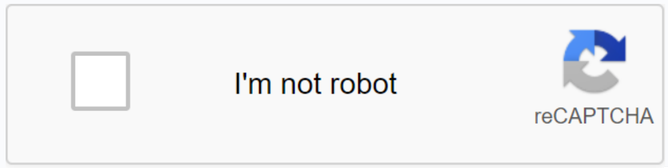

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Physical and chemical structure of dna pdf

For non-technical introductions to the subject, see Introduction to Genetics. For other uses, see Ambiguity. The structure of the molecular DNA double helix that transmits genetic information. The atoms in the structure are color-coded by the elements, and the detailed structure of the two base pairs is displayed in the lower right corner. DNA double helix Deoxyribonucleic acid (/diːˈɒksɪˌraɪboʊnjuːˌkliːɪk, -hleâ-/ (listening); part structure; 1] DNA) is a molecule composed of two polynucleotide chains that form a double spiral that carries genetic instructions for the development, function, growth and regeneration of all known organisms and many viruses. DNA and ribonucleic acid (RNA) is a nucleic acid. Along with proteins, lipids and complex carbohydrates (polysaccharides), nucleic acid is one of the four main types of macromolecules that are essential to every known form of life. Both DNA strands are known as polynucleotides because they consist of a simple monosule unit called nucleotides. [2] [3] each nucleotide is composed of four nitrogen-containing nucleotides (cytosine [C], guanine [G], adenine [A] or thiamine [T]), a sugar and phosphate group called jailbreak liboje. Nucleotides are combined in chains by a shared bond between sugar in one nucleotide and the next phosphate (insandaeaster linkage) to alternate the sugar phosphate backbone. Nitrogen bases in two separate polynucleotide strands are combined with a base pairing rule (A with T and C) with hydrogen bonds to create two separate DNA. Complementary nitrogen itis is divided into two groups: pyrimidine and purin. In DNA, pyrimidin is thymine and cytosine; Purin is adenine and guanine. Two strands of double stranded DNA store the same biological information. This information is replicated, as if the two strands were separated. A large portion of DNA (more than 98% for humans) is non-coding, meaning these sections do not serve as patterns for protein sequences. The two strands of DNA run in the opposite direction to each other, so they cannot be compared. One of four types of nucleobases attached to each sugar (unofficially, base). Encoding genetic information is a sequence of these four nucleome bases along the backbone. RNA strands are created using DNA strands as templates in a process called transcription, and the DNA base is exchanged to that base except for the pleural (T), where the RNA replaces uracil (U). [4] According to the genetic code, these RNA strands specify a sequence of amino acids in the protein in the process of translation. Within eukaryotic cells, DNA is organized into long structures called chromosomes. Before a typical cell division, these chromosomes are replicated in the process of DNA replication, providing a complete set of chromosomes for each daughter cell. Eukaryotes Plants, fungi and protists) store most of the DNA inside the cell nucleus as nuclear DNA, and part of the mitochondria are stored in mitochondrial DNA or chlorophyll cell DNA. [5] In contrast, prokaryotes (bacteria and archaeology) store their DNA only in cytoplasm in circular chromosomes. Within the eukaryotic chromosomes, chromosomal proteins such as histone, small and tissue DNA. These compressed structures lead to interactions between DNA and other proteins, helping to control which parts of DNA are transferred. DNA was first isolated by Friedrich Misher in 1869. The molecular structure was first identified in 1953 by Francis Crick and James Watson of the Cavendish Institute at The University of Cambridge, and his model-building efforts were guided by X-ray diffraction data obtained by Raymond Gosling, a graduate student at King's College London by Rosalind Franklin. DNA is used by researchers as a molecular tool to explore physical laws and theories, such as ergonomic theorems and theories of elasticity. The unique material properties of DNA have made it an attractive molecule for material scientists and engineers interested in micro and nanomanufacturing. Among the notable developments in this field are DNA origami and DNA-based hybrid materials. [6] the chemical structure of the DNA; Hydrogen bonds, represented by dotted DNA, are long polymers made in repeating units called nucleotides, each symbolized by a single character: A, T, C or G.[7]] DNA structures are dynamic along its length, and can solidify into solid loops and other shapes. [9] In all species, it consists of two retinal chains bound to each other by hydrogen bonds. Both chains are coiled around the same axis and have the same pitch of 34 Angstrom (Å) (3.4 nanometers). The chain pair has a radius of 10 pieces (1.0 nanometers). [10] According to other studies, when measured with different solutions, DNA chains measured 22 to 26 anstrom width (2.2 to 2.6 nanometers) and one nucleotide unit measured at a length of 3.3 Å (0.33 nm). [11] Each individual nucleotide is very small, but the DNA polymer can be very large and may contain hundreds of millions of nucleotides, such as chromosome 1. Chromosome 1 is the largest human chromosome with approximately 220 million base pairs, and will be 85 mm long when straightened. [12] DNA generally does not exist as a single strand, but instead exists as a pair of strands that are held tightly together. [10] [13] These two long strands revolve around each other in the shape of a double spiral. Nucleotides include both segments of the backbone of molecules (holding chains together) and nucleobases (which interact with other DNA strands in the helix). Nucleobase connected to sugar is called nucleoside, a base connected to sugar and one or more phosphate groups is called nucleotides. biopolymers containing multiple connected nucleotides (such as DNA) The backbone of the DNA strands is created alternately between phosphate and sugar groups. [15] The sugar in DNA is 2-deoxyboje, a pentos (5 carbon) sugar. Sugar is combined together by a phosphate group that forms a phosphate bond between the third and fifth carbon atoms of the adjacent sugar ring. These are known as 3′end (three prime ends) and 5′ end (five prime ends) carbon, the main symbol used by thalokibos to distinguish them from the carbon atoms at the base, which form a glycodic bond. Thus, some DNA strands have one end with a group of phosphates usually attached to the 5′ carbon (5′ insporyl) of the Ribose, and another end with a free hydroxy group attached to the 3′ carbon (3′ hydiaxyl) of the ribose. The direction of 3′ and 5′ along the sugar phosphate backbone, carbon gives directionality (sometimes referred to as polarity) to each DNA strand. In a double helix of nucleic acid, one strand of nucleotide direction is the opposite of the direction of the other strand: the strands are parallel. The asymmetric end of the DNA strand has the directionality of five prime ends (5′) and three prime ends (3′), and the 5′ end ends the 3′ terminal hydroxyil group with a group of end phosphates. One main difference between DNA and RNA is sugar along with 2-deoxyribose in DNA, which is replaced by alternative pentossugarribose in RNA. [13] Section of DNA. The base lies horizontally between the two spiral strands[16] (animated version). DNA double helix is mainly stabilized by two forces: the hydrogen bond between nucleotides and the primary stacking interaction between the aromatic nucleobase. [17] the four bases found in the DNA are adenine (A), cytosin (C), guanine (G) and thiamine (T). These four bases are attached to sugar phosphate to form a complete nucleotides as shown in adenosine monophosphate. Adenine pairs a Pair of A-T and G-C bases by matching thymine, guanine and cytosine. [18] [19] Nucleobase classification nucleobase is classified into two types: celestial, A and G are 5-6 member heterogeneous compounds and pyrimidine, sixth-person ring C and T. [13] fifth pyrimidine nucleobase, urasil (U) fused to replace the usual RNA tamine and differ from the dimine of the usual RNA. In addition to RNA and DNA, many artificial nucleic acid analogs are designed to study the properties of nucleic acids or for use in biotechnology. [20] The unstyled base deformation base occurs in DNA. The first of these things was 5-methylcytosinfound in the genome of Mycobacterium tuberculosis in 1925. [21] The reason why this amorphitisitis present in bacterial viruses (bacteriophages) is to avoid the restricted enzymes present in the bacteria. This enzyme system acts at least partially as a molecular immune system that protects bacteria from infection. The modification of base cytosine and adenine, a more common and modified DNA base, plays an important role in controlling epigenetic control of gene expression in plants and animals. [23] It is known to occur in the list DNA of the unformal base found in the DNA. [24] Most of these are full base and uracil crystals. Modified adenosine N6-carbamoil methyladenine N6-methyladeined crystal guanine 7-Deazaguanine 7-methyl guanine modified cytosine N4-methylcitozin 5-carboxysine 5-cloud-performing tosin 5-glycotosin 5-glycotosin Cosil hydrocy5-hydroxyshitosin 5-methylcitosin modified timmydine α-glutatisymidin α-putrescinIltamine urasil and modified base J uracil 5-di hydroxypentauracil 5-hydroxymethyl diocioshiosin other deoxysha urasil 2,6-diamiapurusine. The latter is a binding site for Hoechst Stain Dye 33258. Groove twin helical strands form a DNA backbone. Another double spiral can be found to track the space or groove between the strands. These voids are adjacent to the base pair and can provide binding sites. Because strands are not positioned symmetrically with each other, the size of the grooves is sterile. One home, the main groove, 22 angstrom (Å) wide and the other, minor home, 12 Å wide. [25] The width of the main groove means that the edge of the base is more accessible from the main home than the minor groove. As a result, proteins such as transcription factors, which can be bonded to a specific sequence in double-stranded DNA, usually come into contact with the side of the base exposed to the main groove. [26] This situation depends on the unusual suitability of DNA in the cell (see below), but the main and minor grooves are always named to reflect the difference in size that can be seen when the DNA is twisted back into the normal B form. Basic pairing additional information: From the base pair DNA double helix, each type of nucleobase to combine just one type of nucleobase on another strand and one strand. This is called complementary base pairing. Purin forms a hydrogen bond to pyridine, and adenine binds only to thymines with two hydrogen bonds, and only cytosine bonds in guanine in three hydrogen bonds. This array of two nucleotides that bind together across a double helix is called the Watson Creek Base Pair. DNA with a high GC content is more stable than DNA with low GC content. The Hoogsteen Bass Pair is a rare strain of bass pairing. [27] Since hydrogen bonds are not shared, they are cracked and can be re-bonded relatively easily. Two strands of DNA in a double spiral can thus be pulled off like a zipper by mechanical force or high temperature. [28] As a result of the complementaryness of this base pair, all information of the double stranded sequence of the DNA helix is replicated in each strand essential for DNA replication. This reversible and specific interaction between complementary primary pairs is critical in all cases. Of DNA from organisms. [8] Top, three hydrogen bonds and a GC base pair. As mentioned above, most DNA molecules are actually bound together in a helical manner by two polymer strands, non-covalent binding; This dual stranding (dsDNA) structure is largely maintained by the intra-strand base stacking interaction, which is the strongest in the G and C stacks. Two strands can come apart, a process known as melting to form two single-stranded DNA (ssDNA) molecules. Melting occurs at high temperatures, low salts and high pH (low pH melts DNA, but low pH is rarely used because dna is unstable due to acid desperation). Stability in the form of dsDNA depends not only on GC content (%G, C basepair), but also in sequence (because stacking is specific to the sequence) and length (longer molecules are more stable). Stability can be measured in a variety of ways. A common method is the melting temperature, where 50% of the ds molecule is converted into ss molecules. The melting temperature depends on the ionic strength and concentration of DNA. As a result, the percentage and overall length of the GC base pair of DNA double helix to determine the strength of the association between the two strands of DNA. Long DNA helicopters with high GC content have stronger interaction strands, while short helicas with higher AT content have weak interaction strands. [29] In biology, parts of DNA double helix, such as tataat Pribnow boxes in some promoters, tend to have a high AT content, which makes it easier to remove strands. [30] In the laboratory, the intensity of these interactions can be measured by finding the temperature required to break half of the hydrogen bond, their melting temperature (also known as the Tm value). When all the underlying pairs of DNA double helixes melt, the strands are separated and present in the solution. These single stranded DNA molecules do not have a single common form, but some compatibility is more stable than others. [31] Sense and Antisense More Information: Sensory (Molecular Biology) DNA sequences are called sensory sequences when they are the same as a copy of messenger RNA converted into a protein. [32] The sequence of opposite strands is called an antisense sequence. Sense and antisense sequences can be present in different parts of the same strand of DNA (i.e., both strands may contain sense and antisense sequences). In both prokaryotes and eukaryotes, but the antisense RNA sequence is generated, the function of these RNA is not entirely clear. [33] One suggestion is that the antisense RNA is involved in gene expression control through RNA-RNA base pairing. [34] Some DNA sequences of procayotes and eukaryotes, more on plasmids and viruses, blurring the distinction between sensory and antisense strands Gene. [35] In these cases, some DNA sequences perform a double duty, coding one protein when read along one strand, and the second protein when read in the opposite direction along the other strand. In bacteria, this nesting can be involved in the regulation of gene transcription,[36] while in the virus, duplicate genes increase the amount of information that can be encoded within the small viral genome. [37] Supercoil Ing Extra Information: DNA Supercoil DNA can be distorted like a rope in the process of DNA overheating. In a comfortable state of DNA, strands typically circle the axis of a double helix once every 10.4 basic pairs, but when the DNA is distorted the strands are wound more tightly or more loosely. [38] If the DNA twists in the direction of the spiral, this is a positive super-coiling, and the base is held together more firmly. Twisting in the opposite direction is a negative super-coiling, and the base is more easily disassembled. In nature, most DNA has some negative overconfidence introduced by an enzyme called topoimorase. [39] These enzymes are also necessary to alleviate the torsional stress introduced into the DNA strands in the process, such as transcription and DNA replication. [40] From left to right, A, B and Z DNA alternative DNA structure of dna dna structure: molecular structure of nucleic acid: the structure of the jailbreak ribose nucleic acid, molecular model and DNA structure DNA of DNA exists in many possible conformity, including A-DNA, B-DNA and Z DNA form, b DNA and Z DNA only it is directly observed. [15] The form adopted by DNA depends on the level of hydration, dna sequence, quantity and direction of super-coiling, chemical deformation of the base, the type and concentration of metal ions, and the presence of polyamine in the solution. [41] The first published report of A-DNA X-ray diffraction patterns - also b-DNA - provides a limited amount of structural information about dna-oriented fibers that use analysis based on Patterson conversion. [42] [43] Alternative analysis was proposed in 1953 for in vivo B-DNA X-ray diffraction-scattering patterns of high-hydrated DNA fibers in terms of the square of veselfunction, such as Wilkins. [44] In the same journal, James Watson and Frances Crick published molecular modeling analysis of DNA X-ray diffraction patterns, suggesting that the structure was a double spiral. [10] B-DNA forms are the most common under conditions found in cells, but [45] is not a well-defined form, but a family of related DNA conformity that occurs at the high moisture levels present in the cell. Their corresponding X-ray diffraction and scattering patterns are characteristic of molecular parachutes with a significant degree of disorder. [47] [48] Compared to B-DNA, The A-DNA form is a shallow, wider minor groove and a narrower, deeper main and wider right-handed spiral A form occurs under non-physiological conditions in partially dehydrated samples of DNA, while in hybrid pairing of DNA and RNA strands from cells, and in enzyme DNA complexes. [49] [50] Segments of DNA chemically modified by methylation can undergo larger changes in formation and adopt form Z. Here, the strand spun the spiral axis in a left-handed spiral, which is the opposite of the usual B shape. [51] This unusual structure may be recognized by a particular Z-DNA binding protein and may be involved in the regulation of transcription. [52] A 2020 study concluded that DNA was replaced right-handed by ionization by cosmic rays. [53] Over the years, biologists have suggested the existence of shadow biospheres, the earth's supposed microbial biosphere, which uses radically different biochemical and molecular processes than currently known organisms. One of the suggestions was the presence of living organisms that used arsenic instead of being in DNA. A 2010 report on the possibility of the bacterium GFAJ-1, despite the study's objections, published [54][54][55][55], and evidence suggests that it actively prevents bacteria from injecting arsenic into DNA backbones and other biomolecules. [57] Quadruflex structure additional information: a special area of DNA called telomeres at the end of the G-quadruflex linear chromosome. The main function of this area is to allow cells to replicate chromosomal ends using chromosomes as enzymes that normally replicate DNA 3′ ends of chromosomes. [58] These special chromosome caps help protect the END of the DNA and prevent the cell's DNA repair system from being treated with damage to be corrected. [59] In human cells, telomeres are usually the length of a single stranded DNA that contains thousands of repetitions of simple TTAGGG sequences. [60] DNA quadruple formed by telomere repetition. The repeated formation of the DNA backbone is very different from that of a typical DNA helix. The central green sphere represents potassium ions. [61] These guanine-rich sequence sequencing can stabilize the chromosomal end by forming the structure of a laminated set of four units rather than the normal base pairs found in other DNA molecules. Here, four guanine bases, called guanine tetrads, form flat plates. These flat four-base units overlap each other and form a stable G-quadruflex structure. [62] These structures are stabilized by a hydrogen bond between the base and the edge of the metal ion in the center of each four-unit unit. [63] Different structures can also be formed with a central set of four bases coming from a single strand or several different parallel strands folded around the base, each contributing one base to the central structure. In addition to these accumulated structures, telomeres form a large loop structure called telomere loops or T loops. Here At the very end of the T loop, single stranded telomere DNA is held in the area of double stranded DNA by a single stranded telomere strand, paired with one of two strands. This triple-stranded structure is called a displacement loop or a D loop. [62] single branch multi-branch branch DNA can form a network containing multiple branches. Branch DNA More Information: In branch DNA and DNA nanotechnology DNA, wear occurs when non-complementary areas are present at the end of otherwise complementary double strands of DNA. However, the branched DNA may occur when a third strand of DNA is introduced and includes adjacent regions that can be hybridized with the worn area of the existing double strands. The simplest example of branched DNA involves only three strands of DNA, and complexes involving additional strands and multiple branches are also possible. [65] Branch DNA can be used in nanotechnology to construct geometric shapes, see section on the use of the technology below. Artificial base main article: nucleic acid analogs several artificial nucleobases are synthesized, and were successfully incorporated into the eighth-term DNA analogs named hachimoji DNA. Dubbed S, B, P and Z, these artificial bases can be combined with each other in a predictable way (S-B and P-Z), maintaina double helix structure of DNA, and are transferred to RNA. Their presence means that there is nothing special about the four natural nucleobases that have evolved on earth. [66] [67] Chemical deformation and altered DNA-packed cytosin 5-methylcytosin ethymine structure of cytosine structure and without the structure of 5 methyl groups. Talamination converts 5-methylcytosin into thymine. Additional basic modifications and DNA packaging: The expression of DNA methylation and chromamartinis remodeling genes depends on how DNA is packaged on chromosomes. Basic modifications can be involved in packaging with districts with low or no gene expression, which typically contains high levels of methylation of cytosine bases. The impact on DNA packaging and gene expression can also be caused by a shared modification of the histone protein core, which is wrapped in a chromatin structure by DNA, or by remodeling carried out by the Chromatin remodeling complex (see Chromatin Remodeling). Between DNA methylation and histone modifications, chromatin and gene expression can be coordinated. [68] For example, cytosinmethylation produces 5-methylcytosin, which is important for x inactivation of chromosomes. [69] The average level of methylation varies from organism to organism- worms Caenorhabditis elegans lack cytosinmethylation, while vertebrates have higher levels, with up to 1% of their DNA containing 5-methyl cytosine. [70] It can leave the thimine base and recapture it, so methylated cytosine is particularly prone to mutations. [71] Other basic modifications produce j-base in kinetoststried, including adenine methylation in bacteria, the presence of 5-hydroxymethylcytosin, [72] and glycolysis of uracil in the brain. [73] [74] Damage additional information: DNA damage (naturally occurring), DNA damage theory benzo [a] pyrenees of mutations and aging, the main mutant source of tobacco smoke, DNA [75] shared derivatives between DNA can be damaged by many kinds of mutants changing the DNA sequence. Mutants also include high-energy electromagnetic radiation such as oxidizers, al-killing agents, ultraviolet rays and X-rays. The type of DNA damage produced depends on the type of mutant. For example, UV light can damage DNA by creating a timin dimmer, a cross link between pyrimidin bases. [76] On the other hand, oxides such as free radicals or hydrogen peroxide cause many forms of damage, especially guanocin and basic modifications to double-stranded breakage. [77] Typical human cells contain about 150,000 bases that have suffered oxidative damage. [78] Of these oxidative lesions, the most dangerous double strand breaks, these are difficult to repair and can produce point mutations, inserts, deletions from DNA sequences, and chromosomal translocation. [79] These mutations can cause cancer. Because of the limitations inherent in DNA repair mechanisms, if humans lived long enough, they would all eventually develop cancer. [80] [81] DNA damage that occurs naturally due to the normal cell process to generate a reactive oxygen species, hydrolysis activity of the number of cells, etc. also occurs frequently. Although most of these damages are repaired, some DNA damage from some cells may remain despite the effects of the repair process. This remaining DNA damage accumulates with age in the tissues after mammals. This accumulation appears to be an important root cause of aging. [82] [83] [84] Many mutants fit into the space between two adjacent base pairs, which is called interculling. Most intercalators are aromatic and flat molecules. Examples include ethidium bromide, acritin, donomicin and doxorubicin. For interlocks that fit between the base pairs, the base must release a double helix and separate the DNA strands by distorting them. This inhibits both transcription and DNA replication, causing toxicity and mutations. [85] As a result, the DNA intercalator may be a carcinogen and in the case of thalidomide, it may be terratogen. [86] Benzo [a] pyren dior epoxyside and others, such as aflatoxin form DNA derivatives induce errors in replication. [87] Nevertheless due to the ability to inhibit DNA transcription and replication, other similar toxins are used in chemotherapy to inhibit rapidly growing cancer cells. [88] The location of the eukaryotic DNA in biological function DNA usually occurs with linear chromosomes in eukaeotes, and circular chromosomes in prokaryotes. A set of chromosomes in cells constitutes its genome; The human genome has about three billion basal pairs of DNA arranged by 46 chromosomes. [89] The information transmitted by DNA is held in the order of fragments of DNA called genes. The transmission of genetic information in genes is achieved through complementary base pairing. For example, in transcription, when the cells use information in the gene, DNA sequences are copied to a complementary RNA sequence through the attraction between THE DNA and the correct RNA nucleotides. Generally, these RNA copies are then used to make matching protein sequences in a process called translation, which relies on the same interaction between RNA nucleotides. Alternatively, cells can simply copy their genetic information in a process called DNA replication. The details of these functions are covered in other documents. The focus here is on the interaction between DNA and other molecules that neutralize the function of the genome. Gene and genome additional information: cell nuclei, chromatin, chromosomes, genes and non-coding DNA dna is packed in a process called DNA condensation to match a small amount of cells. In eukaryotes, DNA is located in small cell nuclei in mitochondria and chlorophyll. In prokaryotes, DNA is held within irregularly formed bodies in cytoplasm called nucleoids. [90] The genetic information of the genome is maintained within the gene, and the entire set of this information in an organism is called a genotype. Genes are units of anti-inflammatory and are areas of DNA that affect specific characteristics in the organism. The gene contains an open reading frame that can be transferred and regulatory sequences such as promoters and reinforcements to control the transcription of open reading frames. In many species, the total sequence of genome encodes just a small fraction of the protein. For example, only about 1.5% of the human genome consists of protein-coding exons with more than 50% of human DNA consisting of non-coding repeatability sequences. [91] The reason for the presence of too much uncoded DNA in the eukaryotic genome and the special difference in genome size, or C value, represents a long-standing puzzle known as the C-value riddle among species. [92] However, some DNA sequences that do not encode proteins can still encode functional non-coding RNA molecules involved in the regulation of gene expression. [93] T7 RNA polymerase (blue) plays a structural role in the chromosome to produce a mRNA (green) in the DNA template (orange) [94]. Telomeres and centrome typically contain several genes, but they are important for the function and stability of chromosomes. [59] [95] A rich form of non-coded DNA in humans is a pseudo gene, a copy of a gene inactivated by a mutation. [96] These They are usually only molecular fossils, although they can sometimes act as primitive genetic material for the creation of new genes through the process of gene duplication and divergence. [97] Transcription and translation additional information: genetic code, transcription (genetics), and protein biosynthesis A gene is a sequence of DNA that may include genetic information and affect the phenotype of the organism. Within the gene, the sequence of bases along the DNA strands then defines the messenger RNA sequence, which defines one or more protein sequences. The relationship between the nucleotide sequence of the gene and the amino acid sequence of the protein is determined by the translation rules commonly referred to as genetic code. The genetic code consists of a three-letter 'word' called codon formed in a sequence of three nucleotides (e.g. ACT, CAG, TTT). In transcription, the codon of the gene is copied to the messenger RNA by RNA polymerase. These RNA copies are decoded by ribosomes reading the RNA sequence by basal pairing the messenger RNA to deliver the RNA to carry the amino acid. There are 64 codons (43 combinations) because there are four bases in the three-way combination. They encode 20 standard amino acids, giving most amino acids one or more possible codons. There are three 'stop' or 'nonsense' cordons that signify the end of the coding area. These are TAA, TGA and TAG codons. DNA replication: The double spiral is released by a helicopter and topoasorase. Next, one DNA polymerase produces a copy of the main strand. Another DNA polymer binds to a lagging strand. This enzyme creates discrete segments (called okazaki fragments) before DNA ligase binds together. More replication: DNA replication cell division is essential for the organism to grow, but when the cells are divided, dna must be replicated in the genome so that the two daughter cells have the same genetic information as their parents. The double stranded structure of DNA provides a simple mechanism for DNA replication. Here, two strands are separated and complementary DNA sequences of each strand are reproduced by an enzyme called DNA polymerase. This enzyme uses complementary base pairing to find the right base and combine it with the original strands to create complementary strands. Because DNA polymerase can only extend dna strands from 5′ to 3′ in the direction, other mechanisms are used to copy the antimicrobial strands of the double helix. [98] In this way, the base of the old strand directs the base to appear on the new strands, and the cells end up with a perfect copy of DNA. Extracellular nucleic acid naked extracellular DNA (eDNA), most of it is almost ubiquitous in the environment, released by cell death. The concentration of the soil can be as high as 2 µg/L, the concentration in the natural aquatic environment can be high at 88 µg/L.[99], and various possible functions may have been suggested for eDNA. Gene delivery; [100] Can provide nutrients. [101] and may serve as a buffer for recruiting or hitting ions or antibiotics. [102] Extracellular DNA acts as a functional extracellular matrix component in the biofilm of various bacterial species. It can act as a recognition factor for controlling the adhesion and dispersion of a particular cell type of bioperine. [103] may contribute to the formation of biofilm; [104] It can contribute to the stamina and resistance of biofilm to biological stress. [105] Cellless fetal DNA is found in the mother's blood and can be sequenced to determine much information about the developing fetus. [106] In the name of environmental DNA eDNA, we have seen the use in natural sciences as an investigative tool for ecology increase, monitor the movement and presence of species in water, air or land, and evaluate the biodiversity of the region. [107] [108] All functions of interaction dna with proteins depend on interaction with proteins. These protein interactions may be non-specific, proteins can be specifically coupled to a single DNA sequence. Enzymes can also bind to DNA and these, and polymers for copying DNA sequencing in transcription and DNA replication are particularly important. More information about DNA binding proteins: DNA binding protein interactions (orange) and histone (blue). The primary amino acid of this protein binds to the acidphosphate group in DNA. Structural proteins that bind DNA are well-understood examples of non-specific DNA protein interactions. Within chromosomes, DNA is held in complexes with structural proteins. This protein organizes DNA into a miniature structure called chromatin. In eukaryotes, this structure involves DNA binding to a complex of small basic proteins called crashes, while multiple types of proteins from prokaryotes are involved. [109] [110] Histon forms a disk-shaped complex called nucleosis, which includes two complete rotations of double-stranded DNA that surrounds the surface. This non-specific interaction is formed through the basic residue of histone acid sugar of DNA - creates an ion bond to the phosphate backbone, and therefore is largely independent of the basic sequence. [111] chemical modifications of these basic amino acid residues include methylation, phosphorylation and acetylation. [112] These chemical changes change the intensity of the interaction between DNA and histone, allowing THE DNA to approach transcription factors somewhat and change the transcription rate. [113] Other non-specific DNA binding proteins in chromatin contain high-mobility group proteins that bind to bent or distorted DNA. [114] These proteins are important for bending the arrangement of nucleosomes and arranging them into larger structures that make up chromosomes. [115] A separate group of DNA binding proteins is a DNA binding protein that combines a single stranded DNA in particular. In humans, clone protein A Members of this family are used in processes in which double helixes are separated, including DNA replication, recombination, and DNA repair. [116] These binding proteins appear to stabilize single-stranded DNA and prevent stem loops from forming or degrading by nucleases. Lambda suppressor helix-helix transcription factor binds to DNA targets[117] in contrast to other proteins have evolved to bind to specific DNA sequences. The most intensive study of these is the various transcription factors that are proteins that control the transcription. Each transcription factor binds to a specific set of DNA sequences and activates or inhibits the

transcription of genes that have these sequences close to their promoters. Transcription factors do this in two ways. First, they can be combined through RNA polymerase, directly or through other mediator proteins responsible for transcription; This allows the promoter to find the polymer and start the transcription. [118] Alternatively, the transcription factor may combine the enzyme to modify the histone in the promoter. This changes the accessibility of dna templates to polymers. [119] Because these DNA targets can occur throughout the genome of an organism, changes in the activity of one type of transcription factor can affect thousands of genes. [120] Therefore, these proteins are often the target of the signal conversion process, which controls the response to environmental changes or cell differentiation and development. The specificity of the interaction of DNA and these transcription factors came from proteins that make multiple contacts at the edge of the DNA base, allowing them to read DNA sequences. Most of these basic interactions are made in the main home where the base is most accessible. [26] The limiting enzyme EcoRV (green) of the complex with substrate DNA is an enzyme nuclease and ligu enzyme stoic to transform the DNA is an enzyme that cuts the DNA strands by catalysising the hydrolysis of infodister binding. Nuclease to hydrolyz the nucleus at the end of the DNA strand is called exonuclease, and endonicles is cut in the strand. The most frequently used nucleases in molecular biology are limited entonacles, which cut DNA in certain sequences. For example, the EcoRV enzyme shown on the left recognizes the sixth sequence 5′-GATATC-3′ and cuts it from the horizontal line. In nature, these enzymes work as part of a limited fertilization system, because they digest phage DNA and protect bacteria against phage infections. [122] in the technique, these sequence-specific nucleases are used in molecular replication and DNA fingerprints. An enzyme called DNA regasecan be cut or recoupled with broken DNA strands. [123] Ligases are especially important for delaying strand EDD replication because they combine short segments of DNA generated from replication forks into complete copies of DNA templates. It is also used. DNA repair and genetic recombination. [123] topoisomerase and helicase topoisomerase is an enzyme with both the nucleus and liguase activity. This protein changes the amount of fruit in DNA. Some of these enzymes work by cutting dna helixes and reducing super-coiling levels by allowing one section to rotate. Enzymes seal DNA brakes. [39] Before other types of these enzymes rejoin the helix, it is possible to cut the DNA helix through which the second strand of DNA has passed through and then passthrough. [124] Topoisoraseise is necessary for many processes related to DNA, such as DNA replication and transcription. [40] Helicase is a protein that is a type of molecular motor. They use chemical energy in the side triad as nucleus, mainly adenosine triphosphate (ATP), breaking the hydrogen bond between bases and releasing dna double helixes into a single strand. [125] These enzymes are essential for most processes where enzymes need access to the DNA base. Polymerase polymerase is an enzyme that synthesizes polynucleotide chains from nucleosides. Their order is based on an existing polynucleotide chain called a template. These enzymes function by repeatedly adding nucleotides to the 3′ hydroxy group at the end of the growing polynucleotide chain. As a result, all polymers work in 5′ in 3′ directions. [126] A pair of nucleoside trichosite chloride from the active area of these enzymes is inserted into the template. Polymerase is classified according to the type of template used. In DNA replication, DNA-dependent DNA polymerase makes copies of DNA polynucleotide chains. In order to preserve biological information, it is essential that the base sequence sequencing of each copy is accurately complemented by the base sequence of the template strands. Many DNA polymers have corrective activity. Here, the polymer recognizes the occasional mistake in the synthetic reaction by the lack of base pairing between the mismatched nucleotides. When discrepancies are detected, the 3′ to 5′ exonuclease activity is activated and incorrect base removal is removed. [127] In most organisms, DNA polymers function in a large complex called replisome containing several appendages, such as DNA clamps or helicopters. [128] RNA-dependent DNA polymer is a professional polymerase class for copying the sequence sequencing of rna strands to DNA. They contain telomerease, which is a viral enzyme involved in the infection of cells by retroviruses, and telomeres, which are required for replication of telomeres. [58] [129] For example, HIV reversal is an AIDS virus replication enzyme. [129] Telomerase is an unusual polymer because it contains its own RNA template as part of the structure. Synthesize telomeres at the end of the chromosome. Telomeres prevent the fusion of the extremities. Protects chromosomes and chromosomal ends from damage. [59] transcription is carried out by RNA polymerase that depend on the DNA to copy the sequence of the DNA strands to RNA. To initiate gene transfer, RNA polymerase binds to a sequence of DNA called promoters and separates dna strands. The gene sequence is then copied to the messenger RNA transcription until it reaches a DNA site called a terminator, which is interrupted and separated from the DNA. As with human DNA-dependent DNA polymerase, the enzyme RNA polymerase II, which transfers most genes in the human genome, operates as part of a large protein complex with multiple control and accessory sub-units. [130] Genetic recombinant structure of the holiday junction medium in the oil field recombinant. Four separate DNA strands are shown in red, blue, green, and yellow. [131] Additional information: Genetic recombinant recombination produces two rearranged chromosomes (C1 and C2), including destruction and re-joining of two chromosomes (M and F). DNA helixes generally do not interact with other segments of DNA, and in human cells, other chromosomes even occupy separate areas in the nucleus called chromosome territory. [132] physical separation of different chromosomes is important in the ability of DNA to function as a stable repository for information, one of the number of times the chromosome interacts is in the chromosomal crossover that occurs during sexual reproduction when gene recombination occurs. The chromosomal crossover is when two DNA helixes are broken, cross-sectioned, and then re-joined. Recombination allows chromosomes to exchange genetic information, increase the efficiency of natural selection and produce new combinations of genes that can be important in the rapid evolution of new proteins. [133] Genetic recombination may be involved in DNA repair, especially in the reaction of cells to double-stranded breaks. [134] The most common form of chromosomal crossover is allogeneic recombination, in which the two chromosomes share a very similar sequence. Non-frostbite recombination can damage cells because they can produce chromosomal translocation and genetic abnormalities. Recombinant reaction is catalyzed by an enzyme known as a recombinant enzyme, such as RAD51. [135] The first step in recombination is a double stranded break due to endonouklicor damage to DNA. [136] A series of steps partially catalyzed by recombination leads to the bonding of two heliby by at least one holiday intersection. Holiday joints are tetrahedral joints that can move along pairs of chromosomes, allowing one strand to be replaced with another. The reunion reaction is then interrupted by the division of the junction and re-ligation of the DNA released. [137] while only strands of dna in the same polar exchange are reunited. There are two. Division: East-West and North-South divisions. The north-south division nixes both strands of DNA, and the east-west division has one strand of DNA. The formation of holiday junctions during recombination enables genetic diversity, genes that exchange on chromosomes, and the expression of the wild-type virus genome. Evolution More: RNA World Hypothesis DNA contains genetic information that allows all forms of life to function, grow, and reproduce. However, it is unclear how long this function has been performed in the 4 billion-year history of life DNA, suggesting that early forms of life may have used RNA as their genetic material. [138] [139] RNA may have acted as a central part of early cellular metabolism because it can transmit genetic information and perform catalysts as part of ribojime. [140] This ancient RNA world where nucleic acids were used in both catalysts and genetics may have influenced the evolution of the current genetic code based on four nucleotide situ. A number of different bases in these organisms occur because it is a trade-off between a prime number of bases that increase replication accuracy and a large number of bases that increase catalytic efficiency of ribozymes. [141] However, there is no direct evidence of the ancient genetic system, because dna survives in an environment of less than a million years, so the recovery of DNA in most fossils is impossible, and slowly degrades into short pieces of solution. [142] Claims of old DNA have been made, especially in the 250 million-year-old salt crystals, which have been written reports of the isolation of viable bacteria, but these claims are controversial. [144] [145] Building blocks of DNA (adenine, guanine and related organic molecules) may have been formed extraterrestrial in outer space. [146] [147] [148] Complex DNA and RNA organic compounds, including uracil, cytosine and thiamine, were formed in the laboratory under conditions that mimic what is found in outer space using starting chemicals such as pyridine found in meteorites. Pyrimidin may have been formed from red giants or interstellar cosmic dust and gas clouds, such as polycyclic aromatic hydrocarbons (PAHs), a carbon-rich chemical found in space. [149] Additional information used in technical genetic engineering: molecular biology, nucleic acid methods and genetic engineering methods to purify DNA from organisms such as phenolic chloroform extraction, and limited digestion and polymer chain reactions were developed to manipulate them in the laboratory. Modern biology and biochemistry make intensive use of this technique in recombinant DNA technology. Recombinant DNA is an artificial DNA sequence assembled in another DNA sequence. They can be transformed into organisms in the form of plasmids or in an appropriate format using viral vectors. [150] Genetic modification Production can be used to produce products such as recombinant proteins, used in medical research,[151] or grown in agriculture. [152] [153] DNA Profiling More Information: DNA profiling forensic scientists can use DNA from blood, semen, skin, saliva or hair found at the crime scene to determine the matching DNA of an individual, such as the perpetrator. [154] This process is also called DNA profiling, also known as DNA fingerprinting. In DNA profiling, the length of variable sections of repetitive DNA, such as short tandem repetitions and mini satellites, is compared among people. This method is usually a very reliable technique for identifying matching DNA. [155] However, identification can be complicated if the scene is contaminated with the DNA of multiple people. [156] DNA profiling was developed in 1984 by British geneticist Sir Alec Jeffreys[157] and was first used in forensics to convict Colin Pitchfork in the 1988 Enderby murder. [158] The development of forensics and the ability to obtain genetic matching for microscopic samples of blood, skin, saliva or hair led to a re-examination of many cases. Evidence may now be found that the original scan was scientifically impossible at the time. With the removal of the Double Risk Act in some places, this may reopen cases that failed to produce enough evidence to persuade previous trial jurors. Those accused of serious crimes may be required to provide DNA samples for matching purposes. The most obvious defense against forensically obtained DNA matches is the assertion that cross-contamination of evidence has occurred. This resulted in a new case of serious crime, a meticulous and rigorous processing process. DNA profiling is also successfully used to actively identify the body or body parts of a serious accident, and individual victims of mass war graves with their families. DNA profiling is also typically 99.99% when a parent claimed to determine whether someone in a DNA paternity test is a biological parent or grandparent of a child who has a probability of parental involvement is biologically related to the child. Normal DNA sequencing methods occur after birth, but there are new ways to test paternity while the mother is still pregnant. [160] DNA enzyme or catalytic DNA more information: Deoxyribozyme Deoxyribozyme, also called DNAzymes or catalytic DNA, was first discovered in 1994. [161] They are mainly a single stranded DNA sequence separated from a large pool of random DNA sequences through a binding approach called in vitro selection or systematic evolution of ligands by exponential concentration (SELEX). DNAzymes is RNA-DNA division, RNA-DNA ligation, amino acid phosphorylation - catalysis a variety of chemical reactions, including deforylization, carbon binding formation. DNAzymes can improve the catalytic rate of chemical reactions up to 100,000,000,000 times. Reaction. [162] The most extensively studied class of DNAzymes is rna-cleaving type used to detect other metal ions and design therapeutics. Several metal stars have been reported including DNAzyme GR-5 DNAzyme (Lead Star), [161] CA1-3 DNAzymes (Copper Specific), [163] 39E DNAzyme (uranyl-specific) and NaA43 DNAzyme (sodium specific). [164] NaA43 DNAzyme has been selectively reported for sodium more than any other metal ion and has been used to create real-time sodium sensors in cells. Bioinformatics More Information: Bioinformatics Includes the development of technologies for storing, data mining, retrieval, and manipulating biological data, including DNA nucleic acid sequence data. This has led to widespread advances in computer science, especially string search algorithms, machine learning, and database theory. [165] A string search or matching algorithm was developed to detect a specific nucleotide sequence that found that a sequence of characters occurs inside a larger character sequence. [166] DNA sequence sequencing may be aligned with other DNA sequences to find a specific mutation to identify and distinguish the homogeneous sequence. These techniques, especially multi-sequence alignment, are used to study physical genetic relationships and protein functions. [167] A set of data that represents the DNA sequence sequencing of the entire genome, such as the one created by the Human Genome Project, is difficult to use without annotations that identify the location of genes and regulatory elements on each chromosome. The area of DNA sequences with characteristic patterns associated with protein or RNA-coding genes can be identified by gene-finding algorithms, allowing researchers to predict the presence of specific gene products and possible functions in an organism even before they are experimentally isolated. [168] The entire genome can also be compared to illuminate the evolutionary history of a particular organism and allow for examination of complex evolutionary events. The DNA structure (schematic display) on the left side of DNA nanotechnology is self-assembled into a structure visualized by nuclear microscopy from the right. DNA nanotechnology is an area that wants to design nanoscale structures using molecular recognition characteristics of DNA molecules. Image: Strong, 2004. Read more: DNA nanotechnology DNA nanotechnology uses unique molecular recognition characteristics of DNA and other nucleic acids to create self-assembled branch DNA complexes with useful properties. [169] DNA is therefore used as a structural material, not a carrier of biological information. This resulted in the creation of a two-dimensional cycle lattice (using tile-based and DNA origami methods) and a polyhedra-shaped three-dimensional structure. [170] Nanomechanical devices and algorithms self-assembly And these DNA structures have been used as templates for an array of other molecules such as gold nanoparticles and streptococcal proteins. [172] History and anthropology More information: Philogenetics and genetic genealogy are inherited, historical information, and dna sequences, because DNA collects mutations over time, allowing geneticists to deduce the evolutionary history of the organism, their physics. [173] This field of philogenetics is a powerful tool in evolutionary biology. If comparing DNA sequences within a species, population geneticists can learn the history of a particular population. This can be used in studies that range from ecological genetics to anthropology. 정보 저장 주요 기사: DNA 디지털 데이터 저장 DNA 정보를 위한 저장 장치로서 전자 기기에 비해 저장 밀도가 훨씬 높기 때문에 엄청난 잠재력을 가지고 있습니다. However, high cost, read and write time (memory latency) and lack of reliability can prevent practicality. [174] [175] History Extra information: Molecular biology James Watson and Francis Crick (right), co-originator of the dual helix model, Macklin McCarty (left) with a pencil sketch of a double helix DNA by Francis Crick in 1953 DNA was first isolated by Swiss doctor Friedrich Misher, who in 1869, found a fine substance in the disposal of surgery. He resides in the nucleus of the cell and called it the nucleus. [176] [177] In 1878, Albrecht Cossel separated the non-protein components of nucleic acids and nucleic acids and later separated five primary nucleous bases. [178] [179] In 1909, Phoebus Levene identified the base, sugar and phosphate nucleotide units of RNA (then named yeast nucleic acids). [180] [181] [182] In 1929, Leven identified deoxyboos sugar from thoracic acid (DNA). [183] Levene suggested that DNA consists of a string of four nucleotide units connected together through the phosphate group (tetranucleotide hypothesis). Leven thought the chain was short and the base was repeated in a fixed order. In 1927, Nikolai Coulthorpe suggested that he would use each strand as a template to inherit inherited traits through a huge genetic molecule consisting of two mirror strands to replicate in an anti-conservative manner. [184] [185] In 1928, Frederick Griffiths found in an experiment that the characteristics of pneumococcus in a smooth form can be transferred to the coarse form of the same bacteria by mixing the living coarse form with dead smooth bacteria. [186] [187] This system provided the first clear suggestion that DNA transmits genetic information. In 1933, while studying virgin urchin eggs, Jean Brachet suggested that DNA was found in cell nuclei and that RNA exists exclusively in cytoplasm. At the time, yeast nucleic acid (RNA) was thought to occur only in plants, and only animals had thoracic acid (DNA). The latter was thought to be Tetrammer, cellular pH buffering function. [188] [189] In 1937, William Astbury produced the first X-ray diffraction pattern that showed that DNA had a regular structure. [190] In 1943, Oswald Avery, along with his colleagues Colin McLeod and Maclean McCarty, supported Griffith's proposal by identifying DNA as a modified principle. [191] The role of DNA in the oil field was confirmed in 1952 in the Alfred Hershey and Hershey Chase experiments, when Martha Chase showed that DNA was a genetic material of the intestinal bacteria Phage T2. [192] In 1951, francis Creek, who had a blue plaque outside the Eagle Pub celebrating Creek and Watson, started working with James Watson at the Cavendish Institute at the University of Cambridge. In February 1953, Linus Pauling and Robert Cory proposed a nucleic acid model containing three tangled chains, along with phosphates near the axis and an external base. [193] In May 1952, Raymond Gosling, a graduate student who worked under the supervision of Rosalind Franklin, took an X-ray diffraction image marked with 51,[194], a photo of a high moisture level in DNA. This photo was given to Watson and Creek by Maurice Wilkins and was important in obtaining the correct structure of DNA. Franklin told Creek and Watson that the backbone should be on the outside. Before that, Linus Pauling, Watson, and Creek had the wrong model pointing outwards to the inside of the chain and the base. Her identification of the space group for DNA determination revealed to Creek that the two DNA strands are semi-similar. [195] In February 1953, Watson and Crick completed the model, which is now accepted as the first correct model of the double spiral of DNA. On February 28, 1953, Crick stopped for lunch at the Eagle Pub in Cambridge, where he and Watson announced that they had discovered the secrets of their lives. [196] In the April 25, 1953 issue of the journal Nature, a series of five articles and evidence supporting watson and creek double helix structural DNA were published. [197] The structure was reported in a letter titled Structure for Deoxyribose Nucleic Acid, which the molecular structure of nucleic acids did not escape our notice that certain pairs suggest a possible copy mechanism for genetic material. [10] Franklin and Gosling's letter was followed by the first publication of their X-ray diffraction data and the first publication of the original method of analysis. [43] [198] Followed Wilkins' letter, and two of his colleagues, which included analysis of biological B-DNA X-ray patterns, and supported the invivo presence of the Watson and Creek structures. [44] After Franklin's death in 1962, Watson, Crick and Wilkins jointly won the Nobel Prize in Physiology or Medicine. [199] The Nobel Prize is awarded only to living recipients. There is an ongoing debate about who should be recognized for its findings. In [200] In an influential presentation in 1957, Crick presented a central doctrine of molecular biology that predicted the relationship between DNA, RNA and protein, and manifested the adapter hypothesis. [201] The final confirmation of the replication mechanism implied by the dual helic structure was followed by the Messelson-Stahl experiment in 1958. [202] Further work by Creek and colleagues showed that the genetic code was based on a non-overlapping triple of the base called codon, HarGovind Corana, Robert W. Holly, and Marshall Warren Nirenberg to help decipher the genetic code. [203] These findings indicate the birth of molecular biology. [204] Also auto-nucleic acid simulation software crystallography all chromosomes other than comparing sex chromosomes - crystal structure DNA encoding chemical library DNA microarray scientific studies of genetic diseases - health problems caused by one or more in genomic genetic lineage - inferring relationships between individuals and ancestor Haplo The use of DNA testing along with traditional genealogy methods to find type – a group of genes from one parent Meiosis – a type of cell division in sexually regenerated organisms used to produce gametes nucleic acid notation – is a universal notation using the Roman characters A, C, G, And T calls four DNA nucleotide nucleic acid sequences - the succession of nucleotides from nucleic acid pancreatic sissy - a former theory that heritage was based on particles from all parts of the body, inspolamide ribosomal DNA southern stain scattering group genoic acid reference

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