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Catching Catalysis in the Act: Using Single Crystal Kinetics to trap Methylamine Dehydrogenase Reaction Intermediates. Teresa De la Mora-Rey, Arwen R. Pearson, Kevin T. Watts, Ed Hoeffner, Carrie Wilmot, Univ., of Minnesota, Dept. of Biochemistry, Molecular Biology & Biophysics, Minneapolis, MN 55455, USA.

Methylamine dehydrogenase (MADH) is a soluble periplasmic $\alpha_2\beta_2$ heterotetrameric enzyme, present in many methylotropic bacteria, that catalyzes the oxidation of methylamine to formaldehyde and ammonia. It is upregulated by the presence of substrate, and enables bacterial growth on methylamine as the sole carbon and nitrogen source. The redox center is tryptophan tryptophylquinone (TTQ) which is composed of two Trp residues that are posttranslational modified by a covalent cross-link and an addition of an o-quinone group to one of the Trps. Amicyanin (a type I blue copper protein) is the redox partner of MADH and it is also induced in the presence of methylamine. The reaction during turnover gives distinct spectral features in the visible region, which define specific electronic states of the cofactor.

The use of single crystal kinetics, microspectrophotometry and X-ray crystallography of the holo- (with Cu) and apo- (without Cu) complexes of MADH with amicyanin allows the study of the structures of these electronic states of the TTQ cofactor. In this presentation the structural features of N-quinol and N-semiquinone catalytic intermediates are examined.