PTPN12 dephosphorylates ERBB2 on tyrosine Y1248

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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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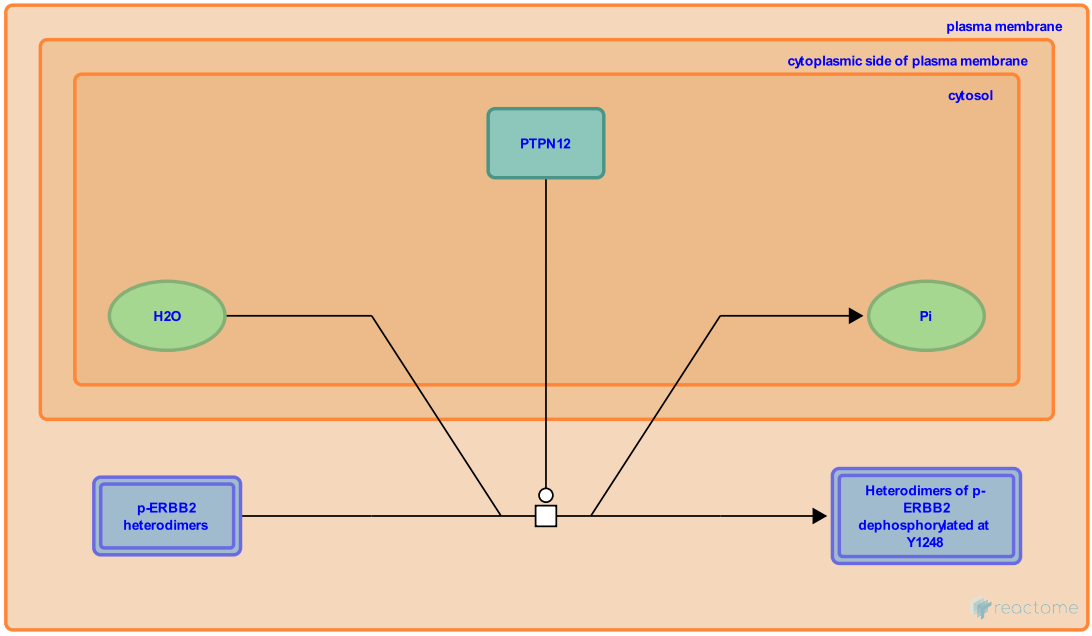
Stable identifier: R-HSA-8863804

Type: transition

Compartments: plasma membrane, cytosol



PTPN12 protein tyrosine phosphatase dephosphorylates activated ERBB2 at tyrosine residue Y1248 and activated EGFR at tyrosine residue Y1148 (Y1148 corresponds to Y1172 of the nascent EGFR, with 24 amino acid signal peptide at the N-terminus). PTPN12-mediated dephosphorylation of ERBB2 attenuates downstream RAS activation, as Y1248 is involved in SHC1 recruitment. Similar to Y1148 of EGFR, Y1248 of ERBB2 is part of the NPXY motif that is, when phosphorylated on the tyrosine residue, recognized by the N-terminal phosphotyrosine interaction domain (PID) of SHC1 (Batzer et al. 1995, Songyang et al. 1995). SHC1 itself could be a target for PTPN12. PTPN12 function is frequently lost in triple negative breast cancer (Sun et al. 2011).

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Editions

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