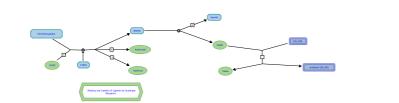
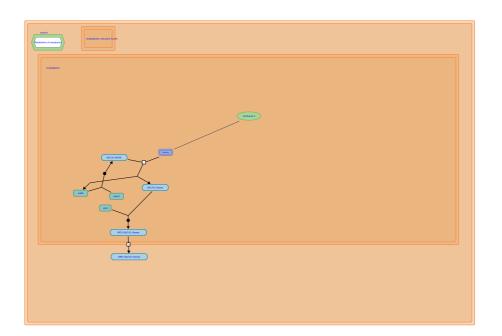


# Heme signaling





European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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05/09/2021

### 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

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- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, *14*, e1005968. *¬*

Reactome database release: 77

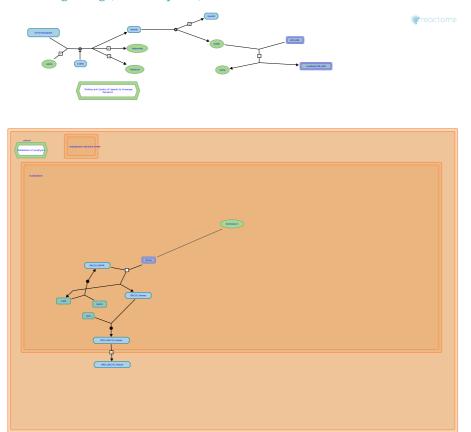
This document contains 1 pathway and 7 reactions (see Table of Contents)

#### Heme signaling **↗**

Stable identifier: R-XTR-9707616

Compartments: cytosol, extracellular region, nuclear envelope, nucleoplasm, plasma membrane

**Inferred from:** Heme signaling (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

<a href='/electronic\_inference\_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

#### H2O2 oxidises ferrohemoglobin to MetHb 7

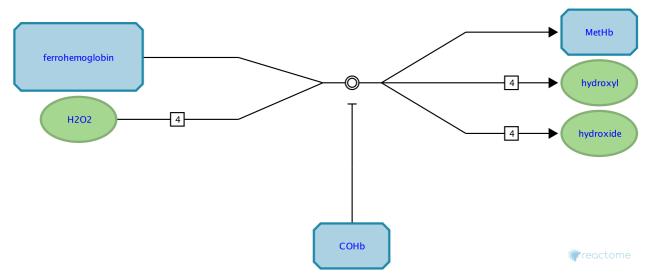
**Location:** Heme signaling

Stable identifier: R-XTR-9707504

Type: dissociation

Compartments: extracellular region

#### Inferred from: H2O2 oxidises ferrohemoglobin to MetHb (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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Followed by: FeHM dissociates from MetHb

#### FeHM dissociates from MetHb 7

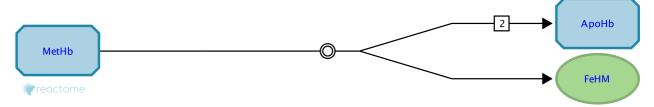
Location: Heme signaling

Stable identifier: R-XTR-9707516

Type: dissociation

Compartments: extracellular region

Inferred from: FeHM dissociates from MetHb (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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Preceded by: H2O2 oxidises ferrohemoglobin to MetHb

Followed by: FeHM oxidises LDL, HDL

#### FeHM oxidises LDL,HDL ↗

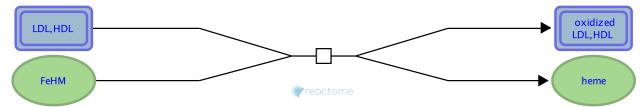
**Location:** Heme signaling

Stable identifier: R-XTR-9707586

Type: transition

Compartments: extracellular region

Inferred from: FeHM oxidises LDL, HDL (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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Preceded by: FeHM dissociates from MetHb

#### BACH1 binds MAFK 7

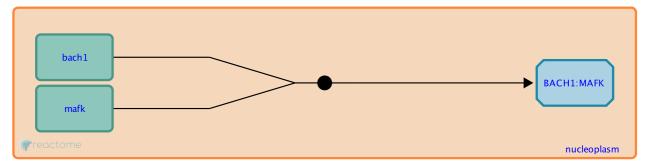
**Location:** Heme signaling

Stable identifier: R-XTR-9707690

Type: binding

Compartments: nucleoplasm

Inferred from: BACH1 binds MAFK (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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Followed by: Hemes bind to BACH1:MAFK

#### Hemes bind to BACH1:MAFK ↗

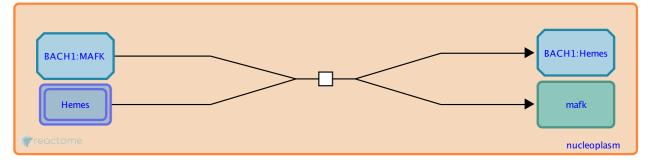
**Location:** Heme signaling

Stable identifier: R-XTR-9707523

Type: transition

Compartments: nucleoplasm

Inferred from: Hemes bind to BACH1:MAFK (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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Preceded by: BACH1 binds MAFK

Followed by: XPO1 (CRM1) binds to BACH1:Hemes

#### XPO1 (CRM1) binds to BACH1:Hemes 7

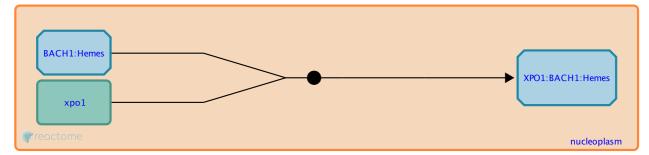
**Location:** Heme signaling

Stable identifier: R-XTR-9708430

Type: binding

Compartments: nucleoplasm

Inferred from: XPO1 (CRM1) binds to BACH1:Hemes (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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Preceded by: Hemes bind to BACH1:MAFK

Followed by: XPO1:BACH1:Hemes are transported out of the nucleus

#### XPO1:BACH1:Hemes are transported out of the nucleus **7**

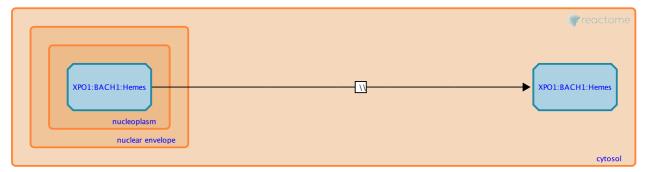
**Location:** Heme signaling

Stable identifier: R-XTR-9708423

Type: omitted

Compartments: cytosol, nucleoplasm

Inferred from: XPO1:BACH1:Hemes are transported out of the nucleus (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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Preceded by: XPO1 (CRM1) binds to BACH1:Hemes

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