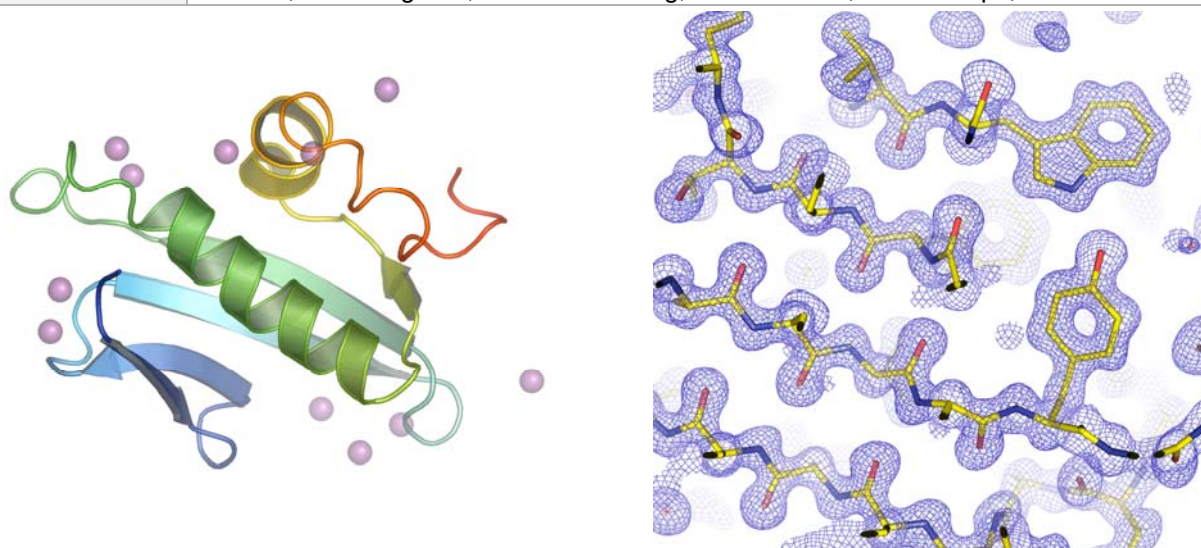




<b>Target ID</b>	GO.6042	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At1g77540.1	
<b>PDB Entry</b>	1XMT	Deposition: 4-Oct-2004
<b>Function</b>	putative acetyltransferase (FF/Refine: 2Q44)	
<b>Produced From</b>	<i>E. coli</i> B834(DE3)	
<b>Structure by X-ray</b>	Resolution: 1.15 Å, Br-MAD	R-value (R-free): 14.9% (17.0%)
	No. of Residues: 103	Subunits/Molecule: 1
<b>Data Collected At</b>	Advanced Photon Source, COM-CAT 32-ID	
<b>Authors</b>	E. Bitto, C.A. Bingman, G.E. Wesenberg, S.T.M. Allard, G.N. Phillips, Jr.	



### Structural Features

The structure of At1g75540.1 was solved by a MAD experiment performed with bromide as the anomalous scatterer. This represents the first successful application of Br phasing at CESG. At1g75540.1 likely functions as acetyl transferase. Its primary structure shows distant homology to proteins with this activity, cataloged within Gcn5-related N-acetyltransferase superfamily. Often, this small domain occurs in multi-domain proteins where it provides substrate acetylation activity. The most similar homolog in the PDB shows 32% sequence identity of 71 aligned residues (1R57, NMR), several others range in 9-13% sequence identity (1BOB, 1NSL, 1KZF, 1YGH, 1GHE, 1QZY). Several of the fold-homologs were co-crystallized with an acetyl coenzyme A, the most common biochemical donor of acetyl groups. The binding site for this cofactor in At1g75540.1 can thus be inferred to reside in the groove delineated by central helix of the domain (green), several loop residues following the helix and smaller perpendicularly oriented helix (yellow). Some of the residues 43-51 are likely to be involved in the binding of acetyl CoA moiety. This protein aligns to two Pfam-B domains, Pfam-B\_34288 over residues 2-29, and Pfam-B\_2135 over residues 30-79. The small N-terminal domain seems to be plant-specific.

*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.

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

Center for Eukaryotic Structural Genomics (CESG), University of Wisconsin-Madison Biochemistry Department, 433 Babcock Drive, Madison, WI 53706-1549; phone: 608.263.2183; fax: 608.890.1942; email: [cesginfo@biochem.wisc.edu](mailto:cesginfo@biochem.wisc.edu); website: <http://www.uwstructuralgenomics.org>. This research funded by NIH / NIGMS Protein Structure Initiative grants U54 GM074901 and P50 GM064598.