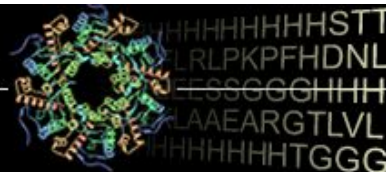
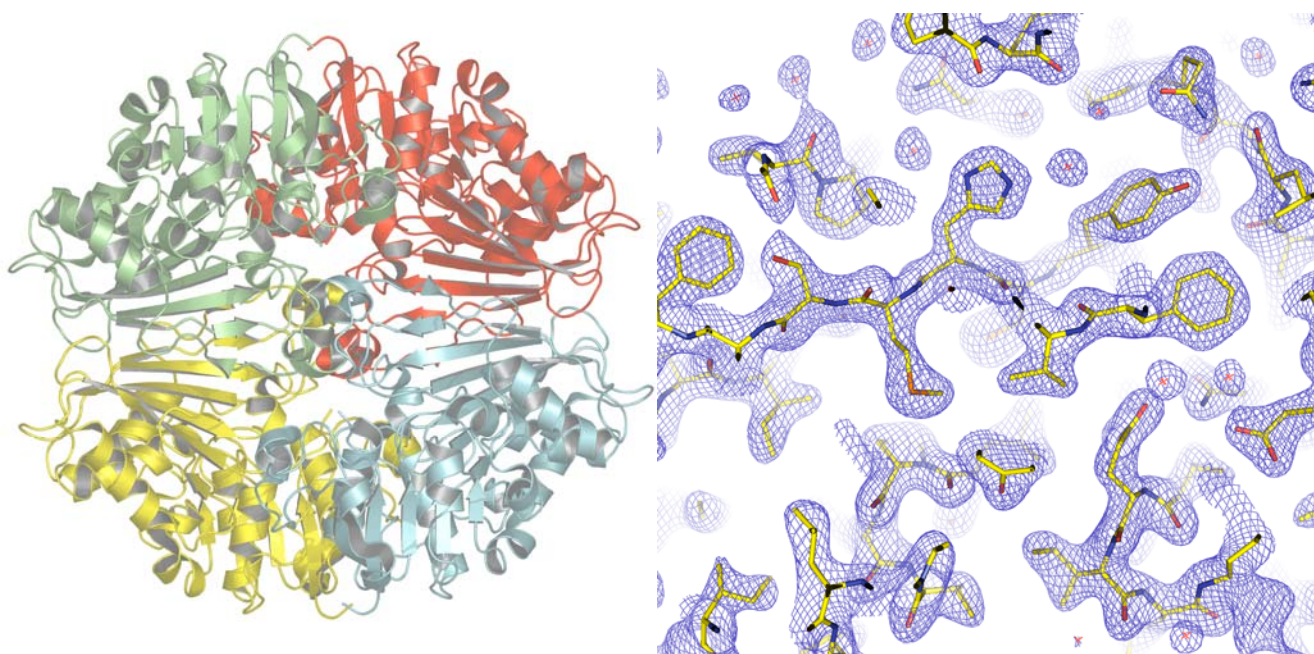


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



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