

Linkage of L1 with treadmilling F-actin

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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

- 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. [↗](#)

Reactome database release: 74

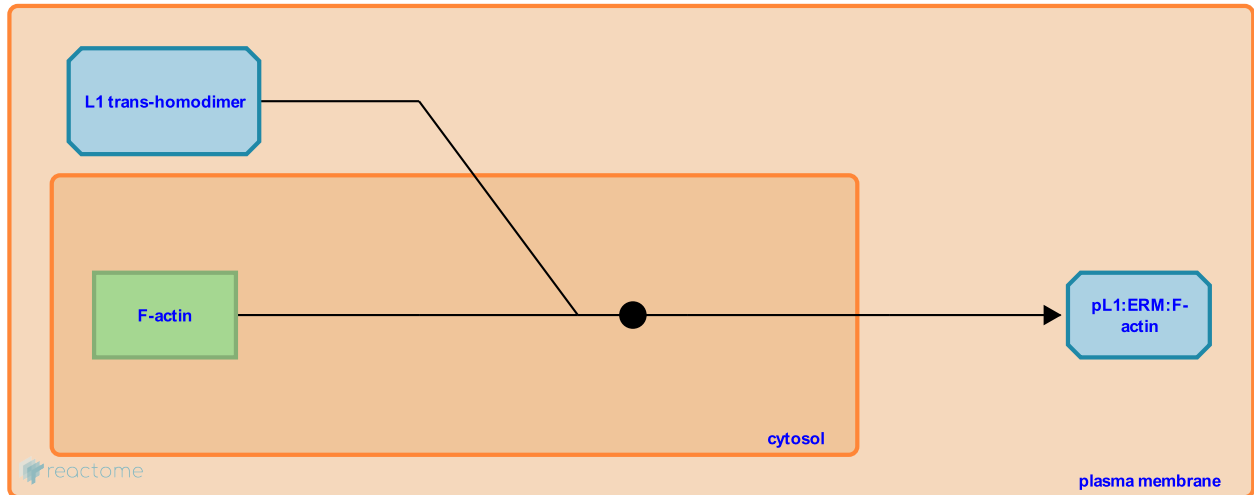
This document contains 1 reaction ([see Table of Contents](#))

Linkage of L1 with treadmilling F-actin [↗](#)

Stable identifier: R-HSA-443779

Type: binding

Compartments: cytosol, plasma membrane



The COOH termini of all ERM proteins have sequence motifs that bind directly to F-actin. The L1 molecules on the cell surface are translocated to the C-domain by coupling with the retrograde F-actin. The force generated by linking L1 clusters with retrograde F-actin flow leads to the migration of the growth cone.

Literature references

Sakurai, T., Gil, OD., Whittard, JD., Gazdoui, M., Joseph, T., Wu, J. et al. (2008). Interactions between the L1 cell adhesion molecule and ezrin support traction-force generation and can be regulated by tyrosine phosphorylation. *J Neurosci Res*, 86, 2602-14. [↗](#)

Editions

2008-07-30	Authored, Edited	Garapati, P V.
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