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Structural Studies of MosA, a Dihydrodipicolinate Synthase from *Sinorhizobium meliloti*. K.H. Nienaber¹, C.P. Phenix², D.R.J. Palmer², L.T.J. Delbaere¹, ¹Dept. of Biochemistry, ²Dept. of Chemistry, Univ. of Saskatchewan, 107 Wiggins Rd., Saskatoon, SK, Canada, S7N 5E5.

Sinorhizobium meliloti L530 is a bacterium found in soil that forms a symbiotic relationship with legumes. MosA has been isolated from *S. meliloti* L530 and was initially identified as an *O*-methyltransferase. Investigation by Dr. David Palmer and his lab has revealed that MosA was mischaracterized and actually acts as a dihydrodipicolinate synthase (DHDPS). MosA is of particular interest as it is a part of the lysine biosynthesis pathway in most plants and bacteria, and thus is a potential drug target. Previous crystallographic structures revealed the presence of pyruvate covalently bound to a lysine residue in a Schiff base form in the active site. New data are being collected on crystals of complexes of MosA with (S)-aspartate- β -semialdehyde, 2-oxobutyrate, lysine and pyruvate, and 2,6-pyridinedicarboxylic acid bound, representing a substrate, substrate analog, inhibitor, and product analog respectively. It is expected these structures will add weight to the argument that MosA is a DHDPS, as well as providing a possible drug target for other more harmful bacterium.