

SEC16 complex binds SAR1B:GTP:SEC23:SEC24

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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: 74

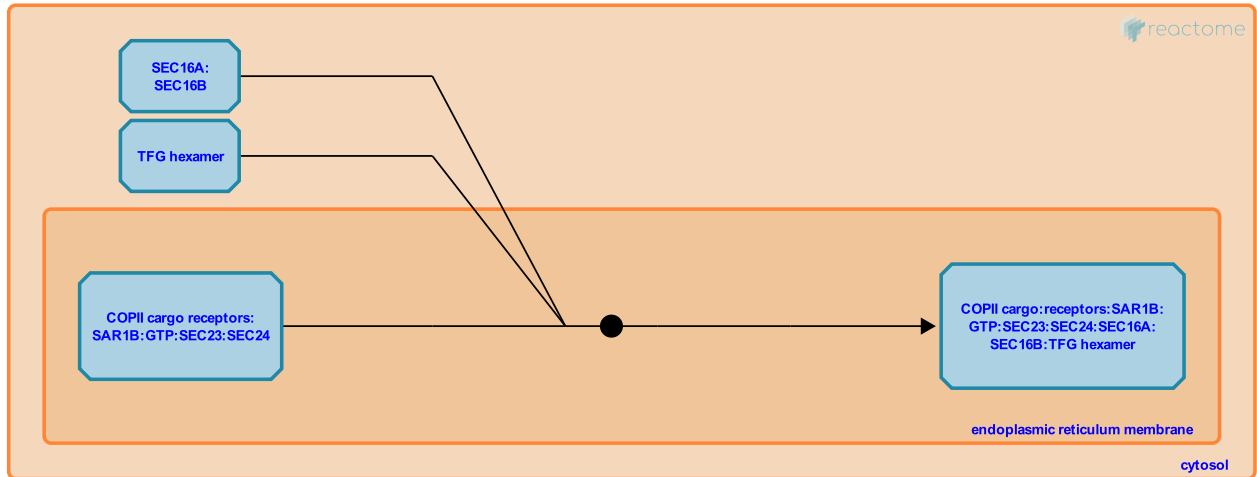
This document contains 1 reaction ([see Table of Contents](#))

SEC16 complex binds SAR1B:GTP:SEC23:SEC24 [↗](#)

Stable identifier: R-HSA-5694417

Type: binding

Compartments: endoplasmic reticulum membrane



The multimeric SEC16 complex marks sites of ER exit (ERES) and helps to localize nascent COPII coat complexes through interaction with SEC23 and SAR1 (Battacharyya et al, 2007; Watson et al, 2006; Hughes et al, 2009; Yorimitsu and Sato, 2012; reviewed in Sprangers and Rabouille, 2015). SEC16 may help to prevent premature dissociation of the COPII coats after activation of SEC13 GTPase (Supek et al, 2002; Kung et al, 2012). SEC16 functions with hexameric TFG1, which is recruited to the ERES through direct interaction with SEC16 and is required for cargo traffic out of the ER and for organization of the ER-to-ERGIC boundary (Witte et al, 2001; Beetz et al, 2012; Johnson et al, 2015).

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Editions

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