DNA structure

Contains
- Sugar – deoxyribose
- Phosphate
- Organic bases
  - Guanine, Cytosine,
  - Thymine, Adenine
DNA
- Polymer of repeating sugars and phosphates, with organic bases attached.

Sugar
- Primary alcohol
- Base attached here
- 5'
- Deoxyribose
- Secondary alcohol
- 3'

Sugar + base = nucleoside
- Adenosine: adenine
- Thymidine: thymine
- Guanosine: guanine
- Cytidine: cytosine

Nucleoside + phosphate = nucleotide
- dATP: deoxyadenosine triphosphate

Oligonucleotide Polynucleotide
**Chargaff’s rules**

- The four nucleotides are not present in the same amounts and the exact ratios differ from one species to another.
- However the number of A = T and G = C
- The purines (A+G) = pyrimidines (C+T)

<table>
<thead>
<tr>
<th>Source</th>
<th>Adenine (A)</th>
<th>Guanine (G)</th>
<th>Cytosine (C)</th>
<th>Thymine (T)</th>
<th>(G + C)</th>
<th>A/T</th>
<th>G/C</th>
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<tr>
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**X-ray diffraction patterns**

- Rosalind Franklin, Maurice Wilkins

Obtained X-ray diffraction patterns on DNA fibres, which provided the fundamental repeating distances in DNA.

• 0.34 nm (3.4 Å) - distance between nucleotides.

**These data were interpreted by James Watson and Francis Crick in 1953 – developing the familiar structure of the DNA double helix**

**Bases are on the inside**

- A pairs with T
  - 2 hydrogen bonds
- G pairs with C
  - 3 hydrogen bonds
• The bases are **hydrophobic** and stack on top of each other in the core of the double helix.

• Separation distance of stacked bases is optimal for **van der Waals interactions**.

• The two bases in each pair are connected by specific **hydrogen bonds**.

• GC and AT pairs are the same size and shape

• Other pairings (e.g. G with T or G with A) do not have the correct hydrogen bonds

• Incorrect pairings are the wrong shape and size.

• The phosphates are on the outside – the molecule is highly **negatively** charged.

• The two strands are **ANTIPARALLEL**. The 5'-end of one strand is opposite the 3'-end of the other

```markdown
5'  3'
3'  5'
```

5'-AAGTCTA pairs with 5'-TAGACTT
**NOT** 5'-TTCAGAT

5'-AAGTCTA-3' **NOT** 5'-AAGTCTA-3'
3'-TTCAGAT-5' **NOT** 3'-TAGACTT-5'

• It is a **right-handed** helix
  - looking down, curls clockwise

• The base pairs are perpendicular to the helix axis

• The centre of the helix runs through the base pairs.

• This is known as **B-DNA**
B-DNA Key features
- predominant form of double stranded DNA
- right-handed
- 0.34 nm between base pairs
- 3.4 nm per turn
- 10 bp per turn
- ~2 nm in diameter (approx. 20 Angstroms)

B-DNA has two grooves of unequal size

Other conformations are also possible though they may not be biologically relevant

DNA melting
- DNA absorbs maximally at 260 nm
- Single stranded DNA has a higher absorbance than double stranded (as the bases are no longer stacked on each). The mid-point of the transition is the $T_m$ ($^{\circ}$C).
- GC-rich DNAs melt at a higher temperature than AT-rich as there are 3 hydrogen bonds in a GC pair, but only 2 in an AT.
- Longer DNA fragments melt at a higher temperature than short ones
- Higher salt concentrations give higher melting temperatures → positive ions neutralise repulsive negative phosphate groups on backbone
DNA packing into a cells nucleus

- 6,000,000,000 base pairs per cell
- Approximately 2 metres long (6x10⁹x0.34nm)
- Approximately 10¹⁴ cells in the body 200,000,000,000 km total length in all the cells in your body.
- 0.6 pg DNA per cell - 600g DNA per person (approx 1% body weight)

In all eukaryotic cells the DNA is condensed in the form of chromatin

The human genome is 2 m long 2 nm wide (one billion times longer than it is wide).

- Chromatin contains five main proteins called Histones
  - H1, H2A, H2B, H3, H4
  - These proteins are very basic (contain lots of positively charged amino acids – arginine and lysine) which interact with the negatively charged DNA (electrostatic interactions).
  - Two copies each of H2A, H2B, H3 and H4 combine to form an octameric, disk-like structure (histone core) around which the DNA is wrapped 1.6 times (nucleosome).

Role of H1 Histone

- Linker histone
- Single H1 histone binds to each nucleosome
- Contacts both protein and DNA
- Changes conformation of DNA as it leaves the nucleosome
- This change in conformation helps compact the DNA
Summary

- What is the molecular composition of DNA?
- How did Chargaff’s rules and X-ray diffraction help develop the structure of DNA?
- How is the DNA helix formed and what are its properties?
- How is DNA packed into the cell nucleus?