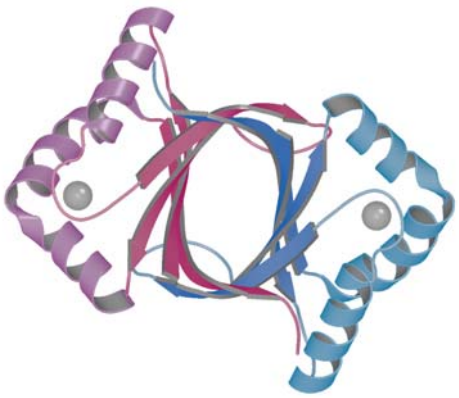
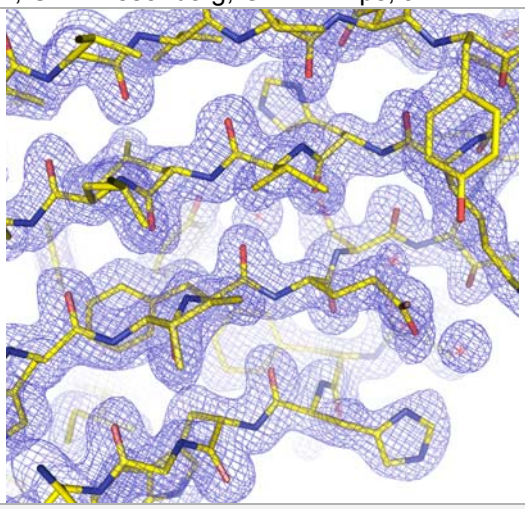
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.13081	
Source Organism	*Arabidopsis thaliana*	
Target Name	At3g17210.1	
PDB Entry	1Q4R	Deposition: 04-Aug-2003
Function	unknown (FF/Refine: 2Q3P)	
Produced From	*E. coli* B834(DE3)	
Structure by X-ray	Resolution: 1.9 Å, Se-MAD	R-value (R-free): 18.5% (23.2%)
	No. of Residues: 112 aa, 12,465x2	Subunits/ASU: 2 + 2 Mg^{++}
Data Collected At	Advanced Photon Source, BioCARS 14-ID-B	
Authors	C.A. Bingman, K.A. Johnson, D.W. Smith, G.E. Wesenberg, G.N. Phillips, Jr.	





Structural Features

At3g17210.1 was a fold-space target and the first structure solved at CESG using seleno-methionyl protein produced using our variant of Studier's autoinducing growth medium. It crystallized in space group $P6_2$ with one half-dimer per asymmetric unit. The monomers have a βαββααβ with antiparallel beta strands with a 2,1,3,4 sheet topology. Strand 2 of one monomer hydrogen bonds with strand 4 of a crystallographically-related monomer to form an elongated 8-stranded beta barrel. The N- and C- termini emerge from the same face of the dimer. Each monomer binds one magnesium ion, shown above. Sequence searches reveal a high degree of similarity to a large number of proteins from plants and bacteria. Some of the similar plant proteins are annotated as stress-response proteins. There is some three-dimensional similarity to 1LQ9, a monooxygenase from *S. coelicolor*, although At3g17210.1 lacks the active site resi-dues of the monooxygenase, and there is little or no apparent sequence similarity between these two proteins. The structure of At3g17210.1 was determined in parallel by NMR spectroscopy, and there is good agreement between the two structures. The presence of bound divalent ions is a unique feature of the X-ray structure, and may present a clue to the function of At3g17210.1.

References: (1) Bingman, C.A., Johnson, K.A., Peterson, F.C., Frederick, R.O., Zhao, Q., Thao, S., Fox, B.G., Volkman, B.F., Jeon, W.B., Smith, D.W., Newman, C.S., Ulrich, E.L., Hegeman, A., Sussman, M.R., Markley, J.L., Phillips, G.N. (2004) Crystal structure of the protein from gene At3g17210 of *Arabidopsis thaliana*. *Proteins* 57(1)**:** 218-220

Percent Identity with Nearest PDB Structure at Time Solved	none better than E=1
Pfam Cluster	B_3438
Protonet Cluster Size : Structures in PDB	67 : 0

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