

SLC46A1 transports hemes from extracellular region to cytosol

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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

- 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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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: 77

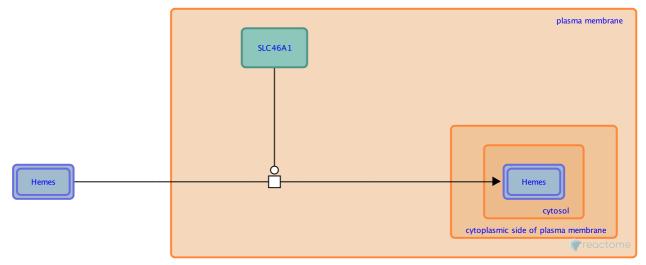
This document contains 1 reaction (see Table of Contents)

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Stable identifier: R-HSA-917870

Type: transition

Compartments: plasma membrane



Uptake of iron from meat happens mostly in the form of ferriheme (FeHM), and via the same transporter that is used for folate. The process is more effective than taking up iron ions (Shayeghi M et al, 2005). In general, heme transporters do not differentiate between ferroheme and ferriheme.

Literature references

Shayeghi, M., Latunde-Dada, GO., Oakhill, JS., Laftah, AH., Takeuchi, K., Halliday, N. et al. (2005). Identification of an intestinal heme transporter. *Cell*, 122, 789-801. ↗

Editions

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