

Cleavage of intergenic spacer RNA to yield fragments of 150-300 nucleotides

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11/05/2024

https://reactome.org

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

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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.
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- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

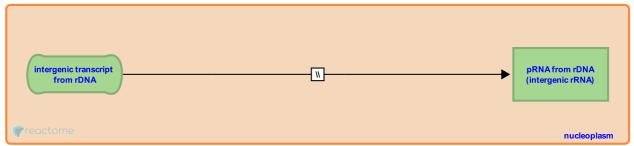
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Stable identifier: R-MMU-573343

Type: omitted

Compartments: nucleoplasm



Long Intergenic Spacer RNA of about 2 Kb is cleaved to yield shorter fragments of 150-300 nucleotides. The enzyme responsible for the cleavage is unknown.

Literature references

Mayer, C., Santoro, R., Grummt, I., Li, J., Schmitz, KM. (2006). Intergenic transcripts regulate the epigenetic state of rRNA genes. *Mol Cell*, 22, 351-61. ↗

Editions

2010-04-06	Authored, Edited	May, B.
2014-02-18	Reviewed	Shiao, YH.