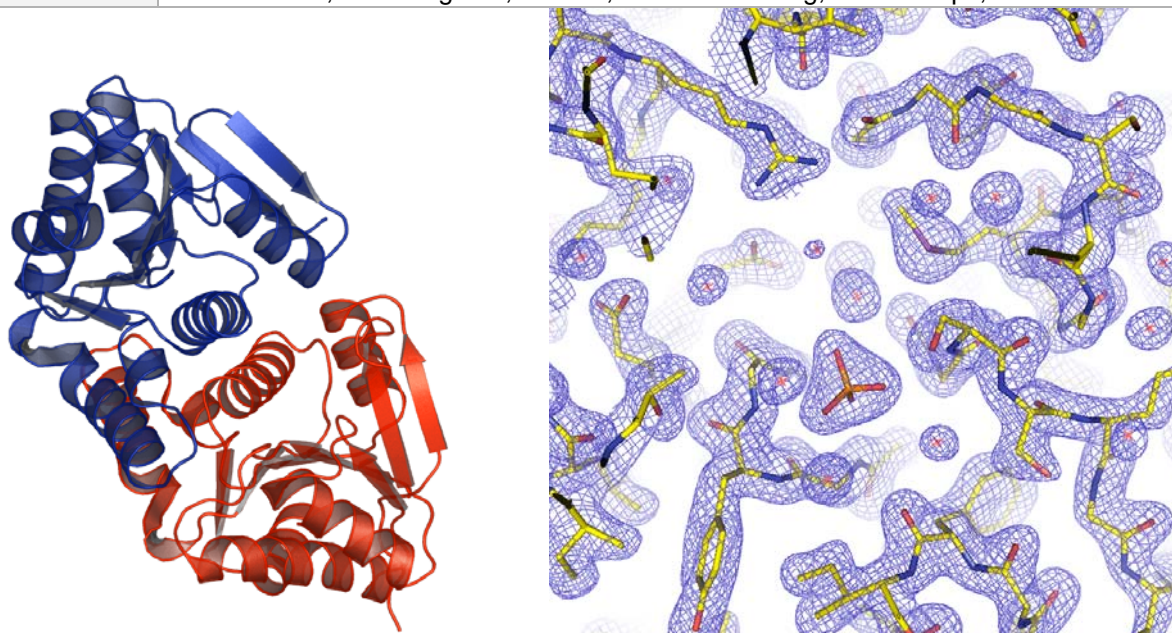


# Center for Eukaryotic Structural Genomics

## Protein Structure Initiative



<b>Target ID</b>	GO.9733	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At2g37210.1	
<b>PDB Entry</b>	2A33	Deposition: 23-Jun-2005
<b>Function</b>	lysine decarboxylase-like protein (FF/Refine: 2Q4O)	
<b>Produced From</b>	<i>E. coli</i> B834(DE3) p(RARE) pVP-13	
<b>Structure by X-ray</b>	Resolution: 1.95 Å	R-value (R-free): 18.3% (23.4%)
	No. of Residues/ASU: 215x2	Subunits/Molecule: 2
<b>Data Collected At</b>	Advanced Photon Source SER-CAT 22-BM	
<b>Authors</b>	S.T.M. Allard, C.A. Bingman, E. Bitto, G.E. Wesenberg, G.N. Phillips, Jr.	



### Structural Features

The gene product of At2g37210.1 from *Arabidopsis thaliana* is a "conserved" "hypothetical" protein belonging to a populous sequence family found in eukaryotes and simpler organisms. It is annotated as a lysine decarboxylase. At2g37210.1, along with other members of this sequence family share a highly conserved motif PGGXGTXXE that is probably functionally important. In addition to a tight dimer of At2g37210.1, the crystallographic asymmetric unit contains one magnesium ion, two sulfate ions, and 222 waters. The functional implications of the bound ions are under consideration. The electron density figure above shows density for one of the two bound sulfates.

*References:* (1) Jeon, W.B., Allard, S.T., Bingman, C.A., Bitto, E., Han, B.W., Wesenberg, G.E., Phillips, G.N., Jr. (2006) X-ray crystal structures of the conserved hypothetical proteins from *Arabidopsis thaliana* gene loci At5g11950 and At2g37210. *Proteins* 65(4):1051-4.

<b>% Identity with Nearest PDB Structure at Time Selected/Solved</b>	1I33 38% (49aa); 1YDH 63% (184aa)
<b>Pfam Cluster</b>	Lysine_decarbox Pfam-B_957
<b>Sequence Family Size</b>	338

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