

PSM scan report

20120906_balliau_extract_1_A01_urnb-1

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

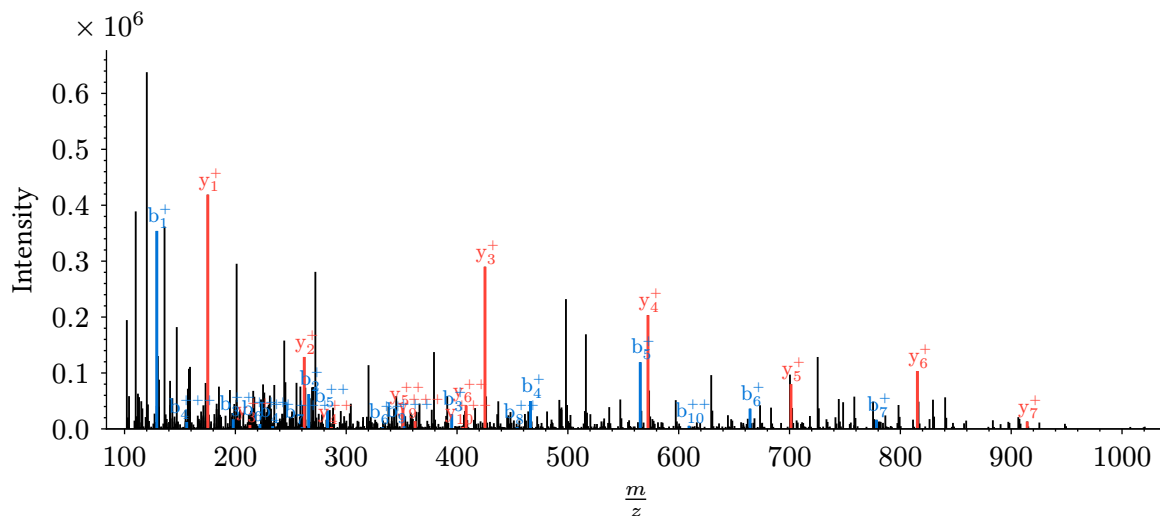
KHEAVVNEFYSR

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

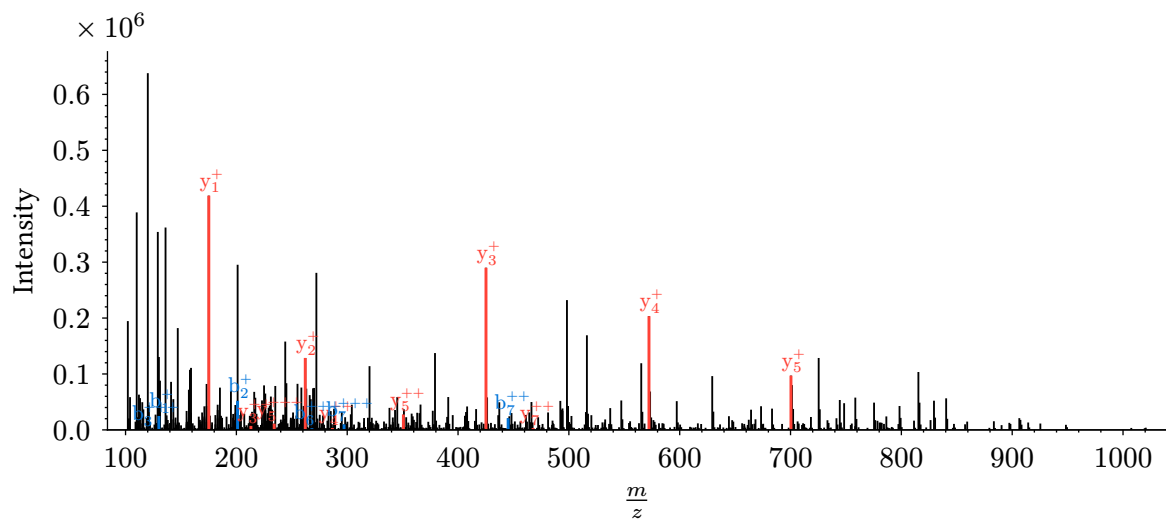
+70 HILQSHDDSIDQRLVPKVGMTFSNVD EAYKFYSR YAYEVGFPLKRYRERKNCKWRLNCSM +129

GRMZM2G156668_P01

+104 VILQRHEVTIDPRLVPKVGMTFSGVD EAYKFYSR YAYEVGFPLKRYRERKNCKWLNCSME +163

GRMZM2G389595_P01

+0 MTFNSNVD EAYKFYSR YAYEVGFPLKRYRERKNCKWLNCSMEGKRAERGNVWIDLIHLEHN +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