

LGI3 binds ADAM22,23,synatxin1

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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: 88

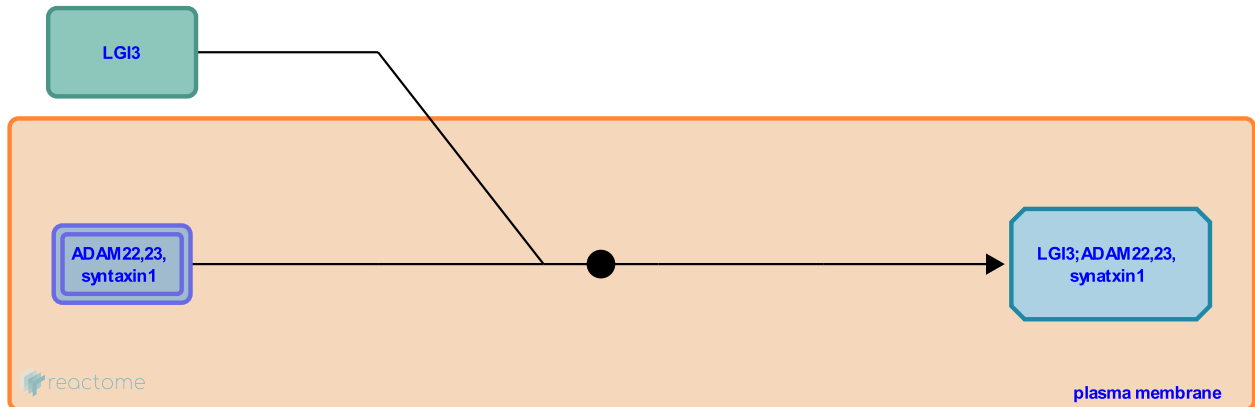
This document contains 1 reaction ([see Table of Contents](#))

LGI3 binds ADAM22,23,syntaxin1 [↗](#)

Stable identifier: R-HSA-5682802

Type: binding

Compartments: extracellular region, plasma membrane



Leucine-rich glioma inactivated 3 (LGI3) is a secreted protein and a member of LGI/epitempin family expressed in the peripheral nerve and interacts with ADAM22 and ADAM23 as well as syntaxin1 in the presynaptic SNARE complex. LGI3 is suggested to be involved in multiple functions. It induces neurite outgrowth and increases phosphorylation of the signal transduction proteins AKT and FAK (focal adhesion kinase) (Park et al. 2010). It appears to promote amyloid beta and syntaxin1 endocytosis (Kimura et al. 2007, Okabayashi & Kimura 2008,2010).

Literature references

- Okabayashi, S., Kimura, N. (2008). Leucine-rich glioma inactivated 3 is involved in amyloid beta peptide uptake by astrocytes and endocytosis itself. *Neuroreport*, 19, 1175-9. [↗](#)
- Okabayashi, S., Kimura, N. (2010). LGI3 interacts with flotillin-1 to mediate APP trafficking and exosome formation. *Neuroreport*, 21, 606-10. [↗](#)
- Negishi, T., Suzaki, S., Ishii, Y., Kyuwa, S., Yoshikawa, Y., Kimura, N. (2007). Abeta upregulates and colocalizes with LGI3 in cultured rat astrocytes. *Cell. Mol. Neurobiol.*, 27, 335-50. [↗](#)
- Baek, KJ., Park, WJ., Yun, HY., Kwon, NS., Kim, DS., Lim, YY. (2010). Leucine-rich glioma inactivated 3 induces neurite outgrowth through Akt and focal adhesion kinase. *Neurochem. Res.*, 35, 789-96. [↗](#)

Editions

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