PTPN12 dephosphorylates EGFR at Y1172 (Y1148)

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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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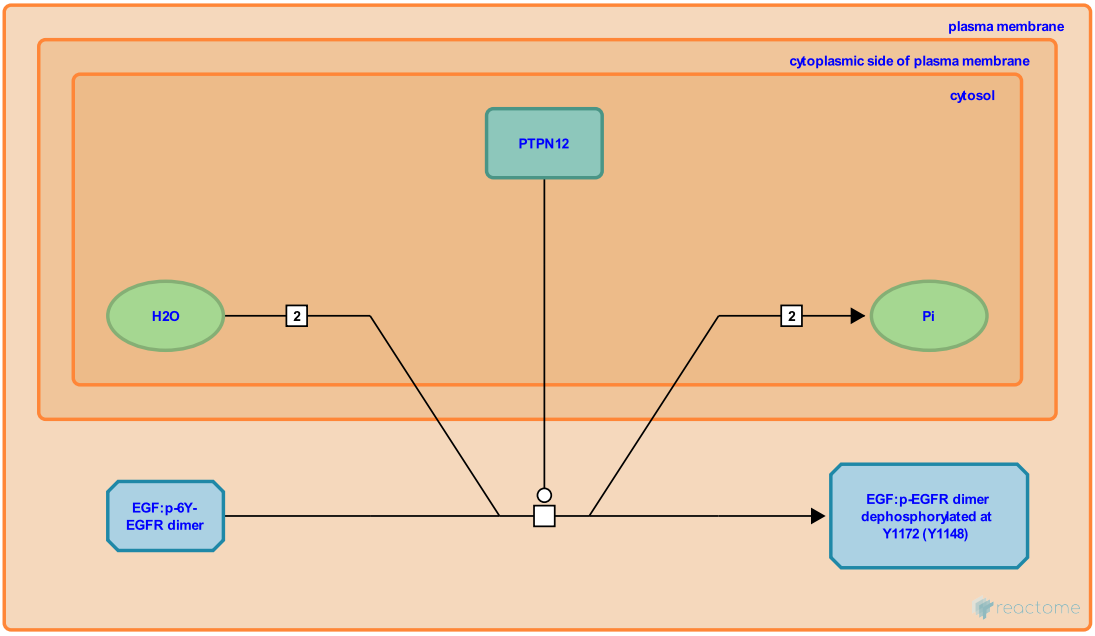
Stable identifier: R-HSA-8864029

Type: transition

Compartments: cytosol, plasma membrane



PTPN12 protein tyrosine phosphatase dephosphorylates activated EGFR at tyrosine residue Y1148 (Y1148 corresponds to Y1172 in the nascent EGFR sequence which includes the 24 amino acid long signal peptide at the N-terminus). PTPN12-mediated dephosphorylation of activated EGFR inhibits SHC1 recruitment to the p-Y1148 (i.e. p-Y1172) docking site, thus attenuating downstream RAS activation (Sun et al. 2011). The recruitment of SHC1 to p-Y1148 (i.e. Y1172) of EGFR is mediated by the N-terminal phosphotyrosine interaction domain (PID) of SHC1 (Batzer et al. 1995, Songyang et al. 1995).

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Editions

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