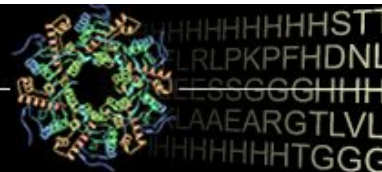
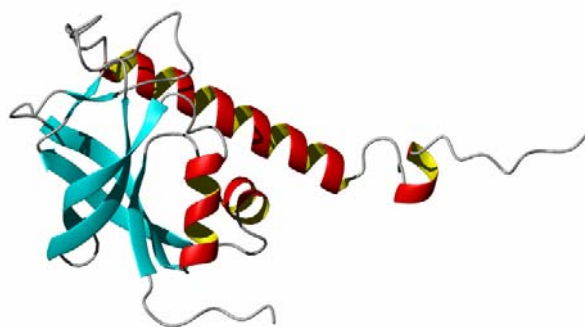


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



Target ID	GO.16211	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At3g28950.1	
PDB Entry	2JQV	Deposition: 07-Jun-2007
BMRB Entry	15295	Deposition: 14-Aug-2007
Function	an AIG-2 like protein	
Produced From	<i>E. coli</i>	
Structure by NMR	Restraints/Residue: 13.1	Subunits/Molecule: 1
	No. of Residues: 165	Molecular Weight: 18.5 kDa
	Backbone RMSD(9-44,60-80,85-111): 0.63 Å	All Heavy Atoms RMSD(9-44,60-80,85-111): 1.05 Å
Data Collected At	Medical College of Wisconsin	
Authors	Volkman, B.F., de la Cruz, N.B., Peterson, F.C.	



Structural Features

We determined the solution structure of At3g28950 from *A. thaliana*, a homolog of At5g39720, whose structure we solved earlier. The secondary structure of the 165-aa protein consists of a 5-strand antiparallel beta-barrel domain flanked by two alpha-helices and a 2-strand beta-sheet; an additional free C-terminal alpha-helix extends into solution. Bioinformatic searches and analyses suggest that members of this growing set of structurally related proteins have been recruited to serve a wide variety of functions ranging from gamma-glutamyl cyclotransferase activity to participation in plant responses to chemical and biotic stimuli. Expression of a human homolog is elevated in bladder cancer tissues. Expression patterns for At3g28950 and its *Arabidopsis* paralogs suggest that each one evolved a different physiological role. The At3g28950 structure was solved as part of a structural genomics effort, and the results demonstrate how such a project can further understanding of genome evolution in addition to sequence-structure and structure-function relationships.

References: (1) de la Cruz NB, Peterson FC, Volkman BF. (2008) Solution structure of At3g28950 from *Arabidopsis thaliana*. *Proteins*.

Percent Identity with Nearest PDB Structure at Time Solved	60.7% over 112 aa (2G0Q)
Pfam Cluster	PF06094
Protonet Cluster Size : Structures in PDB	27 : 1

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