?????A hook departs from the basal body, passing into a filament, which ends with a "cap". The filament is a rigid cylinder formed by the flagellin protein. In the cell membrane there are rings M and S, which are often considered as a single whole. The MS ring is surrounded by several motor proteins that transmit torque to the filament. Gram-negative bacteria, in addition to the M and S rings, have two more rings: P, which lies in the peptidoglycan layer, and L, which is located in the outer membrane. A rigid rod passes through all the rings, transmitting the torque to the filament. The movement of the cell occurs due to the rotation of the flagellum clockwise or counterclockwise. In monotrichs, the cell slowly rotates in the direction opposite to the rotation of the flagellum. If the flagellum rotates clockwise, then the cell moves forward with the flagellum, and if against, then the cell is pushed forward with the flagellum (that is, it moves backward with the flagellum). Some bacteria that have a single flagellum rotate it only clockwise, and in order to change the direction of movement, they need to stop and reorient themselves. In peritrichs, the flagella rotate counterclockwise, and if you need to change the direction of movement, the cell stops and makes a somersault. ????? 30. Pili (also known as fimbriae or villi) are filamentous protein structures located on the cell surface of many bacteria. The size of the pili varies from fractions of microns to more than 20 microns in length and 2-11 nm in diameter. Pili are involved in the transfer of genetic material between bacterial cells (conjugation), the attachment of bacteria to the substrate and other cells, are responsible for the adaptation of organisms, serve as attachment sites for many bacteriophages. Structurally, the saws can be from thin filamentous formations to thick rod-shaped structures with axial holes. Peels consist of one or more types of spirally stacked protein molecules, which are called pilin. ????? 32. How does the replication machinery know where to start? It turns out that there are specific nucleotide sequences called origins of replication where replication begins. E. coli has a single origin of replication on its one chromosome, as do most prokaryotes. The origin of replication is approximately 245 base pairs long and is rich in AT sequences. This sequence of base pairs is recognized by certain proteins that bind to this site. An enzyme called helicase unwinds the DNA by breaking the hydrogen bonds between the nitrogenous base pairs. ATP hydrolysis is required for this process because it requires energy. As the DNA opens up, Y-shaped structures called replication forks are formed. Two replication forks are formed at the origin of replication and these get extended bi-directionally as replication proceeds. ????? 33. Two replication forks are formed at the origin of replication and these get extended bi-directionally as replication proceeds. Single-strand binding proteins (Figure 2) coat the single strands of DNA near the replication fork to prevent the single-stranded DNA from winding back into a double helix. The next important enzyme is DNA polymerase III, also known as DNA pol III, which adds nucleotides one by one to the growing DNA chain (Figure 2). The addition of nucleotides requires energy; this energy is obtained from the nucleotides that have three phosphates attached to them. ATP structurally is an adenine nucleotide which has three phosphate groups attached; breaking off the third phosphate releases energy. In addition to ATP, there are also TTP, CTP, and GTP. Each of these is made up of the corresponding nucleotide with three phosphates attached. When the bond between the phosphates is broken, the energy released is used to form the phosphodiester bond between the incoming nucleotide and the existing chain. In prokaryotes, three main types of polymerases are known: DNA pol I, DNA pol II, and DNA pol III. DNA pol III is the enzyme

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required for DNA synthesis; DNA pol I is used later in the process and DNA pol II is used primarily required for repair (this is another irritating example of naming that was done based on the order of discovery rather than an order that makes sense). DNA polymerase is able to add nucleotides only in the 5? to 3? direction (a new DNA strand can be only extended in this direction). It requires a free 3?–OH group (located on the sugar) to which it can add the next nucleotide by forming a phosphodiester bond between the 3?–OH end and the 5? phosphate of the next nucleotide. This essentially means that it cannot add nucleotides if a free 3?–OH group is not available. Then how does it add the first nucleotide? The problem is solved with the help of a primer that provides the free 3?–OH end. Another enzyme, RNA primase, synthesizes an RNA primer that is about five to ten nucleotides long and complementary to the DNA. RNA primase does not require a free 3?–OH group. Because this sequence primes the DNA synthesis, it is appropriately called the primer. DNA polymerase can now extend this RNA primer, adding nucleotides one by one that are complementary to the template strand. The replication fork moves at the rate of 1000 nucleotides per second. DNA polymerase can only extend in the 5? to 3? direction, which poses a slight problem at the replication fork. As we know, the DNA double helix is anti–parallel; that is, one strand is in the 5? to 3? direction and the other is oriented in the 3? to 5? direction. One strand, which is complementary to the 3? to 5? parental DNA strand, is synthesized continuously towards the replication fork because the polymerase can add nucleotides in this direction. This continuously synthesized strand is known as the leading strand. The other strand, complementary to the 5? to 3? parental DNA, is extended away from the replication fork, in small fragments known as Okazaki fragments, each requiring a primer to start the synthesis. Okazaki fragments are named after the Japanese scientist who first discovered them. The strand with the Okazaki fragments is known as the lagging strand. The leading strand can be extended by one primer alone, whereas the lagging strand needs a new primer for each of the short Okazaki fragments. The overall direction of the lagging strand will be 3? to 5?, and that of the leading strand 5? to 3?. A protein called the sliding clamp holds the DNA polymerase in place as it continues to add nucleotides. The sliding clamp is a ring–shaped protein that binds to the DNA and holds the polymerase in place. Topoisomerase prevents the over–winding of the DNA double helix ahead of the replication fork as the DNA is opening up; it does so by causing temporary nicks in the DNA helix and then resealing it. As synthesis proceeds, the RNA primers are replaced by DNA pol I, which breaks down the RNA and fills the gaps with DNA nucleotides. The nicks that remain between the newly synthesized DNA (that replaced the RNA primer) and the previously synthesized DNA are sealed by the enzyme DNA ligase that catalyzes the formation of phosphodiester linkage between the 3?–OH end of one nucleotide and the 5? phosphate end of the other fragment. ????? 34. ????? I think this process is almost impossible to visualize from reading text. I strongly recommend that you watch a couple of animations / videos like the one available here. ????? 35. DNA unwinds at the origin of replication. Helicase opens up the DNA–forming replication forks; these are extended in both directions. Single–strand binding proteins coat the DNA around the replication fork to prevent rewinding of the DNA. Topoisomerase binds at the region ahead of the replication fork to prevent supercoiling (over–winding). Primase synthesizes RNA primers complementary to the DNA strand. DNA polymerase III starts adding nucleotides to the 3?–OH (sugar) end of the primer. Elongation

of both the lagging and the leading strand continues. RNA primers are removed and gaps are filled with DNA by DNA pol I. The gaps between the DNA fragments are sealed by DNA ligase. ????? 36. Unlike multicellular organisms, in unicellular organisms, including bacteria, cell size increase and reproduction by cell division are closely related. Bacterial cells reach a certain size and then divide by binary division. Under optimal conditions, the bacteria grow and divide very quickly, an example of the marine Pseudomonas aeruginosa is described, the population of which can double every 9.8 minutes. In binary division, two daughter cells are formed, identical to the mother. Some bacteria are capable of budding when the daughter cell forms growths on the mother cell, which subsequently separates and goes on to independent life. In the laboratory, bacteria are grown on solid or liquid media. Solid media, such as agar, are used to isolate pure cultures of bacterial strains. Liquid media are used when it is necessary to measure the growth rate or to obtain a large number of cells. When growing bacteria in a liquid medium with mixing, homogeneous cell cultures are obtained, but it is difficult to notice contamination by other bacteria. To identify individual bacteria, selective media containing antibiotics, specific nutrients, or, conversely, devoid of any compounds are used. Most laboratory methods of growing bacteria require large amounts of nutrients to ensure that large volumes of cells are produced quickly. However, in natural conditions, nutrients are limited, and bacteria cannot multiply indefinitely. Due to the limited amount of nutrients, various growth strategies have evolved. Some species grow extremely fast when nutrients are available, for example, cyanobacteria often cause blooming of organic–rich reservoirs. Other organisms are adapted to harsh environmental conditions, for example, bacteria of the genus Streptomyces secrete antibiotics that inhibit the growth of competing bacteria. In nature, many bacterial species live in communities (for example, in the form of biofilms), which provide each cell with the necessary nutrition and protect it from adverse conditions. Some organisms and groups of organisms grow only as part of communities and cannot be isolated into a pure culture. ????? 37. Biofilm –– a set (conglomerate) of microorganisms located on a surface, the cells of which are attached to each other. Usually, the cells are immersed in the extracellular polymer substance (extracellular matrix) secreted by them –– mucus. Biofilm development, and sometimes the biofilm itself, is also called biofouling. The term "biofilm" is defined in different ways, but in general, we can say that a biofilm is a community (colony) of microorganisms located on the interface of media and immersed in an extracellular polymer matrix with a spatial and metabolic structure.There is no single "natural" (phylogenetic) classification of them, reflecting the kinship relationships between individual groups of bacteria, the evolutionary development of individual species. Bacterial classification systems are essentially artificial, and bacteria are grouped into specific groups based on their similarity in a complex of morphological, physiological, and biochemical features (in particular, in the composition of DNA). As of 2020, about 7,000 species of the bacterium and about 600 species of archaea have been described. It is known that most bacteria and archaea (more than 99%) do not grow on laboratory culture media and, therefore, cannot be studied. Pace and several other scientists proposed extracting, cloning, sequencing, and comparing ribosomal RNAs directly from the environment, which allowed for accurate counting and identification of microorganisms without the need for isolation and cultivation. This is especially important for the completely accurate identification of pathogens of infectious diseases and food poisoning. ????? 5 Systematics (taxonomy) of organisms

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consists in the distribution (classification) of them into certain groups, each of which has a name: class, order, family, genus, species. The species is the main taxonomic unit. In microbiology, the term "strain" is often used.Large and medium-sized straight or slightly curved rods, capable of forming endospores resistant to adverse effects (extreme temperatures, drying, ionizing radiation, chemical agents), most species are mobile and have flagella arranged peritrichially, Bacillus anthracis forms capsules.Those that remain attached can be classified based on cellular arrangement: Diplococci are pairs of cocci Streptococci are chains of cocci Staphylococci are irregular (grape-like) clusters of cocci Tetrads are clusters of four cocci arranged within the same plane Sarcina is a genus of bacteria that are found in cuboidal arrangements of eight cocci ?????The giant ring DNA of prokaryotes, the nucleode (a), using RNA and proteins, is repeatedly folded to form numerous spiral loops protruding from the dense central region (b), resulting in a significant nucleoid compaction.The cell membrane maintains the osmotic balance of the cell, carries out various types of transport, including the secretion of proteins, is involved in the formation of the cell wall and the biosynthesis of extracellular polymers, and also receives regulatory signals from the external environment.The cytoplasm occupies the main volume of the bacterial cell and consists of soluble proteins, ribonucleic acids, inclusions and numerous small granules-ribosomes responsible for the synthesis (translation) of proteins.Spiral bacteria, bacteria spiral (helical) shape, form the third major morphological category prokaryotes along with the rod-shaped bacilli and round cocci.[1][2] Spiral bacteria can be subclassified by the number of twists per cell, cell thickness, cell flexibility, and motility.Termination The newly formed protein, which consists of protranslated amino acids, is disconnected.Maturation-
II.Elongation.??????????????????8.?????9.?????10.?????11.?????12.13.?????14.?????15.?????16.?????17.?????18.?????19.?????20.?????21.?????22.?????23.?????24.?????25.26.?????27.?????28.?????29.?????38.

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