Recruitment of p190RhoGEF to p-FAK

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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. ↗

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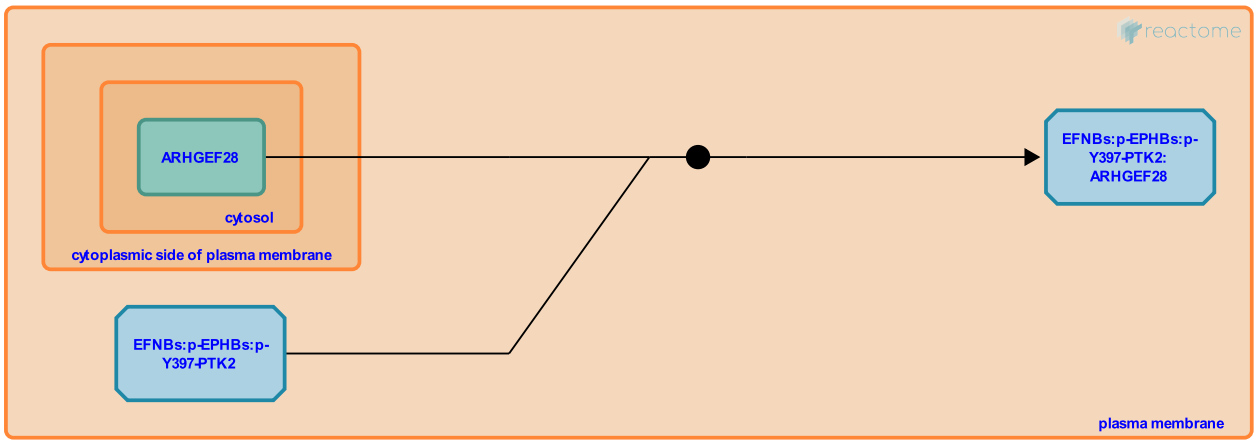
Stable identifier: R-HSA-3928598

Type: binding

Compartments: cytosol, plasma membrane



FAK-mediated spine morphogenesis was shown to occur, in part through Rho guanine nucleotide exchange factor 28 (ARHGEF28, p190RhoGEF), suggesting that FAK-mediated spine maturation might proceed through a FAK-RhoGEF-RHOA mechanism. p190RhoGEF binds directly to phosphorylated PTK2 through a motif in the RhoGEF C-terminal domain, a feature not shared with other GEFs (Moeller et al. 2006, Rico et al. 2004, Zhai et al. 2003).

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Editions

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