

Crystal structures of conserved hypothetical protein YLBA from three different bacteria.

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Keywords: structural genomics; NYSGXRC; crystal structures

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 2.0Å 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 2.4Å 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.