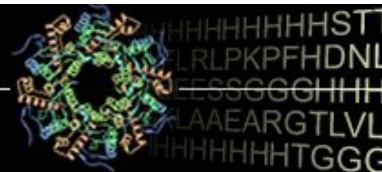
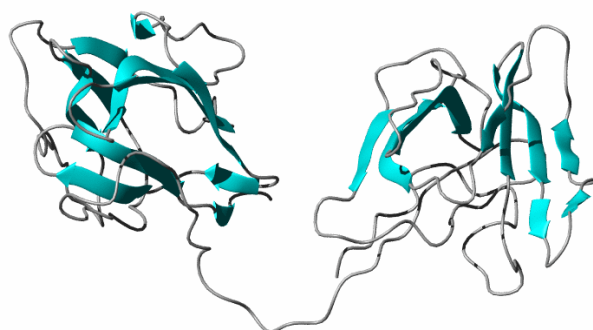


# Center for Eukaryotic Structural Genomics

## Protein Structure Initiative



<b>Target ID</b>	GO.12798	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At3g16450.1	
<b>PDB Entry</b>	2JZ4	Deposition: 28-Dec-2007
<b>BMRB Entry</b>	6140	Deposition: 19-Feb-2008
<b>Function</b>	Putative 32 kDa myrosinase binding protein	
<b>Produced From</b>	GO.12798	
<b>Structure by NMR</b>	Restraints/Residue: N/A	Subunits/Molecule: 1
	No. of Residues: 299	Molecular Weight: 33.0 kDa
	Backbone RMSD(25-295): 14.17 Å	All Heavy Atoms RMSD(14-120,126-152): 14.54 Å
<b>Data Collected At</b>	Nuclear Magnetic Resonance Facility at Madison (NMRFAM)	
<b>Authors</b>	Takeda, N., Sugimori, N., Torizawa, T., Terauchi, T., Ono, A.M., Yagi, H., Yamaguchi, Y., Kato, K., Ikeya, T., Guntert, P., Aceti, D.J., Markley, J.L., Kainosho, M.	



### Structural Features

The flowering brassica *Arabidopsis thaliana* is important as a model for identifying plant genes and determining their functions. At3g16450.1 is a 32 kDa, 299-residue hypothetical protein from *A. thaliana*. At3g16450.1 is expected to be a bifunctional lectin.

*References:* (1) Sugimori, N., Torizawa, T., Aceti, D.J., Thao, S., Markley, J.L., Kainosho, M. (2004) (1)H, (13)C and (15)N backbone assignment of a 32 kDa hypothetical protein from *Arabidopsis thaliana*, At3g16450.1. *J Biomol NMR* 30(3):357-8.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	28% coverage (1ZQR)
<b>Pfam Cluster</b>	JACALIN
<b>Protonet Cluster Size : Structures in PDB</b>	224

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