# Phosphorylation of NEFL by the P-TEFb(Cyclin T1:Cdk9) complex

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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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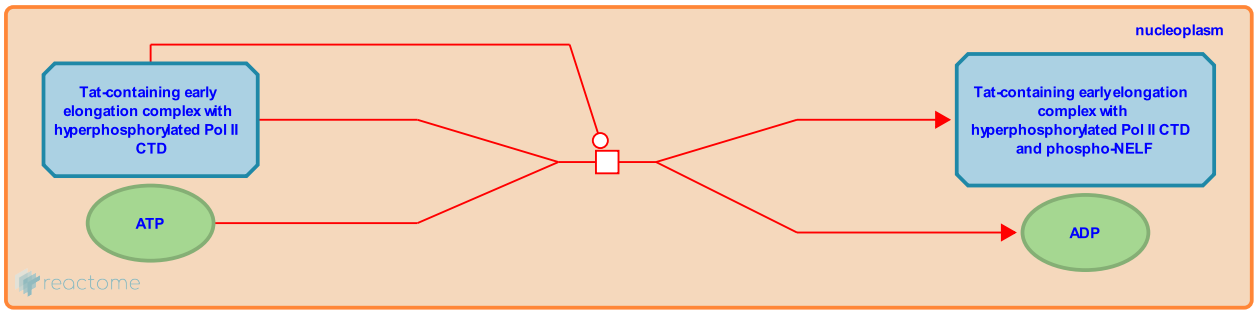
## Phosphorylation of  NEFL by the P-TEFb(Cyclin T1:Cdk9) complex ↗

**Stable identifier:** R-HSA-170706

**Type:** transition

**Compartments:** nucleoplasm

**Diseases:** Human immunodeficiency virus infectious disease




Phosphorylation of the RD subunit of NEFL by P-TEFb(Cyclin T1:Cdk9) results in the dissociation of NEFL from TAR as well as the conversion of NEFL to an elongation factor (Fujinaga et al., 2004)

## Literature references


Peterlin, BM., Irwin, D., Taube, R., Huang, Y., Fujinaga, K., Kurosu, T. (2004). Dynamics of human immunodeficiency virus transcription: P-TEFb phosphorylates RD and dissociates negative effectors from the transactivation response element. *Mol Cell Biol, 24*, 787-95. ↗


## Editions

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