

Poster Presentation

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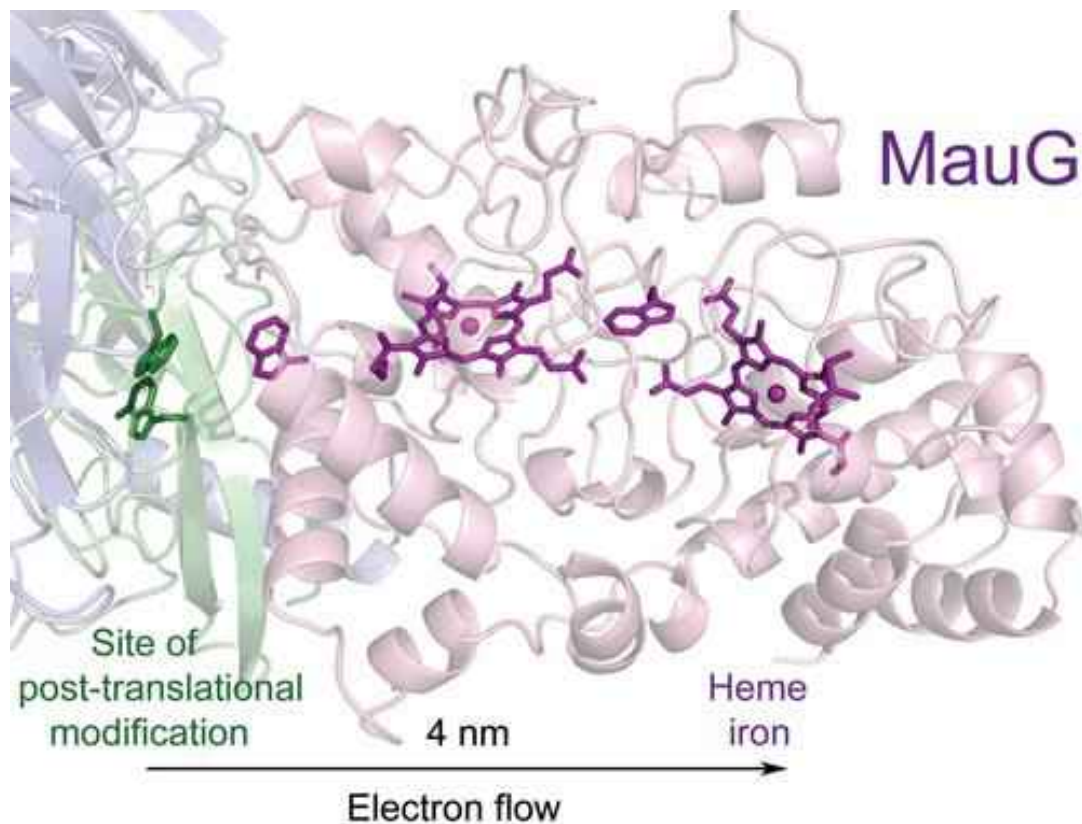
MauG catalysis: a tale of ferryl iron, radicals and long distance hopping

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Methylamine dehydrogenase (MADH) enables some methylotrophic/autotrophic bacteria to grow on methylamine as a sole source of carbon and energy. MADH catalysis depends on the cofactor tryptophan tryptophylquinone (TTQ) that is a posttranslational modification of two Trp residues in the MADH β -subunit. The maturation of MADH depends on four gene products located in the methylamine utilization (*mau*) gene cluster. One of these, *mauG*, encodes a c-type di-heme enzyme that completes synthesis of the TTQ cofactor. The potent oxidant is an unusual bis-Fe(IV) MauG species composed of a ferryl heme (Fe(IV)=O) with an oxidizing equivalent stored as Fe(IV) at the second heme, which has an unusual His, Tyr axial ligation. The bis-Fe(IV) oxidant is formally Fe(V) and equivalent to Compound I. Completion of TTQ to generate active MADH involves long-range electron transfer and a radical hopping mechanism to effect catalysis over a 40 Å distance. The MauG catalyzed reaction occurs in three discrete 2-electron events in a hydrogen peroxide or molecular oxygen (+ reducing equivalents) dependent process. A crystal structure of MauG in complex with its protein substrate, a precursor form of MADH known as preMADH, has been solved. The crystals are catalytically active. The order of the 2-electron chemistry catalyzed by MauG was determined through a series of structures from crystals harvested after different amounts of time following crystallization. Hydrogen peroxide to initiate the reaction was generated by the slow breakdown of polyethylene glycol used in crystallization. These in crystallo data are corroborated by mass spectrometry in solution experiments.

[1] L. Jensen, R. Sanishvili, V. Davidson, C. Wilmot, *Science*, 2010, 327, 1392-1394, [2] E. Yuki, F. Liu, J. Krzystek, S. Shin, L. Jensen, V. Davidson, C. Wilmot, A. Liu, *Proc. Natl. Acad. Sci., USA*, 2013, 110, 4569-4573



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