ZCRB1 binds 5'UTR of SARS-CoV-2 genomic RNA

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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)
ZCRB1 binds 5'UTR of SARS-CoV-2 genomic RNA

**Stable identifier:** R-HSA-9694677

**Type:** binding

**Compartments:** cytosol

**Diseases:** COVID-19

**Inferred from:** ZCRB1 binds 5'UTR of SARS-CoV-1 genomic RNA (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.

Human zinc finger CCHC-type and RNA-binding motif-containing protein 1 (ZCRB1, also known as MADP1) binds to the 5'UTR of the plus strand genomic RNA of the SARS-CoV-1, as well as other coronaviruses, infectious bronchitis virus (IBV) and human coronavirus OC43. ZCRB1 normally localizes to the nucleus, where it is a component of the U12-type spliceosome. Upon infection with a coronavirus, ZCRB1 appears in the cytosol. Binding of ZCRB1 to the 5'UTR stem of coronavirus genomic RNA is thought to be necessary for efficient transcription of viral genes (Tan et al. 2012).

**Literature references**


**Editions**

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