

LCN2:2,5DHBA binds Fe³⁺

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17/05/2024

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

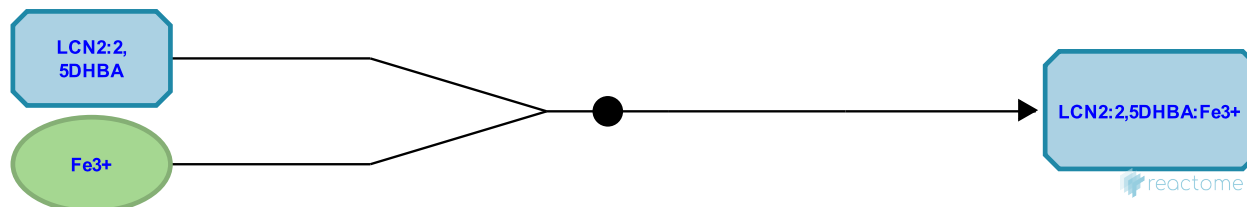
This document contains 1 reaction ([see Table of Contents](#))

LCN2:2,5DHBA binds Fe3+ [↗](#)

Stable identifier: R-HSA-5229273

Type: binding

Compartment: extracellular region



Neutrophil gelatinase associated lipocalin (LCN2, NGAL) is a member of the lipocalin superfamily that is involved in iron trafficking both in and out of cells. LCN2 binds iron via an association with 2,5 dihydroxybenzoic acid (2,5DHBA), a siderophore that shares structural similarities with bacterial enterobactin, and delivers or removes iron from the cell via interacting with different receptors, depending on cellular requirement (Goetz et al. 2002, Devireddy et al. 2010). LCN2 is a potent bacteriostatic agent in iron limiting conditions therefore it is proposed that LCN2 participates in the antibacterial iron depletion strategy of the innate immune system (Flo et al. 2004).

Literature references

Goetz, DH., Hart, DO., Green, MR., Devireddy, LR. (2010). A mammalian siderophore synthesized by an enzyme with a bacterial homolog involved in enterobactin production. *Cell*, 141, 1006-17. [↗](#)

Raymond, KN., Bluhm, ME., Goetz, DH., Strong, RK., Holmes, MA., Borregaard, N. (2002). The neutrophil lipocalin NGAL is a bacteriostatic agent that interferes with siderophore-mediated iron acquisition. *Mol. Cell*, 10, 1033-43. [↗](#)

Aderem, A., Rodriguez, DJ., Flo, TH., Sato, S., Strong, RK., Akira, S. et al. (2004). Lipocalin 2 mediates an innate immune response to bacterial infection by sequestering iron. *Nature*, 432, 917-21. [↗](#)

Editions

2014-01-17	Authored, Edited	Jassal, B.
2014-06-09	Reviewed	Chen, C.