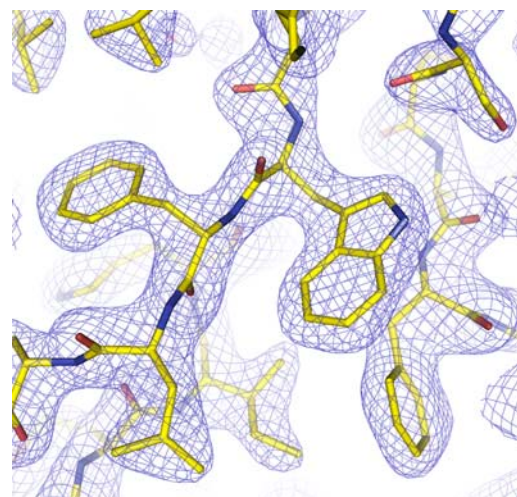


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



Target ID	GO.23169	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At5g18200.1	
PDB Entry	1ZWJ (replaced 1VKV)	Deposition: 24-Jun-2004
Function	putative galactose-1-phosphate uridyl transferase (ADP-glucose + phosphate -> glucose-1-P + ADP) FF/Refine: 1Z84, 2H39 [REPLACED 2GDK], 2Q4H, 2Q4L)	
Produced From	<i>E. coli</i> B834(DE3) p(LacI+RARE)	
Structure by X-ray	Resolution: 2.3 Å	R-value (R-free): 22.0% (27.7%)
	No. of Residues: 351 (39,005)	Subunits/Molecule:
Data Collected At	APS: BioCARS 14-ID-B 11-Feb-2004, COM-CAT 32-ID 04-Apr-2004	
Authors	E. Bitto, S.T.M. Allard, D.W. Smith, G.E. Wesenberg, K.A. Johnson, C.A. Bingman, G.N. Phillips, Jr.	



Structural Features

The gene locus At5g18200.1 was chosen for fold-space investigation, since it had only limited amino acid sequence identity to any known protein. The closest relative whose structure was known was a bacterial galactose uridinylyltransferase (GalT). On the basis of this marginal sequence identity (~22%), the At5g18200.1 gene product was annotated in databases as having the same activity as the bacterial protein. The crystal structure of At5g18200.1 confirmed structural similarity to the bacterial GalT enzyme. However, collaboration with Professor Perry Frey revealed that the enzyme did NOT have appreciable activity for this reaction. This observation underscores the need for actual experimental determination of biological function. Clearly the clues provided by homology in sequence or structure are valuable, but they are just that-clues. Further studies in the Frey laboratory revealed that the enzyme catalyzes a new reaction not previously appreciated in starch metabolism. This finding could have profound effects on our understanding of metabolic pools of ADP-glucose, the first committed step in starch degradation (Frey *et al.*, to be published), potentially improving nutritional or industrial production of starch in plants.

References: (1) McCoy, J.G., Arabshahi, A., Bitto, E., Bingman, C.A., Ruzicka, F.J., Frey, P.A., Phillips, G.N., Jr. (2006) Structure and mechanism of an ADP-glucose phosphorylase from *Arabidopsis thaliana*. *Biochemistry* 45(10):3154-62.

Percent Identity with Nearest PDB Structure at Time Solved	22% of 298 aa (1HXP)
Pfam Cluster	B-7903, B_18006
Protonet Cluster Size : Structures in PDB	89 : 1

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