p-BMAL1:p-CLOCK,NPAS2 binds SER-PINE1 gene

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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. ↗

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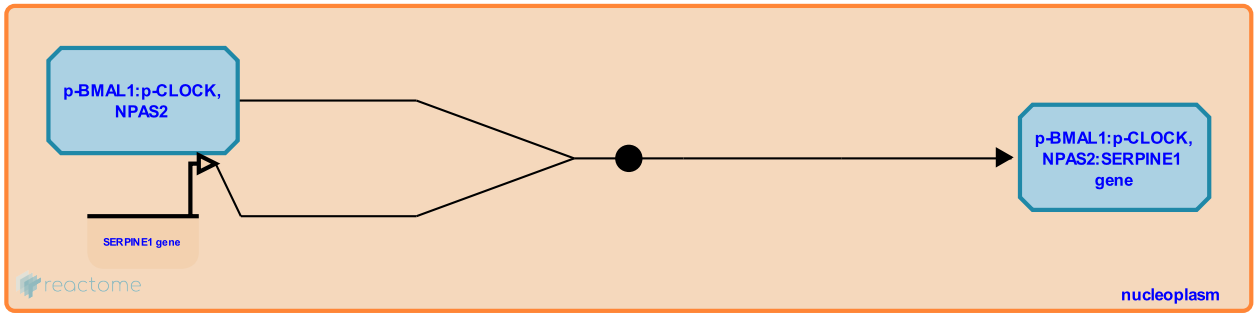
Stable identifier: R-HSA-5663124

Type: binding

Compartments: nucleoplasm



The phosphorylated BMAL1:CLOCK (ARNTL) heterodimer binds an E-box in the promoter of the PAI-1 gene and activate transcription of PAI-1. NPAS2 is predicted to act redundantly with CLOCK.

Literature references

Samani, NJ., Chong, NW., Codd, V., Chan, D. (2006). Circadian clock genes cause activation of the human PAI-1 gene promoter with 4G/5G allelic preference. *FEBS Lett, 580*, 4469-72. ↗

van der Bom, JG., Bots, ML., Kluft, C., Haverkate, F., Grobbee, DE. (2003). The 4G5G polymorphism in the gene for PAI-1 and the circadian oscillation of plasma PAI-1. *Blood, 101*, 1841-4. ↗

Eren, M., Smith, LH., Vaughan, DE., Johnson, CH., Painter, CA., Schoenhard, JA. (2003). Regulation of the PAI-1 promoter by circadian clock components: differential activation by BMAL1 and BMAL2. *J Mol Cell Cardiol, 35*, 473-81. ↗

Editions

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