Crystal Structures of Two Bacillus subtilis Protein YjcG and YflL Dan Li, Lan-Fen Li, Yu-He Liang, Xiao-Dong Su, Department of Biochemistry and Molecular Biology, College of Life Sciences, Peking University, Beijing, China. E-mail: li-dan@pku.edu.cn

YjcG is a putative protein from *Bacillus Subtilis* with 171 amino acids, it was cloned into the vector pET21-DEST by Gateway system. YjcG was expressed in *E. coli* strain BL21(DE3), purified and crystallized by hanging-drop vapor diffusion method. Since there is no homologous structures, MAD (multi-wavelength anomalous diffraction) method was chosen to solve the YjcG structure. The crystal belongs to spacegroup C2 with unit-cell parameters a=99.30 Å, b=73.77 Å, c=61.58 Å,  $\beta$ =113.541°. The structure is refined to R<sub>cryst</sub> 0.237 and R<sub>free</sub> 0.267 at 2.3 Å. Dali search showed that YjcG structure is similar to 2'-5' RNA ligase with Z=14.7, RMSD 2.5 Å with 138 residues.

YflL is a function uncharacterized *B. subtilis* protein with 39.5% identity to acylphosphatase from horse muscle. Crystals suitable for structural studies were obtained from 50 mM potassium phosophate, pH 6.5. The structure was determined by MR (molecular replacement). The crystal diffracted to 1.3 Å and belongs to space group P2<sub>1</sub>2<sub>1</sub>2<sub>1</sub> with unit-cell parameters of a=26.86 Å, b=48.27 Å, c=59.57 Å. The structure is refined to R<sub>cryst</sub> 0.181 and R<sub>free</sub> 0.234. We have identified in vitro that the YflL is not only an acylphosphatase but also an apyrase.

Keywords: Bacillus subtilis, MAD method, MR