Fig. S1. Sequence alignment of the *E. coli* Aer PAS/F1α region and MmoS (PAS-A) from *Methylococcus capsulatus* (Bath) (2).The Aer sequence begins after the N-cap loop and extends through the F1α segment. Aer-F1α aligns with the linker in MmoS that connects PAS-A to PAS-B. Residues identical to those of Aer are highlighted in green, while those similar to Aer are highlighted in magenta. The predicted secondary structural elements for Aer are shown as yellow rectangles for helices and as arrows for β-strands. The asterisks (*) highlight non-reactive (uncrosslinked) cysteine substitutions in Aer that fall on the same face of a helical model (see Fig. 3). The alignment was made with ClustalW (1).

1.   **Larkin, M. A., G. Blackshields, N. P. Brown, R. Chenna, P. A. McGettigan, H. McWilliam, F. Valentin, I. M. Wallace, A. Wilm, R. Lopez, J. D. Thompson, T. J. Gibson, and D. G. Higgins.** 2007. Clustal W and Clustal X version 2.0. Bioinformatics **23:**2947-8.
2.   **Ukaegbu, U. E., and A. C. Rosenzweig.** 2009. Structure of the redox sensor domain of *Methylococcus capsulatus* (Bath) MmoS. Biochemistry **48:**2207-15.