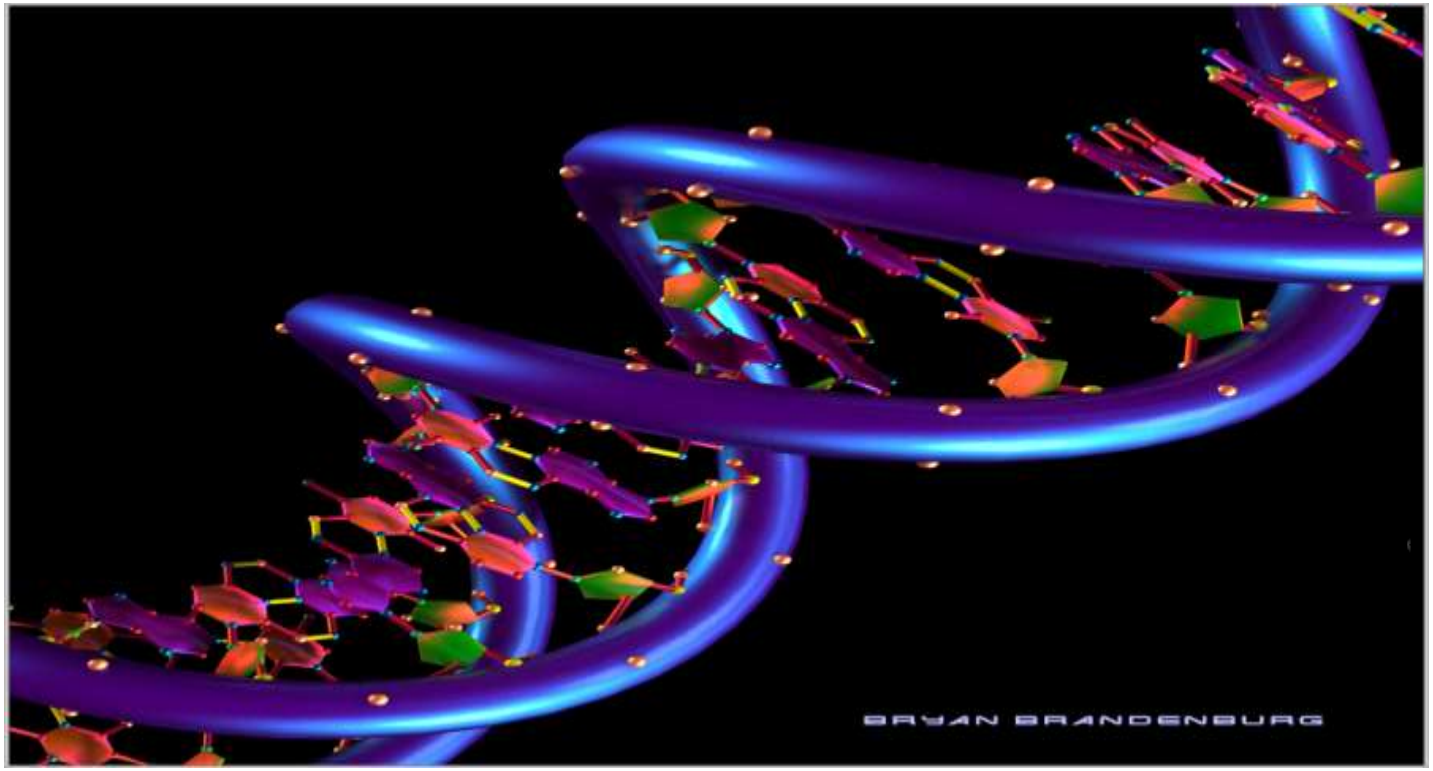
DNA Structure



By
Dr. Walaa Bayoumie El Gazzar

Nucleic acids

- **Polymer of nucleotides.**
- **Two main types:**

DNA

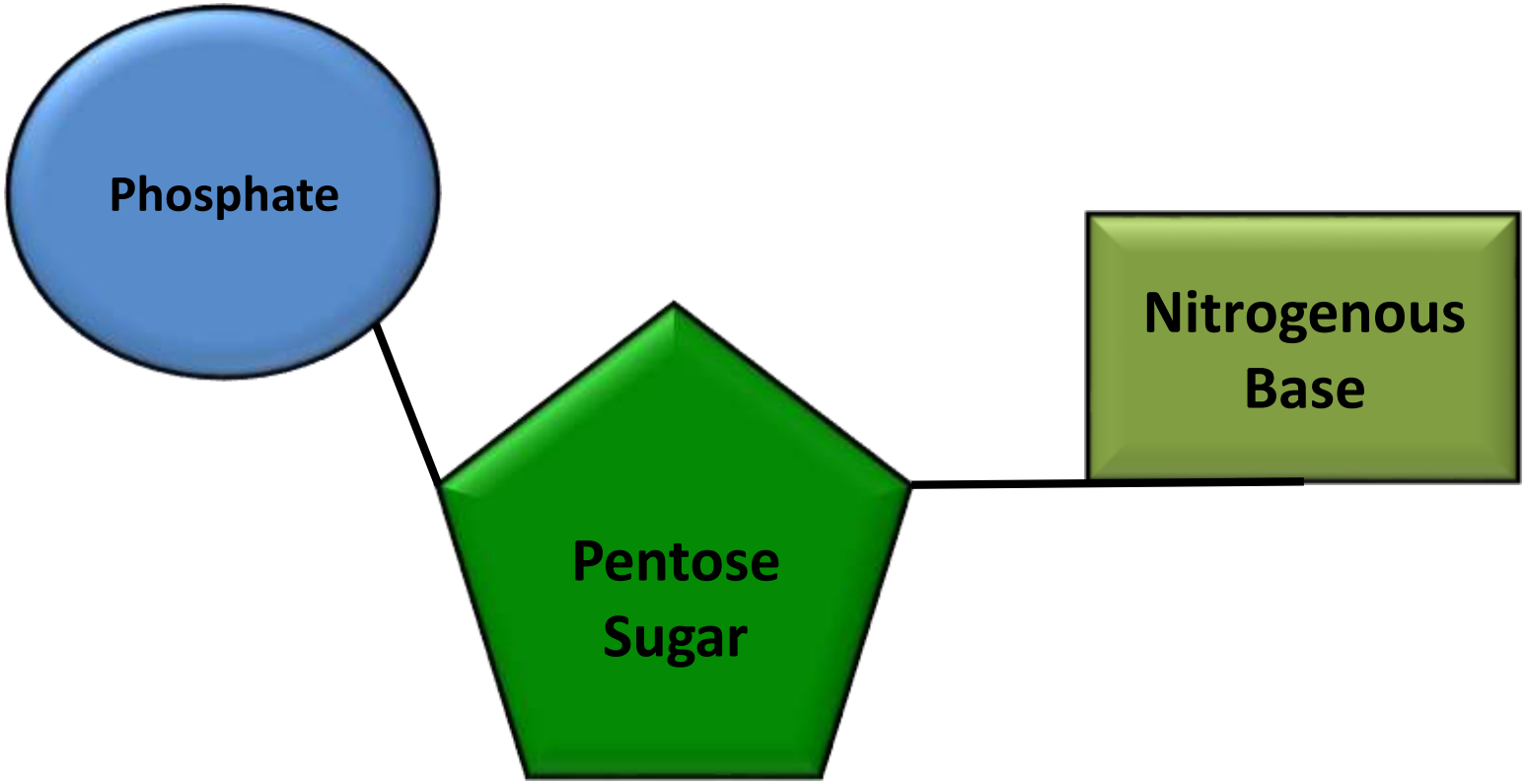
RNA

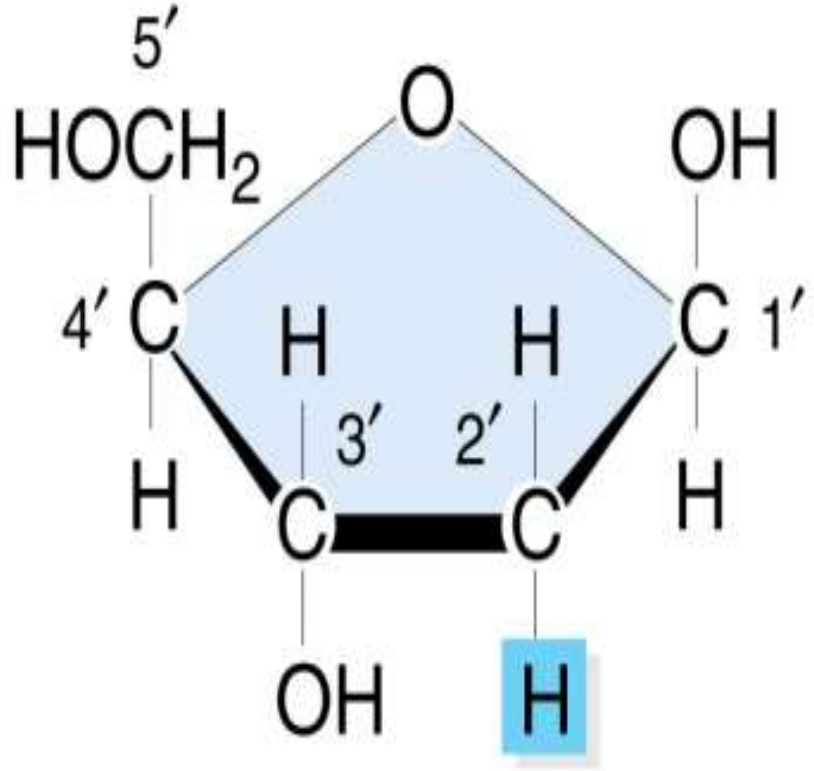
- **All cellular functions depend on proteins which consist of chains of amino acids.**

- **The precise arrangement of these amino acids necessitates certain guiding information.**

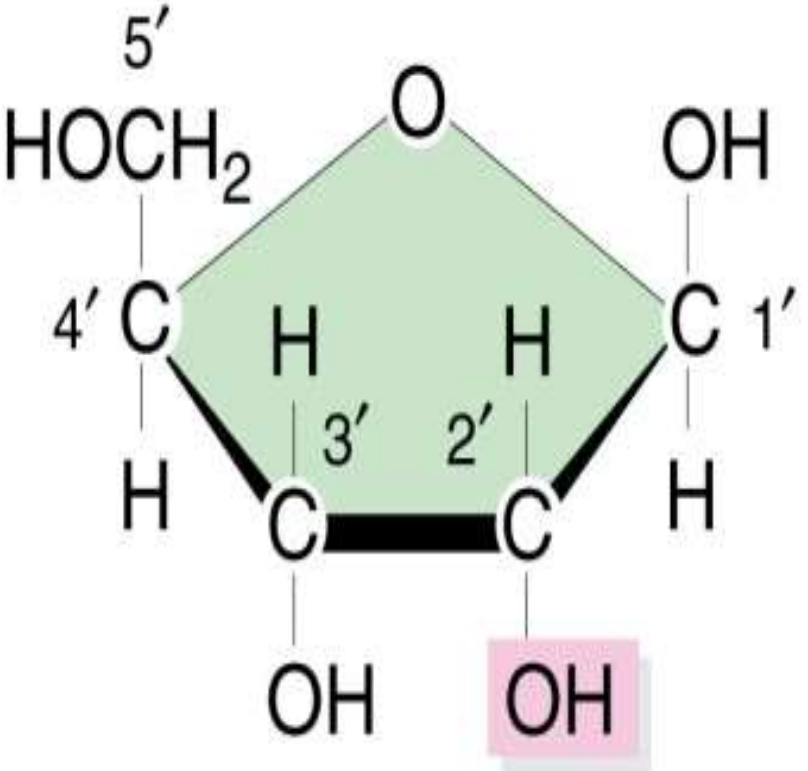
- **Such information is provided by DNA which can convey information through a group of RNA.**

Nucleotides



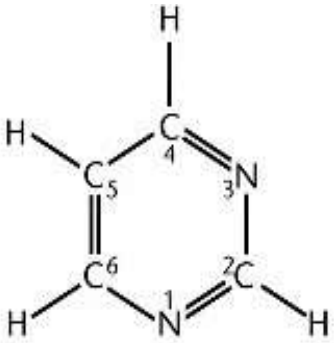


Deoxyribose



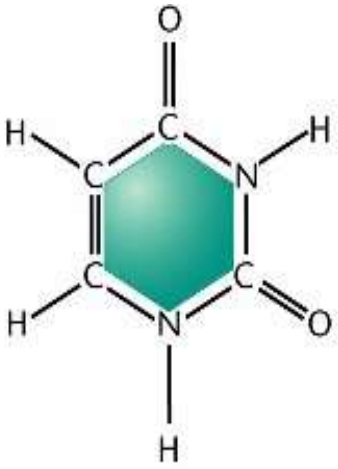
Ribose

Note that the positions on the sugar are designated with primes to distinguish them from positions on the bases.



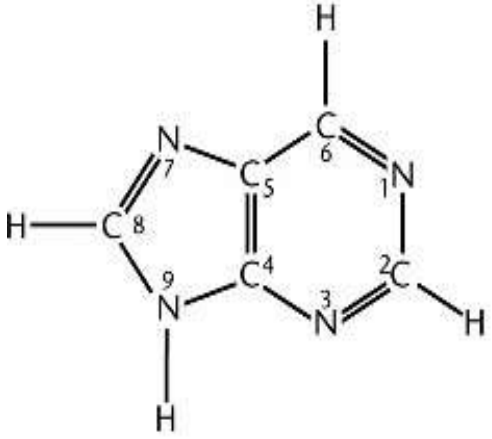
Pyrimidine ring

Cytosine

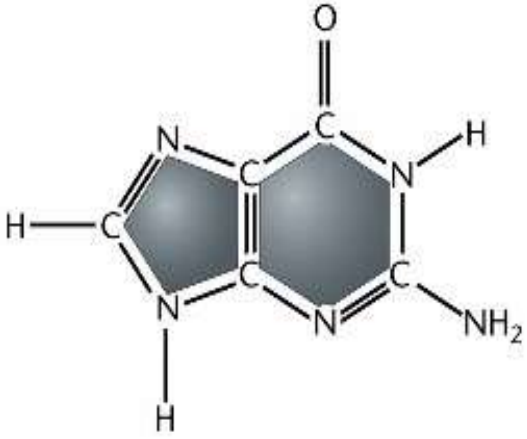


Uracil

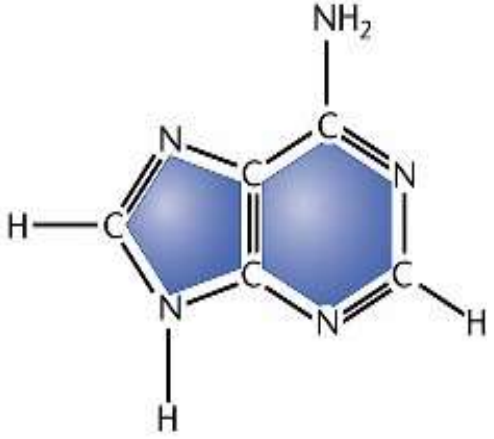
Thymine



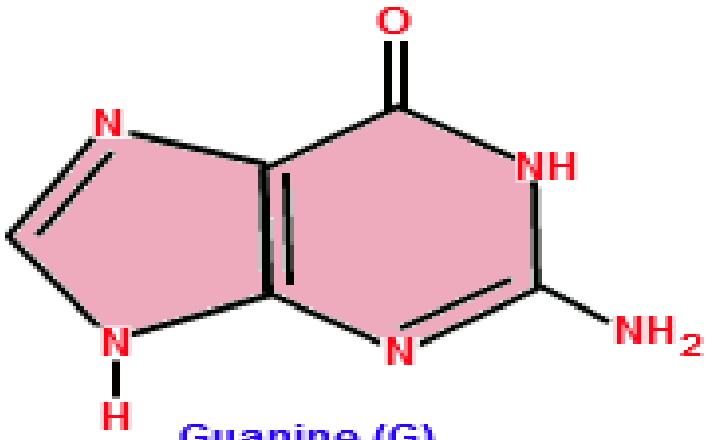
Purine ring



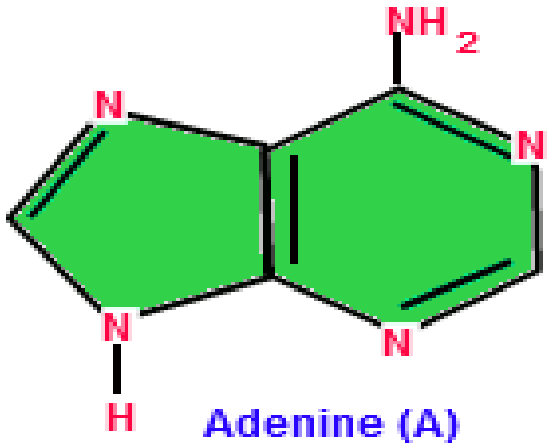
Guanine



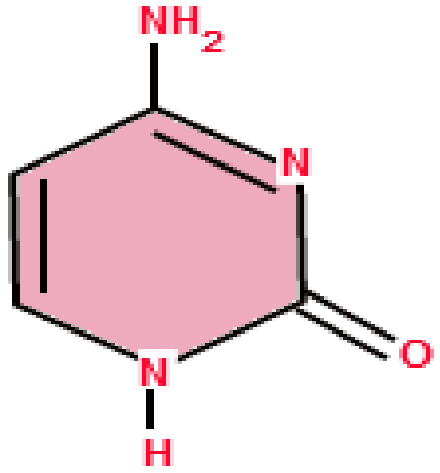
Adenine



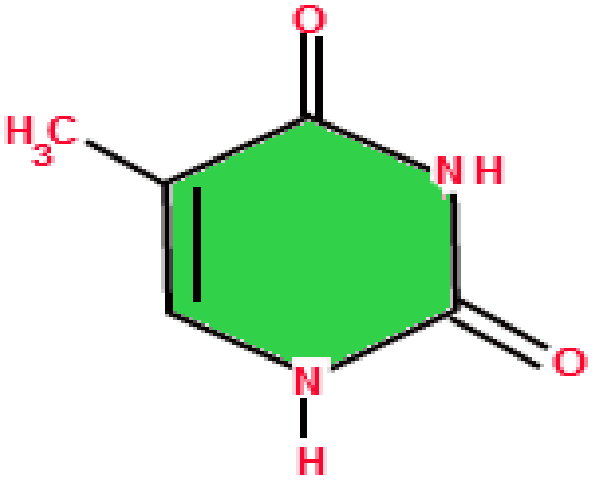
Guanine (G)



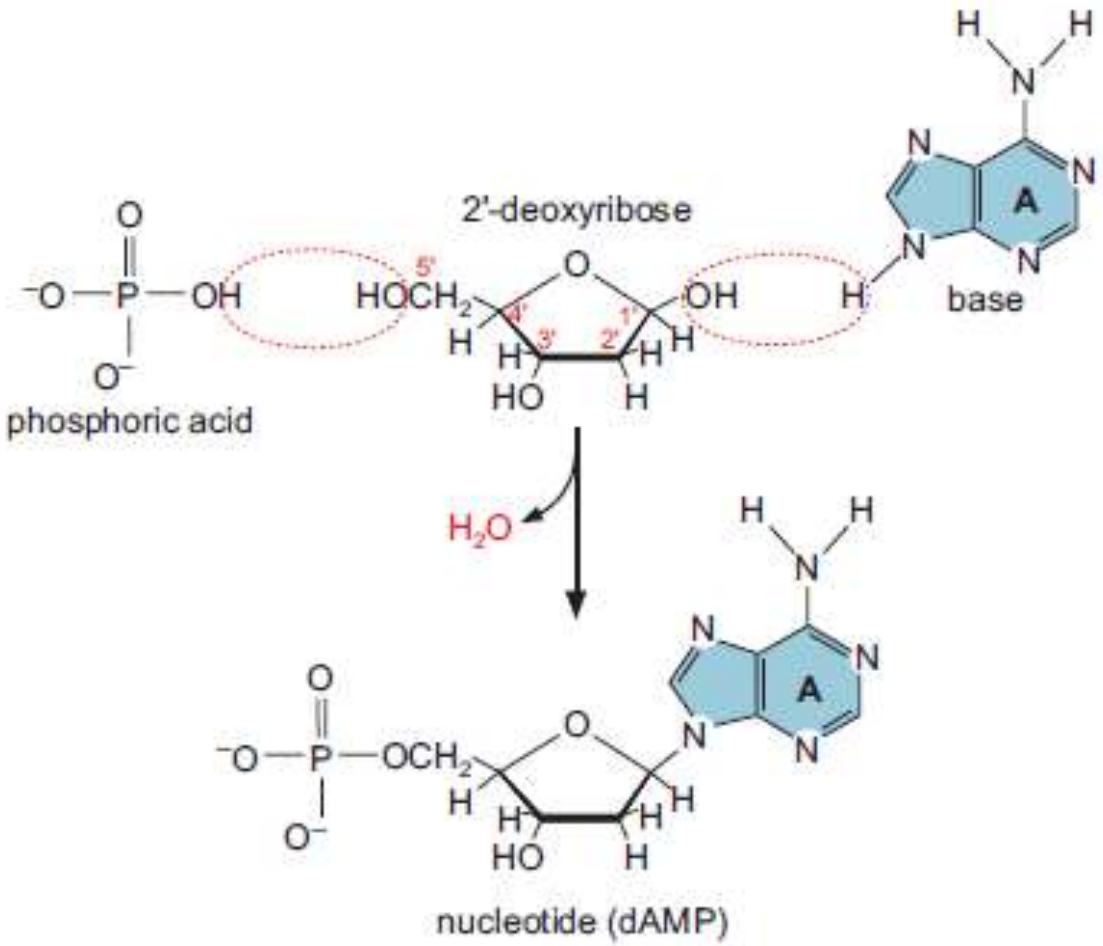
Adenine (A)

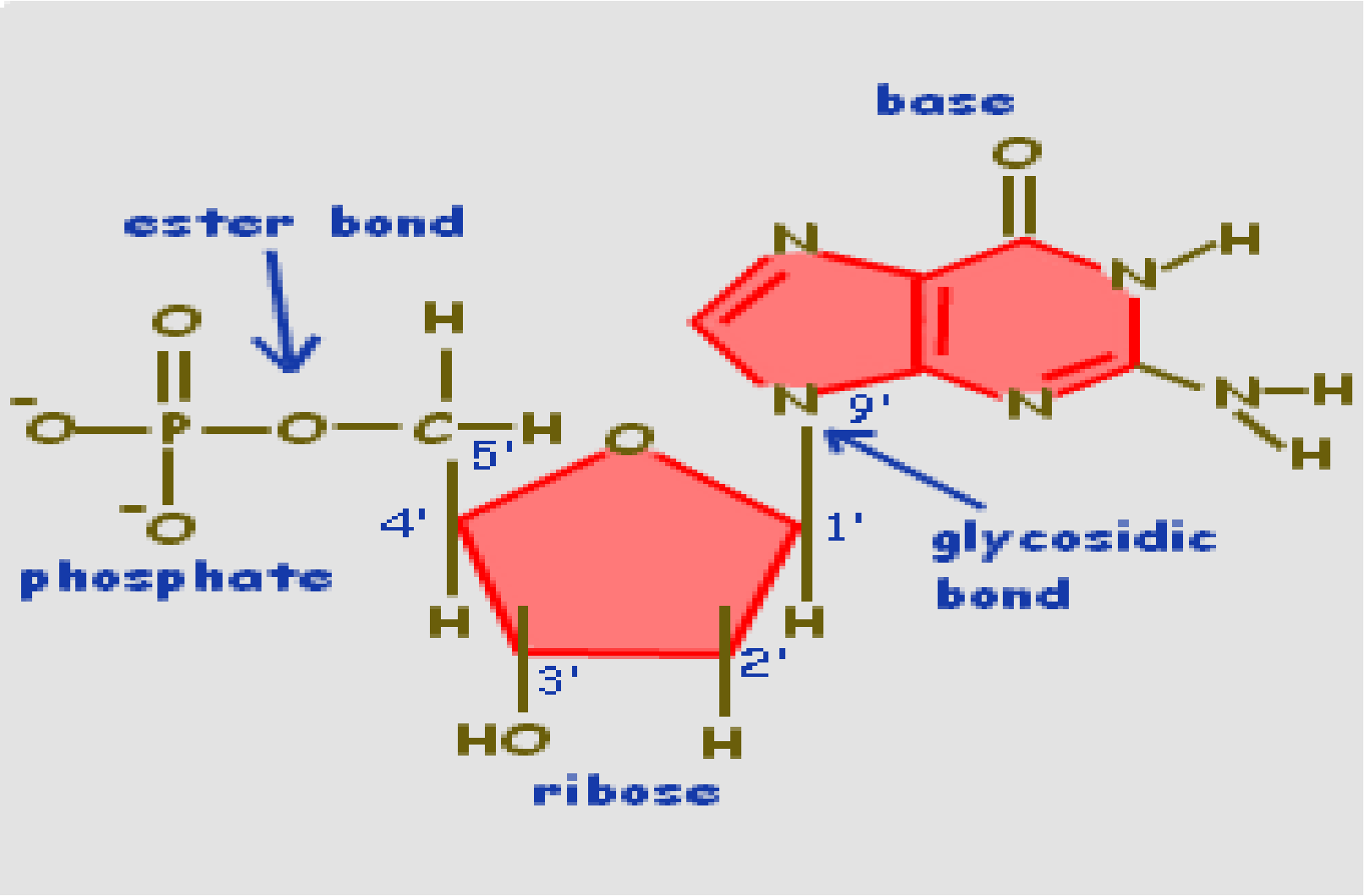


Cytosine (C)

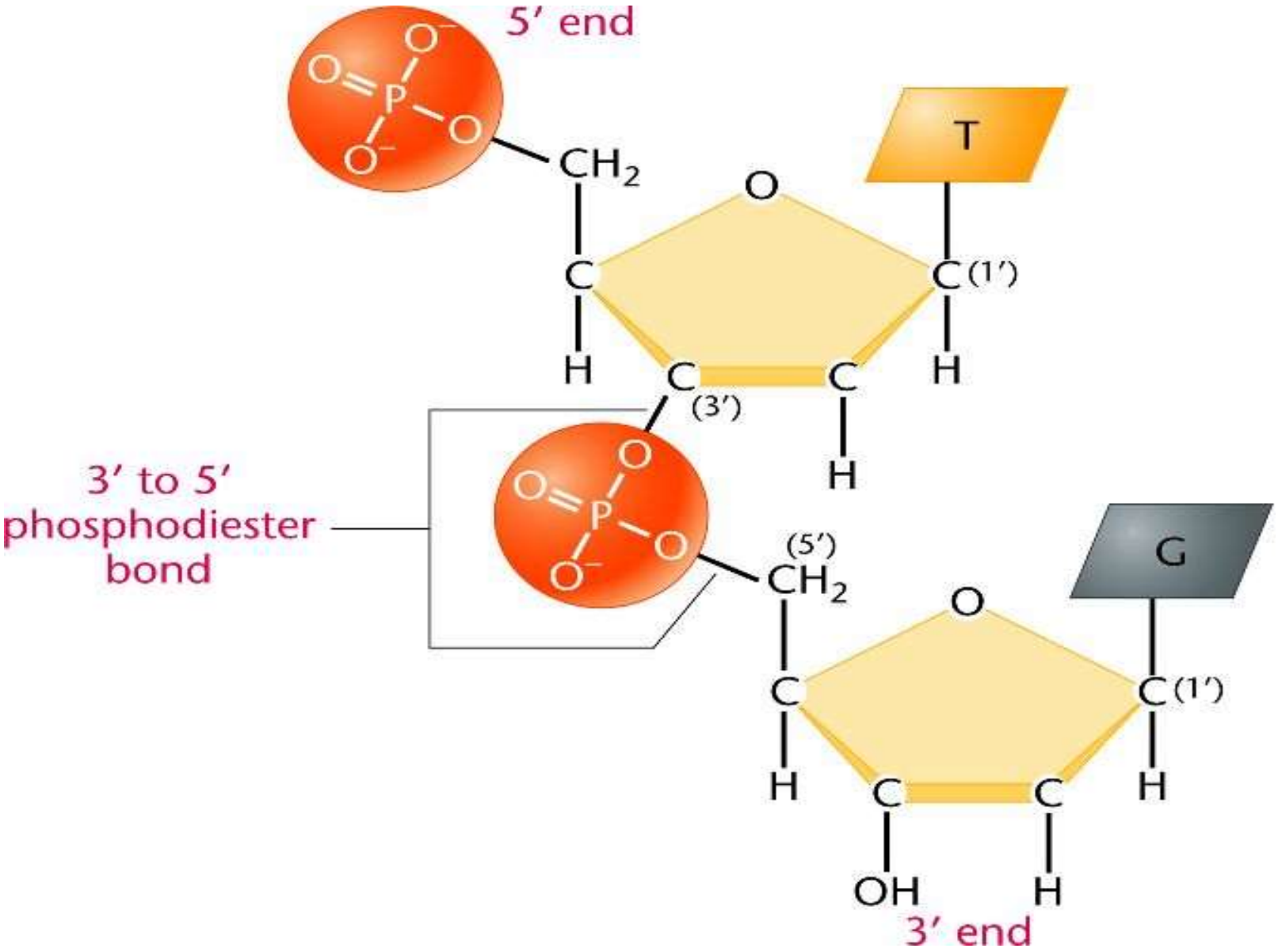


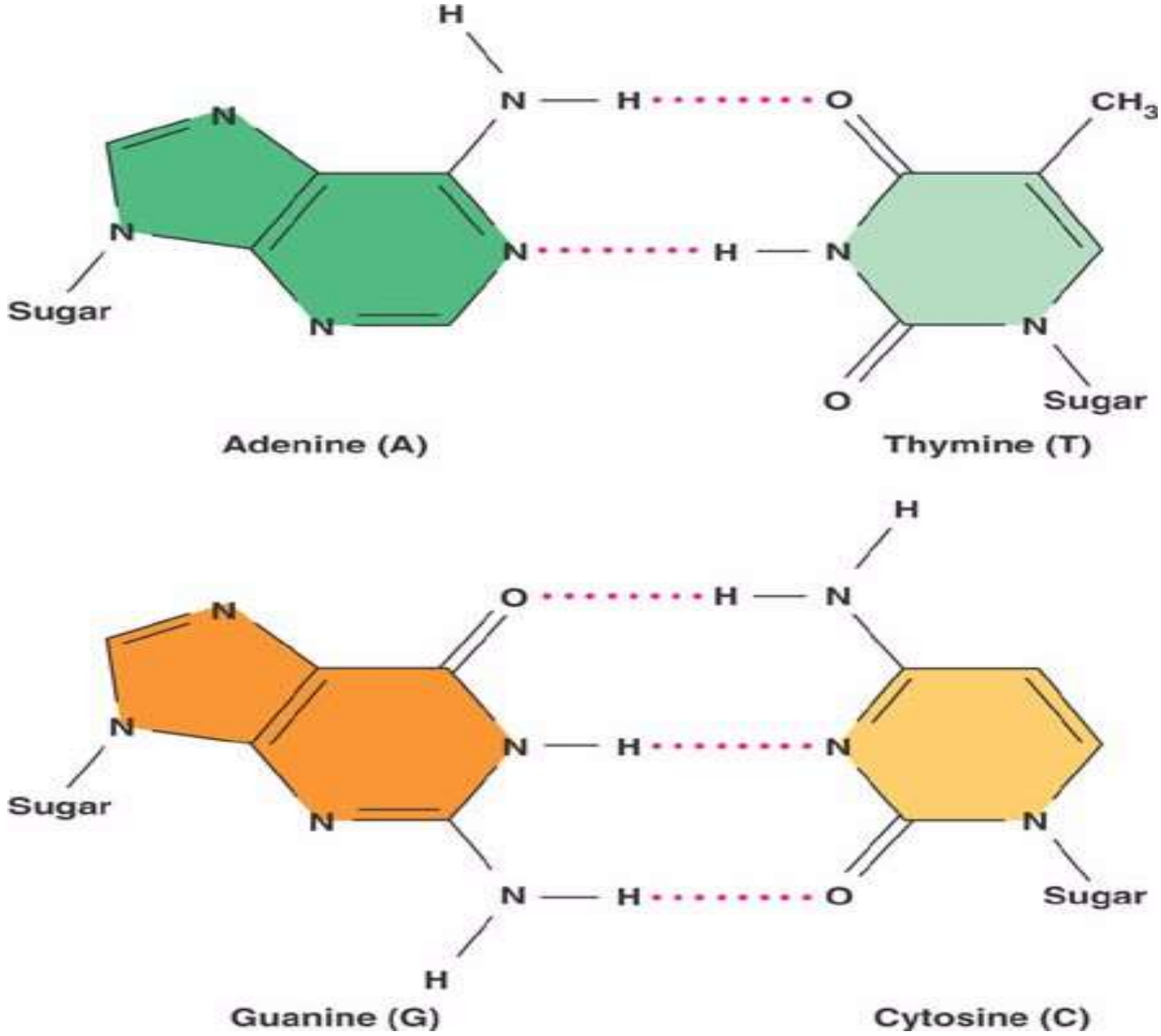
Thymine (T)


2'-deoxyribose
phosphoric acid
base
H_2O
nucleotide (dAMP)



The bases are attached to the deoxyribose by glycosidic linkages at N1 of the pyrimidines or at N9 of the purines.


5′ end
T
G
3′ to 5′
phosphodiester
bond
3′ end


H
N
H
O
CH3
N
N
N
H
N
N
N
Sugar
O
Sugar
Adenine (A)
Thymine (T)
H
O
H
N
N
N
H
N
N
N
Sugar
N
H
O
Sugar
H
Guanine (G)
Cytosine (C)

DNA Structure

- DNA consists of two strands of polynucleotides.

DNA 1ry structure :

- The sequence of nucleotides
- The order of nucleotides in any DNA strand is written in the 5’ to3’ direction

- The nucleotide in each strand covalently linked by phosphodiester bonds between phosphate at 5'of one nucleotide and 3\ hydroxyl group of deoxyribose of the next nucleotide.
- Each strand has two ends, **3** end with free hydroxyl group and **5** end with free 5\ phosphate group.
- The two DNA strands run **antiparallel** direction this means that one strands run from 3\to 5\ while the other strand run from 5\to 3\.

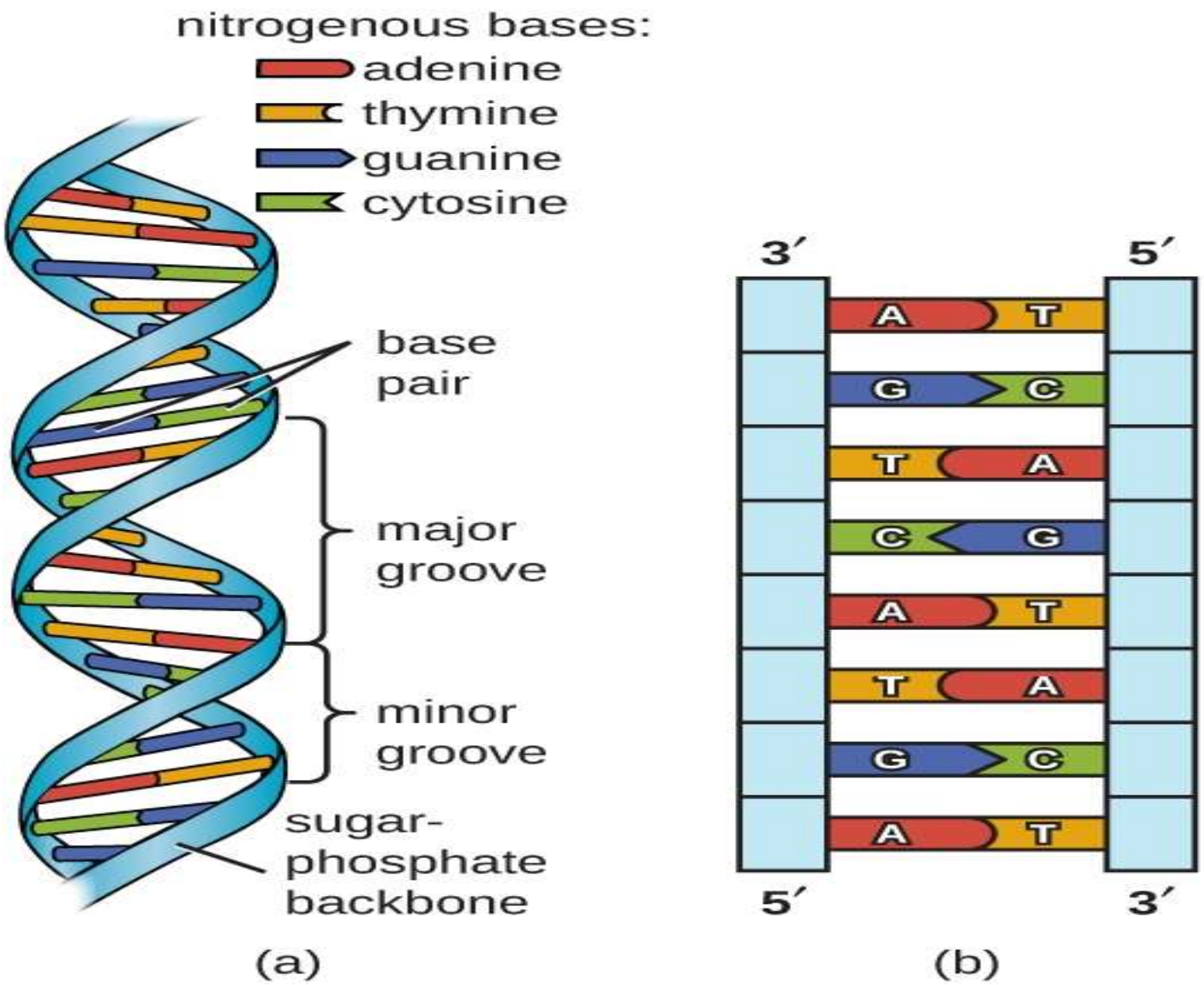
- **The sequence of nucleotide is always read from 5\ to 3\ direction e.g. 5\pGpApCp… 3\ or GAC.**
- **The sugar phosphate unites form the backbone of DNA strand while nitrogenous bases are projecting to the inside in between the two strands.**
- **The sequence of bases determines the coding structure of DNA (genetic information)**

DNA 2ry structure :

- Watson and crick proposed a structure for DNA in the form of a double helix (B form) which is the most common physiological form. It has the following characters:

1-Two antiparallel strands form a right handed helix: one runs in the 5' to3' direction and the other in the 3' to 5' direction. The two strands are paired to each other & coil around a common axis to form a right handed helix.

- **2-complementary base pairing**: The two strands are held together by hydrogen bonds between the complementary base pairs, adenine forms two hydrogen bonds with thymine and guanine forms three hydrogen bonds with cytosine. Thus the number of adenine equals that of thymine and the number of guanine equals that of cytosine in DNA.
- The sequence of bases in one strand determines the sequence of the other during **DNA replication** to transfer genetic information in a correct manner as each of the original DNA strand acts as a template for synthesis of a new complementary strand to form two daughter DNA molecules.


nitrogenous bases:
adenine
thymine
guanine
cytosine
base pair
major groove
minor groove
sugar-phosphate backbone
(a)
3′
5′
A
T
G
C
T
A
C
G
A
T
T
A
G
C
A
T
5′
3′
(b)

- **3- Base stacking: the base pairs are stacked above each other by van der waals forces and hydrophobic interactions so stability of the helix is provided by :**

- **Van der waals forces**
- **Hydrophobic interactions**
- **Hydrogen bonding between complementary base pairs**

- **Van der waals forces:** a class of transient electrostatic interaction. The attraction between molecules is greatest at a distance called the Van der waals distance (0.3 to 0.4 nm). If molecules approach each other more closely, a repulsive force develops, by the negative charges of their outer electron shells.
- **Hydrophobic interactions:** nonpolar molecules cannot form hydrogen bonds with water molecules and tend to cluster together and they are insoluble in water

- **4-Dimensions**:

-2 nm wide, each complete turn is 3.4 nm long in which there is 10.4 base pairs.

-Two grooves are apparent from outside, a major groove (2.2 nm) and a minor groove (1.2 nm), through which many drugs or proteins can make contact with the nitrogenous bases without any need to open the helix as in these grooves the bases are exposed.

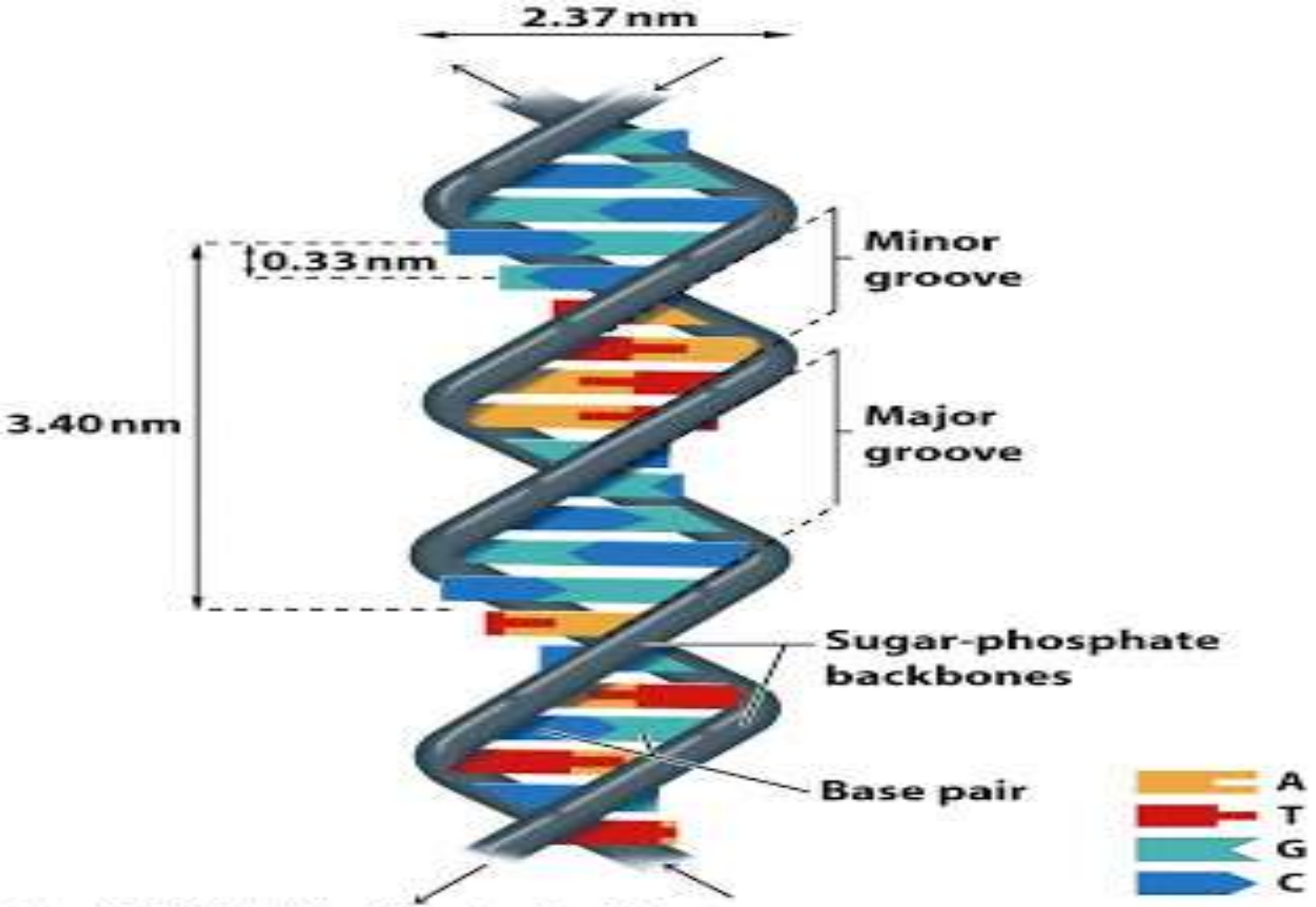
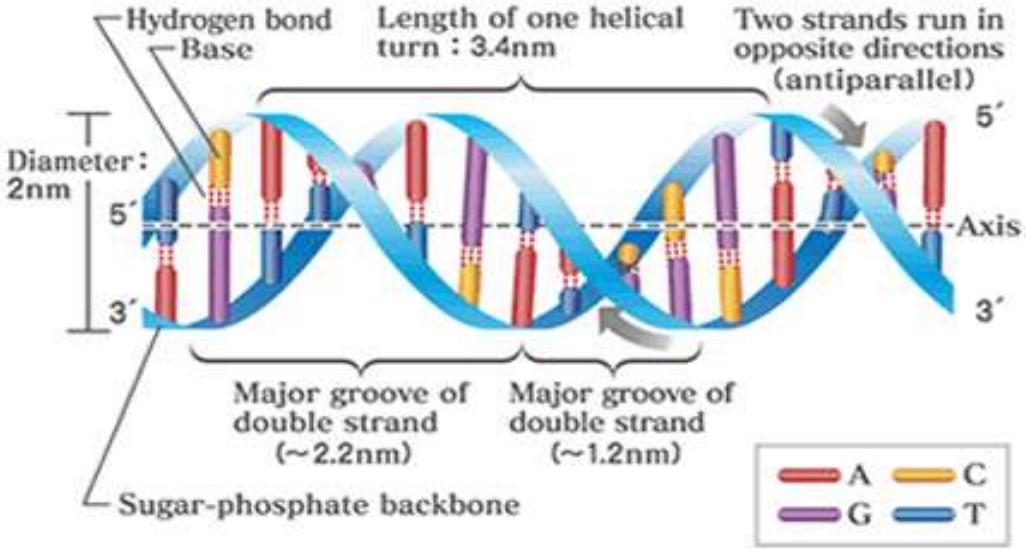


Figure 19-14 Principles of Biochemistry, 4/e

Ribbon model



Space-filling model