Heme signaling

This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

28/04/2024

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

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

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

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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: 88

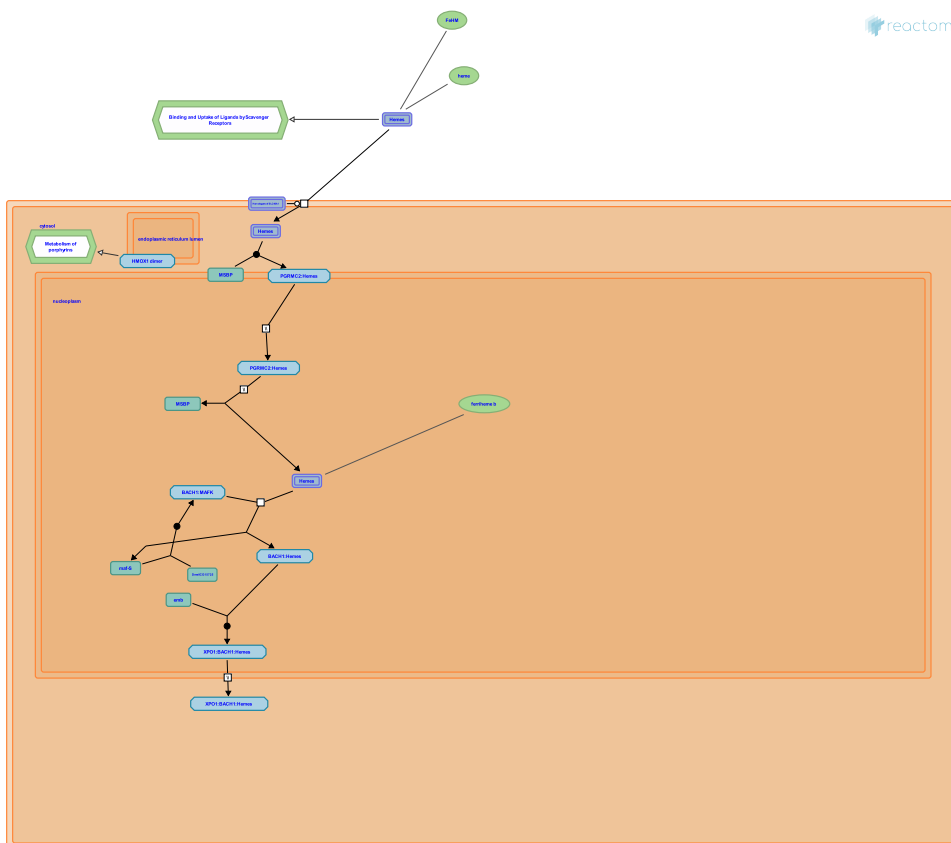This document contains 1 pathway and 8 reactions (see Table of Contents)

Heme signaling ↗

Stable identifier: R-DME-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.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

SLC46A1 transports hemes from extracellular region to cytosol ↗
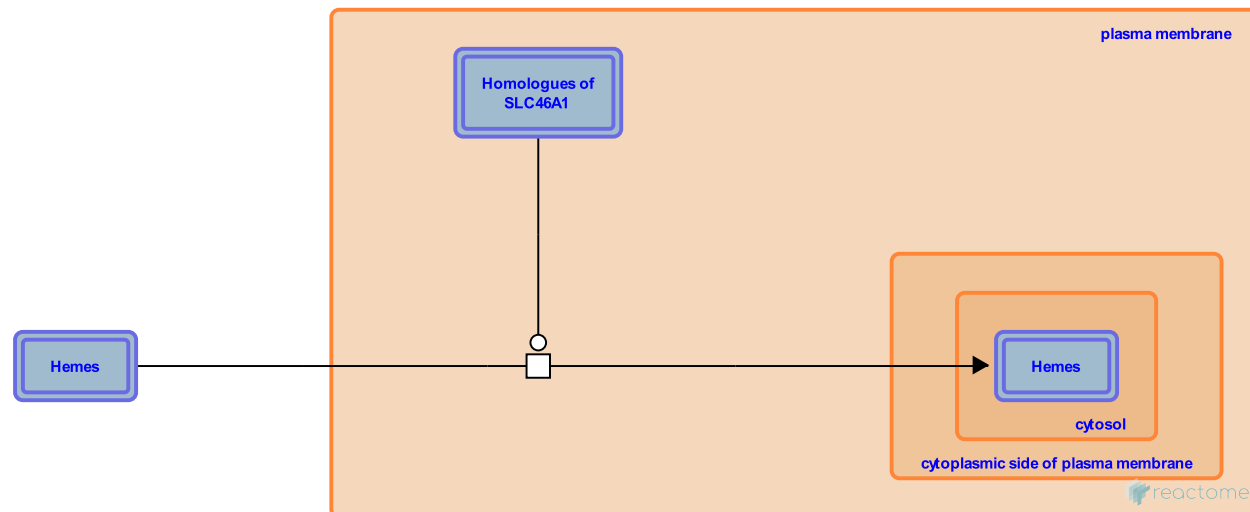
Location: Heme signaling

Stable identifier: R-DME-917870

Type: transition

Compartments: plasma membrane

Inferred from: SLC46A1 transports hemes from extracellular region to cytosol (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.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp
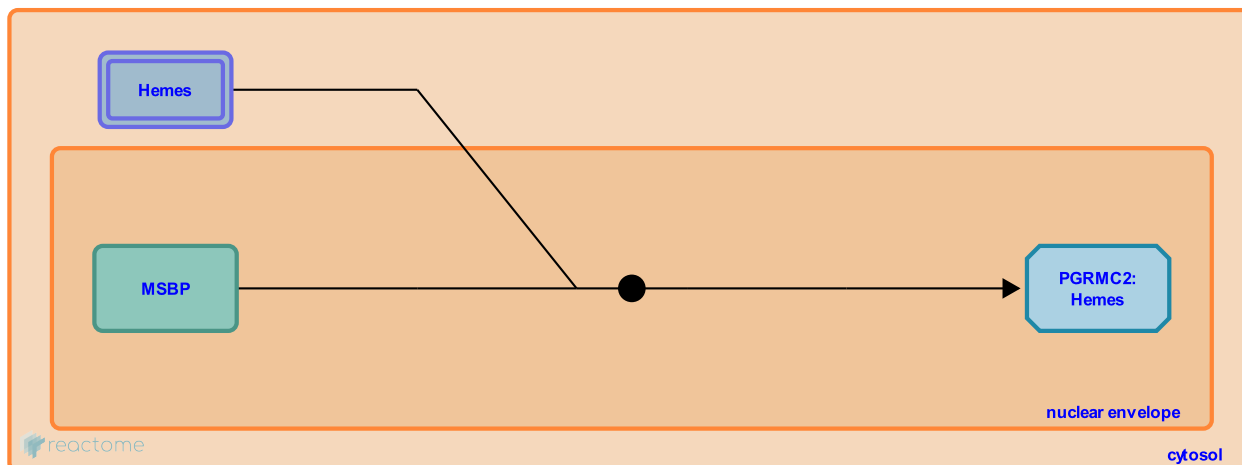
PGRMC2 binds Hemes ↗

Location: Heme signaling

Stable identifier: R-DME-9707683

Type: binding

Compartments: nuclear envelope, cytosol

Inferred from: PGRMC2 binds 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.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: PGRMC2:Hemes translocate to the nucleus

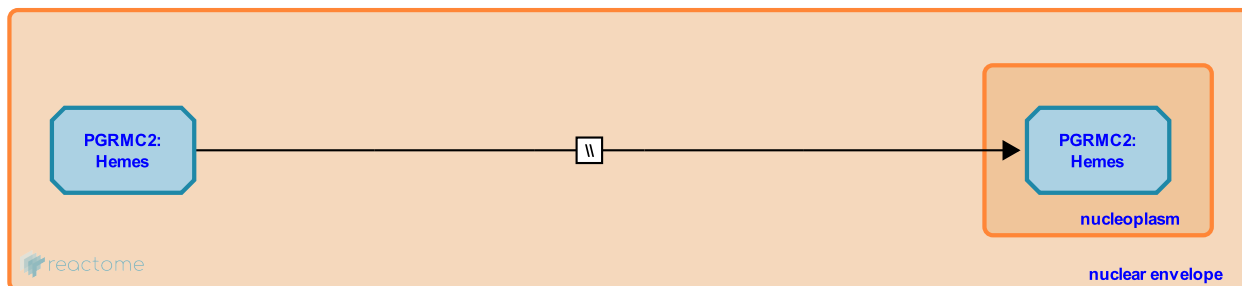## PGRMC2:Hemes translocate to the nucleus ↗

Location: Heme signaling

Stable identifier: R-DME-9707606

Type: omitted

Compartments: nuclear envelope, nucleoplasm

Inferred from: PGRMC2:Hemes translocate to 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.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: PGRMC2 binds Hemes

Followed by: Hemes bind to BACH1:MAFK, PGRMC2:Hemes dissociates
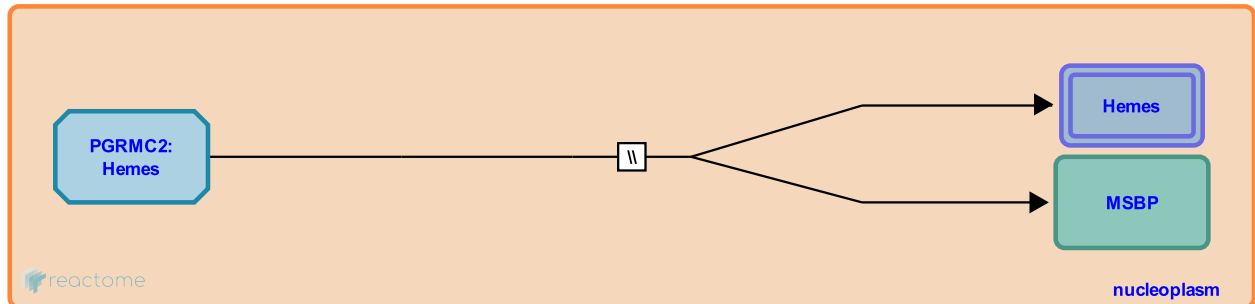
PGRMC2:Hemes dissociates ↗

Location: Heme signaling

Stable identifier: R-DME-9707856

Type: omitted

Compartments: nucleoplasm

Inferred from: PGRMC2:Hemes dissociates (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.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: PGRMC2:Hemes translocate to the nucleus
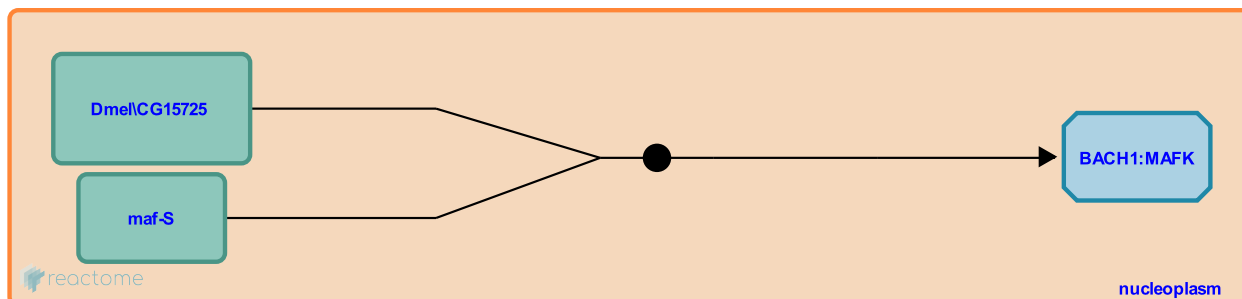
BACH1 binds MAFK ↗

Location: Heme signaling

Stable identifier: R-DME-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.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: Hemes bind to BACH1:MAFK

Hemes bind to BACH1:MAFK ↗
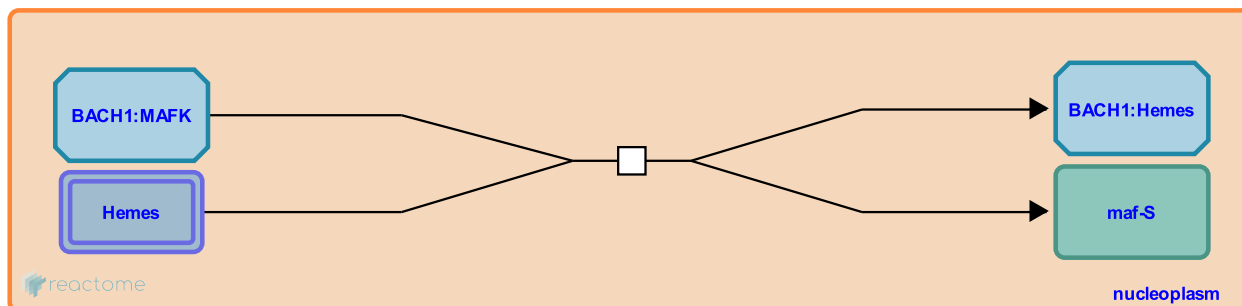
Location: Heme signaling

Stable identifier: R-DME-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.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: BACH1 binds MAFK, PGRMC2:Hemes translocate to the nucleus

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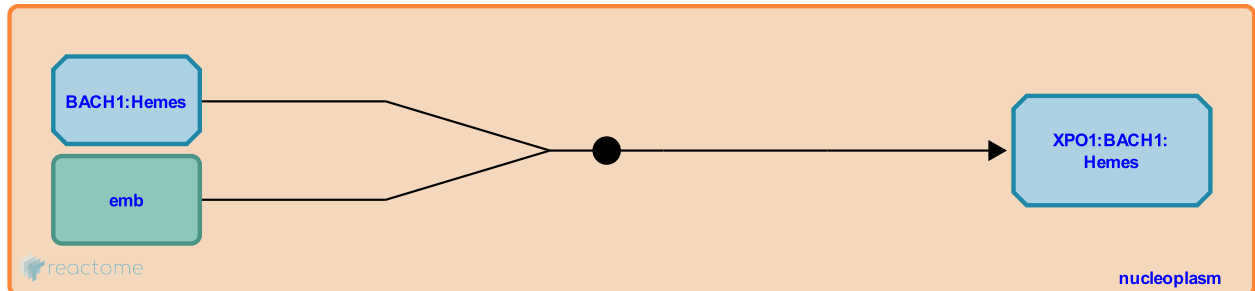
XPO1 (CRM1) binds to BACH1:Hemes ↗

Location: Heme signaling

Stable identifier: R-DME-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.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Hemes bind to BACH1:MAFK

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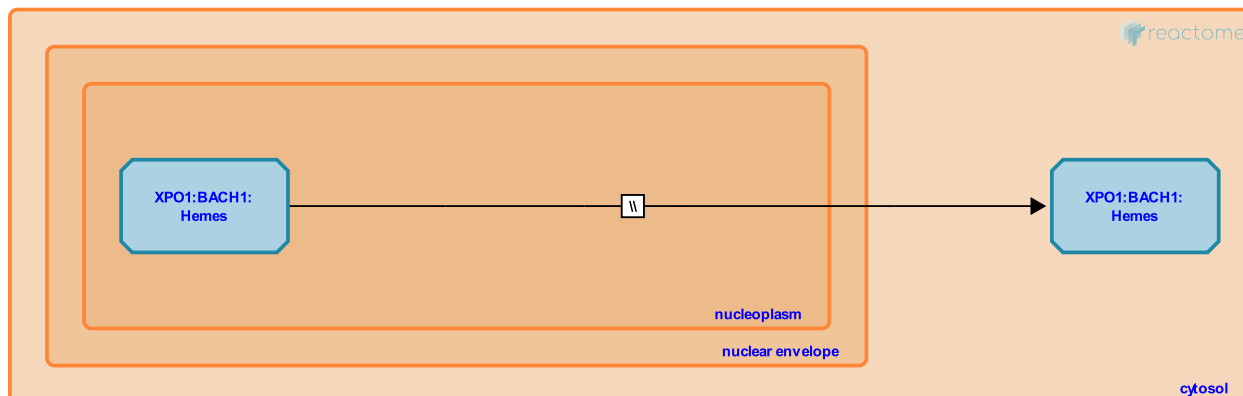
XPO1:BACH1:Hemes are transported out of the nucleus ↗

Location: Heme signaling

Stable identifier: R-DME-9708423

Type: omitted

Compartments: nucleoplasm, cytosol

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.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

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

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