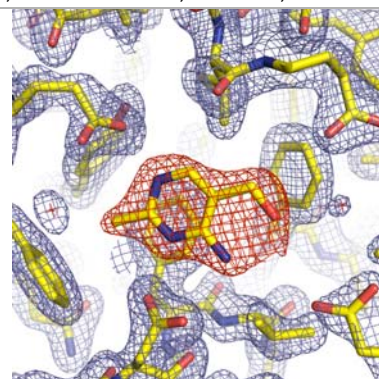
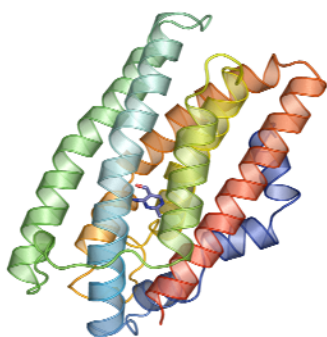




<b>Target ID</b>	GO.12240	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At3g16990.1	
<b>PDB Entry</b>	2F2G (refinement of 1Q4M)	Deposition: 16-Nov-2005
<b>Function</b>	Seed maturation protein pm36 homolog (FF/Refine: 2Q4X)	
<b>Produced From</b>	<i>E. coli</i> ROSETTA, pVP-13	
<b>Structure by X-ray</b>	Resolution: 1.48 Å	R-value (R-free): 17.3% (23.4%)
	No. of Residues/ASU: 426	Monomers/ASU: 2
<b>Data Collected At</b>	Advanced Photon Source 14IDB, 26-Jun-2003	
<b>Authors</b>	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 archaea, 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 subtilis* 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.

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

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