

ISL1 binds the SLIT2 gene enhancer

Jaworski, A., 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](#). For more information see our [license](#).

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](#))

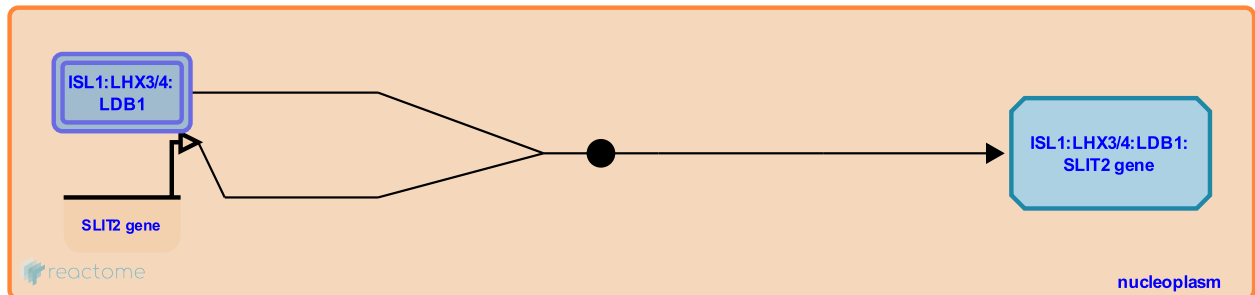
ISL1 binds the SLIT2 gene enhancer [↗](#)

Stable identifier: R-HSA-9010541

Type: binding

Compartments: nucleoplasm

Inferred from: [Isl1 binds the Slit2 gene enhancer \(Mus musculus\)](#)



Based on studies in mice, the transcription factor ISL1, in complex with either LHX3 or LHX4, binds to an evolutionarily conserved LIM-HD binding site in the enhancer of the SLIT2 gene, located in the sixth intron of the SLIT2 gene. The complex of ISL1 and LHX4 regulates SLIT2 expression in branchiomotor neurons, while the complex of ISL1 and LHX3 regulates SLIT2 expression in somatic motor neurons (Kim et al. 2016). From the previous structural studies of the ISL1 complex with LHX3, conducted using mouse and rat proteins, it is known that LDB1 is also part of this complex (Thaler et al. 2002).

Editions

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