botA HC transports botA LC from target cell synaptic vesicle membrane into cytosol

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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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *オ*

This document contains 1 reaction (see Table of Contents)

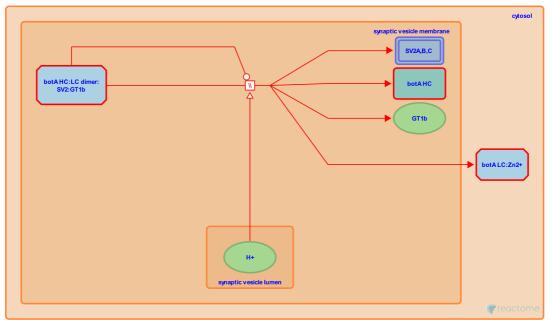
botA HC transports botA LC from target cell synaptic vesicle membrane into cytosol

Stable identifier: R-HSA-5244428

Type: omitted

Compartments: synaptic vesicle membrane, cytosol

Diseases: botulism



Acidification, a normal step in endocytosis causes a conformational change in the botulinum toxin type A disulfide bonded heavy chain - light chain heterodimer ("dichain") (botA HC:LC) it contains, allowing the HC part of the toxin to function as a channel through which its LC part is extruded into the neuronal cytosol. The HC - LC disulfide bond is cleaved (Koriazova & Montal 2003; Montal 2010). Recent studies in vitro suggest that GT1b ganglioside associated with the toxin may play a role in this process (Sun et al. 2012).

Literature references

Tepp, WH., Chapman, ER., Sun, S., Johnson, EA. (2012). Botulinum neurotoxins B and E translocate at different rates and exhibit divergent responses to GT1b and low pH. *Biochemistry*, *51*, 5655-62. *¬*

Montal, M. (2010). Botulinum neurotoxin: a marvel of protein design. Annu. Rev. Biochem., 79, 591-617. 🗷

Koriazova, LK., Montal, M. (2003). Translocation of botulinum neurotoxin light chain protease through the heavy chain channel. *Nat Struct Biol, 10,* 13-8.

Editions

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