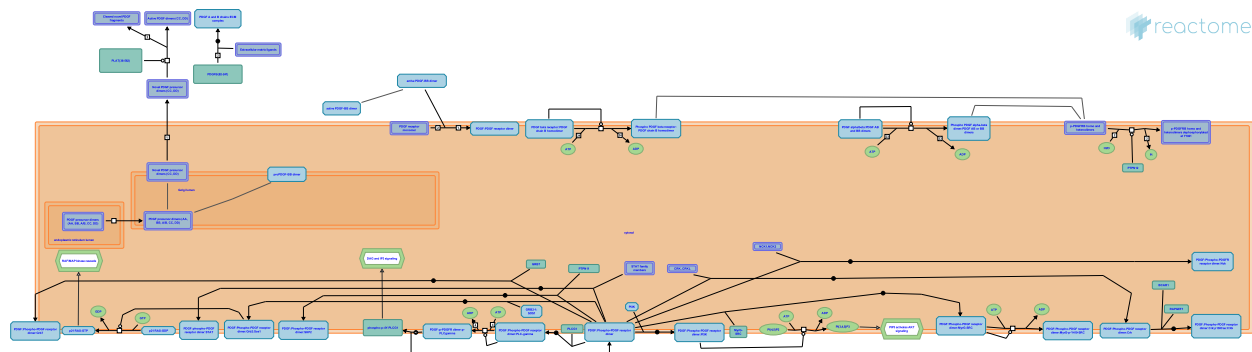


# Signaling by PDGF



European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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.

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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- 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. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

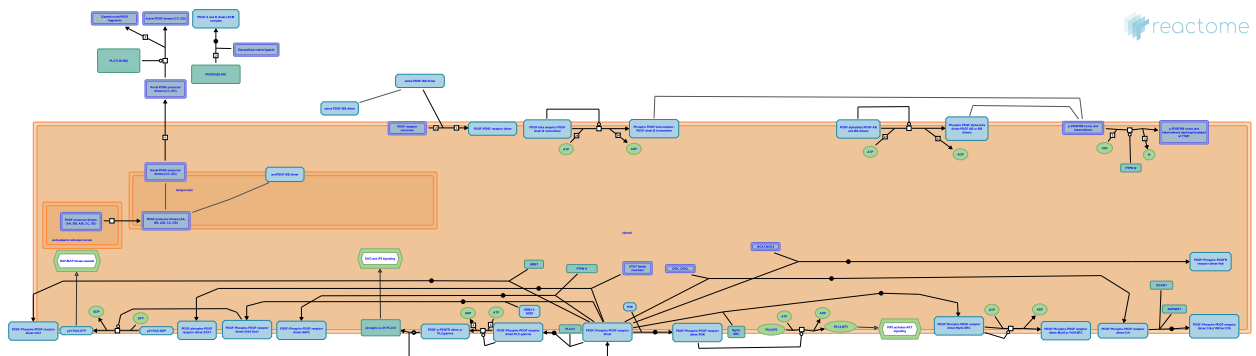
Reactome database release: 70

This document contains 2 pathways and 8 reactions ([see Table of Contents](#))

## Signaling by PDGF ↗

**Stable identifier:** R-BTA-186797

**Inferred from:** Signaling by PDGF (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## Translocation of PDGF from ER to Golgi ↗

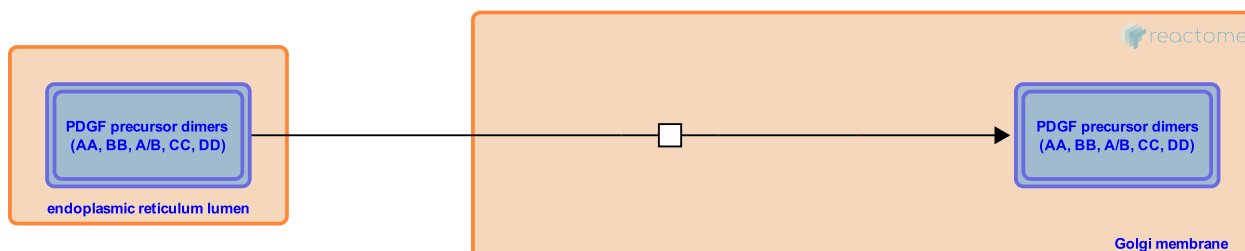
**Location:** [Signaling by PDGF](#)

**Stable identifier:** R-BTA-382053

**Type:** transition

**Compartments:** Golgi membrane, endoplasmic reticulum lumen

**Inferred from:** [Translocation of PDGF from ER to Golgi \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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**Followed by:** [Release of novel PDGFs as latent factors](#)

## Release of novel PDGFs as latent factors ↗

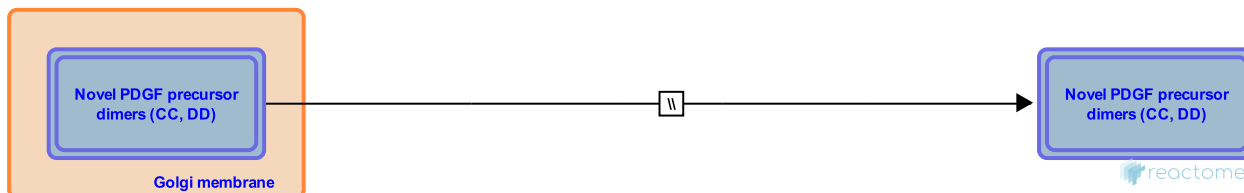
**Location:** [Signaling by PDGF](#)

**Stable identifier:** R-BTA-382057

**Type:** omitted

**Compartments:** extracellular region, Golgi membrane

**Inferred from:** [Release of novel PDGFs as latent factors \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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**Preceded by:** [Translocation of PDGF from ER to Golgi](#)

**Followed by:** [Extracellular processing of novel PDGFs](#)

## Extracellular processing of novel PDGFs ↗

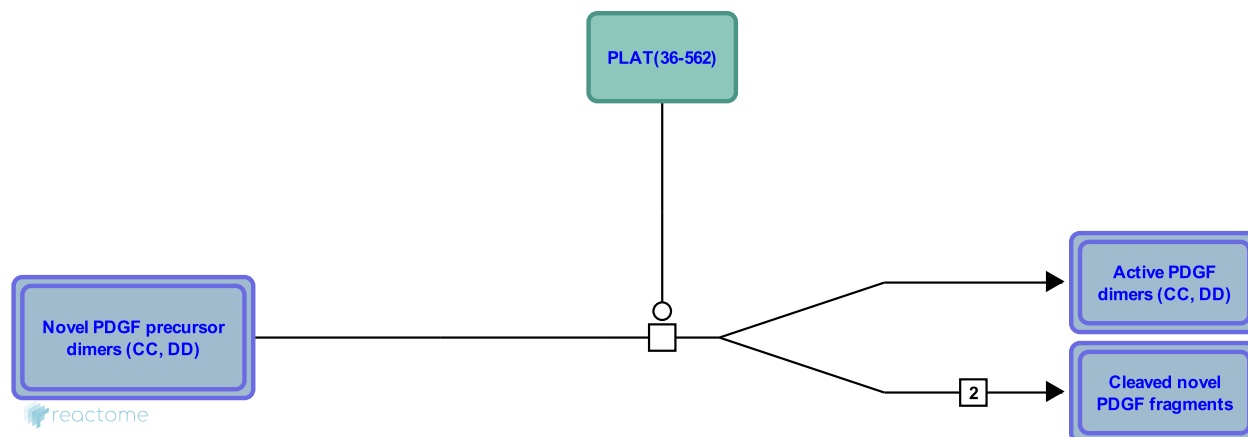
**Location:** [Signaling by PDGF](#)

**Stable identifier:** R-BTA-382061

**Type:** transition

**Compartments:** extracellular region

**Inferred from:** [Extracellular processing of novel PDGFs \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Release of novel PDGFs as latent factors](#)

## PDGF binds to extracellular matrix proteins ↗

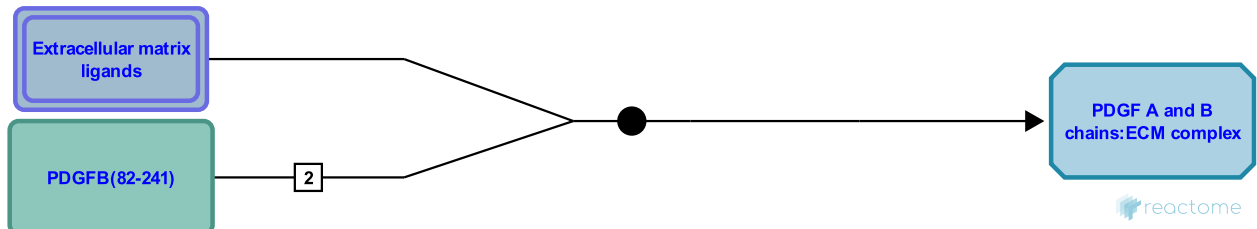
**Location:** Signaling by PDGF

**Stable identifier:** R-BTA-382054

**Type:** binding

**Compartments:** extracellular region

**Inferred from:** PDGF binds to extracellular matrix proteins (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## PDGF dimer binds two receptors simultaneously [↗](#)

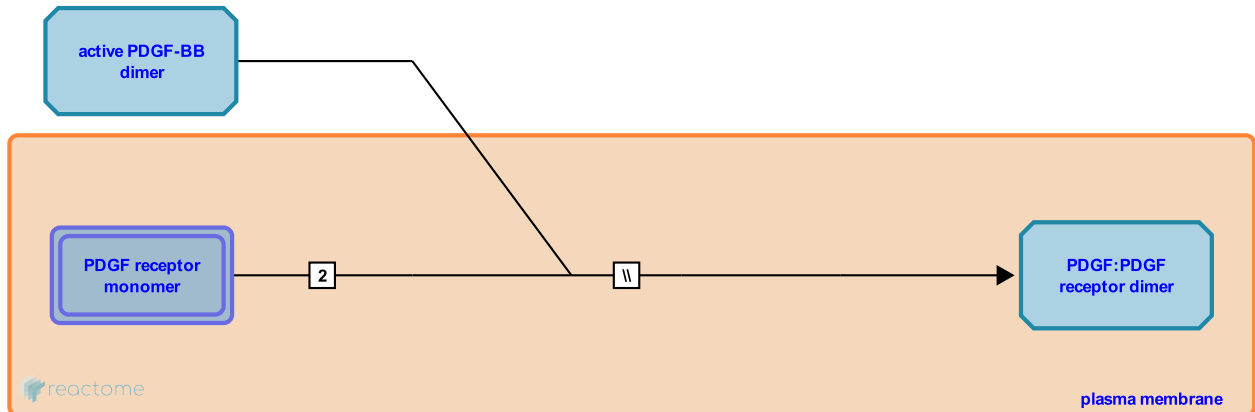
**Location:** [Signaling by PDGF](#)

**Stable identifier:** R-BTA-186773

**Type:** omitted

**Compartments:** plasma membrane

**Inferred from:** [PDGF dimer binds two receptors simultaneously \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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**Followed by:** [Autophosphorylation of PDGF alpha/beta receptors](#), [Autophosphorylation of PDGF beta receptors](#)



## Autophosphorylation of PDGF beta receptors ↗

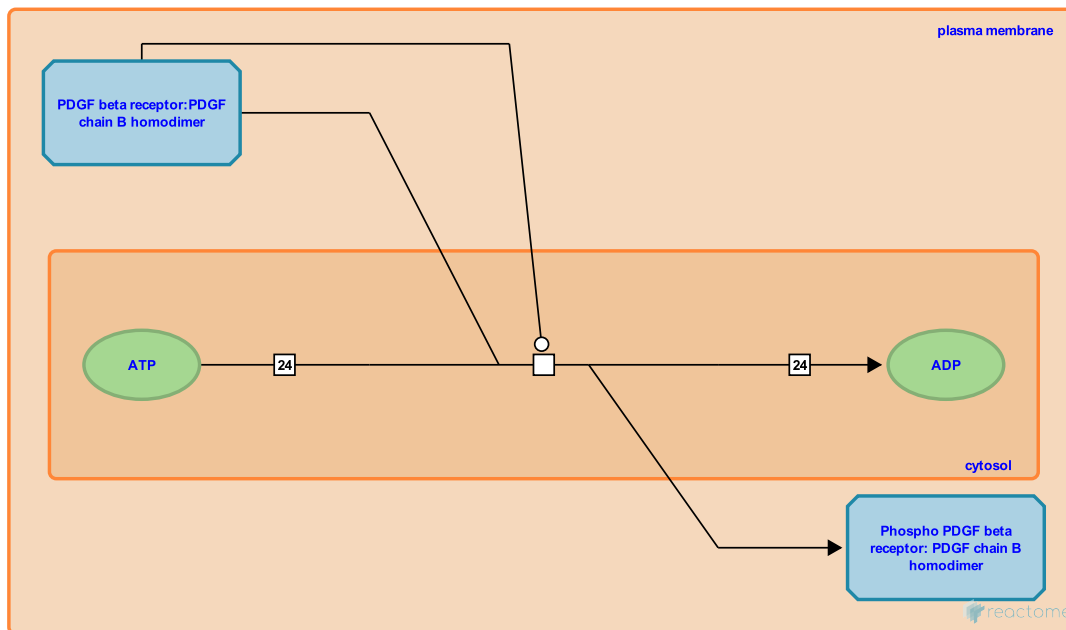
**Location:** Signaling by PDGF

**Stable identifier:** R-BTA-186786

**Type:** transition

**Compartments:** cytosol, plasma membrane

**Inferred from:** Autophosphorylation of PDGF beta receptors (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [PDGF dimer binds two receptors simultaneously](#)

**Followed by:** [PTPN12 dephosphorylates PDGFRB at Y1021](#)

## Autophosphorylation of PDGF alpha/beta receptors ↗

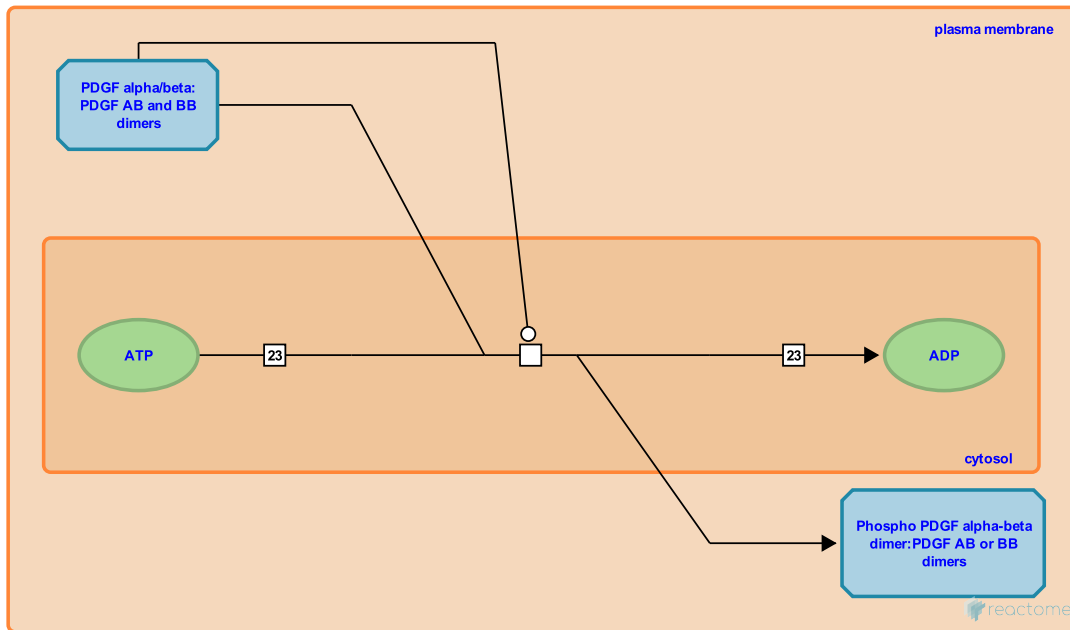
**Location:** Signaling by PDGF

**Stable identifier:** R-BTA-389086

**Type:** transition

**Compartments:** cytosol, plasma membrane

**Inferred from:** [Autophosphorylation of PDGF alpha/beta receptors \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [PDGF dimer binds two receptors simultaneously](#)

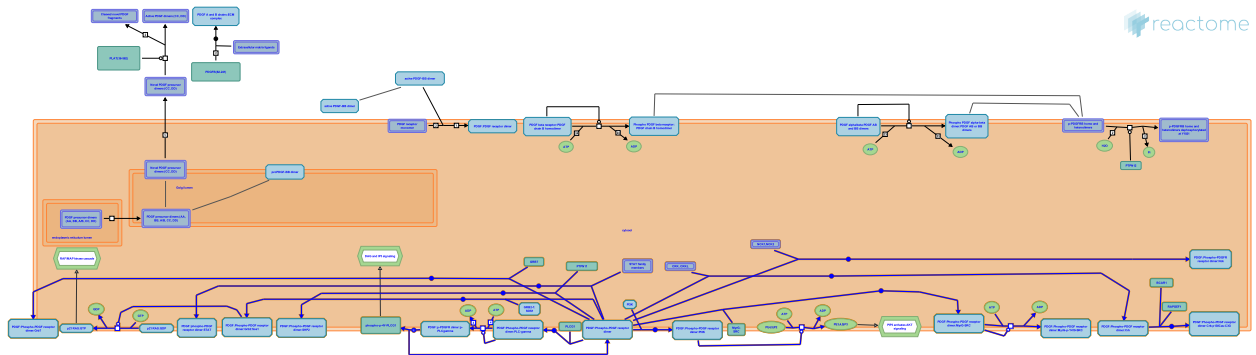
**Followed by:** [PTPN12 dephosphorylates PDGFRB at Y1021](#)

## Downstream signal transduction ↗

**Location:** Signaling by PDGF

**Stable identifier:** R-BTA-186763

**Inferred from:** Downstream signal transduction (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## PTPN12 dephosphorylates PDGFRB at Y1021 [↗](#)

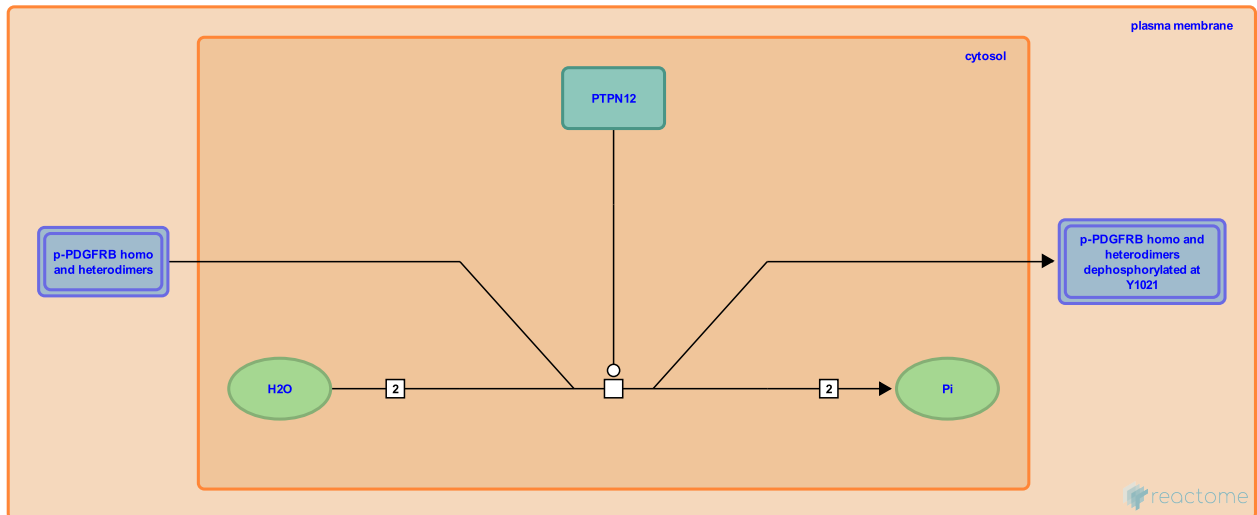
**Location:** [Signaling by PDGF](#)

**Stable identifier:** R-BTA-8864036

**Type:** transition

**Compartments:** cytosol, plasma membrane

**Inferred from:** [PTPN12 dephosphorylates PDGFRB at Y1021 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Autophosphorylation of PDGF beta receptors](#), [Autophosphorylation of PDGF alpha/beta receptors](#)

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