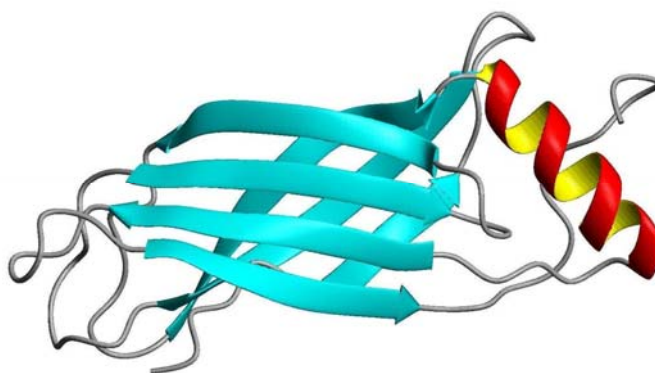




<b>Target ID</b>	GO.2361	
<b>Source Organism</b>	<i>Arabidopsis thaliana</i>	
<b>Target Name</b>	At1g01470.1	
<b>PDB Entry</b>	1XO8	Deposition: 06-Oct-2004
<b>BMRB Entry</b>	6339	Deposition: 06-Oct-2004
<b>Function</b>	LEA14, unknown	
<b>Produced From</b>	<i>E. coli</i> B834(DE3)/pLacIRARE	
<b>Structure by NMR</b>	Restraints/Residue:	Subunits/Molecule: 1
	No. of Residues: 151	Molecular Weight: 16.5 kDa
	Backbone RMSD(23–146): 0.34 Å	All Heavy Atoms RMSD(23–146): 0.67 Å
<b>Data Collected At</b>	Nuclear Magnetic Resonance Facility at Madison (NMRFAM)	
<b>Authors</b>	S. Singh, C.C. Cornilescu, G. Cornilescu, R.C.Tyler, M. Tonelli, M.S. Lee, J.L. Markley	



### Structural Features

The most similar structures in the PDB were human cellular coagulation factor XIII with 6.7% identity over 104 residues (1F13), human Fcari bound to Iga1-Fc with 4.7% over 87 residues (1OWO), and histocompatibility antigen Hla-Dm with 11.9% over 84 residues (1HDM). At1g01470.1 belongs to a class of proteins known as late embryogenesis abundant (LEA) proteins that are expressed at different stages of late embryogenesis in higher plant seed embryos. Different types of these proteins are expressed under stress. The expression of the LEA gene imparts an adaptive mechanism to withstand abiotic stress conditions such as salinity, drought, and high or low temperature. Although extensive studies has been carried out on LEA\_2 proteins, this is the first three-dimensional structure solved for this class of protein. The structural similarity of At1g01470.1 to proteins in the mammalian blood coagulation cascade involved in wound healing is intriguing and suggests that the protein may be involved in a plant system that responds to stress of a wounding nature. However tantalizing this conjecture may be, the true biological function of At1g01470.1 currently is unknown. This target aligns to domains within Pfam trusted matches for LEA\_2 over residues 2–151.

*References:* (1) Singh, S., Cornilescu, C.C., Tyler, R.C., Cornilescu, G., Tonelli, M., Lee, M.S., Markley, J.L. (2005) Solution structure of a late embryogenesis abundant protein (LEA14) from *Arabidopsis thaliana*, a cellular stress-related protein. *Protein Sci* 14(10):2601-9.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	6.7% over 104 aa (1F13)
<b>Pfam Cluster</b>	LEA_2
<b>Protonet Cluster Size : Structures in PDB</b>	24 : 0

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