

## W0413

**Crystal Structure of Nudix Family Proteins BT0354 and EF2700.** C. Chang, E. Duggan, J. Abdullah, A. Joachimiak, Midwest Center for Structural Genomics and Structural Biology Center, Biosciences, Argonne National Laboratory, 9700 South Cass Ave., Bldg 202, Argonne, IL 60439, USA.

The Nudix family is widespread among eukaryotes, bacteria, archaea and viruses and consists mainly of pyrophosphohydrolases that act upon substrates of general structure Nucleoside Diphosphate linked to another moiety, X (NDPX) to yield NMP and P-X. This family is defined by conserved 23 amino acid Nudix sequence motif: GxxxxxExxxx[UA]xRExxEExGU, where U is an aliphatic, hydrophobic residue. Sequence data analysis suggests that BT0354 from *B. thetaiotaomicron* and EF2700 *E. faecalis* belong to Nudix family. The crystal structures of both proteins have been determined by SAD method. The structure of BT0354 (225 residues) was refined to 2.4 Å resolution ( $R=19.8\%$ ,  $R_{\text{free}}=25.1\%$ ) with two dimers in the asymmetric unit. The structure of EF2700 (273 residues) was refined to 2.26 Å resolution ( $R=20.1\%$ ,  $R_{\text{free}}=24.3\%$ ) as dimer. Although these proteins belong to Nudix family, they show some striking differences. The structural comparisons with other Nudix proteins would be presented.

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