mRNA1 is translated to pp1a

Acencio, ML., Stephan, R.
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)
mRNA1 is translated to pp1a

Stable identifier: R-HSA-9694334

Type: omitted

Compartments: cytosol

Diseases: COVID-19

Inferred from: mRNA1 is translated to pp1a (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.

In most translation attempts the genomic viral mRNA1 in the cytosol is translated to a shortened polyprotein, pp1a, that does not contain genome replication enzymes (Baranov et al, 2005).

Literature references


Editions

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