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Structural basis for processive DNA synthesis by yeast DNA polymerase ϵ

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DNA polymerase ϵ (Pol ϵ) is a high-fidelity polymerase that participates in leading-strand synthesis during eukaryotic DNA replication in eukaryotic cells. The 2.2 Å ternary structure of the 142 kDa catalytic core of Pol ϵ from *Saccharomyces cerevisiae* in complex with DNA and an incoming nucleotide has recently been determined [1]. The structure provides information about the selection of the correct nucleotide and the positions of amino acids that might be critical for proofreading activity. Pol ϵ has the highest fidelity among B-family polymerases despite the absence of an extended β -hairpin loop that is required for high-fidelity replication by other B-family polymerases. Moreover, the catalytic core has a new domain (i.e. the P-domain) that allows Pol ϵ to encircle the nascent double-stranded DNA and enhance processivity of the polymerase. The structure provides valuable insights into the similarities and differences between Pol ϵ and other B-family polymerases, and suggests possible mechanisms responsible for the high processivity and fidelity of Pol ϵ .

[1] Hogg *et al.*, 2014, *NSMB*, 21, 49-55



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