Transcription of intergenic spacer of the rRNA gene

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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

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. ↗

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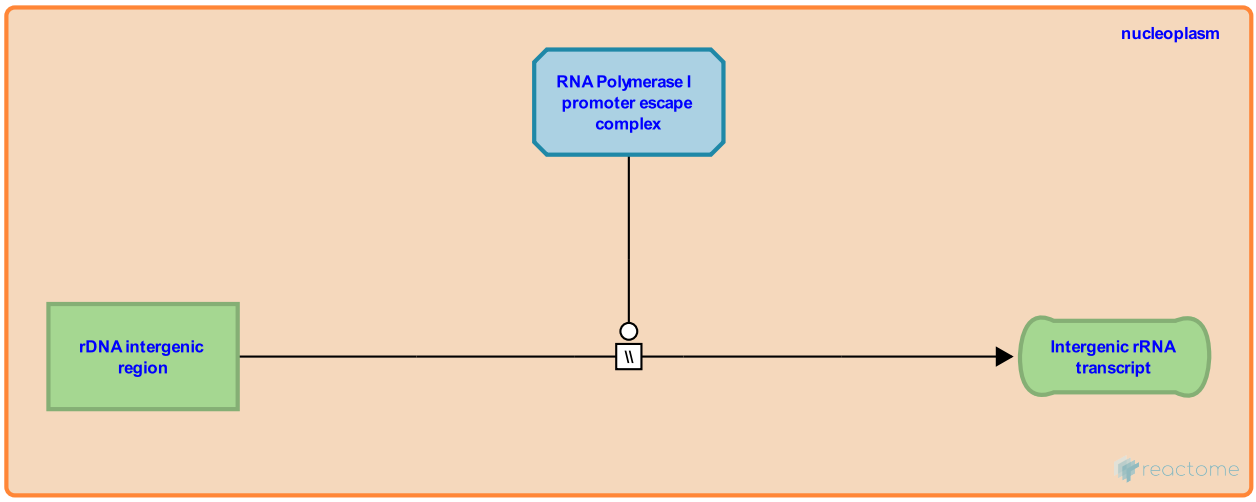
Transcription of intergenic spacer of the rRNA gene ↗

Stable identifier: R-HSA-427366

Type: omitted

Compartments: nucleoplasm

Inferred from: Transcription of intergenic spacer of the rRNA gene (Mus musculus)



As inferred from mouse cell models, intergenic spacer regions (IGS) located between rRNA transcription units contain upstream promoters and are transcribed by RNA Polymerase I. The IGS transcripts originate approximately 2 Kb upstream of the start of rRNA transcription and proceed though the main promoter of the rRNA gene.

Literature references

Alvord, WG., Gu, YD., Hwang, CJ., Anderson, LM., Kasprzak, W., Fields, JR. et al. (2009). An intergenic non-coding rRNA correlated with expression of the rRNA and frequency of an rRNA single nucleotide polymorphism in lung cancer cells. *PLoS One, 4*, e7505. ↗

Editions

2009-06-19	Authored, Edited	May, B.
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