

Expression of Nr1d1 (Rev-erba)

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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

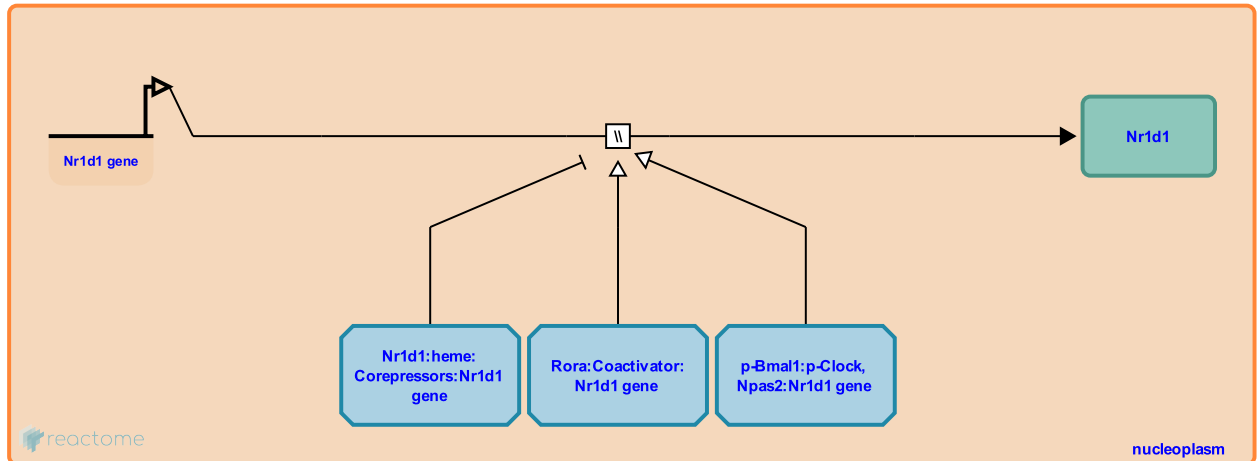
This document contains 1 reaction ([see Table of Contents](#))

Expression of Nr1d1 (Rev-erba) ↗

Stable identifier: R-MMU-549505

Type: omitted

Compartments: nucleoplasm



The Nr1d1 (Rev-erba) gene is transcribed to yield mRNA and the mRNA is translated to yield protein. The Nr1d1 promoter is regulated by the Bmal1:Clock (Arntl:Clock) heterodimer, therefore Nr1d1 shows circadian expression.

Literature references

Antoch, MP., Kakizawa, T., Safi, R., Laudet, V., Triqueneaux, G., Delaunay, F. et al. (2004). The orphan receptor Rev-erbalpha gene is a target of the circadian clock pacemaker. *J Mol Endocrinol*, 33, 585-608. ↗

Albrecht, U., Schibler, U., Preitner, N., Zakany, J., Damiola, F., Duboule, D. et al. (2002). The orphan nuclear receptor REV-ERBalpha controls circadian transcription within the positive limb of the mammalian circadian oscillator. *Cell*, 110, 251-60. ↗

Editions

2010-02-20

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