Removal of remaining Flap from the C-strand

Blackburn, EH., Hayashi, MT., Orlic-Milacic, M., Price, C., Seidel, J.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

22/09/2020

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

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. ↗

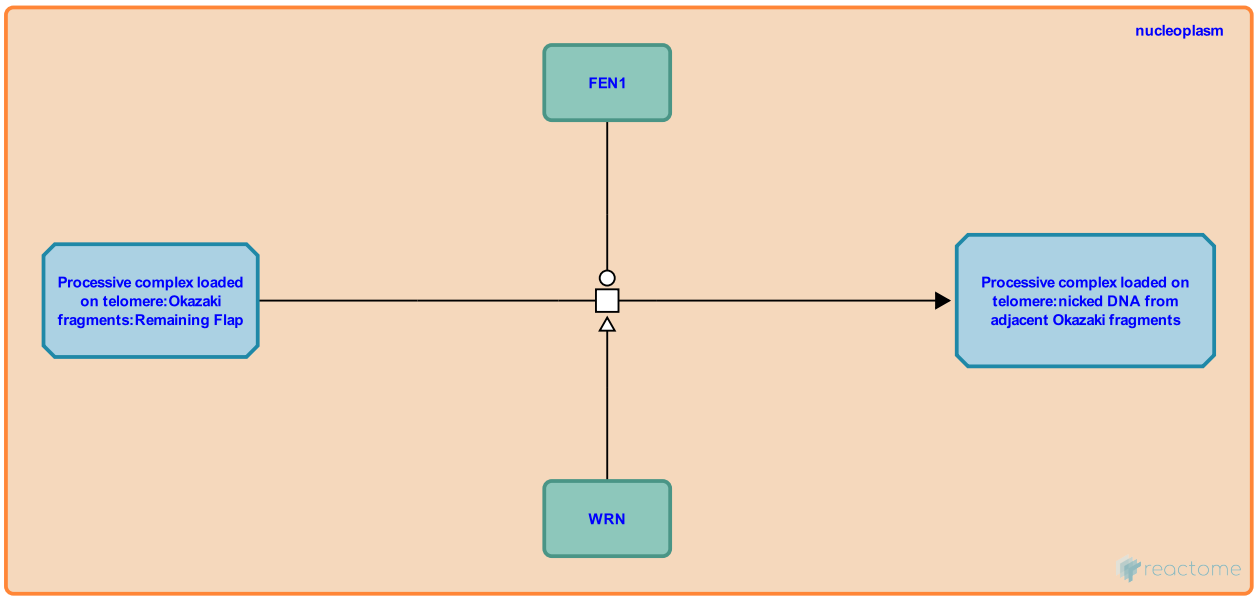
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Removal of remaining Flap from the C-strand ↗

Stable identifier: R-HSA-174446

Type: transition

Compartments: nucleoplasm



The remaining flap, which is too short to support RPA binding, is then processed by FEN1. There is evidence that binding of RPA to the displaced end of the RNA-containing Okazaki fragment prevents FEN1 from accessing the substrate. FEN1 is a structure-specific endonuclease that cleaves near the base of the flap at a position one nucleotide into the annealed region. Biochemical studies have shown that the preferred substrate for FEN1 consists of a one-nucleotide 3'-tail on the upstream primer in addition to the 5'-flap of the downstream primer (Harrington and Lieber 1994, Harrington and Lieber 1995, Murante et al. 1996, Lieber 1997, Kaiser et al. 1999, Xu et al. 2000, Kao et al. 2002). The interaction of FEN1 with WRN, a RECQ family DNA helicase, is needed for successful flap cleavage during telomeric strand displacement synthesis (Saharia et al. 2010, Li et al. 2017).

Literature references

Saharia, A., Teasley, DC., Duxin, JP., Dao, B., Chiappinelli, KB., Stewart, SA. (2010). FEN1 ensures telomere stability by facilitating replication fork re-initiation. *J. Biol. Chem., 285*, 27057-66. ↗

Li, B., Reddy, S., Comai, L. (2017). The Werner Syndrome Helicase Coordinates Sequential Strand Displacement and FEN1-Mediated Flap Cleavage during Polymerase δ Elongation. *Mol. Cell. Biol., 37*. ↗

Editions

2006-03-10	Authored	Blackburn, EH., Seidel, J.
2006-07-13	Reviewed	Price, C.
2020-04-29	Reviewed	Hayashi, MT.
2020-05-04	Edited	Orlic-Milacic, M.