## **Supporting Information**

## New Insight Into the Mechanism of Anaerobic Heme Degradation

Liju G. Mathew, Nathaniel R. Beattie, Clayton Pritchett, and William N. Lanzilotta\*

From the Department of Biochemistry and Molecular Biology & Center for Metalloenzyme Studies, University of Georgia, Athens GA 30602.

\*Corresponding author: phone: 706-542-1324; email: wlanzilo@uga.edu

Table S1. Data collection and refinement statistics for Chu.	X
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Data Collection							
Beamline	APS 22-ID						
Space Group	$P3_2$						
a, b, c (Å) <sup>a</sup> Wavelength (Å) Resolution Range (Å) Outer Shell	50.5, 50.5, 208.9 0.97 50.0-1.5 1.55-1.5						
				Unique Observations	95,633		
				Completeness (%) $R_{\text{svm}}$ (%) <sup>b</sup>	97.3(84.1)		
					6.7(44.1)		
$CC^*$ (CC $\frac{1}{2}$ ) outer shell	0.999(0.995)						
Redundancy	13.3(6.7)						
Ι/σ	36.6(1.8)						
Refinement							
Protein Atoms	4237						
Solvent Atoms	196						
Resolution Limits (Å)	50.0-1.98						
$R_{\rm crvst}$ (%)	19.9						
$R_{\text{free}}$ (%)	24.5						
rmsd bonds (Å)	0.009						
rmsd angles (°)	1.14						
average B factor (Å <sup>2</sup> )	30.2						
PDB ID code	6U9J						

<sup>a</sup>Numbers in parentheses denote values for the outermost resolution shell.  ${}^{b}R_{sym} = \sum_{hkl} [\sum_{I} (|I_{hkl,I} - \langle I_{hkl} \rangle)] / \sum_{hkl,I} \langle I_{hkl} \rangle$ , where  $I_{hkl}$  is the intensity of an individual measurement of the reflection with indices hkl and  $\langle I_{hkl} \rangle$  is the mean intensity of that reflection.

Mathew et al., Figure S1.



**Figure S1. Cartoon representation of the ChuW homology model (green) aligned with the model of HemN (cyan, PDB ID 10LT).** The relative positions of the [4Fe-4S] cluster (ball-and-stick) as well as SAM1, SAM2, and D215 (stick) are also shown. Carbon, nitrogen, oxygen, sulfur, and iron atoms are colored tan, blue, red, cyan, brown, and orange respectively.



Figure S2. Plot showing the specific activity measured for ChuW (0.5  $\mu$ M) in the presence of increasing amounts of either ChuX ( $\triangle$ ) or ChuY ( $\bigcirc$ ). The data is presented as the concentration of ChuX or ChuY (*Panel A*) or the ratio of ChuX or ChuY relative to ChuW (*Panel B*) present in the assay.