

# **Expression of DBP**

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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

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- 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.
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Reactome database release: 88

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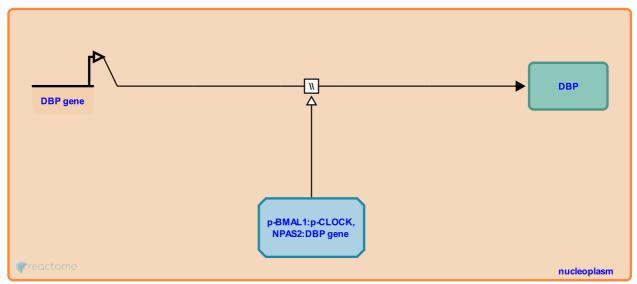
# **Expression of DBP**

**Stable identifier:** R-HSA-879762

Type: omitted

Compartments: nucleoplasm

**Inferred from:** Expression of Dbp (Mus musculus)



The DBP gene is transcribed to yield mRNA and the mRNA is translated to yield protein. As inferred from mouse, BMAL1:CLOCK (ARNTL:CLOCK) heterodimers bind E-boxes in the DBP promoter and activate transcription of DBP.

## Literature references

Inaba, T., Khatib, ZA., Look, AT., Valentine, M. (1994). Chromosomal localization and cDNA cloning of the human DBP and TEF genes. *Genomics*, 23, 344-51. *¬* 

# **Editions**

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