# Loss of Rrn3 from RNA Polymerase I promoter escape 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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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. ↗

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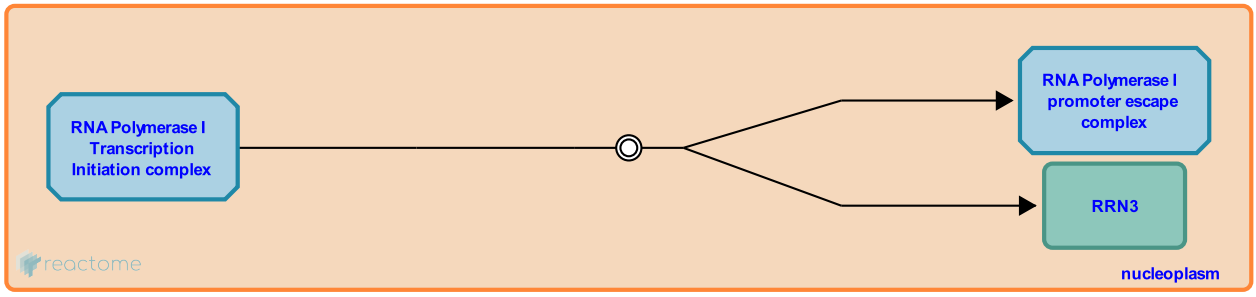
## Loss of Rrn3 from RNA Polymerase I promoter escape complex ↗

**Stable identifier:** R-HSA-73769

**Type:** dissociation

**Compartments:** nucleoplasm




Upon transcription initiation it is thought that RRN3 is inactivated and dissociates from the Loss of Rrn3 from the RNA Polymerase I promoter escape complex. SL1 and UBF are thought to remain bound to the promoter for multiple rounds of transcription initiation

## Literature references

Smink, T., Rothblum, LI., Lun, M., Hu, Q., Cavanaugh, AH., Mirza, A. et al. (2003). Rrn3 becomes inactivated in the process of ribosomal DNA transcription. *J Biol Chem, 278*, 18953-9. ↗

## Editions

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