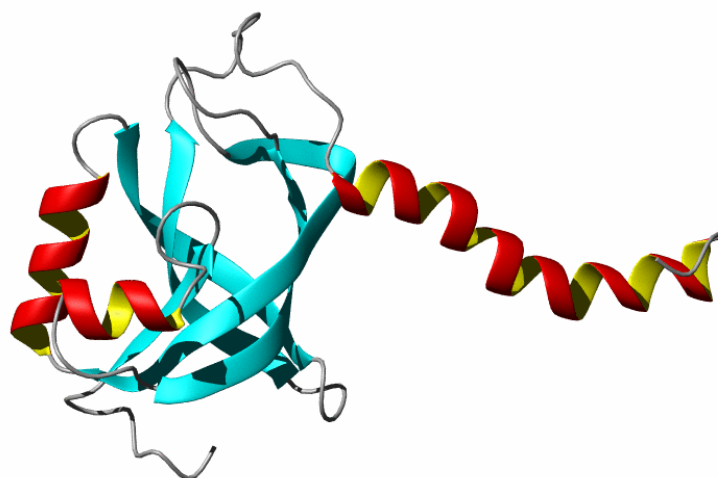


# Center for Eukaryotic Structural Genomics

## Protein Structure Data Summary

<b>Target ID</b>	GO.22446	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At5g39720.1	
<b>PDB Entry</b>	2G0Q	Deposition: 13-Feb-2006
<b>BMRB Entry</b>	7007	Deposition: 28-Feb-2006
<b>Function</b>	unknown	
<b>Produced From</b>	Cell-free	
<b>Structure by NMR</b>	Restrains/Residue: 13.3	Subunits/Molecule: 1
	No. of Residues: 164	Molecular Weight: 20.1 kDa
	Backbone RMSD(17-53,61-121): 0.47 Å	All Heavy Atoms RMSD(17-53,61-121): 0.92 Å
<b>Data Collected At</b>	Medical College of Wisconsin	
<b>Authors</b>	Volkman, B.F., Peterson, F.C., Lytle, B.L.	



### Structural Features

The three-dimensional structure of *Arabidopsis thaliana* protein At5g39720.1 was determined by NMR spectroscopy. It is the first representative structure of Pfam family PF06094, which contains protein sequences similar to that of AIG2, an *A. thaliana* protein of unknown function induced upon infection by the bacterial pathogen *Pseudomonas syringae*. The At5g39720.1 structure consists of a five-stranded beta-barrel surrounded by two alpha-helices and a small beta-sheet. A long flexible alpha-helix protrudes from the structure at the C-terminal end. A structural homology search revealed similarity to three members of Pfam family UPF0131. Conservation of residues in a hydrophilic cavity able to bind small ligands in UPF0131 proteins suggests that this may also serve as an active site in AIG2-like proteins.

*References:* (1) Lytle, B.L., Peterson, F.C., Tyler, E.M., Newman, C.L., Vinarov, D.A., Markley, J.L., Volkman, B.F. (2006) Solution structure of *Arabidopsis thaliana* protein At5g39720.1, a member of the AIG2-like protein family. *Acta Crystallogr Sect F Struct Biol Cryst Commun* 62(Pt 6):490-3.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	25% over 105 aa (1xhs)
<b>Pfam Cluster</b>	PF06094
<b>Protonet Cluster Size : Structures in PDB</b>	27 : 1

Center for Eukaryotic Structural Genomics (CESG), University of Wisconsin-Madison Biochemistry Department, 433 Babcock Drive, Madison, WI 53706-1549; phone: 608.263.2183; fax: 608.890.1942; email: [cesginfo@biochem.wisc.edu](mailto:cesginfo@biochem.wisc.edu); website: <http://www.uwstructuralgenomics.org>. This research funded by NIH / NIGMS Protein Structure Initiative grants U54 GM074901 and P50 GM064598.