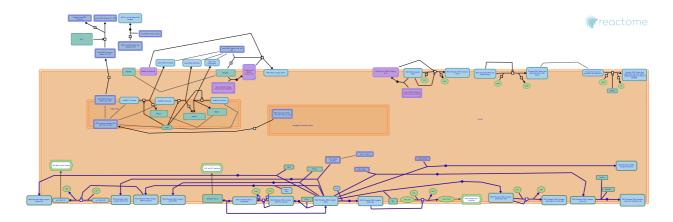


# Downstream signal transduction



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.

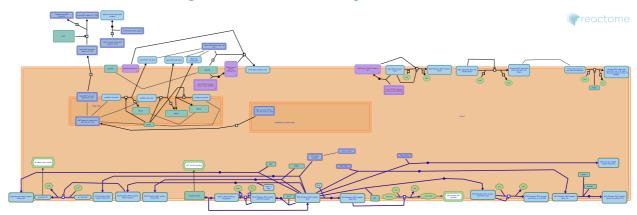
Reactome database release: 77

This document contains 1 pathway and 15 reactions (see Table of Contents)

#### **Downstream signal transduction**

Stable identifier: R-CFA-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.

<a href='/electronic\_inference\_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp</a>

#### PI3-kinase binds to the active receptor **₹**

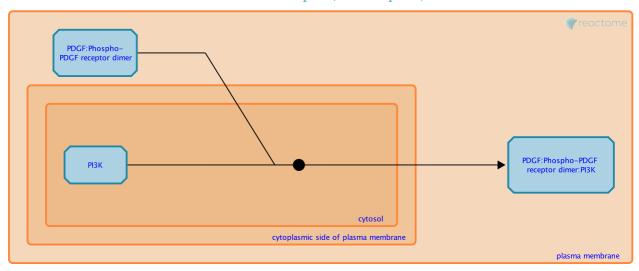
**Location:** Downstream signal transduction

Stable identifier: R-CFA-186780

**Type:** binding

Compartments: cytosol, plasma membrane

Inferred from: PI3-kinase binds to the active receptor (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: PI3K catalyses the phosphorylation of PIP2 to PIP3

### PI3K catalyses the phosphorylation of PIP2 to PIP3

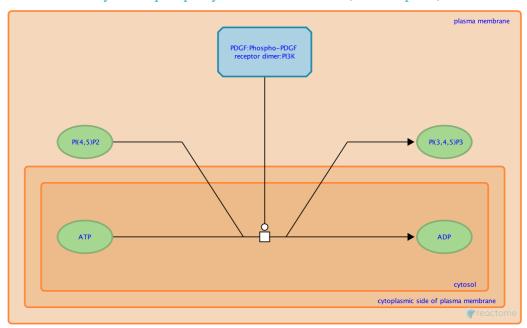
Location: Downstream signal transduction

Stable identifier: R-CFA-186800

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: PI3K catalyses the phosphorylation of PIP2 to PIP3 (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: PI3-kinase binds to the active receptor

#### PLC-gamma binds to the active receptor **₹**

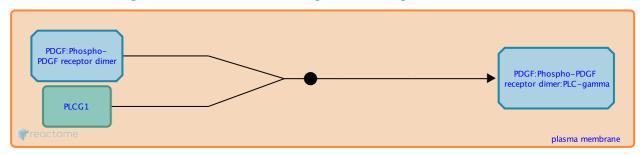
**Location:** Downstream signal transduction

Stable identifier: R-CFA-186765

Type: binding

Compartments: plasma membrane

**Inferred from:** PLC-gamma binds to the active receptor (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: Phosphorylation of PLCgamma by PDGFR

#### Phosphorylation of PLCgamma by PDGFR >

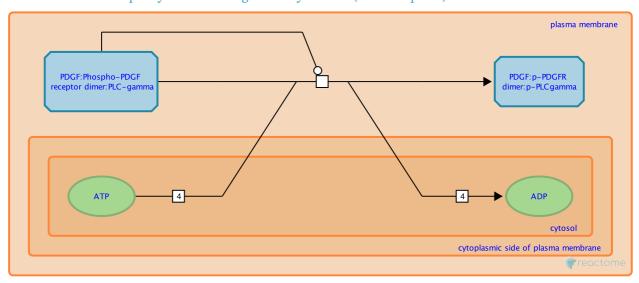
Location: Downstream signal transduction

Stable identifier: R-CFA-1524186

Type: transition

Compartments: plasma membrane

Inferred from: Phosphorylation of PLCgamma by PDGFR (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: PLC-gamma binds to the active receptor

Followed by: Activated PLC gamma dissociates from the PDGF receptor

#### Activated PLC gamma dissociates from the PDGF receptor 7

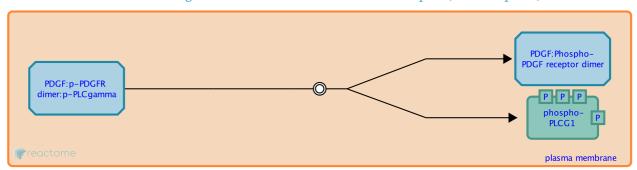
Location: Downstream signal transduction

Stable identifier: R-CFA-1524182

Type: dissociation

Compartments: plasma membrane

Inferred from: Activated PLC gamma dissociates from the PDGF receptor (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: Phosphorylation of PLCgamma by PDGFR

#### SH2 domain of Src binds to the active receptor 7

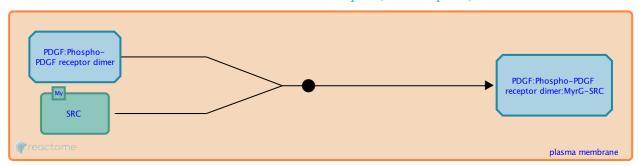
**Location:** Downstream signal transduction

Stable identifier: R-CFA-186819

Type: binding

Compartments: plasma membrane

**Inferred from:** SH2 domain of Src binds to the active receptor (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: Activation of Src

#### **Activation of Src**

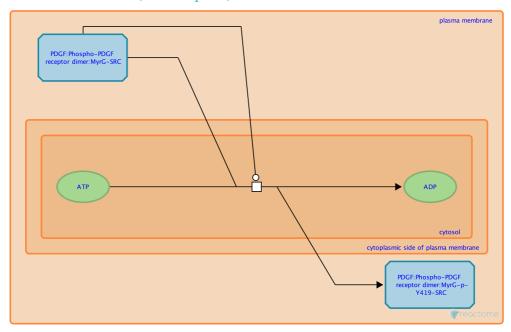
Location: Downstream signal transduction

Stable identifier: R-CFA-380780

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: Activation of Src (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: SH2 domain of Src binds to the active receptor

#### SHP2 binds to the active receptor 7

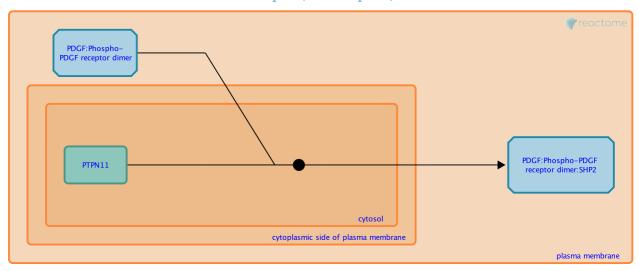
**Location:** Downstream signal transduction

**Stable identifier:** R-CFA-186778

Type: binding

**Compartments:** cytosol, plasma membrane

**Inferred from:** SHP2 binds to the active receptor (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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#### GRB2:SOS1 complex binds to the active receptor **₹**

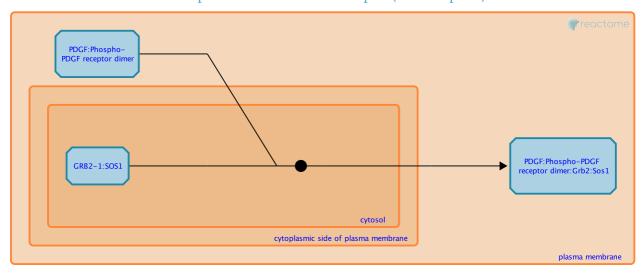
**Location:** Downstream signal transduction

Stable identifier: R-CFA-186826

**Type:** binding

**Compartments:** cytosol, plasma membrane

**Inferred from:** GRB2:SOS1 complex binds to the active receptor (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: SOS-mediated nucleotide exchange on RAS (PDGF receptor:GRB2:SOS)

#### SOS-mediated nucleotide exchange on RAS (PDGF receptor:GRB2:SOS) 7

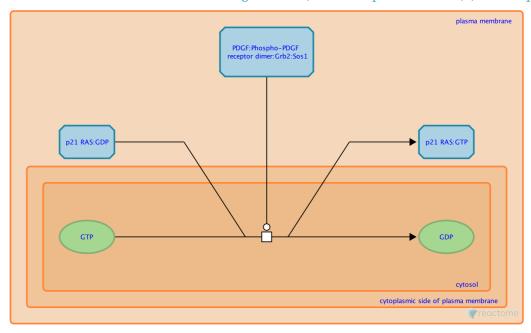
Location: Downstream signal transduction

Stable identifier: R-CFA-186834

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: SOS-mediated nucleotide exchange on RAS (PDGF receptor:GRB2:SOS) (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: GRB2:SOS1 complex binds to the active receptor

#### STAT binds to the active receptor >

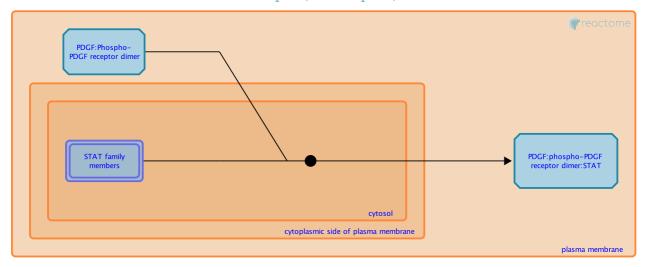
**Location:** Downstream signal transduction

Stable identifier: R-CFA-380782

Type: binding

Compartments: cytosol, plasma membrane

Inferred from: STAT binds to the active receptor (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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#### Crk binds to the active PDGF receptor **₹**

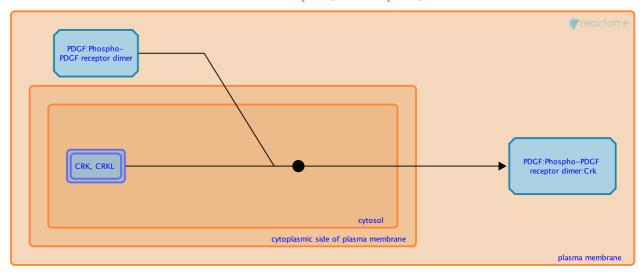
**Location:** Downstream signal transduction

Stable identifier: R-CFA-382056

**Type:** binding

Compartments: cytosol, plasma membrane

**Inferred from:** Crk binds to the active PDGF receptor (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: p130Cas and C3G bind PDGFR bound Crk

#### p130Cas and C3G bind PDGFR bound Crk →

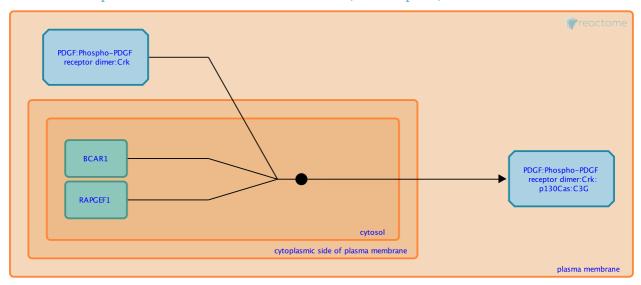
**Location:** Downstream signal transduction

**Stable identifier:** R-CFA-382052

Type: binding

Compartments: cytosol, plasma membrane

Inferred from: p130Cas and C3G bind PDGFR bound Crk (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: Crk binds to the active PDGF receptor

#### Nck binds to the active PDGF receptor **→**

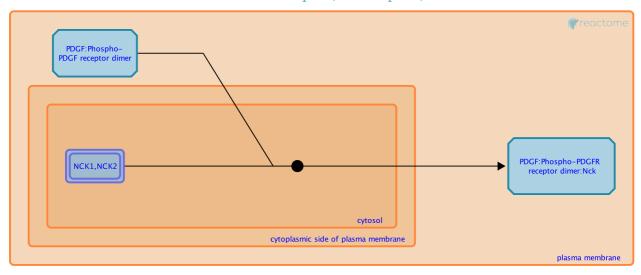
**Location:** Downstream signal transduction

Stable identifier: R-CFA-382058

**Type:** binding

**Compartments:** cytosol, plasma membrane

Inferred from: Nck binds to the active PDGF receptor (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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#### **Grb7 binds to the active PDGF receptor ↗**

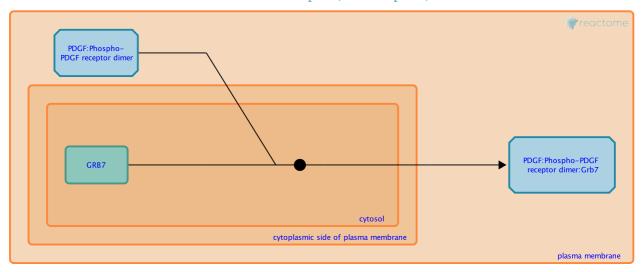
**Location:** Downstream signal transduction

Stable identifier: R-CFA-382055

Type: binding

**Compartments:** cytosol, plasma membrane

**Inferred from:** Grb7 binds to the active PDGF receptor (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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