p-EFNB binds GRB4

Garapati, P V., Ip, NY.

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

23/01/2021

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. ↗

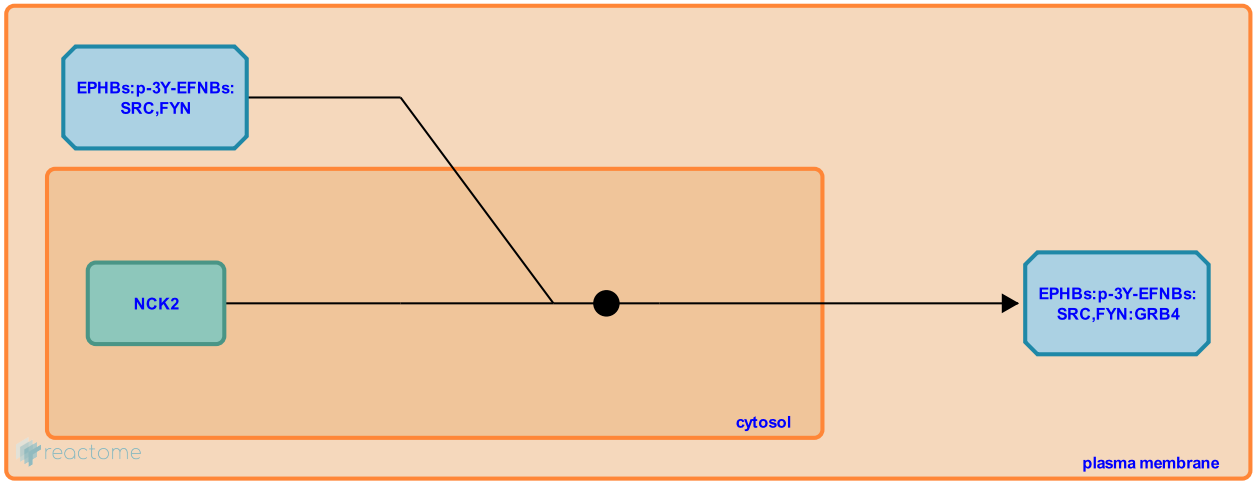
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

p-EFNB binds GRB4

Stable identifier: R-HSA-3928639

Type: binding

Compartments: cytosol, plasma membrane



Unlike EPH receptors, ephrinBs (EFNBs) do not possess intrinsic catalytic activity and thus rely on the recruitment of signaling molecules to signal. Phosphorylated ephrinB (p-EFNB) provides docking site for the SH2/SH3 domain-containing adapter protein cytoplasmic protein NCK2 (NCK2 aka GRB4) (Cowan & Henkemeyer 2001). GRB4 is able to bind to phosphotyrosines in EFNBs through their SH2 domains and 'PxxP' motifs through their SH3 domains. It has been postulated that GRB4 acts as a bridge between EFNBs and G protein-coupled receptor kinase interacting protein (GIT) 1 and Rac at synapses (Segura et al. 2007).

Literature references

Segura, I., Essmann, CL., Weinges, S., Acker-Palmer, A. (2007). Grb4 and GIT1 transduce ephrinB reverse signals modulating spine morphogenesis and synapse formation. *Nat. Neurosci., 10*, 301-10.

Cowan, CA., Henkemeyer, M. (2001). The SH2/SH3 adaptor Grb4 transduces B-ephrin reverse signals. *Nature, 413*, 174-9.

Editions

2013-07-23	Authored, Edited	Garapati, P V.
2014-05-19	Reviewed	Ip, NY.