Polyadenylation of SARS-CoV-2 subgenomic mRNAs (plus strand)

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26/09/2021
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: 77

This document contains 1 reaction (see Table of Contents)

https://reactome.org
Polyadenylation of SARS-CoV-2 subgenomic mRNAs (plus strand)

Stable identifier: R-HSA-9694733

Type: omitted

Compartments: cytosol

Diseases: COVID-19

SARS-CoV-2 transcripts are polyadenylated (Ravindra et al. 2020, Kim et al. 2020), similar to their SARS-CoV-1 counterparts. SARS-CoV-2 subgenomic RNAs (sgRNAs) carry poly(A) tails of the median length of 47 nucleotides. The poly(A) tails of sgRNAs of SARS-CoV-2 are shorter than the poly(A) tails of the full-length SARS-CoV-2 genomic RNA (Kim et al. 2020).

SARS-CoV-1 plus strand sgRNAs share a 3'UTR with the plus strand genomic RNA, and as this 3'UTR possesses a polyadenylation signal, they undergo polyadenylation by an undetermined viral RNA polymerase, possibly nsp8 or nsp12 (Spagnolo and Hogue 2000, Peng et al. 2016, Tvarogova et al. 2019).

Literature references


Editions

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