DNA (nucleic acid)

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DNA is a double-stranded nucleic acid that is the carrier of heredity in cellular organisms. It is found in the nucleus of eukaryotic cells, or in the cytoplasm of prokaryotes. All the information necessary for the growth and survival of the organism is encoded in it. The structure of the double helix was described in 1953 by Mr. James D. Watson and Francis Crick, who received the Nobel Prize in 1962 for this discovery. Structure [✎ edit embedded article] molecule (deoxyribonucleic acid) is made up of two polynucleotide chains . The chains are antiparallel to each other - one chain has the direction of phosphodiester bonds 5' » 3' and the other 3' » 5' - we are talking about the 3' or 5' end. An -OH group is attached to the 3' end , while a phosphate group is attached to the 5' end. General characteristics

Spatial structure of DNA The structure is made up of three components – sugar, phosphate, base . The sugar component consists of the five-carbon sugar 2-deoxy-D-ribose (oxygen is missing in the 2' position of DNA compared to normal ribose). Purine derivatives (Adenine, Guanine) and pyrimidine derivatives (Cytosine, Thymine) are represented as nitrogenous bases in DNA . Bonding interactions occur between N-bases of opposite strands. The law of complementarity Only 2 specific N-bases are always bound together (always 1 pyrimidine base and 1 purine base), namely: • A – T (connected by 2 hydrogen bonds); • C – G (connected by 3 hydrogen bonds). van der Waals forces (stabilization) act between neighboring bases . equation applies : A + CT + G=1

Both polynucleotide strands (primary structure of DNA) create the most common right-handed helix known as double helix (secondary structure of DNA) → the most frequently occurring form is the B-form of DNA = right-handed . DNA molecules can still occur in the right-handed form A and in the left - handed form Z. The transition between individual forms is possible based on a change in physical and chemical conditions. DNA types

Difference between DNA and RNA structure 1. Nuclear (chromosomal)

Cell nucleus → chromosome → stranded DNA From a functional point of view, these are : 1. DNA that encodes the sequence of amino acids in a polypeptide or some RNA . 2. DNA, which has a control and management function. 3. Special types of DNA have specific functions in chromosomes , e.g. in the area of centromeres and telomeres. 4. DNA, the function of which we do not yet know anything. In eukaryotes, approximately 60% of DNA consists of unique (or low-repetition) sequences – this includes, for example, genes encoding polypeptides or similar non-functional pseudogenes . Others represented are repetitive sequences . We divide them into: 1. moderately repetitive sequence – number of copies in the genome 10–10 5 (this includes, for example, genes for rRNA and histone-type proteins); 2. sequence highly repetitive – on the order of 10 6 copies / genome. Repetitive sequences can be scattered throughout the genome. Long repetitive sequences are referred to as LINEs (Long Interspersed Nuclear Elements). Short repetitive sequences are referred to as SINEs (Short Interspersed Nuclear Elements). Most SINEs are derived from tRNA genes → their formation is explained by reposition (transcription) from RNA by reverse transcriptase. The so-called Alu-sequences are specific for primates , where almost every 4kb section of human DNA contains this sequence - their origin is 7SL DNA. Another possibility is the so-called tandem repetitive sequences , where the individual repetitions are one after the other - e.g.: genes for rRNA or so-called satellite DNA. 2. Extrachromosomal

Mitochondrial DNA In humans, it is found in mitochondria . The arrangement of the mitochondrial genome is different from the nuclear genome of a eukaryotic cell, but it is similar to the arrangement of the genome in prokaryotes . DNA has a circular arrangement in mitochondria. In humans, it is 16.6 kb in size. In the human genome, a total of 37 genes code - of which 24 genes are involved in the proteosynthetic apparatus of mitochondria - 16S and 23S genes for rRNA, 22 genes for tRNA. The rest are involved in the enzymatic equipment of mitochondria. Most genes are coded on the H (heavy) strand of DNA. The information is quite strongly compressed, it does not contain introns ! Other differences include that it has 4 triplets with different meanings to those in the nuclear genome, there are also differences in initiation and termination . Replication [✎ edit embedded article] DNA replication is the transfer of information from DNA to DNA . It is therefore a heritable ability . General characteristics During replication, two identical daughter DNAs are formed from one parent DNA molecule - each with one strand from the original DNA, so this is a semi-conservative process , where the newly created double helix always has one original strand and the other newly synthesized strand . It is used during reproduction, when it ensures the identity of the genetic information of both daughter cells (for reproduction, it is necessary for the offspring to receive full genetic information). The rate of replication in animal cells is estimated to be 0.5-0.15 µm/min, it is a really slow process, therefore it takes place in many places at the same time . Replication progress

DNA replication

DNA replication

DNA replication The sites where replication occurs are called replicons . The number of replicons in a cell is not constant , there are more in rapidly multiplying cells than in slowly multiplying cells. Replication does not occur on all replicons at the same time , generally it starts later in replicons located in heterochromatin. Enzymes called DNA polymerases play a key role in DNA replication . There are 5 types of enzymes known as DNA-dependent DNA polymerases in humans (in animal cells there are five types). The following applies to all types of DNA polymerases : • They need a matrix = string to which they make a complement according to the base complementation rules; • in their work they always proceed from the 5' end to the 3' end ; • they need to have available the free end of the 3' nucleotide, to which they attach a phosphodiester bond to the 5' place of the newly

inserted nucleotide. The newly introduced nucleotides are used in the form of nucleotide triphosphates , by splitting two macroergic bonds, the necessary energy is obtained to make the bond; • DNA polymerase cannot initiate synthesis de novo , but only adds a new nucleotide at the 3' position of the previous nucleotide; • in order for DNA polymerase to begin adding nucleotides to the new DNA strand, the hydrogen bonds (i.e., the low-energy bonds between the two strands) must first be broken by the helicase enzyme .

The sites that arise after helicase disruption are referred to as origins of replication . Replication origins are formed by specific sequences of nucleotides that are recognized by initiation proteins (initiation factors). For easy separation of the chains, these sequences contain a high proportion of adenine and thymine . In bacteria , we would find only one such origin . Human DNA creates around 10,000 replication origins, which also enables it to replicate itself in a relatively short time. Primase (DNA-dependent RNA-polymerase) creates a short DNA strand at the beginning of the replicated section of the new strand RNA primer ("eyelet") - DNA polymerase can attach the first nucleotide of a new DNA strand to its 3' end. Since both DNA strands are antiparallel (the 5' end of one strand corresponds to the 3' end of the other strand) and since DNA polymerase synthesizes "unidirectionally" (from 5' to 3'), replication can only proceed continuously on one strand . On this strand, therefore, replication (which is carried out by δ-polymerase) takes place faster and the strand is referred to as the leading strand . On the other (delayed) strand, replication takes place in parts - so-called Okazaki fragments ← replication is slower here, it is carried out by α- polymerase , which has primase activity. addition to the mentioned DNA polymerases, a number of enzymes are involved in the replication process , whose role is : • develop a suprahelical structure - gyrase ; • unfold the Watson-Crick double helix – helicases . After new strands are synthesized to the original (template) strands, DNA replication is complete . DNA polymerase makes 1 mistake in about 10 7 replicated bases (theoretically, G – T and A – C pairs can also form, but they are much less stable). In addition, the DNA polymerase itself has a correction function (in the event of an error, it also performs a correction, consisting of cutting out and adding the correct base), with this method, the RNA loops are probably also removed, and then the enzyme ligase joins the individual fragments into a continuous chain . Transcription Transcription is the transcription of genetic information from DNA into an RNA molecule . It is overwhelmingly a transcription of information from one gene , used to create one specific protein , which the cell needs at a given moment. The RNA strand is formed on the principle of complementarity to the DNA strand. Transcription factors Transcription factors (TF) are proteins that participate in the initiation of transcription (the transcription of hereditary information from a gene from DNA to RNA). Through them, gene expression is adapted to the needs of the cell or the whole organism (e.g. hormones , hypoxia can stimulate the expression - transcription of certain genes).

See the Transcription Factors page for more details .

Posttranscriptional modifications Post-transcriptional modifications occur after the successful transcription of DNA into RNA .

See Post-transcriptional modifications for more detailed information .

Translation Translation , or protein synthesis , is the translation of the nucleotide sequence of mRNA into a sequence of amino acids protein . The process takes place on ribosomes and individual amino acids are classified according to the rules of the genetic code .

More detailed information can be found on the Translation page .

Post-translational modifications Post-translational modifications begin after successful translation .

See the Post-translational modifications page for more detailed information .

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