NR1D1 (REV-ERBA) binds heme, the ARNTL gene, and recruits corepressors.

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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. ↗

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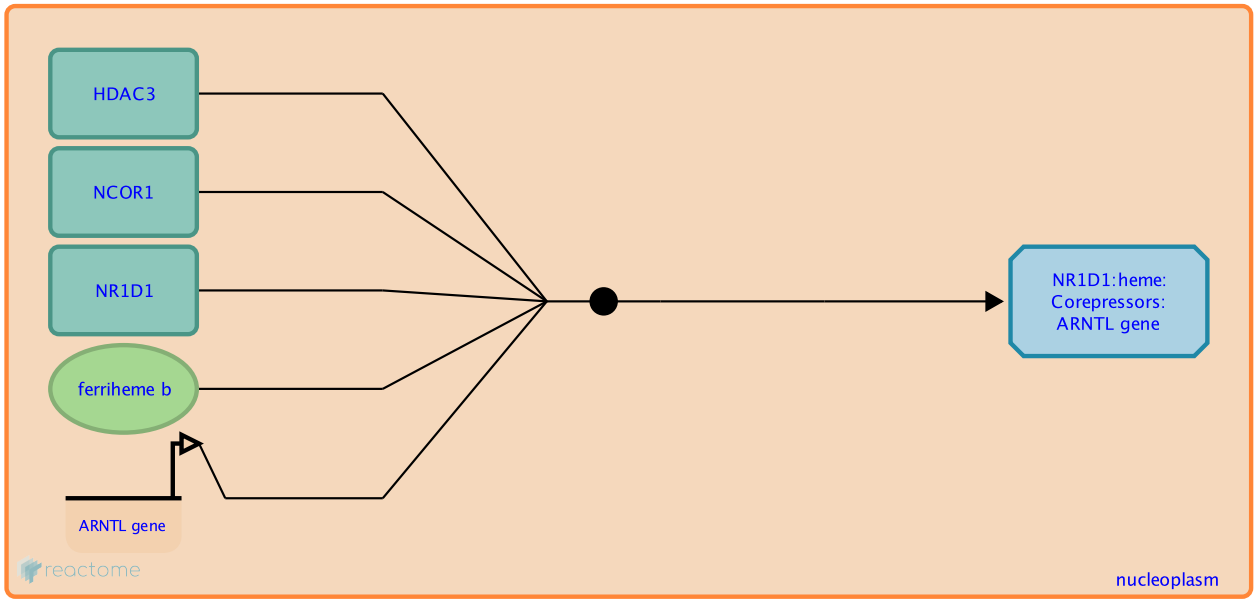
Stable identifier: R-HSA-1368069

Type: binding

Compartments: nucleoplasm



NR1D1 (REV-ERBA) binds heme. The NR1D1:heme complex is then able to recruit the corepressors NCoR and HDAC3. Corepressors do not bind NR1D1 in the absence of heme. NR1D1:heme binds a RRE element in the promoter of the ARNTL (BMAL1) gene, recruits corepressors, and represses transcription.

Literature references

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. ↗

Yin, L., Lazar, MA. (2005). The orphan nuclear receptor Rev-erbalpha recruits the N-CoR/histone deacetylase 3 corepressor to regulate the circadian Bmal1 gene. *Mol Endocrinol, 19*, 1452-9. ↗

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. ↗

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

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