

Elongation and translocation of the extended telomeric chromosome end

D'Eustachio, P., Delany, ME., O'Hare, TH., Swanberg, SE.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

06/05/2024

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. [↗](#)

Reactome database release: 88

This document contains 1 reaction ([see Table of Contents](#))

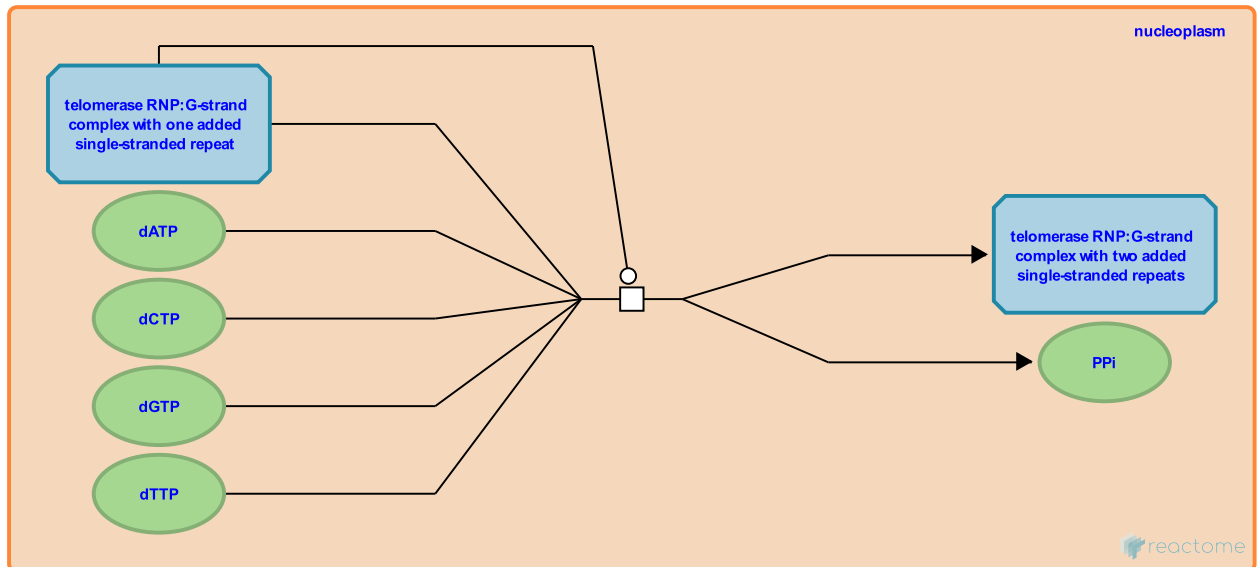
Elongation and translocation of the extended telomeric chromosome end [↗](#)

Stable identifier: R-GGA-417127

Type: transition

Compartments: nucleoplasm

Inferred from: [Elongation of Extended Telomeric Chromosome End \(Homo sapiens\)](#)



TERC directs the sequential addition of nucleotides to the 3' end of a chromosomal DNA strand with one added telomere repeat. After each addition, the template must move relative to the telomerase active site to bring the next template residue into the active site. The product of these additions and translocations is a chromosomal single-stranded end extended by two repeat units (each complementary to the TERC template sequence), positioned on the template so as to allow repetition of the process. The template region of TERC is perfectly conserved between humans and chickens (Chen et al. 2000). The molecular details of the process have been studied in humans; the orthologous chicken event is inferred from those data.

Literature references

Greider, CW., Chen, JL., Blasco, MA. (2000). Secondary structure of vertebrate telomerase RNA. *Cell*, 100, 503-14. [↗](#)

Editions

2009-04-16	Edited	D'Eustachio, P.
2010-06-11	Authored	Delany, ME., Swanberg, SE., O'Hare, TH.