

TSEN complex cleaves the intron from pre-

tRNA

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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.

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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 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)

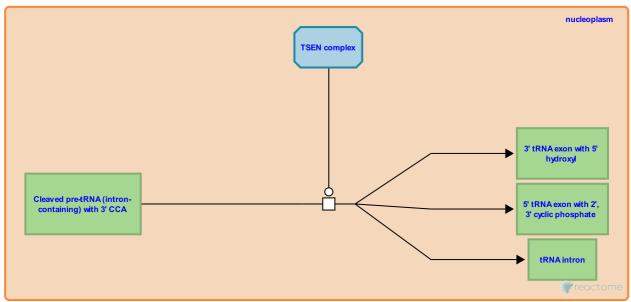
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TSEN complex cleaves the intron from pre-tRNA 7

Stable identifier: R-HSA-5696813

Type: transition

Compartments: nucleoplasm



The TSEN complex endonucleolytically cleaves 5' and 3' of introns in tRNAs, leaving a 2',3' cyclic phosphate on the 5' exon and a 5' hydroxyl on the 3' exon (Paushkin et al. 2004, Trotta et al. 2006).

Literature references

Paushkin, SV., Peltz, SW., Patel, M., Furia, BS., Trotta, CR. (2004). Identification of a human endonuclease complex reveals a link between tRNA splicing and pre-mRNA 3' end formation. *Cell*, 117, 311-21.

Paushkin, SV., Peltz, SW., Patel, M., Li, H., Trotta, CR. (2006). Cleavage of pre-tRNAs by the splicing endonuclease requires a composite active site. *Nature*, 441, 375-7.

Editions

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