botE HC:LC binds SV2A or B and GT1b on the target cell surface

D'Eustachio, P., Gopinathrao, G., Ichtchenko, K., Krupa, S., Sharma, S., Thirunavukkarasu, N.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

03/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. ↗

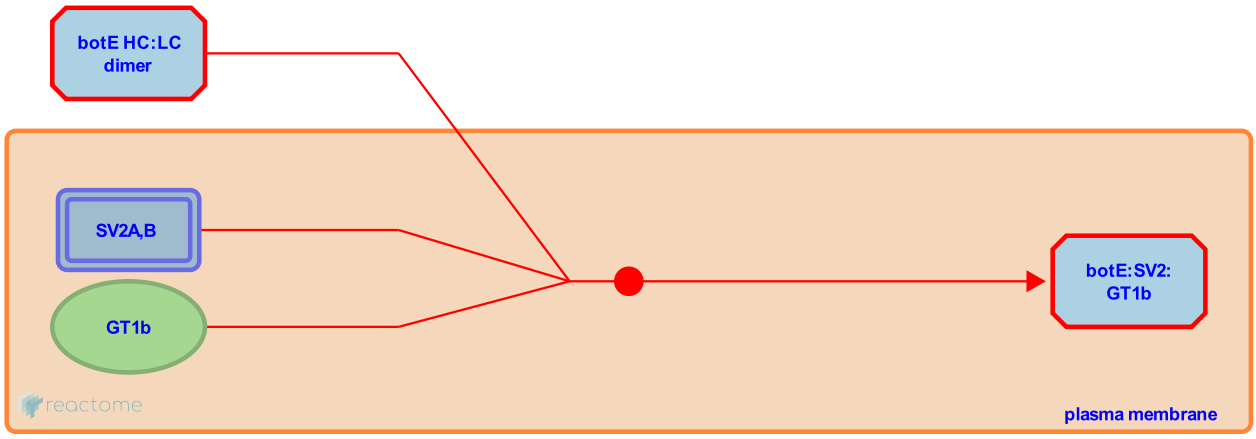
botE HC:LC binds SV2A or B and GT1b on the target cell surface ↗

Stable identifier: R-HSA-5244503

Type: binding

Compartments: extracellular region, plasma membrane

Diseases: botulism



The Botulinum toxin type E disulfide bonded heavy chain - light chain heterodimer (botE HC:LC, encoded by the C. botulinum botE gene) (Kumaran et al. 2009) binds ganglioside GT1b and synaptic vesicle protein 2A (SV2A) or 2B (SV2B) on the plasma membrane of a human target cell. In vivo, this process specifically targets synapses at neuromuscular junctions, where toxin association with ganglioside may position it to bind efficiently to SV2A or B when those proteins are exposed at the cell surface by exocytosis (Dong et al. 2008; Rummel et al. 2009).

Literature references

Mahrhold, S., Darashchonak, N., Häfner, K., Rummel, A., Holt, M., Binz, T. et al. (2009). Botulinum neurotoxins C, E and F bind gangliosides via a conserved binding site prior to stimulation-dependent uptake with botulinum neurotoxin F utilising the three isoforms of SV2 as second receptor. *J. Neurochem., 110*, 1942-54. ↗

Kumaran, D., Swaminathan, S., Sax, M., Navaza, J., Eswaramoorthy, S., Furey, WF. (2009). Domain organization in Clostridium botulinum neurotoxin type E is unique: its implication in faster translocation. *J. Mol. Biol., 386*, 233-45. ↗

Liu, H., Tepp, WH., Chapman, ER., Janz, R., Dong, M., Johnson, EA. (2008). Glycosylated SV2A and SV2B mediate the entry of botulinum neurotoxin E into neurons. *Mol. Biol. Cell, 19*, 5226-37. ↗

Editions

2006-06-15	Authored	Gopinathrao, G., Krupa, S.
2007-08-03	Reviewed	Ichtchenko, K.
2014-02-11	Revised	D'Eustachio, P.
2014-11-18	Reviewed	Sharma, S., Thirunavukkarasu, N.