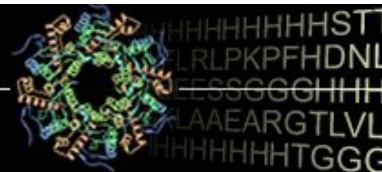
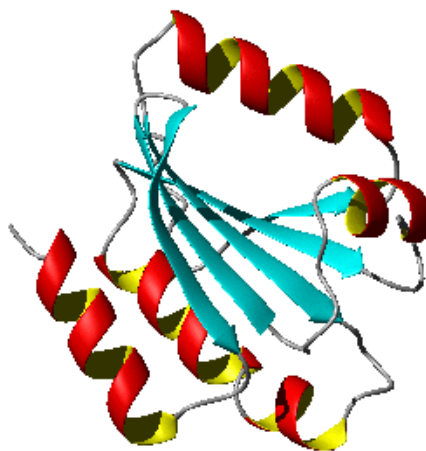


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



Target ID	GO.14751	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At3g51030.1	
PDB Entry	1XFL	Deposition: 15-Sep-2004
BMRB Entry	6318	Deposition: 15-Sep-2004
Function	thioredoxin h1 (FF/Refine: 2Q40)	
Produced From	Cell-Free (wheat germ extract)	
Structure by NMR	Restraints/Residue: 12.8	Subunits/Molecule: 1
	No. of Residues: 124	Molecular Weight: 13.9 kDa
	BackboneRMSD(17–123): 0.6 Å	AllHeavy Atoms RMSD(17–123):1.0. Å
Data Collected At	Medical College of Wisconsin, Milwaukee, WI	
Authors	F.C. Peterson, B.L. Lytle, S. Sampath, D. Vinarov, E. Tyler, M. Shahan, J.L. Markley, B.F. Volkman	



Structural Features

The most similar structure in the PDB to At3g51030.1, thioredoxin h1, was 1ERV, with 45% structure identity over 101 residues. Thioredoxin (Trx) contains an active site disulfide bond and belongs to a structural family that includes bacterial protein disulfide isomerase DsbA, glutaredoxin, glutathione peroxidase, and the N-terminal domain of glutathione transferase. While mammals and bacteria possess only one type of Trx, the plant thioredoxins are unusually diverse, with 19 different Trx proteins found in *Arabidopsis*, organized into six subfamilies. Members of the Trx h subfamily are found in cytosol, nucleus, ER, and mitochondria and are reduced by NADPH via a flavin enzyme, NTR. Reduced (dithiol) Trx in turn functions as an electron donor for the reduction of disulfides or regulation of enzymes. This target aligns to domains within Pfam trusted matches for thioredoxin over residues 17–123.

References: (1) Peterson, F.C., Lytle, B.L., Sampath, S., Vinarov, D., Tyler, E., Shahan, M., Markley, J.L., Volkman, B.F. (2005) Solution structure of thioredoxin h1 from *Arabidopsis thaliana*. *Protein Sci* 2005 Aug;14(8):2195-200.

Percent Identity with Nearest PDB Structure at Time Solved	45% over 101 aa (1ERV)
Pfam Cluster	Thioredoxin
Protonet Cluster Size : Structures in PDB	955 : 11

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