

# Expression of ATF3

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## 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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Reactome database release: 88

This document contains 1 reaction ([see Table of Contents](#))

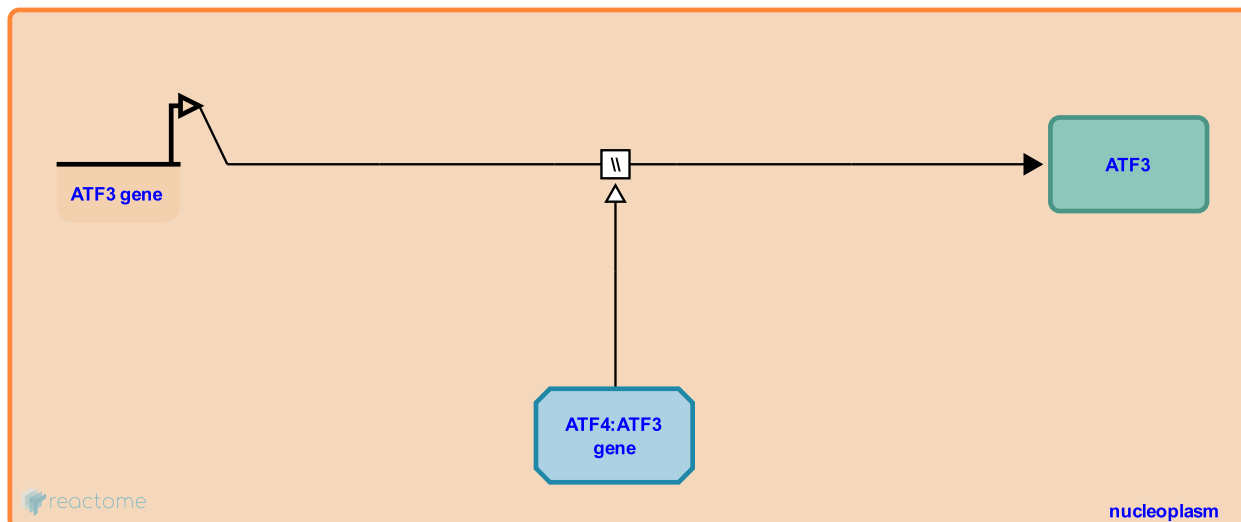
## Expression of ATF3 [↗](#)

**Stable identifier:** R-HSA-1791173

**Type:** omitted

**Compartments:** nucleoplasm

**Inferred from:** [Expression of Atf3 \(Mus musculus\)](#)



The ATF3 gene is transcribed to yield mRNA and the mRNA is translated to yield protein (Chen et al. 2004, Pan et al. 2007, Lee et al. 2008, Armstrong et al. 2010, Sikalidis et al. 2011, Fu and Kilberg 2013, Lee et al. 2013, Hayner et al. 2018). Transcription of ATF3 is enhanced in response to amino acid deficiency (Chen et al. 2004, Pan et al. 2007, Lee et al. 2008, Sikalidis et al. 2011, Fu and Kilberg 2013, Hayner et al. 2018). ATF4 binds a CEBP-ATF response element (CARE) and an additional upstream element in the promoter of the ATF3 gene, resulting in enhanced transcription (Pan et al. 2007, Armstrong et al. 2010, Fu and Kilberg 2013, Lee et al. 2013, Hayner et al. 2018, and inferred from mouse homologs). CEBPB and ATF3 bind later and correlate with reduced expression of ATF4 (Pan et al. 2007)

## Literature references

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## Editions

2008-12-02	Reviewed	Gillespie, ME., D'Eustachio, P., Matthews, L.
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