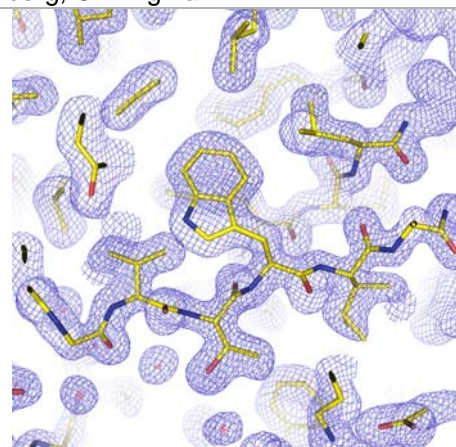
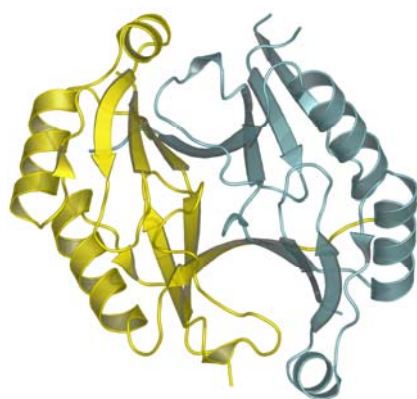




Target ID	GO.22340	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At5g48480.1	
PDB Entry	1XY7	Deposition: 09-Nov-2004
Function	unknown (FF/Refine: 2Q48)	
Produced From	<i>E. coli</i> B834(DE3) p(Lacl+RARE) pVP-13	
Structure by X-ray	Resolution: 1.80 Å	R-value (R-free): 18.4% (22.8%)
	No. of Residues/ASU: 242	Monomers/ASU: 2
Data Collected At	Advanced Photon Source Bio-CARS 14-ID-B	
Authors	E. Bitto, G. N. Phillips, Jr., S. Allard, G. Wesenberg, C. Bingman	



Structural Features

The At5g48480.1 gene encodes a 17kDa protein of unknown function. The crystal structure of At5g48480.1 has been determined and refined to 1.8 Å resolution. The protein crystallizes as a dimer with extensive interface between tightly associated monomers. Each monomer consists of two domains with fold of β - α - β - β - β topology. The fold of At5g48480.1 has been observed in proteins from glyoxalase/bleomycin resistance protein/dioxygenase superfamily (referred to as 'VOC' superfamily). The closest structural homologs of At5g48480.1 include fosfomycin and bleomycin resistance proteins (PDB ID 1R9C and 1QTO, respectively) as well as several proteins from the glyoxalase I family (PDB ID codes 1ZSW, 1F9Z, 2C2, and 1SS4). Many enzymes of VOC-superfamily require metal ion for catalytic activity. The metal binds in the active site, which is located at the dimer interface within the inner cleft formed by the curved 8-stranded β -sheet. The metal coordinating residues are highly conserved despite a low sequence similarity among these proteins. However, structurally equivalent positions in At5g48480.1 are occupied by hydrophobic residues, making metal binding unlikely. The putative substrate-binding cavity in At5g48480.1 is predominantly hydrophobic. The only polar residues in the vicinity of active site are Ser72 and Cys85 and there is no evidence of a catalytic triad that would point toward a hydrolytic activity of this protein. The residues 54-68, located near the active site, were not defined in the electron density map of At5g48480.1. Several residues in this region are charged and may therefore help in substrate binding through electrostatic interactions. Superposition of the two monomers revealed that this loop likely adopts a different conformation in each monomer further pointing toward flexibility in this region. Taken together, the At5g48480.1 protein has been identified as a new member of VOC-superfamily in plants with unknown function and no significant sequence homology to any known protein.

Percent Identity with Nearest PDB Structure at Time Solved	33% (1FFK)
Pfam Cluster	Glyoxalase
Sequence Cluster Size	5

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