



Target ID	GO.33931	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At1g16640.1	
PDB Entry	1YEL	Deposition: 28-Dec-2004
BMRB Entry	6464	Deposition: 18-Jan-2005
Function	Nucleic acid binding	
Produced From	<i>E. coli</i> B834(DE3) p(Lacl+RARE)	
Structure by NMR	Restraints/Residue: 14.2	Subunits/Molecule: 1
	No. of Residues: 102	Molecular Weight: 12.0 kDa
	Backbone RMSD(4-97): 0.71 Å	All Heavy Atoms RMSD(4-97): 1.28 Å
Data Collected At	Medical College of Wisconsin	
Authors	Peterson, F.C., Waltner, J.K., Lytle, B.L., Volkman, B.F.	



Structural Features

A novel DNA binding motif, the B3 domain, has been identified in a number of transcription factors specific to higher plant species, and was recently found to define a new protein fold. Here we report the second structure of a B3 domain, that of the *Arabidopsis thaliana* protein, At1g16640. As part of an effort to 'rescue' structural genomics targets deemed unsuitable for structure determination as full-length proteins, we applied a combined bioinformatic and experimental strategy to identify an optimal construct containing a predicted conserved domain. By screening a series of N- and C-terminally truncated At1g16640 fragments, we isolated a stable folded domain that met our criteria for structural analysis by NMR spectroscopy. The structure of the B3 domain of At1g16640 consists of a seven-stranded beta-sheet arranged in an open barrel and two short alpha-helices, one at each end of the barrel. While At1g16640 is quite distinct from previously characterized B3 domain proteins in terms of amino acid sequence similarity, it adopts the same novel fold that was recently revealed by the RAV1 B3 domain structure. However, putative DNA-binding elements conserved in B3 domains from the RAV, ARF, and ABI3/VP1 subfamilies are largely absent in At1g16640, perhaps suggesting that B3 domains could function in contexts other than transcriptional regulation.

References: Peterson, F.C., Waltner, J.K., Lytle, B.L., Volkman, B.F. (2005) Structure of the B3 domain from *Arabidopsis thaliana* protein At1g16640. *Protein Sci* (9):2478-83.

Percent Identity with Nearest PDB Structure at Time Solved	26% over 102 aa (1WID)
Pfam Cluster	PF02362
Protonet Cluster Size : Structures in PDB	125 : 0

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