Dioxygen Activation in *Hansenula polymorpha* Amine Oxidase

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Copper amine oxidases (CAO) are homodimeric enzymes that convert primary amines to aldehydes and O_2 to H_2O_2. Each monomer contains a Cu(II) ion and a 2,4,5-trihydroxyphenylalanine quinone (TPQ) cofactor. O_2 is 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 O_2 binding in the oxidative half-reaction remains unclear.

The crystal structure of oxidized wild type *H. polymorpha* amine oxidase (wtHPAO) was solved previously [1]. In this study, gas binding is observed in wtHPAO as well as mutants with altered O_2 activation kinetics. Xe can be used to map hydrophobic sites in proteins where molecular O_2 may bind. CO and NO are oxygen mimics used extensively in solution studies to probe dioxygen activation. These gases are complexed to substrate reduced wtHPAO anaerobically in the crystal. The resulting structures give insight into O_2 binding and activation. In addition, parallel structural studies of O_2 binding mutants provide insight into the specific amino acids that play a role in directing and assisting O_2 binding.

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

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