Programa Académico de Bachillerato
Universidad de Chile

Curso Biología C y E

Clase: Estructura de macromoléculas

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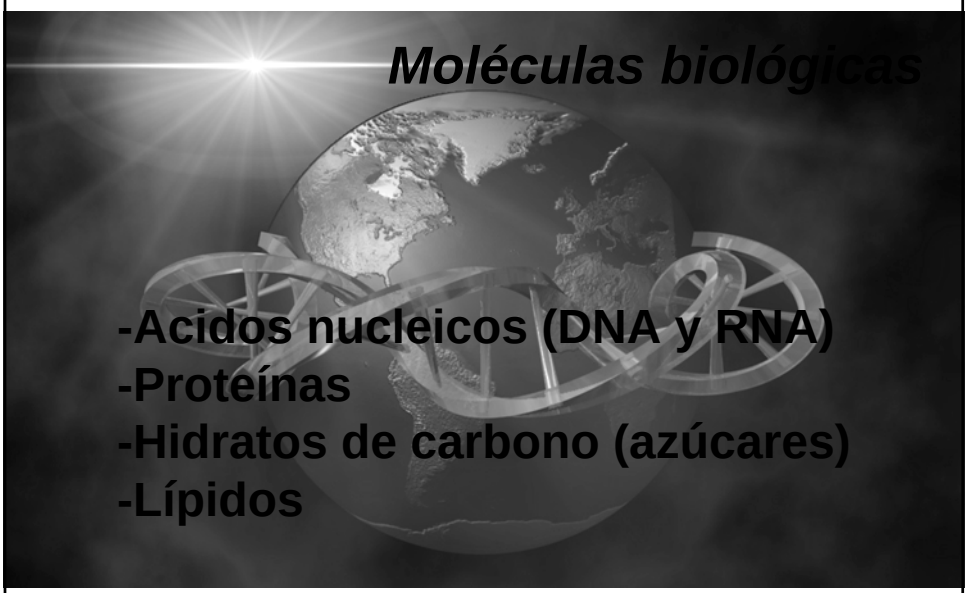
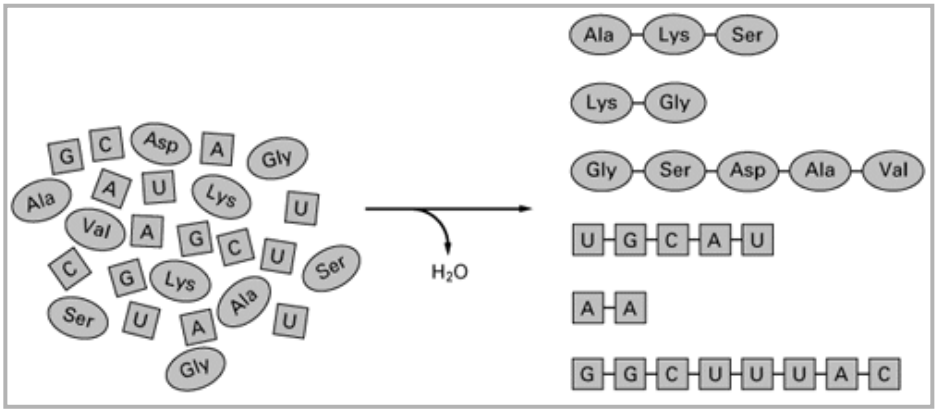
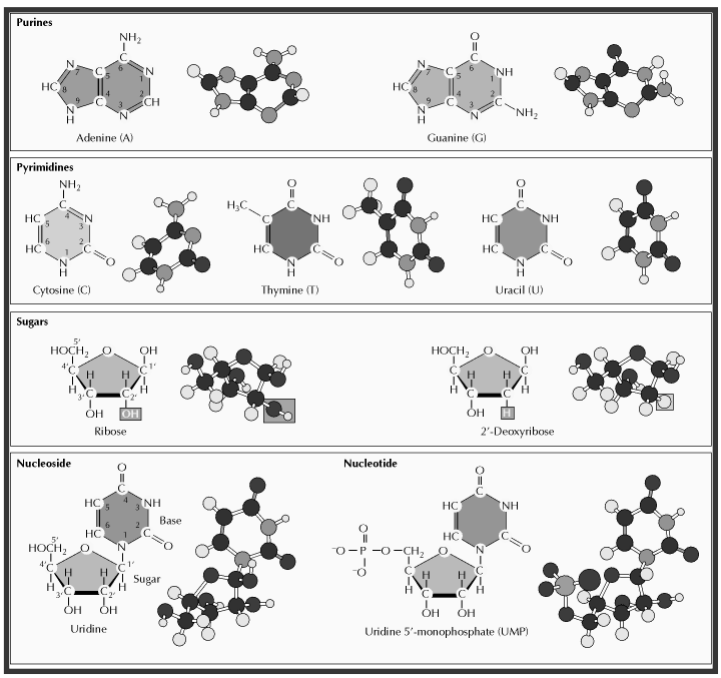
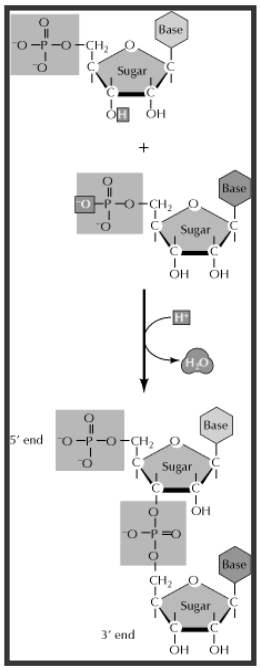
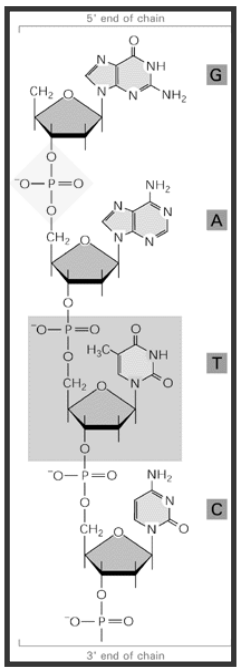
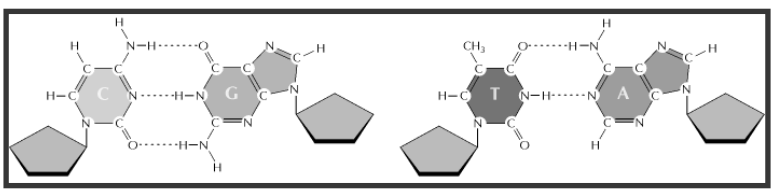


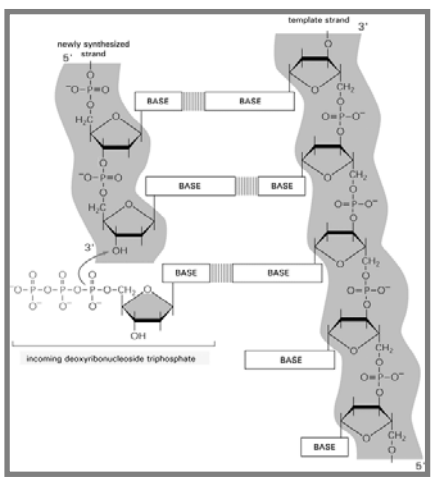

G
C
Asp
A
Gly
Ala
A
U
Lys
U
Val
A
G
C
U
Ser
C
G
Lys
Ala
Ser
U
A
U
Gly
H_2O
Ala Lys Ser
Lys Gly
Gly Ser Asp Ala Val
U G C A U
A A
G G C U U U A C

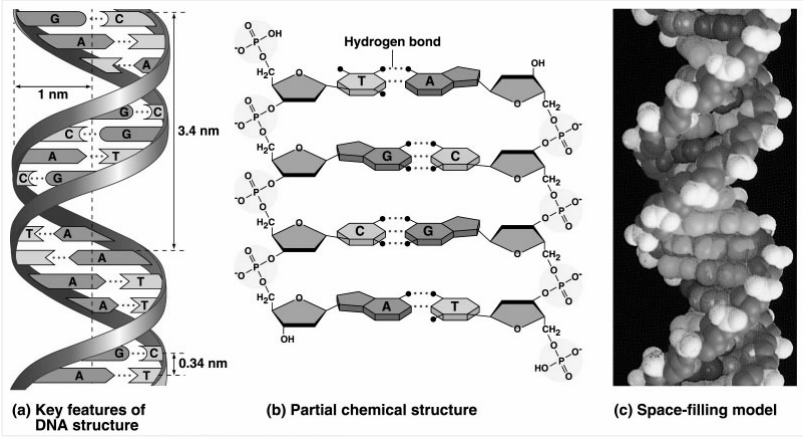

Purines
Adenine (A)
Guanine (G)
Pyrimidines
Cytosine (C)
Thymine (T)
Uracil (U)
Sugars
Ribose
2′-Deoxyribose
Nucleoside
Base
Sugar
Uridine
Nucleotide
Uridine 5′-monophosphate (UMP)

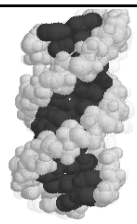

Base
Sugar
OH
+
Base
Sugar
OH OH
H+
H2O
5′ end
Base
Sugar
OH
Base
Sugar
3′ end
OH OH

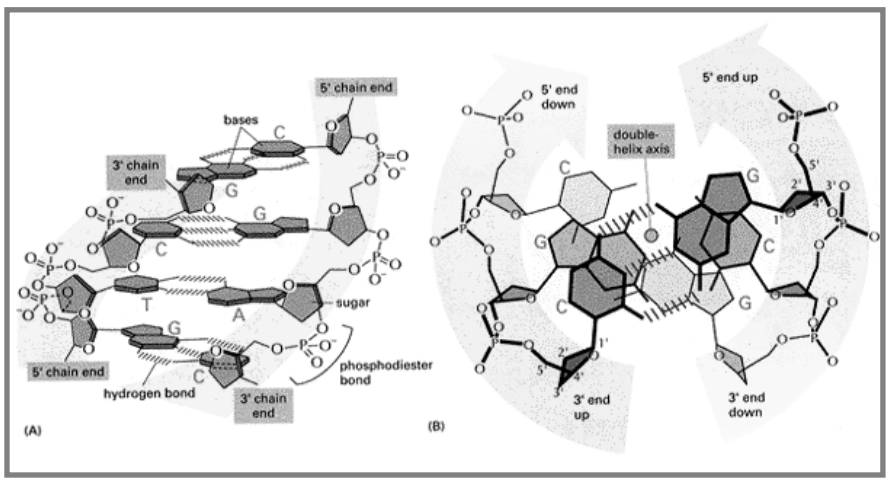

5′ end of chain
G
A
T
C
3′ end of chain

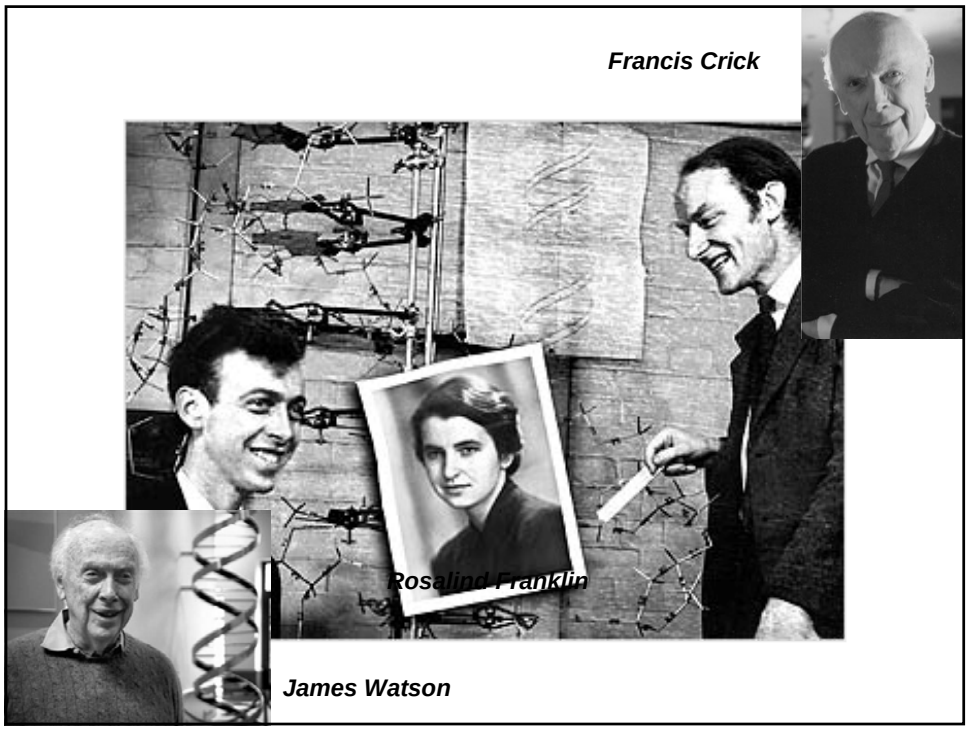

C
G
T
A

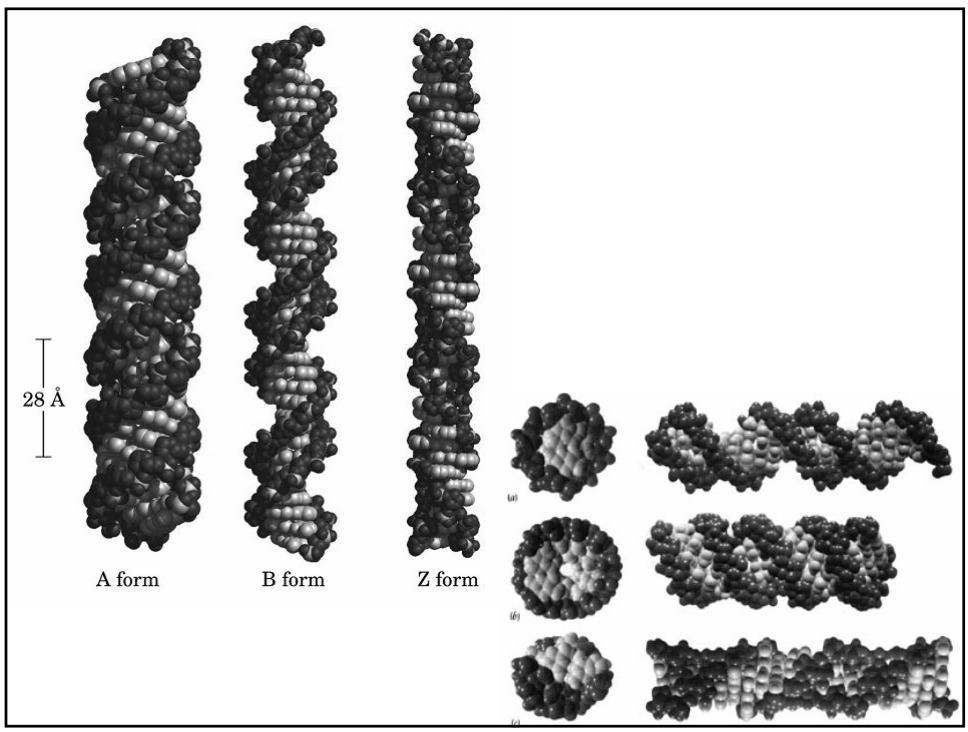

template strand
3′
newly synthesized strand
5′
BASE
BASE
BASE
BASE
BASE
BASE
BASE
BASE
3′
OH
incoming deoxyribonucleoside triphosphate
5′

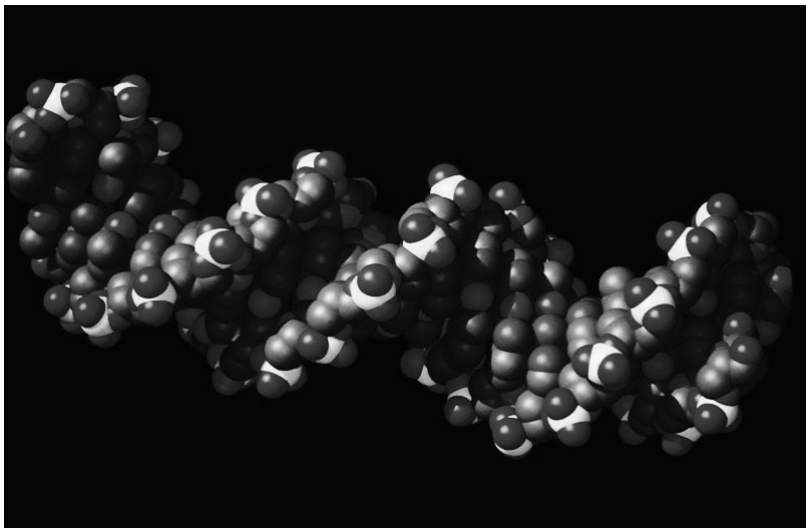

1 nm
3.4 nm
0.34 nm
Hydrogen bond
(a) Key features of DNA structure
(b) Partial chemical structure
(c) Space-filling model

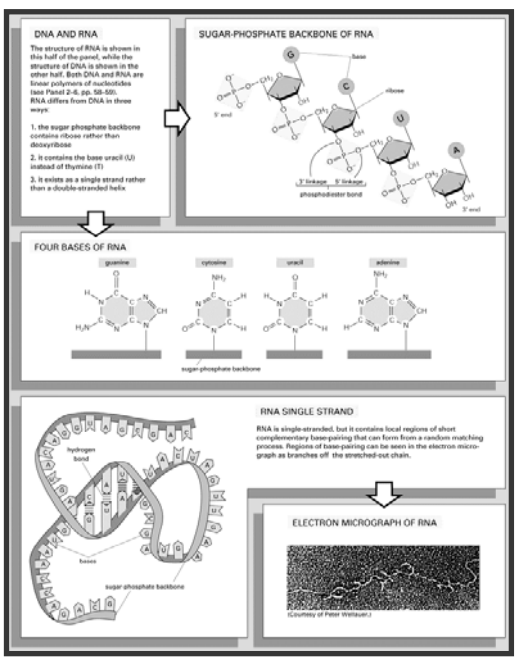


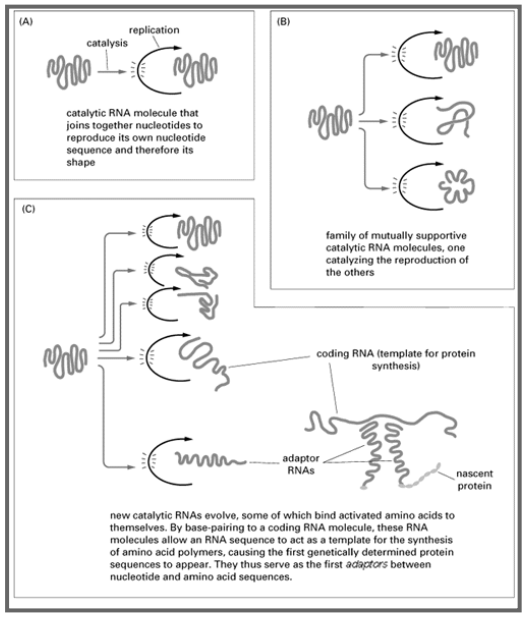

5' chain end
bases
3' chain end
sugar
5' chain end
hydrogen bond
3' chain end
phosphodiester bond
(A)
5' end down
5' end up
double-helix axis
3' end up
3' end down
(B)

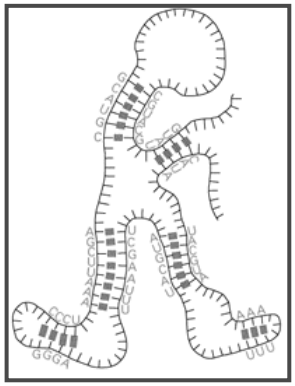

Francis Crick
Rosalind Franklin
James Watson

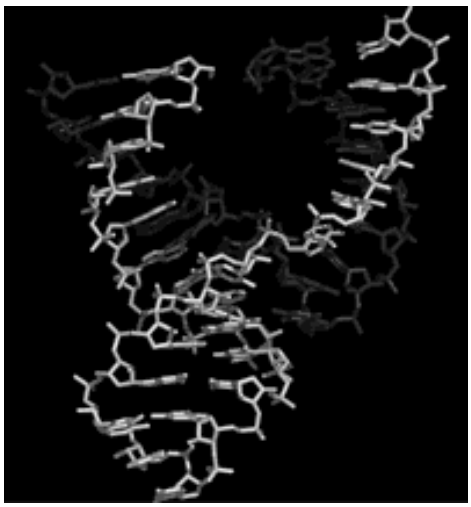

28 Å
A form
B form
Z form

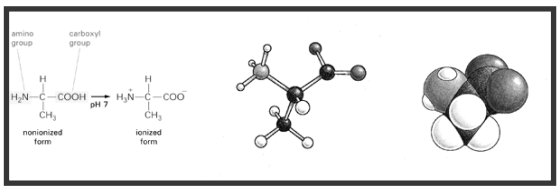


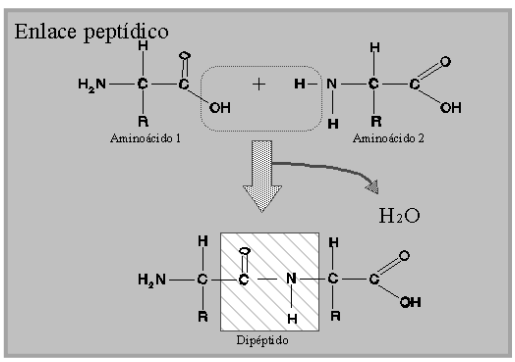

DNA AND RNA
The structure of RNA is shown in this half of the panel, while the structure of DNA is shown in the other half. Both DNA and RNA are linear polymers of nucleotides (see Panel 2-6, pp. 58-59). RNA differs from DNA in three ways:
1. the sugar phosphate backbone contains ribose rather than deoxyribose
2. it contains the base uracil (U) instead of thymine (T)
3. it exists as a single strand rather than a double-stranded helix
SUGAR-PHOSPHATE BACKBONE OF RNA
base
ribose
5' end
3' linkage
5' linkage
phosphodiester bond
3' end
FOUR BASES OF RNA
guanine
cytosine
uracil
adenine
sugar-phosphate backbone
RNA SINGLE STRAND
RNA is single-stranded, but it contains local regions of short complementary base-pairing that can form from a random matching process. Regions of base-pairing can be seen in the electron micrograph as branches off the stretched-out chain.
hydrogen bond
bases
sugar phosphate backbone
ELECTRON MICROGRAPH OF RNA
(Courtesy of Peter Wittauer.)

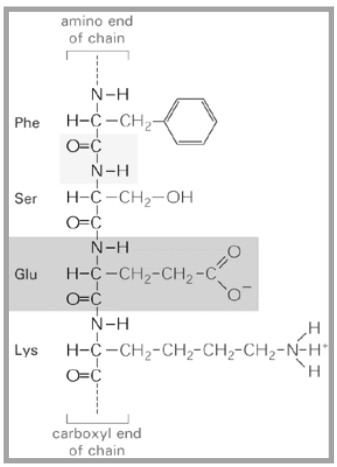

(A)
replication
catalysis
catalytic RNA molecule that joins together nucleotides to reproduce its own nucleotide sequence and therefore its shape
(B)
family of mutually supportive catalytic RNA molecules, one catalyzing the reproduction of the others
(C)
coding RNA (template for protein synthesis)
adaptor RNAs
nascent protein
new catalytic RNAs evolve, some of which bind activated amino acids to themselves. By base-pairing to a coding RNA molecule, these RNA molecules allow an RNA sequence to act as a template for the synthesis of amino acid polymers, causing the first genetically determined protein sequences to appear. They thus serve as the first *adaptors* between nucleotide and amino acid sequences.

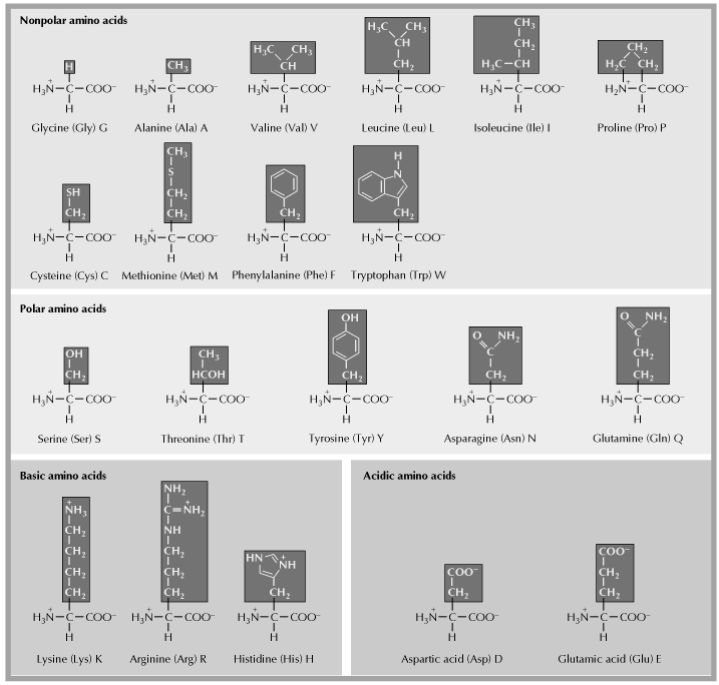





amino group
carboxyl group
pH 7
nonionized form
ionized form


Enlace peptídico
Aminoácido 1
Aminoácido 2
H2O
Dipéptido


amino end of chain
Phe
Ser
Glu
Lys
carboxyl end of chain




```
          5        10        15        20        25        30
  1 A A S X D X S L V E V H X X V F I V P P X I L Q A V V S I A
 31 T T R X D D X D S A A A S I P M V P G W V L K Q V X G S Q A
 61 G S F L A I V M G G G D L E V I L I X L A G Y Q E S S I X A
 91 S R S L A A S M X T T A I P S D L W G N X A X S N A A F S S
121 X E F S S X A G S V P L G F T F X E A G A K E X V I K G Q I
151 T X Q A X A F S L A X L X K L I S A M X N A X F P A G D X X
181 X X V A D I X D S H G I L X X V N Y T D A X I K M G I I F G
211 S G V N A A Y W C D S T X I A D A A D A G X X G G A G X M X
241 V C C X Q D S F R K A F P S L P Q I X Y X X T L N X X S P X
271 A X K T F E K N S X A K N X G Q S L R D V L M X Y K X X G Q
301 X H X X X A X D F X A A N V E N S S Y P A K I Q K L P H F D
331 L R X X X D L F X G D Q G I A X K T X M K X V V R R X L F L
361 I A A Y A F R L V V C X I X A I C Q K K G Y S S G H I A A X
391 G S X R D Y S G F S X N S A T X N X N I Y G W P Q S A X X S
421 K P I X I T P A I D G E G A A X X V I X S I A S S Q X X X A
451 X X S A X X A
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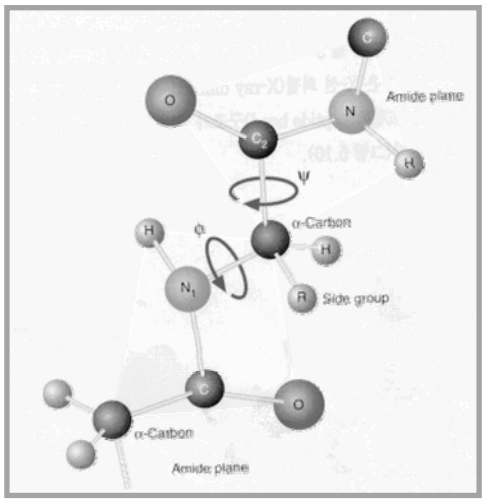
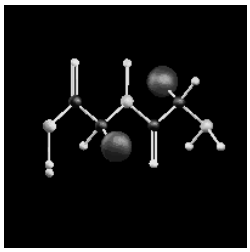
ESTRUCTURA PRIMARIA DE LA HEXOQUINASA (cada aminoácido se simboliza por una letra mayúscula específica)





peptide group in a planar configuration

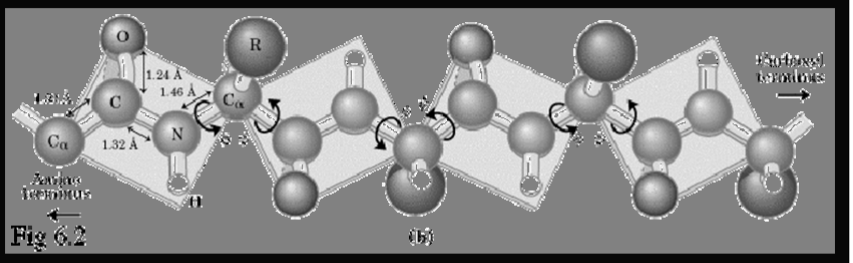
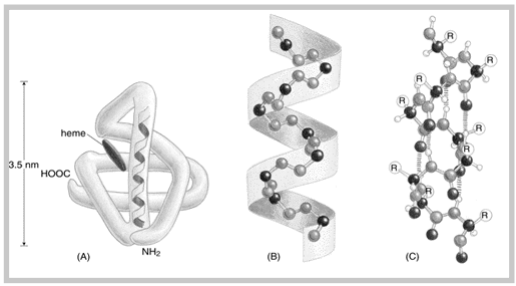
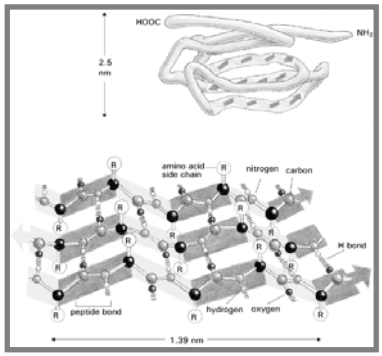
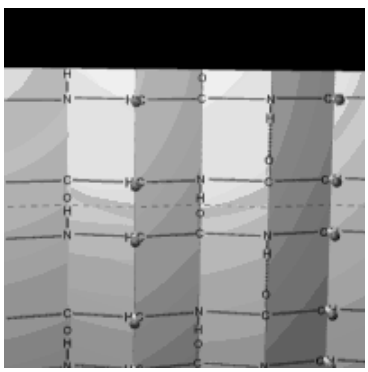


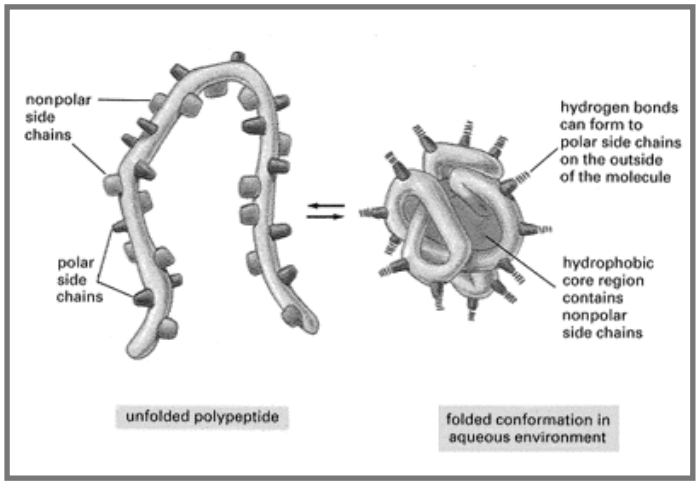
Fig 6.2

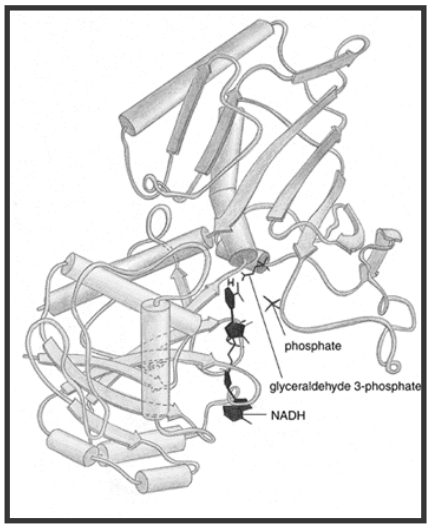
Limits ability of peptide group to rotate - limiting possible protein conformations

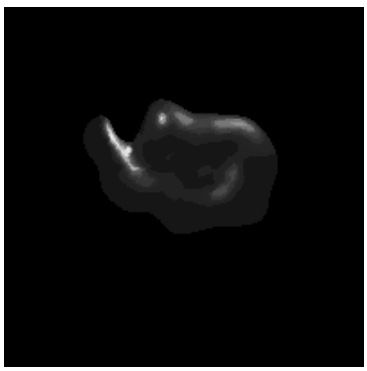

heme
3.5 nm
HOOC
(A)
NH_2
(B)
(C)

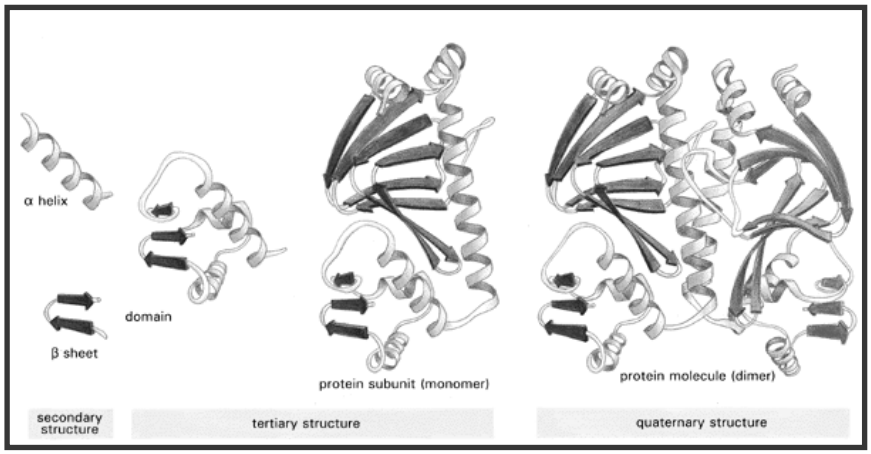

HOOC
NH_2
2.5 nm
amino acid side chain
nitrogen
carbon
H bond
peptide bond
hydrogen
oxygen
1.39 nm

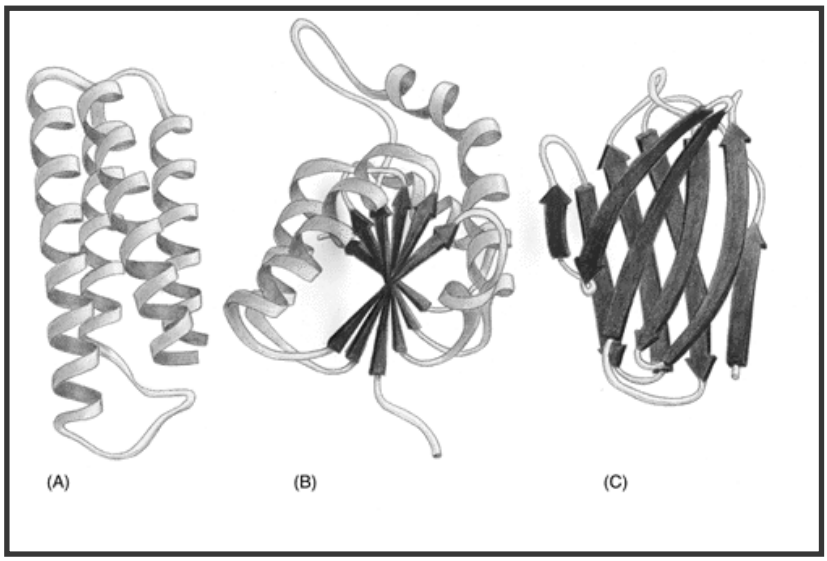


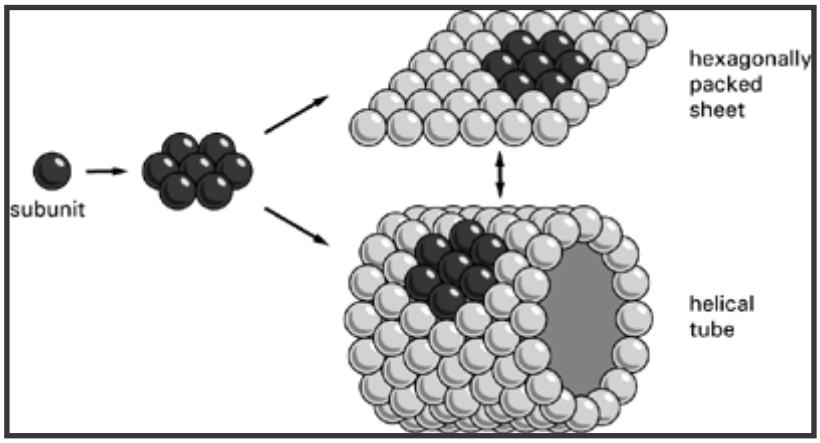

nonpolar
side
chains
polar
side
chains
hydrogen bonds
can form to
polar side chains
on the outside
of the molecule
hydrophobic
core region
contains
nonpolar
side chains
unfolded polypeptide
folded conformation in
aqueous environment

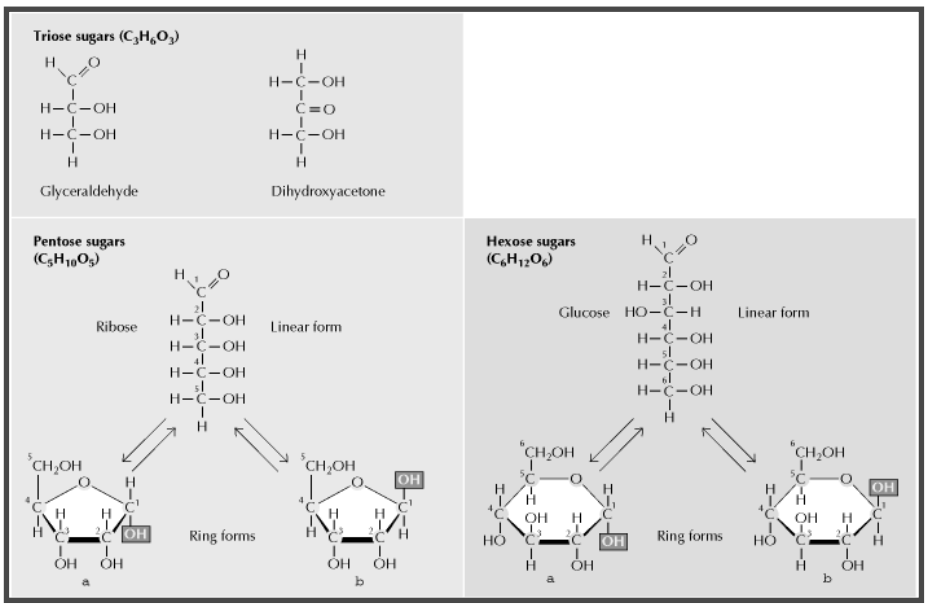

phosphate
glyceraldehyde 3-phosphate
NADH

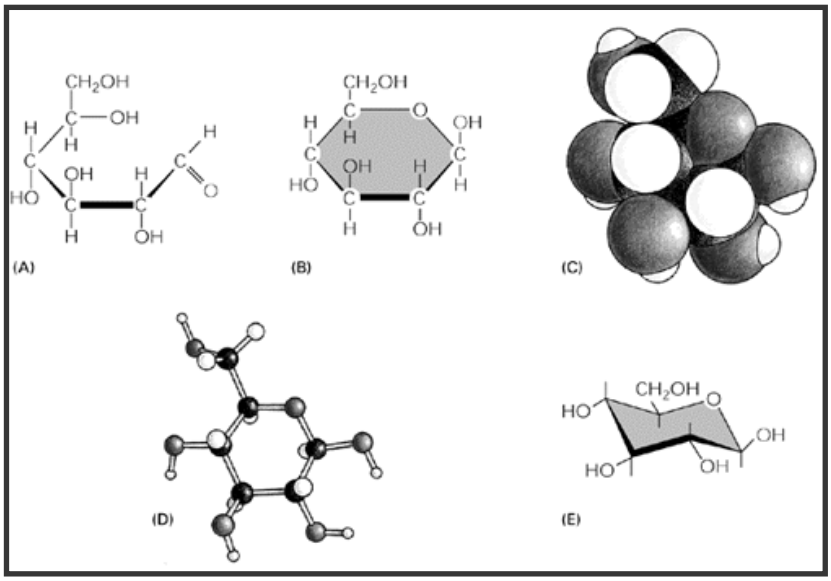


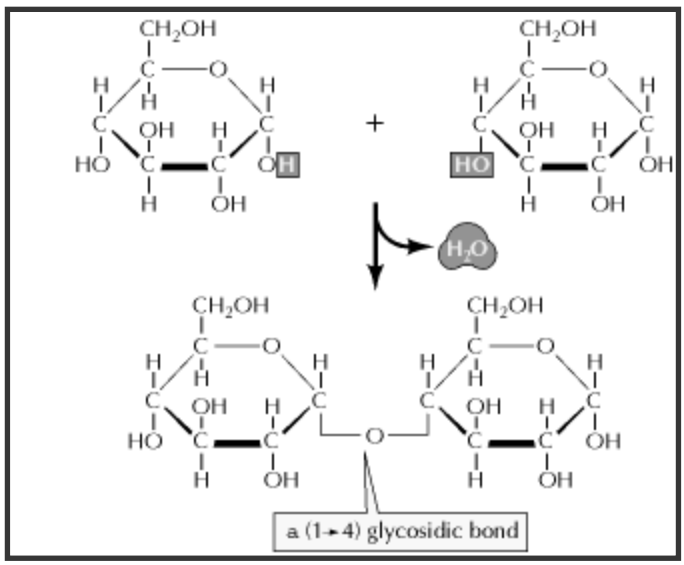

α helix
β sheet
domain
protein subunit (monomer)
protein molecule (dimer)
secondary structure
tertiary structure
quaternary structure

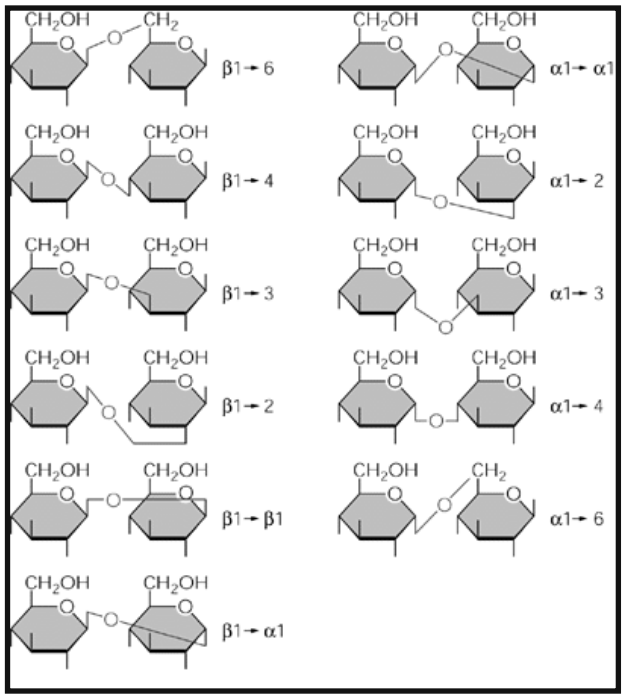

(A)
(B)
(C)

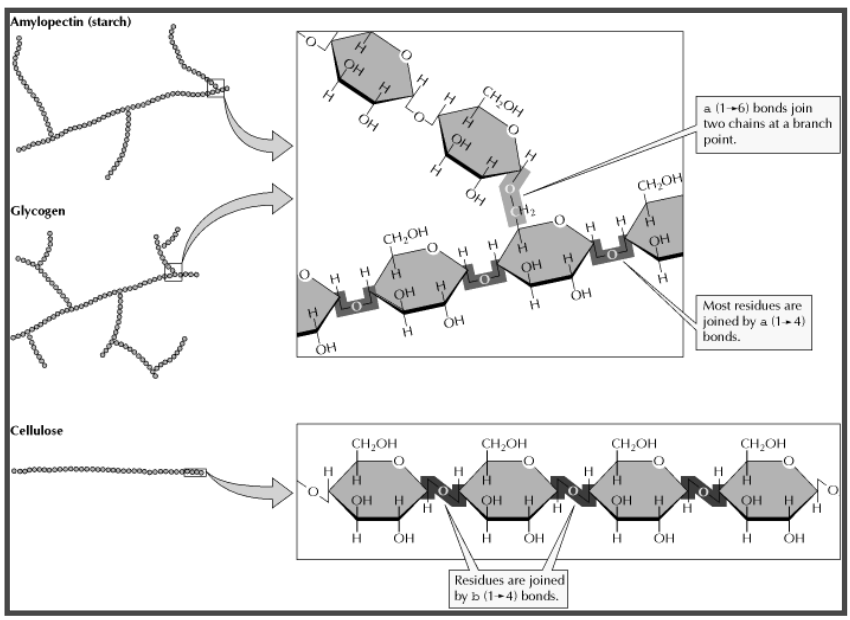

subunit
hexagonally packed sheet
helical tube


Triose sugars ($C_3H_6O_3$)
Glyceraldehyde
Dihydroxyacetone
Pentose sugars ($C_5H_{10}O_5$)
Ribose
Linear form
Ring forms
a
b
Hexose sugars ($C_6H_{12}O_6$)
Glucose
Linear form
Ring forms
a
b


(A)
(B)
(C)
(D)
(E)


+
H_2O
a (1→4) glycosidic bond


β1→6
α1→α1
β1→4
α1→2
β1→3
α1→3
β1→2
α1→4
β1→β1
α1→6
β1→α1


Amylopectin (starch)
Glycogen
Cellulose
α (1→6) bonds join two chains at a branch point.
Most residues are joined by α (1→4) bonds.
Residues are joined by β (1→4) bonds.