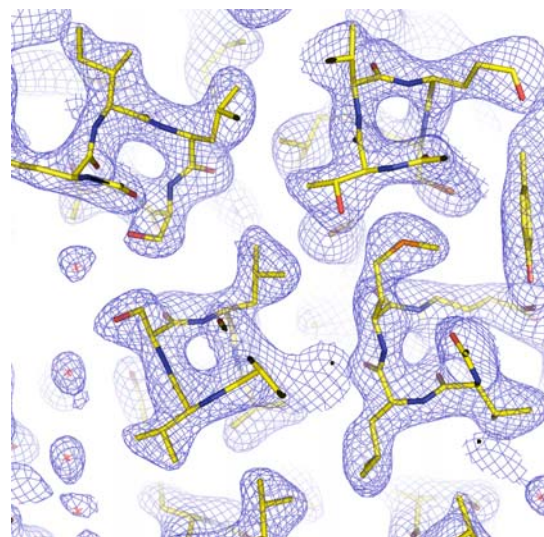
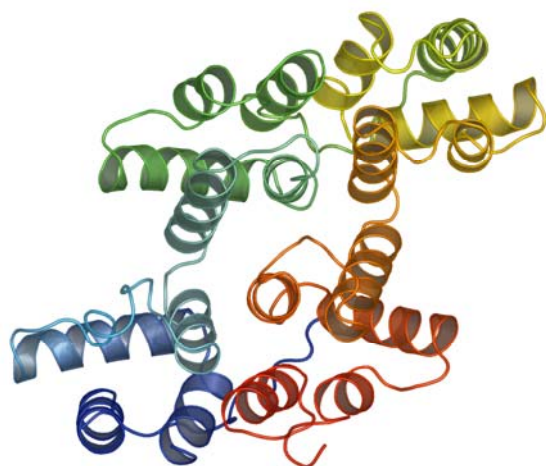


Center for Eukaryotic Structural Genomics

Protein Structure Data Summary

Target ID	GO.4020	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At1g35720.1	
PDB Entry	1YCN	Deposition: 22-Dec-2004
Function	annexin (FF/Refine: 2Q4C)	
Produced From	<i>E. coli</i> B834(DE3) p(LacI+RARE)	
Structure by X-ray	Resolution: 2.51 Å	R-value (R-free): 22.0% (26.8%)
	No. of Residues: 634	Subunits/ASU: 2
Data Collected At	Advanced Photon Source SBC 19-BM 15-Dec-2004	
Authors	E. Bitto, G.N. Phillips, Jr., S.T.M. Allard, G.E. Wesenberg, C.A. Bingman	



Structural Features

Structural studies on At1g35720.1 were initiated by an outside request by Greg Clark, (Department of Botany, University of Texas at Austin). Annexins are a multigene family of proteins expressed in multicellular eukaryotes. Binding of annexins to phospholipids is modulated by free calcium concentration. Previously, only two plant annexins had been crystallized (1,2). The structure of At1g35720.1 was determined by molecular replacement using a cotton annexin (1N00) as the search model. The overall structure of At1g35720.1 is similar to 1N00, but differs significantly in surface loops at the membrane-binding interface. A new buried conformation for the highly conserved Trp99 in domain II was observed. A sulphur cluster hypothesized to be responsible for redox activity is retained in nearly identical conformation to that found in cotton annexin (1,3). However, the positively charged patch leading to the sulphur cluster site is not conserved (1).

References: (1) Hofmann, A., Delmer, D.P., Wlodawer, A. (2003) The crystal structure of annexin Gh1 from *Gossypium hirsutum* reveals an unusual S₃ cluster. *Eur J Biochem* 270(12):2557-2564; (2) Hofmann, A., Prout, J., Dorowski, A., Schantz, R., Huber, R. (2000) Annexin 24 from *Capsicum annuum*: x-ray structure and biochemical characterization. *J Biol Chem* 275(11):8072-8082; (3) Gidrol, X., Sabelli, P.A., Fern, Y.S., Kush, A.K. (1996) Annexin-like protein from *Arabidopsis thaliana* rescues delta oxyR mutant of *Escherichia coli* from H₂O₂ stress. *PNAS* 93(20):11268-73.

Percent Identity with Nearest PDB Structure at Time Solved	73% over 312 aa (1N00)
Pfam Cluster	Annexin
Protonet Cluster Size : Structures in PDB	270 : 11

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