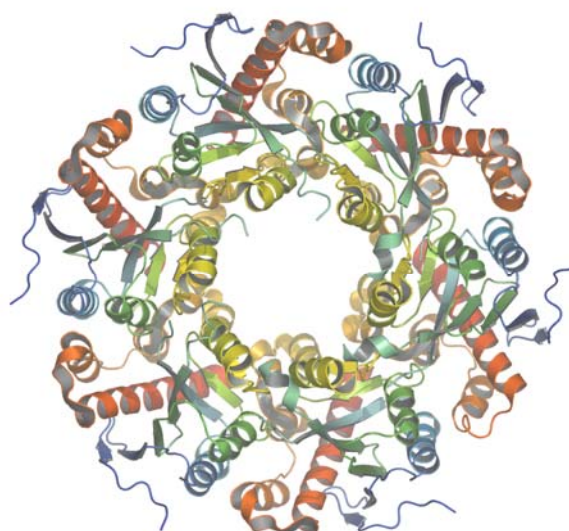


# Center for Eukaryotic Structural Genomics

## Protein Structure Data Summary

<b>Target ID</b>	GO.22116	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At5g06450.1	
<b>PDB Entry</b>	1VK0	Deposition: 12-Apr-2004
<b>Function</b>	exonuclease (FF/Refine: 2Q3S)	
<b>Produced From</b>	<i>E. coli</i> B834(DE3) p(Lacl+RARE)	
<b>Structure by X-ray</b>	Resolution: 2.10	R-value (R-free): 18.3% (23.3%)
	No. of Residues: 206 (23,172x6)	Subunits/Molecule: 6
<b>Data Collected At</b>	Advanced Photon Source BioCARS 14-BM-D 26-Oct-2003	
<b>Authors</b>	D.W. Smith, C.A. Bingman, K.A. Johnson, G.E. Wesenberg, G.N. Phillips, Jr.	



### Structural Features

At5g06450.1 has been assigned to the 35EXOc, a family of proteins that includes the 3'-5' exonuclease proofreading domain present in DNA polymerase I, Werner syndrome helicase, RNase D, and other enzymes. The closest 3D match in DALI is to 1XWL, a 3'-5' exonuclease domain, with an RMSD of 3.6 Å over the aligned regions. At5g06450.1 represents the only structure of a member of this class of proteins with a cyclic quarternary structure. At5g06450.1 has  $C_6$  rotational symmetry. There is a central cavity of variable dimensions, narrowing to 22 Å width between ordered side chains on the N-terminal face of the hexamer. Disordered loops, invisible in the electron density map, would seem to project into this open annulus, further narrowing the cavity. The disordered loops have the sequence YKYKGS, which is highly positively charged, and contains aromatic groups that could stack with nucleic acid. The overall structure is reminiscent of processivity factors in nucleic acid metabolism and viral exonucleases. The size of the Protonet cluster associated with this protein suggests that it may open up a large number of other proteins to modeling efforts.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	none better than E=1
<b>Pfam Cluster</b>	Pfam-B_104596
<b>Protonet Cluster Size : Structures in PDB</b>	61 : 0

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