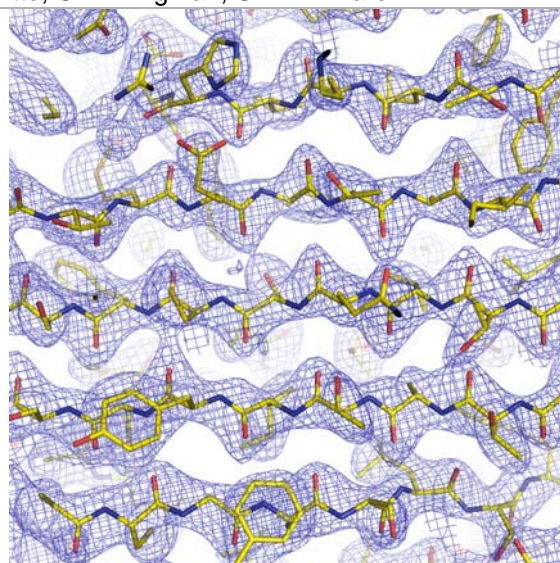
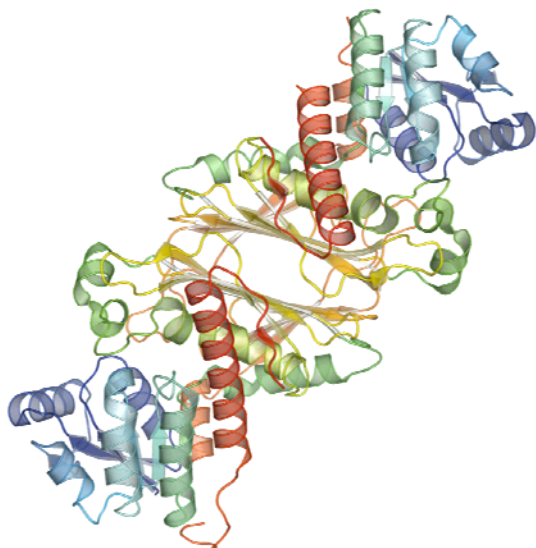


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



Target ID	GO.19812	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At4g09670.1	
PDB Entry	1YDW	Deposition: 28-Nov-2006
Function	putative oxidoreductase (FF/Refine: 2Q4E)	
Produced From	<i>E. coli</i> B834 p(RARE2) pVP-16	
Structure by X-ray	Resolution: 2.49 Å	R-value (R-free): 21.8% (28.3%)
	No. of Residues/ASU: 693	Monomers/ASU: 2
Data Collected At	Advanced Photon Source 14-IDB BIOCARS 24-Oct-2004	
Authors	G.E. Wesenberg, G.N. Phillips, Jr., E. Bitto, C.A. Bingman, S.T.M. Allard	



Structural Features

Based on the amino acid sequence similarity, At4g09670.1 is most closely related to an AX110P-like protein from *A. thaliana* (68% sequence identity). AX110P is an embryogenesis-associated protein of Pfam_01408 oxidoreductase family that was first characterized in carrot. Other closely related proteins include putative oxidoreductases from rice and red grapes. The structure of At4g09670.1 consists two domains with the putative active site located between the two domains in a deep cleft. The N-terminal domain belongs to a class of alpha/beta proteins with NAD(P)-binding Rossmann fold topology. The N-terminal domain harbors so called fingerprint motif of NAD(P)-binding proteins with a consensus sequence GxGxxG/A. In At4g09670.1, the second and third glycine residues are replaced by alanine residues. The C-terminal domain is dominated by large eight-stranded beta-sheet that forms an extensive interface between the two molecules packed in asymmetric unit. The PDB structure most similar to At4g09670.1 is the oxidoreductase (Tm0312) from *Thermotoga maritima* (PDB ID 1ZH8) with 26% sequence identity over 325 residues. The *T. maritima* protein crystallized with NADP+ bound in the active site. Based on structural overlay analysis, At4g09670.1 likely prefers NADP+ because its 2'-phosphate group could be stabilized by electrostatic interaction with Arg39 and Lys43. Interestingly, several of the closest structural homologs of At4g09670.1 are enzymes involved in metabolism of carbohydrates (PDB IDs 2GLX, 1RYD, 2NVW, 2IXA). Although At4g09670.1 has been crystallized in the absence of ligands, it is intriguing to speculate that it could perform similar function in plants.

Percent Identity with Nearest PDB Structure at Time Solved	30% (1EVJ)
Pfam Cluster	GFO_IDH_MocA
Sequence Cluster Size	2246

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