

Mechanisms of Opening and Closing of the Bacterial Replicative Helicase

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Assembly of bacterial ring-shaped hexameric replicative helicases on single-stranded (ss) DNA requires specialized loading factors. However, mechanisms implemented by these factors during opening and closing of the helicase, which enable and restrict access to an internal chamber, are not known. Here, we investigate these mechanisms in the *Escherichia coli* DnaB helicase•bacteriophage λ helicase loader (λ P) complex. We show that five copies of λ P bind at DnaB subunit interfaces and reconfigure the helicase into an open spiral conformation that is intermediate to previously observed closed ring and closed spiral forms; reconfiguration also produces openings large enough to admit ssDNA into the inner chamber. The helicase is also observed in a restrained inactive configuration that poises it to close on activating signal, and transition to the translocation state. Our findings provide insights into helicase opening, ssDNA entry, and closing in preparation for translocation.