

NOTCH1 PEST domain mutants bind DLL4

Haw, R., Jassal, B., Orlic-Milacic, M.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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: 81

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

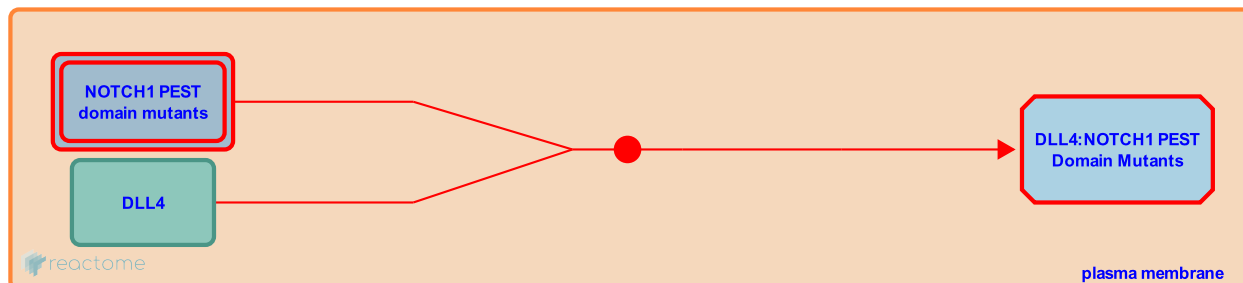
NOTCH1 PEST domain mutants bind DLL4 [↗](#)

Stable identifier: R-HSA-2769000

Type: binding

Compartments: plasma membrane

Diseases: cancer, T-cell leukemia



NOTCH1 PEST domain mutants are expected to bind to DLL4 ligand in an identical fashion to wild-type NOTCH1 (Koch et al. 2008, Hozumi et al. 2008, Benedito et al. 2009).

Literature references

Habu, S., Zuklys, S., Holländer, GA., Hozumi, K., Shima, DT., Hirano, K. et al. (2008). Delta-like 4 is indispensable in thymic environment specific for T cell development. *J Exp Med*, 205, 2507-13. [↗](#)

Benedito, R., Adams, S., Gossler, A., Adams, RH., Fruttiger, M., Roca, C. et al. (2009). The notch ligands Dll4 and Jagged1 have opposing effects on angiogenesis. *Cell*, 137, 1124-35. [↗](#)

Radtke, F., MacDonald, HR., Fiorini, E., Pierres, M., Schuster-Gossler, K., Manley, NR. et al. (2008). Delta-like 4 is the essential, nonredundant ligand for Notch1 during thymic T cell lineage commitment. *J Exp Med*, 205, 2515-23. [↗](#)

Editions

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