

Supplemental Fig. S1. MS/MS spectra from the *Listeria* peptides monitored in the SRM experiments (see Fig. 7 main text). Annotation of the principal fragmentation series (y-carboxy and b-amino series) was performed by the Mascot software (Matrix Science).

MATRIX **SCIENCE** Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEEQPSEVNTGPR**

Found in **lmo0204**, actin-assembly inducing protein precursor (actA) (*Listeria monocytogenes* EGD-e)

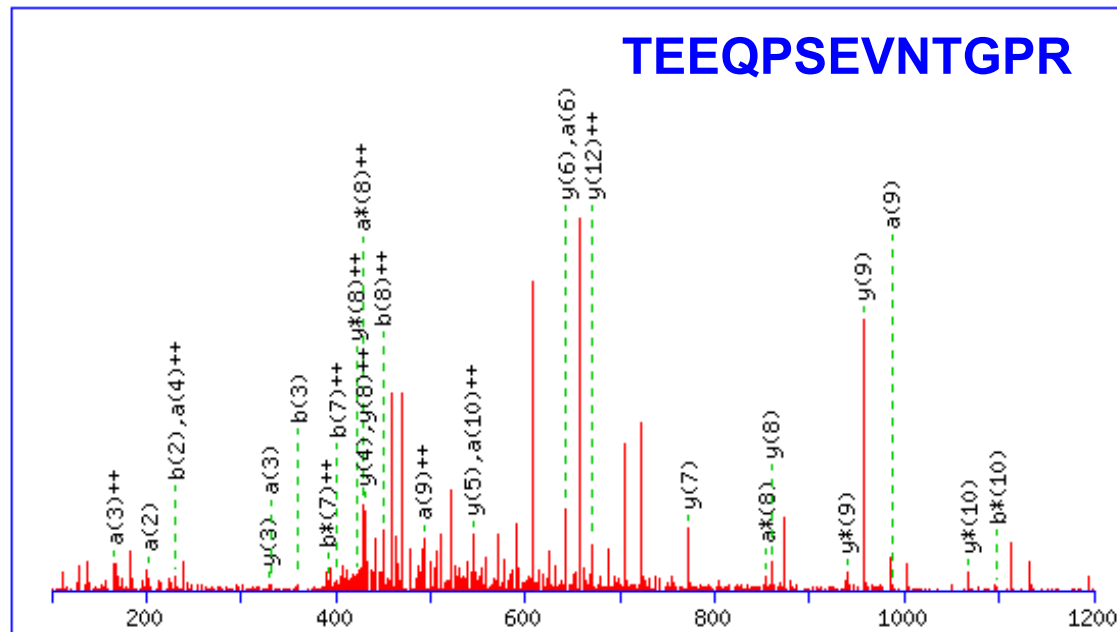
Match to Query 55: 1442.760532 from(722.387542,2+)

Title: File: IMM.wiff, Sample: IMM (sample number 2), Elution: 22.07 to 24.04 min, Period: 1, Cycle(s): 573-577, 579-580, 585 (Experiment 3)

Data file C:\DOCUME~1\ecalvo\LOCALS~1\Temp\mas36.tmp

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da



ActA

Monoisotopic mass of neutral peptide Mr(calc): 1442.6637

Ions Score: 16 Expect: 0.039

Matches (Bold Red): 28/132 fragment ions using 86 most intense peaks

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISAPALISDITK**

Found in **lmo0204**, actin-assembly inducing protein precursor (actA) (*Listeria monocytogenes* EGD-e)

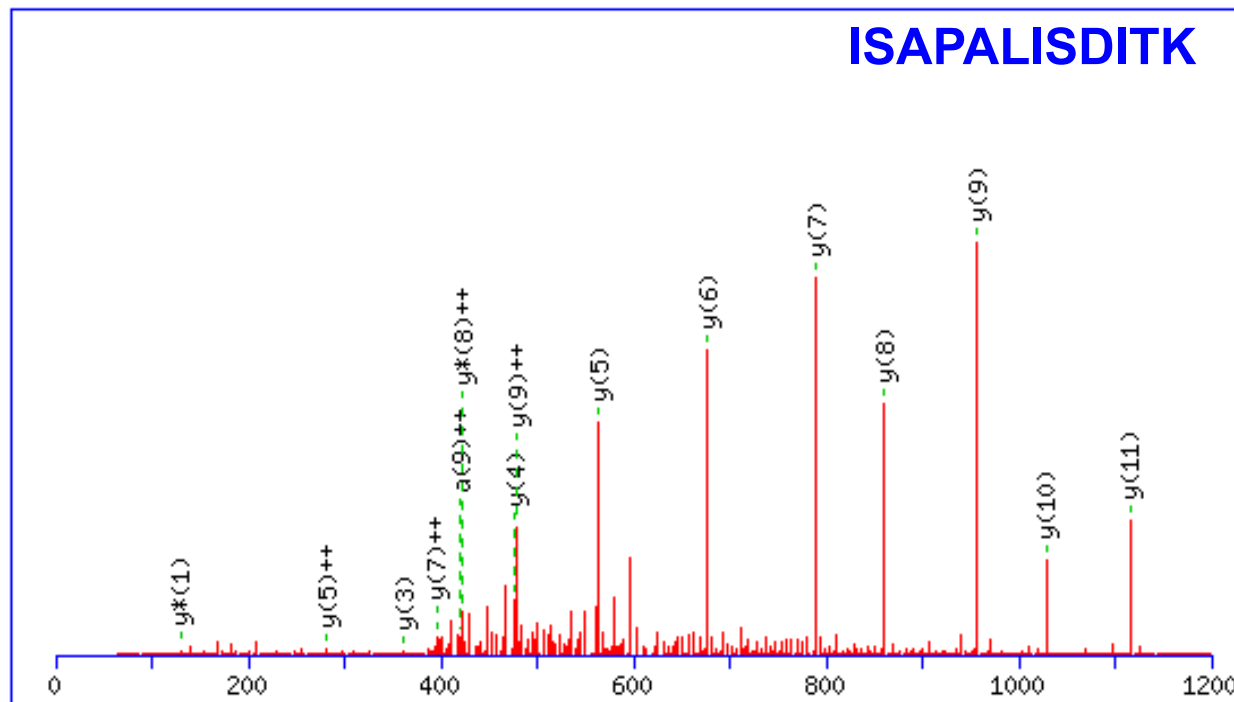
Match to Query 12: 1228.022514 from(615.018533,2+)

Title: File: IMM.wiff, Sample: IMM (sample number 2), Elution: 59.29 to 62.91 min, Period: 1, Cycle(s): 843-853, 855-856, 858, 860, 865

Data file C:\DOCUME~1\ecalvo\LOCALS~1\Temp\mas33.tmp

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da



ActA

Monoisotopic mass of neutral peptide Mr(calc): 1227.7074

Ions Score: 52 **Expect:** 4e-005

Matches (Bold Red): 15/88 fragment ions using 46 most intense peaks

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVEESESANNANGK**

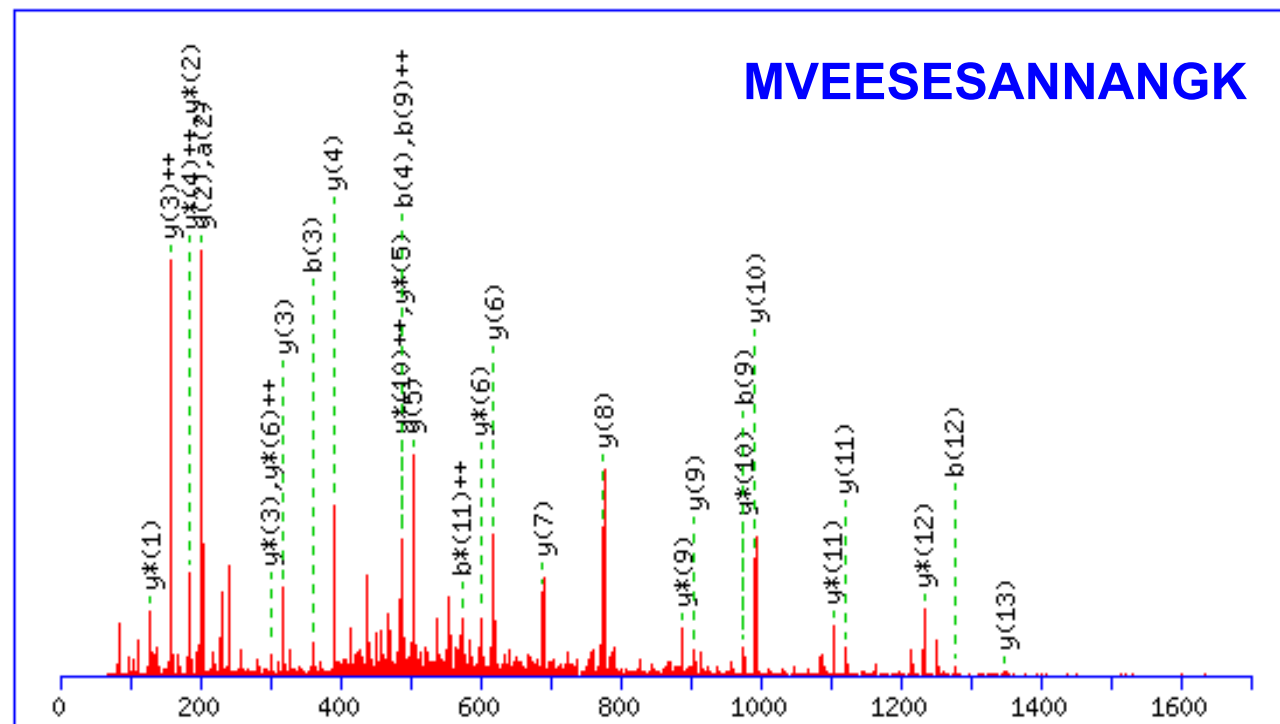
Found in **lmo0204**, actin-assembly inducing protein precursor (actA) (*Listeria monocytogenes* EGD-e)

Match to Query 1: 1479.785448 from(740.900000,2+)

Data file C:\DOCUME~1\ecalvo\LOCALS~1\Temp\mas3B.tmp

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da



ActA

Monoisotopic mass of neutral peptide Mr(calc): 1478.6307

Ions Score: 61 **Expect:** 6.2e-006

Matches (Bold Red): 31/124 fragment ions using 79 most intense peaks

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPPGNHTTLILAMLAIGVFSLGAFIK**

Found in **lmo0204**, actin-assembly inducing protein precursor (actA) (*Listeria monocytogenes* EGD-e)

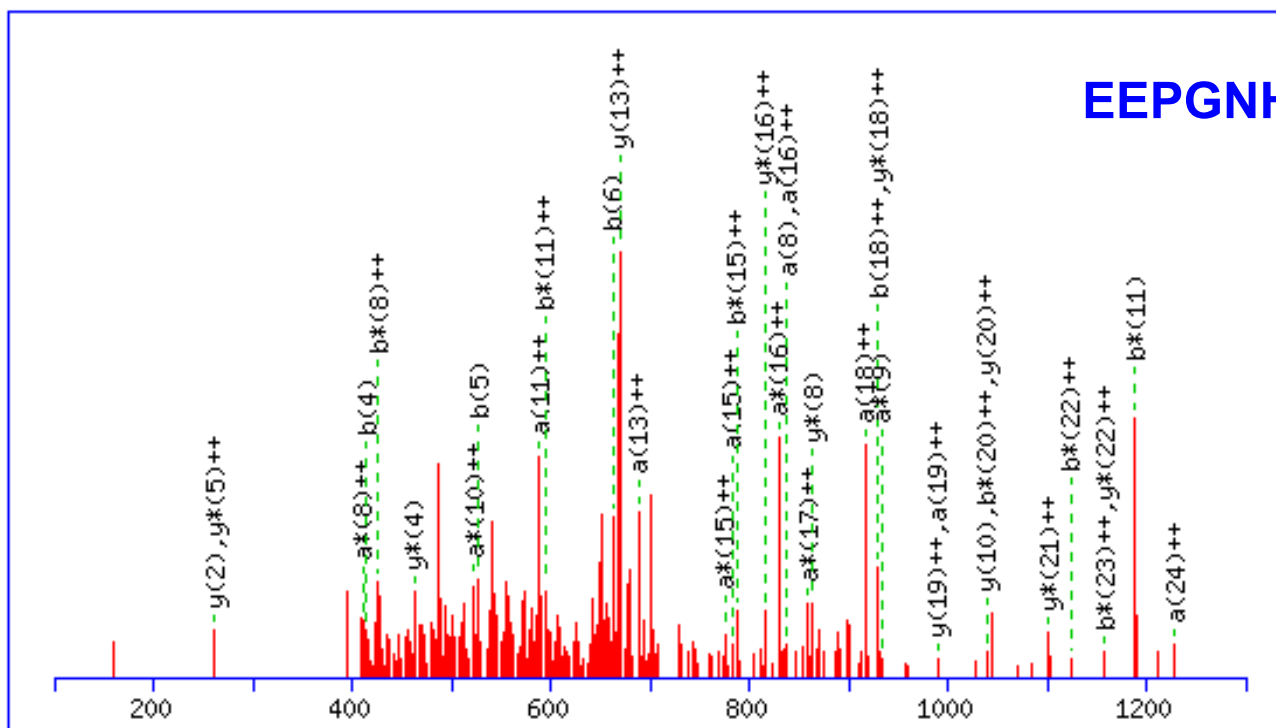
Match to Query 1: 2741.770896 from(686.450000,4+)

Data file C:\DOCUME~1\ecalvo\LOCALS~1\Temp\mas32.tmp

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

ActA



Monoisotopic mass of neutral peptide Mr(calc): 2741.4826

Ions Score: 1 **Expect:** 0.043

Matches (Bold Red): 37/284 fragment ions using 84 most intense peaks

Peptide View

MS/MS Fragmentation of **STTQAVDYQGLLK**

Found in **lmo0433**, Internalin A (InA) (*Listeria monocytogenes* EGD-e)

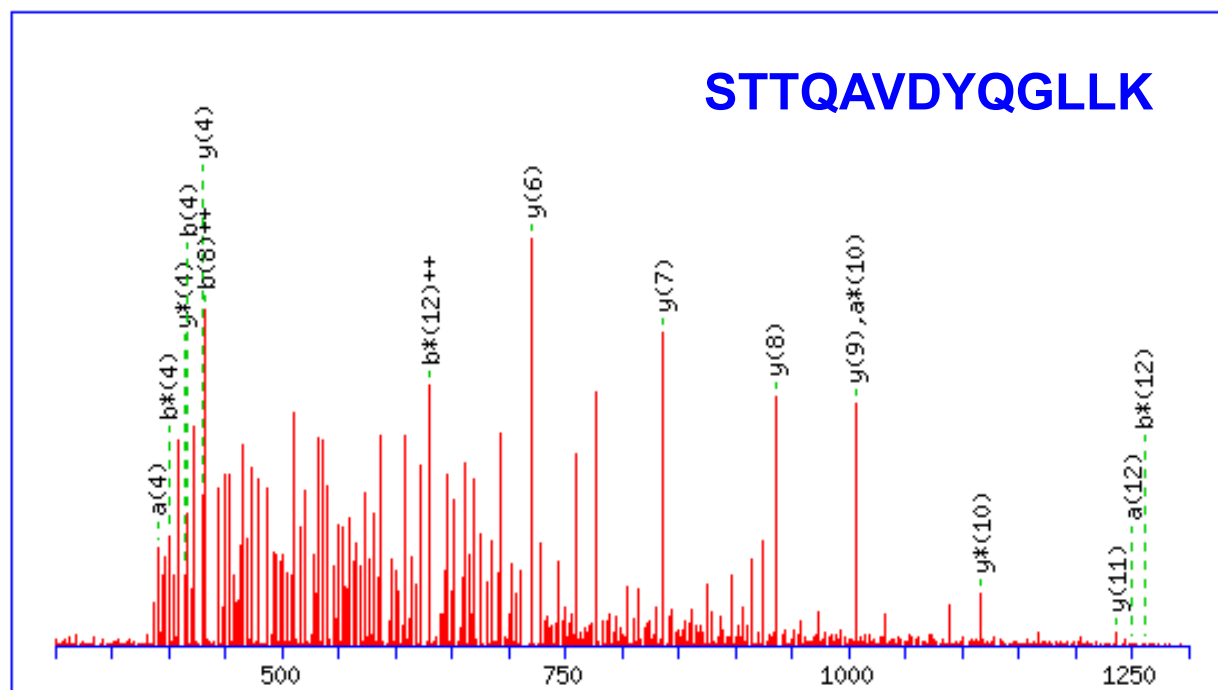
Match to Query 59: 1422.914902 from(712.464727,2+)

Title: File: IMM.wiff, Sample: IMM (sample number 1), Elution: 53.44 to 54.31 min, Period: 1, Cycle(s): 361-366 (Experiment 3)

Data file C:\DOCUME~1\ecalvo\LOCALS~1\Temp\mas44.tmp

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da



Inl-A

Monoisotopic mass of neutral peptide Mr(calc): 1422.7355

Ions Score: 19 **Expect:** 0.034

Matches (Bold Red): 17/132 fragment ions using 39 most intense peaks

Peptide View

MS/MS Fragmentation of **MPANDITLYAQFTK**

Found in **lmo0433**, Internalin A (inlA) (*Listeria monocytogenes* EGD-e)

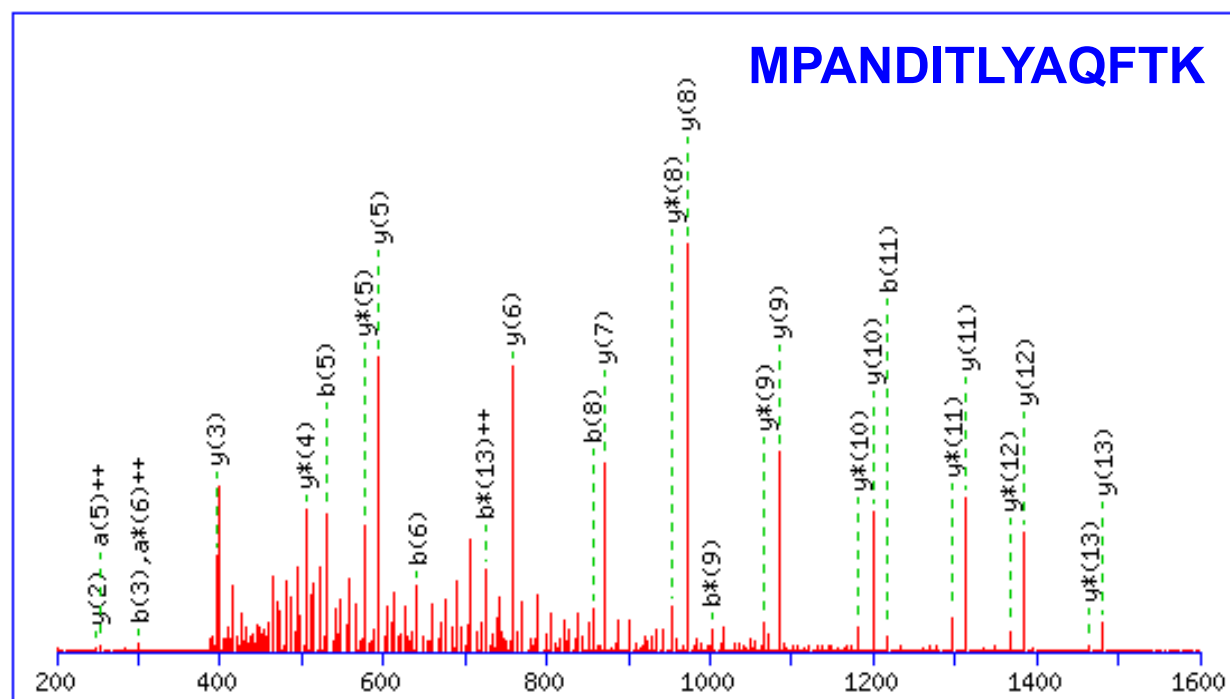
Match to Query 91: 1612.192592 from(807.103572,2+)

Title: File: IMM.wiff, Sample: IMM (sample number 1), Elution: 58.3 to 72.17 min, Period: 1, Cycle(s): 389, 391-398, 403-415, 417-426, 430-431, 450, 452-453, 462, 465, 469 (Experiment 3)

Data file C:\DOCUME~1\ecalvo\LOCALS~1\Temp\mas44.tmp

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da



Inl-A

Monoisotopic mass of neutral peptide Mr(calc): 1611.7967

Ions Score: 73 **Expect:** 8.1e-008

Matches (Bold Red): 29/144 fragment ions using 64 most intense peaks

Peptide View

MS/MS Fragmentation of **NVSAIAGLQSIK**

Found in **lmo0263**, internalin H (InIH) (*Listeria monocytogenes* EGD-e)

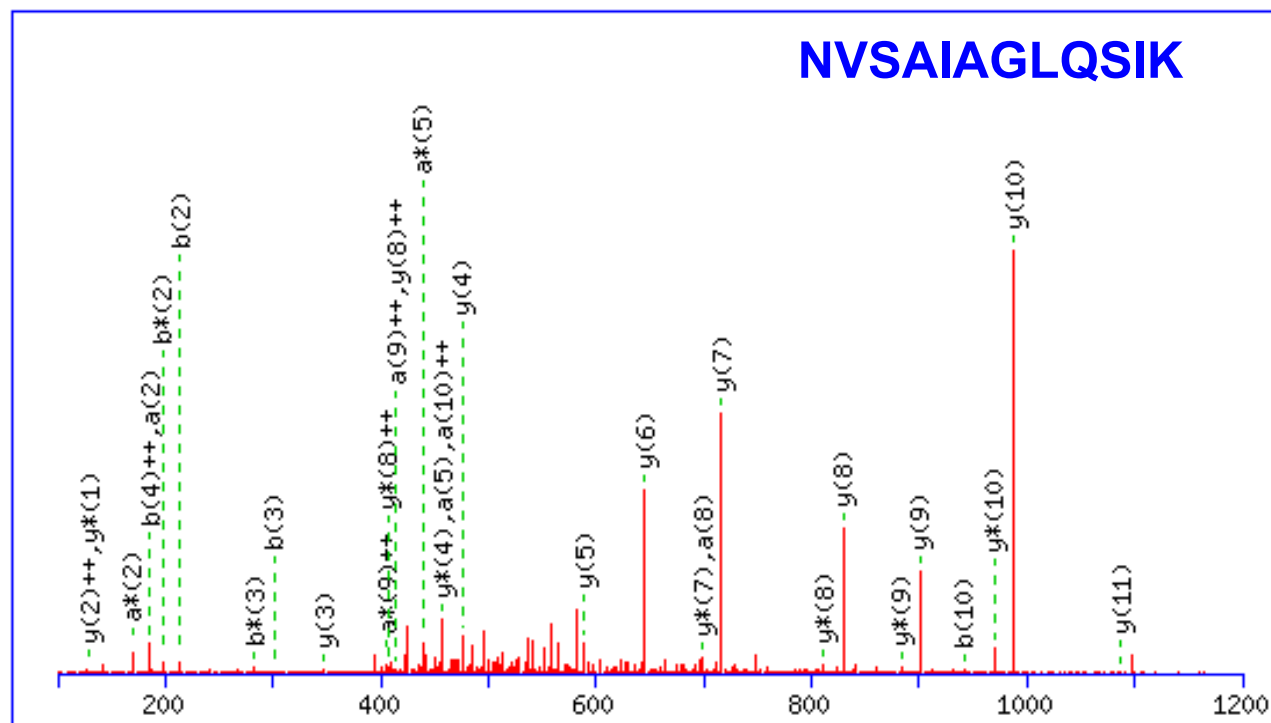
Match to Query 1: 1199.951474 from(600.983013,2+)

Title: File: BHI.wiff, Sample: BHI (sample number 1), Elution: 43.57 to 43.74 min, Period: 1, Cycle(s): 310-311 (Experiment 3)

Data file C:\DOCUME~1\ecalvo\LOCALS~1\Temp\mas45.tmp

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da



InI-H

Monoisotopic mass of neutral peptide Mr(calc): 1199.6874

Ions Score: 60 Expect: 2.8e-006

Matches (Bold Red): 32/132 fragment ions using 46 most intense peaks

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGYTFTGWYDAK**

Found in **lmo0263**, internalin H (inlH) (*Listeria monocytogenes* EGD-e)

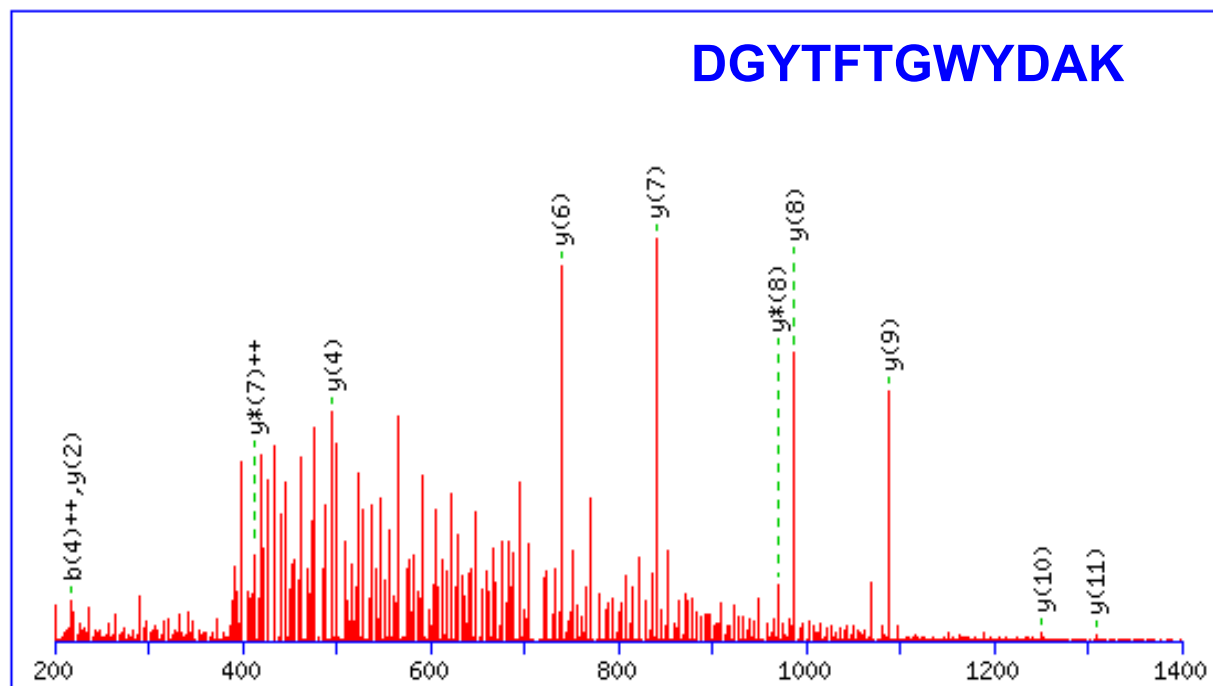
Match to Query 51: 1422.859282 from(712.436917,2+)

Title: File: BHI.wiff, Sample: BHI (sample number 1), Elution: 57.25 to 64 min, Period: 1, Cycle(s): 389, 392-394, 399, 404-405, 407-414, 416-418, 420,

Data file C:\DOCUME~1\ecalvo\LOCALS~1\Temp\mas45.tmp

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da



Inl-H

Monoisotopic mass of neutral peptide Mr(calc): 1422.6092

Ions Score: 53 **Expect:** 1.4e-005

Matches (Bold Red): 11/88 fragment ions using 30 most intense peaks