Spike glycoprotein of SARS-CoV-2 binds ACE2 on host cell

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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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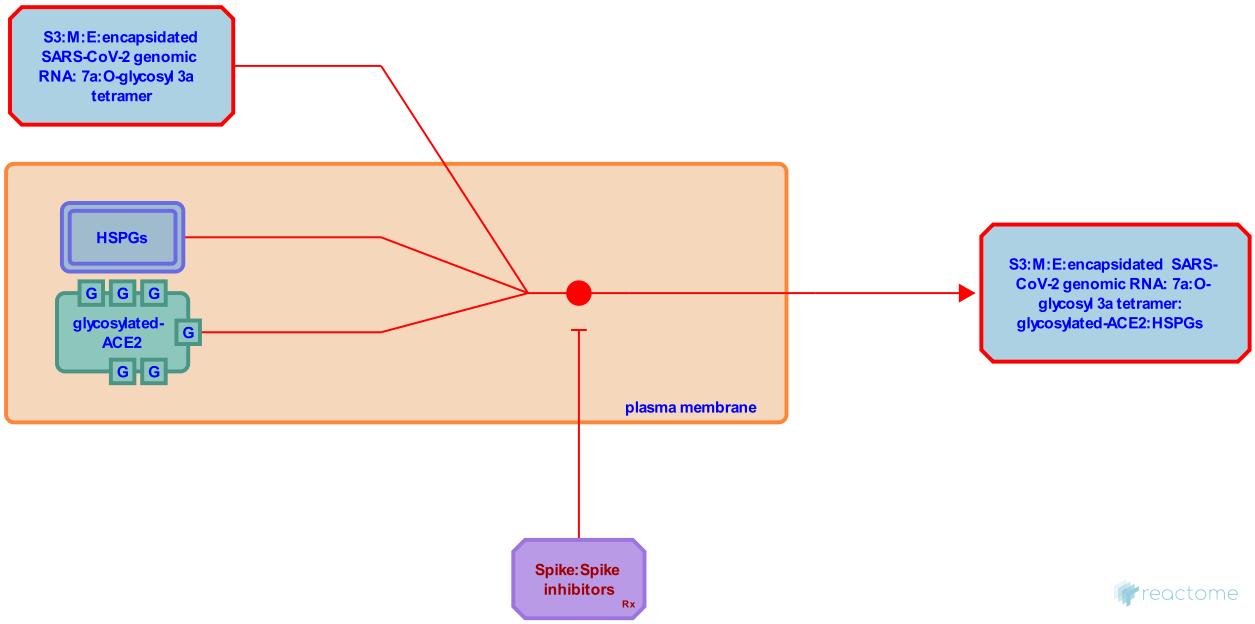
Stable identifier: R-HSA-9694579

Type: binding

Compartments: plasma membrane

Diseases: COVID-19



SARS-CoV-2 spike protein trimer (S3), as a component of the S3:M:E:encapsidated SARS coronavirus-2 genomic RNA: 7a:O-glycosyl 3a tetramer complex, binds to glycosylated angiotensin converting enzyme 2 (ACE2) associated with the human host cell plasma membrane (Zhang et al, 2020; Raghuvamsi et al, 2021; reviewed by Jackson et al, 2022). Glycosylation of both molecules is the most important factor in their interaction (reviewed by Reis et al, 2021; Shajahan et al, 2021; Gong et al, 2021). Spike binding to ACE2 also requires the presence of heparan sulfate (HS) on the cell surface, consistent with the formation of a ternary complex between S, ACE2, and heparan sulfate proteoglycans (HSPGs) (Kim et al, 2020; Zhang et al, 2020; Clausen et al, 2021; Liu et al, 2021; Yue et al, 2021; Bermejo-Jambrina et al, 2021).

In SARS-CoV-1 structural studies of the interaction between human ACE2 protein and the receptor-binding domain of S3 protein have identified key amino acid residues in both proteins responsible for their high-affinity interaction. These residues may be a key factor determining severity (and possibly human-to-human transmission) of SARS-CoV-1 (Li et al. 2003, 2005). 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) and Jackson et al. (2022).

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Editions

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