SALMs 1-3 bind to PSD-95 family members

Garapati, P V., Kim, E., Petralia, RS., Seabold, GK.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

23/09/2024

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.
The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. ↗

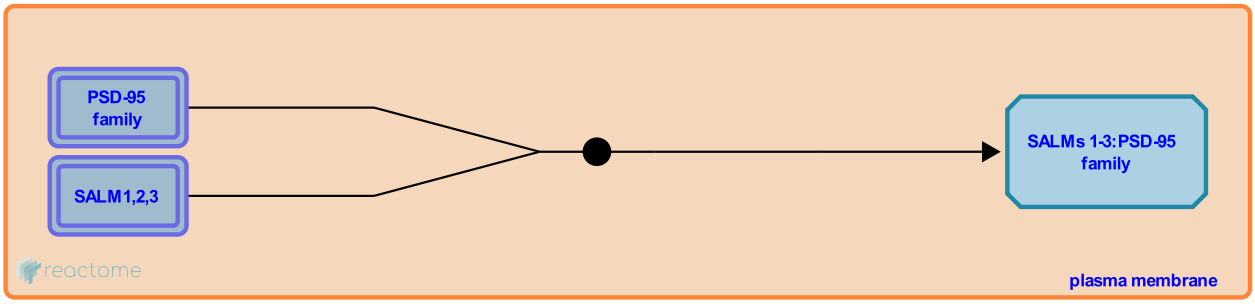
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

SALMs 1-3 bind to PSD-95 family members

Stable identifier: R-HSA-8849891

Type: binding

Compartments: plasma membrane



SALMs 1-3 interact with the PDZ domain containing proteins PSD 95 (DLG4) and synapse associated protein 97 (SAP97 or DLG1) and SAP102 (DLG3), based on yeast 2-hybrid assays (Wang et al. 2006, Ko et al. 2006) and coimmunoprecipitations from detergent solubilized brain (Wang et al. 2006, Ko et al. 2006, Mah et al. 2010) and transiently transfected mammalian cells (Morimura et al., 2006, Wang et al. 2006). PDZ proteins play a central role in organizing functionally diverse membrane proteins at the synapse (Wang et al. 2006, Zheng et al. 2011). PSD-95 family members are abundant postsynaptic scaffolding proteins at excitatory synapses. SALM1 (Wang et al. 2006), SALM2 (Ko et al. 2006), SALM3 and SALM5 (Mah et al. 2010) proteins are enriched in synaptic fractions. SALM5 forms a weak complex with PSD-95, an abundant postsynaptic scaffolding protein at excitatory synapse most likely through indirect interactions (Mah et al. 2010). SALM3 and SALM5, but not other SALMs, induce presynaptic differentiation in contacting axons (Mah et al. 2010).

Literature references

Wang, YX., Wang, CY., Wenthold, RJ., Petralia, RS., Seabold, GK., Chang, K. (2006). A novel family of adhesion-like molecules that interacts with the NMDA receptor. *J. Neurosci., 26*, 2174-83.

Editions

2015-12-18	Authored, Edited	Garapati, P V.
2016-02-04	Reviewed	Kim, E.
2016-05-17	Reviewed	Petralia, RS., Seabold, GK.