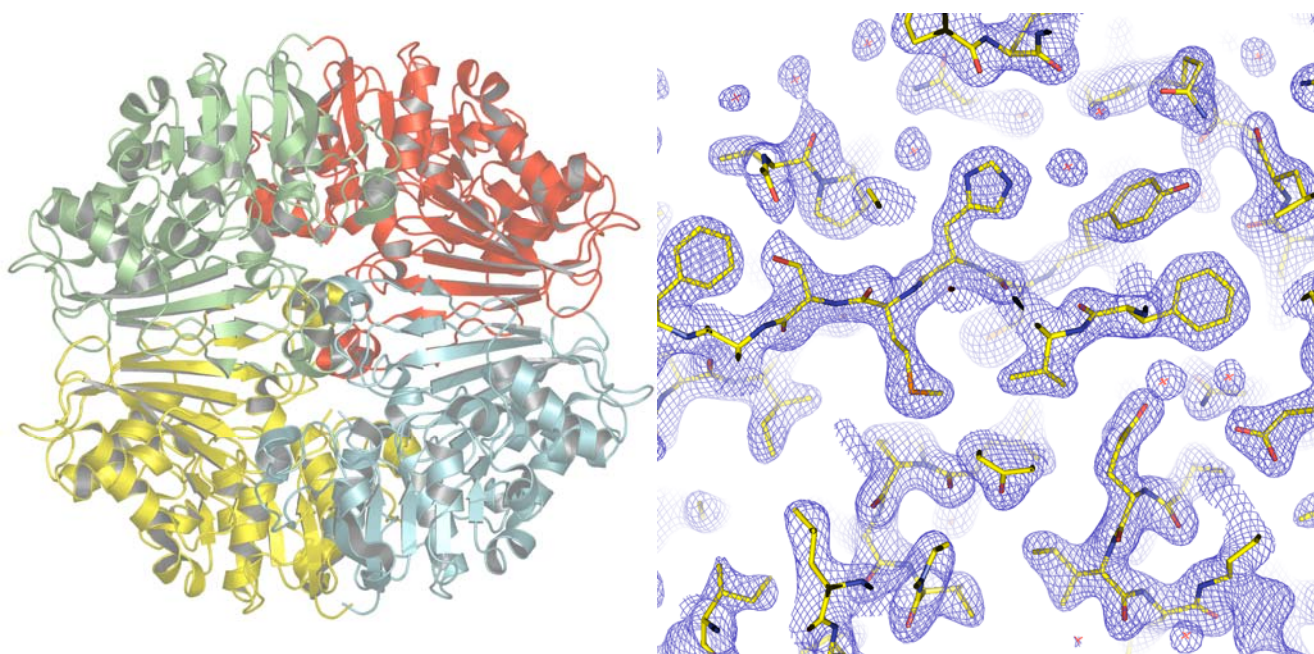


# Center for Eukaryotic Structural Genomics

## Protein Structure Initiative



<b>Target ID</b>	GO.9383	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At2g19940.2	
<b>PDB Entry</b>	1XYG	Deposition: 09-Nov-2004
<b>Function</b>	putative N-acetyl- $\gamma$ -glutamyl-phosphate reductase (FF/Refine: 2Q49)	
<b>Produced From</b>	<i>E. coli</i> B834(DE3) p(Lacl+RARE)	
<b>Structure by X-ray</b>	Resolution: 2.19 Å	R-value (R-free): 26.1% (28.2%)
	No. of Residues: 1436aa, 11676 atoms	Subunits/Molecule: 4
<b>Data Collected At</b>	Advanced Photon Source BioCARS 14-ID-B Oct-2004	
<b>Authors</b>	E. Bitto , G.N. Phillips, Jr., S.T.M. Allard, G.E. Wesenberg, C.A. Bingman	



### Structural Features

The gene product of At2g19940.2 belongs to the semialdehyde dehydrogenase superfamily (PFAM). It participates in arginine biosynthesis, converting N-acetylglutamate-5-phosphate to N-acetylglutamate-5-semialdehyde using NADPH (EC 1.2.1.38). This is the first structure for a eukaryotic N-acetylglutamate-5-phosphate reductase. At2g19940.2 falls within ProtoNet cluster 274710, which is a mixed bacterial, eukaryotic and viral cluster. The structure was solved by molecular replacement using the homolog from *Thematoga maritime* (1VKN) as a search model. The fold and catalytic core are similar to similar to other family members. Displacements in surface loops of several angstroms are observed.

### Percent Identity with Nearest PDB Structure at Time Solved

44.8% over 342 aa (1VKN)

### Pfam Cluster

Semialdhyde\_dh (16-159),  
Semialdhyde\_dhC (172-330),  
Pfam-B\_9629 (192-345)

### Protonet Cluster Size : Structures in PDB

173 : 0

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