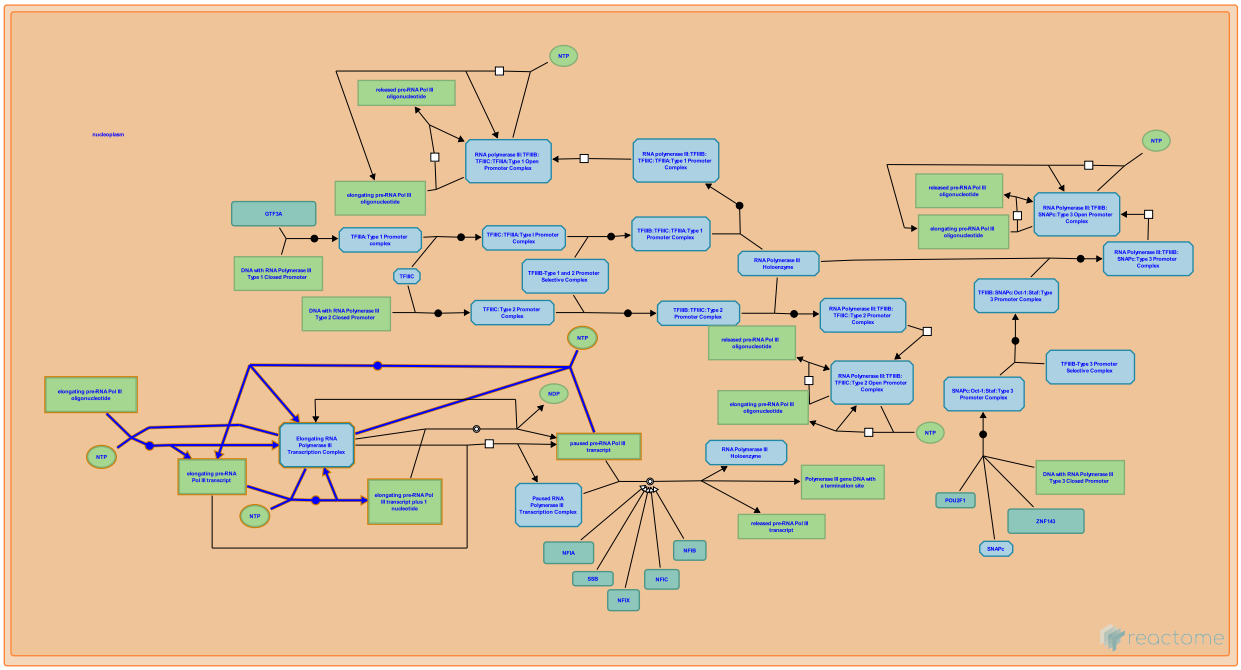
RNA Polymerase III Chain Elongation



Geiduschek, EP., Gillespie, ME., Kassavetis, GA.

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

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.

03/05/2024

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. ↗

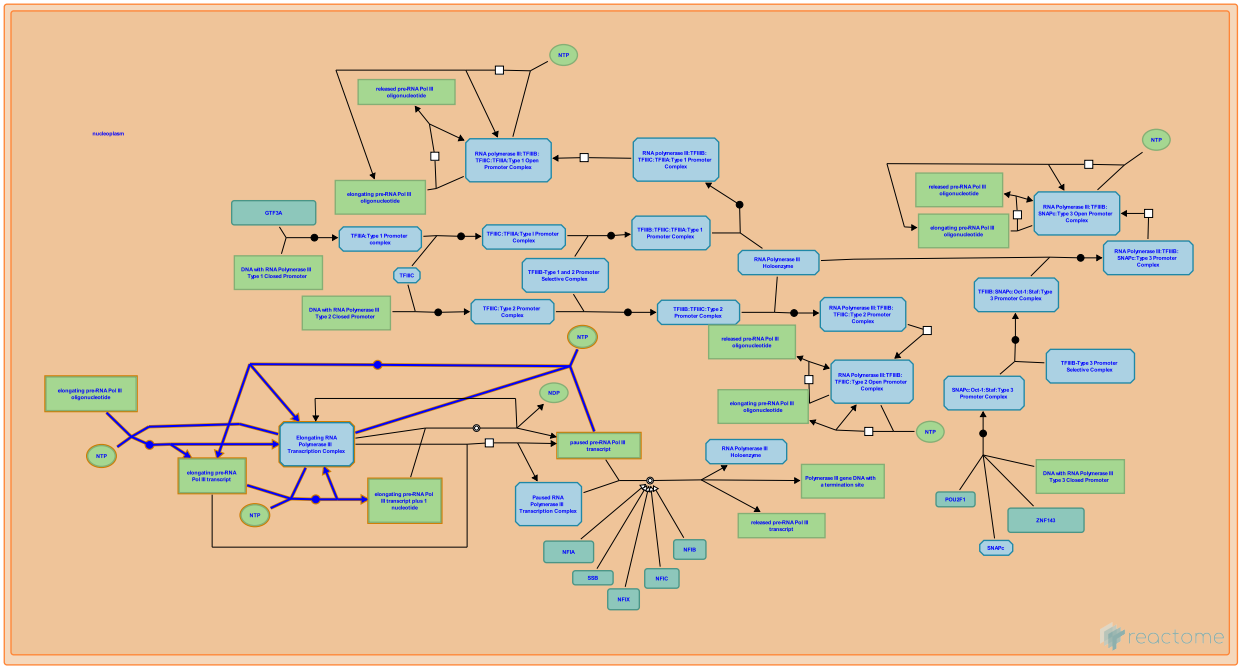
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

RNA Polymerase III Chain Elongation ↗

Stable identifier: R-HSA-73780

Compartments: nucleoplasm



Pol III initiation complexes open the promoter spontaneously similar to the mechanism employed in archaeal and bacterial transcription.

Editions

2004-02-27	Authored	Kassavetis, GA., Geiduschek, EP.
2024-03-06	Edited	Gillespie, ME.

Initiation of RNA Polymerase III Productive Transcription ↗

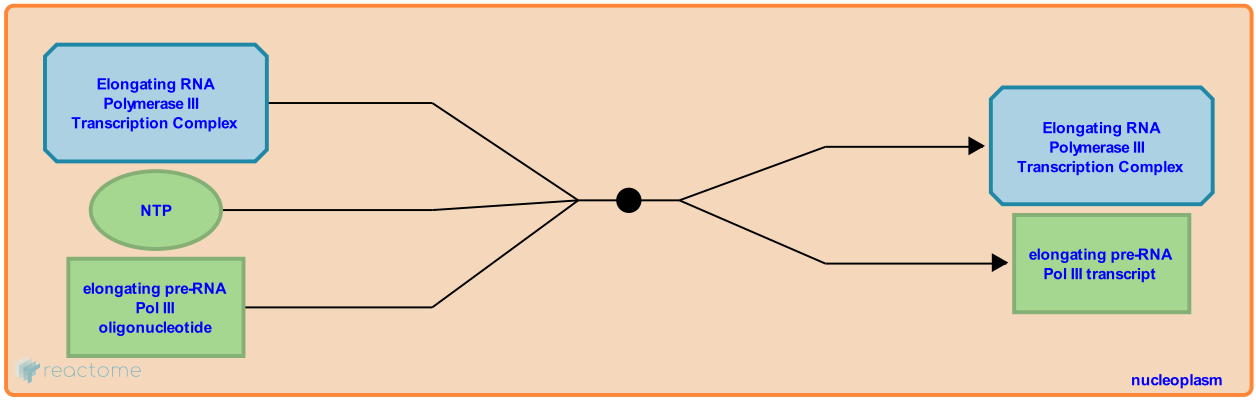
Location: RNA Polymerase III Chain Elongation

Stable identifier: R-HSA-113446

Type: binding

Compartments: nucleoplasm

Inferred from: Beginning of RNA Polymerase III Productive Transcription (Saccharomyces cerevisiae)



The transition from abortive to productive transcription may occur at bp +5. The primary transcripts of pol III-transcribed genes are short, ~90 to 120 nt for tRNA and 5s RNA genes (which constitute the great majority of products) and even the longest transcripts (e.g. the RNA of the signal recognition particles) are only ~500 nt. This event is inferred from an event in Saccharomyces cerevisiae.

Followed by: RNA Polymerase III Productive Transcription

Editions

2004-03-29	Authored	Geiduschek, EP.
2024-03-06	Edited	Gillespie, ME.

RNA Polymerase III Productive Transcription ↗

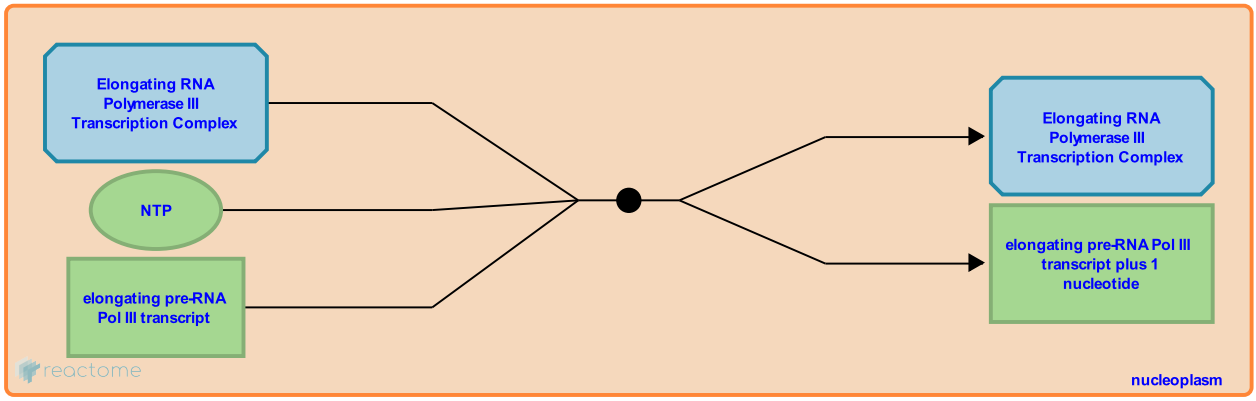
Location: RNA Polymerase III Chain Elongation

Stable identifier: R-HSA-113705

Type: binding

Compartments: nucleoplasm

Inferred from: Beginning of RNA Polymerase III Productive Transcription (Saccharomyces cerevisiae)



The principal cleavage products are dinucleotides, and they are produced in large stoichiometric excess over complete transcripts. Overall productive RNA chain elongation proceeds quite rapidly. This event is inferred from an event in Saccharomyces cerevisiae.

Preceded by: Resumption of RNA Polymerase III Productive Transcription, Initiation of RNA Polymerase III Productive Transcription

Editions

2004-03-29	Authored	Geiduschek, EP.
2024-03-06	Edited	Gillespie, ME.

Resumption of RNA Polymerase III Productive Transcription ↗

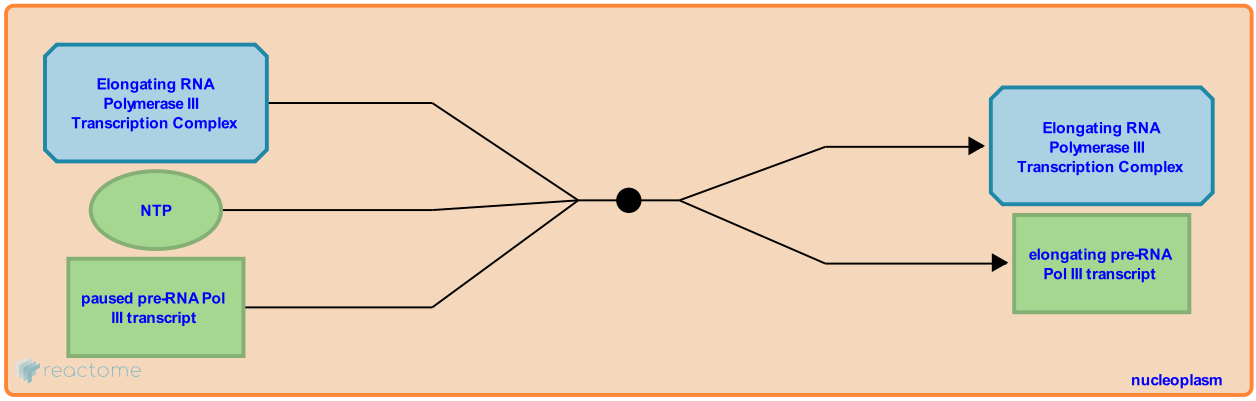
Location: RNA Polymerase III Chain Elongation

Stable identifier: R-HSA-113451

Type: binding

Compartments: nucleoplasm

Inferred from: Beginning of RNA Polymerase III Productive Transcription (Saccharomyces cerevisiae)



The principal cleavage products are dinucleotides, and they are produced in large stoichiometric excess over complete transcripts. Overall productive RNA chain elongation proceeds quite rapidly. This event is inferred from an event in Saccharomyces cerevisiae.

Followed by: RNA Polymerase III Productive Transcription

Editions

2004-03-29	Authored	Geiduschek, EP.
2024-03-06	Edited	Gillespie, ME.

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