

Recruitment of Spike trimer to assembling virion

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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](#))

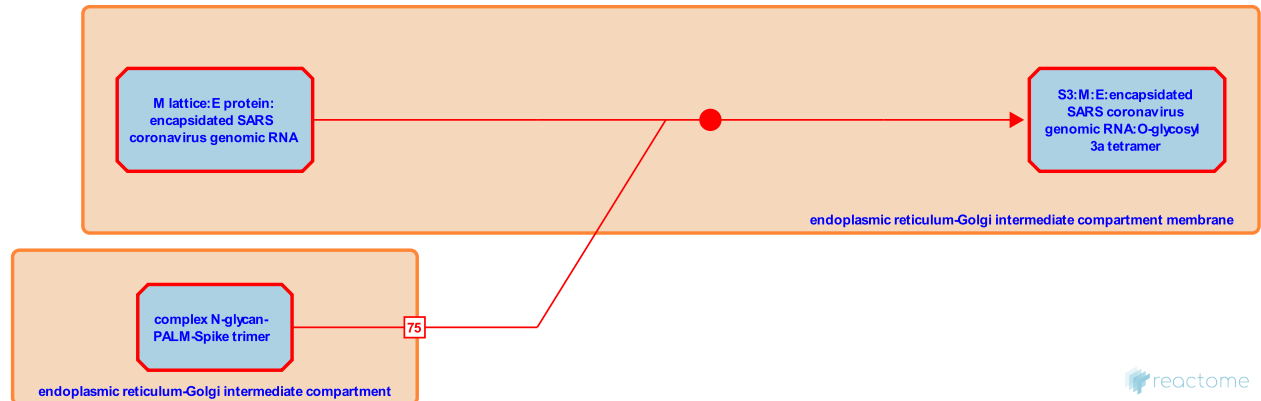
Recruitment of Spike trimer to assembling virion ↗

Stable identifier: R-HSA-9684241

Type: binding

Compartments: endoplasmic reticulum-Golgi intermediate compartment membrane

Diseases: severe acute respiratory syndrome



S trimers are recruited to the assembling virion through interaction with M protein (reviewed in Ujike and Taguchi, 2015). Multiple regions of M contribute to the recruitment of S, with a single tyrosine residue in the C-terminal domain of M playing a critical role (McBride et al, 2010a; Hsieh et al, 2008). Interaction with M is aided by a dibasic motif in the C-terminus of S, which promotes retrieval of the spike protein from the cell surface by binding the COPI coat (McBride et al, 2007; Ujike et al, 2016). Palmitoylation of the C-terminus of S appears dispensable for the interaction with M in SARS-COV-1, unlike the case in other coronaviruses (Ujike et al, 2012; McBride 2010b; reviewed in Ujike and Taguchi, 2015). Size estimates and modelling suggest the mature virion has approximately 300 S trimers (Neuman et al, 2006; reviewed in Chang et al, 2014).

Literature references

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Editions

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