

Transcytosis and dissociation of botA:NT- NHA:HA

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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

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Reactome database release: 88

This document contains 1 reaction ([see Table of Contents](#))

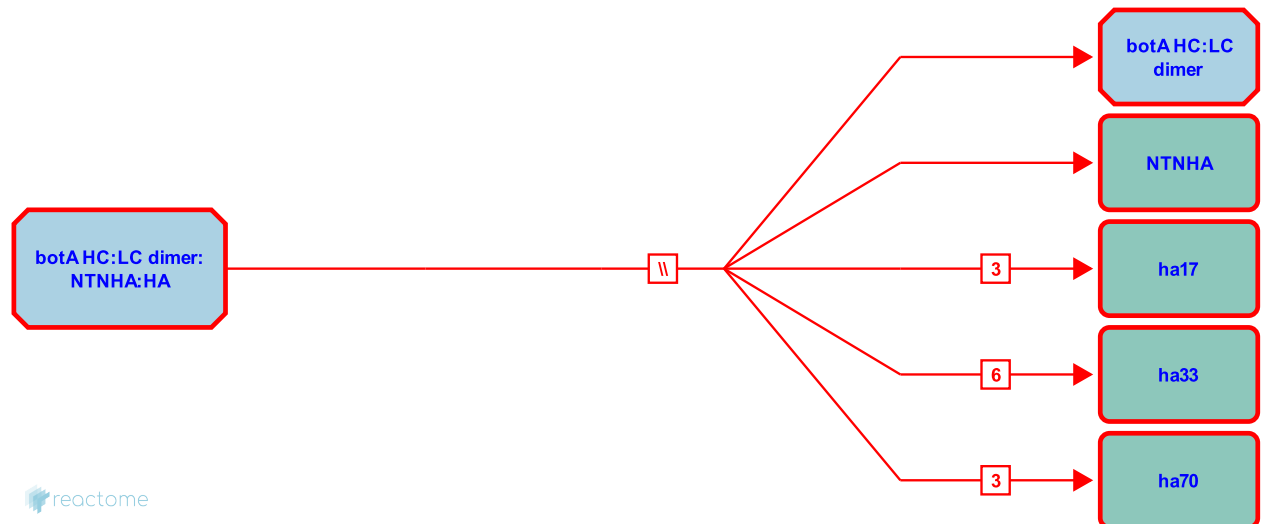
Transcytosis and dissociation of botA:NTNHA:HA [↗](#)

Stable identifier: R-HSA-5228943

Type: omitted

Compartments: extracellular region

Diseases: botulism



The bacterial botA:NTNHA:HA (BoNT/A:NTNHA:HA) complex, consisting of a Botulinum toxin type A (botA) disulfide bonded heavy chain (HC) - light chain (LC) heterodimer ("dichain") associated with nontoxic nonhemagglutinin protein (NTNHA), three molecules of hemagglutinin (ha) 17, six of ha33, and three of ha70 (Lee et al. 2013), associates with the plasma membrane of a human cell (in vivo, the apical surface of a gut epithelial cell) and undergoes transcytosis. While the molecular details of transcytosis remain to be established definitively, the process enables the toxin heterodimer to cross the epithelial cell layer and enter the circulation (Fujinaga et al. 2013; Simpson 2004).

Literature references

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Editions

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