Abortive termination of HIV-1 early transcription elongation by DSIF:NELF

Matthews, L., Rice, AP.

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

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. ↗

Abortive termination of HIV-1 early transcription elongation by DSIF:NELF ↗

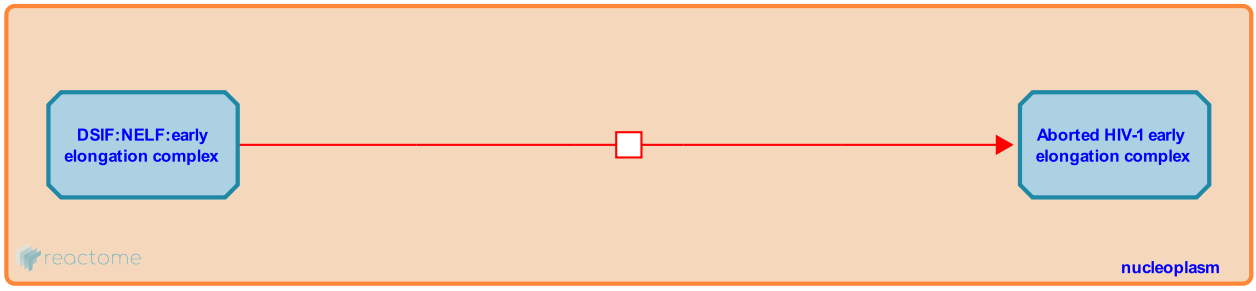
Stable identifier: R-HSA-167478

Type: transition

Compartments: nucleoplasm

Diseases: Human immunodeficiency virus infectious disease

Inferred from: Abortive termination of early transcription elongation by DSIF:NELF (Homo sapiens)



In the early elongation phase, shorter transcripts typically of ~30 nt in length are generated due to random termination of elongating nascent transcripts. This abortive cessation of elongation has been observed mainly in the presence of DSIF-NELF bound to Pol II complex. (Reviewed in Conaway et al.,2000; Shilatifard et al., 2003).

Literature references

Shilatifard, A., Conaway, JW., Dvir, A., Conaway, RC. (2000). Control of elongation by RNA polymerase II. *Trends Biochem Sci, 25*, 375-80. ↗

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.
2005-10-16	Edited	Matthews, L.