Hypusine synthesis from eIF5A-lysine

D'Eustachio, P., Jassal, B., Johansson, HE.

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.

18/03/2022
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: 79

This document contains 1 pathway and 3 reactions (see Table of Contents)
Cytosolic eukaryotic translation initiation factor 5A (eIF5A) undergoes a unique two-step post-translational modification at Lys 50 via deoxyhypusine (Dhp) to hypusine (Hyp). In the first step deoxyhypusine synthase transfers the aminobutyl group of spermidine to the epsilon-amino group of lysine 50, using NAD+ as a cofactor. Hydroxylation of the C2 of the newly added moiety in the second step is catalyzed by deoxyhypusine hydroxylase/monooxygenase with molecular oxygen as the source. The molecular function of eIF5A is unknown, but the protein is required for viability in eukaryotic cells and its normal function requires hypusinylation. eIF5A is the only protein known to undergo hypusinylation (Park 2006).

**Literature references**


**Editions**

<table>
<thead>
<tr>
<th>Date</th>
<th>Action</th>
<th>Author</th>
</tr>
</thead>
<tbody>
<tr>
<td>2007-11-29</td>
<td>Edited</td>
<td>D'Eustachio, P.</td>
</tr>
<tr>
<td>2007-11-29</td>
<td>Authored</td>
<td>Johansson, HE.</td>
</tr>
<tr>
<td>2008-01-28</td>
<td>Reviewed</td>
<td>Jassal, B.</td>
</tr>
</tbody>
</table>
DHPS tetramer synthesizes Dhp-K50-EIF5A from EIF5A and spermidine

Location: Hypusine synthesis from eIF5A-lysine

Stable identifier: R-HSA-204647