Protease nexin-1 (PN1) is a specific and extremely efficient inhibitor of thrombin.

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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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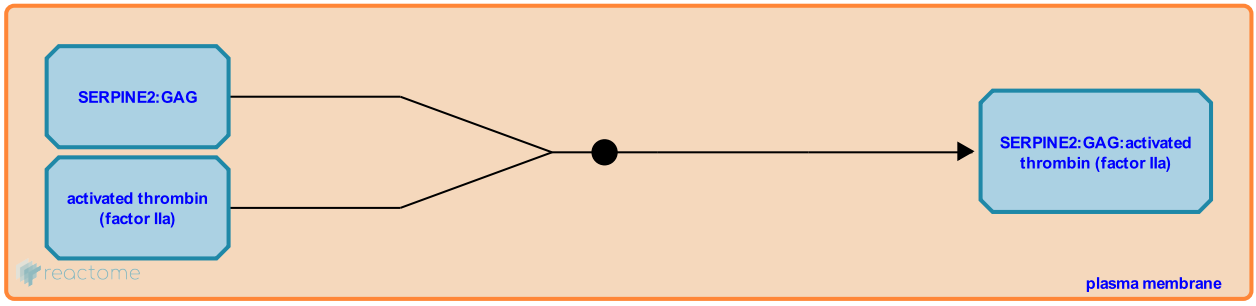
Stable identifier: R-HSA-5602080

Type: binding

Compartments: plasma membrane, extracellular region



SERPINE2 (Protease nexin-1, PN1) is a specific and extremely efficient inhibitor of thrombin. Unlike other thrombin inhibitors belonging to the serpin family, SERPINE2 does not circulate in the blood (Bouton et al. 2012). Rather, it is bound to glycosaminoglycans on the surface of cell types including macrophages, smooth muscle cells and platelets, where it inhibits the signaling functions of thrombin. SERPINE2 sets the threshold for thrombin-induced platelet activation (Gronke et al. 1987, Boulaftali et al. 2010) and has been implicated in atherosclerosis (Bouton et al. 2012). Recent studies have demonstrated an important antithrombotic effect of platelet SERPINE2 in vitro and in vivo (Boulaftali et al. 2010).

Literature references

Li, W., Huntington, JA. (2012). Crystal structures of protease nexin-1 in complex with heparin and thrombin suggest a 2-step recognition mechanism. *Blood, 120*, 459-67.

Editions

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