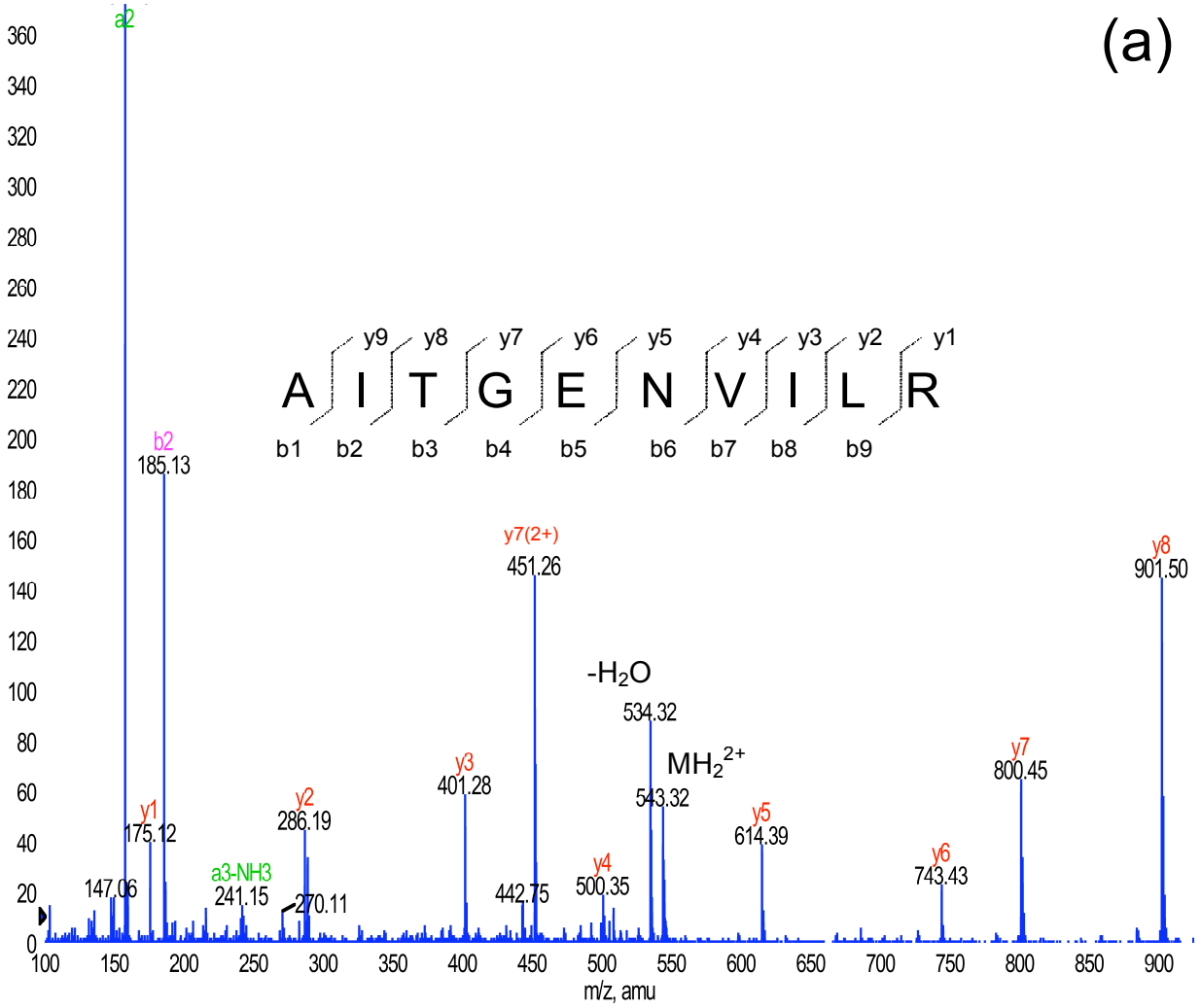
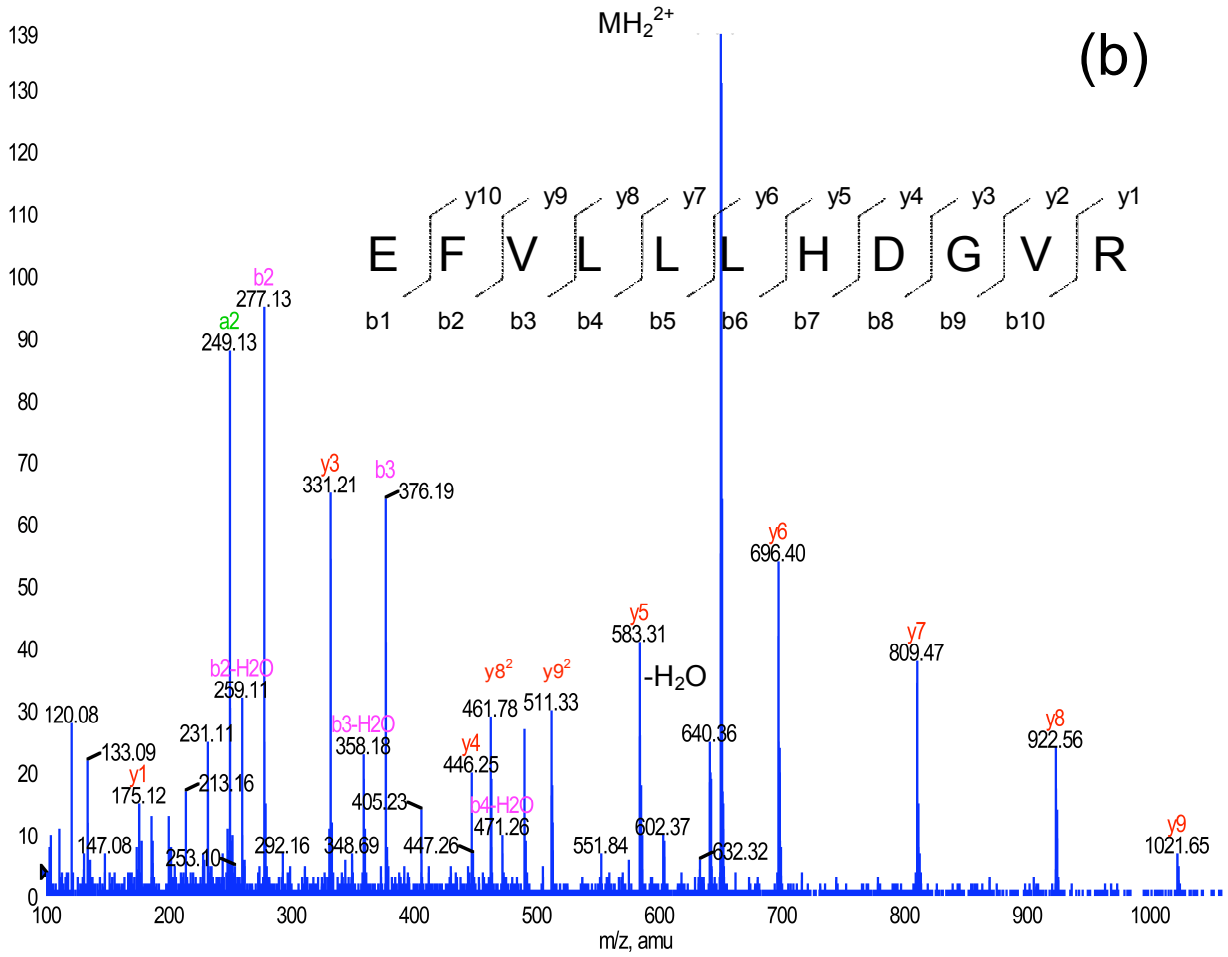
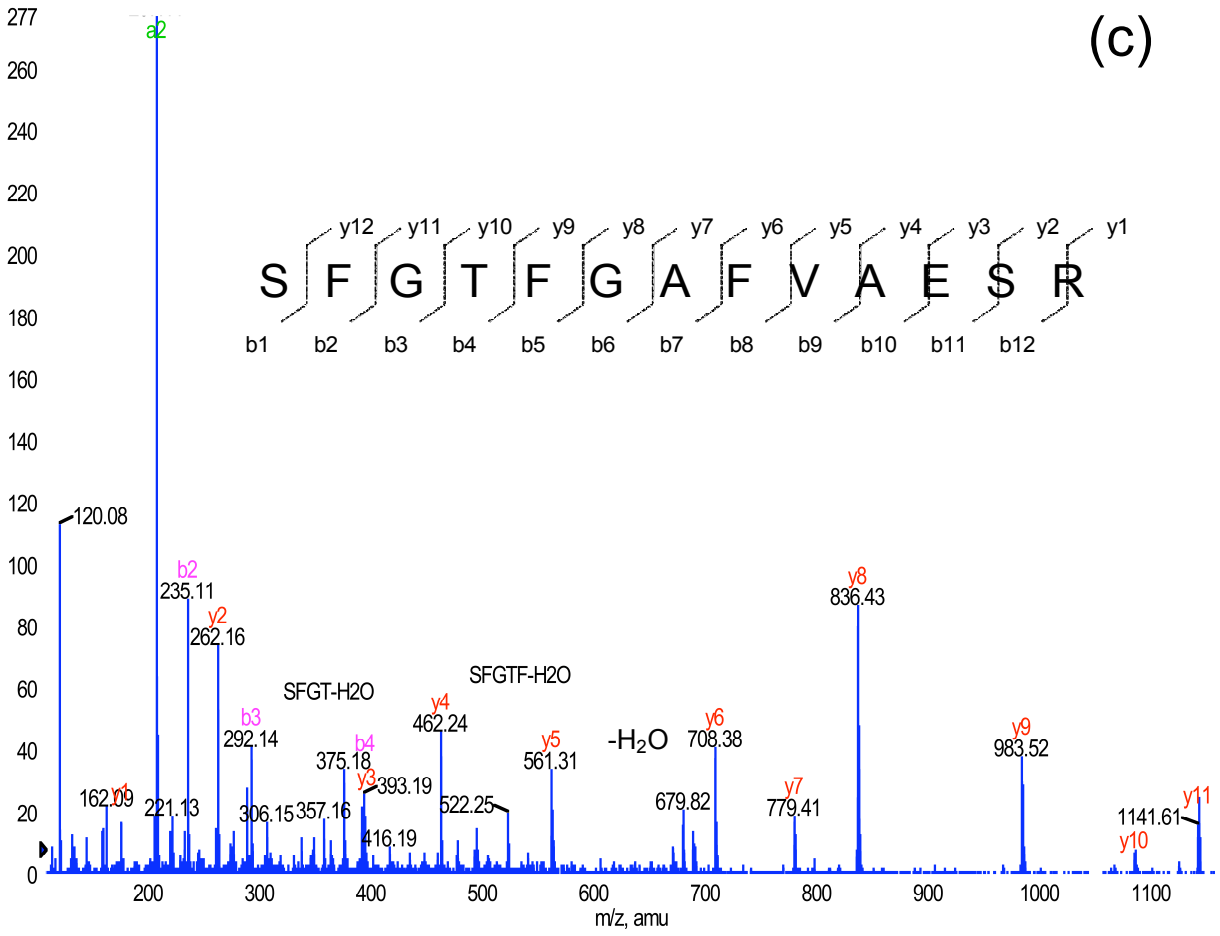
Supplemental Material

Supplemental Figure 1. Representative MS/MS of peptides obtained from in-gel tryptic digest of SDS-PAGE purified Mn oxidase from strain PL-12. MS/MS are acquired by isolating the peptide using a quadrupole mass filter, fragmenting the peptide with collision induced dissociation, and measuring the mass/charge ratio of the fragments produced (1). Fragment ion types are indicated for amide backbone cleavages of (a) *m/z* 543.3, (b) *m/z* 649.4, and (c) *m/z* 688.3 with nomenclature as described by Roepstorff & Fohlman (2). Each peak represents the mass/charge ratio (m/z) of a peptide fragment. The b- and y- type ion series are the result of cleavage at the carbonyl carbon–amide nitrogen bond; b-type ions comprise the N-terminal fragment and y-type ions comprise the C-terminal fragment. The mass difference between successive ions in each series equals the mass of the amino acid at that position, and the order of the ions reveals amino acid sequence. Peak shifts due to loss of water ($-H_2O$) or charge state and protonation of the ion (e.g. MH_2^{2+}) are indicated. For reviews of MS/MS methods and nomenclature, see supplementary references (1-4).


(a)
a2
b2
185.13
y7(2+)
451.26
y8
901.50
-H2O
534.32
MH2 2+
543.32
y3
401.28
y2
286.19
y1
175.12
y5
614.39
y7
800.45
y6
743.43
y4
500.35
a3-NH3
241.15
147.06
270.11
442.75
y9 y8 y7 y6 y5 y4 y3 y2 y1
A I T G E N V I L R
b1 b2 b3 b4 b5 b6 b7 b8 b9
m/z, amu


(b)
MH2 2+
E F V L L L H D G V R
y10 y9 y8 y7 y6 y5 y4 y3 y2 y1
b1 b2 b3 b4 b5 b6 b7 b8 b9 b10
b2 277.13
a2 249.13
y3 331.21
b3 376.19
y6 696.40
y5 583.31
-H2O
y7 809.47
y8 922.56
y9 1021.65
b2-H2O 259.11
y8 2 461.78
y9 2 511.33
b3-H2O 358.18
y4 446.25
b4-H2O 471.26
120.08
133.09
y1 175.12
231.11
213.16
405.23
147.08
253.10
292.16
348.69
447.26
551.84
602.37
640.36
632.32
m/z, amu


(c)
S F G T F G A F V A E S R
y12 y11 y10 y9 y8 y7 y6 y5 y4 y3 y2 y1
b1 b2 b3 b4 b5 b6 b7 b8 b9 b10 b11 b12
277
260
240
220
200
180
160
140
120
100
80
60
40
20
0
120.08
a2
b2
235.11
y2
262.16
b3
292.14
SFGT-H2O
y4
462.24
SFGTF-H2O
b4
375.18
y3
393.19
y5
561.31
-H2O
y6
708.38
y8
836.43
y9
983.52
y7
779.41
y11
1141.61
y10
162.09
y1
221.13
306.15
357.16
416.19
522.25
679.82
200
300
400
500
600
700
800
900
1000
1100
m/z, amu

Supplemental References

1. **Chernushivich, I.V., A.V. Loboda, and B.A. Thomson.** 2001. An introduction to quadropole-time-of-flight mass spectrometry. J. Mass Spectrom. **36**:849-865.
2. **Roepstorff, P., and J. Fohlman.** 1984. Proposal for a common nomenclature for sequence ions in mass spectra of peptides. Biomed. Mass. Spectrom. **11**:601.
3. **Marcotte, E.M.** 2007. How do shotgun proteomics algorithms identify proteins? Nat. Biotechnol. 25:755-757.
4. **Perkins, D.N., D.J.C. Pappin, D.M. Creasy, and J.S. Cottrell.** 1999. Probability-based protein identification by searching databases using mass spectrometry data. Electrophor., **20:**3551-3567.