Crystal Structure of Conserved Hypothetical Protein YBEY from *Escherichia Coli*

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The crystal structure of protein YBEY of unknown function from Escherichia Coli was determined by X-ray crystallography methods. The structure was solved by SeMet MAD method and refined to Rcryst=0.234, Rfree=0.273 at 2.7A resolution. Diffraction data sets were collected at NSLS beam lines X29A and X9A.

The protein YBEY is a member of uncharacterized protein family UPF0054 consisting of 70 similar sequences. The fold of the protein consists of one central helix surrounded by a four-stranded sheet and four other helices. The structure revealed fold similarity to matrix mettalloproteinases. They share a conserved zink-binding motif, which represents the active site of metalloproteinases. The Zn position is occupied by Ni in YBEY structure. Details of the structure and presumptions about possible function of protein YBEY will be presented.

Keywords: structural genomics, NYSGRC, metalloproteinase