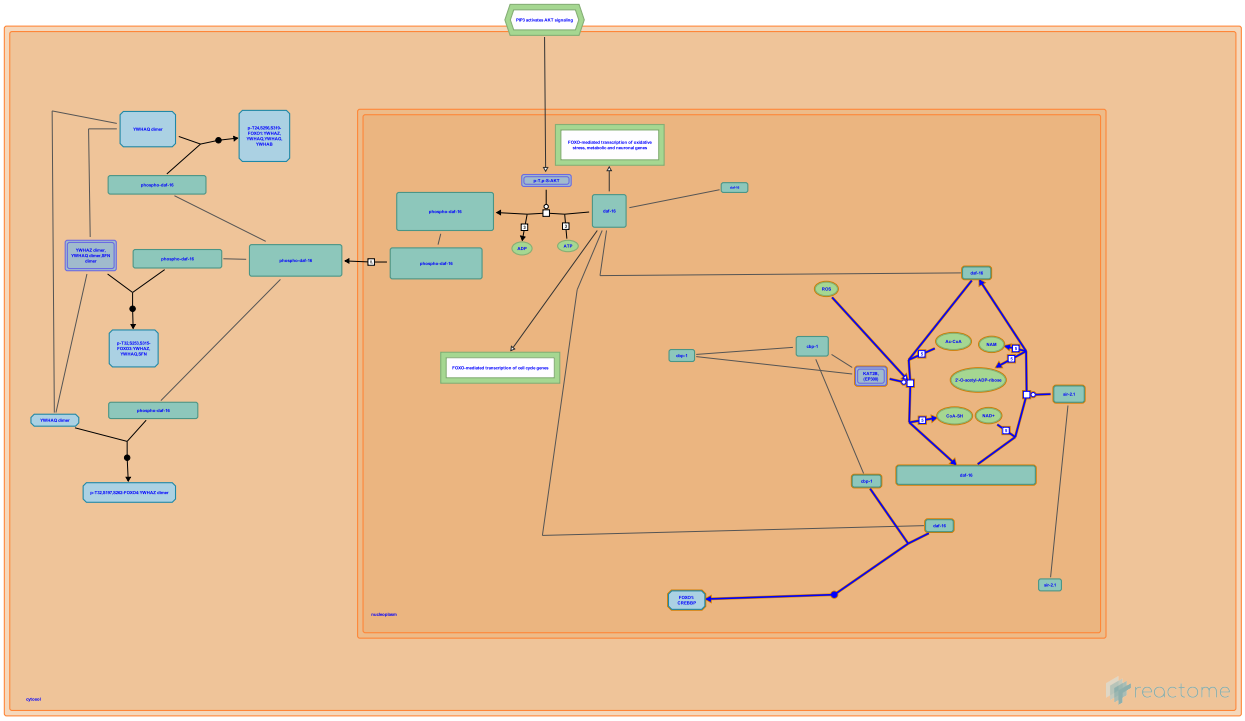
Regulation of FOXO transcriptional activity by acetylation



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27/09/2020

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.

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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. ↗

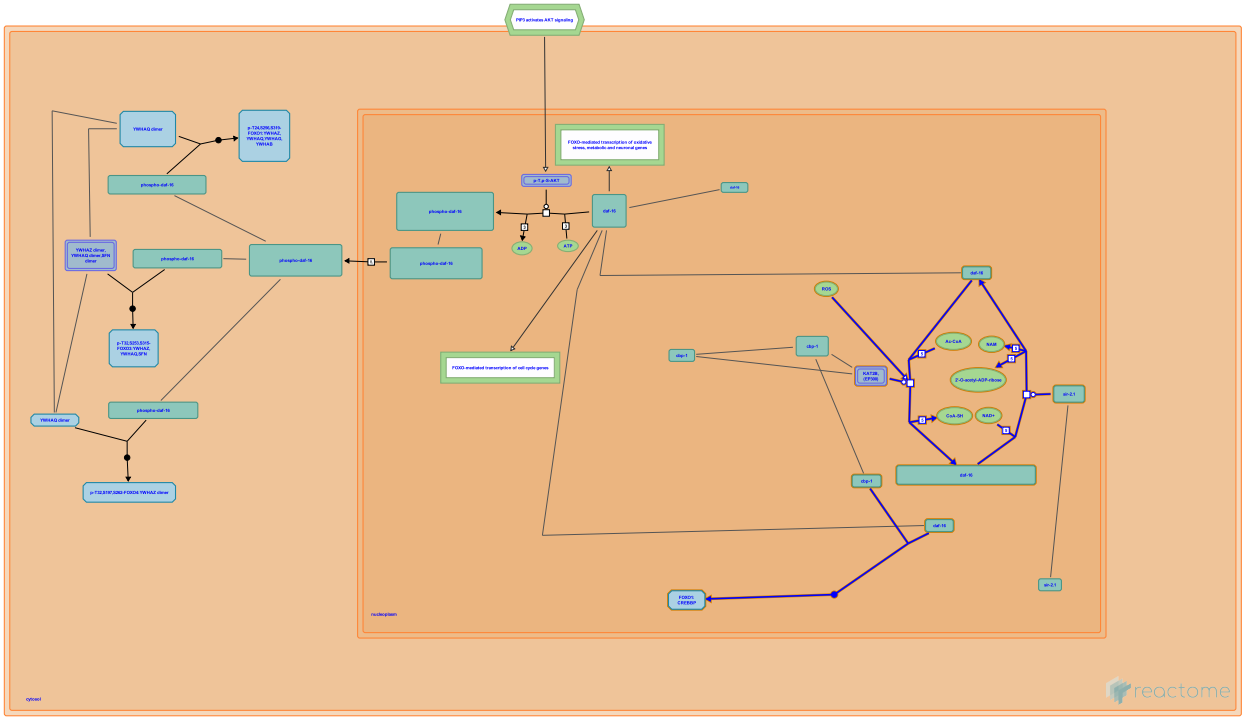
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Regulation of FOXO transcriptional activity by acetylation ↗

Stable identifier: R-CEL-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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

KAT2B,EP300 acetylate FOXO3 under oxidative stress ↗

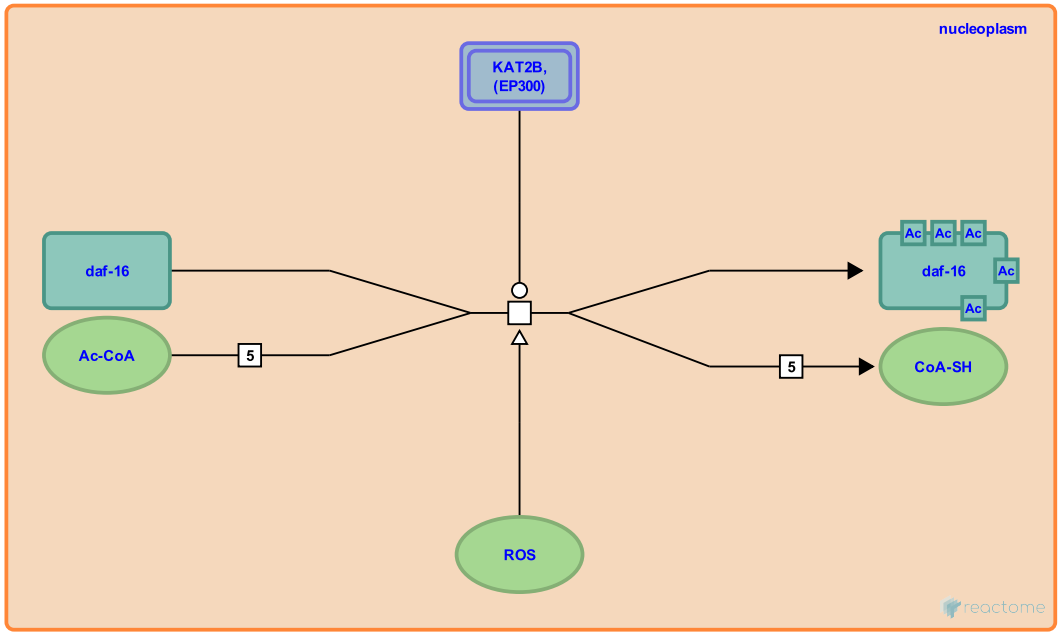
Location: Regulation of FOXO transcriptional activity by acetylation

Stable identifier: R-CEL-9620515

Type: transition

Compartments: nucleoplasm

Inferred from: KAT2B,EP300 acetylate FOXO3 under oxidative stress (Homo sapiens)



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Followed by: SIRT1,SIRT3 deacetylate FOXO3

SIRT1,SIRT3 deacetylate FOXO3 ↗

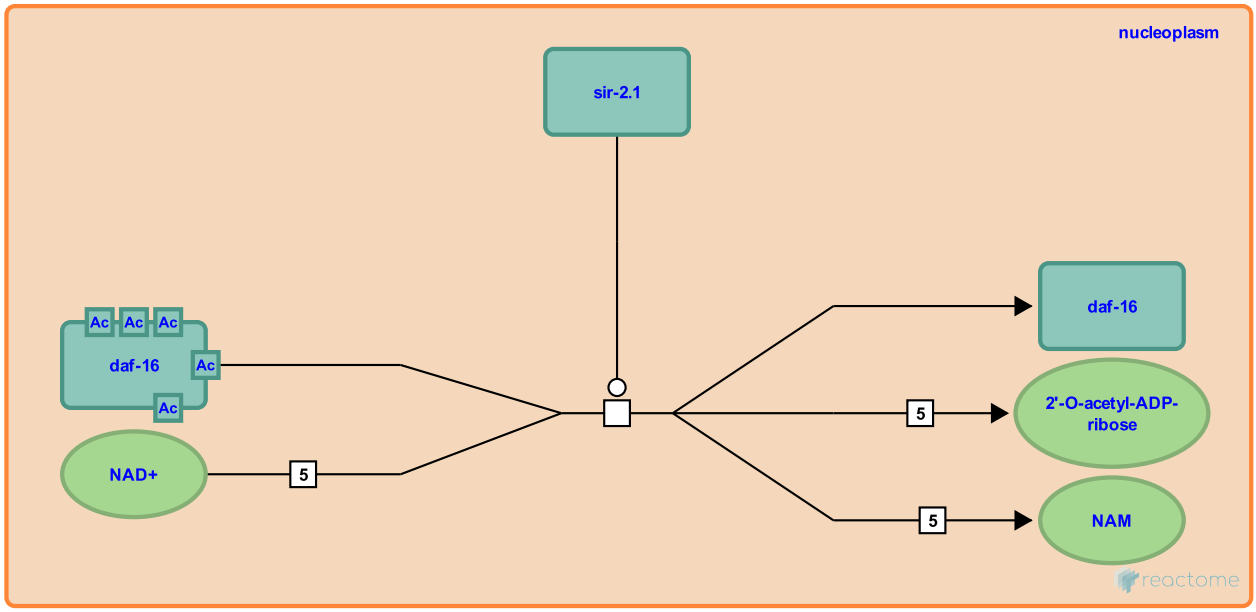
Location: Regulation of FOXO transcriptional activity by acetylation

Stable identifier: R-CEL-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.

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Preceded by: KAT2B,EP300 acetylate FOXO3 under oxidative stress

CREBBP binds FOXO1 ↗

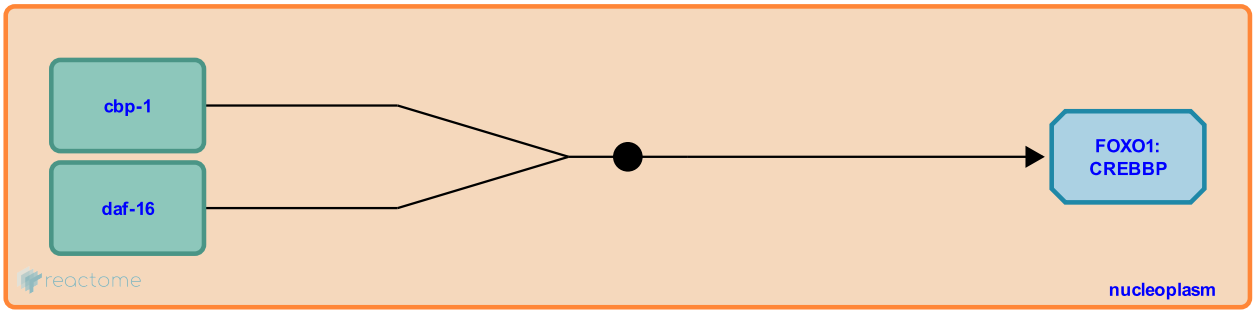
Location: Regulation of FOXO transcriptional activity by acetylation

Stable identifier: R-CEL-9626928

Type: binding

Compartments: nucleoplasm

Inferred from: CREBBP binds FOXO1 (Homo sapiens)



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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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