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Structural Studies of Gas Binding in *Hansenula Polymorpha* Copper Amine Oxidase. B. J. Johnson[#], B. J. Brazeau[#], D. L. Wertz^{*}, J. Klinman^{*}, C. M. Wilmot[#], [#]Univ. of Minnesota, Dept. of Biochem., Mol. Biol. and Biophys., Minneapolis, MN 55455, ^{*}Univ. of California, Depts. of Chem. and Mol. and Cell Biol., Berkeley, CA 94720.

Copper amine oxidases (CAO) are homodimeric enzymes that convert primary amines to aldehydes, ammonia and H₂O₂. Each monomer contains a Cu(II) ion and a 2,4,5-trihydroxyphenylalanine quinone (TPQ) cofactor. Studies of TPQ biogenesis have shown it to be autocatalytic, requiring only the presence of copper and O₂. O₂ is also key in the oxidative-half reaction of CAO, returning the substrate reduced aminoquinol TPQ back to the oxidized quinone state. However, the exact location and timepoint of O₂ binding in the catalytic mechanism remains unclear.

The crystal structure of oxidized wild type *H. polymorpha* amine oxidase (wtHPAO) was solved previously.¹ In this study, gas binding will be observed in wtHPAO as well as mutants with altered O₂ binding. Diatomic O₂ mimics Xe, CO, NO and NO₂ will be complexed to substrate reduced wtHPAO anaerobically to investigate O₂ binding. In addition, parallel studies of O₂ binding mutants will provide insight into the specific amino acids that play a role in directing and assisting O₂ binding. We will present preliminary x-ray data from these studies.

¹R. Li, J.P. Klinman, F.S. Mathews, *Structure*, 1998 Mar 15;6(3):293-307