Clustering of Integrin alphaIIb beta3 complexes

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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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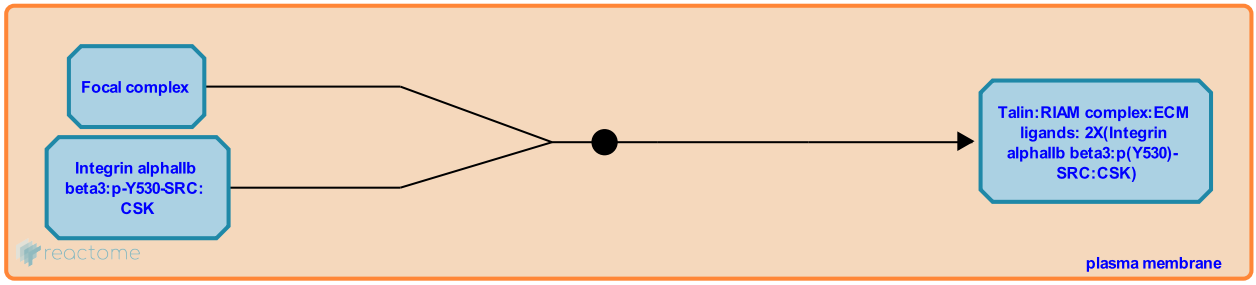
Stable identifier: R-HSA-377641

Type: binding

Compartments: plasma membrane



The fibrinogen-bound integrin alphaIIb beta3 clusters platelets together to form a platelet plug and generates intracellular signals (outside-in) causing further platelet activation and platelet plug retraction.
Intracellular integrin alphaIIb beta3 clustering brings SRCs bound to integrin beta3 chains into proximity. SRC associates constitutively with integrin alphaIIb beta3. In unstimulated cells this SRC is inactive, auto-inhibited by an internal interaction between phosphorylated Y530 and the SH2 domain. CSK is selective for the Y530 residue and prevents access to SRC of PTP1B, a protein tyrosine phosphatase that is capable of de-phosphorylating Y530.

Literature references

DeGrado, WF., Li, R., Bennett, JS. (2004). Structural basis for integrin alphaIIbbeta3 clustering. *Biochem Soc Trans, 32*, 412-5. ↗

Shattil, SJ. (2005). Integrins and Src: dynamic duo of adhesion signaling. *Trends Cell Biol, 15*, 399-403. ↗

Editions

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