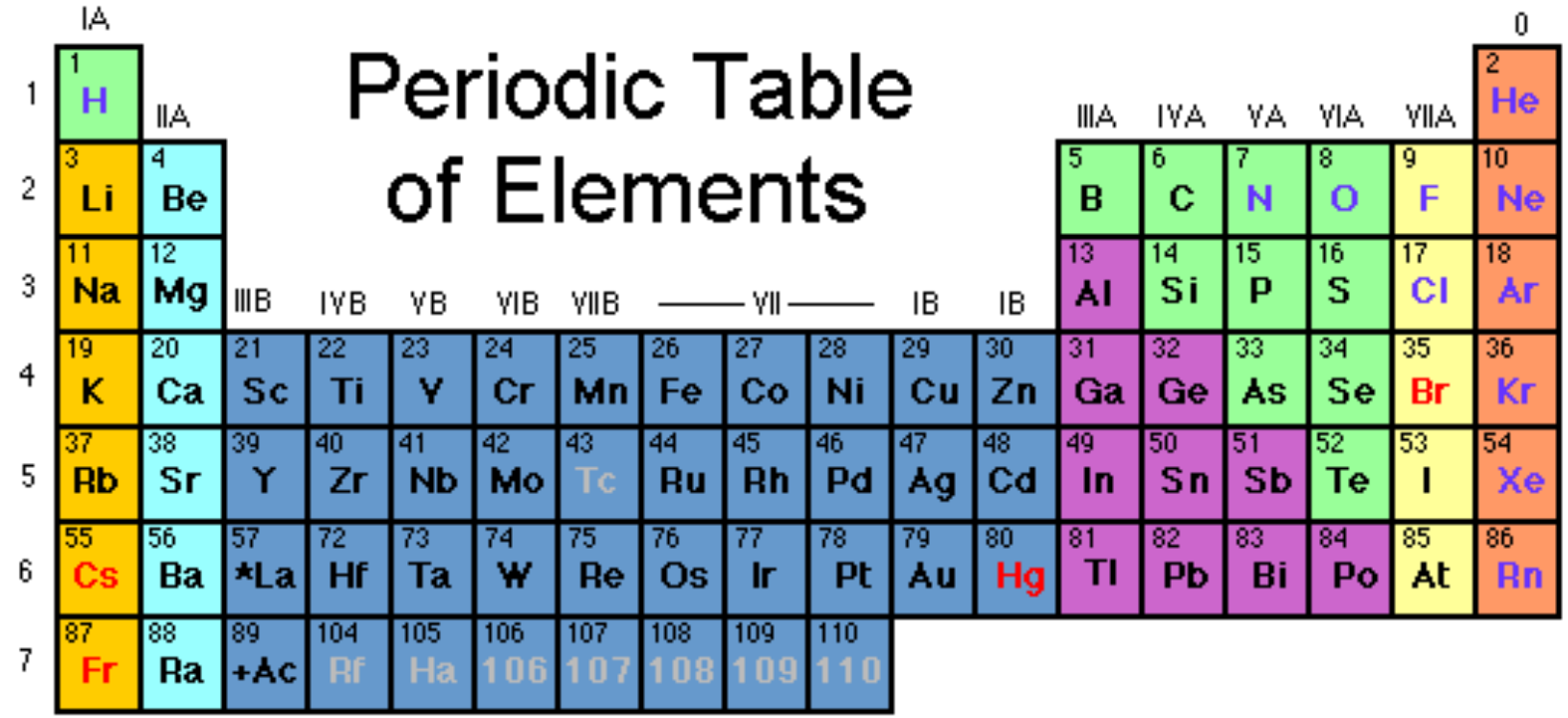
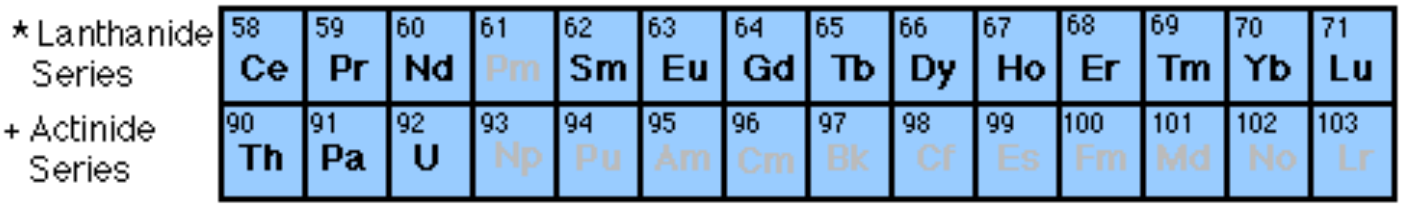
Review of Biochemistry

Periodic Table of Elements





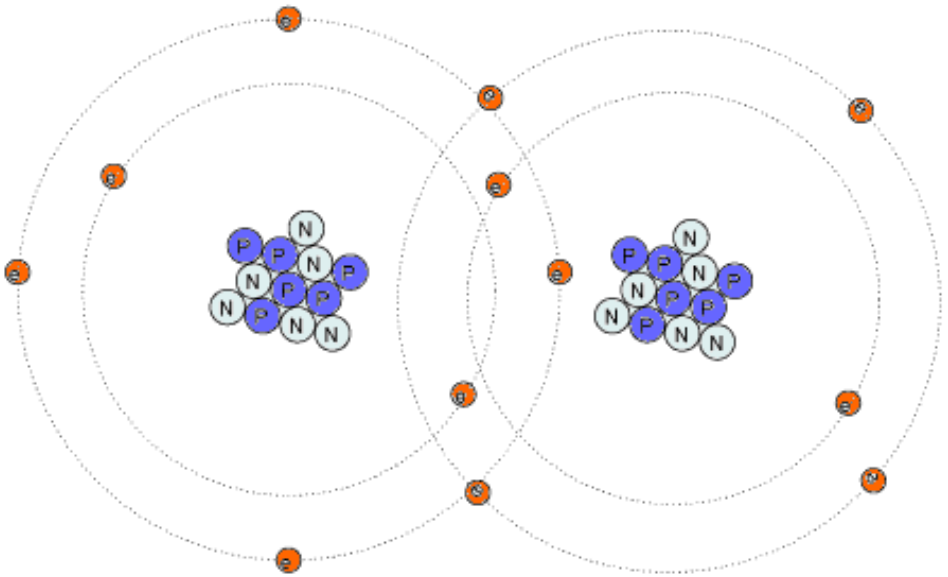
Legend - click to find out more...

H - gas | **Li - solid** | **Br - liquid** | **Tc - synthetic**

- Non-Metals
- Transition Metals
- Rare Earth Metals
- Halogens
- Alkali Metals
- Alkali Earth Metals
- Other Metals
- Inert Elements

Chemical bond

Hydrogen	H•	H•
Carbon	•Ċ•	•Ċ•
Water	H:Ö:H	H-Ö-H
Ethylene	H H C::C H H	H H C=C H H
Acetylene	H:C:::C:H	H-C≡C-H



Functional Groups

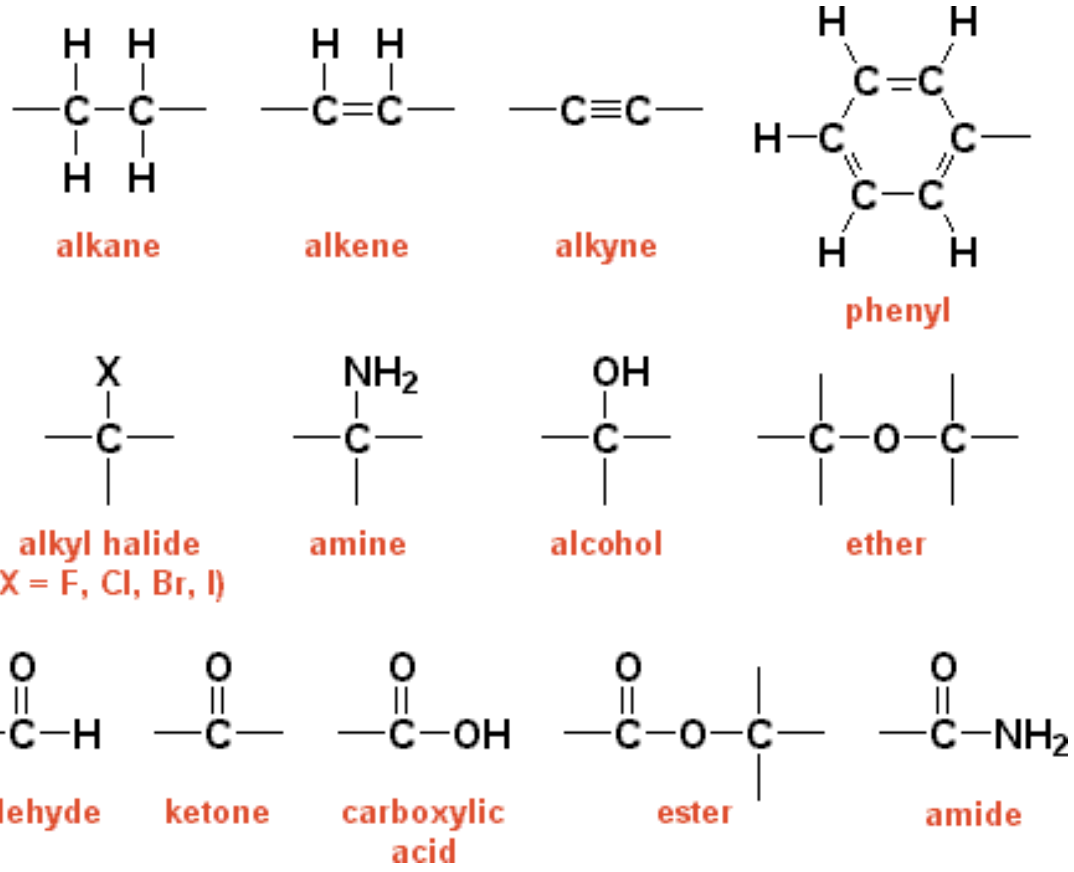
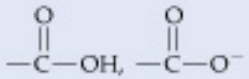
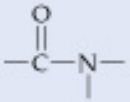
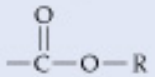
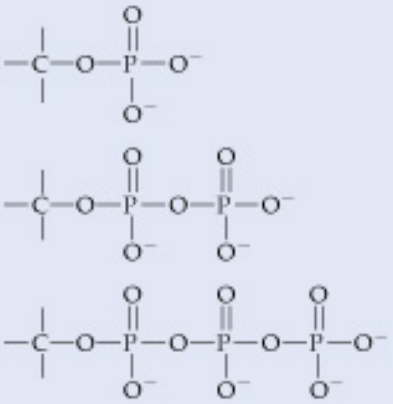
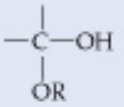
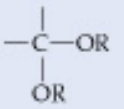
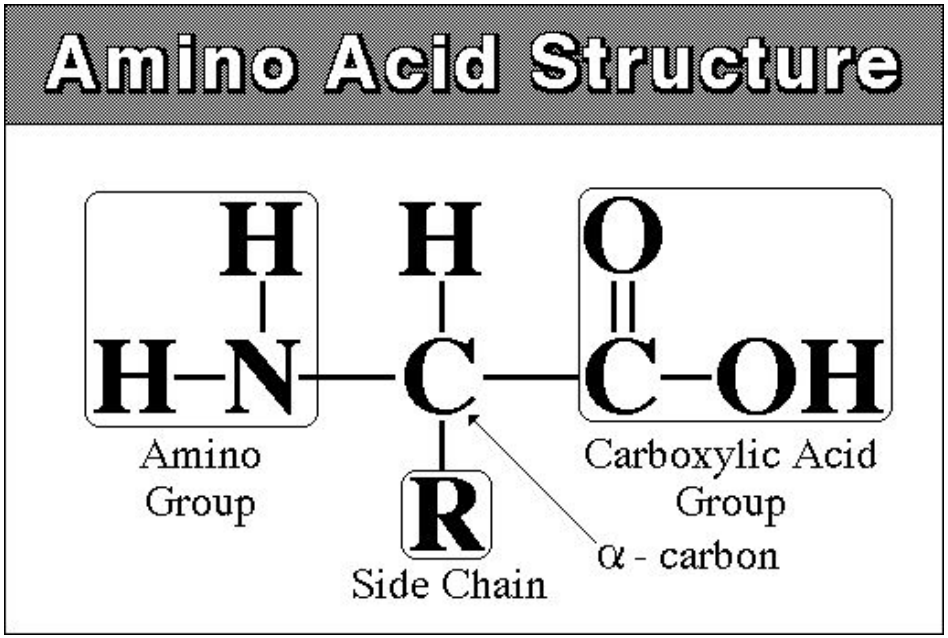
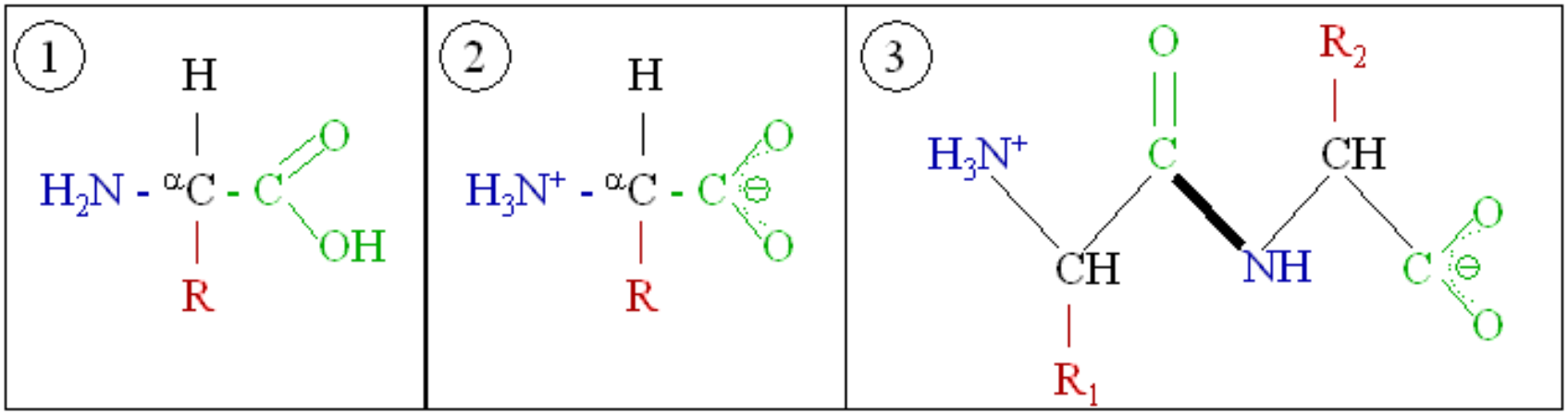


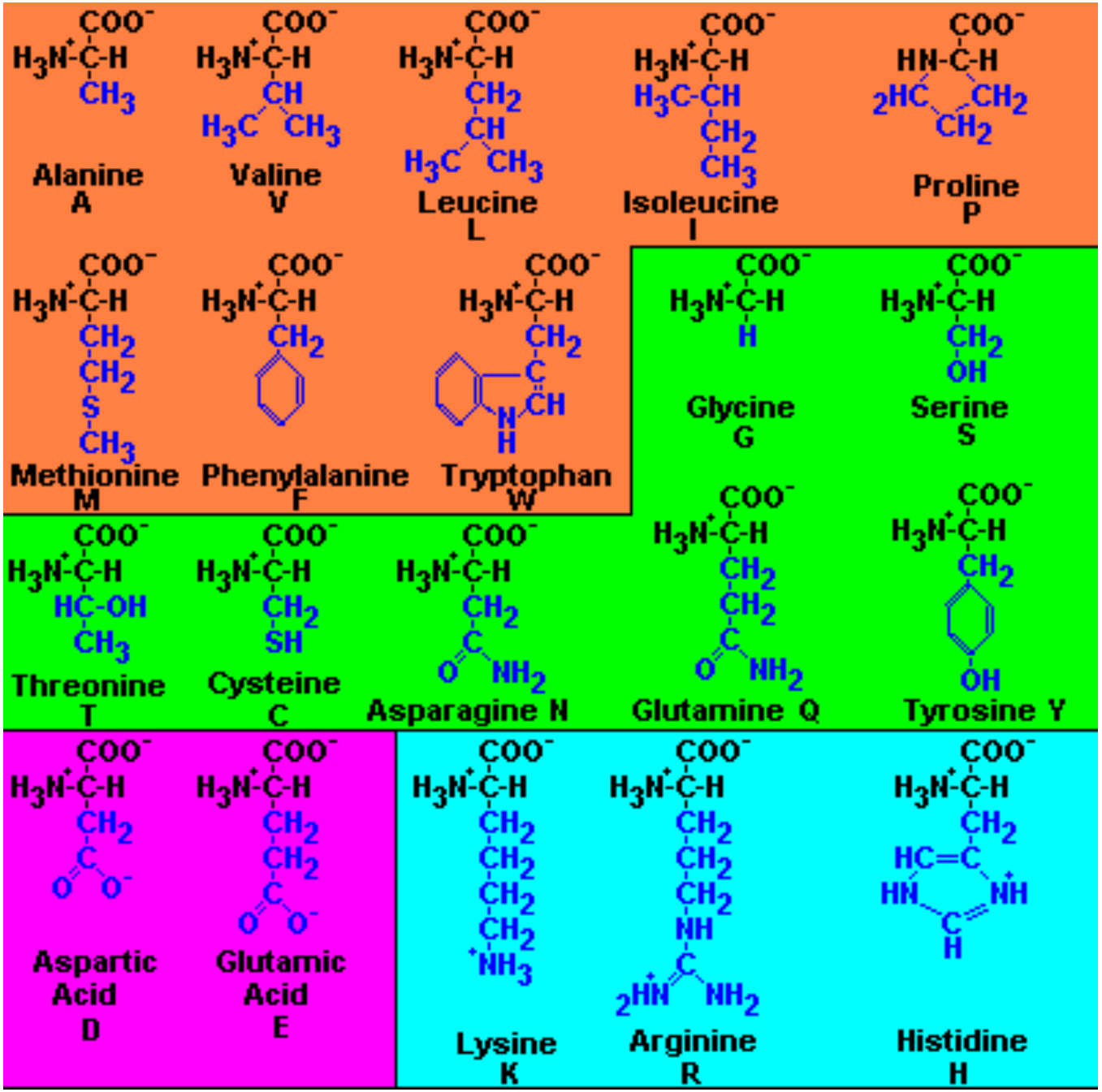
TABLE 18.1 Functional Groups of Importance in Biochemical Molecules

Functional Group	Structure	Type of Biomolecule
Amino group	$-NH_3^+$, $-NH_2$	Amino acids and proteins (Sections 18.3, 18.7)
Hydroxyl group	$-OH$	Monosaccharides (carbohydrates) and glycerol: a component of triacylglycerols (lipids) (Sections 22.4, 24.2)
Carbonyl group		Monosaccharides (carbohydrates); in acetyl group (CH_3CO) used to transfer carbon atoms during catabolism (Sections 22.4, 21.4, 21.8)
Carboxyl group		Amino acids, proteins, and fatty acids (lipids) (Sections 18.3, 18.7, 24.2)
Amide group		Links amino acids in proteins; formed by reaction of amino group and carboxyl group (Section 18.7)
Carboxylic acid ester		Triacylglycerols (and other lipids); formed by reaction of carboxyl group and hydroxyl group (Section 24.2)
Phosphates, mono-, di-, tri-		ATP and many metabolism intermediates (Sections 17.8, 21.5, and throughout metabolism sections)
Hemiacetal group		Cyclic forms of monosaccharides; formed by a reaction of carbonyl group with hydroxyl group (Sections 16.7, 22.4)
Acetal group		Connects monosaccharides in disaccharides and larger carbohydrates; formed by reaction of carbonyl group with hydroxyl group (Sections 16.7, 22.7, 22.9)

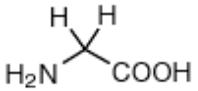
Amino Acid


Amino Acid Structure
H
H
O
H–N–C–C–OH
Amino Group
Carboxylic Acid Group
R
Side Chain
α - carbon

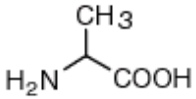

1
H
H2N - αC - C
O
OH
R
2
H
H3N+ - αC - C
O
O
R
3
O
R2
H3N+
C
CH
CH
NH
C
O
O
R1


Alanine
A
Valine
V
Leucine
L
Isoleucine
I
Proline
P
Methionine
M
Phenylalanine
F
Tryptophan
W
Glycine
G
Serine
S
Threonine
T
Cysteine
C
Asparagine N
Glutamine Q
Tyrosine Y
Aspartic
Acid
D
Glutamic
Acid
E
Lysine
K
Arginine
R
Histidine
H

Small

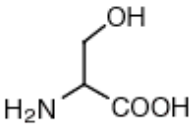


Glycine (Gly, G)
MW: 57.05

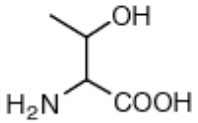


Alanine (Ala, A)
MW: 71.09

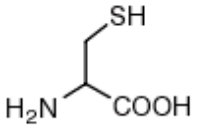
Nucleophilic



Serine (Ser, S)
MW: 87.08, pK_a ~ 16

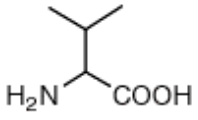


Threonine (Thr, T)
MW: 101.11, pK_a ~ 16

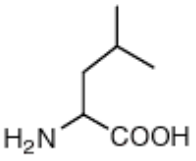


Cysteine (Cys, C)
MW: 103.15, pK_a = 8.35

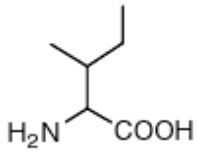
Hydrophobic



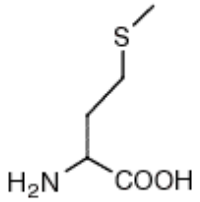
Valine (Val, V)
MW: 99.14



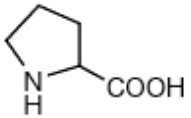
Leucine (Leu, L)
MW: 113.16



Isoleucine (Ile, I)
MW: 113.16

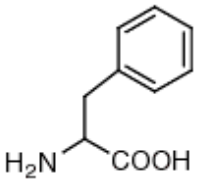


Methionine (Met, M)
MW: 131.19

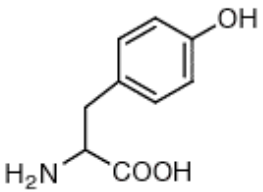


Proline (Pro, P)
MW: 97.12

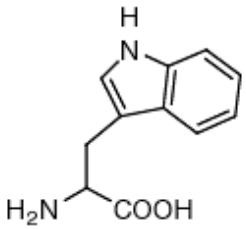
Aromatic



Phenylalanine (Phe, F)
MW: 147.18

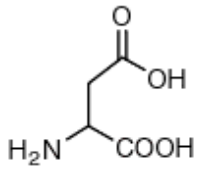


Tyrosine (Tyr, Y)
MW: 163.18

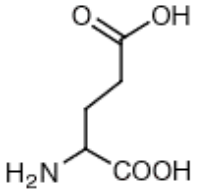


Tryptophan (Trp, W)
MW: 186.21

Acidic

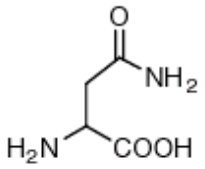


Aspartic Acid (Asp, D)
MW: 115.09, pK_a = 3.9

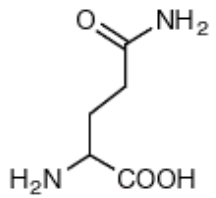


Glutamic Acid (Glu, E)
MW: 129.12, pK_a = 4.07

Amide

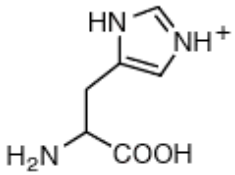


Asparagine (Asn, N)
MW: 114.11

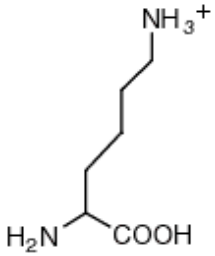


Glutamine (Gln, Q)
MW: 128.14

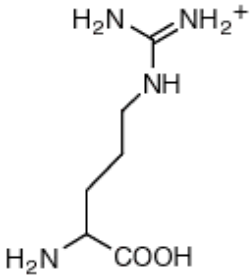
Basic



Histidine (His, H)
MW: 137.14, pK_a = 6.04



Lysine (Lys, K)
MW: 128.17, pK_a = 10.79

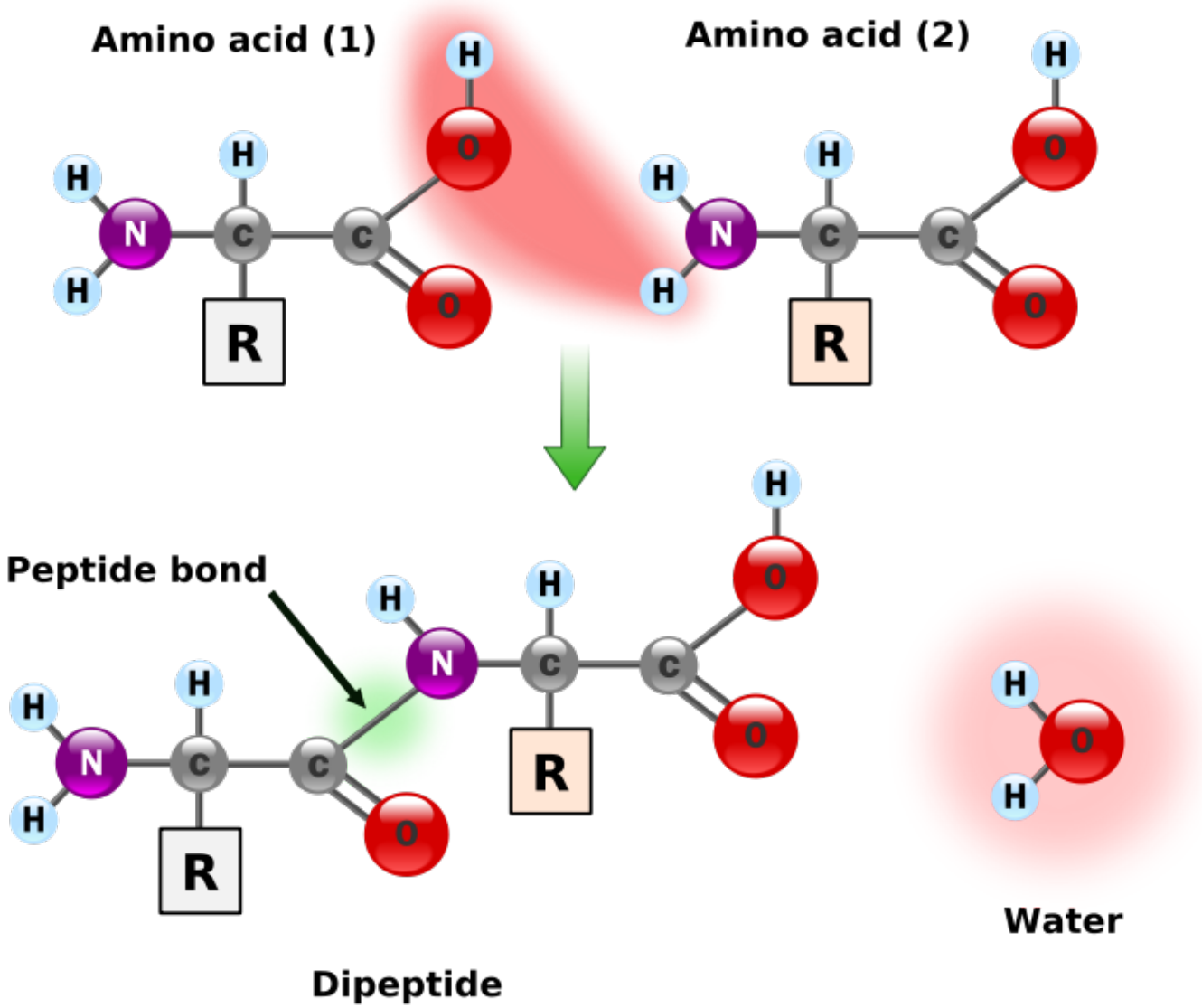


Arginine (Arg, R)
MW: 156.19, pK_a = 12.48

Protein Structure and Function

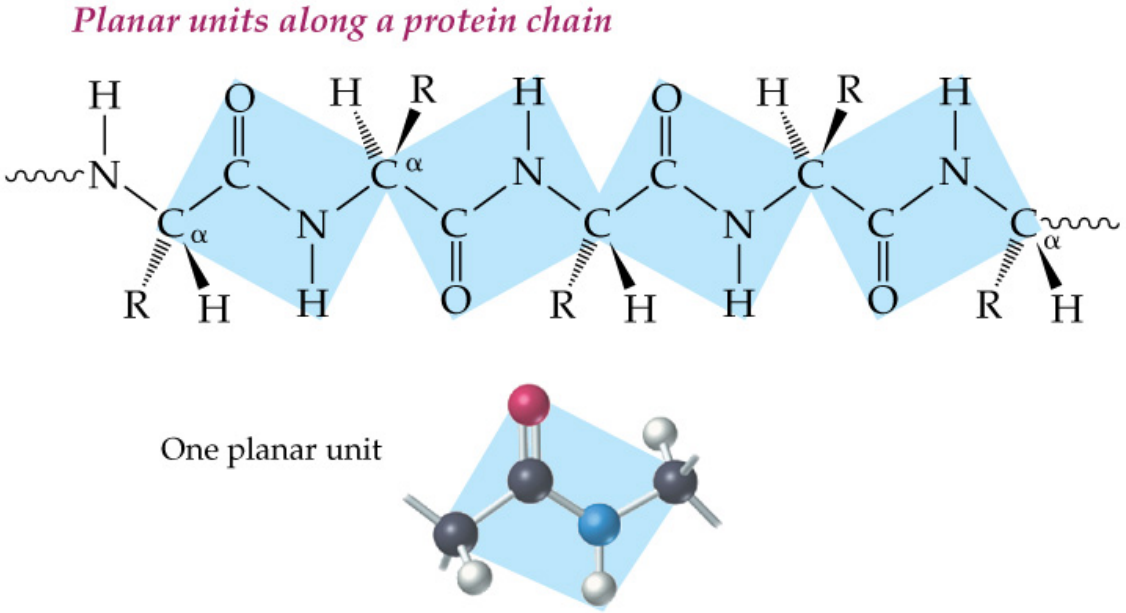
- Proteins are polymers of amino acids.
- Each amino acids in a protein contains a amino group, -NH_2, a carboxyl group, -COOH, and an R group, all bonded to the central carbon atom. The R group may be a hydrocarbon or they may contain functional group.
- All amino acids present in a proteins are *α-amino acids* in which the amino group is bonded to the carbon next to the carboxyl group.
- Two or more amino acids can join together by forming amide bond, which is known as a ***peptide bond*** when they occur in proteins.

Peptide bond



Primary Protein Structure

- Primary structure of a proteins is the sequence of amino acids connected by peptide bonds. Along the backbone of the proteins is a chain of alternating peptide bonds and α-carbons and the amino acid side chains are connected to these

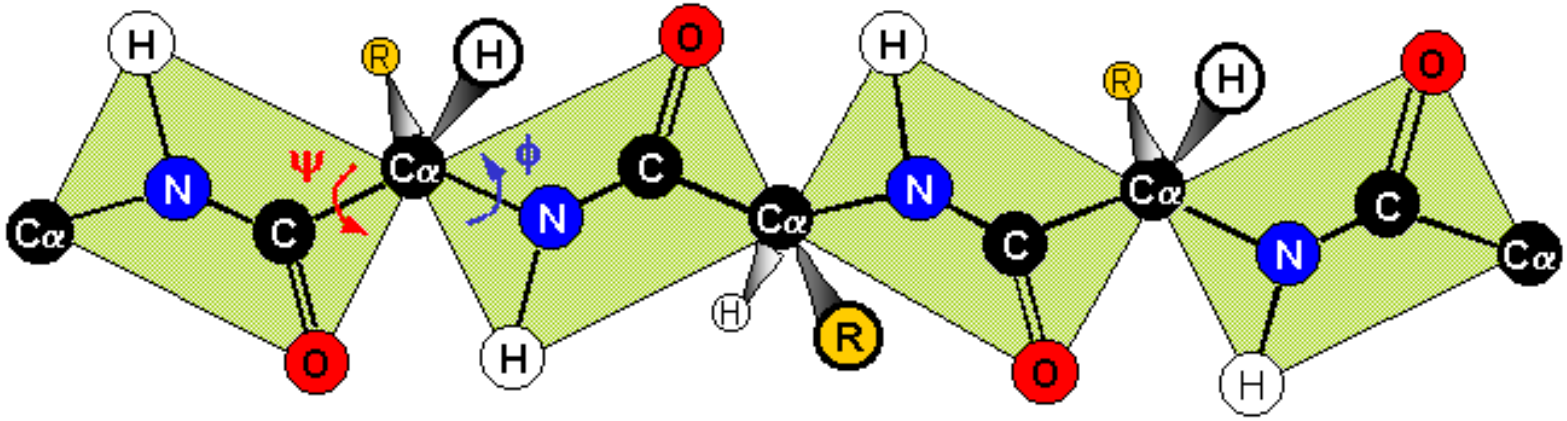


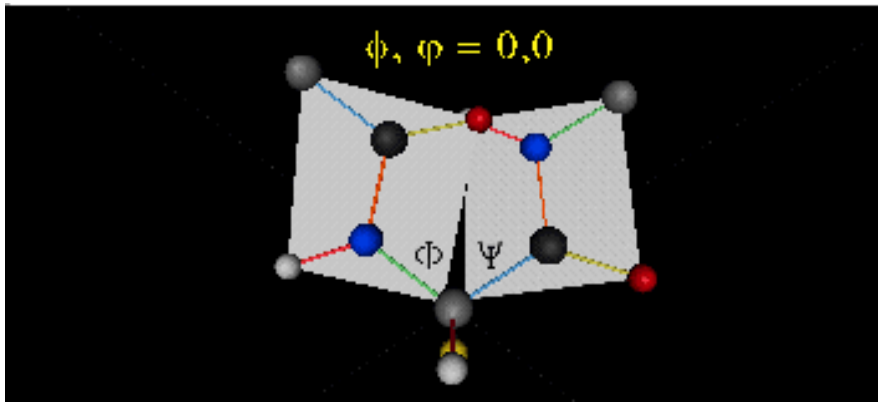
- By convention, peptides and proteins are always written with the amino terminal amino acid (N-terminal) on the left and carboxyl-terminal amino acid (C-terminal) on the right.

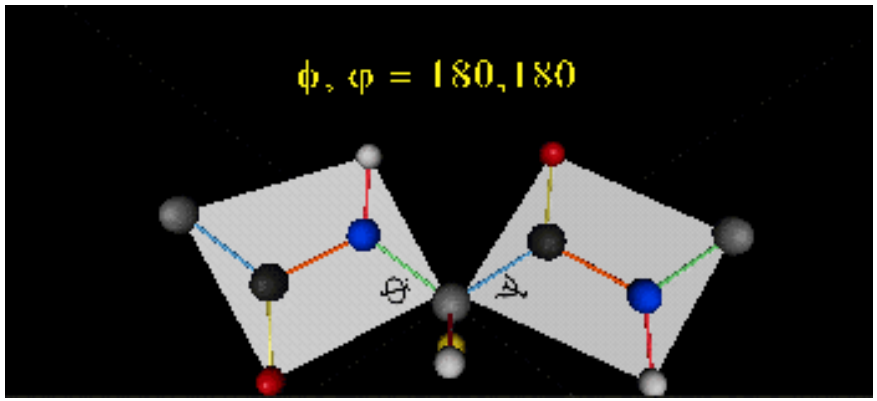
Secondary Protein Structure

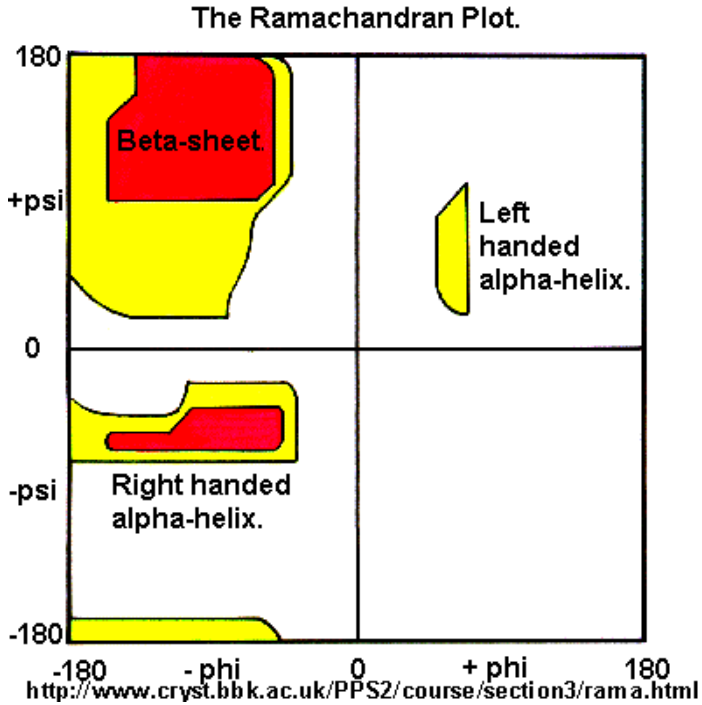
- Secondary structure of a protein is the arrangement of polypeptide backbone of the protein in space. The secondary structure includes two kinds of repeating pattern known as the *α-helix* and *β-sheet*.
- Hydrogen bonding between backbone atoms are responsible for both of these secondary structures.

FULLY EXTENDED POLYPEPTIDE CHAIN

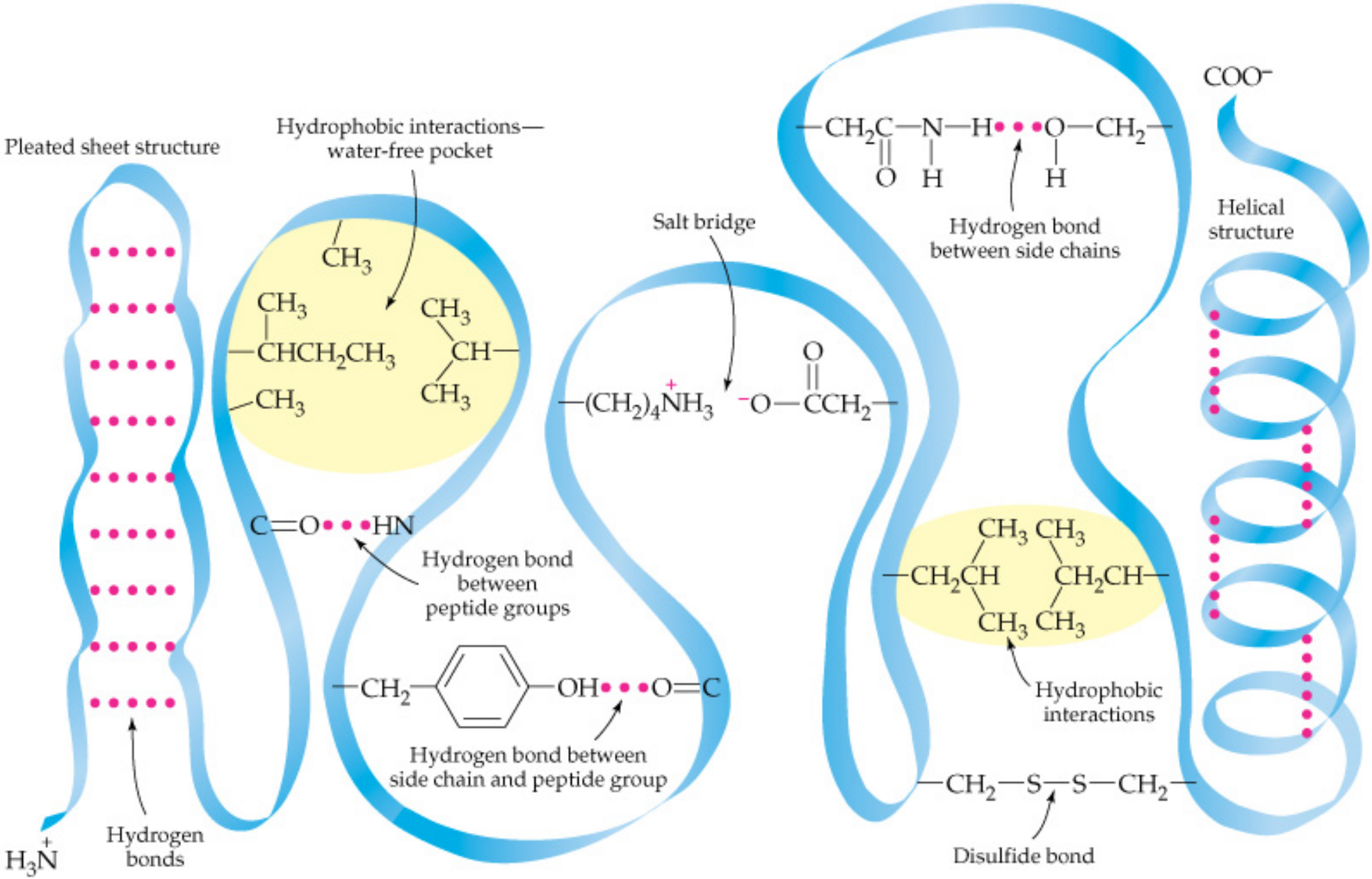








- Protein shape determining interactions are summarized below:
- Hydrogen bond between neighboring backbone segments.
- Hydrogen bonds of side chains with each other or with backbone atoms.
- Ionic attractions between side chain groups or salt bridge.
- Hydrophobic interactions between side chain groups.
- Covalent sulfur-sulfur bonds.

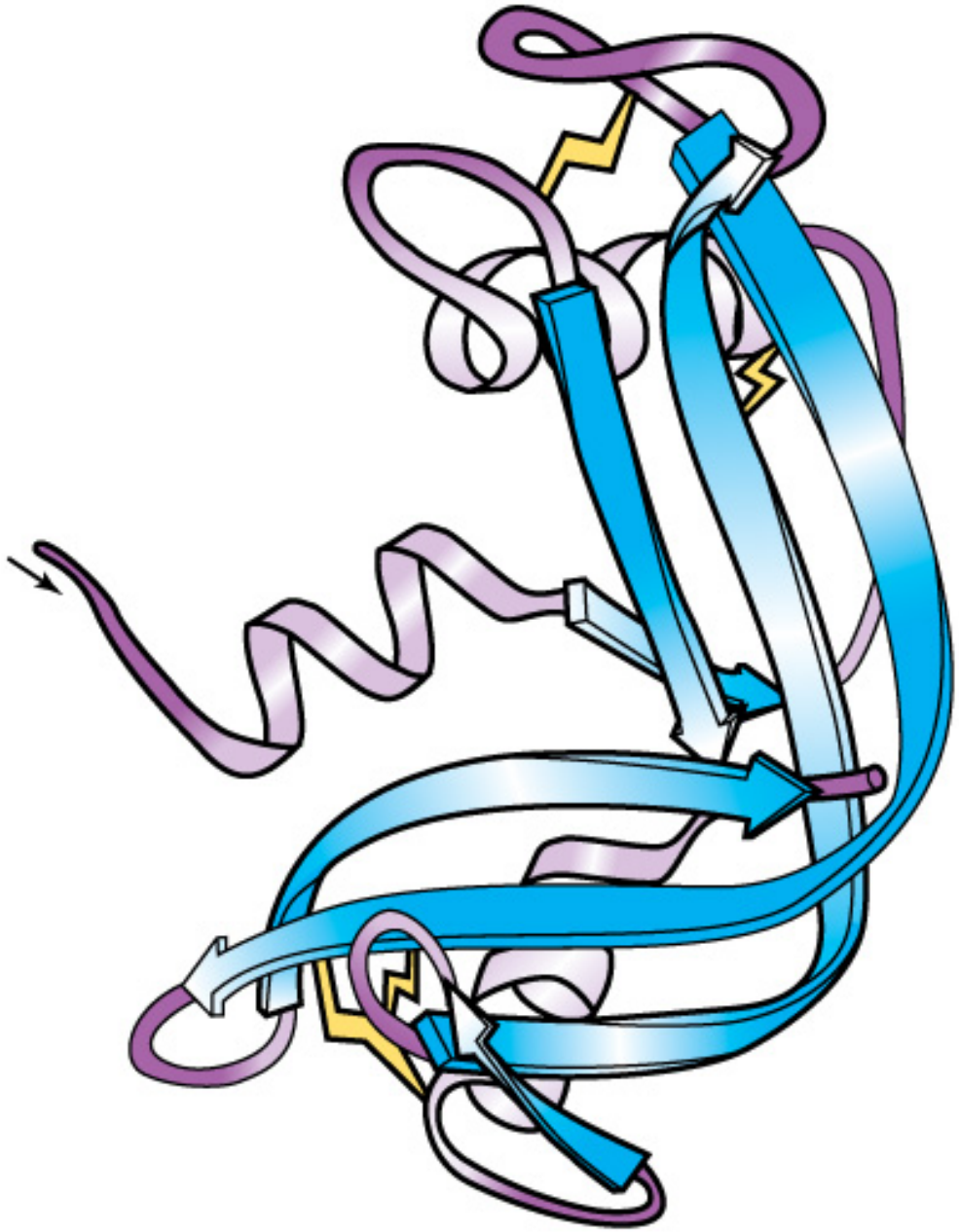

Pleated sheet structure
Hydrophobic interactions—
water-free pocket
Salt bridge
Hydrogen bond
between side chains
Helical
structure
Hydrogen bond
between
peptide groups
Hydrogen bond between
side chain and peptide group
Hydrophobic
interactions
Hydrogen
bonds
Disulfide bond

α Helix

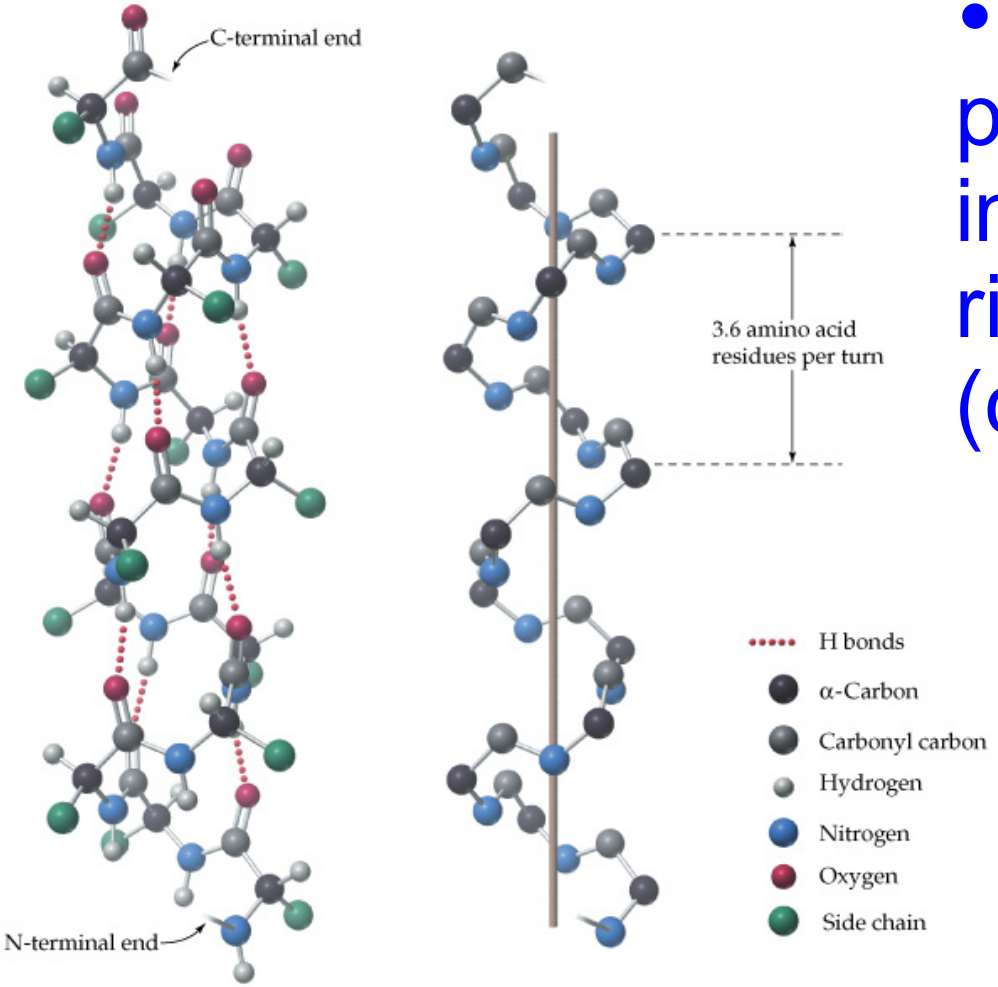
β Sheet

Connecting loop

—S—S— links

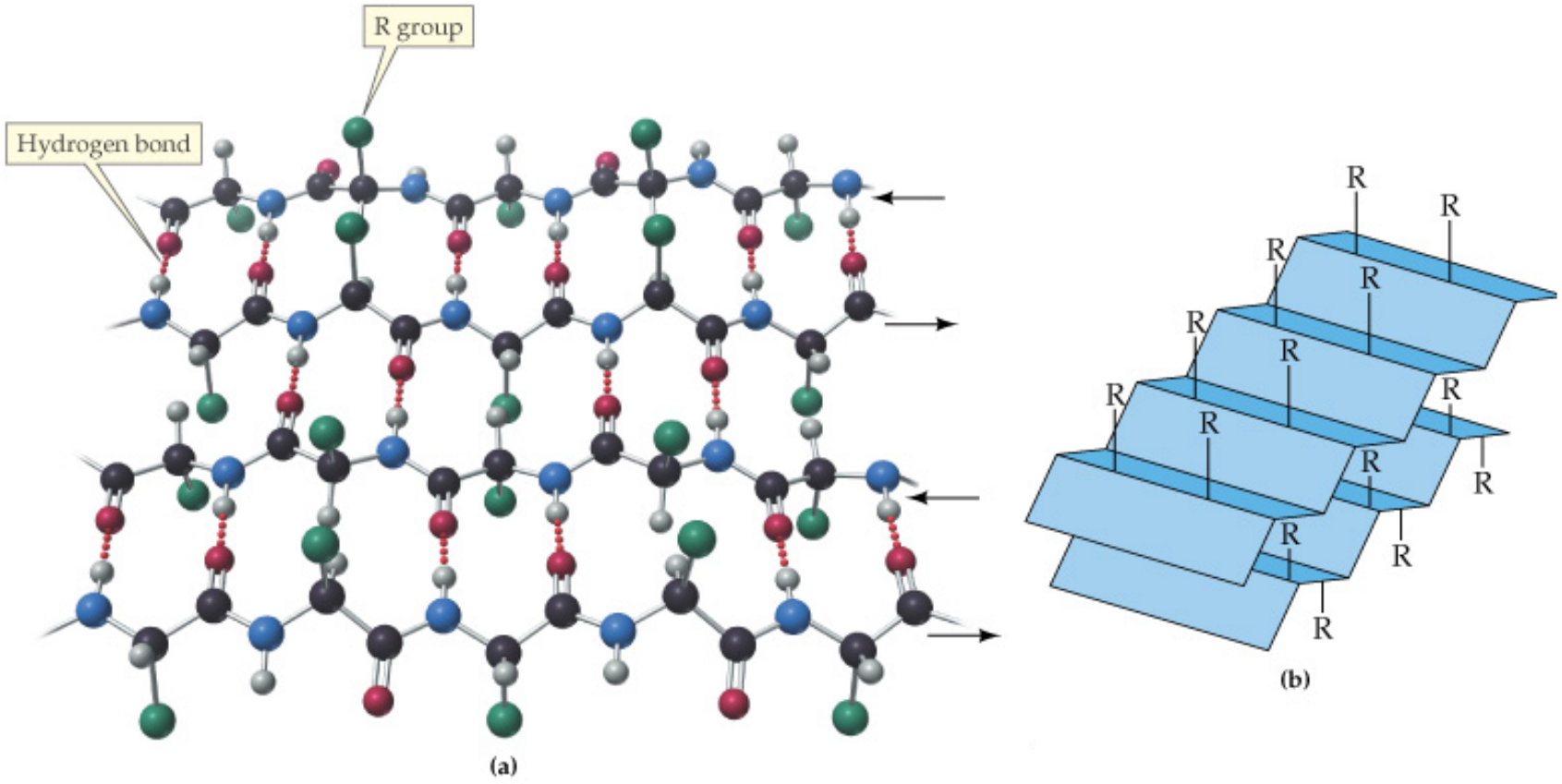


Ribonuclease

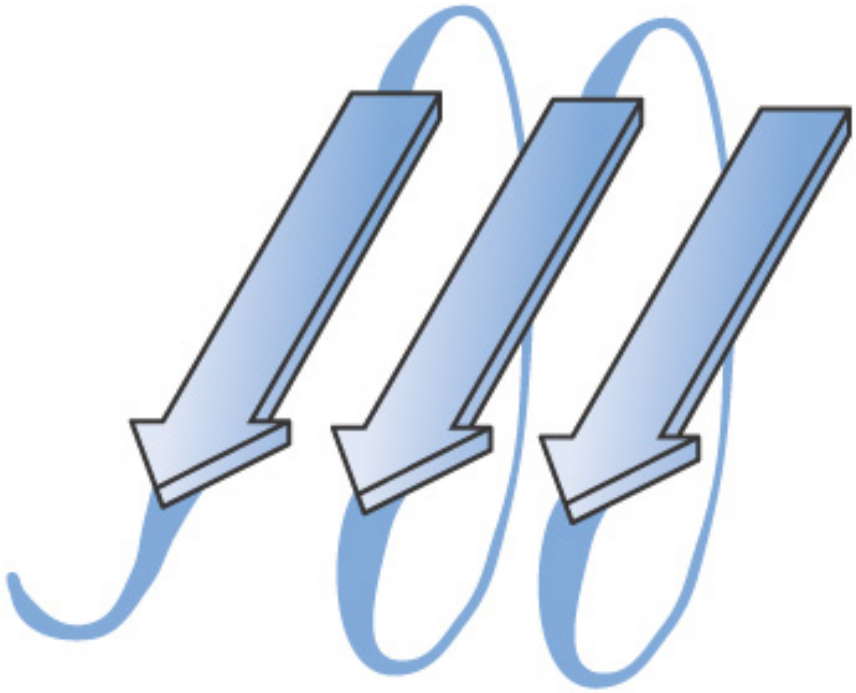


- ***α-Helix:*** A single protein chain coiled in a spiral with a right-handed (clockwise) twist.

•***β-Sheet:*** The polypeptide chain is held in place by hydrogen bonds between pairs of peptide units along neighboring backbone segments.



α helix



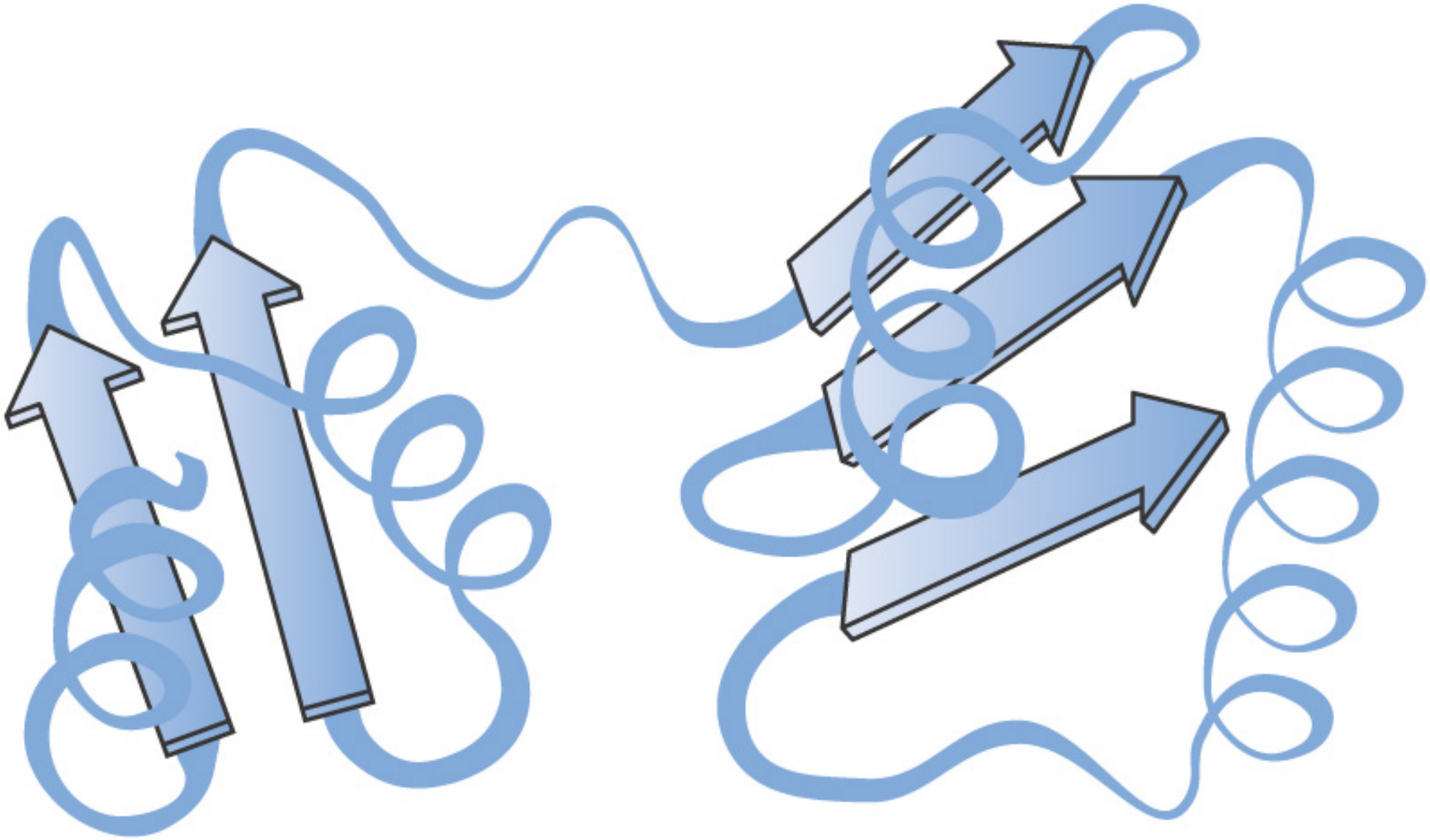
β sheet

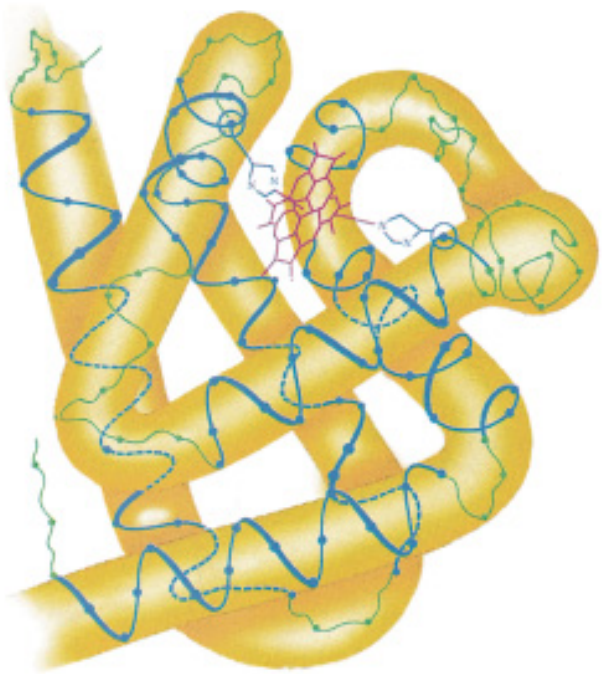
Shape-Determining Interactions in Proteins

- The essential structure-function relationship for each protein depends on the polypeptide chain being held in its necessary shape by the interactions of atoms in the side chains.

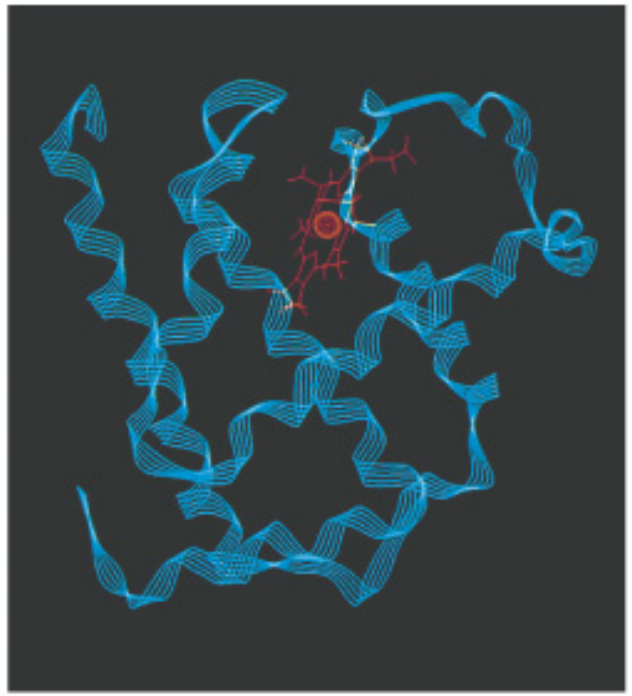
Tertiary Protein Structure

- ***Tertiary Structure of a proteins*** The overall three dimensional shape that results from the folding of a protein chain. Tertiary structure depends mainly on attractions of amino acid side chains that are far apart along the same backbone. Non-covalent interactions and disulfide covalent bonds govern tertiary structure.
- A protein with the shape in which it exist naturally in living organisms is known as a *native protein.*

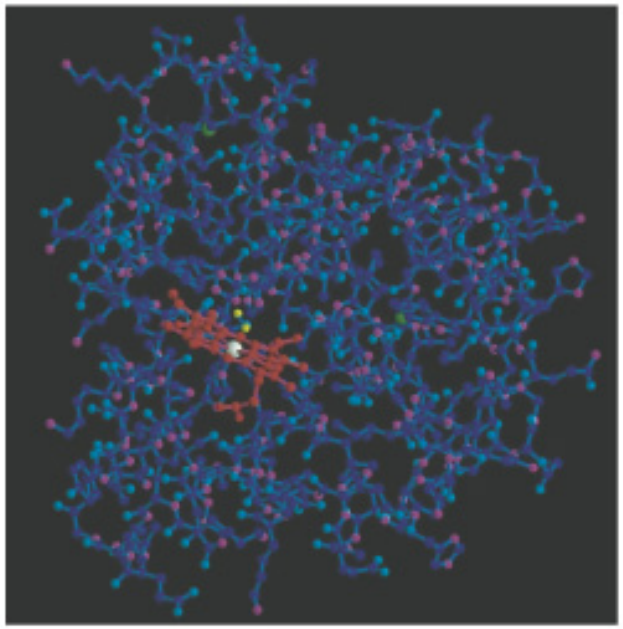




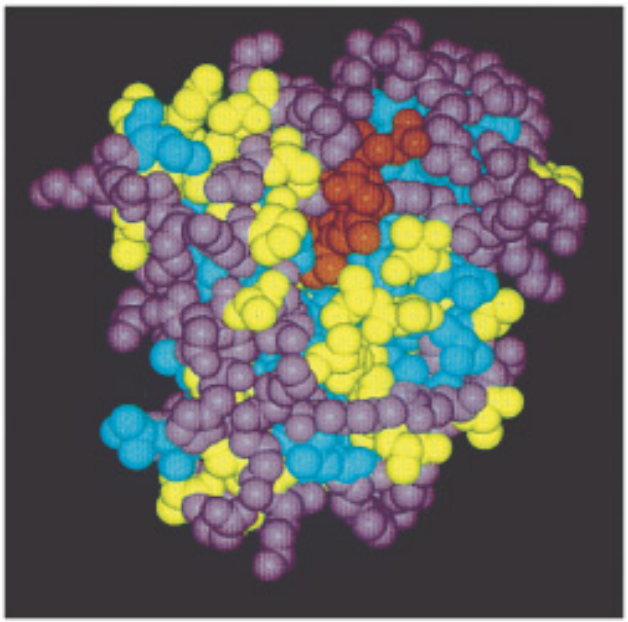
(a)



(b)



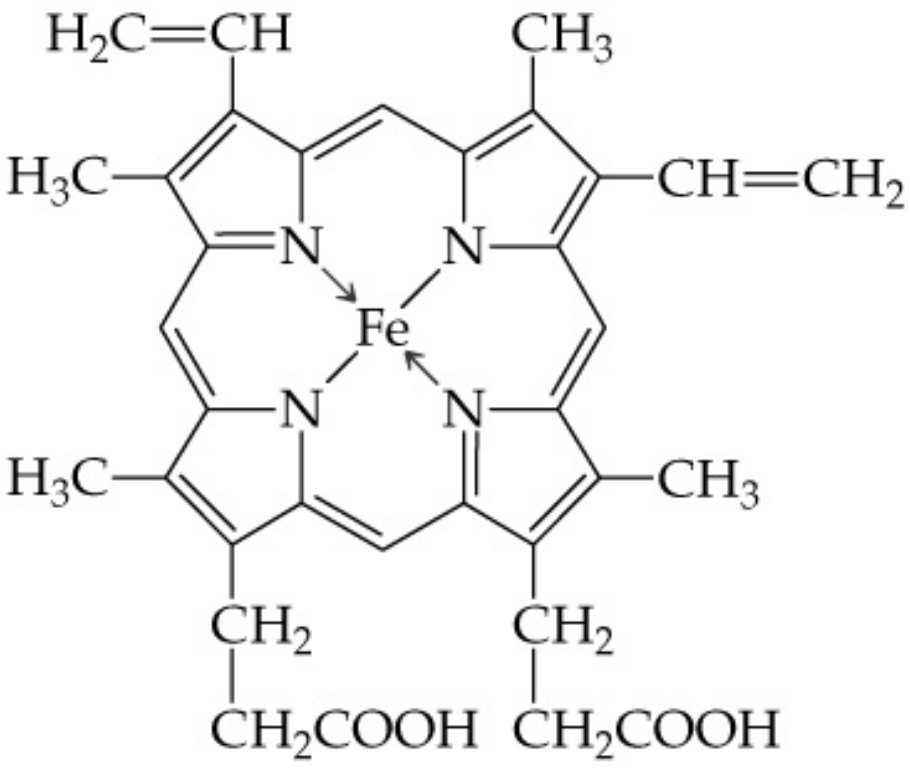
(c)



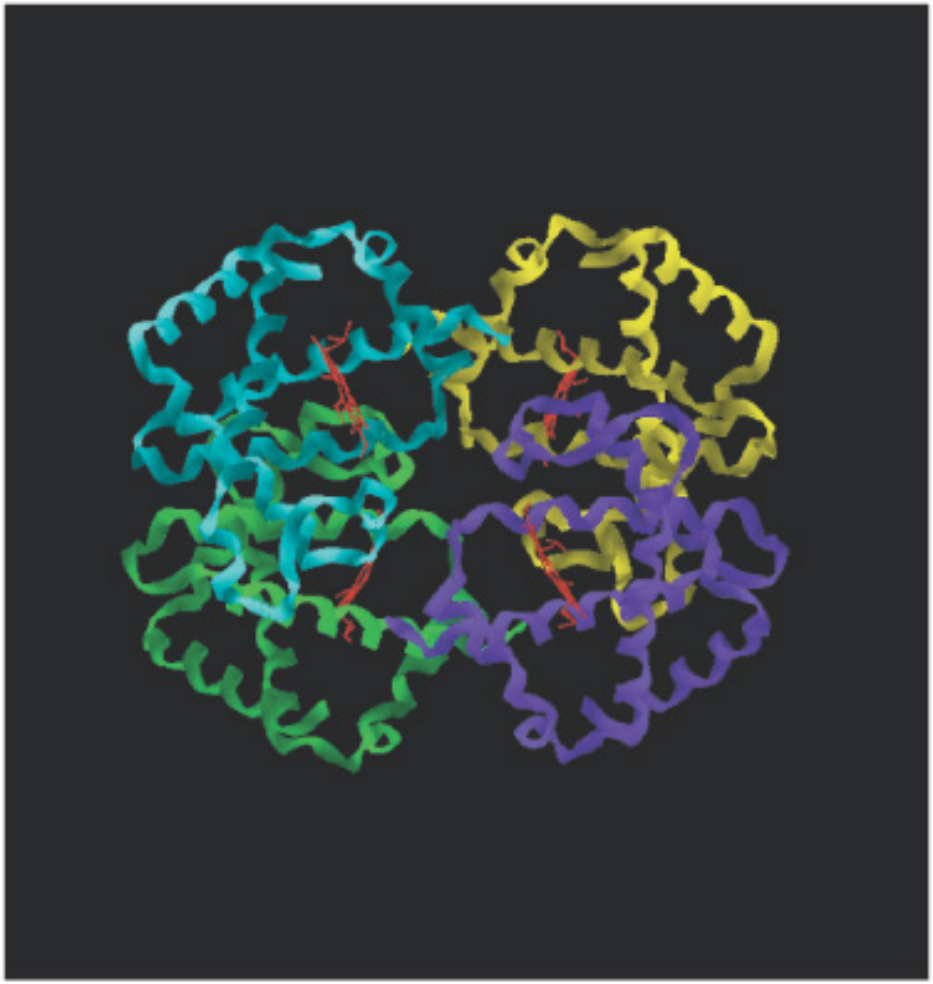
(d)

Quaternary Protein Structure

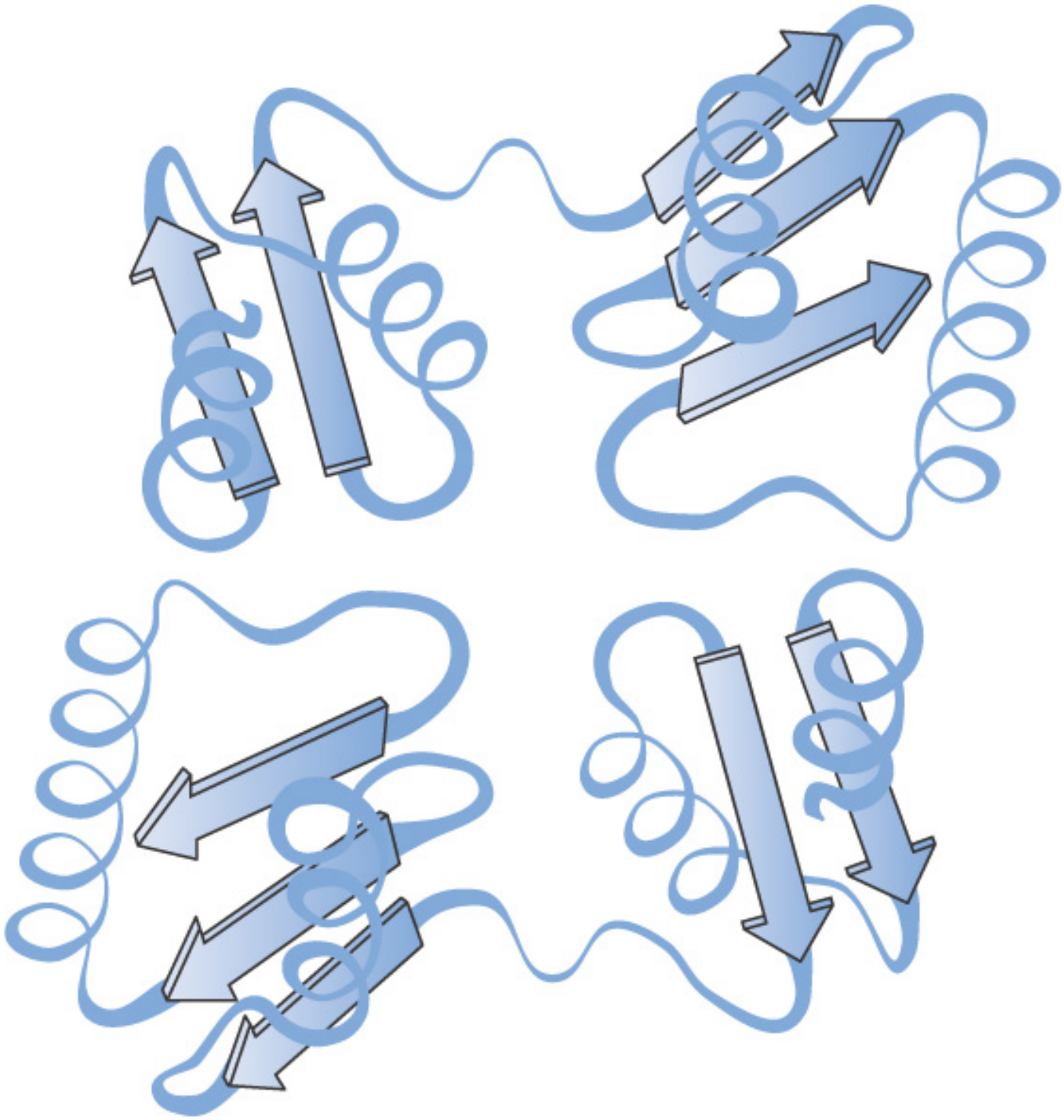
- ***Quaternary protein structure***: The way in which two or more polypeptide sub-units associate to form a single three-dimensional protein unit. Non-covalent forces are responsible for quaternary structure essential to the function of proteins.

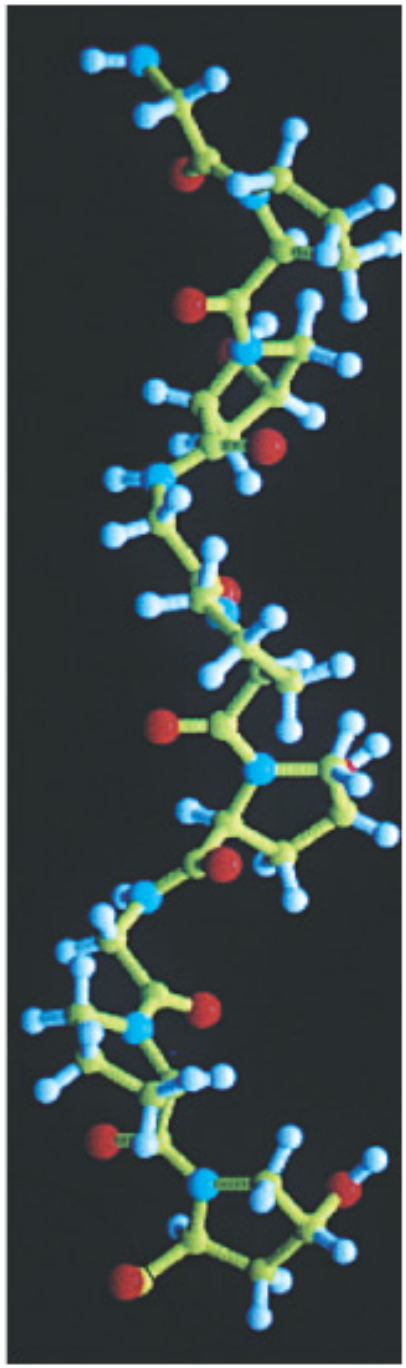


(a)

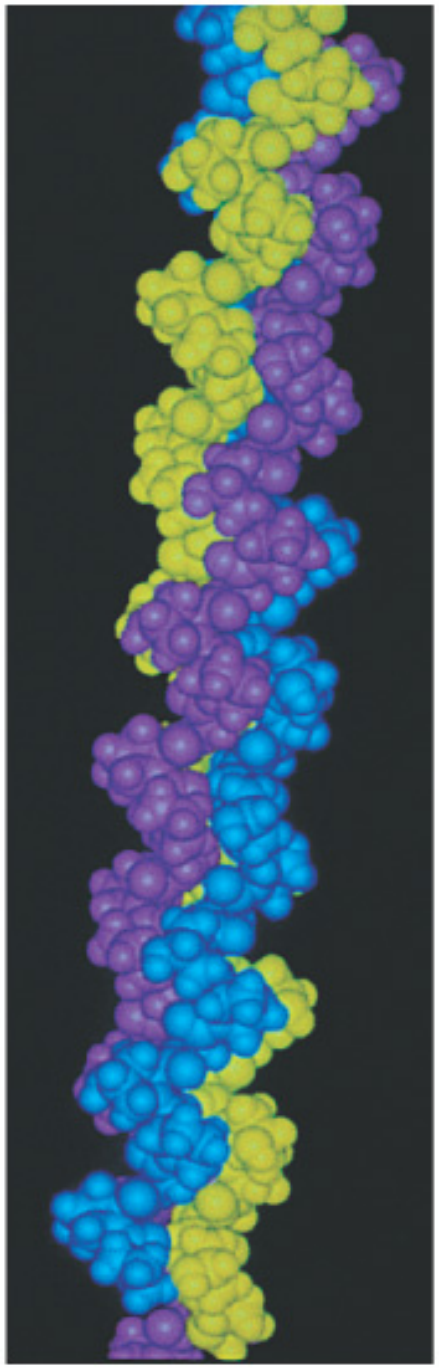


(b)

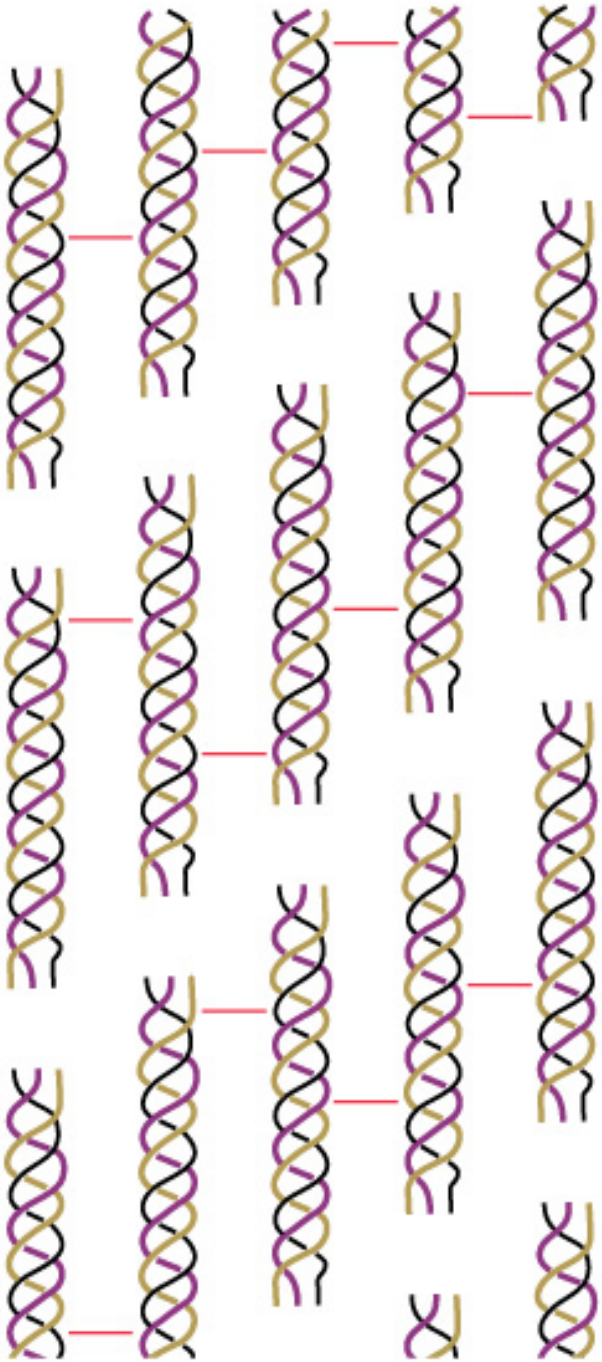




(a)



(b)

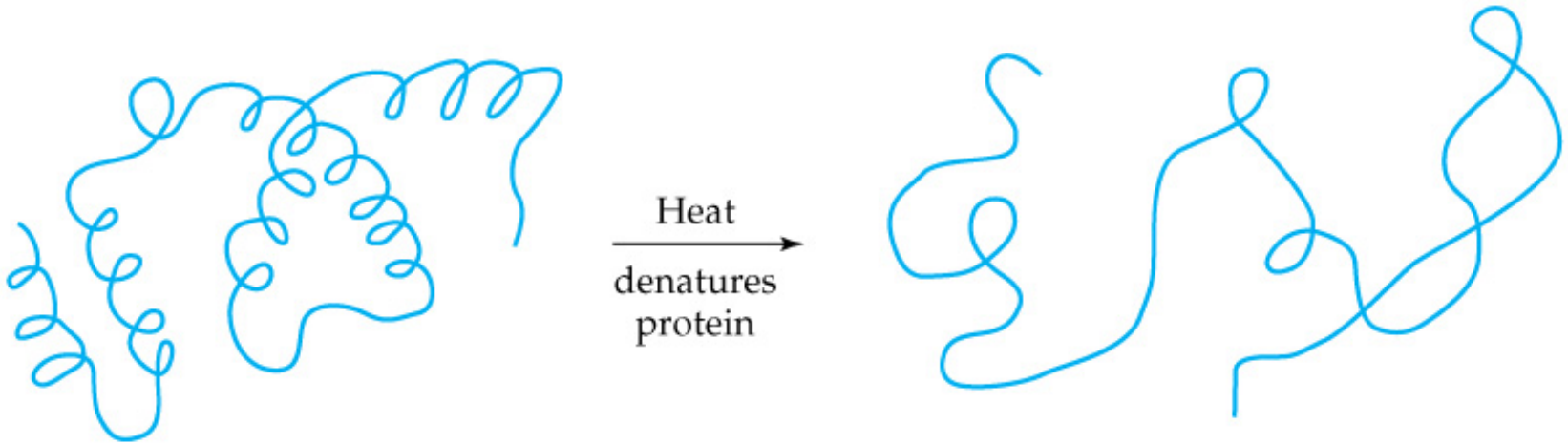


(c)

Chemical Properties of Proteins

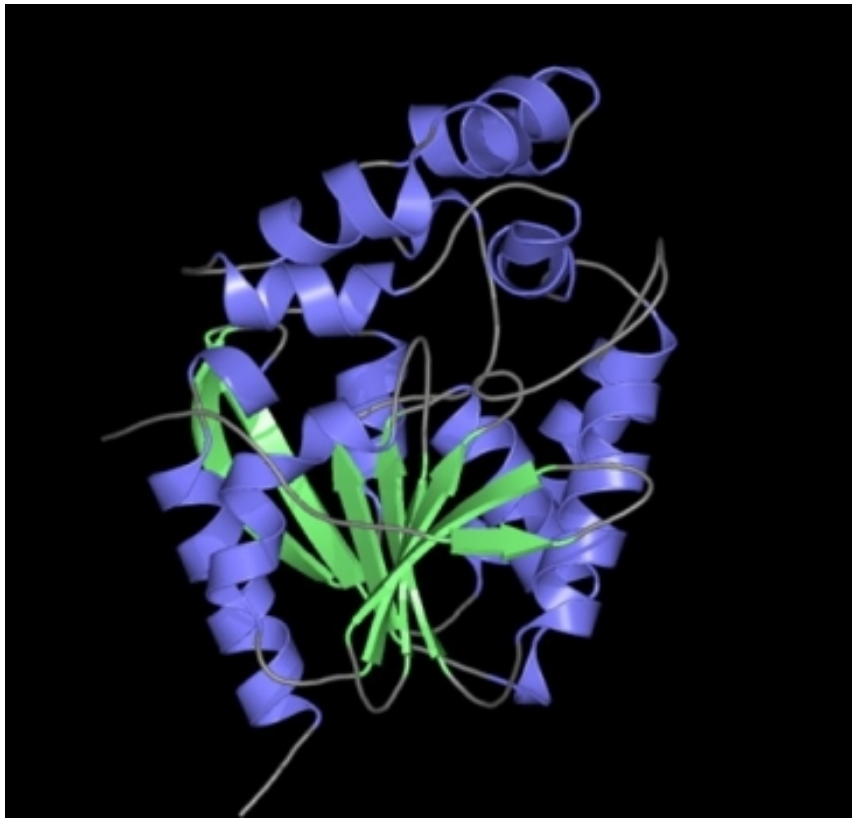
- *Protein hydrolysis:* In protein hydrolysis, peptide bonds are hydrolyzed to yield amino acids. This is reverse of protein formation.

- *Protein denaturation*: The loss of secondary, tertiary, or quaternary protein structure due to disruption of non-covalent interactions and or disulfide bonds that leaves peptide bonds and primary

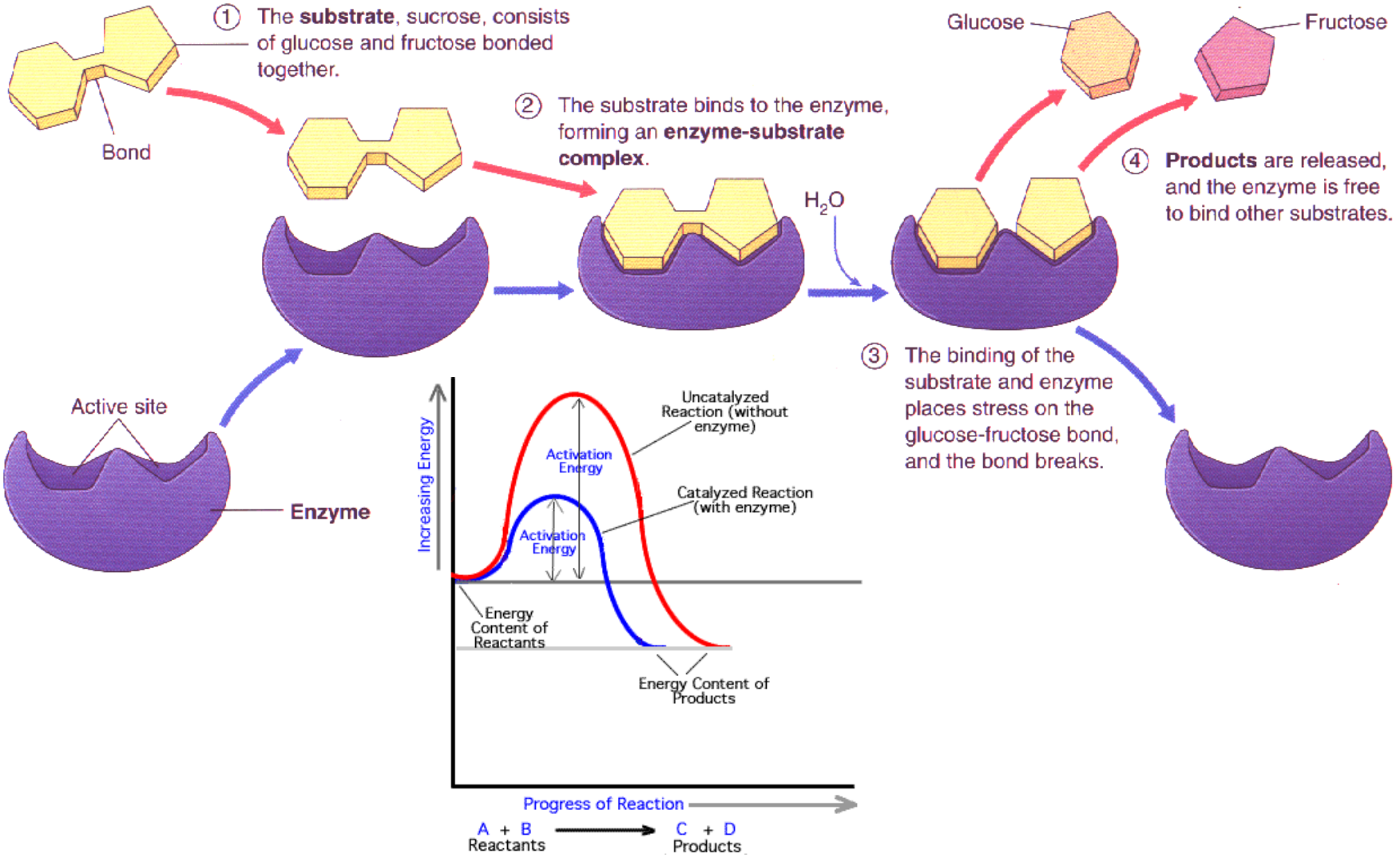


Catalysis by Enzymes

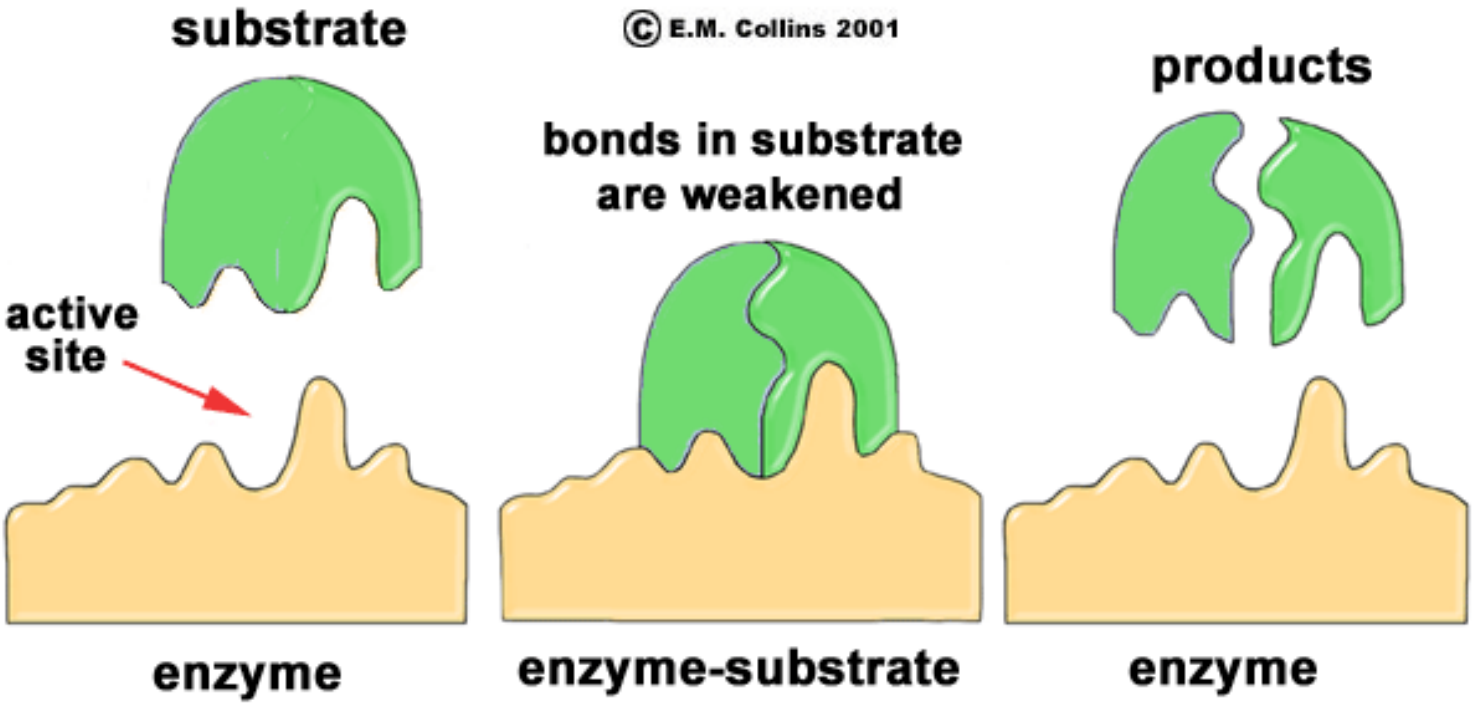
- ***Enzyme*** A protein that acts as a catalyst for a biochemical reaction.



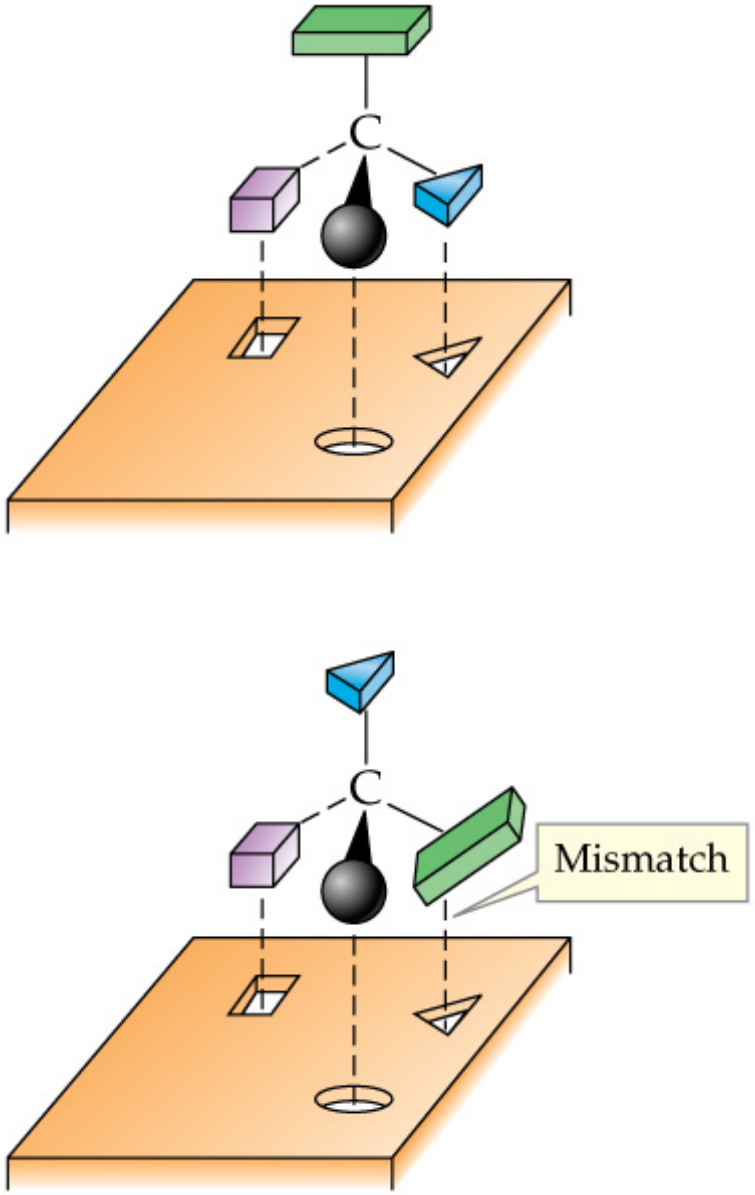
Enzymatic Reaction



Specificity



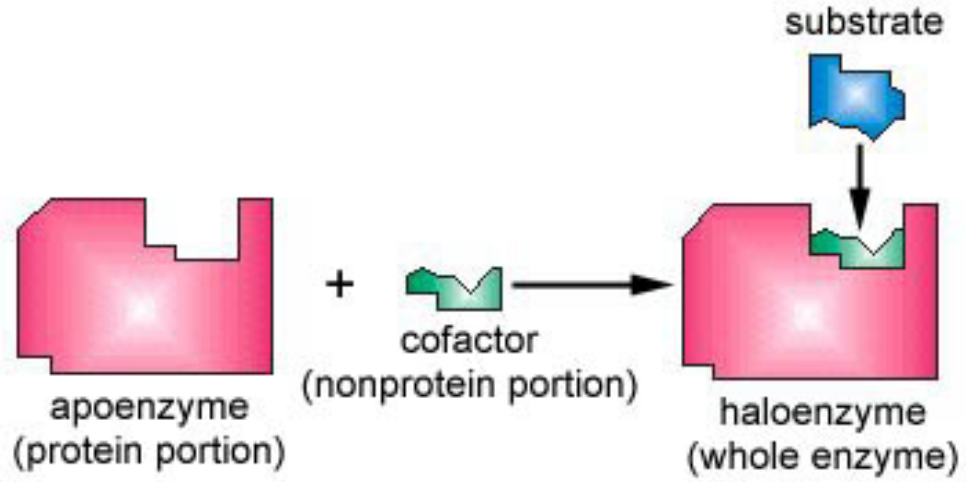
The specificity of an enzyme for one of two enantiomers is a matter of fit. One enantiomer fits better into the active site of the enzyme than the other enantiomer. Enzyme catalyzes reaction of the enantiomer that fits better into the active site of the enzyme.

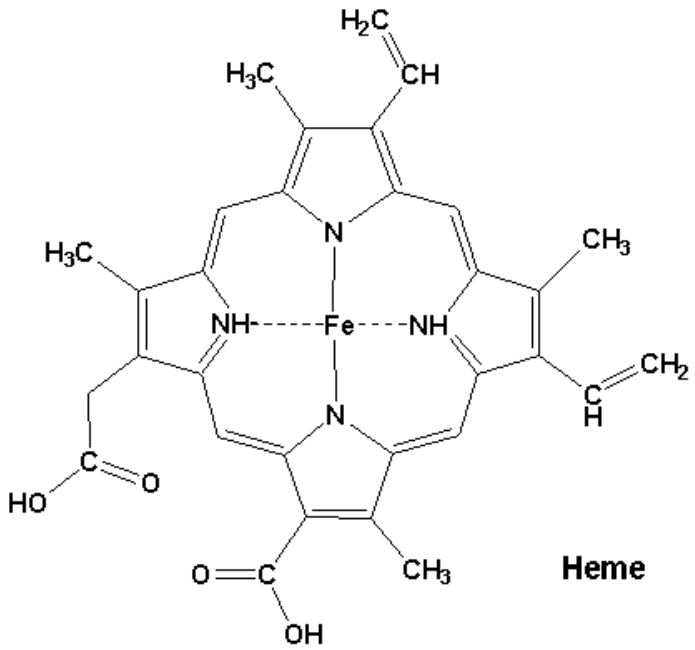


Enzyme Cofactors

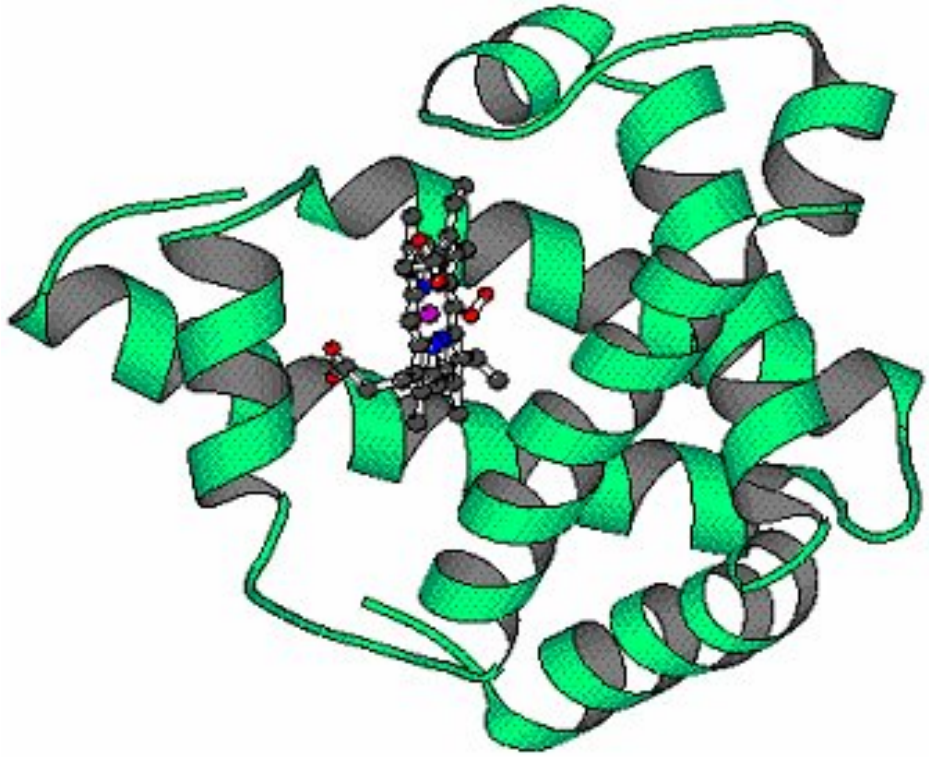
- Many enzymes are conjugated proteins that require nonprotein portions known as ***cofactors***.
- Some cofactors are metal ions, others are nonprotein organic molecules called ***coenzymes***.
- An enzyme may require a metal-ion, a coenzyme, or both to function.

Cofactor





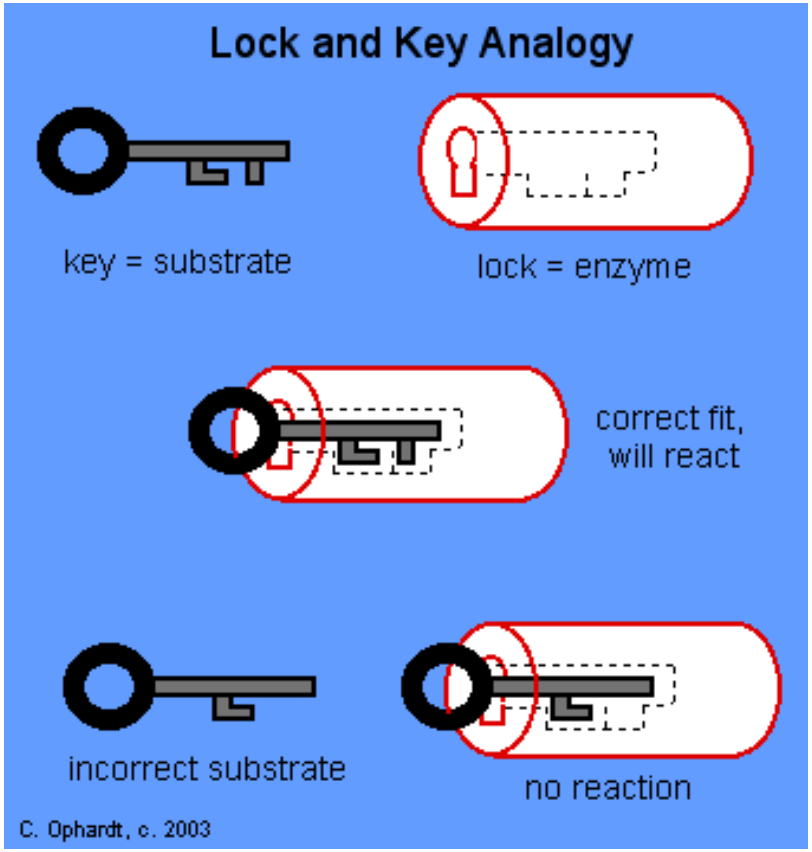
Heme

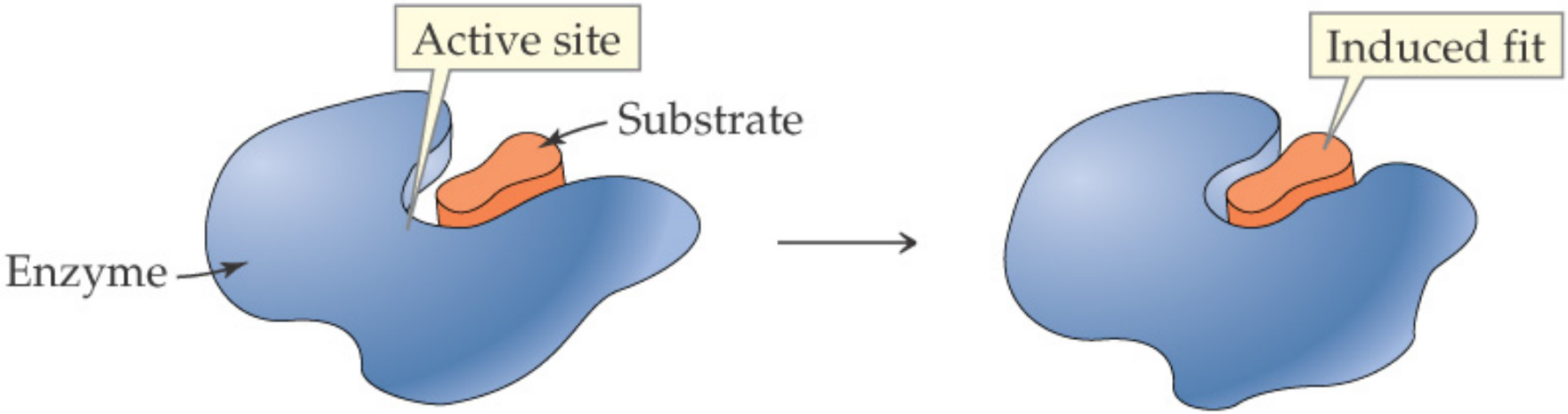


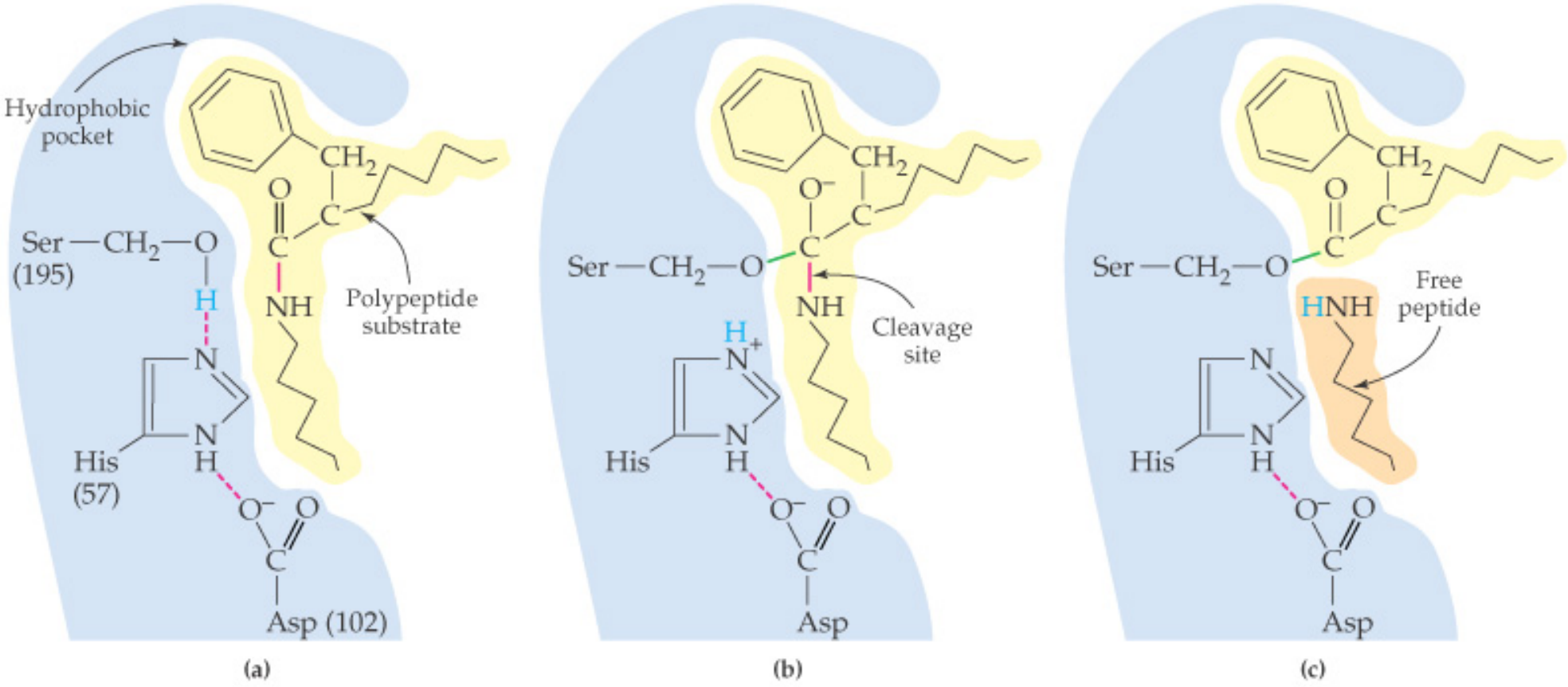
- Cofactors provide additional chemically active functional groups which are not present in the side chains of amino acids that made up the enzyme.
- Metal ions may anchor a substrate in the active site or may participate in the catalyzed reaction.

How Enzyme Work

- Two modes are invoked to represent the interaction between substrate and enzymes. These are:
- ***Lock-and-key model***: The substrate is described as fitting into the active site as a key fit into a lock.
- ***Induced-fit-model***: The enzyme has a flexible active site that changes shape to accommodate the substrate and facilitate the reaction.


Lock and Key Analogy
key = substrate
lock = enzyme
correct fit,
will react
incorrect substrate
no reaction
C. Ophardt, c. 2003


Active site
Substrate
Enzyme
Induced fit


Hydrophobic pocket
Ser —CH2—O
(195)
His
(57)
Asp (102)
Polypeptide substrate
(a)
Cleavage site
(b)
Free peptide
HNH
(c)

19.5 Effect of Concentration on Enzyme Activity

- Variation in concentration of enzyme or substrate alters the rate of enzyme catalyzed reactions.
- *Substrate concentration*: At low substrate concentration, the reaction rate is directly proportional to the substrate concentration. With increasing substrate concentration, the rate drops off as more of the active sites are occupied.

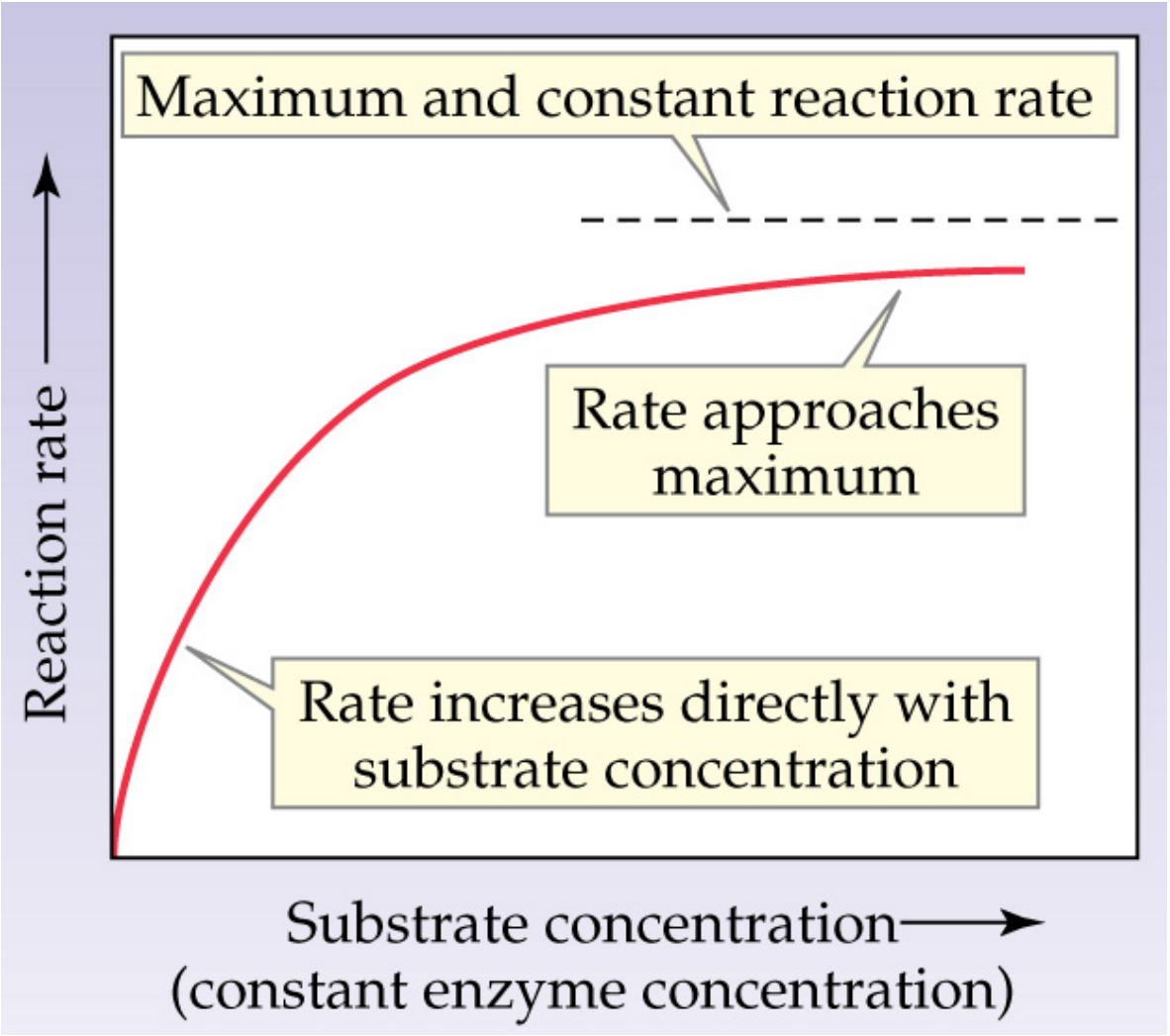
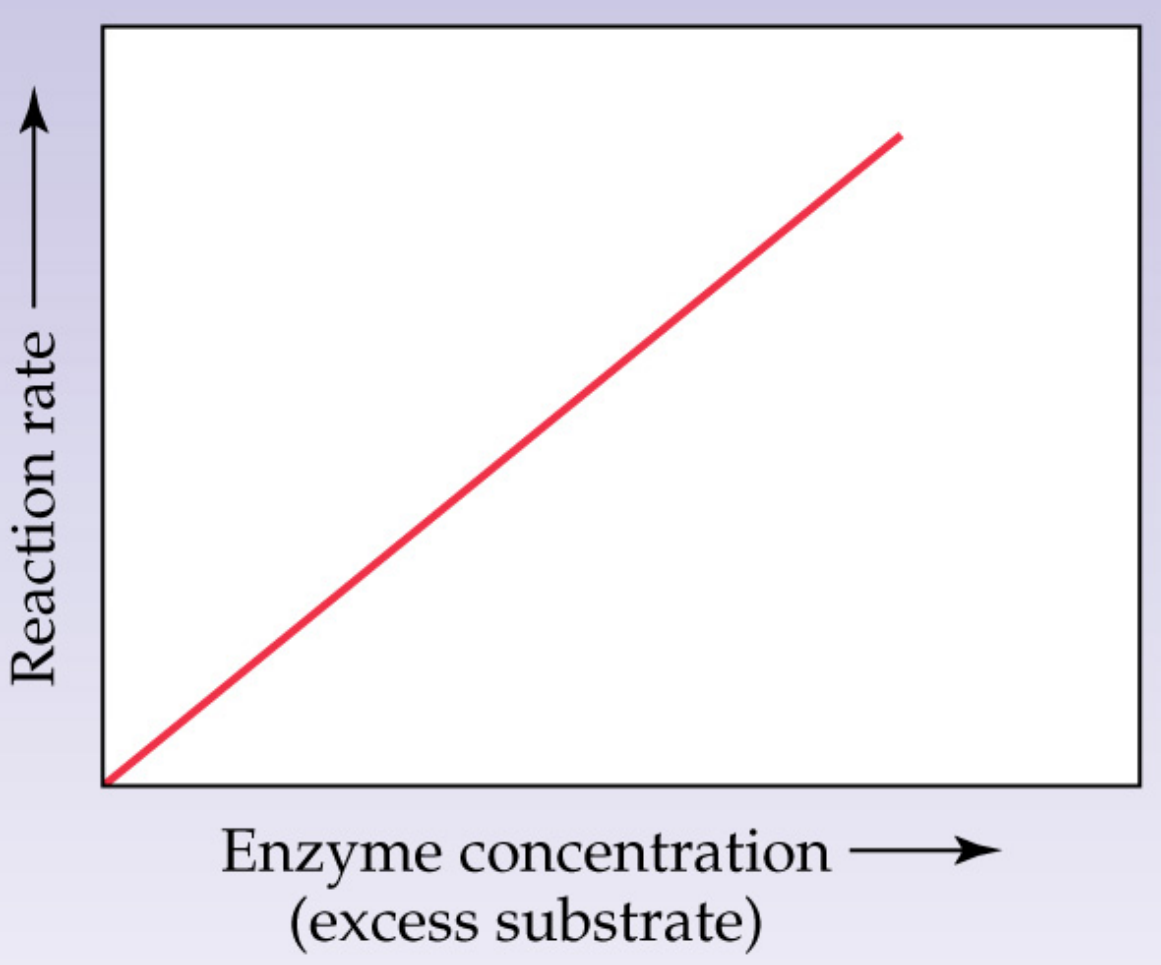


Fig 19.5 Change of reaction rate with substrate concentration when enzyme concentration is constant.

- *Enzyme concentration*: The reaction rate varies directly with the enzyme concentration as long as the substrate concentration does not become a limitation, Fig 19.6 below.



19.6 Effect of Temperature and pH on Enzyme Activity

- Enzymes maximum catalytic activity is highly dependent on temperature and pH.
- Increase in temperature increases the rate of enzyme catalyzed reactions. The rates reach a maximum and then begins to decrease. The decrease in rate at higher temperature is due to denaturation of enzymes.

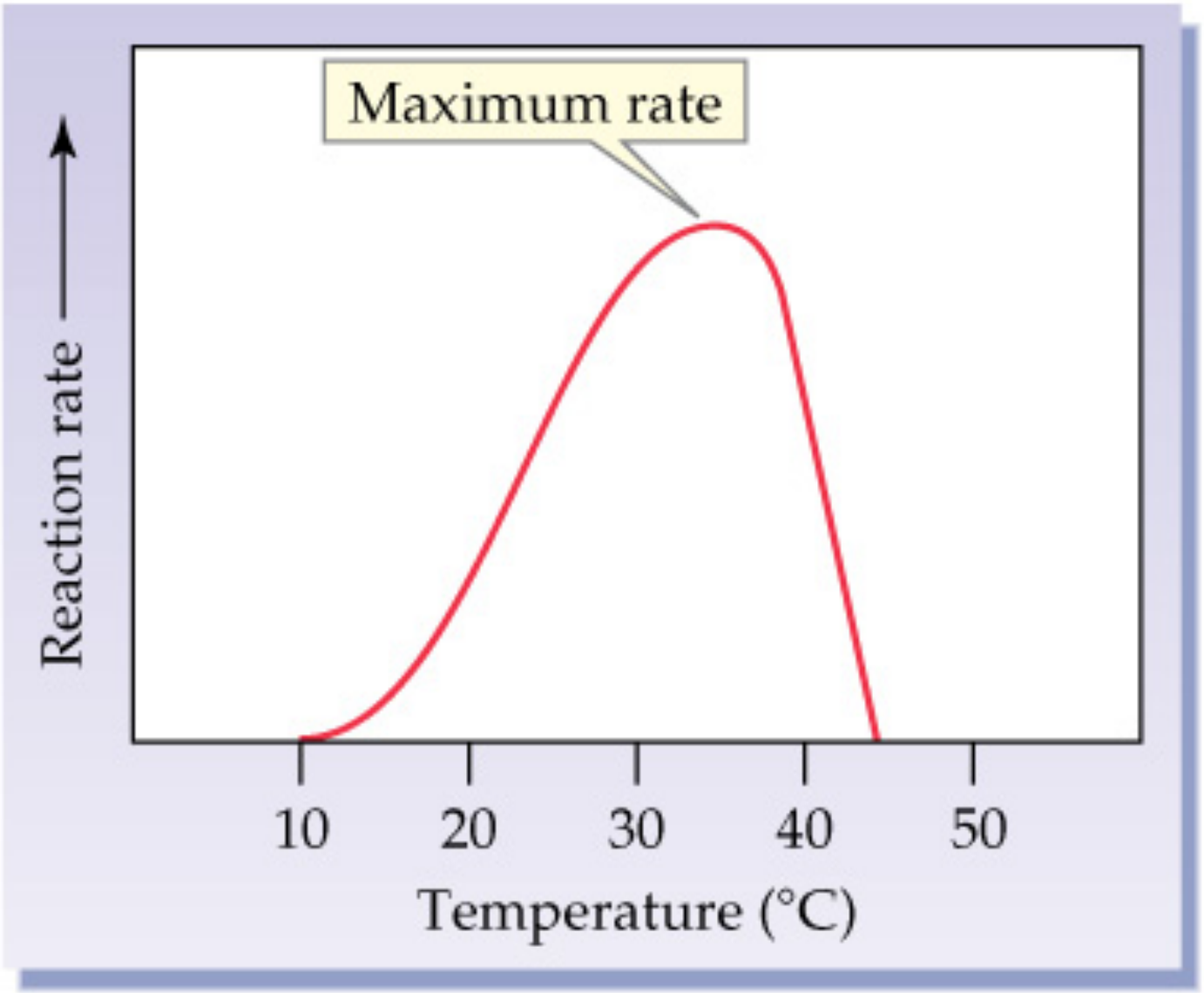
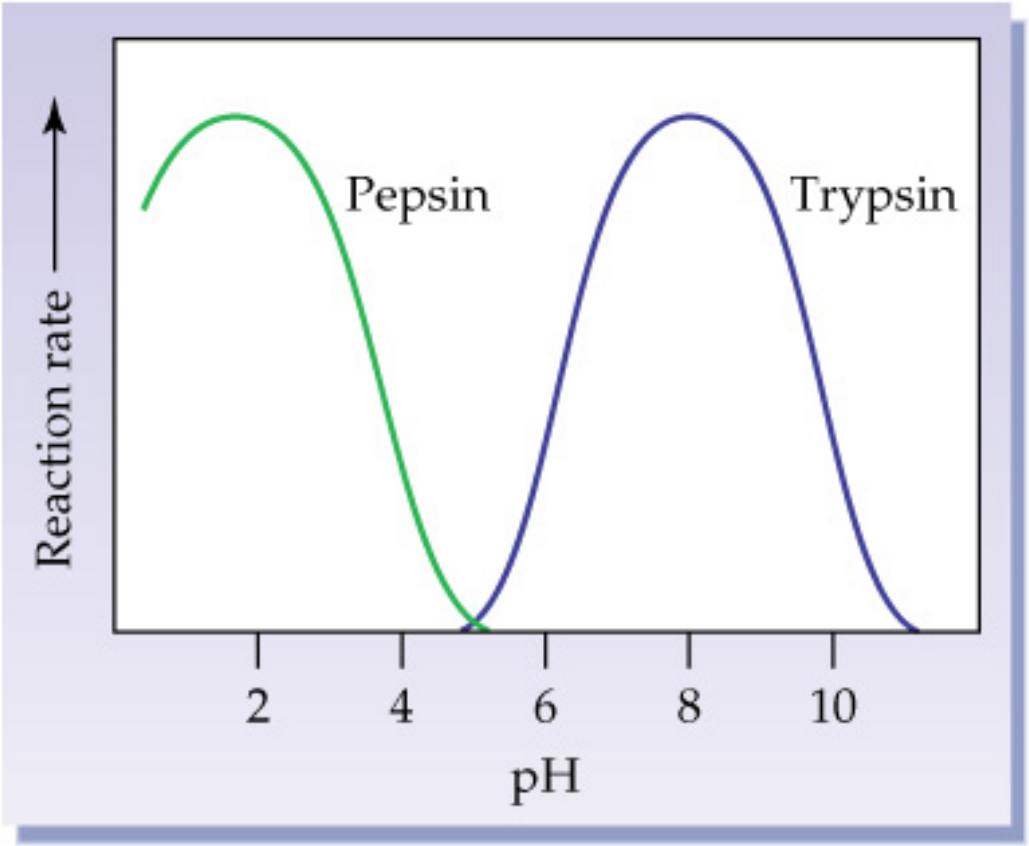


Fig 19.7 (a) Effect of temperature on reaction rate

- Effect of pH on Enzyme activity: The catalytic activity of enzymes depends on pH and usually has a well defined optimum point for maximum catalytic activity Fig 19.7 (b) below.

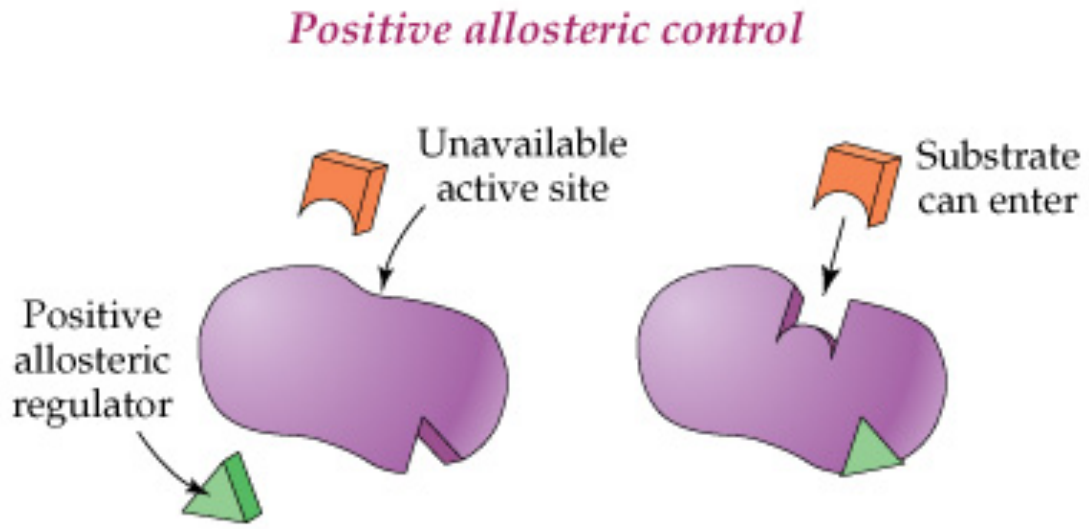


19.7 Enzyme Regulation: Feedback and Allosteric Control

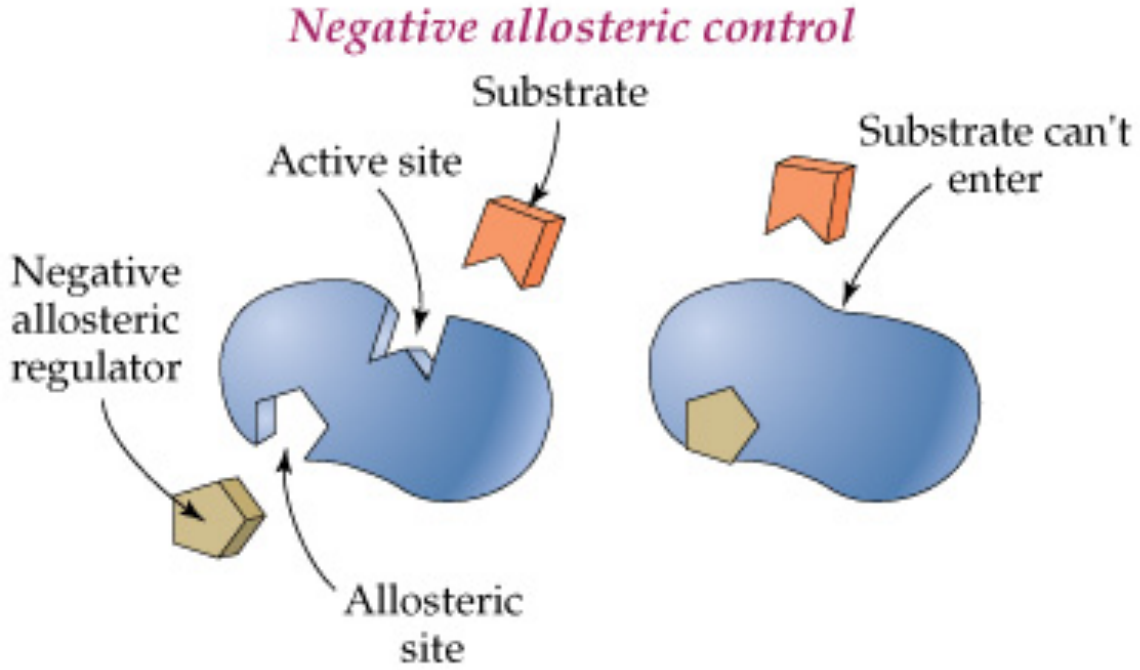
- Concentration of thousands of different chemicals vary continuously in living organisms which requires regulation of enzyme activity.
- Any process that starts or increase the activity of an enzyme is ***activation.***
- Any process that stops or slows the activity of an enzyme is ***inhibition.***

Two of the mechanism

- ***Feedback control***: Regulation of an enzyme's activity by the product of a reaction later in a pathway.
- ***Allosteric control***: Activity of an enzyme is controlled by the binding of an activator or inhibitor at a location other than the active site. Allosteric controls are further classified as positive or negative.
  - A positive regulator changes the activity site so that the enzyme becomes a better catalyst and rate accelerates.
  - A negative regulator changes the activity site so that the enzyme becomes less effective catalyst and rate slows down.



A positive regulator changes the activity site so that the enzyme becomes a better catalyst and rate accelerates.

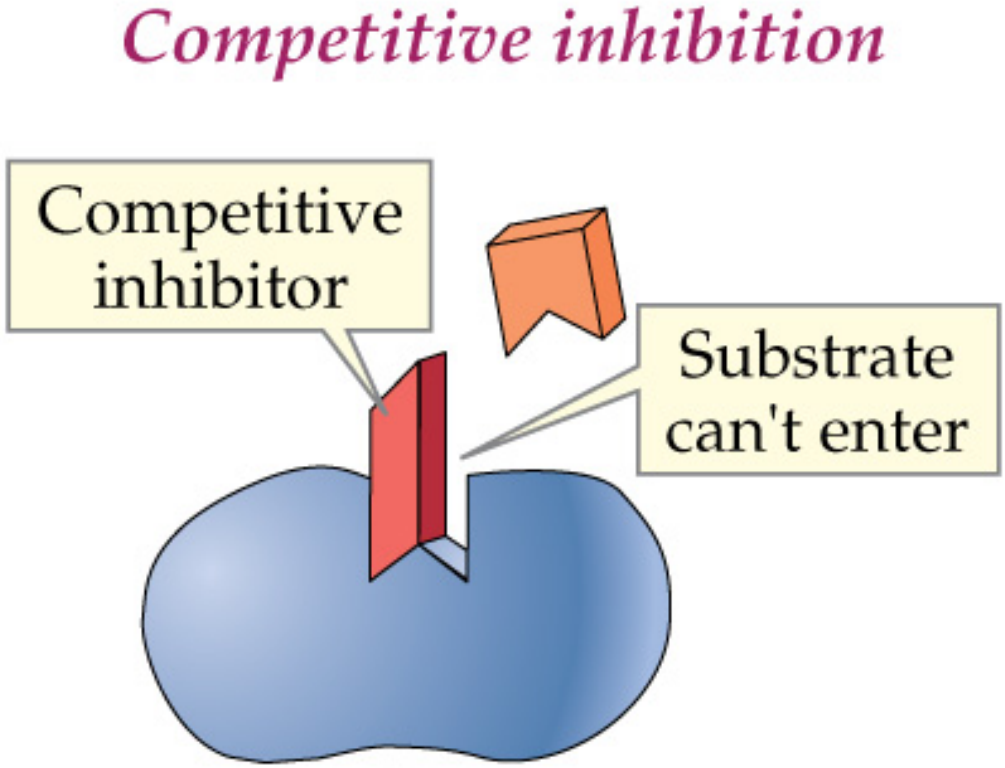


A negative regulator changes the activity site so that the enzyme becomes less effective catalyst and rate slows down.

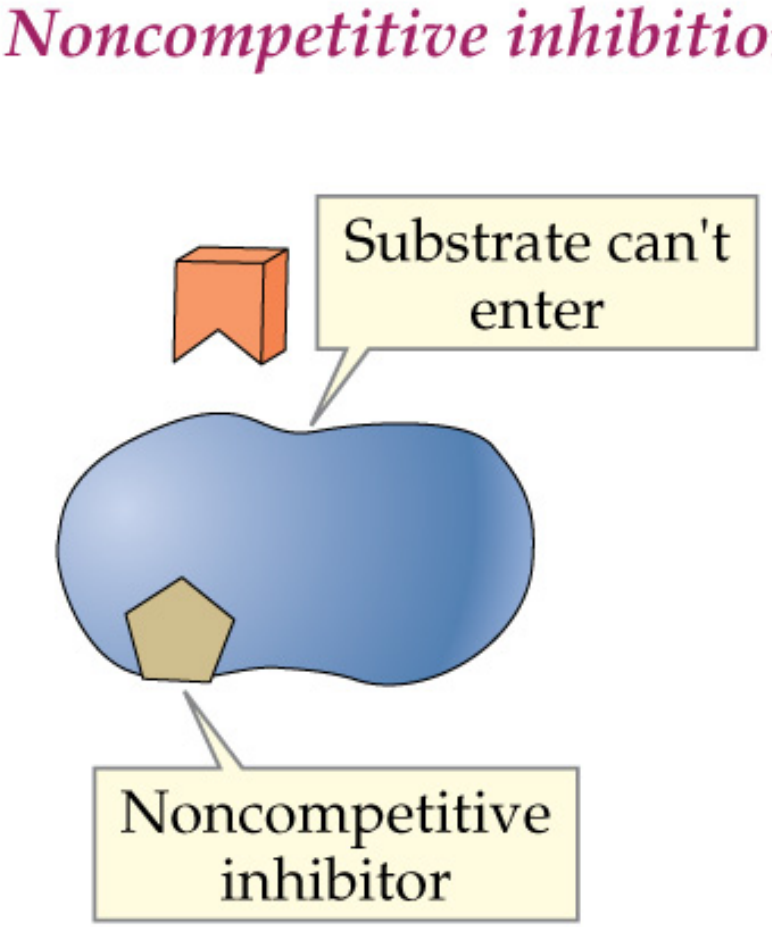
19.8 Enzyme Regulation: Inhibition

- The inhibition of an enzyme can be *reversible* or *irreversible.*
- In *reversible inhibition,* the inhibitor can leave, restoring the enzyme to its uninhibited level of activity.
- In *irreversible inhibition,* the inhibitor remains permanently bound to the enzyme and the enzyme is permanently inhibited.

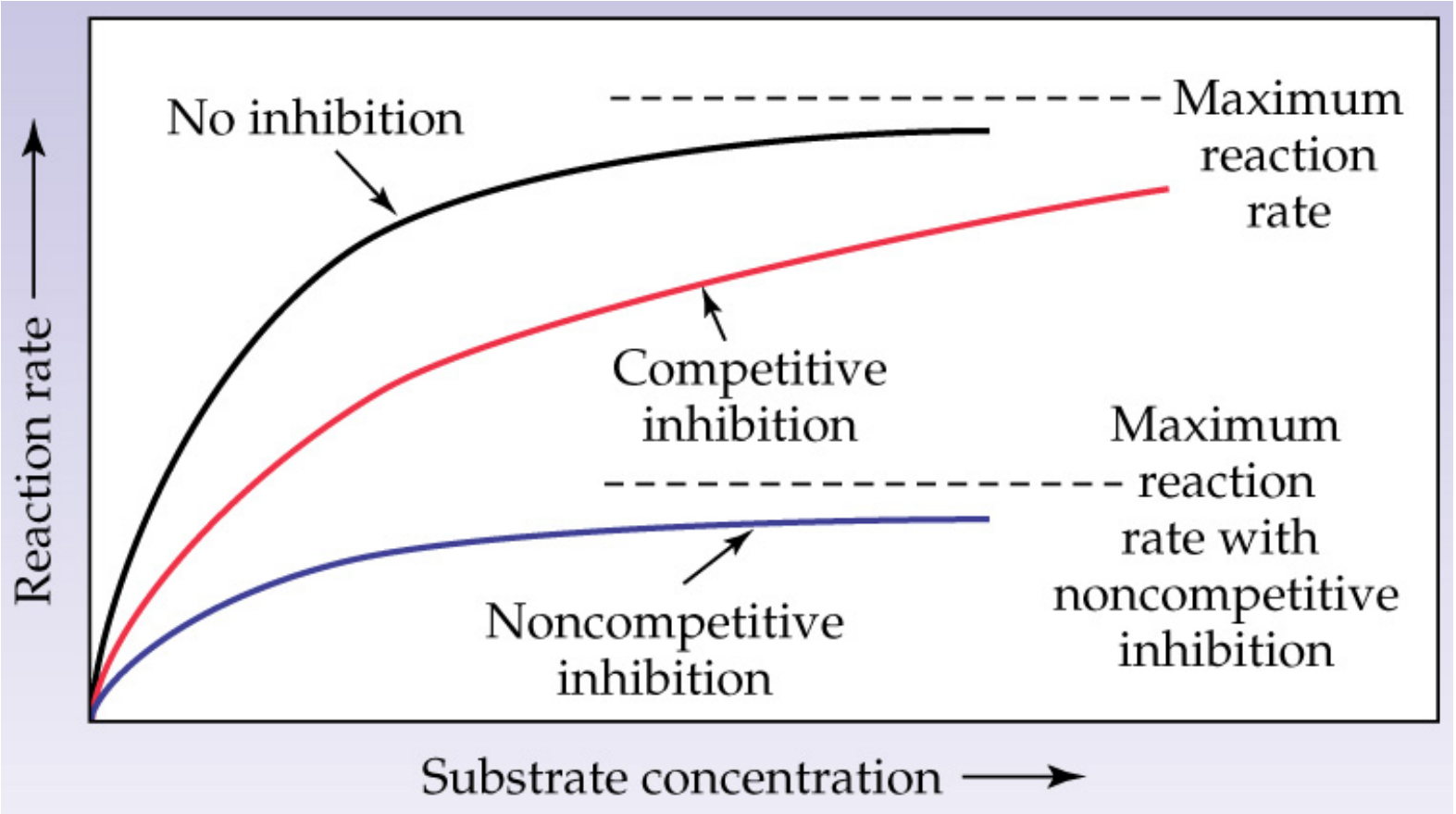
- Inhibitions are further classified as:
- *Competitive inhibition if* the inhibitor binds to the active site.

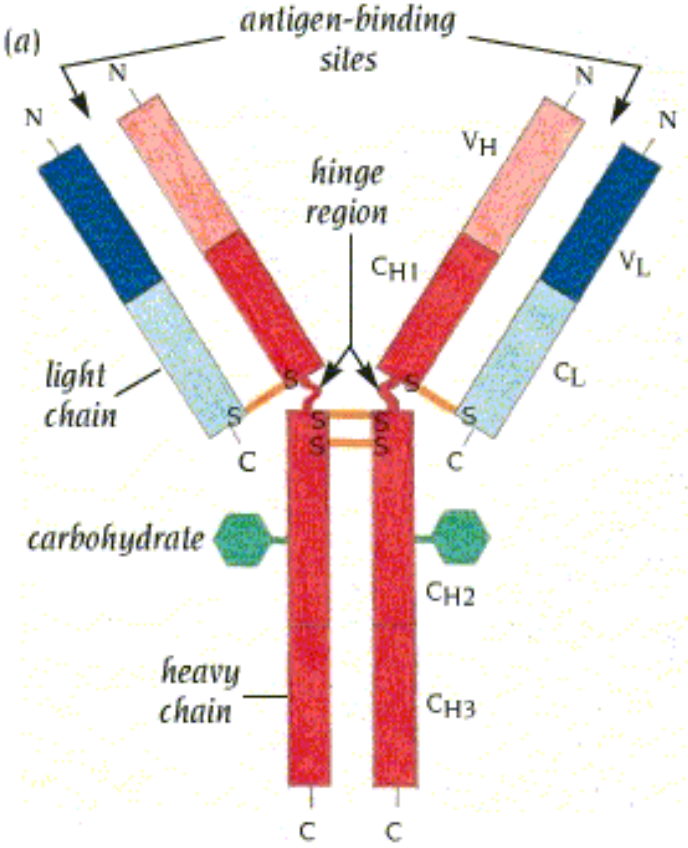


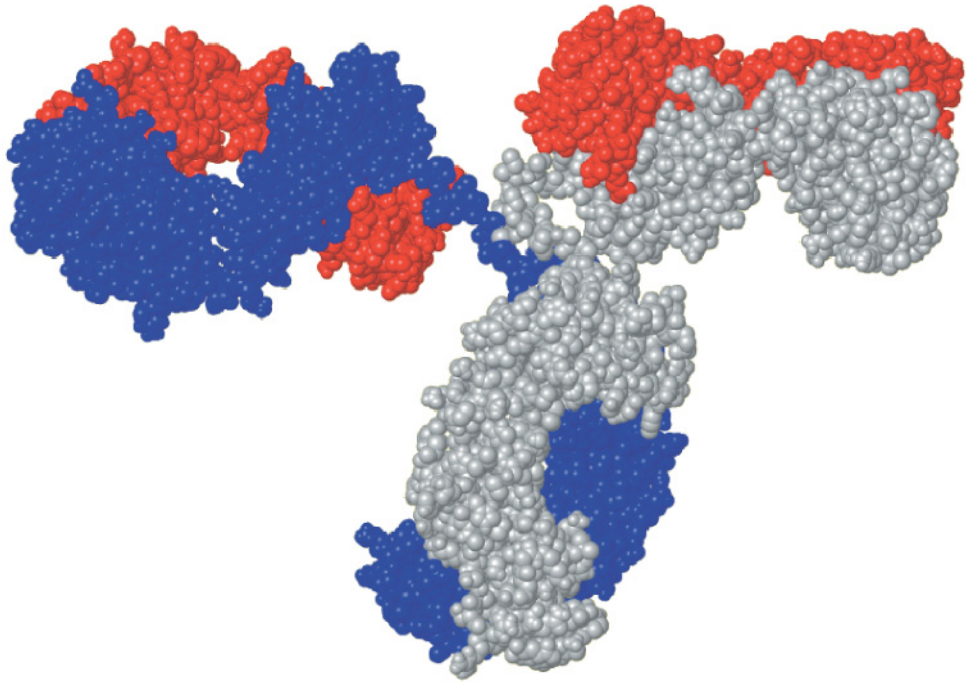
- *Noncompetitive inhibition,* if the inhibitor binds elsewhere and not to the active site.



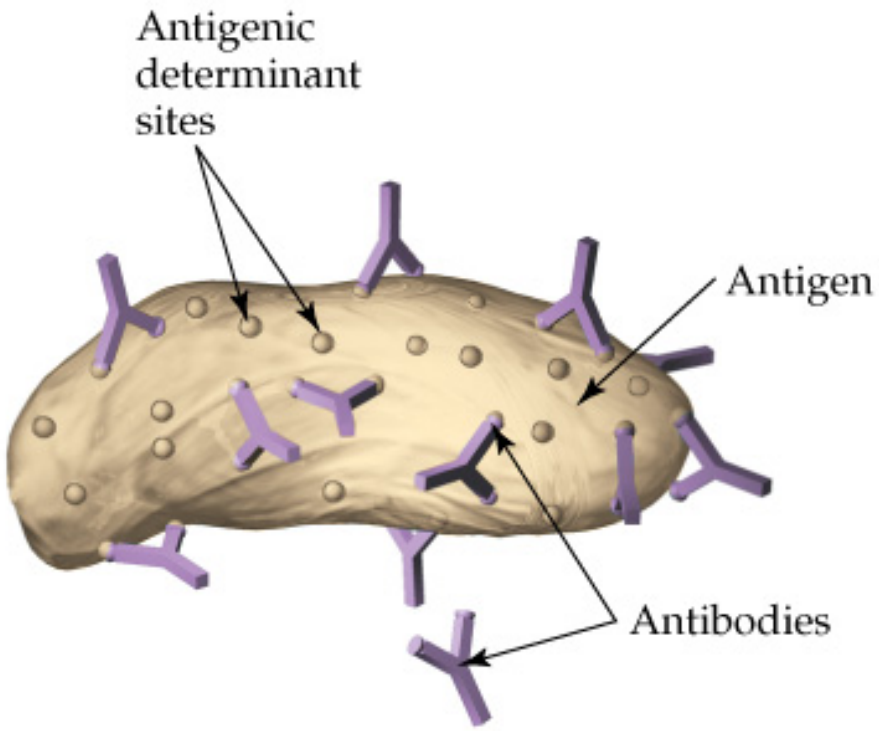
•The rates of enzyme catalyzed reactions with or without a competitive inhibitor are shown in the Fig 19.9 below.



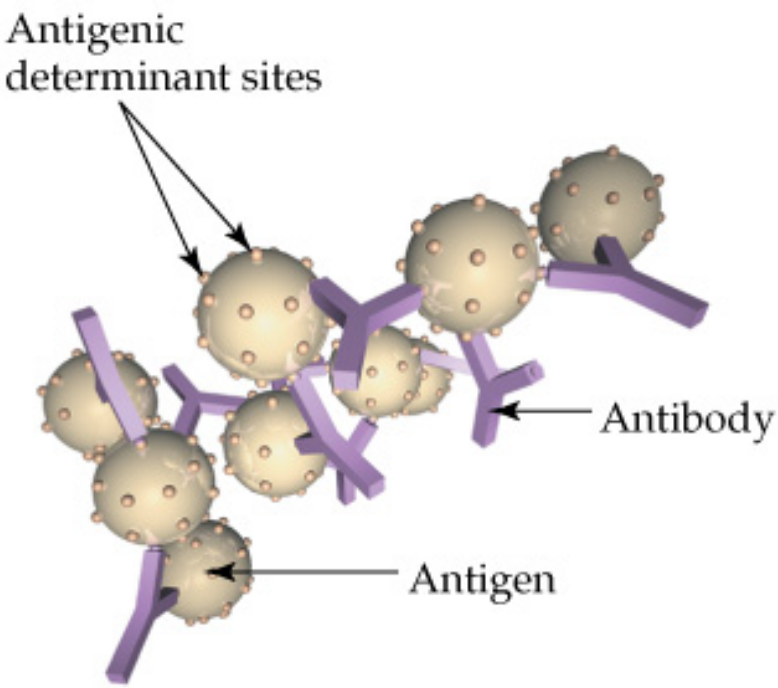

(a)
antigen-binding sites
N
N
N
N
V_H
hinge region
C_{H1}
V_L
light chain
C_L
S
S
S
S
S
S
S
S
C
C
carbohydrate
C_{H2}
heavy chain
C_{H3}
C
C



(b)


Antigenic determinant sites
Antigen
Antibodies

(a)

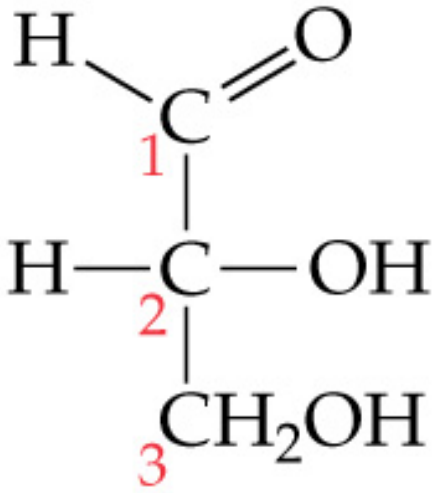

Antigenic determinant sites
Antibody
Antigen

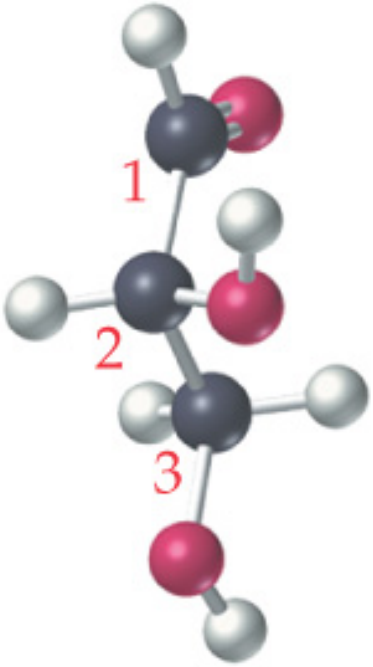
(b)

An Introduction to Carbohydrates

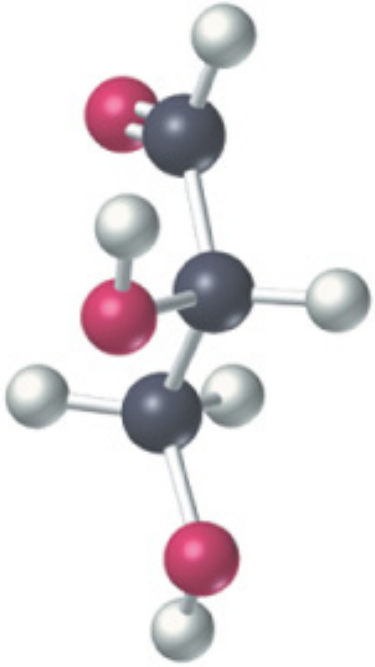
- *Carbohydrates* are a large class of naturally occurring polyhydroxy aldehydes and ketones.
- Monosaccharides also known as simple sugars, are the simplest carbohydrates containing 3-7 carbon atoms.
- sugar containing an aldehydes is known as an aldose.
- sugar containing a ketones is known as a ketose.

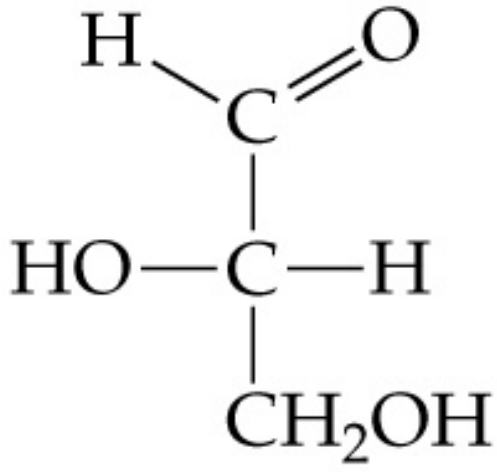
- The number of carbon atoms in an aldose or ketose may be specified as by tri, tetr, pent, hex, or hept. For example, glucose is aldohexose and fructose is ketohexose.
- Monosaccharides react with each other to form disaccharides and polysaccharides.
- Monosaccharides are chiral molecules and exist mainly in cyclic forms rather than the straight chain.



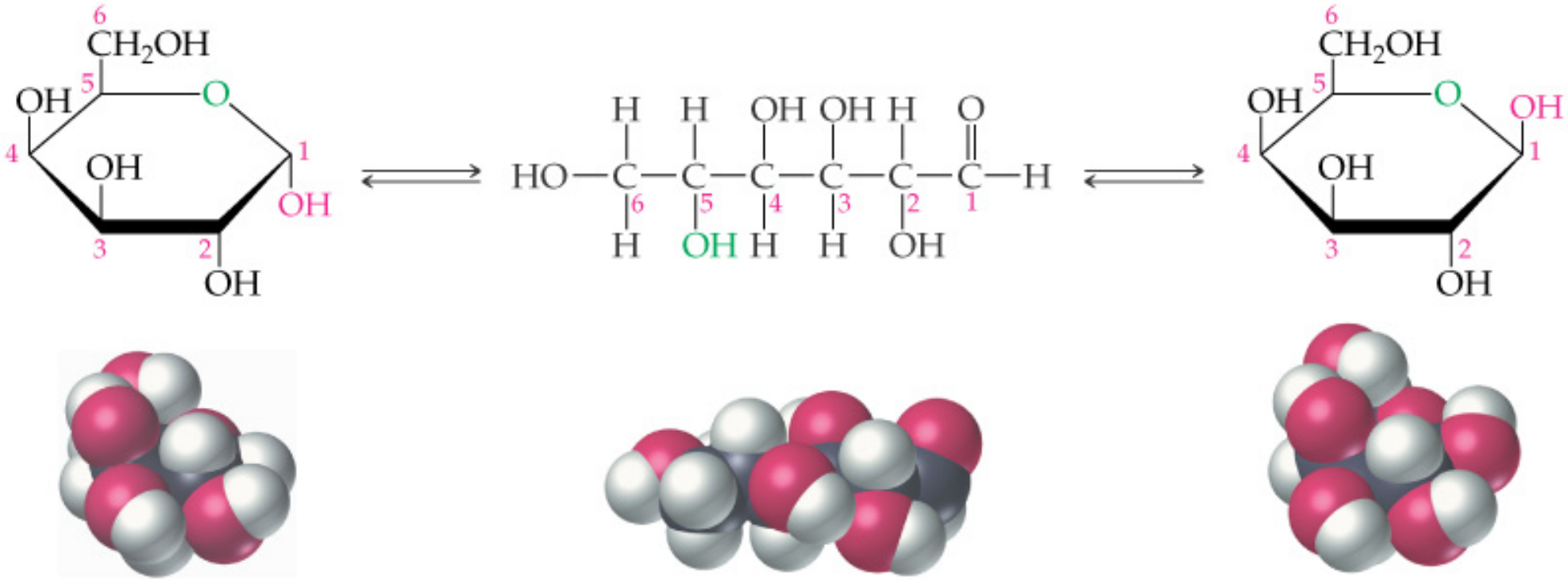


D-Glyceraldehyde
Right-handed





L-Glyceraldehyde
Left-handed

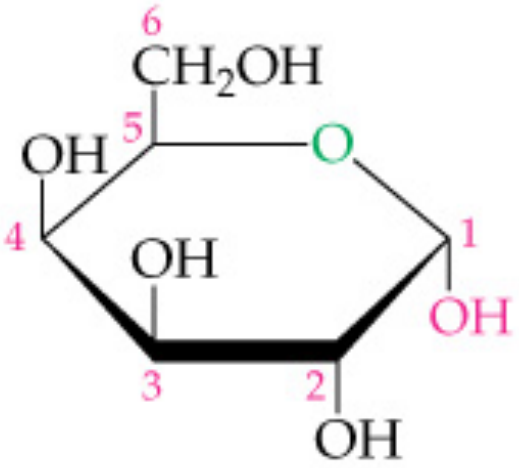


α-D-Galactose

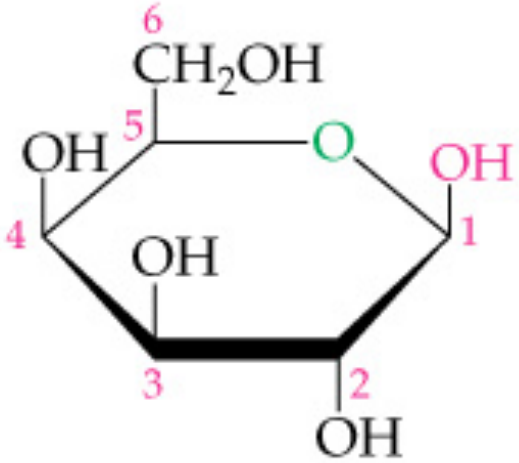
Open-chain galactose

β-D-Galactose

- *Anomers:* Cyclic sugars that differs only in positions of substituents at the hemiacetal carbon; the α-form has the –OH group on the opposite side from the $–CH_2OH$; the β-form the –OH group on the same side as the $–CH_2OH$ group.



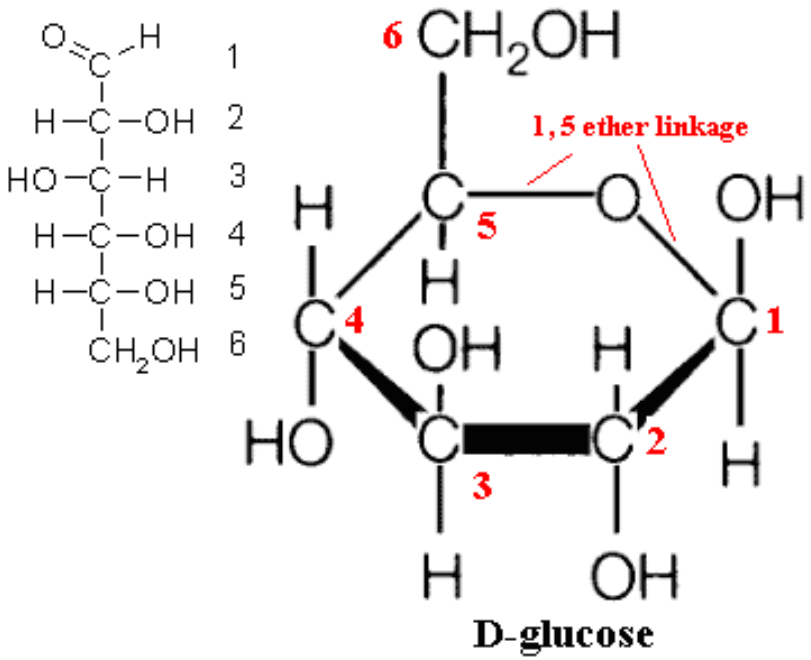
α-D-Galactose

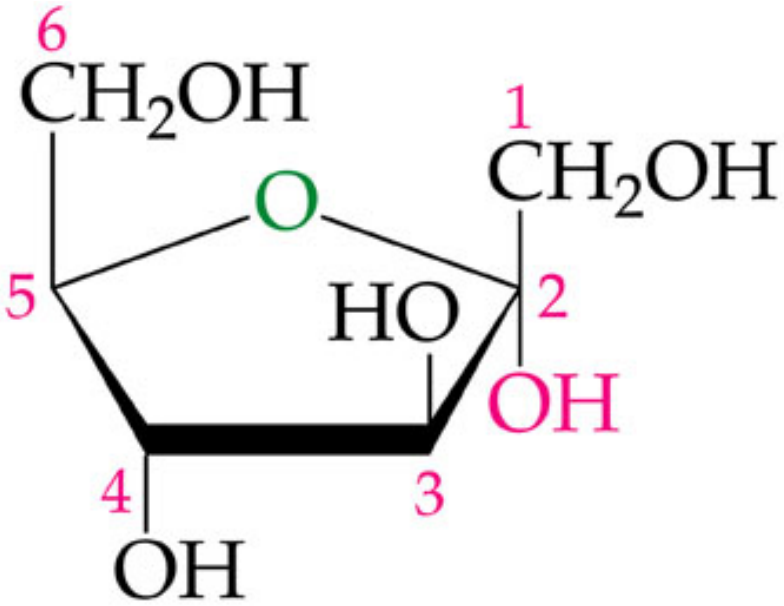


β-D-Galactose

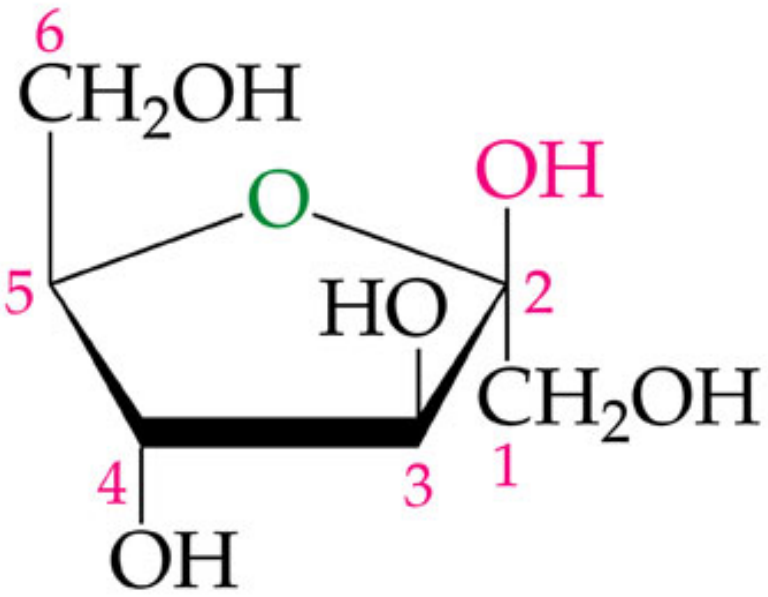
Some Important Monosaccharides

Monosaccharides are generally high-melting, white, crystalline solids that are soluble in water and insoluble in nonpolar solvents. Most monosaccharides are sweet tasting, digestible, and nontoxic.

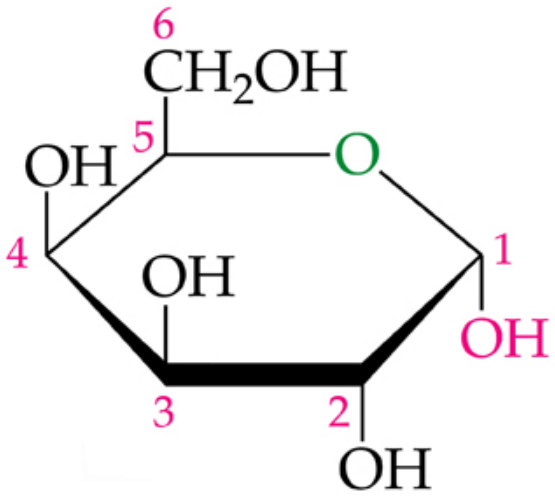




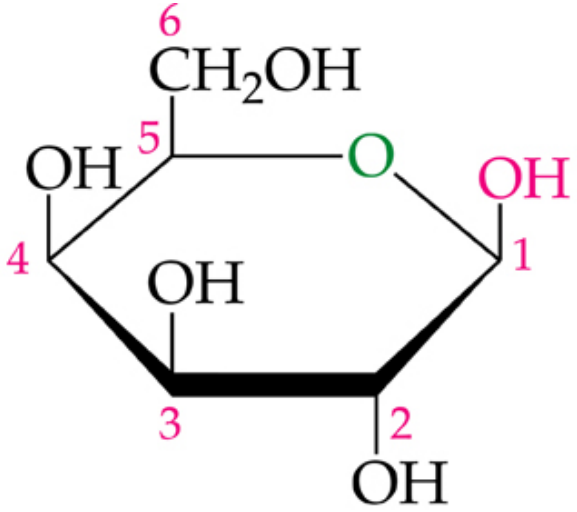
α-D-Fructose



β-D-Fructose

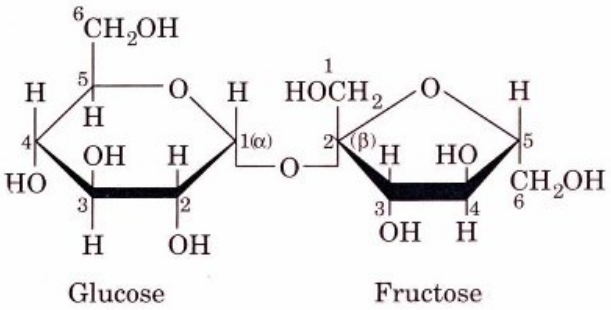


α-D-Galactose

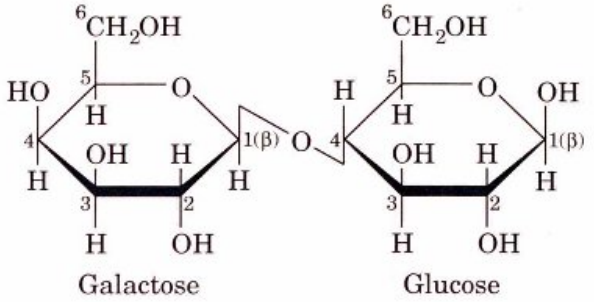


β-D-Galactose

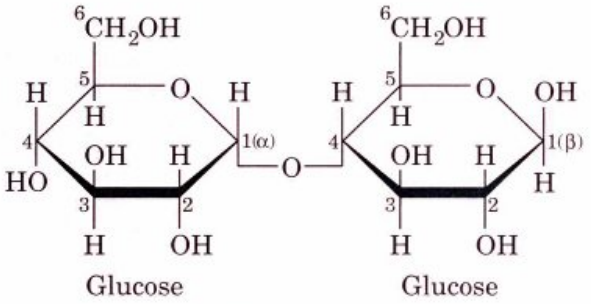
Some Common Disaccharides



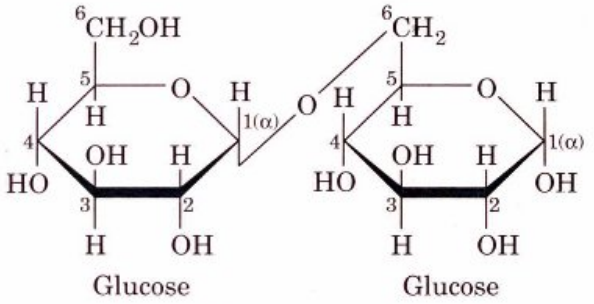
Sucrose



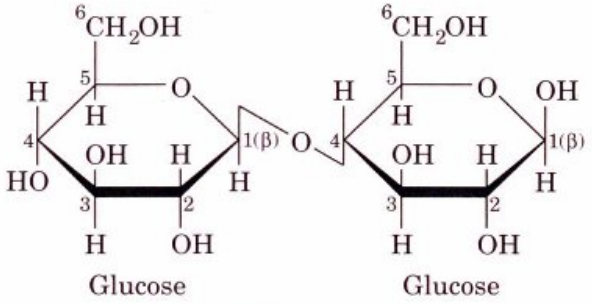
Lactose



Maltose

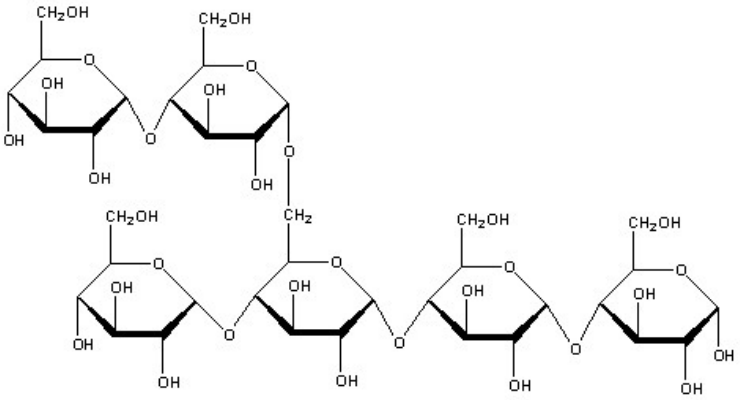


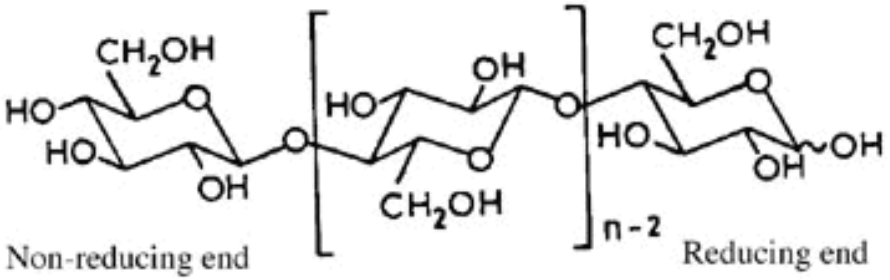
Isomaltose



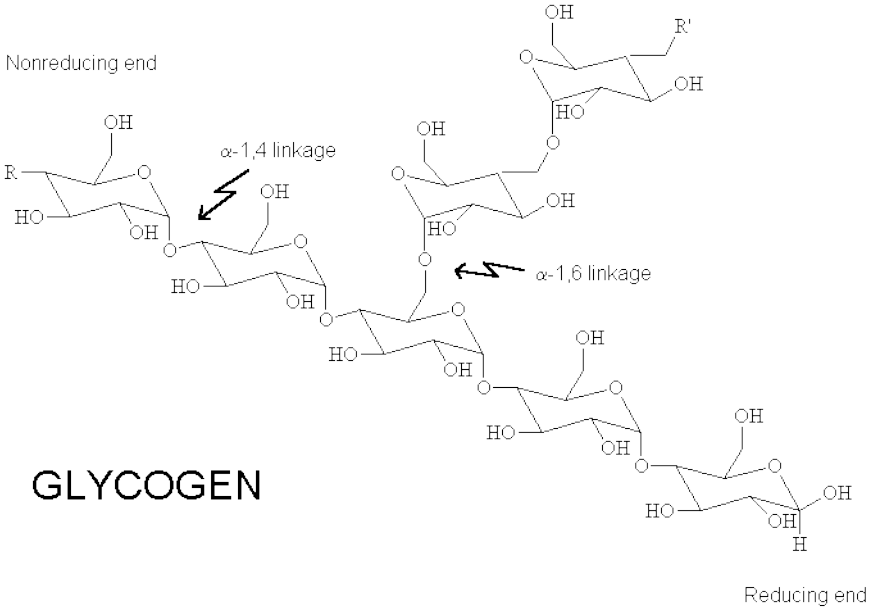
Cellobiose

Polysaccharides

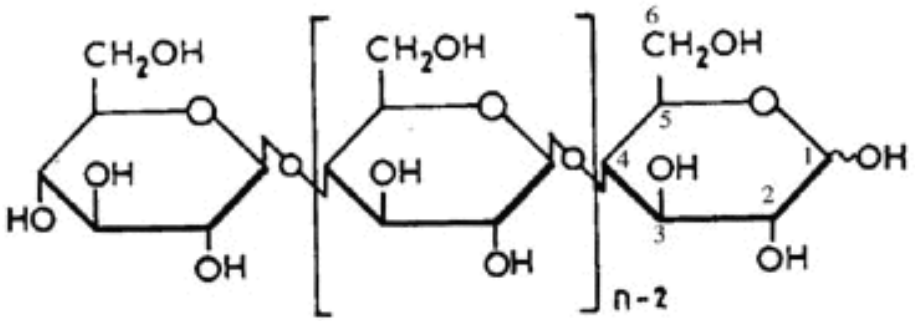




Sometimes shown as

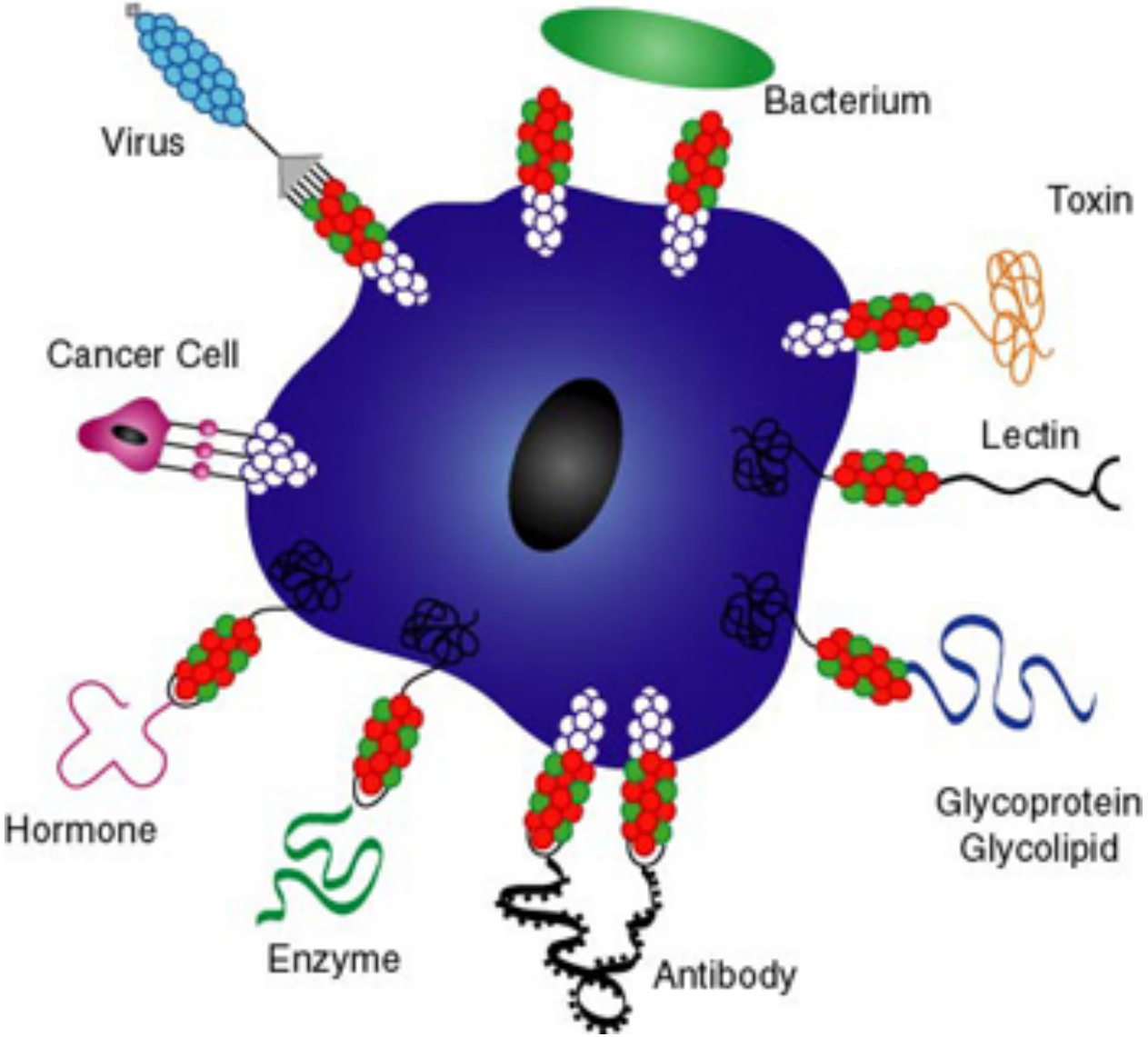


GLYCOGEN



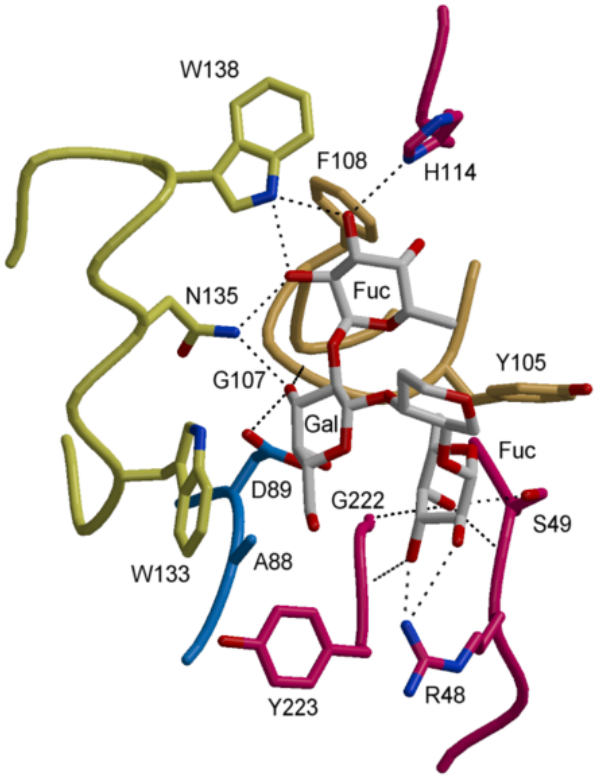
Cellulose

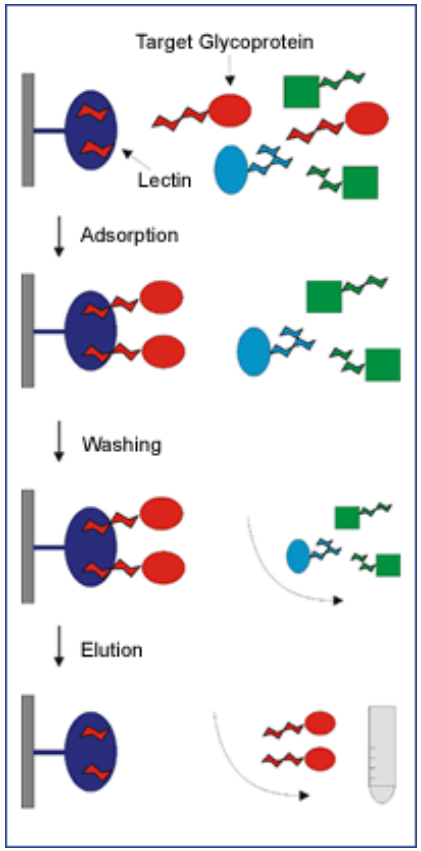
Cell-Surface Carbohydrates Involved in Molecular Recognition



Lectin

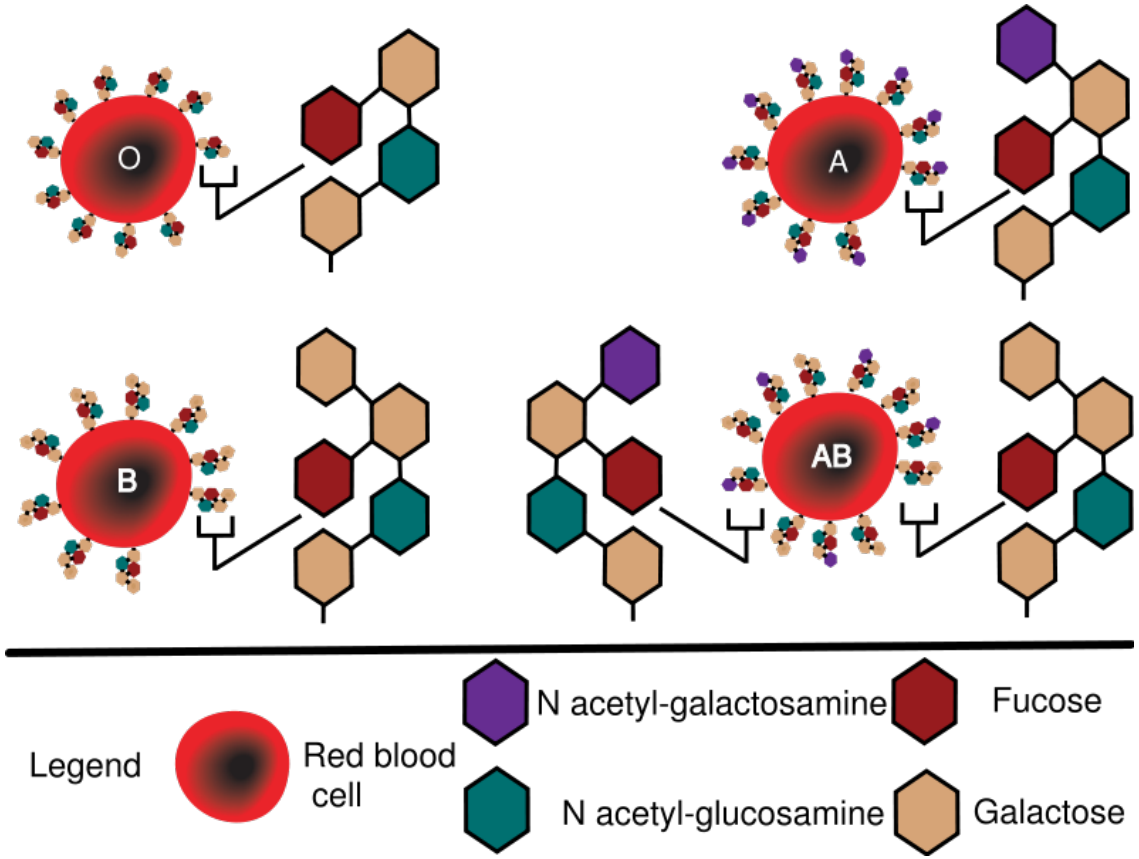
Lectins are sugar-binding proteins which are highly specific for their sugar moieties. They typically play a role in biological recognition phenomena involving cells and proteins. For example, some bacteria use lectins to attach themselves to the cells of the host organism during infection.



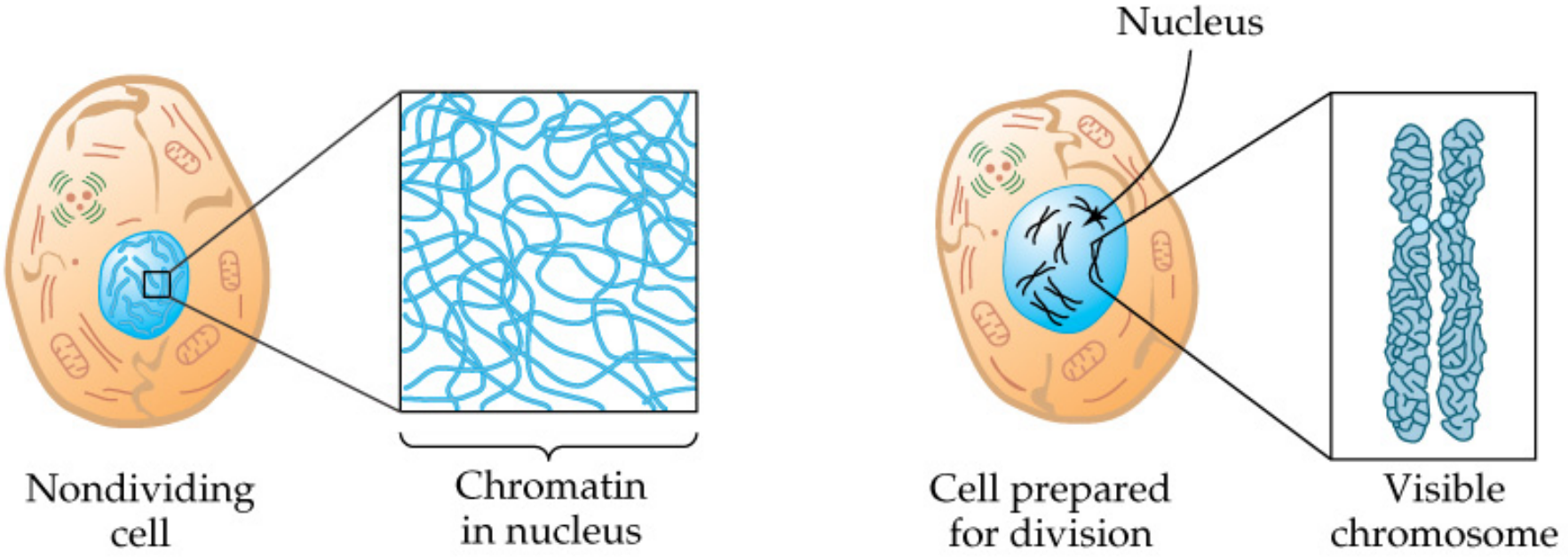


Blood Type

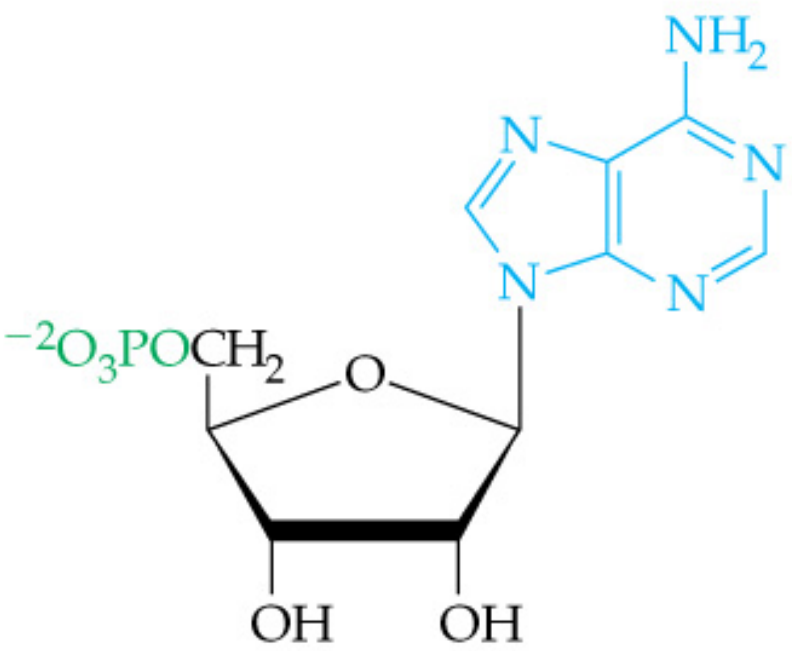
	Group A	Group B	Group AB	Group O
Red blood cell type	A	B	AB	O
Antibodies present	Anti-B	Anti-A	None	Anti-A and Anti-B
Antigens present	A antigen	B antigen	A and B antigens	No antigens



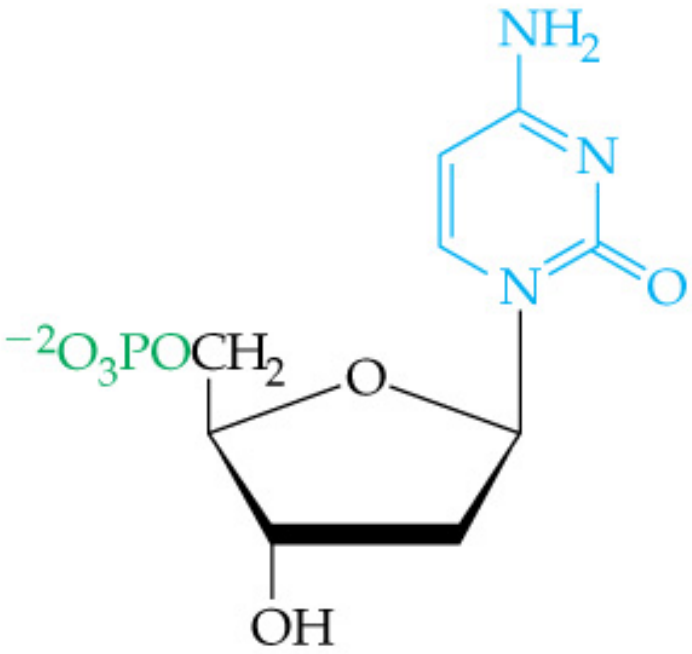
DNA


Nucleus
Nondividing cell
Chromatin in nucleus
Cell prepared for division
Visible chromosome

- In RNA, the sugar is ribose.
- In DNA, the sugar is deoxyribose.



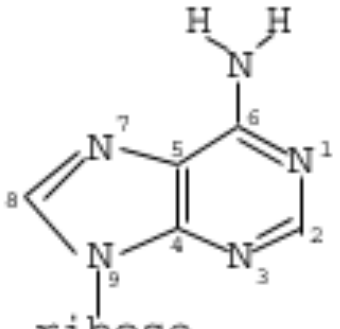
Adenosine 5′-monophosphate (AMP)
(a ribonucleotide)



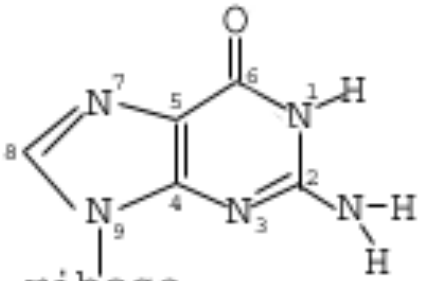
Deoxycytidine 5′-monophosphate (dCMP)
(a deoxyribonucleotide)

Base

Purines

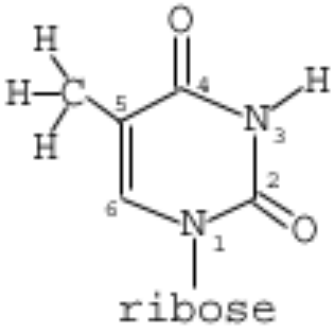


adenosine

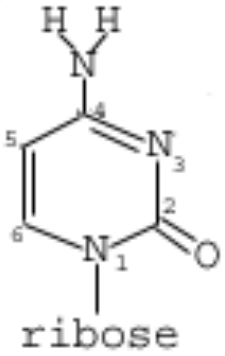


guanine

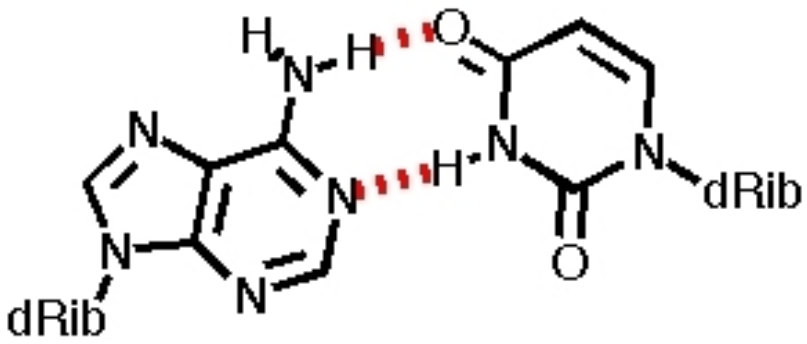
Pyrimidines



thymine



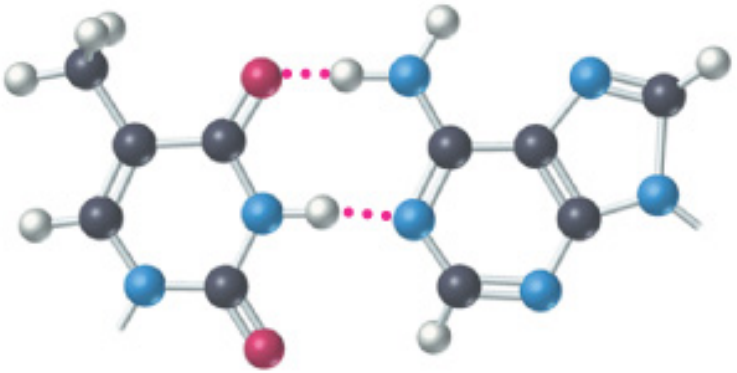
cytosine

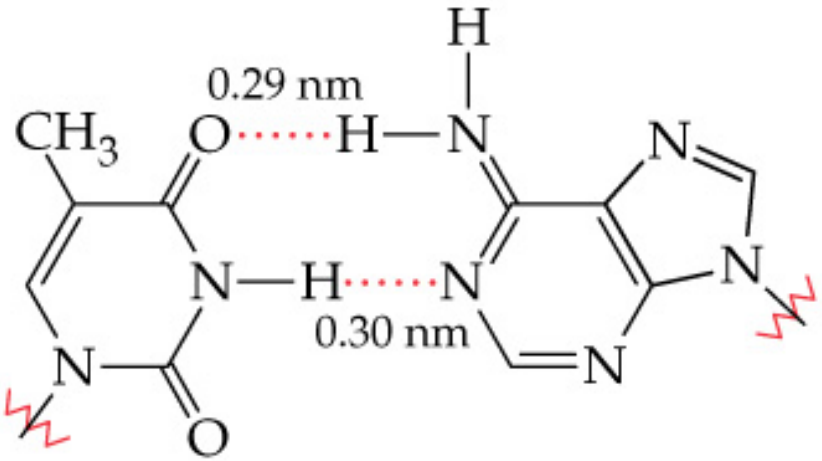


Adenine

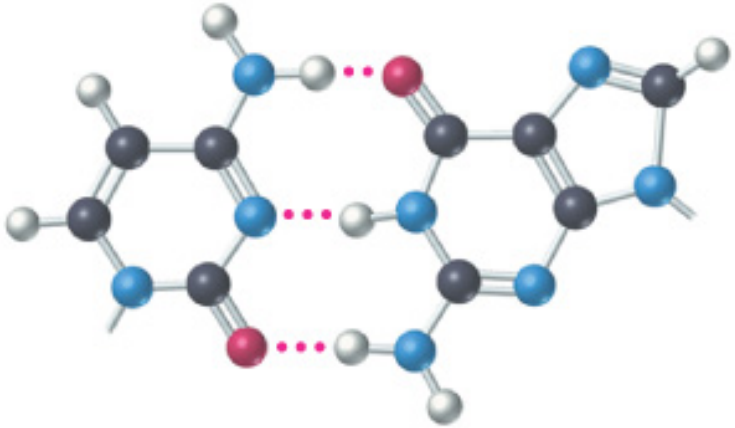
Uracil

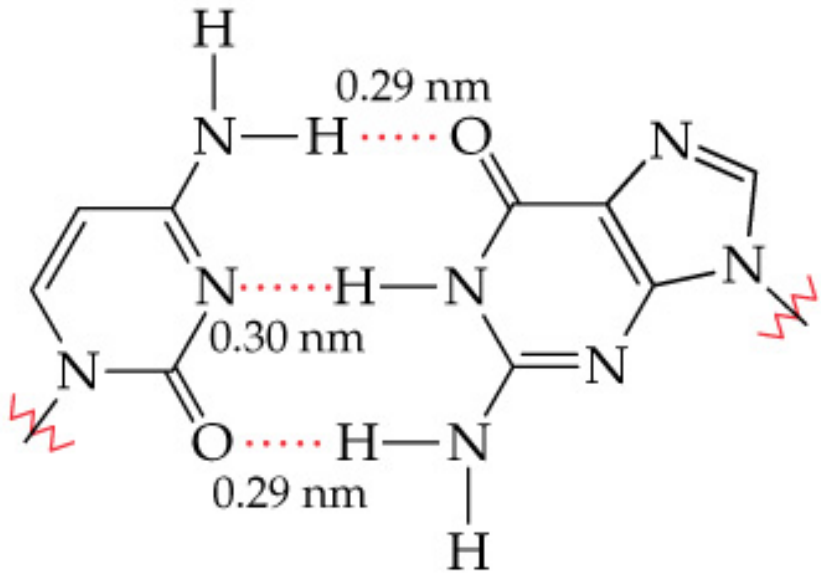
Thymine–Adenine

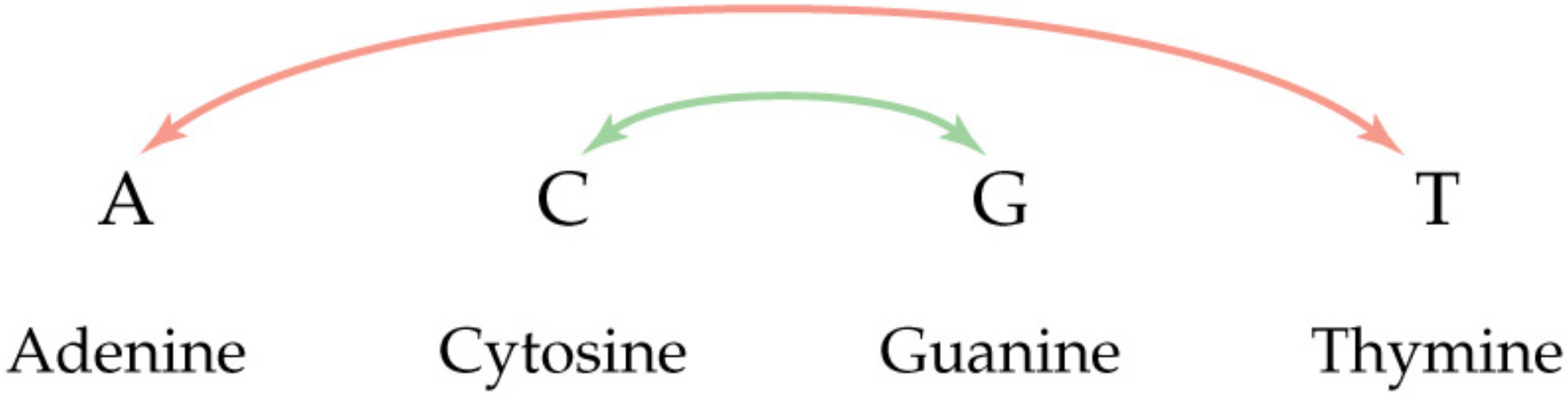


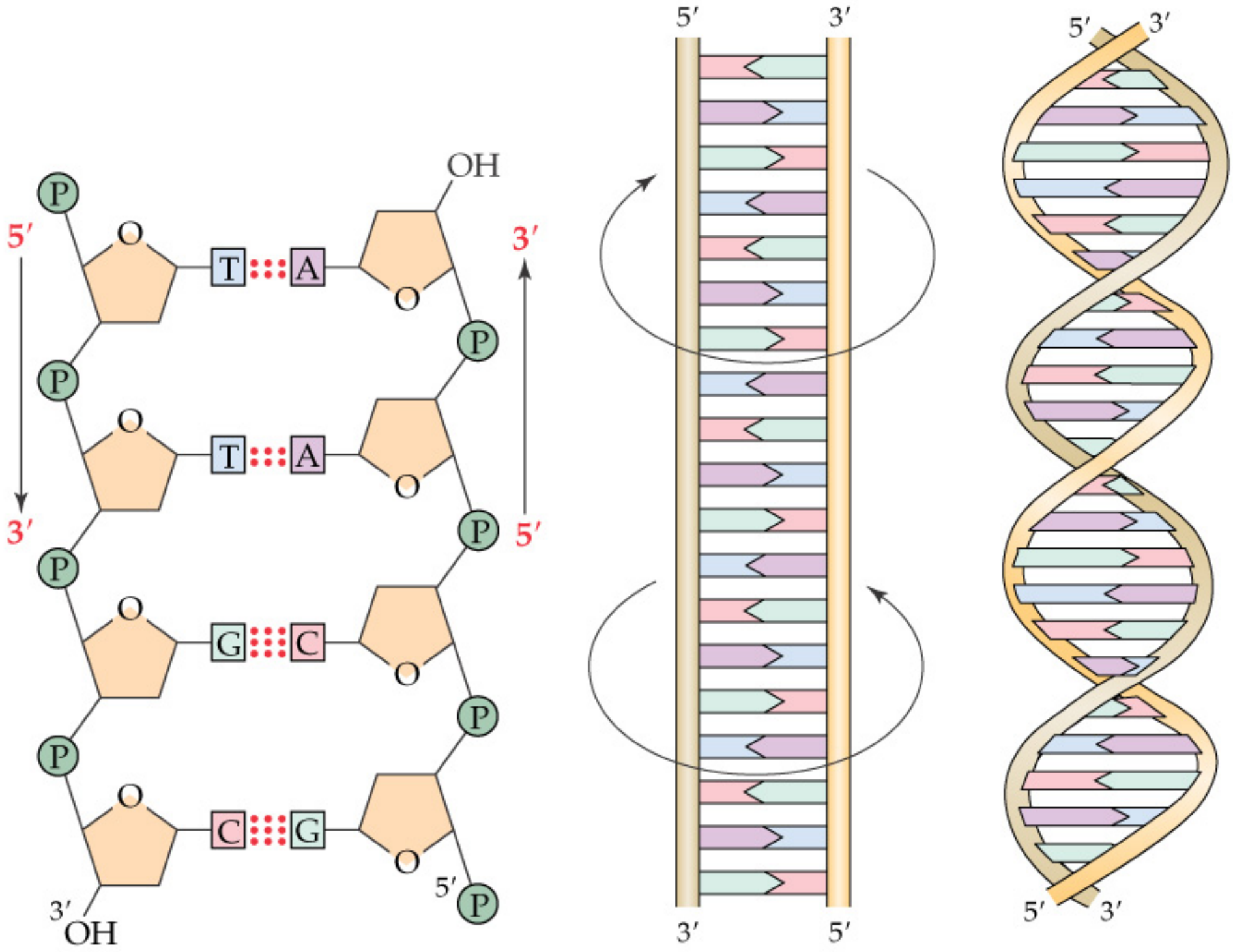


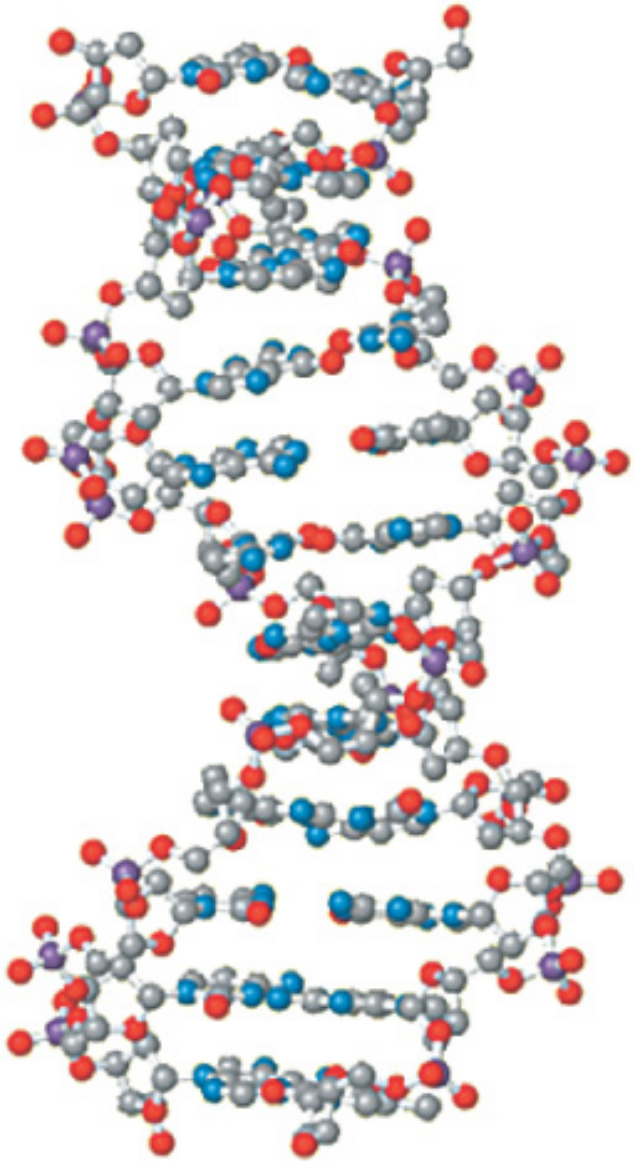
Cytosine–Guanine



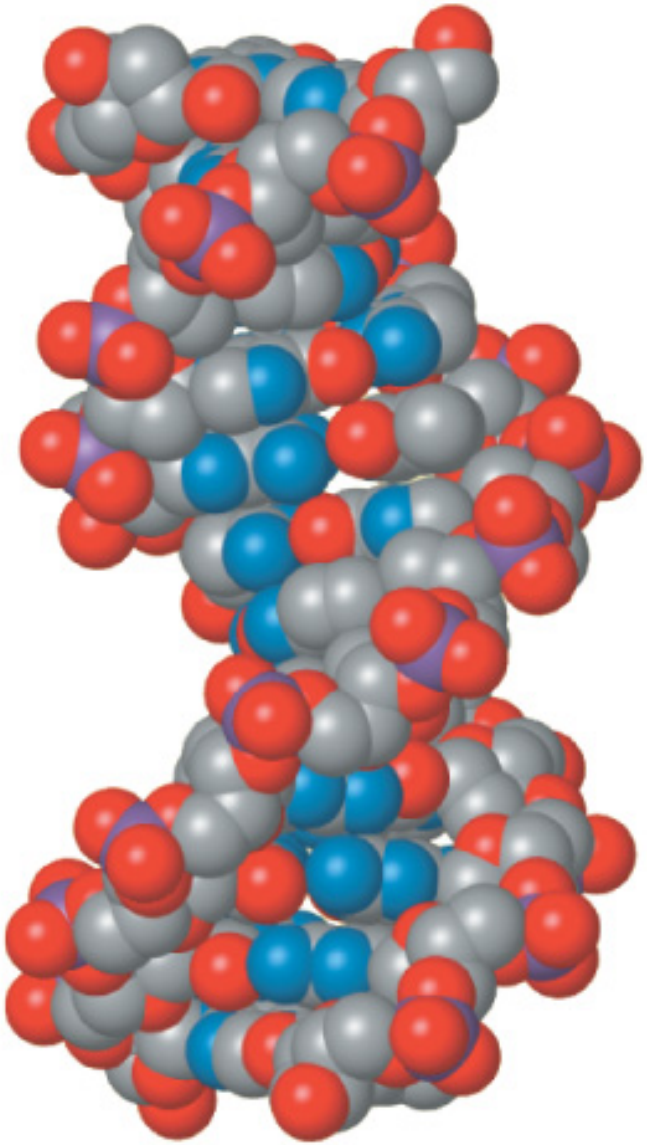



A
C
G
T
Adenine
Cytosine
Guanine
Thymine


5′
3′
OH
P
O
T
A
G
C
3′
OH
5′
3′
5′
3′
5′
3′
5′
3′



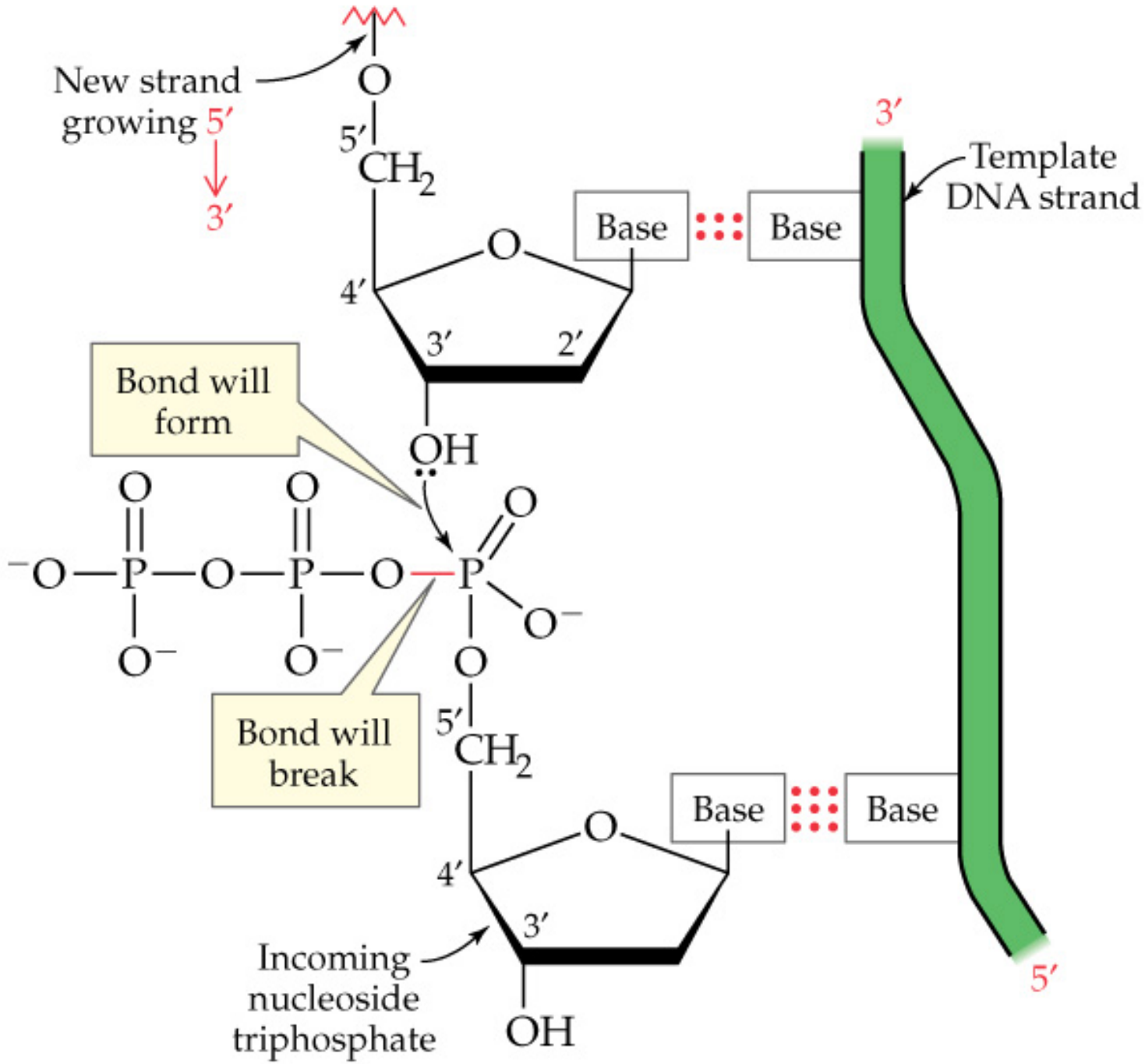
(a)

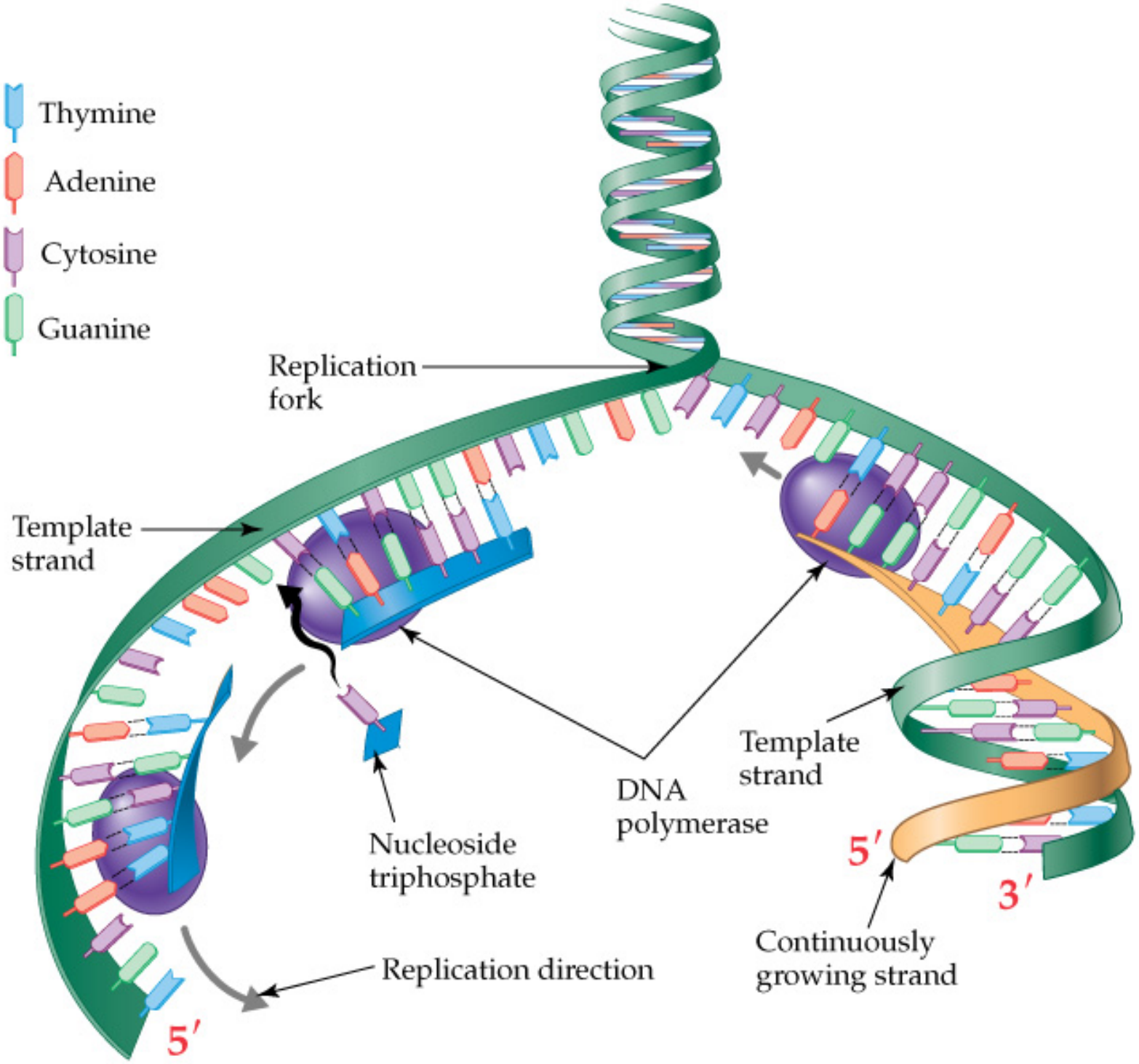


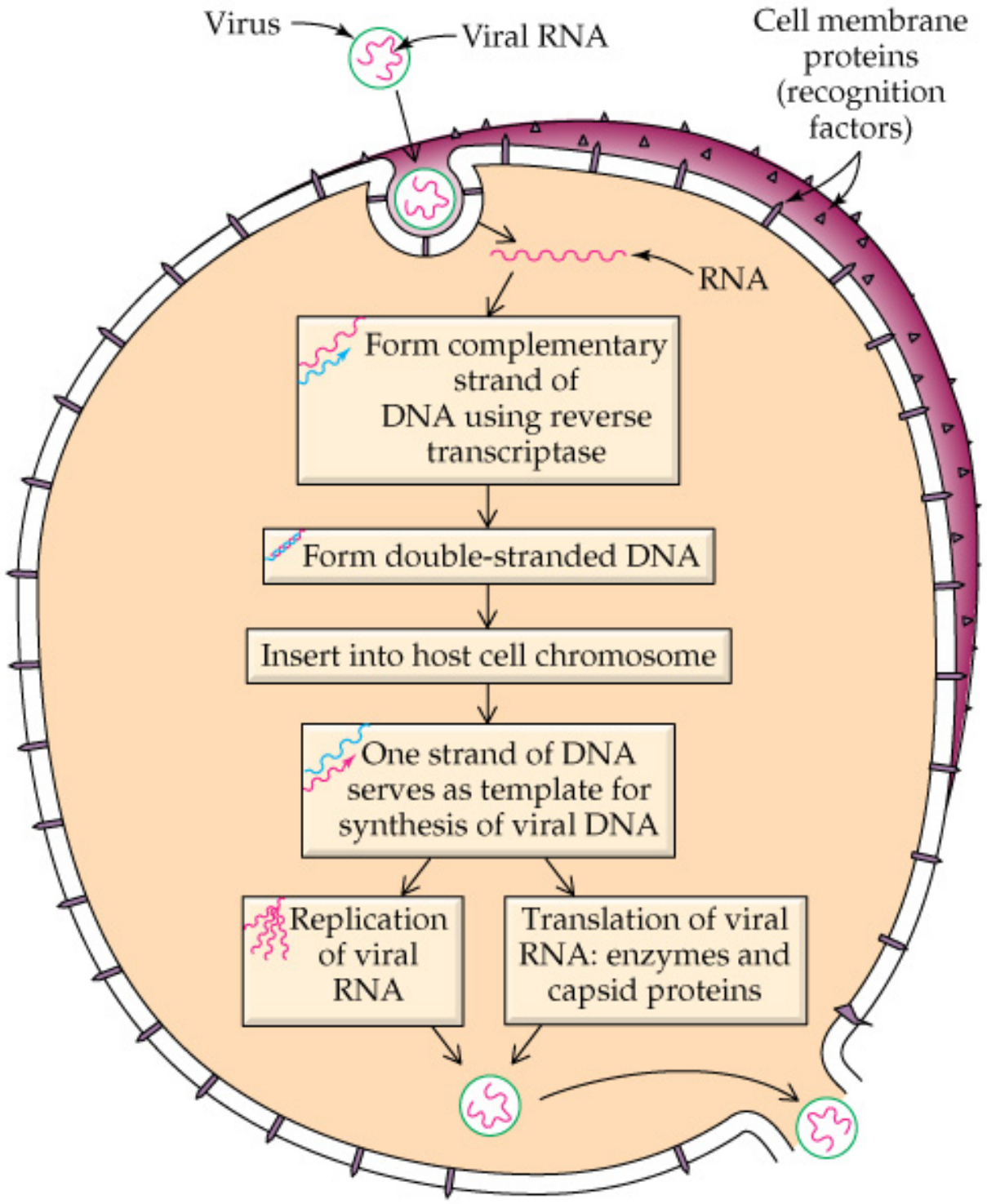
(b)

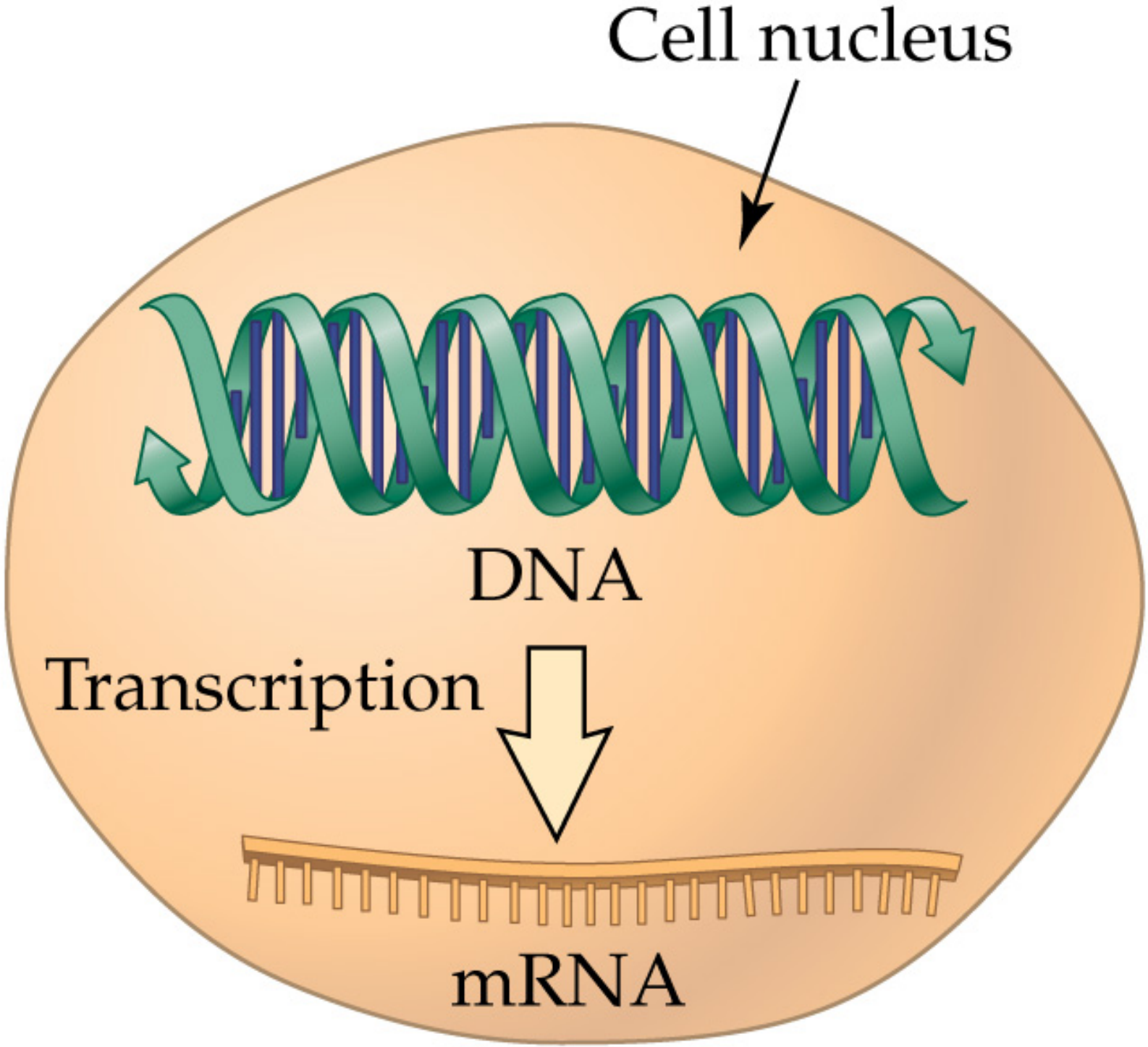
(c)

Bond formation in DNA replication

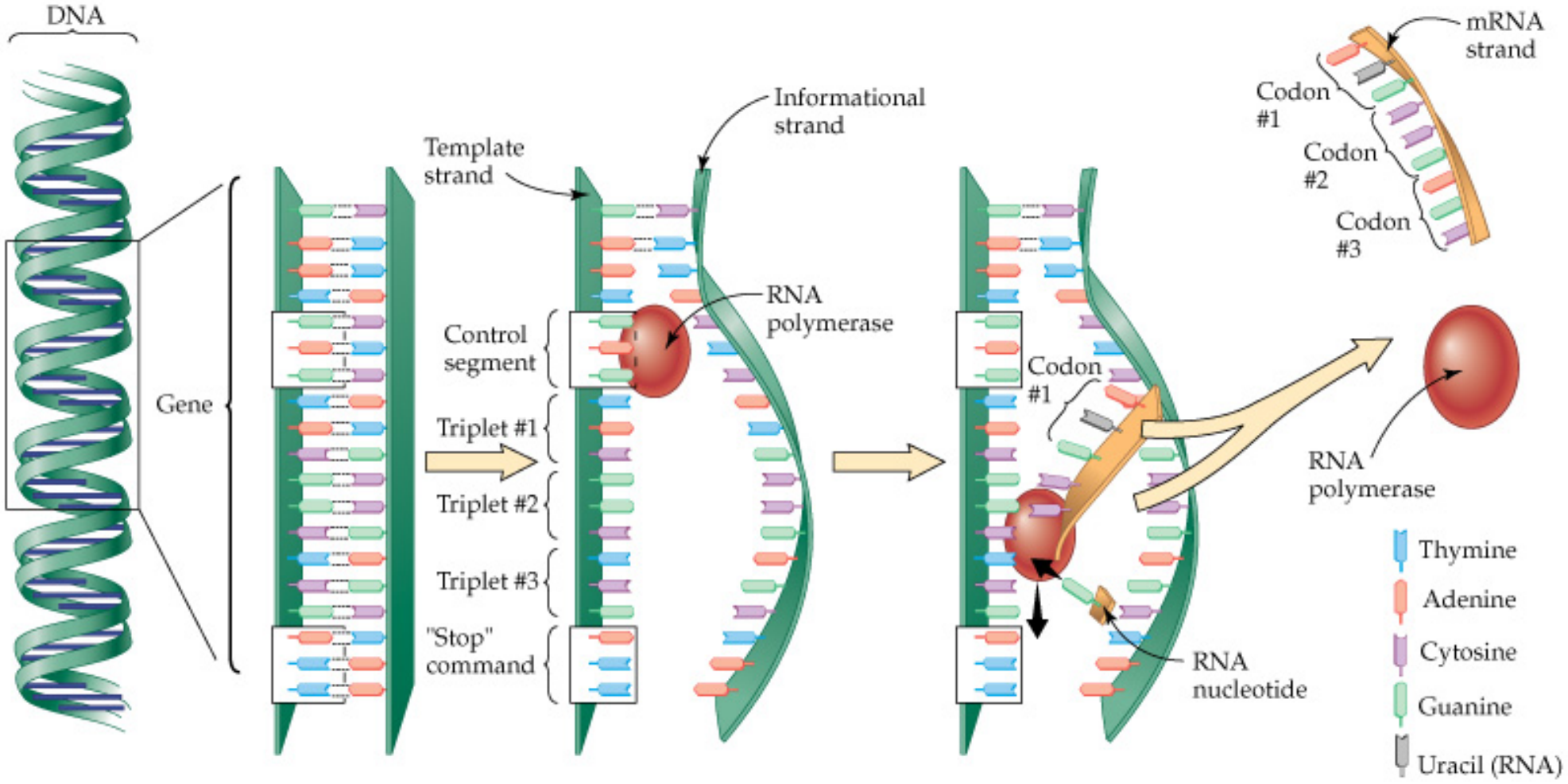


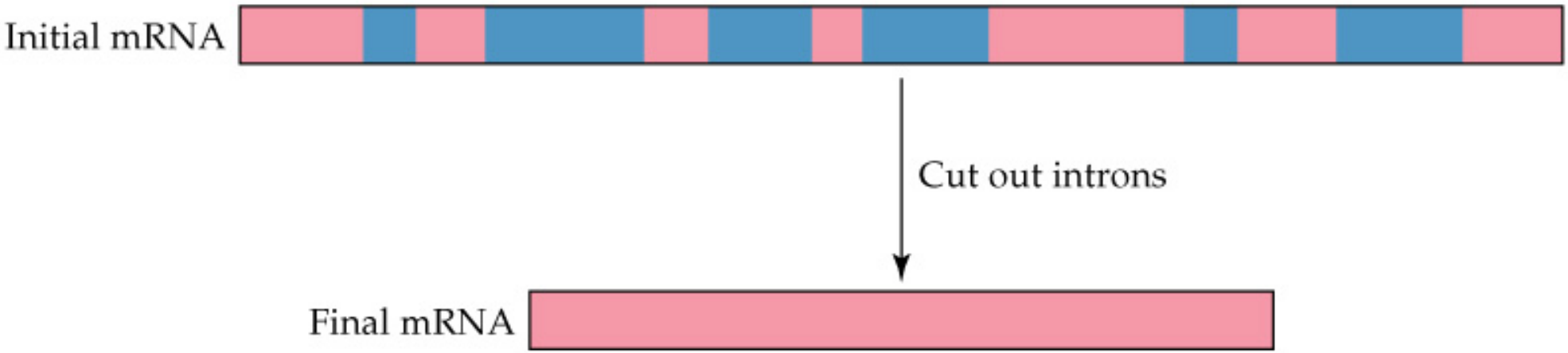

Thymine
Adenine
Cytosine
Guanine
Replication fork
Template strand
Nucleoside triphosphate
DNA polymerase
Template strand
5′
3′
Continuously growing strand
Replication direction
5′

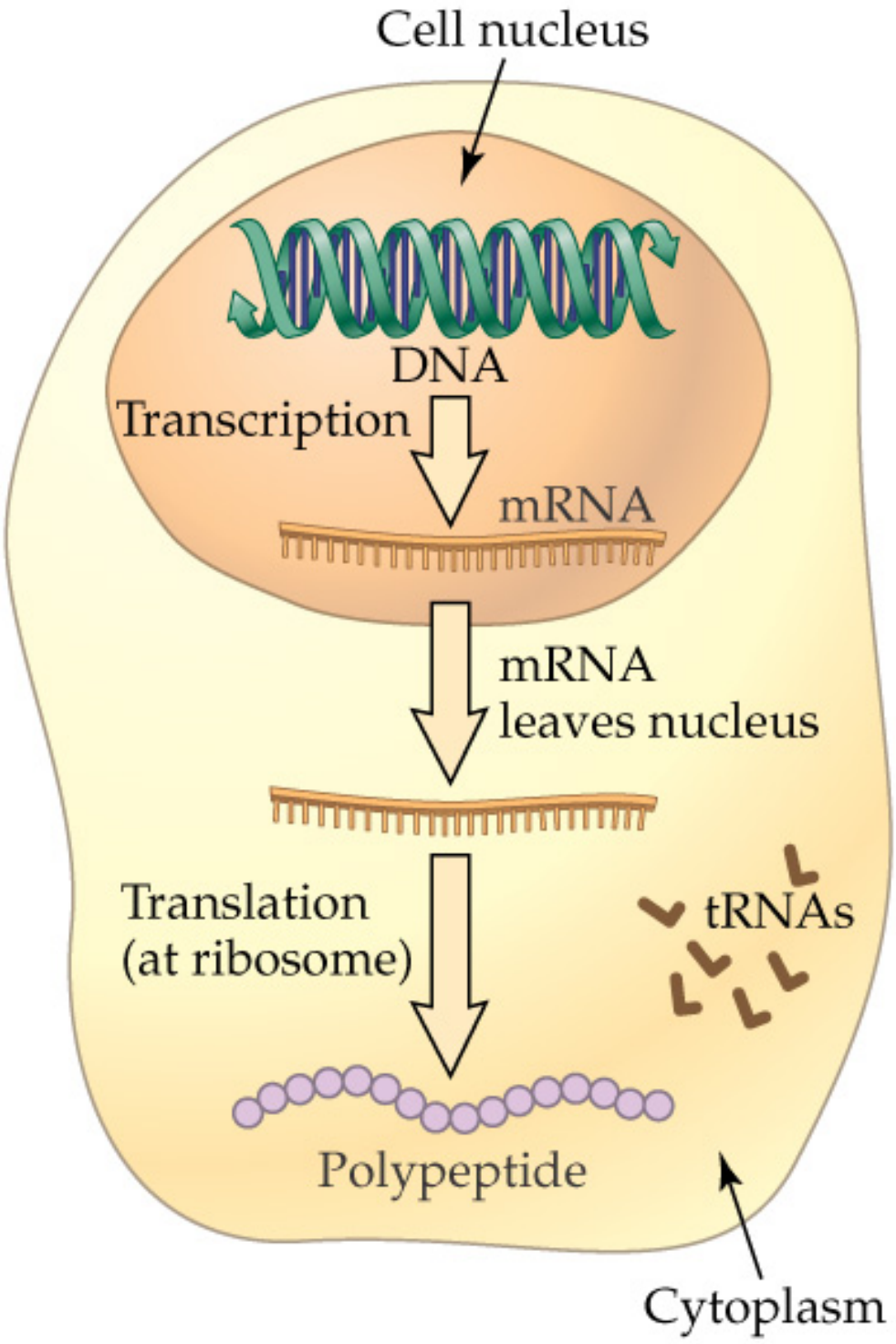

Virus
Viral RNA
Cell membrane proteins (recognition factors)
RNA
Form complementary strand of DNA using reverse transcriptase
Form double-stranded DNA
Insert into host cell chromosome
One strand of DNA serves as template for synthesis of viral DNA
Replication of viral RNA
Translation of viral RNA: enzymes and capsid proteins

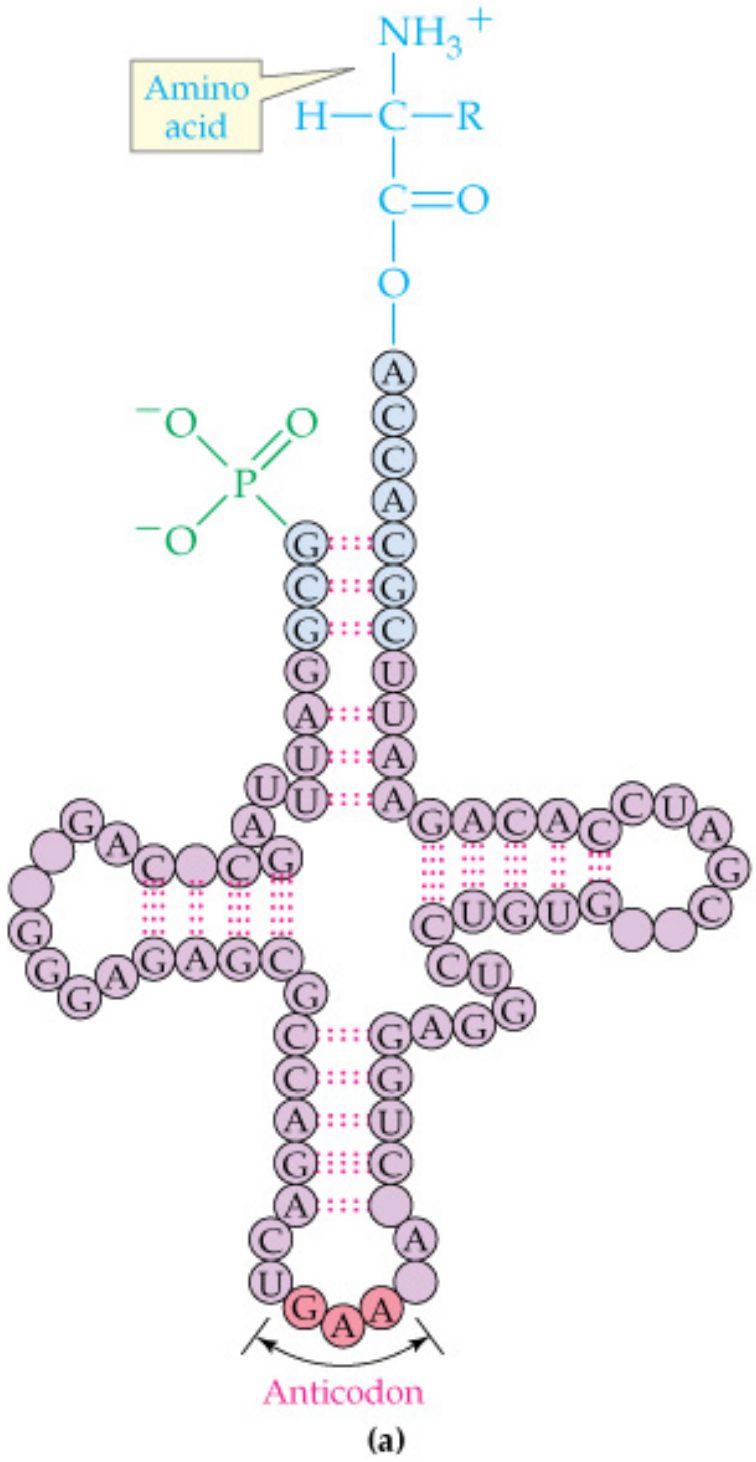

Cell nucleus
DNA
Transcription
mRNA

- The following three RNA make it possible for the encoded information carried by the DNA to be put to use in the synthesis of proteins.
- ***Ribosome RNA***: The granular organelles in the cell where protein synthesis takes place. These organelles are composed of protein and ribosomal RNA (rRNA).
- ***Messenger RNA (mRNA)***: The RNA that carries the code transcribed from DNA and directs protein synthesis.
- ***Transfer RNA (tRNA)***: The smaller RNA that delivers amino acids one by one to protein chains growing at ribosomes. Each tRNA recognizes and carries only one amino acid.

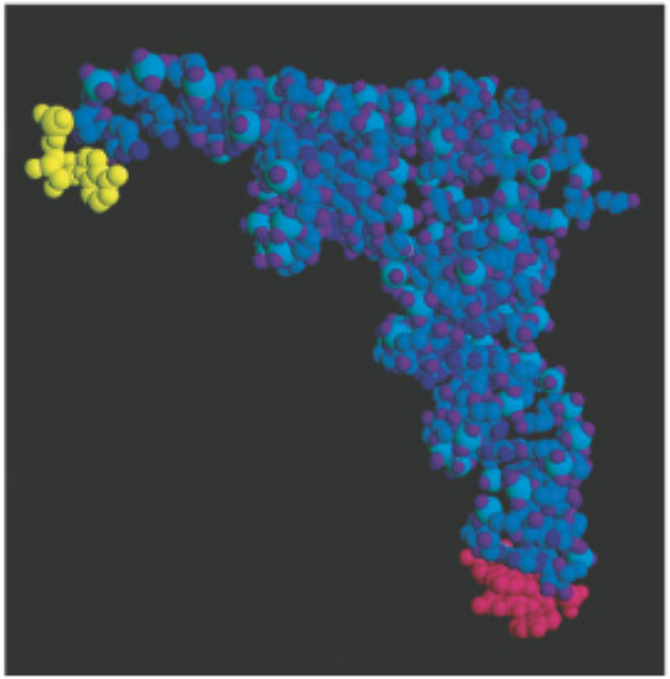

DNA
Gene
Template strand
Informational strand
RNA polymerase
Control segment
Triplet #1
Triplet #2
Triplet #3
"Stop" command
Codon #1
Codon #2
Codon #3
mRNA strand
RNA polymerase
RNA nucleotide
Thymine
Adenine
Cytosine
Guanine
Uracil (RNA)


Initial mRNA
Cut out introns
Final mRNA

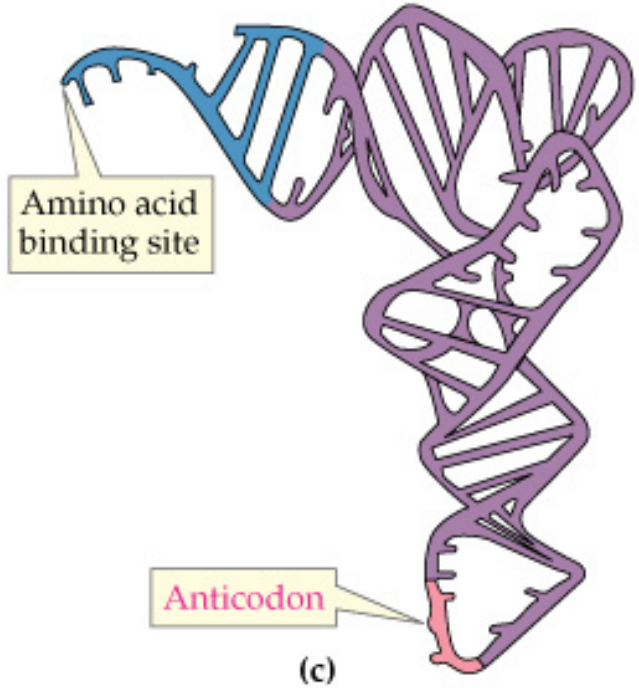

Cell nucleus
DNA
Transcription
mRNA
mRNA
leaves nucleus
Translation
(at ribosome)
tRNAs
Polypeptide
Cytoplasm


Amino acid
NH_3^+
H—C—R
C=O
O
^-O
O
P
^-O
Anticodon

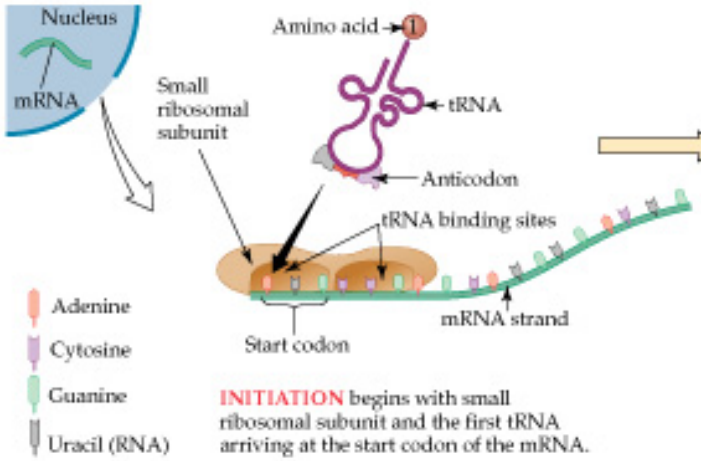
(a)



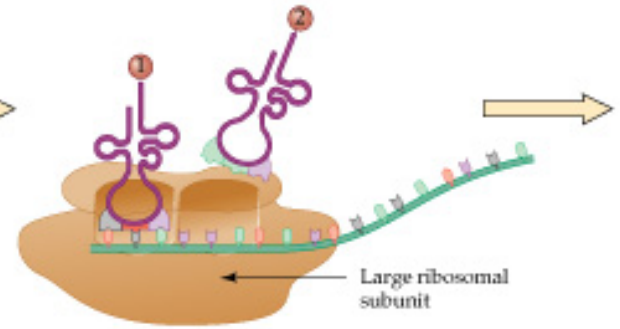
(b)


Amino acid binding site
Anticodon

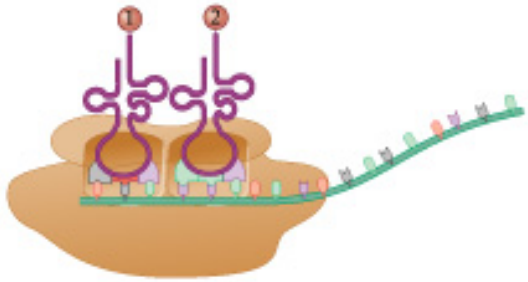
(c)



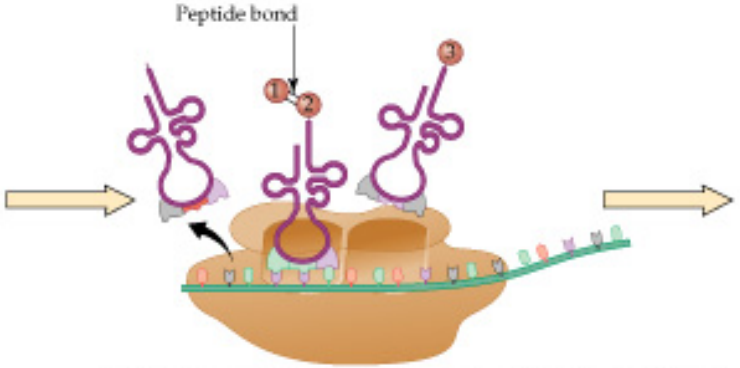
INITIATION begins with small ribosomal subunit and the first tRNA arriving at the start codon of the mRNA.



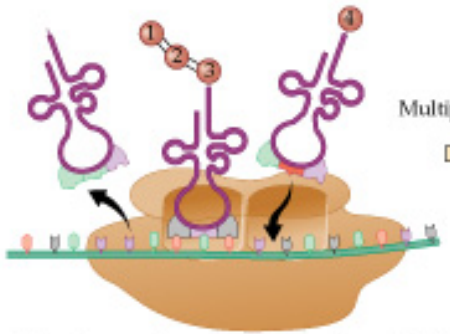
The small and large ribosomal units interlock around the mRNA, with the first tRNA in place at the start codon, completing the initiation stage. The tRNA with amino acid 2 is approaching.



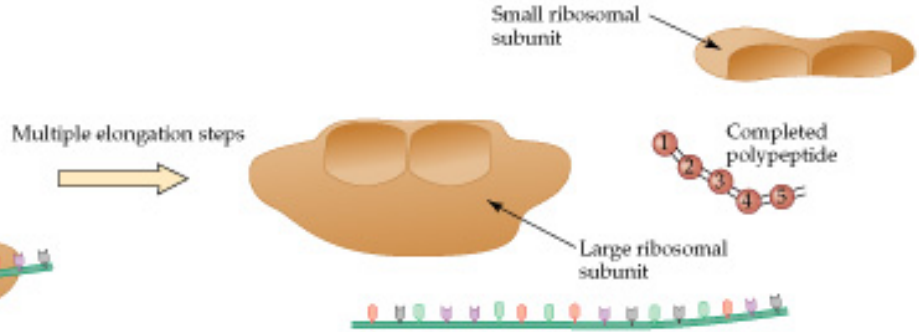
ELONGATION begins as the tRNA with amino acid 2 binds to its codon at the second site within the ribosome.



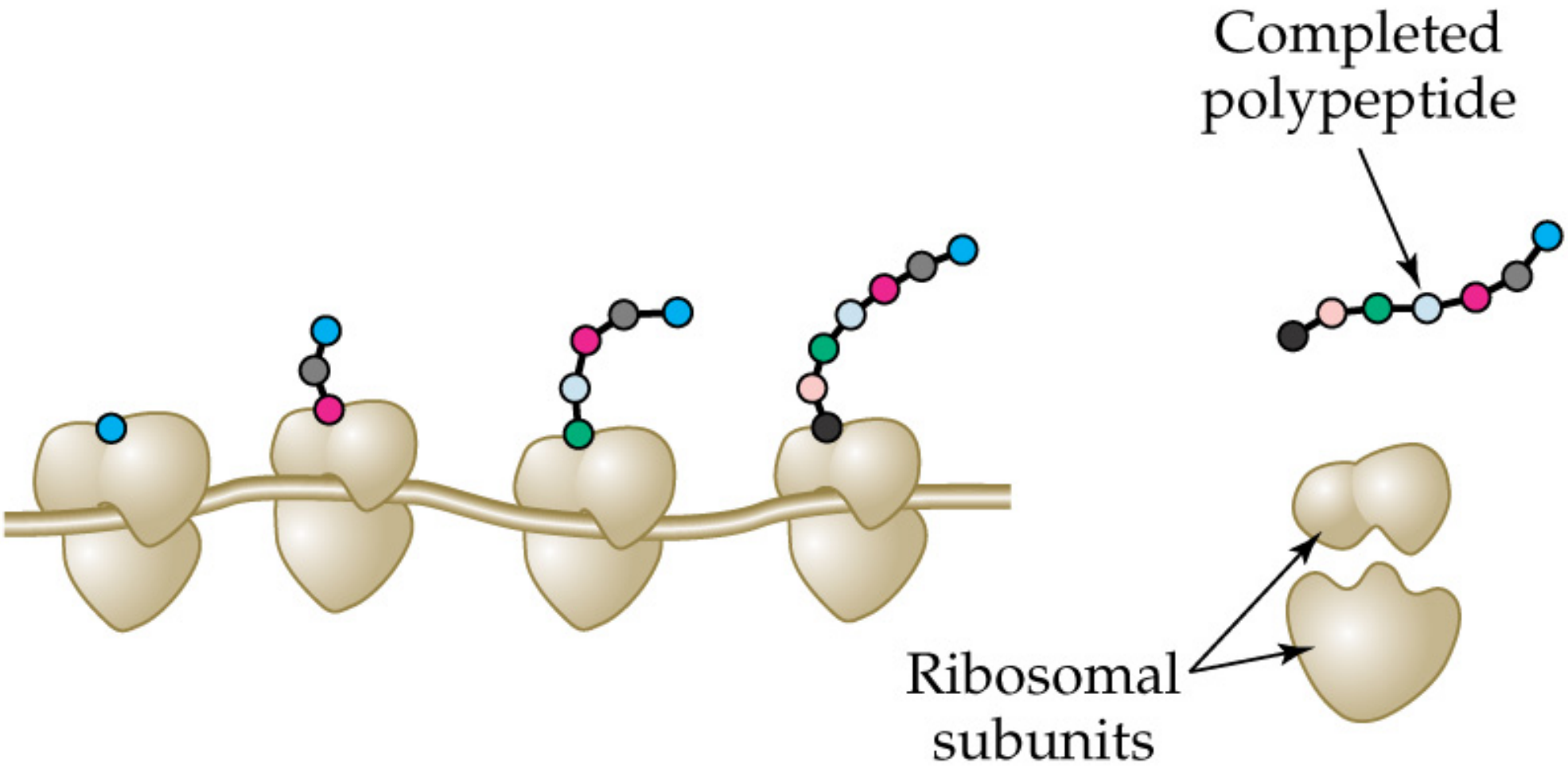
A peptide bond forms between amino acid 1 and 2, the first tRNA is released, the ribosome moves one codon to the right, and the tRNA with amino acid 3 is arriving.

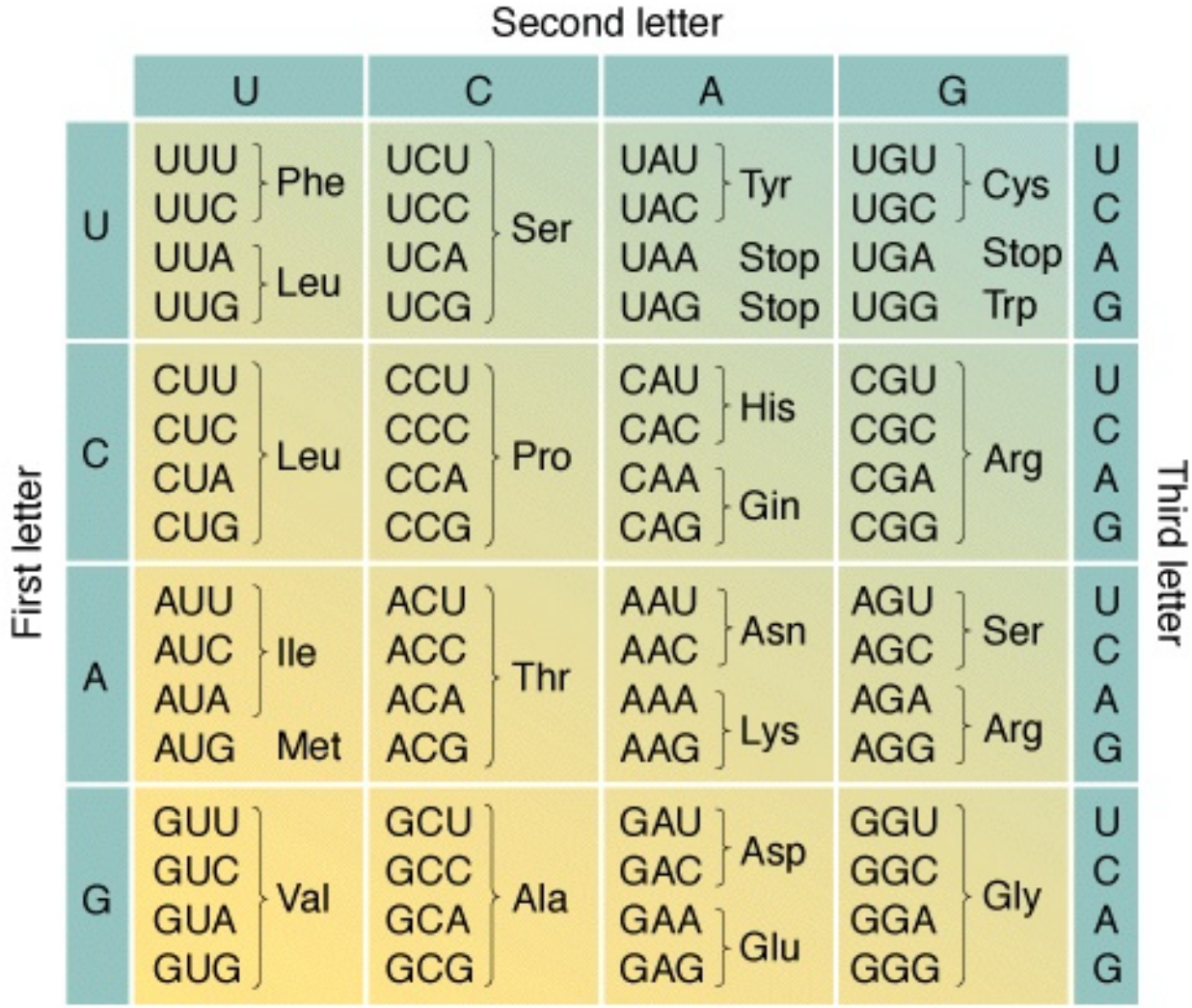


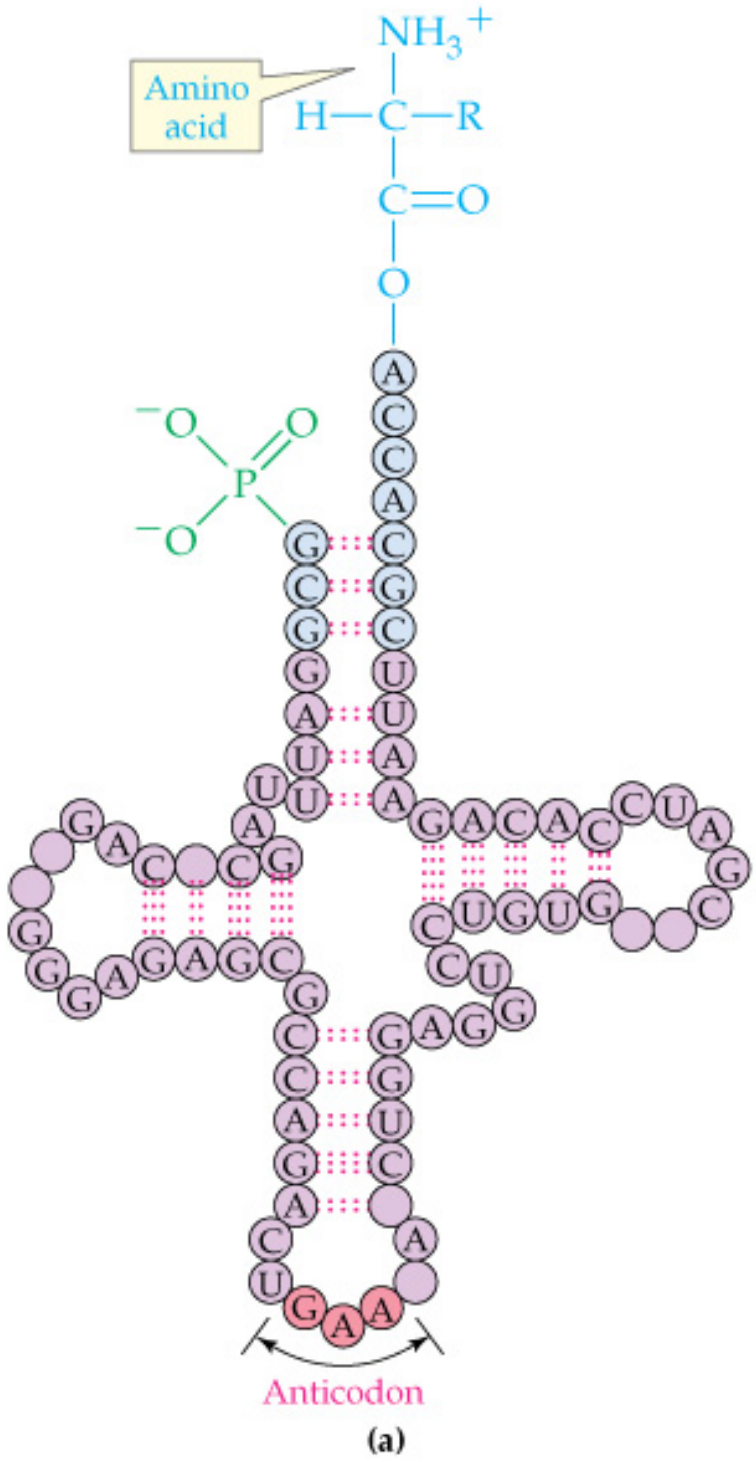
Elongation continues with three amino acids in the growing chain and the fourth one arriving with its tRNA



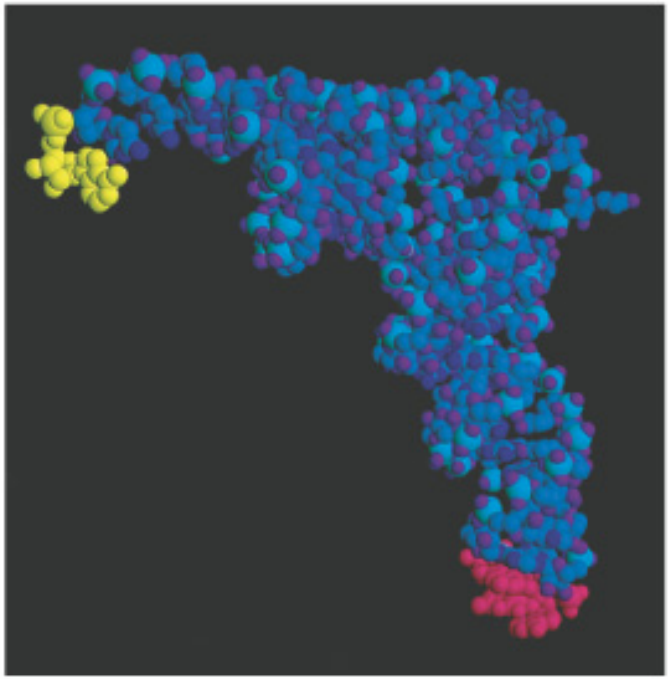
TERMINATION occurs after the elongation steps have been repeated until the stop codon is reached. The ribosomal units, the mRNA, and the polypeptide separate.


Completed
polypeptide
Ribosomal
subunits

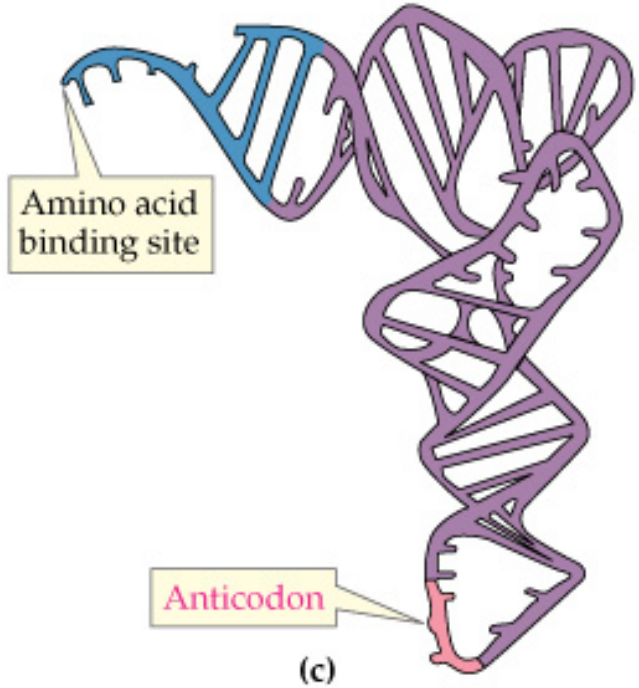

Second letter
U
C
A
G
First letter
U
C
A
G
UUU Phe
UUC
UUA Leu
UUG
UCU Ser
UCC
UCA
UCG
UAU Tyr
UAC
UAA Stop
UAG Stop
UGU Cys
UGC
UGA Stop
UGG Trp
CUU Leu
CUC
CUA
CUG
CCU Pro
CCC
CCA
CCG
CAU His
CAC
CAA Gln
CAG
CGU Arg
CGC
CGA
CGG
AUU Ile
AUC
AUA
AUG Met
ACU Thr
ACC
ACA
ACG
AAU Asn
AAC
AAA Lys
AAG
AGU Ser
AGC
AGA Arg
AGG
GUU Val
GUC
GUA
GUG
GCU Ala
GCC
GCA
GCG
GAU Asp
GAC
GAA Glu
GAG
GGU Gly
GGC
GGA
GGG
Third letter
U C A G


Amino acid
NH_3^+
H—C—R
C=O
O
^-O
O
P
^-O
Anticodon

(a)

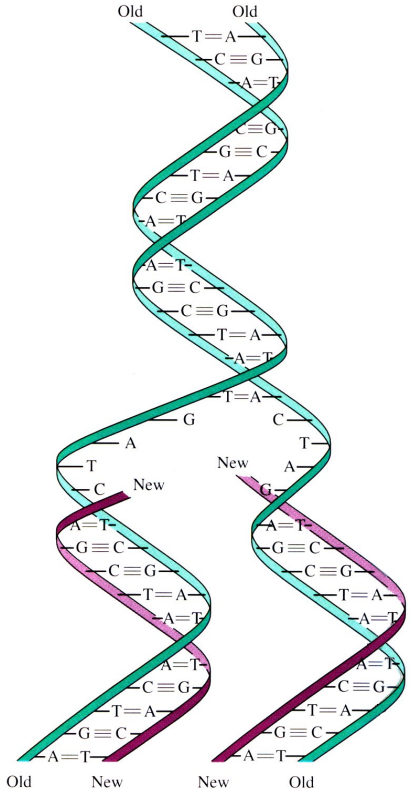


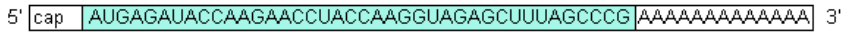
(b)


Amino acid binding site
Anticodon

(c)

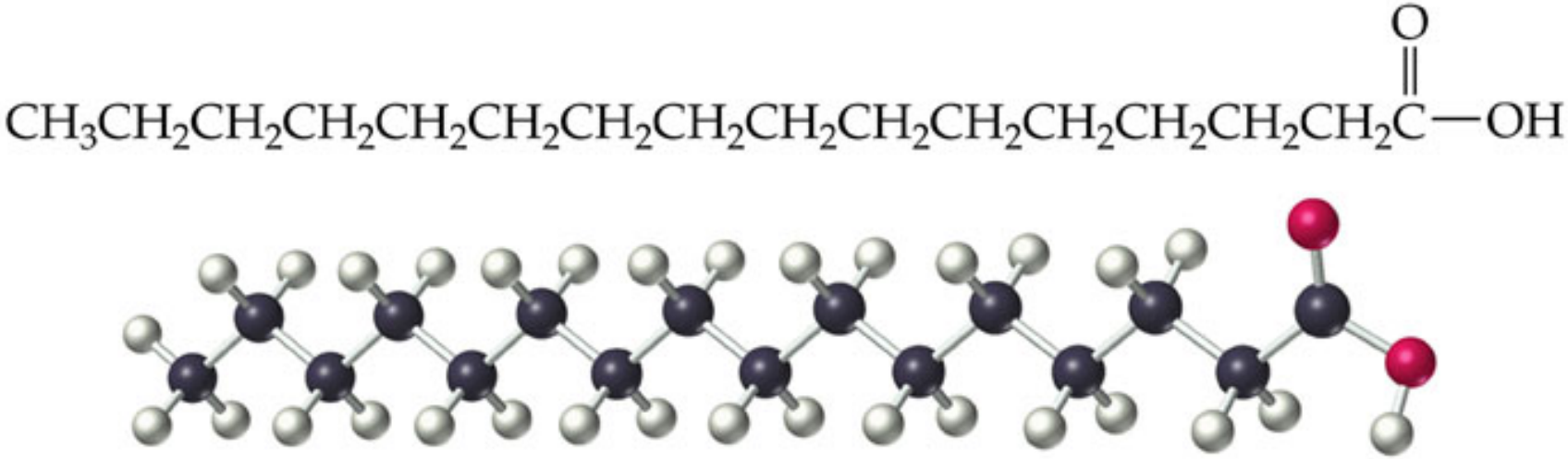
Self-Assembly Process in Nature



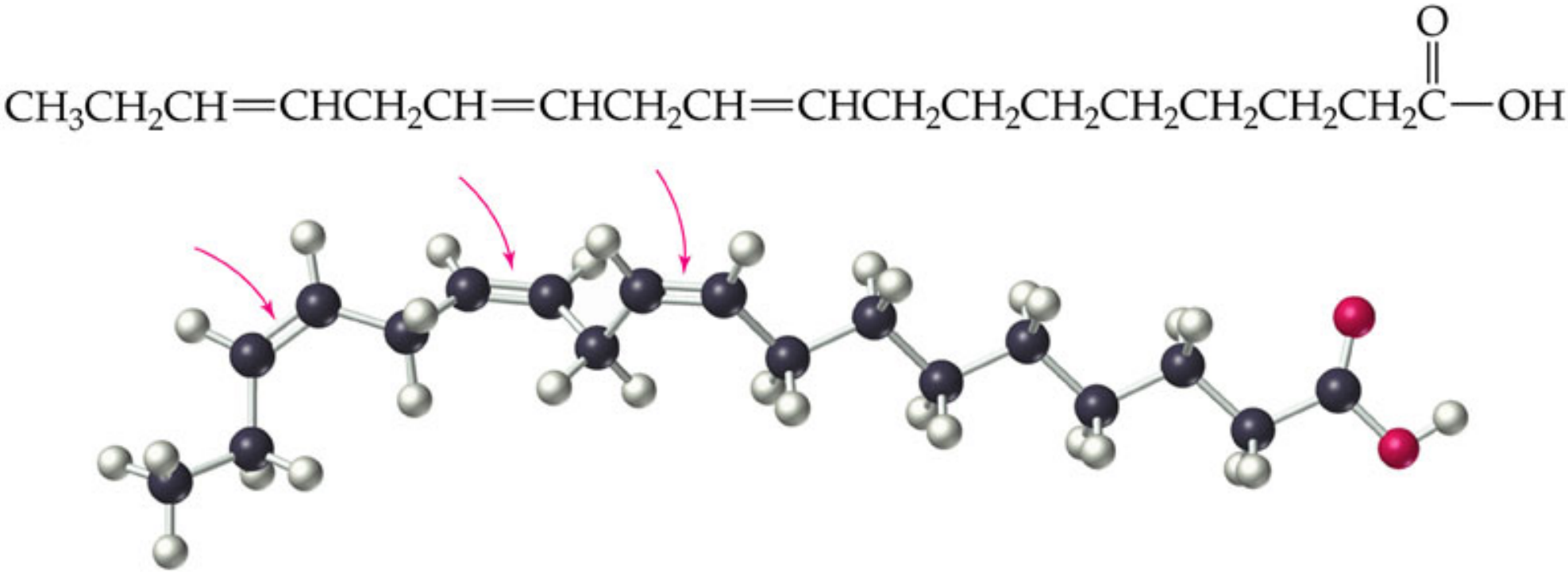


Lipid

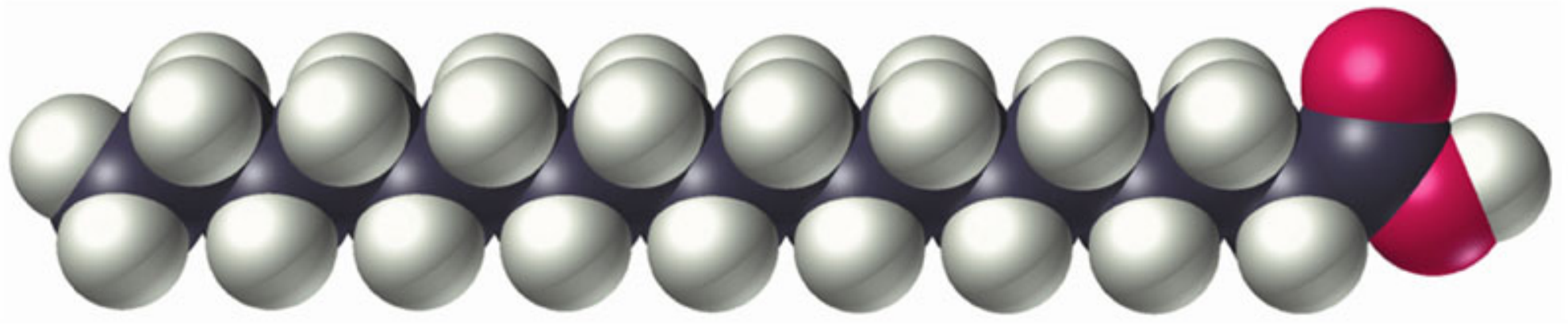
- ***Lipids*** are naturally occurring molecules from plants or animals that are soluble in nonpolar organic solvents.
- Lipid molecules contain large hydrocarbon portion and not many polar functional group, which accounts for their solubility behavior.



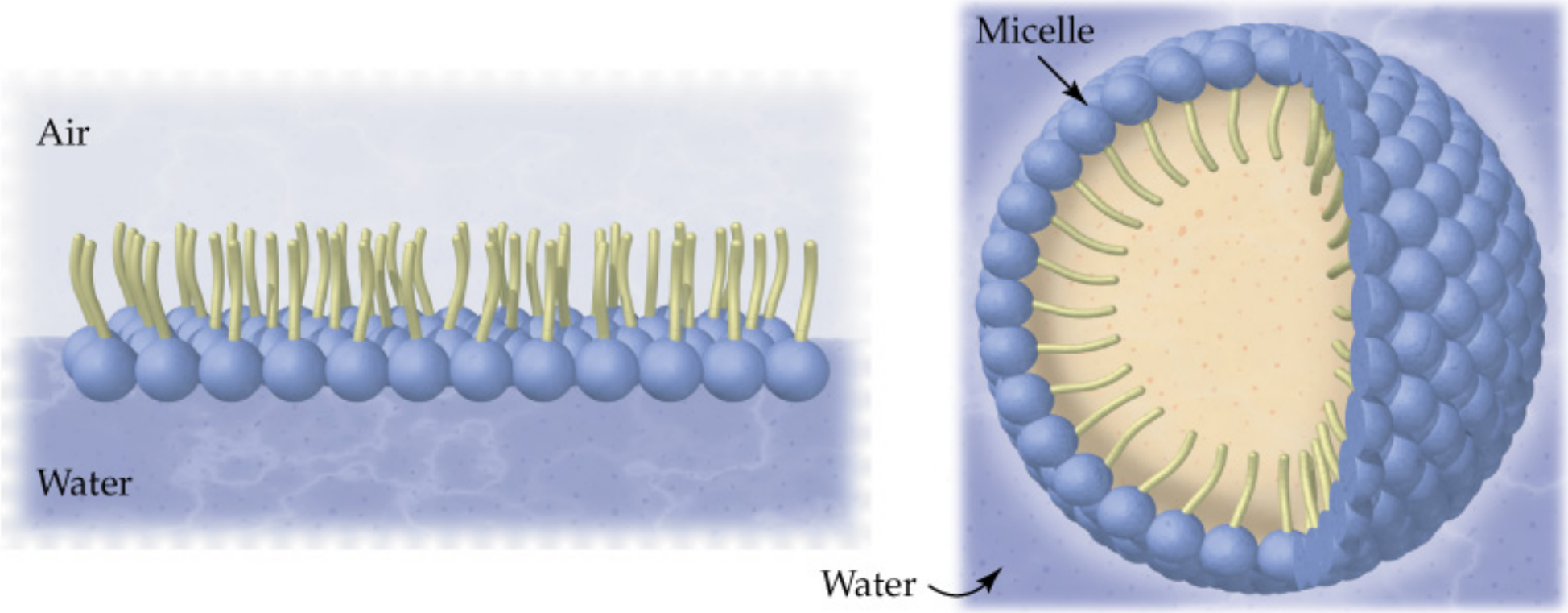
A saturated fatty acid
(palmitic acid)

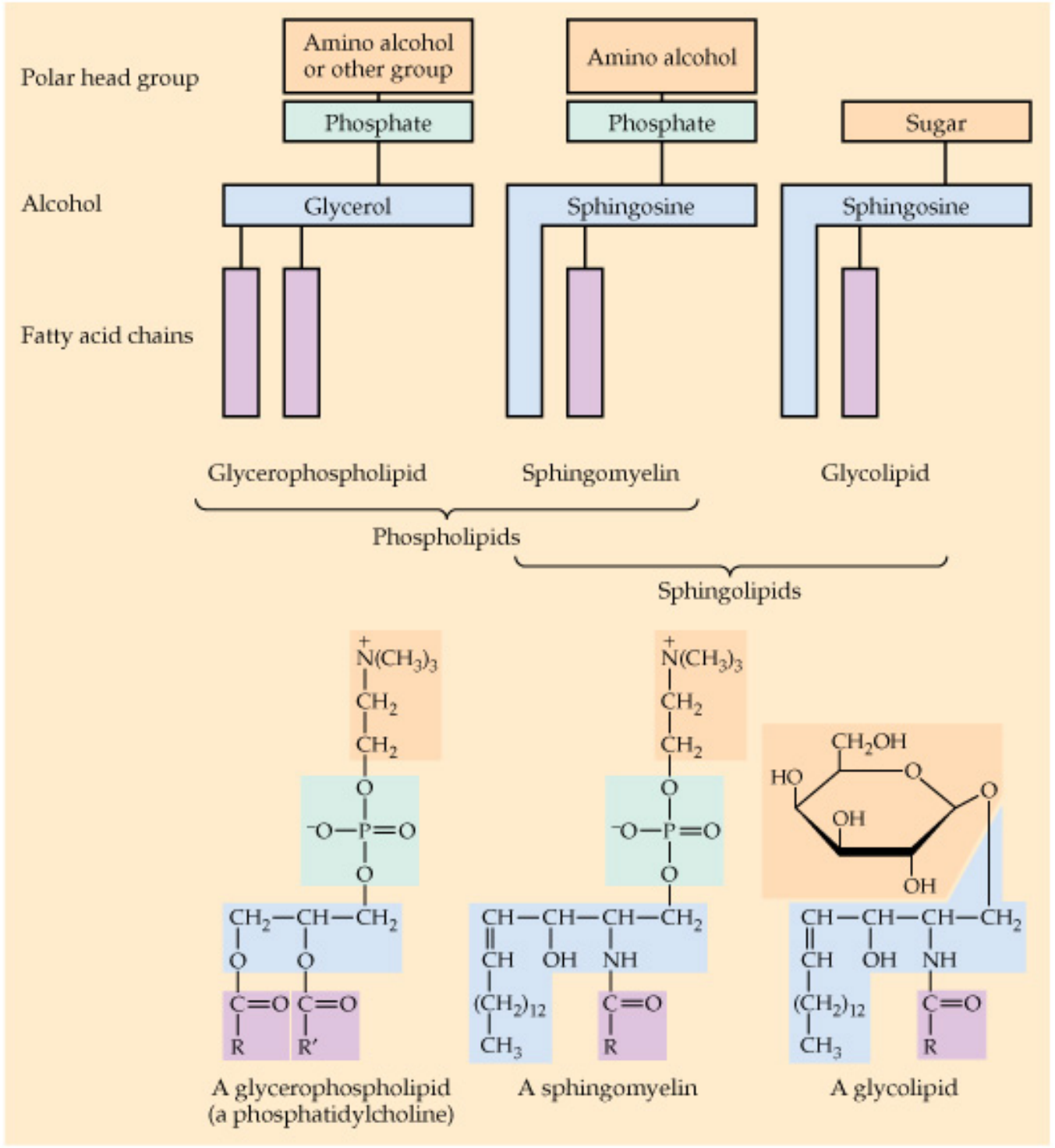


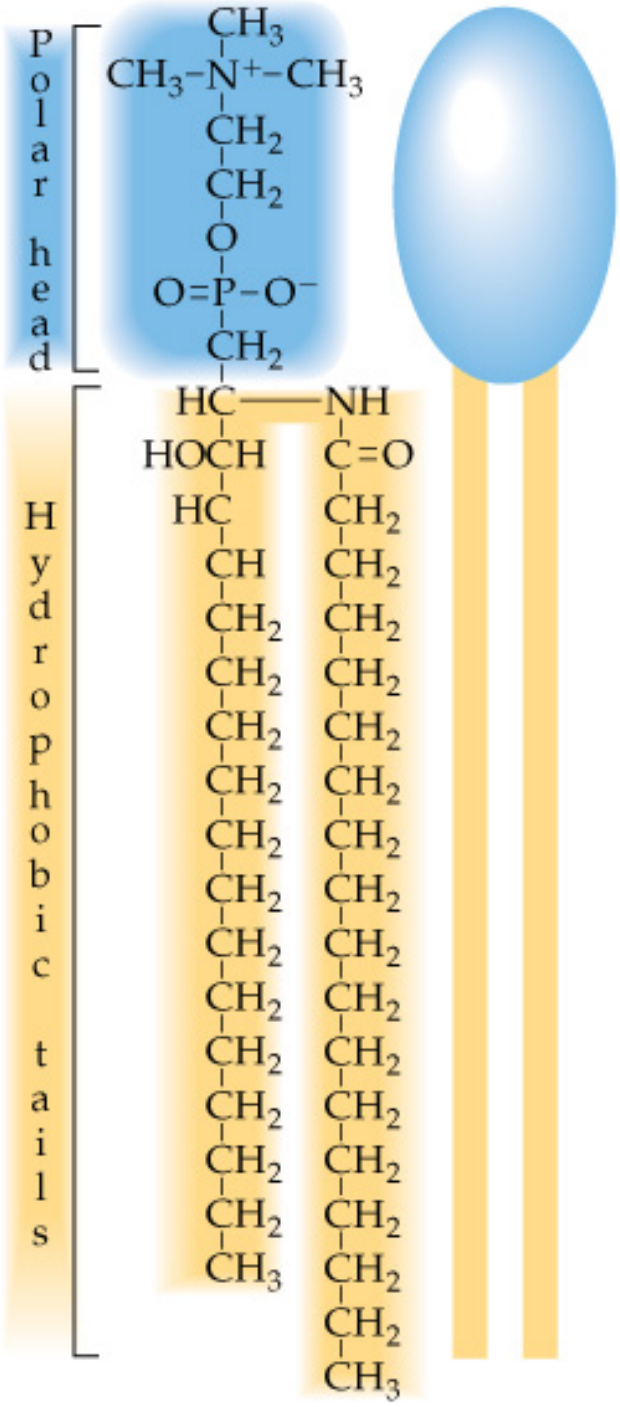
A *cis* unsaturated fatty acid
(linolenic acid)



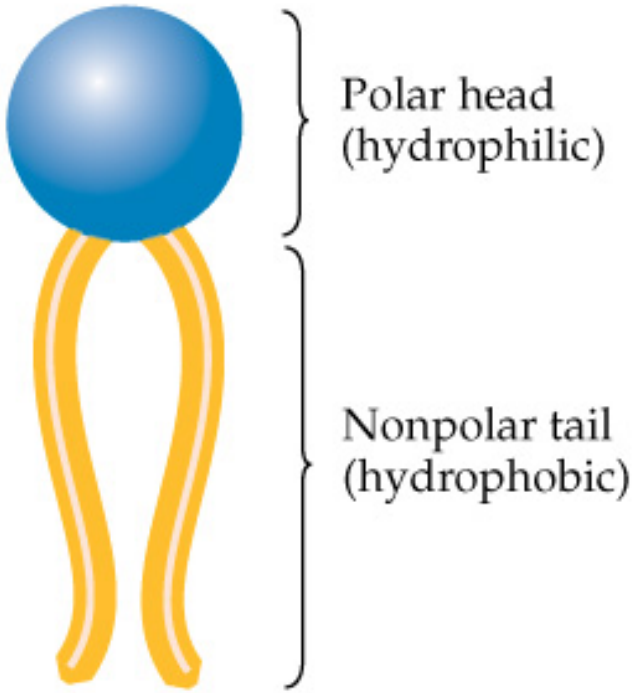
Stearic acid, an 18-carbon saturated fatty acid


Air
Water
Micelle
Water

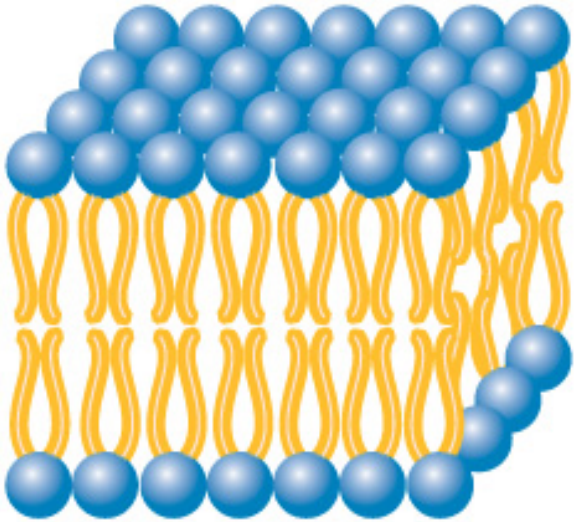

Polar head group
Alcohol
Fatty acid chains
Amino alcohol or other group
Phosphate
Glycerol
Amino alcohol
Phosphate
Sphingosine
Sugar
Sphingosine
Glycerophospholipid
Sphingomyelin
Glycolipid
Phospholipids
Sphingolipids
A glycerophospholipid (a phosphatidylcholine)
A sphingomyelin
A glycolipid



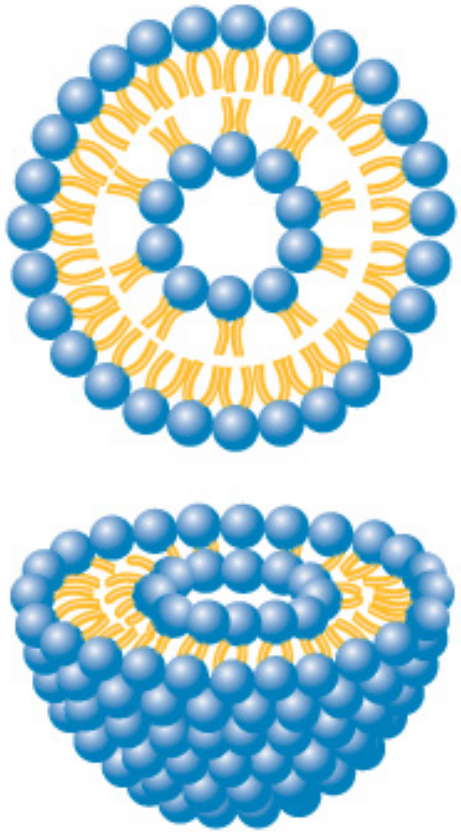
A sphingomyelin



Membrane lipid



Lipid bilayer

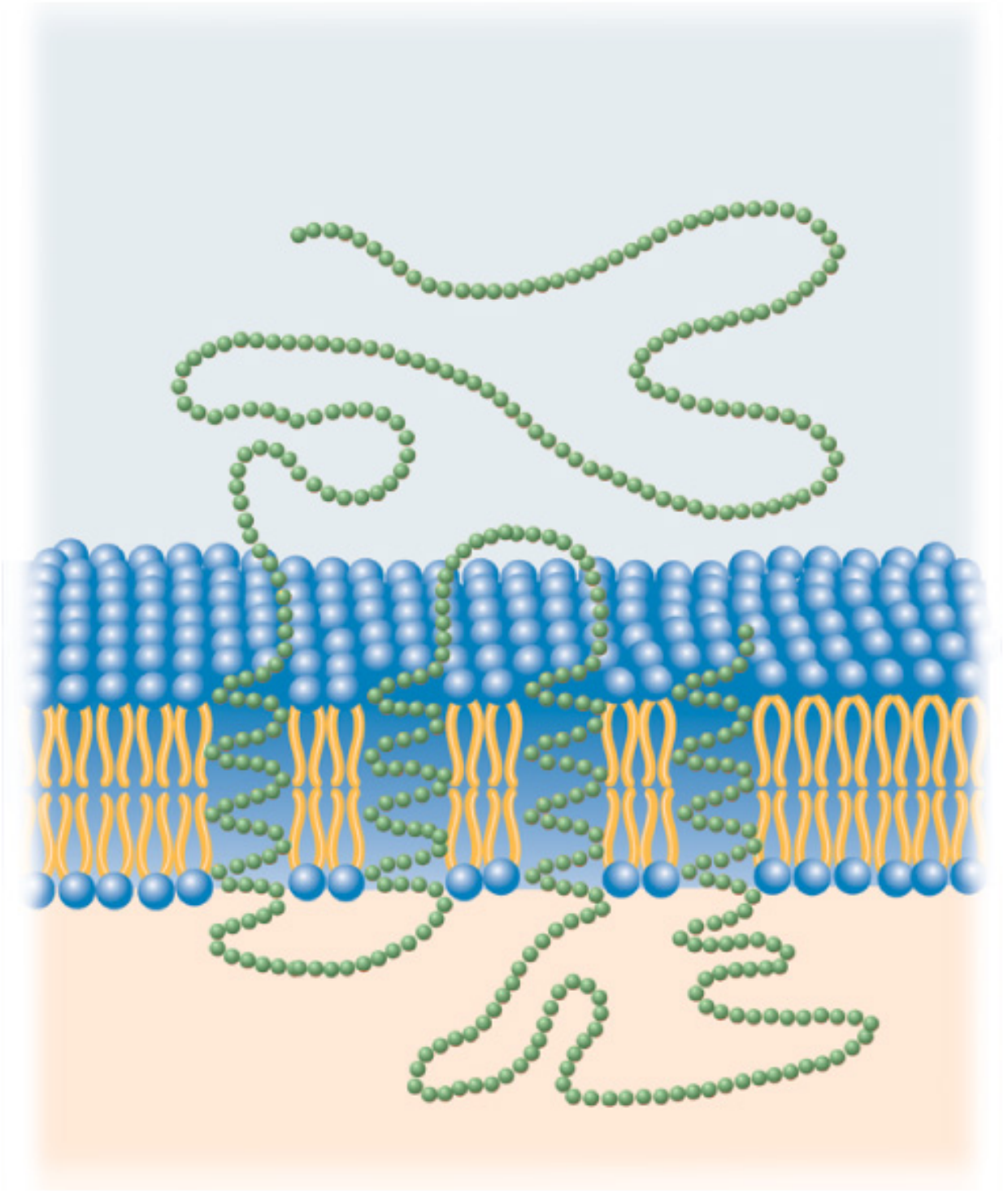


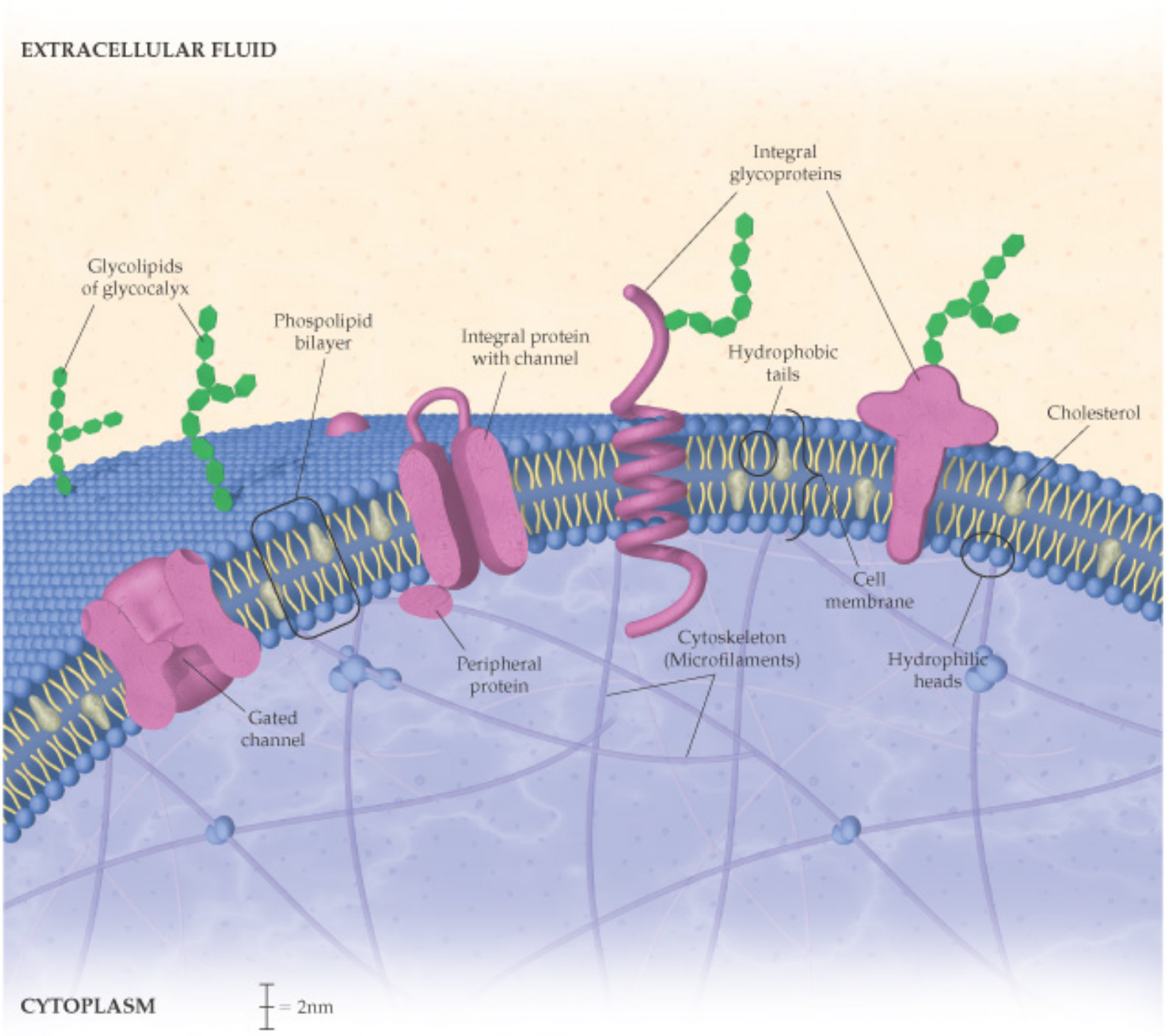
Liposome

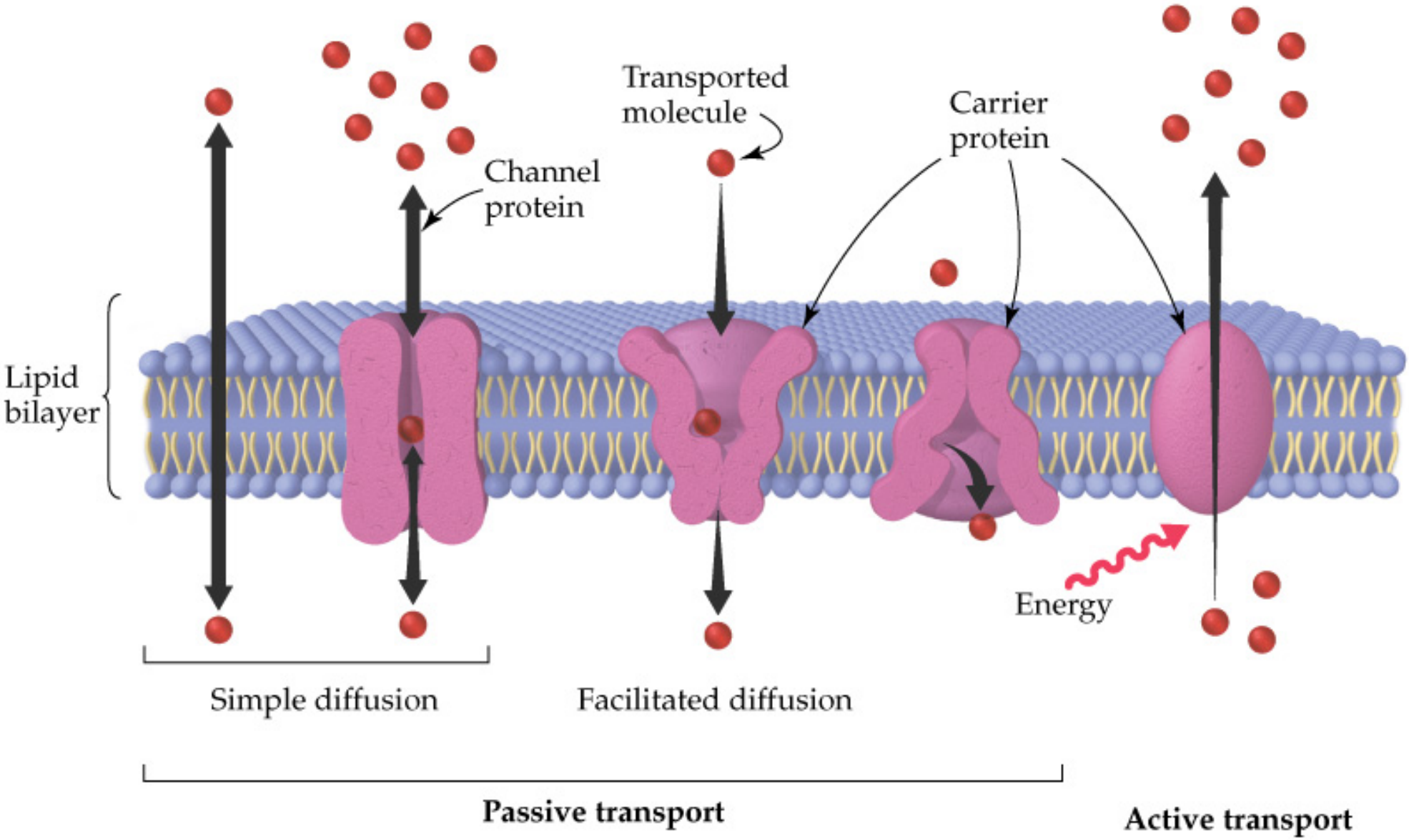
Properties of cell membranes:

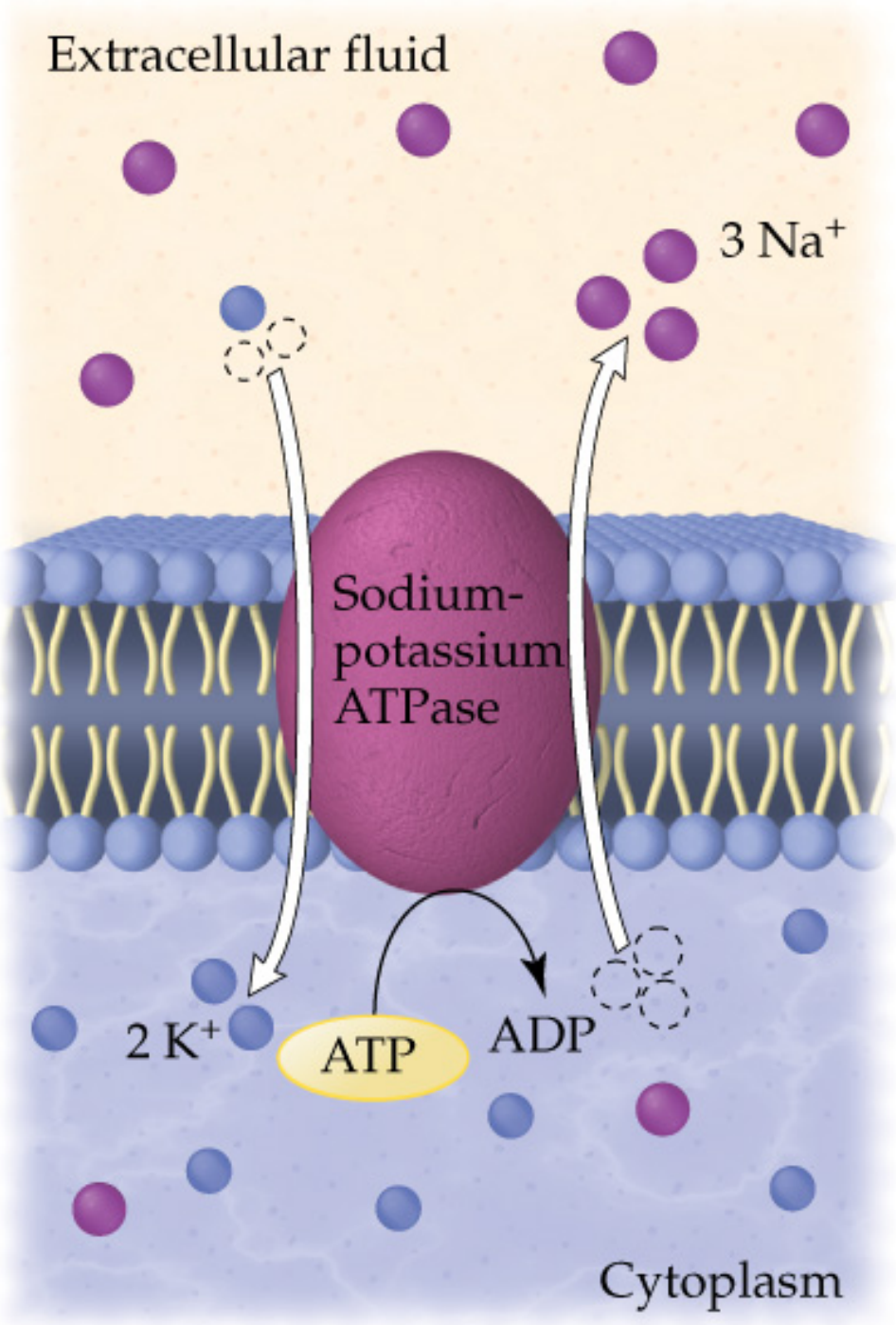
- Cell membranes are composed of a fluid like phospholipid bilayer.
- The bilayer incorporates cholesterol, proteins, and glycolipids.
- Small nonpolar molecules cross by diffusion through the lipid bilayer.
- Small ions and polar molecules diffuse through the aqueous media in protein pores.
- Glucose and certain other substances cross with the aid of proteins without energy input.
- Na^+, K^+, and other substances that maintain concentration gradients inside and outside the cell cross with expenditure of energy and the aid of proteins.

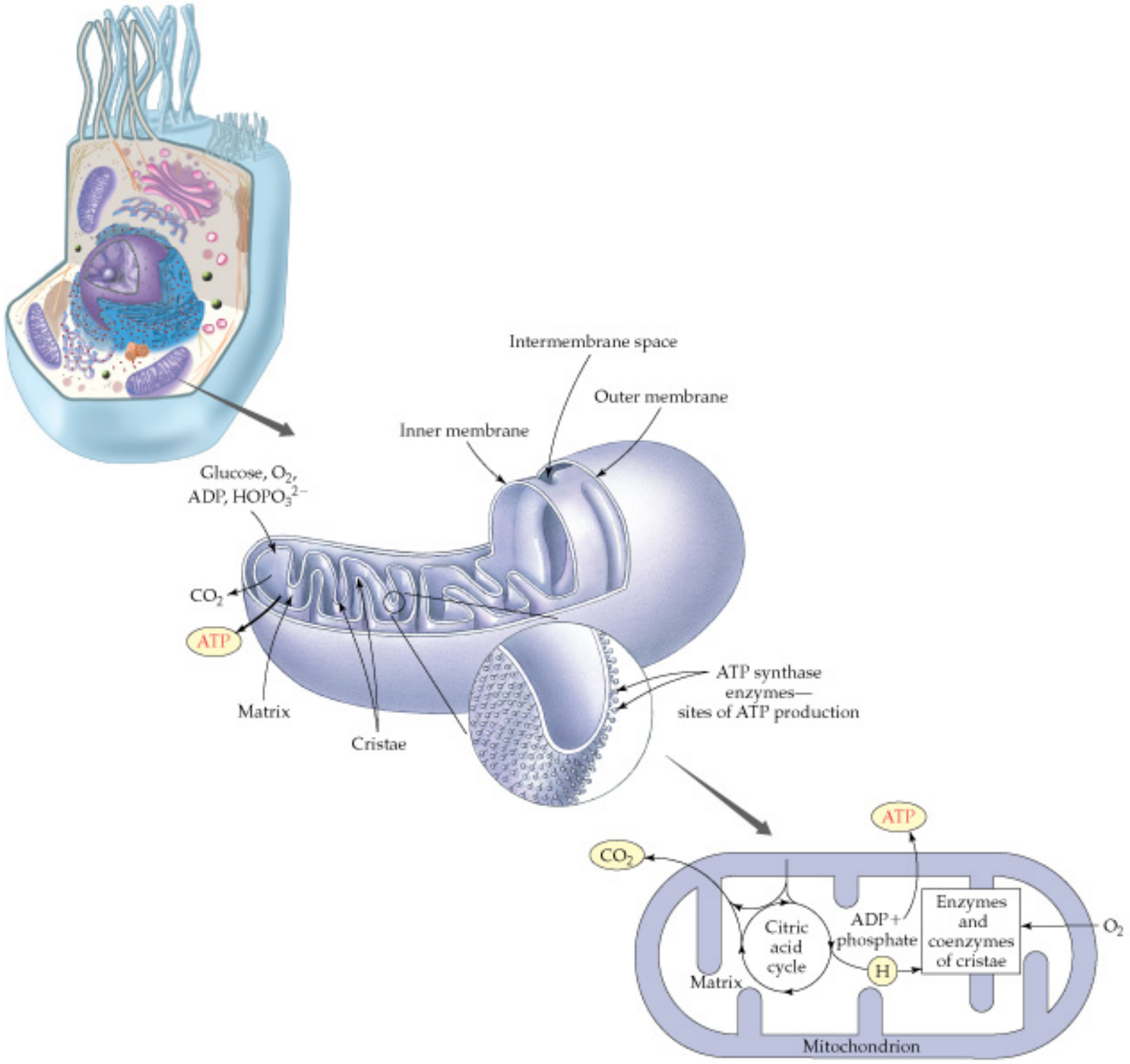
- Small ions and polar molecules diffuse through the aqueous media in protein pores.
- Glucose and certain other substances cross with the aid of proteins without energy input.
- Na^+, K^+, and other substances that maintain concentration gradients inside and outside the cell cross with expenditure of energy and the aid of proteins.




EXTRACELLULAR FLUID
Integral glycoproteins
Glycolipids of glycocalyx
Phospolipid bilayer
Integral protein with channel
Hydrophobic tails
Cholesterol
Cell membrane
Cytoskeleton (Microfilaments)
Peripheral protein
Hydrophilic heads
Gated channel
CYTOPLASM
= 2nm


Transported molecule
Carrier protein
Channel protein
Lipid bilayer
Energy
Simple diffusion
Facilitated diffusion
Passive transport
Active transport

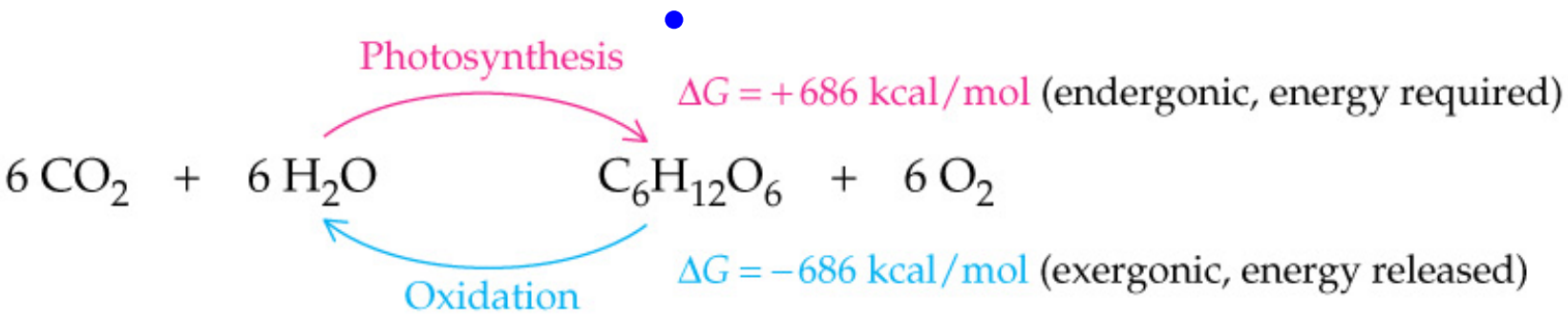

Extracellular fluid
3 Na+
Sodium-
potassium
ATPase
2 K+
ATP
ADP
Cytoplasm


Intermembrane space
Outer membrane
Inner membrane
Glucose, O_2, ADP, $HOPO_3^{2-}$
CO_2
ATP
Matrix
Cristae
ATP synthase enzymes— sites of ATP production
ATP
CO_2
Citric acid cycle
ADP + phosphate
H
Enzymes and coenzymes of cristae
O_2
Matrix
Mitochondrion

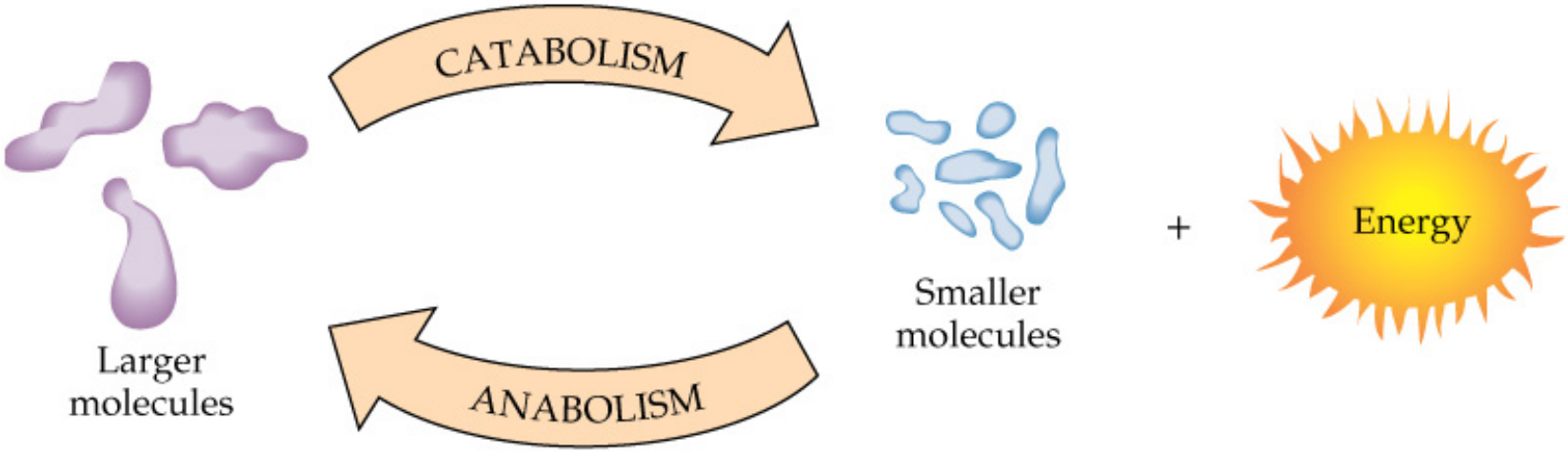
Energy and Biochemical Reactions

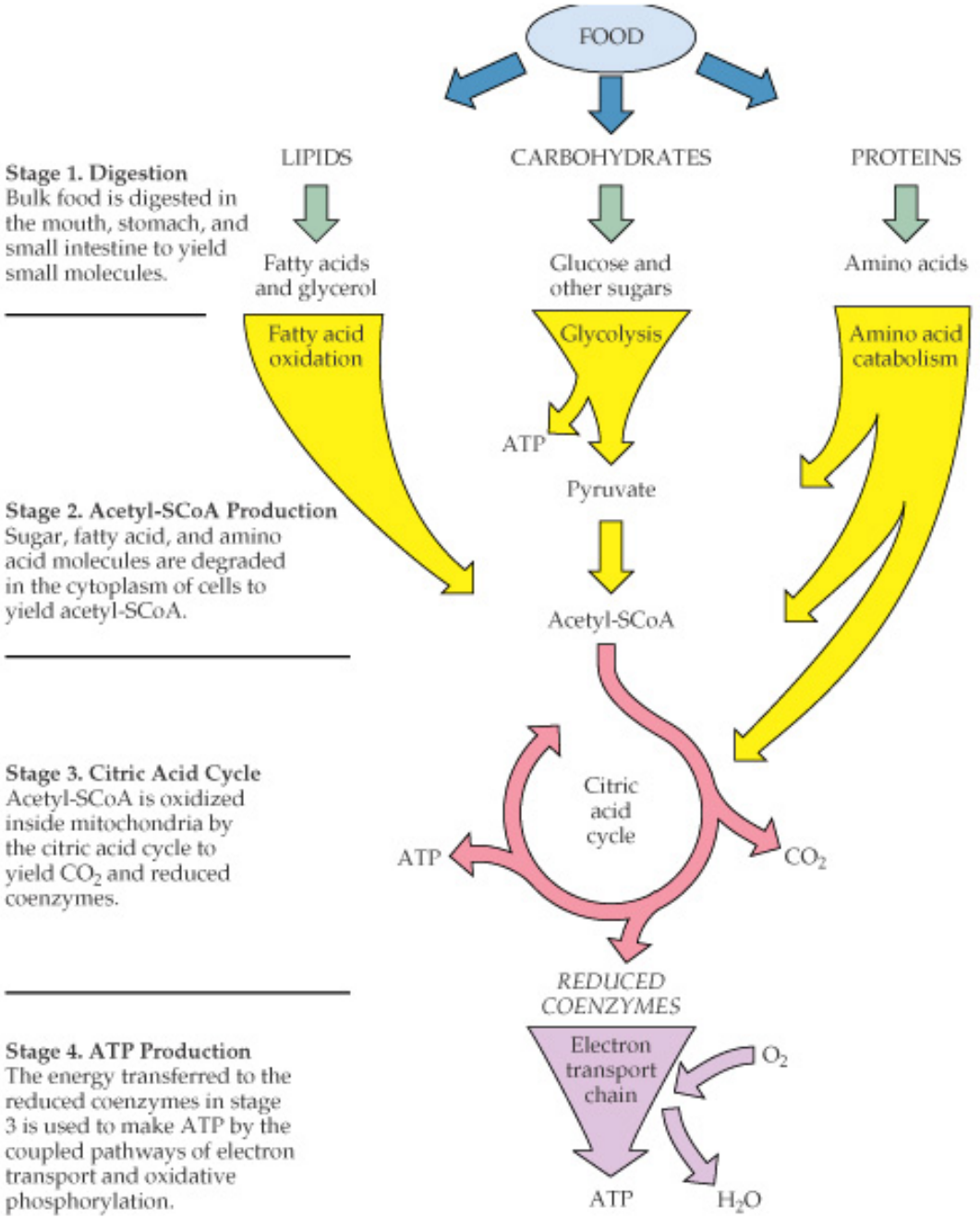
- Reactions in living organisms are similar to reactions in a chemical laboratory.
- Spontaneous reactions, those are favorable in the forward direction, release free energy and the energy released is available to do work.
- Spontaneous reactions , also known as *exergonic* reactions, are the source of our biochemical energy.
- Products of exergonic reactions are more stable than the reactants and the free energy change ΔG has a negative value.

- *Photosynthesis* in plants, converts CO_2 and H_2O to glucose plus O_2 which is the reverse of oxidation of glucose. The sun provides the necessary external energy for photosynthesis (686 kcal of free energy per mole of glucose formed).



- The *mitochondria* is often called the cell's power plants. Within the mitochondria, small molecules are broken down to provide the energy for an organism and also the principle energy carrying molecule adenosine triphosphate (ATP) is produced.


CATABOLISM
ANABOLISM
Larger molecules
Smaller molecules
+
Energy



Stage 1. Digestion
Bulk food is digested in the mouth, stomach, and small intestine to yield small molecules.

Stage 2. Acetyl-SCoA Production
Sugar, fatty acid, and amino acid molecules are degraded in the cytoplasm of cells to yield acetyl-SCoA.

Stage 3. Citric Acid Cycle
Acetyl-SCoA is oxidized inside mitochondria by the citric acid cycle to yield CO_2 and reduced coenzymes.

Stage 4. ATP Production
The energy transferred to the reduced coenzymes in stage 3 is used to make ATP by the coupled pathways of electron transport and oxidative phosphorylation.

ATP and Energy Transfer

- Adenosine triphosphate (ATP) transport energy in living organisms.
- ATP has three $-PO_3^-$ groups.
- Removal of one of the $-PO_3^-$ groups from ATP by hydrolysis produces adenosine diphosphate (ADP). Since this reaction is an exergonic process, it releases energy.
- The reverse of ATP hydrolysis reaction is known as phosphorylation reaction. Phosphorylation reactions are endergonic.

•Biochemical energy production, transport, and use all depends on the ATP $\rightleftharpoons$ ADP interconversions.

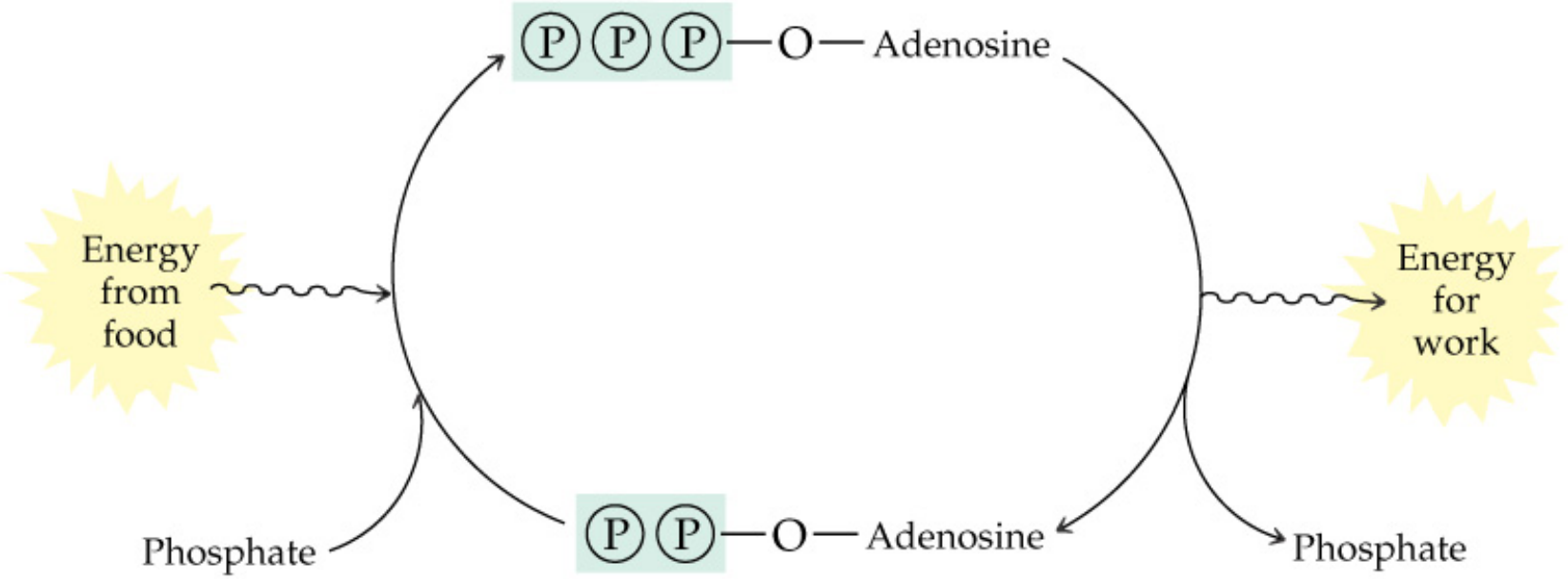
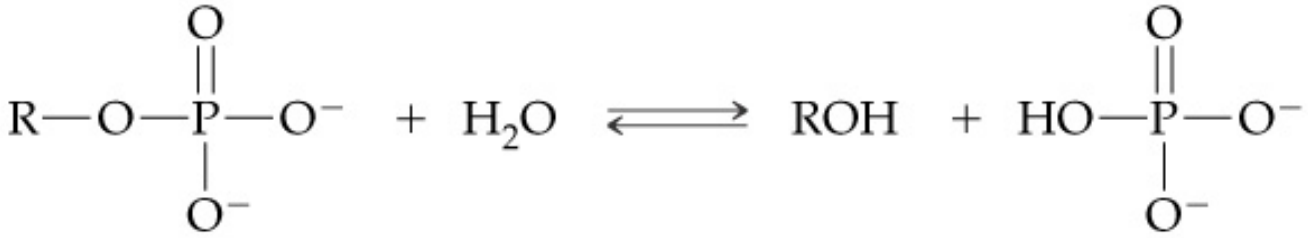


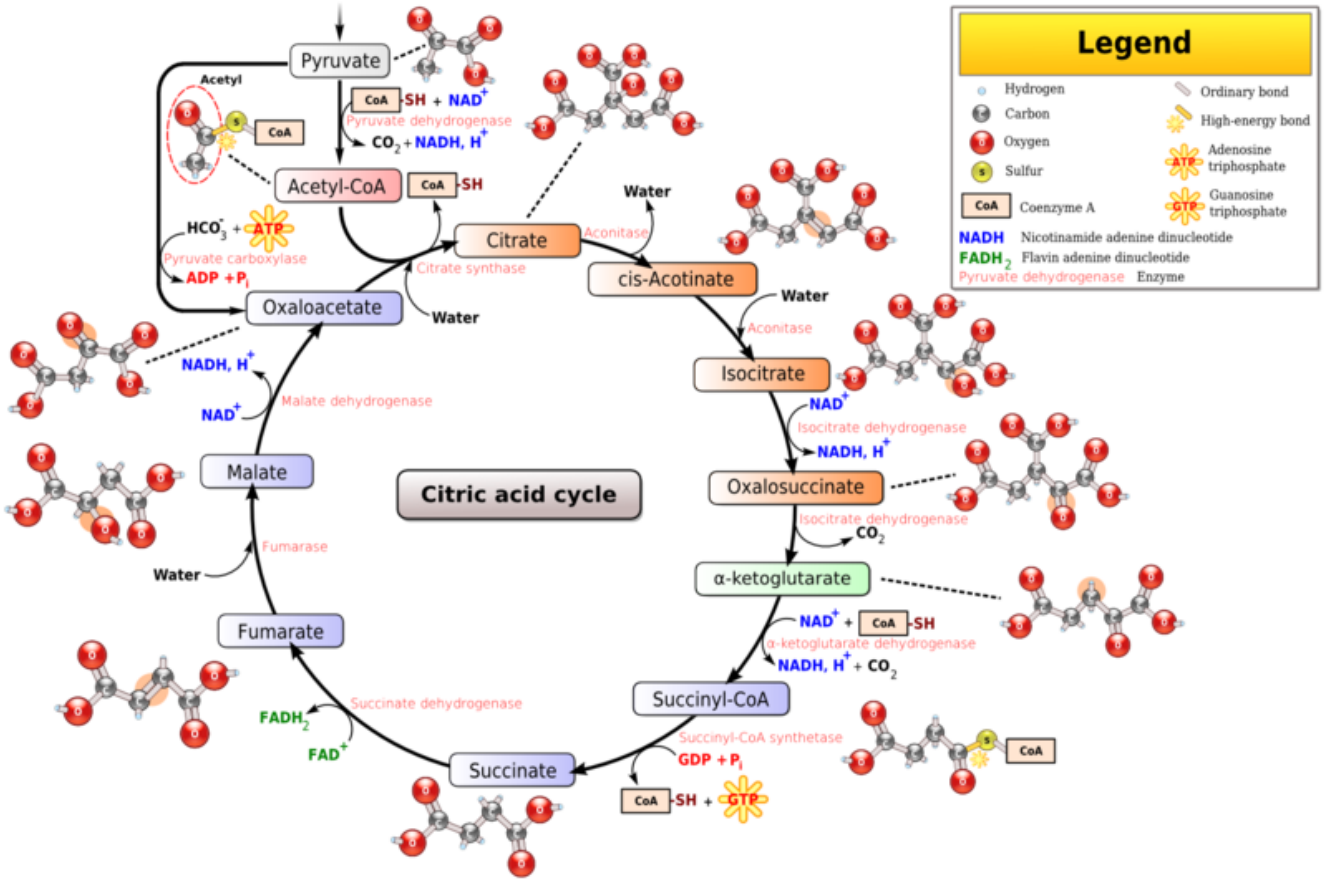
TABLE 21.1 Free Energies of Hydrolysis of Some Phosphates



Compound Name	Function	ΔG (kcal/mol)
Phosphoenol pyruvate	Final intermediate in conversion of glucose to pyruvate (glycolysis)—stage 2, Figure 21.5	−14.8
1, 3-Bisphosphoglycerate	Another intermediate in glycolysis	−11.8
Creatine phosphate	Energy storage in muscle cells	−10.3
ATP (⟶ ADP)	Principal energy carrier	−7.3
Glucose 1-phosphate	First intermediate in breakdown of carbohydrates stored as starch or glycogen	−5.0
Glucose 6-phosphate	First intermediate in glycolysis	−3.3
Fructose 6-phosphate	Second intermediate in glycolysis	−3.3

- A few enzymes continuously cycle between their oxidized and reduced forms

Coenzyme	As Oxidizing Agent	As Reducing Agent
Nicotinamide adenine dinucleotide	NAD^+	$NADH/H^+$
Nicotinamide adenine dinucleotide phosphate	$NADP^+$	$NADPH/H^+$
Flavin adenine dinucleotide	FAD	$FADH_2$
Flavin mononucleotide	FMN	$FMNH_2$

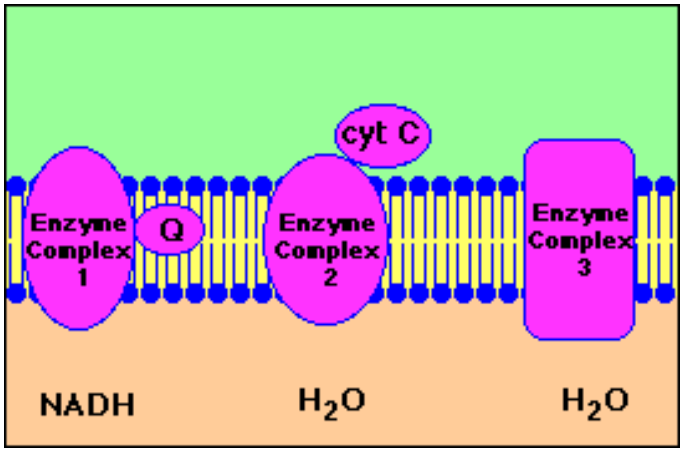


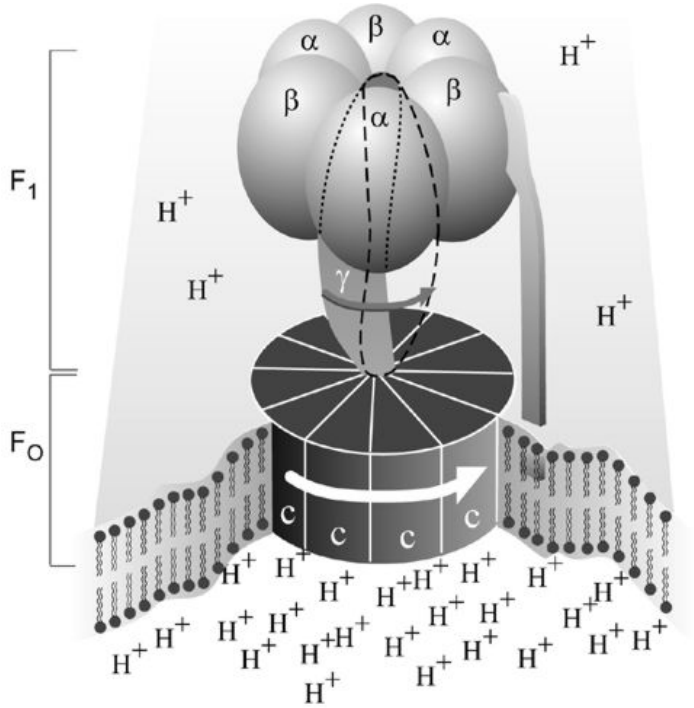
Acetyl-CoA + 3 NAD+ + FAD + GDP + Pi + 2H20
<==> CoASH + 3 NADH + FADH2 + GTP + 2CO2 + 3H

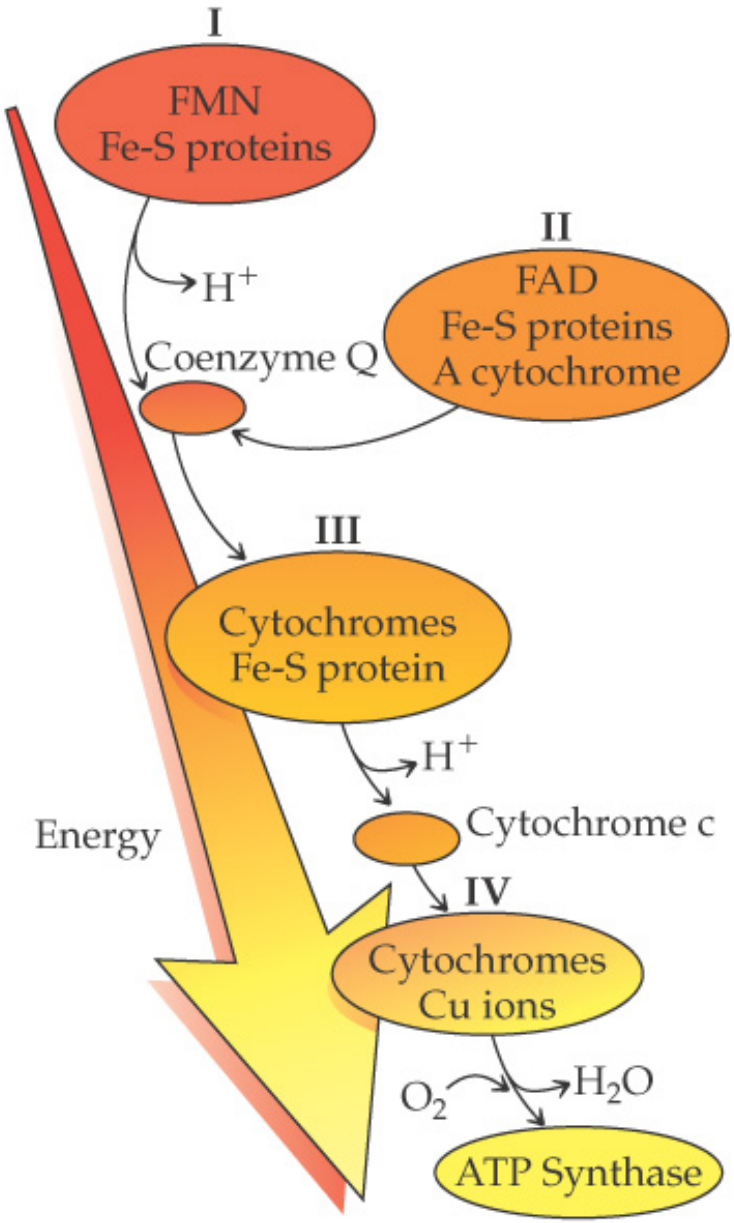
The citric acid cycle

The Electron-Transport Chain and ATP Production

- Electron transport chain: The series of biochemical reactions that passes electrons from reduced coenzymes to oxygen and is coupled to ATP formation. The electrons combine with the oxygen we breathe and with hydrogen ions from their surrounding to produce water.
- Electron transport involves four enzyme complexes held in fixed positions within the inner membrane of mitochondria and two electron carriers move from one complex to another.



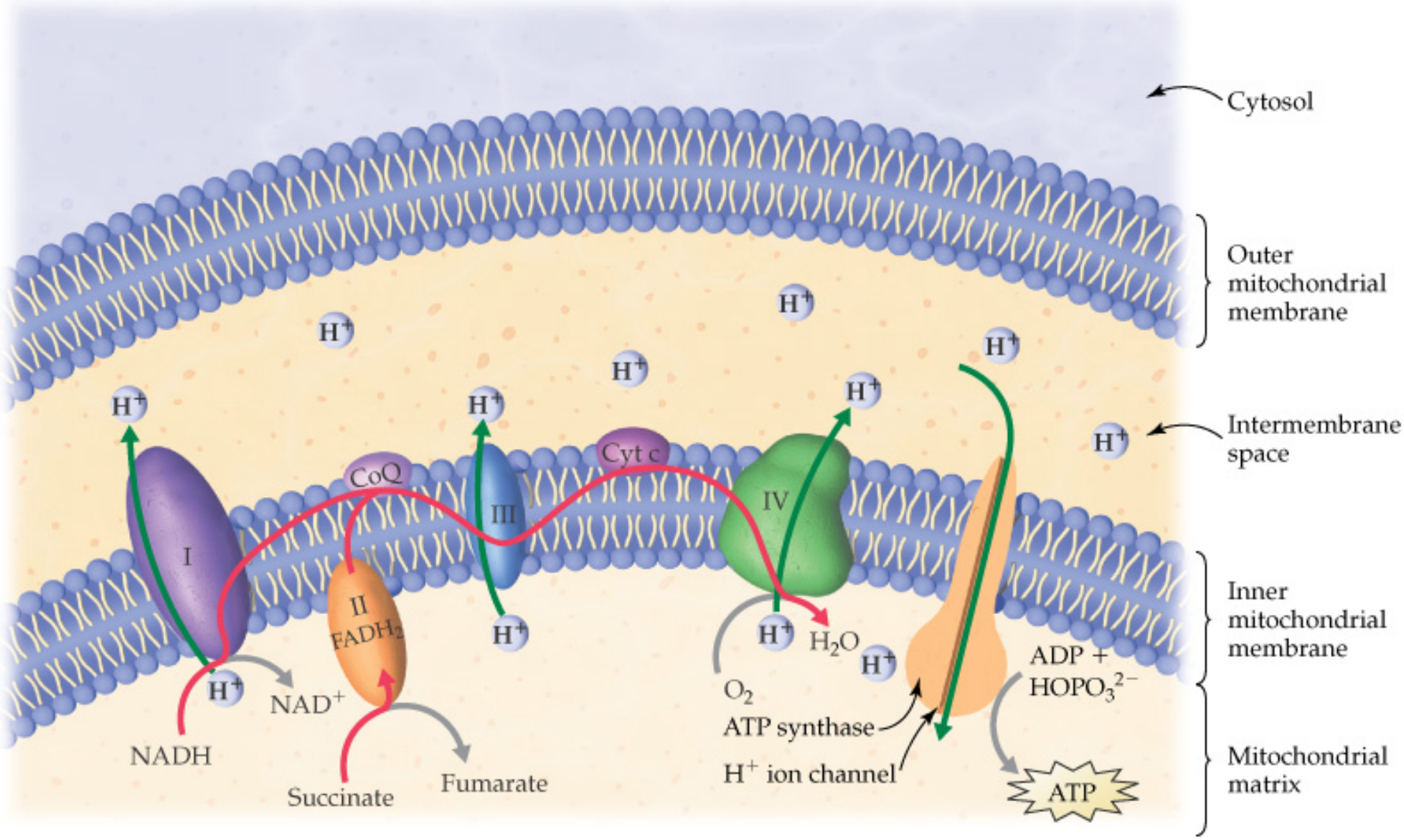


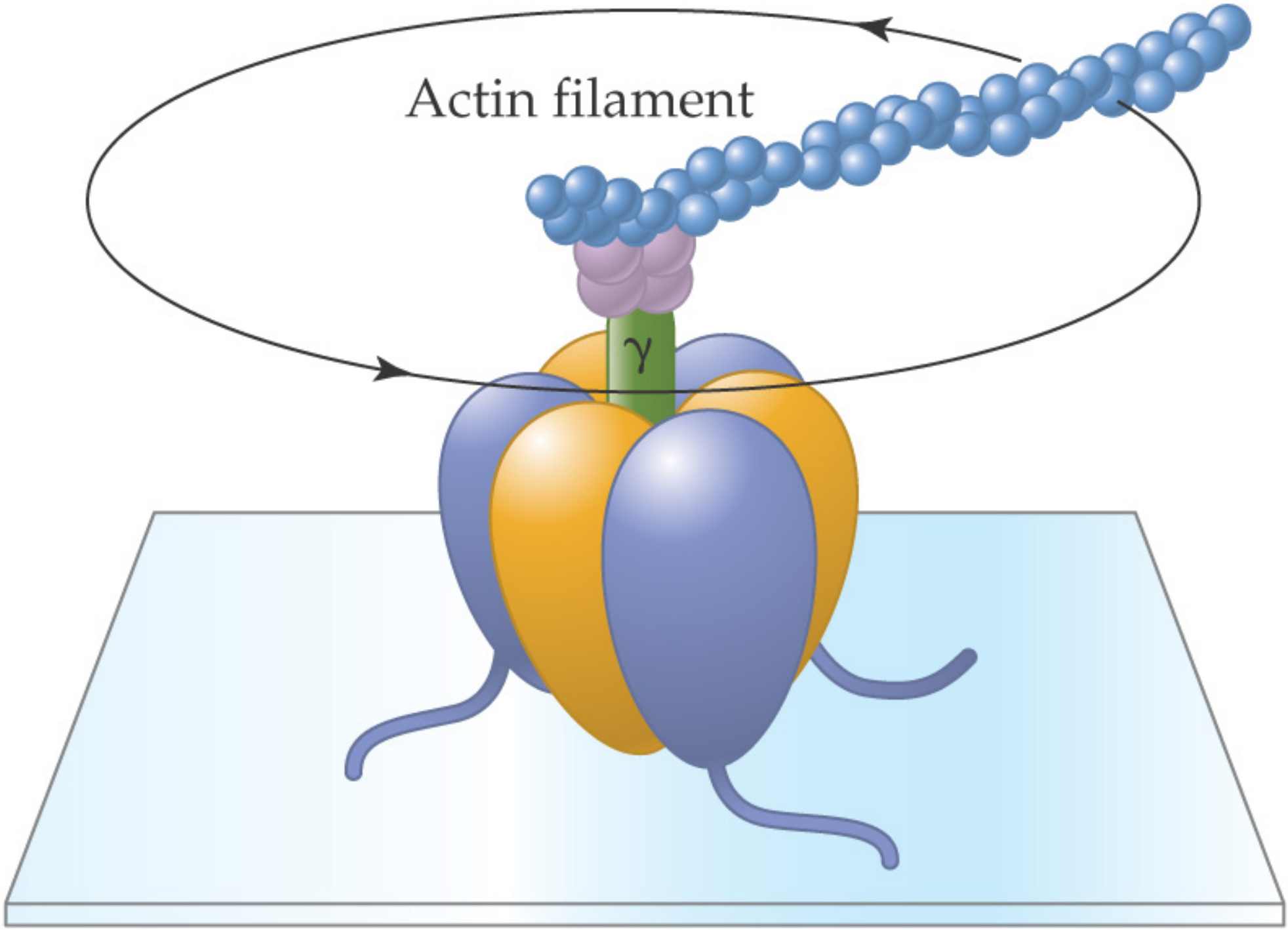


- Pathway of electrons in electron transport

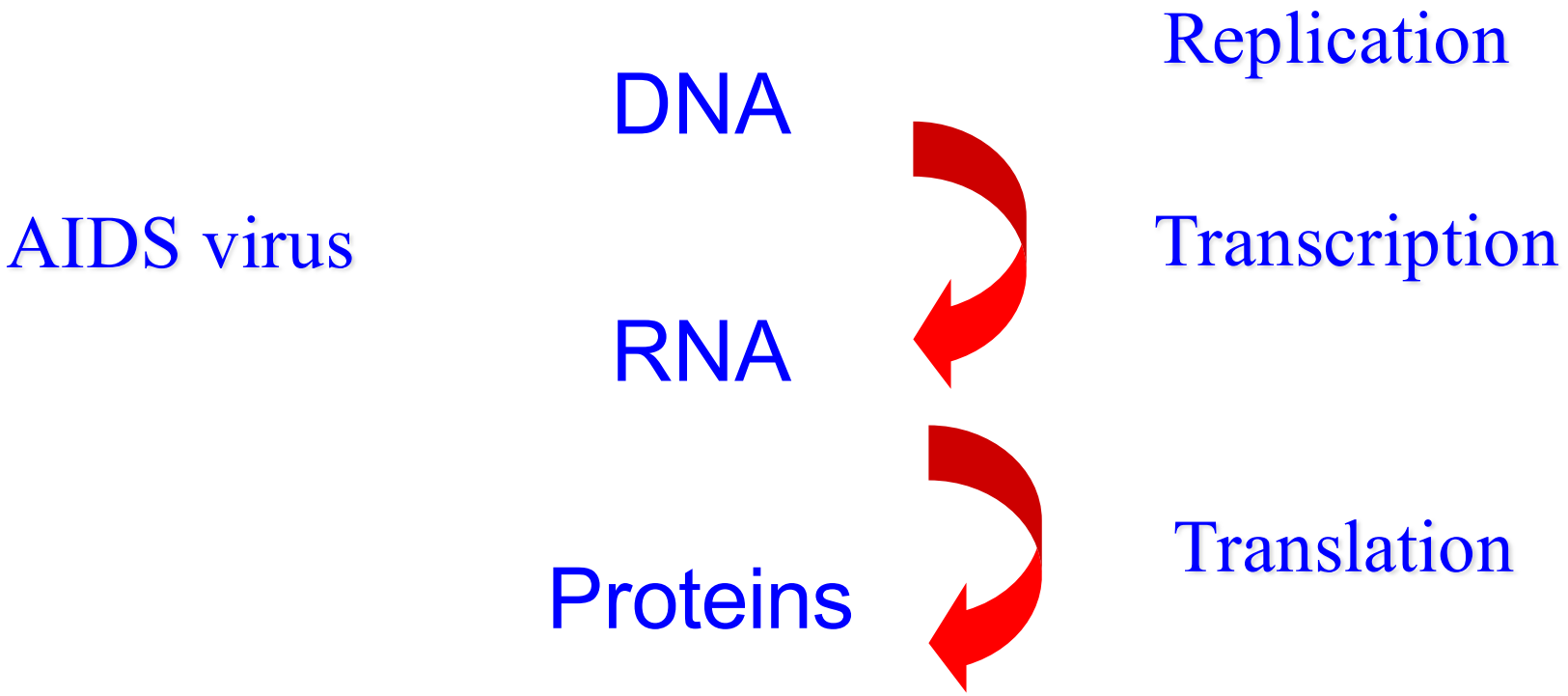
- **ATP Synthesis**
- ADP is converted to ATP by a reaction between ADP and hydrogen phosphate ion. This is both an oxidation and phosphorylation reaction. Energy released in the electron transport chain drives this reaction forward.

Vedio: http://www.iubmb-nicholson.org/swf/ATPSynthase.swf

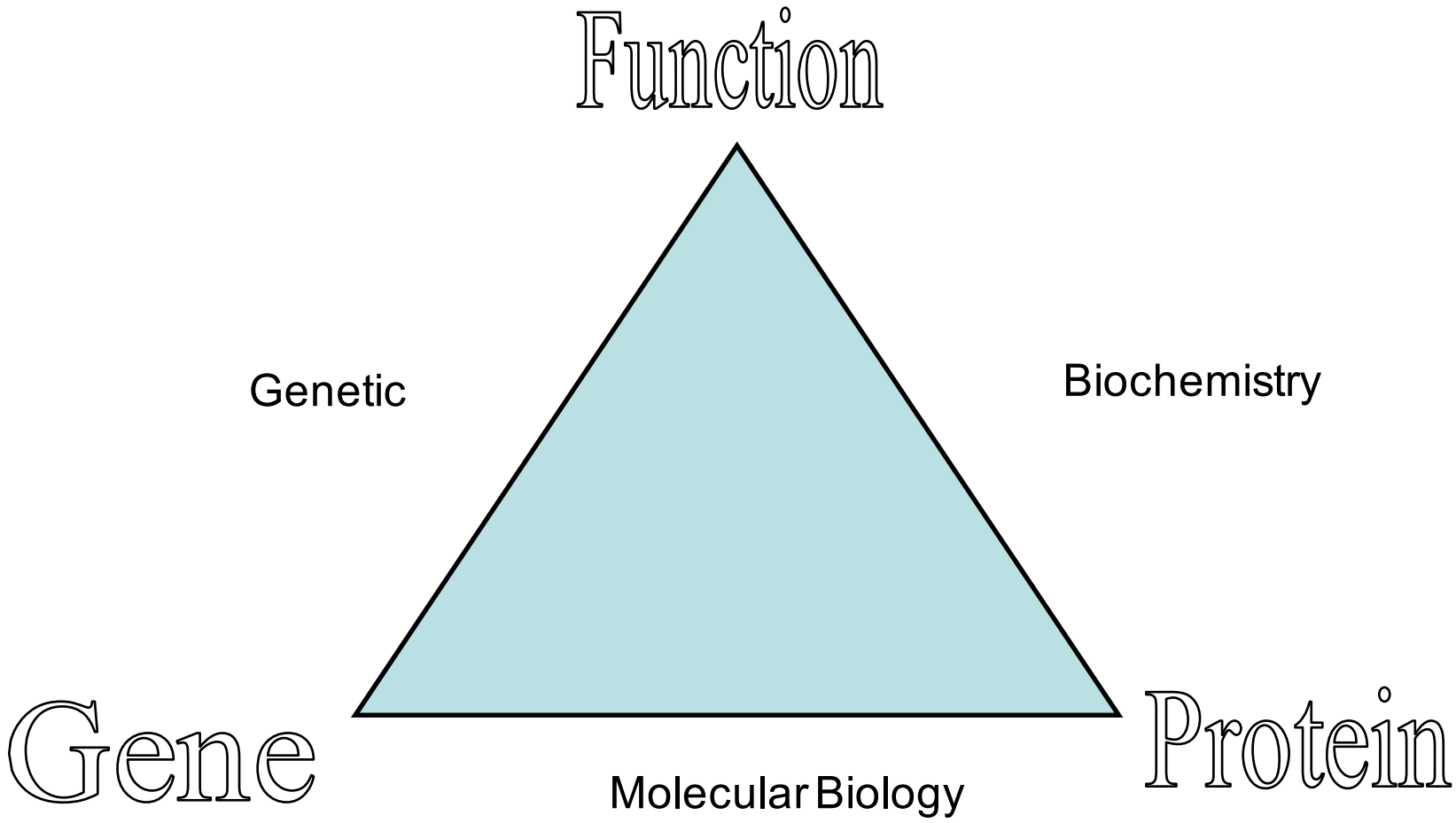

Cytosol
Outer mitochondrial membrane
Intermembrane space
Inner mitochondrial membrane
Mitochondrial matrix
H+
I
II
FADH2
III
IV
CoQ
Cyt c
NADH
NAD+
Succinate
Fumarate
O2
H2O
ATP synthase
H+ ion channel
ADP + HOPO3 2−
ATP

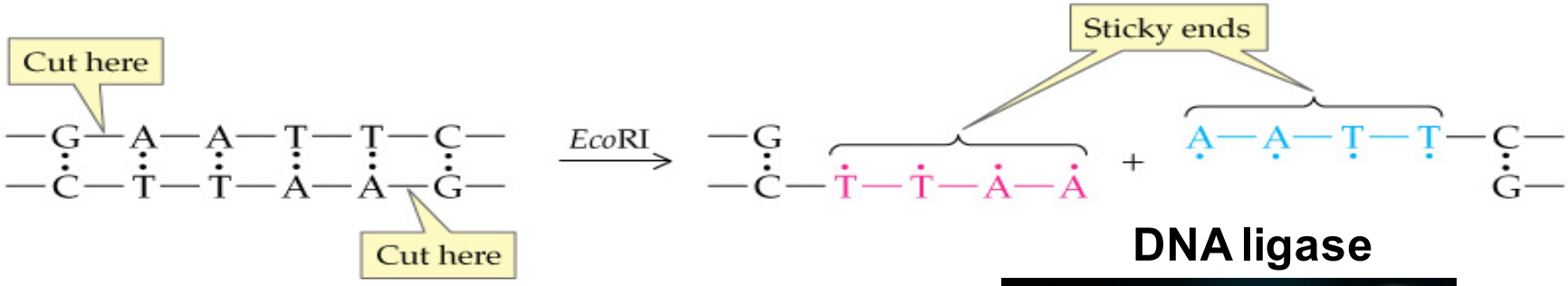

Actin filament
γ

Central Dogma

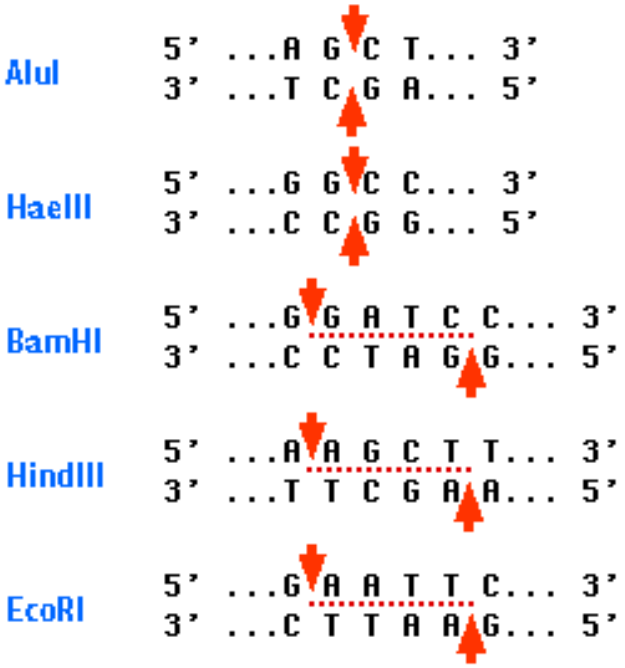


Recombinant DNA





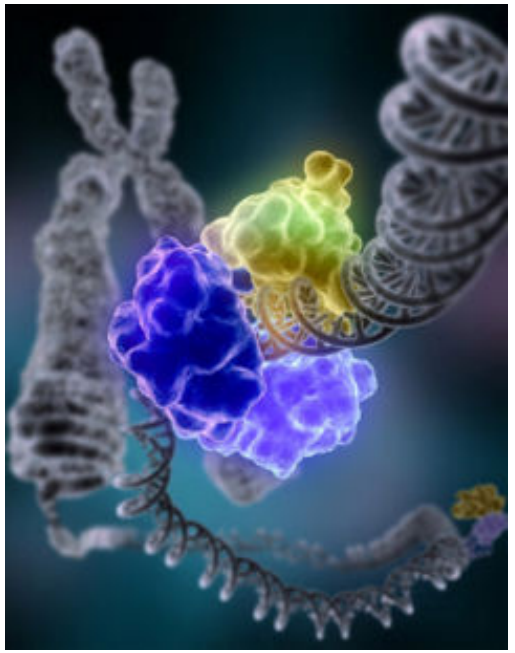
Restriction Enzyme

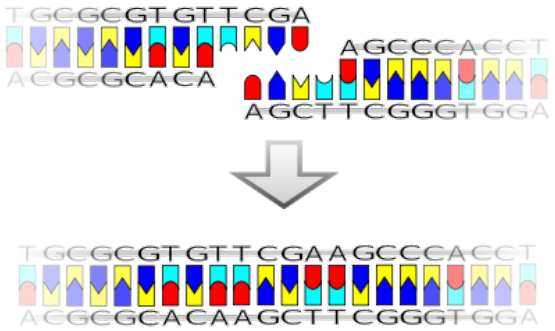


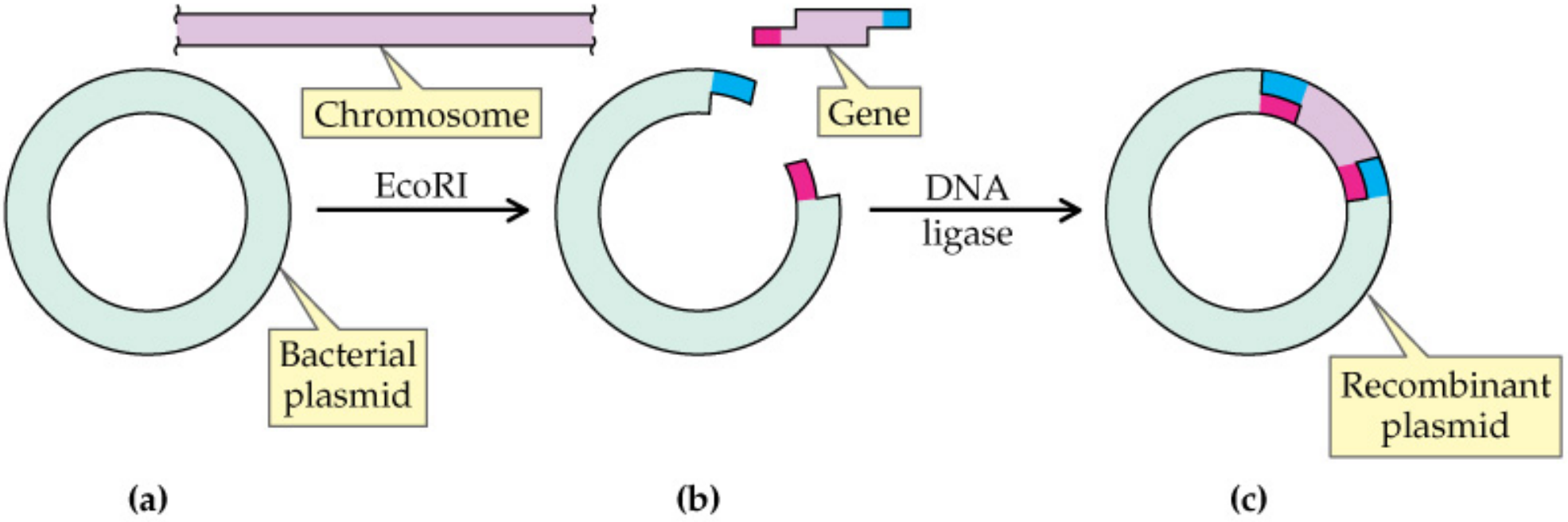
AluI and **HaeIII** produce blunt ends

BamHI **HindIII** and **EcoRI** produce "sticky" ends

DNA ligase

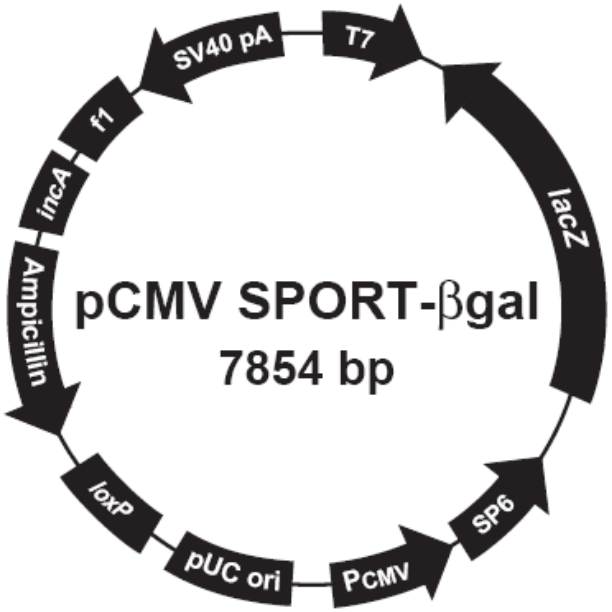


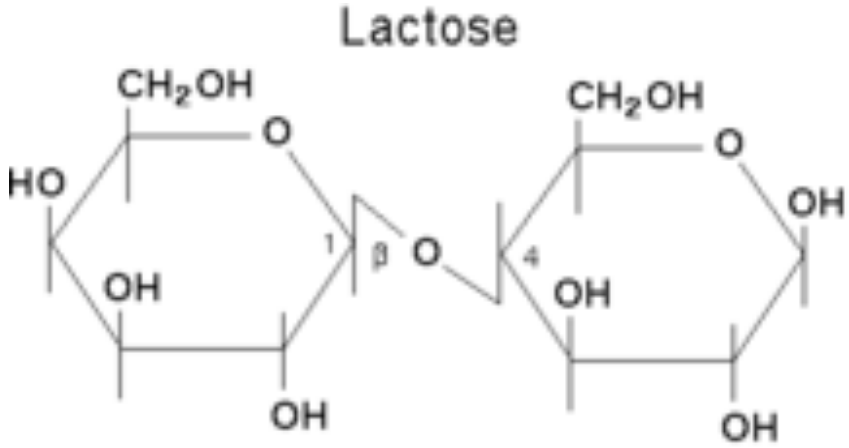



Chromosome
Gene
EcoRI
DNA
ligase
Bacterial
plasmid
Recombinant
plasmid
(a)
(b)
(c)

β-Galactosidase

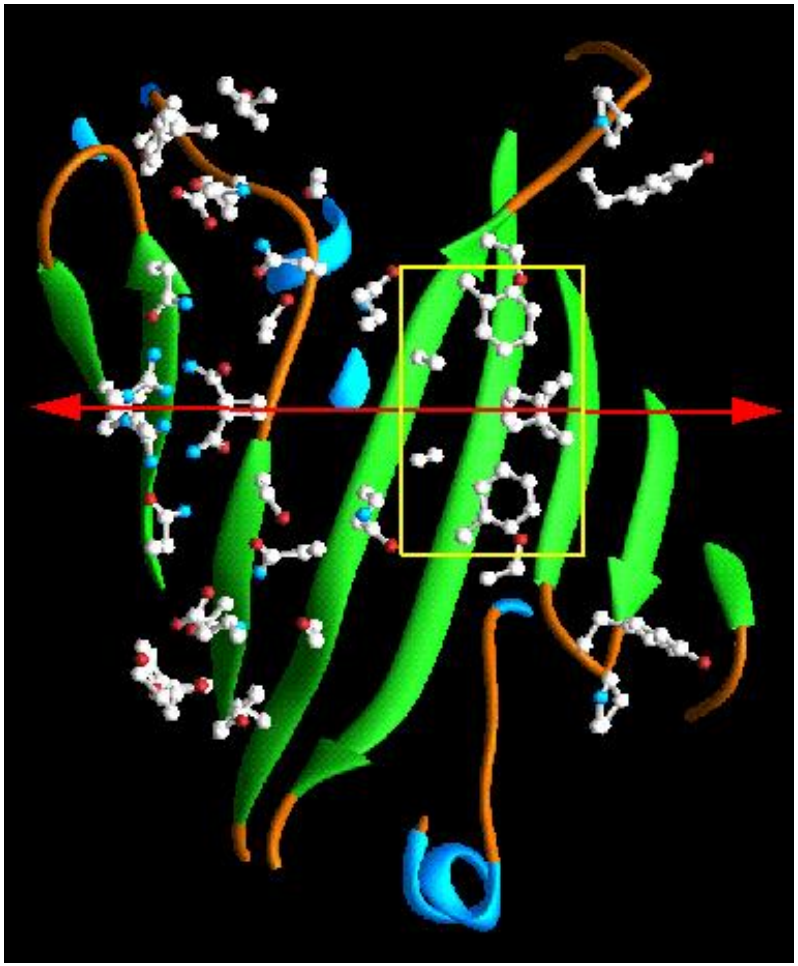
The enzyme that splits lactose into glucose and galactose. Coded by a gene (lacZ) in the lac operon of Escherichia coli.



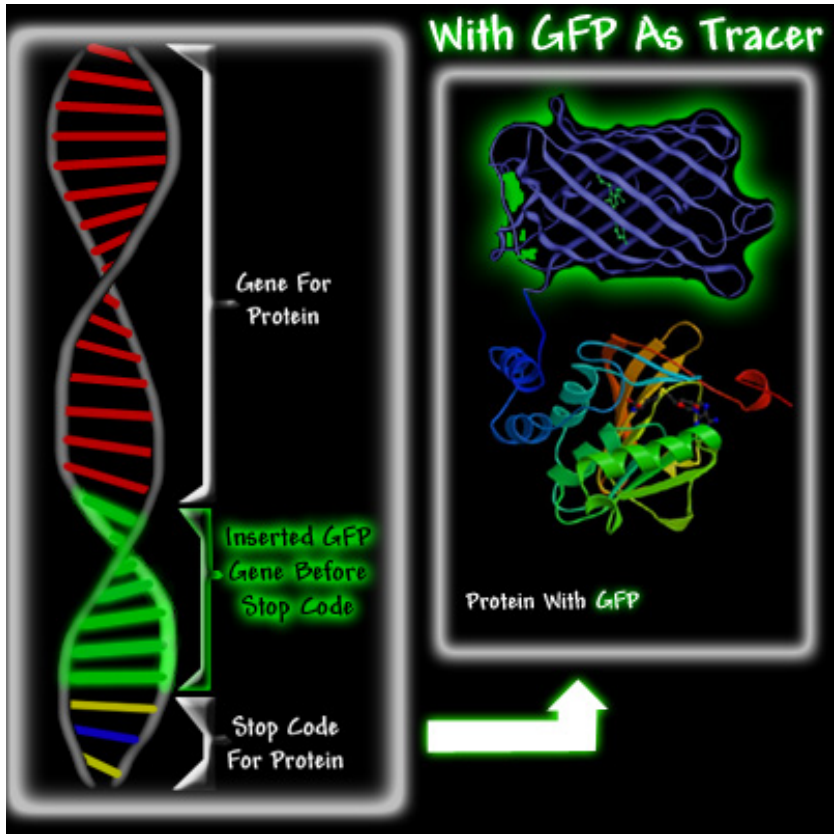


PUC is a family of plasmids that have an ampicillin resistance gene and more importantly a *lacZ* gene. A functional lacZ gene will produce the protein β - galactosidase. Bacterial colonies in which β - galactosidase is produced, will form blue colonies in the presence of the substrate 5 - bromo - 4 - chloro - 3 - indolyl - b - D - galactoside or as it is more commonly referred to, X-gal.

Green Fluorescent Protein (GFP)



The **green fluorescent protein** (**GFP**) is a protein from the jellyfish *Aequorea victoria* that fluoresces green when exposed to blue light.

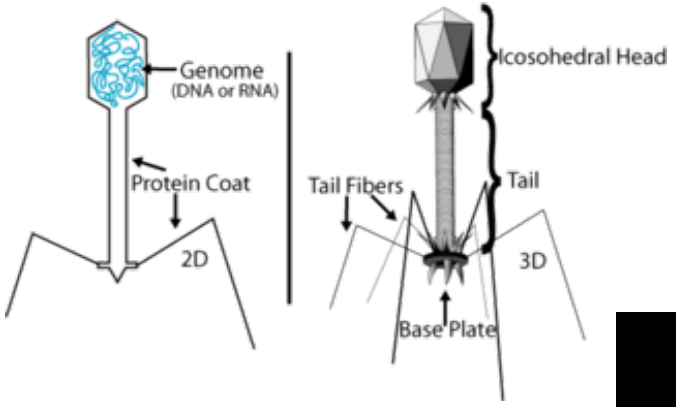


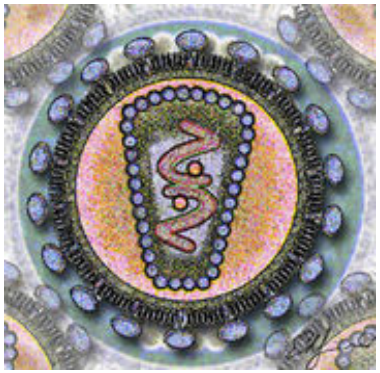
GFP Rats

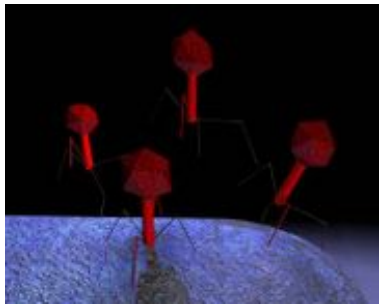
Life

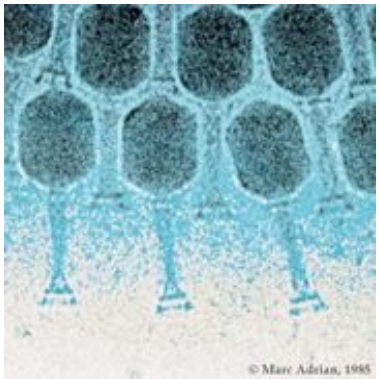
- Replication: reproduction
- Function: catalytic functions
- RNA world:
- Virus is not alive

Virus


Genome
(DNA or RNA)
Protein Coat
2D
Icosohedral Head
Tail Fibers
Tail
3D
Base Plate






© Marc Adrian, 1985

Virus Reproduction