Encapsidation of SARS coronavirus genomic RNA

Acencio, ML., Rothfels, K.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of Creative Commons Attribution 4.0 International (CC BY 4.0) License. For more information see our license.

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
Encapsidation of SARS coronavirus genomic RNA

Stable identifier: R-HSA-9694281

Type: binding

Compartments: endoplasmic reticulum-Golgi intermediate compartment membrane, cytosol

Diseases: COVID-19

Inferred from: Encapsidation of SARS coronavirus genomic RNA (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.

Based on studies in other coronaviruses, the final SARS-COV-2 ribonucleoprotein complex is predicted to be a hollow helical structure with an approximate diameter of 9-16nm, with the C-terminal domain of N protein forming the inner core and the N-terminal domain forming the outer surface (Neuman et al, 2006; Chen et al, 2007). Oliomerization of the N protein capsid coat is likely nucleated through both protein-RNA and protein-protein interactions by the first few N-protein dimers on the genomic RNA (Saikatendu et al, 2007; Chang et al, 2013; reviewed in Chang et al, 2014). Each N dimer may make contact with up to 7 bases of the RNA (reviewed in Chang et al, 2014).

Literature references


Editions

<table>
<thead>
<tr>
<th>Date</th>
<th>Author/Editor</th>
</tr>
</thead>
<tbody>
<tr>
<td>2020-07-30</td>
<td>Authored, Edited</td>
</tr>
<tr>
<td>2020-09-09</td>
<td>Reviewed</td>
</tr>
</tbody>
</table>

Rothfels, K.

Acencio, ML.