CRYSTALLIZATION OF PREPHENATE DEHYDRATASE OF *MYCOBACTERIUM TUBERCULOSIS* H37RV

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The aromatic amino-acid pathway is essential for the survival of *M.tuberculosis* and represents a target for structure-based drug design. The prephenate dehydratase catalyses the decarboxylation and dehydratation of prephenate to form phenylpyruvate. The structure of prephenate dehydratase may provide a structural model to be used in structural based drug design of a new generation of antiTB drugs. Crystallization trials were performed by the hanging-drop vapour diffusion method at 19ºC. The protein concentration was brought to 10mg/mL^{-1}. Small crystals of prephenate dehydratase appeared seven days after the drops were done. The well solution contained 0.1M HEPES buffer pH 7.5, 28% PEG 400, 0.2M calcium chloride. The crystal diffracted 3.2 Å of resolution and belongs to the orthorhombic space group I222 or $I2_12_12_1$. Assuming the asymmetric unit content to be four monomers of molecular weight 33,600Da, the Vm value is 2,7 Å^3 Da $^{-1}$. Molecular replacement was used to solve the structure with program *AMoRe*. As a model research was used phenyalanine hydroxylase (2PHM), but did not yield any meaningful results. This could be due the low identity between the search model and the structure under study. Heavy-atom screening is in progress to try to solve the structure by multiple isomorphous replacement.

Keywords: prephenate dehydratase; crystallization; *M.tuberculosis*.