Structural Basis of Glycogen Synthesis

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Glycogen and starch are the major carbon and energy storage compounds in most living organisms. Glycogen synthase (GS) [EC 2.4.1.21] is a key component of the enzymatic machinery involved in glycogen metabolism, catalyzing the successive addition of α-1,4-linked glucose residues to the non-reducing end of glycogen. The other components of this machinery are glycogen phosphorylase (GP) and the branching/debranching enzymes. GSs from bacteria and higher plants (starch synthases) are α-retaining family GT5 that use ADP-glucose as sugar donor and have MW around 50 kDa. We now report the first 3D structure of GS at 2.3 Å resolution in the presence and absence of adenosine diphosphate [1]. The recombinant enzyme from *A. tumefaciens* was purified to homogeneity and crystallized [2]. The overall fold and the active site architecture of the protein are remarkably similar to those of GP, indicating a common catalytic mechanism and comparable substrate-binding properties.

[1] Buschiazzo A., et al., *EMBO J*, 2004, **23**, 3196. [2] Guerin M.E., et al., *Acta Crystallogr. D*, 2003, **59**, 526.

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