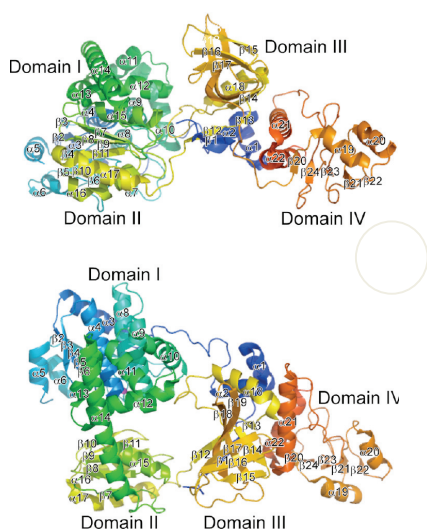
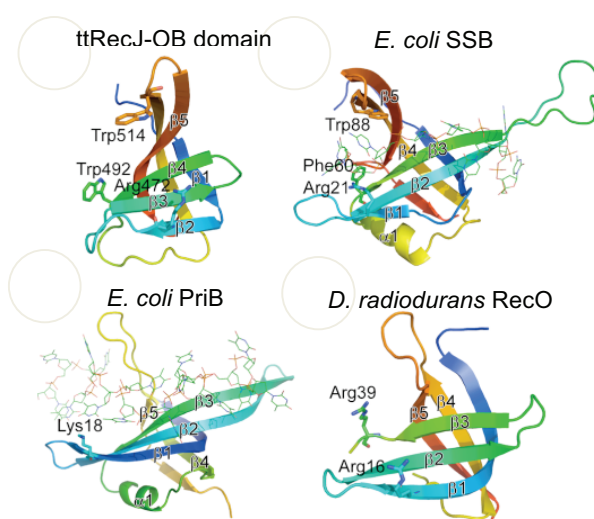


RecJ エキソヌクレアーゼの一本鎖 DNA 特異性の構造的基盤の解明

**Structure of RecJ exonuclease defines its specificity for single-stranded DNA**若松泰介<sup>1</sup>, 小寺祐太郎<sup>2</sup>, 中川紀子<sup>2,3</sup>, 倉光成紀<sup>1,2,3</sup>, 増井良治<sup>2,3</sup>Taisuke Wakamatsu<sup>1</sup>, Yutaro Kotera<sup>2</sup>, Noriko Nakagawa<sup>2,3</sup>, Seiki Kuramitsu<sup>1,2,3</sup> and Ryoji Masui<sup>2,3</sup><sup>(1</sup> 阪大・院生命機能, <sup>2</sup> 阪大・院理, <sup>3</sup> 理研・播磨研)<sup>(1</sup>Grad. Sch. Frontier Biosci., Osaka Univ., <sup>2</sup>Grad. Sch. Sci., Osaka Univ., <sup>3</sup>RIKEN SPring-8 Center, Harima Inst.)e-mail: [taisuke@bio.sci.osaka-u.ac.jp](mailto:taisuke@bio.sci.osaka-u.ac.jp)

RecJ is single-stranded DNA (ssDNA) specific 5'-3' exonuclease and deoxyribophosphodiesterase (dRPase), functions in DNA repair and recombination systems in almost bacteria and archaea. As far, our group have reported the crystal structure of the catalytic core domain of RecJ from *Thermus thermophilus* HB8 (cd-ttRecJ) containing motif I-IV and DHHA1 motif bound to one Mn<sup>2+</sup> and showed that cd-ttRecJ folded into two domains. However, none of the intact RecJ structure had been reported so far. To elucidate how RecJ achieves its high specificity for ssDNA, we determined the 2.15 to 2.50 Å resolution crystal structures of the intact ttRecJ alone, in complex with Mg<sup>2+</sup>, and with Mn<sup>2+</sup>. The entire RecJ consists of four domains which forms a molecule with an O-like structure (Fig. 1). One of two newly identified domains had structural similarities to an oligonucleotide/oligosaccharide-binding (OB)-fold (Fig. 2). The OB-fold domain alone could bind to DNA, indicating that this domain is a novel member of the OB-fold superfamily. The truncated RecJ containing only the core domain exhibited much lower affinity for the ssDNA substrate compared with intact RecJ. These results support the hypothesis that these structural features allow specific binding of RecJ to ssDNA. In addition, the structure of RecJ-Mn<sup>2+</sup> complex suggests that the hydrolysis reaction catalyzed by RecJ proceeds through a two-metal ion mechanism.

**Fig. 1 Overall structure of ttRecJ****Fig. 2 Structural comparison between ttRecJ-OB domain and the OB-fold domains of other proteins**