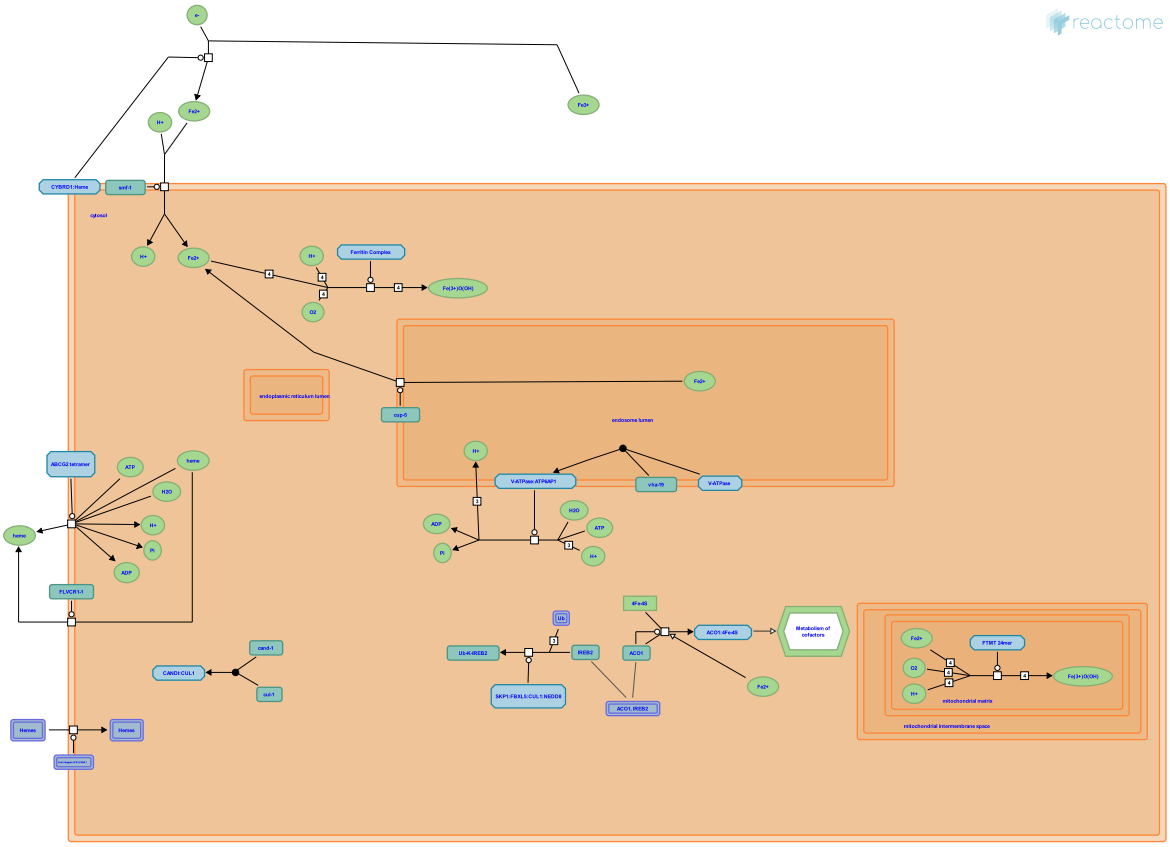
Iron uptake and transport



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

04/05/2024

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. ↗

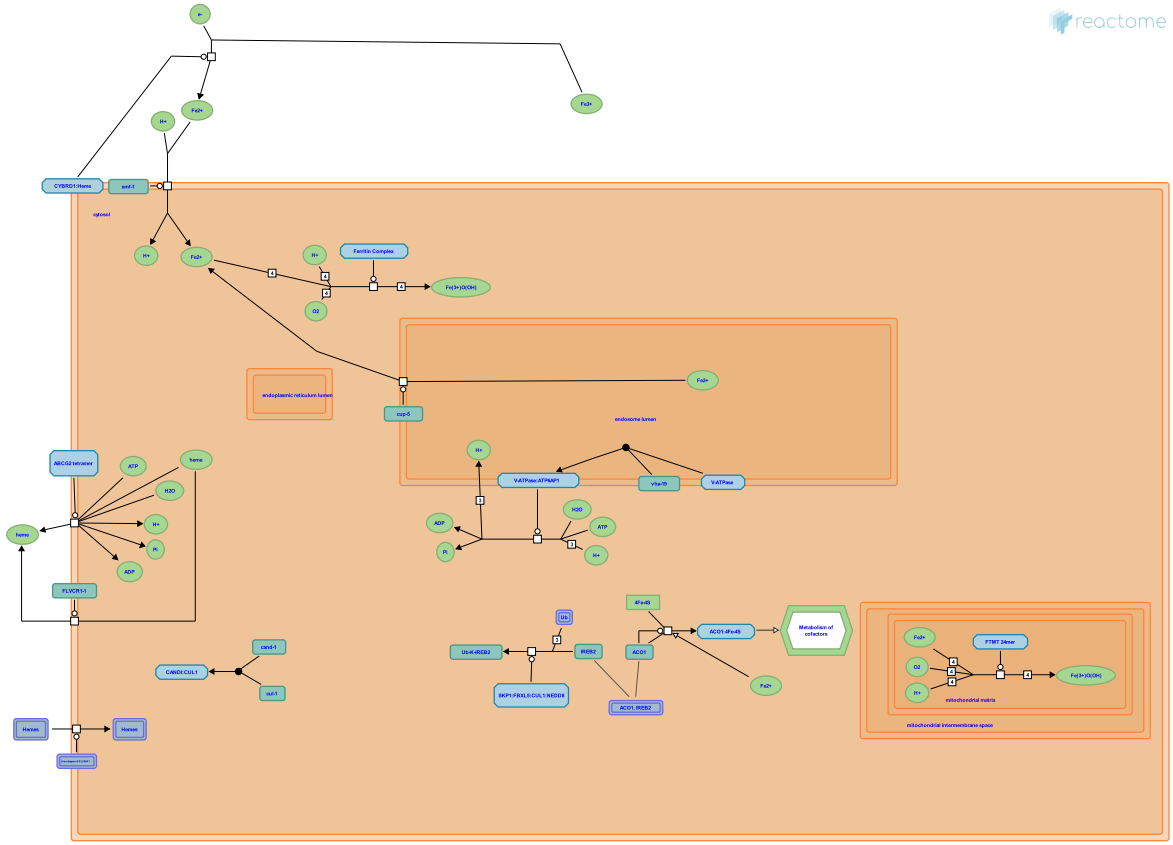
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Iron uptake and transport ↗

Stable identifier: R-CEL-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+ ↗

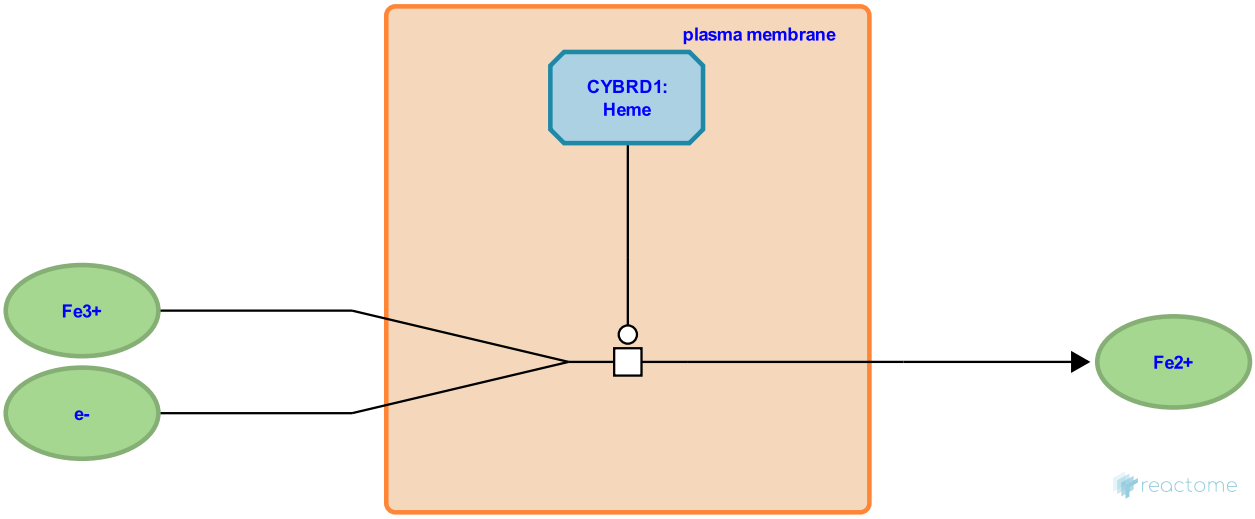
Location: Iron uptake and transport

Stable identifier: R-CEL-917805

Type: transition

Compartments: plasma membrane, extracellular region

Inferred from: CYBRD1:Heme reduces Fe3+ to Fe2+ (Homo sapiens)



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

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

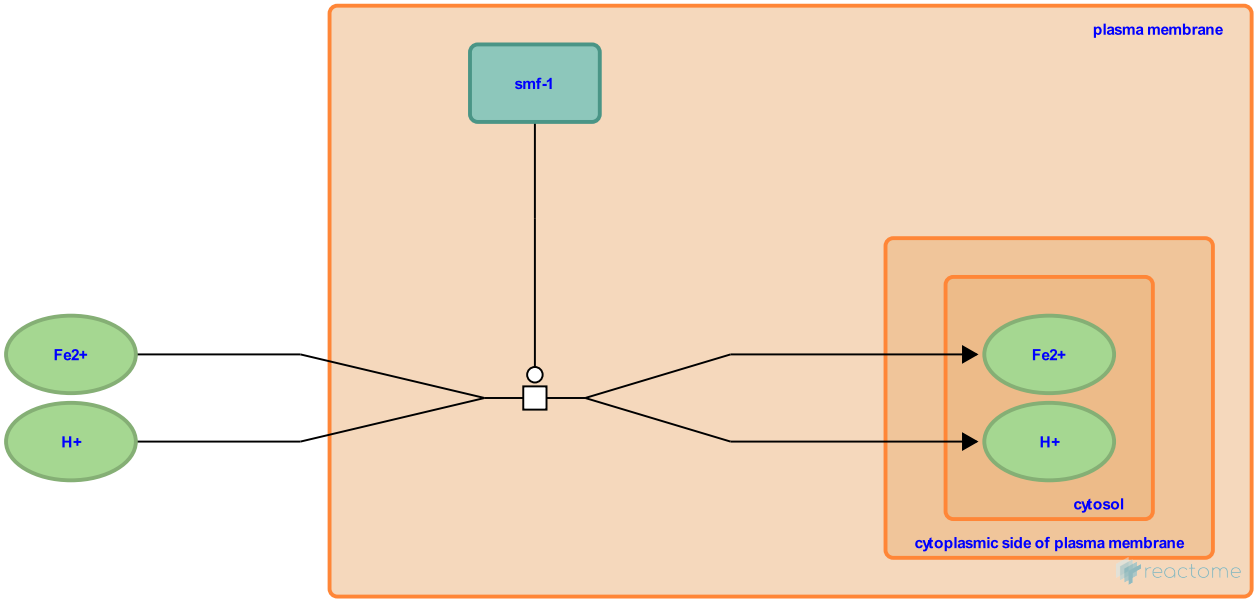
Location: Iron uptake and transport

Stable identifier: R-CEL-435349

Type: transition

Compartments: plasma membrane

Inferred from: SLC11A2 cotransports Fe2+, H+ from extracellular region to cytosol (Homo sapiens)



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

SLC46A1 transports hemes from extracellular region to cytosol ↗

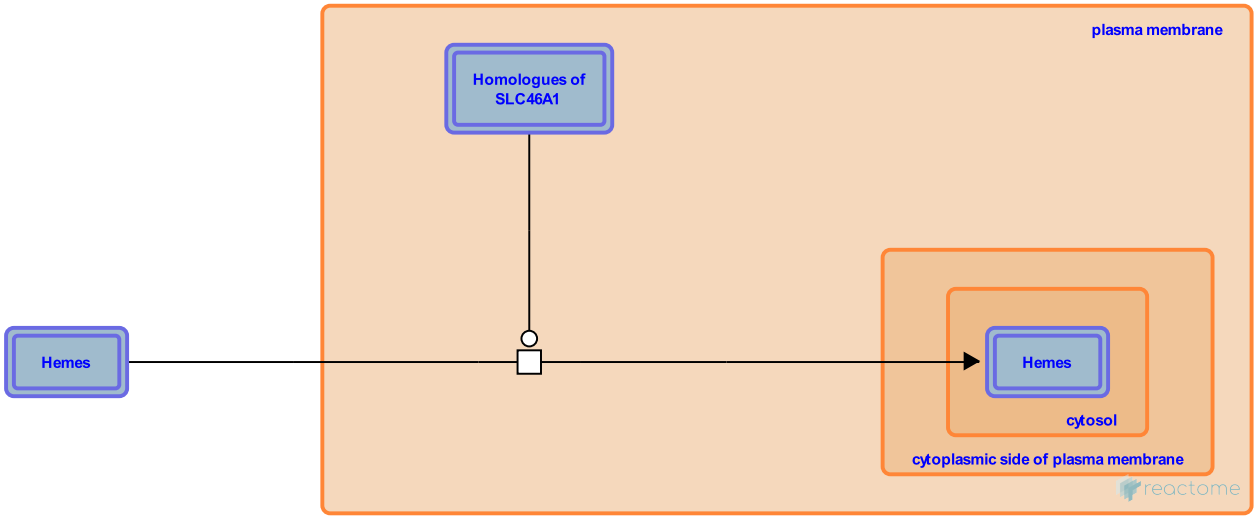
Location: Iron uptake and transport

Stable identifier: R-CEL-917870

Type: transition

Compartments: plasma membrane

Inferred from: SLC46A1 transports hemes from extracellular region to cytosol (Homo sapiens)



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FLVCR1-1 transports heme from cytosol to extracellular region ↗

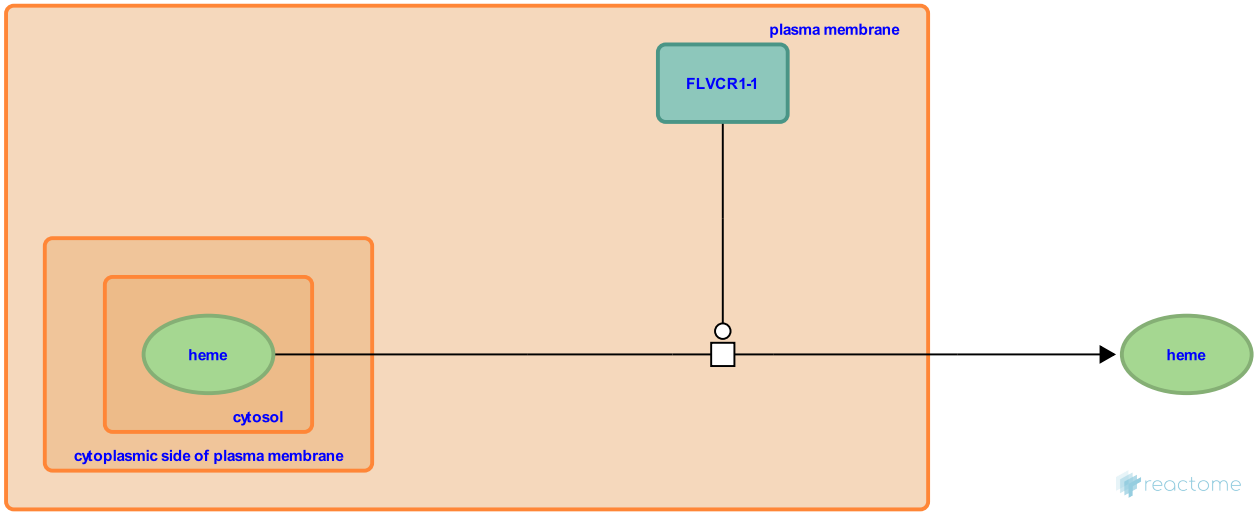
Location: Iron uptake and transport

Stable identifier: R-CEL-917892

Type: transition

Compartments: plasma membrane

Inferred from: FLVCR1-1 transports heme from cytosol to extracellular region (Homo sapiens)



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ABCG2 tetramer transports heme from cytosol to extracellular region ↗

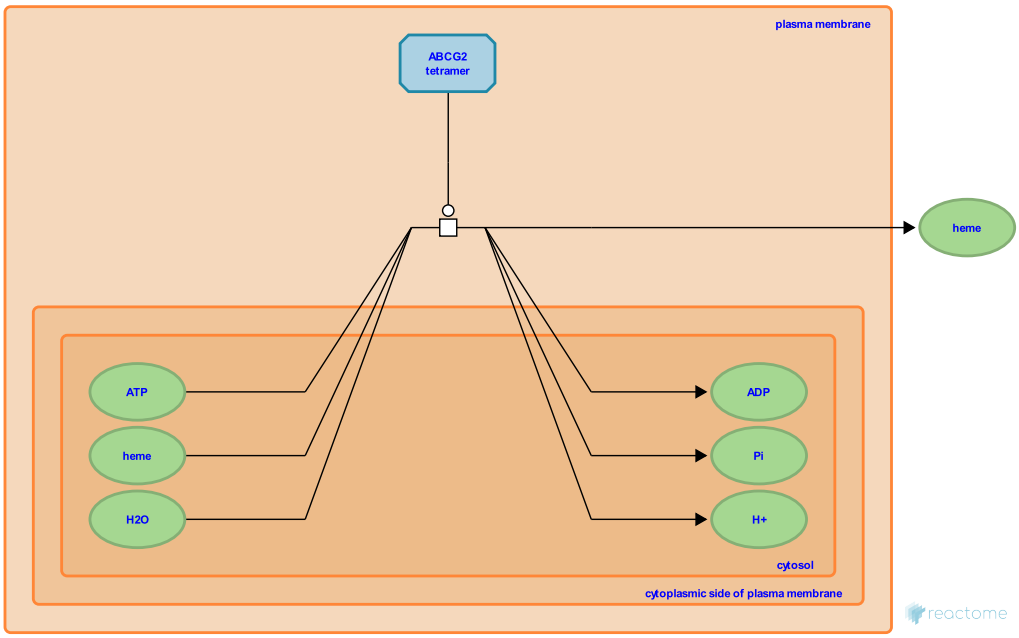
Location: Iron uptake and transport

Stable identifier: R-CEL-917979

Type: transition

Compartments: plasma membrane

Inferred from: ABCG2 tetramer transports heme from cytosol to extracellular region (Homo sapiens)



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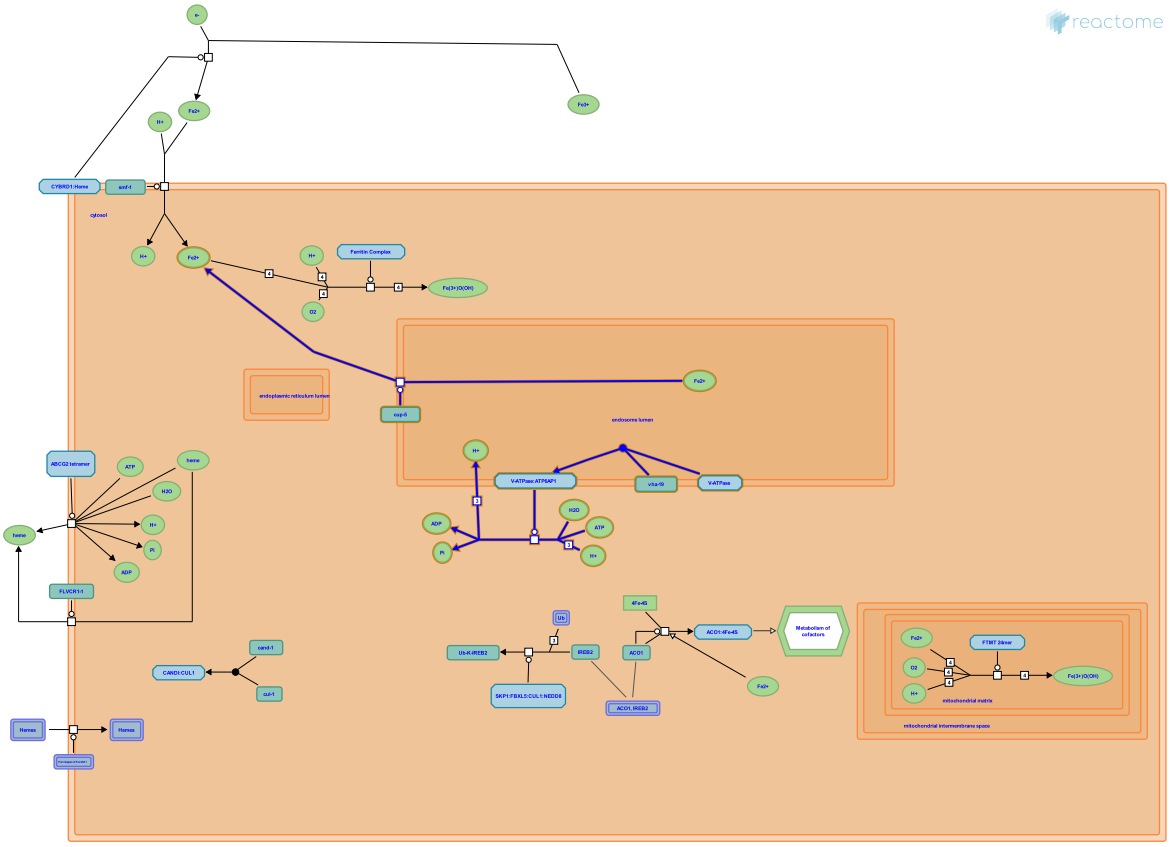
Transferrin endocytosis and recycling ↗

Location: Iron uptake and transport

Stable identifier: R-CEL-917977

Inferred from: Transferrin endocytosis and recycling (Homo sapiens)



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Ferritin Complex oxidises 4Fe2+ to Fe(3+)O(OH) ↗

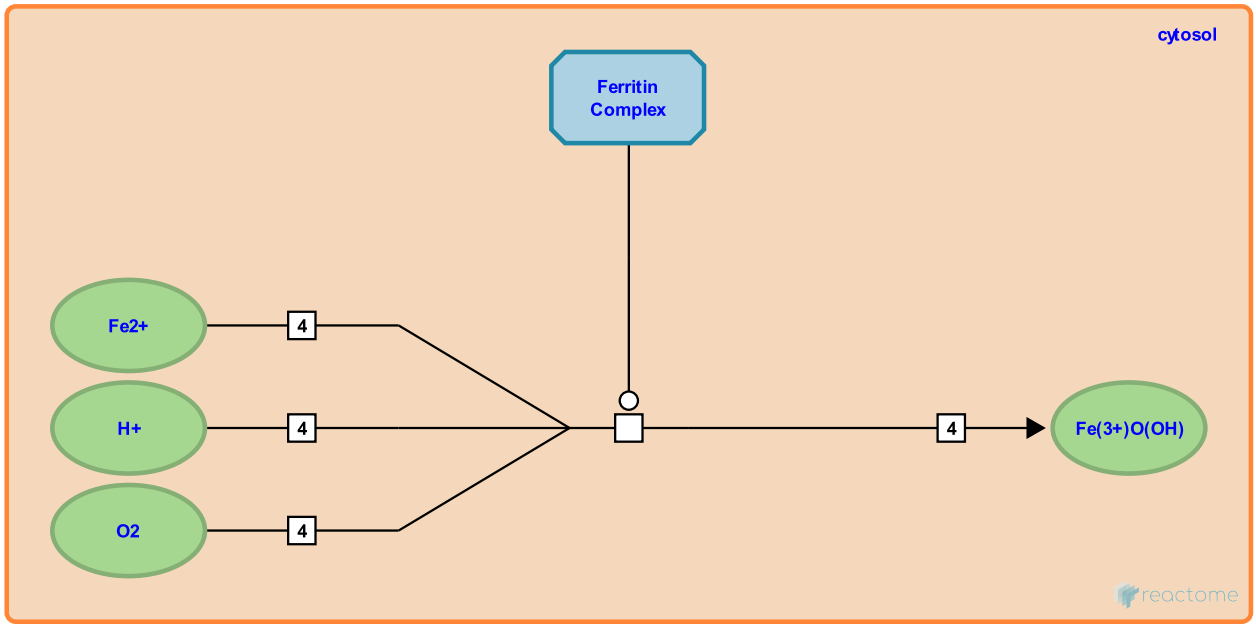
Location: Iron uptake and transport

Stable identifier: R-CEL-1562626

Type: transition

Compartments: cytosol

Inferred from: Ferritin Complex oxidises 4Fe2+ to Fe(3+)O(OH) (Homo sapiens)



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ACO1 binds 4Fe-4S ↗

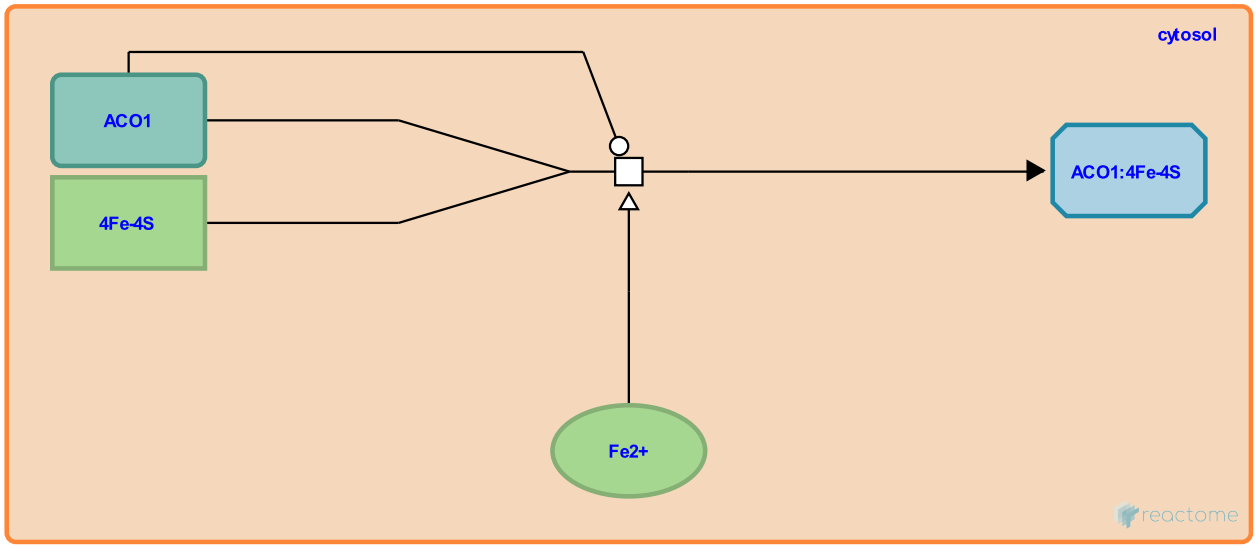
Location: Iron uptake and transport

Stable identifier: R-CEL-5690873

Type: transition

Compartments: cytosol

Inferred from: ACO1 binds 4Fe-4S (Homo sapiens)



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

CANDI binds CUL1 ↗

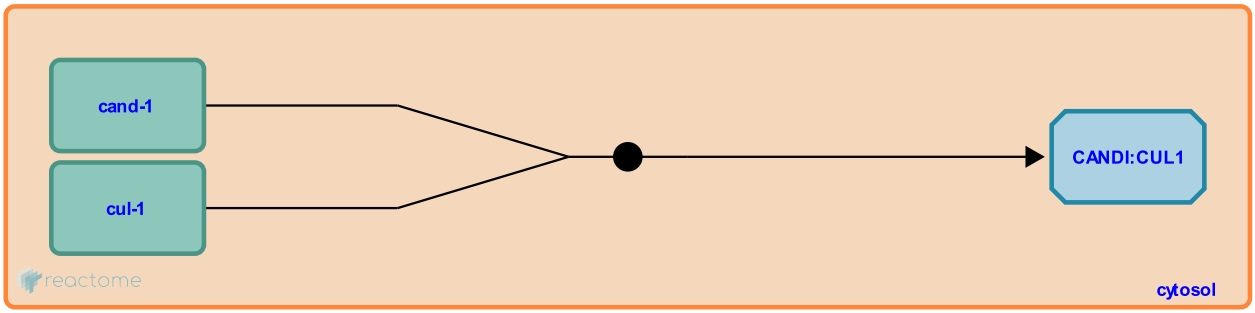
Location: Iron uptake and transport

Stable identifier: R-CEL-5691131

Type: binding

Compartments: cytosol

Inferred from: CANDI binds CUL1 (Homo sapiens)



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SKP1:FBXL5:CUL1:NEDD8 ubiquitinylates IREB2 ↗

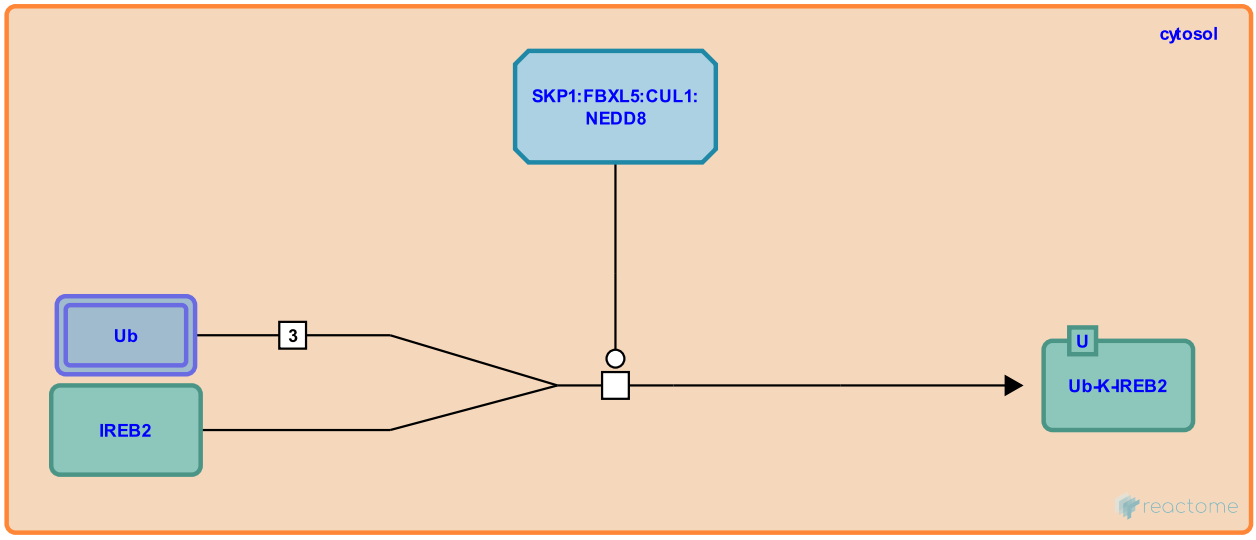
Location: Iron uptake and transport

Stable identifier: R-CEL-5691108

Type: transition

Compartments: cytosol

Inferred from: SKP1:FBXL5:CUL1:NEDD8 ubiquitinylates IREB2 (Homo sapiens)



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FTMT 24mer oxidises 4Fe2+ to 4Fe(3+)O(OH) ↗

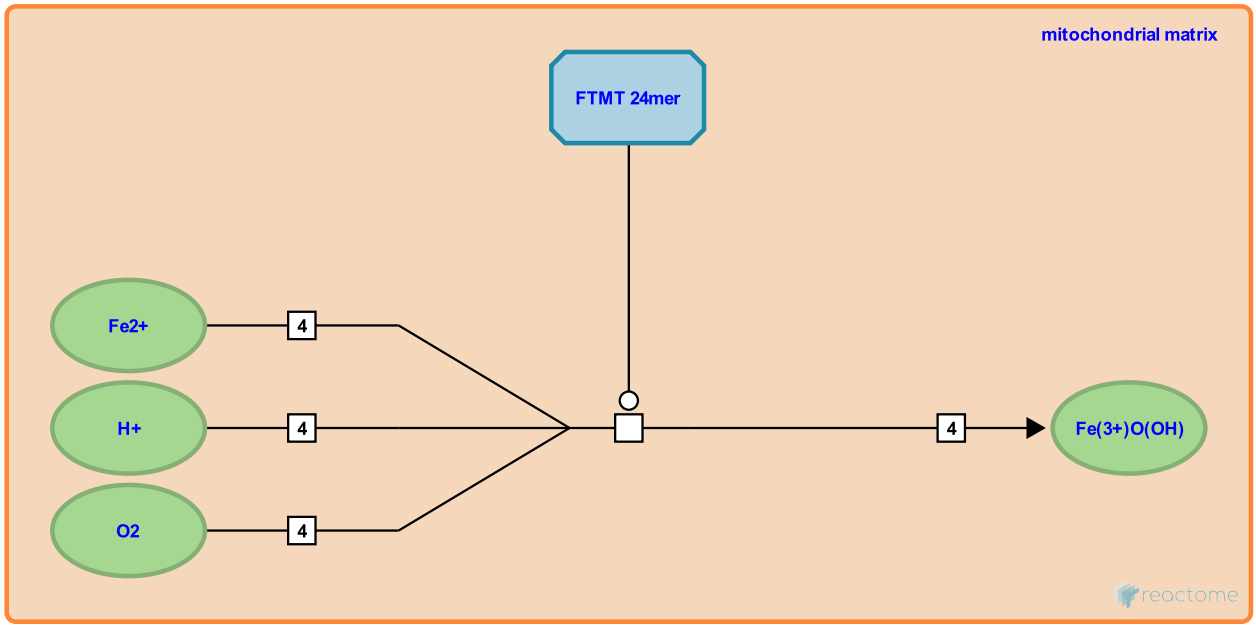
Location: Iron uptake and transport

Stable identifier: R-CEL-5691107

Type: transition

Compartments: mitochondrial matrix

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



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