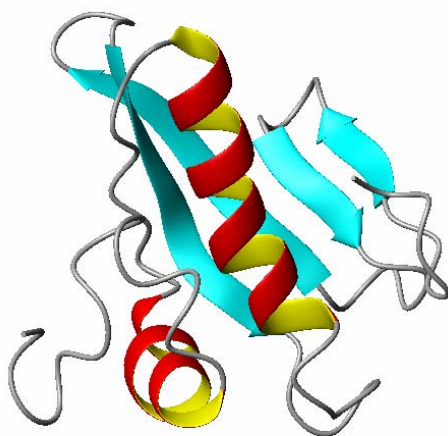


Center for Eukaryotic Structural Genomics

Protein Structure Data Summary

Target ID	GO.6042	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At1g77540.1	
PDB Entry	2EVN (replaced 1XO4)	Deposition: 5-Oct-2004
BMRB Entry	6338	Deposition: 5-Oct-2004
Function	putative acetyltransferase (FF/Refine: 2IL4 [REPLACED 2GDB], 2Q4Y)	
Produced From	<i>E. coli</i> B834(DE3)/pLacIRARE	
Structure by NMR	Restraints/Residue: 19	Subunits/Molecule: 1
	No. of Residues: 103	Molecular Weight: 11.7 kDa
	Backbone RMSD(7-87): 0.48 Å	All Heavy Atoms RMSD(7-87): 0.86 Å
Data Collected At	Nuclear Magnetic Resonance Facility at Madison (NMRFAM)	
Authors	R.C. Tyler, S. Singh, M.S. Lee, J.L. Markley	



Structural Features

The most similar structure in the PDB was GCN5-like putative N-acetyltransferase from *Staphylococcus aureus* (1R57) with 32% sequence identity over 71 residues. Several other targets with similar fold were co-crystallized with acetyl coenzyme A or coenzyme A with or without putative substrate. In view of these findings, the titration of ¹⁵N-At1g77540.1 with coenzyme A was followed by NMR spectroscopy. The ¹H-¹⁵N HSQC chemical shift perturbation clearly demonstrated the binding and the location of this ligand. The coenzyme A binding site was mapped to At1g77540.1 residues in the cavity formed by C-terminal residue of β -sheet 4 (β 4), loop residues spanning β 4 and the N-terminal central helix (α 1), N-terminal residues of α 1 and residues of smaller perpendicularly oriented helix (α -2) in agreement with the X-ray co-crystal structures. Thus, it is most likely that At1g77540.1 functions as acetyl transferase. This target aligns to two Pfam domains of Pfam-B_34288 over residues 2-29 and Pfam-B_2135 over residues 30-79.

References: (1) Tyler, R.C., Bitto, E., Berndsen, C.E., Bingman, C.A., Singh, S., Lee, M.S., Wesenberg, G.E., Denu, J.M., Phillips, G.N., Jr, Markley J.L. (2006) Structure of *Arabidopsis thaliana* At1g77540 protein, a minimal acetyltransferase from the COG2388 family. *Biochemistry* 45(48):14325-36.

Percent Identity with Nearest PDB Structure at Time Solved	32% over 71 aa (1R57)
Pfam Cluster	B_34288, B_2135
Protonet Cluster Size : Structures in PDB	22 : 0

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