Structural Analysis of the N-terminal Domain of PriA from *E. coli*

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PriA, a DEXH-type DNA helicase, is essential for restoration of stalled replication forks and is a candidate sensor protein that recognizes arrested replication forks in bacteria [1]. The N-terminal domain binds to a free 3' terminus through the putative 3'-terminus recognition pocket [2]. We analyzed the interaction between N-terminal minimum binding domain of PriA[1-105] and oligonucleotides by using the single molecule fluorescence detection system MF20 (Olympus, Tokyo). The results indicated that PriA[1-105] recognized only the 3' terminal nucleotide portion of oligonucleotides.

We determined the crystal structure of the N-terminal domain of PriA to reveal the structural basis of the 3' terminal nucleotide recognition. Single crystals of native and SeMet PriA[1-105] were grown in hanging drops with a reservoir solution consisting of 0.1 M sodium citrate pH 3.6-3.8 and 0.15-0.35 M ammonium sulfate. Data sets were collected on BL38B1 at the SPring8 and PF-BL6A at the KEK. Native crystal diffracted to 2.8 Å and belongs to space group *R32*, with unit cell parameters, $a=b=111$Å, $c=260$Å.

[1] Tanaka T., et al., *J. Biol. Chem.*, 2002, **277**, 38062. [2] Mizukoshi T., et al., *J. Biol. Chem.*, 2003, **278**, 42234.

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