Cooper gm the cell a molecular approach

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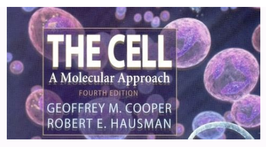

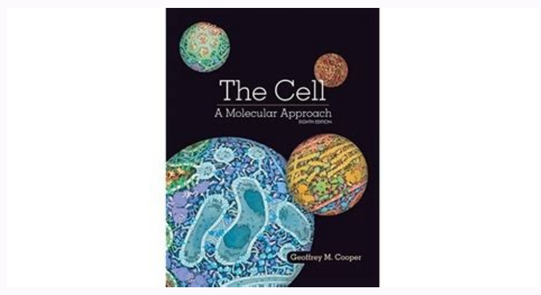

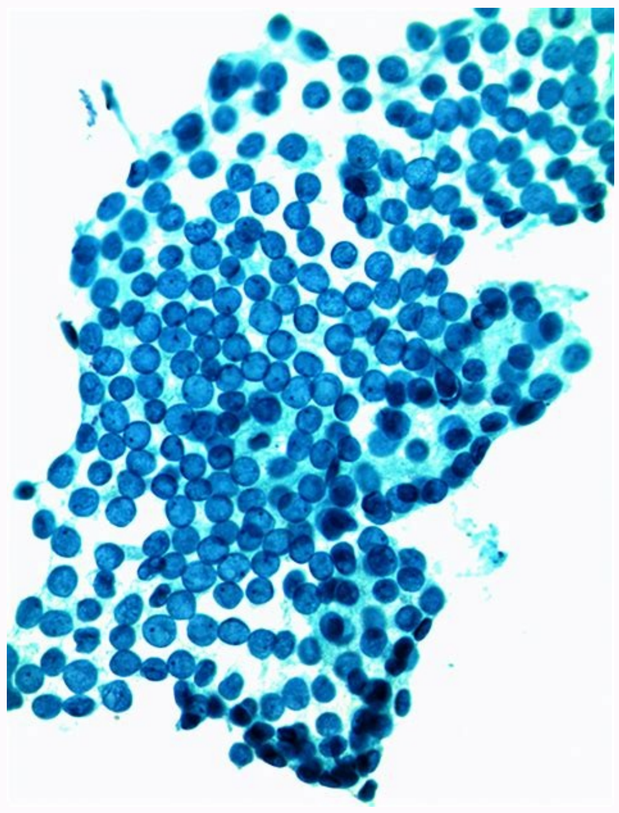

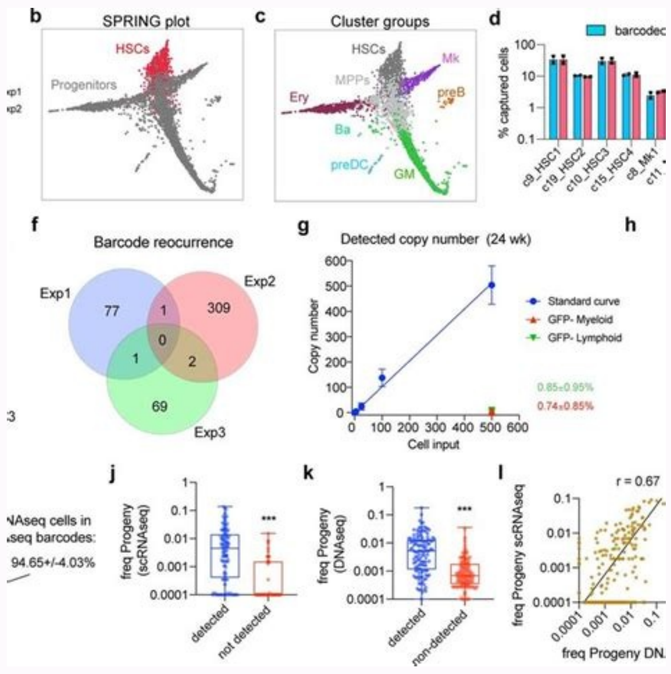

The cell a molecular approach. 2nd edition. cooper gm. What is gm in chemistry. What is molecular biology used for. What is the molecular structure of copper. Is co(g) a molecular compound.

Peroxisomes are small membrane-bound organelles (Fig. 10.24) that contain enzymes that participate in a variety of metabolic reactions, including several aspects of energy metabolism. Although morphologically similar to lysosomes such as mitochondria and chloroplasts, peroxisomes are composed of proteins synthesized on free ribosomes and then imported into peroxisomes as finished polypeptide chains. Although peroxisomes do not contain their own genome, they are similar to mitochondria and chloroplasts in that they replicate by dividing. Peroxisomes contain at least 50 different enzymes involved in various biochemical pathways in different cell types. Peroxisomes were originally defined as organelles that carry out oxidation reactions that produce hydrogen peroxide. Because hydrogen peroxide is harmful to the cell, peroxisomes also contain the enzyme catalase, which breaks down hydrogen peroxide, turning it into water or oxidizing another organic compound. Various substrates, including uric acid, amino acids, and fatty acids, are broken down in peroxisomes by such oxidation reactions. Fatty acid oxidation (Fig. 10.25) is a particularly important example because it is an important source of metabolic energy. In animal cells, fatty acids are oxidized in both peroxisomes and mitochondria, but in yeast and plants, fatty acid oxidation is restricted to peroxisomes. In addition to providing a compartment for oxidation reactions, peroxisomes are involved in lipid biosynthesis. In animal cells, cholesterol and dolichol are synthesized in both peroxisomes and the ER. In the liver, peroxisomes are also involved in the synthesis of cholesterol-derived bile acids. In addition, peroxisomes contain enzymes necessary for the synthesis of plasmalogens, a family of phospholipids in which one of the hydrocarbon chains is linked to glycerol by an ether bond rather than a single one.connection (Fig. 10.26). Plasmalogens are important membrane components in some tissues, especially the heart and brain, although they are absent in others. Peroxisomes have two particularly important roles in plants. First, peroxisomes in seeds are responsible for converting stored fatty acids into carbohydrates, which are essential to provide energy and raw materials for the growth of the germinating plant. This occurs through a series of reactions called the glyoxylate cycle, a variant of the citric acid cycle (Figure 10.27). The peroxisomes in which this occurs are sometimes called glyoxysomes. Second, peroxisomes in leaves participate in photorespiration, which serves to metabolize the by-product obtained during photosynthesis (Figure 10.28). CO2 is converted to carbohydrates during photosynthesis through a series of reactions called the Calvin cycle (see Figure 2.39). The first step is the addition of CO2 to the five-carbon sugar ribulose-1,5-bisphosphate to form two molecules of 3-phosphoglycerate (each with three carbons). However, the enzyme involved (ribulose bisphosphate carboxylase or rubisco) sometimes catalyzes the addition of O2 instead of CO2, producing one molecule of 3-phosphoglycerate and one molecule of phosphoglycolate (two carbons). This is an adverse reaction and phosphoglycolate is not a useful metabolite. It is first converted to glycolate and then transferred to peroxisomes where it is oxidized and converted to glycine. Glycine is then transported to the mitochondria where two molecules of glycine are converted to one molecule of serine with the loss of CO2 and NH3. The serine then returns to the peroxisomes where it is converted to glycerate. Finally, glycerate is transported back to the chloroplasts, where it reenters the Calvin cycle. Photorespiration does not appear to benefit the plant because it is essentially the opposite of photosynthesis: O2 is consumed and CO2 is released without increasing ATP. Sometimes thoughO2, not CO2, appears to be the property of rubisco, so photorespiration is a common companion of photosynthesis. Thus, peroxisomes play an important role in the recovery and utilization of most of the carbon present in glycolate. As already mentioned, the assembly of peroxisomes is essentially similar to the assembly of mitochondria and chloroplasts, rather than the endoplasmic reticulum, Golgi apparatus and lysosomes. Proteins destined for peroxisomes are translated onto free cytosolic ribosomes and then transported to peroxisomes as complete polypeptide chains (Fig. 10.29). Phospholipids are also imported into peroxisomes by phospholipid transport proteins from their main site of synthesis in the ER. The import of proteins and phospholipids causes the growth of peroxisomes, and then the breakdown of old ones leads to the formation of new peroxisomes. Proteins are trafficked into peroxisomes by at least two pathways that are conserved from yeast to humans. Most proteins are targeted to peroxisomes with a simple Ser-Lys-Leu amino acid sequence at their carboxyl terminus (peroxisome targeting signal 1 or PTS1). Other proteins are directed by a sequence of nine amino acids (PTS2) at their amino terminus, and some proteins may be directed by alternative signals that are not yet well defined. PTS1 and PTS2 are recognized by different receptors and then transferred to the translocation complex, which enables their transport across the peroxisome membrane. However, the mechanism of protein import into peroxisomes is less studied than the mechanisms of protein translocation across the membranes of other subcellular organelles. In contrast to the translocation of polypeptide chains across the membranes of the endoplasmic reticulum, mitochondria, and chloroplasts, targeting signals are not normally cleaved when proteins are imported into peroxisomes. Cytosolic Hsp70 is involved in protein import into peroxisomes, but a possible rolemolecular chaperones in peroxisomes are unclear. Furthermore, it appeared that proteins can be transported in peroxisomes in at least partially folded conformations, rather than as extended polypeptide chains. Some peroxisome membrane proteins are similarly synthesized by cytosolic ribosomes and are targeted to the peroxisome membrane by various internal signals. However, other experiments show that some peroxisomal membrane proteins can be synthesized in membrane-bound endoplasmic reticulum polysomes and then transported to peroxisomes, suggesting a role for the endoplasmic reticulum in peroxisome maintenance. Thus, protein import into peroxisomes appears to have several novel properties, making it an active area of research. Interestingly, several components of the peroxisomal import pathways have been identified not only as yeast mutants but also as mutations associated with serious human disease-related disorders. peroxisomes. In some of these diseases, only one peroxisomal enzyme is missing. However, in other diseases caused by defects in peroxisome function, several peroxisomal enzymes cannot be imported into peroxisomes but are localized in the cytosol. The last group of diseases results from a deficiency in the PTS1 or PTS2 pathways responsible for the import of peroxisomal proteins. A typical example is Zellweger syndrome, which is fatal in the first ten years of life. Zellweger syndrome can be caused by mutations in at least ten different genes that affect peroxisomal protein import, one of which has been identified as the gene encoding the peroxisomal targeting signal receptor PTS1. Cell structure and function depend critically on membranes, which not only separate the inside of the cell from the outside, but also define the internal compartments of eukaryotic cells, including the nucleus and cytoplasmic organelles. The formation of biological membranes is based on the properties of lipids,all cell membranes share a common structural organization: phospholipid bilayers with associated proteins. These membrane proteins are responsible for many specialized functions; some act as receptors that allow the cell to respond to external signals, some are responsible for the selective transport of molecules across the membrane, and others are involved in electron transport and oxidative phosphorylation. In addition, membrane proteins control the interactions between the cells of multicellular organisms. Thus, the general structural organization of membranes underlies many of the biological processes and specialized functions of membranes, which will be discussed in detail in the following sections. The basic building blocks of all cell membranes are phospholipids, which are amphipathic molecules composed of two hydrophobic fatty acids. chains linked to a hydrophilic phosphate-containing head group (see Fig. 2.7). Since their fatty acid ends are poorly soluble in water, phospholipids spontaneously form bilayers in aqueous solutions, with hydrophobic ends immersed in the membrane and polar end groups opening on both sides upon contact with water (Fig. 2.45). Such phospholipid bilayers form a stable barrier between two water compartments and are the basic structure of all biological membranes. Lipids make up about 50% of the mass of most cell membranes, although the proportion varies depending on the type of membrane. For example, plasma membranes contain about 50% lipids and 50% proteins. On the other hand, the inner mitochondrial membrane contains an extremely high percentage (about 75%) of protein, reflecting the abundance of protein complexes involved in electron transport and oxidative phosphorylation. The lipid composition of different cell membranes is also varied (Table 2.3). The plasma membrane of E. coli consists mainly of phosphatidylethanolamine, which accounts for 80% of all lipids. Mammal plasmathey are more complex and contain four main phospholipids – phosphatidylcholine, phosphatidylserine, phosphatidylethanolamine and sphingomyelin, which together make up 50 to 60% of all membrane lipids. In addition to phospholipids, plasma membranes of animal cells contain glycolipids and cholesterol, which usually make up about 40% of all lipid molecules. An important property of lipid bilayers is that they behave as two-dimensional fluids in which individual molecules (lipids and proteins) can freely rotate and move sideways (Fig. 2.46). Such fluidity is an important property of membranes and depends on both temperature and lipid composition. For example, the interaction between shorter fatty acid chains is weaker than between longer chains, so membranes containing shorter fatty acid chains are less rigid and remain liquid at lower temperatures. Lipids containing unsaturated fatty acids similarly increase membrane fluidity because the presence of double bonds leads to twisting of the fatty acid chains, making their packing more difficult. Because of its hydrocarbon ring structure (see Figure 2.9), cholesterol plays a special role in determining membrane fluidity. Cholesterol molecules are stored in a bilayer and their polar hydroxyl groups are close to the hydrophilic head groups of phospholipids (Fig. 2.47). Thus, the rigid hydrocarbon rings of cholesterol interact with the regions of the fatty acid chains that are adjacent to the phospholipid head groups. This interaction reduces the mobility of the outer parts of the fatty acid chains, making this part of the membrane more rigid. On the other hand, the introduction of cholesterol prevents the interaction between the fatty acid chains, thereby maintaining membrane fluidity at lower temperatures. Proteins are the second major component of cell membranes, making up 25 to 75% of the weight of various cell membranes. current modelThe membrane structure, proposed by Jonathan Singer and Garth Nicolson in 1972, views membranes as a fluid mosaic where proteins are embedded in a lipid bilayer (Fig. 2.48). While phospholipids provide the basic structural organization of membranes, membrane proteins perform specific functions of various cell membranes. These proteins are divided into two general classes based on the nature of their membrane-association. Integral membrane proteins are incorporated directly into the lipid bilayer. Peripheral membrane proteins are not embedded in the lipid bilayer, but are indirectly associated with the membrane, generally by interacting with integral membrane proteins. Many integral membrane proteins (called transmembrane proteins) span the lipid bilayer, with portions on either side of the membrane exposed. The membrane portions of these proteins are typically ±-helical regions of 20 to 25 non-polar amino acids. The hydrophobic side chains of these amino acids interact with the fatty acid chains of membrane lipids, and the formation of the α-helix neutralizes the polar nature of the peptide bonds, as discussed earlier in this chapter in relation to protein folding. Like phospholipids, transmembrane proteins are amphipathic molecules whose hydrophilic portions on both sides of the membrane are exposed to the aqueous environment. Some transmembrane proteins cross the membrane only once; others have multiple membrane regions. Most transmembrane proteins of eukaryotic plasma membranes have been modified by the addition of carbohydrates that are exposed on the cell surface and can participate in cell-cell interactions. Proteins can also be anchored to membranes by lipids covalently attached to a polypeptide chain (see Chapter 7). Significant lipid modifications anchor proteins to the cytosolic and extracellular surfaces of the plasma membrane. Proteins can be anchored to the surface of the cytosoleither by adding a 14-carbon fatty acid (myristic acid) to its amino terminus, or by adding a 16-carbon fatty acid (palmitic acid) or 15- or 20-carbon prenyl groups to the cysteine side chains of the residue. Alternatively, proteins are anchored to the extracellular surface of the plasma membrane through the addition of glycolipids to their carboxy terminus. The selective permeability of biological membranes to small molecules allows the cell to control and maintain its internal composition. Only small, uncharged molecules can diffuse unhindered through the phospholipid bilayers (Fig. 2.49). Small non-polar molecules such as O2 and CO2 are soluble in the lipid bilayer and can therefore easily cross cell membranes. Small uncharged polar molecules like H2O can also diffuse through membranes, but larger uncharged polar molecules like glucose cannot. Charged molecules such as ions, regardless of their size, cannot diffuse across the phospholipid bilayer; even H+ ions cannot pass through the lipid bilayer by free diffusion. Although ions and most polar molecules cannot diffuse across the lipid bilayer, many such molecules (such as glucose) are able to penetrate cell membranes. These molecules cross membranes under the action of specific transmembrane proteins that act as carriers. Such transport proteins determine the selective permeability of cell membranes and thus play a key role in the functioning of membranes. They contain multiple transmembrane regions that form a lipid bilayer junction that allows polar or charged molecules to cross the membrane through protein pores without interacting with the hydrophobic fatty acid chains of membrane phospholipids. As discussed in detail in Chapter 12, there are two main classes of membrane transport proteins (Figure 2.50). Channel proteins create open pores across the membrane, allowing any molecule of the right size to flow freely. For example ion channelsions such as Na+, K+, Ca2+ and Cl- across the plasma membrane. Once opened, the channel proteins form small pores through which ions of the appropriate size and charge can pass through the membrane by free diffusion. The pores formed by these protein channels are not permanently open; rather, they can selectively open and close in response to extracellular signals, allowing the cell to control the movement of ions across the membrane. Ion channels regulated in this way are particularly well known in nerve and muscle cells, where they mediate electrochemical signaling. Unlike channel proteins, carrier proteins selectively bind and transport specific small molecules such as glucose. Instead of creating open channels, carrier proteins act like enzymes and facilitate the passage of certain molecules across membranes. Specifically, carrier proteins bind certain molecules and then undergo conformational changes that open channels through which the transported molecule can pass through the membrane and be released on the other side. through the membrane in an energetically favorable direction determined by concentration and electrochemical gradients, a process called passive transport. However, carrier proteins also provide a mechanism by which energy changes associated with the transport of molecules across the membrane can be linked to the use or production of other forms of metabolic energy, just as enzymatic reactions can be linked to the hydrolysis of ATP or synthesis. For example, molecules can be transported along the membrane in an energetically unfavorable direction (for example, against the concentration gradient), if their transport in this direction is associated with the hydrolysis of ATP as an energy source - a process called active transport (Fig. 2.51). . Thus, the free energy stored as ATP can also be used to control the internal composition of the cellcontrol the biosynthesis of cellular components. . .