CRYSTALLIZATION AND STRUCTURE DETERMINATION OF A PNGM FROM *BACILLUS ANTHRACIS*

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The enzyme phosphoglucosamine mutase catalyzes the conversion of glucosamine 6-phosphate to glucosamine 1-phosphate, an early step in the formation of the nucleotide sugar UDP-N-acetylglucosamine. In bacteria UDP-*N*-acetylglucosamine (UDP-GlcNAc) is not only an essential peptidoglycan precursor but is also used in the synthesis of many other cell wall *N*-acetylglucosamine-containing macromolecules, such as teichoic acids in Gram-positive organisms and lipopolysaccharides in Gram-negative organisms. The phosphoglucosamine mutases are part of the large α-D-phosphohexomutase enzyme superfamily, but to date no proteins from the phosphoglucosamine mutase sub-group have been structurally characterized. Here we report crystallization of phosphoglucosamine mutase from *Bacillus anthracis* by hanging drop vapor diffusion in space group $P3_221$. Crystals diffract to 2.85 Å resolution under cryocooling conditions. A selenomethionine-substituted version of the enzyme has also been purified and crystallizes isomorphously with the native protein. Structure determination by multiwavelength anomalous diffraction and molecular replacement is underway. The crystal structure of *B. anthracis* phosphoglucosamine mutase should shed light on the substrate specificity of this enzyme and will also serve as a template for inhibitor design. Inhibitors of high specificity and affinity may have clinical utility for treating bacterial infections.