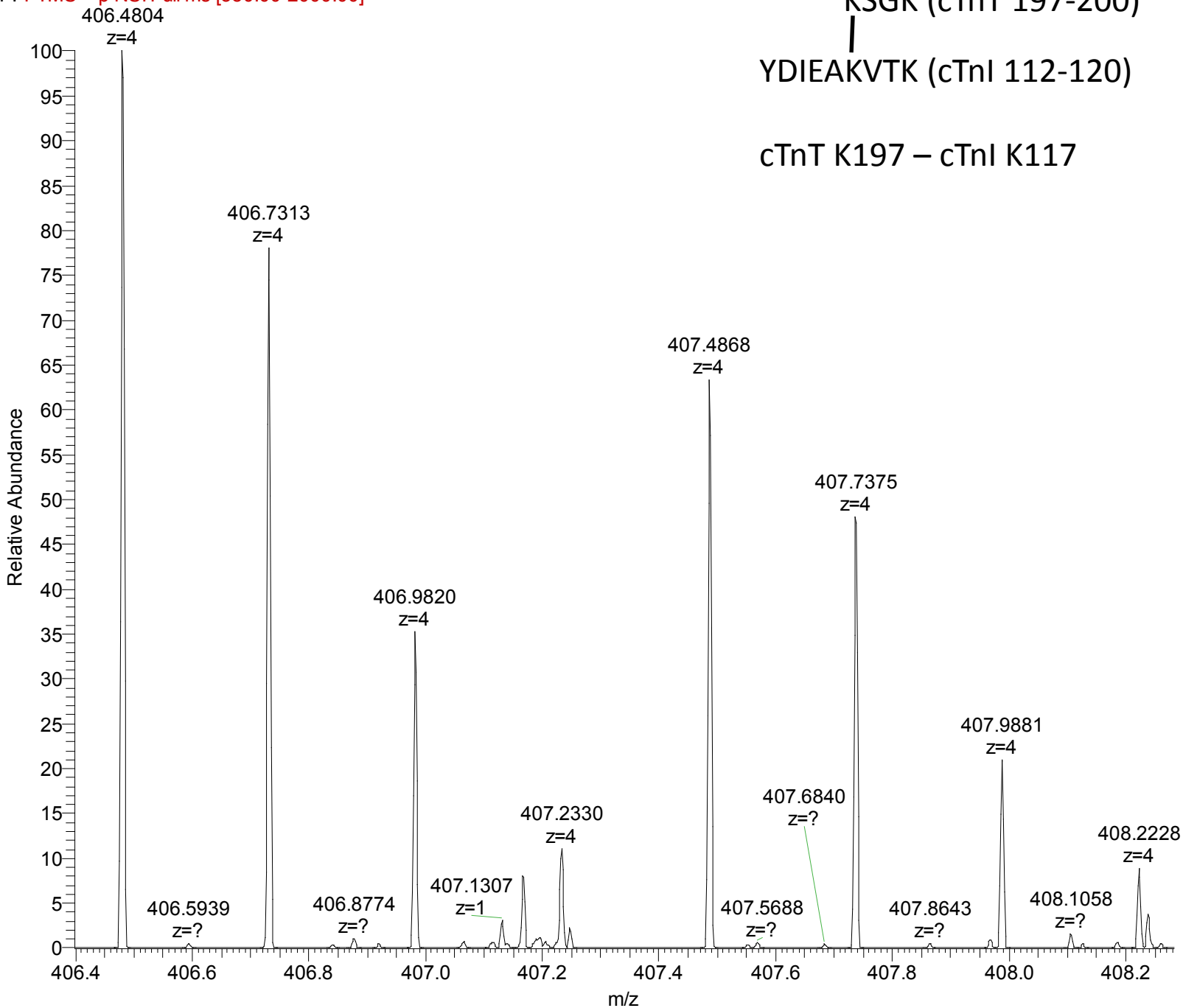


KSGK (cTnT 197-200)

YDIEAKVTK (cTnI 112-120)

cTnT K197 – cTnI K117

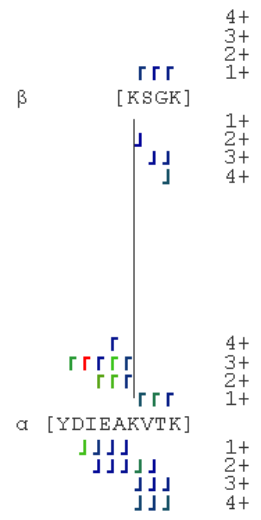
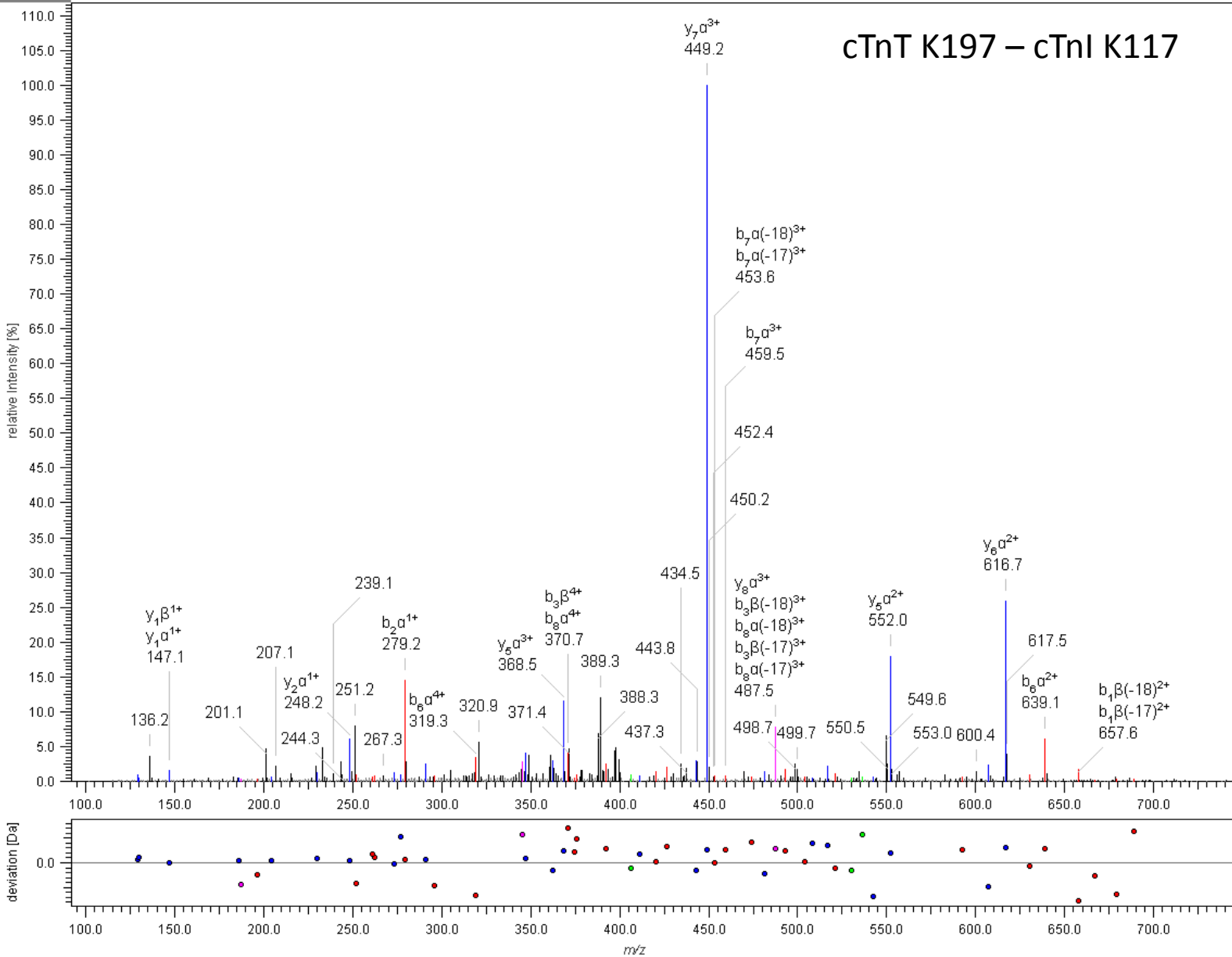


File: F:\Proje ... rad_4uL_1.mzXML_9.zhrs
 Scan: 7462
 theor. Mass (M + H+): 1622.9
 meas. Mass (M + H+): 1622.8975
 Deviation -1.5 ppm
 m/z: 406.479827880859
 Charge: +4

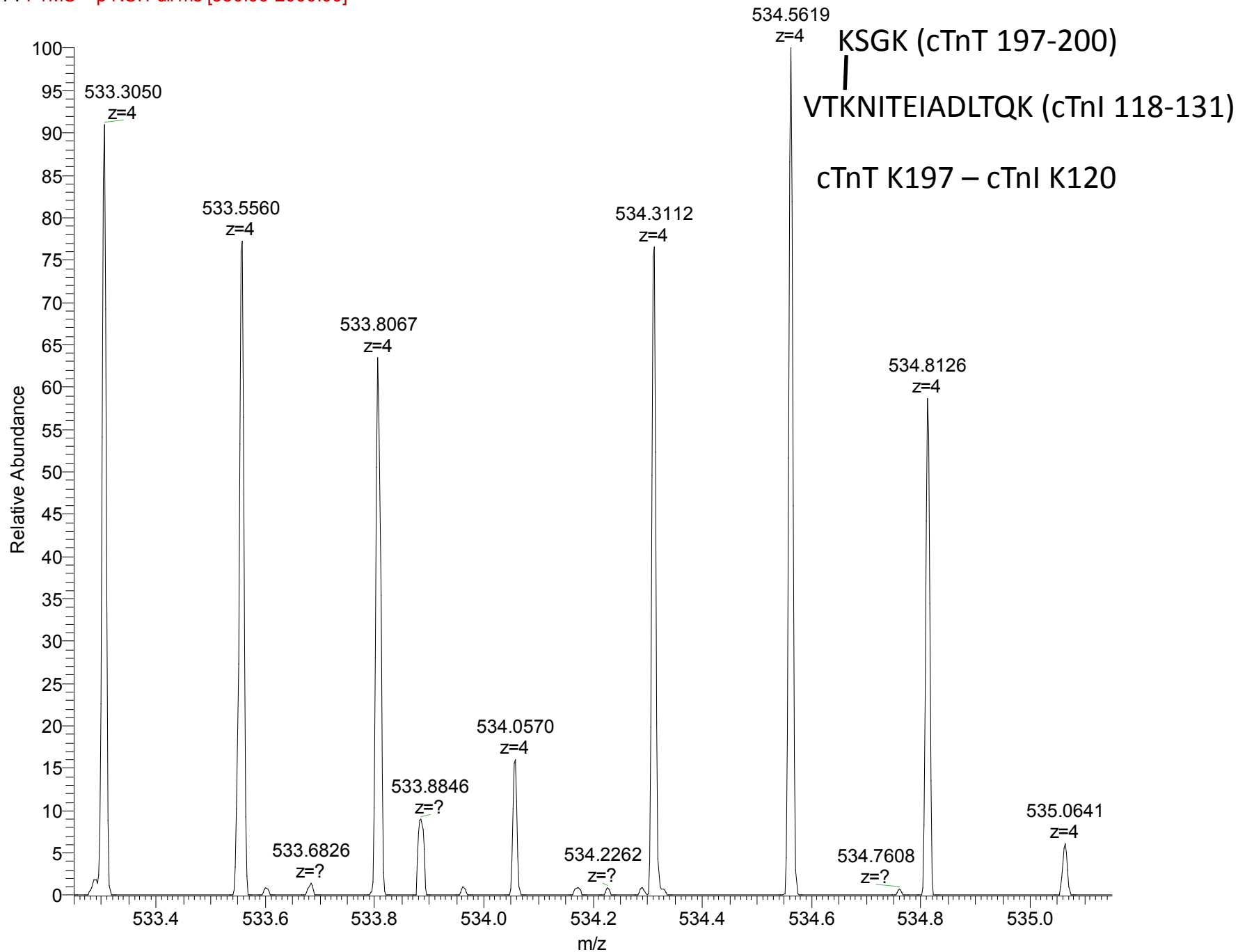
Peptide β : [KSGK] (K1)
 (\rightarrow sp|P453.. from 197 to 200)
 Peptide α : [YDIEAKVTK] (K6)
 (\rightarrow sp|P194.. from 112 to 120)
 Crosslinker: DSS/BS3

Score (102)
 identified signals (0.003)
 ion series (0.002)
 intensity Ratio (0.005)
 hits/possible ions (0.0)

KSGK (cTnT 197-200)
 |
 YDIEAKVTK (cTnI 112-120)



0% rel. intensity 100%



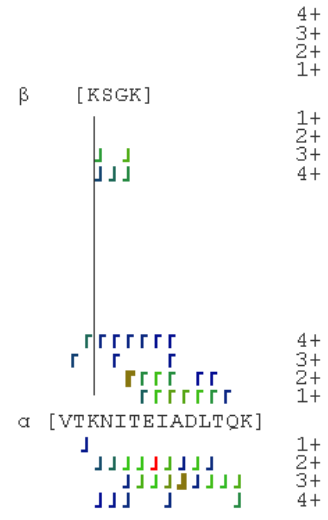
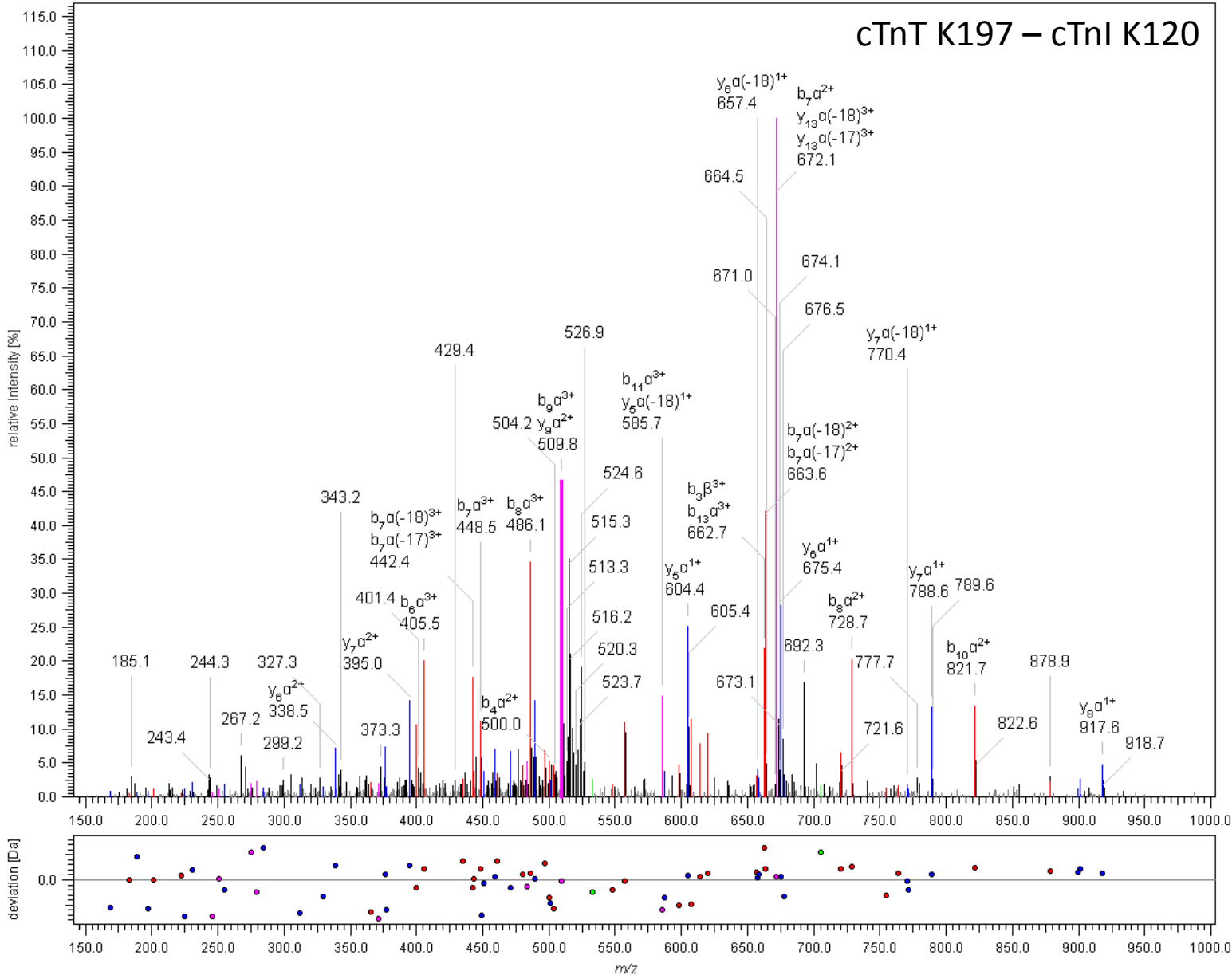
File: F:\Proje ... rad_4uL_1.mzXML_5.zhrs
 Scan: 10339
 theor. Mass (M + H⁺): 2130.2016
 meas. Mass (M + H⁺): 2130.203
 Deviation 0.7 ppm
 m/z: 533.306213378906
 Charge: +4

Peptide β: [KSGK] (K1)
 (>sp)P453.. from 197 to 200)
 Peptide α: [VTKNITEIADLTQK] (K3)
 (>sp)P194.. from 118 to 131)
 Crosslinker: DSS/BS3

Score (145)
 identified signals (0.0)
 ion series (0.0)
 intensity Ratio (0.001)
 hits/possible ions (0.0)

KSGK (cTnT 197-200)
VTKNITEIADLTQK (cTnI 118-131)

cTnT K197 – cTnI K120

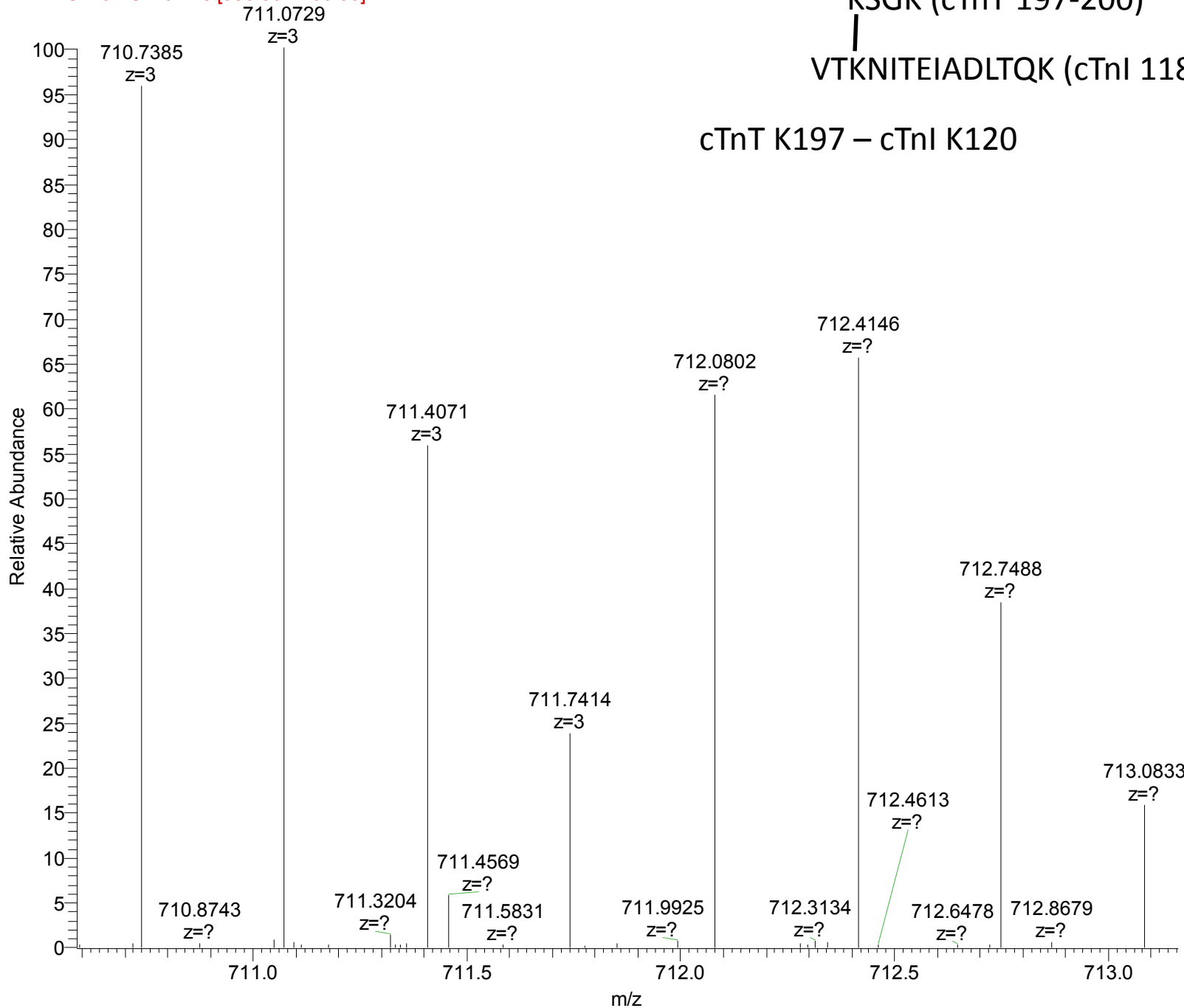


0% rel. intensity 100%

KSGK (cTnT 197-200)

VTKNITEIADLTQK (cTnI 118-131)

cTnT K197 – cTnI K120



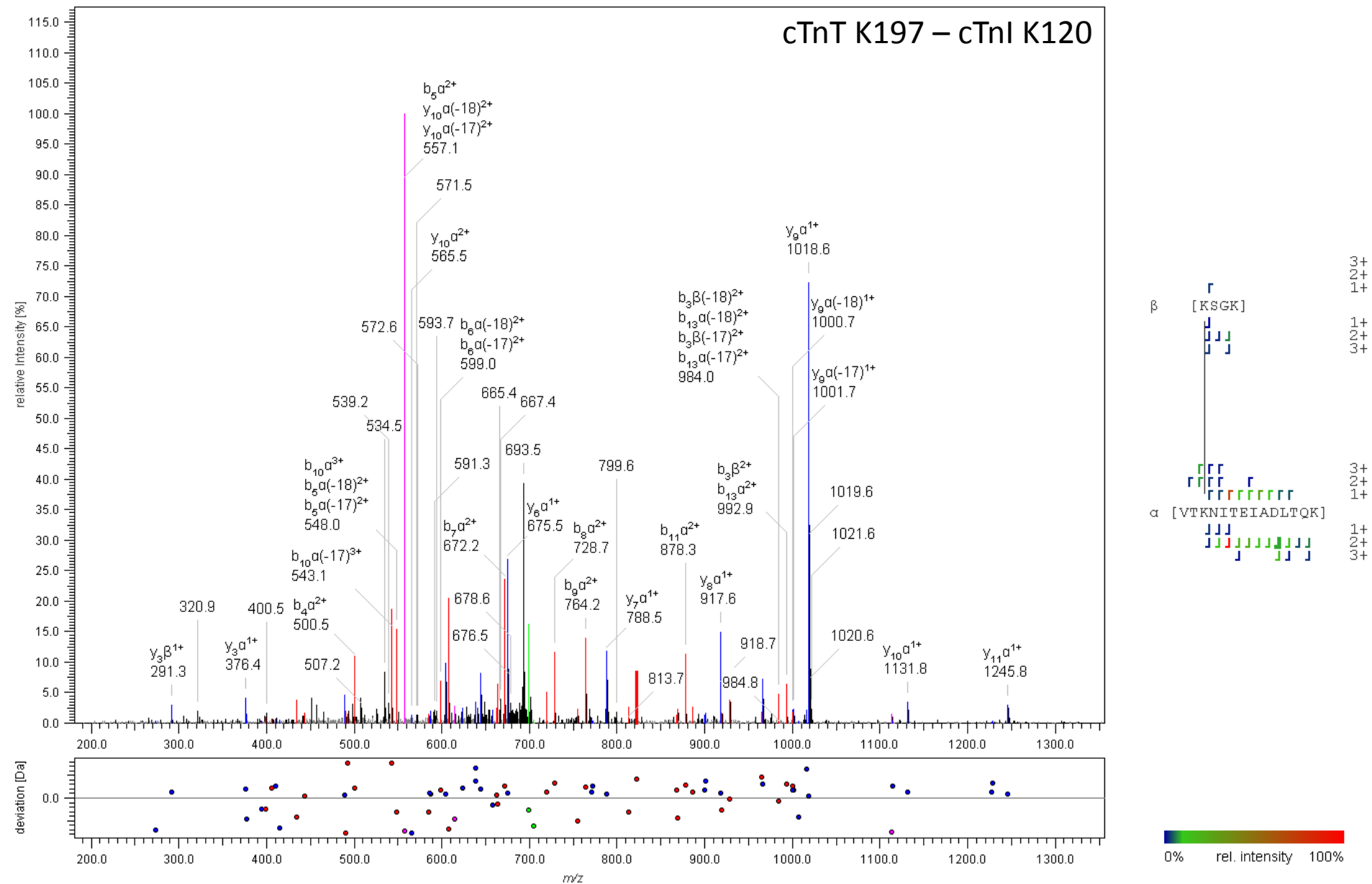
File: F:\Proje ... rad_5uL_1.mzXML_1.zhrs
 Scan: 16009
 theor. Mass (M + H⁺): 2130.2016
 meas. Mass (M + H⁺): 2130.2018
 Deviation 0.1 ppm
 m/z: 710.73876953125
 Charge: +3

Peptide β : [KSGK] (K1)
 (>sp)P453.. from 197 to 200)
 Peptide α : [VTKNITEIADLTQK] (K3)
 (>sp)P194.. from 118 to 131)
 Crosslinker: DSS/BS3

Score (111)
 identified signals (0.007)
 ion series (0.002)
 intensity Ratio (0.001)
 hits/possible ions (0.0)

KSGK (cTnT 197-200)
 |
 VTKNITEIADLTQK (cTnI 118-131)

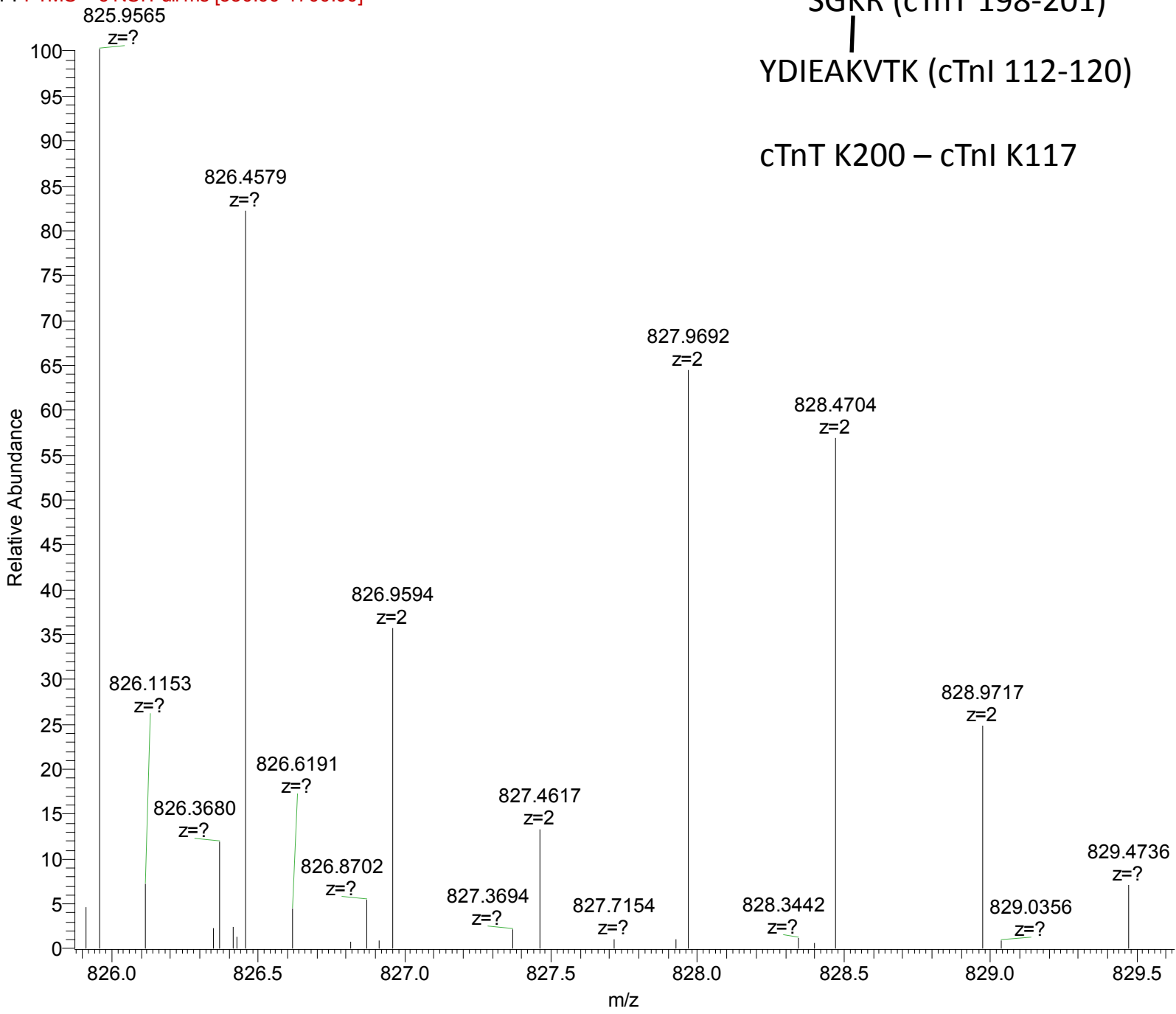
cTnT K197 – cTnI K120



SGKR (cTnT 198-201)

YDIEAKVTK (cTnI 112-120)

cTnT K200 – cTnI K117



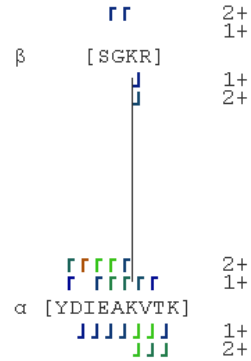
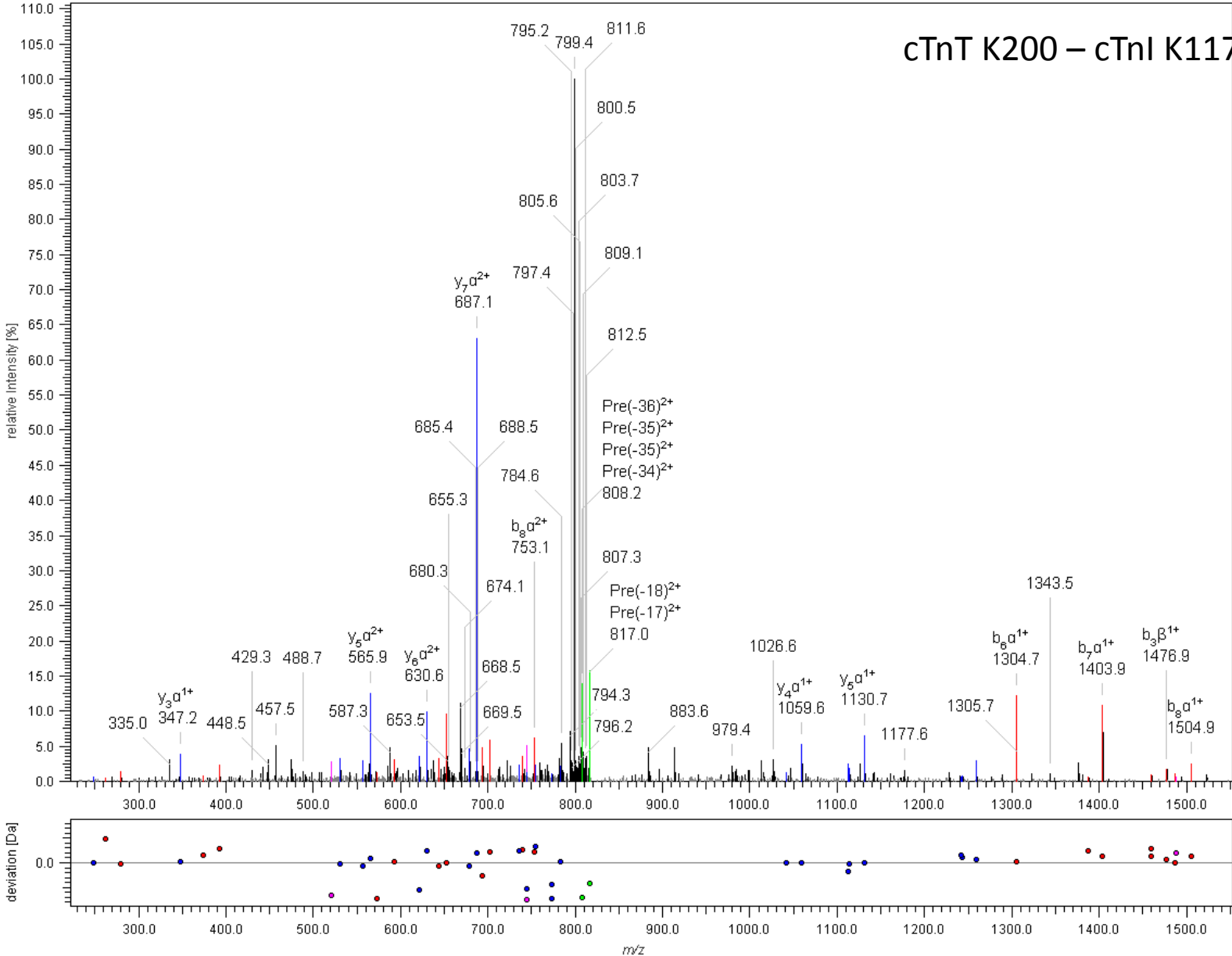
File: F:\Proje ... rad_5uL_1.mzXML_9.zhrs
 Scan: 11933
 theor. Mass (M + H+): 1650.9061
 meas. Mass (M + H+): 1650.9083
 Deviation 1.3 ppm
 m/z: 825.957763671875
 Charge: +2

Peptide β : [SGKR] (K3)
 (>sp)P453.. from 198 to 201
 Peptide α : [YDIEAKVTK] (K6)
 (>sp)P194.. from 112 to 120
 Crosslinker: DSS/BS3

Score (112)
 identified signals (0.013)
 ion series (0.006)
 intensity Ratio (0.002)
 hits/possible ions (0.0)

SGKR (cTnT 198-201)
 |
 YDIEAKVTK (cTnI 112-120)

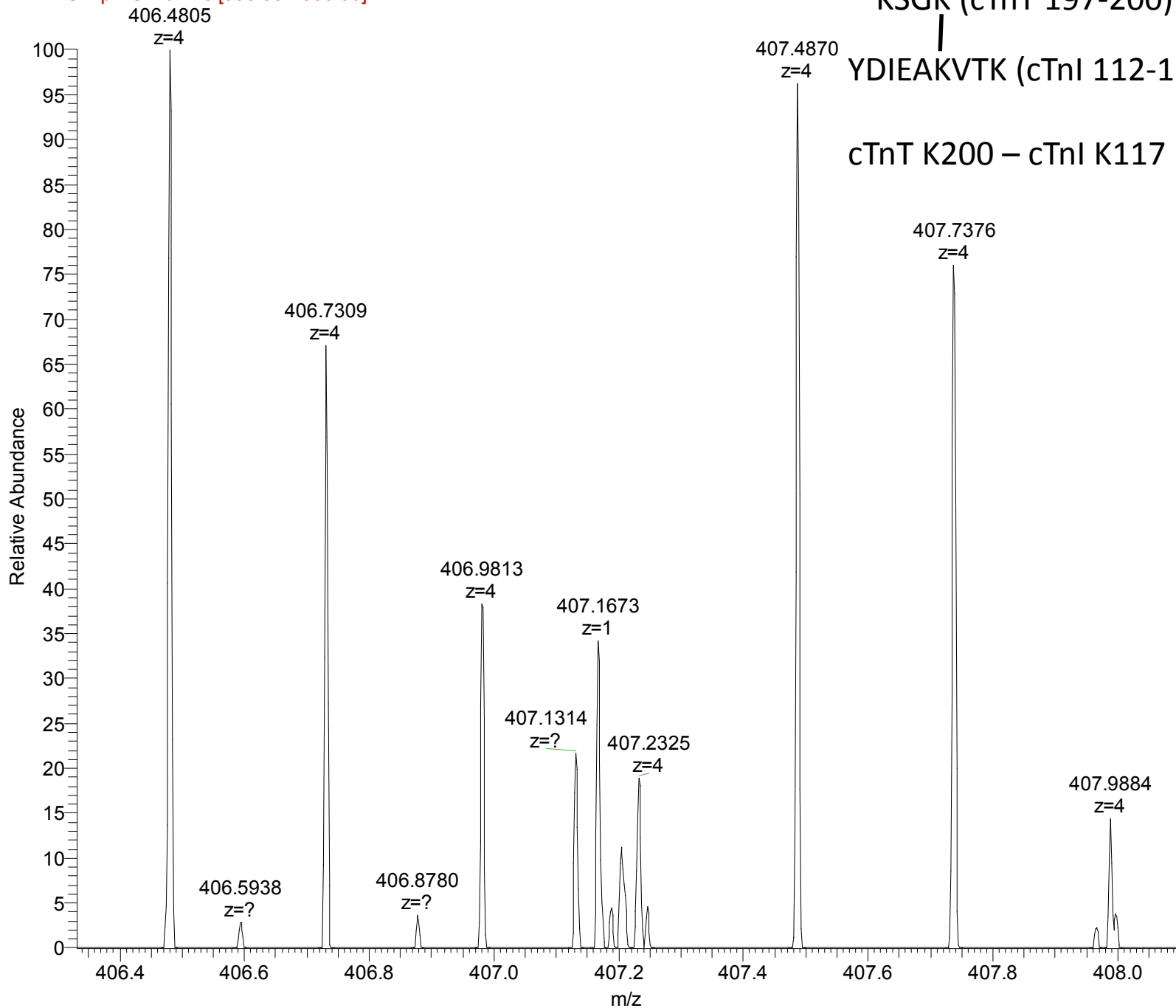
cTnT K200 – cTnI K117



KSGK (cTnT 197-200)

YDIEAKVTK (cTnI 112-120)

cTnT K200 – cTnI K117



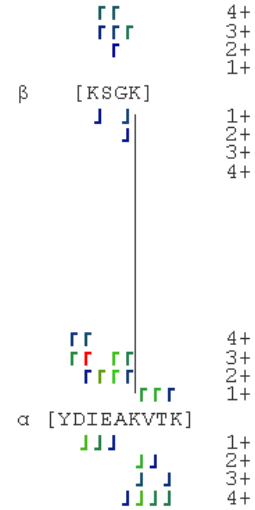
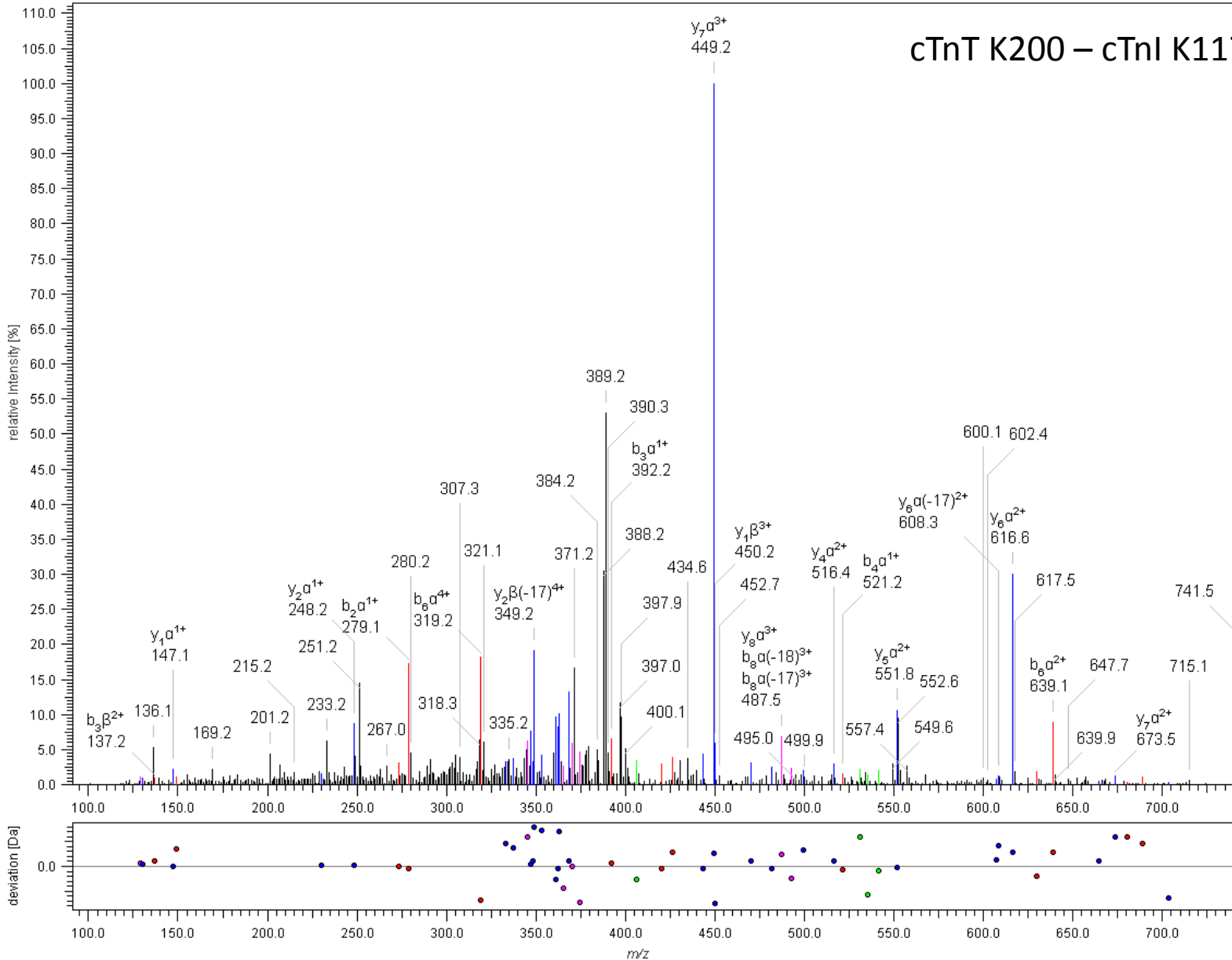
File: F:\Proje ... rad_4uL_1.mzXML_6.zhrs
 Scan: 6212
 theor. Mass (M + H+): 1622.9
 meas. Mass (M + H+): 1622.9011
 Deviation 0.7 ppm
 m/z: 406.480743408203
 Charge: +4

Peptide β : [KSGK] (K4)
 (>sp)P453.. from 197 to 200
 Peptide α : [YDIEAKVTK] (K6)
 (>sp)P194.. from 112 to 120
 Crosslinker: DSS/BS3

Score (105)
 identified signals (0.002)
 ion series (0.0)
 intensity Ratio (0.022)
 hits/possible ions (0.001)

KSGK (cTnT 197-200)
 |
 YDIEAKVTK (cTnI 112-120)

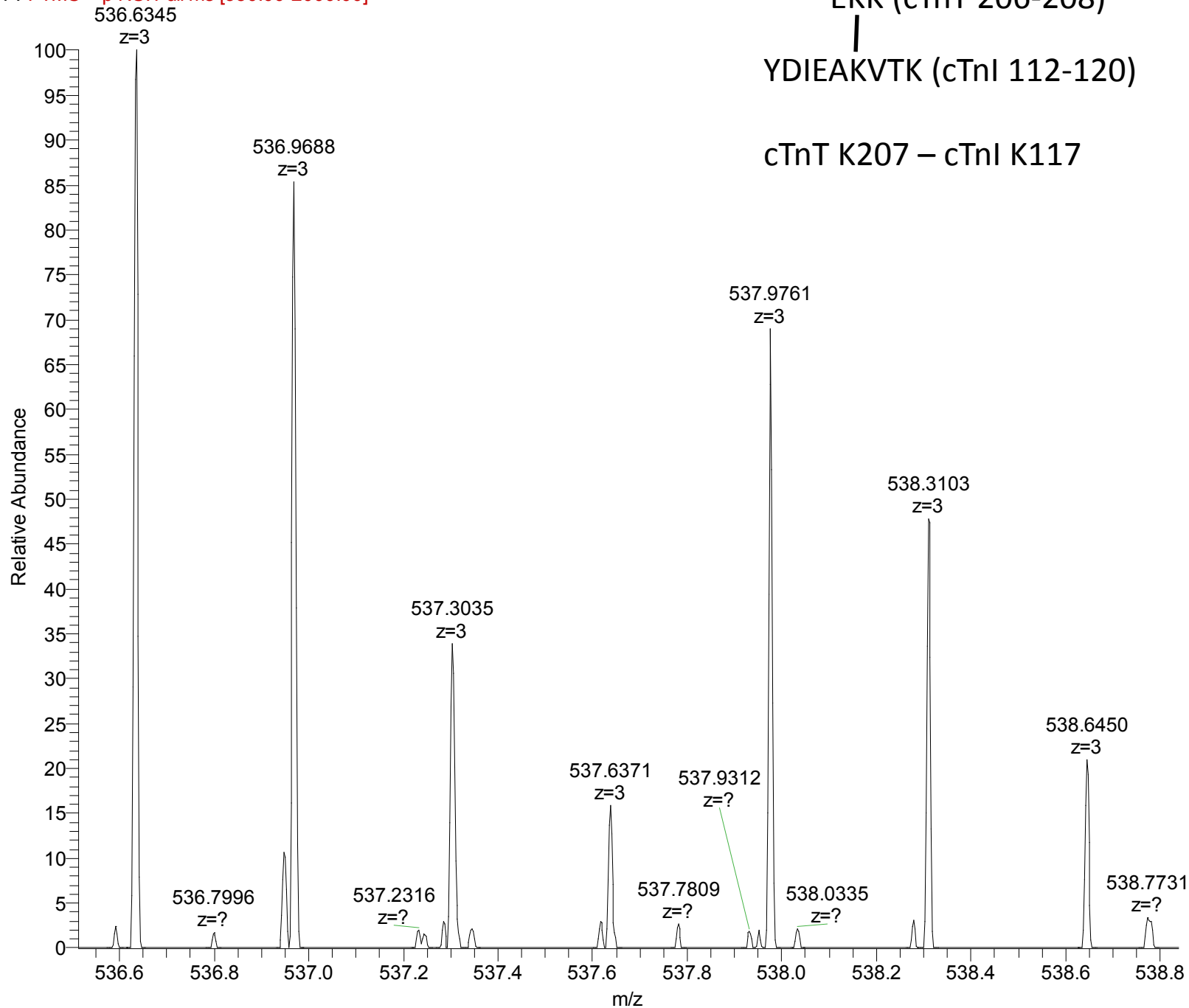
cTnT K200 – cTnI K117



EKK (cTnT 206-208)

YDIEAKVTK (cTnI 112-120)

cTnT K207 – cTnI K117



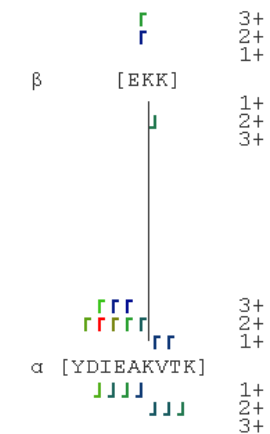
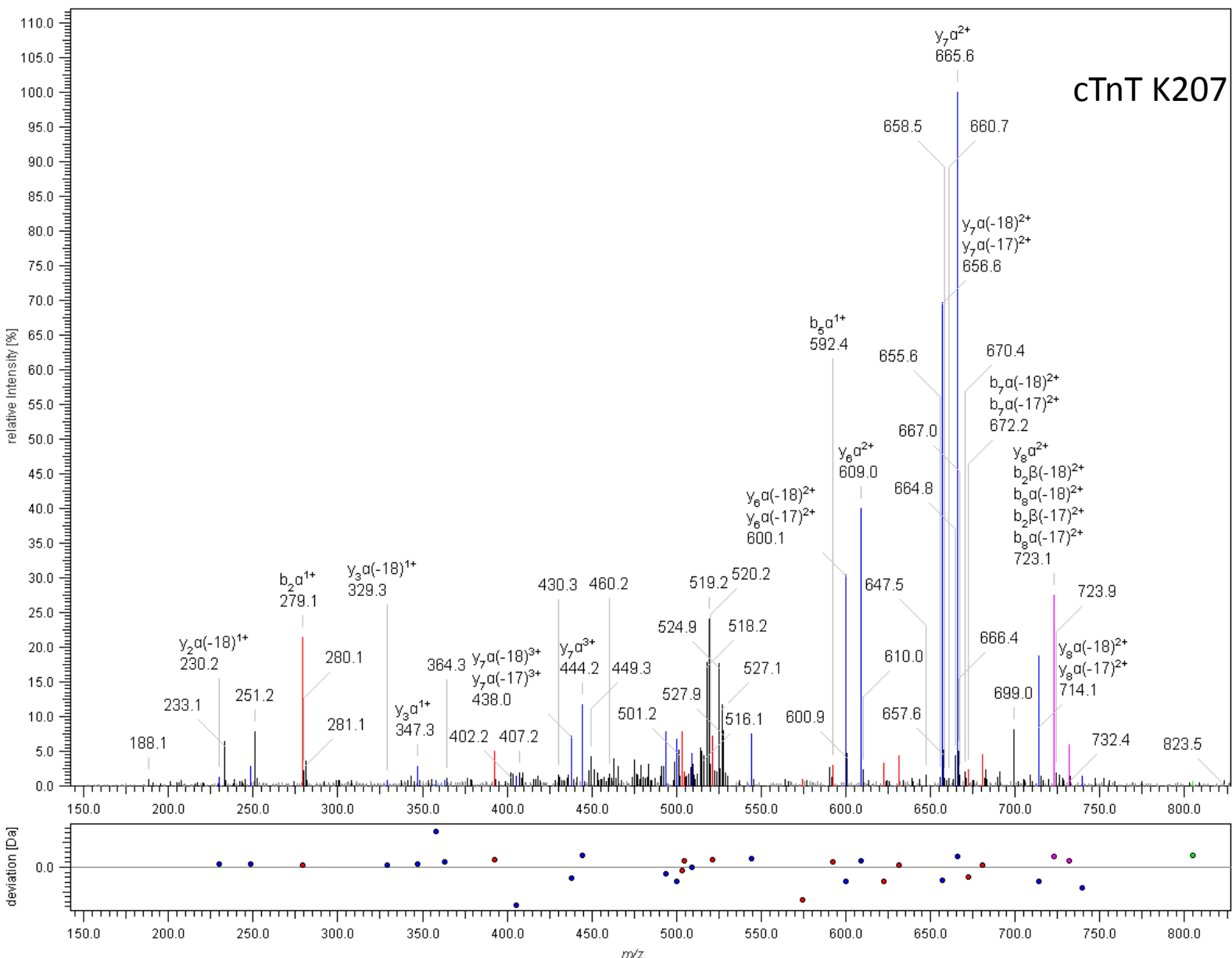
File: F:\Proje ... rad_4uL_1.mzXML_0.zhrs
 Scan: 7820
 theor. Mass (M + H+): 1607.8891
 meas. Mass (M + H+): 1607.8868
 Deviation -1.4 ppm
 m/z: 536.6337890625
 Charge: +3

Peptide β : [EKK] (K2)
 (>sp)P453.. from 206 to 208
 Peptide α : [YDIEAKVTK] (K6)
 (>sp)P194.. from 112 to 120
 Crosslinker: DSS/BSS

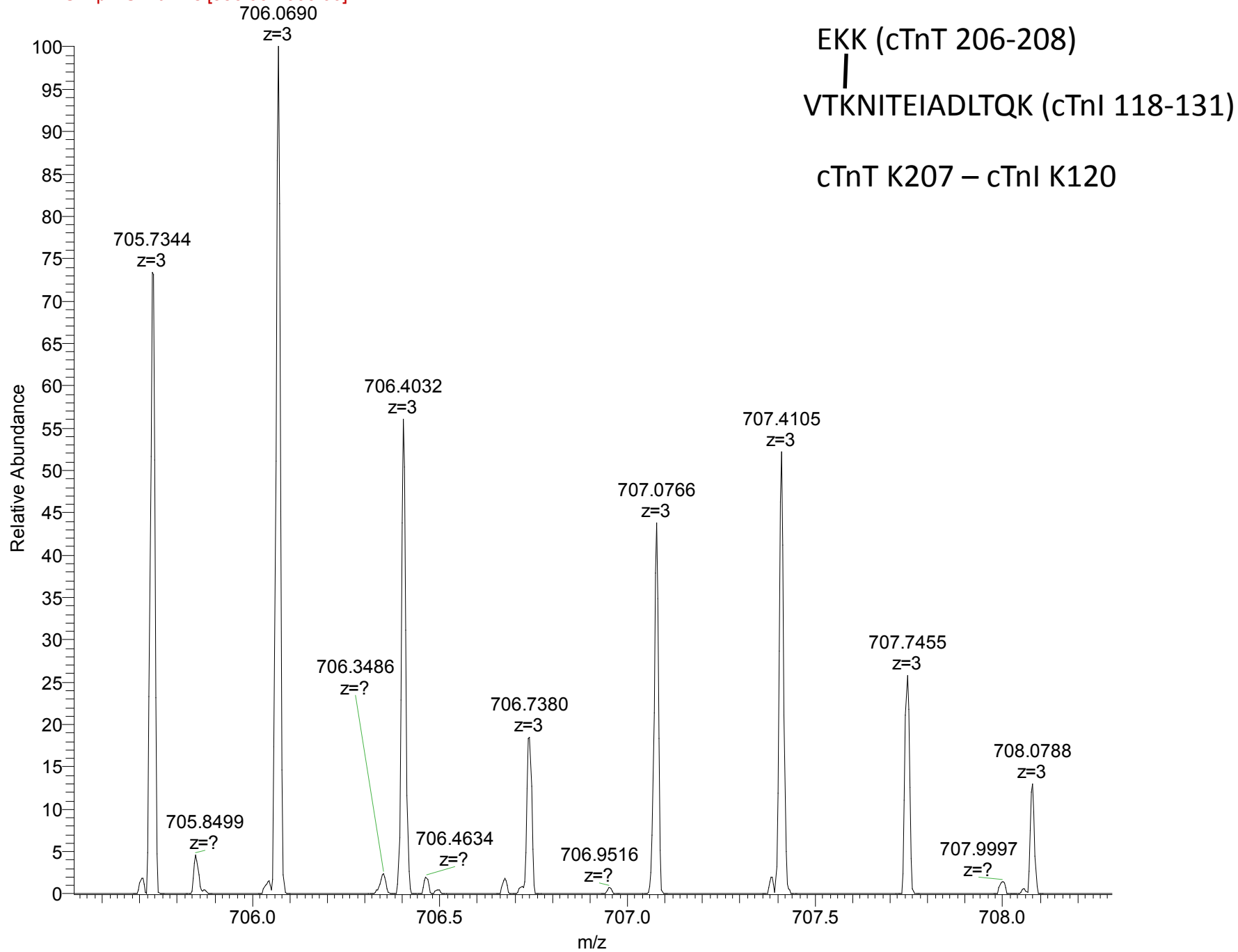
Score (73)
 identified signals (0.019)
 ion series (0.091)
 intensity Ratio (0.001)
 hits/possible ions (0.0)

EKK (cTnT 206-208)
 |
 YDIEAKVTK (cTnI 112-120)

cTnT K207 – cTnI K117



0% rel. intensity 100%

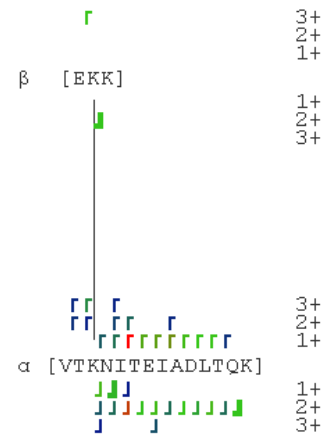
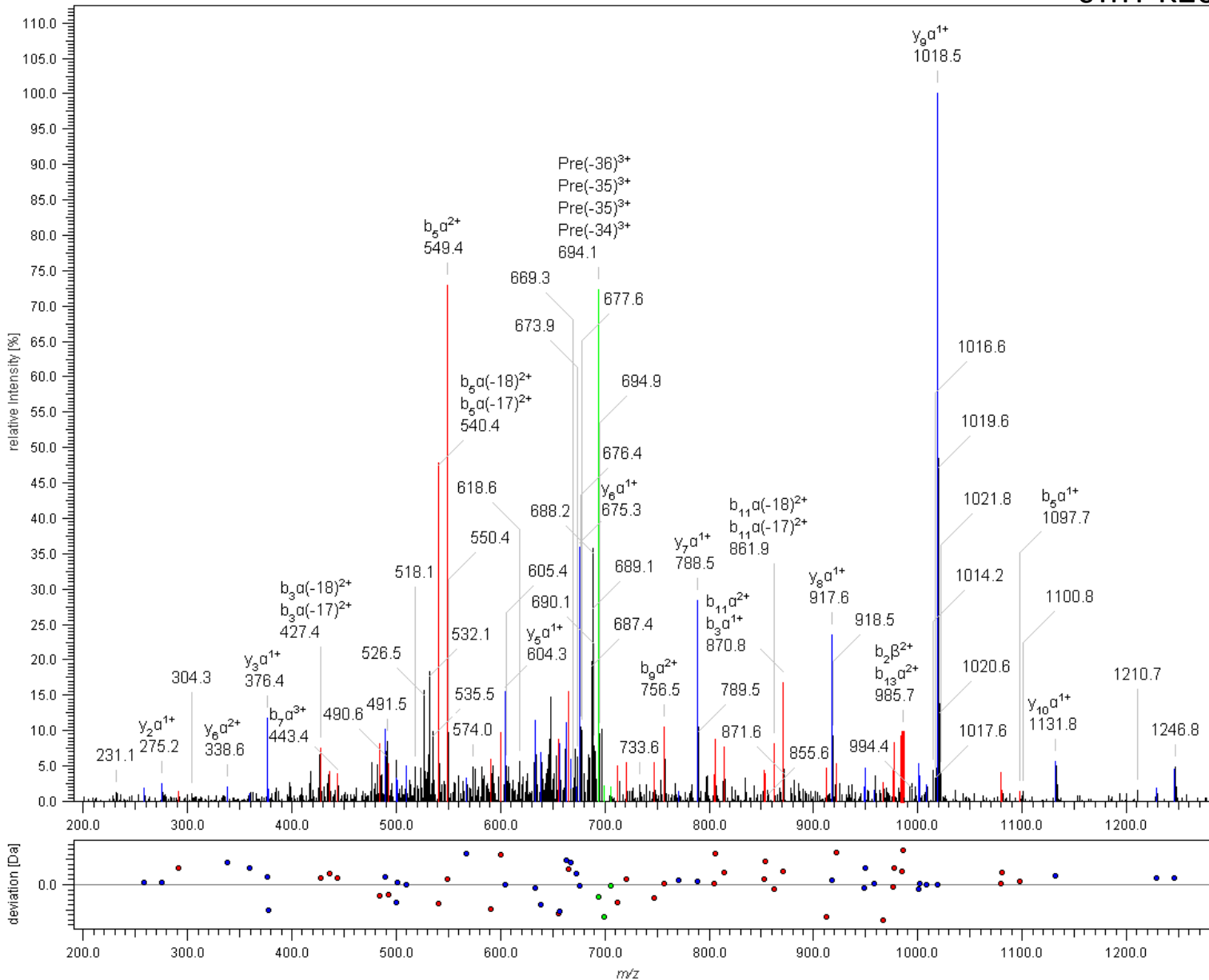


File: F:\Proje ... rad_4uL_1.mzXML_3.zhrs
 Scan: 10627
 theor. Mass (M + H+): 2115.1907
 meas. Mass (M + H+): 2115.1886
 Deviation -1.0 ppm
 m/z: 705.734375
 Charge: +3

Peptide β : [EKK] (K2)
 (>sp)P453.. from 206 to 208)
 Peptide α : [VTKNITEIADLTQK] (K3)
 (>sp)P194.. from 118 to 131)
 Crosslinker: DSS/BBS3

Score (106)
 identified signals (0.002)
 ion series (0.091)
 intensity Ratio (0.001)
 hits/possible ions (0.0)

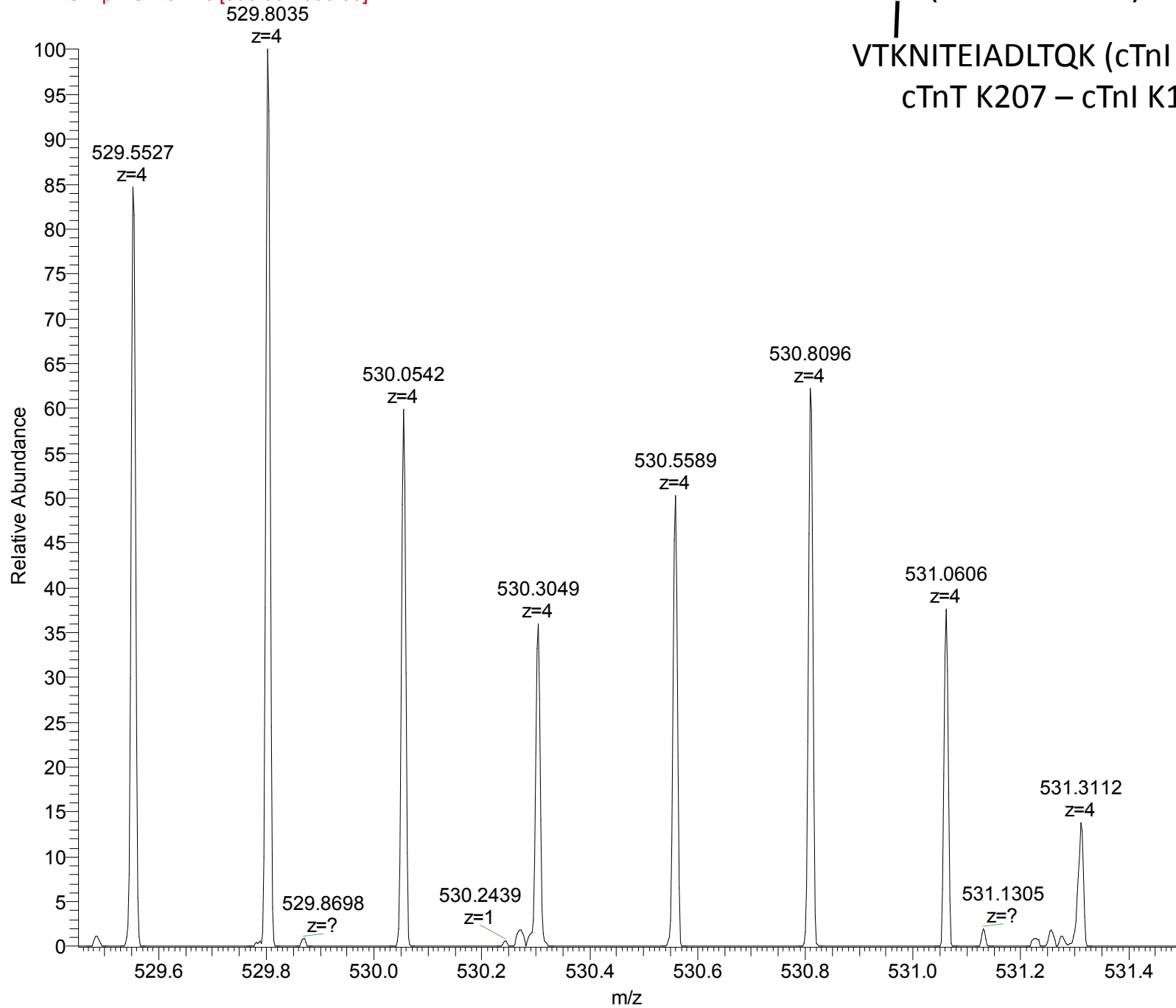
EKK (cTnT 206-208)
 |
 VTKNITEIADLTQK (cTnI 118-131)
 cTnT K207 – cTnI K120



EKK (cTnT 206-208)

VTKNITEIADLTQK (cTnI 118-131)

cTnT K207 – cTnI K120



File: F:\Proje ... rad_4uL_1.mzXML_8.zhrs
 Scan: 10651
 theor. Mass (M + H+): 2115.1907
 meas. Mass (M + H+): 2115.1903
 Deviation -0.2 ppm
 m/z: 529.553039550781
 Charge: +4

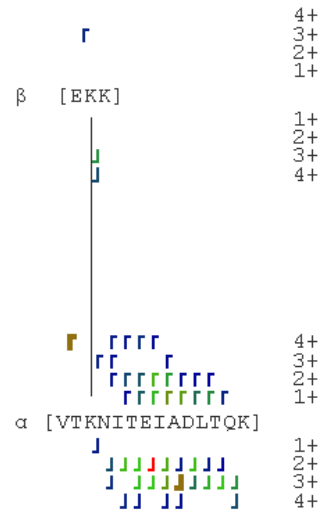
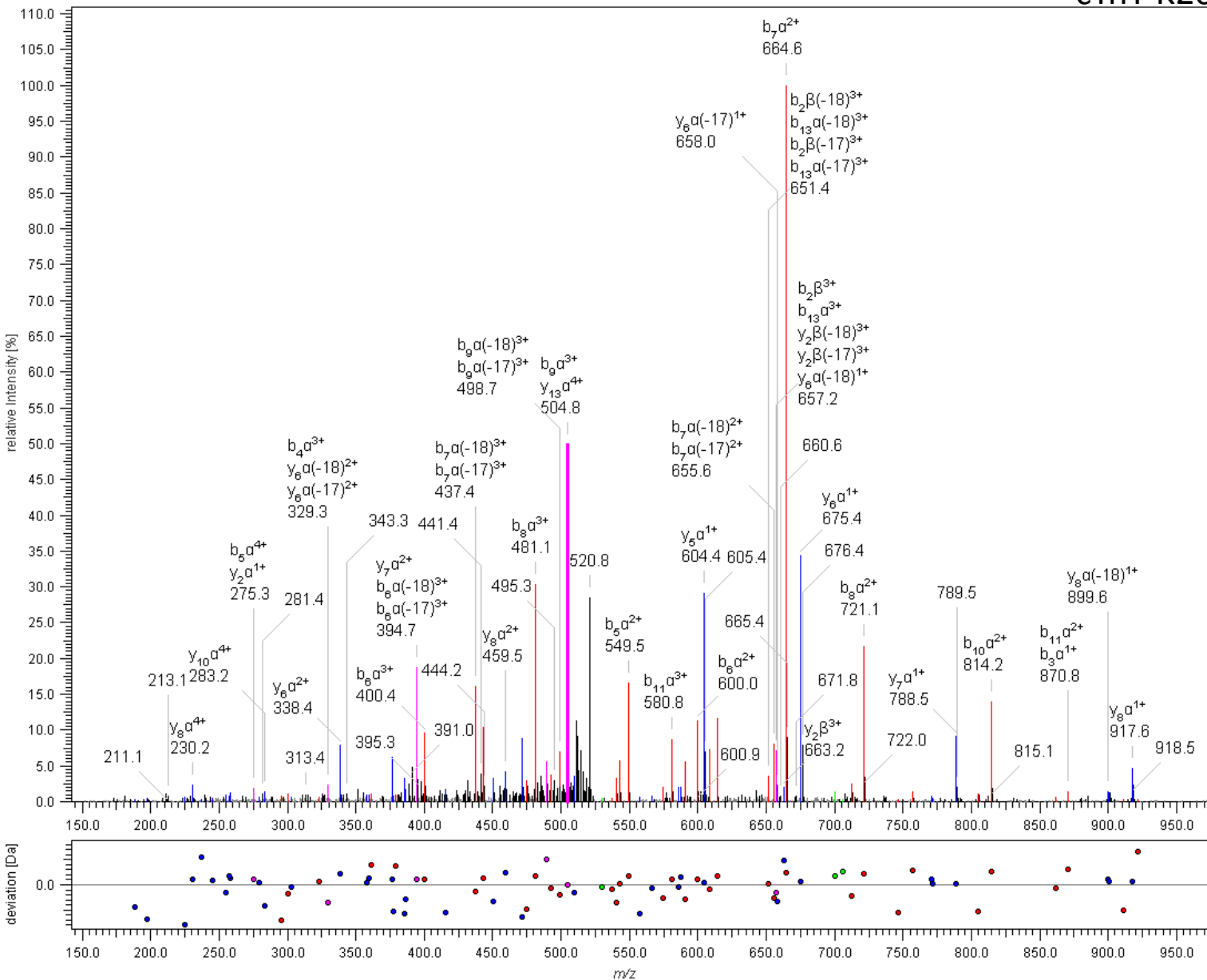
Peptide β : [EKK] (K2)
 (>sp)P453.. from 206 to 208
 Peptide α : [VTKNITEIADLTQK] (K3)
 (>sp)P194.. from 118 to 131
 Crosslinker: DSS/B53

Score (117)
 identified signals (0.0)
 ion series (0.091)
 intensity Ratio (0.0)
 hits/possible ions (0.0)

EKK (cTnT 206-208)

VTKNITEIADLTQK (cTnI 118-131)

cTnT K207 – cTnI K120

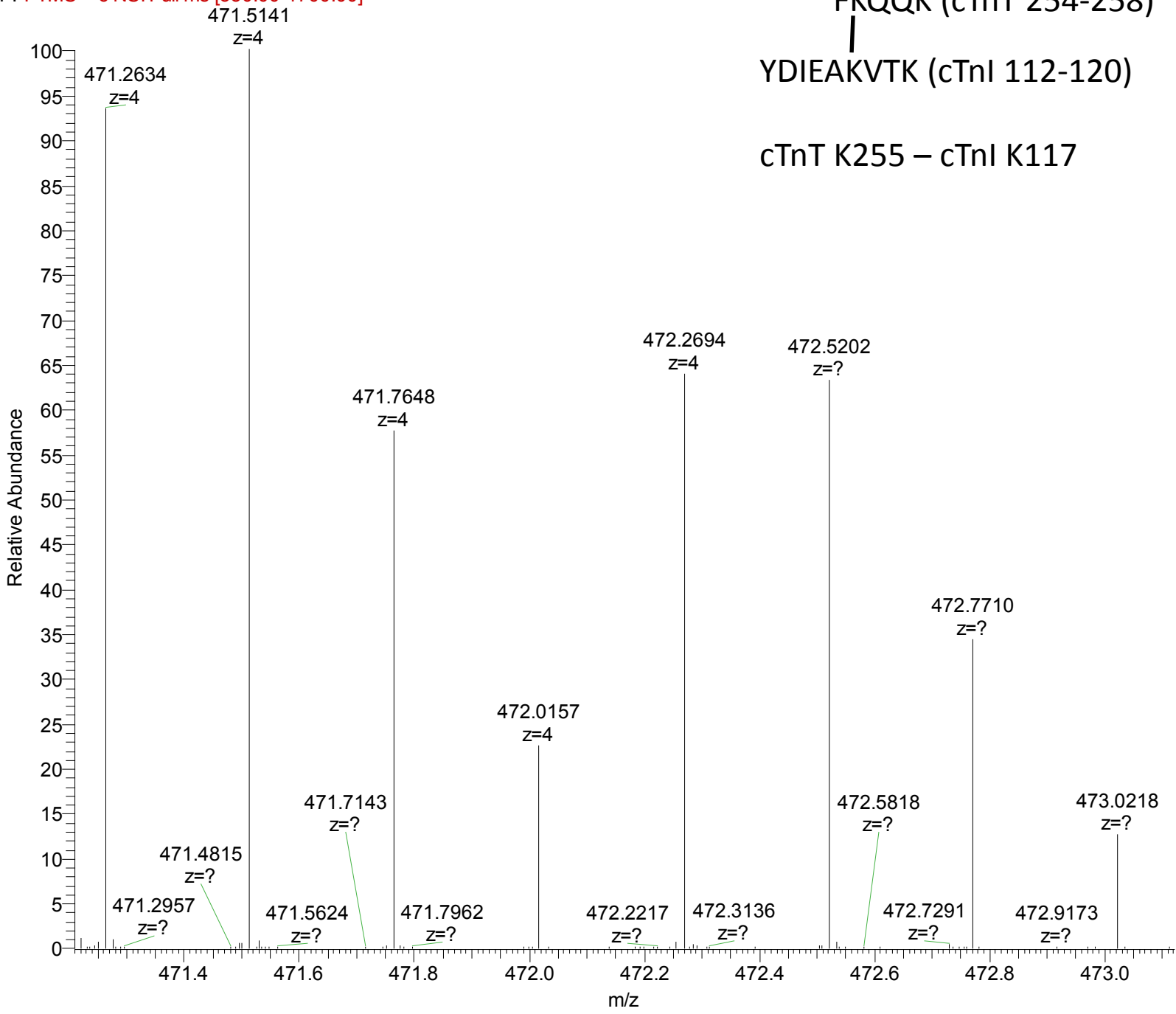


0% rel. intensity 100%

FKQVK (cTnT 254-258)

YDIEAKVTK (cTnI 112-120)

cTnT K255 – cTnI K117

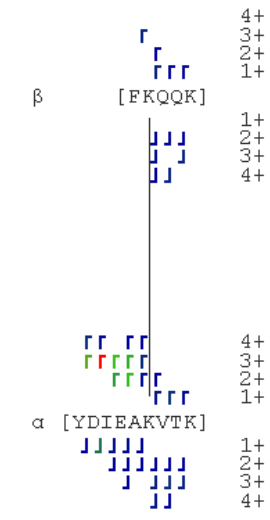
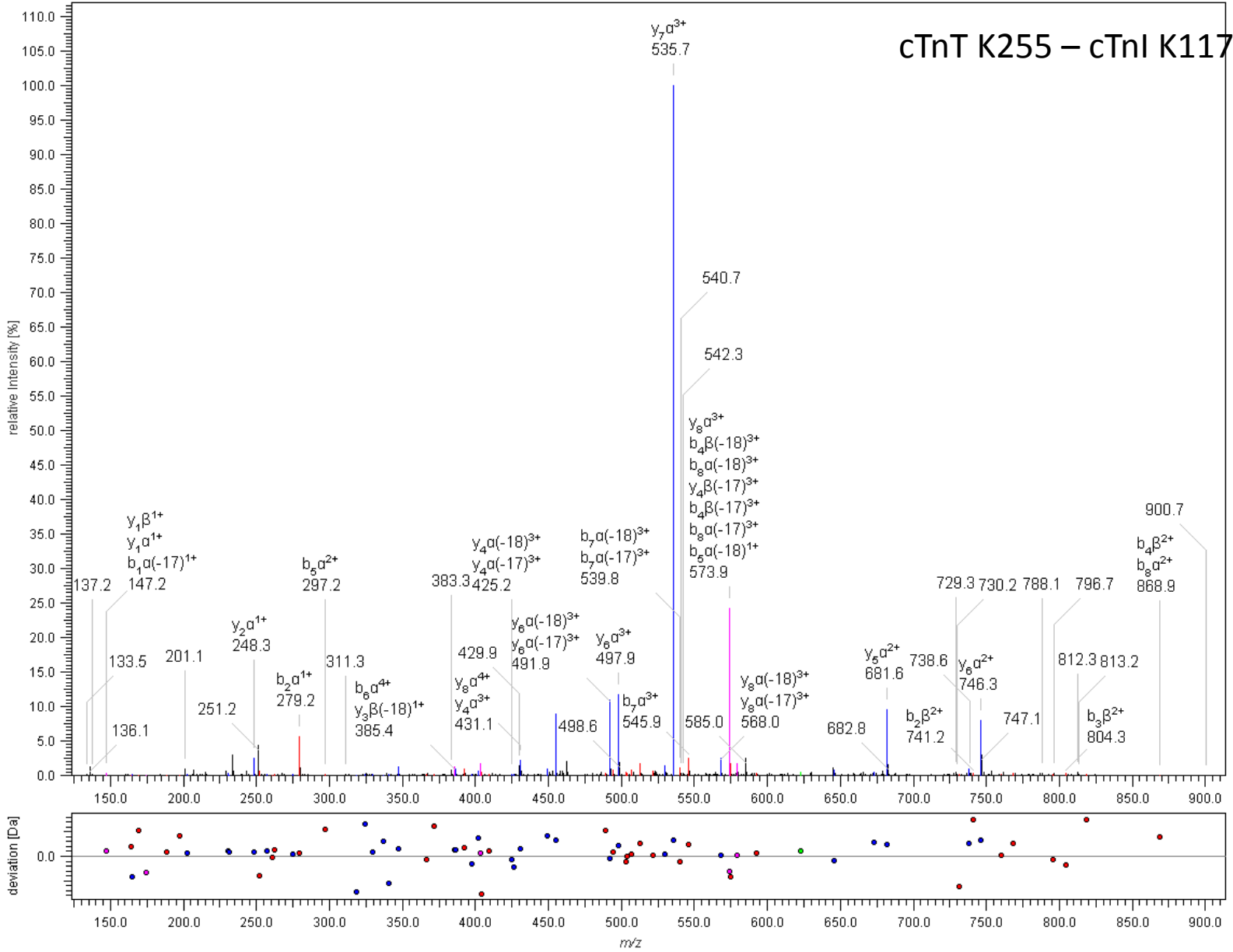


File: F:\Proje ... rad_5uL_1.mzXML_5.zhrs
 Scan: 12960
 theor. Mass (M + H+): 1882.032
 meas. Mass (M + H+): 1882.0297
 Deviation -1.3 ppm
 m/z: 471.262878417969
 Charge: +4

Peptide β: [FKQQK] (K2)
 (→sp|P453.. from 254 to 258)
 Peptide α: [YDIEAKVTK] (K6)
 (→sp|P194.. from 112 to 120)
 Crosslinker: DSS/BS3

Score (172)
 identified signals (0.0)
 ion series (0.0)
 intensity Ratio (0.002)
 hits/possible ions (0.0)

FKQQK (cTnT 254-258)
|
YDIEAKVTK (cTnI 112-120)

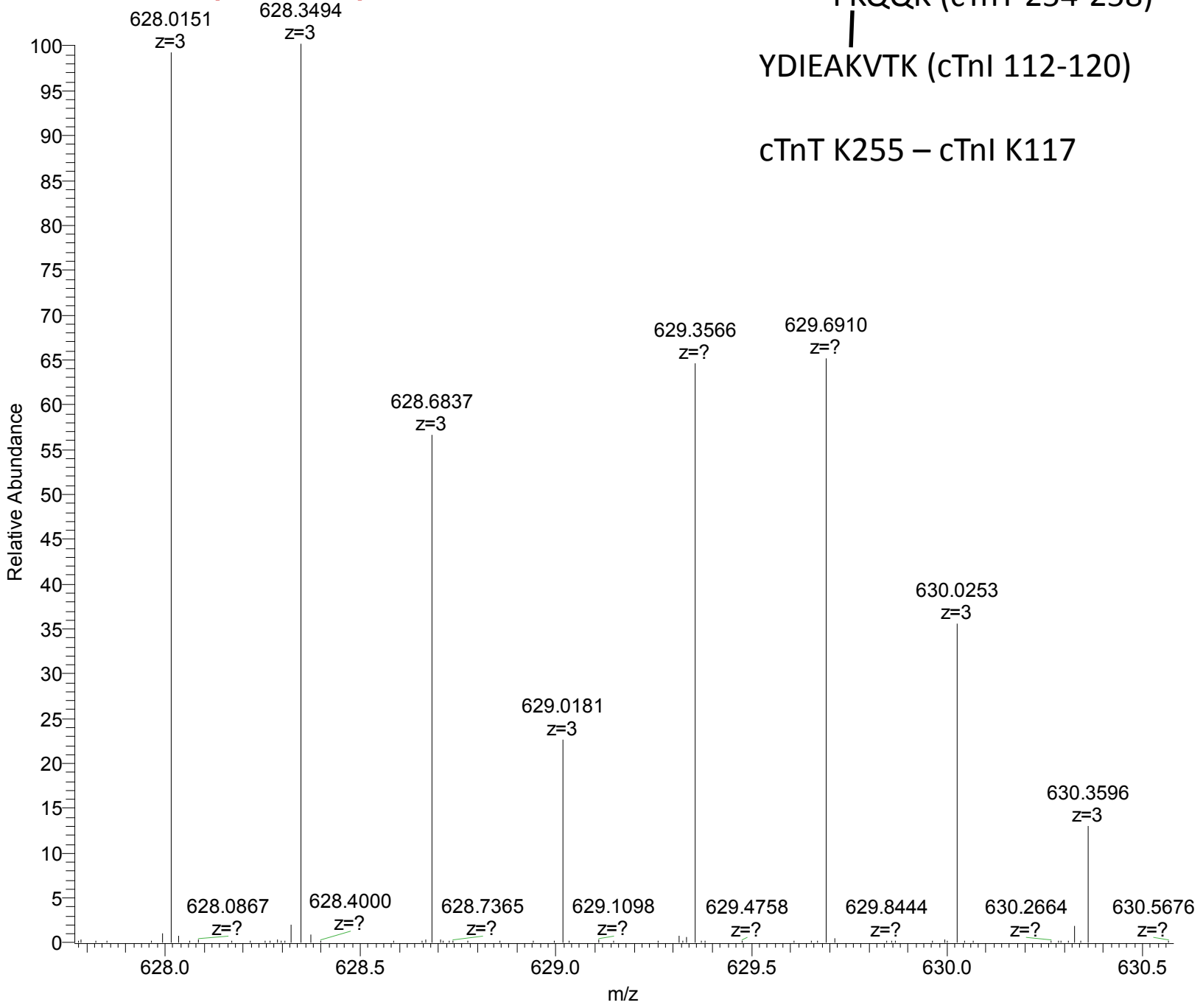


0% rel. intensity 100%

FKQQK (cTnT 254-258)

YDIEAKVTK (cTnI 112-120)

cTnT K255 – cTnI K117



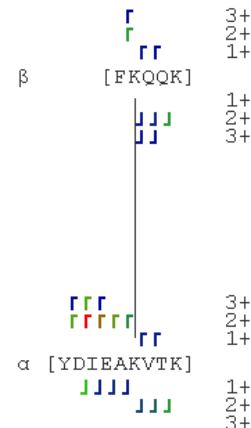
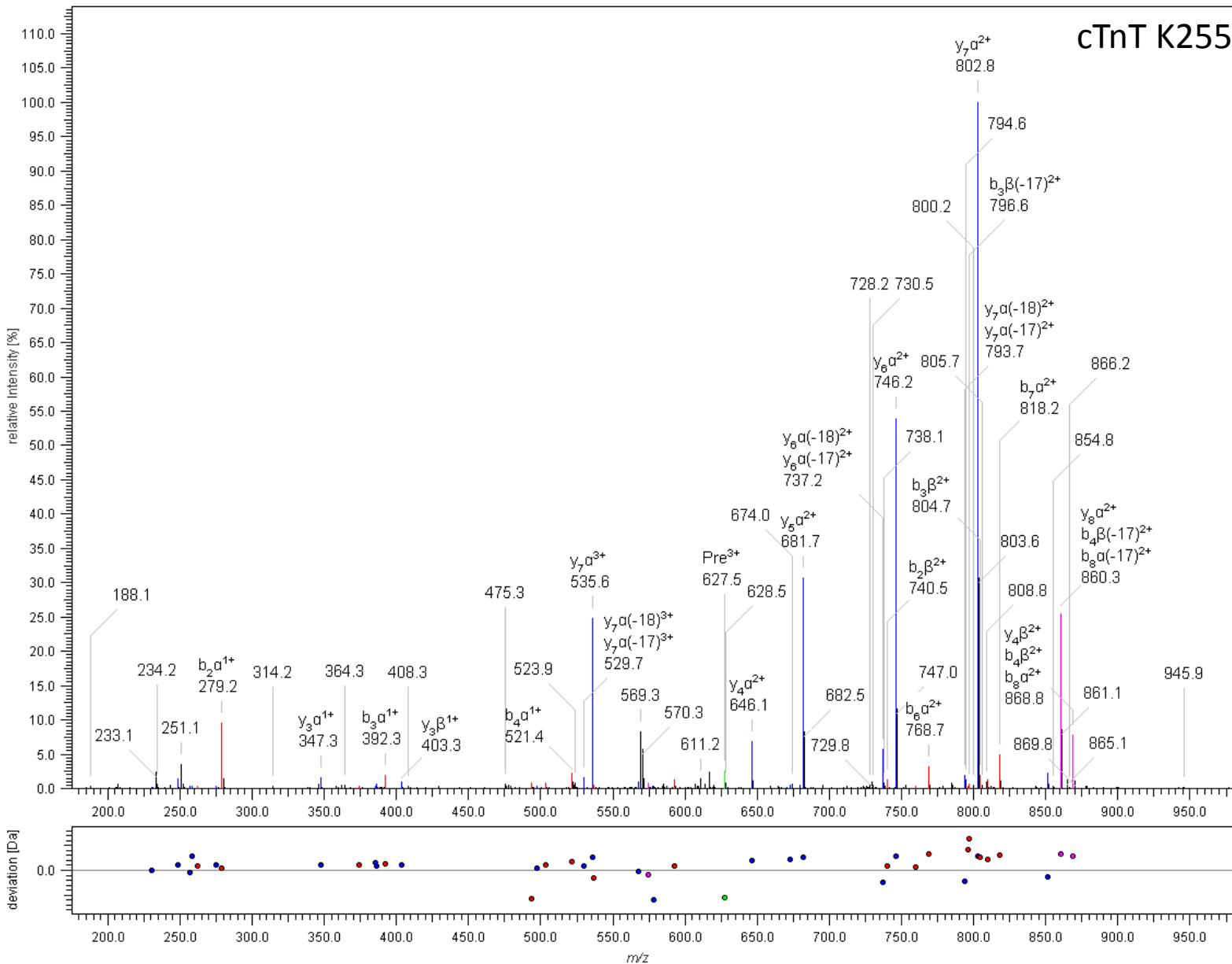
File: F:\Proje ... rad_5uL_1.mzXML_2.zhrs
 Scan: 12968
 theor. Mass (M + H+): 1882.032
 meas. Mass (M + H+): 1882.0327
 Deviation 0.3 ppm
 m/z: 628.015747070313
 Charge: +3

Peptide β : [FKQQK] (K2)
 (\rightarrow sp|P453.. from 254 to 258)
 Peptide α : [YDIEAKVTK] (K6)
 (\rightarrow sp|P194.. from 112 to 120)
 Crosslinker: DSS/BS3

Score (145)
 identified signals (0.001)
 ion series (0.0)
 intensity Ratio (0.002)
 hits/possible ions (0.0)

FKQQK (cTnT 254-258)
 |
 YDIEAKVTK (cTnI 112-120)

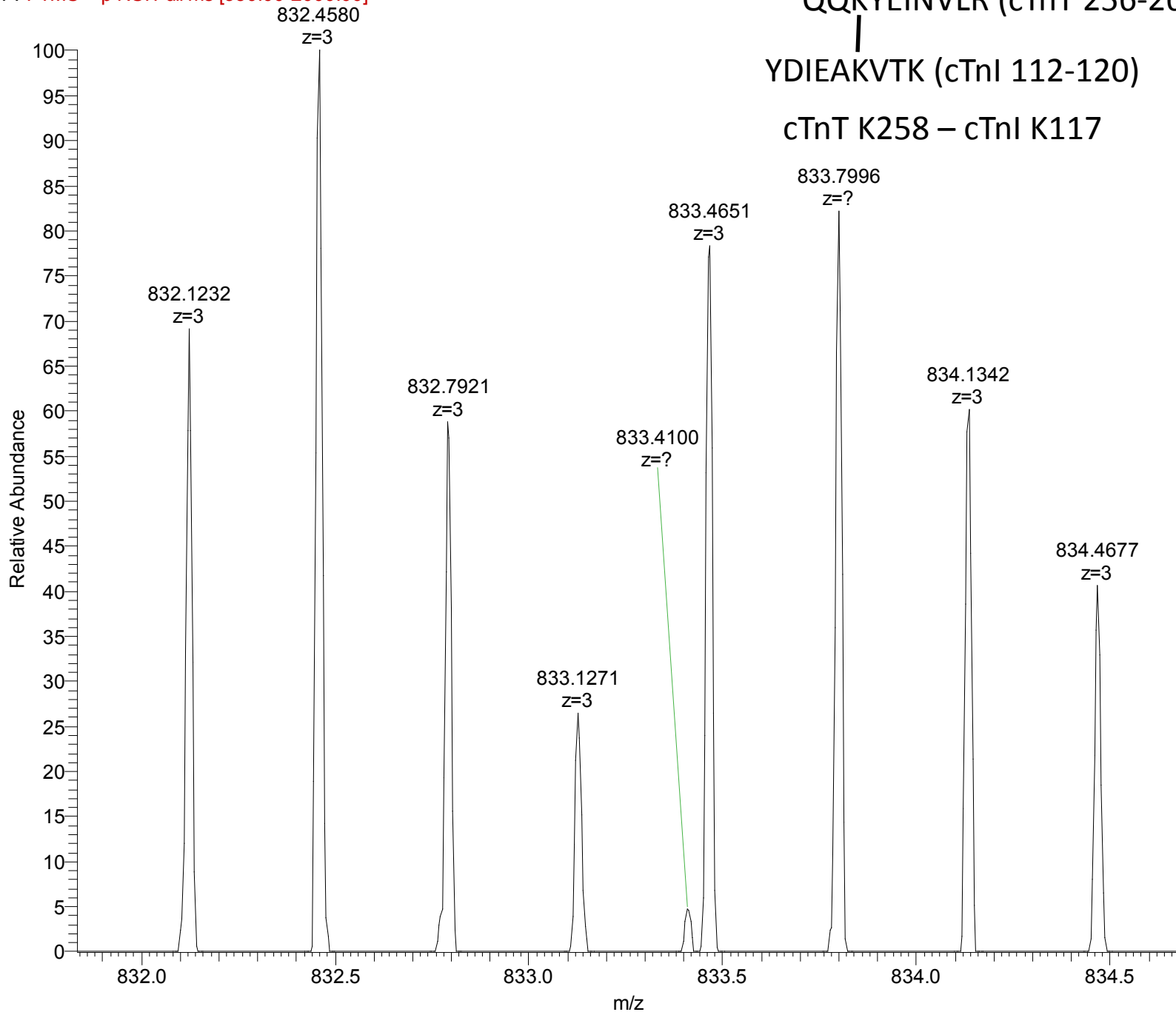
cTnT K255 – cTnI K117



QQKYEINVLR (cTnT 256-265)

YDIEAKVTK (cTnI 112-120)

cTnT K258 – cTnI K117

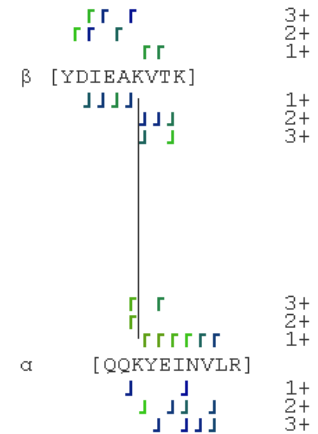
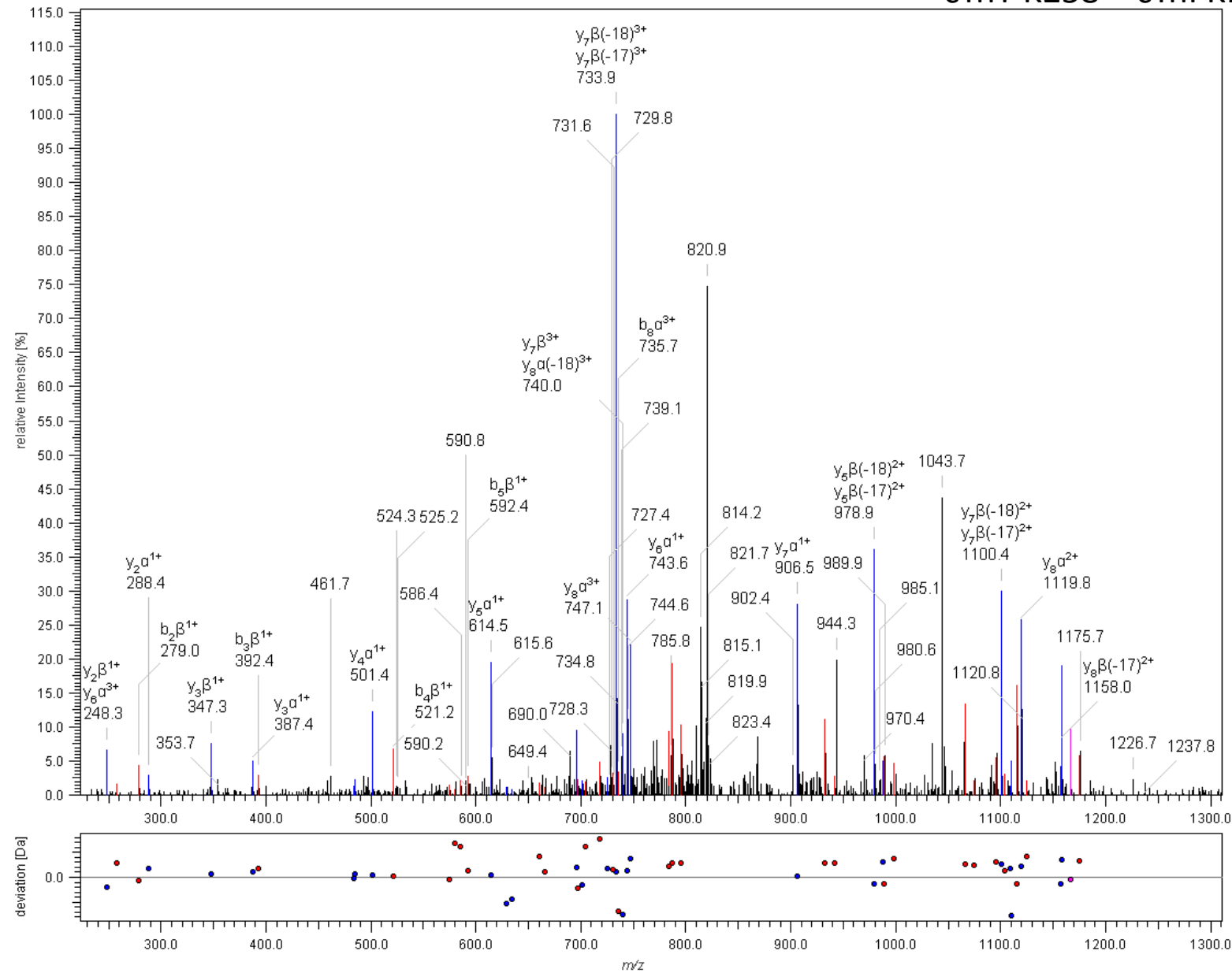


File: F:\Proje ... rad_4uL_1.mzXML_3.zhrs
 Scan: 9988
 theor. Mass (M + H+): 2494.3552
 meas. Mass (M + H+): 2494.3515
 Deviation -1.5 ppm
 m/z: 832.122009277344
 Charge: +3

Peptide β : [YDIEAKVTK] (K6)
 (>sp)P194.. from 112 to 120
 Peptide α : [QQKYEINVLR] (K3)
 (>sp)P453.. from 256 to 265
 Crosslinker: DSS/BS3

Score (99)
 identified signals (0.012)
 ion series (0.0)
 intensity Ratio (0.011)
 hits/possible ions (0.001)

QQKYEINVLR (cTnT 256-265)
 |
 YDIEAKVTK (cTnI 112-120)
 cTnT K258 – cTnI K117

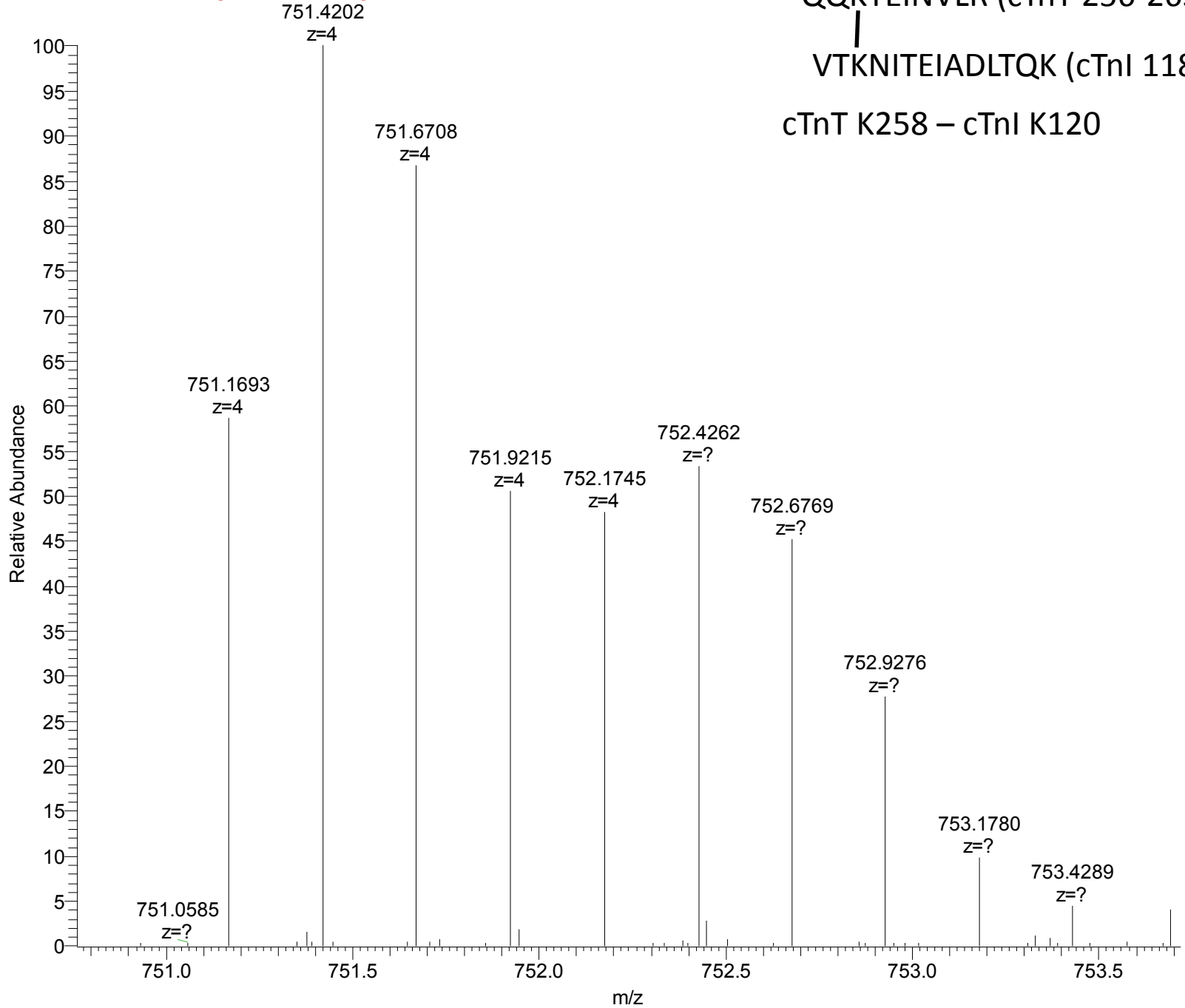


0% rel. intensity 100%

QQKYEINVLR (cTnT 256-265)

VTKNITEIADLTQK (cTnI 118-131)

cTnT K258 – cTnI K120

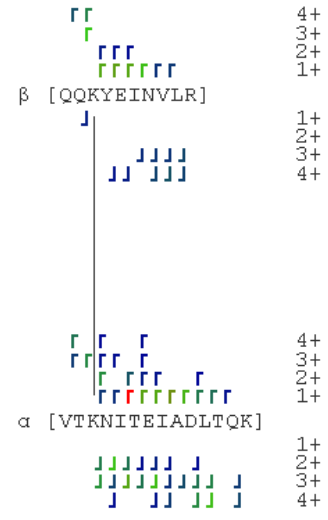
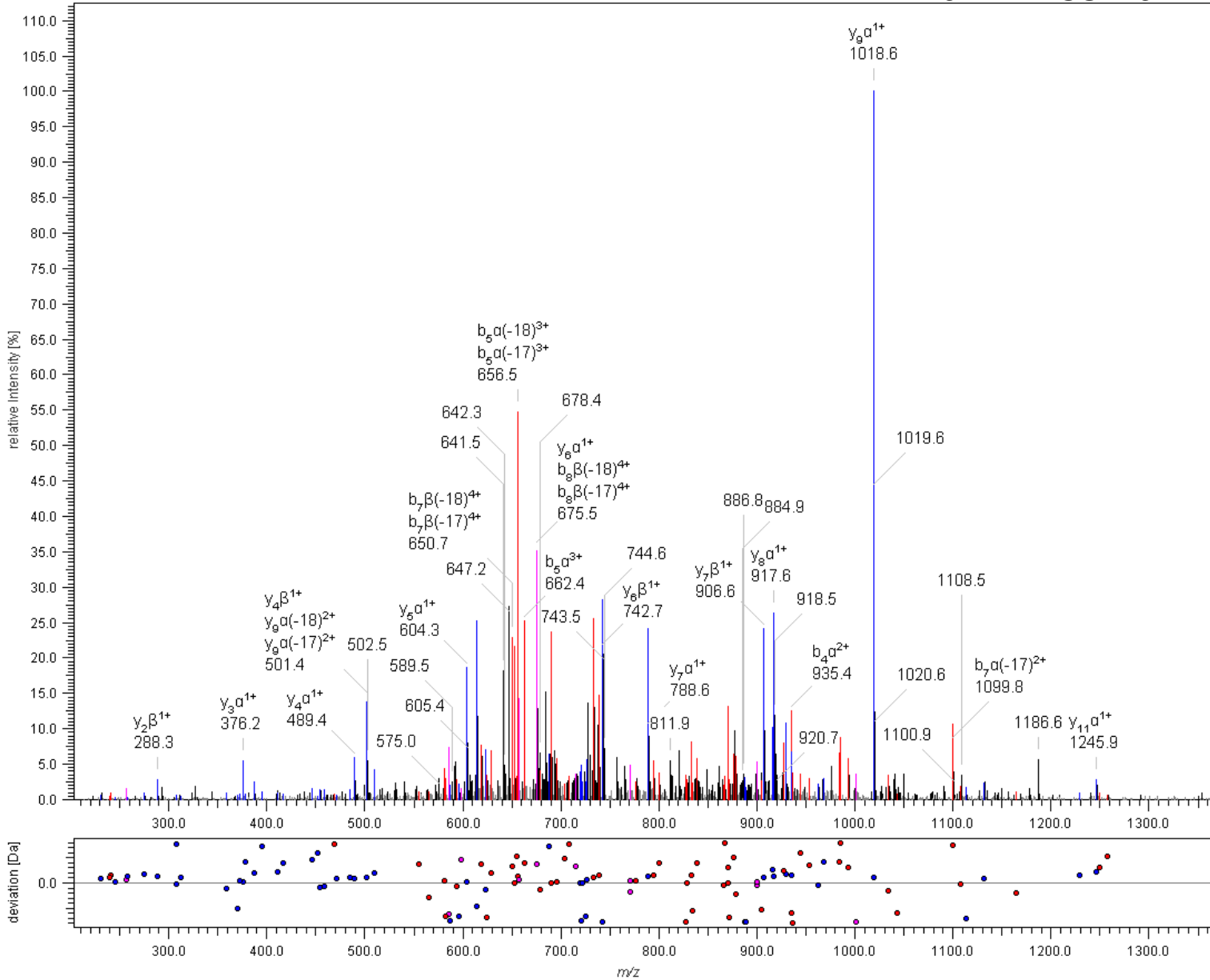


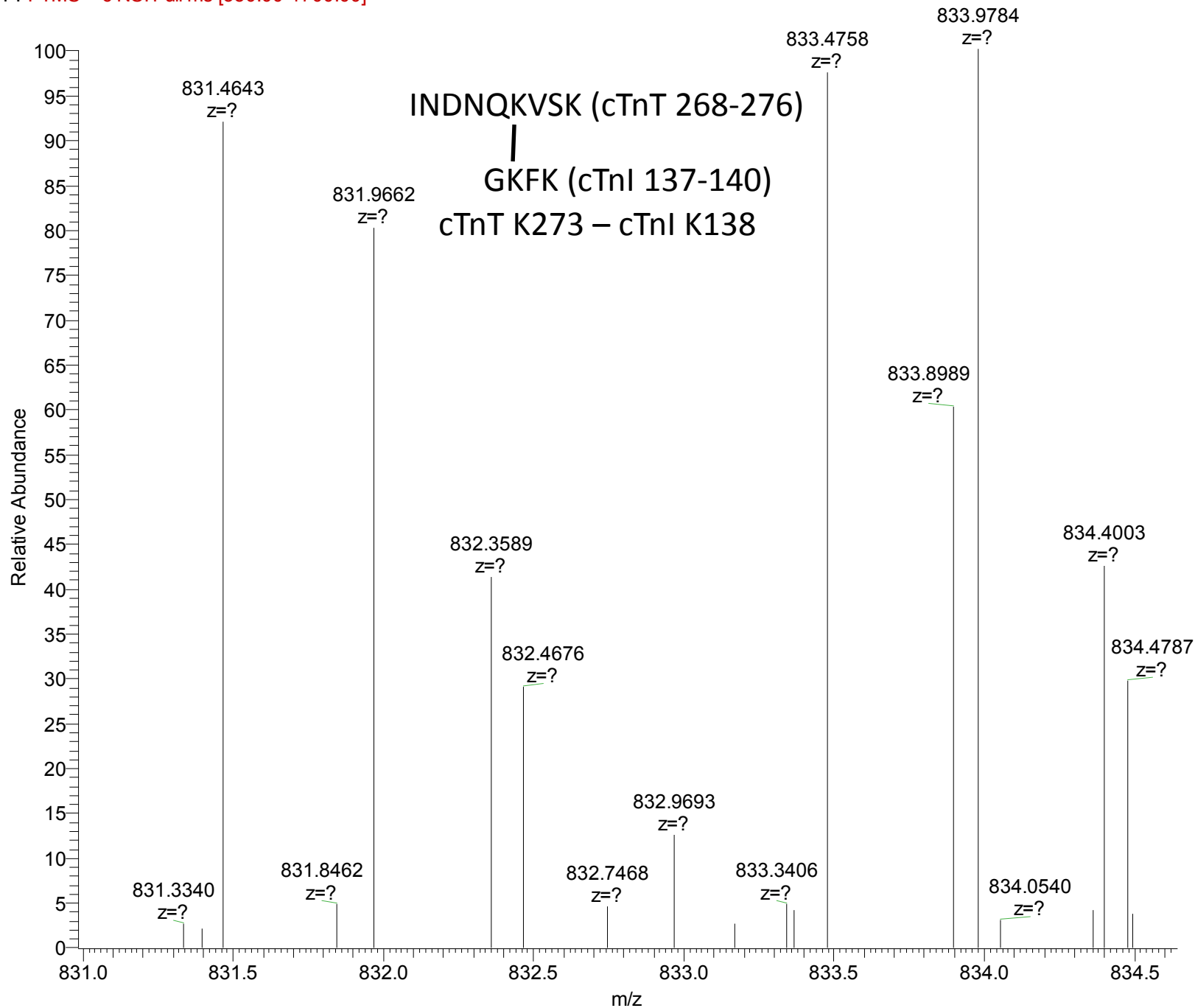
File: F:\Proje ... rad_5uL_1.mzXML_9.zhrs
 Scan: 21981
 theor. Mass (M + H⁺): 3001.6568
 meas. Mass (M + H⁺): 3001.6542
 Deviation -0.9 ppm
 m/z: 751.169006347656
 Charge: +4

Peptide β : [QQKYEINVLR] (K3)
 (>sp|P453.. from 256 to 265)
 Peptide α : [VTKNITEIADLTQK] (K3)
 (>sp|P194.. from 118 to 131)
 Crosslinker: DSS/BBS3

Score (127)
 identified signals (0.006)
 ion series (0.0)
 intensity Ratio (0.003)
 hits/possible ions (0.001)

QQKYEINVLR (cTnT 256-265)
 |
 VTKNITEIADLTQK (cTnI 118-131)
 cTnT K258 – cTnI K120





File: F:\Proje ... rad_5uL_1.mzXML_0.zhrs
 Scan: 8270
 theor. Mass (M + H+): 1661.9221
 meas. Mass (M + H+): 1661.9188
 Deviation -1.9 ppm
 m/z: 831.463073730469
 Charge: +2

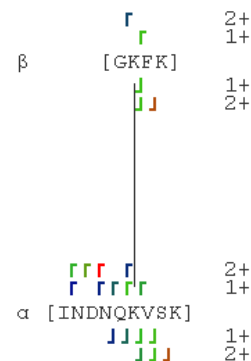
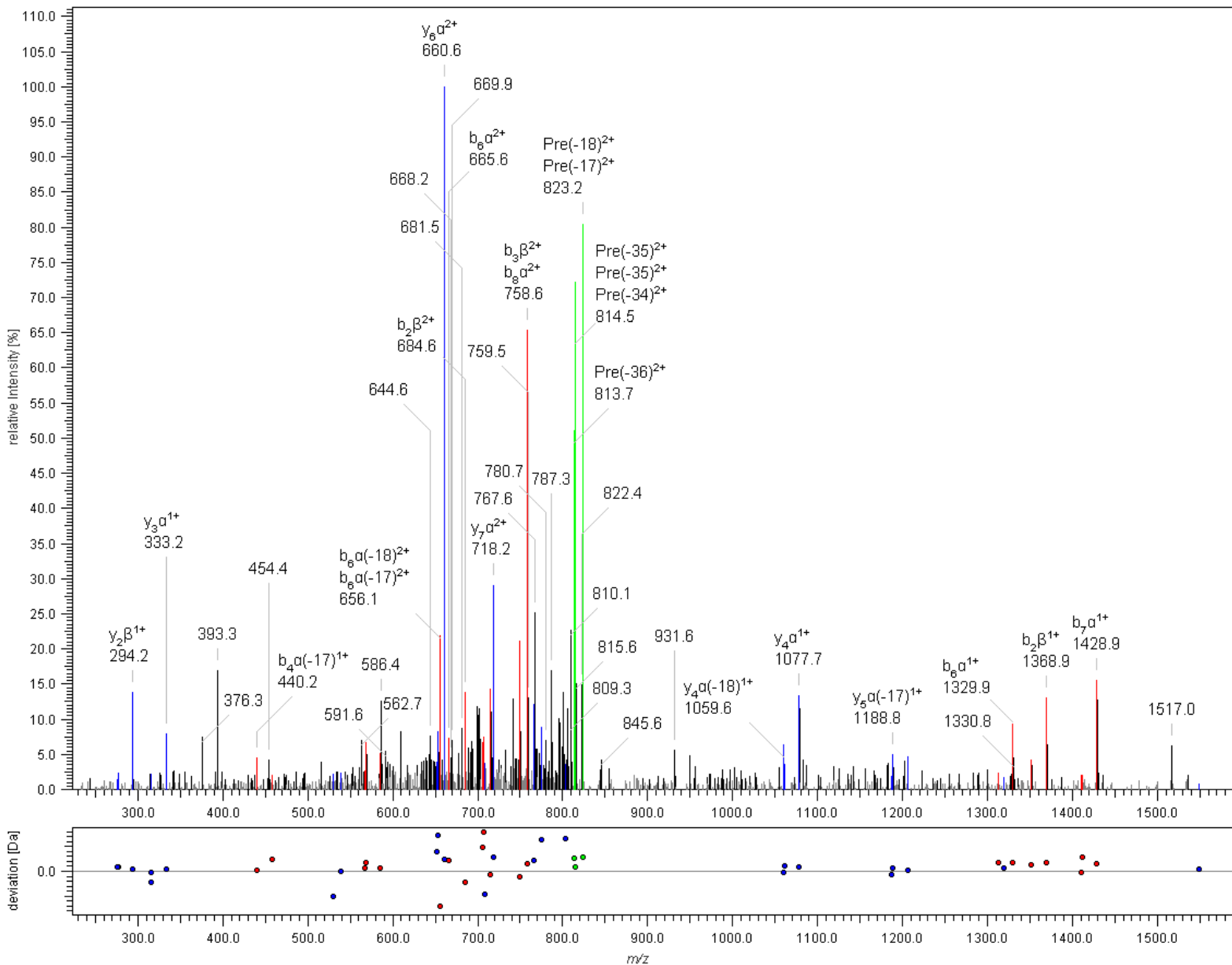
Peptide β : [GKFK] (K2)
 (\rightarrow sp|P194... from 137 to 140)
 Peptide α : [INDNQKVS] (K6)
 (\rightarrow sp|P453... from 268 to 276)
 Crosslinker: DSS/BS3

Score (107)
 identified signals (0.014)
 ion series (0.016)
 intensity Ratio (0.002)
 hits/possible ions (0.0)

INDNQKVS (cTnT 268-276)

GKFK (cTnI 137-140)

cTnT K273 – cTnI K138



[AKVTGR] - {MDDIYK} TnT K282 – TnC K6

[M+3H]³⁺ *m/z* exptl. 518.2721

[M+H]⁺ *m/z* exptl. 1552.8019, calc. 1552.8040

Mass error -1.32 ppm

518.2721

518.6067

519.6145

519.9487

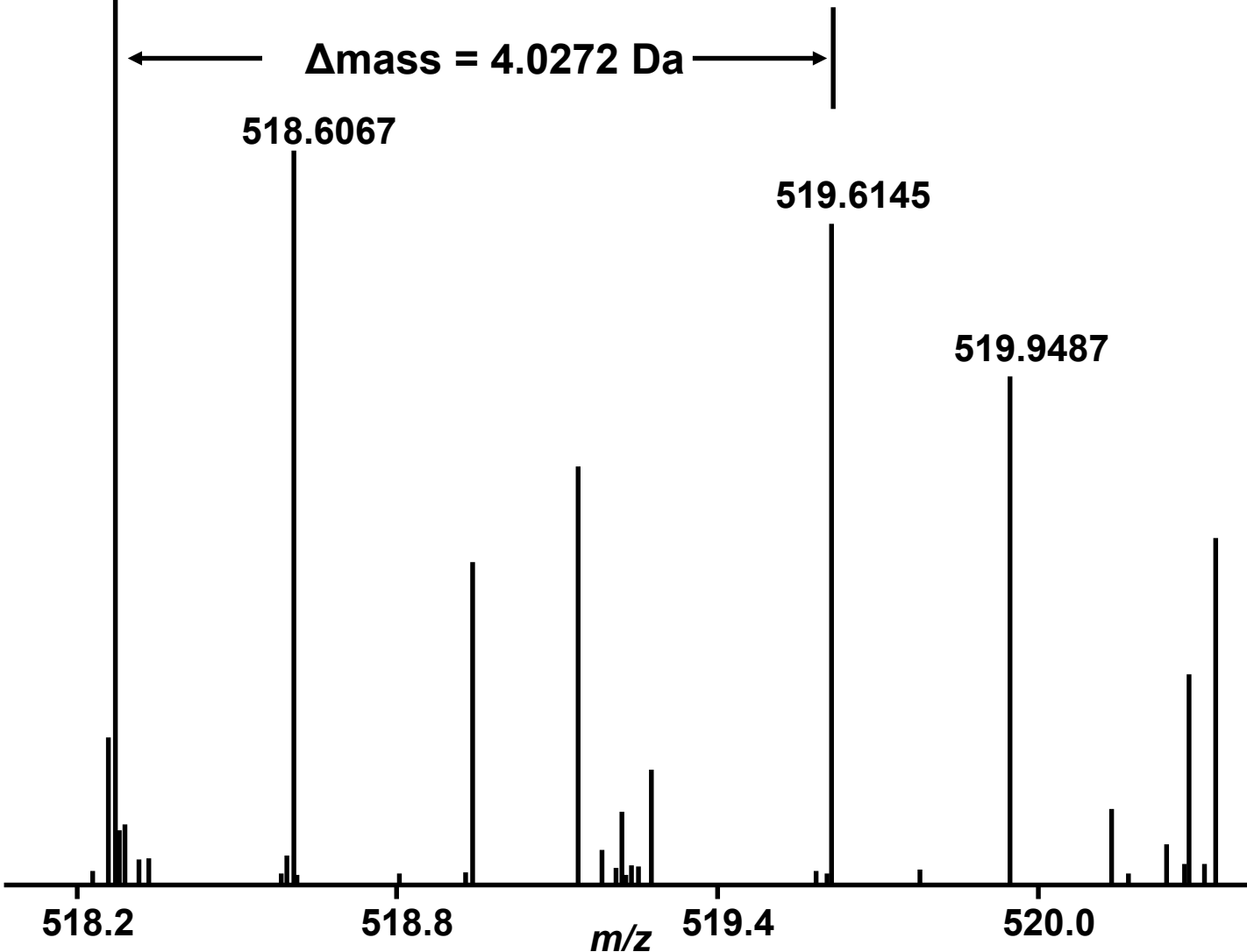
← $\Delta\text{mass} = 4.0272 \text{ Da}$ →

518.2

518.8

m/z 519.4

520.0

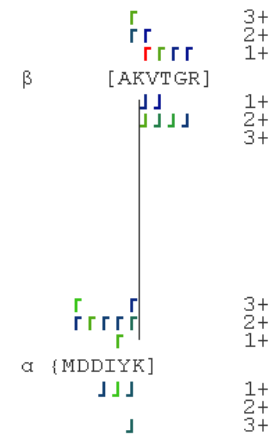
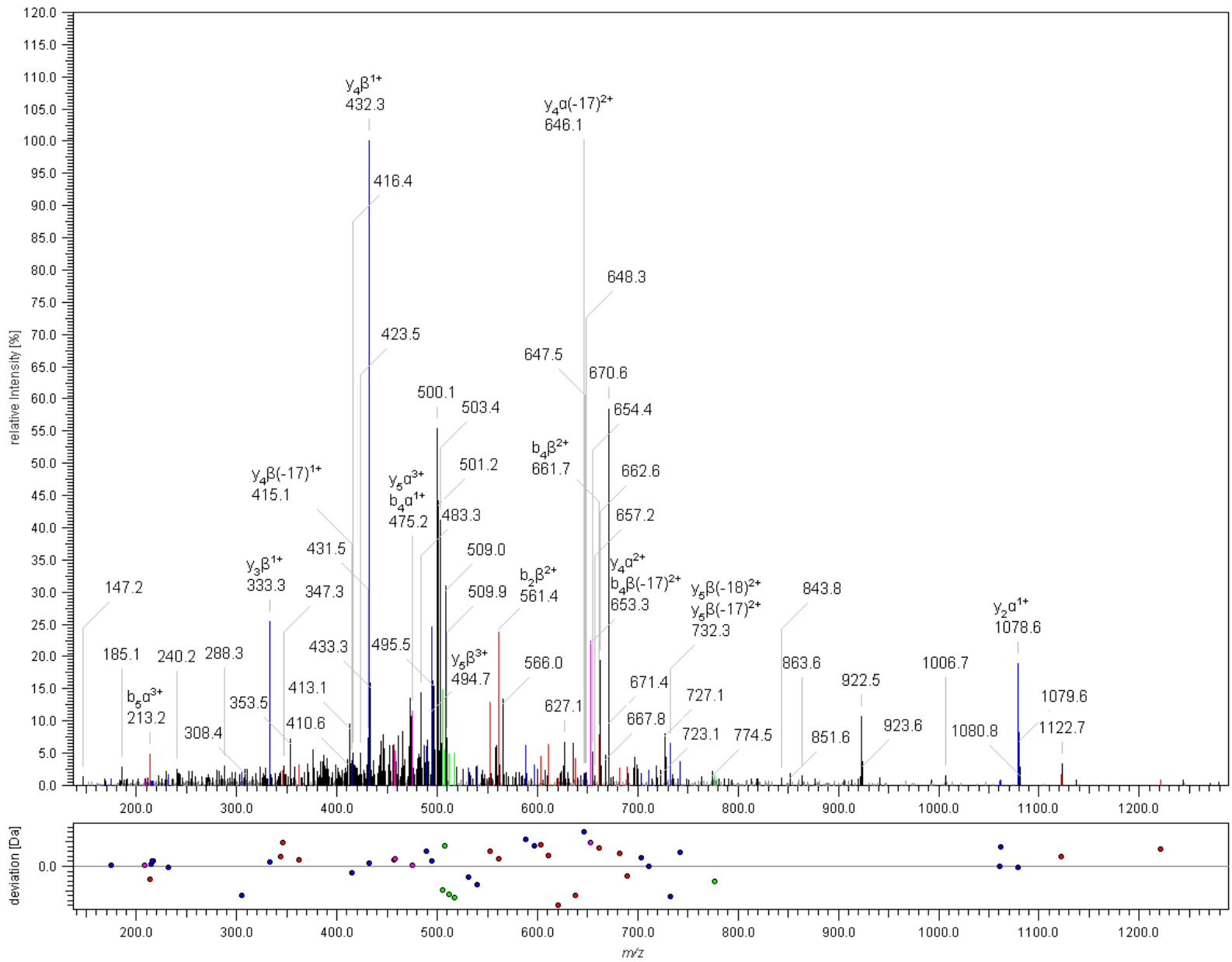


Detail Window

File: C:\Users ... rad_5uL_1.mzXML_7.zhrs
 Scan: 12778
 theor. Mass (M + H+): 1552.804
 meas. Mass (M + H+): 1552.8037
 Deviation -0.1 ppm
 m/z: 518.272766113281
 Charge: +3

Peptide β : [AKVTGR] (K2)
 (>sp)P453.. from 281 to 286
 Peptide α : [MDDIYK] (K6)
 (>sp)P633.. from 0 to 6
 Crosslinker: DSS/BS3

Score (129)
 identified signals (0.01)
 ion series (0.0)
 intensity Ratio (0.008)
 hits/possible ions (0.0)



0% rel. intensity 100%