

PSM scan report

20120906_balliau_extract_1_A01_urnb-1

Scan index=5694 mh=1478.7379 mz=493.5842 charge=3
rt=1299.98s

FDGAVPEPR

GRMZM2G029262_P03

+257 LWSLDQVKENINTQTHQLIDARSKPRFDGAVPEPRKGIRSGHVPGSKCVPFPQVLDSSQK +316

GRMZM2G029262_P04

+278 LWSLDQVKENINTQTHQLIDARSKPRFDGAVPEPRKGIRSGHVPGSKCVPFPQVLDSSQK +337

GRMZM2G029262_P05

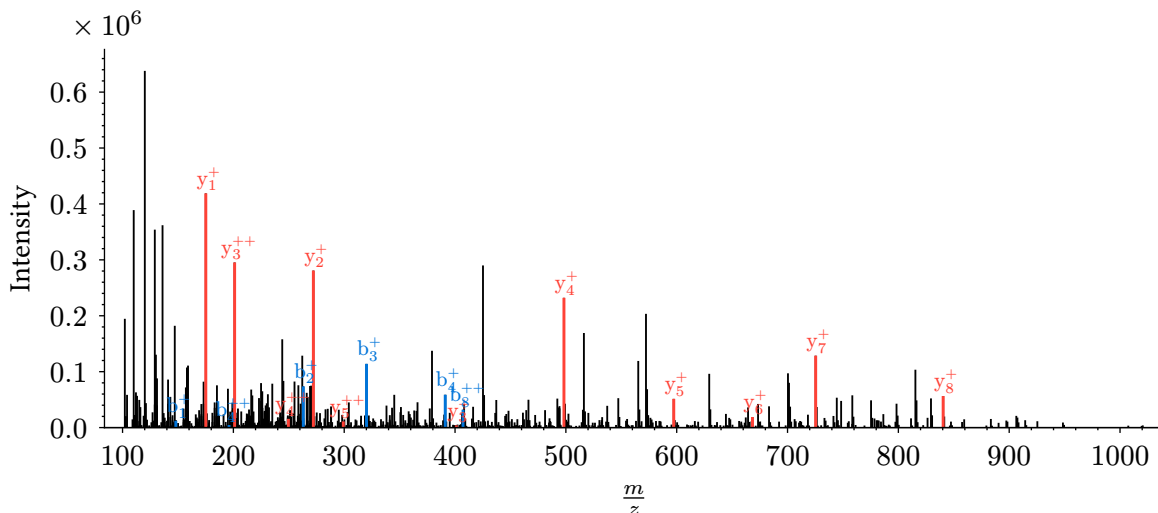
+144 LWSLDQVKENINTQTHQLIDARSKPRFDGAVPEPRKGIRSGHVPGSKCVPFPQVLDSSQK +203

GRMZM2G400704_P01

+22 LHAFGSFYDYLKPLSALLTDLKLLFRFDGAVPEPRNGIRSGHVPGSKCVPFPQVLDSSQK +81

GRMZM2G460900_P01

+27 LHAFGSSYDYLKPLSALLTDLKLLFRFDGAVPEPRNGIRSGHVPGSKCVPFPQVLDSSQK +86



hyperscore 51.64
peptide length 9
peptide mh 987.48942
charge 3
 Δ mz 163.74951
 Δ mh 491.24853

Spoms
isotope error -
bracket FDGAV[P][E]PR
nam 0.005011191271023563
spc 10
score 52

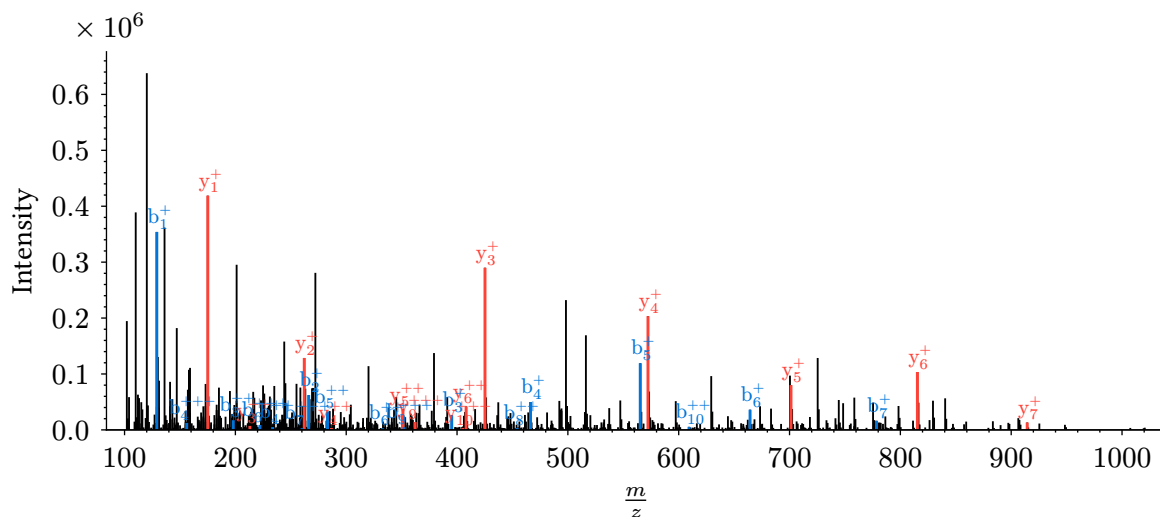
KHEAVVNEFYSR

GRMZM2G029055_P01

+130 SSSYRTLWADLDIEYDKFIRTTDRKHEAVVNEFYSRVLNNGDIYRADYEGLYCVSCEEYK +189

GRMZM2G029055_P02

+130 SSSYRTLWADLDIEYDKFIRTTDRKHEAVVNEFYSRVLNNGDIYRADYEGLYCVSCEEYK +189



hyperscore 107.45

peptide length 12

peptide mh 1478.73865

charge 3

Δ mz -0.00023

Δ mh -0.0007

Spoms

isotope error 0

bracket [K][H][E][A]VVNEFYSR

nam -0.000703633488910782

spc 10

score 56

[+415.22]?EAYKFYSR

GRMZM2G063239_P01

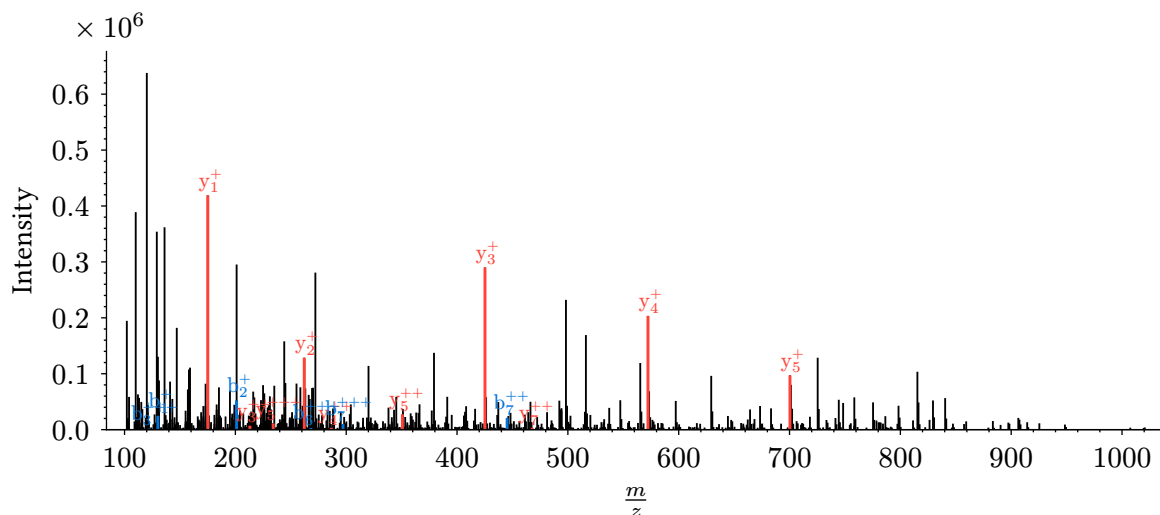
+70 HILQSHDDSIDQRLVPKVGMTFSNVDEAYKFYSRYAYEVGFPLKRYRERKNCKWRLNCSM +129

GRMZM2G156668_P01

+104 VILQRHEVTIDPRLVPKVGMTFSGVDEAYKFYSRYAYEVGFPLKRYRERKNCKWLNCSME +163

GRMZM2G389595_P01

+0 MTFSNVDEAYKFYSRYAYEVGFPLKRYRERKNCKWLNCSMEGKRAERGNVWIDLIHLEHN +59



hyperscore 46.91

peptide length 8

peptide mh 1063.52072

charge 3

Δ mz 138.40574

Δ mh 415.21723

Spoms**isotope error** 0**bracket** [778.35]KFYSR**nam** 0.012267566912896656**spc** 6**score** 35**Spoms post****bracket** [E][A]YKFYSR**nam** 415.21722805245986**spc** 8**score** 42