

## W0142

**Dioxygen Activation in *Hansenula polymorpha* Amine Oxidase.** B.J. Johnson<sup>a</sup>, A. Pearson<sup>a</sup>, J. Klinman<sup>b</sup>, C. Wilmot<sup>a</sup>, <sup>a</sup>Dept. of Biochem., Mol. Biol. and Biophys., Univ. of Minnesota, Minneapolis, MN 55455, <sup>b</sup>Depts. of Chem. and Mol. and Cell Biol., Univ. of California, Berkeley, CA 94720 USA.

Copper amine oxidases (CAO) are homodimeric enzymes that convert primary amines to aldehydes and O<sub>2</sub> to H<sub>2</sub>O<sub>2</sub>. Each monomer contains a Cu(II) ion and a 2,4,5-trihydroxyphenylalanine quinone (TPQ) cofactor. O<sub>2</sub> is essential 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 O<sub>2</sub> binding and activation in the oxidative half-reaction remains unclear.

The crystal structure of oxidized *H. polymorpha* amine oxidase (HPAO) was solved previously [1]. In this study, gas binding is observed in freeze-trapped HPAO. Xe can be used to map hydrophobic sites in proteins where molecular O<sub>2</sub> may bind. CO and NO are oxygen mimics used extensively in solution studies to probe dioxygen activation. These gases are complexed to oxidized HPAO as well as anaerobically methylamine reduced HPAO in the crystal. The resulting structures give insight into O<sub>2</sub> binding and activation.

[1] Li R., Klinman J.P., Mathews F.S., *Structure*. 1998, 6(3), 293.