

Second strand transfer by annealing complementary PBS sequences

D'Eustachio, P., Gopinathrao, G., Hughes, SH.

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](#).

02/05/2024

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](#))

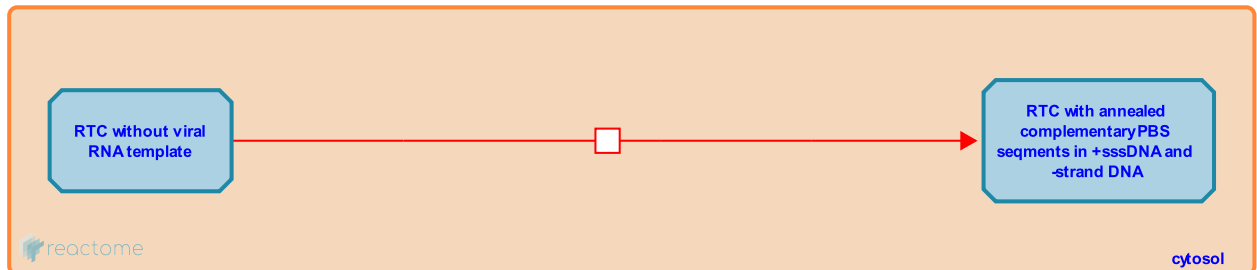
Second strand transfer by annealing complementary PBS sequences [↗](#)

Stable identifier: R-HSA-164512

Type: transition

Compartments: cytosol

Diseases: Human immunodeficiency virus infectious disease



With the removal of all viral genomic RNA and tRNA, the PBS sequence at the 3' end of the plus-strand strong-stop DNA (+ssDNA) is free to pair with the complementary PBS sequence at the 3' end of the minus-strand DNA, to generate a circular structure (Telesnitsky and Goff 1997).

Literature references

De Clercq, E., Anne, J., Jonckheere, H. (2000). The HIV-1 reverse transcription (RT) process as target for RT inhibitors. *Med Res Rev*, 20, 129-54. [↗](#)

Varmus, HE., Hughes, SH., Coffin, JM. (1997). Reverse Transcriptase and the Generation of Retroviral DNA, Retroviruses. *Cold Spring Harbor Laboratory Press*, 121-160.

Editions

2006-05-19	Authored, Edited	Gopinathrao, G., D'Eustachio, P.
2006-10-31	Reviewed	Hughes, SH.