

# Structural Similarities of Hypothetical Protein MTH1747 from *Methanobacterium Thermoautotrophicum* with 3-Hydroxyacid Dehydrogenases

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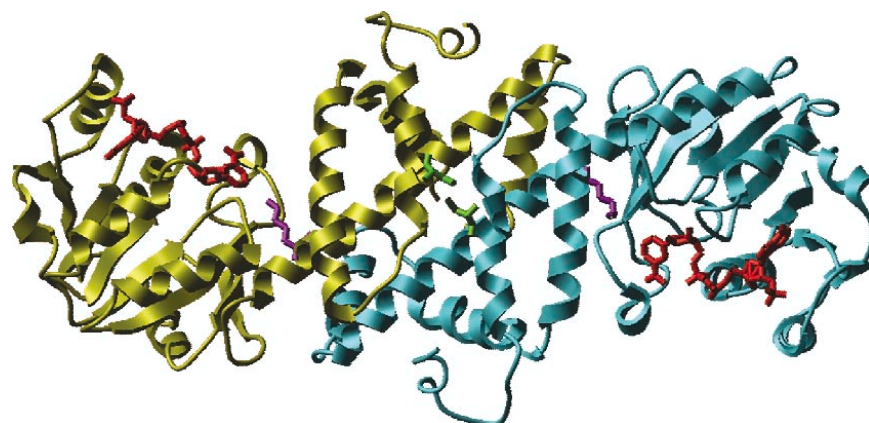


FIG. 1. Ribbon representation of MTH1747 dimer. Protein monomers are shown in yellow and cyan. NADP molecules bound to each monomer are shown in red, and catalytic lysine residues are shown in magenta.

## Abstract

The crystal structure of hypothetical conserved protein MTH-1747 from *Methanobacterium thermoautotrophicum* was solved at 2.0 Å resolution using multiple-wavelength anomalous dispersion (MAD) analysis and SeMet labeled protein. All data were collected at SBC CAT, Sector 19-ID.

Two molecules in an asymmetric unit form a homodimer with one intersubunit disulfate bridge. Each monomer comprises two domains: a large N-terminal NADP-binding domain and a smaller C-terminal  $\alpha$ -helical domain. There is a strong electron density corresponding to an NADP molecule bound to the nucleotide-binding domain of the protein. Although MTH1747 shows low sequence similarity, it has high structural homology with 6-phosphogluconate dehydrogenase (PGP), 1-3-hydroxyacyl CoA dehydrogenase (HDH), and UDP-glucose dehydrogenase (DLJ).

While the overall domain structure and dimer architecture are similar to HDH, MTH1747 lacks catalytic residues proposed for HDH. In contrast, Lys159, one of the catalytic residues found in PGP and DLJ, is preserved in MTH1747 structure, while the quaternary structures are different. The closest sequence homologue of MTH1747 is a 3-hydroxyisobutyrate dehydrogenase, which also has similar catalytic site and, together with PGP and DLJ, belongs to the 3-hydroxyacid dehydrogenases family. The structure of hypothetical protein MTH-1747 provides a considerably focused functional hypothesis that can be verified experimentally.

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