STRUCTURAL STUDIES OF PMM/PGM FROM *PSEUDOMONAS AERUGINOSA*

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ABSTRACT

The human pathogen *Pseudomonas aeruginosa* expresses a variety of cell surface polysaccharides, including alginate, lipopolysaccharide (LPS), and rhamnolipid. *P. aeruginosa* is the primary cause of chronic lung infections in cystic fibrosis (CF) patients, and these molecules contribute to its virulence. This dual-specificity enzyme phosphomannomutase/phosphoglucomutase (PMM/PGM) is required for the production of these molecules. The structure of PMM/PGM was previously solved in our laboratory, showing that the protein has four domains organized in a "heart shape," with the active site in a deep cleft formed by residues from each domain. Recently, we have determined the structures of PMM/PGM bound to its two substrates, two products, and an intermediate at 2.0 Å resolution or higher. These structures reveal the structural basis for diverse substrate recognition by the enzyme and pinpoint residues important for accomplishing the dynamic reorientation step of the reaction.