

## E0010

**Preliminary structural studies of MauG, a novel di-heme protein involved in tryptophan tryptophylquinone (TTQ) biogenesis.** A.R. Pearson<sup>\*</sup>, Y. Wang<sup>†</sup>, M.E. Graichen<sup>†</sup>, T. De la Mora-Rey<sup>\*</sup>, A. Liu<sup>†</sup>, V.L. Davidson<sup>†</sup>, C.M. Wilmot<sup>\*</sup>, <sup>\*</sup>Dept. of Biochem., Mol. Biol. and Biophys., Univ. of Minnesota, Minneapolis, MN 55455, <sup>†</sup>Dept. of Biochem., Univ. of Mississippi Medical Center, Jackson, MS 39216.

MauG catalyses the final stages of tryptophan tryptophylquinone (TTQ) biosynthesis. TTQ is the protein derived cofactor of the *P. denitrificans* enzyme, methylamine dehydrogenase (MADH) which is induced in response to growth on methylamine. TTQ is derived from two tryptophan residues in a multi-step biosynthesis which involves the incorporation of two carbonyl oxygens into  $\beta$ W57 and crosslinking of  $\beta$ W57 to  $\beta$ W108. Unlike other protein derived cofactors the biogenesis of TTQ is not autocatalytic and requires the co-expression of four other genes, *mauD*, *E*, *F* & *G* which are also induced by methylamine. Mutation of *mauG* results in MADH containing a mono-hydroxylated, uncrosslinked intermediate in TTQ biogenesis. Incubation of this biogenesis intermediate with recombinant wt *mauG* and oxygen results in formation of the complete cofactor and reconstitution of MADH activity.

MauG has been recombinantly expressed and characterised, revealing a di-heme protein with unexpected properties. We will report this characterisation here, as well as crystallization conditions and preliminary structural data.