

ATF2 acetylates histone H2B, H4

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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

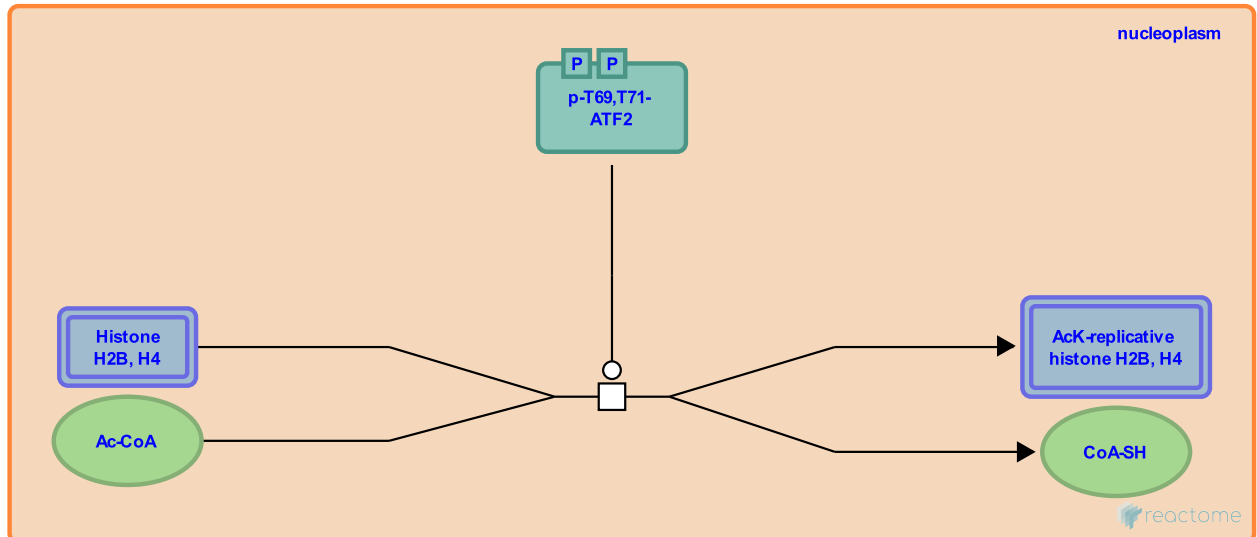
This document contains 1 reaction ([see Table of Contents](#))

ATF2 acetylates histone H2B, H4 [↗](#)

Stable identifier: R-HSA-3318415

Type: transition

Compartments: nucleoplasm



ATF2 (activating transcription factor 2) is a basic leucine zipper (bZIP) protein and member of the activator protein-1 (AP-1) family (Wagner et al. 2001). The basic region of ATF2 binds DNA while the leucine zipper region allows dimerization with partners. ATF2 is a histone acetyltransferase (HAT), which specifically acetylates histones H2B and H4 in vitro. ATF2 is sequentially phosphorylated on threonine residues T69 and T71 by protein kinases ERK1/2 and p38 (van Dam et al. 1995, Livingstone et al. 1995, Ouwens et al. 2002, Baan et al. 2009). This phosphorylated form has increased HAT activity (Kawasaki et al. 2000).

Literature references

Kawasaki, H., Chiu, R., Yokoyama, KK., Taira, K., Itakura, K., Schiltz, L. et al. (2000). ATF-2 has intrinsic histone acetyltransferase activity which is modulated by phosphorylation. *Nature*, 405, 195-200. [↗](#)

Editions

2013-03-12	Authored	Jupe, S.
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