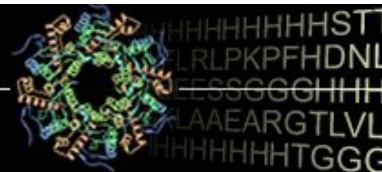
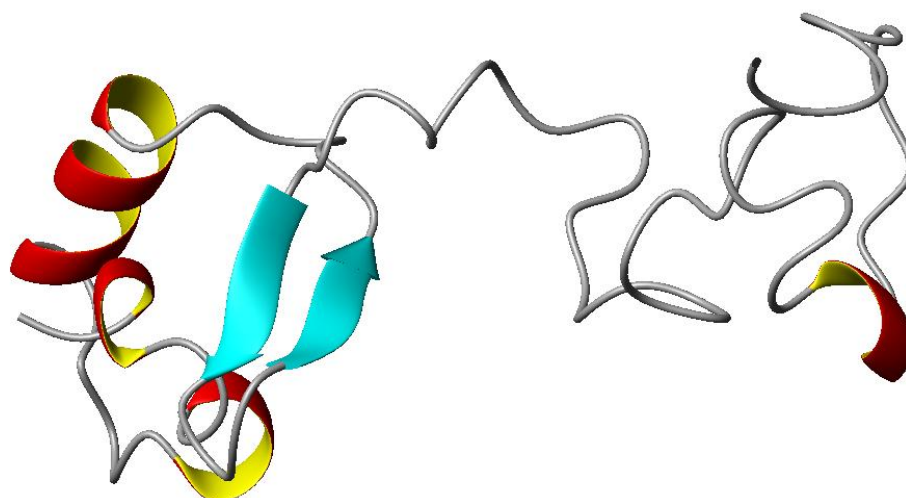


# Center for Eukaryotic Structural Genomics

## Protein Structure Initiative



<b>Target ID</b>	GO.7474	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i> Columbia	
<b>Target Name</b>	At2g23090.1	
<b>PDB Entry</b>	1WVK	1WVK
<b>BMRB Entry</b>	6432	6432
<b>Function</b>	unknown	
<b>Produced From</b>	Cell free (wheat germ extract)	
<b>Structure by NMR</b>	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
<b>Data Collected At</b>	Nuclear Magnetic Resonance Facility at Madison (NMRFAM)	
<b>Authors</b>	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.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	28% coverage with 1tjn
<b>Pfam Cluster</b>	DUF1909
<b>Protonet Cluster Size : Structures in PDB</b>	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: <a href="mailto:cesginfo@biochem.wisc.edu">cesginfo@biochem.wisc.edu</a> ; website: <a href="http://www.uwstructuralgenomics.org">http://www.uwstructuralgenomics.org</a> . This research funded by NIH / NIGMS Protein Structure Initiative grants U54 GM074901 and P50 GM064598.	