

ROBO3.1 antagonizes ROBO1/ROBO2 to allow floor plate crossing

Garapati, P V., Jaworski, A., Kidd, T., Orlic-Milacic, M.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

06/05/2024

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. [↗](#)

Reactome database release: 88

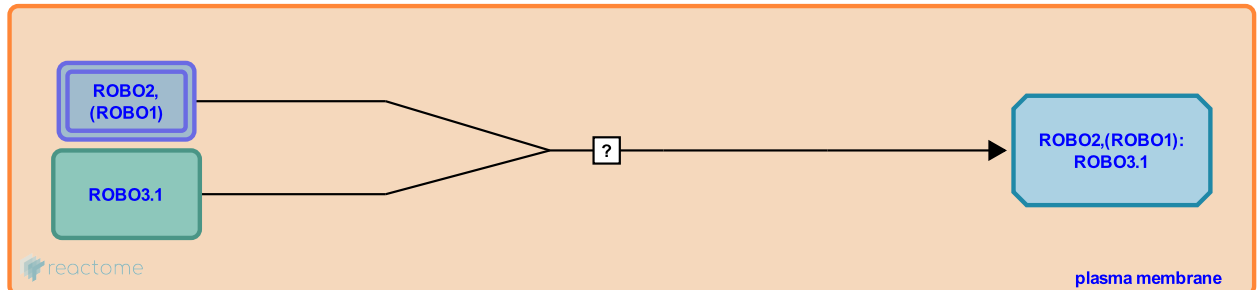
This document contains 1 reaction ([see Table of Contents](#))

ROBO3.1 antagonizes ROBO1/ROBO2 to allow floor plate crossing ↗

Stable identifier: R-HSA-428510

Type: uncertain

Compartments: plasma membrane



ROBO3 antagonizes ROBO1/ROBO2 function to prevent their response to SLIT, thus allowing cells that are expressing ROBO1/ROBO2 to progress towards and across the floor plate. Exactly how ROBO3 interferes with ROBO1/ROBO2 function is not yet clear (Chen et al. 2008). It was shown that ROBO3 isoform ROBO3.1 reduces the amount of ROBO1 and ROBO2 at the cell surface and suggested that ROBO3.1 acts by directing ROBO1 and ROBO2 to late endosome- and lysosome-dependent degradation pathway (Li et al. 2014). Direct binding of ROBO3.1 to ROBO2 was demonstrated (Li et al. 2014).

During commissural axon midline crossing in *Drosophila*, Robo1 signaling can also be antagonized with Robo2 expressed in trans. Extracellular domains of Robo1 and Robo2 may interact through their Ig domains, preventing Robo1 activation by Slits and interfering with axon repulsion (Evans et al. 2015).

Literature references

Lei, Y., Cheng, Y., Li, L., Zhen, X., Liu, S., Yao, C. (2014). Robo3.1A suppresses slit-mediated repulsion by triggering degradation of Robo2. *J. Neurosci. Res.*, 92, 835-46. ↗

Editions

2008-09-05	Authored, Edited	Garapati, P V.
2009-08-18	Reviewed	Kidd, T.
2017-06-23	Edited	Orlic-Milacic, M.
2017-07-31	Reviewed	Jaworski, A.