RORA activates gene expression

Delaunay, F., Kersten, S., May, B.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

18/11/2022

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.

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


Reactome database release: 82

This document contains 1 pathway and 4 reactions (see Table of Contents)
**RORA activates gene expression**

**Stable identifier:** R-HSA-1368082

**Compartments:** nucleoplasm, plasma membrane, endoplasmic reticulum membrane

As inferred from mouse, RORA binds ROR elements (ROREs) in DNA and recruits the coactivators PPAR-GC1A (PGC-1alpha) and p300 (EP300, a histone acetylase) to activate transcription.

**Literature references**


**Editions**

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As inferred from mouse homologs, RORA binds RRE DNA elements in the promoter of CPT1A and recruits the coactivators PGC-1alpha (PPARGC1A) and p300 (EP300, a histone acetylase) to enhance transcription of CPT1A.

Followed by: Expression of CPT1A

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Expression of CPT1A

Location: RORA activates gene expression

Stable identifier: R-HSA-1801587

Type: omitted

Compartments: nucleoplasm, mitochondrial outer membrane

Inferred from: Expression of Cpt1a (Mus musculus)

As inferred from mouse homologs, RORA binds RRE DNA elements in the promoter of CPT1A and recruits the coactivators PGC-1alpha (PPARGC1A) and p300 (EP300, a histone acetylase) to enhance transcription of CPT1A.

The CPT1A gene is transcribed to yield mRNA and the mRNA is translated to yield protein.

Preceded by: RORA, EP300 bind CPT1A gene

Literature references


Editions

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RORA, EP300 bind SREBF1 gene

**Location:** RORA activates gene expression

**Stable identifier:** R-HSA-5663293

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** Rora, Ep300 bind Srebf1 gene (Mus musculus)

As inferred from mouse, RORA binds the promoter of the SREBF1 gene and recruits coactivators to enhance transcription.

**Followed by:** Expression of SREBF1 (SREBP1)

**Editions**

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Expression of SREBF1 (SREBP1)

Location: RORA activates gene expression

Stable identifier: R-HSA-1368081

Type: omitted

Compartments: endoplasmic reticulum membrane, nucleoplasm

Inferred from: Expression of Srebf1 (Mus musculus)

As inferred from mouse, RORA (ROR-alpha) enhances expression of SREBP1 (SREBF1).

The SREBF1 (SREBP1) gene is transcribed to yield mRNA and the mRNA is translated to yield protein.

Preceded by: RORA, EP300 bind SREBF1 gene

Literature references


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