

W0420

Crystal Structure of HI0607 Identifies a novel Shikimate Dehydrogenase from *Haemophilus Influenzae*. S. Singh¹, S. Korolev^{2,3}, O. Koroleva², T. Zarembinski², F. Collart², A. Joachimiak², D. Christendat¹, ¹Univ. of Toronto, Ontario; ²Argonne National Laboratory, Structural Biology Center, Argonne, IL; ³ Saint Louis Univ. School of Medicine, USA.

The enzyme shikimate dehydrogenase catalyzes the reversible reduction of dehydroshikimate to shikimate in the presence of NADPH. We have determined the structure of YdiB protein from *H. influenzae* (HI0607) which is thought to reduce dehydroquininate to quinate and dehydroshikimate to shikimate in the presence of a reductive cofactor. However, HI0607 can catalyze the oxidation of shikimate in the presence of NADP⁺, but not the oxidation of quinate, indicating that this protein does not have YdiB properties. Comparison of the substrate binding sites of YdiB versus AroE shikimate dehydrogenase indicated that a number of residues are conserved across both types of dehydrogenases, and the subtle variations amongst the binding sites were insufficient to implicate residue(s) for their respective substrate specificities. Mutagenesis analysis of two active site residues, Asp103 and Lys67, indicated that they are important catalytic groups and that they may function as a catalytic pair. We present a detailed analysis of HI0607, which indicates that it belongs to a novel functional class of shikimate dehydrogenases.