Supporting Information

Structure and interactions of the C-terminal metal binding domain of Archaeoglobus $fulgidus \ {\tt CopA}$

Sorabh Agarwal,¹ Deli Hong,² Nirav K. Desai,¹ Matthew H. Sazinsky,^{1,3} José M. Argüello,^{2*} and Amy C. Rosenzweig^{1*}

¹Departments of Biochemistry, Molecular Biology, and Cell Biology and of Chemistry, Northwestern University, Evanston, Illinois 60208

²Department of Chemistry and Biochemistry, Worcester Polytechnic Institute, Worcester, Massachusetts 01609

³Present address: Department of Chemistry, Pomona College, Claremont, California 91711

*Correspondence to: Amy C. Rosenzweig, Dept. BMBCB, Northwestern University, 2205 Tech Drive, Evanston, IL 60208, e-mail, amyr@northwestern.edu or José M. Argüello, Dept. of Chemistry and Biochemistry, Worcester Polytechnic Institute, 100 Institute Rd., Worcester, MA 01609, e-mail, arguello@wpi.edu.

Grant sponsor: NIH; Grant number: GM58518 (A. C. R.). NSF; Grant number: MCB-0743901 (J. M. A). NIH; Grant number: GM8382 (S. A). NIH; Grant number: GM073457 (M. H. S).

Running title: The C-terminal metal binding domain of CopA

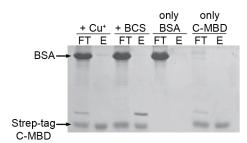


Figure S1 Absence of interaction between C-MBD and BSA. SDS-PAGE of a representative co-purification assay using streptactin resin. 40% of unbound protein (FT) and 40% of bound protein (E) fractions were loaded in each lane.

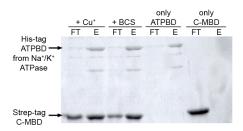


Figure S2 Interaction assay between C-MBD (20 μ g) and Na⁺/K⁺-ATPase ATP-BD (49 μ g). SDS-PAGE of a representative co-purification assay between Na⁺/K⁺-ATPase and either C-MBD or Cu⁺-loaded C-MBD. 40% of unbound protein (FT) and 40% of bound protein (E) fractions were loaded in each lane.