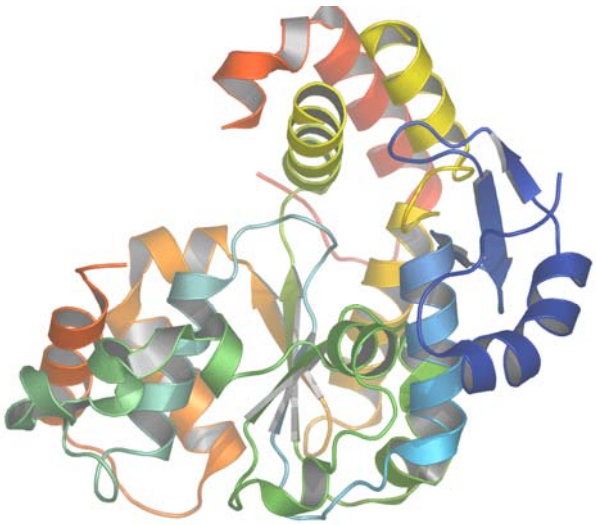
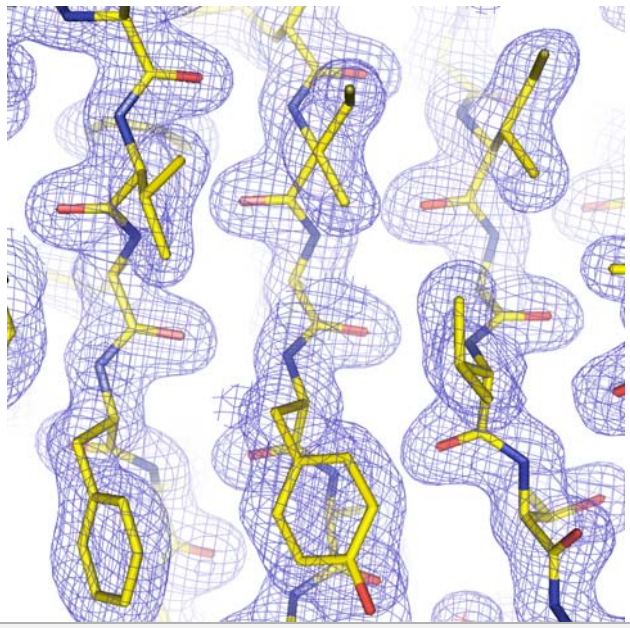
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.7312	
Source Organism	*Arabidopsis thaliana*	
Target Name	At2g03760.1	
PDB Entry	1Q44	Deposition: 1-Aug-2003
Function	putative sulfotransferase (FF/Refine: 2Q3M)	
Produced From	*E. coli* BL21 Rosetta	
Structure by X-ray	Resolution: 1.90 Å	R-value (R-free): 19.3% (22.2%)
	No. of Residues: 326	Subunits/Molecule: 1
Data Collected At	Advanced Photon Source BioCARS 14-ID-B 27-Jun-2003	
Authors	D.W. Smith, K.A. Johnson, C.A. Bingman, G.N. Phillips, Jr.	





Structural Features

PFAM matches known Sulfotransfer_1 domain, as well as Pfam-B_43929 over residues 4-59. For this smaller PFAM domain, electron density for residues 6-59 are modeled in 1Q44. Steroid sulfotransferases are present in plants as well as in mammals. In plants, sulfonation may also deactivate steroids, or have alternative functions in activating the molecule or serving as a defense response to pathogens. It is known that seedlings treated with salicylic acid or methyl jasmonate, or mature plants subjected to avirulent pathogens accumulate mRNA for At2g03760.1. 1Q44 represents the first structure of a plant sulfotransferase.

References: (1) Varin, L., Marsolais, F., Richard, M., Roleau, M. (1997) Sulfation and sulfotransferases 6: Biochemistry and molecular biology of plant sulfotransferases. *FASEB J* 11(7):517-25.

Percent Identity with Nearest PDB Structure at Time Solved	33% over 279 aa (1CJM)
Pfam Cluster	Sulfotransfer_1, B_43929
Protonet Cluster Size : Structures in PDB	192 : 5

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