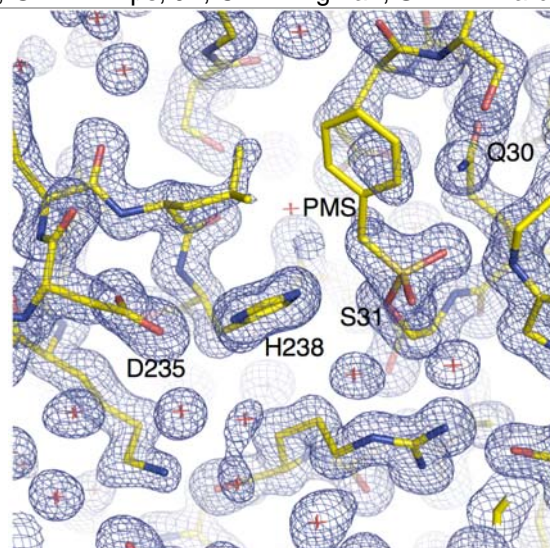
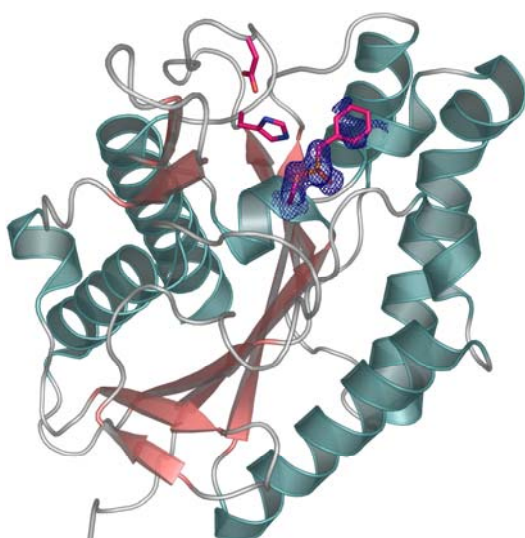


# Center for Eukaryotic Structural Genomics

## Protein Structure Initiative



<b>Target ID</b>	GO.22797	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At4g34215.1	
<b>PDB Entry</b>	2APJ (replaced 1AEA)	Deposition: 16-Aug-2005
<b>Function</b>	Putative esterase	
<b>Produced From</b>	<i>E. coli</i> B834 p(RARE2) pVP-16	
<b>Structure by X-ray</b>	Resolution: 1.60 Å	R-value (R-free): 14.7% (18.3%)
	No. of Residues/ASU: 966	Monomers/ASU: 4
<b>Data Collected At</b>	Advanced Photon Source 22-ID 10-Aug-2005, 10-Jul-2005	
<b>Authors</b>	E. Bitto, G.E. Wesenberg, J.G. McCoy, G.N. Phillips, Jr., C.A. Bingman, S.T.M. Allard	



### Structural Features

The crystal structure of the At4g34215.1 protein of *Arabidopsis thaliana* was determined by molecular replacement and refined to 1.6Å resolution (1). The crystal structure confirms that At4g34215.1 belongs to the SGNH-hydrolase superfamily of enzymes with three-layer  $\alpha\beta\alpha$ -sandwich architecture and Rossmann fold topology. The catalytic triad of the enzyme comprises residues Ser31, His238, and Asp235. The crystal structure revealed that the catalytic serine residue was covalently modified by phenylmethyl-sulfonyl fluoride. The structure also reveals a previously undescribed variation within the active site. A conserved asparagine, found in block III of conserved residues in the SGNH-hydrolase superfamily enzymes, which provides a hydrogen bond for an oxyanion hole, is missing in At4g34215.1 and is functionally replaced by Gln30 in block I. This residue is positioned in a catalytically competent conformation by nearby residues, including Gln159, Gly160, and Glu161, which are fully conserved in the carbohydrate esterase family 6 enzymes.

*References:* (1) Bitto, E., Bingman, C.A., McCoy, J.G., Allard, S.T.M., Wesenberg, G.E., Phillips, G.N., Jr. (2005) The structure at 1.6 Angstroms resolution of the protein product of the At4g34215 gene from *Arabidopsis thaliana*. *Acta Crystallogr D Biol Crystallogr* 61(Pt 12):1655-61.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	27% (1ZMB)
<b>Pfam Cluster</b>	DUF303
<b>Sequence Cluster Size</b>	77

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