

# DLL4 binds NOTCH2

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## 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.

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## 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

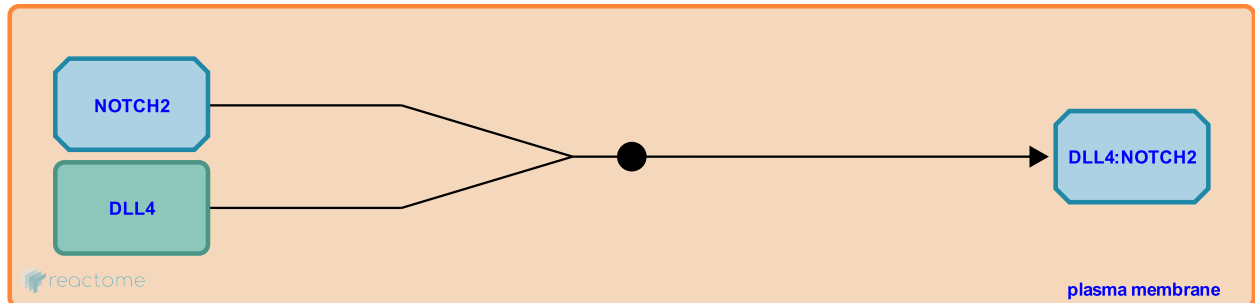
This document contains 1 reaction ([see Table of Contents](#))

## DLL4 binds NOTCH2 [↗](#)

**Stable identifier:** R-HSA-1980051

**Type:** binding

**Compartments:** plasma membrane



DLL4, expressed on a neighboring cell, binds NOTCH2 receptor and activates NOTCH2 intracellular signaling. The study used recombinant NOTCH2 and DLL4, exogenously expressed in Chinese hamster ovary cells. The species origin of NOTCH2 and DLL4 is not specified in the manuscript by Ji et al. 2004. The impact of fringe-mediated modification of NOTCH2 on activation by DLL4 has not been examined.

### Literature references

Zhang, MH., Ji, CY., Zhao, JQ., Ma, DX., Cui, CS., Guo, NJ. (2004). Function of Delta4 gene and its effects on 32D cell differentiation. *Chin Med J (Engl)*, 117, 1687-92. [↗](#)

### Editions

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