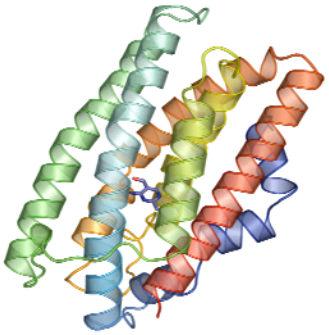
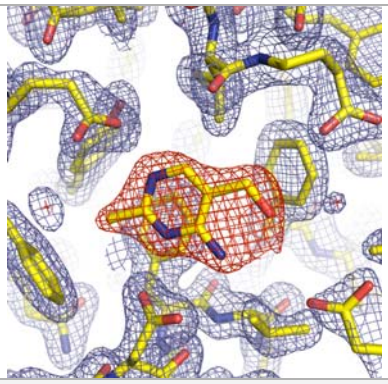
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.12240	
Source Organism	*Arabidopsis thaliana*	
Target Name	At3g16990.1	
PDB Entry	2F2G (refinement of 1Q4M)	Deposition: 16-Nov-2005
Function	Seed maturation protein pm36 homolog (FF/Refine: 2Q4X)	
Produced From	*E. coli* ROSETTA, pVP-13	
Structure by X-ray	Resolution: 1.48 Å	R-value (R-free): 17.3% (23.4%)
	No. of Residues/ASU: 426	Monomers/ASU: 2
Data Collected At	Advanced Photon Source 14IDB, 26-Jun-2003	
Authors	G.E. Wesenberg, D.W. Smith, G.N. Phillips, Jr., K.A. Johnson, E. Bitto, C.A. Bingman	





Structural Features

The protein product of At3g16990.1 gene (hereafter referred to as AtHp25k) is a plant homolog of TenA (transcriptional enhancer A). TenA homologues are widely distributed in eubacteria and archea, however the biological function of TenA remains unclear. It has been proposed to act as a transcriptional regulator and/or an enzyme involved in thiamine (vitamin B1) biosynthesis. The structure of AtHp25k reveals an all alpha-helical protein with a tertiary structure similar to heme oxygenase. Each monomer consists of a seven-helix bundle with a solvent-sequestered inner core. The central cavity forms a putative ligand binding site. In the originally published structure of AtHp25k (PDB ID 1Q4M), the core of the protein harbored an unassigned electron density. Recently, the TenA homolog from *Pyrococcus furiosus* (PDB ID 1RTW) has been crystallized with 4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate (HMP-P) bound in the active site. HMP-P is an intermediate in thiamine metabolism that can be synthesized by ThiD kinase via phosphorylation of 4-amino-5-hydroxymethyl-2-methylpyrimidine (HMP) or through a reaction catalyzed by ThiC enzyme using 5'-phosphoribosyl-5-aminoimidazole (AIR) as a substrate. Based on this information, the originally unexplained electron density at the core of the AtHp25k could be assigned as HMP supporting the role of this protein in thiamine biosynthesis. The TenA homolog from *Bacillus subtillis* have been also crystallized in complex with HMP (PDB ID 1YAK) and has been shown to have thiaminase II activity, hydrolyzing thiamine to HMP and thiazole. Although certain residues in the putative active site are conserved among the TenA homologues there are some important differences. The cysteine residue proposed to act as a nucleophile in the thiamine cleavage reaction in 1YAK is replaced by isoleucine in 2F2G and shifted in 1RTW making them unlikely to function as thiaminases. It is possible that TenA homologues share a common ancestor protein that later diversified to perform different catalytical functions.

References: (1) Blommel, P.G., Smith, D.W., Bingman, C.A., Dyer, D.H., Rayment, I., Holden, H.M., Fox, B.G., Phillips, G.N., Jr. (2004) Crystal structure of the gene locus At3g16690 from *Arabidopsis thaliana*. *Proteins* 57(1):221-2.

Percent Identity with Nearest PDB Structure at Time Solved	23% (1WWM)
Pfam Cluster	TENA_THI-4
Sequence Cluster Size	48

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