

Expression of Clock

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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

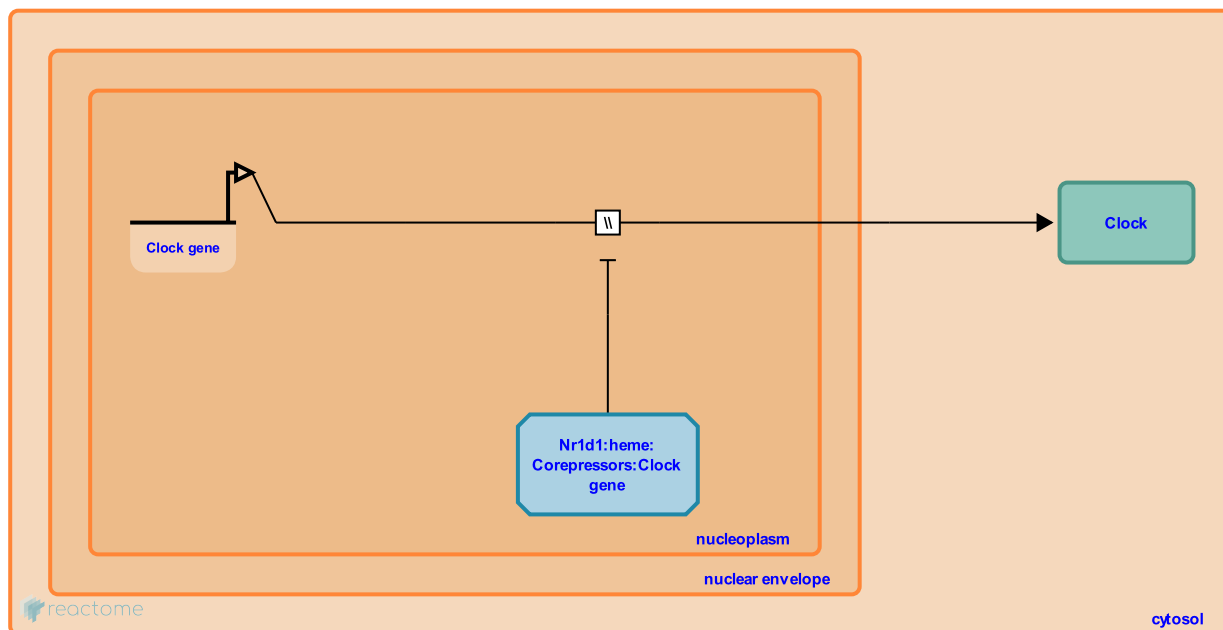
This document contains 1 reaction ([see Table of Contents](#))

Expression of Clock [↗](#)

Stable identifier: R-MMU-5667072

Type: omitted

Compartments: nucleoplasm, cytosol



The Clock gene is transcribed to yield mRNA and the mRNA is translated to yield protein. The promoter of the Clock gene contains a RRe element that confers circadian expression, possibly through binding Rora or Rev-erba.

Literature references

Hayashi, S., Hashimoto, S., Iino, M., Chen, W., Machida, M., Shigeyoshi, Y. et al. (2005). System-level identification of transcriptional circuits underlying mammalian circadian clocks. *Nat. Genet.*, 37, 187-92. [↗](#)

Hogenesch, JB., Nishio, J., Ueda, HR., Uno, KD., Masumoto, KH., Nagano, M. et al. (2008). Analysis and synthesis of high-amplitude Cis-elements in the mammalian circadian clock. *Proc Natl Acad Sci U S A*, 105, 14946-51. [↗](#)

Editions

2012-01-28	Reviewed	Delaunay, F.
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