

Unknown nuclease cleaves cleaved transposon RNA bound in MeR-PIWIL4:cleaved transposon RNA:TDRD9:MAEL:TDRKH

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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: 77

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

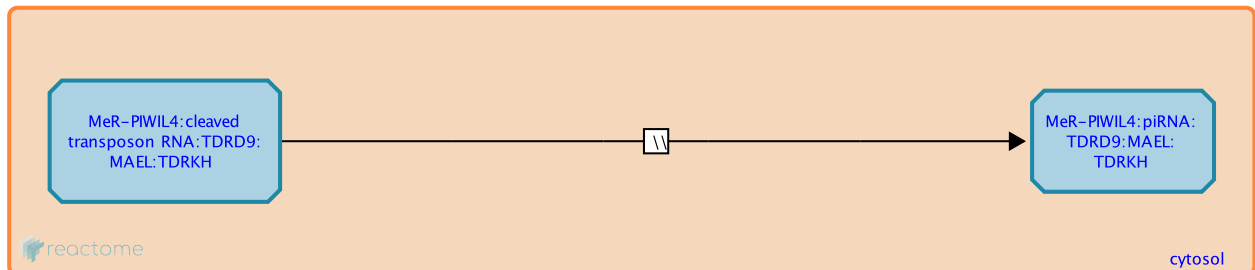
Unknown nuclease cleaves cleaved transposon RNA bound in MeR-PIWIL4:cleaved transposon RNA:TDRD9:MAEL:TDRKH ↗

Stable identifier: R-HSA-5601919

Type: omitted

Compartments: cytosol

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After the cleaved RNA binds PIWIL4 the 3' end is trimmed by an unknown nuclease to generate a mature piRNA.

Editions

2014-06-14	Authored, Edited	May, B.
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