

Shootin-1 links L1 and retrograde actin

flow

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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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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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- 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: 70

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

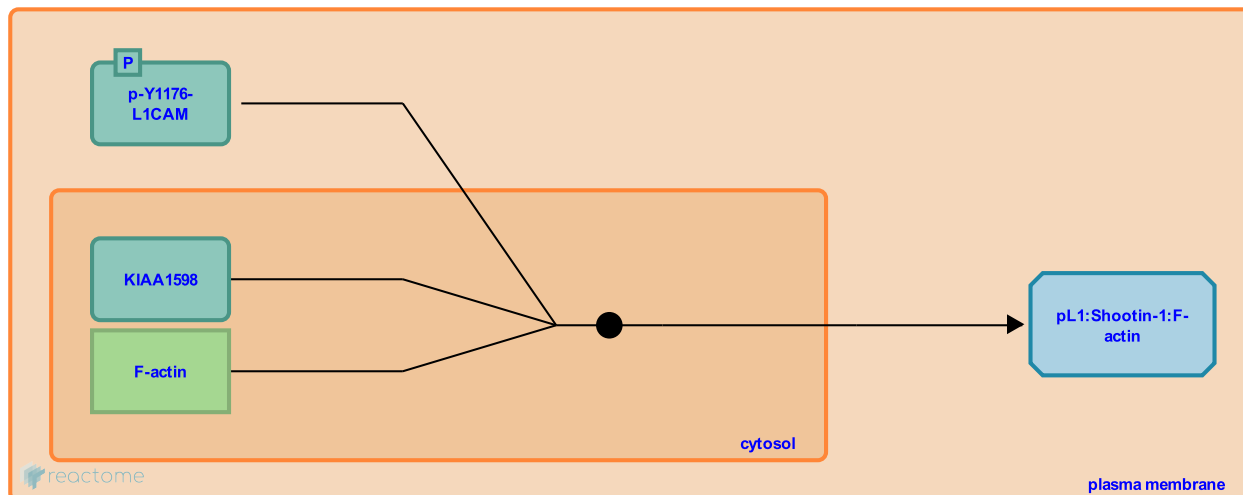
Shootin-1 links L1 and retrograde actin flow [↗](#)

Stable identifier: R-HSA-373736

Type: binding

Compartments: cytosol, plasma membrane

Inferred from: [Shootin-1 links L1 and retrograde actin flow \(Rattus norvegicus\)](#)



Shootin-1 acts as a linker protein, binding L1 to moving actin filaments in axonal growth cones. This interaction mediates the migration of L1 on the plasma membrane from P-domain to the C-domain of the growth cone and enhances neurite elongation.

Editions

2008-07-30	Authored, Edited	Garapati, P V.
2010-02-16	Reviewed	Maness, PF.