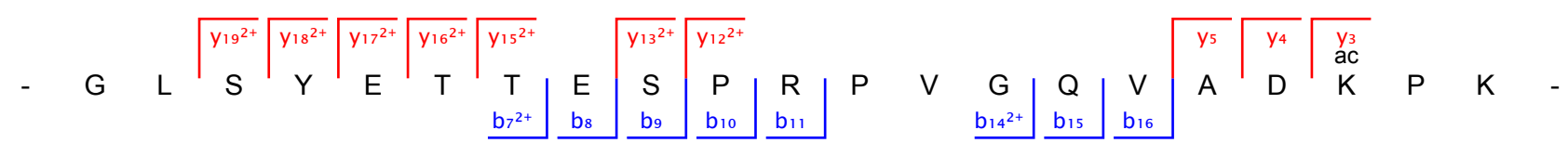
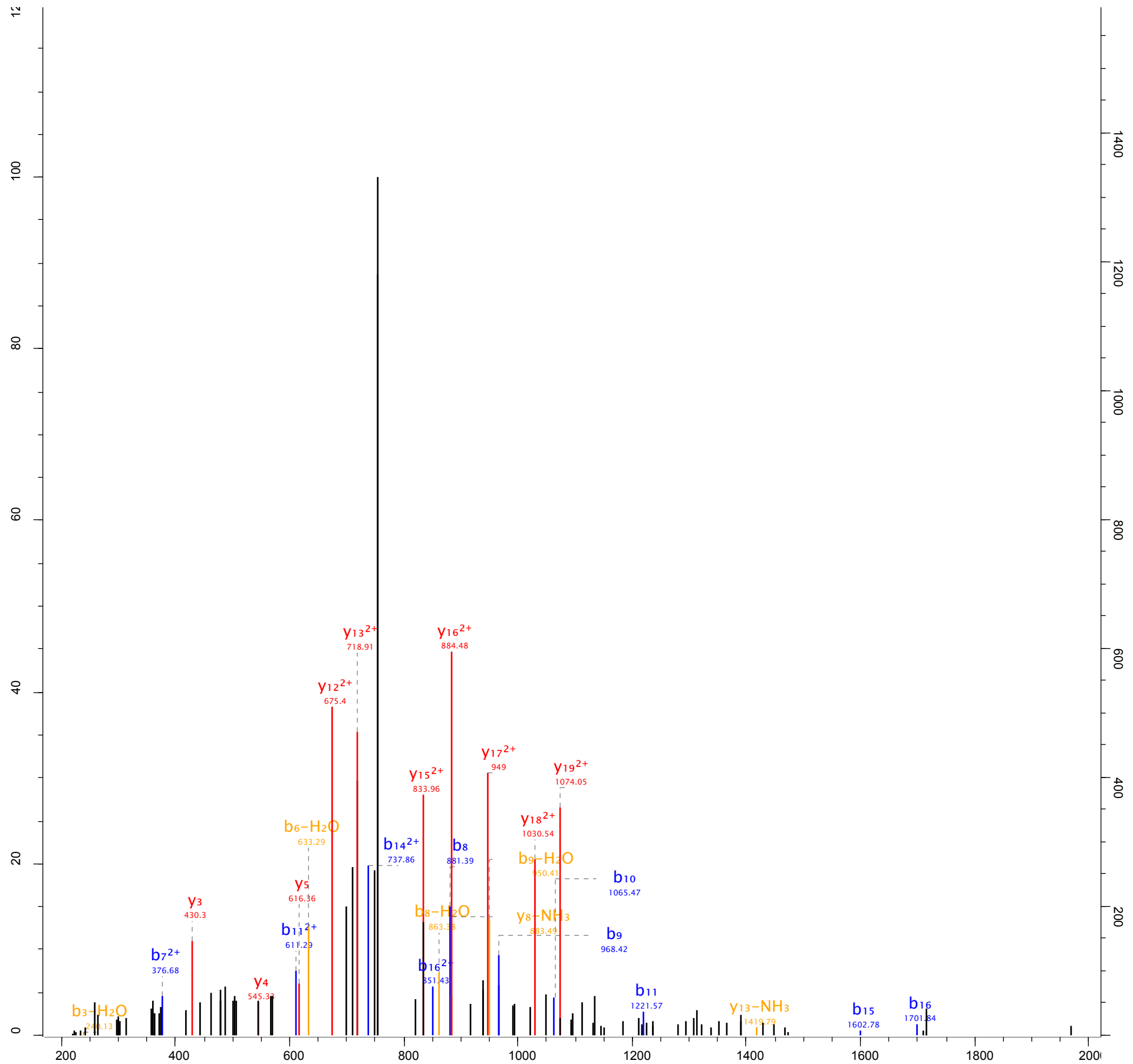


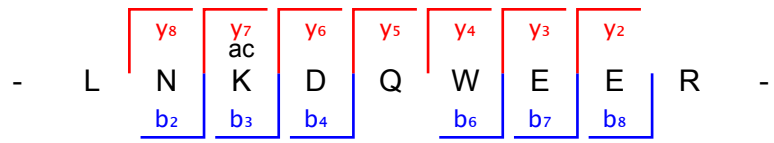
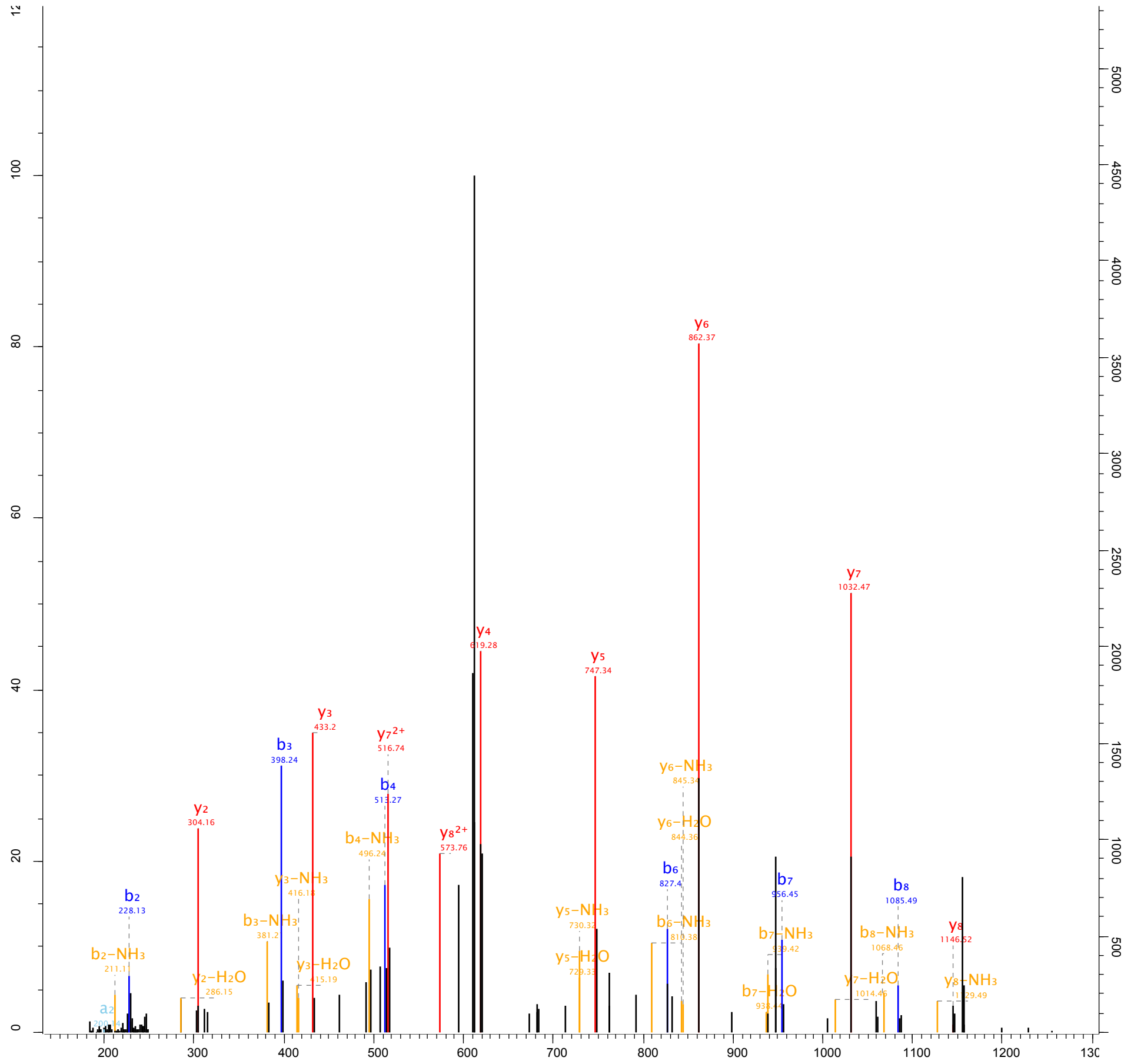


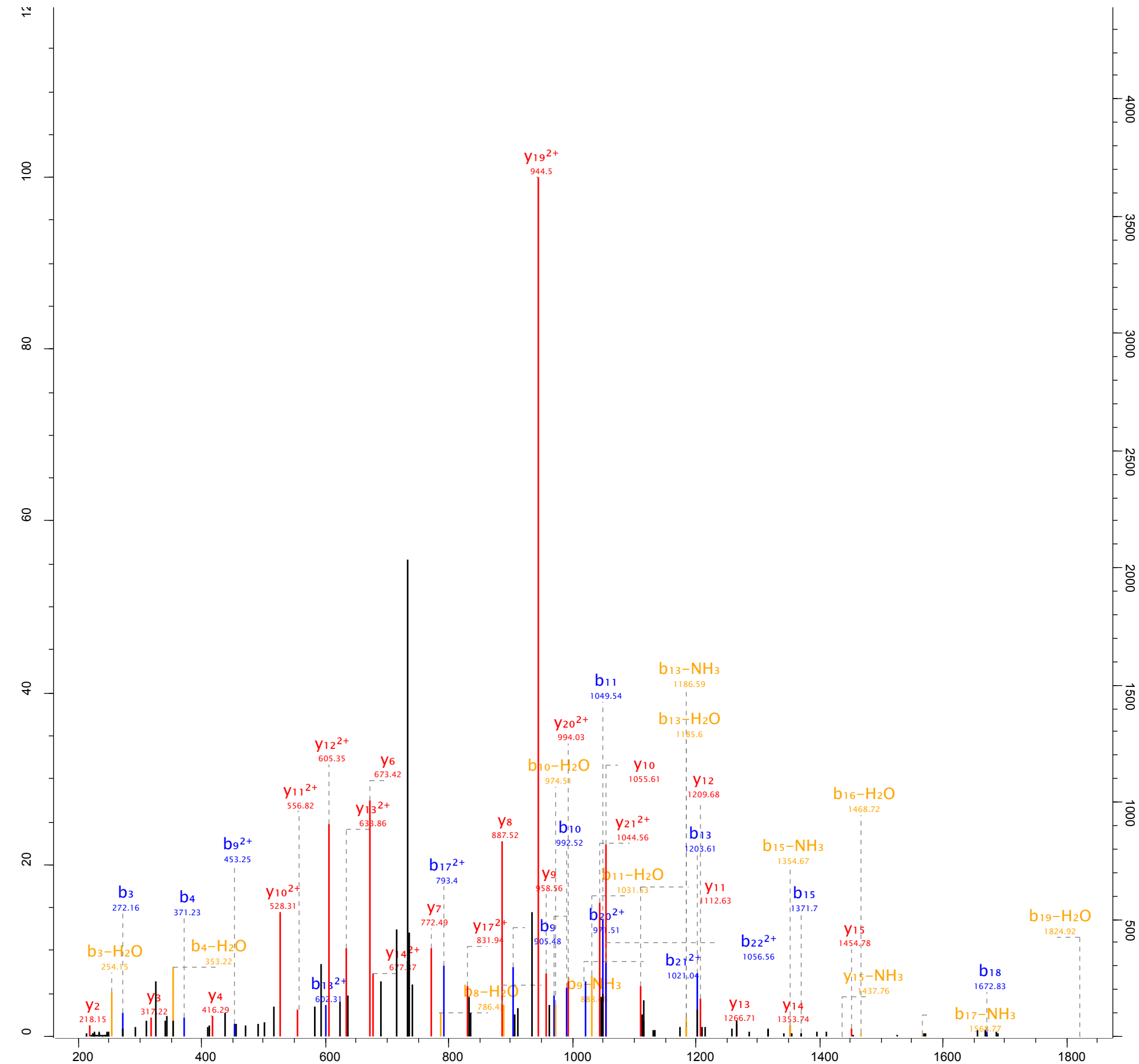






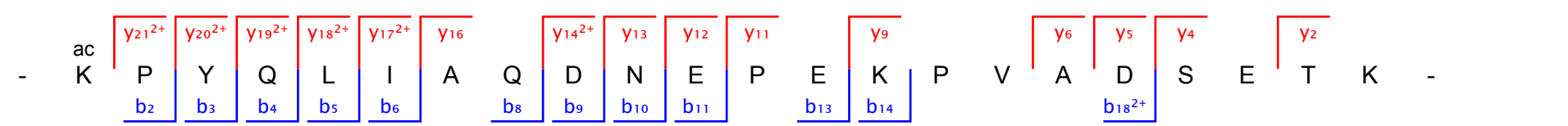
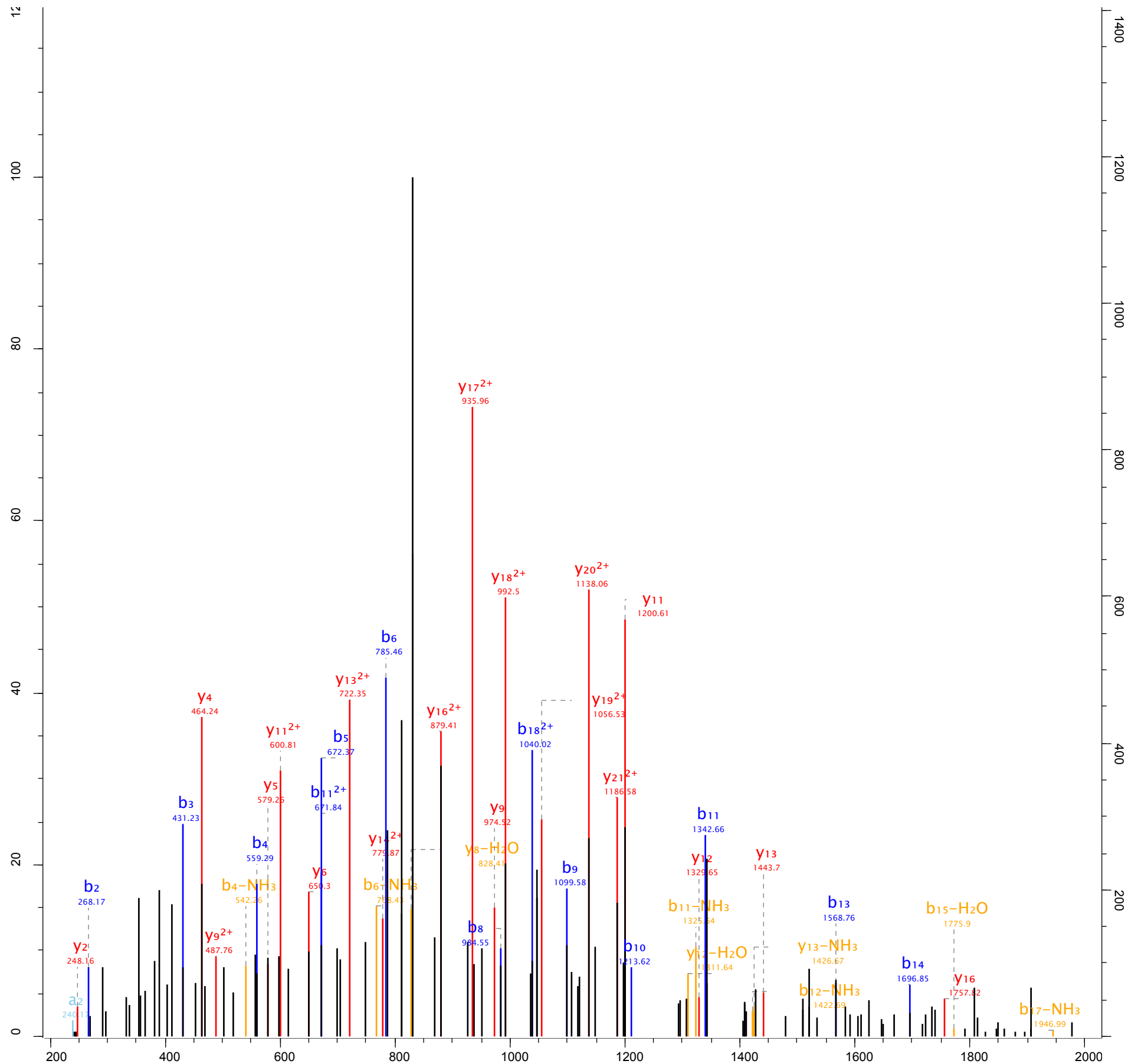


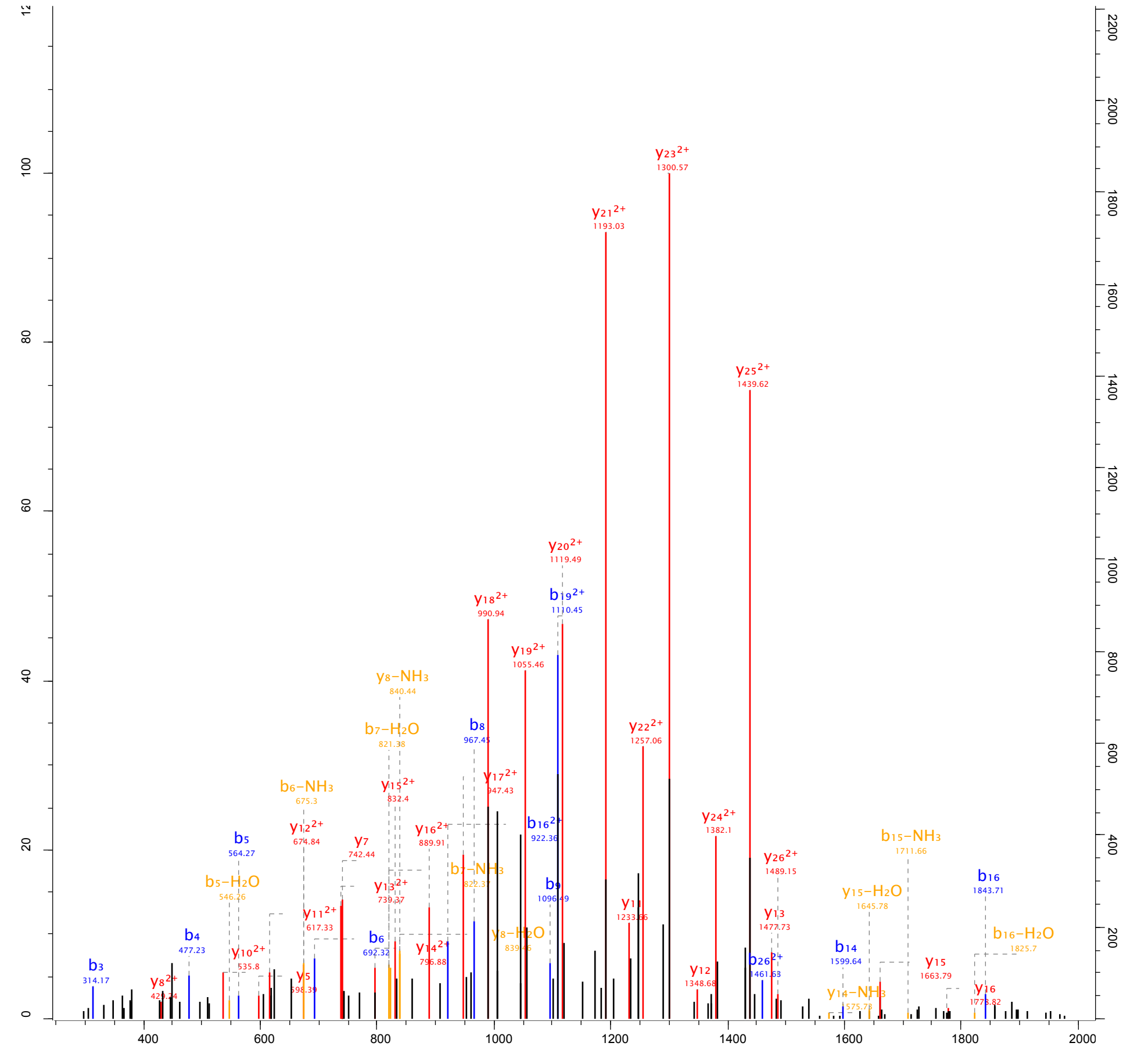




- V A T V P Q H A T S G P G P A D V S K V V A K -

b3 b4 b9 b10 b11 b13 b15 b17 2+ b18 b20 2+ b21 2+ b22 2+





- V V D Y S Q F Q E S D D A D E D Y G R D S G P P

ac
A K | K -

Fragmentation labels: b₃, b₄, b₅, b₆, b₈, b₉, b₁₄, b₁₆, b₁₉^{2+, y₅, y₇, y₈²⁺, y₁₀²⁺, y₁₁, y₁₂, y₁₃, y₁₄²⁺, y₁₅, y₁₆, y₁₇²⁺, y₁₈²⁺, y₁₉²⁺, y₂₀²⁺, y₂₁²⁺, y₂₂²⁺, y₂₃²⁺, y₂₄²⁺, y₂₅²⁺, y₂₆²⁺}

062513_SCW_II_53_6_Vargas_Enriched

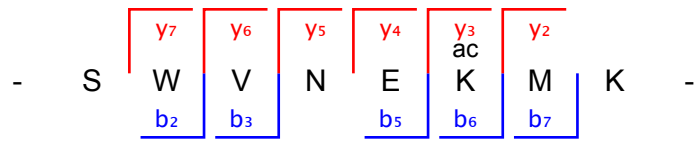
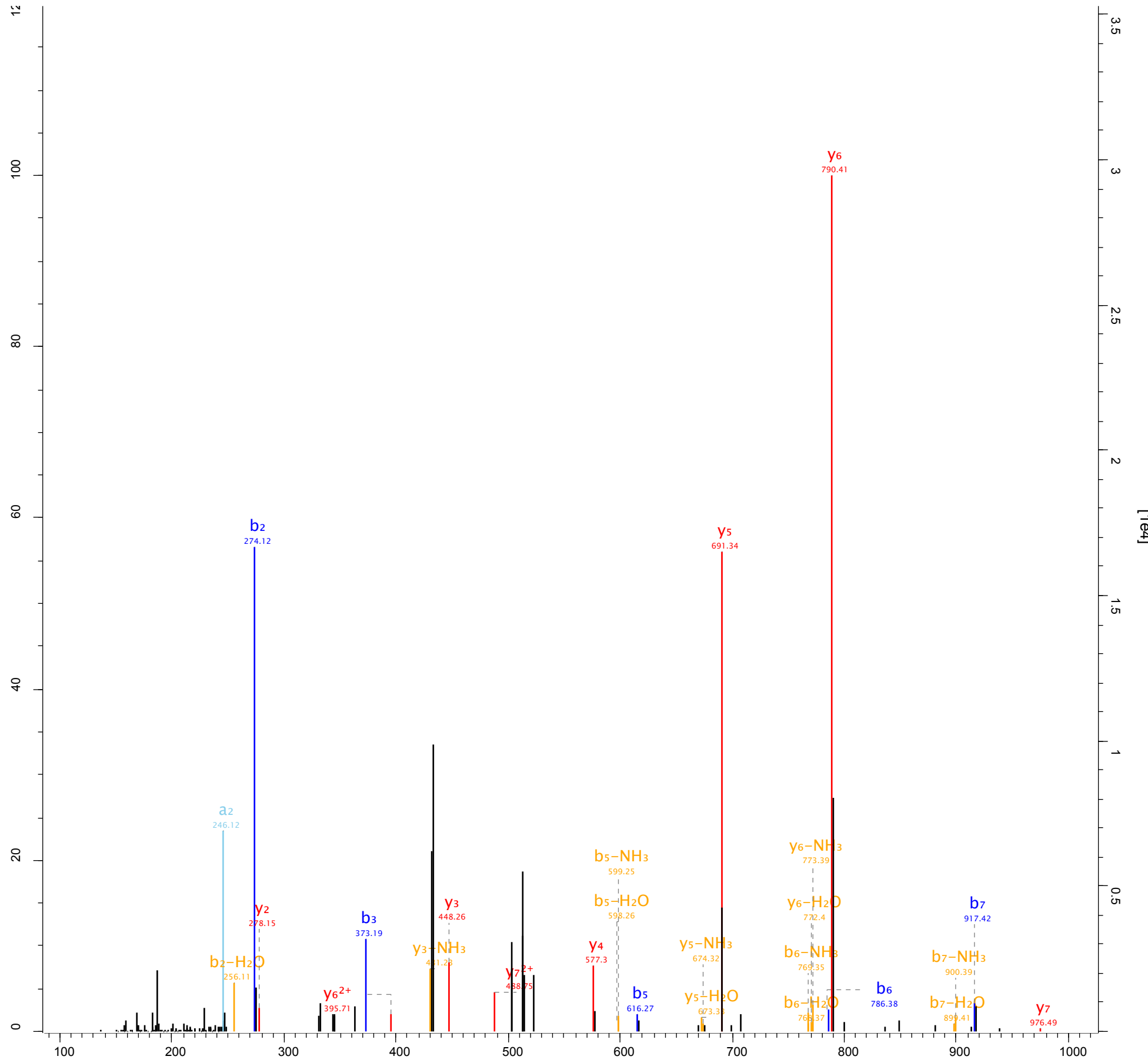
16265

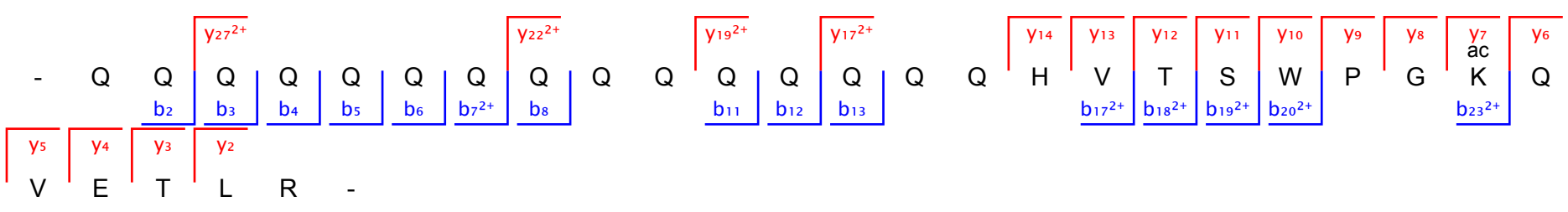
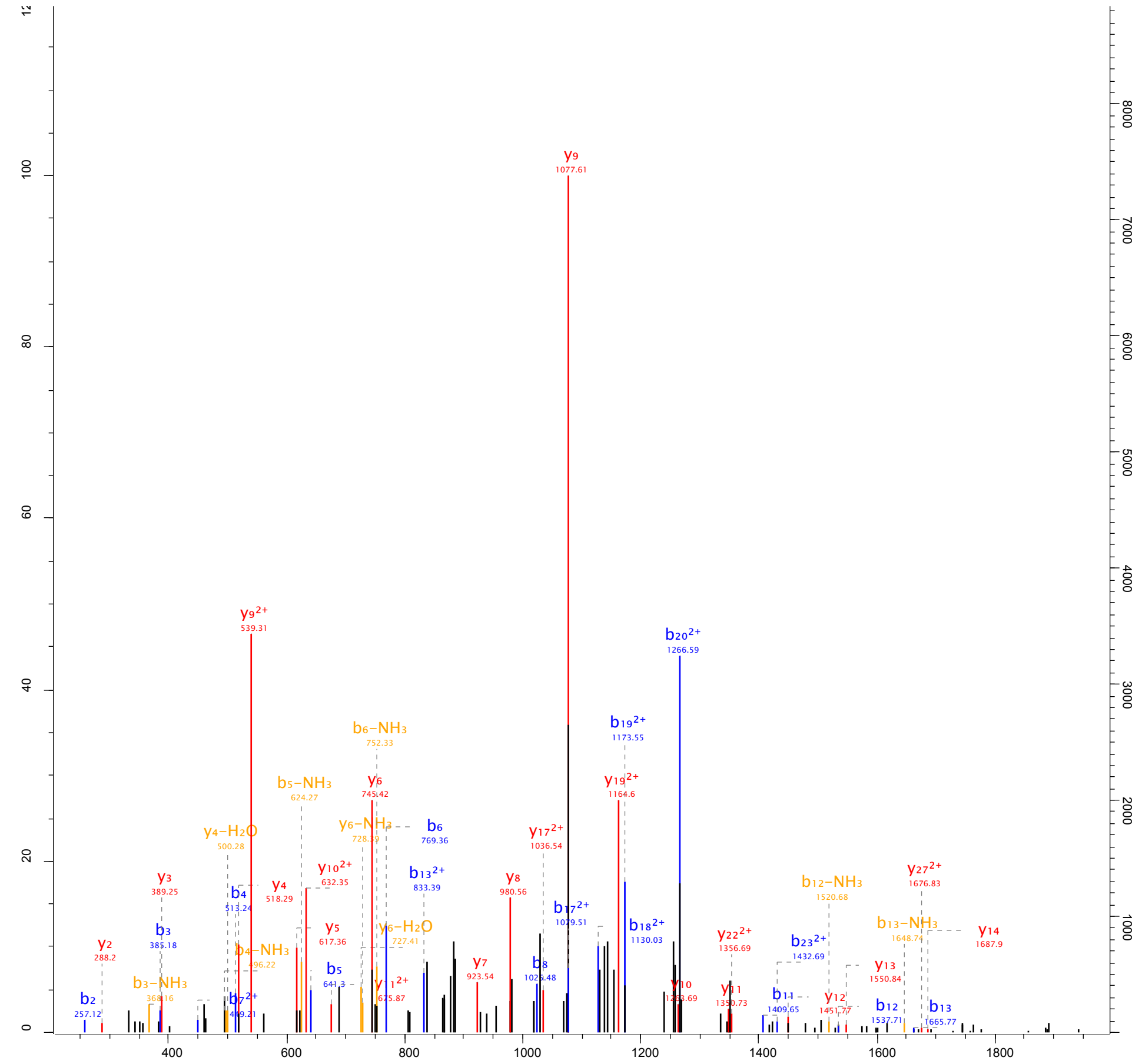
ITMS; CID

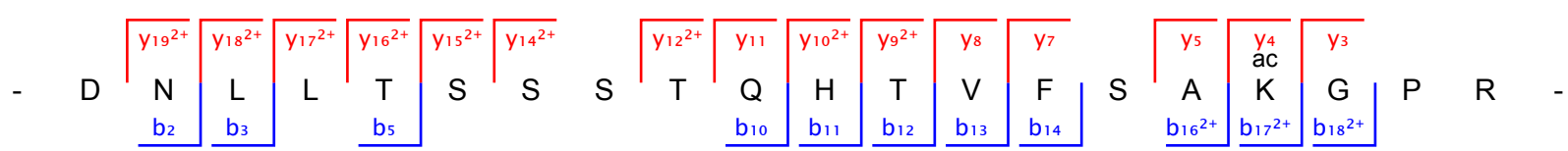
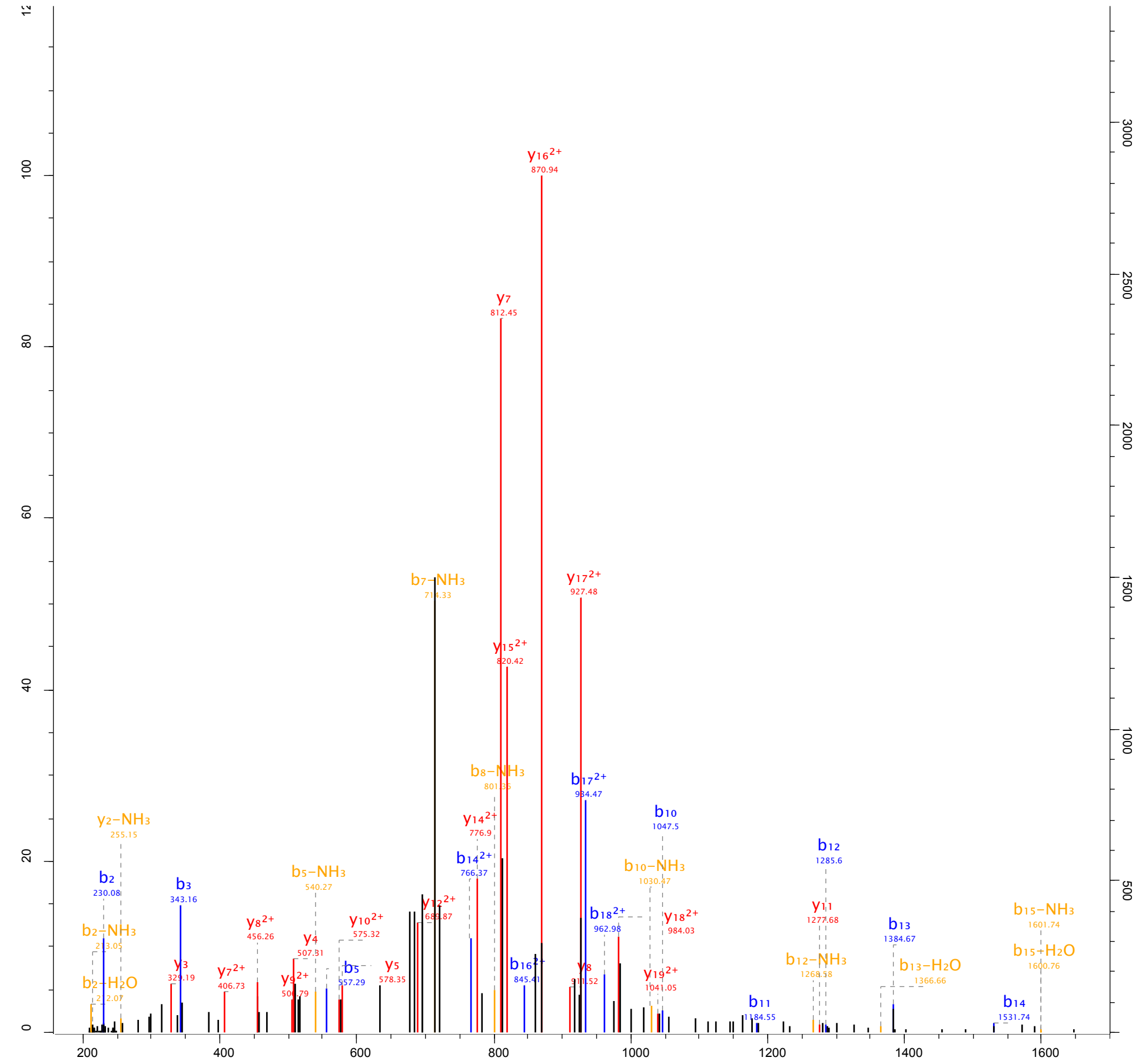
168.26

532.27

Sptan1







062513_SCW_II_53_6_Vargas_Enriched

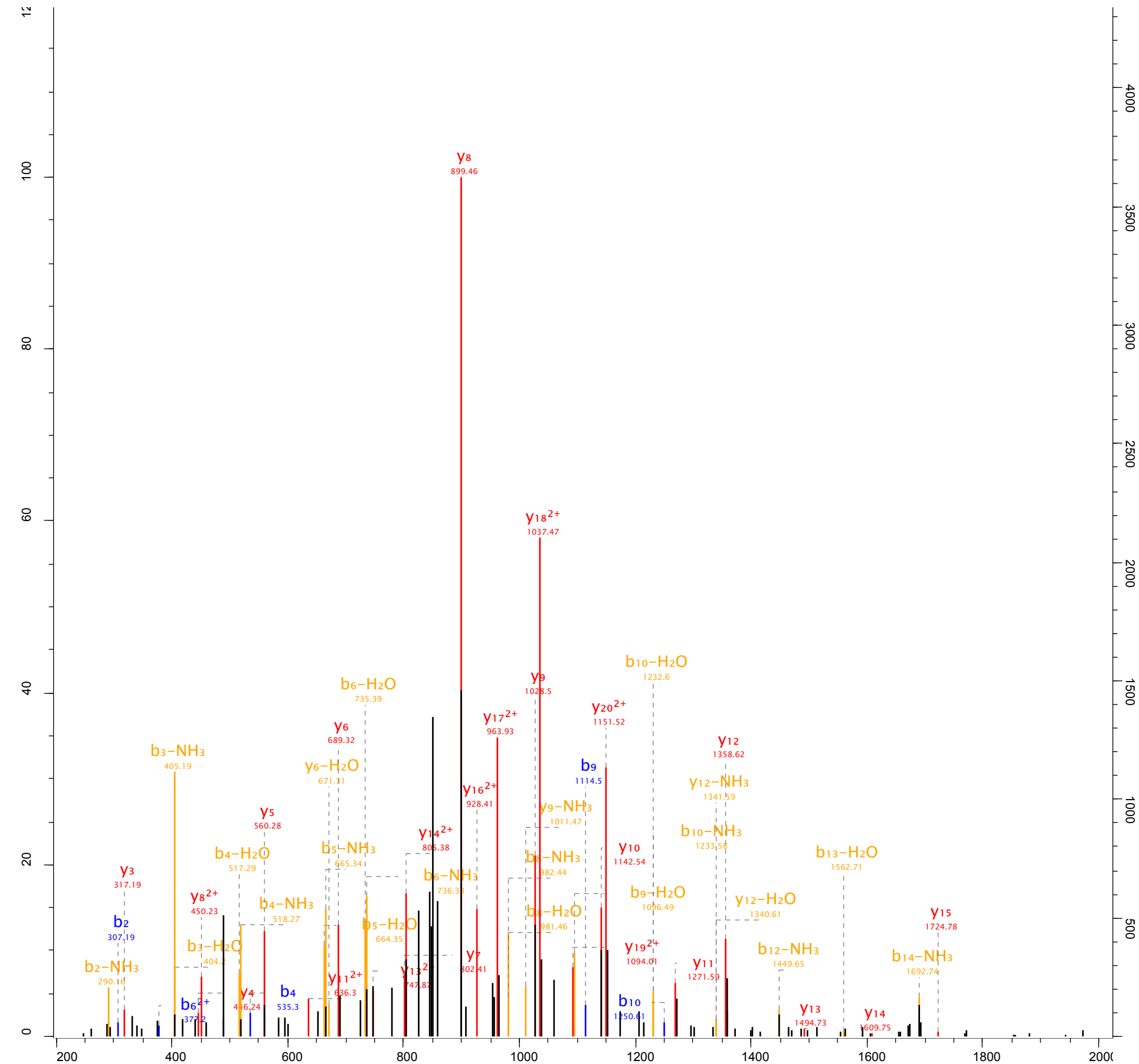
18264

ITMS; CID

126.09

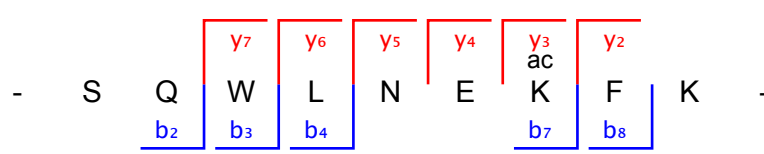
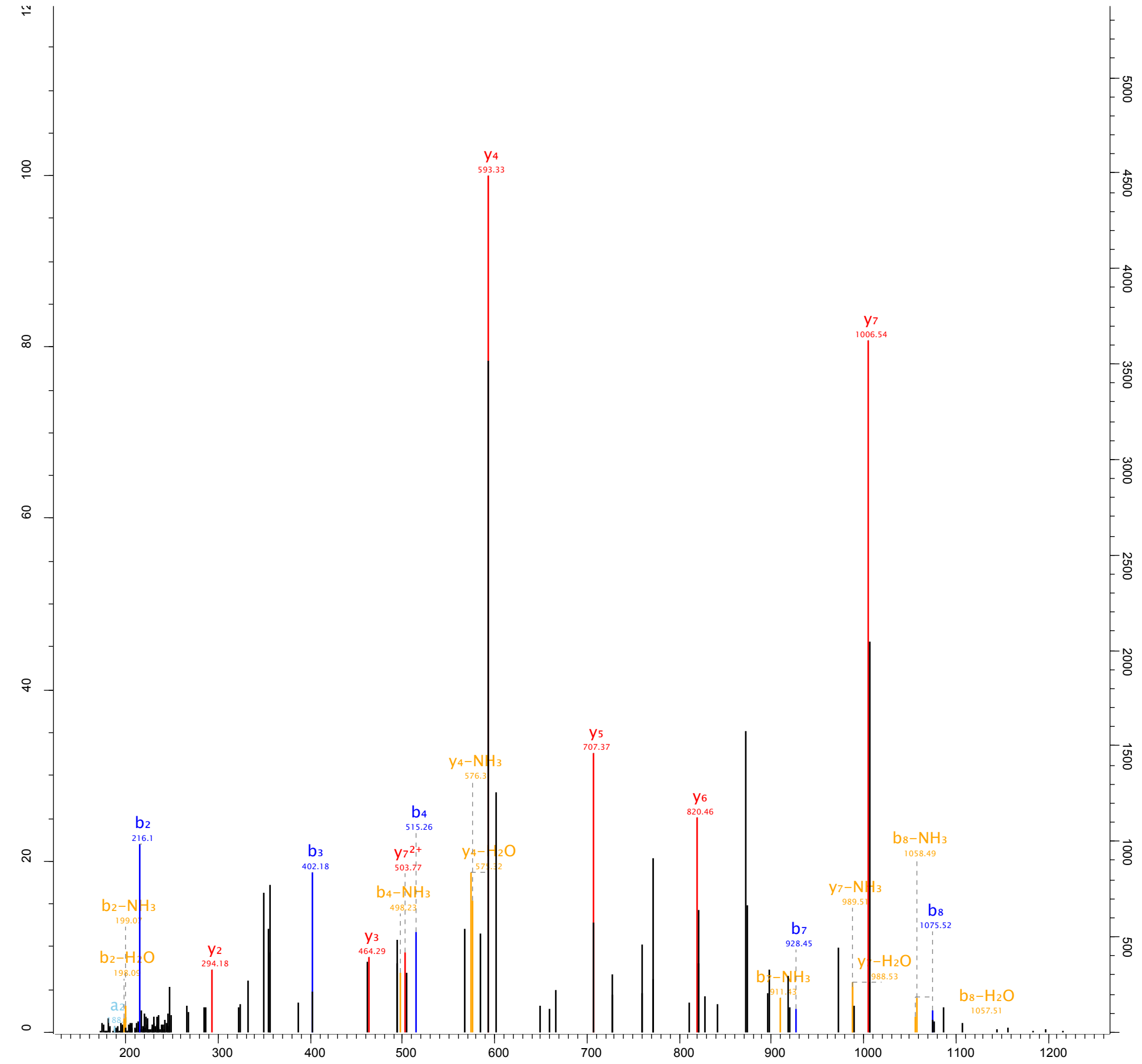
870.41

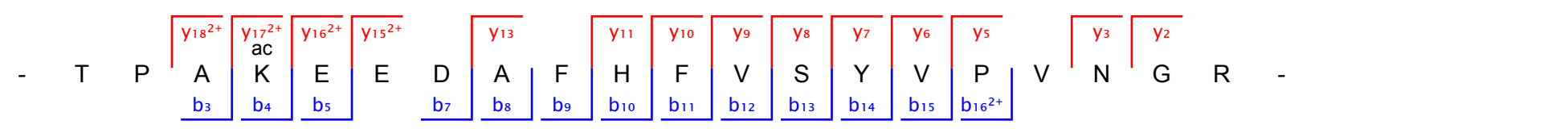
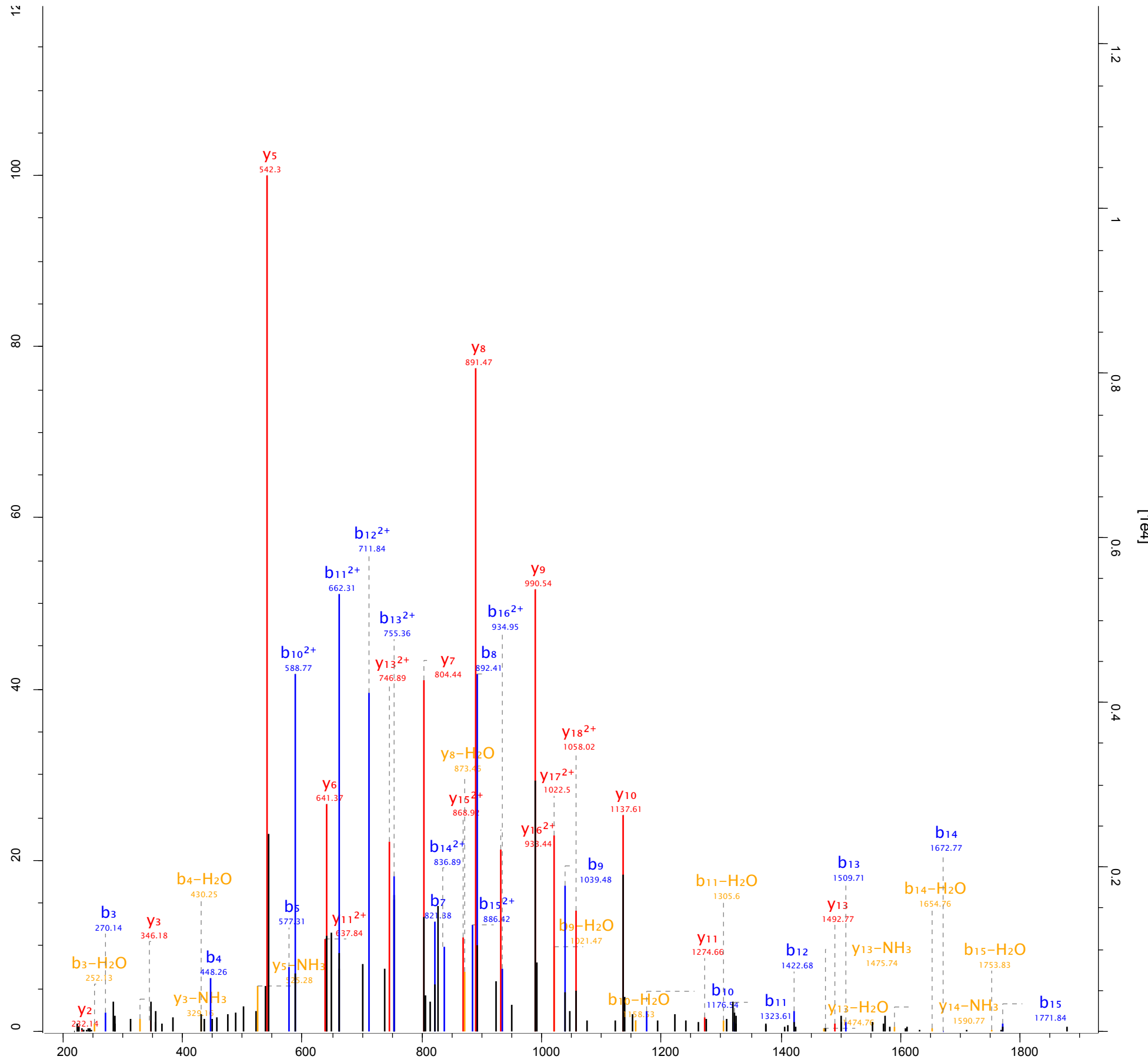
Suclg2

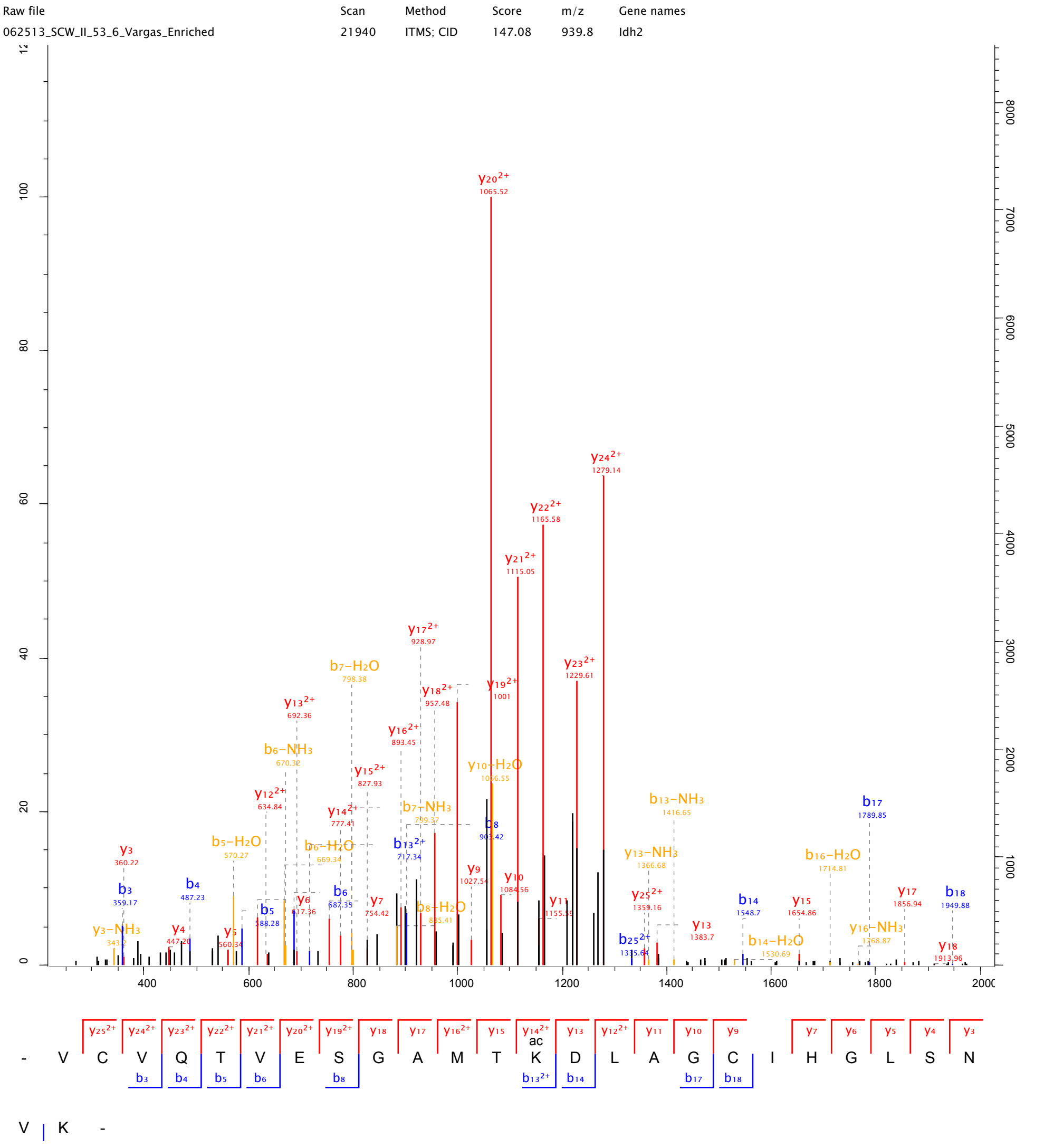


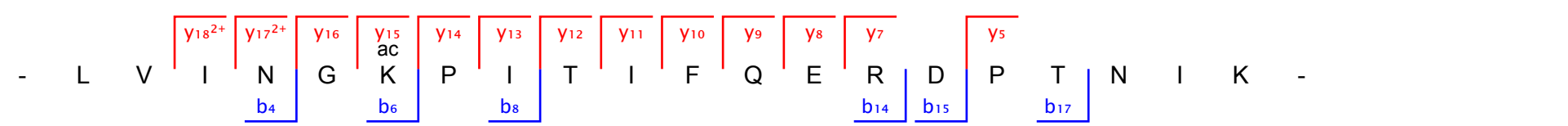
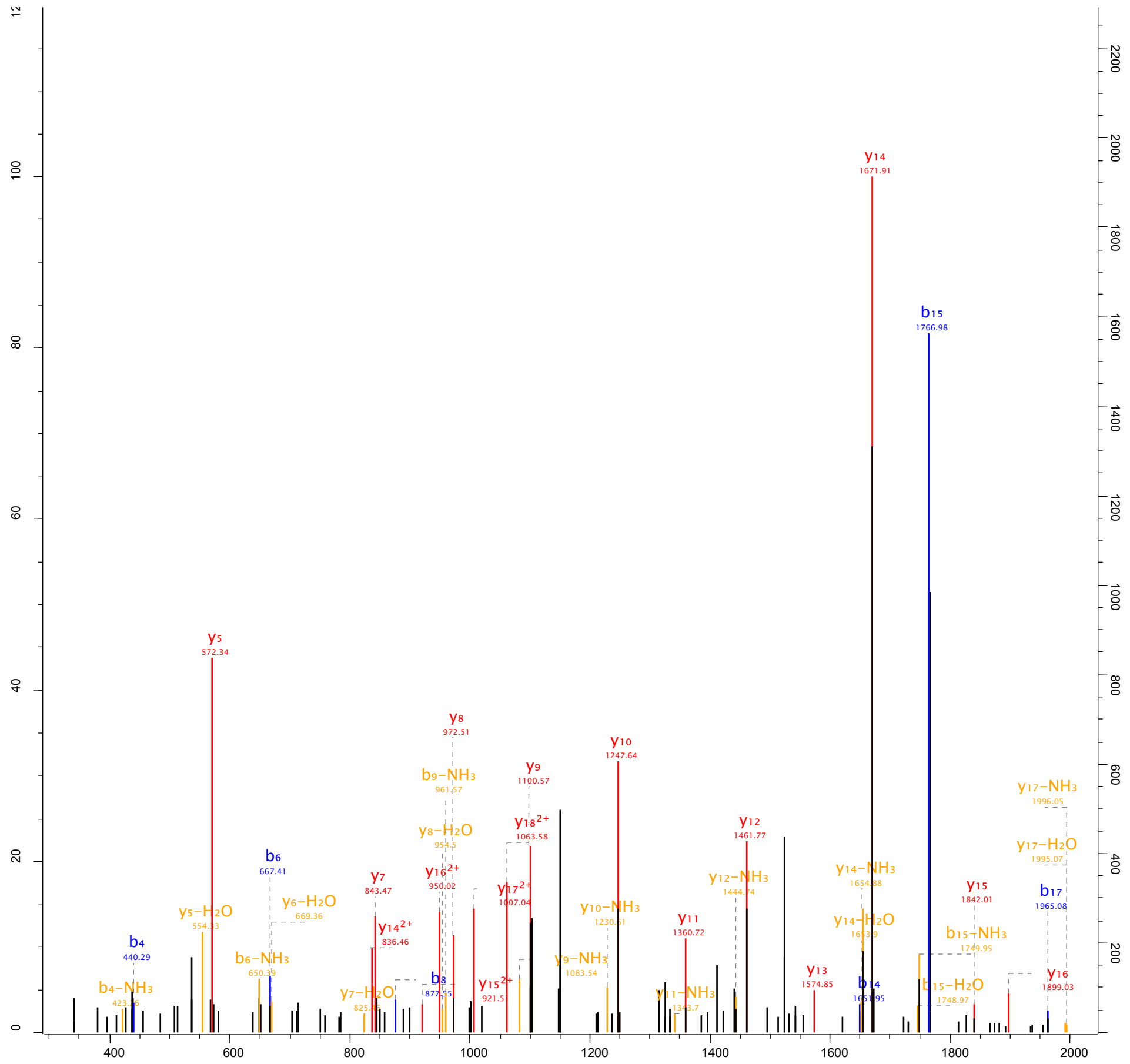
- Q ac K D I F A M D D K S E N E P I E N E A A R -

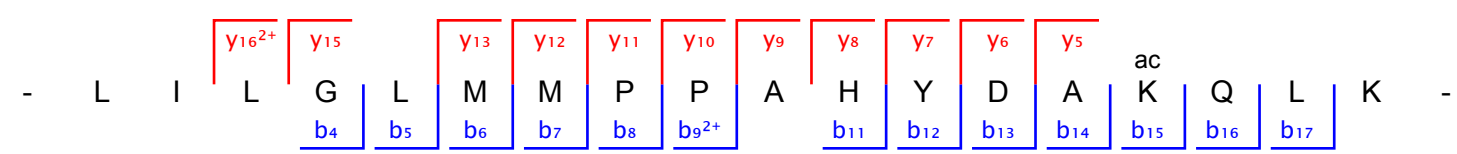
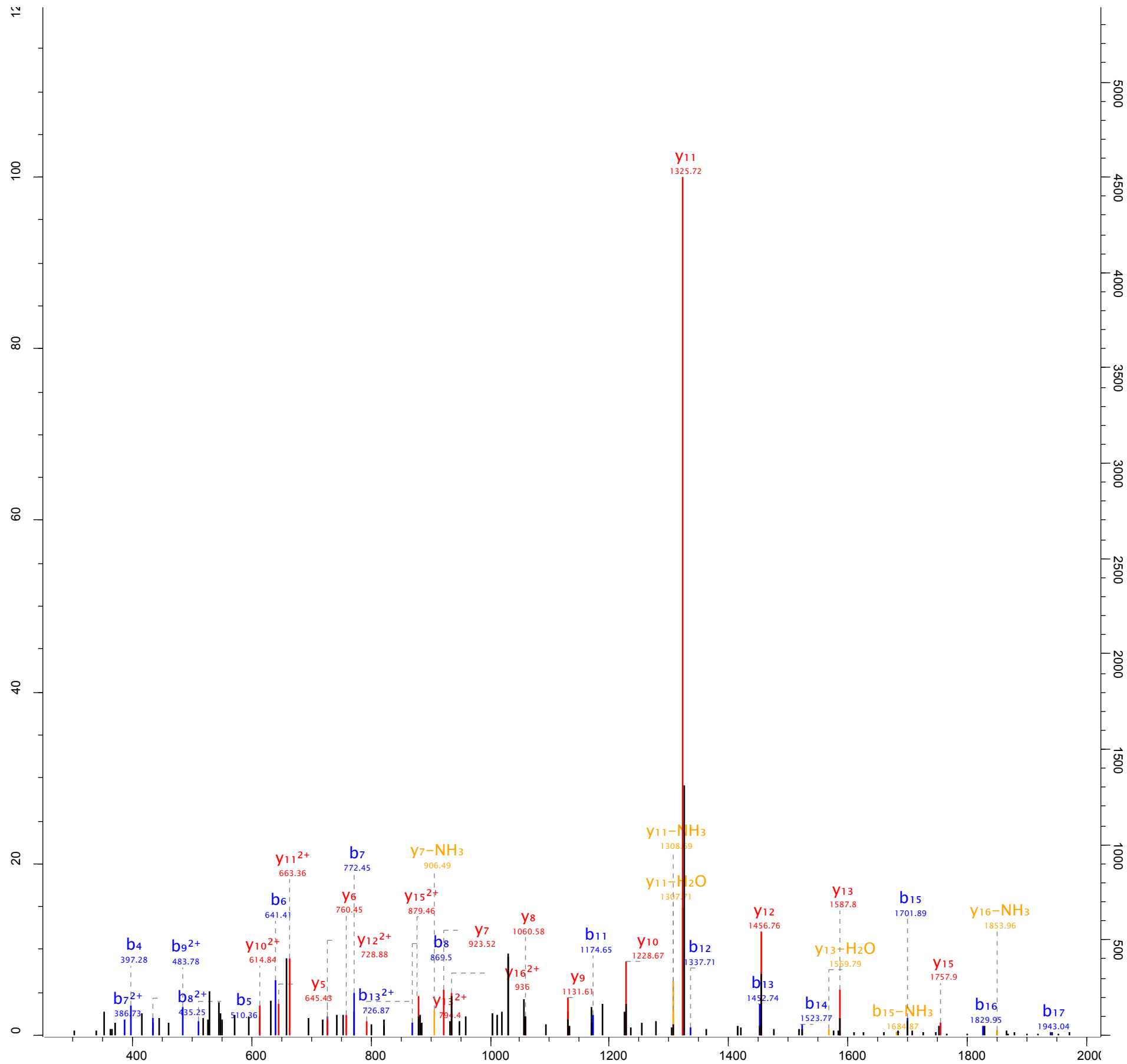
b₂
y₂₀²⁺
y₁₉²⁺
y₁₈²⁺
y₁₇²⁺
y₁₆²⁺
y₁₅
y₁₄
y₁₃
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
b₄
b₆²⁺
b₉
b₁₀

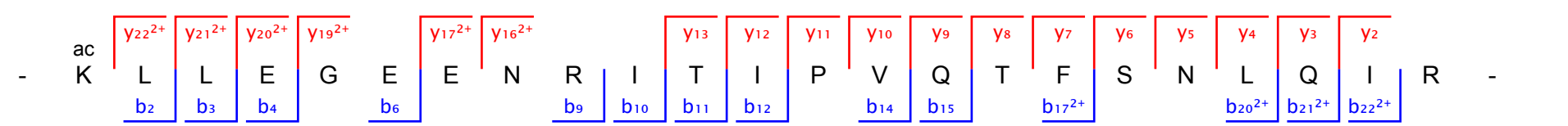
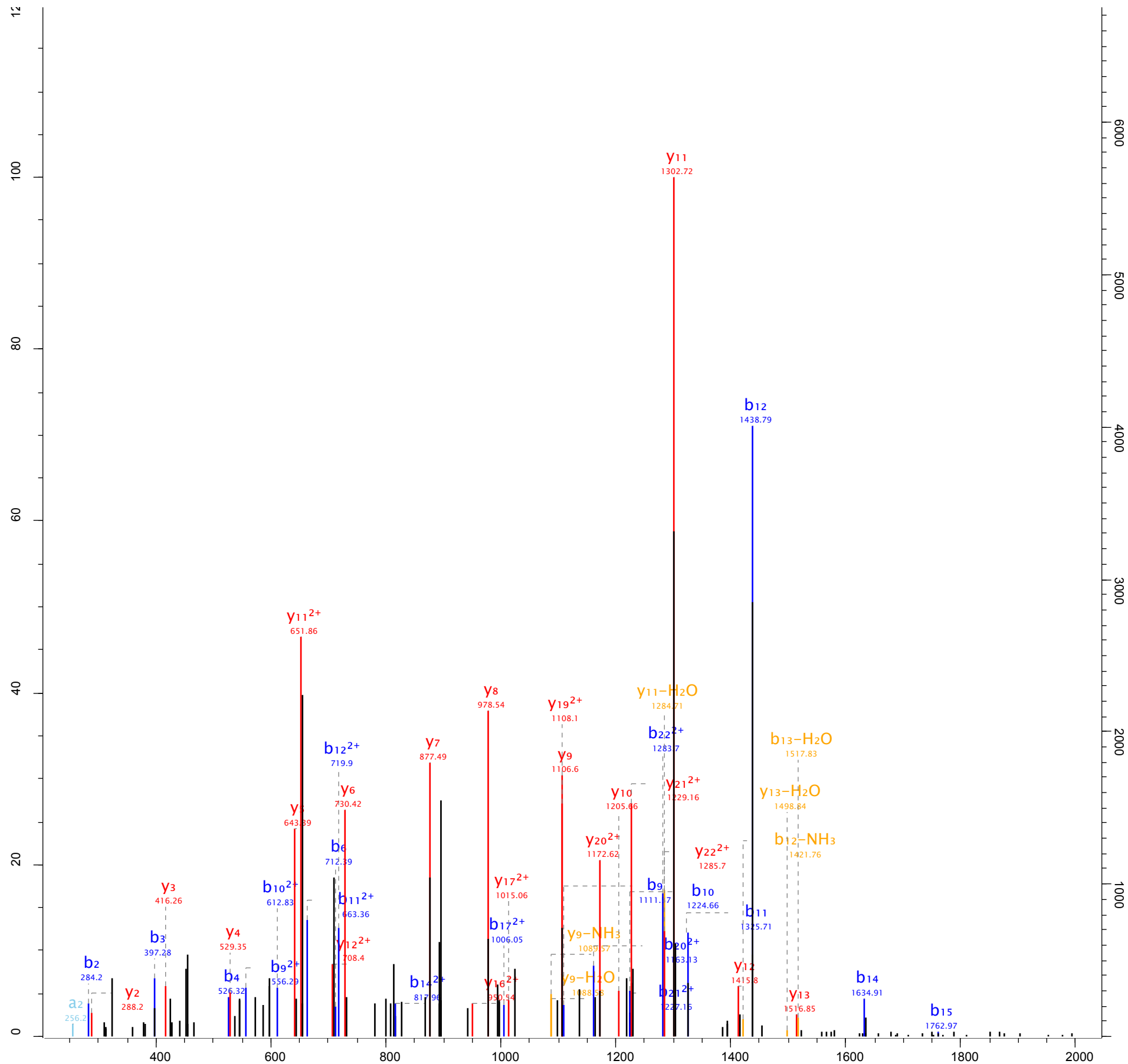


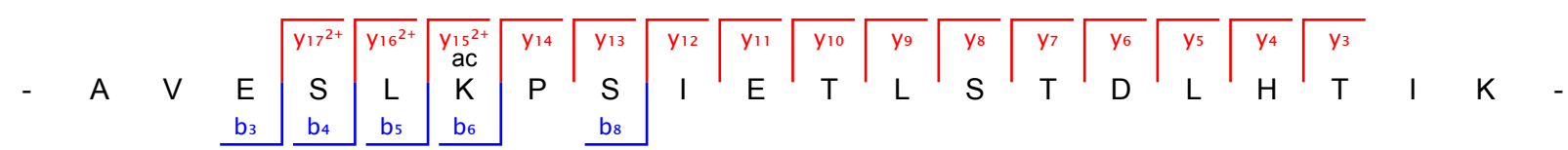
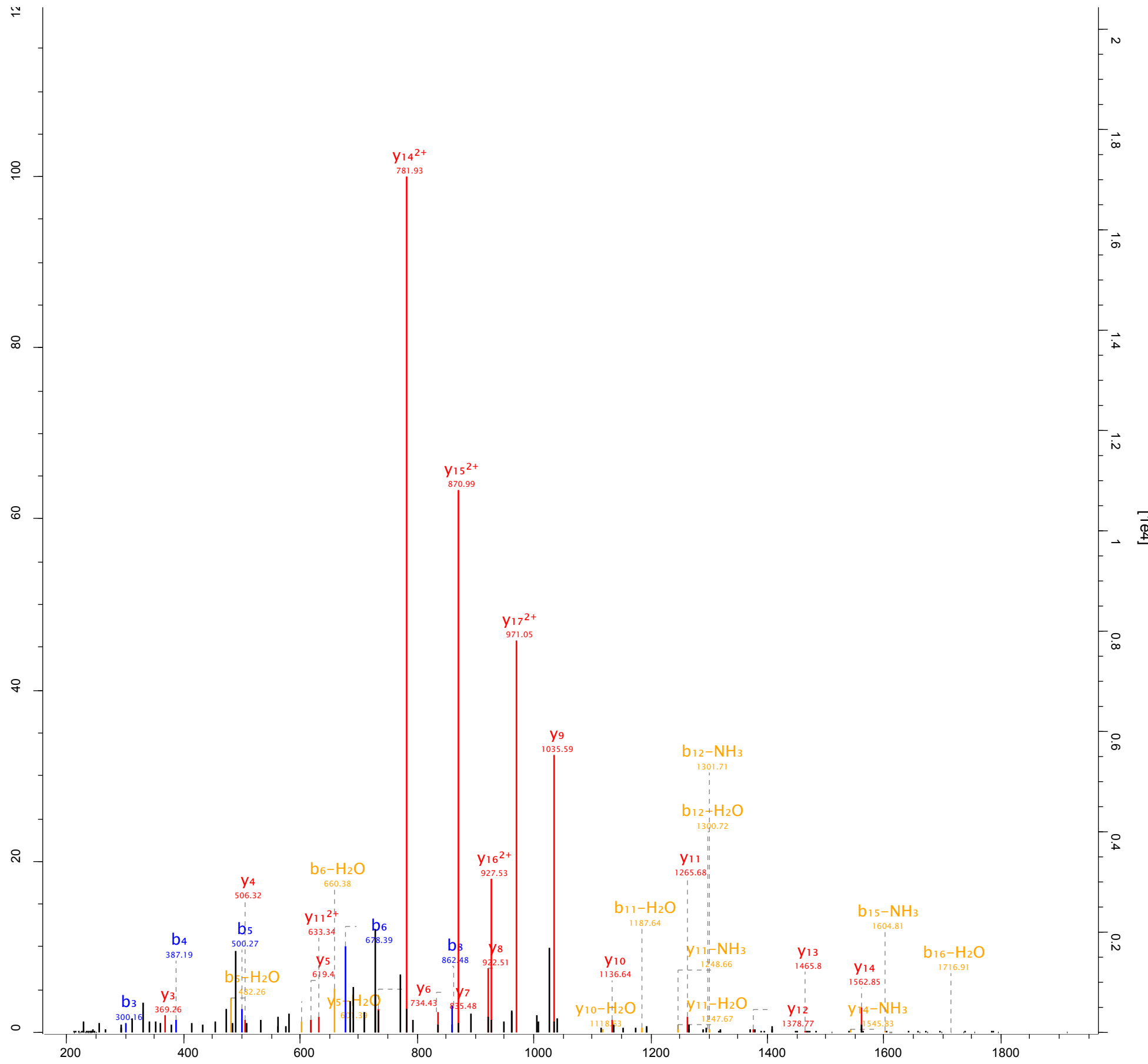


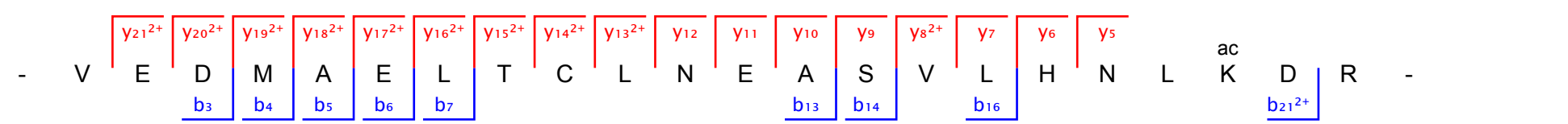
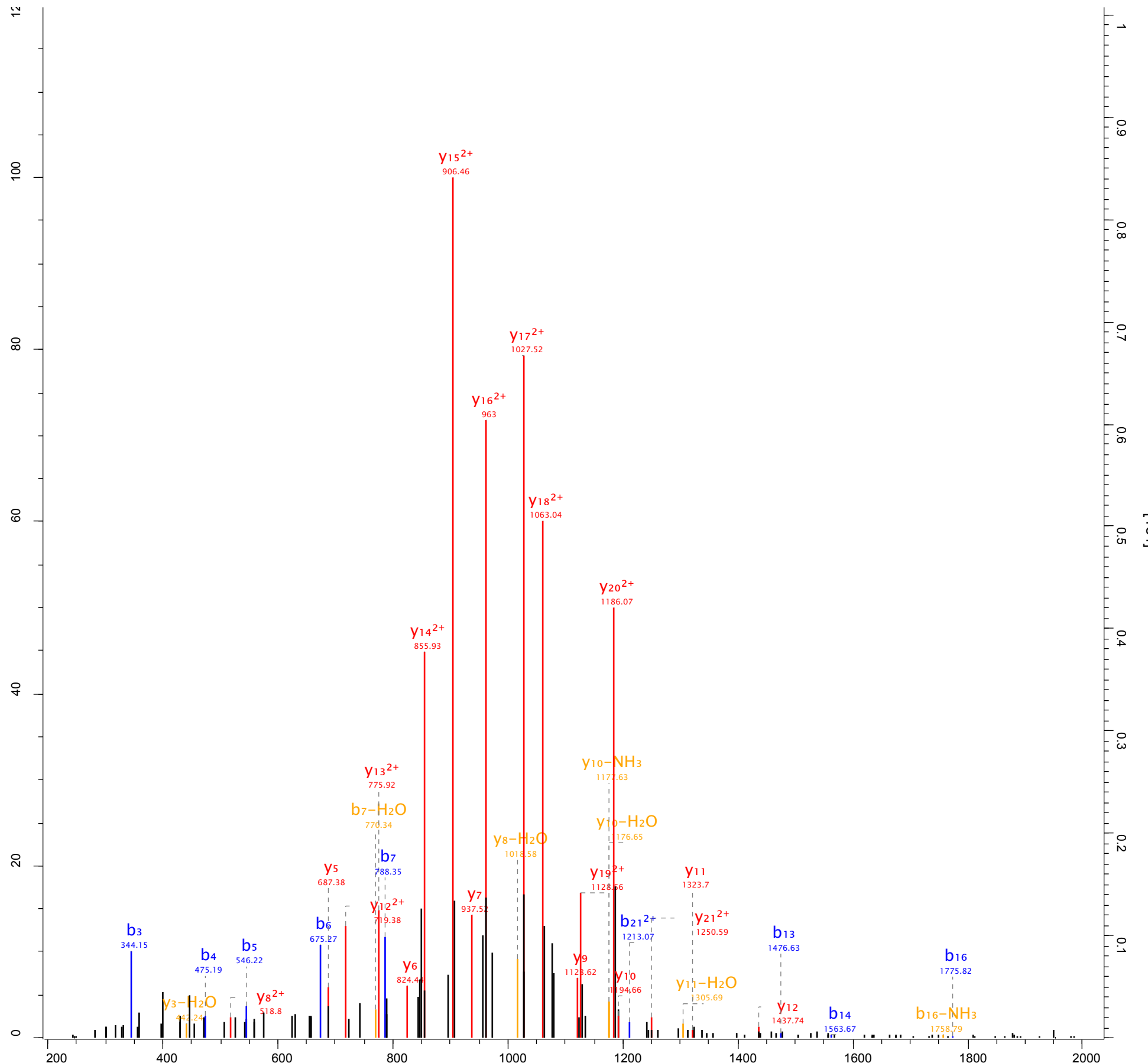


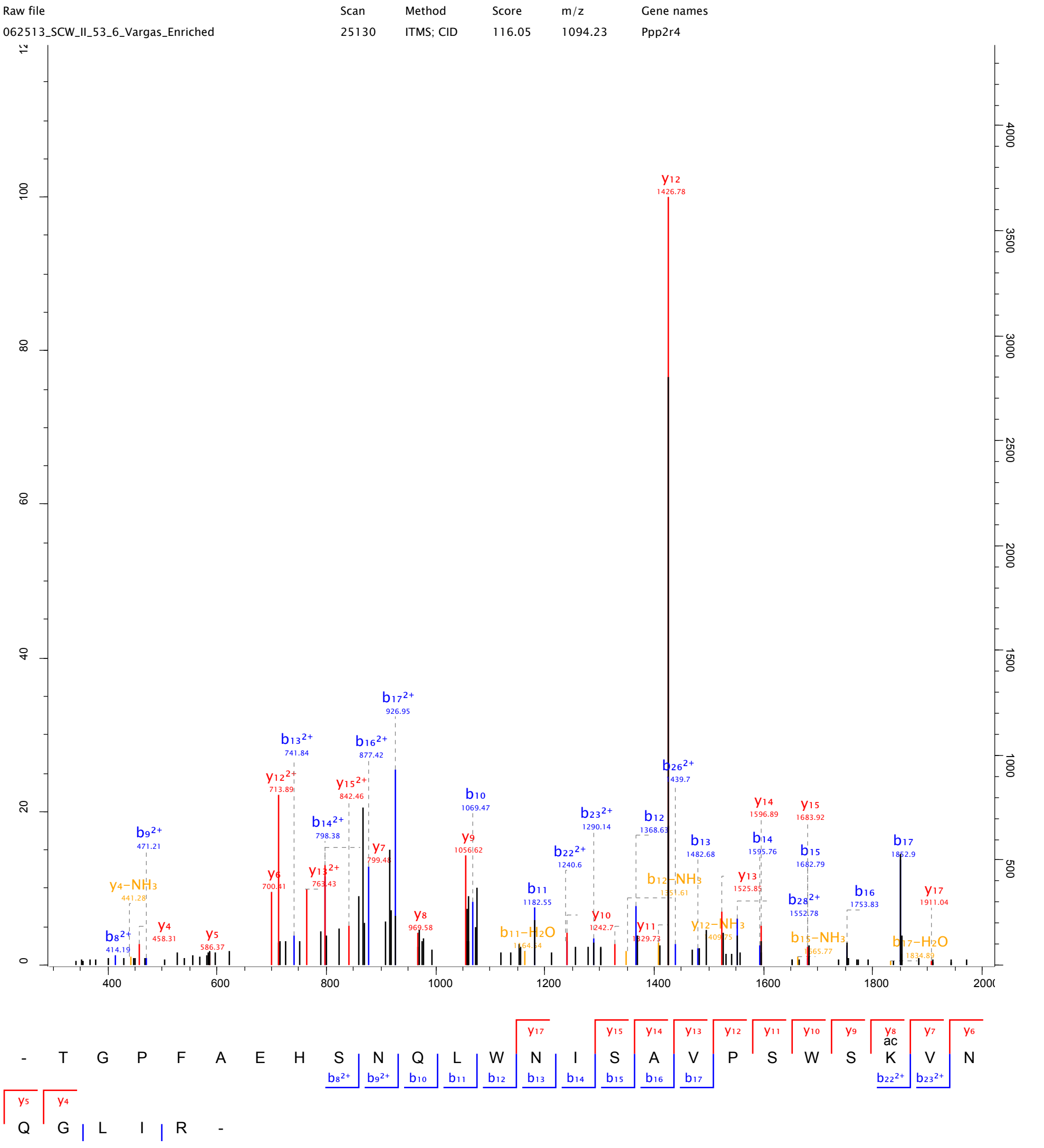


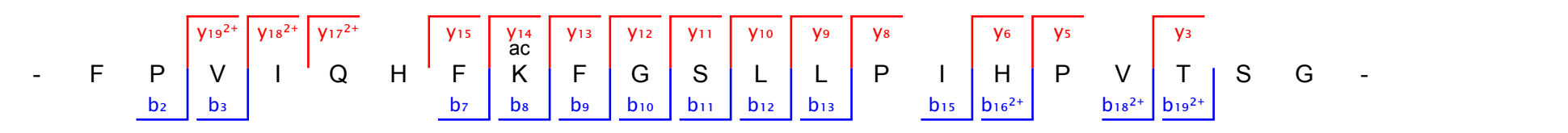
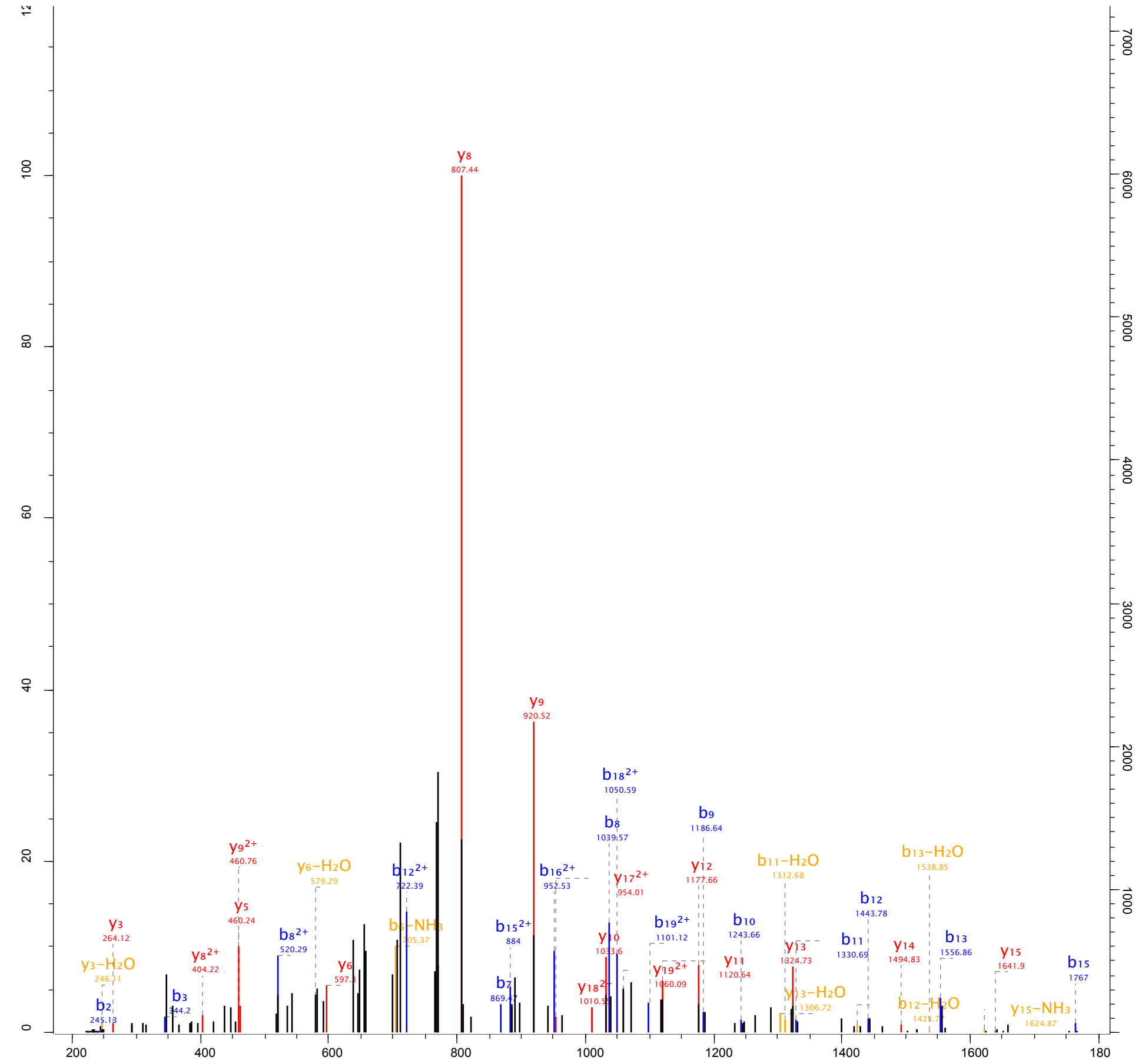


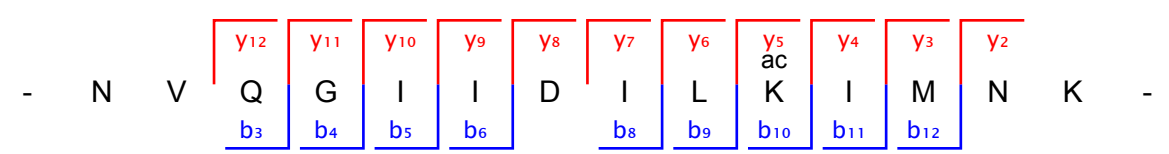
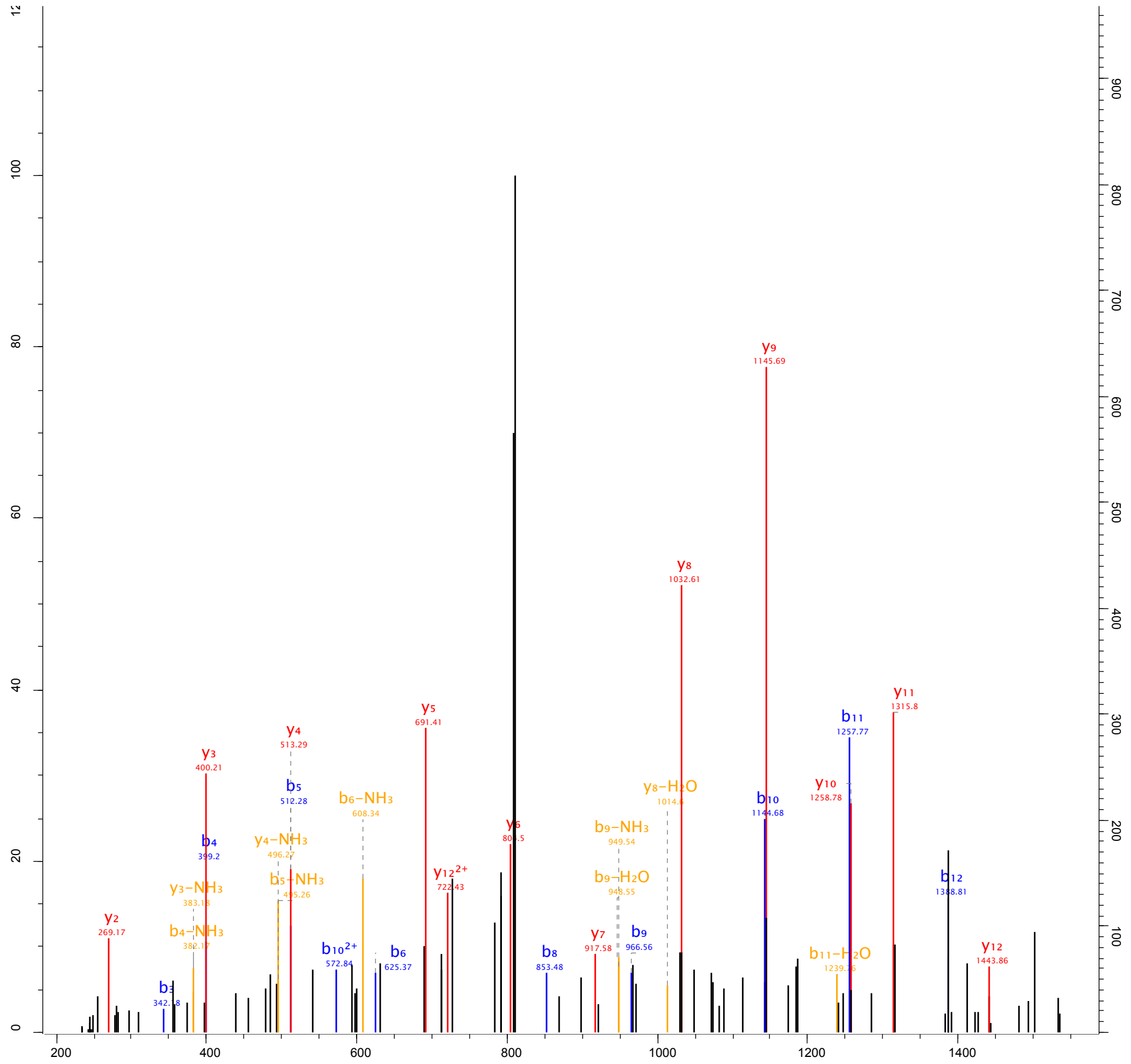


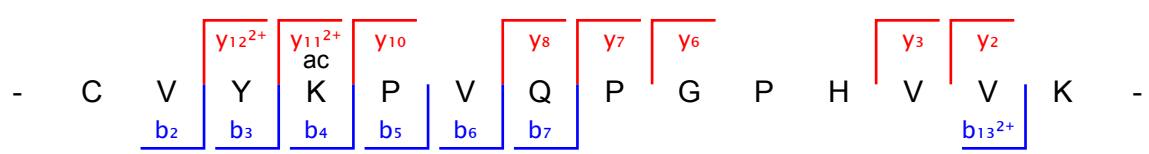
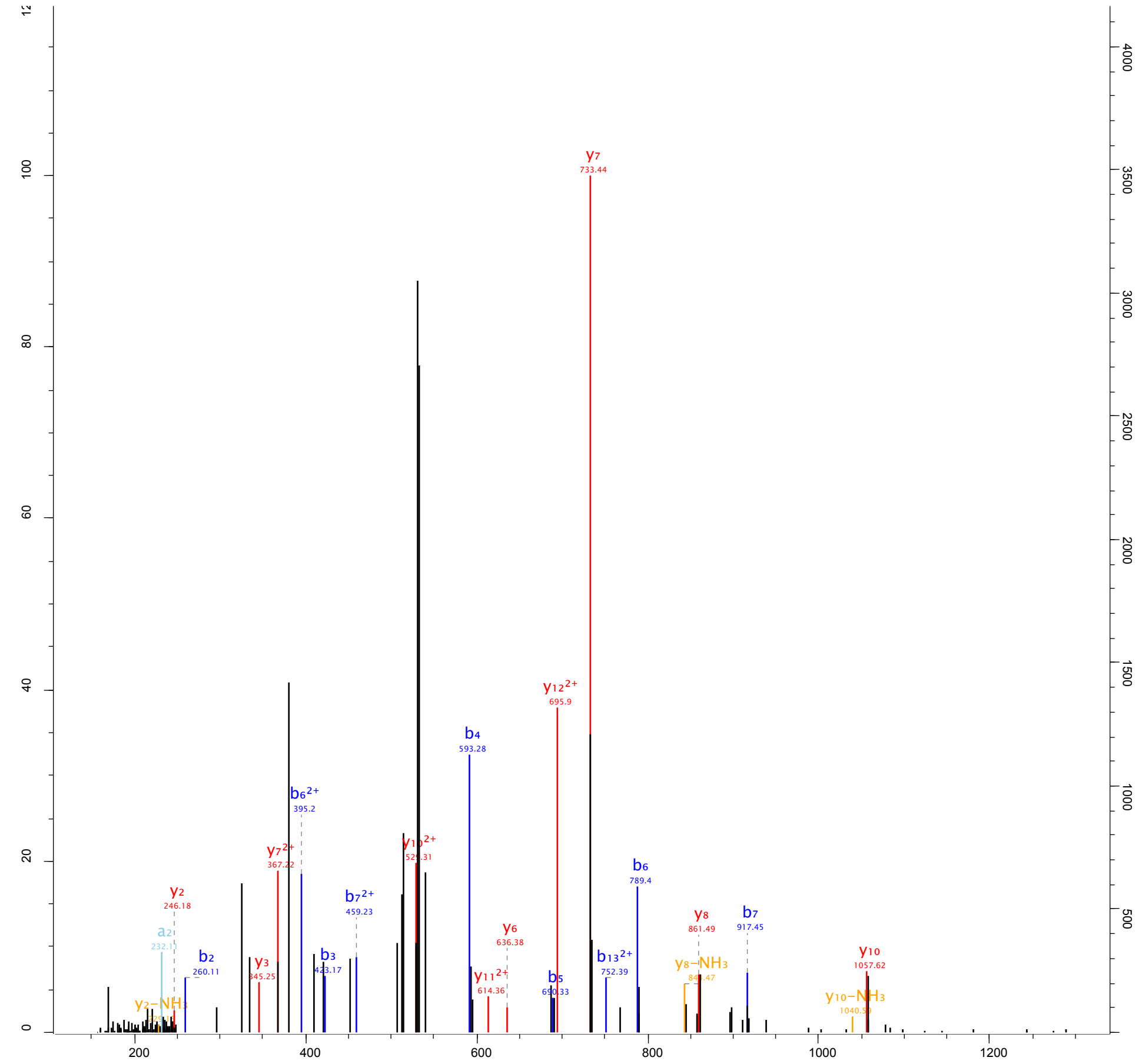


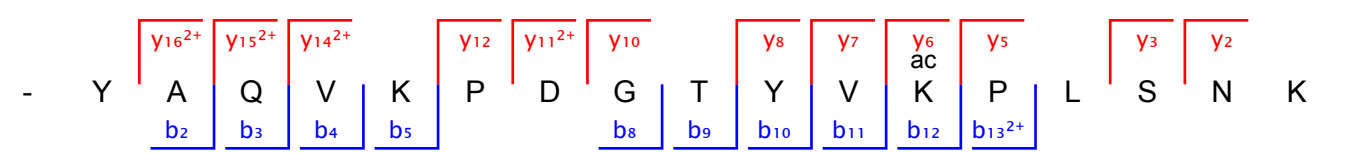
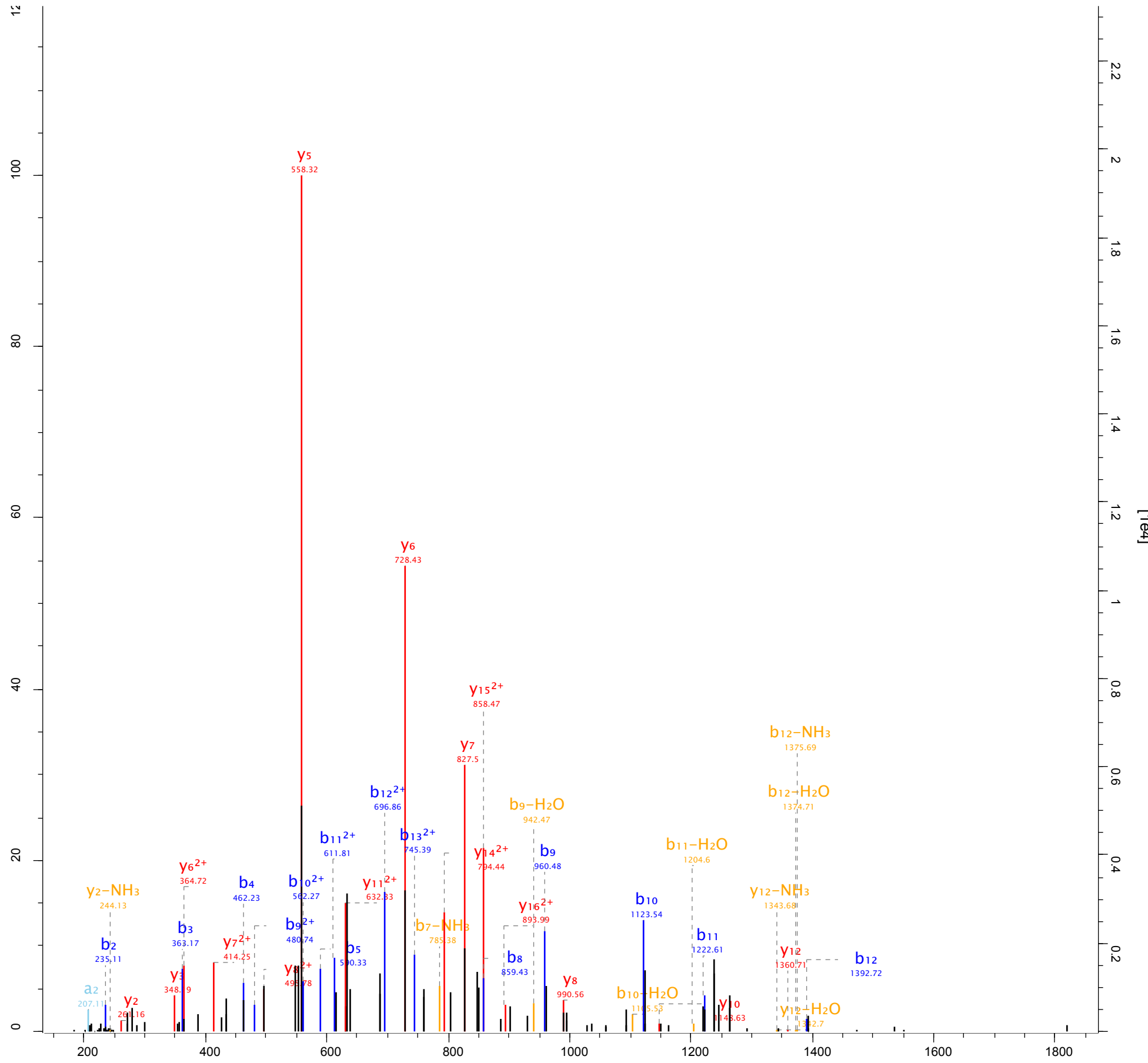


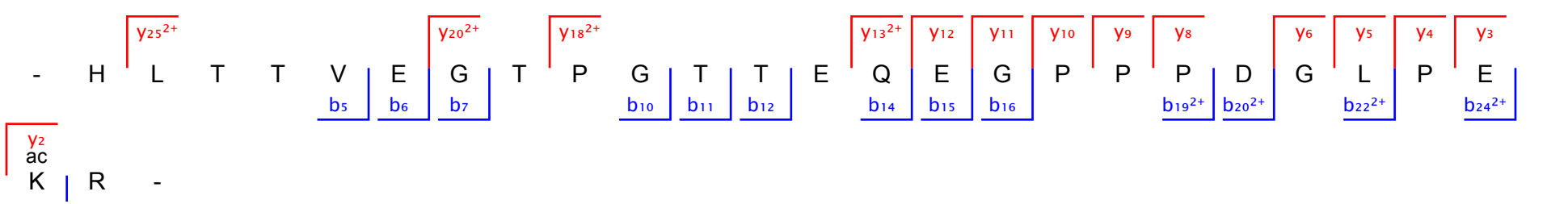
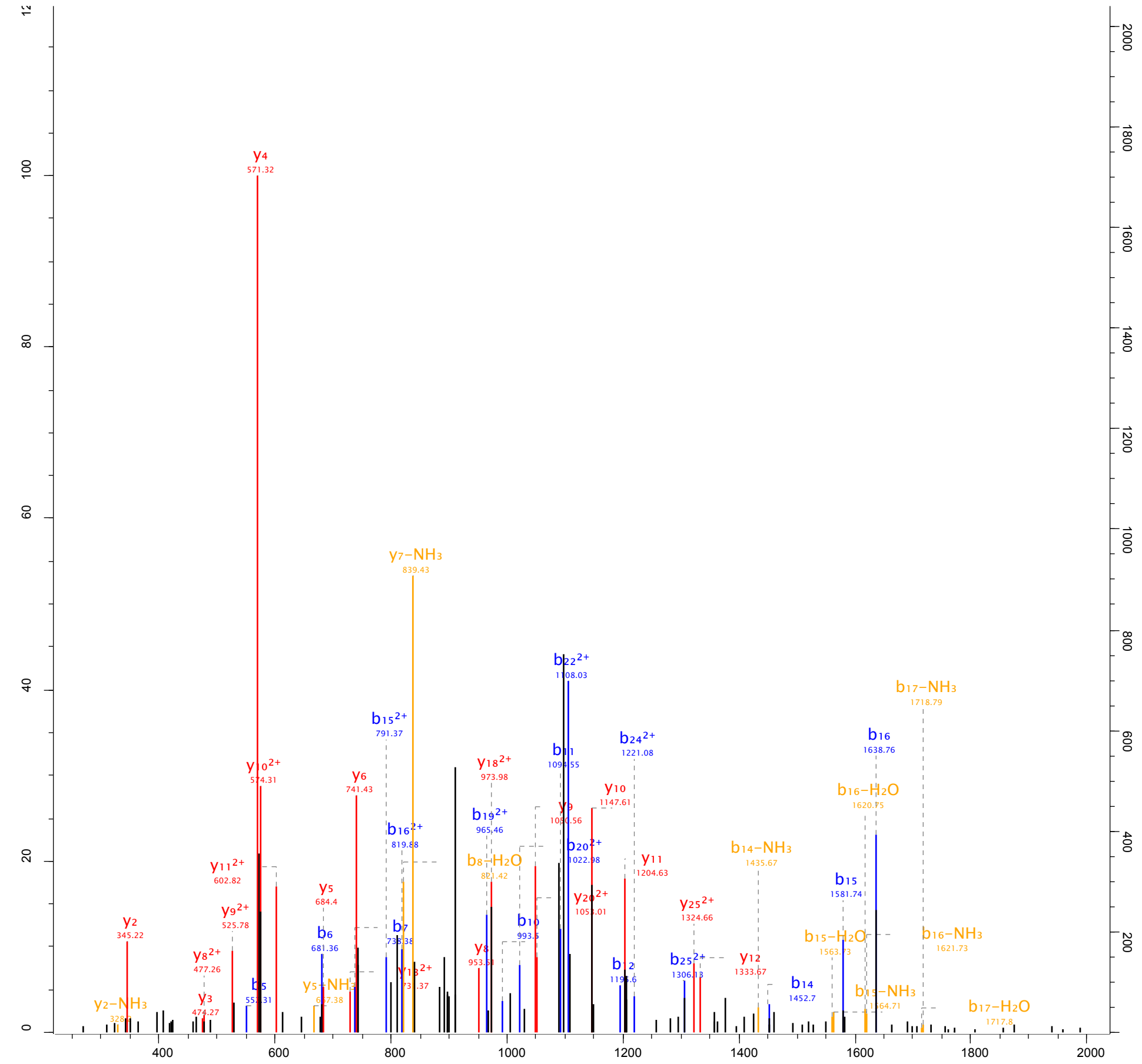




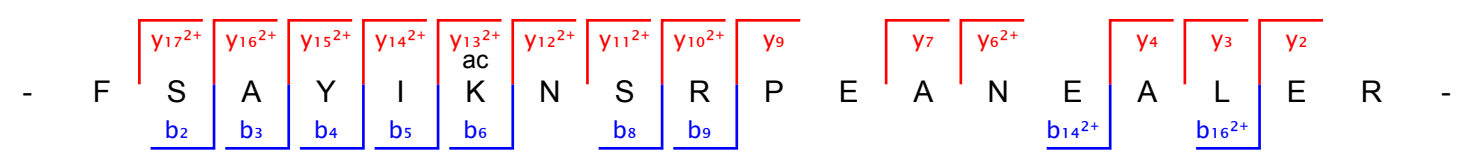
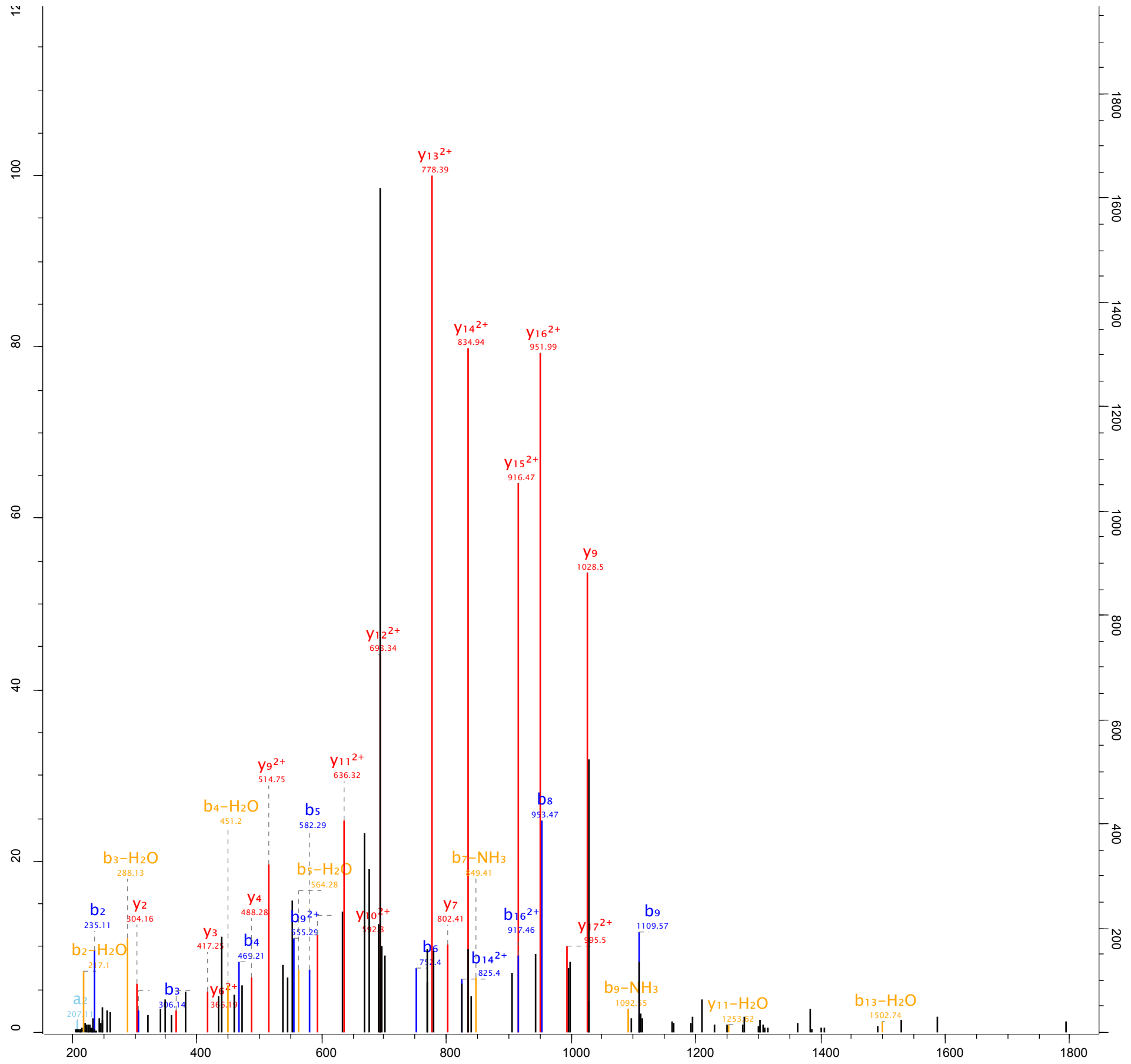


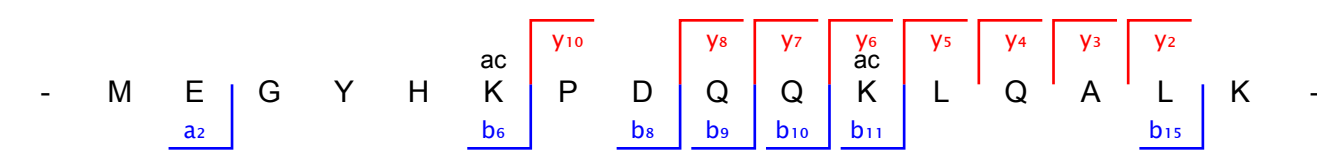
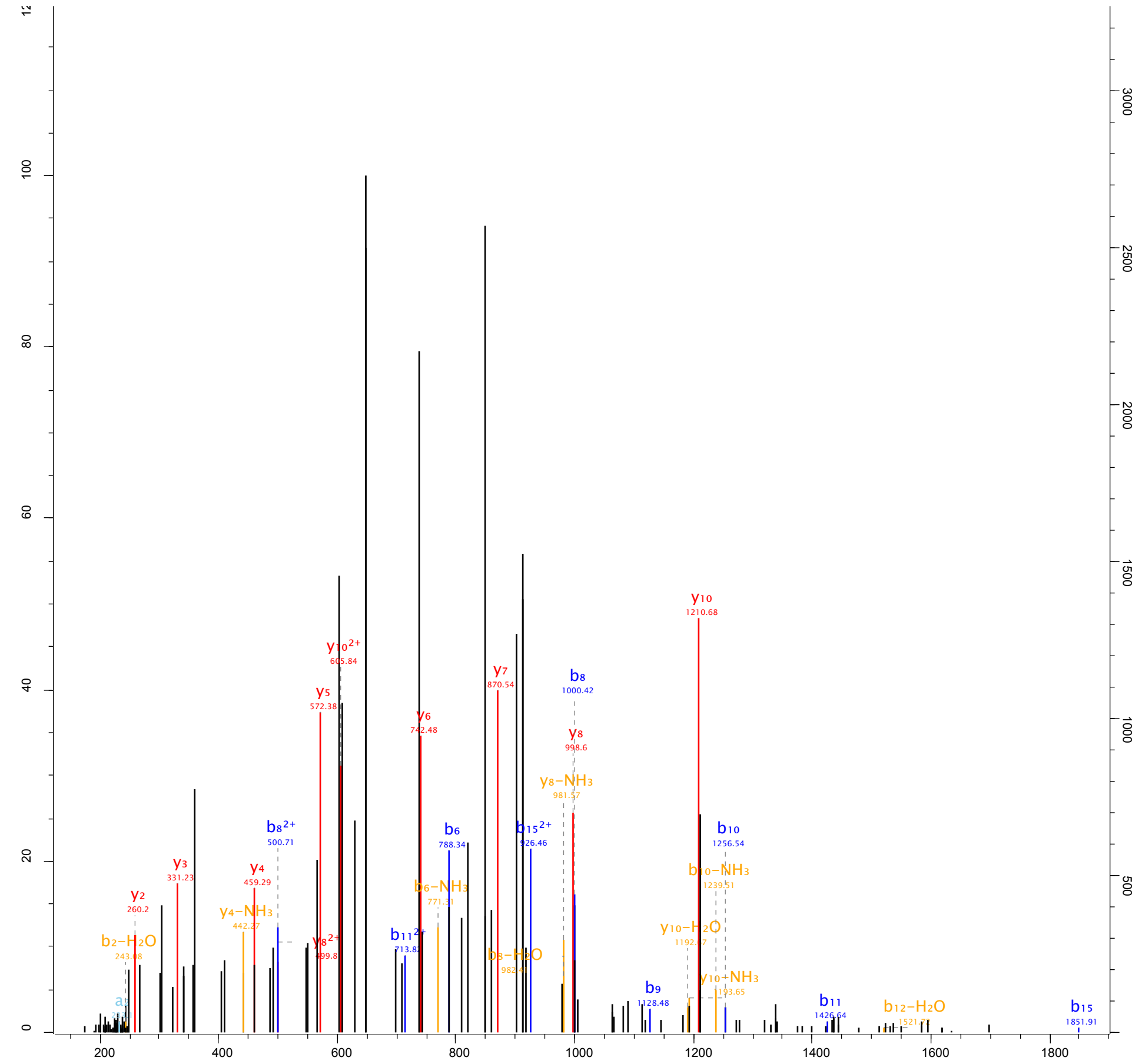




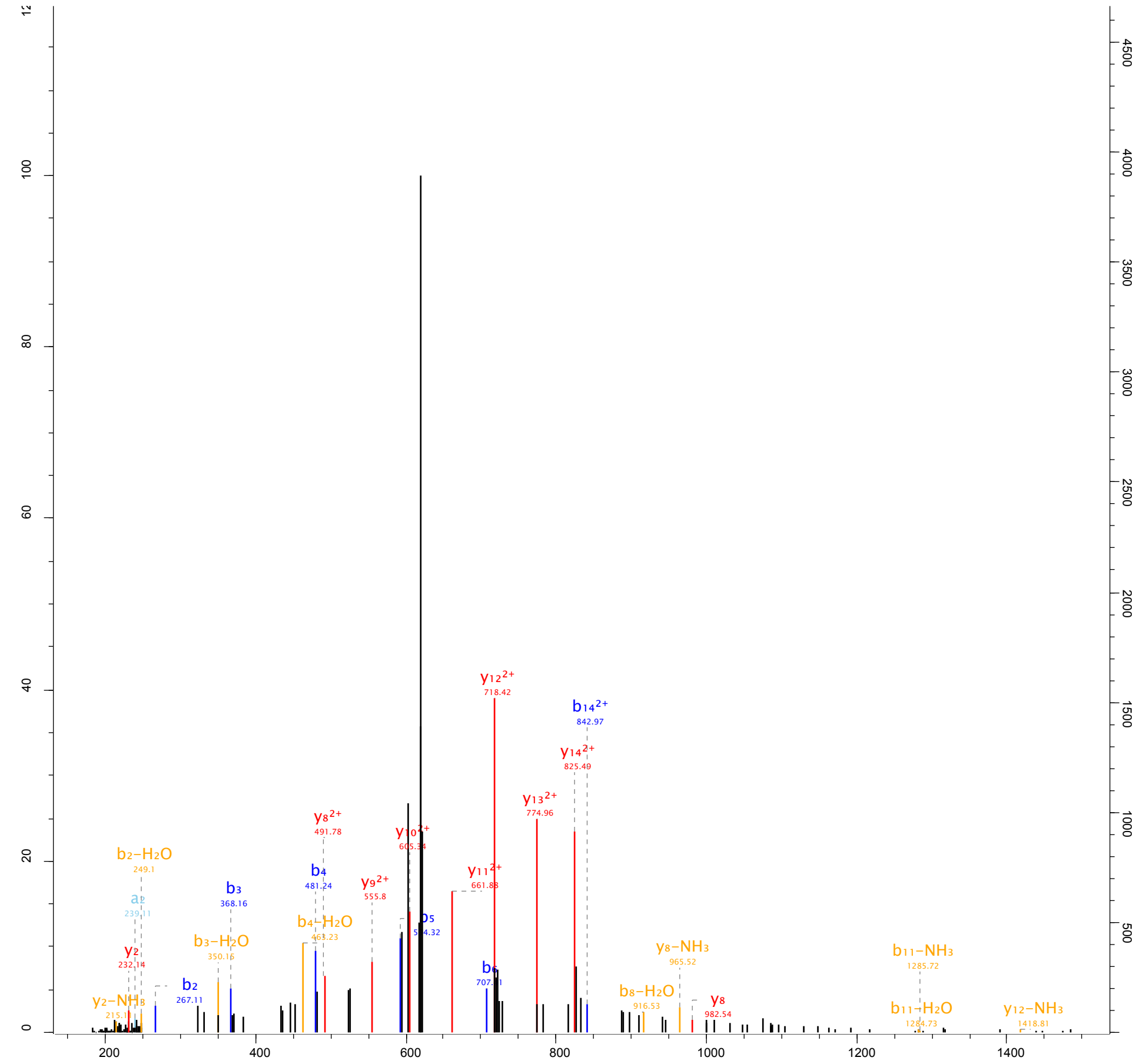


Raw file: 062513_SCW_II_53_7_Vargas_Enriched
 Scan: 16253 Method: ITMS; CID Score: 118.71 m/z: 713.36 Gene names: Clic4





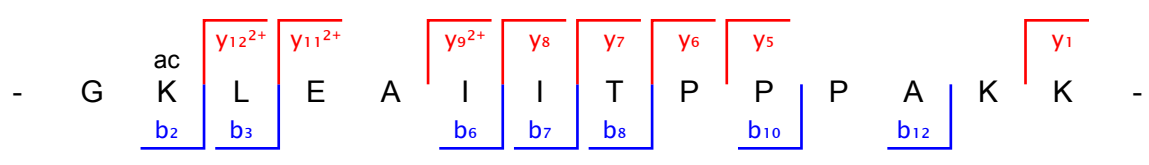
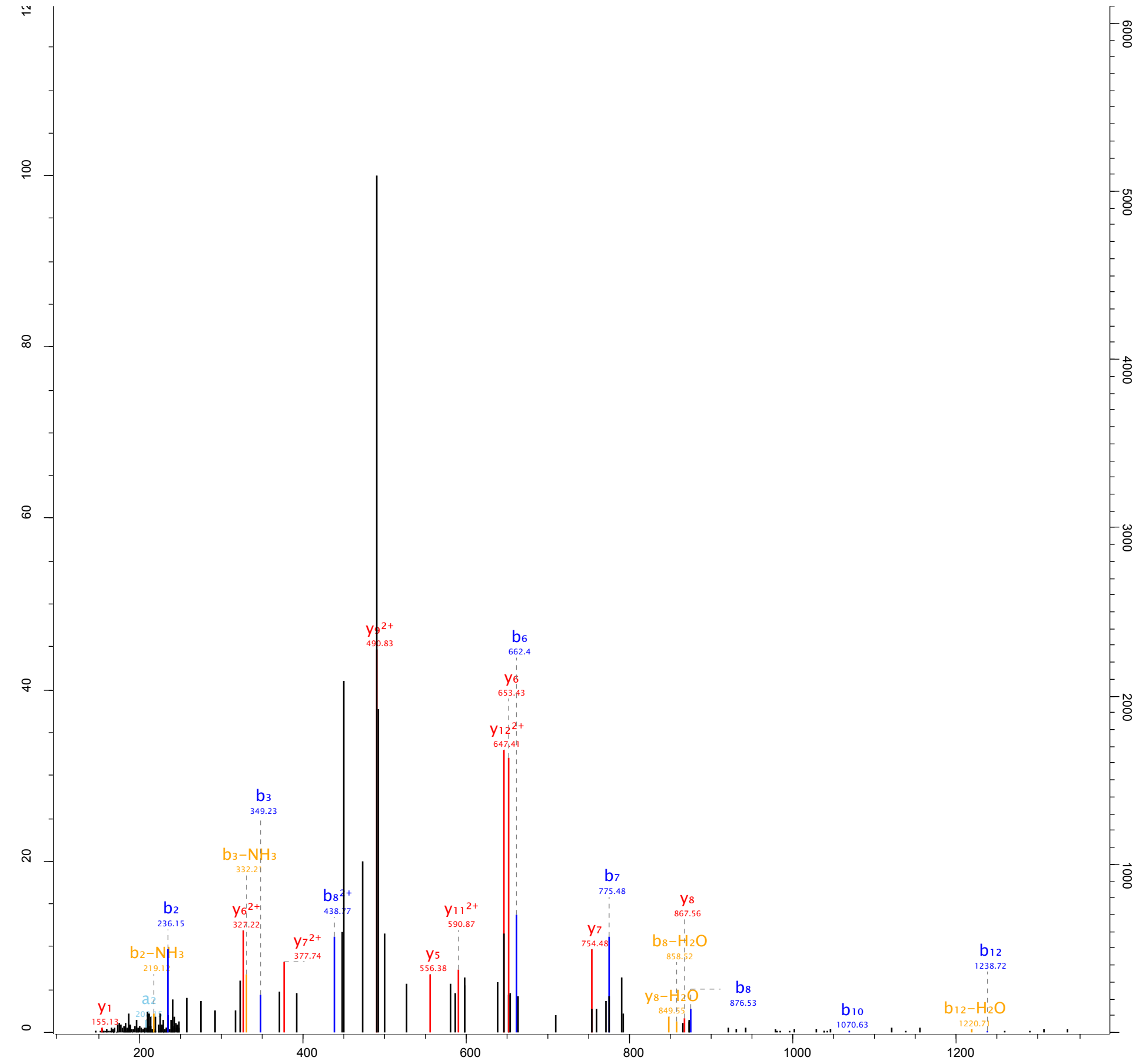
Raw file: 062513_SCW_II_53_7_Vargas_Enriched
 Scan: 17032
 Method: ITMS; CID
 Score: 84.3
 m/z: 639.36
 Gene names: Erh

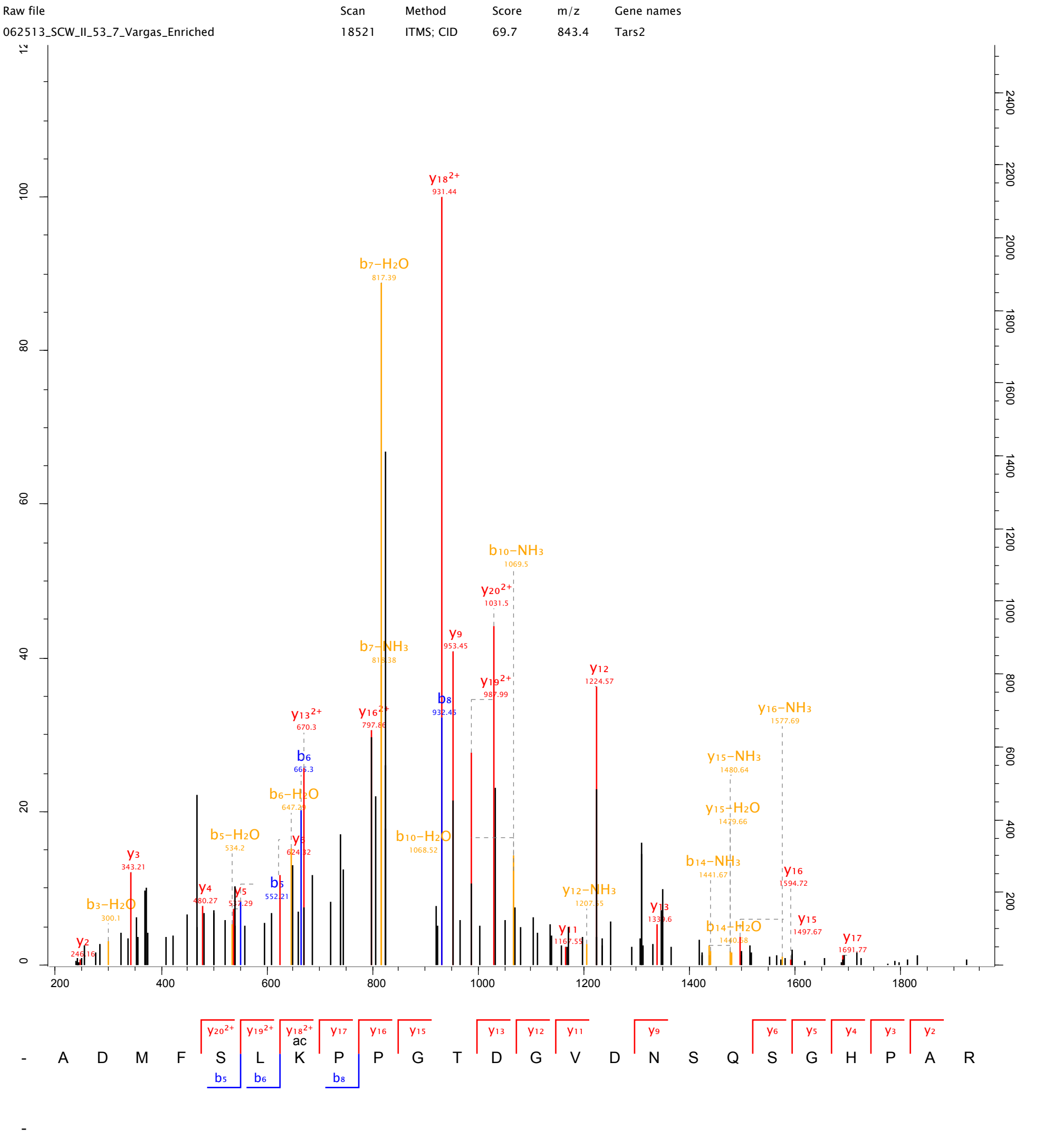


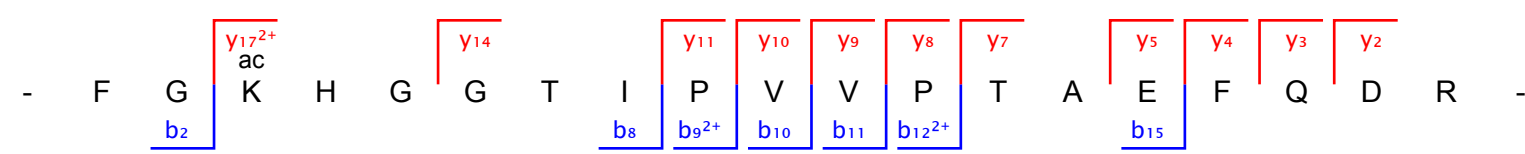
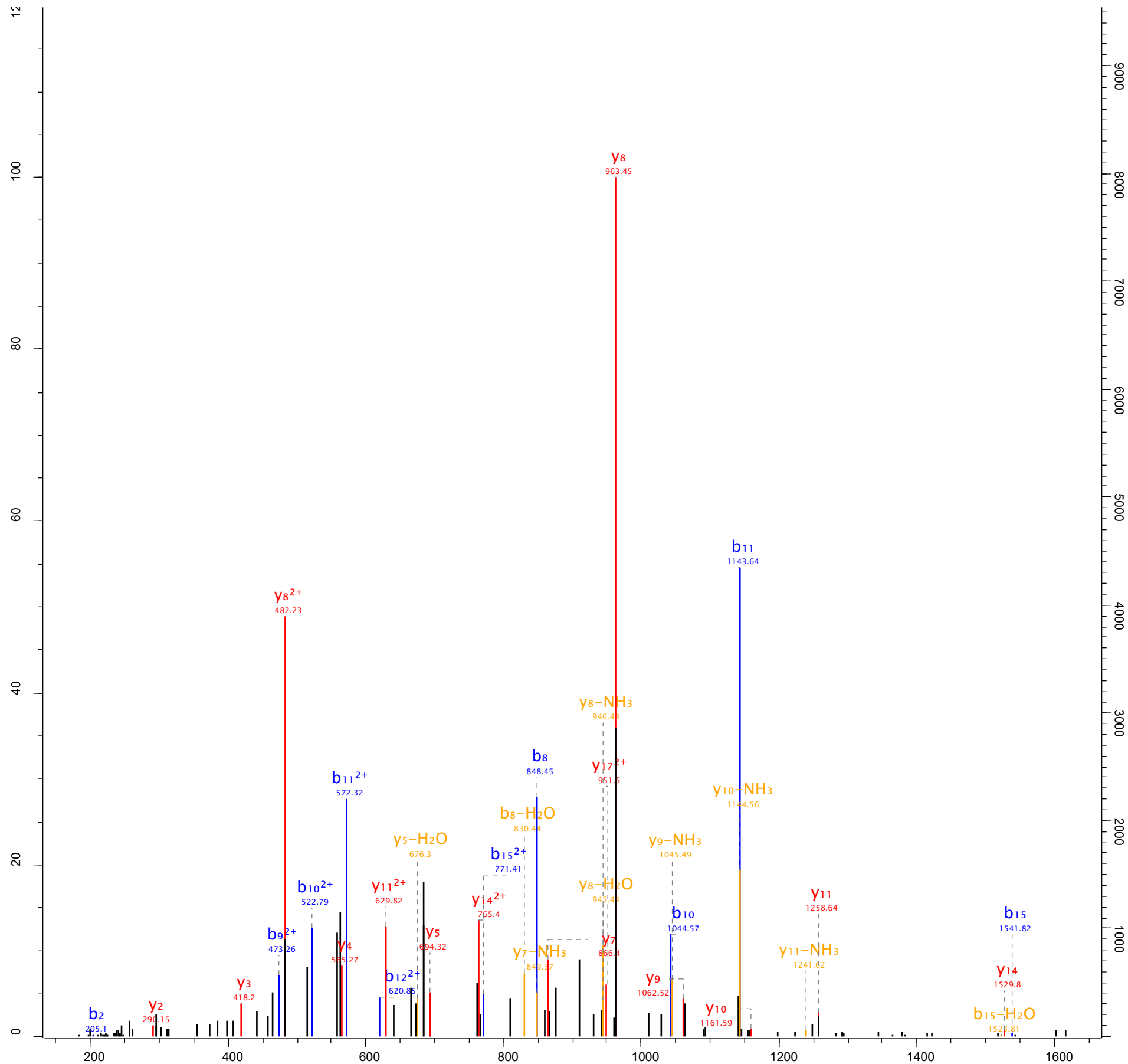
ac - S H T I L L V Q P T K R P E G R -

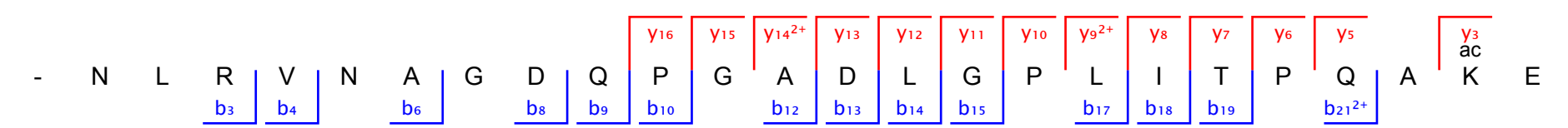
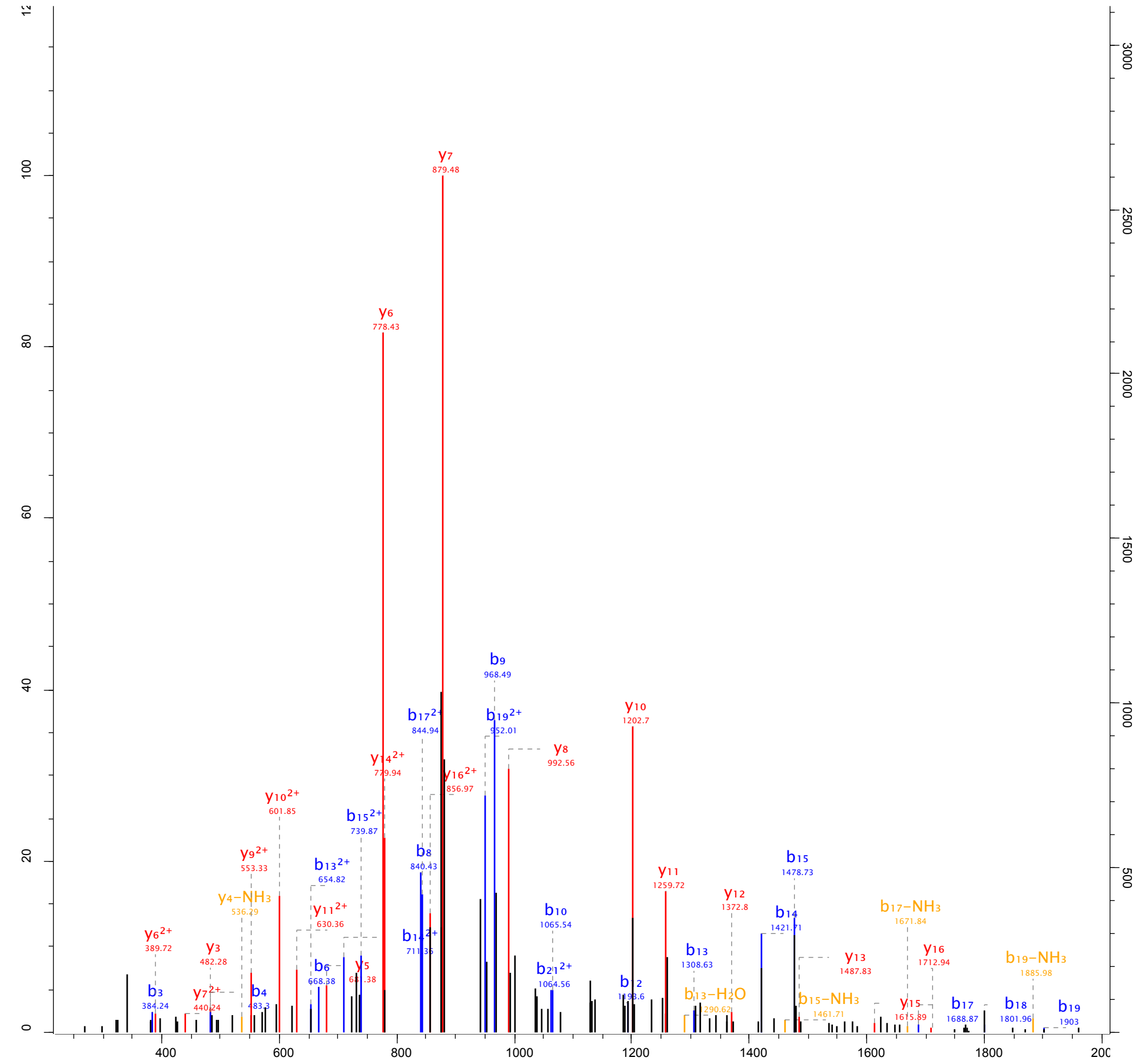
Fragmentation labels below the sequence:

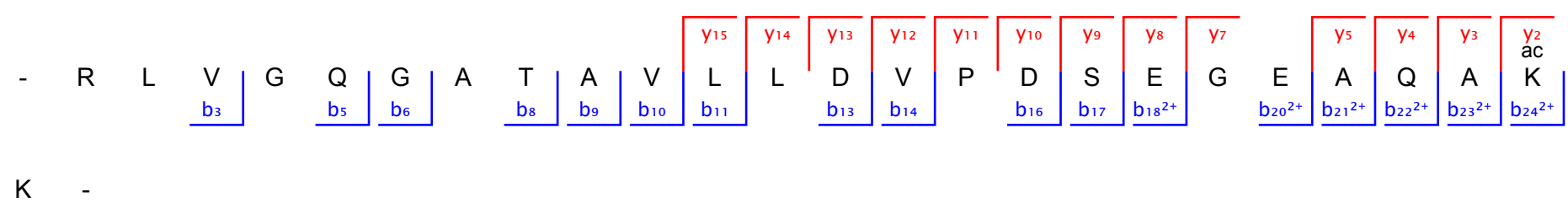
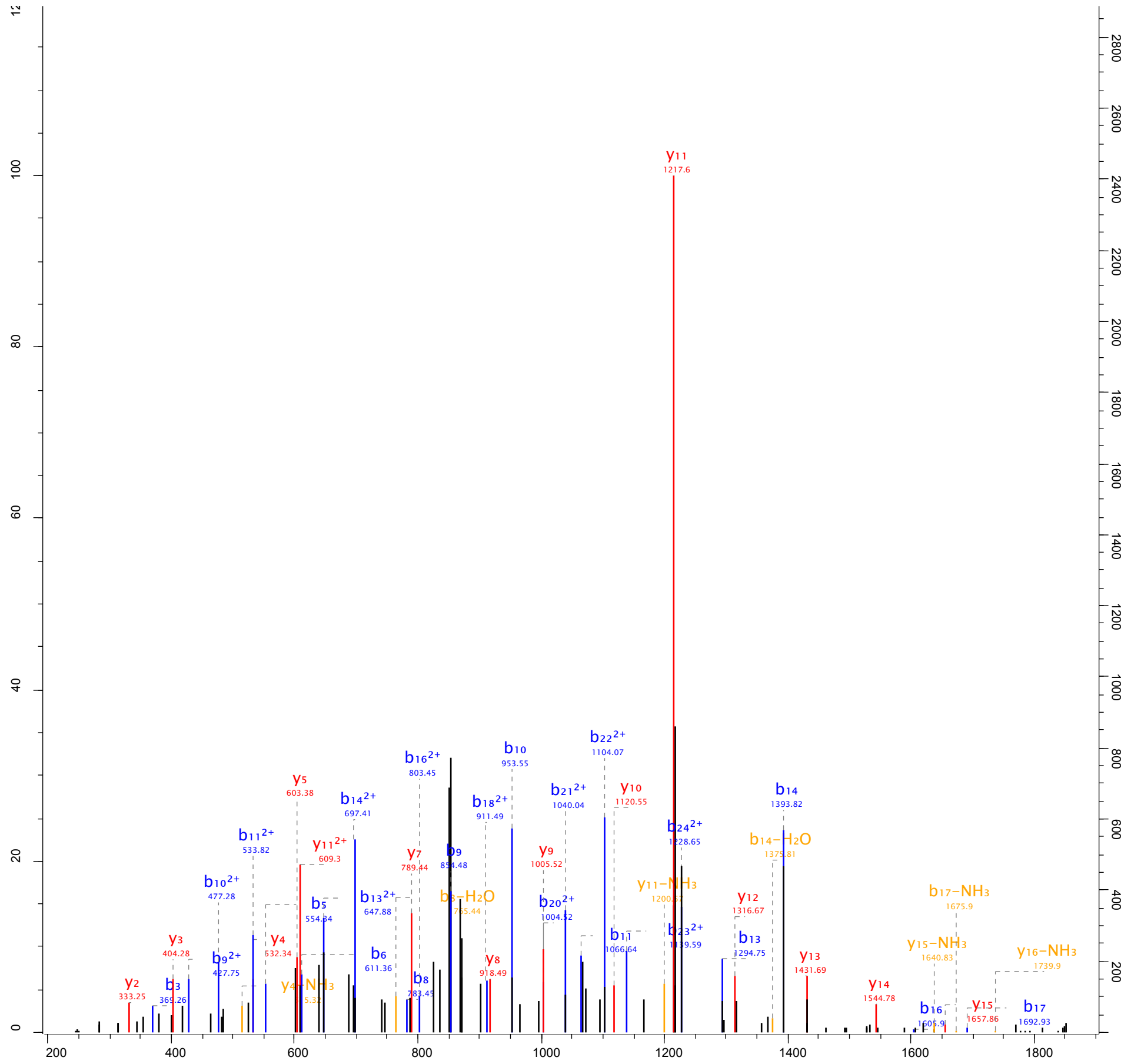
- ac - S
- b₂ - H
- b₃ - T
- b₄ - I
- b₅ - L
- b₆ - L
- y₁₄²⁺ - T
- y₁₃²⁺ - I
- y₁₂²⁺ - L
- y₁₁²⁺ - L
- y₁₀²⁺ - V
- y₉²⁺ - Q
- y₈ - P
- ac - T
- b₁₄²⁺ - E
- y₂ - G
- R -

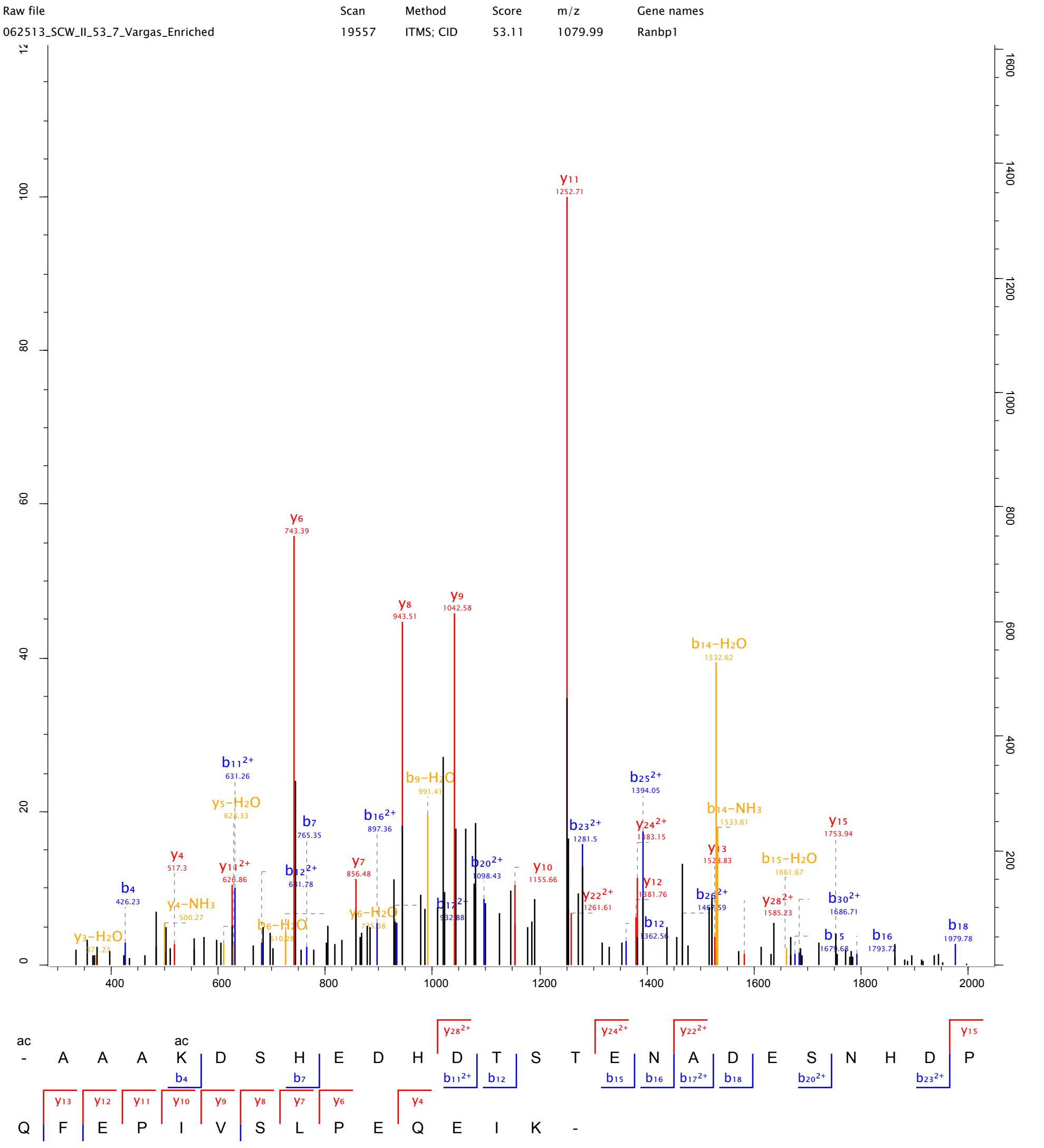


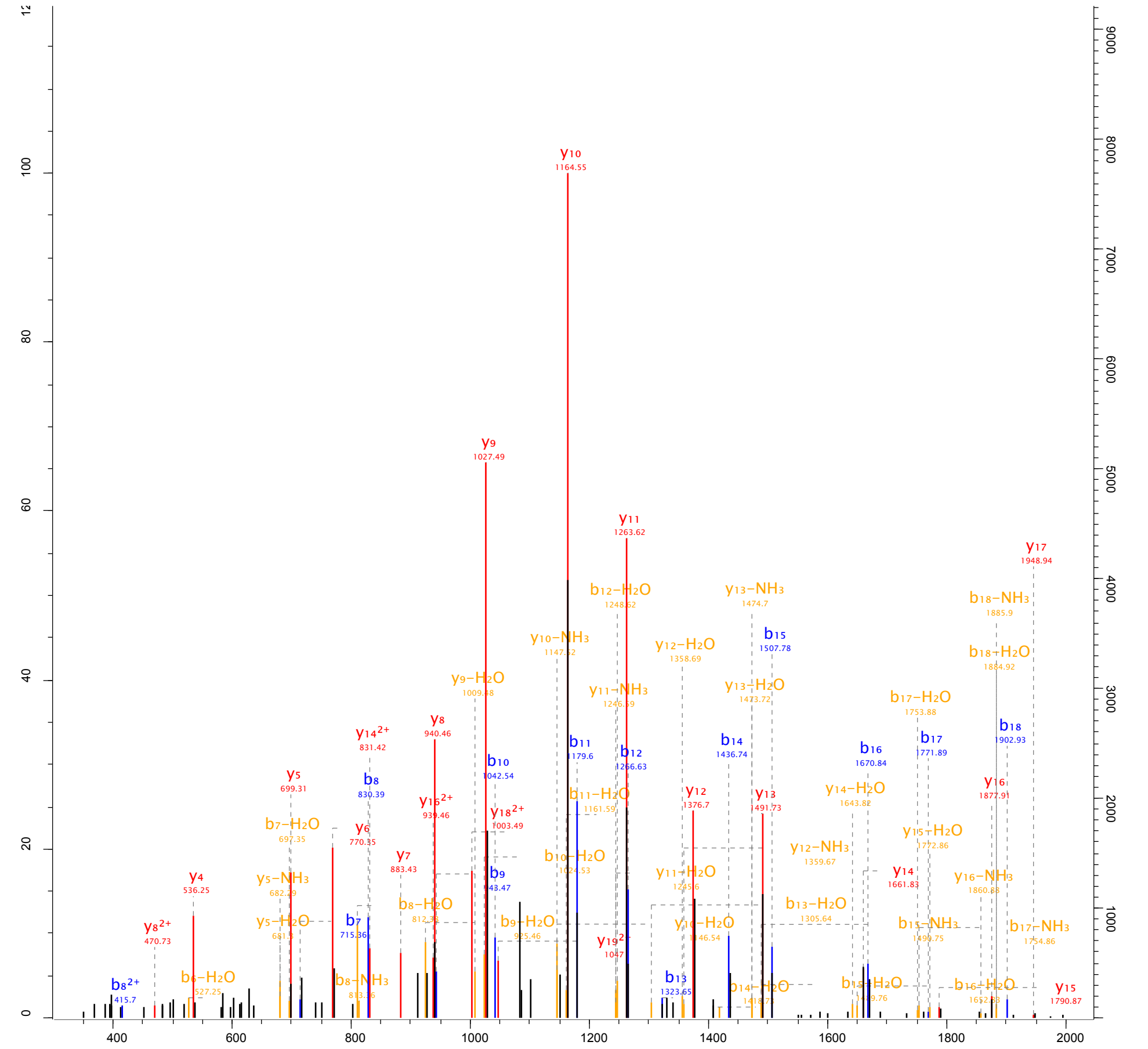












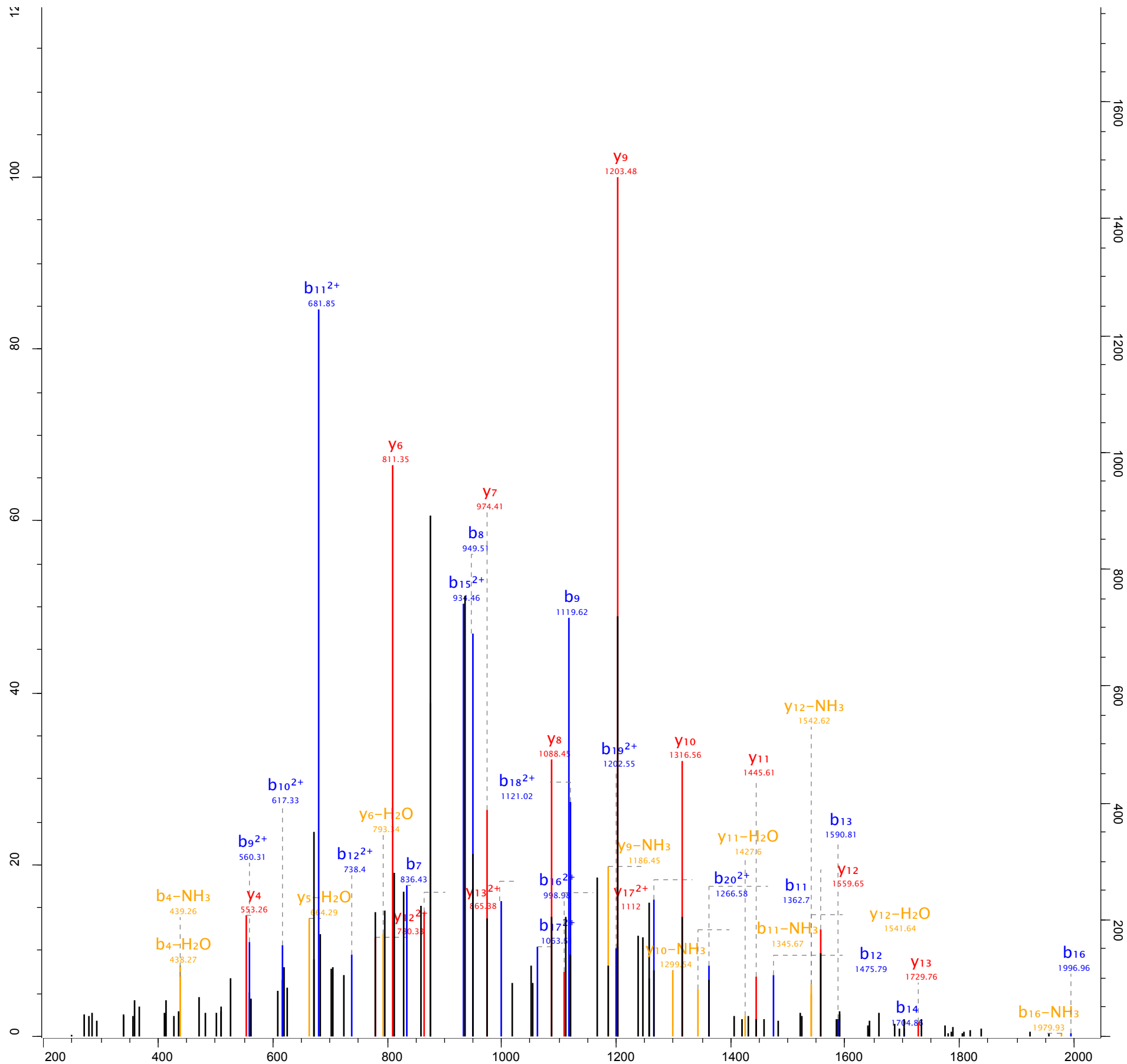
- I S G A S E K D I V H S G L A Y T M E R -

y19²⁺
y18²⁺
y17
y16
y15
y14
y13
y12
y11
y10
y9
y8
y7
y6
y5
y4

b7
b8
b9
b10
b11
b12
b13
b14
b15
b16
b17
b18

Raw file
062513_SCW_II_53_7_Vargas_Enriched

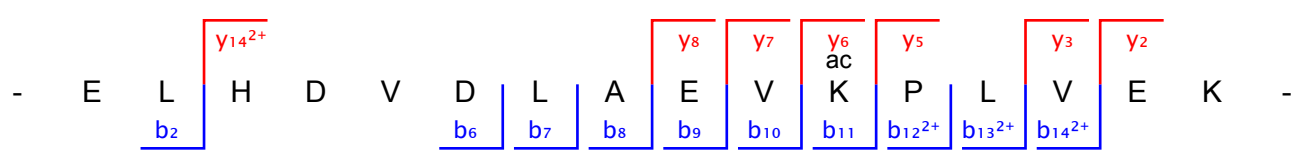
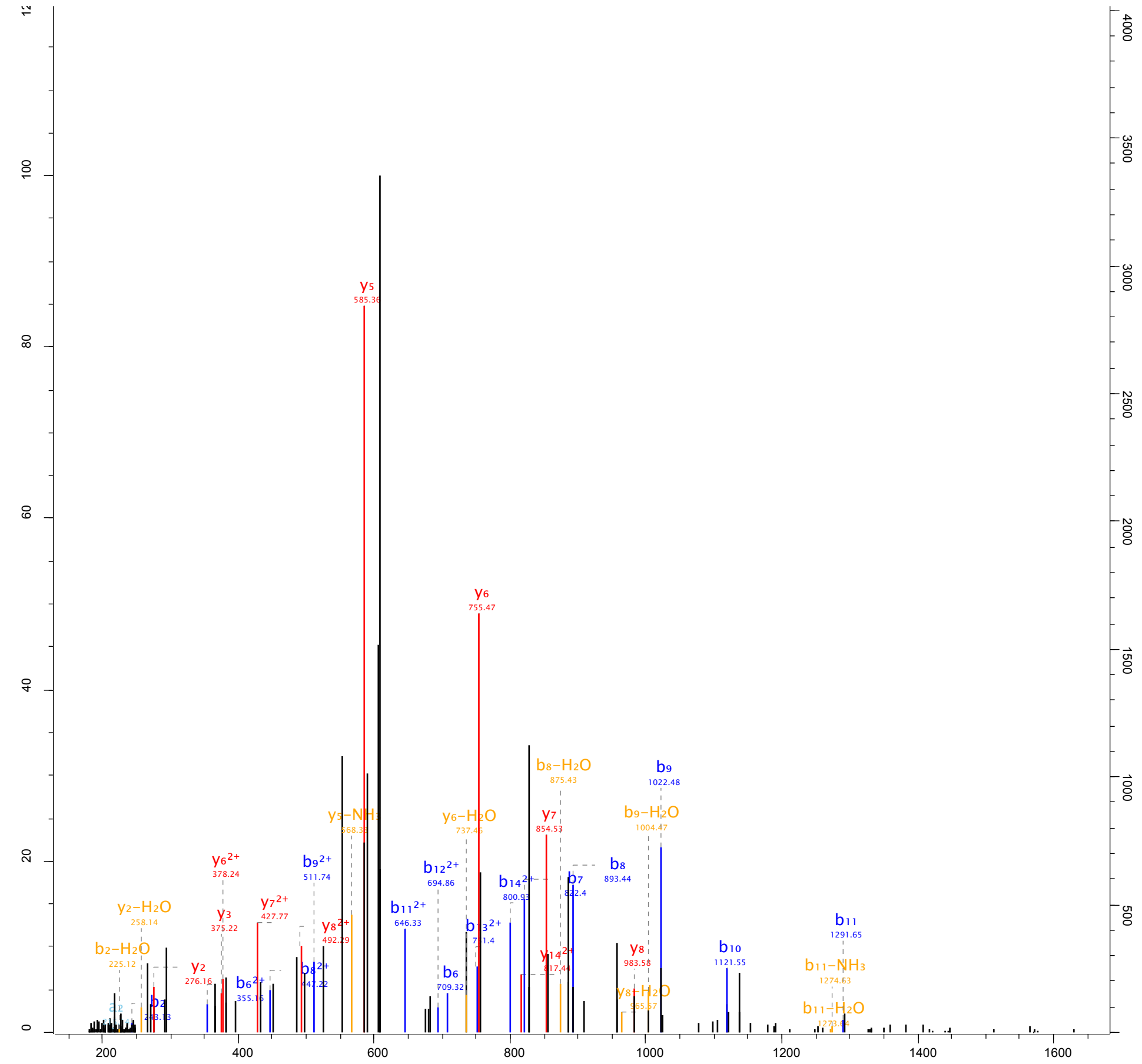
Scan Method Score m/z Gene names
19717 ITMS; CID 146.13 893.76 Sptbn1

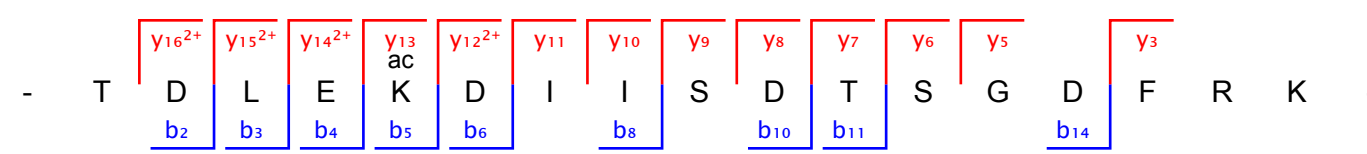
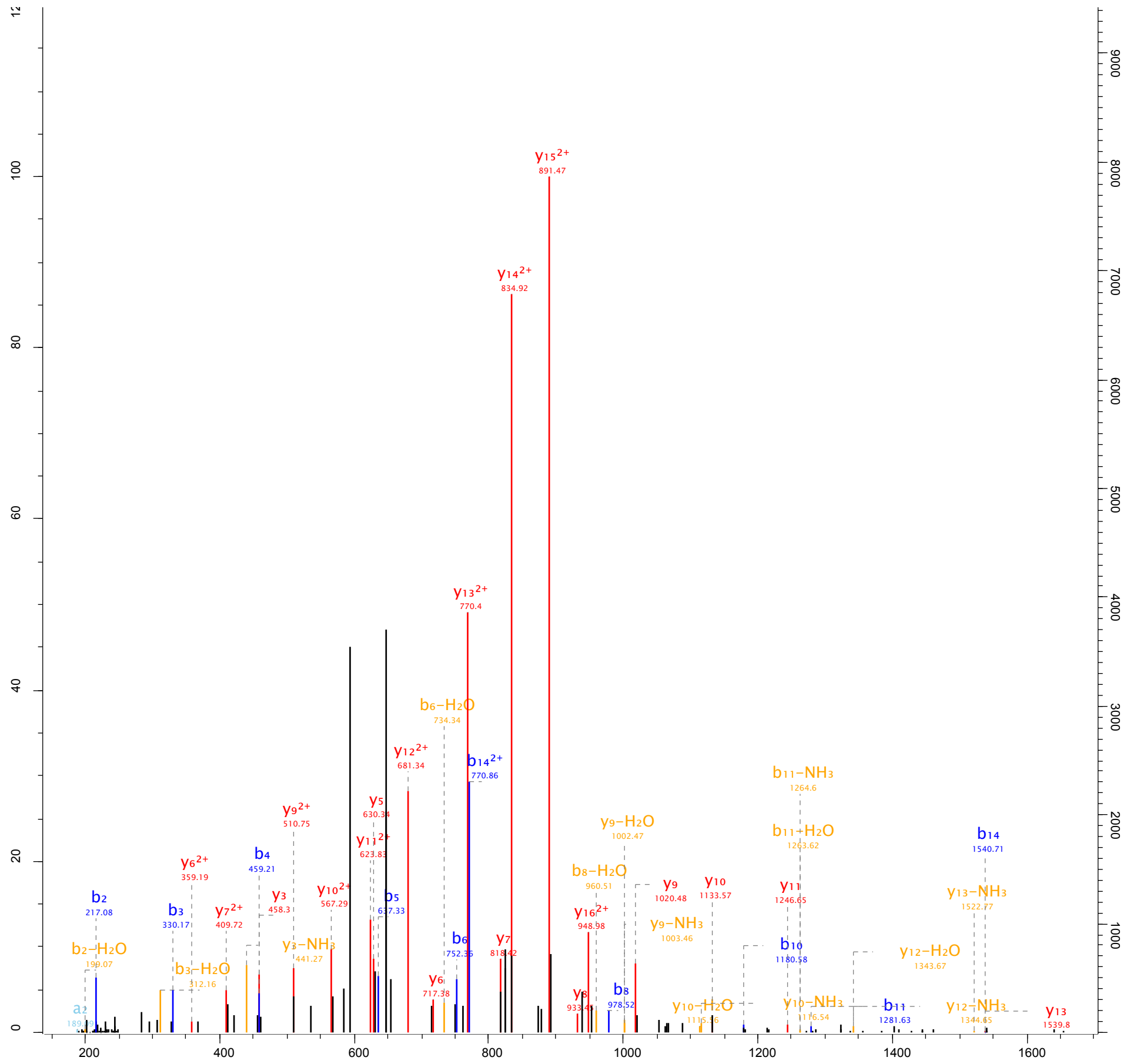


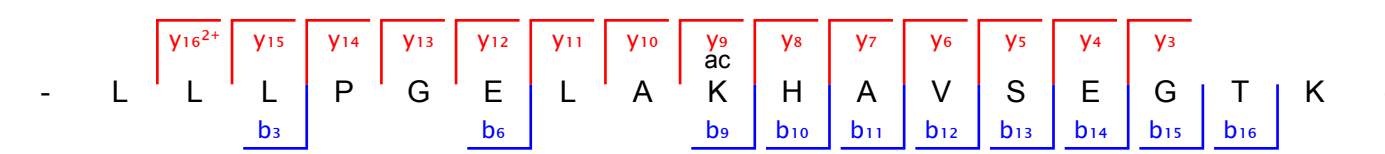
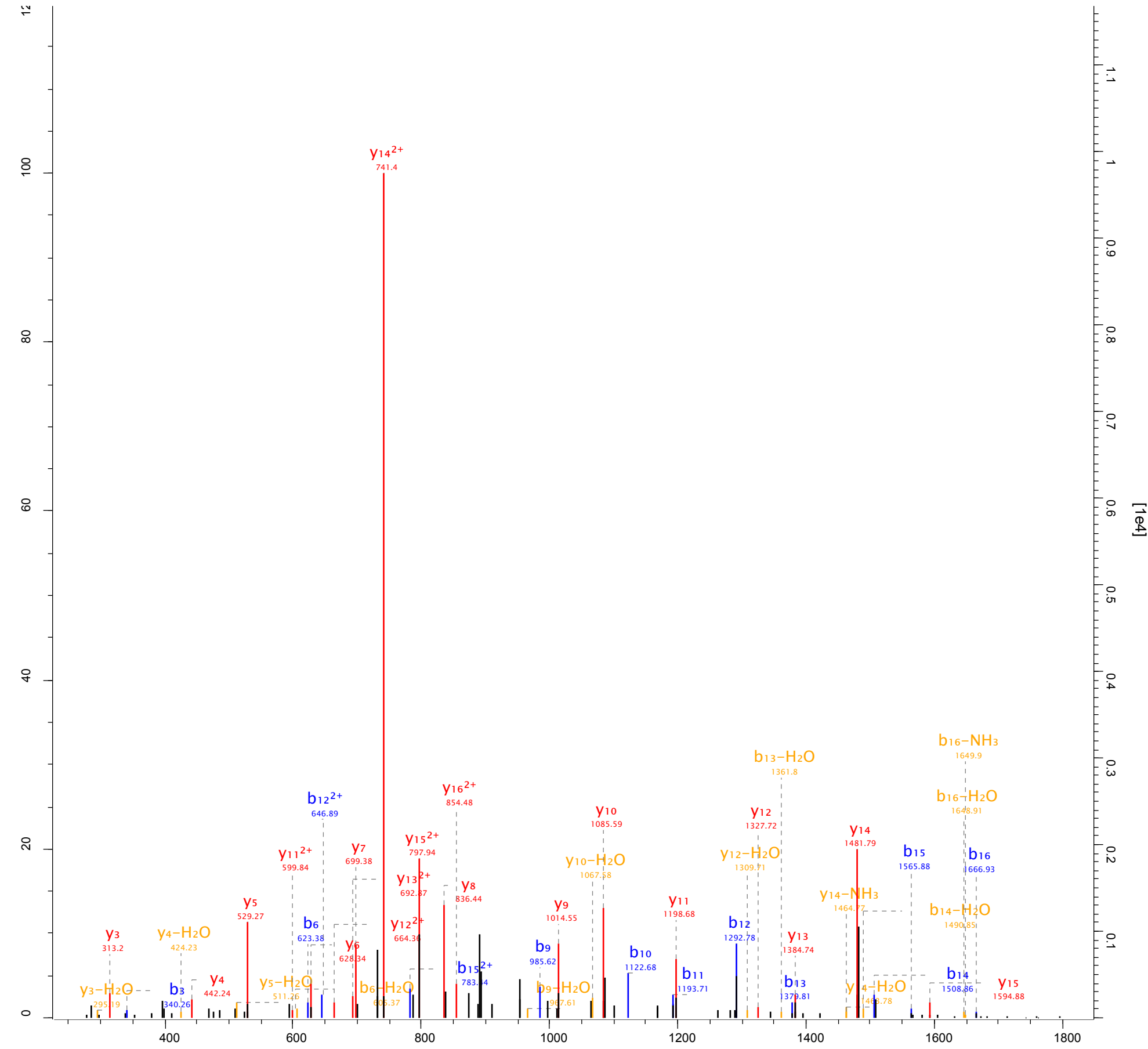
- L L T Q H E N I K N E I D N Y E E D Y Q K -

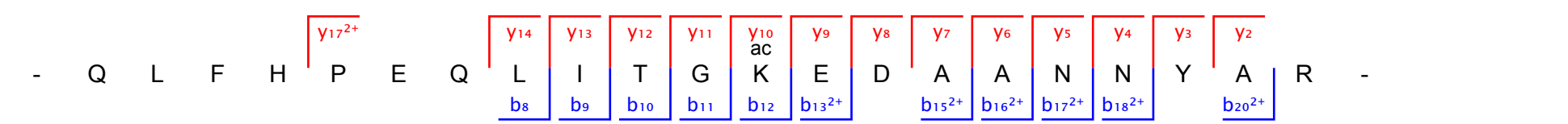
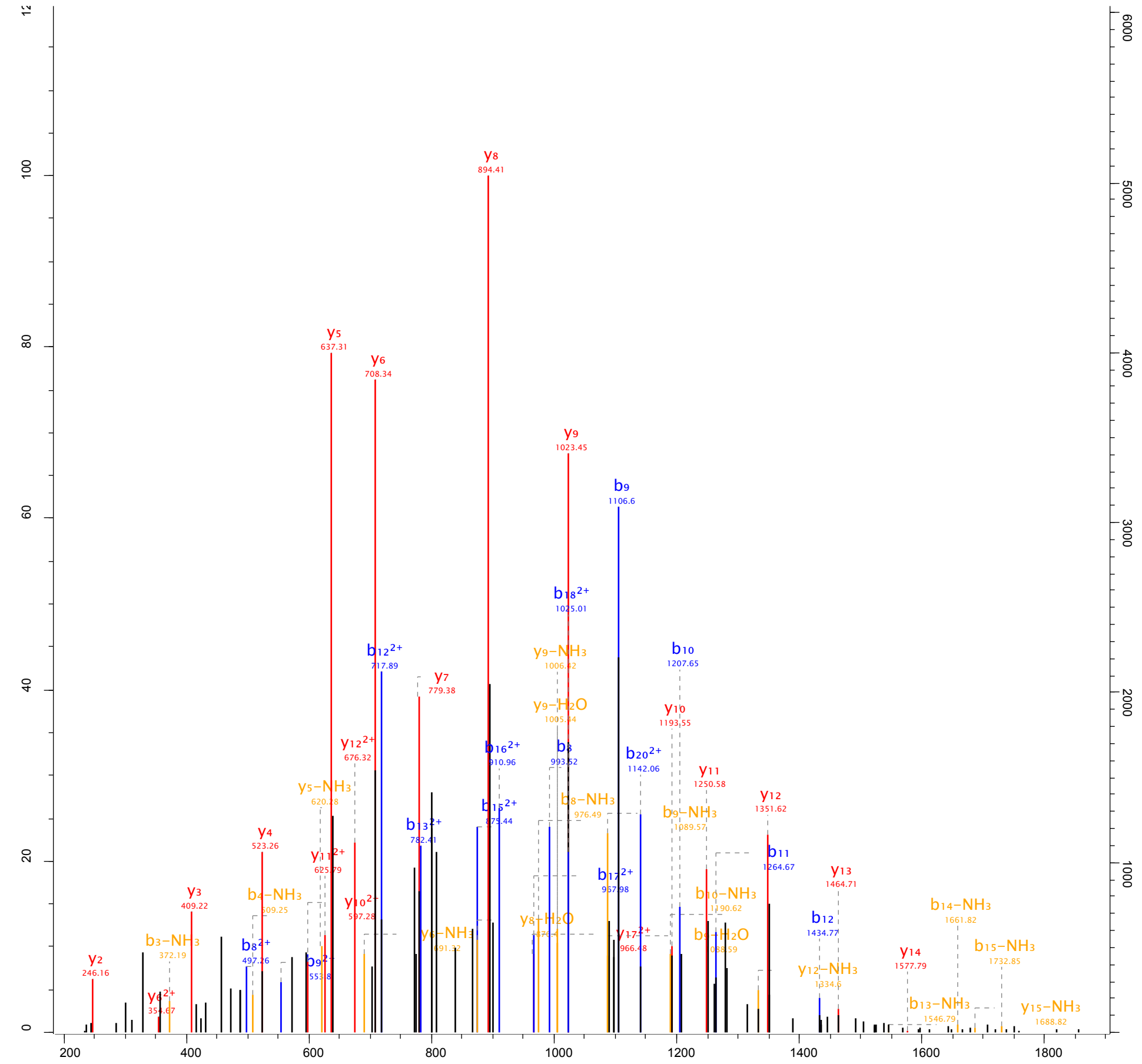
Fragmentation labels below the sequence:
- b7 b8 b9 b10²⁺ b11 b12 b13 b14 b15²⁺ b16 b17²⁺ b18²⁺ b19²⁺ b20²⁺ -

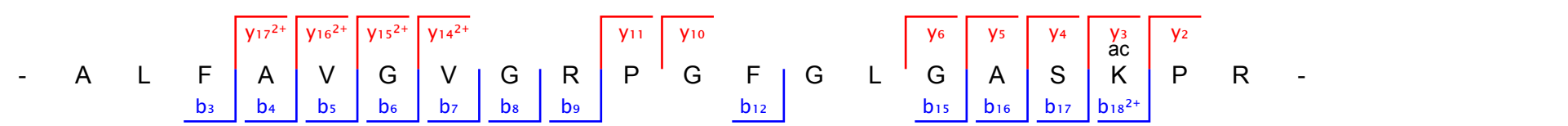
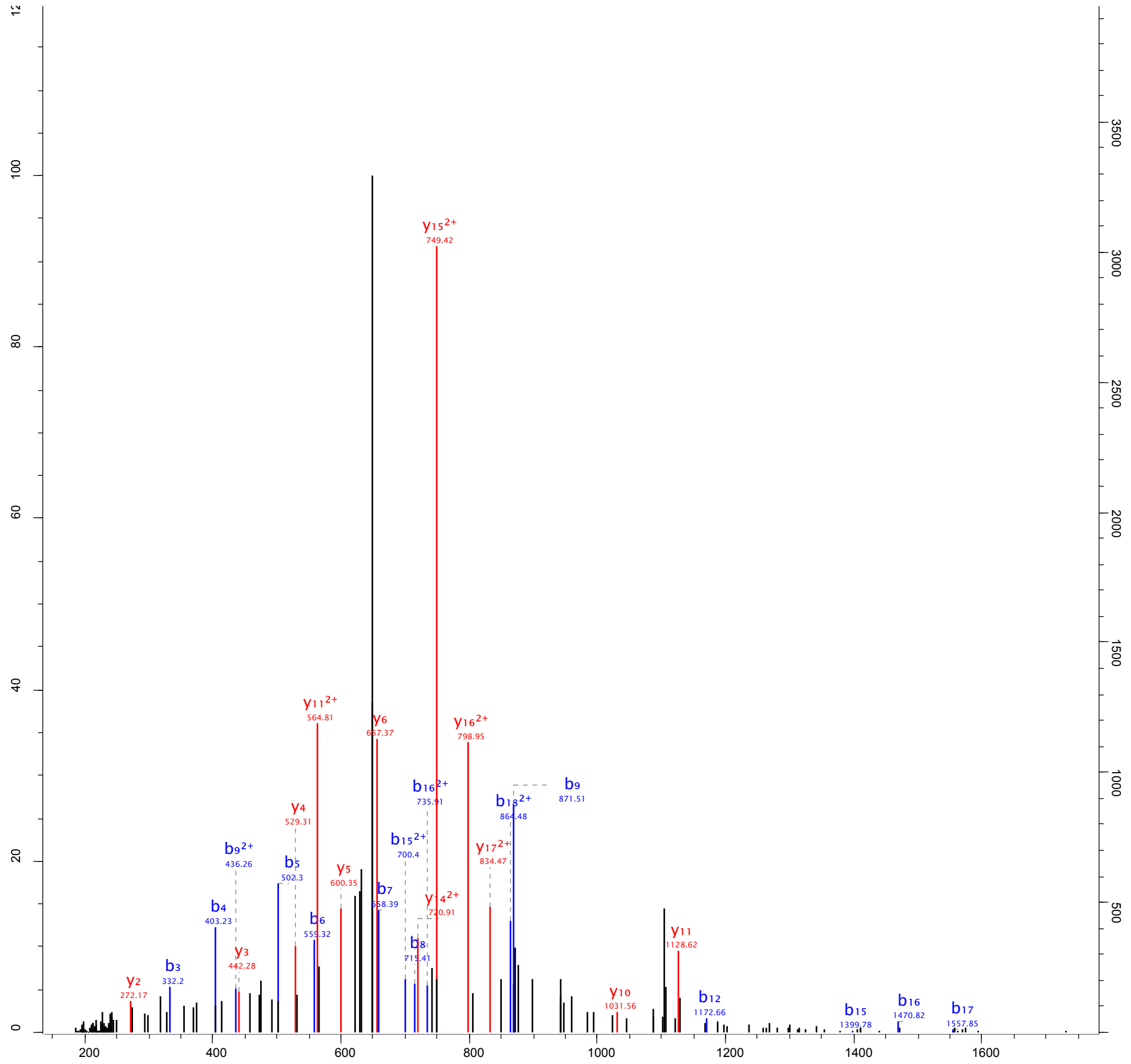
Fragmentation labels above the sequence:
- y17²⁺ y13 ac y12 y11 y10 y9 y8 y7 y6 y4 -

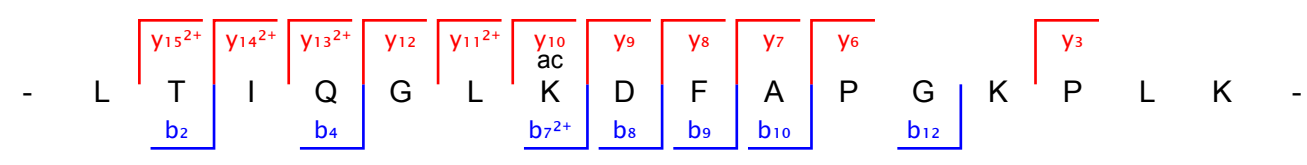
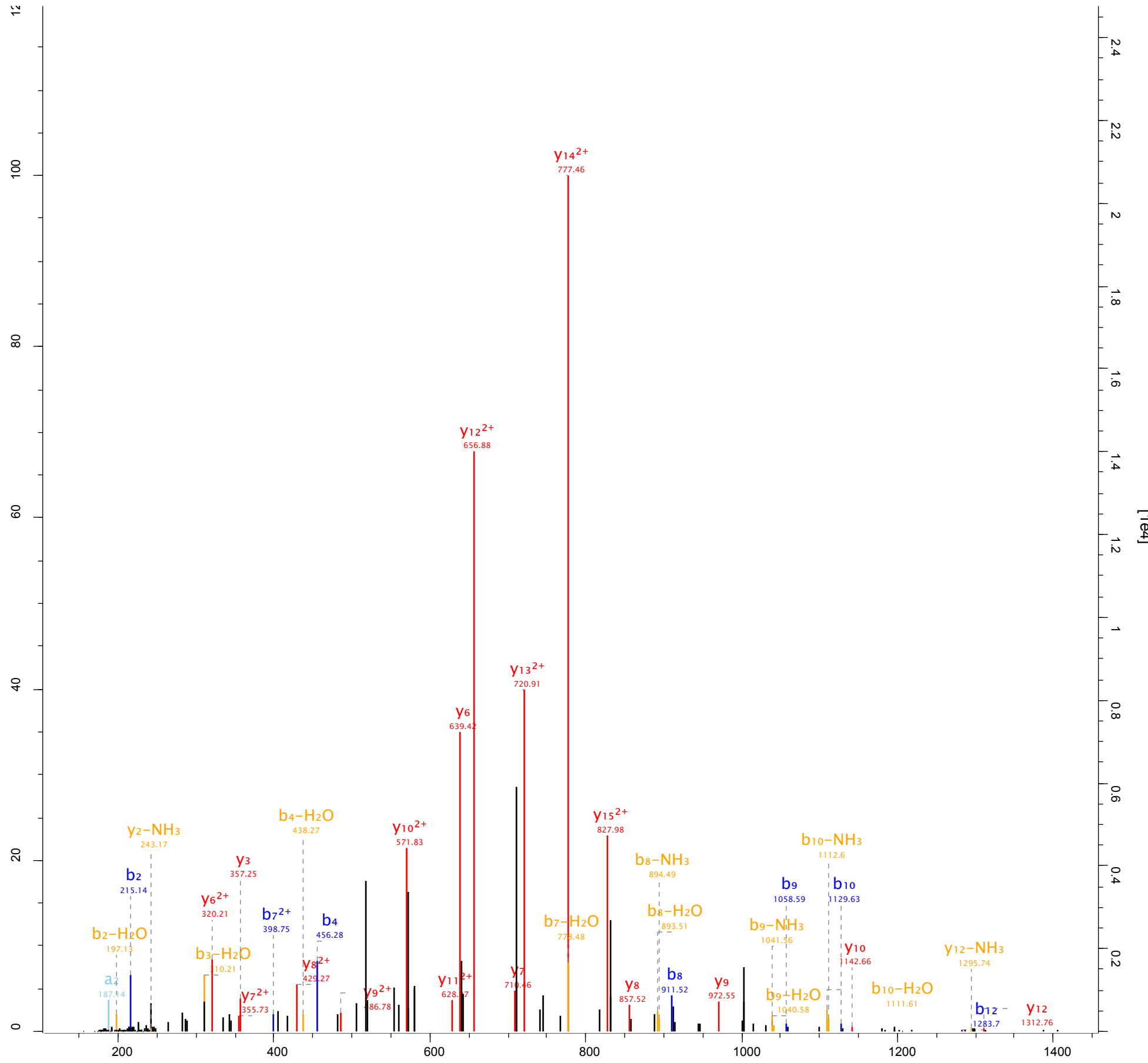


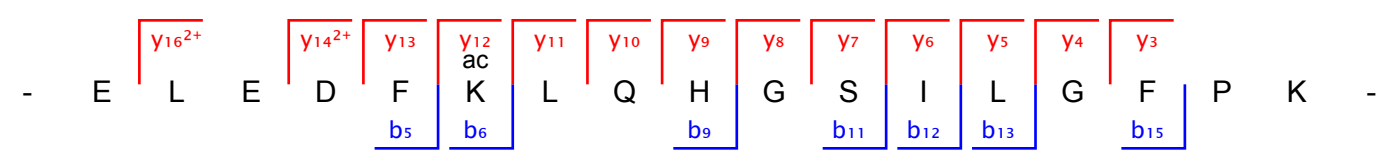
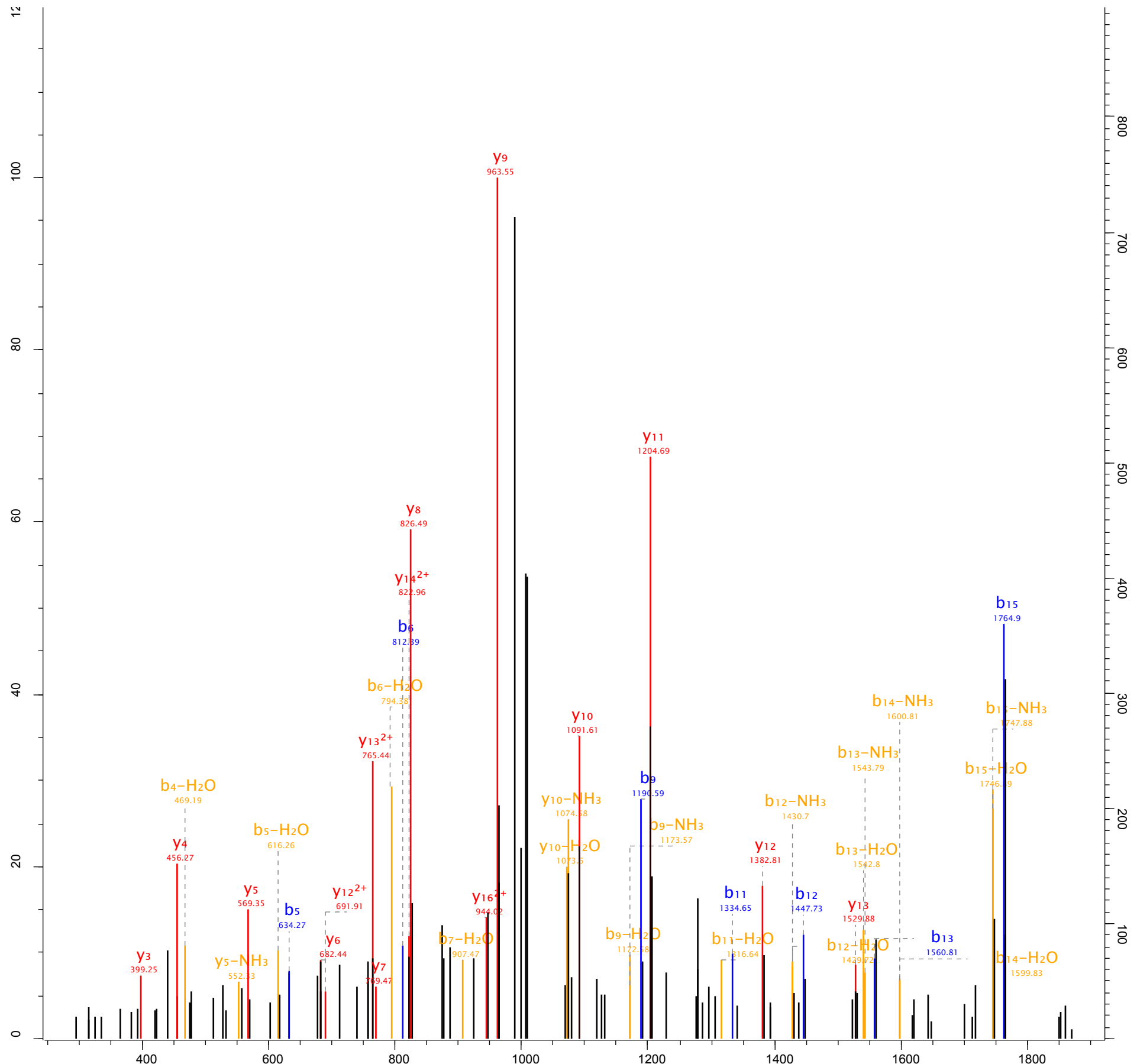


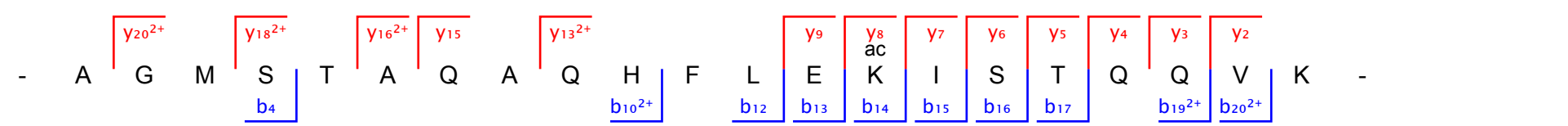
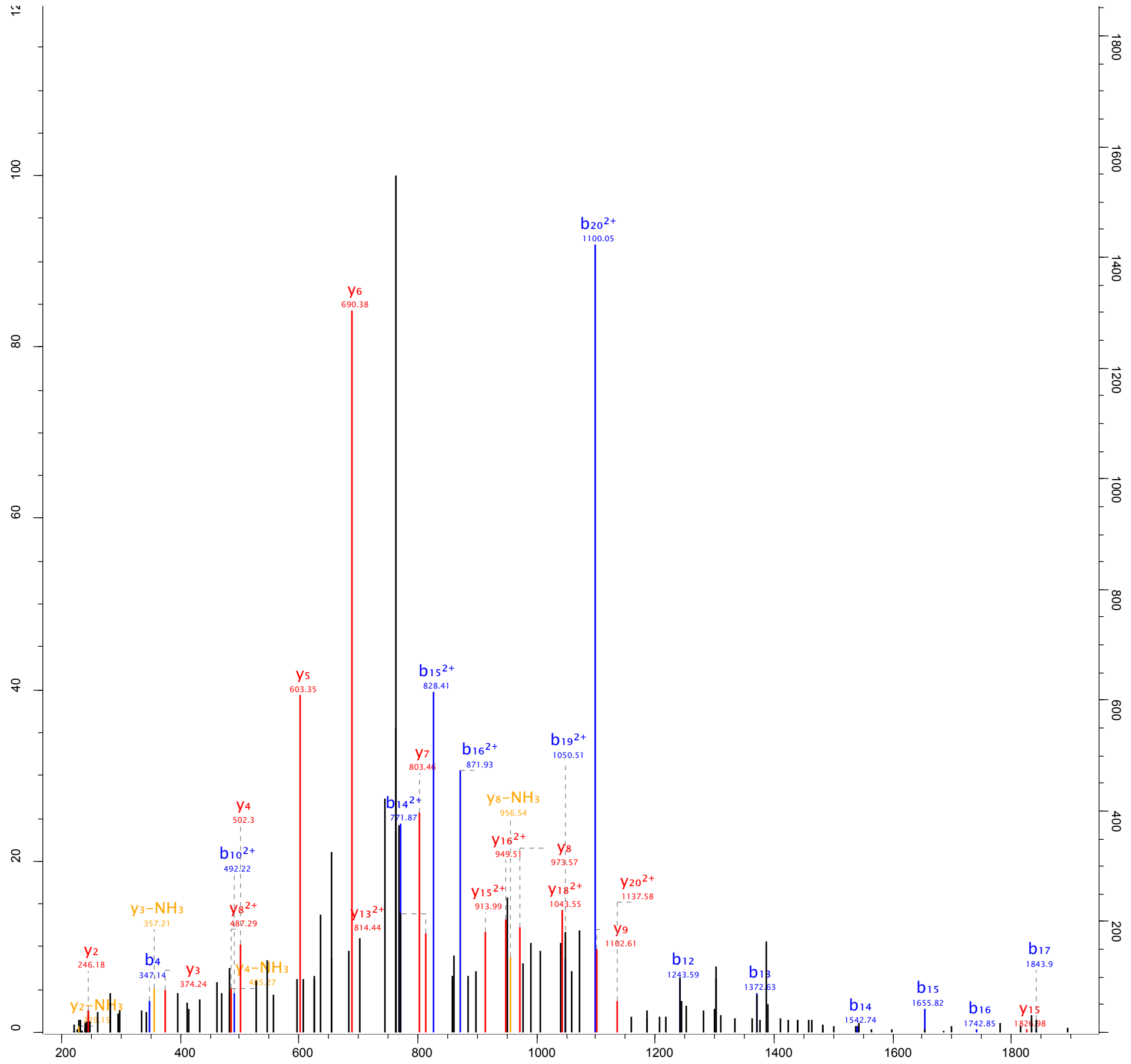




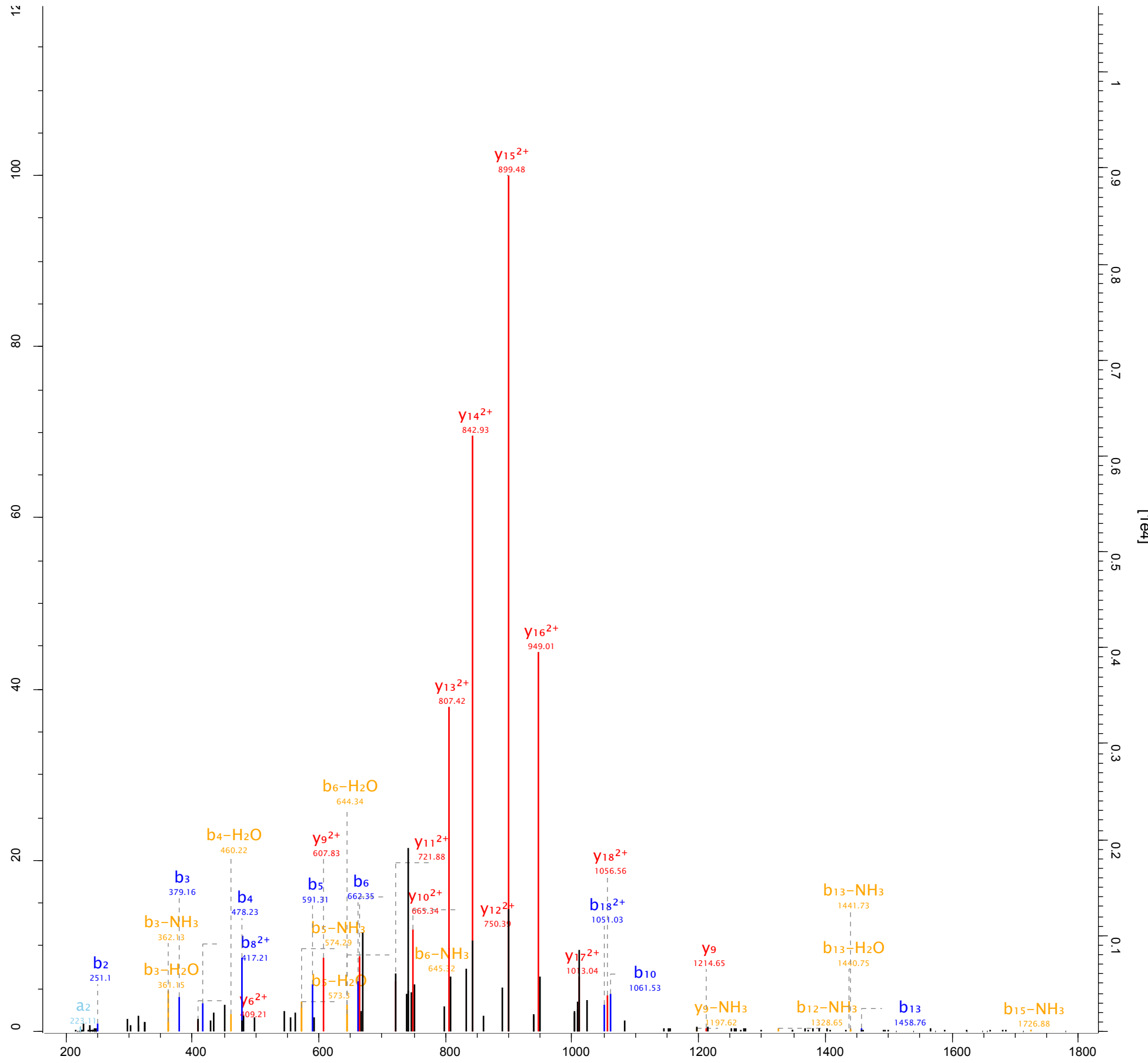








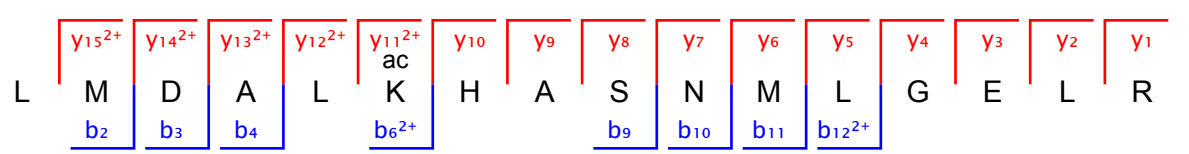
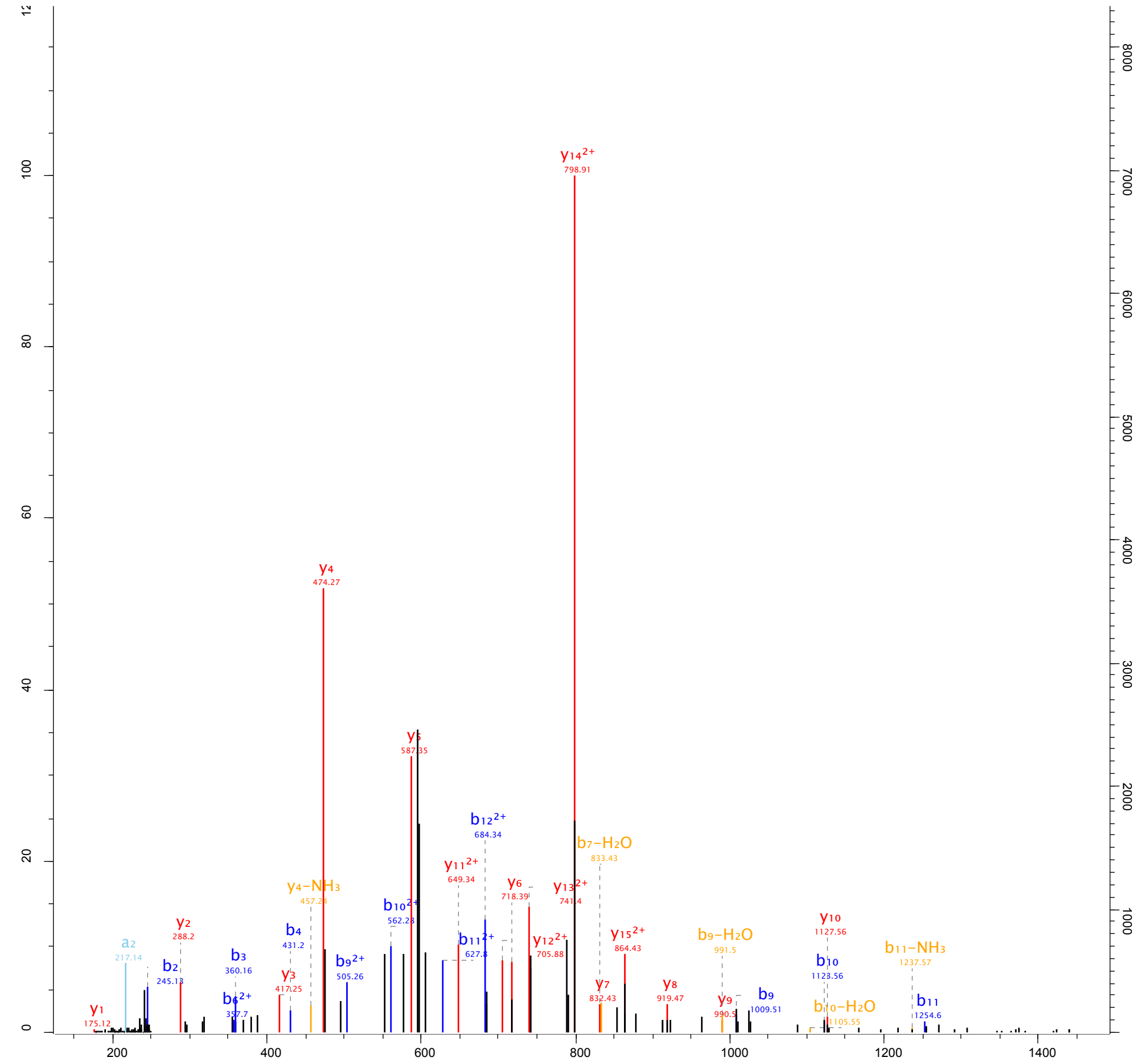
Raw file: 062513_SCW_II_53_7_Vargas_Enriched
 Scan: 22030 Method: ITMS; CID Score: 142.57 m/z: 759.4 Gene names: Rps18;Gm10260

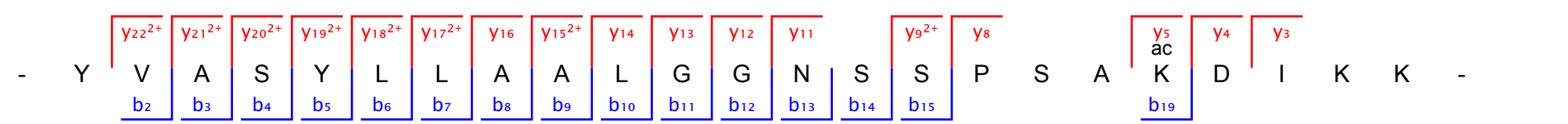
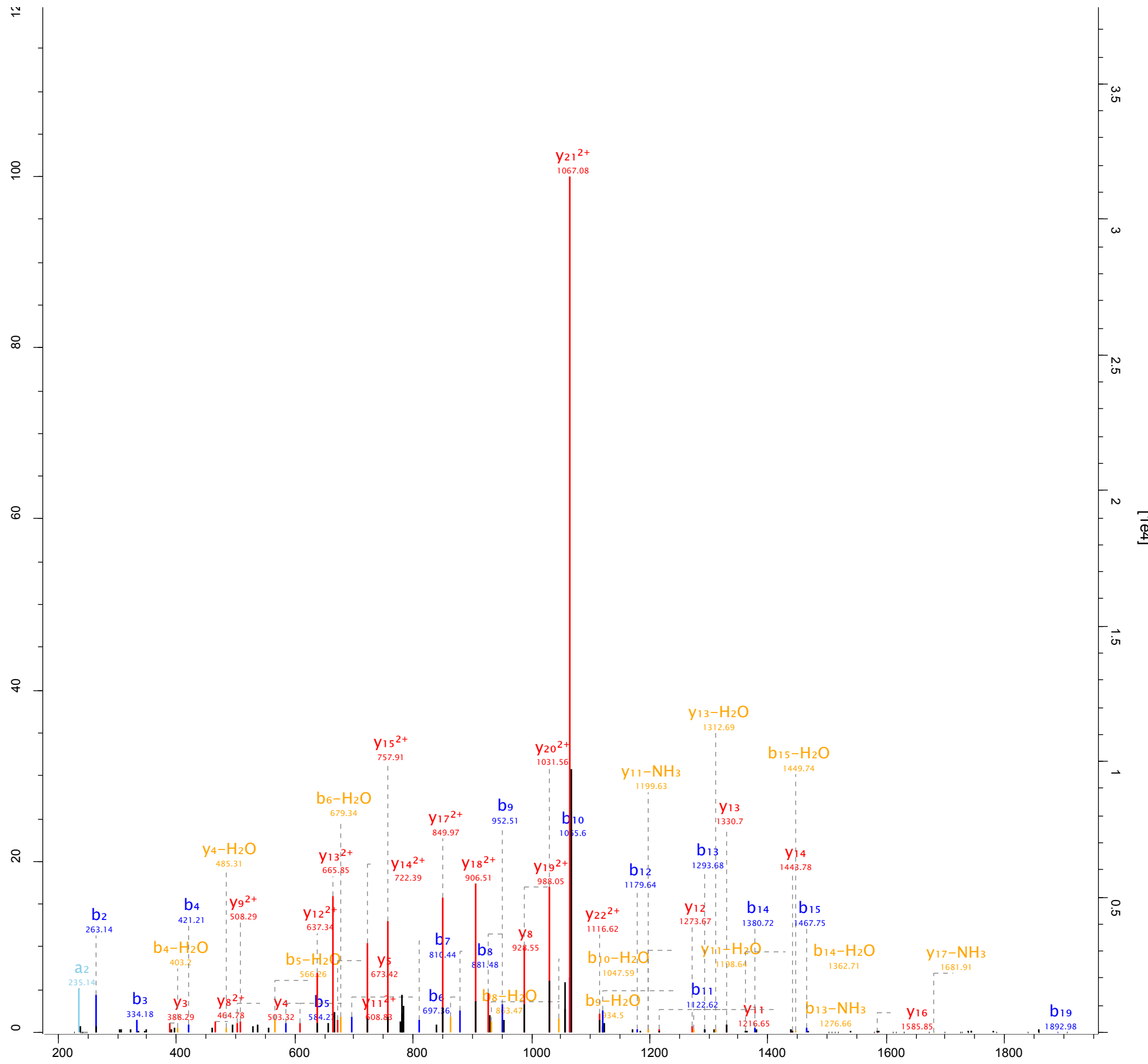


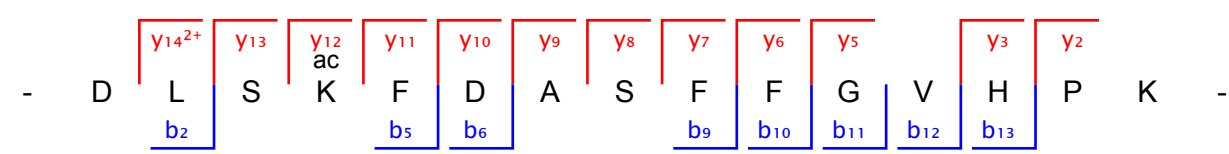
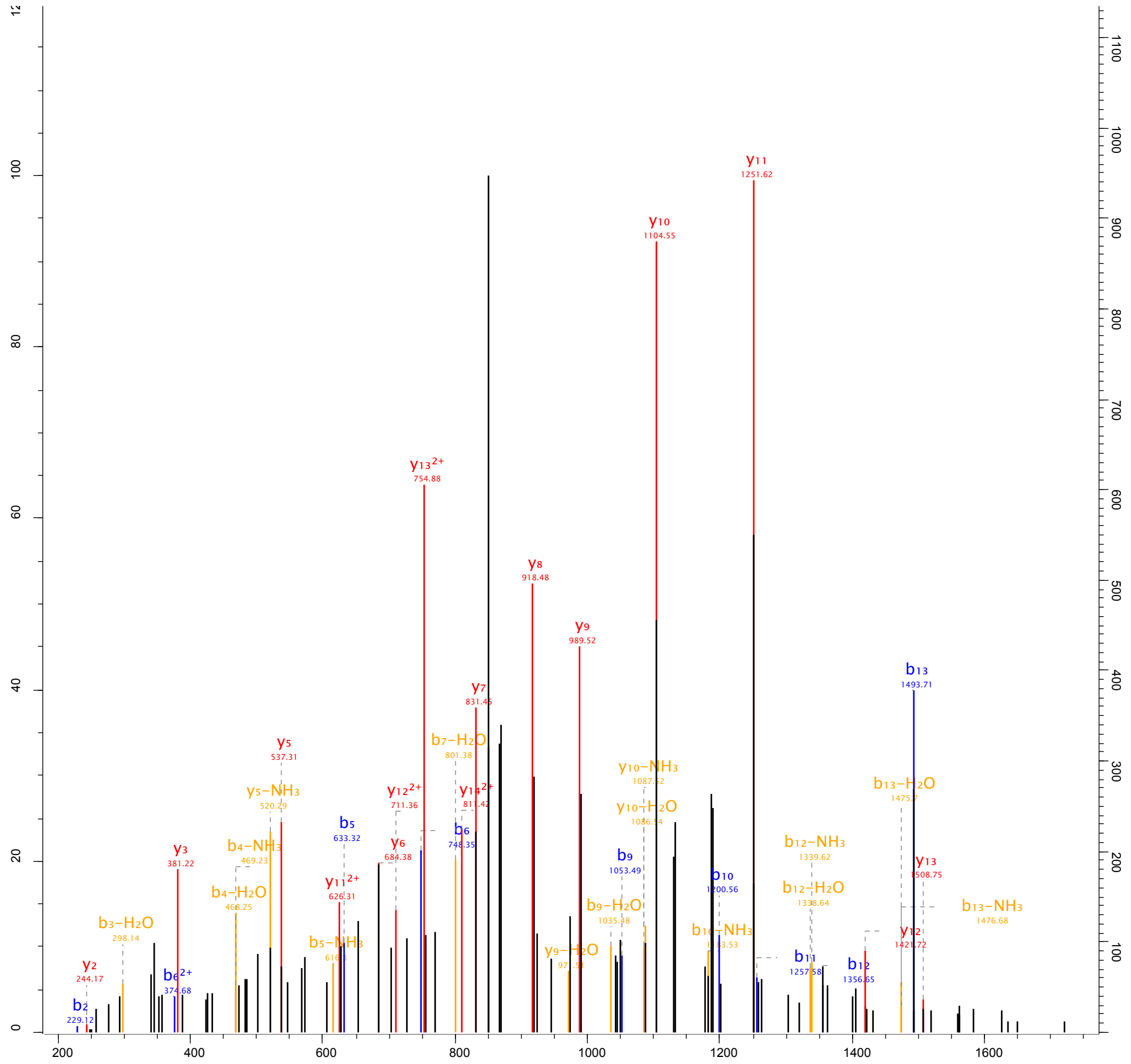
Sequence: - Y S Q V L A N G L D N ac K L R E D L E R -

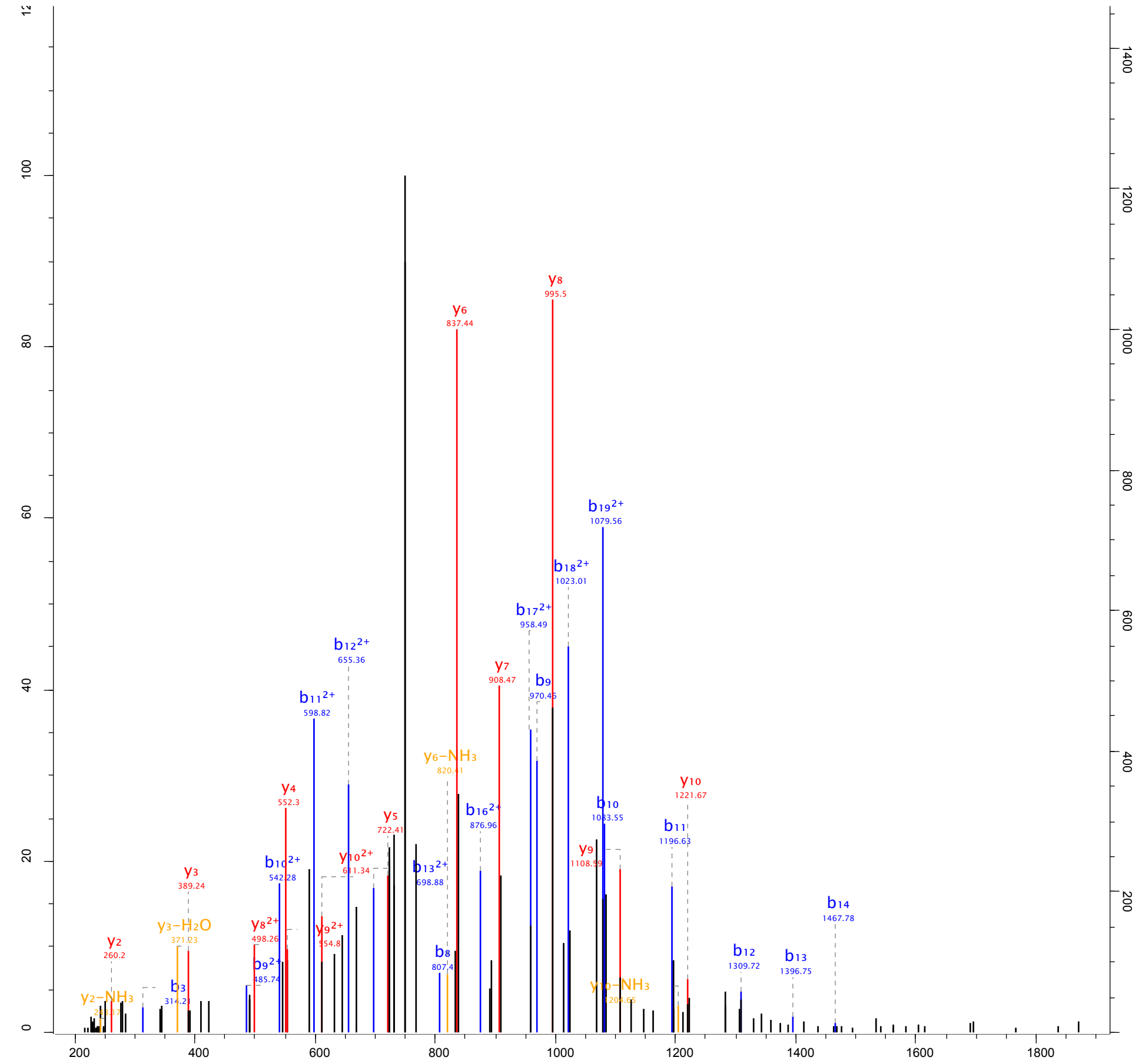
Fragmentation sites (b and y ions) are indicated by boxes below the sequence:

- Red boxes above: y_{18}^{2+} , y_{17}^{2+} , y_{16}^{2+} , y_{15}^{2+} , y_{14}^{2+} , y_{13}^{2+} , y_{12}^{2+} , y_{11}^{2+} , y_{10}^{2+} , y_9
- Blue boxes below: b₂, b₃, b₄, b₅, b₆, b₈²⁺, b₁₀, b₁₃, b₁₈²⁺



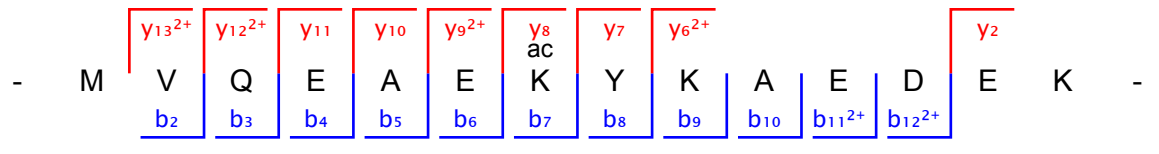
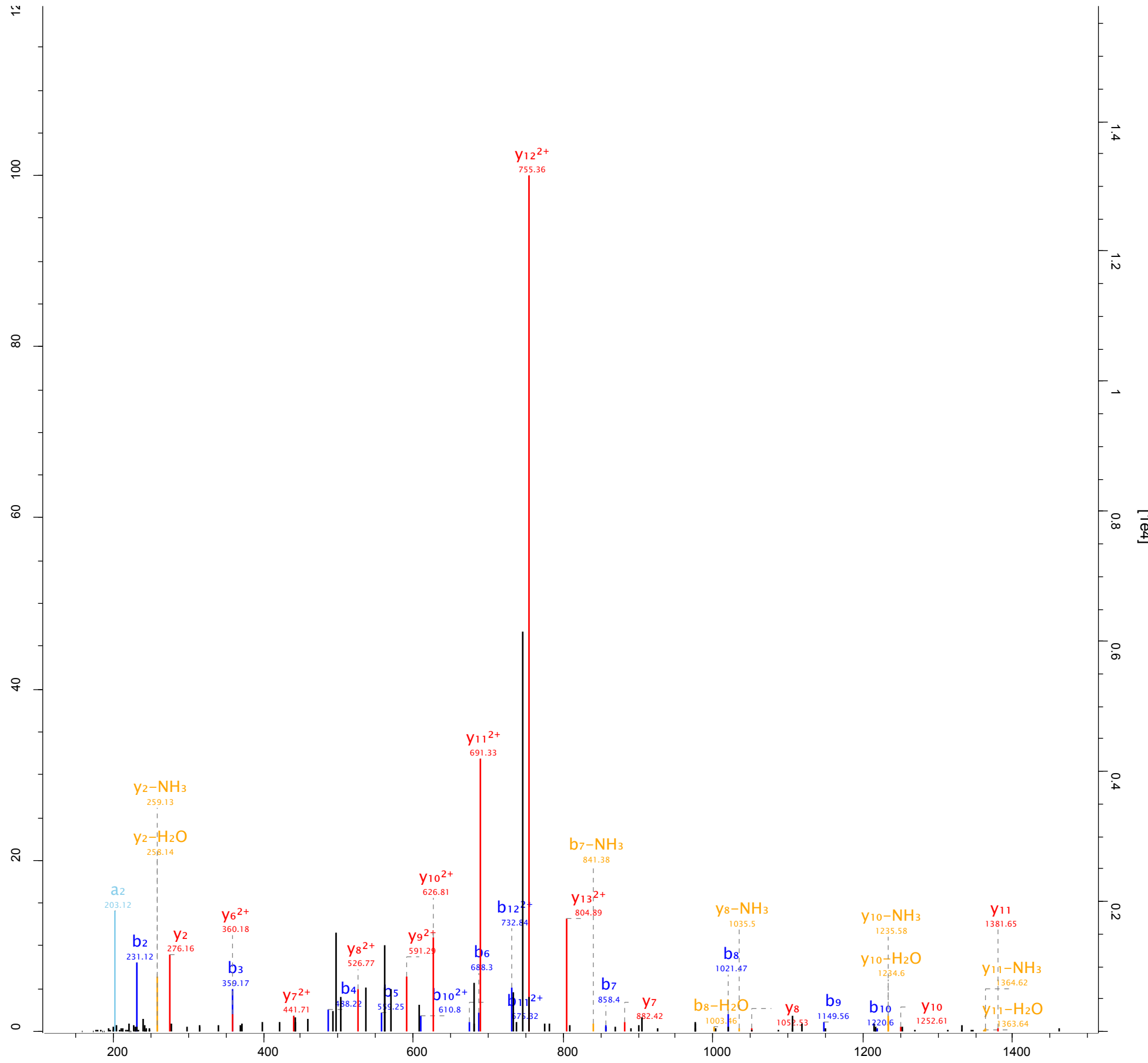


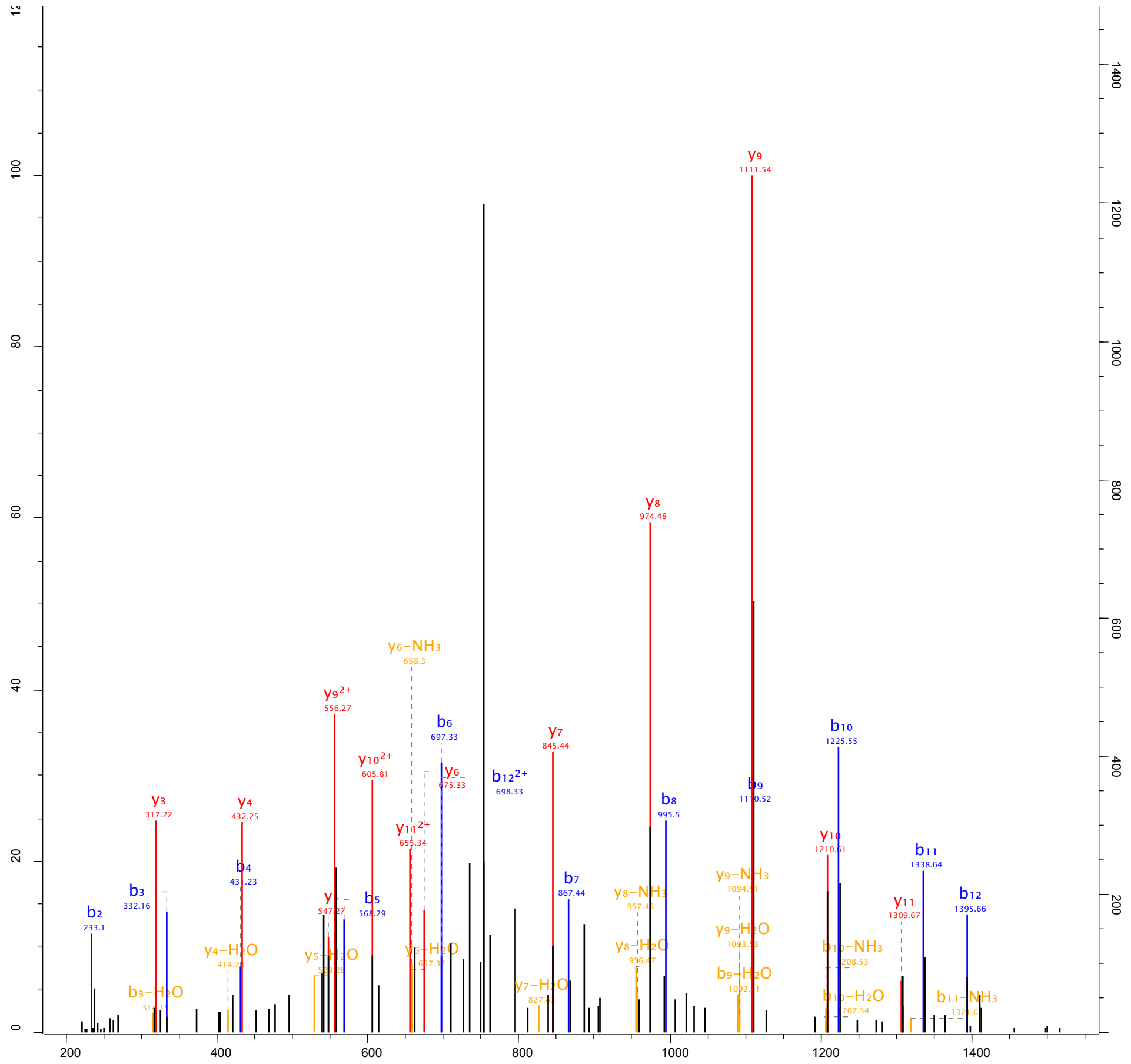




- S L L H S P G D Y I L L S A D K Y E I K -

b3 b8 b9 b10 b11 b12 b13 b14 b16²⁺ b17²⁺ b18²⁺ b19²⁺ y10 y9 y8 y7 y6 y5 ac y4 y3 y2

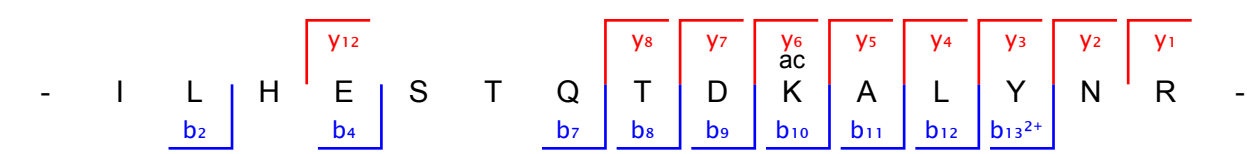
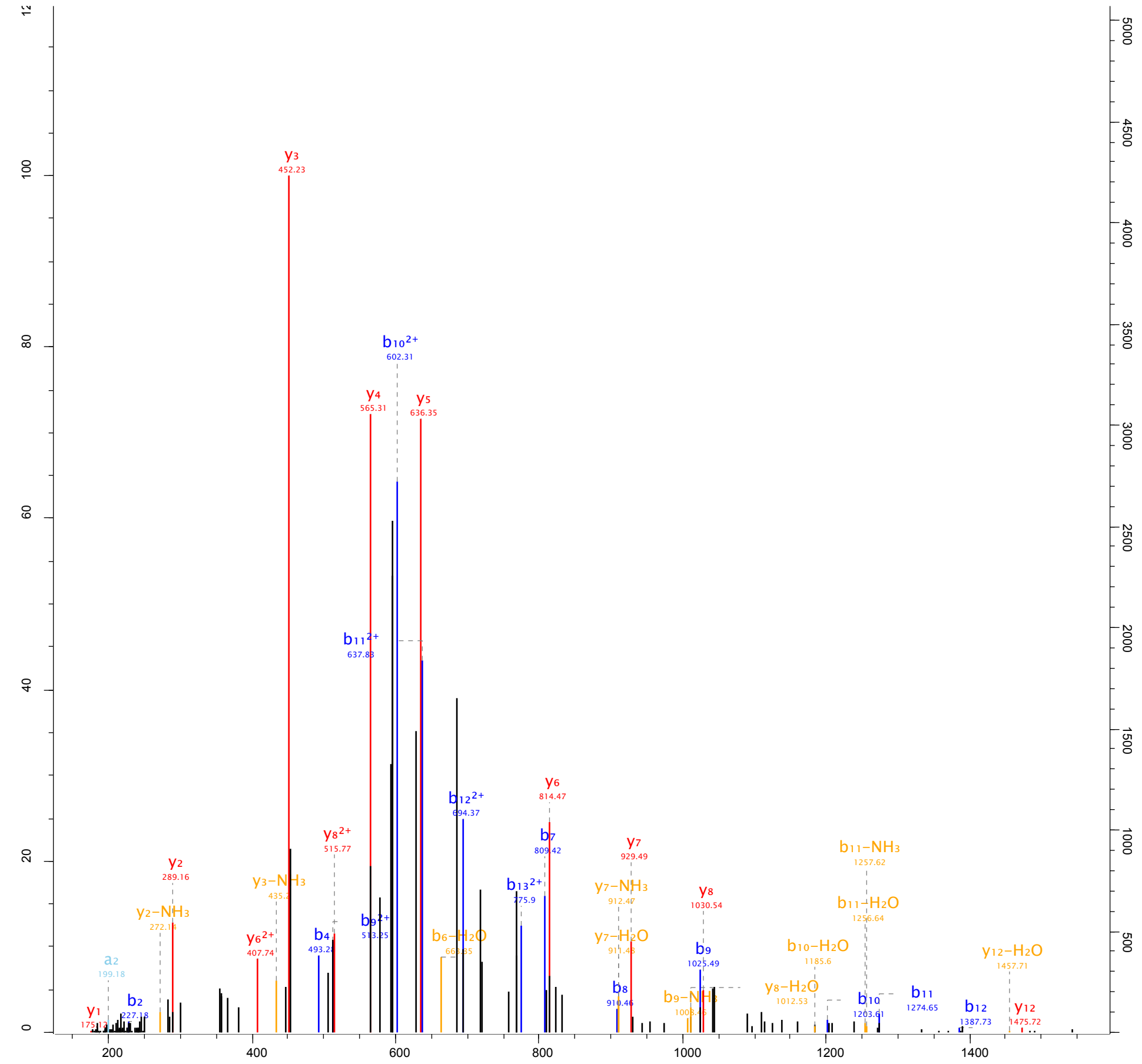


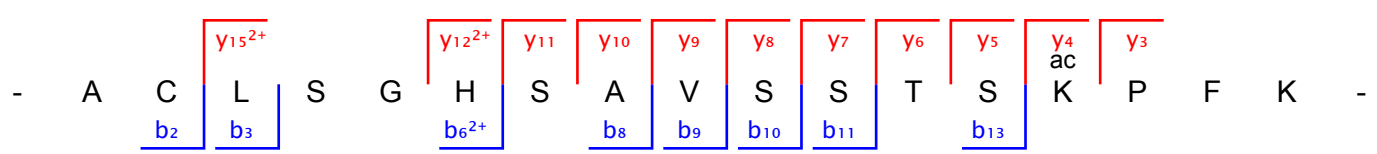
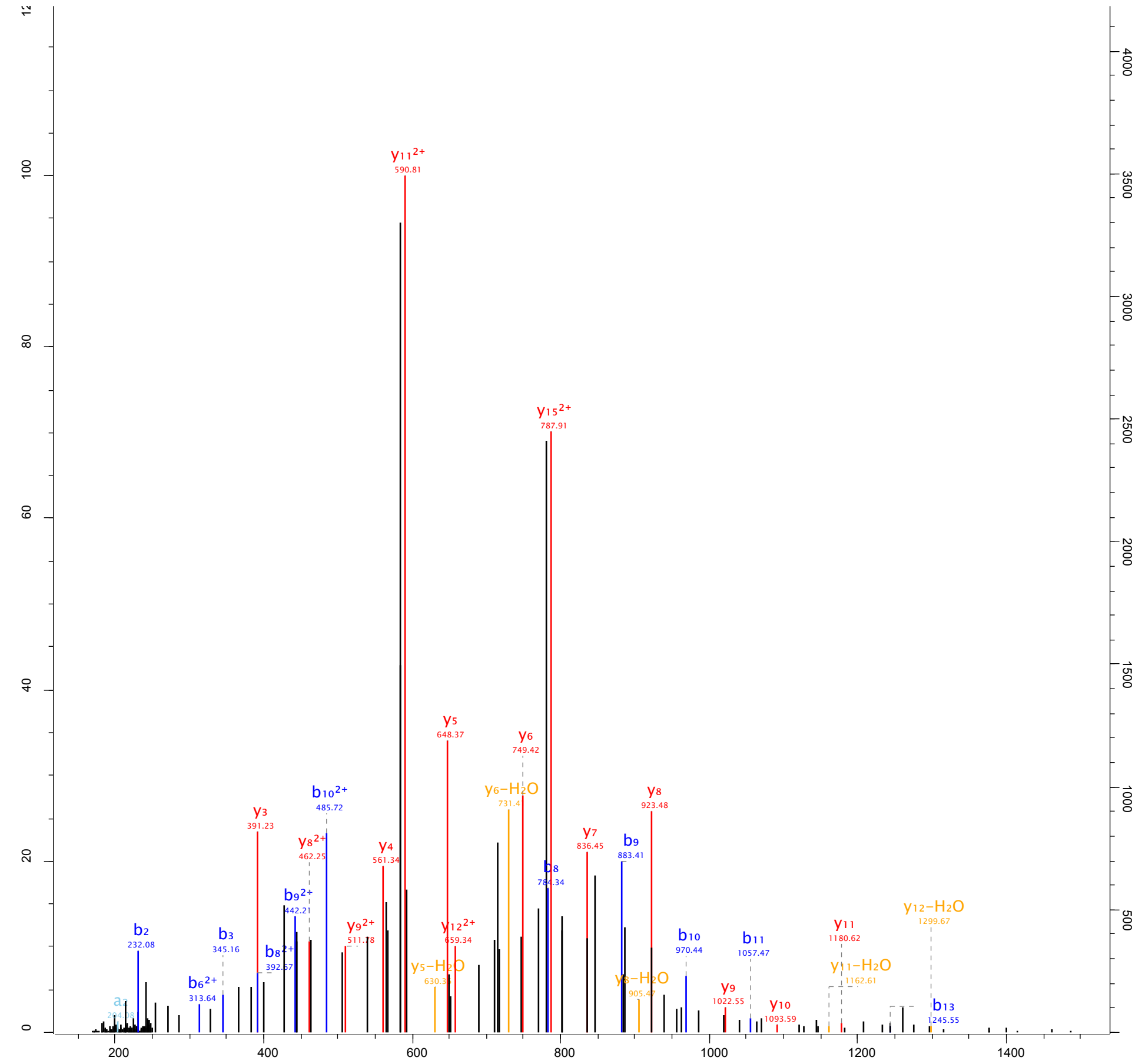


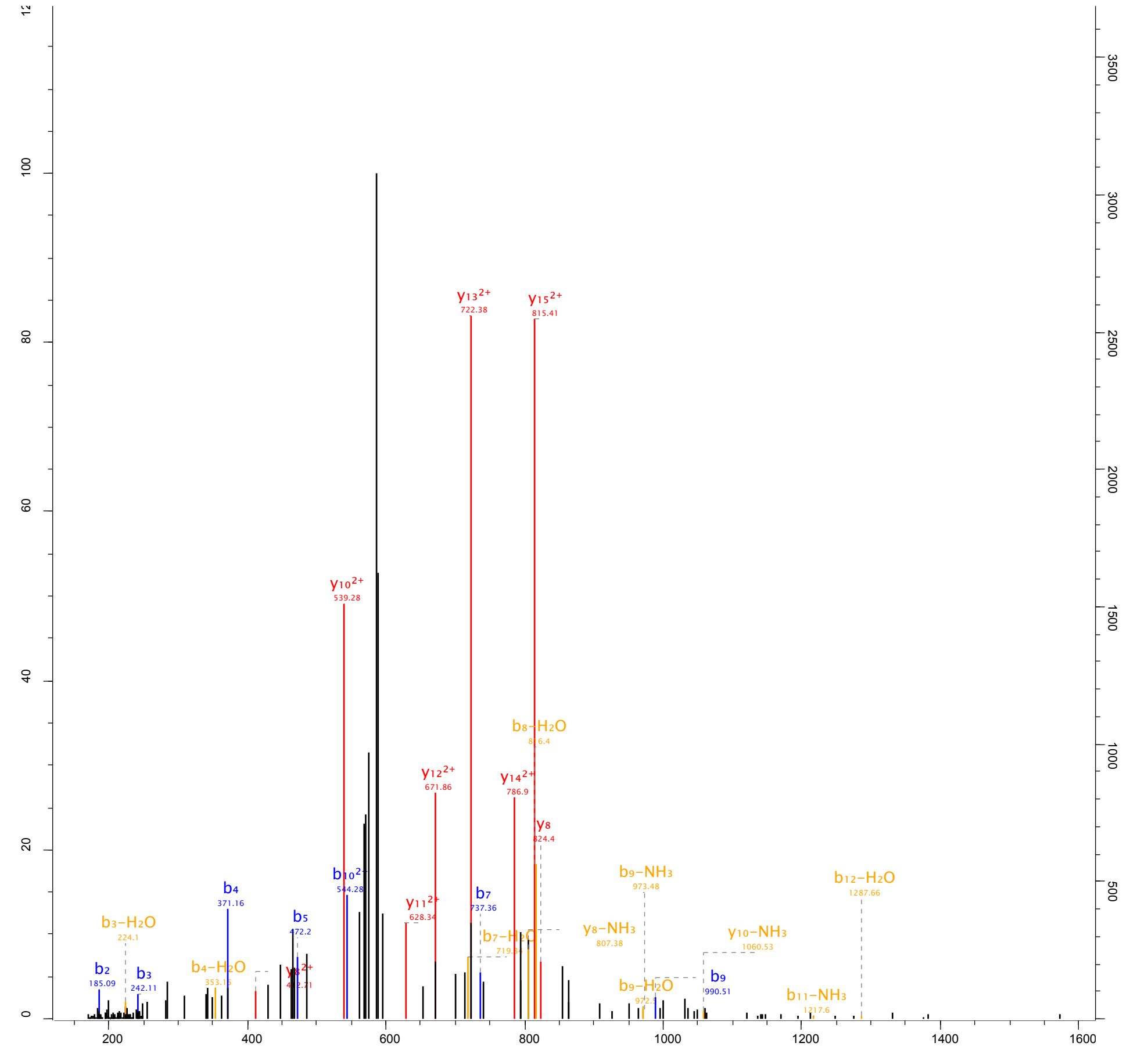
- T M V V H E K Q D D L G K -

y₁₁
y₁₀
y₉
y₈
y₇
ac
y₆
y₅
y₄
y₃

b₂
b₃
b₄
b₅
b₆
b₇
b₈
b₉
b₁₀
b₁₁
b₁₂







- S P G E T S K P R P F A G G G Y R -

b₂
b₃
b₄
b₅
b₇
b₉
b₁₀²⁺
y₁₅²⁺
y₁₄²⁺
y₁₃²⁺
y₁₂²⁺
y₁₁²⁺
ac
y₁₀²⁺
y₈

062513_SCW_II_53_8_Vargas_Enriched

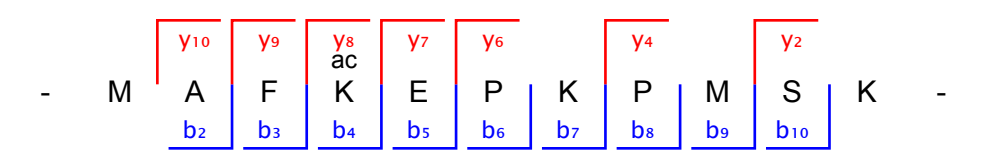
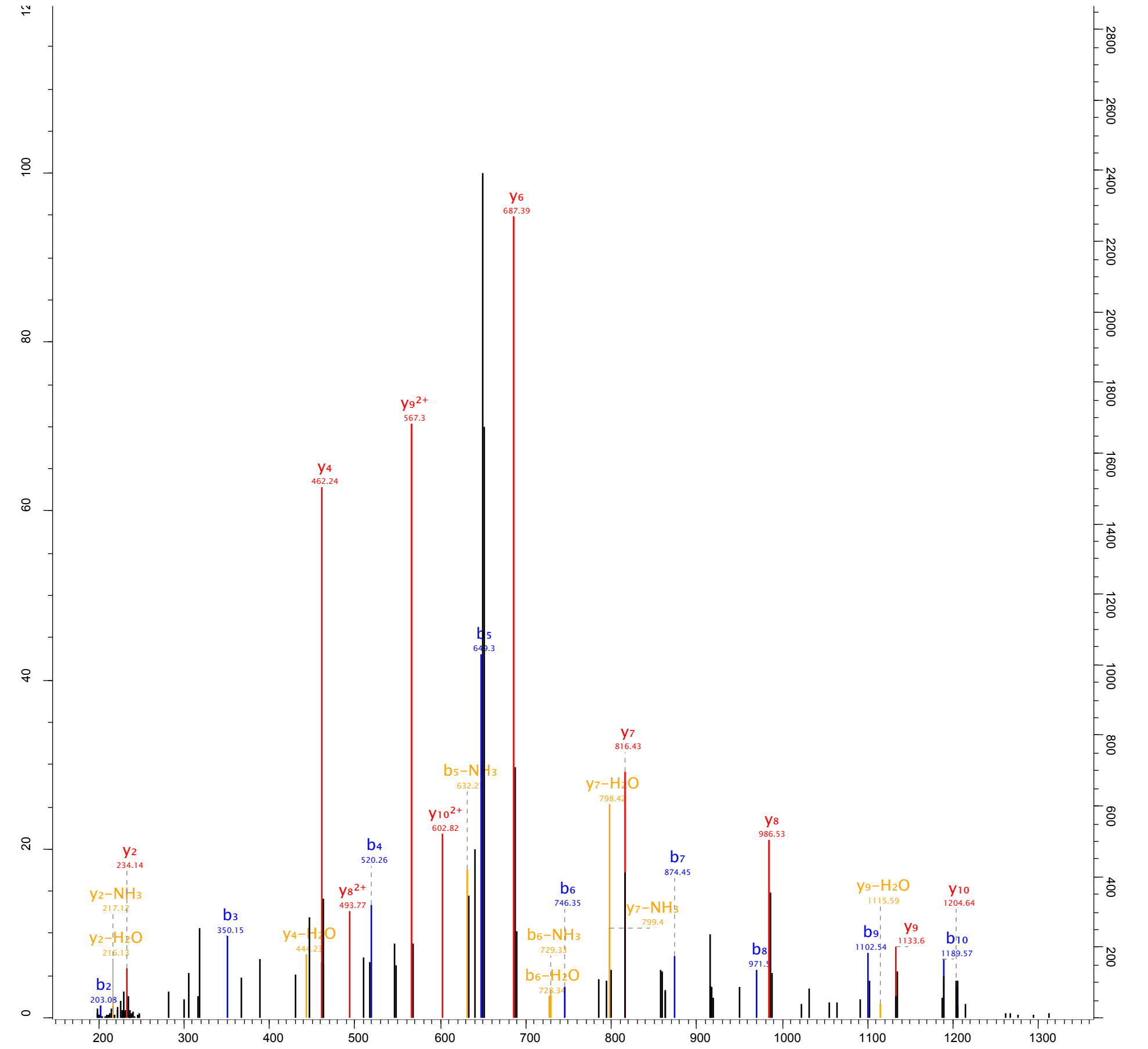
14287

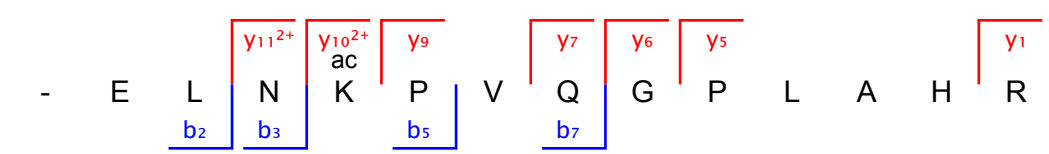
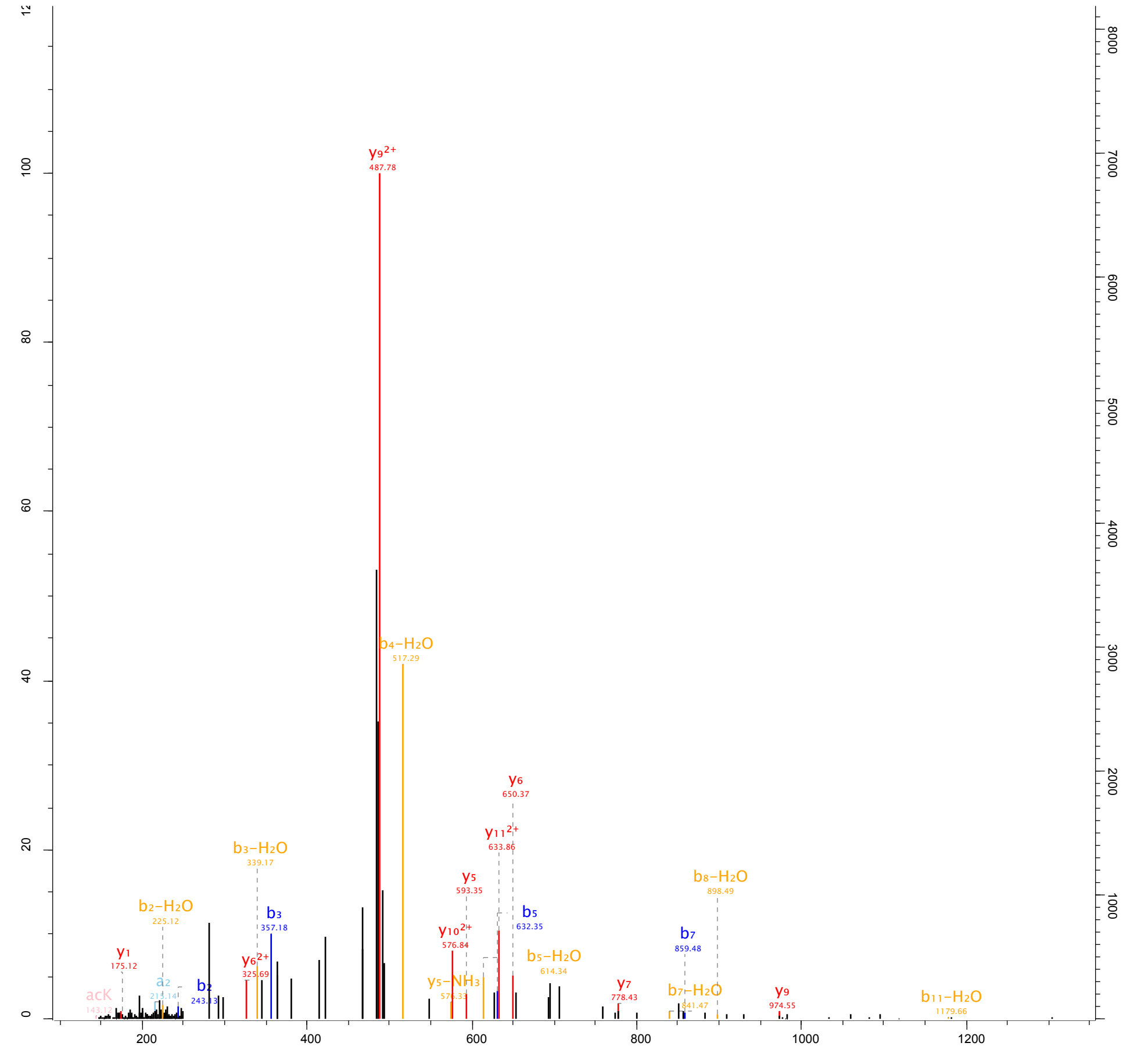
ITMS; CID

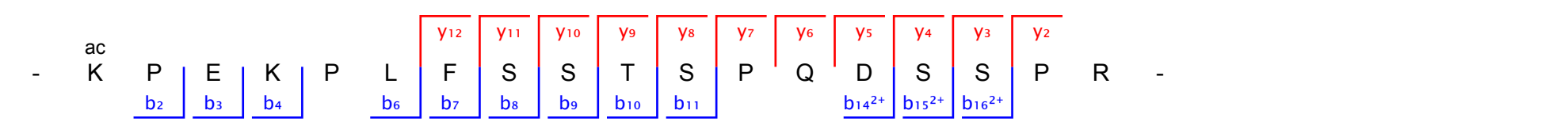
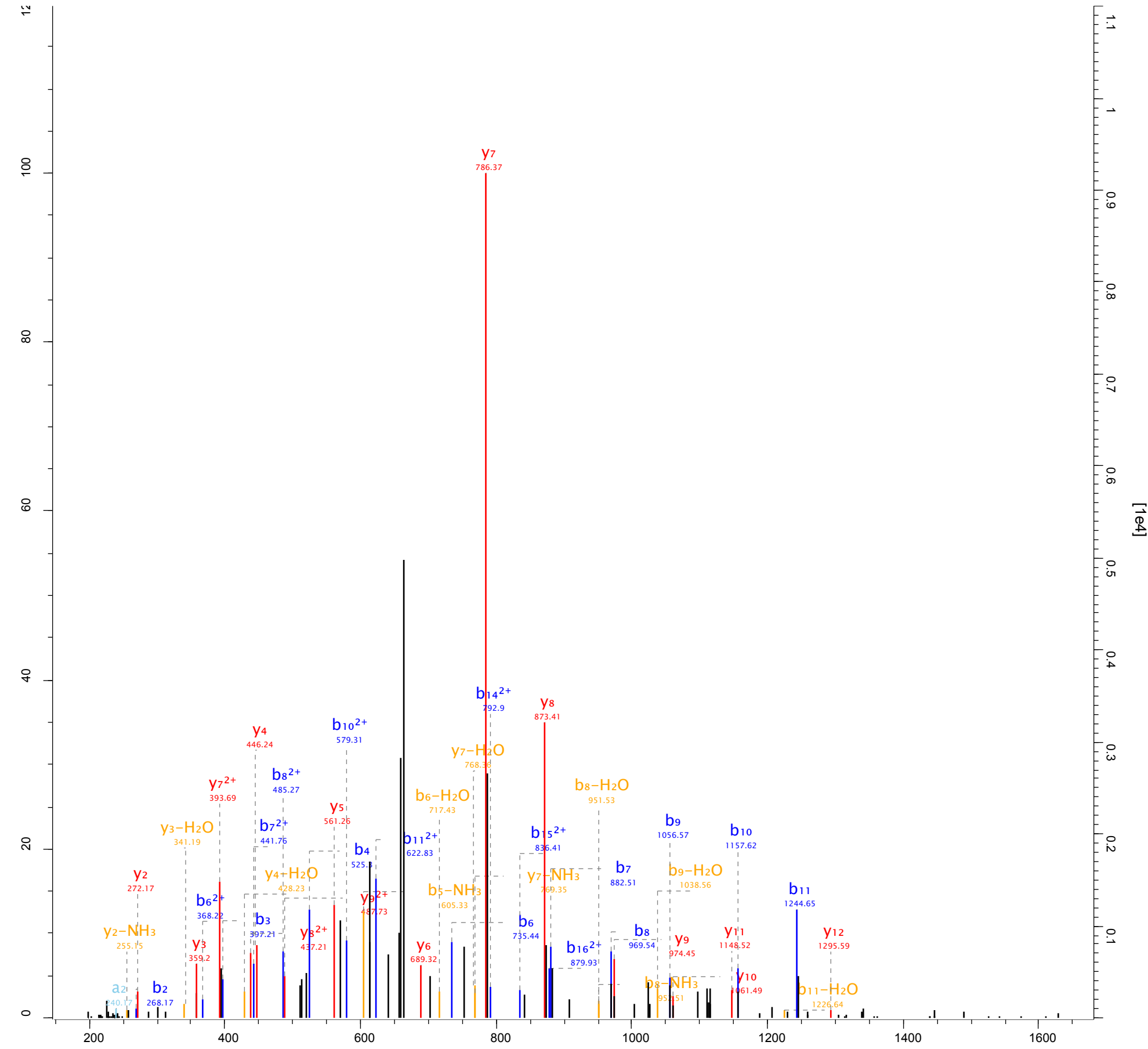
140.45

668.85

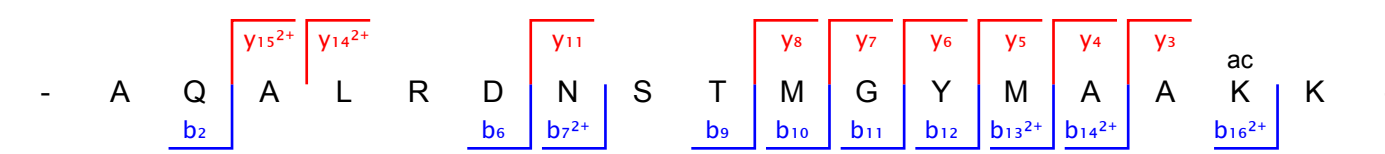
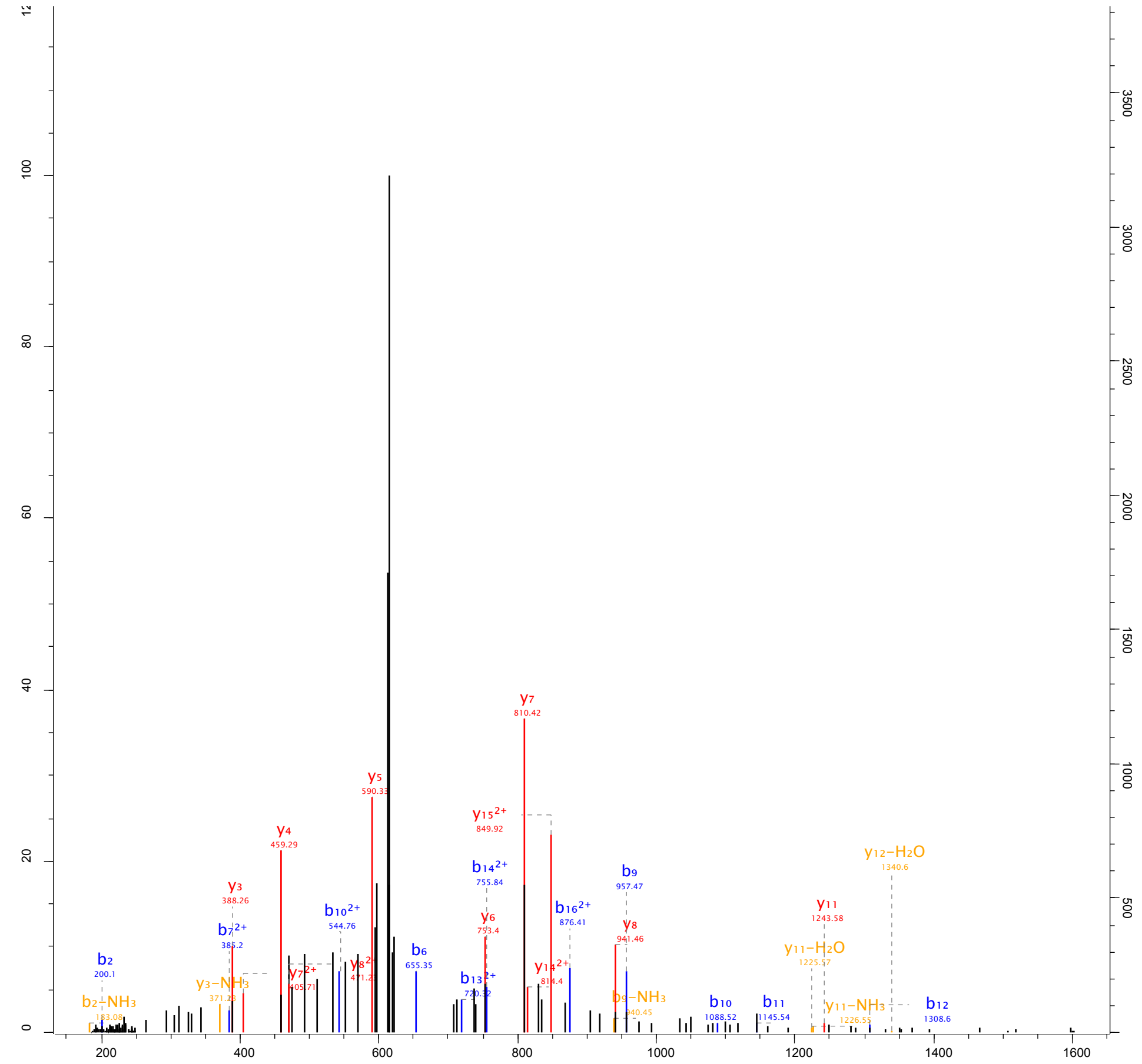
MIIt3

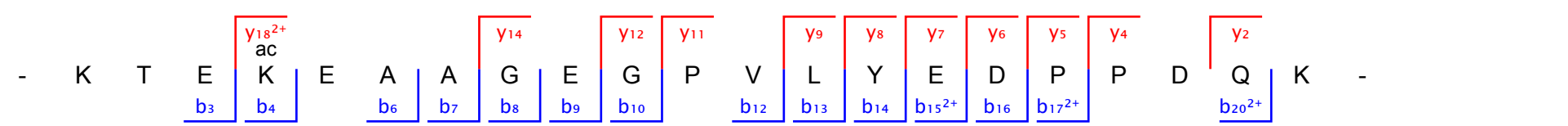
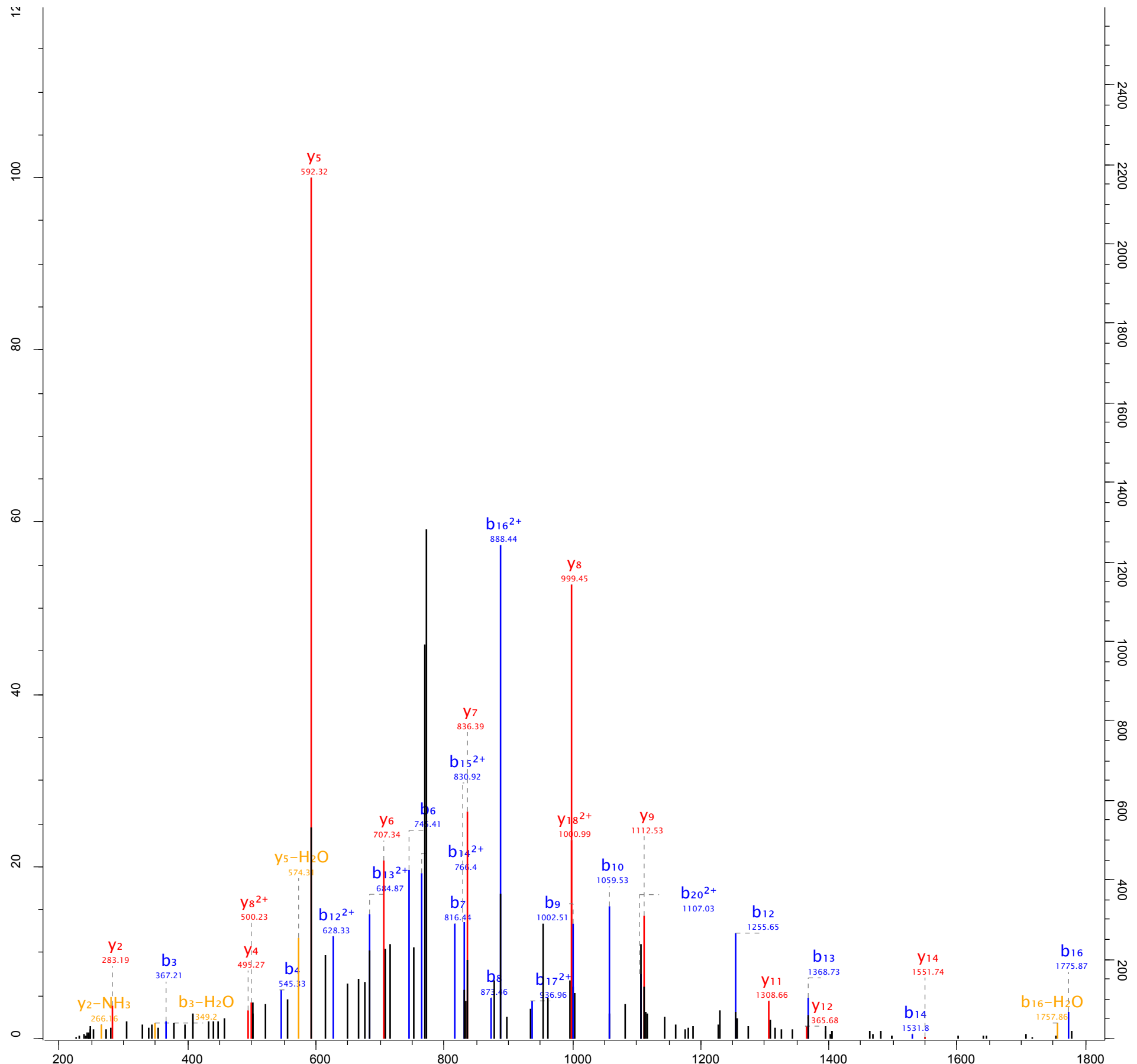


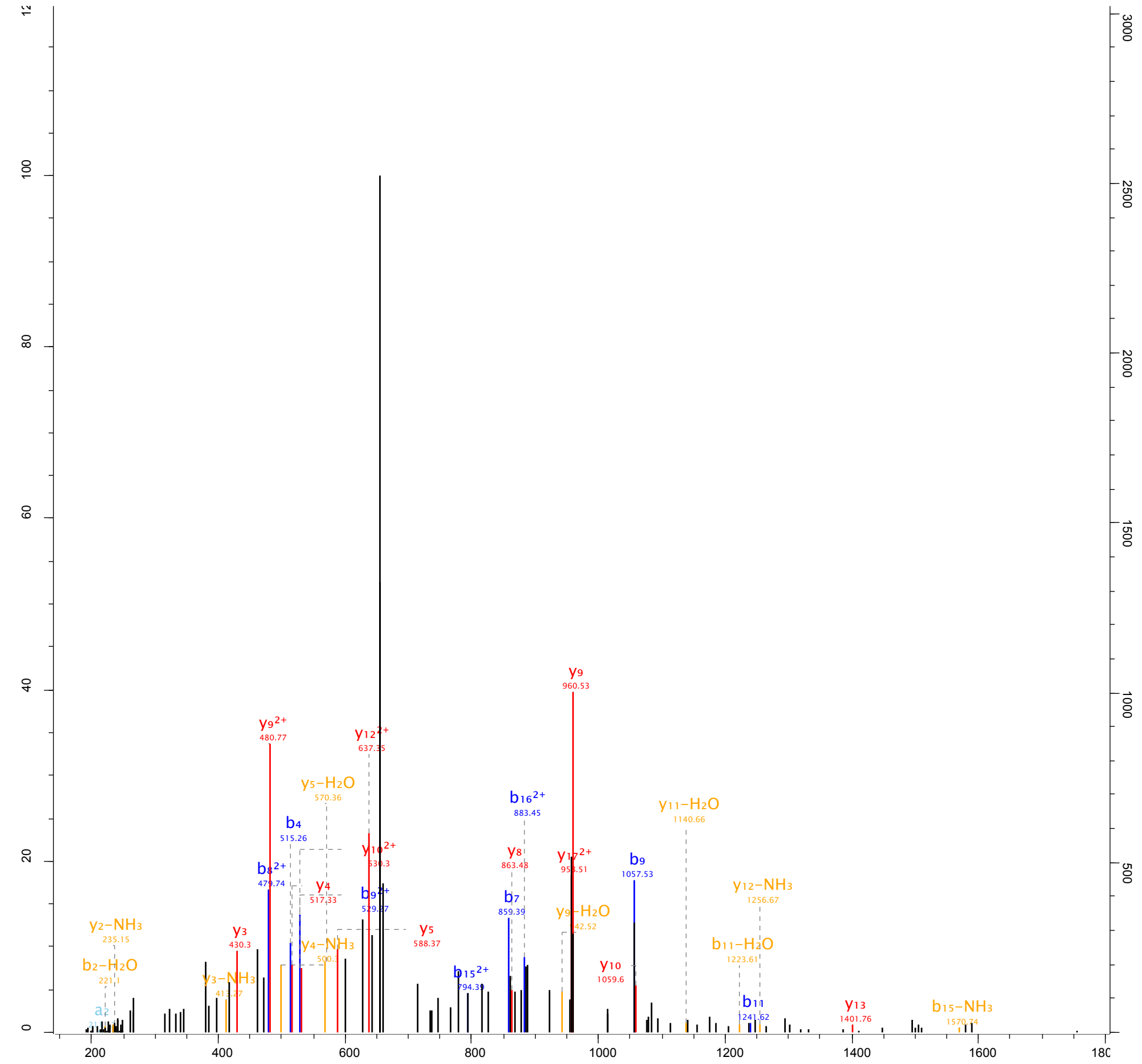




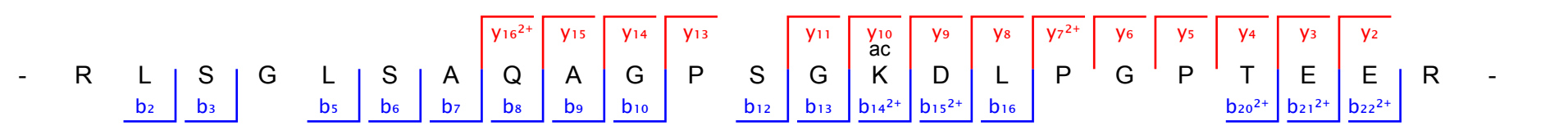
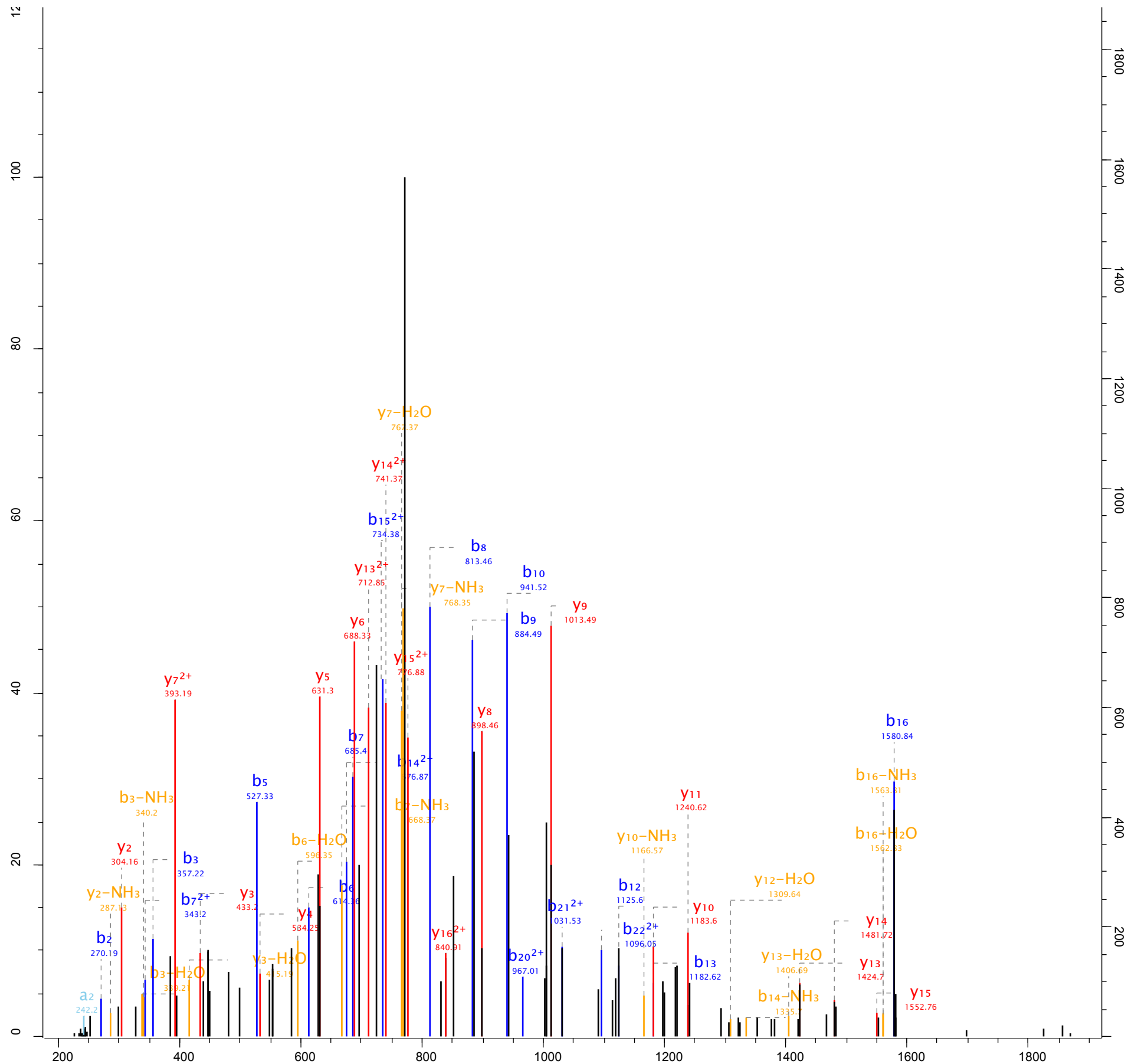
Raw file: 062513_SCW_II_53_8_Vargas_Enriched
 Scan: 14731 Method: ITMS; CID Score: 94.34 m/z: 633.31 Gene names: Hsp90aa1

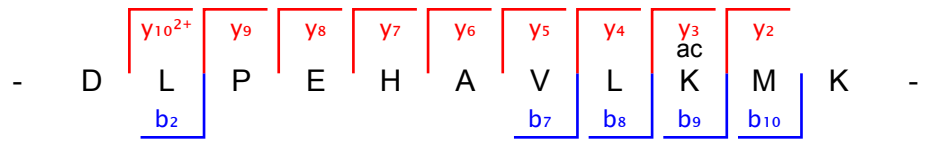
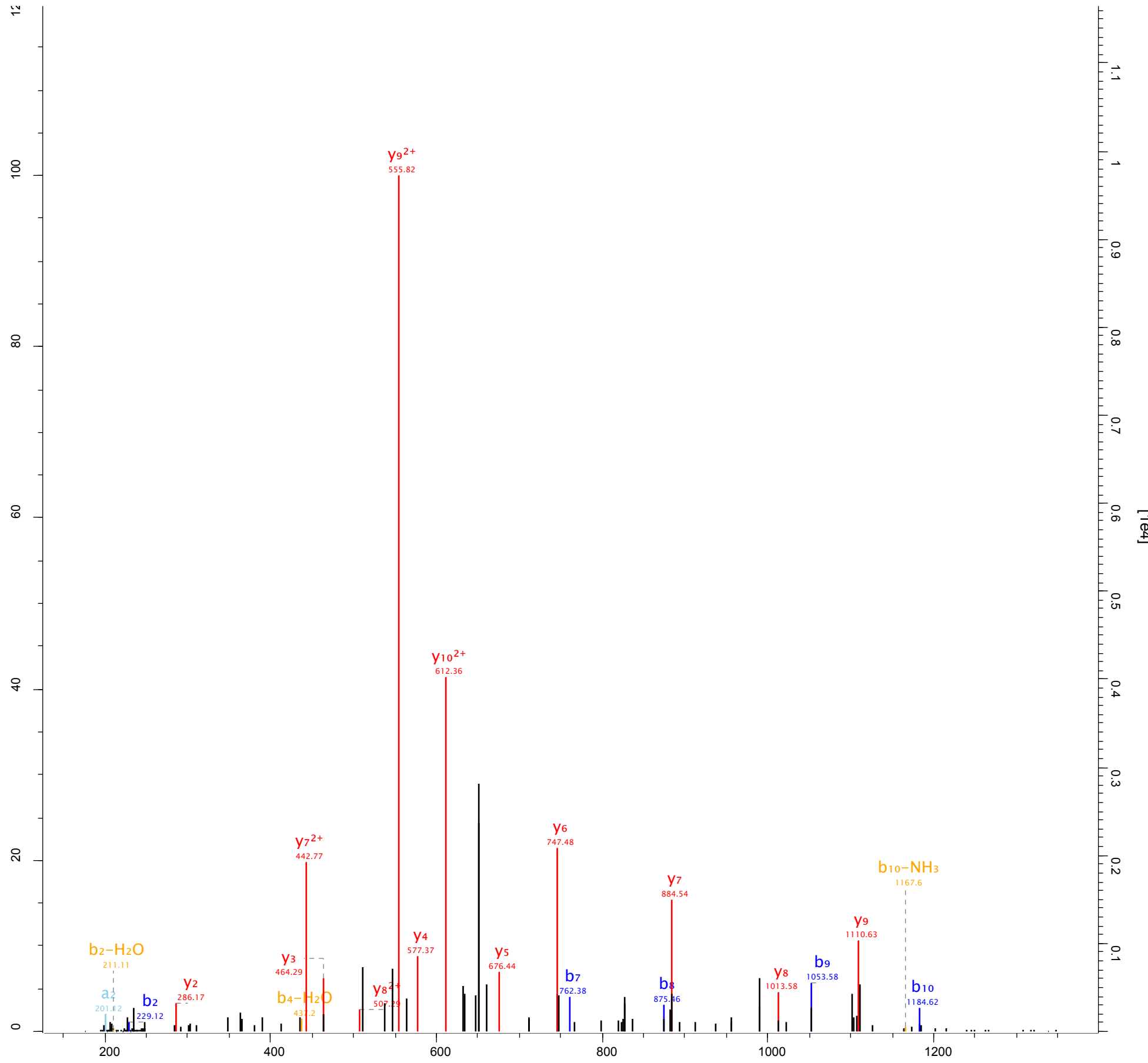


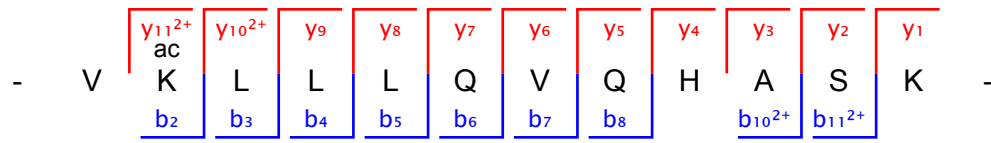
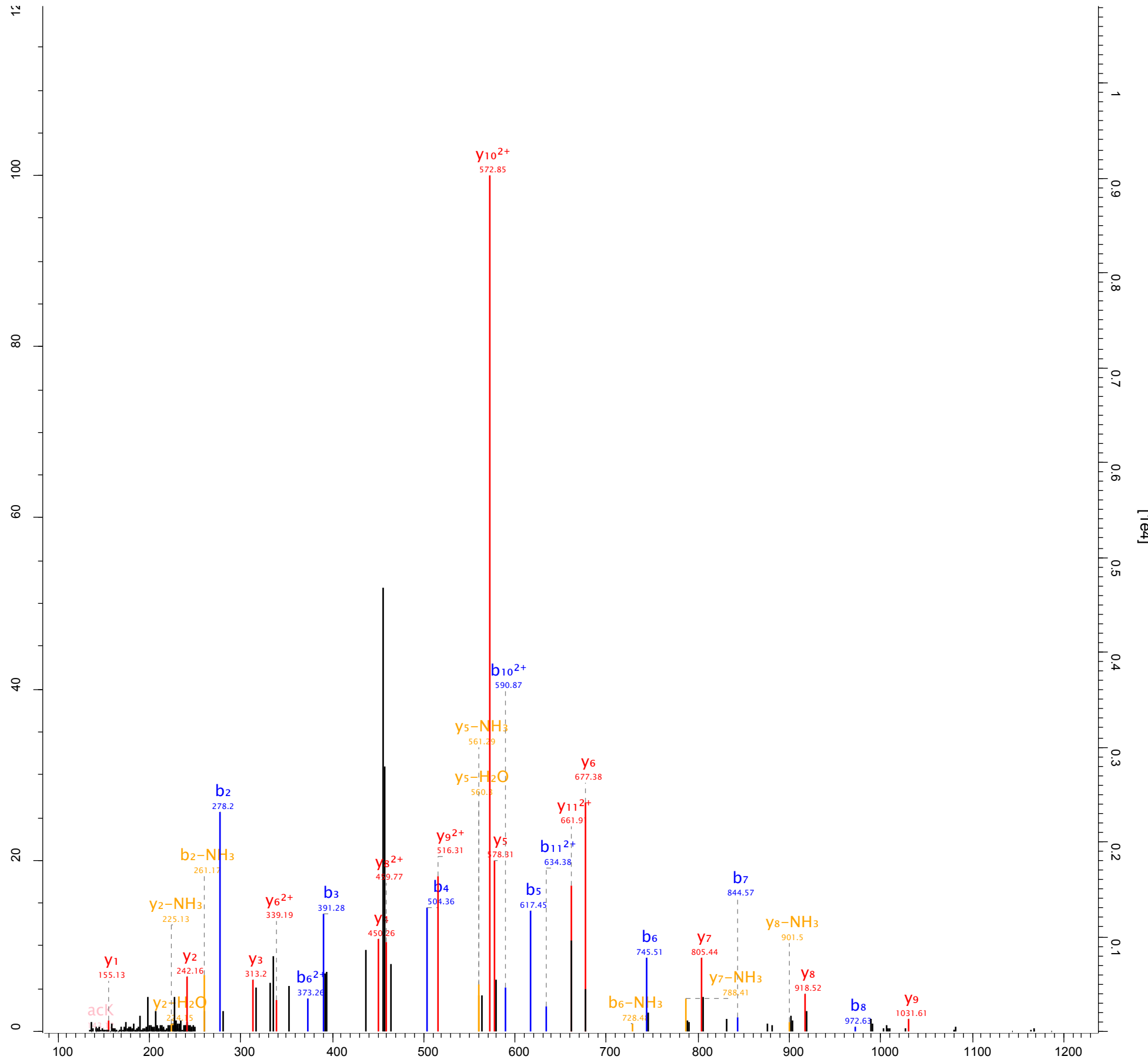


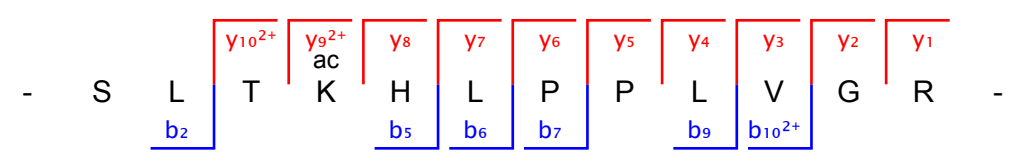
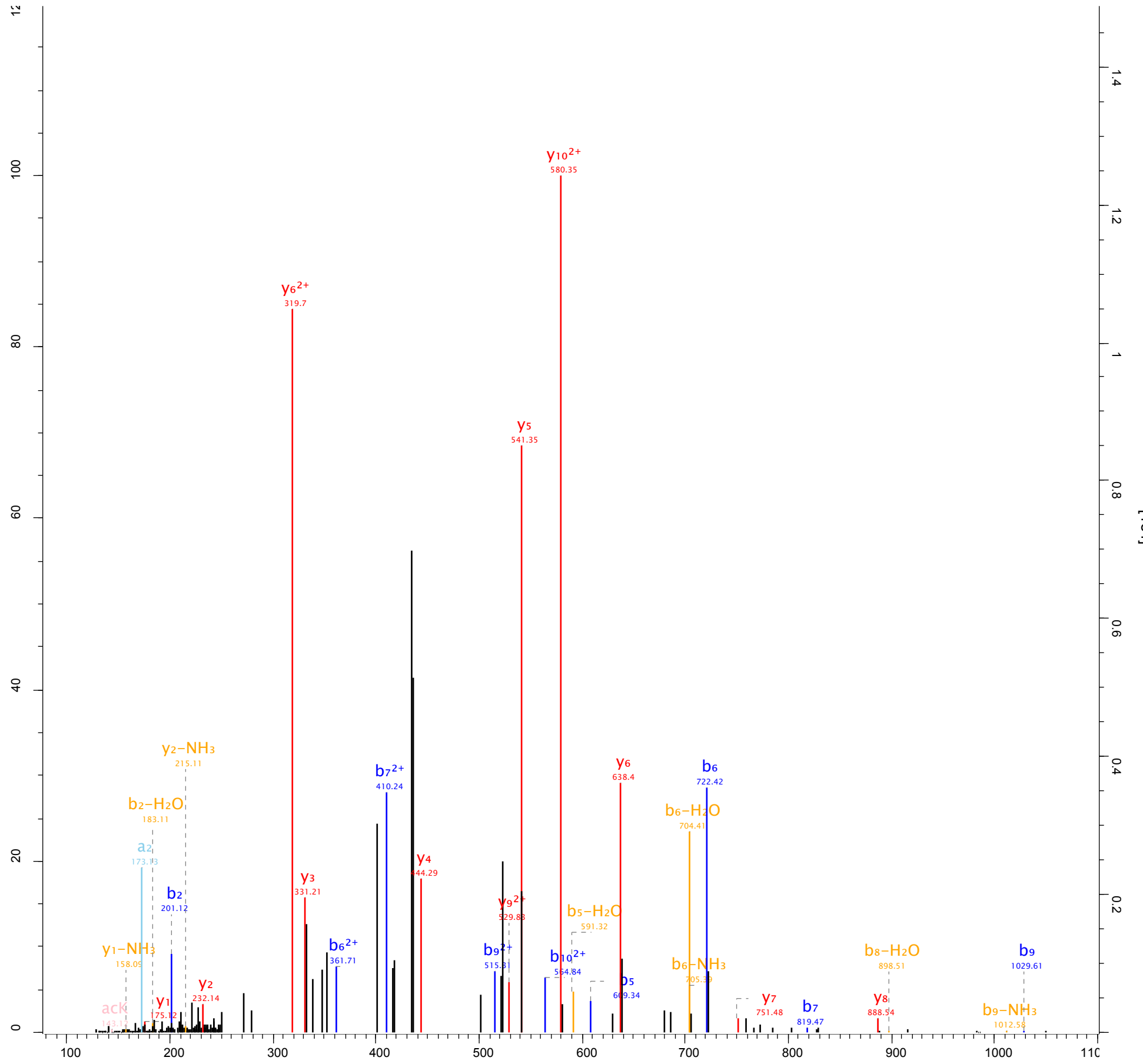


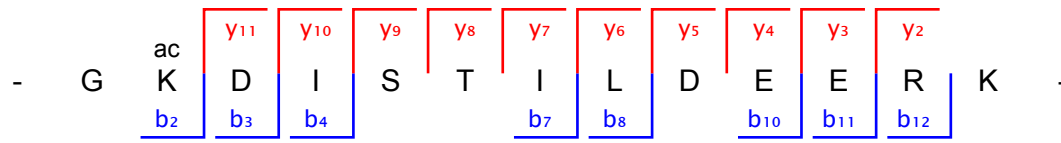
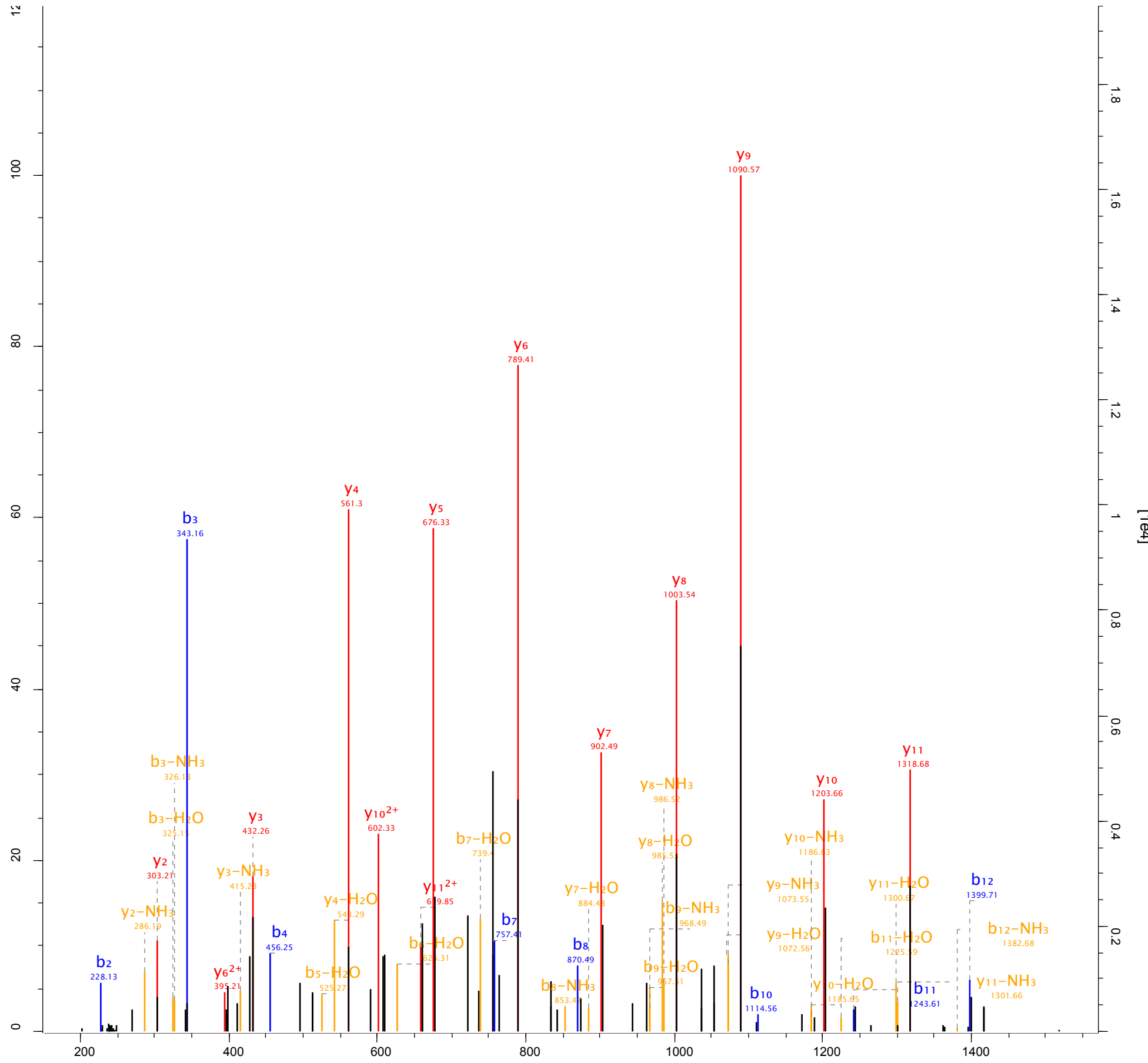
- T y₁₇²⁺ H a₂ Y L b₄ T y₁₃ Q y₁₂²⁺ D b₇ V y₁₀ V y₉ P y₈ S b₁₁ T S y₅ A y₄ S b₁₅²⁺ y₃
ac K b₁₆²⁺ P K -

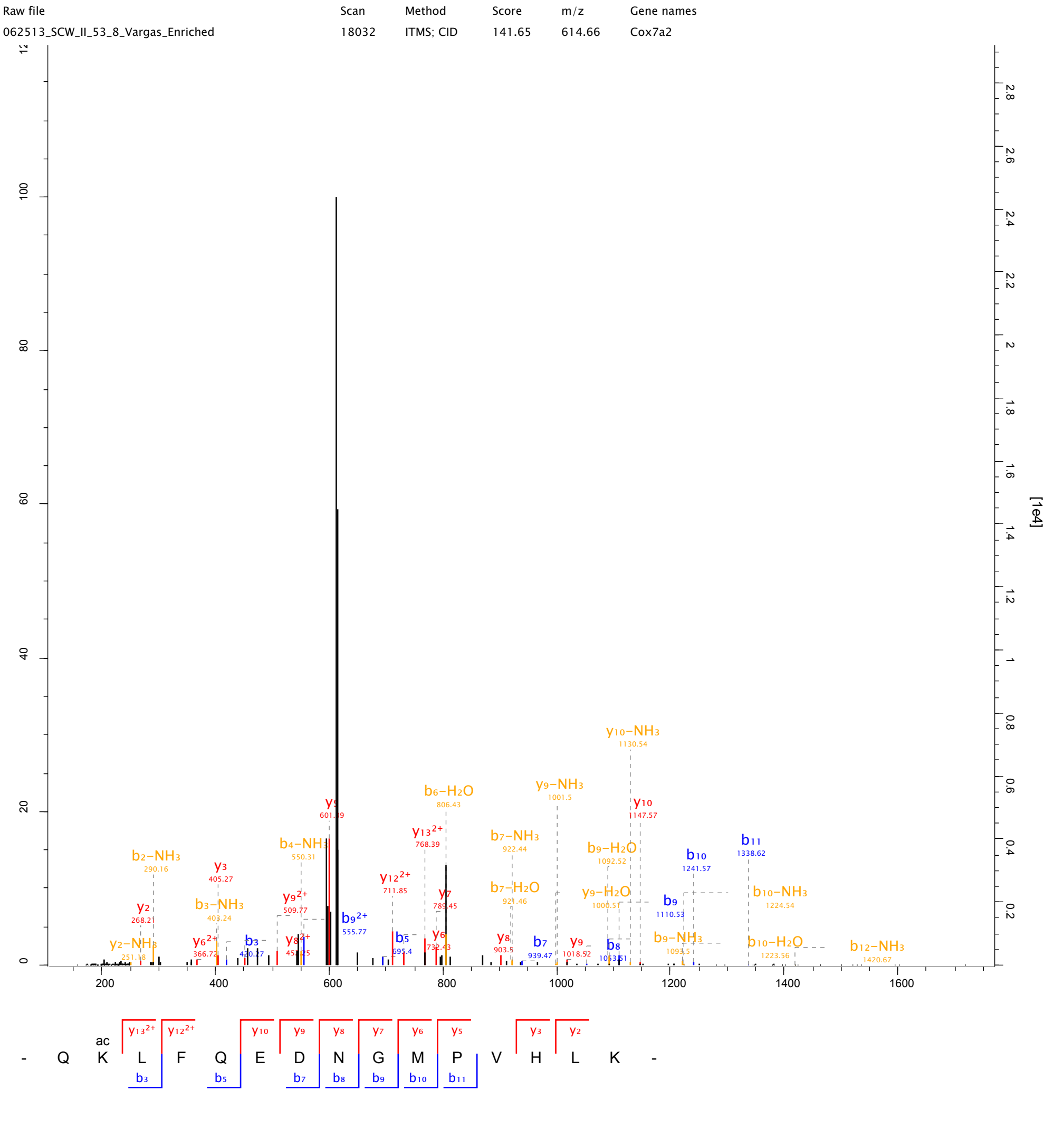




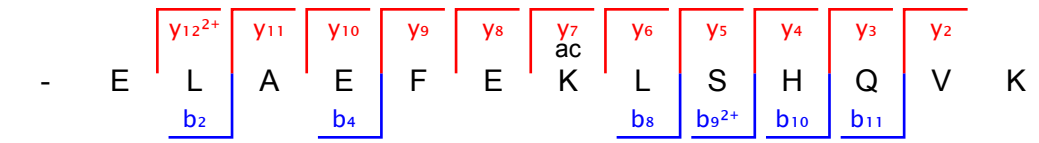
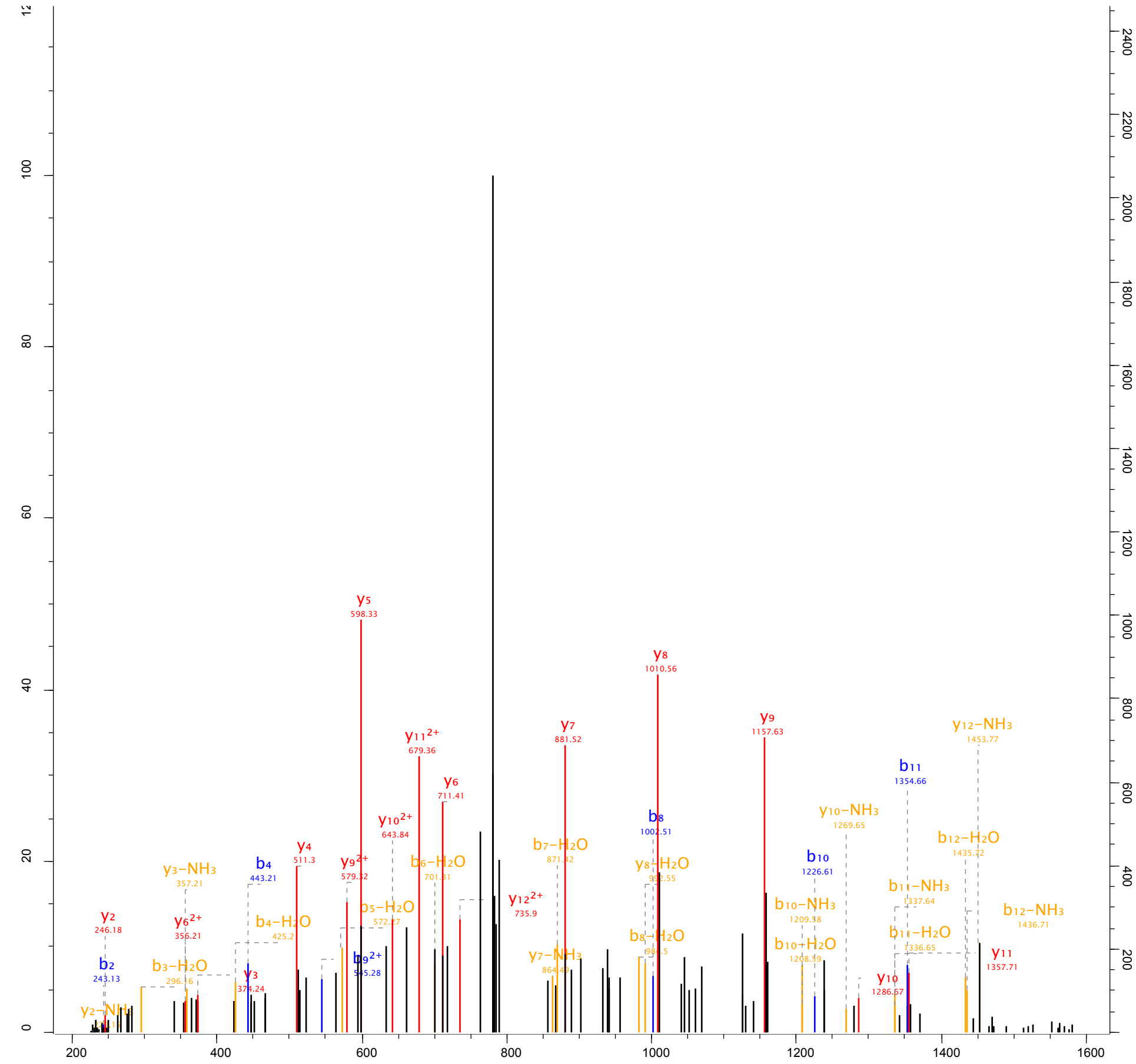


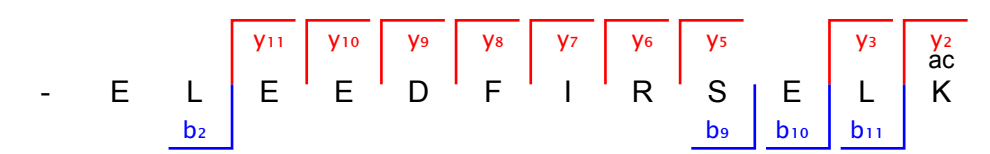
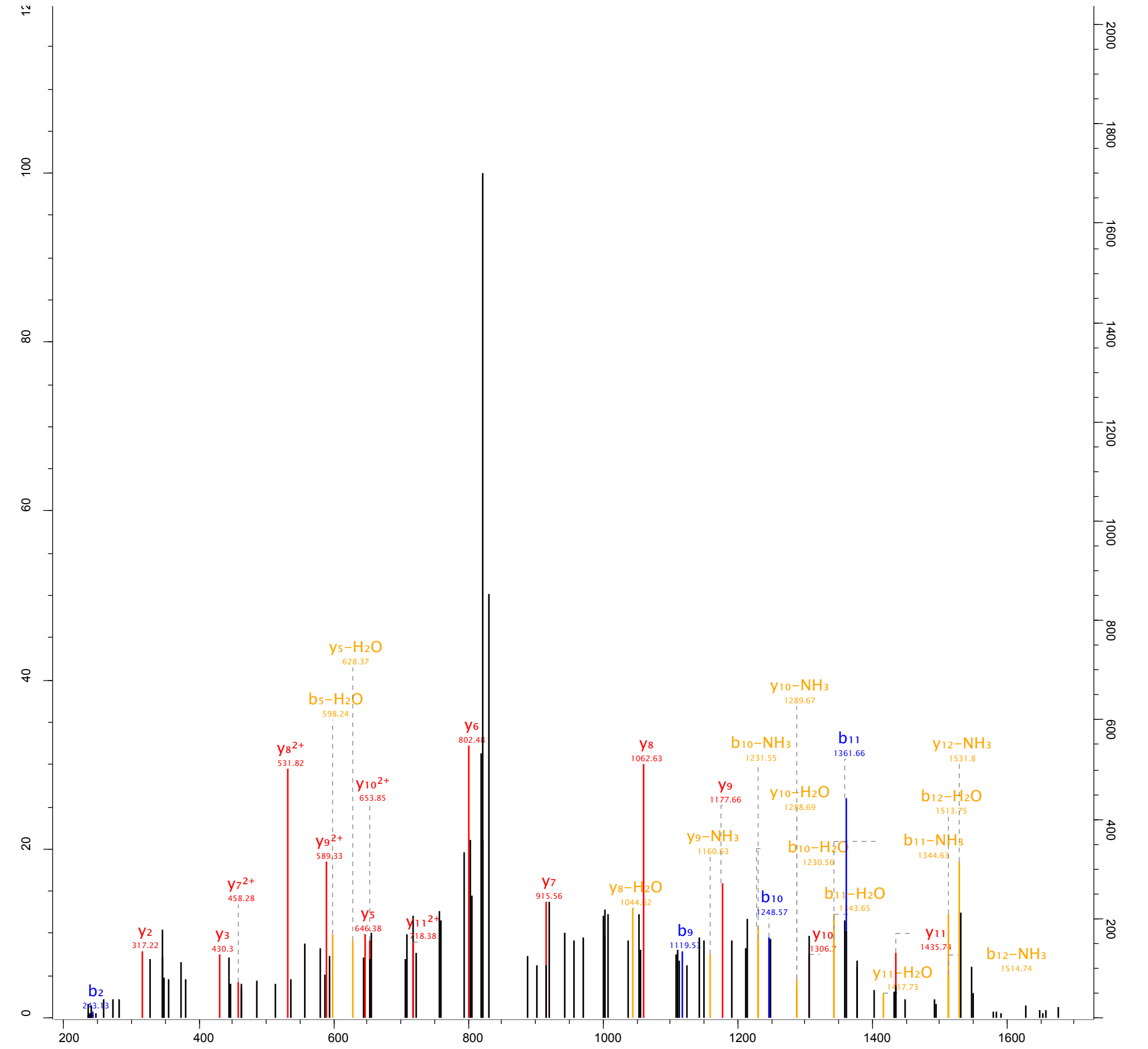




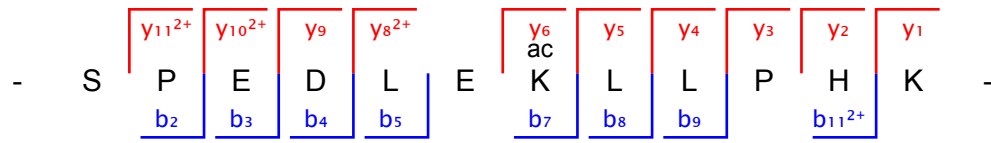
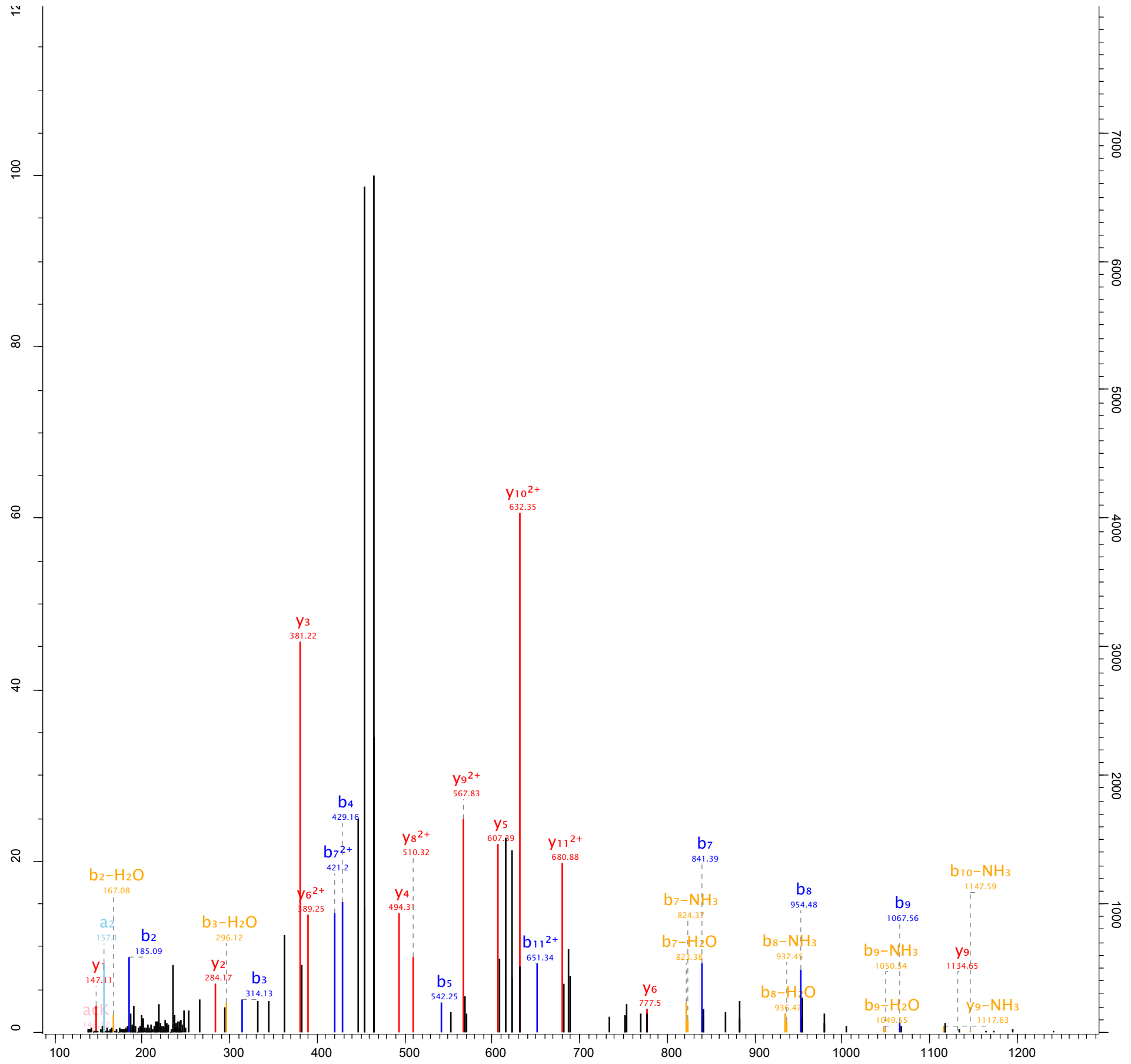


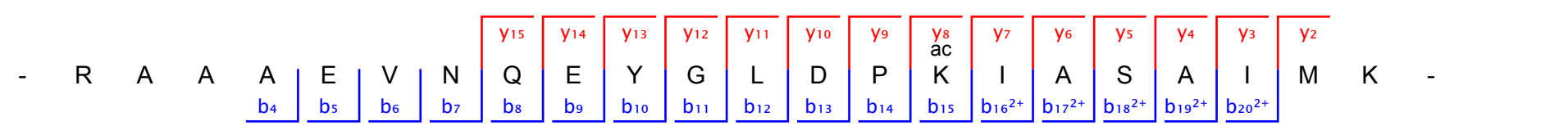
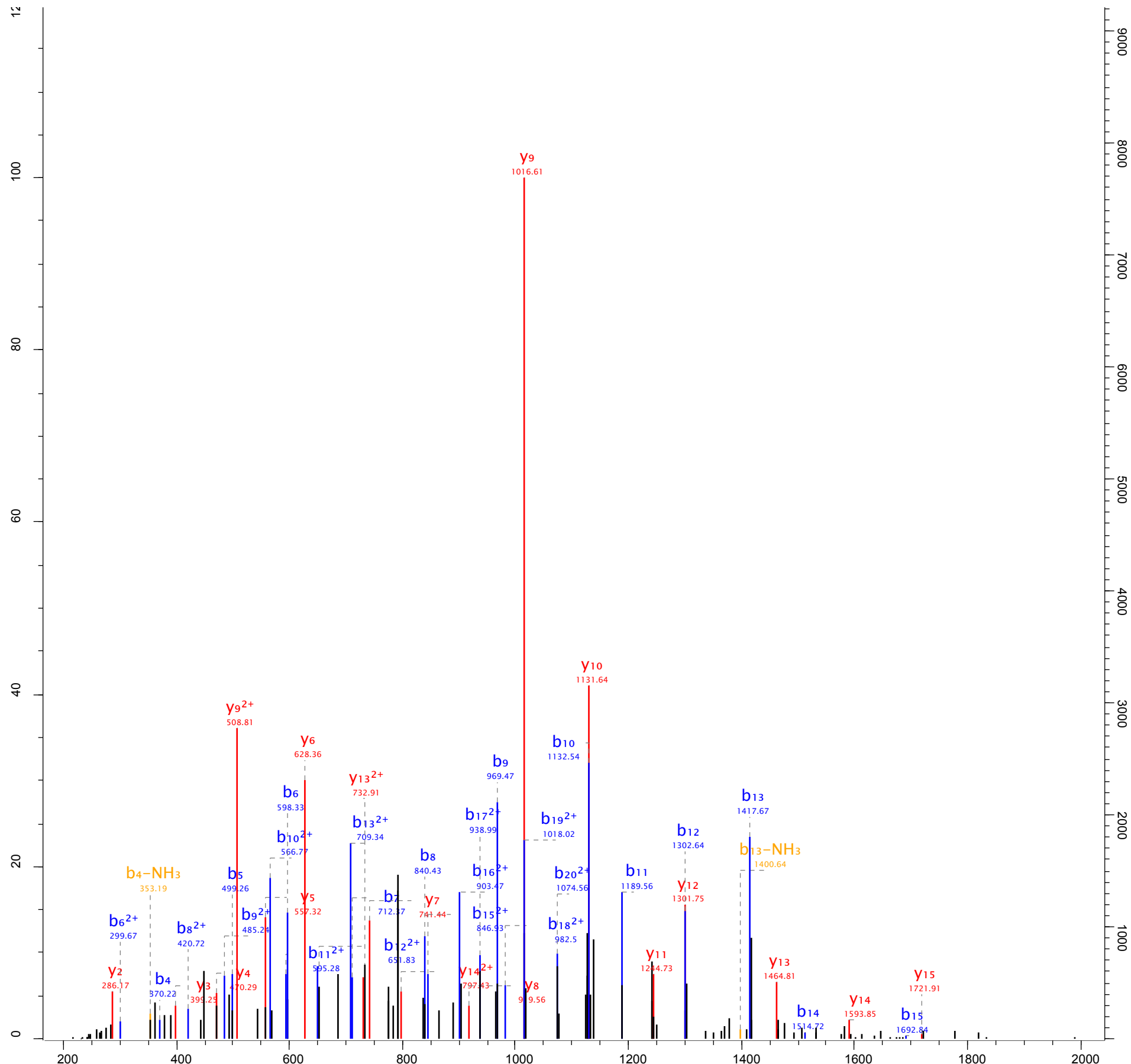
Raw file 062513_SCW_II_53_8_Vargas_Enriched Scan 18540 Method ITMS; CID Score 157.5 m/z 800.42 Gene names Sat2

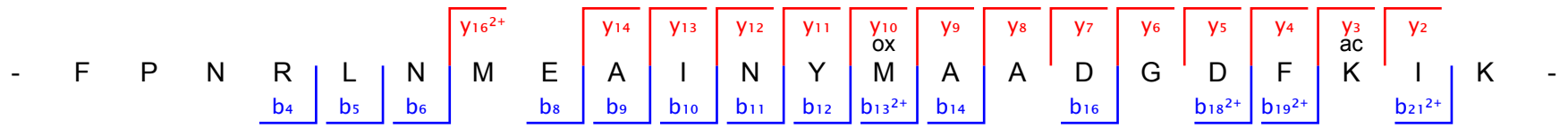
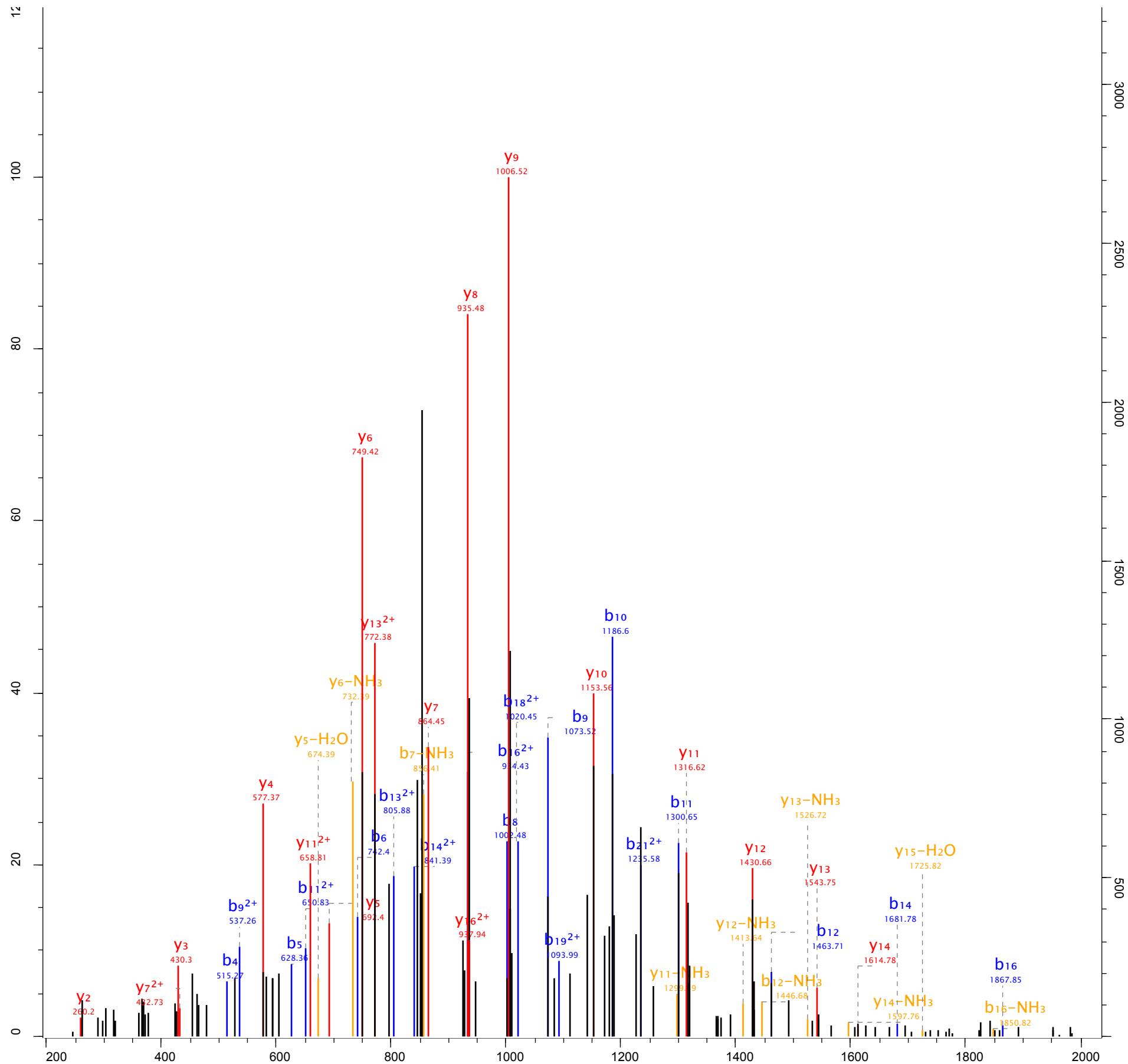


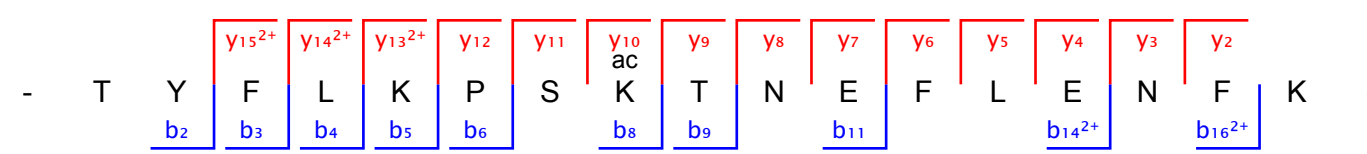
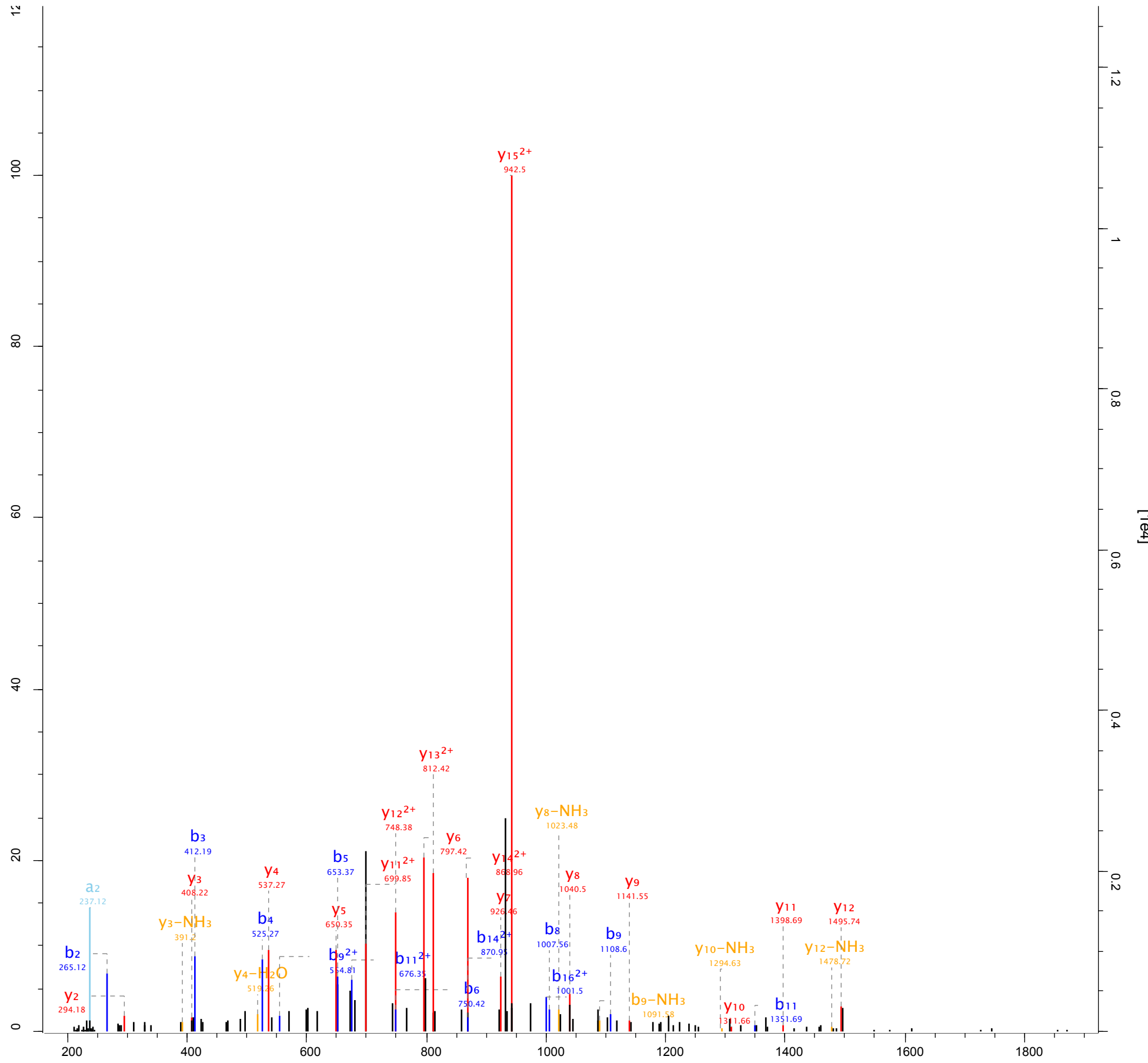


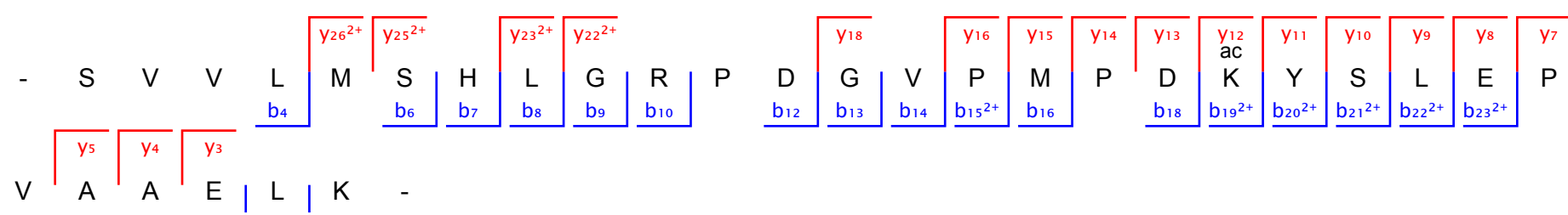
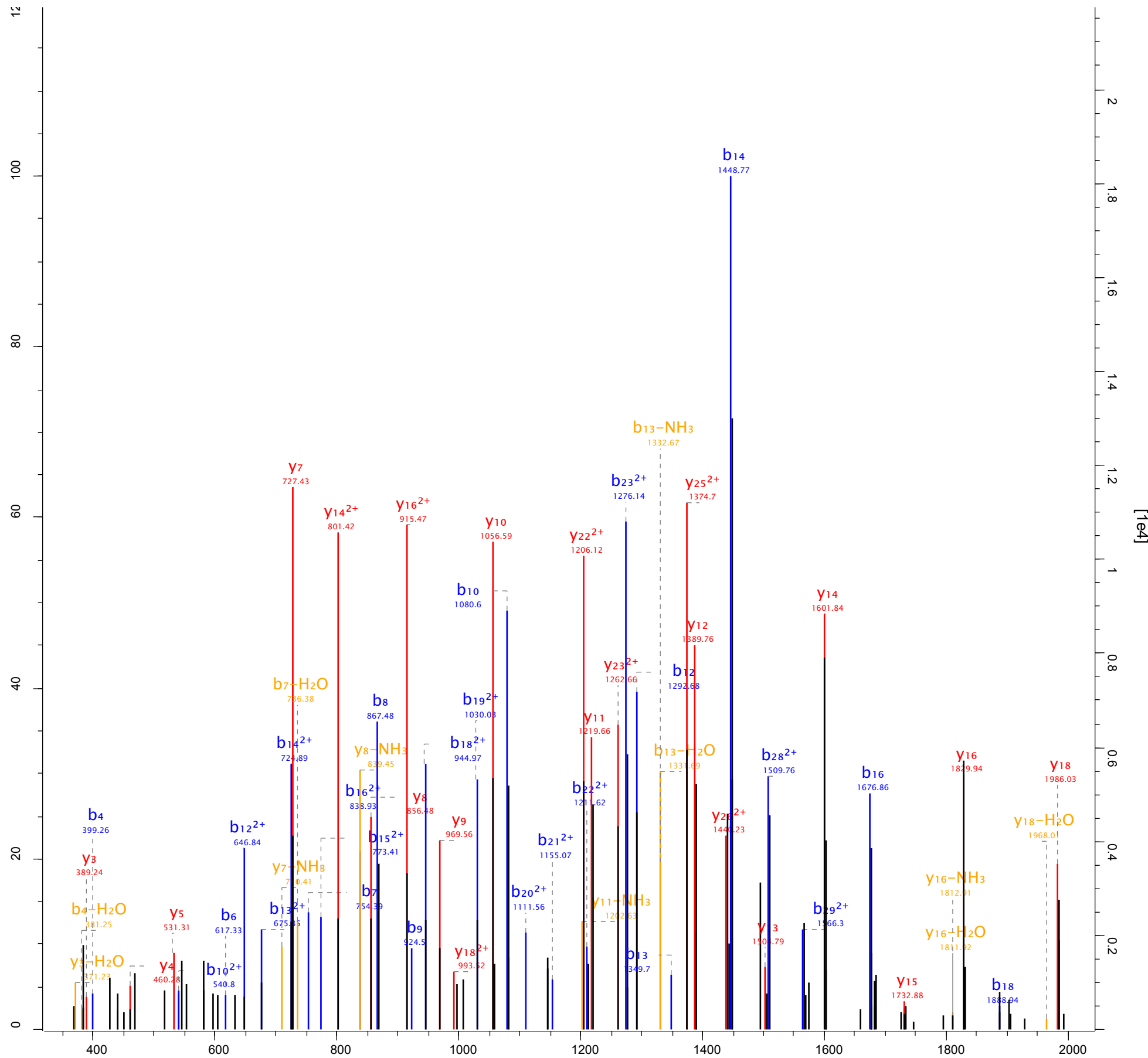
Raw file: 062513_SCW_II_53_8_Vargas_Enriched
 Scan: 19469 Method: ITMS; CID Score: 163.46 m/z: 483.6 Gene names: Gpi;Gm1840

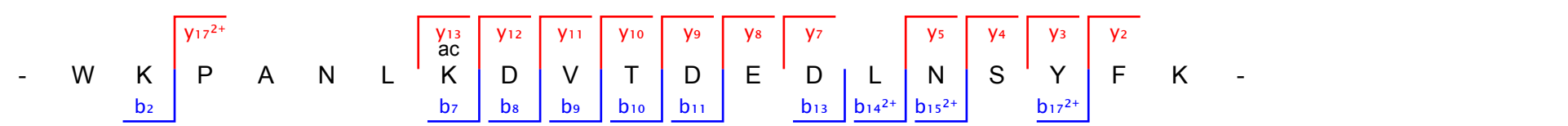
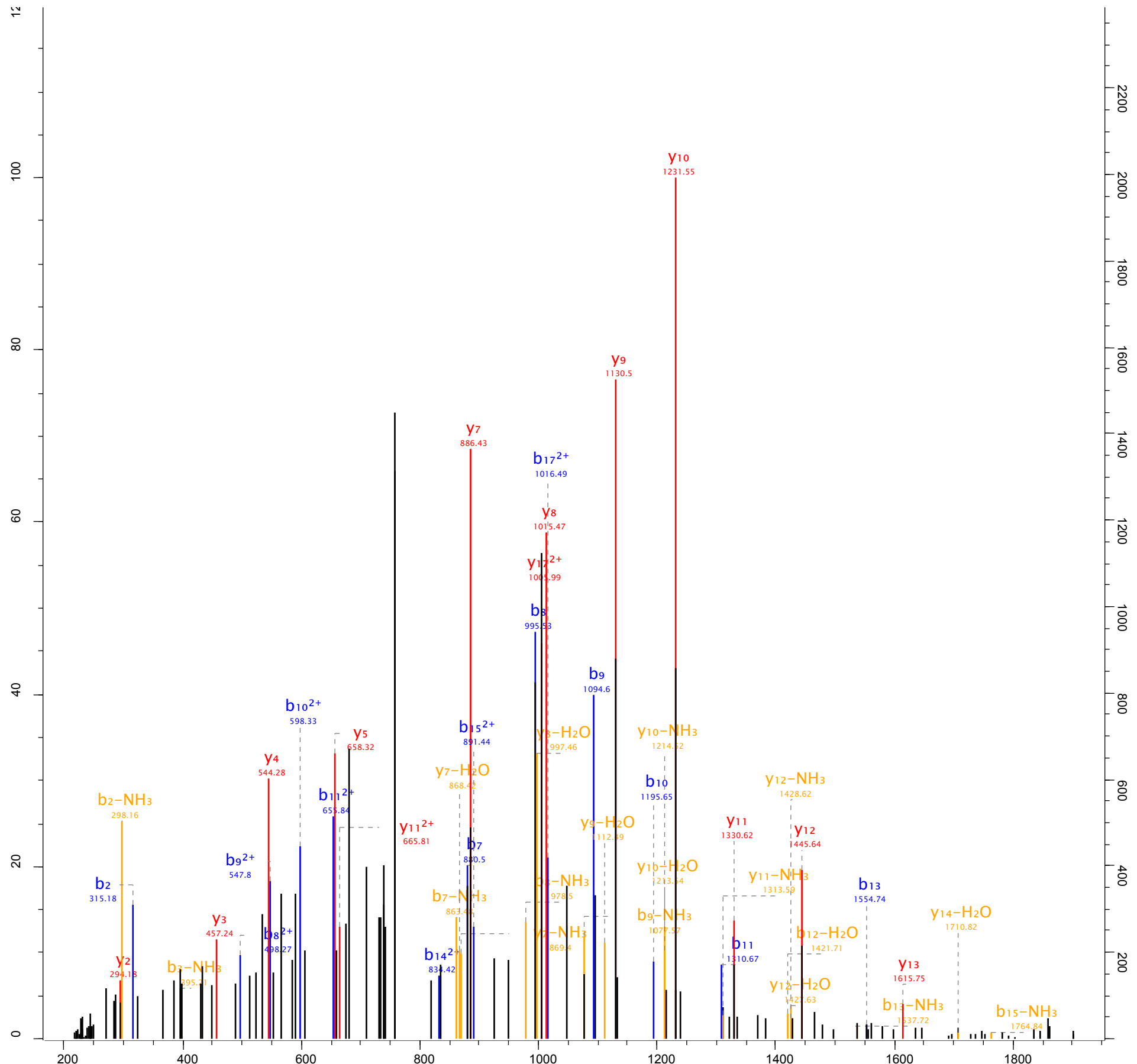


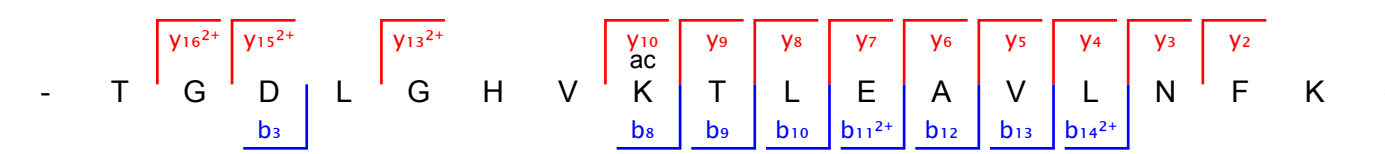
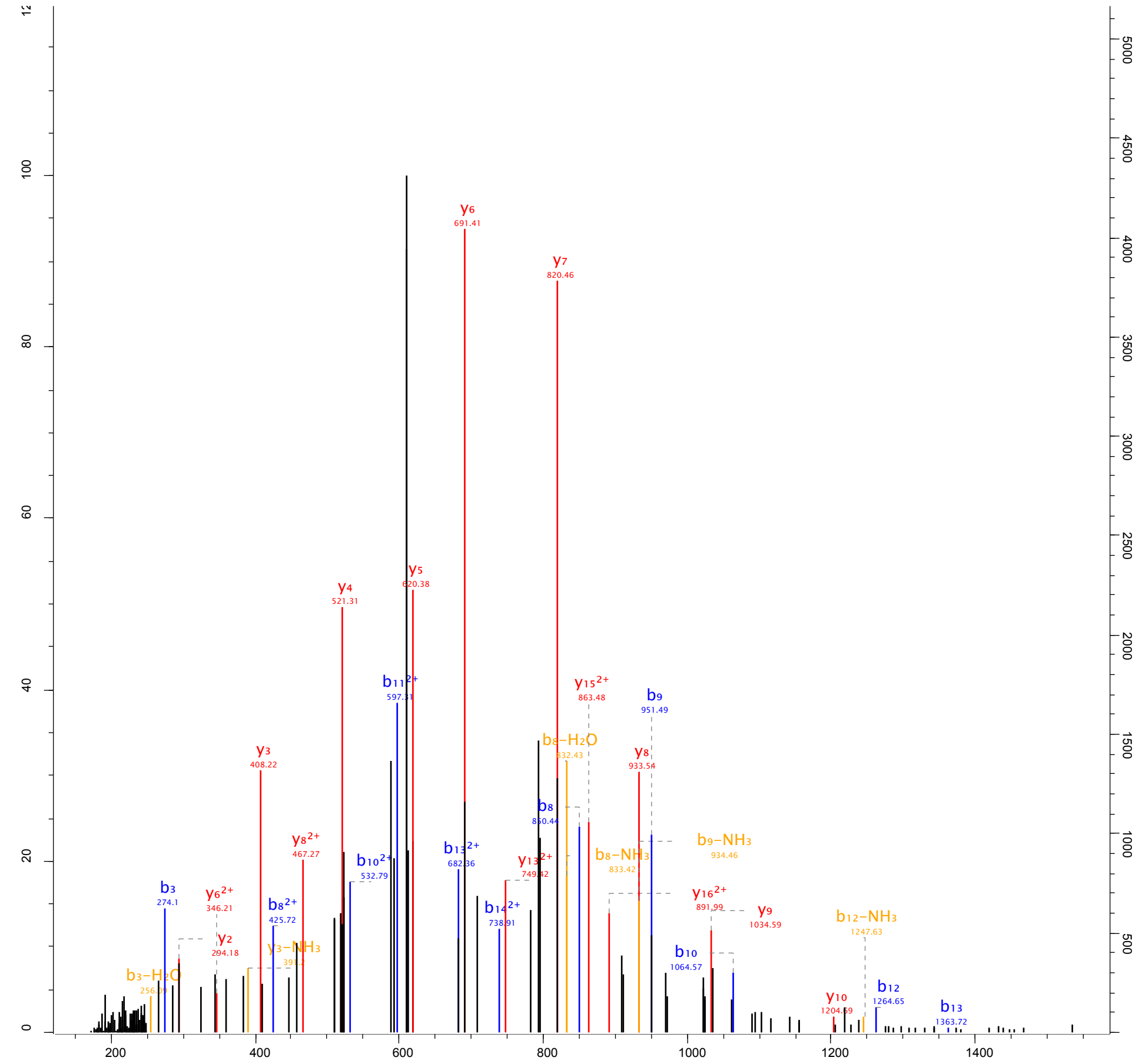


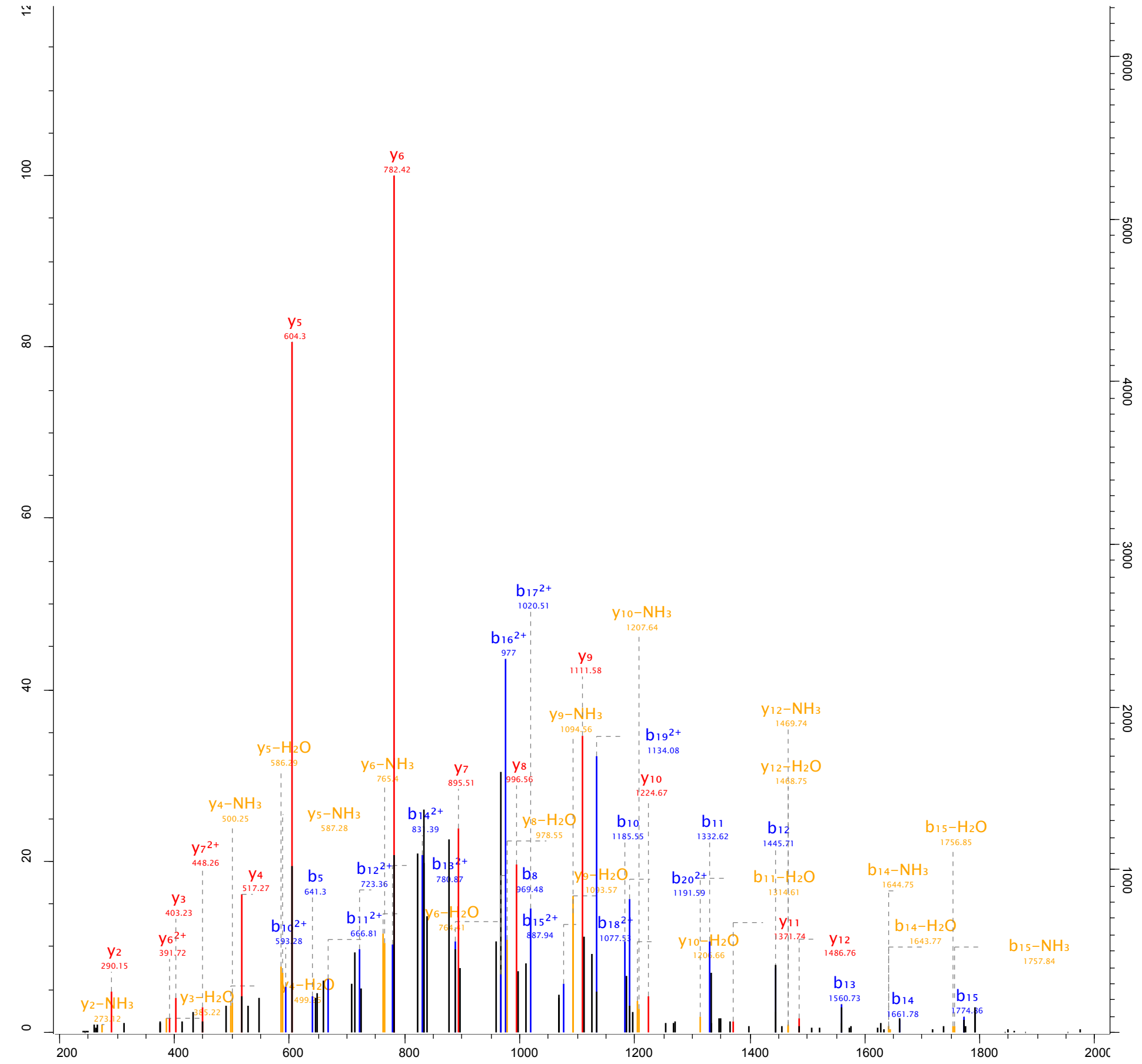








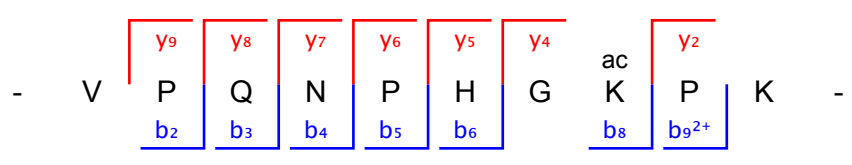
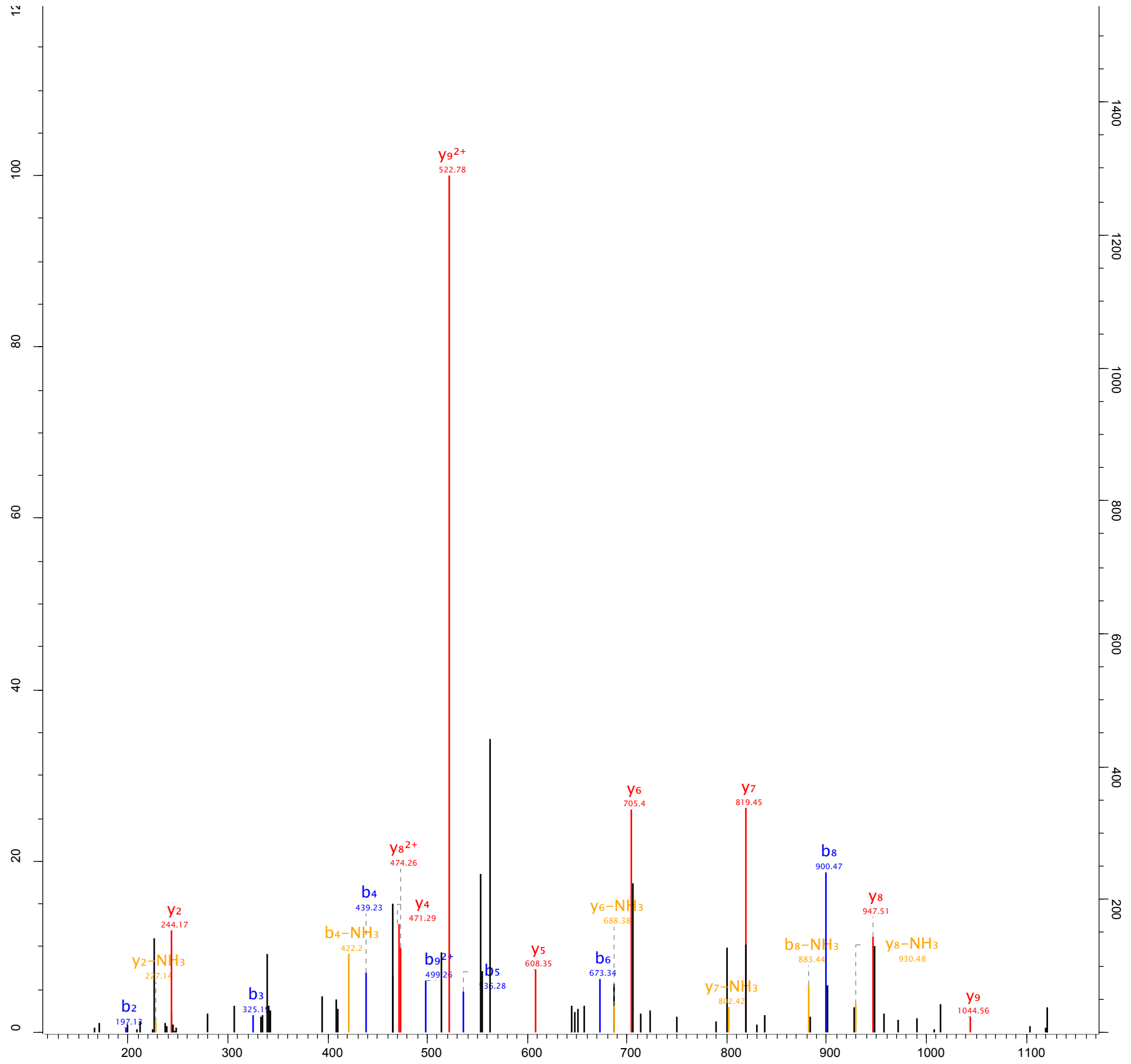


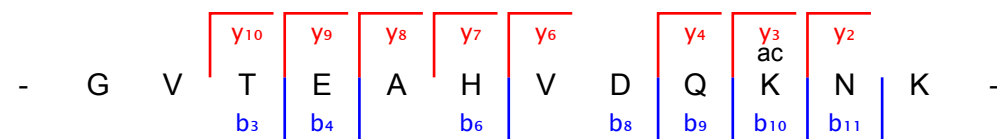
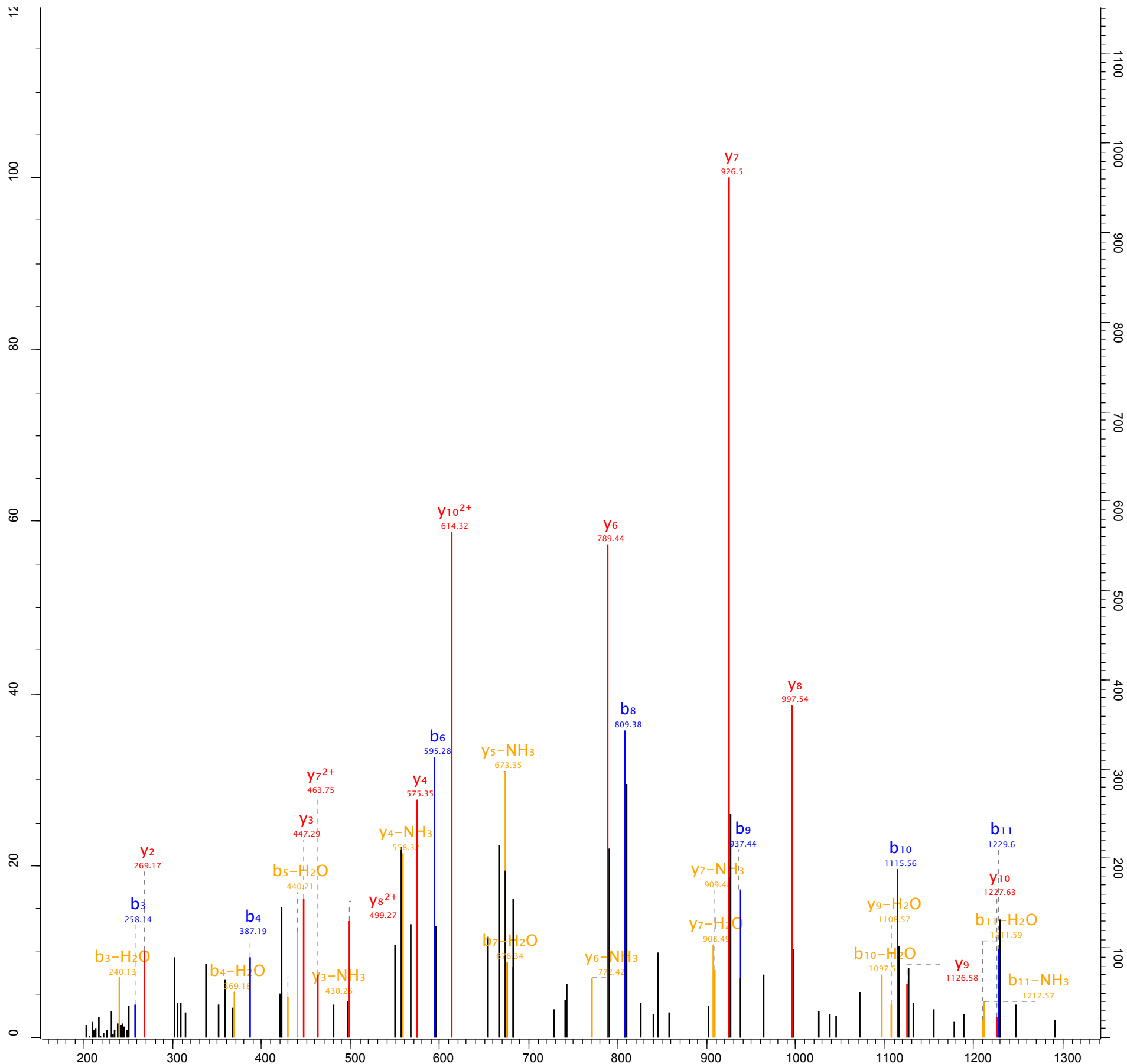


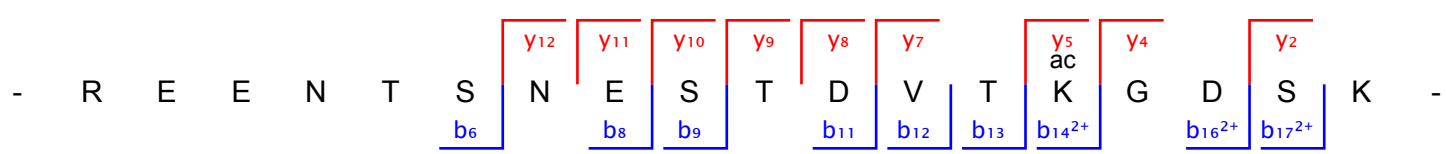
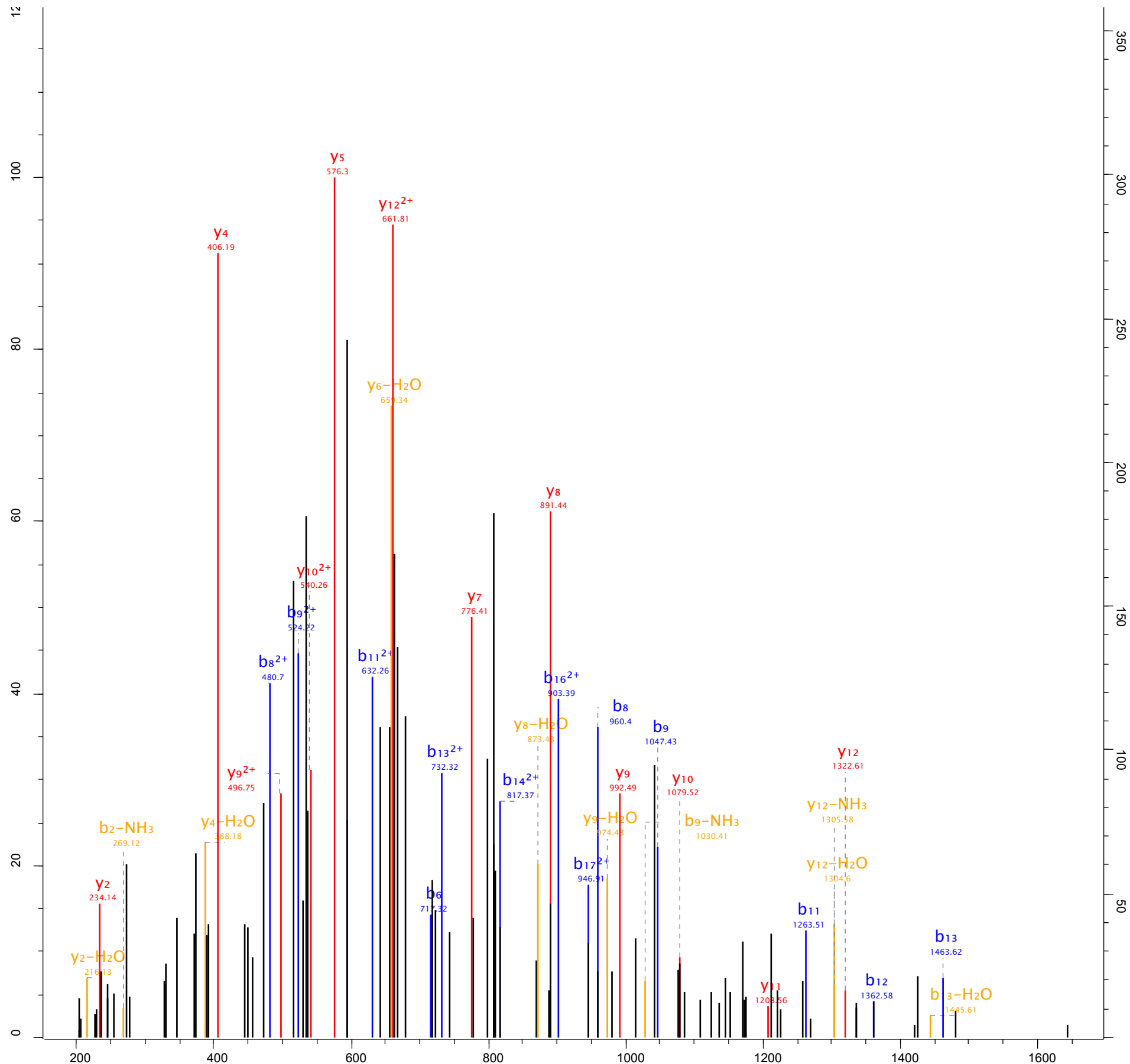
- L N E H F L N T T D F L D T I K S N L D R -

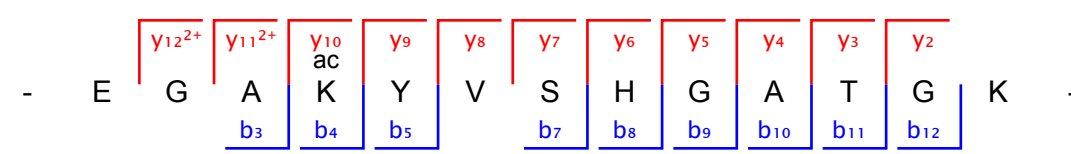
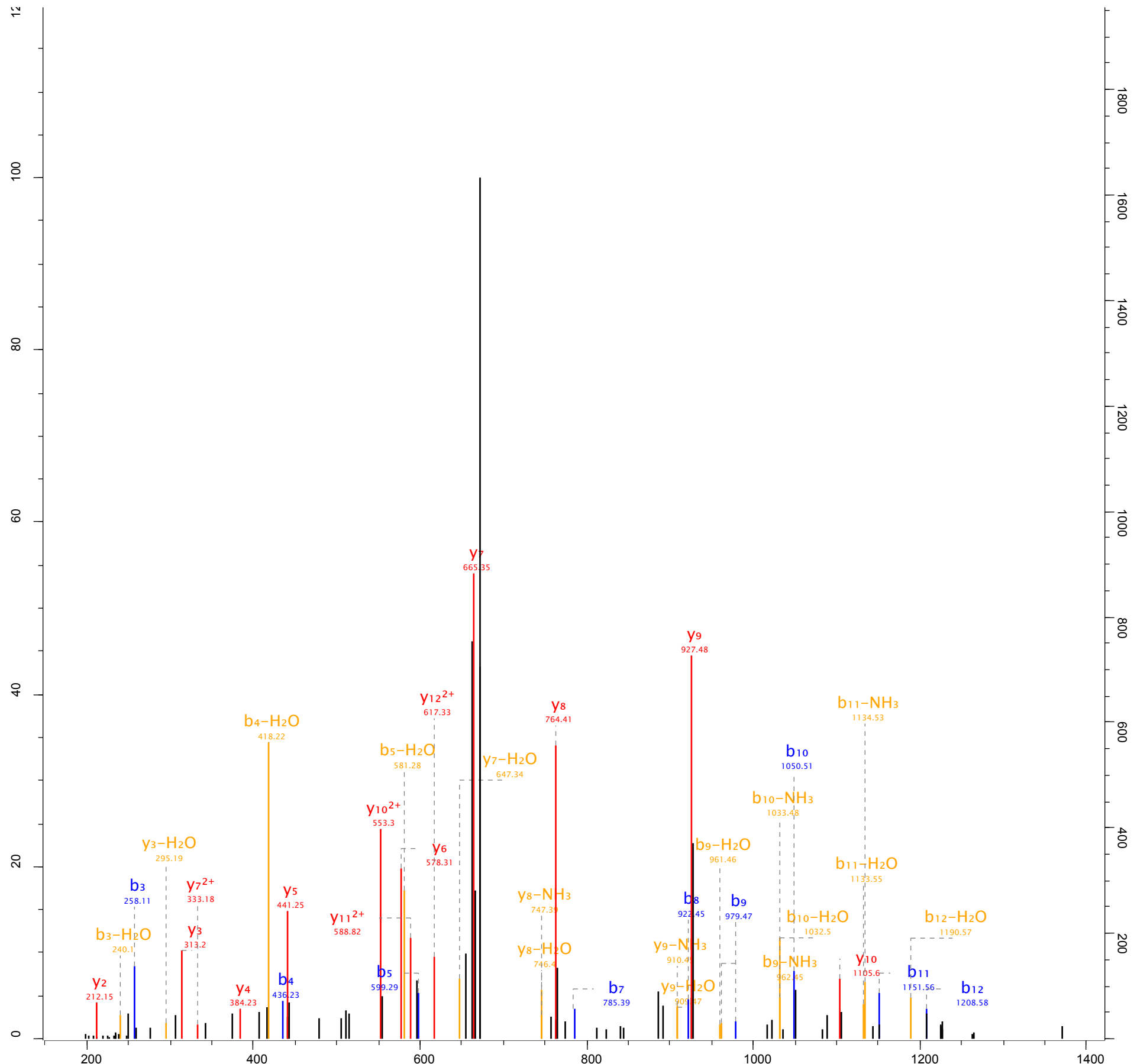
b₅ b₈ b₁₀ b₁₁ b₁₂ b₁₃ b₁₄ b₁₅ b₁₆²⁺ b₁₇²⁺ b₁₈²⁺ b₁₉²⁺ b₂₀²⁺

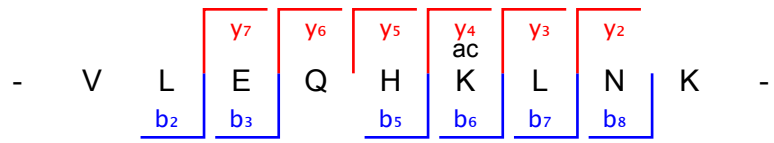
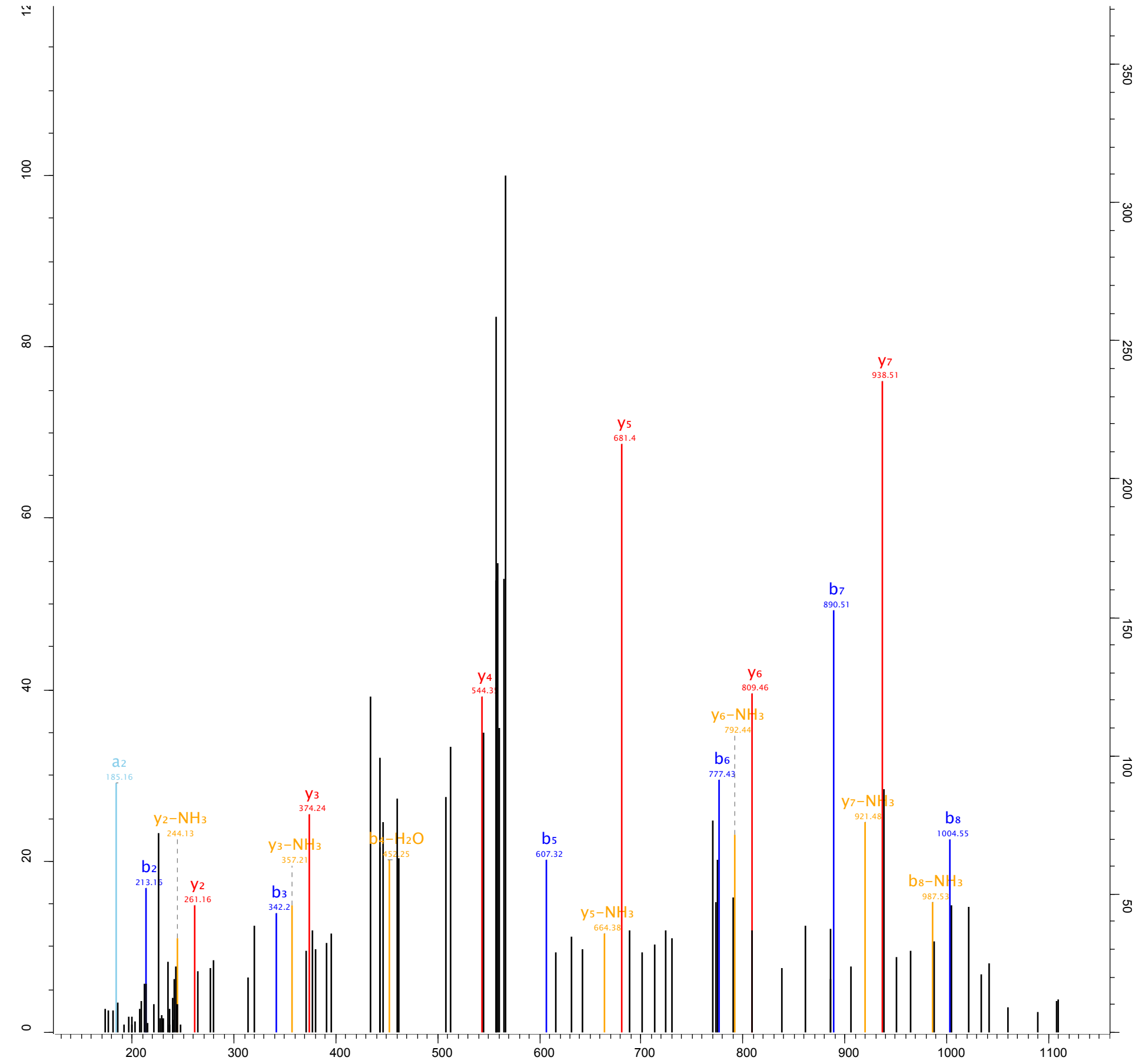
y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ ac y₅ y₄ y₃ y₂

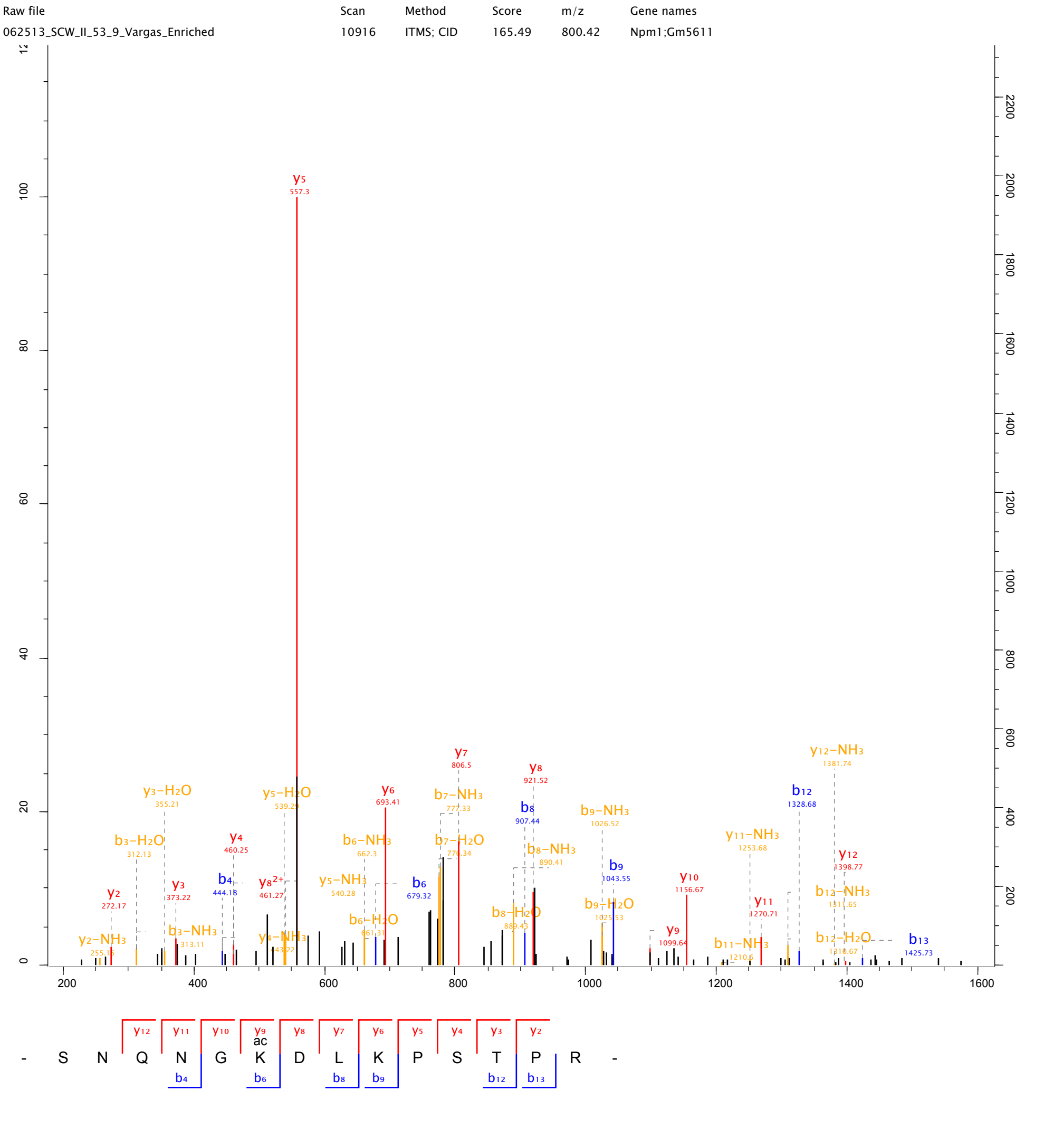


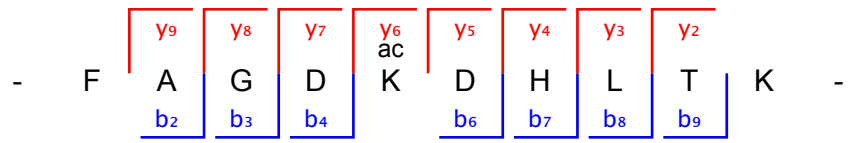
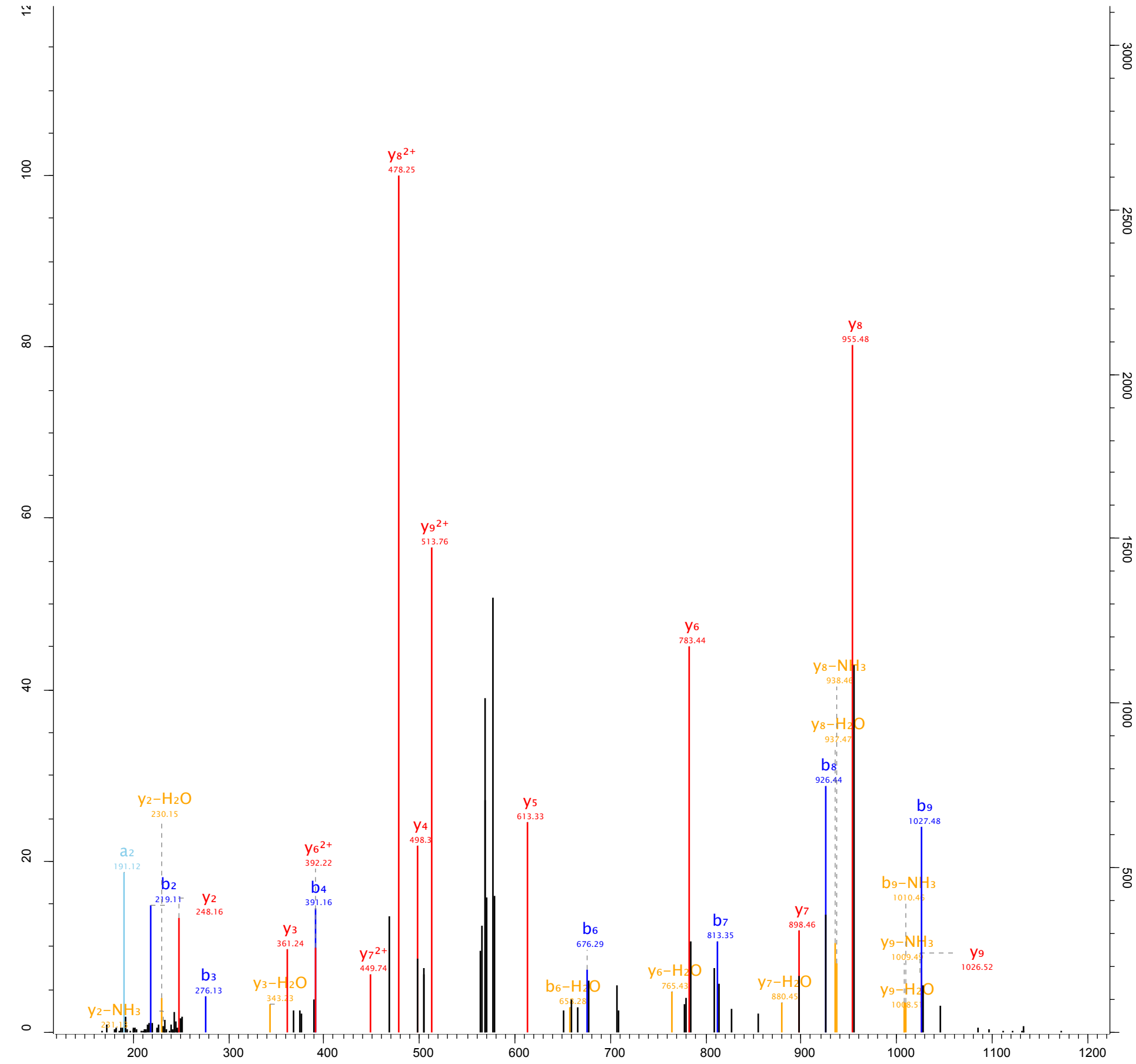


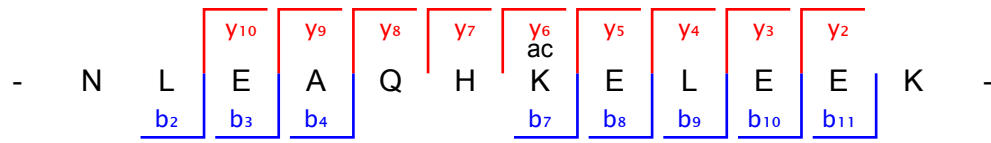
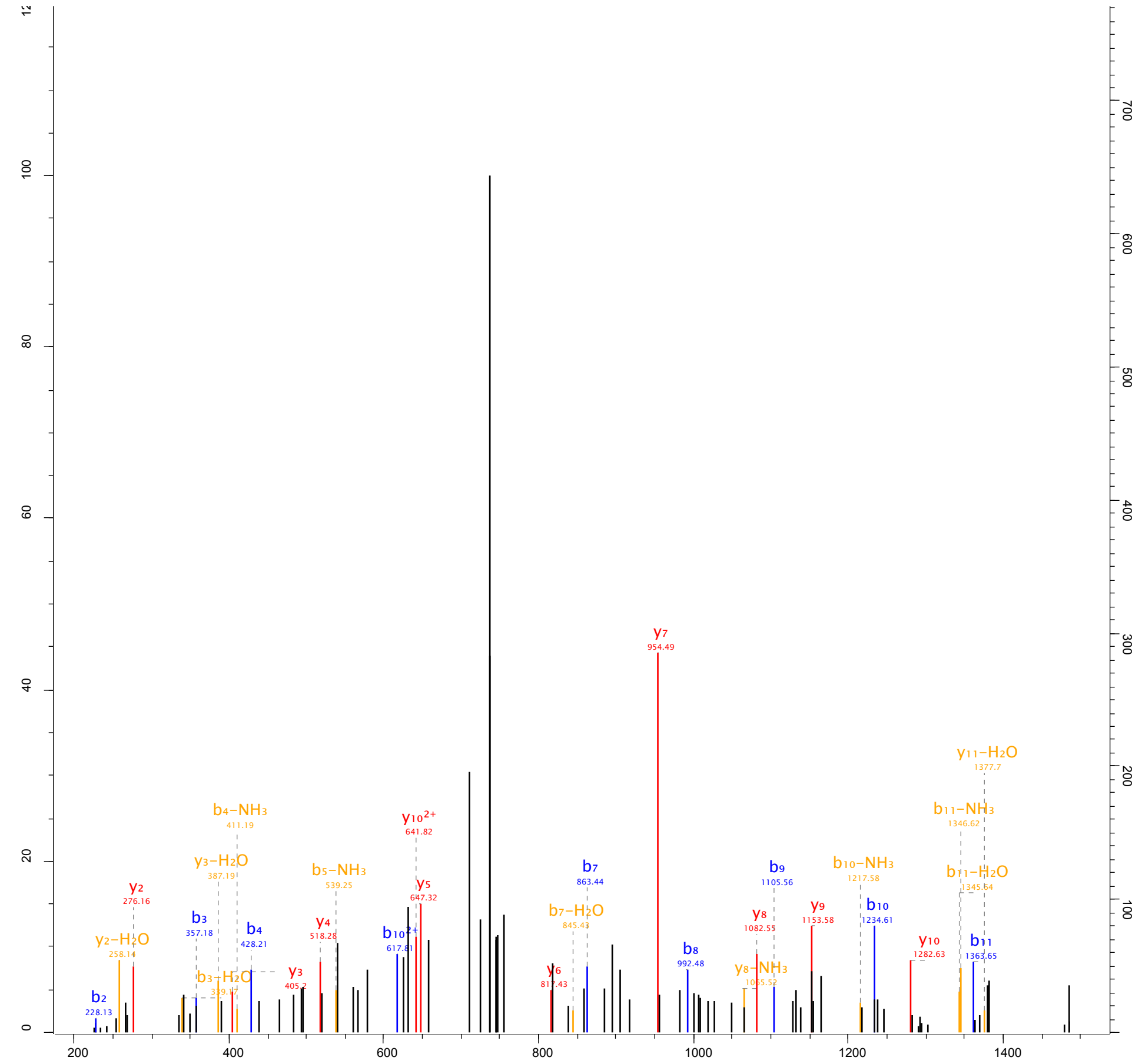




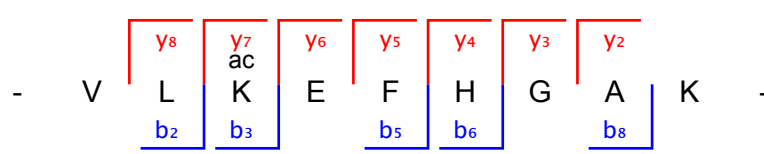
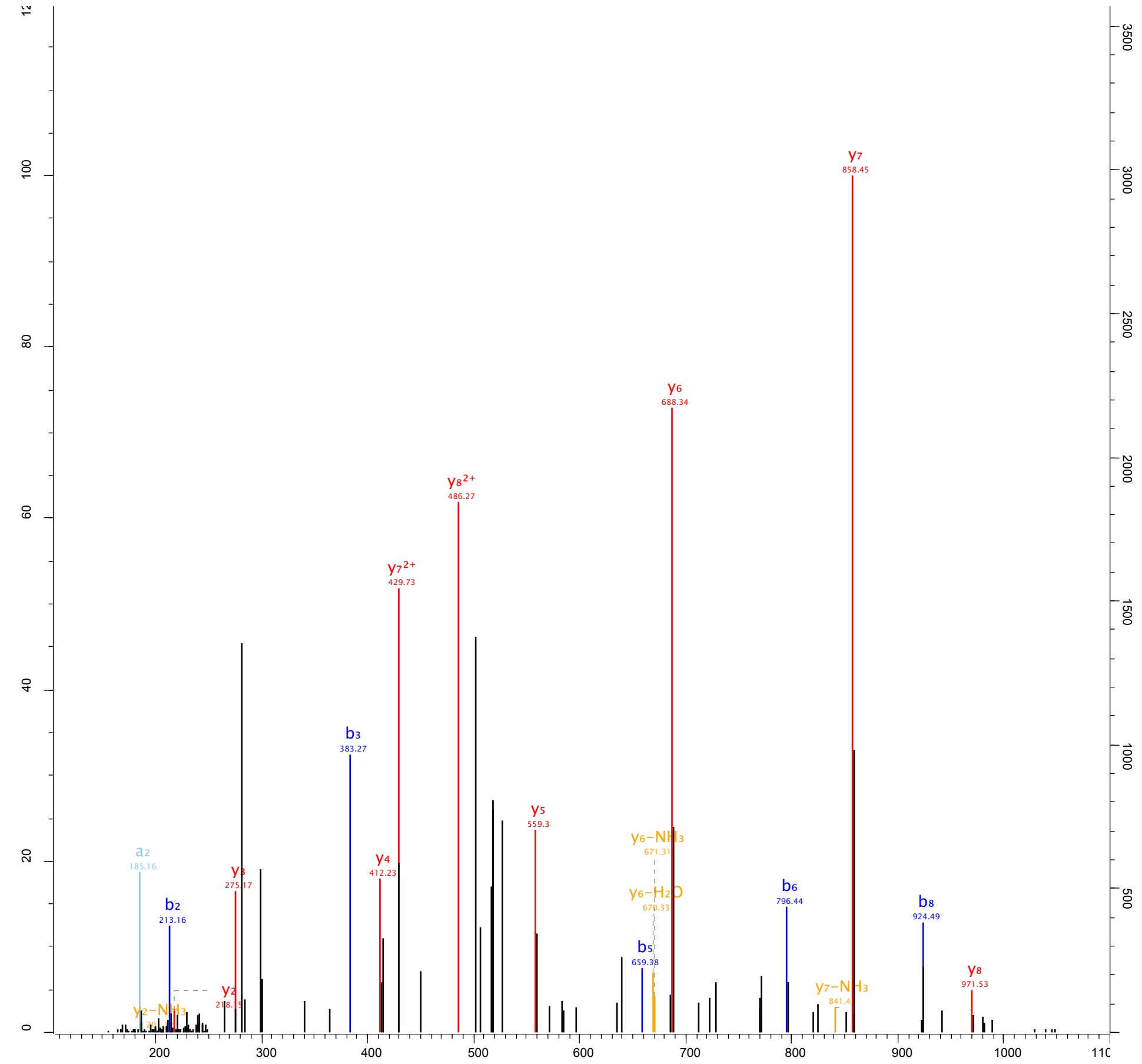








Raw file: 062513_SCW_II_53_9_Vargas_Enriched
 Scan: 12528 Method: ITMS; CID Score: 103.26 m/z: 535.8 Gene names: D10Jhu81e



062513_SCW_II_53_9_Vargas_Enriched

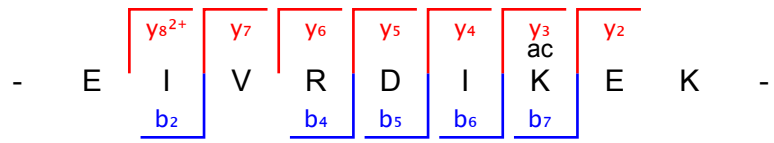
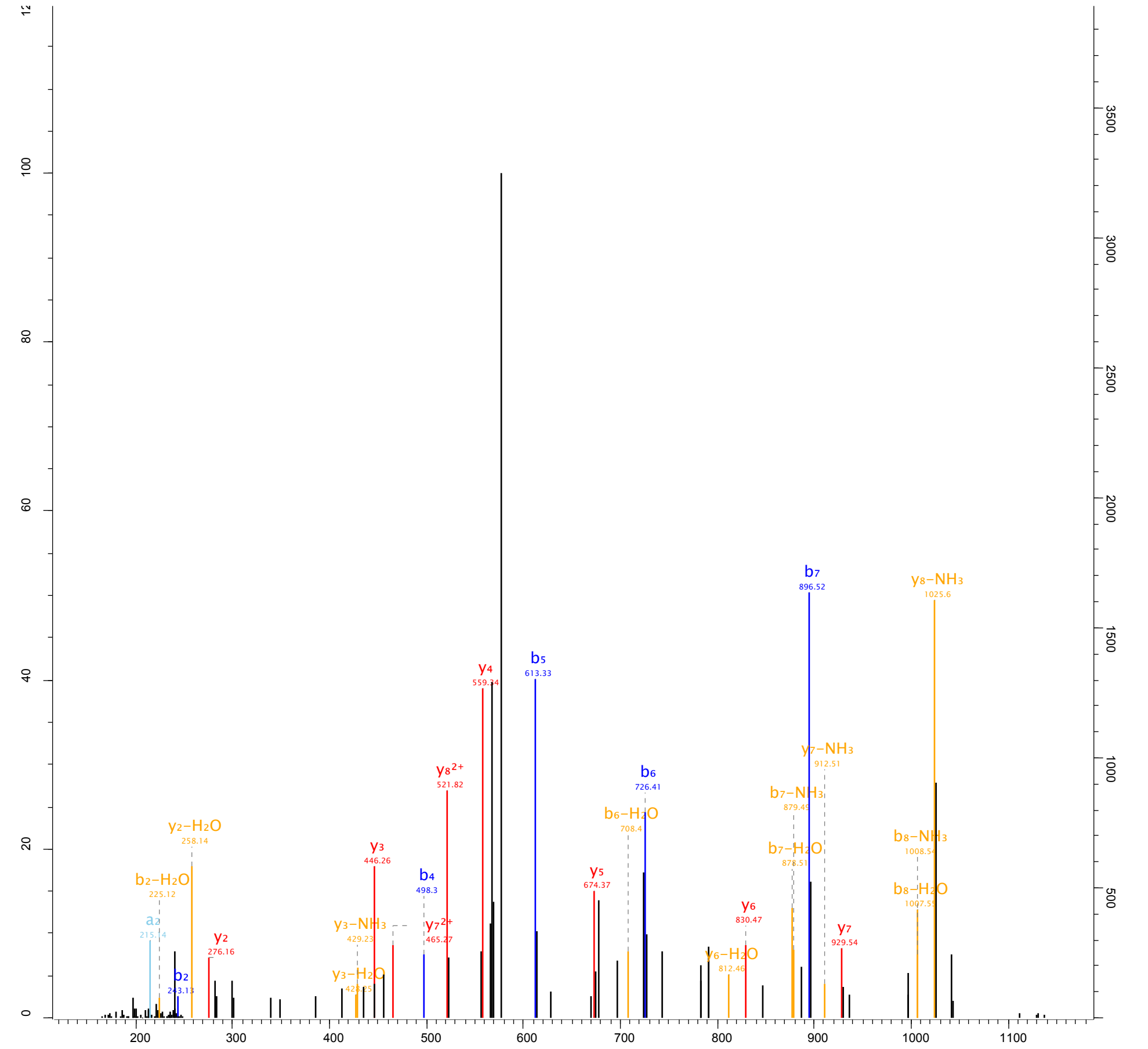
12760

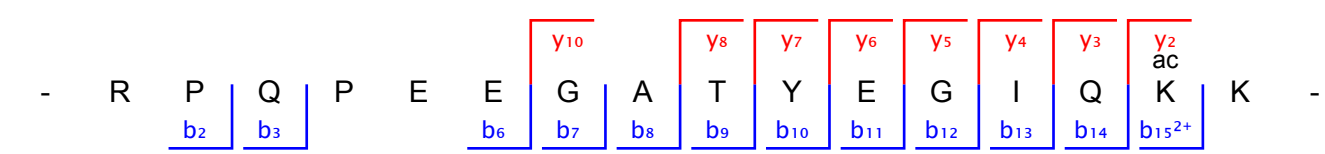
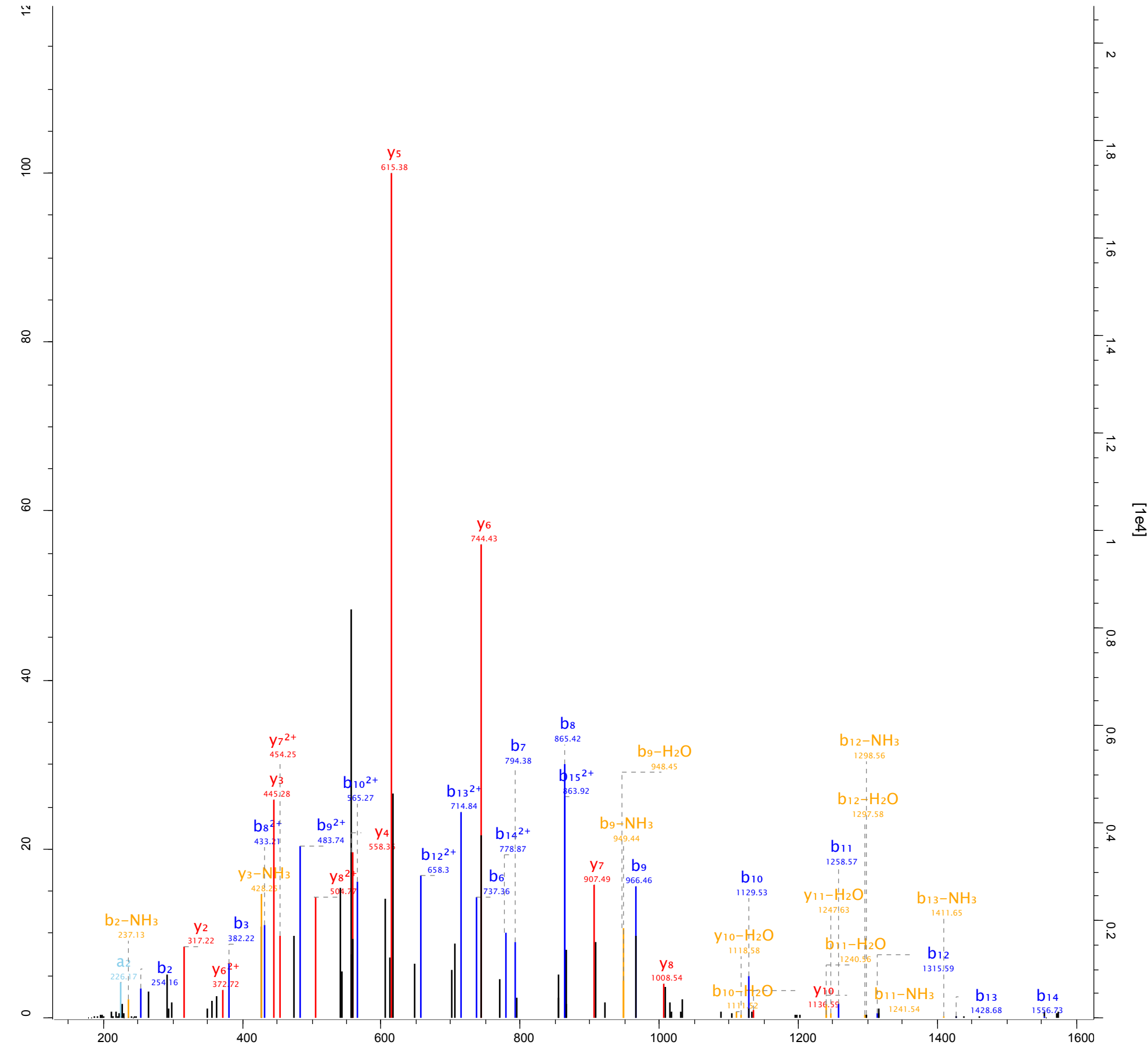
ITMS; CID

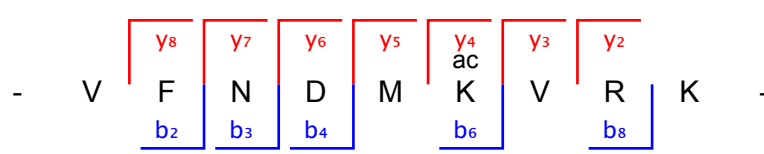
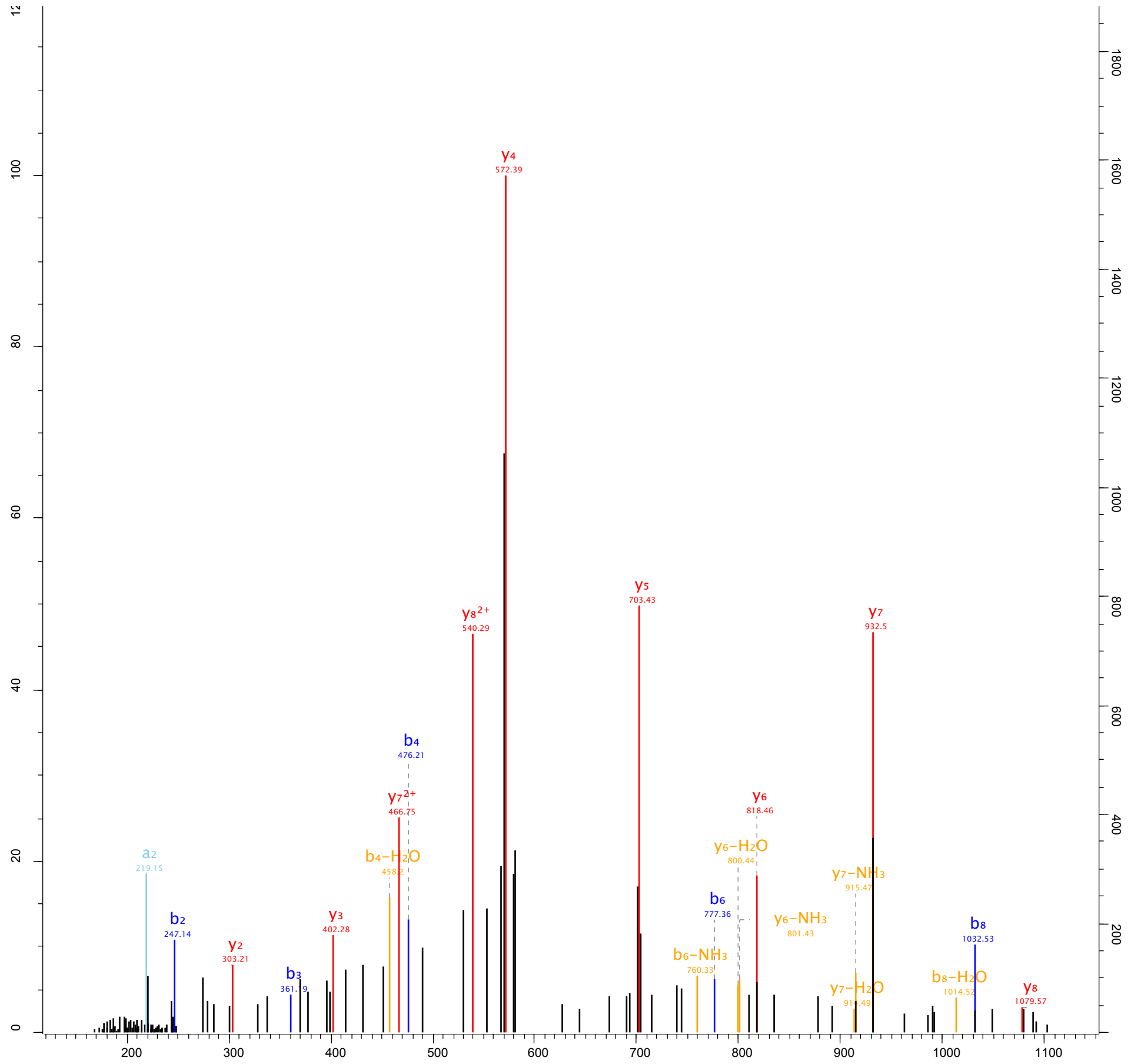
163.66

586.34

Actb;Actg1;Actc1;Acta1;Acta2;Actg2







062513_SCW_II_53_9_Vargas_Enriched

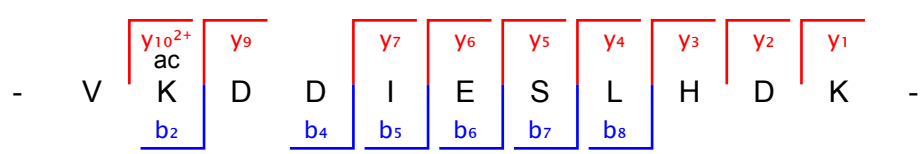
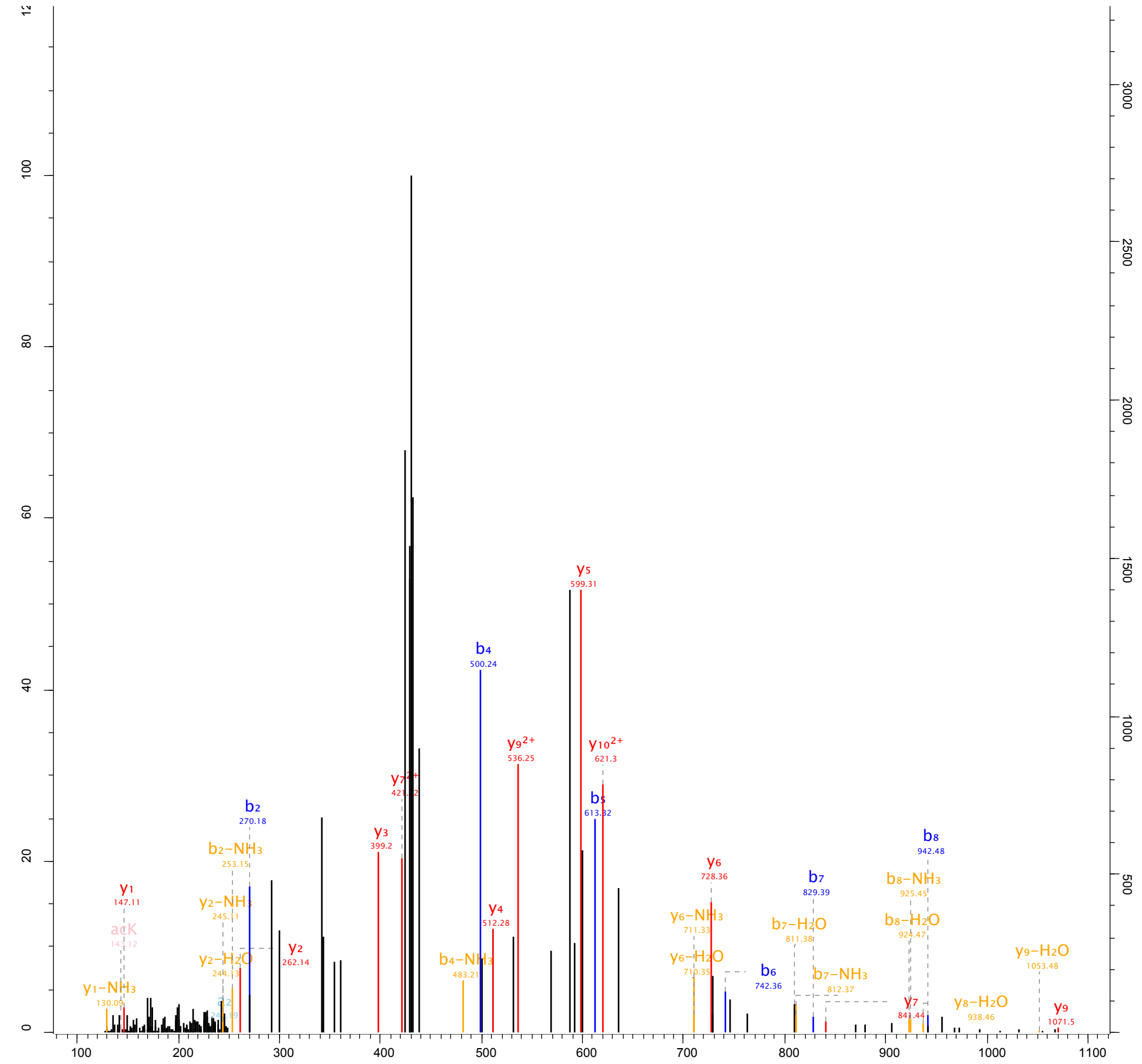
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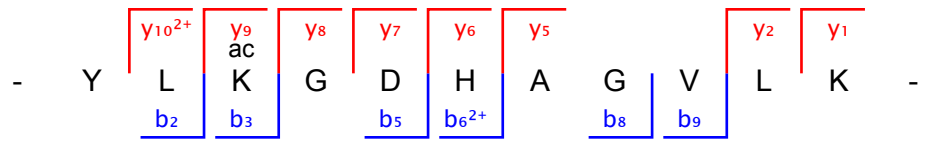
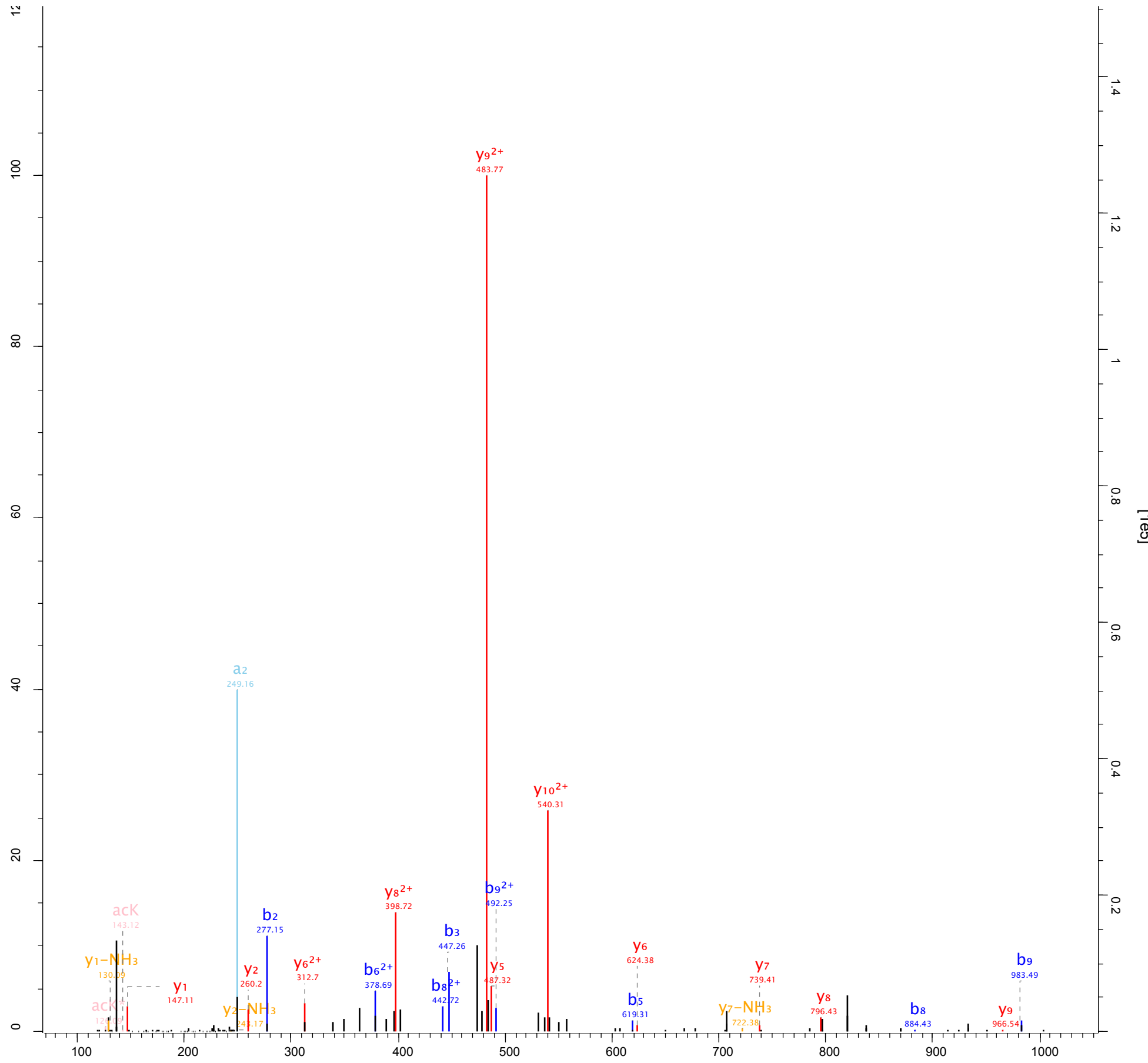
ITMS; CID

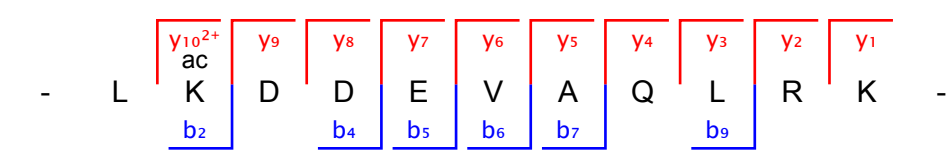
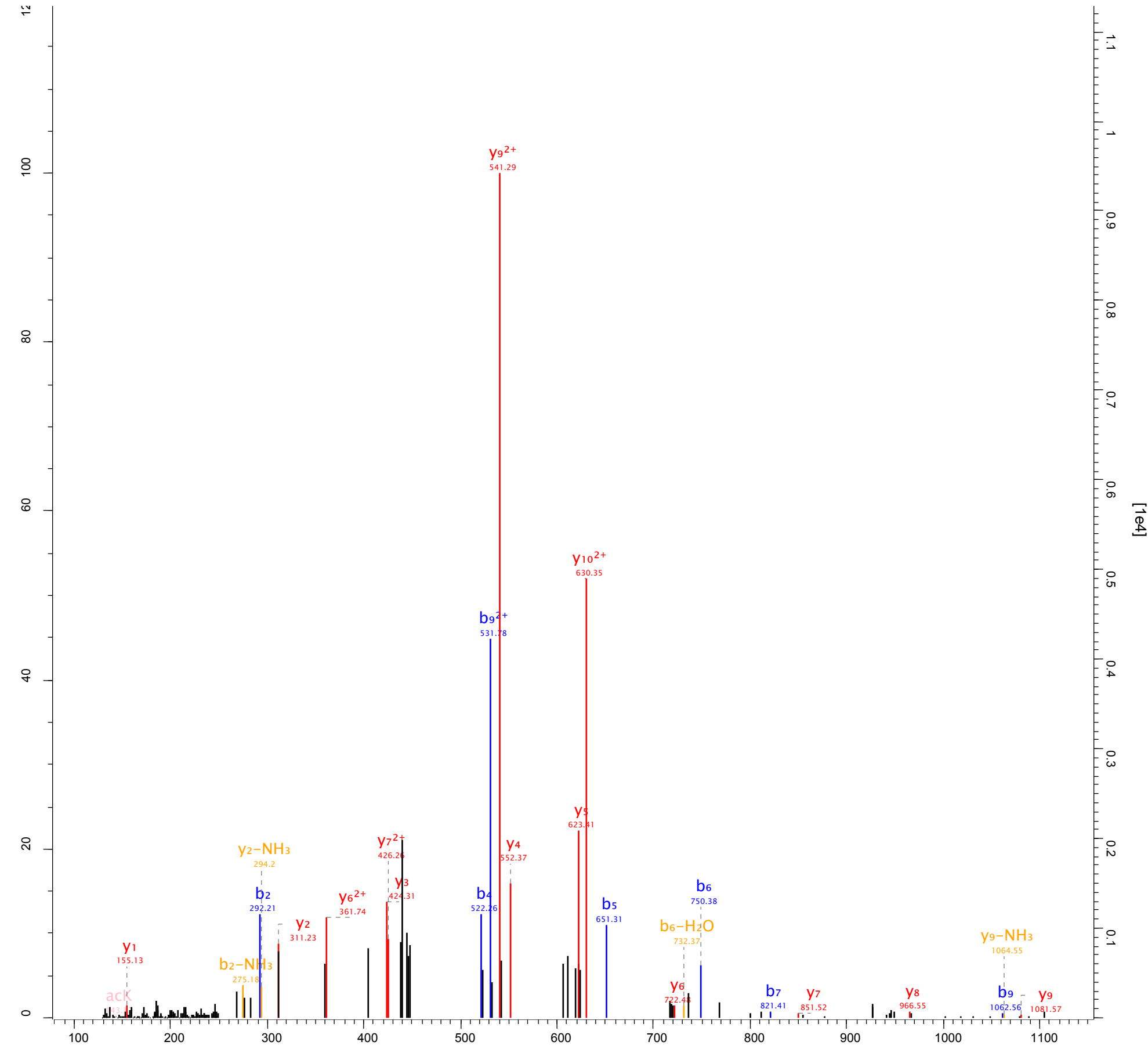
132.86

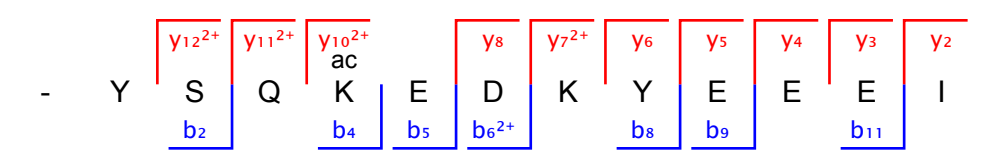
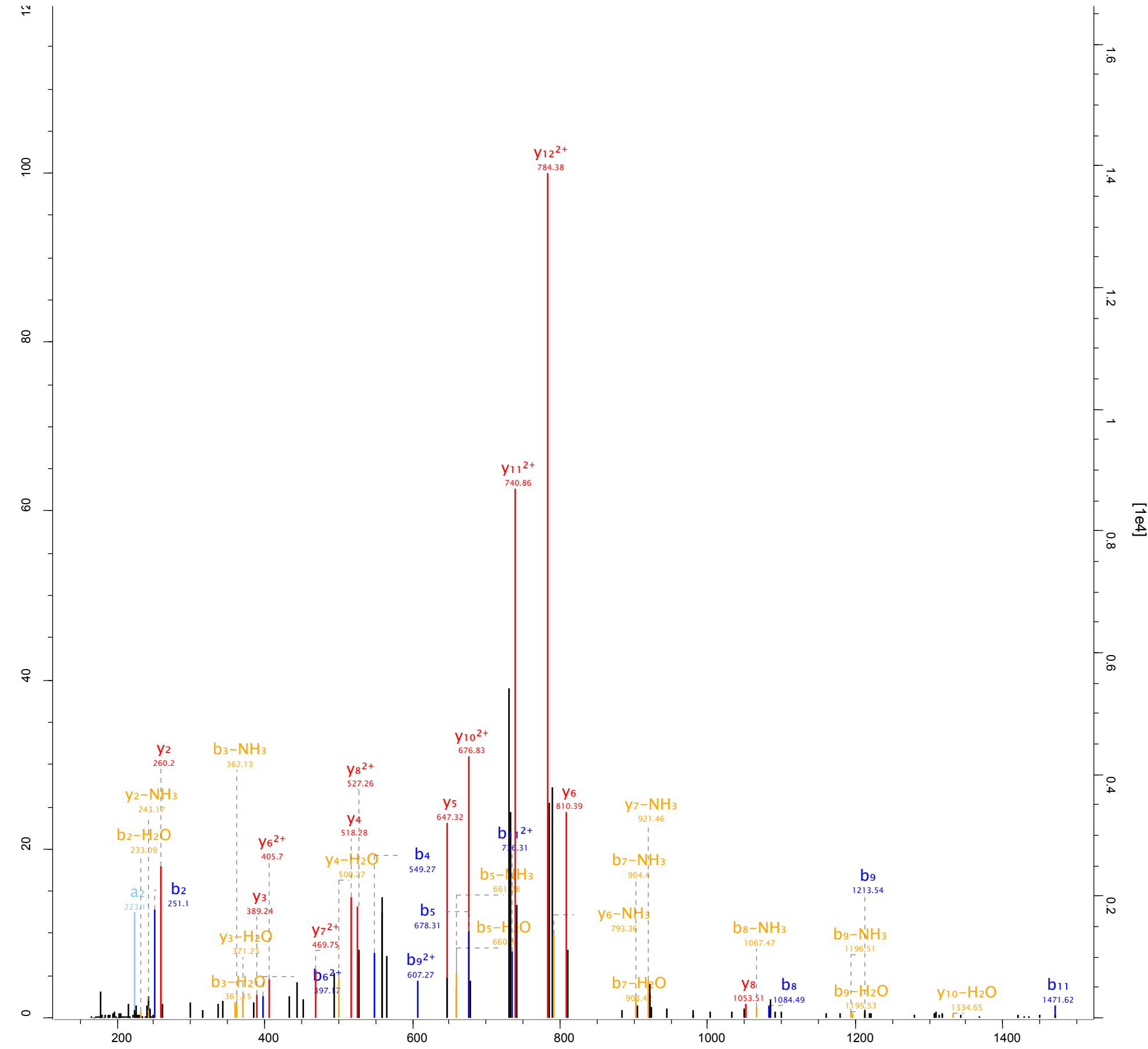
447.9

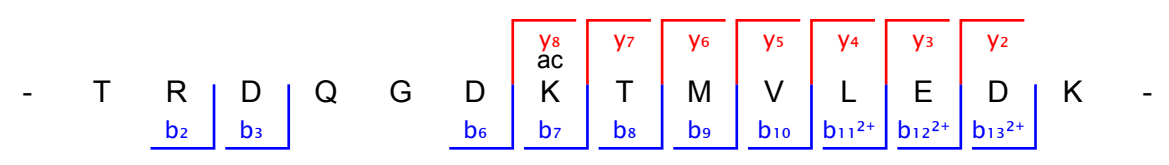
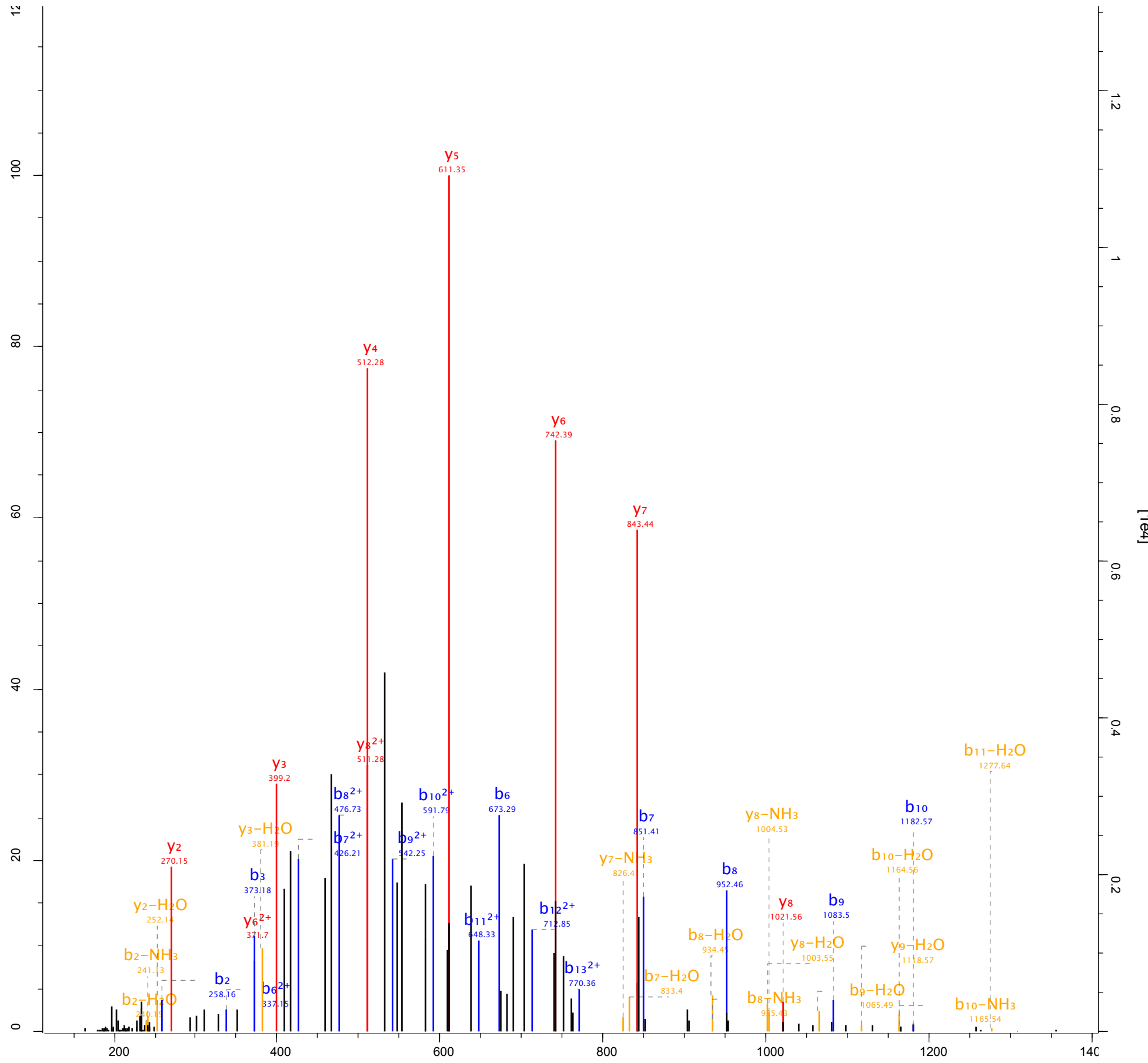
Dync1h1

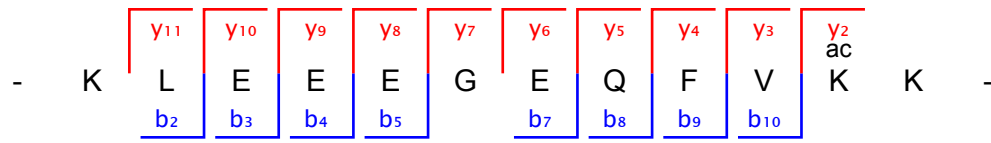
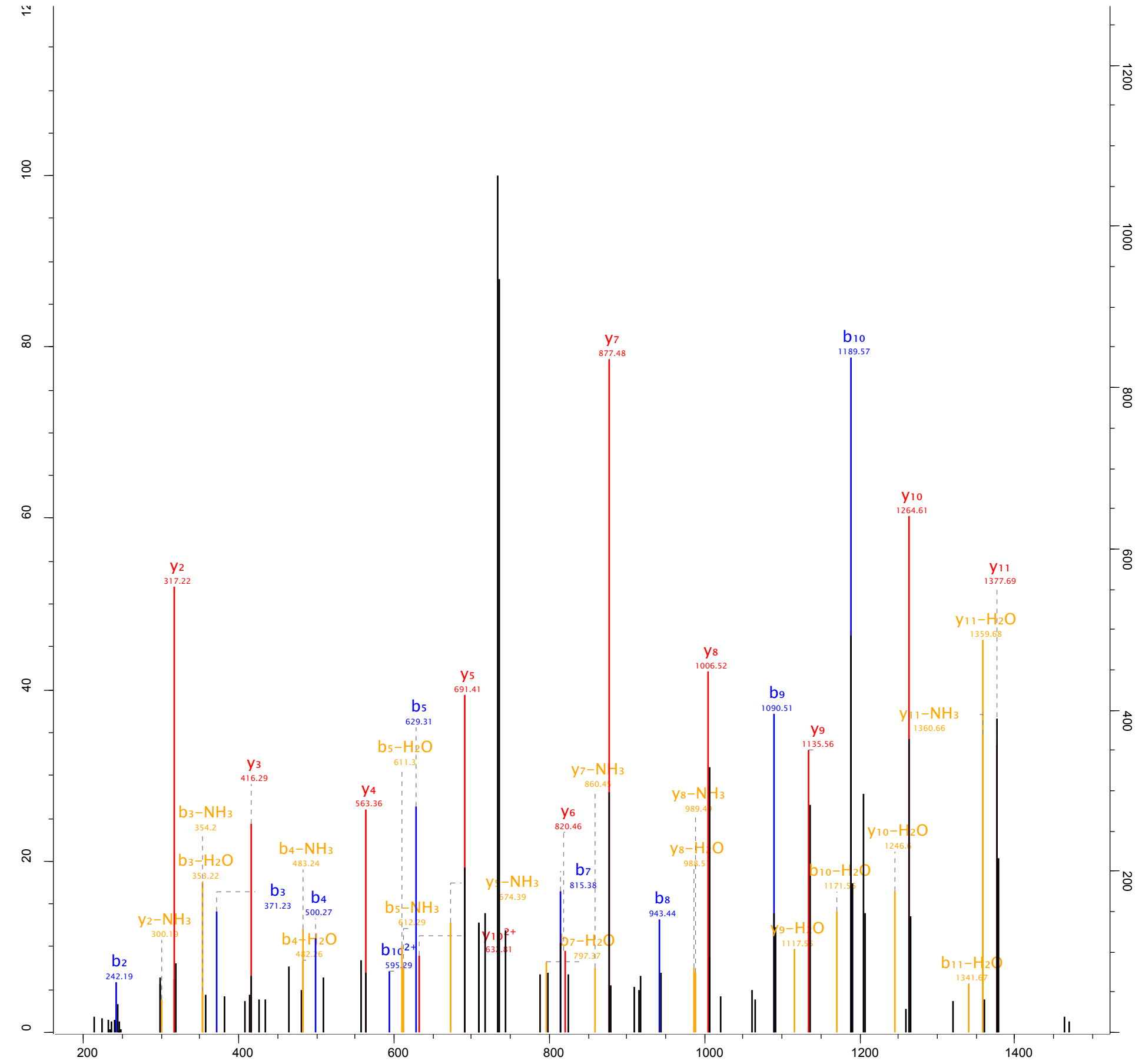


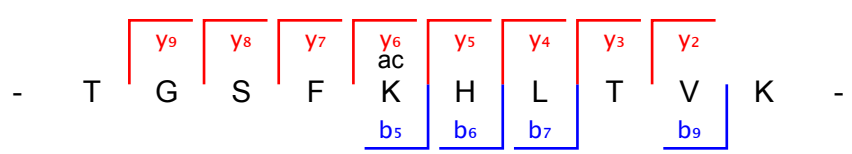
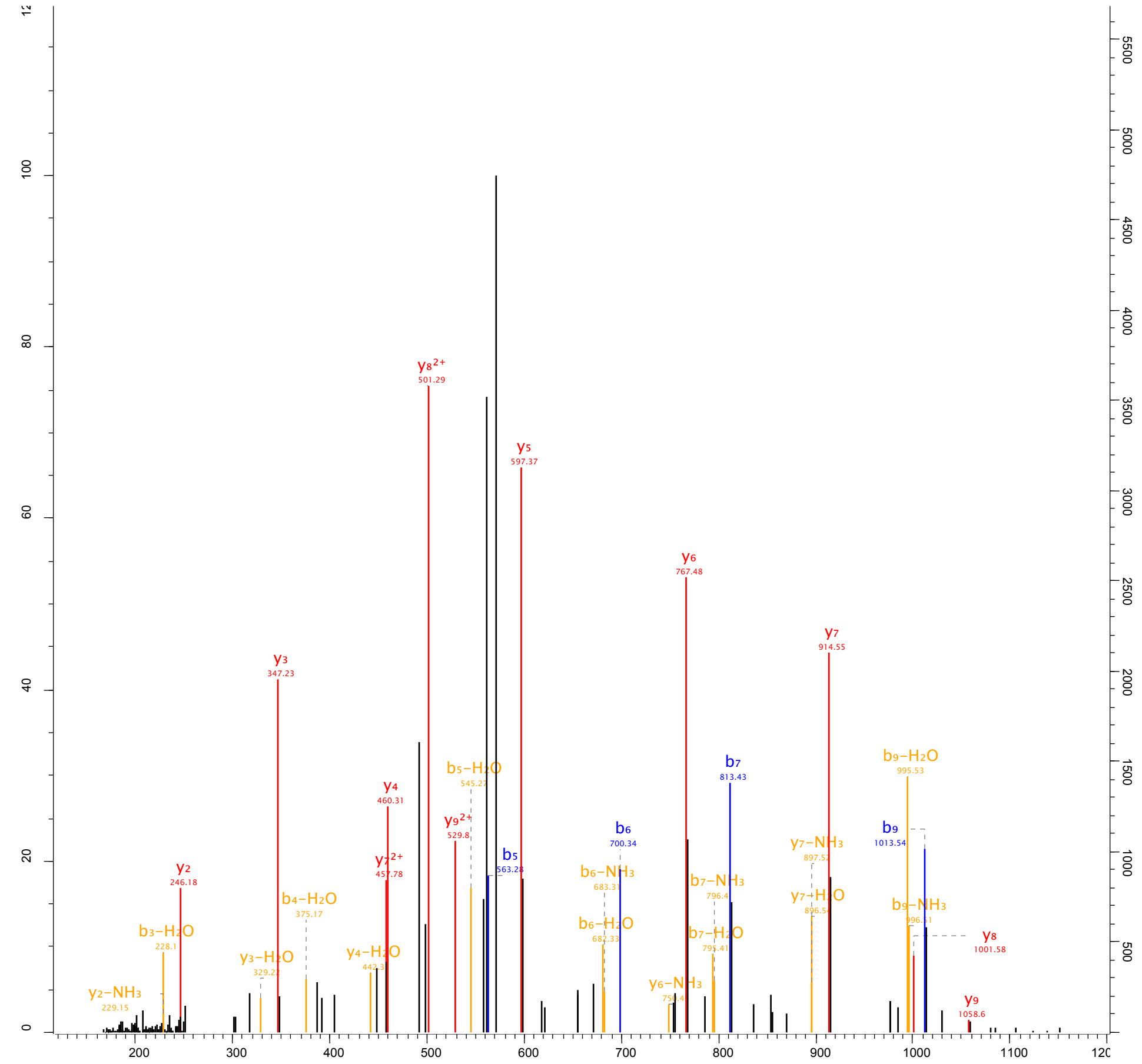


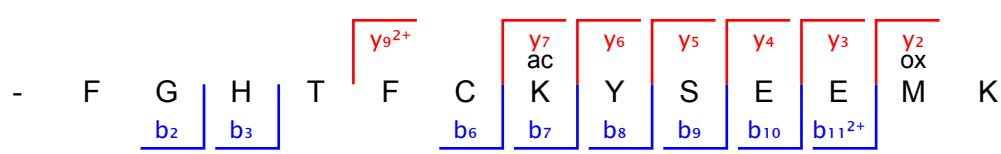
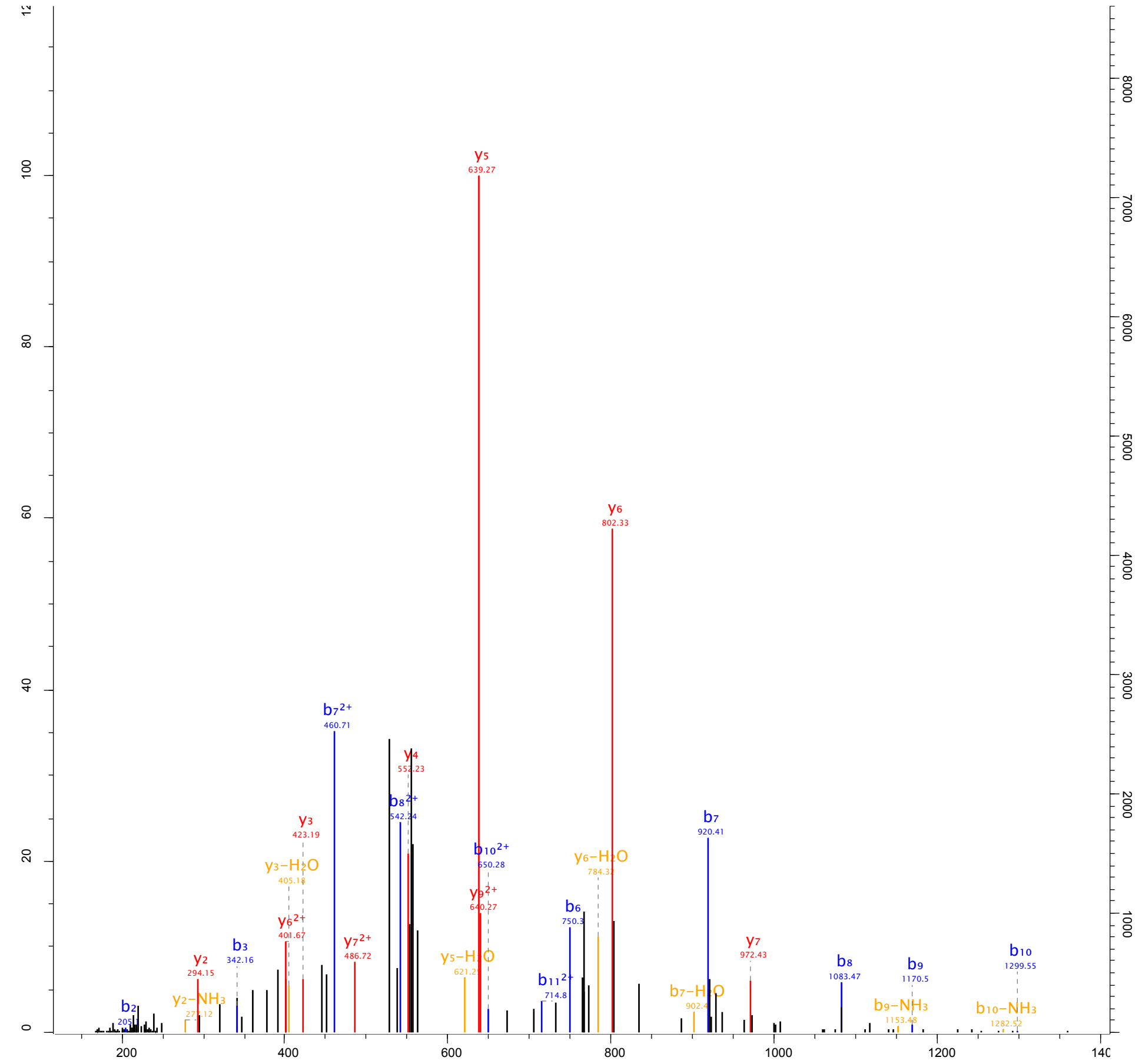


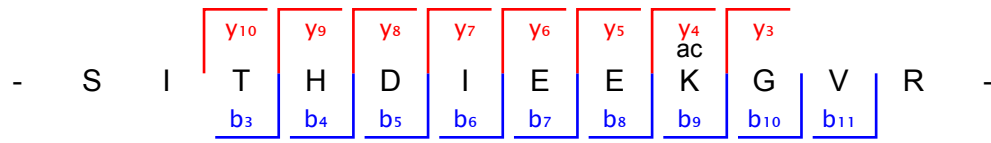
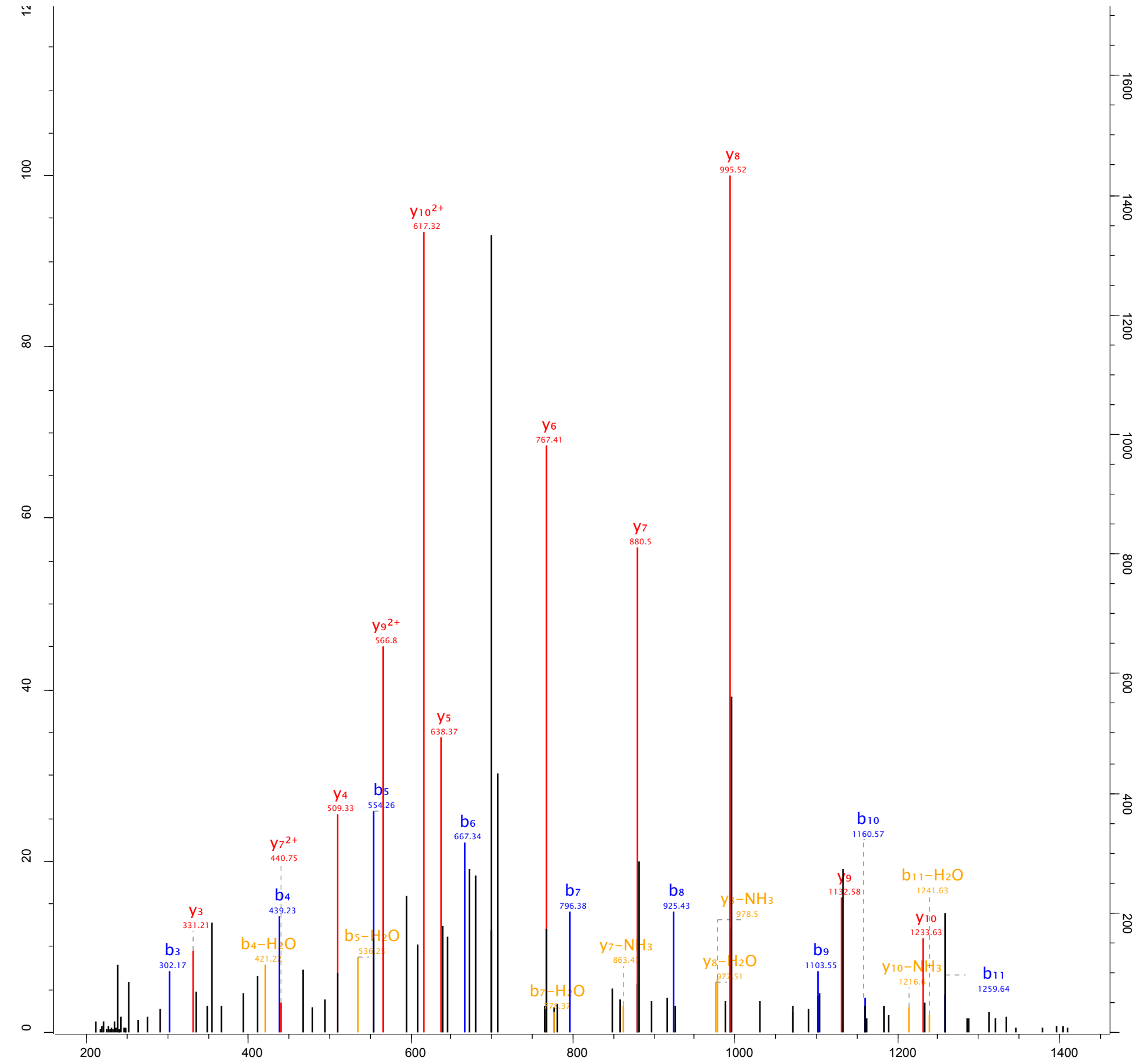


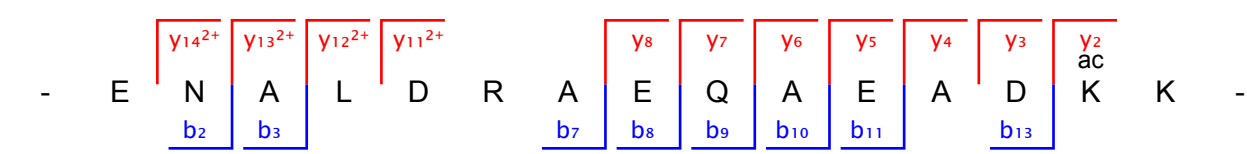
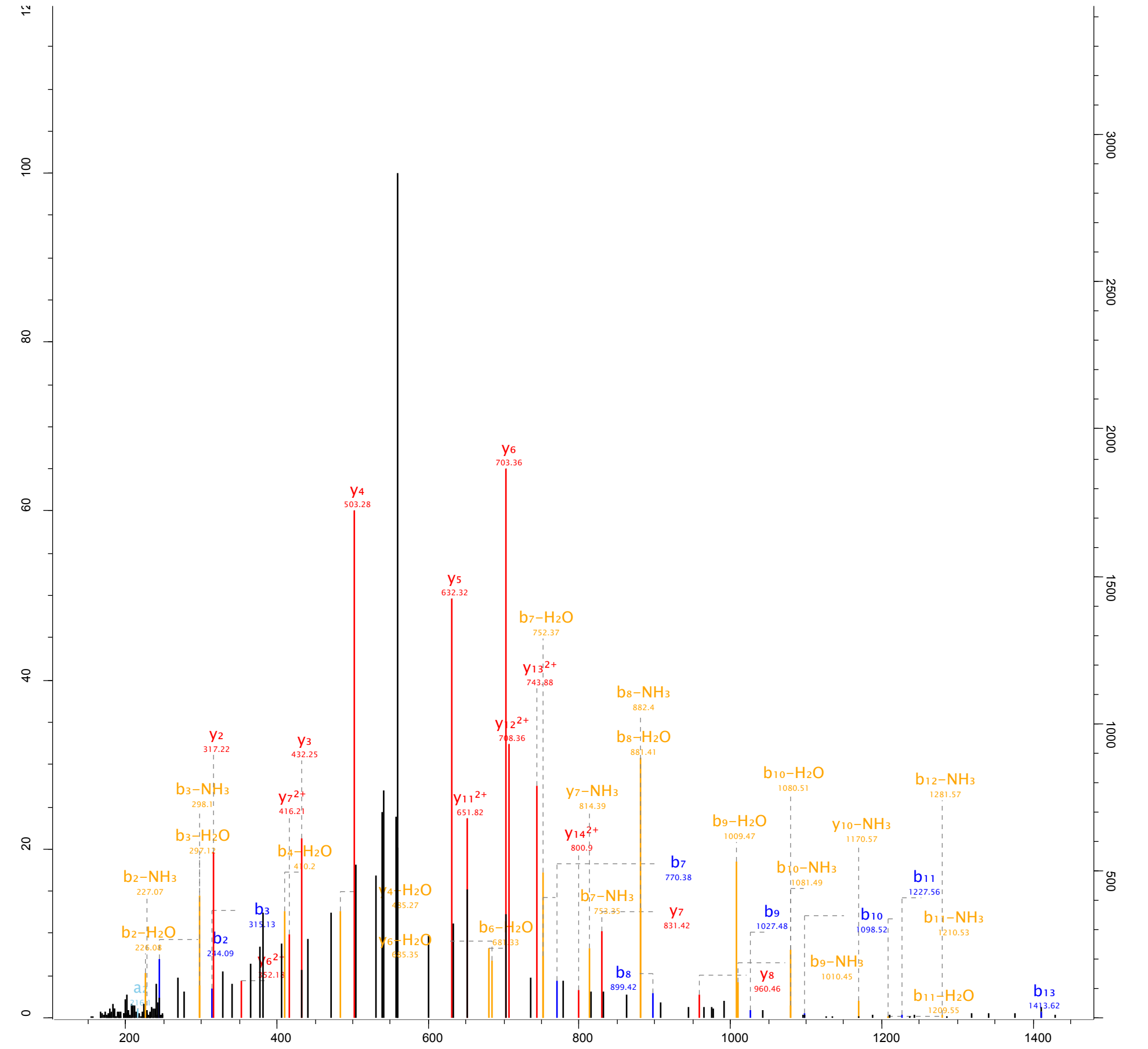


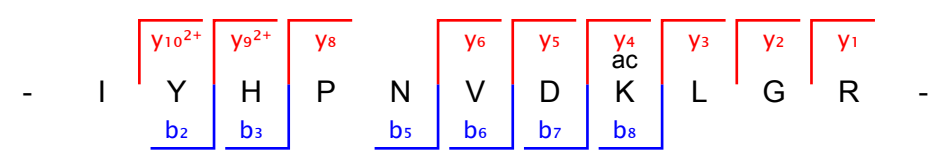
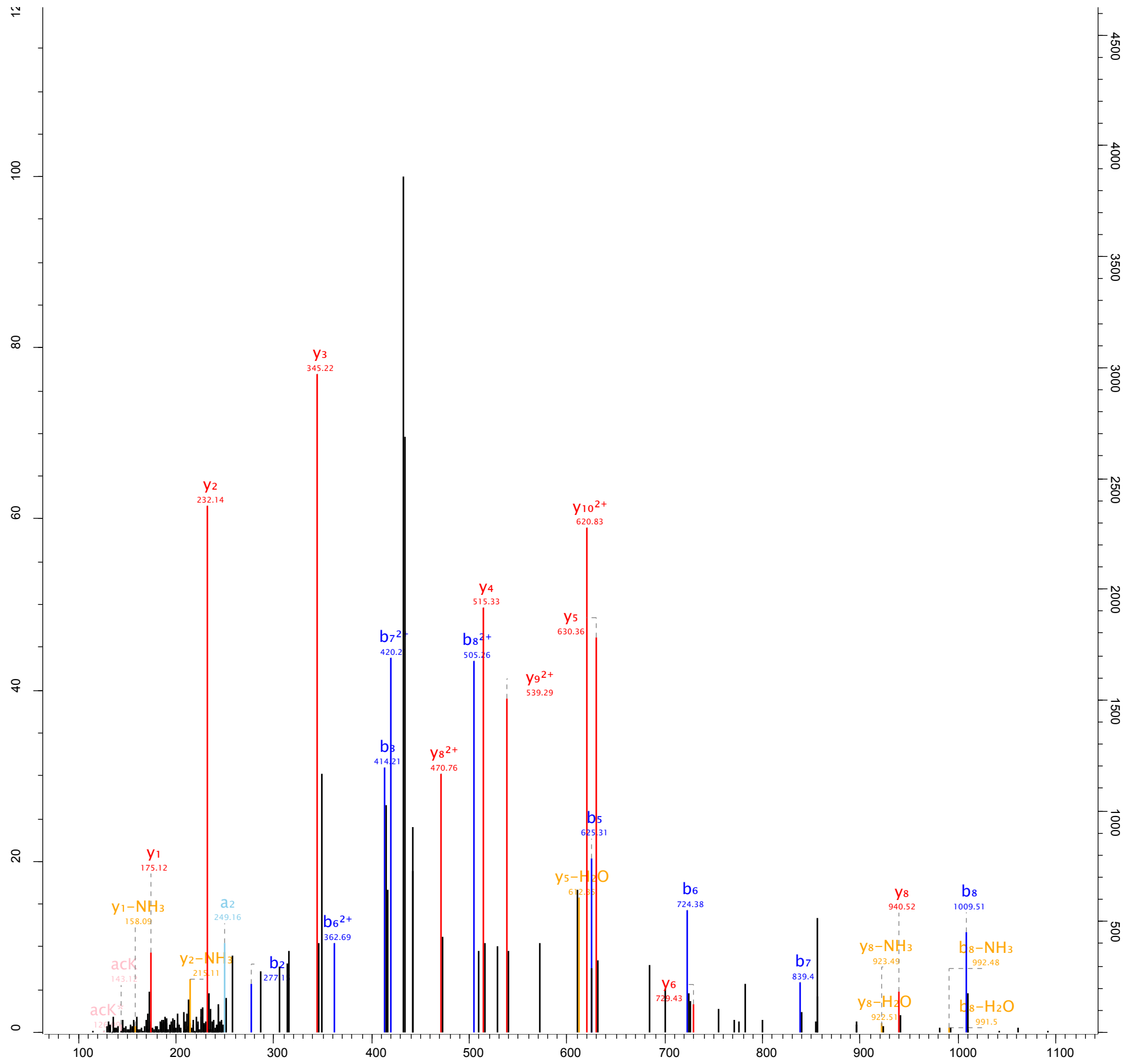


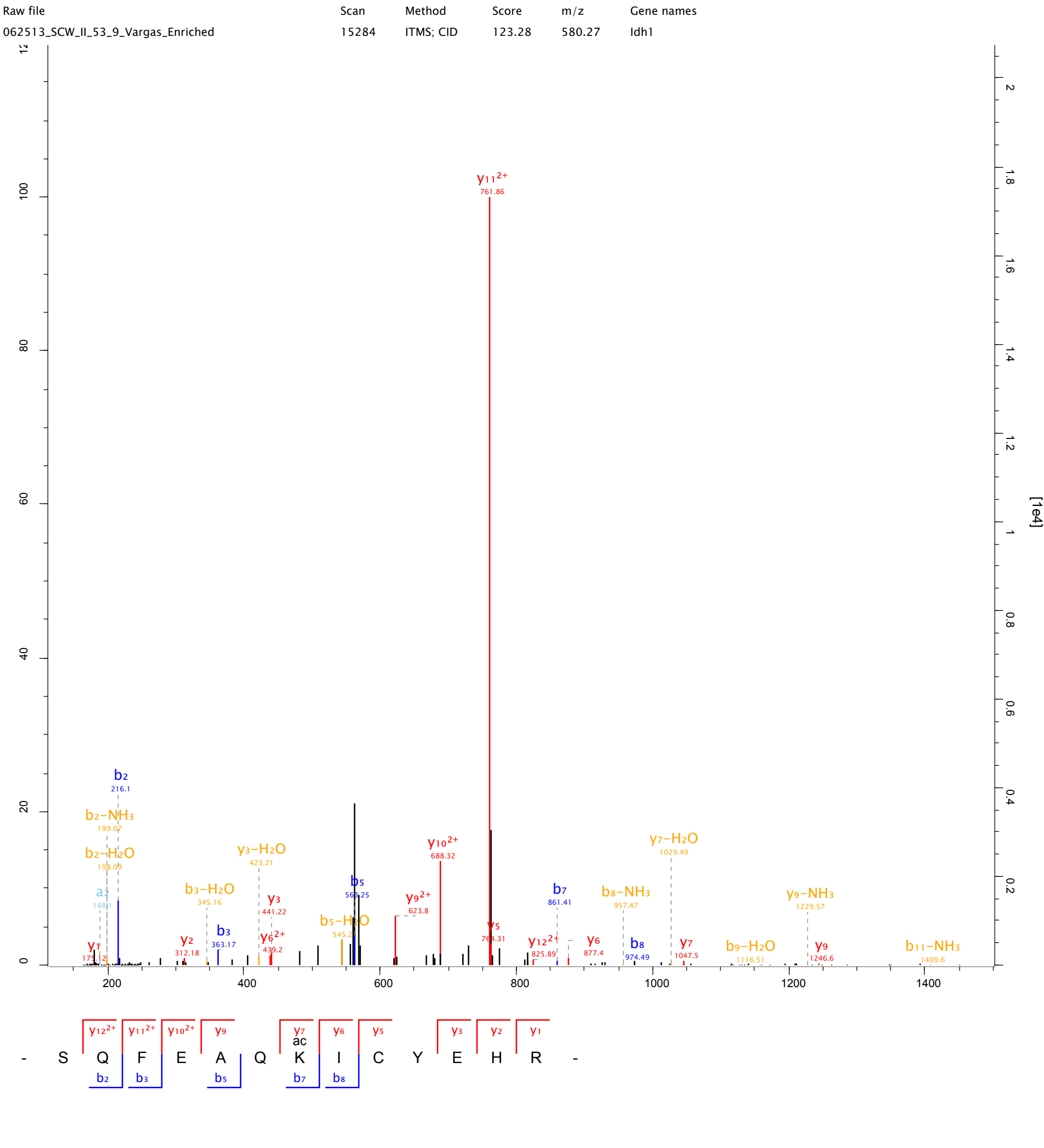


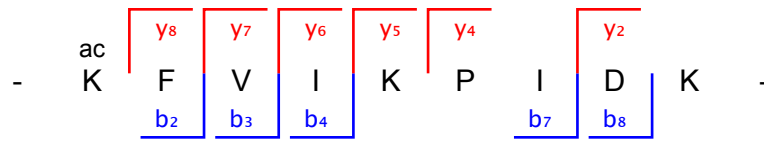
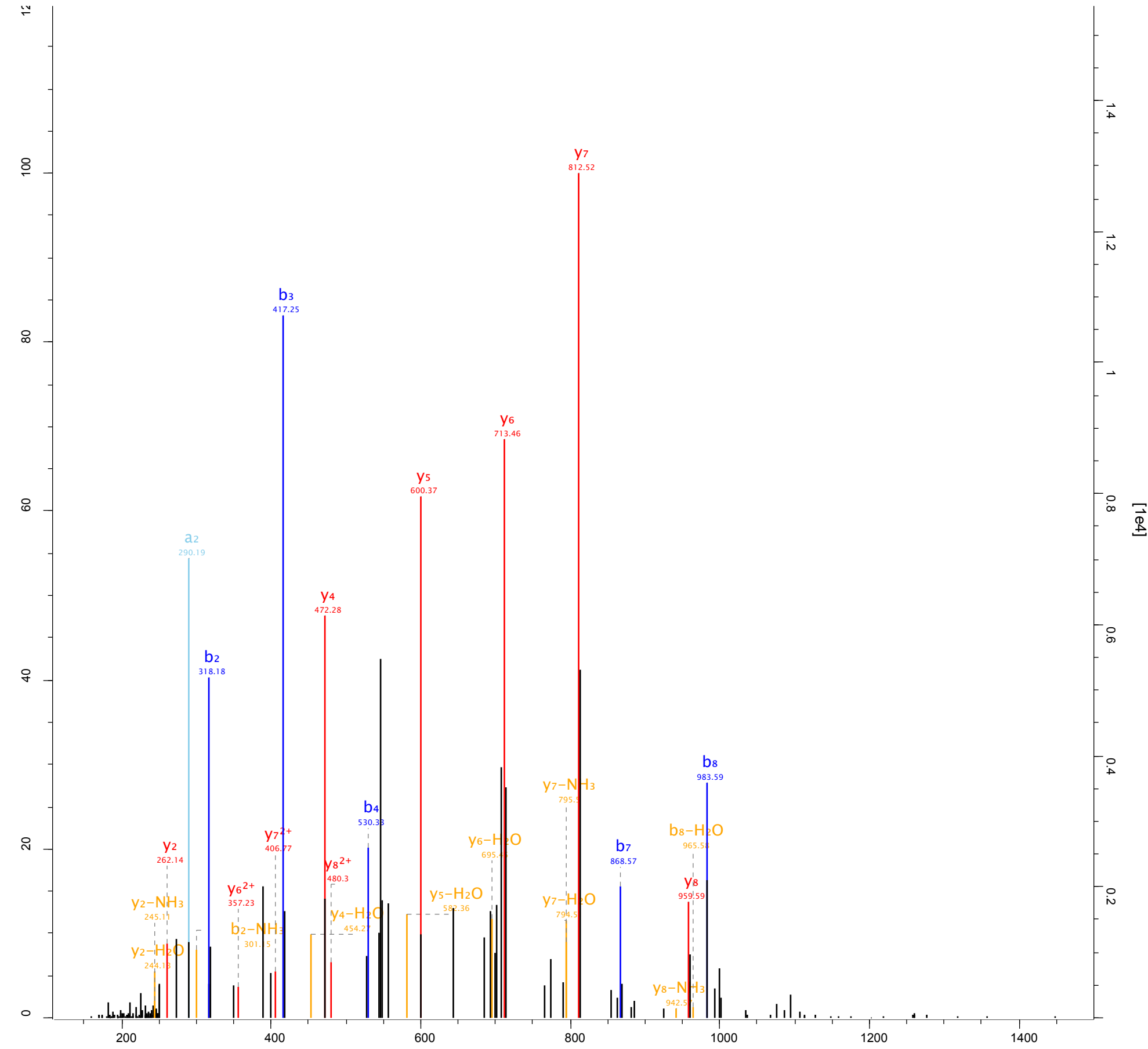


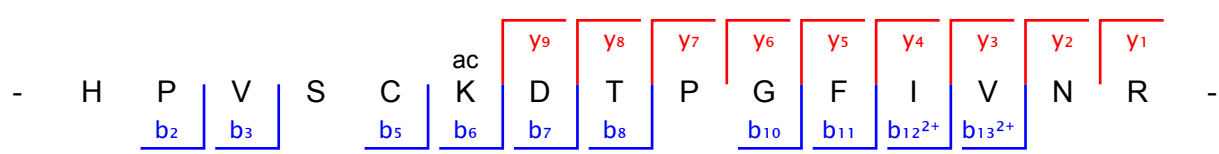
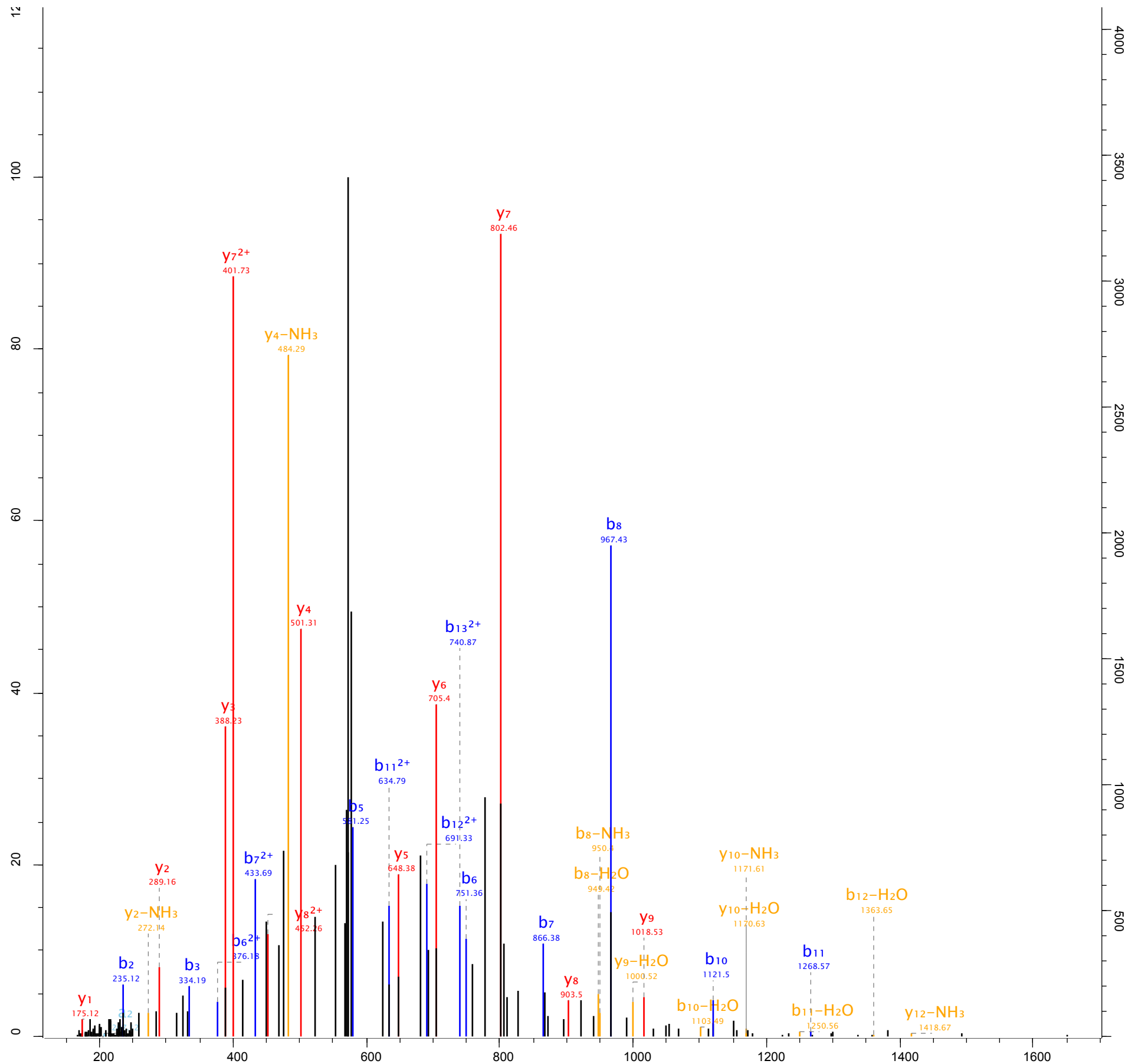




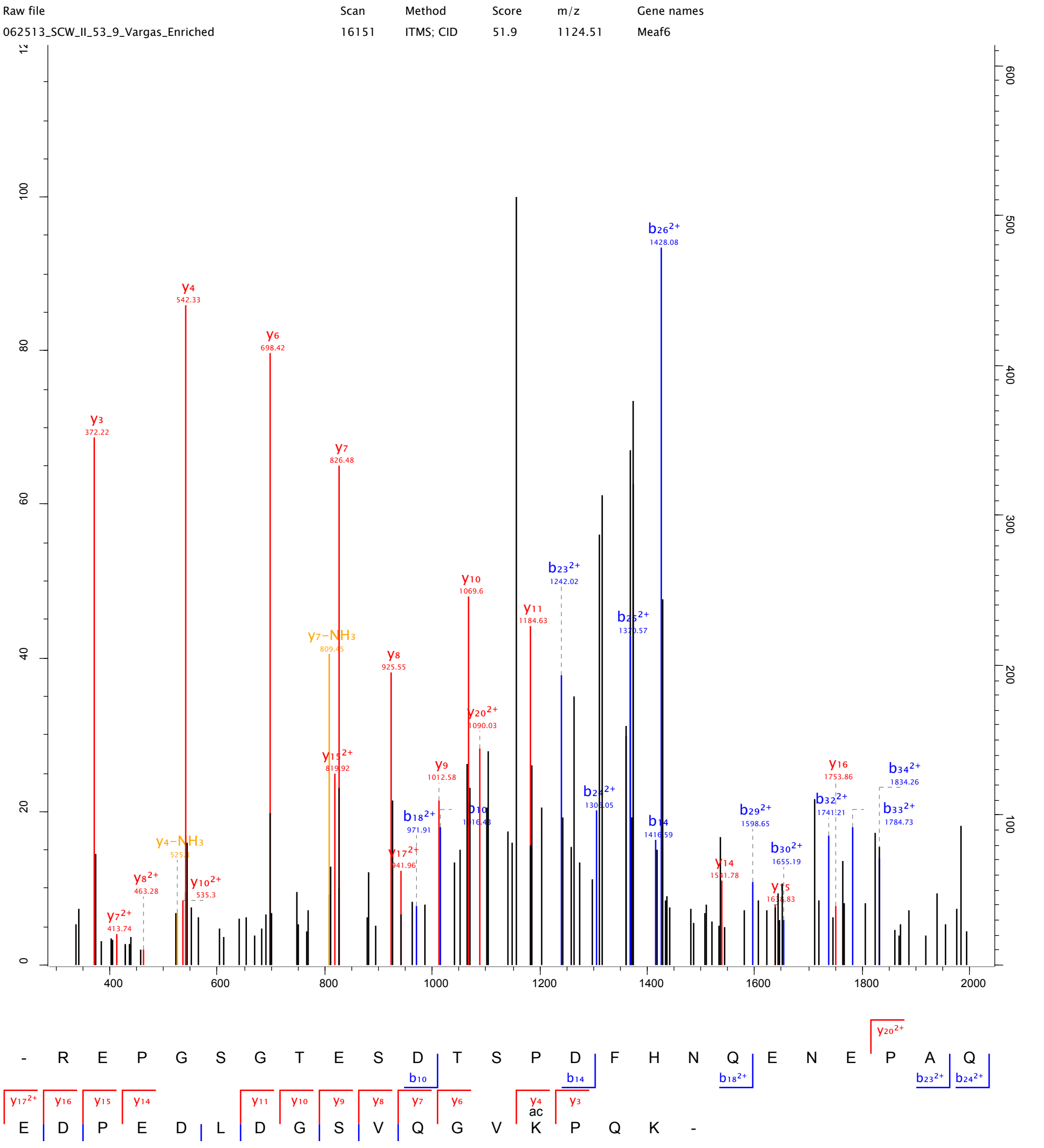


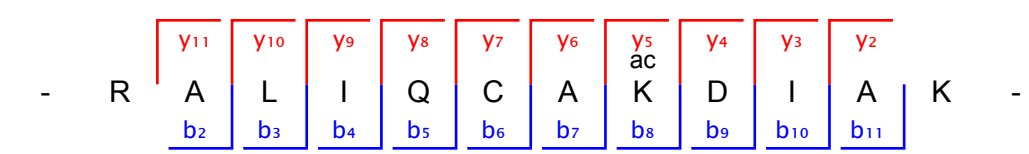
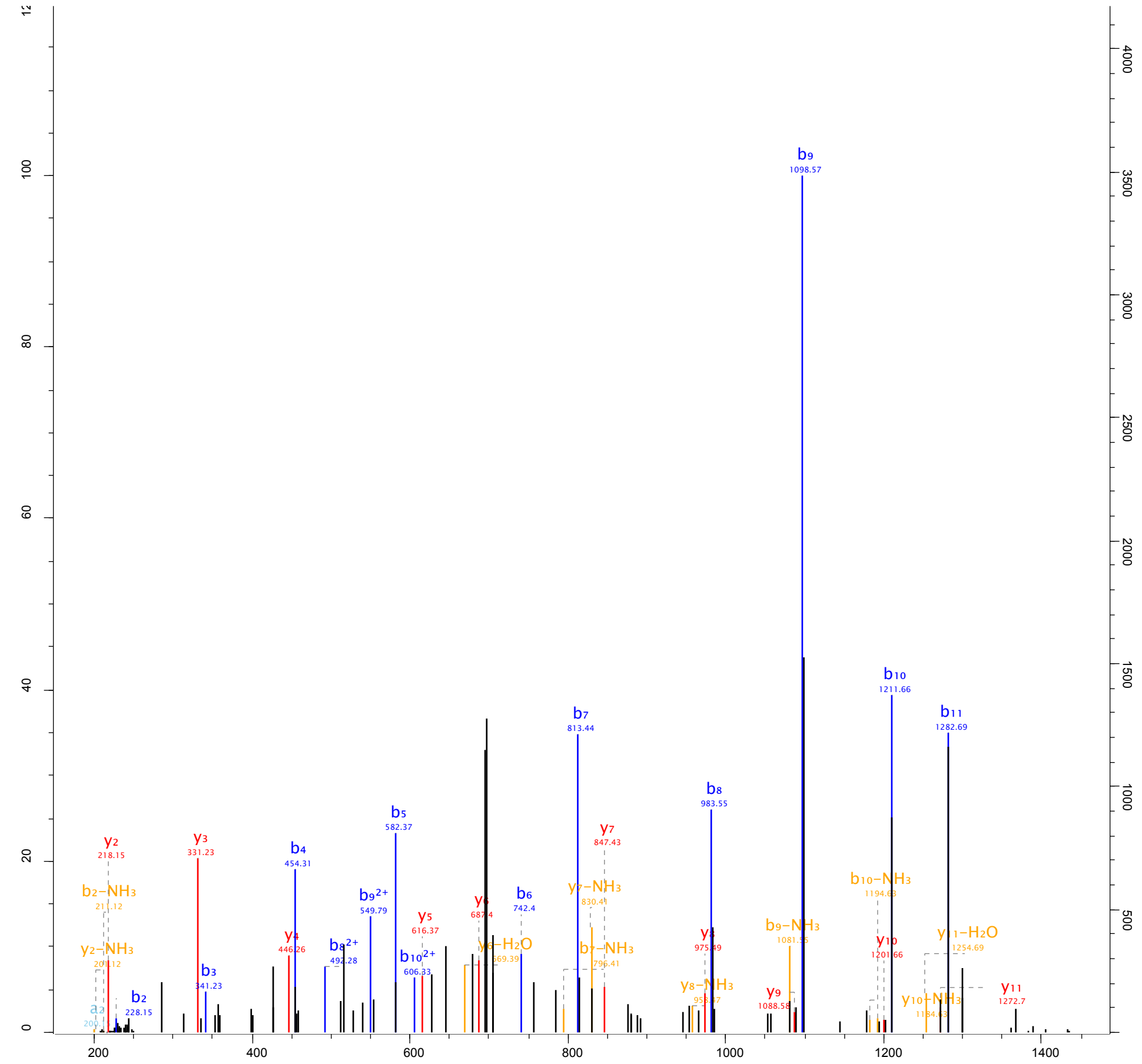






- H P V S C K ac D T P G F I V N R -





062513_SCW_II_53_9_Vargas_Enriched

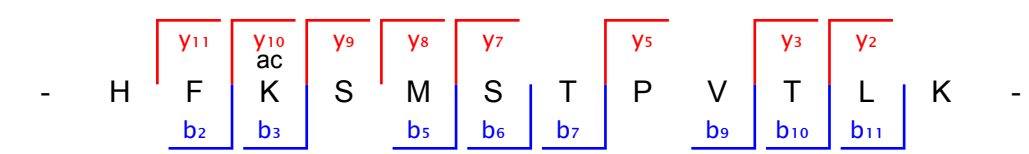
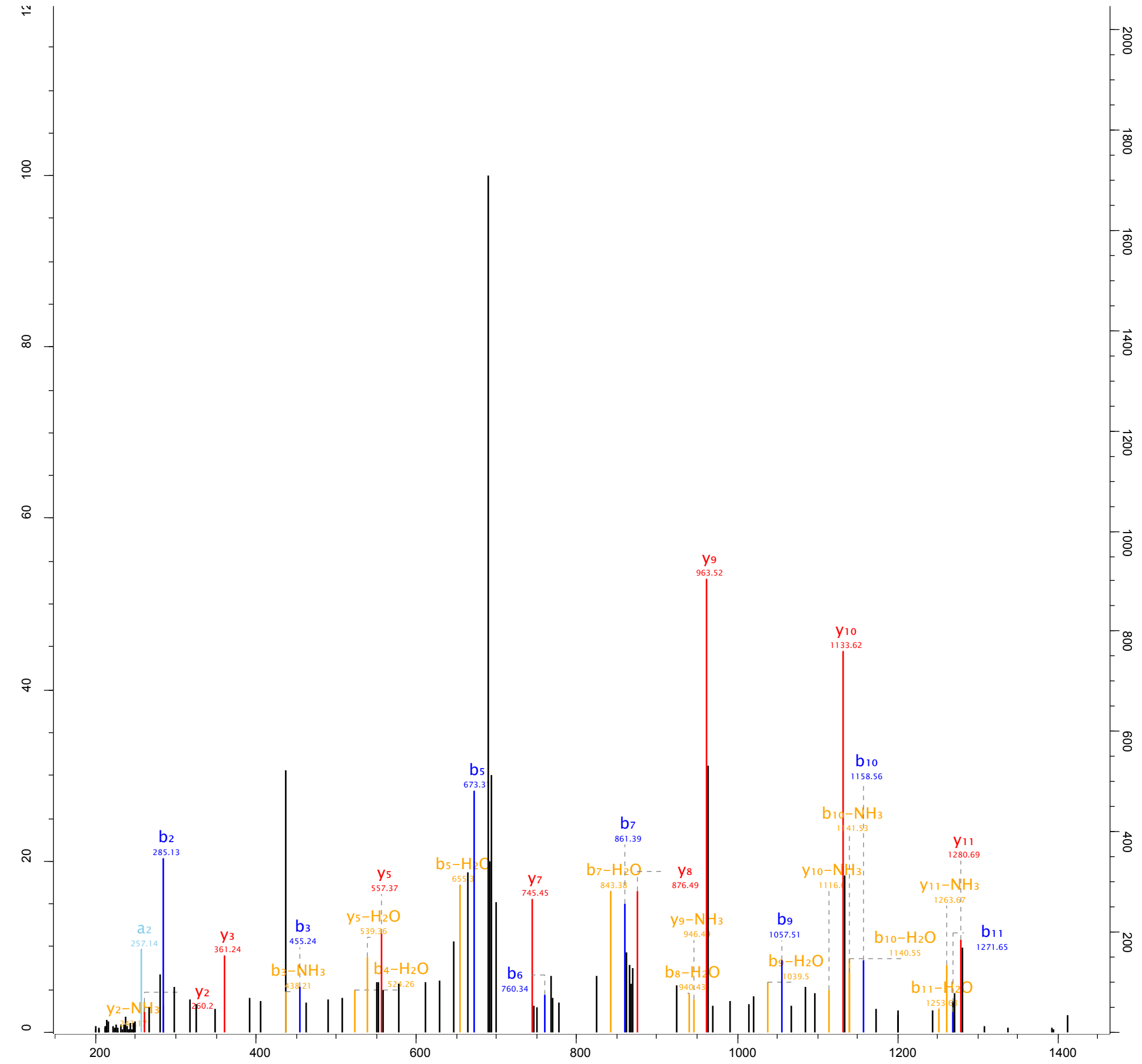
16250

ITMS; CID

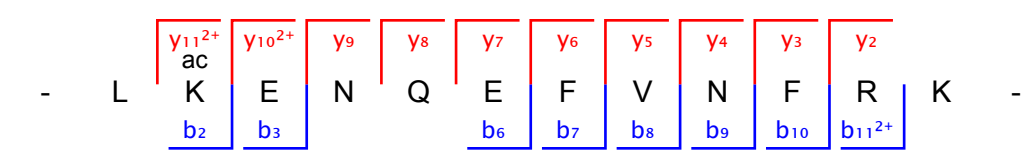
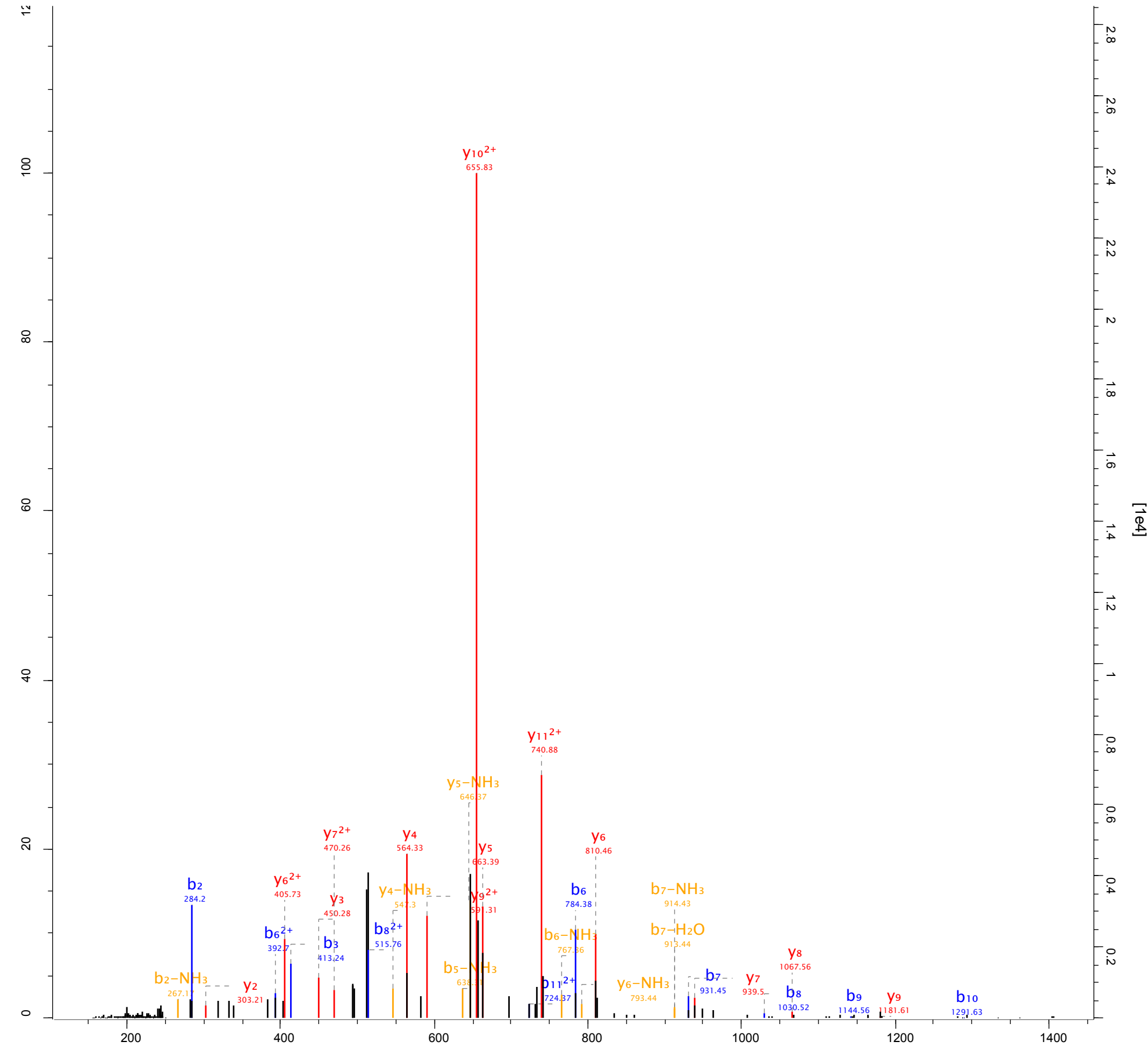
139.48

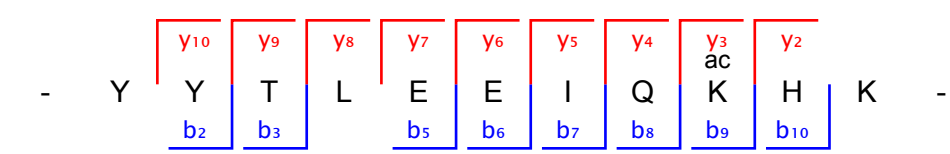
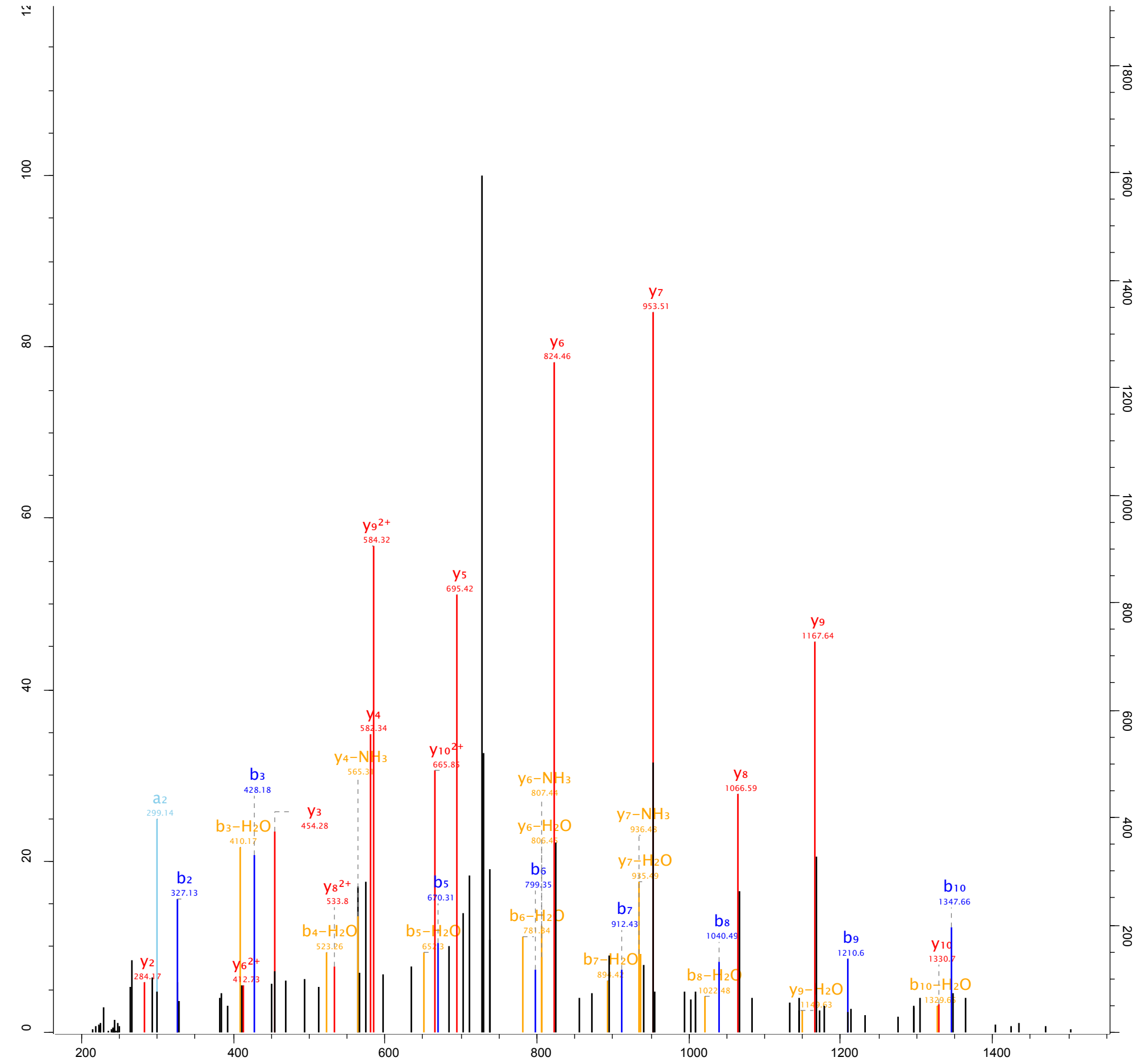
709.38

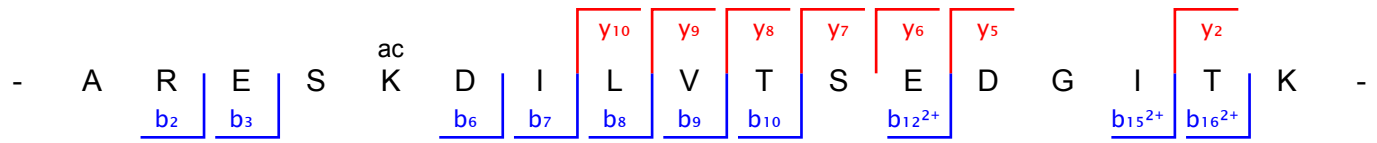
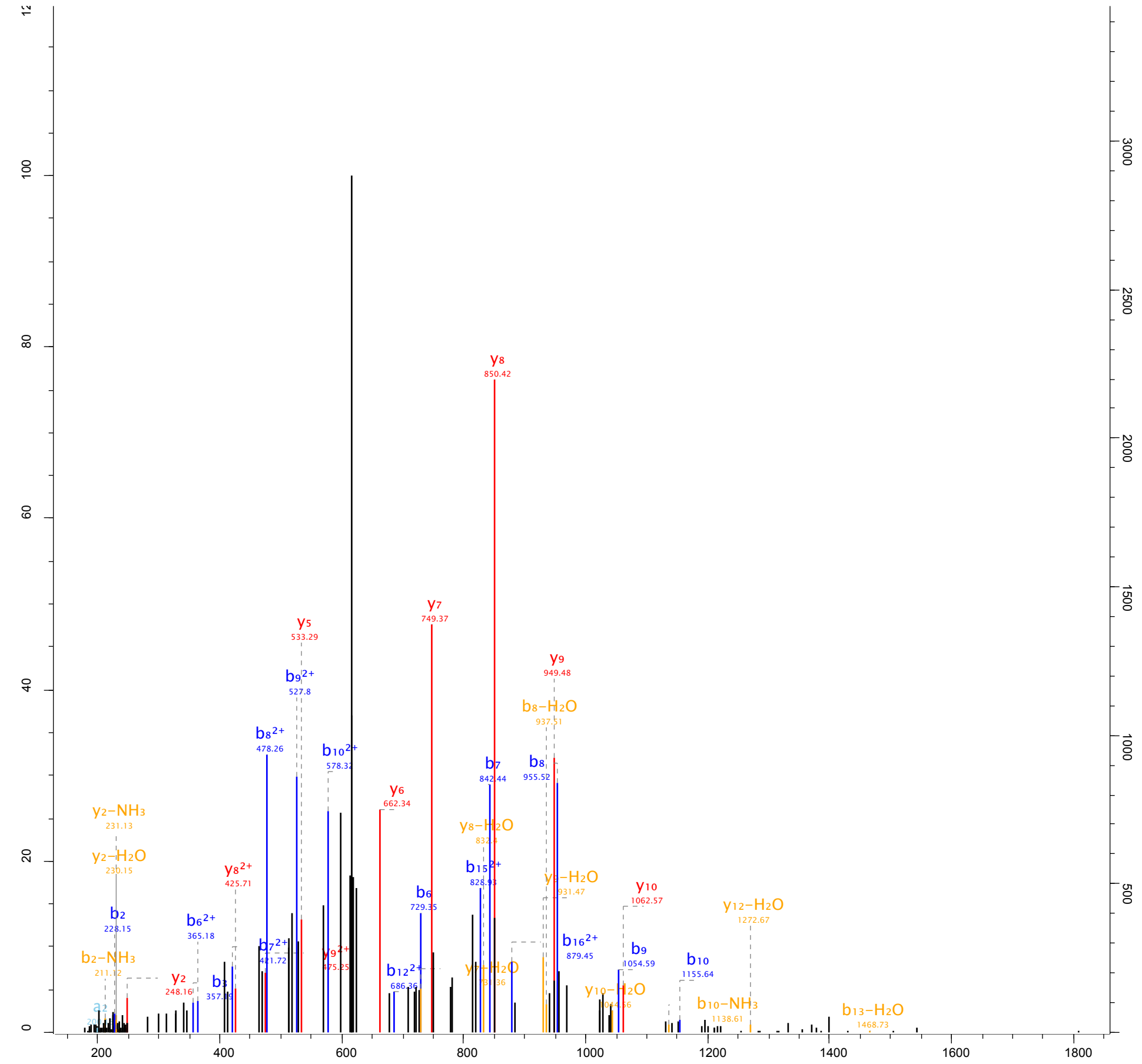
Acot9;Acot10

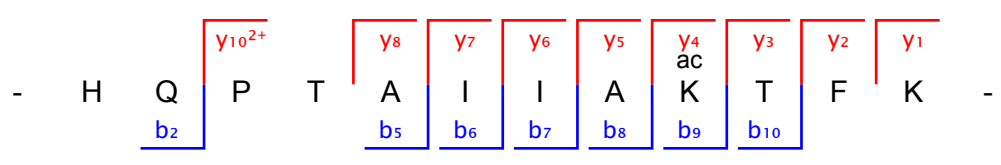
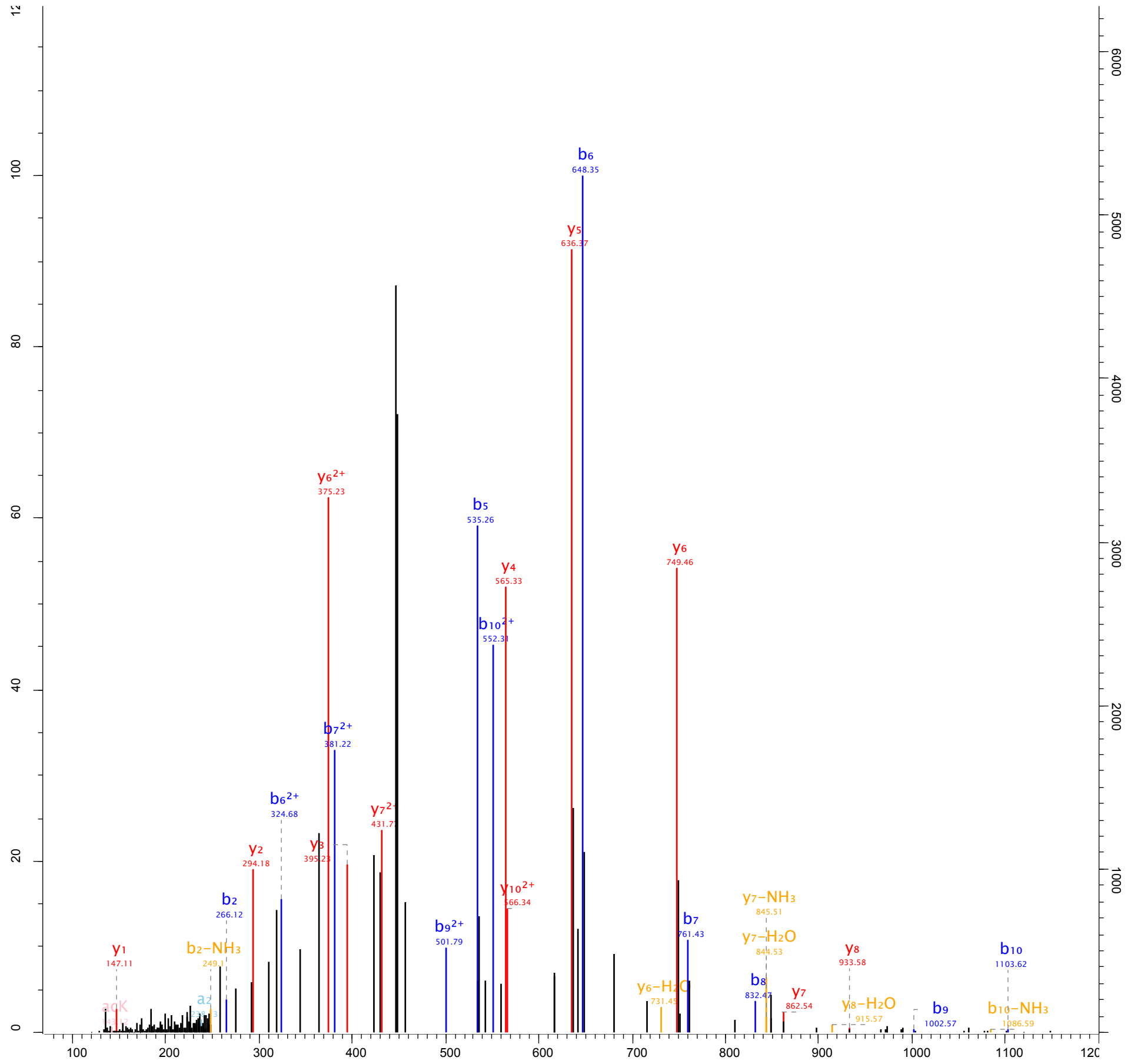


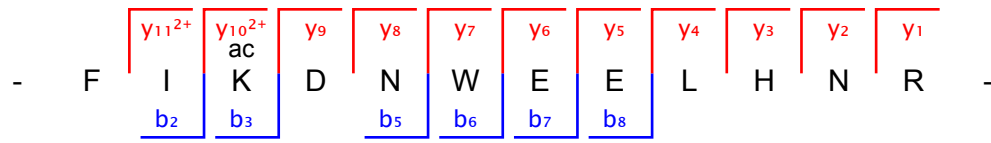
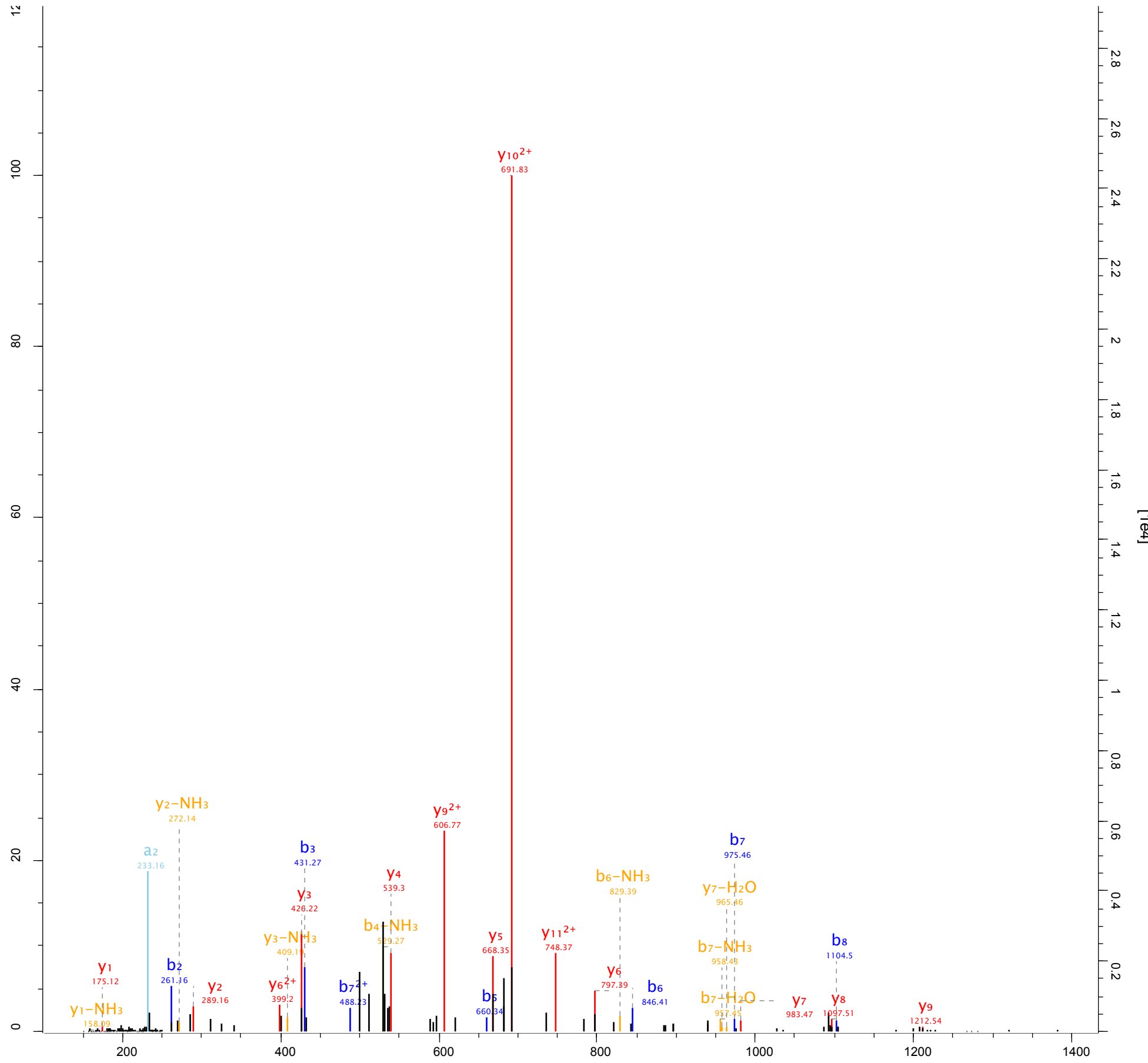
Raw file 062513_SCW_II_53_9_Vargas_Enriched Scan 16259 Method ITMS; CID Score 138.2 m/z 531.95 Gene names Gbas

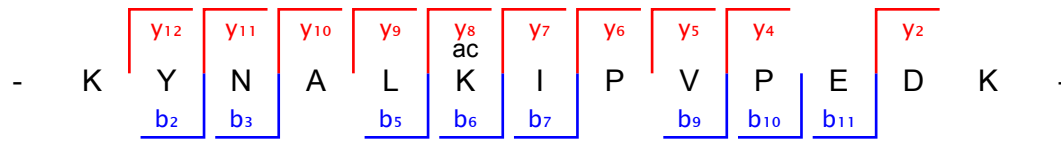
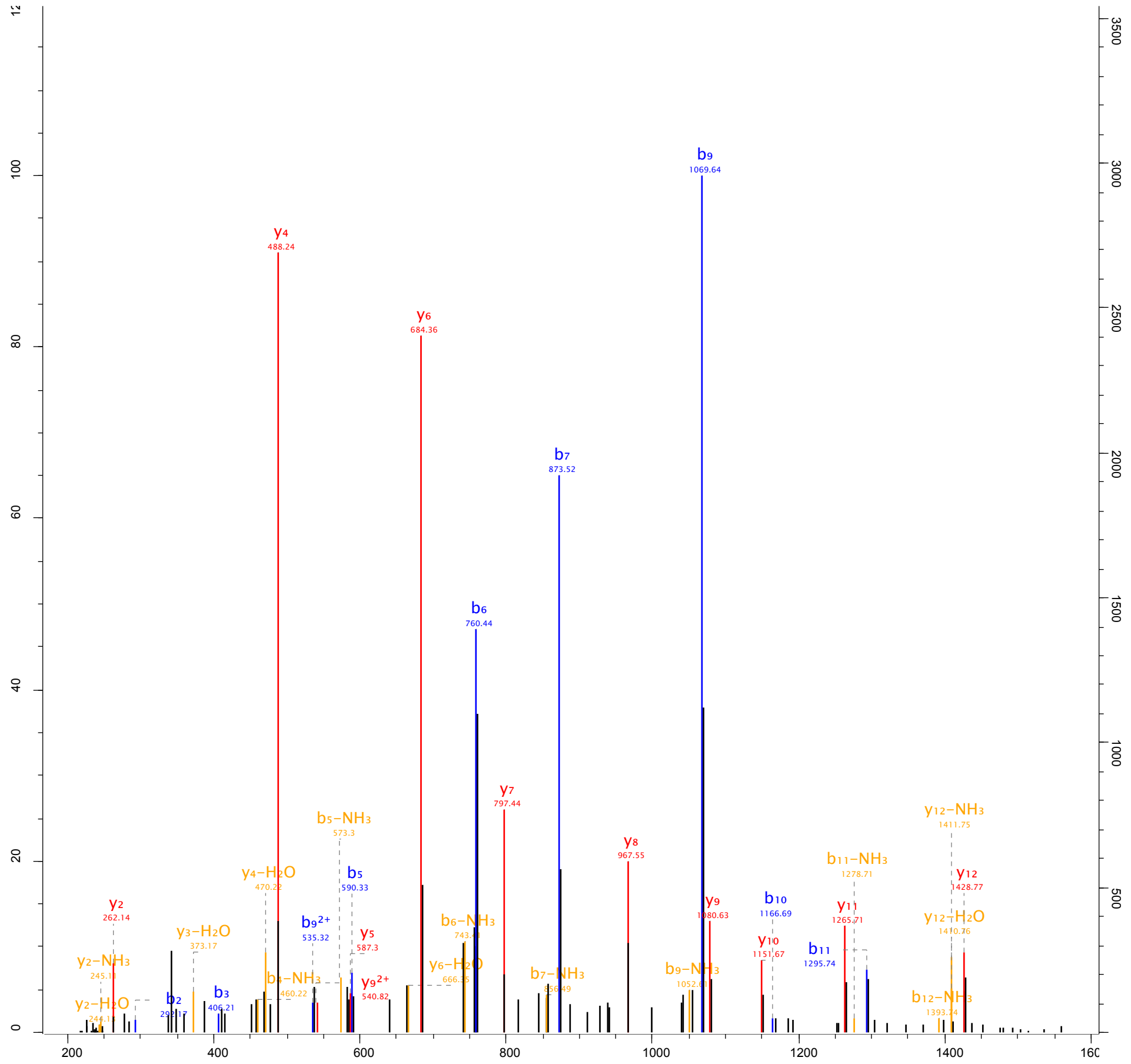


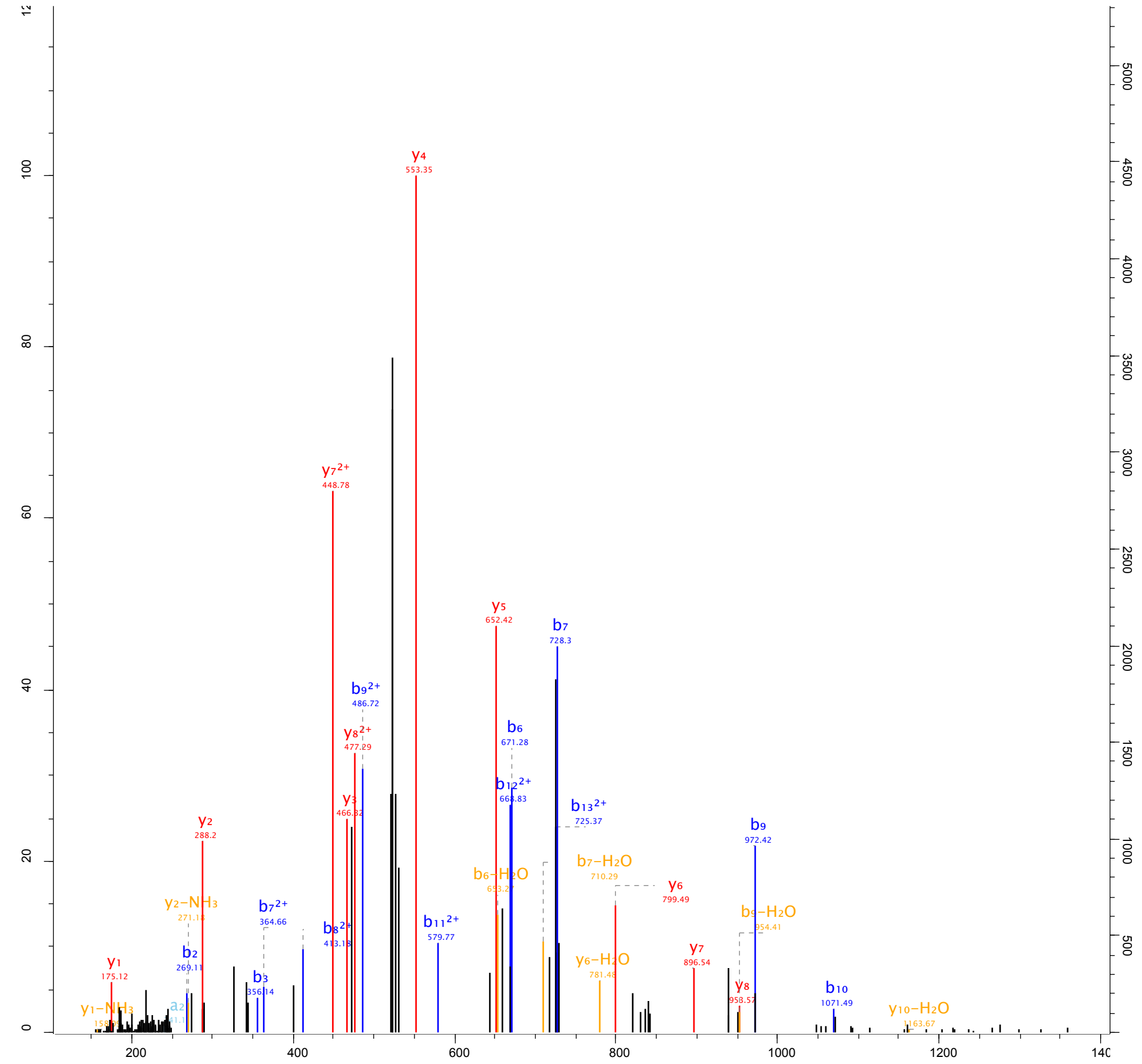






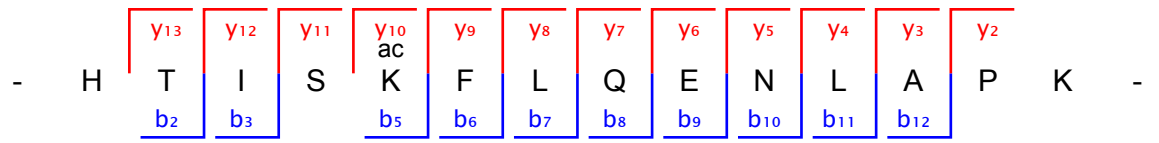
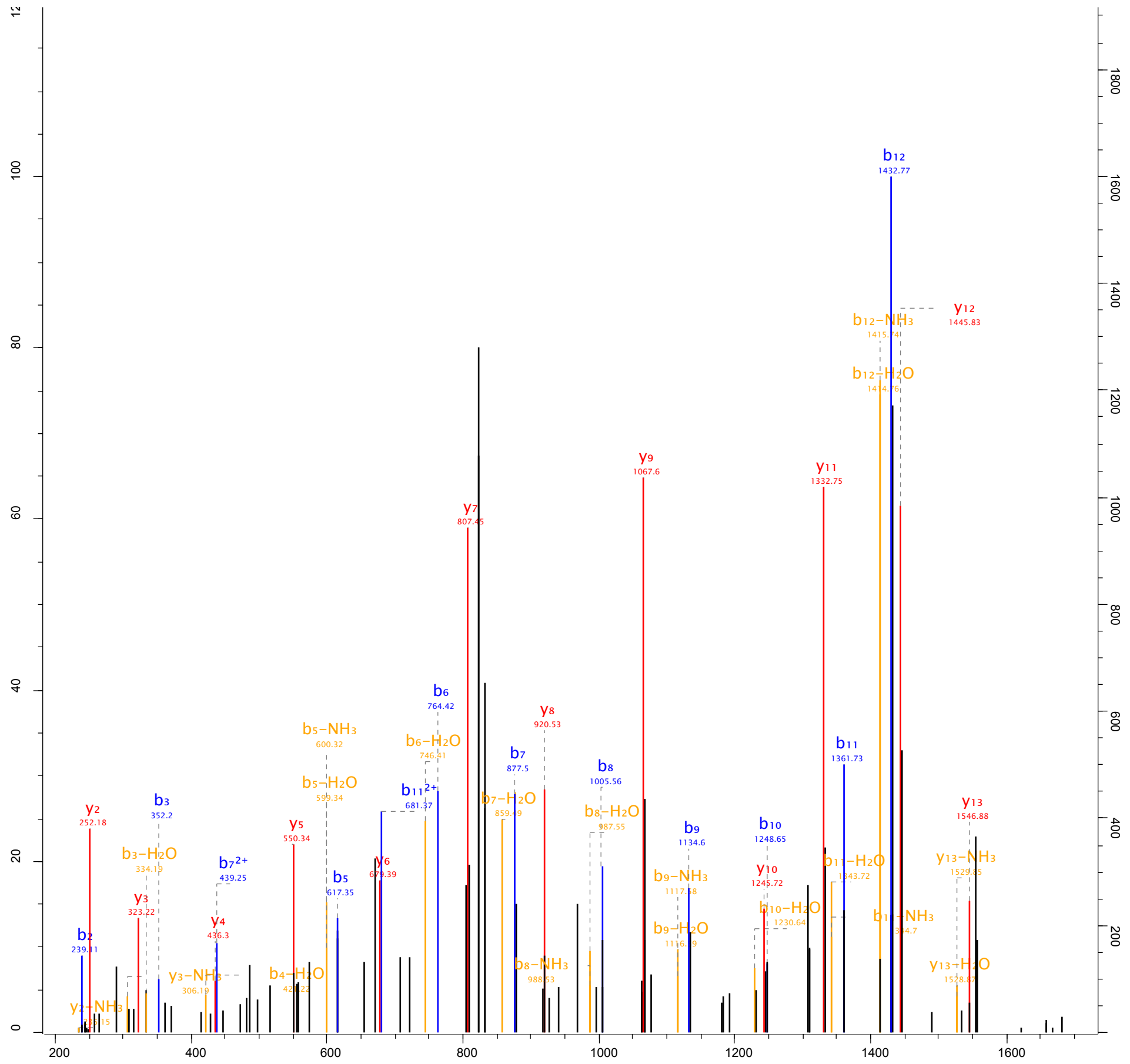


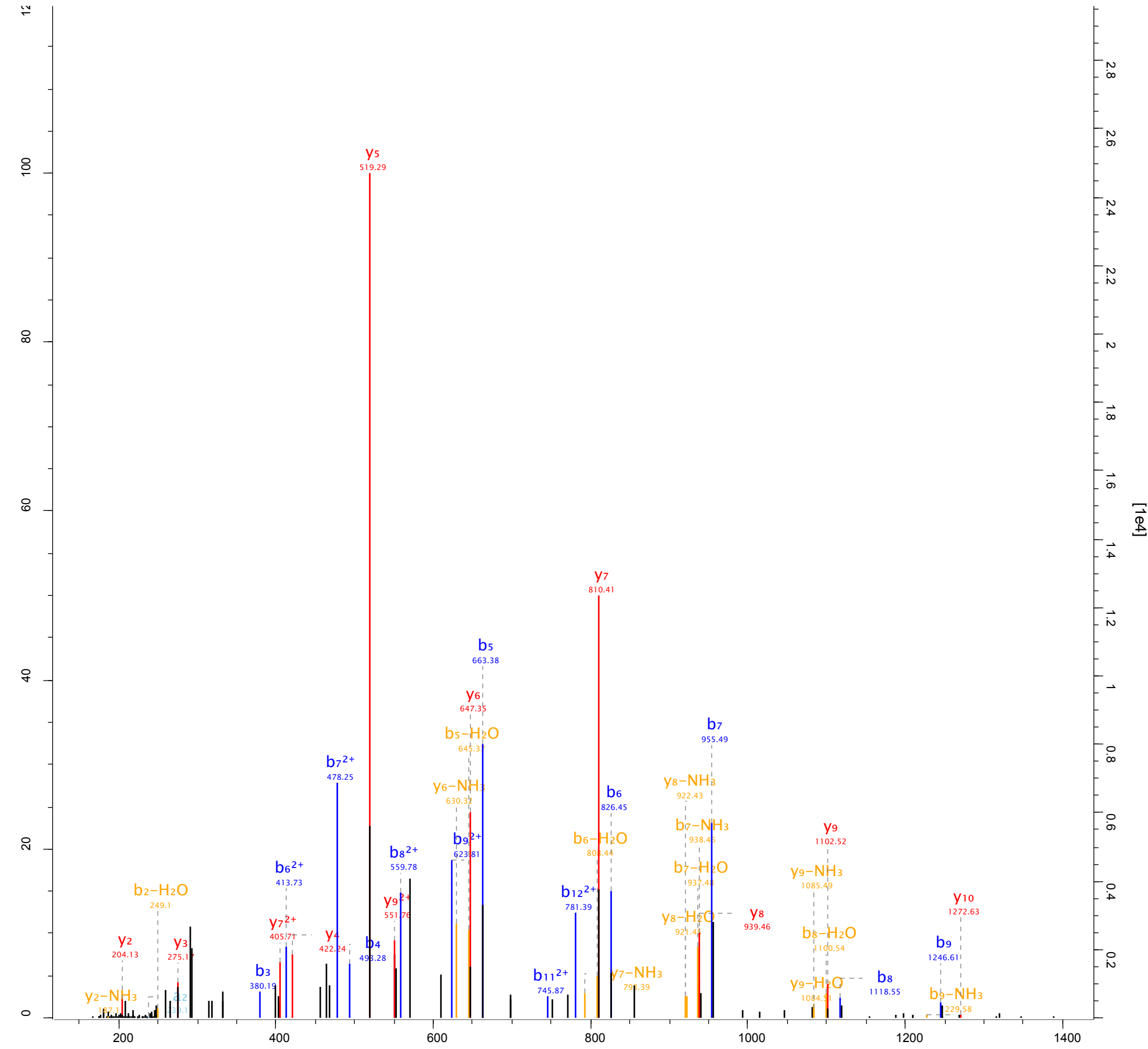




- M H S S E V G P F V S K I R -

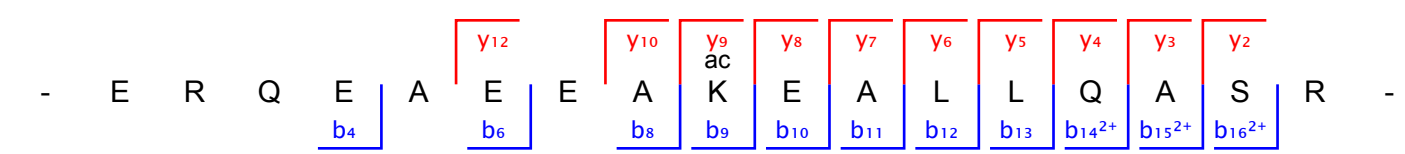
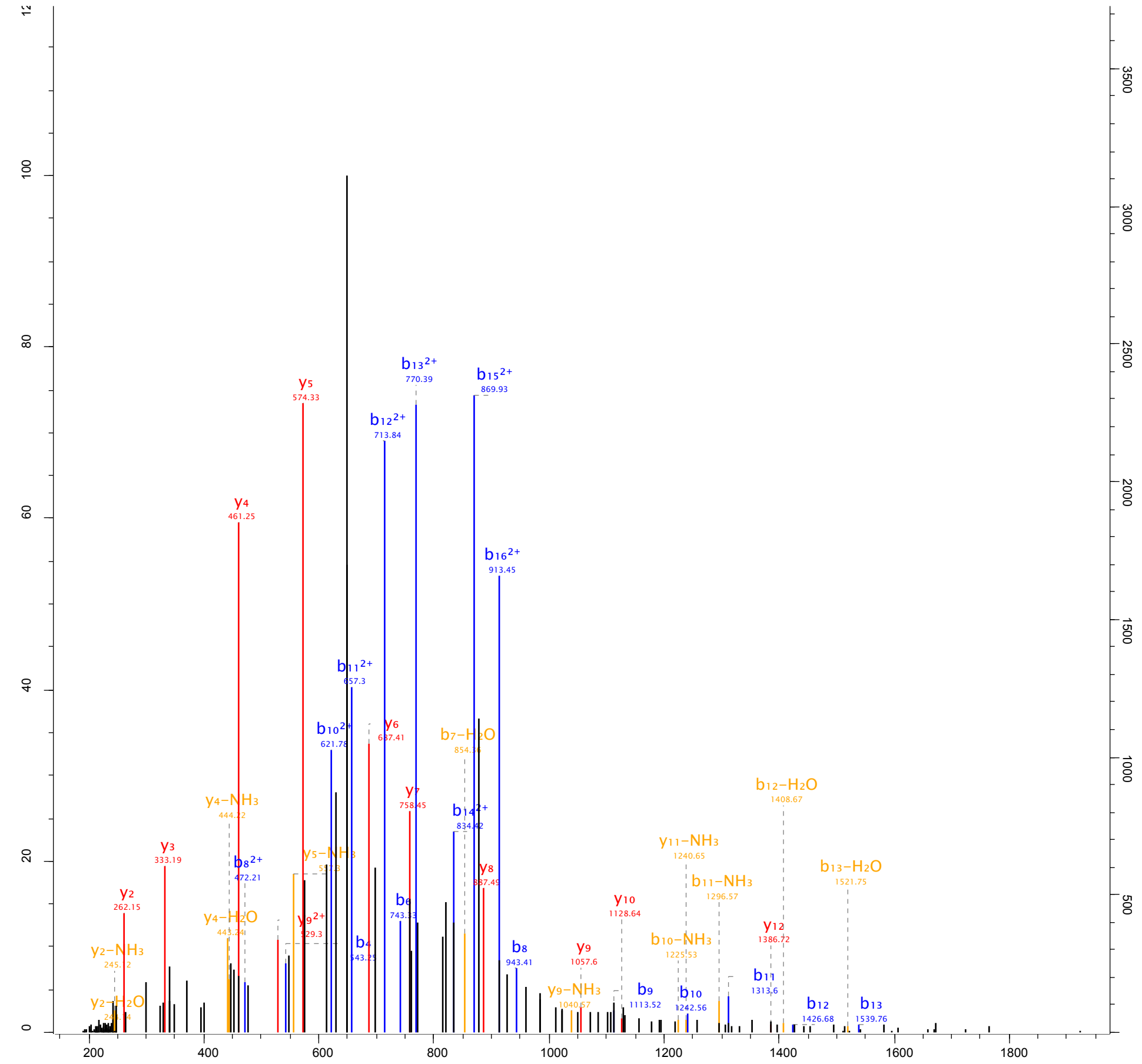
b₂
b₃
b₆
b₇
b₈²⁺
b₉
b₁₀
b₁₁²⁺
b₁₂²⁺
b₁₃²⁺
y₈
y₇
y₆
y₅
y₄
y₃
y₂
y₁

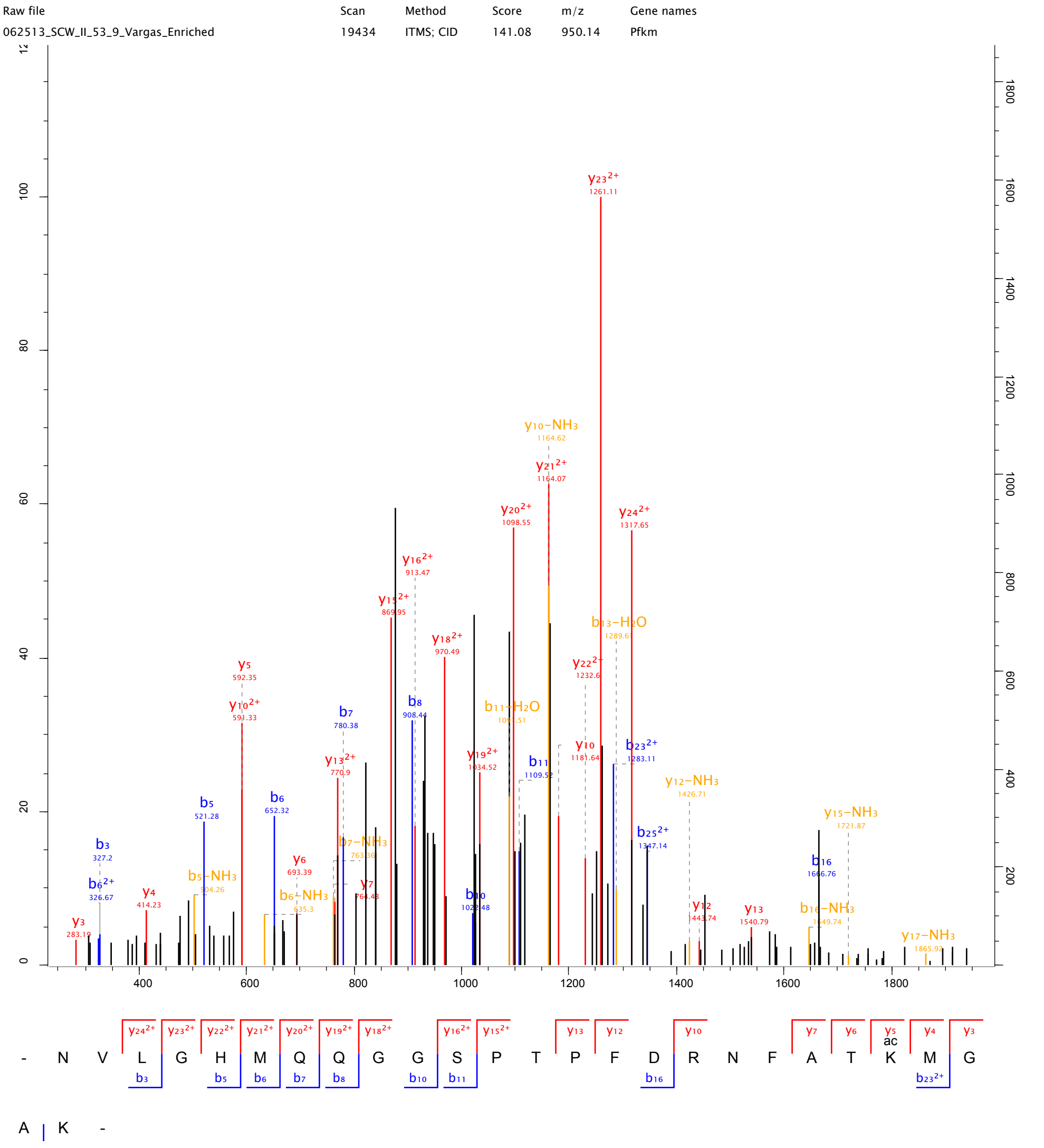


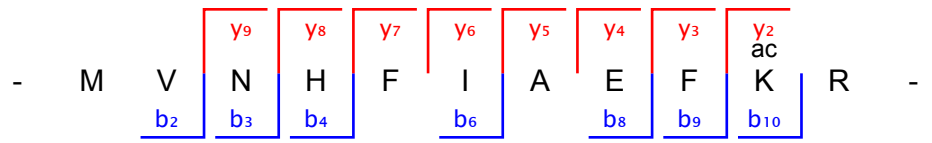
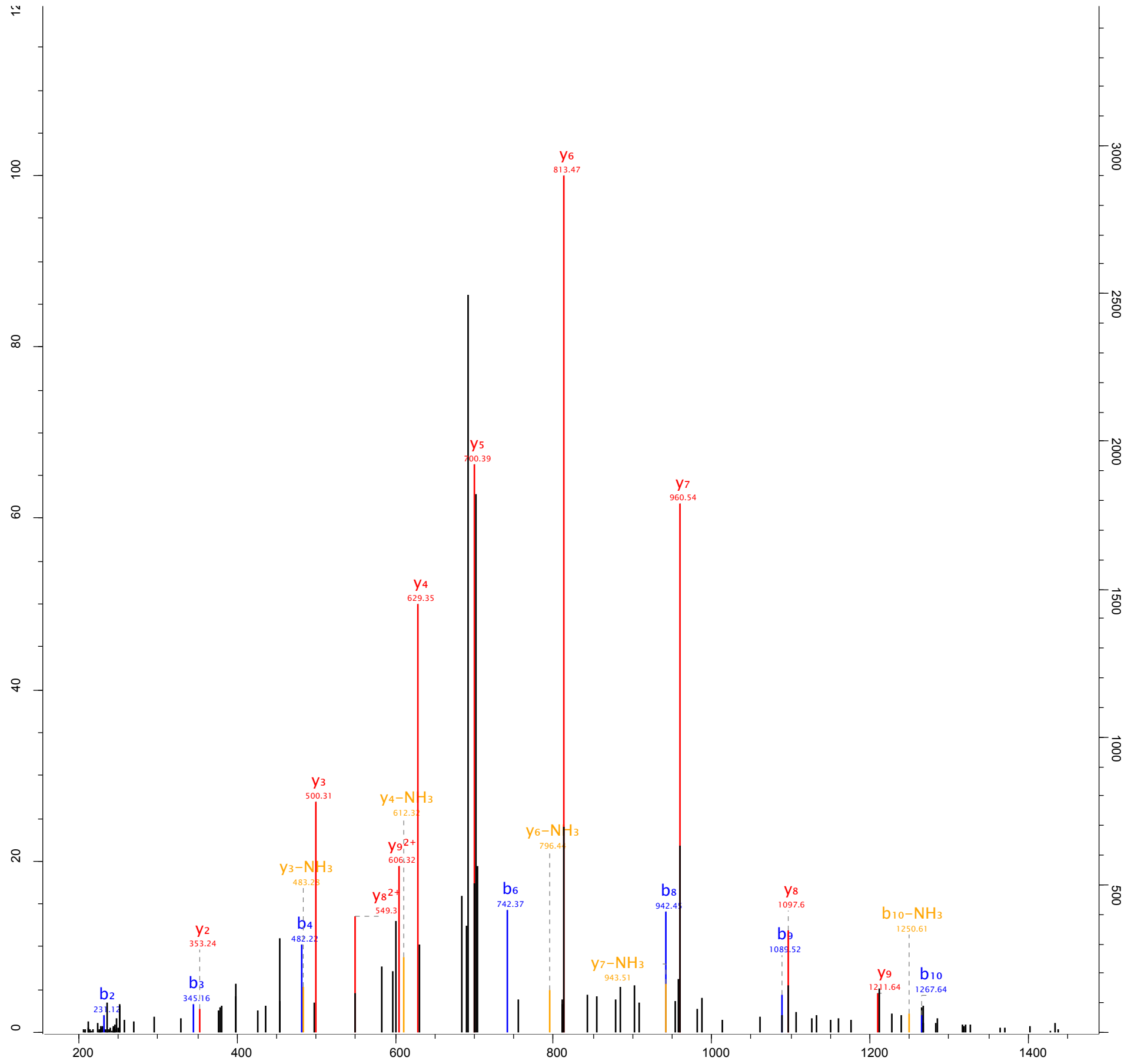


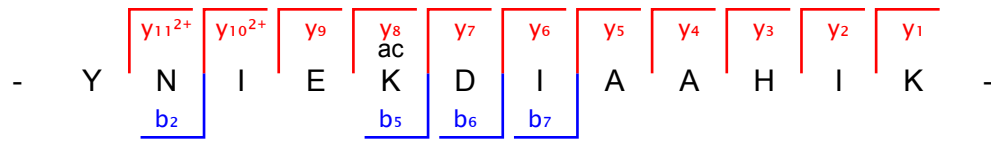
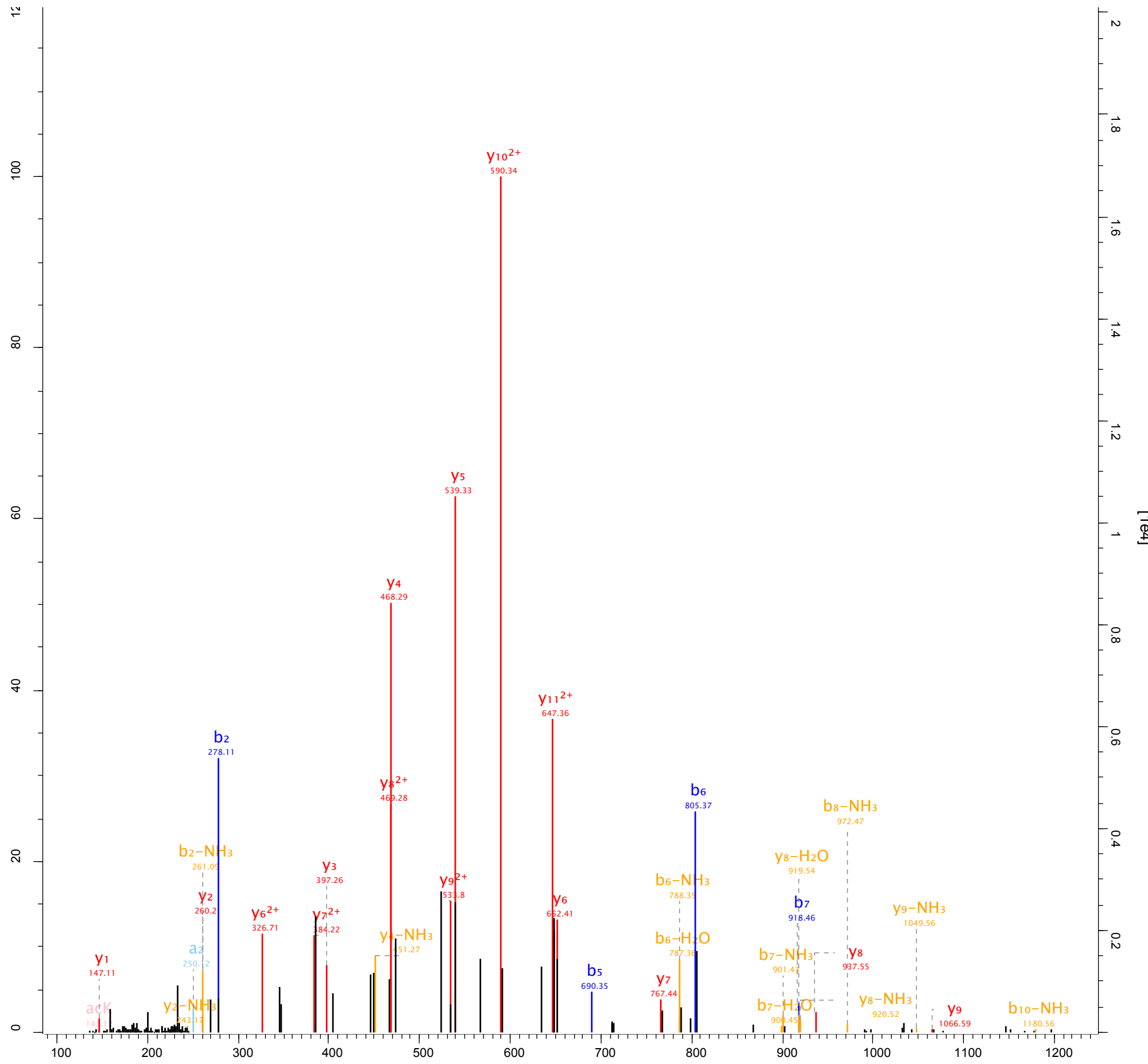
- E H L L K Y E Y Q P F A G K -

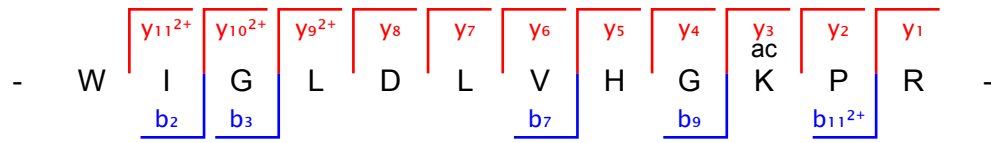
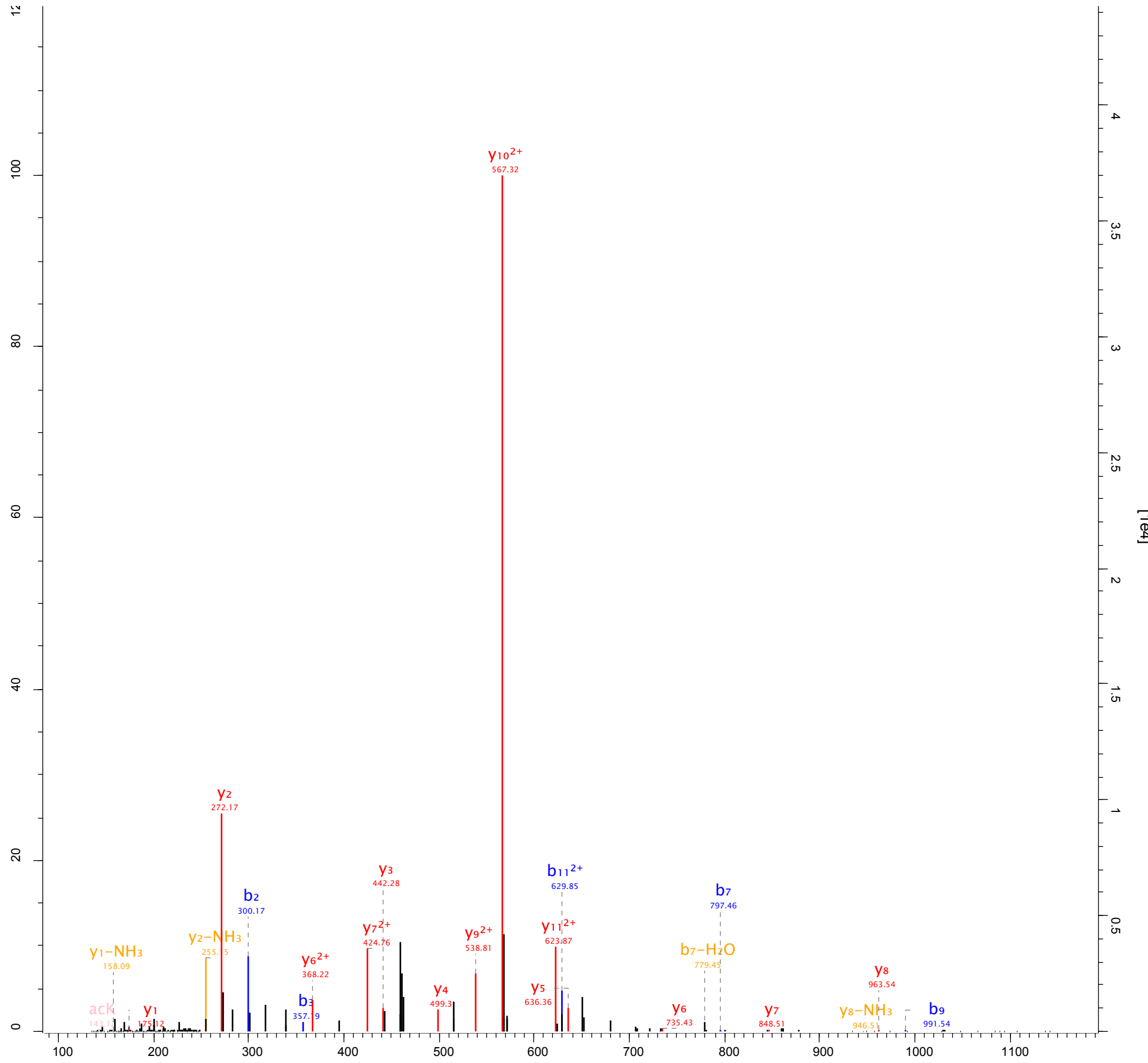
a₂
b₃
b₄
b₅
b₆
b₇
b₈
b₉
b₁₁²⁺
b₁₂²⁺

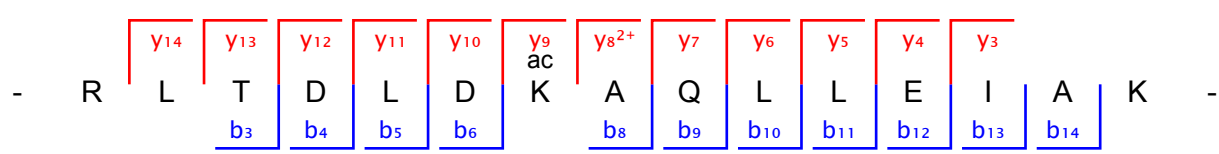
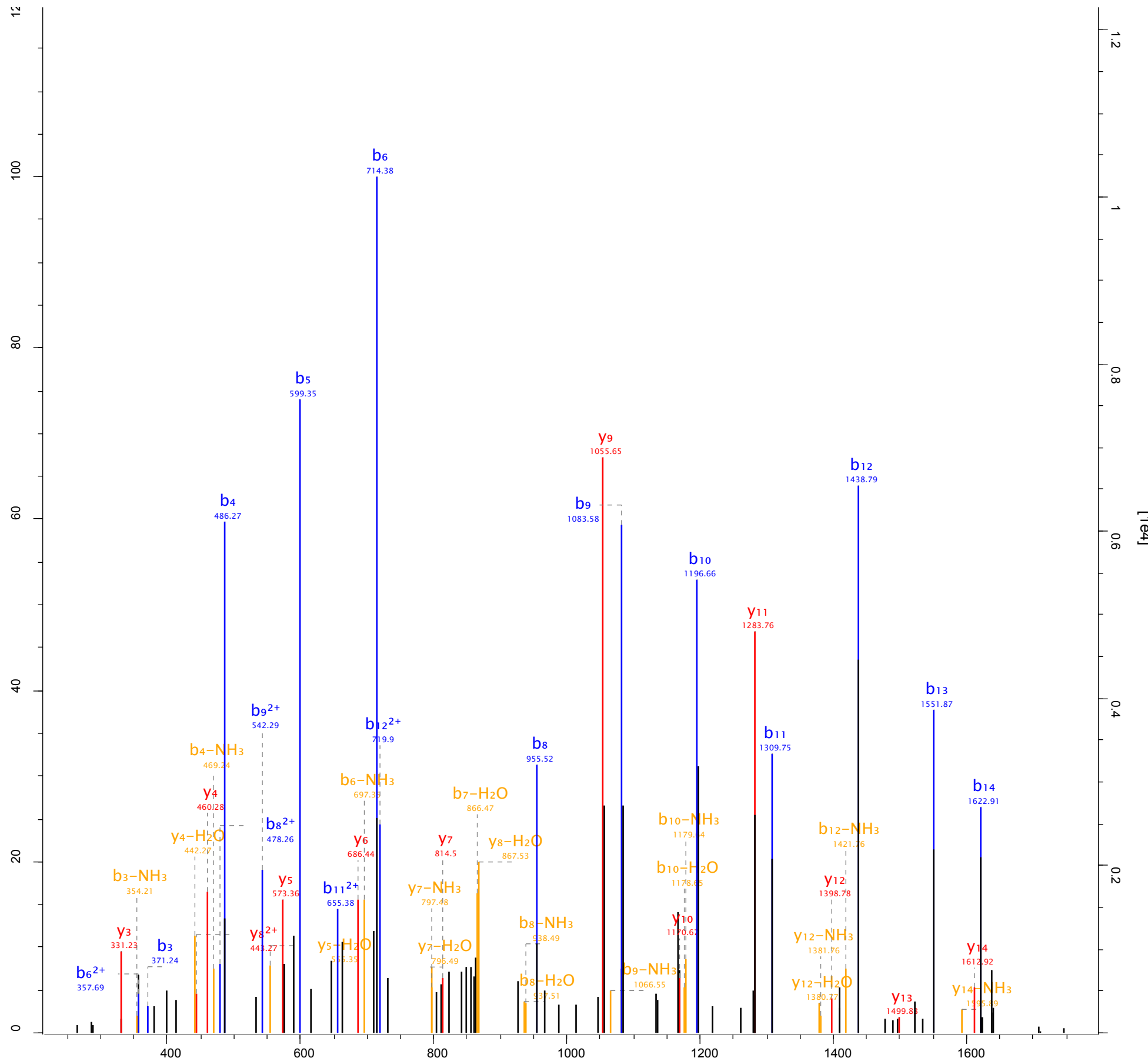


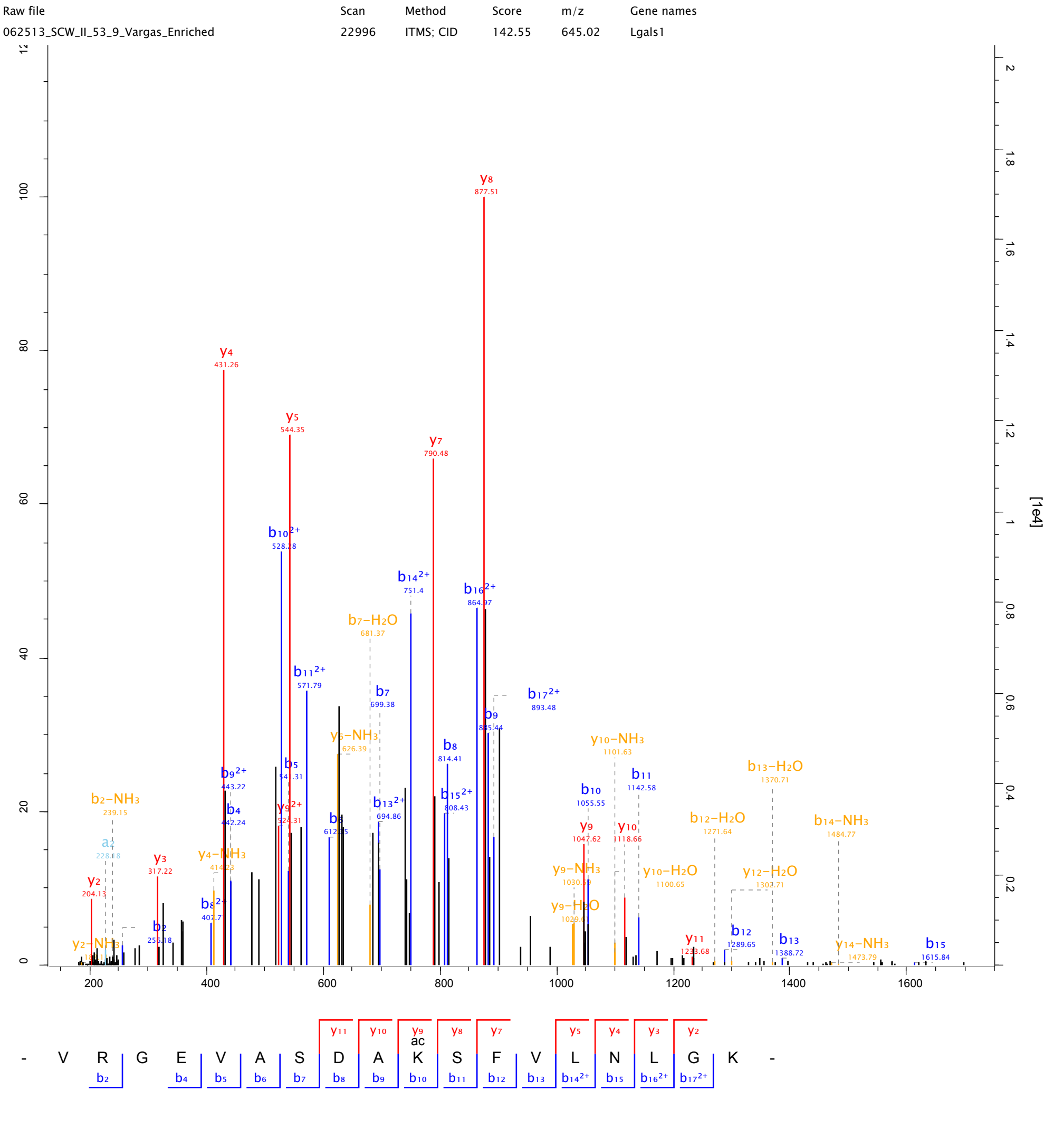


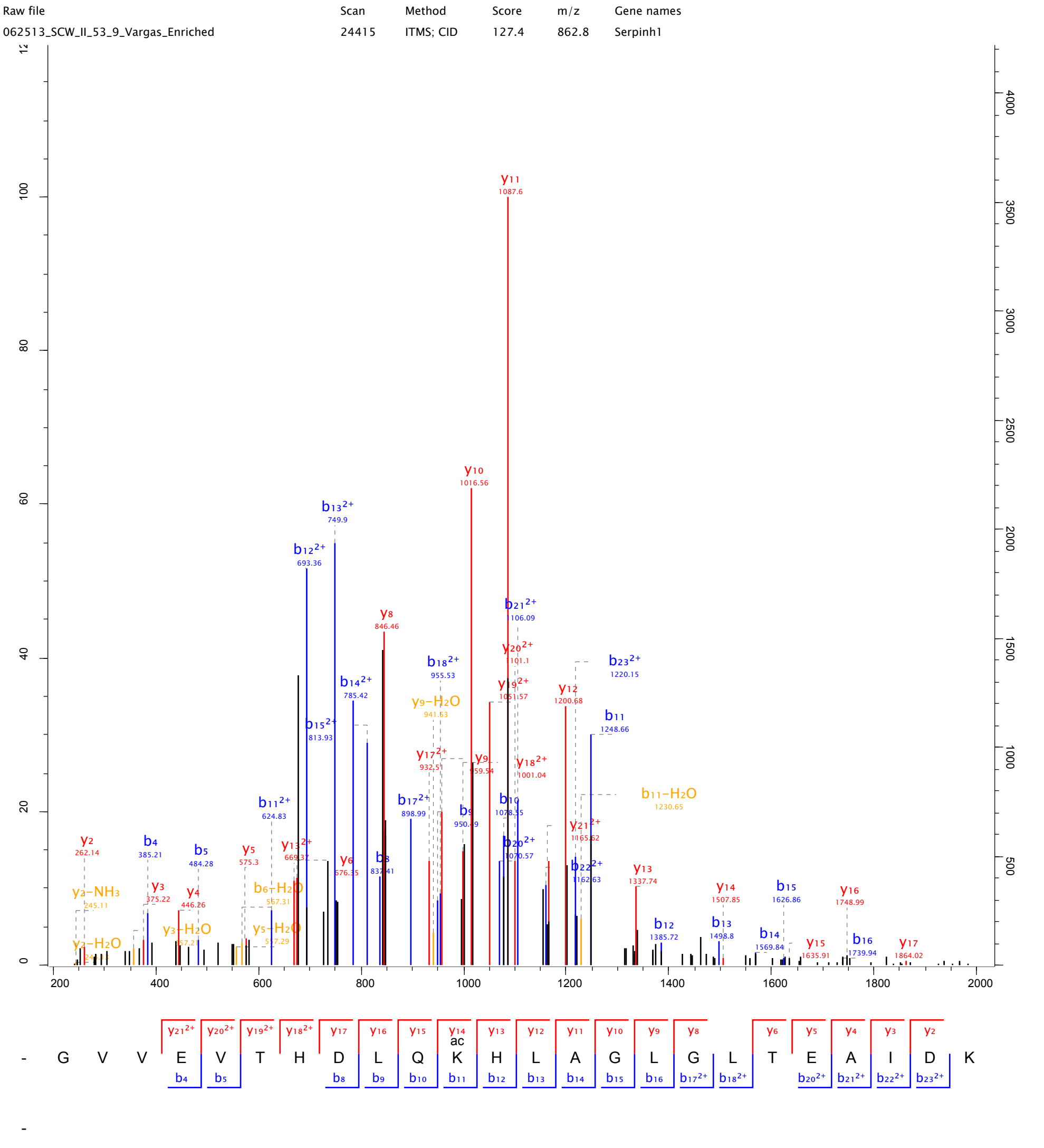


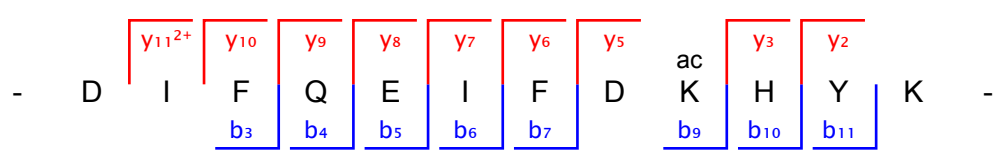
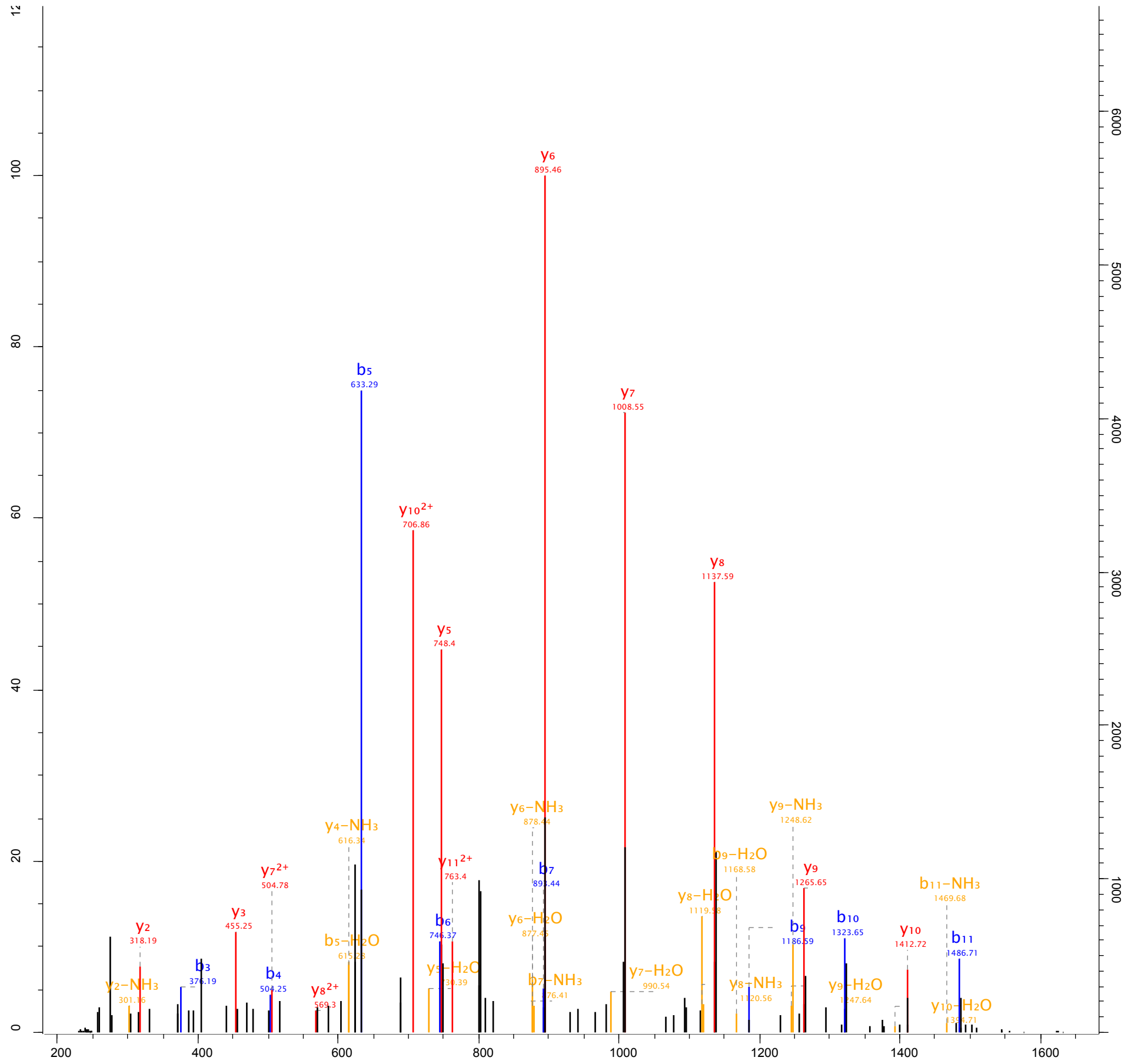


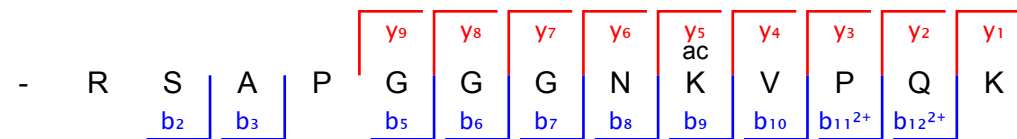
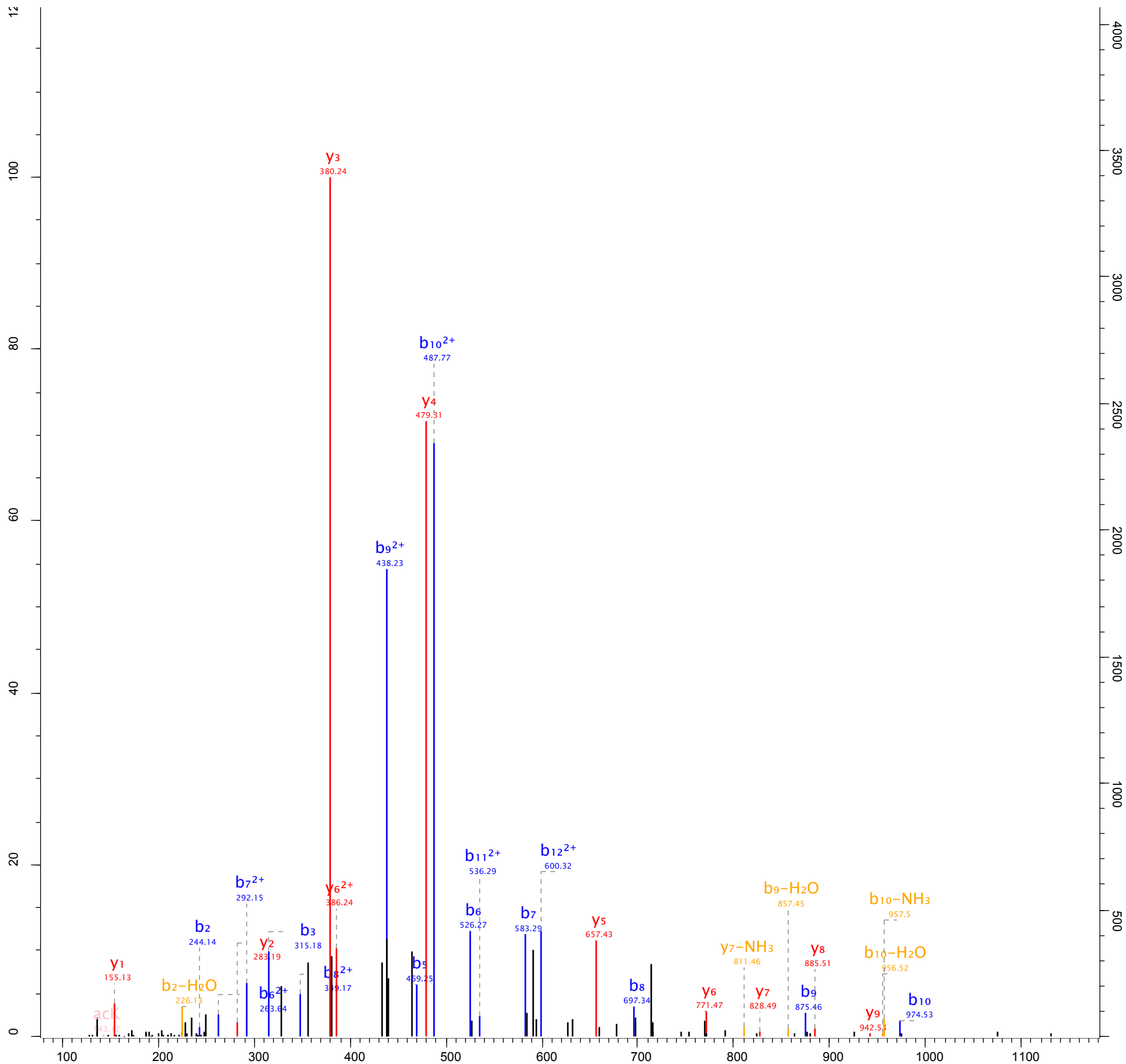












062513_SCW_II_53_10_Vargas_Enriched

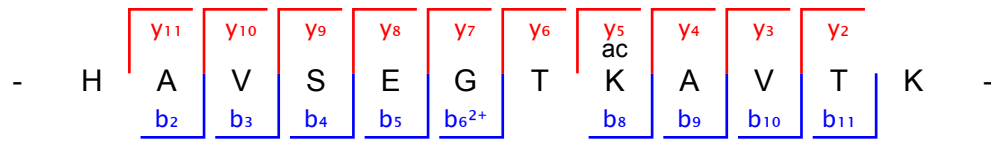
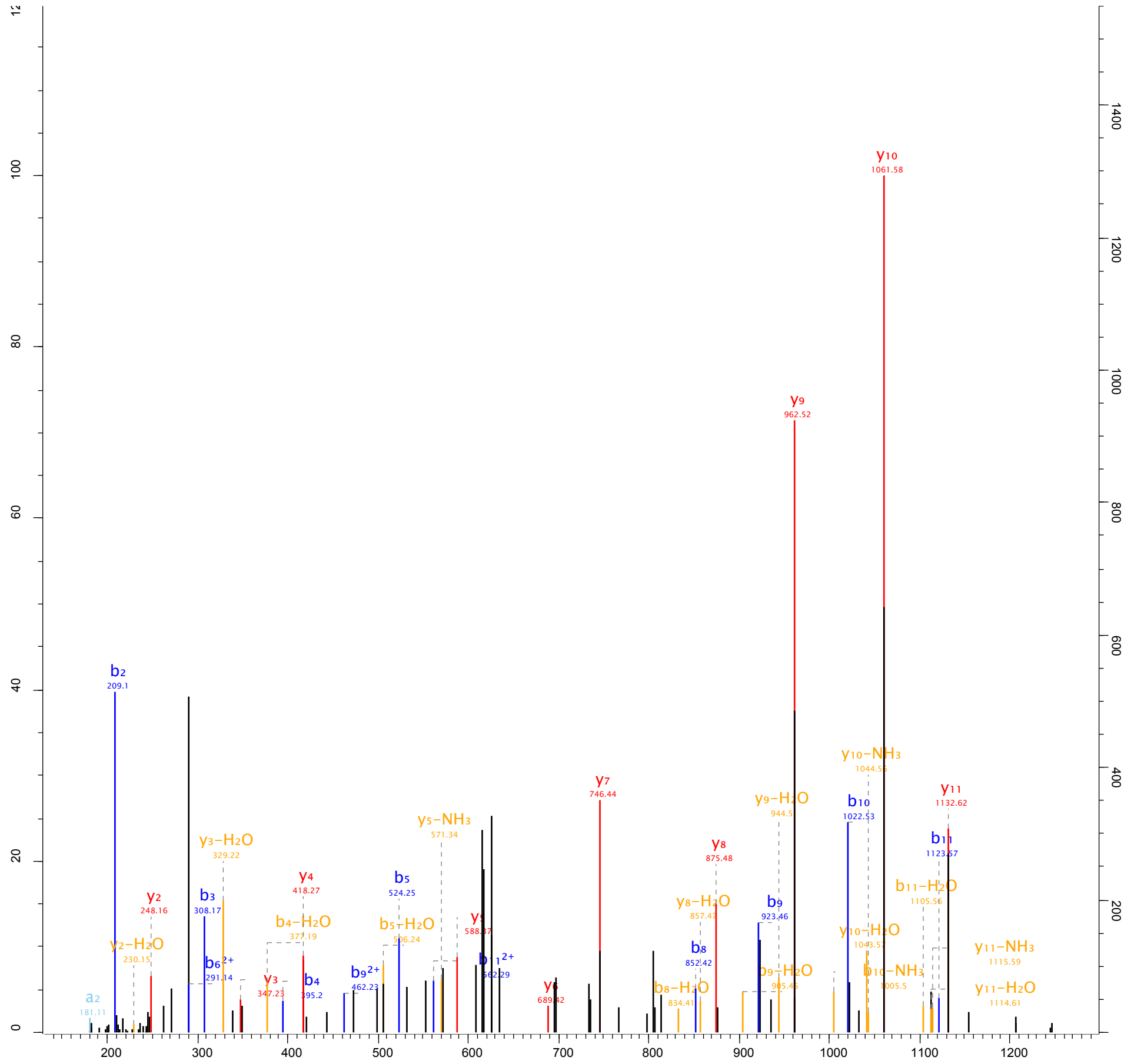
9552

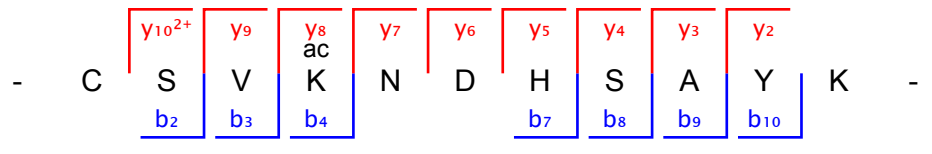
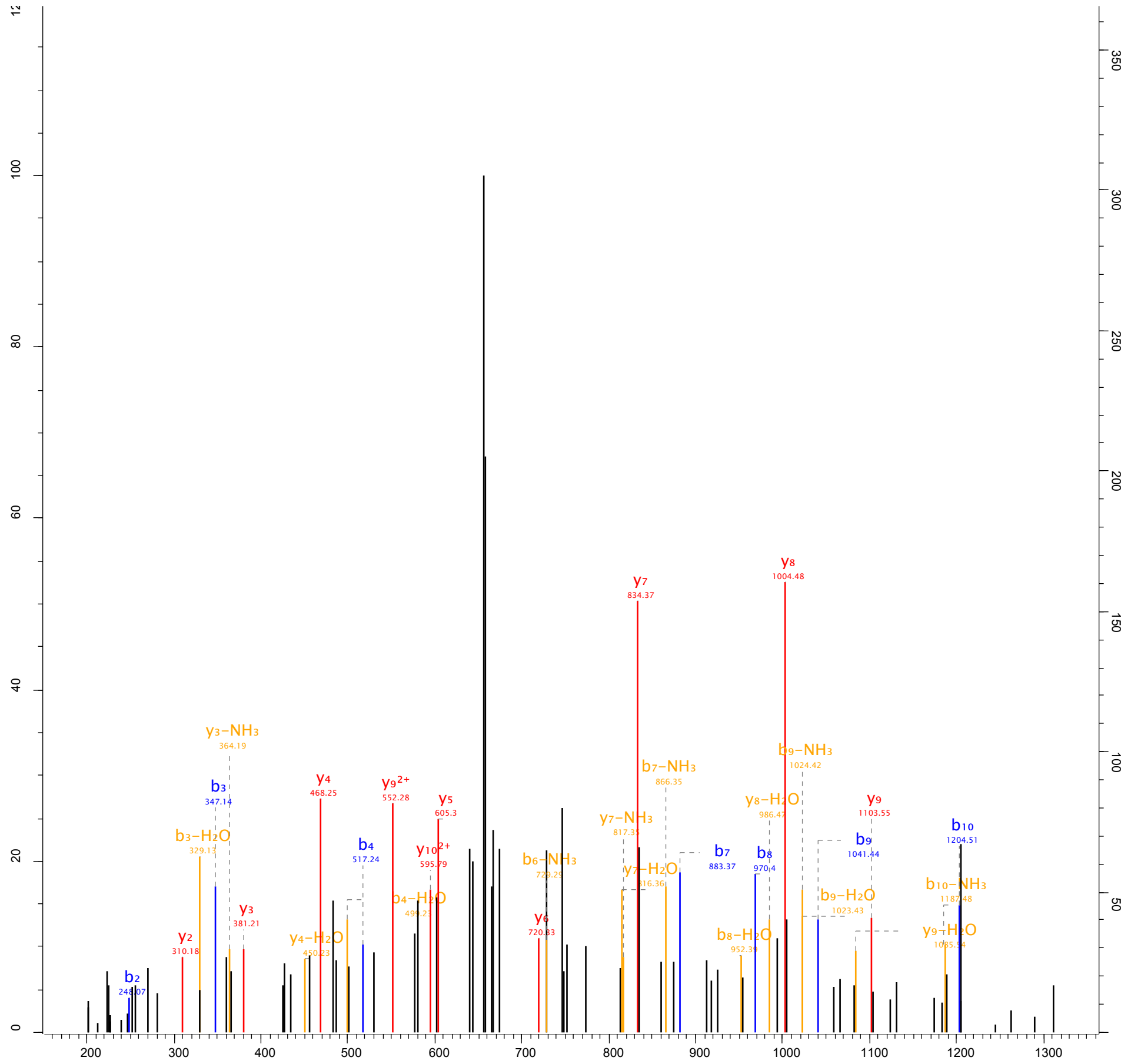
ITMS; CID

144.51

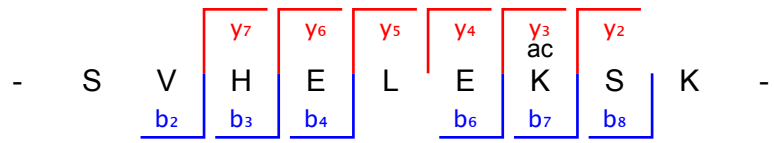
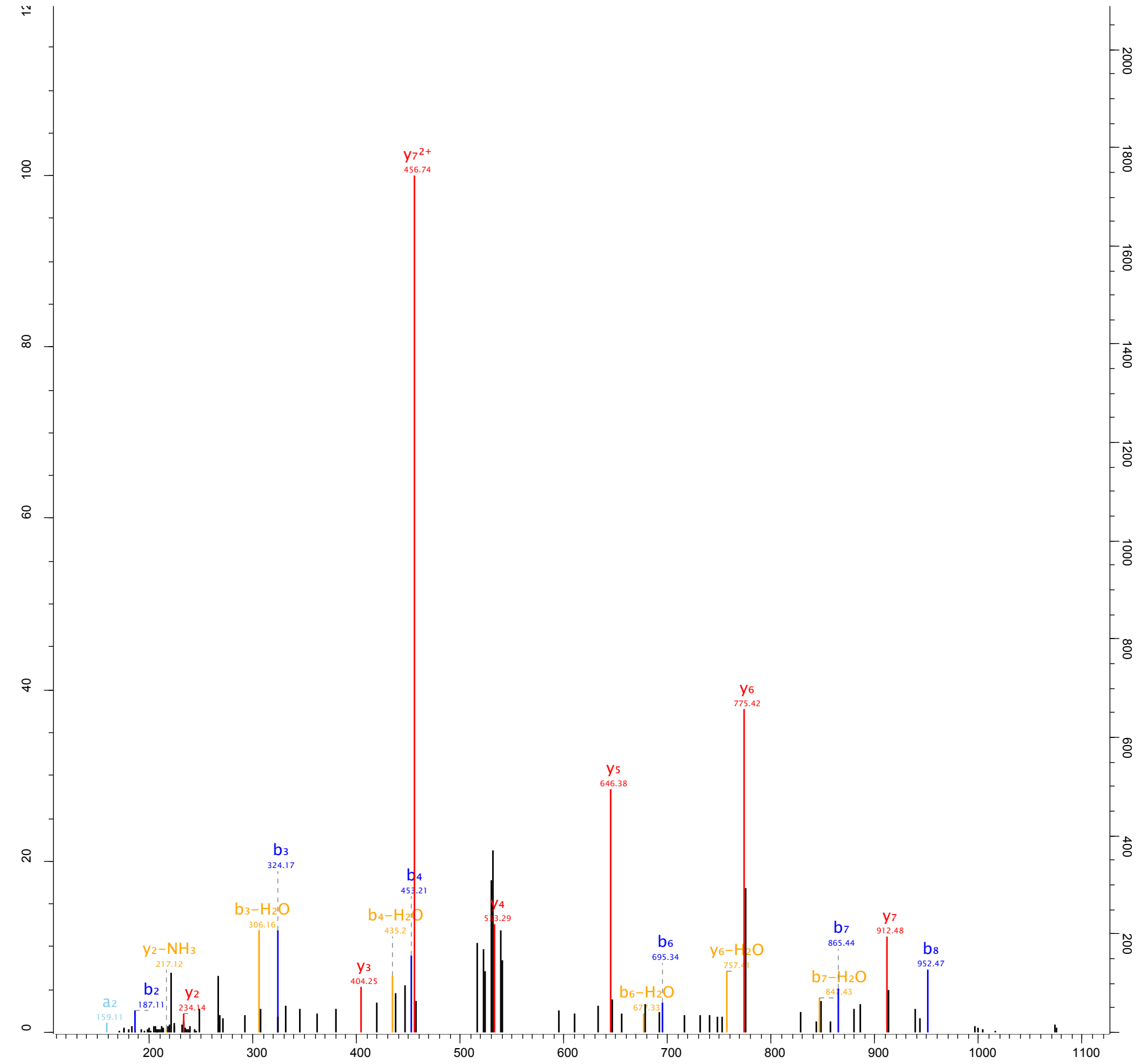
635.34

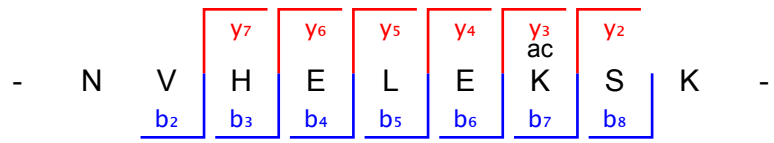
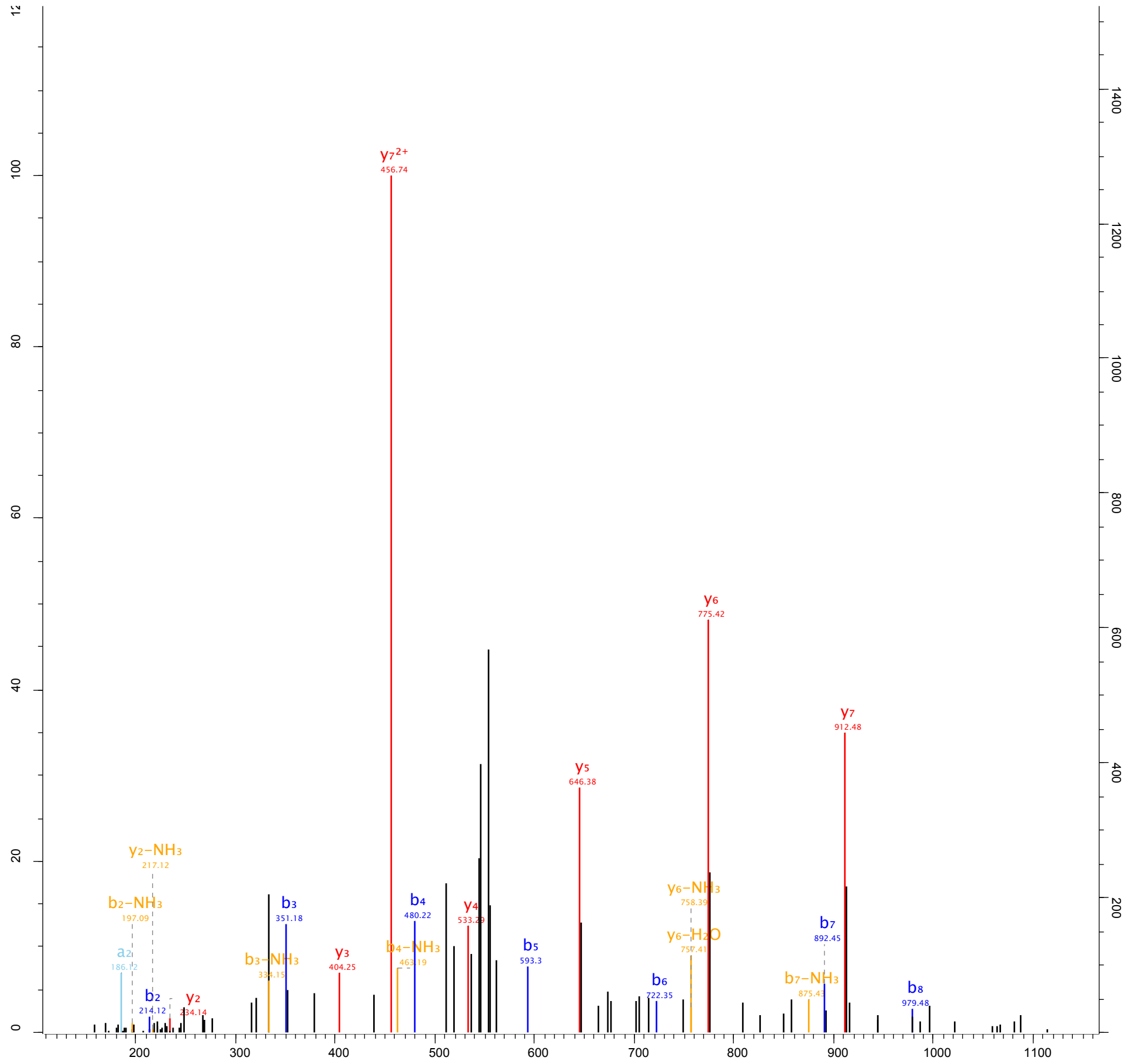
Hist1h2bb;Hist1h2ba;Hist1h2bm;Hist1h2bj;Hist1h2bp;Hist2h2bb;Hist1h2bh;Hist1h2b

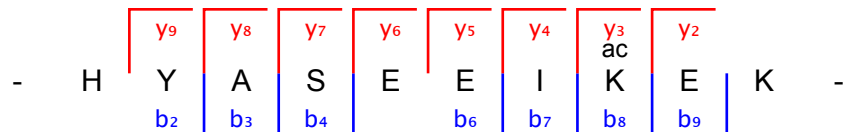
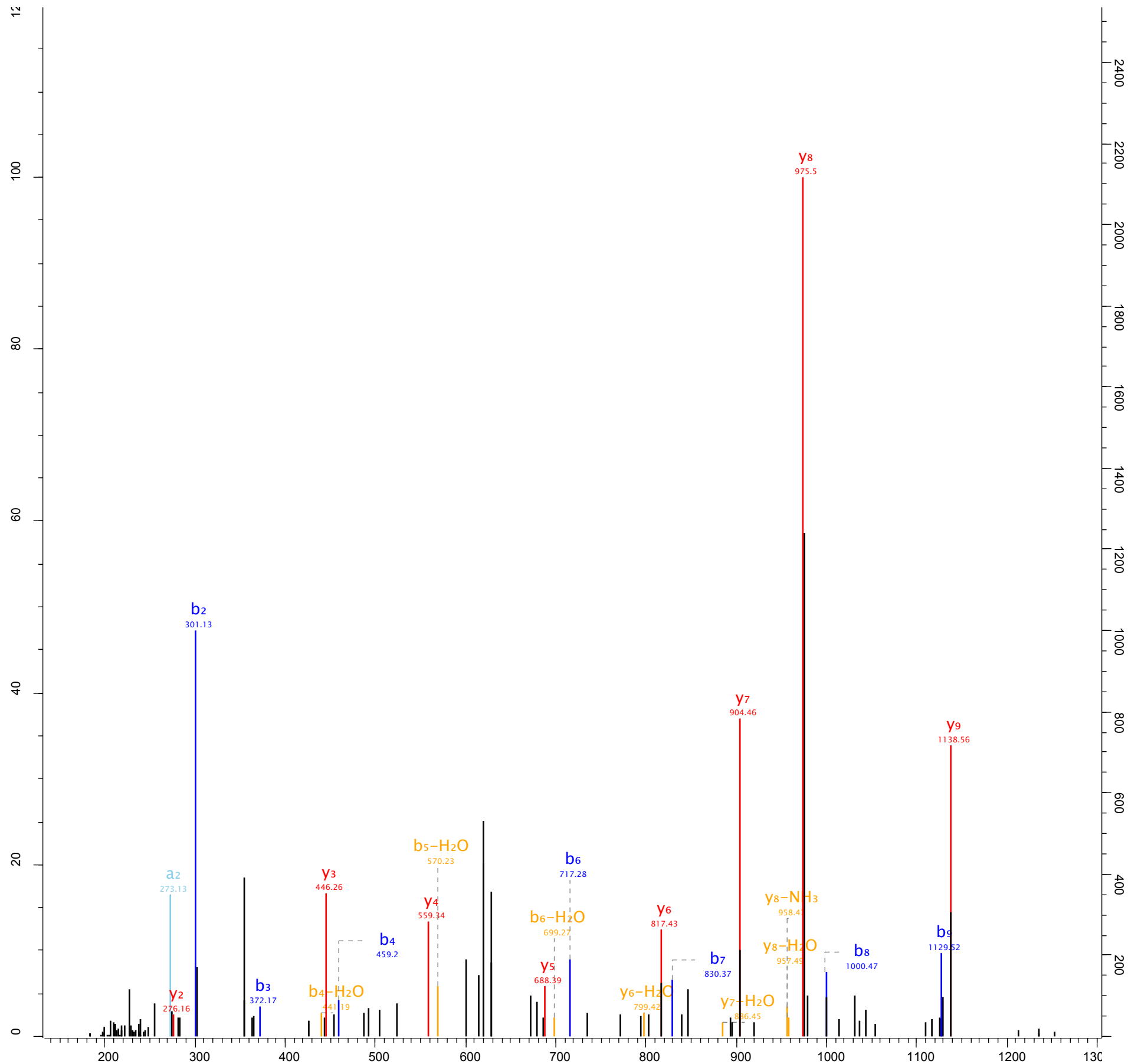


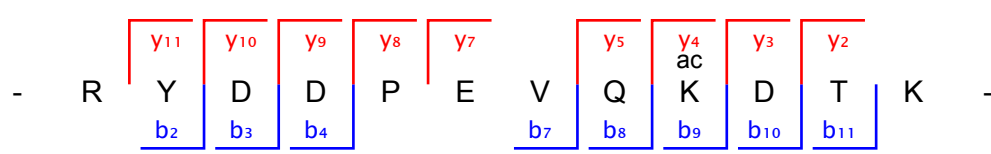
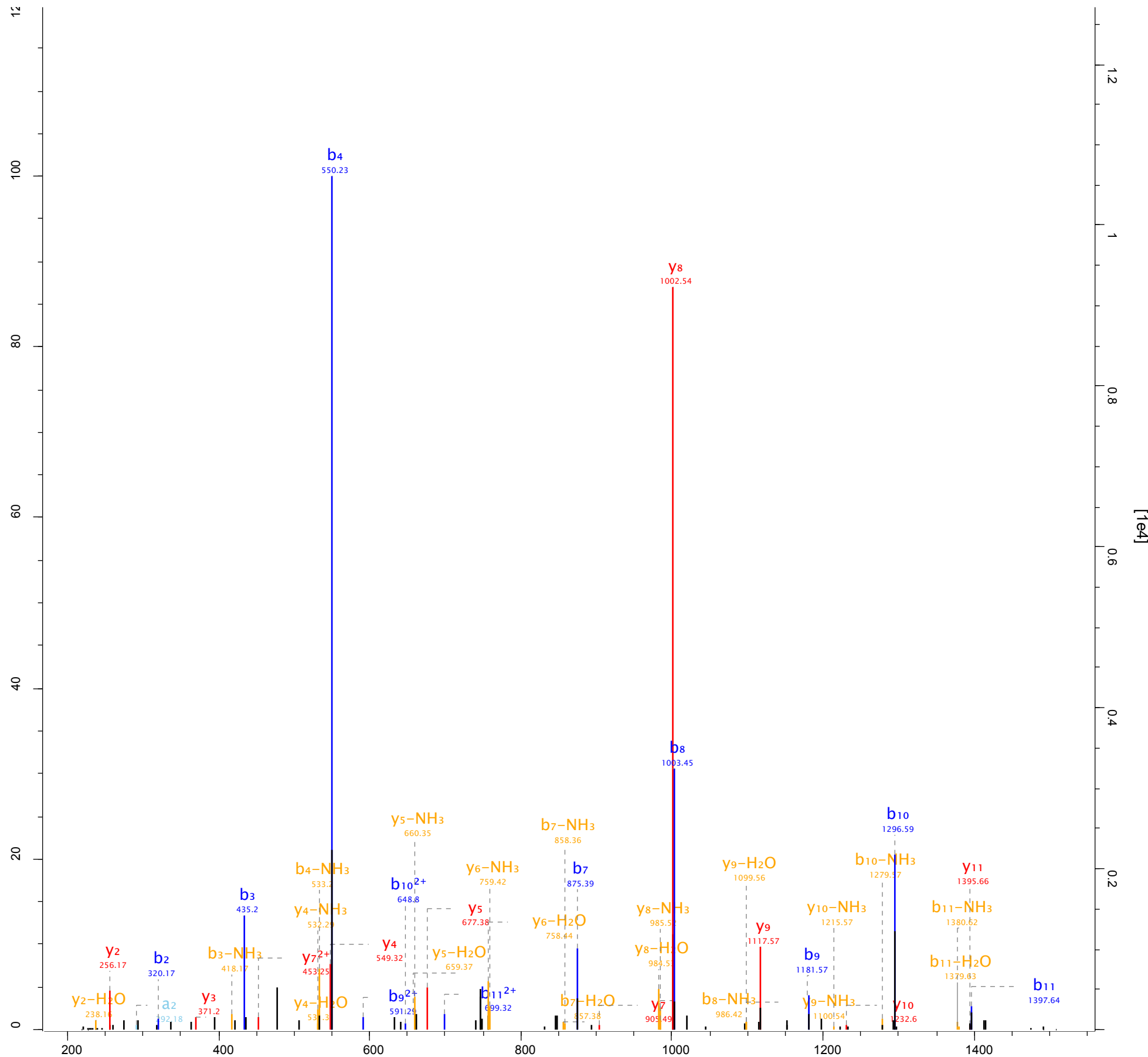


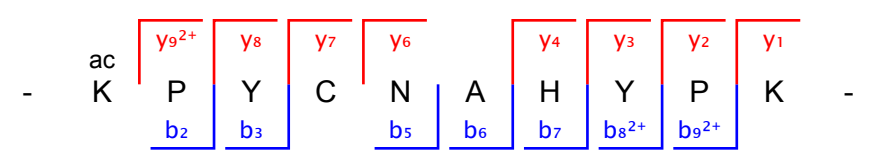
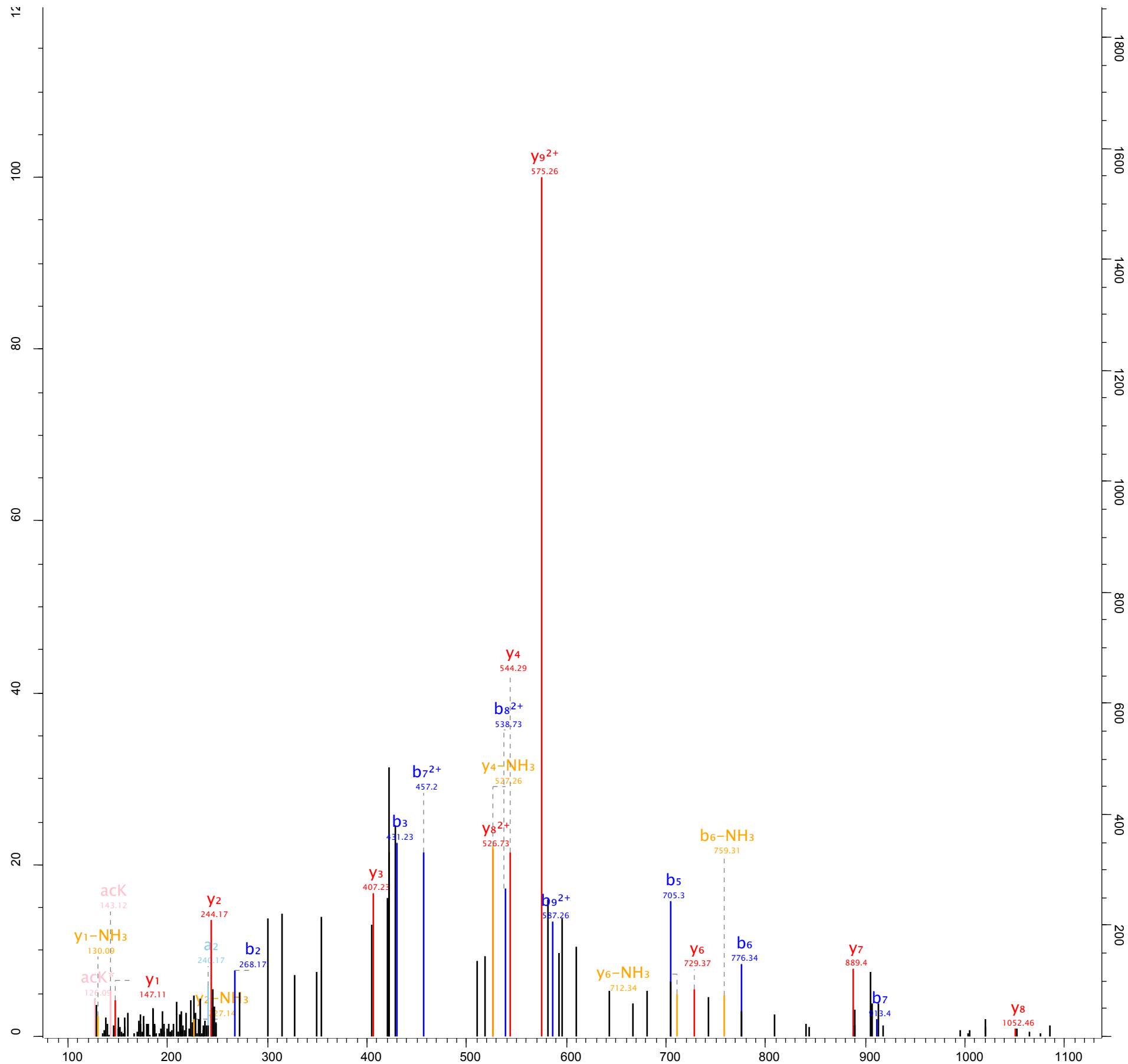
Raw file: 062513_SCW_II_53_10_Vargas_Enriched
 Scan: 10143 Method: ITMS; CID Score: 105.4 m/z: 549.79 Gene names: Myh9

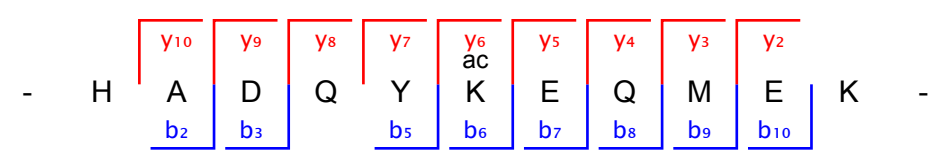
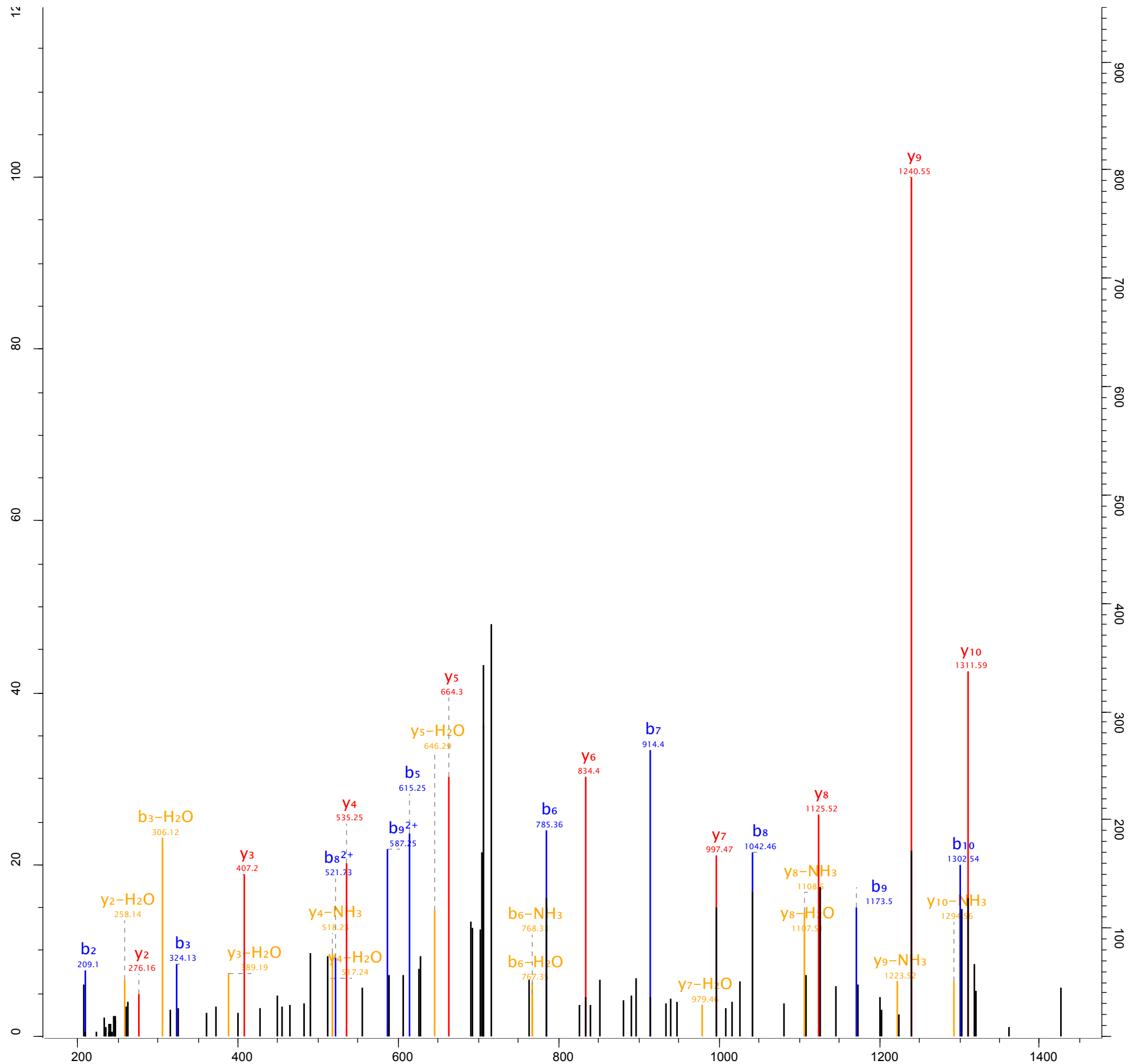


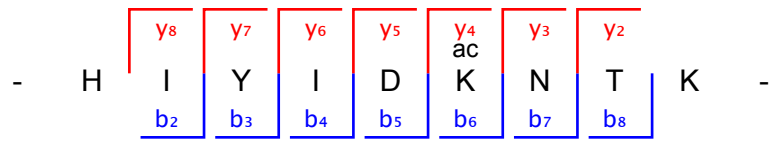
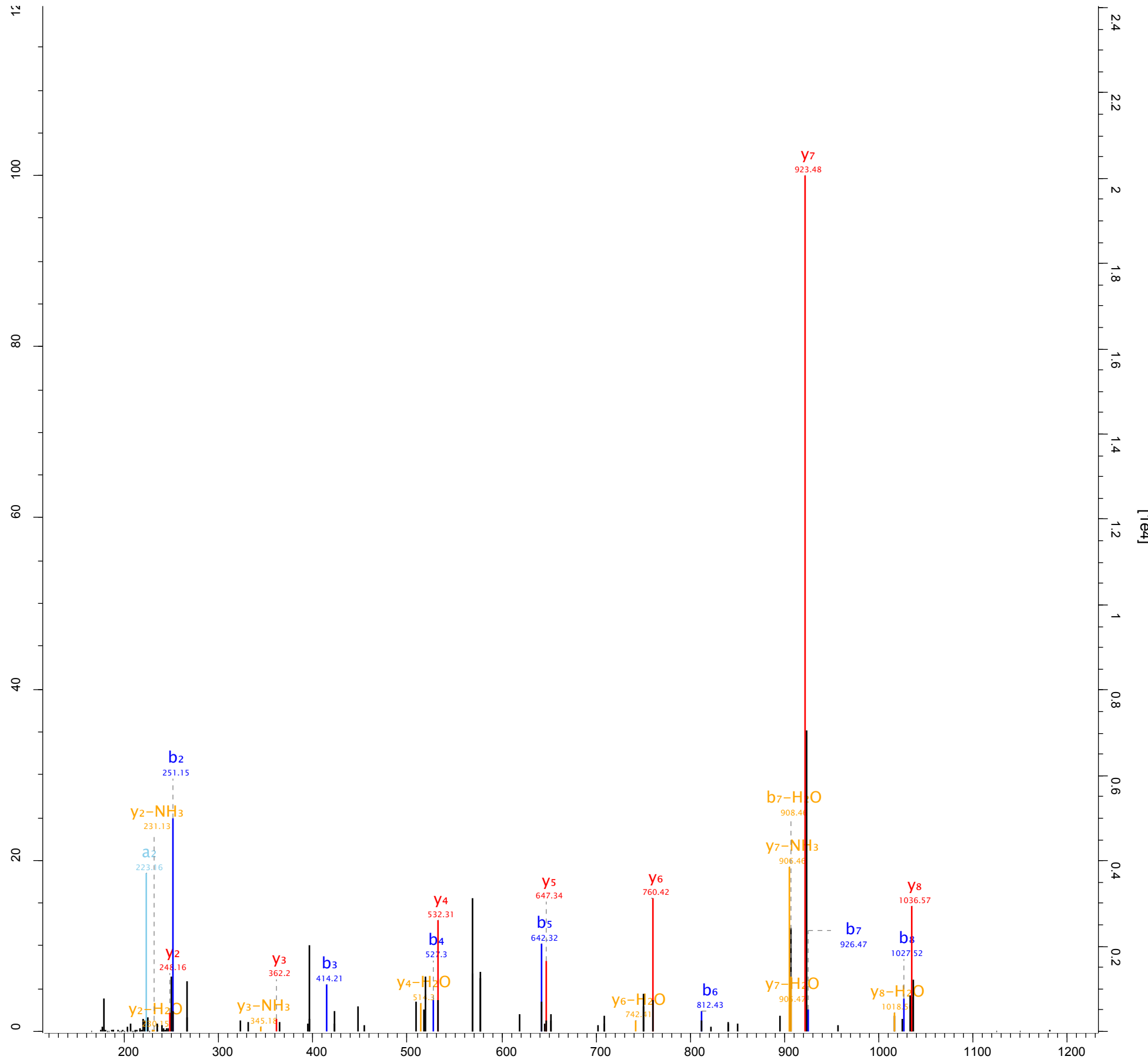


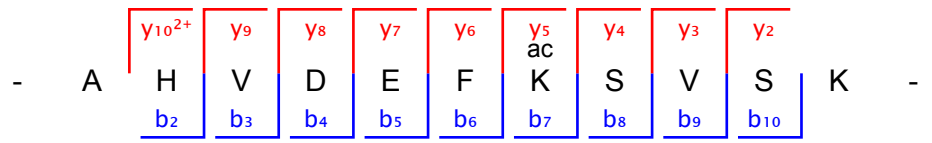
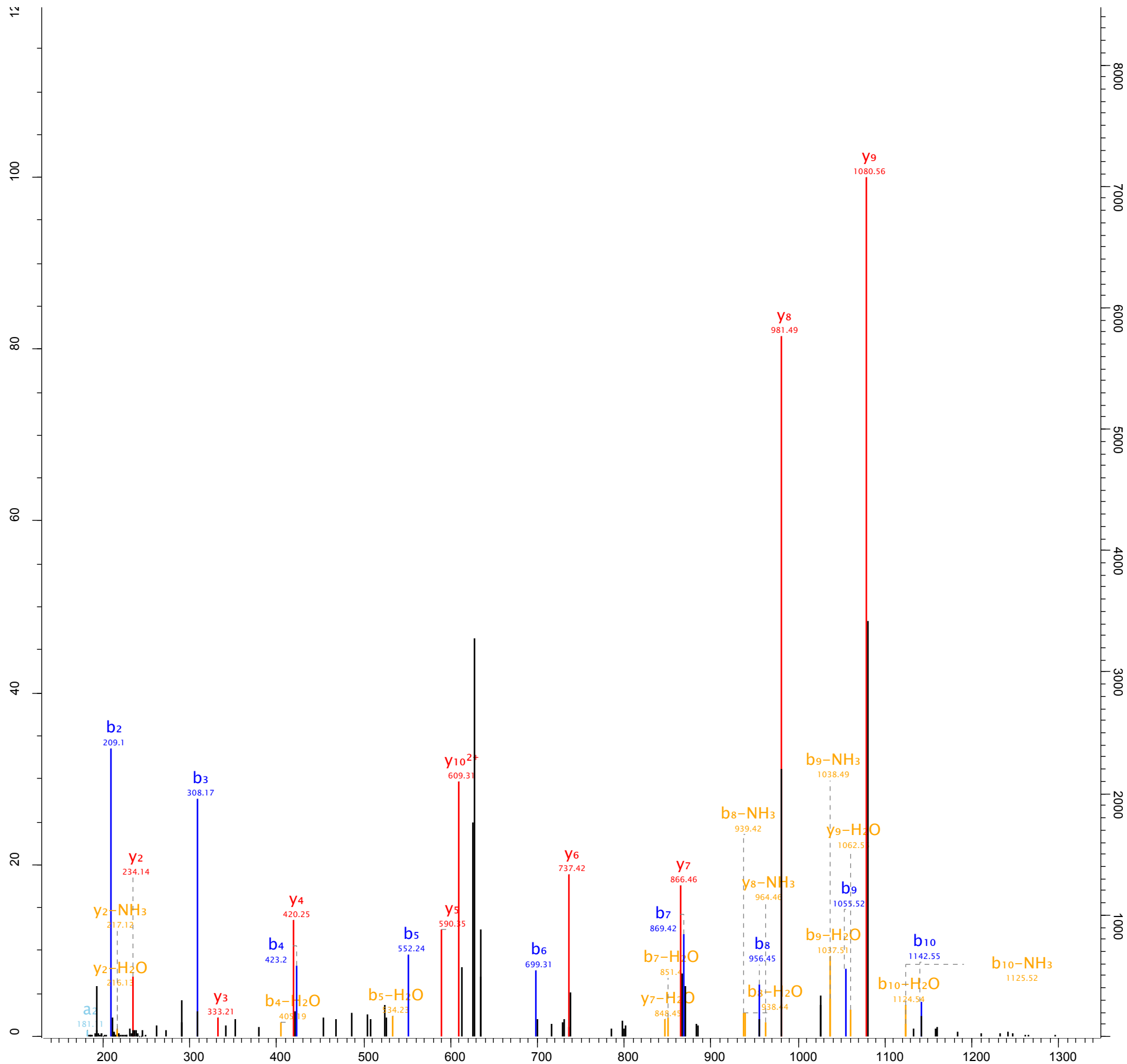


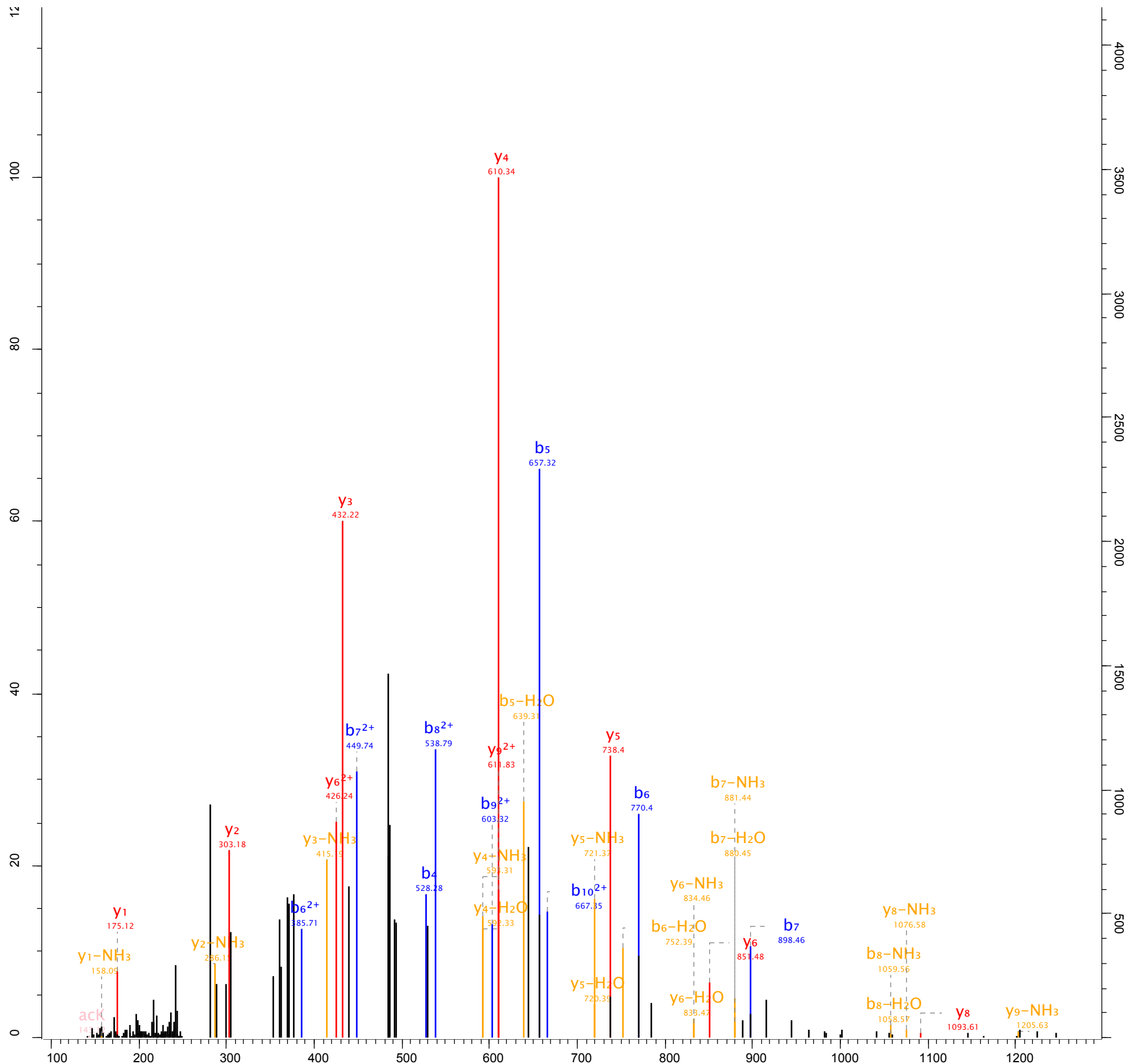








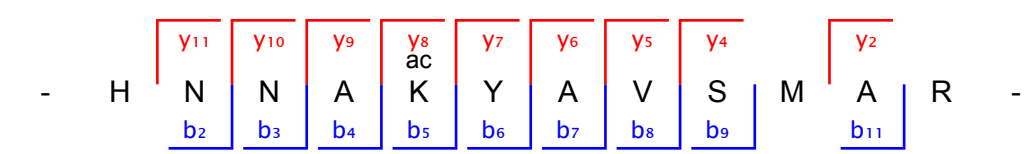
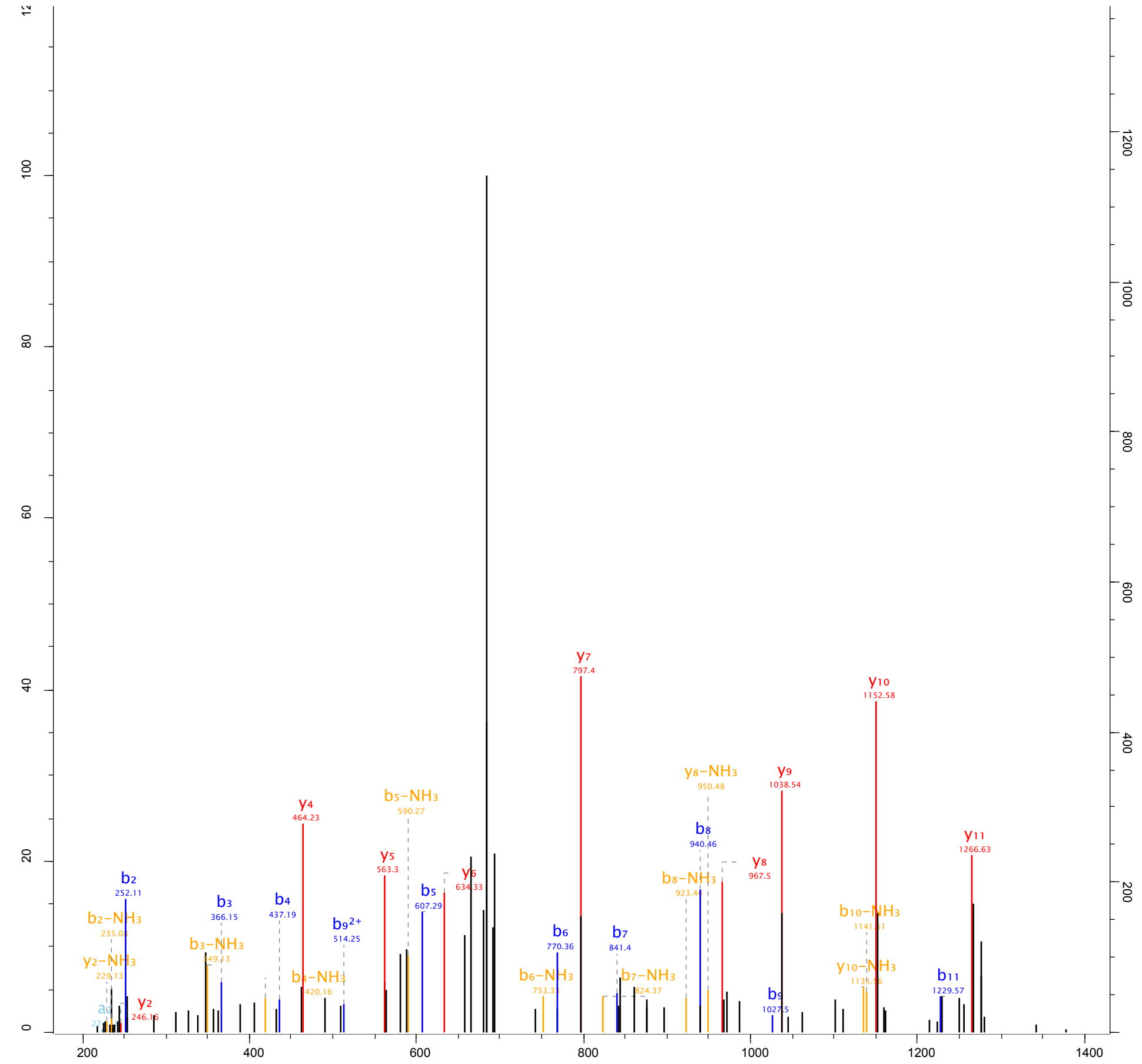


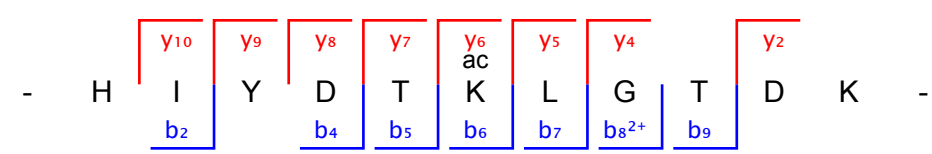
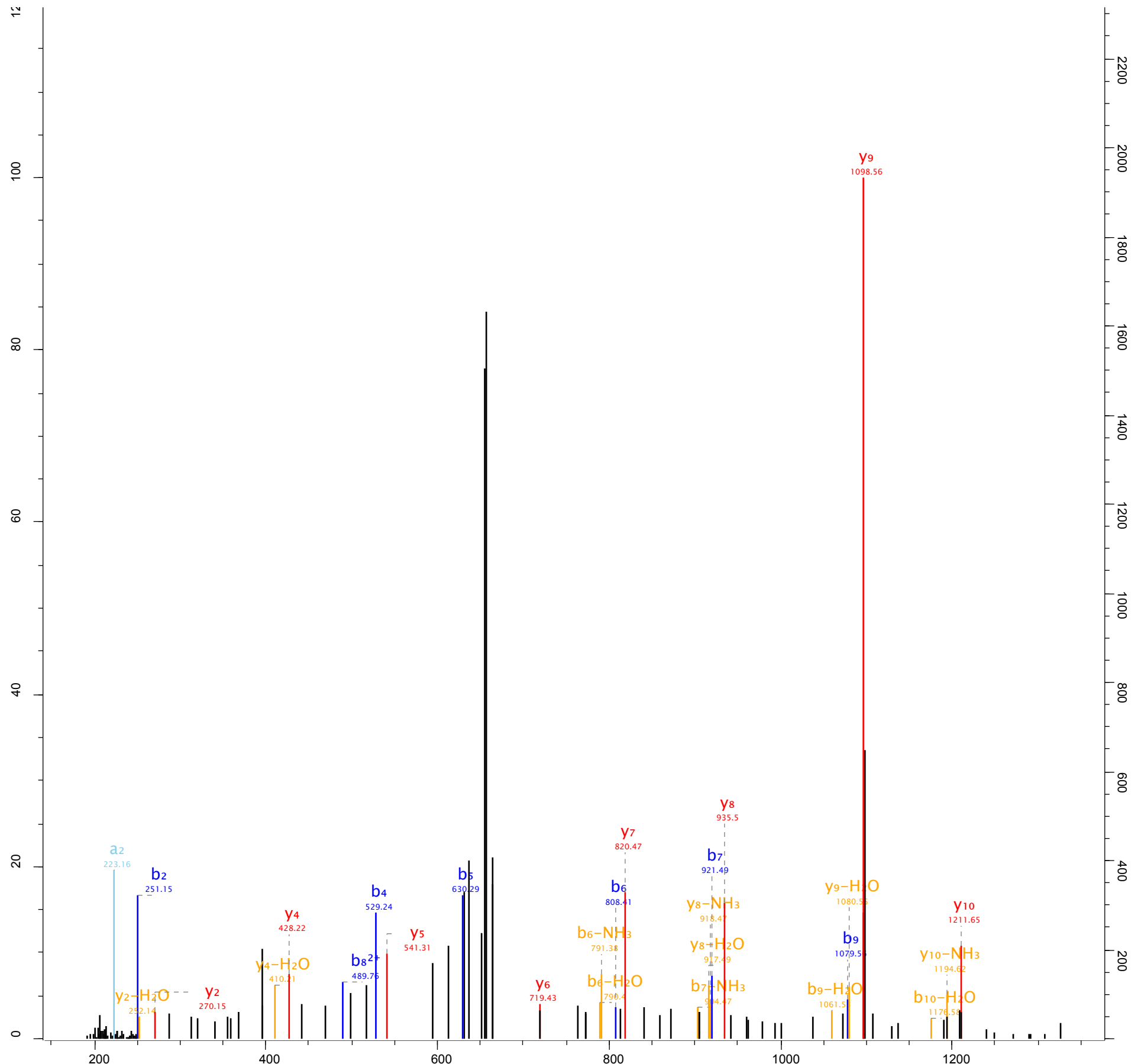


- E R E L E L Q K E Q R -

y₉²⁺
y₈
y₆
y₅
y₄
ac
y₃
y₂
y₁

b₄
b₅
b₆
b₇
b₈²⁺
b₉²⁺
b₁₀²⁺





062513_SCW_II_53_10_Vargas_Enriched

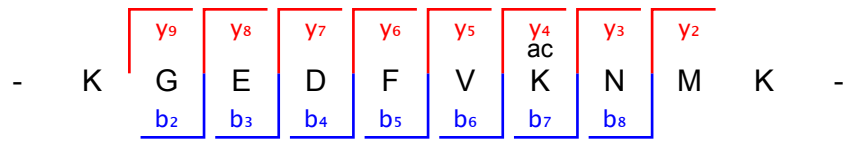
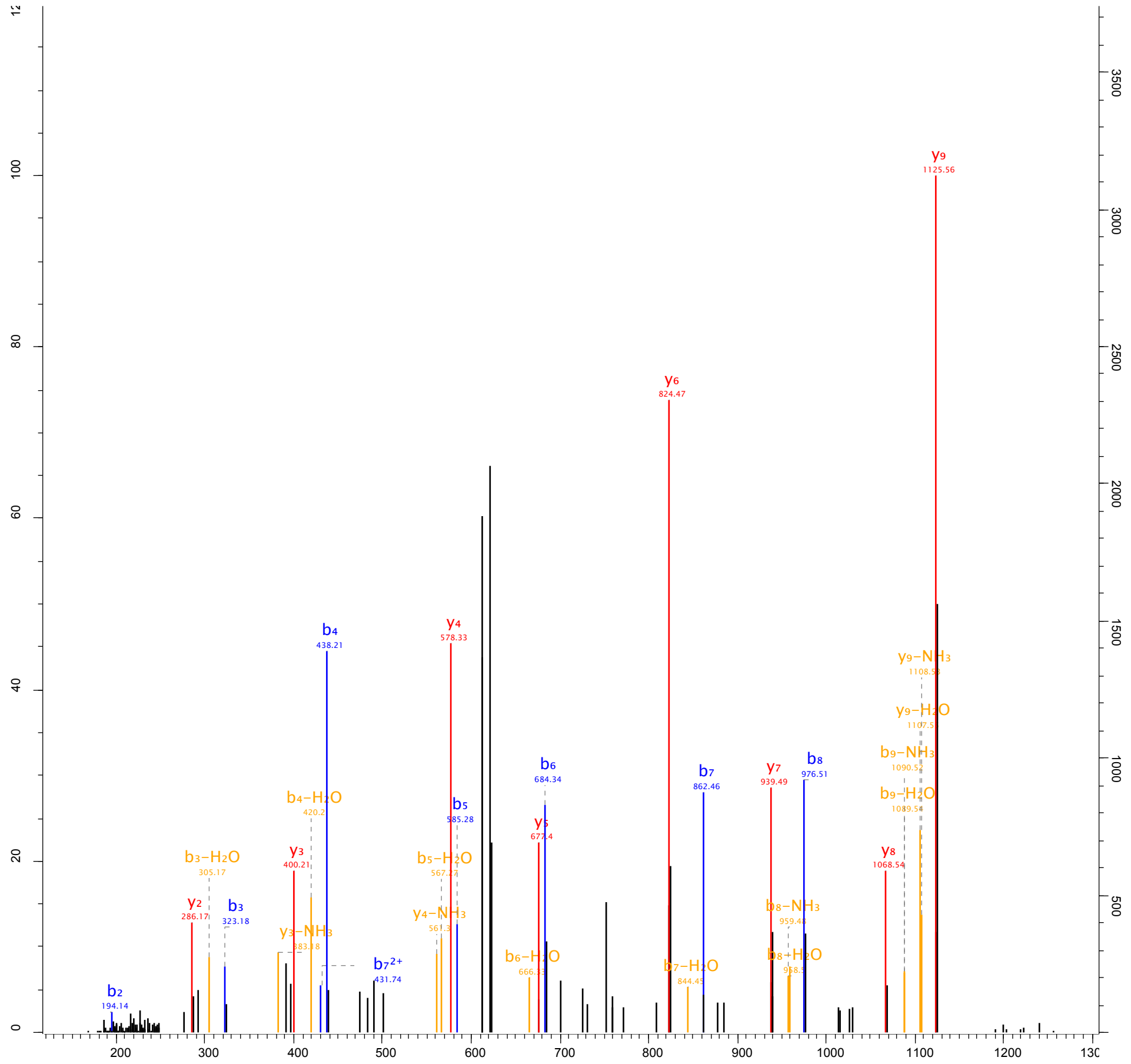
14139

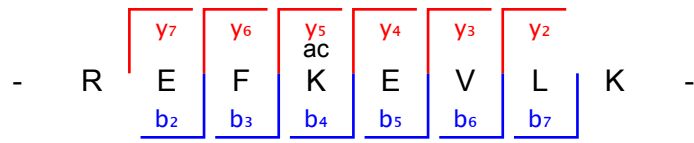
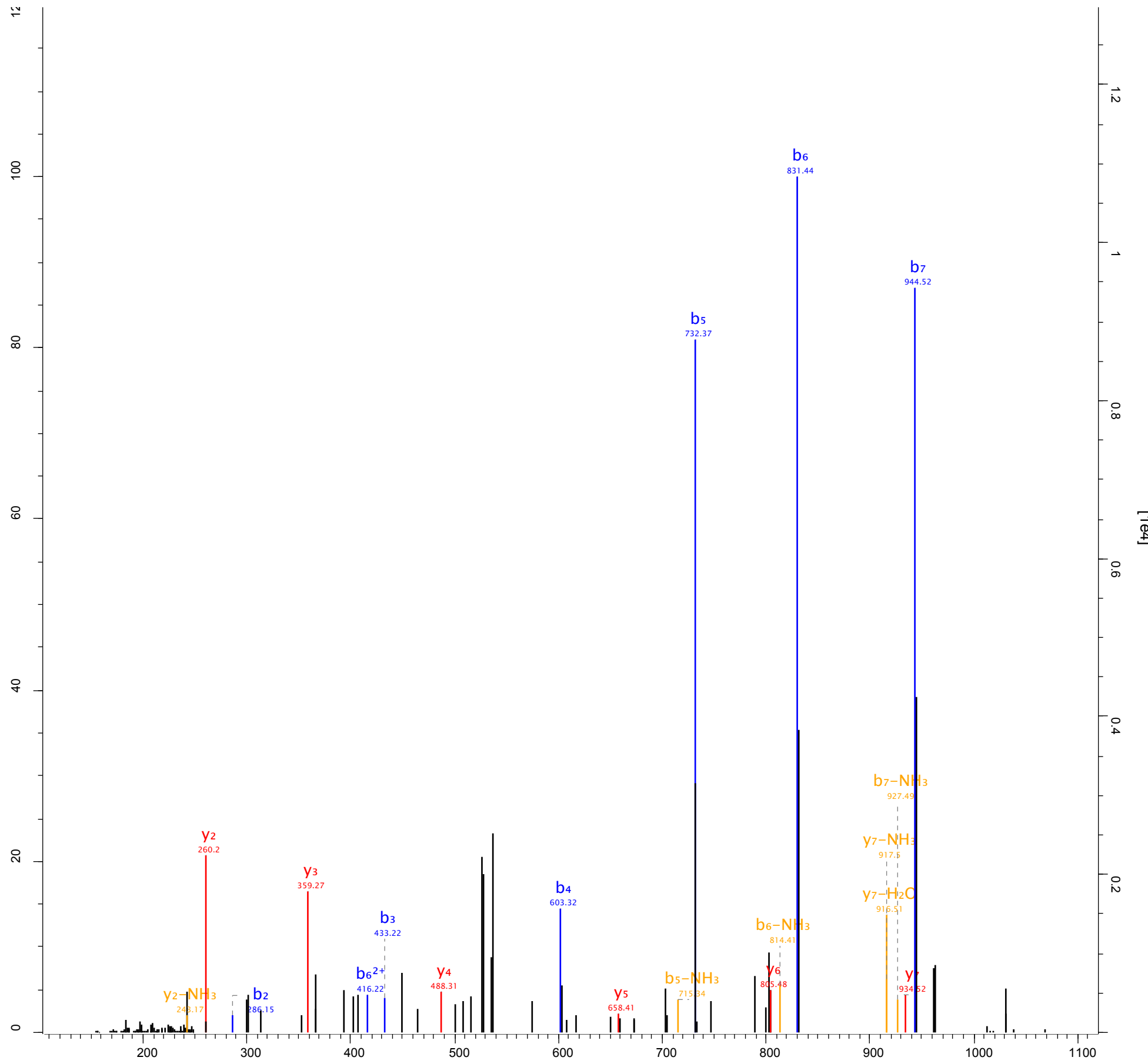
ITMS; CID

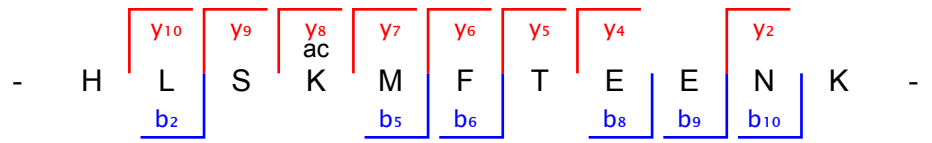
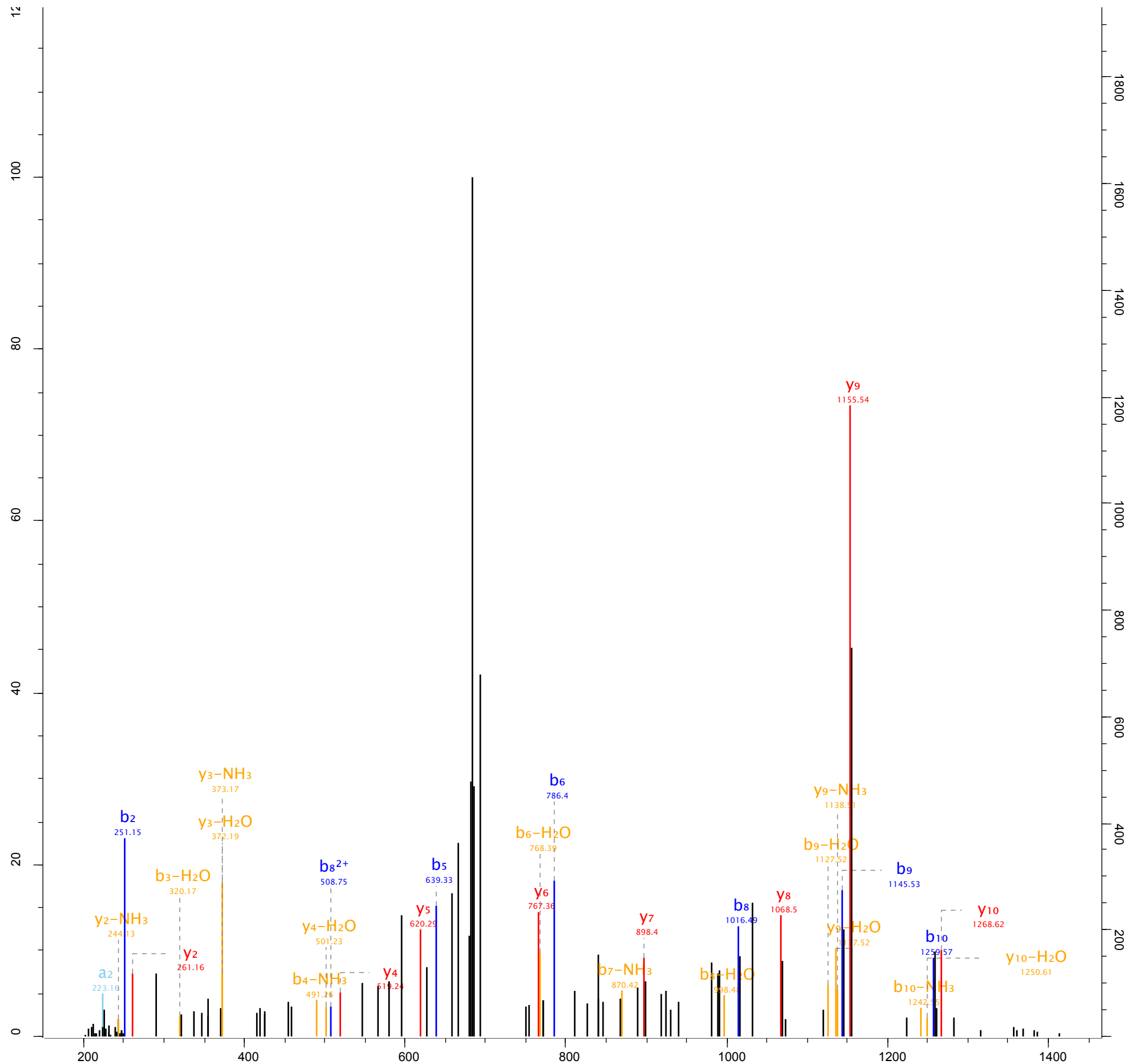
156.01

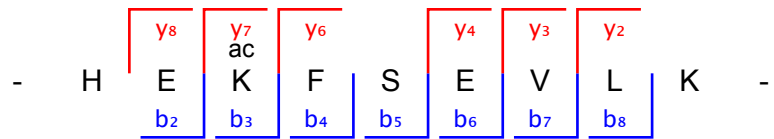
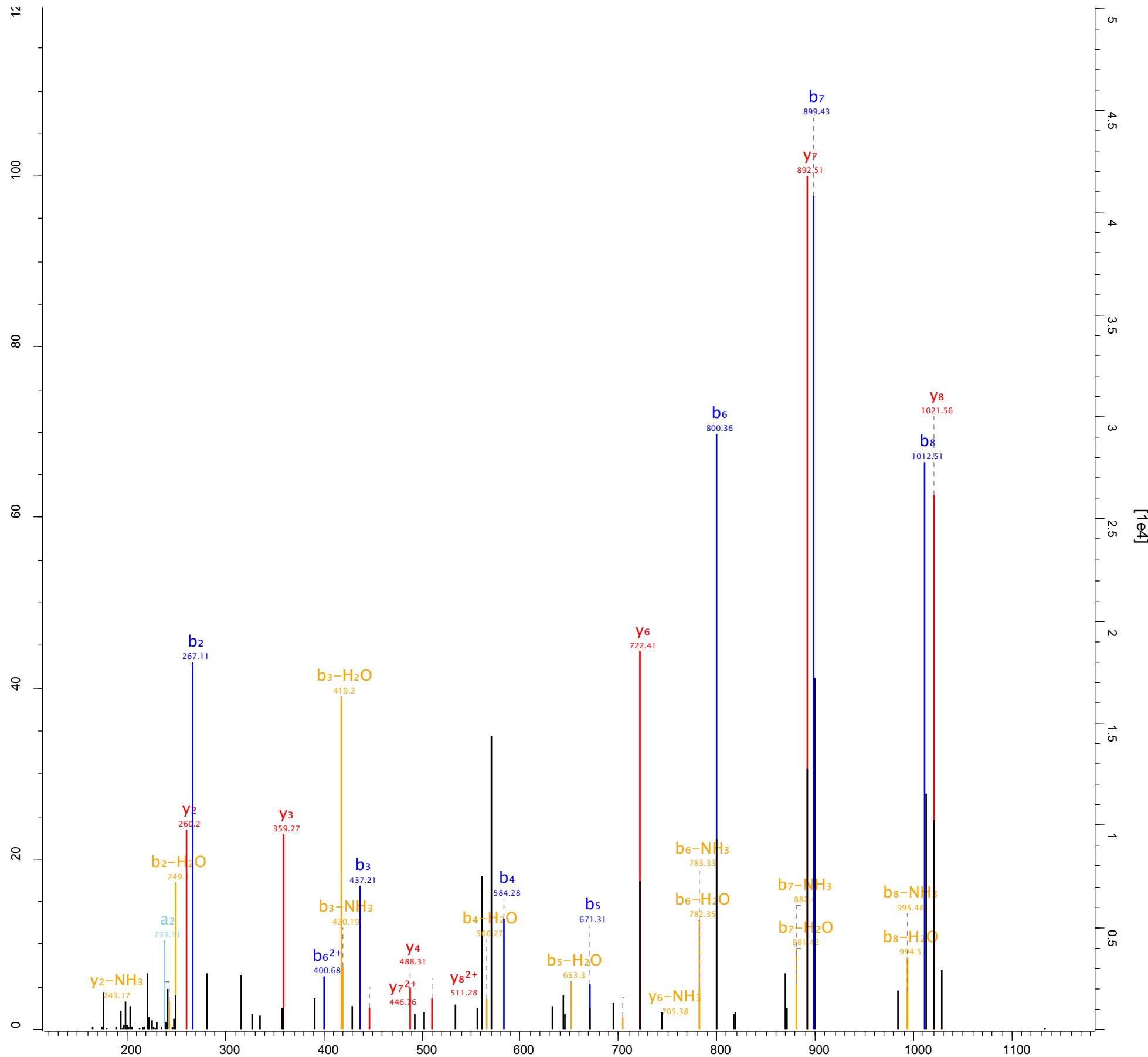
631.34

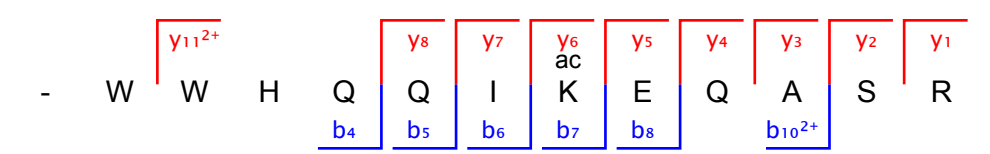
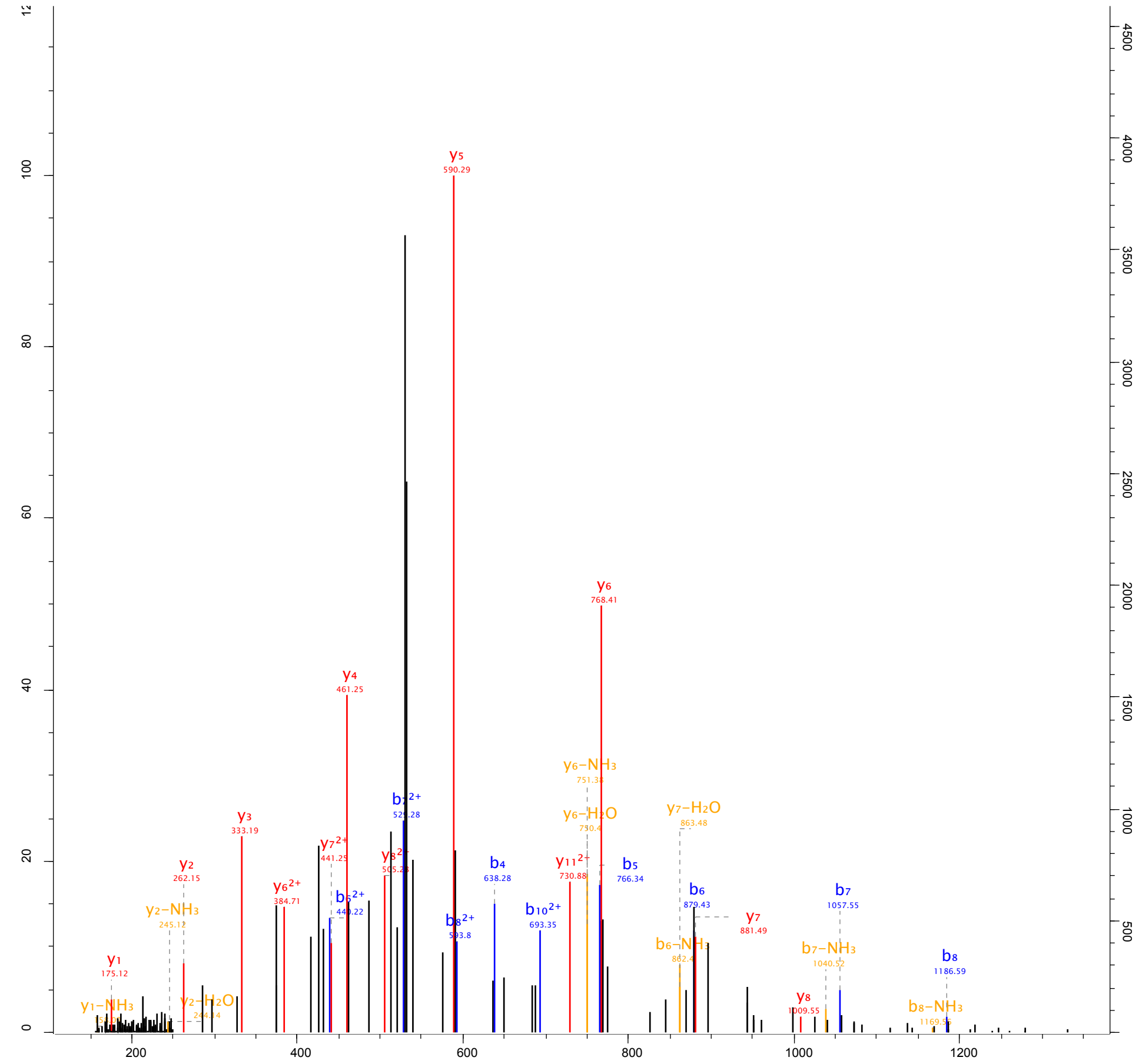
Mdh2

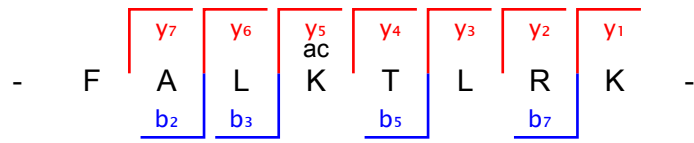
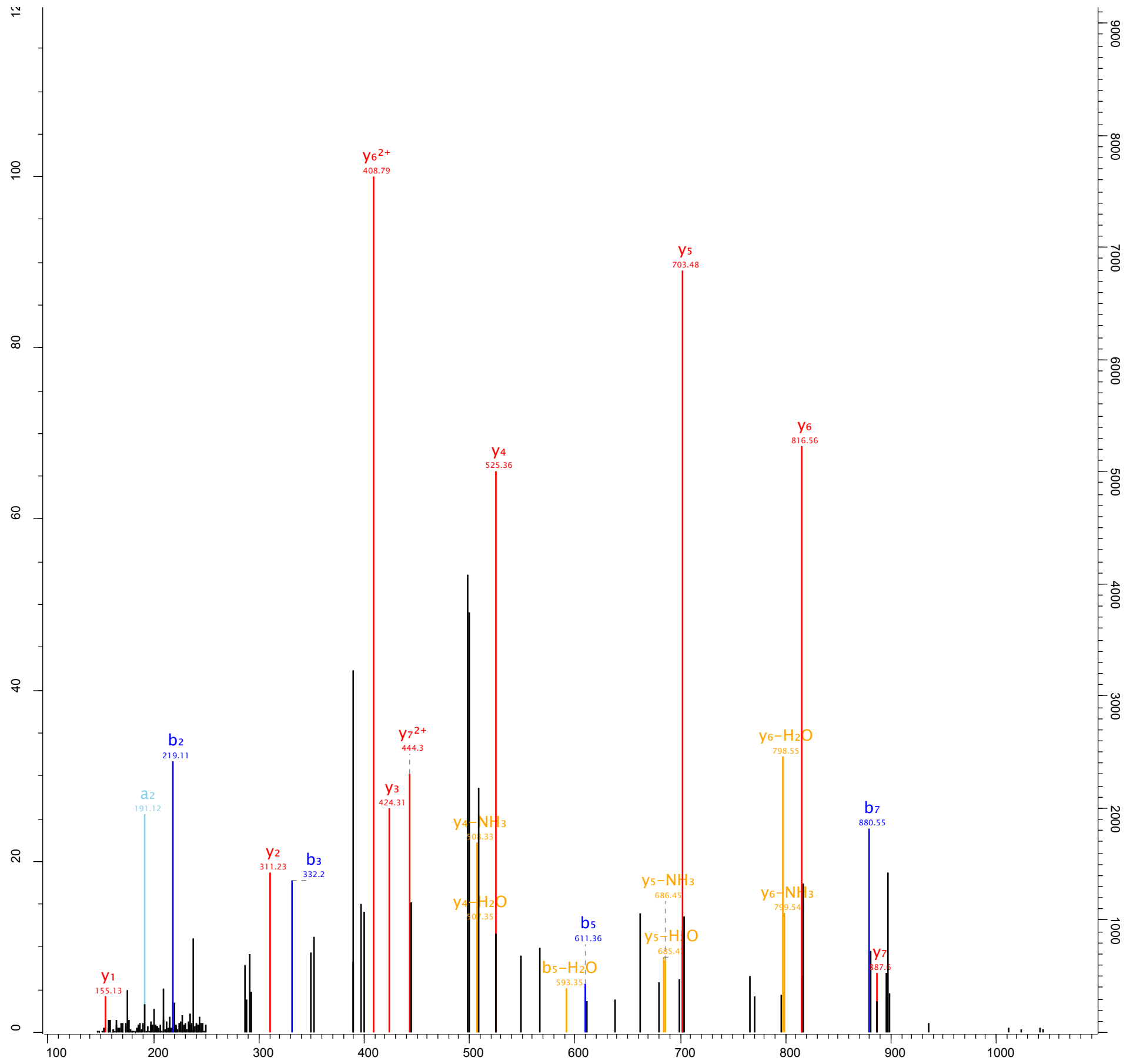


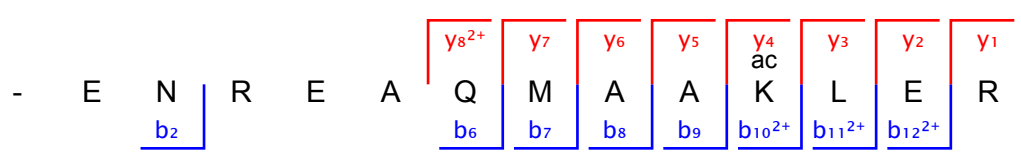
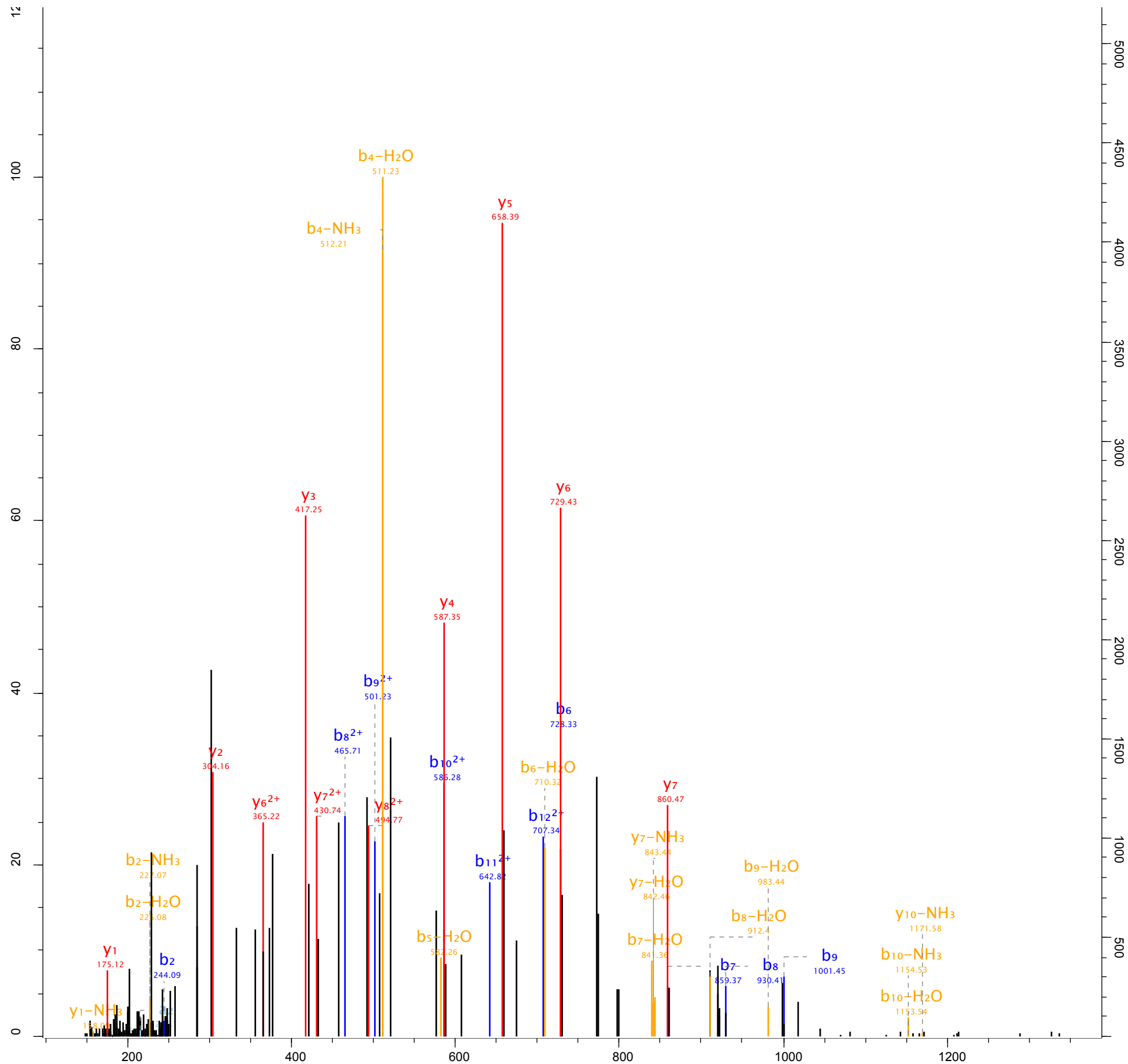


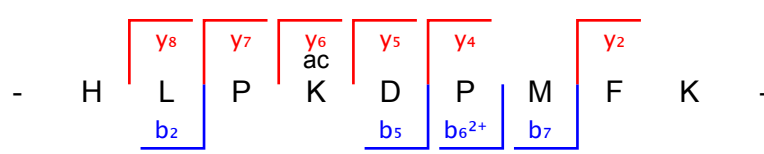
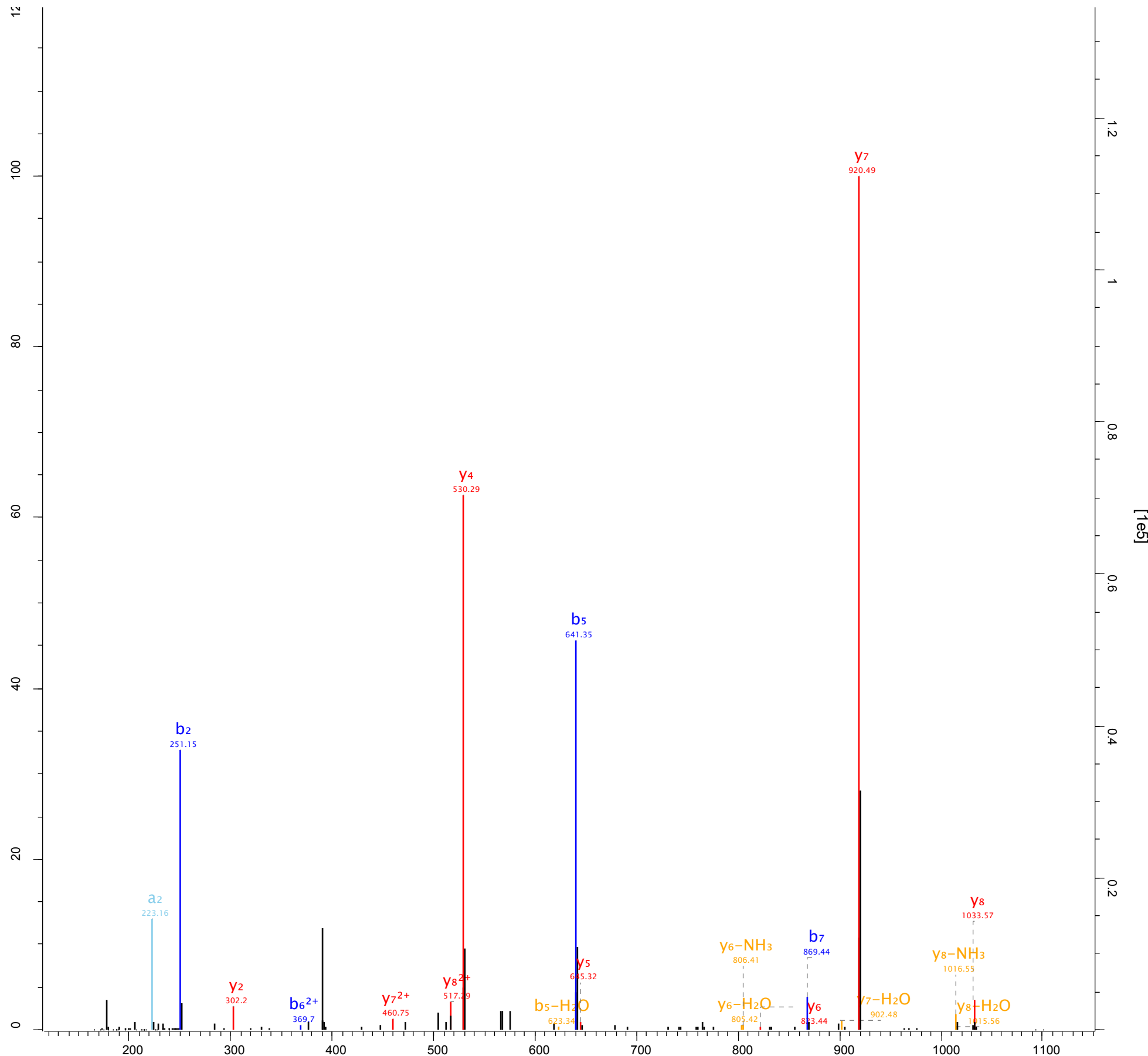


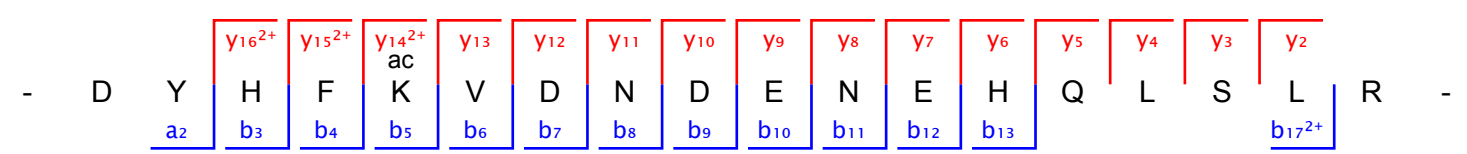
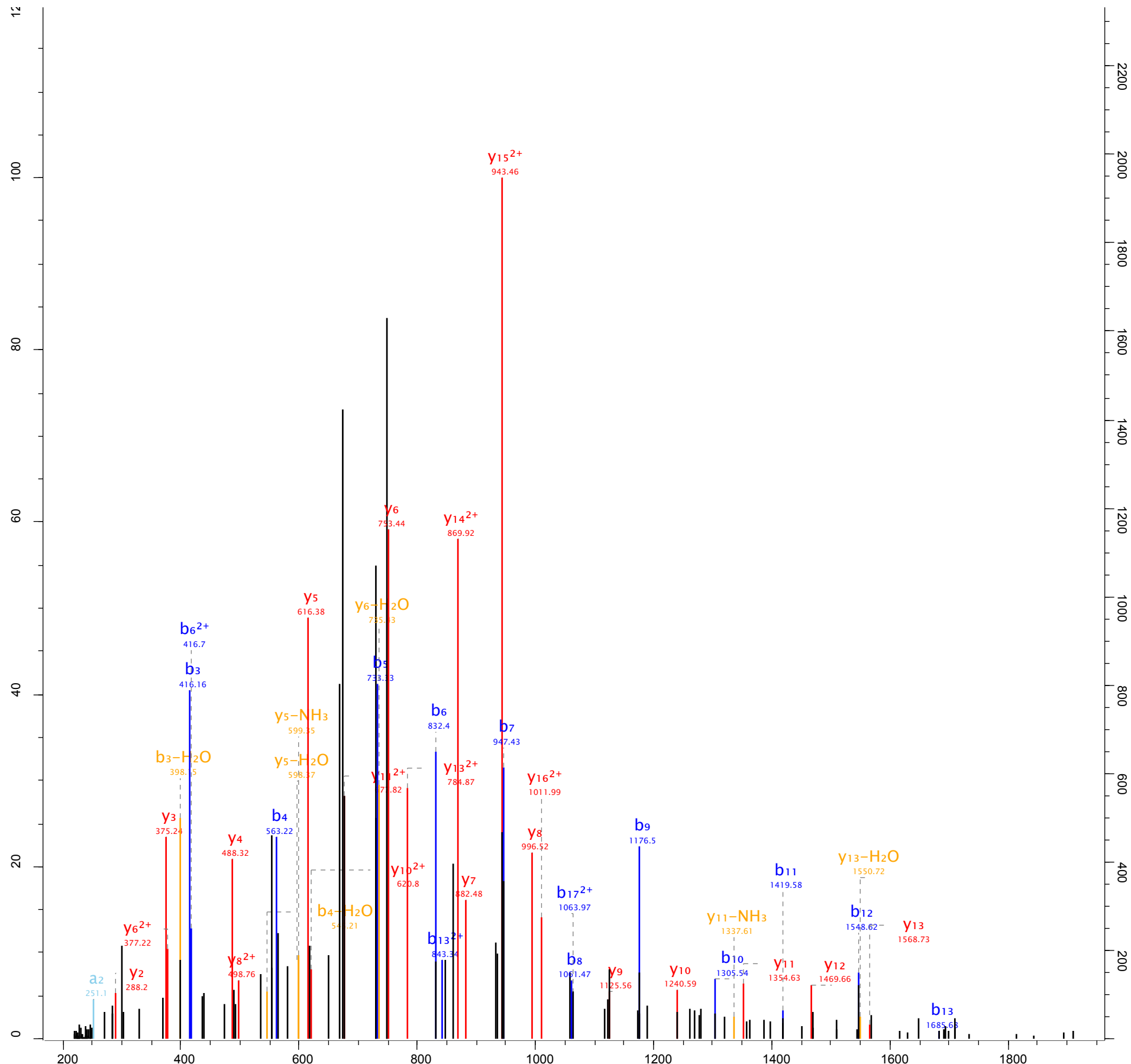


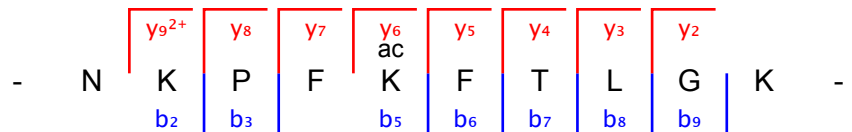
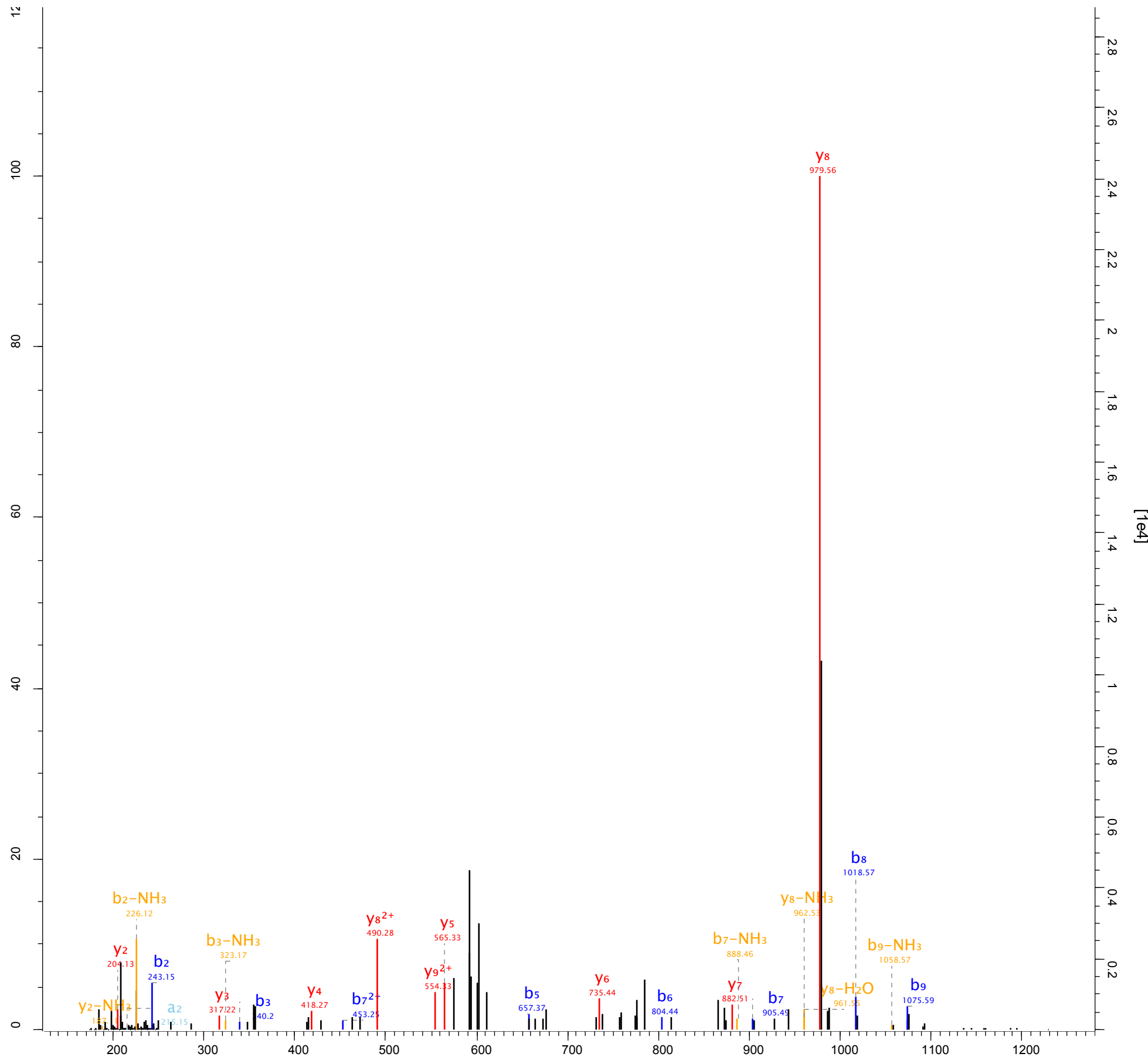


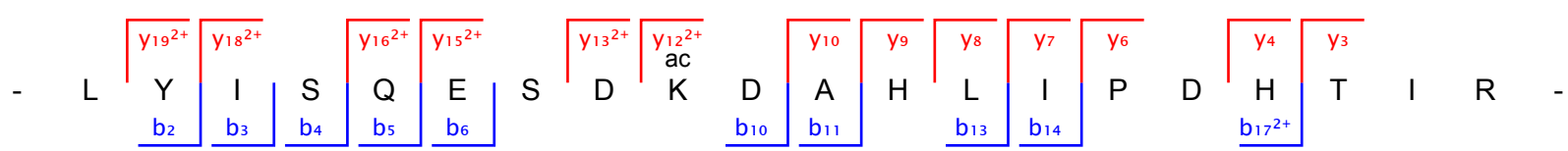
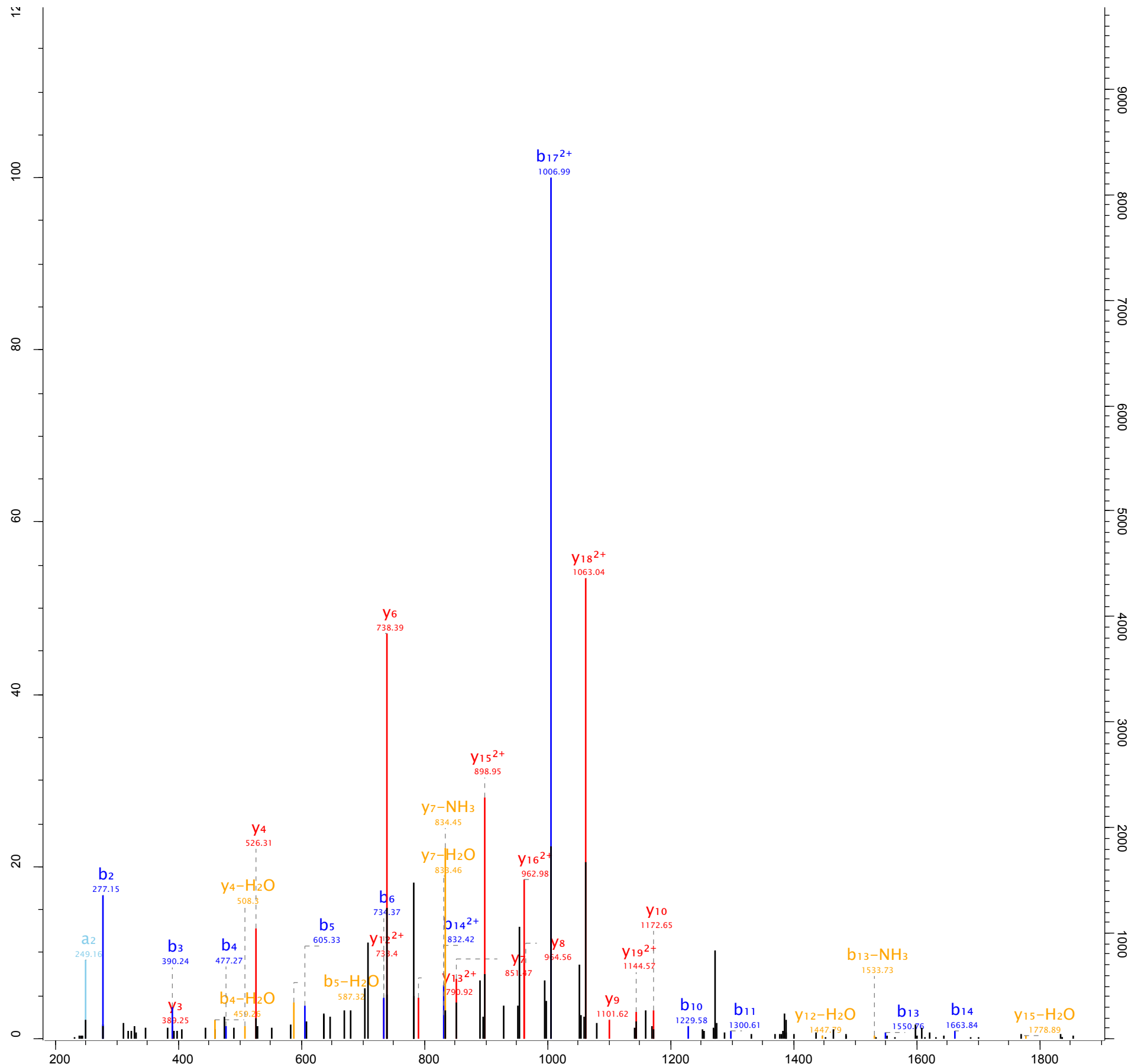


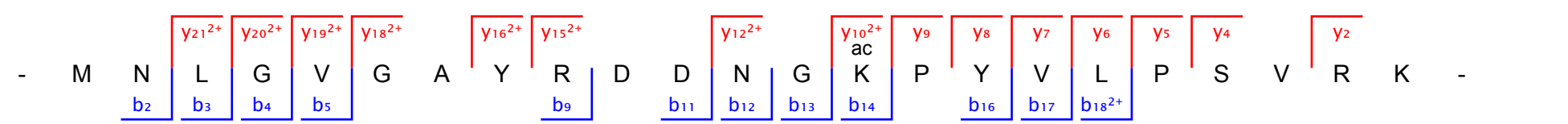
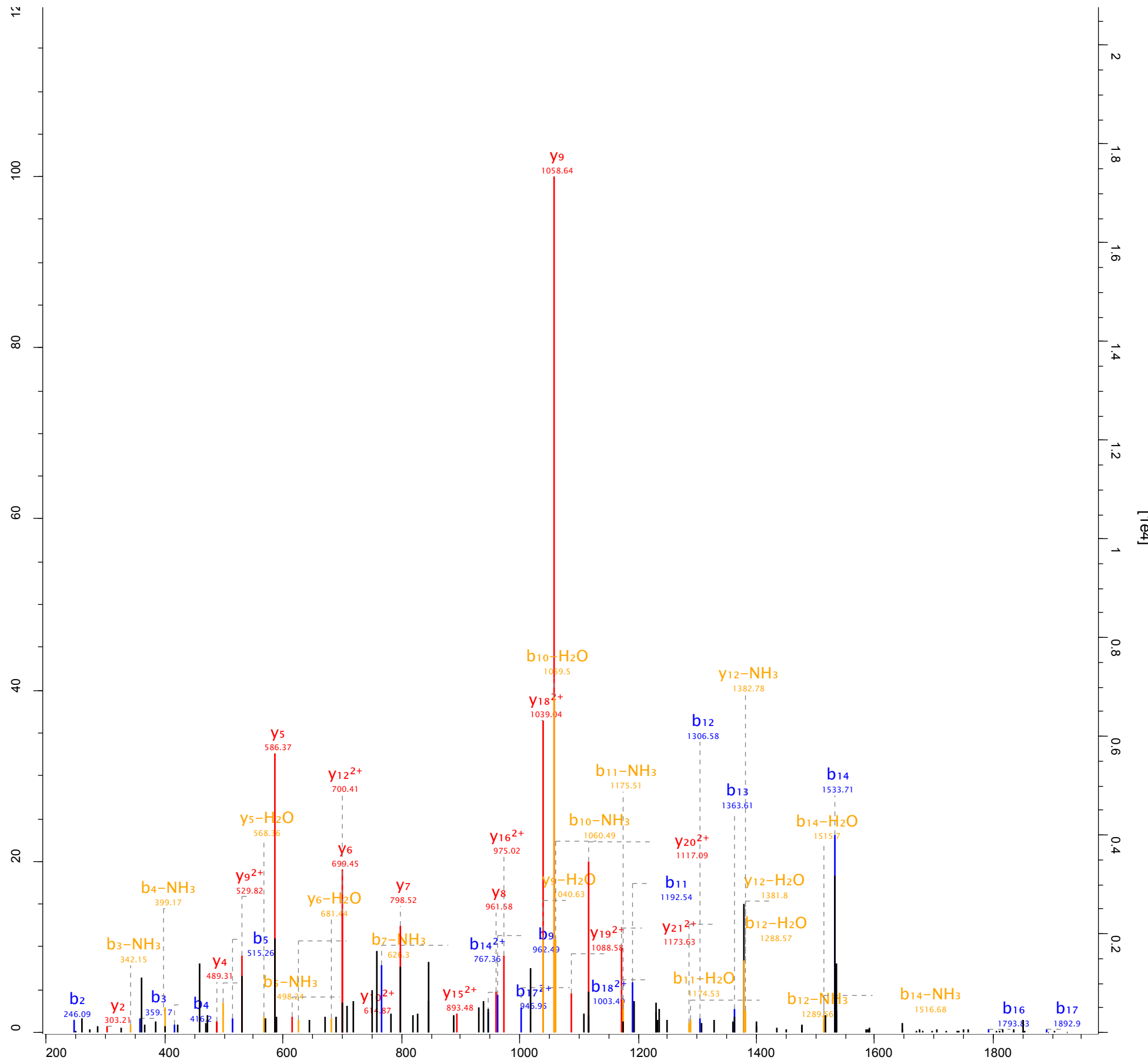












062513_SCW_II_53_10_Vargas_Enriched

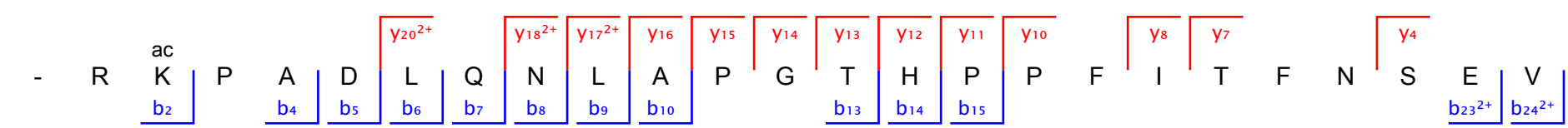
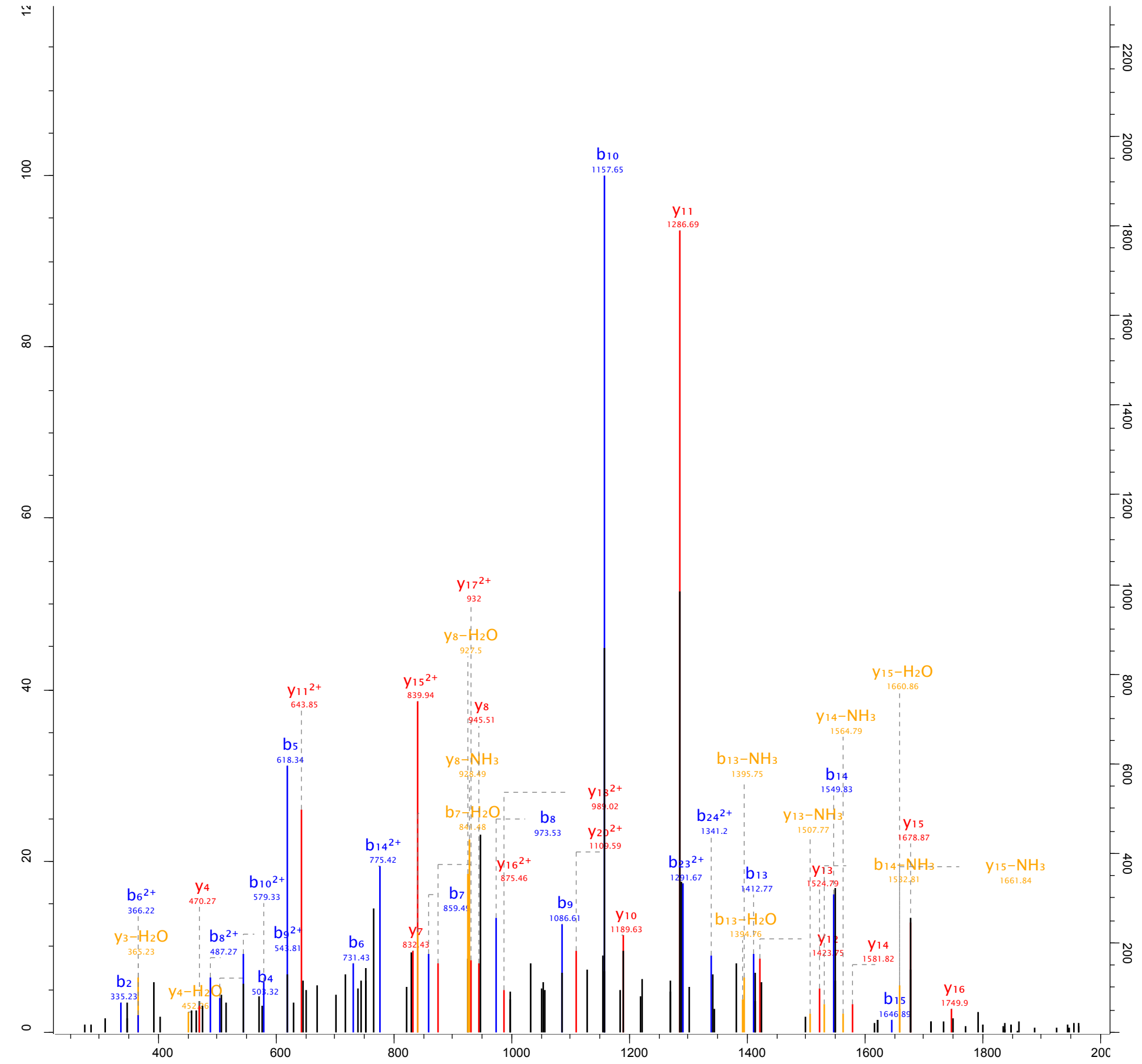
21419

ITMS; CID

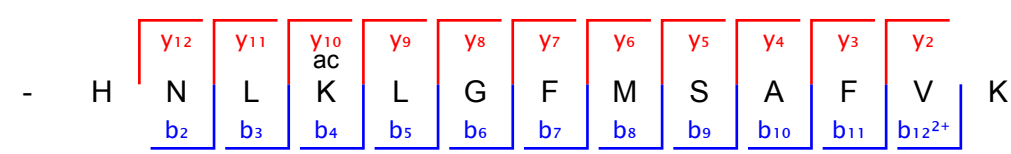
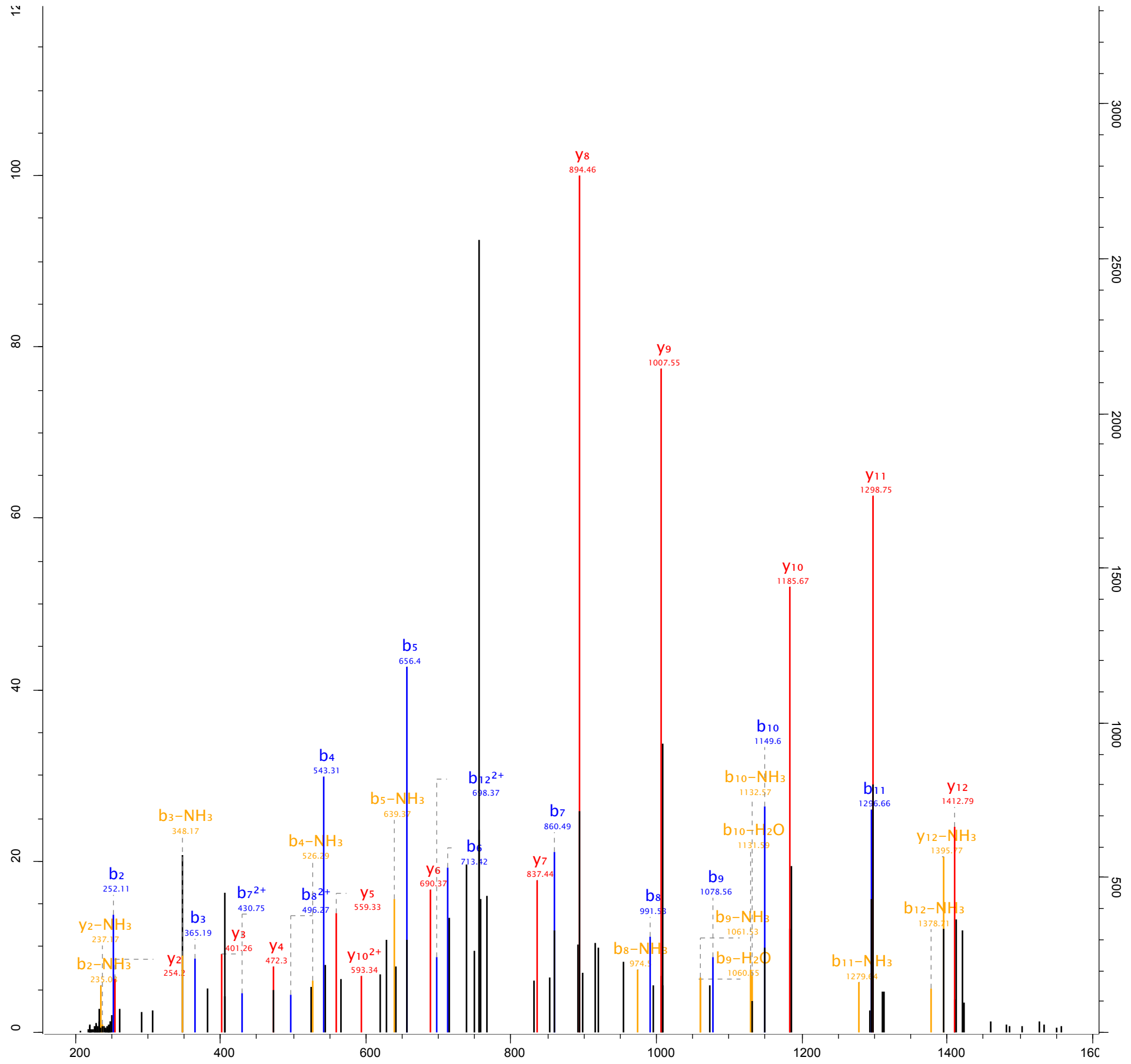
168.12

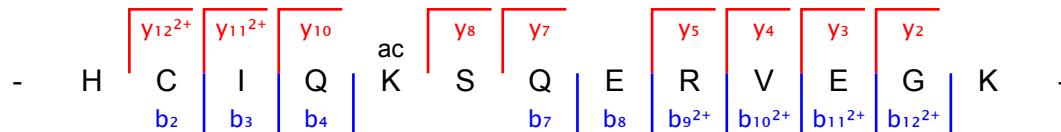
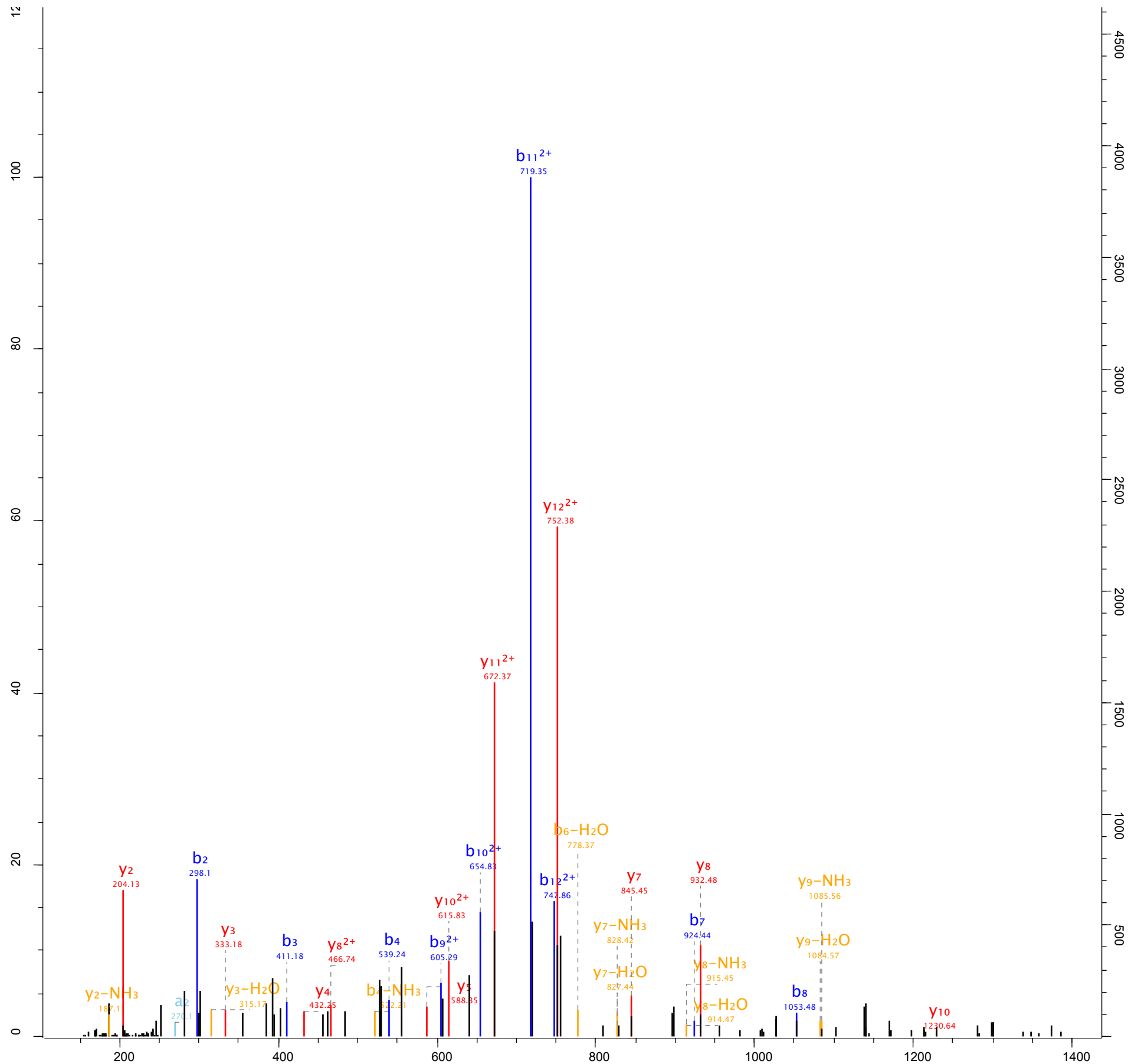
946.17

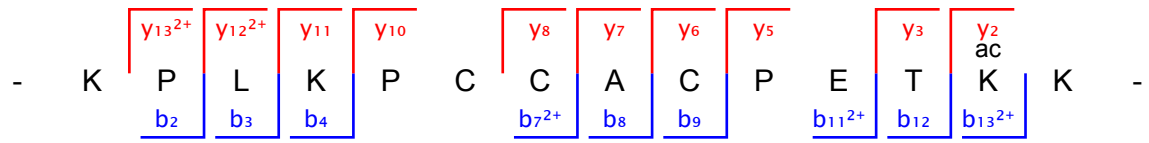
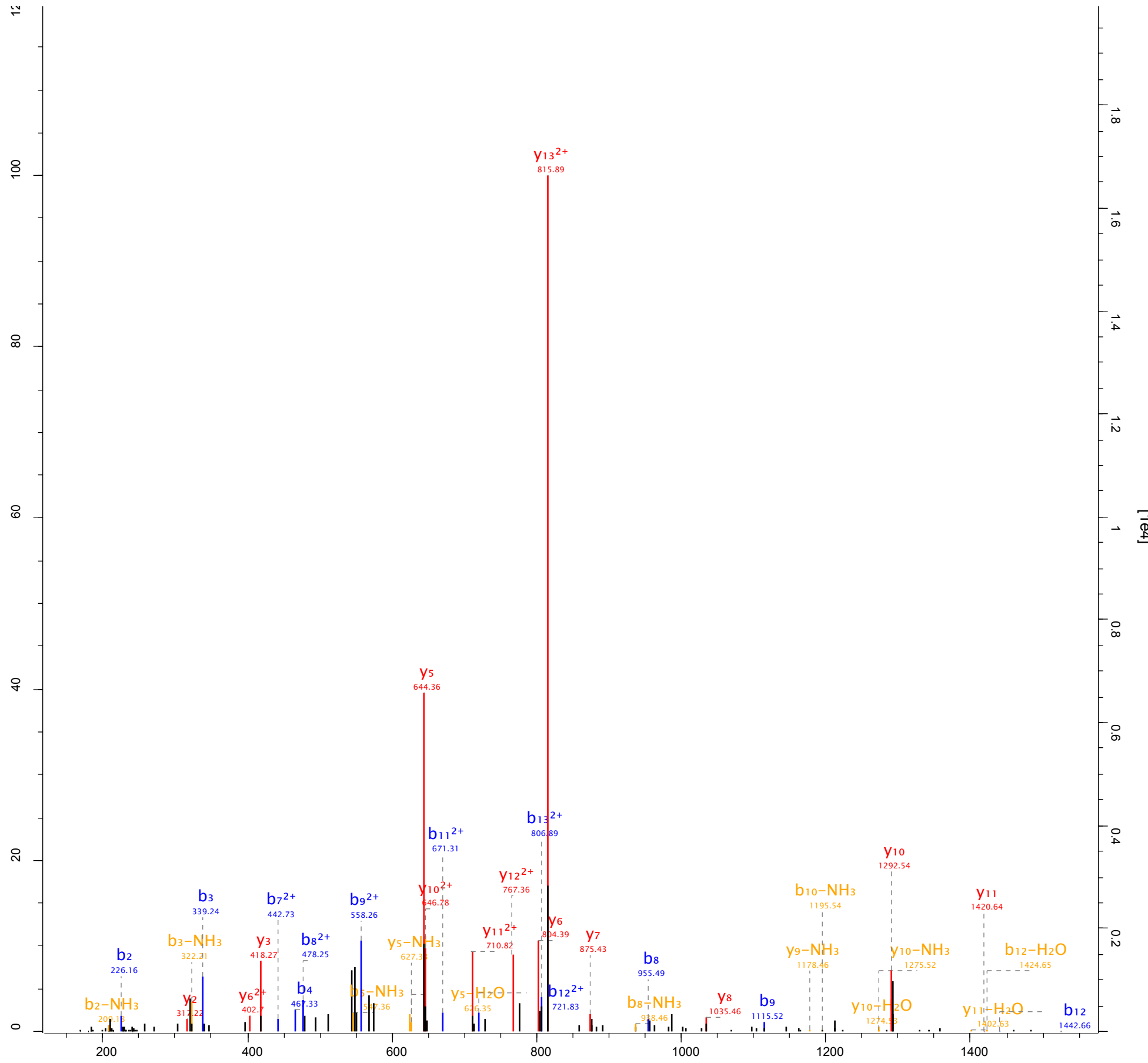
Clic4

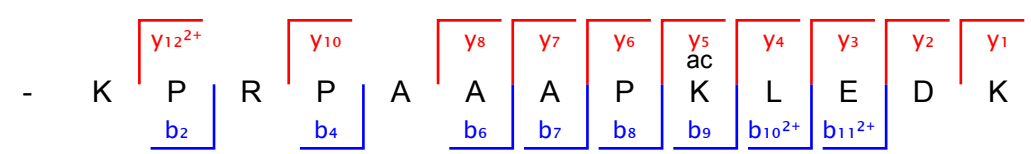
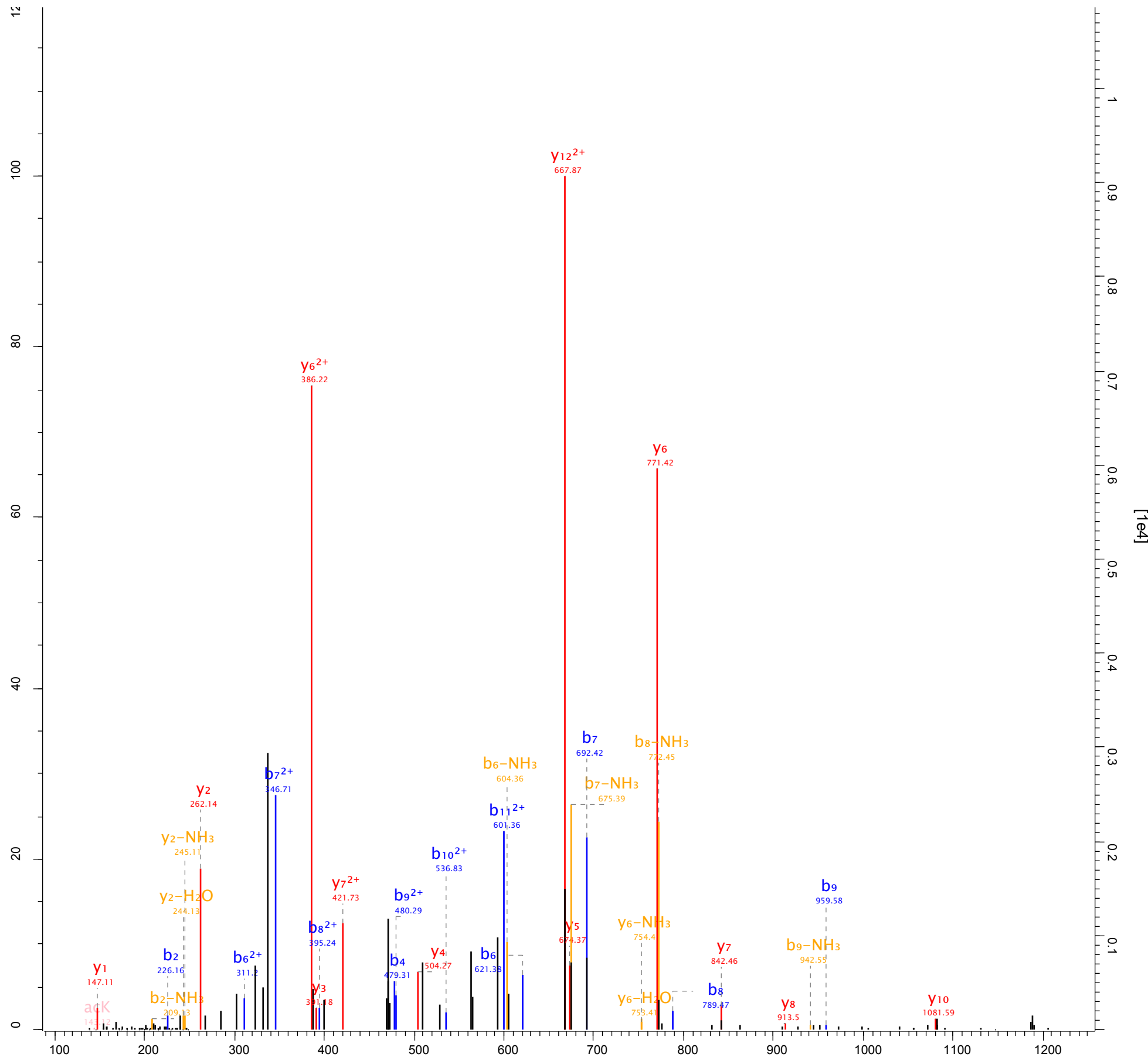


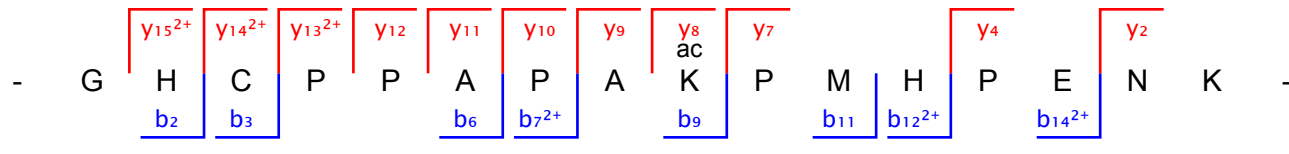
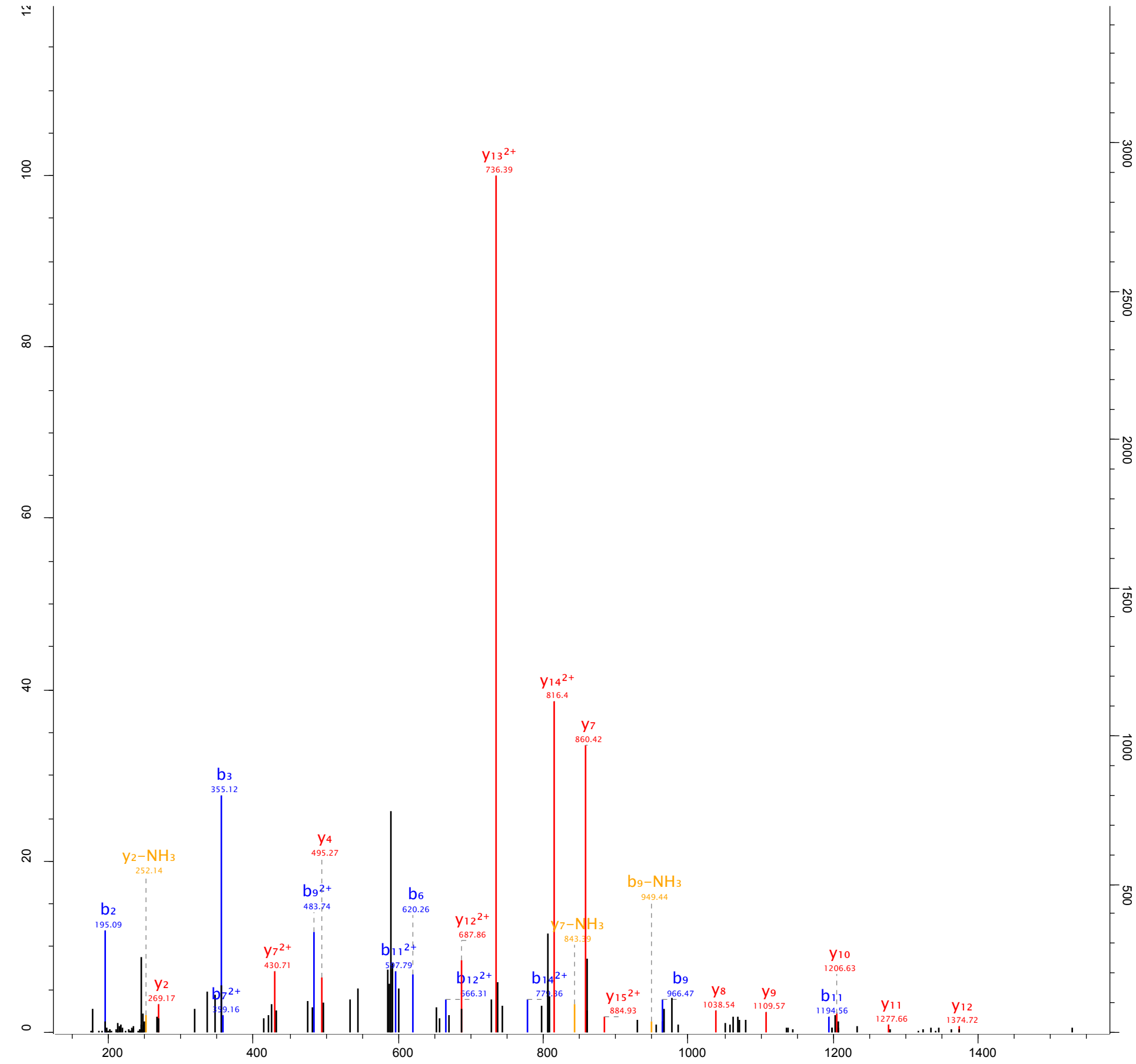
K -

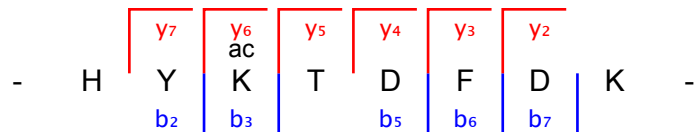
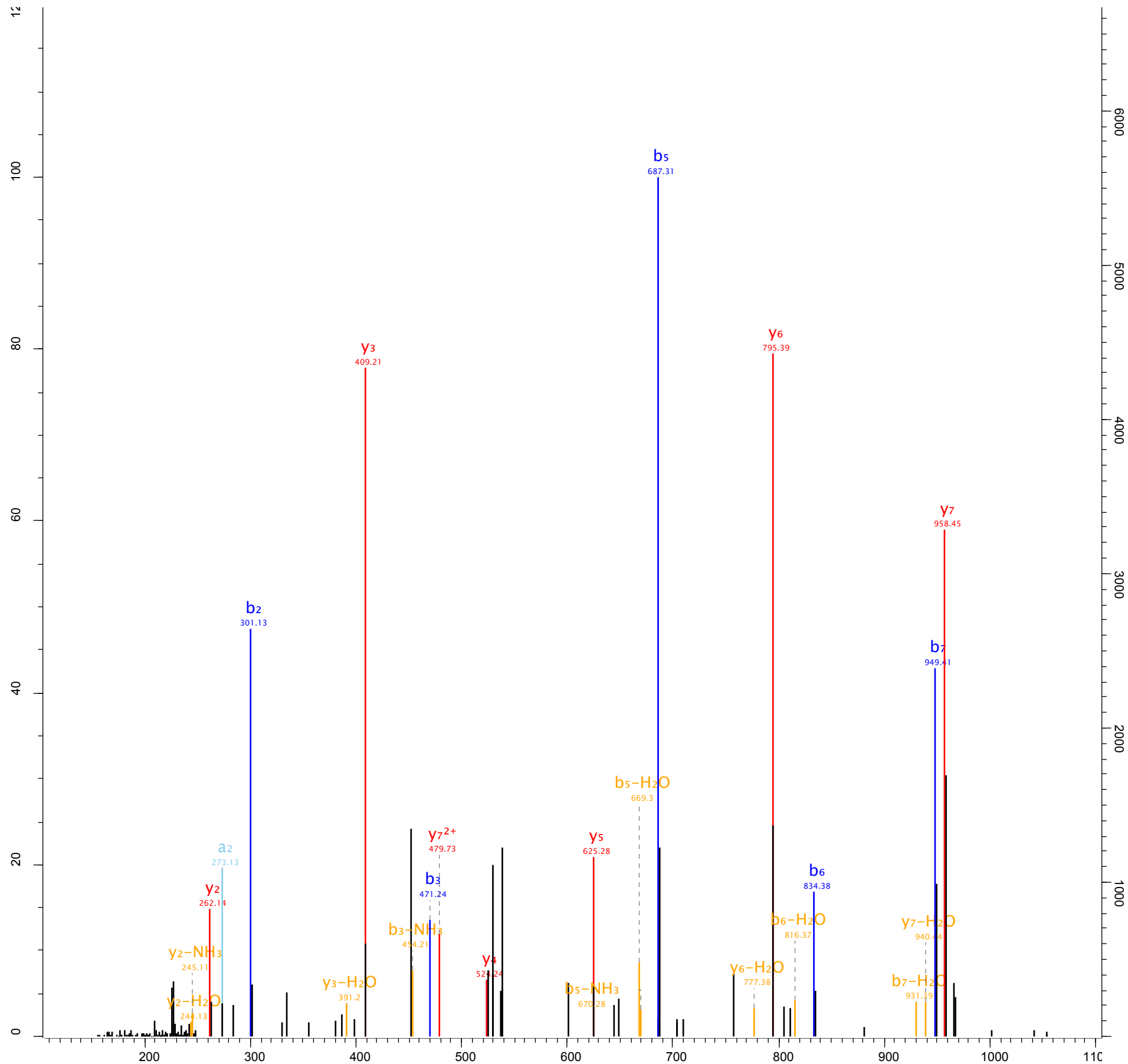


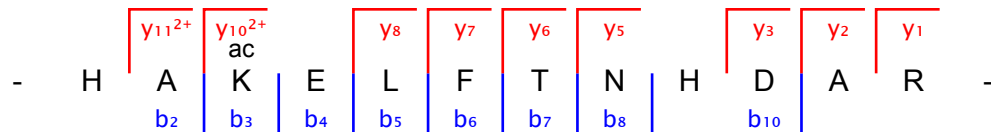
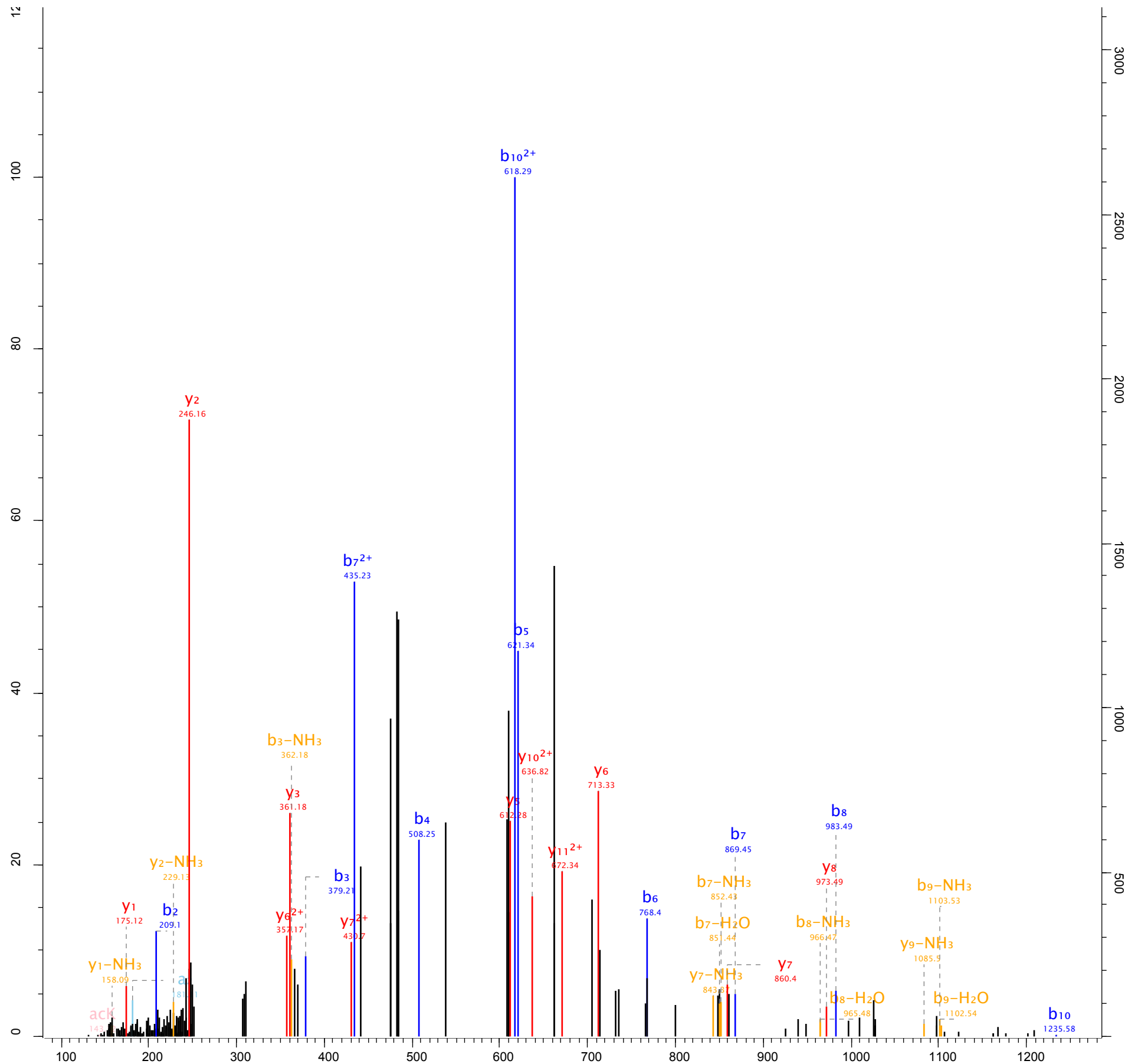


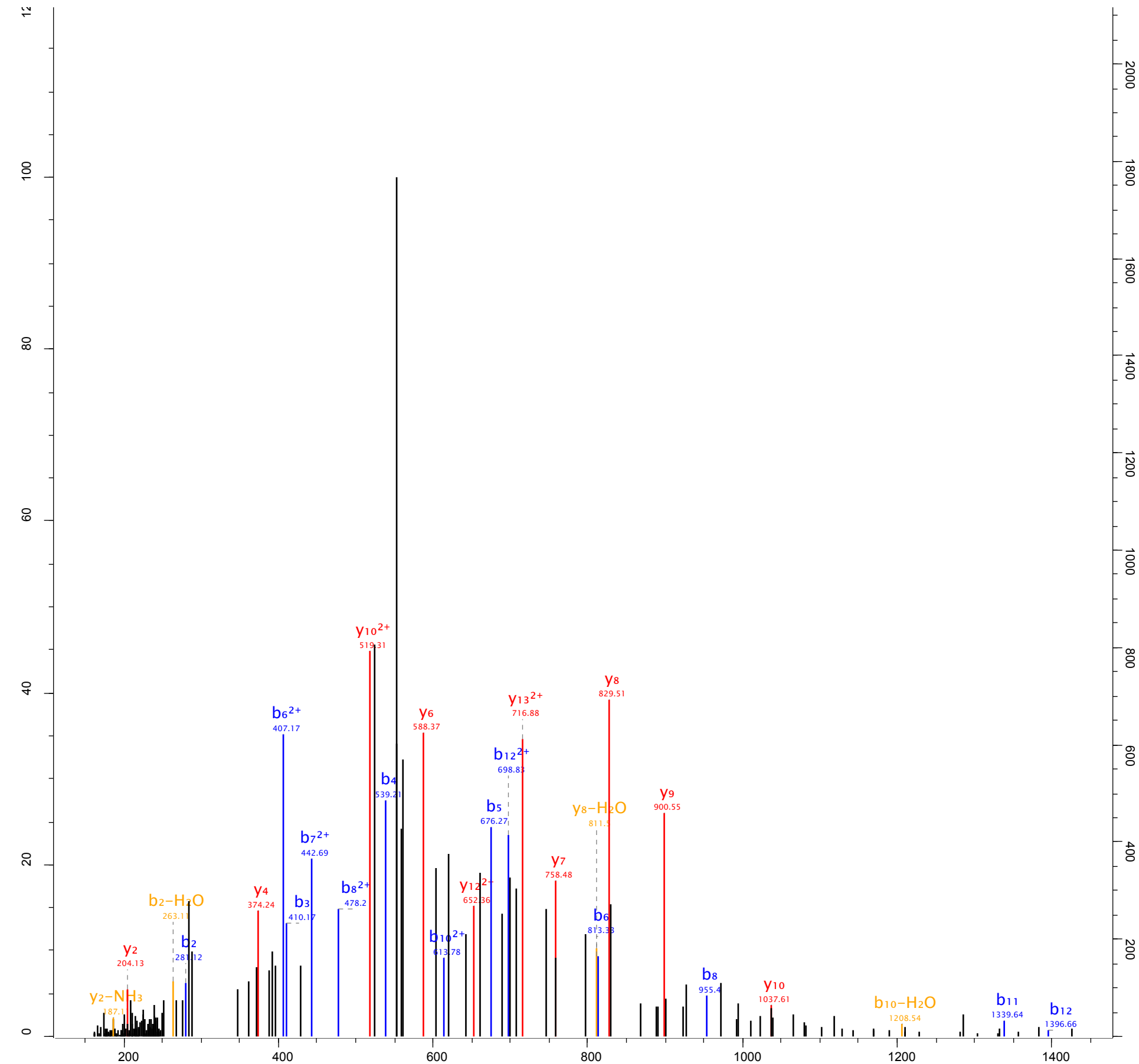








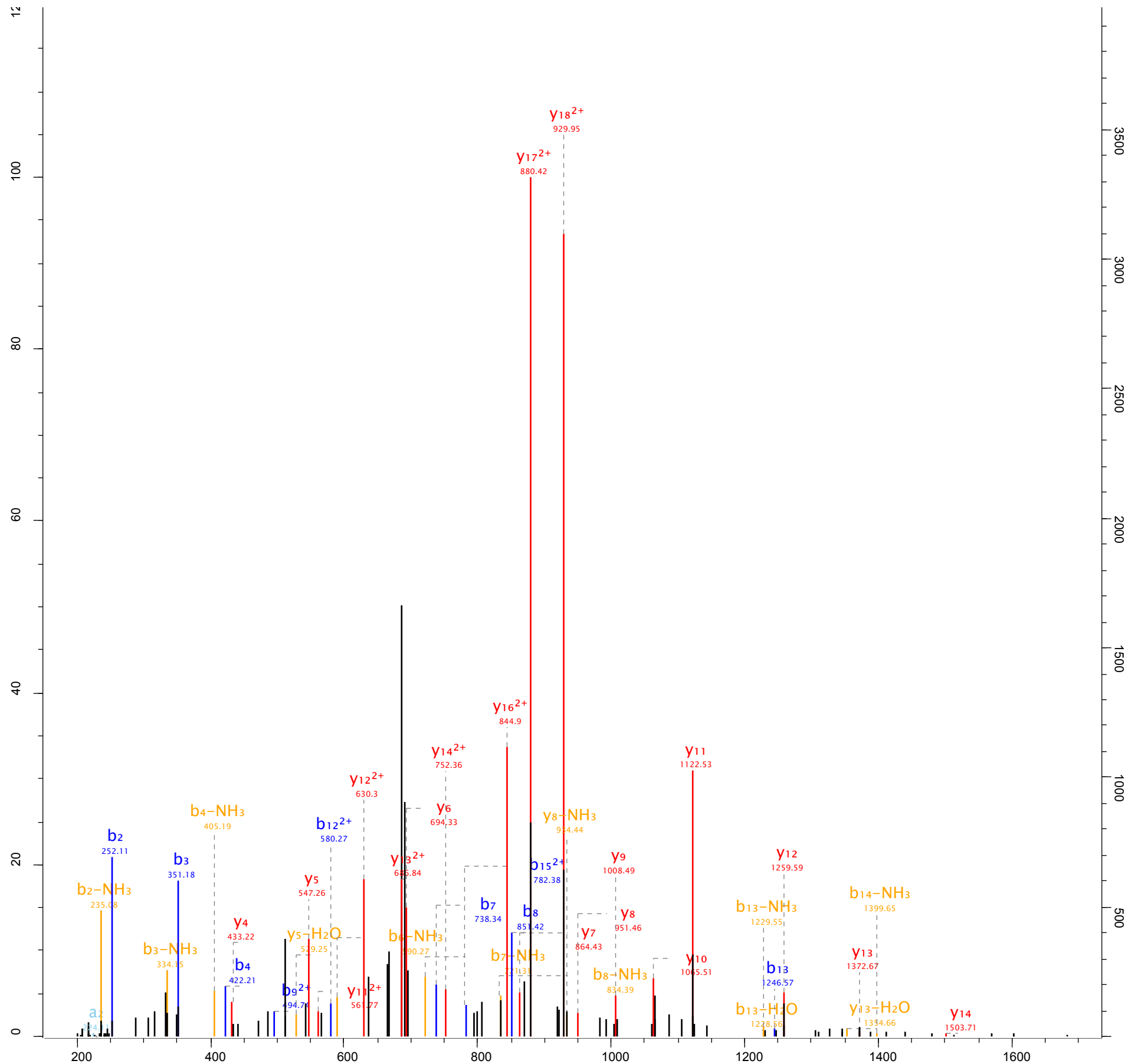




ac
- T H E E H H A A K T L G I G K -

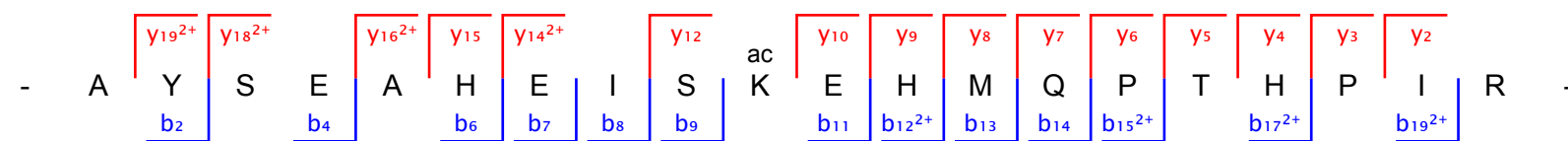
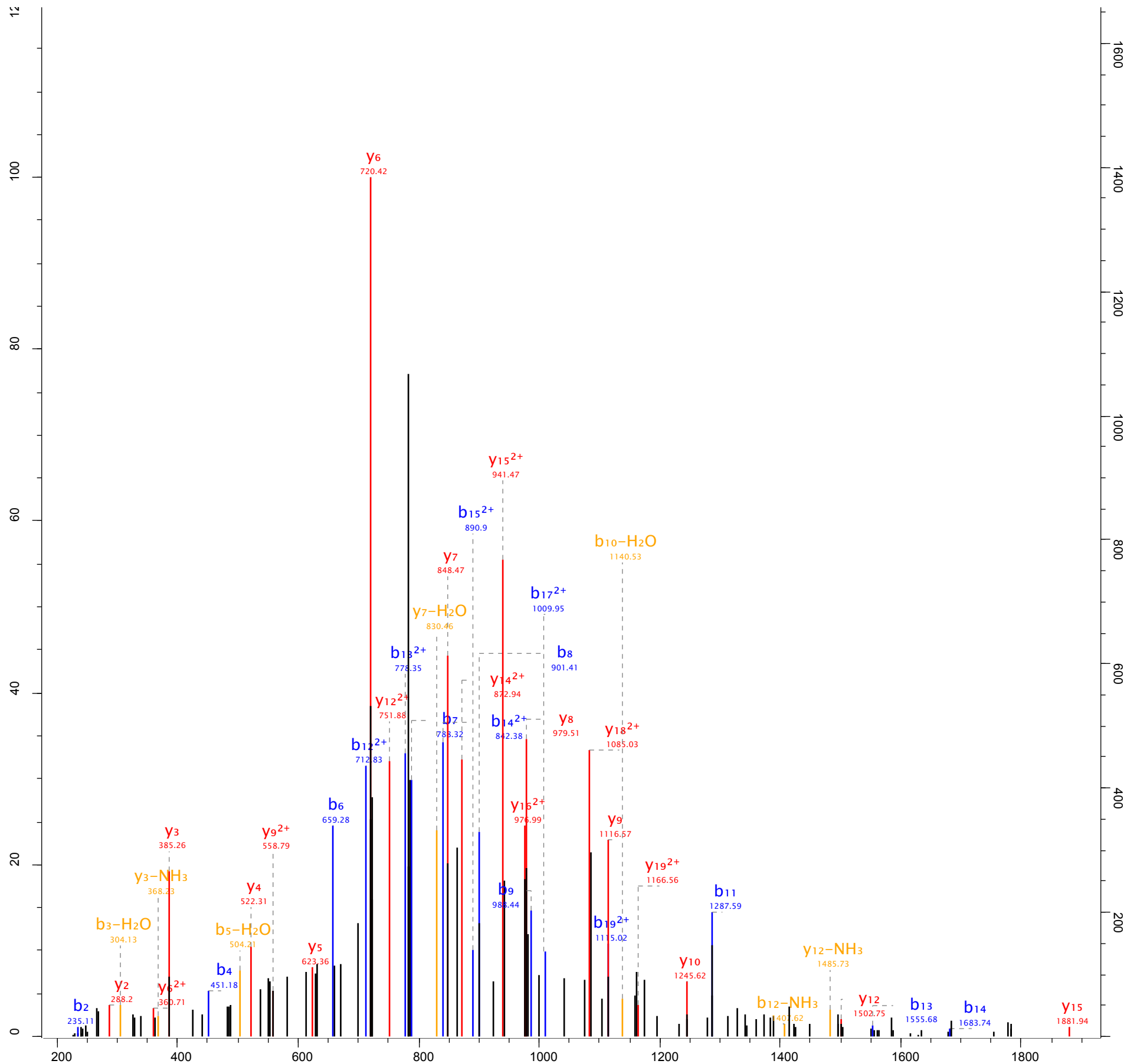
Fragmentation mapping (b and y ions):

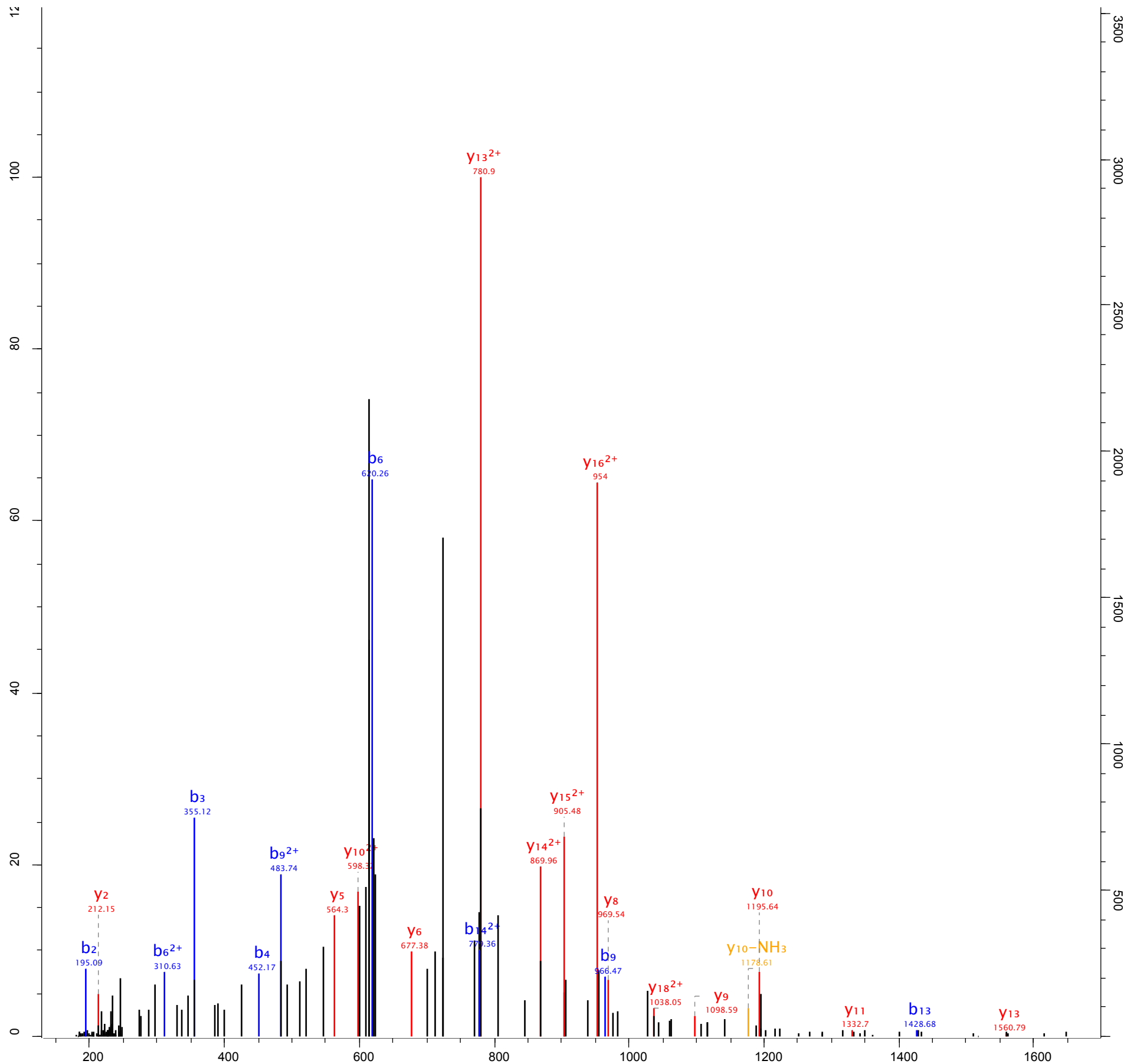
- b₂ (under H)
- b₃ (under E)
- b₄ (under E)
- b₅ (under H)
- b₆ (under H)
- b₇²⁺ (under A)
- b₈ (under A)
- b₁₀²⁺ (under T)
- b₁₁ (under L)
- b₁₂ (under G)
- y₂ (above G)
- y₄ (above I)
- y₆ (above T)
- y₇ (above K)
- y₈ (above A)
- y₉ (above A)
- y₁₀ (above H)
- y₁₂²⁺ (above E)
- y₁₃²⁺ (above E)



- N H V A G Q M L H G G S K F N S G N R -

b₂
b₃
b₄
b₇
b₈
b₉²⁺
b₁₂²⁺
b₁₃
b₁₅²⁺
y₄
y₅
y₆
y₇
y₈
y₉
y₁₀
y₁₁
y₁₂
y₁₃
y₁₄
y₁₆²⁺
y₁₇²⁺
y₁₈²⁺

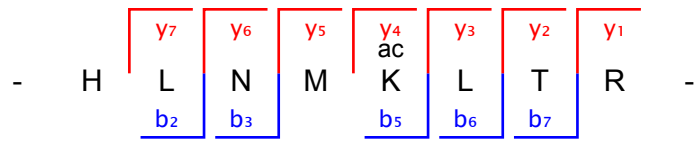
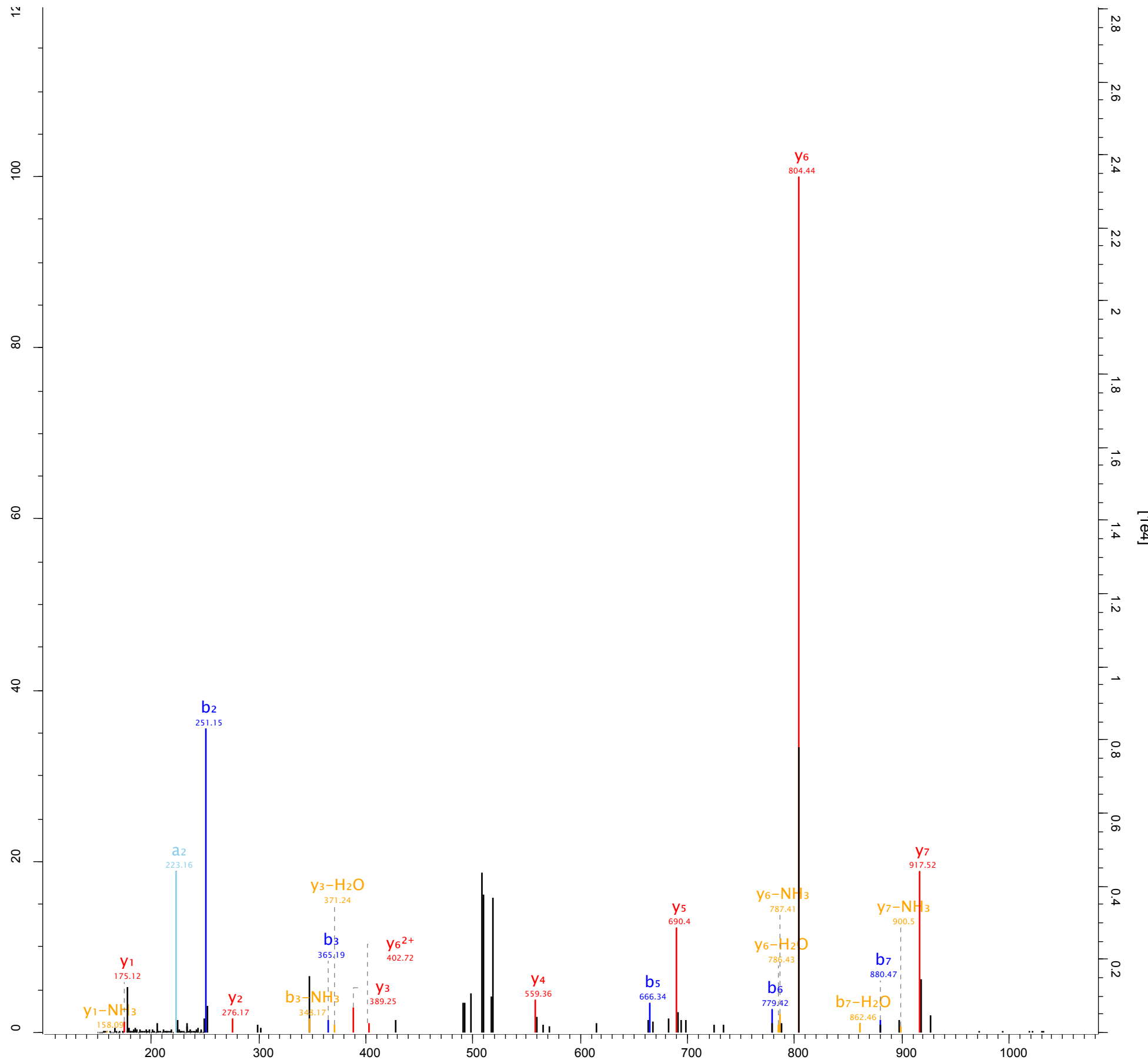




- G H C P P A P A K P M H P E N ac K L T N H G K -

Fragmentation mapping (b and y ions):

- b_2 (H), b_3 (C), b_4 (P), b_6 (A), b_9 (K), b_{13} (P), b_{14}^{2+} (E)
- y_2 (G), y_5 (T), y_6 (L), y_8 (N), y_9 (E), y_{10} (P), y_{11} (H), y_{13} (P), y_{14}^{2+} (K), y_{15}^{2+} (A), y_{16}^{2+} (P), y_{18}^{2+} (P)



062513_SCW_II_53_11_Vargas_Enriched

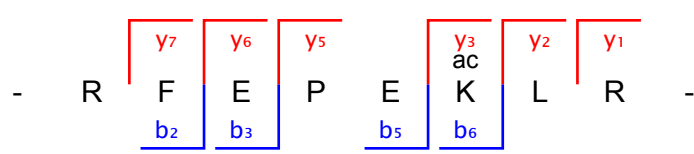
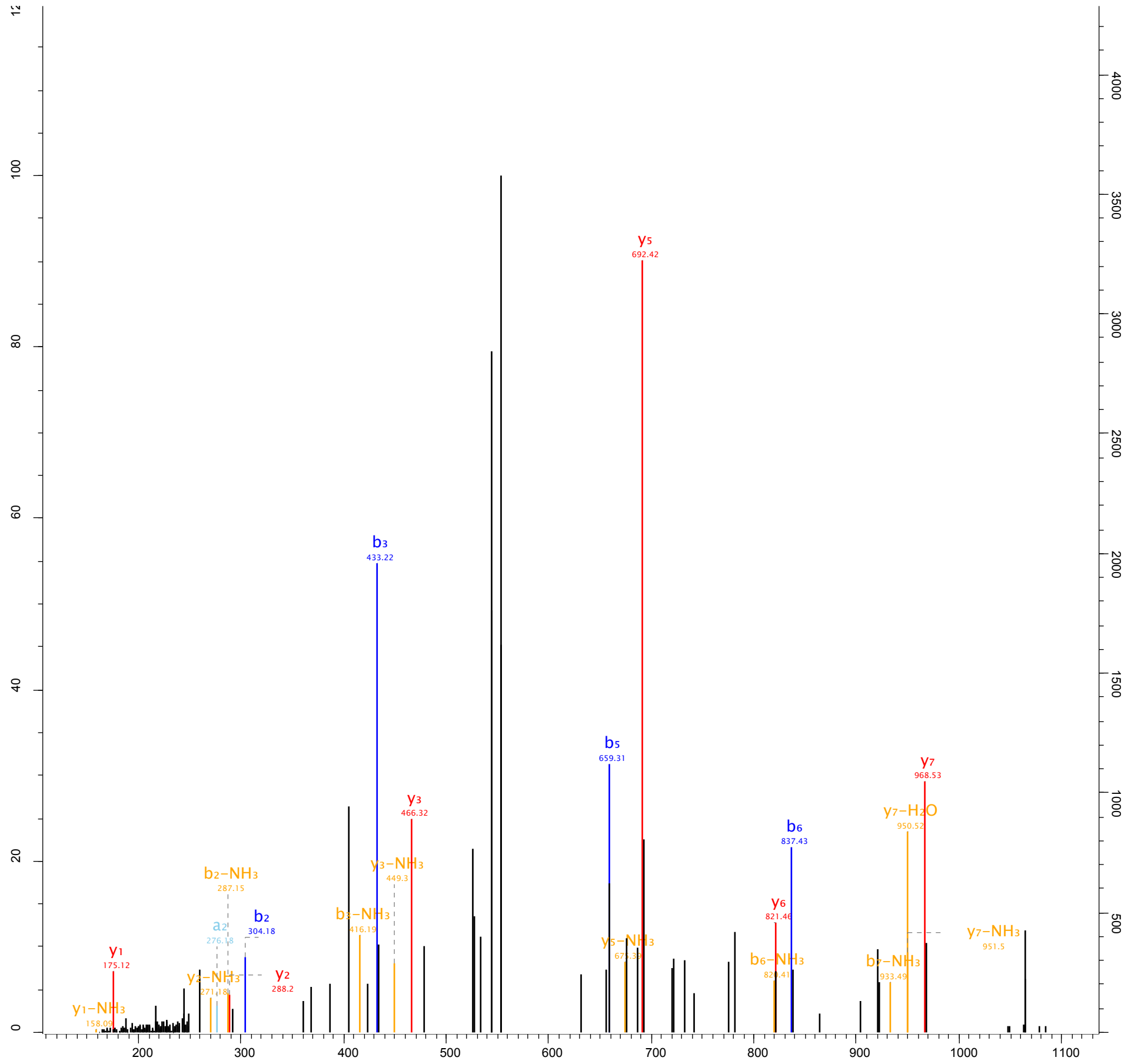
14200

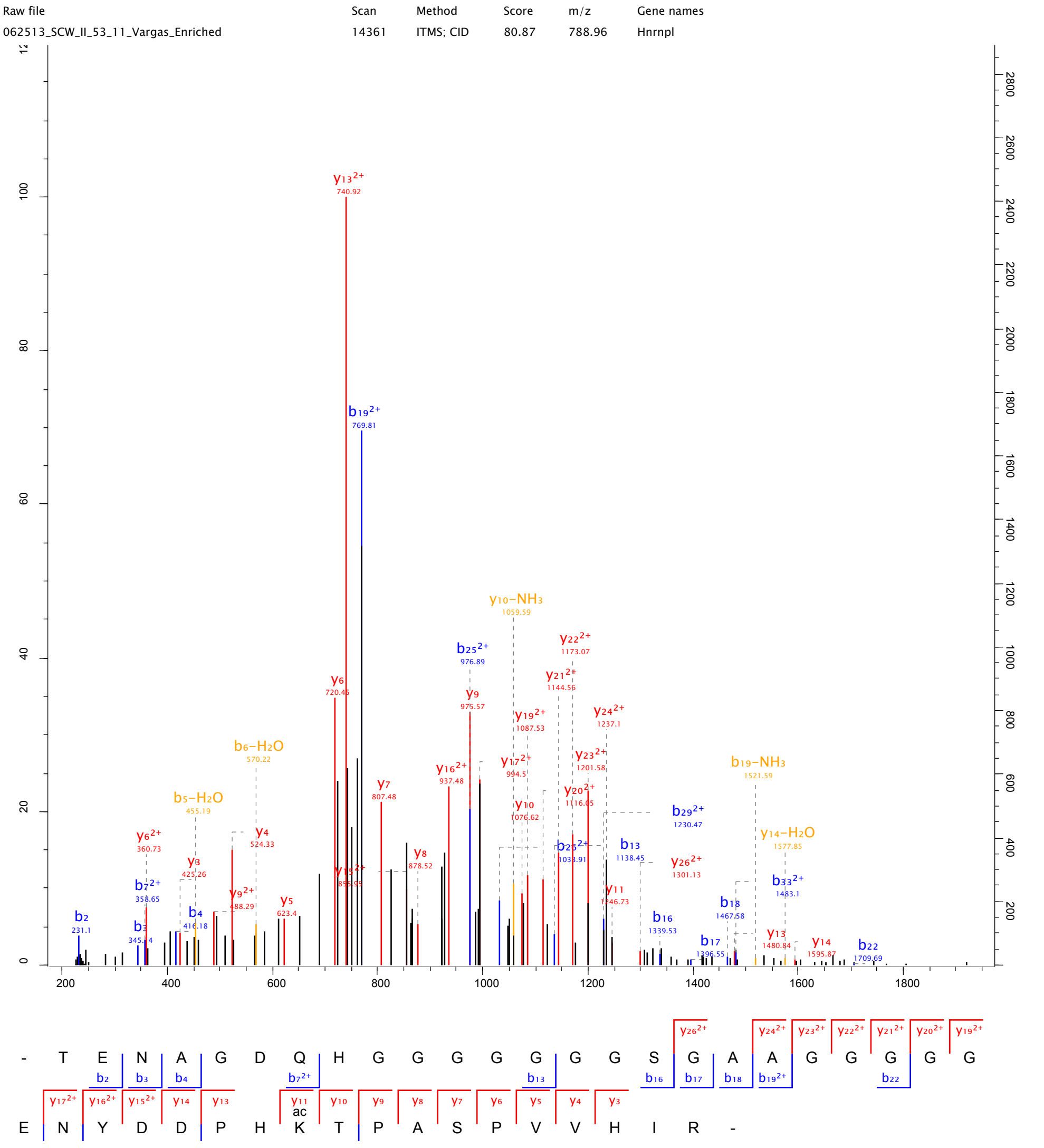
ITMS; CID

109.44

562.82

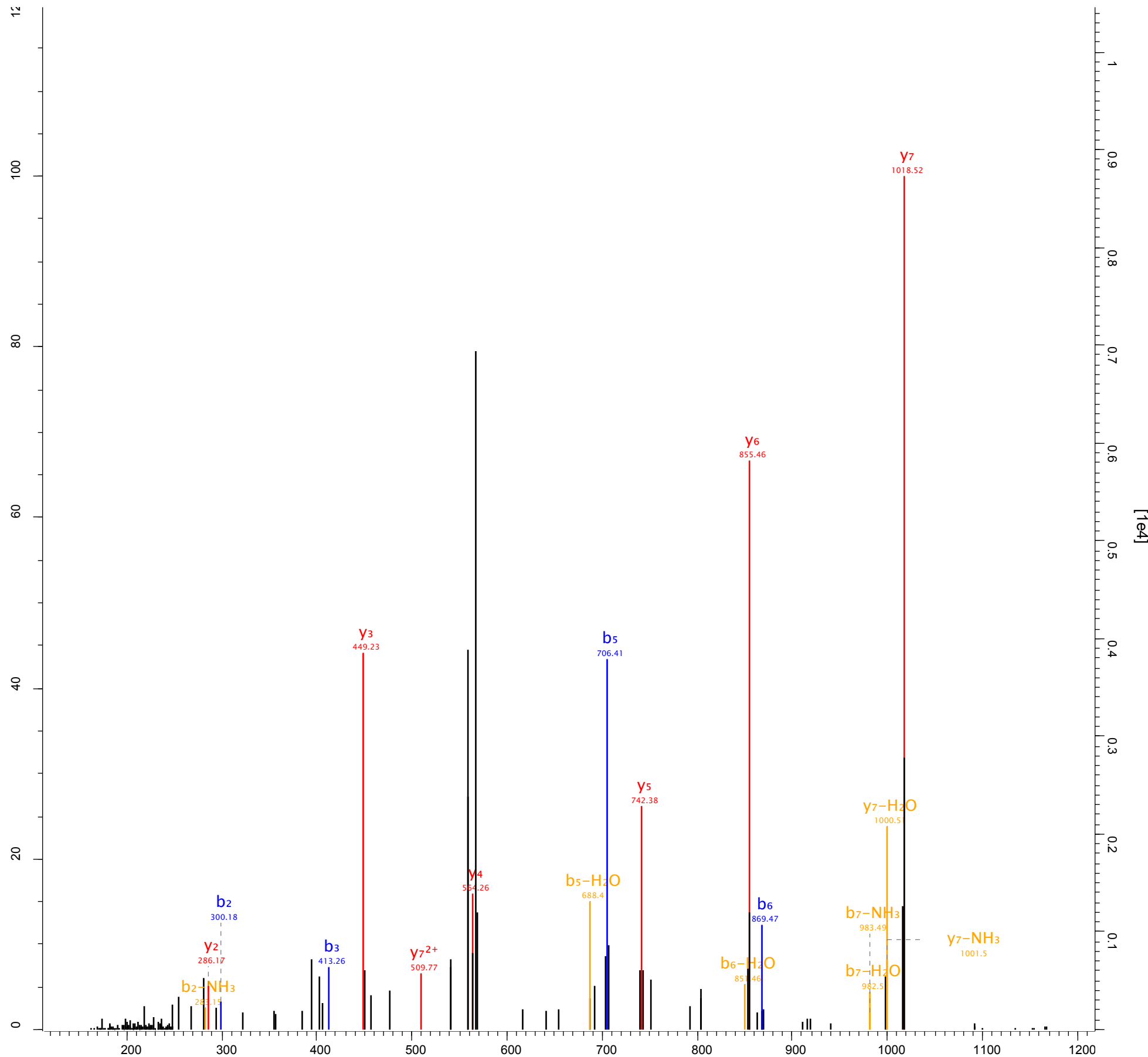
Cnn1





Raw file
062513_SCW_II_53_11_Vargas_Enriched

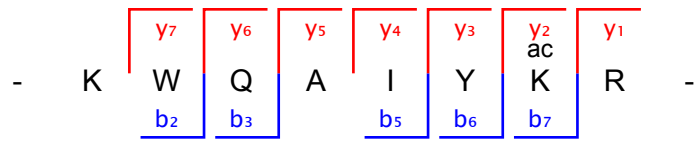
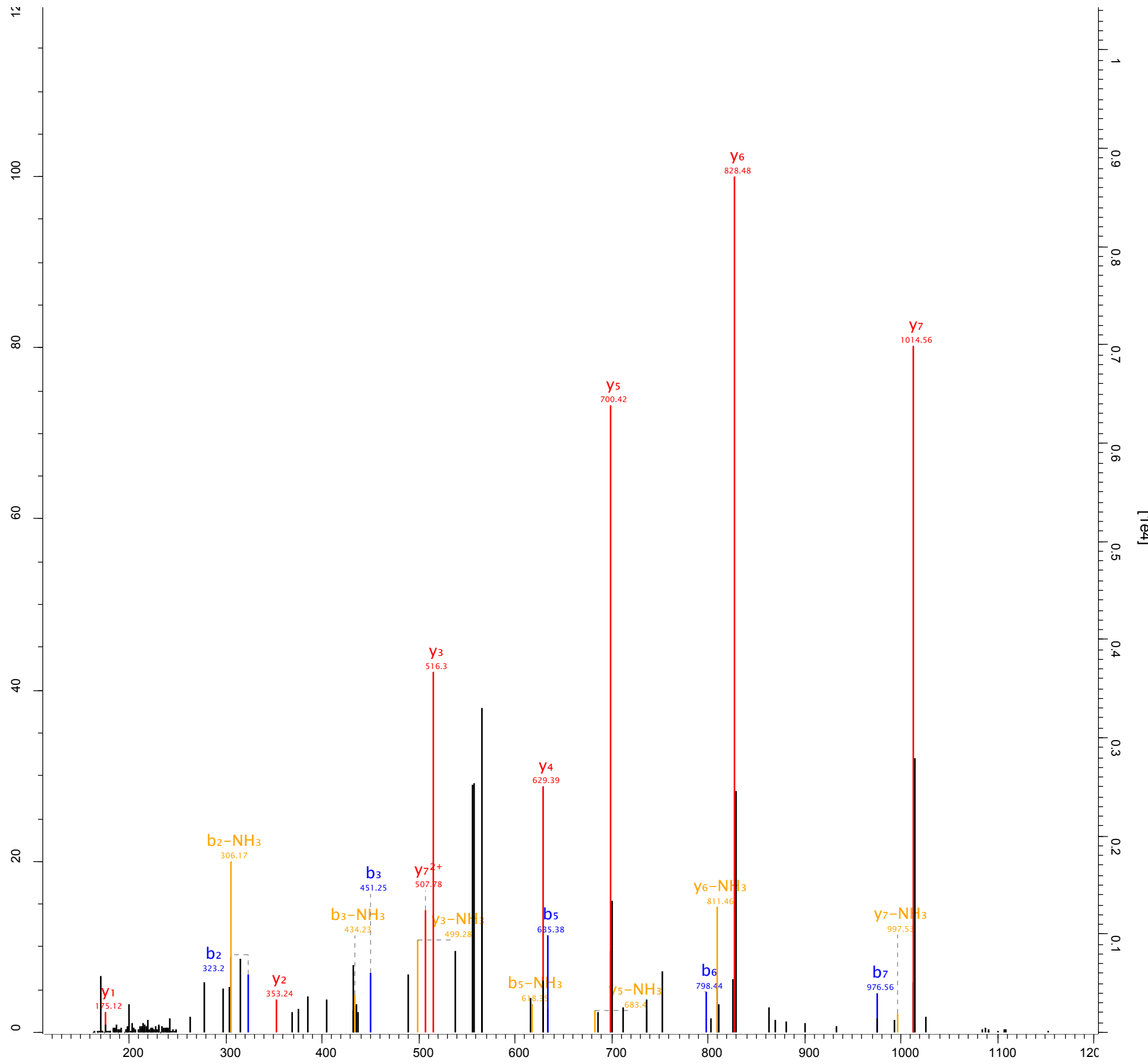
Scan Method Score m/z Gene names
14706 ITMS; CID 109.29 577.82 Tpt1

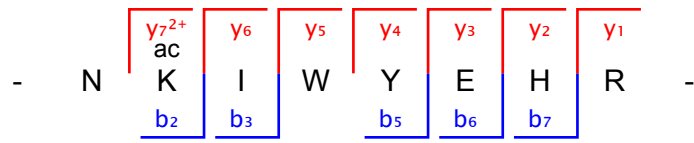
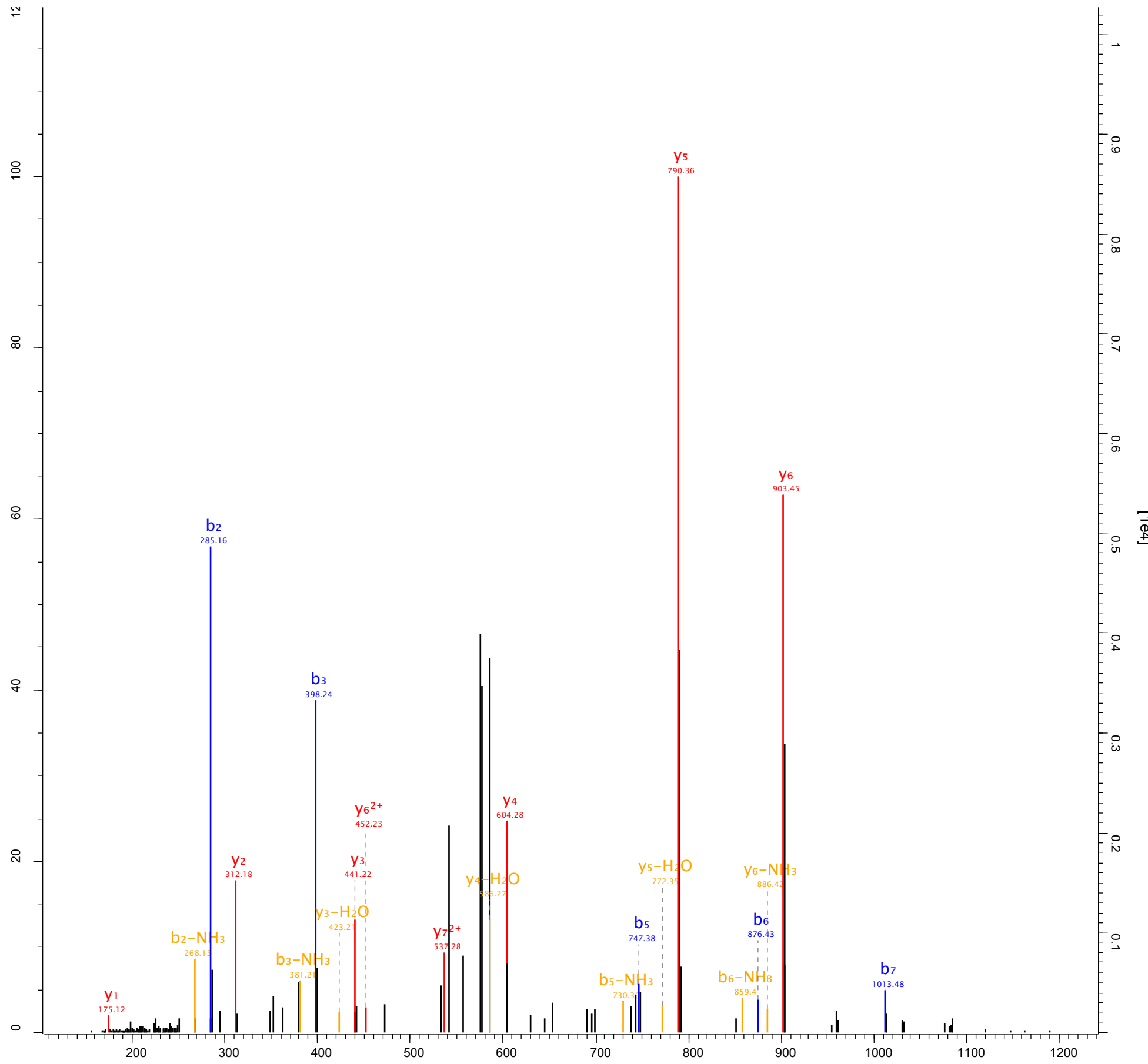


- K Y I K D Y M K -

b2 b3 b5 b6

y7 y6 y5 ac y4 y3 y2





062513_SCW_II_53_11_Vargas_Enriched

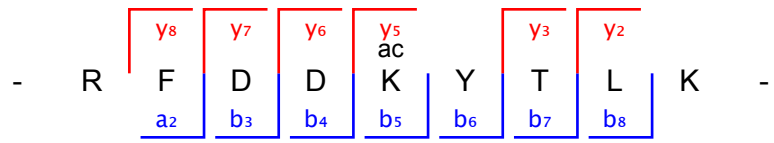
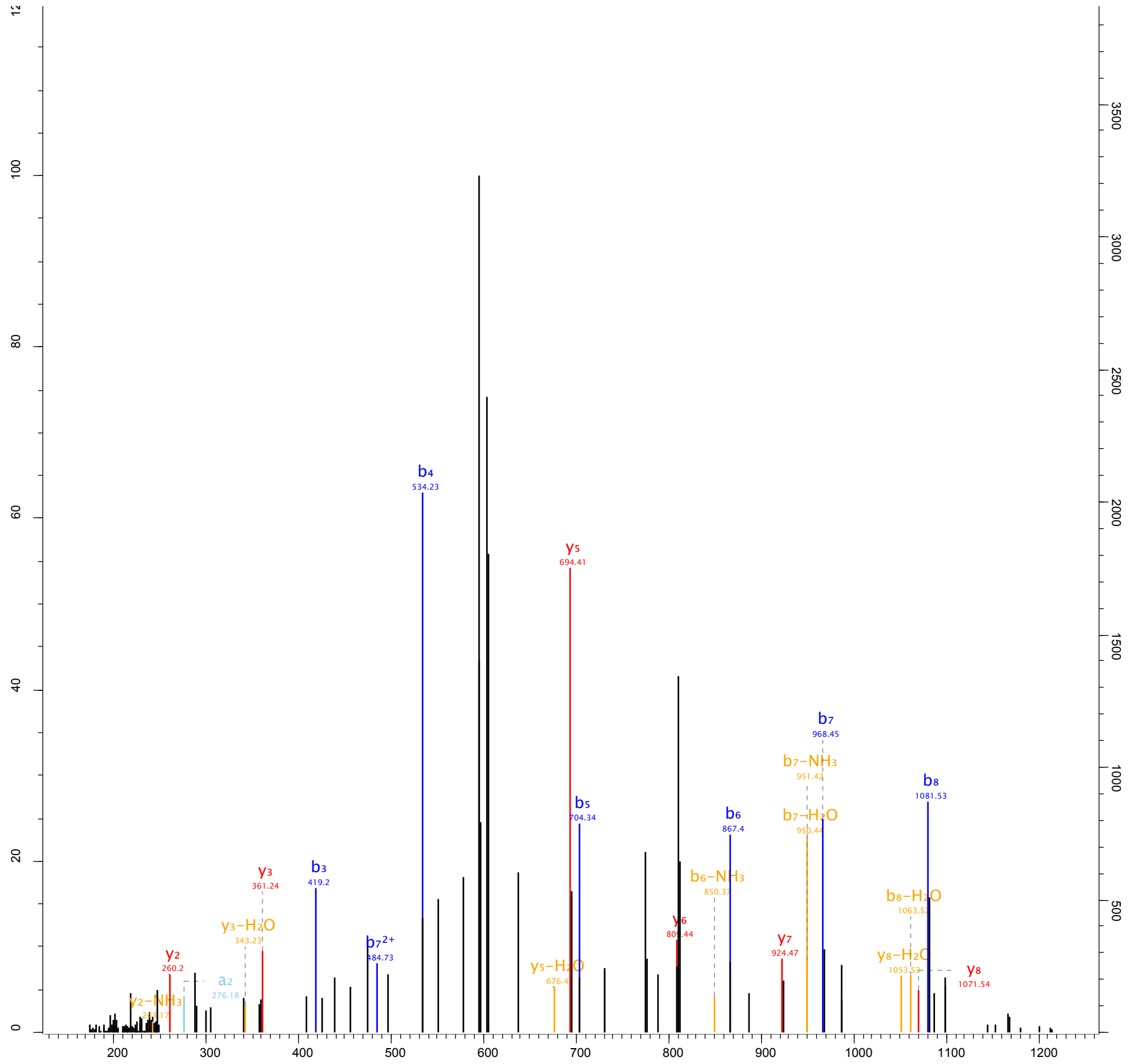
15456

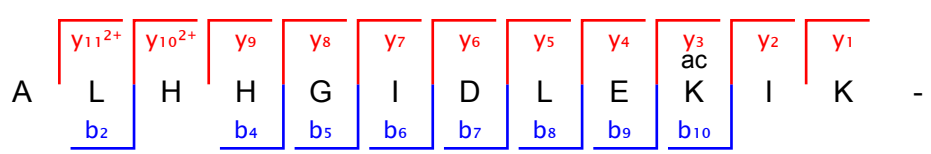
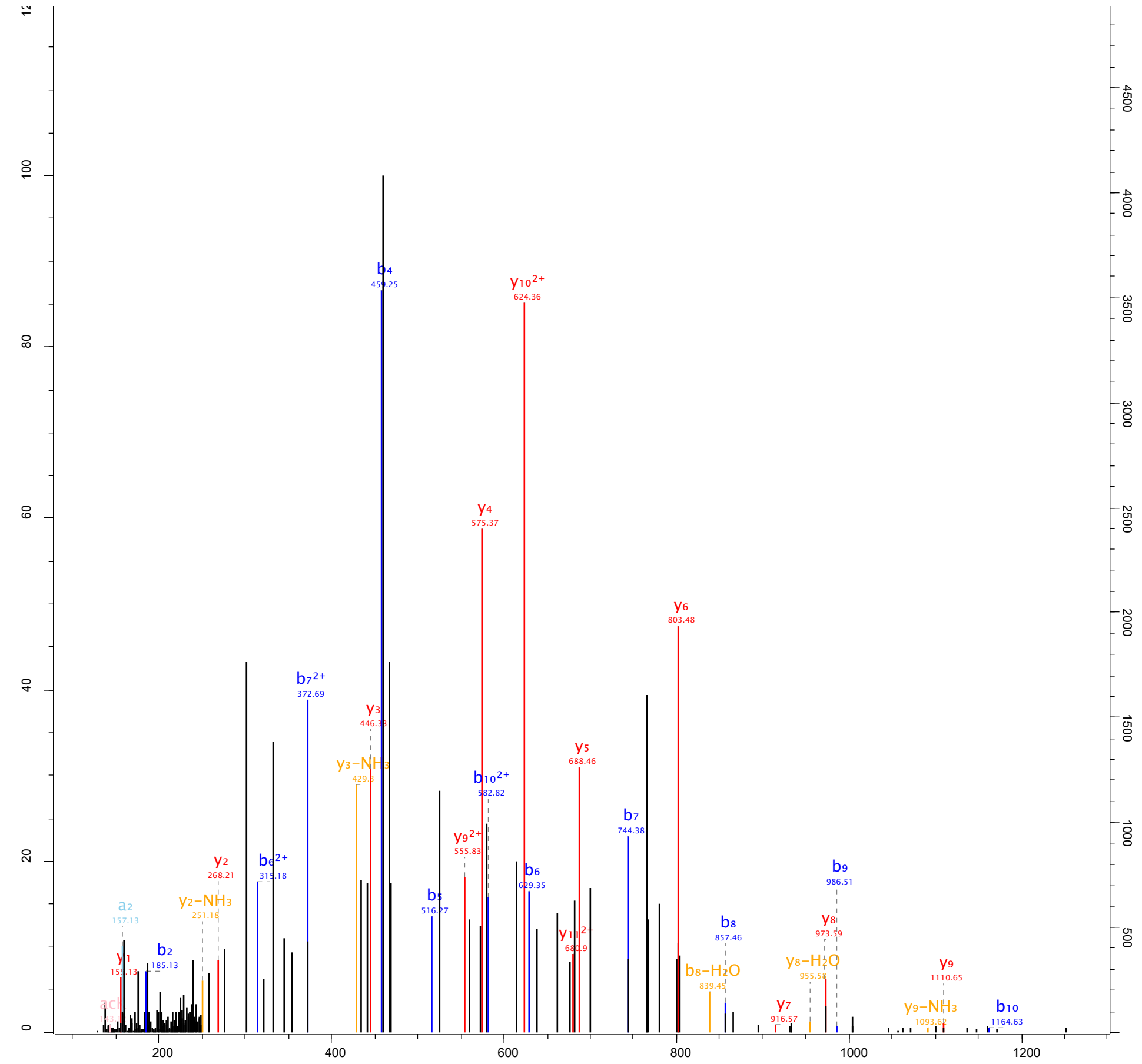
ITMS; CID

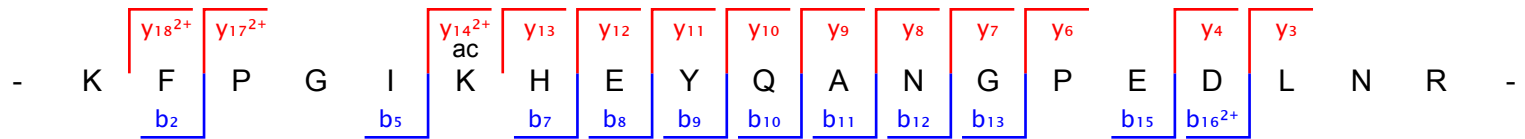
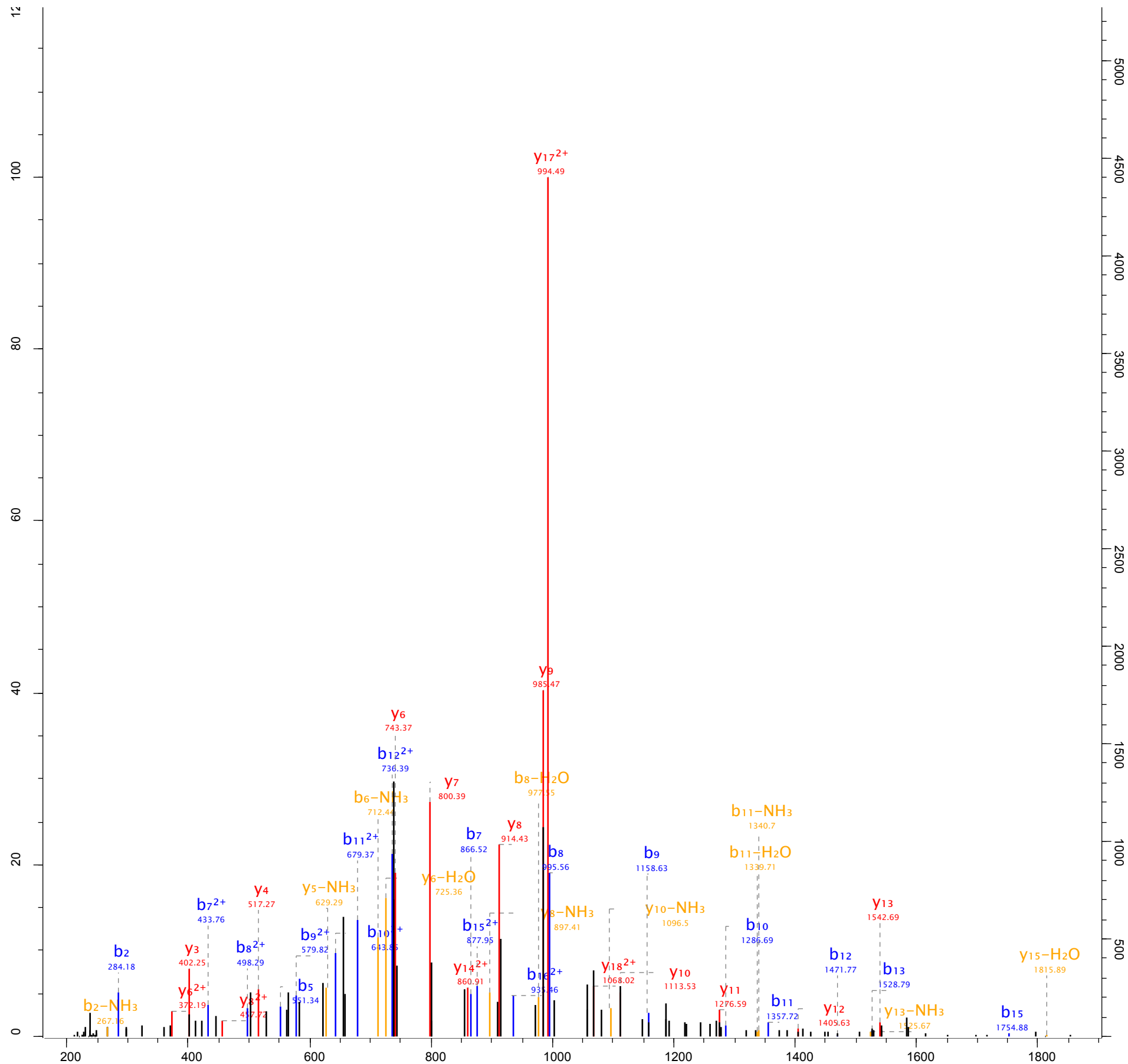
100.69

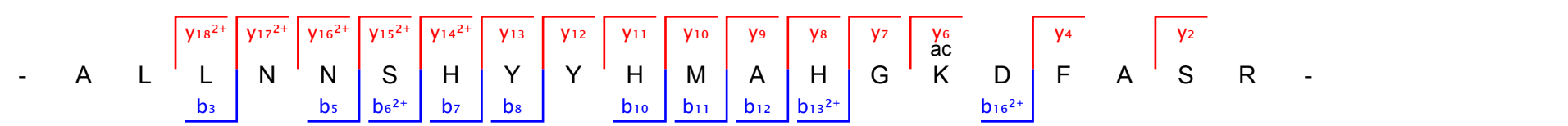
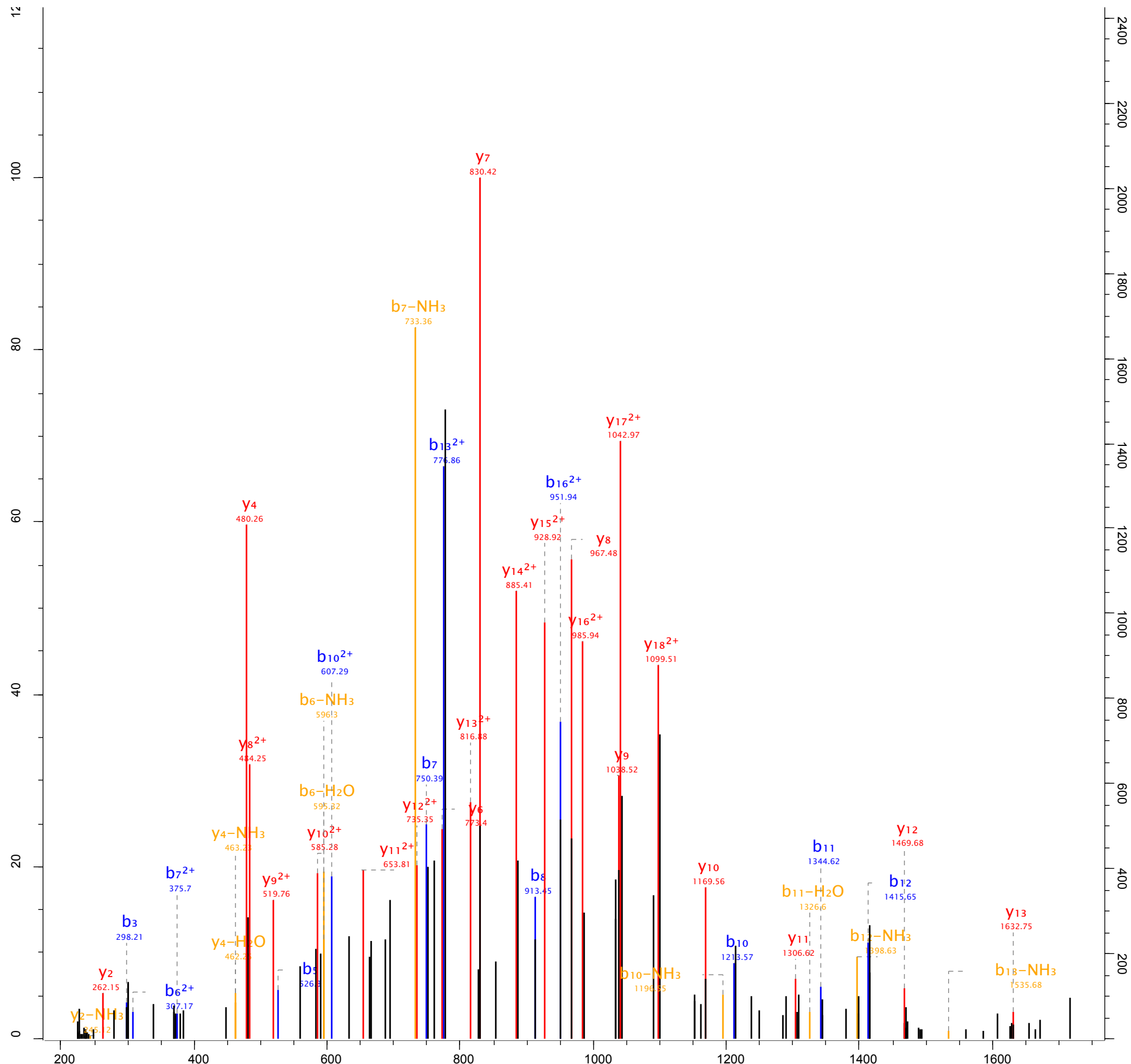
614.32

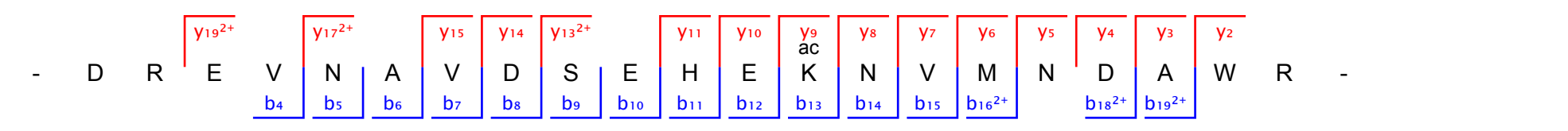
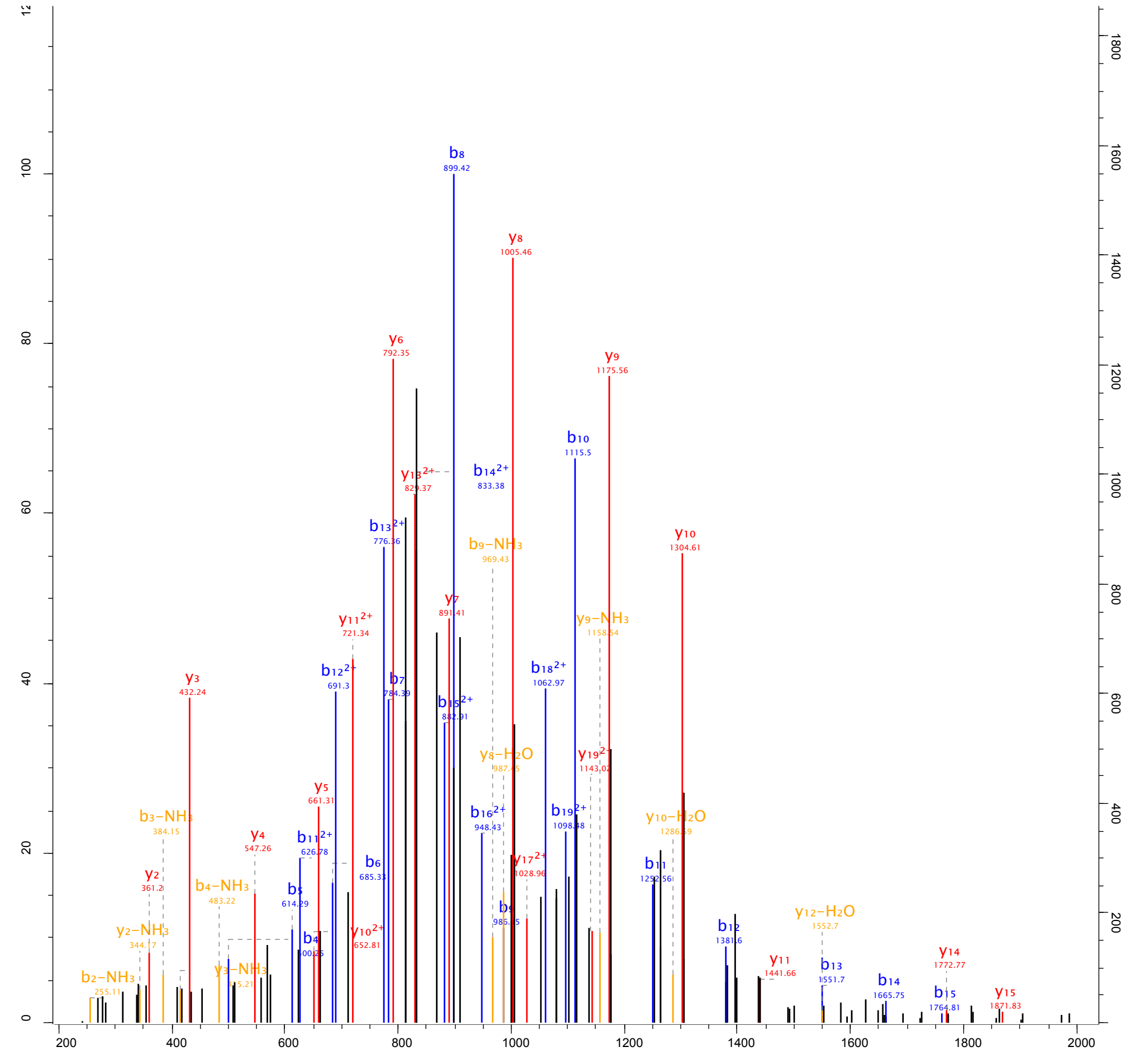
Spcs2

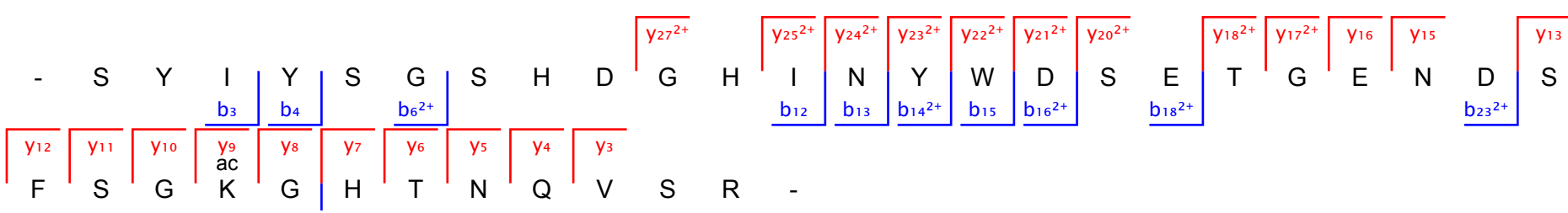
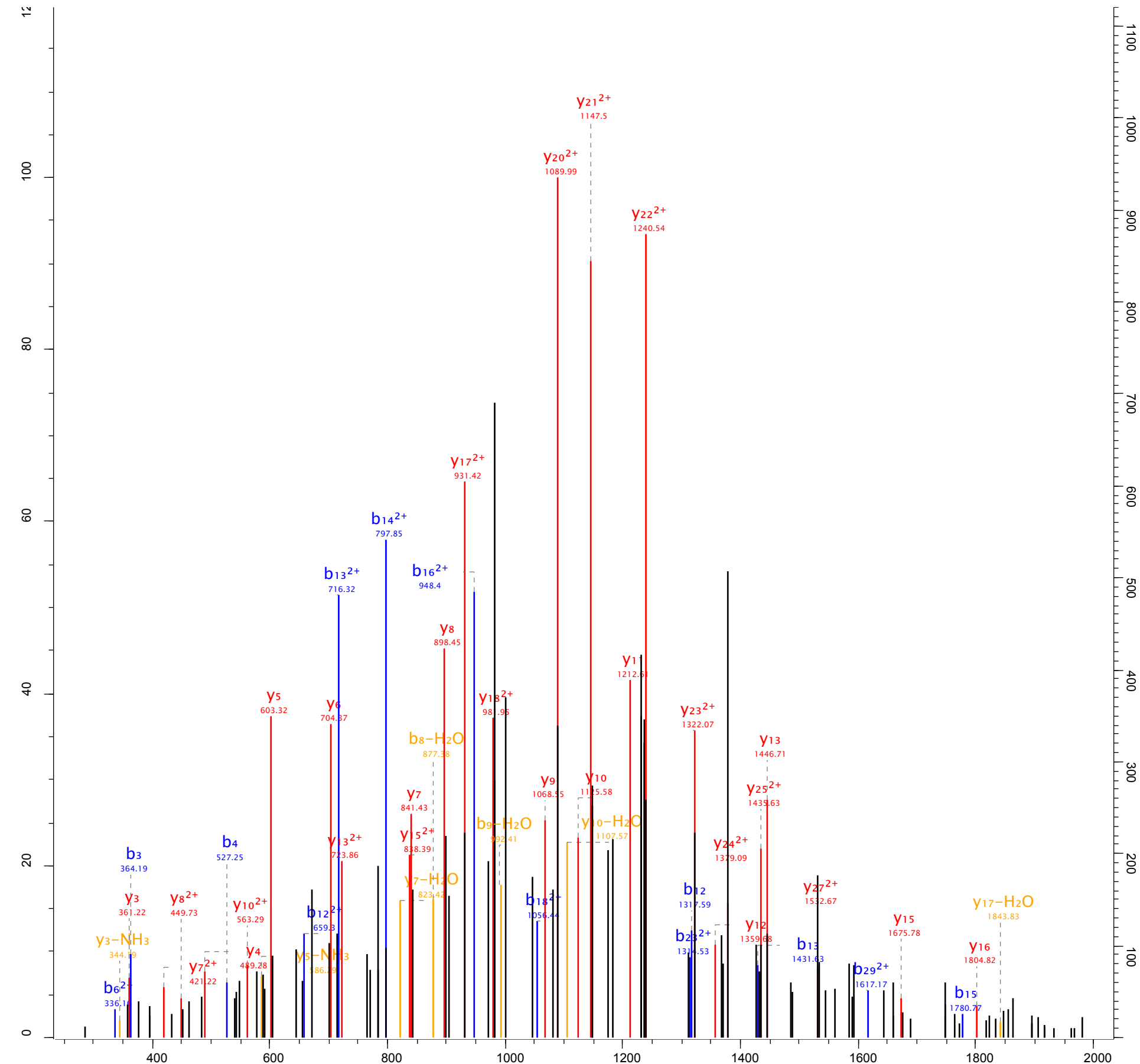


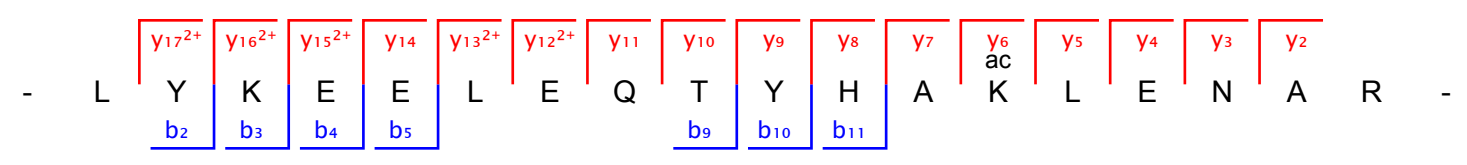
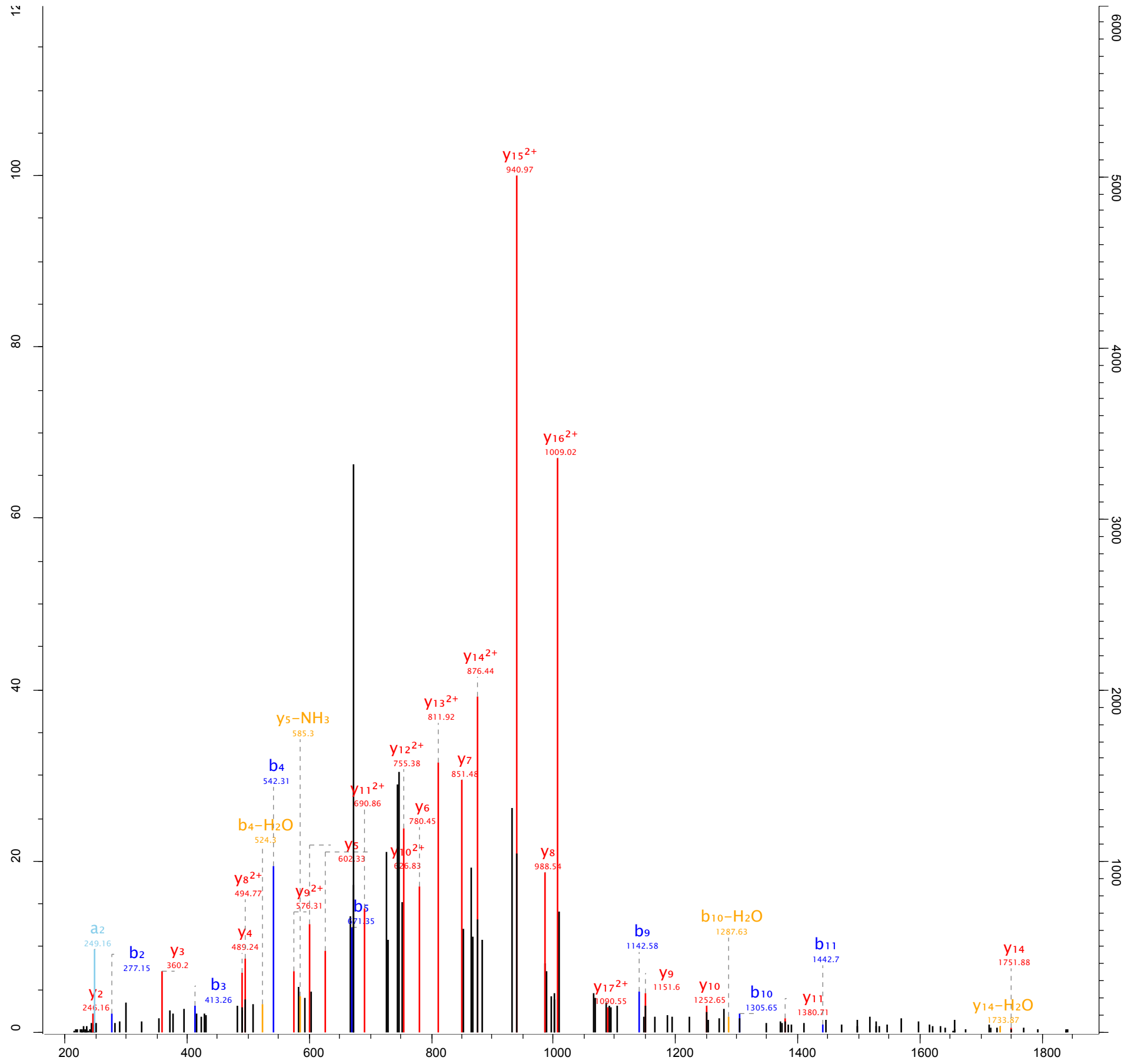


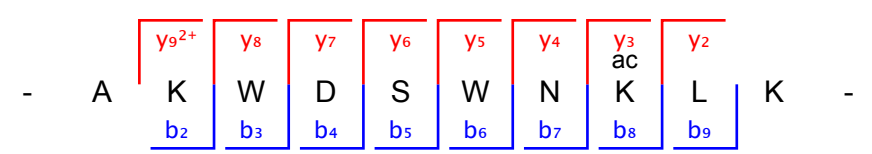
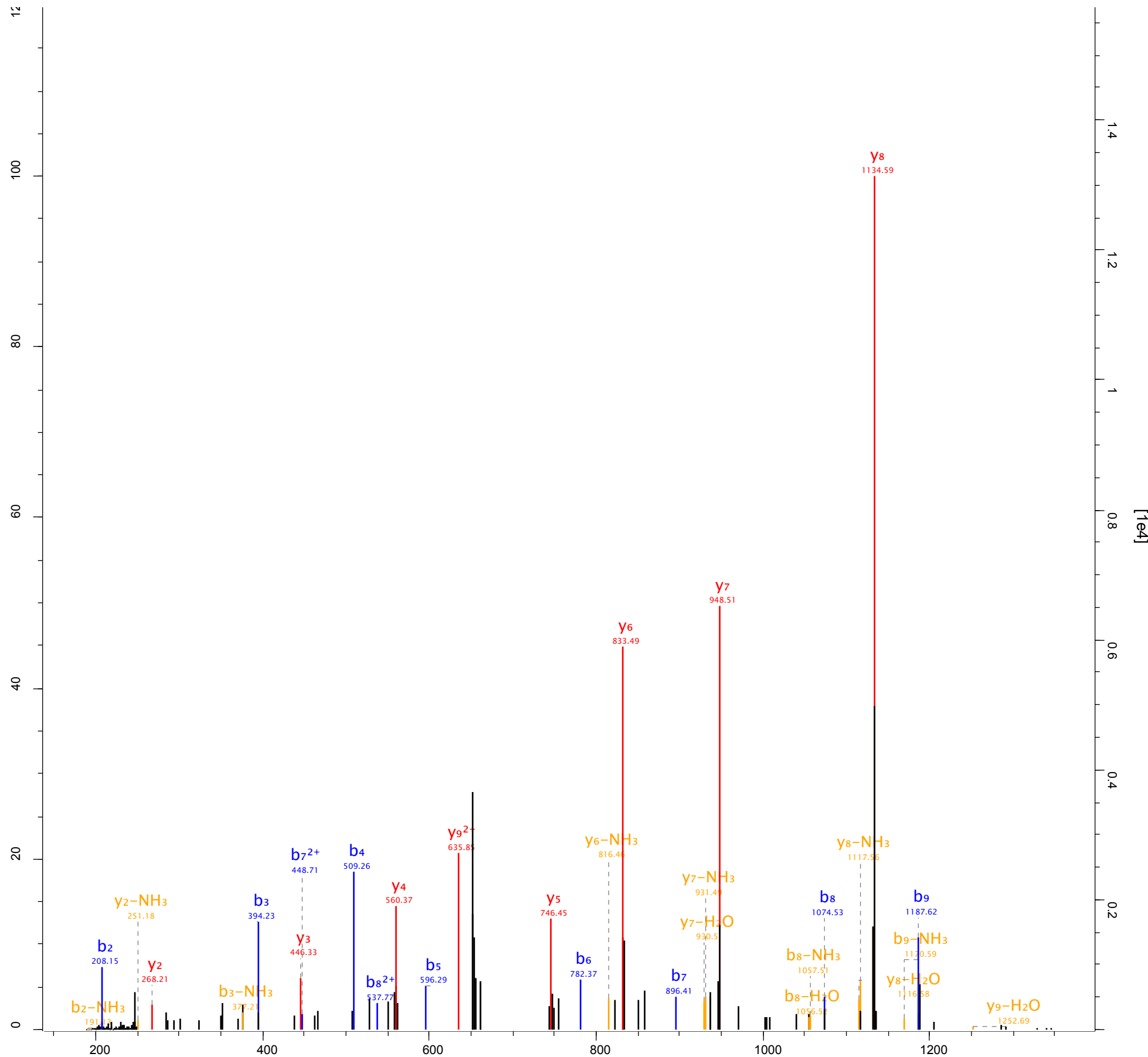


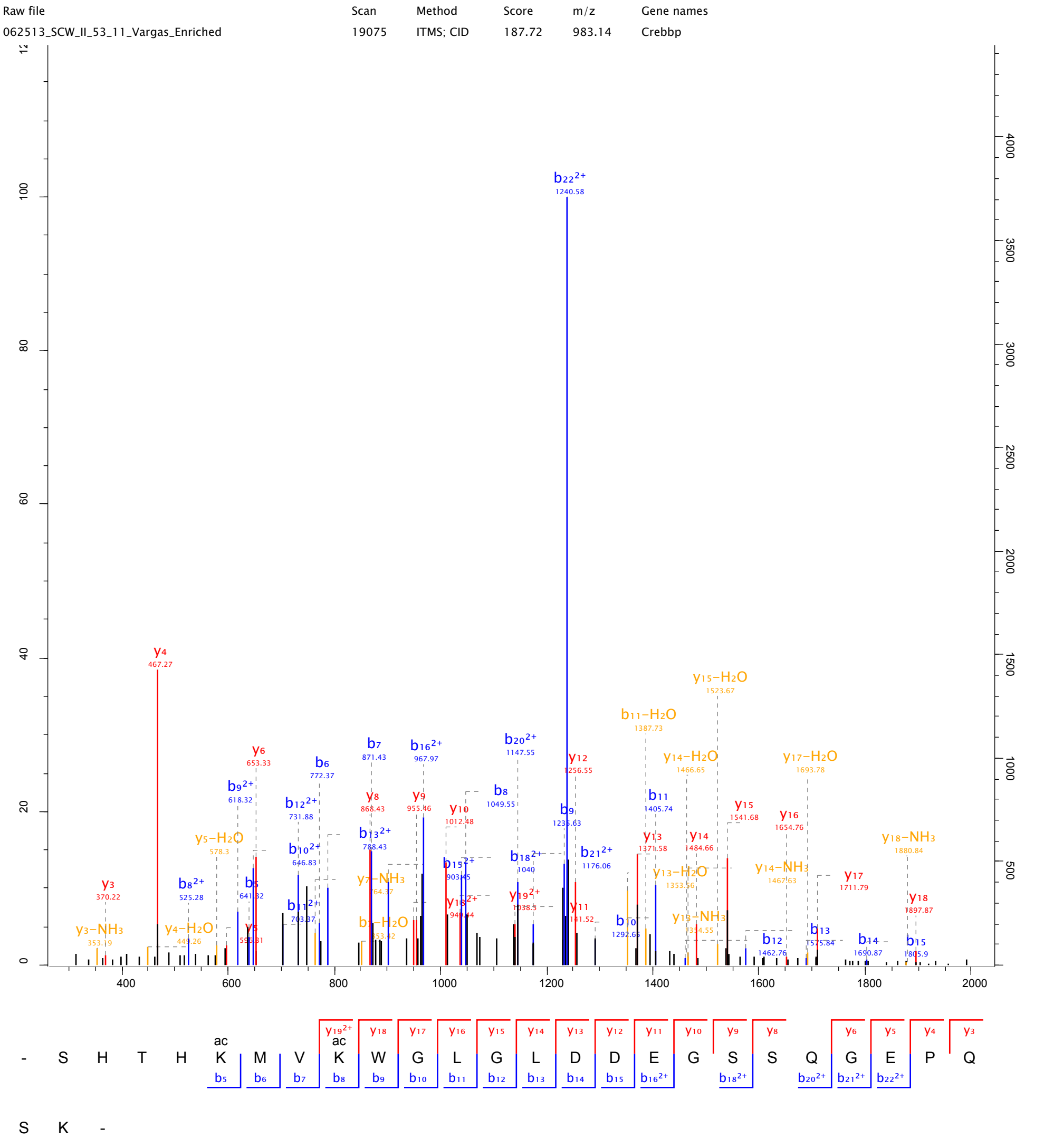


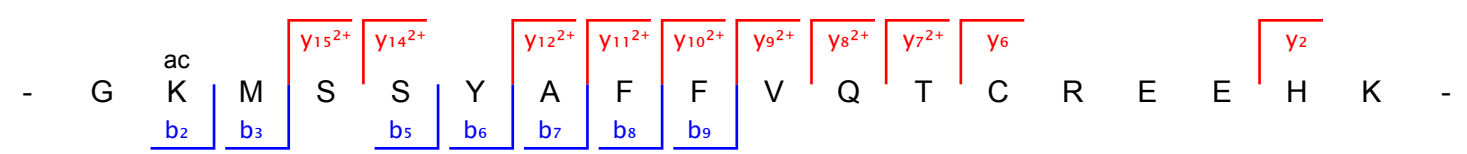
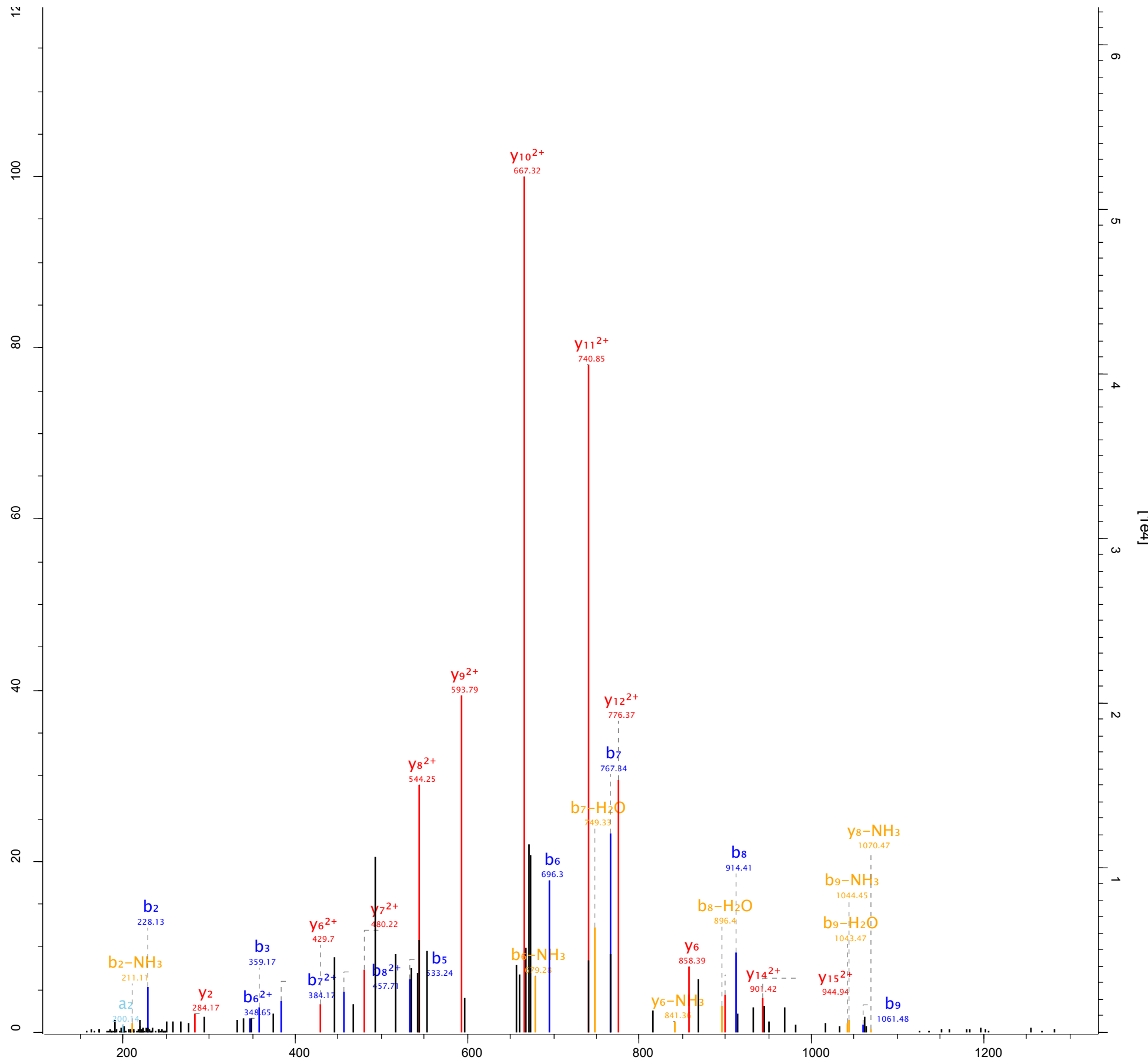


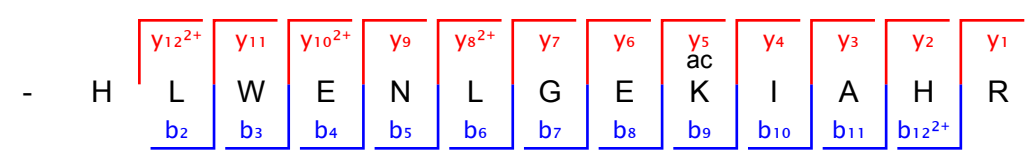
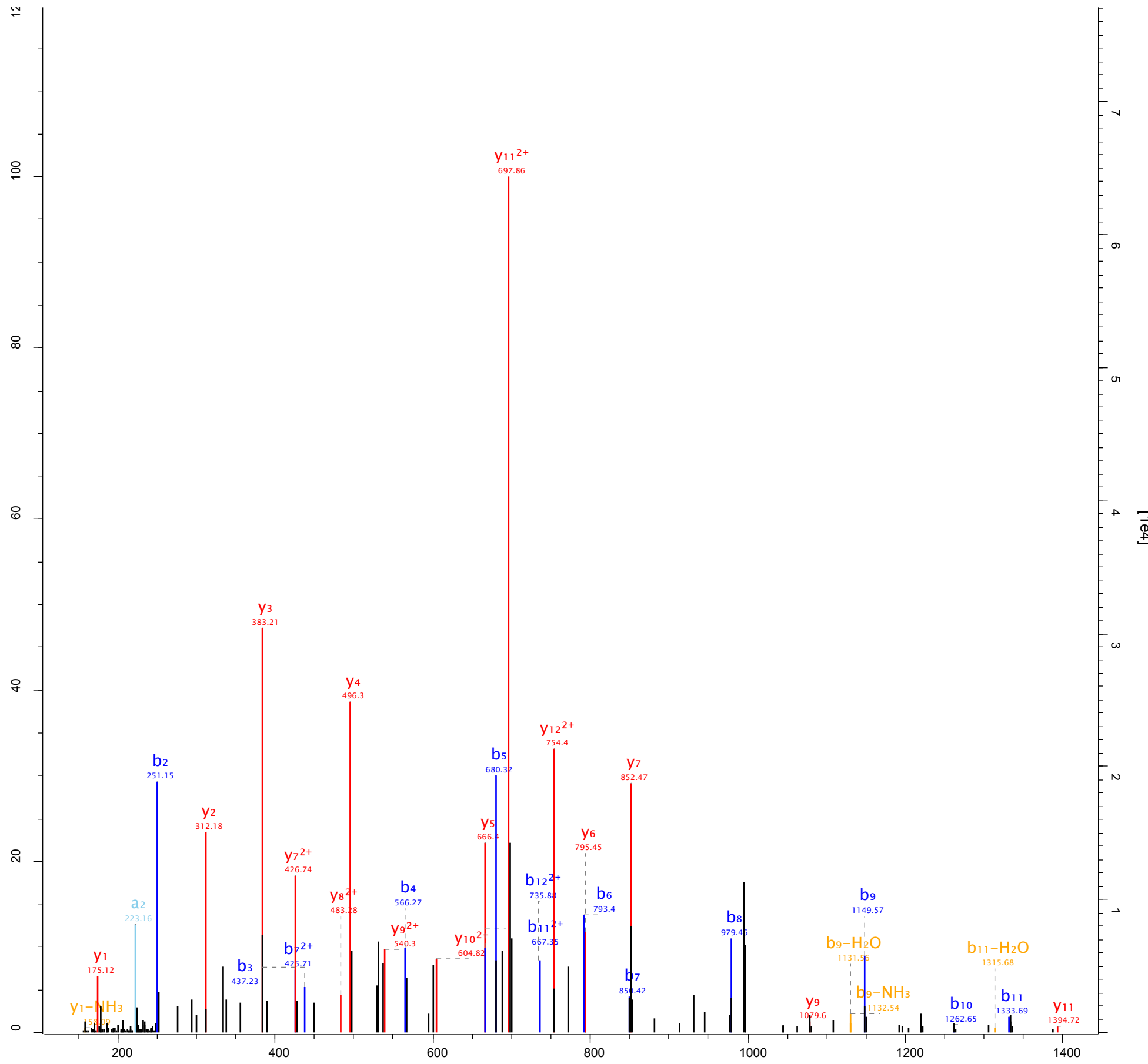


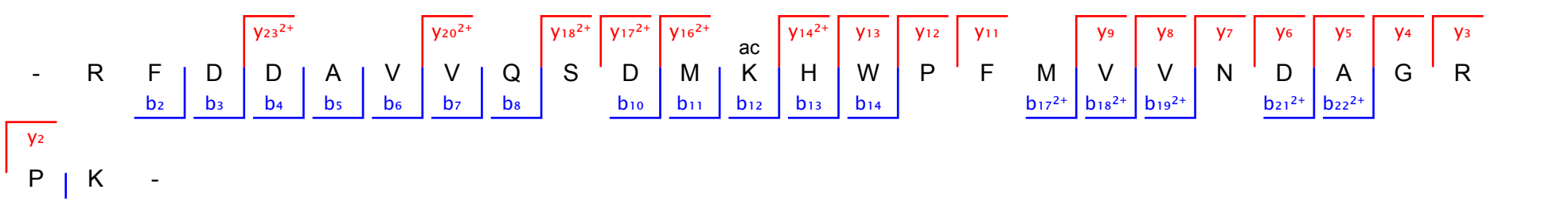
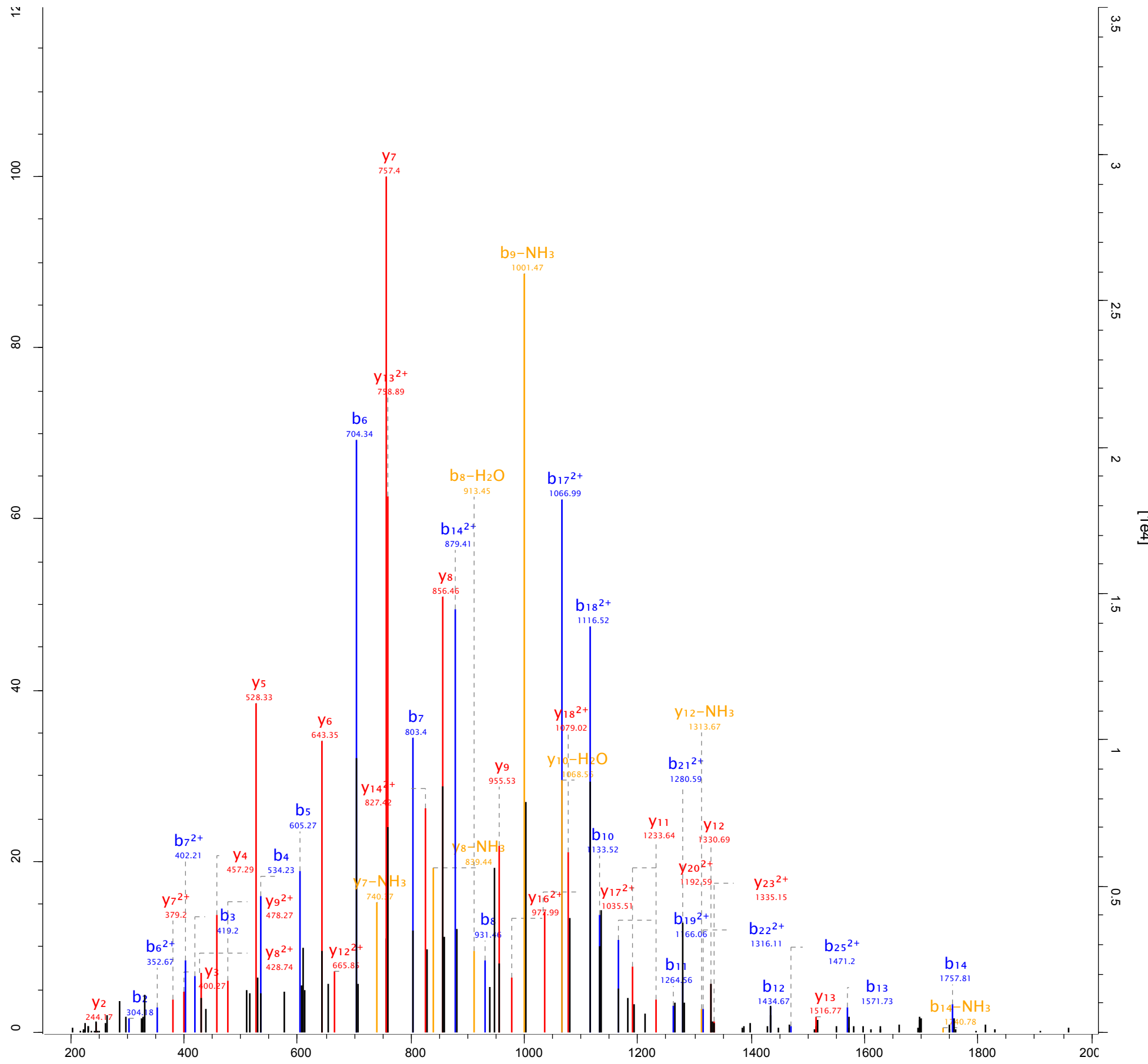


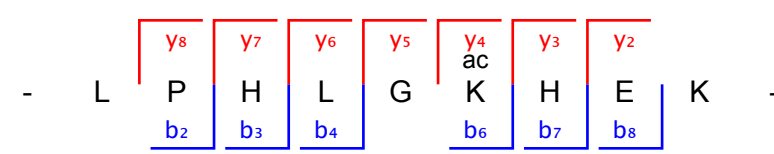
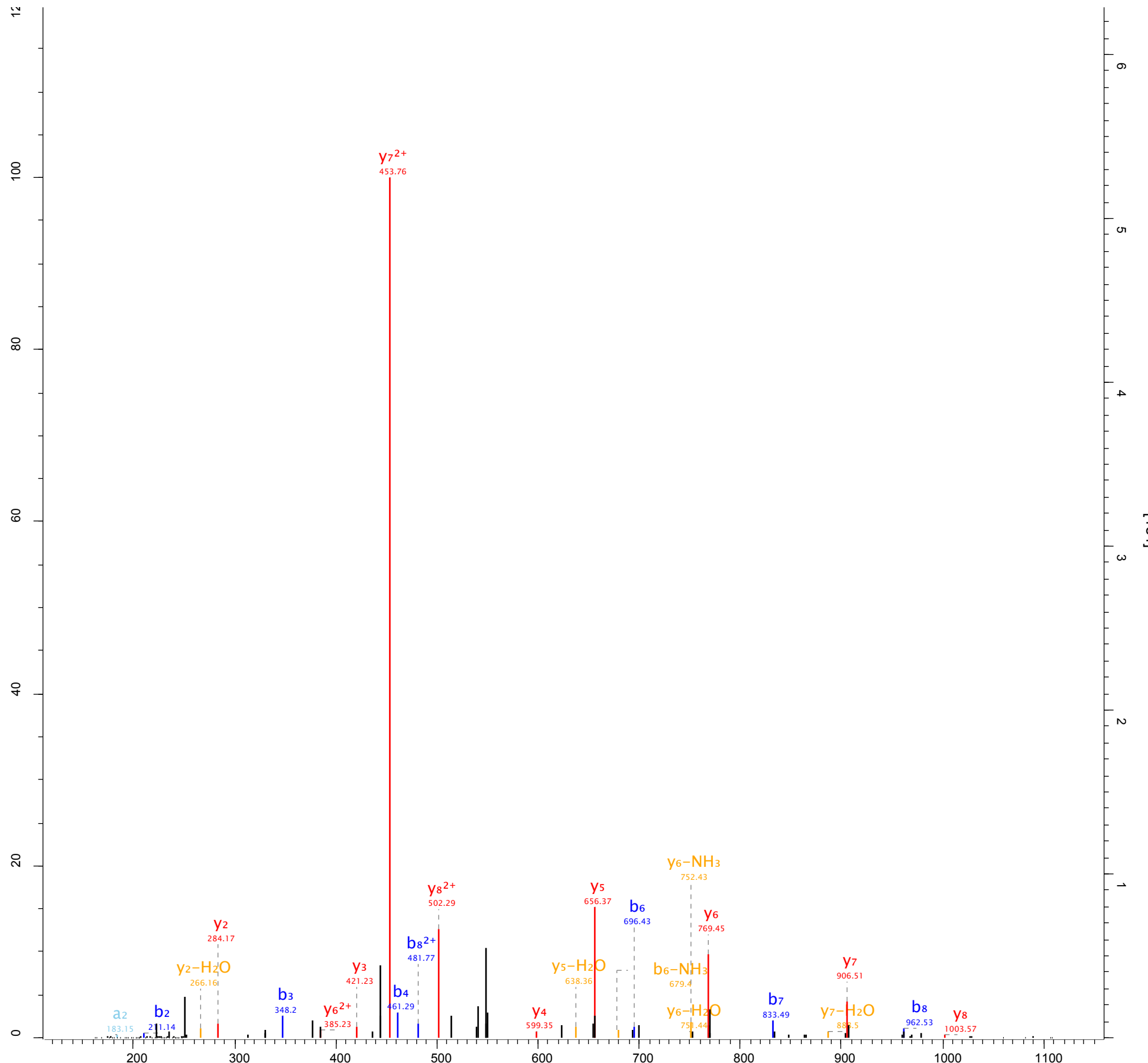


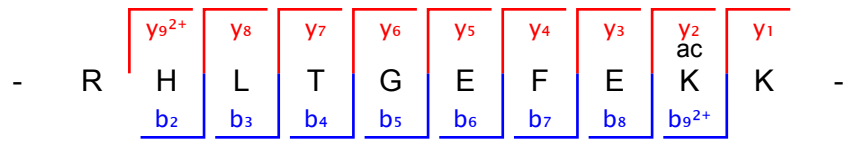
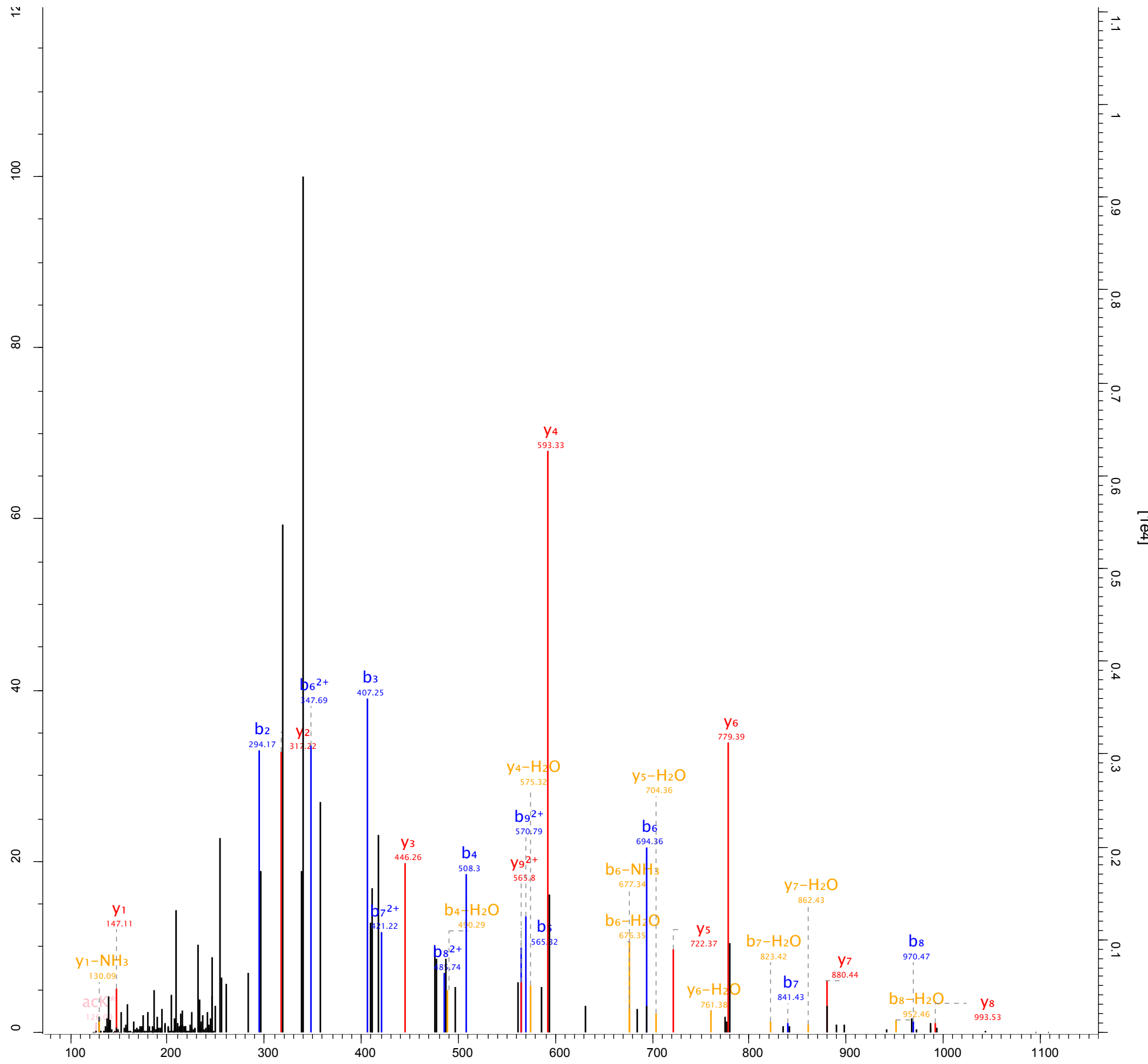






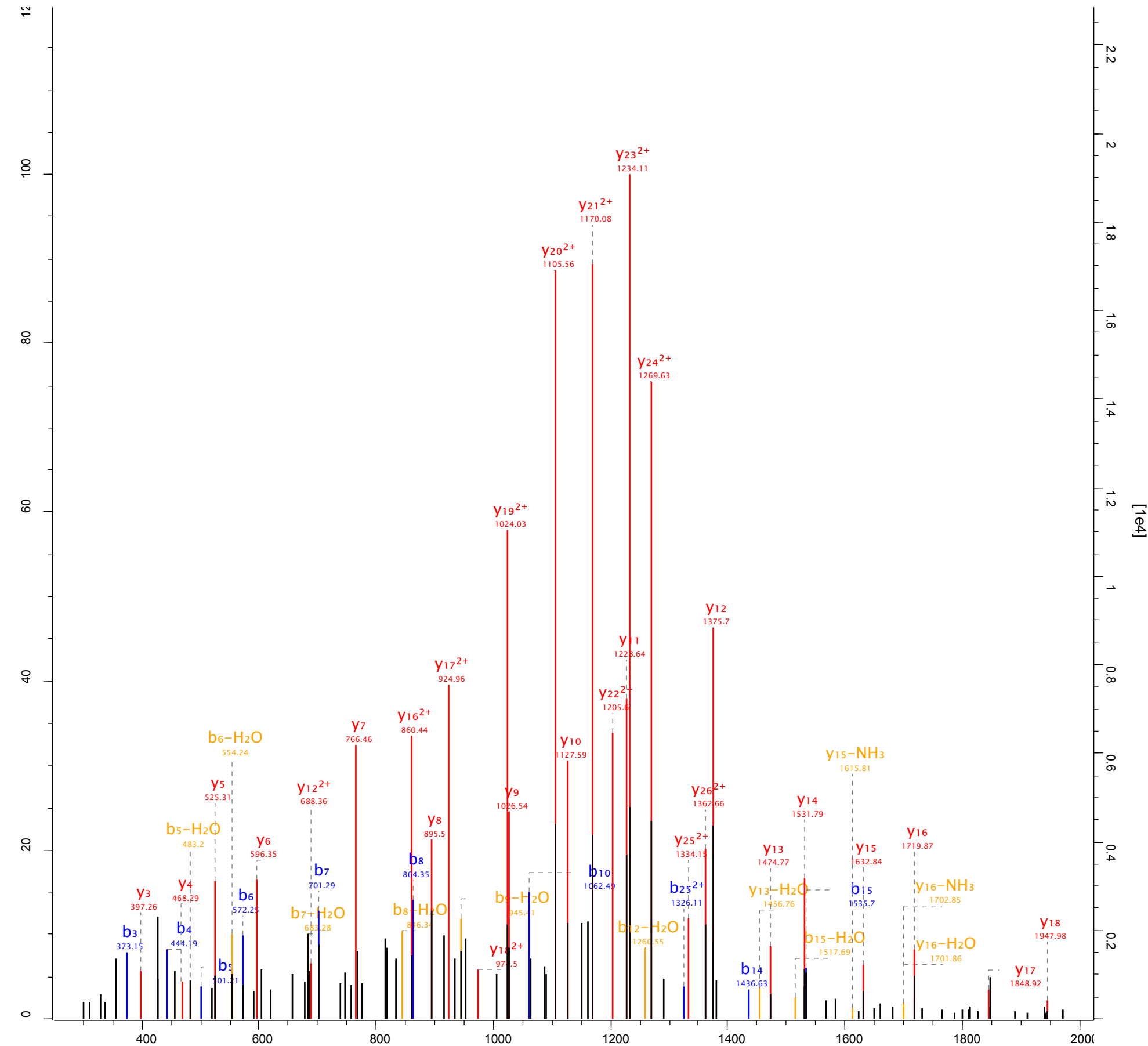






Raw file
062513_SCW_II_53_12_Vargas_Enriched

Scan Method Score m/z Gene names
28310 ITMS; CID 194.97 971.14 Gapdh



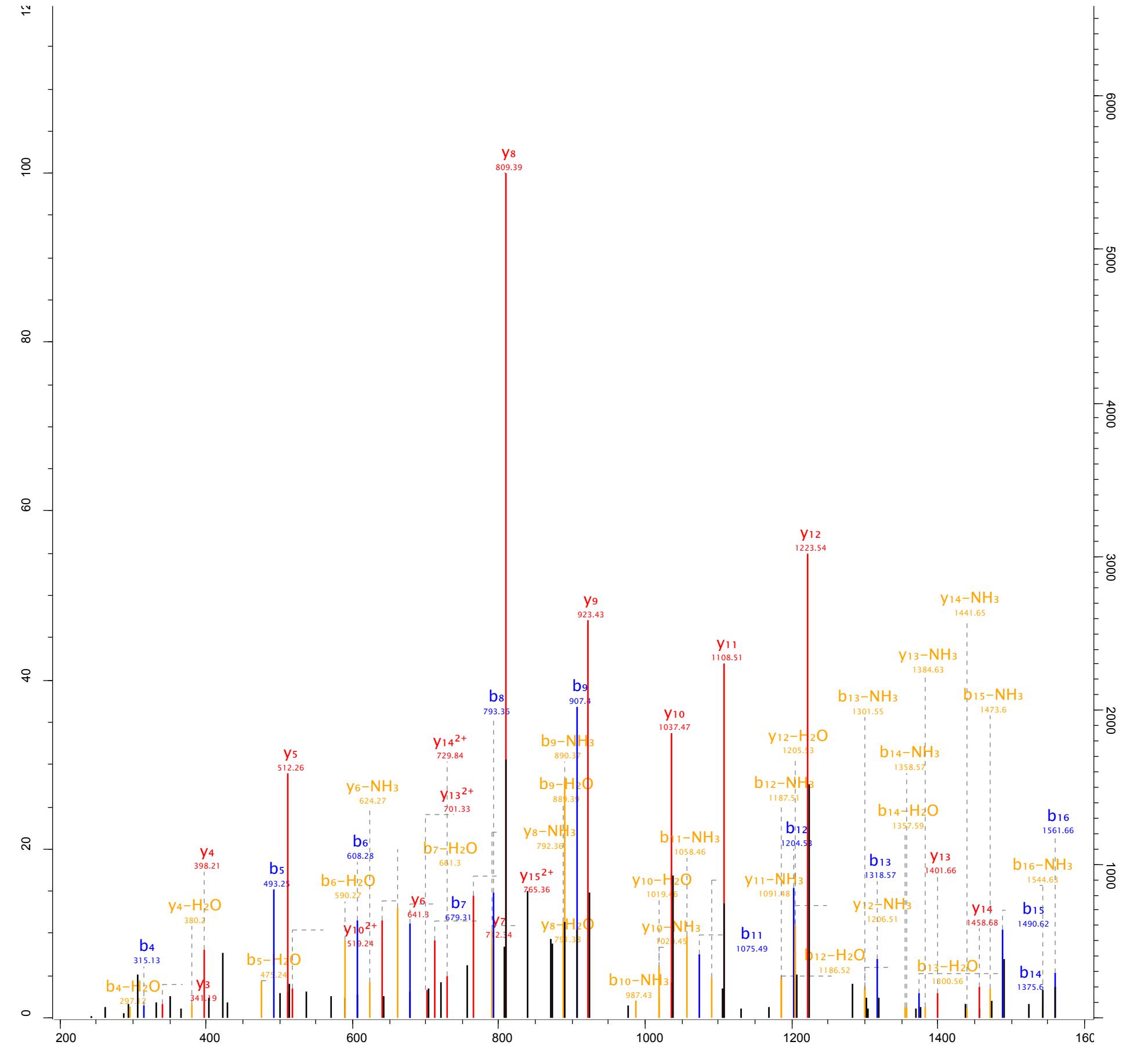
- W G E A G A E Y V V E S T G V F T T M E K A G A

 y₂₆²⁺ y₂₅²⁺ y₂₄²⁺ y₂₃²⁺ y₂₂²⁺ y₂₁²⁺ y₂₀²⁺ y₁₉²⁺ y₁₈ y₁₇ y₁₆ y₁₅ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄

 b₃ b₄ b₅ b₆ b₇ b₈ b₁₀ b₁₄ b₁₅

 y₃

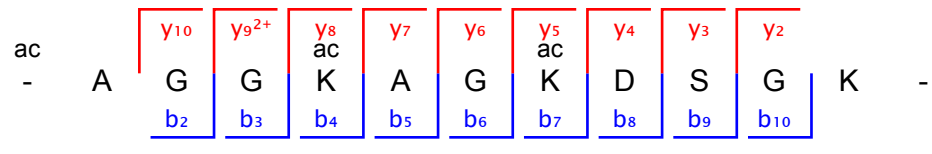
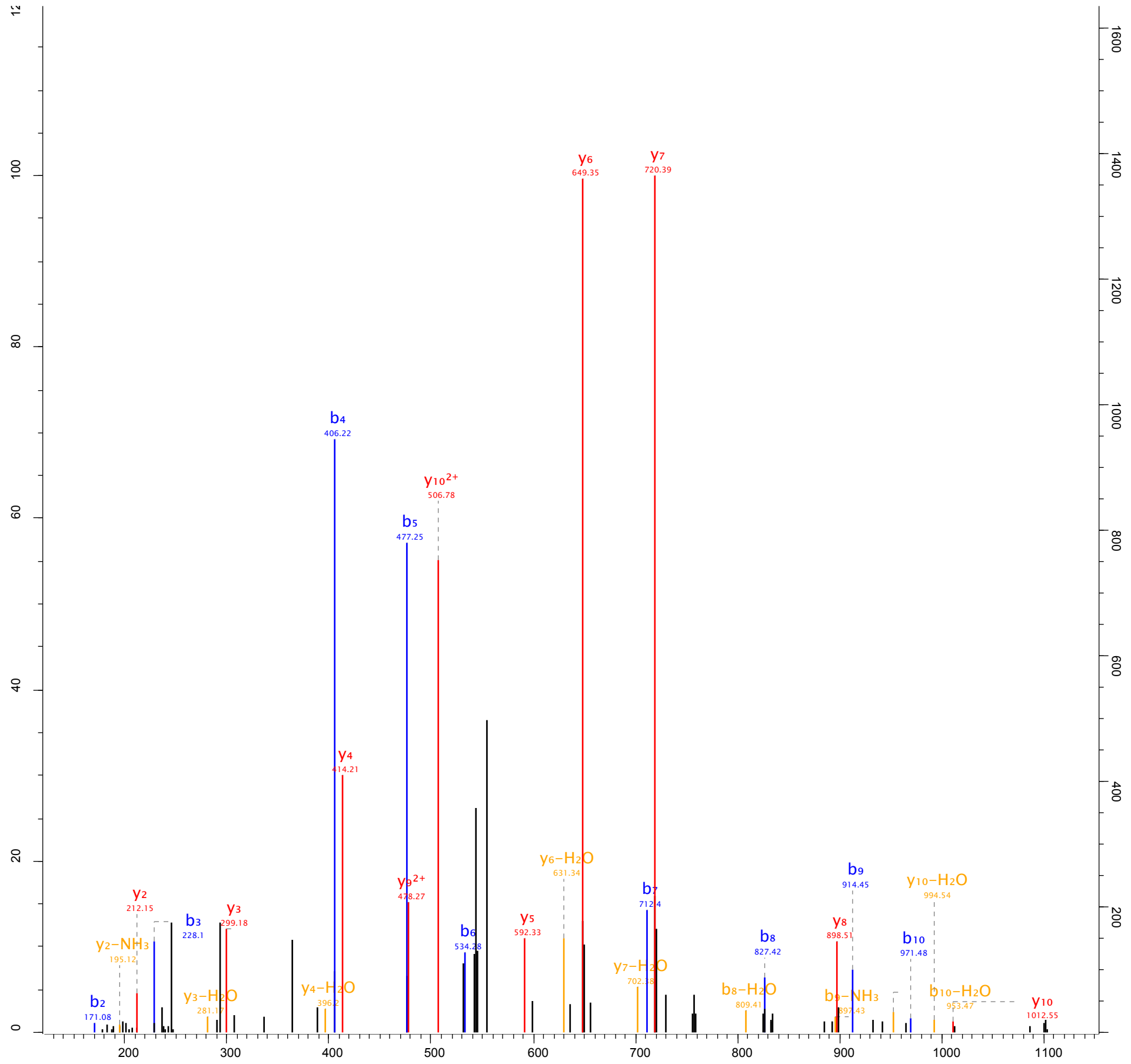
H | L K -



- A D A G K D A N N P A E N G D A K -

y15²⁺
y14
y13 ac
y12
y11
y10
y9
y8
y7
y6
y5
y4
y3

b4
b5
b6
b7
b8
b9
b11
b12
b13
b14
b15
b16



072613_SCW_II_68_Enriched_1

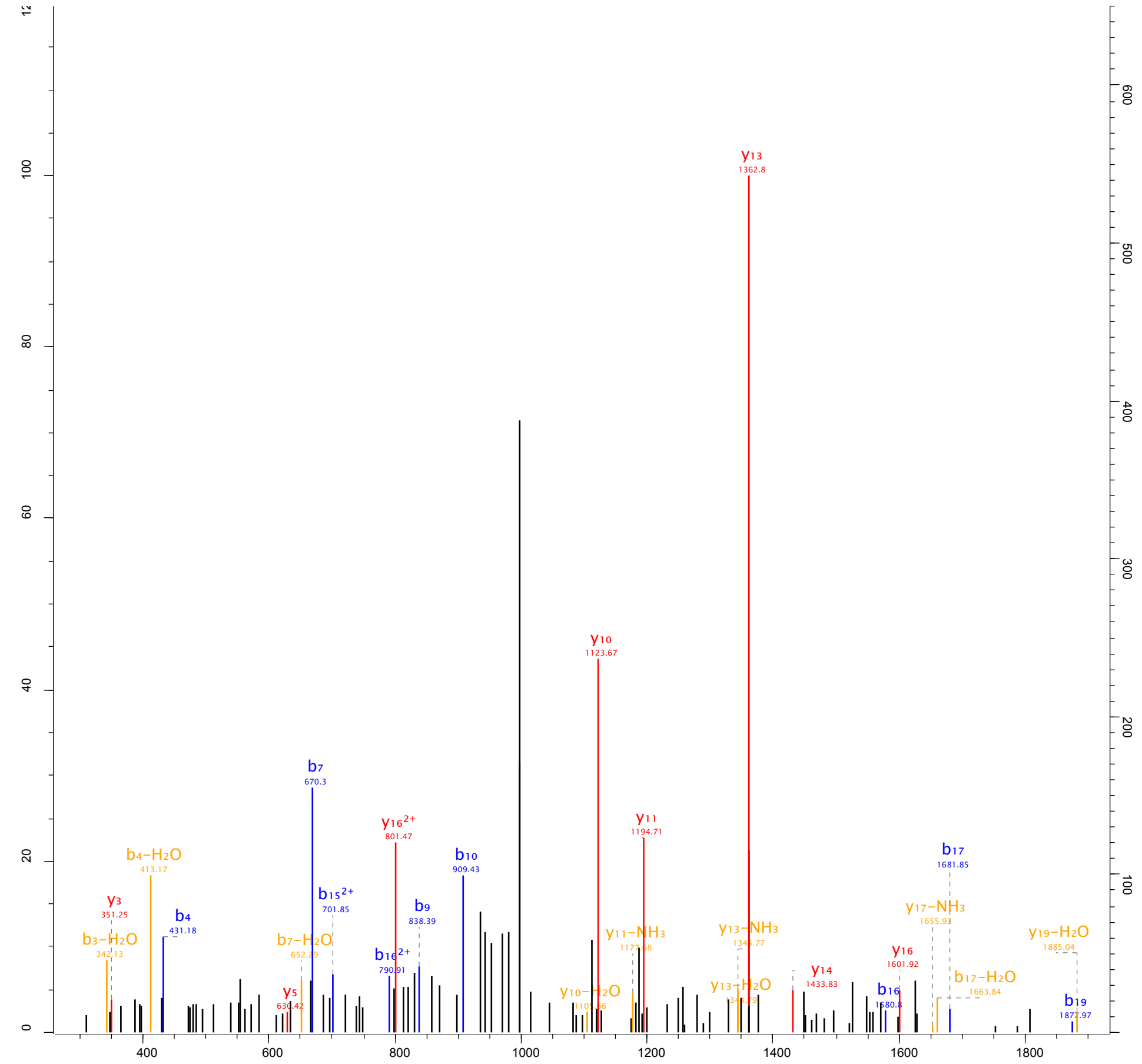
18365

ITMS; CID

93.37

1016.55

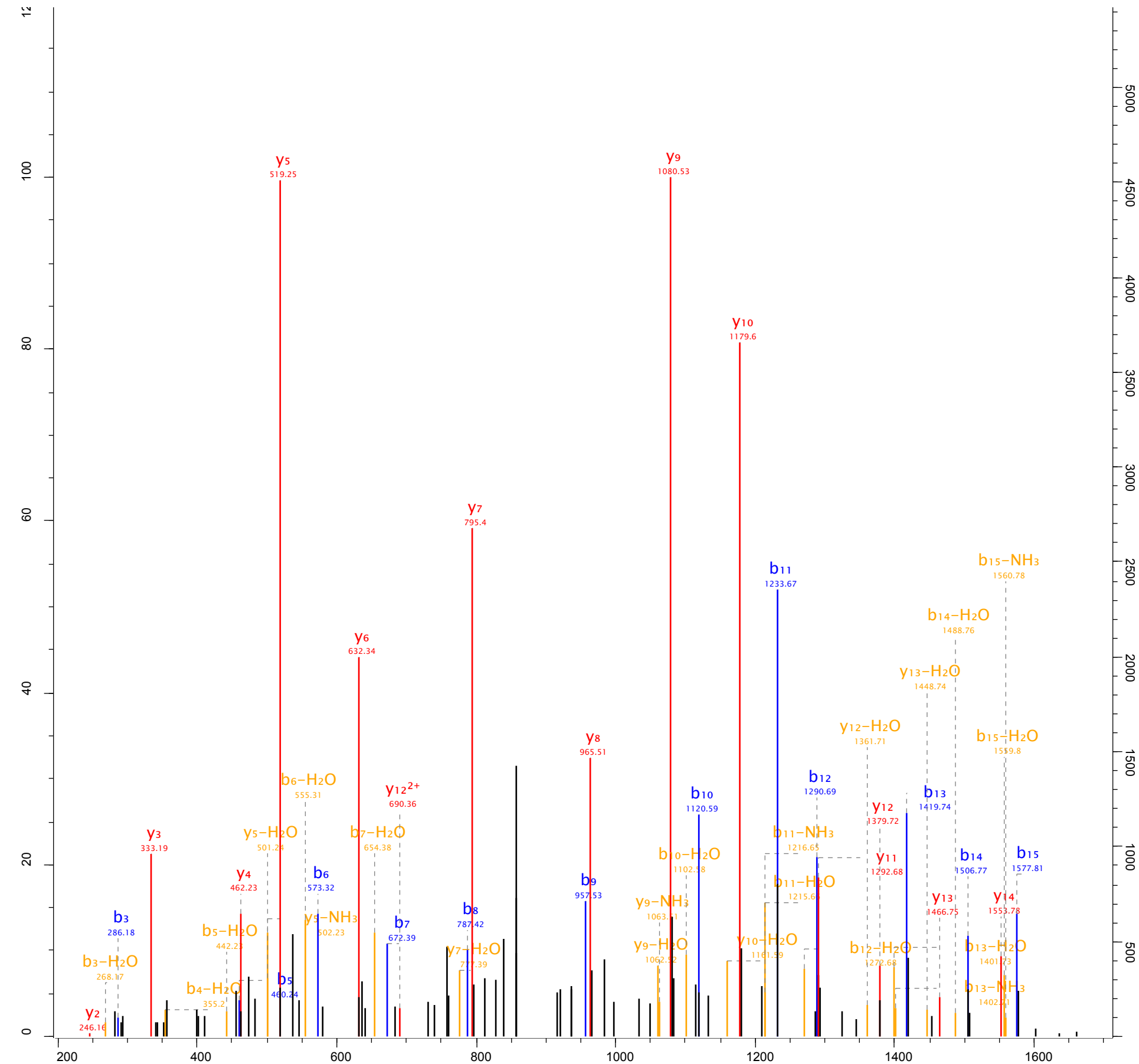
Hist1h1d



ac - S E T A P A A P A A P A P V E K T P V K -

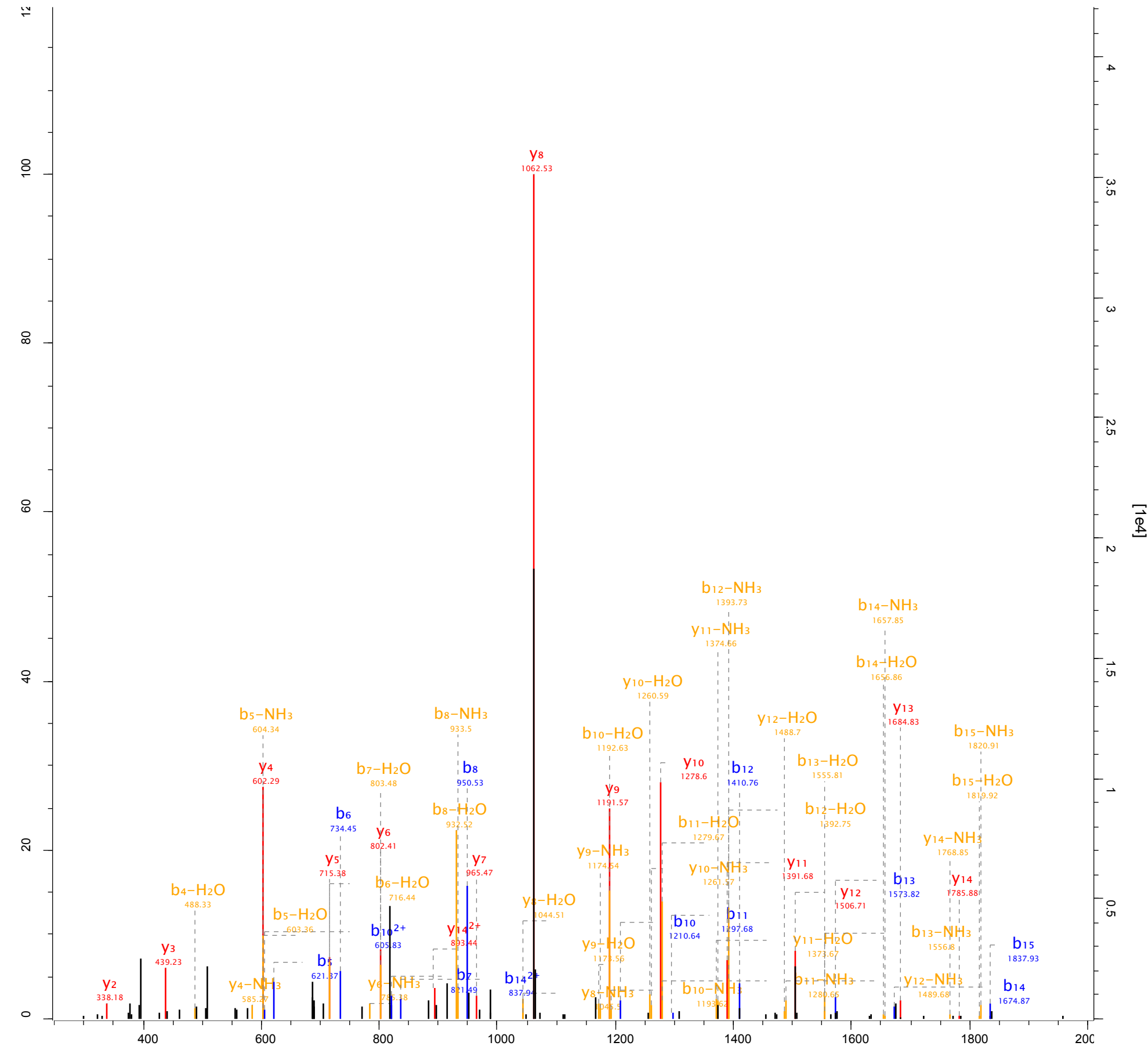
Fragmentation mapping (b and y ions):

- b4: A
- y16: P
- b7: A
- y14: A
- y13: P
- b9: A
- y11: A
- y10: P
- b15²⁺: V
- b16: K
- y5: ac
- b17: T
- y3: P
- b19: V



- V V S^{y₁₄} S^{y₁₃} S^{y₁₂} I^{y₁₁} V^{y₁₀} D^{y₉} K^{y₈ ac} Y^{y₇} I^{y₆} G^{y₅} E^{y₄} S^{y₃} A^{y₂} R -

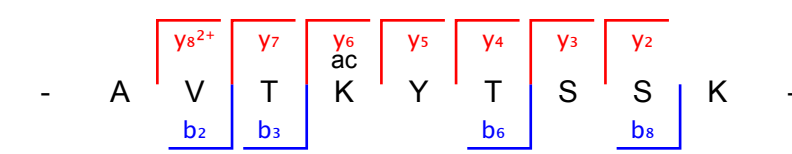
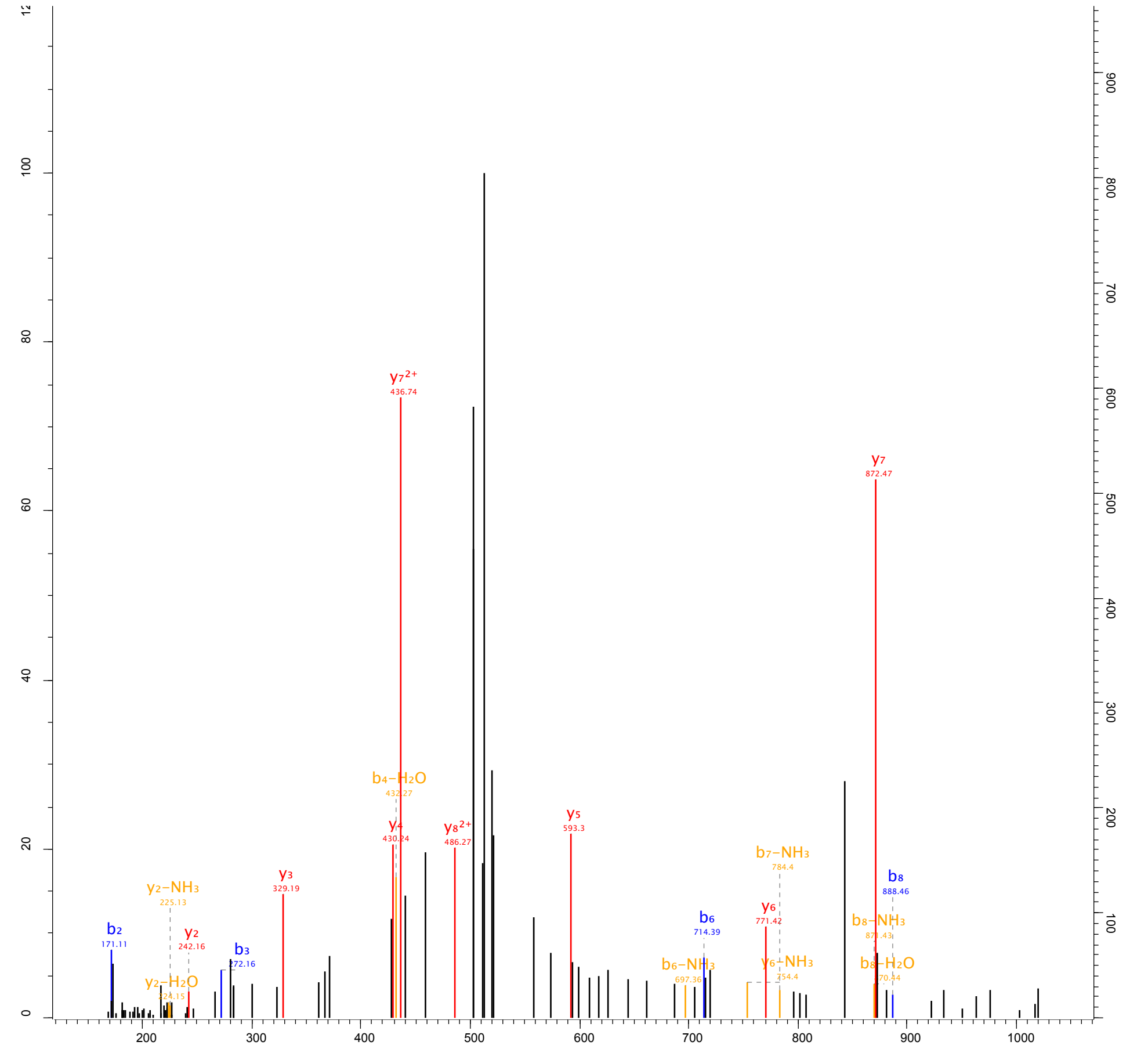
b₃ b₅ b₆ b₇ b₈ b₉ b₁₀ b₁₁ b₁₂ b₁₃ b₁₄ b₁₅



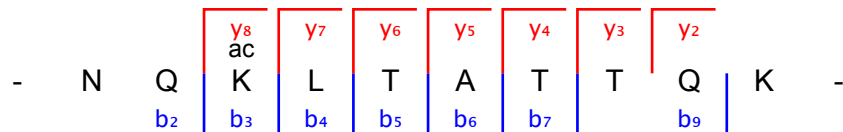
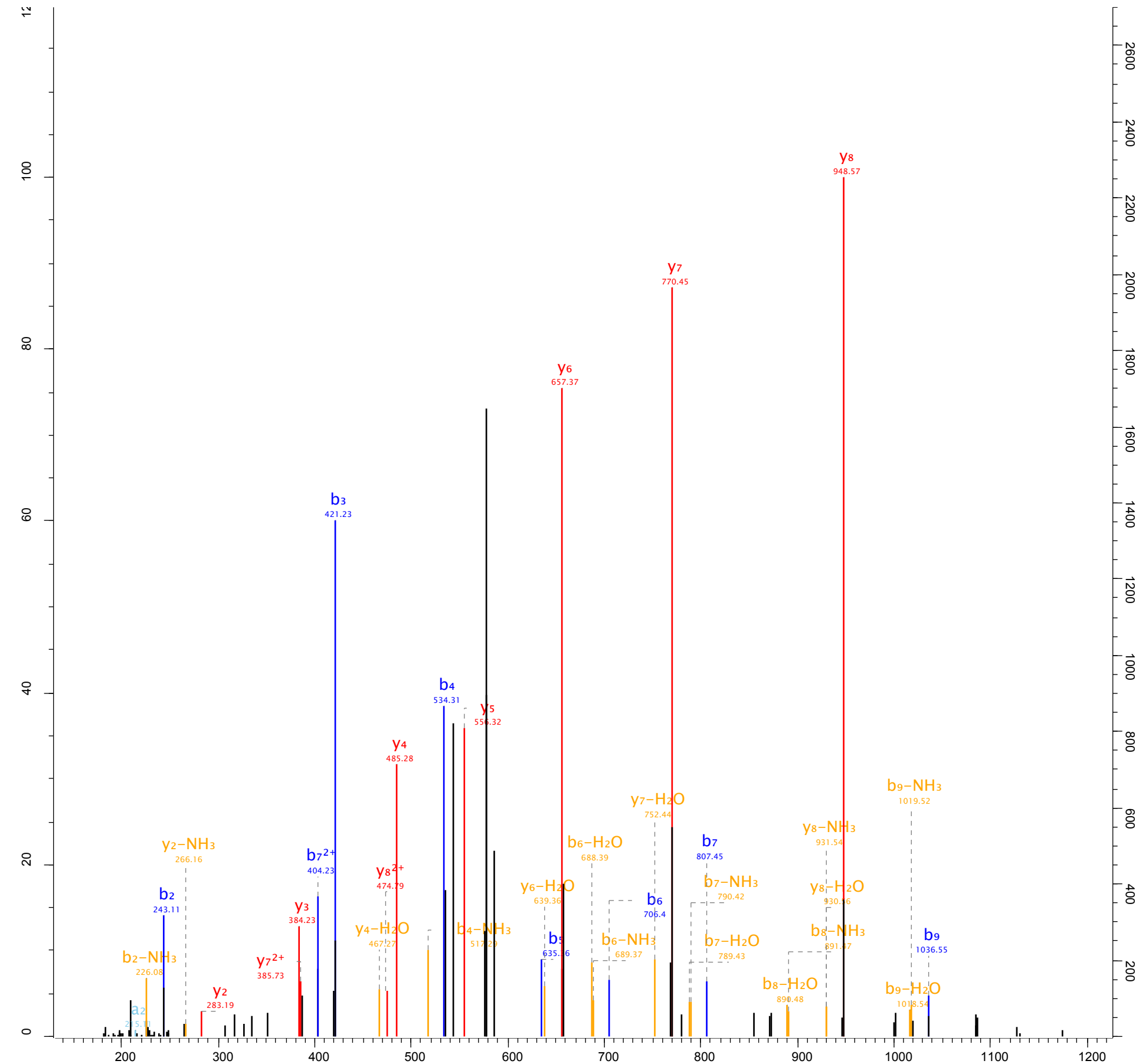
Y14
Y13 ac
Y12
Y11
Y10
Y9
Y8
Y7
Y6
Y5
Y4
Y3
Y2

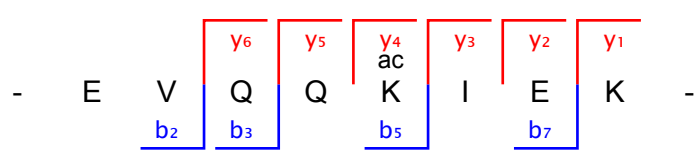
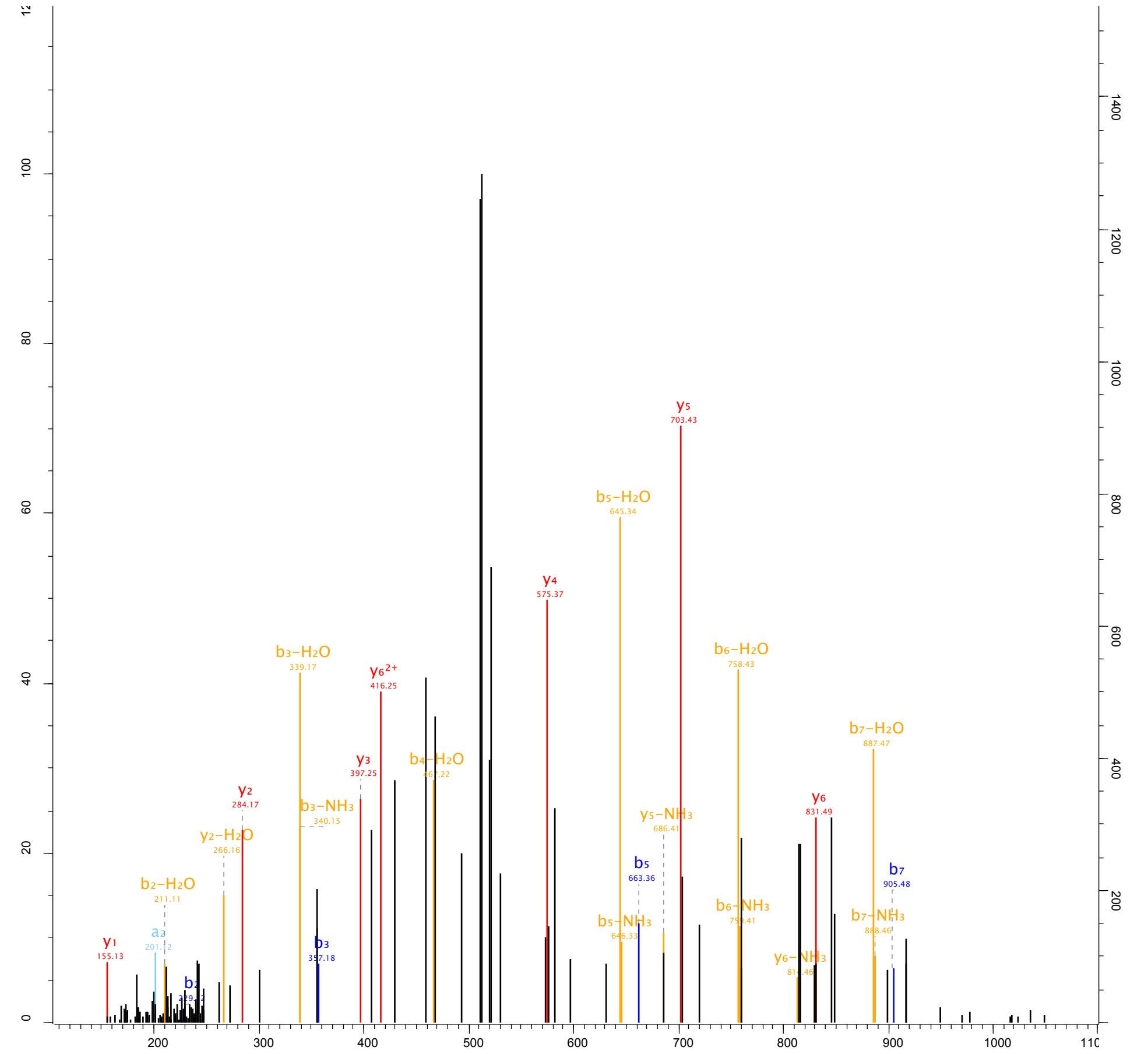
b5
b6
b7
b8
b10
b11
b12
b13
b14
b15

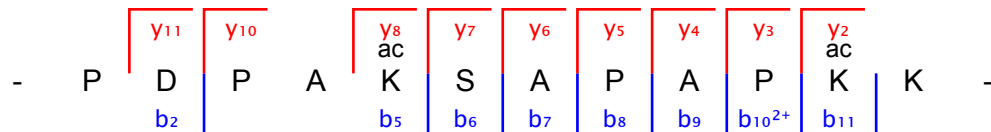
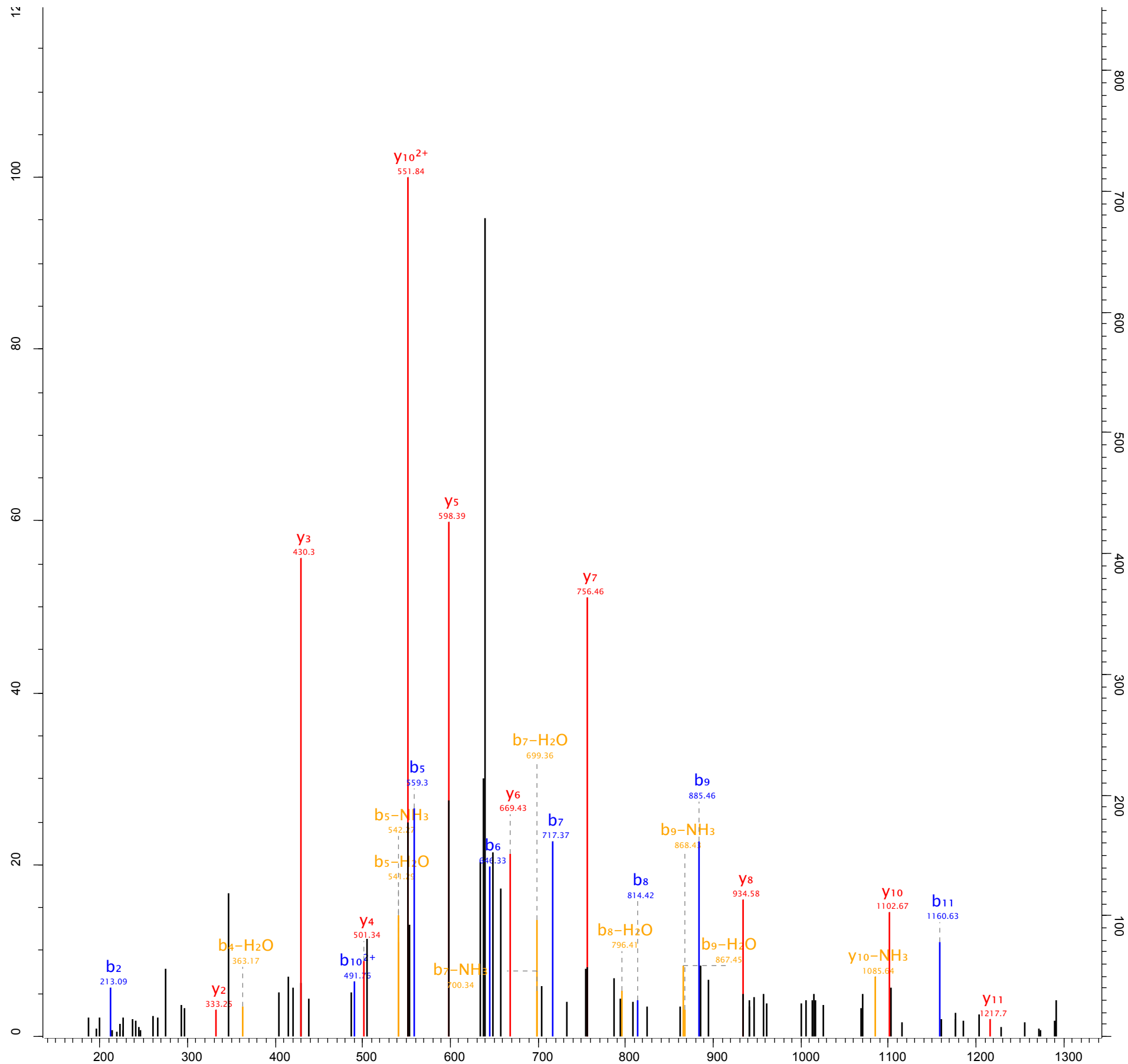
- L I T K D L S E P Y S I Y T Y R -



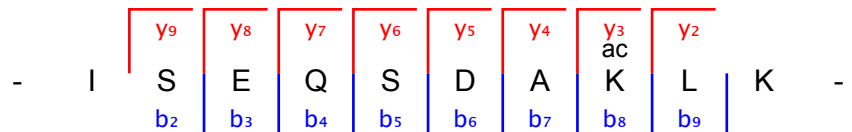
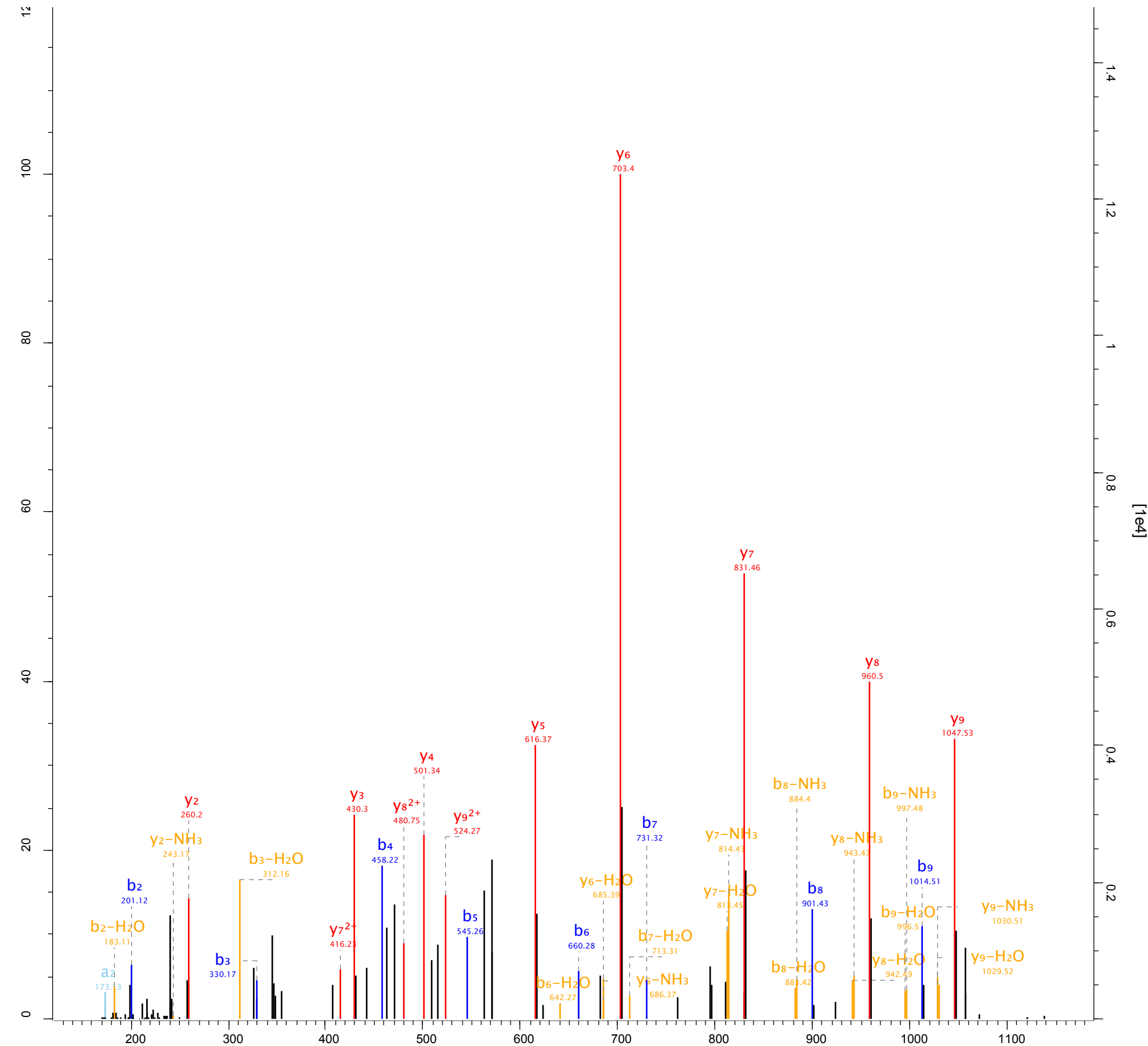
Raw file 072613_SCW_II_68_Enriched_4 Scan 12385 Method ITMS; CID 204.56 m/z 595.84 Gene names Tpr

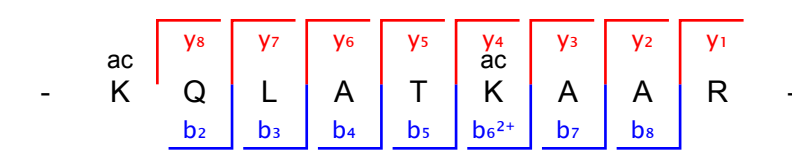
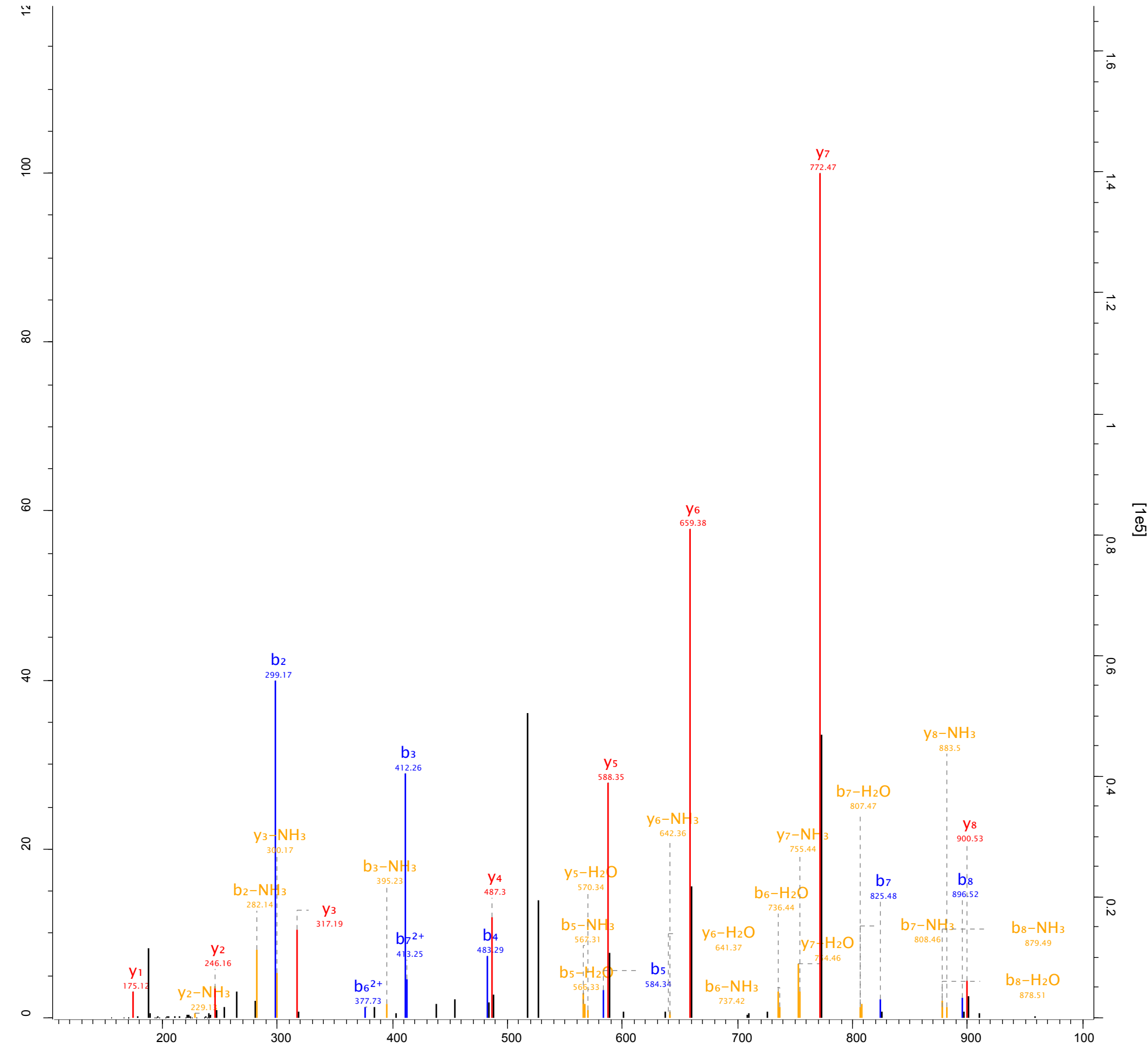


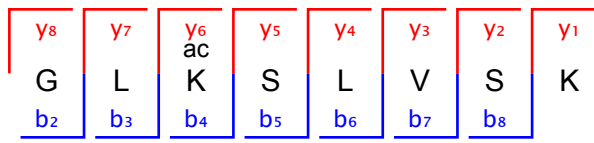
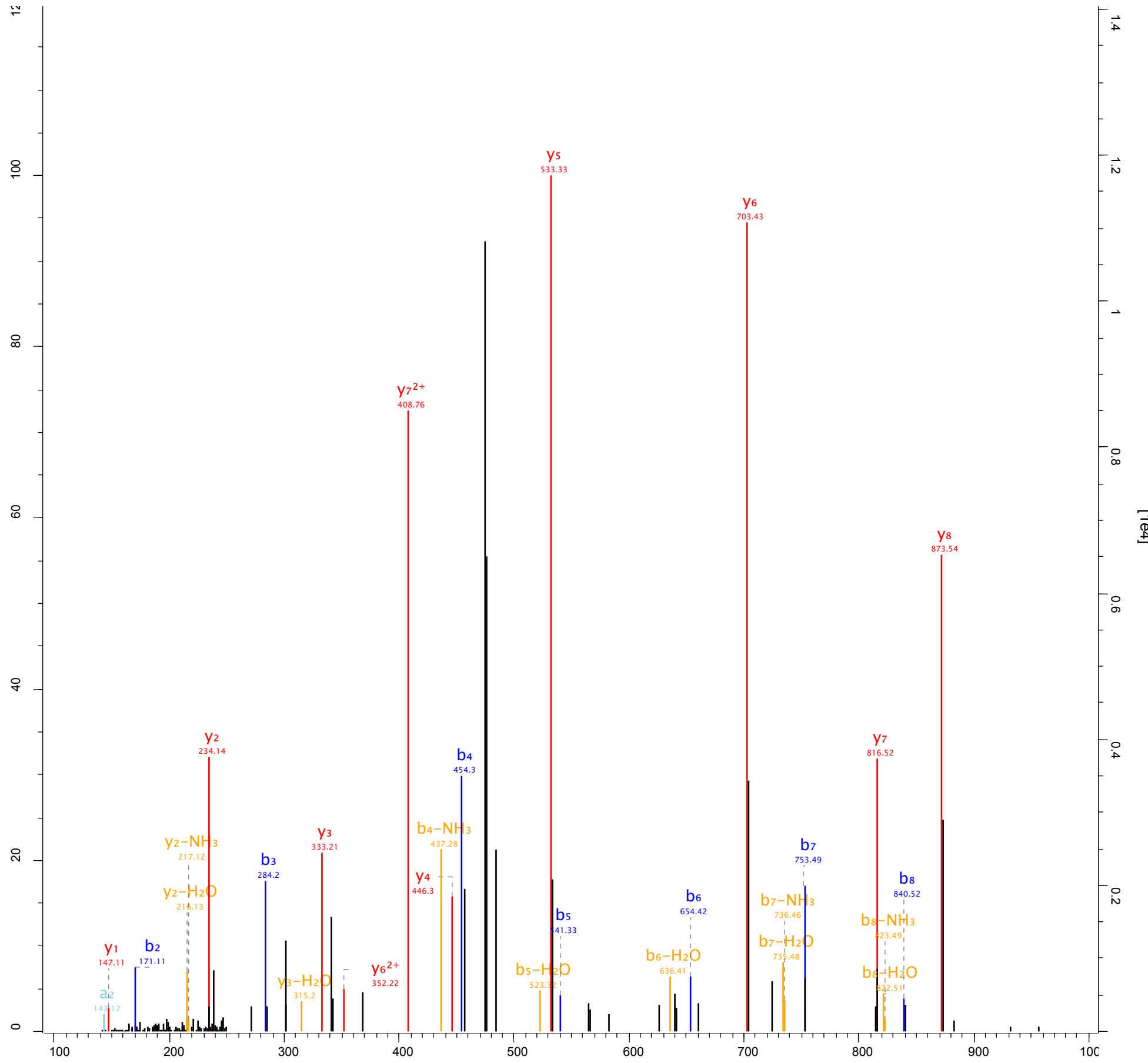




Raw file 072613_SCW_II_68_Enriched_4 Scan 13880 Method ITMS; CID Score 243.91 m/z 580.81 Gene names Atp5a1

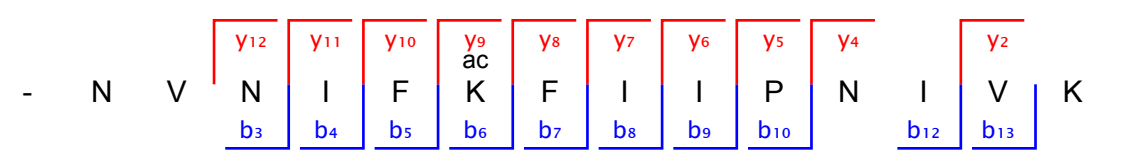
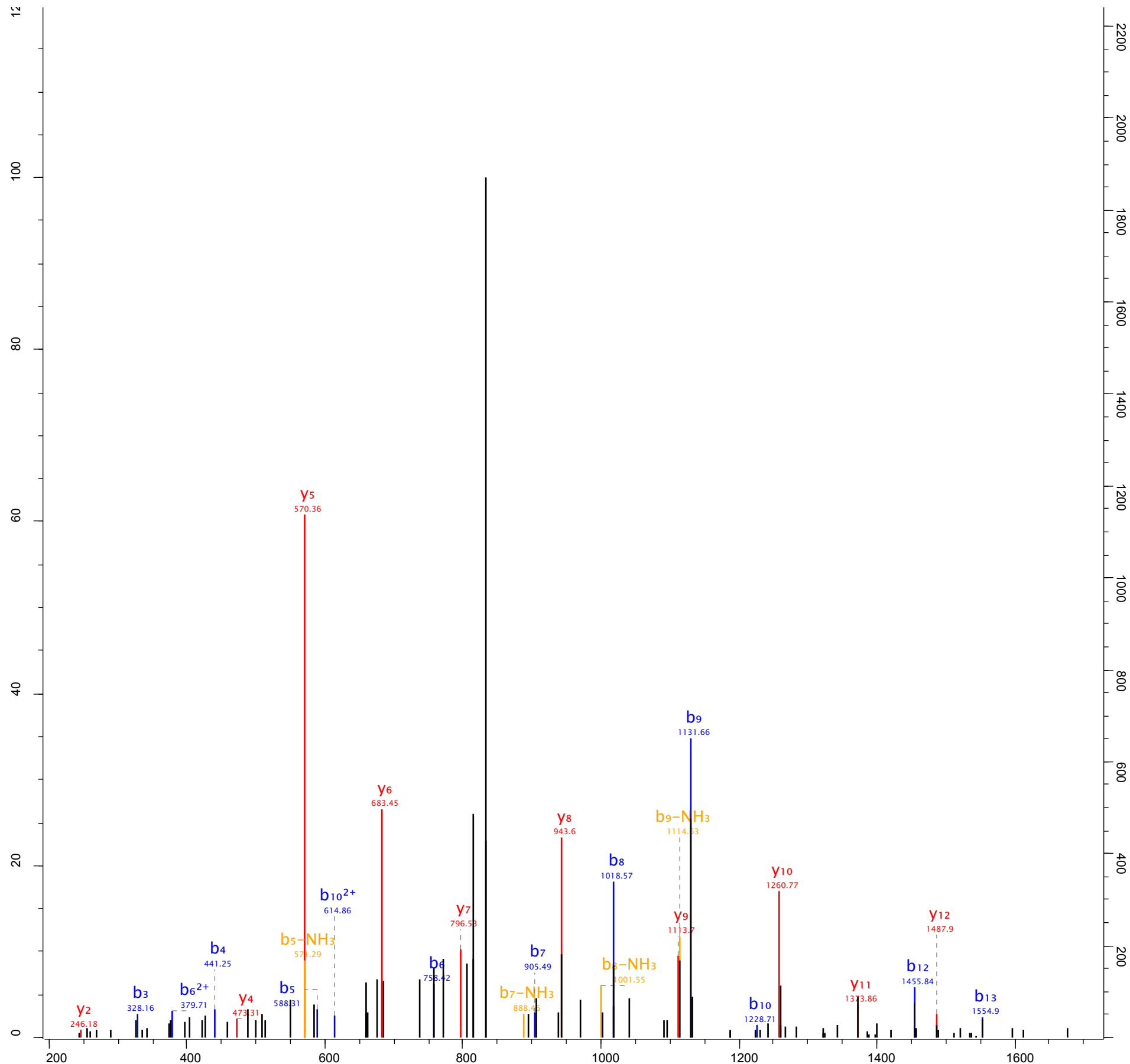


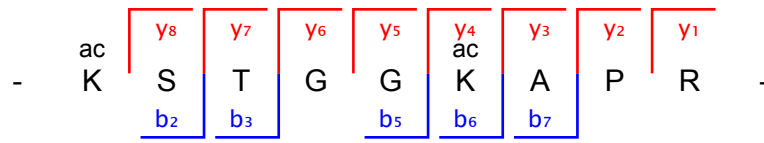
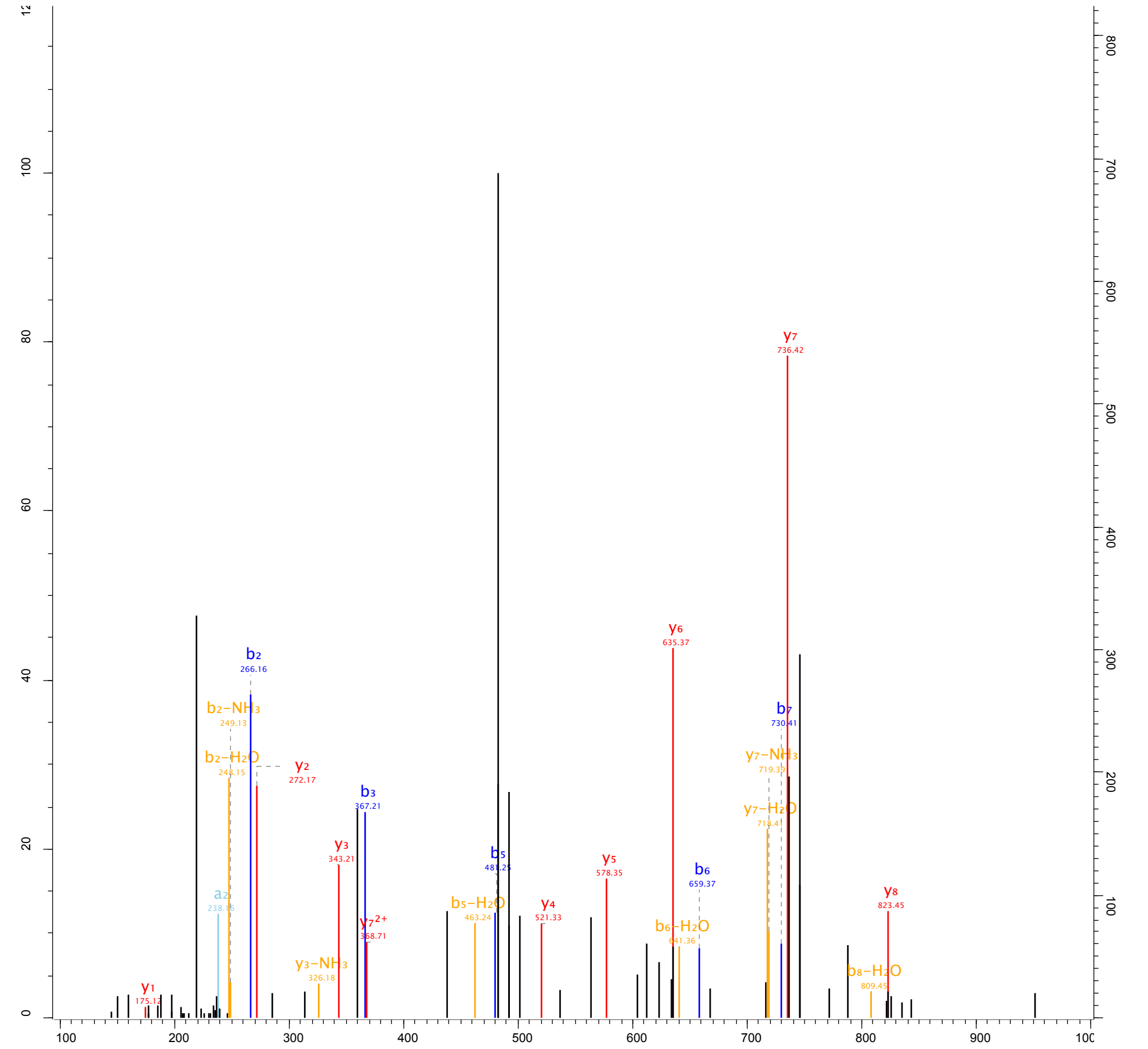




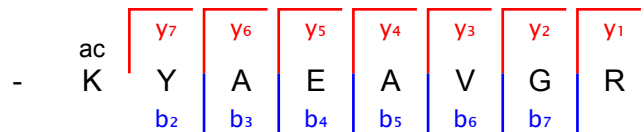
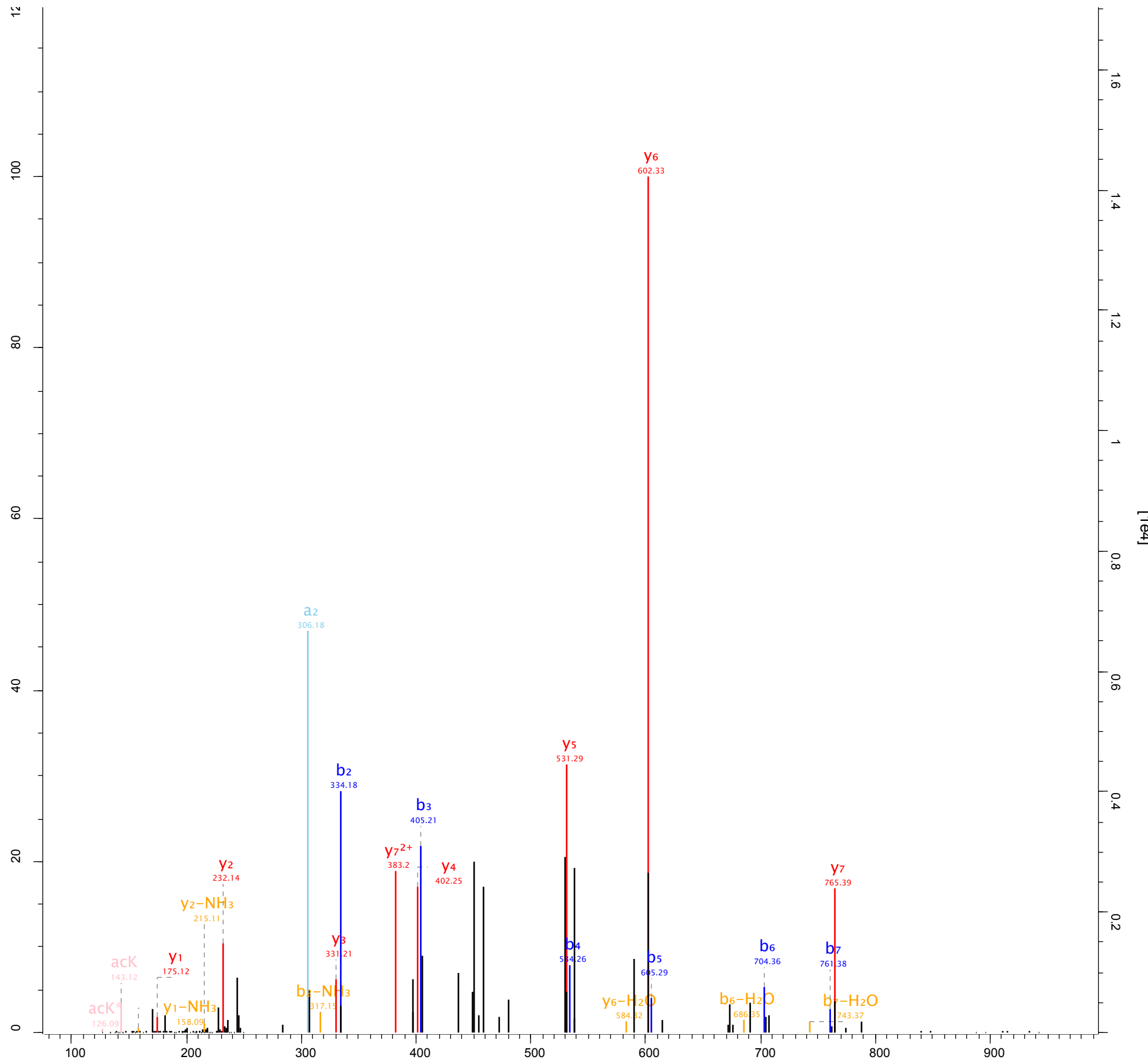
Raw file
072613_SCW_II_68_Enriched_4

Scan 31183 Method ITMS; CID Score 124.47 m/z 851.51 Gene names Ldha

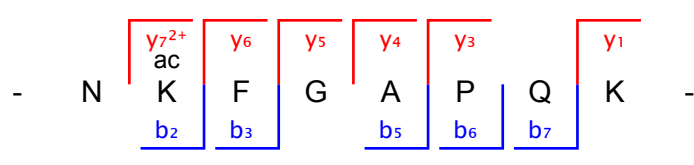
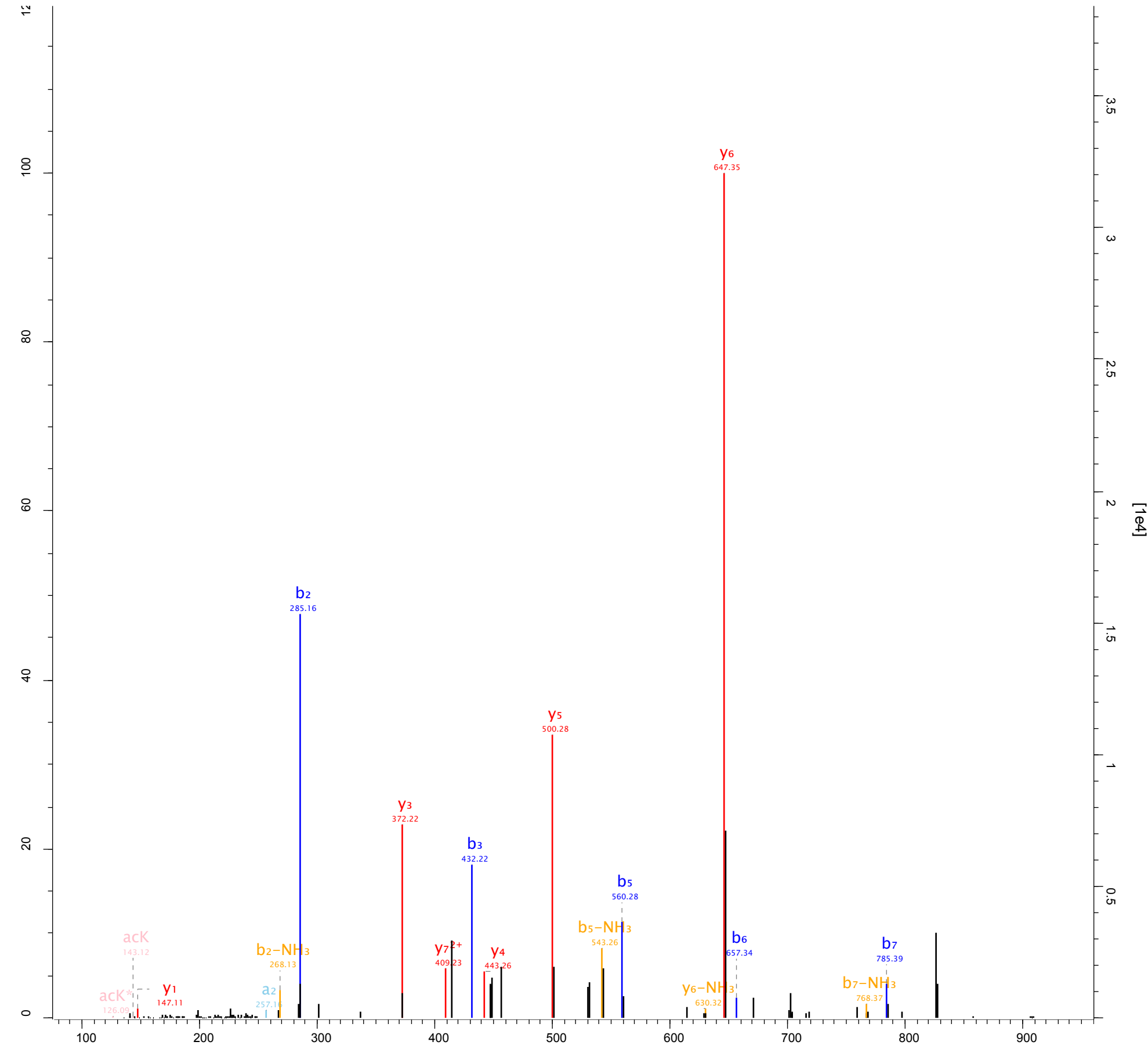




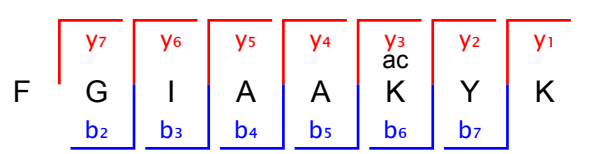
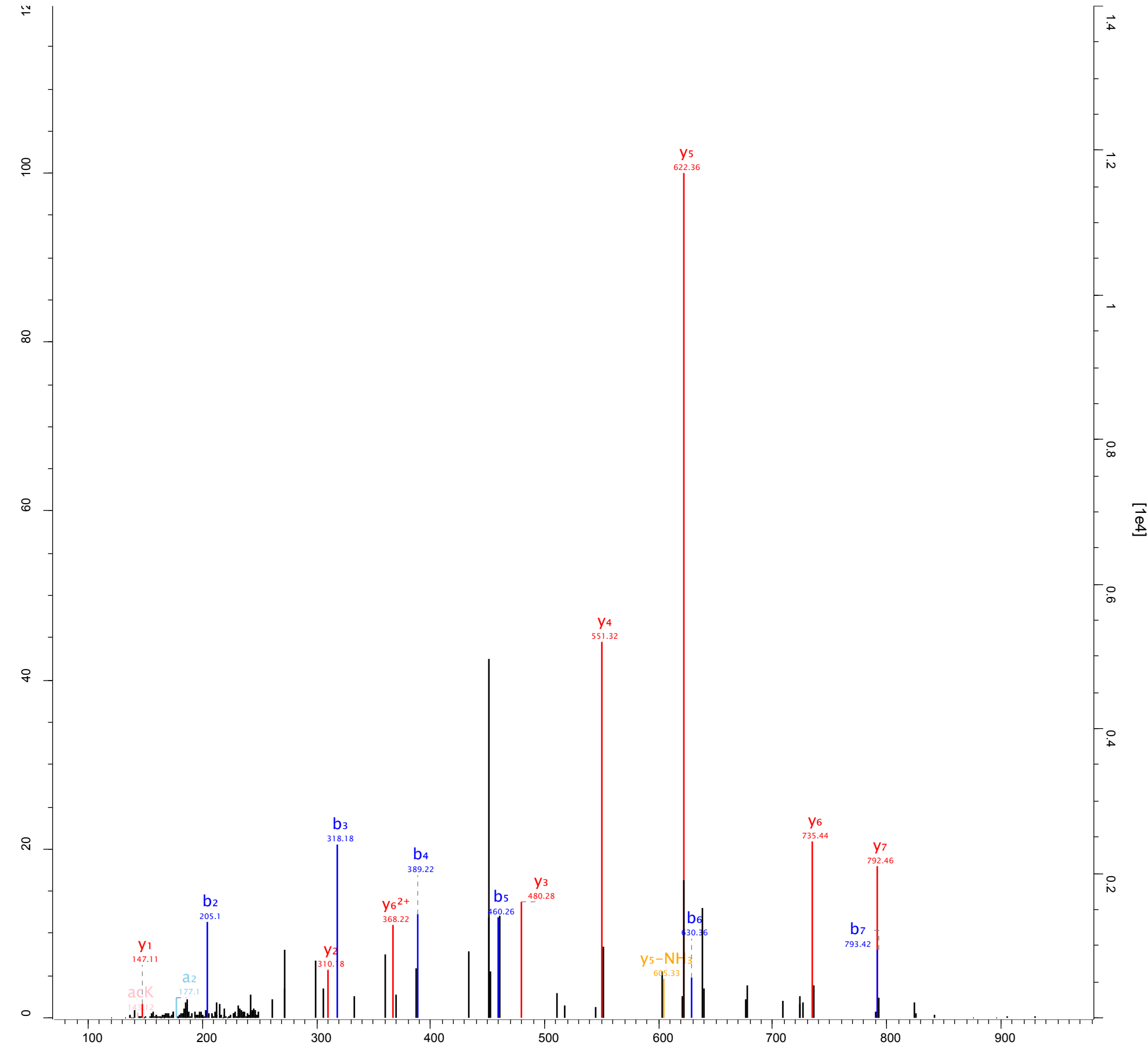
Raw file 072613_SCW_II_68_Enriched_5 Scan 12950 Method ITMS; CID Score 125.71 m/z 468.25 Gene names Pgk1

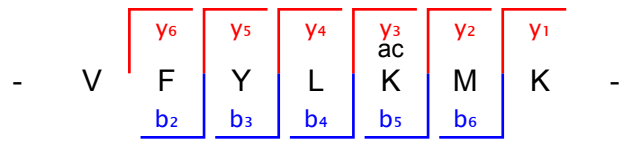
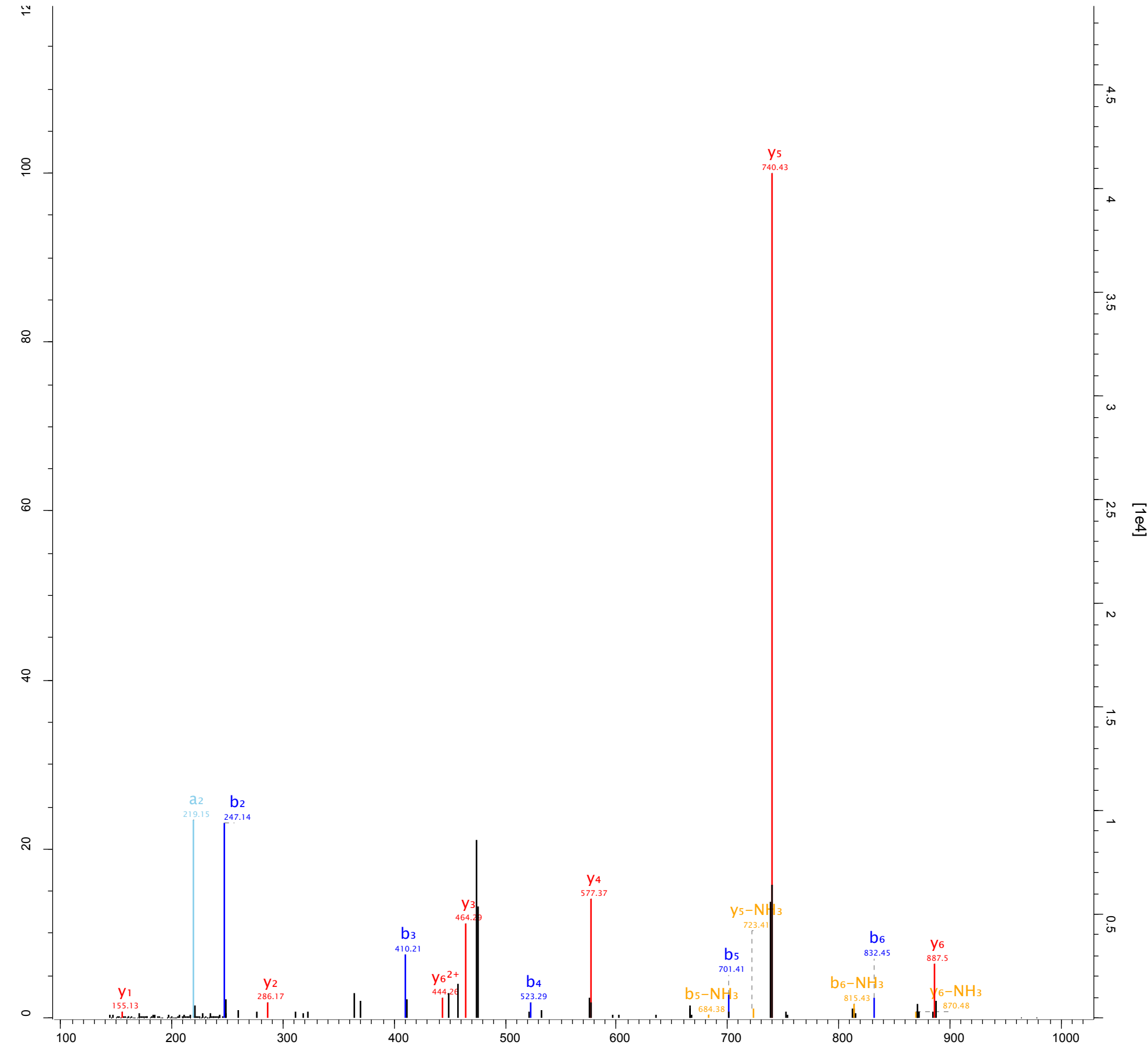


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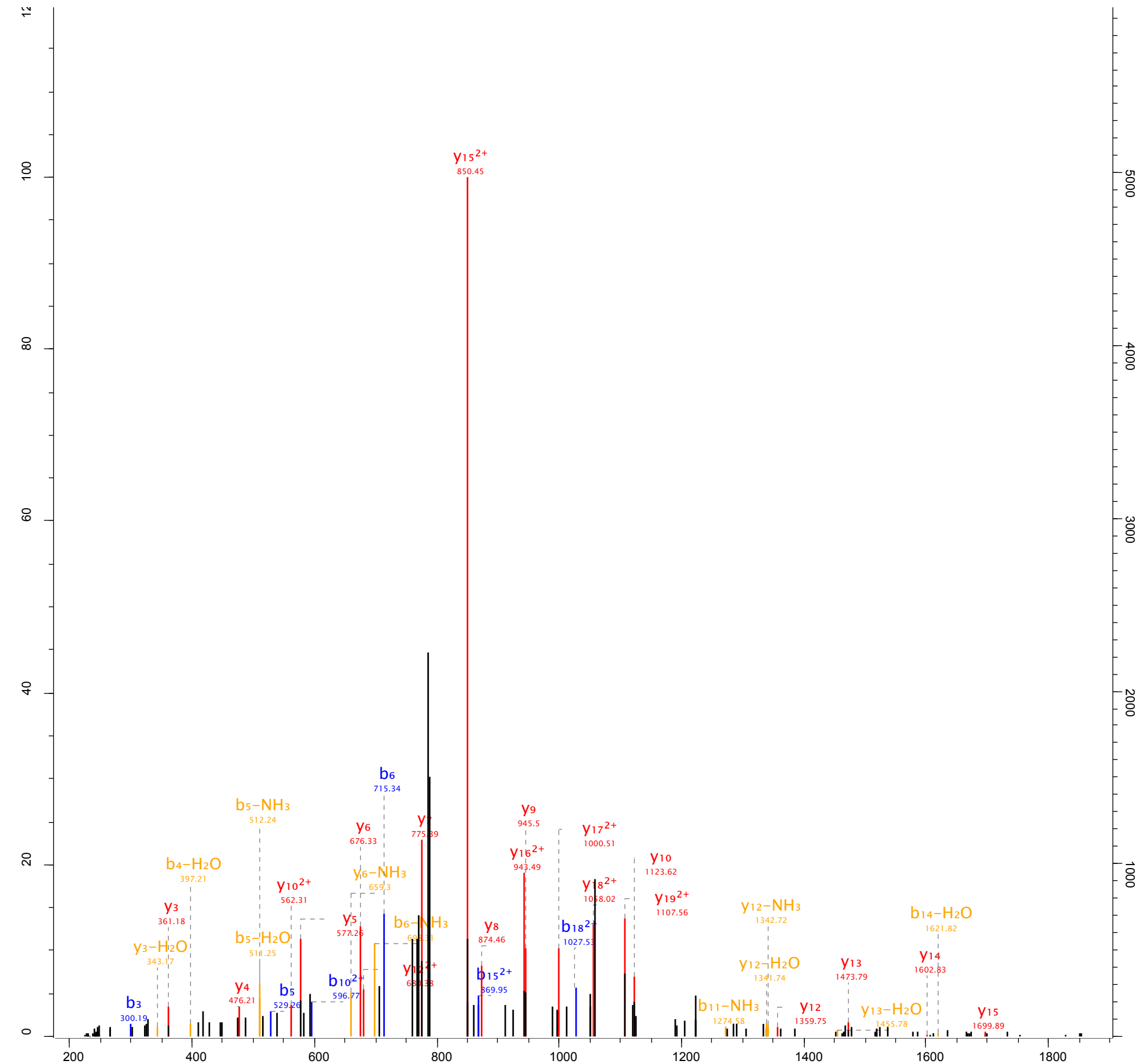


Raw file 072613_SCW_II_68_Enriched_5 Scan 18536 Method ITMS; CID Score 120.46 m/z 470.27 Gene names Vdac3





Raw file 072613_SCW_II_68_Enriched_6 Scan 22130 Method ITMS; CID Score 122.94 m/z 805.75 Gene names Me2



- S I V D N W P E N H V K A V V V T D G E R -

b₃ b₅ b₆ b₁₀²⁺ b₁₅²⁺ b₁₈²⁺ y₁₉²⁺ y₁₈²⁺ y₁₇²⁺ y₁₆²⁺ y₁₅ y₁₄ y₁₃ y₁₂ y₁₀ ac y₉ y₈ y₇ y₆ y₅ y₄ y₃

072613_SCW_II_68_Enriched_6

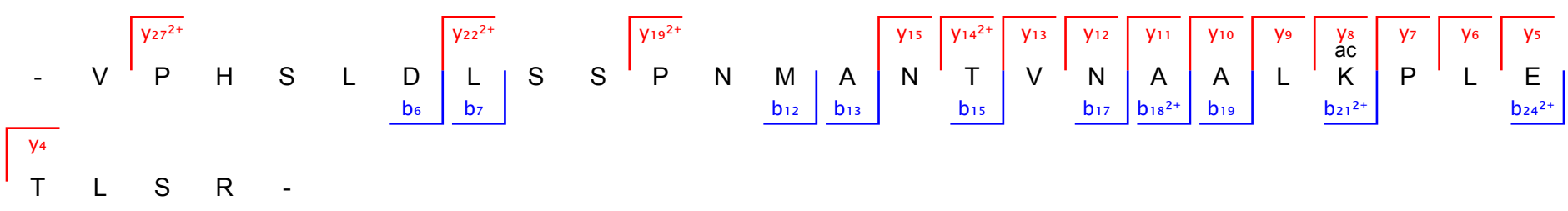
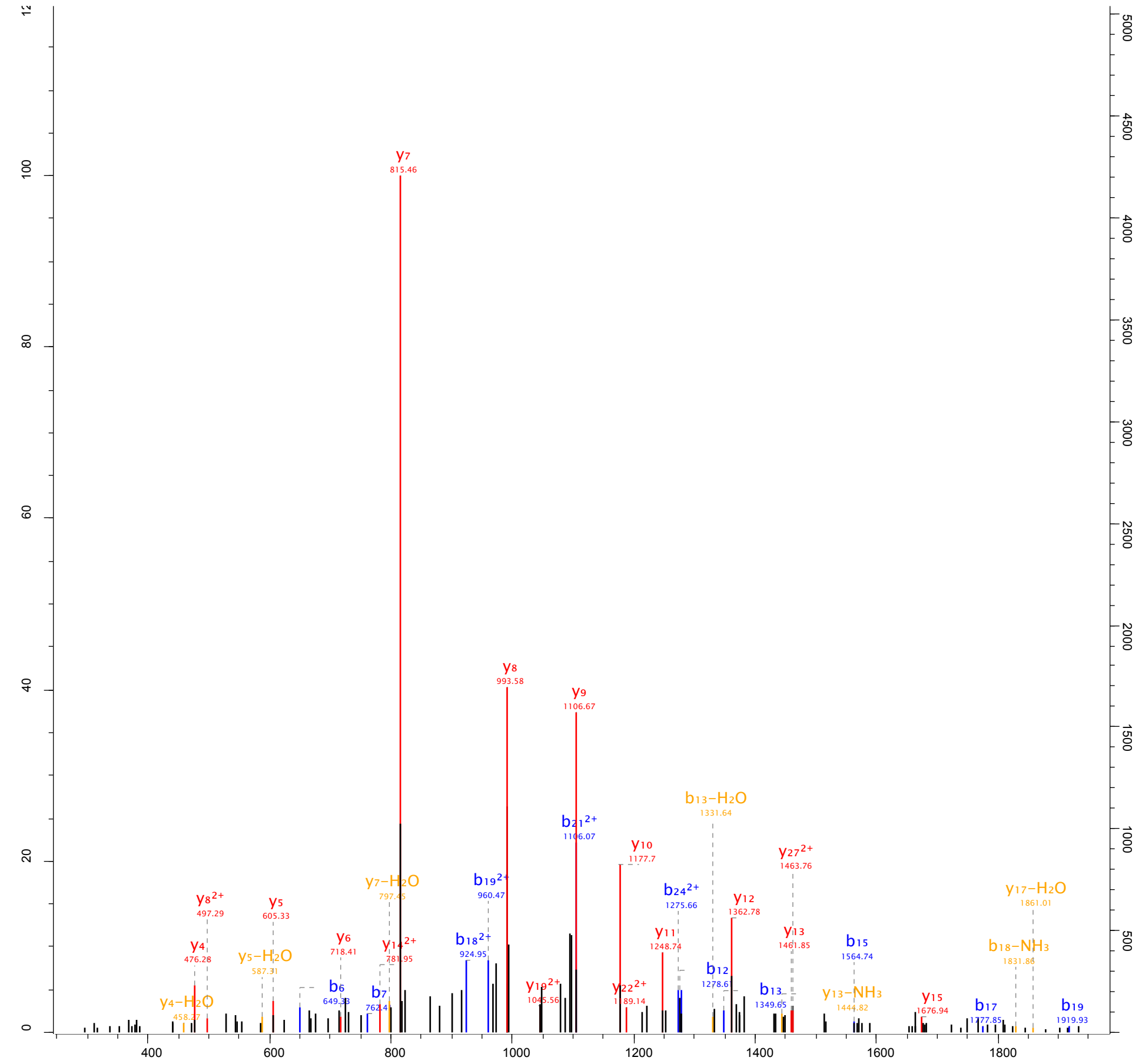
28190

ITMS; CID

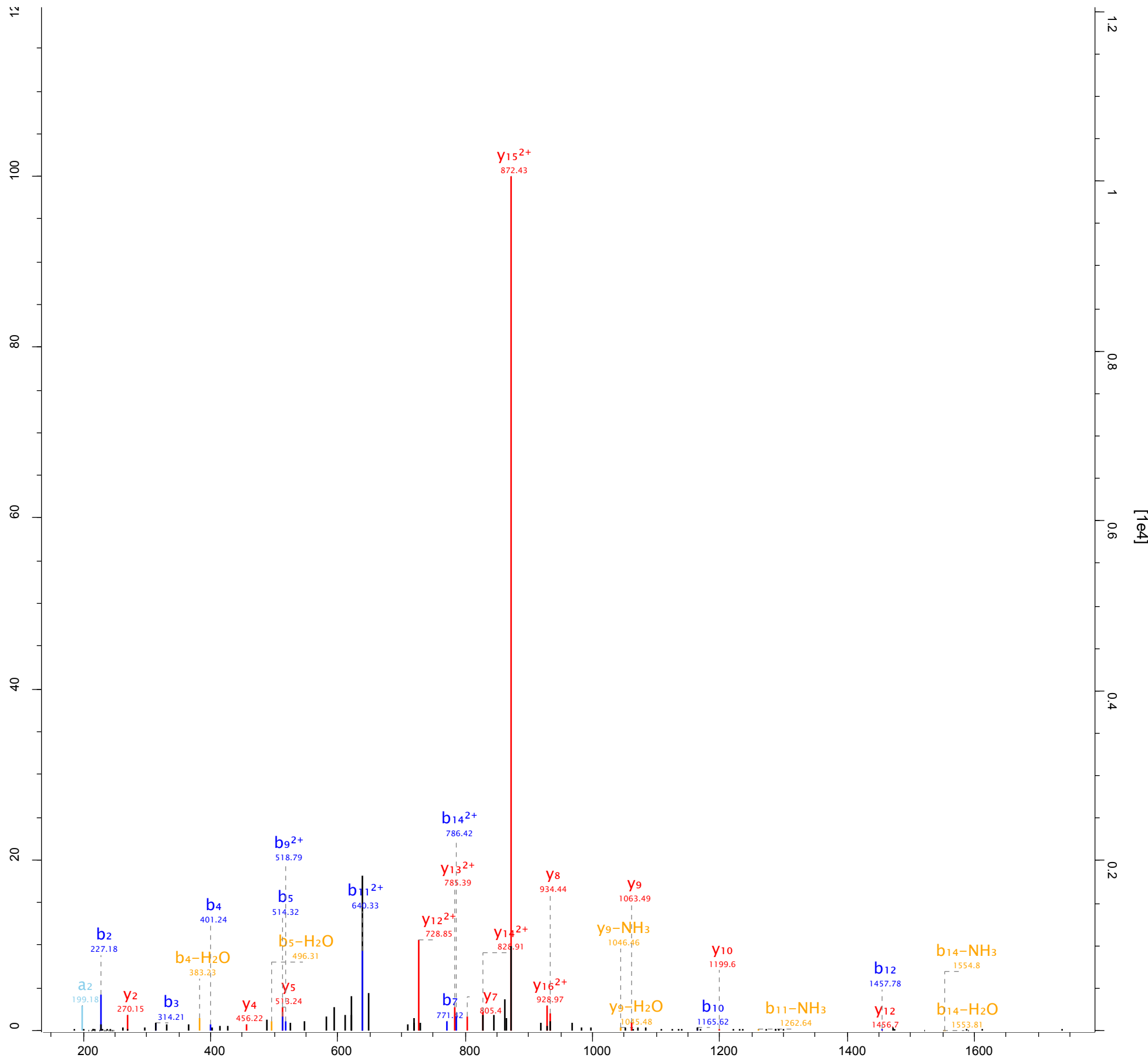
69.02

1009.54

Huwe1



Raw file: 072613_SCW_II_68_Enriched_7
 Scan: 14544 Method: ITMS; CID Score: 121.32 m/z: 657.68 Gene names: Ywhae



- I y16²⁺ y15²⁺ y14²⁺ y13²⁺ y12 Q y10 y9 y8 y7 ac y5 y4 y2 -
b2 b3 b4 b5 b7 K b9²⁺ b10 b11²⁺ b12 b14²⁺ E D K -

072613_SCW_II_68_Enriched_7

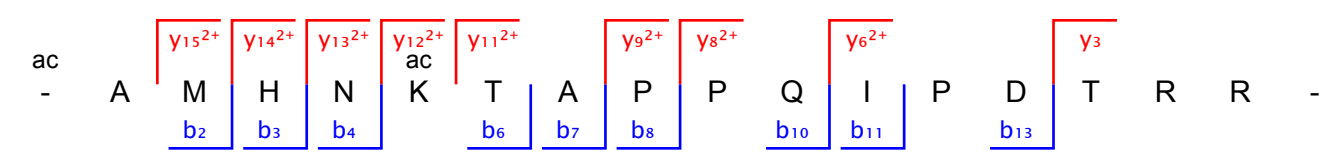
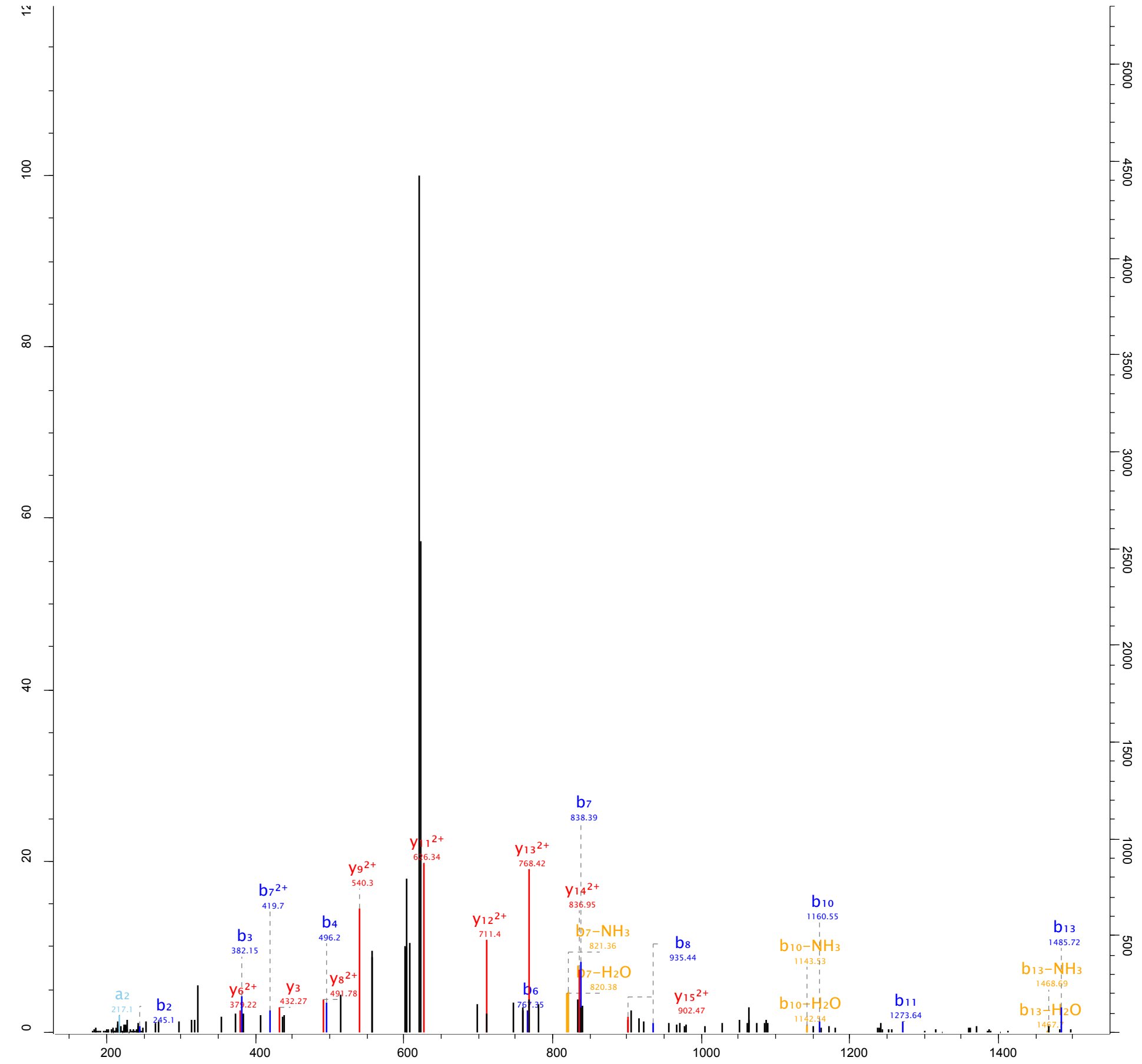
16355

ITMS; CID

102.5

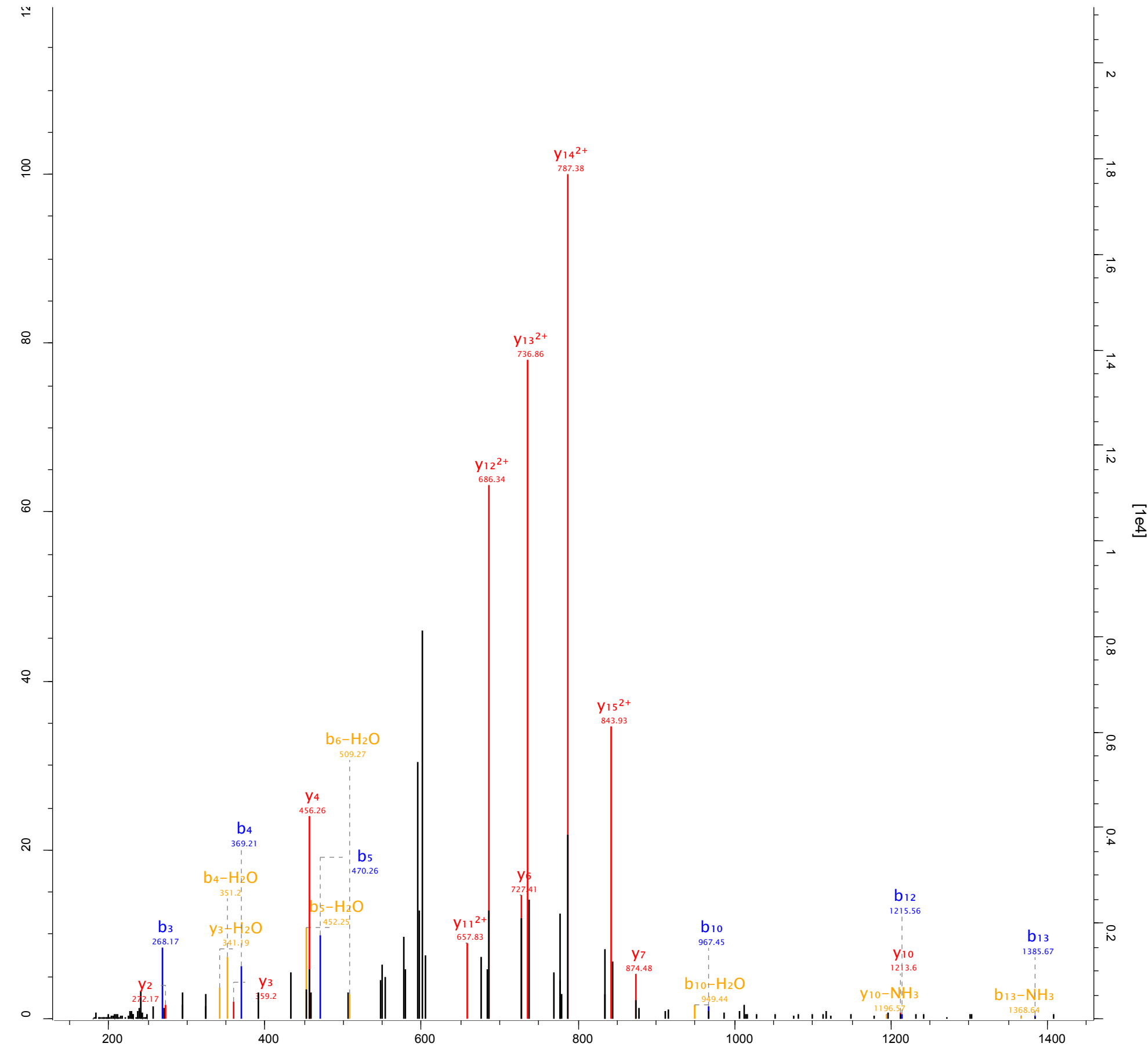
639.67

Meaf6

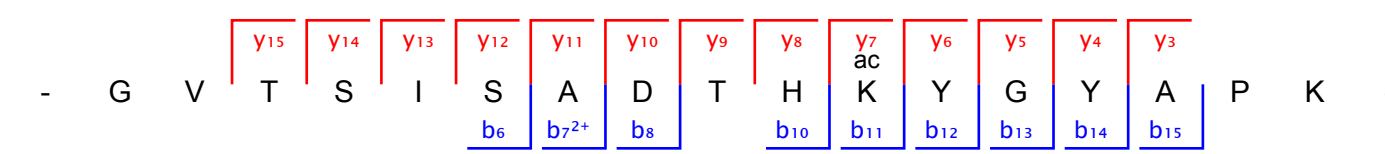
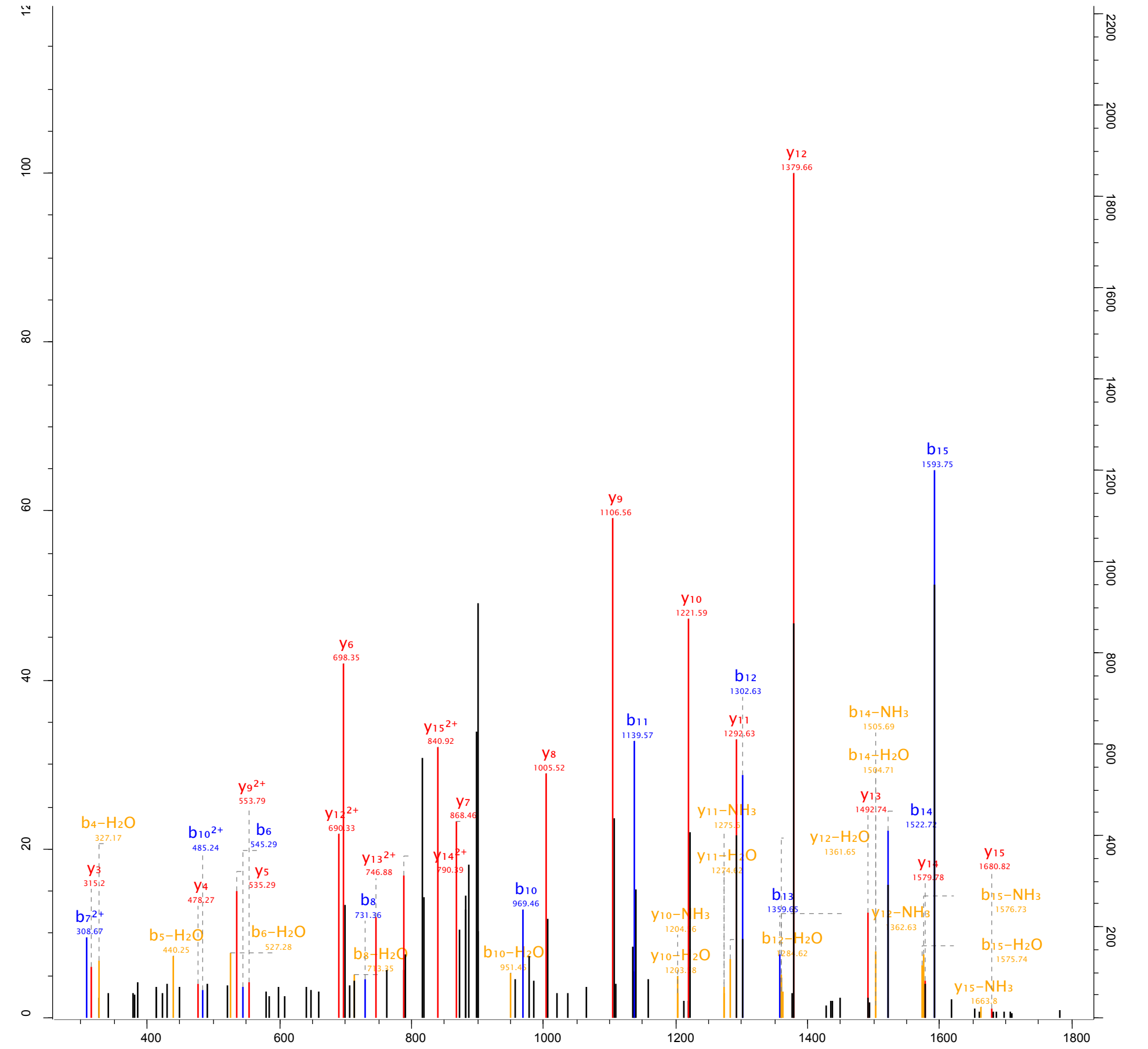


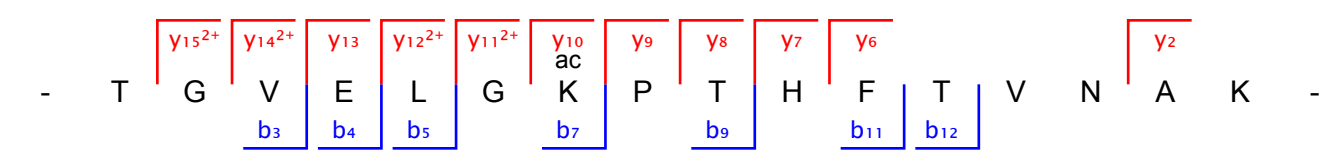
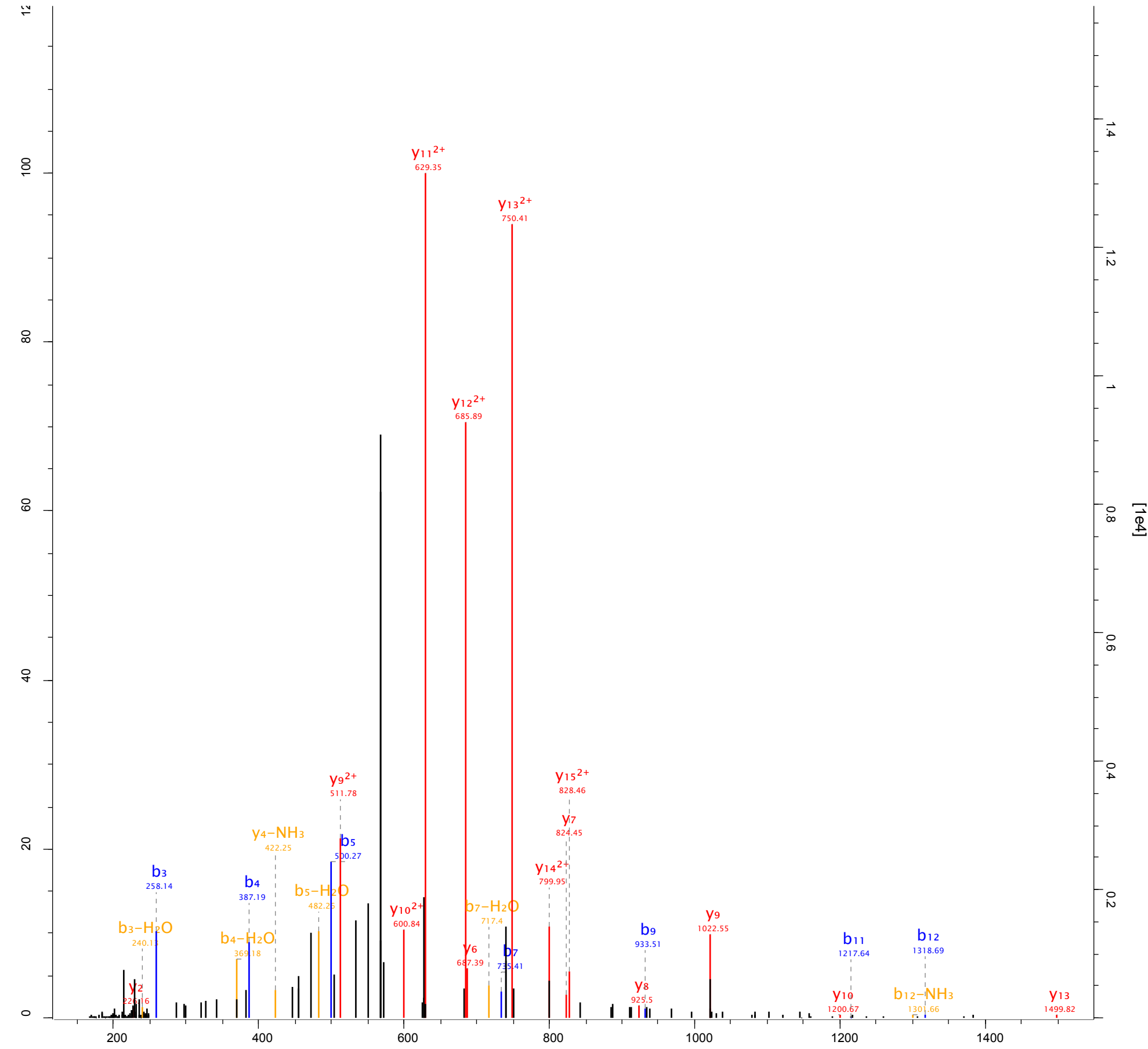
Raw file
072613_SCW_II_68_Enriched_7

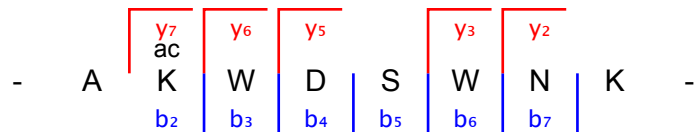
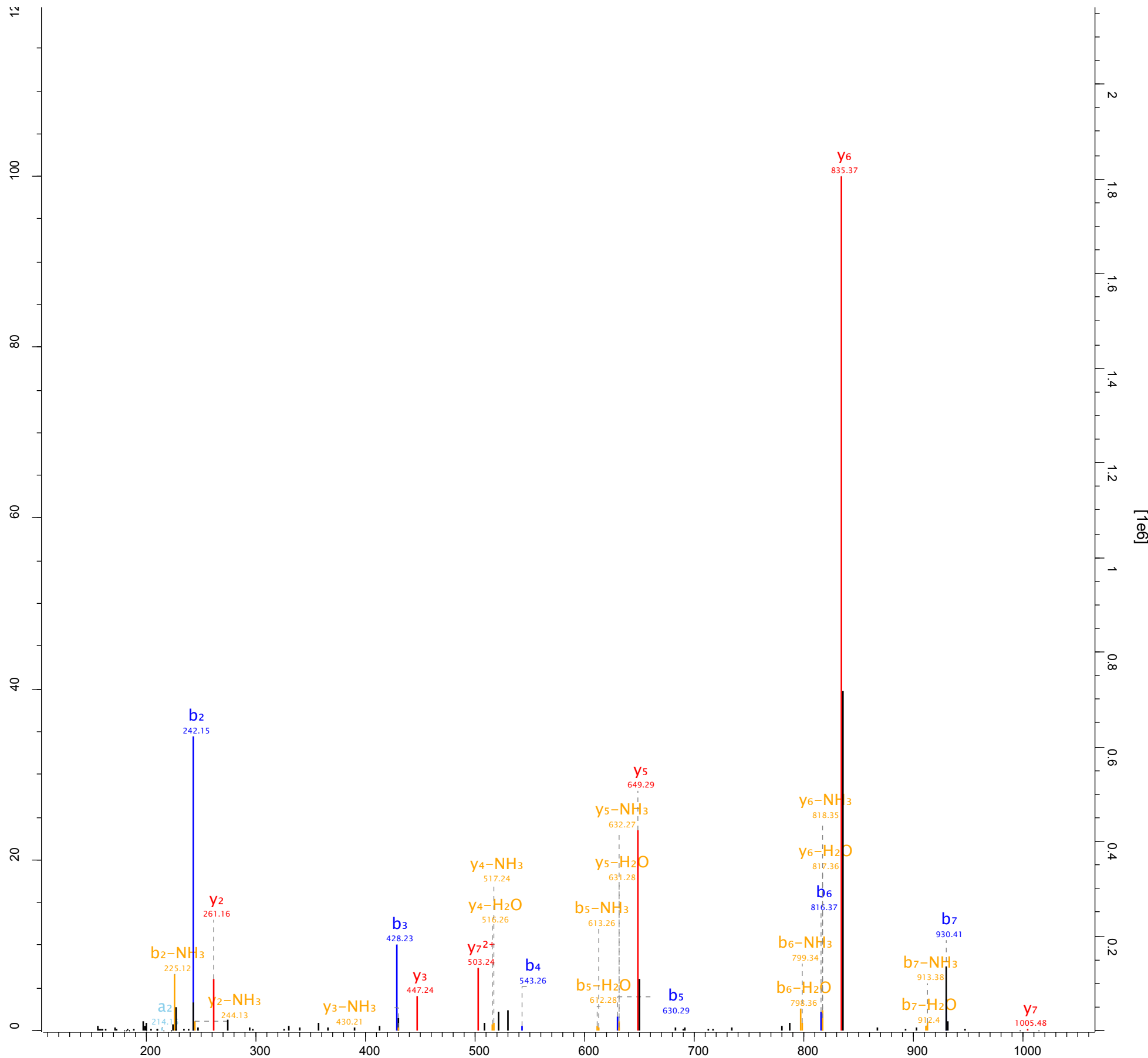
Scan 16803 Method ITMS; CID Score 95.07 m/z 614.65 Gene names Kmt2c



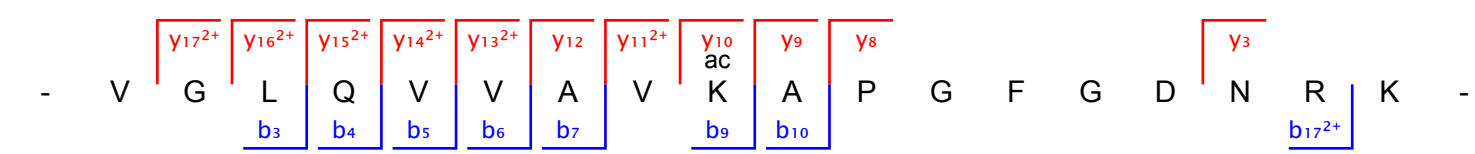
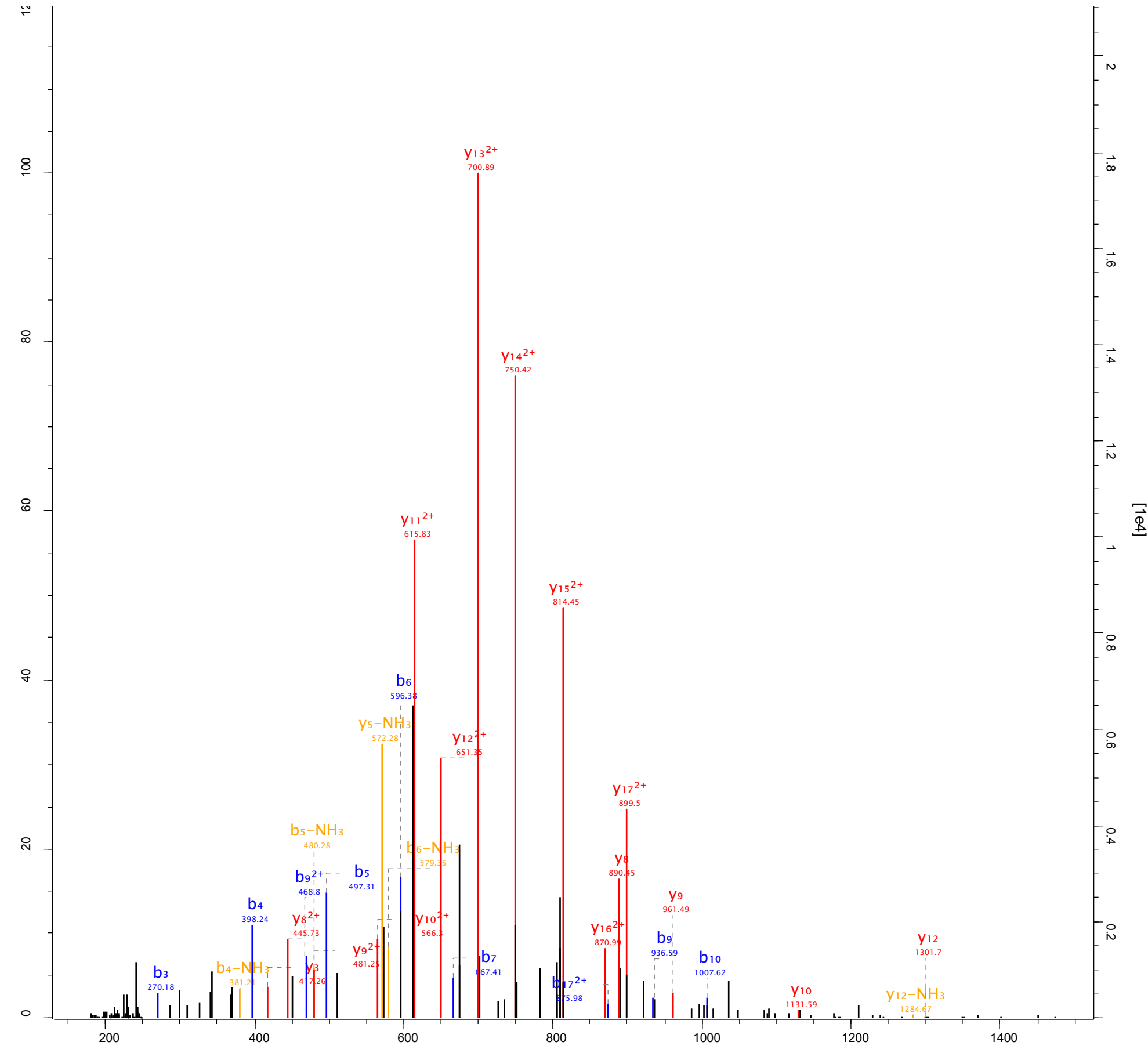
- G P L T T G T S D H F T ac K P S P R -
b3 b4 b5 b10 b12 b13

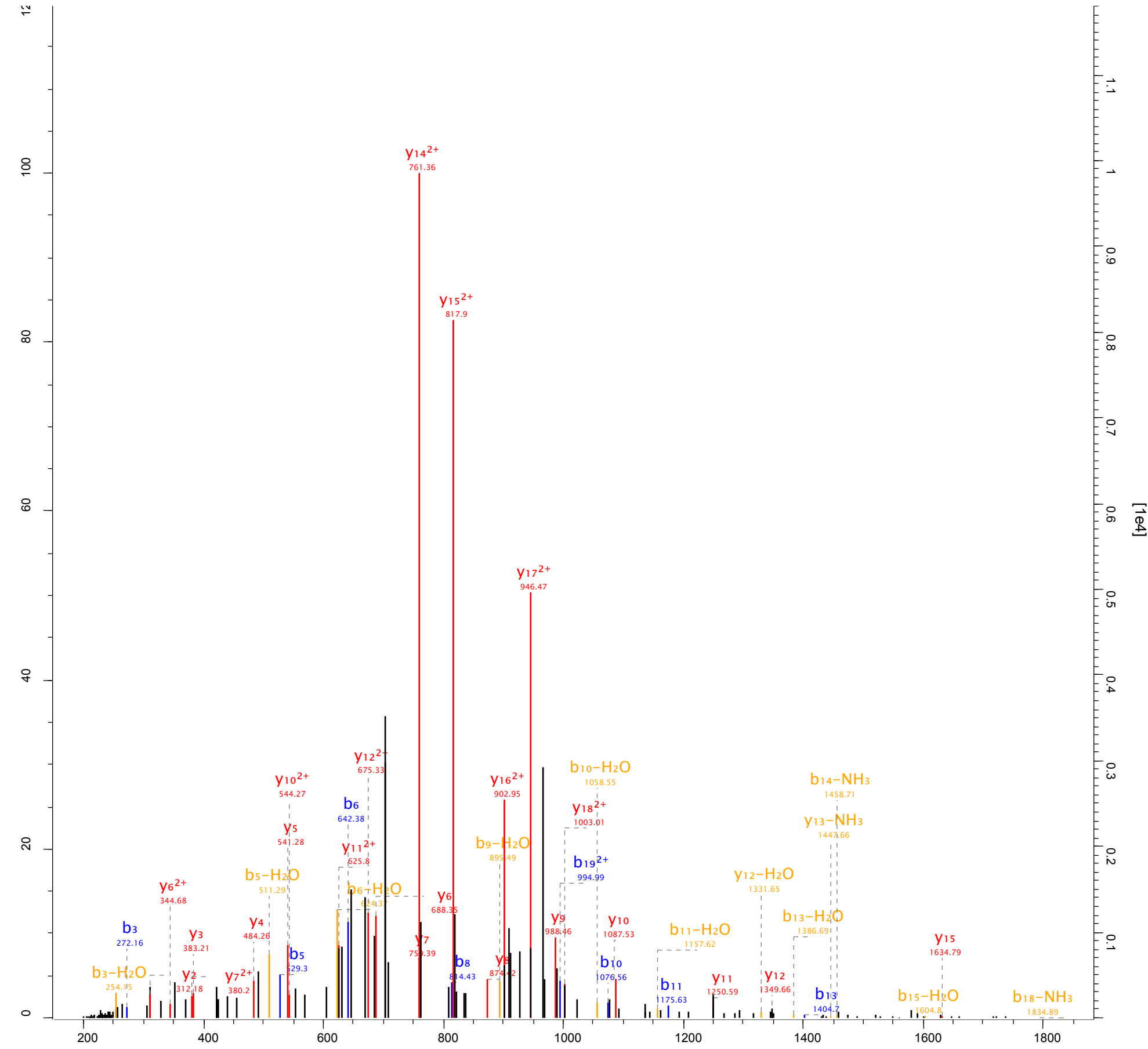






Raw file 072613_SCW_II_68_Enriched_7 Scan 20843 Method ITMS; CID Score 121.13 m/z 633.03 Gene names Hspd1

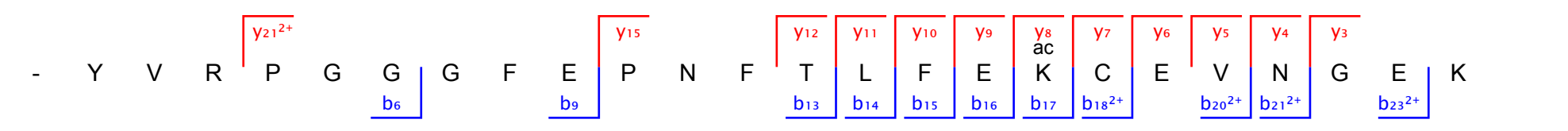
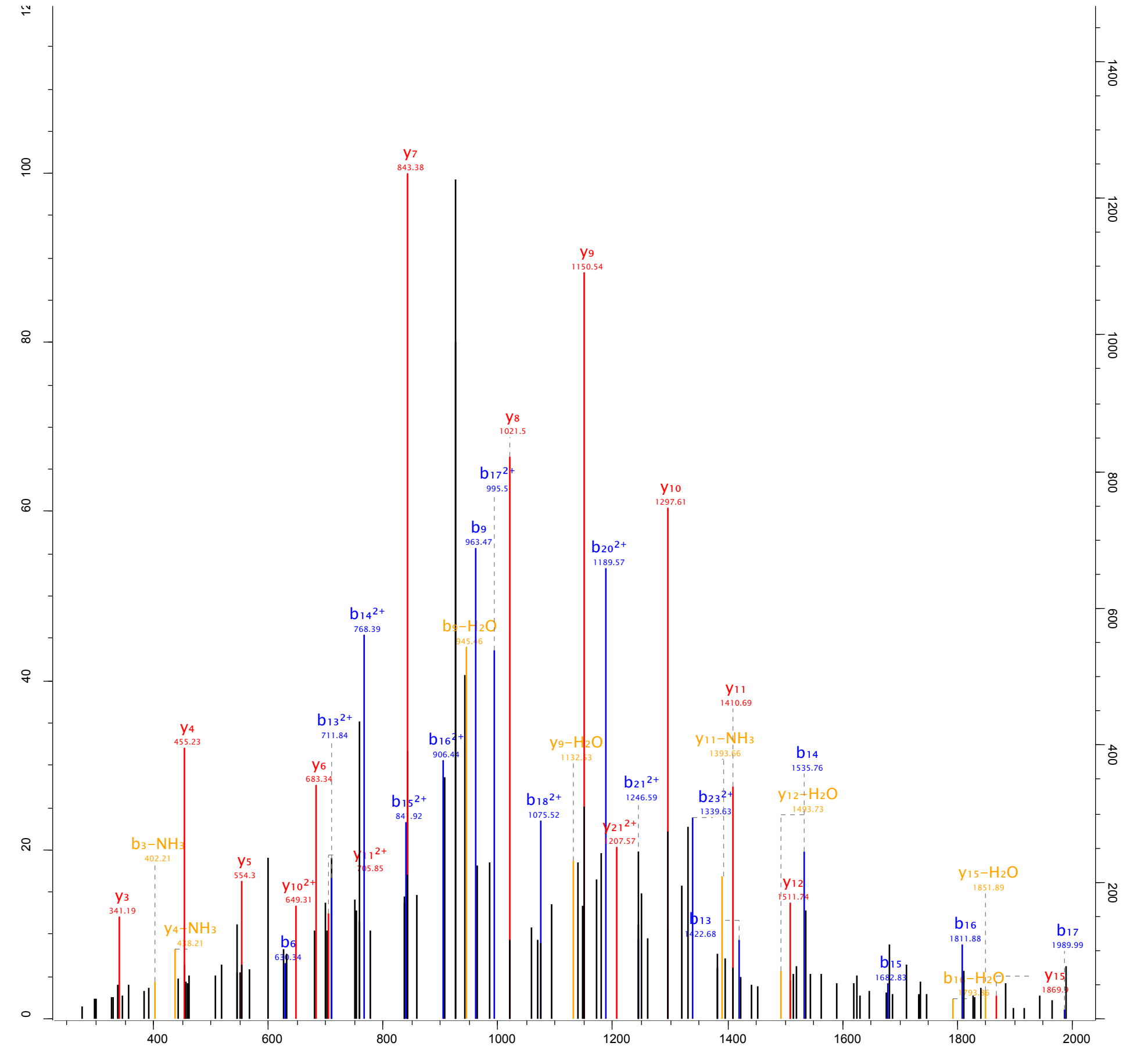


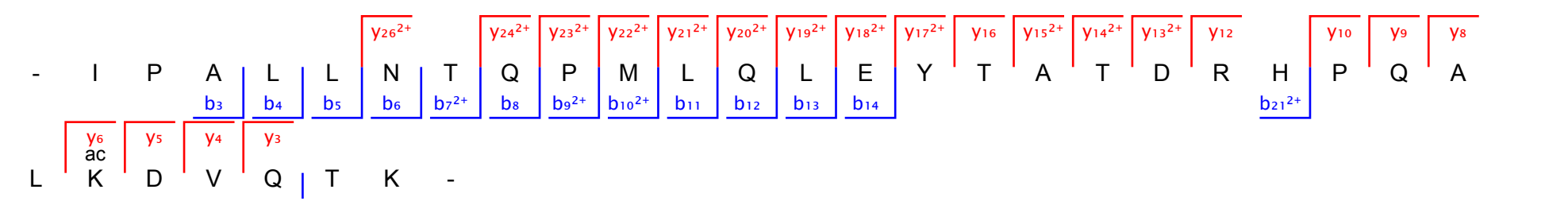
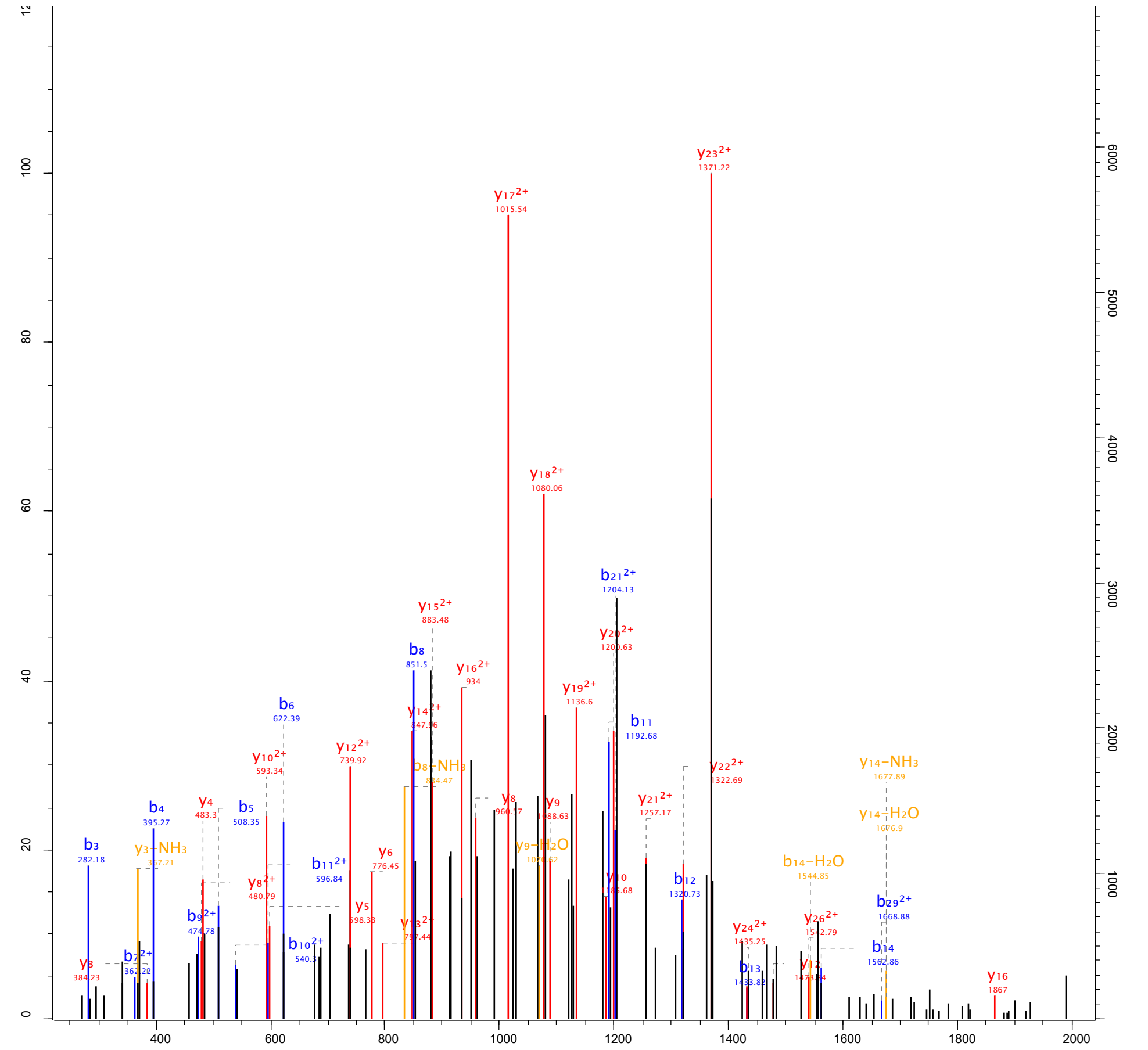


- A S L S K L G D V Y V N D A F G T A H R -

y₁₈²⁺
y₁₇²⁺
y₁₆²⁺
y₁₅
y₁₄²⁺
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₂

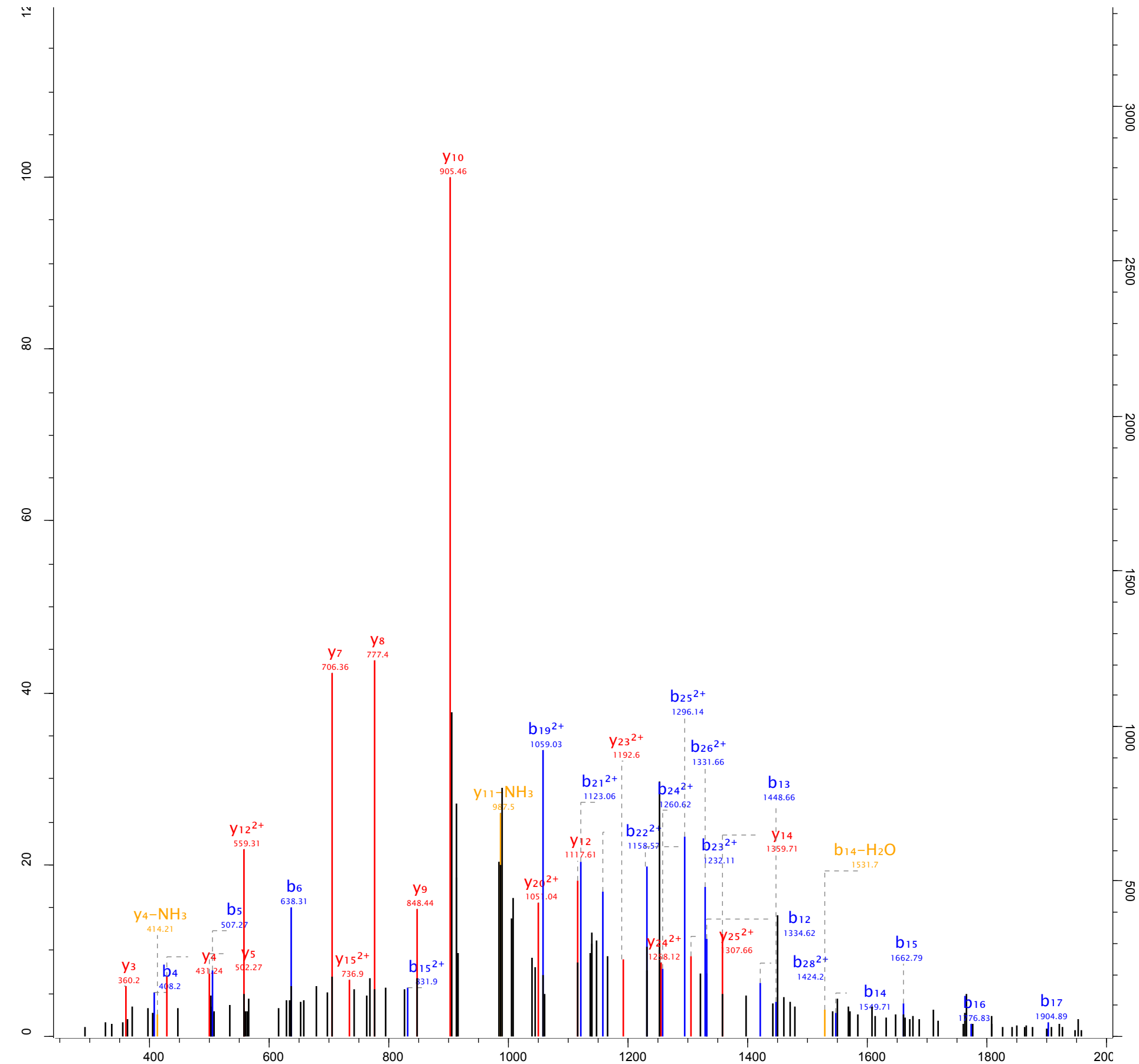
b₃
b₅
b₆
b₈
b₁₀
b₁₁
b₁₃
b₁₉²⁺



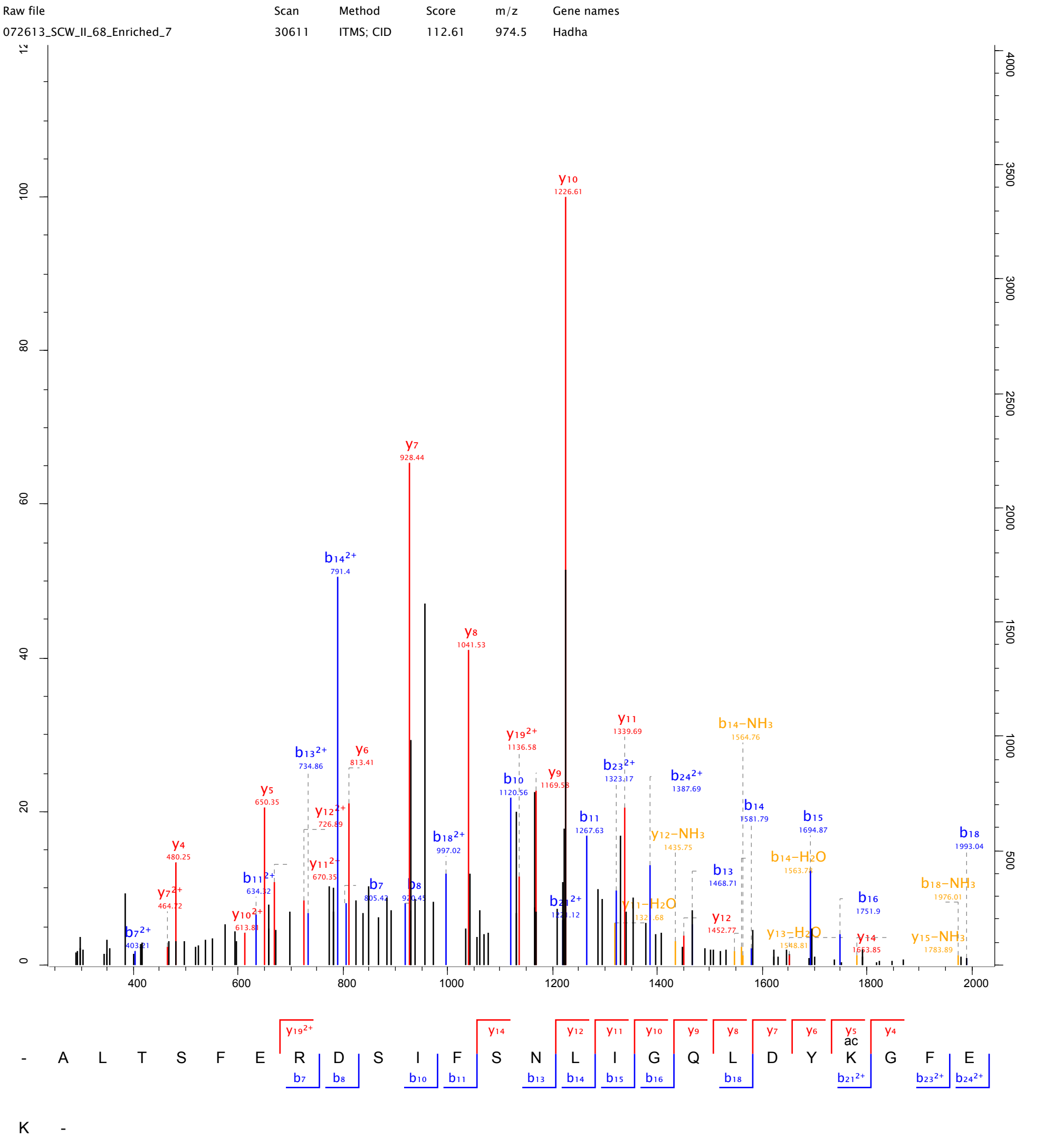


Raw file
072613_SCW_II_68_Enriched_7

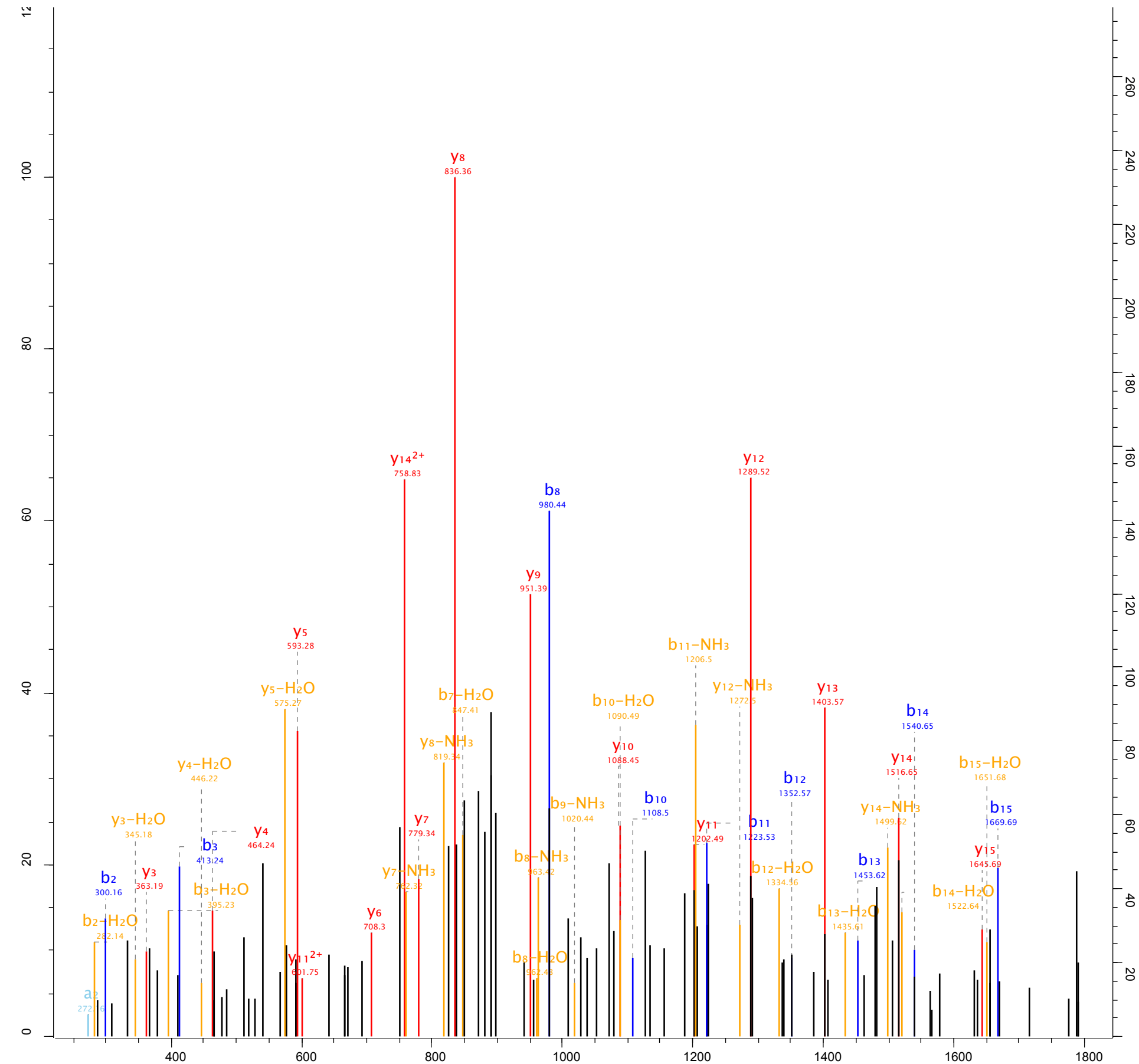
Scan 28685 Method ITMS; CID Score 110.03 m/z 1008.17 Gene names Aldh6a1



- N H G V V M P D A N K E N T L N Q L V G A A F G
b4 b5 b6 b12 b13 b14 b15 b16 b17 b19²⁺ b21²⁺ b22²⁺ b23²⁺ b24²⁺
y5 y4 y3 y25²⁺ y24²⁺ y23²⁺ y20²⁺ y15²⁺ y14 y12 y10 y9 y8 y7
A A G Q R -



Raw file 072613_SCW_II_68_Enriched_8 Scan 10965 Method ITMS; CID Score 171.29 m/z 908.41 Gene names Set



ac K E L N S N H D G A D E T S E K -

b2 b3 b8 b10 b11 b12 b13 b14 b15

072613_SCW_II_68_Enriched_8

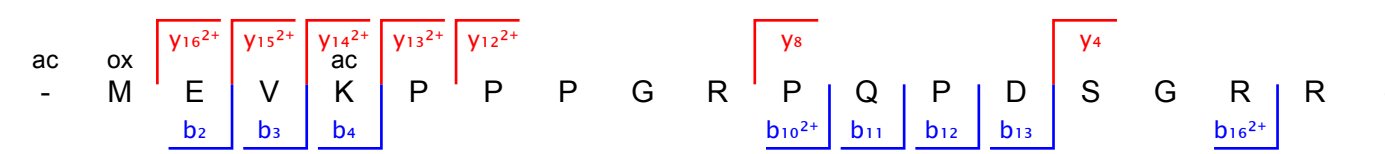
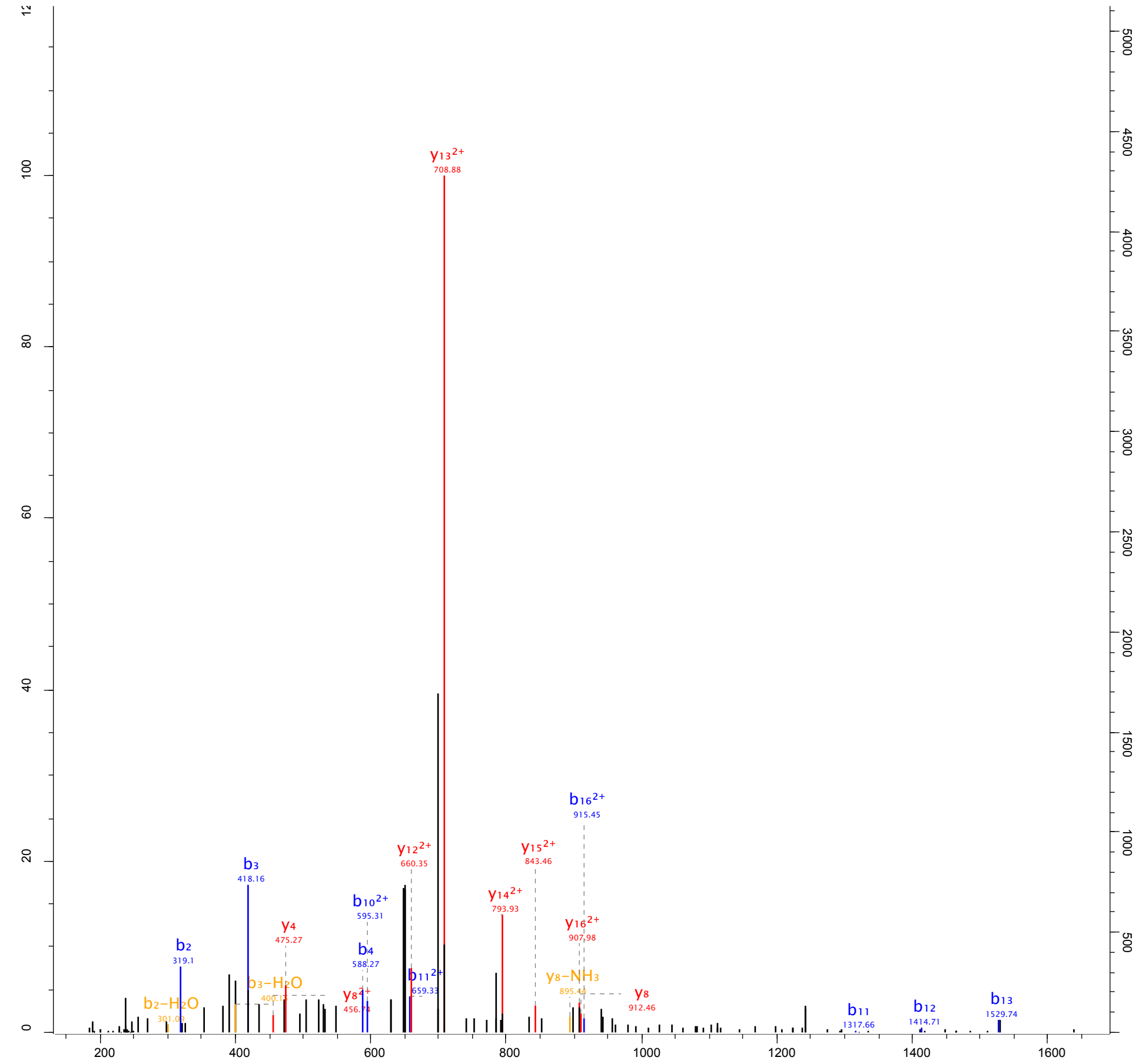
13539

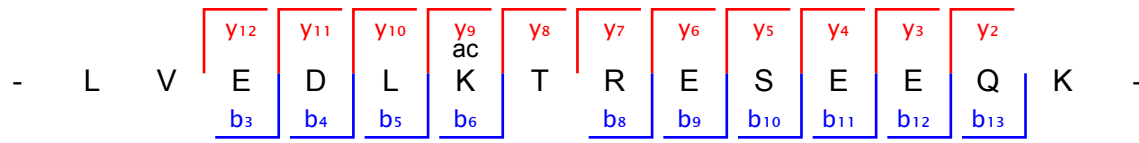
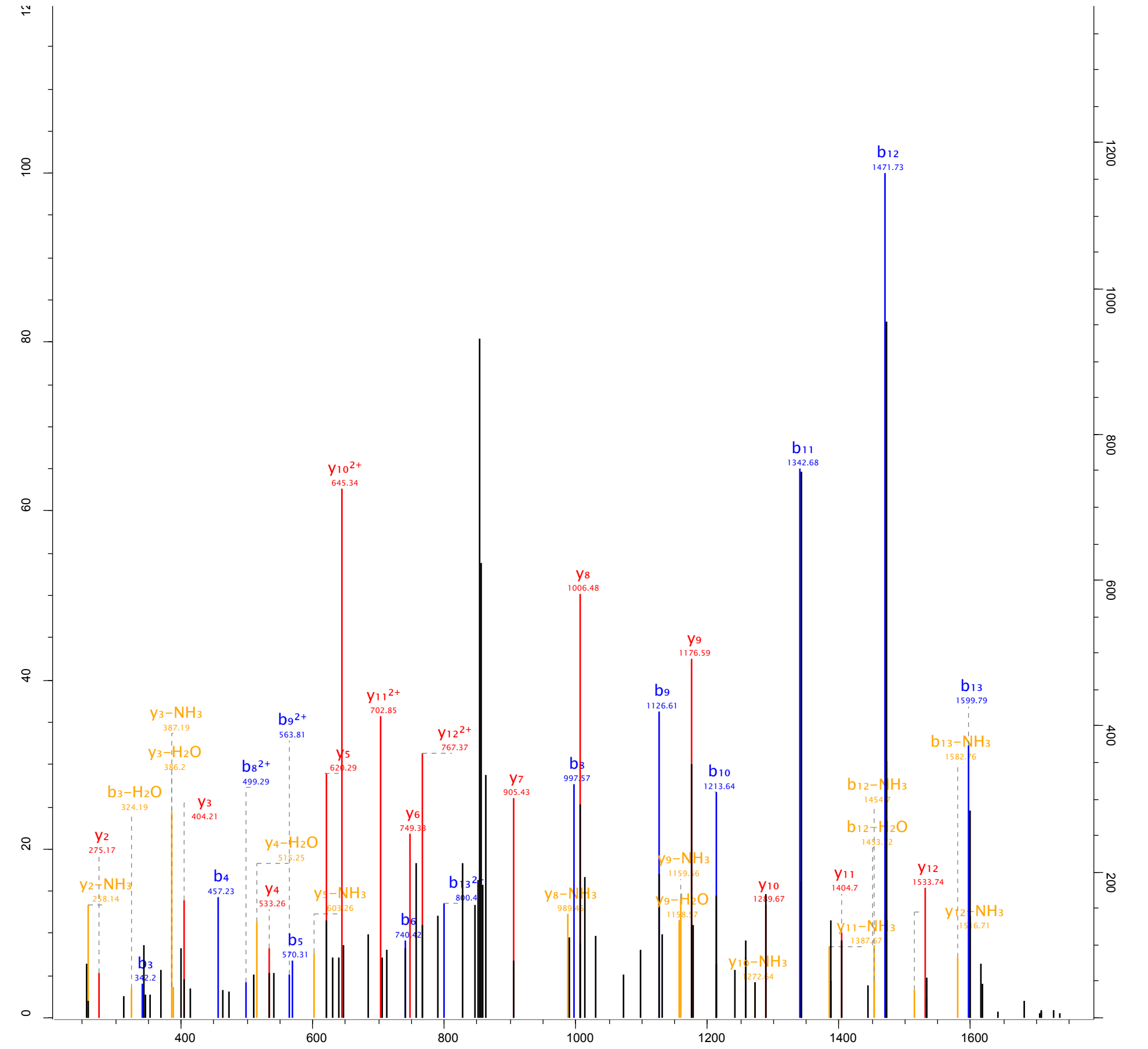
ITMS; CID

57.97

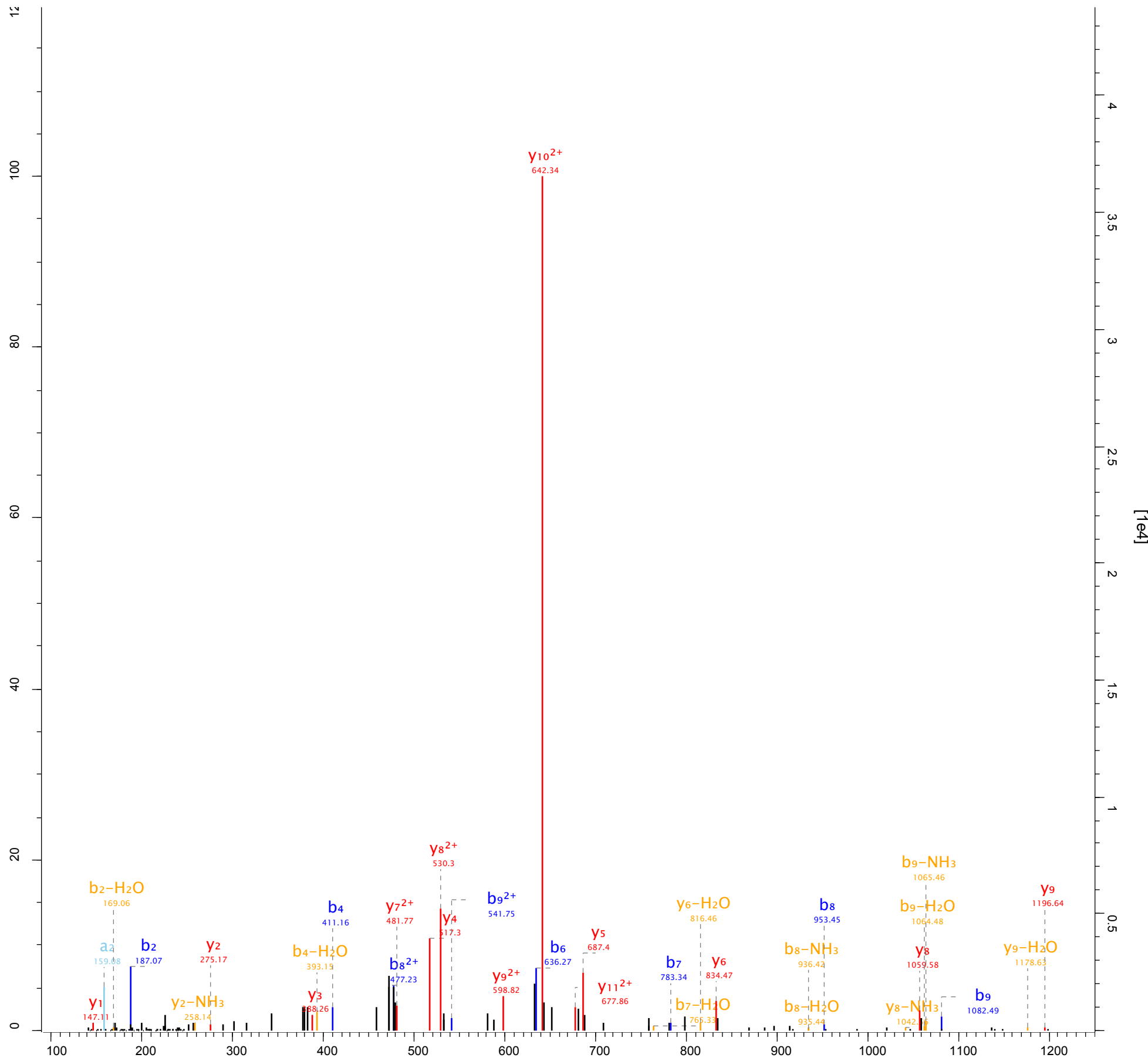
668.68

Hnrnpa3





Raw file 072613_SCW_II_68_Enriched_8 Scan 15625 Method ITMS; CID 165.35 m/z 490.59 Gene names Isoc2a

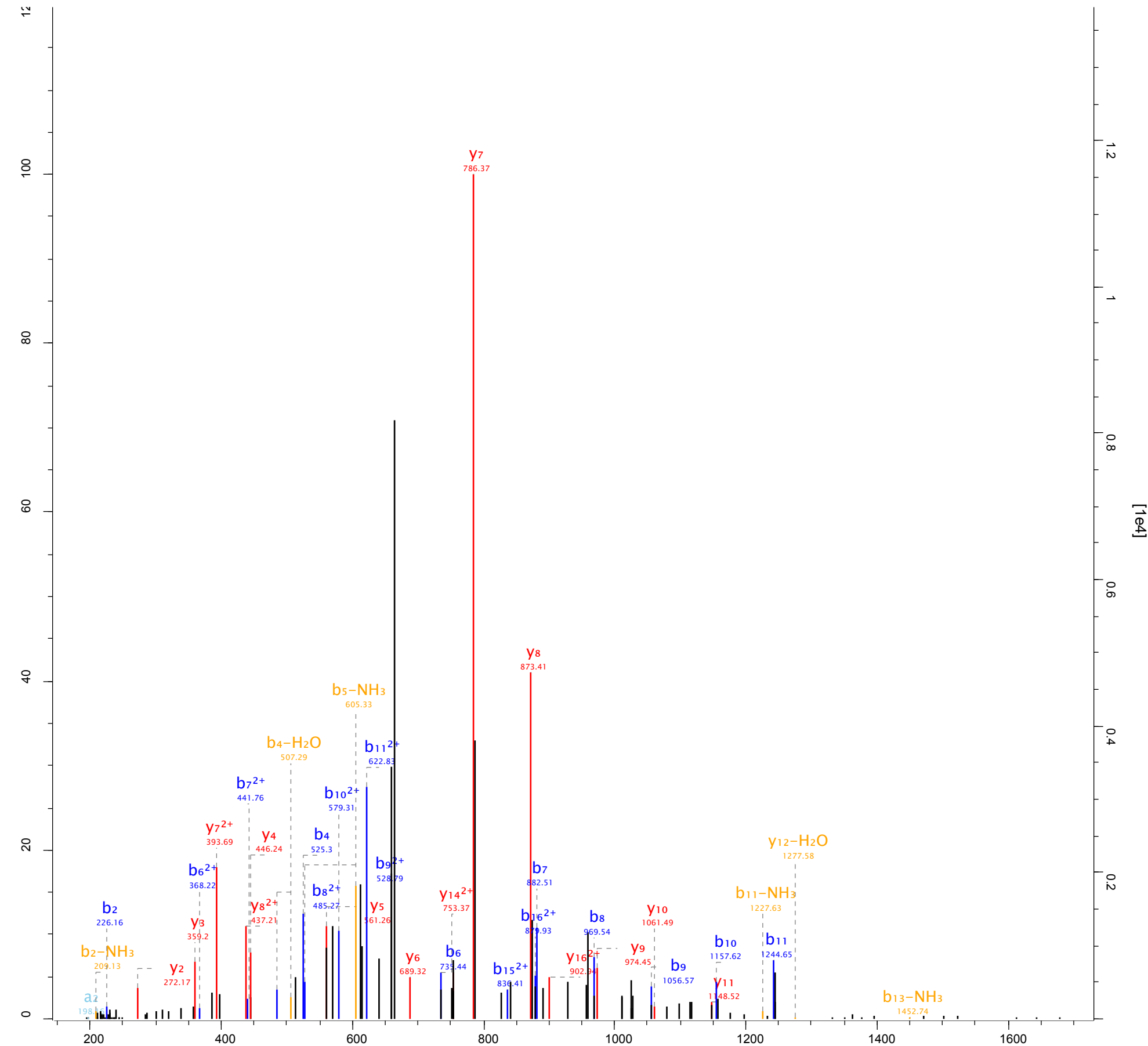


- D A S H P Q F K E I Q K -

y_{11}^{2+}
 y_{10}^{2+}
 y_9
 y_8
 y_7^{2+}
 y_6
 y_5
ac
 y_4
 y_3
 y_2
 y_1

b_2
 b_4
 b_6
 b_7
 b_8
 b_9

Raw file 072613_SCW_II_68_Enriched_8 Scan 16740 Method ITMS; CID Score 113.86 m/z 677.68 Gene names Nfib

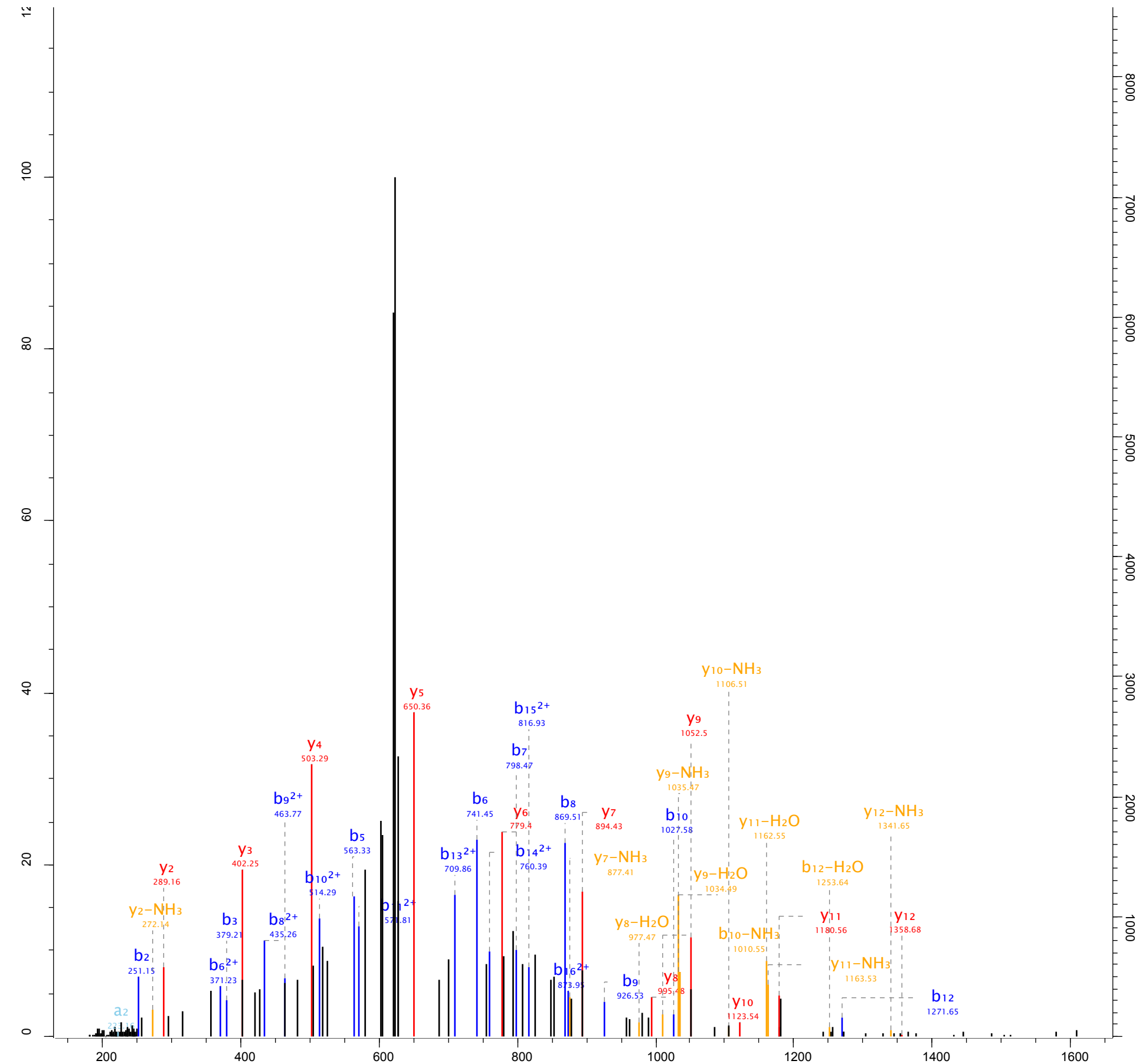


- K P E K P L F S S T S P Q D S S P R -

b₂
b₄
b₆
b₇
b₈
b₉
b₁₀
b₁₁
b_{15²⁺}
b_{16²⁺}
y₂
y₃
y₄
y₅
y₆
y₇
y₈
y₉
y₁₀
y₁₁
y_{14²⁺}
y_{16²⁺}

Raw file
072613_SCW_II_68_Enriched_8

Scan 18811 Method ITMS; CID Score 199.15 m/z 641.01 Gene names Anxa3



- L H Q A L K G A G T D E F T L N R -

Peptide sequence: LHLQALKGATDEFTLNR

Fragmentation sites (b and y ions):

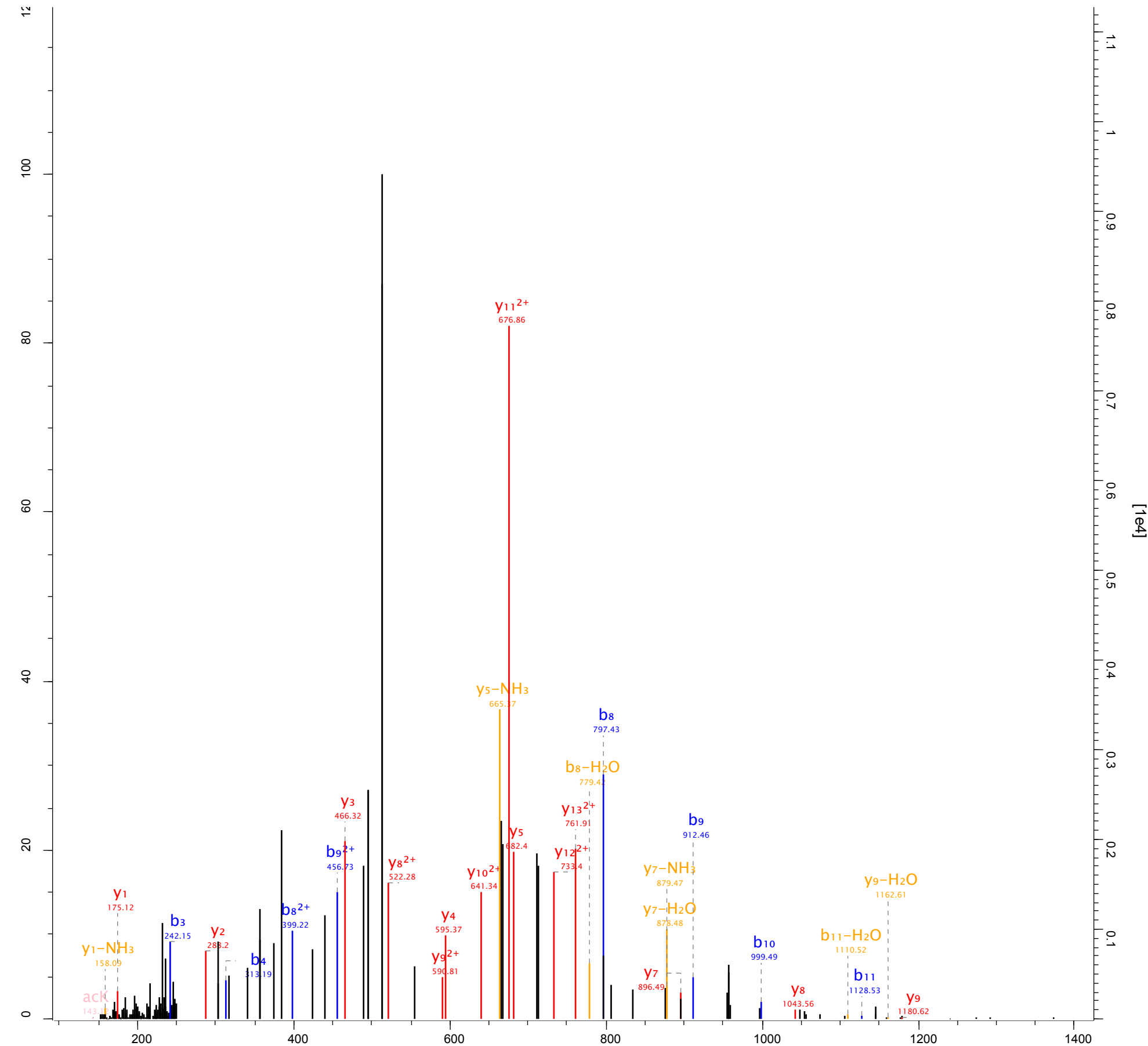
- b₂ (H), b₃ (Q)
- b₅ (L)
- b₆ (K), b₆ ac (K)
- b₇ (G)
- b₈ (A)
- b₉ (G)
- b₁₀ (T)
- b₁₁²⁺ (D)
- b₁₂ (E)
- b₁₃²⁺ (F)
- b₁₄²⁺ (T)
- b₁₅²⁺ (L)
- b₁₆²⁺ (N)

Fragmentation sites (b and y ions):

- y₂ (N)
- y₃ (L)
- y₄ (T)
- y₅ (F)
- y₆ (E)
- y₇ (D)
- y₈ (T)
- y₈ (F)
- y₉ (G)
- y₁₀ (A)
- y₁₁ (K)
- y₁₁ ac (K)
- y₁₂ (L)

Raw file
072613_SCW_II_68_Enriched_8

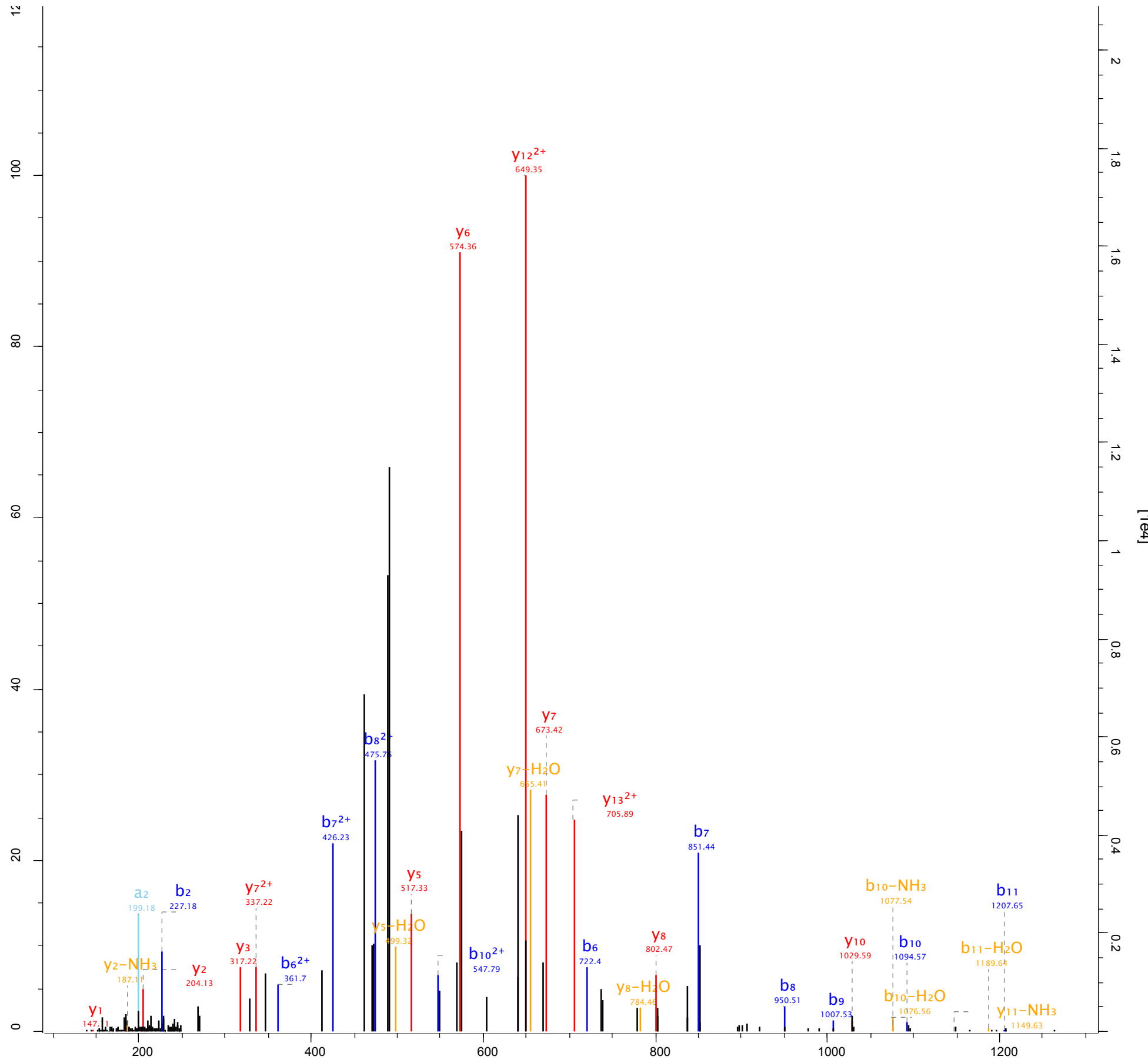
Scan 19296 Method ITMS; CID Score 141.34 m/z 531.95 Gene names Hibch



- A G I A T H F V D S E K L R -

Fragmentation mapping showing y and b ions corresponding to the peptide sequence. Red boxes indicate y ions (y1 to y13) and blue boxes indicate b ions (b3 to b11). The sequence is: A G I A T H F V D S E K L R.

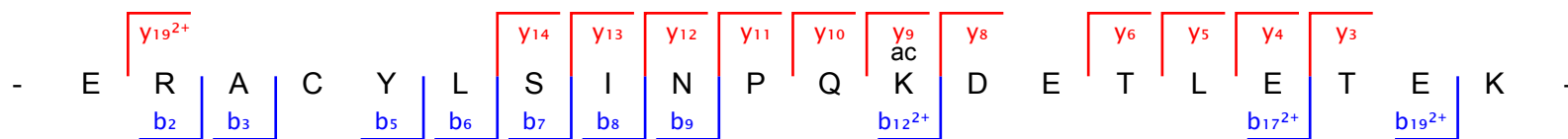
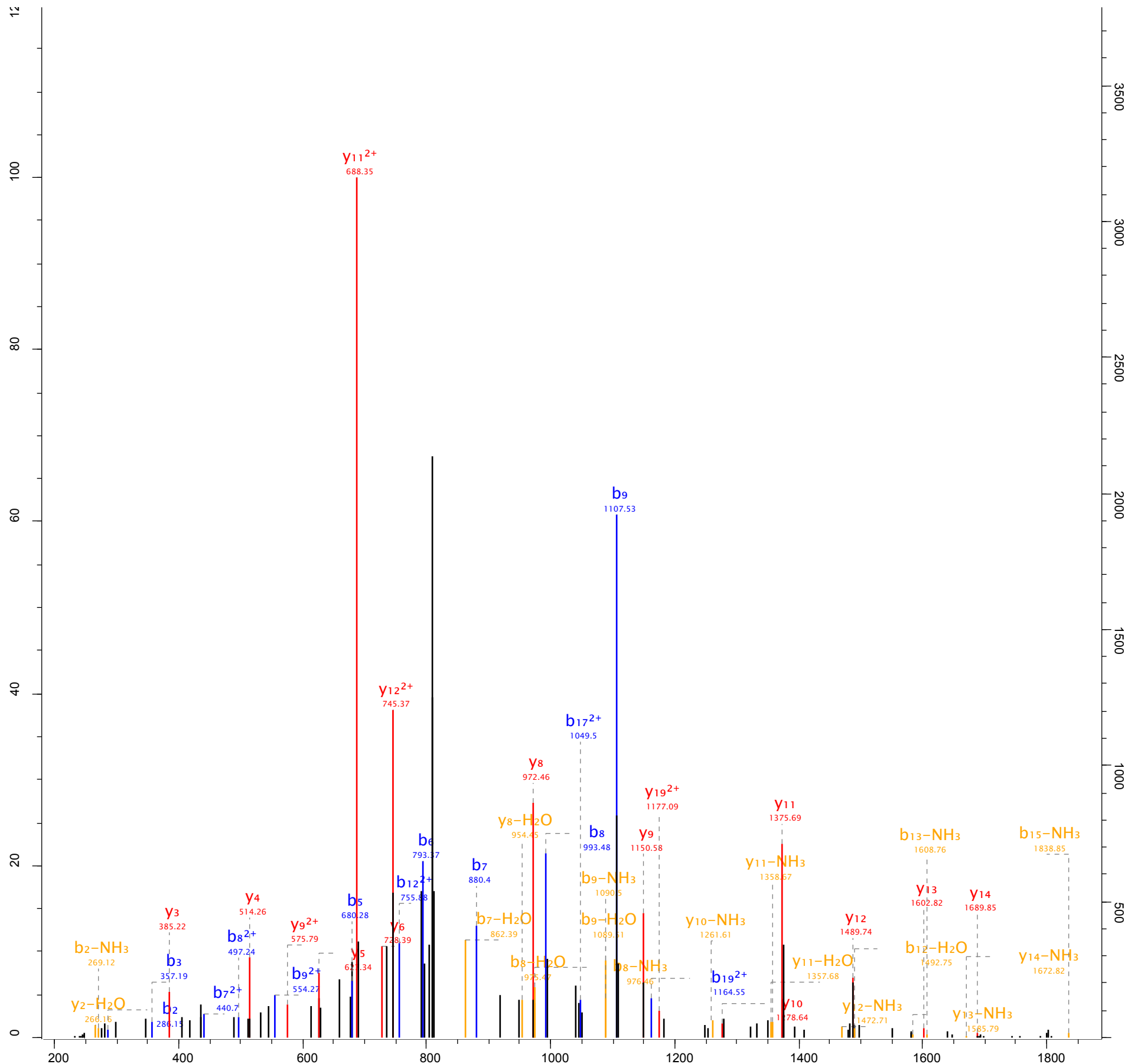
Raw file: 072613_SCW_II_68_Enriched_8
 Scan: 19691 Method: ITMS; CID Score: 150.22 m/z: 508.96 Gene names: Pcbp2;Pcbp3;Pcbp1

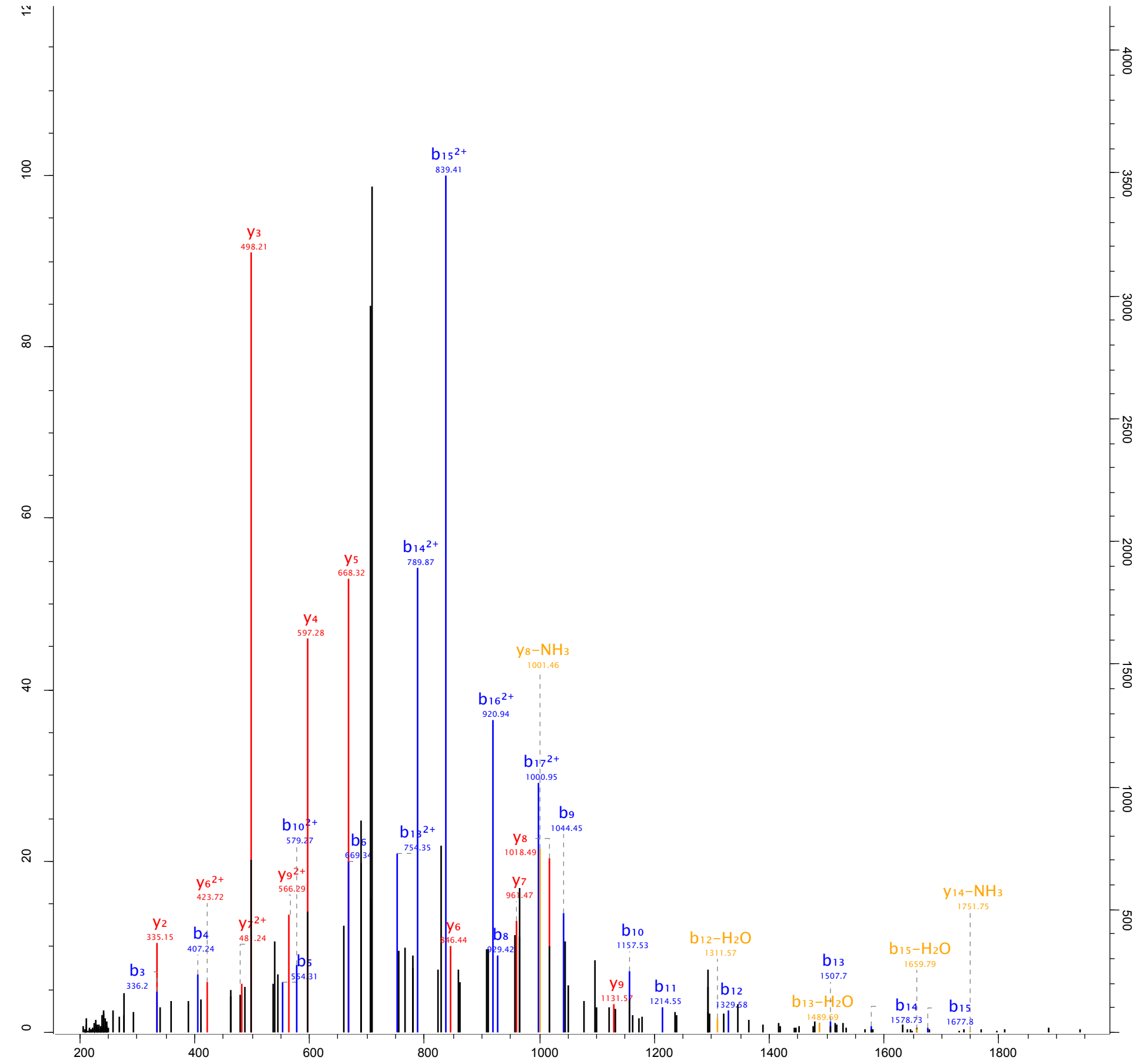


- L L M H G ac K E V G S I I G K -

y₁₃²⁺
y₁₂²⁺
y₁₀
y₈
y₇
y₆
y₅
y₃
y₂
y₁

b₂
b₆
b₇
b₈
b₉
b₁₀
b₁₁

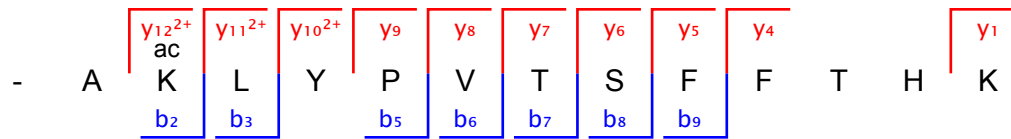
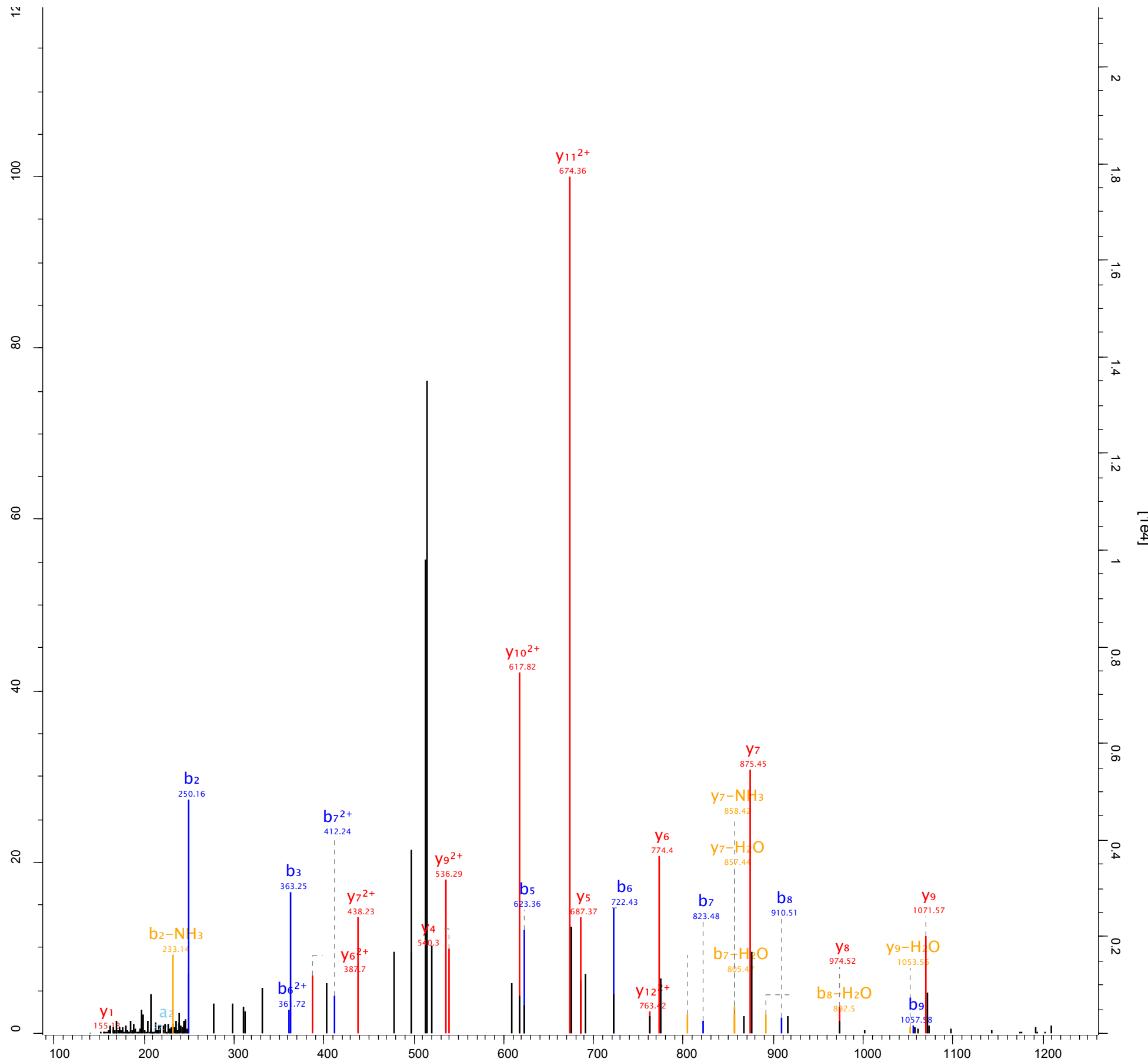




- V V H A F D M E D L G D K A V Y C R -

b₃
b₄
b₅
b₆
b₈
b₉
b₁₀
b₁₁
b₁₂
b₁₃
b₁₄
b₁₅
b₁₆²⁺
b₁₇²⁺

y₉
y₈
y₇
y₆
ac
y₅
y₄
y₃
y₂



072613_SCW_II_68_Enriched_8

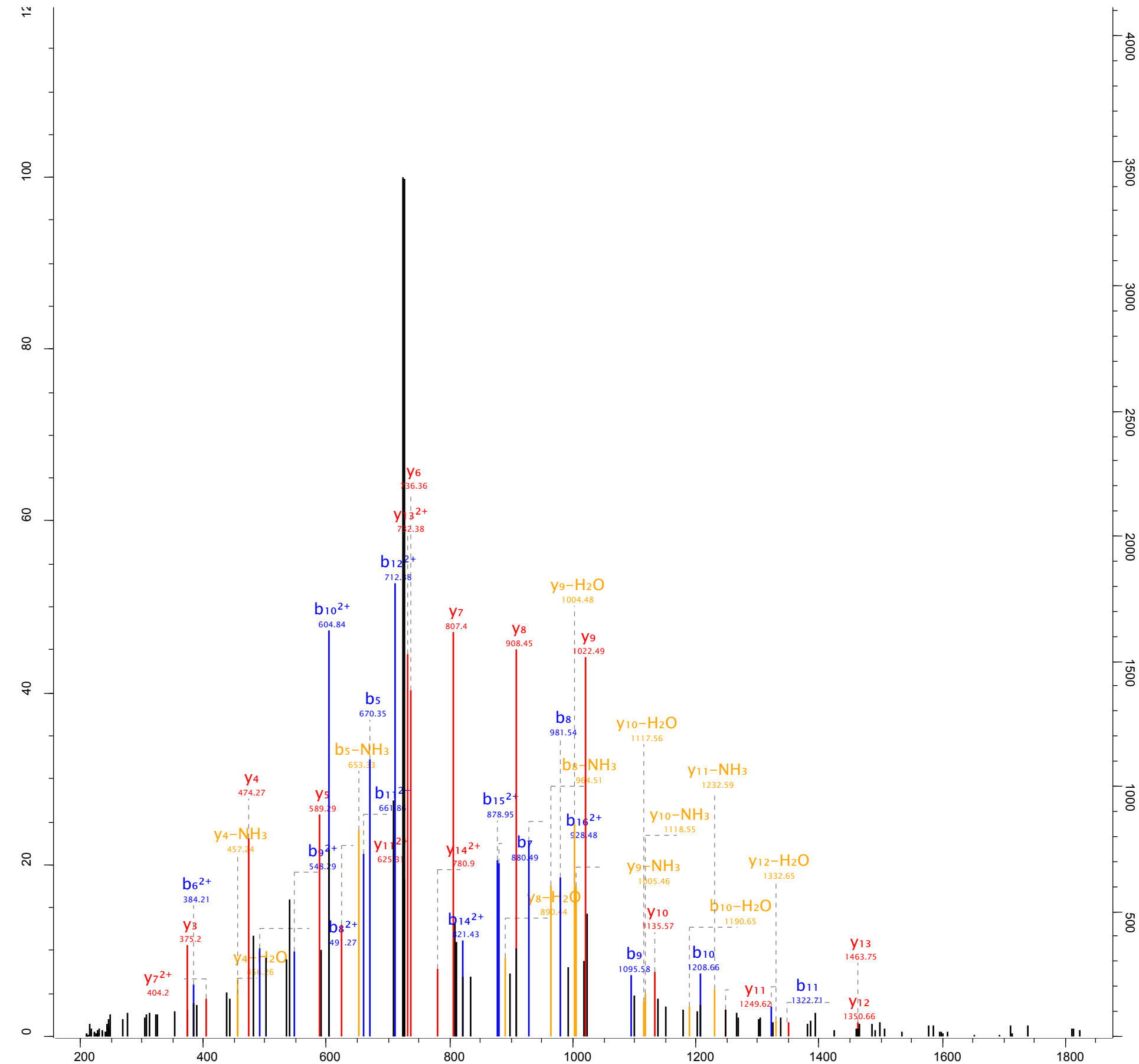
24595

ITMS; CID

182.17

744.05

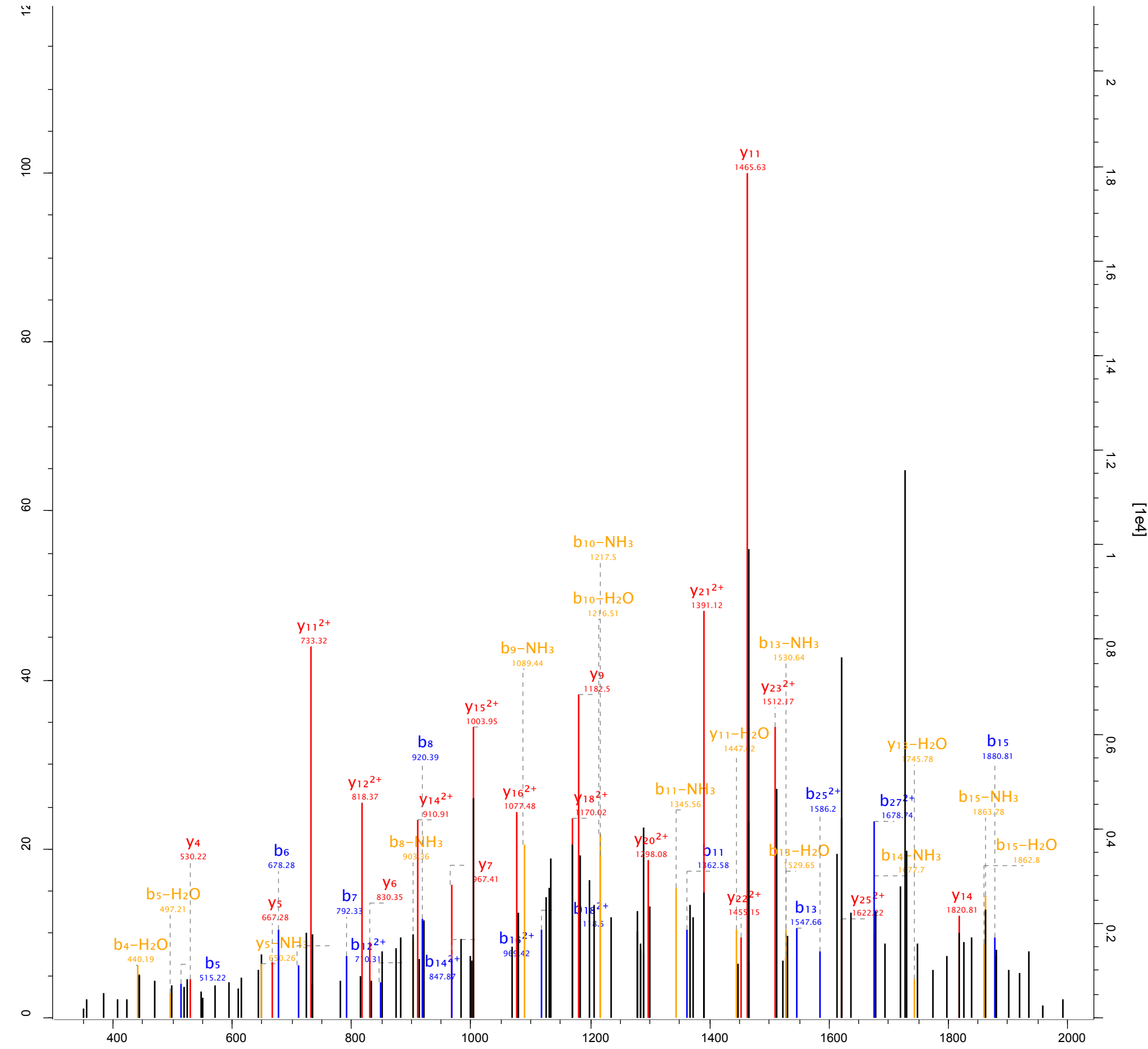
Actn1



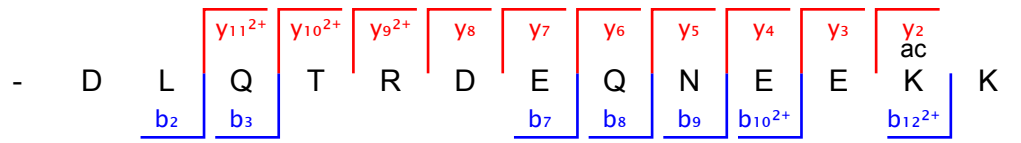
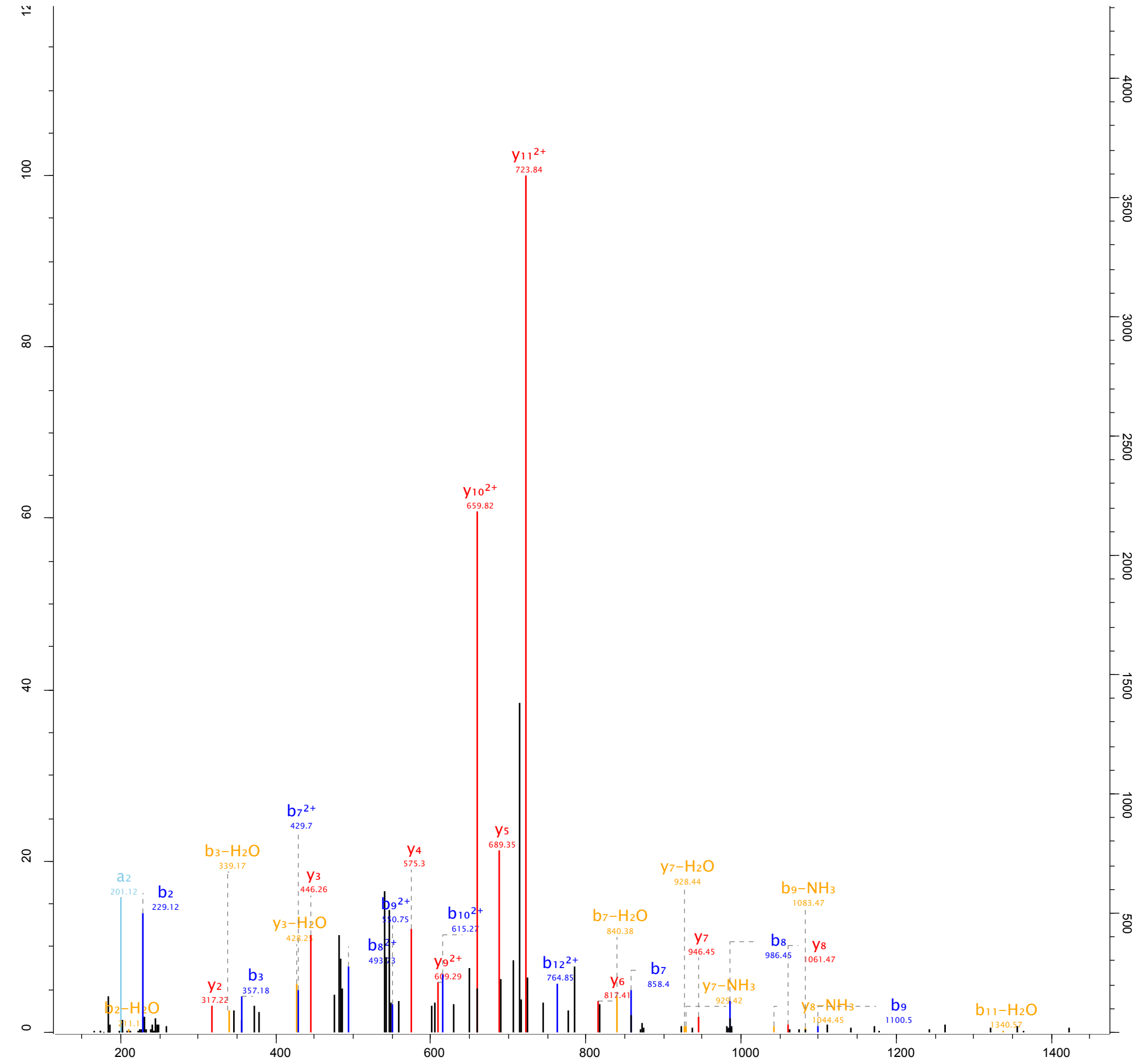
- L R ac K D D P L T N L N T A F D V A E R -

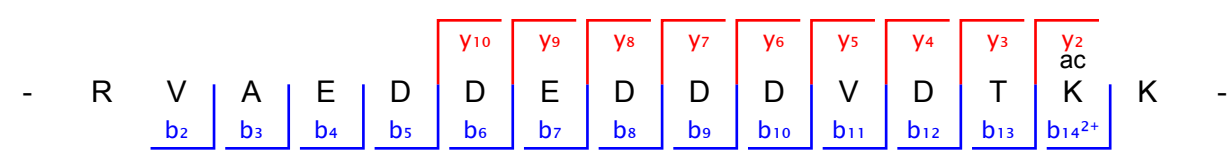
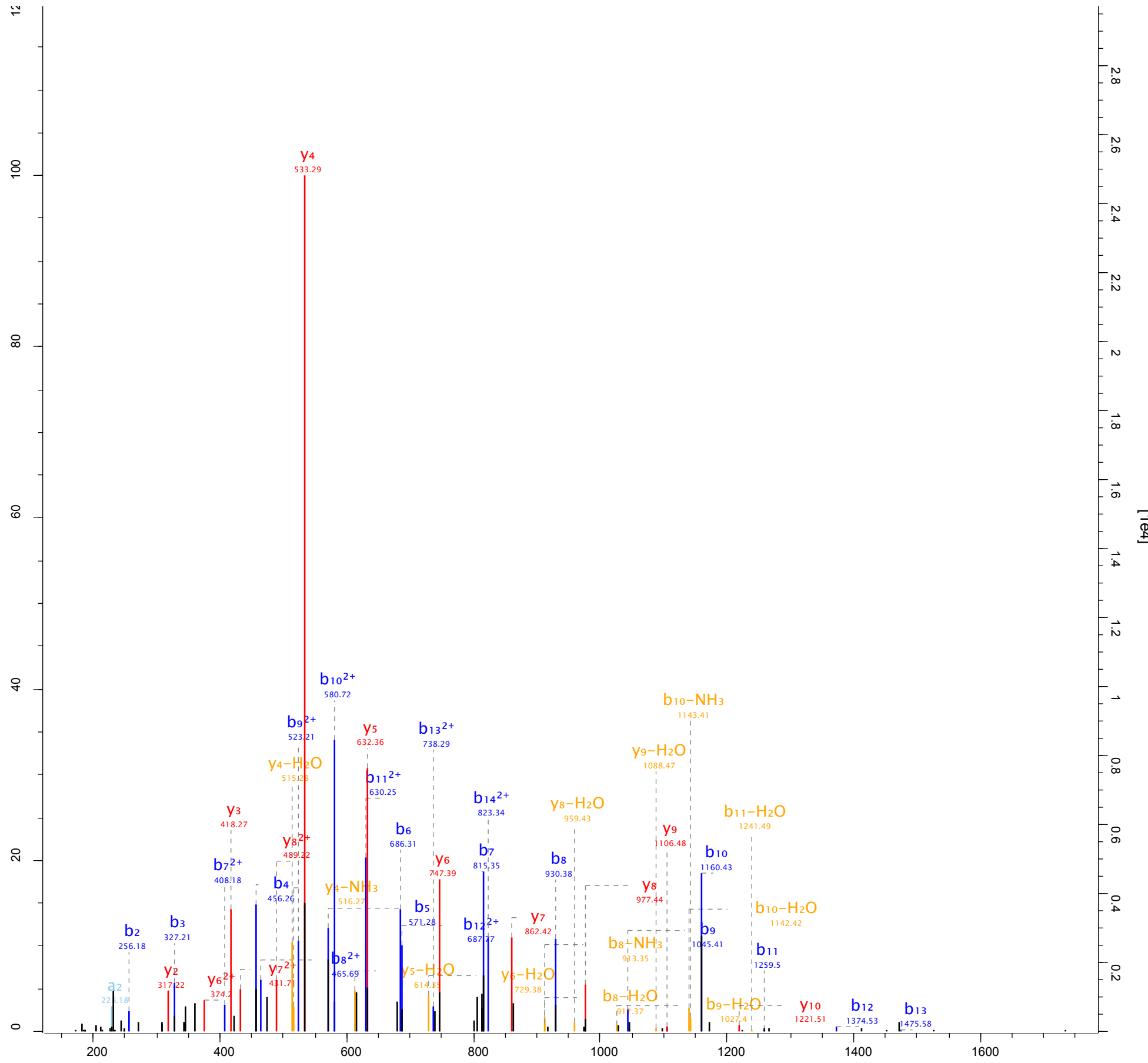
b₅ b₆²⁺ b₇ b₈ b₉ b₁₀ b₁₁ b₁₂²⁺ b₁₄²⁺ b₁₅²⁺ b₁₆²⁺

y₁₄²⁺ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃



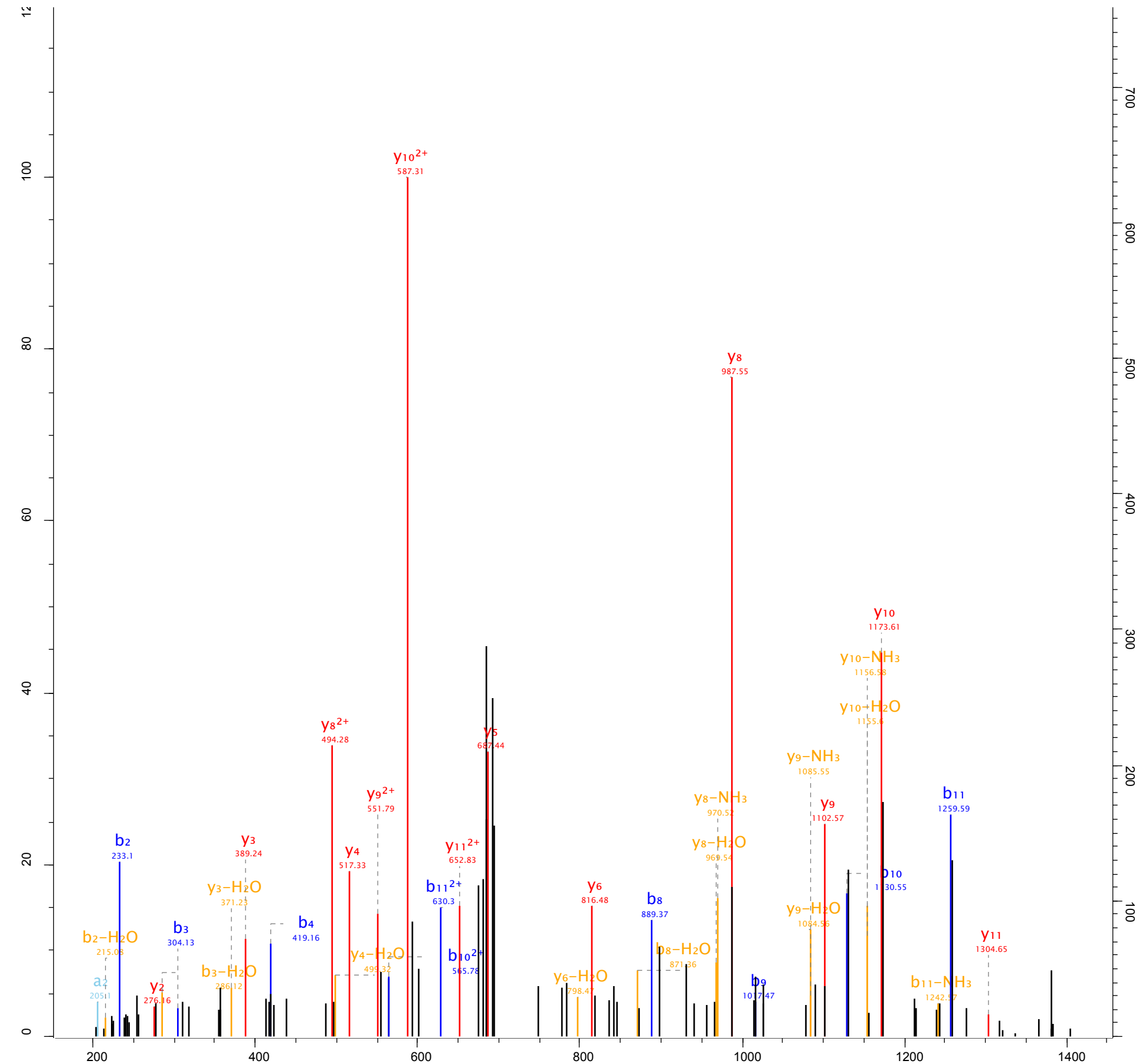
y₂₅²⁺ y₂₃²⁺ y₂₂²⁺ y₂₁²⁺ y₂₀²⁺ y₁₈²⁺ y₁₆²⁺ y₁₅²⁺ y₁₄ y₁₂²⁺ y₁₁ y₉ y₇ y₆
 - N Q S Q G Y N Q W Q Q G Q F W G Q K P W S Q H Y
b₅ b₆ b₇ b₈ b₁₁ b₁₂²⁺ b₁₃ b₁₄²⁺ b₁₅ b₁₆²⁺ b₁₈²⁺ b₁₈²⁺
H Q G Y Y -





Raw file
072613_SCW_II_68_Enriched_9

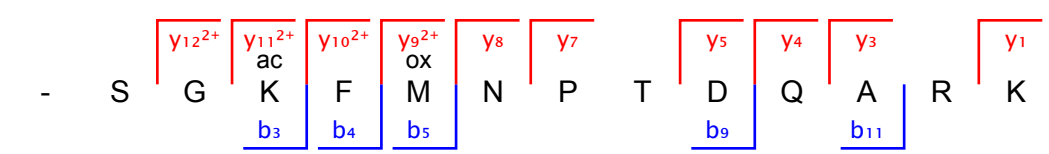
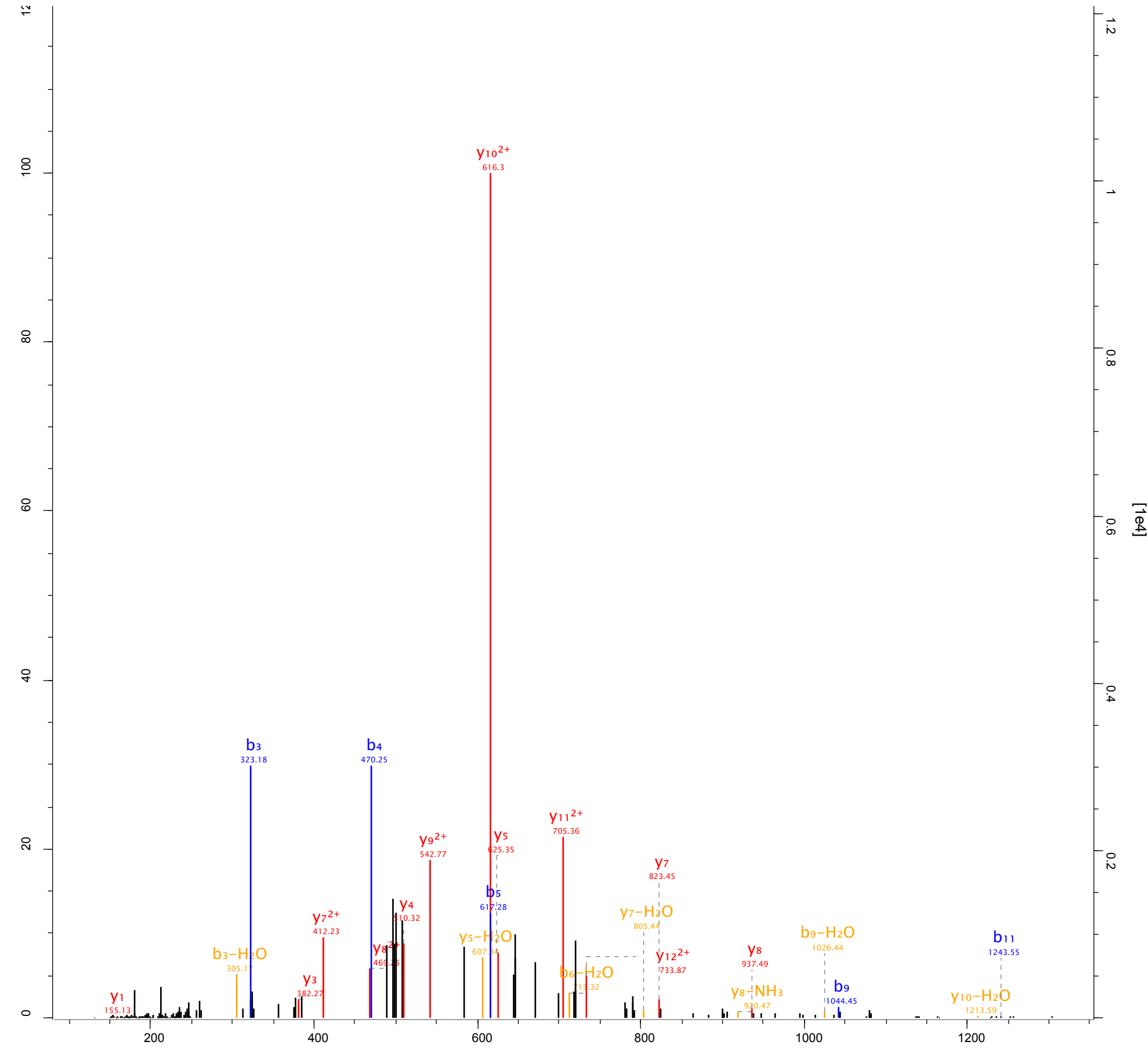
Scan 12809 Method ITMS; CID Score 187.62 m/z 703.36 Gene names Ywhah

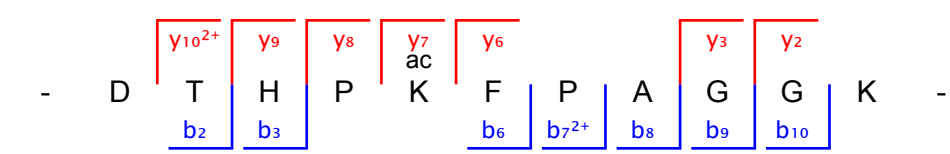
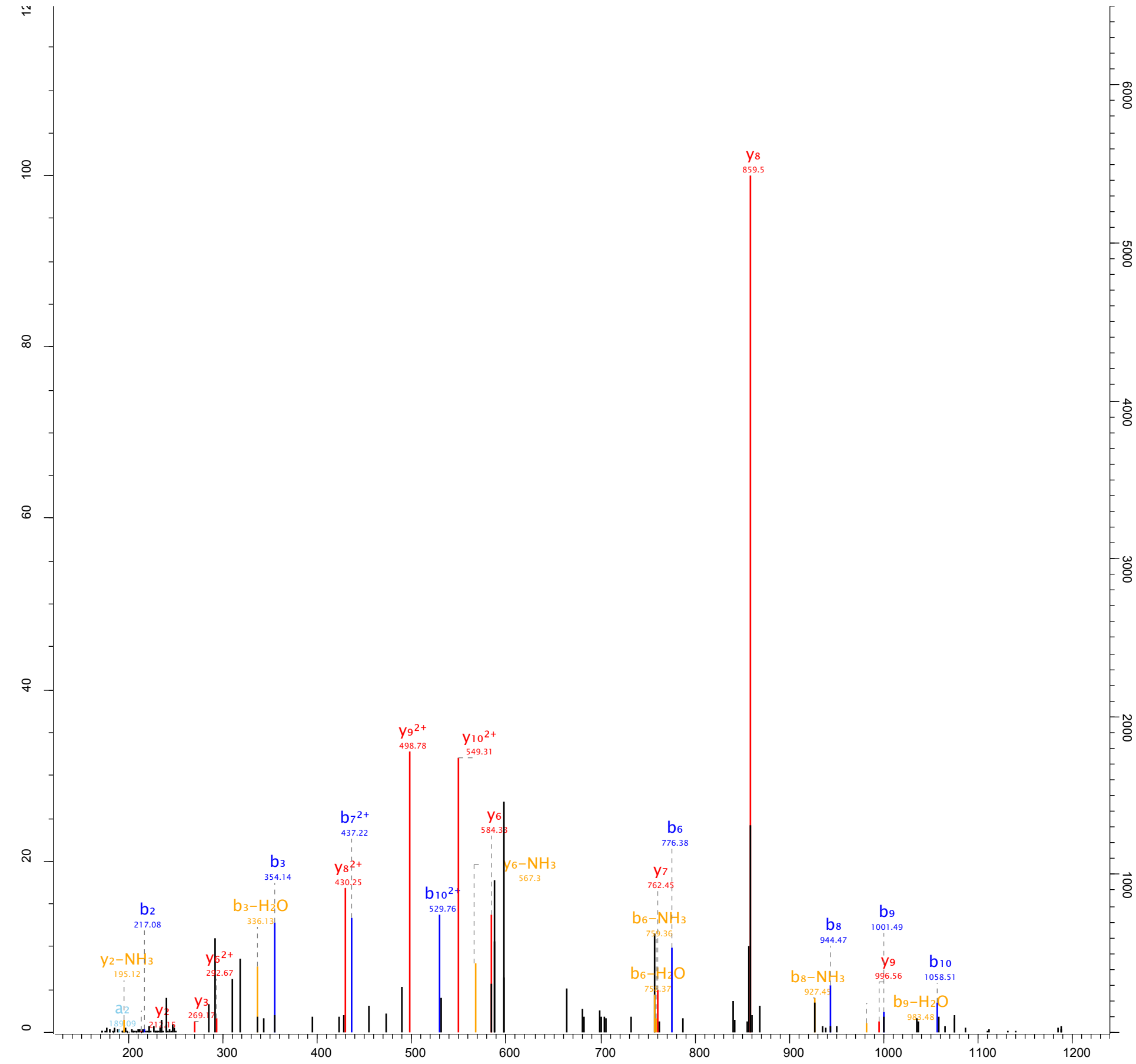


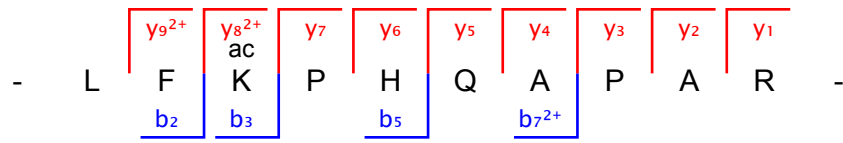
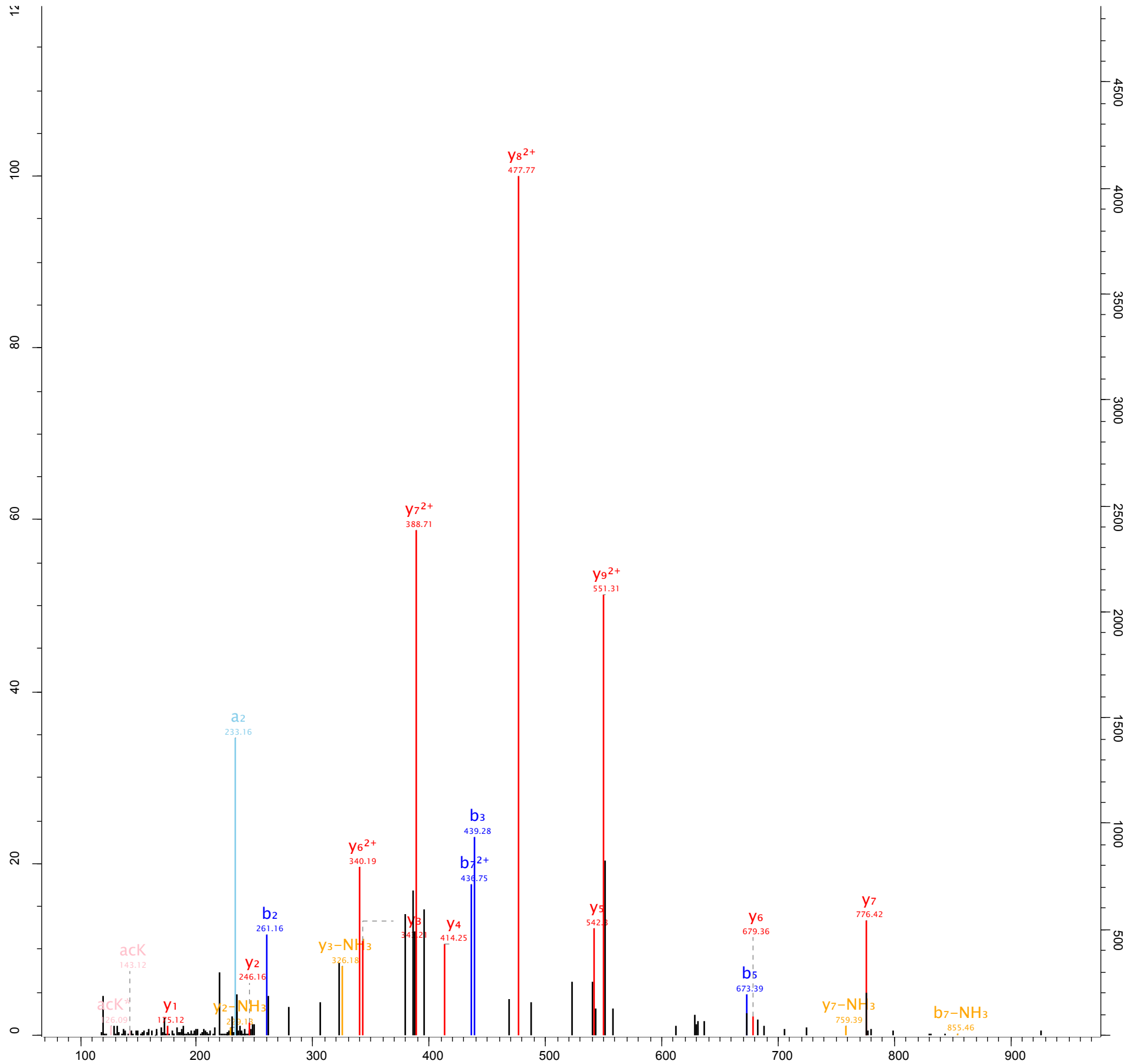
- T M A D G N E K K L E K -

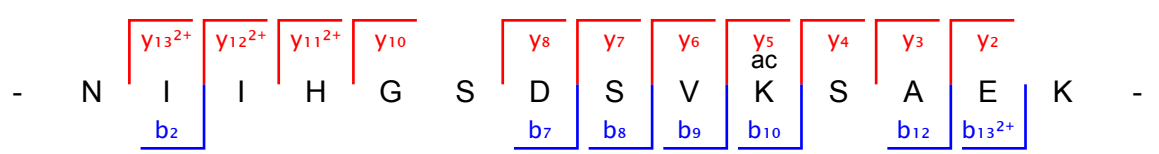
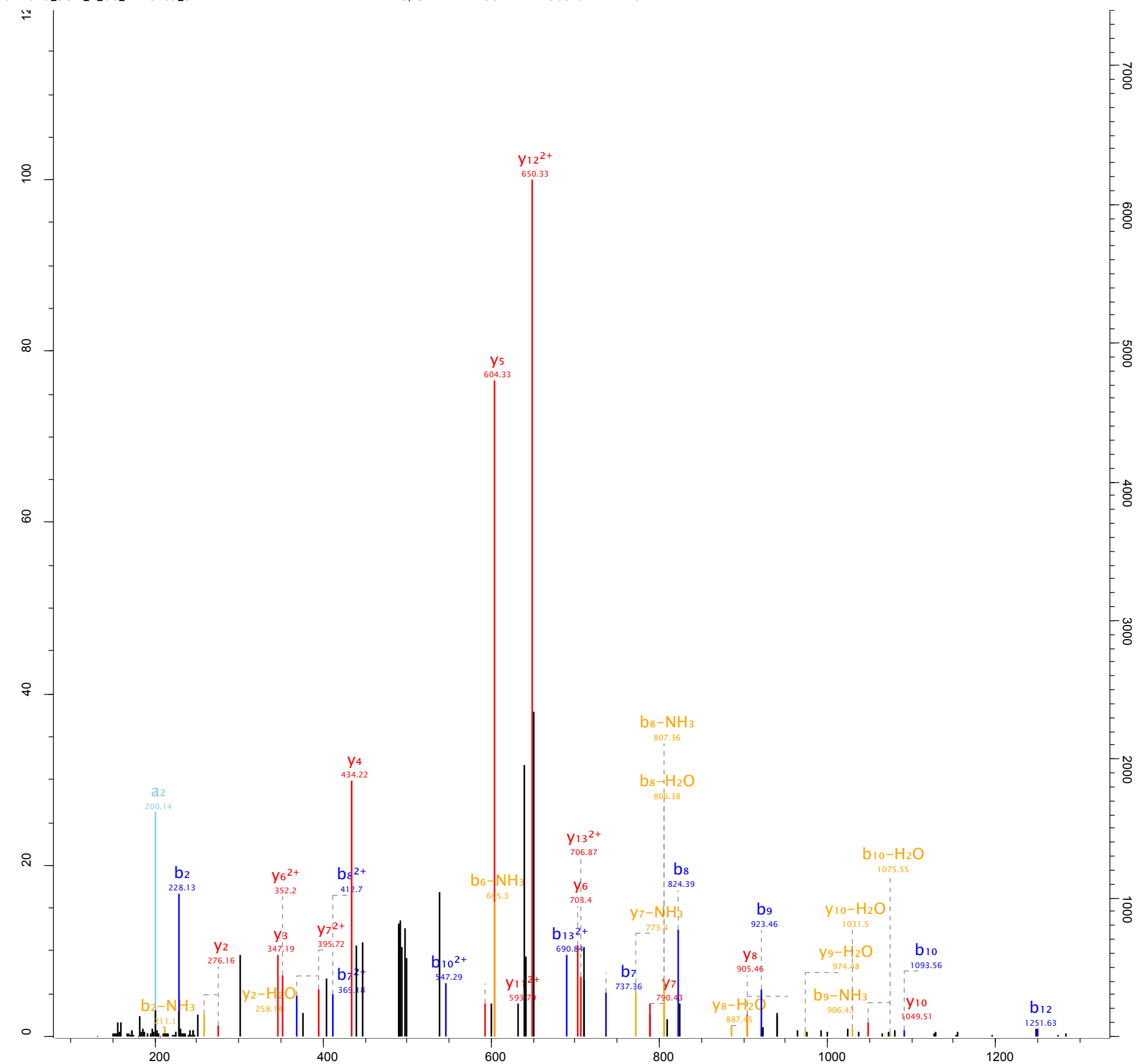
Fragmentation mapping:
- y_{11} (M) - y_{10} (A) - y_9 (D) - y_8 (G) - N - y_6 (E) - y_5 (K) - y_4 (K) - y_3 (L) - y_2 (E) - K -
- b_2 (M) - b_3 (A) - b_4 (D) - G - N - E - b_8 (K) - b_9 (K) - b_{10} (L) - b_{11} (E) - K -

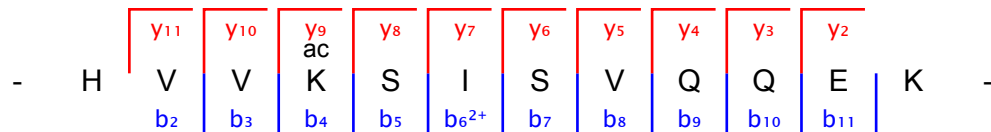
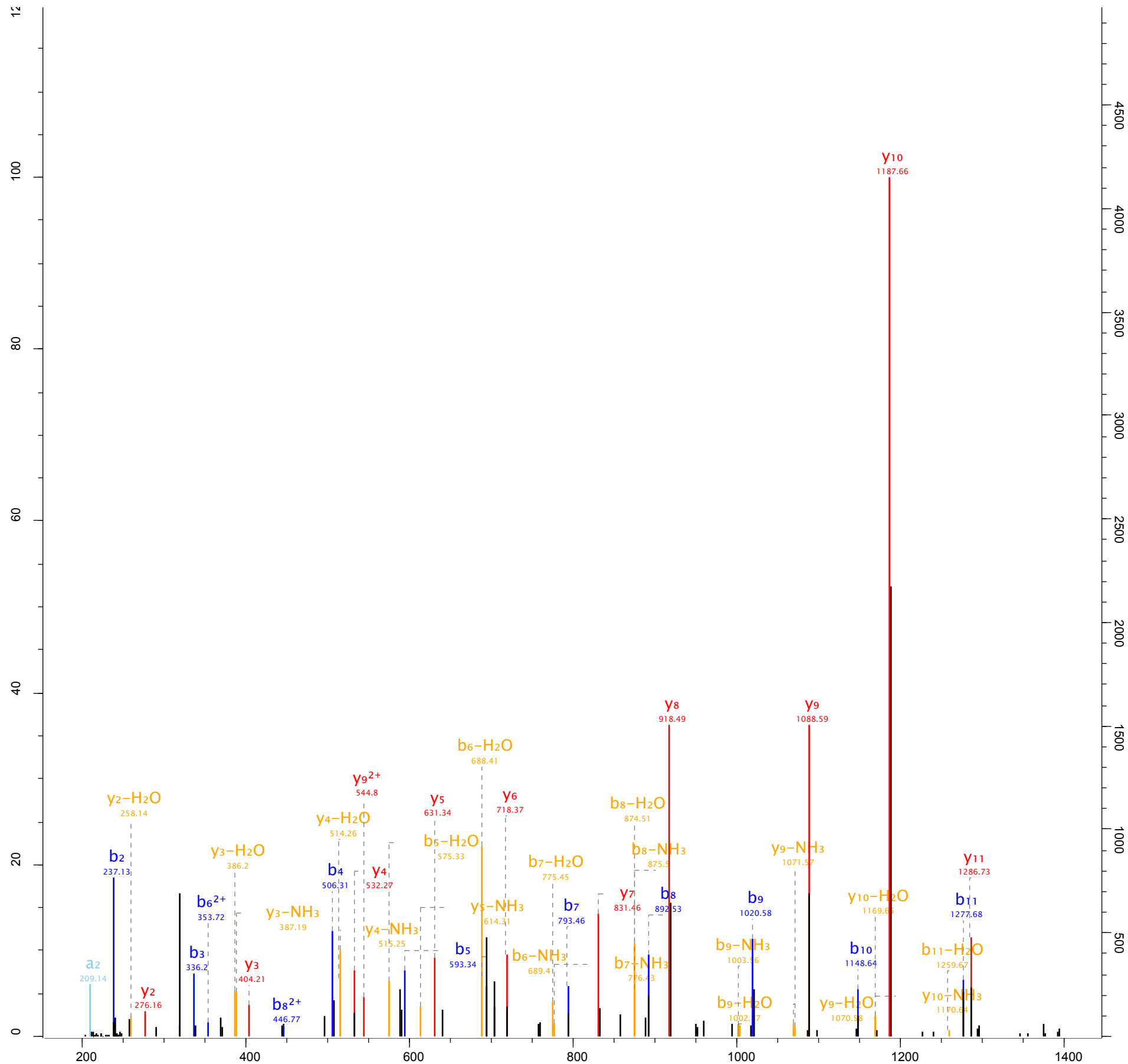
Raw file 072613_SCW_II_68_Enriched_9 Scan 13669 Method ITMS; CID Score 94.69 m/z 518.6 Gene names Wbp11











072613_SCW_II_68_Enriched_9

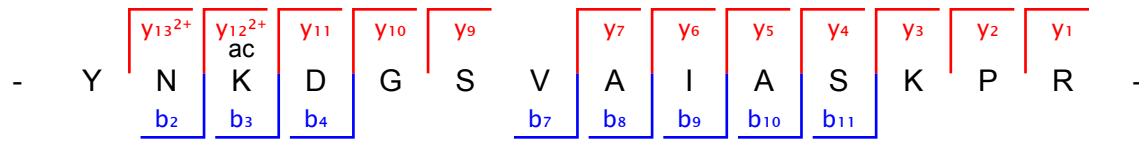
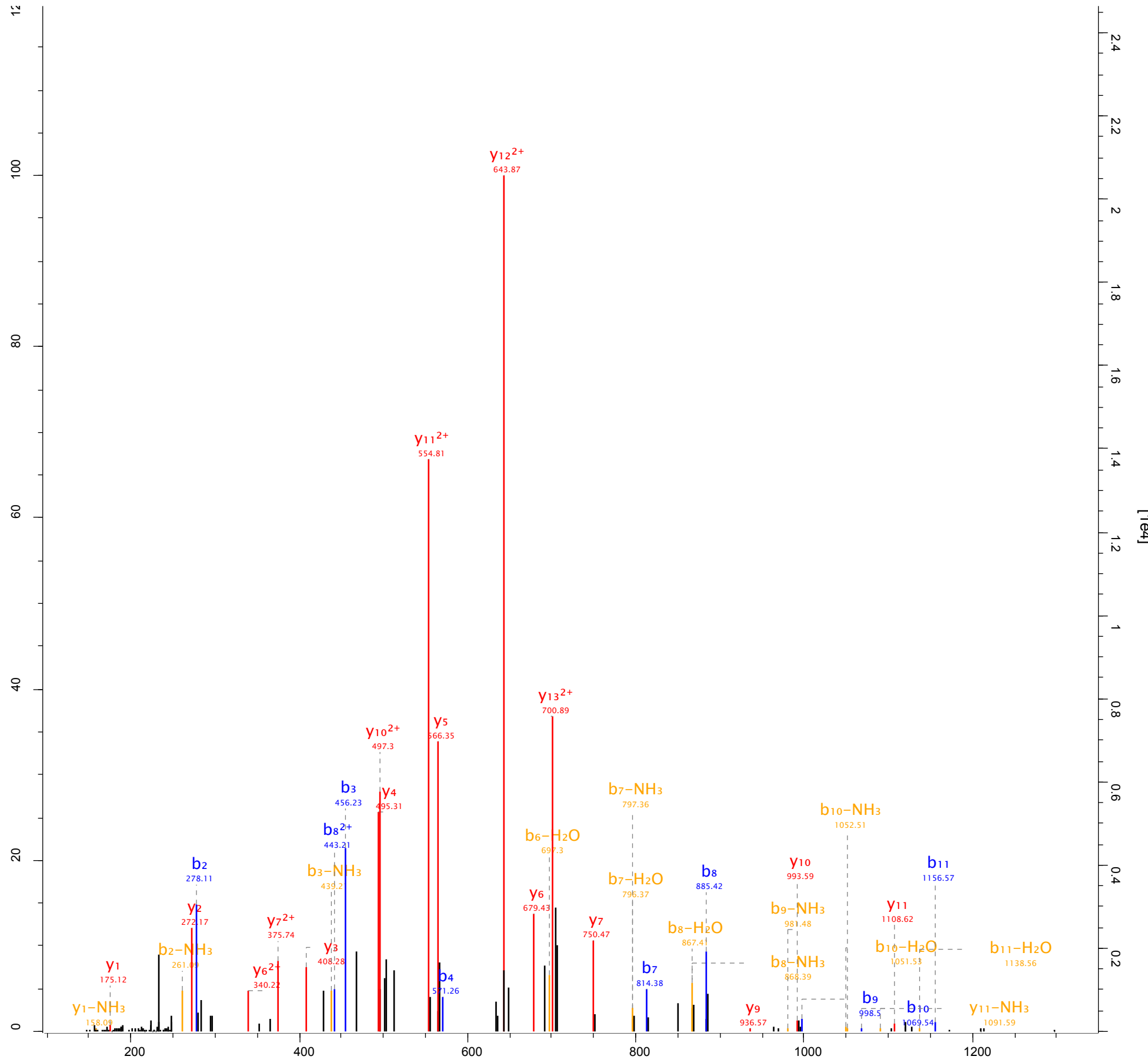
14538

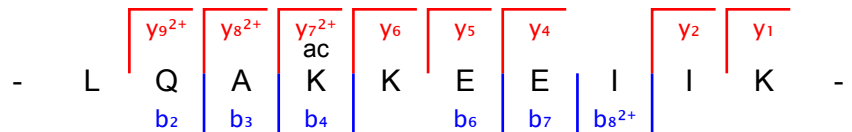
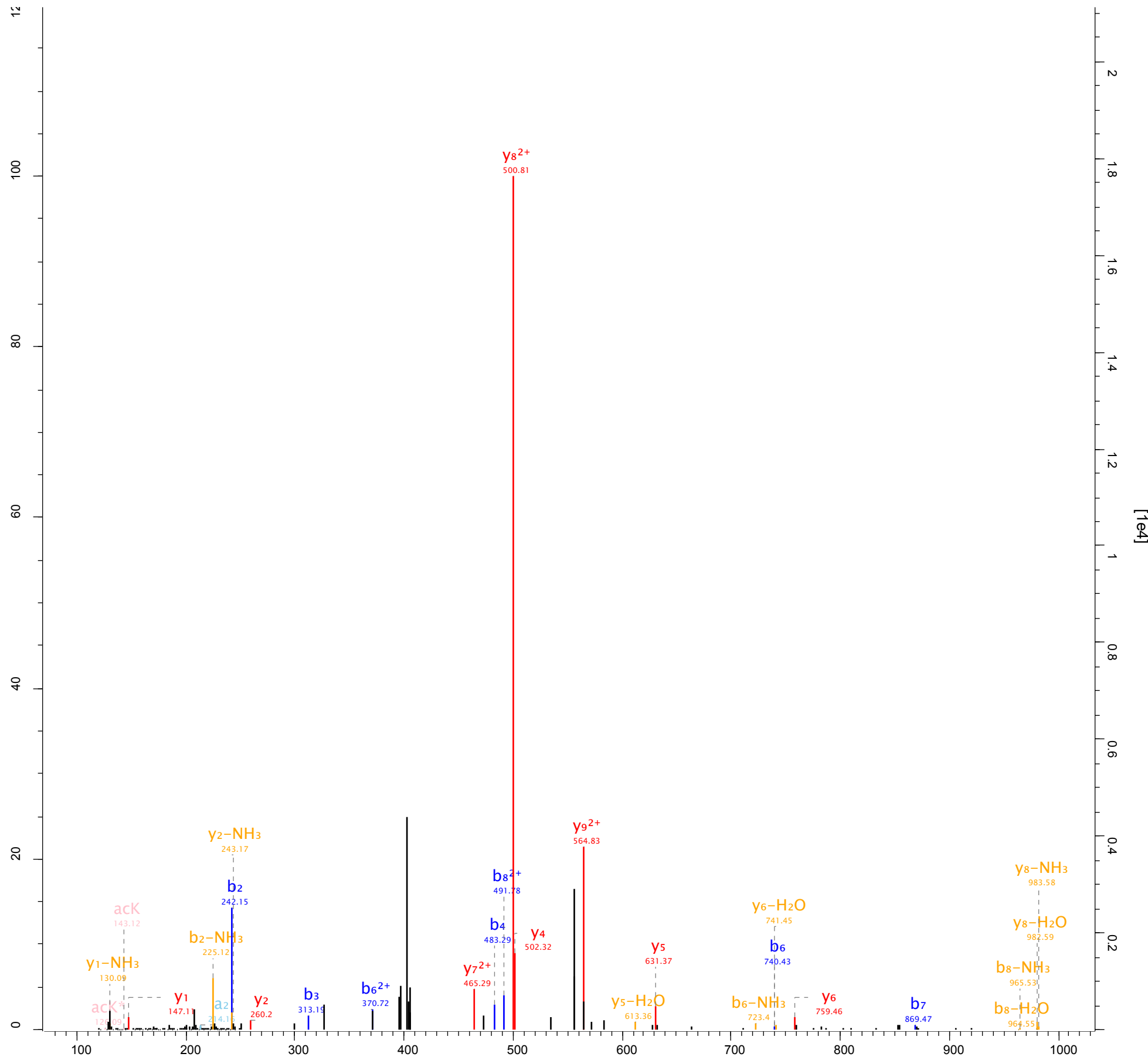
ITMS; CID

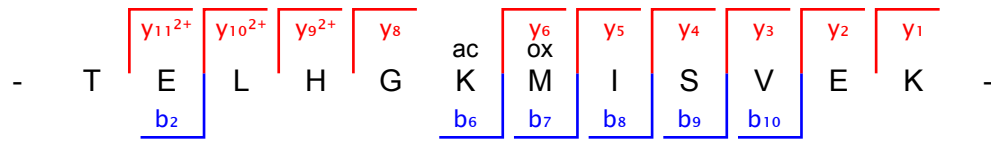
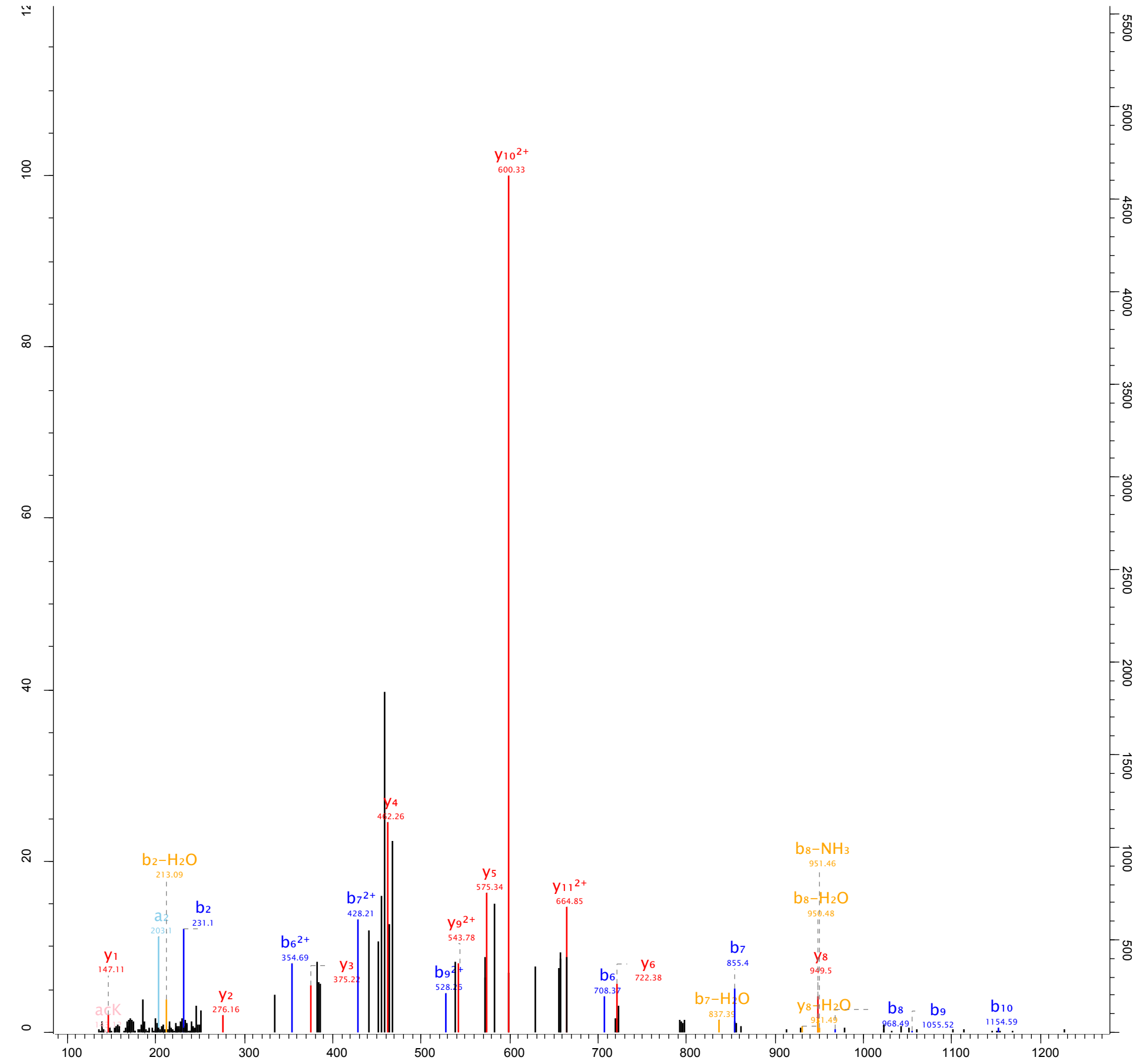
173.33

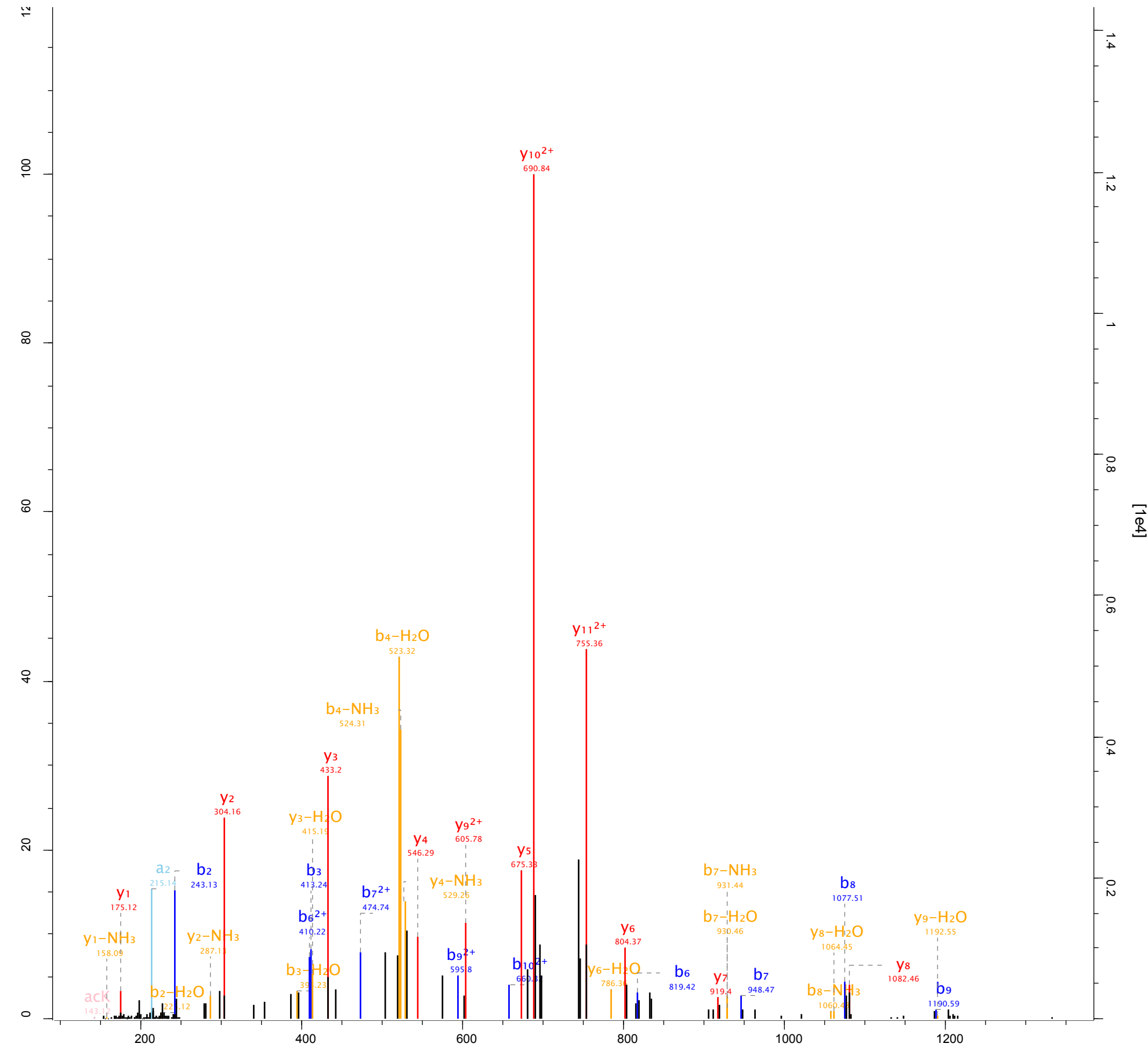
521.95

Oxct1





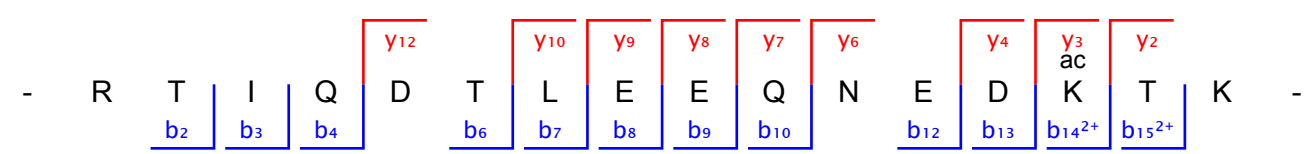
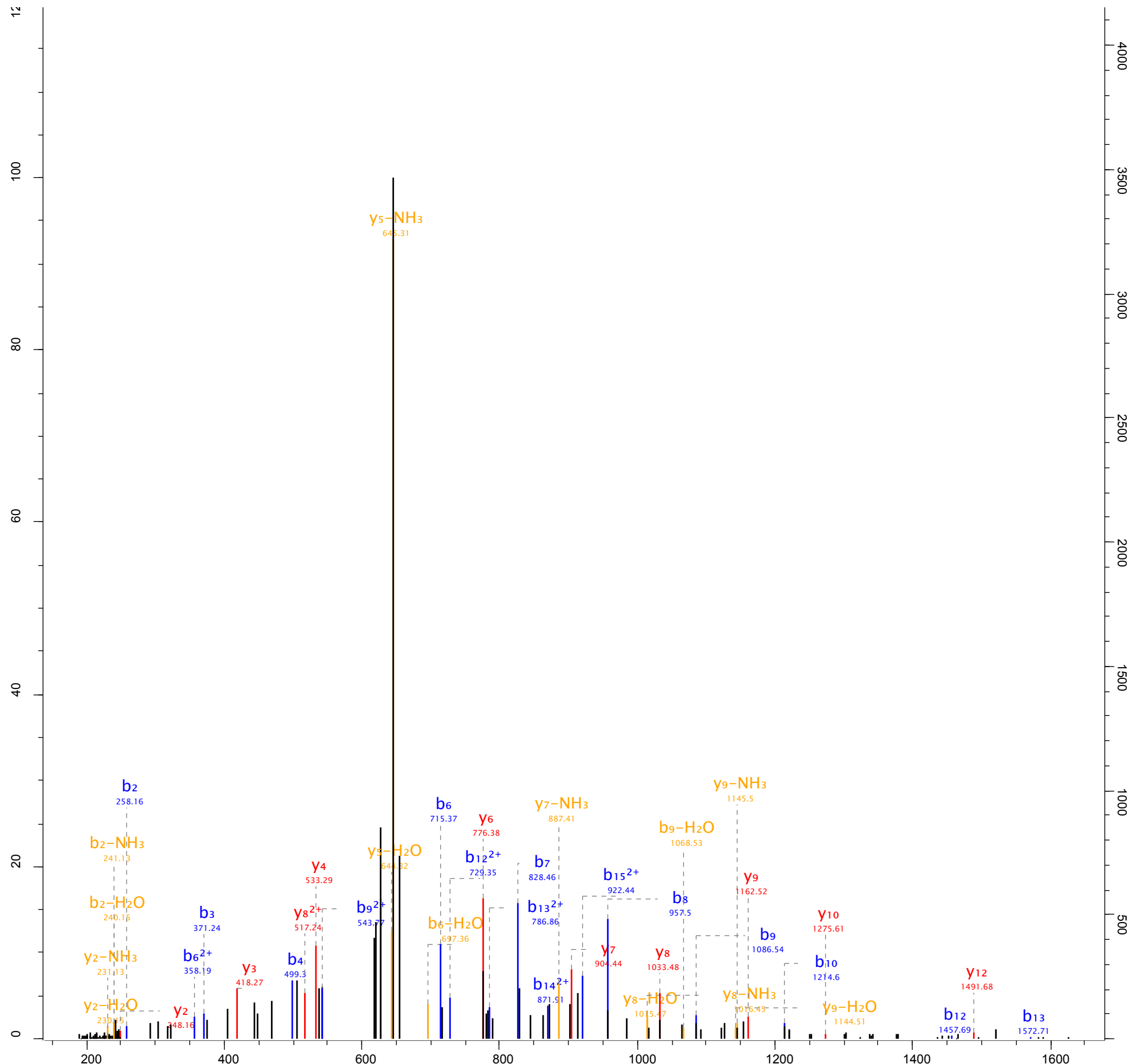


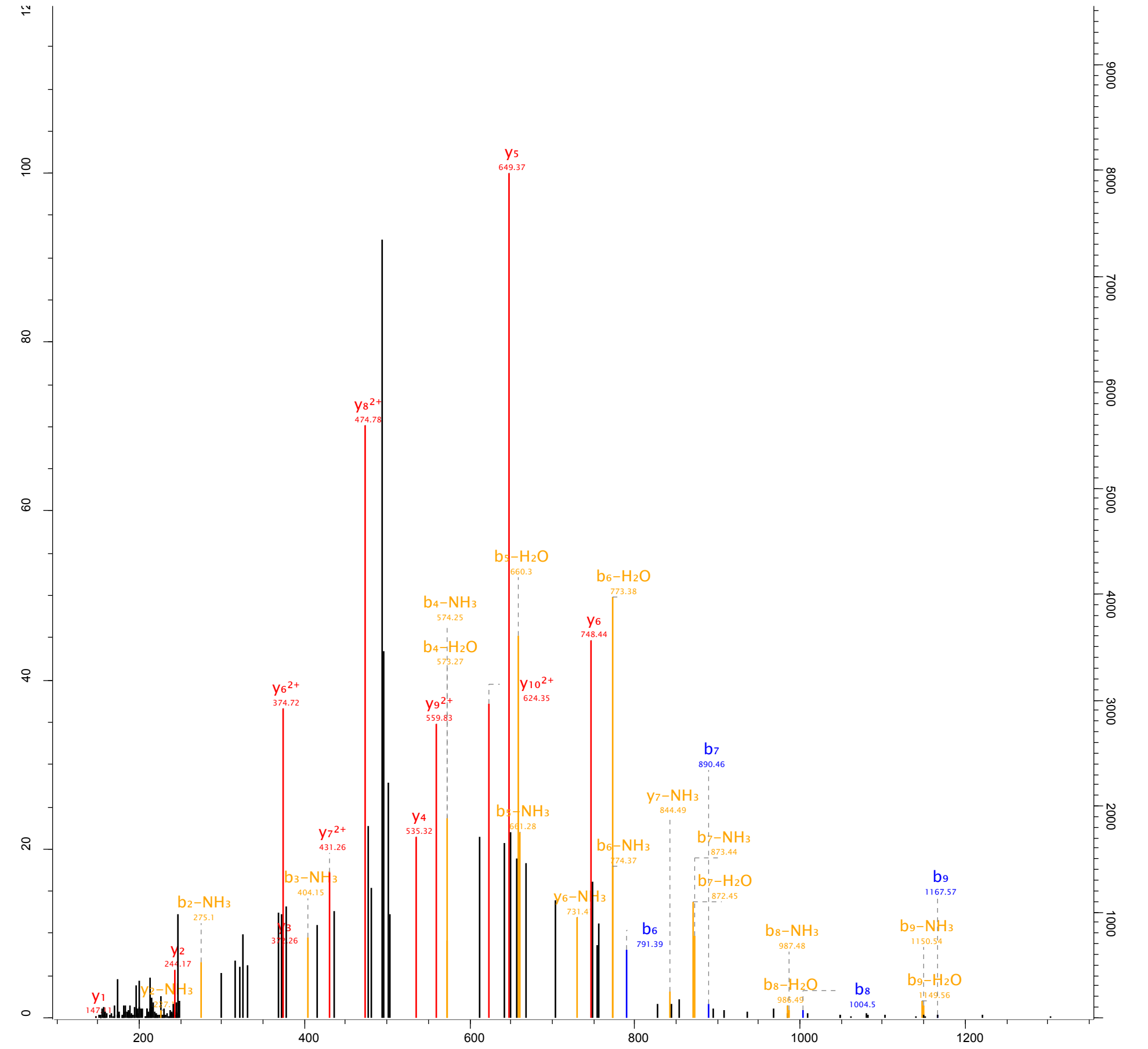


- I E K K Y D E E L E E R -

y_{11}^{2+}
 y_{10}^{2+}
 y_9^{2+}
 y_8
 y_7
 y_6
 y_5
 y_4
 y_3
 y_2
 y_1

b_2
ac
 b_3
 b_6
 b_7
 b_8
 b_9
 b_{10}^{2+}

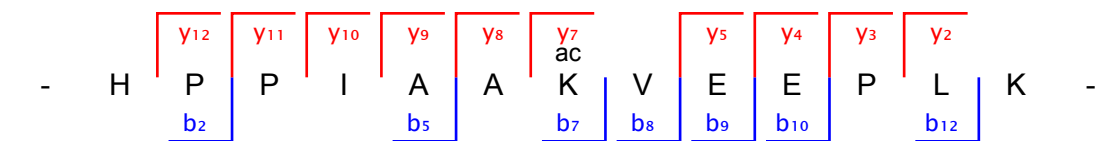
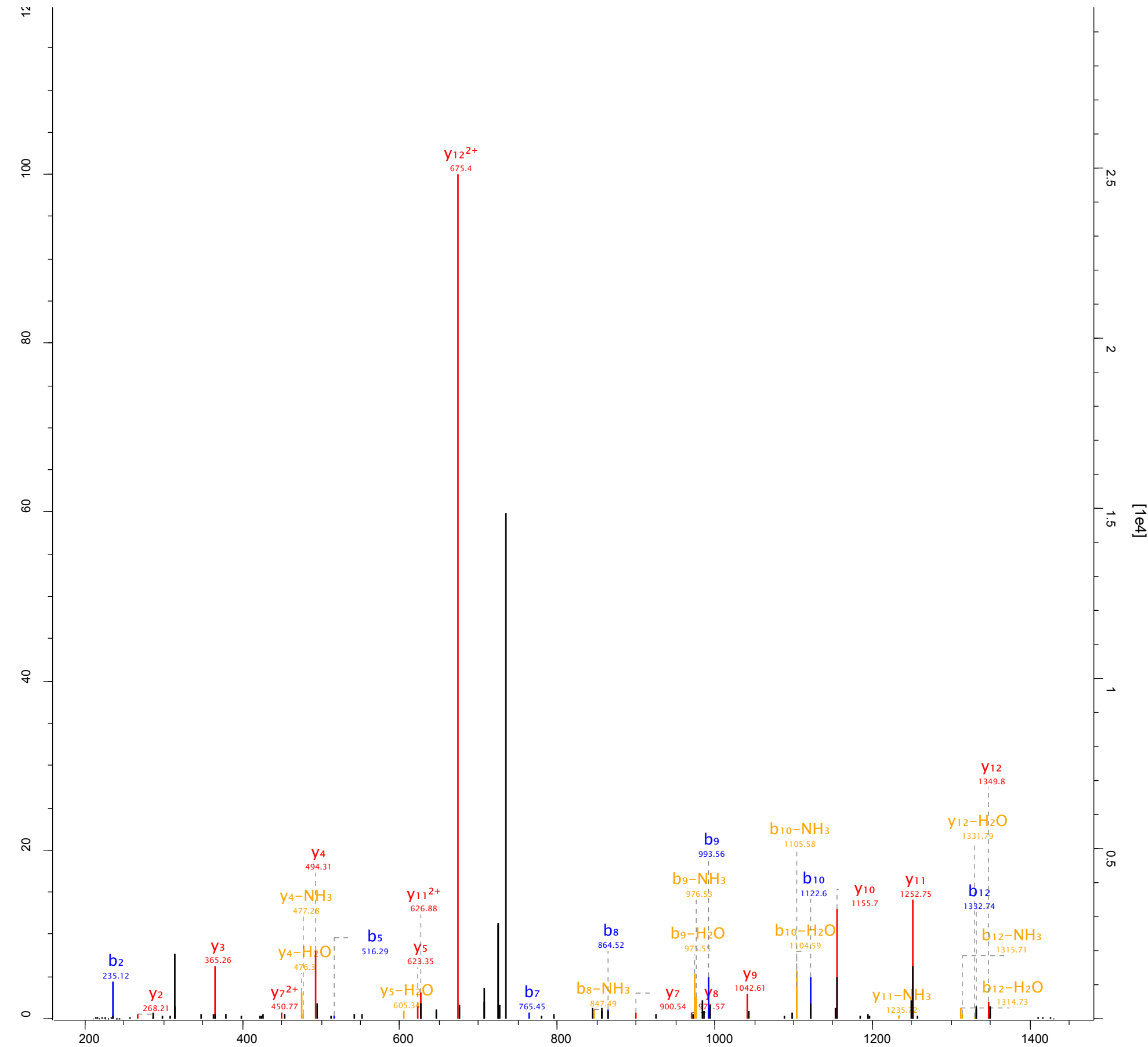


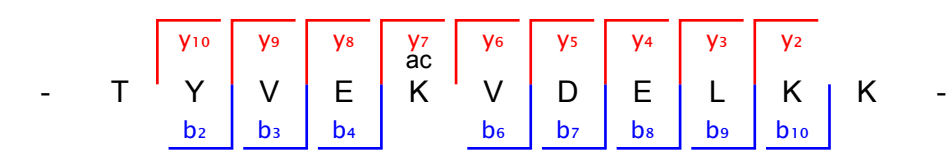
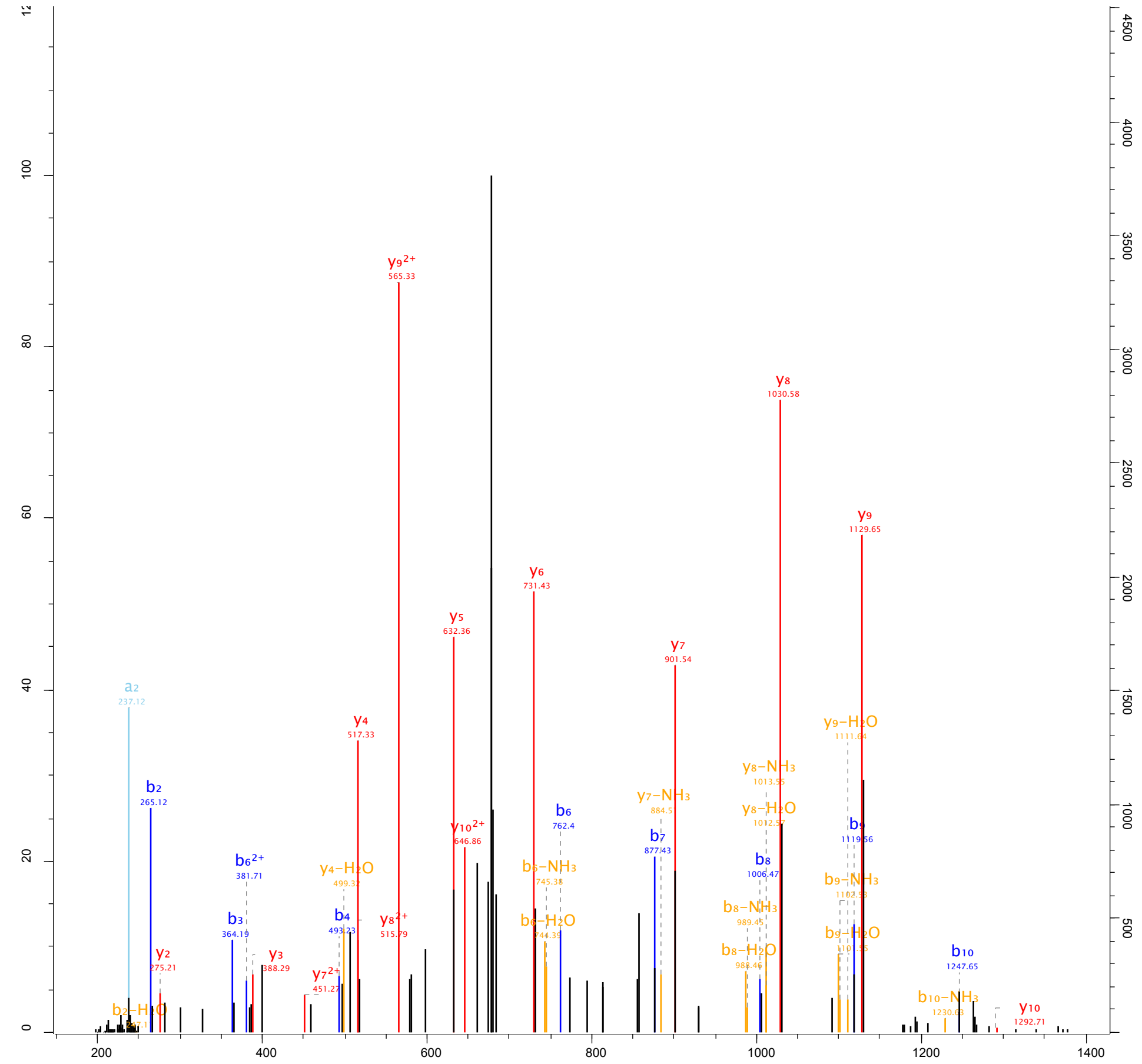


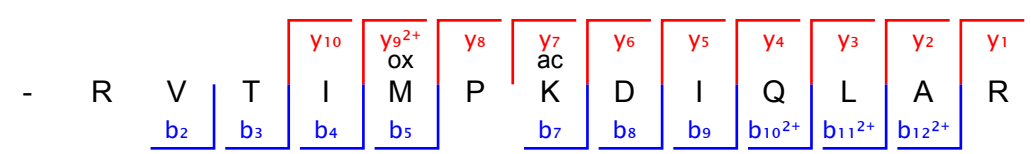
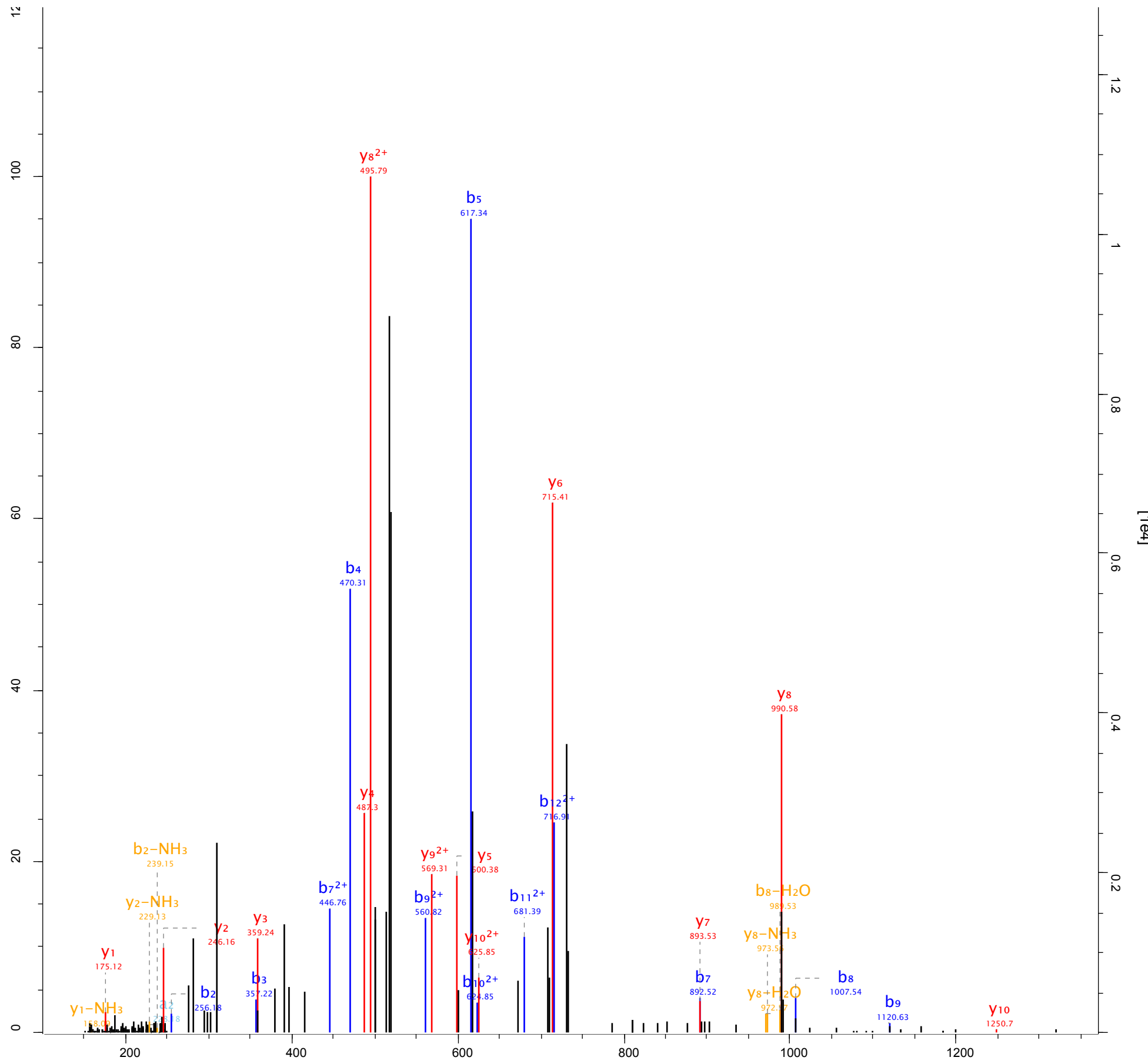
- Q Y E K S I V N Y K P K -

y10 2+
y9 2+ ac
y8 2+
y7 2+
y6
y5
y4
y3
y2
y1

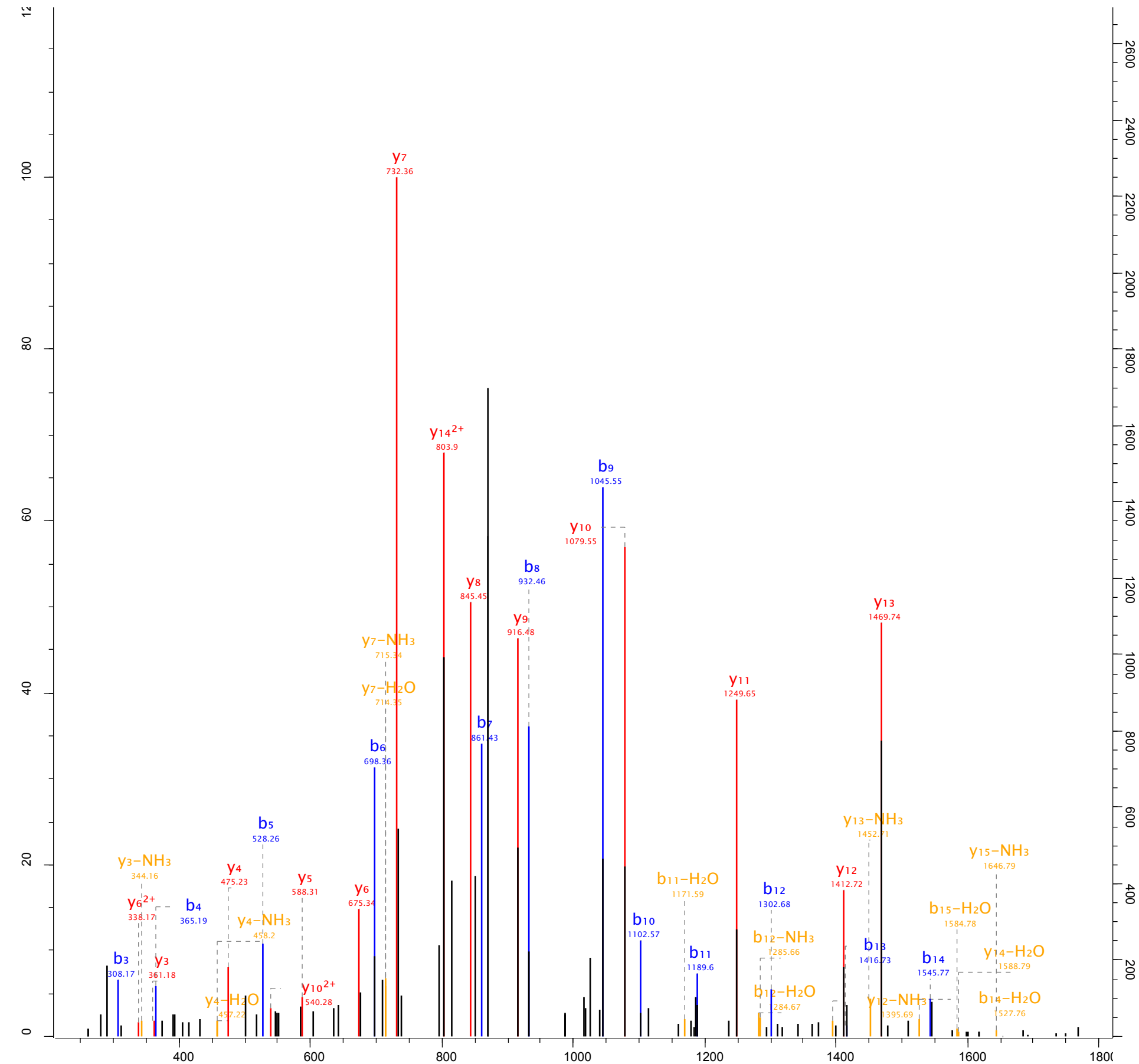
b6
b7
b8
b9







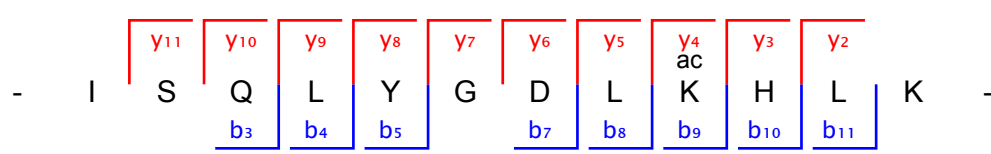
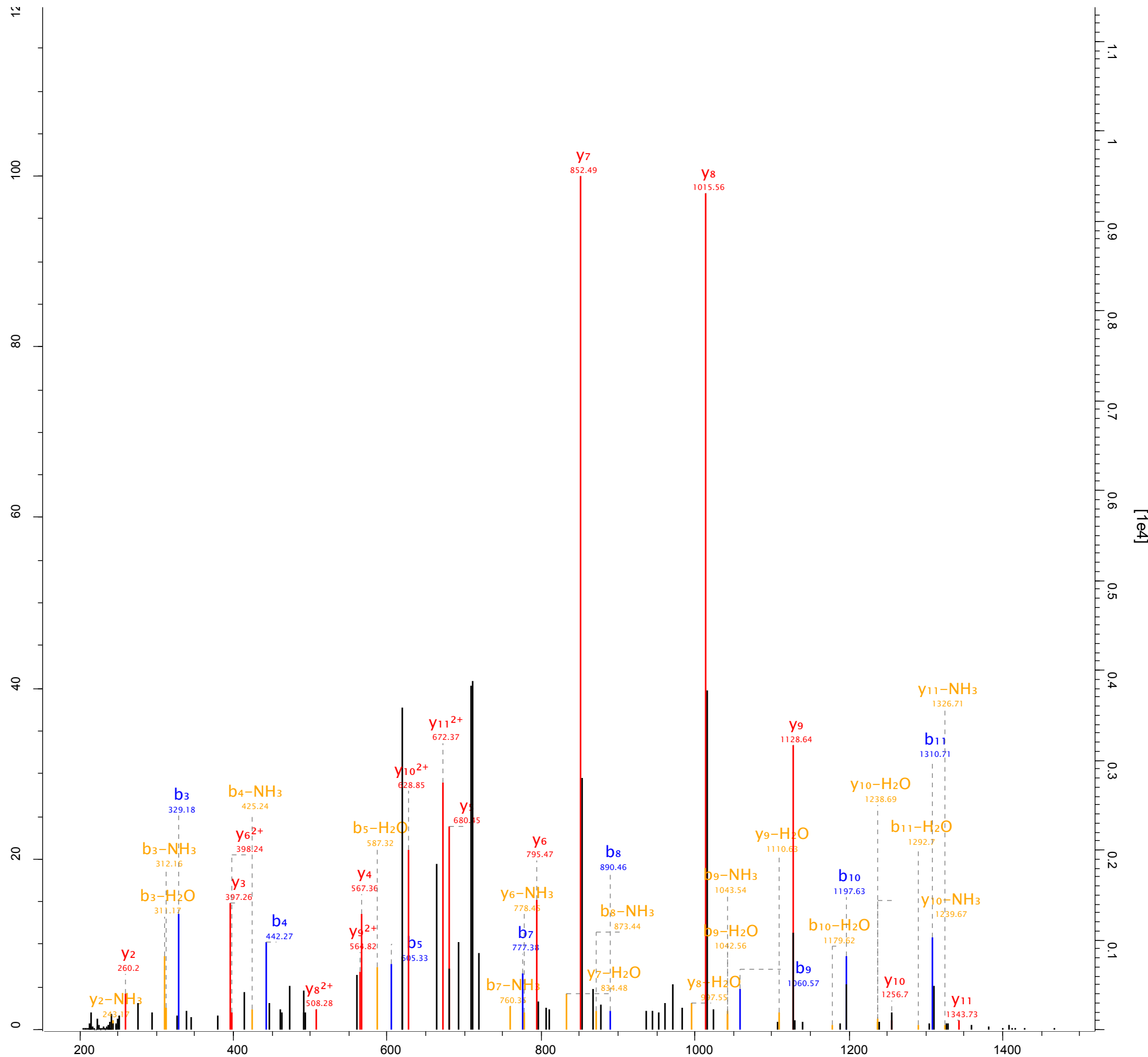
Raw file 072613_SCW_II_68_Enriched_9 Scan 19485 Method ITMS; CID Score 176.08 m/z 888.96 Gene names Acadsb

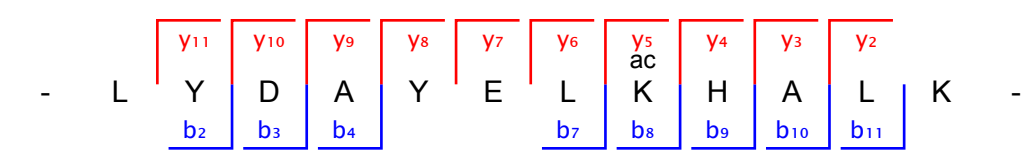
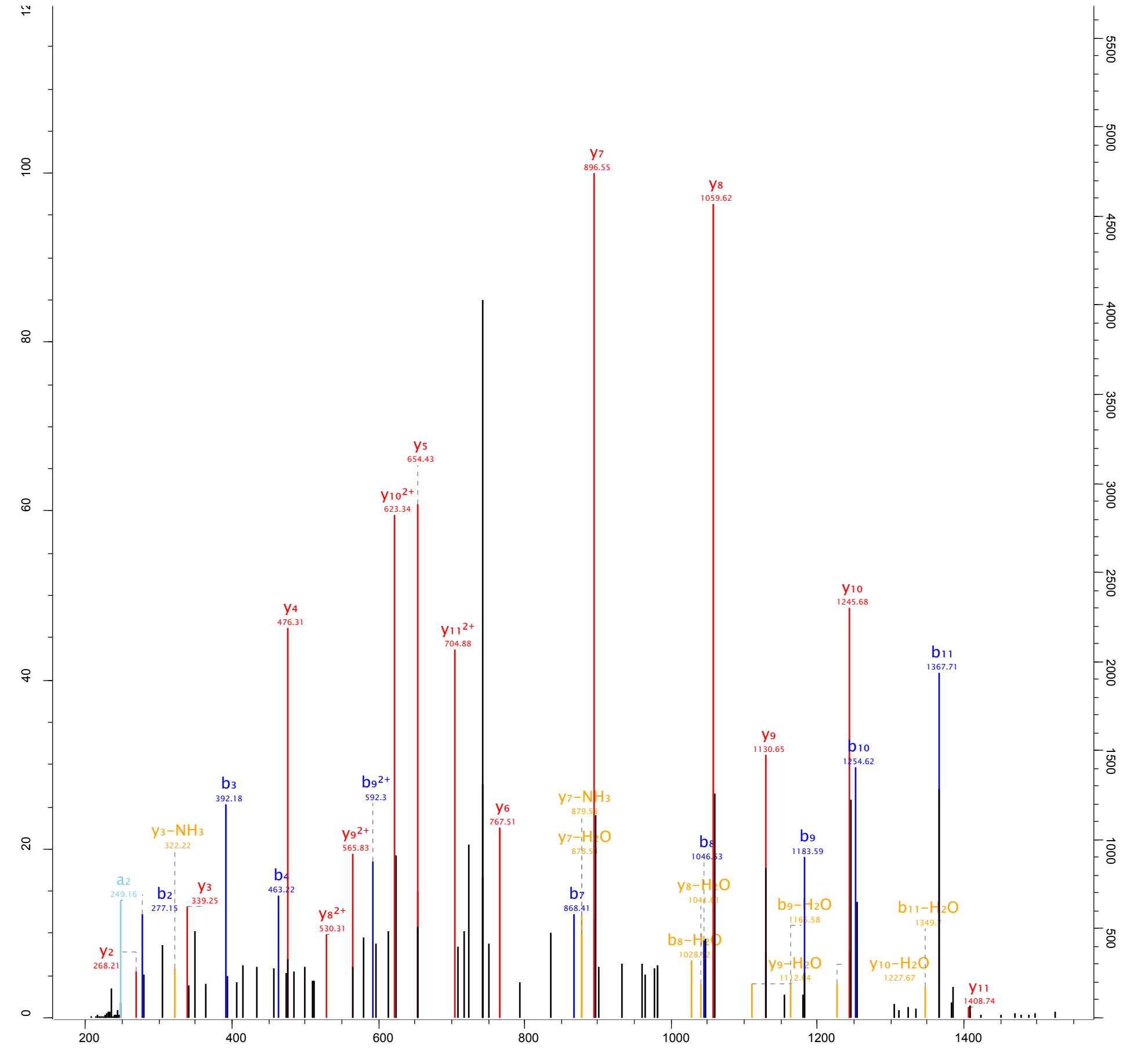


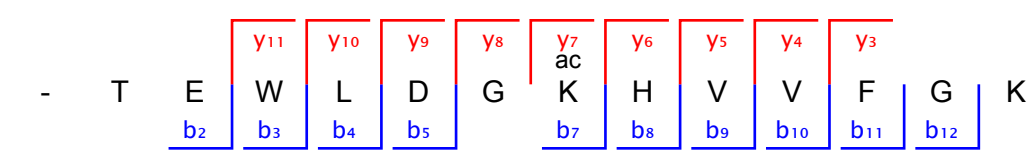
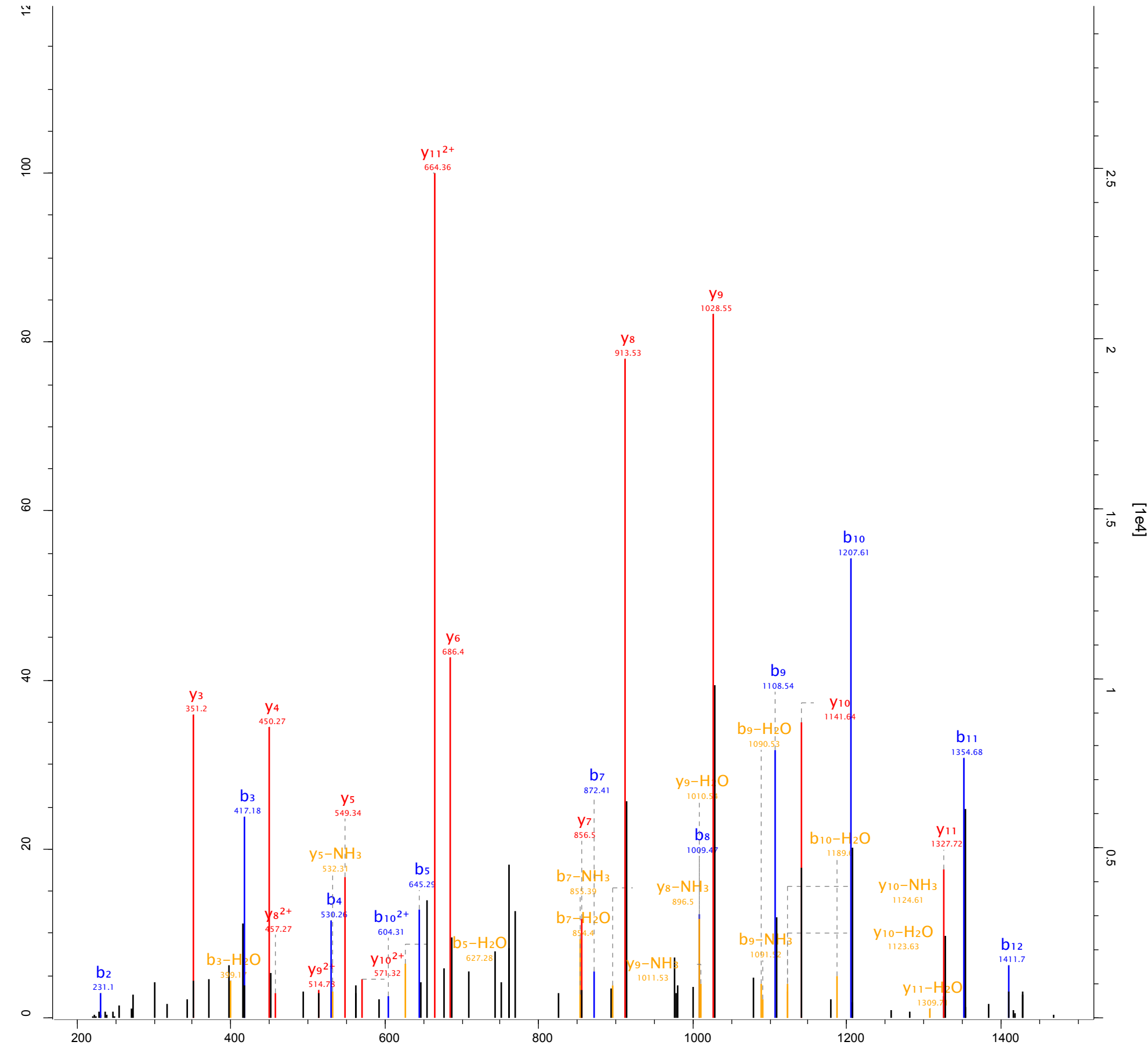
y14²⁺
y13
y12
y11 ac
y10
y9
y8
y7
y6
y5
y4
y3

b3
b4
b5
b6
b7
b8
b9
b10
b11
b12
b13
b14

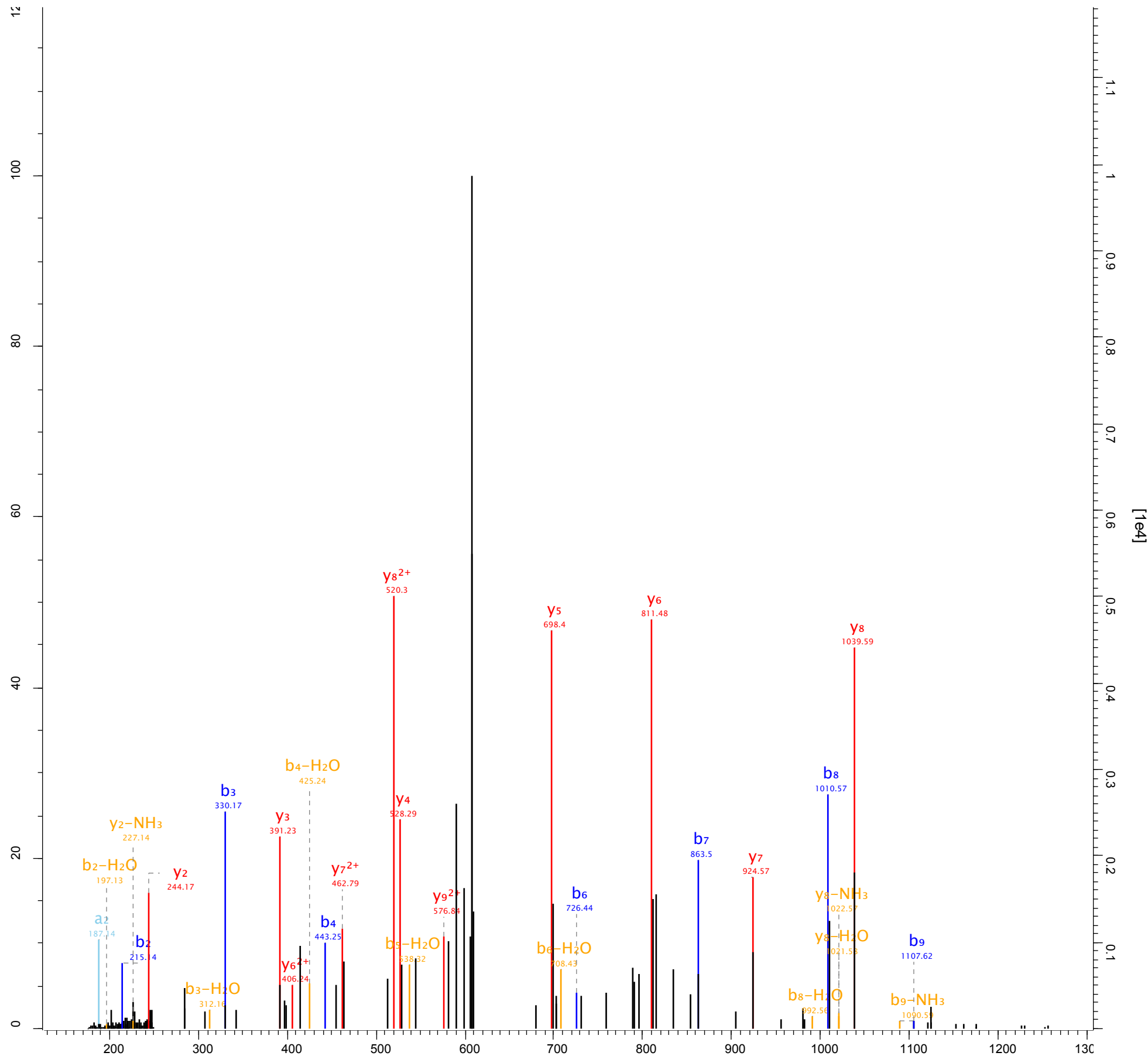
- I G H G Y K Y A I G S L N E G R -







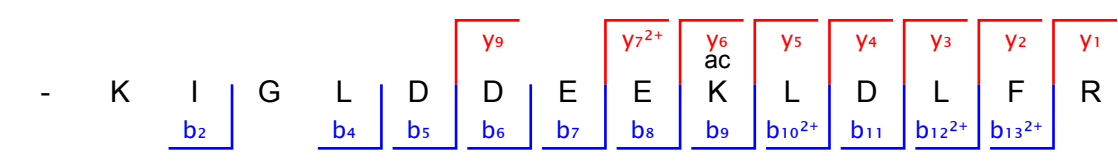
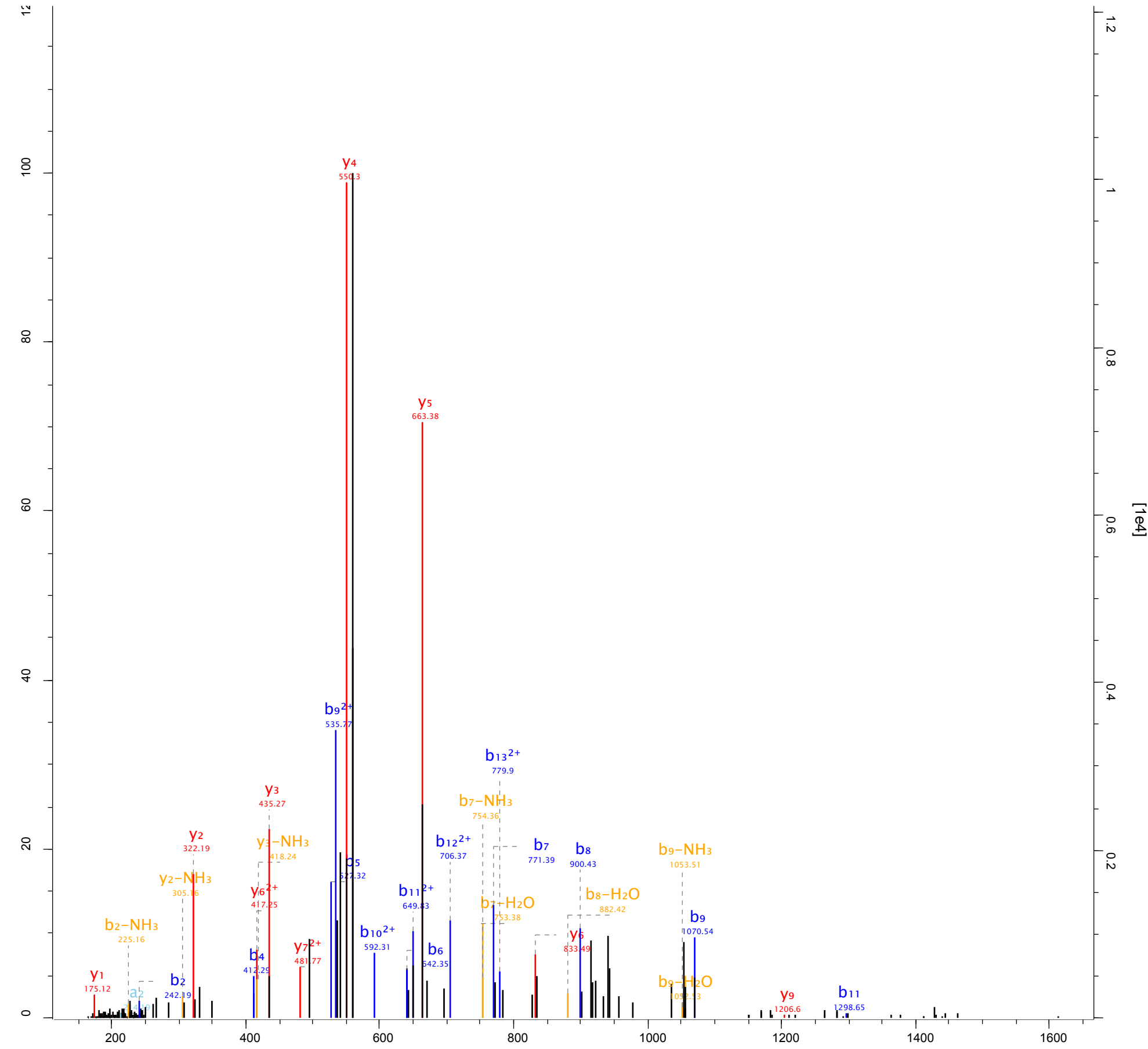
Raw file 072613_SCW_II_68_Enriched_9 Scan 23027 Method ITMS; CID Score 161.51 m/z 627.37 Gene names Ndufa5

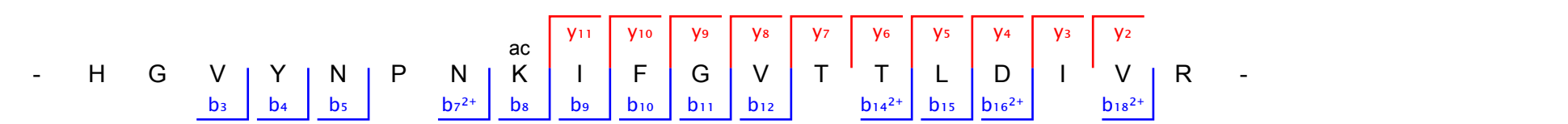
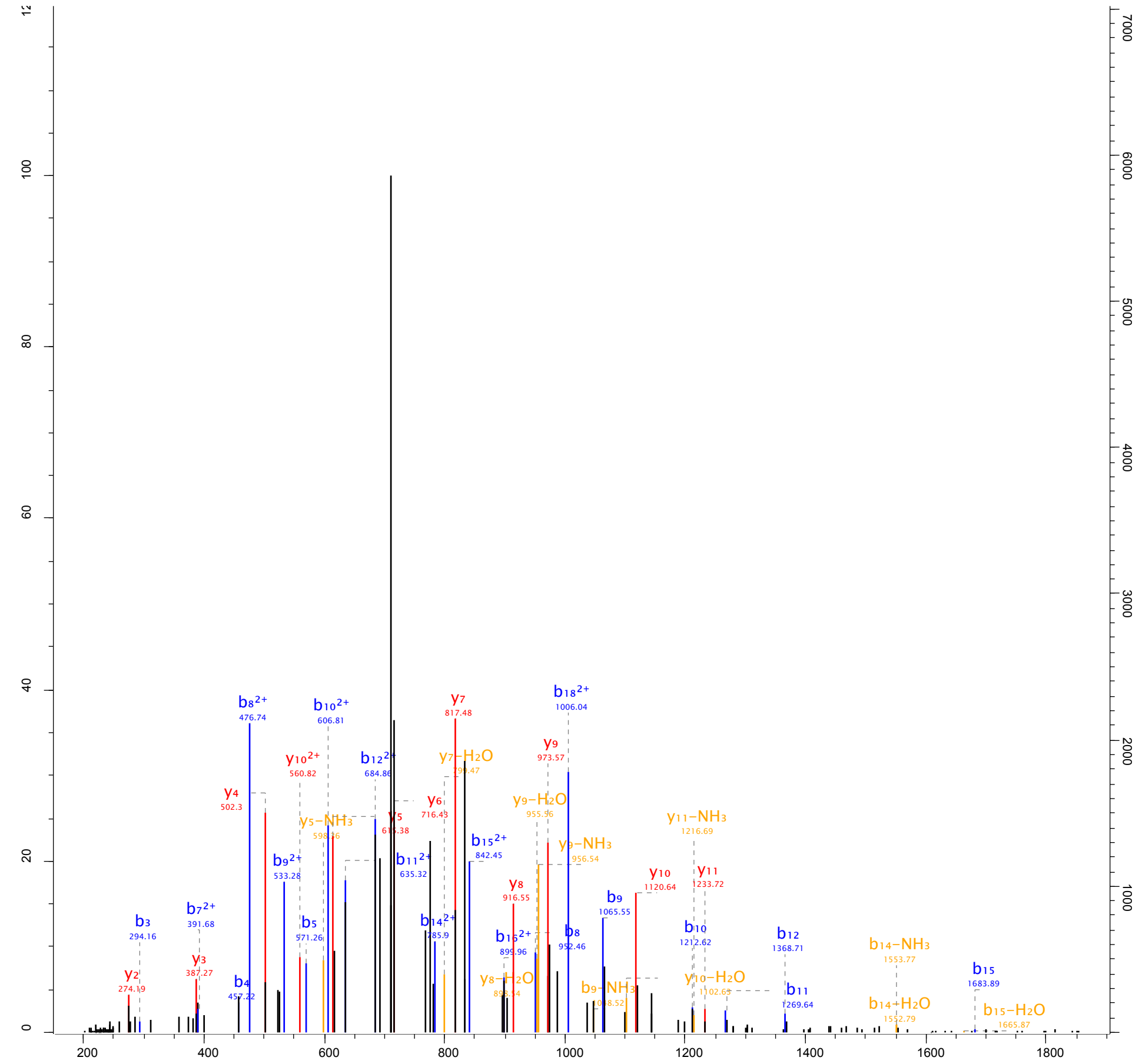


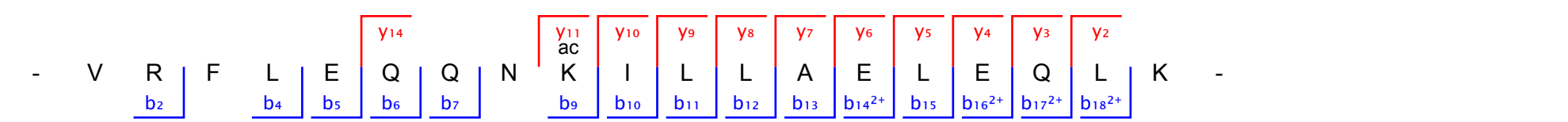
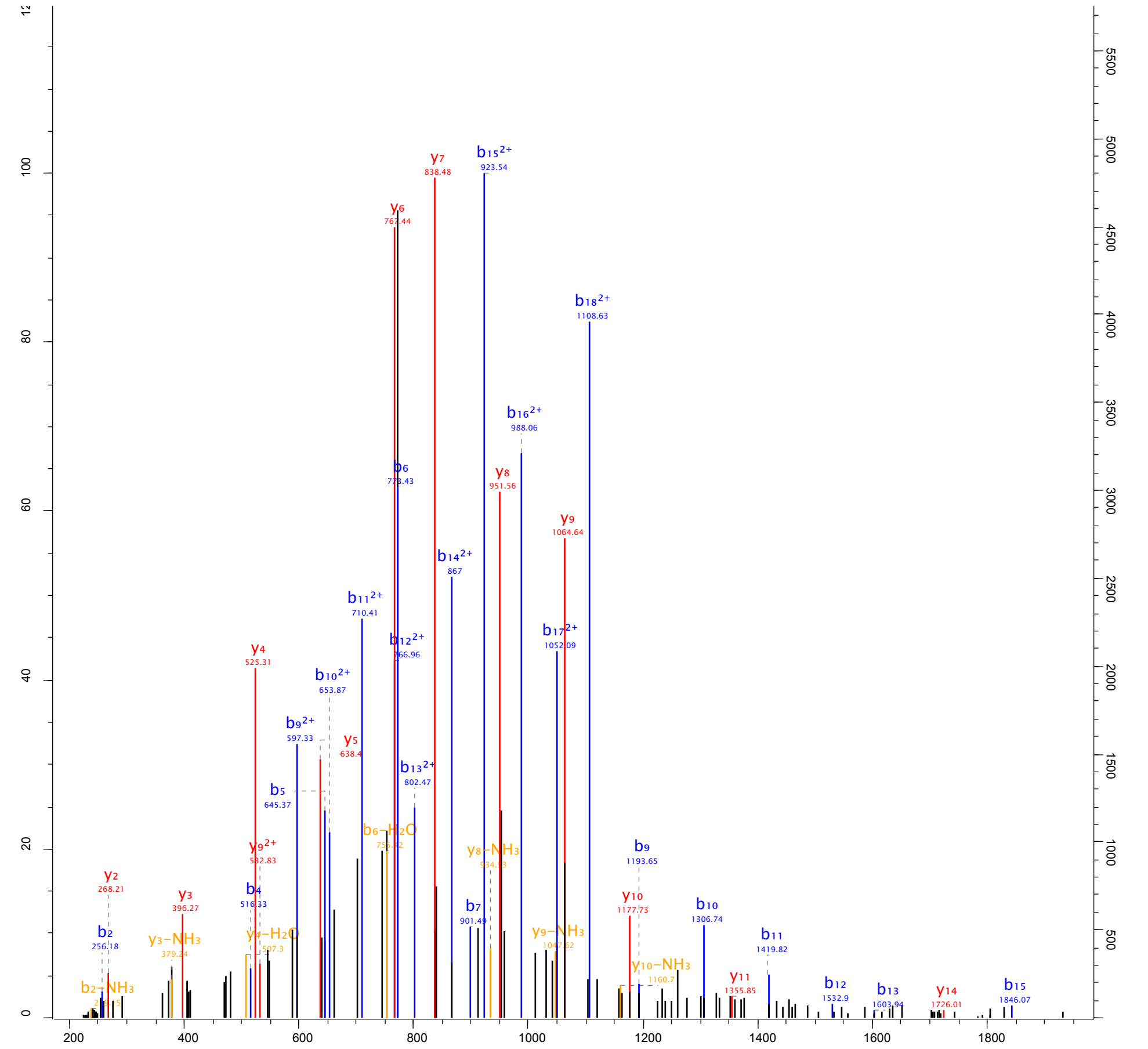
- T L D I L K H F P K -

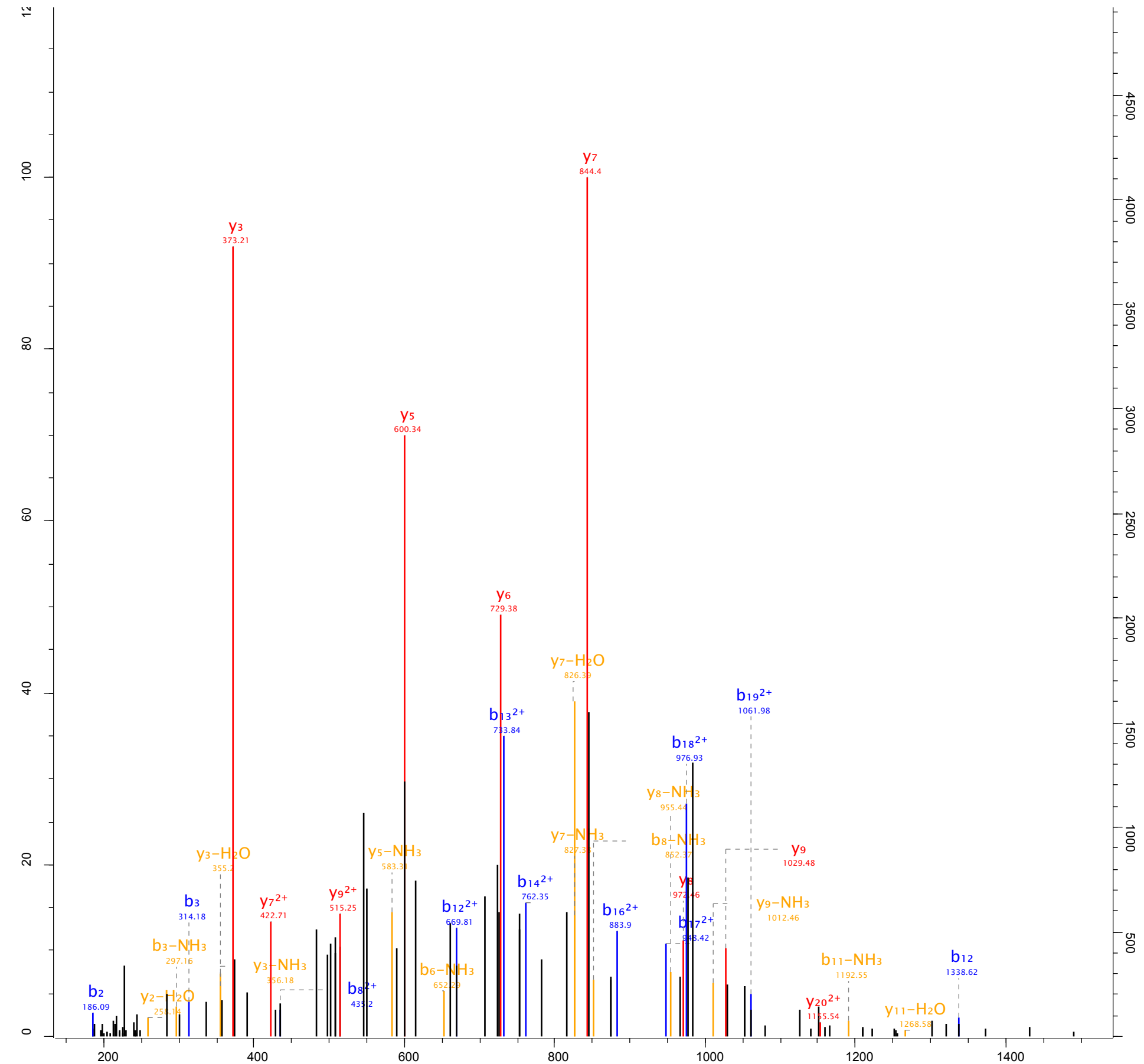
y9²⁺
y8
y7
y6
y5
y4
y3
y2

b2
b3
b4
b6
b7
b8
b9





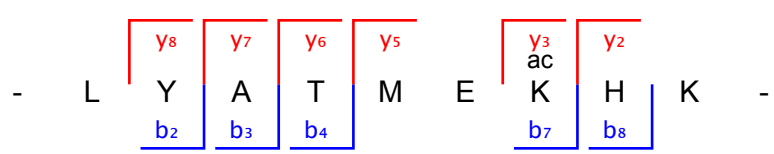
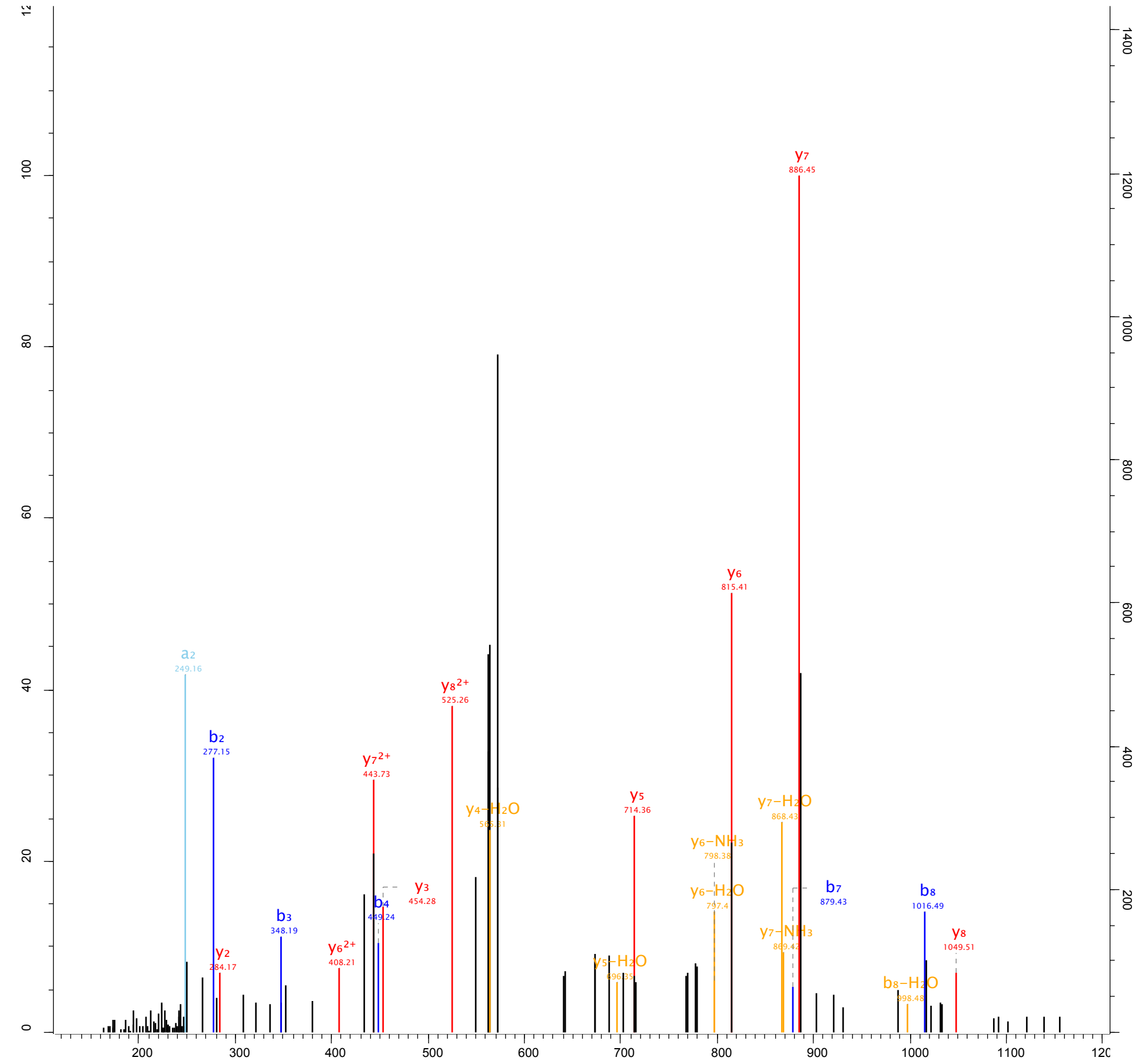


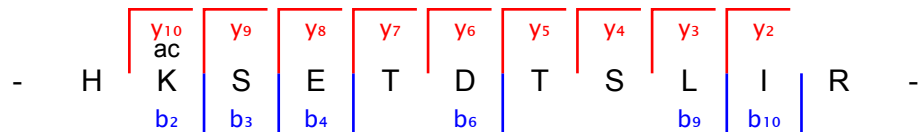
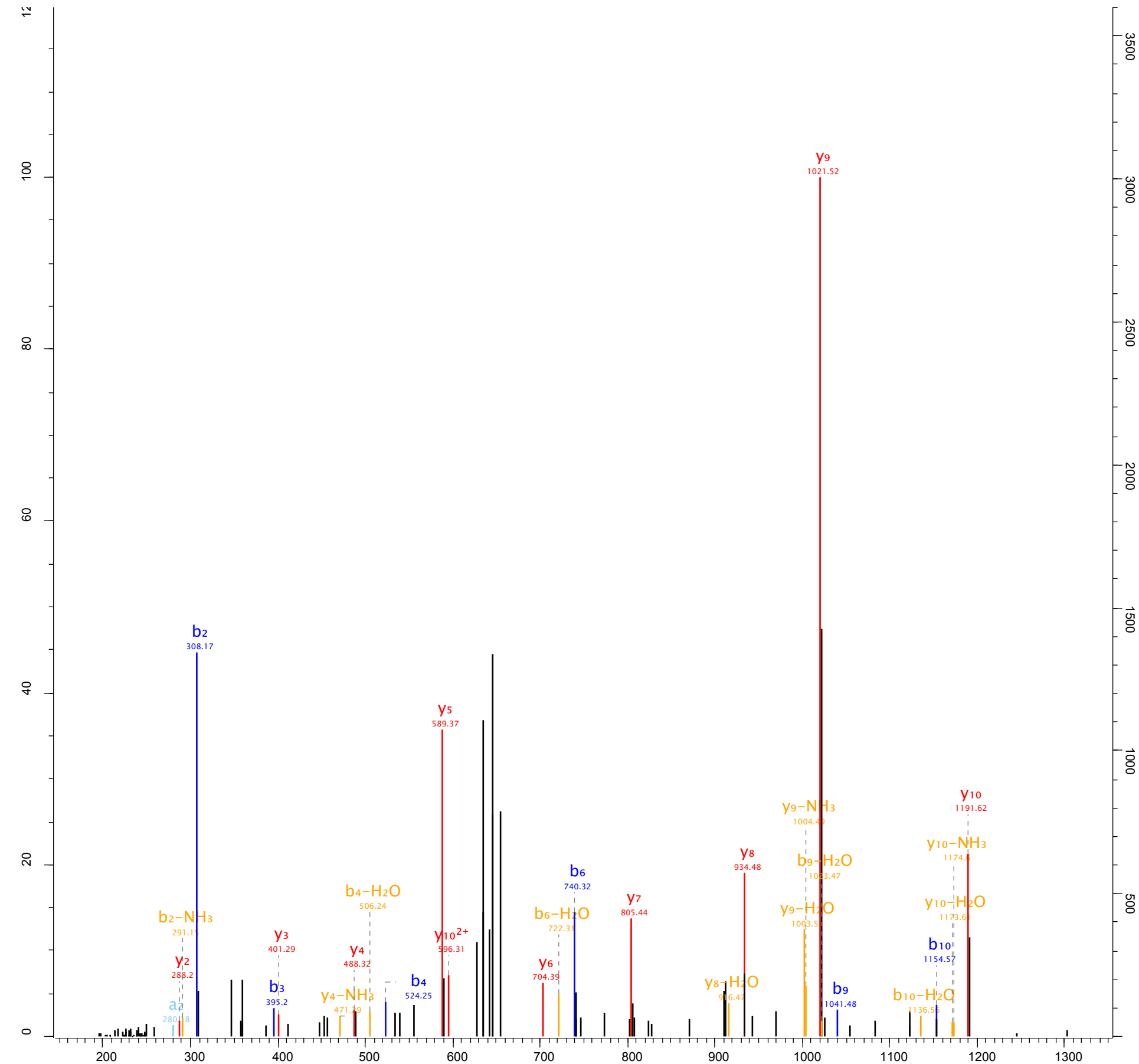


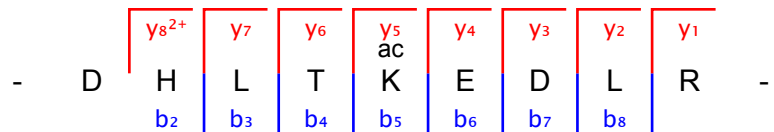
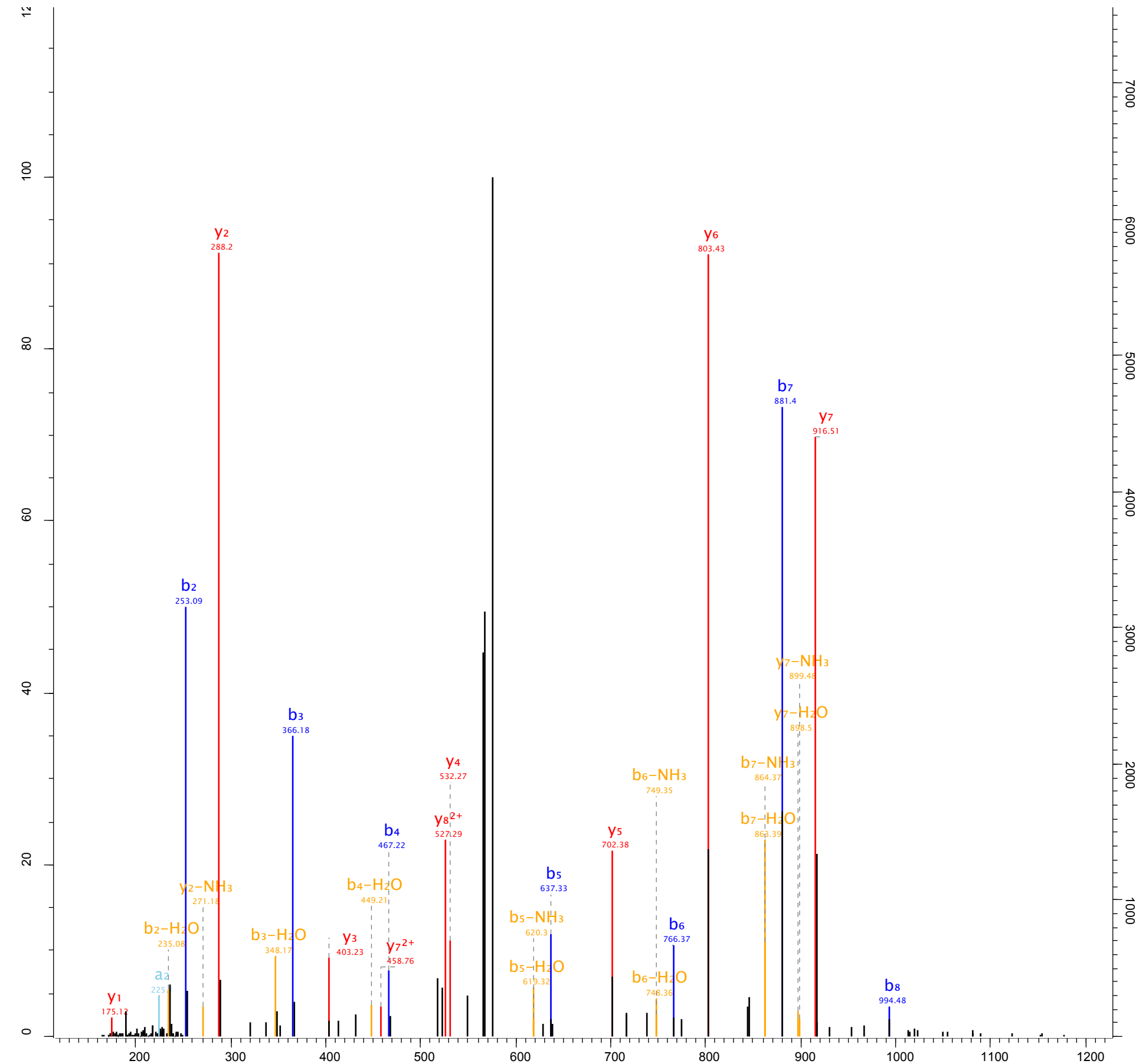
- Q G K P E E E A K P D E Q G Q D E G K P E K -

b₂
b₃
b₈²⁺
b₁₂
b₁₃²⁺
b₁₄²⁺
b₁₆²⁺
b₁₇²⁺
b₁₈²⁺
b₁₉²⁺
y₂₀²⁺
y₉
y₈
y₇
y₆
y₅
ac
y₃

Raw file 072613_SCW_II_68_Enriched_10 Scan 13872 Method ITMS; CID Score 106.88 m/z 581.8 Gene names Crebbp;Ep300







072613_SCW_II_68_Enriched_10

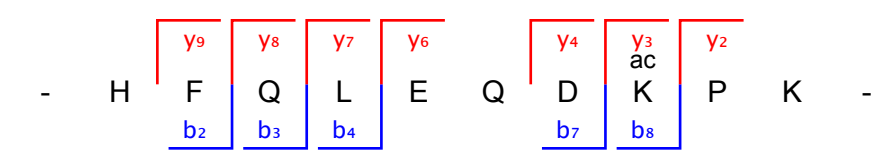
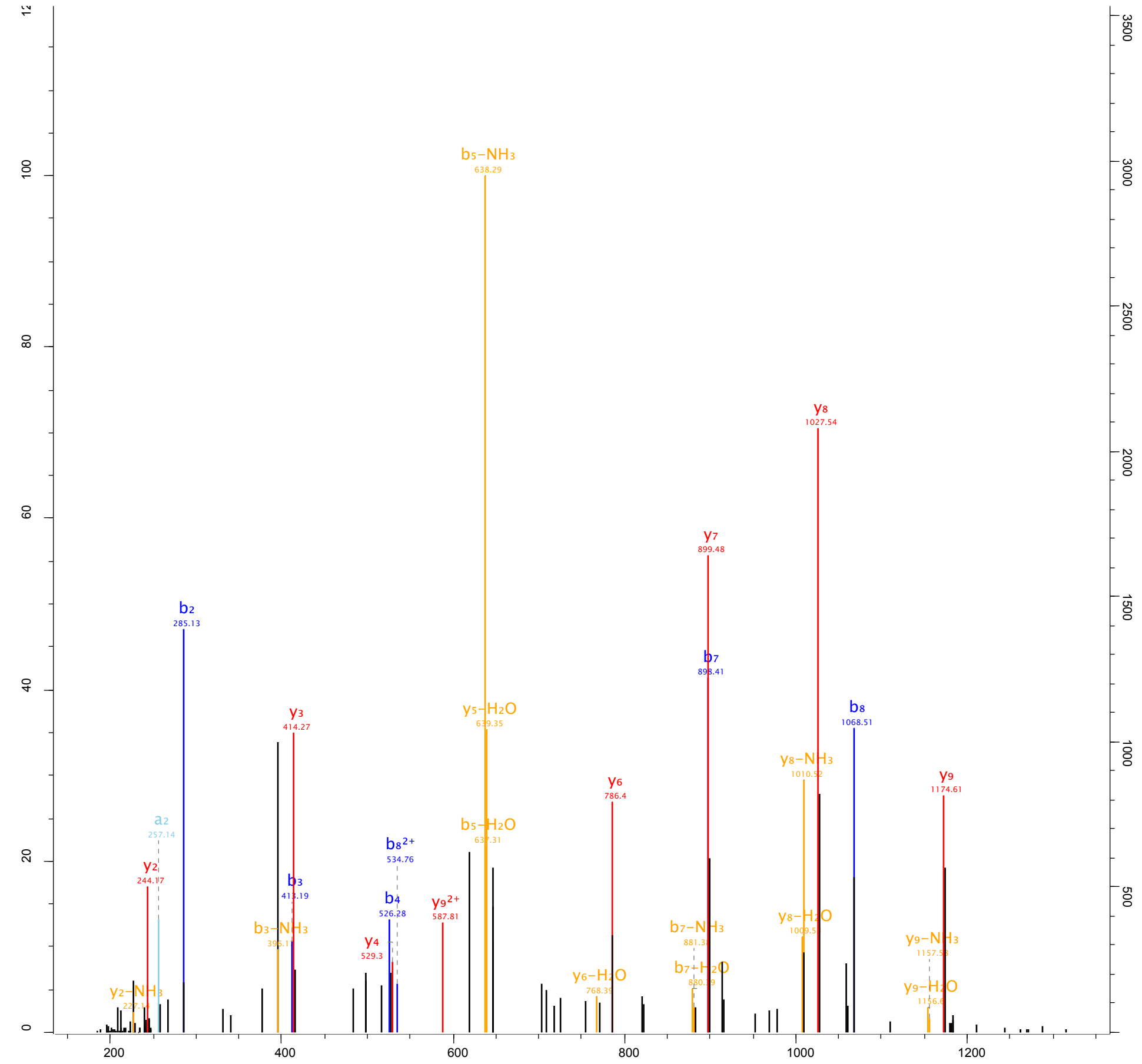
15908

ITMS; CID

156.48

656.34

Fasn



Raw file 072613_SCW_II_68_Enriched_10 Scan 16236 Method ITMS; CID Score 154.84 m/z 602.83 Gene names Tkt

