

The Role of Cell Membranes in Cell Traffic

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1. Introduction

Membrane means the boundary of the cell. Whether they surround the cell or enclose intracellular organelles, membranes are crucial for normal physiological function because they control the composition of the spaces or compartments, they cover. They can expel a wide variety of molecules, and because of their selective transport system, they can move molecules into or out of spaces. By controlling the movement of substances from one compartment to another, membranes exert a strong influence on metabolic pathways. The main components of cell membranes are lipids and proteins. The basic structure of the cell membrane and cell is a lipid bilayer, consisting of two adjacent and continuous leaflets and proteins that span the bilayer or interact with lipids on either side of the leaflet. The lipid bilayer

ABSTRACT

The cell membrane plays an important role in cell traffic because it functions to secrete various molecules. The selective transport system allows the movement of molecules into or out of the cell compartment. By controlling the movement of substances from one compartment to another, membranes exert a strong influence on metabolic pathways. Cell membranes are composed of proteins and lipids with a very important function in maintaining the rhythm of circulation and cell transport. In addition, the cell membrane also plays a role in maintaining the integrity and relationship, and communication of cells.

> provides the basic fluid structure of the membrane and is mostly an impenetrable barrier for watersoluble molecules. Individual lipid molecules can diffuse swiftly through their monolayer. Most membrane proteins span the lipid bilayer and mediate many functions of the membrane including the transport of molecules across the membrane and the synthesis of ATP.¹⁻³

Composition of the cell membrane

Previously, the plasma membrane was described as a fluid lipid bilayer composed of a uniform lipid with the movement of the introduced protein. Whether the lipid molecules in the plasma membrane of living cells separate into domains called lipid-rafts is a controversial topic. It is known that many lipids and proteins are not uniformly distributed but appear to be transiently concentrated, a dynamic pathway aided by protein-protein interactions that enable the transient formation of pleated domains or assemblies. The organization of lipid assemblies in living cells may be important for cell communication where proteins together convert extracellular signals into intracellular signals. The larger co-operation of the cluster is the caveola, a flask-shaped invagination thought to form from lipid assembly and is important for endocytosis. Carbohydrates are primarily associated with the plasma membrane, where they combine chemically with lipids to form glycolipids and proteins to form glycoproteins.⁴⁻⁵

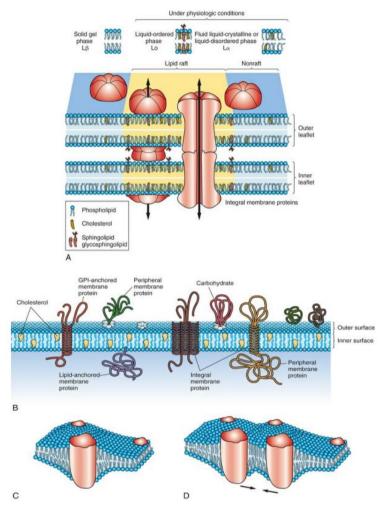


Figure 1. Lipid Bilayer Membrane. A, The biological concept of membranes marks the change in the last two decades, from the classical fluid mosaic model to the current model in which lipids and proteins are not evenly distributed but can isolate into small domains, having different proteins and different lipid compositions. An example is a small domain filled with lipid assembly (yellow color). Assemblies are dynamic domain structures composed of cholesterol, sphingolipids, and membrane proteins important in different cellular processes. Various models exist to clarify the function of the domain. The three main phases of lipid bilayer organization include the solid gel phase (eg, low temperature), the ordered liquid phase (high temperature), and the crystalline liquid phase. B, Several membrane associated proteins are integrated into a lipid bilayer; other proteins are weakly bound to the outer and inner surfaces of the membrane. Intermembrane proteins protrude across the entire outer and inner surfaces of the membrane and can be attracted to small domains by specific interactions with lipids. The interactions of membrane proteins with lipids differ depending on the hydrophobic thickness of the membrane, the lateral pressure of the membrane (mechanical forces can change a protein channel from open to closed), the polarity or electrical changes at the lipidprotein interface, and the presence of protein sites with amino acid chains. Important in pathophysiology is the suggestion that lipid-protein interactions can be important for the proper insertion, folding, and orientation of membrane proteins. For example, lipid-related diseases affected by protein folding are becoming more prevalent. C, Observers are studying the cooperative nature of lipids, membrane fluctuations, and domains that affect protein organization and consequent protein function. This is a disturbed region that develops between integral proteins. D, Two proteins are withdrawn due to the division of the disturbed region of the lipid bilayer.

Lipids

Cell membranes may contain many different classes of lipids, but in animals, the main forms are phospholipids, cholesterol, and glycolipids. The most abundant lipids are phospholipids. Phospholipids are key to membrane repair-they tend to reassemble spontaneously to prevent tearing (the water-free boundary) by folding on themselves and forming a sealed compartment. Inositol phospholipids are a subclass of phospholipids that are important for cell signaling because of the cytosolic lipid leaflet of the bilayer to which they respond to extracellular signals. Lipids together with proteins act as "glue molecules" for the structural integrity of the membrane. Individual lipid molecules are said to be polar, or amphipathic. An amphipathic molecule is one part hydrophobic (uncharged, or "water-fearing") and another part hydrophilic (charged, or "water-loving") membrane (figure 2) The organizes itself spontaneously into a bilayer due to these two incompatible solubilities. The hydrophobic area (hydrophobic tail) of each lipid is protected from water, whereas the hydrophilic area (hydrophilic head) sinks into it. The bilayer structure provides one of the essential functions of the plasma membrane: it is not easy for most water-soluble molecules to pass because they do not dissolve in areas with an oily core. The bilayer provides a barrier for the diffusion of water and hydrophilic substances while fat-soluble molecules, such as oxygen and carbon dioxide, pass through them swiftly. Because the bilayer is a liquid at temperatures greater than freezing, components of the cellular environment move slowly and selectively across the membrane over time.¹⁻⁶

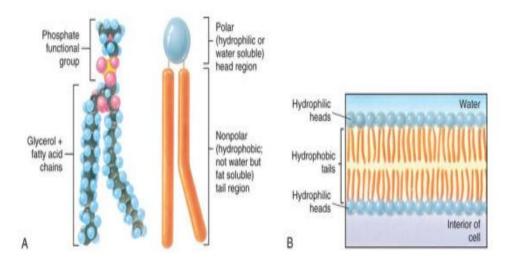


Figure 2. Phospholipid Molecular Structure. A, Each phospholipid molecule contains a phosphate functional group and two fatty acid chains bonded to a glycerol molecule. B, The fatty acid and glycerol chains of the non-polar, hydrophobic "tail" and the phosphate functional group of the polar, hydrophilic "heads". When placed in water, the hydrophobic tails of the molecules move inward away from the water, and the hydrophilic heads move outwards, toward the water.

Proteins

Proteins perform the specific actions of most plasma membranes. The amount and type of protein vary. A protein is made of a chain of amino acids, known as a polypeptide. There are 20 types of amino acids in a protein, and each type of protein has a unique strand of amino acids. Proteins are the main workers of cells.^{2,3}

Membrane proteins relate to the lipid bilayer in different ways (figure 3) including (1) intermembrane proteins extend across the bilayer and are exposed to the liquid environment from both sides (figure 3A); (2) proteins are located almost throughout the cytosol and are linked to half of the lipid bilayer by alpha chains exposed to the protein surface (Figure 3B); (3) proteins that lie outside the bilayer, on one side or the other, and are bound to the membrane by one or more covalent lipid-binding groups (Figure 3C); and (4) the protein binds indirectly to one or more surfaces of the bilayer membrane and is held in position by interactions with other proteins (Figure 3D). Membrane proteins are amphiphilic, with both hydrophobic and hydrophilic areas.

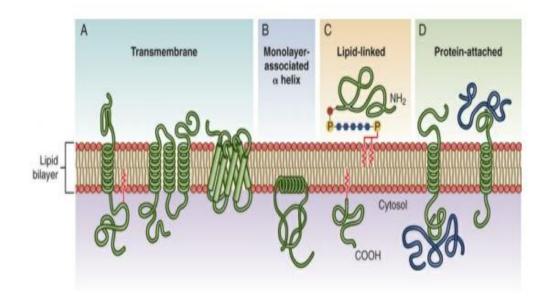


Figure 3. Proteins Bind to Plasma Membranes in Different Ways. A, Intermembrane proteins extend across the membrane as single alpha chains, multiple alpha chains, or as barrel-like coiled layers called beta barrels. B, Several membrane proteins are anchored to the cytosolic side of the lipid bilayer by amphiphilic alpha chains. C, Several proteins are linked on both sides of the membrane by covalent lipid molecular linkages. D, Proteins are linked by weak noncovalent interactions with other membrane proteins.

Proteins exist in a tightly folded molecular configuration rather than straight chains; So excess hydrophilic units are located on the surface of the molecule and excess hydrophobic units are located inside. Membrane proteins, like other proteins, are synthesized mainly by ribosomes in the cytosol and then travel, called traffic. Their fate hinges on their amino acid strand, which contains the building blocks of signals that direct their delivery to locations outside the cytosol or to the surface of organelles. A simple illustration of protein traffic in a cell is depicted in figure 4.

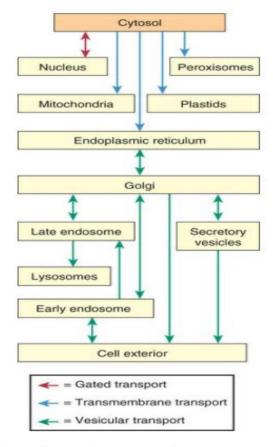


Figure 4. A simple "skeleton" of protein traffic. Proteins can move from one compartment to another by gate transport (red), intermembrane transport (blue), or vesicle transport (green). The sequence of signals directs the movement of proteins through the cell and determines their final destination. This journey begins with protein synthesis on the ribosomes in the cytosol and ends when the protein reaches its final destination. Signal arrays are required either for retention in the intermediate box or for exiting the box or compartment.

Proteins move from one compartment to another via (1) gate transport, (2) protein translocation, or (3) vesicle transport. In gate transport, the selected gate directs the movement of proteins and RNA molecules between the cytosol and the nucleus across the nuclear cleft complex in the nuclear envelope. In protein translocation, intermembrane protein translocators directly transmit proteins across the membrane from the cytosol to different locations. To perform exploration through the translocator, the protein molecule usually folds. In transport vesicles, spherical vesicles are closed intermediate membranes of small transport vesicles or fragments of large organelles. These vesicles release their charge into different compartments by fusion with the membranes of these compartments. The transfer of dissolved proteins from the ER to the Golgi apparatus occurs via transport vesicles. The protein lacks signaling sequences to persist in the cytosol. Traffic takes a unique place depending on the demand for membrane proteins for folding, translocation, and stability. Thus, much research is currently underway to understand misfolded proteins, for example, as the cause of disease.

Proteins facilitate transport across membranes by providing receptors, enzymes, or transporters. Proteins act as (1) recognition and binding units (receptors) for substances moving in and out of cells; (2) gaps or transport channels for various electrical signals releasing particles called ions or electrolytes and specific carriers for amino acids and monosaccharides; (3) a specific enzyme that drives an

active pump that promotes the concentration of certain ions, especially potassium (K⁺), inside the cell while keeping the concentration of other ions, for example, sodium (Na⁺), below those found in the extracellular environment; (4) cell surface markers, such glycoproteins (proteins bound as to carbohydrates), that identify cells to their neighbors; (5) cell adhesion molecule (CAM), or proteins that enable cells to link together and form links to the cytoskeleton to maintain cellular shape; and (6) the catalysis of chemical reactions, for example, the conversion of lactose to glucose. Membrane proteins are the key to energy transduction, converting chemical energy into electrical energy, or electrical energy into mechanical energy or ATP synthesis.

The interactions of plasma membrane proteins with lipids are complex and are the subject of many studies. The role of proteins in the onset and progression of the disease is important because they control communication between cells through enzymatic functions, transport, and receptor recognition in cellular physiology.¹⁻⁵

Regulation of proteins in a cell: Proteostasis

Proteostasis (or proteome homeostasis [the complete collection of cell proteins]) is a state of equilibrium in the cell of the processes of protein synthesis, folding, and degradation. Proteostasis is vital for cell health. The cellular protein field is in constant change or flux. The amount of protein in a cell depends on how quickly they are made and how they survive or break down. The system of protein homeostasis can be adapted and defined by a "proteostatic" network consisting of ribosomes (makers); companion (helper); and two proteindestroying or proteolytic systems, the lysosomes and the proteosome-ubiquitin (UPS) system. Molecular companions called heat-shock proteins (hsp) are important and so named because they increase after the cell is exposed to elevated temperatures (proteotoxic stress). The increase in hsp is part of a feedback system that responds to an increase in the misfolded protein and helps this protein to refold. This companion also facilitates the transport and ubiquitination or tagging of proteins with a small molecule, ubiquitin, which signals proteins to proteosomes for degradation. Together, these systems regulate protein homeostasis under a wide variety of conditions including variations in nutrient supply, oxidative stress, cell differentiation, temperature changes, presence of heavy metal ions, and other stressors. Malfunction or failure of the proteostatic network is associated with human disease (figure 5).

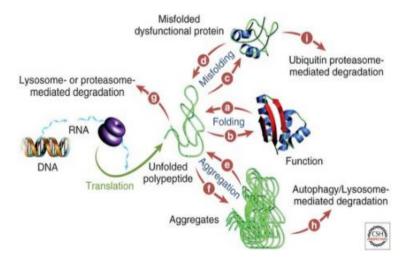


Figure 5. Protein Homeostasis System and Its Results. A major role of protein homeostasis (proteostasis) is to minimize protein misfolding and protein aggregation. This network involves ribosome-mediated protein synthesis, companion (helper folding in the ER) and enzyme-mediated folding, lysosomal breakdown and proteosome-mediated protein degradation, and vesicular traffic. These networks integrate biological pathways that balance protein folding, traffic, and degradation marked by arrows b, d, ef, g, h, and i.

Protease is an enzyme that causes the breakdown of proteins. Certain proteases can be tethered to cell membranes. Proteases are involved in the physiological regulation of essential processes by participating in dense orchestral-like strands of events called the proteolytic cascade. Four major proteolytic cascades of disease relevance are candidates for treatment modalities, including (1) cell death or caspase-mediated apoptosis, (2) the blood coagulation cascade, (3) membrane-degrading enzymes or matrix metalloproteinases, and (4) the complement cascade. Several proteases in the proteolytic cascade act as initiators; the other is involved in amplification and propagation and execution. Understanding the various stages involved is important for designing drug interventions. Dysregulation of proteases is prominent in human diseases, including cancer, autoimmunity, and neurodegenerative disorders.1-3

Short chains of sugars and carbohydrates (oligosaccharides) contained in the plasma membrane are generally bound to membrane proteins (glycoproteins) and lipids (glycolipids). Long polysaccharide chains bound to protein membranes are called proteoglycans. All of the carbohydrates in glycoproteins, proteoglycans, and glycolipids are located outside the plasma membrane, and the webbed carbohydrates are called the glycocalyx (or cell envelope). The glycocalyx protects cells from mechanical damage. Also, the carbohydrate laver provides cells with a slimy surface that aids the mobility of other cells, such as leukocytes, to squeeze through narrow slits. The function of carbohydrates goes beyond protection and lubrication and involves cell-specific recognition and adhesion. Intercellular recognition is а function of membrane oligosaccharides; for example, intermembrane proteins, called lectins that are bound to certain oligosaccharides, recognize neutrophils at the site of bacterial infection. This recognition enables

neutrophils to accumulate in the vessel walls and migrate from the blood to infected tissues to aid in the elimination of invading bacteria.

Cellular Receptors

Cellular receptors are protein molecules in the plasma membrane, in the cytoplasm, or in the nucleus that can recognize and bind to smaller molecules called ligands (Latin ligare "to bind) (figure 6). The area of the protein associated with the ligand is called the bound site. Hormones, for example, are ligands. Recognition and binding depend on the chemical configuration of the receptor and its smaller ligands, which must fit together like a puzzle. Selectively binding to protein receptors with a high affinity for ligands depends on the formation of weak, interactions-hydrogen noncovalent bonds. electrostatic attractions, and van der Waals attractions-and good hydrophobic drive. Some receptors are found in many cells, and ligands bound to receptors activate or inhibit receptor-binding signaling or biochemical pathways.

Although the chemical structure of the ligands and the receptors to which they bind differ, receptors are classified according to their location and function. The cellular type determines the overall function of the cell. but the plasma membrane receptors determine which ligands the cell will bind to and how the cell will respond to these bindings. For example, the ability of a hormone or neurotransmitter to stimulate cells is regulated by the specificity and number of receptors presHSPent on the plasma membrane. Specific processes also control intracellular mechanisms. Hormone binding, for example, relies on special messenger molecules that regulate protein synthesis in cells. Neurotransmitters also operate because they are special messengers to react with specific receptors.1

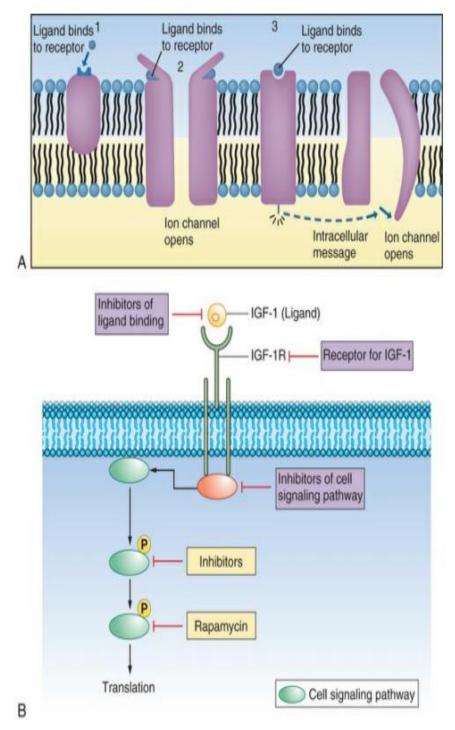


Figure 6. Cellular Receptors. (A) 1, Plasma membrane receptors for ligands (here, a hormone molecule) on the surface of integral proteins. A neurotransmitter can produce its effects in postsynaptic cells using two fundamentally different types of receptor proteins; 2, channel-connected receptors, and 3, channel-disconnected receptors. Channel-connected receptors are also known as ligand-gated channels. (B) An example of ligand-receptor interaction. Insulin-like growth factor 1 (IGF-1) is a ligand and binds to its receptor. By binding to the cell membrane, intracellular signaling pathways are activated, causing the translation of new proteins to work as intracellular communicators. This pathway is important for cancer growth. Researchers are developing pharmacological strategies to reduce signaling at and downregulate the IGF-1 receptor, hoping this will lead to a useful component for cancer treatment. P, the phosphate group of ATP.

Receptors for different drugs are found on the plasma membrane, in the cytoplasm, and in the nucleus. Membrane receptors have been found for specific anesthetics. opiates. endorphins. enkephalins, antibiotics, cancer chemotherapeutic agents, digitalis, and other drugs. Membrane receptors for endorphins, in which opiate-like peptides are isolated from the pituitary gland, are found in large numbers in pain pathways and the nervous system. By binding, endorphins (or drugs such as morphine) convert cellular permeability to ions, increase the concentration of molecules that regulate intracellular protein synthesis, and initiate molecular events that modulate pain perception.²

Receptors for infectious microorganisms, or antigen receptors, bind to bacteria, viruses, and parasites. Antigen receptors on white blood cells (lymphocytes, monocytes, macrophages, granulocytes) recognize and bind to antigenic microorganisms and activate immune and inflammatory responses.

Cell-to-cell adhesion

Cells are small and slippery, unlike bricks. They are enclosed only by a thin membrane, but cells depend on the integrity of this membrane to survive. How could cells be combined so tightly, with their membranes intact, to form the muscle that could lift this book? The plasma membrane not only serves as the outer boundary of the entire cell but also allows groups of cells to hold together tightly, in cell-to-cell adhesion, to form tissues and organs. Once assembled, cells are held together for three distinct purposes: (1) the extracellular matrix, (2) cell adhesion molecules in the cell plasma membrane, and (3) specialized cell junctions.³

Extracellular matrix and basement membrane

Cells can be bound together by links with each other or through the extracellular matrix (ECM); also involve the basement membrane), which cells secrete around them. The ECM is an intricate web of interstitial protein fibers embedded in a watery, gellike substance composed of complex carbohydrates (figure 7). A special type of ECM is called the basement membrane (also known as the basement membrane). The molecular layer of this matrix is very thin, hard, and flexible; located under epithelial cells; and surrounds individual muscle cells, fat cells, and Schwann cells (with sheaths around the axons of peripheral nerve cells) (figure 8). ECM is like glue; however, it provides a pathway for the diffusion of nutrients, waste, and dissolved water traffic between blood and tissue cells. Overall, the matrix helps regulate cell growth, migration, and differentiation. In particular, the main functions of the ECM include (1) mechanical support, (2) control of cell proliferation, (3) formation of a scaffold for tissue regeneration, and (4) generating a small environment. for the network (Box 1.1). Interwoven within the matrix are three groups of macromolecules: (1) fibrous structural proteins, including collagen and elastin; (2) a distinct group of adhesive glycoproteins, such as fibronectin; and (3) proteoglycans and hyaluronic acid.4

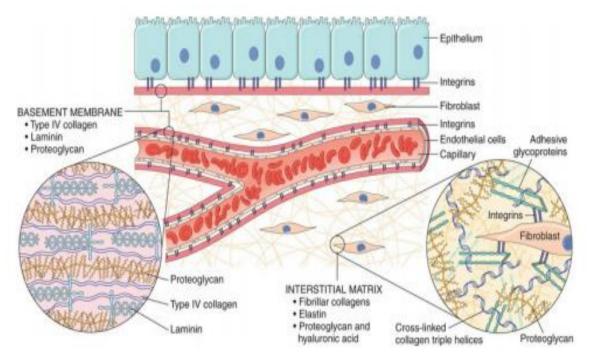


Figure 7. The Extracellular Matrix. Tissues are not only cells but also extracellular spaces. The extracellular cleft is a complex network of macromolecules called the extracellular matrix (ECM). ECM-associated macromolecules are secreted locally (mostly by fibroblasts) and aggregate into a mesh in close association with the surface of the cells that produce them. The two main classes of macromolecules include proteoglycans, which are bound to polysaccharide chains called glycosaminoglycans; and fibrous proteins (eg collagen, elastin, fibronectin, and laminin), which have structural and adhesive properties. Together, the proteoglycan molecules form a gel-like substance in which the fibrous proteins are present. The gel enables the rapid diffusion of nutrients, metabolites, and hormones between blood and tissue cells. Matrix proteins modulate cell-matrix interactions including normal tissue repair (which can become abnormal, for example, with chronic inflammation), embryogenesis, wound healing, and angiogenesis. Disruption of this balance results in serious illnesses such as arthritis, tumor growth, and others.

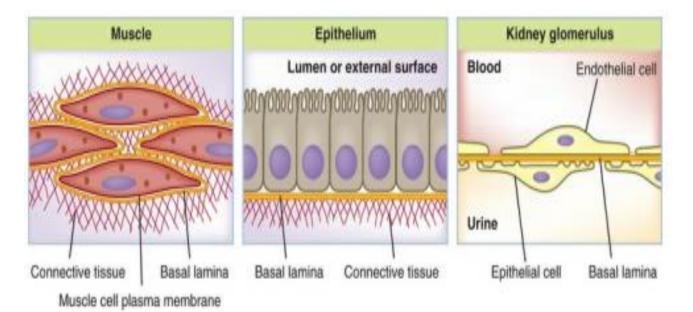


Figure 8. Three Ways The Basal Membrane (Basic Lamina) Is Arranged. Lamina basalis (yellow) surrounds certain cells such as skeletal muscle cells, under the epithelium, and lies between two layers of cells (renal glomerulus).

Functions of the extracellular matrix

The extracellular matrix has several functions. The mechanical support function provides anchorage for cells, cell migration, and the defense of cell polarity. The cell proliferation control function Provides a storehouse for growth factors and cell signaling via receptors in the integrin family (Figure 7). Latent growth factors can be activated from injury or inflammation. functions Scaffold For tissue regeneration-ongoing defense of normal tissue structures requires a basement membrane (stromal scaffold); The integrity of the basement membrane is important for structuring tissue regeneration. It provides a guide for cellular regeneration migration. Modified after injury, promotes cell migration for wound healing. Structurally, the basement membrane acts as a bond between the epithelium and the underlying connective tissue, but it is also functional. For example, at a neuromuscular synapse, the synaptic basal lamina (or basement membrane) is important for the reconstruction of the synapse after nerve or muscle damage.5-7

Collagen forms cable-like fibers or layers that provide tensile strength or resistance to longitudinal stress. The breakdown of collagen, as occurs in osteoarthritis, damages the fibers that provide tensile strength to cartilage. Elastin is a gum-rubber-like protein fiber that is abundant in tissues capable of stretching and coiling, such as the lungs. Fibronectin, a large glycoprotein, promotes cell adhesion and anchorage for cells. Decreased numbers were found in certain types of cancer cells; This allows cancer cells to travel or metastasize to other parts of the body.

The extracellular matrix is secreted by fibroblasts ("fiber-formers"), local cells that arise in the matrix. The matrix and the cells within it are known collectively as *connective tissue* because they link cells together by forming tissues and organs. Human connective tissue is highly variable. They can be solid and loose, like bones; flexible, like tendons in the dermis of the skin; ductile and able to absorb shocks, such as cartilage; or soft and transparent, like a jellylike substance that fills the eye. Of these examples, the majority of the tissue is composed of the ECM, and the matrix-producing cells are scattered within it like raisins in the pudding (Figure 7).

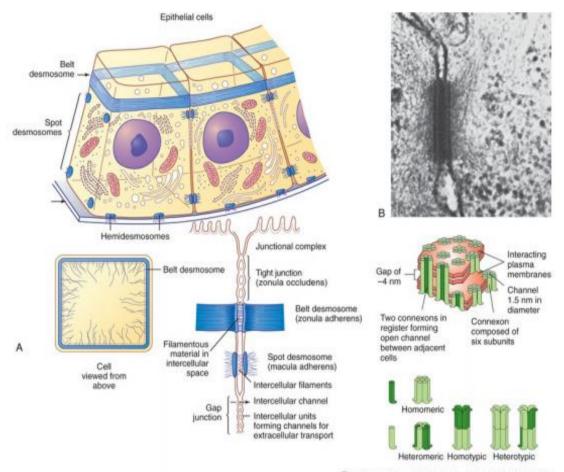
The matrix is not just a passive frame for mobile links; it also helps regulate the function of the cells within which it interacts. The matrix helps regulate cell growth, movement, and differentiation.^{7.8}

Cell Adhesion Molecules (CAMs)

Cell adhesion molecules (CAMs) are cell-surface proteins that bind cells to subsequent cells and components of the ECM. CAMs include four protein families: integrins, cadherins, selecins, and the large immunoglobulin (Ig) family. Integrins are a major receptor class in the ECM and regulate ECM cell interactions with collagen, fibronectin, vitronectin, and fibrinogen. Cadherin is a Cadependent glycoprotein⁺⁺ and has a unique pattern of distribution of tissues, for example, epithelial (E-cadherin). Selectins are a family of proteins that bind to certain carbohydrates, for example, mucin. The large family of immunoglobulin CAMs (IgSF CAMs) binds to integrins or other IgSF CAMs.⁹

Cell-specific junctions

Cells in direct physical contact with neighboring cells are often linked together at special areas of their plasma membranes called cell junctions. Cell joints are classified according to their function: (1) to hold cells together, forming a strong seal (strong joint); (2) provide strong mechanical links (adherent junctions, desmosomes, hemidesmosomes); (3) provide a special type of chemical communication, for example, inorganic ions and small water-soluble molecules to move from the cytosol of one cell to the cytosol of another cell, causing an electric wave (gap junction); and (4) maintain the apicobasal polarity of individual epithelial cells (strong junction) (figure 9). Overall, cell junctions make the epithelium leak-proof (mediate mechanical linkage from one cell to another), allow communication tunnels, and maintain cell polarity.



C Connexins Connexons Intercellular channels

Figure 9. Types of Cell Relationships. A, Schematic image of the desmosome belt between epithelial cells. These junctions, also called adherent zonules, surround each cell interaction. The points of desmosomes and hemidesmosomes, like belt desmosomes, are adherent junctions. These strong junctions are impermeable junctions that hold cells together but seal them in such a way that molecules cannot leak between them. Splice gaps, as communication junctions, mediate the passage of small molecules from one cell interaction to another. B, Electron micrograph of a desmosome. C, Connexons.

Cell junctions can be classified as symmetrical and asymmetrical. Symmetrical junctions include strong junctions (occlusion zonules), desmosome belts (adherent zonules), desmosomes (adherent macules), and junction gaps which are also known as intercellular canals or communication junctions. Asymmetric junctions include hemidesmosomes (see figure 9). Together with the zones between the epithelial cells—commonly containing the occlusive zonules, adherent zonules, and adherent macules from the junction complex. Desmosomes hold cells together with either by forming junctional bands or belts of the epithelial lining or by developing buttonlike contact points. Desmosomes also act as a wired system to maintain structural stability. Strong junctions act as a barrier for diffusion, prevent the movement of substances across transport proteins in the plasma membrane, and prevent the leakage of small molecules between the plasma membranes of adjacent cells. The junction gap is a cluster of communication tunnels or connexons that allow small ions and molecules to pass directly from within the cell into other cells. connexons are one-sided canals that extend outward from each of the plasma membranes of adjacent cells (figure 9C).¹⁰⁻¹²

The junction complex is a highly permeable part of the plasma membrane. Permeability is controlled by a process called gatekeeping, which depends on the concentration of calcium ions in the cytoplasm. An increase in the cytoplasmic calcium concentration causes a decrease in the permeability of the junction complex. The gate is an important defense mechanism for cells because it enables an uninjured cell to seal itself from injury to neighboring cells. Cell damage releases calcium, which travels across the junction complex and raises calcium levels in neighboring cells, causing the damaging effect. An increase in calcium concentration decreases the permeability of the neighboring cell junction complexes, which form a relatively impermeable wall around the injured area. 13-15

2. Conclusion

Cell membranes are composed of proteins and lipids with very important functions in maintaining the rhythm of circulation and cell transport. In addition, the cell membrane also plays a role in maintaining the integrity and relationship communication of cells.

3. References

- Ozbabacan SEA, Engin HB, Gursoy A, Keskin,
 O. Transient protein-protein interactions.
 Proteins Eng. Dec. Cell. 2011; 24:635–48.
- Bacia K, Schwille P. Practical guidelines for dual-color fluorescence cross-correlation spectroscopy. Nat. Protoc. 2007; 2:2842–56.
- Adhikary S, Deredge DJ, Nagarajan A, Forrest LR, Wintrode, PL, et al. Conformational dynamics of a neurotransmitter:sodium symporter in a lipid bilayer. Proc. Natl. Acad. Sci. USA. 2017; 114: E1786–E1795.
- Ahuja S, Jahr N, Im S-C, Vivekanandan S, Popovych N, et al. A model of the membranebound cytochrome b5-cytochrome P450 complex from NMR and mutagenesis data. J. Biol. Chem. 2013; 288:22080–95.

- Bolmatov D, Soloviov D, Zhernenkov M, Zav'yalov D, Mamontov E, et al. Molecular picture of the transient nature of lipid rafts. Langmuir. 2020; 36:4887–96.
- Contreras F-X, Ernst AM, Haberkant P, Björkholm P, Lindahl E, et al. Molecular recognition of a single sphingolipid species by a protein's transmembrane domain. Nature. 2012; 481:525–9.
- Bagheri Y, Chedid S, Shafiei F, Zhao B, You M. A quantitative assessment of the dynamic modification of lipid–DNA probes on live cell membranes. Chem. Sci. 2019a; 10: 11030–40.
- Bakht O, Pathak P, London E. Effect of the structure of lipids favoring disordered domain formation on the stability of cholesterolcontaining ordered domains (lipid rafts): identification of multiple raft-stabilization mechanisms. Biophys. J. 2007; 93: 4307–18.
- Dannatt HRW, Felletti M, Jehle S, Wang Y, Emsley L, Dixon NE, et al. Weak and transient protein interactions determined by solid-state NMR. Angew. Chemie Int. Ed. 2016; 55:6638– 41.
- De Keersmaecker H, Camacho R, Rantasa DM, Fron E, Uji-I H, et al. Mapping transient protein interactions at the nanoscale in living mammalian cells. ACS Nano. 2018; 12:9842– 54.
- Dürr UHN, Gildenberg M, Ramamoorthy A. The magic of bicelles lights up membrane protein structure. Chem. Rev. 2012; 112: 6054–74.
- Furukawa A, Konuma T, Yanaka S, Sugase K. Quantitative analysis of protein-ligand interactions by NMR. Prog. Nucl. Magn. Reson. Spectrosc. 2016; 96:47–57.
- Gagnon E, Connolly A, Dobbins J, Wucherpfennig KW. Studying dynamic plasma membrane binding of TCR-CD3 chains during immunological synapse formation using donor-quenching FRET and

FLIM-FRET. Methods Mol. Biol. 2017; 1584: 259–89.

- 14. Fantini J, Yahi N. Molecular insights into amyloid regulation by membrane cholesterol and sphingolipids: common mechanisms in neurodegenerative diseases. Expert Rev. Mol. Med. 2010; 12:e27.
- Frick M, Schmidt C. Mass spectrometry—A versatile tool for characterising the lipid environment of membrane protein assemblies. Chem. Phys. Lipids. 2019; 221, 145–157