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**Structure of Homolog of F420-0: $\gamma$ -Glutamyl Ligase from *Archaeoglobus fulgidus* Reveals a Novel Fold.** B. Nocek<sup>1</sup>, E. Evdokimova<sup>2</sup>, M. Kudritska<sup>2</sup>, A. Savchenko<sup>2</sup>, A. Edwards<sup>2</sup>, A. Joachimiak<sup>1</sup>,<sup>1</sup>Midwest Center for Structural Genomics, Biosciences, Argonne National Laboratory, Argonne, IL 60439 USA, <sup>2</sup>Banting and Best Dept. of Med. Res., Univ. of Toronto, Toronto, Ontario, Canada.

Coenzyme F420 (8-hydroxy-5-deazaflavin) is a group of redox-active cofactors playing a crucial role in biosynthesis of diverse metabolic reactions in methanoarchaea and some eubacteria. The biosynthesis of this coenzyme has been studied unveiling six-step pathway. The fifth step of the F420 biosynthesis, the GTP-dependent addition of two L-Glu to the L-lactyl phosphodiester of 7,8-didemethyl-8-hydroxy-5-deazariboflavine is catalyzed by F420-0: $\gamma$ -glutamyl ligase (CofE). CofE is a 54kD homodimeric protein showing no sequence similarity to any previously characterized protein. Here we report first crystal structure of CofE from *A. fulgidus* determined using the SAD method and refined to 2.5 Å resolution. The protein structure has mixed alpha/beta fold with monomer organized into two domains. The structural similarity search using DALI server indicates that the structure of CofE homolog represents a novel fold. The structural analysis of this enzyme will be presented.

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