

SecA2 transports SapM from cytoplasm to cytosol

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https://reactome.org

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

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

Reactome database release: 88

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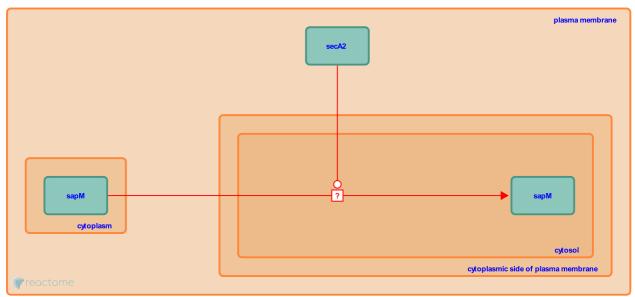
SecA2 transports SapM from cytoplasm to cytosol **₹**

Stable identifier: R-HSA-9636375

Type: uncertain

Compartments: cytosol

Diseases: tuberculosis



Mtb protein translocase subunit (SecA2) transports phosphatidylinositol-3-phosphatase (SapM) from Mtb's cytosol (called cytoplasm here) to the host's cytosol (Zulauf et al. 2018).

Literature references

Braunstein, M., Sullivan, JT., Zulauf, KE. (2018). The SecA2 pathway of Mycobacterium tuberculosis exports effectors that work in concert to arrest phagosome and autophagosome maturation. *PLoS Pathog.*, 14, e1007011.

Editions

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