

Watson and Crick model of DNA (1953)



James Watson



Francis Crick



Maurice Wilkins



Rosalind Franklin

The data available to Watson and Crick, crucial to the development of their proposal, came primarily from two sources:

- (1) base composition analysis of hydrolyzed samples of DNA done by Austrian biochemist Erwin Chargaff and
- (2) X-ray diffraction studies of DNA conducted by Rosalind Franklin.

Chargaff's rule:

1. The base composition of DNA generally varies from one species to another.
2. DNA specimens isolated from different tissues of the same species have the same base composition.
3. The base composition of DNA in a given species does not change with an organism's age, nutritional state, or changing environment.
4. In all cellular DNAs, regardless of the species, the number of adenosine residues is equal to the number of thymidine residues (that is, $A = T$), and the number of guanosine residues is equal to the number of cytidine residues ($G = C$). From these relationships it follows that the sum of the purine residues equals the sum of the pyrimidine residues; that is, $A + G = T + C$. (**Pu = Py**)

These quantitative relationships, are called Chargaff's rule.

The Watson–Crick Model

Watson and Crick published their analysis of DNA structure in 1953. By building models based on the above-mentioned parameters, they arrived at the double-helical form of DNA.

This model has the following major features:

1. DNA consists of **two strands** of polynucleotides. These two long polynucleotide chains are coiled around a central axis, forming a right-handed double helix (**clockwise turning**).
2. The two chains are **antiparallel**; that is, their 5'-P and 3'-OH ends run in opposite directions.
3. Sugar – phosphate backbone lies on the outer side. The bases of both chains are flat structures lying perpendicular to the axis; they are “stacked” on one another, **3.4 Å (0.34 nm) apart**, on the inside of the double helix.
4. The nitrogenous bases of opposite chains are *paired* as the result of the formation of hydrogen bonds; in DNA, only A-T and C-G pairs occur. (Watson and Crick pairing). These bases are complementary bases and strands are complementary strands. Hydrogen bonds between the bases (A-T and G-C) of the two strands and the base stacking interactions hold the two strands together.
5. Each complete turn of the helix is **34 Å (3.4 nm)** long; thus, each turn of the helix is the length of a series of 10 base pairs.
6. A larger **major groove** alternating with a smaller **minor groove** winds along the length of the molecule.
7. The double helix has a **diameter of 20 Å (2.0 nm)**.



Right-handed double helix



Left-handed double helix

FIGURE 10.13 The right- and left-handed helical forms of DNA. Note that they are mirror images of one another.

Right handed :

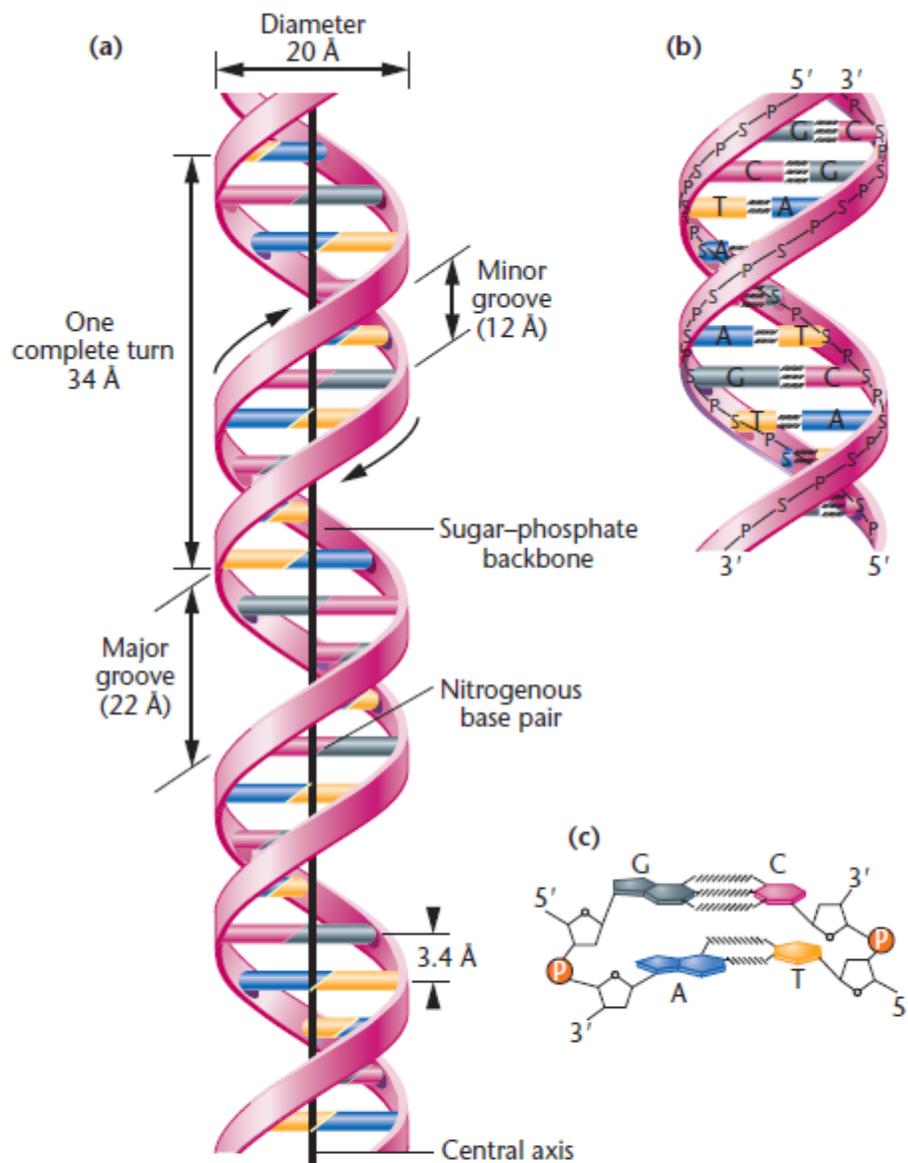


FIGURE 10.12 (a) The DNA double helix as proposed by Watson and Crick. The ribbon-like strands represent the sugar-phosphate backbones, and the horizontal rungs depict the nitrogenous base pairs, of which there are 10 per complete turn. The major and minor grooves are apparent. A solid vertical line shows the central axis. (b) A detailed view depicting the bases, sugars, phosphates, and hydrogen bonds of the helix. (c) A demonstration of the antiparallel arrangement of the chains and the horizontal stacking of the bases.