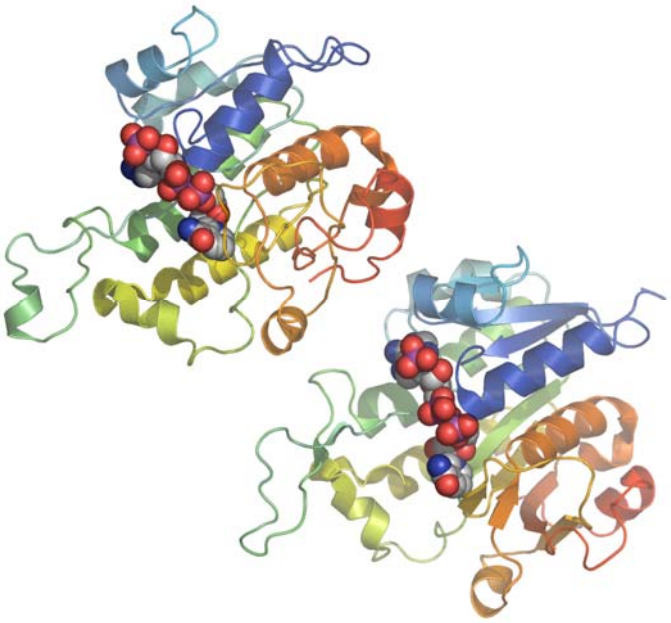
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.23662	
Source Organism	*Arabidopsis thaliana*	
Target Name	At5g02240.1	
PDB Entry	1XQ6 and 1YBM	Deposition: 12-Oct-2004
Function	short-chain dehydrogenase (FF/Refine: 2Q46, 2Q4B)	
Produced From	*E. coli* B834(DE3) p(LacI+RARE)	
Structure by X-ray	Resolution: 1.8 Å	R-value (R-free): 22.1% (27.8%)
	No. of Residues: 253 (27,059x2)	Subunits/ASU: 2
Data Collected At	Advanced Photon Source Bio-CARS 14-ID-B	
Authors	D.W. Smith, G.E. Wesenberg, C.A. Bingman, S.T.M. Allard, E. Bitto, G.N. Phillips, Jr.	



Structural Features

At5g02240.1 was a fold-space target, with weak similarity to small segments of dehydrogenases in the PDB (22% over 90 aa to 1HD0). All of the weak matches were less significant than E=2. The structure was determined by SeMet MAD, and the protein has a classic dehydrogenase core, with additional N- and C-terminal domains, which match to Pfam-B_27474 and Pfam-B_11732. This structure will enable more confident modeling of the 16 structural neighbors in Protonet, and the 128 proteins with domains in PFam-B_227. DALI searches show good structural overlap to a number of oxidoreductases. The closest match, with a Z score of 24.3, is to biliverdin-IX beta reductase (1HE2). The crystal structure clearly shows that this protein is an oxidoreductase, since it came through protein purification and crystallization with tightly bound NADPH co-factors (see ribbon plot above).

Percent Identity with Nearest PDB Structure at Time Solved	26% over 90 aa 1HD0 (E=2.2)
Pfam Cluster	Pfam-B_27474 2-116 Pfam-B_227 117-176 Pfam-B_11732 203-248
Protonet Cluster Size : Structures in PDB	16 : 0

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