

# Center for Eukaryotic Structural Genomics

## Protein Structure Data Summary

<b>Target ID</b>	GO.15176	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At3g01050.1	
<b>PDB Entry</b>	1SE9	Deposition: 16-Feb-2004
<b>BMRB Entry</b>	6128	Deposition: 03-Mar-2004
<b>Function</b>	trypsin inhibitor	
<b>Produced From</b>	Cell-Free (wheat germ extract)	
<b>Structure by NMR</b>	Restraints/Residue: 10.7	Subunits/Molecule: 1
	No. of Residues: 126	Molecular Weight: 12.8 kDa
	Backbone RMSD(7-93): 1.14 Å	All Heavy Atoms RMSD(7-93): 1.60 Å
<b>Data Collected At</b>	Medical College of Wisconsin, Milwaukee, WI	
<b>Authors</b>	B.F. Volkman, B.L. Lytle, F.C. Peterson	



### Structural Features

The most similar structure in the PDB was the ubiquitin-like protein Rub1 (1BT0), the plant homolog of NEDD8, with 27% structure identity over 76 residues. The beta-grasp fold is ~80 amino acid in length, and is composed of a 5-stranded beta sheet that wraps around a single alpha helix. Ub and ubiquitin-like proteins (UBL) generally serve as covalent modifiers of other proteins in the cell, tagging them for proteasomal degradation or altering their functional behavior. Based on sequence analysis, At3g01050.1 probably does not function as a Ub-like covalent modifier, but instead may be prenylated at a putative C-terminal CAAX box motif, thus targeting the protein and its binding partners to a membrane compartment of the cell. This target aligns to Pfam domain of Pfam-B\_16300 over residues 1-99.

*References:* (1) Vinarov, D.A., Lytle, B.L., Peterson, F.C., Tyler, E.M., Volkman, B.F., Markley, J.L. (2004) Cell-free protein production and labeling protocol for NMR-based structural proteomics. *Nat Methods* 1(2):149-53.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	27% over 76 aa (1BT0)
<b>Pfam Cluster</b>	B_16300
<b>Protonet Cluster Size : Structures in PDB</b>	613 : 7

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