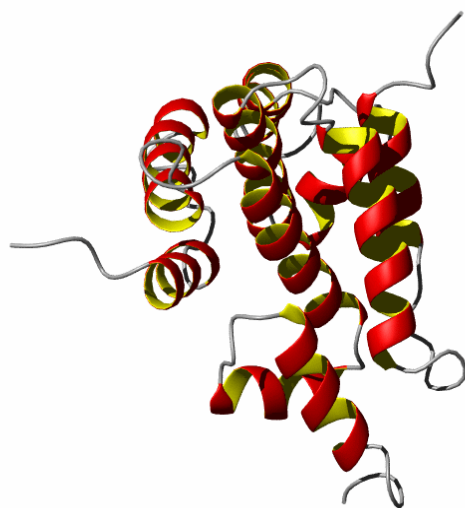




Target ID	GO.79132	
Source Organism	<i>Homo sapiens</i>	
Target Name	NM_003422b	
PDB Entry	2FI2	Deposition: 27-Dec-2005
BMRB Entry	6957	Deposition: 17-Jan-2006
Function	zinc finger protein 42	
Produced From	<i>E. coli</i>	
Structure by NMR	Restraints/Residue: 25	Subunits/Molecule: 2
	No. of Residues: 92	Molecular Weight: 10.5 kDa
	Backbone RMSD(40-122): 0.62 Å	All Heavy Atoms RMSD(40-122): 0.95 Å
Data Collected At	Medical College of Wisconsin	
Authors	Volkman, B.F., Peterson, F.C., Sander, T.L., Waltner, J.K.	



Structural Features

The SCAN domain mediates interactions between members of a subfamily of zinc-finger transcription factors and is found in more than 60 C2H2 zinc finger genes in the human genome, including the tumor suppressor gene myeloid zinc finger 1 (MZF1). Glutathione-S-transferase pull-down assays showed that the MZF1 SCAN domain self-associates, and a K_d value of 600 nM was measured by intrinsic tryptophan fluorescence polarization. The MZF1 structure determined by NMR spectroscopy revealed a domain-swapped dimer. Each monomer consists of five alpha helices in two subdomains connected by the alpha2-alpha3 loop. Residues from helix 3 of each monomer compose the core of the dimer interface, while the alpha1-alpha2 loop and helix 2 pack against helices 3 and 5 from the opposing monomer. Comprehensive sequence analysis is coupled with the first high-resolution structure of a SCAN dimer to provide an initial view of the recognition elements that govern dimerization for this large family of transcription factors.

References: (1) Peterson, F.C., Hayes, P.L., Waltner, J.K., Heisner, A.K., Jensen, D.R., Sander, T.L., Volkman, B.F. (2006) Structure of the SCAN domain from the tumor suppressor protein MZF1. *J Mol Biol* 363(1):137-47.

Percent Identity with Nearest PDB Structure at Time Solved	57.5% over 92 aa (1y7q)
Pfam Cluster	PF02023
Protonet Cluster Size : Structures in PDB	5312 : 42

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