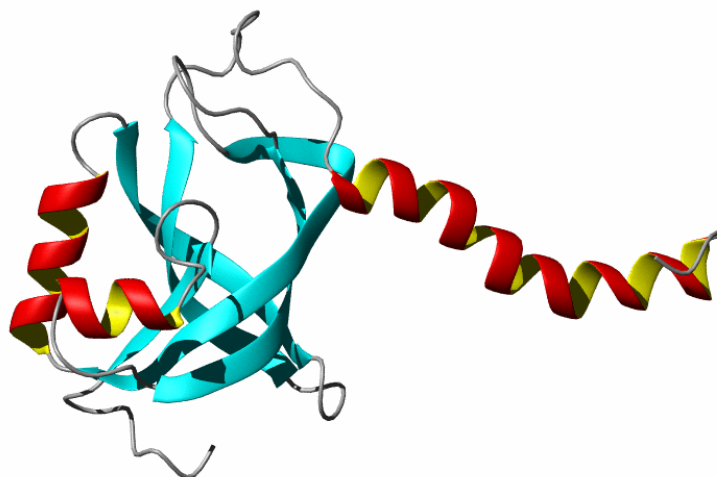


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|--------------------------|--|---|
| Target ID | GO.22446 | |
| Source Organism | <i>Arabidopsis thaliana</i> | |
| Target Name | At5g39720.1 | |
| PDB Entry | 2G0Q | Deposition: 13-Feb-2006 |
| BMRB Entry | 7007 | Deposition: 28-Feb-2006 |
| Function | unknown | |
| Produced From | Cell-free | |
| Structure by NMR | Restraints/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 |
| Data Collected At | Medical College of Wisconsin | |
| Authors | 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.

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

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