Glucosylation of Pre-Notch by Poglut1

D'Eustachio, P., Egan, SE., Haw, R., Orlic-Milacic, M.
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


Reactome database release: 78

This document contains 1 reaction (see Table of Contents)

https://reactome.org
Glucosylation of Pre-Notch by Poglut1

Stable identifier: R-MMU-2023179

Type: transition

Compartments: endoplasmic reticulum lumen, endoplasmic reticulum membrane

In addition to fucosylation of Notch receptor precursors, glucosylation is another crucial step in Notch processing, required for the receptor to be fully functional. Endoplasmic reticulum O-glucosyl transferase Poglut1, homolog of Drosophila Rumi, adds a glucosyl group to conserved serine residues within EGF repeats of Notch. The consensus sequence of Poglut1 glucosylation sites is C1-X-S-X-P-C2, where C1 and C2 are the first and second cysteine residue in the EGF repeat, respectively, while X represents any amino acid. Only those glucosylation sites that are conserved between human, mouse and rat isoforms are shown.

Literature references


Editions

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