LIM kinase phosphorylation by ROCK

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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

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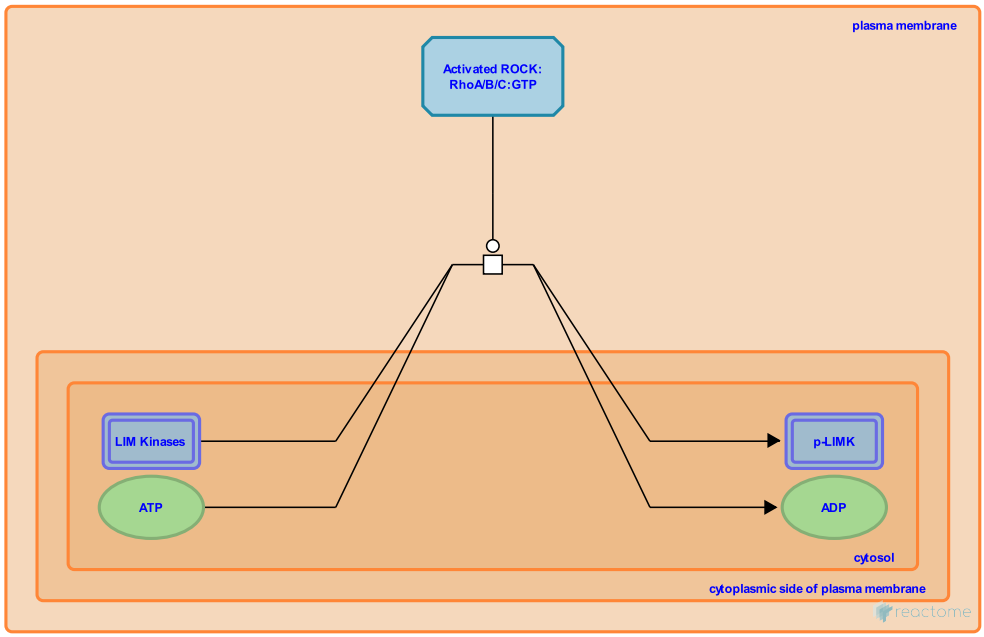
Stable identifier: R-HSA-419087

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: ROCK1 phosphorylates LIMK2 (rat) (Homo sapiens)



LIM kinases are serine protein kinases with a unique combination of two N-terminal LIM motifs, a central PDZ domain, and a C-terminal protein kinase domain. ROCK1 and ROCK2 phosphorylate and activate LIM kinases LIMK1 and LIMK2 at Thr508 and Thr505, respectively (Ohashi et al. 2000, Sumi et al. 2001). These threonine residues lay within the activation loop of the kinase domain. LIMKs phosphorylate and inactivate cofilin, an actin depolymerizing factor, resulting in stabilization of the actin cytoskeleton (Pandey et al. 2006).

Literature references

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Editions

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