

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

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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. [↗](#)
- 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. [↗](#)

Reactome database release: 88

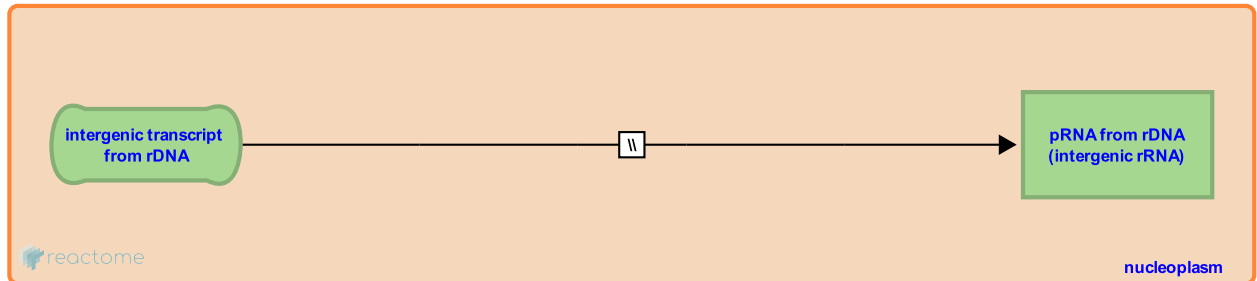
This document contains 1 reaction ([see Table of Contents](#))

## Cleavage of intergenic spacer RNA to yield fragments of 150-300 nucleotides [↗](#)

**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.
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