

Abortive termination of early transcription elongation by DSIF:NELF

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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

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Reactome database release: 88

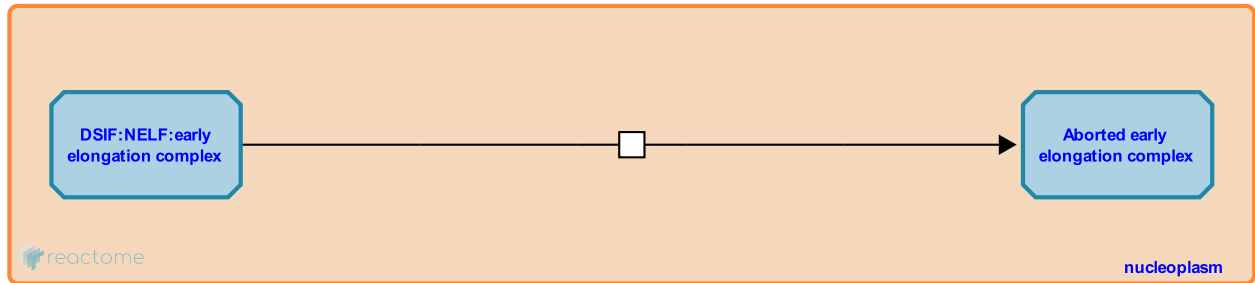
This document contains 1 reaction ([see Table of Contents](#))

Abortive termination of early transcription elongation by DSIF:NELF [↗](#)

Stable identifier: R-HSA-113409

Type: transition

Compartments: nucleoplasm



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

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

Editions

2004-04-28

Authored

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