Expression of CLOCK

Delaunay, F., May, B., Somers, J.

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. ↗

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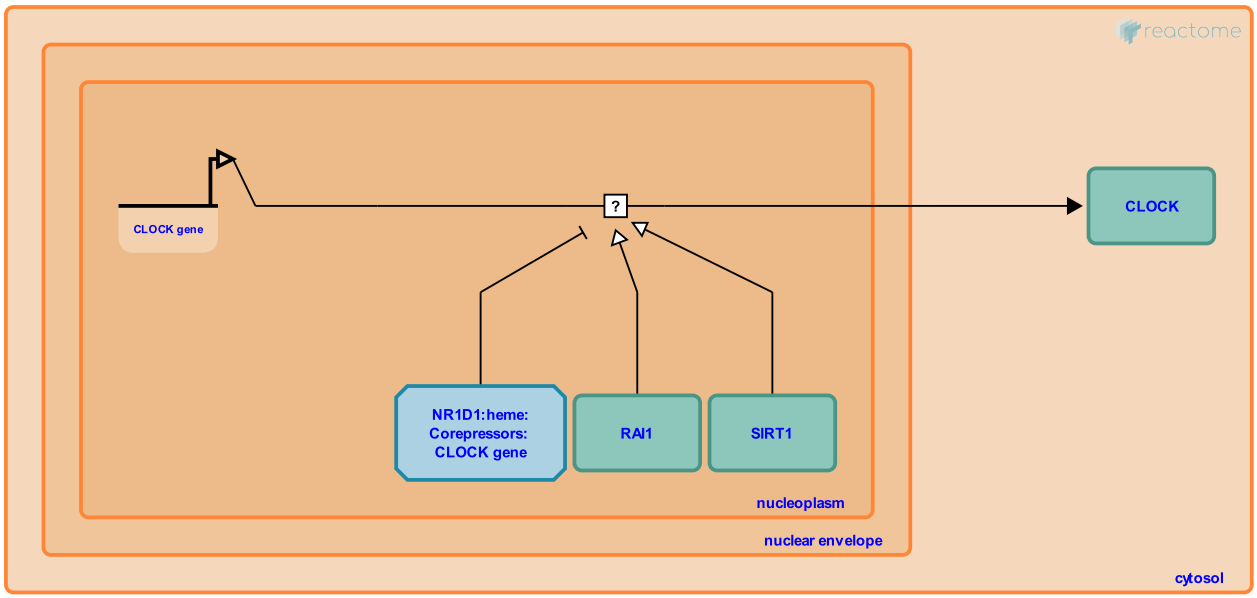
Expression of CLOCK ↗

Stable identifier: R-HSA-1368119

Type: uncertain

Compartments: nucleoplasm, cytosol

Inferred from: Expression of Clock (Mus musculus)



The CLOCK gene is transcribed to yield mRNA and the mRNA is translated to yield CLOCK protein (Steeves et al. 1999, Ueda et al. 2005, also inferred from mouse homologs). Transcription of CLOCK is repressed by REV-ERBA. The promoter of CLOCK contains an RRE element that may bind REV-ERBA and RORA.
Inferred from mouse homologs, RAI1 increases transcription of the CLOCK gene (Williams et al. 2012).

Literature references

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Editions

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