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Crystal Structure of IMP Dehydrogenase from *Bacillus anthracis*. R-g. Zhang¹, R-y. Wu¹, L.E. Volkart¹, G. Joachimiak¹, P. Gornicki², A. Joachimiak¹, ¹Structural Biology Center, Biosciences, Argonne National Laboratory, 9700 South Cass Ave., Bldg 202, Argonne, IL 60439, ²Dep. of Mol. Gen. and Cell Biol., Univ. of Chicago, 920 E. 58th St., Chicago, IL 60637.

IMP dehydrogenase (IMPDH) is an essential enzyme that catalyzes the conversion of IMP to XMP, a unique step in GTP synthesis. IMPDH inhibitors have broad clinical utility in the treatment of malignancy, viral diseases and as immunosuppressive agents. To provide a basis for the evaluation of IMPDH inhibitors as antimicrobial agents, we have determined the crystal structures IMPDH from *B. anthracis* at 2.2 Å with substrate and product bound in the active site. The IMPDH is a tetramer with its four subunits related by a crystallographic fourfold axis. The enzyme is composed of two domains: a TIM barrel domain that embodies the catalytic site and a CBS dimer domain. The structure of *B. anthracis* IMPDH is similar to *S. pyogenes* IMPDH which we reported earlier. Structural comparisons of IMPDH from bacterial and eukaryotic sources will contribute to understanding of their distinct properties and the design of specific bacterial IMPDH inhibitors.

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