

(Frs2)C3G stimulates nucleotide exchange on Rap1

Annibali, D., Greene, LA., Jassal, B., Nasi, S.

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](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

09/05/2024

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: 88

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

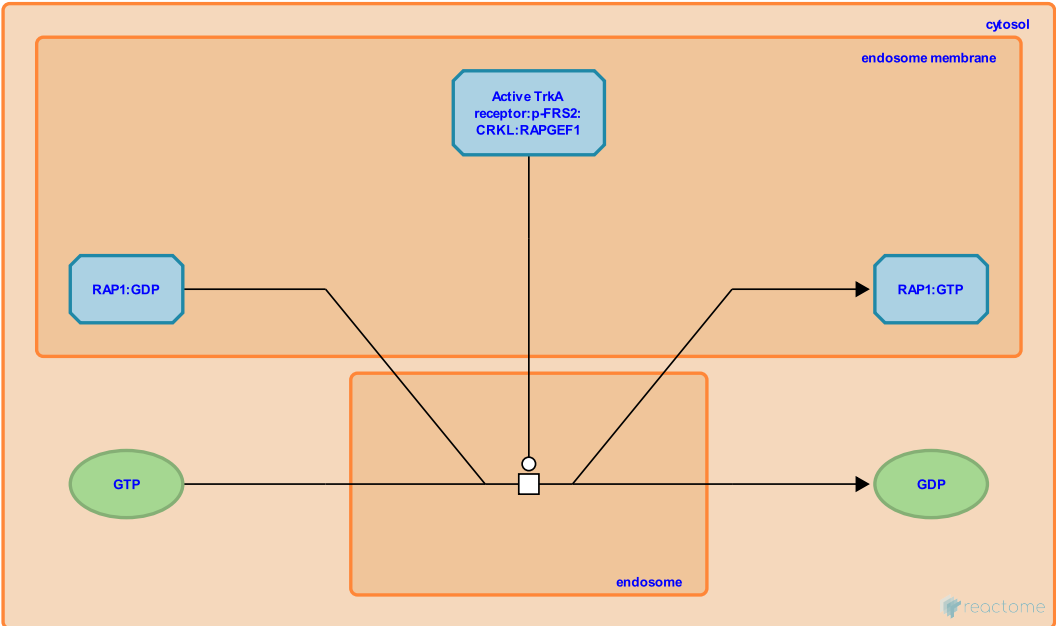
(Frs2)C3G stimulates nucleotide exchange on Rap1

Stable identifier: R-HSA-170979

Type: transition

Compartments: endosome

Inferred from: C3G stimulates nucleotide exchange on Rap1 (Rattus norvegicus)



Rap1 is a small G protein, necessary for prolonged ERK activity in PC12 cells. In such cells, NGF triggers a program of neuronal differentiation through the activation of a Rap1:B-RAF:ERK module. Rap1 is activated by NGF, but not by epidermal growth factor (EGF), although both growth factors cause transient activation of RAS. Activation of Rap1 by NGF requires internalization of TRKA to intracellular vesicles, mostly endosomes, containing Rap1, B-RAF, MEK and ERKs. Rap1 does not co-localize with RAS. Therefore, the ability of Rap1 to bind RAF-1 without activating it might sequester RAF-1 from RAS. Activation of GEFs that couple to Rap1 as well as RAS might provide a mechanism to limit signals to RAS.

Literature references

Stork, P.J., McCleskey, E.W., Dillon, T., Eckert, S.P., Yao, H., York, R.D. et al. (1998). Rap1 mediates sustained MAP kinase activation induced by nerve growth factor. *Nature*, 392, 622-6. [↗](#)

Editions

2006-10-10	Edited	Jassal, B.
2006-10-10	Authored	Annibali, D., Nasi, S.
2007-11-08	Reviewed	Greene, L.A.