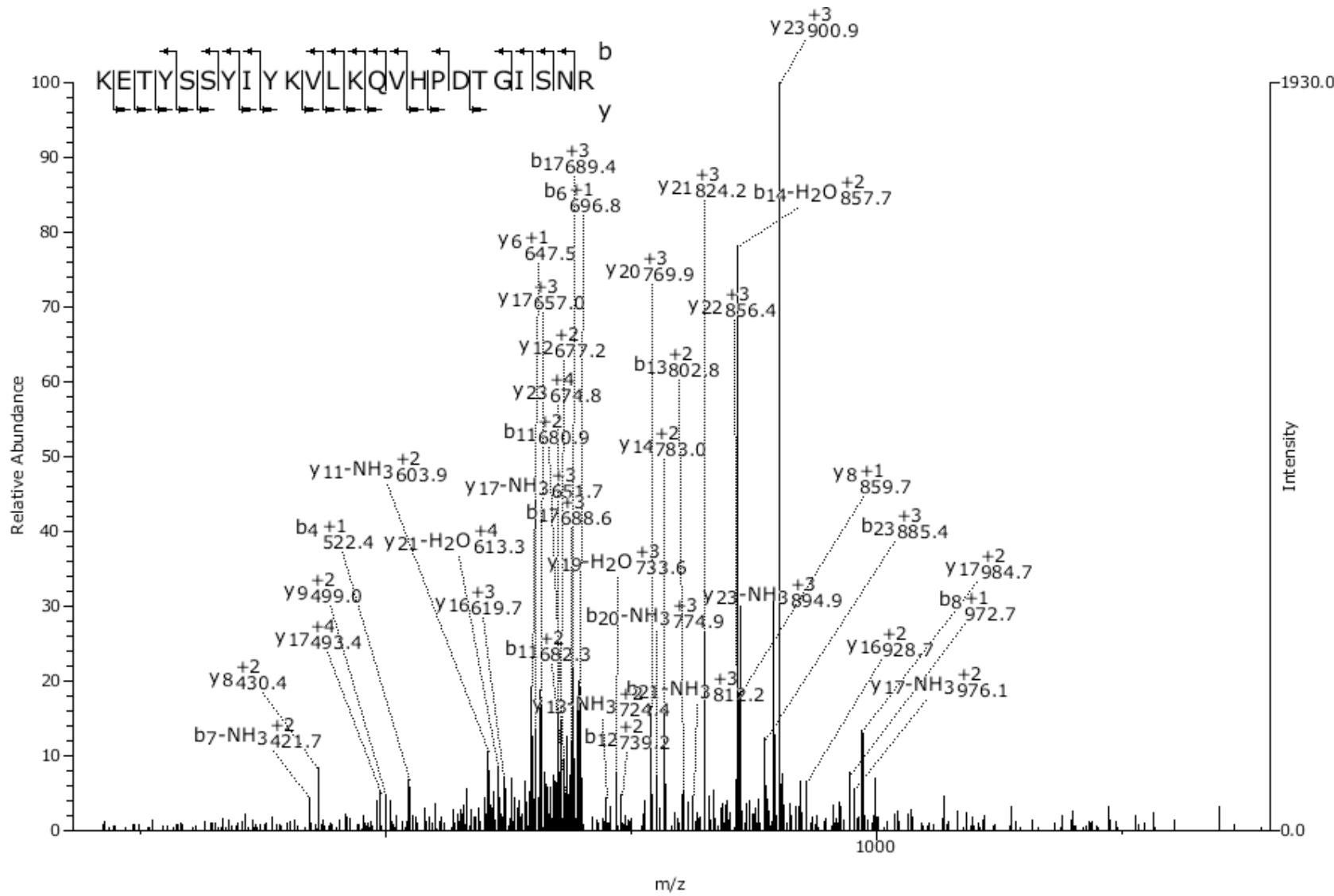
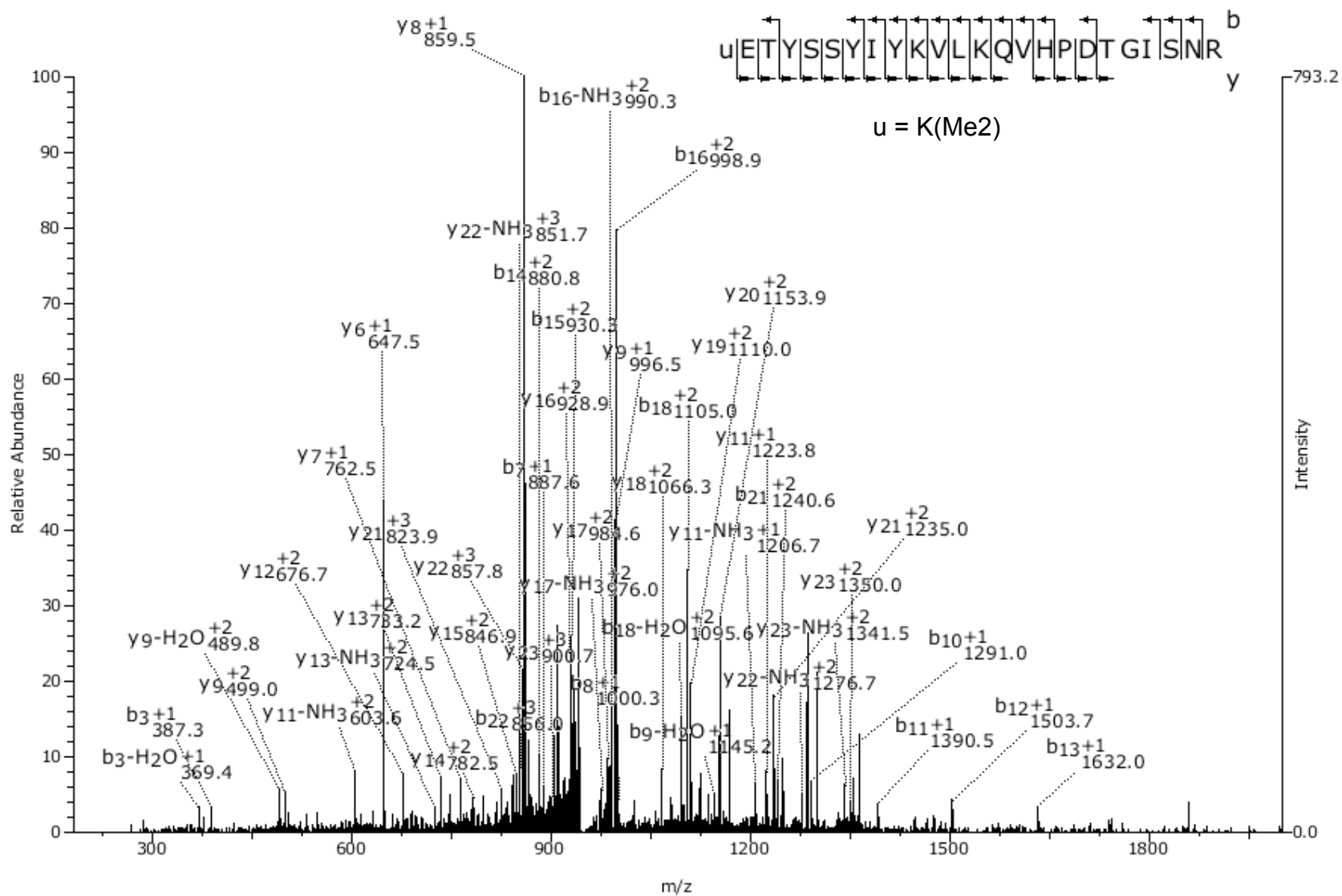


Table 3 MS/MS spectra, in order presented in table. Fragment uncertainty for fit is 1 m/z or less. Protein Prospector/MS-Product is used to annotate spectra.

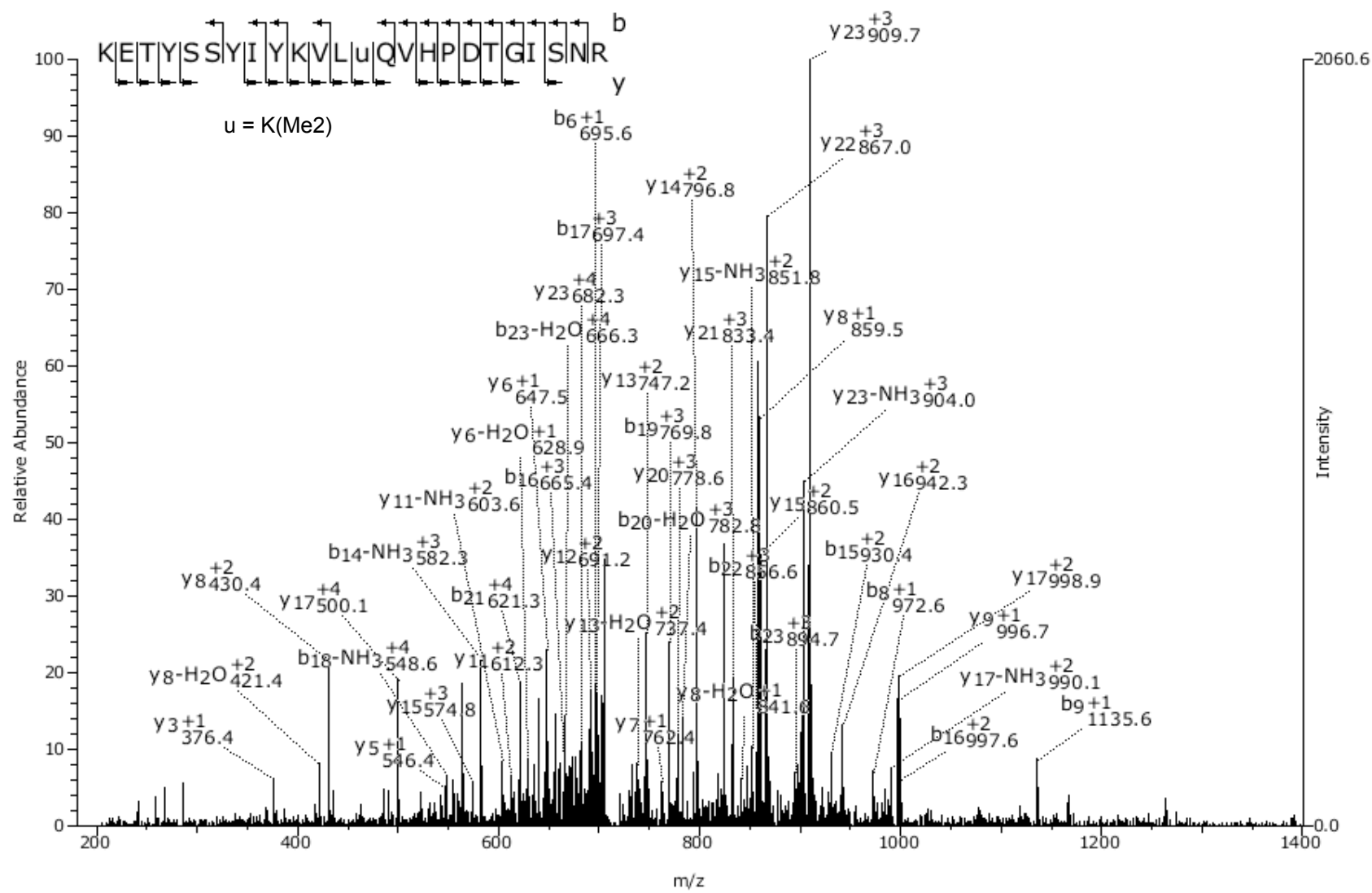
WT K₄₅ETYS₅₄SYI₅₄YKVLKQVHPDTGISNR



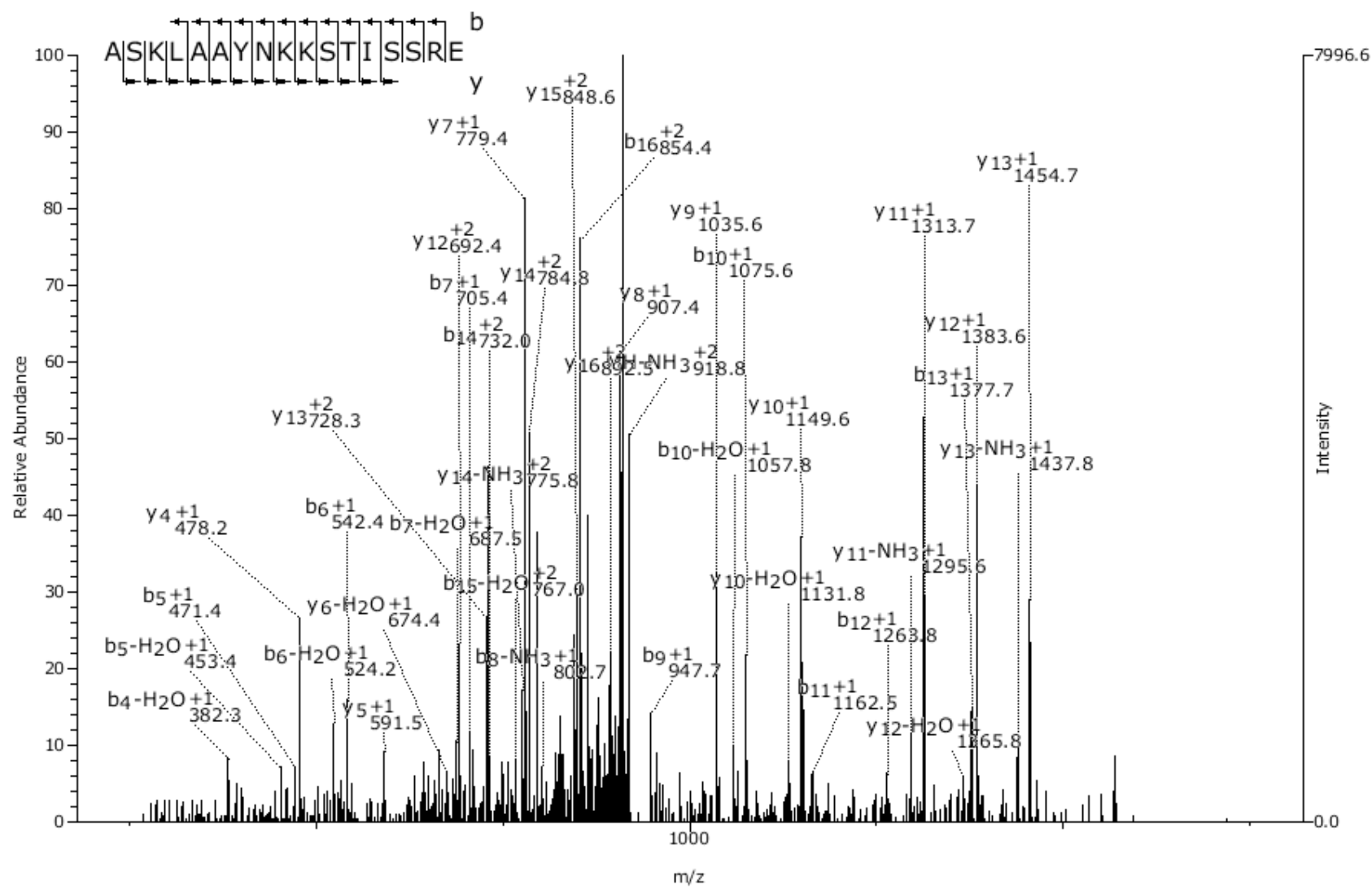
WT K₄₅(Me₂)ETYSSYIYKVLKQVHPDTGISNR; data consistent with K45 or K54 -Me₂



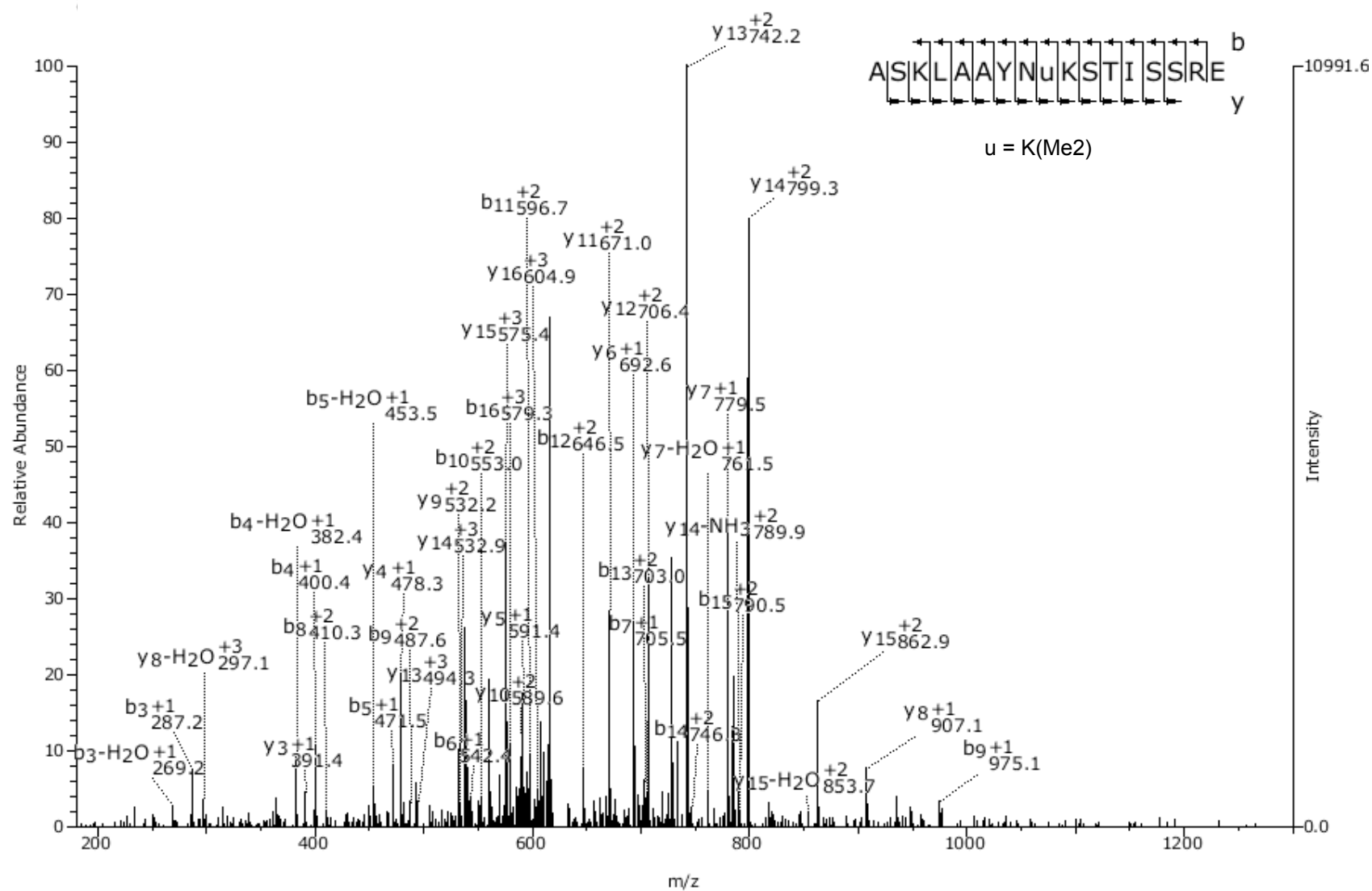
WT K₄₅ETYS₅₄SYI₅₇YKVL₅₇uQVHPDTGISNR



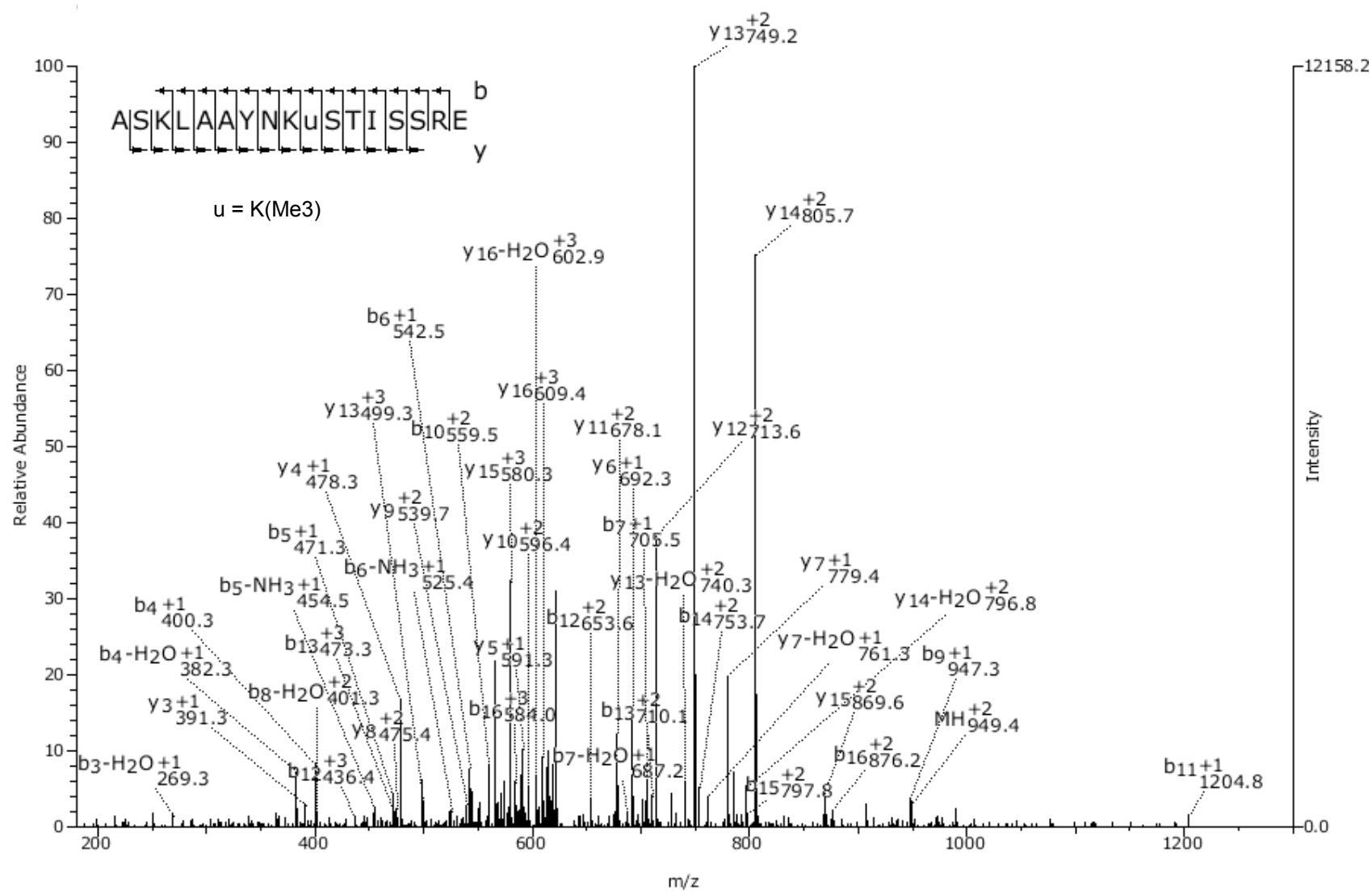
WT ASK₉₀LAAYNK₉₆K₉₇STISSRE



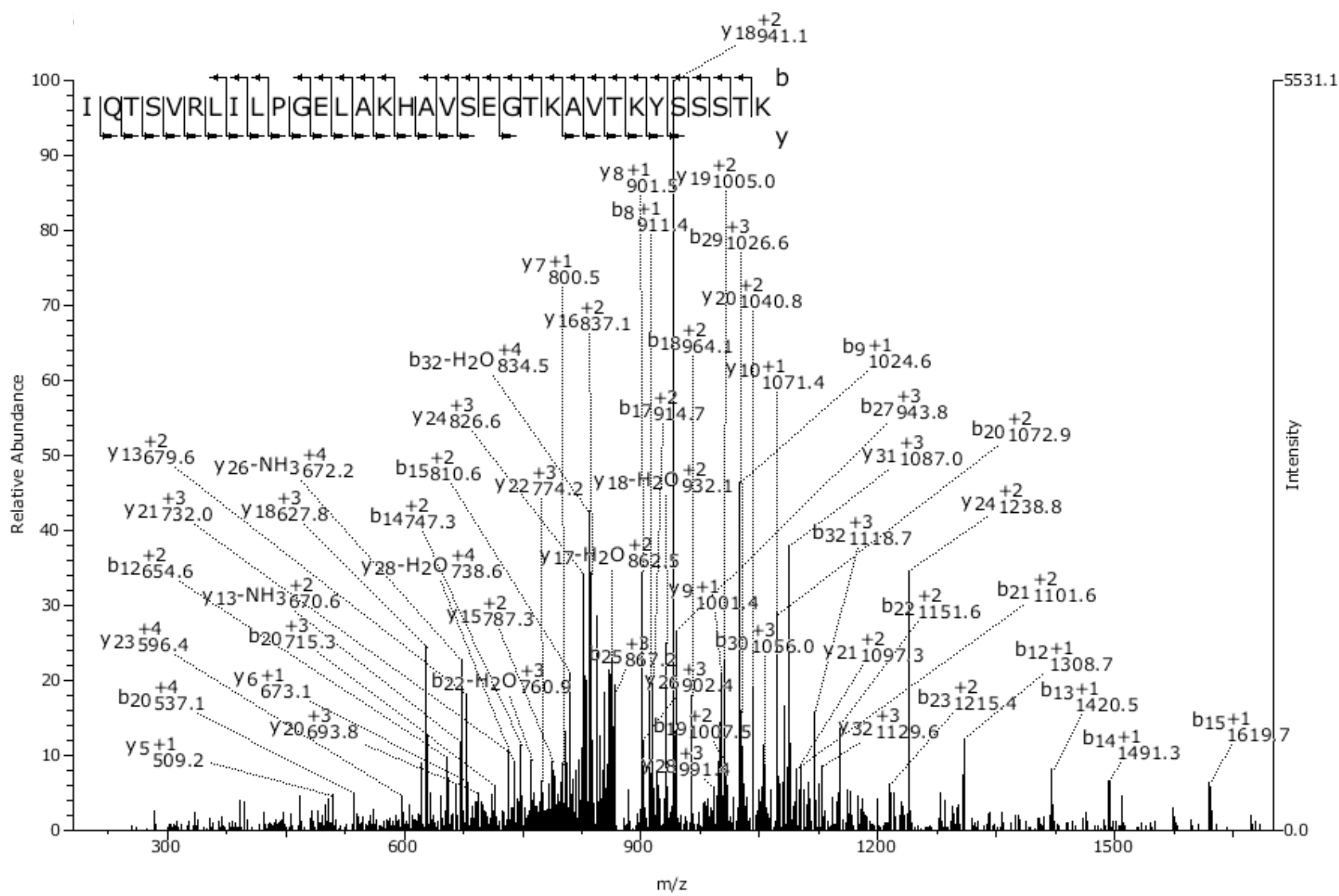
WT ASK₉₀LAAYNK₉₆(Me₂)K₉₇STISSRE; data can't distinguish K96- vs. K97-Me2



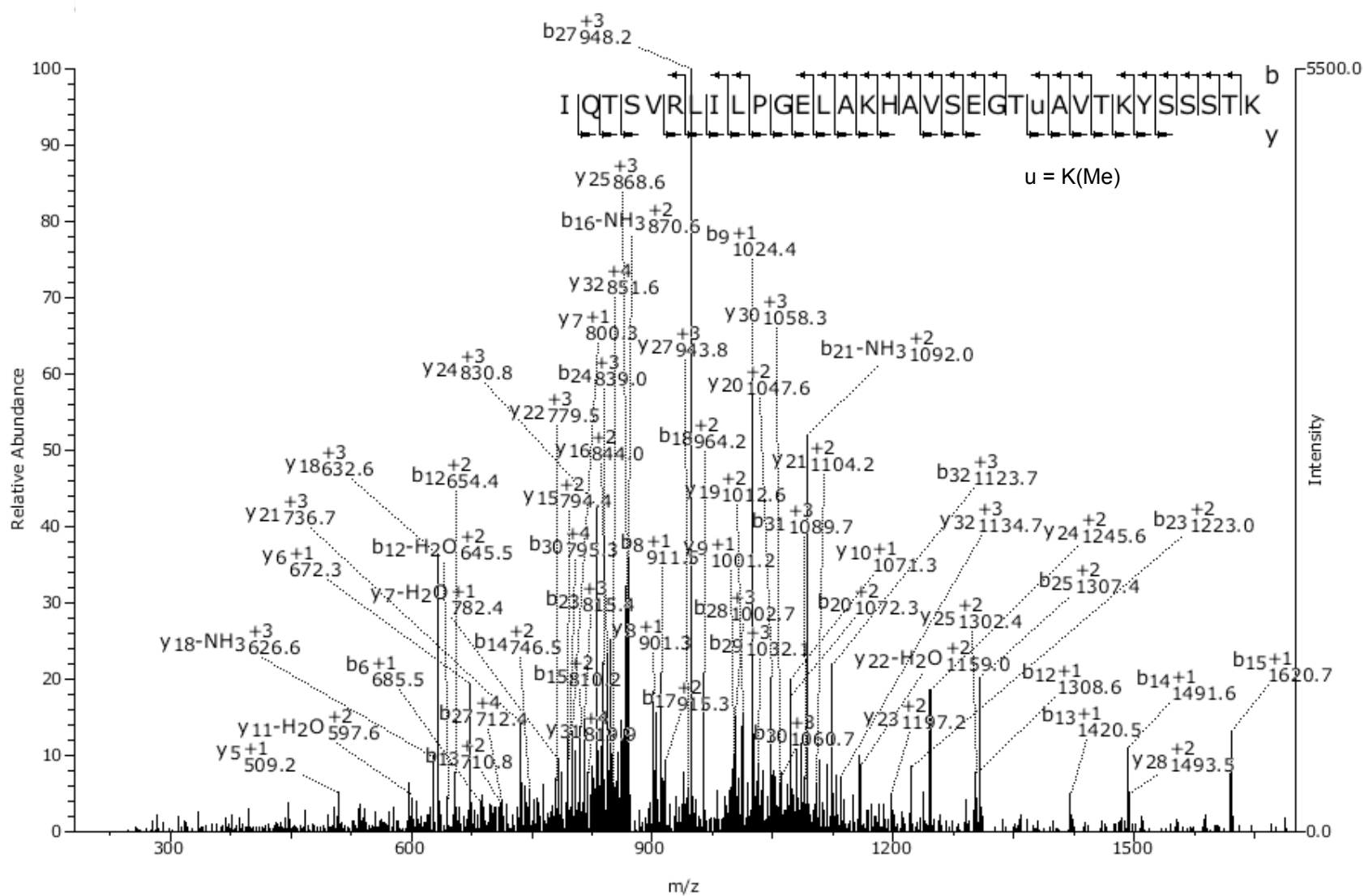
WT ASK₉₀LAAYNK₉₆K₉₇(Me₃)STISSRE;



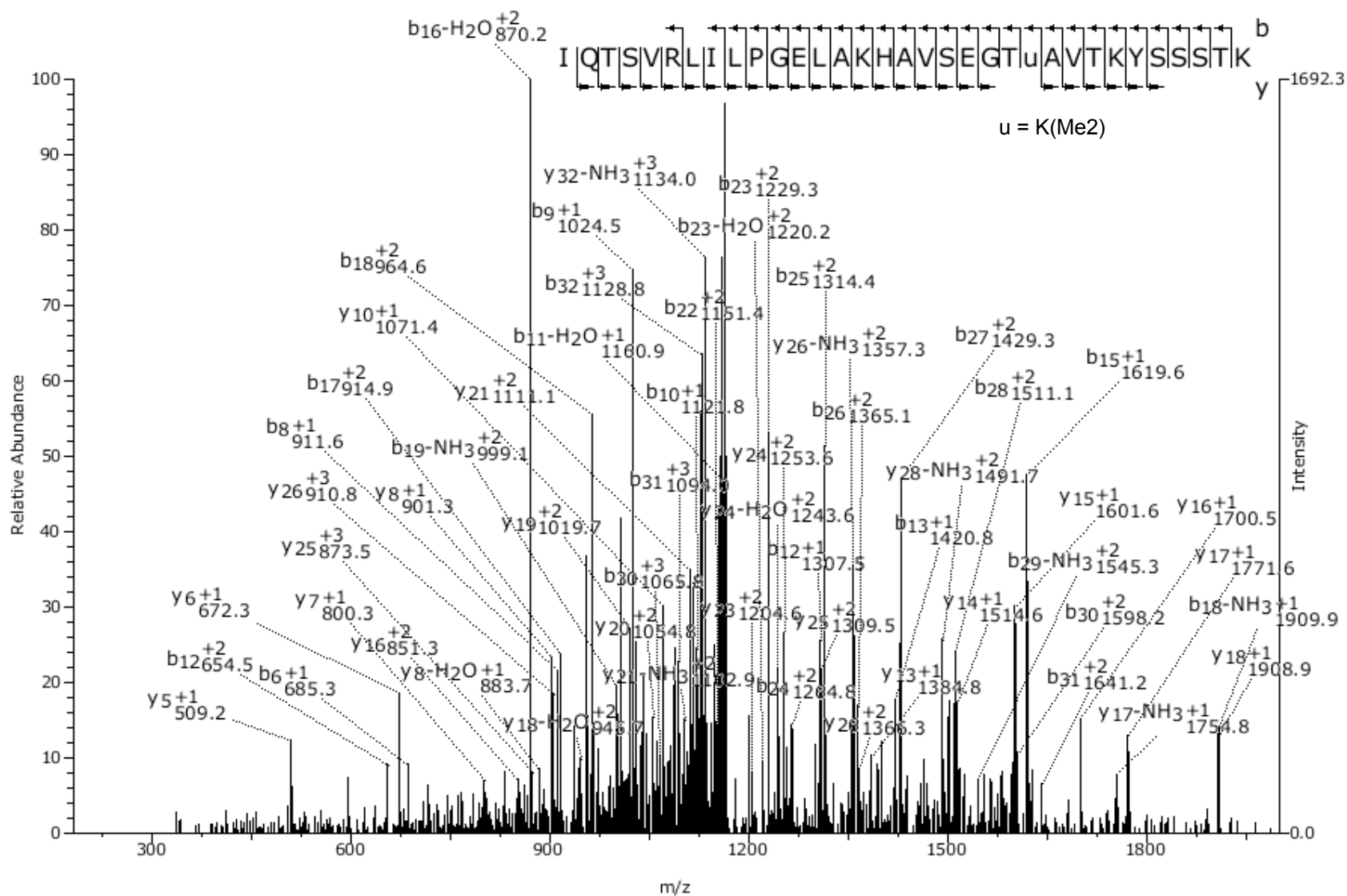
WT IQTSVRLILPGELAKHAVSEGK₁₂₇AVTKYSSSTY



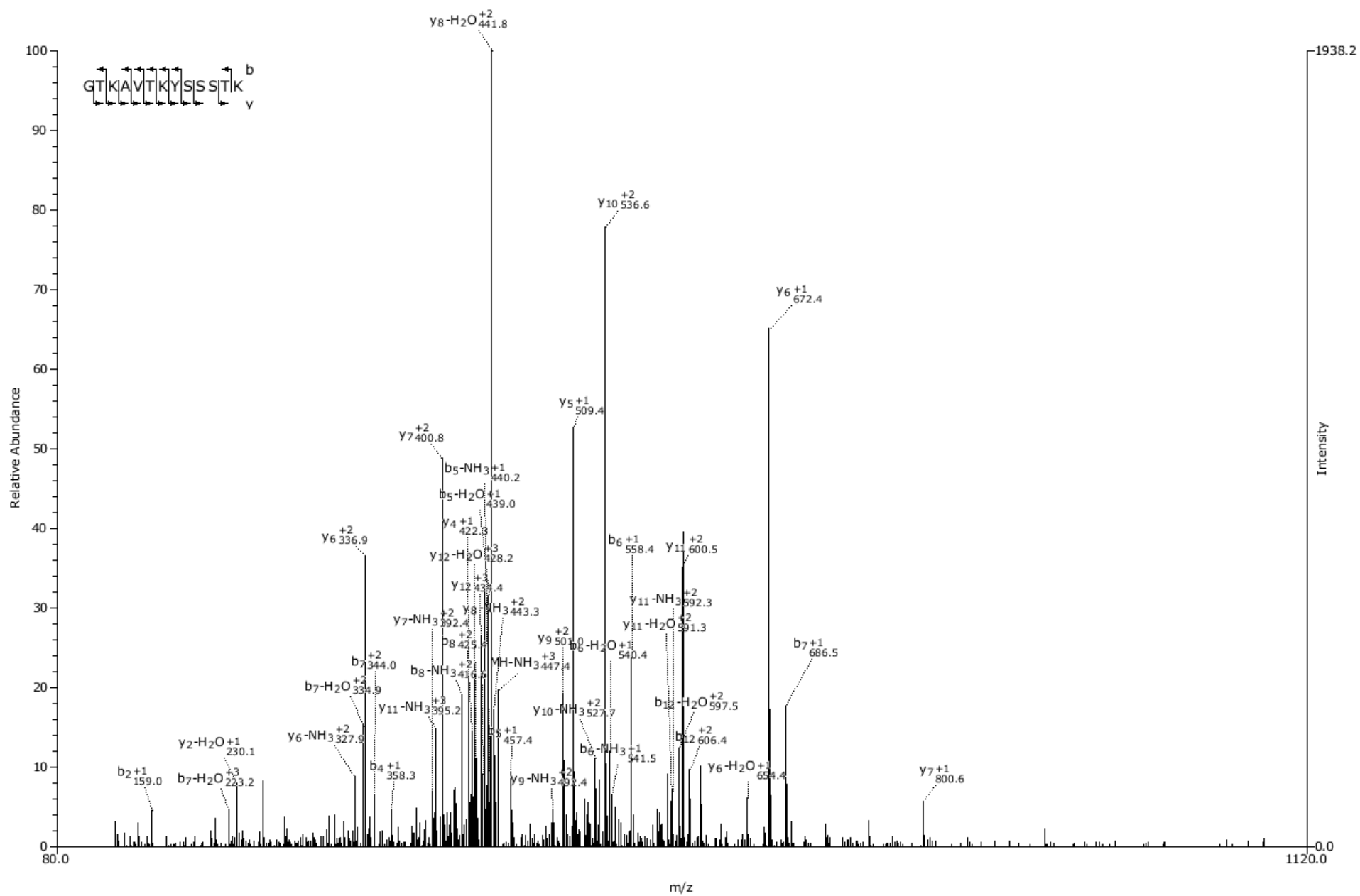
WT IQTSVRLILPGELAKHAVSEGTK₁₂₇(Me)AVTKYSSSTK



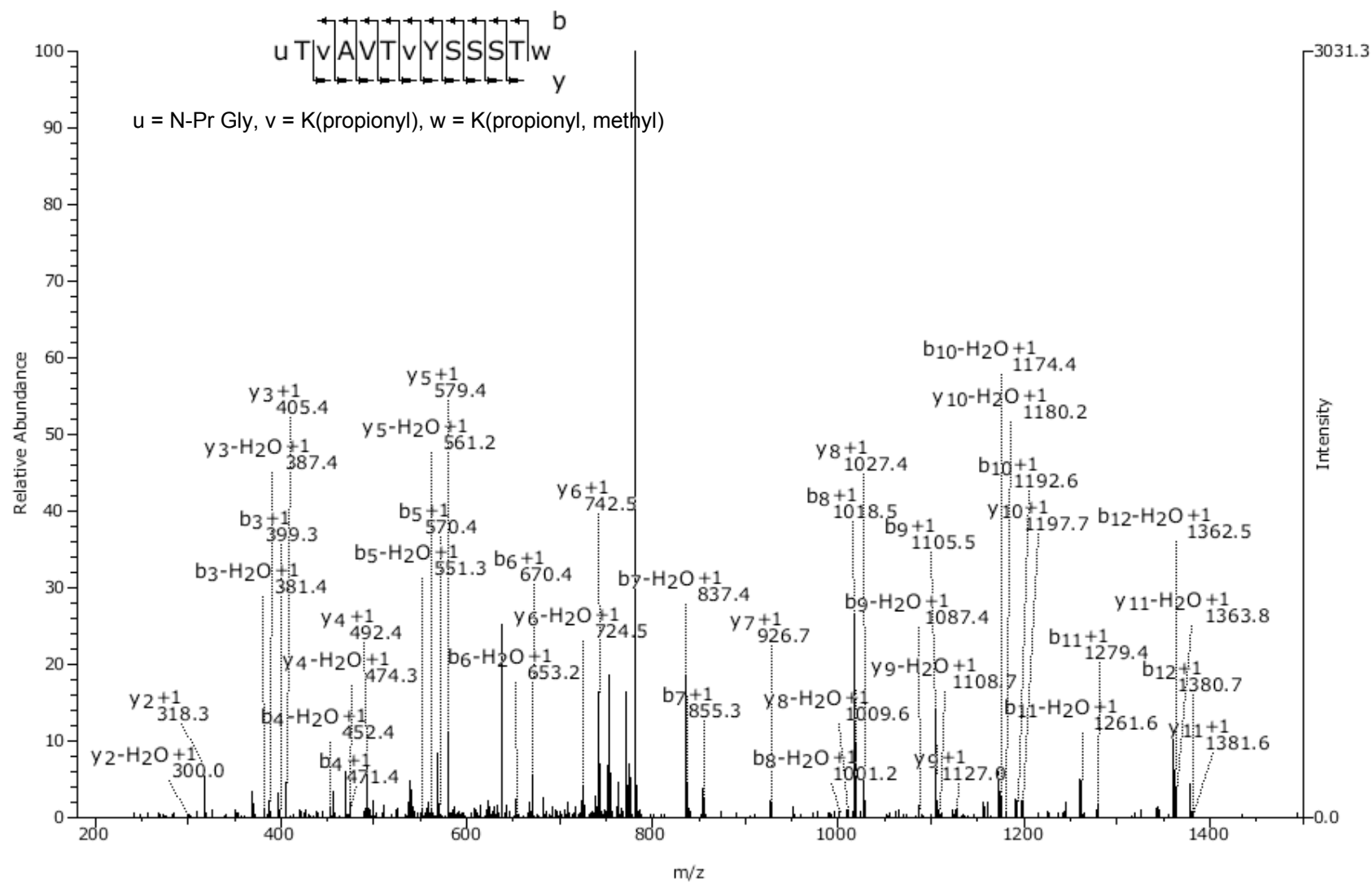
WT IQTSVRLILPGELAKHAVSEGTK₁₂₇(Me₂)AVTKYSSSTK



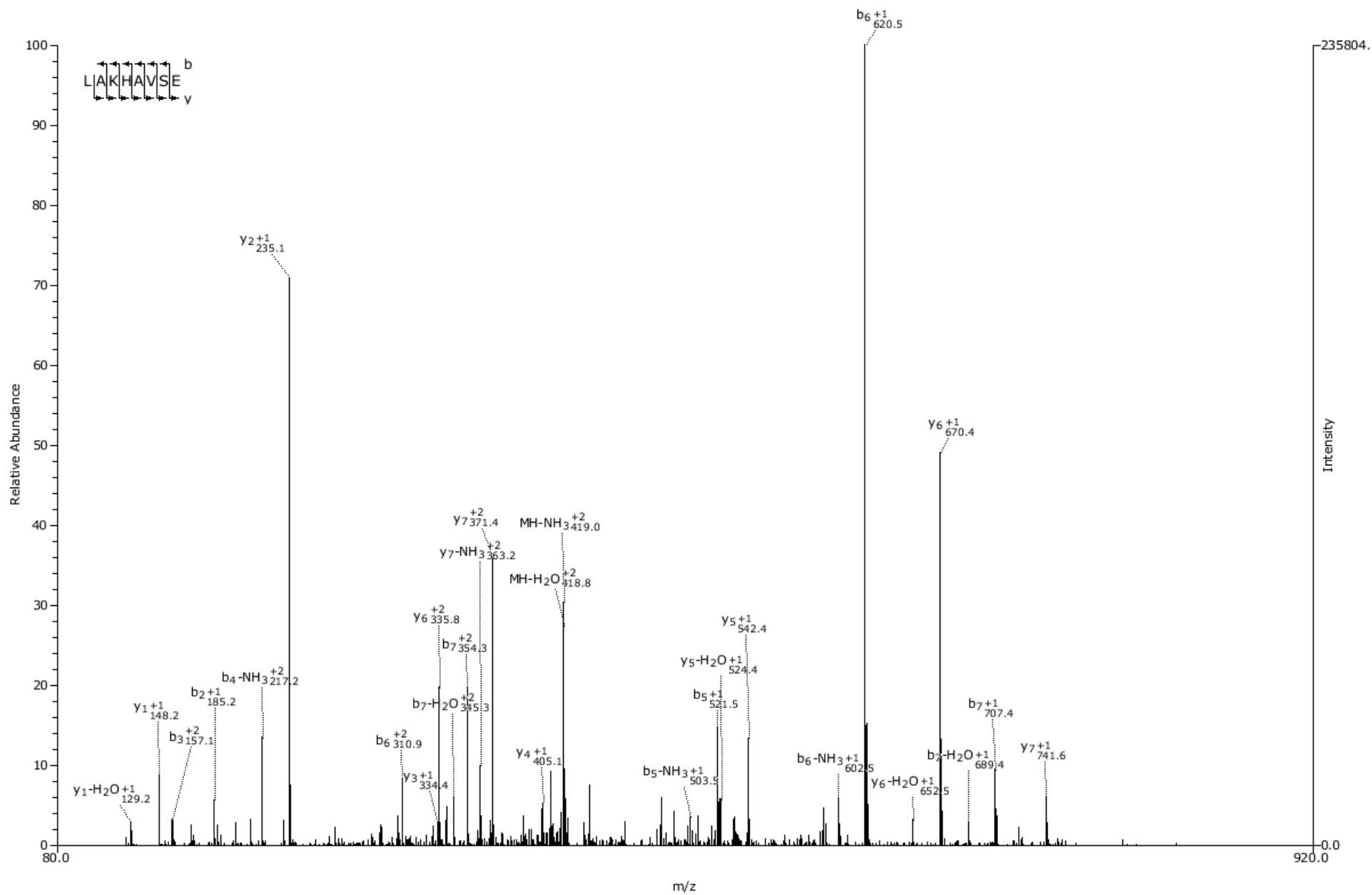
WT GTKAVTKYSSSTK₁₃₇



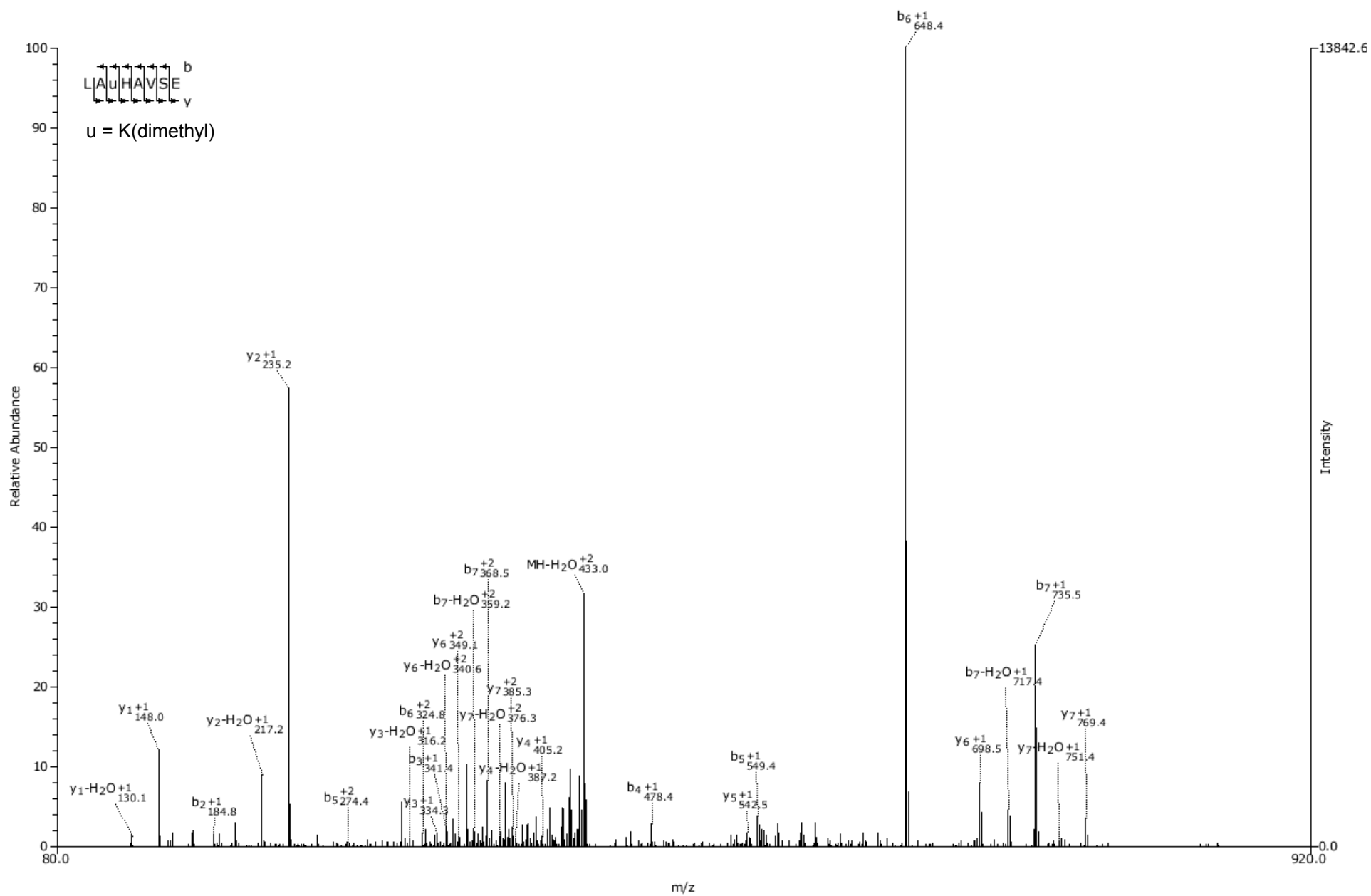
WT (Pr)GTK(Pr)AVTK(Pr)YSSSTK₁₃₇(Pr,Me), Pr = propyl



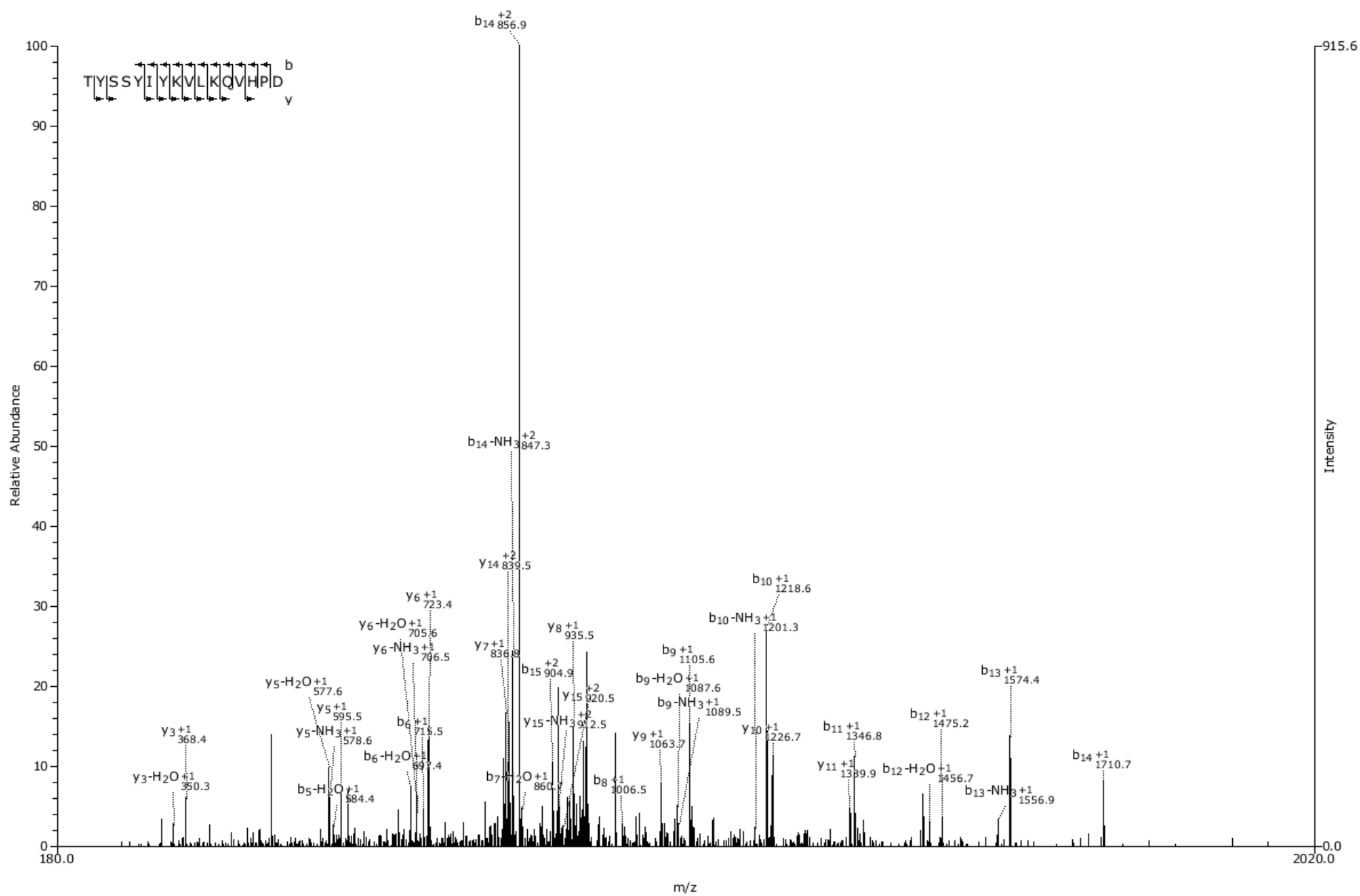
HDA LAK₁₁₉HAVSE



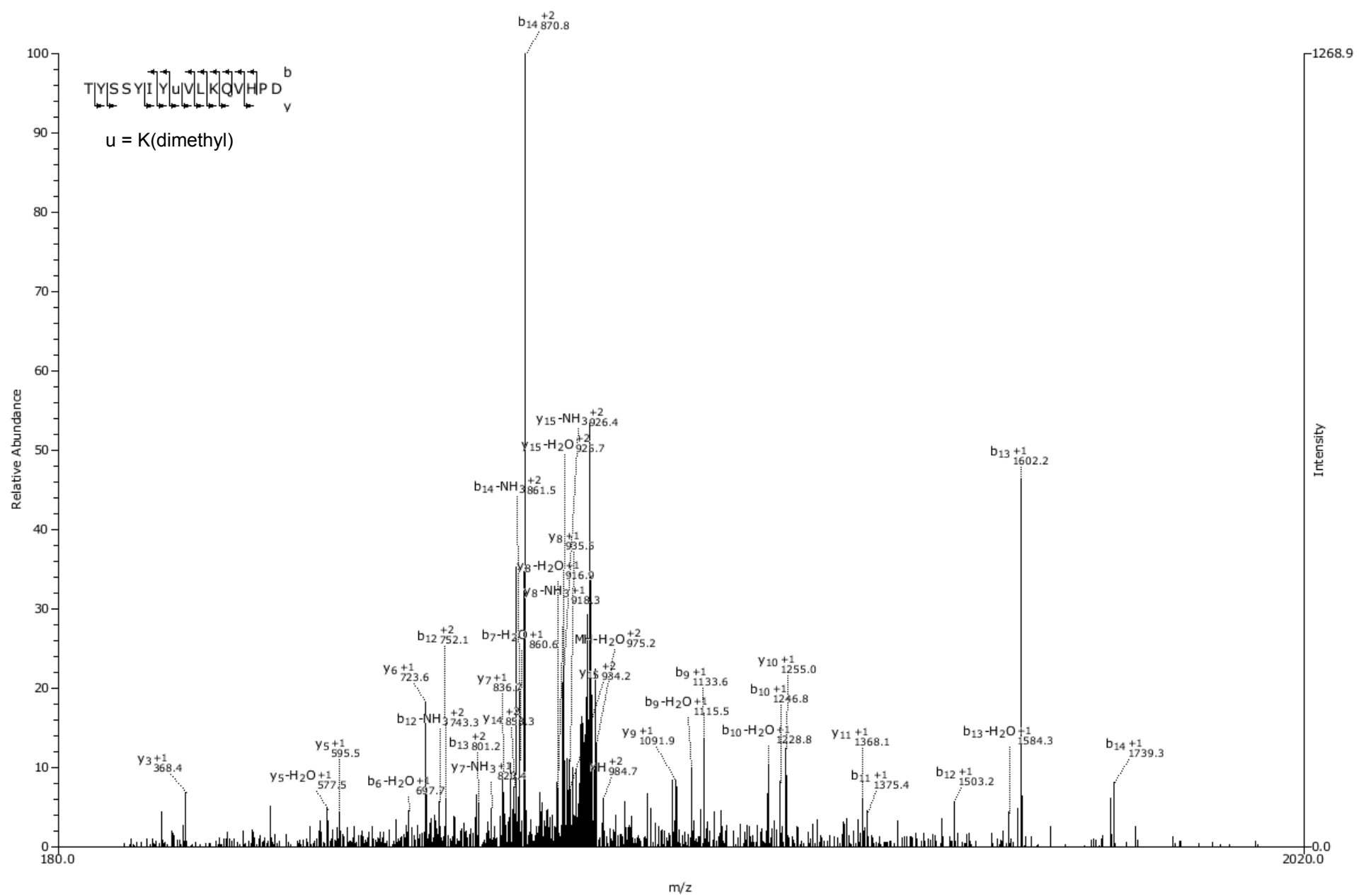
HDA LAK₁₁₉(Me₂)HAVSE



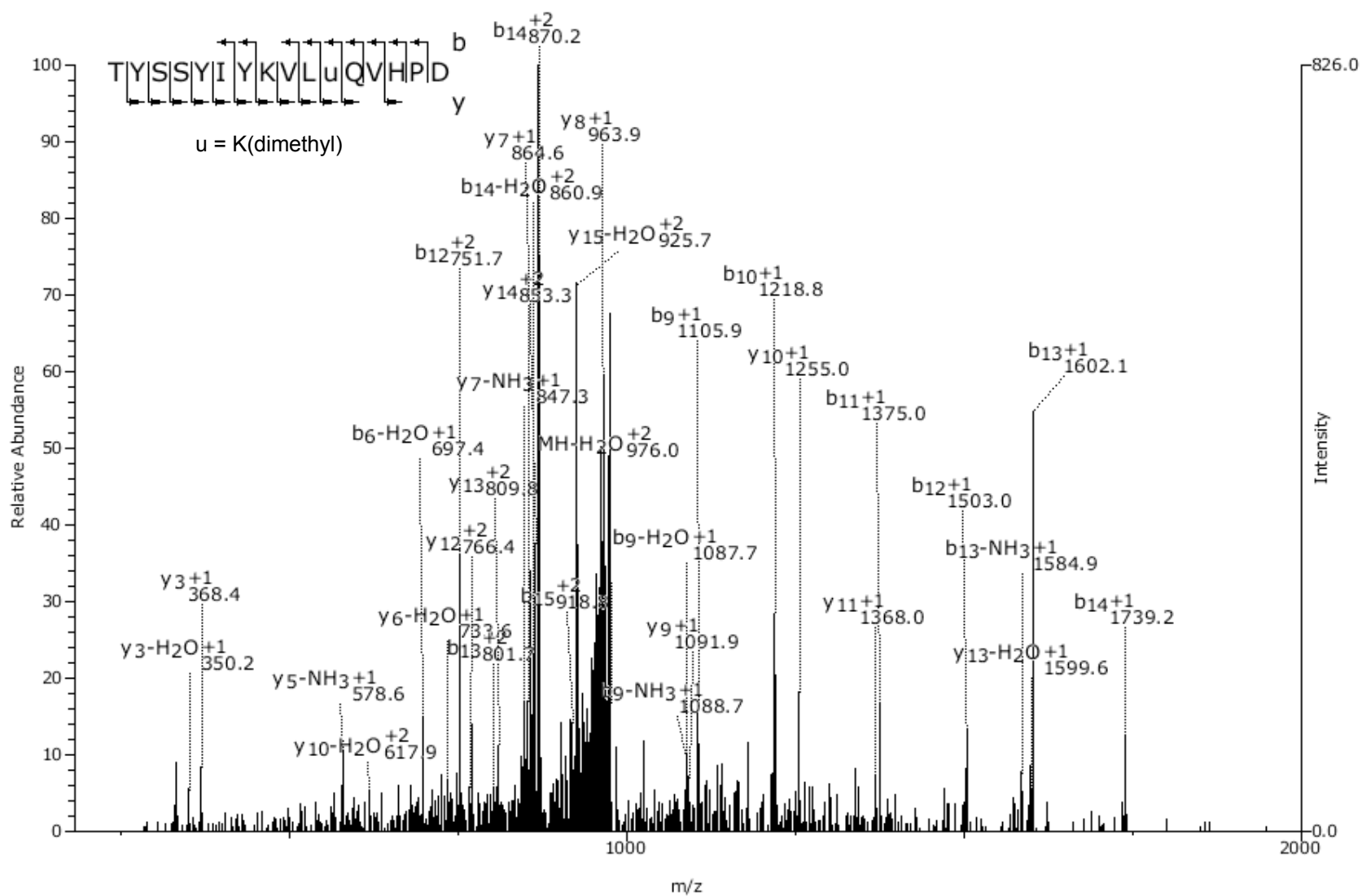
HDA TYSSYIK₅₄VLK₅₇QVHPD



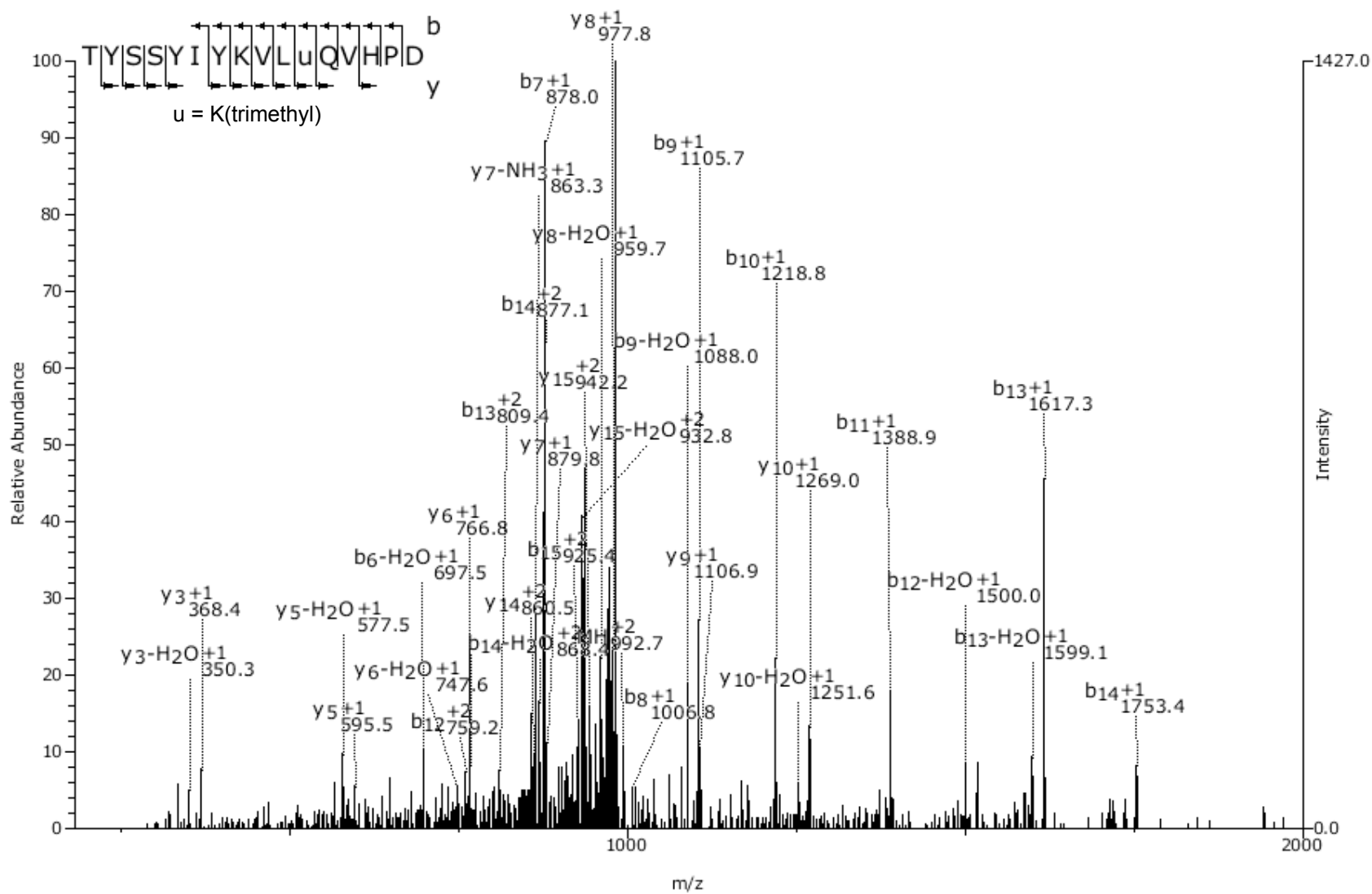
HDA TYSSYIK₅₄(Me₂)VLK₅₇QVHPD

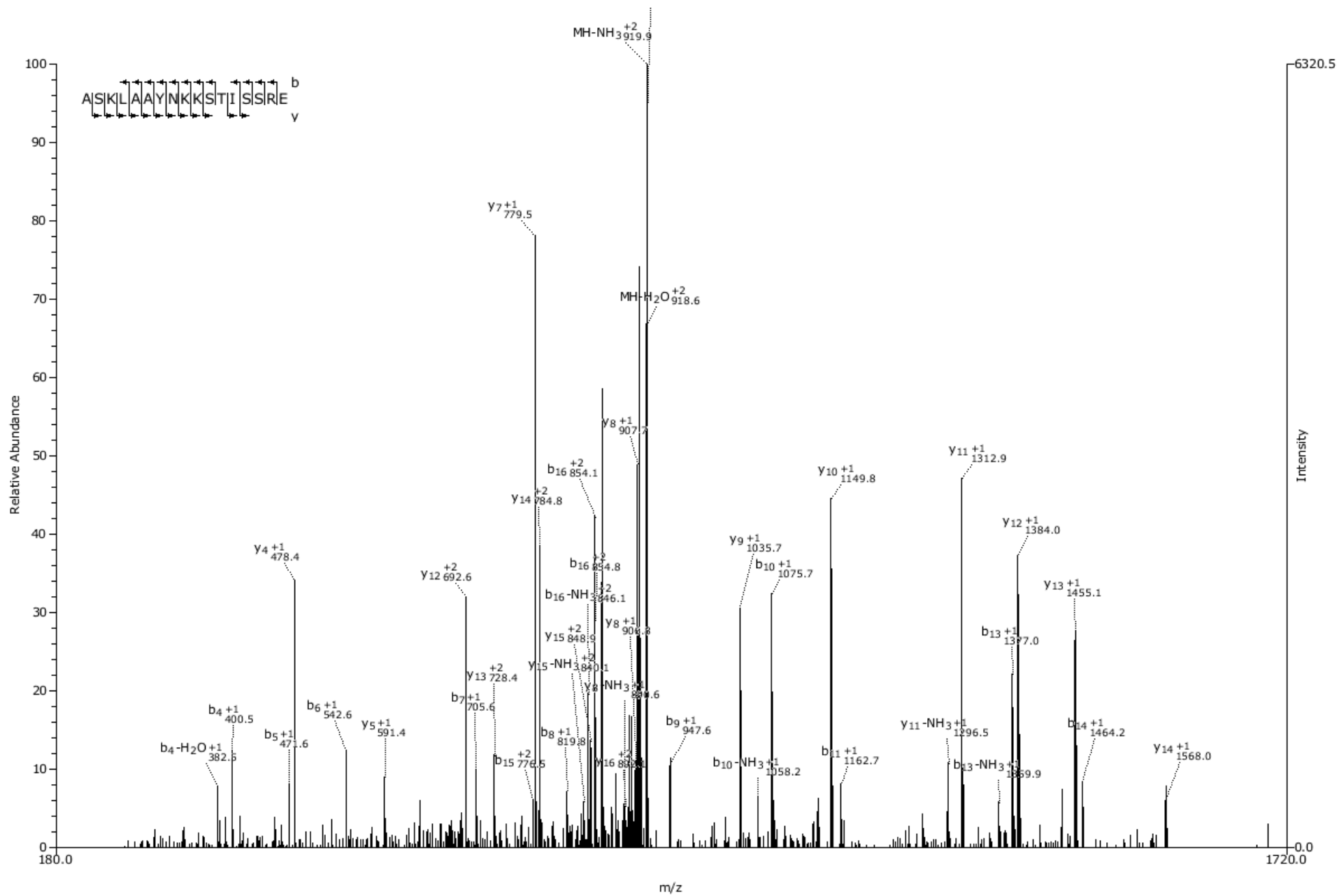


HDA TYSSYIYKVLK₅₇(Me₂)QVHPD



HDA TYSSYIKVLK₅₇(Me₃)QVHPD



HDA ASK₉₀LAAYNK₉₆K₉₇STISSRE

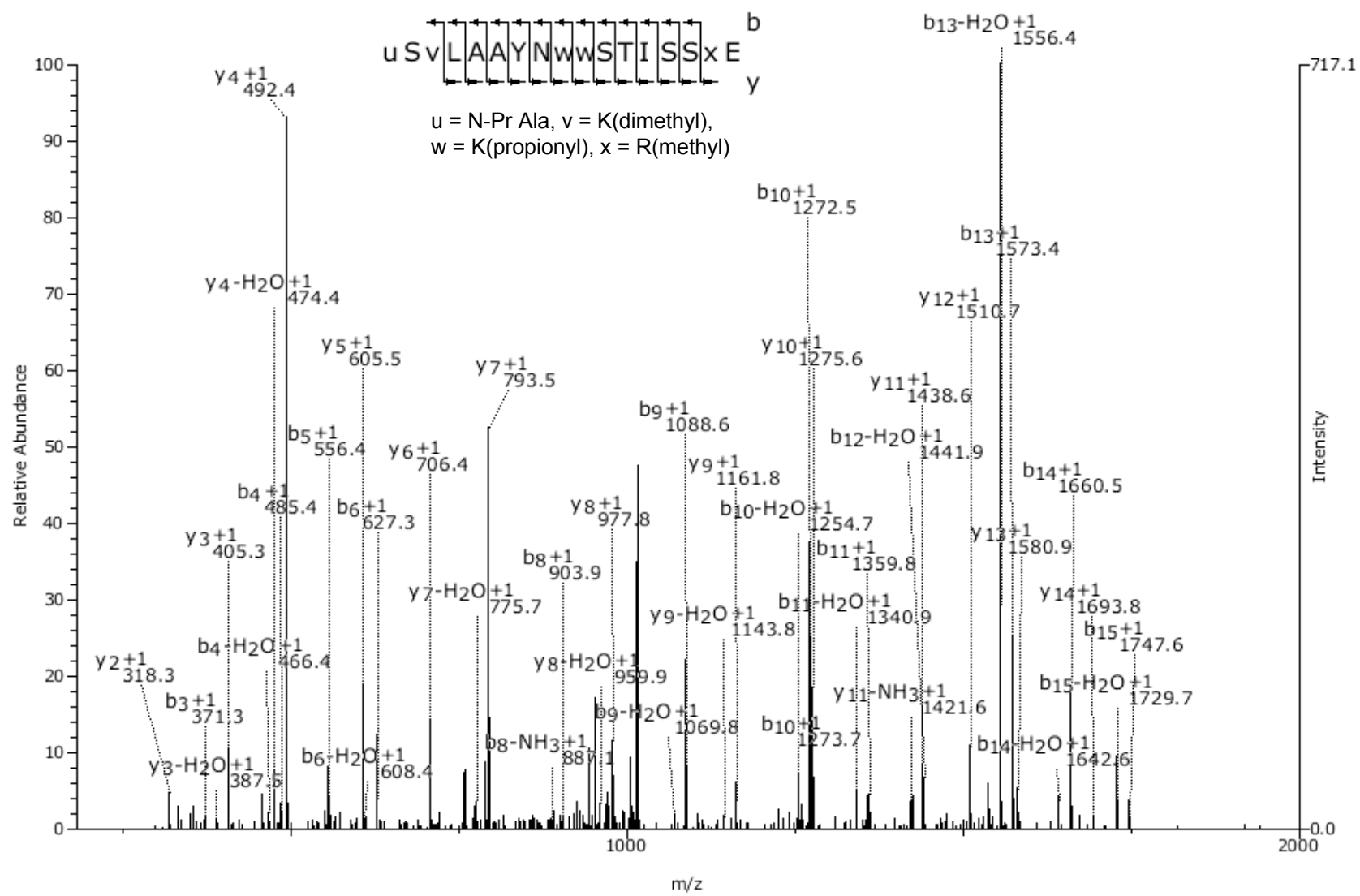
Mass spectrum of the tryptic digest of protein 14-3-3. The x-axis is m/z (400-1800) and the y-axis is Relative Abundance (0-100). The base peak is at m/z 907.6 ($y8+1$). Other significant peaks are labeled with b and y ion series and their m/z values. A sequence diagram at the top shows the protein sequence ASuLAAYNKKSTISSRE with tryptic cleavage sites indicated by arrows. The modification u = K(dimethyl) is noted.

Sequence: ASuLAAYNKKSTISSRE
 Cleavage sites: A|S|u|L|A|A|Y|N|K|K|S|T|I|S|S|R|E
 Modification: u = K(dimethyl)

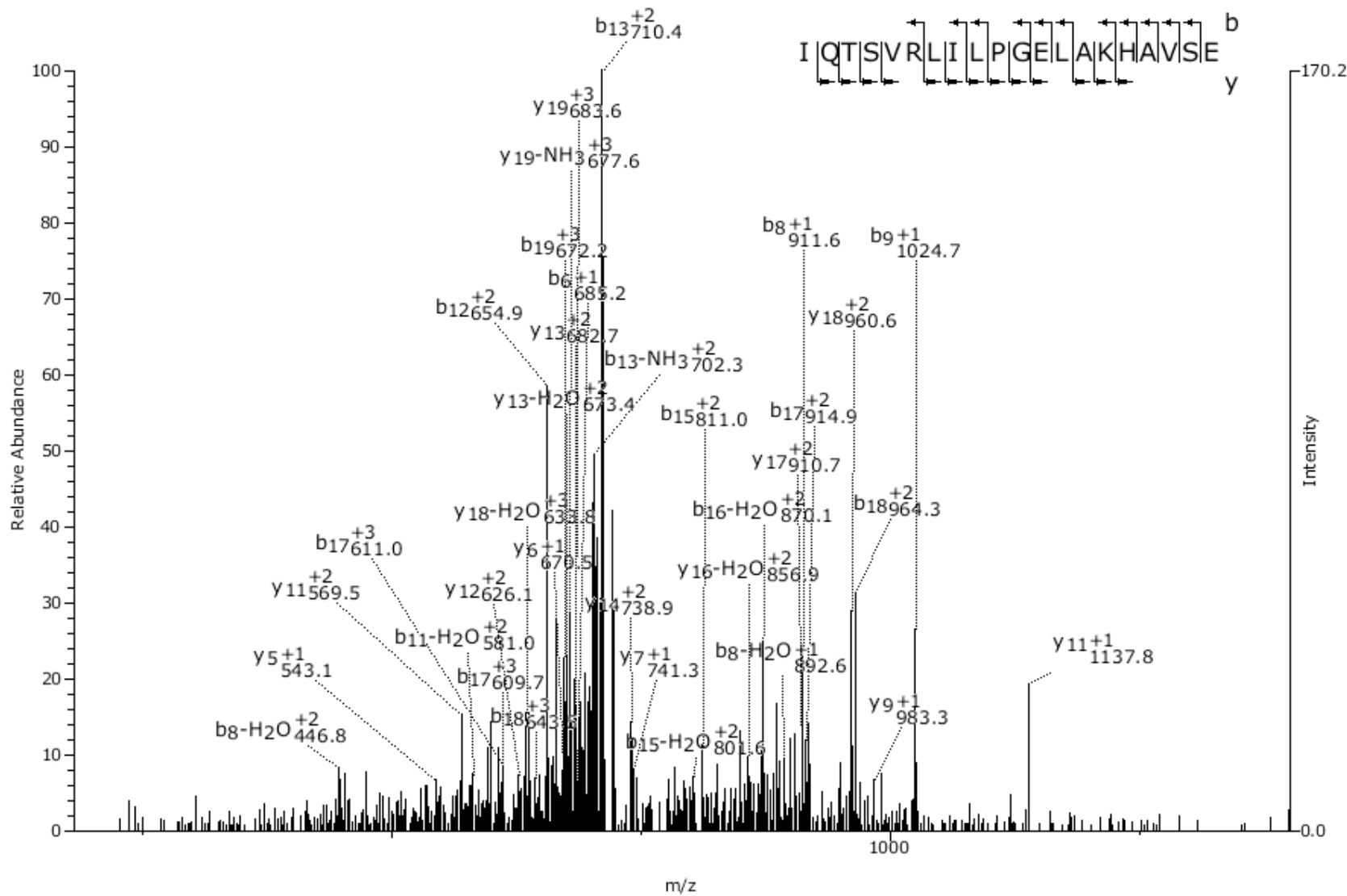
Key peaks (b and y ions):

- $b4-H_2O+1$: 410.4
- $b4+1$: 428.5
- $y4+1$: 478.3
- $b5-H_2O+1$: 552.5
- $y5+1$: 591.5
- $b7-H_2O+1$: 715.5
- $y7+1$: 779.6
- $y12+2$: 692.6
- $b13+2$: 702.2
- $y13+2$: 728.2
- $y14+2$: 785.0
- $b8+1$: 846.6
- $b8-NH_3+1$: 830.3
- $b15-H_2O+2$: 780.6
- $y16+2$: 905.8
- $y8+1$: 907.6 (Base Peak)
- $b9+1$: 975.6
- $y9+1$: 1035.8
- $MH-H_2O+2$: 932.4
- $y10+1$: 1149.8
- $b10+1$: 1103.7
- $y10-NH_3+1$: 1132.8
- $b12-NH_3+1$: 1275.6
- $y11-NH_3+1$: 1296.0
- $y12-NH_3+1$: 1367.0
- $b13+1$: 1404.9
- $y13-NH_3+1$: 1438.0
- $y13+1$: 1454.9
- $y12+1$: 1383.9
- $b14+1$: 1492.3
- $y14+1$: 1568.8
- $y11+1$: 1312.8
- $y12+1$: 1383.9
- $y13+1$: 1454.9
- $y14+1$: 1568.8
- $y15+1$: 1639.8
- $y16+1$: 1710.8
- $y17+1$: 1781.8
- $y18+1$: 1852.8

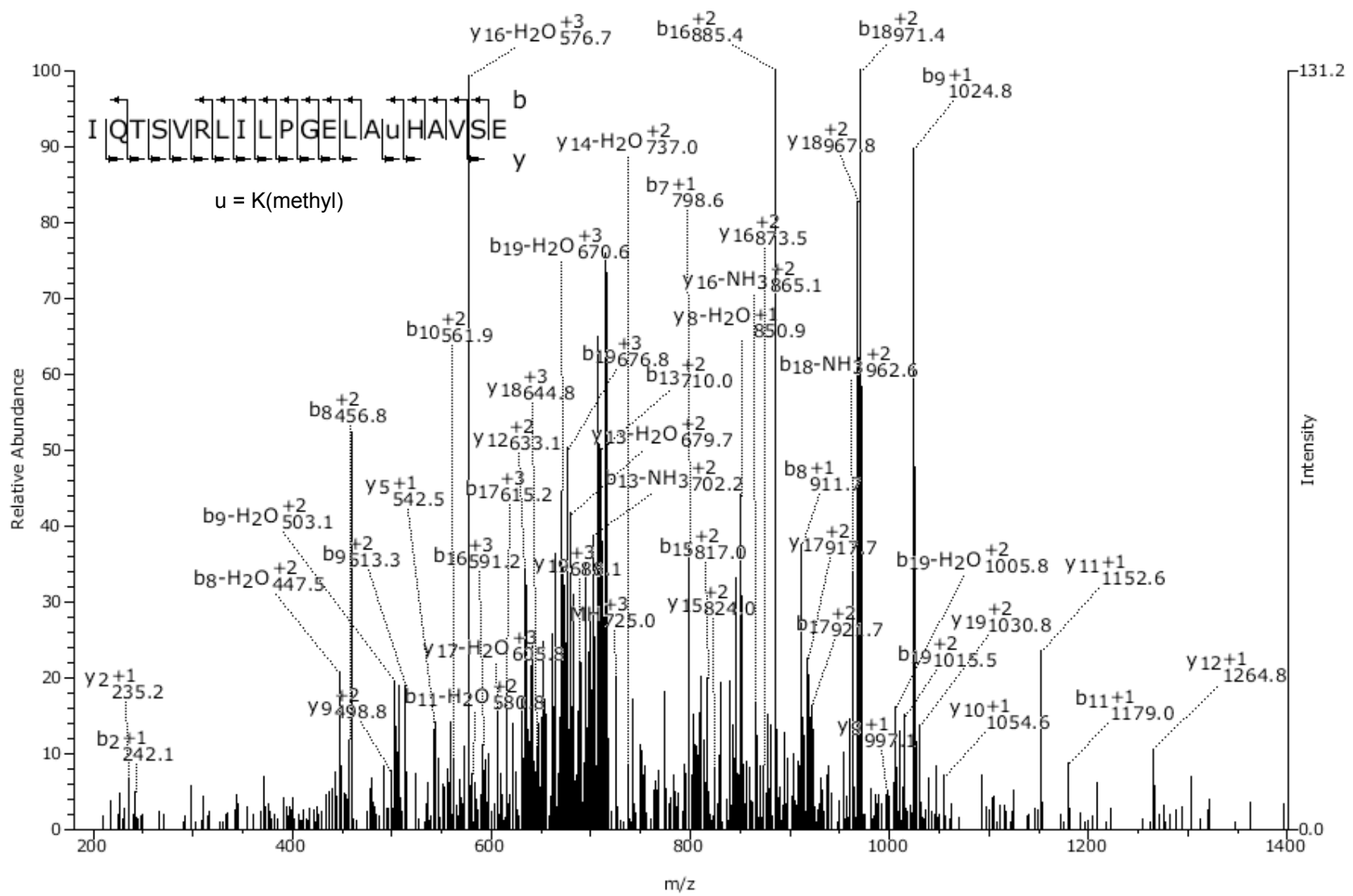
HDA (Pr)ASK₉₀(Me₂)LAAYNK₉₆(Pr)K₉₇(Pr)STISSR(Me)E, Pr = propyl



HDA IQTSVRLILPGELAK₁₁₉HAVSE



HDA IQTSVRLILPGELAK₁₁₉(Me)HAVSE



HDA IQTSVRLILPGELAK₁₁₉(Me₂)HAVSE

