Activation of PAK by Rac1

Garapati, P V., Kikutani, H., Kumanogoh, A.

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

29/04/2024

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. ↗

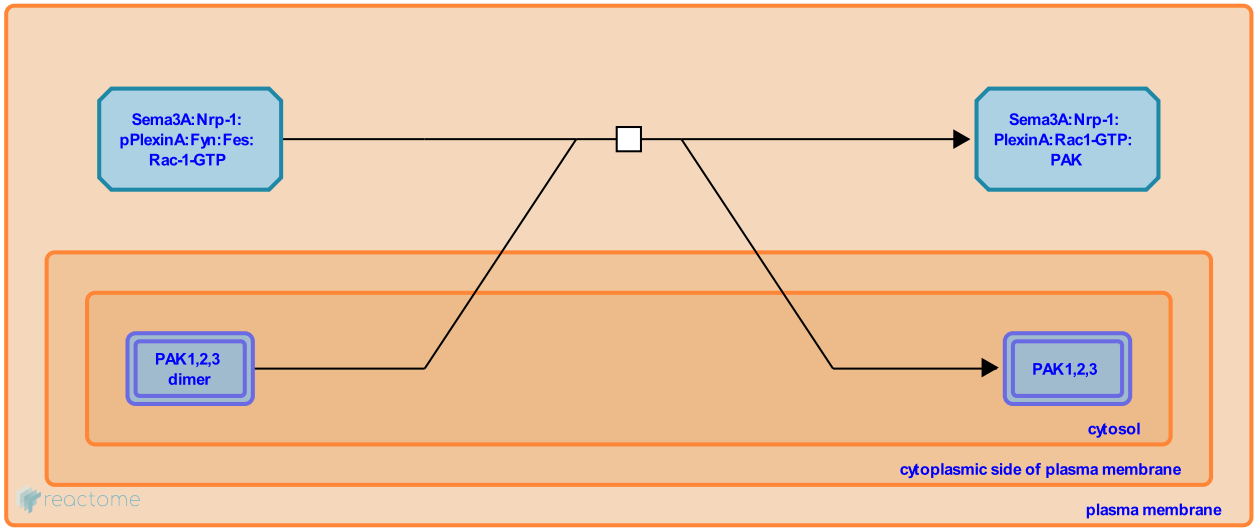
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Activation of PAK by Rac1

Stable identifier: R-HSA-399930

Type: transition

Compartments: cytosol, plasma membrane



Plexin-bound Rac1 binds to and stimulates the kinase activity of PAK. PAK dimers are arranged in head-to-tail fashion, in which the catalytic domain binds the kinase inhibitory (KI) domain and is supported by associated PAK-interacting exchange factor (PIX) dimers. Upon Rac1 binding the kinase undergoes conformational change that allows autophosphorylation. Phosphorylation of serine residues disables the KI-domain-kinase interaction and thereby reduces the affinity of PIX.

Literature references

Whitford, KL., Ghosh, A. (2001). Plexin signaling via off-track and rho family GTPases. *Neuron, 32*, 1-3.

Editions

2009-03-23	Authored, Edited	Garapati, P V.
2009-09-02	Reviewed	Kikutani, H., Kumanogoh, A.