

The HHM Motif at the CuH-site of Peptidylglycine Monooxygenase is a pH-Dependent Conformational Switch†.

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Supporting Information

Table S1. Oligonucleotides used in the construction of PHM H-site H108A and M109I variants.

PHMcc Mutant Oligos	
	Oligos
H108A	AGCATGGATACTGTCCAC GCT ATGCTGCTGTTTGGATGC
M109I	AGCATGGATACTGTCCACCAT ATA CTGCTGTTTGGATGC
WT	AGCATGGATACTGTCCACCATATGCTGCTGTTTGGATGC

The forward primers are shown above with the mutated codon in bold while the reverse primers are complementary. WT PHMcc sequence is available for comparison.

Figure S1. Experimental (black) and simulated (red) EXAFS and Fourier transforms for reduced forms of PHM H-site variants at pH 7.5.

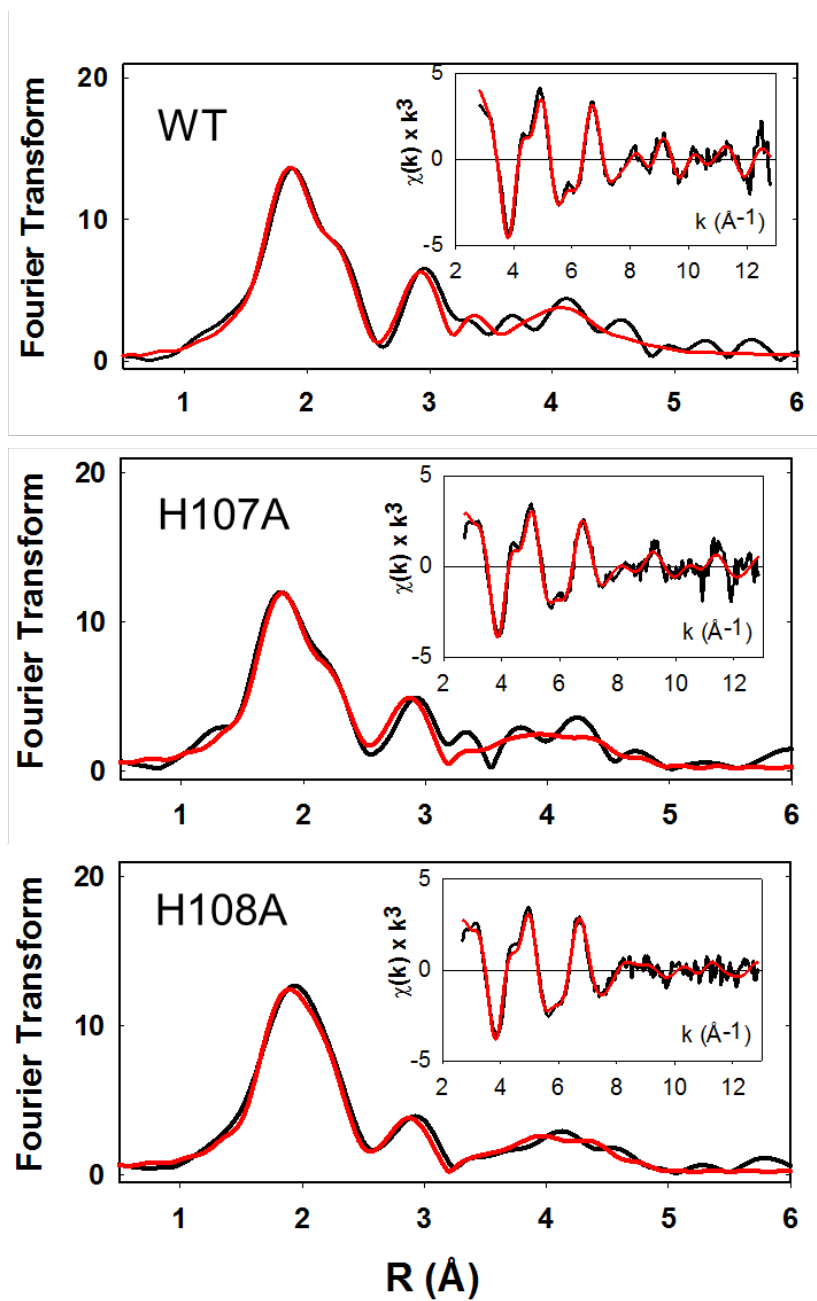


Figure S2. Experimental (black) and simulated (red) EXAFS and Fourier transforms for reduced forms of PHM H-site variants at pH 3.5.

