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

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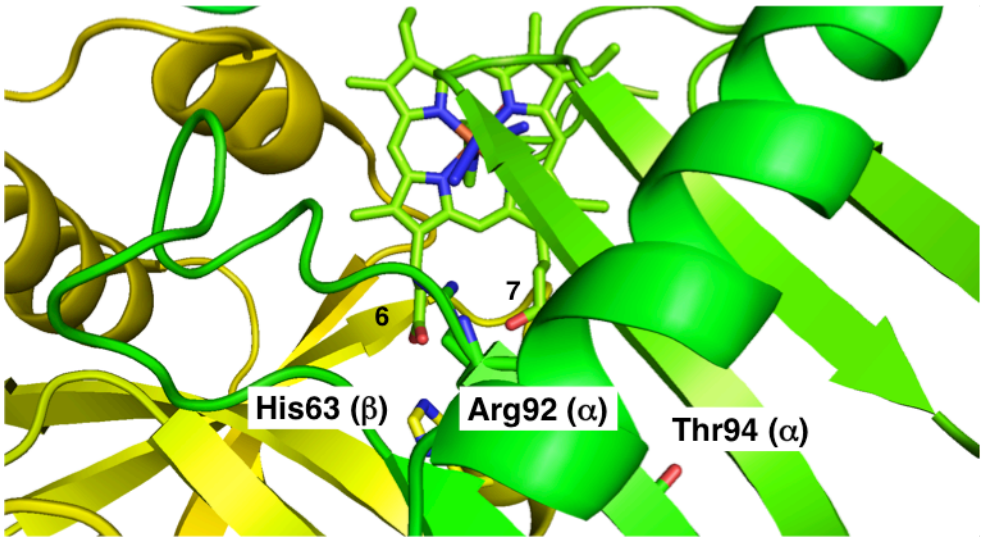


Fig. S1 Top view of HugZ from *Helicobacter pylori* (PDB ID code 3GAS).

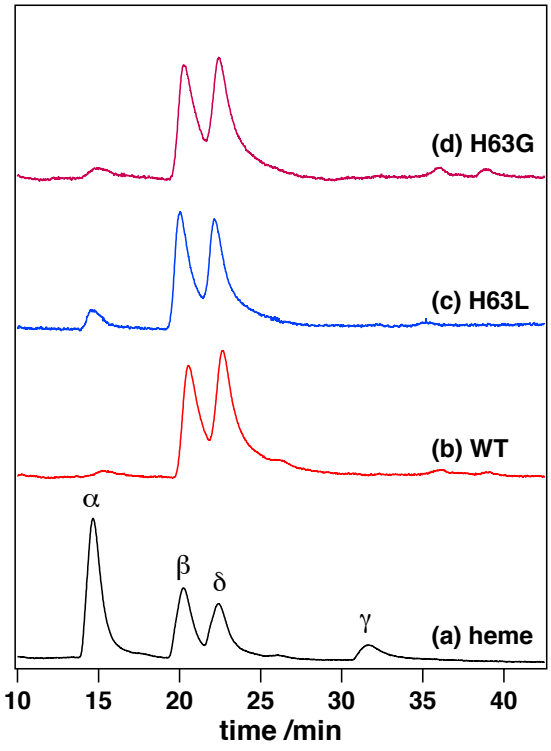


Fig. S2 Regiospecificity of heme degradation by HutZ. HPLC chromatography of products from reaction of free heme (a), heme-WT (b), heme-H63L mutant (c) and heme-H63G mutant (d) with 0.1 mM H_2O_2 and 1 mM ascorbic acid.

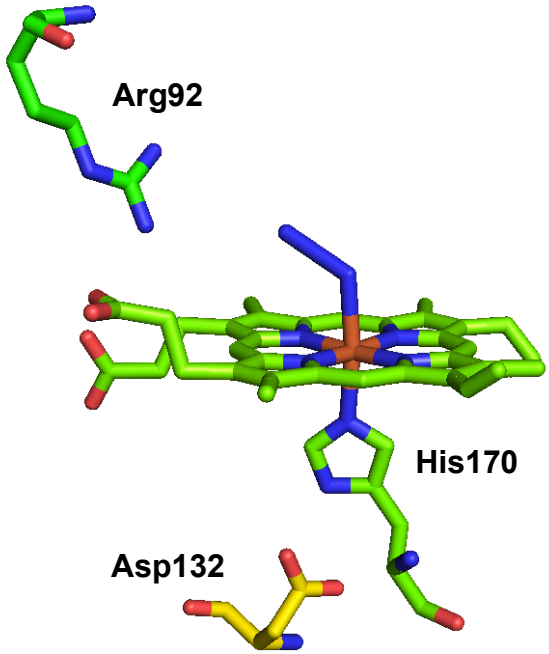


Fig. S3 Crystal structure of HugZ from *H. pylori* (PDB 3GAS) at the heme-binding site. Residues are numbered according to the amino acid sequence of HutZ from *V. cholerae*..

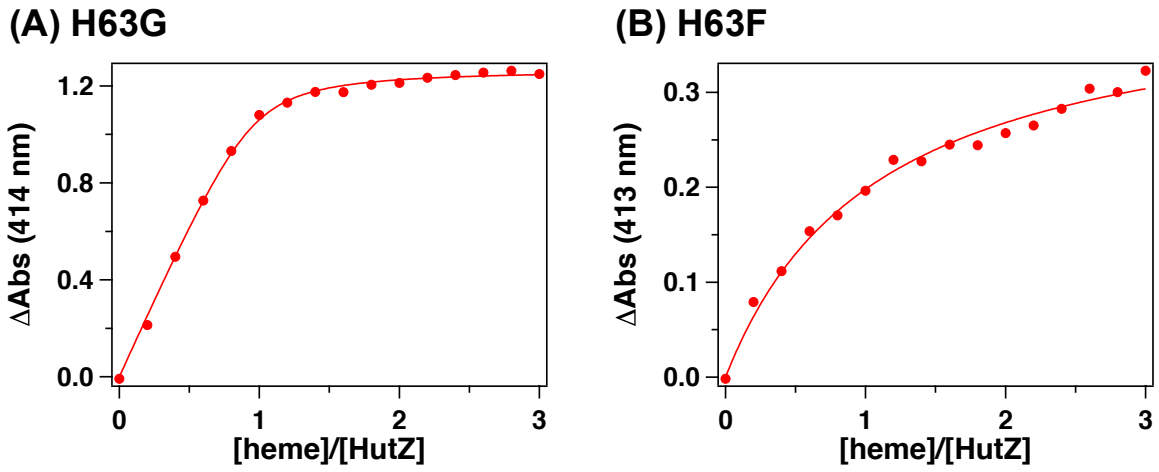


Fig. S4 Heme titration plots of H63G and H63F mutant HutZ proteins. Heme binding curve generated from the difference absorbance of the Soret maximum by plotting ΔA_{Soret} vs. molar ratios of heme to protein, specifically, H63G (A) and H63F at pH 8.0 (B) at pH 8.0 (D). The protein was in 10 μM in 50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

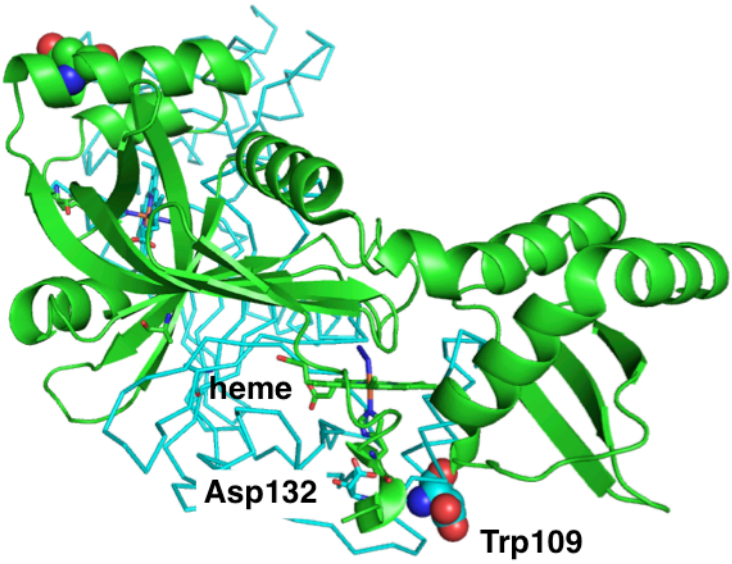


Fig. S5 Location of Trp109 and heme on the HugZ crystal structure (PBD 3GAS). Residues are numbered according to the amino acid sequence of HutZ from *V. cholerae*. Green and cyan show each protomer. Trp109 is present in a different protomer (green) from that (cyan) containing nearby Asp132