

W0417

**Decoding the Phenazine Biosynthesis Pathway: Structural Characterization of the proteins PhzA & G from *Pseudomonas fluorescens* 2-79.** Ekta G Ahuja<sup>1</sup>, Dimitri V Mavrodi<sup>2</sup>, Linda S Thomashow<sup>2</sup>, Wulf Blankenfeldt<sup>1</sup>, <sup>1</sup>Max-Planck Institute of Molecular Physiology, Dortmund, Germany, <sup>2</sup>USDA-ARS, Washington State Univ. Pullman, WA.

Phenazines are broad-spectrum antibiotic metabolites synthesized by species like *Pseudomonas*, *Streptomyces* etc. They are thought to act by causing an accumulation of fatal superoxide radicals. Phenazine production contributes to virulence in *Pseudomonas aeruginosa* infections and suppresses fungal root pathogens in case of biocontrol agent *Pseudomonas fluorescens*. An operon of seven phenazine (*phz*) genes (named PhzA-G), conserved across a number of species (*P.chlororaphis*, *P. aeruginosa* etc.) is involved in the production of phenazines. Phenazine-1-carboxylic acid is the end product of phenazine biosynthesis pathway in *Pseudomonas fluorescens*. Both PhzG and PhzA are thought to catalyse reactions specific to this pathway. PhzA shows a high level of fold similarity with  $\Delta^5$ -3-ketosteroid isomerase while PhzG shares 32% sequence identity with *Escherichia coli* pyridoxine 5'-phosphate oxidase. The exact function of both of these proteins is yet to be elucidated.

This poster presents the structures of PhzA and PhzG determined at a resolution of 2.1 Å and 1.4 Å respectively, using the Multiwavelength Anomalous Dispersion (MAD) method.