

Synthesis of SARS-CoV-2 plus strand sub-genomic mRNAs

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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](#))

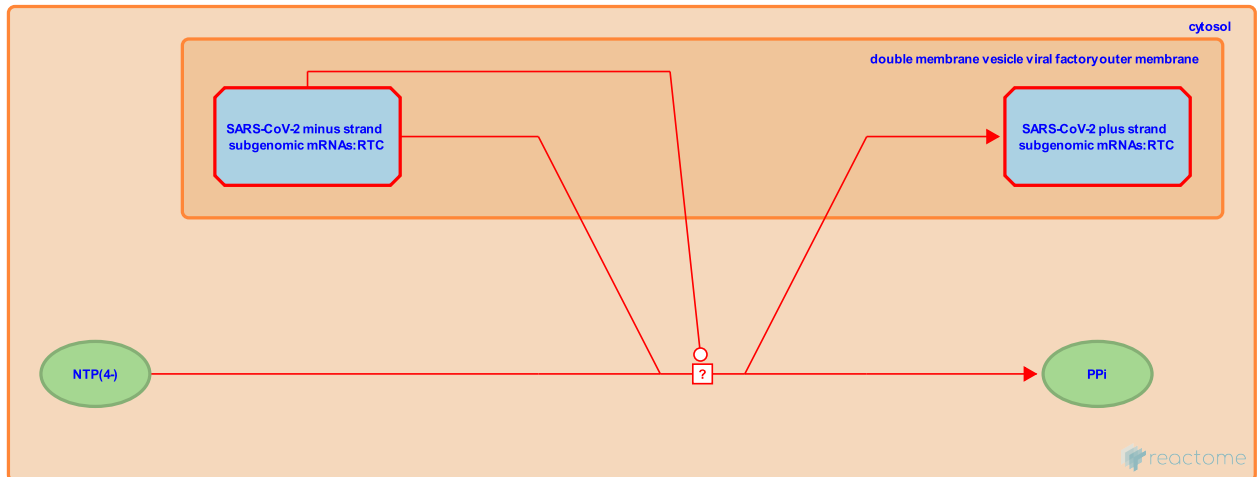
Synthesis of SARS-CoV-2 plus strand subgenomic mRNAs ↗

Stable identifier: R-HSA-9694506

Type: uncertain

Compartments: cytosol, double membrane vesicle viral factory outer membrane

Diseases: COVID-19



SARS-CoV-2 produces nine subgenomic RNAs (sgRNAs). N protein-encoding mRNA (mRNA9) is most abundantly expressed, followed by mRNAs encoding proteins S (mRNA2), 7a (mRNA7a), 3a (mRNA3), 8 (mRNA8), M (mRNA5), E (mRNA4), 6 (mRNA6) and 7b (mRNA7b) (Kim et al. 2020).

SARS-CoV-1 encodes eight subgenomic RNAs, mRNA2 to mRNA9. mRNA1 corresponds to the genomic RNA. mRNA2 encodes the S protein. mRNA3 is bicistronic and encodes proteins 3a and 3b. mRNA4 encodes the E protein. mRNA5 encodes the M protein. mRNA6 encodes the protein 6. mRNA7, mRNA8 and mRNA9 are bicistronic, with mRNA7 encoding proteins 7a and 7b, mRNA8 encoding proteins 8a and 8b, and mRNA 9 encoding proteins 9a and N. The 5' and 3' ends of subgenomic RNAs are identical, in accordance with the template switch model of coronavirus RNA transcription (Snijder et al. 2003, Thiel et al. 2003, Yount et al. 2003). Based on studies of the murine hepatitis virus (MHV), which is closely related to SARS-CoV-1, positive-sense virus mRNAs are present at much higher amounts than negative-sense mRNAs (Irigoyen et al. 2016).

Literature references

Kim, JW., Kim, D., Lee, JY., Yang, JS., Chang, H., Kim, VN. (2020). The Architecture of SARS-CoV-2 Transcriptome. *Cell*, 181, 914-921.e10. ↗

Editions

2020-08-12	Authored	Orlic-Milacic, M., Senff-Ribeiro, A.
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