# Intrinsic nucleotide exchange on RAS

Gavathiotis, E., Rothfels, K.

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



06/05/2024

# 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. ↗

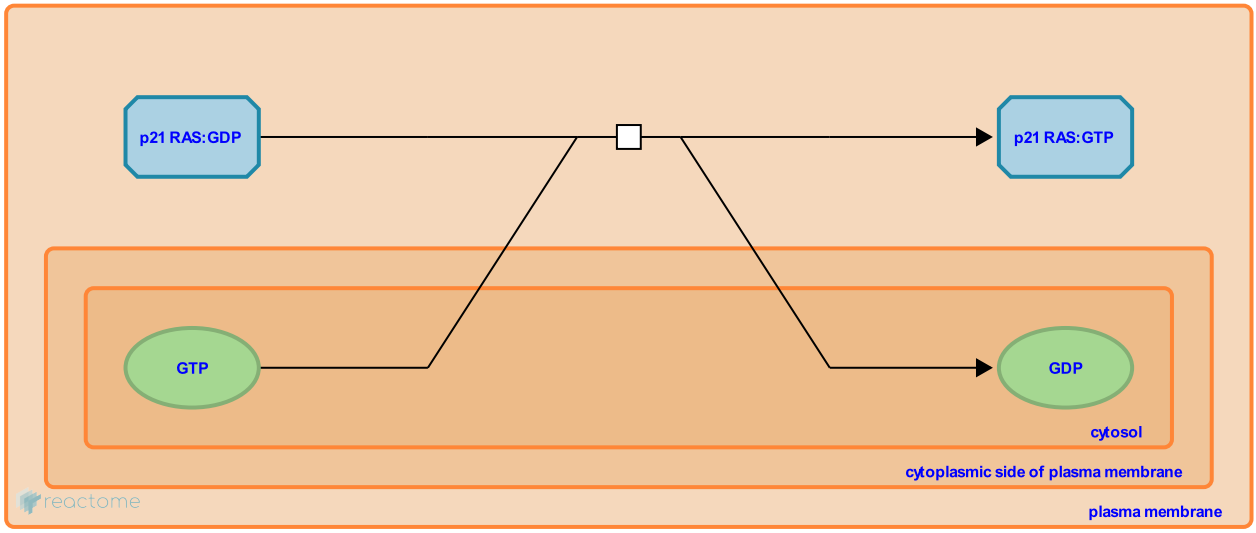
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

## Intrinsic nucleotide exchange on RAS ↗

**Stable identifier:** R-HSA-9649735

**Type:** transition

**Compartments:** plasma membrane, cytosol




Inactive RAS:GDP is converted at a low rate to the active GTP-bound state through release of GDP and binding of GTP. This intrinsic GEF activity is weak due to the picomolar affinity of the protein for both nucleotides, but is stimulated by the interaction of RAS proteins with guanine nucleotide exchange factors (Marshall et al, 2012; reviewed in Bourne et al, 1991; Hennig et al, 2015; Pei et al, 2018).

## Literature references


Markwart, R., Esparza-Franco, MA., Ladds, G., Rubio, I., Hennig, A. (2015). Ras activation revisited: role of GEF and GAP systems. *Biol. Chem., 396*, 831-48. ↗

McCormick, F., Bourne, HR., Sanders, DA. (1991). The GTPase superfamily: conserved structure and molecular mechanism. *Nature, 349*, 117-27. ↗

Chen, K., Liao, H., Pei, D. (2018). Targeting Ras with Macromolecules. *Cold Spring Harb Perspect Med, 8*. ↗

Marshall, CB., Rottapel, R., Smith, MJ., Gasmi-Seabrook, GM., Meiri, D., Stambolic, V. et al. (2012). Probing the GTPase cycle with real-time NMR: GAP and GEF activities in cell extracts. *Methods, 57*, 473-85. ↗


## Editions

| | | |
|---|---|---|
| 2019-10-25 | Authored | Rothfels, K. |
| 2020-05-04 | Reviewed | Gavathiotis, E. |
| 2020-05-26 | Edited | Rothfels, K. |