nsp14 acts as a cap N7 methyltransferase to modify SARS-CoV-2 mRNAs

Acencio, ML., Orlic-Milacic, M.
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


Reactome database release: 77

This document contains 1 reaction (see Table of Contents)
nsp14 acts as a cap N7 methyltransferase to modify SARS-CoV-2 mRNAs

Stable identifier: R-HSA-9694476

Type: omitted

Compartments: cytosol, double membrane vesicle viral factory outer membrane

Diseases: COVID-19

Inferred from: nsp14 acts as a cap N7 methyltransferase to modify SARS-CoV-1 mRNAs (Homo sapiens)

This COVID-19 event has been created by a combination of computational inference (see https://reactome.org/documentation/inferred-events) from SARS-CoV-1 data and manual curation, as described in the summation for the overall SARS-CoV-2 infection pathway.

The genomic and subgenomic (sg) mRNAs of SARS-CoV-1 coronavirus are presumed to be capped at their 5' end, based on studies of the mouse hepatitis virus (MHV) (Lai and Stohlman 1981) and the equine torovirus (van Vliet et al. 2002). Non-structural protein 14 (nsp14) acts as an RNA guanine-N7-methyltransferase (N7-MTase) that completes the synthesis of the cap-0 on SARS-CoV-1 mRNAs. The cap-0 represents N7-methyl guanosine connected to the 5' nucleotide through a 5' to 5' triphosphate linkage, and is also known as m7G cap or m7Gppp cap. The N7-MTase domain maps to the carboxy-terminal part of nsp14 (Chen et al. 2009). Cap-0 formation requires three sequential reactions catalyzed by RNA triphosphatase (TPase), guanylyltransferase (GTase), and N7-MTase. There is no evidence that nsp14 possesses TPase and GTase activities, and no other SARS-CoV-1 proteins with these activities have been identified, so the identities of the enzymes that mediate these required steps remain unknown. Based on the study of the human coronavirus 229E, non-structural protein 13 (nsp13) may have a TPase activity in addition to its established helicase activity (Ivanov and Ziebuhr 2004).

Editions

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