ROBO2 gene transcription is stimulated by HOXA2 and inhibited by LHX2

Jaworski, A., Orlic-Milacic, M.

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

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. ↗

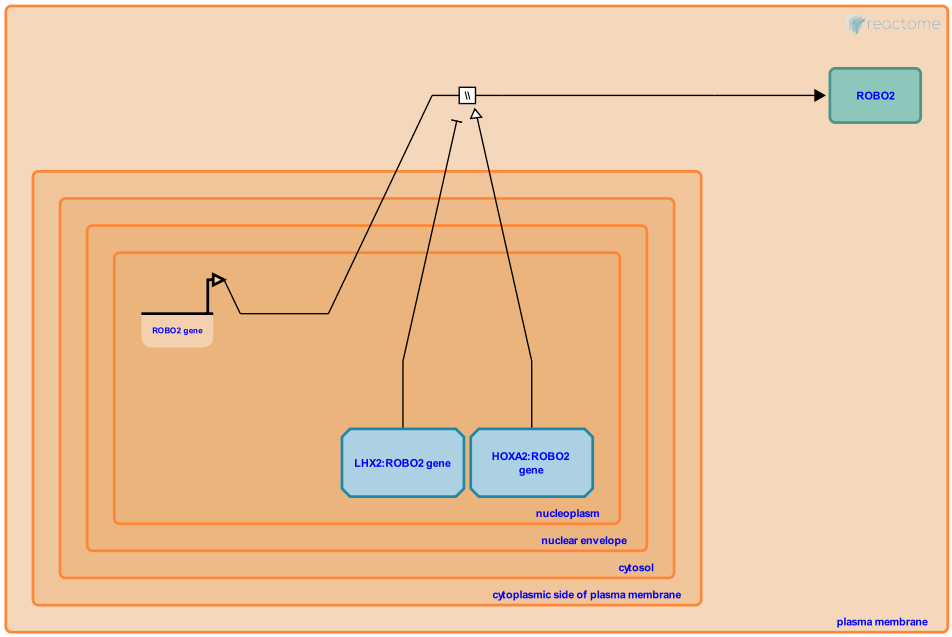
ROBO2 gene transcription is stimulated by HOXA2 and inhibited by LHX2 ↗

Stable identifier: R-HSA-9010523

Type: omitted

Compartments: nucleoplasm, plasma membrane

Inferred from: Robo2 gene expression is stimulated by Hoxa2 and inhibited by Lhx2 (Mus musculus)



Based on studies in mice, the homeobox transcription factor HOXA2, which directly binds to an evolutionarily conserved site in the second intron of the ROBO2 gene, is needed for the maintenance of ROBO2 expression during pontine neuron migration (Geisen et al. 2008).

Also based on mouse studies, LHX2, a LIM-homeodomain transcription factor, directly represses transcription of the ROBO2 gene by binding to evolutionarily conserved LHX2 binding sites about 50 kb downstream from the ROBO2 gene transcription start site. LHX2 is involved in thalamocortical axon guidance (Marcos-Mondejar et al. 2012). In commissural relay neurons of the dorsal spinal cord, however, ROBO2 expression is not affected by LHX2 (Wilson et al. 2008).

In zebrafish, transcription of Robo2 is directly stimulated by Mecp2 (Leong et al. 2015).

Editions

2017-06-23	Authored	Orlic-Milacic, M.
2017-07-31	Reviewed	Jaworski, A.
2017-08-04	Edited	Orlic-Milacic, M.