Cell-extracellular matrix interactions

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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.

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: 74

This document contains 3 pathways and 4 reactions (see Table of Contents)
Cell-extracellular matrix interactions

Stable identifier: R-HSA-446353

Cell-extracellular matrix (ECM) interactions play a critical role in regulating a variety of cellular processes in multicellular organisms including motility, shape change, survival, proliferation and differentiation. Cell-ECM contact is mediated by transmembrane cell adhesion receptors, such as integrins, that interact with extracellular matrix proteins as well as a number of cytoplasmic adaptor proteins. Many of these adaptor proteins physically interact with the actin cytoskeleton or function in signal transduction.

Several protein complexes interact with the cytoplasmic tail of integrins and function in transducing bidirectional signals between the ECM and intracellular signaling pathways (reviewed in Sepulveda et al., 2005).

Early events that are triggered by interactions with ECM, such as formation/turnover of Focal Adhesions, regulation of actin dynamics and protrusion of lamellipodia to promote cellular spreading and motility are modulated by PINCH-ILK-parvin complexes (see Sepulveda et al., 2005). A number of partners of the PINCH-ILK-parvin complex components have been identified that regulate and/or mediate the functions of these complexes (reviewed in Wu, 2004). Interactions with some of these partners modulate cytoskeletal remodeling and cell spreading.

Literature references


Editions

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The PINCH-ILK-parvin complex (Tu et al., 2001; Zhang et al., 2002; Li et al., 1999) localizes to focal adhesions and plays a critical role in the regulation of cell adhesion, cell shape modulation, motility and ECM deposition (Velyvis et al., 2001; Braun et al, 2003). ILK binds PINCH through its N-terminal domain and binds PARVA or PARVB through its C-terminal domain, resulting in formation of the ternary PINCH-ILK-parvin complex (Tu et al., 2001). These complexes form before they are localized to integrin-rich adhesion sites (Zhang et al., 2002). Formation of the ILK-PINCH-parvin complexes stabilizes these proteins by protecting them from degradation by the proteasome (Fukuda et al., 2003).

Followed by: Localization of the PINCH-ILK-PARVIN complex to focal adhesions

Literature references

Localization of the PINCH-ILK-PARVIN complex to focal adhesions

Location: Cell-extracellular matrix interactions

Stable identifier: R-HSA-446343

The interactions among ILK, PINCH, and parvins are necessary but not sufficient for localization of ILK to cell-ECM adhesions (Zhang et al., 2002). Additional proteins that interact with PINCH-ILK-parvin complex components likely participate in mediating its localization (reviewed in Wu, 2004).

Literature references


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Regulation of cytoskeletal remodeling and cell spreading by IPP complex components

Location: Cell-extracellular matrix interactions

Stable identifier: R-HSA-446388

The PINCH-ILK-Parvin complexes function in transducing diverse signals from ECM to intracellular effectors. Interacting partners for components of these complexes have been identified, a number of which regulate and/or mediate its functions in cytoskeletal remodeling and cell spreading (reviewed in Wu, 2004).

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Mig-2 recruits Migfilin to the cell-ECM adhesions

Location: Cell-extracellular matrix interactions

Stable identifier: R-HSA-430341

Type: binding

Compartments: cytosol

Migfilin functions in cell shape modulation regulating filamin-mediated cross-linking and stabilization of actin filaments. Migfilin is recruited to cell–Extra Cellular Matrix adhesion sites in a variety of fibroblasts, epithelial, and endothelial cells by interaction with Mig-2 (Tu et al., 2003).

Literature references


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Migfilin associates with Filamin and F-actin

Location: Cell-extracellular matrix interactions

Stable identifier: R-HSA-430347

Type: binding

Compartments: cytosol

Migfilin associates with actin filaments as a result of its interaction with filamin (Tu et al., 2003). Migfilin associates with actin filaments and loss of migfilin decreases the level of F-actin suggesting that, in addition to providing an anchoring site for actin filaments at cell-ECM adhesions, migfilin also functions in the regulation of filamin-mediated cross-linking and stabilization of actin filaments (Tu et al., 2003).

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Migfilin interacts with VASP

**Location:** Cell-extracellular matrix interactions

**Stable identifier:** R-HSA-446364

**Type:** binding

**Compartments:** cytosol

Migfilin interacts with VASP and regulates VASP localization to cell-matrix adhesions (Zhang et al., 2006). Interaction between migfilin and VASP is critical for migfilin-mediated regulation of cell migration (Zhang et al., 2006).

**Literature references**


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