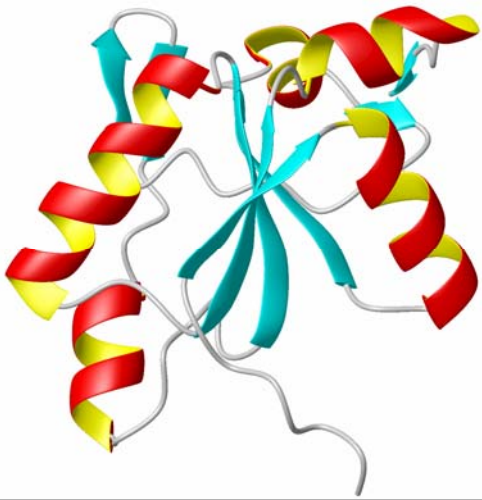
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.20862	
Source Organism	*Arabidopsis thaliana*	
Target Name	At5g66040.1	
PDB Entry	1TQ1	Deposition: 16-Jun-2004
BMRB Entry	6240	Deposition: 15-Jun-2004
Function	putative sulfotransferase/phosphatase	
Produced From	Cell-Free (wheat germ extract)	
Structure by NMR	Restraints/Residue: 16.5	Subunits/Molecule: 1
	No. of Residues: 129	Molecular Weight: 13. 8 kDa
	Backbone RMSD: 1.05 Å (16–56, 85–128)	All Heavy Atoms RMSD: 1.59 Å (16–56, 85–128)
Data Collected At	Nuclear Magnetic Resonance Facility at Madison (NMRFAM)	
Authors	C. C. Cornilescu, G. Cornilescu, S. Singh, M.S. Lee, E.M. Tyler, M.N. Shahan, D. Vinarov, J.L. Markley	



Structural Features

The most similar structure in the PDB was a prototype sulfotransferase for the single-domain Rhodanese Homology Superfamily GlpE from *Escherichia coli* (1GMX) with 22% sequence identity over 77 residues. The rhodanese homology domain has an alpha beta fold domain duplicated internally in the rhodanese protein. The enzymatically active cysteine containing domain can be found in CDC25 class of phosphatases, sulfide dehydrogenases and stress protein such as senescence specific protein 1 in plants, PspE and GlpE in bacteria and cyanide and arsenate resistance proteins. Additionally, this domain can be found as a single copy in other proteins such as phosphatases and ubiquitin C-terminal hydrolases. Although At5g66040.1 falls within the Rhodanese Superfamily, the true biological function of At5g66040.1 currently is unknown. This target aligns to domains within Pfam trusted matches for rhodanese over residues 13–114.

References: (1) Cornilescu, G., Vinarov, D.A., Tyler, E.M., Markley, J.L., Cornilescu, C.C. (2006) Solution structure of a single-domain thiosulfate sulfurtransferase from *Arabidopsis thaliana*. *Protein Sci* 15(12):2836-41.

Percent Identity with Nearest PDB Structure at Time Solved	22% over 77 aa (1GMX)
Pfam Cluster	Rhodanese
Protonet Cluster Size : Structures in PDB	53 : 0

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