Autophosphorylation of cytosolic PDGFRA and PDGFRB fusion proteins

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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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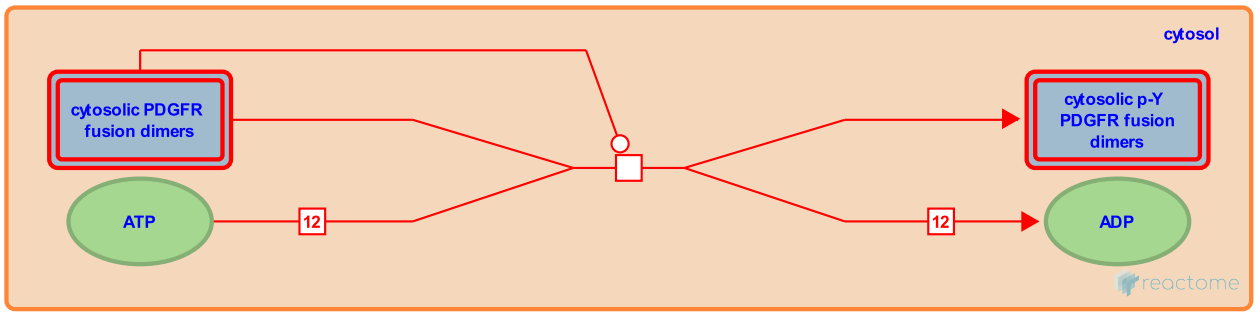
Stable identifier: R-HSA-9673756

Type: transition

Compartments: cytosol

Diseases: cancer



Where examined, cytosolic fusion proteins of PDGFRA and B have been shown to undergo constitutive trans-autophosphorylation in the absence of ligand (Cools et al, 2003; Stover et al, 2006; Salemi et al, 2009; reviewed in Reilly et al, 2003; Wang et al, 2016; Appiah-Kubi et al, 2017). Although downstream signaling has not been investigated in detail, the FIP1L1-PDGFRA fusion has been shown to signal through STAT5 and its expression in Ba/F3 murine cell line promotes oncogenic transformation (Cools et al, 2003).

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Editions

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