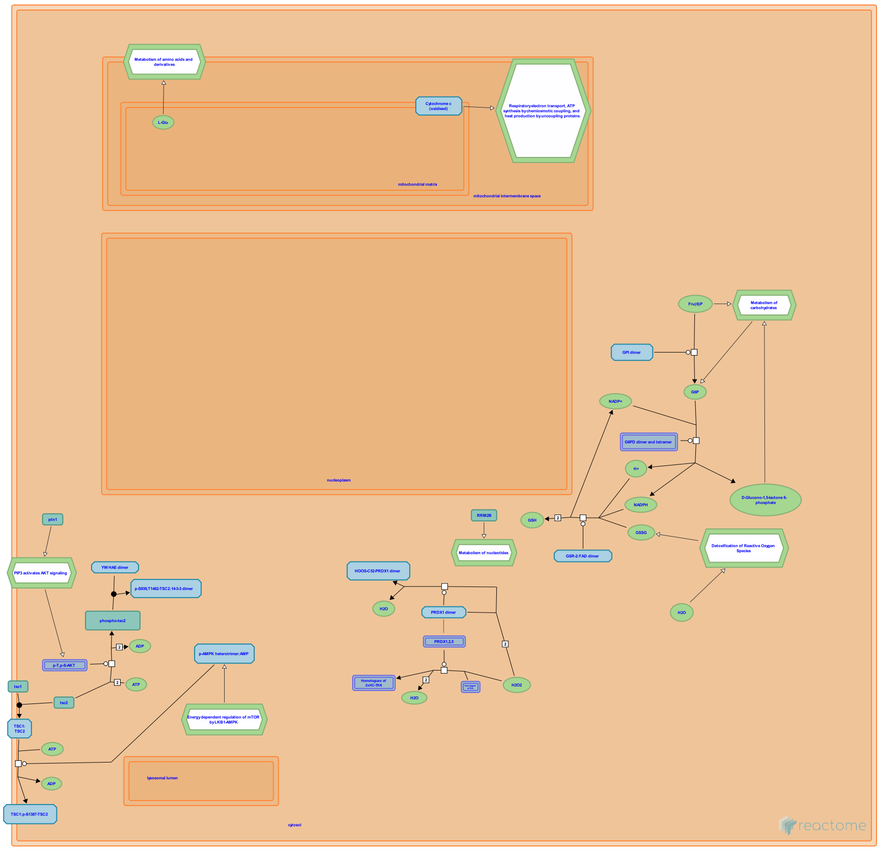
TP53 Regulates Metabolic Genes



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

06/05/2024

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. ↗

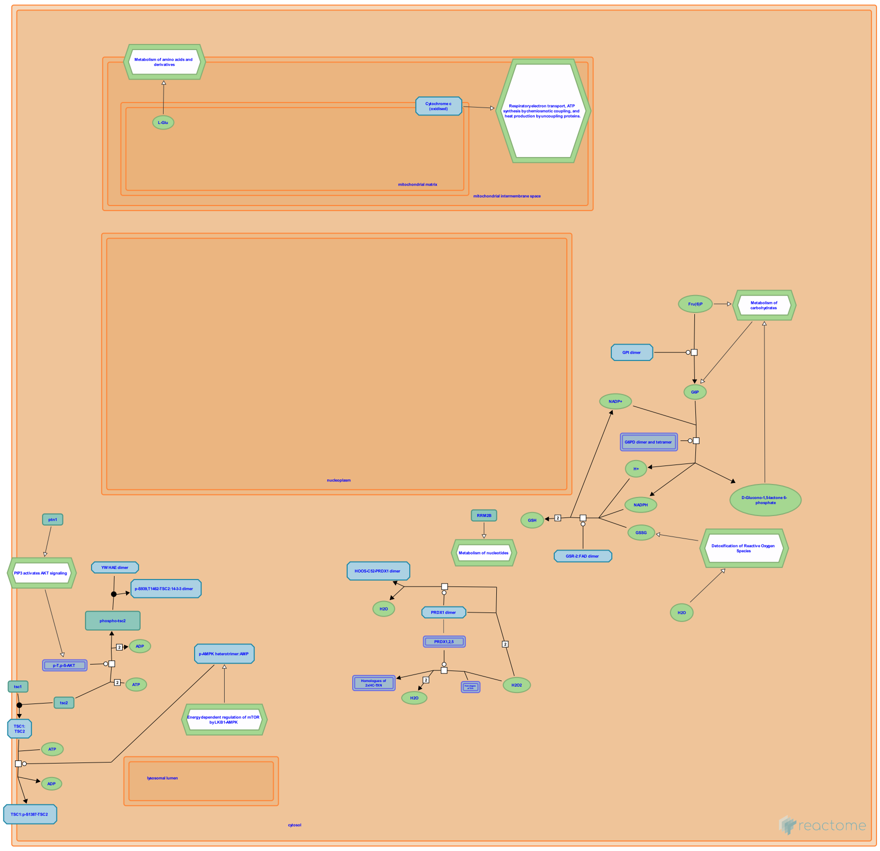
Reactome database release: 88

This document contains 1 pathway and 9 reactions (see Table of Contents)

TP53 Regulates Metabolic Genes ↗

Stable identifier: R-SPO-5628897

Inferred from: TP53 Regulates Metabolic Genes (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

GPI dimer isomerizes Fru(6)P to G6P ↗

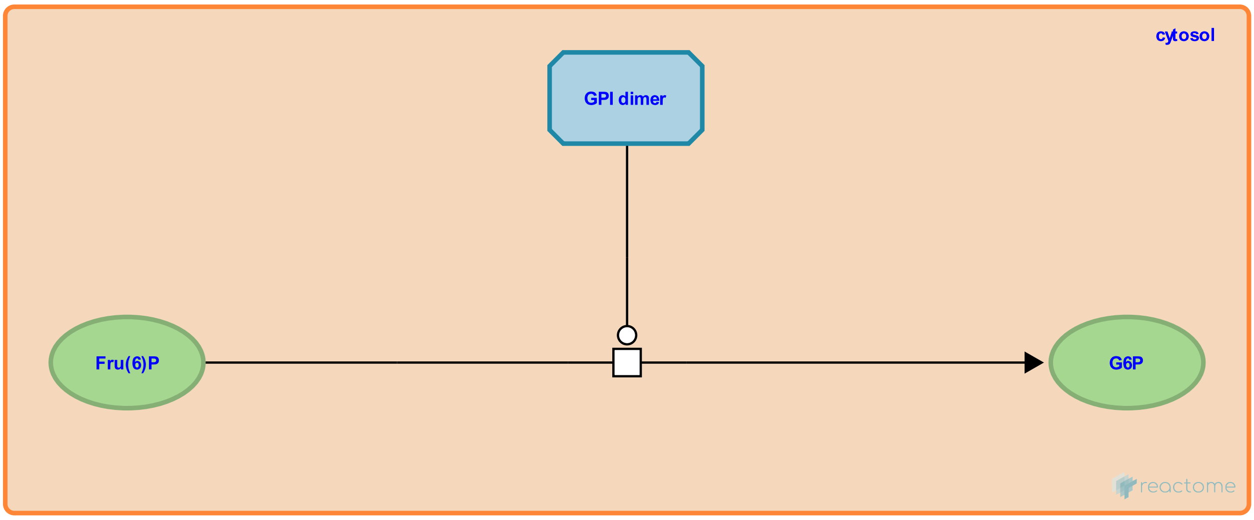
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-SPO-70475

Type: transition

Compartments: cytosol

Inferred from: GPI dimer isomerizes Fru(6)P to G6P (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: alpha-D-glucose 6-phosphate + NADP+ => D-glucono-1,5-lactone 6-phosphate + NADPH + H+

alpha-D-glucose 6-phosphate + NADP+ => D-glucono-1,5-lactone 6-phosphate + NADPH + H+ ↗

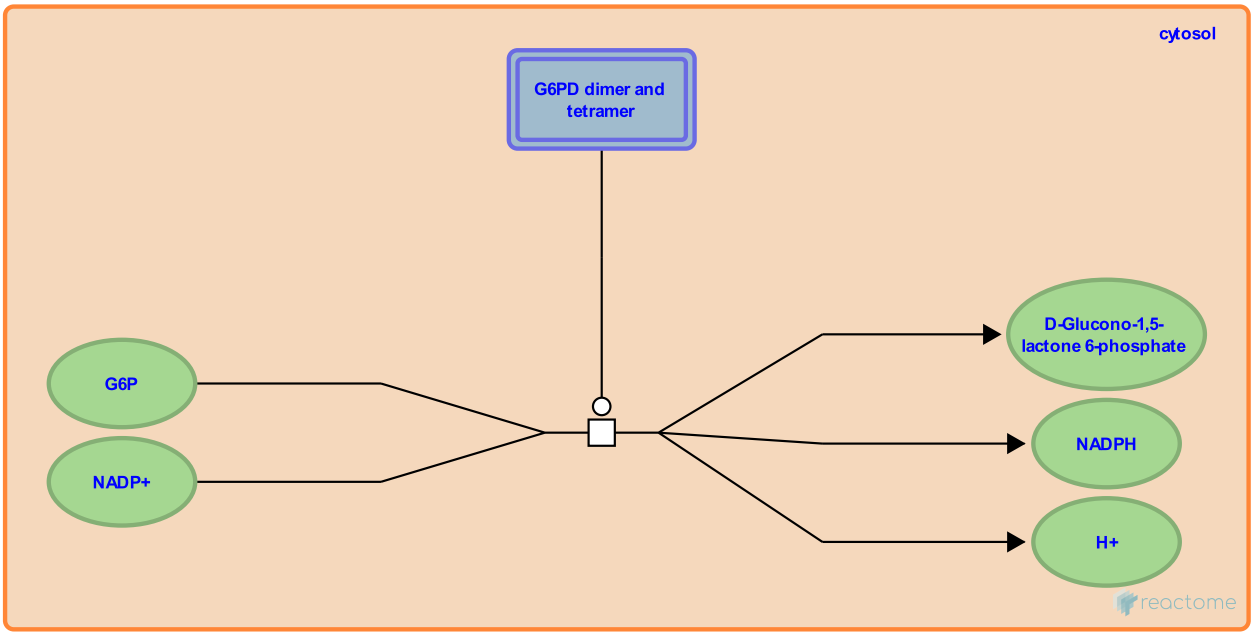
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-SPO-70377

Type: transition

Compartments: cytosol

Inferred from: alpha-D-glucose 6-phosphate + NADP+ => D-glucono-1,5-lactone 6-phosphate + NADPH + H+ (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: GPI dimer isomerizes Fru(6)P to G6P

Followed by: glutathione (oxidized) + NADPH + H+ => 2 glutathione (reduced) + NADP+

glutathione (oxidized) + NADPH + H+ => 2 glutathione (reduced) + NADP+ ↗

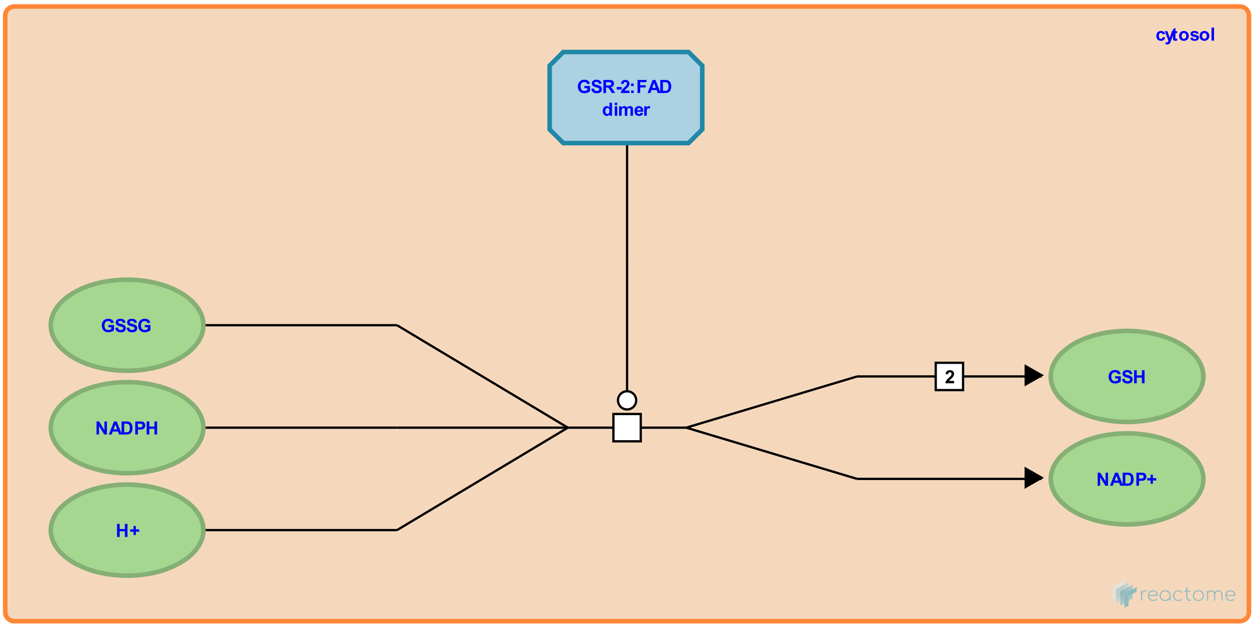
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-SPO-71682

Type: transition

Compartments: cytosol

Inferred from: glutathione (oxidized) + NADPH + H+ => 2 glutathione (reduced) + NADP+ (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: alpha-D-glucose 6-phosphate + NADP+ => D-glucono-1,5-lactone 6-phosphate + NADPH + H+

PRDX1,2,5 catalyze TXN reduced + H2O2 => TXN oxidized + 2H2O ↗

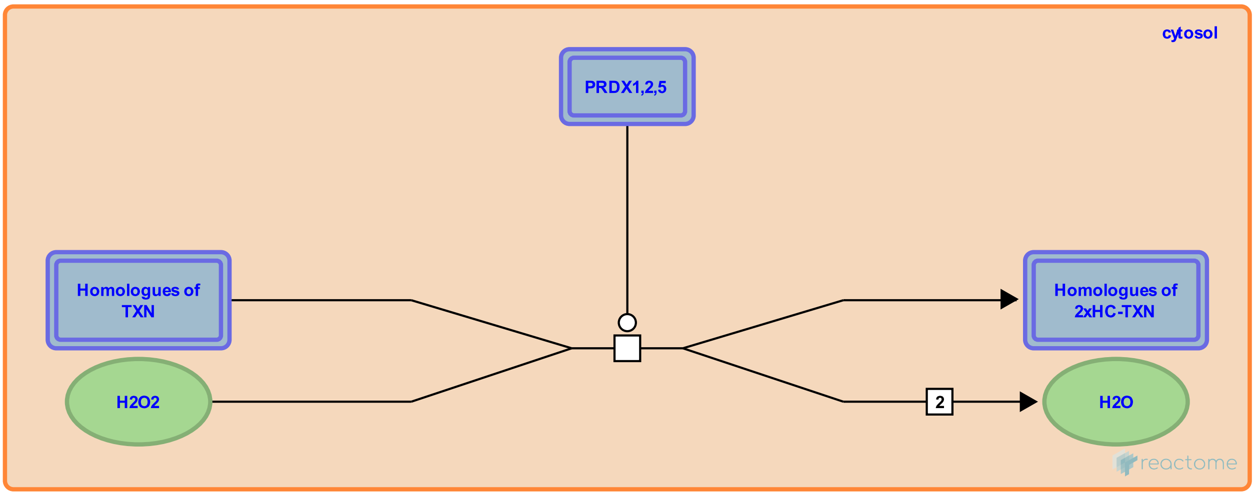
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-SPO-3341343

Type: transition

Compartments: cytosol

Inferred from: PRDX1,2,5 catalyze TXN reduced + H2O2 => TXN oxidized + 2H2O (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: PRDX1 overoxidizes

PRDX1 overoxidizes ↗

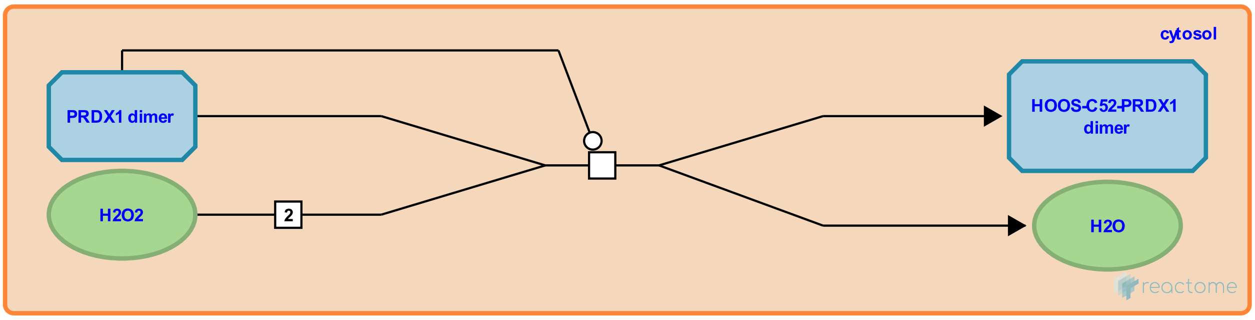
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-SPO-5631885

Type: transition

Compartments: cytosol

Inferred from: PRDX1 overoxidizes (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: PRDX1,2,5 catalyze TXN reduced + H2O2 => TXN oxidized + 2H2O

p-AMPK phosphorylates TSC1:TSC2 ↗

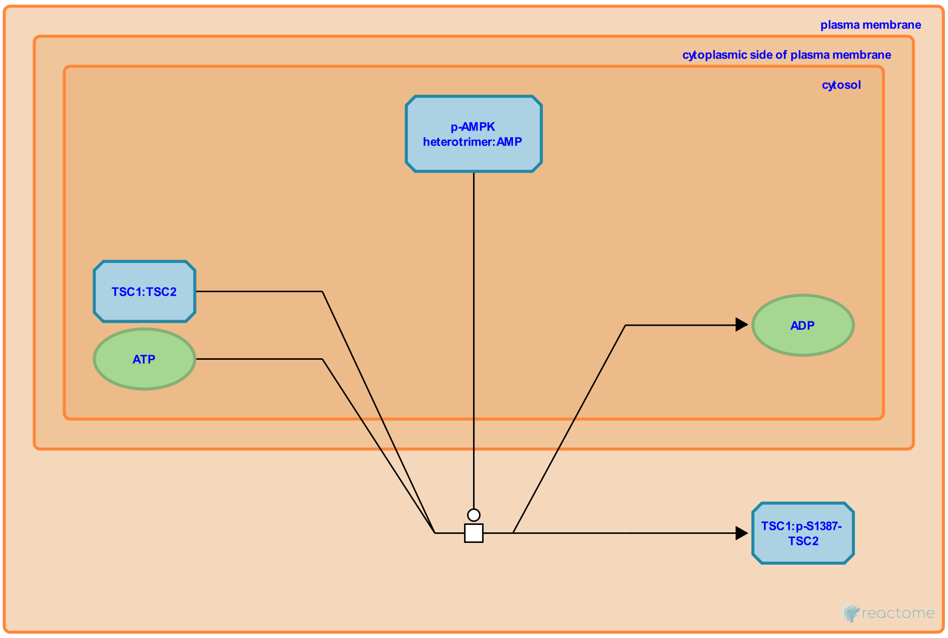
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-SPO-380927

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: p-AMPK phosphorylates TSC1:TSC2 (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: Formation of TSC1:TSC2 complex

Formation of TSC1:TSC2 complex ↗

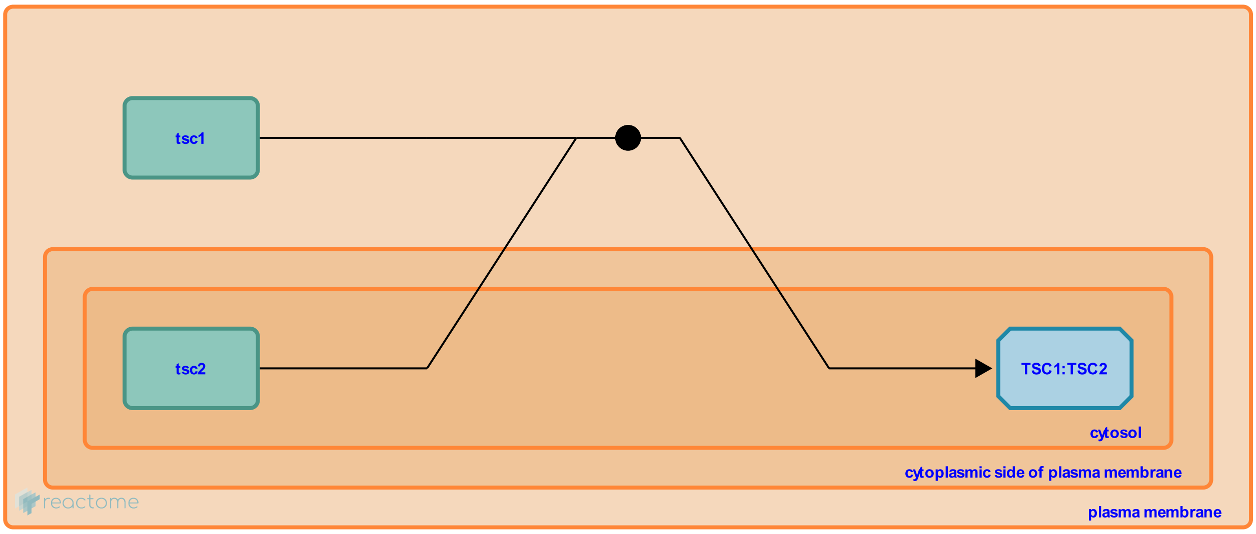
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-SPO-165179

Type: binding

Compartments: plasma membrane, cytosol

Inferred from: Formation of TSC1:TSC2 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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: p-AMPK phosphorylates TSC1:TSC2

AKT phosphorylates TSC2, inhibiting it ↗

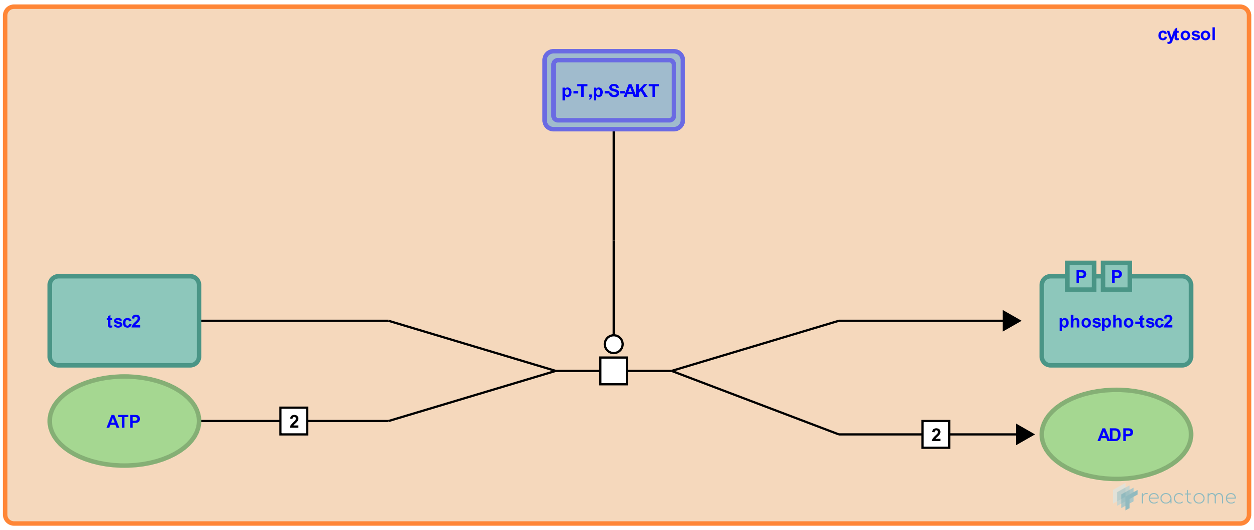
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-SPO-198609

Type: transition

Compartments: cytosol

Inferred from: AKT phosphorylates TSC2, inhibiting it (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: p-S939,T1462-TSC2 binding to 14-3-3 dimer is negatively regulated by DDIT4

p-S939,T1462-TSC2 binding to 14-3-3 dimer is negatively regulated by DDIT4 ↗

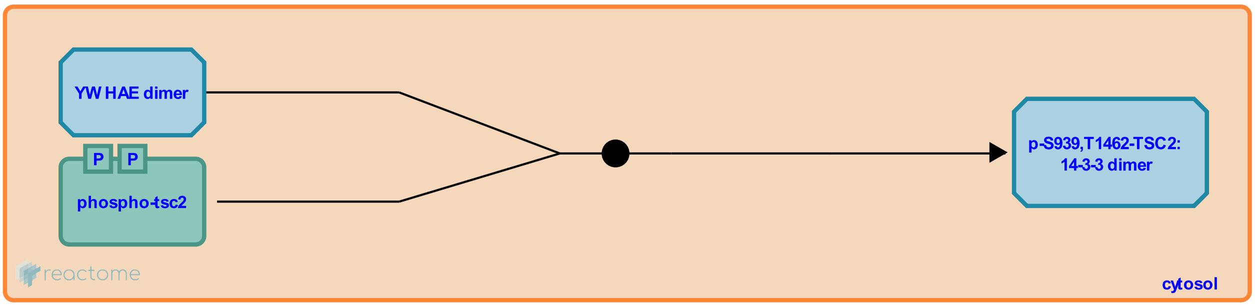
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-SPO-5632732

Type: binding

Compartments: cytosol

Inferred from: p-S939,T1462-TSC2 binding to 14-3-3 dimer is negatively regulated by DDIT4 (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: AKT phosphorylates TSC2, inhibiting it

Table of Contents