

FOXOA2-, MAFA-, and PAX6-dependent synthesis of PDX1 protein

D'Eustachio, P., Ferrer, J., Jensen, J., Tello-Ruiz, MK.

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.

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Literature references

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- 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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Reactome database release: 82

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

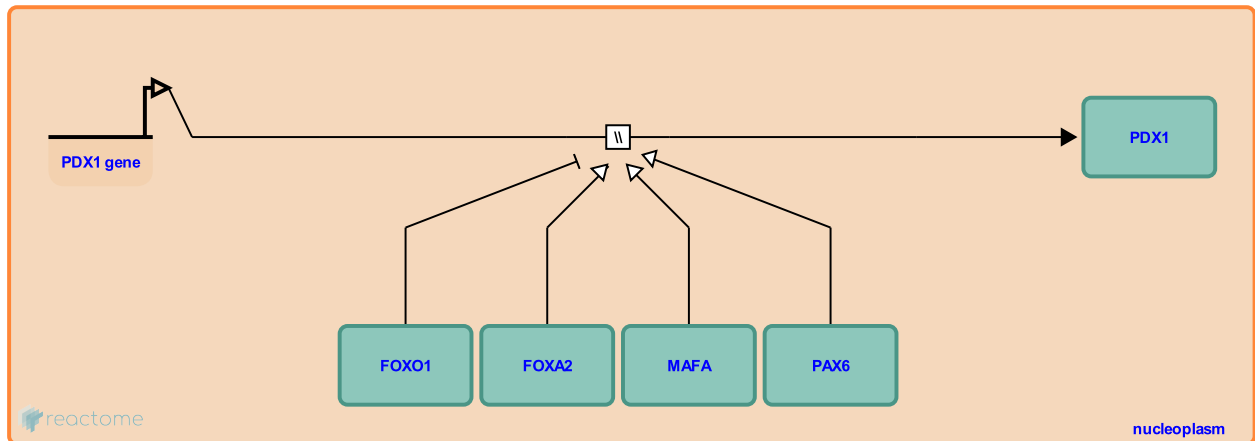
FOXOA2-, MAFA-, and PAX6-dependent synthesis of PDX1 protein ↗

Stable identifier: R-HSA-211272

Type: omitted

Compartments: nucleoplasm

Inferred from: FOXa2/HNF3b-, MafA-, and PAX6-dependent synthesis of Pdx1 protein (Mus musculus)



The PDX1 (IPF1) gene is transcribed, its mRNA is translated, and the protein product is transported to the nucleus. PDX1 transcription is positively regulated by the activities of the FOXA2, MAFA, and PAX6 transcription factors. It is negatively regulated by FOXO1A, so events that deplete the nucleoplasmic pool of FOXO1A increase expression of PDX1. These events and interactions have not been studied directly in humans, but are inferred from corresponding ones worked out in the mouse.

Editions

2008-05-13	Edited	D'Eustachio, P.
2008-05-13	Reviewed	Jensen, J.
2008-05-24	Authored	Tello-Ruiz, MK., Ferrer, J.