

# Autophosphorylation of PDGFR mutant dimers

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18/05/2024

## 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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

## Literature references

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Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)

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Reactome database release: 88

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

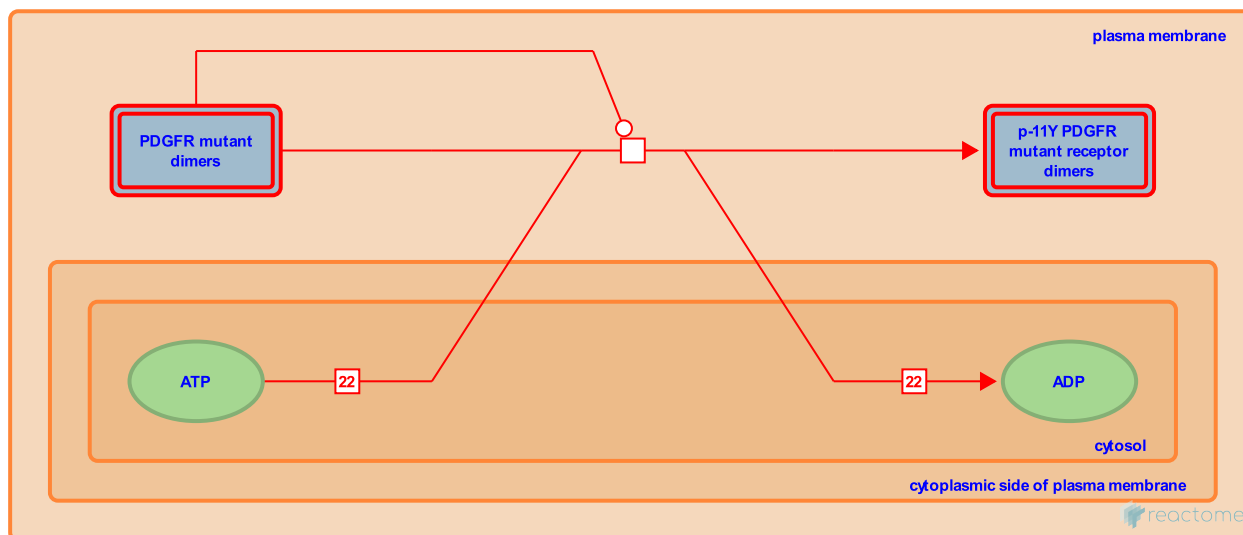
## Autophosphorylation of PDGFR mutant dimers ↗

**Stable identifier:** R-HSA-9672175

**Type:** transition

**Compartments:** cytosol, plasma membrane

**Diseases:** cancer



Activating mutations in the kinase, juxtamembrane and transmembrane domains of PDGFRA lead to constitutive, ligand-independent dimerization and trans-autophosphorylation, and stimulate downstream signaling pathways (Heinrich et al, 2003; Hirota et al, 2003; Corless et al, 2005; Velghe et al, 2014; reviewed in Roskoski et al, 2018; Klug et al, 2018).

### Literature references

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### Editions

2020-02-06	Reviewed	Ip, CKM.
2020-02-25	Authored, Edited	Rothfels, K.