RABGGTA and RABGGTB bind

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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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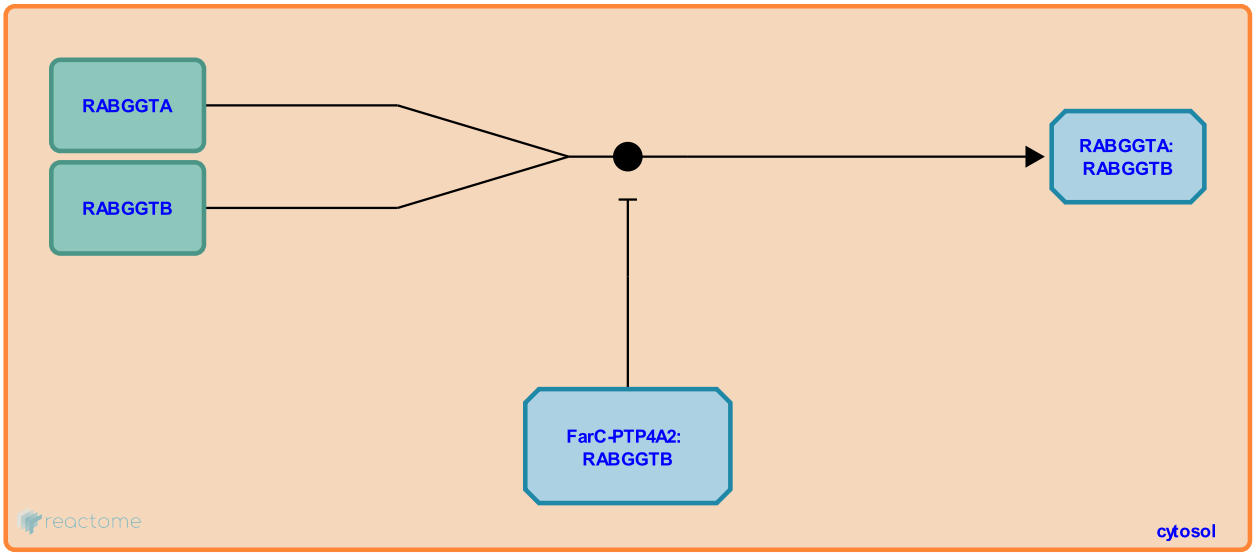
Stable identifier: R-HSA-8870461

Type: binding

Compartments: cytosol



RABGGTA and RABGGTB are the two catalytic subunits of a trimeric RAB geranylgeranyl transferase complex (GGTase); the third subunit is the RAB binding subunit CHM or CHML (reviewed in Leung et al, 2006; Gutkowska and Swiezewska, 2012). RABGGTB also interacts in a mutually exclusive way with PTP4A2, preventing formation of a functional gernanylgeranyl transferase complex (Si et al, 2001; Baron and Seabra, 2008). Newly synthesized RAB proteins are singly or more commonly doubly geranylgeranylated near their C-termini by the GGTase. Geranylgeranylation promotes association of active RAB proteins with membranes. Membrane association is additionally modulated by the nucleotide state of the GTPase through regulatory proteins such as guanine nucleotide exchange factors (GEFs), GTPase activating proteins (GAPs) and GDP Dissocation Inhibitors (GDIs), among others (reviewed in Stenmark et al, 2009; Wandinger-Ness and Zerial, 2014). An exception to this is RAB13, which has recently been shown to be membrane-associated even in the inactive state and to traffic on vesicles independently of geranylgeranylation (Ioannou et al, 2016).

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Editions

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