

DICER1 cleaves tRNA Lys TTT 3' in tRNA:HIV RNA hybrid

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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](#))

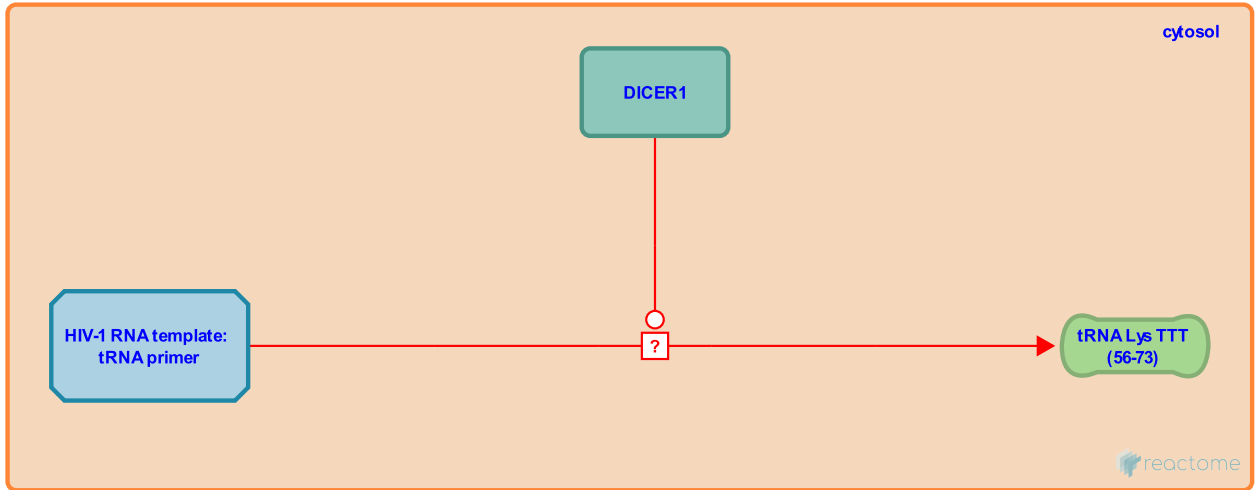
DICER1 cleaves tRNA Lys TTT 3 in tRNA:HIV RNA hybrid ↗

Stable identifier: R-HSA-9708408

Type: uncertain

Compartments: cytosol

Diseases: Human immunodeficiency virus infectious disease



DICER1 cleaves the double-stranded RNA hybrid formed by the primer binding site (PBS) of HIV genomic RNA and tRNA Lys UUU, the tRNA that primes reverse transcription of the HIV genome. The products are a tsRNA, PBSncRNA, that is 18 nt of the 3' end of tRNA Lys UUU and an uncharacterized fragment of the HIV genome (Yeung et al. 2009).

Literature references

Yeung, ML., Jeang, KT., Houzet, L., Bennasser, Y., Watashi, K., Le, SY. (2009). Pyrosequencing of small non-coding RNAs in HIV-1 infected cells: evidence for the processing of a viral-cellular double-stranded RNA hybrid. *Nucleic Acids Res*, 37, 6575-86. ↗

Editions

2020-11-29	Authored, Edited	May, B.
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