8b binds MAP1LC3B

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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

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

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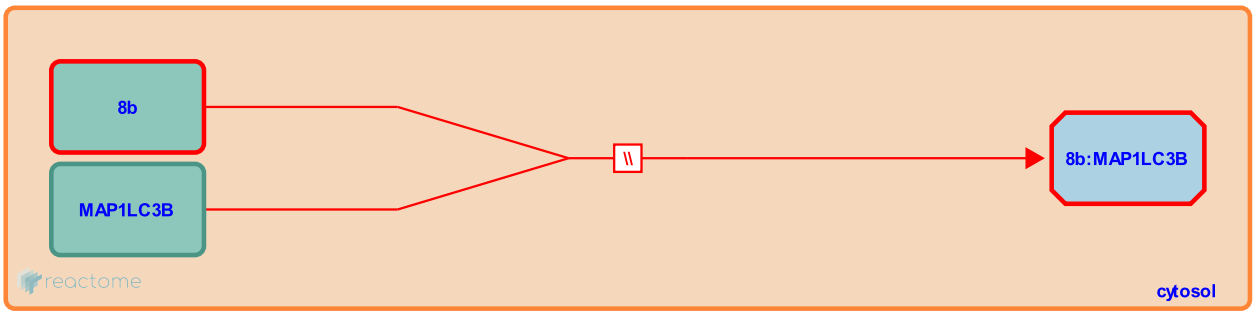
Stable identifier: R-HSA-9687109

Type: omitted

Compartments: cytosol

Diseases: severe acute respiratory syndrome



It is known that non-structural proteins (nsp) in SARS-CoV viruses induce the formation of ER-bound double membrane vesicles (DMV) in host cells post infection. These DMVs are decorated with 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. Studies show that in some cells sars8b (8b) colocalizes with MAP1LC3B. However, little is known about underlying molecular mechanisms (Shi C S. et al 2019).

Literature references

Shi, CS., Kehrl, JH., Huang, NN., Nabar, NR. (2019). SARS-Coronavirus Open Reading Frame-8b triggers intracellular stress pathways and activates NLRP3 inflammasomes. *Cell Death Discov, 5*, 101.

Editions

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