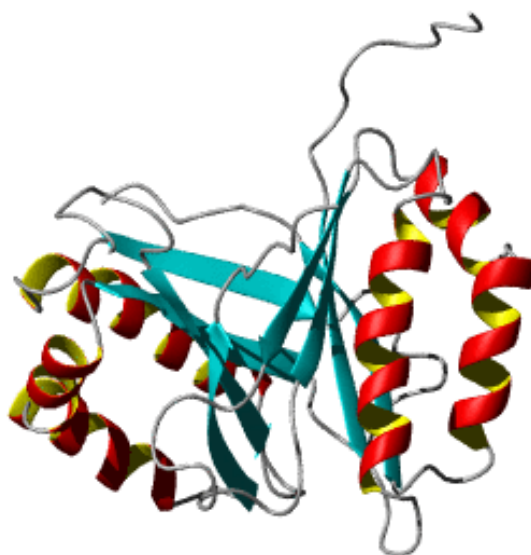


# Center for Eukaryotic Structural Genomics

## Protein Structure Data Summary

<b>Target ID</b>	GO.13081	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At3g17210.1	
<b>PDB Entry</b>	1Q53 (replaced 1NWJ)	Deposition: 06-Aug-2003
<b>BMRB Entry</b>	5843	Deposition: 07-Aug-2003
<b>Function</b>	unknown (FF/Refine: 2Q3P)	
<b>Produced From</b>	<i>E. coli</i> Rosetta(DE3)/pLysS	
<b>Structure by NMR</b>	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
<b>Data Collected At</b>	Medical College of Wisconsin, Milwaukee, WI	
<b>Authors</b>	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.

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

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