

p-BMAL1:p-CLOCK,NPAS2 binds PPARA

gene

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30/04/2024

https://reactome.org

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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

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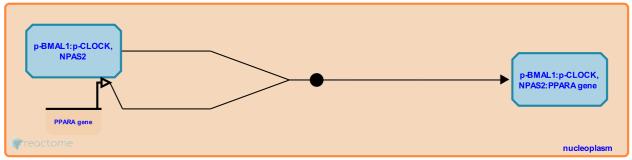
p-BMAL1:p-CLOCK,NPAS2 binds PPARA gene **ブ**

Stable identifier: R-HSA-5663156

Type: binding

Compartments: nucleoplasm

Inferred from: p-Bmal1:p-Clock,Npas2 binds Ppara gene (Mus musculus)



As inferred from mouse, BMAL1:CLOCK (ARNTL:CLOCK) heterodimers bind E-boxes 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. *对*

Editions

2009-05-27	Reviewed	D'Eustachio, P.
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