

# NOTCH1 stimulates HES1 transcription

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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

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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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Reactome database release: 88

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

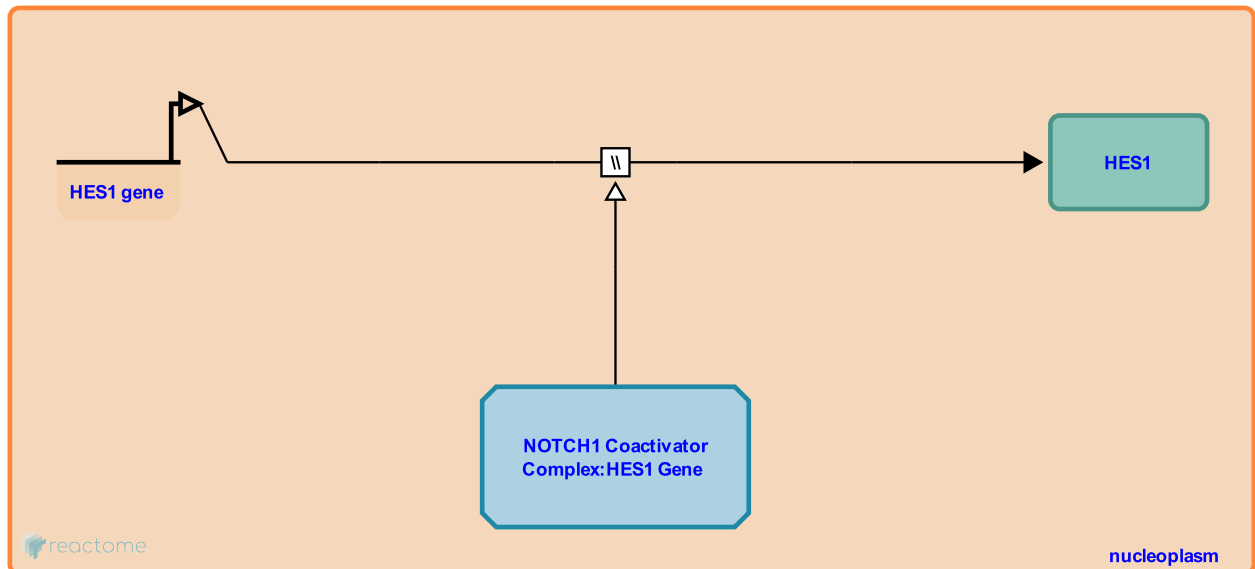
## NOTCH1 stimulates HES1 transcription [↗](#)

**Stable identifier:** R-HSA-1980047

**Type:** omitted

**Compartments:** nucleoplasm

**Inferred from:** [mNICD1 stimulates Hes1 transcription \(Homo sapiens\)](#)



NOTCH1 coactivator complex binds the promoter of HES1 gene and directly stimulates HES1 transcription. HES1 belongs to the bHLH family of transcription factors (Jarriault et al. 1995).

### Literature references

Kopan, R., Schroeter, EH., Brou, C., Israel, A., Jarriault, S., Logeat, F. (1995). Signalling downstream of activated mammalian Notch. *Nature*, 377, 355-8. [↗](#)

### Editions

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