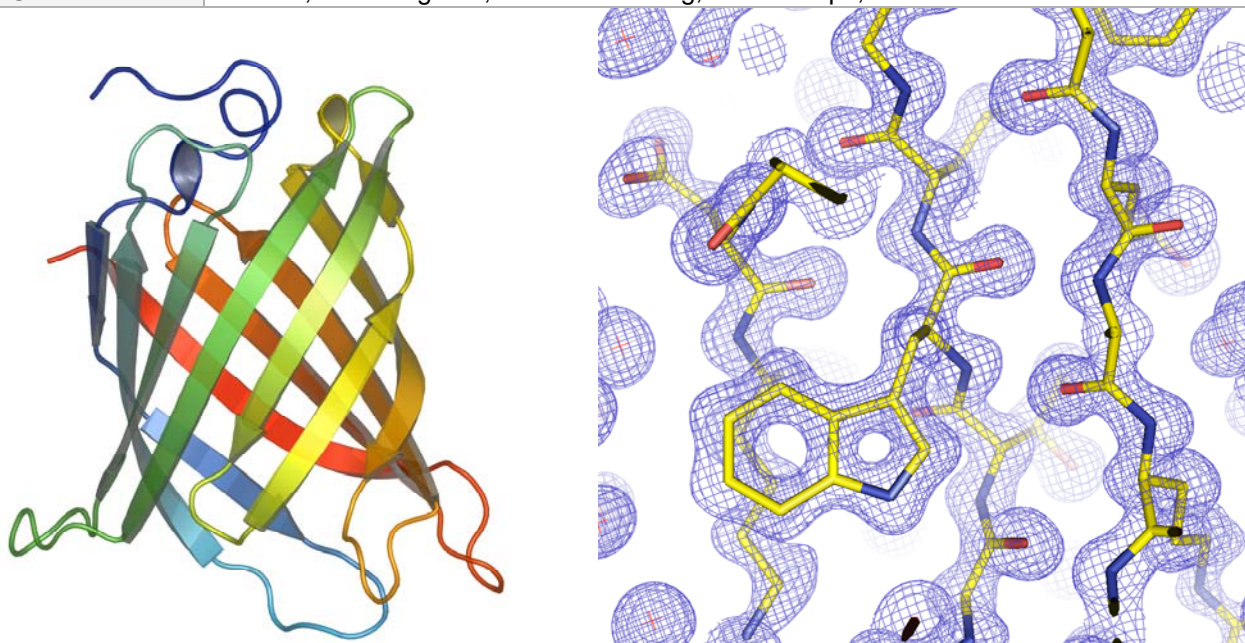


Center for Eukaryotic Structural Genomics

Protein Structure Initiative



Target ID	GO.6462	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At1g79260.1	
PDB Entry	2A13	Deposition: 17-Jun-2005
Function	structurally similar to fatty acid binding proteins (FF/Refine: 2Q4N)	
Produced From	<i>E. coli</i> B834(DE3) p(RARE) pVP-13	
Structure by X-ray	Resolution: 1.32 Å	R-value (R-free): 15.6% (18.6%)
	No. of Residues: 166	Subunits/ASU: 1
Data Collected At	Advanced Photon Source SER-CAT 22-ID	
Authors	E. Bitto, C.A. Bingman, G.E. Wesenberg, G.N. Phillips, Jr.	



Structural Features

The gene At1g79260.1 of *Arabidopsis thaliana* encodes a protein with molecular mass of 18.5 kDa (residues 1-166). The function of this protein is not yet established. At1g79260.1 does not show a detectable sequence-family relationship to any previously annotated protein family based on a SUPERFAMILY server search. A search of Pfam database revealed that residues 7-103 of At1g79260.1 match the profile of Pfam-B 3693 domain family. The profile-profile alignment tool FFAS03 confirmed that no PDB entry showed a sequence relationship to At1g79260.1. This protein thus represents a valuable structural genomics fold-space target. The protein forms a 10-stranded beta-barrel that was previously observed in a range of fatty-acid binding proteins and bacterial outer membrane proteins. The fully conserved residues of At1g79260.1 are clustered mainly around the large cavity found on the one side of the barrel.

Percent Identity with Nearest PDB Structure at Time Solved	2HSD 28% (66aa)
Pfam Cluster	Pfam-B_3693
Sequence Family Size	65

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