

Hemes bind to BACH1:MAFK

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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

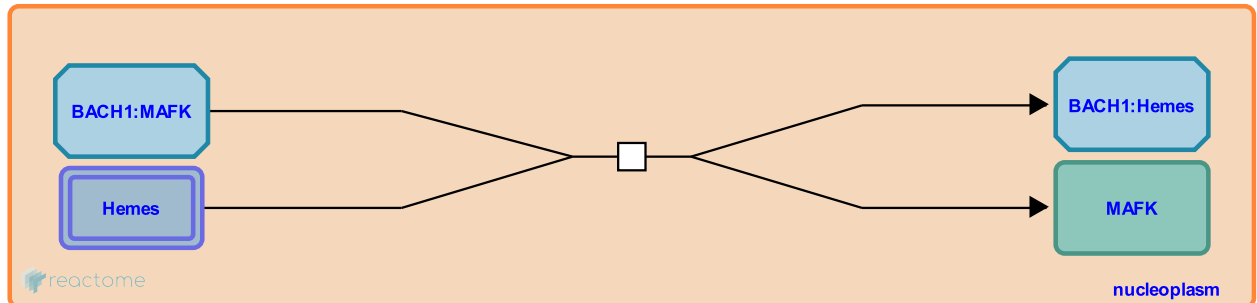
This document contains 1 reaction ([see Table of Contents](#))

Hemes bind to BACH1:MAFK [↗](#)

Stable identifier: R-HSA-9707523

Type: transition

Compartments: nucleoplasm



Heme binds to four cysteine-proline motifs in the C-terminal region of BACH1 and inhibits the DNA-binding activity of BACH1-MAFK heterodimers resulting in HMOX1 induction. MAFK separates from the complex, and heme recruits nuclear exporters for BACH1 (Yoshida et al, 1988; Ogawa et al, 2001; Suzuki et al, 2004).

Literature references

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Editions

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