ATF4 activates genes in response to endoplasmic reticulum stress

Bruhat, A., Chen, JJ., D'Eustachio, P., Gillespie, ME., Matthews, L., May, B., Staschke, KA., Urano, F.

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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.

19/12/2022
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: 83

This document contains 1 pathway and 7 reactions (see Table of Contents)
ATF4 activates genes in response to endoplasmic reticulum stress

Stable identifier: R-HSA-380994

ATF4 is a transcription factor and activates expression of IL-8, MCP1, IGFBP-1, CHOP, HERP1 and ATF3.

Literature references


Editions

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https://reactome.org
Expression of ATF3

Location: ATF4 activates genes in response to endoplasmic reticulum stress

Stable identifier: R-HSA-1791173

Type: omitted

Compartments: nucleoplasm

Inferred from: Expression of Atf3 (Mus musculus)


Literature references


Kilberg, M.S., Fu, L. (2013). Elevated cJUN expression and an ATF/CRE site within the ATF3 promoter contribute to activation of ATF3 transcription by the amino acid response. Physiol. Genomics, 45, 127-37.


## Editions

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Expression of ASNS (Asparagine Synthetase)

**Location:** ATP4 activates genes in response to endoplasmic reticulum stress

**Stable identifier:** R-HSA-1791118

**Type:** omitted

**Compartments:** nucleoplasm, cytosol

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

The Asparagine Synthetase (ASNS) gene is transcribed to yield mRNA and the mRNA is translated to yield protein (Chen et al. 2004, Lee et al. 2008, Gjymishka et al. 2009, Sikalidis et al. 2011, Balasubramanian et al. 2013, inferred from the mouse homolog). Transcription of ASNS is activated by the unfolded protein response (Gjymishka et al. 2009), amino acid deficiency (Chen et al. 2004, Lee et al. 2008, Sikalidis et al. 2011, Balasubramanian et al. 2013, inferred from the mouse homolog), and heme deficiency (inferred from the mouse homolog).

**Literature references**


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**Expression of CCL2**

**Location:** ATF4 activates genes in response to endoplasmic reticulum stress

**Stable identifier:** R-HSA-1791056

**Type:** omitted

**Compartments:** nucleoplasm, extracellular region

The CCL2 gene is transcribed to yield mRNA and the mRNA is translated to yield protein.

**Literature references**


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**Literature references**


**Expression of HERPUD**

**Location:** ATP4 activates genes in response to endoplasmic reticulum stress

**Stable identifier:** R-HSA-1791095

**Type:** omitted

**Compartments:** endoplasmic reticulum membrane, nucleoplasm

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

**Literature references**


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**Expression of IGFBP1**

**Location:** ATP4 activates genes in response to endoplasmic reticulum stress

**Stable identifier:** R-HSA-1791180

**Type:** omitted

**Compartments:** nucleoplasm, extracellular region

The IGFBP1 gene is transcribed to yield mRNA and the mRNA is translated to yield protein.

**Literature references**


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Expression of IL-8

Location: ATF4 activates genes in response to endoplasmic reticulum stress

Stable identifier: R-HSA-517731

Type: omitted

Compartments: nucleoplasm, extracellular region

The IL-8 gene is transcribed to yield mRNA which is translated to yield protein.

KSRP binds an AU-rich element in the mRNA encoding IL-8 and destabilizes the mRNA.

Literature references


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