

Expression of Ppara

Albrecht, U., Delaunay, F., Hirota, T., Kay, SA., May, B.

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

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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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Reactome database release: 88

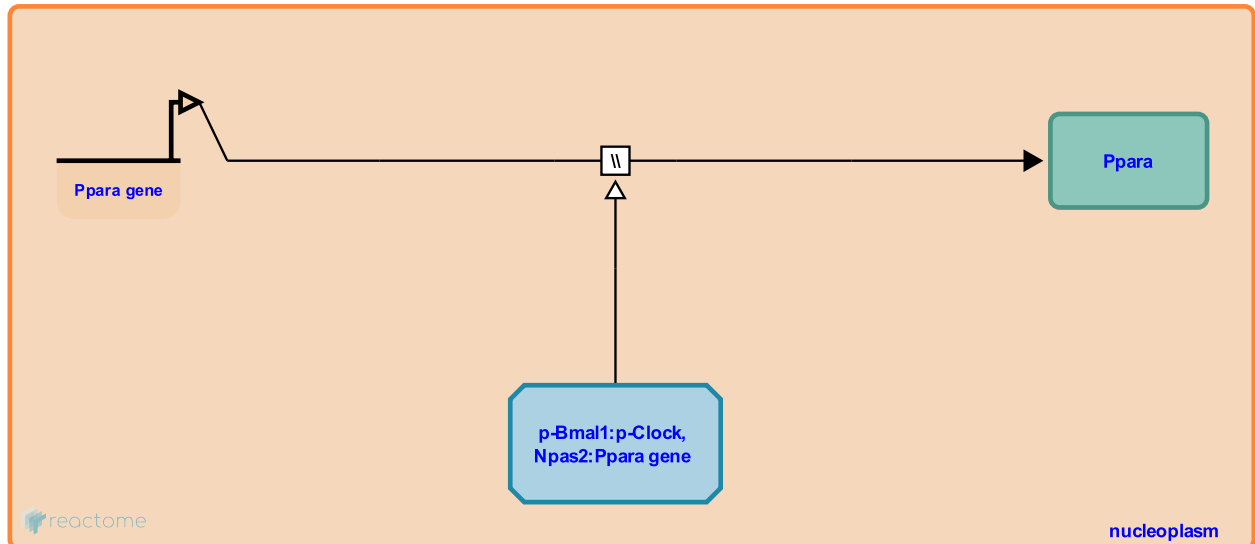
This document contains 1 reaction ([see Table of Contents](#))

Expression of Ppara [↗](#)

Stable identifier: R-MMU-879764

Type: omitted

Compartments: nucleoplasm



The Ppara gene is transcribed to yield mRNA and the mRNA is translated to yield protein. Bmal1:Clock (Arntl:Clock) heterodimers bind to E-box elements in the second intron of the Ppara gene and activate transcription of Ppara.

Literature references

Ishida, N., Oishi, K., Shirai, H. (2005). CLOCK is involved in the circadian transactivation of peroxisome-proliferator-activated receptor alpha (PPARalpha) in mice. *Biochem J*, 386, 575-81. [↗](#)

Editions

2010-06-18	Authored, Edited	May, B.
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