E protein gets N-glycosylated

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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


Reactome database release: 77

This document contains 1 reaction (see Table of Contents)
E protein gets N-glycosylated

Stable identifier: R-HSA-9694790

Type: omitted

Compartments: endoplasmic reticulum lumen

Diseases: COVID-19

Inferred from: E protein gets N-glycosylated (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.

A minor proportion of the E protein is modified by N-linked glycosylation. This variant appears to be more likely to form multimers, and it shows a different membrane topology than the main variant (Yuan et al, 2006).

Literature references


Editions

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