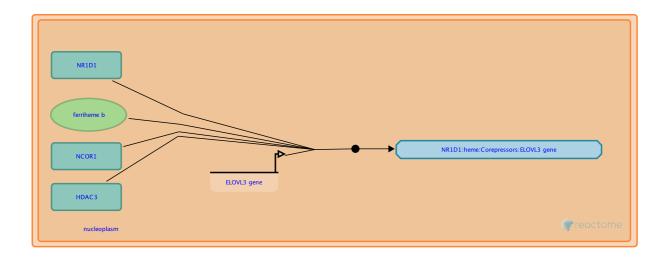


NR1D1 (REV-ERBA) represses gene expres-

sion



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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: 77

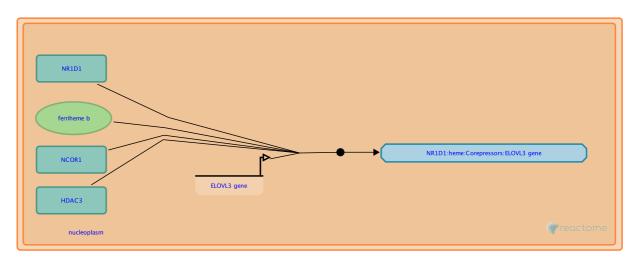
This document contains 1 pathway and 1 reaction (see Table of Contents)

https://reactome.org Page 1

NR1D1 (REV-ERBA) represses gene expression 7

Stable identifier: R-HSA-1368071

Compartments: nucleoplasm



REV-ERBA binds DNA elements very similar to those bound by the transcription activator RORA. ROR-AREV-ERBA bound to DNA and heme recruits the corepressors NCoR and HDAC3 to repress transcription. Thus REV-ERBA and RORA appear to compete to repress or activate genes, repectively.

Literature references

Yin, L., Wu, N., Curtin, JC., Qatanani, M., Szwergold, NR., Reid, RA. et al. (2007). Rev-erbalpha, a heme sensor that coordinates metabolic and circadian pathways. *Science*, 318, 1786-9.

Raghuram, S., Stayrook, KR., Huang, P., Rogers, PM., Nosie, AK., McClure, DB. et al. (2007). Identification of heme as the ligand for the orphan nuclear receptors REV-ERBalpha and REV-ERBbeta. *Nat Struct Mol Biol, 14*, 1207-13.

Phelan, CA., Gampe RT, Jr., Lambert, MH., Parks, DJ., Montana, V., Bynum, J. et al. (2010). Structure of Rev-erbal-pha bound to N-CoR reveals a unique mechanism of nuclear receptor-co-repressor interaction. *Nat Struct Mol Biol*, 17, 808-14.

Yin, L., Wu, N., Lazar, MA. (2010). Nuclear receptor Rev-erbalpha: a heme receptor that coordinates circadian rhythm and metabolism. *Nucl Recept Signal*, 8, e001.

Editions

| 2011-06-22 | Authored, Edited | May, B. |
|------------|------------------|--------------|
| 2012-01-28 | Reviewed | Delaunay, F. |
| 2015-01-17 | Revised | May, B. |

https://reactome.org Page 2

NR1D1 (REV-ERBA) binds heme, the ELOVL3 gene, and recruits corepressors 7

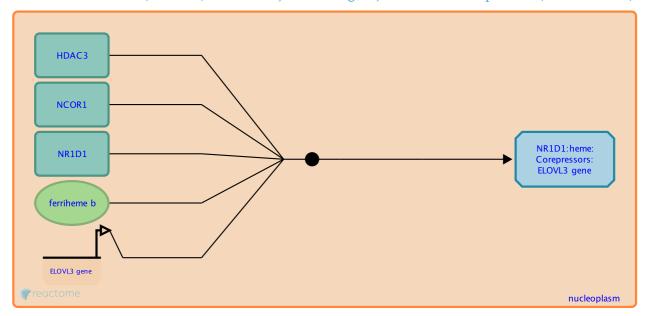
Location: NR1D1 (REV-ERBA) represses gene expression

Stable identifier: R-HSA-5663252

Type: binding

Compartments: nucleoplasm

Inferred from: Nr1d1 (Rev-erba) binds heme, the Elovl3 gene, and recruits corepressors (Mus musculus)



As inferred from mouse homologs, REV-ERBA (NR1D1) binds the promoter of the ELOVL3 gene and represses transcription, possibly by recruiting corepressors.

Editions

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https://reactome.org

Table of Contents

| Introduction | 1 |
|---|---|
| NR1D1 (REV-ERBA) represses gene expression | 2 |
| NR1D1 (REV-ERBA) binds heme, the ELOVL3 gene, and recruits corepressors | 3 |
| Table of Contents | 4 |

https://reactome.org Page 4