CEBPA mRNA is translated to yield CEBPA protein

May, B., Skokowa, J.
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


Reactome database release: 73

This document contains 1 reaction (see Table of Contents)
CEBPA mRNA is translated to yield CEBPA protein

Stable identifier: R-HSA-9622367

Type: omitted

Compartments: cytosol, nucleoplasm

Inferred from: Cebpa mRNA is translated to yield Cebpa protein (Mus musculus)

In the cytosol, 80S ribosomes translate the CEBPA mRNA to yield CEBPA protein (Pabst et al. 2001, Timchenko et al. 2002, Haefliger et al. 2011). Depending on which initiation codon is used, the CEBPA mRNA can be translated to yield a 35.9 kDa protein (p42) or a 25.5 kDa protein (p30). CEBPA protein is then imported into the nucleus. The p30 isoform is not antimitotic (inferred from mouse homologs).

Literature references


Editions

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