Beginning of RNA Polymerase III Productive Transcription

Geiduschek, EP., Gillespie, ME.

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

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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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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. ↗

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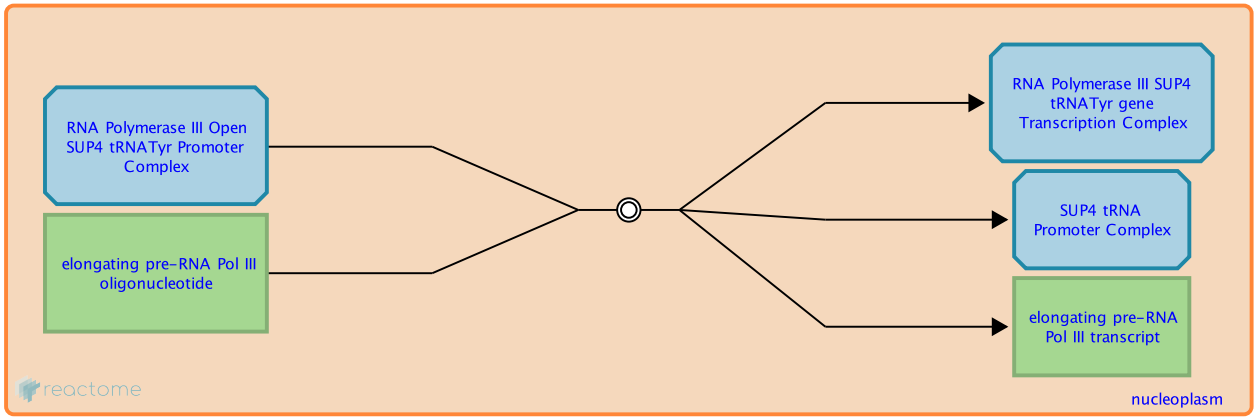
Stable identifier: R-SCE-111945

Type: dissociation

Compartments: nucleoplasm



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 5 sRNA 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. The special feature of this transcription is the presence of initiation factors bound within the transcription unit – TFIIIA within class 1 genes (NH section) and TFIIIC in class 1 and class 2 genes. Transcript elongation, which has been analyzed at single-step resolution on a single sc tRNA gene, is rapid with highly purified components (TFIIIC, TFIIIB and pol III), and also in crude extracts (Matsuzaki et al., 1994; Shaaban et al., 1996). In particular, TFIIIC does not present a barrier to transcript elongation, generating a delay at only a single site of only 0.15-0.2 s duration at 20C. In other words, the requirement to displace TFIIIC during transcript elongation is not rate-limiting for tRNA gene activity. On the other hand, transcript elongation slows down when short U-tracts, e.g. UUU, are laid down, even at high concentrations of NTPs. These pauses exceed the TFIIIC-imposed delay on transcription of the sc SUP4 gene by a factor of ~3 or greater.

Sc TFIIIC is entirely displaced from a tRNA gene during multiple cycles of transcription in vitro (Bardeleben et al., 1994) and its occupancy of pol III genes in vivo during active cell growth is also low (Roberts et al., 2003).

Literature references

Matsuzaki, H., Kassavetis, GA., Geiduschek, EP. (1994). Analysis of RNA chain elongation and termination by Saccharomyces cerevisiae RNA polymerase III. *J Mol Biol, 235*, 1173-92. ↗

Editions

2004-03-29	Authored	Geiduschek, EP.
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