Pro-HNP1-4 are cleaved to biologically active defensin

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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. ↗

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. ↗

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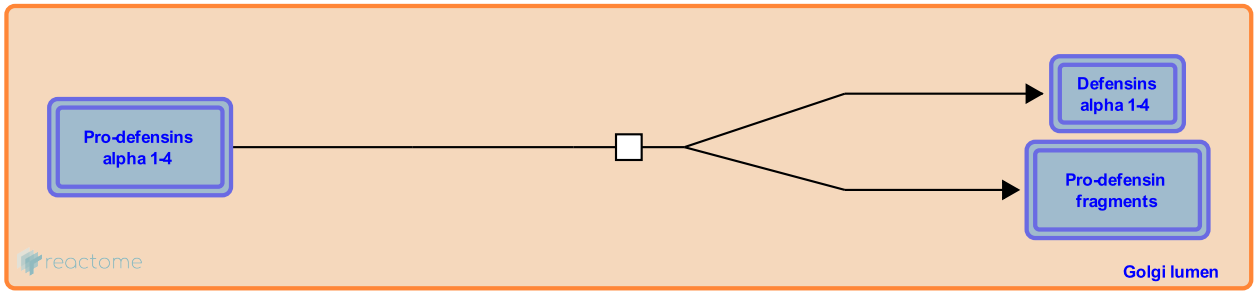
Stable identifier: R-HSA-1462039

Type: transition

Compartments: Golgi lumen



Synthesis of alpha defensins takes place in neutrophil precursor cells, the promyelocytes, in the bone marrow. Pro HNP1-4 are cleaved in the Golgi body, with HNP-2 being derived from cleavage of the N-terminal amino acid from HNP-1 or HNP-3. The defensin propiece is not only important for correct sub-cellular trafficking and sorting but also inhibits HNP activity (Valore et al. 1996, Wu et al. 2007). The resulting mature peptides are sorted to primary neutrophil (azurophil) granules for storage (Valore & Ganz 1992, Harwig et al. 1992, Cowland & Borregaard).

Literature references

Harwig, SS., Lehrer, RI., Park, AS. (1992). Characterization of defensin precursors in mature human neutrophils. *Blood, 79*, 1532-7. ↗

Ganz, T., Valore, EV. (1992). Posttranslational processing of defensins in immature human myeloid cells. *Blood, 79*, 1538-44. ↗

Editions

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