

## **Structure of the Bacterial YhcH Protein, a Putative Copper Aminosugar Epimerase**

Alexey Teplyakov, Galina Obmolova, Gary L. Gilliland, *Center for Advanced Research in Biotechnology, University of Maryland, Rockville, Maryland, U.S.A.* E-mail: teplyako@umbi.umd.edu

Nine-carbon sugars sialic acids are located at the end of a glycan chain in vertebrate glycoconjugates and involved in molecular and cellular recognition. Bacteria can use sialic acid of the host cell as the sole carbon or nitrogen source and as a source of amino sugars for cell wall synthesis. In many pathogenic bacteria, proteins involved in sialic acid catabolism are encoded by the *nan* operon that includes a specific transporter, lyase, kinase, epimerase, and the *yhcH* gene of unknown function. The crystal structure determination of YhcH from *Haemophilus influenzae* was undertaken as part of a structural genomics effort in order to assist with the functional assignment of the protein. The structure was determined at 2.2 Å resolution by the MAD method. The protein fold is a variation of the double-stranded β-helix. Two antiparallel β-sheets form a funnel opened at one side, where a putative active site contains a copper ion coordinated to two histidines and an aspartic acid. Comparison to other proteins with a similar fold, and analysis of the genomic context suggest that YhcH may be a sugar isomerase involved in degradation of exogenous sialic acid.

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