

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

May, B., Shiao, YH.

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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- 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](#))

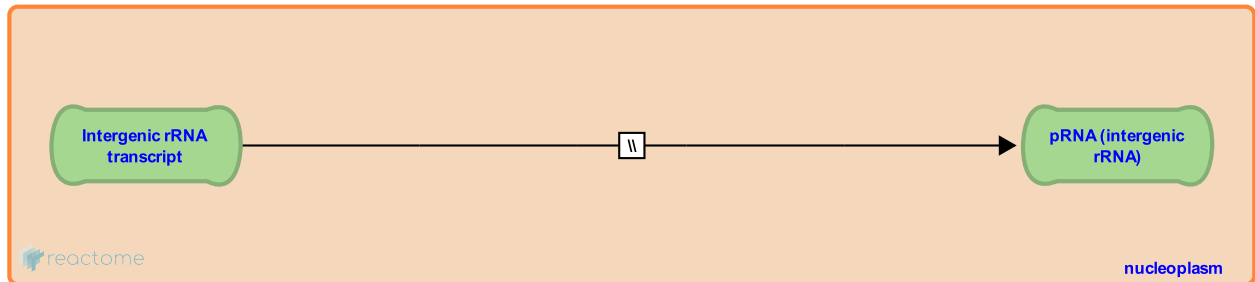
## Cleavage of intergenic spacer RNA to yield fragments of 150-300 nucleotides [↗](#)

**Stable identifier:** R-HSA-427394

**Type:** omitted

**Compartments:** nucleoplasm

**Inferred from:** [Cleavage of intergenic spacer RNA to yield fragments of 150-300 nucleotides \(Mus musculus\)](#)



As inferred from mouse cell models, 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.

### Editions

2009-06-19	Authored, Edited	May, B.
2014-02-18	Reviewed	Shiao, YH.