# EGFR phosphorylates NOTCH3

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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. ↗

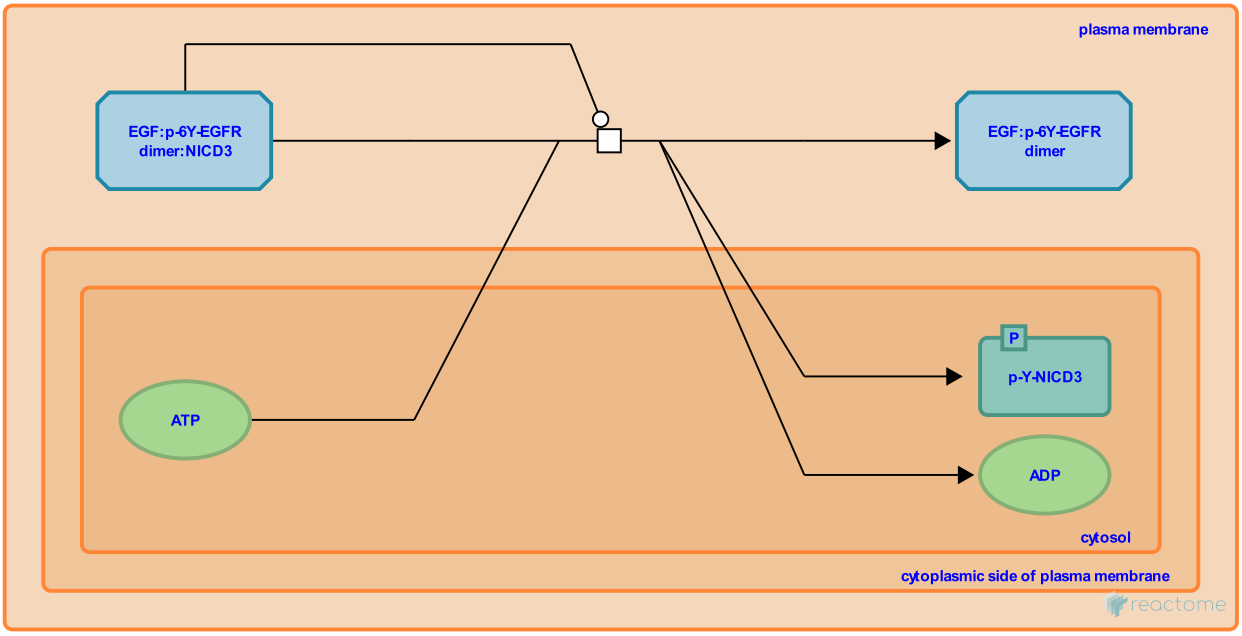
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

## EGFR phosphorylates NOTCH3 ↗

**Stable identifier:** R-HSA-9018572

**Type:** transition

**Compartments:** plasma membrane




EGFR phosphorylates intracellular domain of NOTCH3 (NICD3) on an unknown tyrosine residue. EGFR signaling inhibits NICD3-mediated transcription. It is not known whether EGFR-mediated phosphorylation of NICD3 affects NICD3 nuclear translocation or the formation of the NOTCH3 coactivator complex. Erlotinib treatment, which inhibits EGFR activation, results in increased NOTCH3 signaling and induction of stem-like phenotype in treated cells (Arasada et al. 2014).

## Literature references

Huppert, SS., Carbone, DP., Arasada, RR., Rahman, MA., Amann, JM. (2014). EGFR blockade enriches for lung cancer stem-like cells through Notch3-dependent signaling. *Cancer Res., 74*, 5572-84. ↗

## Editions

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