

PTPN12 dephosphorylates PDGFRB at Y1021

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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

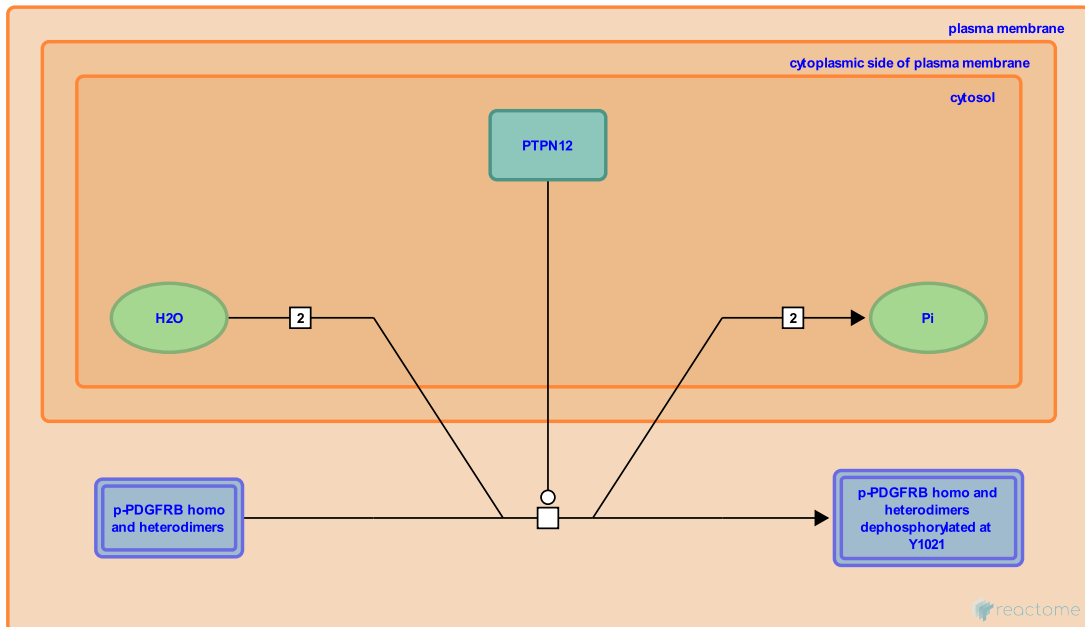
This document contains 1 reaction ([see Table of Contents](#))

PTPN12 dephosphorylates PDGFRB at Y1021 [↗](#)

Stable identifier: R-HSA-8864036

Type: transition

Compartments: cytosol, plasma membrane



Protein tyrosine phosphatase PTNP12 dephosphorylates activated PDFRB (PDGF receptor beta) at tyrosine residue Y1021, which contributes to the tumor suppressor role of PTPN12 in triple negative breast cancer in addition to PTPN12-mediated dephosphorylation of ERBB2 (HER2) at Y1248 (Sun et al. 2011).

Literature references

Schmitt, E., Creighton, CJ., Hilsenbeck, SG., Gygi, SP., Bernardi, RJ., Osborne, CK. et al. (2011). Activation of multiple proto-oncogenic tyrosine kinases in breast cancer via loss of the PTPN12 phosphatase. *Cell*, 144, 703-18. [↗](#)

Editions

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