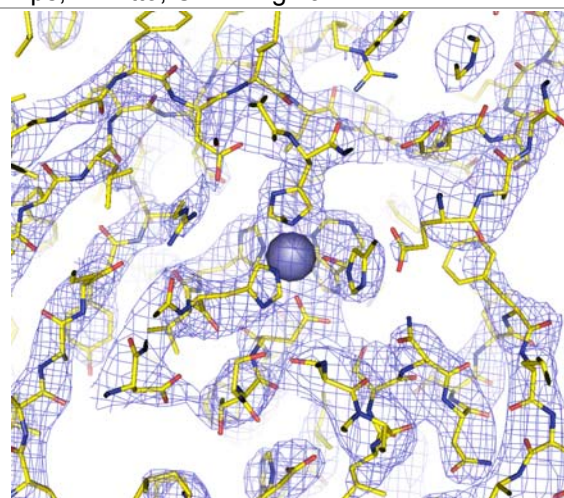
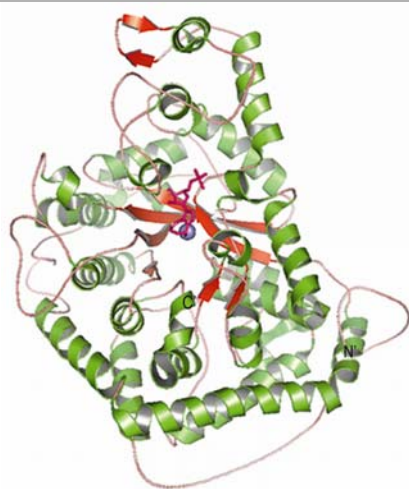


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



Target ID	GO.11648	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At2g38280.1	
PDB Entry	2A3L	Deposition: 25-Jun-2005
Function	Adenosine 5'-monophosphate deaminase (AMPD), <i>Arabidopsis</i> embryonic factor 1 (FAC1)	
Produced From	<i>Spodoptera frugiperda</i> (Sf9) – Baculovirus (BaculoGold)	
Structure by X-ray	Resolution: 3.34Å	R-value (R-free): 23.7 % (32.3%)
	No. of Residues/ASU: 701 (617)	Monomers/ASU: 1
Data Collected At	Advanced Photon Source 22-ID 13-Mar-2005	
Authors	B.W. Han, G.E. Wesenberg, G.N. Phillips, E. Bitto, C.A. Bingman	



Structural Features

AMP deaminase is a ubiquitous enzyme in eukaryotic cells, catalyzing the hydrolytic deamination of AMP to inosine 5'-monophosphate and ammonia. While higher eukaryotes such as humans have three AMPD genes, plants, and lower eukaryotes contain only one. It has been observed that abnormally high levels of ammonia are observed in the brains of Alzheimer's disease patients, and along with elevated AMPD enzyme levels. Dysfunctions in AMPD are also observed to cause disorders of skeletal muscle, known as myoadenylate deaminase deficiency (MADD). In plants, AMPD is an identified herbicide target. This protein used in this structure was expressed in insect cells, from a truncated variant of the AtAMPD, lacking the N-terminal membrane anchor sequence. The presence of a specific inhibitor of AMPD, coformycin 5'-phosphate, was important in growing diffraction quality crystals. The protein was observed to contain an incomplete TIM barrel. The protein crystallized as a dimer. This structure represents the only publicly available structure of an AMP deaminase.

References: (1) Han, B.W., Bingman, C.A., Mahnke, D.K., Bannen, R.M., Bednarek, S.Y., Sabina, R.L., Phillips, G.N., Jr. (2006) Membrane association, mechanism of action, and structure of *Arabidopsis* embryonic factor 1 (FAC1). *J Biol Chem* 281(21):14939-47. (2) Han, B.W., Bingman, C.A., Mahnke, D.K., Sabina, R.L., Phillips, G.N., Jr. (2005) Crystallization and preliminary X-ray crystallographic analysis of adenosine 5'-monophosphate deaminase (AMPD) from *Arabidopsis thaliana* in complex with coformycin 5'-phosphate. *Acta Crystallogr Sect F Struct Biol Cryst Commun* 61(Pt 8):740-2.

Percent Identity with Nearest PDB Structure at Time Solved	No significant hits
Pfam Cluster	A_deaminase
Sequence Cluster Size : Structures in PDB	225:1

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