Laminin interactions

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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

02/11/2022
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


Reactome database release: 82

This document contains 1 pathway and 15 reactions (see Table of Contents)
Laminin interactions

Stable identifier: R-HSA-3000157

Laminins are a large family of conserved, multidomain trimeric basement membrane proteins. There are many theoretical trimer combinations but only 18 have been described (Domogatskaya et al. 2012, Miner 2008, Macdonald et al. 2010) and the existence of isoforms laminin-212 and/or laminin-222 (Durbbeej et al. 2010) awaits further confirmation. The chains assemble through coiled-coil domains at their C-terminal end. Alpha chains additionally have a large C-terminal globular domain containing five LG subdomains (LG1-5). The N termini are often referred to as the short arms. These have varying numbers of laminin-type epidermal growth factor-like (LE) repeats. Trimer assembly is controlled by highly specific coiled-coil interactions (Domogatskaya et al. 2012). Some laminin isoforms are modified extracellularly by proteolytic processing at the N- or C-terminal ends prior to their binding to cellular receptors or other matrix molecules (Tzu & Marinkovitch 2008).

The cell adhesion properties of laminins are mediated primarily through the alpha chain G domain to integrins, dystroglycan, Lutheran glycoprotein, or sulfated glycolipids. The N-terminal globular domains of the alpha-1 (Colognato-Pyke et al. 1995) and alpha-2 chains (Colognato et al. 1997) and globular domains VI (Nielsen & Yamada 2001) and IVa (Sasaki & Timpl 2001) of the alpha-5 chain can bind to several integrin isoforms (alpha1beta1, alpha2beta1, alpha3beta1, and alphaVbeta3), which enables cell binding at both ends of laminins with these alpha chains.

Literature references


Editions

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The principal structural elements of basement membrane are laminin (LM) and collagen IV. These form distinct networks that become noncovalently interconnected by nidogen and perlecan, both of which are able to form irregular polymers (Breitkreutz et al. 2013).

LM polymeric networks can self-assemble even in the absence of other basement membrane components (Yurchenco et al. 1992) suggesting a key developmental role. Polymerization in vivo occurs at the cell surface, to which LMs are anchored through direct or indirect interactions with cellular receptors, dystroglycan or integrins, and possibly other receptors (Hohenester & Yurchenco 2013).

Receptor-engaged LM exceeds the critical concentration for self-assembly (Colognato & Yurchenco 2000).

The three short arms of the cross-shaped LM molecule form the nodes in the polymeric network, with a strict requirement for one each of alpha, beta and gamma arms (Hohenester & Yurchenco 2013). A surface loop, strictly conserved in the LN domains of all alpha chains, is required for stable ternary association with the beta and gamma short arms (Hussain et al. 2011).

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Integrins alpha3beta1, alpha6beta4 bind laminin-332, 511, 521, (211, 221)

Location: Laminin interactions

Stable identifier: R-HSA-216048

Type: binding

Compartments: plasma membrane, extracellular region