nsp12 misincorporates a nucleotide in nascent RNA minus strand

Acencio, ML., Orlic-Milacic, M.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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26/09/2021
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)

https://reactome.org
**nsp12 misincorporates a nucleotide in nascent RNA minus strand**

**Stable identifier:** R-HSA-9694792

**Type:** omitted

**Compartments:** cytosol, double membrane vesicle viral factory outer membrane

**Diseases:** COVID-19

**Inferred from:** nsp12 misincorporates a nucleotide in nascent RNA minus strand (Homo sapiens)

This COVID-19 event has been created by a combination of computational inference (see [https://reactome.org/documentation/inferred-events](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 the presence of functional nsp14, which acts as a 3'-to-5' exonuclease, the mutation rate during human SARS coronavirus 1 (SARS-CoV-1) replication is $9 \times 10^{-7}$ (9E-7) per nucleotide per replication cycle or $2.2 \times 10^{-5}$ (2.2E-5) non-redundant substitutions per nucleotide, which translates into 2-3 nucleotide substitutions for each replicated SARS-CoV-1 genome. When nsp14 is defective, the mutation rate during SARS-CoV-1 replication increases to $1.2 \times 10^{-5}$ (1.2E-5) mutations per nucleotide per replication cycle or $3.34 \times 10^{-4}$ (3.34E-4) non-redundant substitutions per nucleotide, which translates into 12-23 nucleotide substitutions for each replicated SARS-CoV-1 genome (Eckerle et al. 2010). Here the process is annotated in two steps, nsp12-mediated misincorporation of a base (this reaction) and nsp14-mediated detection and removal of that base (next reaction).

**Editions**

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