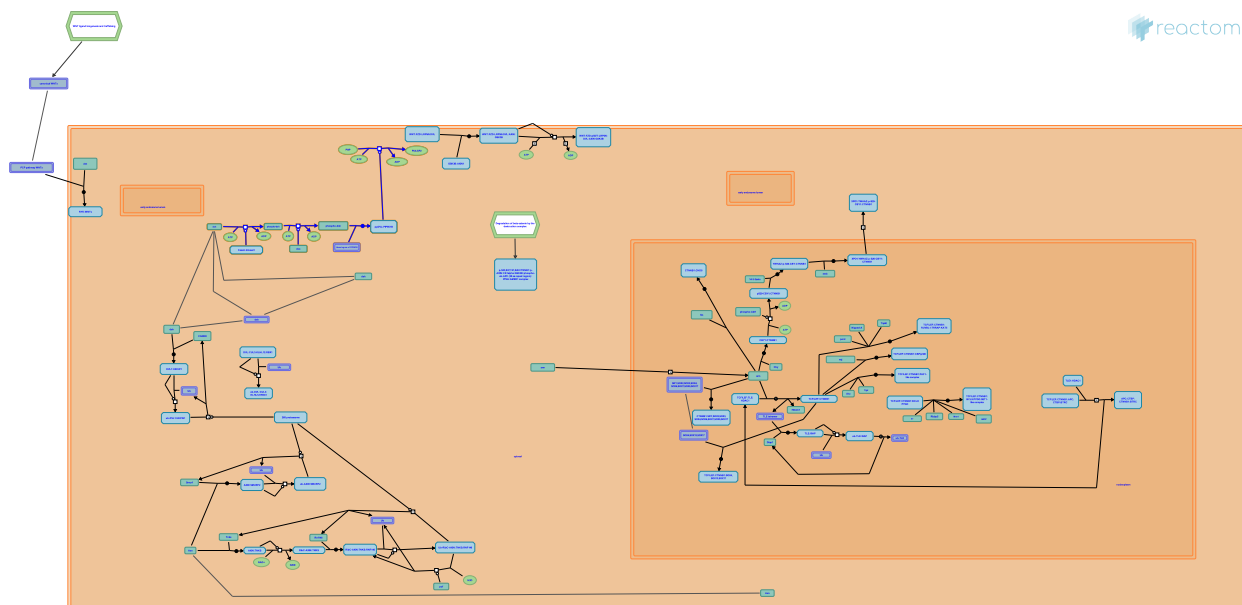


WNT mediated activation of DVL



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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

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. [↗](#)

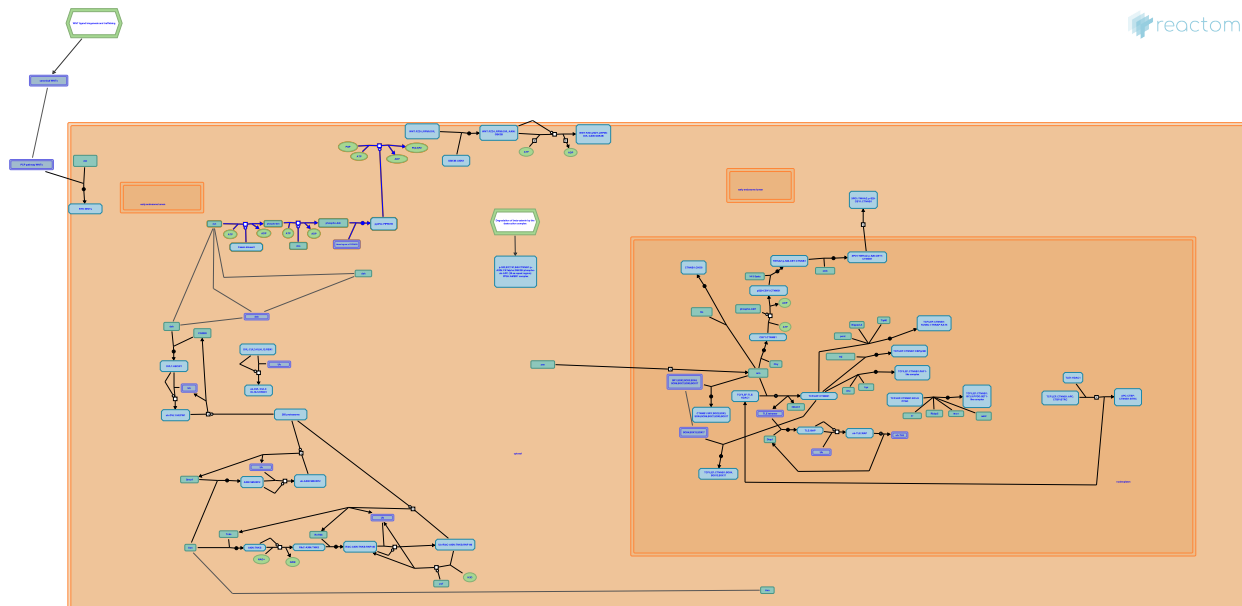
Reactome database release: 75

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

WNT mediated activation of DVL ↗

Stable identifier: R-DME-201688

Inferred from: [WNT mediated activation of DVL \(Homo sapiens\)](#)



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>

CSNK2-mediated phosphorylation of DVL ↗

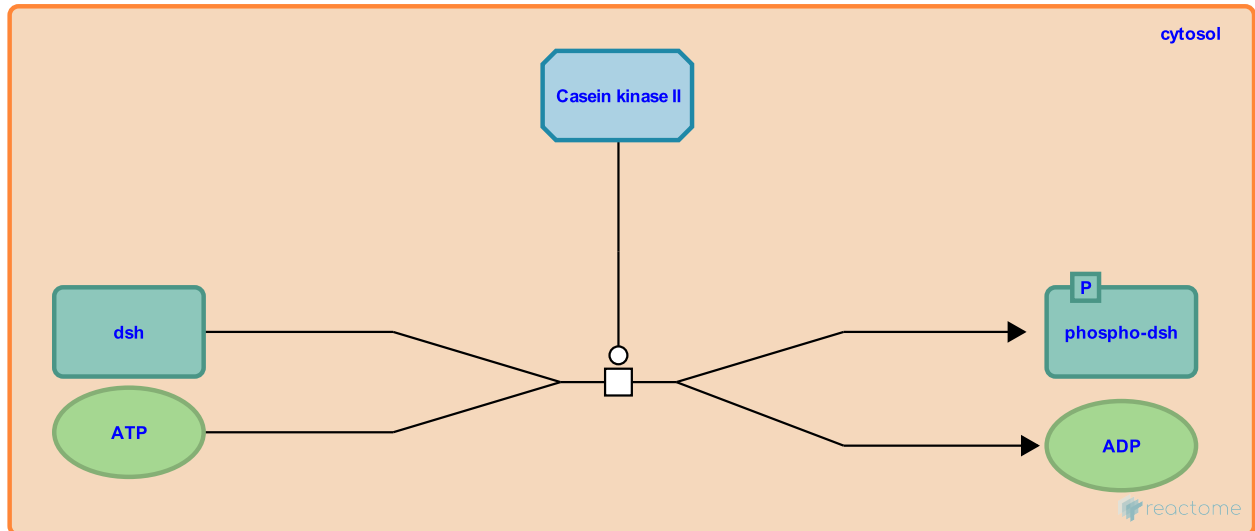
Location: [WNT mediated activation of DVL](#)

Stable identifier: R-DME-201717

Type: transition

Compartments: cytosol

Inferred from: [CSNK2-mediated phosphorylation of DVL \(Homo sapiens\)](#)



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: [WNT signaling stimulates CSNK1-dependent phosphorylation of DVL](#)

WNT signaling stimulates CSNK1-dependent phosphorylation of DVL ↗

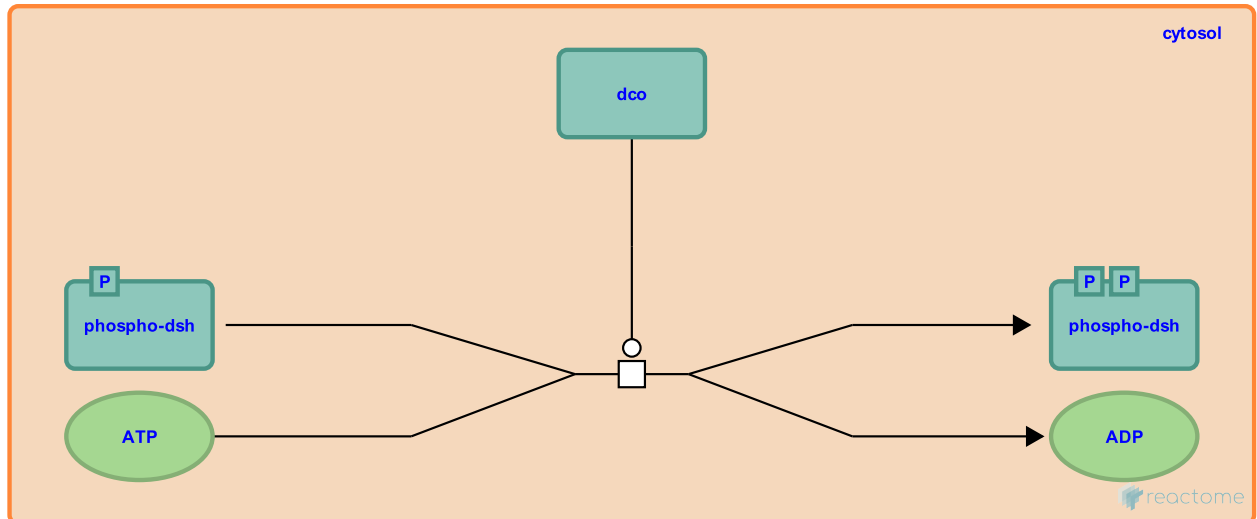
Location: [WNT mediated activation of DVL](#)

Stable identifier: R-DME-3772435

Type: transition

Compartments: cytosol

Inferred from: [WNT signaling stimulates CSNK1-dependent phosphorylation of DVL \(Homo sapiens\)](#)



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: [CSNK2-mediated phosphorylation of DVL](#)

Followed by: [Phosphorylated DVL recruits PIP5K1B to the plasma membrane](#)

Phosphorylated DVL recruits PIP5K1B to the plasma membrane ↗

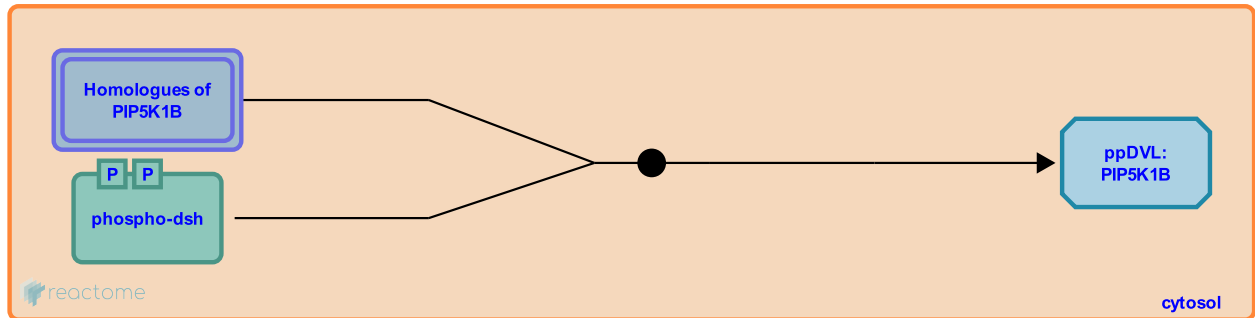
Location: [WNT mediated activation of DVL](#)

Stable identifier: R-DME-3772434

Type: binding

Compartments: cytosol

Inferred from: [Phosphorylated DVL recruits PIP5K1B to the plasma membrane \(Homo sapiens\)](#)



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: [WNT signaling stimulates CSNK1-dependent phosphorylation of DVL](#)

Followed by: [DVL-associated PIP5K1B phosphorylates PI4P to PI\(4,5\)P2](#)

DVL-associated PIP5K1B phosphorylates PI4P to PI(4,5)P2 ↗

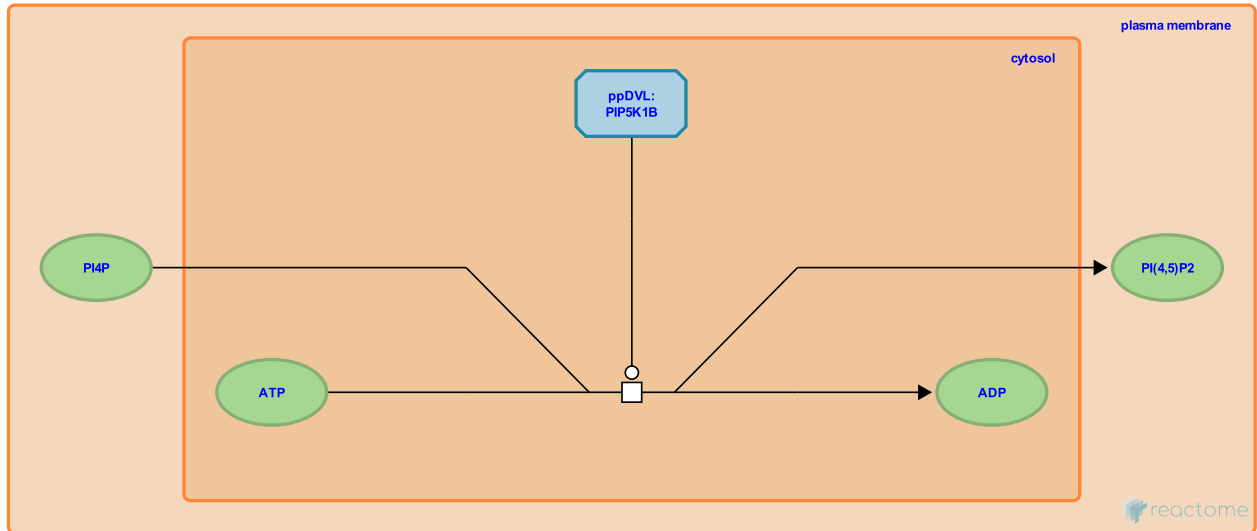
Location: [WNT mediated activation of DVL](#)

Stable identifier: R-DME-3772436

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: [DVL-associated PIP5K1B phosphorylates PI4P to PI\(4,5\)P2 \(Homo sapiens\)](#)



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: [Phosphorylated DVL recruits PIP5K1B to the plasma membrane](#)

Table of Contents

Introduction	1
❏ WNT mediated activation of DVL	2
↳ CSNK2-mediated phosphorylation of DVL	3
↳ WNT signaling stimulates CSNK1-dependent phosphorylation of DVL	4
↳ Phosphorylated DVL recruits PIP5K1B to the plasma membrane	5
↳ DVL-associated PIP5K1B phosphorylates PI4P to PI(4,5)P2	6
Table of Contents	7