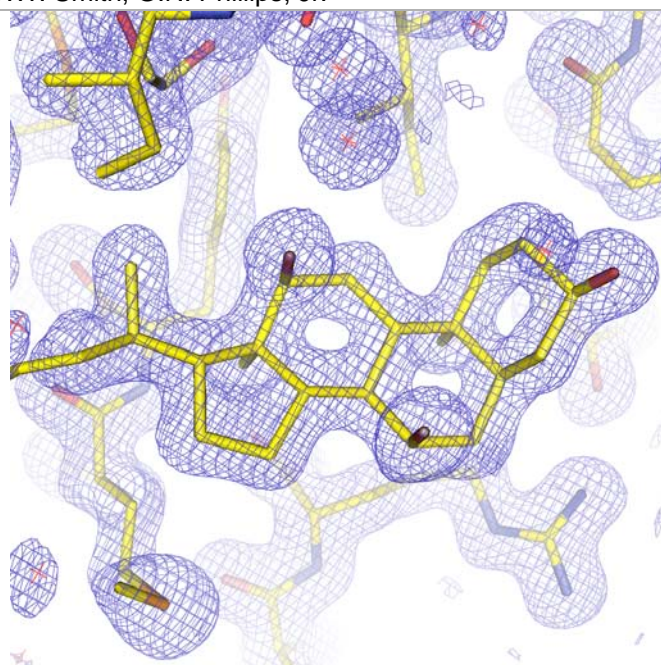
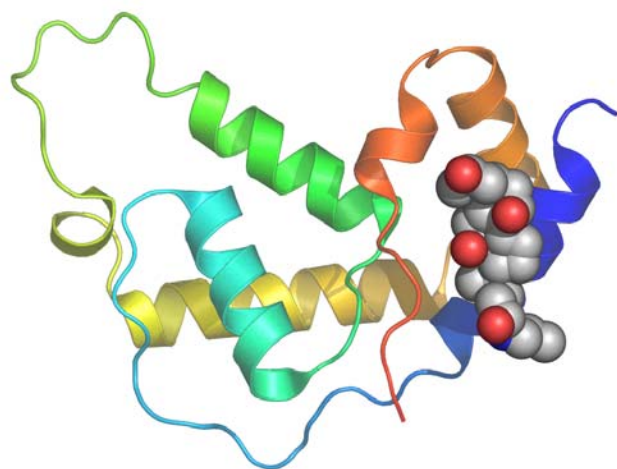


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



Target ID	GO.13974	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At3g22680.1	
PDB Entry	1VK5	Deposition: 06-May-2004
Function	binds CHAPS detergent in crystal (FF/Refine: 2Q3T)	
Produced From	<i>E. coli</i> B834(DE3) p(Lacl+RARE)	
Structure by X-ray	Resolution: 1.60	R-value (R-free): 16.1% (18.4%)
	No. of Residues: 157 (17,924)	Subunits/Molecule: 1
Data Collected At	Advanced Photon Source BioCARS 14-BM-D 14-Feb-2004, COM-CAT 32-IDB 27-Feb-2004	
Authors	S.T.M. Allard, C.A. Bingman, D.W. Smith, G.N. Phillips, Jr.	



Structural Features

At3g22680.1 appears to represent a new protein fold. The structure was solved by Se-Met MAD. At the time of selection and deposition, there was no significant sequence similarity to structures in the PDB. DALI searches revealed no significant structural similarity to any known protein fold. The quality of crystals of this protein was dramatically improved by including the detergent CHAPS. The above left figure shows CHAPS bound to At3g22680.1.

References: (1) Allard, S.T., Bingman, C.A., Johnson, K.A., Wesenberg, G.E., Bitto, E., Jeon, W.B., Phillips, G.N. Jr. (2005) Structure at 1.6 Å resolution of the protein from gene locus At3g22680 from *Arabidopsis thaliana*. *Acta Crystallogr Sect F Struct Biol Cryst Commun* 61(Pt 7):647-50.

Percent Identity with Nearest PDB Structure at Time Solved	none better than E=1
Pfam Cluster	Pfam-B_96548
Protonet Cluster Size : Structures in PDB	108 : 1

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