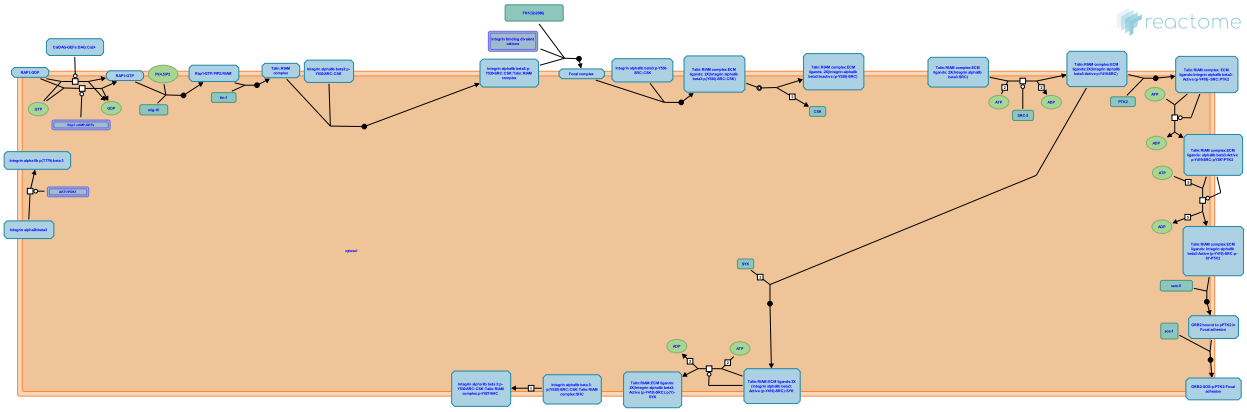
Integrin signaling



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

This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

19/05/2024

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

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. ↗

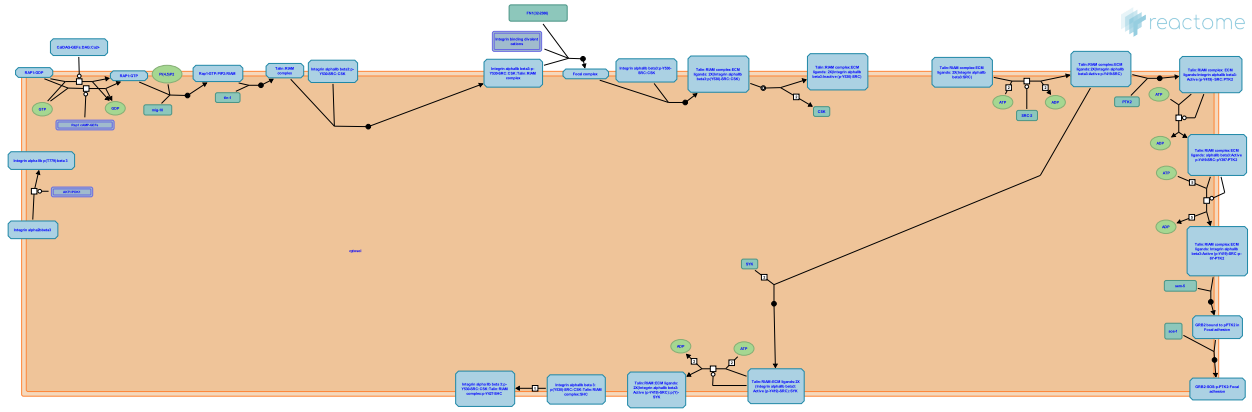
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Integrin signaling ↗

Stable identifier: R-CEL-354192

Inferred from: Integrin signaling (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Activation of Rap1 by cytosolic GEFs ↗

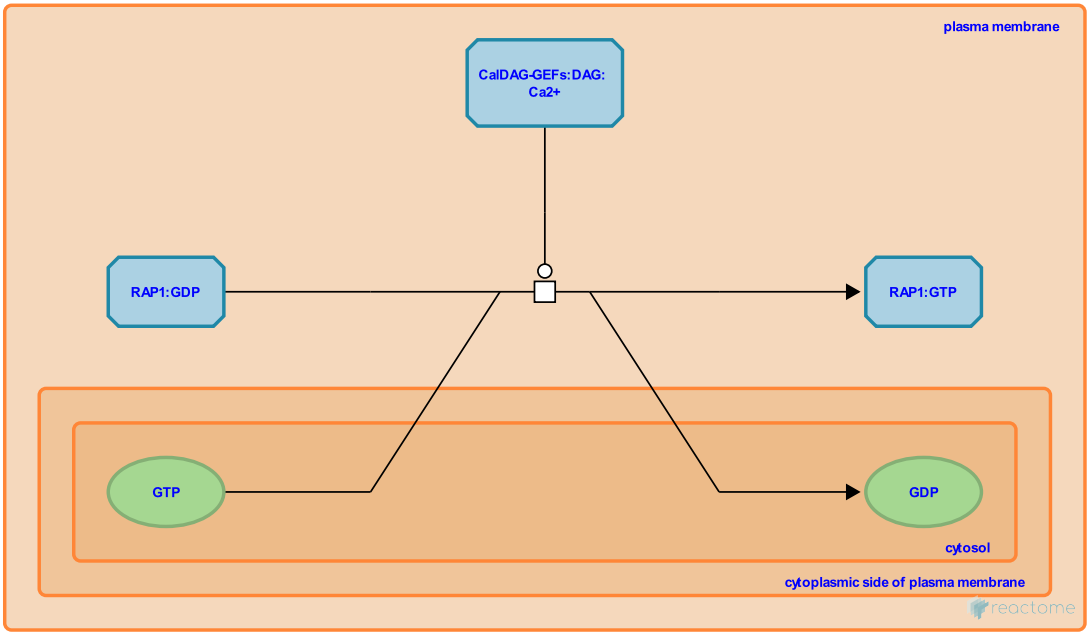
Location: Integrin signaling

Stable identifier: R-CEL-354173

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Activation of Rap1 by cytosolic GEFs (Homo sapiens)



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Followed by: Translocation of RIAM to plasma membrane

Activation of Rap1 by membrane-associated GEFs ↗

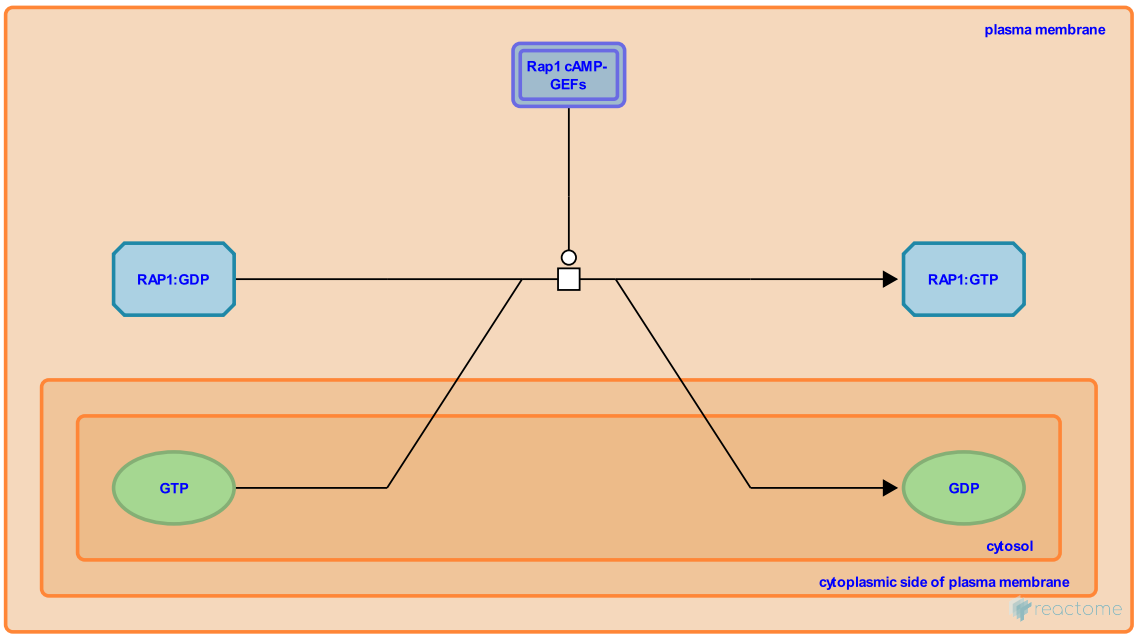
Location: Integrin signaling

Stable identifier: R-CEL-939265

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Activation of Rap1 by membrane-associated GEFs (Homo sapiens)



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Followed by: Translocation of RIAM to plasma membrane

Translocation of RIAM to plasma membrane ↗

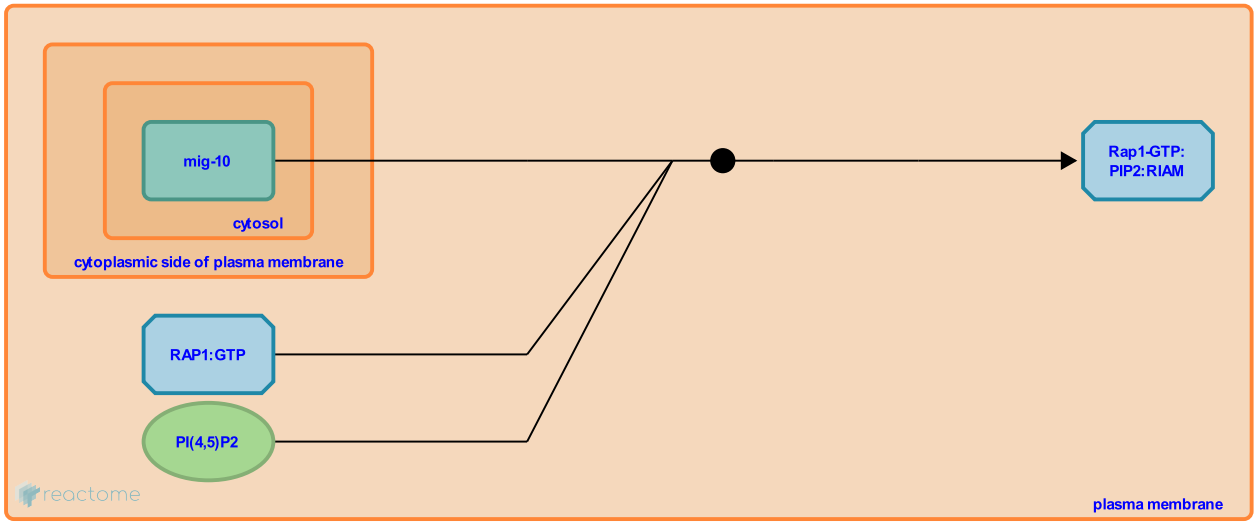
Location: Integrin signaling

Stable identifier: R-CEL-354060

Type: binding

Compartments: plasma membrane, cytosol

Inferred from: Translocation of RIAM to plasma membrane (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Activation of Rap1 by membrane-associated GEFs, Activation of Rap1 by cytosolic GEFs

Followed by: Activation of Talin

Activation of Talin ↗

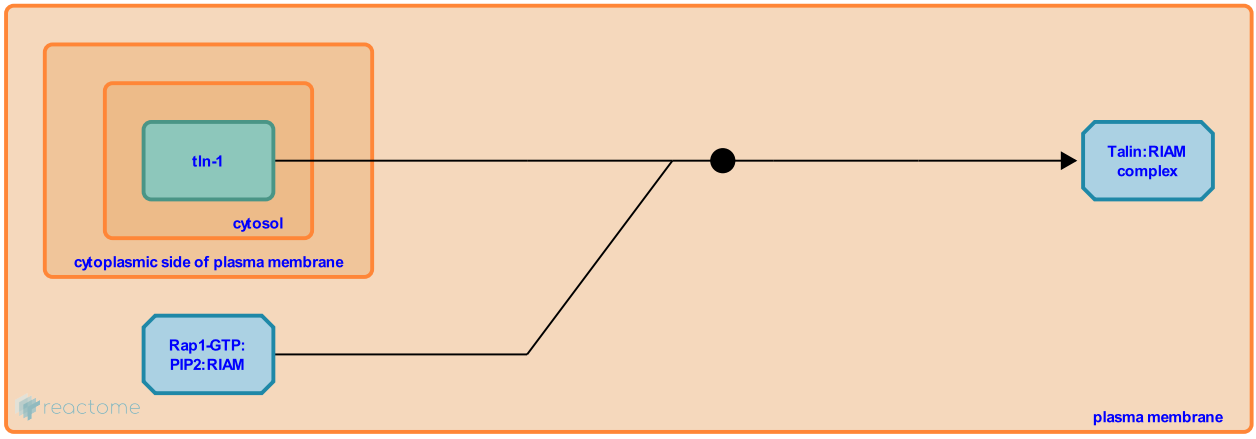
Location: Integrin signaling

Stable identifier: R-CEL-354097

Type: binding

Compartments: plasma membrane, cytosol

Inferred from: Activation of Talin (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Translocation of RIAM to plasma membrane

Followed by: Integrin alphaIIb beta3 activation

Integrin alphaIIb beta3 activation ↗

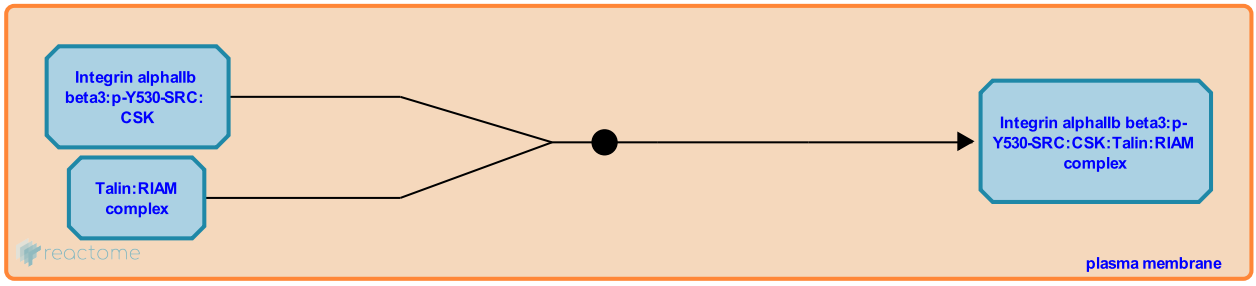
Location: Integrin signaling

Stable identifier: R-CEL-354077

Type: binding

Compartments: plasma membrane

Inferred from: Integrin alphaIIb beta3 activation (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Activation of Talin

Followed by: Interaction of integrin alphaIIb beta3 with Fibrinogen

Interaction of integrin alphaIIb beta3 with Fibrinogen ↗

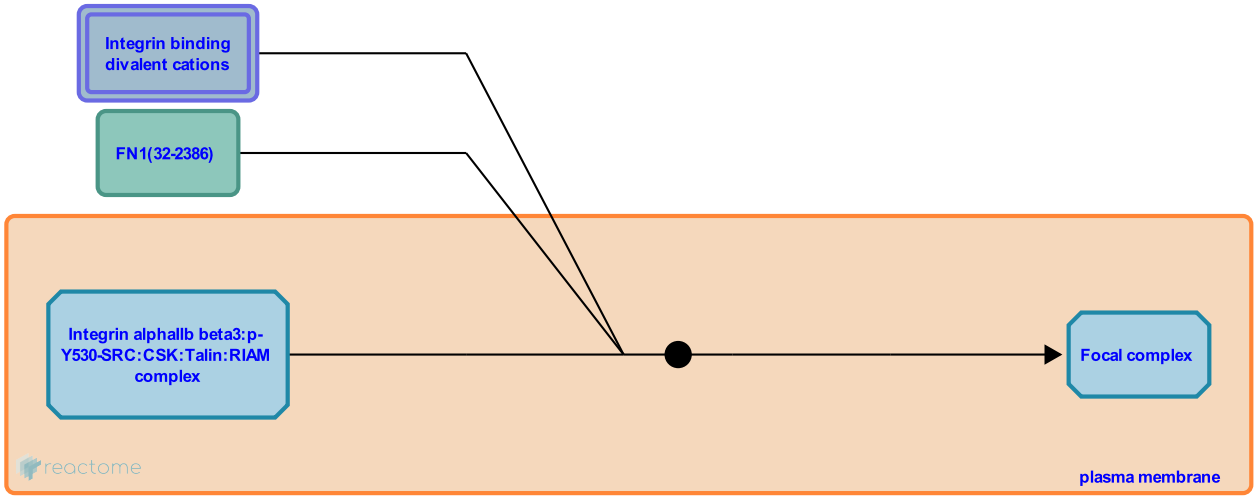
Location: Integrin signaling

Stable identifier: R-CEL-354149

Type: binding

Compartments: plasma membrane, extracellular region

Inferred from: Interaction of integrin alphaIIb beta3 with Fibrinogen (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Integrin alphaIIb beta3 activation

Followed by: Clustering of Integrin alphaIIb beta3 complexes

Clustering of Integrin alphaIIb beta3 complexes ↗

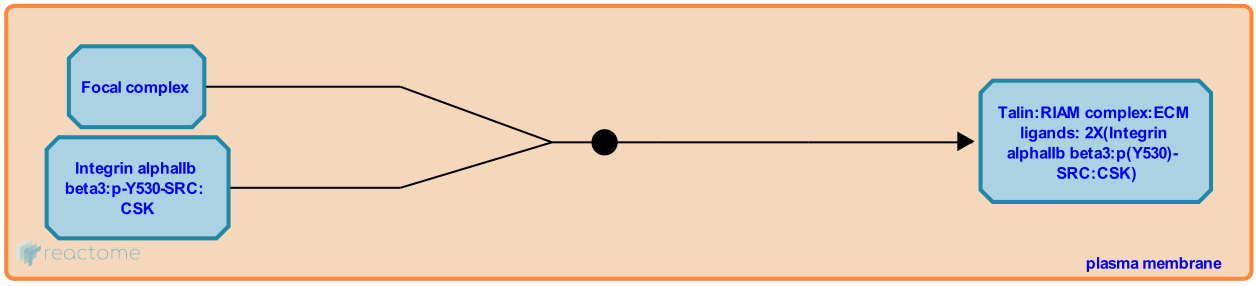
Location: Integrin signaling

Stable identifier: R-CEL-377641

Type: binding

Compartments: plasma membrane

Inferred from: Clustering of Integrin alphaIIb beta3 complexes (Homo sapiens)



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

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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Interaction of integrin alphaIIb beta3 with Fibrinogen

Followed by: Release of CSK from SRC

Release of CSK from SRC ↗

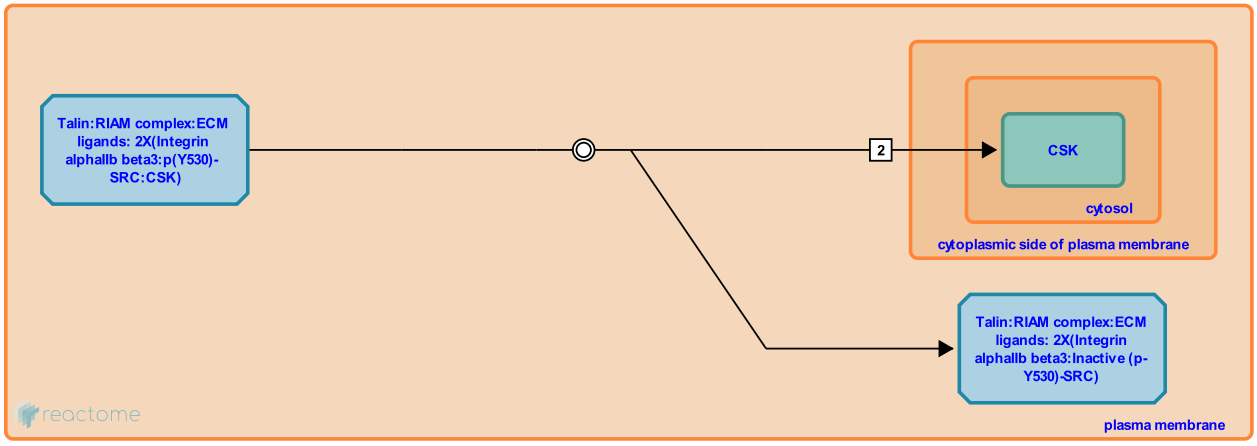
Location: Integrin signaling

Stable identifier: R-CEL-377644

Type: dissociation

Compartments: plasma membrane, cytosol

Inferred from: Release of CSK from SRC (Homo sapiens)



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

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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Clustering of Integrin alphaIIb beta3 complexes

Autophosphorylation of SRC ↗

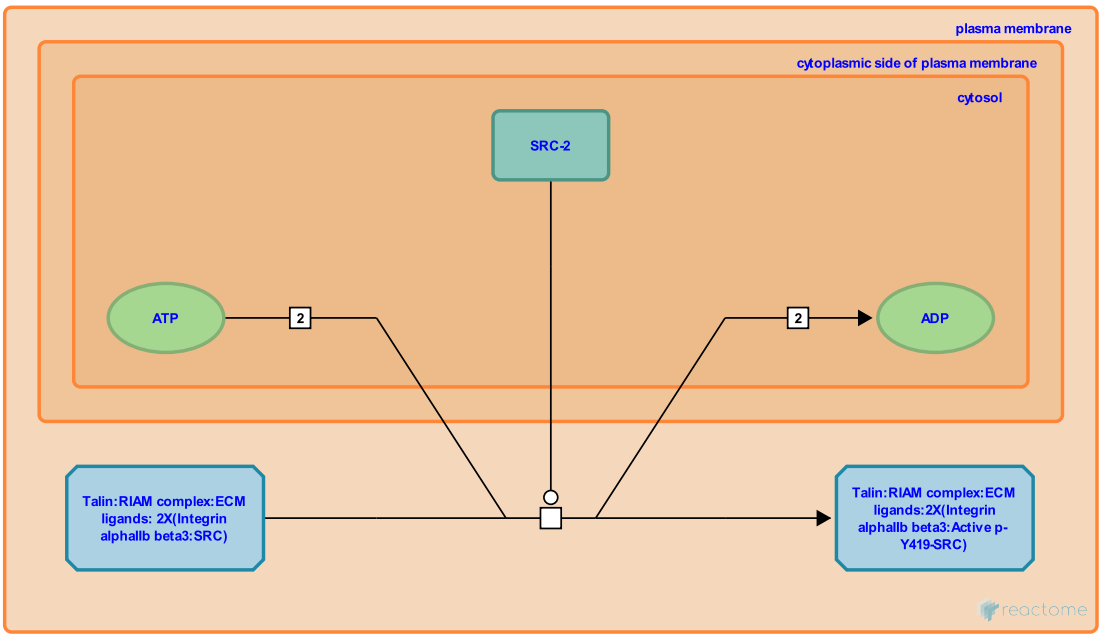
Location: Integrin signaling

Stable identifier: R-CEL-377640

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Autophosphorylation 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.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: SYK binds to integrin alphaIIb beta3, Translocation of PTK2 to Focal complexes

Translocation of PTK2 to Focal complexes ↗

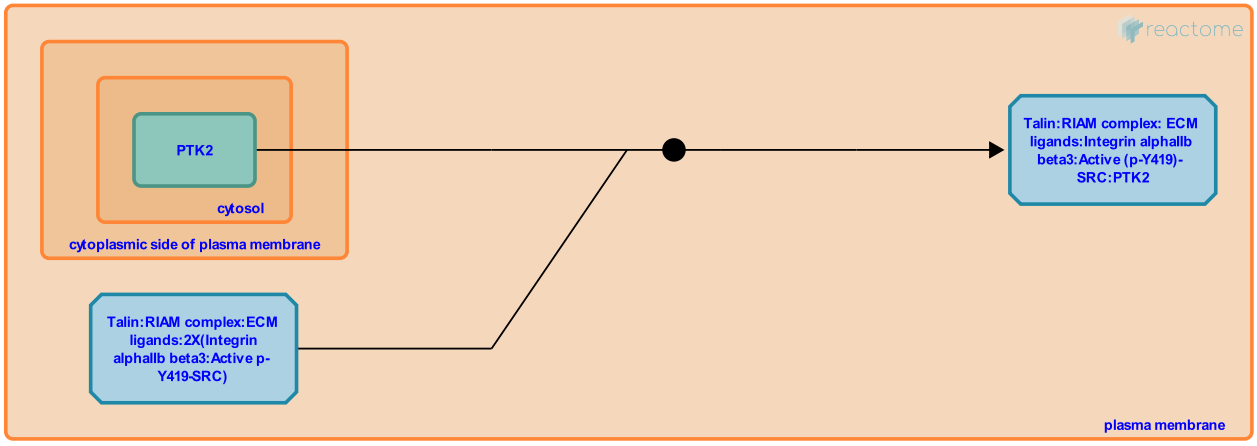
Location: Integrin signaling

Stable identifier: R-CEL-354066

Type: binding

Compartments: plasma membrane, cytosol

Inferred from: Translocation of PTK2 to Focal complexes (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Autophosphorylation of SRC

Followed by: Autophosphorylation of PTK2 at Y397

Autophosphorylation of PTK2 at Y397 ↗

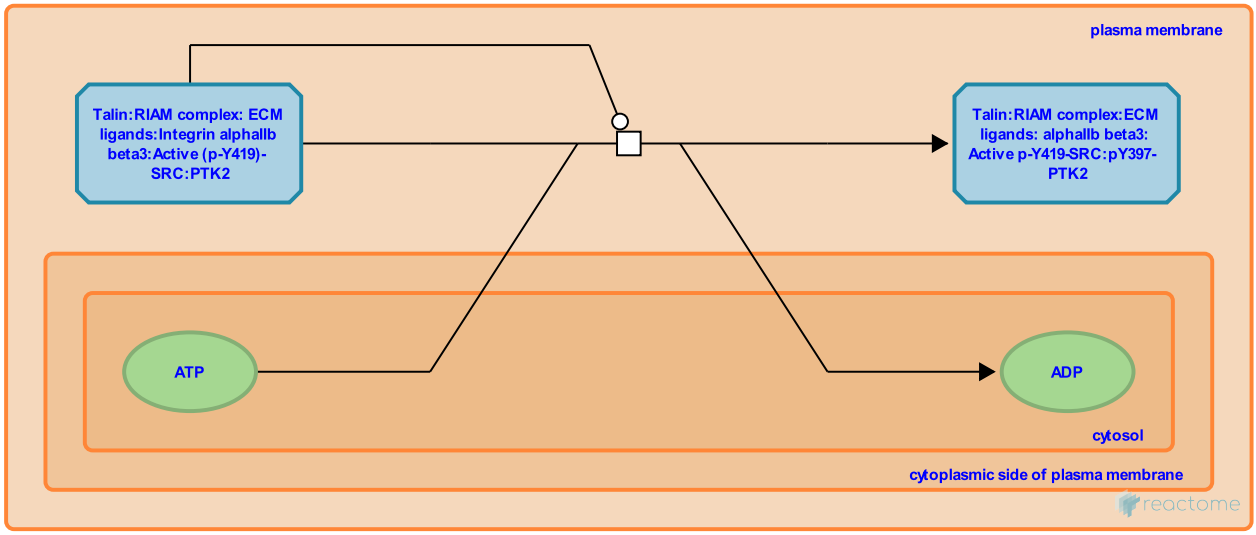
Location: Integrin signaling

Stable identifier: R-CEL-354073

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Autophosphorylation of PTK2 at Y397 (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Translocation of PTK2 to Focal complexes

Followed by: Phosphorylation of pPTK2 by SRC

Phosphorylation of pPTK2 by SRC ↗

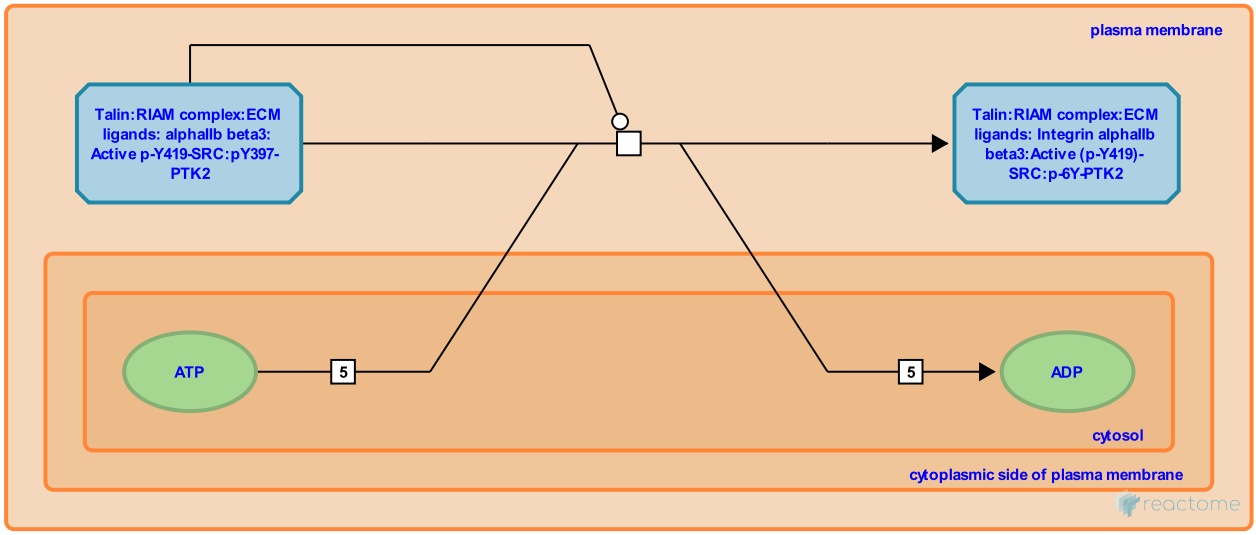
Location: Integrin signaling

Stable identifier: R-CEL-354124

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Phosphorylation of pPTK2 by 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.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

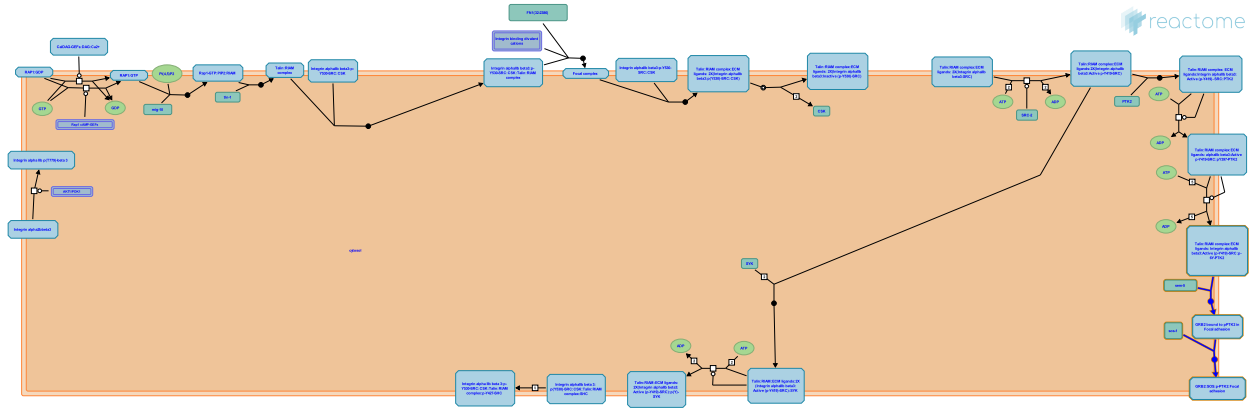
Preceded by: Autophosphorylation of PTK2 at Y397

GRB2:SOS provides linkage to MAPK signaling for Integrins ↗

Location: Integrin signaling

Stable identifier: R-CEL-354194

Inferred from: GRB2:SOS provides linkage to MAPK signaling for Integrins (Homo sapiens)



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Integrin alpha IIb beta3 T779 phosphorylation blocks SHC binding ↗

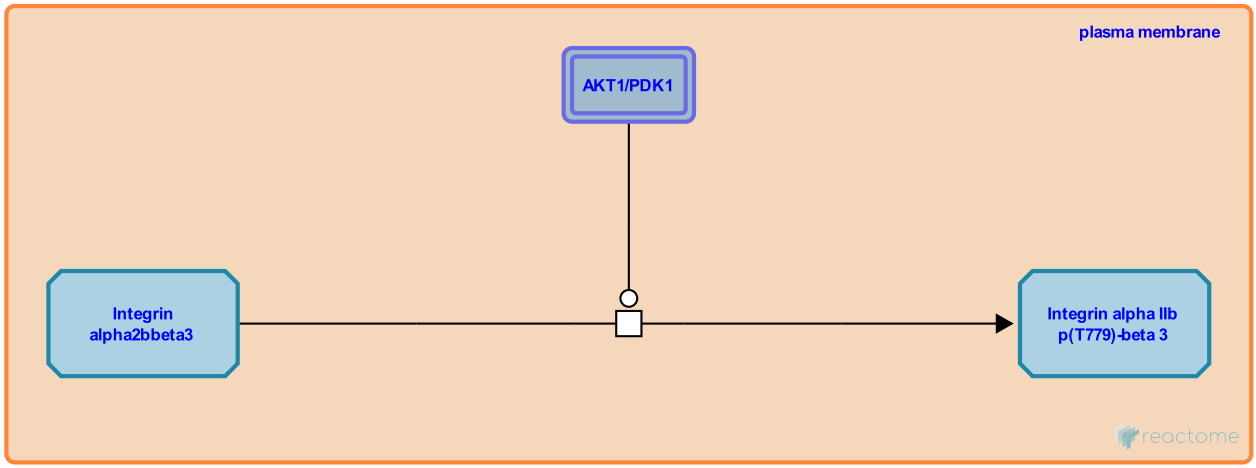
Location: Integrin signaling

Stable identifier: R-CEL-432110

Type: transition

Compartments: plasma membrane

Inferred from: Integrin alpha IIb beta3 T779 phosphorylation blocks SHC binding (Homo sapiens)



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SHC1 bound to integrin alphaIIb beta3 is phosphorylated somehow ↗

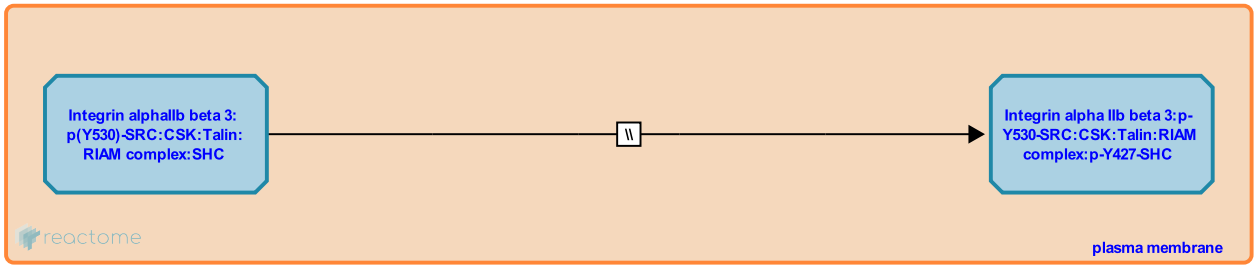
Location: Integrin signaling

Stable identifier: R-CEL-443905

Type: omitted

Compartments: plasma membrane

Inferred from: SHC1 bound to integrin alphaIIb beta3 is phosphorylated somehow (Homo sapiens)



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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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SYK binds to integrin alphaIIb beta3 ↗

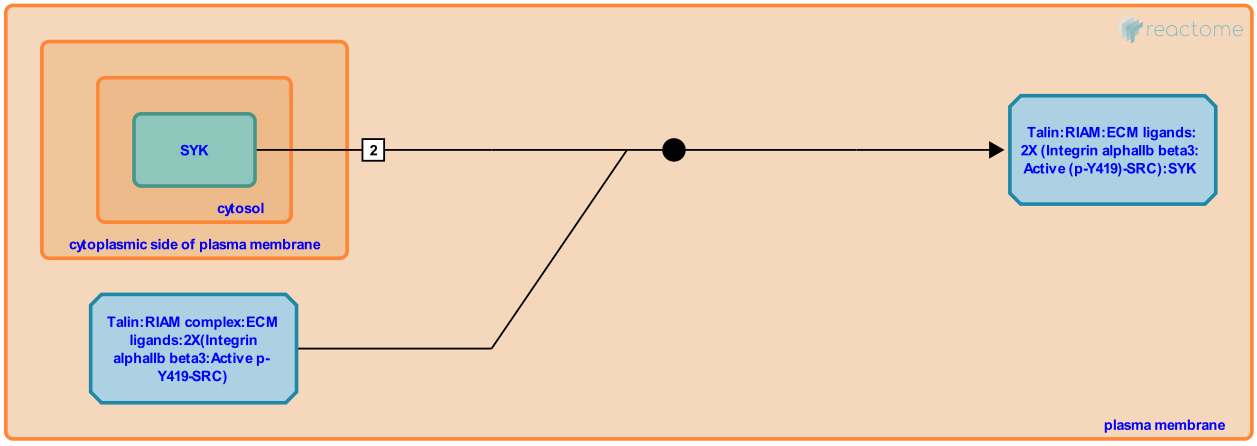
Location: Integrin signaling

Stable identifier: R-CEL-429415

Type: binding

Compartments: plasma membrane, cytosol

Inferred from: SYK binds to integrin alphaIIb beta3 (Homo sapiens)



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

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Preceded by: Autophosphorylation of SRC

Followed by: SYK activation by SRC

SYK activation by SRC ↗

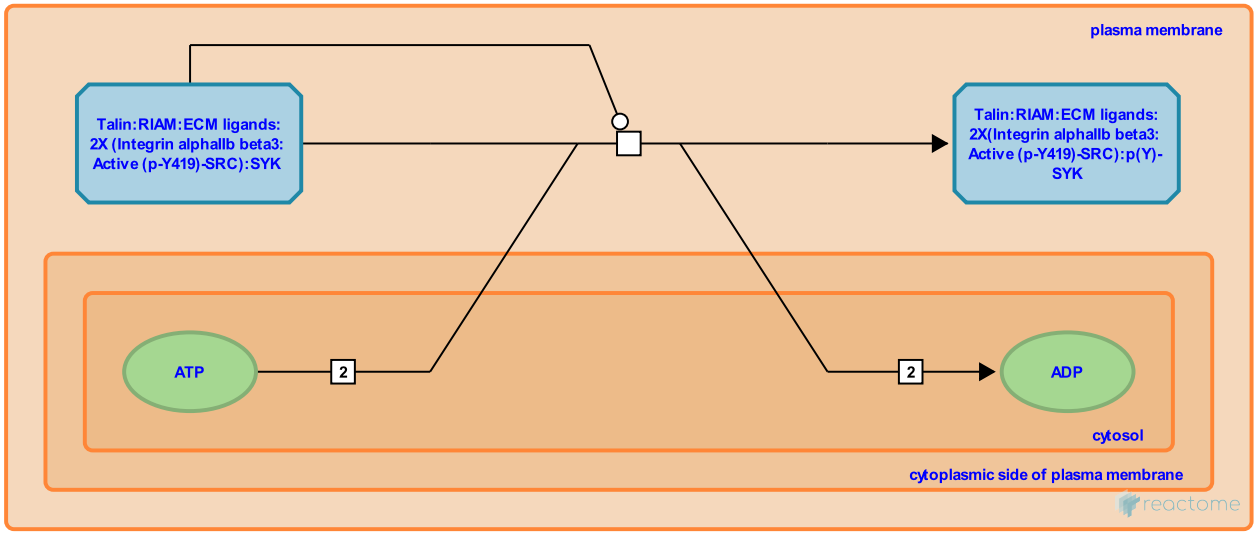
Location: Integrin signaling

Stable identifier: R-CEL-429441

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: SYK activation by SRC (Homo sapiens)



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Preceded by: SYK binds to integrin alphaIIb beta3

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