Interaction of SOS-1 to Tie2 bound Grb2

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29/04/2024

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. ↗

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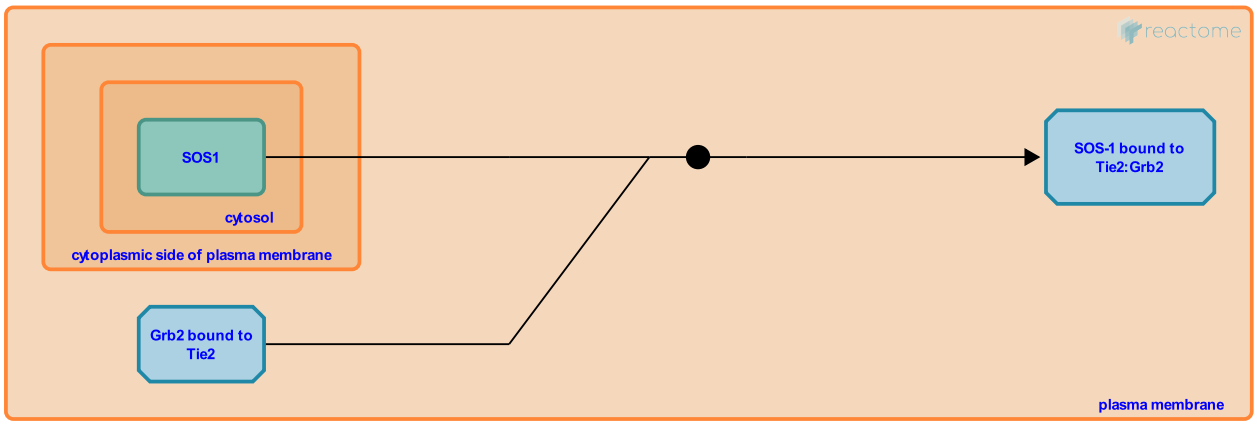
Stable identifier: R-HSA-210974

Type: binding

Compartments: cytosol, plasma membrane



Grb2 binds directly to autophosphorylated Tie2 receptor. GRB2 also contains two SH3 domains, which bring various ligands to the sites of active signaling. One of the SH3 domains on Tie2-bound Grb2 recruits SOS1, an activating nucleotide exchange factor for Ras. This interaction of Sos1 to Grb2 brings Sos1 towards Ras molecules leading to Ras activation. Ras is implicated in the MAP kinase cascade, a pathway in cell growth stimulation, migration and differentiation.

Literature references

Dumont, DJ., Jones, N. (2000). Tek/Tie2 signaling: new and old partners. *Cancer Metastasis Rev, 19*, 13-7.

Peters, KG., Turck, CW., Huang, L., Rao, P. (1995). GRB2 and SH-PTP2: potentially important endothelial signaling molecules downstream of the TEK/TIE2 receptor tyrosine kinase. *Oncogene, 11*, 2097-103.

Editions

2008-02-26	Reviewed	Trowsdale, J.
2008-03-05	Authored	de Bono, B., Garapati, P V.