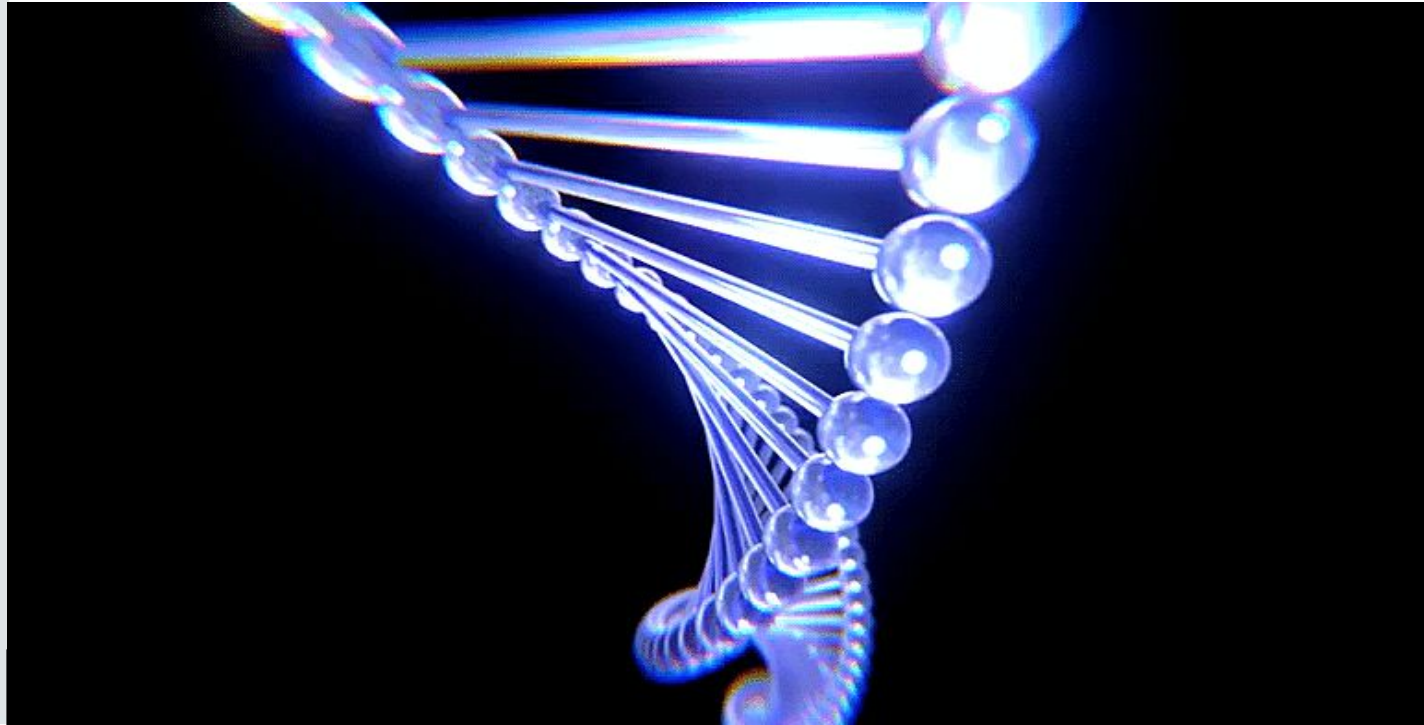


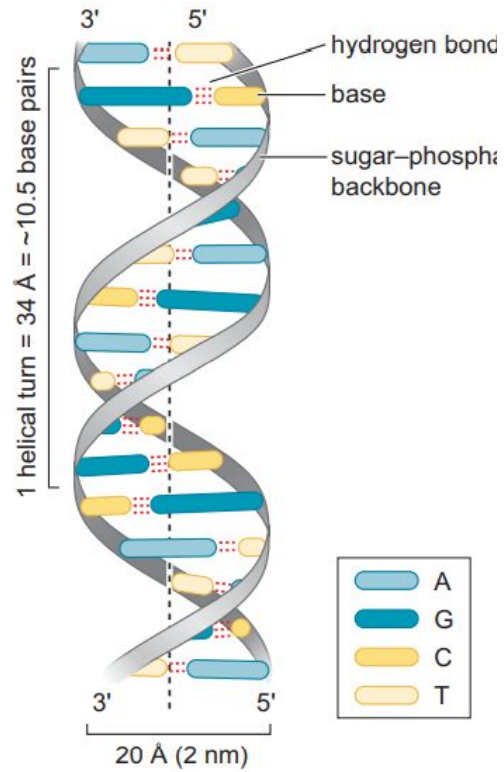
DNA

Vysakh V G

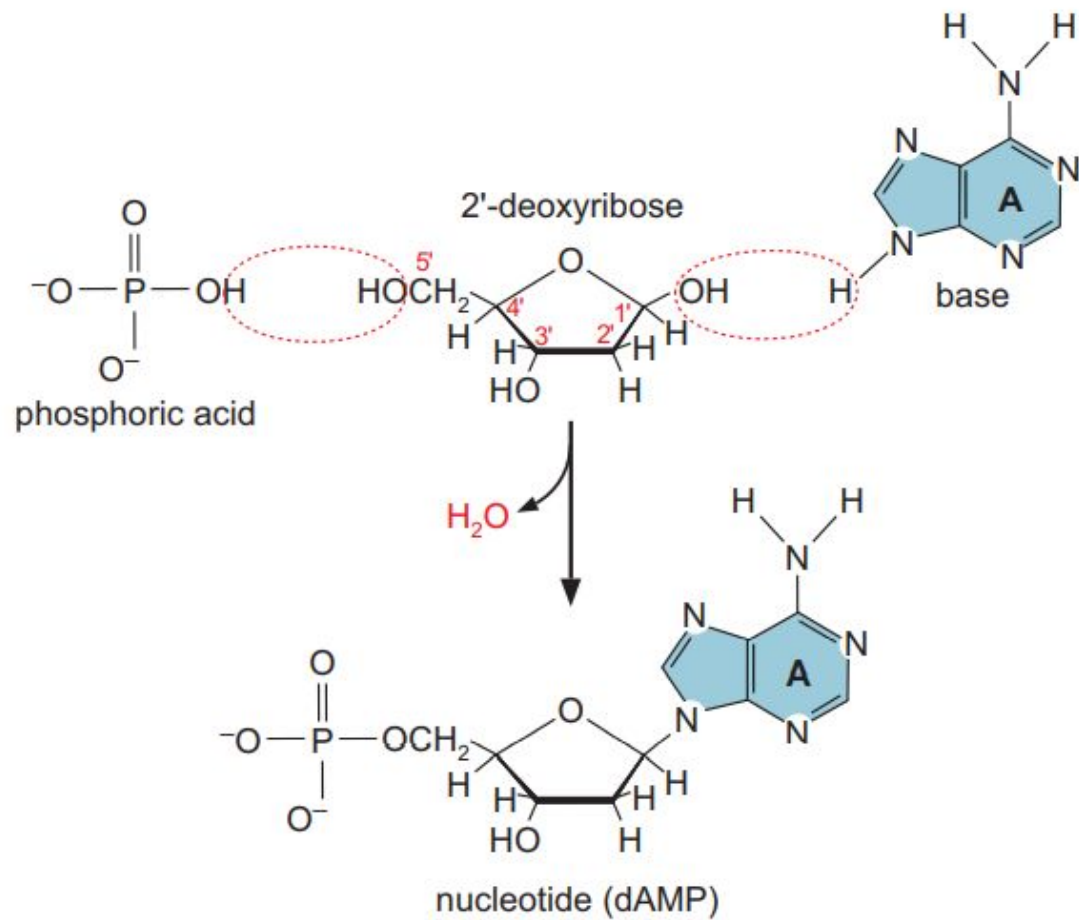


DNA Is Composed of Polynucleotide Chains

- Composed of two polynucleotide chains
- **Nucleotide:** Fundamental building block of DNA
- Phosphate joined to a sugar, 2' -deoxyribose,
- To which base attached.
- There is no hydroxyl at position 2'



- The sugar and base alone are called a **nucleoside.**
- Adding a phosphate to a nucleoside creates a nucleotide.

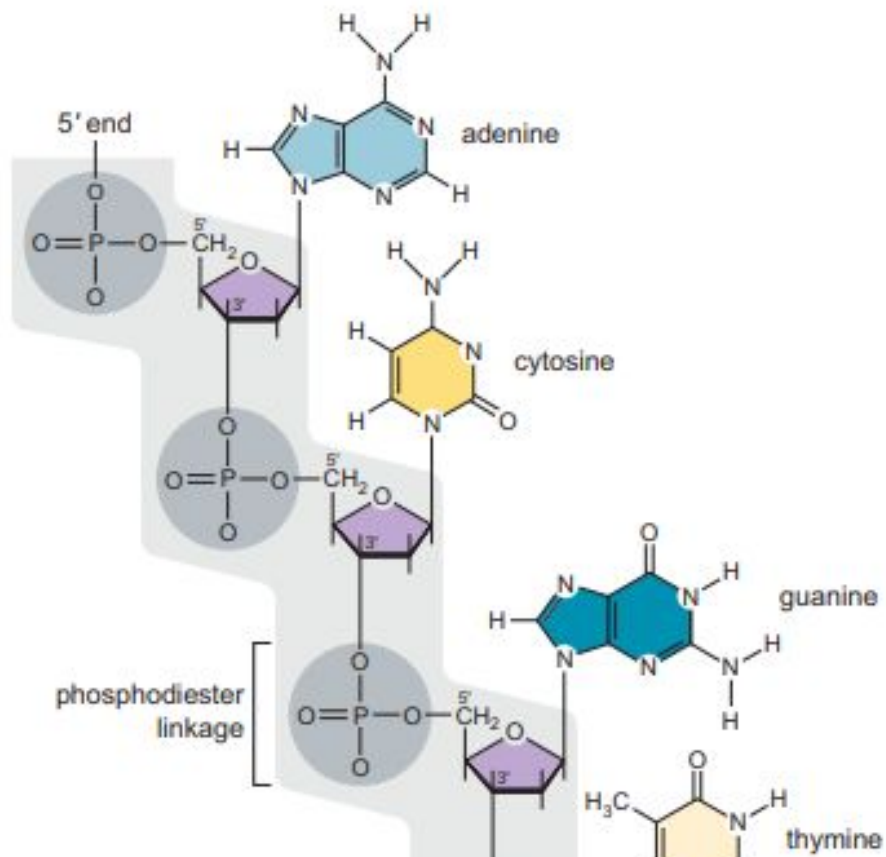


The Structure of a Nucleotide

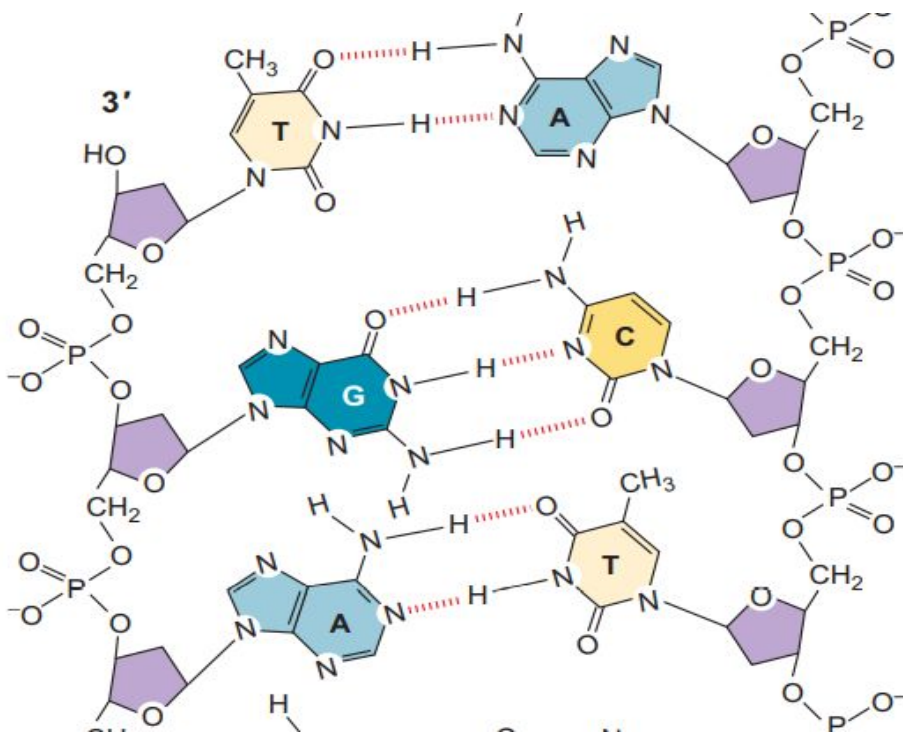


→ Nucleic acids are polymers of nucleotides.

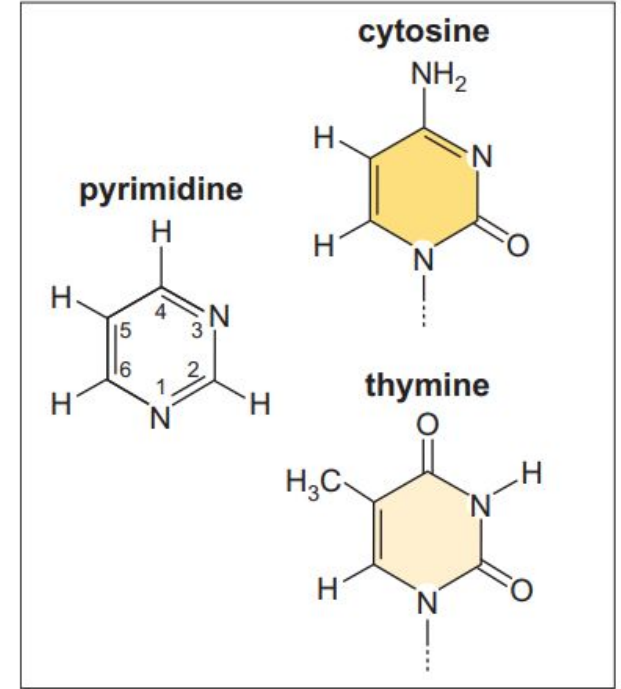
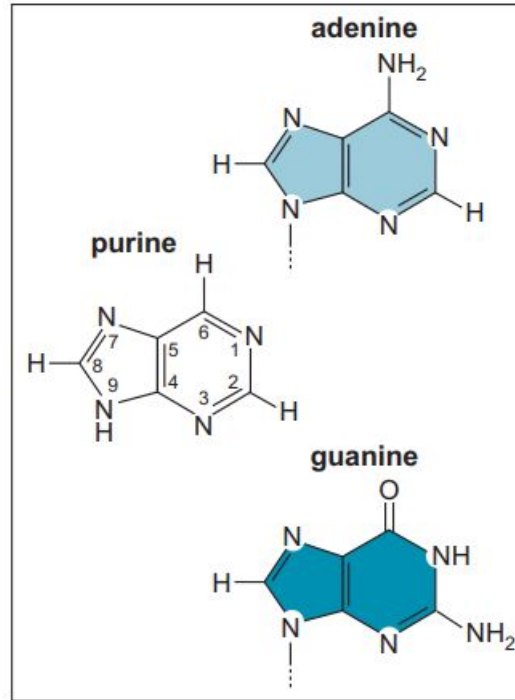
- Nucleotides are, joined to each other in polynucleotide chains through the 3' -hydroxyl of 2' -deoxyribose of one nucleotide and the phosphate attached to the 5' -hydroxyl of another nucleotide



- The order of the bases along the polynucleotide chain is irregular
- The basis for the enormous information content of DNA.
- The phosphodiester linkages impart an inherent polarity to the DNA chain.



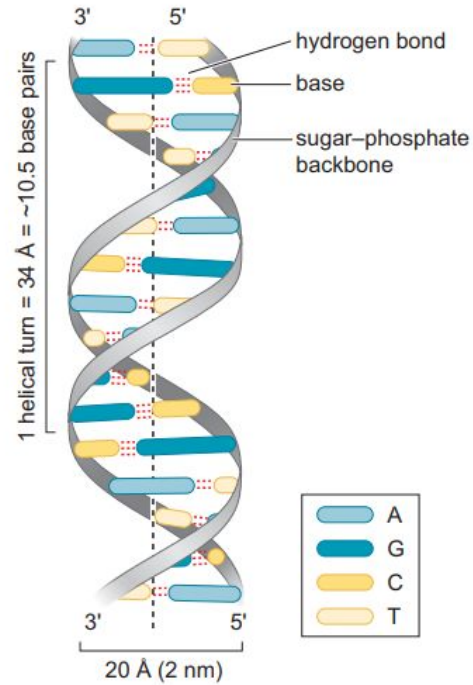
Purines & Pyrimidines



The Two Strands of the Double Helix Are Wound around Each Other in an Antiparallel Orientation

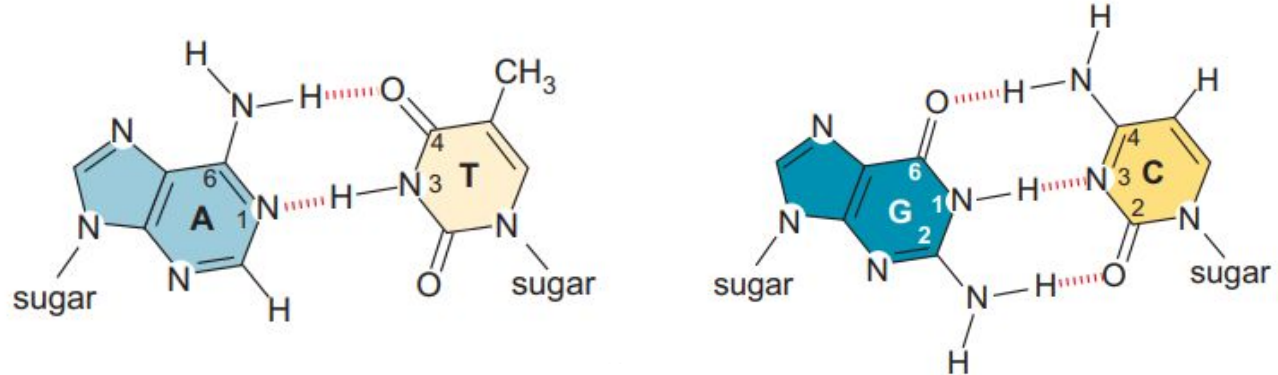
- The two chains have the same helical geometry but have **opposite 5' to 3'** orientations.
- The two chains interact with each other by pairing between the bases

Polarity



Base pairing

- **Adenine** on one chain pairing with **thymine** on the other chain
- **Guanine** pairing with **cytosine**
- Base at the 5' end of one strand is paired with the base at the 3' end of the other strand



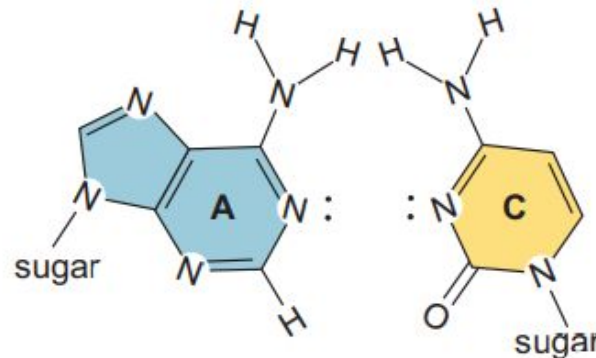
- Results in a complementary relationship between the sequence of bases on the two intertwined chains and gives DNA its self-encoding character
- Sequence 5' -ATGTC-3' on one chain,
- Sequence 3' ??????? 5'
- **“Watson–Crick” Pairing**
- Derives from the complementarity both of shape and of hydrogen-bonding properties between adenine and thymine and between guanine and cytosine

The Double Helix Is Stabilized by Base Pairing and Base Stacking

- **Hydrogen bonding**
- A second important contribution comes from **stacking interactions** between the bases.
- The bases are flat, relatively water-insoluble molecules, and they tend to stack above each other roughly perpendicular to the direction of the helical axis.
- Electron cloud interactions (p-p) between bases in the helical stacks contribute significantly to the stability of the double helix

Hydrogen Bonding Is Important for the Specificity of Base Pairing

- Tried to pair an adenine with a cytosine
- Hydrogen-bond acceptor (N1 of adenine) lying opposite a hydrogen-bond acceptor (N3 of cytosine) with no room to put a water molecule in between to satisfy the two acceptors

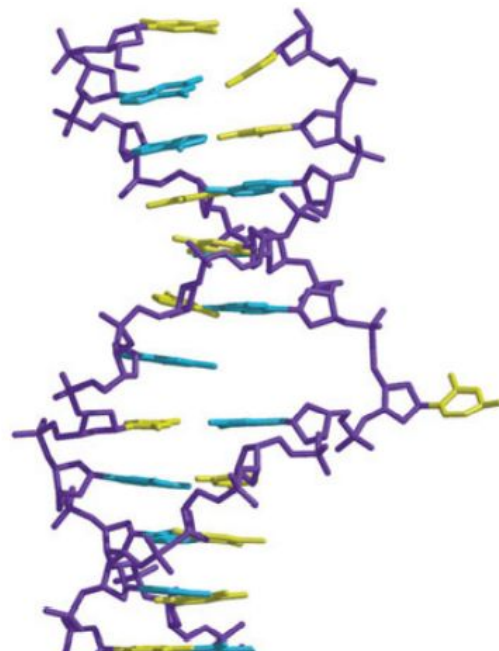


Bases Can Flip Out from the Double Helix

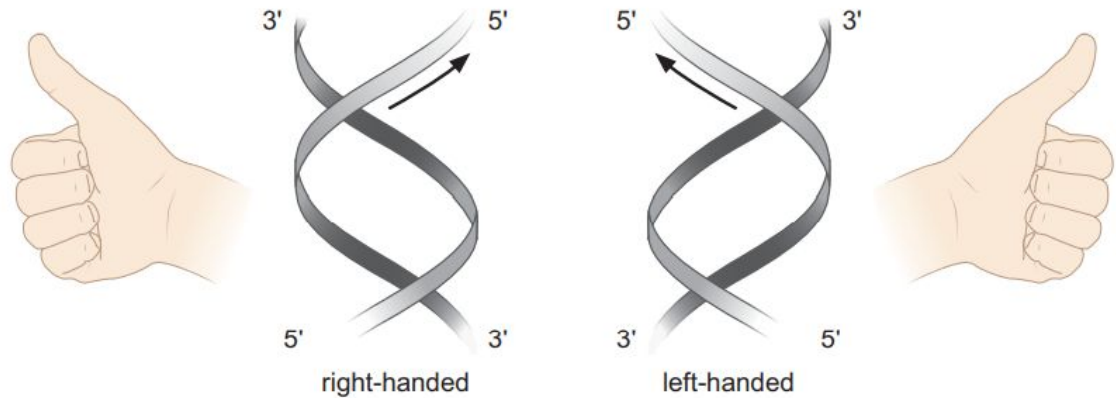
- Individual bases can protrude from the double helix in a remarkable phenomenon known as **base flipping**
- Certain enzymes that methylate bases or remove damaged bases do so with the base in an extrahelical configuration in which it is **flipped out from the double helix, enabling the base to sit in the catalytic cavity of the enzyme**



ENTRI

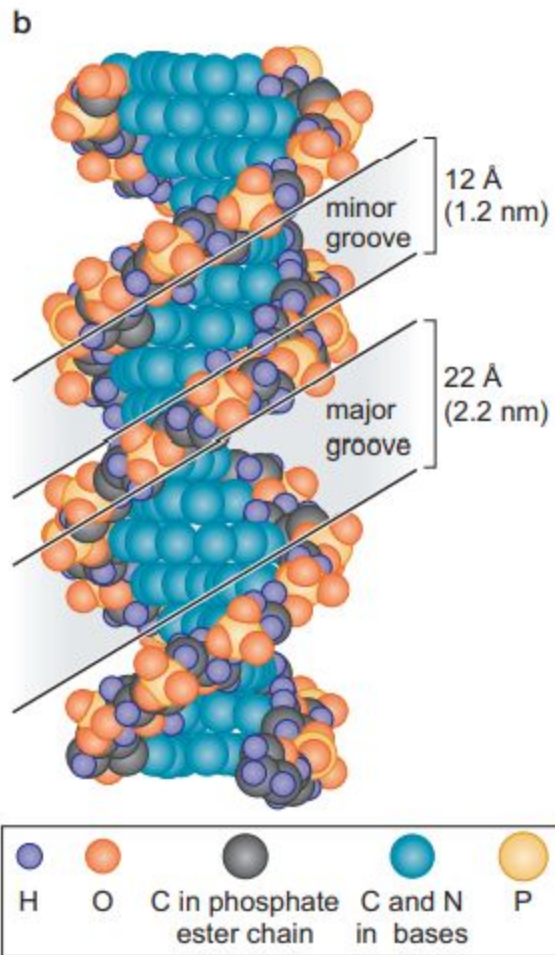


DNA Is Usually a Right-Handed Double Helix

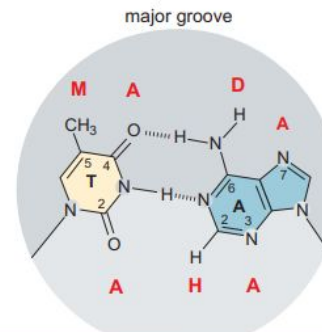
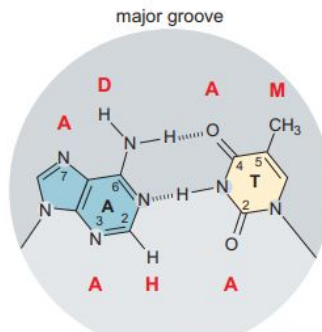
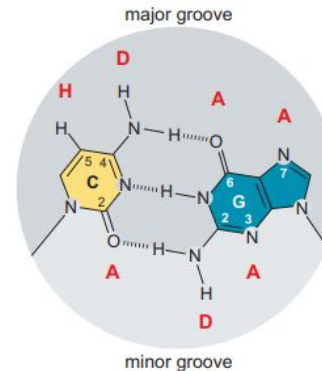
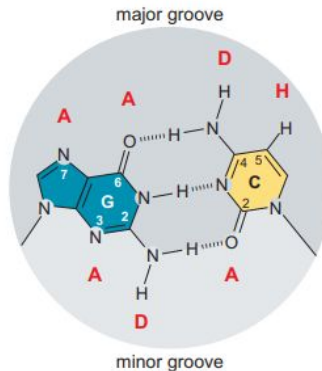


The Double Helix Has Minor and Major Grooves

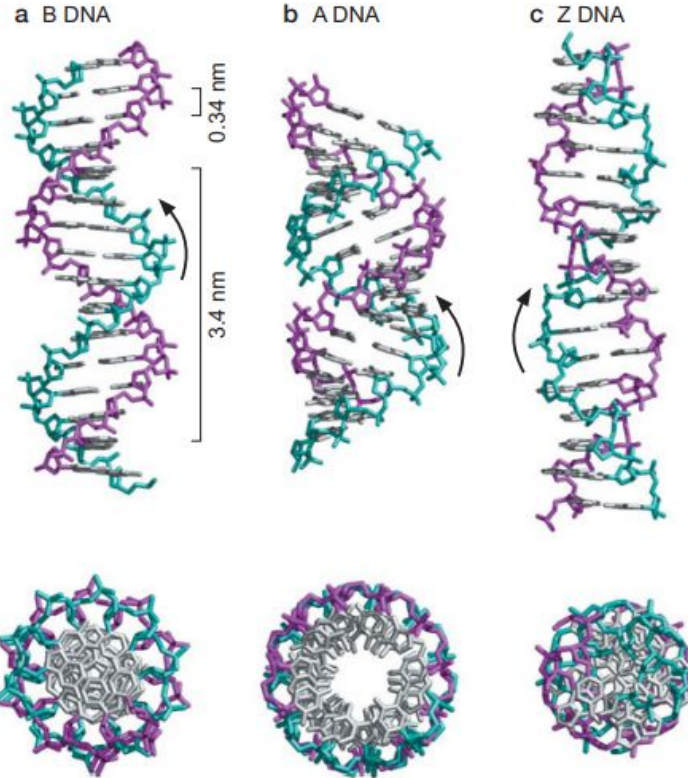
- As a result of the double-helical structure of the two chains, the DNA molecule is a long, extended polymer with two grooves that are not equal in size to each other.
- The narrow angle between the sugars on one edge of the base pairs generates a minor groove
- The large angle on the other edge generates a major groove



The Major Groove Is Rich in Chemical Information



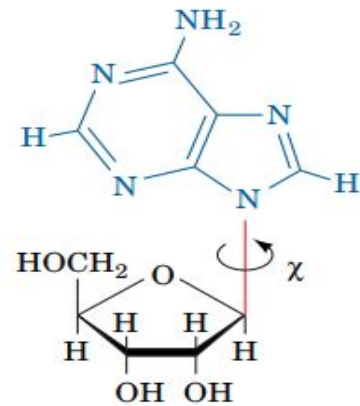
The Double Helix Exists in Multiple Conformations



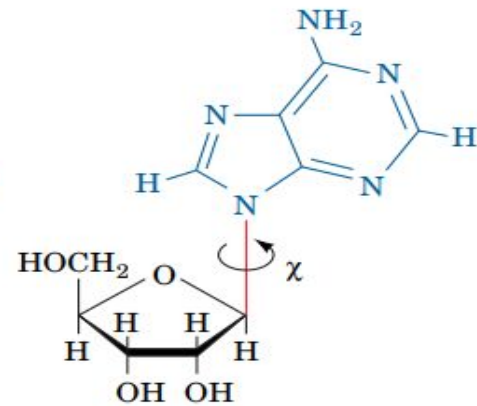
	A	B	Z
Helical sense	Right handed	Right handed	Left handed
Diameter	~26 Å	~20 Å	~18 Å
Base pairs per helical turn	11.6	10	12 (6 dimers)
Helical twist per base pair	31°	36°	9° for pyrimidine–purine steps; 51° for purine–pyrimidine steps
Helix pitch (rise per turn)	34 Å	34 Å	44 Å
Helix rise per base pair	2.9 Å	3.4 Å	7.4 Å per dimer
Base tilt normal to the helix axis	20°	6°	7°
Major groove	Narrow and deep	Wide and deep	Flat
Minor groove	Wide and shallow	Narrow and deep	Narrow and deep
Sugar pucker	C3'-endo	C2'-endo	C2'-endo for pyrimidines; C3'-endo for purines
Glycosidic bond conformation	Anti	Anti	Anti for pyrimidines; syn for purines

Source: Mainly Arnott, S., in Neidle, S. (Ed.), *Oxford Handbook of Nucleic Structure*, p. 35, Oxford University Press (1999).

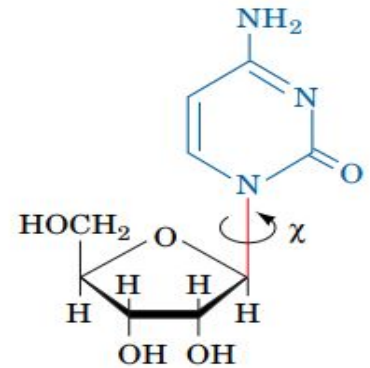
- Glycosidic bond that connects the base to the 1' position of 2' deoxyribose.
- This bond can be in one of two conformations **syn and anti**



syn-Adenosine



anti-Adenosine



anti-Cytidine

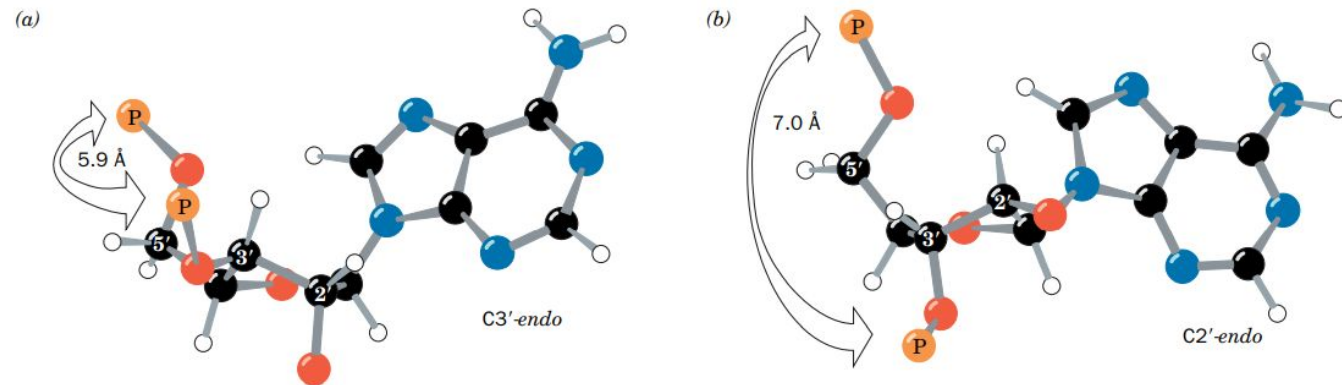


FIG. 24-7 Nucleotide sugar conformations. (a) The *C3'-endo* conformation ($C3'$ is displaced to the same side of the ring as $C5'$), which occurs in A-DNA. (b) The *C2'-endo* conformation, which occurs

in B-DNA. The distances between adjacent P atoms in the sugar-phosphate backbone are indicated. [After Saenger, W., *Principles of Nucleic Acid Structure*, p. 237, Springer-Verlag (1983).]

**Which of the following statement
is true regarding DNA ?**

B

Which of the following statement is true regarding DNA ?

- a. DNA Is Usually a Right-Handed Double Helix
- b. Bases Can Flip Out from the Double Helix
- c. The Major Groove Is Rich in Chemical Information
- d. Minor groove is rich in Chemical Information

