

SHARPIN binds SHANK proteins

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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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- 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: 88

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

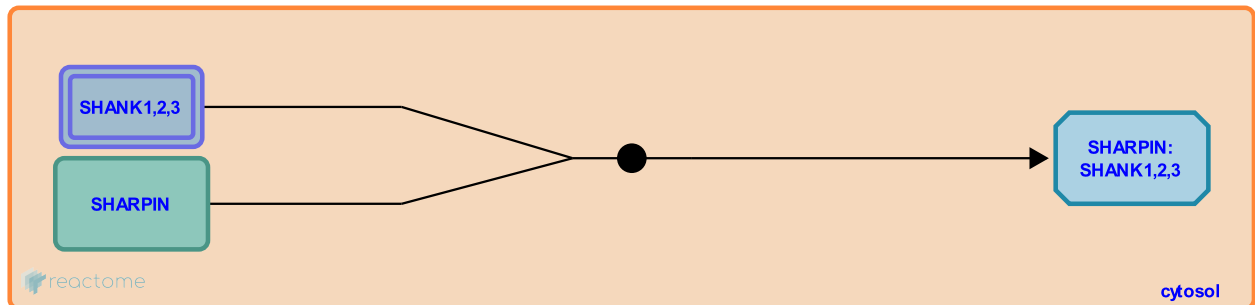
SHARPIN binds SHANK proteins [↗](#)

Stable identifier: R-HSA-6794351

Type: binding

Compartments: cytosol

Inferred from: [Shank1 binds Sharpin \(Rattus norvegicus\)](#)



SHANK with its ankyrin repeats has been found to bind SHARPIN a molecule that can form homomers. SHARPIN is another PSD protein enriched at synaptic sites in mature neurons and may be involved in the formation and maintenance of excitatory synaptic structures (Lim et al. 2001).

Editions

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Washbourne, P.