

TRMT44 2'-O-methylates uridine-44 in tRNA(Ser)

Jarrous, N., Levinger, L., May, B., Motorin, Y.

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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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467.

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Reactome database release: 77

This document contains 1 reaction (see Table of Contents)

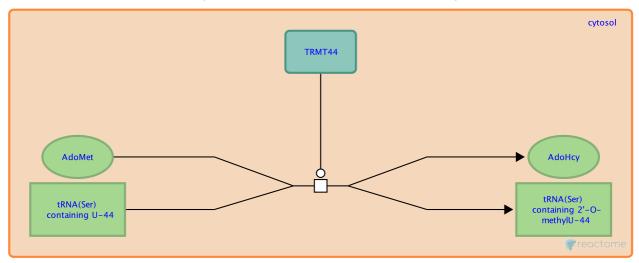
https://reactome.org Page 1

Stable identifier: R-HSA-6788707

Type: transition

Compartments: cytosol

Inferred from: TRM44 2'-O-methylates uridine-44 in tRNA(Ser) (Saccharomyces cerevisiae)



As inferred from the yeast homolog, TRMT44 methylates the 2' hydroxyl group of uridine-44 in tRNA(Ser). In yeast 2'-O-methyluridine-44 together with N(4)-acetylcytidine appears to be required to maintain abundance of tRNA(Ser).

Editions

2015-07-23	Authored, Edited	May, B.
2015-08-11	Reviewed	Levinger, L.
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