nsp8 binds MAP1LC3B

Acencio, ML., Varusai, TM.
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)
**nsp8 binds MAP1LC3B**

**Stable identifier:** R-HSA-9694580

**Type:** omitted

**Compartments:** cytosol

**Diseases:** COVID-19

**Inferred from:** nsp8 binds MAP1LC3B (Homo sapiens)

This COVID-19 event has been created by a combination of computational inference from SARS-CoV-1 data (https://reactome.org/documentation/inferred-events) and manual curation, as described in the summation for the overall SARS-CoV-2 infection pathway.

The replicase polyprotein 1a of the human severe acute respiratory syndrome coronavirus is post-translationally cleaved by virally encoded proteases to generate non-structural proteins (nsps). Viral nsps induce the formation of ER-bound double membrane vesicles (DMV) in host cells post infection. These DMVs are decorated with host microtubule-associated proteins 1A/1B light chain 3B (MAP1LC3B) proteins that are involved in autophagosome formation. However, there is no evidence that DMVs are recruited to the autophagy machinery. Immunofluorescence studies show that nsp8 colocalizes with MAP1LC3B suggesting a binding event (Prentice E. et al 2004).

**Literature references**


**Editions**

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