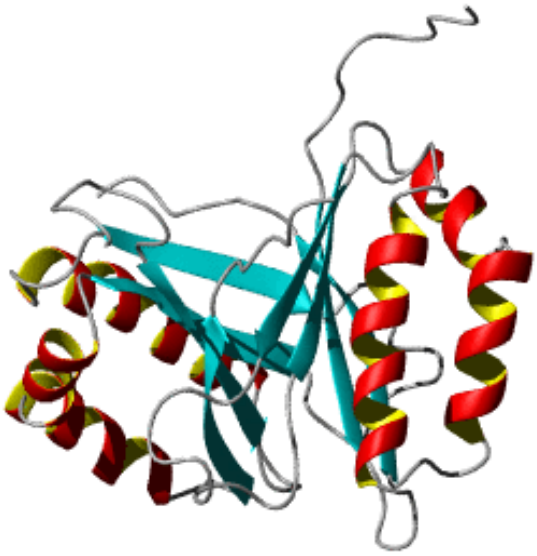
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.13081	
Source Organism	*Arabidopsis thaliana*	
Target Name	At3g17210.1	
PDB Entry	1Q53 (replaced 1NWJ)	Deposition: 06-Aug-2003
BMRB Entry	5843	Deposition: 07-Aug-2003
Function	unknown (FF/Refine: 2Q3P)	
Produced From	*E. coli* Rosetta(DE3)/pLysS	
Structure by NMR	Restraints/Residue: 18.4	Subunits/Molecule: 2
	No. of Residues: 224	Molecular Weight: 24.4 kDa
	Backbone RMSD: 0.95 Å	All Heavy Atoms RMSD: 1.30 Å
Data Collected At	Medical College of Wisconsin, Milwaukee, WI	
Authors	B.L. Lytle, F.C. Peterson, B.F. Volkman	



Structural Features

The most similar structure in the PDB to homodimeric (112 residues/monomer) At3g17210.1 shows 35% identity over 108 aligned residues (1RJJ). Additionally, ActVA-Orf6, a bacterial monooxygenase from *Streptomyces coelicolor* (1LQ9) and a protein of unknown function from *Thermus thermophilus* (1IUJ) show structural similarity. Although the two proteins, ActVA-Orf6 and At3g17210.1, share only 10% sequence identity, their tertiary and quaternary structures are very similar. Because none of the active site residues of ActVA-Orf6 are retained in At3g17210.1, the latter protein probably has a different function, which remains to be elucidated. This target aligns to Pfam-B domain of Pfam-B_3438 over residues 8–102.

References: (1) Lytle, B.L., Peterson, F.C., Kjer, K.L., Frederick, R.O., Zhao, Q., Thao, S., Bingman, C., Johnson, K.A., Phillips, G.N. Jr, Volkman, B.F. (2004) Structure of the hypothetical protein At3g17210 from *Arabidopsis thaliana*. *J Biomol NMR* (4):397-400.

Percent Identity with Nearest PDB Structure at Time Solved	10% over 109 aa (1LQ9)
Pfam Cluster	B_3438
Protonet Cluster Size : Structures in PDB	67 : 0

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