

	10	20	30	40	50	60	
<i>P.a.</i> BfrB							
<i>A.vinelandii</i>	MKGDKKVIQHLNKILGNELIAINQYFLHSRMWNDWGLKRLGAHEYHESIDE EMK HADKLIE						
<i>E. coli</i>	MKGDKIVIQHLNKILGNELIAINQYFLHARMYEDWGLEKLGKHEYHESIDE EMK HADKLIK						
<i>M.smegmatis</i>	MKGDTKVINYLNKLLGNELVAINQYFLHARMFKNWGLKRLNDVEYHESIDE EMK HADRYIE						
<i>R.capsulatus</i>	MQGDPDVLKLLNEQLTSELTAINQYFLHSKMQDNWGFTELAEHTRAESFE EMR HAETITD						
	70	80	90	100	110	120	
<i>P.a.</i> BfrB							
<i>A.vinelandii</i>	RILFLEGLPNLQDLGKLLIGENTQEMLQCDLNLE E LKATKDLREAIHVCEQVHDYVSRDLL						
<i>E. coli</i>	RILFLEGLPNLQELGKLLIGEHTKEMLECDLK E QAGLPDLKAIAYCESVGDYASRELL						
<i>M.smegmatis</i>	RILFLEGLPNLQDLGKLNIGEDVEEMLRSDL E LDGAKNLREAIGYADSVHDYVSRDMM						
<i>R.capsulatus</i>	RILLDGLPNYQRIFSLRVGQTLREQFEADLA E YEVLERLKP G I I LCREKQDATSARLL						
	130	140	150				
<i>P.a.</i> BfrB							
<i>A.vinelandii</i>	KDILESE E EE H IDYLETQLGLI Q KVGLENLY Q SHMHEDD---						
<i>E. coli</i>	EDILESE E ED H IDWLETQLDL I D K IGLENLY Q SQMDE-----						
<i>M.smegmatis</i>	IEILRD E EG H IDWLETELDL I Q K MG L Q N YL Q A Q IREEG---						
<i>R.capsulatus</i>	EQILAD E E T HIDYLETQLQLMDKLGDALYAAQCVRPPGS A						

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

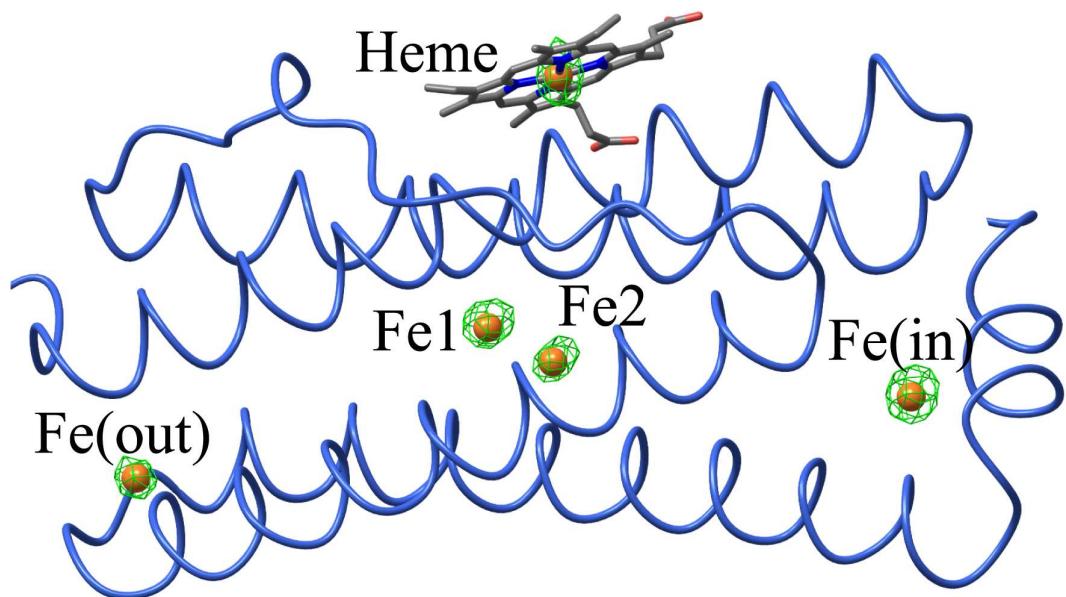


Figure S2. Single subunit of BfrB showing the anomalous difference map (green mesh) calculated from data collected at $\lambda = 1.6314 \text{ \AA}$ contoured at 6σ . Fe atoms are represented as gold spheres and the neighboring heme atoms are drawn as sticks.

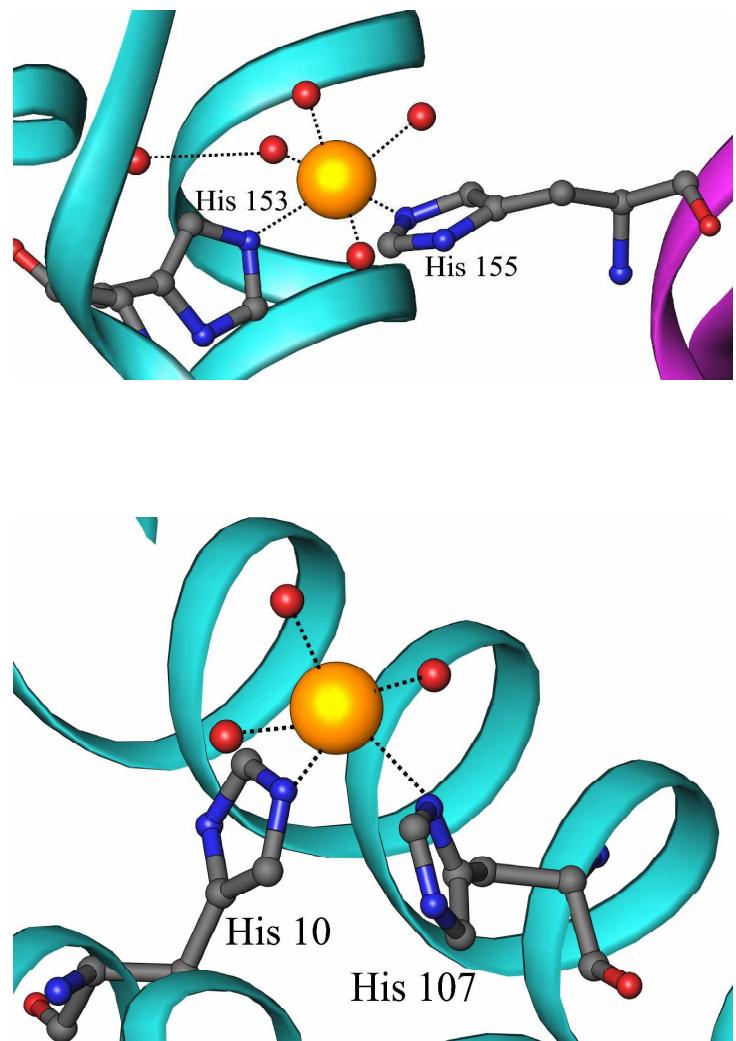


Figure S3. Non-bonded contacts between Fe ions and histidine residues. Fe ions and water molecules are represented as gold and red spheres, respectively. (A) Fe_{in} and His 153 from subunit J and His 155 from subunit E. (B) Fe_{out} and surface residues His 10 and His 107.