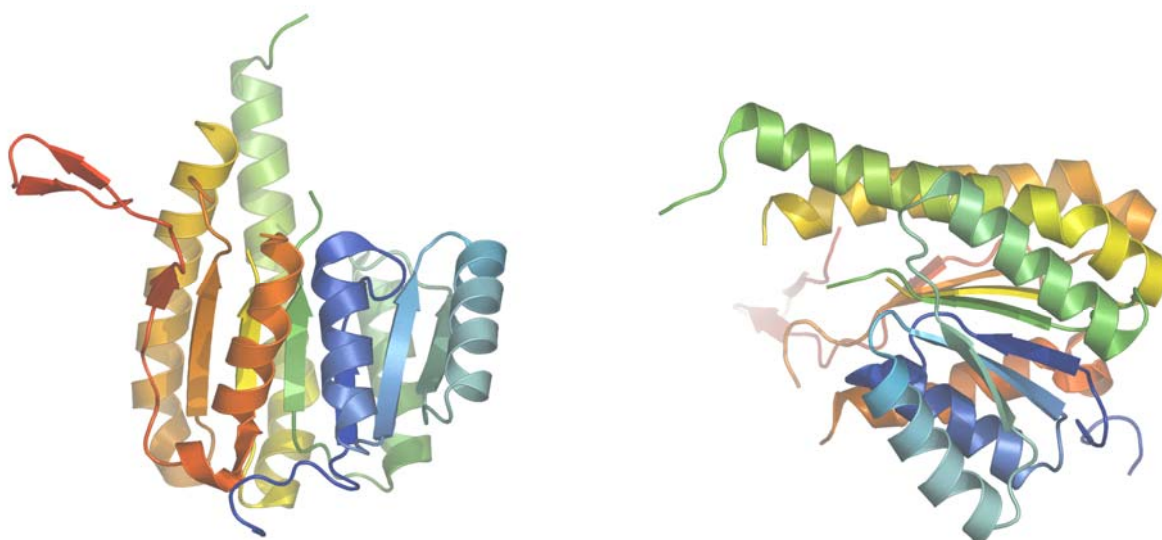


<b>Target ID</b>	GO.2303	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At1g07440.1	
<b>PDB Entry</b>	1XQ1	Deposition: 11-Oct-2004
<b>Function</b>	putative tropinone reductase-like (oxidoreductase) (FF/Refine: 2Q45)	
<b>Produced From</b>	<i>E. coli</i> B834(DE3) p(LacI+RARE)	
<b>Structure by X-ray</b>	Resolution: 2.1 Å	R-value (R-free): 25.5% (31.6%)
	No. of Residues: 266 (28,288)	Subunits/Molecule: 1
<b>Data Collected At</b>	Advanced Photon Source SBC 19-BM 31-Jul-2004	
<b>Authors</b>	G.N. Phillips, Jr., S.T.M. Allard, E. Bitto, D.W. Smith, G.E. Wesenberg, C.A. Bingman	



### Structural Features

First CESH structure solved with a reductively methylated protein sample. This is one of the few apoprotein structures in this class of dehydrogenase. The protein did not give good crystals without reductive methylation. This suggests that in some cases, reductive methylation may compensate for the absence of a cofactor (which is often, unfortunately, the case for unknown fold-space targets) in addition to merely modifying the surface properties of the protein to promote crystallization.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	58.6% over 256 aa (1AE1)
<b>Pfam Cluster</b>	adh_short
<b>Protonet Cluster Size : Structures in PDB</b>	2130 : 18

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