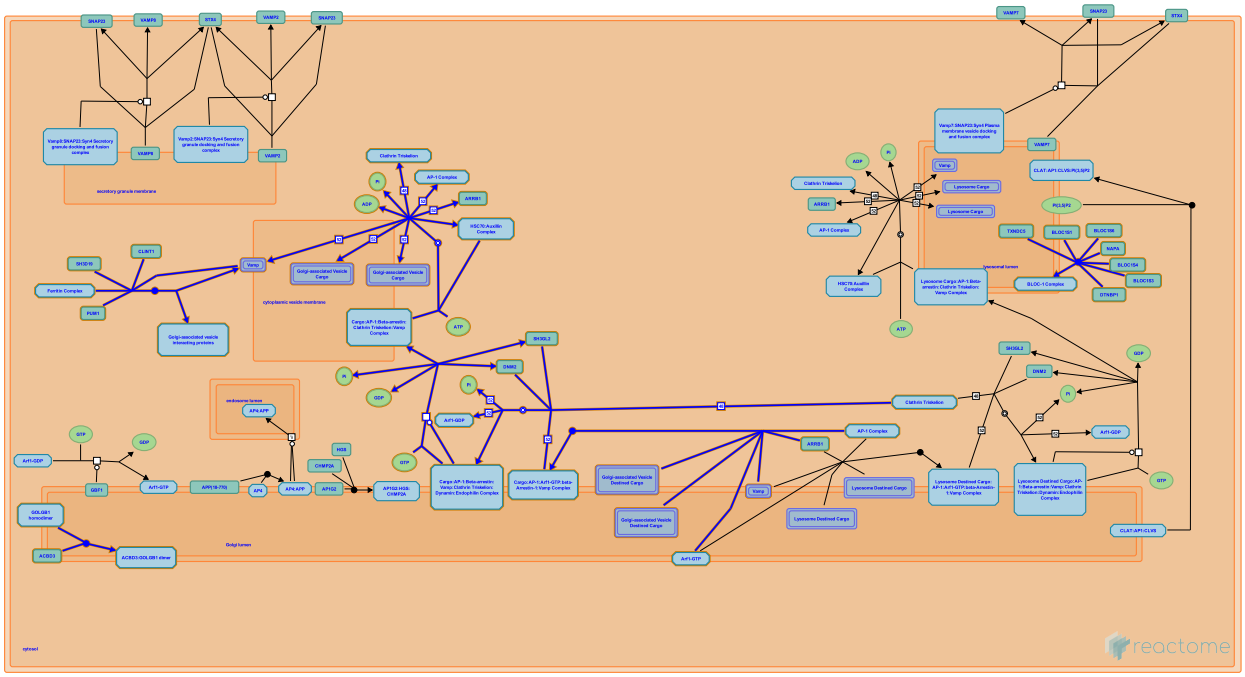
Golgi Associated Vesicle Biogenesis



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18/01/2021

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.

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. ↗

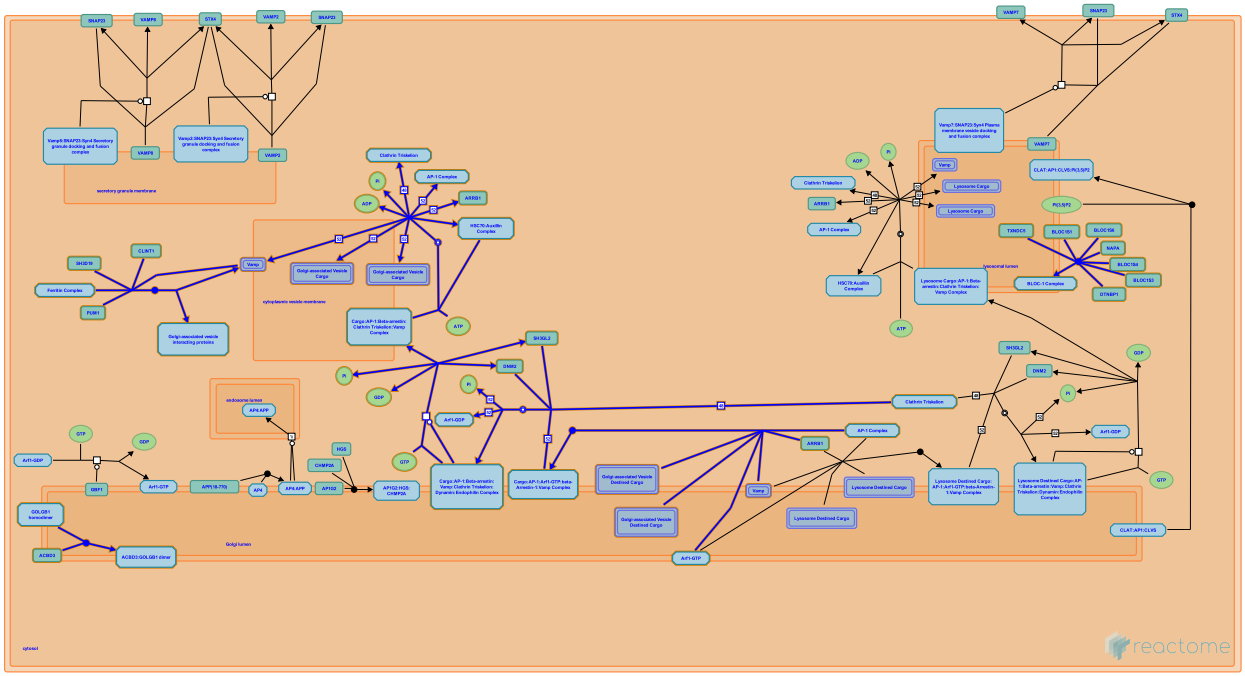
Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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. ↗

Golgi Associated Vesicle Biogenesis ↗

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

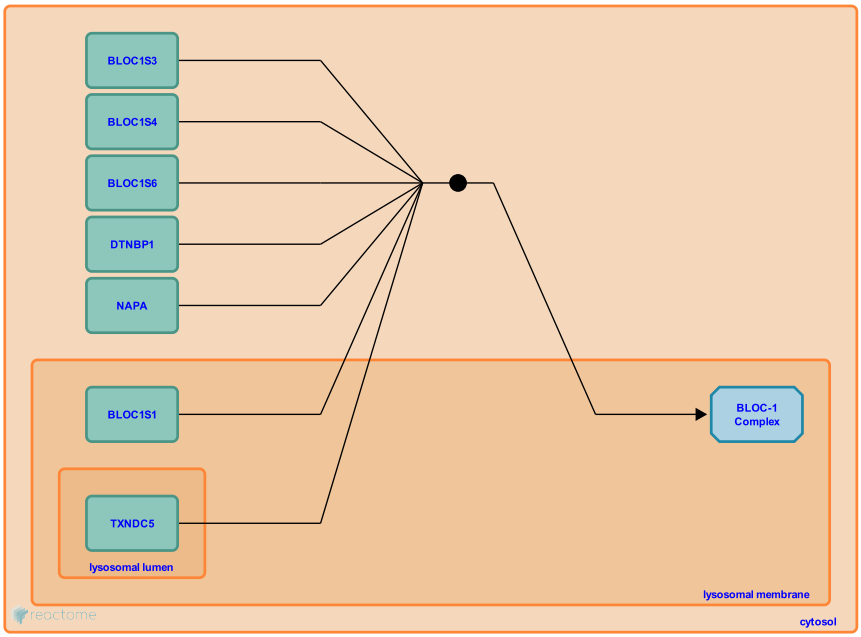
Formation Of Bloc-1 Complex ↗

Location: Golgi Associated Vesicle Biogenesis

Stable identifier: R-HSA-429815

Type: binding

Compartments: cytosol



The ubiquitously expressed protein complexes, named biogenesis of lysosome-related organelles complex or BLOC are required for normal biogenesis of specialized organelles of the endosomal-lysosomal system, such as melanosomes and platelet dense granules.

Preceded by: trans-Golgi Network Derived Vesicle Uncoating

Literature references

Borner, GH., Harbour, M., Hester, S., Lilley, KS., Robinson, MS. (2006). Comparative proteomics of clathrin-coated vesicles. *J Cell Biol, 175*, 571-8. ↗

Starcevic, M., Dell'Angelica, EC. (2004). Identification of snapin and three novel proteins (BLOS1, BLOS2, and BLOS3/reduced pigmentation) as subunits of biogenesis of lysosome-related organelles complex-1 (BLOC-1). *J Biol Chem, 279*, 28393-401. ↗

Editions

2009-08-27	Authored	Gillespie, ME.
2009-08-28	Reviewed	Simpson, JC.
2009-09-09	Edited	Gillespie, ME.

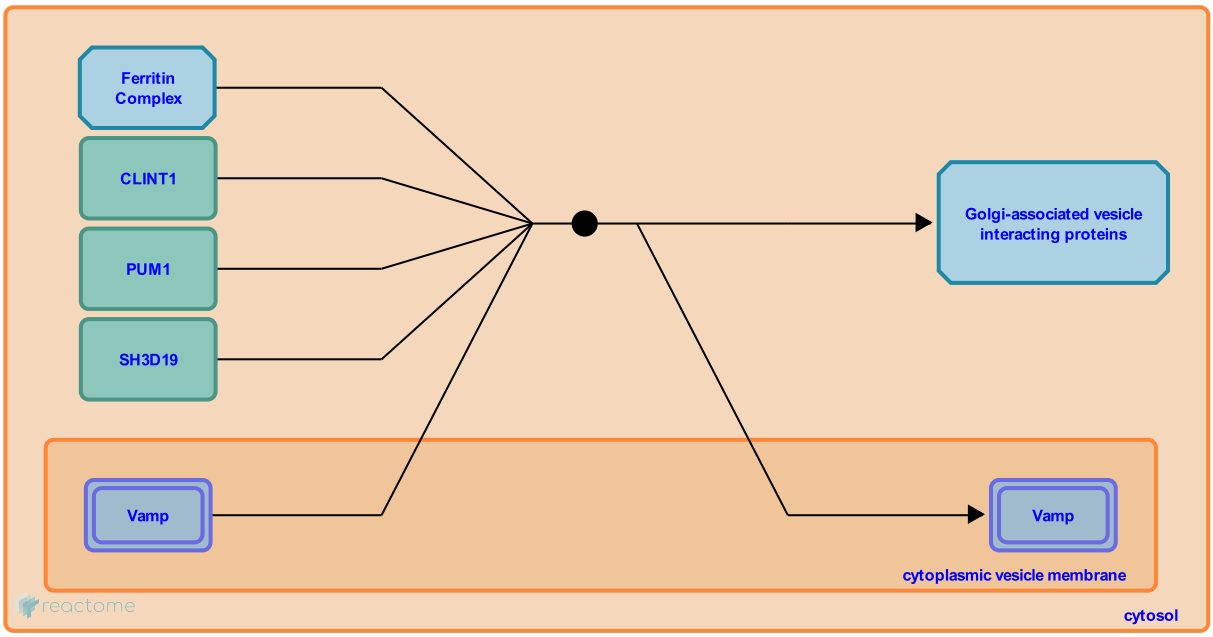
Recruitment Of Cytoplasmic Proteins To Vesicles ↗

Location: Golgi Associated Vesicle Biogenesis

Stable identifier: R-HSA-434362

Type: binding

Compartments: cytosol



Cytosolic proteins are also recruited to the cytoplasmic face of newly formed vesicles.

Preceded by: trans-Golgi Network Derived Vesicle Uncoating

Literature references

Borner, GH., Harbour, M., Hester, S., Lilley, KS., Robinson, MS. (2006). Comparative proteomics of clathrin-coated vesicles. *J Cell Biol, 175*, 571-8. ↗

Editions

2008-09-08	Edited	Gillespie, ME.
2009-08-13	Authored	Gillespie, ME.
2009-08-28	Reviewed	Simpson, JC.

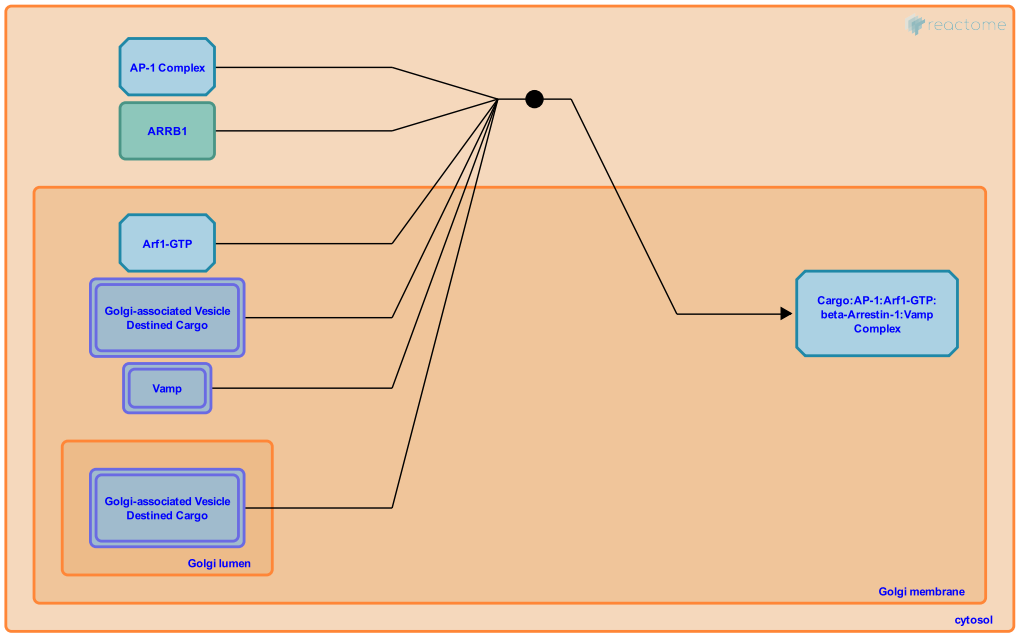
Vamp And trans-Golgi Network AP-1 Binding Coupled With Cargo Capture ↗

Location: Golgi Associated Vesicle Biogenesis

Stable identifier: R-HSA-421833

Type: binding

Compartments: cytosol



Once AP-1 is recruited to the trans-Golgi Network membrane the complex of functional vesicle building proteins is joined by the cargo that will be within that vesicle. As with other types of vesicles the cargo itself is part of the vesicle development. Here the cargo is destined for the Golgi-associated vesicle membrane. It is at this stage that a specific Synaptobrevin (Vamp) molecule also joins the complex. It should be noted that only certain Vamp molecules will be found with specific cargo molecules on the newly forming vesicles. However here we represent this reaction in bulk, without specific Vamp and cargo molecule pairings.

Followed by: trans-Golgi Network Coat Assembly

Literature references

Hirst, J., Lindsay, MR., Robinson, MS. (2001). GGAs: roles of the different domains and comparison with AP-1 and clathrin. *Mol Biol Cell, 12*, 3573-88. ↗

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

Borner, GH., Harbour, M., Hester, S., Lilley, KS., Robinson, MS. (2006). Comparative proteomics of clathrin-coated vesicles. *J Cell Biol, 175*, 571-8. ↗

Editions

2008-05-22	Edited	Gillespie, ME.
2009-08-27	Authored	Gillespie, ME.
2009-08-28	Reviewed	Simpson, JC.

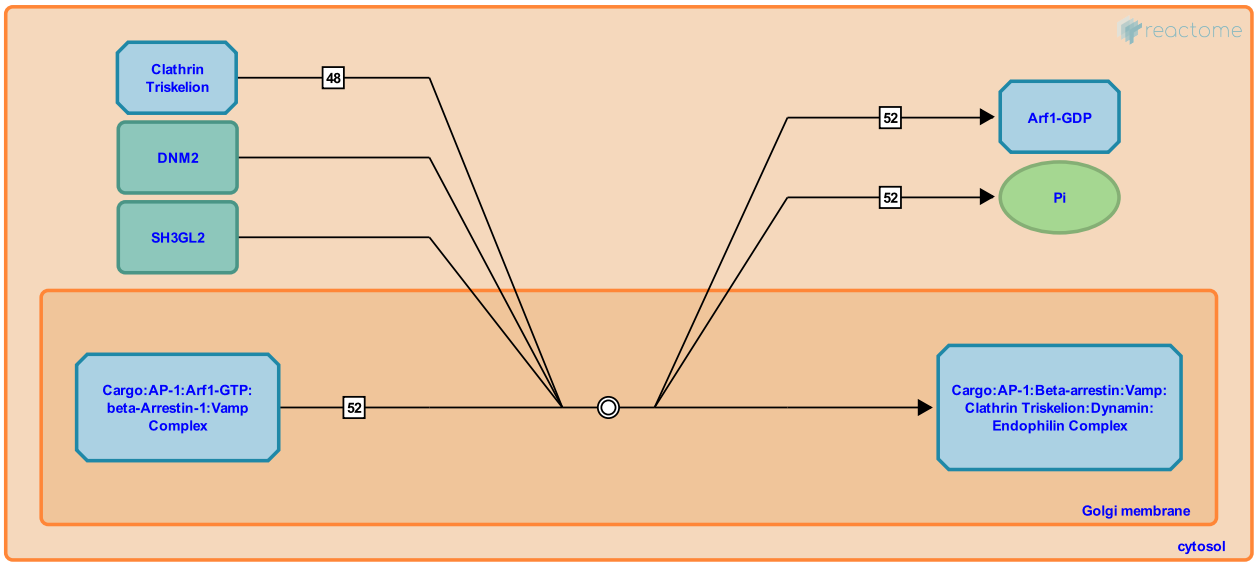
trans-Golgi Network Coat Assembly ↗

Location: Golgi Associated Vesicle Biogenesis

Stable identifier: R-HSA-421831

Type: dissociation

Compartments: Golgi membrane, cytosol



Once the basic components of the docking complex are assembled with one end of AP-1 bound to cargo molecules, the other end binds to clathrin. Clathrin triskelions polymerize into hexagons and pentagons, forming a cage, which leads to membrane deformation. This polymerization step drives the sculpting of the vesicle. The number of clathrin triskelions required to sculpt a vesicle appears to be variable, but has been estimated to require 36 - 60 triskelions assocaited with 30 - 66 AP-1 complexes. Here a ~380 angstroms vesicle is represented with 48 clathrin triskelions and 52 AP-1 complexes.

Preceded by: Vamp And trans-Golgi Network AP-1 Binding Coupled With Cargo Capture

Followed by: trans-Golgi Network Vesicle Scission

Literature references

Musacchio, A., Smith, CJ., Roseman, AM., Harrison, SC., Kirchhausen, Tomas., Pearse, BM. (1999). Functional organization of clathrin in coats: combining electron cryomicroscopy and X-ray crystallography. *Mol Cell, 3*, 761-70. ↗

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

Editions

2008-05-22	Edited	Gillespie, ME.
2009-08-27	Authored	Gillespie, ME.
2009-08-28	Reviewed	Simpson, JC.

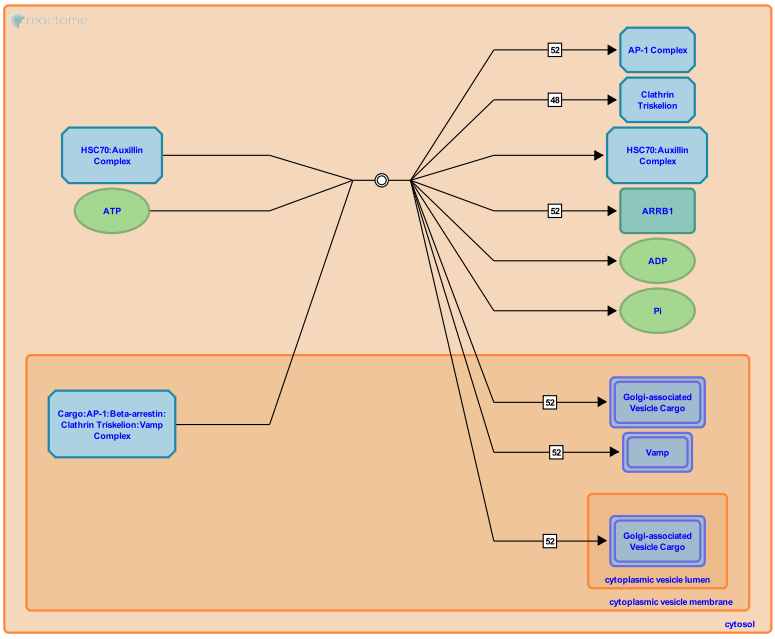
trans-Golgi Network Derived Vesicle Uncoating ↗

Location: Golgi Associated Vesicle Biogenesis

Stable identifier: R-HSA-421836

Type: dissociation

Compartments: cytosol



The heat shock protein Hsc70 and auxilin, a J-domain containing protein, are responsible for clathrin disassembly through an ATP-dependent reaction. This uncoating step may be a point in the pathway subject to regulation. This final step releases the vesicle from the clathrin cage. The vesicle still contatins a specific Vamp molecule, part of the targeting and fusion mechanism that delivers the vesicle to its ultimate destination. This vesicle also contains its cargo, membrane proteins embeded in the Golgi-associated vesicle membrane.

Preceded by: trans-Golgi Network Vesicle Scission

Followed by: Recruitment Of Cytoplasmic Proteins To Vesicles, Formation Of Bloc-1 Complex

Literature references

Ungewickell, E., Ungewickell, H., Holstein, SE., Lindner, R., Prasad, K., Barouch, W. et al. (1995). Role of auxilin in uncoating clathrin-coated vesicles. *Nature, 378*, 632-5. ↗

Acton, SL., Wong, DH., Parham, P., Brodsky, FM., Jackson, AP. (1993). Alteration of clathrin light chain expression by transfection and gene disruption. *Mol Biol Cell, 4*, 647-60. ↗

Lee, DW., Zhao, X., Zhang, F., Eisenberg, E., Greene, LE. (2005). Depletion of GAK/auxilin 2 inhibits receptor-mediated endocytosis and recruitment of both clathrin and clathrin adaptors. *J Cell Sci, 118*, 4311-21. ↗

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

Borner, GH., Harbour, M., Hester, S., Lilley, KS., Robinson, MS. (2006). Comparative proteomics of clathrin-coated vesicles. *J Cell Biol, 175*, 571-8. ↗

Editions

2008-05-22	Edited	Gillespie, ME.
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2009-08-28	Reviewed	Simpson, JC.

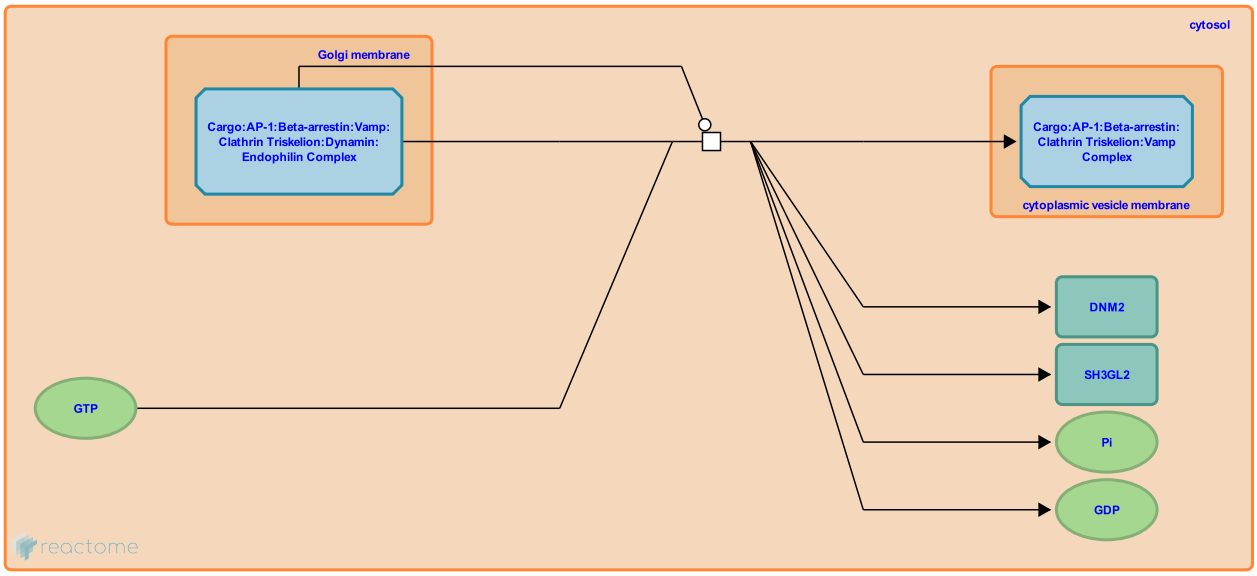
trans-Golgi Network Vesicle Scission ↗

Location: Golgi Associated Vesicle Biogenesis

Stable identifier: R-HSA-421835

Type: transition

Compartments: cytosol



Dynamin is recruited to the growing vesicle and, under conditions that interfere with its GTPase activity, dynamin forms a collar or ring around the neck of the budding vesicle. It is unclear whether dynamin acts as a mechanochemical transducer to generate fission or as a recruiter to attach other proteins that are directly responsible for the fission step. Lipid-modifying enzymes such as endophilin are also involved in vesicle formation. Endophilin is an acyltransferase that interacts with dynamin and that generates lysophosphatidic acid. The current view is that this reaction produces a negative curvature at the neck of the vesicle.

Preceded by: trans-Golgi Network Coat Assembly

Followed by: trans-Golgi Network Derived Vesicle Uncoating

Literature references

Maier, O., Knoblich, M., Westermann, P. (1996). Dynamin II binds to the trans-Golgi network. *Biochem Biophys Res Commun, 223*, 229-33. ↗

Farsad, K., Ringstad, N., Takei, K., Floyd, SR., Rose, K., De Camilli, P. (2001). Generation of high curvature membranes mediated by direct endophilin bilayer interactions. *J Cell Biol, 155*, 193-200. ↗

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

Editions

2008-05-22	Edited	Gillespie, ME.
2009-08-27	Authored	Gillespie, ME.
2009-08-28	Reviewed	Simpson, JC.

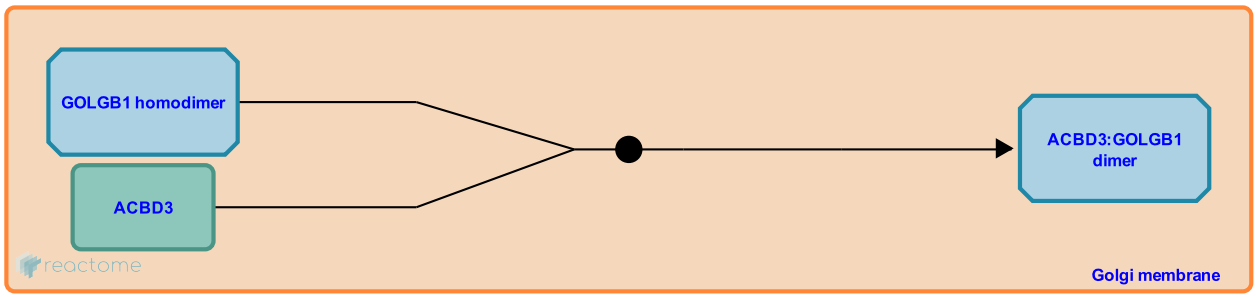
ACBD3 binds GOLGB1 ↗

Location: Golgi Associated Vesicle Biogenesis

Stable identifier: R-HSA-8874979

Type: binding

Compartments: Golgi membrane



Golgi resident protein GCP60 (ACBD3) is a Golgi membrane-associated protein thought to be involved in the maintenance of the Golgi structure by interacting with Golgin subfamily B member 1 (GOLGB1, giantin), which may mediate protein transport between the endoplasmic reticulum and the Golgi (Sohda et al. 2001).

Literature references

Sohda, M., Misumi, Y., Yamamoto, A., Yano, A., Nakamura, N., Ikehara, Y. (2001). Identification and characterization of a novel Golgi protein, GCP60, that interacts with the integral membrane protein giantin. *J. Biol. Chem., 276* , 45298-306. ↗

Editions

2016-05-31	Authored, Edited	Jassal, B.
2016-07-15	Reviewed	D'Eustachio, P.

Table of Contents