

NOTCH1 associates with negative regulators NUMB and ITCH

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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: 82

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

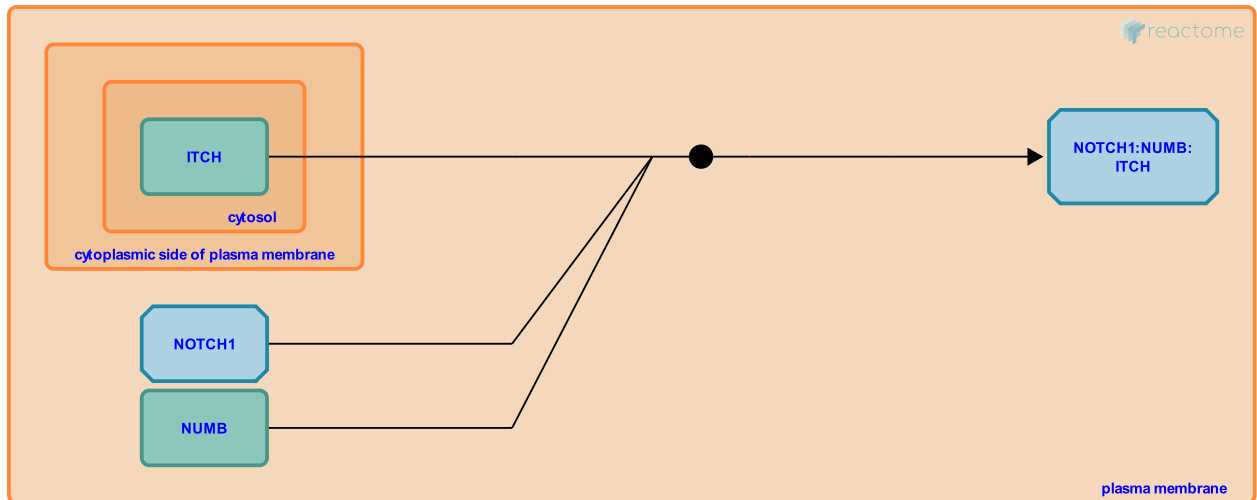
NOTCH1 associates with negative regulators NUMB and ITCH [↗](#)

Stable identifier: R-HSA-1980128

Type: binding

Compartments: cytosol, plasma membrane

Inferred from: [Numb recruits Itch to Notch1 \(Mus musculus\)](#)



Genetic studies in *Drosophila* have identified Numb as an inhibitor of Notch signaling during development of the peripheral and central nervous systems as well as muscle cell differentiation. Both *Drosophila* and mammalian Numb are asymmetrically localized in dividing precursor cells, ensuring that cells adopt distinct cell fates through suppression of Notch signaling in one daughter cell (Rhyu et al. 1994). NUMB recruits E3 ubiquitin ligase ITCH (AIP4) to NOTCH1 and promotes sorting of NOTCH1 through late endosomes for degradation (McGill et al. 2009).

Literature references

Rhyu, MS., Jan, LY., Jan, YN. (1994). Asymmetric distribution of numb protein during division of the sensory organ precursor cell confers distinct fates to daughter cells. *Cell*, 76, 477-91. [↗](#)

McGill, MA., McGlade, CJ., Weinmaster, G., Dho, SE. (2009). Numb regulates post-endocytic trafficking and degradation of Notch1. *J Biol Chem*, 284, 26427-38. [↗](#)

Editions

2011-11-14	Authored	Egan, SE., Orlic-Milacic, M.
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