PSM scan report

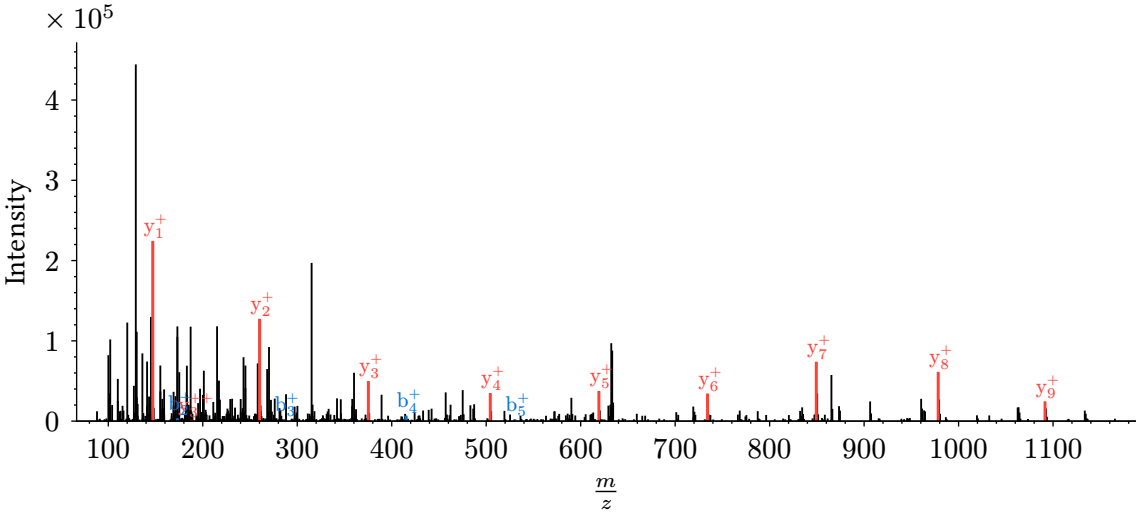
20120906_balliau_extract_1_A01_urnb-1

Scan index=5734 mh=1263.558 mz=632.2827 charge=2 rt=1305.67s

ATLEDDDEDLK

GRMZM2G103197_P01

+275 CMRNTKDTKDLARRAIGGAVVAFLR**ATLEDDDEDLK**VVLENRPGLSPAVLDPVGHDL +331



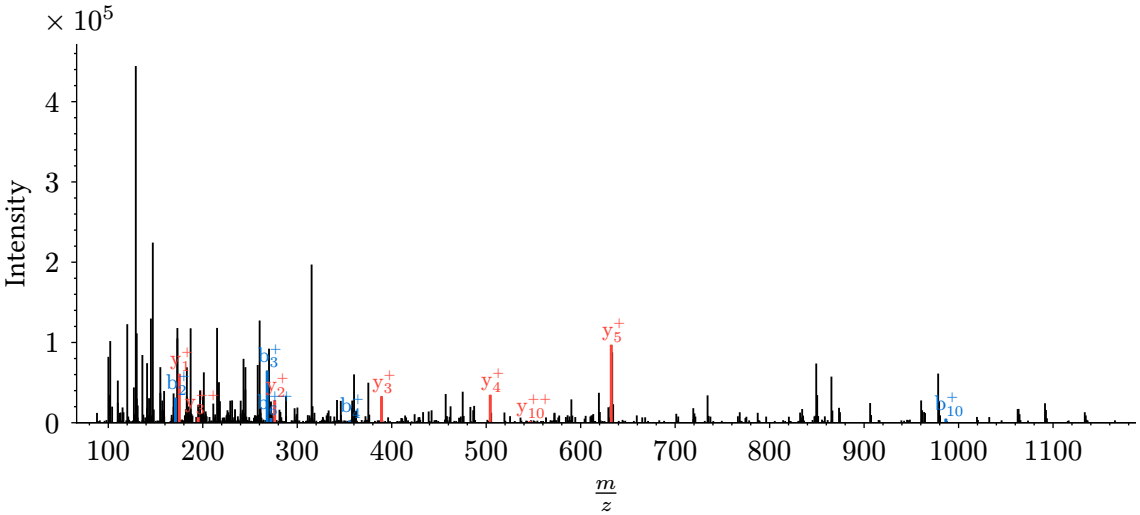
hyperscore 40.51
peptide length 11
peptide mh 1263.55868
charge 2
Δ mz −0.00032
Δ mh −0.00065

Spoms
isotope error 0
bracket [A][T]LEDDDED[L][K]
nam −0.000651506931944823
spc 11
score 52

AVPSTSSKDITR

GRMZM2G313909_P01

+4 ARQGNTVRRKAERPGATSVWPPAL**AVPSTSSKDITR**ATKSPSTMQKSNNLSTRPGIEKAA +63

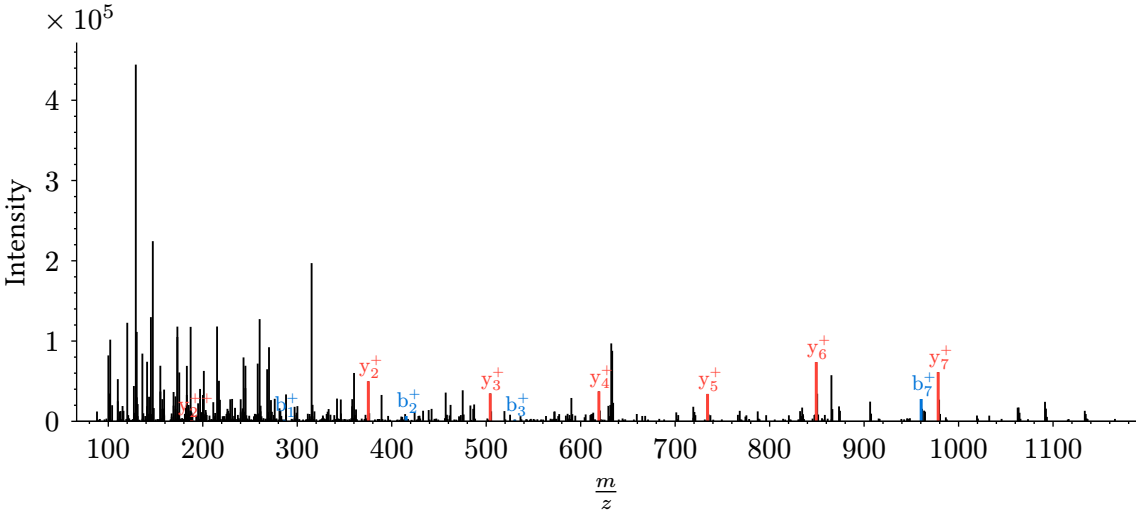


hyperscore 30.82
peptide length 12
peptide mh 1261.67465
charge 2
Δ mz 0.94169
Δ mh 1.88338

Spoms
isotope error -
bracket [A][V]P[S][T][S][S]KDITR
nam 0.004224858632369433
spc 10
score 45

[+172.08]-LEDDDEAF[+138.10]

GRMZM2G074314_P01
+360 EAYAIYDQEIGYCQGMSDLLAPLLAVLEDDDEAFWCFAGFMRKARHNFRLDEVGIRRQLN +419
GRMZM2G074314_P02
+355 EAYAIYDQEIGYCQGMSDLLAPLLAVLEDDDEAFWCFAGFMRKARHNFRLDEVGIRRQLN +414

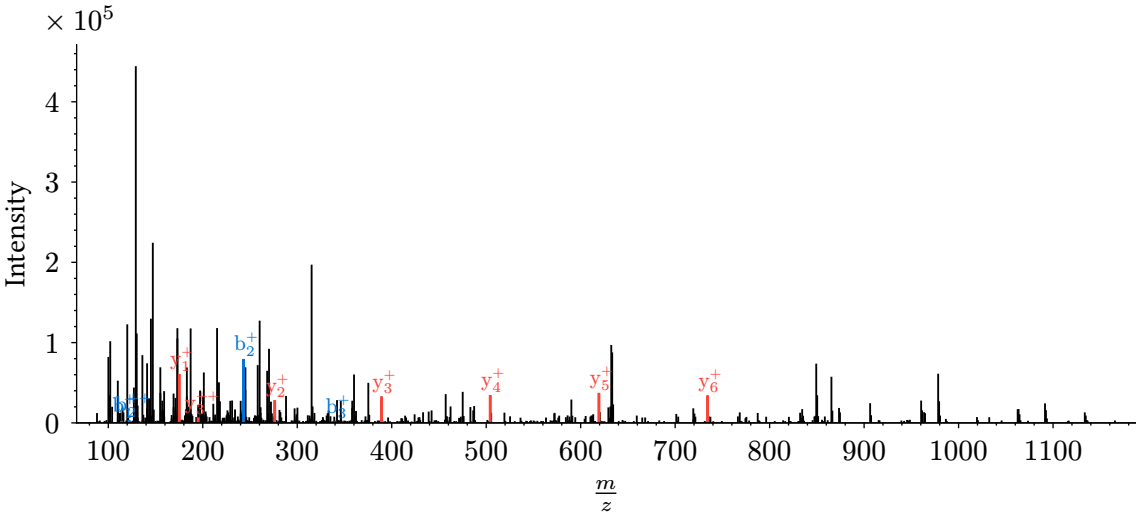


hyperscore 27.82
peptide length 8
peptide mh 1263.55344
charge 2
Δ mz 0.00229
Δ mh 0.00459

Spoms
isotope error 0
bracket [172.08]LEDDDEAF[138.10]
nam −0.00197573180935251
spc 10
score 44

[+188.17]?LEPDDDLTR

GRMZM5G878378_P01
+67 SSSSTPSLYLSHLALERLGLPAGAAVLEPDDDLTRLQGEVARDEVAARPPATARASLSSS +126



hyperscore 27.77
peptide length 9
peptide mh 1073.51094
charge 2
Δ mz 95.02355
Δ mh 190.04709

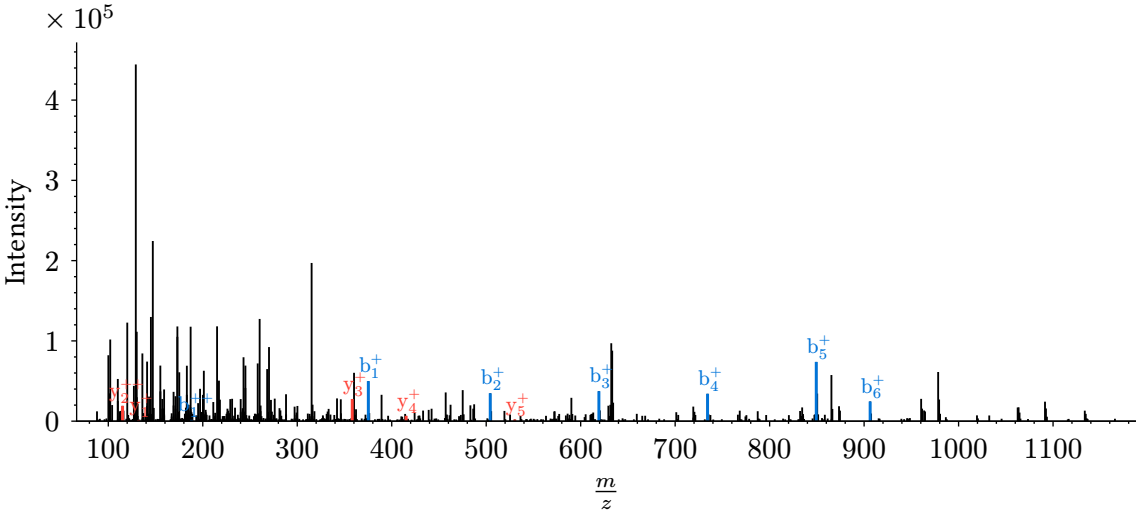
Spoms
isotope error -
bracket [527.36]DDDLTR
nam −0.015971941433690517
spc 8
score 45

Spoms post
bracket [L][E]PDDDLTR
nam 188.16793614221228
spc 10
score 49

[+259.19]-DEDDDGEPI

GRMZM2G023418_P01

+44 KGKKGGKAAAPDDDDYEPPPPPPPAADEDDDGEPINLVFTGKKKKKKGATPAAPFSAFSA +103



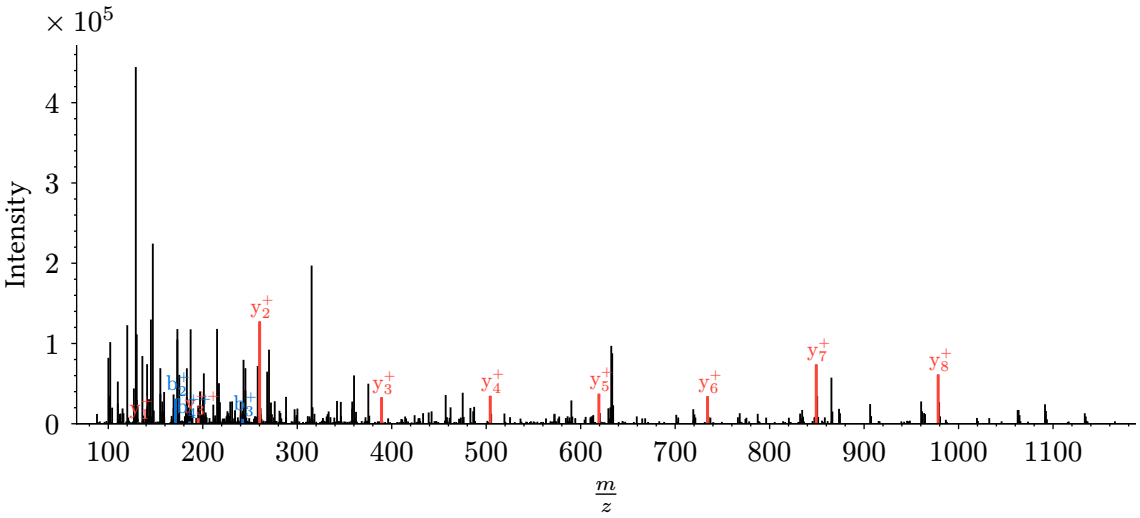
hyperscore 30.52
peptide length 9
peptide mh 1263.55909
charge 2
Δ mz −0.00053
Δ mh −0.00106

Spoms
isotope error 0
bracket [259.19]DEDDDG[E][P][I]
nam −0.00025552891725055815
spc 9
score 42

[+42.15]?AVAEDDDDEKL

AC189744.3_FGP002

+20 SDSVVGIMNAEPELDVLPDGTQGVAAVAEDDDDEKLSSDQHTLSRRNATEARRRPVCSST +79



hyperscore 33.37
peptide length 11
peptide mh 1219.53246
charge 2
Δ mz 22.01278
Δ mh 44.02557

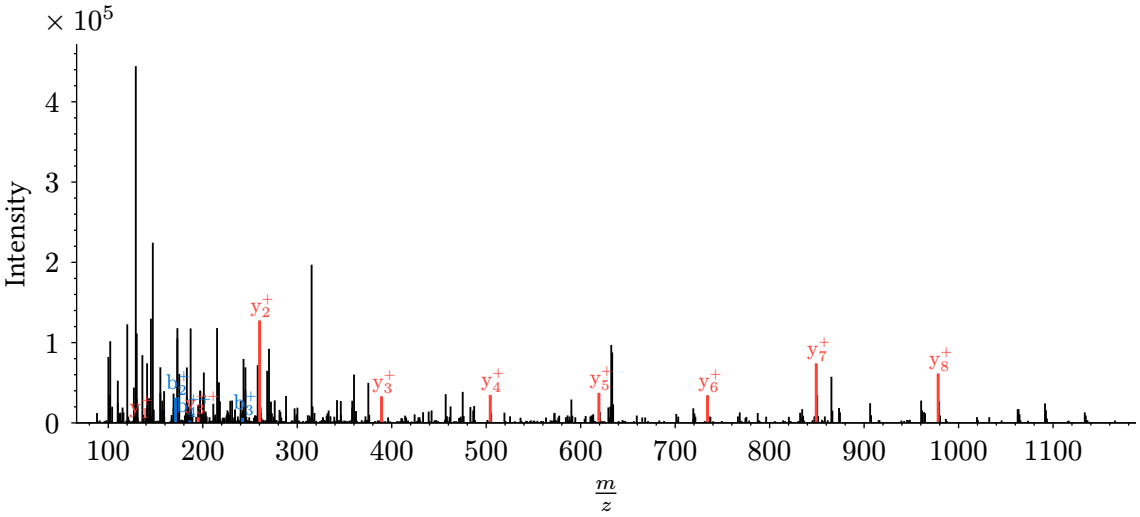
Spoms
isotope error -
bracket [283.29]EDDDDE[K][L]
nam −0.001276618370638971
spc 9
score 45

Spoms post
bracket [A][V]AEDDDDE[K][L]
nam 42.1464128509665
spc 10
score 49

[+44.03]?AVAEDDDDEKL

AC189744.3_FGP002

+20 SDSVVGIMNAEPELDVLPDGTQGVAAVAEDDDDEKLSSDQHTLSRRNATEARRRPVCSST +79



hyperscore 33.37
peptide length 11
peptide mh 1219.53246
charge 2
Δ mz 22.01278
Δ mh 44.02557

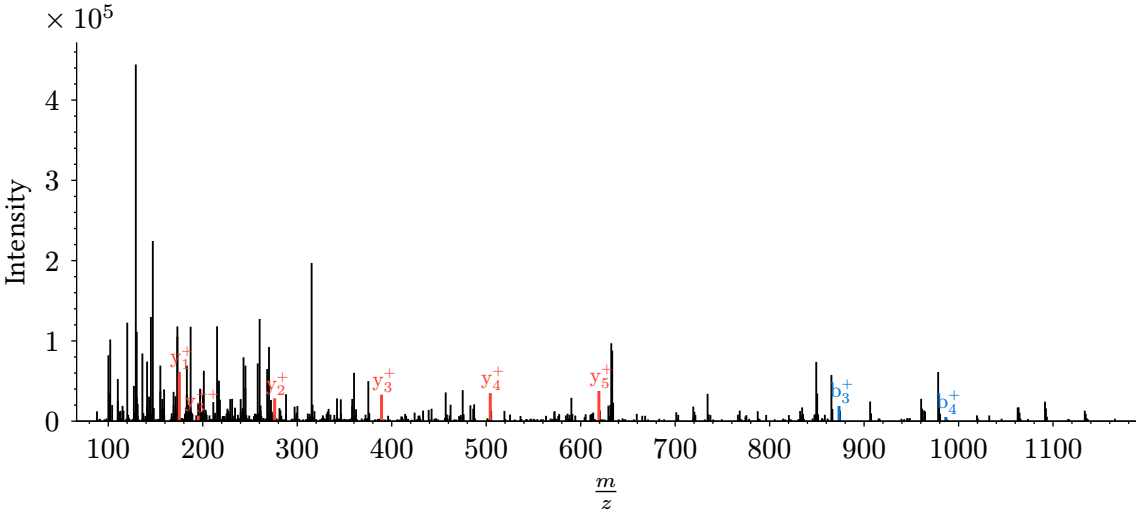
Spoms
isotope error 0
bracket [214.13]AEDDDDE[K][L]
nam −0.00038076038049439376
spc 9
score 49

Spoms post
bracket [A][V]AEDDDDE[K][L]
nam 44.025563241591954
spc 10
score 49

[+527.36]-DDDLTR

GRMZM2G119566_P01

+318 GPAPAPGPSGPSKRTVLDDDSSSDDSSDDDLTRTAPYRTPAFTQGIGRLFRCLCNPAYDV +377

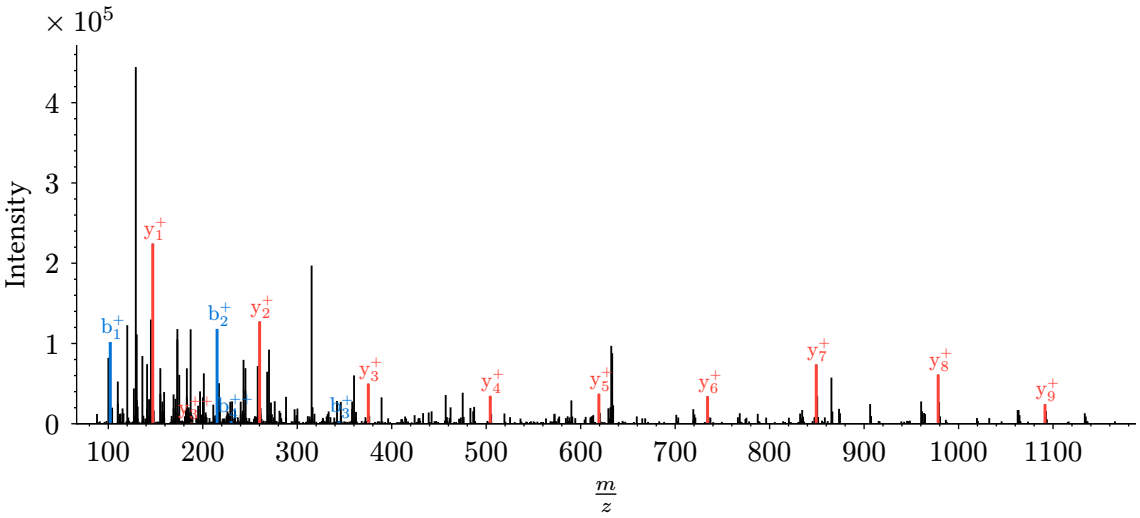


hyperscore 19.45
peptide length 6
peptide mh 1261.69152
charge 2
Δ mz 0.93326
Δ mh 1.86651

Spoms
isotope error -
bracket [527.36]DDDLTR
nam −0.015971941433690517
spc 8
score 45

[+69.16]?TLEDDDEDLK

GRMZM2G103197_P01
+276 MRNTKDTKDLARRAIGGAVVAFLRATLEDDDEDLKVVLENRPGLSPAVLDPVGHDL +331



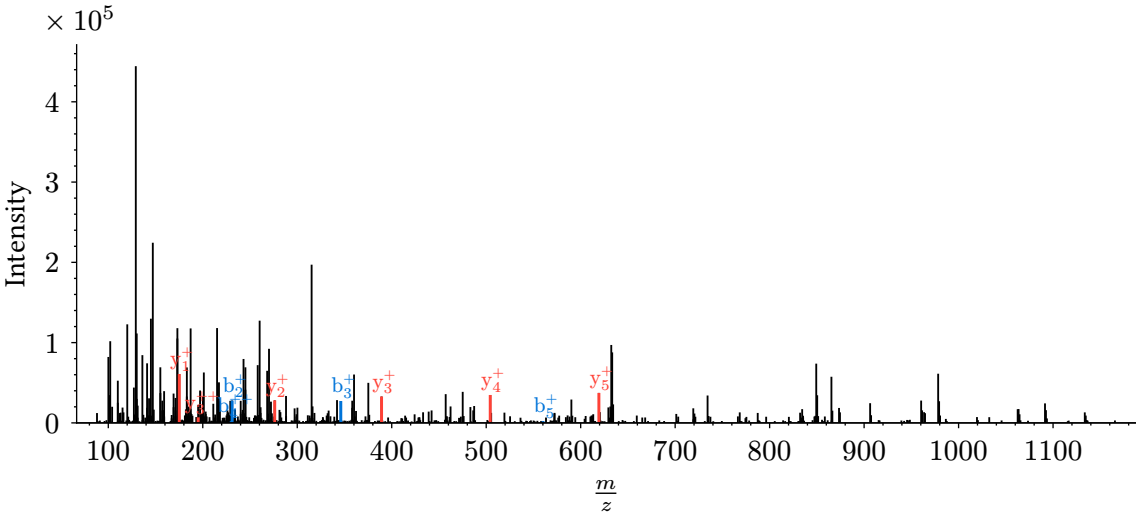
hyperscore 40.98
peptide length 10
peptide mh 1192.52156
charge 2
Δ mz 35.51823
Δ mh 71.03647

Spoms
isotope error -
bracket [170.21]LEDDDED[L][K]
nam −0.0005017301939460594
spc 9
score 49

Spoms post
bracket TLEDDDED[L][K]
nam 69.1573118880076
spc 11
score 59

[-101.95]?DDDLTR

GRMZM2G119566_P01
+318 GPAPAPGPSGPSKRTVLDDDSSSDDSSDDDLTRTAPYRTPAFTQGIGRLFRCLCNPAYDV +377
GRMZM5G878378_P01
+69 SSTPSLYLSHLALERLGLPAGAAVLEPDDDLTRLQGEVARDEVAARPPATARASLSSSSS +128



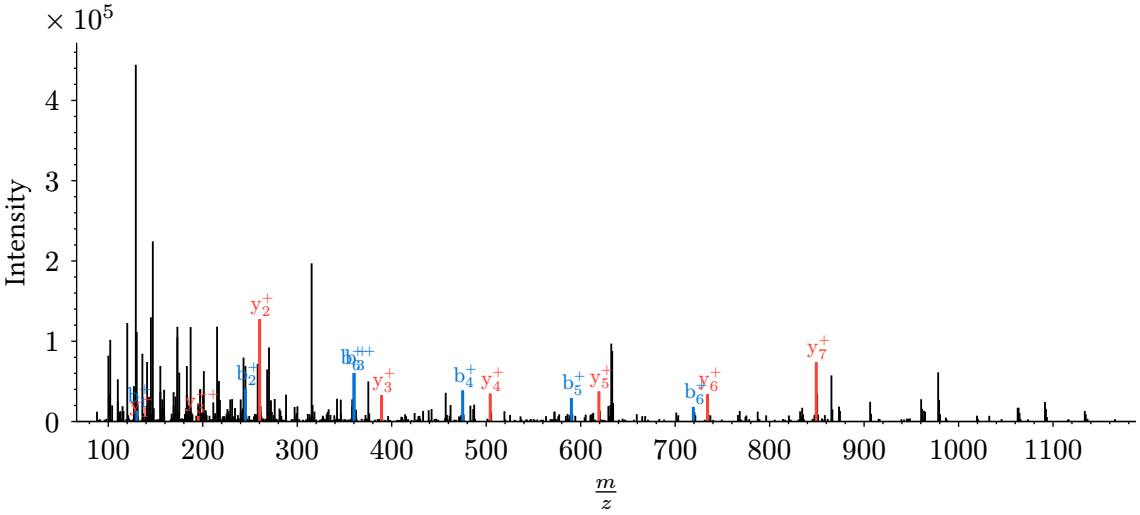
hyperscore 24.02
peptide length 6
peptide mh 734.33152
charge 2
Δ mz 264.61326
Δ mh 529.22651

Spoms
isotope error -
bracket DDDLTR
nam −101.95499782033994
spc 7
score 42

[-346.01]?EDDDDEKL

AC189744.3_FGP002

+22 SVVGIMNAEPELDVLPDGTQGVAAVAEDDDDEKLSSDQHTLSRRNATEARRRPVCSSTIA +81



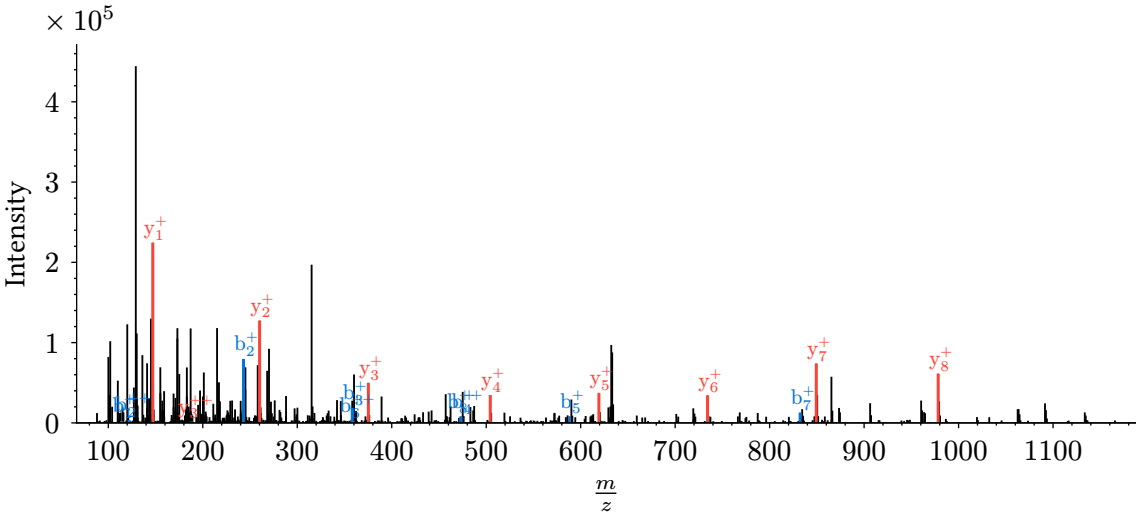
hyperscore 41.78
peptide length 8
peptide mh 978.38982
charge 2
Δ mz 142.5841
Δ mh 285.16821

Spoms
isotope error -
bracket EDDDDE[K][L]
nam −346.0133005441519
spc 8
score 42

[-459.10]?LEDDDEDLK

GRMZM2G103197_P01

+276 MRNTKDTKDLARRAIGGAVVAFLRATLEDDDEDLKVVLENRPGLSPAVLDPVGHDL +331



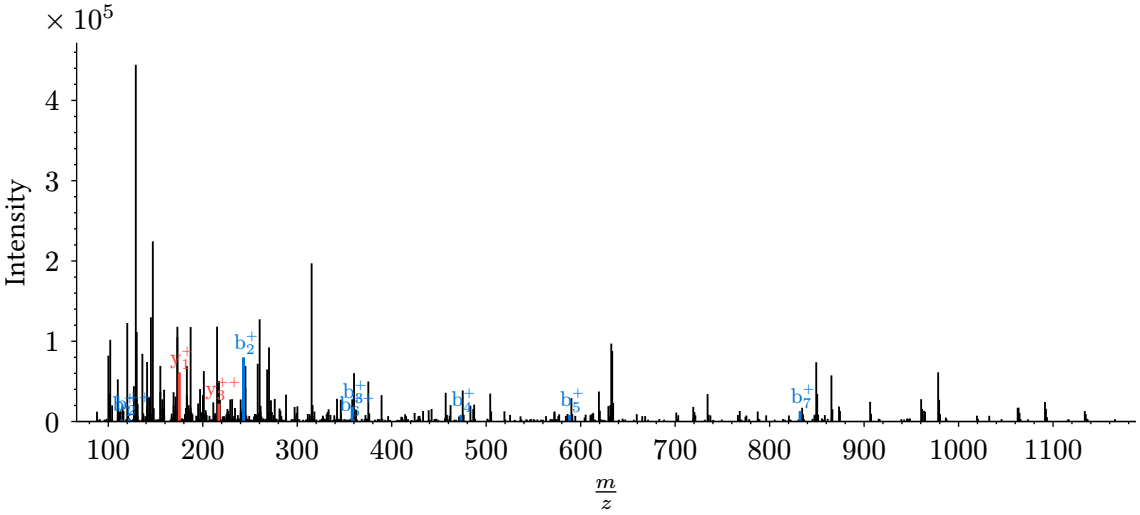
hyperscore 53.47
peptide length 9
peptide mh 1091.47389
charge 2
Δ mz 86.04207
Δ mh 172.08415

Spoms
isotope error -
bracket LEDDDED[L][K]
nam −459.0973645231628
spc 10
score 52

[-459.10]?LEDDDEDN[-28.97]R

GRMZM2G445523_P01

+273 KAMKVVHHASLSKAGNDRALAVMDELLEDDDEDNRDIERDGELGERNGNEIQEVSNILEG +332



hyperscore 26.4
peptide length 9
peptide mh 1149.4089
charge 2
Δ mz 57.07457
Δ mh 114.14913

Spoms
isotope error -
bracket LEDDDED[N][-28.97]R
nam −459.0970740105121
spc 11
score 39