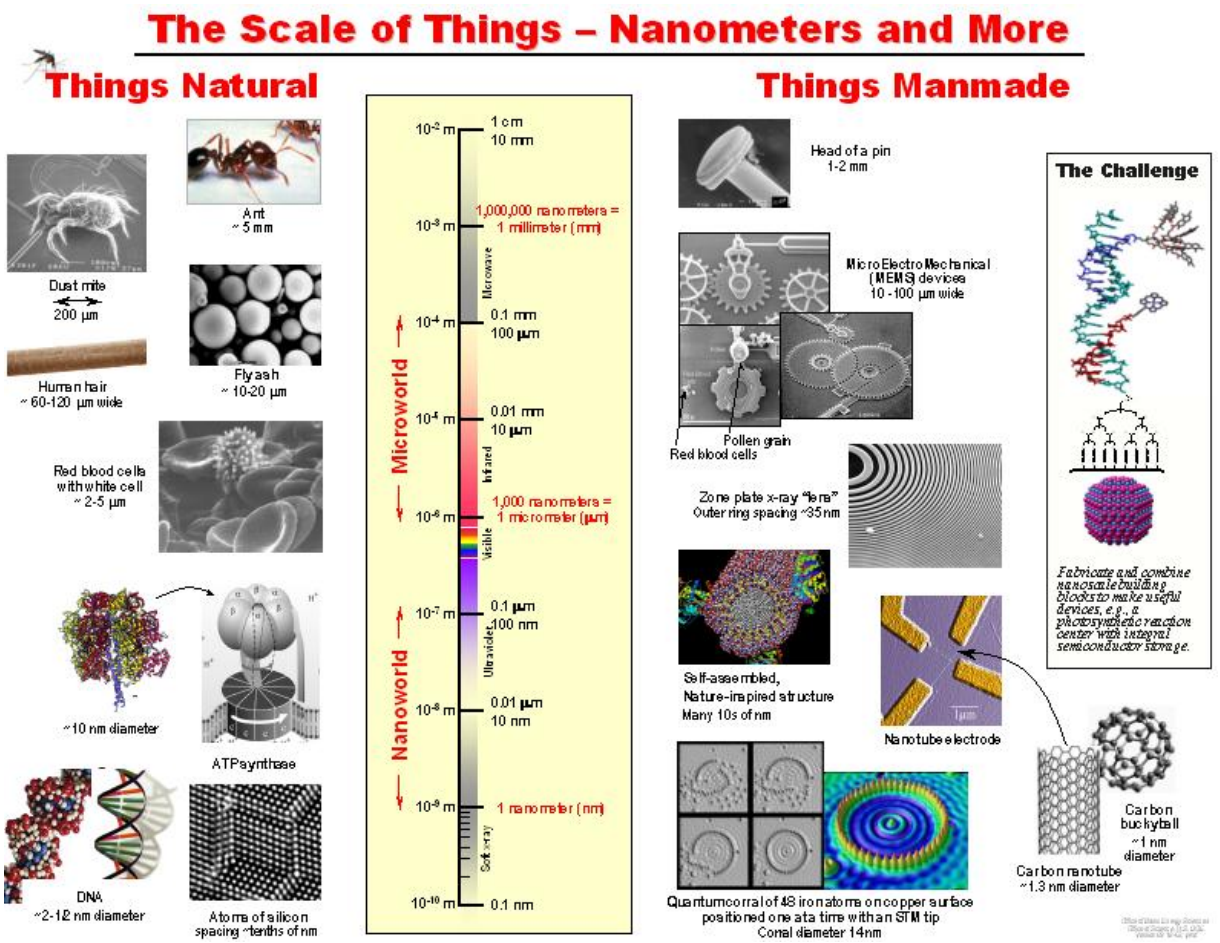
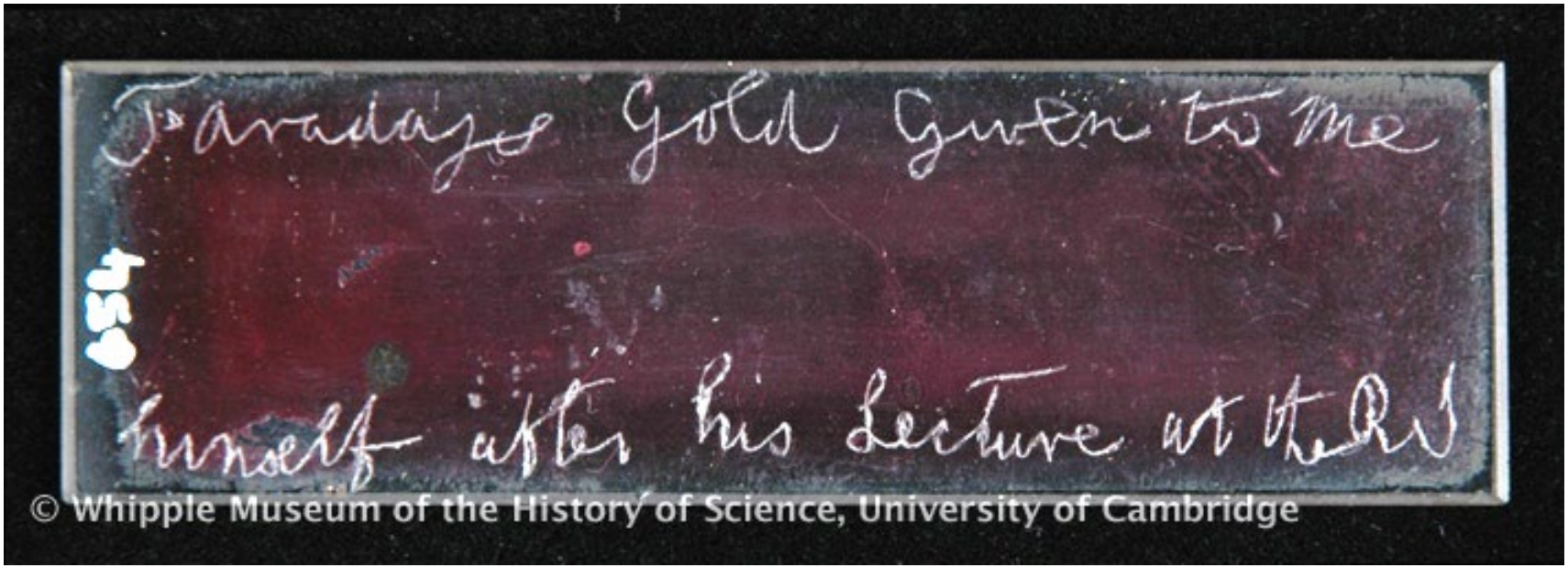
What is nano?



http://cohesion.rice.edu/CentersAndInst/CNST/emplibrary/Scale%20of%20Nanotechnology.jpg

Faraday's Gold Sol



1856
20-40 nm gold

Topics

Fundamental Knowledge and Current Literatures

- Analytical Chemistry
- Spectroscopic tools
- Microarray
- Cell-surface interaction
  Ultrasensitive detection
- Physical Chemistry
- Single molecular behavior (Optical and AFM)
- Optical properties of Q-dot
- SERS
- Surface plasmon
- Material Chemistry:
- Nanomaterials: Q-dot, nanoparticle, DNA assembly
- Surface functionalization
- Drug delivery
- DNA, Protein, Cell interactions
-

New Development in Nanobiotechnology

Method of the Year 2020: spatially resolved transcriptomics

Spatially resolved transcriptomics methods are changing the way we understand complex tissues.

Method of the Year 2019: Single-cell multimodal omics

Multimodal omics measurement offers opportunities for gaining holistic views of cells one by one.

Method of the Year 2018: Imaging in freely behaving animals

Neuronal imaging in unrestrained animals has expanded the range of behaviors amenable to circuit-level studies in several model organisms.

Imaging: 2018, 2015, 2014, 2010, 2008
DNA Sequencing: 2020, 2019, 2016, 2013
Organoid: 2017

Method of the Year 2017: Organoids

The ability to prod stem cells into three-dimensional tissue models makes for a powerful way to study human biology. But these exciting tools are still works in progress.

Method of the Year 2014

Light-sheet fluorescence microscopy can image living samples in three dimensions with relatively low phototoxicity and at high speed.

Method of the Year 2016: Epitranscriptome analysis

Chemical modifications on ribonucleotides are being profiled with increased efficiency and appreciated as important regulatory features.

Method of the Year 2013

Methods to sequence the DNA and RNA of single cells are poised to transform many areas of biology and medicine.

Method of the Year 2010

With the capacity to control cellular behaviors using light and genetically encoded light-sensitive proteins, optogenetics has opened new doors for experimentation across biological fields.

Method of the Year 2015

The end of 'blob-ology': single-particle cryo-electron microscopy (cryo-EM) is now being used to solve macromolecular structures at high resolution.

Method of the Year 2008

With its tremendous potential for understanding cellular biology now poised to become a reality, super-resolution fluorescence microscopy is our choice for Method of the Year.

Review of General Chemistry, Biochemistry and Cell Biology

Synthesis of Nanoparticles and Surface Modifications

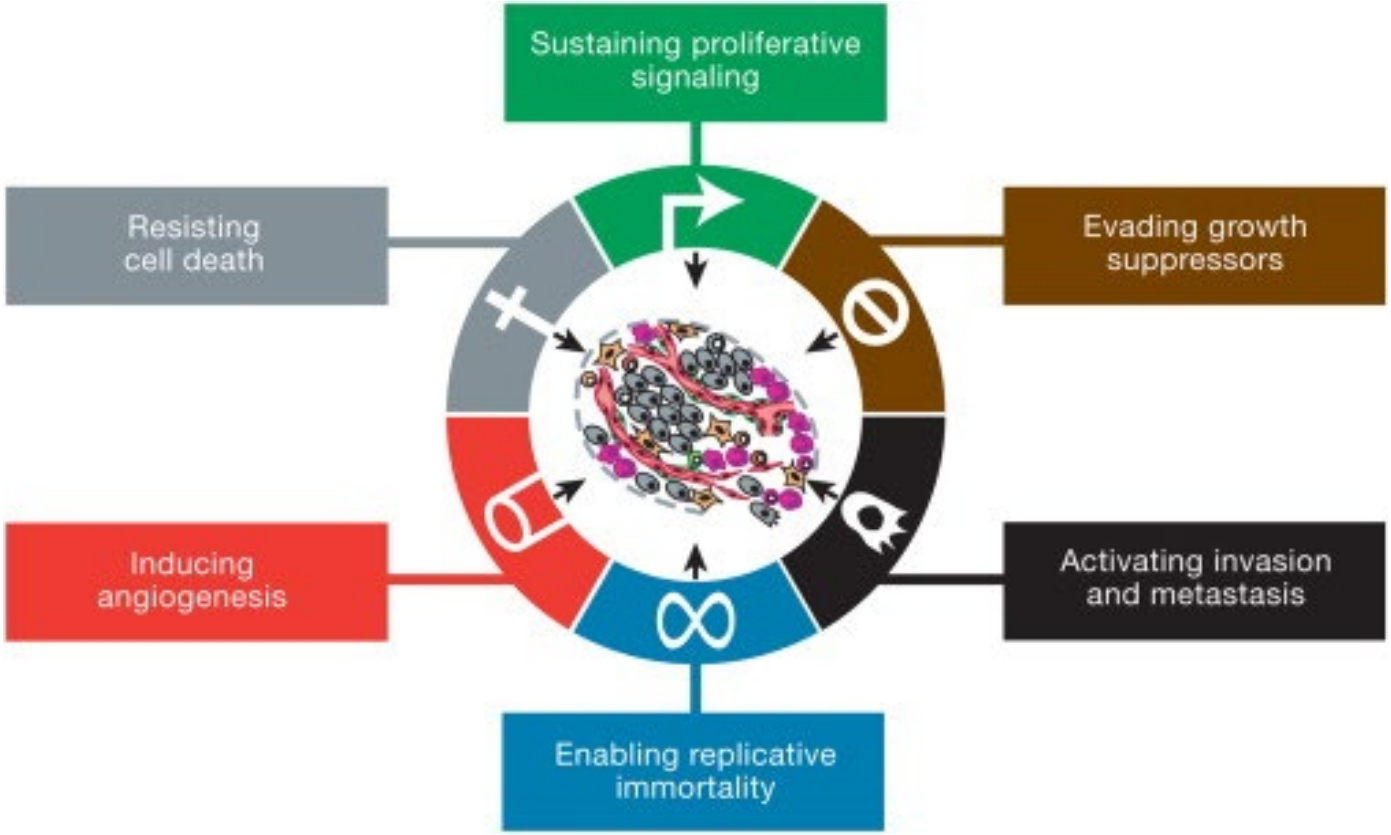
Properties of Nanomaterials

Nanomaterials for Biodiagnostic

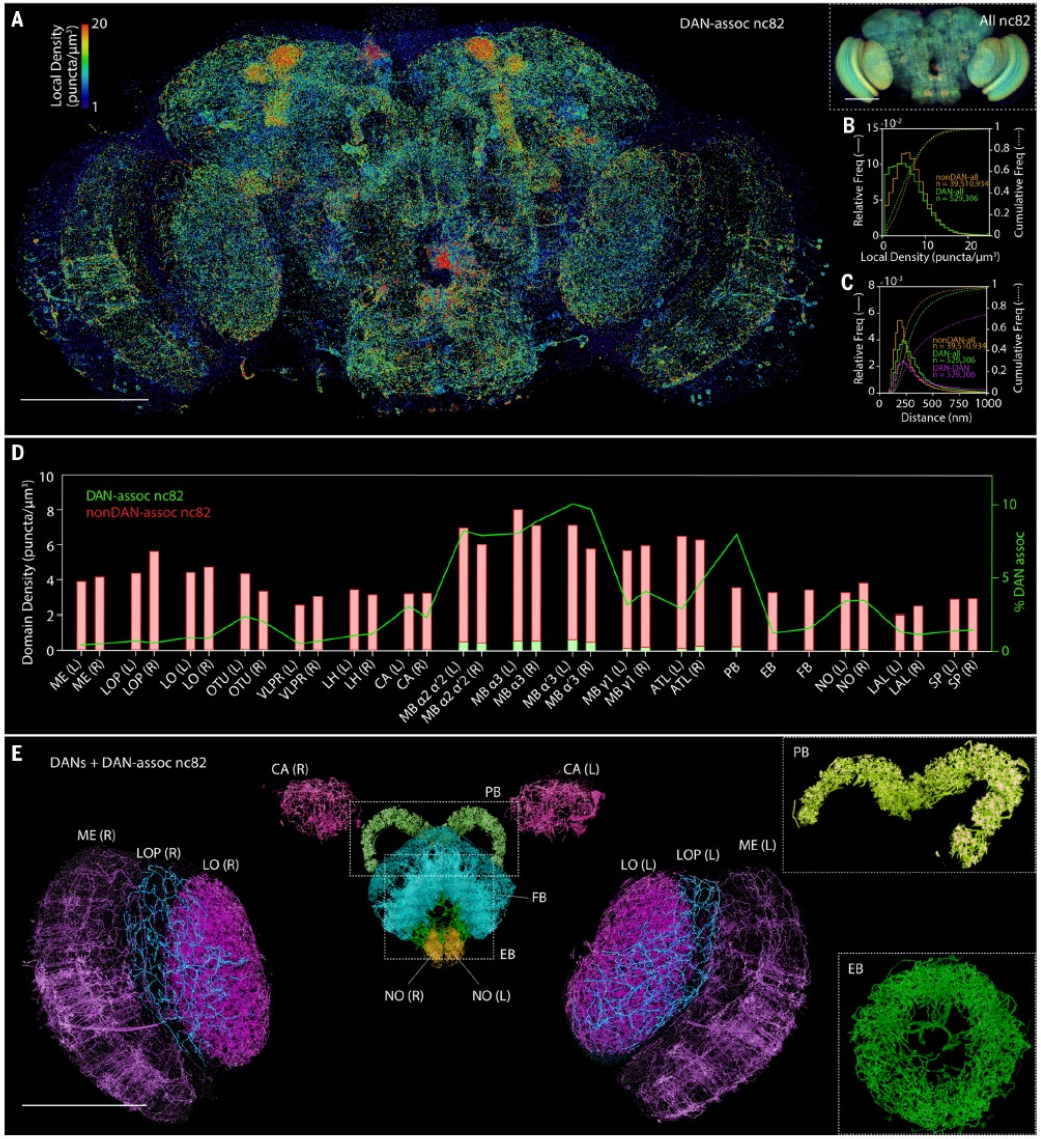
- Nucleic Acid
  - Genetic information for identification
  - Diseases, bacterium, virus, pathogen
  - PCR with molecular fluorophore, State of the Art
  - Expansive, Non-portable, Non-multiplexing
- Proteins
  - Cancers and diseases, unusual high concentration of marker
  - ELISA (~pM) with molecular fluorophore
  - No PCR version

Nanomedicine

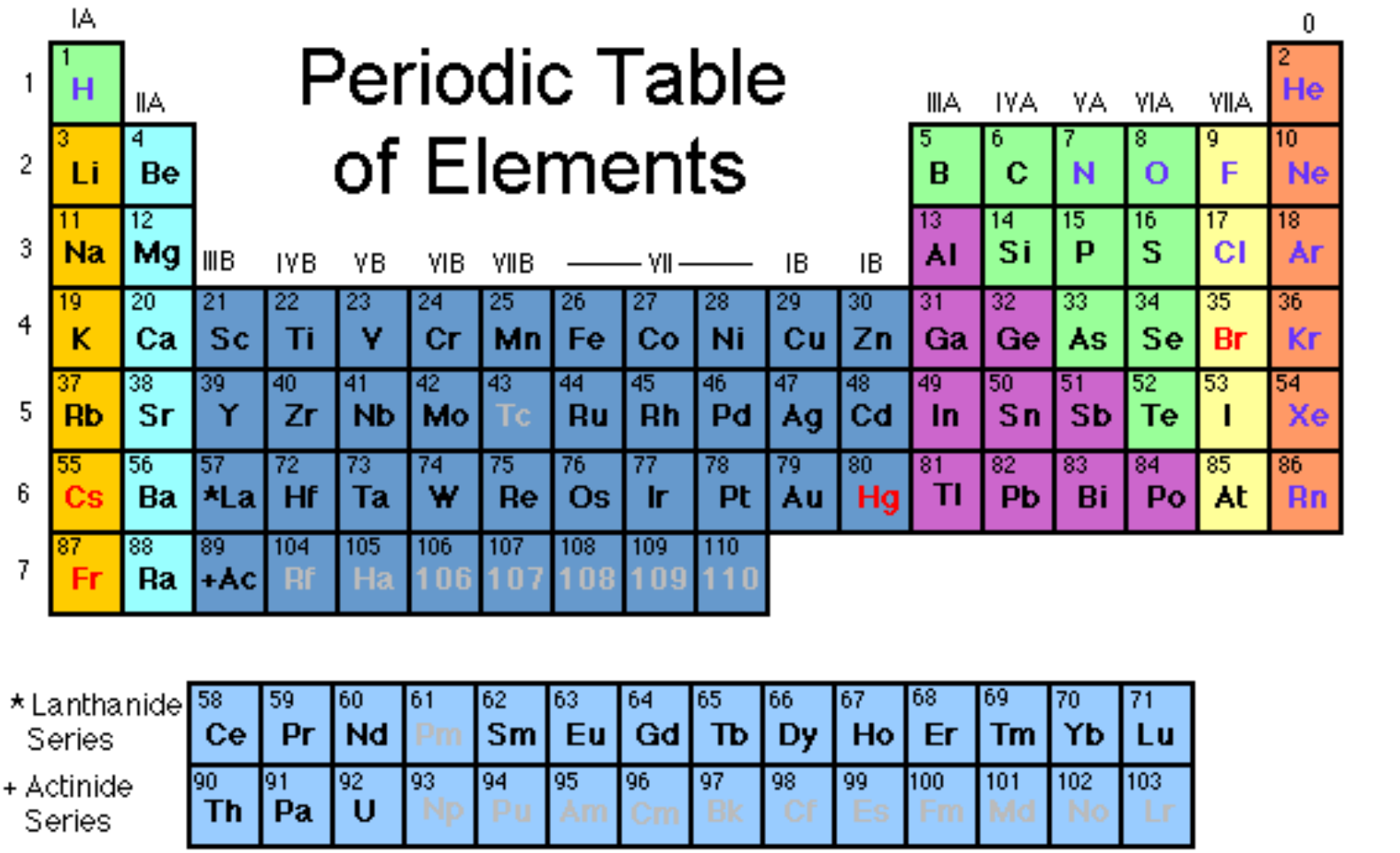
Cancer Hallmark



Imaging and Sequencing

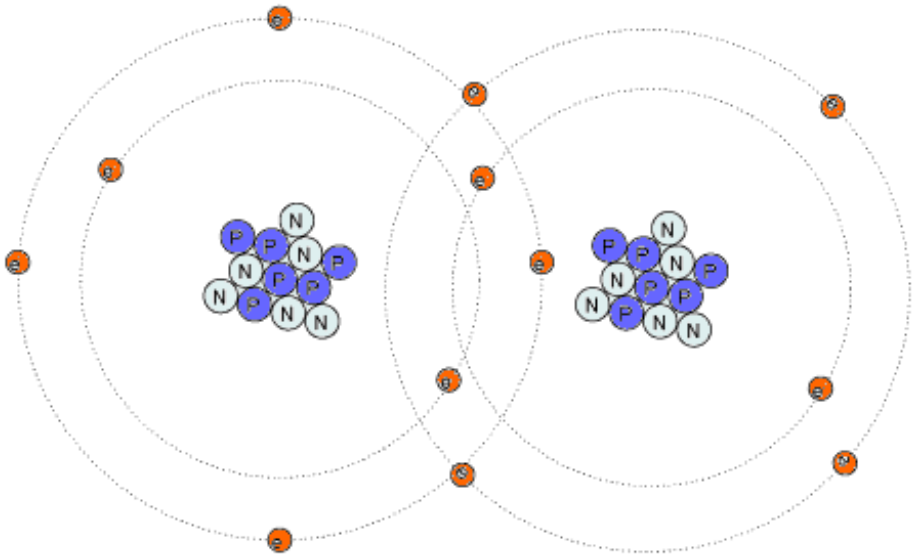


Review of General Chemistry

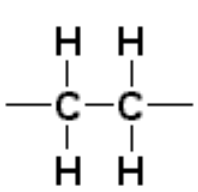

Periodic Table of Elements
IA
IIA
IIIB
IVB
VB
VIB
VIIB
VII
IB
IB
IIIA
IVA
VA
VIA
VIIA
0
1 H
2 He
3 Li
4 Be
5 B
6 C
7 N
8 O
9 F
10 Ne
11 Na
12 Mg
13 Al
14 Si
15 P
16 S
17 Cl
18 Ar
19 K
20 Ca
21 Sc
22 Ti
23 V
24 Cr
25 Mn
26 Fe
27 Co
28 Ni
29 Cu
30 Zn
31 Ga
32 Ge
33 As
34 Se
35 Br
36 Kr
37 Rb
38 Sr
39 Y
40 Zr
41 Nb
42 Mo
43 Tc
44 Ru
45 Rh
46 Pd
47 Ag
48 Cd
49 In
50 Sn
51 Sb
52 Te
53 I
54 Xe
55 Cs
56 Ba
57 *La
72 Hf
73 Ta
74 W
75 Re
76 Os
77 Ir
78 Pt
79 Au
80 Hg
81 Tl
82 Pb
83 Bi
84 Po
85 At
86 Rn
87 Fr
88 Ra
89 +Ac
104 Rf
105 Ha
106 106
107 107
108 108
109 109
110 110
* Lanthanide Series
58 Ce
59 Pr
60 Nd
61 Pm
62 Sm
63 Eu
64 Gd
65 Tb
66 Dy
67 Ho
68 Er
69 Tm
70 Yb
71 Lu
+ Actinide Series
90 Th
91 Pa
92 U
93 Np
94 Pu
95 Am
96 Cm
97 Bk
98 Cf
99 Es
100 Fm
101 Md
102 No
103 Lr
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

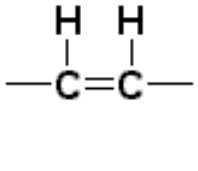
Hydrogen	H•	H•
Carbon	•Ċ•	•Ċ•
Water	H:Ö:H	H-Ö-H
Ethylene	H H C::C H H	H H C=C H H
Acetylene	H:C:::C:H	H-C≡C-H



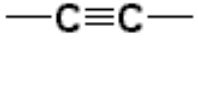
Functional Groups



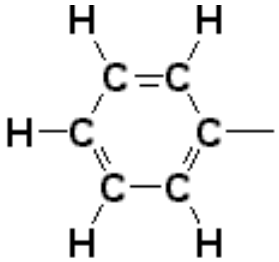
alkane



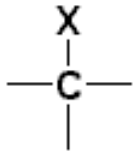
alkene



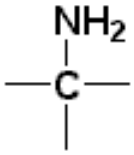
alkyne



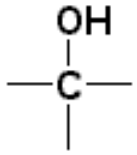
phenyl



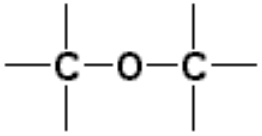
alkyl halide
(X = F, Cl, Br, I)



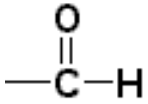
amine



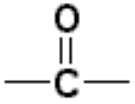
alcohol



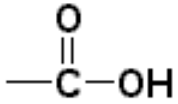
ether



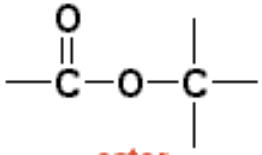
aldehyde



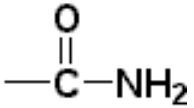
ketone



carboxylic
acid

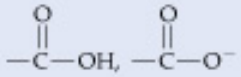
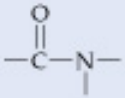
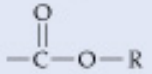
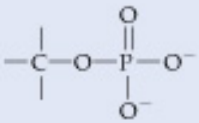
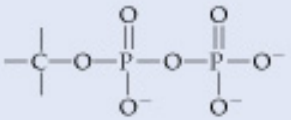
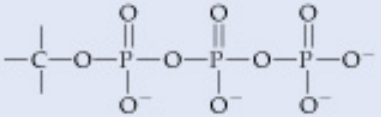
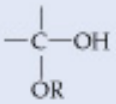
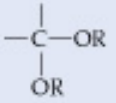


ester

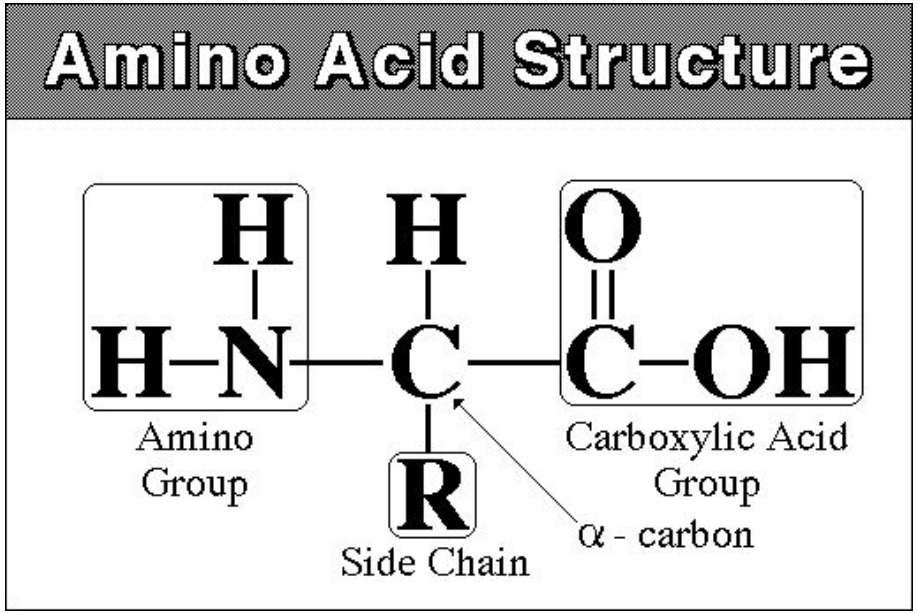


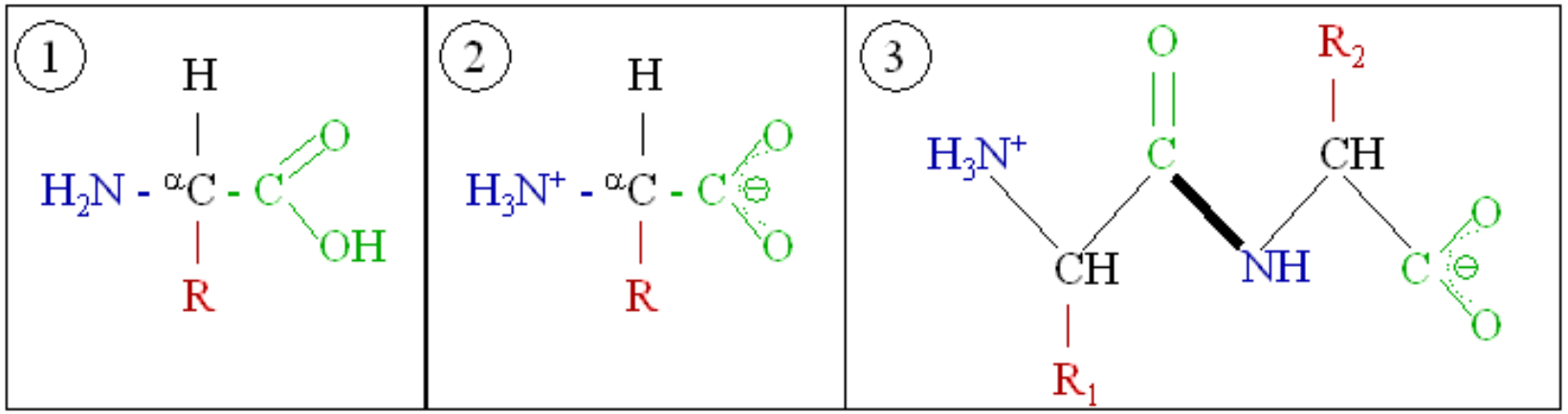
amide

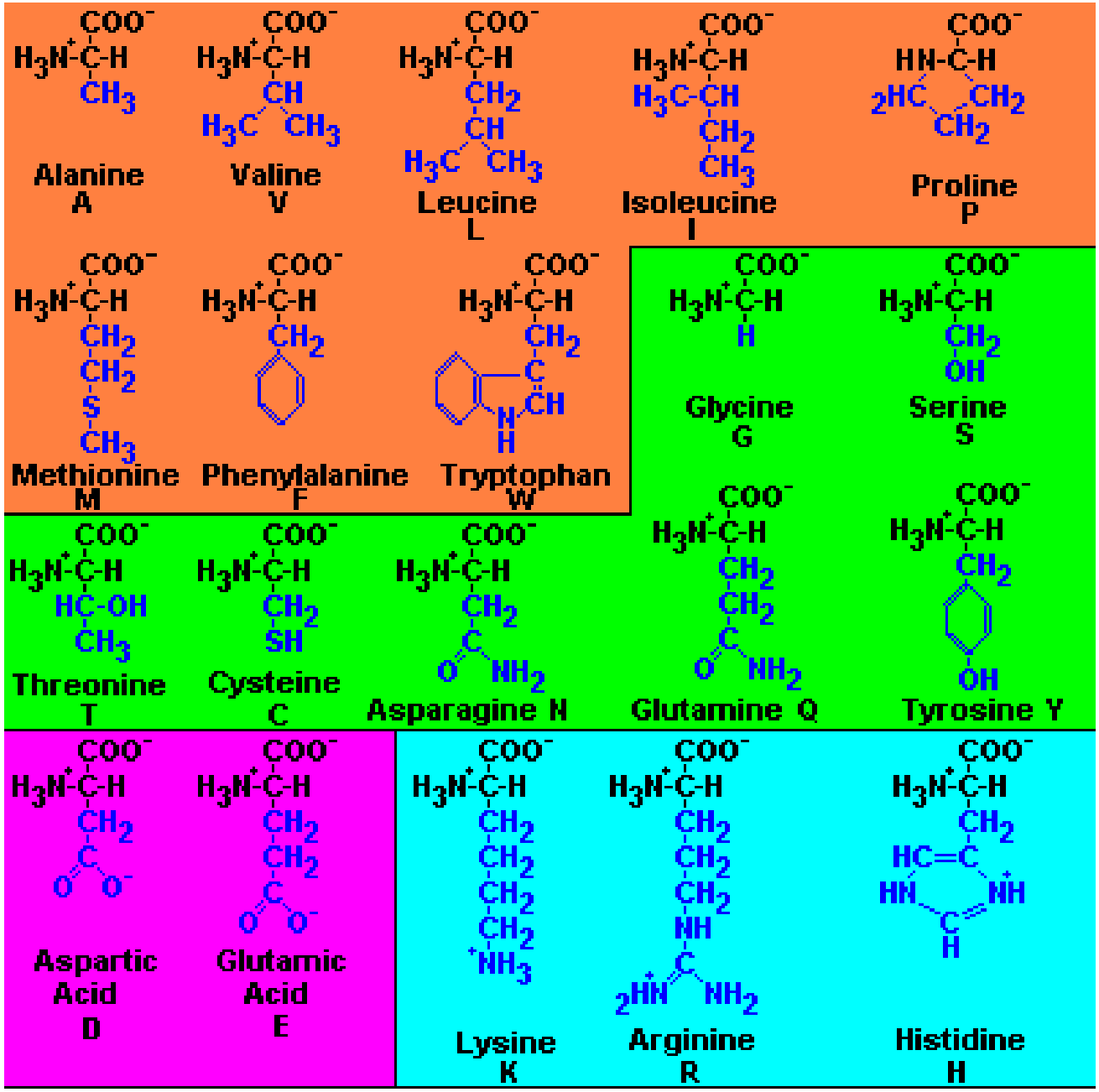
TABLE 18.1 Functional Groups of Importance in Biochemical Molecules

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)

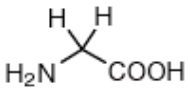
Amino Acid


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

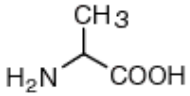

1
H
H_2N - $^{\alpha}C$ - C
O
OH
R
2
H
H_3N^+ - $^{\alpha}C$ - C
O
O
R
3
O
R_2
H_3N^+
C
CH
CH
NH
C
O
O
R_1


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

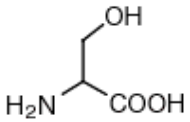


Glycine (Gly, G)
MW: 57.05

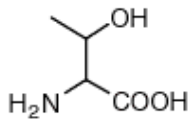


Alanine (Ala, A)
MW: 71.09

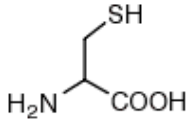
Nucleophilic



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

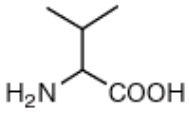


Threonine (Thr, T)
MW: 101.11, pK_a ~ 16

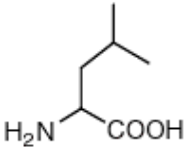


Cysteine (Cys, C)
MW: 103.15, pK_a = 8.35

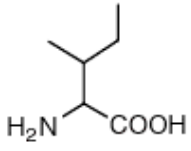
Hydrophobic



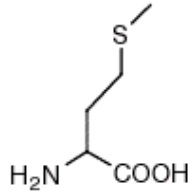
Valine (Val, V)
MW: 99.14



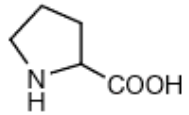
Leucine (Leu, L)
MW: 113.16



Isoleucine (Ile, I)
MW: 113.16

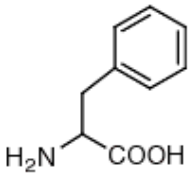


Methionine (Met, M)
MW: 131.19

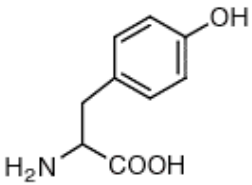


Proline (Pro, P)
MW: 97.12

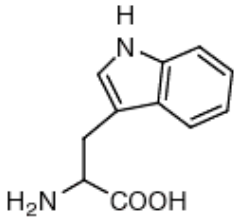
Aromatic



Phenylalanine (Phe, F)
MW: 147.18

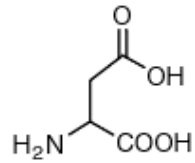


Tyrosine (Tyr, Y)
MW: 163.18

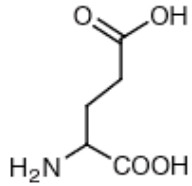


Tryptophan (Trp, W)
MW: 186.21

Acidic

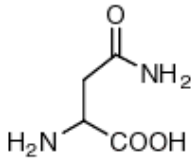


Aspartic Acid (Asp, D)
MW: 115.09, pK_a = 3.9

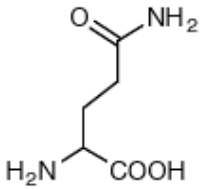


Glutamic Acid (Glu, E)
MW: 129.12, pK_a = 4.07

Amide

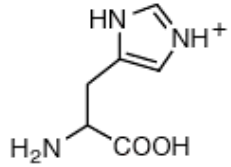


Asparagine (Asn, N)
MW: 114.11

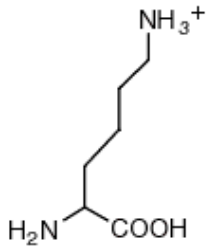


Glutamine (Gln, Q)
MW: 128.14

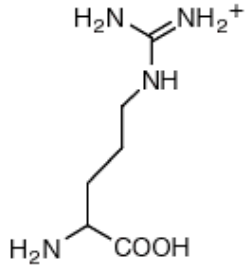
Basic



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



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

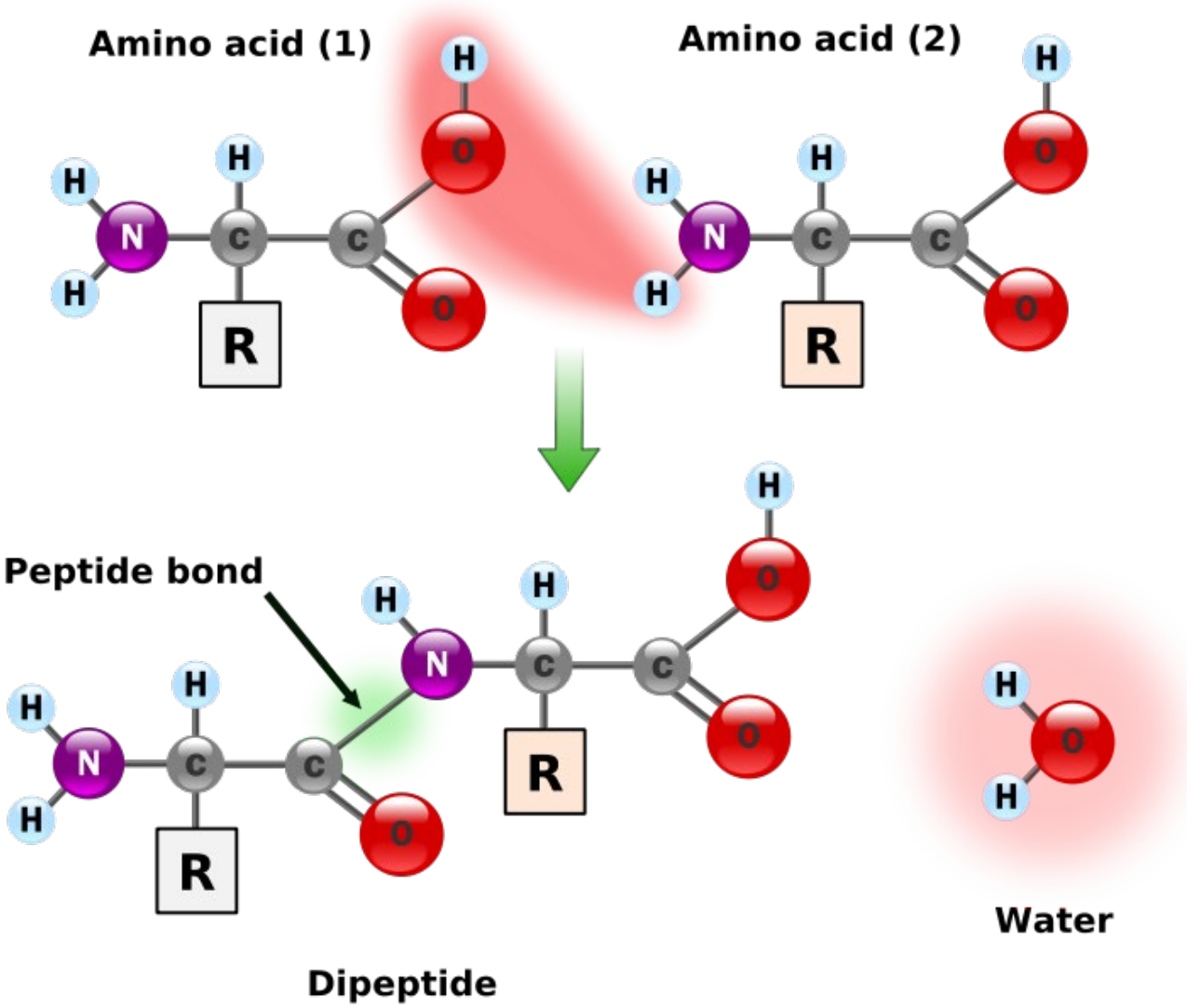


Arginine (Arg, R)
MW: 156.19, pK_a = 12.48

Protein Structure and Function

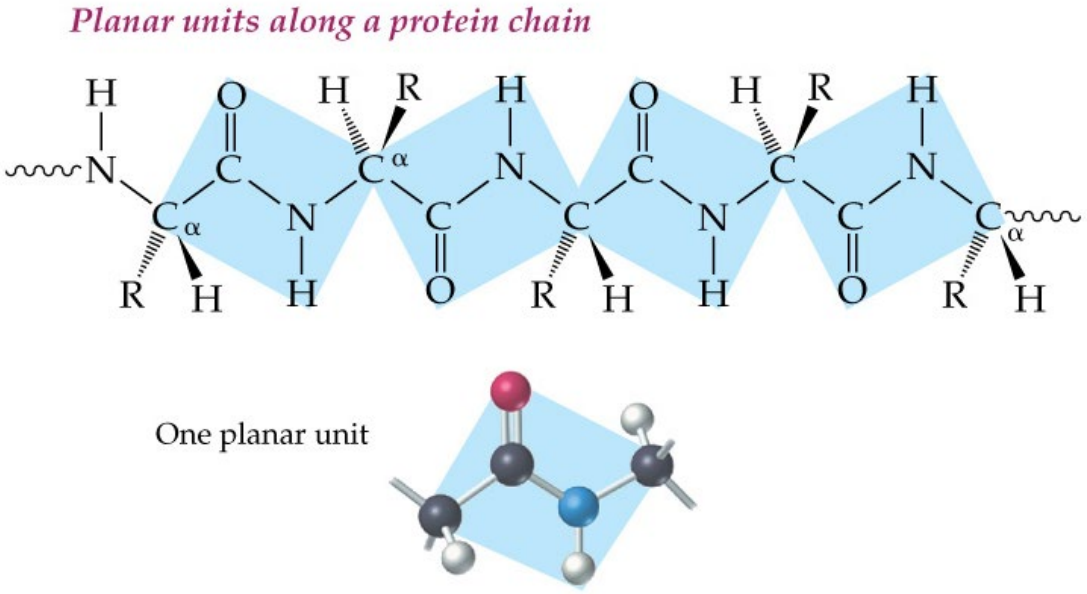
- Proteins are polymers of amino acids.
- Each amino acids in a protein contains a amino group, -NH_2, a carboxyl group, -COOH, and an R group, all bonded to the central carbon atom. The R group may be a hydrocarbon or they may contain functional group.
- All amino acids present in a proteins are *α-amino 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

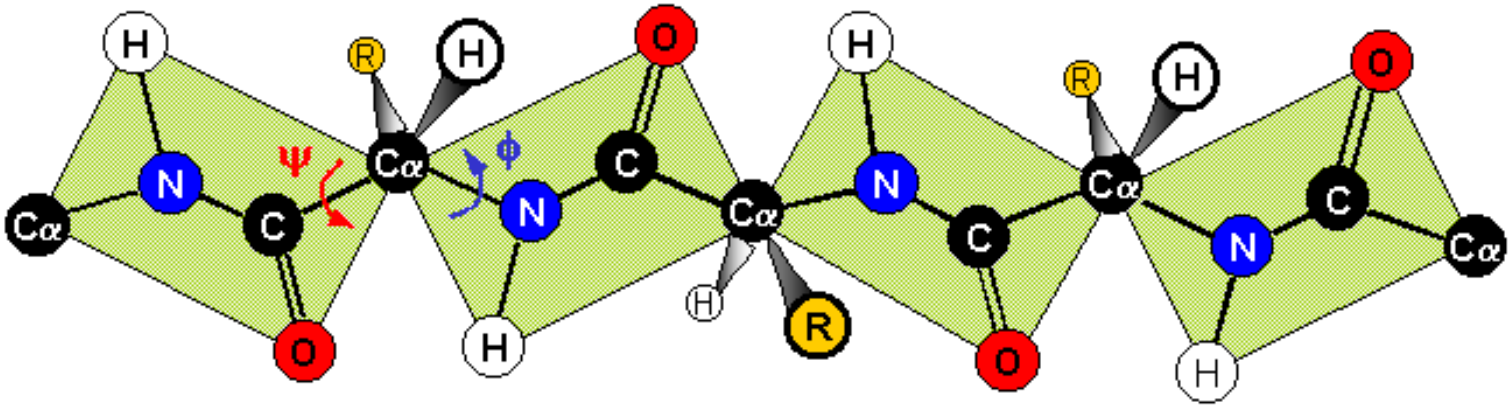


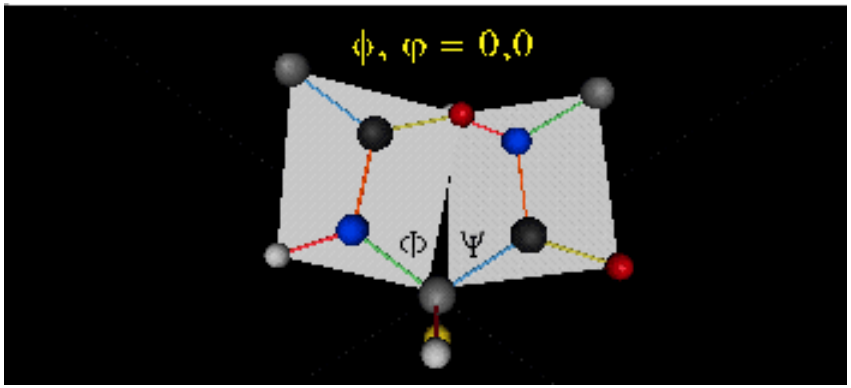
- By convention, peptides and proteins are always written with the amino terminal amino acid (N-terminal) on the left and carboxyl-terminal amino acid (C-terminal) on the right.

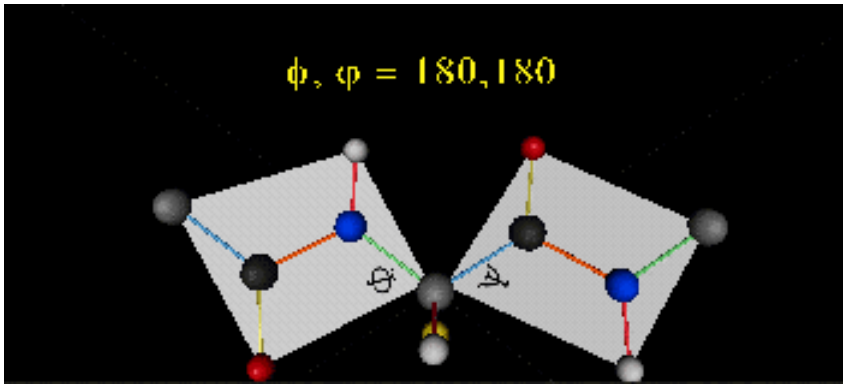
Secondary Protein Structure

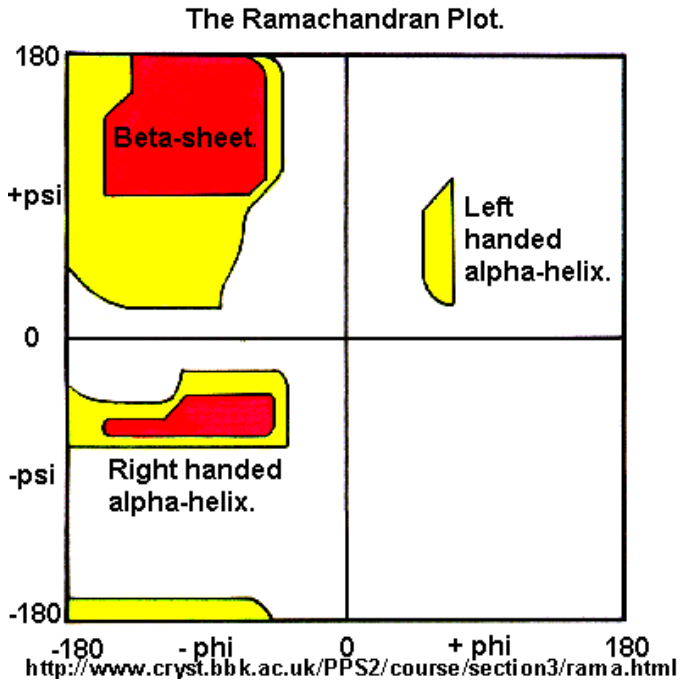
- Secondary structure of a protein is the arrangement of polypeptide backbone of the protein in space. The secondary structure includes two kinds of repeating pattern known as the *α-helix* and *β-sheet*.
- Hydrogen bonding between backbone atoms are responsible for both of these secondary structures.

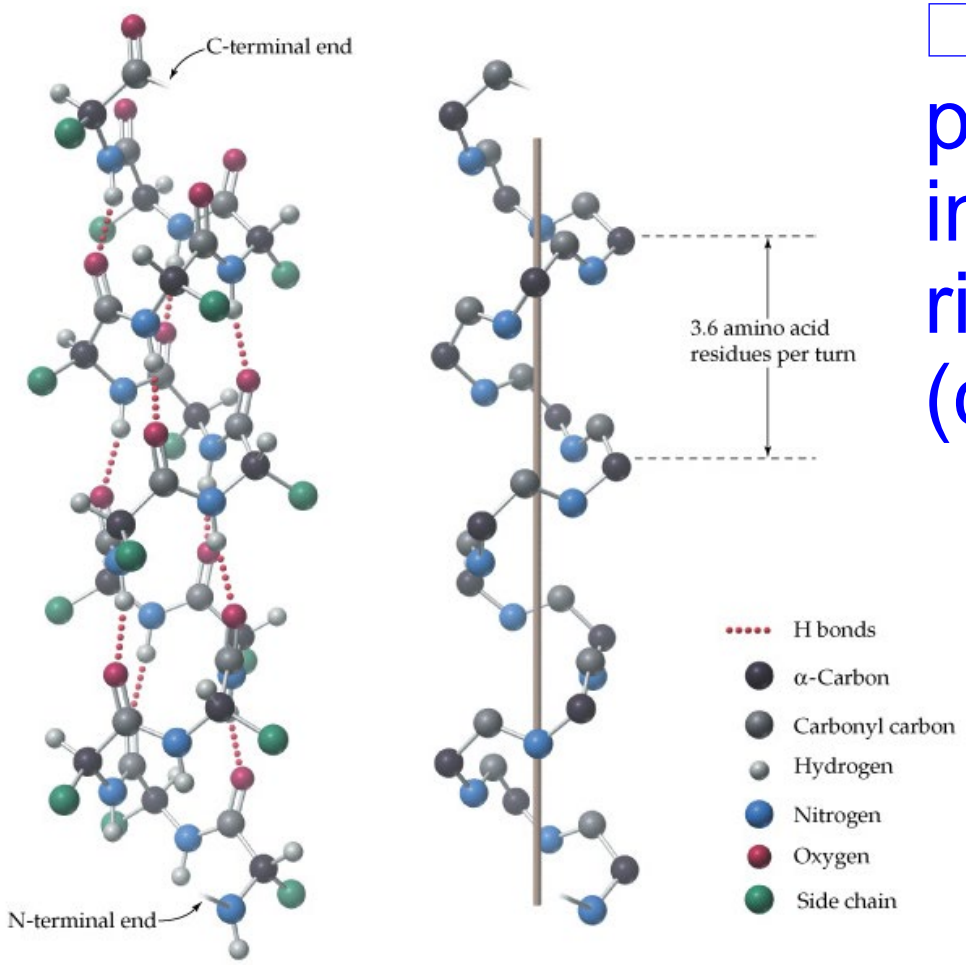
FULLY EXTENDED POLYPEPTIDE CHAIN





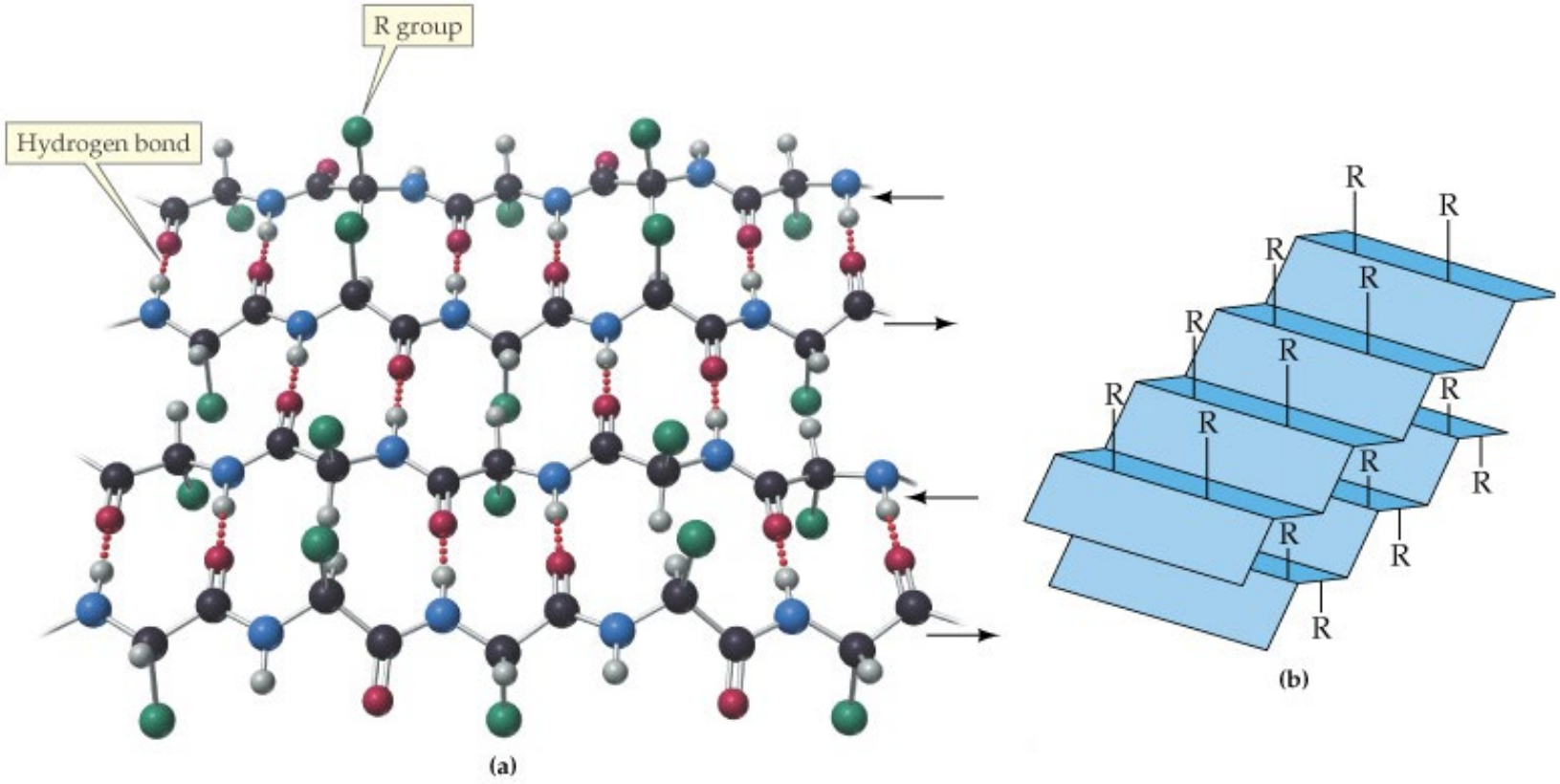




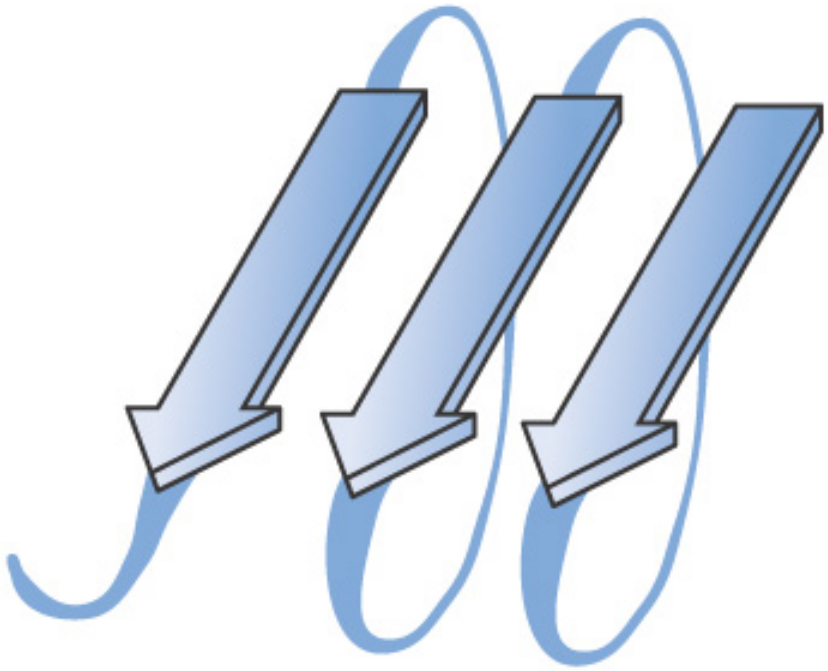


- ***α-Helix:*** A single protein chain coiled in a spiral with a right-handed (clockwise) twist.

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



α helix

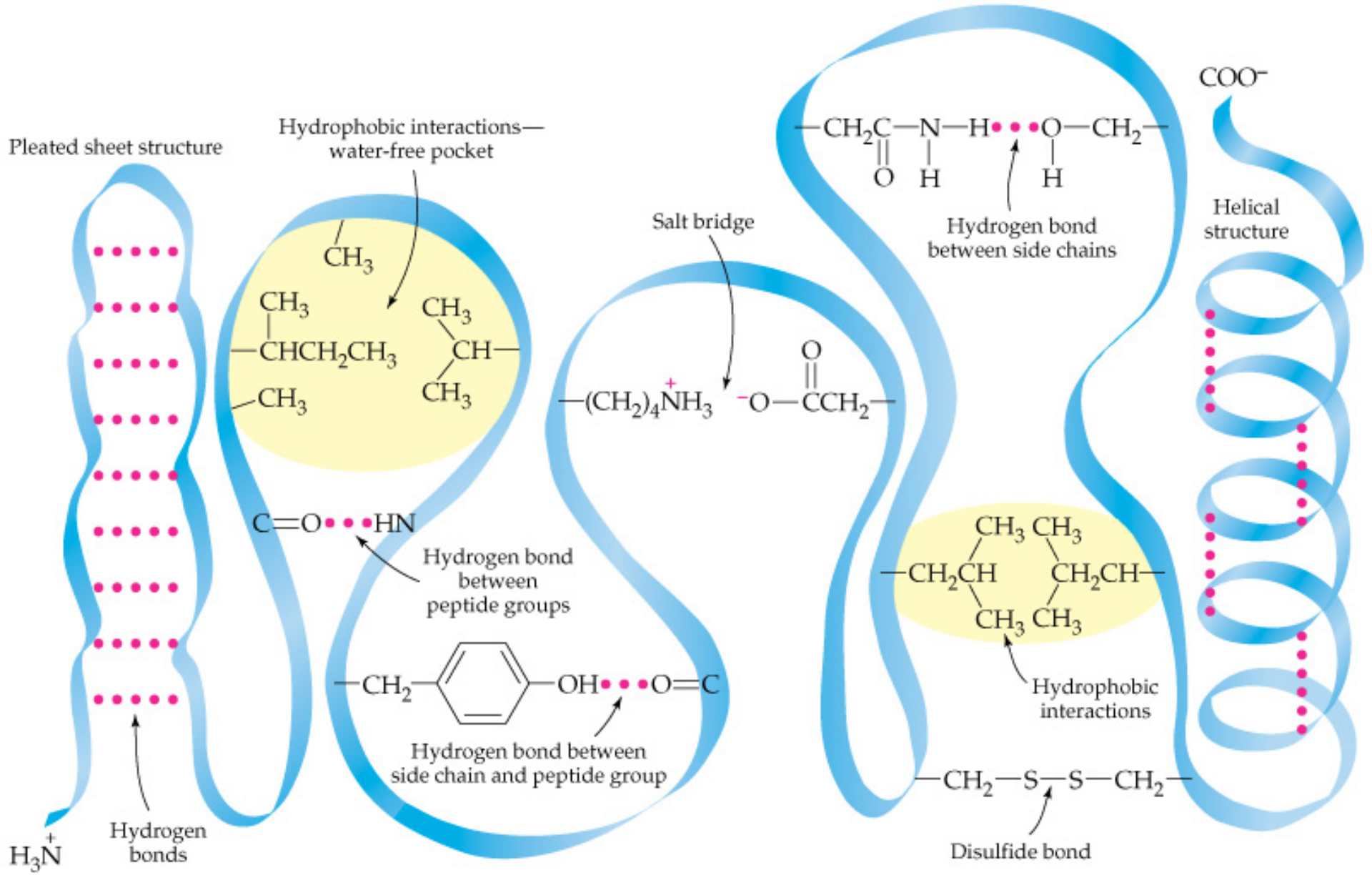


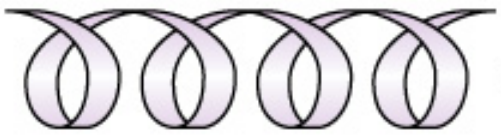
β sheet

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.*

- 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

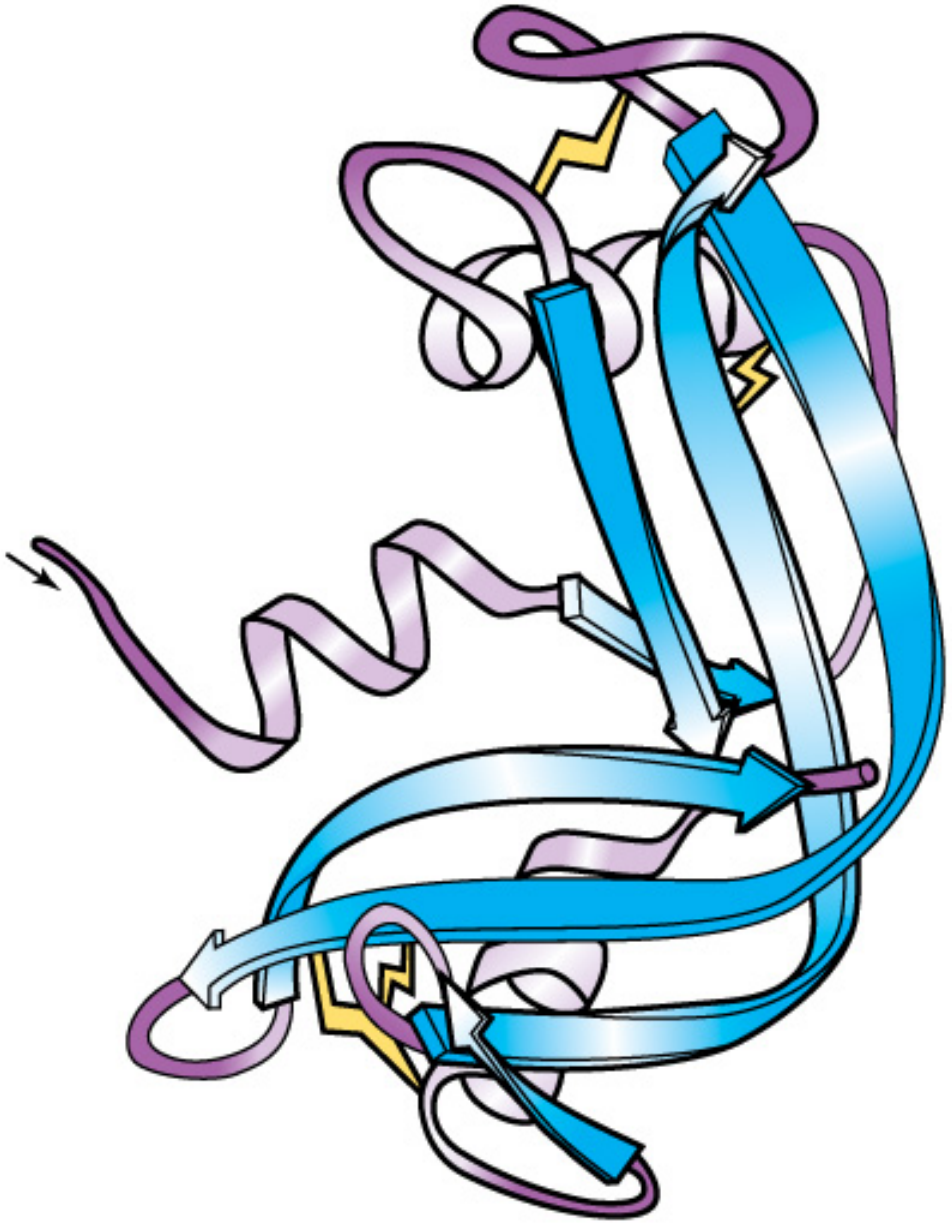


α Helix

β Sheet

Connecting loop

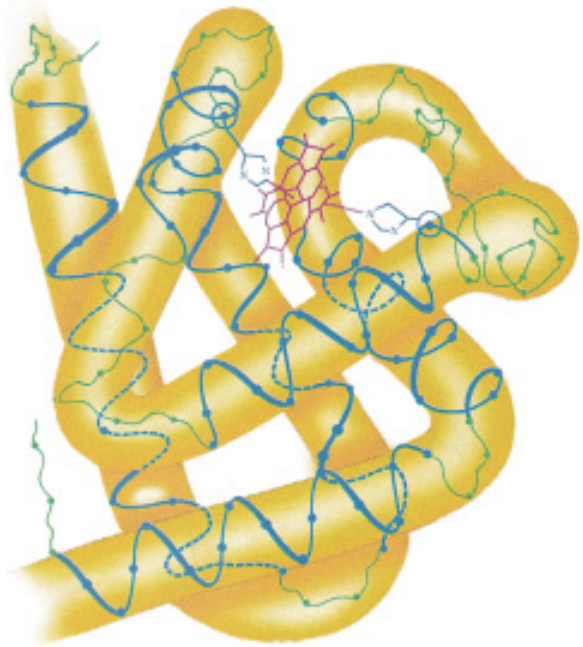
—S—S— links



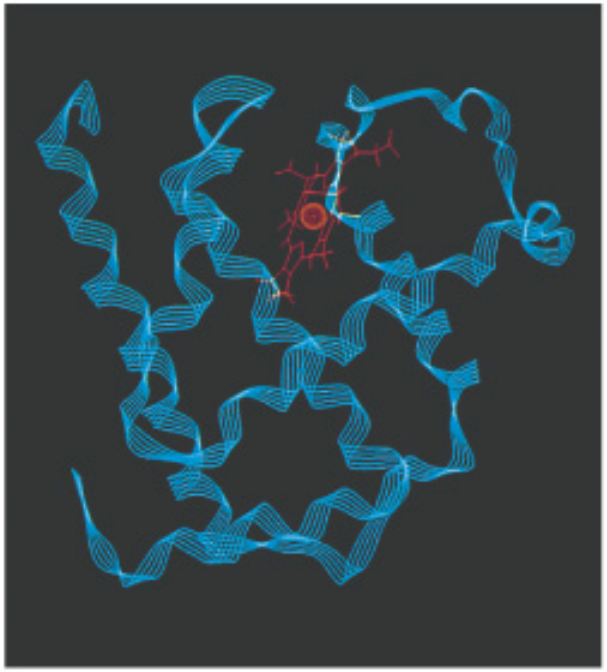
Ribonuclease

Shape-Determining Interactions in Proteins

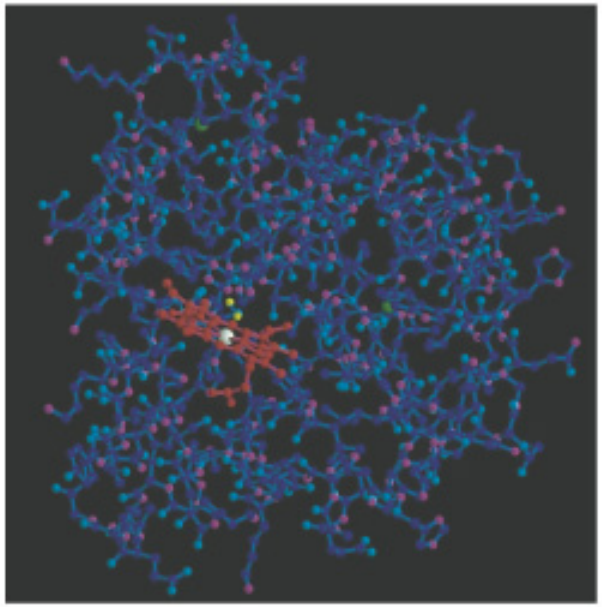
- The essential structure-function relationship for each protein depends on the polypeptide chain being held in its necessary shape by the interactions of atoms in the side chains.



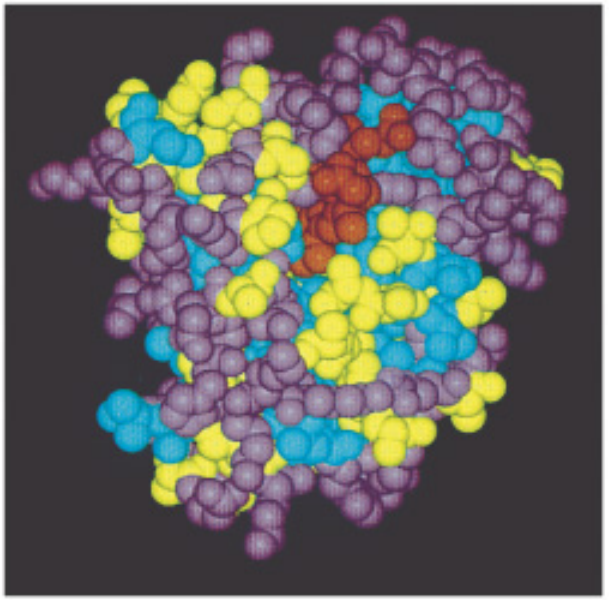
(a)



(b)



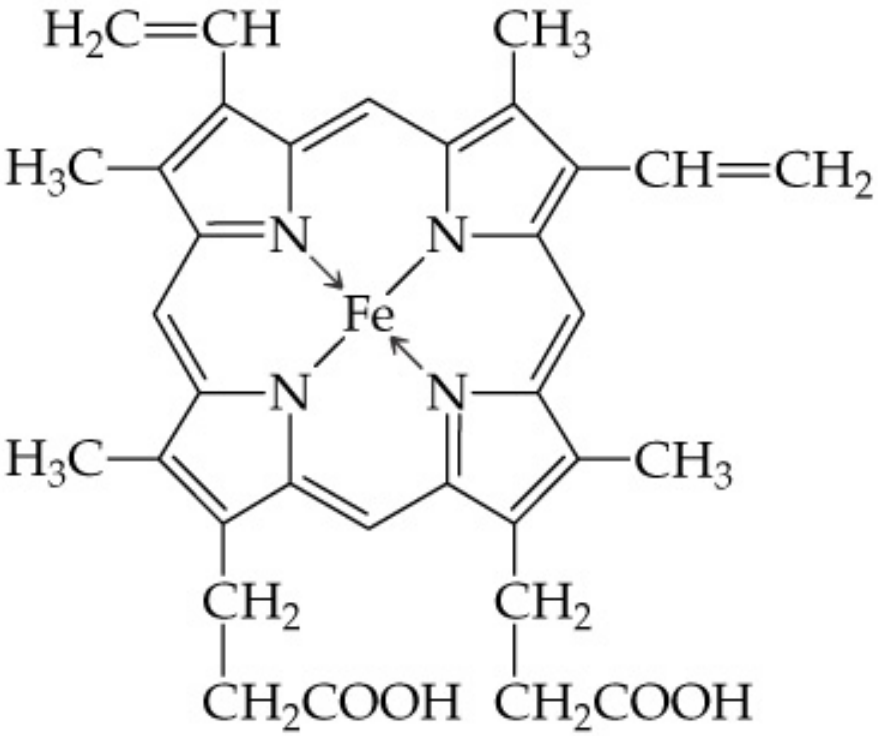
(c)



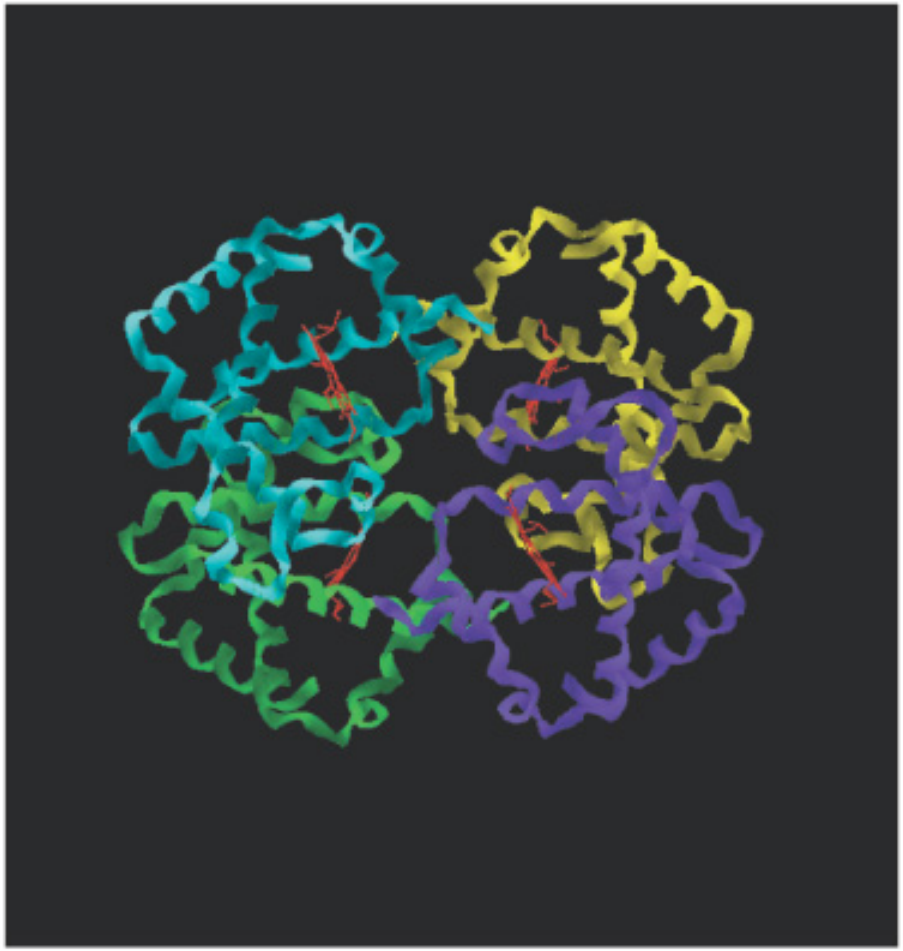
(d)

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)



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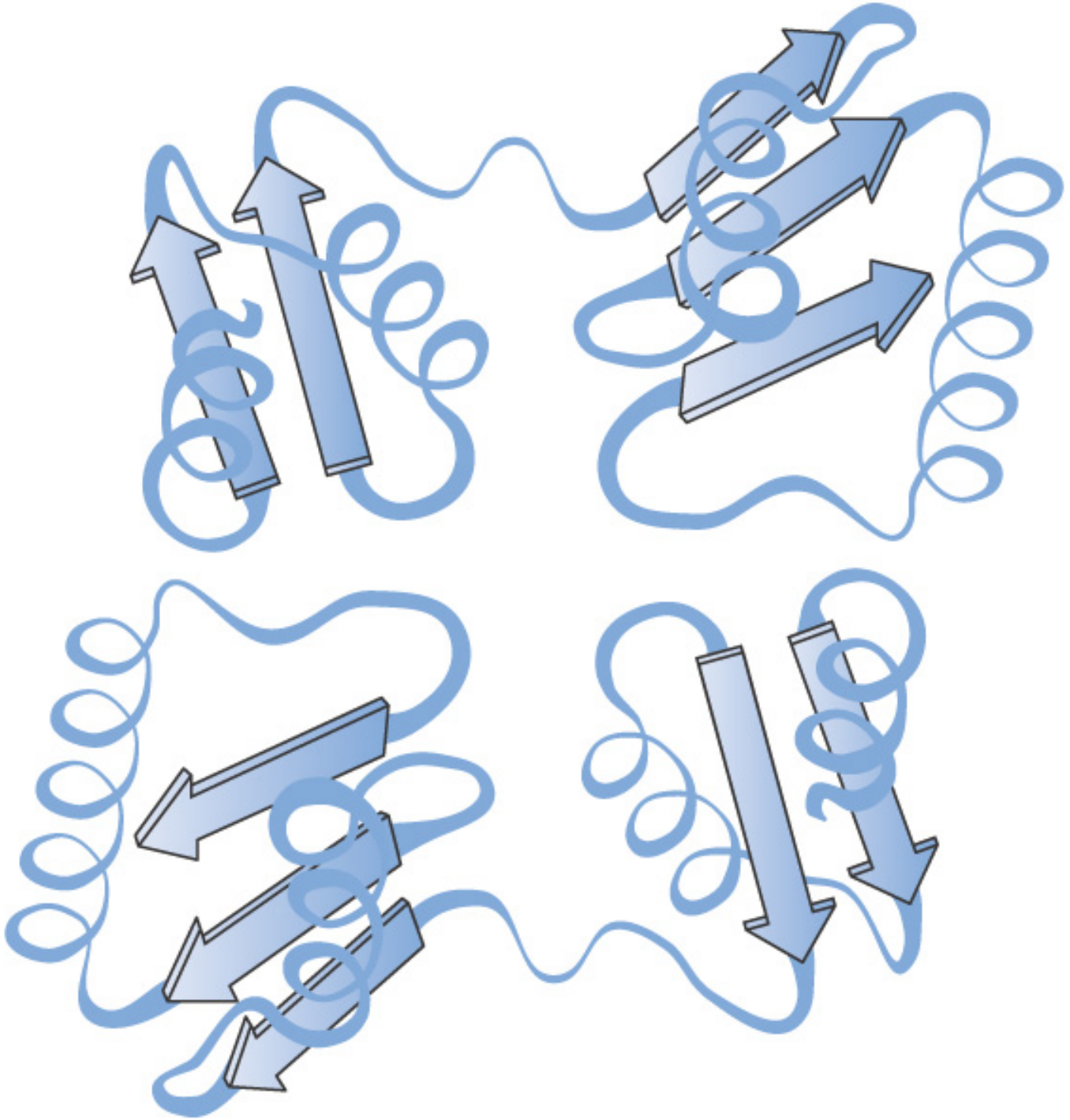
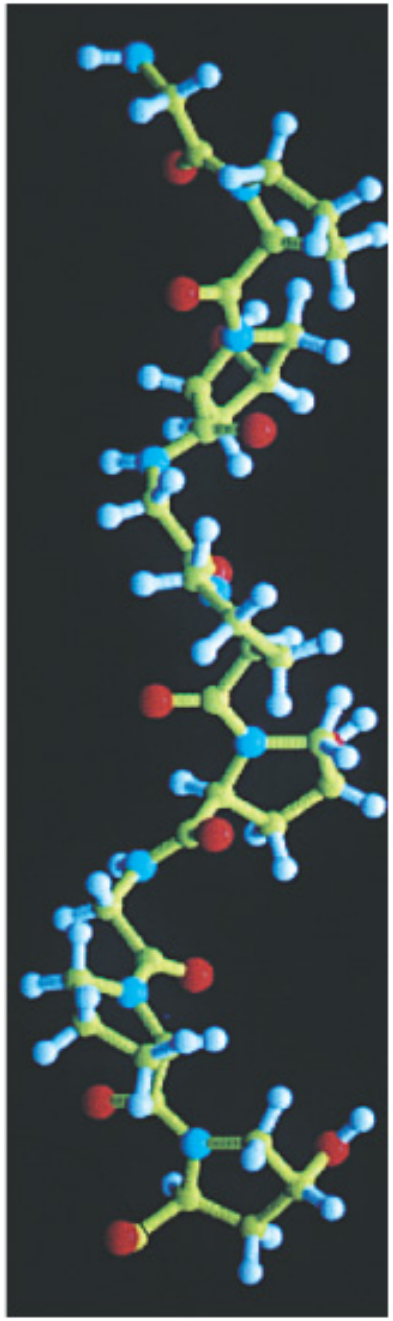
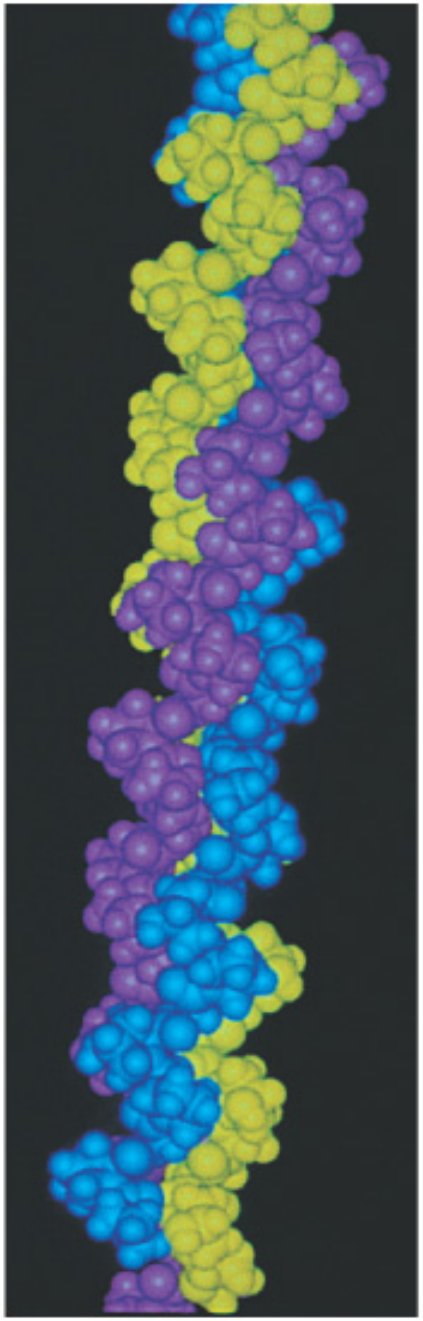
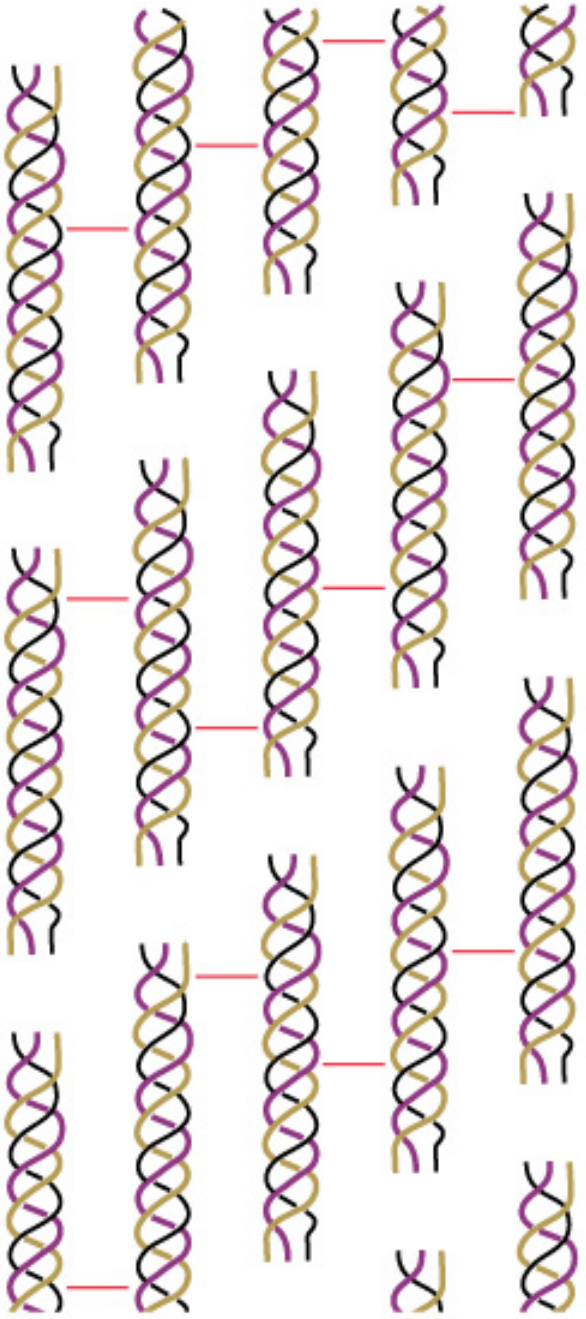




(a)



(b)

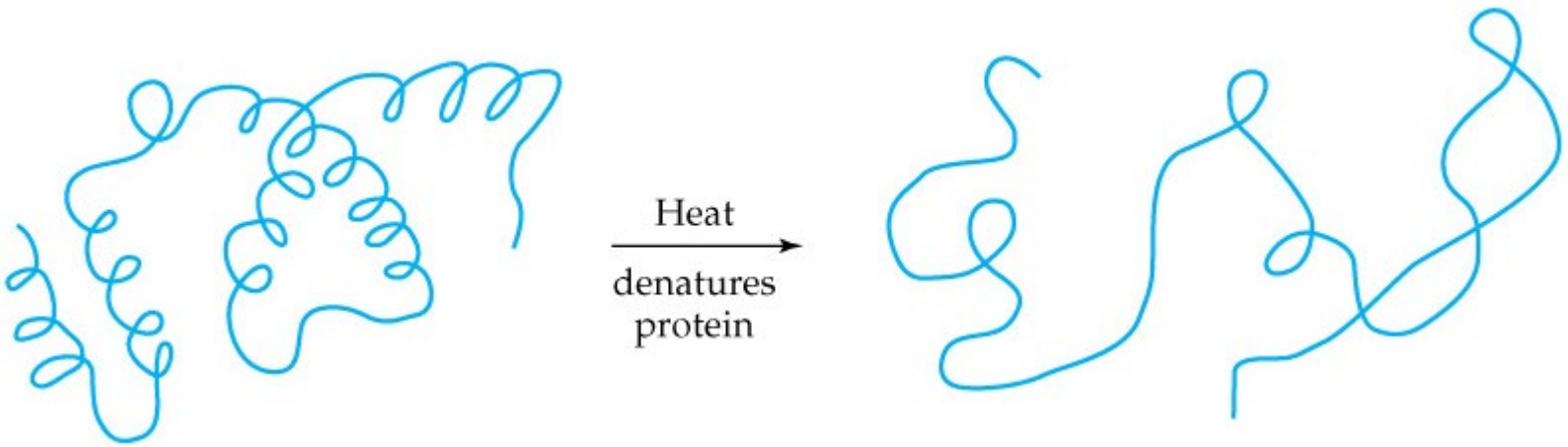


(c)

Chemical Properties of Proteins

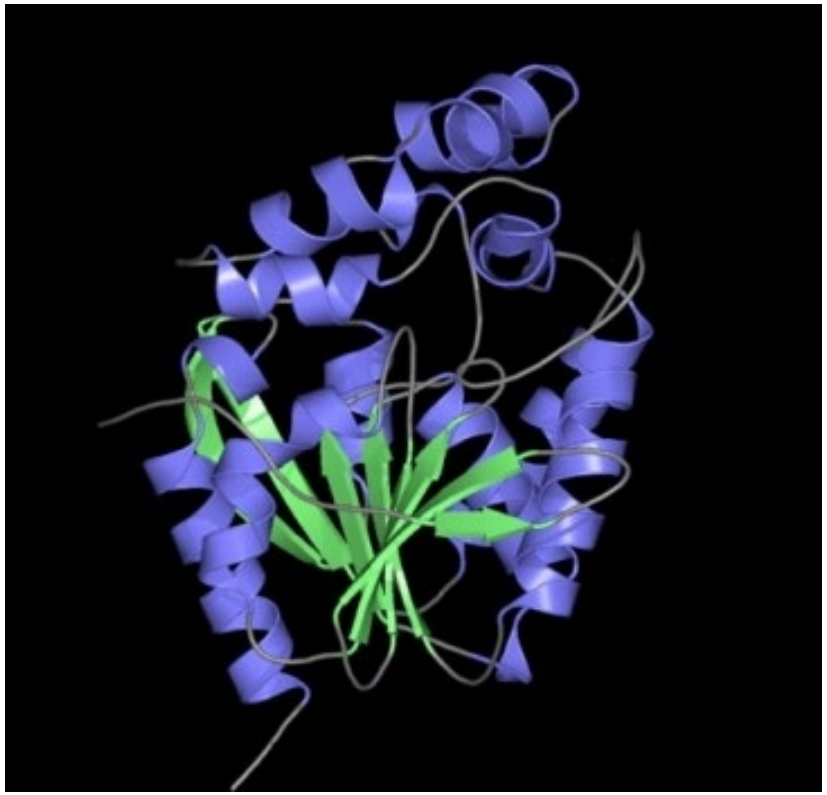
- *Protein hydrolysis:* In protein hydrolysis, peptide bonds are hydrolyzed to yield amino acids. This is reverse of protein formation.

- *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

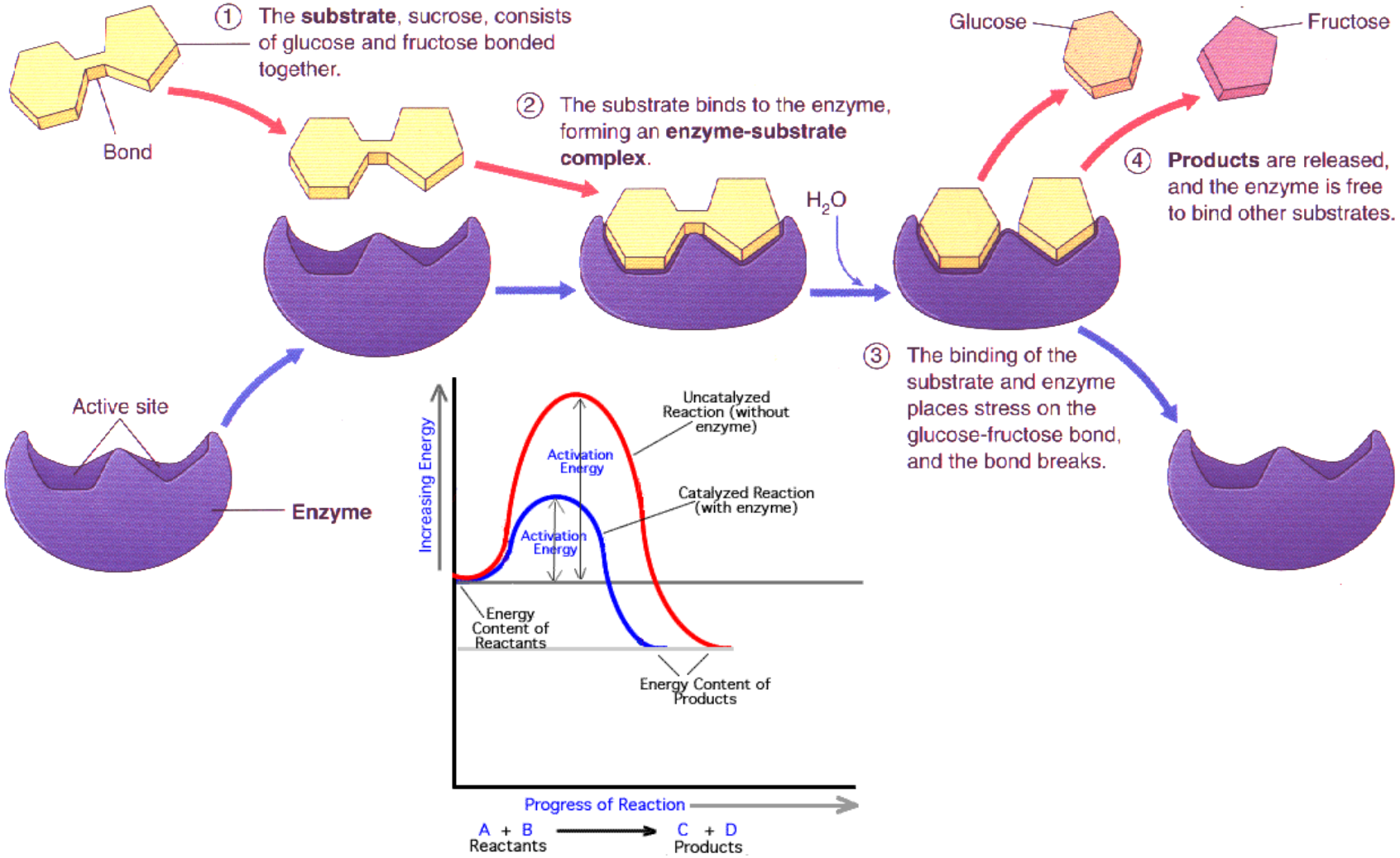


Catalysis by Enzymes

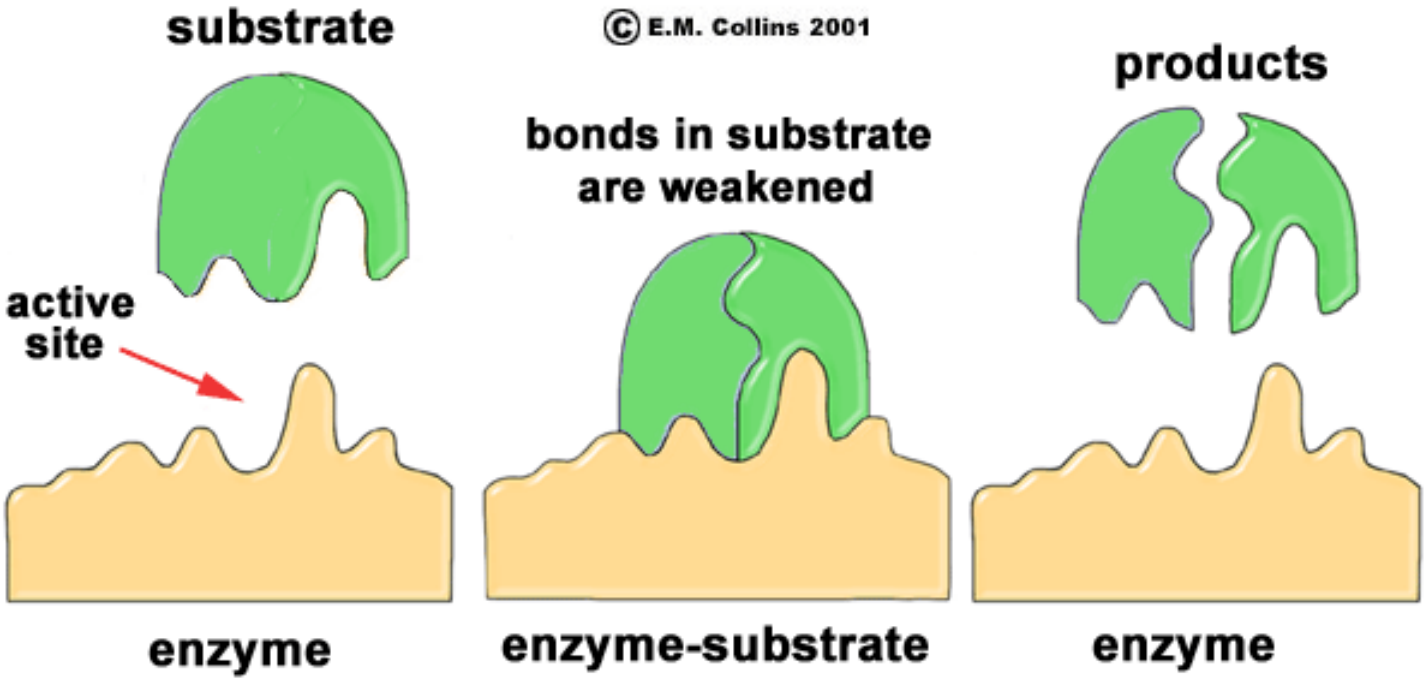
- ***Enzyme*** A protein that acts as a catalyst for a biochemical reaction.



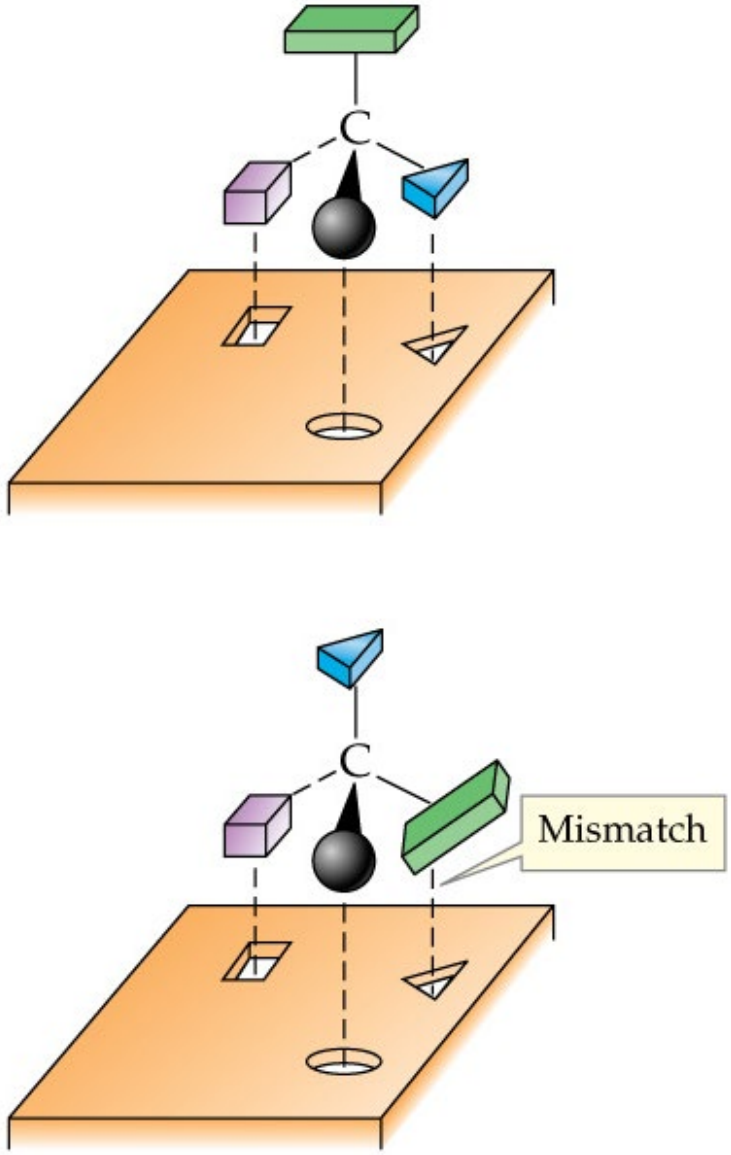
Enzymatic Reaction



Specificity



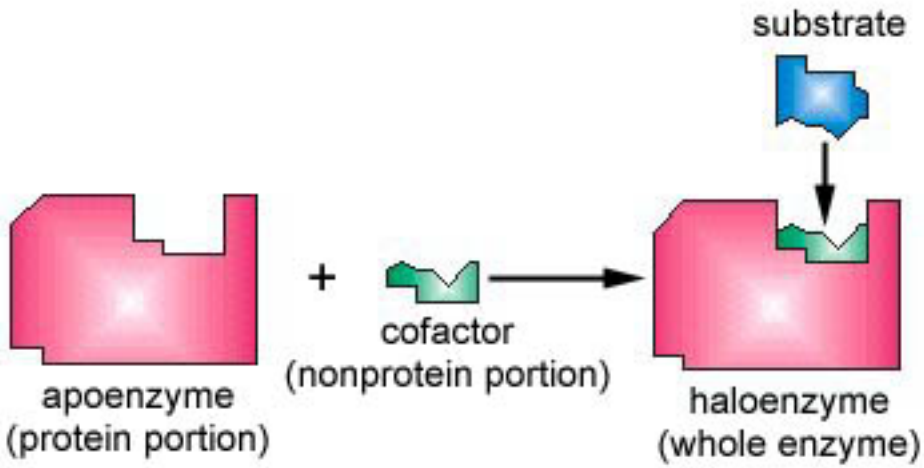
The specificity of an enzyme for one of two enantiomers is a matter of fit. One enantiomer fits better into the active site of the enzyme than the other enantiomer. Enzyme catalyzes reaction of the enantiomer that fits better into the active site of the enzyme.

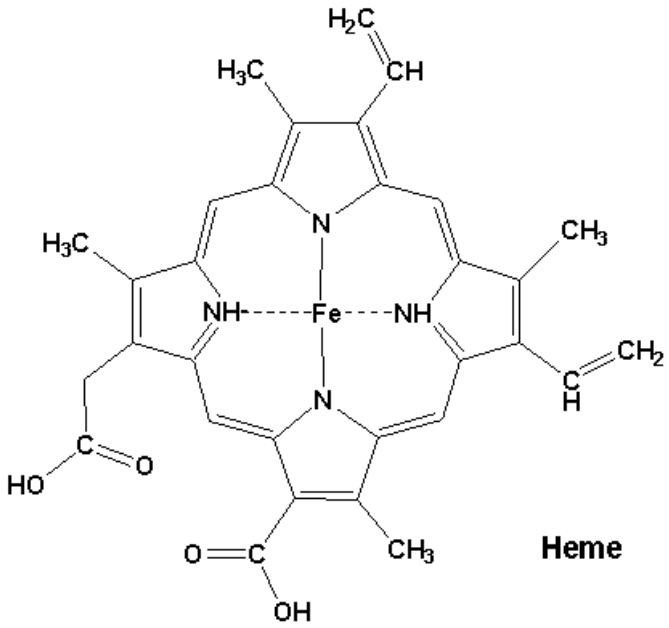


Enzyme Cofactors

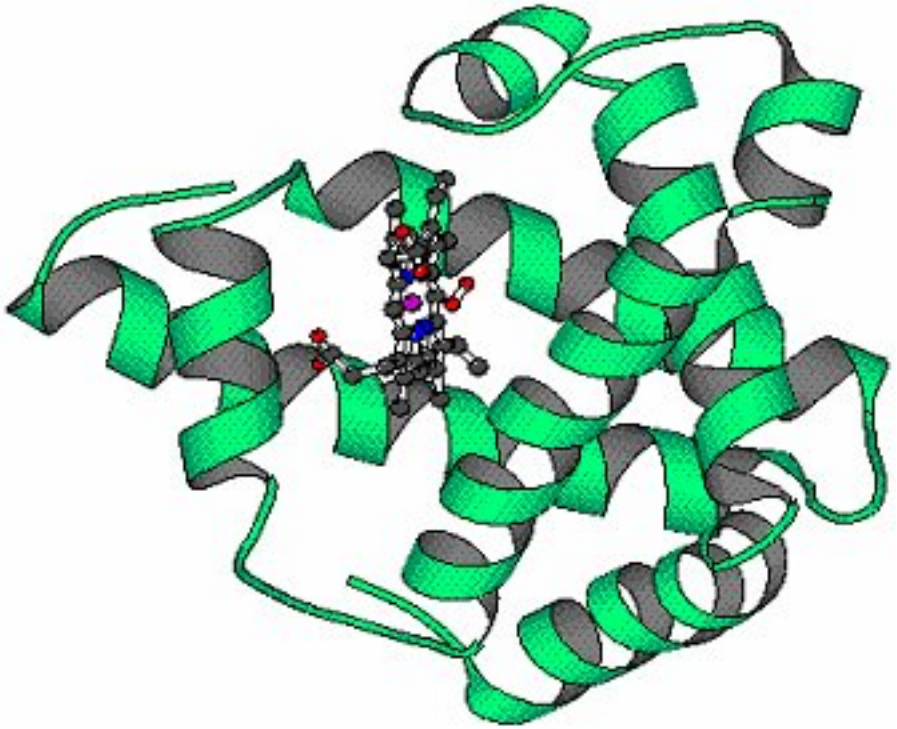
- Many enzymes are conjugated proteins that require nonprotein portions known as ***cofactors***.
- Some cofactors are metal ions, others are nonprotein organic molecules called ***coenzymes***.
- An enzyme may require a metal-ion, a coenzyme, or both to function.

Cofactor





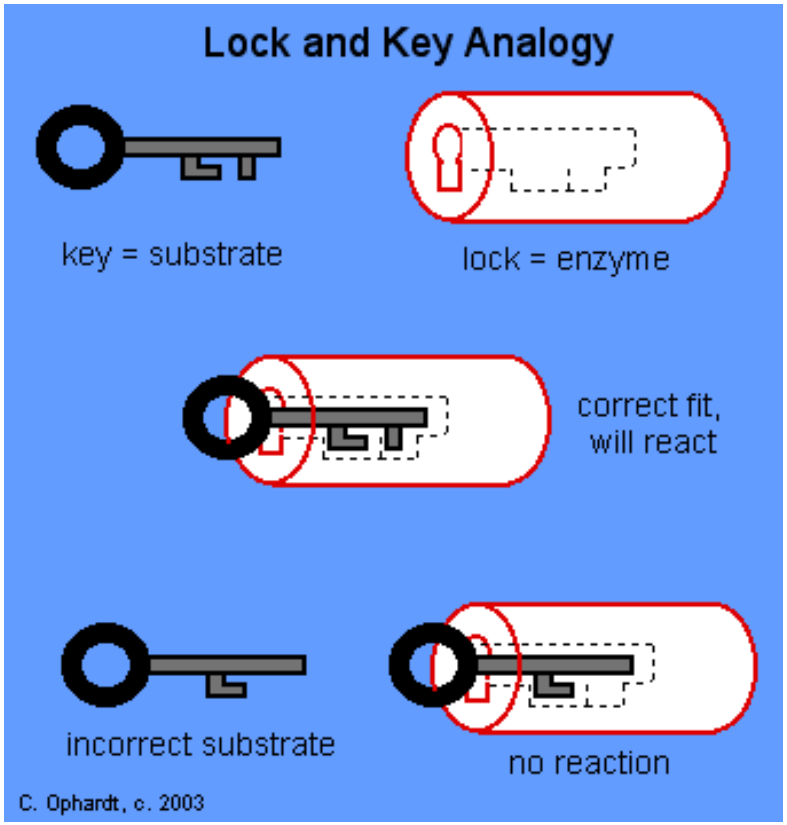
Heme

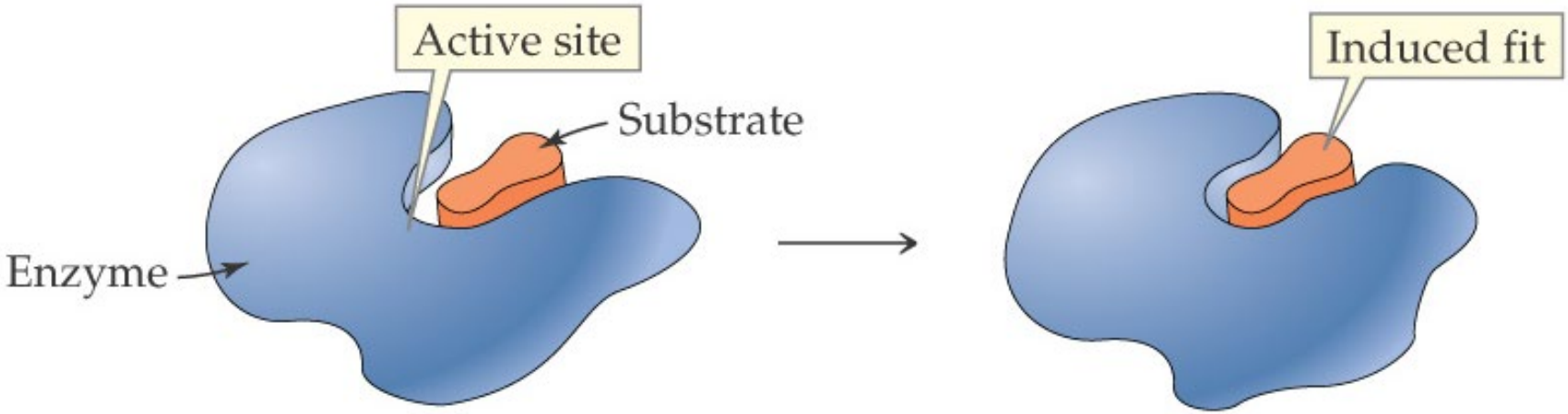


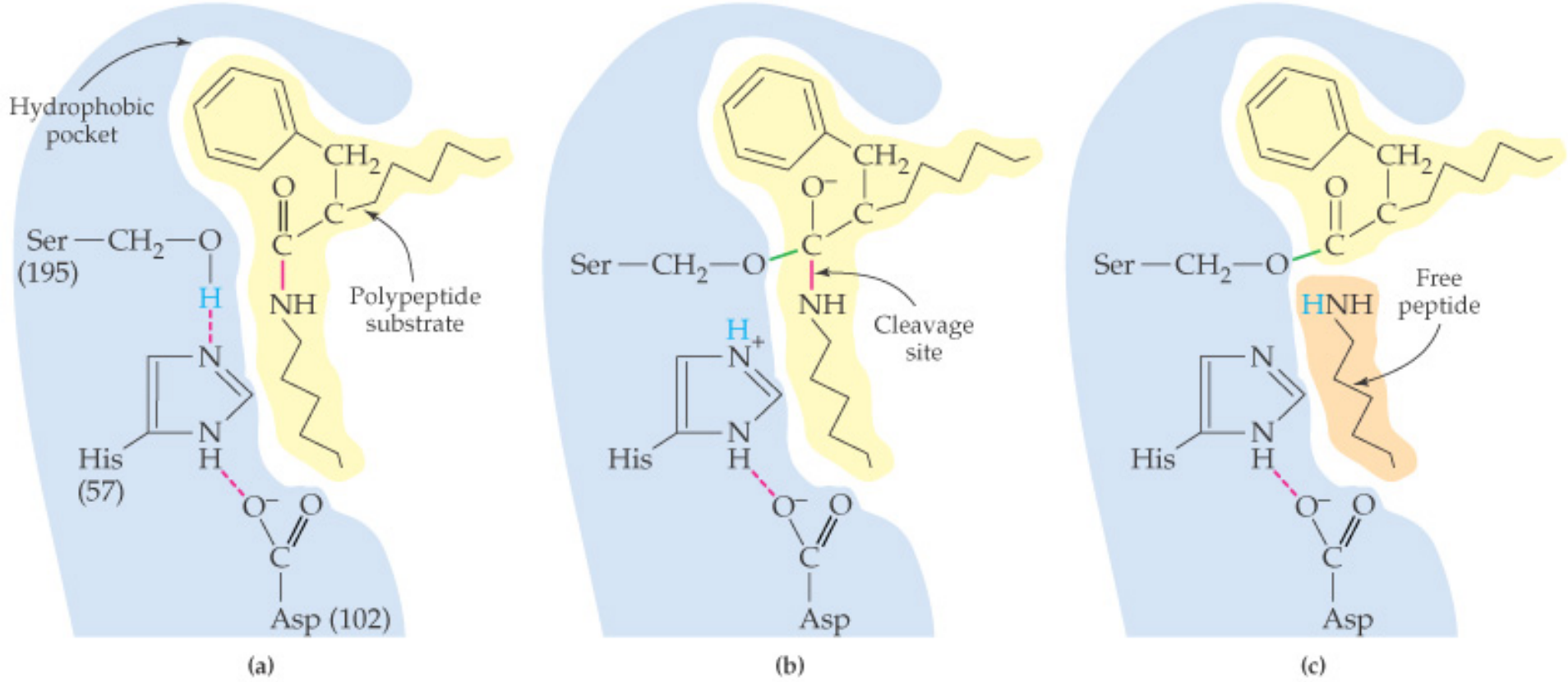
- Cofactors provide additional chemically active functional groups which are not present in the side chains of amino acids that made up the enzyme.
- Metal ions may anchor a substrate in the active site or may participate in the catalyzed reaction.

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)
H
N
N
H
His
(57)
O⁻ O
C
Asp (102)
CH2
O
C
C
NH
Polypeptide substrate
(a)
O⁻
C
Ser —CH2—O
NH
Cleavage site
H+
N
N
H
His
O⁻ O
C
Asp
(b)
HNH
Free peptide
(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.

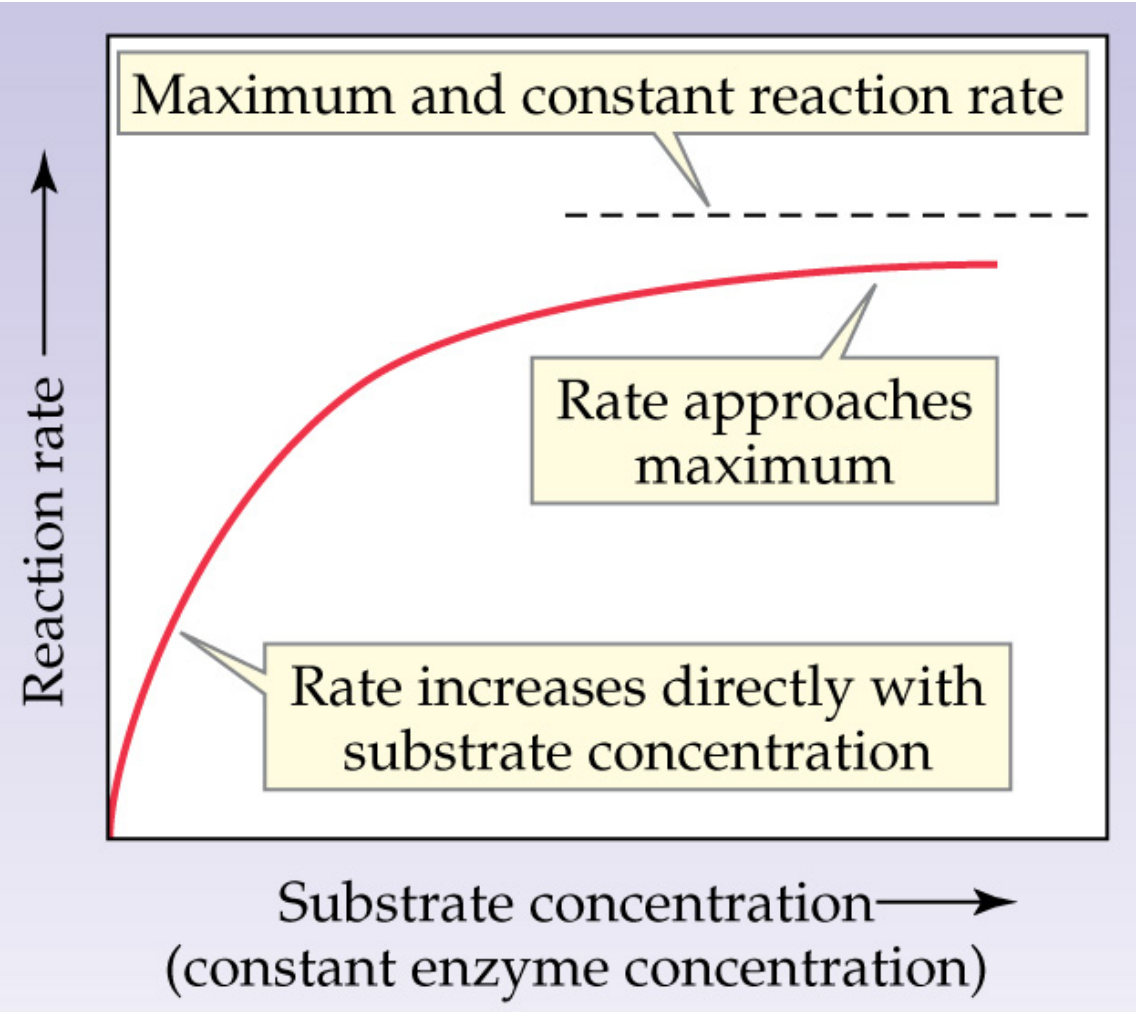
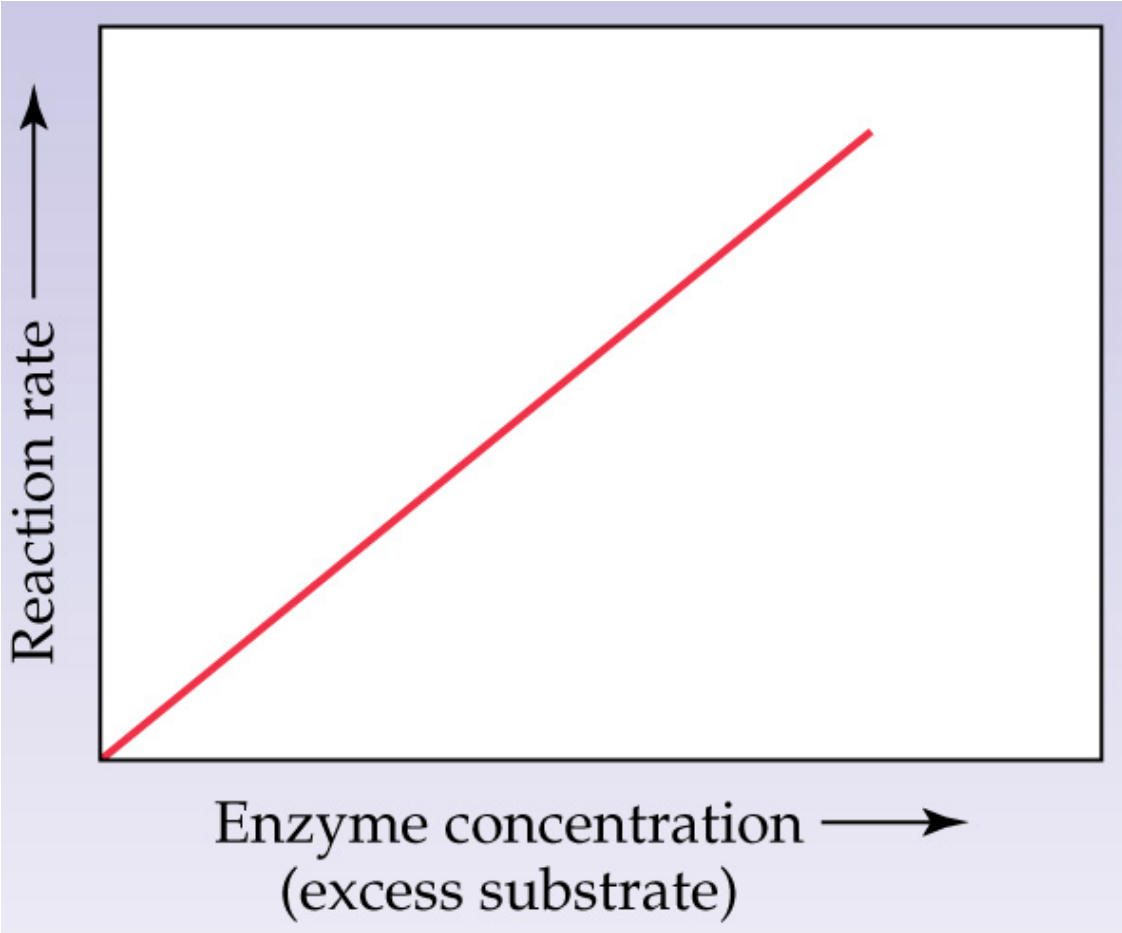


Fig 19.5 Change of reaction rate with substrate concentration when enzyme concentration is constant.

- *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.

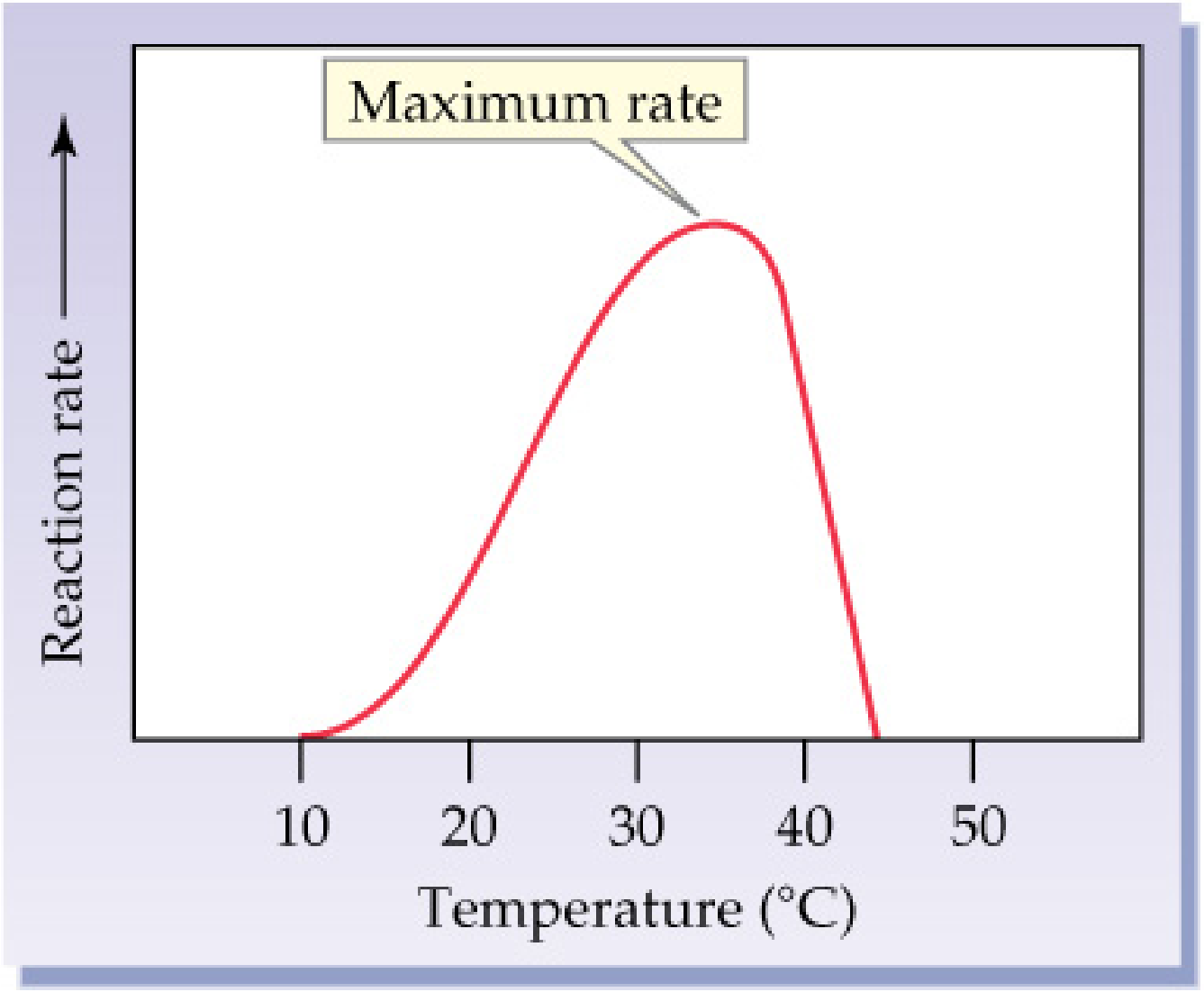
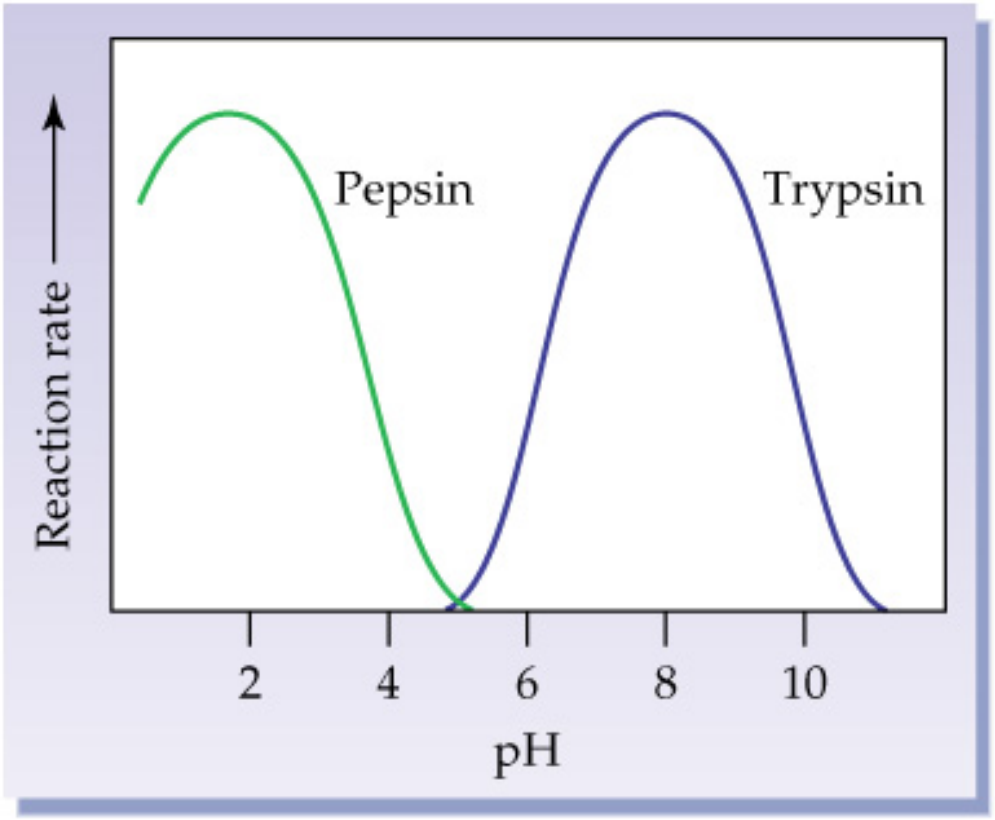


Fig 19.7 (a) Effect of temperature on reaction rate

- 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.

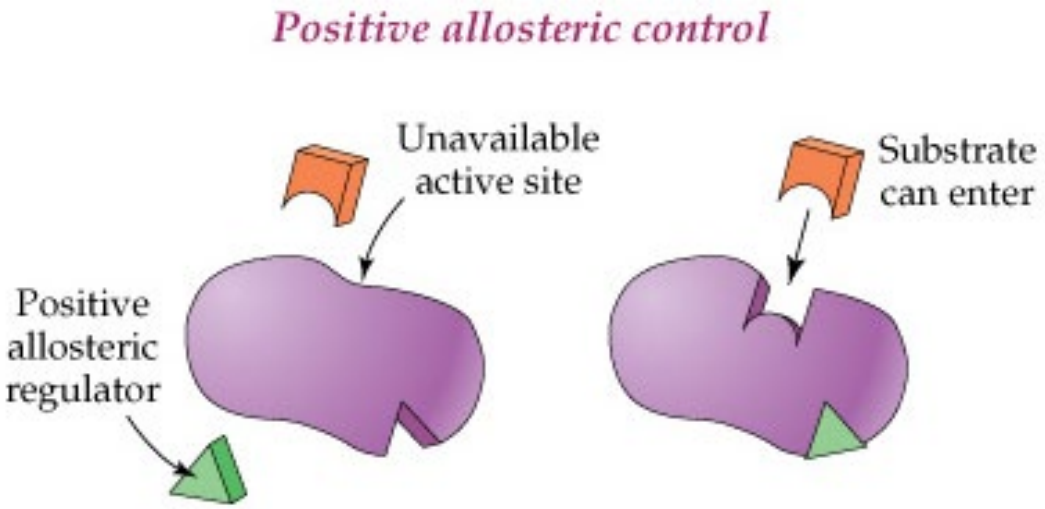


19.7 Enzyme Regulation: Feedback and Allosteric Control

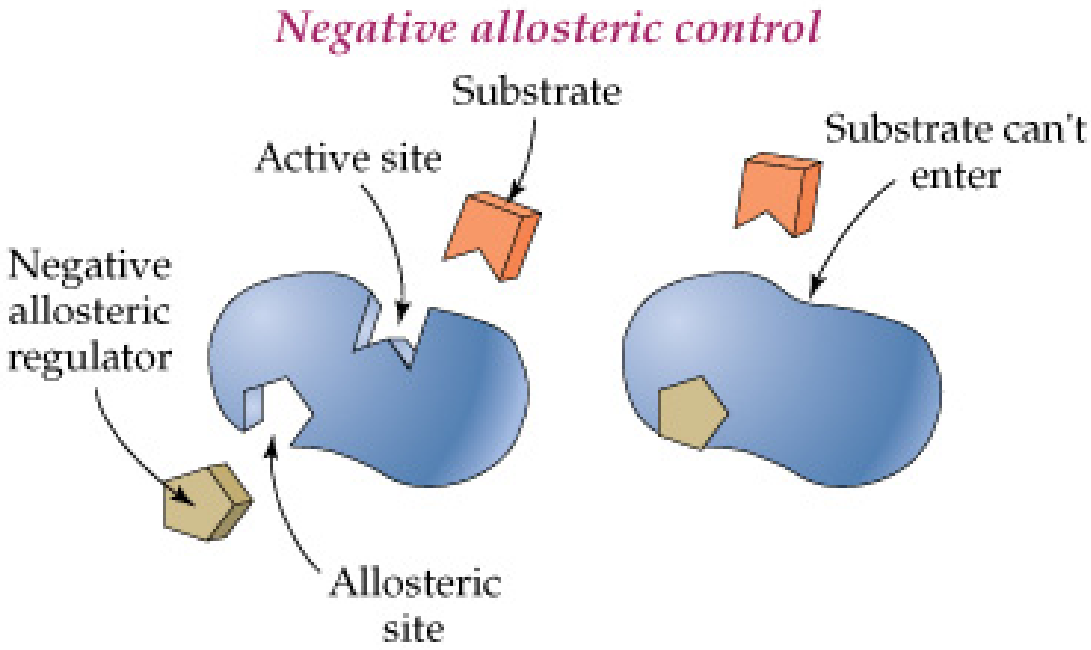
- Concentration of thousands of different chemicals vary continuously in living organisms which requires regulation of enzyme activity.
- Any process that starts or increase the activity of an enzyme is ***activation.***
- Any process that stops or slows the activity of an enzyme is ***inhibition.***

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.

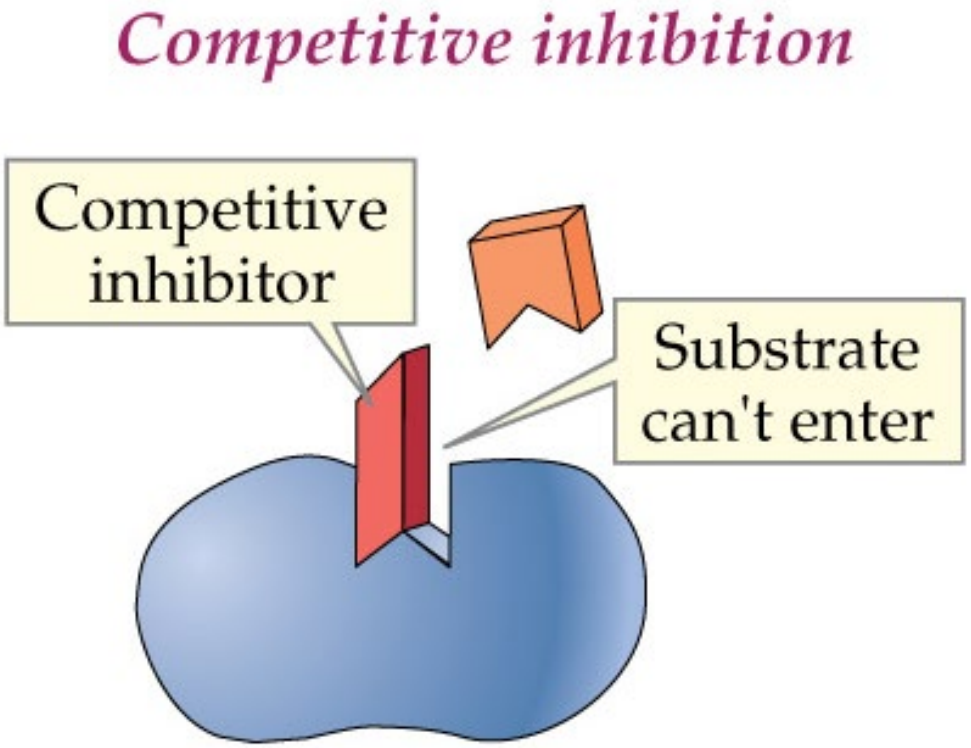


A negative regulator changes the activity site so that the enzyme becomes less effective catalyst and rate slows down.

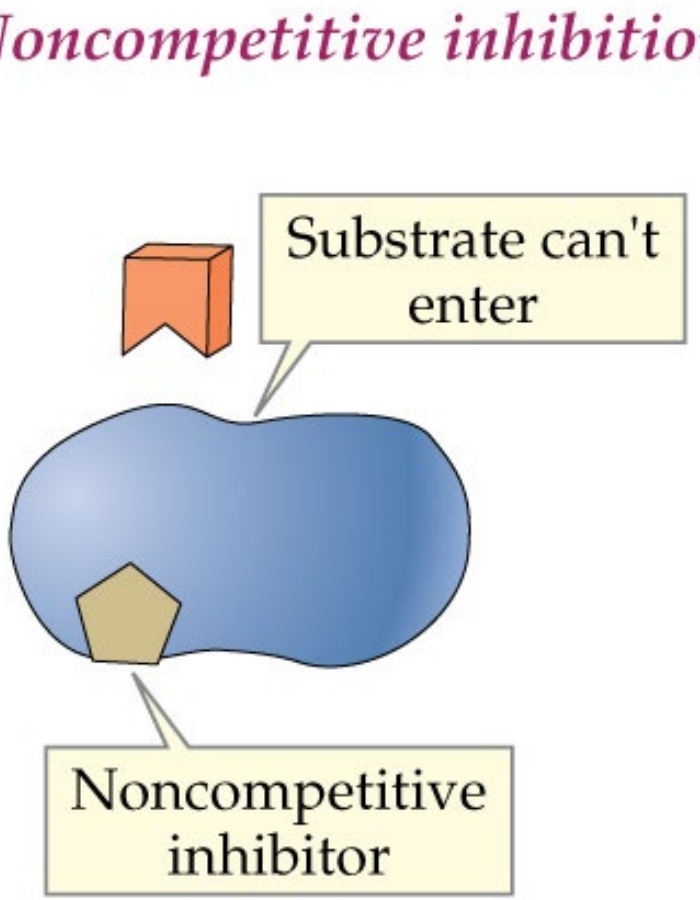
19.8 Enzyme Regulation: Inhibition

- 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.

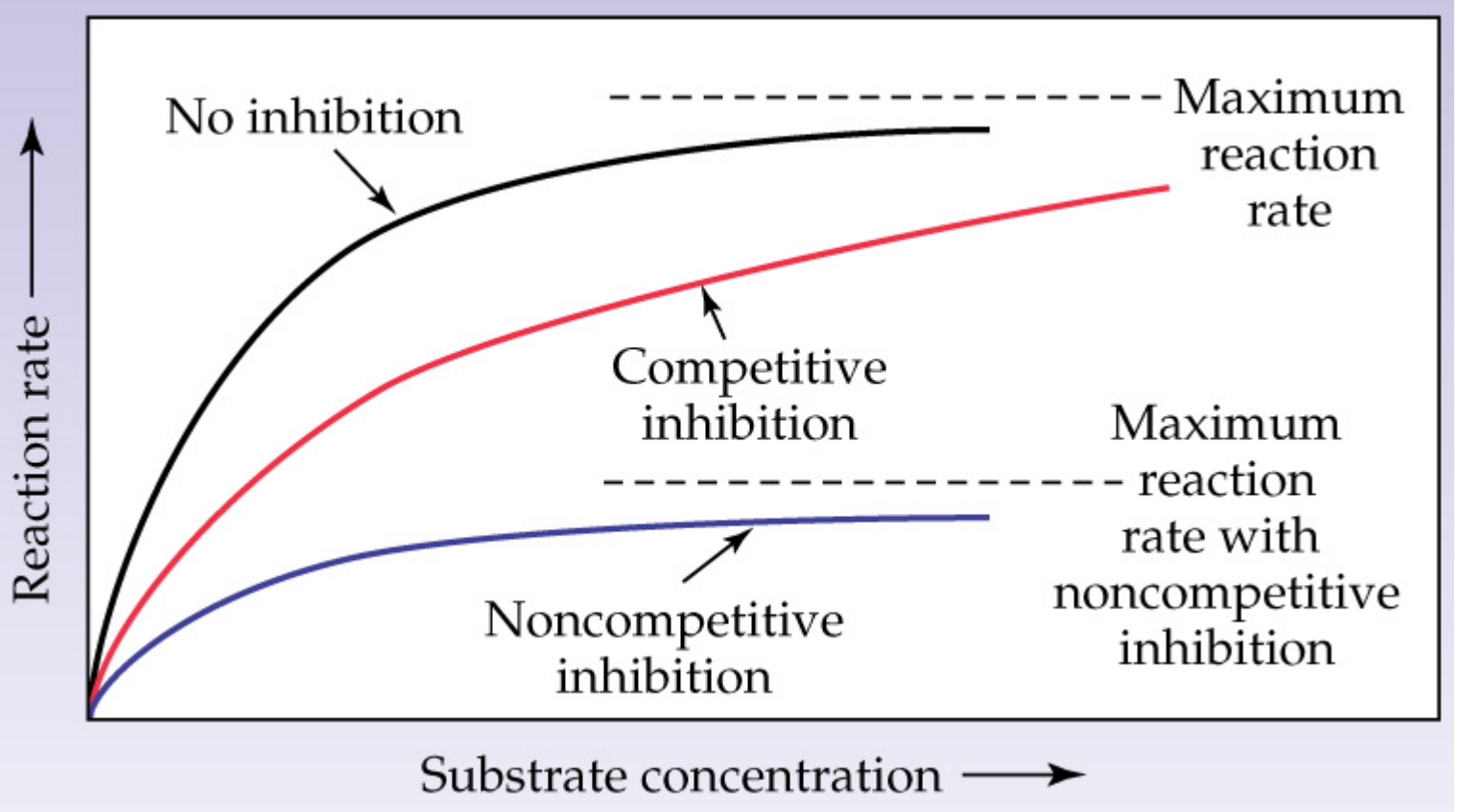
- Inhibitions are further classified as:
- *Competitive inhibition if* the inhibitor binds to the active site.

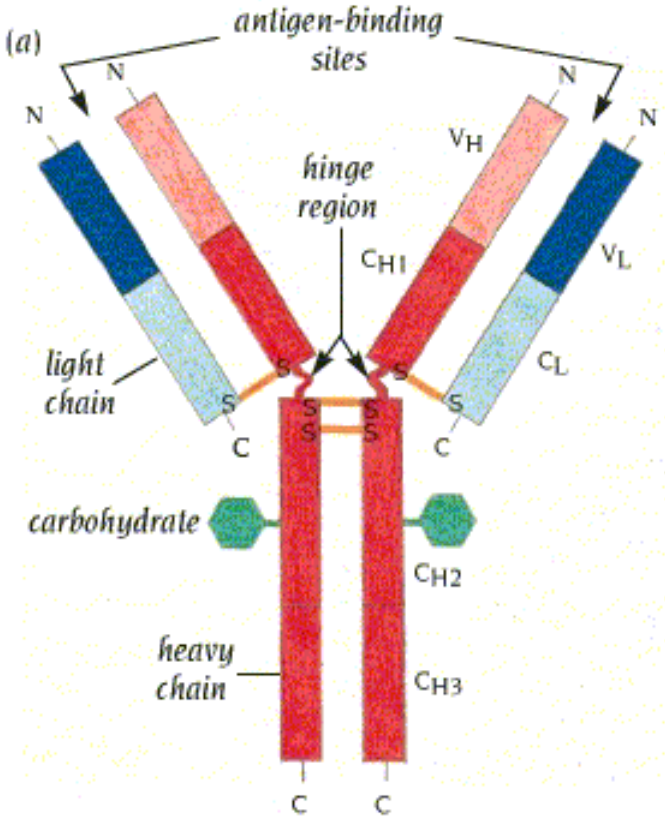


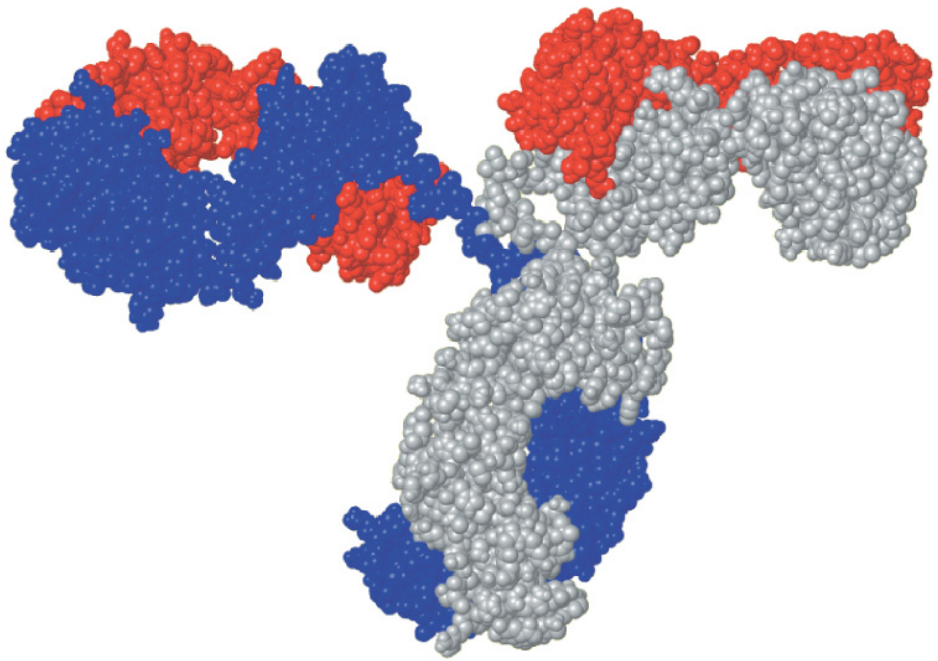
- *Noncompetitive inhibition,* if the inhibitor binds elsewhere and not to the active site.



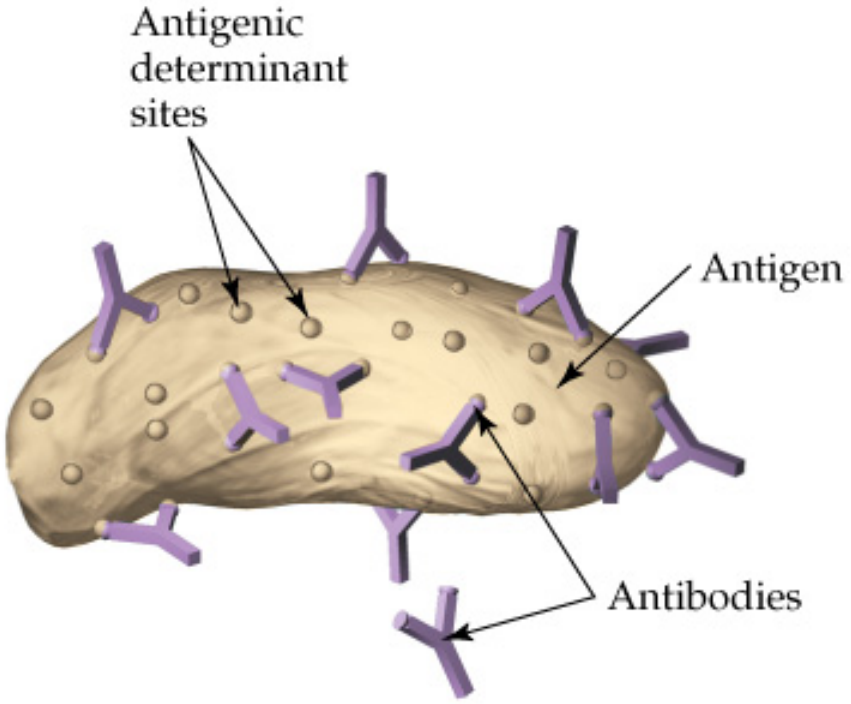
•The rates of enzyme catalyzed reactions with or without a competitive inhibitor are shown in the Fig 19.9 below.



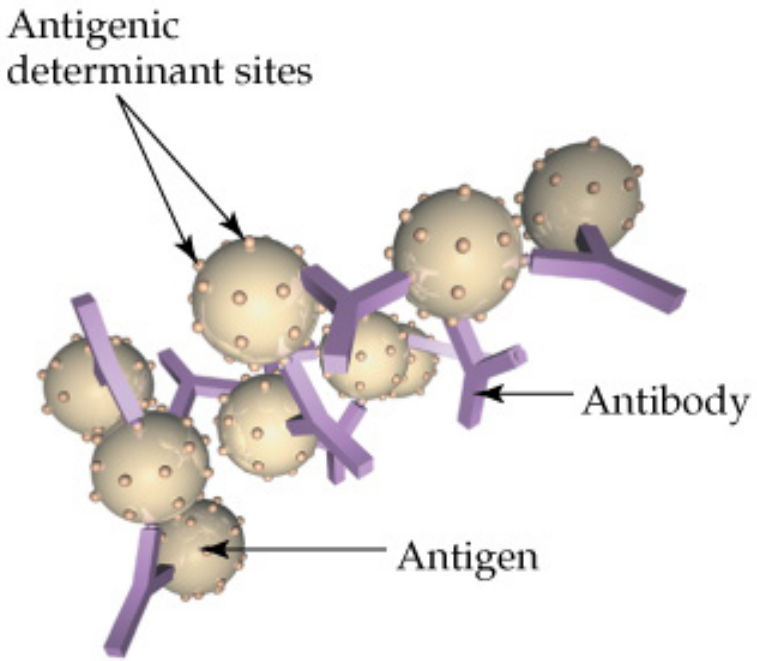

(a)
antigen-binding sites
N
N
N
N
VH
VL
hinge region
CH1
CL
light chain
S
S
S
S
S
S
S
S
C
C
carbohydrate
CH2
heavy chain
CH3
C
C



(b)


Antigenic determinant sites
Antigen
Antibodies

(a)

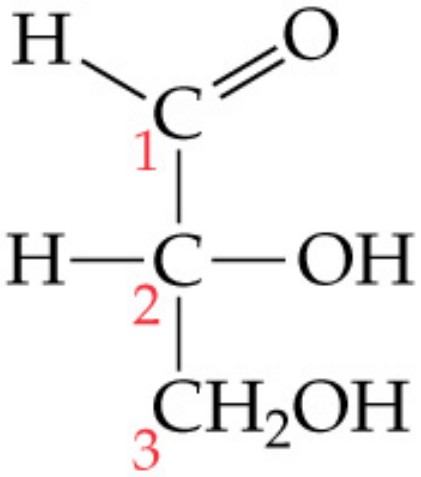

Antigenic determinant sites
Antibody
Antigen

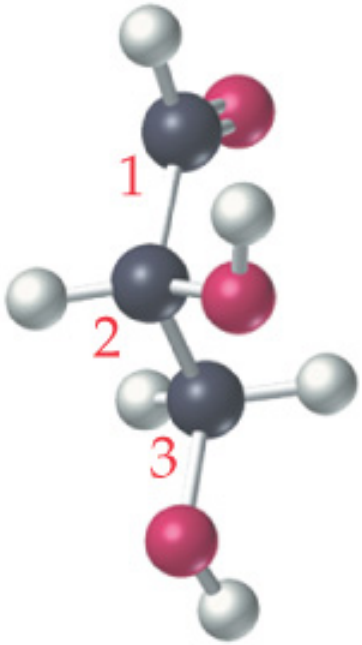
(b)

An Introduction to Carbohydrates

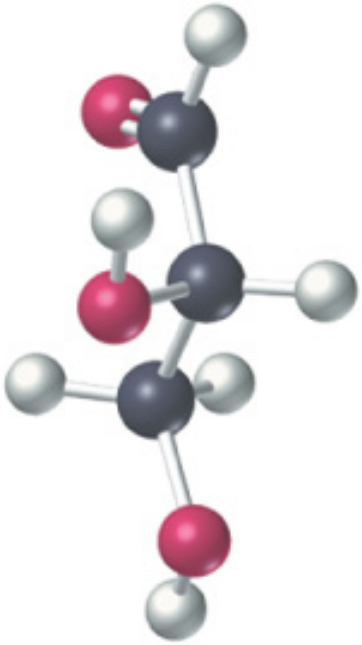
- *Carbohydrates* are a large class of naturally occurring polyhydroxy aldehydes and ketones.
- Monosaccharides also known as simple sugars, are the simplest carbohydrates containing 3-7 carbon atoms.
- sugar containing an aldehydes is known as an aldose.
- sugar containing a ketones is known as a ketose.

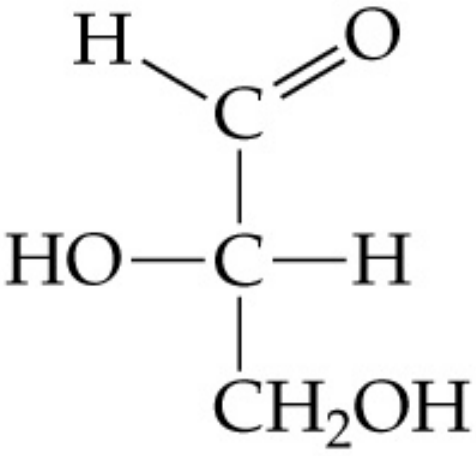
- The number of carbon atoms in an aldose or ketose may be specified as by tri, tetr, pent, hex, or hept. For example, glucose is aldohexose and fructose is ketohexose.
- Monosaccharides react with each other to form disaccharides and polysaccharides.
- Monosaccharides are chiral molecules and exist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



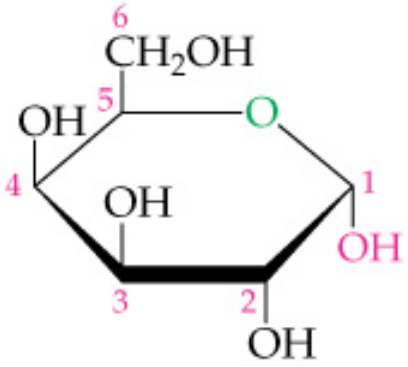


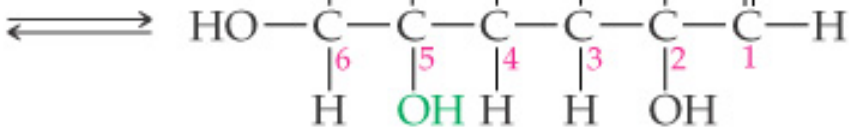
D-Glyceraldehyde
Right-handed

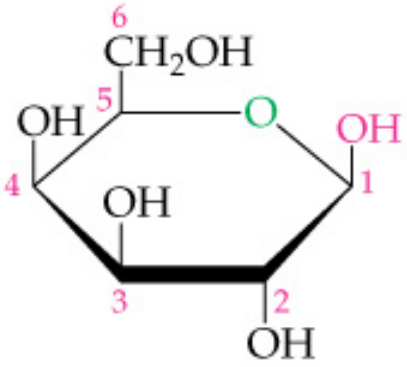


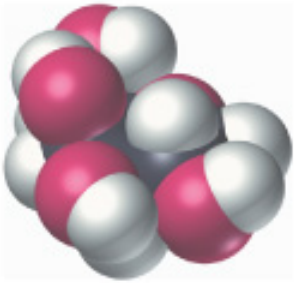


L-Glyceraldehyde
Left-handed

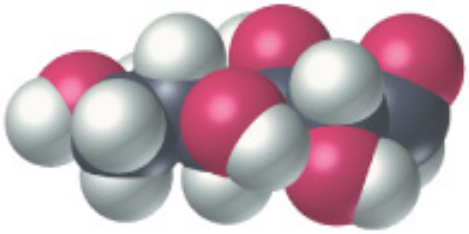




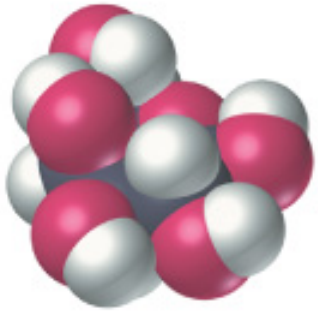




α-D-Galactose

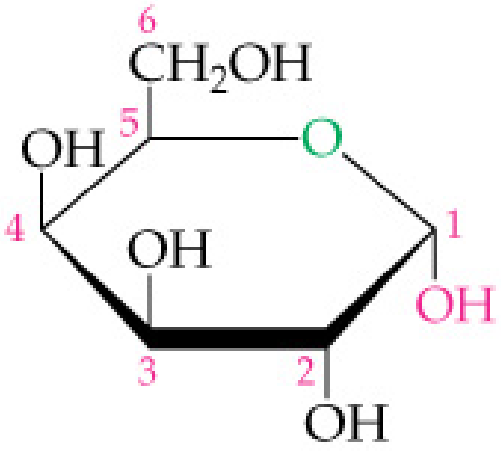


Open-chain galactose

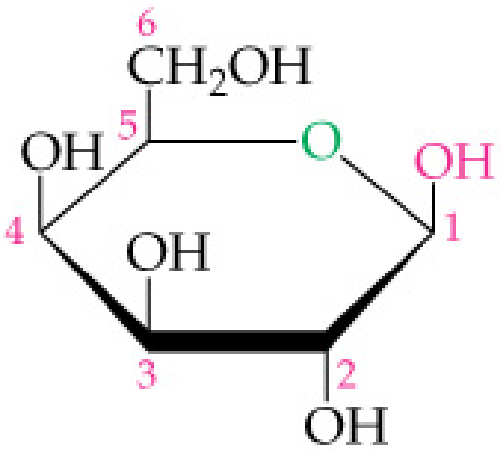


β-D-Galactose

- *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.



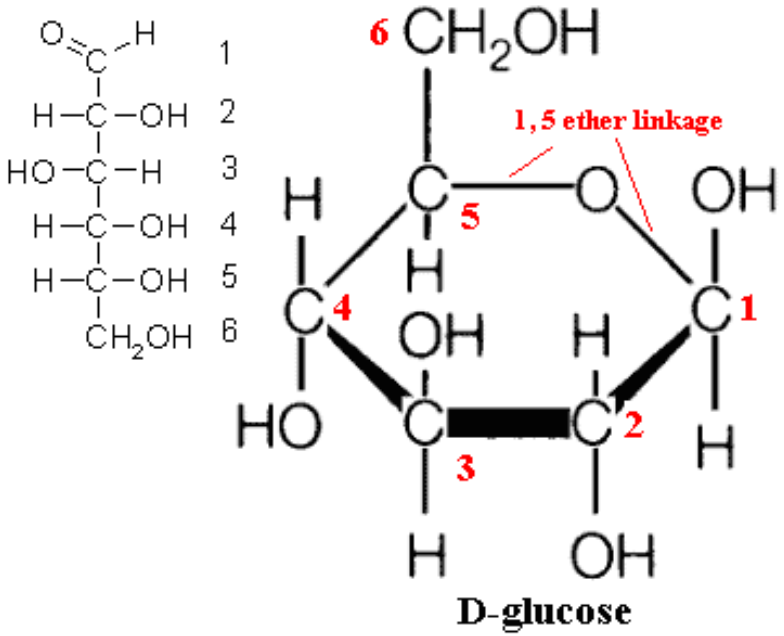
α-D-Galactose

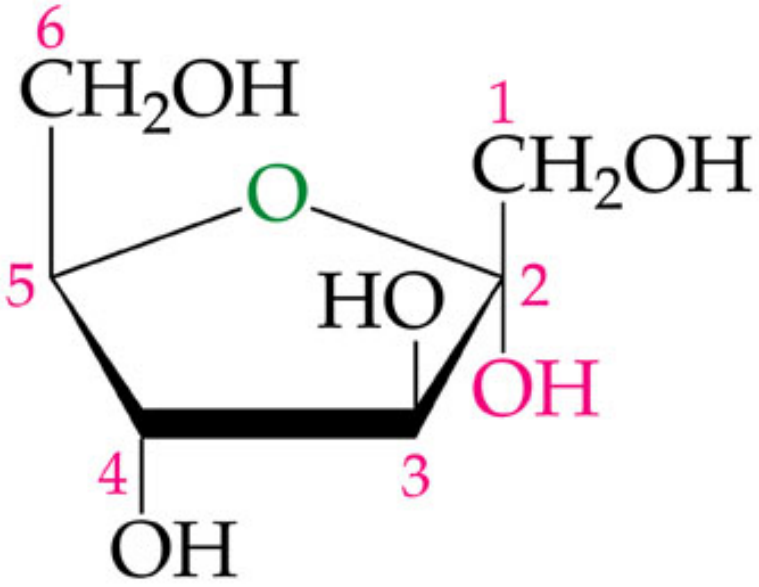


β-D-Galactose

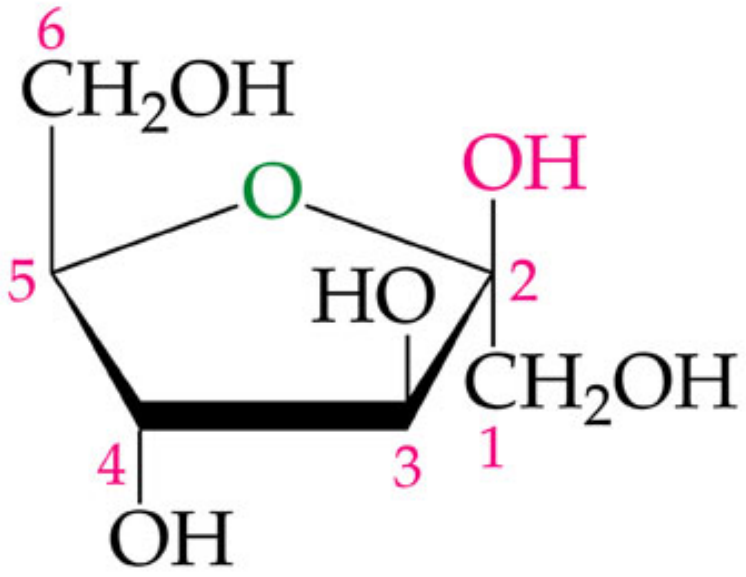
Some Important Monosaccharides

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.

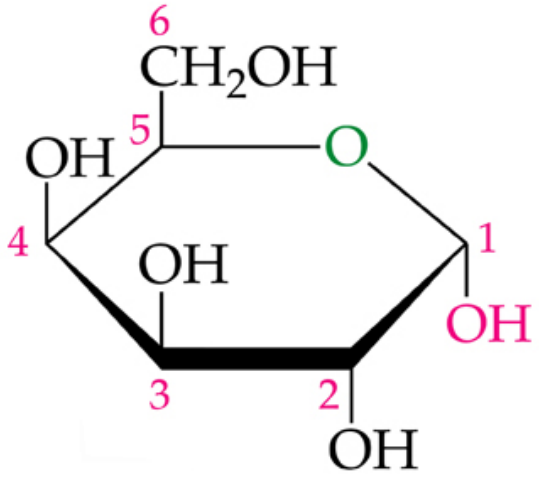




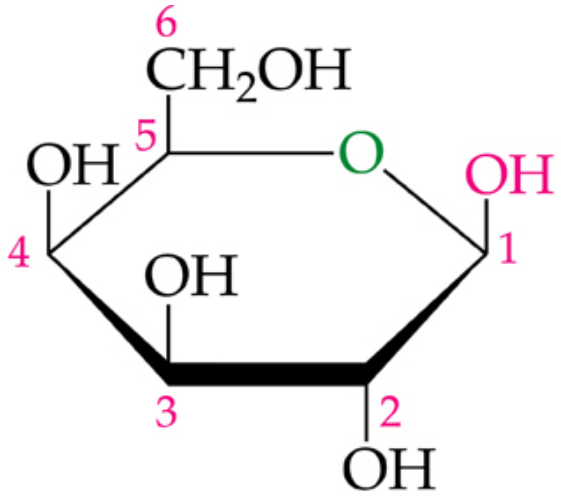
α-D-Fructose



β-D-Fructose

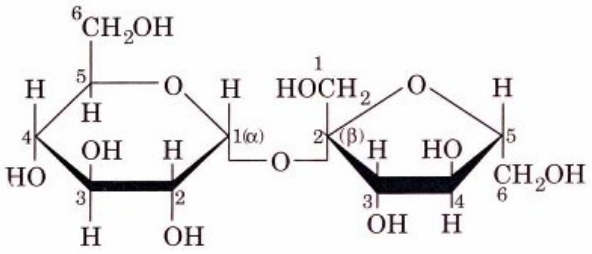


α-D-Galactose

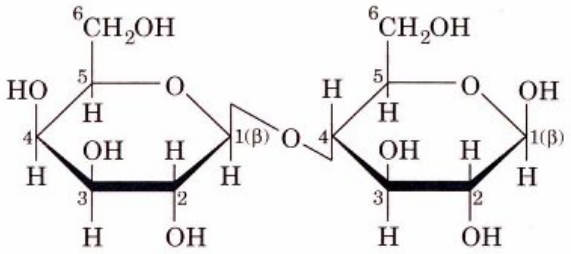


β-D-Galactose

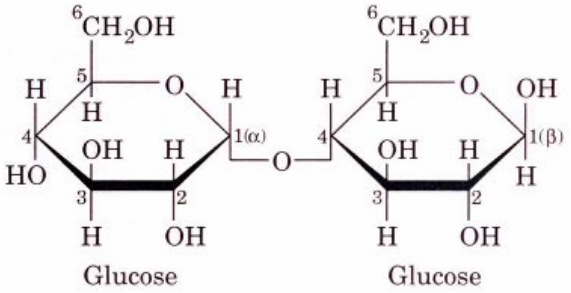
Some Common Disaccharides



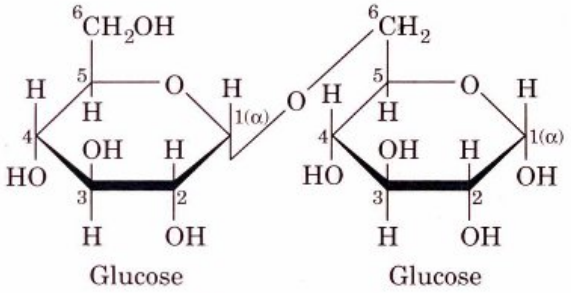
Sucrose



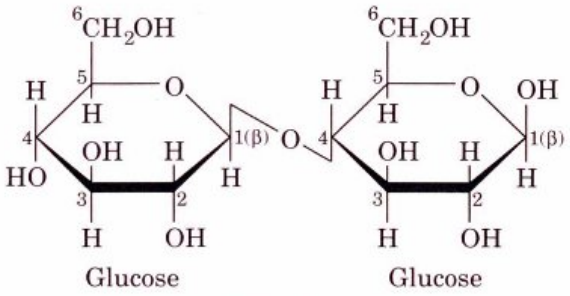
Lactose



Maltose

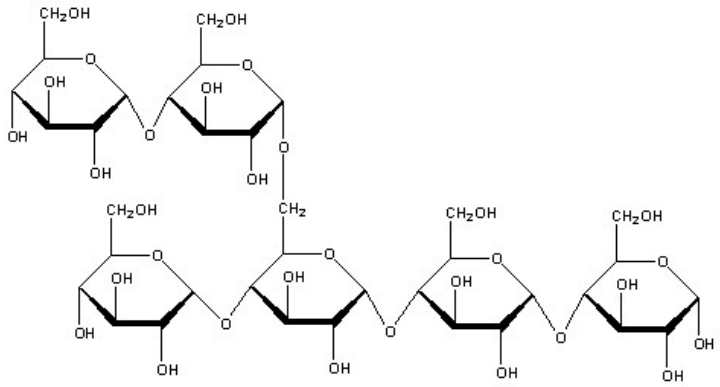


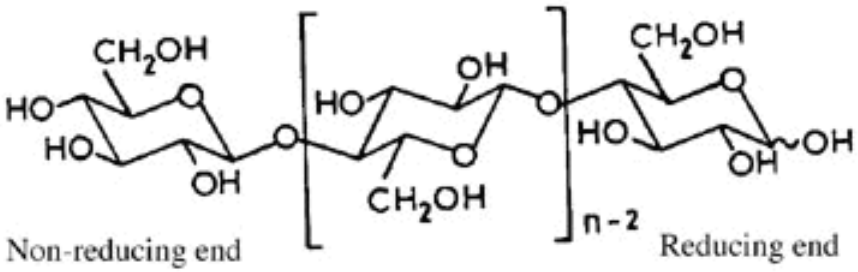
Isomaltose



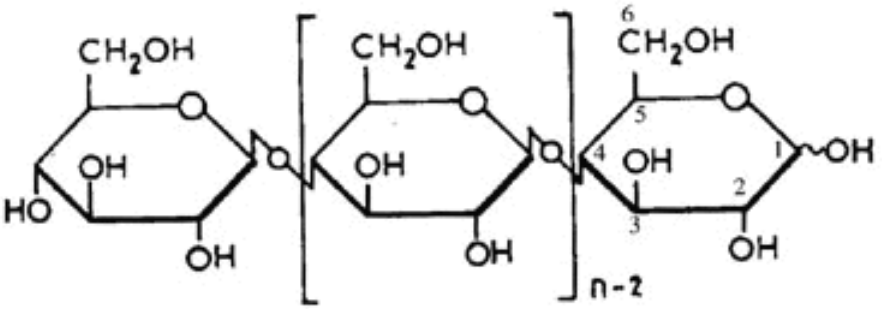
Cellobiose

Polysaccharides

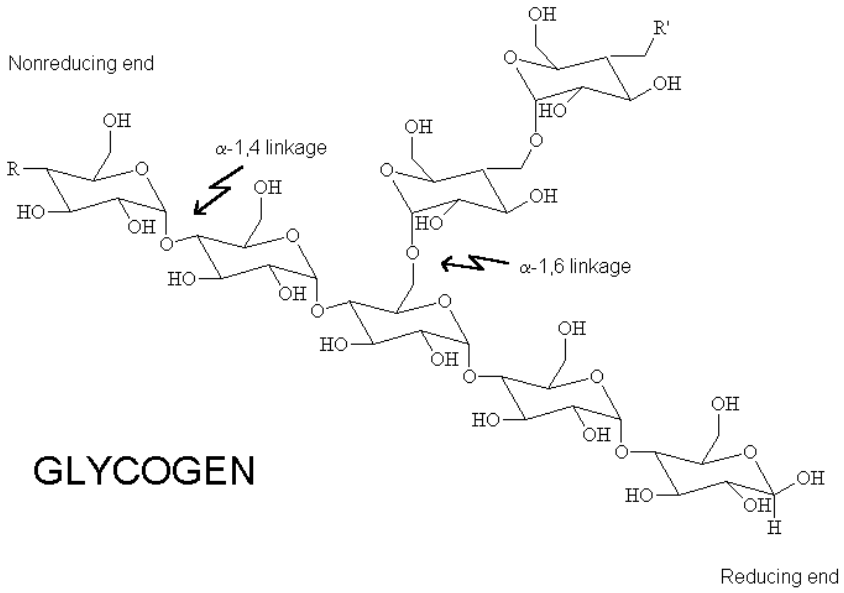




Sometimes shown as

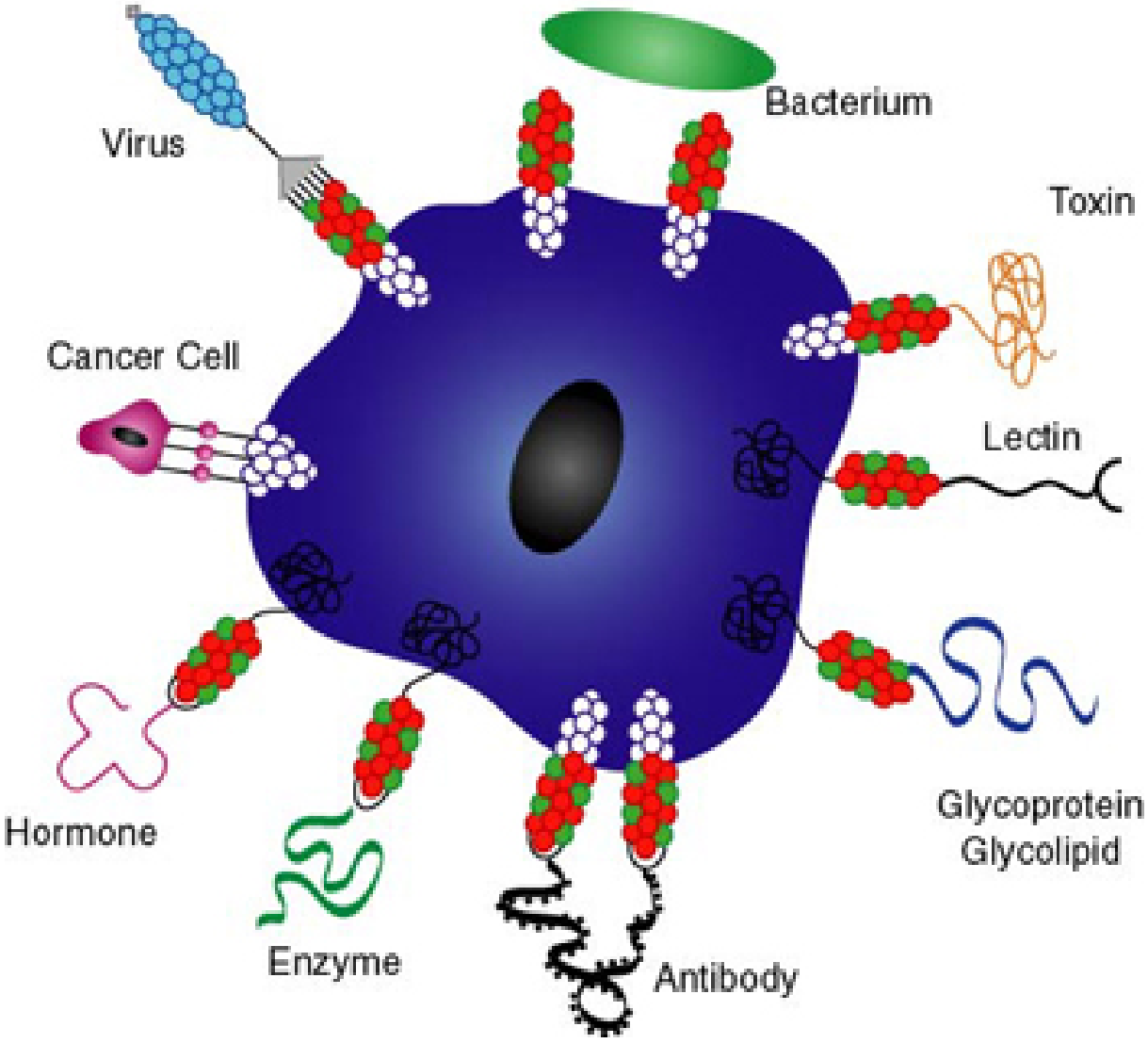


Cellulose



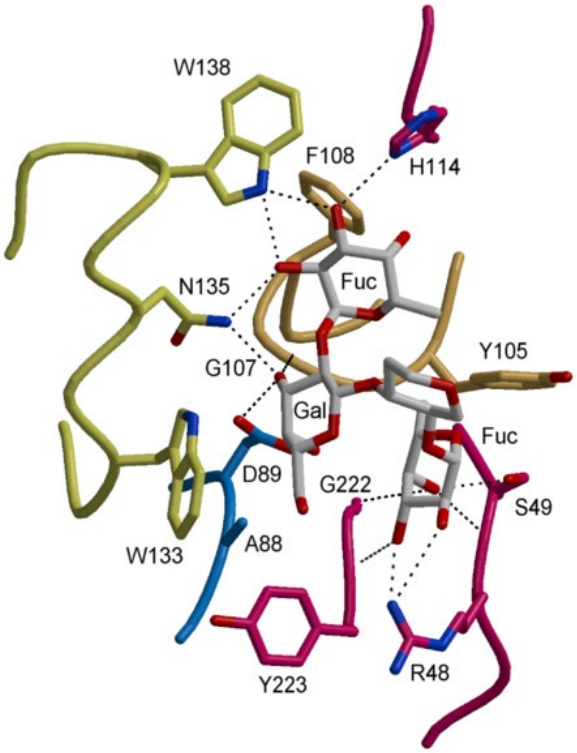
GLYCOGEN

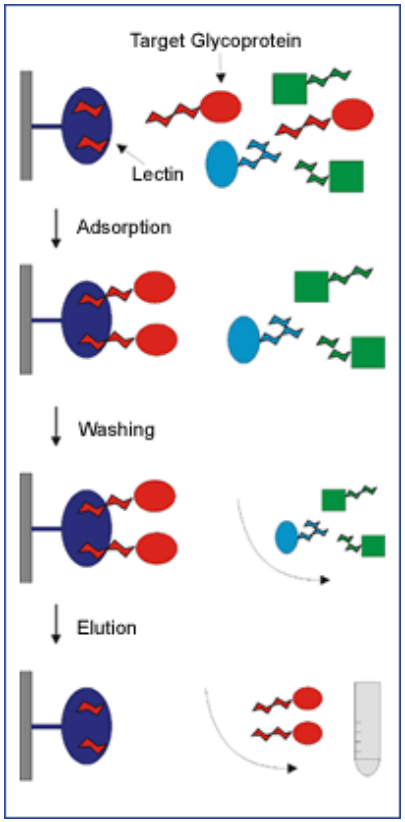
Cell-Surface Carbohydrates Involved in Molecular Recognition



Lectin

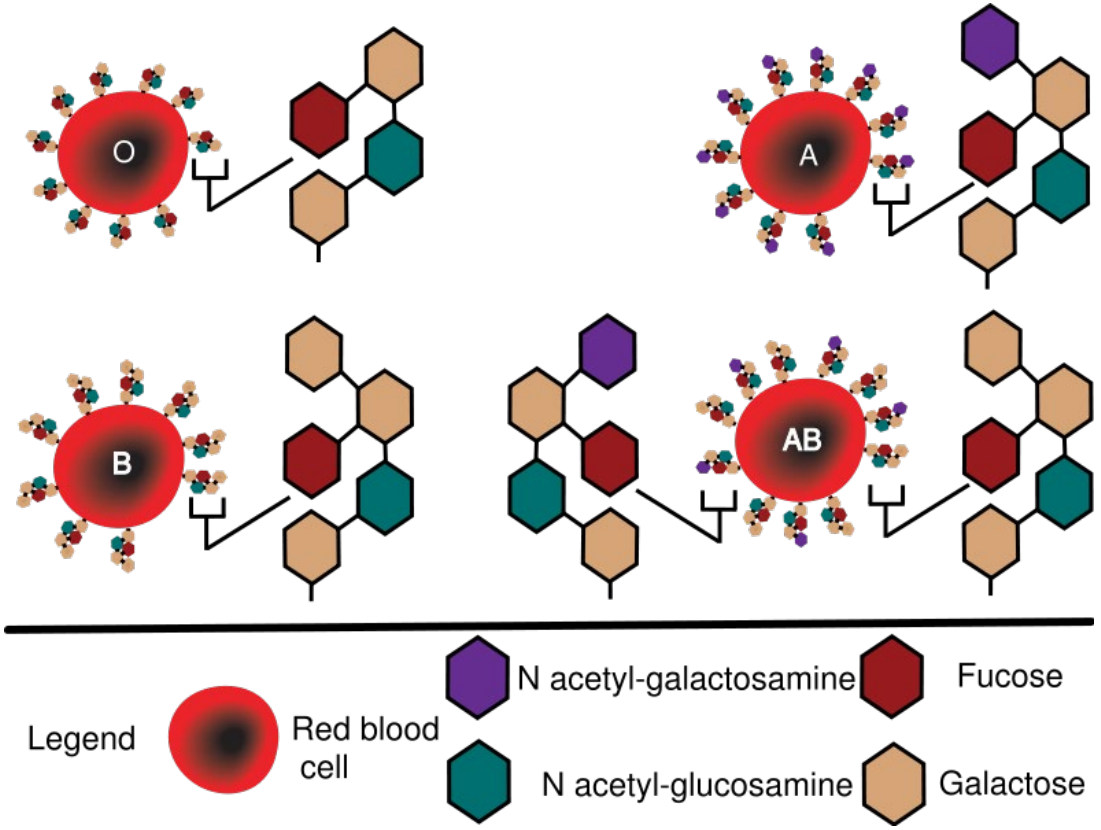
Lectins are sugar-binding proteins which are highly specific for their sugar moieties. They typically play a role in biological recognition phenomena involving cells and proteins. For example, some bacteria use lectins to attach themselves to the cells of the host organism during infection.





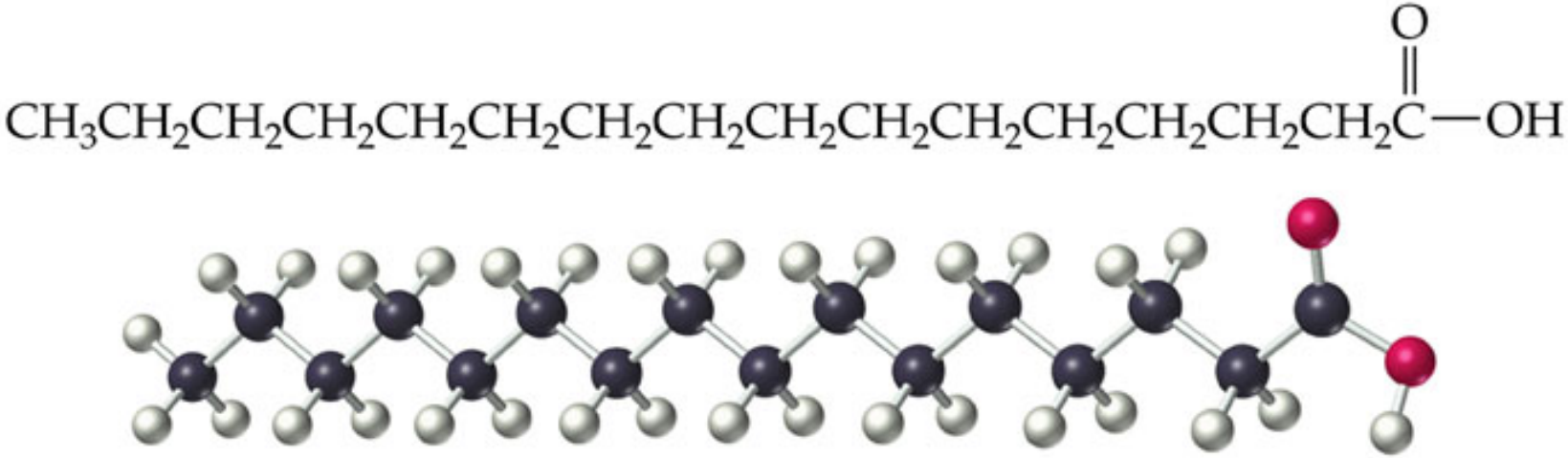
Blood Type

	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

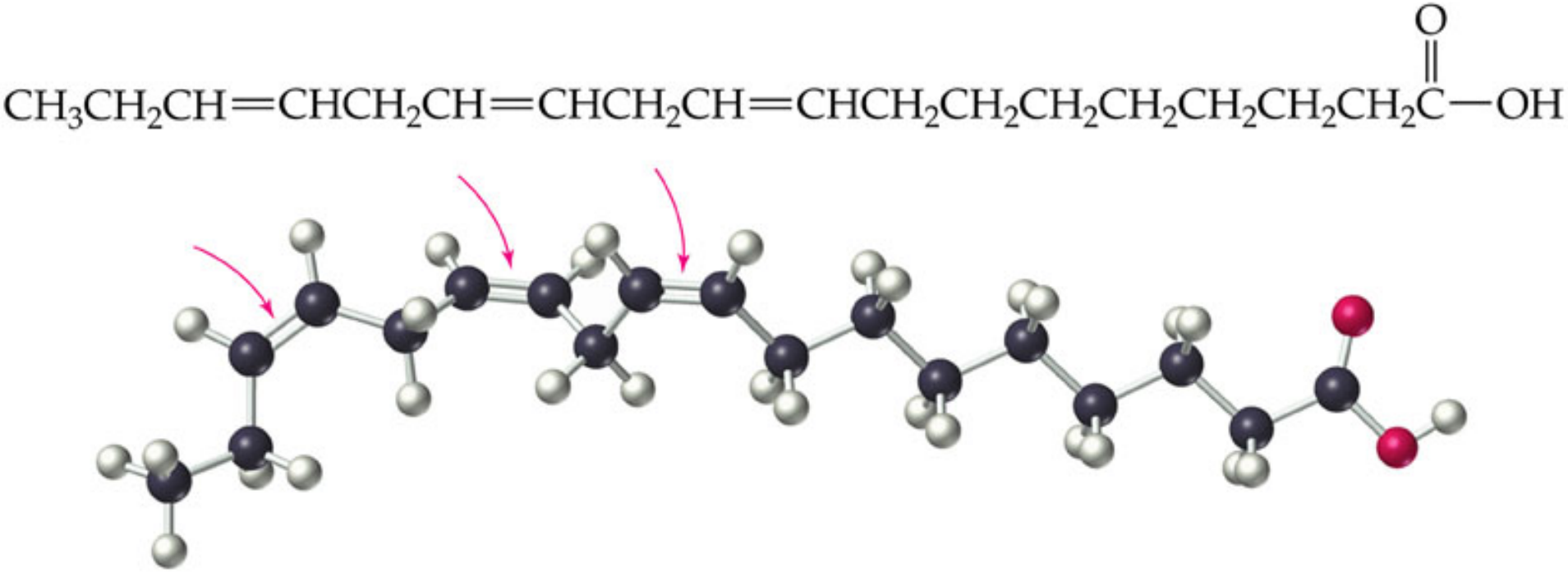


Lipid

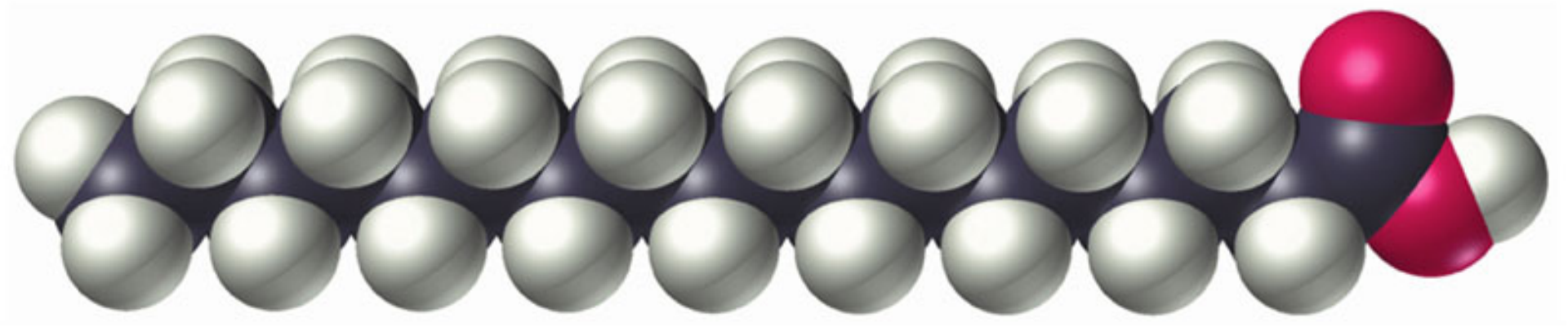
- ***Lipids*** are naturally occurring molecules from plants or animals that are soluble in nonpolar organic solvents.
- Lipid molecules contain large hydrocarbon portion and not many polar functional group, which accounts for their solubility behavior.



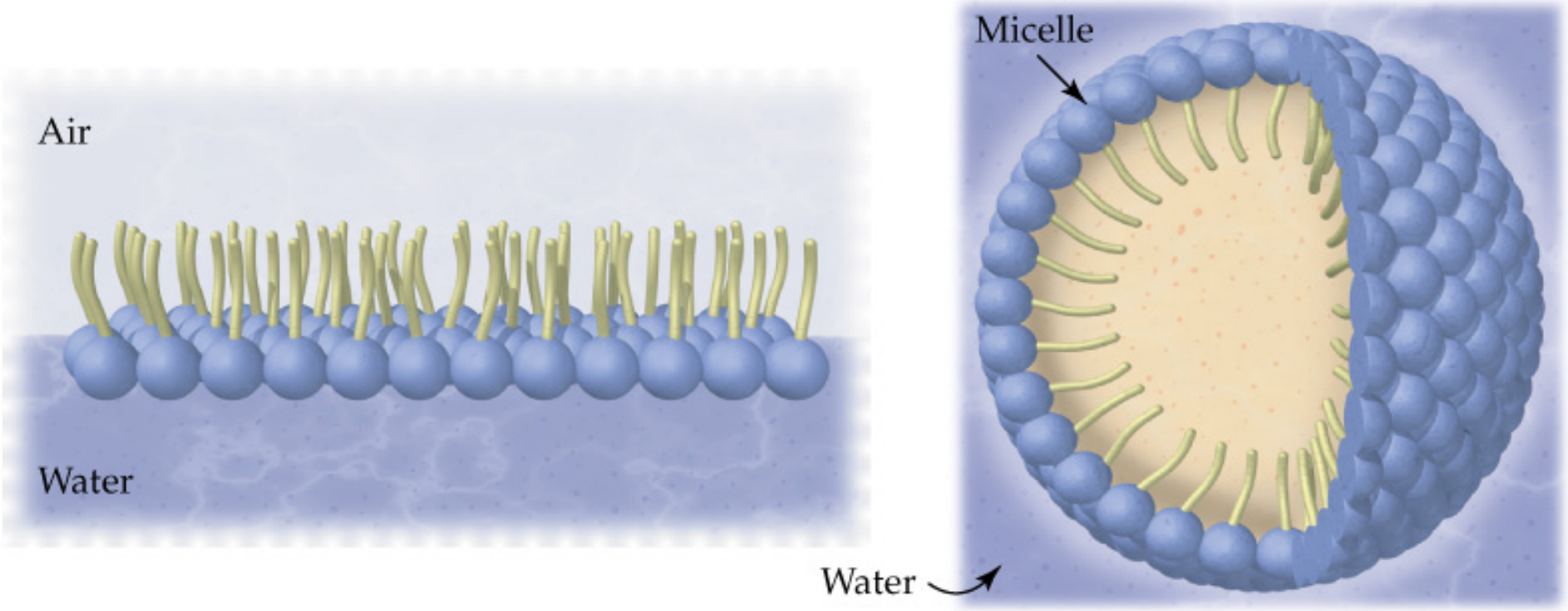
A saturated fatty acid
(palmitic acid)

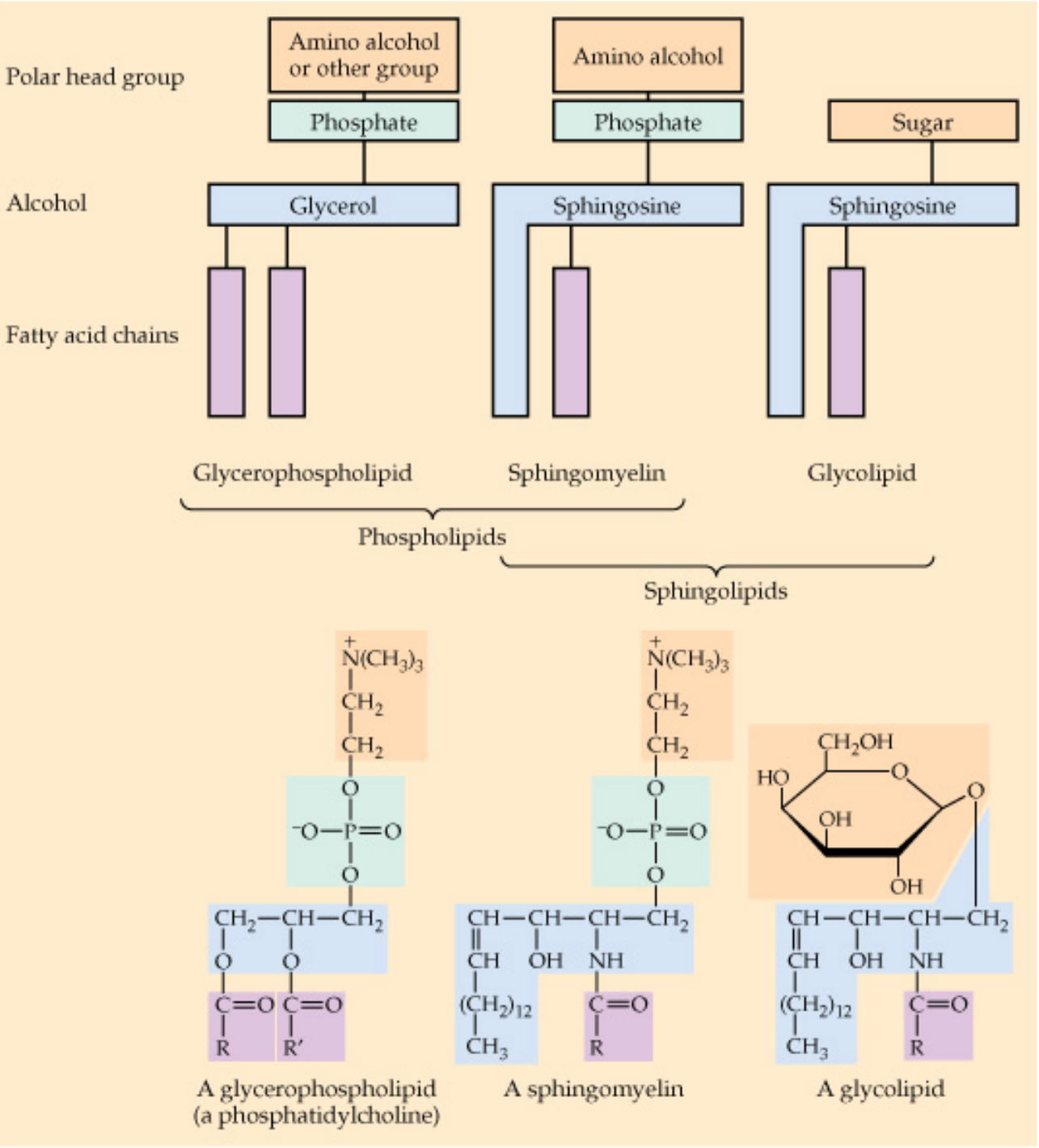


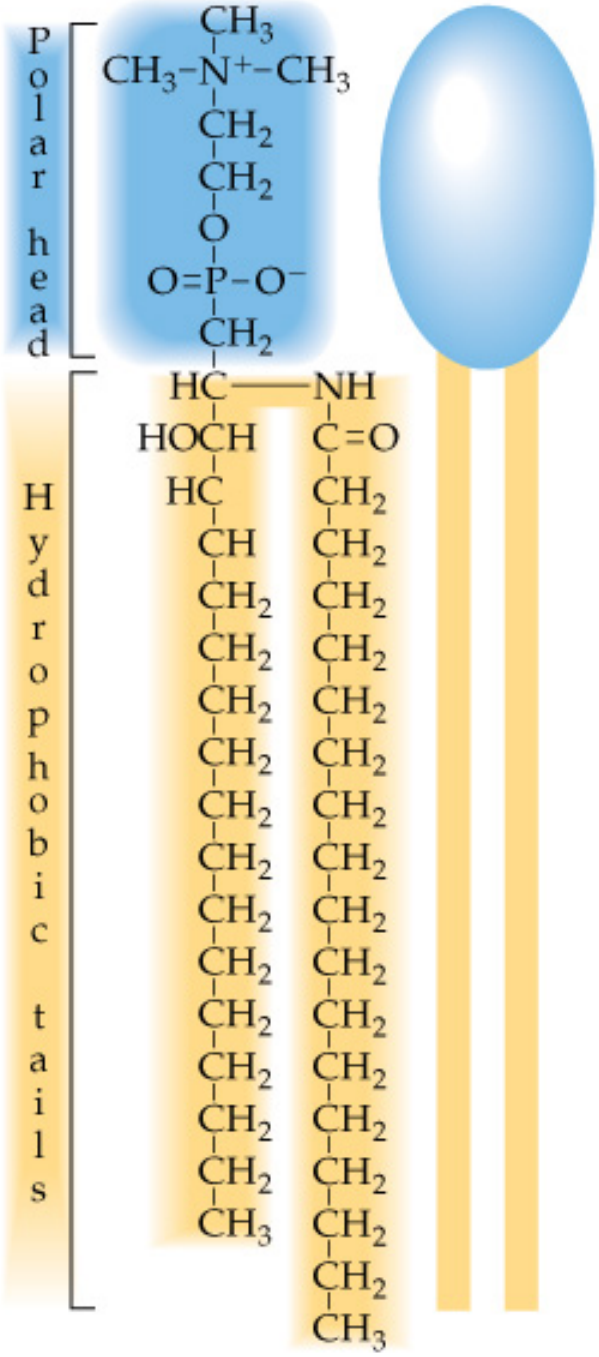
A *cis* unsaturated fatty acid
(linolenic acid)



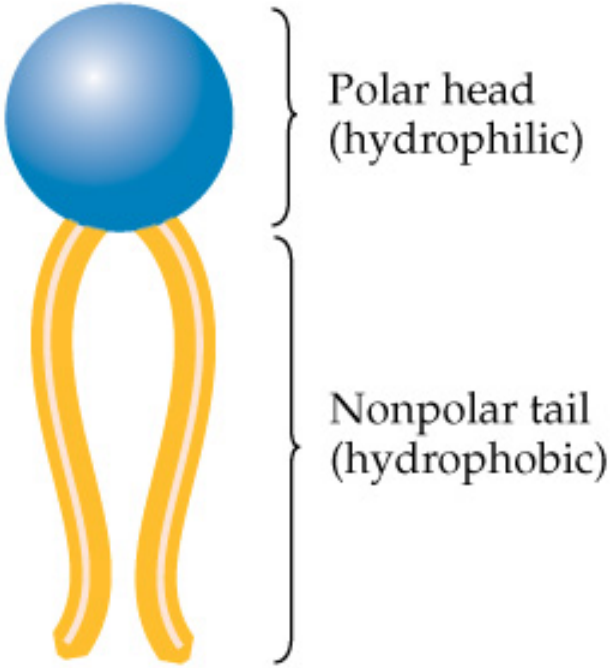
Stearic acid, an 18-carbon saturated fatty acid


Air
Water
Micelle
Water

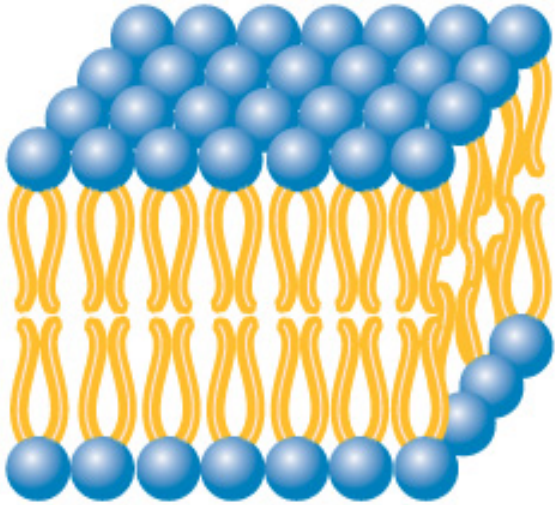

Polar head group
Alcohol
Fatty acid chains
Amino alcohol or other group
Phosphate
Glycerol
Amino alcohol
Phosphate
Sphingosine
Sugar
Sphingosine
Glycerophospholipid
Sphingomyelin
Glycolipid
Phospholipids
Sphingolipids
A glycerophospholipid (a phosphatidylcholine)
A sphingomyelin
A glycolipid



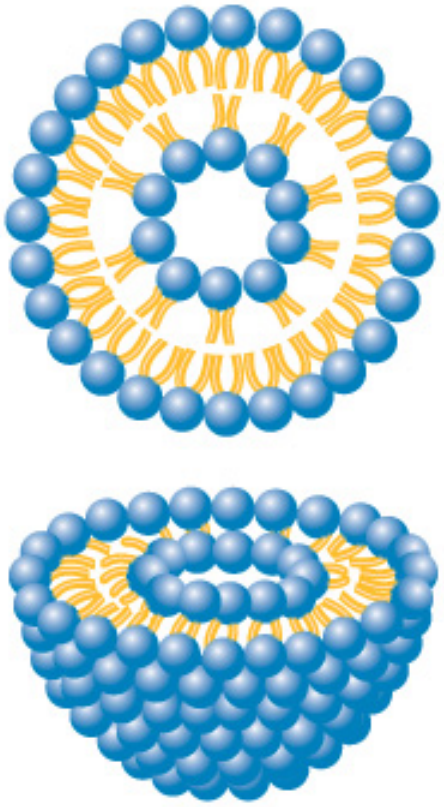
A sphingomyelin



Membrane lipid



Lipid bilayer

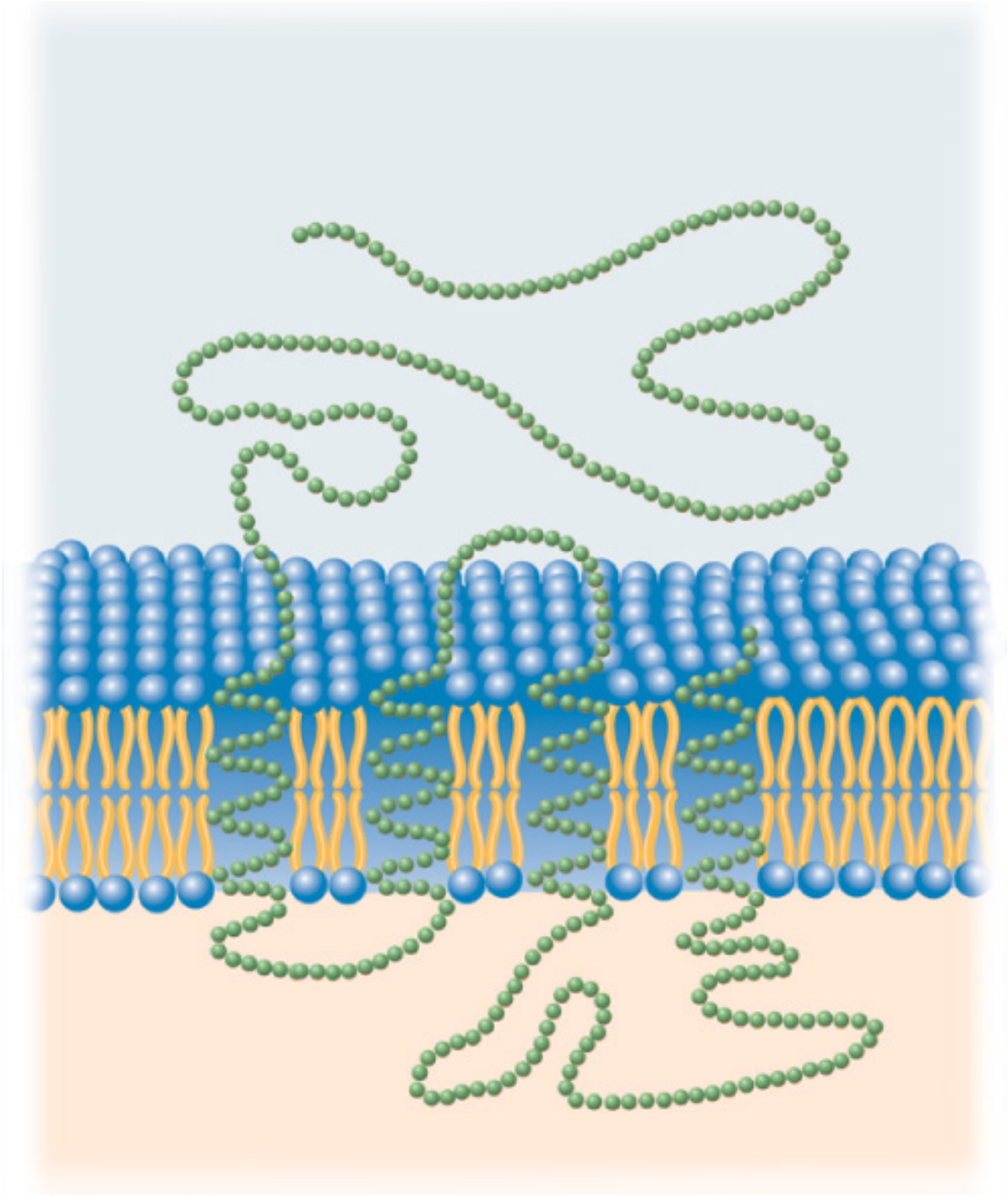


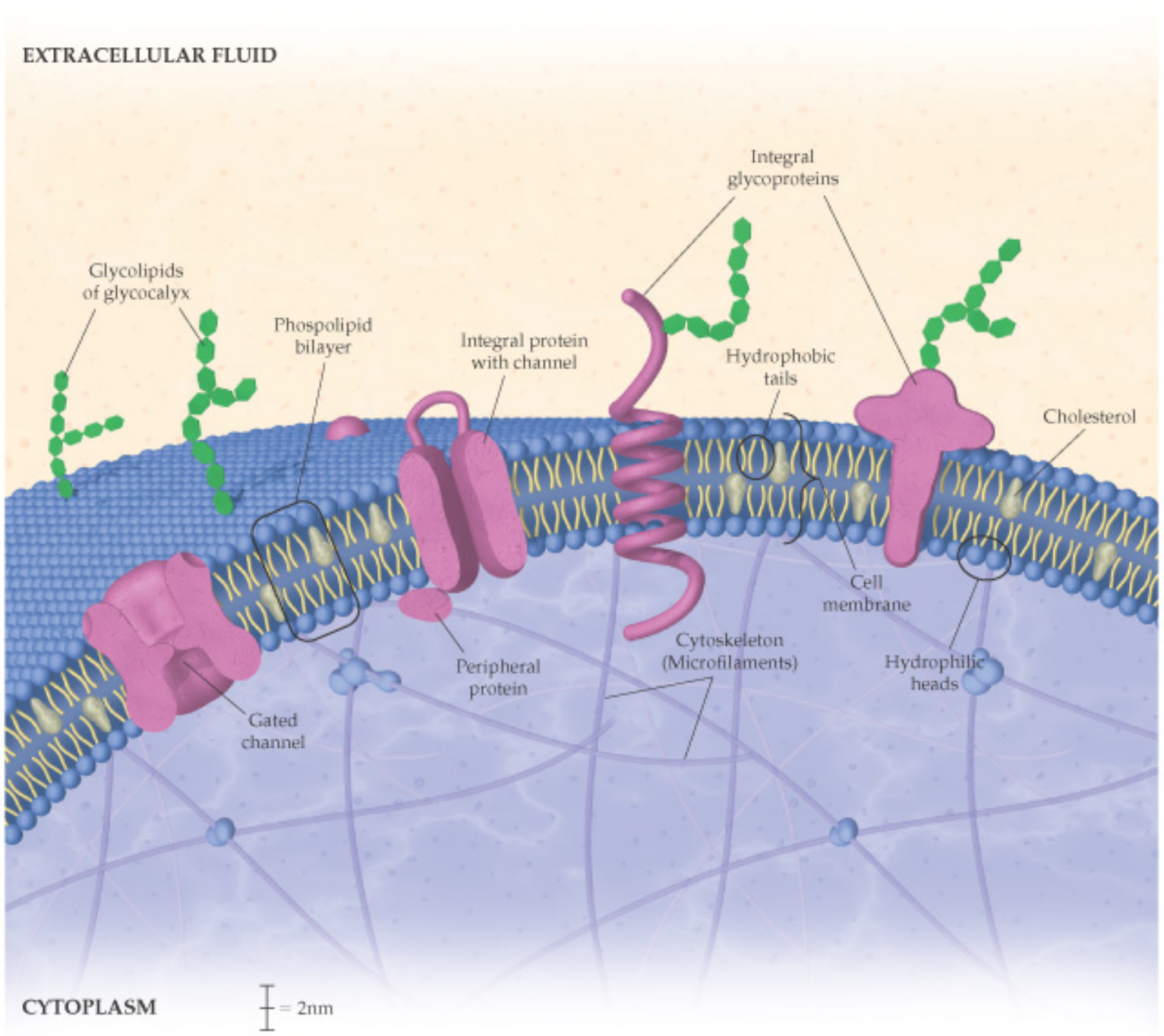
Liposome

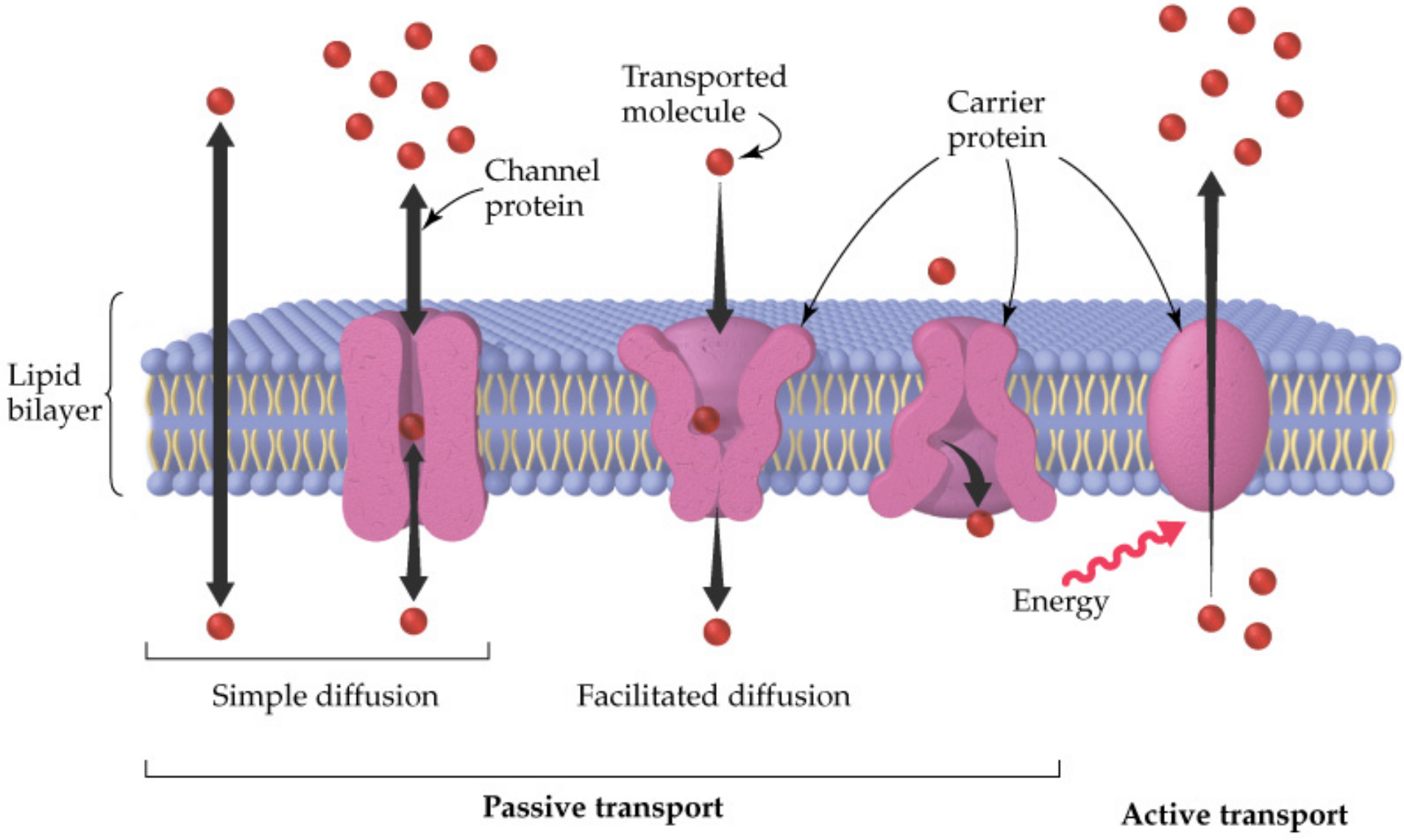
Properties of cell membranes:

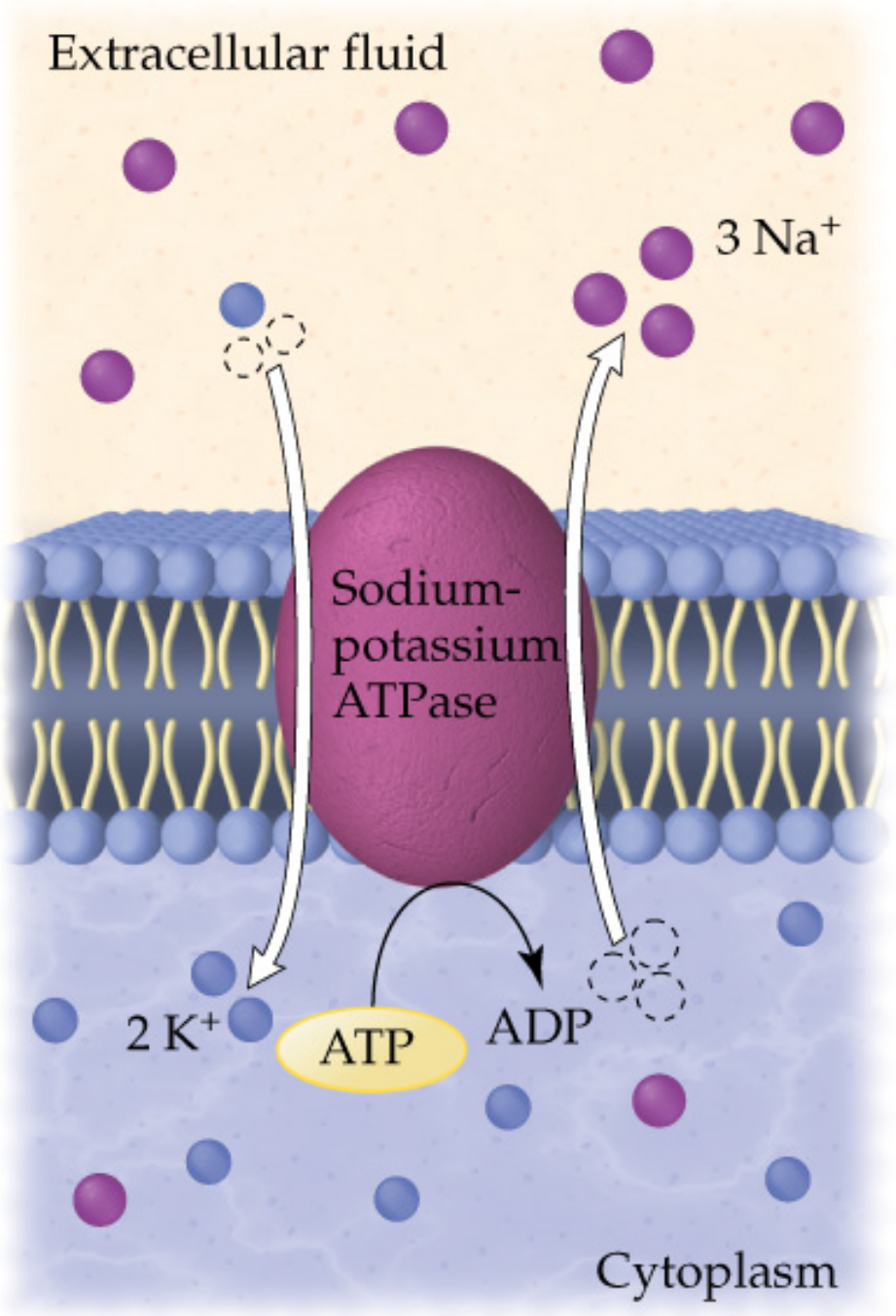
- Cell membranes are composed of a fluid like phospholipid bilayer.
- The bilayer incorporates cholesterol, proteins, and glycolipids.
- Small nonpolar molecules cross by diffusion through the lipid bilayer.
- Small ions and polar molecules diffuse through the aqueous media in protein pores.
- Glucose 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