

PROCR binds Protein C

Jupe, S., Mumford, D.

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

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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. [↗](#)

Reactome database release: 70

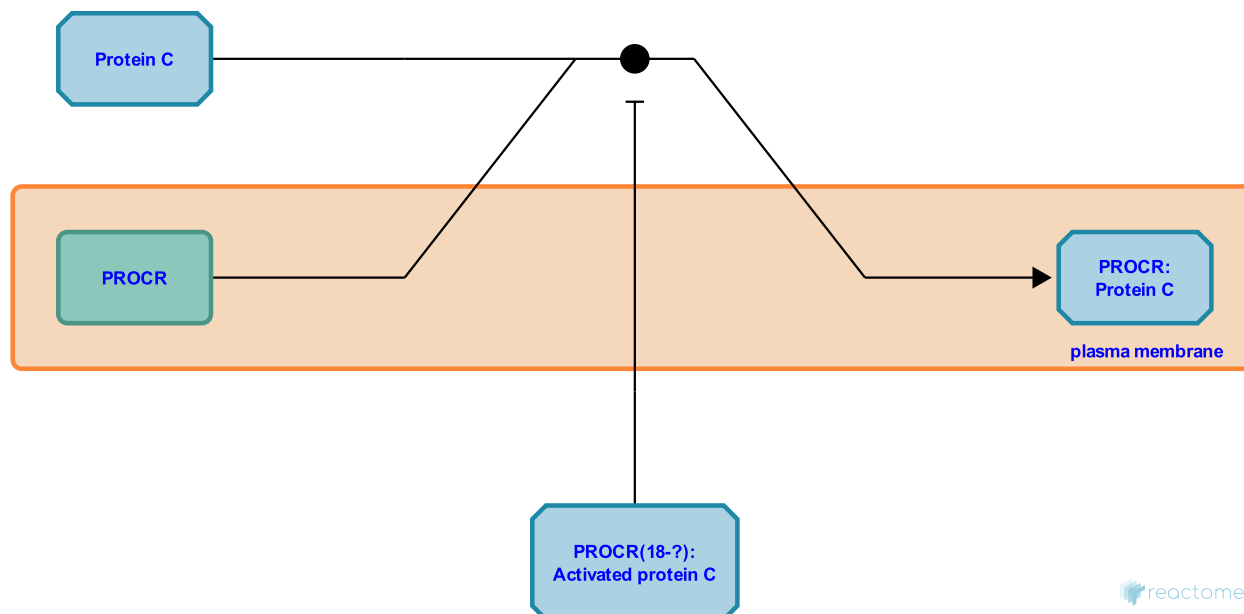
This document contains 1 reaction ([see Table of Contents](#))

PROCR binds Protein C ↗

Stable identifier: R-HSA-5591052

Type: binding

Compartments: extracellular region, plasma membrane



Physiological activation of protein C on the endothelial cell surface requires the binding of protein C to the endothelial protein C receptor PROCr (EPCR) as well as binding of thrombin to thrombomodulin (TM) (Stavenuiter et al. 2013). PROCr binding to protein C (Fukudome & Esmon 1994) augments by at least 5-fold the effect of thrombin-thrombomodulin on the rate of protein C activation (Stearns-Kurosawa et al. 1996, Taylor et al. 2001).

Literature references

Taylor, FB., Peer, GT., Lockhart, MS., Ferrell, G., Esmon, CT. (2001). Endothelial cell protein C receptor plays an important role in protein C activation in vivo. *Blood*, 97, 1685-8. ↗

Editions

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