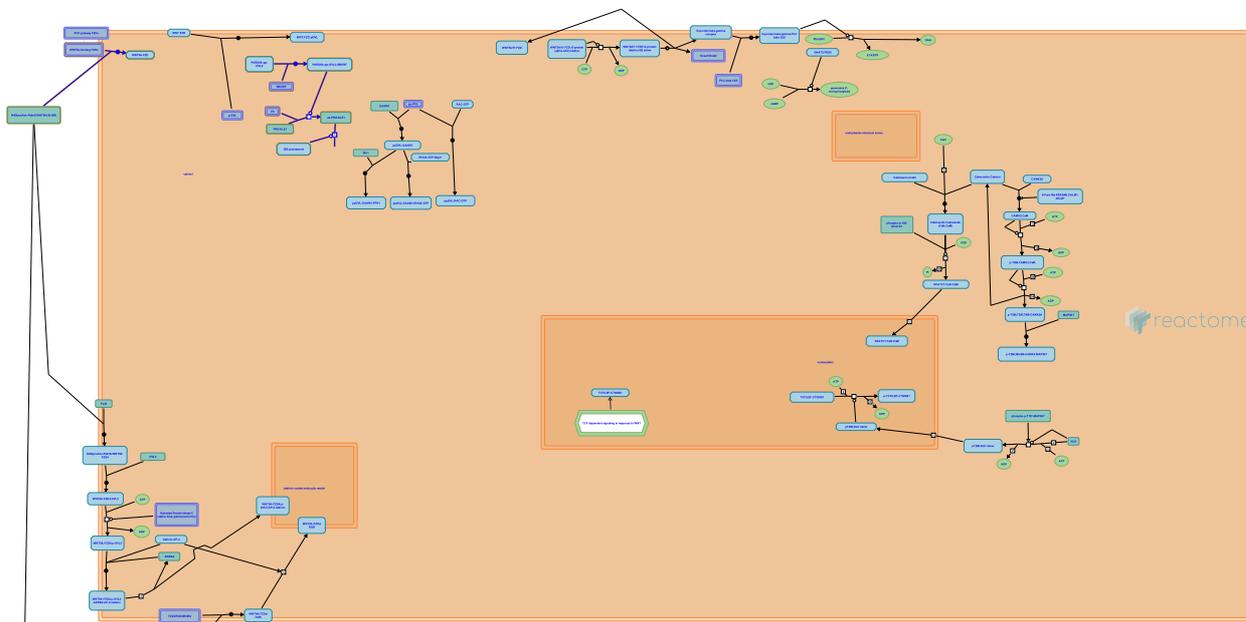


Asymmetric localization of PCP proteins



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.

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Literature references

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- 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

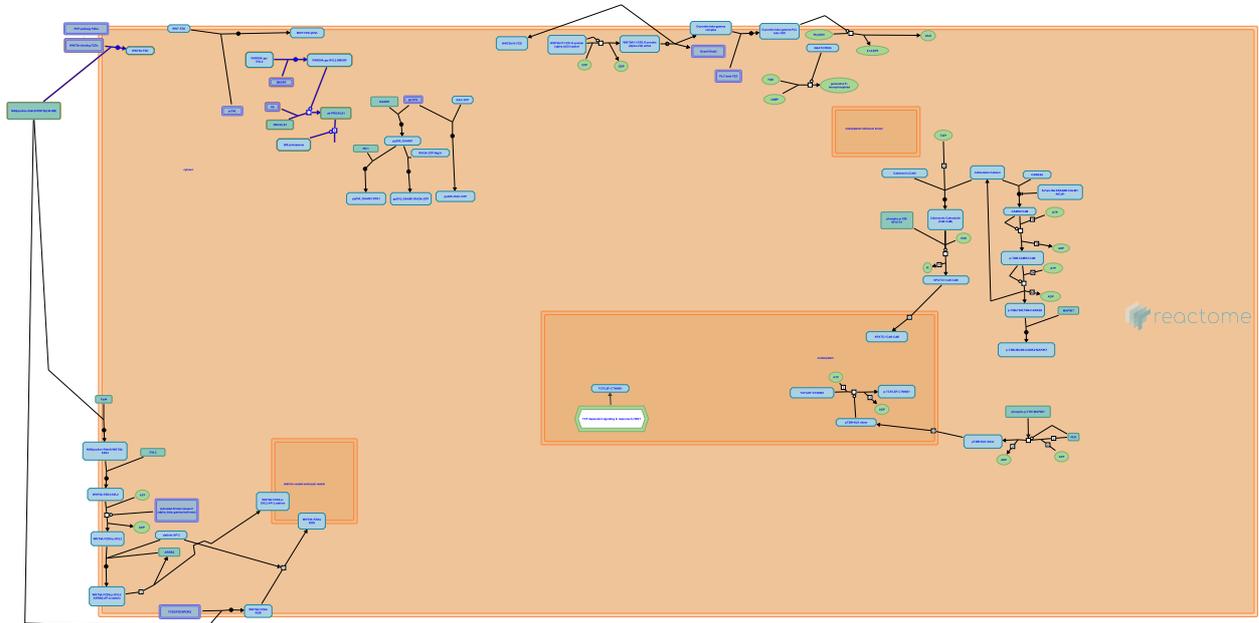
This document contains 1 pathway and 4 reactions ([see Table of Contents](#))

Asymmetric localization of PCP proteins ↗

Stable identifier: R-MMU-4608870

Compartments: cytosol, plasma membrane

Inferred from: [Asymmetric localization of PCP 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>

WNT5A binding to FZD promotes PRICKLE1 degradation ↗

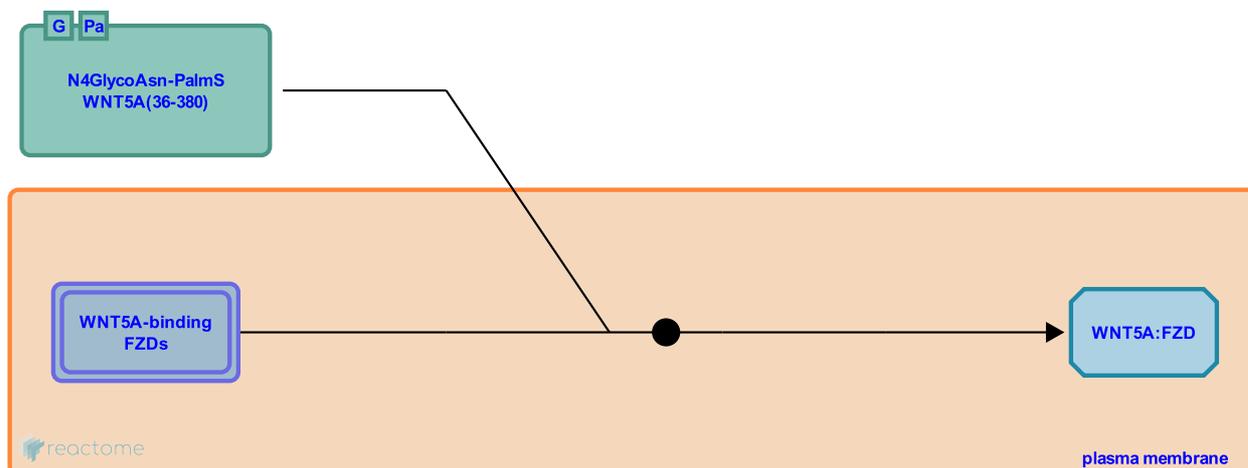
Location: [Asymmetric localization of PCP proteins](#)

Stable identifier: R-MMU-5099886

Type: binding

Compartments: plasma membrane, extracellular region

Inferred from: [WNT5A binding to FZD promotes PRICKLE1 degradation \(Homo sapiens\)](#)



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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SMURF1/2 are recruited to the DVL2:PARD6A complex ↗

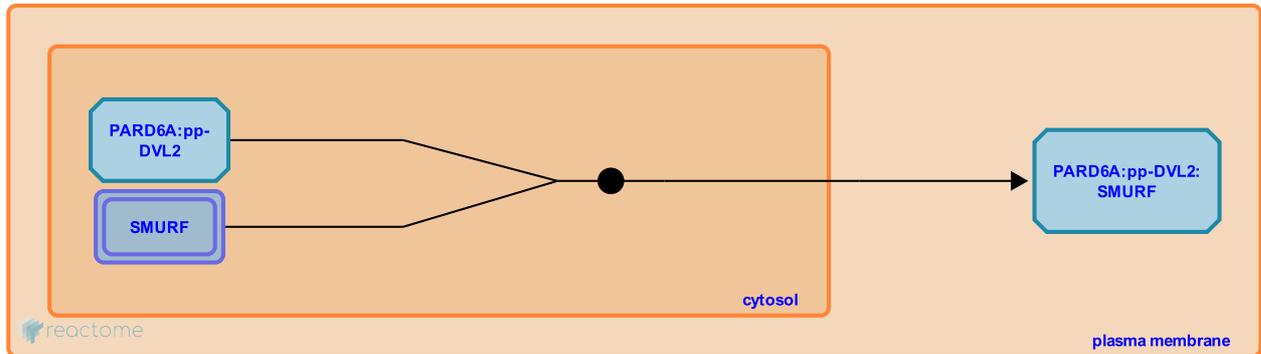
Location: [Asymmetric localization of PCP proteins](#)

Stable identifier: R-MMU-4608854

Type: binding

Compartments: cytosol, plasma membrane

Inferred from: [SMURF1/2 are recruited to the DVL2:PARD6A complex \(Homo sapiens\)](#)



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>

Followed by: [SMURF1/2 ubiquitinates PRICKLE1](#)

SMURF1/2 ubiquitinates PRICKLE1 ↗

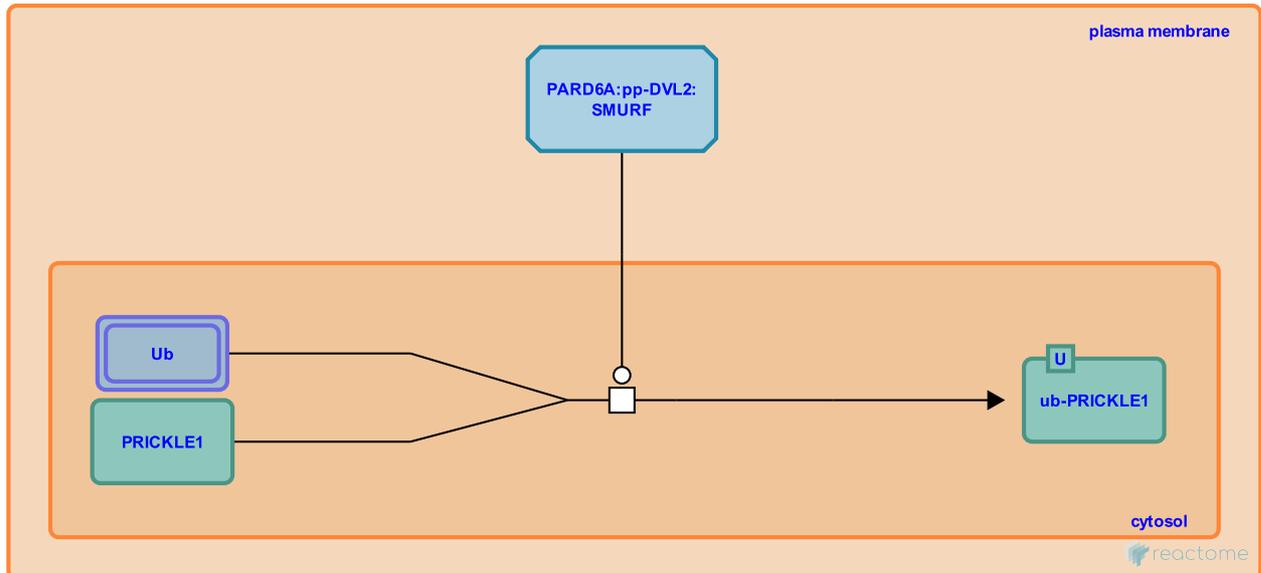
Location: [Asymmetric localization of PCP proteins](#)

Stable identifier: R-MMU-4608852

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: [SMURF1/2 ubiquitinates PRICKLE1 \(Homo sapiens\)](#)



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: [SMURF1/2 are recruited to the DVL2:PAR6A complex](#)

Followed by: [PRICKLE1 is degraded by the proteasome](#)

PRICKLE1 is degraded by the proteasome ↗

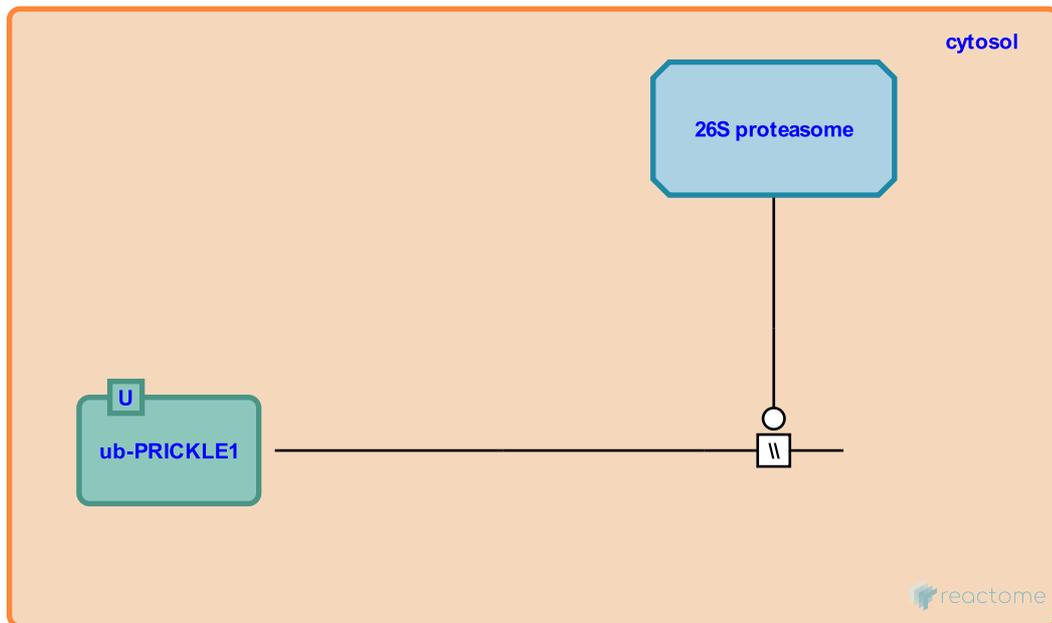
Location: [Asymmetric localization of PCP proteins](#)

Stable identifier: R-MMU-4608855

Type: omitted

Compartments: cytosol, plasma membrane

Inferred from: [PRICKLE1 is degraded by the proteasome \(Homo sapiens\)](#)



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: [SMURF1/2 ubiquitinates PRICKLE1](#)

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