3CLp cleaves 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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references


Reactome database release: 77

This document contains 1 reaction (see Table of Contents)
3CLp cleaves pp1a

Stable identifier: R-HSA-9694441

Type: transition

Compartments: cytosol

Diseases: COVID-19

Inferred from: 3CLp cleaves 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.

Main protease cleaves all cleavage sites of pp1a and ppa1b starting with nsp4/5, thus cleaving itself, and all the cytosolic RTC proteins (Fan et al, 2004)

Literature references


Editions

<table>
<thead>
<tr>
<th>Date</th>
<th>Author/Editor</th>
<th>Reviewer</th>
</tr>
</thead>
<tbody>
<tr>
<td>2020-08-28</td>
<td>Authored, Edited</td>
<td>Stephan, R.</td>
</tr>
<tr>
<td>2020-09-09</td>
<td>Reviewed</td>
<td>Acencio, ML.</td>
</tr>
</tbody>
</table>