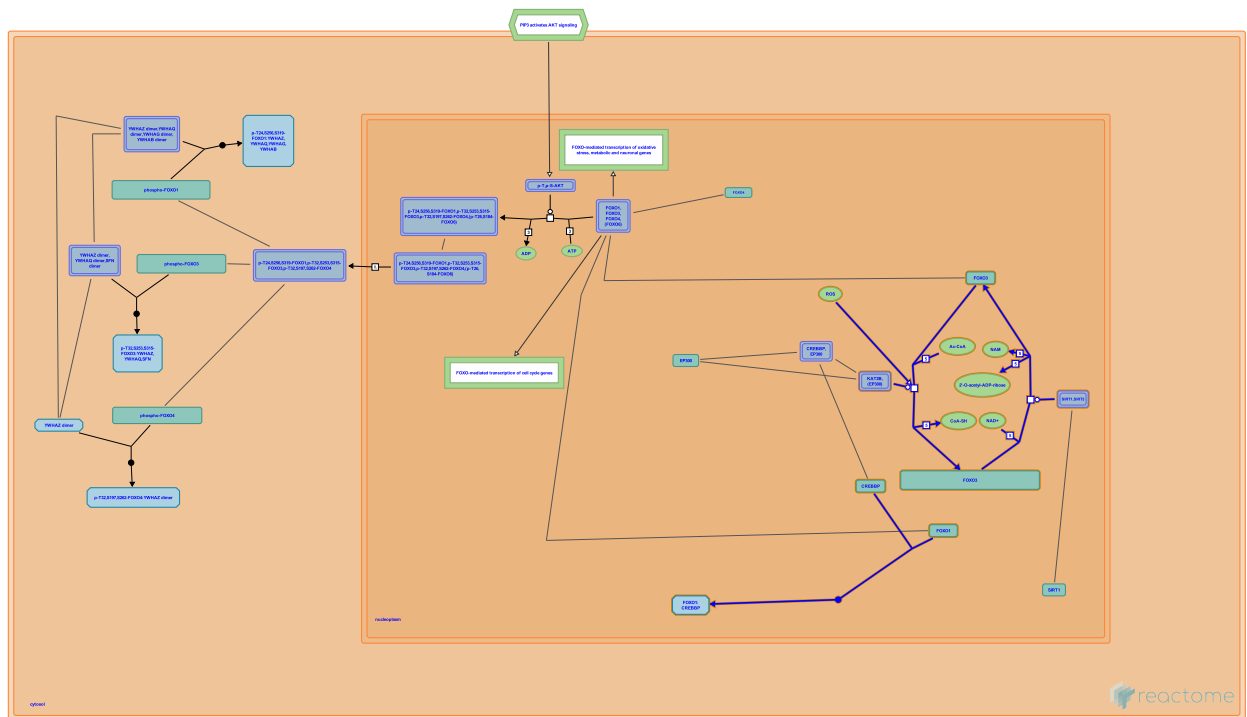


# Regulation of FOXO transcriptional activity by acetylation



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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

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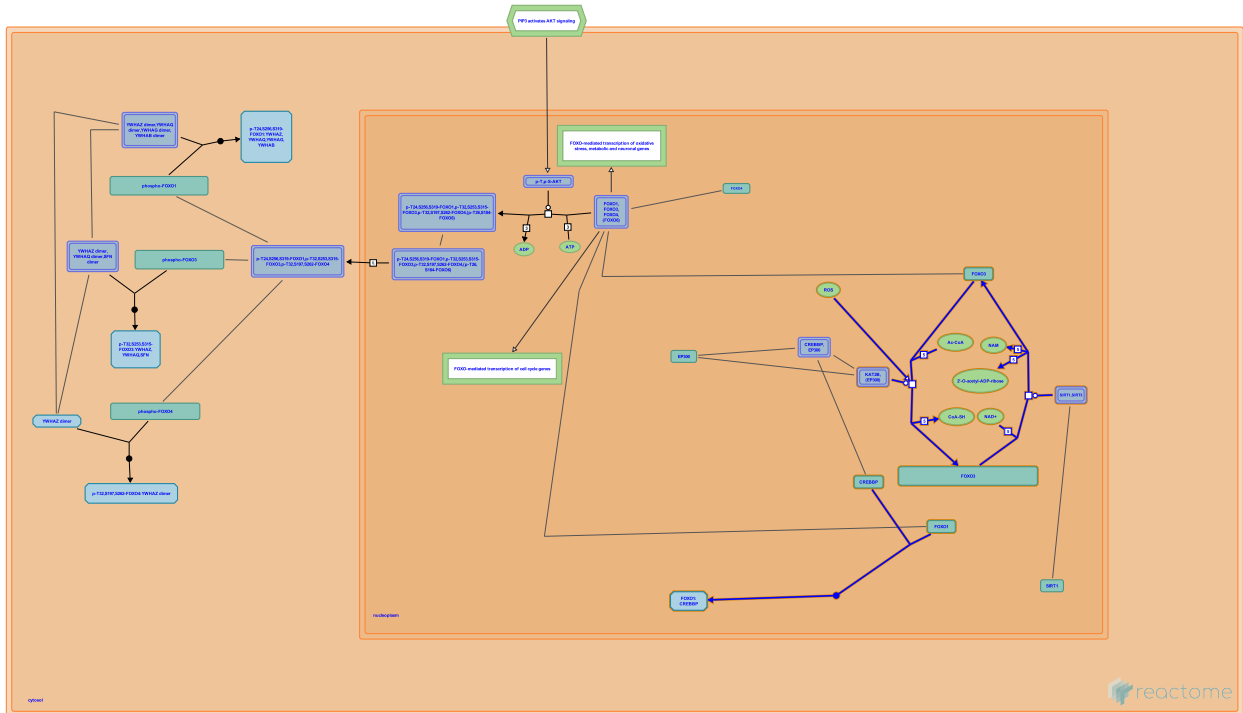
Reactome database release: 73

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

## Regulation of FOXO transcriptional activity by acetylation ↗

**Stable identifier:** R-CFA-9617629

**Inferred from:** Regulation of FOXO transcriptional activity by acetylation (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>

## KAT2B,EP300 acetylate FOXO3 under oxidative stress ↗

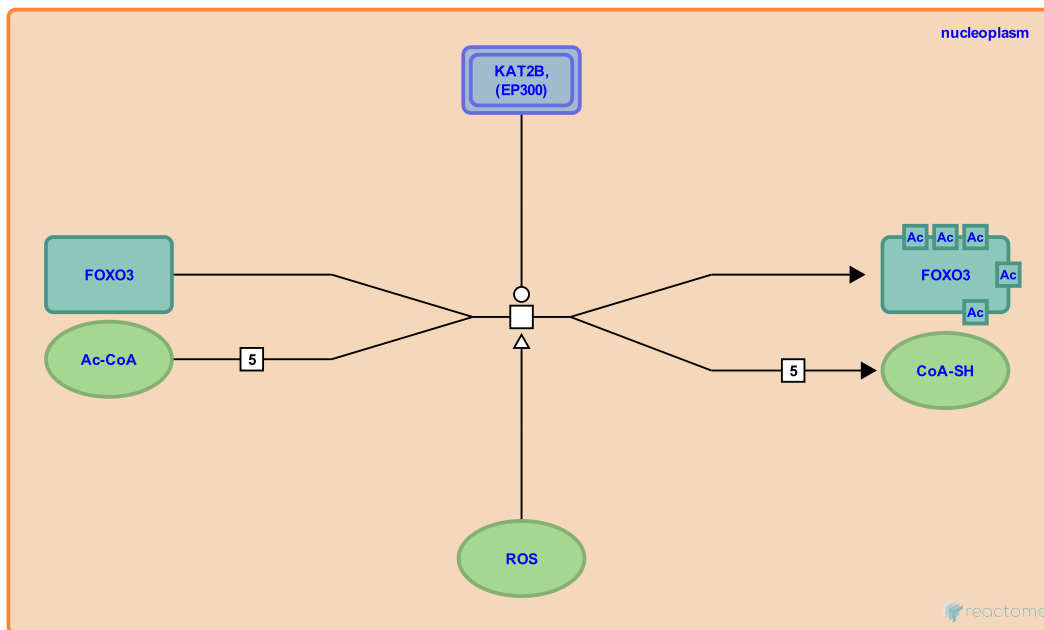
**Location:** Regulation of FOXO transcriptional activity by acetylation

**Stable identifier:** R-CFA-9620515

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** KAT2B,EP300 acetylate FOXO3 under oxidative stress (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:** SIRT1,SIRT3 deacetylate FOXO3

## SIRT1,SIRT3 deacetylate FOXO3 ↗

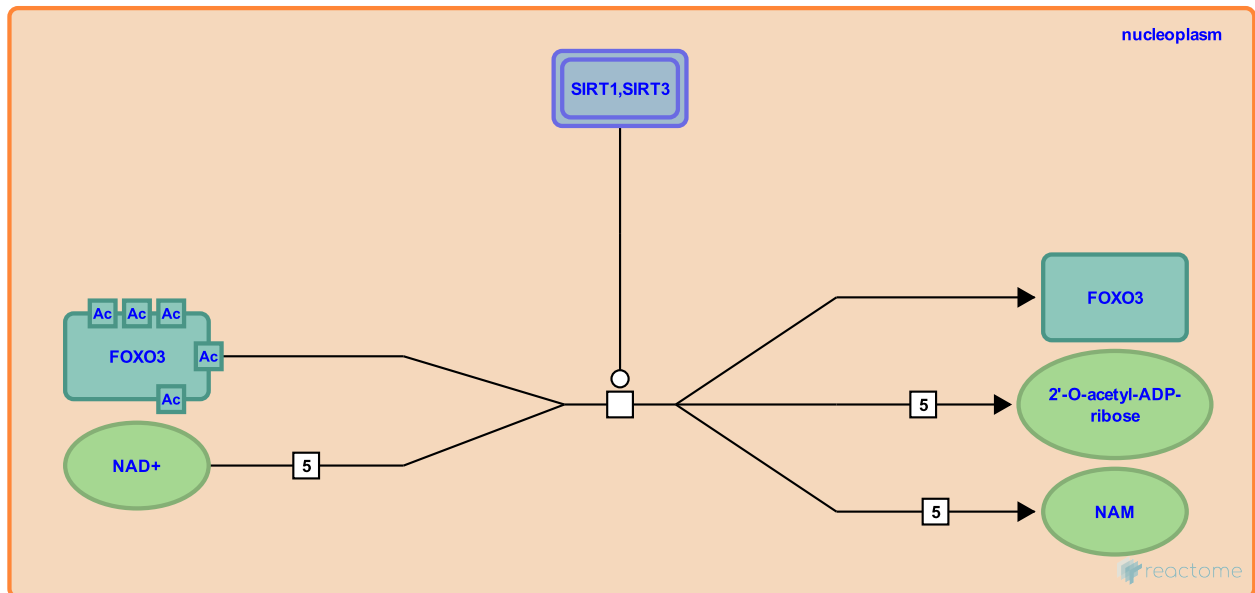
**Location:** [Regulation of FOXO transcriptional activity by acetylation](#)

**Stable identifier:** R-CFA-9620532

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [SIRT1,SIRT3 deacetylate FOXO3 \(Homo sapiens\)](#)



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:** [KAT2B,EP300 acetylate FOXO3 under oxidative stress](#)

## CREBBP binds FOXO1 ↗

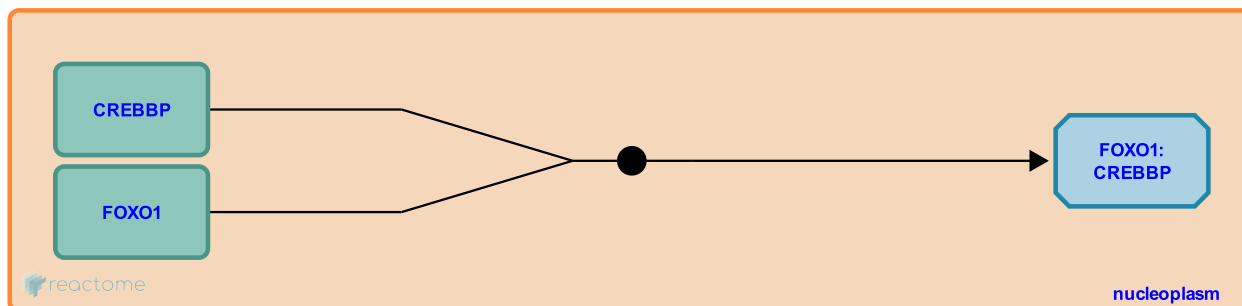
**Location:** [Regulation of FOXO transcriptional activity by acetylation](#)

**Stable identifier:** R-CFA-9626928

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [CREBBP binds FOXO1 \(Homo sapiens\)](#)



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>

# Table of Contents

Introduction	1
☛ Regulation of FOXO transcriptional activity by acetylation	2
☛ KAT2B,EP300 acetylate FOXO3 under oxidative stress	3
☛ SIRT1,SIRT3 deacetylate FOXO3	4
☛ CREBBP binds FOXO1	5
Table of Contents	6