

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 12 reactions ([see Table of Contents](#))

TIGAR converts D-fructose-2,6-bisphosphate to D-fructose 6-phosphate ↗

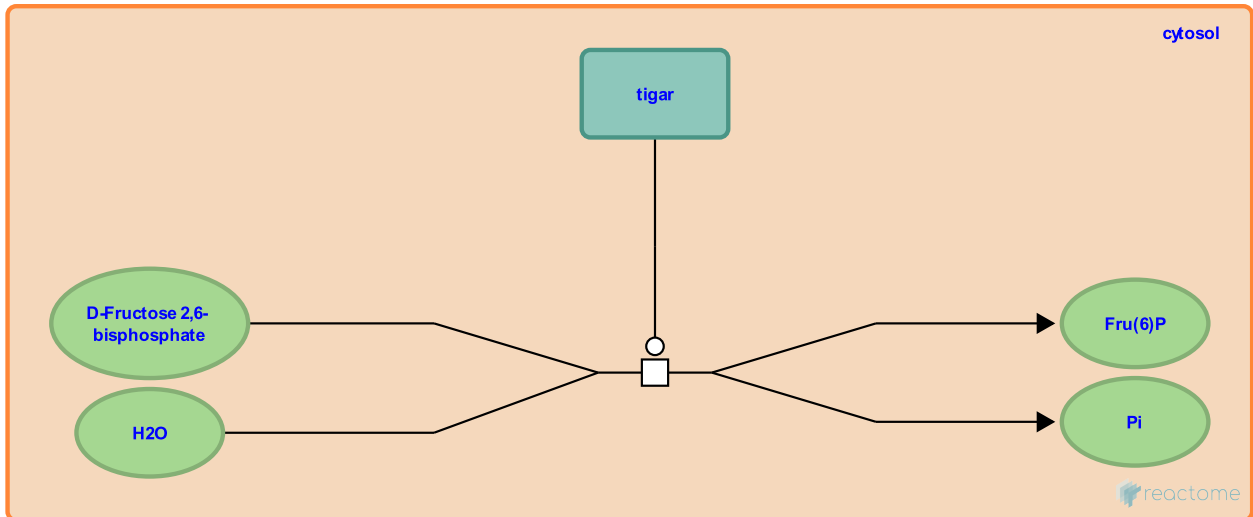
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-XTR-5628905

Type: transition

Compartments: cytosol

Inferred from: TIGAR converts D-fructose-2,6-bisphosphate to D-fructose 6-phosphate (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: GPI dimer isomerizes Fru(6)P to G6P

GPI dimer isomerizes Fru(6)P to G6P ↗

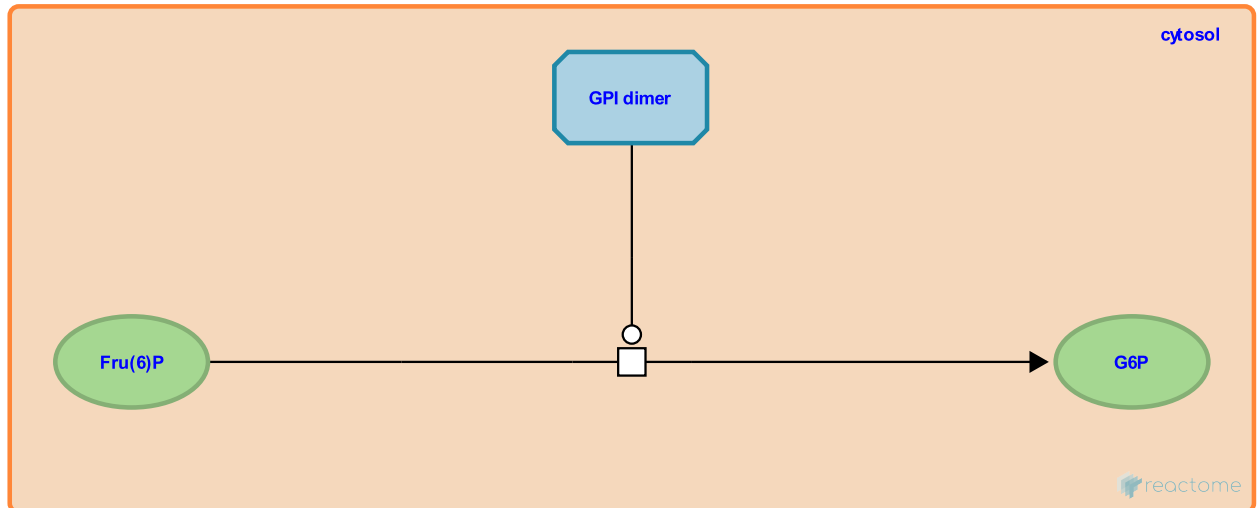
Location: [TP53 Regulates Metabolic Genes](#)

Stable identifier: R-XTR-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>

Preceded by: [TIGAR converts D-fructose-2,6-bisphosphate to D-fructose 6-phosphate](#)

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+ ↗

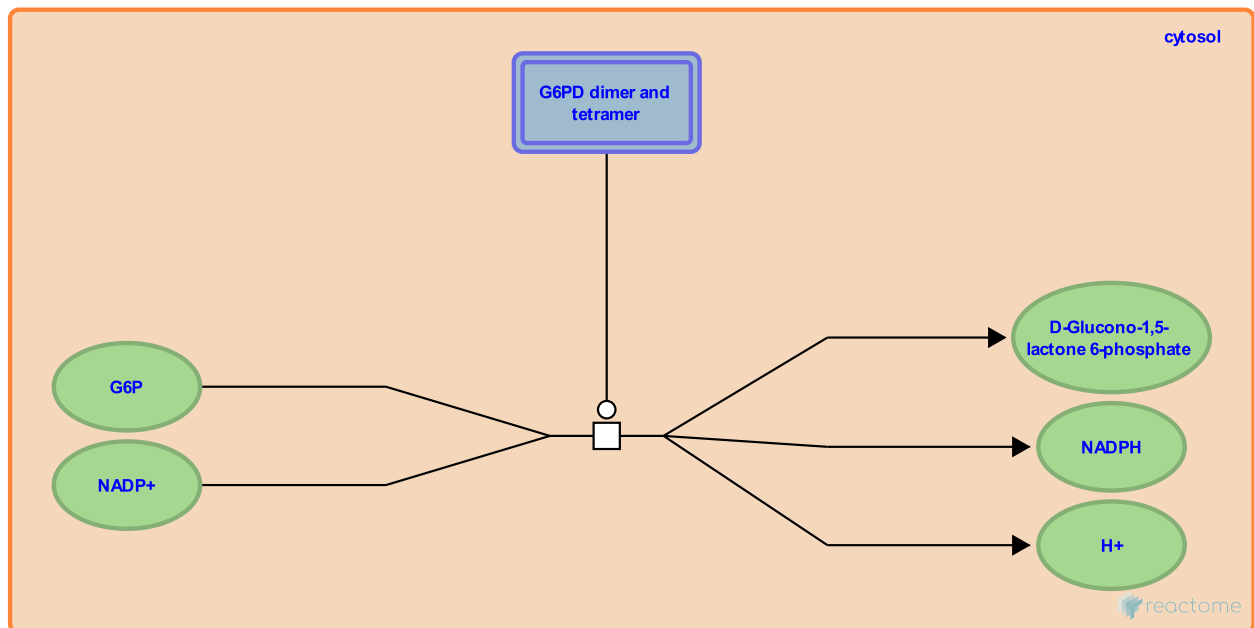
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-XTR-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.](http://www.pantherdb.org/about.jsp) 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+ ↗

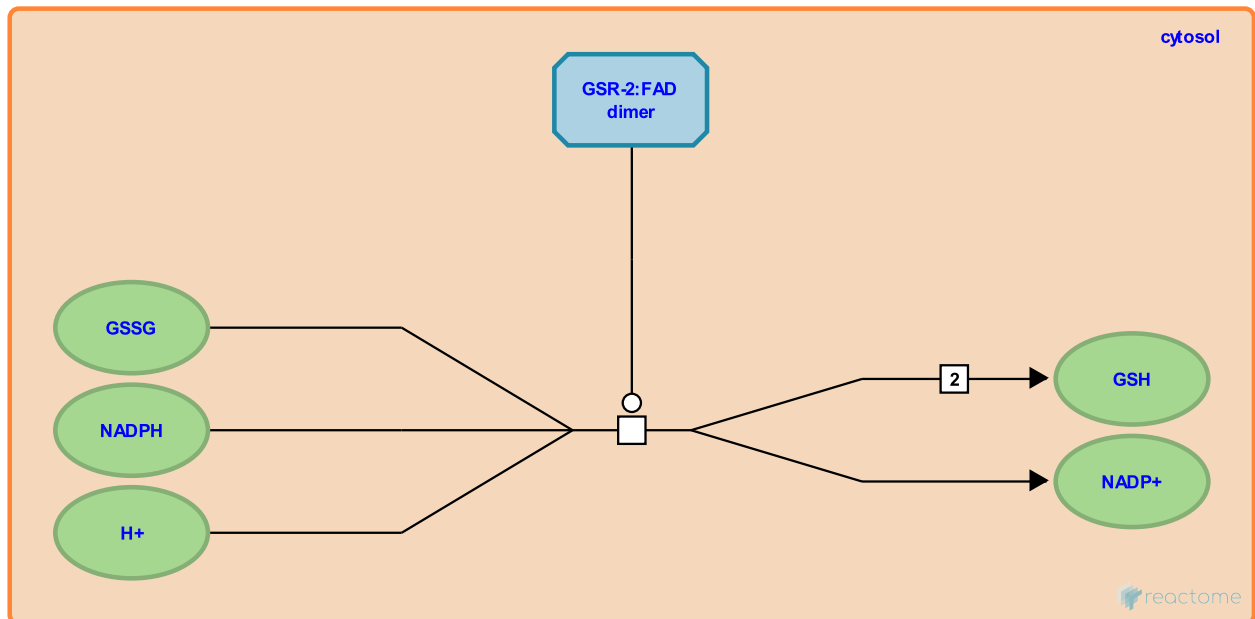
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-XTR-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.](http://www.pantherdb.org/about.jsp) 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 overoxidizes ↗

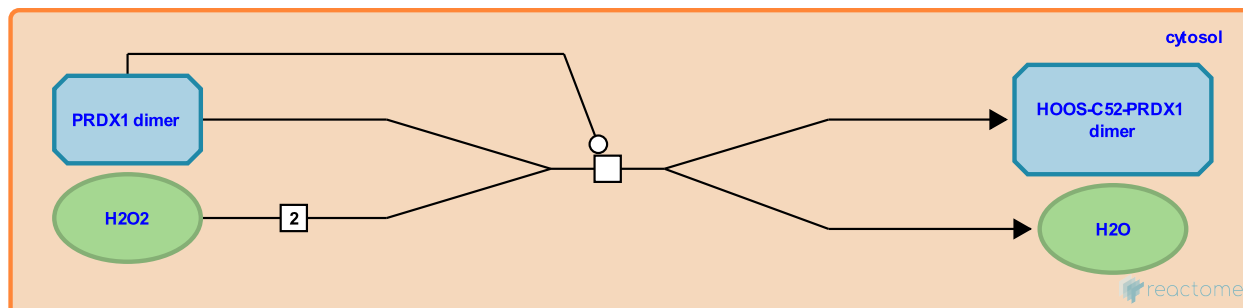
Location: [TP53 Regulates Metabolic Genes](#)

Stable identifier: R-XTR-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>

Followed by: [SESN1,2,3 bind overoxidized PRDX1](#)

SESN1,2,3 bind overoxidized PRDX1 ↗

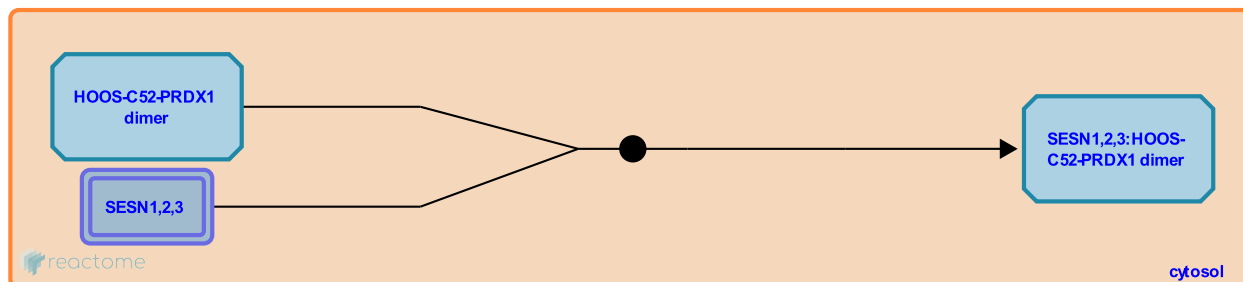
Location: [TP53 Regulates Metabolic Genes](#)

Stable identifier: R-XTR-5631903

Type: binding

Compartments: cytosol

Inferred from: [SESN1,2,3 bind overoxidized PRDX1 \(Homo sapiens\)](#)



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 overoxidizes](#)

RHEB in mTORC1:RHEB:GTP hydrolyses GTP ↗

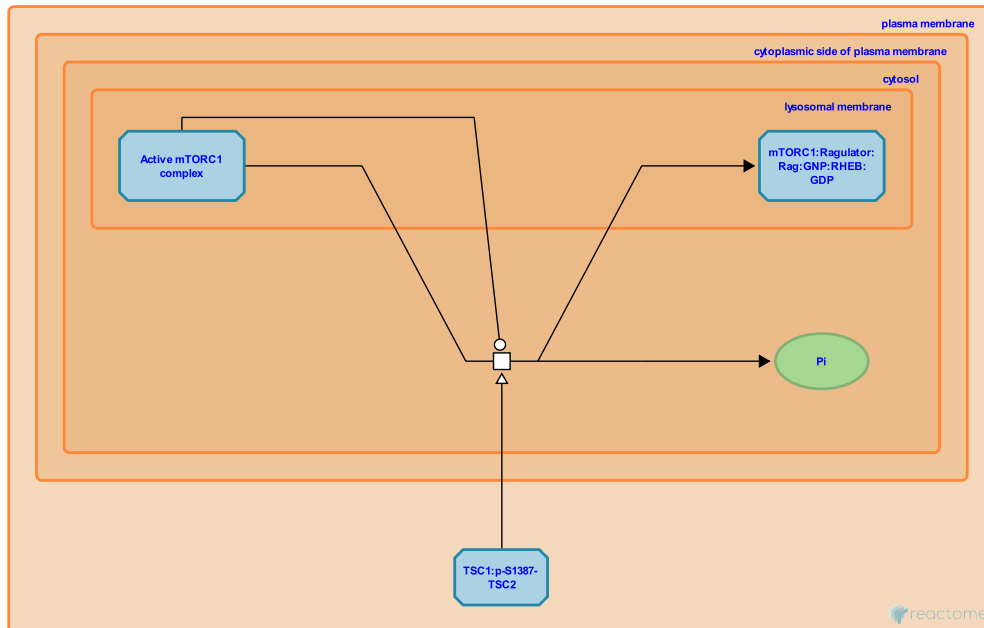
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-XTR-380979

Type: transition

Compartments: cytosol, lysosomal membrane

Inferred from: RHEB in mTORC1:RHEB:GTP hydrolyses GTP (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Formation of TSC1:TSC2 complex ↗

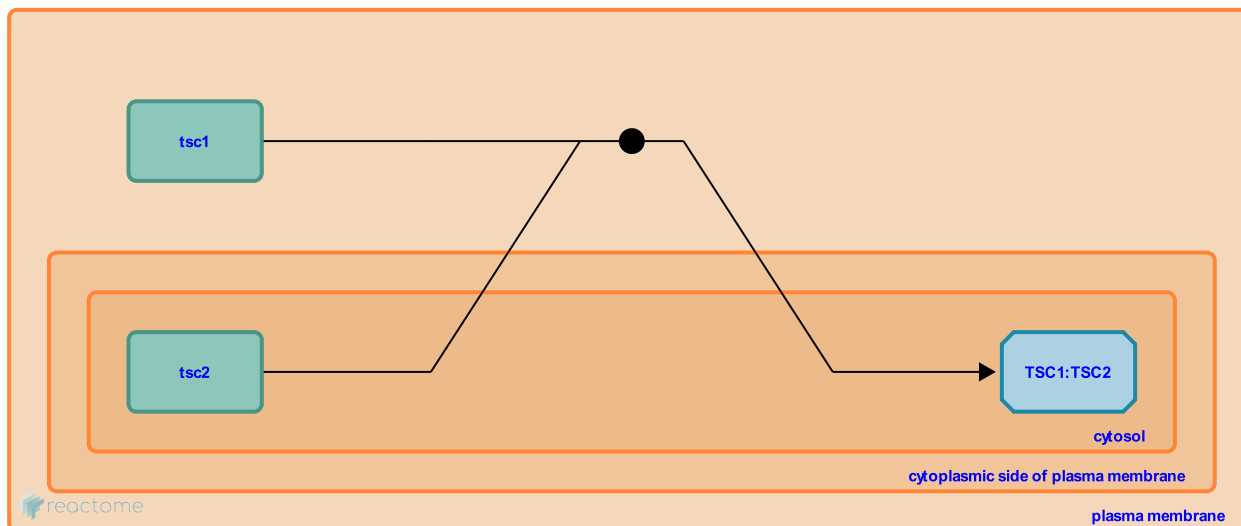
Location: [TP53 Regulates Metabolic Genes](#)

Stable identifier: R-XTR-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>

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

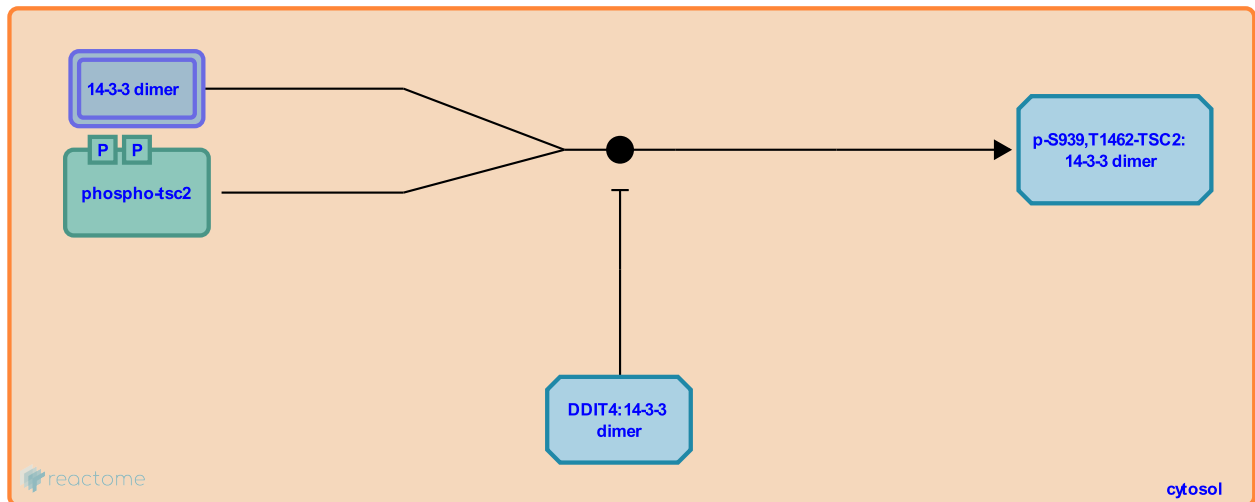
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-XTR-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.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

DDIT4 binds 14-3-3 dimer ↗

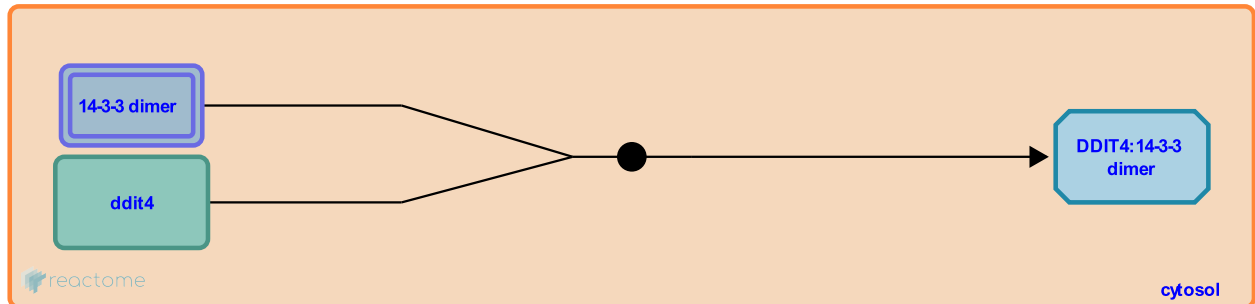
Location: [TP53 Regulates Metabolic Genes](#)

Stable identifier: R-XTR-5632738

Type: binding

Compartments: cytosol

Inferred from: [DDIT4 binds 14-3-3 dimer \(Homo sapiens\)](#)



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>

Electron transfer from reduced cytochrome c to molecular oxygen ↗

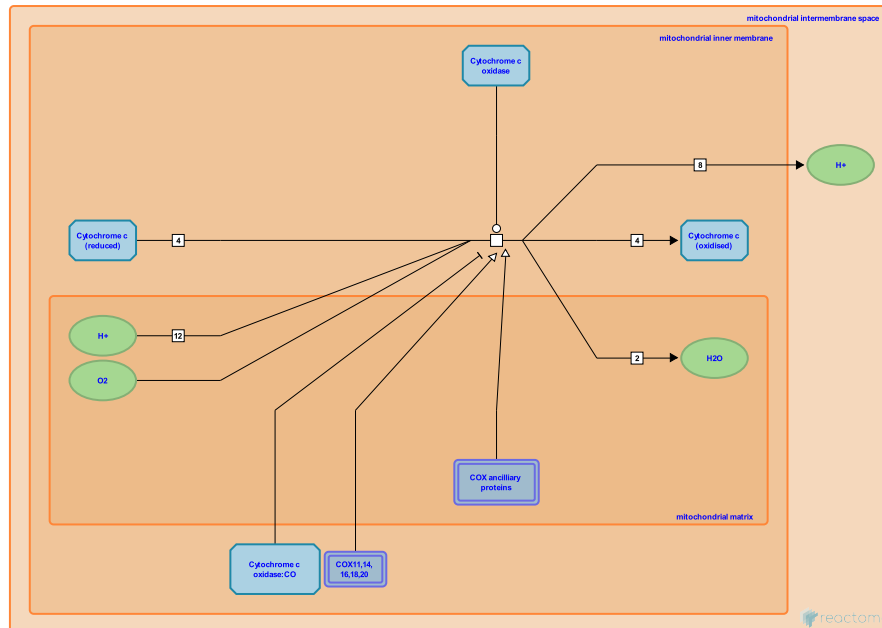
Location: TP53 Regulates Metabolic Genes

Stable identifier: R-XTR-163214

Type: transition

Compartments: mitochondrial inner membrane, mitochondrial intermembrane space, mitochondrial matrix

Inferred from: Electron transfer from reduced cytochrome c to molecular oxygen (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.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

glutamine + H₂O => glutamate + NH₄⁺ [GLS] ↗

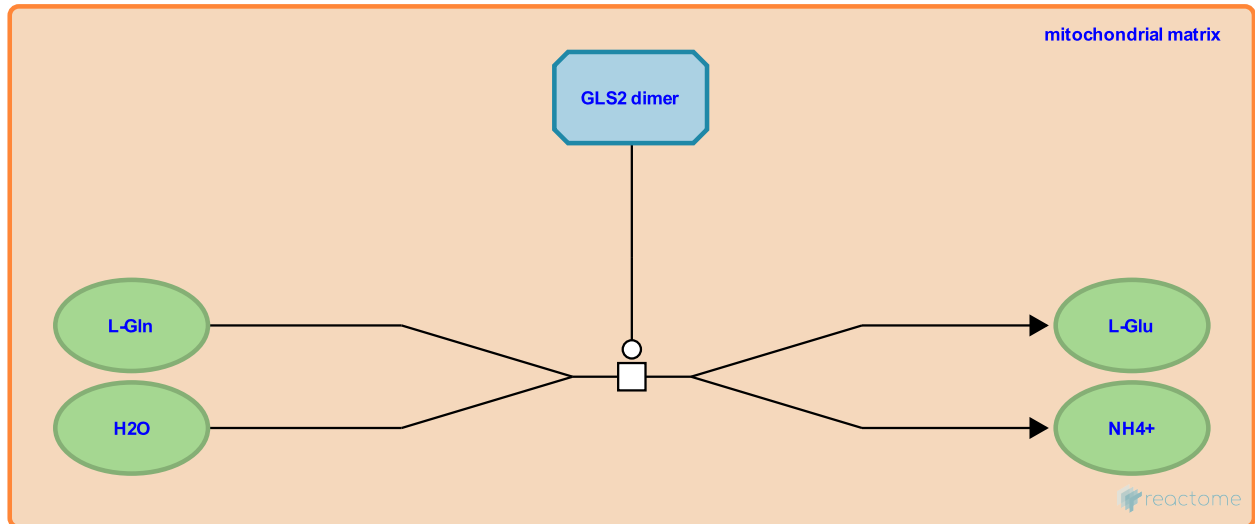
Location: [TP53 Regulates Metabolic Genes](#)

Stable identifier: R-XTR-70609

Type: transition

Compartments: mitochondrial matrix

Inferred from: [glutamine + H₂O => glutamate + NH₄⁺ \[GLS\]](#) (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>

Table of Contents

Introduction	1
☒ TP53 Regulates Metabolic Genes	2
↳ TIGAR converts D-fructose-2,6-bisphosphate to D-fructose 6-phosphate	3
↳ GPI dimer isomerizes Fru(6)P to G6P	4
↳ α -D-glucose 6-phosphate + NADP ⁺ => D-glucono-1,5-lactone 6-phosphate + NADPH + H ⁺	5
↳ glutathione (oxidized) + NADPH + H ⁺ => 2 glutathione (reduced) + NADP ⁺	6
↳ PRDX1 overoxidizes	7
↳ SESN1,2,3 bind overoxidized PRDX1	8
↳ RHEB in mTORC1:RHEB:GTP hydrolyses GTP	9
↳ Formation of TSC1:TSC2 complex	10
↳ p-S939,T1462-TSC2 binding to 14-3-3 dimer is negatively regulated by DDIT4	11
↳ DDIT4 binds 14-3-3 dimer	12
↳ Electron transfer from reduced cytochrome c to molecular oxygen	13
↳ glutamine + H ₂ O => glutamate + NH ₄ ⁺ [GLS]	14
Table of Contents	15