tRNA modification in the nucleus and cytosol

Alkuraya, FS., Bohnsack, MT., Jarrous, N., Levinger, L., May, B., Motorin, Y., Phizicky, EM.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of Creative Commons Attribution 4.0 International (CC BY 4.0) License. For more information see our license.
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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references


Reactome database release: 72

This document contains 2 pathways and 29 reactions (see Table of Contents)

https://release.reactome.org
At least 92 distinct tRNA nucleotide base modifications have been found. The modifications are made post-transcriptionally by a large group of disparate enzymes located in the nucleus, cytosol, and mitochondria (reviewed in Boschi-Muller and Motorin 2013, Jackman and Alfonzo 2013, Gu et al. 2014, Helm and Alfonzo 2014, Li and Mason 2014). Modifications near the anticodon and near the 3' end affect interaction of the tRNA with ribosomes and tRNA synthetases, respectively, while modifications in other regions of the tRNA affect folding and stability of the tRNA (reviewed in Hou et al. 2015). Mutations in tRNA modification enzymes are associated with human diseases (reviewed in Sarin and Leidel 2014, Torres et al. 2014).

**Literature references**


### Editions

<table>
<thead>
<tr>
<th>Date</th>
<th>Action</th>
<th>Author</th>
</tr>
</thead>
<tbody>
<tr>
<td>2015-05-30</td>
<td>Authored, Edited</td>
<td>May, B.</td>
</tr>
<tr>
<td>2015-08-11</td>
<td>Reviewed</td>
<td>Levinger, L.</td>
</tr>
<tr>
<td>2015-08-25</td>
<td>Reviewed</td>
<td>Motorin, Y.</td>
</tr>
<tr>
<td>2015-10-24</td>
<td>Reviewed</td>
<td>Jarrous, N.</td>
</tr>
</tbody>
</table>
ADAT1 deaminates adenosine-37 in tRNA(Ala)

**Location:** tRNA modification in the nucleus and cytosol

**Stable identifier:** R-HSA-6782336