

PSM scan report

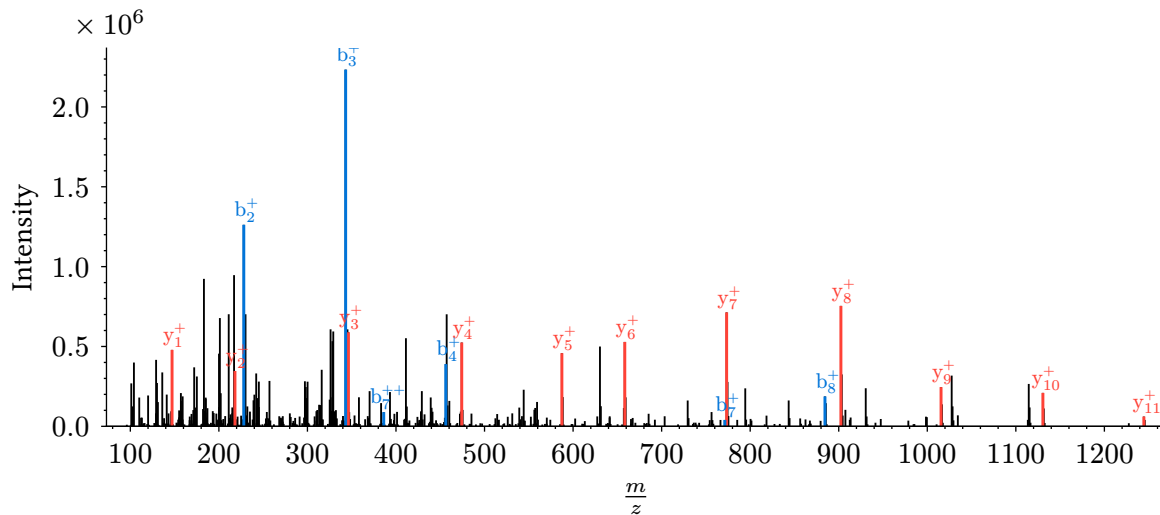
20120906_balliau_extract_1_A01_urnb-1

Scan index=10017 mh=1357.696 mz=679.3516 charge=2
rt=1918.88s

LNDLEDALQQAK

conta|P04264|K2C1_HUMAN

+418 SNLQQSISDAEQRGENALKDAKNK**LNDLEDALQQAKE**EDLARLLRDYQELMNTKLALDLEI +477



hyperscore 52.28

peptide length 12

peptide mh 1357.69578

charge 2

Δ mz 0.0001

Δ mh 0.00019

Spoms

isotope error 0

bracket [L][N]DLEDALQ[Q][A][K]

nam 0.0001853342980666639

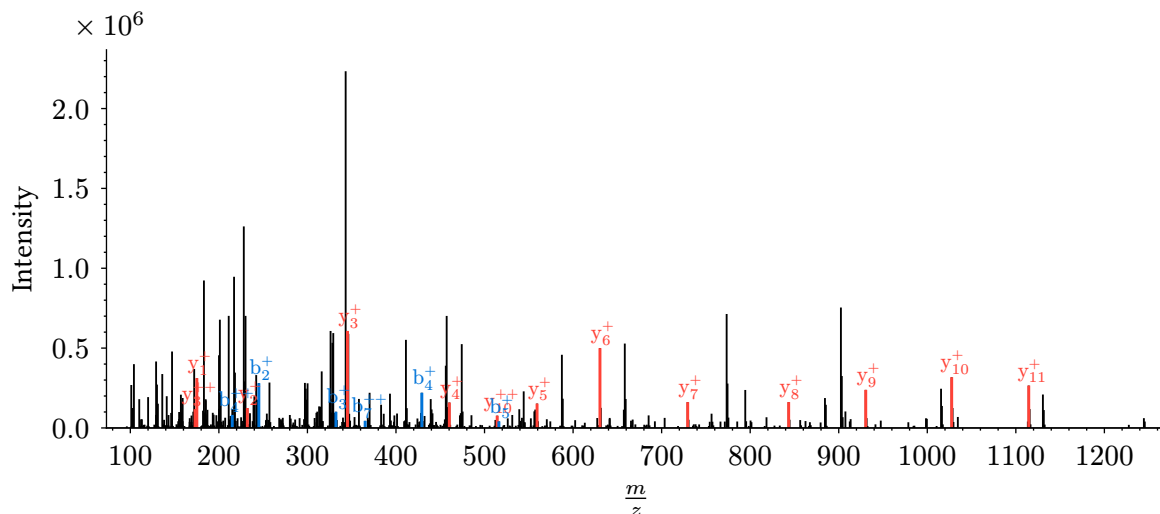
spc 14

score 61

MISPSNVAVDIGR

GRMZM2G105644_P01

+86 IPLCMVSEFDLPLDLVDRKVRKMK**MISPSNVAVDIGR**TLAPHEYIGMVRREVLDAYLRSR +145



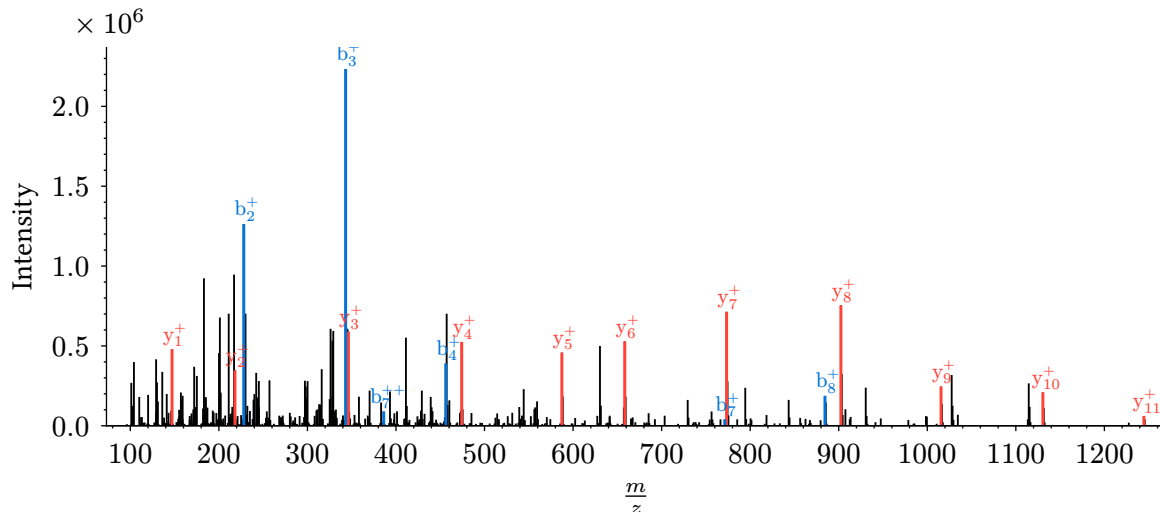
hyperscore 59.6
peptide length 13
peptide mh 1358.70966
charge 2
 Δ **mz** -0.50684
 Δ **mh** -1.01369

Spoms
isotope error +1
bracket [M][I]SPSNVAVD[I][G]R
nam -0.007953777956799968
spc 14
score 69

[+1.01]?LNDLEDALQQAK

conta|P04264|K2C1_HUMAN

+418 SNLQQSISDAEQRGENALKDAKN**LNDLEDALQQAKE**DLARLLRDYQELMNTKLALDLEI +477



hyperscore 52.28
peptide length 12
peptide mh 1357.69578
charge 2
 Δ **mz** 0.0001
 Δ **mh** 0.00019

Spoms
isotope error +1
bracket [228.13]DLEDALQ[Q][A][K]
nam -0.0005565432704770501
spc 10
score 52

Spoms post
bracket [L][N]DLEDALQ[Q][A][K]
nam 1.0059226389860214
spc 14
score 61

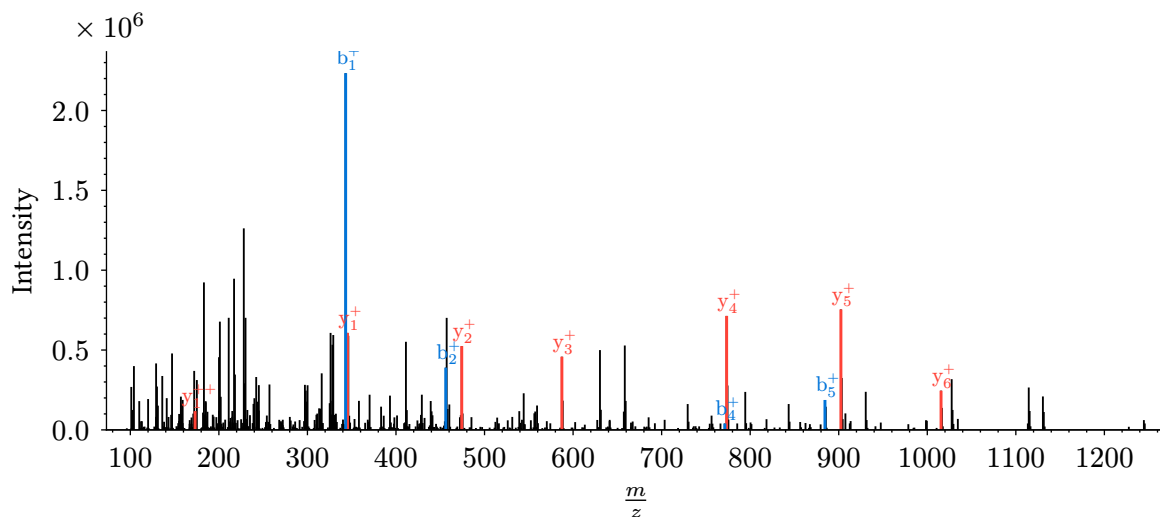
[+227.13]-DLEWLEK[+198.11]

GRMZM2G138624_P01

+91 DTHYPDKPEPPYPPHCIIGTGEEDFVP**DLEWLEKE**PNVTIKRKSCIDGYISCIKDGSSV +150

GRMZM2G138624_P02

+91 DTHYPDKPEPPYPPHCIIGTGEEDFVP**DLEWLEKE**PNVTIKRKSCIDGYISCIKDGSSV +150



hyperscore 30.12

peptide length 7

peptide mh 1357.71237

charge 2

Δ **mz** -0.0082

Δ **mh** -0.0164

Spoms

isotope error 0

bracket [227.13]DLEWLEK[198.11]

nam -0.01517924347058397

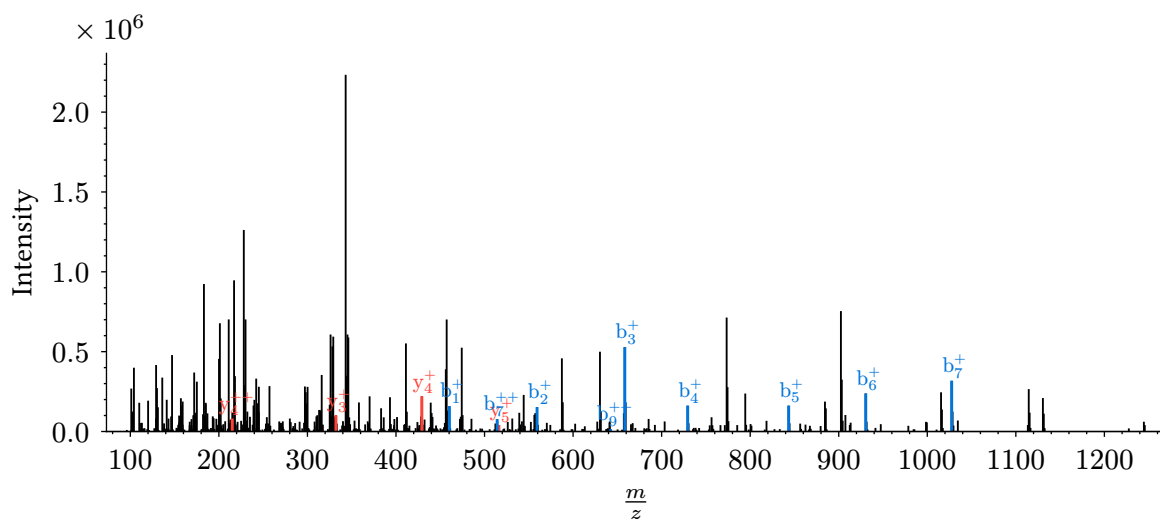
spc 12

score 46

[+344.22]-DVVANSPQQG

GRMZM2G062777_P03

+0 MLIHIFSLPNVTPKKTEETALIS **DVVANSPQQG** FHSGHCWSDL +43



hyperscore 35.78

peptide length 10

peptide mh 1358.70506

charge 2

Δ **mz** -0.50454

Δ **mh** -1.00909

Spoms

isotope error +1

bracket [344.22]DVVANSP[Q][Q][G]

nam 0.00007371750712081848

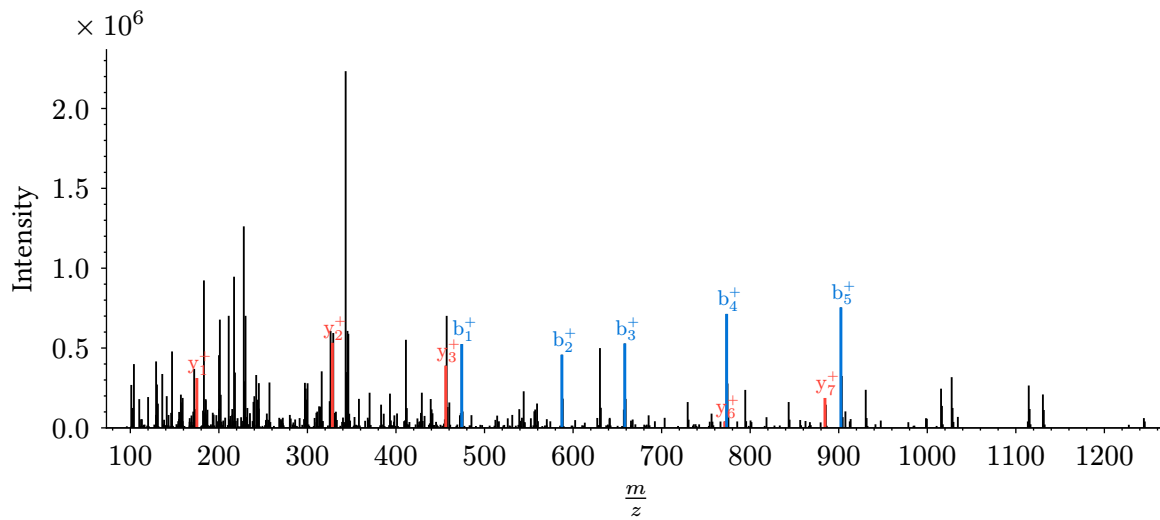
spc 10

score 52

[+344.22]-ELADEQQ[+25.02]R

GRMZM2G436312_P01

+66 QKDNKWLENIKKWD AEDKERIQKRRE **ELADEQQ** RVEEQEMRRVAECREEKGEE +118



hyperscore 25.83

peptide length 8

peptide mh 1357.70941

charge 2

Δ mz -0.00672

Δ mh -0.01344

Spoms

isotope error 0

bracket [344.22]ELADEQQ[25.02]R

nam -0.010049297301065964

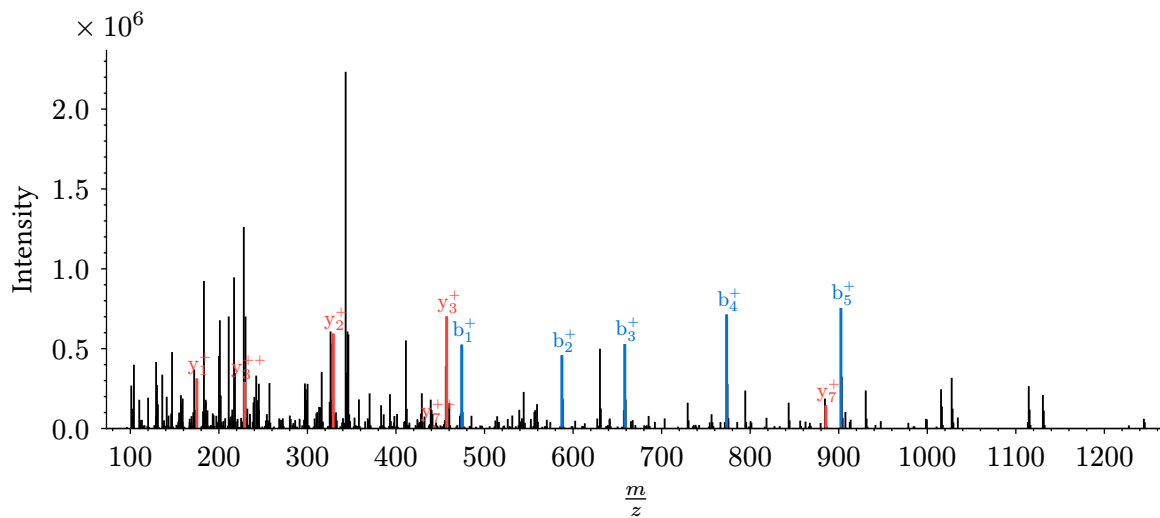
spc 12

score 47

[+344.22]-ELADEQQ[+26.00]R

GRMZM2G436312_P01

+66 QKDNKWLNIKKWDAEDKERIQKRREELADEQQRVVEEQEMRRVAECREEKGEE +118



hyperscore 29.16

peptide length 8

peptide mh 1358.68941

charge 2

Δ mz -0.49672

Δ mh -0.99344

Spoms

isotope error +1

bracket [344.22]ELADEQQ[26.00]R

nam 0.012808368715013785

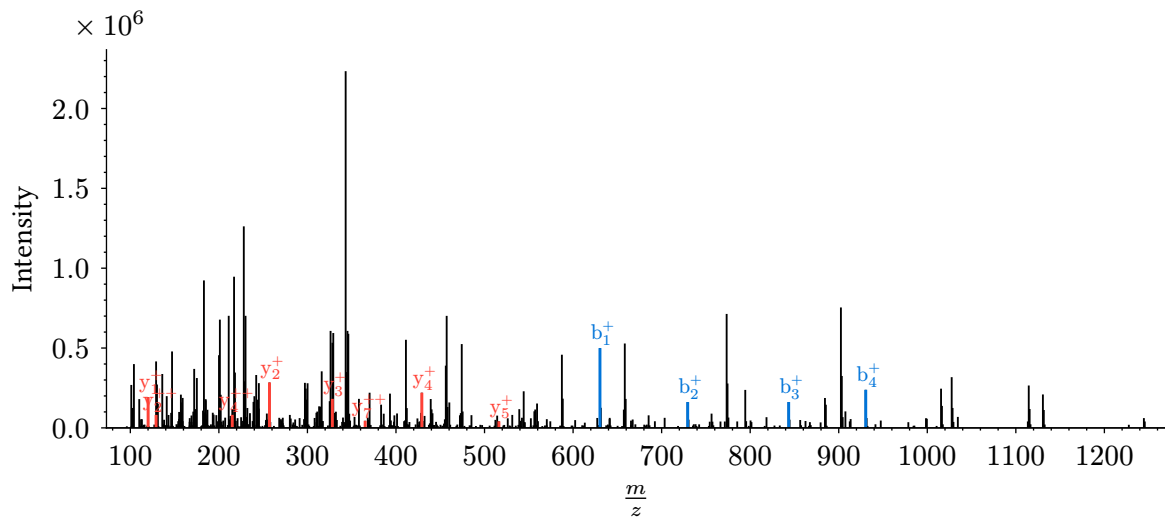
spc 11

score 44

[+473.26]-RVNSTAHT

AC215611.3_FGP011

+825 KLKARKSIPPNFVPRRSRRVAKLPPLRVNSTAHTICLKLGLKNGEAPVSADDLDRCAREF +884



hyperscore 31.91

peptide length 8

peptide mh 1358.7137

charge 2

Δ **mz** -0.50886

Δ **mh** -1.01773

Spoms

isotope error +1

bracket [473.26]RVNSTA[H][T]

nam -0.011260675162930056

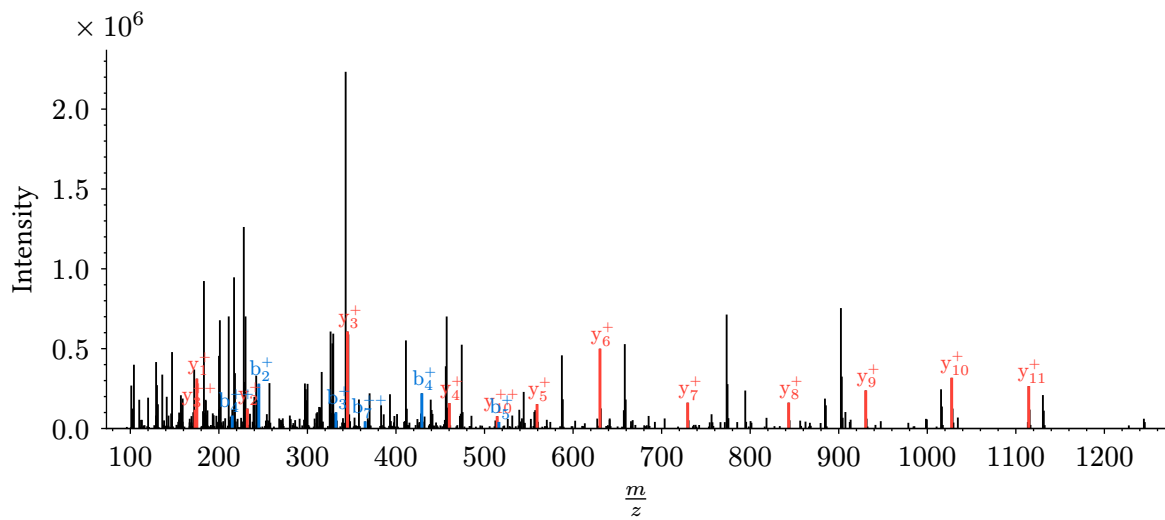
spc 9

score 45

[-1.01]?MISPSNVAVDIGR

GRMZM2G105644_P01

+86 IPLCMVSEFDLPLDLVDRKVRKMK**MISPSNVAVDIGR**TLAPHEYIGMVRREVLDAYLRSR +145



hyperscore 59.6

peptide length 13

peptide mh 1358.70966

charge 2

Δ **mz** -0.50684

Δ **mh** -1.01369

Spoms**isotope error** 0**bracket** [243.11]SPSNVAVD[I][G]R**nam** -0.001982735625688292**spc** 11**score** 63**Spoms post****bracket** [M][I]SPSNVAVD[I][G]R**nam** -1.0136910826447547**spc** 13**score** 66