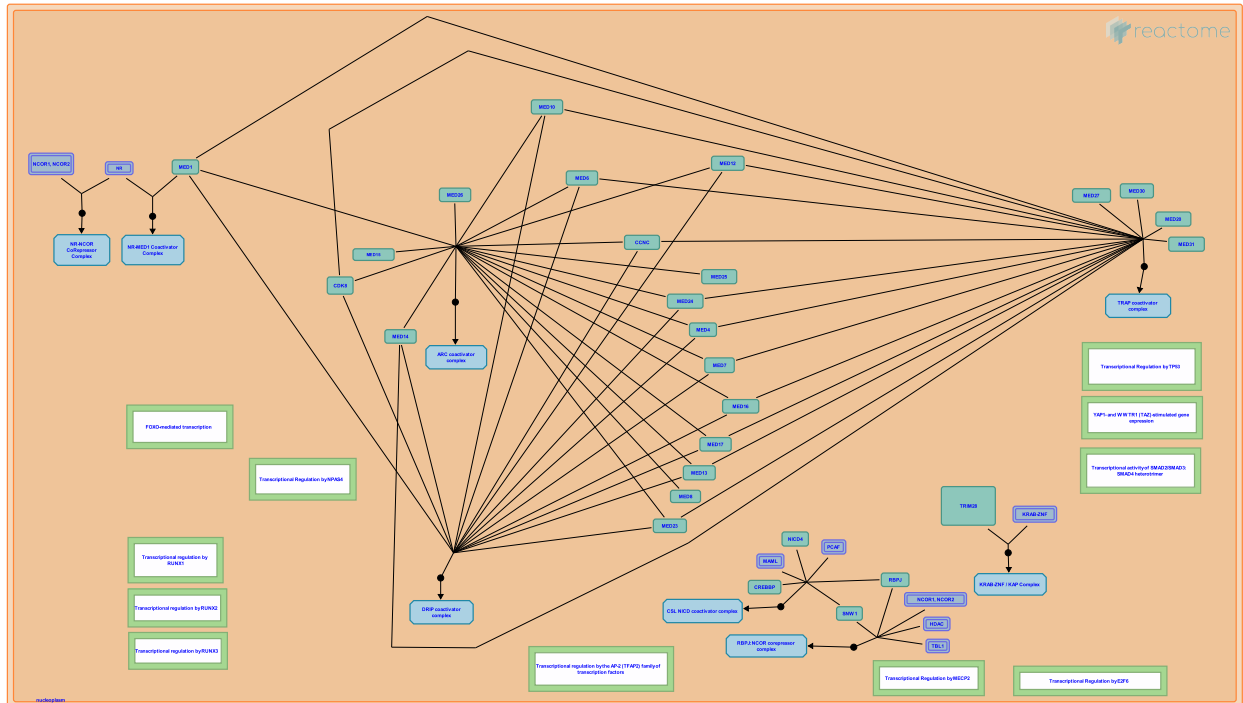


Generic Transcription Pathway



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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://reactome.org/Textbook).

20/05/2024

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. [↗](#)
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- 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 14 pathways and 4 reactions ([see Table of Contents](#))

Formation of ARC coactivator complex ↗

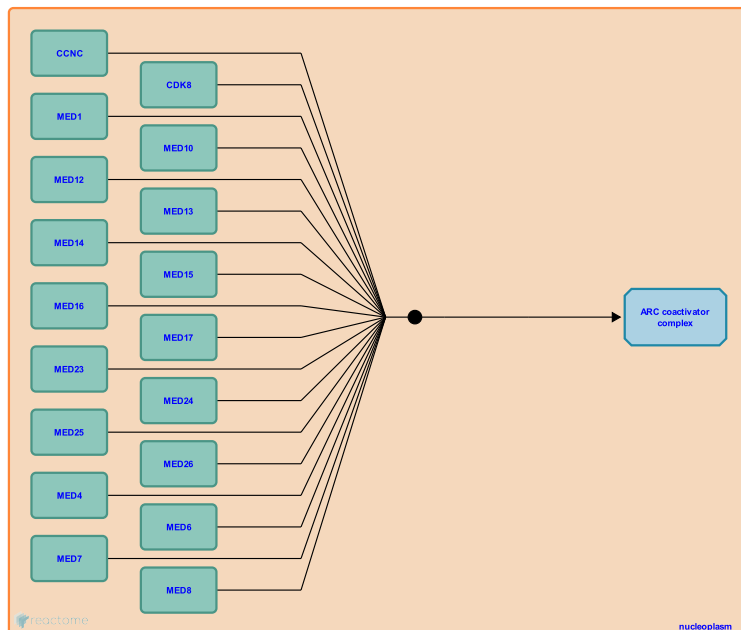
Location: [Generic Transcription Pathway](#)

Stable identifier: R-SSC-212352

Type: binding

Compartments: nucleoplasm

Inferred from: [Formation of ARC coactivator 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>

Formation of DRIP coactivator complex ↗

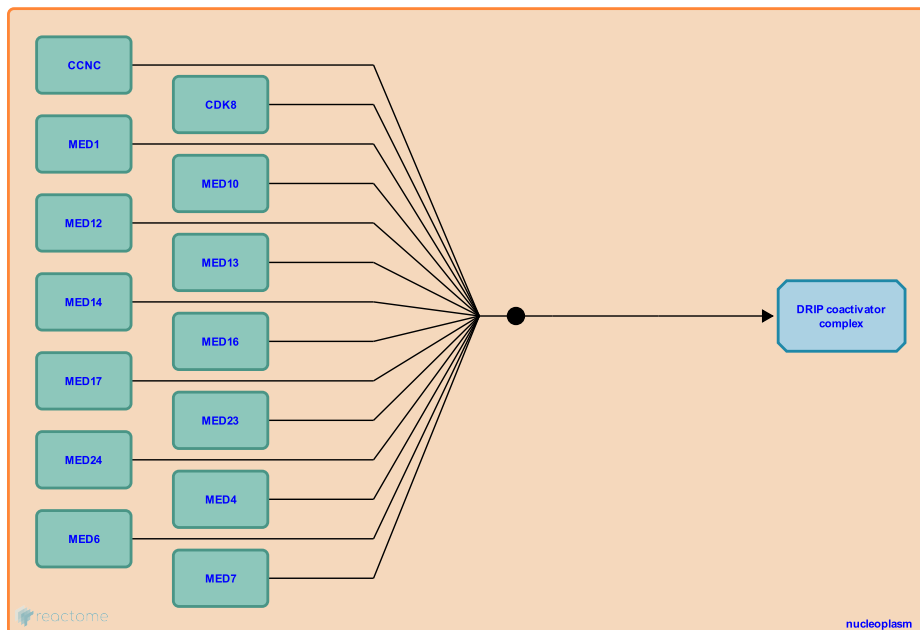
Location: [Generic Transcription Pathway](#)

Stable identifier: R-SSC-212432

Type: binding

Compartments: nucleoplasm

Inferred from: [Formation of DRIP coactivator 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>

Formation of TRAP coactivator complex ↗

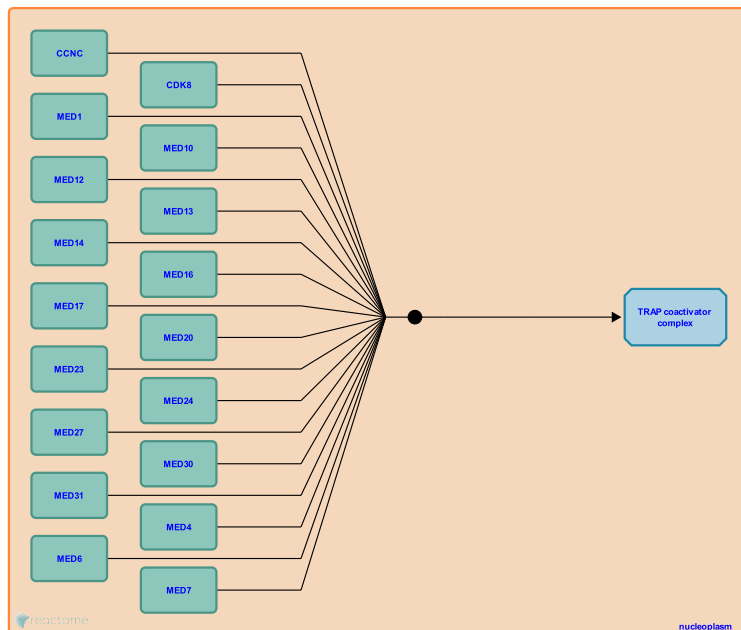
Location: [Generic Transcription Pathway](#)

Stable identifier: R-SSC-212380

Type: binding

Compartments: nucleoplasm

Inferred from: [Formation of TRAP coactivator 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.

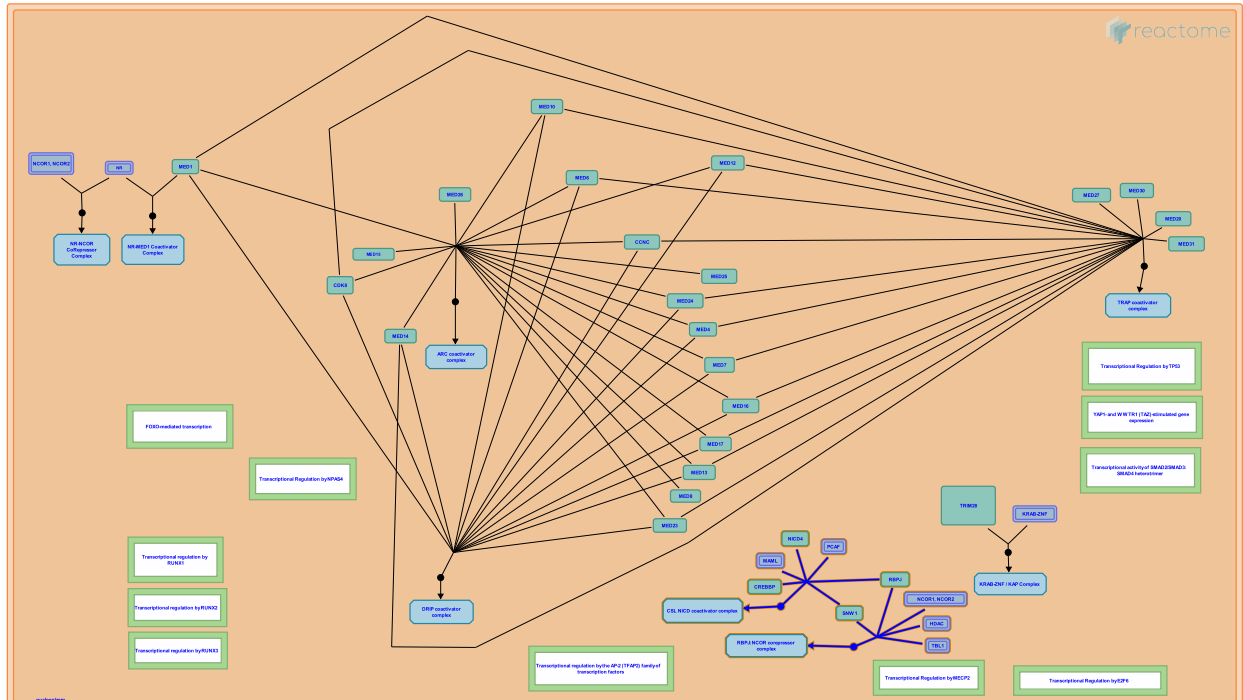
[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Notch-HLH transcription pathway ↗

Location: Generic Transcription Pathway

Stable identifier: R-SSC-350054

Inferred from: Notch-HLH transcription pathway (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.

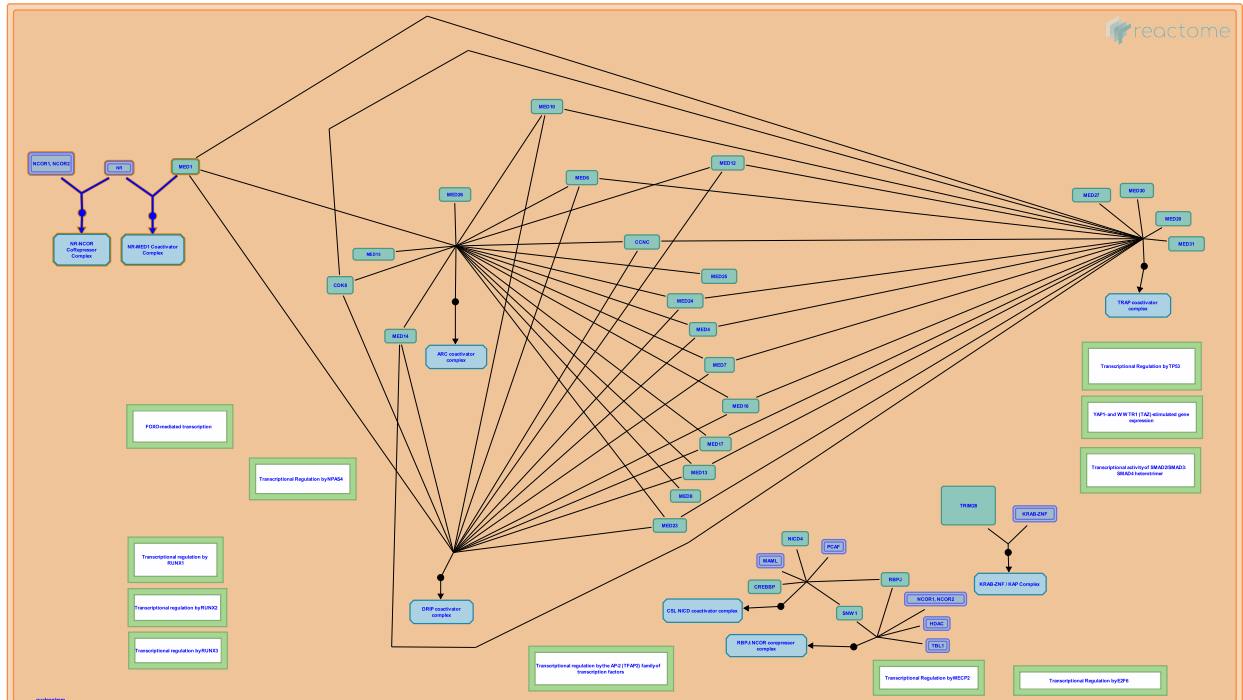
[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Nuclear Receptor transcription pathway ↗

Location: Generic Transcription Pathway

Stable identifier: R-SSC-383280

Inferred from: Nuclear Receptor transcription pathway (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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KRAB-ZNF / KAP Interaction ↗

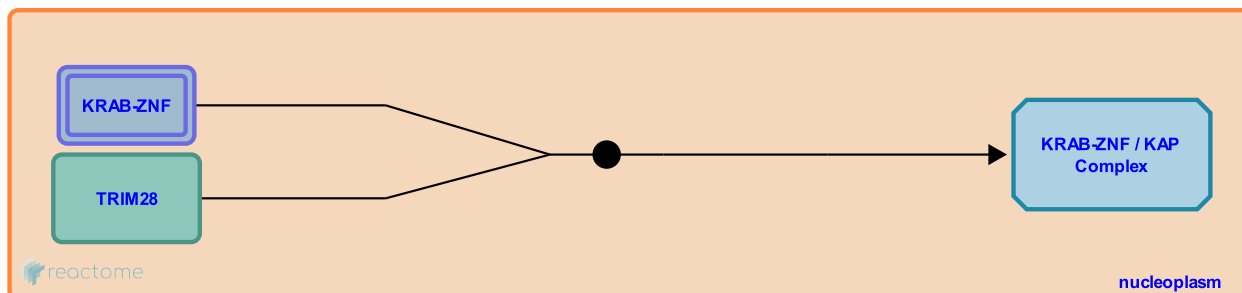
Location: [Generic Transcription Pathway](#)

Stable identifier: R-SSC-975040

Type: binding

Compartments: nucleoplasm

Inferred from: [KRAB-ZNF / KAP Interaction \(Homo sapiens\)](#)



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>

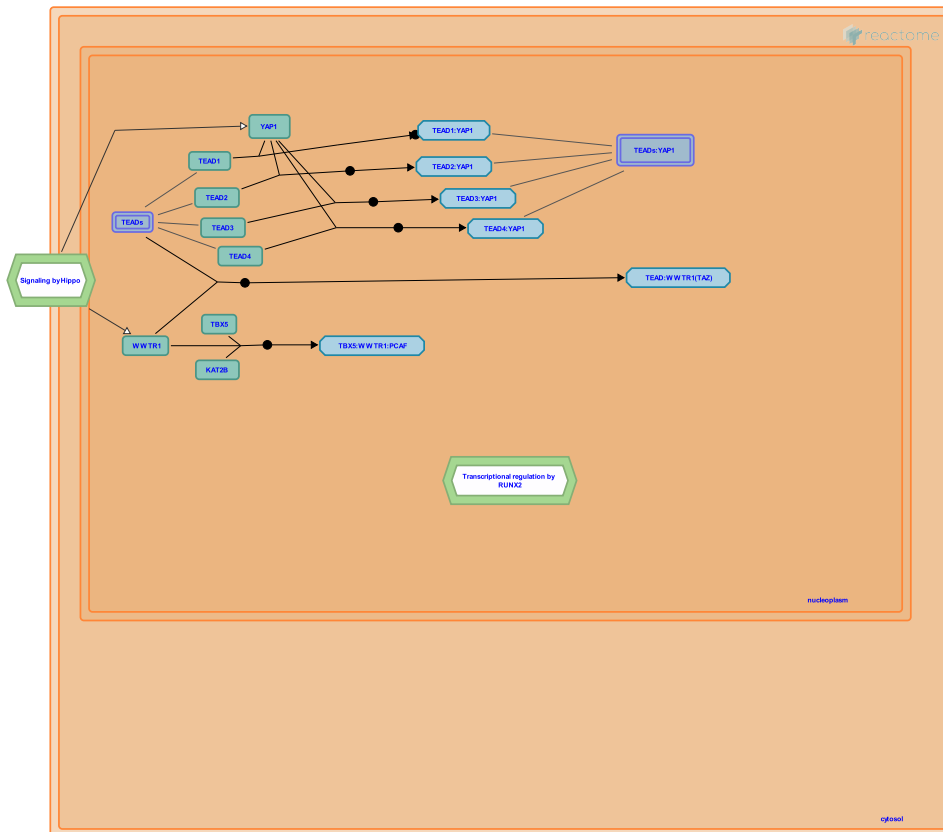
YAP1- and WWTR1 (TAZ)-stimulated gene expression ↗

Location: [Generic Transcription Pathway](#)

Stable identifier: R-SSC-2032785

Compartments: nucleoplasm, cytosol

Inferred from: [YAP1- and WWTR1 \(TAZ\)-stimulated gene expression \(Homo sapiens\)](#)



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.

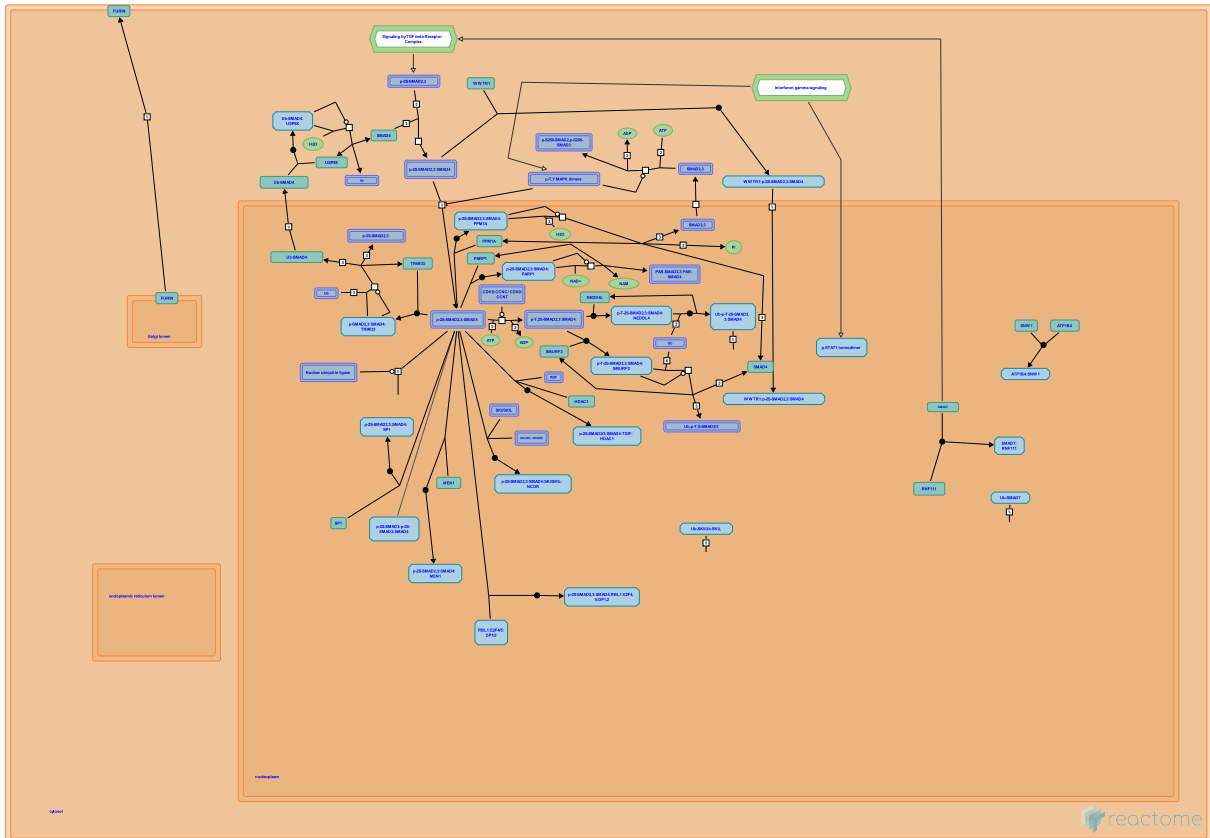
[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer ↗

Location: Generic Transcription Pathway

Stable identifier: R-SSC-2173793

Inferred from: Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer (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.

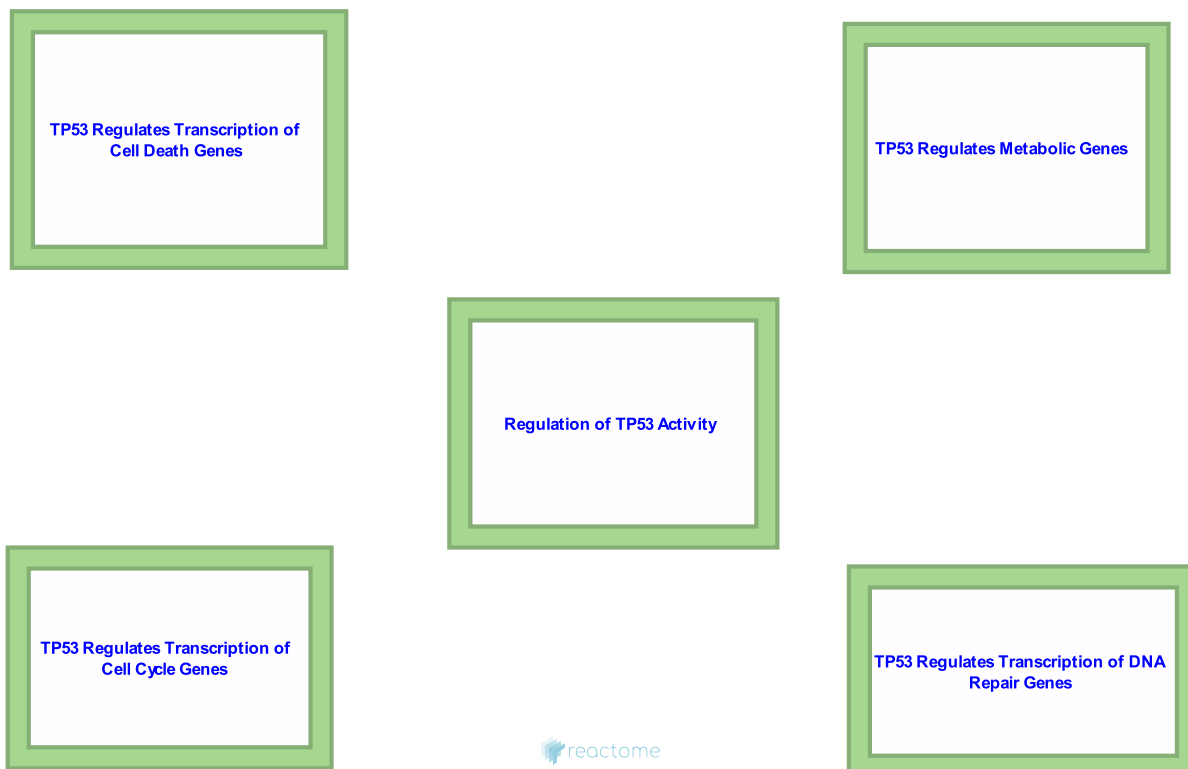
[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Transcriptional Regulation by TP53 ↗

Location: [Generic Transcription Pathway](#)

Stable identifier: R-SSC-3700989

Inferred from: [Transcriptional Regulation by TP53 \(Homo sapiens\)](#)



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.

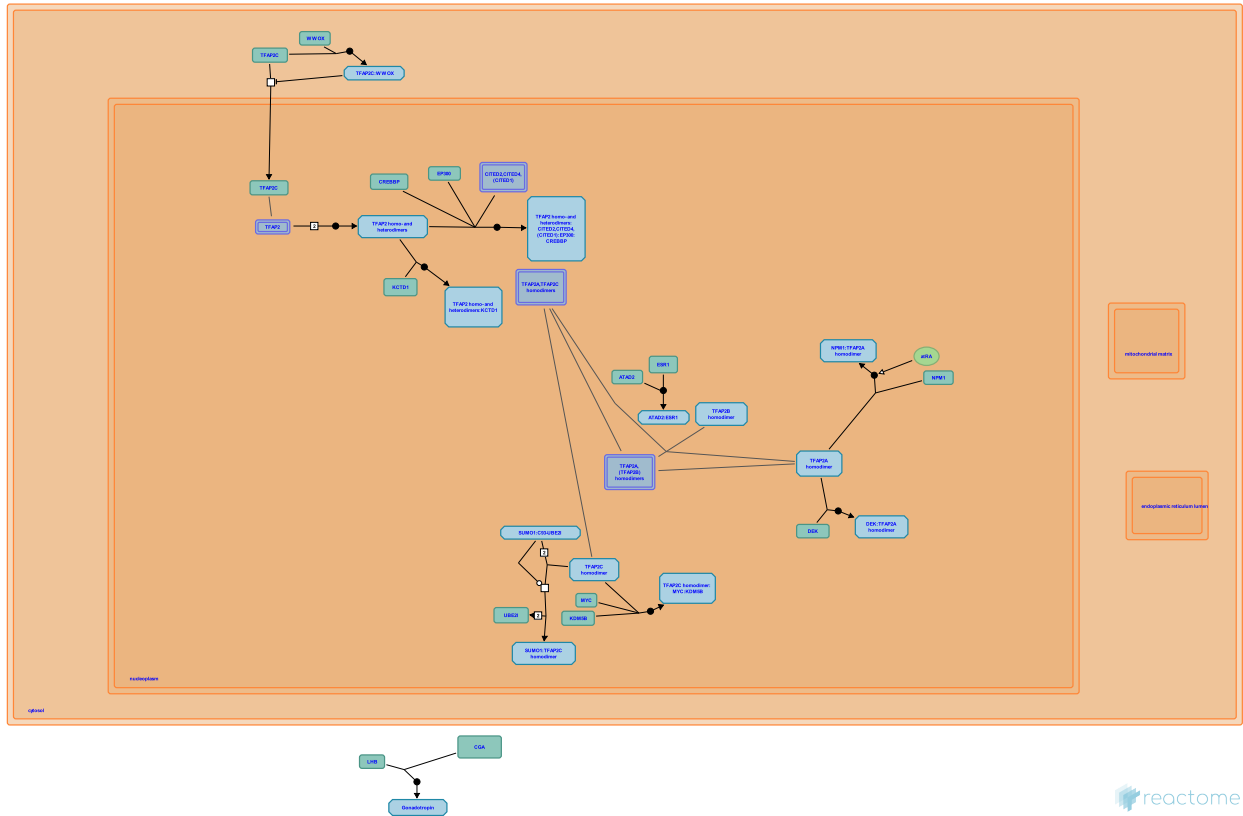
[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors ↗

Location: Generic Transcription Pathway

Stable identifier: R-SSC-8864260

Inferred from: Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors (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.

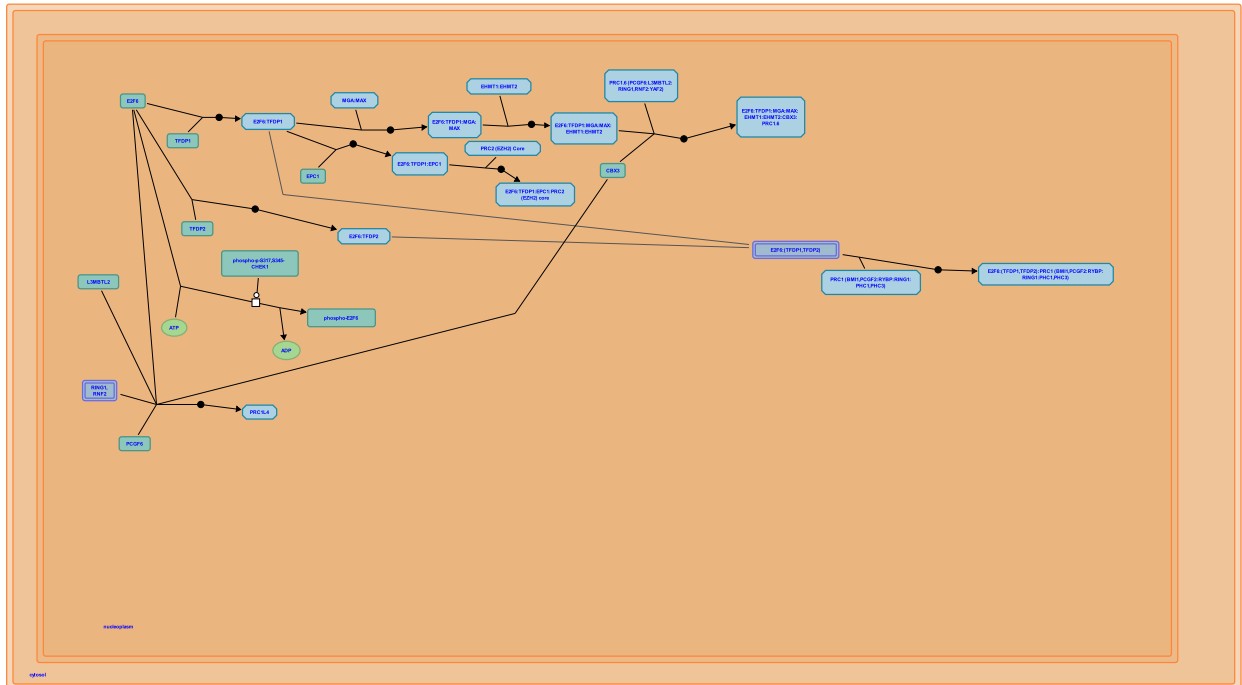
[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Transcriptional Regulation by E2F6 ↗

Location: Generic Transcription Pathway

Stable identifier: R-SSC-8953750

Inferred from: Transcriptional Regulation by E2F6 (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.

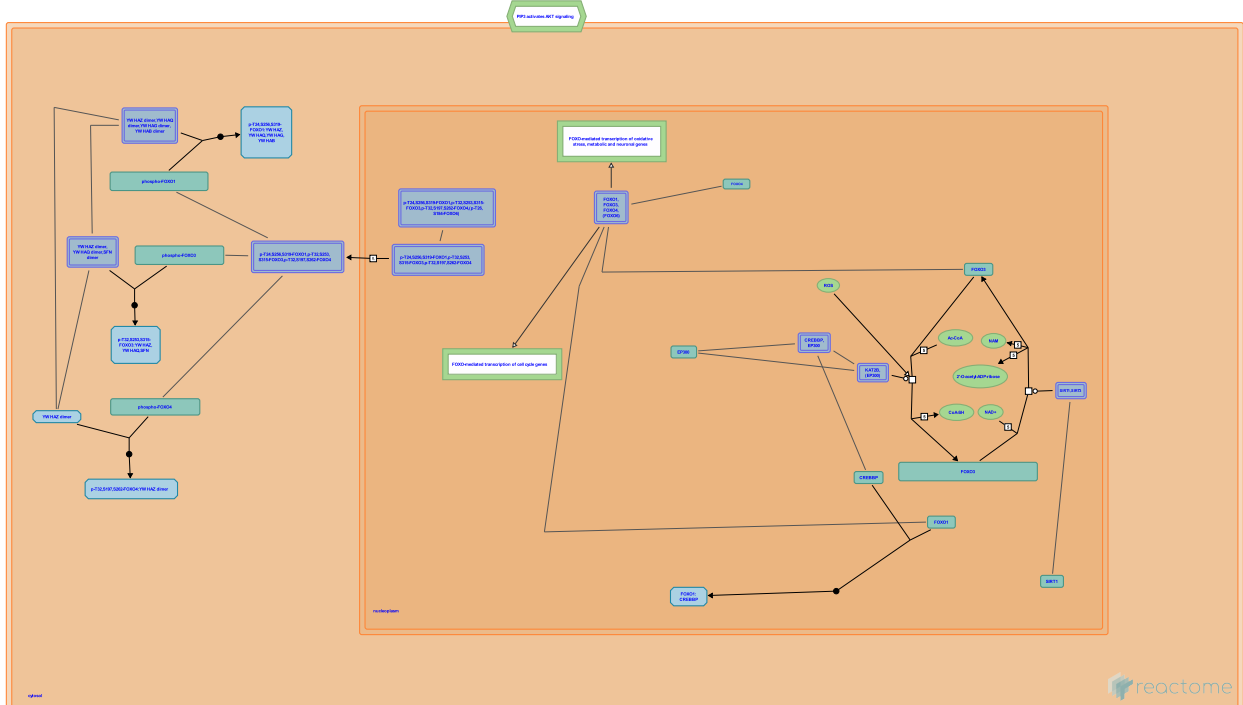
[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

FOXO-mediated transcription ↗

Location: Generic Transcription Pathway

Stable identifier: R-SSC-9614085

Inferred from: FOXO-mediated transcription (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>

Table of Contents

Introduction	1
❏ Generic Transcription Pathway	2
➤ Formation of ARC coactivator complex	3
➤ Formation of DRIP coactivator complex	4
➤ Formation of TRAP coactivator complex	5
❏ Notch-HLH transcription pathway	6
❏ Nuclear Receptor transcription pathway	7
➤ KRAB-ZNF / KAP Interaction	8
❏ YAP1- and WWTR1 (TAZ)-stimulated gene expression	9
❏ Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer	10
❏ Transcriptional Regulation by TP53	11
❏ Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors	12
❏ Transcriptional regulation by RUNX1	13
❏ Transcriptional regulation by RUNX2	14
❏ Transcriptional regulation by RUNX3	15
❏ Transcriptional Regulation by MECP2	16
❏ Transcriptional Regulation by E2F6	17
❏ FOXO-mediated transcription	18
❏ Transcriptional Regulation by NPAS4	19
Table of Contents	20