PSM scan report

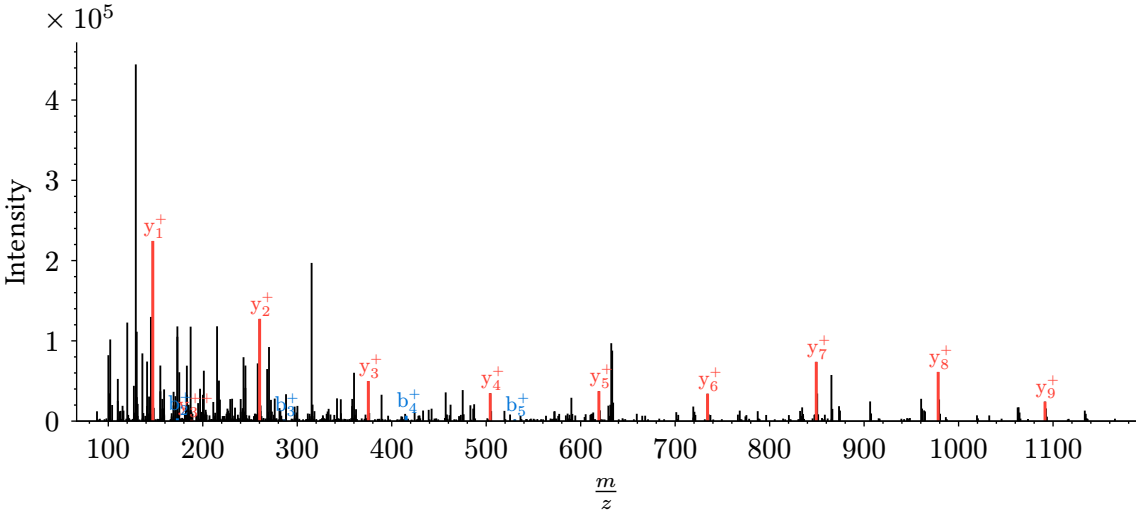
20120906_balliau_extract_1_A01_urnb-1

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

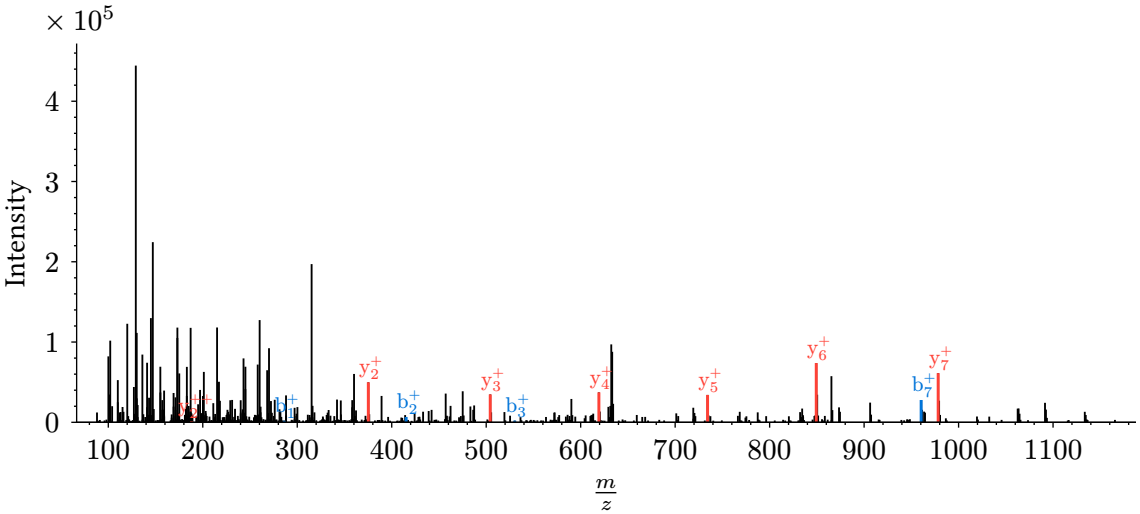
[+172.08]-LEDDDEAF[+138.10]

GRMZM2G074314_P01

+360 EAYAIYDQEIGYCQGMSDLLAPLLAV**LEDDDEAF**WCFAGFMRKARHNFRLDEVGIRRQLN +419

GRMZM2G074314_P02

+355 EAYAIYDQEIGYCQGMSDLLAPLLAV**LEDDDEAF**WCFAGFMRKARHNFRLDEVGIRRQLN +414



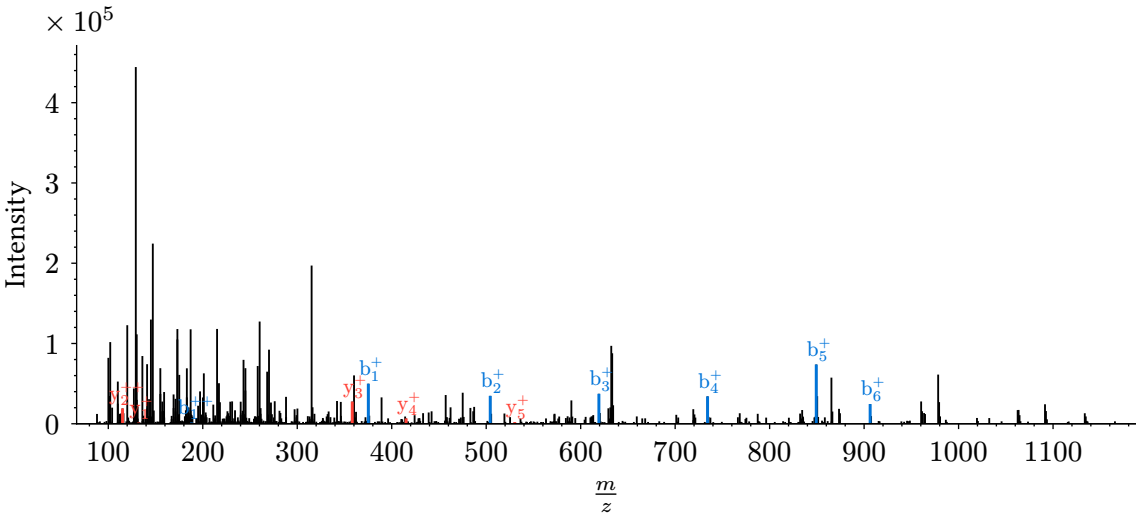
hyperscore 27.82
peptide length 8
peptide mh 1263.55344
charge 2
Δ mz 0.00229
Δ mh 0.00459

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

[+259.19]-DEDDDGEPI

GRMZM2G023418_P01

+44 KGKKGGKAAAPDDDDYEPPPPPPPAADEDDDGEPINLVFTGKKKKKKGATPAAPFSAFSA +103



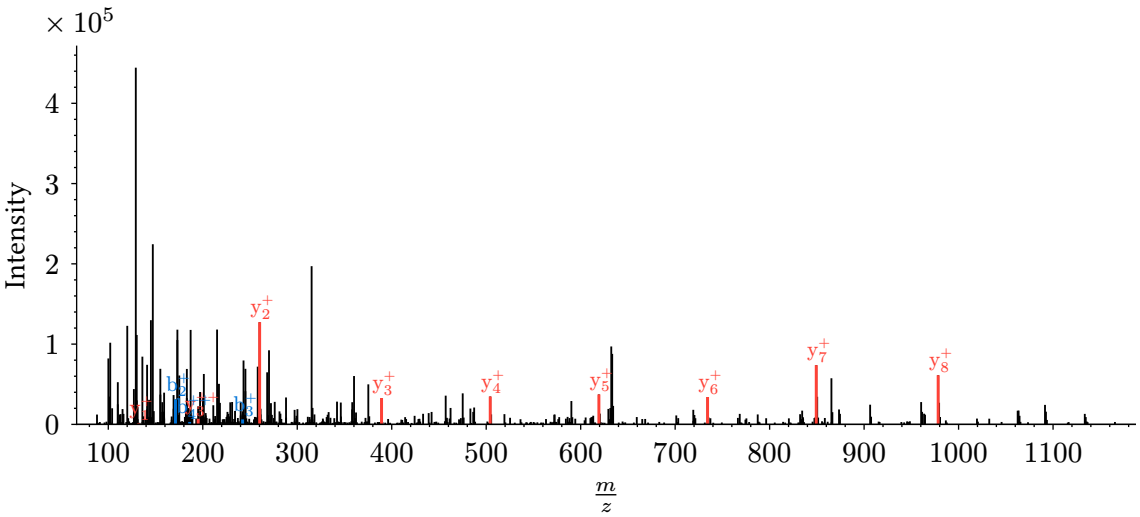
hyperscore 30.52
peptide length 9
peptide mh 1263.55909
charge 2
Δ mz −0.00053
Δ mh −0.00106

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

[+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