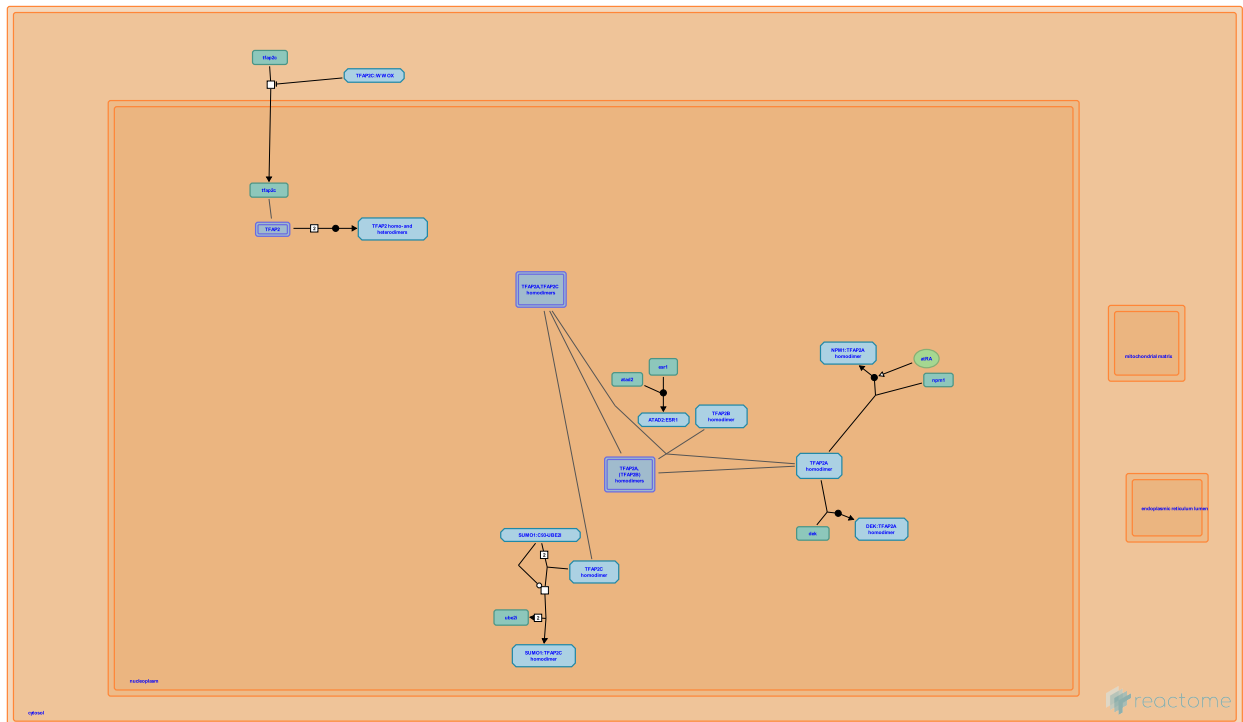


# Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors



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

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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/).

08/05/2024

## 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

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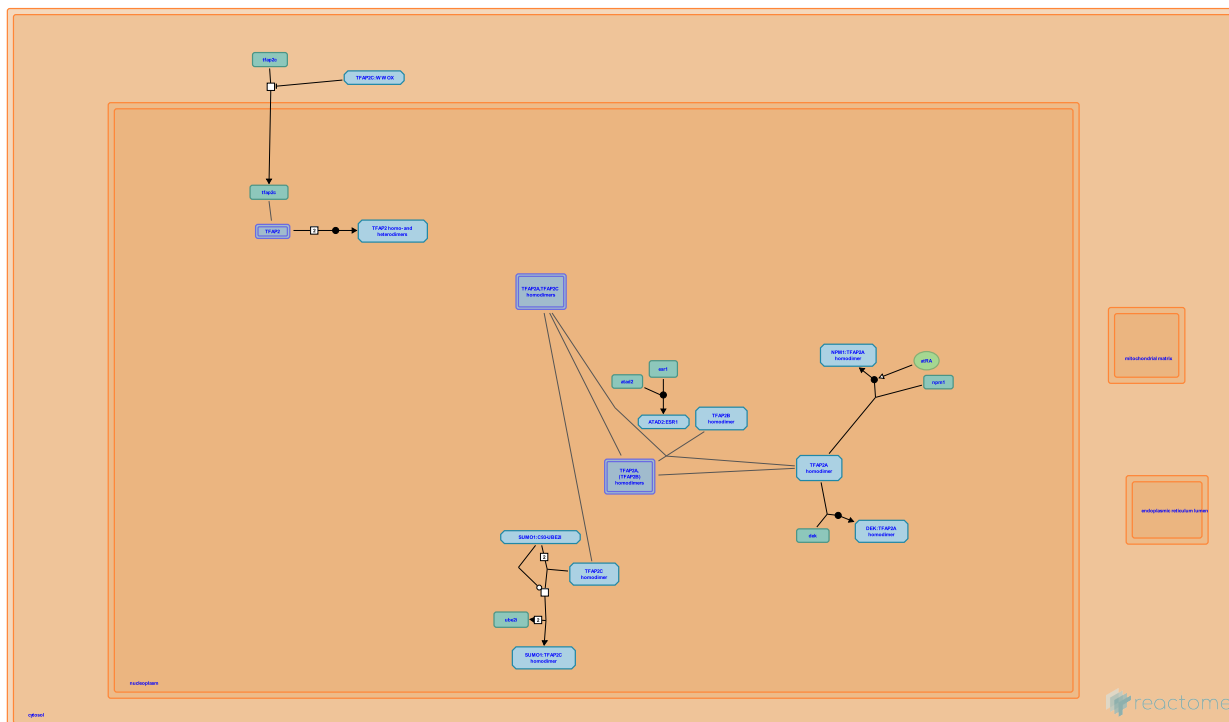
Reactome database release: 88

This document contains 5 pathways and 1 reaction ([see Table of Contents](#))

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

**Stable identifier:** R-XTR-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.

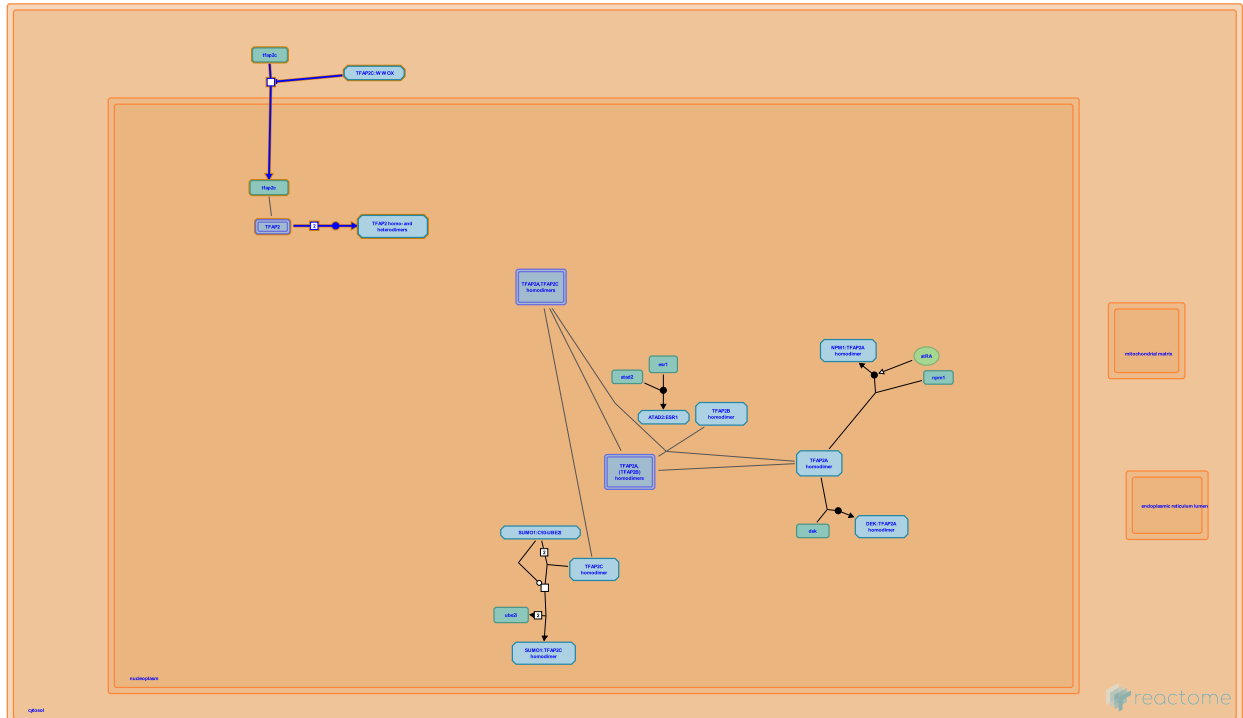
[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## Activation of the TFAP2 (AP-2) family of transcription factors ↗

**Location:** Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors

**Stable identifier:** R-XTR-8866907

**Inferred from:** Activation of the TFAP2 (AP-2) 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.

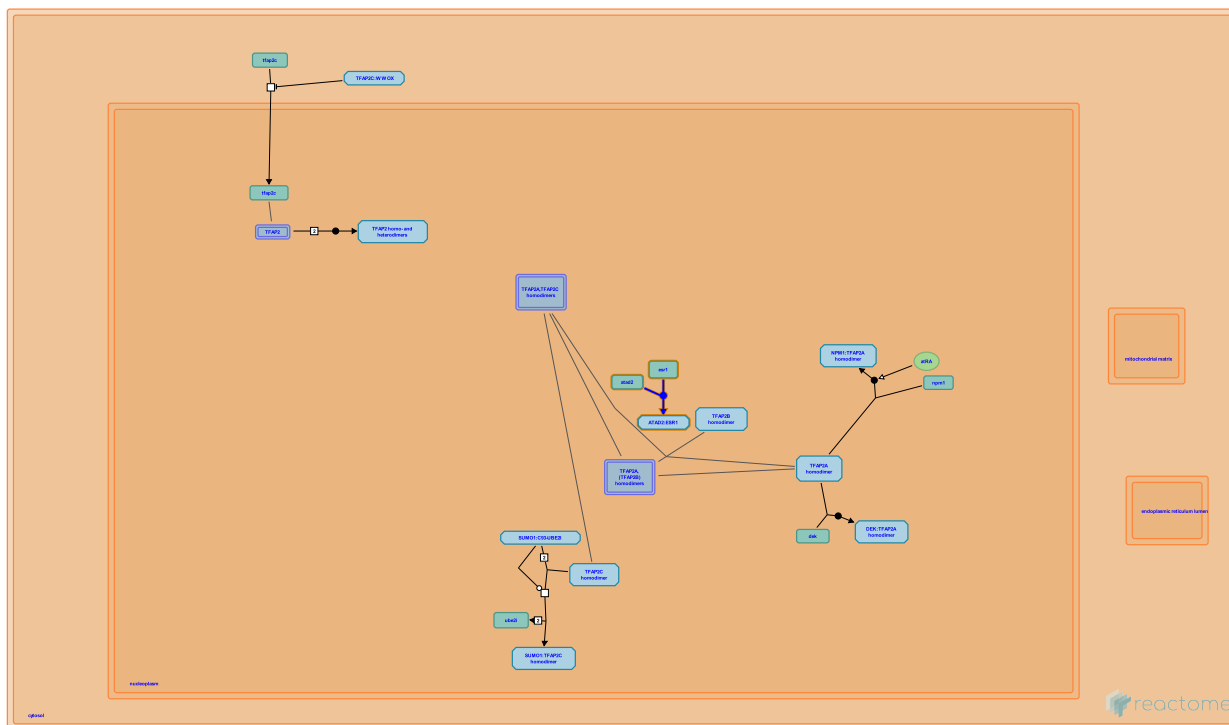
[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## TFAP2 (AP-2) family regulates transcription of growth factors and their receptors ↗

**Location:** Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors

**Stable identifier:** R-XTR-8866910

**Inferred from:** TFAP2 (AP-2) family regulates transcription of growth factors and their receptors (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>

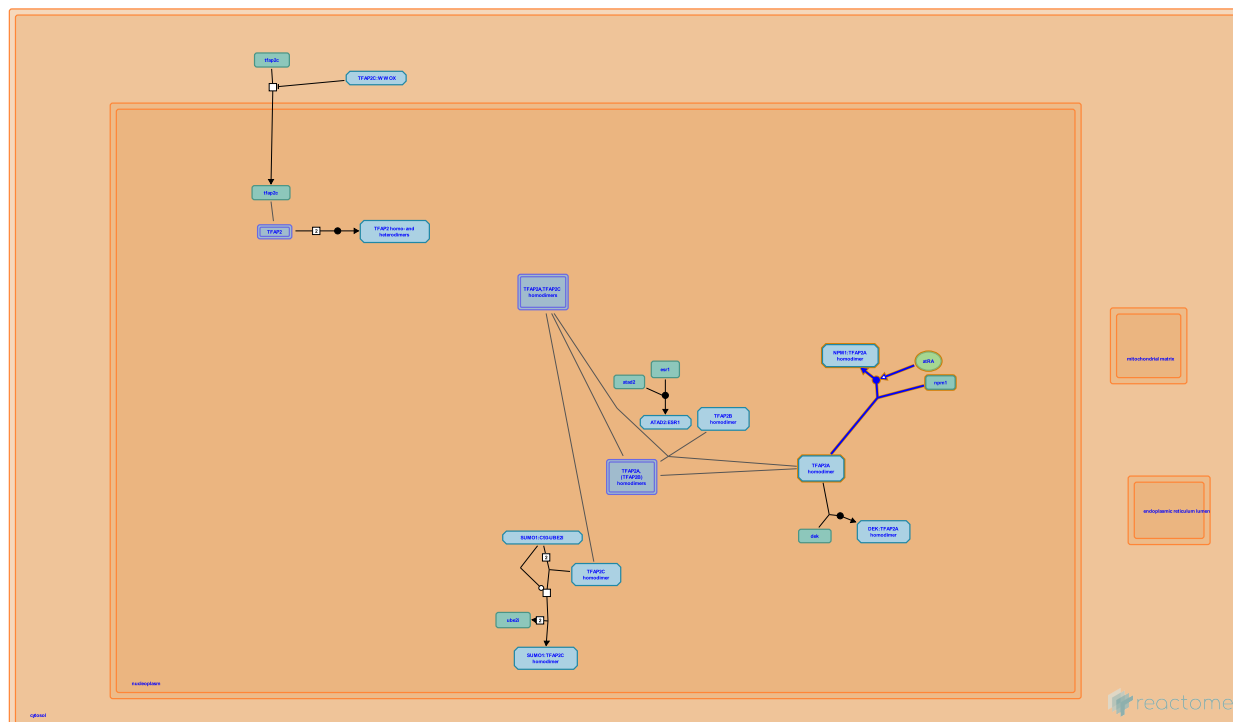
## TFAP2A acts as a transcriptional repressor during retinoic acid induced cell differentiation ↗

**Location:** Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors

**Stable identifier:** R-XTR-8869496

**Compartments:** nucleoplasm

**Inferred from:** TFAP2A acts as a transcriptional repressor during retinoic acid induced cell differentiation (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>

## DEK binds TFAP2A homodimers ↗

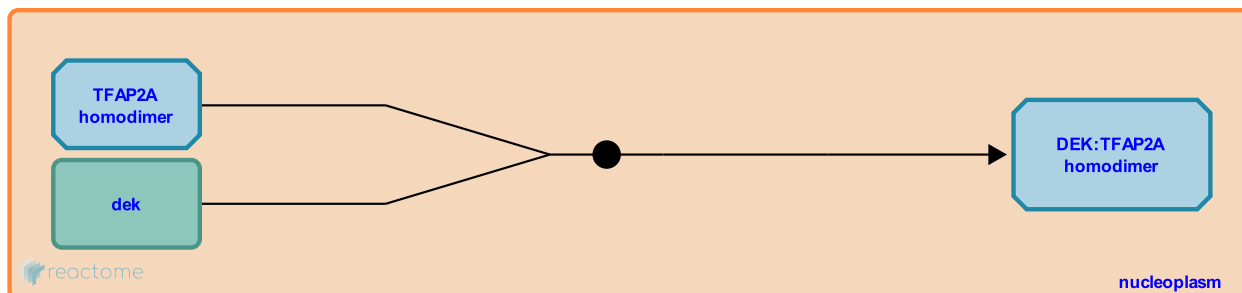
**Location:** Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors

**Stable identifier:** R-XTR-8869580

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** DEK binds TFAP2A homodimers (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.

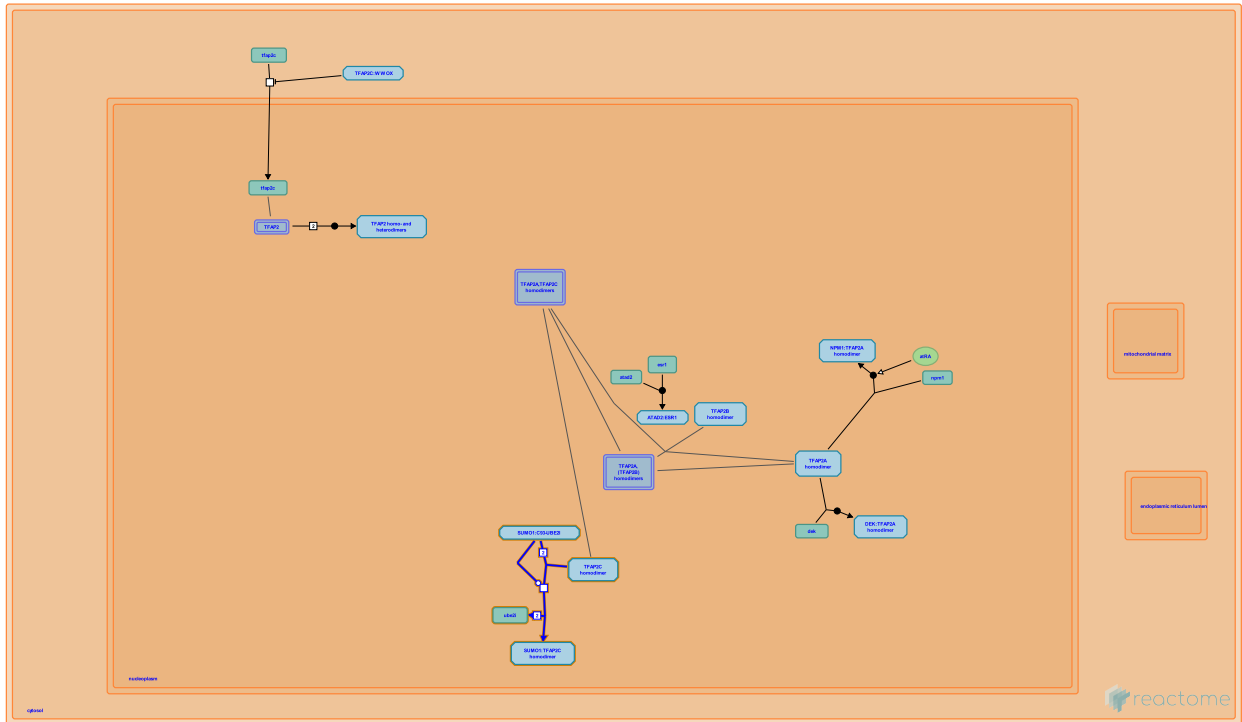
[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## Negative regulation of activity of TFAP2 (AP-2) family transcription factors ↗

**Location:** Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors

**Stable identifier:** R-XTR-8866904

**Inferred from:** Negative regulation of activity of TFAP2 (AP-2) family 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>



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