

Activation of Talin

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https://reactome.org

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

- 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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

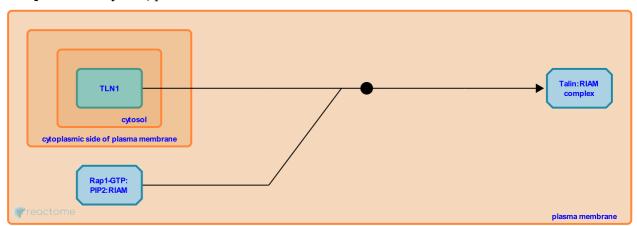
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Activation of Talin ₹

Stable identifier: R-HSA-354097

Type: binding

Compartments: cytosol, plasma membrane



Talin is one of the major cytoskeletal proteins involved in integrin activation and linking the resulting focal adhesion (FA) with cytoskeleton. Talin comprises an N-ter head region and a flexible rod domain. The head region has the FERM domain (subdivided into F1, F2 and F3 subdomains), which has the binding sites for beta integrin cytoplasmic regions and actin binding sites close to the C-terminal rod domain.

Talin exists in closed inactive conformation, where the head region interacts with the rod domain masking the integrin binding sites. At the plasma membrane the RIAM bound to active Rap1 recruits talin to form the integrin activation complex. This interaction exposes the integrin-binding site in talin F3 domain leading to integrin activation.

Literature references

Kasirer-Friede, A., Kahn, ML., Shattil, SJ. (2007). Platelet integrins and immunoreceptors. *Immunol Rev, 218*, 247-64.

Gingras, AR., Critchley, DR. (2008). Talin at a glance. J Cell Sci, 121, 1345-7.

Editions

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