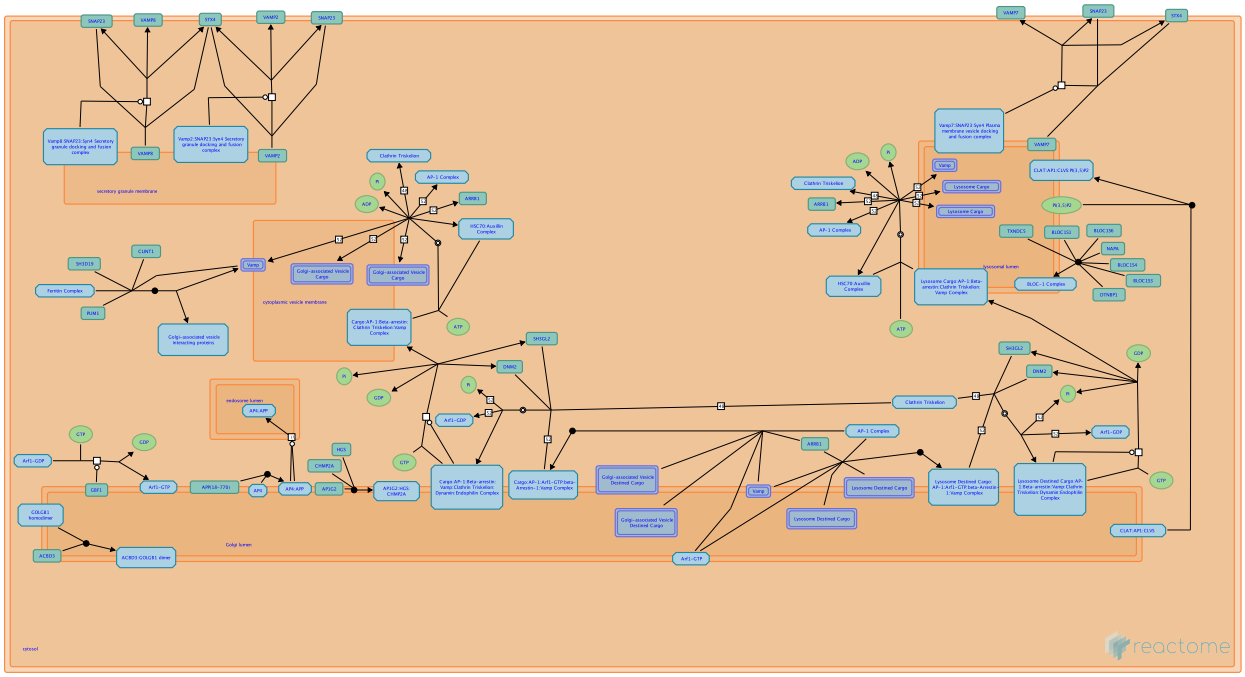
trans-Golgi Network Vesicle Budding



Gillespie, ME., Rush, MG., Simpson, JC.

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

07/09/2021

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. ↗

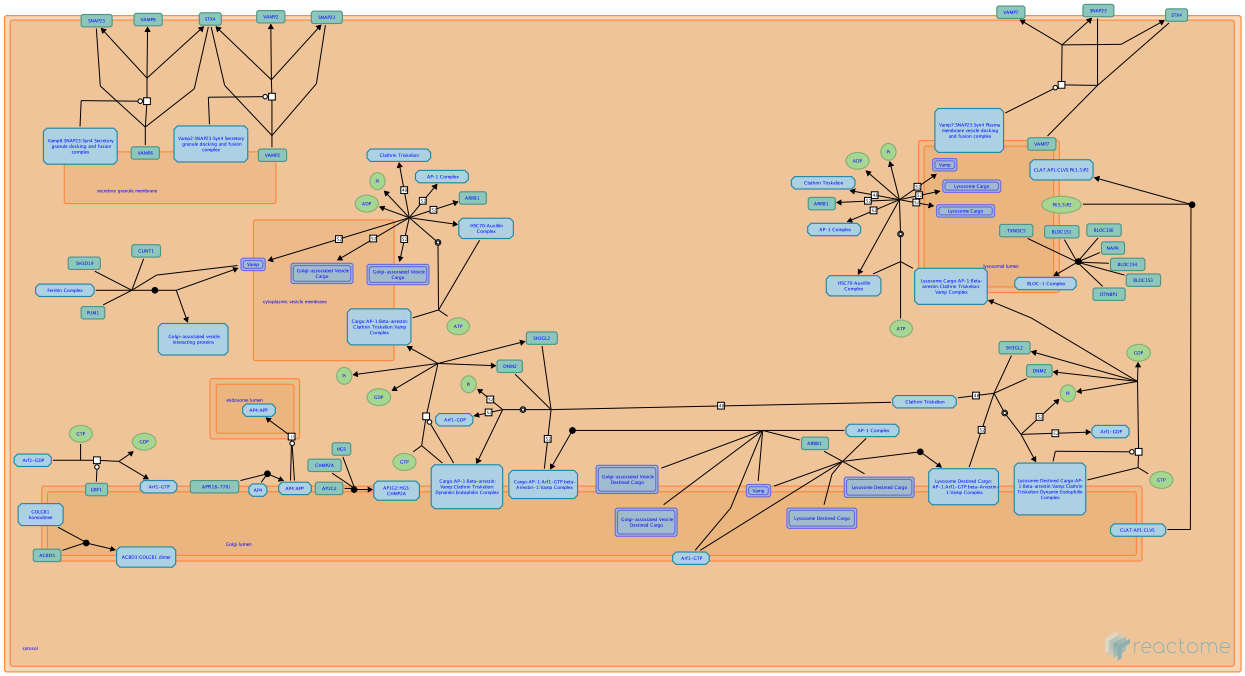
Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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 database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

trans-Golgi Network Vesicle Budding ↗

Stable identifier: R-HSA-199992



After passing through the Golgi complex, secretory cargo is packaged into post-Golgi transport intermediates (post-Golgi), which translocate plus-end directed along microtubules to the plasma membrane.

There at least two classes of clathrin coated vesicles in cells, one predominantly Golgi-associated, involved in budding from the trans-Golgi network and the other at the plasma membrane. Here the clathrin-coated vesicles emerging from the Golgi apparatus are triggered by the heterotetrameric adaptor protein complex, AP-1 at the trans-Golgi network membrane. The cargo can be transmembrane, membrane associated or golgi luminal proteins. Each step in the vesicle sculpting pathway, gathers cargo and clathrin triskeletons, until a complete vesicular sphere is formed. With the scission of the membrane the vesicle is released and eventually losses its clathrin coat.

Literature references

Kirchhausen, Tomas. (2000). Three ways to make a vesicle. *Nat Rev Mol Cell Biol, 1*, 187-98. ↗

Editions

2008-01-11	Reviewed	Rush, MG.
2008-05-22	Authored, Edited	Gillespie, ME.
2009-08-28	Reviewed	Simpson, JC.

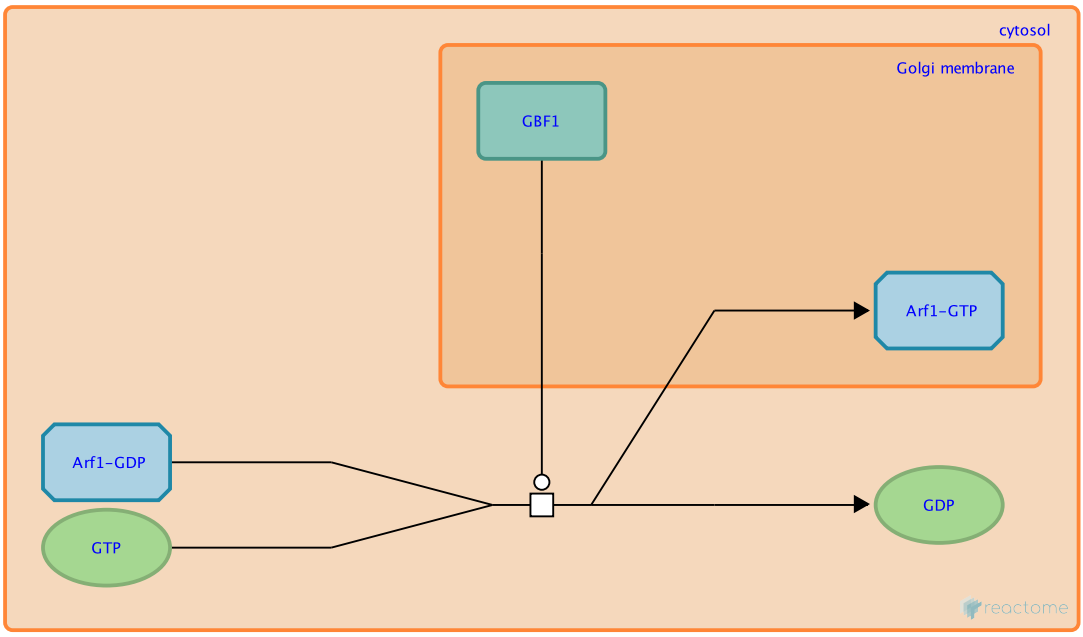
trans-Golgi Network Coat Activation ↗

Location: trans-Golgi Network Vesicle Budding

Stable identifier: R-HSA-350769

Type: transition

Compartments: cytosol



ARF1 helps to recruit AP-1 to Golgi membrane. AP-1 is not alone in this process of establishing a docking complex at the trans-Golgi Network. This section of the Golgi membrane will be where the new vesicle will be built and loaded.

Literature references

Seaman, MN., Sowerby, PJ., Robinson, MS. (1996). Cytosolic and membrane-associated proteins involved in the recruitment of AP-1 adaptors onto the trans-Golgi network. *J Biol Chem, 271*, 25446-51. ↗

Zhu, Y., Traub, LM., Kornfeld, S. (1998). ADP-ribosylation factor 1 transiently activates high-affinity adaptor protein complex AP-1 binding sites on Golgi membranes. *Mol Biol Cell, 9*, 1323-37. ↗

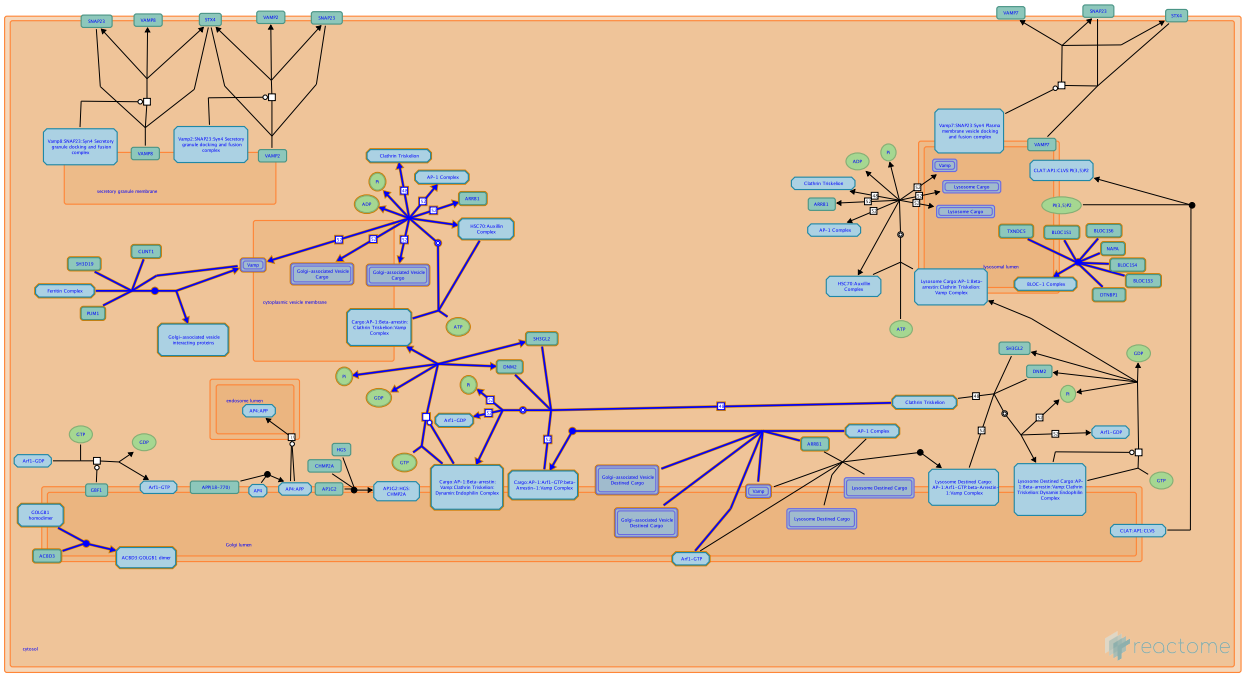
Editions

2008-01-11	Reviewed	Rush, MG.
2008-05-22	Edited	Gillespie, ME.
2009-08-27	Authored	Gillespie, ME.

Golgi Associated Vesicle Biogenesis ↗

Location: trans-Golgi Network Vesicle Budding

Stable identifier: R-HSA-432722



Proteins that have been synthesized, processed and sorted eventually reach the final steps of the secretory pathway. This pathway is responsible not only for proteins that are secreted from the cell but also enzymes and other resident proteins in the lumen of the ER, Golgi, and lysosomes as well as integral proteins transported in the vesicle membranes.

Editions

2009-08-15	Edited	Gillespie, ME.
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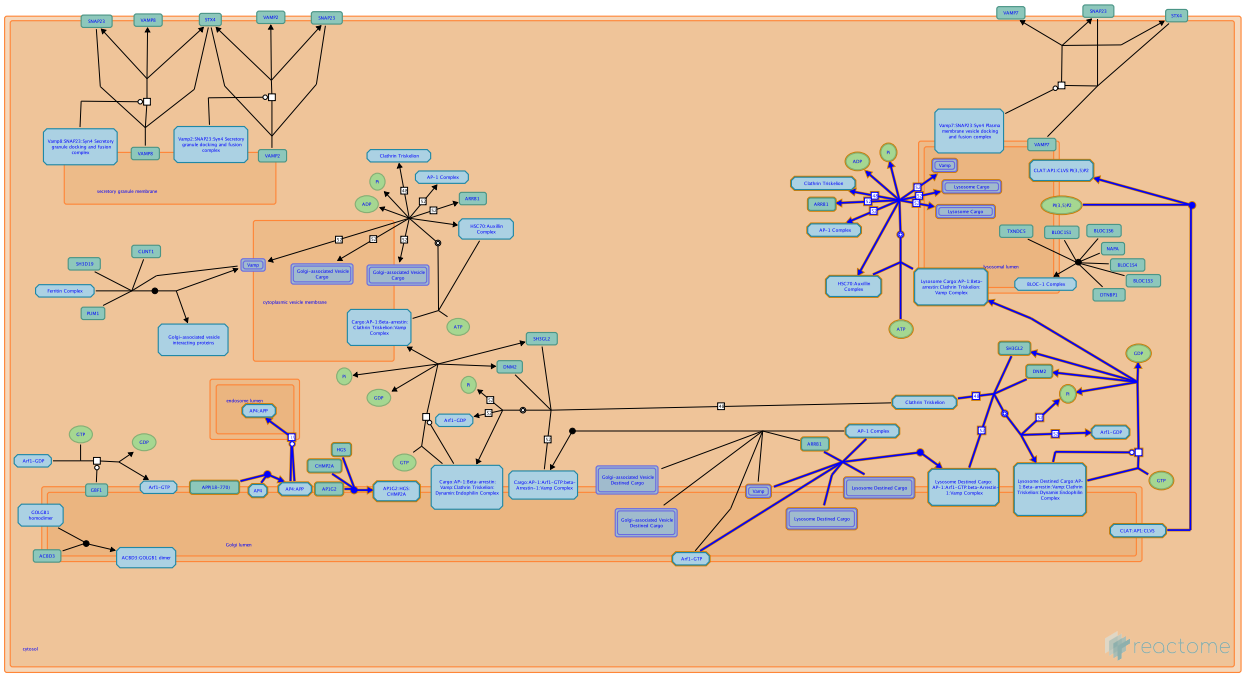
2009-08-28	Reviewed	Simpson, JC.

Lysosome Vesicle Biogenesis ↗

Location: trans-Golgi Network Vesicle Budding

Stable identifier: R-HSA-432720



Proteins that have been synthesized, processed and sorted eventually reach the final steps of the secretory pathway. This pathway is responsible not only for proteins that are secreted from the cell but also enzymes and other resident proteins in the lumen of the ER, Golgi, and lysosomes as well as integral proteins transported in the vesicle membranes. Here the proteins in this secretory pathway are ultimately found in lysososmes.

Editions

2009-08-13	Edited	Gillespie, ME.
2009-08-27	Authored	Gillespie, ME.
2009-08-28	Reviewed	Simpson, JC.

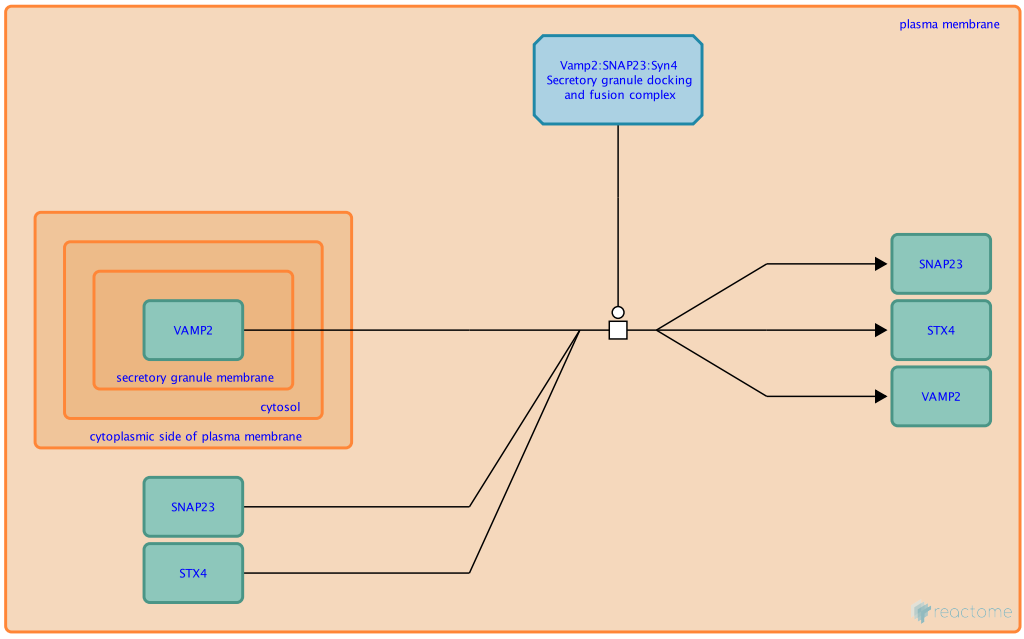
Vamp2 associated secretory vesicle to plasma membrane transport ↗

Location: trans-Golgi Network Vesicle Budding

Stable identifier: R-HSA-376369

Type: transition

Compartments: plasma membrane



The vamp2 associated vesicle docks and fuses with the plasma membrane.

Literature references

Bryant, NJ., Govers, R., James, DE. (2002). Regulated transport of the glucose transporter GLUT4. *Nat Rev Mol Cell Biol, 3*, 267-77. ↗

Editions

2008-01-11	Reviewed	Rush, MG.
2009-08-27	Authored	Gillespie, ME.

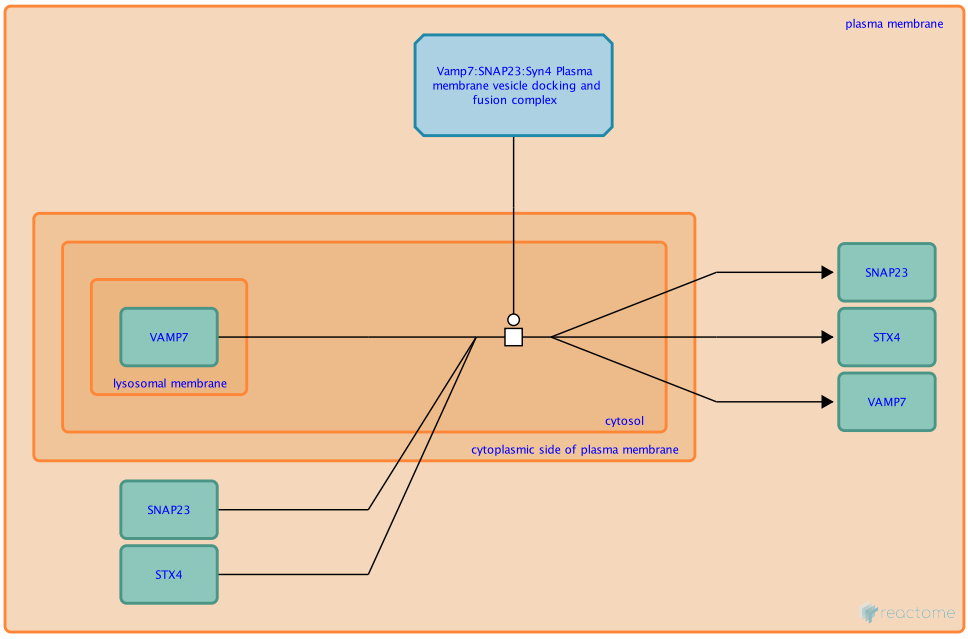
Vamp7 associated Lysosome to Plasma membrane transport ↗

Location: trans-Golgi Network Vesicle Budding

Stable identifier: R-HSA-376357

Type: transition

Compartments: cytosol



The lysosomal vesicle is targeted to and fused with the plasma membrane, releasing its contents into the extracellular space.

Literature references

Antonin, W., Holroyd, C., Fasshauer, D., Pabst, S., Von Mollard, GF., Jahn, R. (2000). A SNARE complex mediating fusion of late endosomes defines conserved properties of SNARE structure and function. *EMBO J, 19*, 6453-64. ↗

Rao, SK., Huynh, C., Proux-Gillardeaux, V., Galli, T., Andrews, NW. (2004). Identification of SNAREs involved in synaptotagmin VII-regulated lysosomal exocytosis. *J Biol Chem, 279*, 20471-9. ↗

Editions

2008-01-11	Reviewed	Rush, MG.
2009-08-27	Authored	Gillespie, ME.

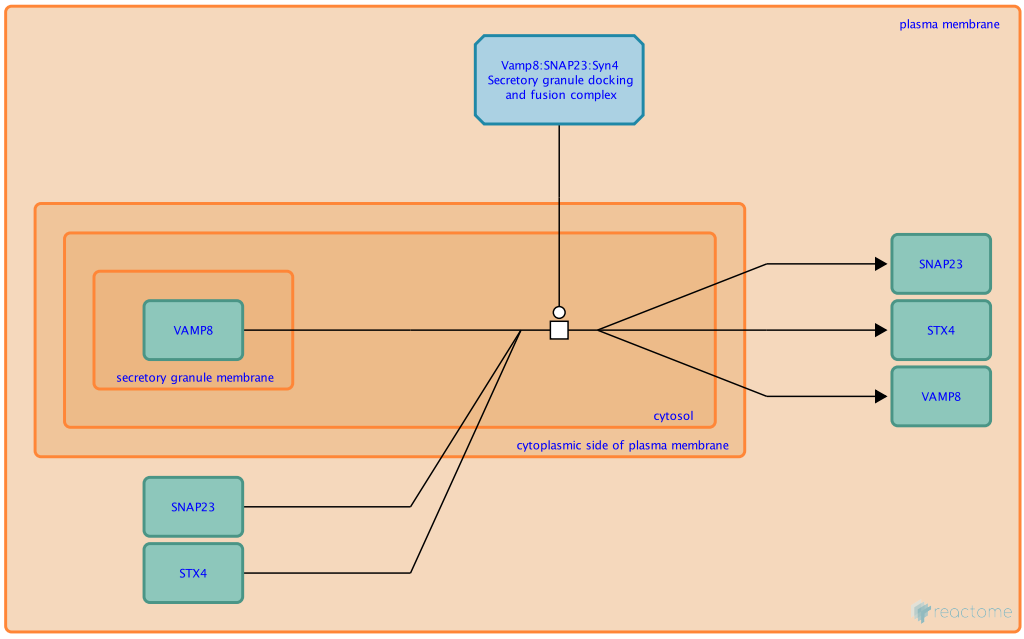
Vamp8 associated secretory vesicle to plasma membrane transport ↗

Location: trans-Golgi Network Vesicle Budding

Stable identifier: R-HSA-376364

Type: transition

Compartments: cytosol



The vamp8 associated vesicle docks and fuses with the plasma membrane.

Literature references

Wesolowski, J., Paumet, F. (2014). Escherichia coli exposure inhibits exocytic SNARE-mediated membrane fusion in mast cells. *Traffic, 15*, 516-30. ↗

Suzuki, K., Verma, IM. (2008). Phosphorylation of SNAP-23 by IkappaB kinase 2 regulates mast cell degranulation. *Cell, 134*, 485-95. ↗

Salinas, E., Quintanar-Stephano, A., Córdova, LE., Ouintanar, JL. (2008). Allergen-sensitization increases mast-cell expression of the exocytotic proteins SNAP-23 and syntaxin 4, which are involved in histamine secretion. *J Investig Allergol Clin Immunol, 18*, 366-71. ↗

Puri, N., Roche, PA. (2006). Ternary SNARE complexes are enriched in lipid rafts during mast cell exocytosis. *Traffic, 7*, 1482-94. ↗

Guo, Z., Turner, C., Castle, D. (1998). Relocation of the t-SNARE SNAP-23 from lamellipodia-like cell surface projections regulates compound exocytosis in mast cells. *Cell, 94*, 537-48. ↗

Editions

2008-01-11	Reviewed	Rush, MG.
2009-08-27	Authored	Gillespie, ME.

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