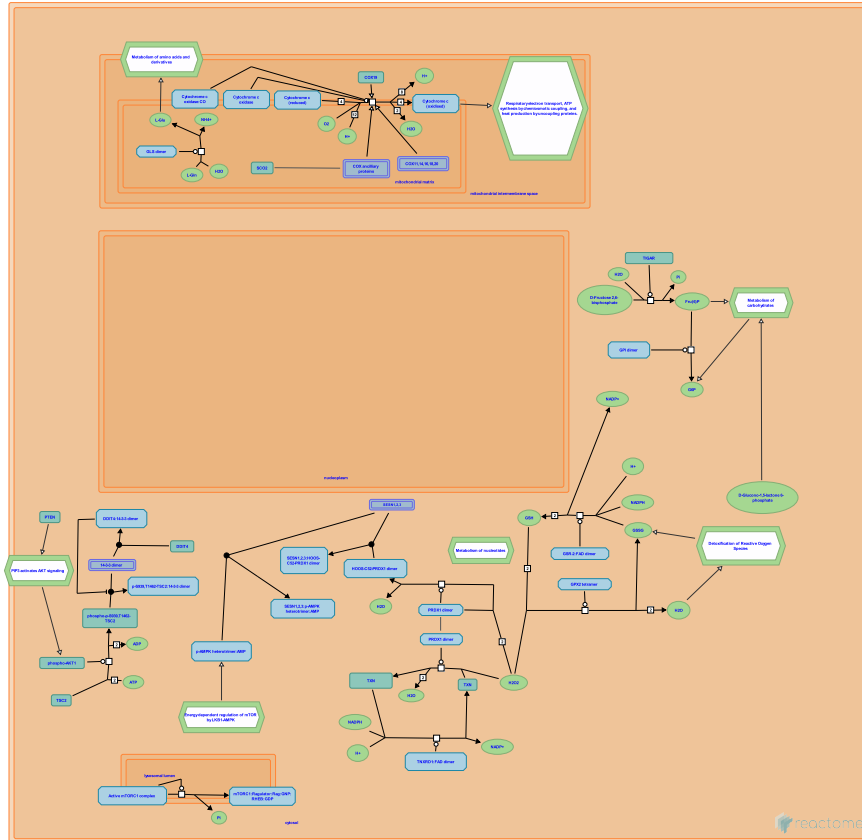


# TP53 Regulates Metabolic Genes



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](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/faq).

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://reactome.org/Textbook).

03/04/2024

## 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. [↗](#)

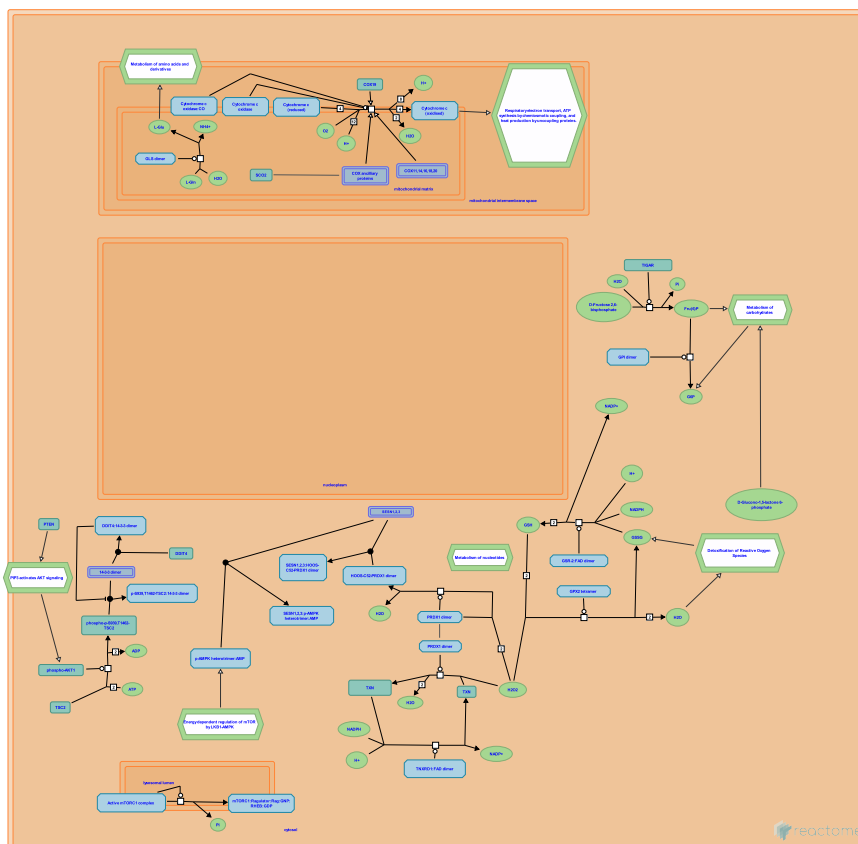
Reactome database release: 88

This document contains 1 pathway and 15 reactions ([see Table of Contents](#))

## TP53 Regulates Metabolic Genes ↗

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

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

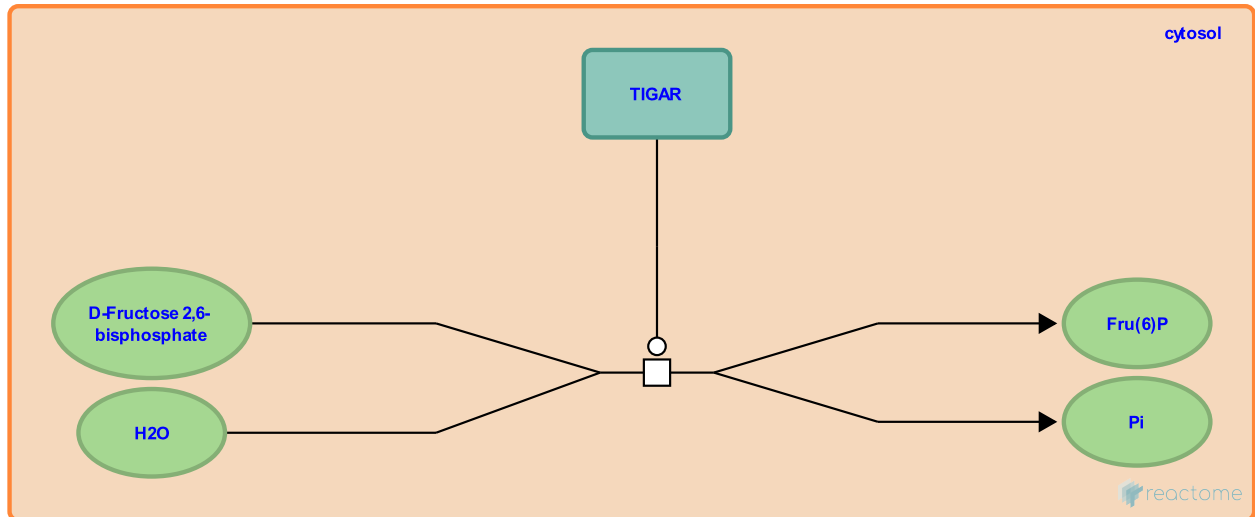
**Location:** TP53 Regulates Metabolic Genes

**Stable identifier:** R-GGA-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.](#) 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 ↗

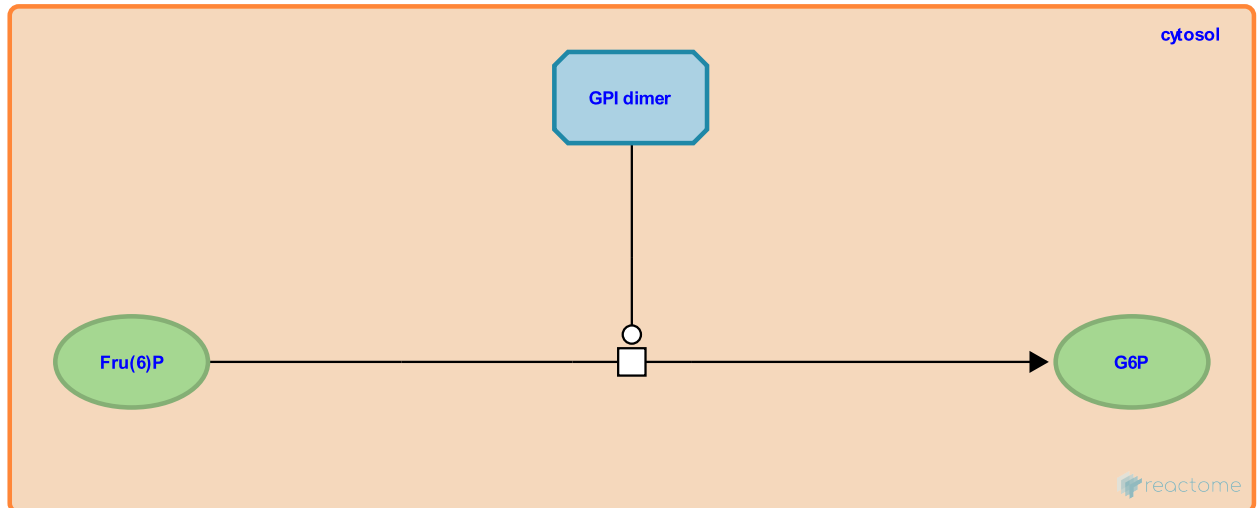
**Location:** [TP53 Regulates Metabolic Genes](#)

**Stable identifier:** R-GGA-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](#)

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

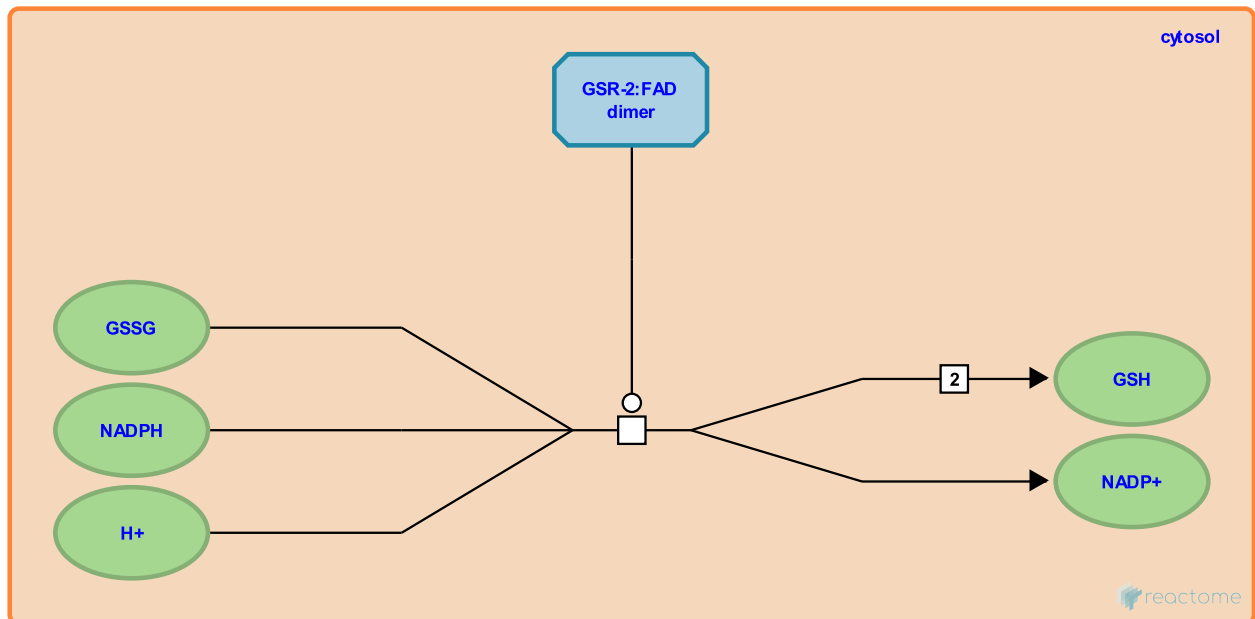
**Location:** TP53 Regulates Metabolic Genes

**Stable identifier:** R-GGA-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>

**GPX2 catalyzes 2 glutathione, reduced + H2O2 => glutathione, oxidized + 2 H2O** ↗

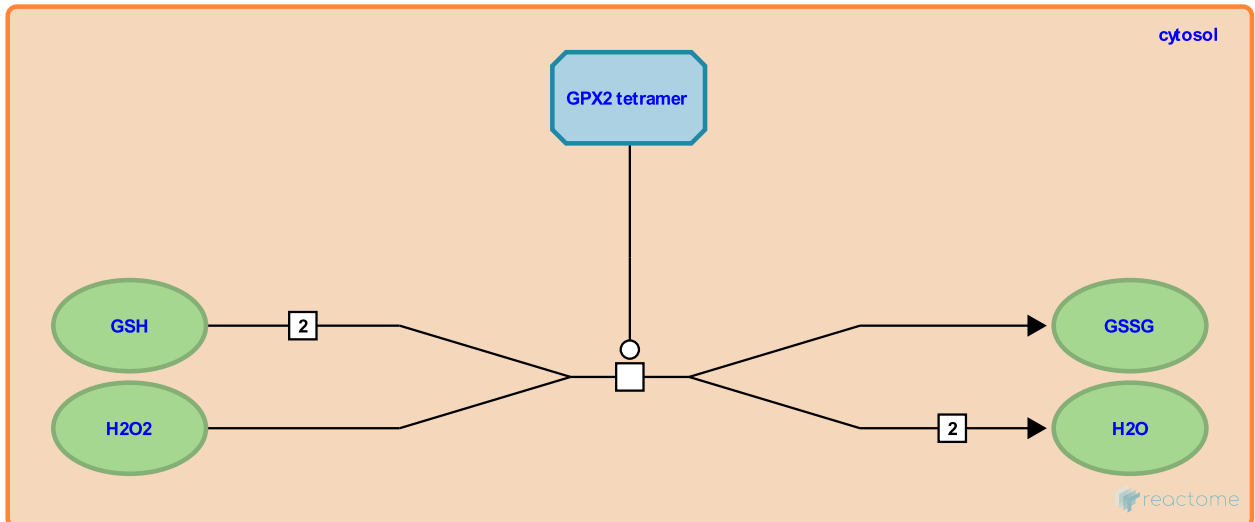
**Location:** TP53 Regulates Metabolic Genes

**Stable identifier:** R-GGA-3341277

**Type:** transition

**Compartments:** cytosol

**Inferred from:** GPX2 catalyzes 2 glutathione, reduced + H2O2 => glutathione, oxidized + 2 H2O (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>

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

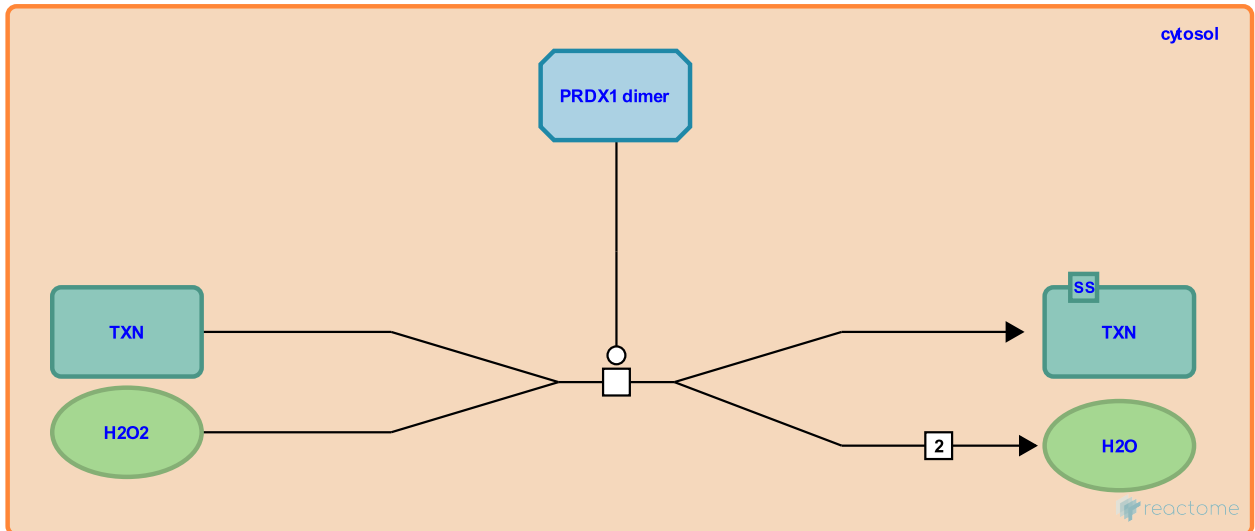
**Location:** TP53 Regulates Metabolic Genes

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

**Preceded by:** thioredoxin, oxidized + NADPH + H+ => thioredoxin, reduced + NADP+

**Followed by:** PRDX1 overoxidizes



**thioredoxin, oxidized + NADPH + H+ => thioredoxin, reduced + NADP+ ↗**

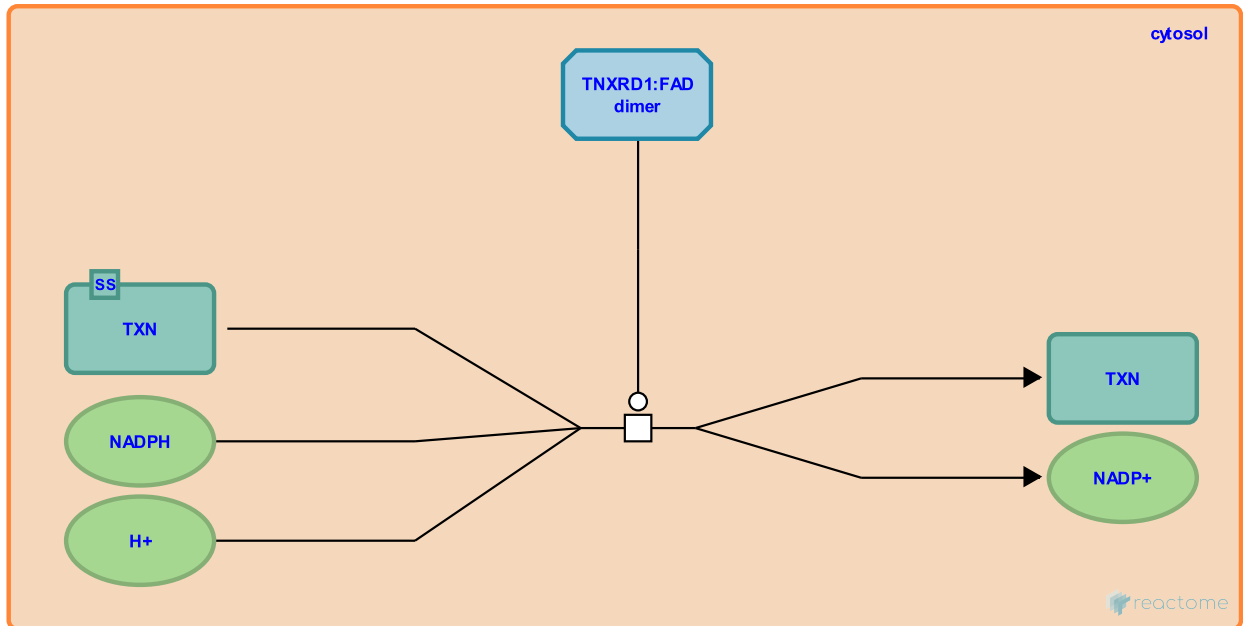
**Location:** TP53 Regulates Metabolic Genes

**Stable identifier:** R-GGA-73646

**Type:** transition

**Compartments:** cytosol

**Inferred from:** thioredoxin, oxidized + NADPH + H+ => thioredoxin, 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>

**Followed by:** PRDX1 overoxidizes, PRDX1,2,5 catalyze TXN reduced + H<sub>2</sub>O<sub>2</sub> => TXN oxidized + 2H<sub>2</sub>O

## PRDX1 overoxidizes ↗

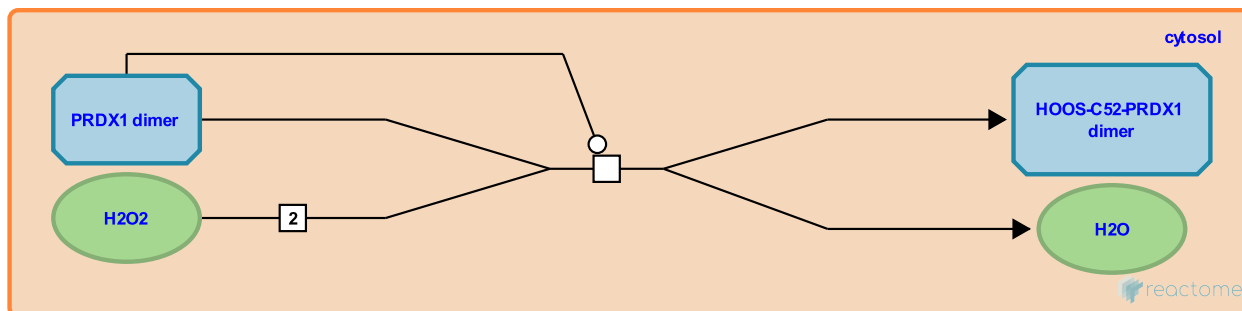
**Location:** TP53 Regulates Metabolic Genes

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

**Preceded by:** PRDX1,2,5 catalyze TXN reduced + H2O2 => TXN oxidized + 2H2O, thioredoxin, oxidized + NADPH + H+ => thioredoxin, reduced + NADP+

**Followed by:** SESN1,2,3 bind overoxidized PRDX1

## SESN1,2,3 bind overoxidized PRDX1 ↗

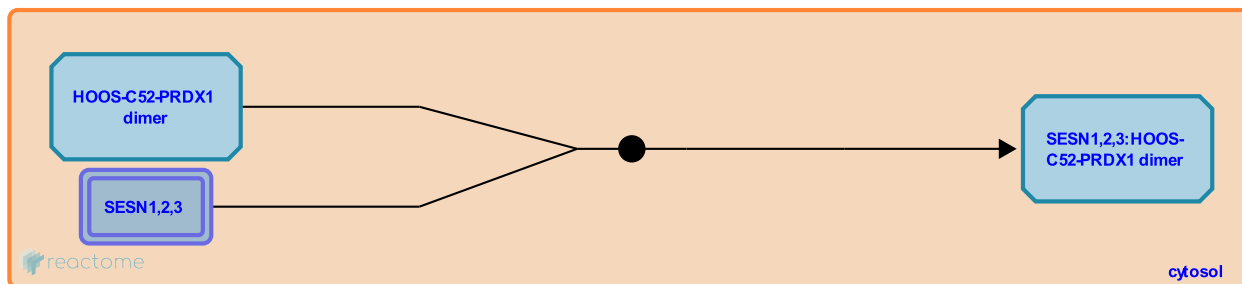
**Location:** [TP53 Regulates Metabolic Genes](#)

**Stable identifier:** R-GGA-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 ↗

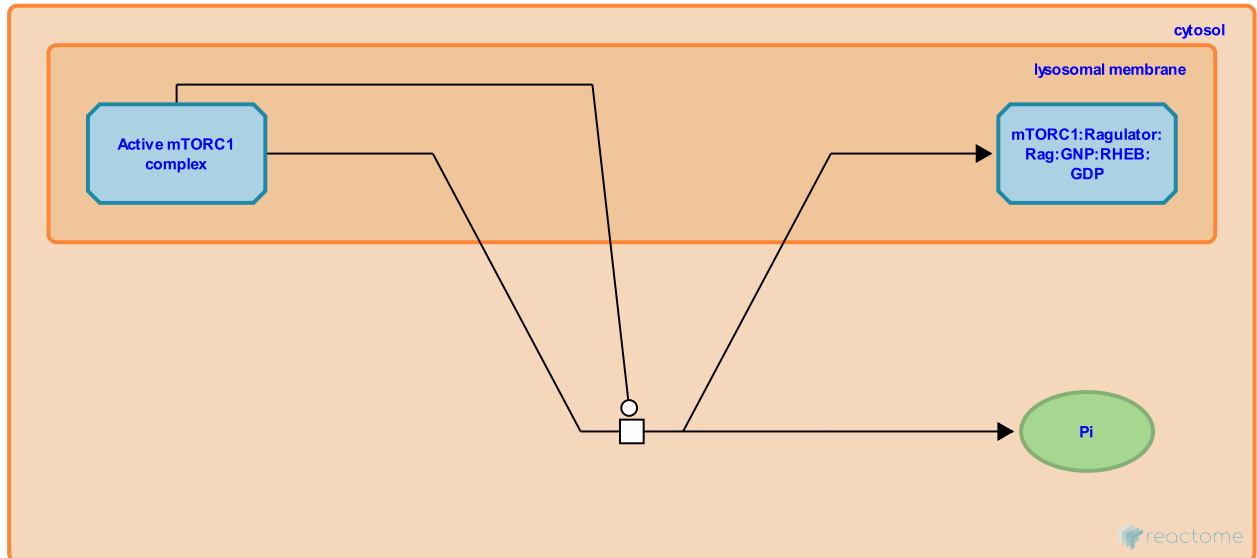
**Location:** [TP53 Regulates Metabolic Genes](#)

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

## SESN1,2,3 bind AMPK ↗

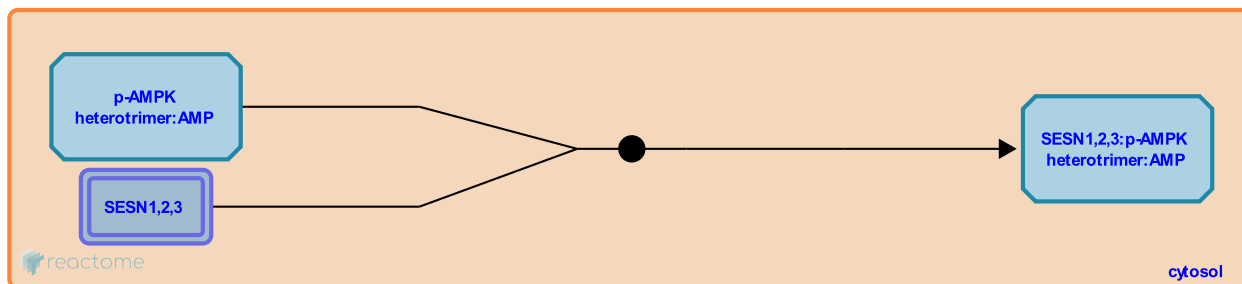
**Location:** TP53 Regulates Metabolic Genes

**Stable identifier:** R-GGA-5631941

**Type:** binding

**Compartments:** cytosol

**Inferred from:** SESN1,2,3 bind AMPK (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>

## AKT phosphorylates TSC2, inhibiting it ↗

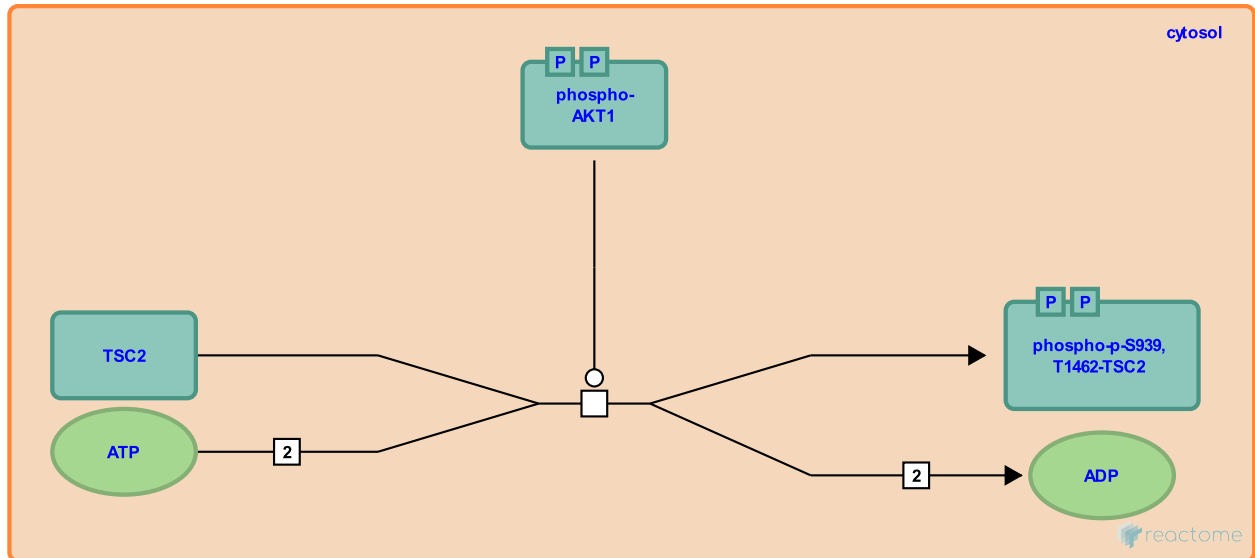
**Location:** TP53 Regulates Metabolic Genes

**Stable identifier:** R-GGA-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.](http://www.pantherdb.org/about.jsp) 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 [↗](#)

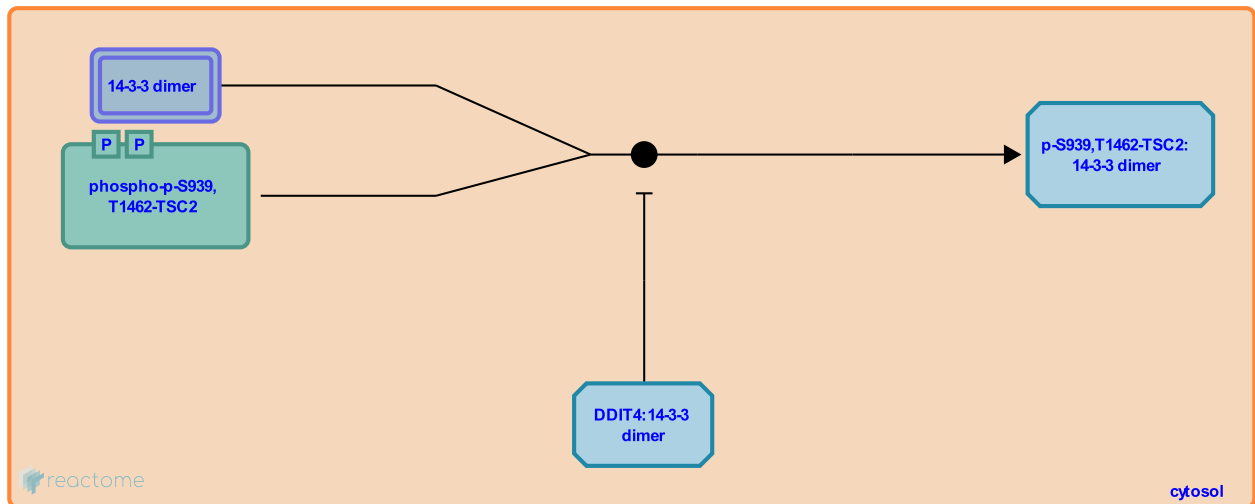
**Location:** TP53 Regulates Metabolic Genes

**Stable identifier:** R-GGA-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

## DDIT4 binds 14-3-3 dimer ↗

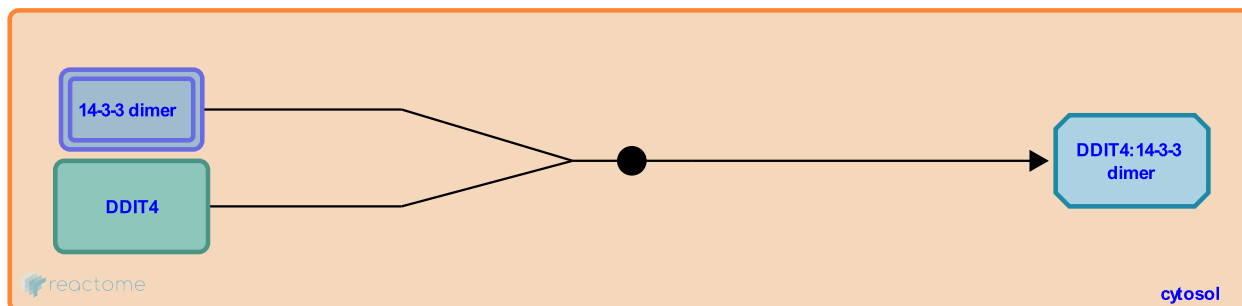
**Location:** [TP53 Regulates Metabolic Genes](#)

**Stable identifier:** R-GGA-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 ↗

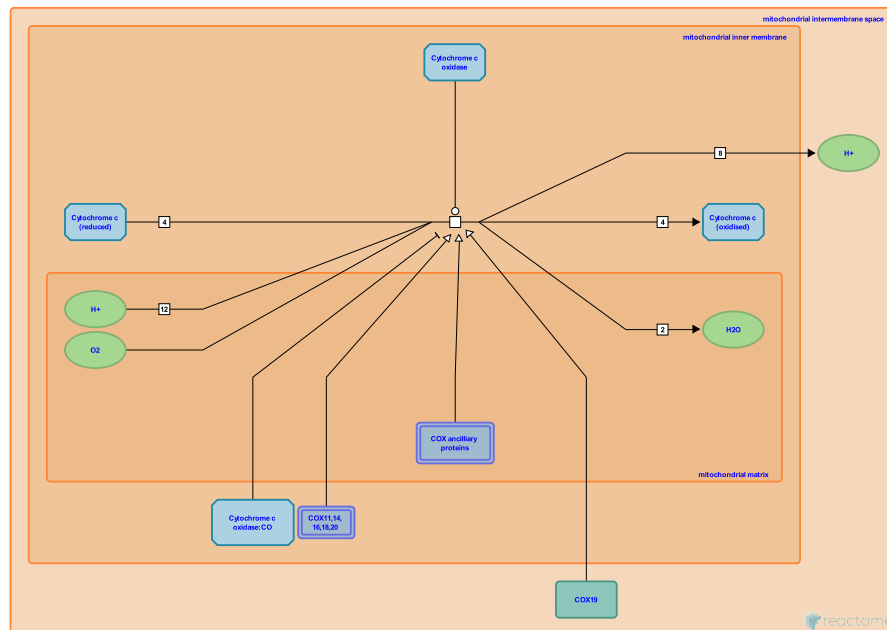
**Location:** TP53 Regulates Metabolic Genes

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

**glutamine + H<sub>2</sub>O => glutamate + NH<sub>4</sub><sup>+</sup> [GLS]** ↗

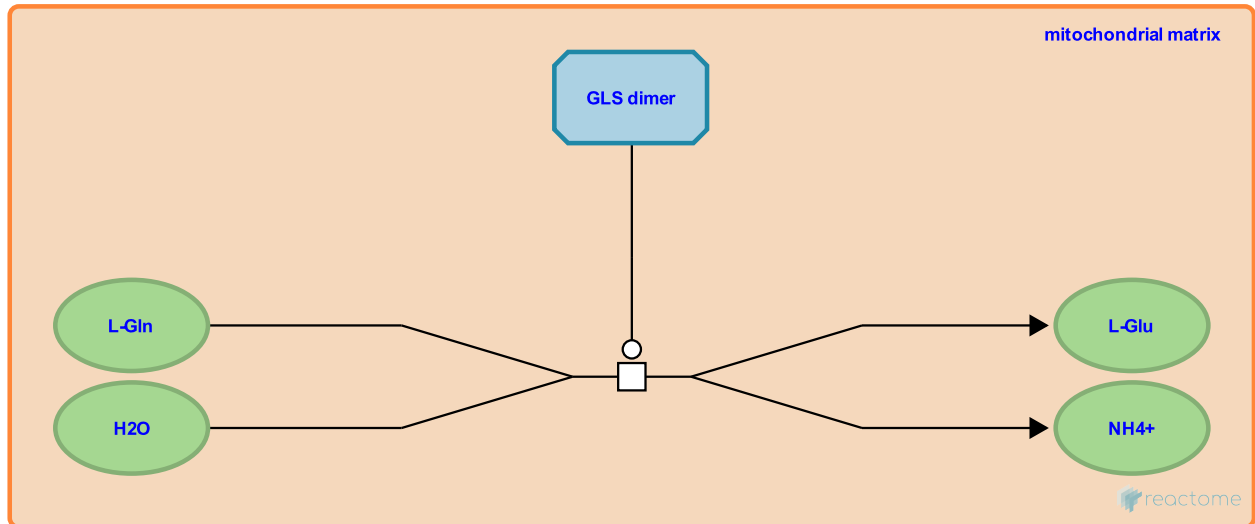
**Location:** [TP53 Regulates Metabolic Genes](#)

**Stable identifier:** R-GGA-70609

**Type:** transition

**Compartments:** mitochondrial matrix

**Inferred from:** [glutamine + H<sub>2</sub>O => glutamate + NH<sub>4</sub><sup>+</sup> \[GLS\]](#) (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
↳ glutathione (oxidized) + NADPH + H <sup>+</sup> => 2 glutathione (reduced) + NADP <sup>+</sup>	5
↳ GPX2 catalyzes 2 glutathione, reduced + H <sub>2</sub> O <sub>2</sub> => glutathione, oxidized + 2 H <sub>2</sub> O	6
↳ PRDX1,2,5 catalyze TXN reduced + H <sub>2</sub> O <sub>2</sub> => TXN oxidized + 2H <sub>2</sub> O	7
↳ thioredoxin, oxidized + NADPH + H <sup>+</sup> => thioredoxin, reduced + NADP <sup>+</sup>	8
↳ PRDX1 overoxidizes	9
↳ SESN1,2,3 bind overoxidized PRDX1	10
↳ RHEB in mTORC1:RHEB:GTP hydrolyses GTP	11
↳ SESN1,2,3 bind AMPK	12
↳ AKT phosphorylates TSC2, inhibiting it	13
↳ p-S939,T1462-TSC2 binding to 14-3-3 dimer is negatively regulated by DDIT4	14
↳ DDIT4 binds 14-3-3 dimer	15
↳ Electron transfer from reduced cytochrome c to molecular oxygen	16
↳ glutamine + H <sub>2</sub> O => glutamate + NH <sub>4</sub> <sup>+</sup> [GLS]	17
Table of Contents	18