

Disassembly of COPII coated vesicle

Elliott, T., Garapati, P V.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

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. [↗](#)

Reactome database release: 76

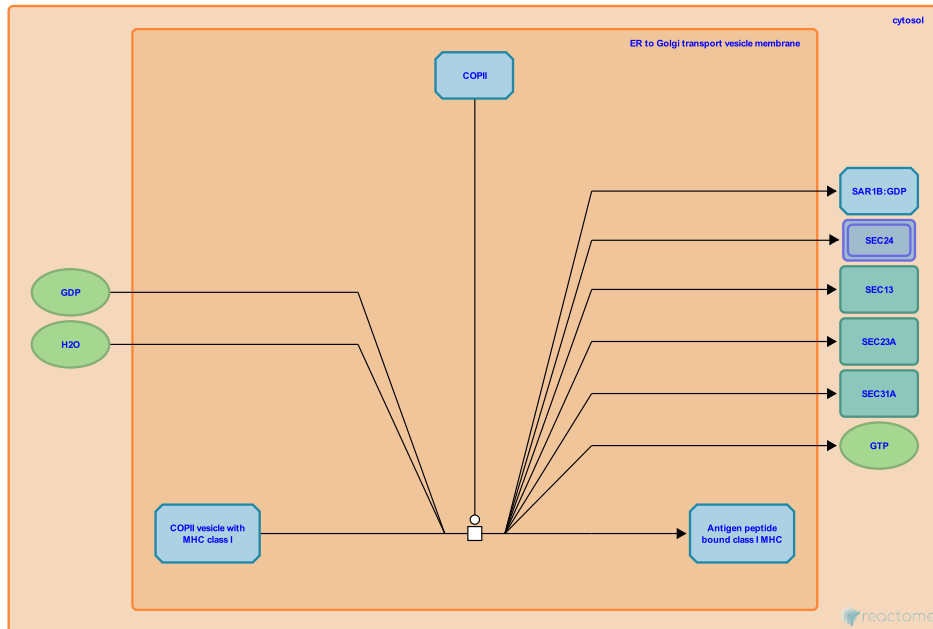
This document contains 1 reaction ([see Table of Contents](#))

Disassembly of COPII coated vesicle ↗

Stable identifier: R-HSA-983422

Type: transition

Compartments: ER to Golgi transport vesicle membrane, cytosol



Before the cargo vesicle can fuse with target membrane, the COPII protein coat must be disassembled and its components released into cytosol. This uncoating is triggered by hydrolysis of the bound GTP to produce Sar1p-GDP, which has decreased affinity for the vesicle membrane. Disassociation of Sar1p-GDP from the membrane is followed by the release of the other COPII subunits.

Literature references

- Hammond, AT., Glick, BS. (2000). Dynamics of transitional endoplasmic reticulum sites in vertebrate cells. *Mol Biol Cell*, 11, 3013-30. ↗
- Sato, K., Nakano, A. (2007). Mechanisms of COPII vesicle formation and protein sorting. *FEBS Lett*, 581, 2076-82. ↗
- Stephens, DJ., Lin-Marq, N., Pagano, A., Pepperkok, R., Paccaud, JP. (2000). COPI-coated ER-to-Golgi transport complexes segregate from COPII in close proximity to ER exit sites. *J Cell Sci*, 113, 2177-85. ↗

Editions

2010-10-29	Authored, Edited	Garapati, P V.
2011-02-11	Reviewed	Elliott, T.