

Internal Methylation of mRNA

Joshi-Tope, G.

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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Reactome database release: 88

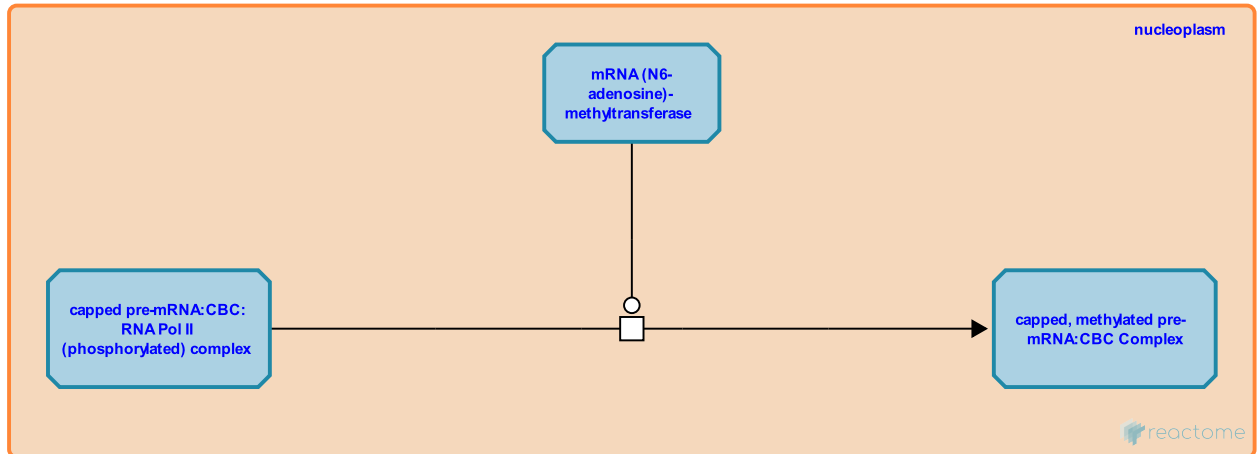
This document contains 1 reaction ([see Table of Contents](#))

Internal Methylation of mRNA [↗](#)

Stable identifier: R-HSA-72095

Type: transition

Compartments: nucleoplasm



In addition to the methylation of the 5'-cap, there is methylation of internal nucleotides in the mRNA. This methylation can occur in translated and untranslated regions. One to three methyl groups have been seen per mRNA molecule, but methylation is non-stoichiometric. The most frequent methylation observed is at the N6 position of adenosine. The function of mRNA internal methylation, if any, is unknown.

Literature references

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Editions

2024-03-06

Edited

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