ADP-Ribosylation of HNP-1

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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. ↗

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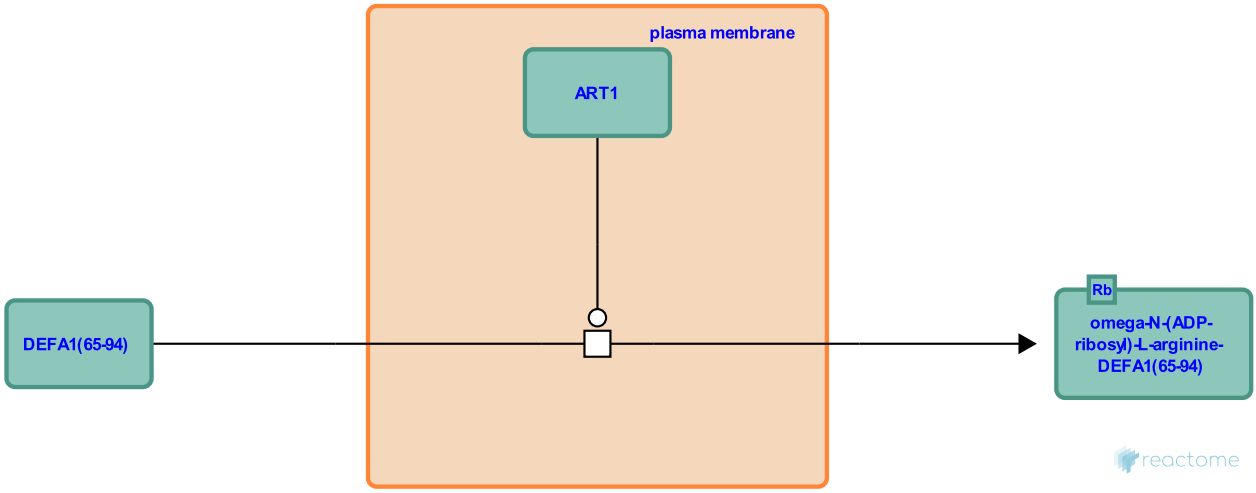
Stable identifier: R-HSA-1972385

Type: transition

Compartments: extracellular region, plasma membrane



HNP-1 is recognized as a substrate by arginine-specific ADP-ribosyltransferase-1 which ribosylates Arg-14 of the peptide. The modified defensin has reduced antimicrobial and cytotoxic activities but its chemotactic properties remain unchanged whilst its ability to induced the chemokine IL-8 is enhanced.

Literature references

Moss, J., Wada, A., Paone, G., Hirayama, T., Matin, A., Stevens, LA. et al. (2002). ADP ribosylation of human neutrophil peptide-1 regulates its biological properties. *Proc Natl Acad Sci U S A, 99*, 8231-5.

Editions

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