3D Structure Determination of the Cpn60-2 Protein from *Mycobacterium tuberculosis*

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Heat shock proteins (HSP) are a large super-family of proteins which are highly conserved throughout evolution and are necessary for the correct folding of proteins inside the cell. Cpn60-2 from *Mycobacterium tuberculosis (Mt)* belongs to the HSP60 family which is also called Chaperonins. These proteins are involved in folding of a large number of proteins in an ATP dependent manner. In addition, Cpn60-2 is one of the most immunogenic of all *Mt* proteins, eliciting a significant immune response when whole cells are used in vaccination. Due to its high immunogenity, Cpn60-2 has a medical importance.

We have isolated Cpn60-2 by over expression of the cloned gene encoding for Cpn60-2 into pQE60 vector to enable metal chelate affinity purification. The recombinant protein was shown to protect *E. coli* cells from heat shock stress. Crystals of His-Cpn60-2 grow in 2-14 days and were improved by different methodologies. The crystallization conditions are 10% 2-propanol, 20% PEG 4K, 0.1M Hepes pH 7.5. Crystallographic analysis shows the crystals to be monoclinic ($P2_1$) with unit cell parameters of a=58.460, b=112.209, c=77.5, β=95.482° and containing a dimer in the asymmetric unit. We have collected a complete 2.75Å data on ESRF beamline ID14-1. The structure has been solved by the molecular replacement method using a lower resolution model recently published. At present, the structure of the Cpn60-2 has been refined to R/R_{free} factors of 23.69/31.79%.

Keywords: protein crystallography chaperones, stress, bacteria