Target ID: GO.11624  
Source Organism: Arabidopsis thaliana  
Target Name: At3g04780.1  
PDB Entry: 1XOY  
Deposition: 07-Oct-2004  
BMRB Entry: 6341  
Deposition: 06-Oct-2004  
Function: unknown  
Produced From: E. coli B834(DE3)/pLacIRARE  
Structure by NMR:  
- Restraints/Residue: 12  
- No. of Residues: 161  
- Backbone RMSD(9-161): 0.92 Å  
- All Heavy Atoms RMSD(9-161): 1.43 Å  
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 pl of 4.3, which is also a distinct feature for At3g04780.1 (calculated pl 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.


**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