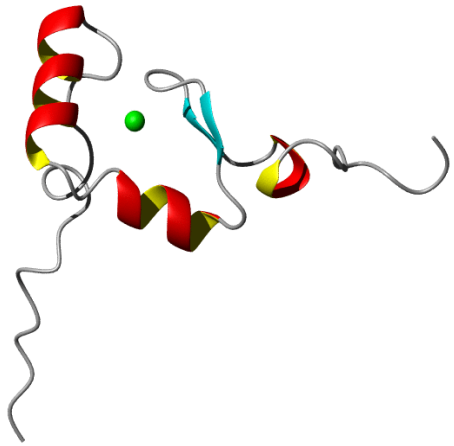
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.33810	
Source Organism	*Homo sapiens*	
Target Name	BC019267	
PDB Entry	1ZR9	Deposition: 19-May-2005
BMRB Entry	6682	Deposition: 07-Jun-2005
Function	zinc finger protein 593	
Produced From	Cell-free (wheat germ extract)	
Structure by NMR	Restraints/Residue: 12.9	Subunits/Molecule: 1
	No. of Residues: 115	Molecular Weight: 13.2 kDa
	Backbone RMSD(36-71): 0.52 Å	All Heavy Atoms RMSD(36-71): 1.07 Å
Data Collected At	Medical College of Wisconsin	
Authors	Lytle, B.L., Peterson, F.C., Volkman, B.F.	



Structural Features

Here, we report the solution structure of ZNF593, a protein identified in a functional study as a negative modulator of the DNA-binding activity of the Oct-2 transcription factor. ZNF593 contains a classic C(2)H(2) zinc finger domain flanked by about 40 disordered residues on each terminus. Although the protein contains a high degree of intrinsic disorder, the structure of the zinc finger domain was resolved by NMR spectroscopy without a need for N- or C-terminal truncations. The tertiary structure of the zinc finger domain is composed of a beta-hairpin that positions the cysteine side chains for zinc coordination, followed by an atypical kinked alpha-helix containing the two histidine side chain ligands. The structural topology of ZNF593 is similar to a fragment of the double-stranded RNA-binding protein Zfa and the C-terminal zinc finger of MBP-1, a human enhancer binding protein. The structure presented here will provide a guide for future functional studies of how ZNF593 negatively modulates the DNA-binding activity of Oct-2, a POU domain-containing transcription factor. Our work illustrates the unique capacity of NMR spectroscopy for structural analysis of folded domains in a predominantly disordered protein.

References: (1) Hayes, P.L., Lytle, B.L., Volkman, B.F., Peterson, F.C. (2008) The solution structure of ZNF593 from *Homo sapiens* reveals a zinc finger in a predominantly unstructured protein. *Protein Sci* 17(3):571-6.

Percent Identity with Nearest PDB Structure at Time Solved	21% over 38 aa (1ZU1)
Pfam Cluster	None
Protonet Cluster Size : Structures in PDB	12 : 1

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