Formation of C-strand Okazaki fragments

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references

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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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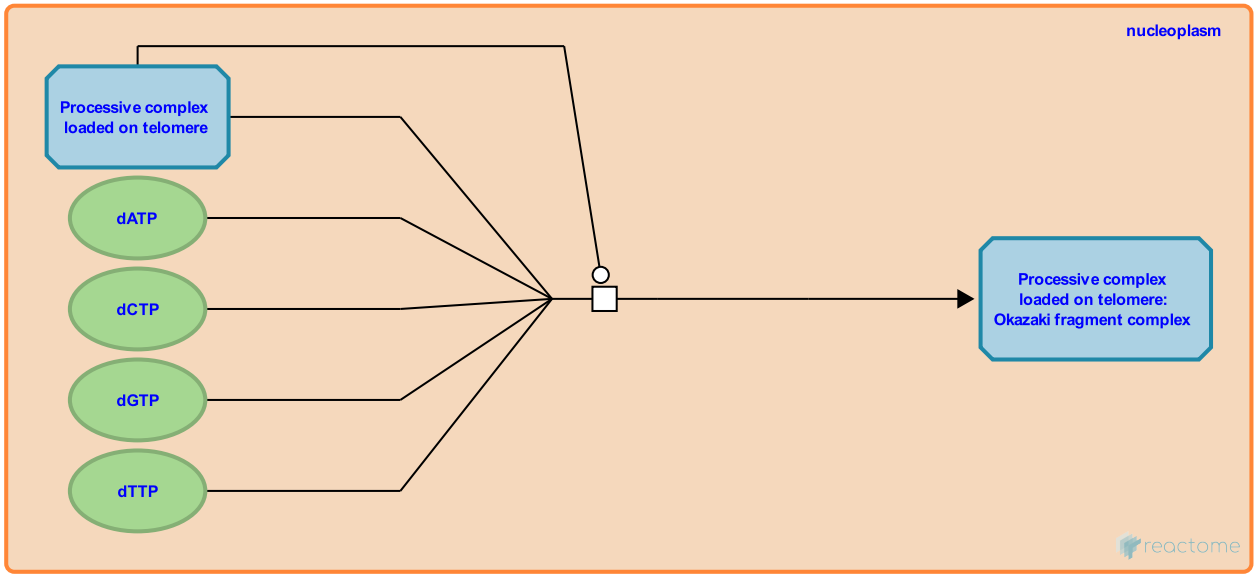
Stable identifier: R-HSA-174444

Type: transition

Compartments: nucleoplasm



After RFC initiates the assembly of the primer recognition complex, the complex of pol delta and PCNA is responsible for incorporating the additional nucleotides prior to the position of the next downstream initiator RNA primer. On the lagging strand, short discontinuous segments of DNA, called Okazaki fragments, are synthesized on RNA primers. The average length of the Okazaki fragments is 100 nucleotides. Polymerase switching is a key event that allows the processive synthesis of DNA by the pol delta and PCNA complex (Lee and Hurwitz 1990, Tsurimoto and Stillman 1991, Nethanel et al. 1992, Brown and Campbell 1993, Waga et al.1994, Bambara et al. 1997). PCNA increases the processivity of the DNA polymerase delta during telomeric C-strand synthesis in a human telomere replication model, but it does not eliminate the DNA polymerase delta stalling on the G-rich template (Lormand et al. 2013).

Literature references

Opresko, PL., Kaur, P., Wang, H., Kunkel, TA., Buncher, N., Lee, MY. et al. (2013). DNA polymerase δ stalls on telomeric lagging strand templates independently from G-quadruplex formation. *Nucleic Acids Res., 41*, 10323-33.

Editions

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