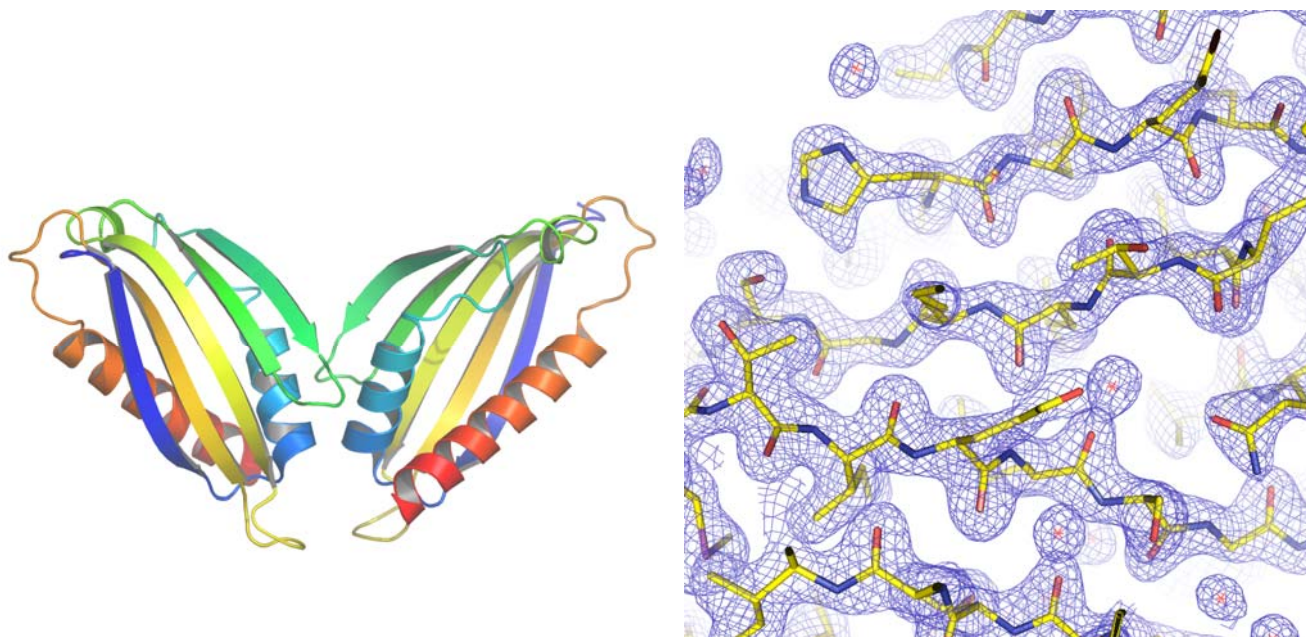


# Center for Eukaryotic Structural Genomics

## Protein Structure Data Summary

<b>Target ID</b>	GO.5358	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At1g24000.1	
<b>PDB Entry</b>	1VJH	Deposition: 20-Feb-2004
<b>Function</b>	allergen, binding pocket (FF/Refine: 2Q3Q)	
<b>Produced From</b>	<i>E. coli</i> B834(DE3)	
<b>Structure by X-ray</b>	Resolution: 2.1 Å, Se-MAD	R-value (R-free): 18.6% (23.9%)
	No. of Residues: 122 aa, (13,758x2)	Subunits/ASU: 2
<b>Data Collected At</b>	Advanced Photon Source, BioCARS 14-BM-D	
<b>Authors</b>	C.A. Bingman, K.A. Johnson, D.W. Smith, G.E. Wesenberg, G.N. Phillips, Jr.	



### Structural Features

At1g24000.1 was annotated at the time of selection as a member of the Bet\_v\_1 allergin family, but at the time of selection and deposition, there were no significant sequence matches to anything in the PDB. The protein has a  $\beta\alpha\beta\beta\alpha\beta\beta\alpha$ , with the five beta strands forming an antiparallel beta sheet. The structure was solved by a 3-wavelength SeMet MAD experiment. There are two copies of the protein in the asymmetric unit, probably indicating a dimer as the biological unit. The crystal structure reveals extra density that may be a low molecular weight polyethylene glycol, pointing to a binding site for low molecular weight hydrophobic ligands. At1g24000.1 has a high degree of sequence similarity to five other hypothetical proteins in *Arabidopsis*. A DALI search reveals only structural similarity to itself, so At1g24000.1 probably represents a new fold. In addition to the gene complex in *Arabidopsis*, At1g24000.1 also displays significant sequence similarity to genes from tobacco, peach, grape, and sugar beet.

**References:** (1) Song, J., Zhao, Q., Lee, M.S., Markley, J.L. (2005)  $^1\text{H}$ ,  $^{15}\text{N}$  and  $^{13}\text{C}$  resonance assignments of the putative Bet v 1 family protein At1g24000.1 from *Arabidopsis thaliana*. *J Biomol NMR* 32(4):335.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	none better than E=1
<b>Pfam Cluster</b>	B_68483
<b>Protonet Cluster Size : Structures in PDB</b>	78 : 0

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