Iron uptake and transport

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.

18/05/2024

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.

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

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 2 pathways and 20 reactions (see Table of Contents)

Iron uptake and transport ↗

Stable identifier: R-BTA-917937

Inferred from: Iron uptake and transport (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

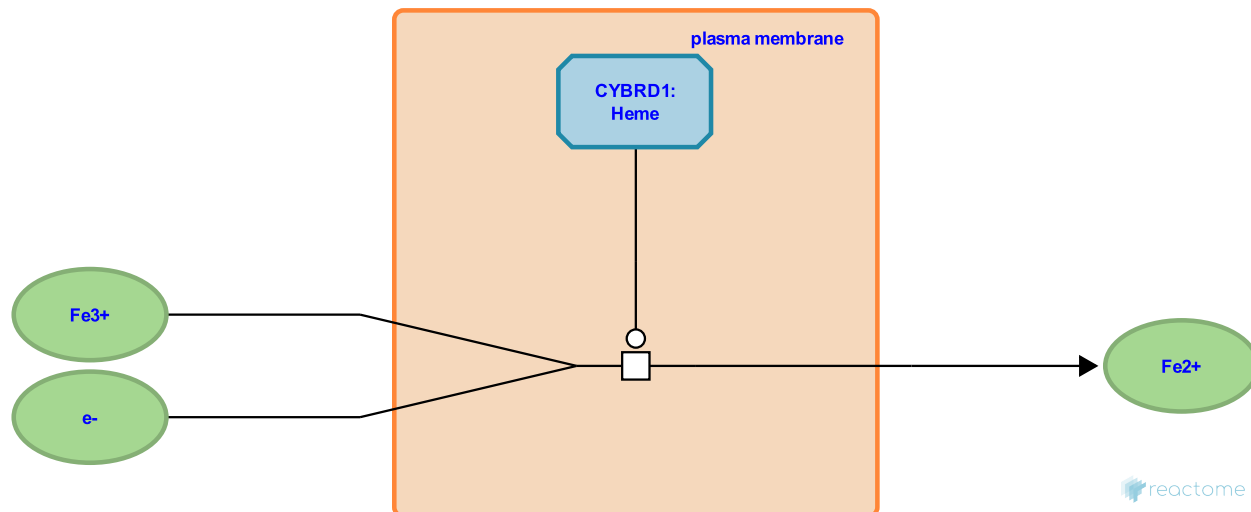# CYBRD1:Heme reduces Fe3+ to Fe2+ ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-917805

Type: transition

Compartments: plasma membrane, extracellular region

Inferred from: CYBRD1:Heme reduces Fe3+ to Fe2+ (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: SLC11A2 cotransports Fe2+, H+ from extracellular region to cytosol

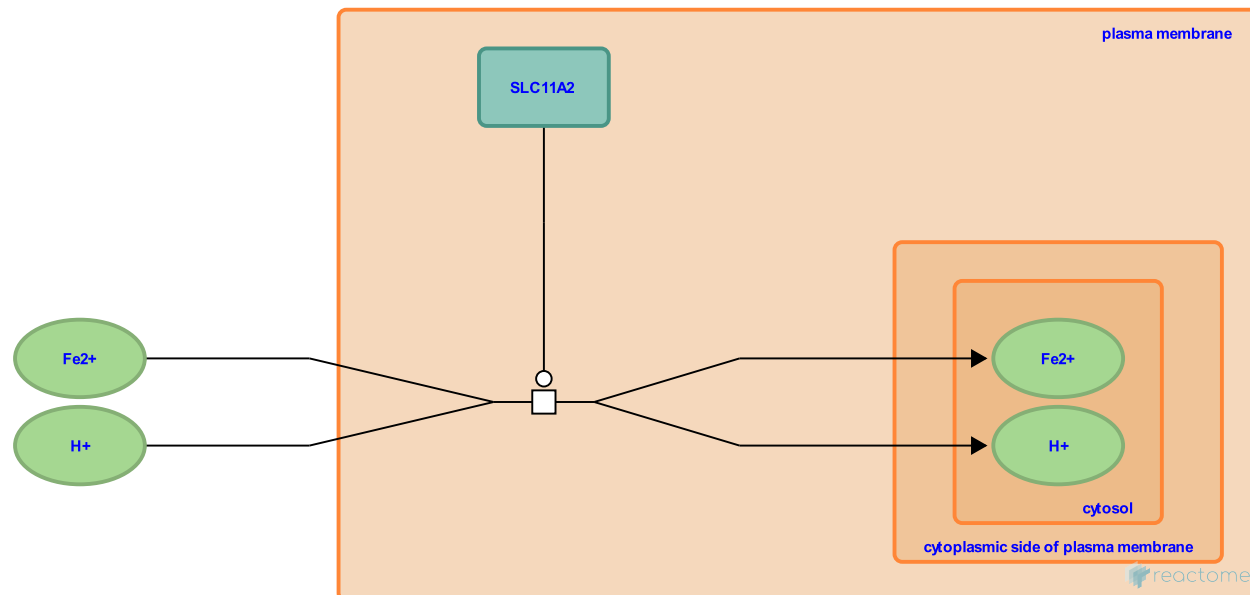# SLC11A2 cotransports Fe2+, H+ from extracellular region to cytosol ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-435349

Type: transition

Compartments: plasma membrane

Inferred from: SLC11A2 cotransports Fe2+, H+ 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.

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Preceded by: CYBRD1:Heme reduces Fe3+ to Fe2+

Followed by: SLC40A1:CP:6Cu2+ transports Fe2+ from cytosol to extracellular region

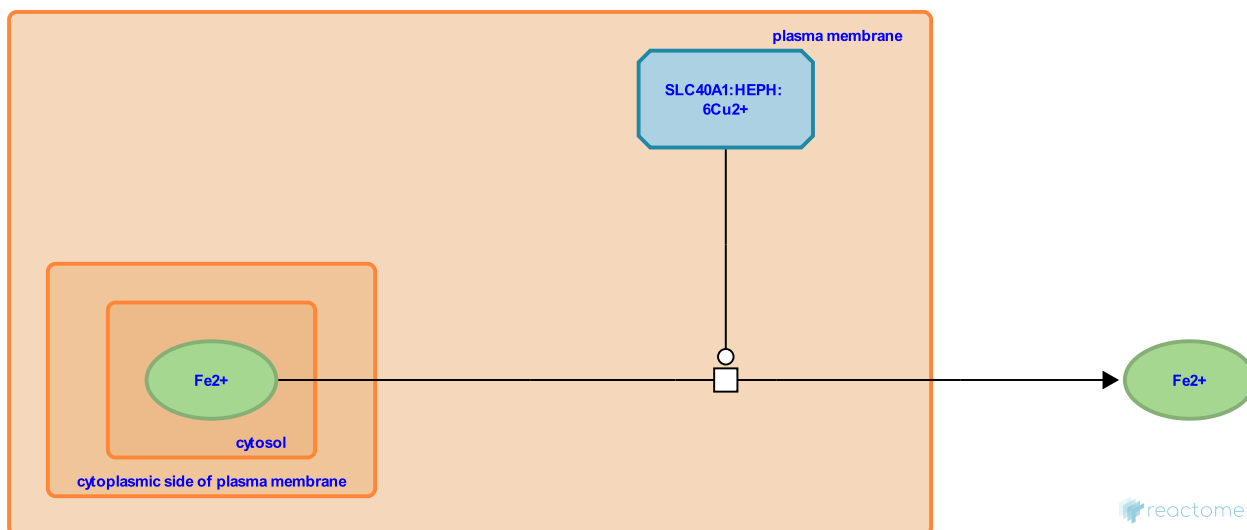# SLC40A1:HEPH:6Cu2+ transports Fe2+ from cytosol to extracellular region ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-442368

Type: transition

Compartments: plasma membrane

Inferred from: SLC40A1:HEPH:6Cu2+ transports Fe2+ from cytosol to extracellular region (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: SLC40A1:HEPH:6Cu2+ oxidises 4Fe2+ to 4Fe3+

SLC40A1:CP:6Cu2+ transports Fe2+ from cytosol to extracellular region ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-904830

Type: transition

Compartments: plasma membrane

Inferred from: SLC40A1:CP:6Cu2+ transports Fe2+ from cytosol to extracellular region (Homo sapiens)
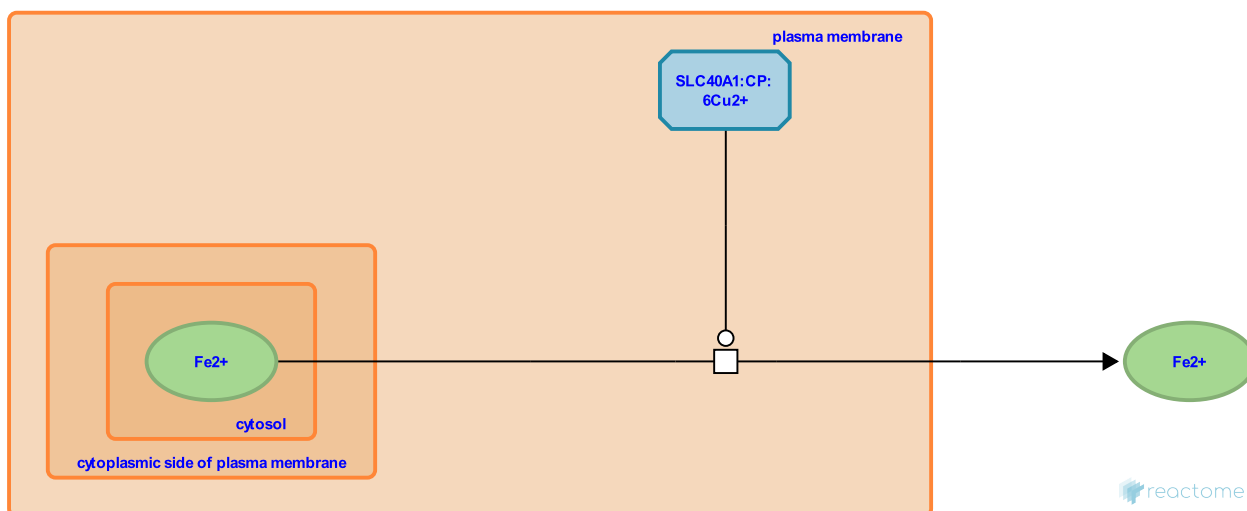
This event has been computationally inferred from an event that has been demonstrated in another species.

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: SLC11A2 cotransports Fe2+, H+ from extracellular region to cytosol

SLC40A1:CP:6Cu2+ oxidises Fe2+ to Fe3+ ↗
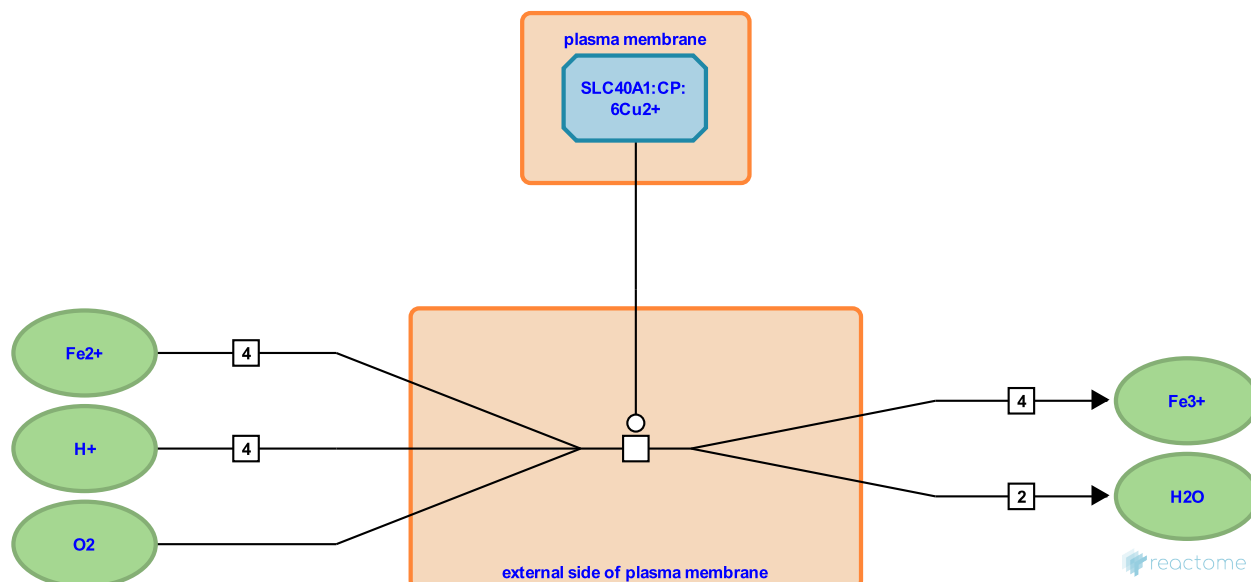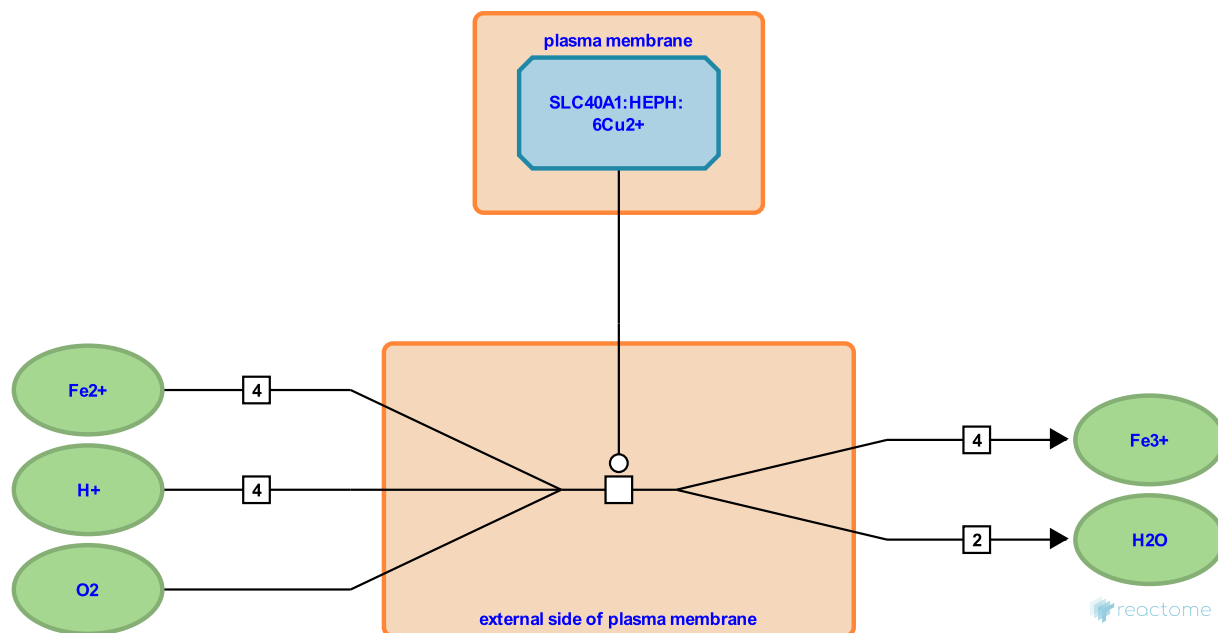
Location: Iron uptake and transport

Stable identifier: R-BTA-917891

Type: transition

Compartments: external side of plasma membrane

Inferred from: SLC40A1:CP:6Cu2+ oxidises Fe2+ to Fe3+ (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: apoTF binds 2Fe3+ to form holoTF

SLC40A1:HEPH:6Cu2+ oxidises 4Fe2+ to 4Fe3+ ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-917933

Type: transition

Compartments: external side of plasma membrane

Inferred from: SLC40A1:HEPH:6Cu2+ oxidises 4Fe2+ to 4Fe3+ (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: SLC40A1:HEPH:6Cu2+ transports Fe2+ from cytosol to extracellular region

Followed by: apoTF binds 2Fe3+ to form holoTF
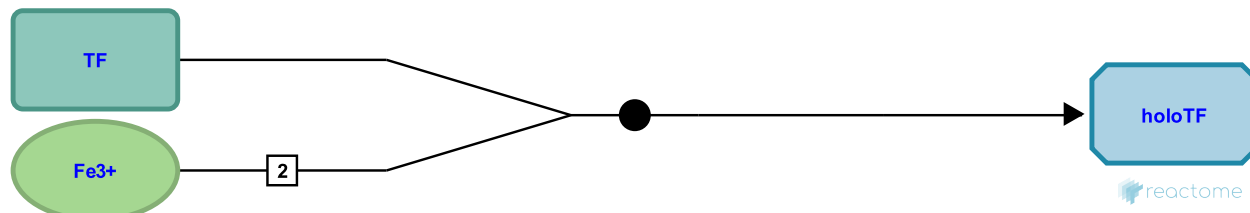
apoTF binds 2Fe3+ to form holoTF ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-917888

Type: binding

Compartments: extracellular region

Inferred from: apoTF binds 2Fe3+ to form holoTF (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: SLC40A1:HEPH:6Cu2+ oxidises 4Fe2+ to 4Fe3+, SLC40A1:CP:6Cu2+ oxidises Fe2+ to Fe3+

Followed by: Transferrin endocytosis and recycling

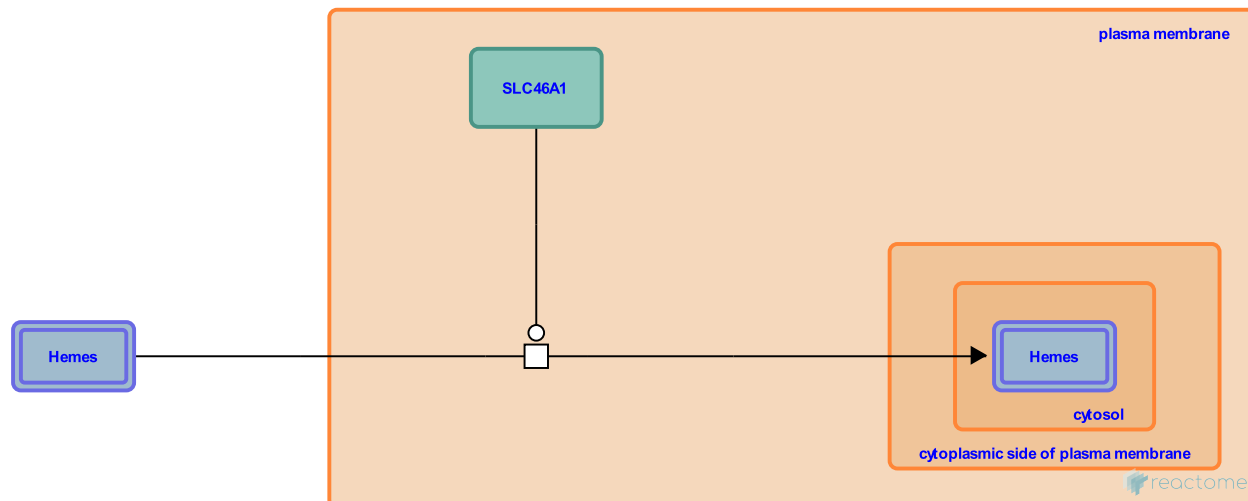# SLC46A1 transports hemes from extracellular region to cytosol ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-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
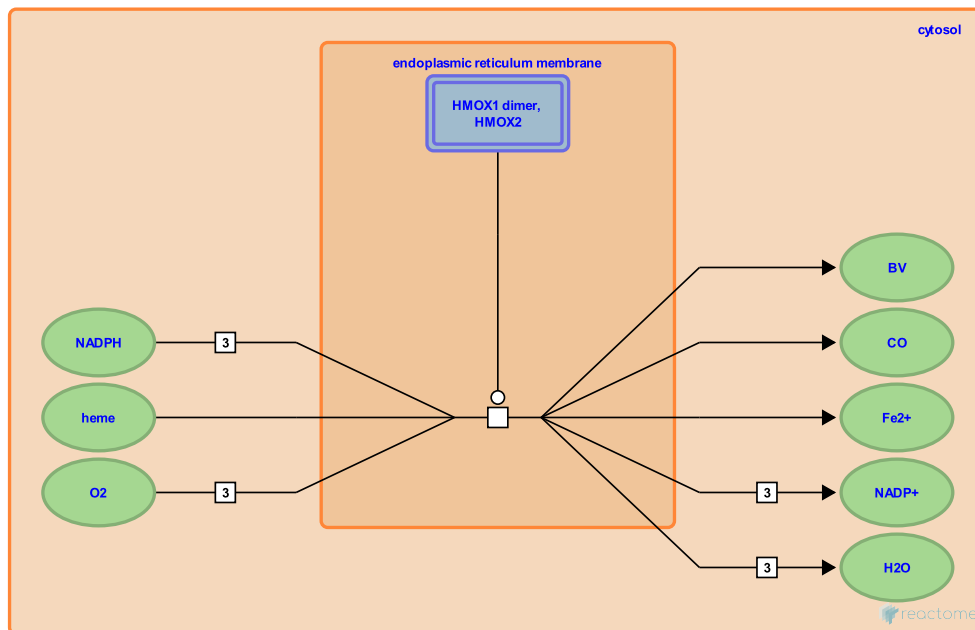
HMOX1 dimer, HMOX2 cleave heme ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-189398

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: HMOX1 dimer, HMOX2 cleave heme (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

FLVCR1-1 transports heme from cytosol to extracellular region ↗
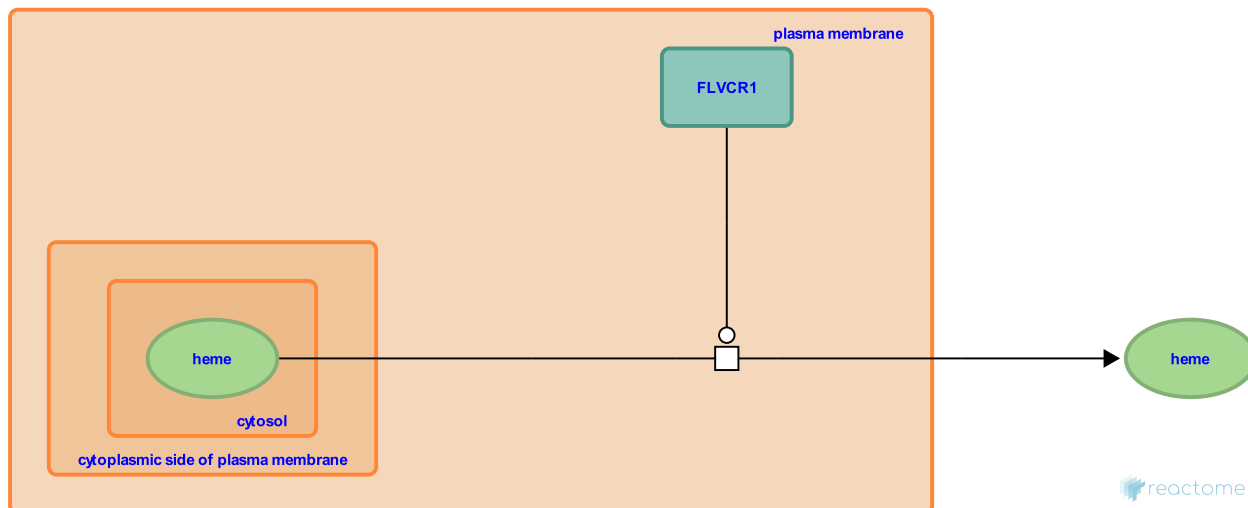
Location: Iron uptake and transport

Stable identifier: R-BTA-917892

Type: transition

Compartments: plasma membrane

Inferred from: FLVCR1-1 transports heme from cytosol to extracellular region (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.
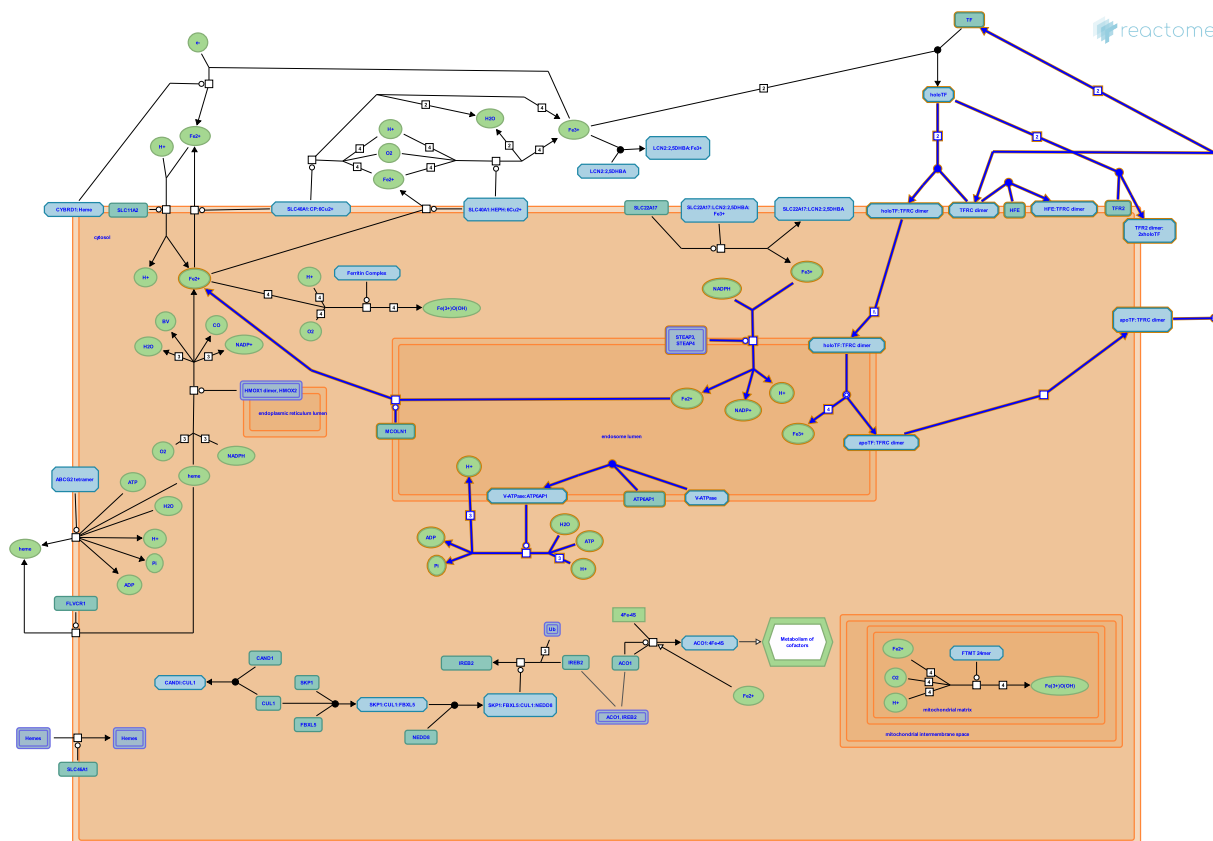
More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

ABCG2 tetramer transports heme from cytosol to extracellular region ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-917979

Type: transition

Compartments: plasma membrane

Inferred from: ABCG2 tetramer transports heme from cytosol to extracellular region (Homo sapiens)
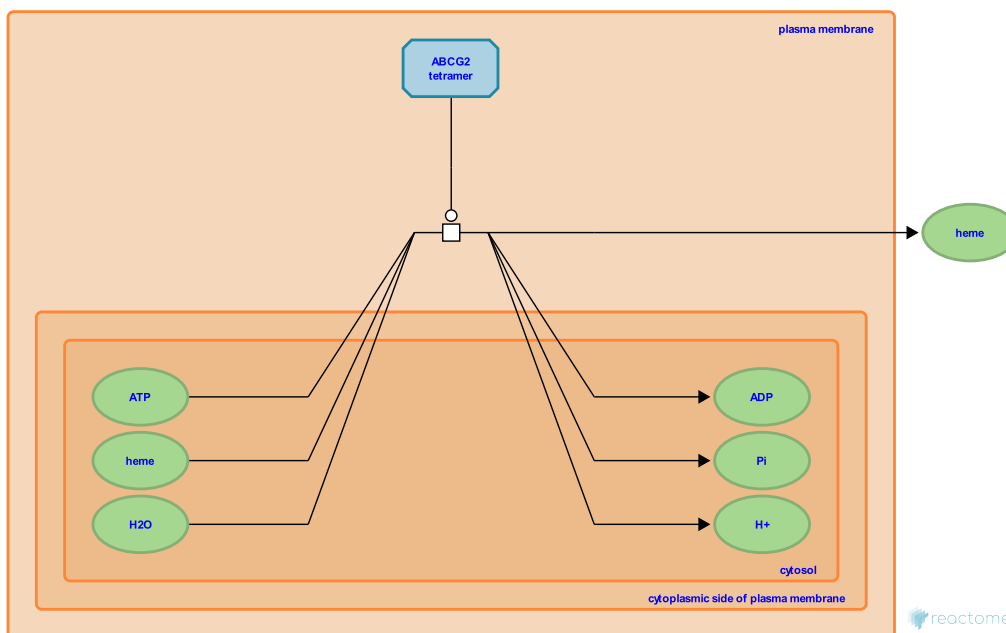
This event has been computationally inferred from an event that has been demonstrated in another species.

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

Transferrin endocytosis and recycling ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-917977

Inferred from: Transferrin endocytosis and recycling (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

Ferritin Complex oxidises 4Fe2+ to Fe(3+)O(OH) ↗
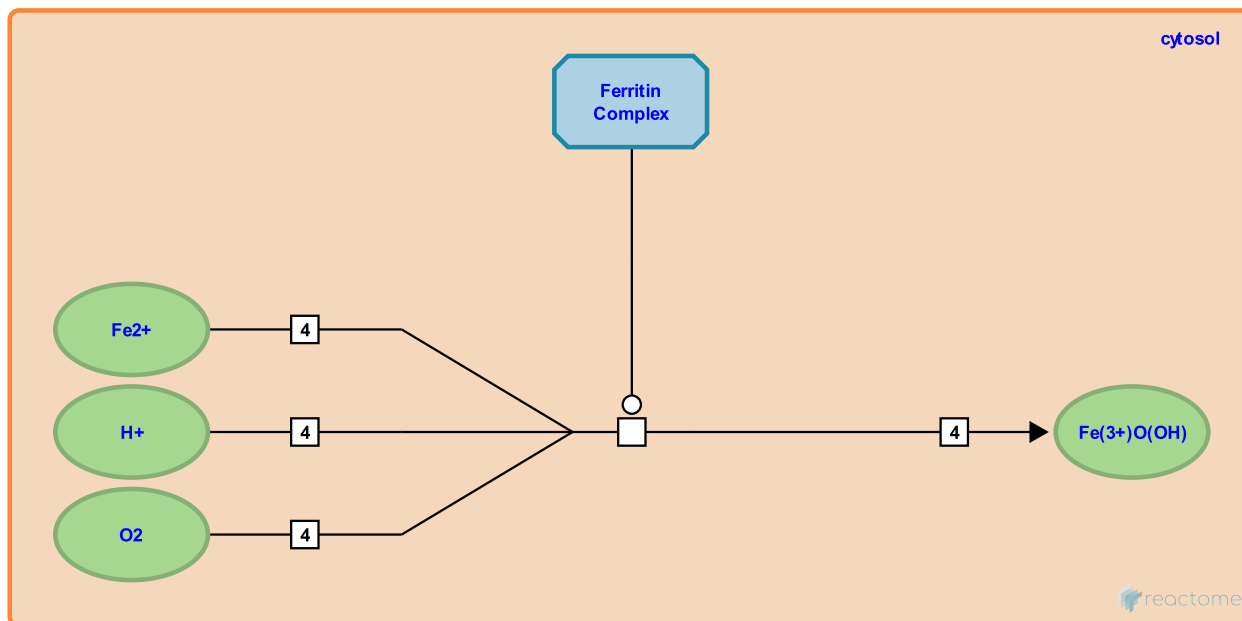
Location: Iron uptake and transport

Stable identifier: R-BTA-1562626

Type: transition

Compartments: cytosol

Inferred from: Ferritin Complex oxidises 4Fe2+ to Fe(3+)O(OH) (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
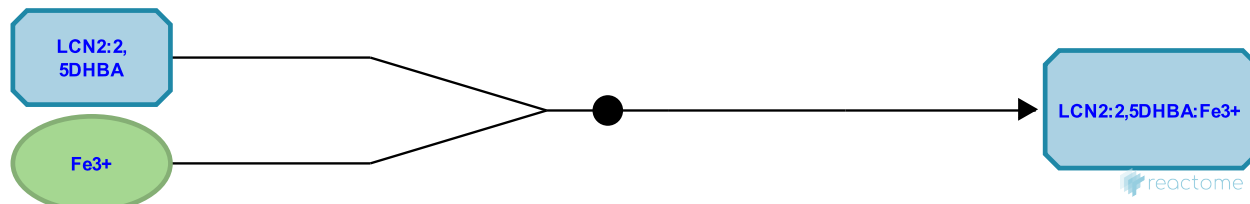
LCN2:2,5DHBA binds Fe3+ ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-5229273

Type: binding

Compartments: extracellular region

Inferred from: LCN2:2,5DHBA binds Fe3+ (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

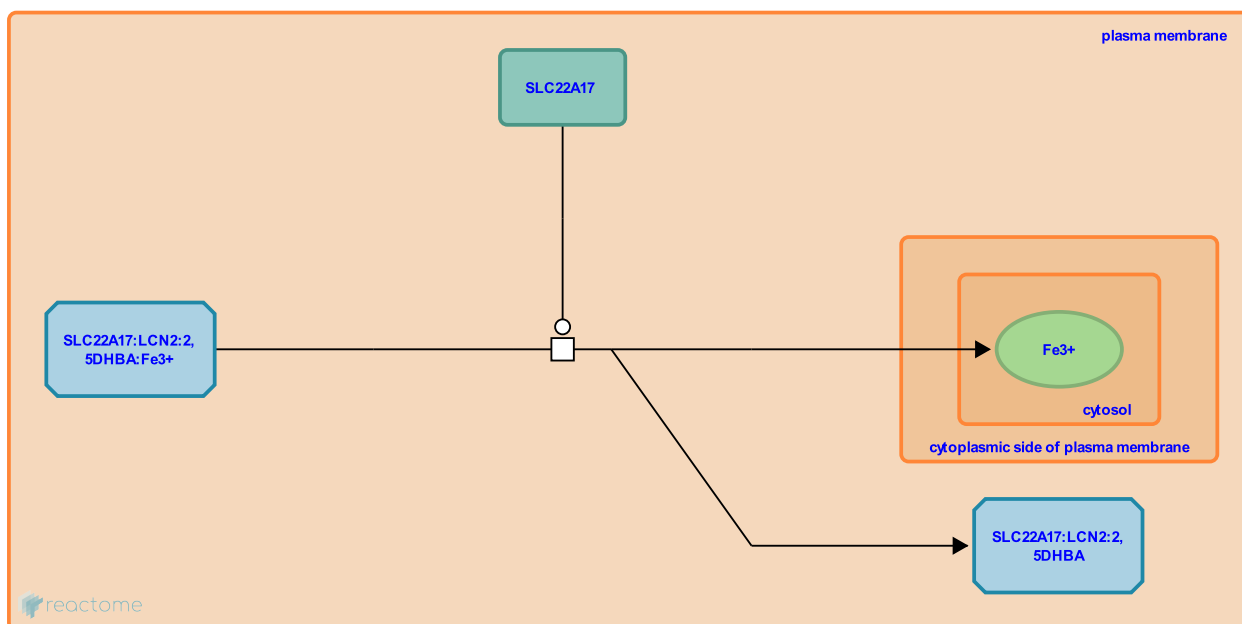# Fe3+ dissociates from SLC22A17:LCN2:2,5DHBA ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-5671707

Type: transition

Compartments: plasma membrane, extracellular region, cytosol

Inferred from: Fe3+ dissociates from SLC22A17:LCN2:2,5DHBA (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

ACO1 binds 4Fe-4S ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-5690873

Type: transition

Compartments: cytosol

Inferred from: ACO1 binds 4Fe-4S (Homo sapiens)
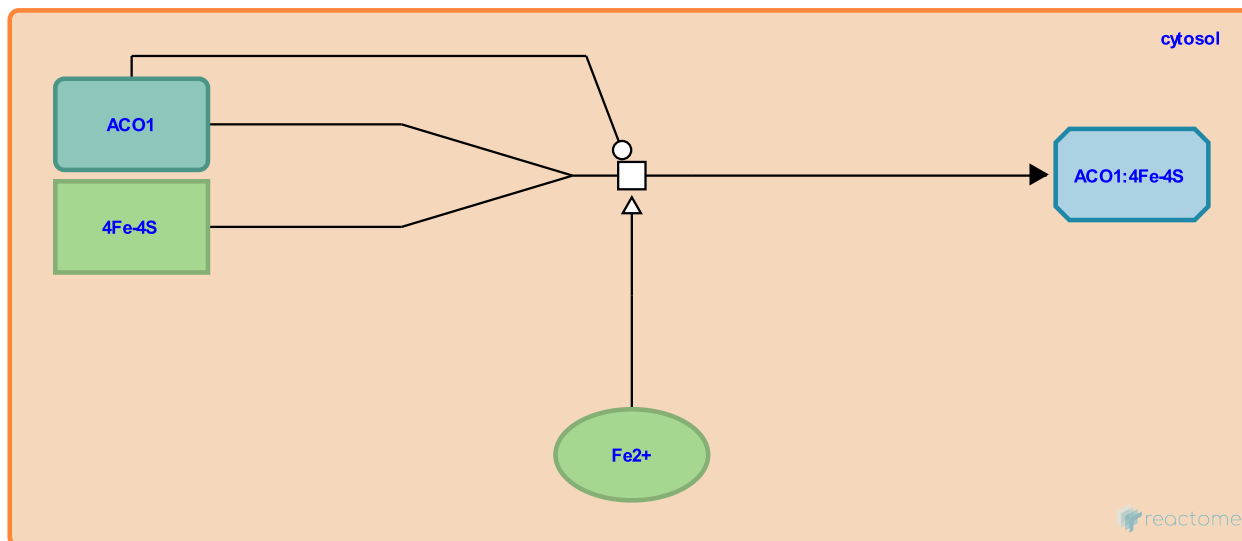
This event has been computationally inferred from an event that has been demonstrated in another species.

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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CANDI binds CUL1 ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-5691131

Type: binding

Compartments: cytosol

Inferred from: CANDI binds CUL1 (Homo sapiens)
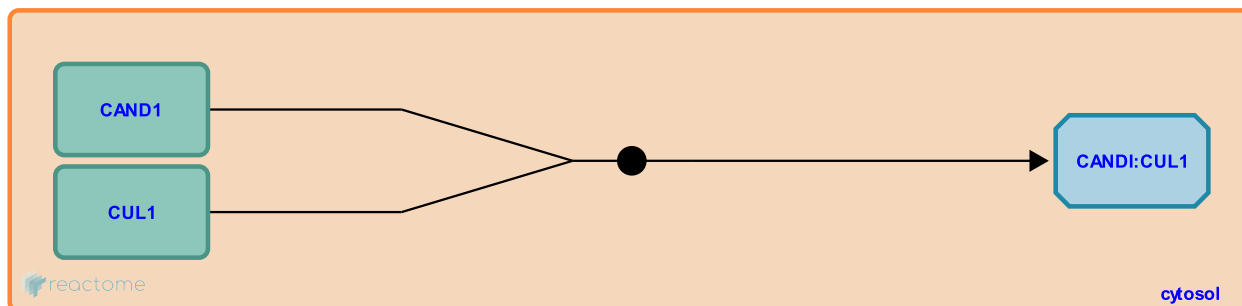
This event has been computationally inferred from an event that has been demonstrated in another species.

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
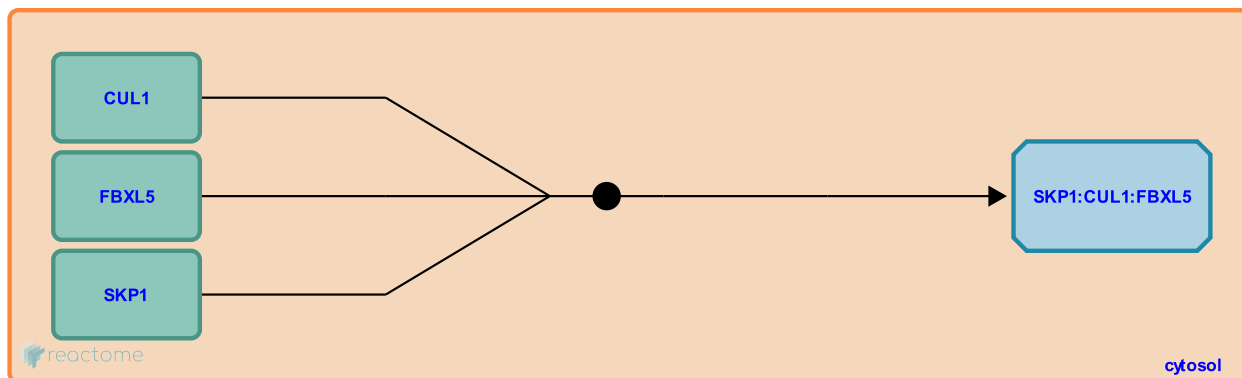
CUL1, SKP1, FBXL5 bind ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-5691167

Type: binding

Compartments: cytosol

Inferred from: CUL1, SKP1, FBXL5 bind (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: NEDD8 binds CUL1 (in SKP1:CUL1:FXBL5)

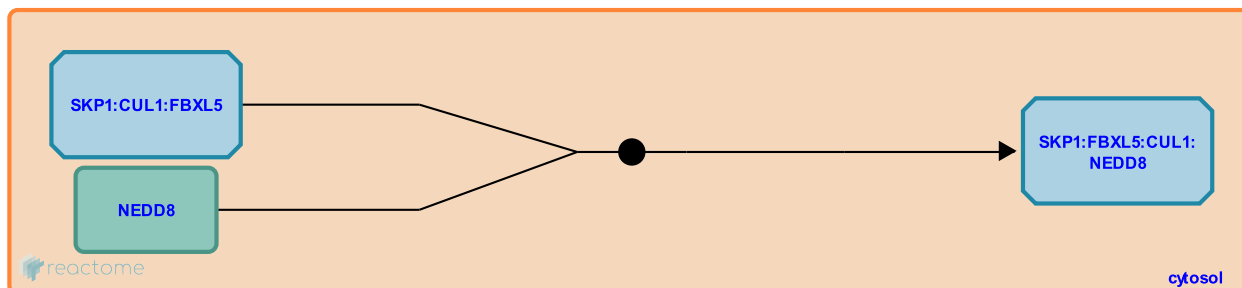# NEDD8 binds CUL1 (in SKP1:CUL1:FXBL5) ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-5691176

Type: binding

Compartments: cytosol

Inferred from: NEDD8 binds CUL1 (in SKP1:CUL1:FXBL5) (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: CUL1, SKP1, FBXL5 bind

Followed by: SKP1:FBXL5:CUL1:NEDD8 ubiquitinylates IREB2
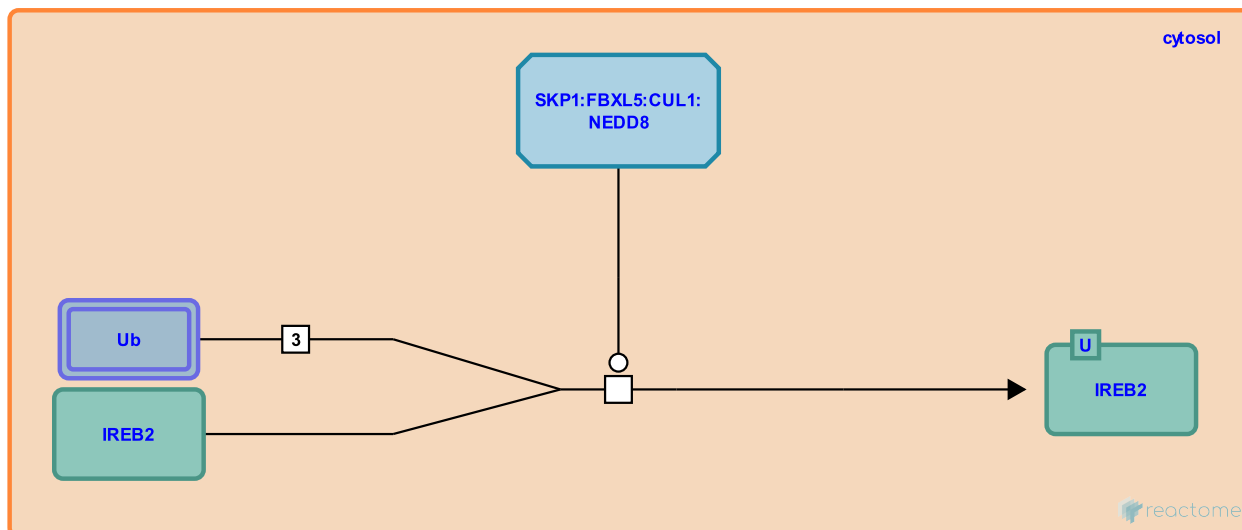
SKP1:FBXL5:CUL1:NEDD8 ubiquitinylates IREB2 ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-5691108

Type: transition

Compartments: cytosol

Inferred from: SKP1:FBXL5:CUL1:NEDD8 ubiquitinylates IREB2 (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: NEDD8 binds CUL1 (in SKP1:CUL1:FXBL5)
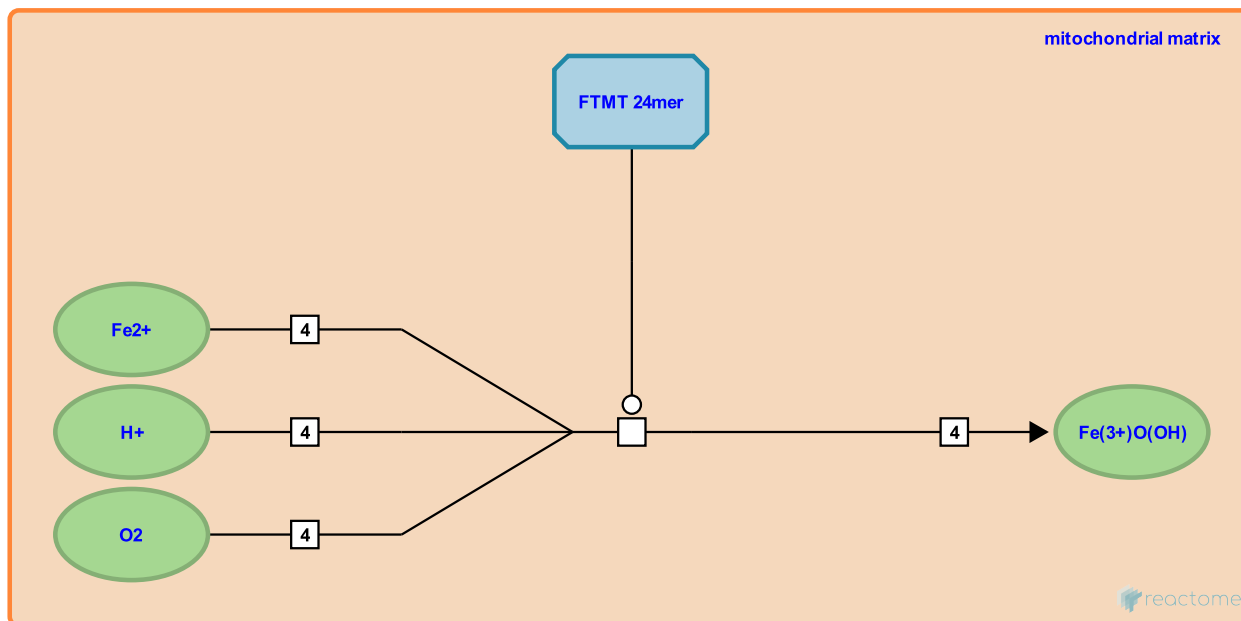
FTMT 24mer oxidises 4Fe2+ to 4Fe(3+)O(OH) ↗

Location: Iron uptake and transport

Stable identifier: R-BTA-5691107

Type: transition

Compartments: mitochondrial matrix

Inferred from: FTMT 24mer oxidises 4Fe2+ to 4Fe(3+)O(OH) (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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