

DICER1 cleaves tRNA

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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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Reactome database release: 88

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

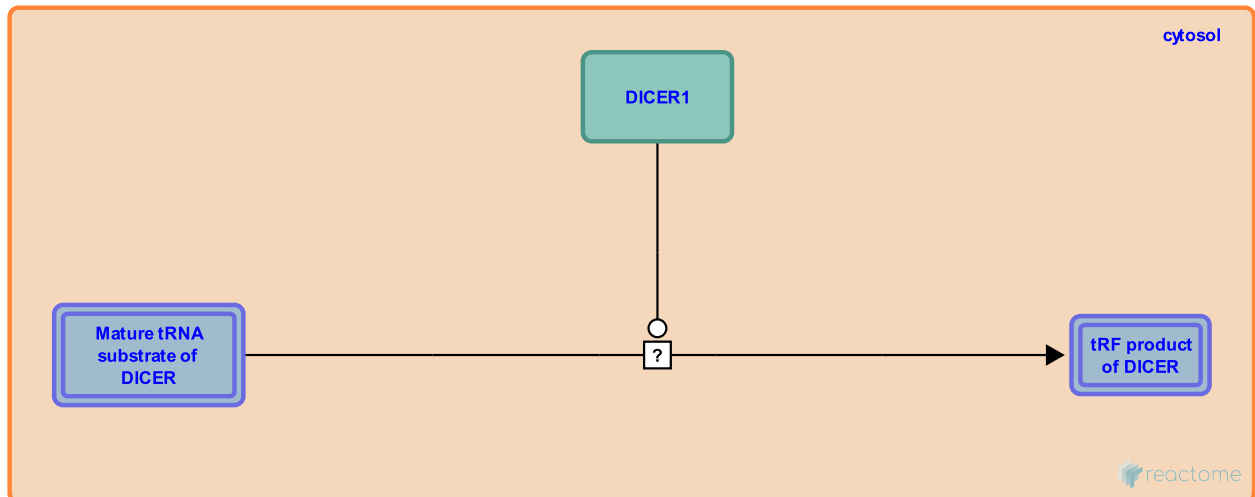
DICER1 cleaves tRNA [↗](#)

Stable identifier: R-HSA-9708292

Type: uncertain

Compartments: cytosol

Inferred from: [Dicer1 cleaves tRNA Ile TAT to yield miR-1983 \(Mus musculus\)](#)



DICER1 cleaves: tRNA Gln CTG in the D-loop, releasing a 19 nt fragment from the 5' end of the tRNA (Cole et al. 2009); tRNA Gly GCC, releasing a 22 nt fragment, tRF-3b (tRF-3027b), from the 3' end of the tRNA (Maute et al. 2013); precursor tRNA Ile TAT, releasing a 21 nt fragment, known as sRNA-Ile or miR-1983, from the 3' end of the tRNA (Hasler et al. 2016, and inferred from mouse homologs). Most tRFs are thought to arise in a DICER1 independent manner, however, as deletion of DICER1 does not significantly alter tRF expression (Kumar et al. 2014, Kuscu and Kumar et al. 2018).

Literature references

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Editions

2020-11-27	Authored, Edited	May, B.
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