RHOA:GTP binds ROCK, activating it

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28/04/2024

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

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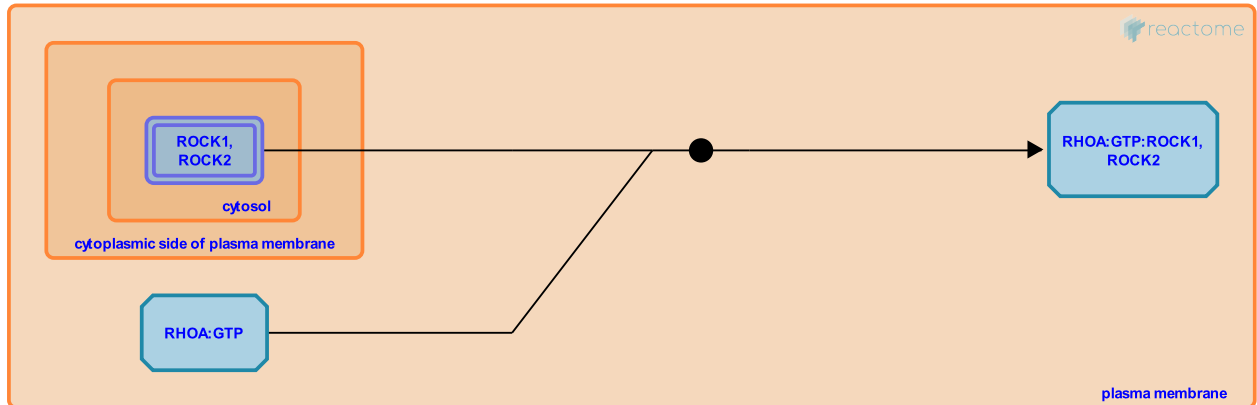
Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

RHOA:GTP binds ROCK, activating it ↗

Stable identifier: R-HSA-3928576

Type: binding

Compartments: plasma membrane, cytosol

EPHB receptor-induced phosphorylation of coffin is at least partially controlled by Rho-associated kinase (ROCK) and LIM domain kinase (LIMK) activities (Shi et al. 2009). ROCK structure comprises a kinase domain located at the amino terminus of the protein, a coiled-coil region containing the Rho-binding domain (RBD), and a pleckstrin-homology (PH) domain with a cysteine-rich domain (CRD). In resting cells ROCKs exist in an autoinhibition state where the kinase domain interacts with the C-terminal inhibitory region. Binding of active RHOA:GTP to RBD stimulates the phosphotransferase activity of ROCK by disrupting the interaction between the catalytic and the inhibitory C-terminal region of the enzyme (Khalil 2010).

Literature references

Reichardt, LF., Shi, Y., Pontrello, CG., DeFea, KA., Ethell, IM. (2009). Focal adhesion kinase acts downstream of EphB receptors to maintain mature dendritic spines by regulating cofilin activity. *J. Neurosci., 29*, 8129-42. ↗

Editions

2013-07-23	Authored, Edited	Garapati, P V.
2014-05-19	Reviewed	Ip, NY.