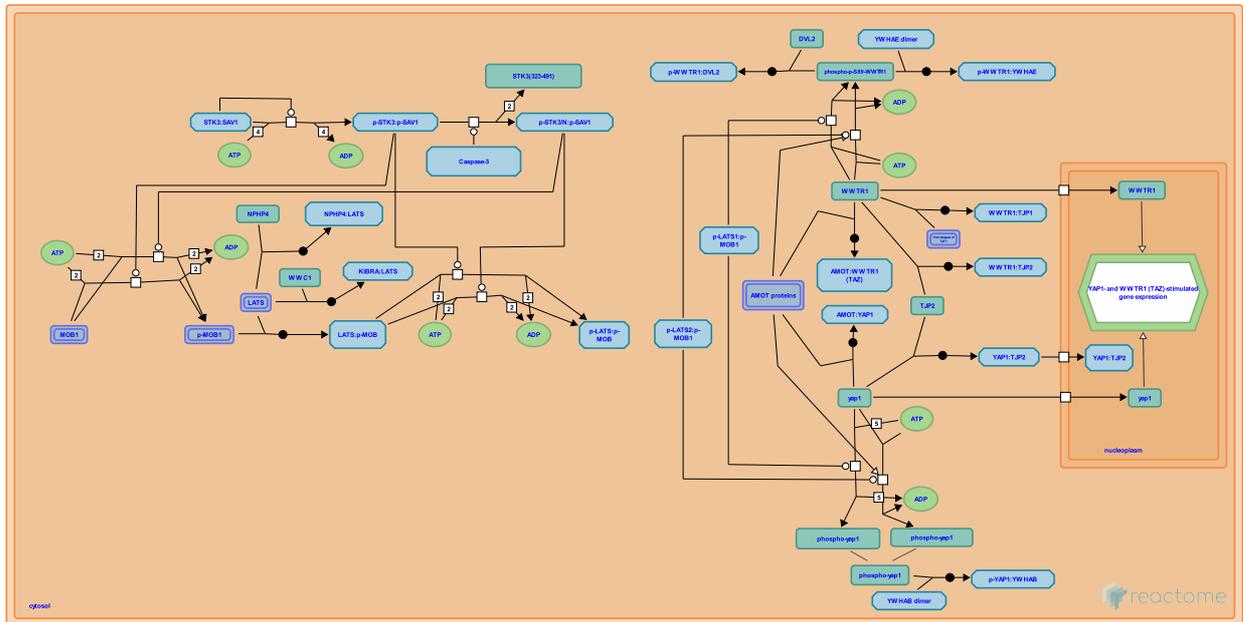


Signaling by Hippo



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

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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](https://www.reactome.org/textbook/).

30/09/2022

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

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- 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: 82

This document contains 1 pathway and 24 reactions ([see Table of Contents](#))

Phosphorylation of STK3 (MST2) and SAV1 by STK3 ↗

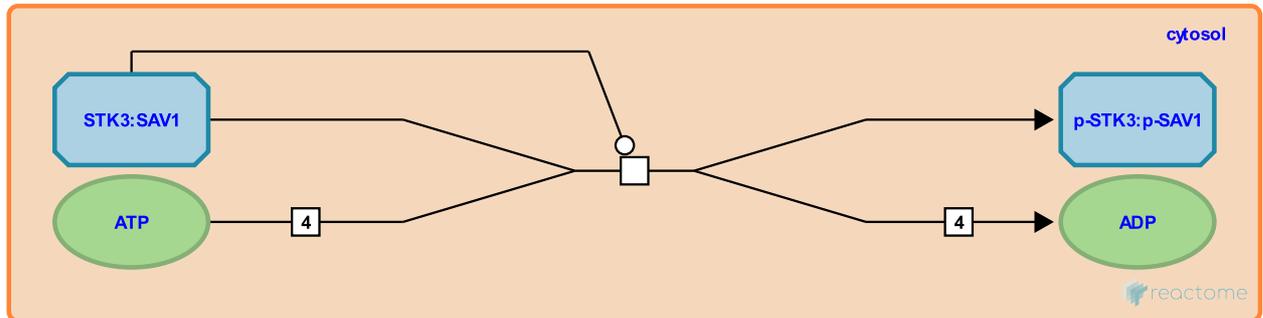
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2028591

Type: transition

Compartments: cytosol

Inferred from: [Phosphorylation of STK3 \(MST2\) and SAV1 by STK3 \(Homo sapiens\)](#)



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: [Phosphorylation of LATS1 and 2 by p-STK3 \(p-MST2\)](#), [Phosphorylation of MOB1A and B by p-STK3 \(p-MST2\)](#), [Cleavage of p-STK3 \(p-MST2\) by caspase 3](#)

Cleavage of p-STK3 (p-MST2) by caspase 3 [↗](#)

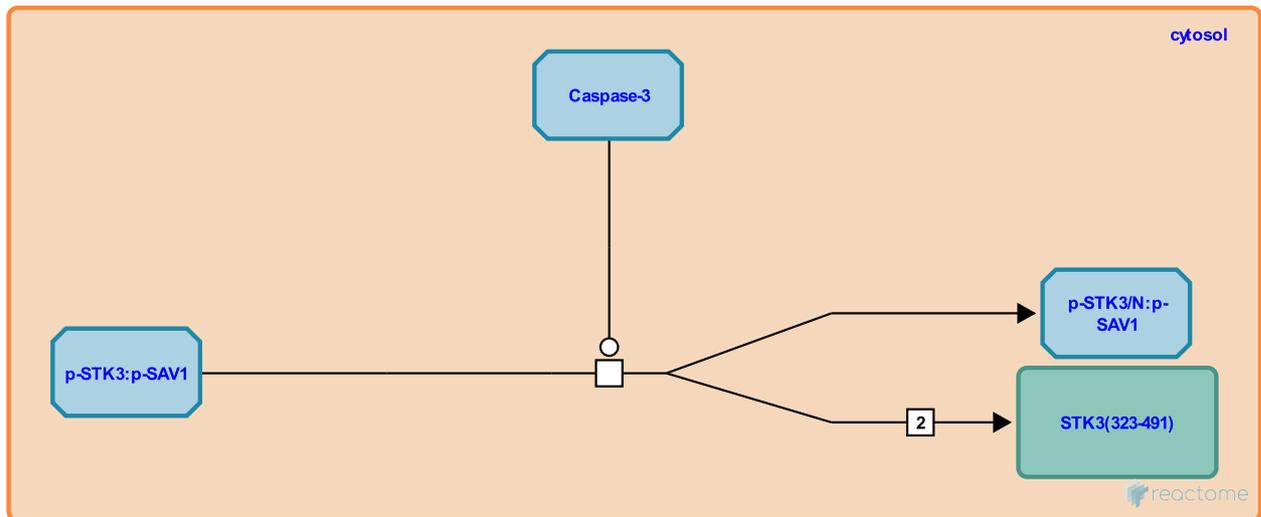
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2028697

Type: transition

Compartments: cytosol

Inferred from: [Cleavage of p-STK3 \(p-MST2\) by caspase 3 \(Homo sapiens\)](#)



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: [Phosphorylation of STK3 \(MST2\) and SAV1 by STK3](#)

Followed by: [Phosphorylation of LATS1 and 2 by p-STK3 \(MST2\)/N](#), [Phosphorylation of MOB1A and B by p-STK3\(MST2\)/N](#)

KIBRA (WWC1) binds LATS proteins ↗

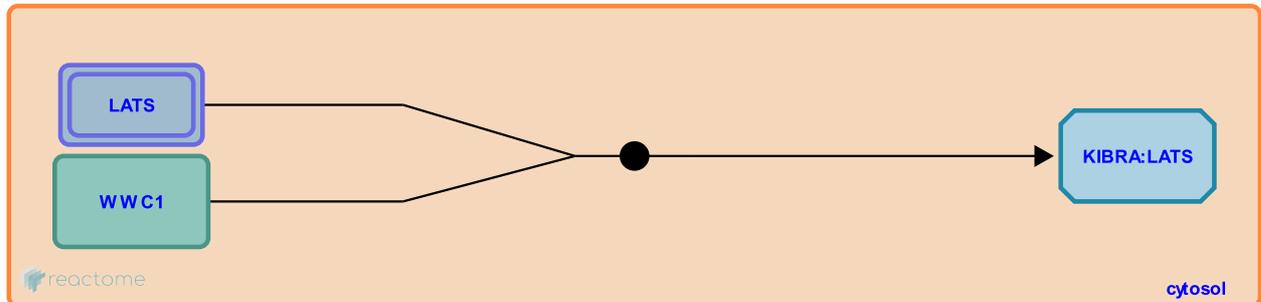
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2038398

Type: binding

Compartments: cytosol

Inferred from: [KIBRA \(WWC1\) binds LATS 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>

NPHP4 protein binds LATS proteins ↗

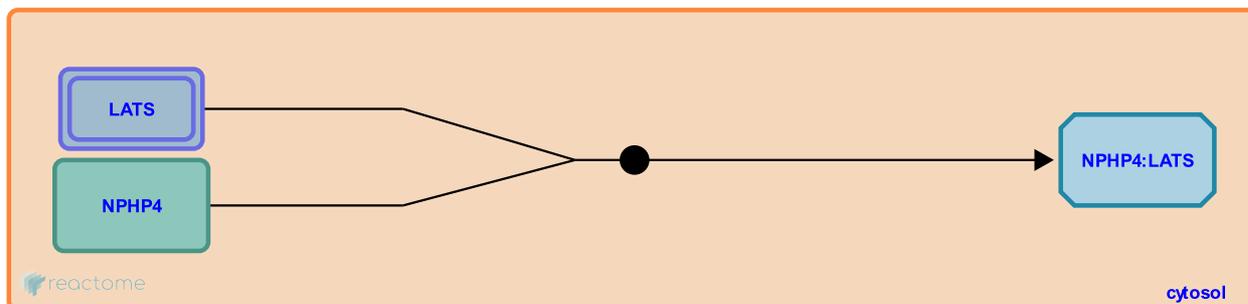
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2059926

Type: binding

Compartments: cytosol

Inferred from: [NPHP4 protein binds LATS 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>

Phosphorylation of LATS1 and 2 by p-STK3 (p-MST2) ↗

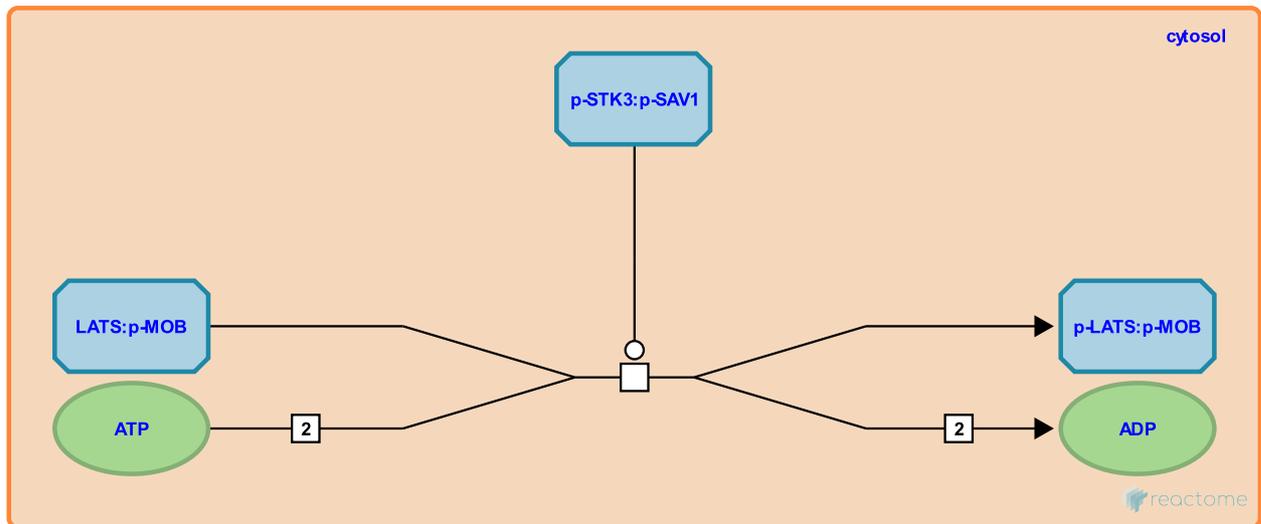
Location: Signaling by Hippo

Stable identifier: R-DRE-2028589

Type: transition

Compartments: cytosol

Inferred from: Phosphorylation of LATS1 and 2 by p-STK3 (p-MST2) (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 MOB1A proteins associate with LATS proteins](#), [Phosphorylation of STK3 \(MST2\) and SAV1 by STK3](#)

Followed by: [Phosphorylation of YAP by LATS2](#), [Phosphorylation of YAP by LATS1](#), [Phosphorylation of WWTR1 \(TAZ\) by LATS1](#), [Phosphorylation of WWTR1 \(TAZ\) by LATS2](#)

Phosphorylation of LATS1 and 2 by p-STK3 (MST2)/N ↗

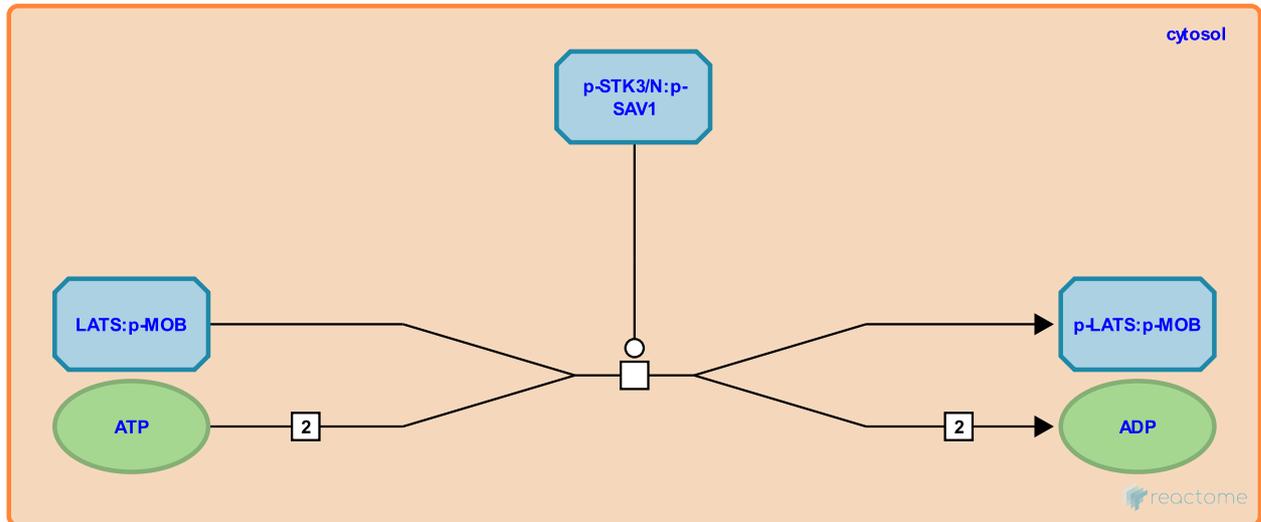
Location: Signaling by Hippo

Stable identifier: R-DRE-2028673

Type: transition

Compartments: cytosol

Inferred from: Phosphorylation of LATS1 and 2 by p-STK3 (MST2)/N (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 MOB1A proteins associate with LATS proteins](#), [Cleavage of p-STK3 \(p-MST2\) by caspase 3](#)

Followed by: [Phosphorylation of YAP by LATS2](#), [Phosphorylation of YAP by LATS1](#)

Phosphorylation of MOB1A and B by p-STK3 (p-MST2) ↗

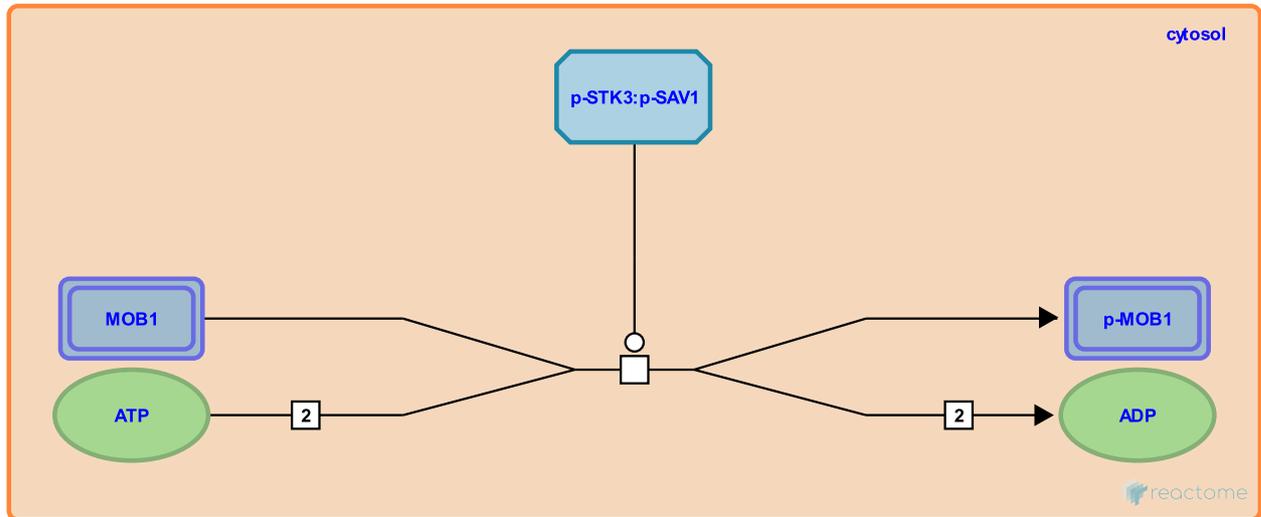
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2028635

Type: transition

Compartments: cytosol

Inferred from: [Phosphorylation of MOB1A and B by p-STK3 \(p-MST2\) \(Homo sapiens\)](#)



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: [Phosphorylation of STK3 \(MST2\) and SAV1 by STK3](#)

Followed by: [Phosphorylated MOB1A proteins associate with LATS proteins](#)

Phosphorylation of MOB1A and B by p-STK3(MST2)/N ↗

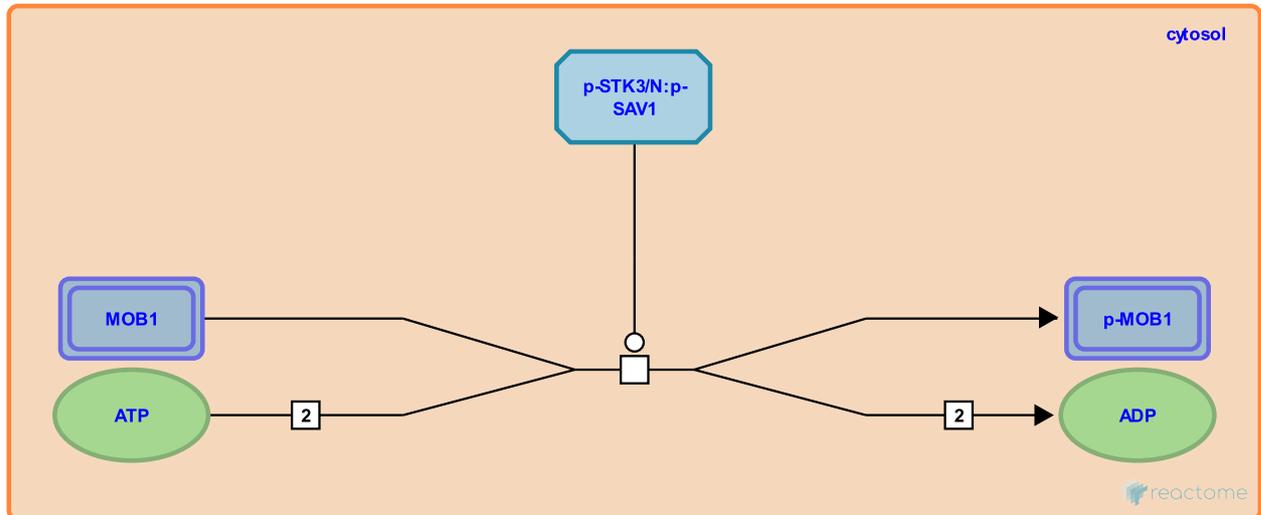
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2028675

Type: transition

Compartments: cytosol

Inferred from: [Phosphorylation of MOB1A and B by p-STK3\(MST2\)/N \(Homo sapiens\)](#)



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: [Cleavage of p-STK3 \(p-MST2\) by caspase 3](#)

Followed by: [Phosphorylated MOB1A proteins associate with LATS proteins](#)

Phosphorylated MOB1A proteins associate with LATS proteins ↗

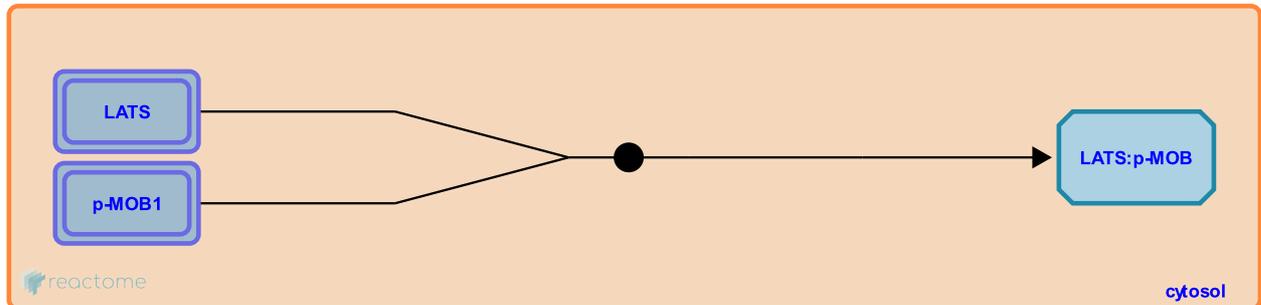
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2028626

Type: binding

Compartments: cytosol

Inferred from: [Phosphorylated MOB1A proteins associate with LATS 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>

Preceded by: [Phosphorylation of MOB1A and B by p-STK3\(MST2\)/N](#), [Phosphorylation of MOB1A and B by p-STK3 \(p-MST2\)](#)

Followed by: [Phosphorylation of LATS1 and 2 by p-STK3 \(p-MST2\)](#), [Phosphorylation of LATS1 and 2 by p-STK3 \(MST2\)/N](#)

Translocation of YAP1 to the nucleus ↗

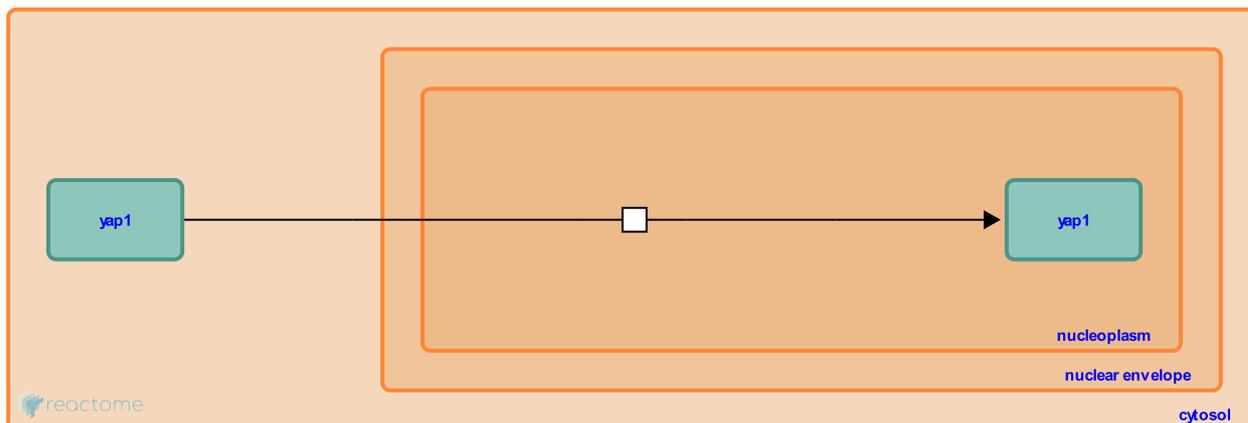
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2032770

Type: transition

Compartments: nucleoplasm, cytosol

Inferred from: [Translocation of YAP1 to the nucleus \(Homo sapiens\)](#)



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>

YAP1 binds ZO-2 (TJP2) ↗

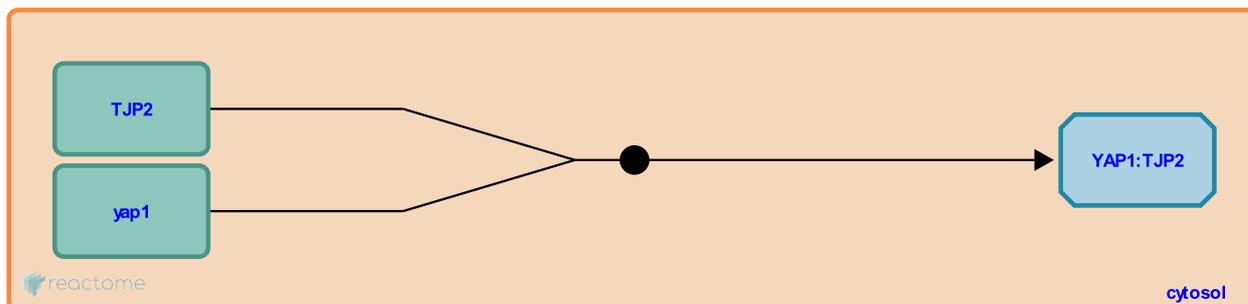
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2064421

Type: binding

Compartments: cytosol

Inferred from: [YAP1 binds ZO-2 \(TJP2\) \(Homo sapiens\)](#)



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: [Translocation of YAP1:ZO-2 \(TJP2\) to the nucleus](#)

Translocation of YAP1:ZO-2 (TJP2) to the nucleus ↗

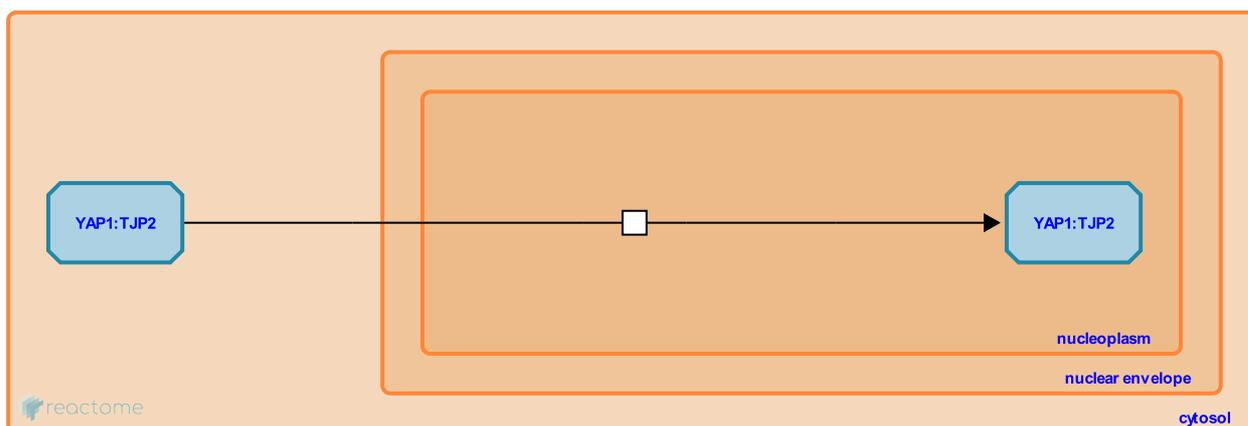
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2064406

Type: transition

Compartments: nucleoplasm, cytosol

Inferred from: [Translocation of YAP1:ZO-2 \(TJP2\) to the nucleus \(Homo sapiens\)](#)



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: [YAP1 binds ZO-2 \(TJP2\)](#)

AMOT proteins bind YAP1 ↗

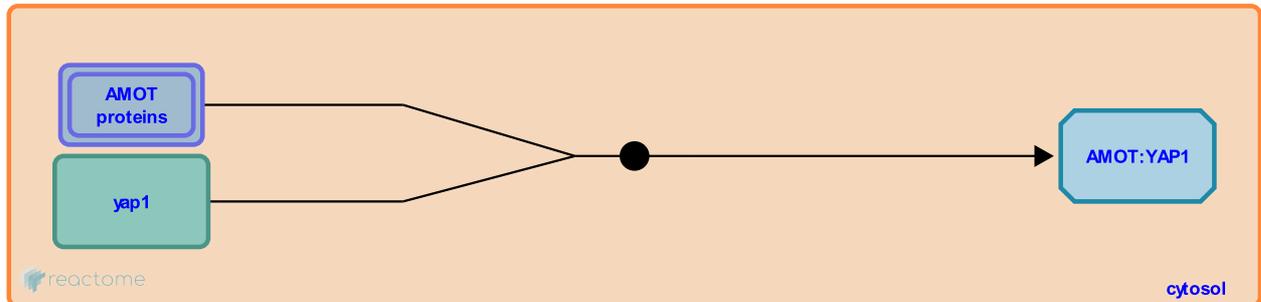
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2028724

Type: binding

Compartments: cytosol

Inferred from: [AMOT proteins bind YAP1 \(Homo sapiens\)](#)



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>

Phosphorylation of YAP by LATS1 ↗

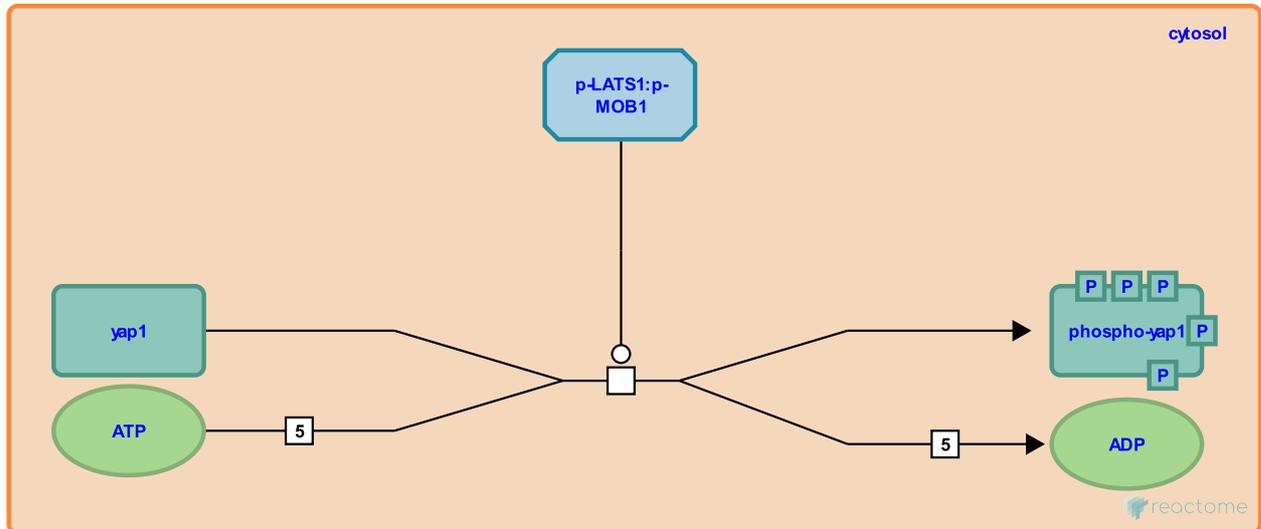
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2028598

Type: transition

Compartments: cytosol

Inferred from: [Phosphorylation of YAP by LATS1 \(Homo sapiens\)](#)



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: [Phosphorylation of LATS1 and 2 by p-STK3 \(MST2\)/N](#), [Phosphorylation of LATS1 and 2 by p-STK3 \(p-MST2\)](#)

Followed by: [YWHAB \(14-3-3 beta/alpha\) dimer binds phosphorylated YAP1](#)

Phosphorylation of YAP by LATS2 ↗

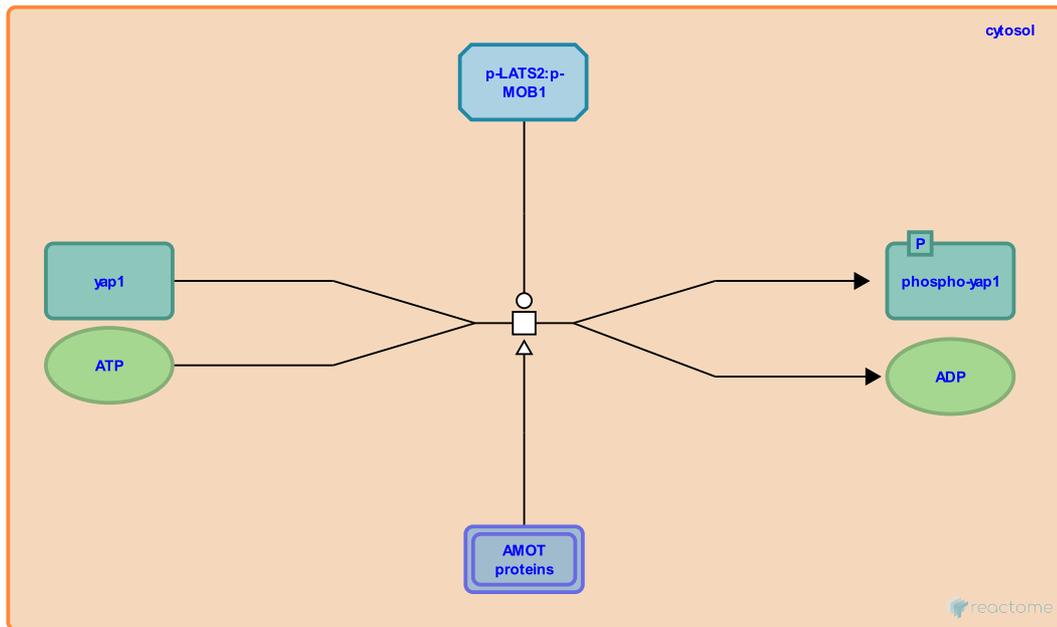
Location: Signaling by Hippo

Stable identifier: R-DRE-2028583

Type: transition

Compartments: cytosol

Inferred from: Phosphorylation of YAP by LATS2 (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: Phosphorylation of LATS1 and 2 by p-STK3 (MST2)/N, Phosphorylation of LATS1 and 2 by p-STK3 (p-MST2)

Followed by: YWHAB (14-3-3 beta/alpha) dimer binds phosphorylated YAP1

YWHAB (14-3-3 beta/alpha) dimer binds phosphorylated YAP1 [↗](#)

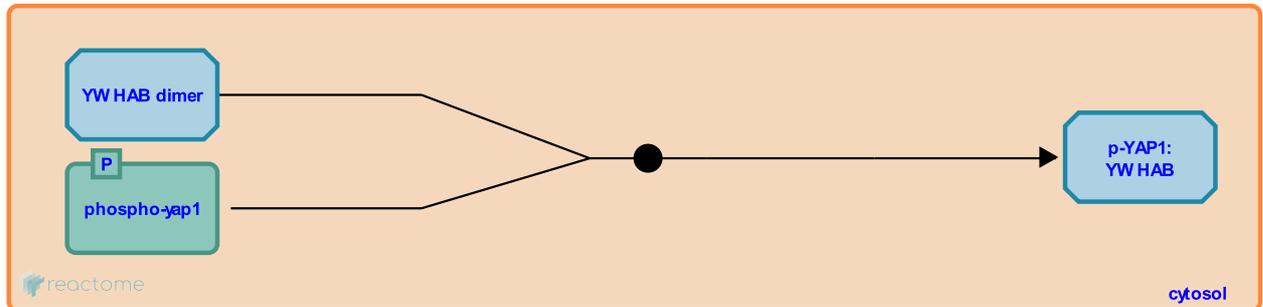
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2028644

Type: binding

Compartments: cytosol

Inferred from: [YWHAB \(14-3-3 beta/alpha\) dimer binds phosphorylated YAP1 \(Homo sapiens\)](#)



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: [Phosphorylation of YAP by LATS1](#), [Phosphorylation of YAP by LATS2](#)

Translocation of WWTR1 (TAZ) to the nucleus ↗

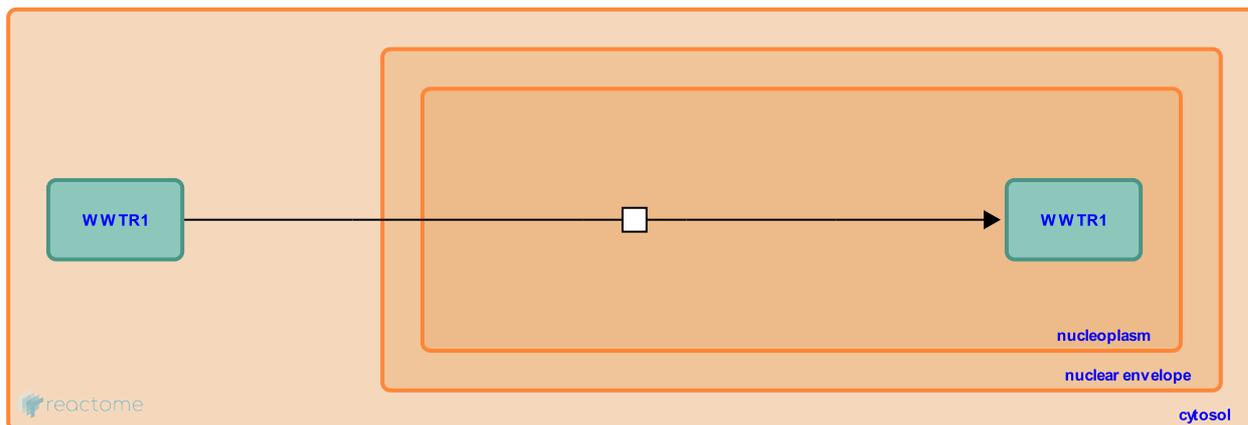
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2032768

Type: transition

Compartments: nucleoplasm, cytosol

Inferred from: [Translocation of WWTR1 \(TAZ\) to the nucleus \(Homo sapiens\)](#)



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>

WWTR1 (TAZ) binds ZO-1 (TJP1) ↗

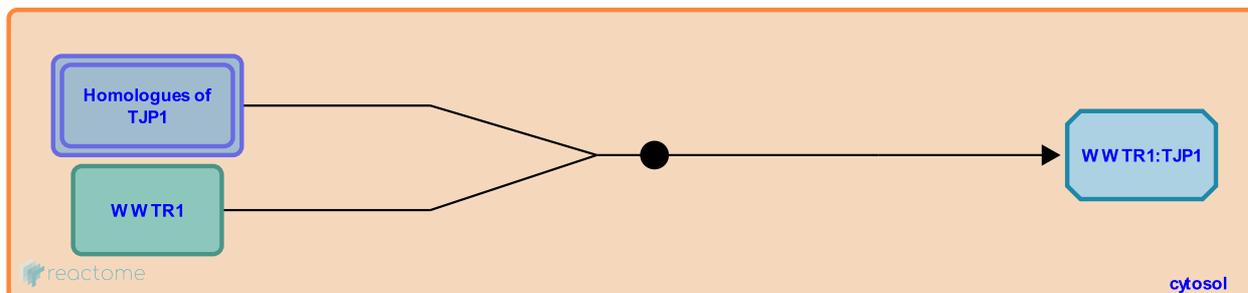
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2064417

Type: binding

Compartments: cytosol

Inferred from: [WWTR1 \(TAZ\) binds ZO-1 \(TJP1\) \(Homo sapiens\)](#)



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>

WWTR1 (TAZ) binds ZO-2 (TJP2) ↗

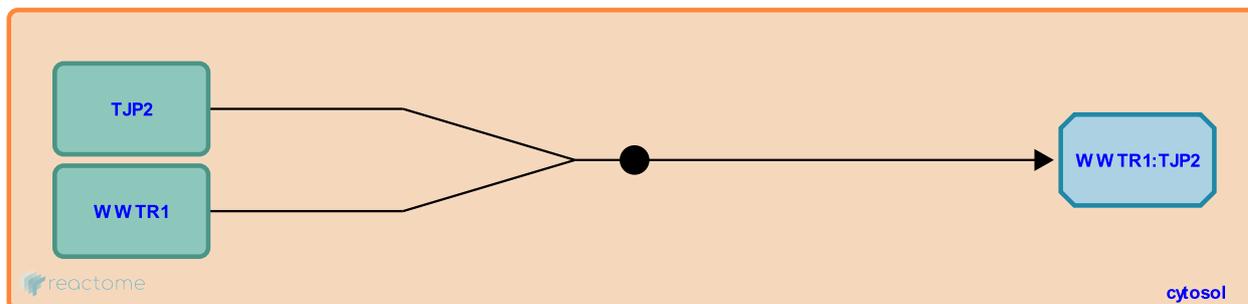
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2064418

Type: binding

Compartments: cytosol

Inferred from: [WWTR1 \(TAZ\) binds ZO-2 \(TJP2\) \(Homo sapiens\)](#)



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>

AMOT proteins bind WWTR1 (TAZ) ↗

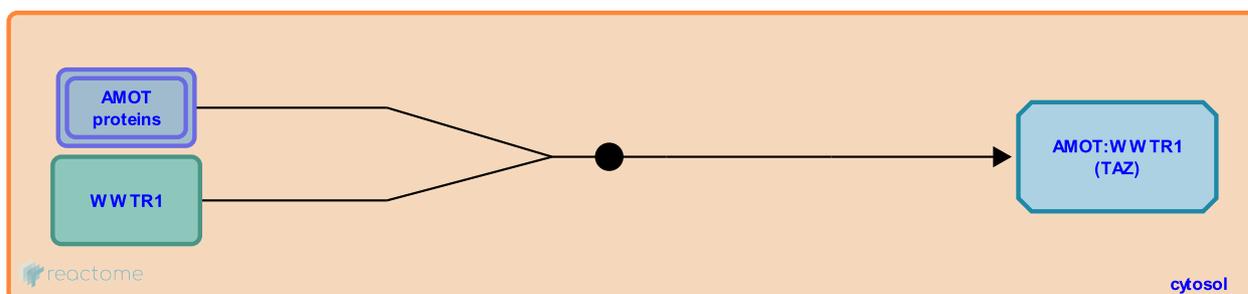
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2028735

Type: binding

Compartments: cytosol

Inferred from: [AMOT proteins bind WWTR1 \(TAZ\) \(Homo sapiens\)](#)



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>

Phosphorylation of WWTR1 (TAZ) by LATS1 ↗

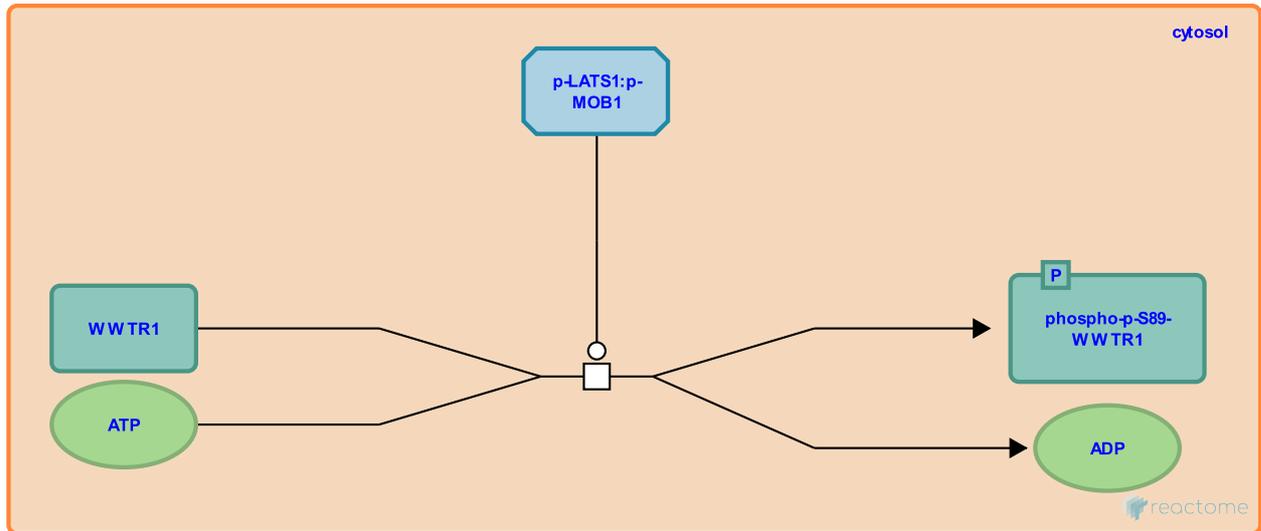
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2060328

Type: transition

Compartments: cytosol

Inferred from: [Phosphorylation of WWTR1 \(TAZ\) by LATS1 \(Homo sapiens\)](#)



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: [Phosphorylation of LATS1 and 2 by p-STK3 \(p-MST2\)](#)

Followed by: [DVL2 binds phosphorylated WWTR1 \(TAZ\)](#)

Phosphorylation of WWTR1 (TAZ) by LATS2 ↗

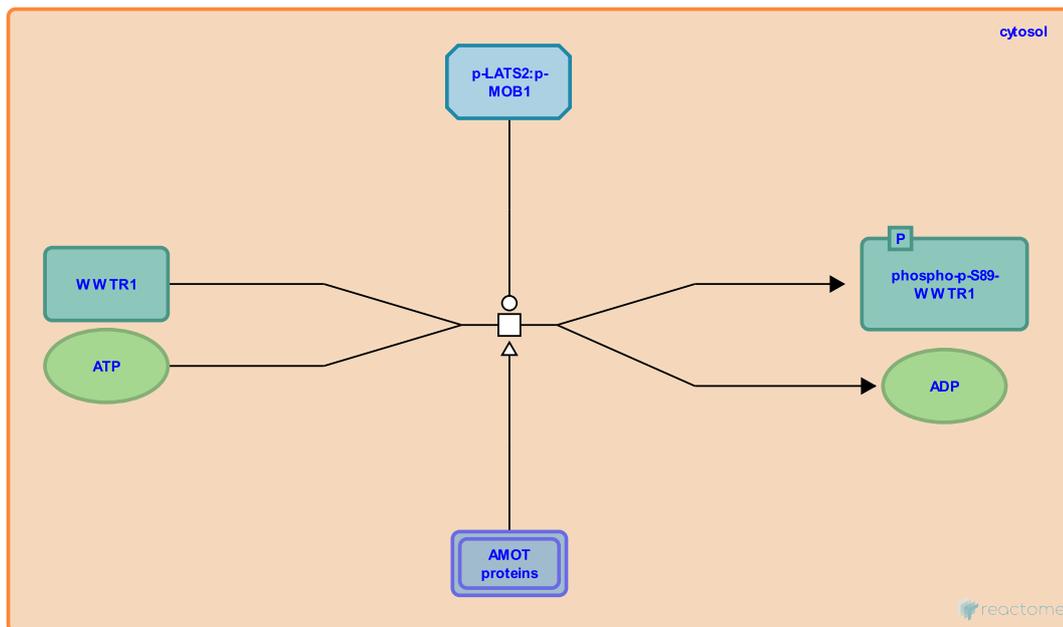
Location: Signaling by Hippo

Stable identifier: R-DRE-2028661

Type: transition

Compartments: cytosol

Inferred from: Phosphorylation of WWTR1 (TAZ) by LATS2 (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: Phosphorylation of LATS1 and 2 by p-STK3 (p-MST2)

Followed by: YWHAE (14-3-3 epsilon) dimer binds phosphorylated WWTR1 (TAZ), DVL2 binds phosphorylated WWTR1 (TAZ)

DVL2 binds phosphorylated WWTR1 (TAZ) ↗

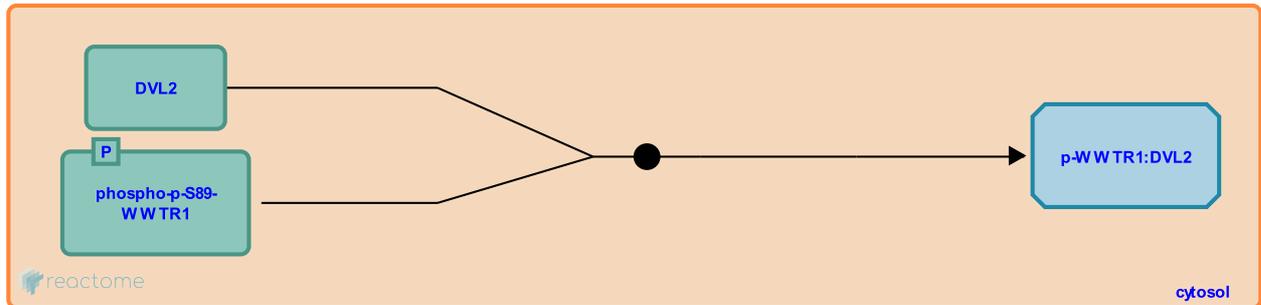
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2066299

Type: binding

Compartments: cytosol

Inferred from: [DVL2 binds phosphorylated WWTR1 \(TAZ\) \(Homo sapiens\)](#)



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: [Phosphorylation of WWTR1 \(TAZ\) by LATS1](#), [Phosphorylation of WWTR1 \(TAZ\) by LATS2](#)

YWHAE (14-3-3 epsilon) dimer binds phosphorylated WWTR1 (TAZ) ↗

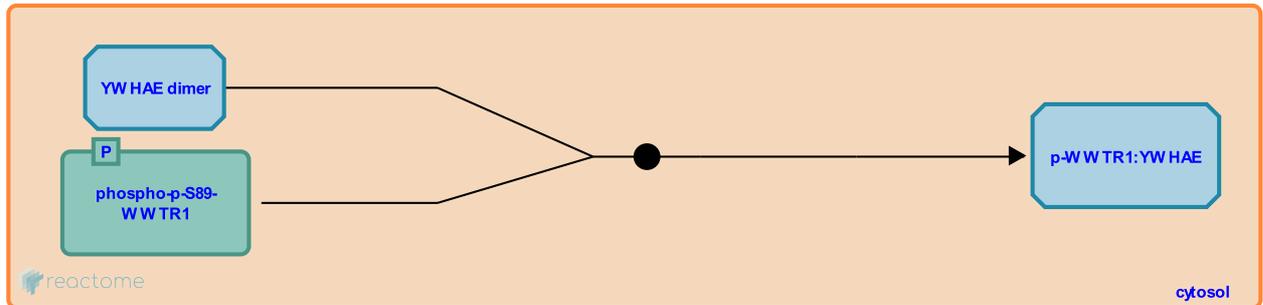
Location: [Signaling by Hippo](#)

Stable identifier: R-DRE-2028651

Type: binding

Compartments: cytosol

Inferred from: [YWHAE \(14-3-3 epsilon\) dimer binds phosphorylated WWTR1 \(TAZ\) \(Homo sapiens\)](#)



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: [Phosphorylation of WWTR1 \(TAZ\) by LATS2](#)

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