FGFRL1 binds SPRED1/2

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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. ↗

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. ↗

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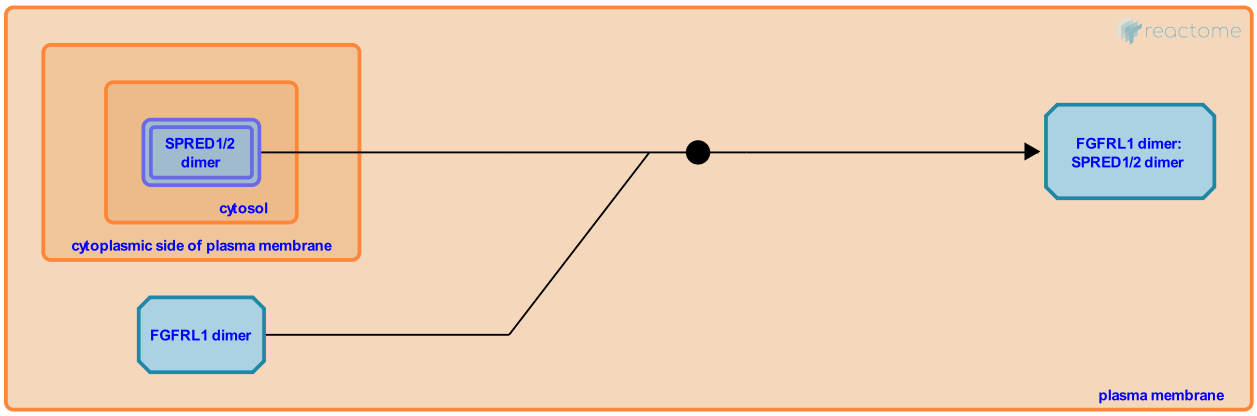
Stable identifier: R-HSA-5654510

Type: binding

Compartments: plasma membrane



FGFRL1 binds to SPRED1 and 2 and Sprouty1 as assessed by co-immunoprecipitation, although the exact stoichiometry of the complex remains to be determined. The interaction requires the C-terminal residues of the short intracellular domain of FGFRL1 (Zhuang et al, 2011). The SPRED proteins are members of the Sprouty family, with established roles as negative regulators of the Ras/Raf/Erk signaling pathway (reviewed in McClatchey and Cichowski, 2012).

Literature references

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Editions

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