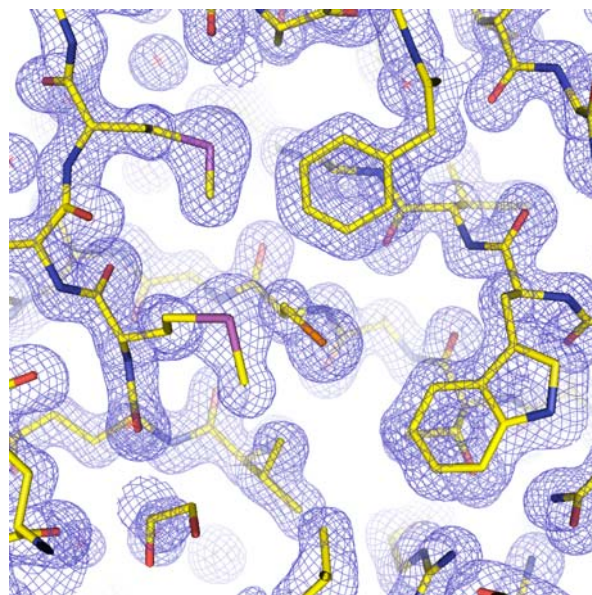
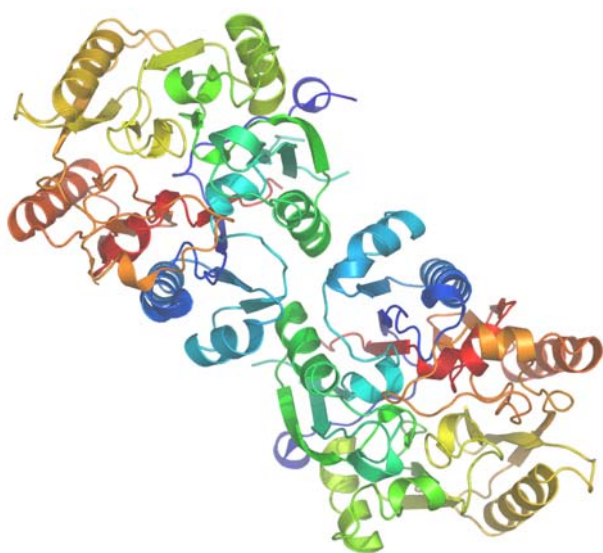


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



Target ID	GO.24674	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At5g08170.1	
PDB Entry	1VKP	Deposition: 15-Jun-2004
Function	agmatine iminohydrolase (EC:3.5.3.12) (FF/Refine: 2Q3U)	
Produced From	<i>E. coli</i> B834(DE3) p(Lacl+RARE)	
Structure by X-ray	Resolution: 1.53 Å	R-value (R-free): 14.8% (17.4%)
	No. of Residues: 383 (43,053)	Subunits/Molecule: 2
Data Collected At	Advanced Photon Source COM-CAT 32-ID-B 04-Apr-2004	
Authors	D.W. Smith, S.T.M. Allard, E. Bitto, C.A. Bingman, G.N. Phillips, Jr.	



Structural Features

This target was nominated by David Meinke of Oklahoma State University and was the first externally nominated target solved by X-ray crystallography. It was selected based on an interesting phenotype in *Arabidopsis* seedlings, identified by genetic screens. Subsequent biochemical characterization by Piotrowski and coworkers established At5g08170.1 as agmatine iminohydrolase, the final uncharacterized step in polyamine biosynthesis in plants. At5g08170.1 represents the first structure of an agmatine deiminase, and the first representative of the PPAD family. It is a member of the same superfamily as aminotransferase, unifies the PPAD and known arginine deiminase family, will allow the modeling of a large number of proteins and will facilitate the elucidation of the mechanism of this enzyme.

References: (1) Janowitz, T., Kneifel, H., Piotrowski, M. (2003) Identification and characterization of plant agmatine iminohydrolase, the last missing link in polyamine biosynthesis of plants. *FEBS Lett* 544(1-3):258-61.

Percent Identity with Nearest PDB Structure at Time Solved	none higher than E=1
Pfam Cluster	PAD_porph
Protonet Cluster Size : Structures in PDB	261 : 1

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