Replication transcription complex binds SARS-CoV-2 genomic RNA

Acencio, ML., Orlic-Milacic, M., Senff-Ribeiro, A.
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)
Replication transcription complex binds SARS-CoV-2 genomic RNA

Stable identifier: R-HSA-9694454

Type: binding

Compartments: cytosol, double membrane vesicle viral factory outer membrane

Diseases: COVID-19

The cryo-electron microscopy (cryoEM) structure of the SARS-CoV-2 replication transcription complex (RTC) components nsp7, nsp8 and nsp12, bound to more than two turns of RNA template-product duplex, indicates that the active cleft of nsp12 binds to the first turn of RNA, while two copies of nsp8 bind to opposite sides of the cleft and position the second turn of RNA. Long helical extensions in nsp8 protrude along exiting RNA, forming positively charged "sliding poles". These sliding poles may confer processivity to the RTC (Hillen et al. 2020). Binding of nsp12 to the template RNA is markedly increased by the presence of nsp7 and nsp8 (Yin et al. 2020). Notable structural rearrangements occur in nsp12, nsp8 and nsp7 to accommodate the RNA (Wang et al. 2020).

Based on studies in SARS-CoV-1, the RTC binds to the 3' end of the viral plus strand genomic RNA to initiate synthesis of the complementary minus strand. A 36 nucleotide sequence from the 3'-UTR of the plus strand, predicted to form a stable stem-loop structure, seems to be the minimal cis-acting RNA element required for the viral RNA-directed RNA polymerase (nsp12) to initiate RNA synthesis. The polyA tail also seems to play a role in the initiation of replication of viral genomic RNA (Ahn et al. 2012).

Literature references


Editions

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<tr>
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