

FarC-PTP4A2 binds RABGGTB

Palsuledesai, CC., Rothfels, K.

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

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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

- 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: 88

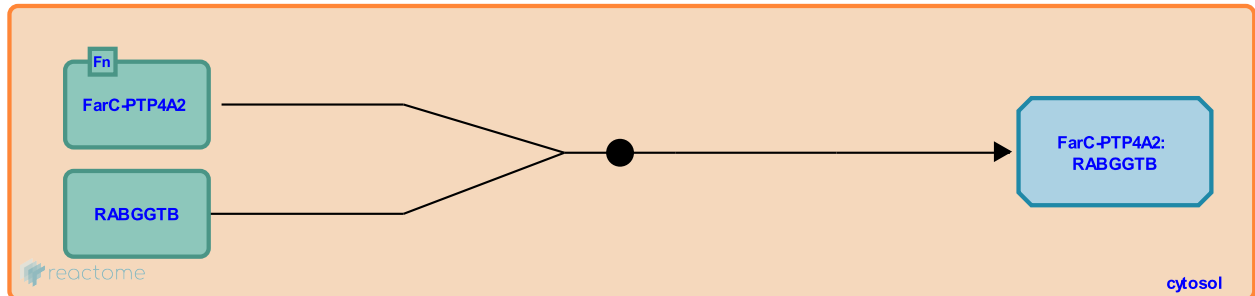
This document contains 1 reaction ([see Table of Contents](#))

FarC-PTP4A2 binds RABGGTB [↗](#)

Stable identifier: R-HSA-8870457

Type: binding

Compartments: cytosol



PTP4A2, also known as PRL2, is a member of the protein tyrosine phosphatase family. Farnesylated PTP4A2 interacts with RABGGTB, one of the two catalytic subunits of the RAB geranylgeranyl transferase complex and prevents its association with the other catalytic subunit RABGBTA (Si et al, 2001). In this way, binding of PTP4A2 acts as a negative regulator of RAB geranylgeranylation (reviewed in Gutkowska and Swiezewska, 2012).

Literature references

Swiezewska, E., Gutkowska, M. (2012). Structure, regulation and cellular functions of Rab geranylgeranyl transferase and its cellular partner Rab Escort Protein. *Mol. Membr. Biol.*, 29, 243-56. [↗](#)

Hong, W., Si, X., Ng, CH., Pallen, CJ., Zeng, Q. (2001). Interaction of farnesylated PRL-2, a protein-tyrosine phosphatase, with the beta-subunit of geranylgeranyltransferase II. *J. Biol. Chem.*, 276, 32875-82. [↗](#)

Editions

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