

NGEF binds EPHA

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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](#))

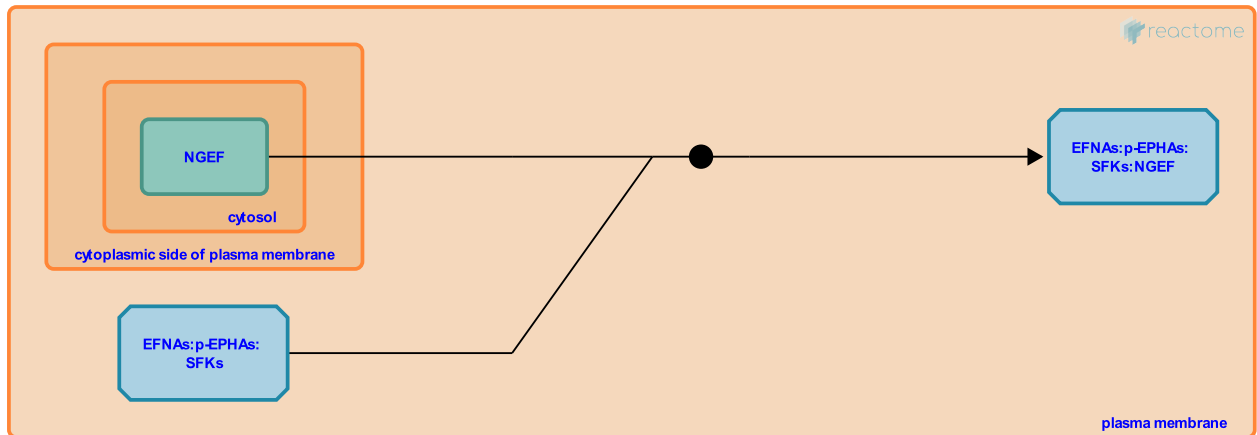
NGEF binds EPHA ↗

Stable identifier: R-HSA-3928602

Type: binding

Compartments: plasma membrane, cytosol

Inferred from: Ephexin1 binds to EphA4 (Mus musculus)



Ephexin1/NGEF (Neuronal guanine nucleotide exchange factor) is a member of the Dbl family of guanine nucleotide exchange factors (GEFs) for Rho GTPases, which interacts with cytoplasmic domain of EPHAs. NGEF is highly expressed in the CNS during development and is enriched in neuronal growth cones. NGEF binds to the kinase domain of EPHA through its Dbl homology (DH)-pleckstrin-homology (PH) domains and this binding does not require activation of the receptor. EPHA activation by ephrinA ligands increases the catalytic activity of ephexin1 resulting in enhanced RHOA activation in cortical neurons (Noren & Pasquale 2004, Shamah et al. 2001). Ephrin-A1 also induces the dispersal of acetylcholine receptors clusters at the neuromuscular junction through the activation of NGEF and RhoA (Shi et al., 2010). NGEF is involved in both axonal growth, growth cone collapse, dendritic spine elimination and stabilization of the neuromuscular junction. In the absence of ephrin stimulation, NGEF promotes actin polymerization and axonal growth by stimulating RHOA, RAC1 and CDC42. Whereas in the presence of ephrin stimulation, NGEF induces growth cone collapse by activating RHOA, but not RAC1 and CDC42 (Shamah et al. 2001, Sahin et al. 2005).

Editions

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