SUPPORTING INFORMATION

Modification of Heme Peptides by Reverse Proteolysis:
Spectroscopy of Microperoxidase-10 with C-Terminal Histidine,
Tyrosine, and Methionine Residues

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Figure Captions for Supporting Information

Figure 1: Laser-desorption mass spectra of (A) H23MP10; (B) M23MP10; (C) Y23MP10. All experimental masses correspond to the values expected for the peptide with His18-aquo coordination.

Figure 2: FPLC traces for purification of (A) H23MP10; (B) M23MP10; (C) Y23MP10. Reaction mixtures were applied to a Pharmacia PepRPC 16/10 column and eluted with an increasing gradient of acetonitrile containing buffer (buffer A: 0.1% trifluoroacetic acid (TFA), buffer B: 60% acetonitrile; 40% water; 0.1% TFA). Flow rate 5 mL/min. Peaks labelled 1 correspond to the desired X23MP10 product; peaks labelled 2 correspond to MP9 starting material. Peak 3 in the H23 chromatogram does not contain heme.

Figure 3: Low frequency region Raman spectra of (A) Fe(III) Y23MP10; (B) Fe(II) Y23MP10; (C) Fe(III) H23MP10; (D) Fe(II) H23MP10. Arrows in the Y23 spectra indicate vibrations that are not present or significantly less intense in the corresponding Raman spectra of other microperoxidases.
Figure 1C

AVERAGE MASS VALUES

[179.1, 181.2, 184.5]
Figure 3A
Figure 3B
Figure 3D
Figure 3C