

E0005

Crystal Structures of Conserved Hypothetical Protein YLBA from Three Different Bacteria. A.A. Fedorov, E.V. Fedorov, S.C. Almo, Albert Einstein College of Medicine, Bronx, NY 10461 USA

The structures of three functionally uncharacterized YLBA homologs from *Escherichia Coli*, *Enterococcus faecalis* and *Deinococcus radiodurans* are described. The first structure was solved by SeMet MAD and refined to $R(\text{cryst}) = 0.232$, $R(\text{free}) = 0.267$ at 2.6Å resolution. The second structure was solved by molecular replacement using first structure as the search model (~55% identity) and refined to $R(\text{cryst}) = 0.208$, $R(\text{free}) = 0.220$ at 2.0 Å resolution. The third structure (~28% identity with first two) was solved by Hg SAD and refined to $R(\text{cryst}) = 0.229$, $R(\text{free}) = 0.278$ at 2.4 Å resolution. All data were collected at NSLS beam line X9A. All three structures have a common fold and differ only in the placement of outer loops segments. The molecule is composed of two similar domains positioned face to face around a pseudo two-fold axis. Each domain contains two antiparallel beta-sheets forming a beta-sandwich. Details of the structures and functional predictions will be presented.