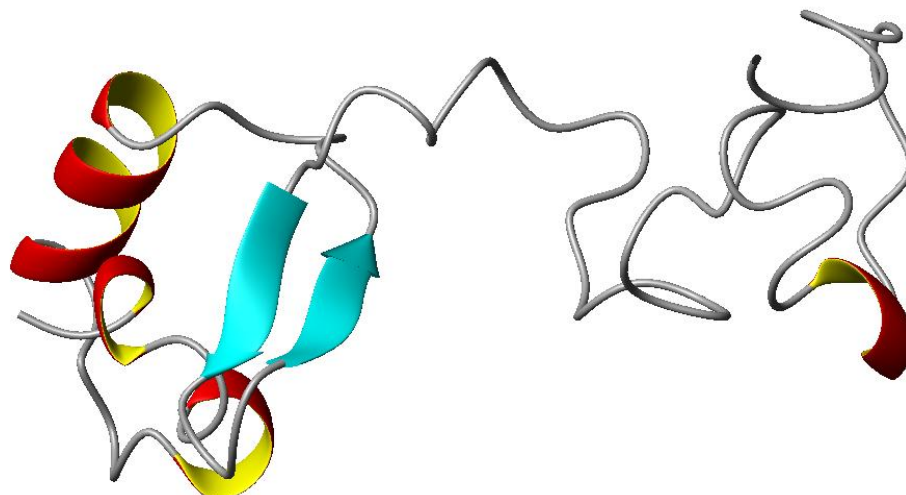


Center for Eukaryotic Structural Genomics

Protein Structure Data Summary

Target ID	GO.7474	
Source Organism	<i>Arabidopsis thaliana</i> Columbia	
Target Name	At2g23090.1	
PDB Entry	1WVK	1WVK
BMRB Entry	6432	6432
Function	unknown	
Produced From	Cell free (wheat germ extract)	
Structure by NMR	Restraints/Residue: N/A	Restraints/Residue: N/A
	No. of Residues: 86	No. of Residues: 86
	Backbone RMSD (46-48,53-55,62-69,76-78,82-84): 1.02 Å	Backbone RMSD (46-48,53-55,62-69,76-78,82-84): 1.02 Å
Data Collected At	Nuclear Magnetic Resonance Facility at Madison (NMRFAM)	
Authors	Tyler, R. C., Tonelli, M., Lee, M., Markley, J.L.	



Structural Features

Title: NMR solution Structure of a partially diordered protein from *Arabidopsis thaliana* At2g23090
 The N-terminal of this protein is disorder whereas the C-terminus forms a two stranded beta-sheet (Residues: 46-48 and 53-55) and three small helices (Residues: 62-69, 76-78 and 82-84).

References: Tyler, Robert C., Tonelli, M., Lee, M., Markley, J. L. (2008) NMR solution Structure of a partially diordered protein from *Arabidopsis thaliana* At2g23090, in press.

Percent Identity with Nearest PDB Structure at Time Solved	28% coverage with 1tjn
Pfam Cluster	DUF1909
Protonet Cluster Size : Structures in PDB	47
Center for Eukaryotic Structural Genomics (CESG), University of Wisconsin-Madison Biochemistry Department, 433 Babcock Drive, Madison, WI 53706-1549; phone: 608.263.2183; fax: 608.890.1942; email: cesginfo@biochem.wisc.edu ; website: http://www.uwstructuralgenomics.org . This research funded by NIH / NIGMS Protein Structure Initiative grants U54 GM074901 and P50 GM064598.	