Expression of NPAS2

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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


Expression of NPAS2

Stable identifier: R-HSA-1368065

Type: uncertain

Compartments: nucleoplasm, cytosol

Inferred from: Expression of Npas2 (Mus musculus)

The NPAS2 gene is transcribed to yield mRNA and the mRNA is transcribed to yield NPAS2 protein (Zhou et al. 1997, Matsumura et al. 2013, also inferred from mouse homologs). Transcription of NPAS2 is enhanced by the RORA:Coactivator complex and repressed by the REV-ERBA:Corepressor complex.

As inferred from mouse, RORA binds RRE DNA elements and recruits the coactivators PGC-1alpha (PPARGC1A) and p300 (EP300, a histone acetylase). As inferred from mouse, ROR-alpha binds the promoter of the NPAS2 gene and enhances transcription.

Literature references


Editions

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