
**Figure S1.** Bacterioferritin sequences from different organisms aligned against *P. aeruginosa* BfrB (Pa BfrB): Residues involved in the ferroxidase center, as well as Met-52, which coordinates the heme axially, are highlighted. The sequences were aligned with the aid of ClustalW

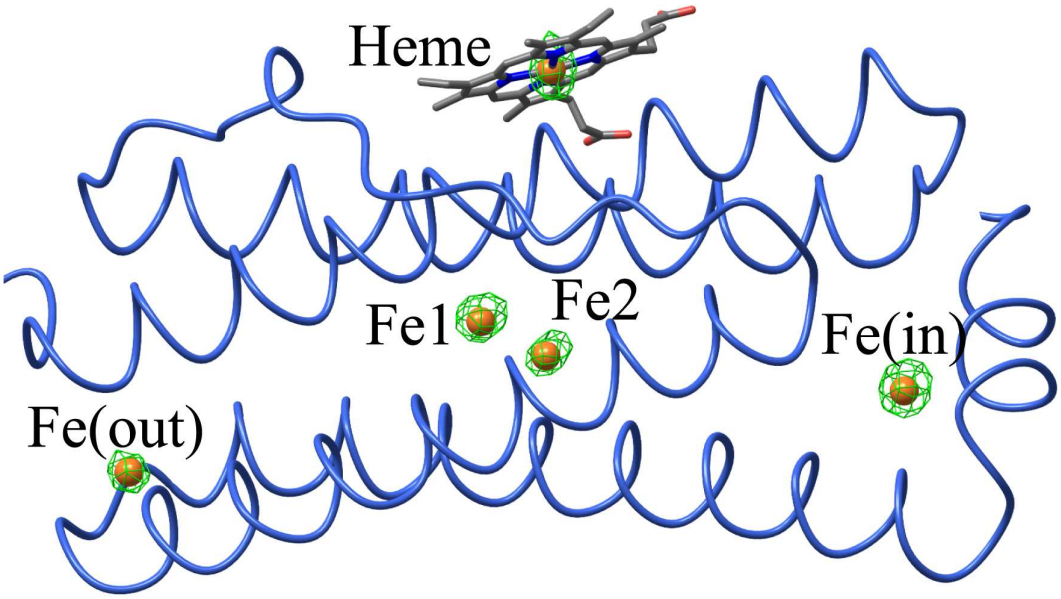


**Figure S2.** Single subunit of BfrB showing the anomalous difference map (green mesh) calculated from data collected at $\lambda$ = 1.6314 Å contoured at 6$\sigma$. Fe atoms are represented as gold spheres and the neighboring heme atoms are drawn as sticks.

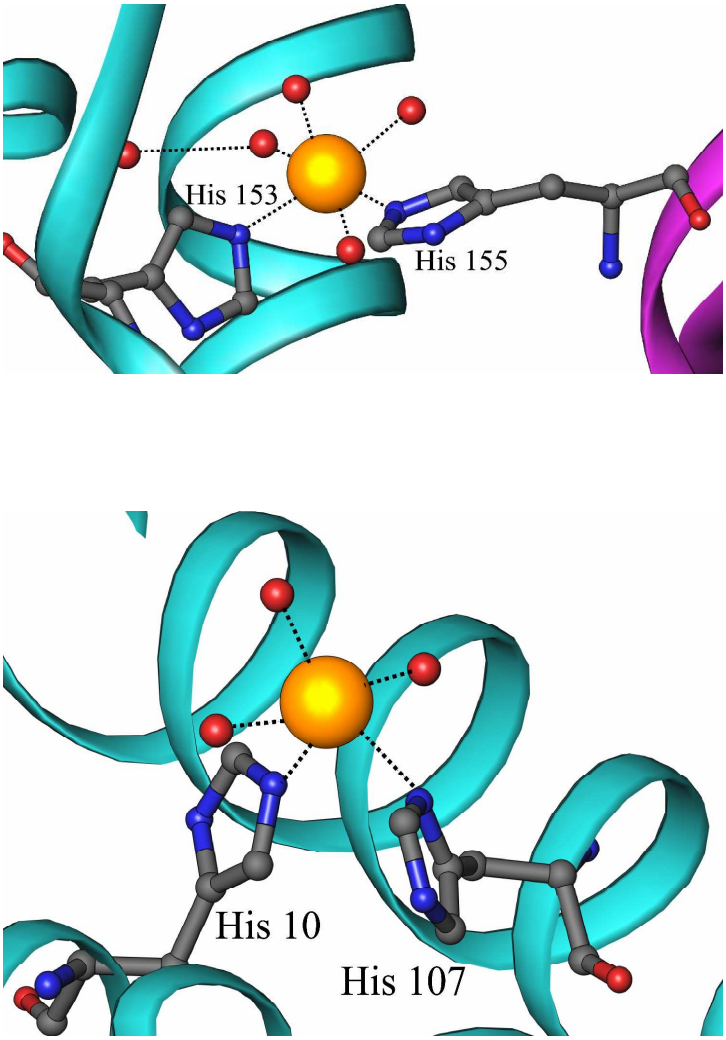


**Figure S3.** Non-bonded contacts between Fe ions and histidine residues. Fe ions and water molecules are represented as gold and red spheres, respectively. (A) $Fe_{in}$ and His 153 from subunit J and His 155 from subunit E. (B) $Fe_{out}$ and surface residues His 10 and His 107.