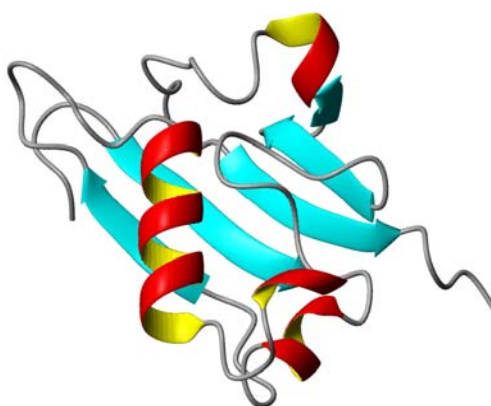


<b>Target ID</b>	GO.34198	
<b>Source Organism</b>	<i>Mus musculus</i>	
<b>Target Name</b>	Mm.20273	
<b>PDB Entry</b>	1XO3	Deposition: 05-Oct-2004
<b>BMRB Entry</b>	6337	Deposition: 05-Oct-2004
<b>Function</b>	ubiquitin-like	
<b>Produced From</b>	<i>E. coli</i> B834(DE3)/pLacIRARE	
<b>Structure by NMR</b>	Restraints/Residue: 23	Subunits/Molecule: 1
	No. of Residues: 101	Molecular Weight: 11.2 kDa
	Backbone RMSD(4–98): 0.28 Å	All Heavy Atoms RMSD(4–98): 0.69 Å
<b>Data Collected At</b>	Nuclear Magnetic Resonance Facility at Madison (NMRFAM)	
<b>Authors</b>	S. Singh, M. Tonelli, R.C. Tyler, C.C. Cornilescu, M.S. Lee, J.L. Markley	



### Structural Features

The most similar structure in the PDB were the MoaD related protein from *Thermus thermophilus* Hb8 with 13.2% identity over 68 residues (1V8C) and molybdopterin synthase with 23.4% identity over 64 aligned residues. Molybdenum cofactor biosynthesis is an evolutionarily conserved pathway over eubacteria, archaea, and eukaryotes. In humans, genetic deficiencies of this enzyme lead to a severe and usually fatal disease. Serious neurological symptoms include attenuated growth of the brain and untreatable seizures. Molybdopterin synthase is a heterotetramer with large and small subunits known as MoaE and MoaD, respectively. The small subunit, MoaD, is ubiquitin-like, and the insertion of the C-terminus of this subunit into a large subunit forms the active site. The active form of MoaD is thiocarboxylated at the invariant C-terminal Gly residue that serves as the sulfur donor in the biosynthetic pathway. As expected, similar to MoaD, the structure of Mm.20273 differs from that of ubiquitin (Ub) largely in the regions outside of the well defined Ub signature secondary structure fold. This target aligns to Pfam domains of Pfam-B\_45334 over residues 2–63 and Pfam-B\_14998 over residues 64–101.

*References:* (1) Singh, S., Tonelli, M., Tyler, R.C., Bahrami, A., Lee, M.S., Markley, J.L. (2005) Three-dimensional structure of the AAH26994.1 protein from *Mus musculus*, a putative eukaryotic Urm1. *Protein Sci* 14(8):2095-102.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	13.2 % over 68 aa (1V8C)
<b>Pfam Cluster</b>	B_45334, B_14998
<b>Protonet Cluster Size : Structures in PDB</b>	11 : 0

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