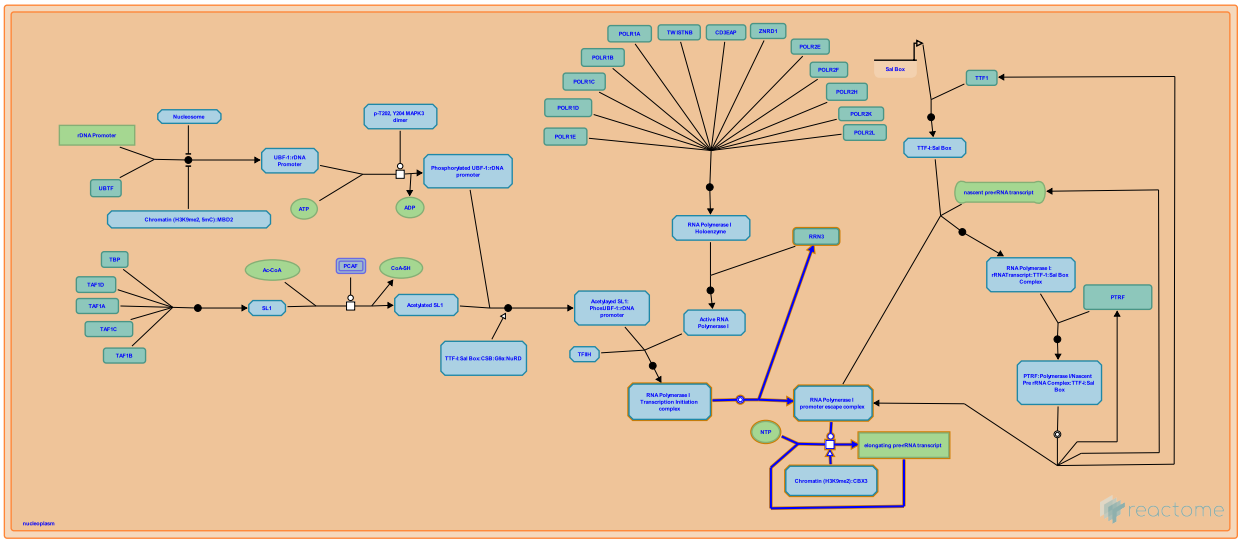
RNA Polymerase I Promoter Escape



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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

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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.
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. ↗

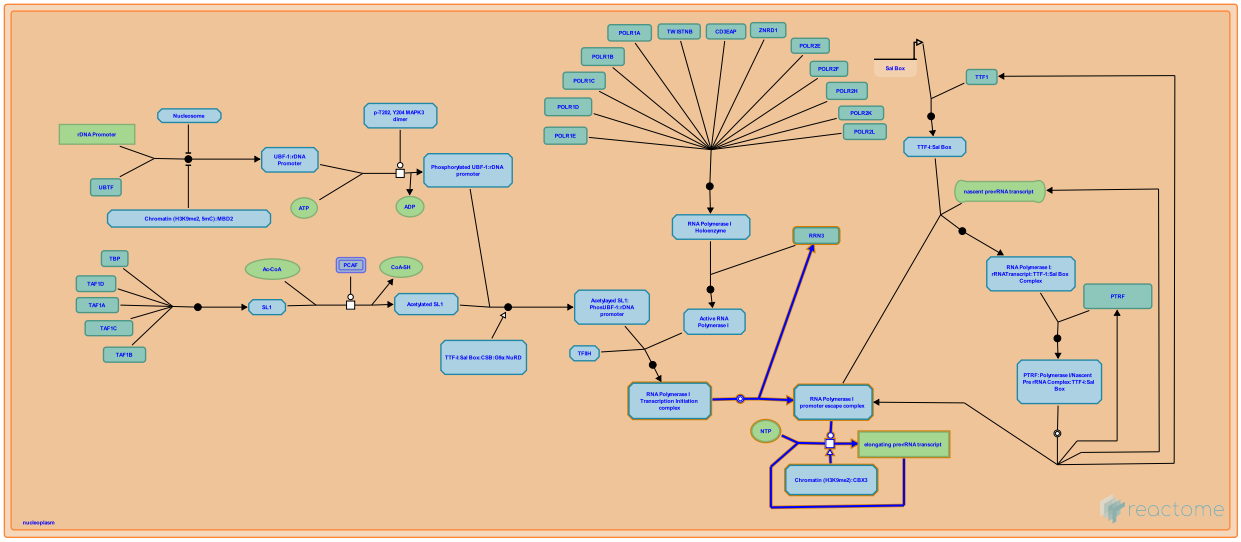
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

RNA Polymerase I Promoter Escape ↗

Stable identifier: R-HSA-73772

Compartments: nucleolus



As the active RNA Polymerase I complex leaves the promoter Rrn3 dissociates from the complex. RNA polymerase I Promoter Clearance is complete and Chain Elongation begins (Milkereit and Tschochner, 1998). The assembly of the initiation complex on the promoter and the transition from a closed to an open complex is then followed by promoter clearance and transcription elongation by RNA Pol I. Unlike the RNA polymerase II system, RNA polymerase I transcription does not require a form of energy such as ATP for initiation and elongation. Regulatory mechanisms operating at both the level of transcription initiation and elongation probably concurrently to adjust the level of rRNA synthesis to the need of the cell.

Literature references

Tschochner, H., Milkereit, P. (1998). A specialized form of RNA polymerase I, essential for initiation and growth-dependent regulation of rRNA synthesis, is disrupted during transcription. *EMBO J., 17*, 3692-703. ↗

Carles, C., Sentenac, A., Schultz, P., Riva, M., Tschochner, H., Peyroche, G. et al. (2000). The recruitment of RNA polymerase I on rDNA is mediated by the interaction of the A43 subunit with Rrn3. *EMBO J., 19*, 5473-82. ↗

Editions

2003-07-03	Authored	Comai, L.
2024-03-06	Edited	Gillespie, ME.

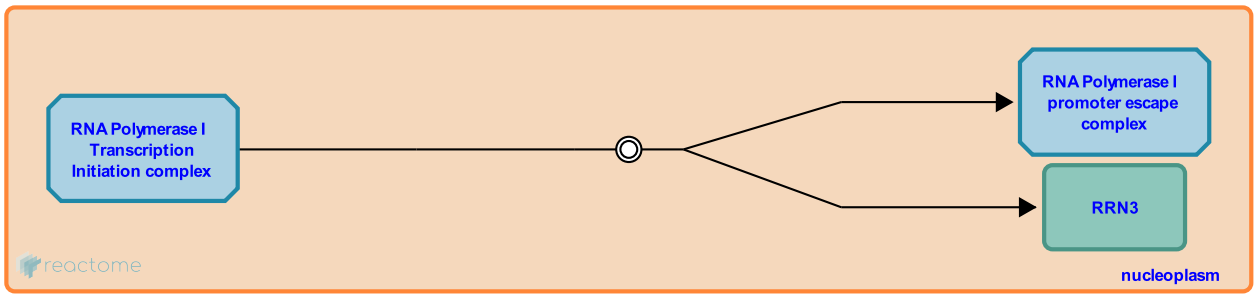
Loss of Rrn3 from RNA Polymerase I promoter escape complex ↗

Location: RNA Polymerase I Promoter Escape

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

Followed by: Elongation of pre-rRNA transcript

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

2003-07-03	Authored	Comai, L.
2024-03-06	Edited	Gillespie, ME.

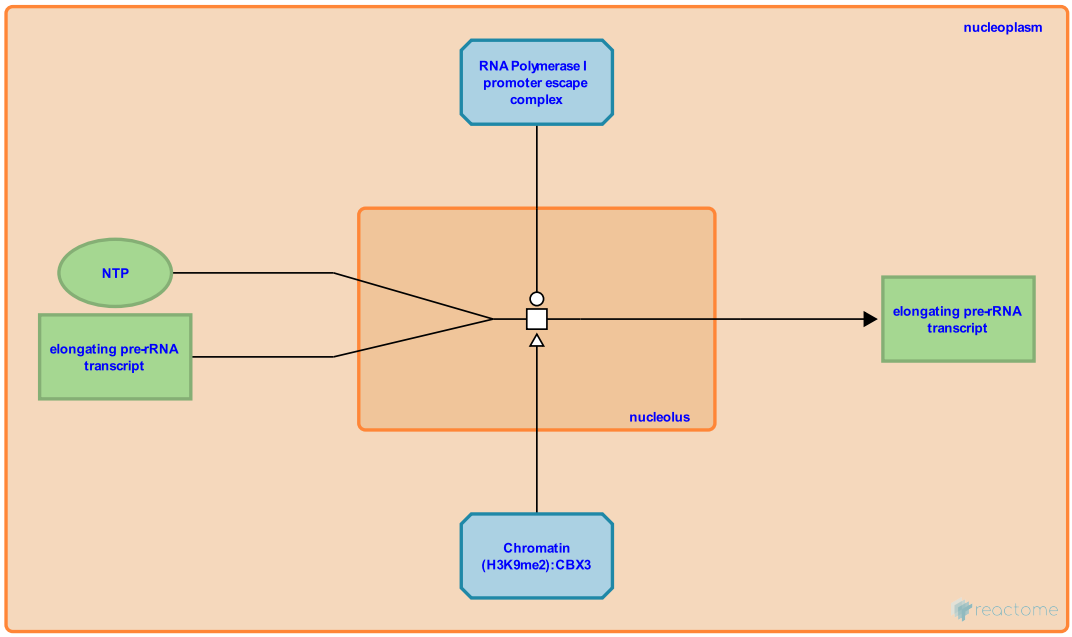
Elongation of pre-rRNA transcript ↗

Location: RNA Polymerase I Promoter Escape

Stable identifier: R-HSA-74986

Type: transition

Compartments: nucleolus



At the beginning of this reaction, 1 molecule of 'elongating pre-rRNA transcript', and 1 molecule of 'NTP' are present. At the end of this reaction, 1 molecule of 'elongating pre-rRNA transcript' is present.

This reaction takes place in the 'nucleolus' and is mediated by the 'DNA-directed RNA polymerase activity' of 'RNA Polymerase I promoter escape complex'.

Preceded by: Loss of Rrn3 from RNA Polymerase I promoter escape complex

Literature references

Comai, L. (2004). Mechanism of RNA polymerase I transcription. *Adv. Protein Chem., 67*, 123-55. ↗

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