

## Electronic supplementary information

### **Role of Hydrogen Bonding to a Heme Propionate Group in the Heme Degradation Reaction by HutZ from *Vibrio cholerae*\***

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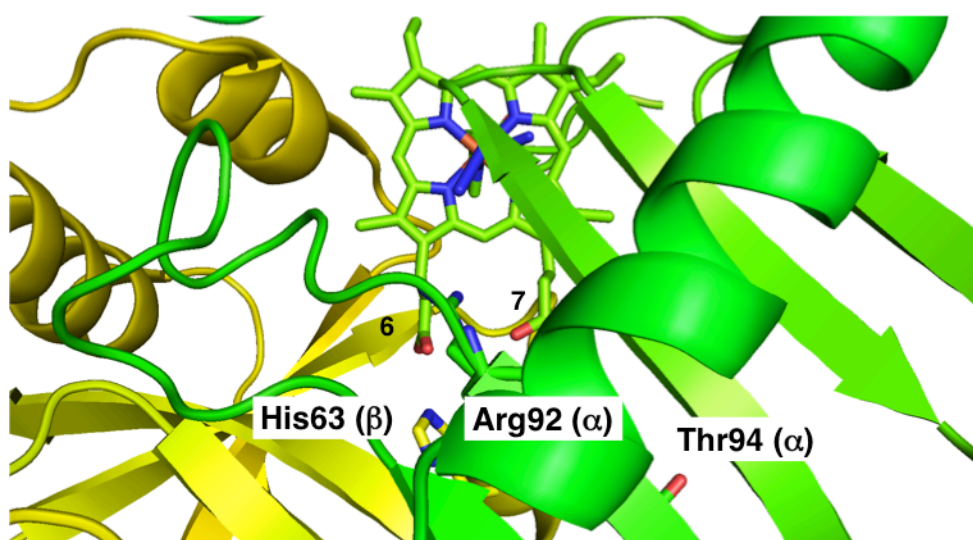
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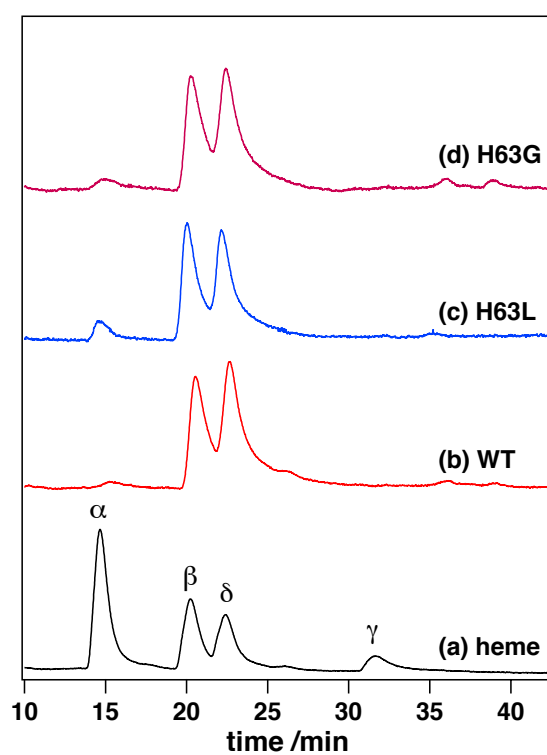
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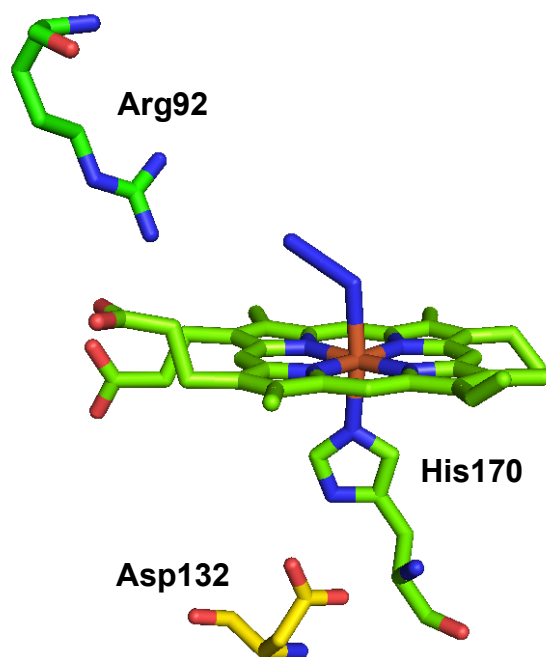
S2-S4



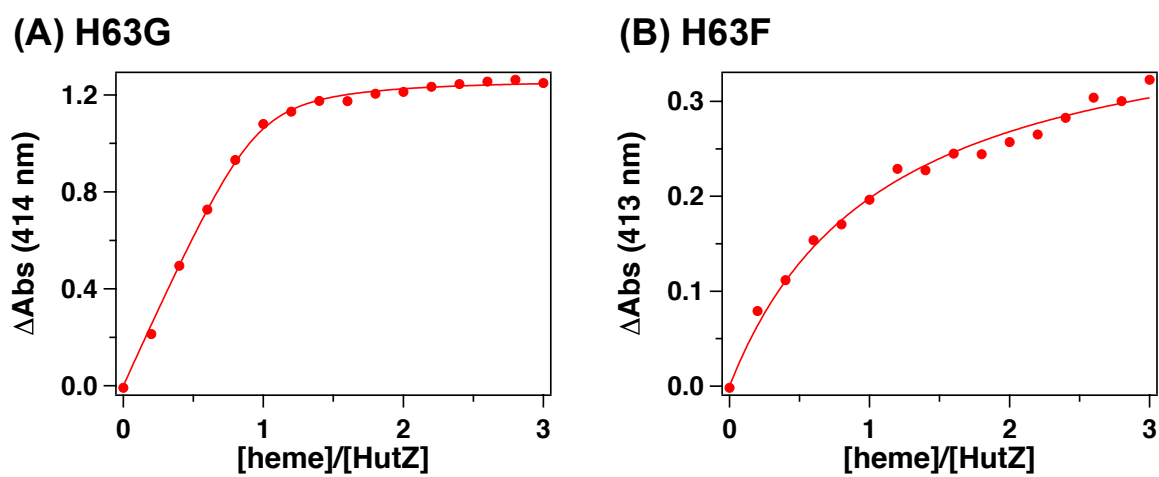
**Fig. S1** Top view of HugZ from *Helicobacter pylori* (PDB ID code 3GAS).



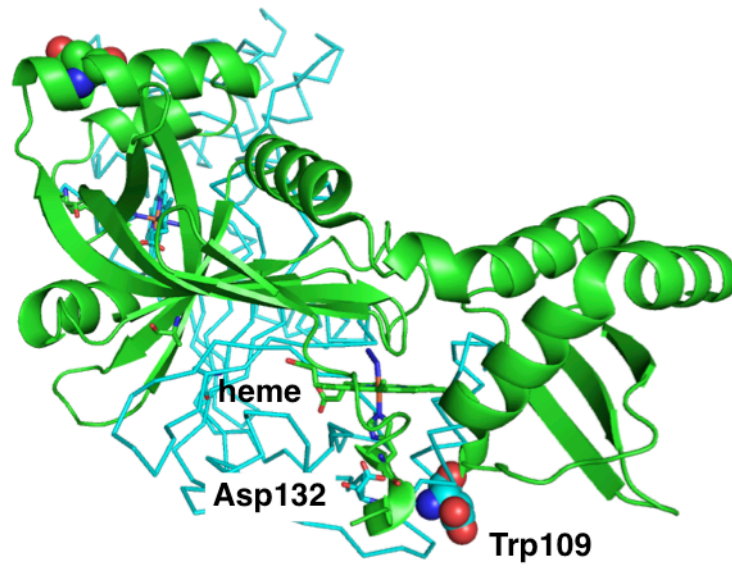
**Fig. S2** Regiospecificity of heme degradation by HutZ. HPLC chromatography of products from reaction of free heme (a), heme-WT (b), heme-H63L mutant (c) and heme-H63G mutant (d) with 0.1 mM  $\text{H}_2\text{O}_2$  and 1 mM ascorbic acid.



**Fig. S3** Crystal structure of HugZ from *H. pylori* (PDB 3GAS) at the heme-binding site. Residues are numbered according to the amino acid sequence of HutZ from *V. cholerae*..



**Fig. S4** Heme titration plots of H63G and H63F mutant HutZ proteins. Heme binding curve generated from the difference absorbance of the Soret maximum by plotting  $\Delta A_{\text{Soret}}$  vs. molar ratios of heme to protein, specifically, H63G (A) and H63F at pH 8.0 (B) at pH 8.0 (D). The protein was in 10  $\mu\text{M}$  in 50 mM Tris-HCl, 150 mM NaCl (pH 8.0).



**Fig. S5** Location of Trp109 and heme on the HugZ crystal structure (PDB 3GAS). Residues are numbered according to the amino acid sequence of HutZ from *V. cholerae*. Green and cyan show each protomer. Trp109 is present in a different protomer (green) from that (cyan) containing nearby Asp132