RGGT:CHM binds RABs

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16/09/2021

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.

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

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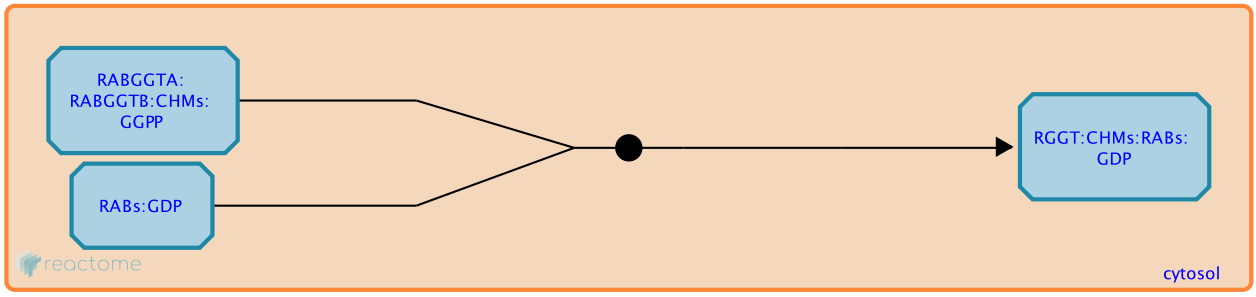
Stable identifier: R-HSA-8870466

Type: binding

Compartments: cytosol



CHM and CHML are the substrate-binding subunits of the RAB geranylgeranyltransferase (GGTase) complex. CHMs, also known as RAB escort proteins (REPs) bind to unprenylated RAB proteins in the GDP bound state (Seabra, 1996). In the classical model of RAB recruitment, CHM proteins first bind the unprenylated RAB alone and then present it to the catalytic dimer of the RAB GGTase, while in the alternative model, depicted here, RAB recruitment occurs after the GGPP-dependent formation of a highly stable trimeric GGTase complex (Andres et al, 1993; Thoma et al, 2001a; Thoma et al 2001b; Baron and Seabra, 2008). After geranylgeranylation, binding of additional GGPP to the GGTase promotes release of the CHM:RAB complex, possibly through an allosteric mechanism (Baron and Seabra, 2008). CHM proteins remain in complex with the RABs after geranylgeranylation, dissociating after the RAB has been transferred to the target membrane (Alexandrov et al, 1994; Shen and Seabra, 1996; Baron and Seabra, 2008).

Literature references

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Editions

2016-06-08	Authored, Edited	Rothfels, K.
2016-08-04	Reviewed	Palsuledesai, CC.