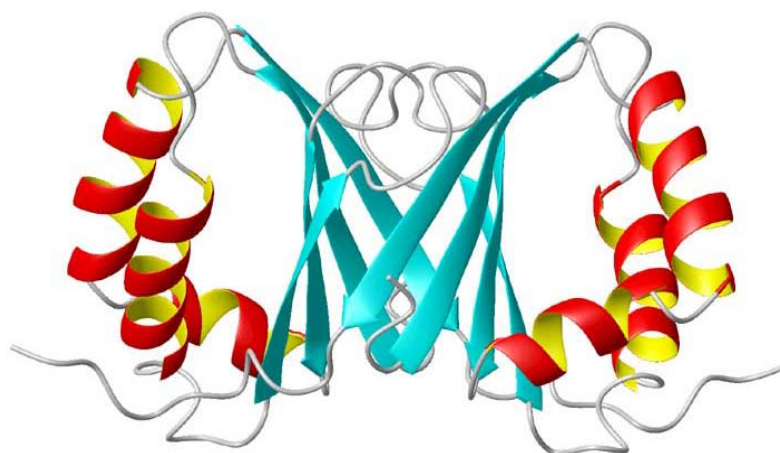


# Center for Eukaryotic Structural Genomics

## Protein Structure Data Summary

<b>Target ID</b>	GO.22997	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At5g22580.1	
<b>PDB Entry</b>	1RJJ	Deposition: 19-Nov-2003
<b>BMRB Entry</b>	6011	Deposition: 19-Nov-2003
<b>Function</b>	monooxygenase	
<b>Produced From</b>	<i>E. coli</i> Rosetta(DE3)/pLysS	
<b>Structure by NMR</b>	Restraints/Residue: 21.5	Subunits/Molecule: 2
	No. of Residues: 222	Molecular Weight: 24.7 kDa
	Backbone RMSD(6–102): 0.61 Å	All Heavy Atoms RMSD(6–102): 1.25 Å
<b>Data Collected At</b>	Nuclear Magnetic Resonance Facility at Madison (NMRFAM)	
<b>Authors</b>	G. Cornilescu, C.C. Cornilescu, Q. Zhao, R.O. Frederick, F.C. Peterson, S. Thao, J. L. Markley	



### Structural Features

The structure of homodimeric (111 residues/monomer) At5g22580.1 was solved by starting with a monomeric structure obtained using CANDID/CYANA in the XPLOR simulated annealing protocol. A dimeric model with the correct relative orientation of its monomeric subunits was obtained using ambiguous inter-subunit NOE assignments, radius of gyration and RDC constraints. The dimeric NOE contacts were then refined by consideration of incompatibility of distances within the monomer. Each monomer adopts a  $\beta$ - $\alpha$ - $\beta$ - $(3_{10})$ - $\beta$ - $\alpha$ - $\alpha$ - $\beta$  fold. The most similar structure in the PDB shows 36% sequence identified over 88 aligned residues (1Q53 and 1Q4R). Additionally, the bacterial monooxygenase from *Streptomyces coelicolor* (1LQ9) and a protein of unknown function from *Thermus thermophilus* (1IUJ) show structural similarity. This target aligns to Pfam-B domain of Pfam-B\_3438 over residues 7–98.

*References:* (1) Cornilescu, G., Cornilescu, C.C., Zhao, Q., Frederick, R.O., Peterson, F.C., Thao, S., Markley, J.L.(2004) Solution structure of a homodimeric hypothetical protein, At5g22580, a structural genomics target from *Arabidopsis thaliana*. *J Biomol NMR* (3):387-90.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	36% over 88 aa (1Q53)
<b>Pfam Cluster</b>	B_3438
<b>Protonet Cluster Size : Structures in PDB</b>	582 : 2

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