Endocytosis of SARS-CoV-2 Virion

Acencio, ML., Gillespie, ME.

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

25/08/2021

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

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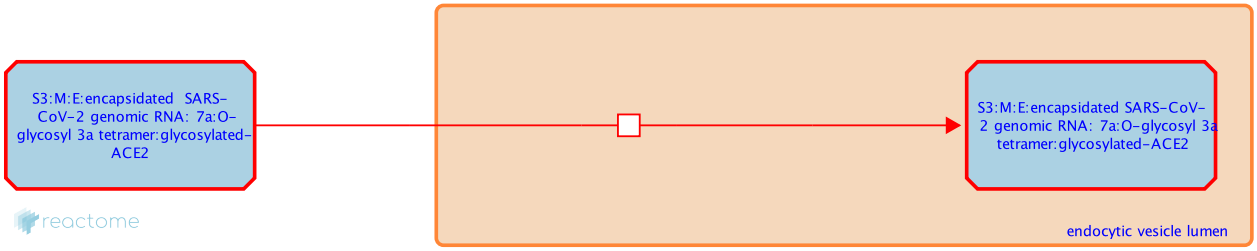
Stable identifier: R-HSA-9697423

Type: transition

Compartments: endocytic vesicle lumen

Diseases: COVID-19

Inferred from: Endocytois of SARS-CoV-1 Virion (Homo sapiens)



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

Based on SARS-CoV-1 experiments, SARS-CoV-2 virions attached to the host cell surface via a complex involving viral spike (S) protein and host angiotensin-converting enzyme 2 (ACE2) are inferred to undergo endocytosis. In the case of SARS-CoV-1, studies with pseudoviruses have established that S protein is necessary and sufficient for mediating viral attachment and entry. Inhibition of this SARS-CoV-1 S protein-mediated transduction by two different classes of lysosomotropic agents in multiple cell lines strongly suggests that acidification of endosomes is needed for viral entry (Hofmann et al. 2004; Simmons et al. 2004; Yang et al. 2004). The roles of S protein in viral binding to the host cell membrane and fusion of viral and host cell membranes and thus the central role of S protein in determining the host range and tissue tropisms of the virus are reviewed by Belouzard et al. (2012).

Literature references

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Editions

2020-09-05	Edited	Gillespie, ME.
2020-09-09	Reviewed	Acencio, ML.
2020-09-09	Authored	Gillespie, ME.