nsp14 binds nsp12

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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)
**nsp14 binds nsp12**

**Stable identifier:** R-HSA-9694304

**Type:** binding

**Compartments:** cytosol

**Diseases:** COVID-19

**Inferred from:** nsp14 binds nsp12 (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.

Non-structural protein 14 (nsp14) of the human SARS coronavirus is a bifunctional enzyme bearing 3'-5' exoribonuclease activity involved in replication fidelity and RNA cap N7-guanine methyltransferase activity involved in 5'-RNA capping. nsp14 binds to the minimal replication and transcription complex (RTC), composed of nsp7, nsp8, and nsp12, by directly binding to nsp12 (the main RNA-dependent RNA polymerase). Binding of nsp14 does not affect the processivity of the RTC (Minskaia et al. 2006, Subissi et al. 2014).

**Editions**

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