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Funded by: Life Sciences Undergraduate Research Opportunity Program

Structural basis for substrate specificity of the alpha-D-phosphohexomutase superfamily

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Phosphoacetylglucosamine mutase (PAGM) is a human enzyme that is the key to the formation of the essential metabolite UDP-N-acetylglucosamine. Bacterial phosphoglucomutase (PGM) from *Acetobacter xylinum* catalyzes the interconversion of glucose 1-phosphate and glucose 6-phosphate. PAGM and PGM are members of the alpha-D-phosphohexomutase superfamily which all catalyze intramolecular phosphoryl transfer on sugar substrates. These two analogs are similar in their mechanism, but dissimilar in their substrate specificity, not only to each other, but also to other well characterized (structurally and mechanistically) members of their superfamily. Protein expression and purification techniques were used to attempt to produce crystals to determine the three dimensional structures of human PAGM and bacterial PGM by X-ray diffraction in order to clarify the structural explanation for substrate specificity within the alpha-D-phosphohexomutase superfamily.