p-Bmal1:p-Clock,Npas2 binds Nr1d1 gene

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

05/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. ↗
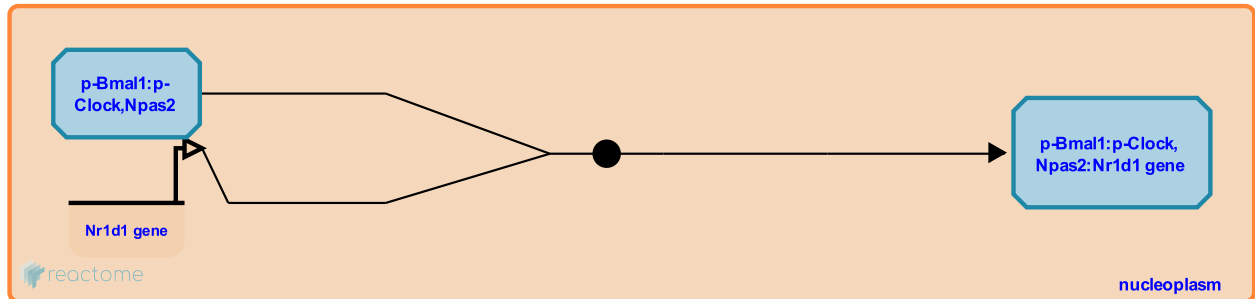
Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

p-Bmal1:p-Clock,Npas2 binds Nr1d1 gene ↗

Stable identifier: R-MMU-5663147

Type: binding

Compartments: nucleoplasm

Bmal1:Clock (Arntl:Clock) and Bmal1:Npas2 (Arntl:Npas2) heterodimers bind E-box elements (consensus CACGTG) in the promoters of target genes. Two E-box elements separated by 6 bp are sufficient to confer circadian transcription on a reporter gene. The Rev-erba (Nr1d1) promoter has an E-box and is regulated by Bmal1:Clock. Regulation by Bmal1:Npas2 has also been demonstrated, leading to the conclusion that Clock and Npas2 are at least partially redundant.

Literature references

Antoch, MP., Kakizawa, T., Safi, R., Laudet, V., Triqueneaux, G., Delaunay, F. et al. (2004). The orphan receptor Rev-erbalpha gene is a target of the circadian clock pacemaker. *J Mol Endocrinol, 33*, 585-608. ↗

Albrecht, U., Schibler, U., Preitner, N., Zakany, J., Damiola, F., Duboule, D. et al. (2002). The orphan nuclear receptor REV-ERBalpha controls circadian transcription within the positive limb of the mammalian circadian oscillator . *Cell, 110*, 251-60. ↗

Reppert, SM., DeBruyne, JP., Weaver, DR. (2007). CLOCK and NPAS2 have overlapping roles in the suprachiasmatic circadian clock. *Nat Neurosci, 10*, 543-5. ↗

Editions

2010-06-23	Reviewed	Hirota, T., Kay, SA., Delaunay, F., Albrecht, U.
2015-01-15	Authored, Edited	May, B.