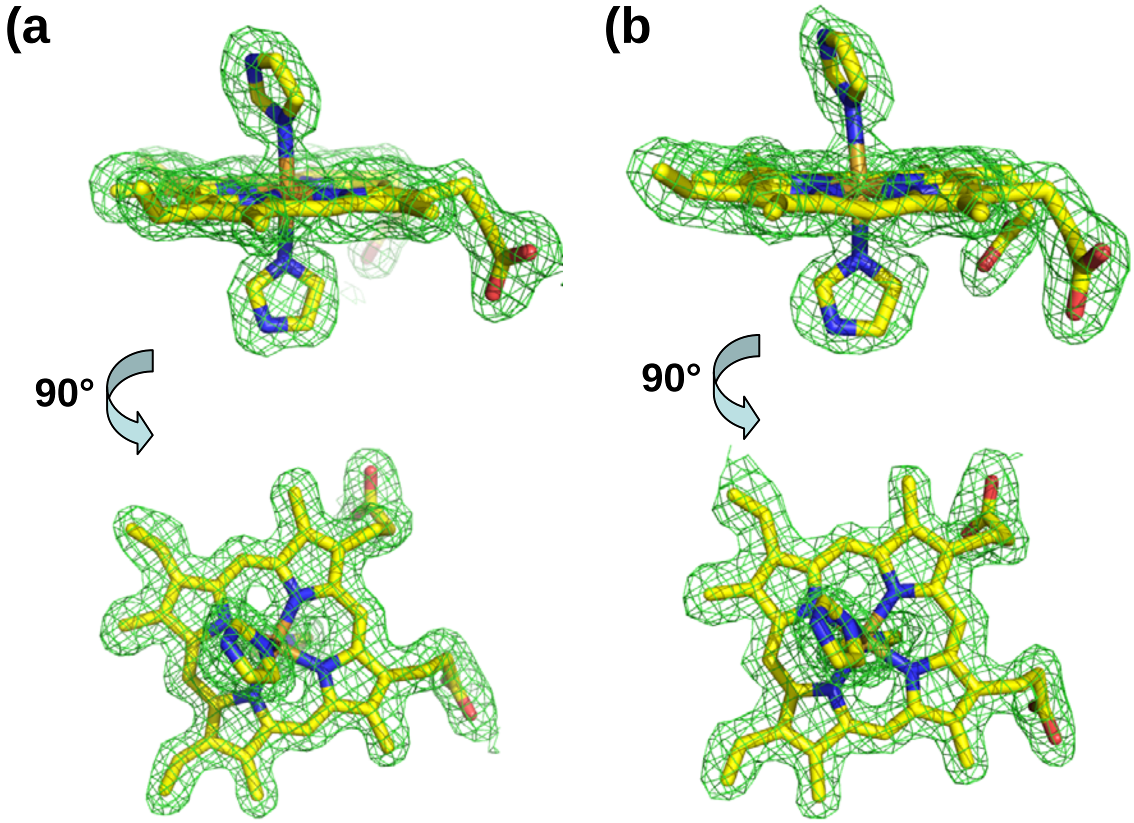
SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure 1. Model and electron density revealing a metallated protoporphyrin IX bound within the active site of the B monomer for the wild-type human ferrochelatase enzyme treated with protoporphyrin IX and either Hg (*Panel a*) or Cd (*Panel b*). The model is shown in stick format and the $2F_o$-F_c composite omit map (*green cage*) was generated using the simulated annealing protocol with 7% of the model omitted per cycle. The lower image in both panels is the same data shown in the top image rotated by 90°. Carbon, nitrogen, oxygen, and iron atoms are colored tan, blue, red, and orange respectively and the composite omit map is contoured at 1 σ.

Supplemental Figure 2. Alignment of the previously published models for the protoporphyrin-bound (*Panel a;* PDB ID 2HRE "Closed" conformation) and the heme bound (*Panel b;* PDB ID 2QD2 "Release" conformation) forms of human ferrochelatase. *Panel a;* Cartoon representation of secondary structure showing an overlay of the 2HRE (Green) and 2QD2 (Light Blue) models. For clarity the structurally conserved π helix is labeled and the regions of the 2HRE and 2QD2 models that differ significantly are highlighted by dark green and dark blue coloring respectively.. *Panel b;* Model in stick format for the porphyrin macrocycles and the relative positions of S130, Y123, and R115. Carbon atoms in the closed model are shown in green while the carbon atoms in the NI-DEUT model are shown in blue. Oxygen, nitrogen, and iron atoms are colored red, blue and dark orange, respectively.

Supplemental Figure 1, Medlock et al.



Supplemental Figure 2, Medlock et al.