

HNF1A-dependent synthesis of FOXA3

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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

- 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. [↗](#)

Reactome database release: 82

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

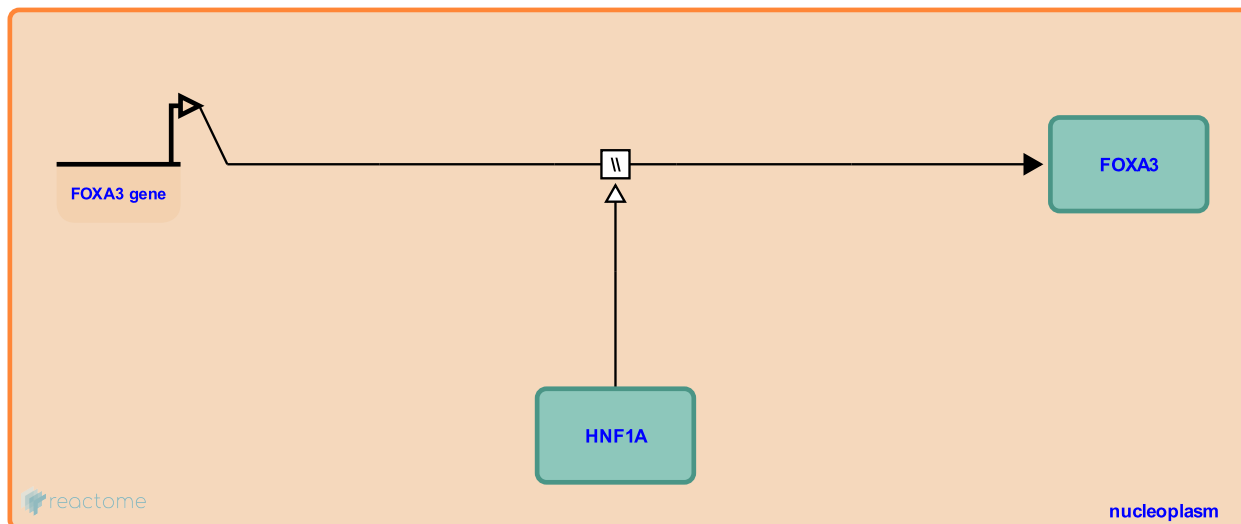
HNF1A-dependent synthesis of FOXA3 [↗](#)

Stable identifier: R-HSA-211482

Type: omitted

Compartments: nucleoplasm

Inferred from: [HNF1a regulates Foxa3 \(Mus musculus\)](#)



The FOXA3 gene is transcribed, its mRNA is translated, and the protein product is localized to the nucleoplasm. FOXA3 expression is positively regulated by HNF1A. The molecular details of FOXA3 expression in intact pancreatic beta cells have not been studied in humans, but are inferred from corresponding ones worked out in the mouse (Boj et al. 2001).

Editions

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