

# Fibrillin-1 binds integrins

Jupe, S., Muiznieks, LD.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

28/11/2024

## 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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

## 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: 90

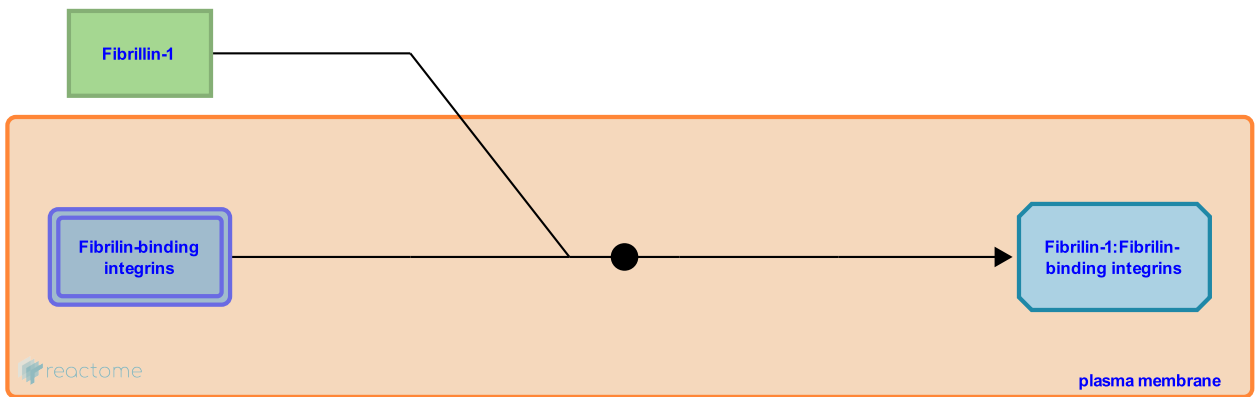
This document contains 1 reaction ([see Table of Contents](#))

**Fibrillin-1 binds integrins** ↗

**Stable identifier:** R-HSA-2328037

**Type:** binding

**Compartments:** plasma membrane



Fibrillin-1 splice variants that include the RGD sequence located in the fourth 8-cysteine domain mediate cell adhesion, binding integrin alphaVbeta3 (Pfaff et al. 1996), alpha5beta1 (Bax et al. 2003) and alphaVbeta6 (Jovanovic et al. 2008). AlphaVbeta3 has the highest affinity for fibrillin-1. Integrin alphaVbeta3 is a high-affinity fibrillin-1 receptor (K(d) approximately 40 nM), whereas integrins alphaVbeta6 and alpha5beta1 show moderate-affinity (K(d) approximately 450 nM) and low-affinity (K(d) >1 microM) binding respectively (Jovanovic et al. 2008).

**Literature references**

Pfaff, M., Timpl, R., Sakai, LY., Reinhardt, DP. (1996). Cell adhesion and integrin binding to recombinant human fibrillin-1. *FEBS Lett.*, 384, 247-50. ↗

**Editions**

2012-04-30	Authored	Jupe, S.
2012-11-02	Reviewed	Muiznieks, LD.
2012-11-12	Edited	Jupe, S.