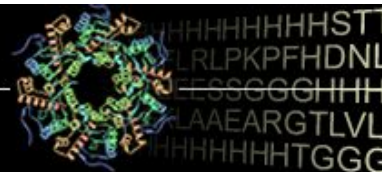


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



Target ID	GO.74365	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At1g70830.1	
PDB Entry	2I9Y	Deposition: 06-Sep-2006
BMRB Entry	N/A	Deposition: N/A
Function	member of the major latex protein family	
Produced From	Cell-free	
Structure by NMR	Restraints/Residue: 11.2	Subunits/Molecule: 1
	No. of Residues: 157	Molecular Weight: 17.5 kDa
	Backbone RMSD(21-43,70-78,86-128,132-171): 0.78 Å	All Heavy Atoms RMSD(21-43,70-78,86-128,132-171): 1.21 Å
Data Collected At	Medical College of Wisconsin	
Authors	Volkman, B.F., de la Cruz, N.B., Lytle, B.L., Peterson, F.C.	



Structural Features

At1g70830.1, also known as MLP28, is a member of the major latex protein (MLP) family comprised of proteins that were first identified in the latex of opium poppy. The MLPs are members of Pfam family PF00407 (Pathogenesis-related protein Bet v 1), which also includes the cytokinin-specific binding proteins (CSBPs) and the Bet v 1/PR-10 allergen proteins. The structure consists of a six-stranded β -sheet enfolding a 21-amino acid C-terminal α -helix, defining a hydrophobic pocket. Residues 45-65 comprise a long, flexible loop. A search for homologous structures yielded At1g24000.1, also solved by CESH, as the closest match. The two structures can be superimposed with an rmsd of 1.6 Å for 102 aligned C α atoms. While the function of MLP28 is unknown, homology to other Bet v 1 proteins indicates that its hydrophobic pocket could play a functional role in binding plant hormones or other small metabolites.

Percent Identity with Nearest PDB Structure at Time Solved	33% over 102 aa (1VJH)
Pfam Cluster	Bet_v_1 (PF00407)
Protonet Cluster Size : Structures in PDB	78 : 0

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