Activated CIT phosphorylates MRLCs

Orlic-Milacic, M., Rivero Crespo, F.

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

20/09/2019

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. ↗

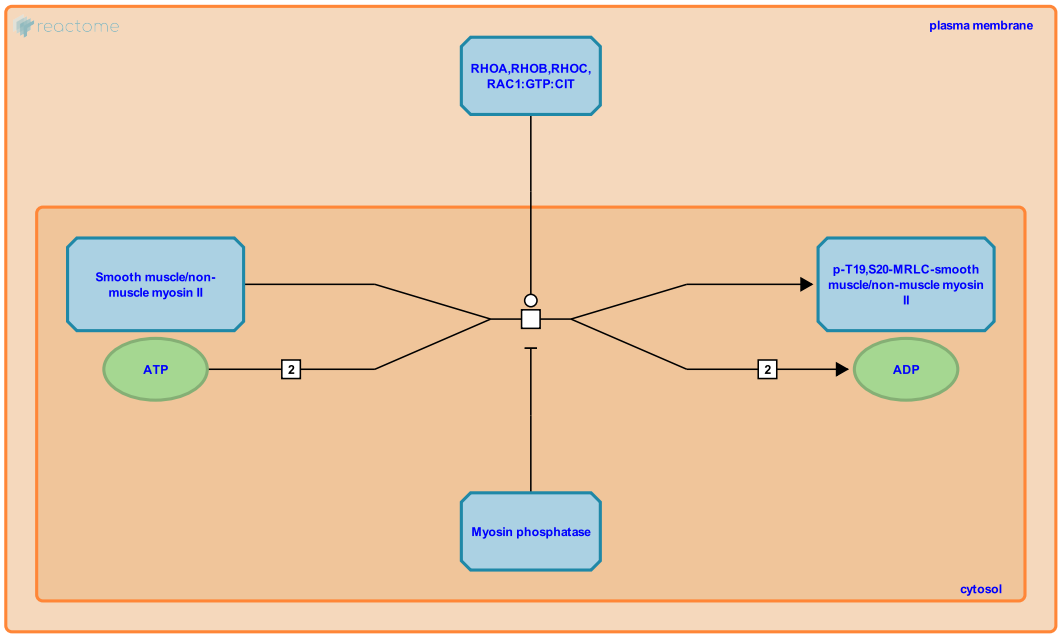
Activated CIT phosphorylates MRLCs ↗

Stable identifier: R-HSA-5671919

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: Activated Cit phosphorylates MRLCs of myosin II complex (Bos taurus)



Activated CIT phosphorylates MRLCs (mysoin regulatory light chains) at threonine T19 and serine S20 (also labeled in the literature as T18 and S19), and can restore stress fibre assembly when ROCKs are inhibited, although ROCKs play the dominant role in stress fiber formation-related phosphorylation of MRLCs. CIT-mediated phosphorylation of MRLCs may be important during cytokinesis. Unlike ROCKs, CIT does not phosphorylate the myosin binding subunit of the myosin phosphatase complex (Yamashiro et al. 2003).

Literature references

Yamashiro, S., Totsukawa, G., Yamakita, Y., Sasaki, Y., Madaule, P., Ishizaki, T. et al. (2003). Citron kinase, a Rho-dependent kinase, induces di-phosphorylation of regulatory light chain of myosin II. *Mol. Biol. Cell, 14*, 1745-56. ↗

Editions

2014-10-24	Authored	Orlic-Milacic, M.
2014-12-26	Authored	Rivero Crespo, F.
2015-02-02	Edited	Orlic-Milacic, M.