Estrutura de ácido nucléicos e cromatina
Os componentes básicos dos ácidos nucléicos são os nucleotídeos
Figure 4.4  Pyrimidines have a six carbon ring.

Pyrimidine

Cytosine

Uracil

Thymine

Figure 4.5  Purines consist of two joined carbon rings, with five and six members.

Purine

Adenine

Guanine
**Figure 4.6** 2-Deoxyribose is the sugar in DNA and ribose is the sugar in RNA. The carbon atoms are numbered as indicated for deoxyribose. The sugar is connected to the nitrogenous base via position 1′.

**Table 4.1** Bases, nucleosides, and nucleotides have related names. Abbreviations of the form NMP stand for nucleoside monophosphate; "d" indicates the 2'-deoxy form.

<table>
<thead>
<tr>
<th>Base</th>
<th>Nucleoside</th>
<th>Nucleotide</th>
<th>Abbreviation RNA</th>
<th>Abbreviation DNA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adenine</td>
<td>adenosine</td>
<td>adenylic acid</td>
<td>AMP</td>
<td>dAMP</td>
</tr>
<tr>
<td>Guanine</td>
<td>guanosine</td>
<td>guanylic acid</td>
<td>GMP</td>
<td>dGMP</td>
</tr>
<tr>
<td>Cytosine</td>
<td>cytidine</td>
<td>cytidylic acid</td>
<td>CMP</td>
<td>dCMP</td>
</tr>
<tr>
<td>Thymine</td>
<td>thymidine</td>
<td>thymidylic acid</td>
<td>UMP</td>
<td>dTMP</td>
</tr>
<tr>
<td>Uracll</td>
<td>uridine</td>
<td>uridylic acid</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Figure 4.9** A nucleoside-5′-triphosphate has energy-rich phosphate bonds.
Figure 4.7 A polynucleotide chain consists of a series of 5'-3' sugar-phosphate links that form a backbone from which the bases protrude.

Figure 4.8 Nucleotides may carry phosphate in the 5' or 3' position.
Desvendando a estrutura do DNA:

Chargaff e colaboradores:

1. O DNA de todas as espécies vivas e constituído de 4 base nitrogenadas
2. A composição de bases varia de uma espécie para outra
3. DNA isolado de diferentes tecidos de uma mesma espécie tem a mesma composição de bases
4. Composição de bases não muda com a idade, estado nutricional ou mudanças ambientais
5. Em todas as espécies, independente da composição e base, o numero de timinas é igual ao numero de adeninas, e o numero de guaninas é igual ao numero de citosinas

\[ A = T \]
\[ C = G \]

Primeira indicação de uma estrutura em que bases formam pares
Molecular Structure of Nucleic Acids

A Structure for Deoxyribose Nucleic Acid

We wish to suggest a structure for the deoxyribose nucleic acid (D.N.A.). This structure is based upon the following observations:

1. In the absence of acid, D.N.A. is a crystalline material, which is obtained in the form of discrete, rod-like crystals.
2. The structure of these crystals is such that they can be separated into two distinct components, each of which is capable of forming a separate crystalline structure.
3. The two components are related to each other by a simple mathematical relationship.
4. The structure is such that it can be represented by a series of interconnected rings, each of which is composed of a single deoxyribose molecule.
5. The structure is such that it can be represented by a series of interconnected rings, each of which is composed of a single deoxyribose molecule.

The structure is such that it can be represented by a series of interconnected rings, each of which is composed of a single deoxyribose molecule. The rings are connected by a series of covalent bonds, which are themselves connected by a series of hydrogen bonds.

Molecular Structure of Deoxyribose Nucleic Acid

The biological properties of deoxyribose nucleic acid are such that it can form a double helix, which is the structure proposed by Crick and Watson. This structure is composed of two parallel strands of nucleotides, each of which is composed of a single deoxyribose molecule.

The two strands are connected by hydrogen bonds, which are formed between the bases of the nucleotides. The structure is such that it can be represented by a series of interconnected rings, each of which is composed of a single deoxyribose molecule.

Molecular Configuration in Sodium Thymonucleate

In the presence of sodium ions, the structure of deoxyribose nucleic acid changes, and it forms a helical structure. This structure is such that it can be represented by a series of interconnected rings, each of which is composed of a single deoxyribose molecule.

The structure is such that it can be represented by a series of interconnected rings, each of which is composed of a single deoxyribose molecule. The rings are connected by a series of covalent bonds, which are themselves connected by a series of hydrogen bonds.

We wish to thank Prof. J. T. Randall for assistance in the preparation of this manuscript.
FIGURE 8.15 Watson-Crick model for the structure of DNA. The original model proposed by Watson and Crick had 10 base pairs, or 34 Å (3.4 nm), per turn of the helix; subsequent measurements revealed 10.5 base pairs or 36 Å (3.6 nm), per turn. (a) Schematic representation, showing dimensions of the helix. (b) Stick representation showing the backbone and stacking of the bases. (c) Space-filling model.
Em solução, DNA pode assumir 3 conformationes distintas:

**Figure 8-18** Structural variation in DNA. (a) The conformation of a nucleotide in DNA is affected by rotation about seven different bonds. Six of the bonds rotate freely. The limited rotation about the bond of given rise to the puckering of the other four. This conformation is either **A** or **B**, depending on whether the atom is displaced to the same side of the plane as C-3' or to the opposite side (see Fig. 8-30). (b) For pairs of bases in nucleotides, only two conformations with respect to the attached base unit are sterically permitted, anti or syn. Pyrimidines generally occur in the anti conformation.
A sequência de nucleotídeos em um ácido nucléico pode também determinar que esse assuma conformações espaciais distintas.

**FIGURE 9-21** Hairpins and cruciforms. Palindromic DNA (or RNA) sequences can form alternative structures with intramolecular base pairing. (a) When only a single DNA (or RNA) strand is involved, the structure is called a hairpin. (b) When both strands of a duplex DNA are involved, it is called a cruciform. Blue shading highlights asymmetric sequences that can pair with the complementary sequence either in the same strand or in the complementary strand.
As duas principais interações que mantêm a dupla fita são:

1. Pontes de hidrogênio

2. Empilhamento de bases
RNAs também podem assumir conformações espaciais em formato de hélices.

**FIGURE 8–25** Typical right-handed stacking pattern of single-stranded RNA. The bases are shown in gray, the phosphate atoms in yellow, and the riboses and phosphate oxygens in green. Green is used to represent RNA strands in succeeding chapters, just as blue is used for DNA.

**FIGURE 8–26** Secondary structure of RNAs. (a) Bulge, internal loop, and hairpin loop. (b) The paired regions generally have an A-form right-handed helix, as shown for a hairpin.
FIGURE 8-27  Base-paired helical structures in an RNA. Shown here is the possible secondary structure of the M1 RNA component of the enzyme RNase P of *E. coli*, with many hairpins. RNase P, which also contains a protein component (not shown), functions in the processing of transfer RNAs (see Fig. 26-23). The two brackets indicate additional complementary sequences that may be paired in the three-dimensional structure. The blue dots indicate non-Watson-Crick G–U base pairs (boxed inset). Note that G–U base pairs are allowed only when presynthesized strands of RNA fold up or anneal with each other. There are no RNA polymerases (the enzymes that synthesize RNAs on a DNA template) that insert a U opposite a template G, or vice versa, during RNA synthesis.
Ácidos nucléicos de fita dupla podem ser reversivelmente DNA desnaturados.

A hibridização de moléculas heterólogas de ácidos nucléicos depende apenas da homologia de sequência, o que pode ser utilizado como "diagnostico" de "parentesco" molecular.
Os DNAs celulares são altamente compactados

Genoma humano = 3,4x10⁹ pares de bases, alinhados em 46 cromossomos

Esticados e enfileirados, isso corresponde a quase 2 m

O que as células fizeram para resolver esse problema?
Compactação do DNA na forma de cromatina:
Os nucleossomas são a unidade básica da cromatina eucariótica

146 nt por volta do core de histonas
Aaron Klug

The Nobel Prize in Chemistry 1982 was awarded to Aaron Klug "for his development of crystallographic electron microscopy and his structural elucidation of biologically important nucleic acid-protein complexes".

Photos: Copyright © The Nobel Foundation
The following is a list of human histone proteins:

<table>
<thead>
<tr>
<th>Super family</th>
<th>Family</th>
<th>Subfamily</th>
<th>Members</th>
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</thead>
<tbody>
<tr>
<td>Linker</td>
<td>H1</td>
<td>H1F</td>
<td>H1F0, H1FNT, H1FOO, H1FX</td>
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<td>H2AF</td>
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Interações entre proteínas e DNA estabelecem e mantêm a estrutura da cromatina.
Eucromatina × heterocromatina
A estrutura da cromatina é dinâmica.

**TABLE 28-2** Some Enzyme Complexes Catalyzing Chromatin Structural Changes Associated with Transcription

<table>
<thead>
<tr>
<th>Enzyme complex*</th>
<th>Oligomeric structure (number of polypeptides)</th>
<th>Source</th>
<th>Activities</th>
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</thead>
<tbody>
<tr>
<td>GCN5-ADA2-ADA3</td>
<td>3</td>
<td>Yeast</td>
<td>GCN5 has type A HAT activity</td>
</tr>
<tr>
<td>SAGA/PCAF</td>
<td>&gt;20</td>
<td>Eukaryotes</td>
<td>Includes GCN5-ADA2-ADA3</td>
</tr>
<tr>
<td>SWI/SNF</td>
<td>11; total M, $2 \times 10^6$</td>
<td>Eukaryotes</td>
<td>ATP-dependent nucleosome remodeling</td>
</tr>
<tr>
<td>NURF</td>
<td>4; total M, 500,000</td>
<td>Drosophila</td>
<td>ATP-dependent nucleosome remodeling</td>
</tr>
<tr>
<td>CAFI</td>
<td>&gt;2</td>
<td>Humans; Drosophila</td>
<td>Responsible for binding histones H3 and H4 to DNA</td>
</tr>
<tr>
<td>NAP1</td>
<td>1; $M$, 125,000</td>
<td>Widely distributed in eukaryotes</td>
<td>Responsible for binding histones H2A and H2B to DNA</td>
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</tbody>
</table>
Modificações pós-traducionais de componentes protéicos da cromatina