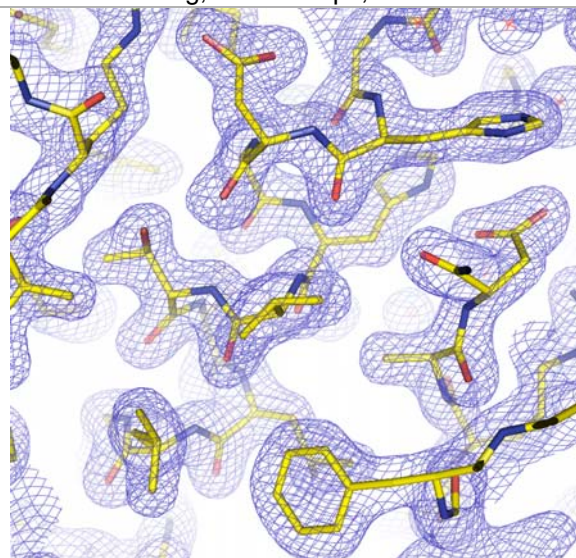
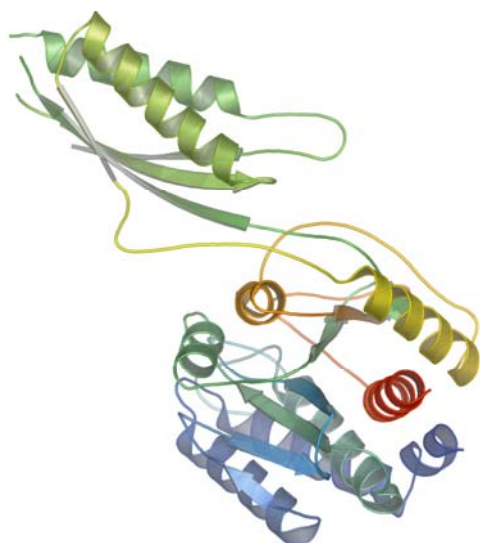


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



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|---------------------------|---|---------------------------------|
| Target ID | GO.22207 | |
| Source Organism | <i>Arabidopsis thaliana</i> | |
| Target Name | At5g56660.1 | |
| PDB Entry | 1XMB | Deposition: 01-Oct-2004 |
| Function | indole acetic acid (IAA) amino acid hydrolase (ILL2) (FF/Refine: 2Q43) | |
| Produced From | <i>E. coli</i> B834(DE3) p(Lacl+RARE) | |
| Structure by X-ray | Resolution: 2.0 Å SeMet SAD | R-value (R-free): 15.9% (20.4%) |
| | No. of Residues: 439 (47,811) | Subunits/ASU: 1 |
| Data Collected At | Advanced Photon Source SBC 19-BM | |
| Authors | E. Bitto, C.A. Bingman, S.T.M. Allard, G.E. Wesenberg, G.N. Phillips, Jr. | |



Structural Features

At5g56660.1 (1XMB) represents the first structure of an IAA-amino acid hydrolase. It is involved in the hydrolysis of amide-linked conjugates of auxin (IAA, indole-3-acetic acid). Highest activity was found for IAA-Ala as a substrate, followed by IAA-Ser and IAA-Thr (1). Auxin is one of the most important plant hormones. Auxin levels are regulated by several mechanisms, among them hydrolysis of amide-linked auxin conjugates. BLAST searches reveal over 200 related proteins. There are a large number of closely related IAA-hydrolases (>50% identity) in other plants as rice, wheat, and poplar trees. There are also five closely related *Arabidopsis* IAA-aminocid hydrolases that show 40-85% identity in primary sequence (IR3, ILL5, ILL1, ILL6, ILR1). At lower primary structure identities (~30-50%) At5g56660.1 is similar to a large number of peptidases from microorganisms and eukaryotes. In addition to the known Peptidase_M20 domain (108-421) and M20_dimer domain (213-317), At5g56660.1 matches Pfam-B_1745, which is found in proteins from Eukaryota, Eubacteria, and Archaea.

References: (1) LeClere, S., Tellez, R., Rampey, R.A., Matsuda, S.P., Bartel, B. (2002) Characterization of a family of IAA-amino acid conjugate hydrolases from *Arabidopsis*. *J Biol Chem* 277(23):20446-52.

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|---|--------------------------|
| Percent Identity with Nearest PDB Structure at Time Solved | 23.8% over 361 aa (1VGY) |
| Pfam Cluster | Peptidase_M20, B_1745 |
| Protonet Cluster Size : Structures in PDB | 189 : 0 |

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