HMOX1 gene produces HMOX1 dimer

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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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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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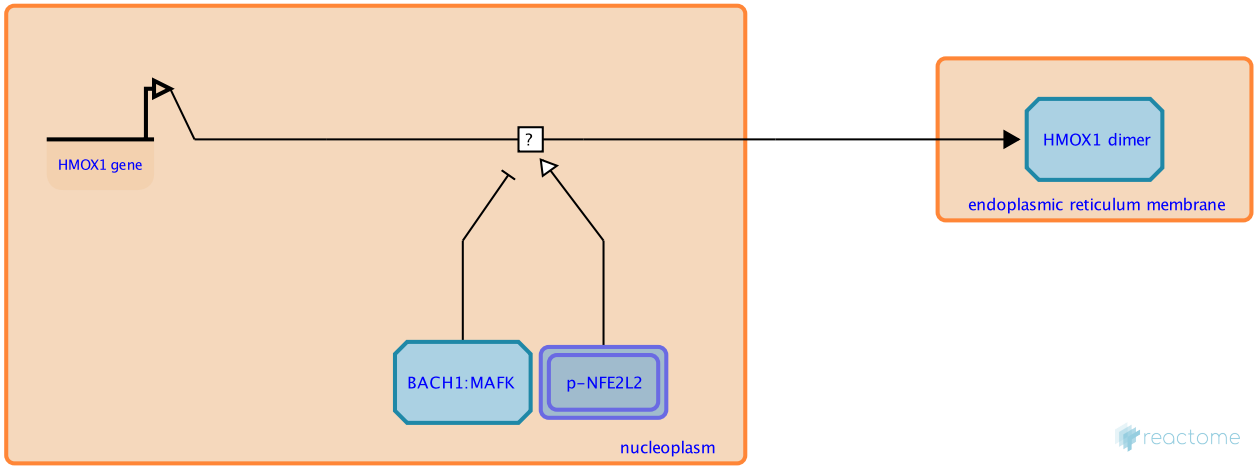
Stable identifier: R-HSA-9707645

Type: uncertain

Compartments: nucleoplasm, endoplasmic reticulum membrane



Transcription regulator protein BACH1 is a critical physiological repressor of heme oxygenase 1 (HMOX1). BACH1 binds to the multiple Maf recognition elements (MAREs) of HMOX1 enhancer MafK in vitro and represses its activity in vivo. BACH1 is inducible by hypoxia and IFN-gamma (Kitamuro et al, 2003; Sun et al, 2002).

NFE2L2 (nuclear factor erythroid 2-related factor 2) is a transcription factor that activates transcription of a battery of cytoprotective genes by binding to the ARE (antioxidant response element). It is considered not only as a cytoprotective factor regulating the expression of genes coding for anti-oxidant, anti-inflammatory and detoxifying proteins, but it is also a powerful modulator of species longevity. HMOX1 is one of the genes whose expression it activates (Huang et al, 2000; Reichard et al, 2007).

Literature references

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Editions

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