

W0364

Crystal Structure of Potato Tuber ADP-Glucose Pyrophosphorylase. James H. Geiger, Xiangshu Jin, Dept. of Chemistry, Michigan State Univ. & Jack Preiss, Dept. of Biochemistry & Molecular Biology, Michigan State Univ.

We report the first atomic resolution structure of an ADP-glucose pyrophosphorylase, the first and rate limiting step in the biosynthesis of starch in plants and glycogen in bacteria. Crystals were grown in high concentrations of sulfate ion, resulting in the sulfate-bound, allosterically inhibited form of the enzyme. Structures were also obtained of the sulfate/ATP-bound and sulfate/ADP-glucose-bound enzyme. Together, these structures lead to a reasonable hypothesis for the mechanism that involves metal-mediated catalysis and strongly suggest an allosteric regulation that involves both local changes around the active site and significant structural changes between the four subunits of the tetramer. Communication between the inhibitor/activator binding sites and the active site of the enzyme are both subtle and complex and involve several distinct regions of the enzyme including the n-terminus, the glucose-1-phosphate binding site and the ATP binding site.