

PTPN11 dephosphorylates RUNX1

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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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Reactome database release: 74

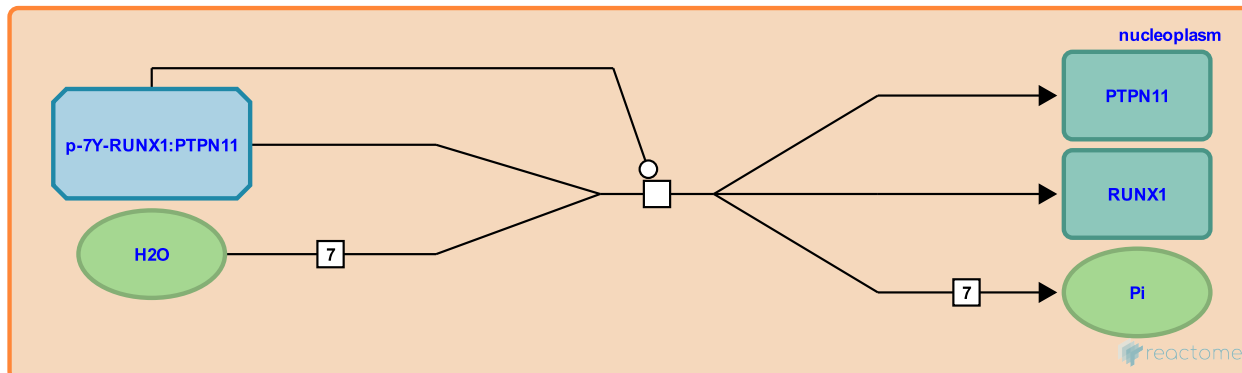
This document contains 1 reaction ([see Table of Contents](#))

PTPN11 dephosphorylates RUNX1 ↗

Stable identifier: R-HSA-8937767

Type: transition

Compartments: nucleoplasm



Based on mouse studies, PTPN11 (SHP2) protein tyrosine phosphatase dephosphorylates SRC-phosphorylated RUNX1 (Huang et al. 2012).

Literature references

Huang, H., Woo, AJ., Waldon, Z., Schindler, Y., Moran, TB., Zhu, HH. et al. (2012). A Src family kinase-Shp2 axis controls RUNX1 activity in megakaryocyte and T-lymphocyte differentiation. *Genes Dev.*, 26, 1587-601. ↗

Editions

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