

GKAPs bind PSD-95 members

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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](#))

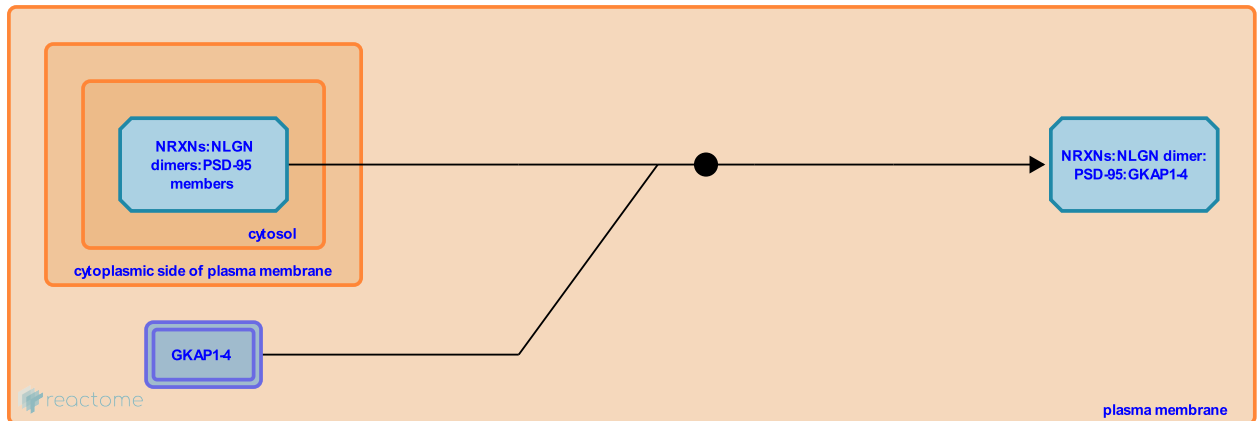
GKAPs bind PSD-95 members ↗

Stable identifier: R-HSA-6794338

Type: binding

Compartments: plasma membrane, cytosol

Inferred from: GKAP bind Psd-95 (Rattus norvegicus)



Guanylate kinase-associated protein (GKAP; also known as synapse-associated 42 protein 90-postsynaptic density-95-associated protein (SAPAP) and Discs-large-associated 43 protein (DAP) family proteins) a synaptic protein is one of the major constituent of the postsynaptic density (PSD). GKAP binds directly to the GK (guanylate kinase-like) domain of the four known members of the PSD-95 (postsynaptic density protein 95) family (Kim et al. 1997, Naisbitt et al. 1997, Takeuchi et al. 1997). GKAP is therefore one of the major scaffold proteins organizing glutamate receptors in the PSD.

Editions

2015-09-04	Authored, Edited	Garapati, P V.
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