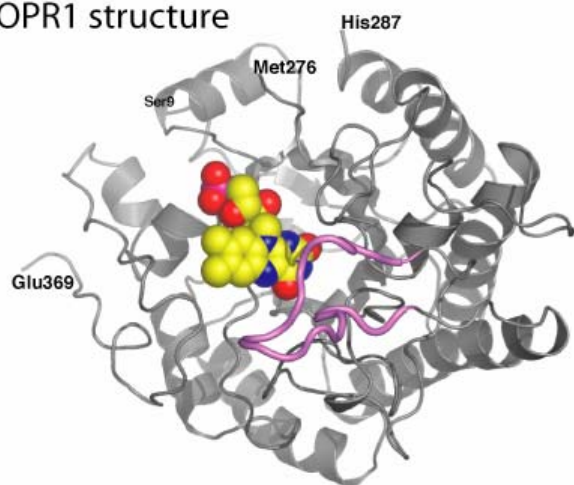


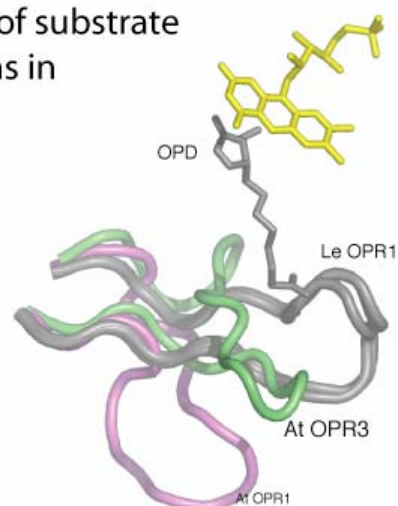


<b>Target ID</b>	GO.3073	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At1g76680.1	
<b>PDB Entry</b>	1VJI	Deposition: 24-Feb-2004
<b>Function</b>	12-oxophytodienoate reductase isoform 1 (FF/Refine: 2Q3R)	
<b>Produced From</b>	<i>Escherichia coli</i> Rosetta pLacI RARE	
<b>Structure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

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

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