



J. Am. Chem. Soc., 1998, 120(13), 3247-3248, DOI:[10.1021/ja972968+](https://doi.org/10.1021/ja972968+)

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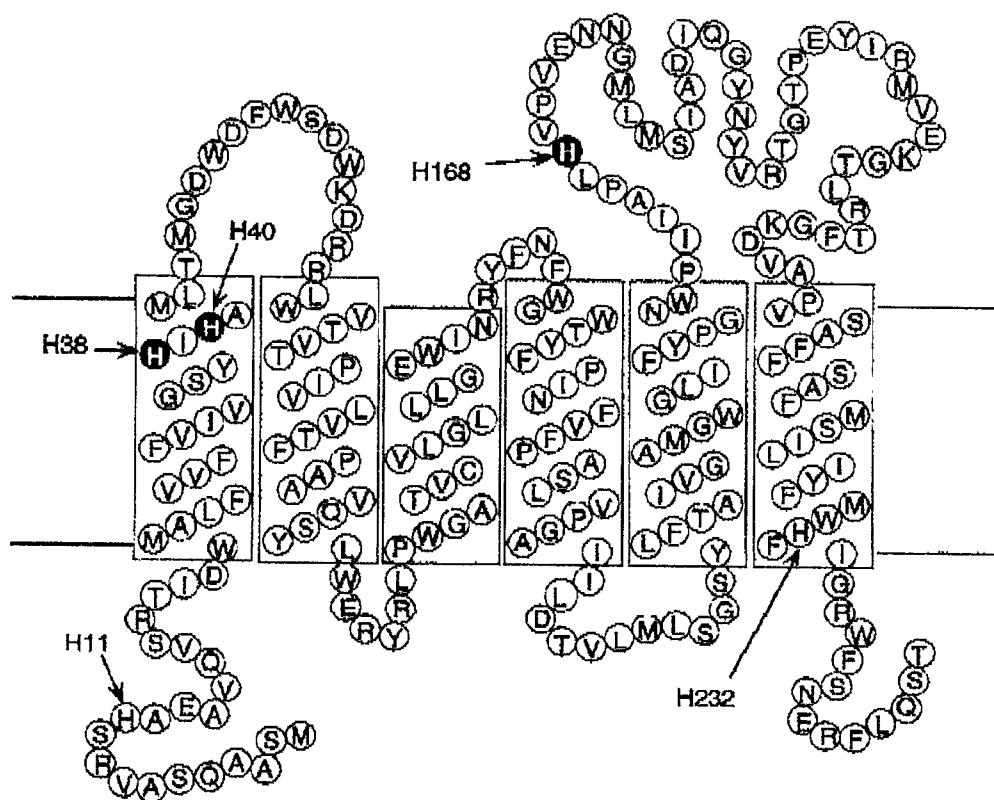
Figure S1

Figure S1. Schematic of the amino acid sequence of the PmoA protein, with assignment of transmembrane helices via analogy to Hooper and coworkers model of AmoA (ref. 25, main text). Histidines are indicated as identical in the sequences published to date (black circles) or variable (white circle; from ref. 24, main text).

Pulsed EPR Studies of Particulate Methane Monooxygenase from *Methylococcus capsulatus* (Bath): Evidence for Histidine Ligation

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Table S1

Sample	e^2qQ (MHz)	η	ref.
pMMO	1.60	0.98	--
dopamine β -hydroxylase	1.44	0.98	1
amine oxidase ^a	1.73	0.48	2
stellacyanin	1.49	0.94	3
$\text{Ag}^{\text{I}}_2\text{Cu}^{\text{II}}_2$ -superoxide dismutase	1.44	0.94	4
T2-laccase	1.47	0.83	5
T2-ascorbate oxidase ^a	1.56	0.83	6
Cu(II)-hemocyanin	1.52	0.92	7
galactose oxidase ^a	1.70	0.65	8
phenylalanine hydroxylase	1.68	0.55	9
coalbumin ^a	1.53	0.91	10

^a As quoted in reference 3.

Table S1. Summary of ^{14}N nqi parameters for copper(II) proteins, and the nqi parameters from pMMO ESEEM shown in Figure 1.

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