

Separation of abortive HIV-1 transcript from template

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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

- 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](#))

Separation of abortive HIV-1 transcript from template [↗](#)

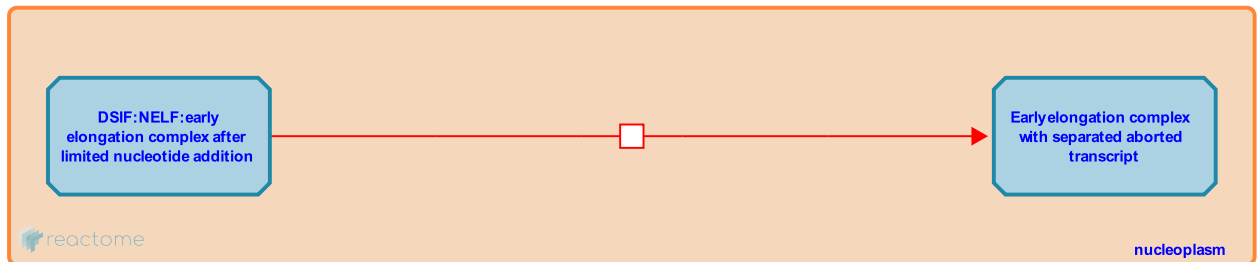
Stable identifier: R-HSA-167147

Type: transition

Compartments: nucleoplasm

Diseases: Human immunodeficiency virus infectious disease

Inferred from: [Separation of elongating transcript from template \(Homo sapiens\)](#)



At the beginning of this reaction, 1 molecule of 'DSIF:NELF:early elongation complex after limited nucleotide addition' is present. At the end of this reaction, 1 molecule of 'Early elongation complex with separated aborted transcript' is present.

This reaction takes place in the 'nucleus'.

Literature references

Conaway, JW., Shilatifard, A., Conaway, RC. (2003). The RNA polymerase II elongation complex. *Annu Rev Biochem*, 72, 693-715. [↗](#)

Editions

2005-07-27	Authored	Matthews, L., Rice, AP.
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