

Human fetuin: MS/MS spectra of all PTM modified peptides

Glycosylation site

N156

VCQDCPLLAPLND
VCQDCPLLAPLNDTRVVHAAK
VCQDCPLLAPLNDTRVVHAAK

N176

AALAAFNAQNNGSNFQLEE

T256

VAVTCTVFQTQPVTSQPQPE

T270

GANEAVPTPVVDPDAPPSPLGAPGLPPAGSPPDSHVLLAAPPQHQLHRAHYD

S346

TVVQPSVGAAAGPVVPPCPGRIRHFK

Phosphorylation site

S138

SSPDSAEDVRK

S330

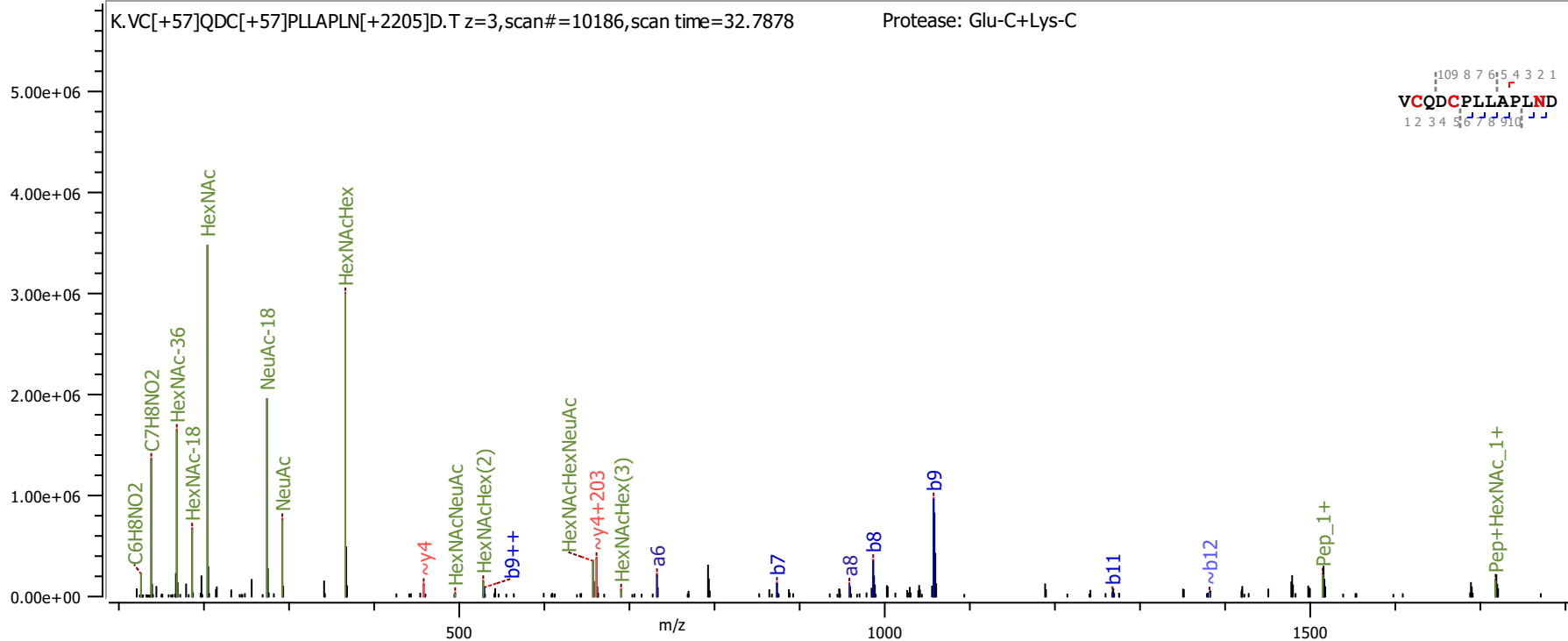
LRHTFMGVVSLGSPSGE

K.VC[+57]QDC[+57]PLLAPLN[+2205]D.T z=3,scan#=10186,scan time=32.7878

Protease: Glu-C+Lys-C

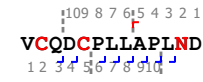
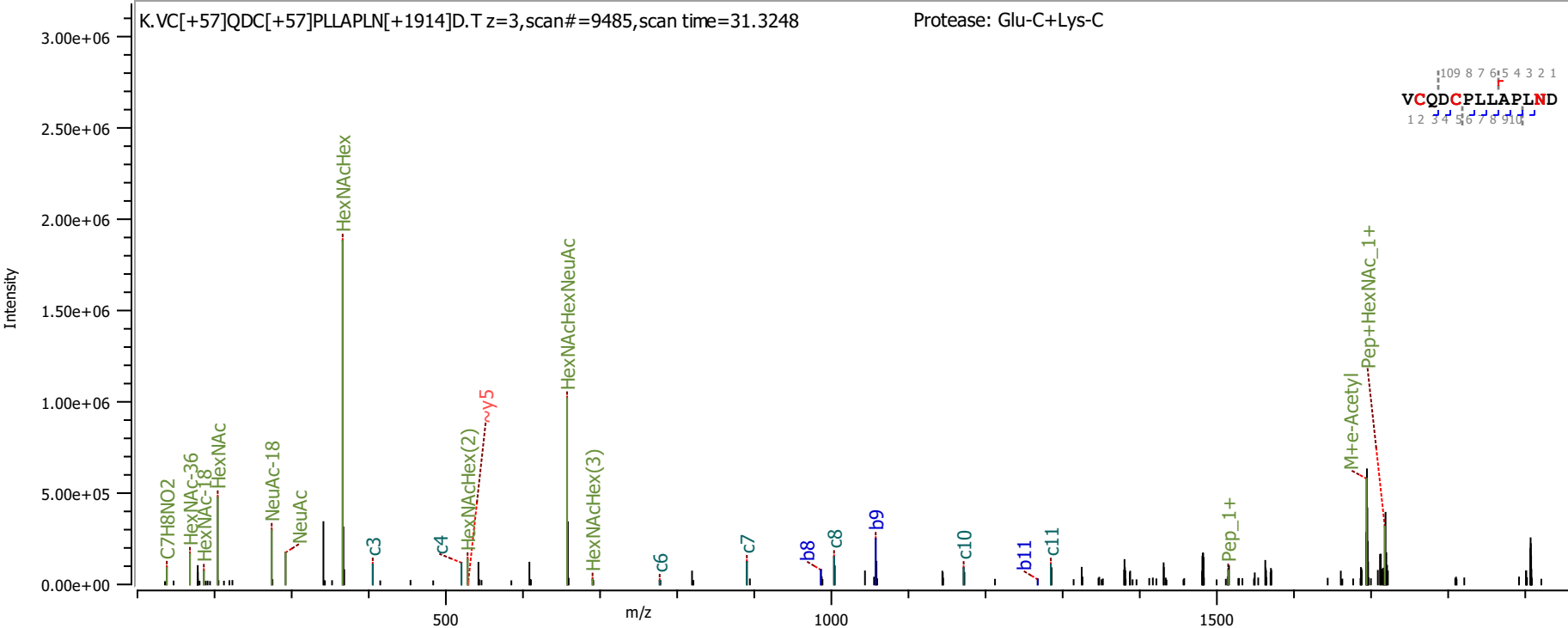
109 8 7 6 5 4 3 2 1
VCQDCPLLAPLND
1 2 3 4 5 6 7 8 9 10

Intensity



K.VC[+57]QDC[+57]PLLAPLN[+1914]D.T z=3,scan# =9485,scan time=31.3248

Protease: Glu-C+Lys-C



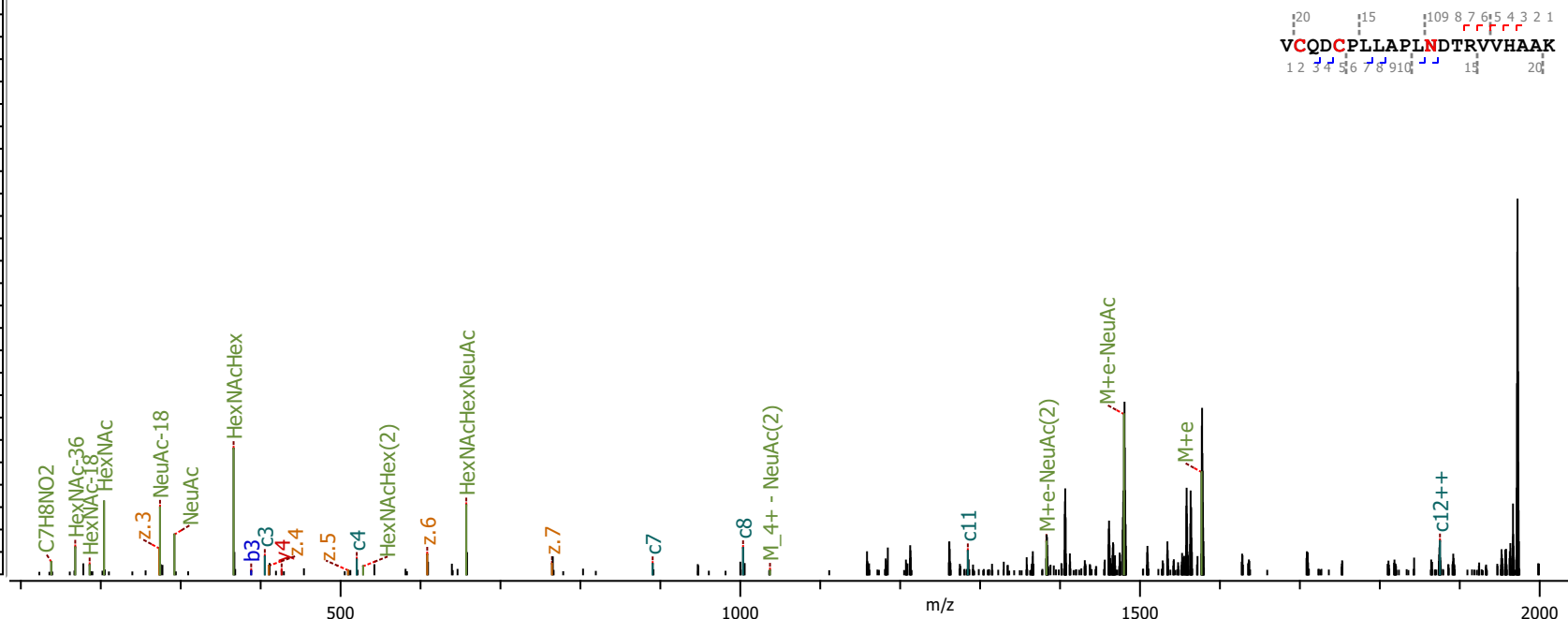
K.VC[+57]QDC[+57]PLLAPLN[+2351]DTRVHAAK.A z=4,scan#=8352,scan time=29.0167

Protease: Glu-C+Lys-C

20 15 109 8 7 6 5 4 3 2 1
VCQDCPLLAPLNDRVHAAK
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Intensity

5.00e+06
4.00e+06
3.00e+06
2.00e+06
1.00e+06
0.00e+00



m/z

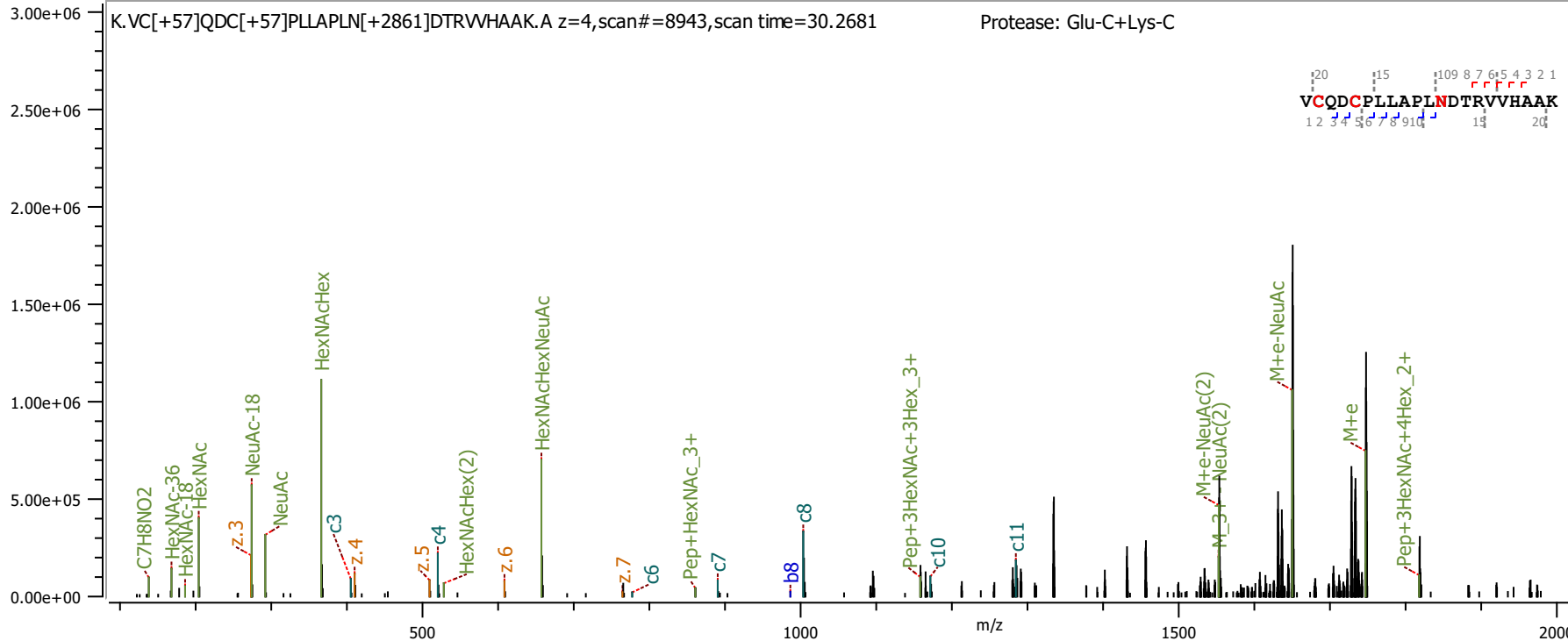
2000

K.VC[+57]QDC[+57]PLLAPLN[+2861]DTRVHAAK.A z=4,scan#=8943,scan time=30.2681

Protease: Glu-C+Lys-C

20 15 109 8 7 6 5 4 3 2 1
VCQDCPLLAPLNDRVVHAAK
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Intensity



Intensity

1.20e+06
1.00e+06
8.00e+05
6.00e+05
4.00e+05
2.00e+05
0.00e+00

109 8 7 6 5 4 3 2 1
VCQDCPLLAPLND
12 3 4 5 6 7 8 9 10

0.00e+00

500

m/z

1000

1500

C7H8NO2

HexNAc-36

HexNAc-18

HexNAc

NeuAc-18

NeuAc

HexNAcHex

c3

HexHexNAcFuc

c4

HexNAcHex(2)

HexNAcHexNeuAc

c6

c7

b8

b9

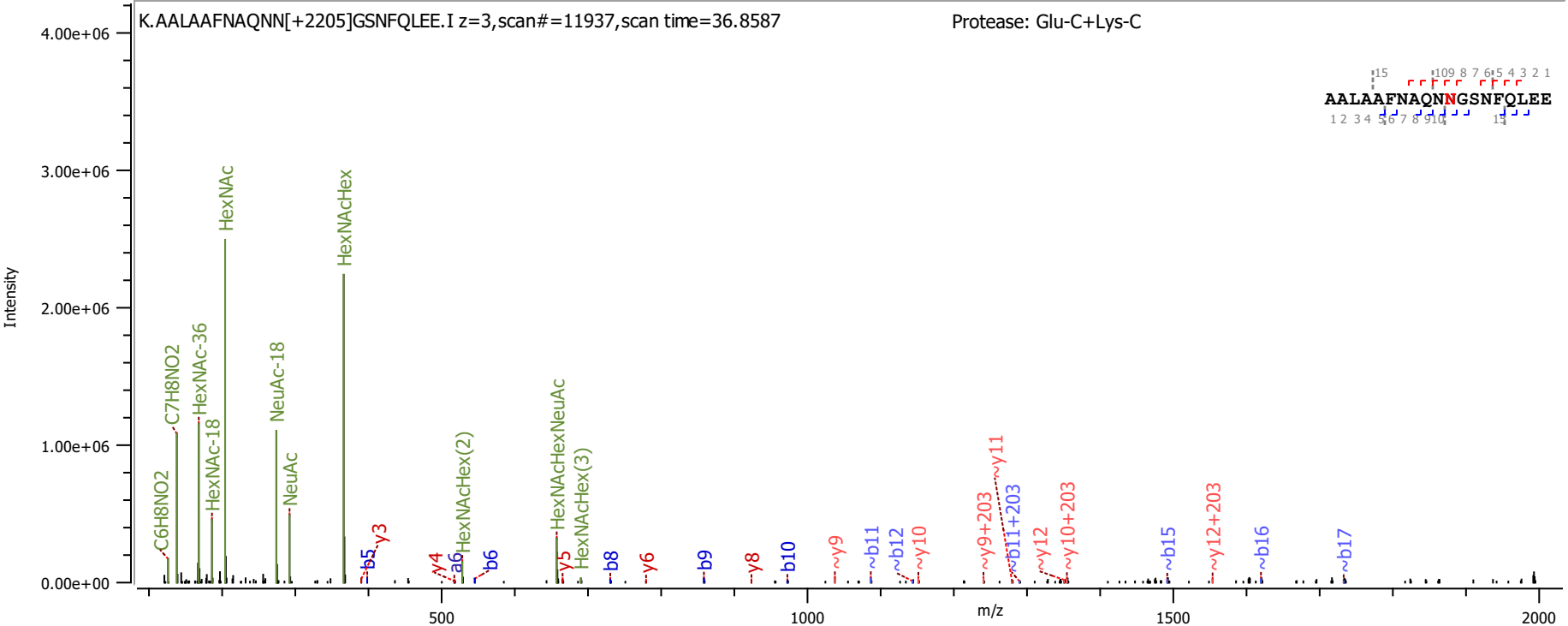
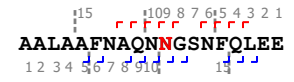
M_4+ - NeuAc

b11

Pep+HexNAc_1+

K.AALAAFNAQNN[+2205]GSNFQLEE.I z=3,scan#=11937,scan time=36.8587

Protease: Glu-C+Lys-C



15 109 8 7 6 5 4 3 2 1
A A L A A F N A Q N N G S N F Q L E E
1 2 3 4 5 6 7 8 9 10 11 12 13 14

Intensity

2.50e+6
2.00e+6
1.50e+6
1.00e+6
5.00e+5
0.00e+0

m/z

500

1000

1500

2000

C6H8NO2

C7H8NO2

c2

HexNAc-36

HexNAc-18

HexNAc

b3

c3

y2

NeuAc-18

NeuAc

b4

z.3-43

y3

c8++

y5

b5

y4

HexNAcHex(2)

b6

c6

z.5

b7

HexNAcHexNeuAc

y5

HexNAcHex(3)

b6

b8

c8

z.6

y6

a9

b9

y7

c9

y8

c10

Pep_2+

Pep+HexNAc_2+

Pep+2HexNAc_2+

M+e-45

Pep+2HexNAc+2Hex_2+

Pep+2HexNAc+3Hex_2+

Pep+3HexNAc+3Hex_2+

c16++

M+2e-NeuAc

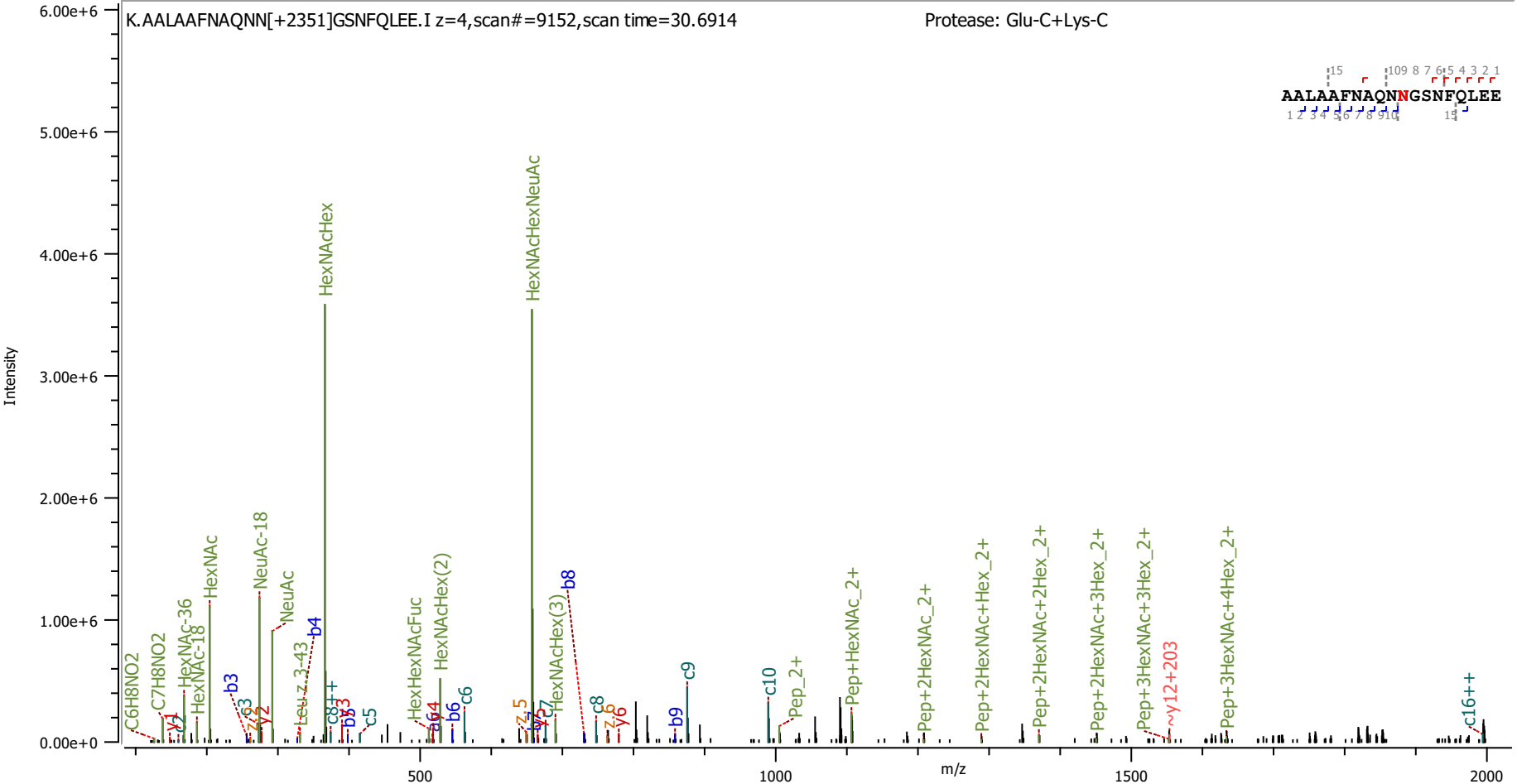
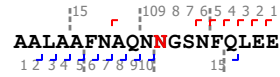
M+2e-Acetyl

M+2e

M+2e-17

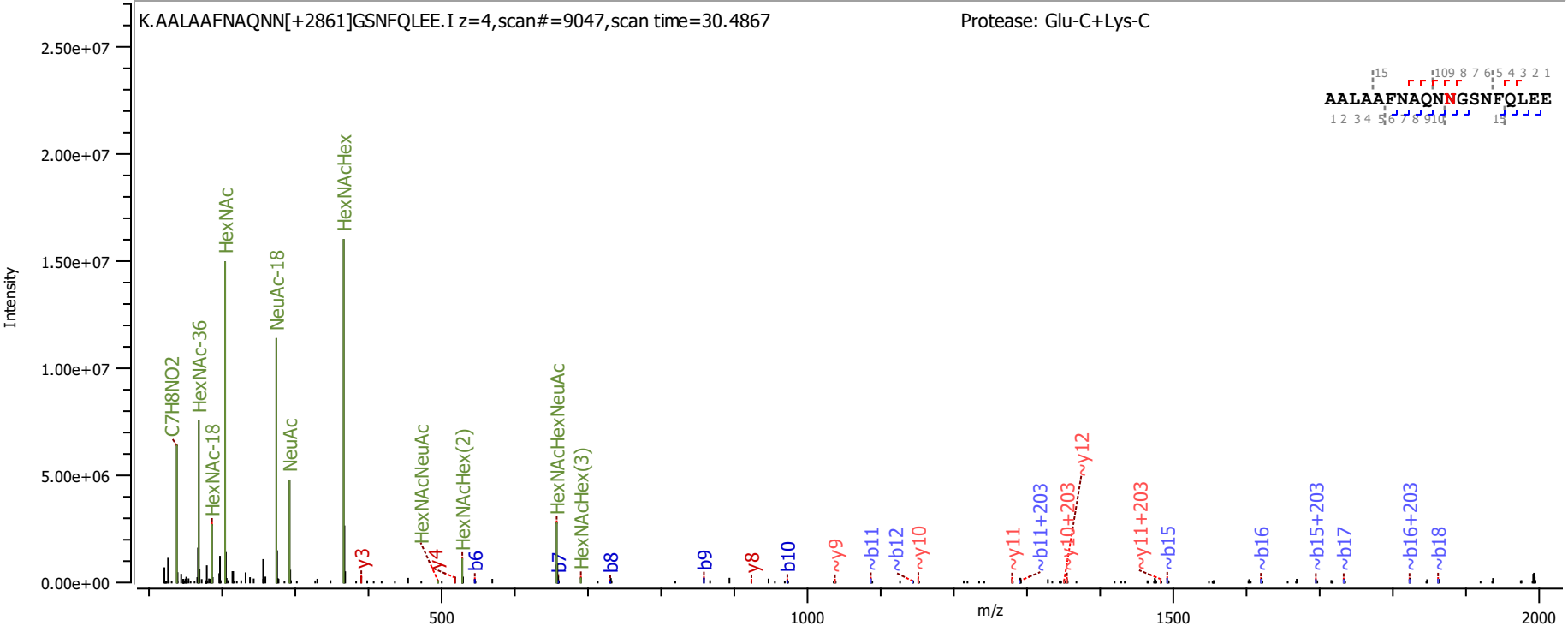
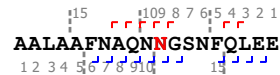
M+2e-45

M



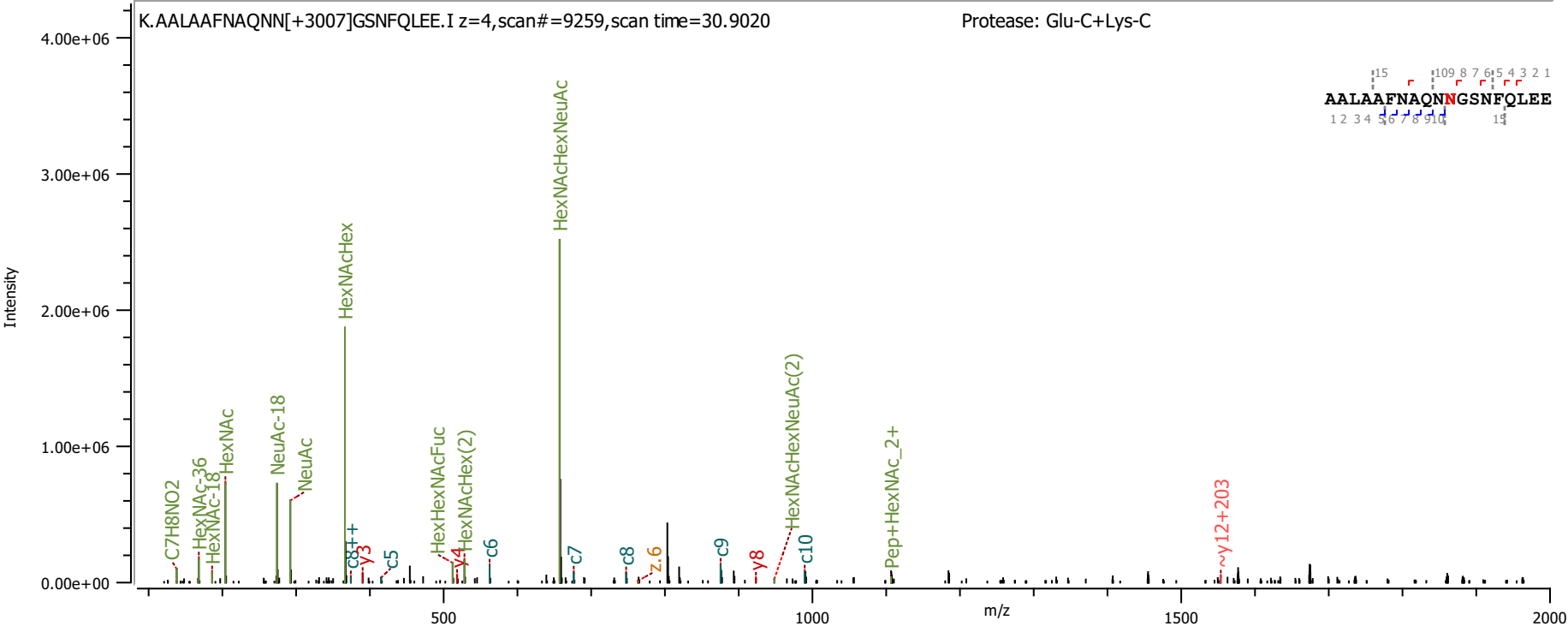
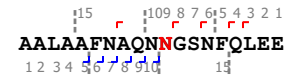
K.AALAAFNAQNN[+2861]GSNFQLEE.I z=4,scan#=9047,scan time=30.4867

Protease: Glu-C+Lys-C



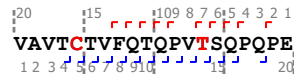
K.AALAAFNAQNN[+3007]GSNFQLEE.I z=4,scan#=9259,scan time=30.9020

Protease: Glu-C+Lys-C

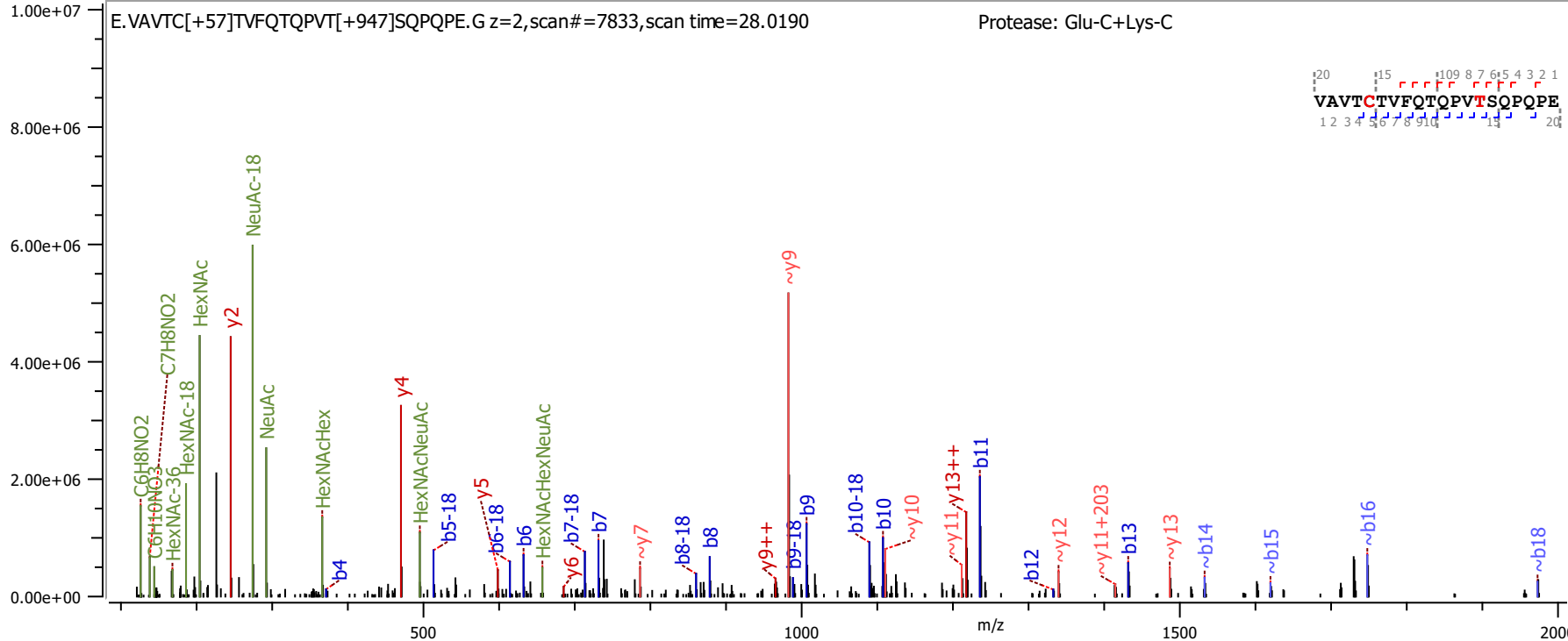


E. VAVTC[+57]TVFQTQPVT[+947]SQPQPE.G z=2, scan#=7833, scan time=28.0190

Protease: Glu-C+Lys-C

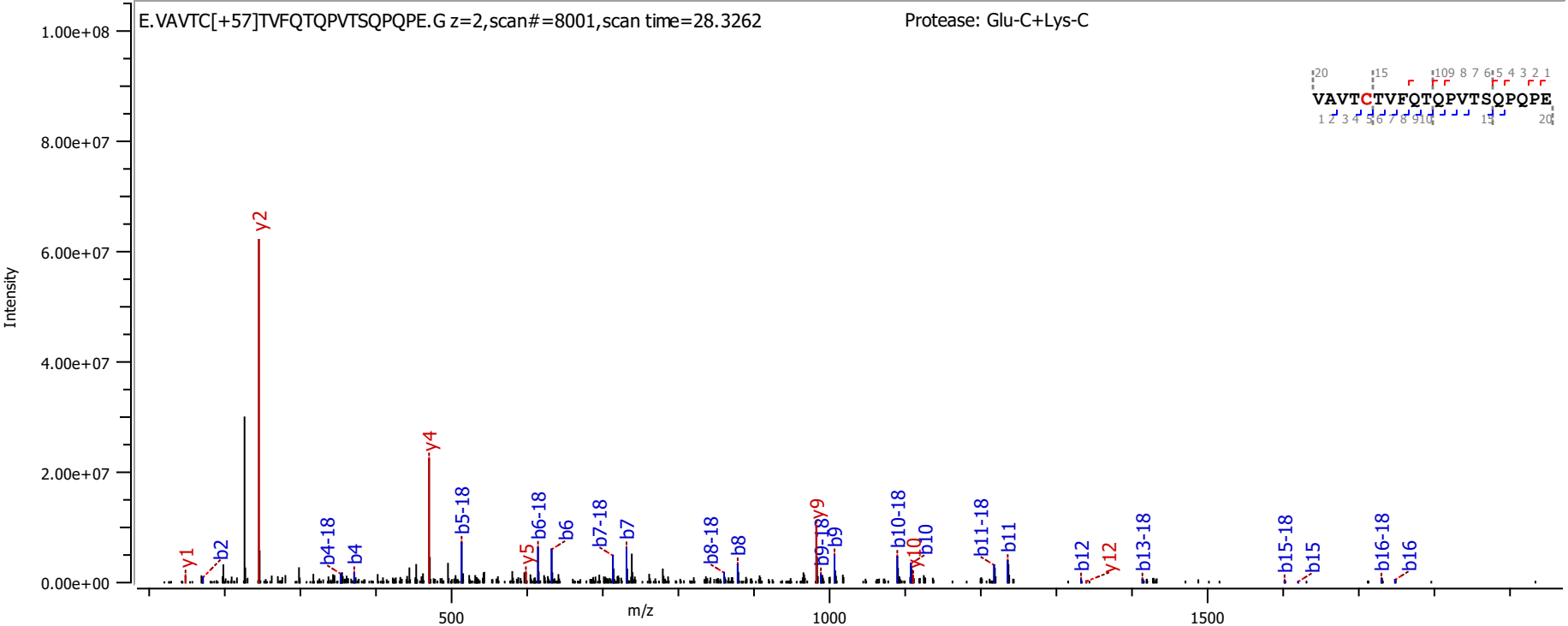
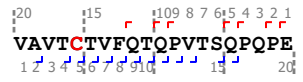


Intensity



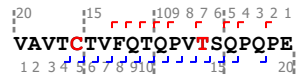
E. VAVTC[+57]TVFQTQPVTSPQPE.G z=2, scan#=8001, scan time=28.3262

Protease: Glu-C+Lys-C

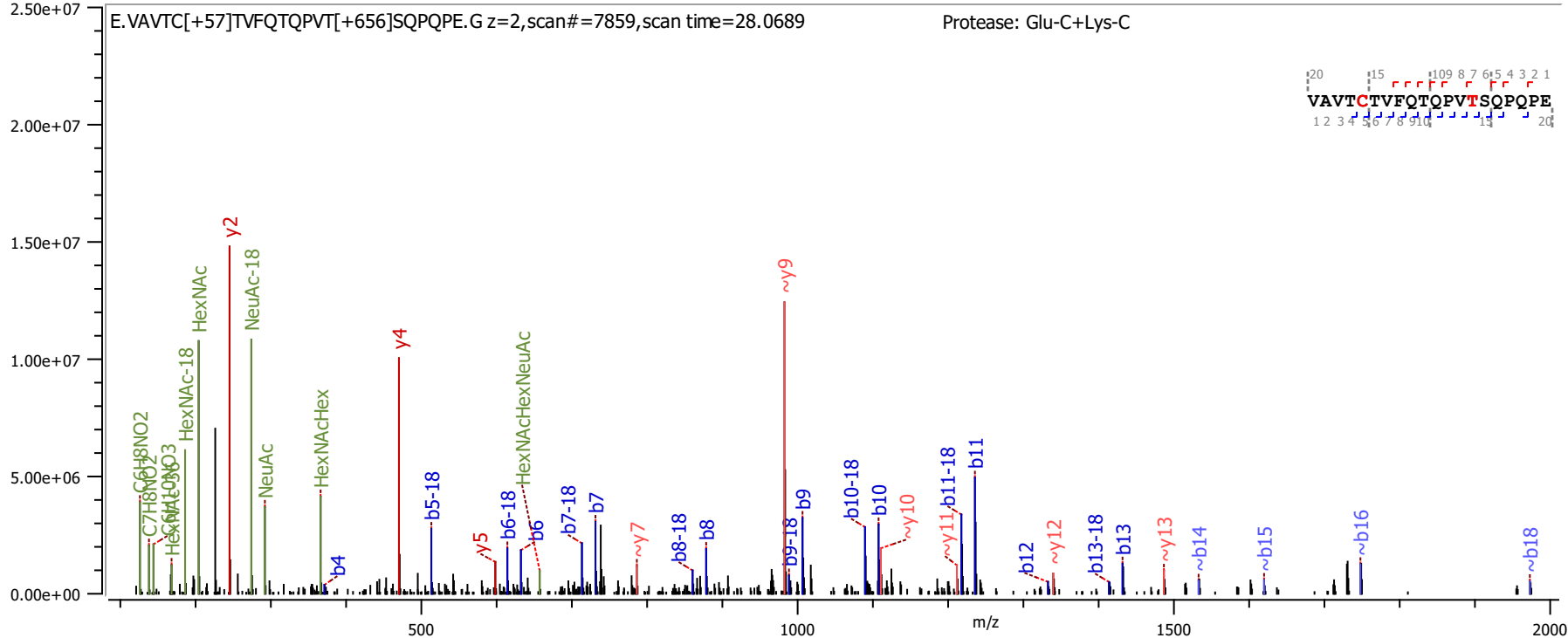


E. VAVTC[+57]TVFQTQPVT[+656]SQPQPE. G z=2, scan# = 7859, scan time = 28.0689

Protease: Glu-C+Lys-C

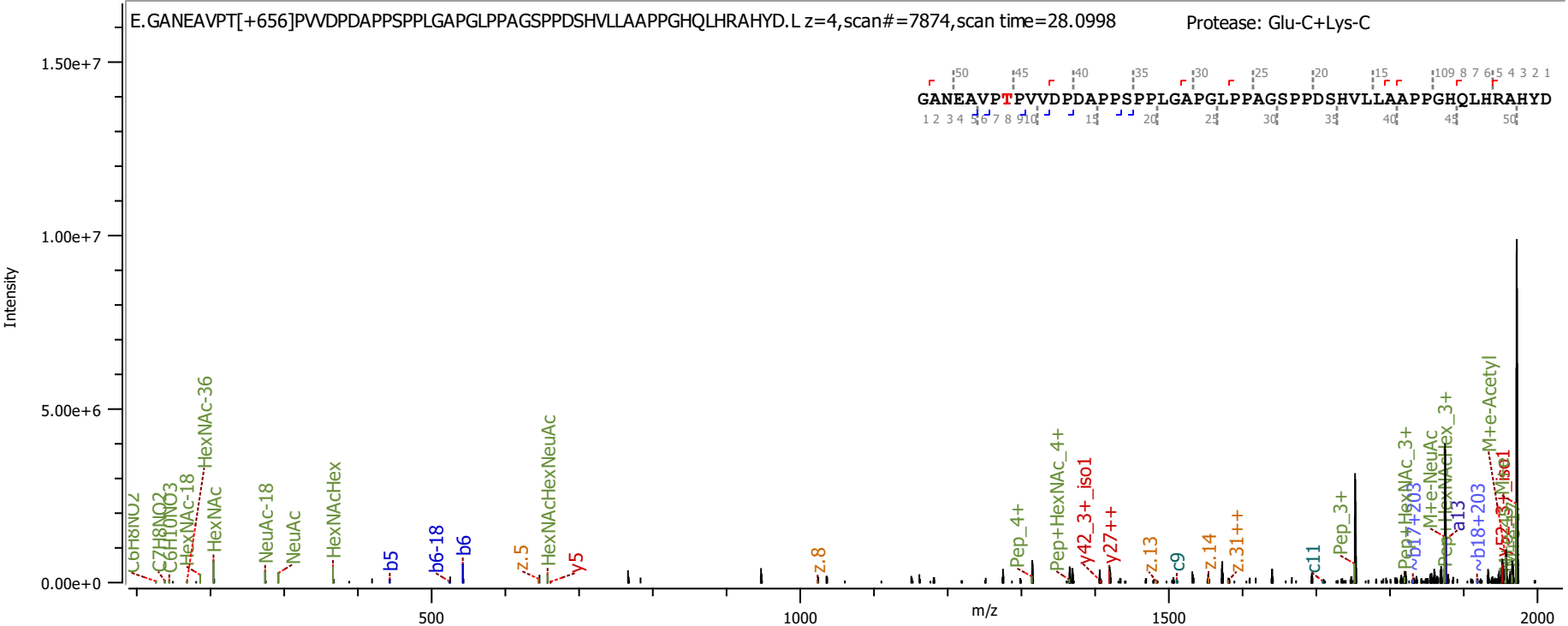


Intensity



E. GANEAVPT[+656]PVVDPDAPPSPLGAPGLPPAGSPDASHVLLAAPPGLHRAHYD. L z=4, scan#=7874, scan time=28.0998

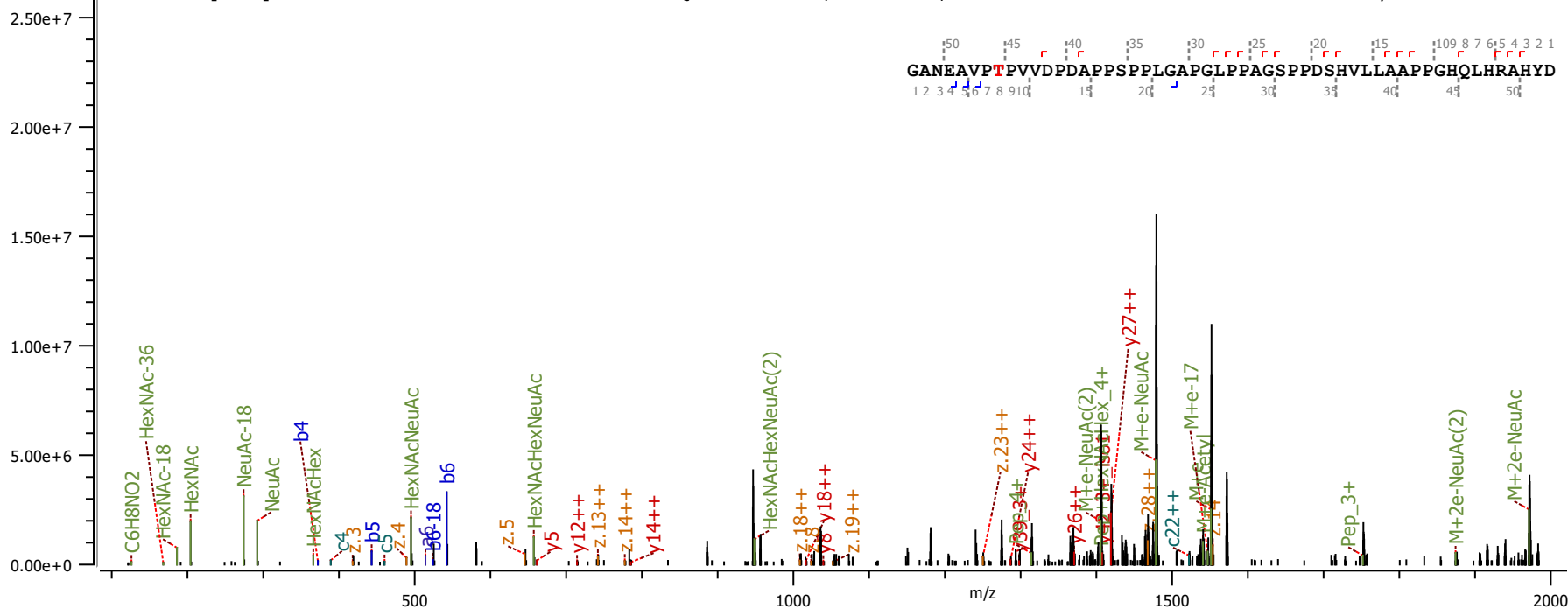
Protease: Glu-C+Lys-C



E. GANEAVPT[+947]PVVDPDAPPSPLGAPGLPPAGSPDShVLLAAPPGLHRAHYD. L z=5, scan#=7896, scan time=28.1402

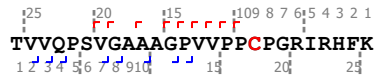
Protease: Glu-C+Lys-C

Intensity



R. TVVQPSVGAAAGPVWPPC[+57]PGRIRHFK.V z=4, scan#=5322, scan time=23.4344

Protease: Glu-C+Lys-C



Intensity

3.50e+06
3.00e+06
2.50e+06
2.00e+06
1.50e+06
1.00e+06
5.00e+05
0.00e+00

m/z

200

400

600

800

1000

1200

a2

b2

b3

b8++

b4

b10++

y11++

a7

y12++

y13++

y14++

y15++

y17++

y19++

b12

y20++

b13

y10

y11

R.TVVQPS[+656]VGAAAGPVWPPC[+57]PGRIRHFK.V z=5,scan#=5880,scan time=24.3679

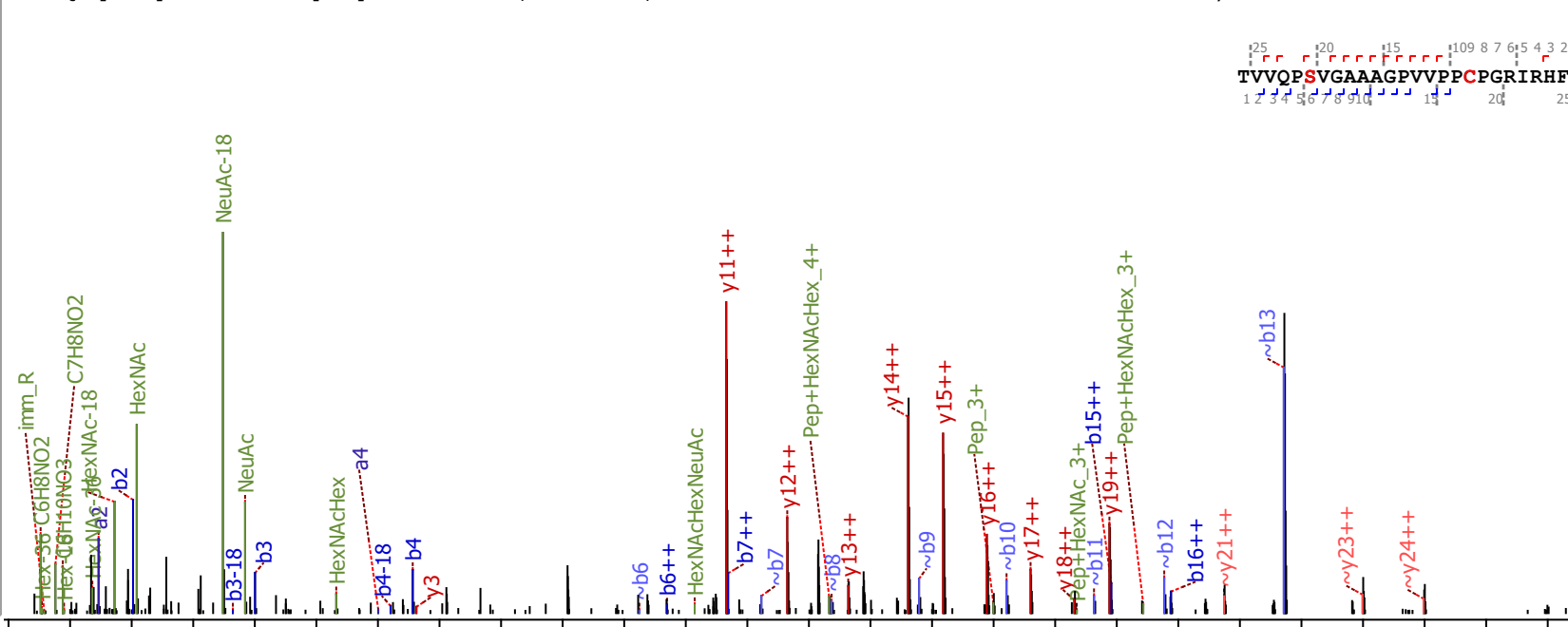
Protease: Glu-C+Lys-C

25 20 15 109 8 7 6 5 4 3 2 1
TVVQPSVGAAAGPVWPPCPGRIRHFK
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25

Intensity

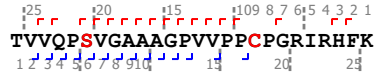
7.00e+7
6.00e+7
5.00e+7
4.00e+7
3.00e+7
2.00e+7
1.00e+7
0.00e+0

200 400 600 800 1000 1200
m/z



R.TVVGPS[+947]VGAAAGPVPPC[+57]PGRIRHFK.V z=5,scan#=5991,scan time=24.5560

Protease: Glu-C+Lys-C



Intensity

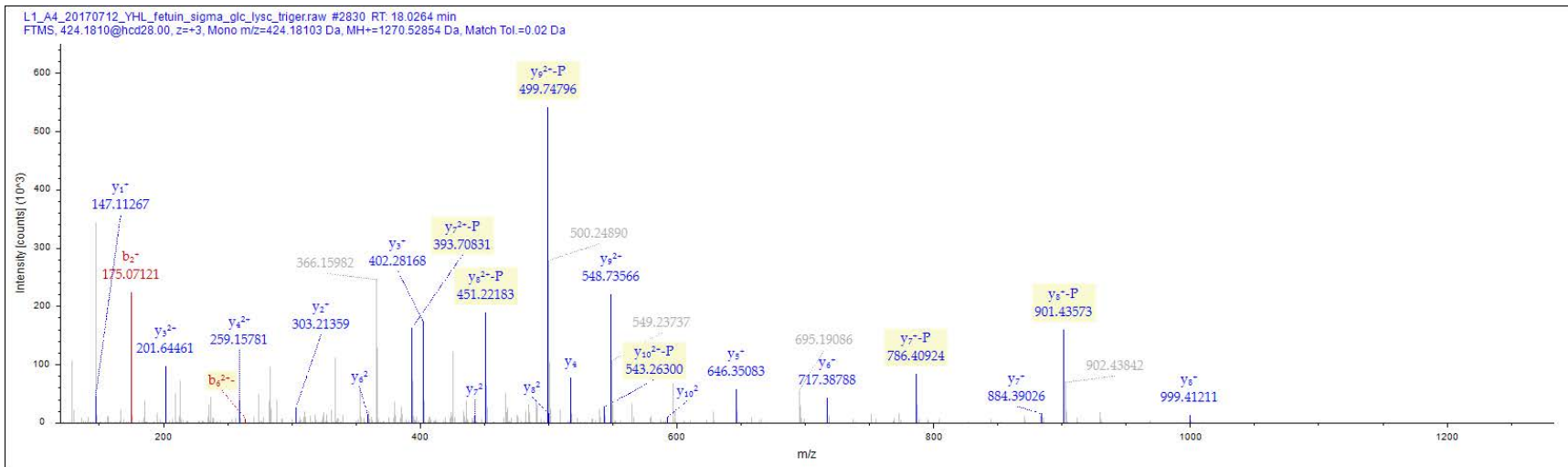
1.00e+8
8.00e+7
6.00e+7
4.00e+7
2.00e+7
0.00e+0

imm_F
Hex-36
C6H8NO2
C6H10NO3
HexNAC-18
HexNAC-36
HexNAC
b3-18
y2
b3
HexNACHex
b4-18
b4
y3
HexNACNeuAc
b5-18
b5
Pep_5+
y15_3+
b6
y10++
HexNACHexNeuAc
b7
y12++
Pep+HexNACHex_4+
b8
y13++
b9
y14++
y15++
Pep_3+
y16++
y17++
HexNACHexNeuAc(2)
Pep+HexNAC_3+
y19++
Pep+HexNACHex_3+
b12
y20++
y21++
b13
y23++
b17++
y24++
b15
Pep_2+
y11

m/z

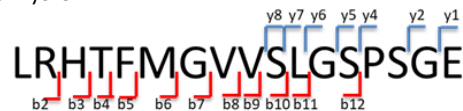
Sequence: SSPDS[+79.9]AEDVRK z=3, scan=2830, scan time=18.0264

Protease: Glu-C+Lys-C



Sequence: LRHTFMGVVSLGSPS[79.9]GE z=3, scan=10547, scan time=33.5

Protease: Glu-C+Lys-C



L1_A4_20170712_YHL_fetuin_sigma_glc_lysc_trigger.raw #10547 RT: 33.5043 min
FTMS, 618.6243@hcd28.00, z=+3, Mono m/z=618.62433 Da, MH+=1853.85843 Da, Match Tol.=0.02 Da

