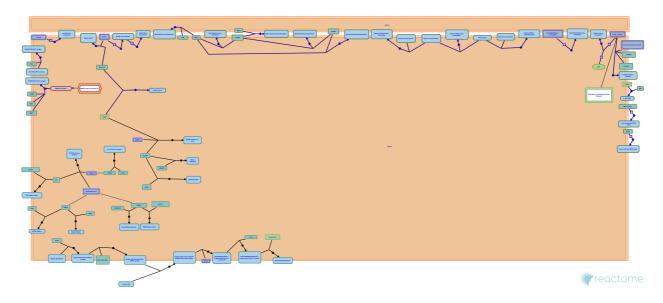


Cell-cell junction organization



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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.

10/04/2024

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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.

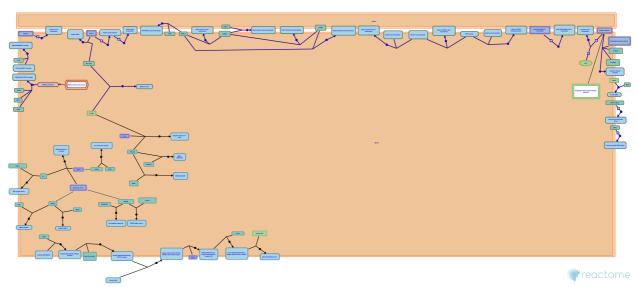
Reactome database release: 88

This document contains 4 pathways (see Table of Contents)

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Cell-cell junction organization 对

Stable identifier: R-HSA-421270



Epithelial cell-cell contacts consist of three major adhesion systems: adherens junctions (AJs), tight junctions (TJs), and desmosomes. These adhesion systems differ in their function and composition. AJs play a critical role in initiating cell-cell contacts and promoting the maturation and maintenance of the contacts (reviewed in Ebnet, 2008; Hartsock and Nelson, 2008). TJs form physical barriers in various tissues and regulate paracellular transport of water, ions, and small water soluble molecules (reviewed in Rudini and Dejana, 2008; Ebnet, 2008; Aijaz et al., 2006; Furuse and Tsukit, 2006). Desmosomes mediate strong cell adhesion linking the intermediate filament cytoskeletons between cells and playing roles in wound repair, tissue morphogenesis, and cell signaling (reviewed in Holthofer et al., 2007).

Literature references

Matter, K., Balda, MS., Aijaz, S. (2006). Tight junctions: molecular architecture and function. *Int Rev Cytol*, 248, 261-98

Lynch, RD., Schneeberger, EE. (1992). Structure, function, and regulation of cellular tight junctions. *Am J Physiol*, 262, L647-61. *¬*

Tsukita, S., Furuse, M. (2006). Claudins in occluding junctions of humans and flies. Trends Cell Biol, 16, 181-8.

Rudini, N., Dejana, E. (2008). Adherens junctions. Curr Biol, 18, R1080-2.

Nelson, WJ., Hartsock, A. (2008). Adherens and tight junctions: structure, function and connections to the actin cyto-skeleton. *Biochim Biophys Acta*, 1778, 660-9.

Editions

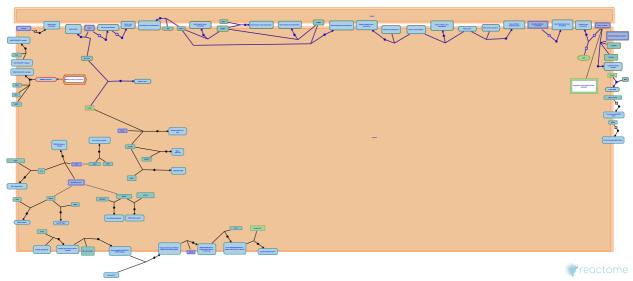
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2009-05-19 Edited Matthews, L.	
2009-08-26 Edited Matthews, L.	
2009-08-27 Reviewed Ebnet, K.	

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Adherens junctions interactions

Location: Cell-cell junction organization

Stable identifier: R-HSA-418990



The adherens junctions (AJ) are multiprotein complexes that promote homotypic cell adhesion in nearly all types of tissue by linking membrane and cytoskeletal components at discrete contact regions (reviewed in Hartsock & Nelson 2008; Gumbiner 2005; Ebnet, 2008). The molecular constituents of adherens junctions form adhesive units which are organized into higher order junctional adhesions that create a zipper-like seal between adjacent cells. Junctional adhesions function in epithelial cell polarization and in the coupling of cytoskeletons in adjacent cells that allow coordinated movements. During embryonic development, AJs function in specifying adhesion between cells and contribute in the sorting of different cell types. AJs also regulate cell polarity and shape, promote cell-cell communication and help mediate contact inhibition of cell growth. This module covers transdimerization events involving AJ transmembrane proteins (cadherins and nectins) (Gumbiner 2005; Ebnet 2008; Hartsock & Nelson 2008).

Literature references

Ebnet, K. (2008). Organization of multiprotein complexes at cell-cell junctions. Histochem Cell Biol, 130, 1-20.

Rudini, N., Dejana, E. (2008). Adherens junctions. Curr Biol, 18, R1080-2.

Editions

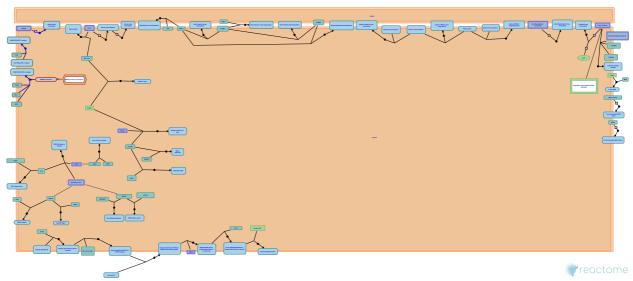
2009-04-21	Edited	Matthews, L.
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Tight junction interactions

Location: Cell-cell junction organization

Stable identifier: R-HSA-420029



Tight junctions (TJs) are the most apical component of the epithelial junctional complex forming a belt-like structure at the cellular junction. When visualized by freeze-fracture electron microscopy they appear as a branched network of intramembrane strands that correspond to the sites of direct membrane contacts and that are composed of the integral membrane claudin proteins. The TJs act as a primary barrier to the diffusion of solutes through the paracellular space (barrier function) (Tsukita et al., 2001). They also prevent the intermixing of intramembrane proteins and lipids and thus create a boundary between the apical and the basolateral membrane domains of polarized epithelial cells (fence function) (Tsukita et al., 2001). Interestingly, the fence function seems not to depend on TJ strands (Umeda et al., 2006). Recents evidence indicates that the TJs also participate in signal transduction mechanisms which regulate cell proliferation and morphogenesis (Matter and Balda, 2003; Matter and Balda, 2007). This module describes the major molecular interactions responsible for the formation of TJ strands and for the rectruitment of the PAR-3-PKC-PAR-6 and CRB3-Pals1-PATJ complexes that function in tight junction formation (Ebnet, 2008).

Literature references

Tsukita, S., Tsukita, S., Furuse, M., Umeda, K., Furuse, K., Ikenouchi, J. et al. (2006). ZO-1 and ZO-2 independently determine where claudins are polymerized in tight-junction strand formation. *Cell*, 126, 741-54.

Ebnet, K. (2008). Organization of multiprotein complexes at cell-cell junctions. Histochem Cell Biol, 130, 1-20.

Matter, K., Balda, MS. (2003). Signalling to and from tight junctions. Nat Rev Mol Cell Biol, 4, 225-36.

Tsukita, S., Furuse, M., Itoh, M. (2001). Multifunctional strands in tight junctions. Nat Rev Mol Cell Biol, 2, 285-93.

Matter, K., Balda, MS. (2007). Epithelial tight junctions, gene expression and nucleo-junctional interplay. *J Cell Sci*, 120, 1505-11.

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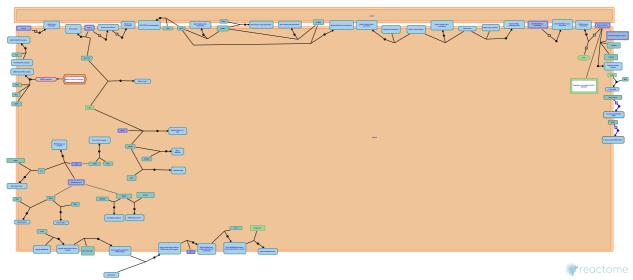
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SDK interactions

Location: Cell-cell junction organization

Stable identifier: R-HSA-373756

Compartments: plasma membrane



Sidekick-1 (SDK1) and sidekick-2 (SDK2) are cell adhesion molecules of the immunoglobulin superfamily expressed by nonoverlapping subsets of retinal neurons. They have been shown to function as neuronal targeting molecules, guiding developing neurons to specific synapses.

SDKs are concentrated at synapses that connect SDK-expressing pre- and postsynaptic partners, suggesting that their homophilic adhesion properties promote formation or stabilization of synapses.

SDKs promotes lamina-specific synaptic connections in the retina and are specifically required for the formation of neuronal circuits that detect motion (Krishnaswamy et al. 2015).

Literature references

Kurihara, H., Potla, U., Kaufman, L., Hata, Y., Dikiy, S., Coleman, S. et al. (2010). Up-regulation of the homophilic adhesion molecule sidekick-1 in podocytes contributes to glomerulosclerosis. *J. Biol. Chem.*, 285, 25677-85.

Weiner, JA., Sanes, JR., Yamagata, M. (2002). Sidekicks: synaptic adhesion molecules that promote lamina-specific connectivity in the retina. *Cell*, 110, 649-60.

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Honig, B., Goodman, KM., Katsamba, PS., Sanes, JR., Sergeeva, AP., Jin, X. et al. (2016). Molecular basis of sidekick-mediated cell-cell adhesion and specificity. *Elife, 5.*

Sanes, JR., Yamagata, M. (2008). Dscam and Sidekick proteins direct lamina-specific synaptic connections in vertebrate retina. *Nature*, 451, 465-9.

Kaufman, L., Hayashi, K., Klotman, PE., Ross, MD. (2005). Definition of the critical domains required for homophilic targeting of mouse sidekick molecules. *FASEB J.*, 19, 614-6. *¬*

Editions

2008-02-26	Authored	de Bono, B., Garapati, P V.
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