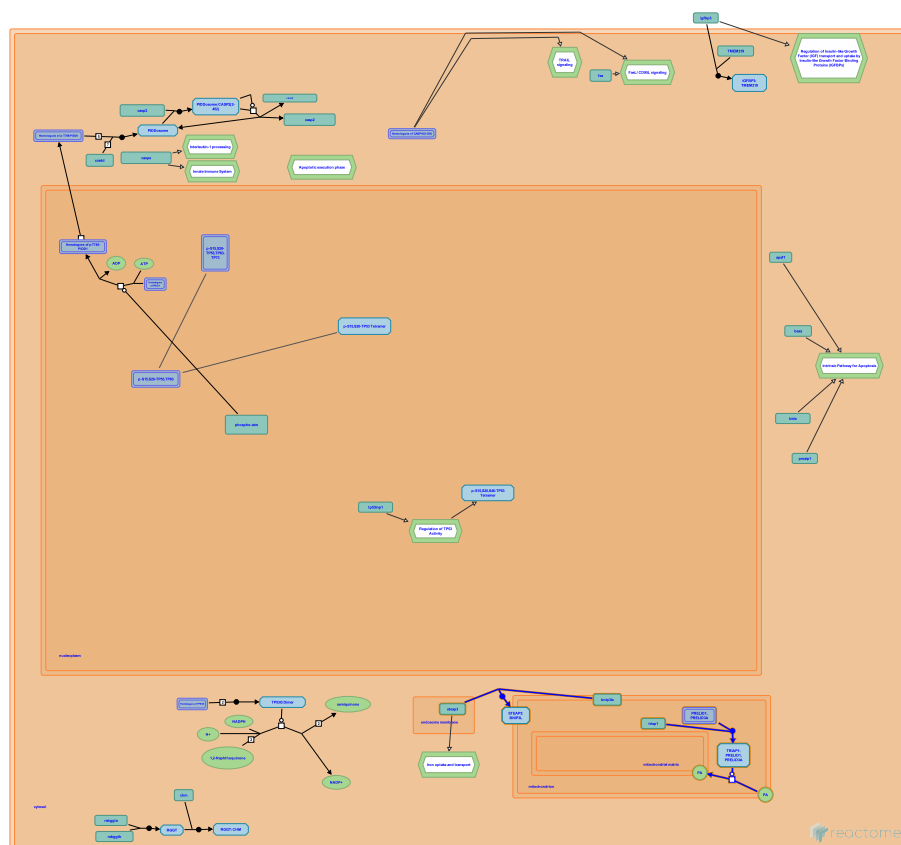


# TP53 Regulates Transcription of Genes Involved in Cytochrome C Release



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

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## 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. [↗](#)
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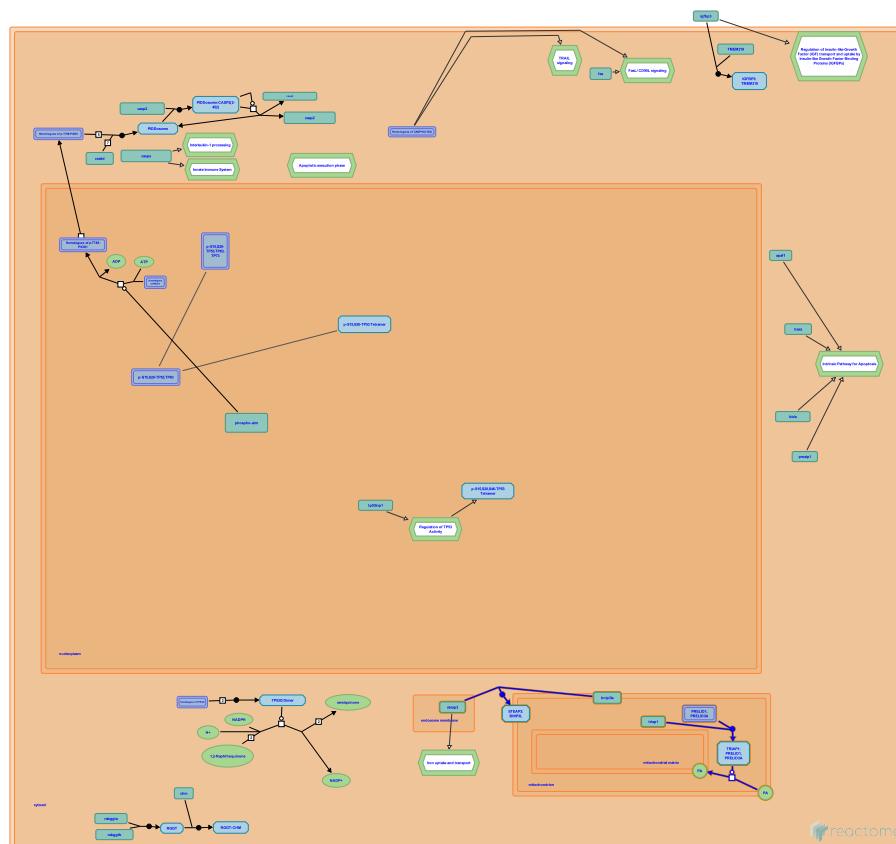
Reactome database release: 73

This document contains 1 pathway and 3 reactions ([see Table of Contents](#))

## TP53 Regulates Transcription of Genes Involved in Cytochrome C Release ↗

Stable identifier: R-DRE-6803204

Inferred from: TP53 Regulates Transcription of Genes Involved in Cytochrome C Release (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>

## STEAP3 binds BNIP3L ↗

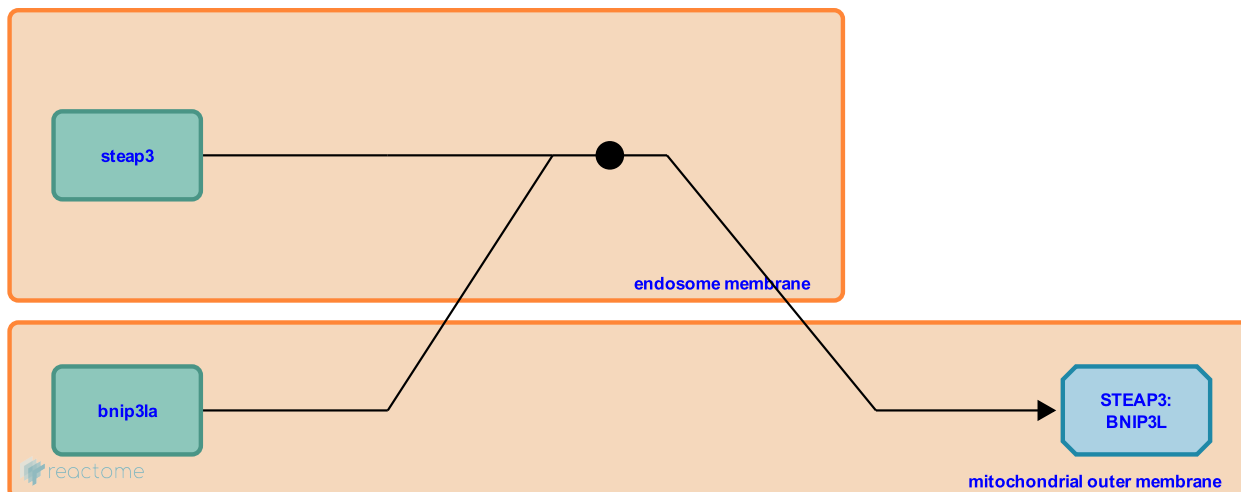
**Location:** [TP53 Regulates Transcription of Genes Involved in Cytochrome C Release](#)

**Stable identifier:** R-DRE-6801195

**Type:** binding

**Compartments:** endosome membrane, mitochondrial outer membrane

**Inferred from:** [STEAP3 binds BNIP3L \(Homo sapiens\)](#)



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.

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## TRIAP1 binds PRELID1, PRELID3A ↗

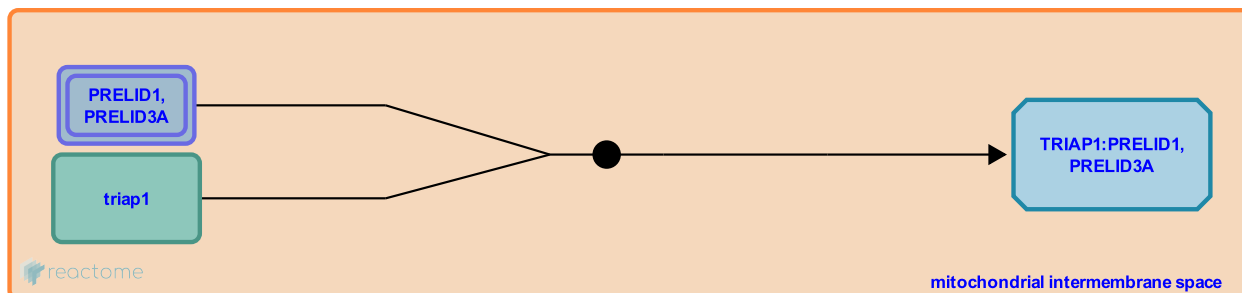
**Location:** [TP53 Regulates Transcription of Genes Involved in Cytochrome C Release](#)

**Stable identifier:** R-DRE-6801242

**Type:** binding

**Compartments:** mitochondrial intermembrane space

**Inferred from:** [TRIAP1 binds PRELID1, PRELID3A \(Homo sapiens\)](#)



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:** [TRIAP1:PRELID1, PRELID3A transports PA from the outer to the inner mitochondrial membrane](#)

## TRIAP1:PRELID1, PRELID3A transports PA from the outer to the inner mitochondrial membrane ↗

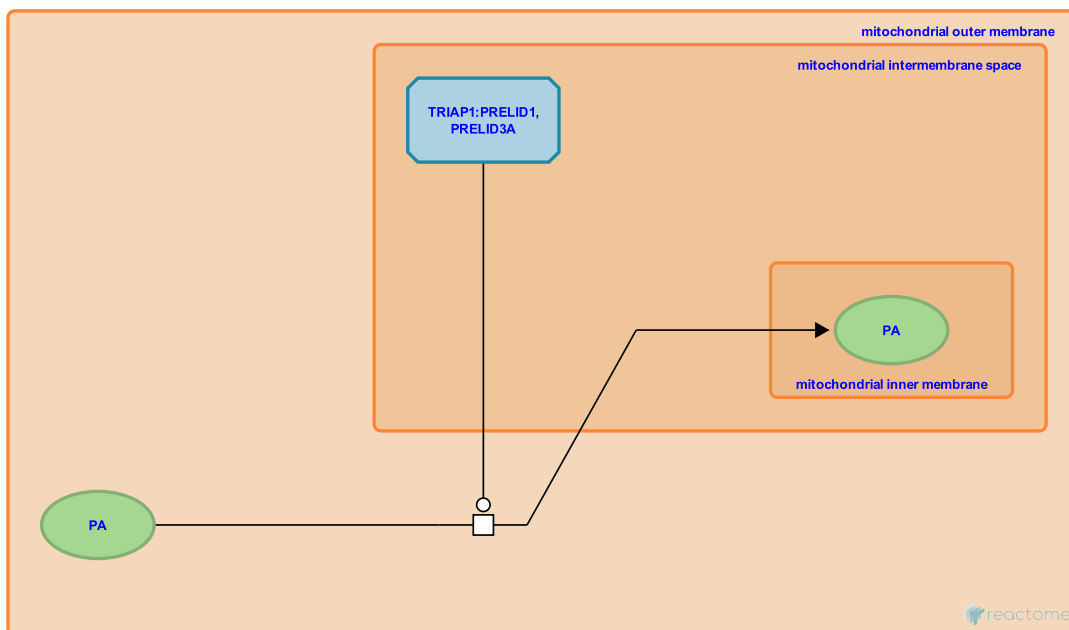
**Location:** [TP53 Regulates Transcription of Genes Involved in Cytochrome C Release](#)

**Stable identifier:** R-DRE-6801250

**Type:** transition

**Compartments:** mitochondrial outer membrane, mitochondrial inner membrane, mitochondrial intermembrane space

**Inferred from:** [TRIAP1:PRELID1, PRELID3A transports PA from the outer to the inner mitochondrial 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:** [TRIAP1 binds PRELID1, PRELID3A](#)

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