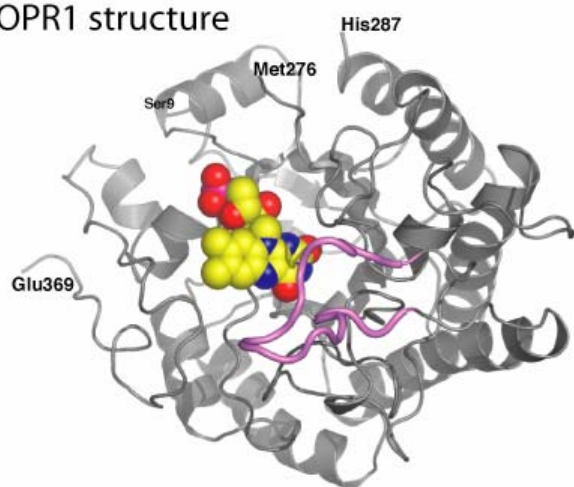


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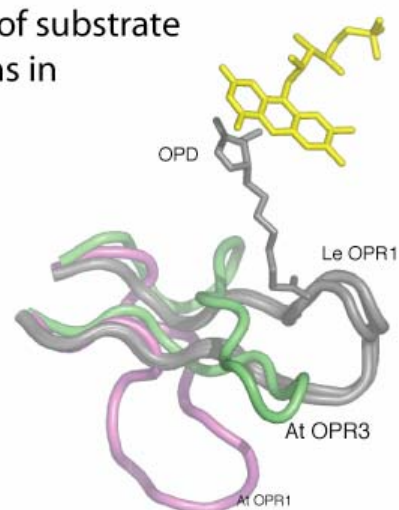
Protein Structure Data Summary

Target ID	GO.3073	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At1g76680.1	
PDB Entry	1VJI	Deposition: 24-Feb-2004
Function	12-oxophytodienoate reductase isoform 1 (FF/Refine: 2Q3R)	
Produced From	<i>Escherichia coli</i> Rosetta pLacI RARE	
Structure by X-ray	Resolution: 2.0 Å, Mol rep	R-value (R-free): 20.6% (29.3%)
	No. of Residues: 372 (41,168)	Subunits/Molecule: 1
Data Collected At	Advanced Photon Source BioCARS 14-BM-D	
Authors	K.A., Johnson, C.A. Bingman, D.W. Smith, G.N. Phillips, Jr.	

OPR1 structure



Comparison of substrate loop positions in three OPR structures



Structural Features

This work reports the 2.0 Å X-ray structure of *Arabidopsis* OPR1, identified to be encoded by At1g76680.1 (PDB 1VJI). Comparison of the *Arabidopsis* OPR1 structure (*violet*) with the *Arabidopsis* OPR3 (1Q45, *green*) and tomato OPR1 (1ICQ, *grey*) structures revealed a third backbone conformation at the putative substrate-binding loop in the newest structure. The variability in configuration observed at this critical region of the protein structure further emphasizes the need for detailed structural analysis to understand the role of each OPR isoform in the octadecanoid-dependent signaling pathways.

References: (1) Fox, B.G., Malone, T.E., Johnson, K.A., Madson, S.E., Aceti, D., Bingman, C.A., Blommel, P.G., Buchan, B., Burns, B., Cao, J., Cornilescu, C., Doreleijers, J., Ellefson, J., Frederick, R., Geetha, H., Hruby, D., Jeon, W.B., Kimball, T., Kunert, J., Markley, J.L., Newman, C., Olson, A., Peterson, F.C., Phillips, G.N. Jr, Primm, J., Ramirez, B., Rosenberg, N.S., Runnels, M., Seder, K., Shaw, J., Smith, D.W., Sreenath, H., Song, J., Sussman, M.R., Thao, S., Troestler, D., Tyler, E., Tyler, R., Ulrich, E., Vinarov, D., Vojtik, F., Volkman, B.F., Wesenberg, G., Wrobel, R.L., Zhang, J., Zhao, Q., Zolnai, Z. (2005) X-ray structure of *Arabidopsis* At1g77680, 12-oxophytodienoate reductase isoform 1. *Proteins* 61(1):206-8.

Percent Identity with Nearest PDB Structure at Time Solved	74% over 374 aa (1ICQ)
Pfam Cluster	Oxidored_FMN, B_5997
Protonet Cluster Size : Structures in PDB	290 : 5

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