

Retrograde transport of internalized tetX

HC:LC:gangliosides

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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

- 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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

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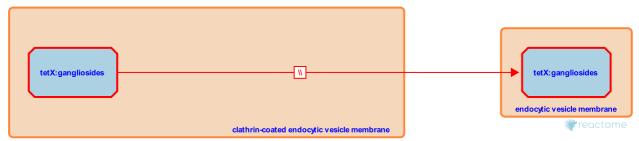
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Stable identifier: R-HSA-5228408

Type: omitted

Compartments: clathrin-coated endocytic vesicle membrane, endocytic vesicle membrane

Diseases: tetanus



Vesicles containing ganglioside-bound tetanus toxin disulfide-bonded heavy chain - light chain dimer (tetX HC:LC) are transported in a retrograde fashion away from the target cell synapse where they were formed into the cell body (Lalli et al. 2003).

Literature references

Verastegui, C., Schiavo, G., Lalli, G., Deinhardt, K., Bohnert, S. (2003). The journey of tetanus and botulinum neurotoxins in neurons. *Trends Microbiol*, 11, 431-7. ↗

Editions

2007-08-03	Reviewed	Ichtchenko, K.
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