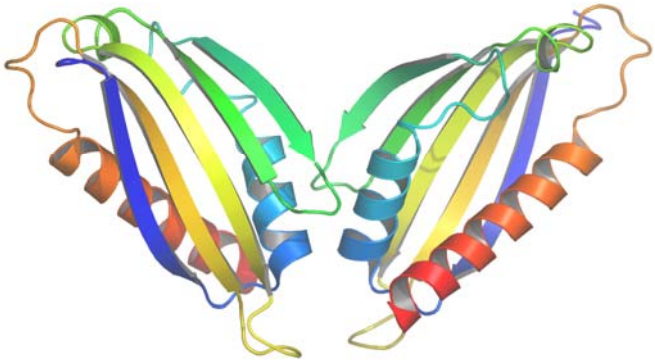
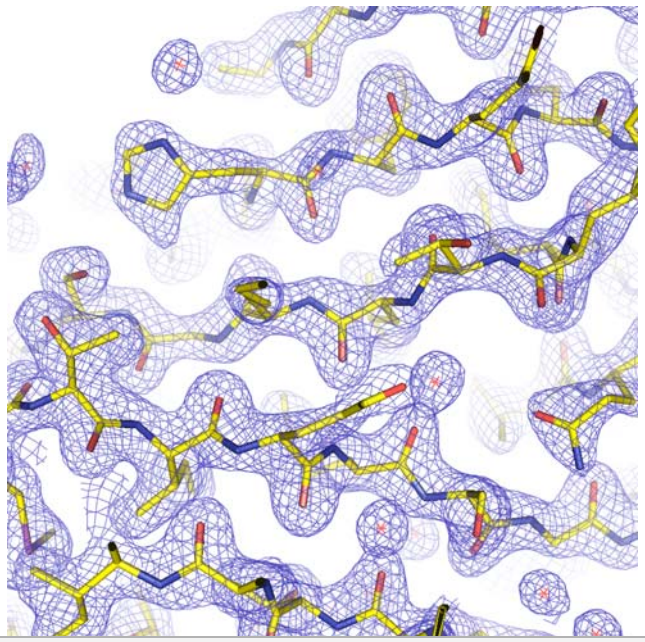
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.5358	
Source Organism	*Arabidopsis thaliana*	
Target Name	At1g24000.1	
PDB Entry	1VJH	Deposition: 20-Feb-2004
Function	allergen, binding pocket (FF/Refine: 2Q3Q)	
Produced From	*E. coli* B834(DE3)	
Structure by X-ray	Resolution: 2.1 Å, Se-MAD	R-value (R-free): 18.6% (23.9%)
	No. of Residues: 122 aa, (13,758x2)	Subunits/ASU: 2
Data Collected At	Advanced Photon Source, BioCARS 14-BM-D	
Authors	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 *βαββαββα*, 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}H, ^{15}N and ^{13}C resonance assignments of the putative Bet v 1 family protein At1g24000.1 from *Arabidopsis thaliana*. *J Biomol NMR* 32(4):335.

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

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