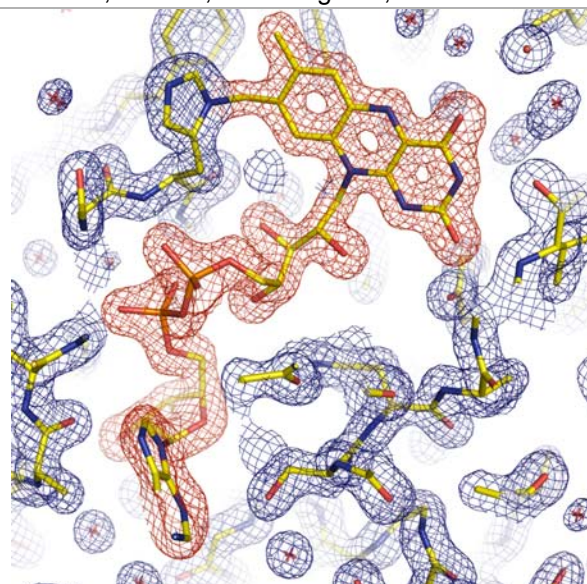
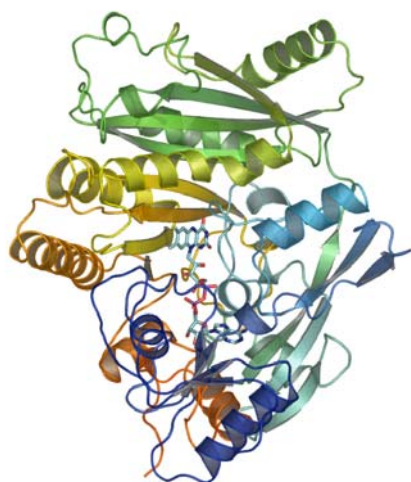




Target ID	GO.29544	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At5g21482.1	
PDB Entry	2EXR	Deposition: 08-Nov-2005
Function	Cytokinin dehydrogenase (FF/Refine: 2Q4W)	
Produced From	<i>E. coli</i> B834 p(RARE2) pVP-16	
Structure by X-ray	Resolution: 1.70 Å	R-value (R-free): 17.3% (21.4%)
	No. of Residues/ASU: 491	Monomers/ASU: 1
Data Collected At	Advanced Photon Source 22-ID 10-Oct-2005	
Authors	G.E. Wesenberg, G.N. Phillips, Jr., B.W. Han, E. Bitto, C.A. Bingman, E. Bae	



Structural Features

Cytokinins are a class of plant hormones regulating cell division and a variety of developmental events. Cytokinin homeostasis is important in many aspects of plant growth, and their control has economic significance in agriculture. These hormones are adenine derivatives with variable substituents at N6. Most of their catabolism is regulated by cytokinin dehydrogenase (CKX, EC 1.5.99.12), which is involved in oxidative cleavage of cytokinins back to the adenine and the substituent. CKX genes have been identified in many plants including corn, rice and *Arabidopsis thaliana*. *Arabidopsis* has seven CKX homologs (AtCKX1-AtCKX7). The crystal structure of AtCKX7 is highly similar to that of *Zea mays* CKX (ZmCKX1, PDB ID 1W1O). These two CKX structures superimpose with root mean square deviation of 1.9Å and share 43% sequence identity for 467 aligned residues. AtCKX7, like ZmCKX1, displays two-domain topology found in the members of the vanillyl-alcohol oxidase family. The FAD-binding domain (residues 34-237 and 480-514) forms a binding site for the cofactor, which is covalently linked to the protein via conserved His96. FAD-binding residues are conserved in both CKX proteins. The second domain consists of one antiparallel beta-sheet and surrounding alpha-helices. In the structures of ZmCKX1 substrate complexes (PDB ID codes 1W1Q, 1W1R, 1W1S), the corresponding domain is involved in substrate binding. The substrate-binding cavity of the ZmCKX1 is conserved both in structure and sequence in the AtCKX7. The conserved residues include the carboxylate-carboxylate pair (Asp162 and Glu275 in AtCKX7), which has been suggested to be a key element in catalysis. Therefore, it is most likely that this domain is in fact involved in substrate binding, and that AtCKX7 and ZmCKX1 share the same catalytic mechanism.

Percent Identity with Nearest PDB Structure at Time Solved	41% (1W1S)
Pfam Cluster	FAD_binding_4; Cytokinin-bind
Sequence Cluster Size	1771

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