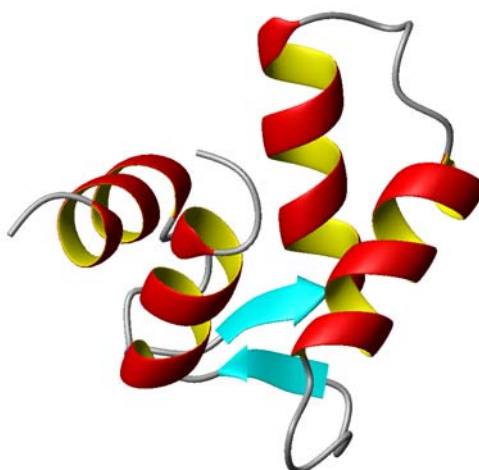


# Center for Eukaryotic Structural Genomics

## Protein Structure Initiative



<b>Target ID</b>	GO.33909	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At3g03410.1	
<b>PDB Entry</b>	1TIZ	Deposition: 02-Jun-2004
<b>BMRB Entry</b>	6209	Deposition: 19-May-2004
<b>Function</b>	EF-hand/Ca binding sensors or signal modulators	
<b>Produced From</b>	<i>E. coli</i> Rosetta(DE3)/pLysS	
<b>Structure by NMR</b>	Restraints/Residue: 25.5	Subunits/Molecule: 1
	No. of Residues: 67	Molecular Weight: 7.8 kDa
	Backbone RMSD(2-67): 0.27 Å	All Heavy Atoms RMSD(2-67): 0.87 Å
<b>Data Collected At</b>	Nuclear Magnetic Resonance Facility at Madison (NMRFAM)	
<b>Authors</b>	J. Song, Q. Zhao, S. Thao, R.O. Frederick, J.L. Markley	



### Structural Features

The most similar structures in the PDB were the canonical EF-hands, including the N-terminal domains of calmodulin and calbindin. These calcium binding motifs comprise a diverse superfamily of calcium sensors and calcium signal modulators. Binding of  $\text{Ca}^{2+}$  induces a conformational change in the EF-hand motif, leading to the activation or inactivation of target proteins. Unlike most of the other canonical EF-hands, the second EF-hand of N-terminal domain of At3g03410.1 shows closed conformation in the presence of calcium. Although At3g03410.1 falls within the EF-hand superfamily, the true biological function of At3g03410.1 currently is unknown. This target aligns to domains within Pfam trusted matches for ehand over residues 2-30 and 38-66.

*References:* (1) Song, J., Zhao, Q., Thao, S., Frederick, R.O., Markley, J.L. (2004) Solution structure of a calmodulin-like calcium-binding domain from *Arabidopsis thaliana*. *J Biomol NMR* 30(4):451-6.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	31% over 67 aa (1J7O)
<b>Pfam Cluster</b>	efhand
<b>Protonet Cluster Size : Structures in PDB</b>	794 : 12

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