

Exocytosis of azurophil granule lumen proteins

Heegaard, N., Jupe, S.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

01/04/2024

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

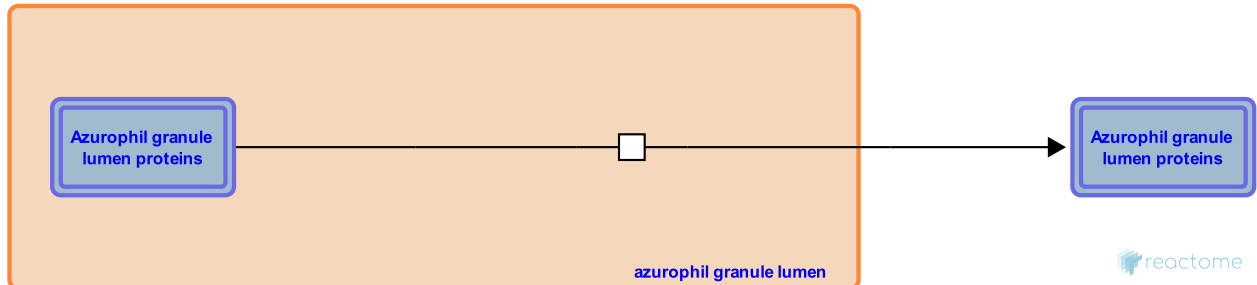
This document contains 1 reaction ([see Table of Contents](#))

Exocytosis of azurophil granule lumen proteins [↗](#)

Stable identifier: R-HSA-6798751

Type: transition

Compartments: azurophil granule lumen, extracellular region



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). MPO reacts with H₂O₂ formed by NADPH oxidase, increasing its toxicity by formation of hypochlorous acid and other chlorination products, tyrosine radicals and reactive nitrogen intermediates which attack the surface of microbes (Klebanoff et al. 2013).

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

2015-09-21	Authored	Jupe, S.
2016-06-13	Reviewed	Heegaard, N.
2016-06-13	Edited	Jupe, S.