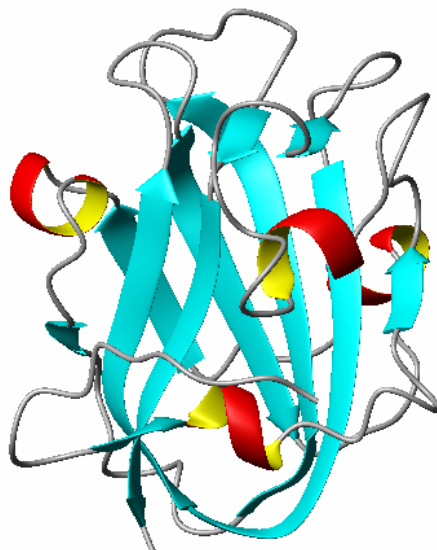


Target ID	GO.11624	
Source Organism	<i>Arabidopsis thaliana</i>	
Target Name	At3g04780.1	
PDB Entry	1XOY	Deposition: 07-Oct-2004
BMRB Entry	6341	Deposition: 06-Oct-2004
Function	unknown	
Produced From	<i>E. coli</i> B834(DE3)/pLacIRARE	
Structure by NMR	Restrains/Residue: 12	Subunits/Molecule: 1
	No. of Residues: 161	Molecular Weight: 17.9 kDa
	Backbone RMSD(9–161): 0.92 Å	All Heavy Atoms RMSD(9–161): 1.43Å
Data Collected At	Nuclear Magnetic Resonance Facility at Madison (NMRFAM)	
Authors	J. Song, R.C. Tyler, M.S. Lee, J.L. Markley	



Structural Features

The most similar structures in the PDB were *Saccharomyces cerevisiae* anaphase-promoting complex subunit DOC1/Apc10 (1GQP) with 13.5 % sequence identity over 126 residues. Additionally, At3g04780.1 shares a 42% sequence identity with the C-terminal domain of the 32 kD human thioredoxin-like protein (TXNL). The C-terminal domain of the TXNL is rich in acidic residues and has a calculated pI of 4.3, which is also a distinct feature for At3g04780.1 (calculated pI of 4.9). Although its molecular function has not been revealed, the genomic location of TXNL protein suggests that it is related to the cell apoptosis and cancer. The X-ray structure of the N-terminal thioredoxin domain of TXNL has been determined. However, the structure of the C-terminal domain has not been solved. Thus, the structure of At3g04780.1 as determined here may help in delineation of function of this target. This target aligns to domains within Pfam trusted matches for DUF1000 over residues 12–161.

References: (1) Song, J., Tyler, R.C., Wrobel, R.L., Frederick, R.O., Vojtek, F.C., Jeon, W.B., Lee, M.S., Markley, J.L. (2005) Solution structure of At3g04780.1-des15, an *Arabidopsis thaliana* ortholog of the C-terminal domain of human thioredoxin-like protein. *Protein Sci* 14(4):1059-63.

Percent Identity with Nearest PDB Structure at Time Solved	13.5% over 126aa (1GQP)
Pfam Cluster	DUF1000
Protonet Cluster Size : Structures in PDB	23 : 1

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