

NEUROD1- and PDX1-dependent synthesis of glucokinase (GCK) 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

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: 88

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

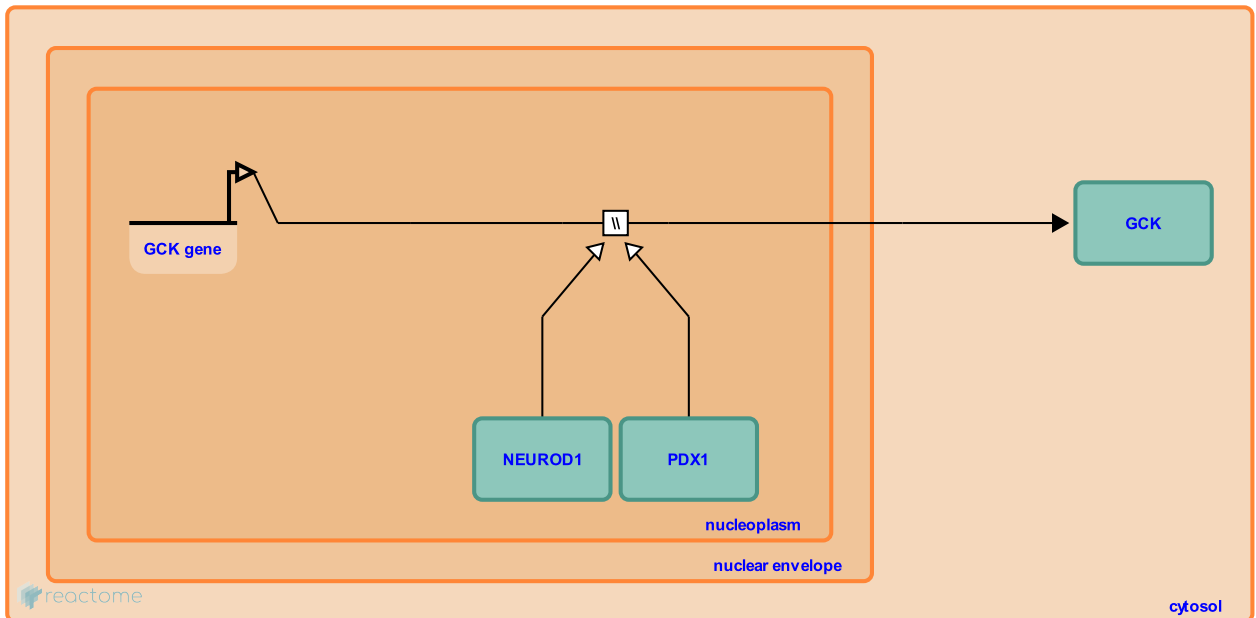
NEUROD1- and PDX1-dependent synthesis of glucokinase (GCK) protein ↗

Stable identifier: R-HSA-211346

Type: omitted

Compartments: nucleoplasm, cytosol

Inferred from: [NeuroD1- and Pdx1-dependent synthesis of glucokinase \(Gck\) protein \(Mus musculus\)](#)



The glucokinase (GCK) gene is transcribed and its mRNA is translated. GCK transcription is positively regulated by the activity of the NEUROD1 and PDX1 transcription factors. These events and interactions are inferred from corresponding ones studied in molecular detail 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.