Exocytosis of azurophil granule membrane proteins

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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., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Sidiropoulos, K., Sidiropoulos, K., Sidiropoulos, K., Sidiropoulos, K., Sidiropoulos, K. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Reactome database release: 92

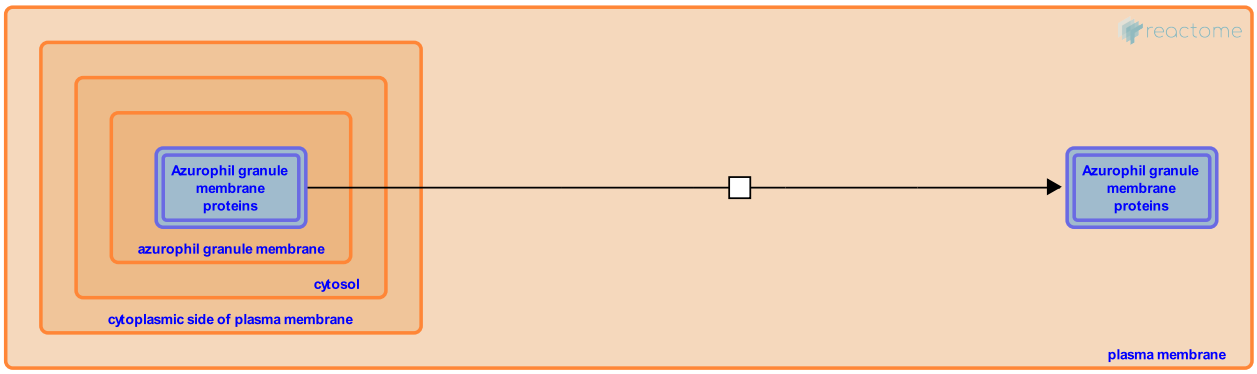
This document contains 1 reaction (see Table of Contents)

Exocytosis of azurophil granule membrane proteins ↗

Stable identifier: R-HSA-6798739

Type: transition

Compartments: azurophil granule membrane, plasma membrane



Azurophil or primary granules were originally defined by their high content of myeloperoxidase (MPO) and their affinity for the basic dye azure A (Spicer & Hardin 1969). Azurophil granules are generally described as spherical. Like lysosomes, they contain CD63 in their membrane (Cham et al. 1994) but are regarded as specialized secretory granules rather than lysosomes (Cieutat et al. 1998). Azurophil granules undergo limited exocytosis in response to stimulation (Sengelov et al. 1993, Faurschou et al. 2002), their primary role is believed to be killing and degradation of engulfed microbes in the phagolysosome (Joiner et al. 1989).

Literature references

Le Cabec, V., Borregaard, N., Calafat, J., Cowland, JB. (1996). Targeting of proteins to granule subsets is determined by timing and not by sorting: The specific granule protein NGAL is localized to azurophil granules when expressed in HL-60 cells. *Proc. Natl. Acad. Sci. U.S.A., 93*, 6454-7. ↗

Editions

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