

LIM kinase phosphorylation by ROCK

Akkerman, JW., Jupe, S., Kikutani, H., Kumanogoh, A., Rivero Crespo, F.

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 <u>Creative Commons Attribution 4.0 International (CC BY 4.0)</u> <u>License</u>. For more information see our <u>license</u>.

10/05/2024

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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *オ*

This document contains 1 reaction (see Table of Contents)

LIM kinase phosphorylation by ROCK 7

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

- Nakamura, T., Matsumoto, K., Sumi, T. (2001). Specific activation of LIM kinase 2 via phosphorylation of threonine 505 by ROCK, a Rho-dependent protein kinase. *J Biol Chem*, 276, 670-6.
- Siess, W., Bamburg, JR., Pandey, D., Goyal, P. (2006). Regulation of LIM-kinase 1 and cofilin in thrombin-stimulated platelets. *Blood, 107*, 575-83.
- Ohashi, K., Narumiya, S., Mizuno, K., Ishizaki, T., Nagata, K., Maekawa, M. (2000). Rho-associated kinase ROCK activates LIM-kinase 1 by phosphorylation at threonine 508 within the activation loop. *J Biol Chem*, 275, 3577-82.

Editions

2009-04-28	Edited	Jupe, S.
2009-06-03	Authored	Akkerman, JW.
2009-09-02	Reviewed	Kikutani, H., Kumanogoh, A.
2014-12-26	Reviewed	Rivero Crespo, F.