

PSM scan report

20120906_balliau_extract_1_A01_urnb-1

Scan index=5737 mh=1240.4975 mz=620.7524 charge=2
rt=1306.13s

MKEMAPDNFR

GRMZM2G059083_P01

+247 YTGLAWLFLGVPTSDTLLYKEELEKMKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAE +306

GRMZM2G059083_P02

+221 YTGLAWLFLGVPTSDTLLYKEELEKMKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAE +280

GRMZM2G059083_P03

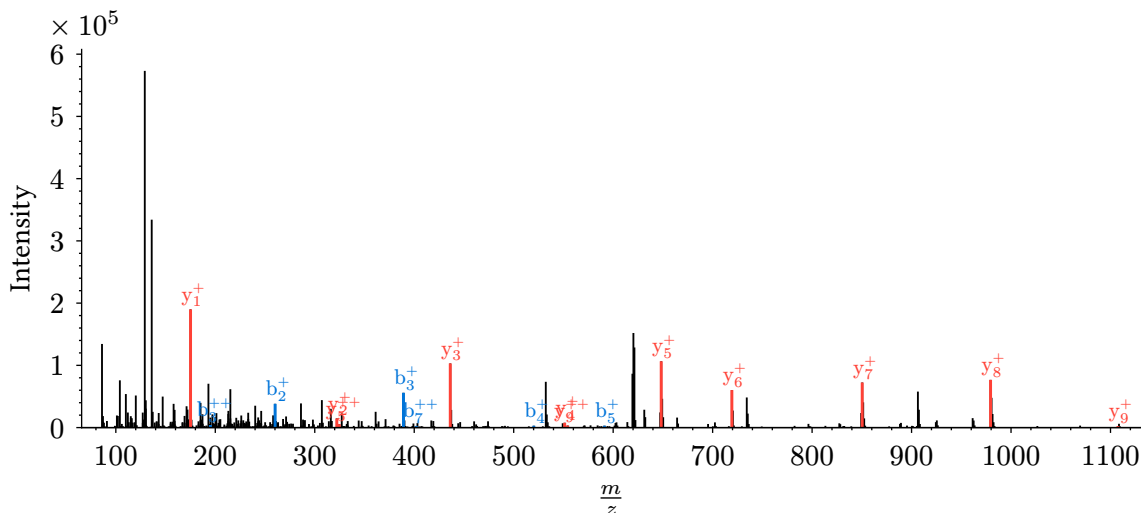
+247 YTGLAWLFLGVPTSDTLLYKEELEKMKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAE +306

GRMZM2G059083_P04

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GRMZM2G059083_P05

+0 MKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAEYKEELWELLKKDNTYVVMCGLKGME +59



hyperscore 50.3

peptide length 10

peptide mh 1238.56564

charge 2

Δ mz 0.96592

Δ mh 1.93185

Spoms

isotope error -

bracket [M][K]EMA[P][D]NFR

nam -0.00040717729598327423

spc 11

score 48

[+132.97]?KEMAPDNFR

GRMZM2G059083_P02

+221 YTGLAWLFLGVPTSDTLLYKEELEKMKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAE +280

GRMZM2G059083_P03

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GRMZM2G059083_P04

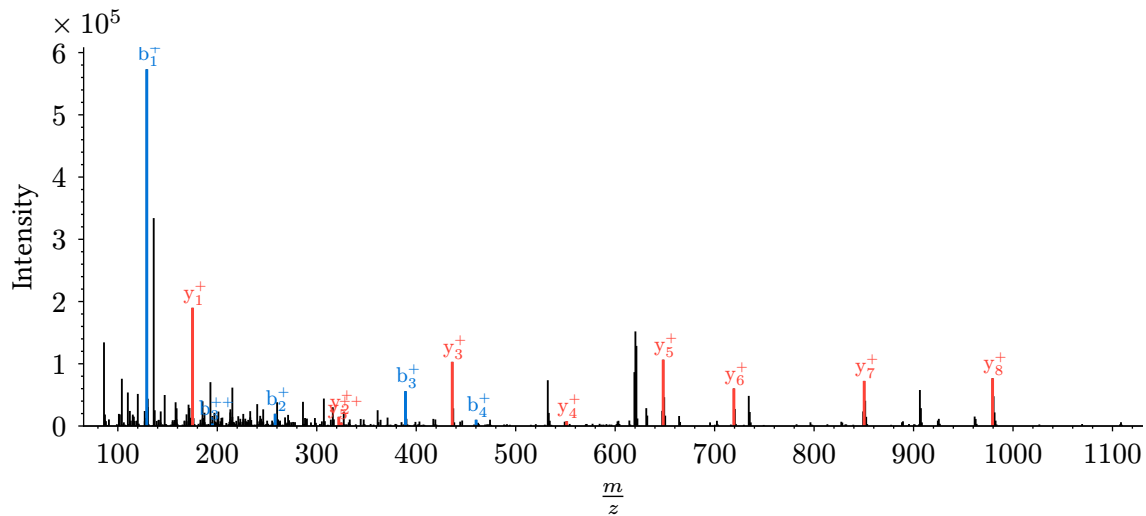
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GRMZM2G059083_P05

+0 MKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAEYKEELWELLKKDNTYVVMCGLKGME +59

GRMZM2G059191_P01

+248 FSGLAWLFLGVPTSDSLLYKEELEKMKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAE +307



hyperscore 39.98

peptide length 9

peptide mh 1107.52515

charge 2

Δ mz 66.48617

Δ mh 132.97233

Spoms

isotope error 0

bracket [261.07]EMA[P][D]NFR

nam -0.000871082298544934

spc 8

score 42

Spoms post

bracket KEMA[P][D]NFR

nam 132.97232888789586

spc 11

score 55

[-360.07]?EMAPDNFR

GRMZM2G059083_P01

+248 TGLAWLFLGVPTSDTLLYKEELEKMKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAEY +307

GRMZM2G059083_P02

+222 TGLAWLFLGVPTSDTLLYKEELEKMKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAEY +281

GRMZM2G059083_P03

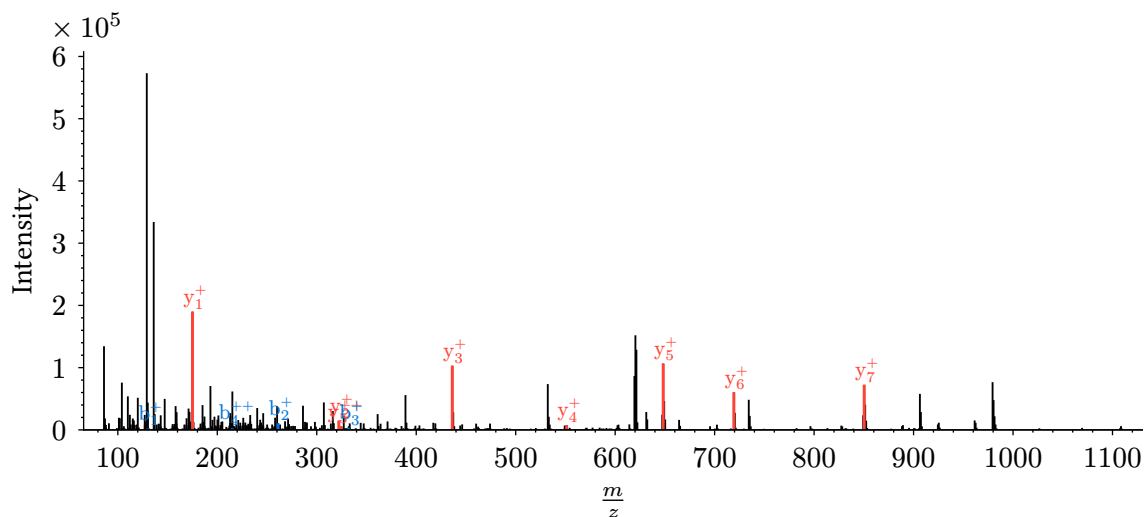
+248 TGLAWLFLGVPTSDTLLYKEELEKMKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAEY +307

GRMZM2G059083_P04

+248 TGLAWLFLGVPTSDTLLYKEELEKMKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAEY +307

GRMZM2G059191_P01

+249 SGLAWLFLGVPTSDSLLYKEELEKMKEMAPDNFRLDFAVSREQTNAAGEKMYIQTRMAEY +308



hyperscore 31.96

peptide length 8

peptide mh 979.43019

charge 2

Δ mz 130.53365

Δ mh 261.0673

Spoms

isotope error -

bracket EMA[P][D]NFR

nam -360.07020701979866

spc 8

score 42

[-360.10]?EMAPDNFR

GRMZM2G059083_P01

+248 TGLAWLFLGVPTSDTLLYKEELEKMK**EMAPDNFR**LDFAVSREQTNAAGEKMYIQTRMAEY +307

GRMZM2G059083_P02

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GRMZM2G059083_P03

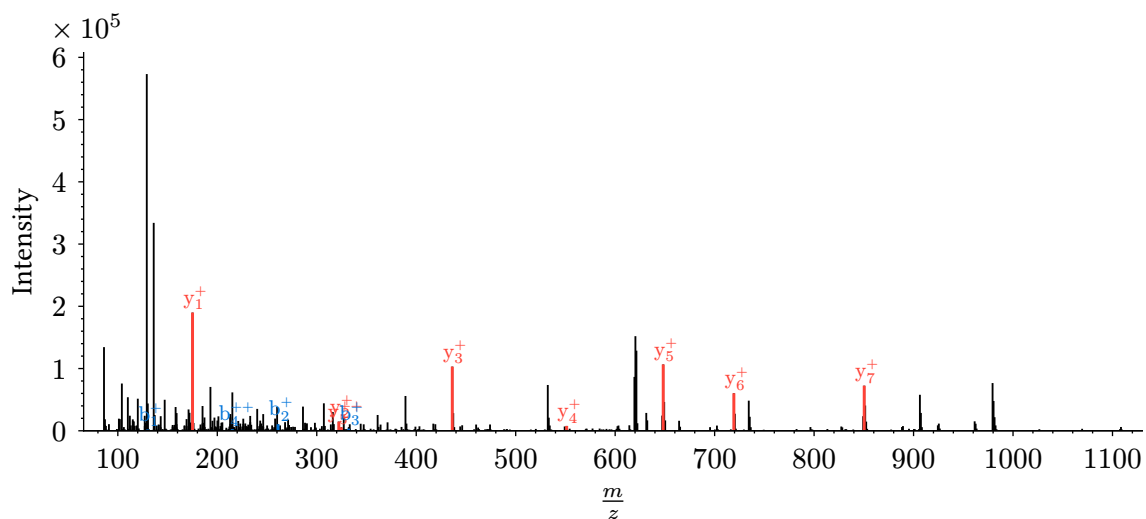
+248 TGLAWLFLGVPTSDTLLYKEELEKMK**EMAPDNFR**LDFAVSREQTNAAGEKMYIQTRMAEY +307

GRMZM2G059083_P04

+248 TGLAWLFLGVPTSDTLLYKEELEKMK**EMAPDNFR**LDFAVSREQTNAAGEKMYIQTRMAEY +307

GRMZM2G059191_P01

+249 SGLAWLFLGVPTSDSLLYKEELEKMK**EMAPDNFR**LDFAVSREQTNAAGEKMYIQTRMAEY +308



hyperscore 31.96
peptide length 8
peptide mh 979.43019
charge 2
 Δ mz 130.53365
 Δ mh 261.0673

Spoms
isotope error -
bracket EMA[P][D]NFR
nam -360.10121287917366
spc 9
score 45