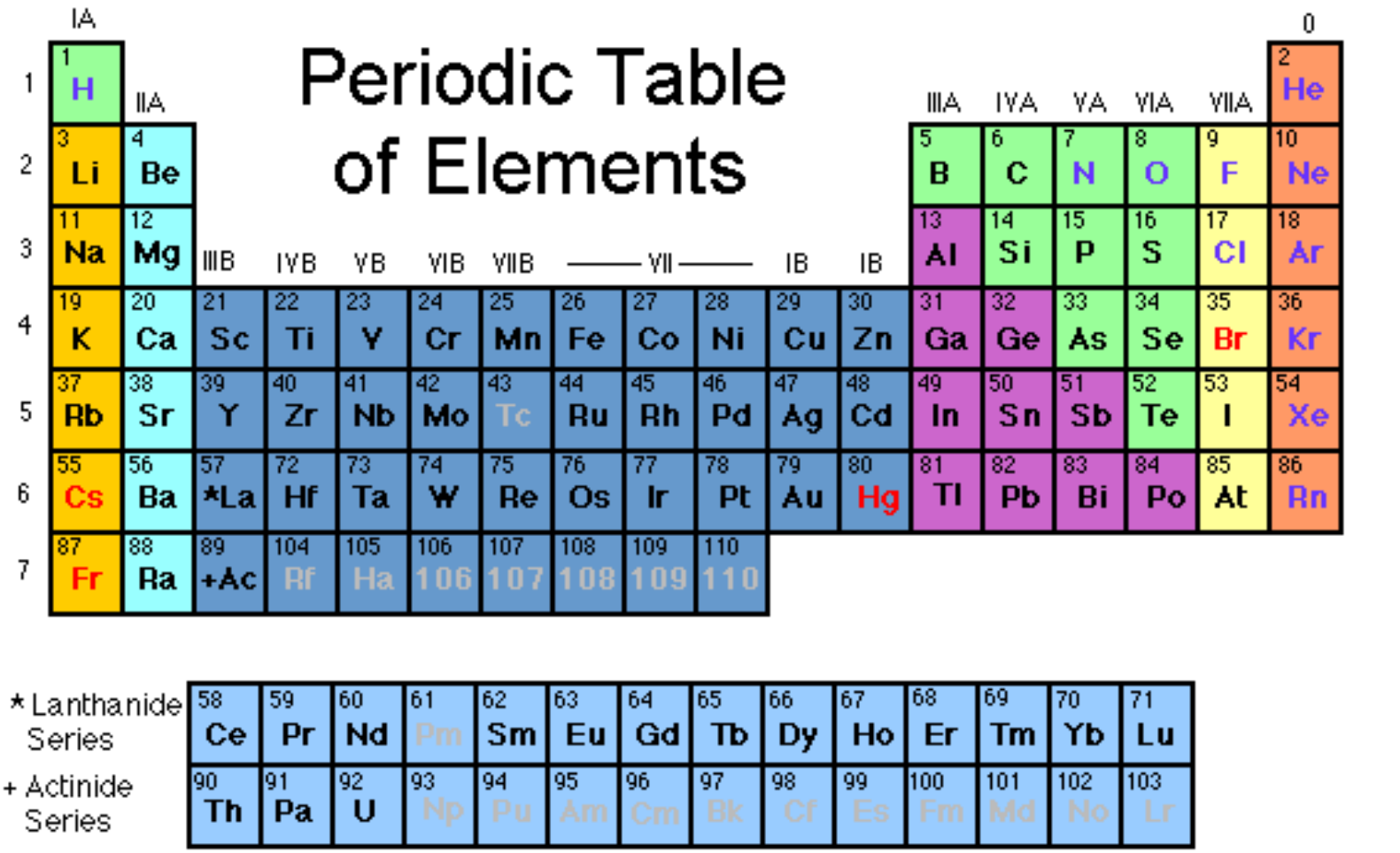
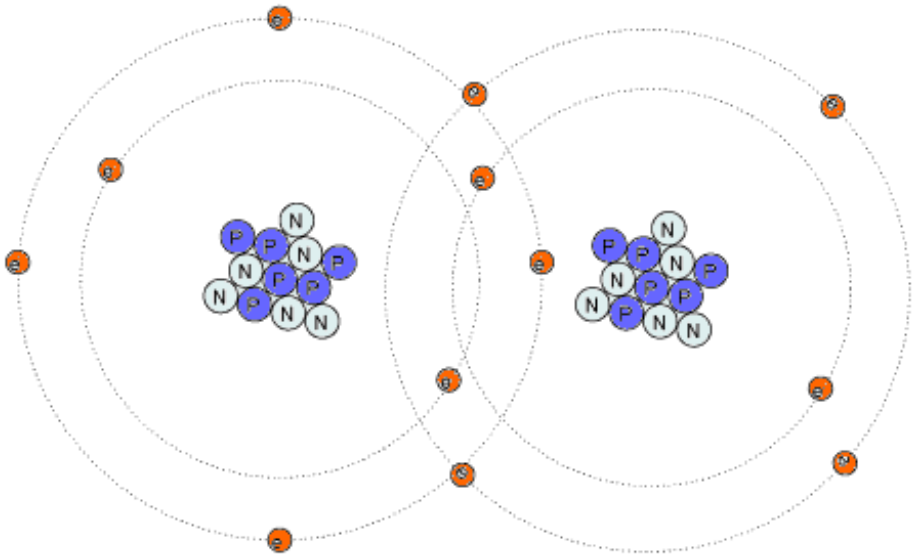
Review of General Chemistry

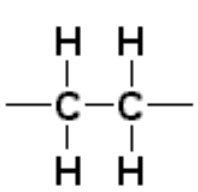

Periodic Table of Elements
IA
IIA
IIIB
IVB
VB
VIB
VIIB
VII
IB
IB
IIIA
IVA
VA
VIA
VIIA
0
1 H
2 He
3 Li
4 Be
5 B
6 C
7 N
8 O
9 F
10 Ne
11 Na
12 Mg
13 Al
14 Si
15 P
16 S
17 Cl
18 Ar
19 K
20 Ca
21 Sc
22 Ti
23 V
24 Cr
25 Mn
26 Fe
27 Co
28 Ni
29 Cu
30 Zn
31 Ga
32 Ge
33 As
34 Se
35 Br
36 Kr
37 Rb
38 Sr
39 Y
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

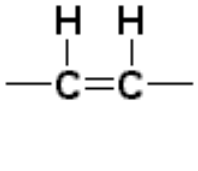
Hydrogen	H•	H•
Carbon	•Ċ•	•Ċ•
Water	H:Ö:H	H-Ö-H
Ethylene	H H C::C H H	H H C=C H H
Acetylene	H:C:::C:H	H-C≡C-H



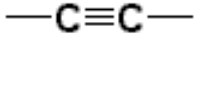
Functional Groups



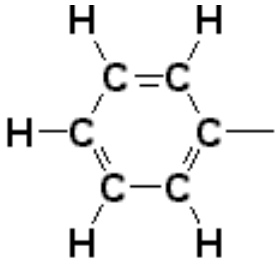
alkane



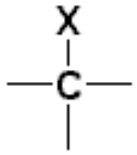
alkene



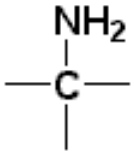
alkyne



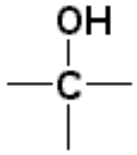
phenyl



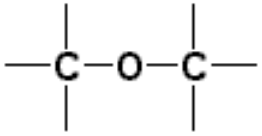
alkyl halide
(X = F, Cl, Br, I)



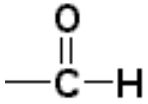
amine



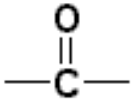
alcohol



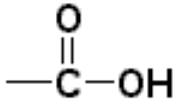
ether



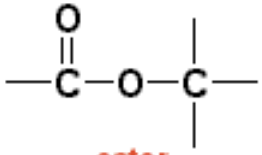
aldehyde



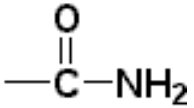
ketone



carboxylic
acid

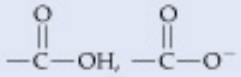
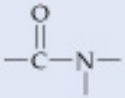
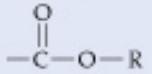
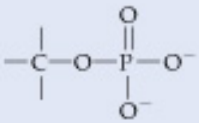
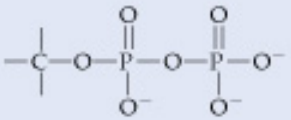
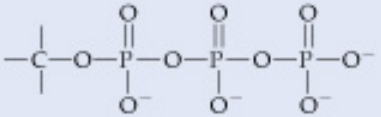
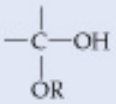
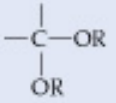


ester

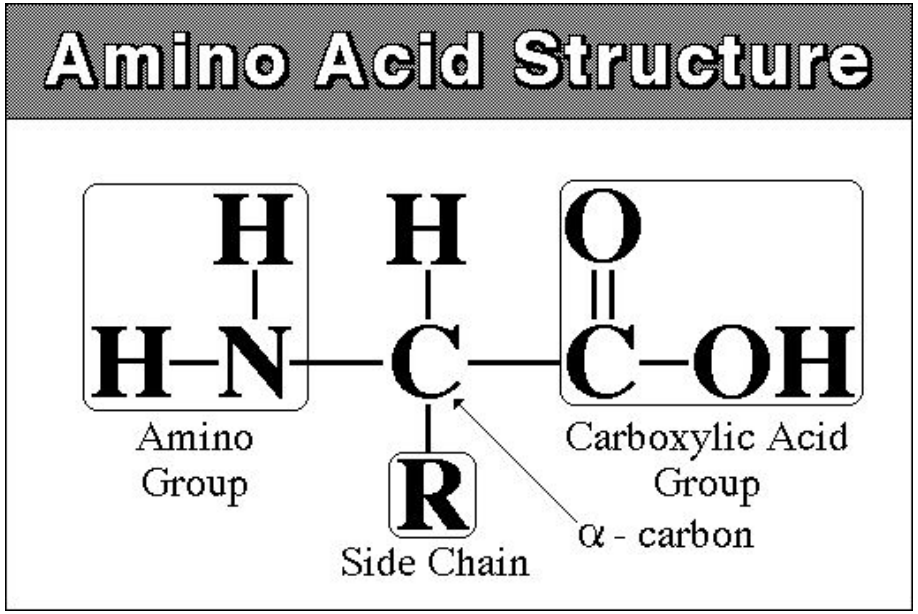


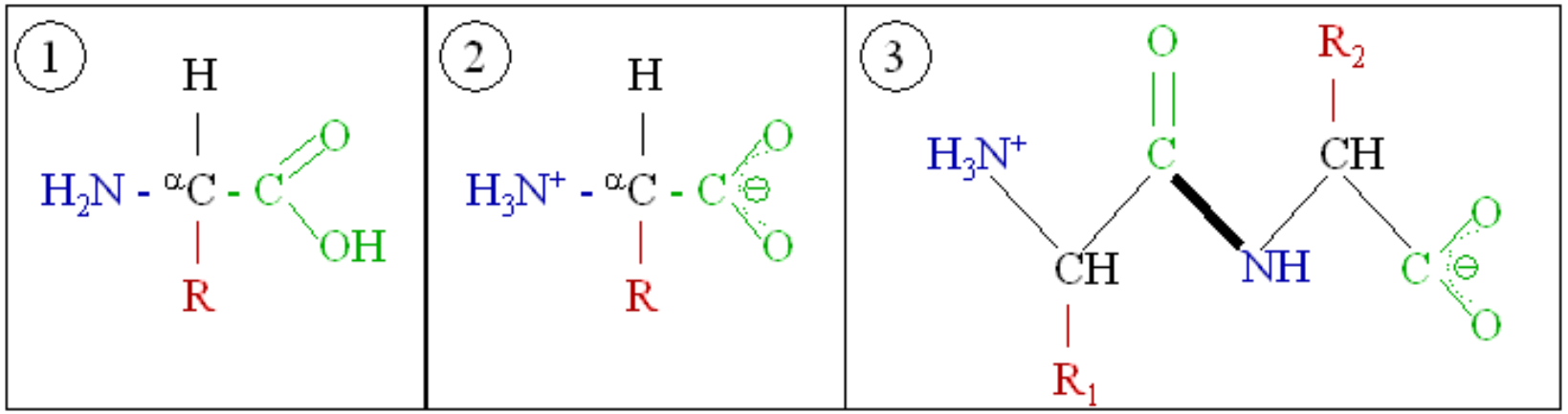
amide

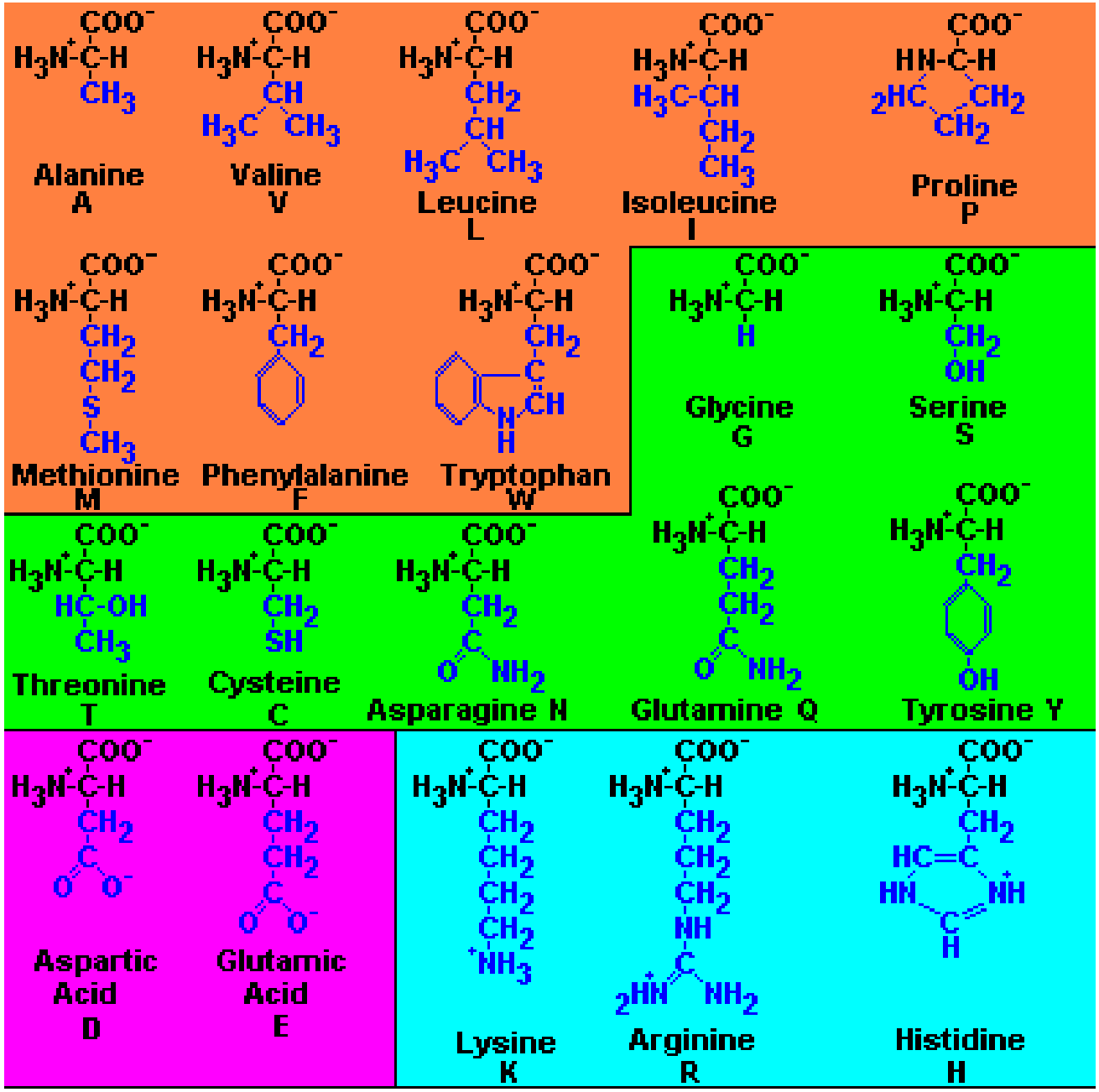
TABLE 18.1 Functional Groups of Importance in Biochemical Molecules

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)

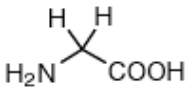
Amino Acid


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

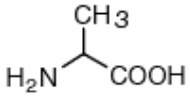

1
H
H_2N - $^{\alpha}C$ - C
O
OH
R
2
H
H_3N^+ - $^{\alpha}C$ - C
O
O
R
3
O
R_2
H_3N^+
C
CH
CH
NH
C
O
O
R_1


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

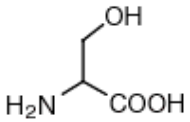


Glycine (Gly, G)
MW: 57.05

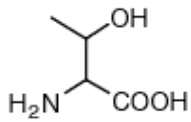


Alanine (Ala, A)
MW: 71.09

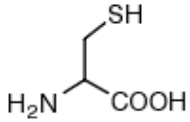
Nucleophilic



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

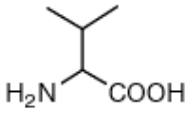


Threonine (Thr, T)
MW: 101.11, pK_a ~ 16

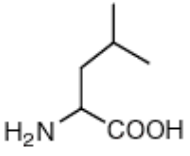


Cysteine (Cys, C)
MW: 103.15, pK_a = 8.35

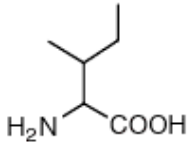
Hydrophobic



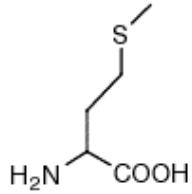
Valine (Val, V)
MW: 99.14



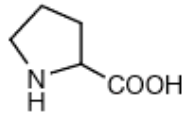
Leucine (Leu, L)
MW: 113.16



Isoleucine (Ile, I)
MW: 113.16

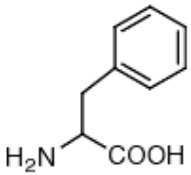


Methionine (Met, M)
MW: 131.19

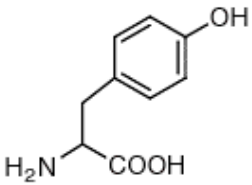


Proline (Pro, P)
MW: 97.12

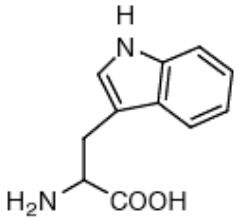
Aromatic



Phenylalanine (Phe, F)
MW: 147.18

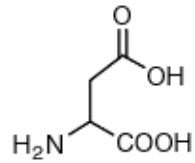


Tyrosine (Tyr, Y)
MW: 163.18

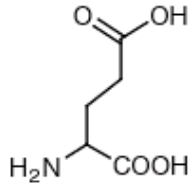


Tryptophan (Trp, W)
MW: 186.21

Acidic

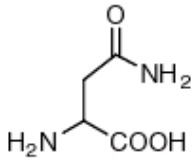


Aspartic Acid (Asp, D)
MW: 115.09, pK_a = 3.9

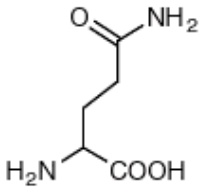


Glutamic Acid (Glu, E)
MW: 129.12, pK_a = 4.07

Amide

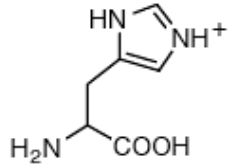


Asparagine (Asn, N)
MW: 114.11

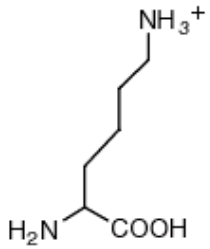


Glutamine (Gln, Q)
MW: 128.14

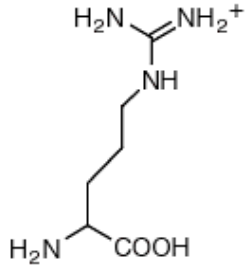
Basic



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



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

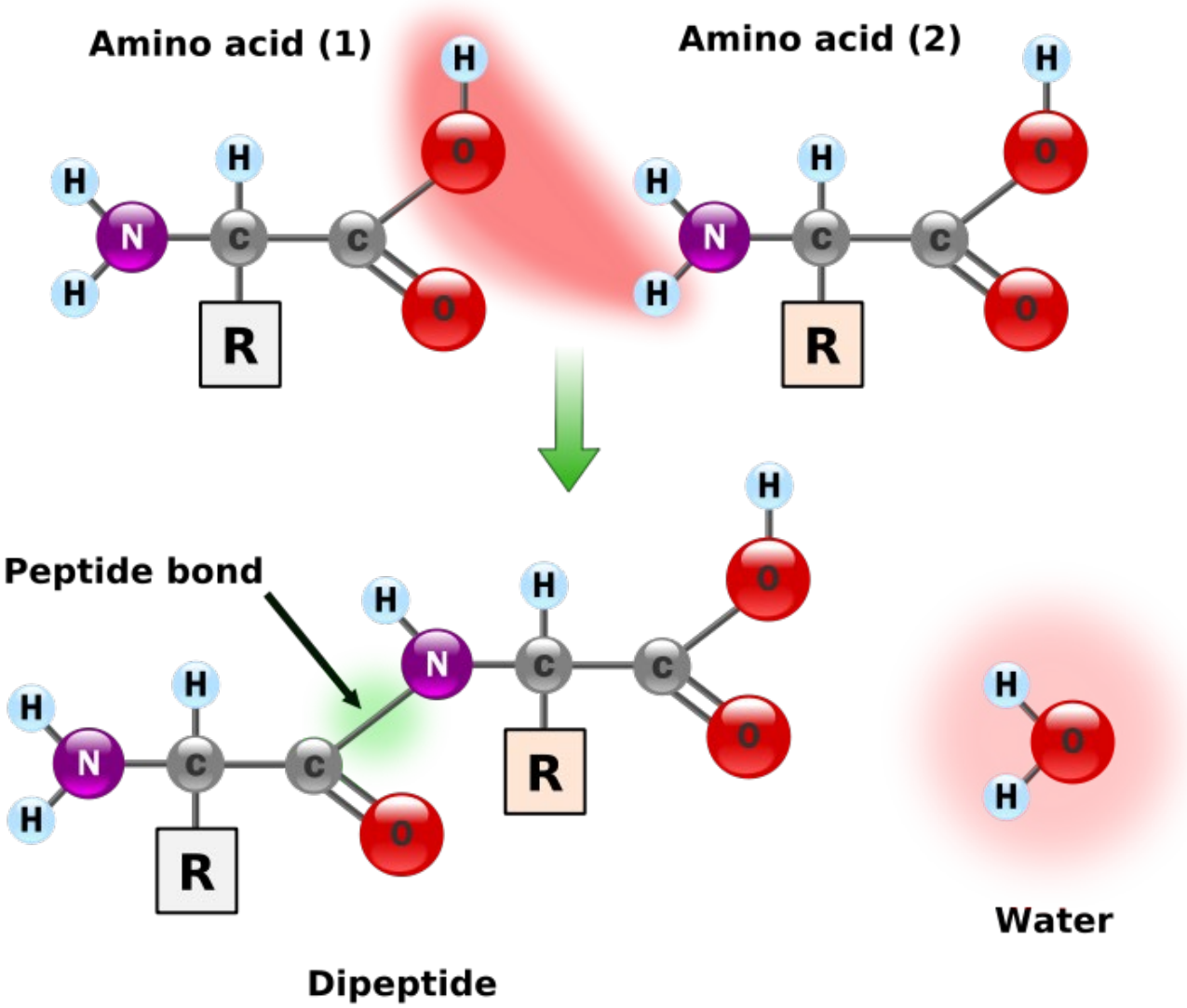


Arginine (Arg, R)
MW: 156.19, pK_a = 12.48

Protein Structure and Function

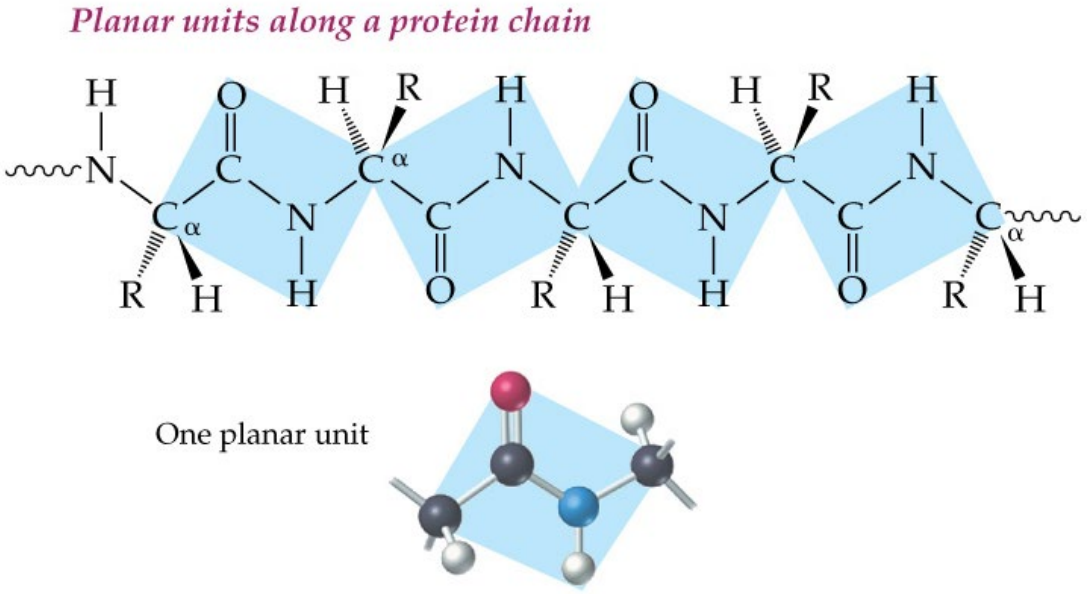
- Proteins are polymers of amino acids.
- Each amino acids in a protein contains a amino group, -NH_2, a carboxyl group, -COOH, and an R group, all bonded to the central carbon atom. The R group may be a hydrocarbon or they may contain functional group.
- All amino acids present in a proteins are *α-amino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

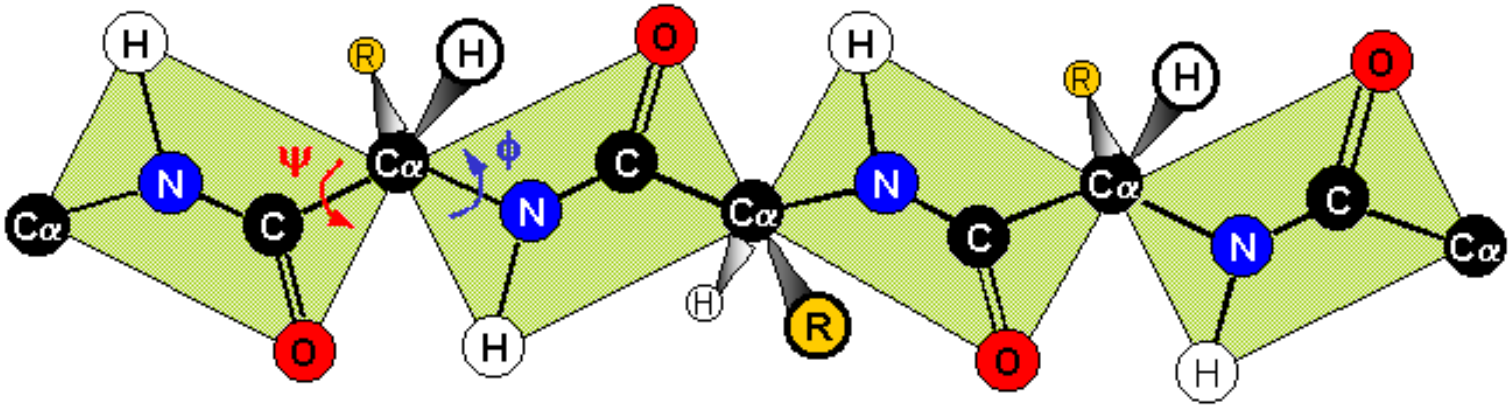


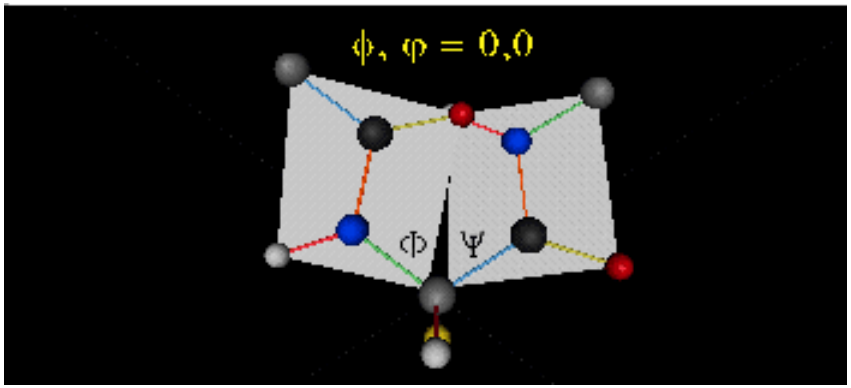
- By convention, peptides and proteins are always written with the amino terminal amino acid (N-terminal) on the left and carboxyl-terminal amino acid (C-terminal) on the right.

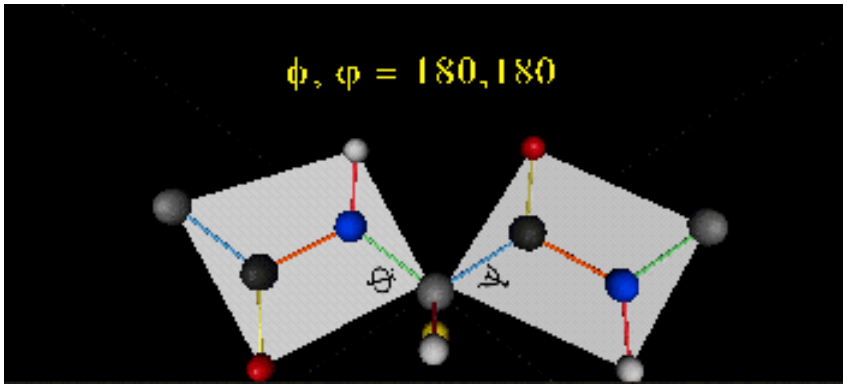
Secondary Protein Structure

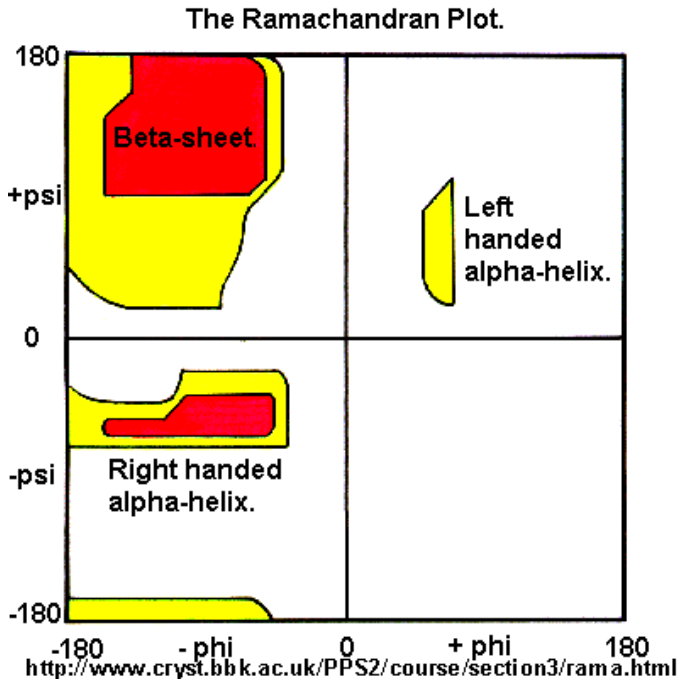
- Secondary structure of a protein is the arrangement of polypeptide backbone of the protein in space. The secondary structure includes two kinds of repeating pattern known as the *α-helix* and *β-sheet*.
- Hydrogen bonding between backbone atoms are responsible for both of these secondary structures.

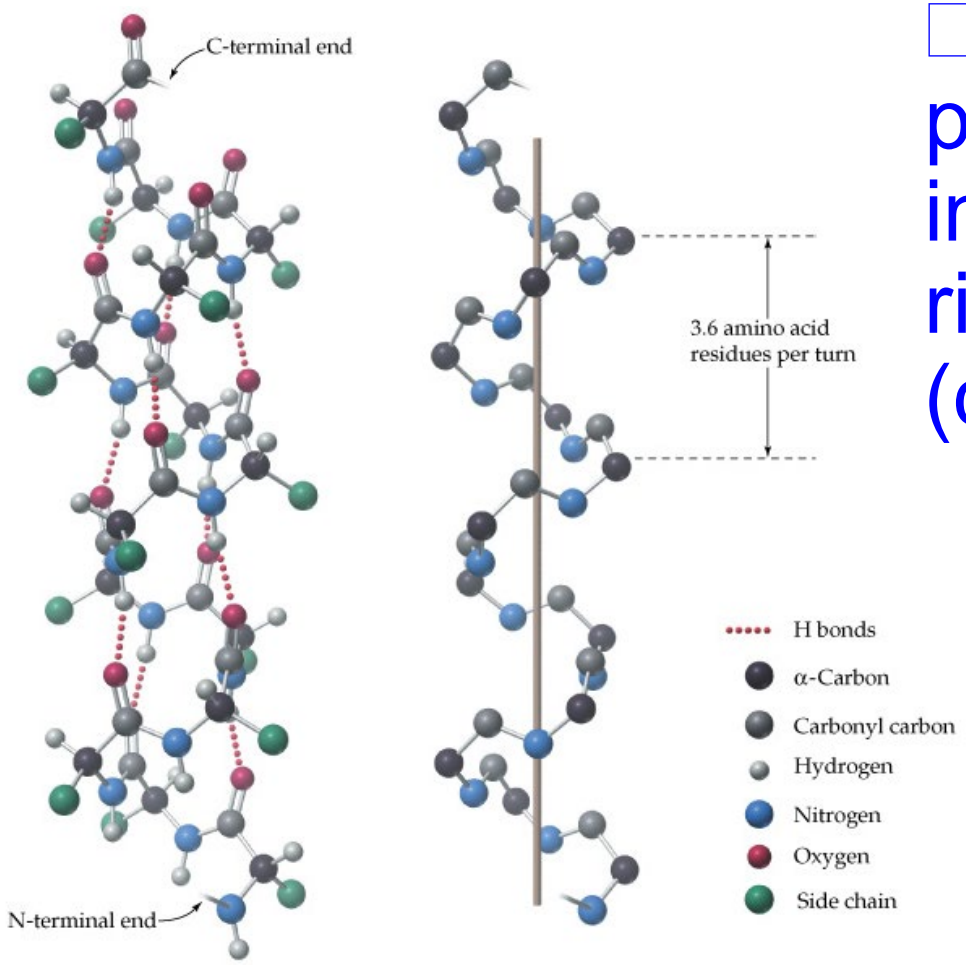
FULLY EXTENDED POLYPEPTIDE CHAIN





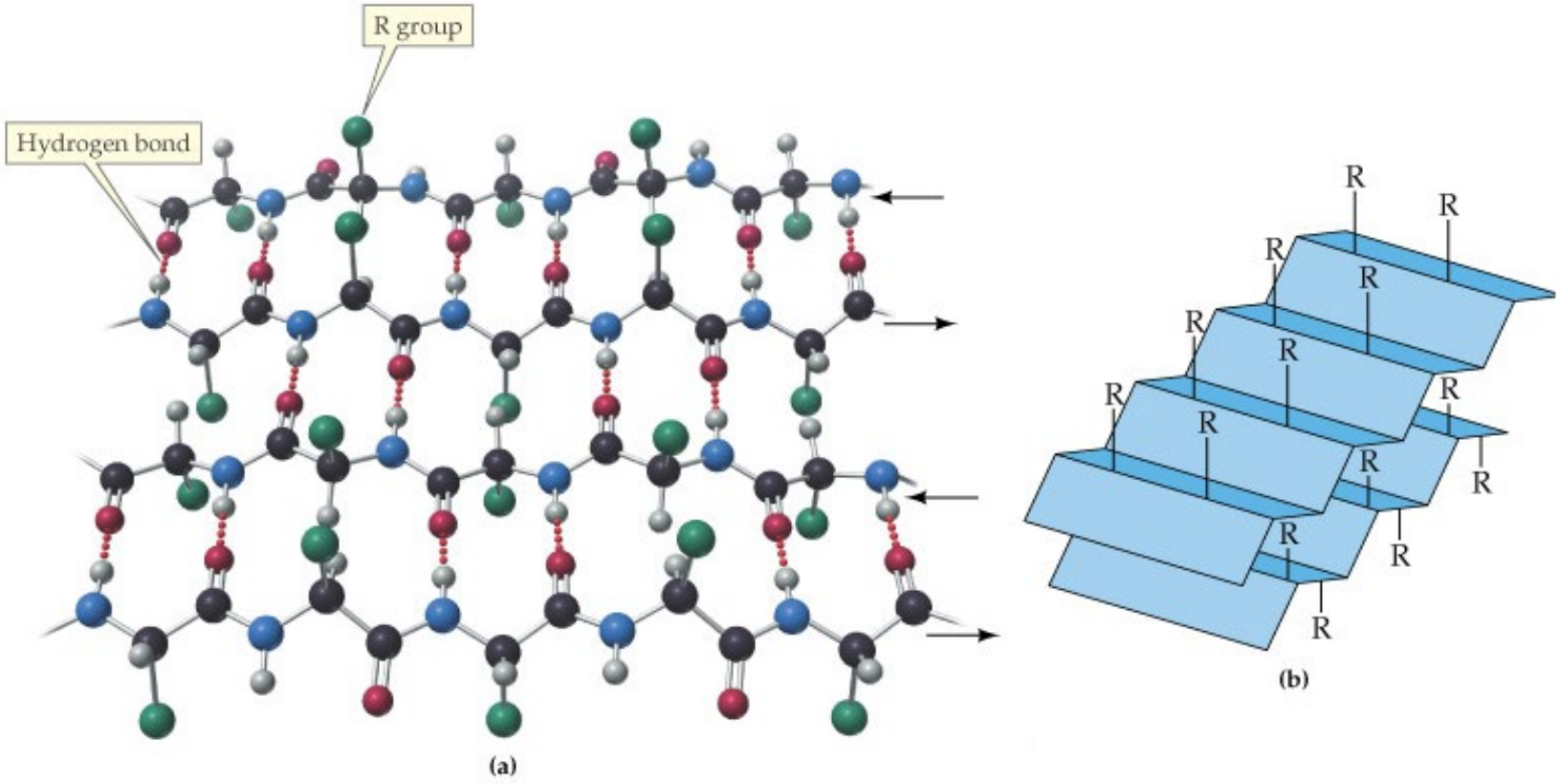




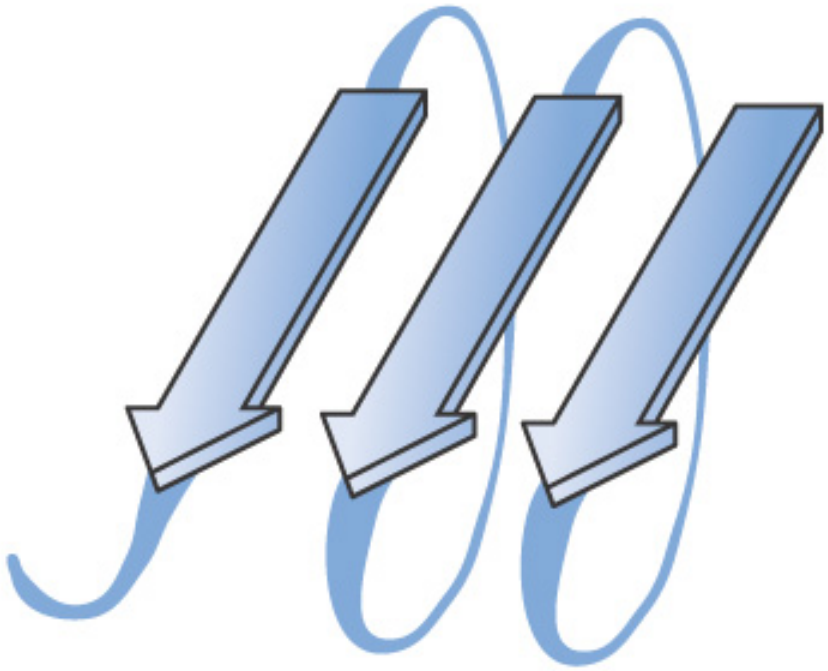


- ***α-Helix:*** A single protein chain coiled in a spiral with a right-handed (clockwise) twist.

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

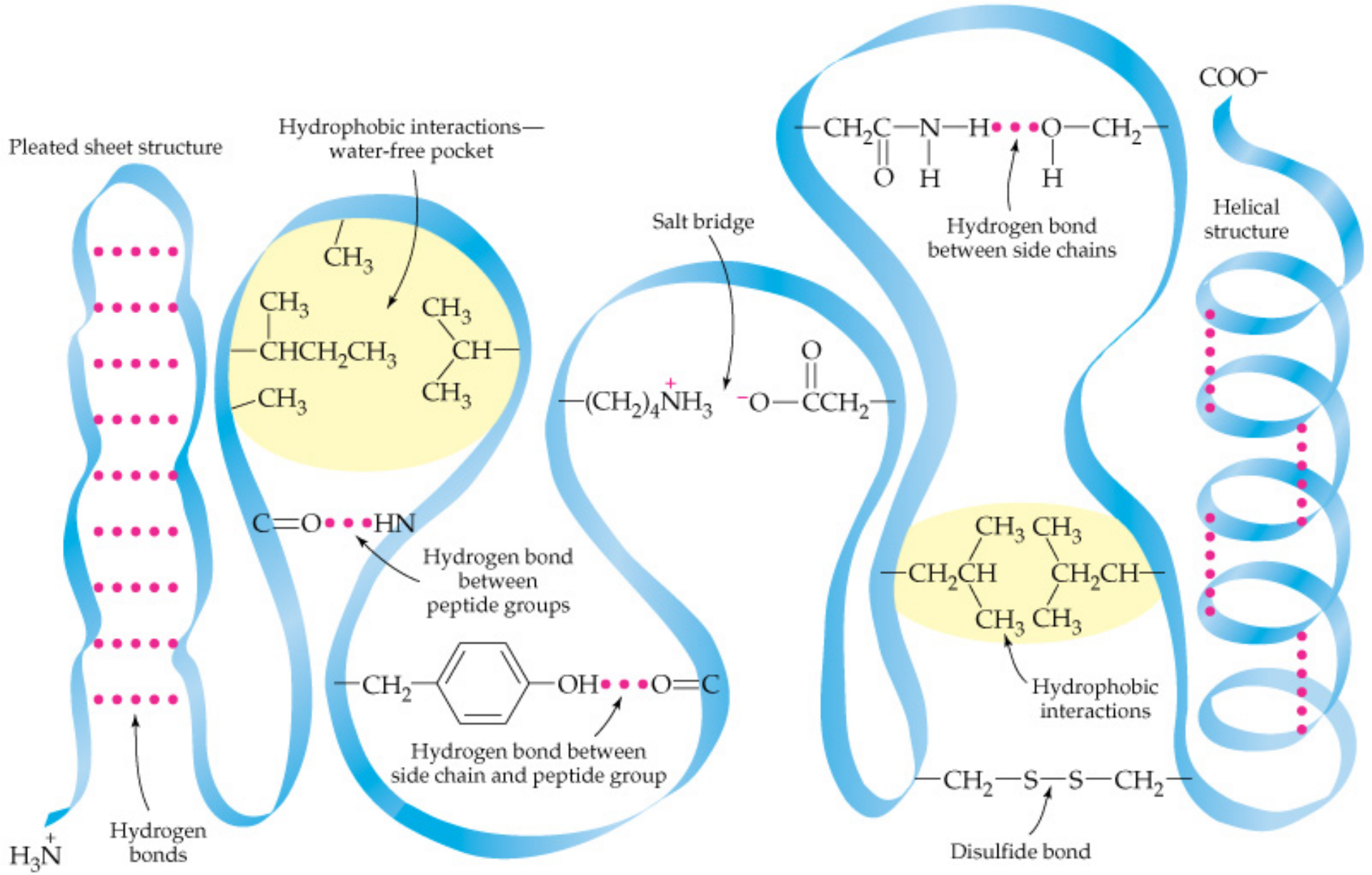
Tertiary Protein Structure

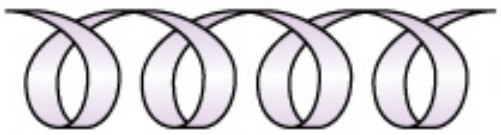
- ***Tertiary Structure of a proteins*** The overall three dimensional shape that results from the folding of a protein chain. Tertiary structure depends mainly on attractions of amino acid side chains that are far apart along the same backbone. Non-covalent interactions and disulfide covalent bonds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

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.

- 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

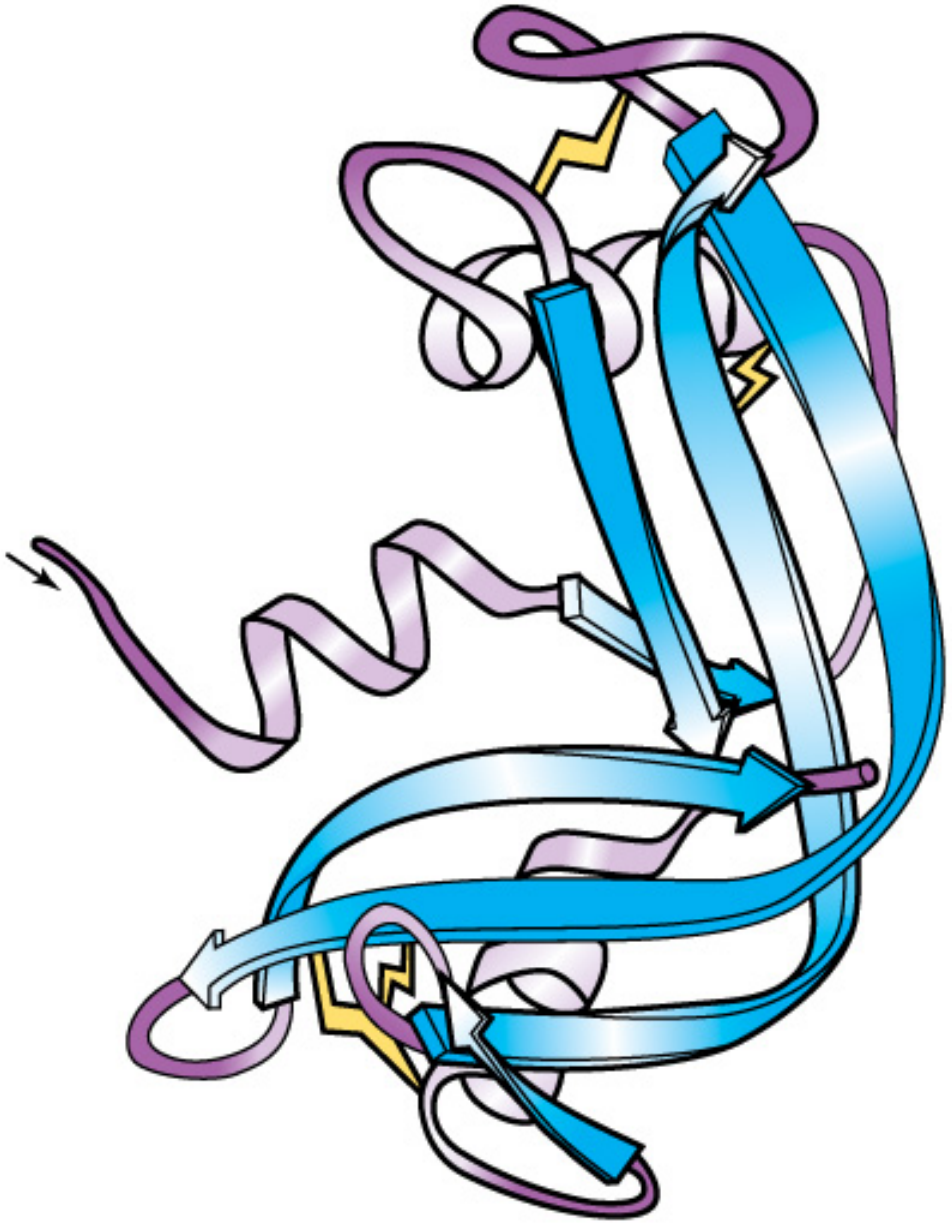


α Helix

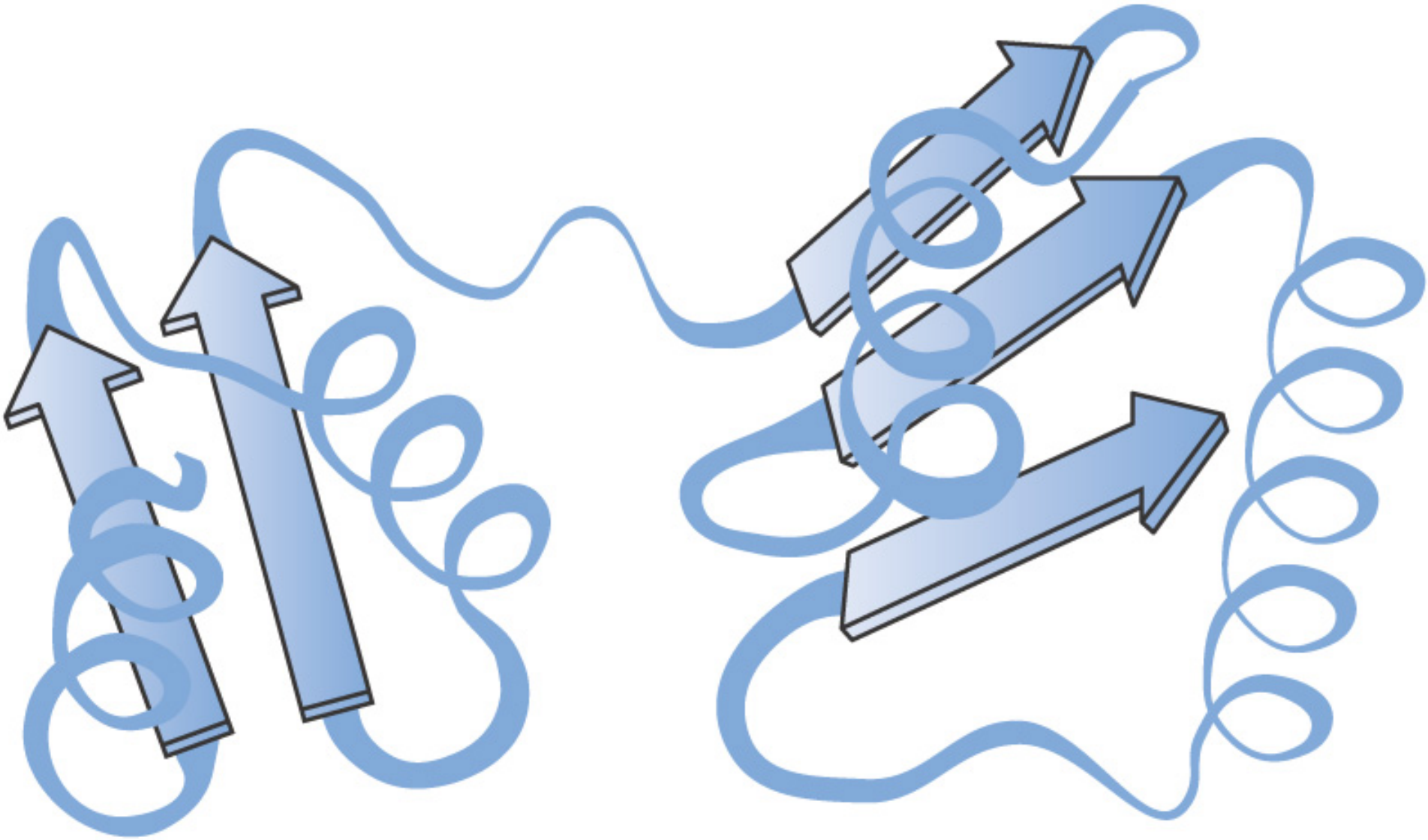
β Sheet

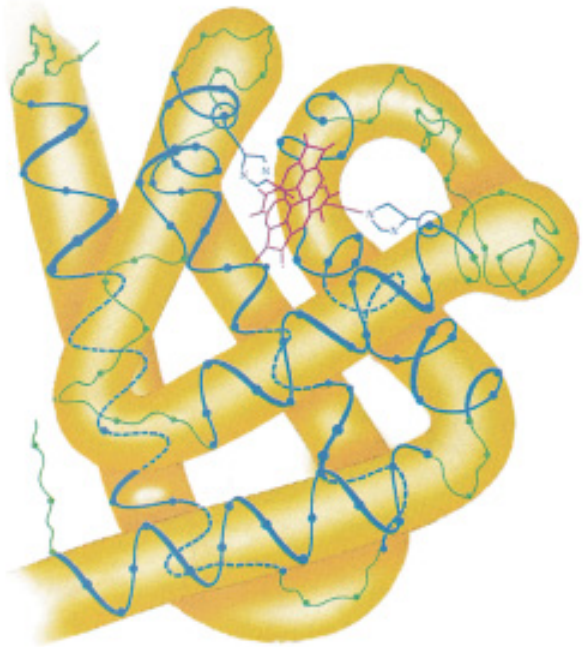
Connecting loop

—S—S— links

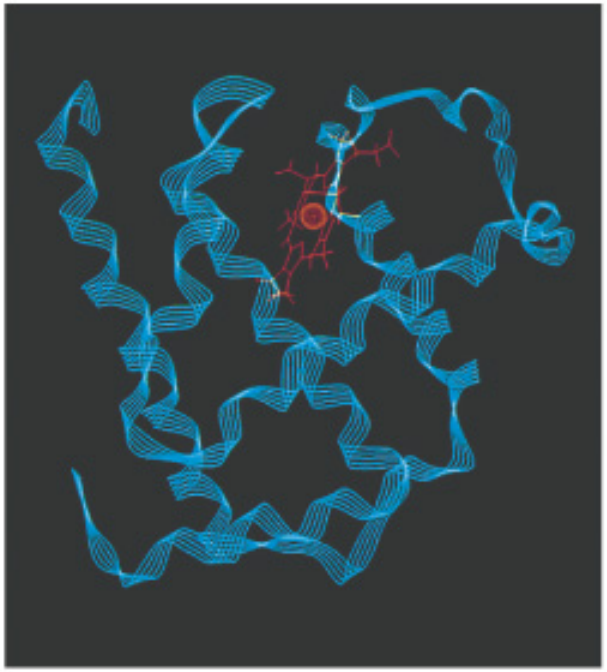


Ribonuclease

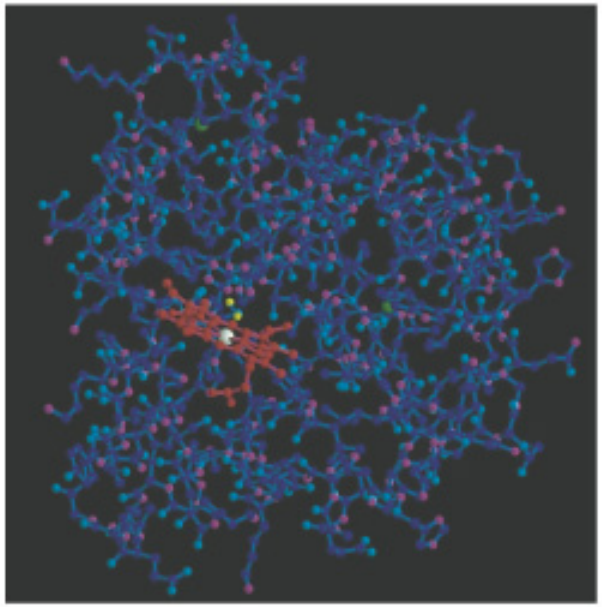




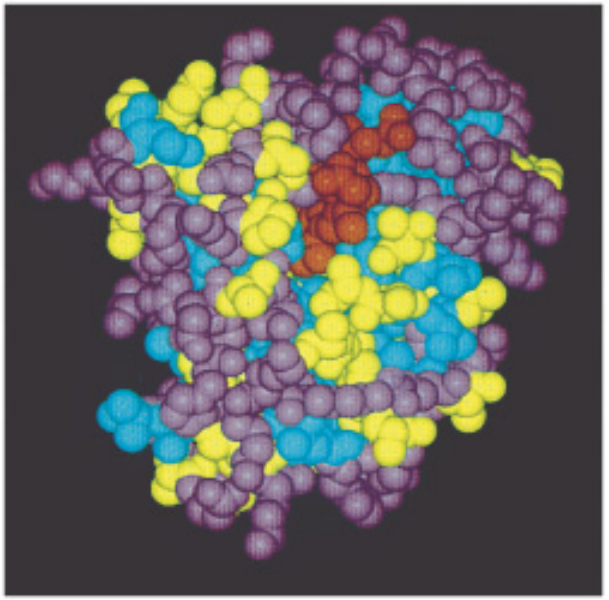
(a)



(b)



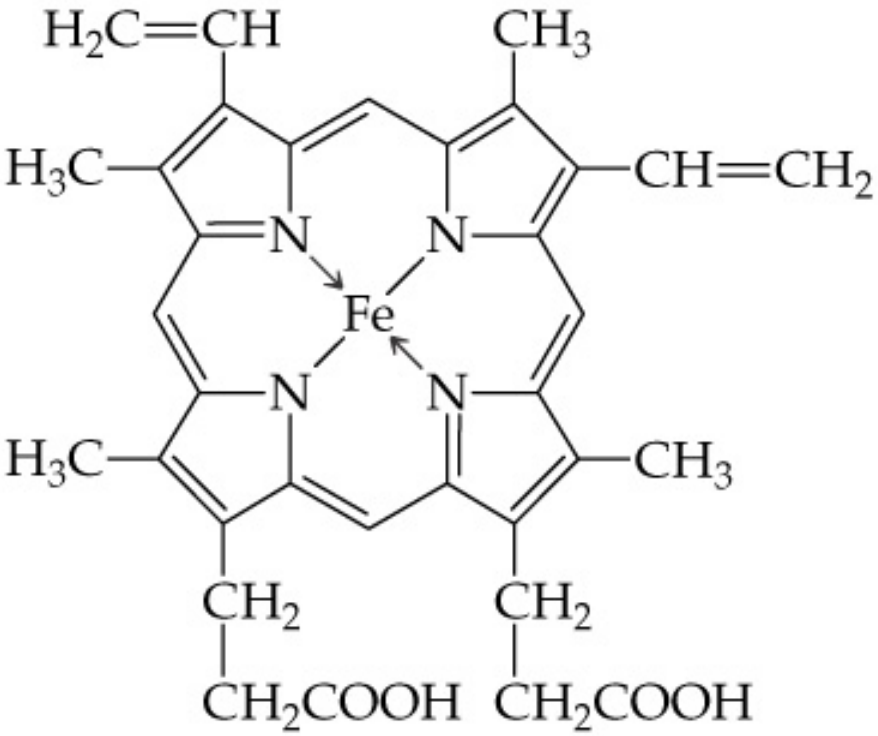
(c)



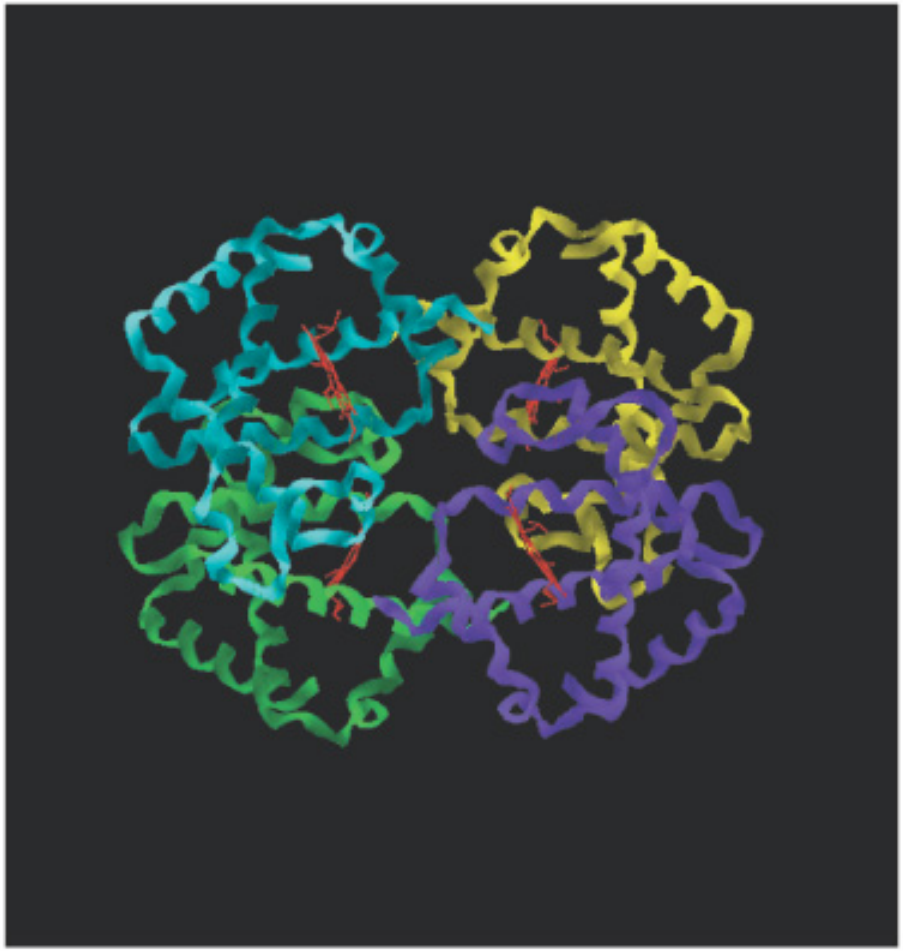
(d)

Quaternary Protein Structure

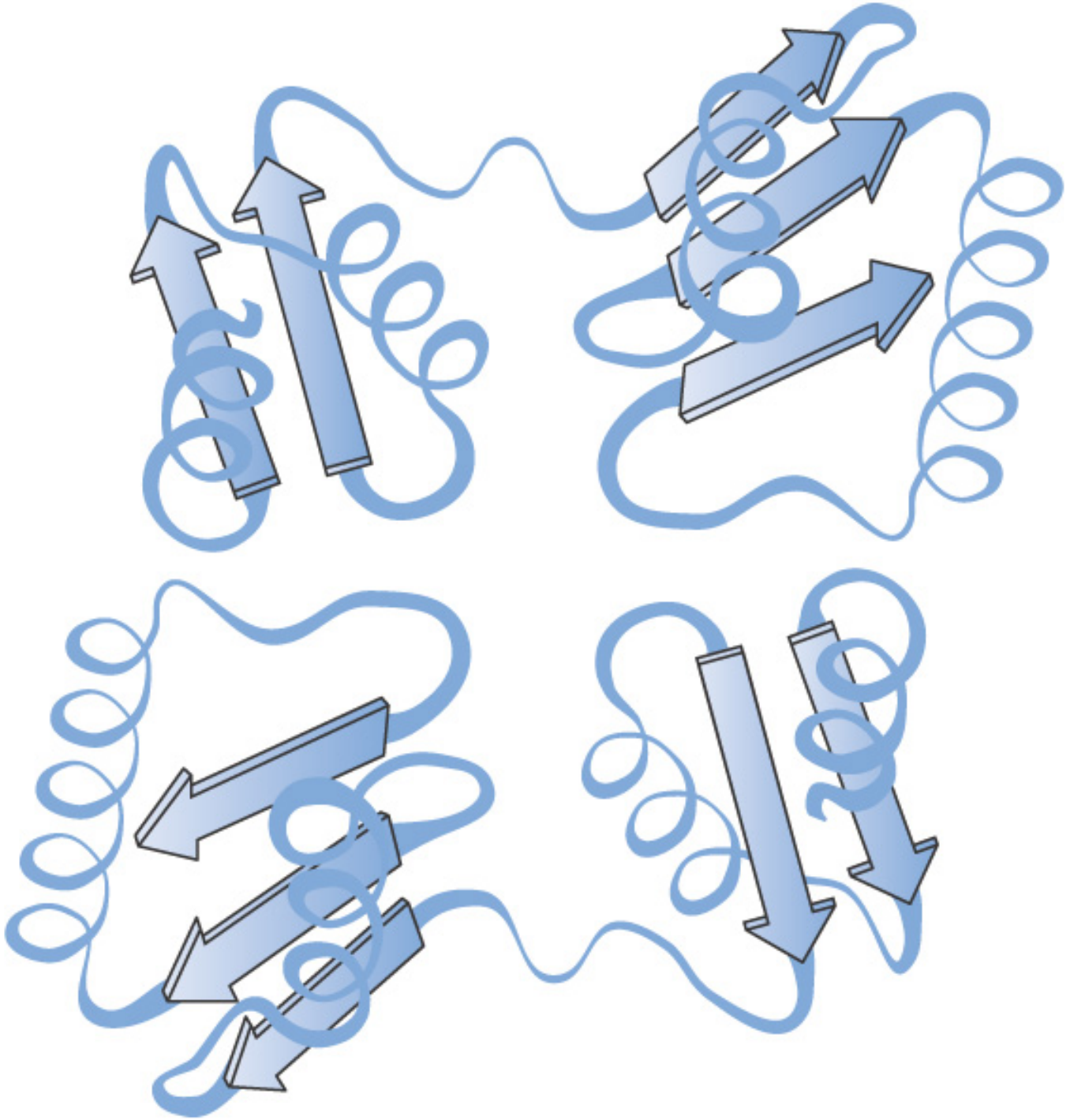
- ***Quaternary protein structure***: The way in which two or more polypeptide sub-units associate to form a single three-dimensional protein unit. Non-covalent forces are responsible for quaternary structure essential to the function of proteins.

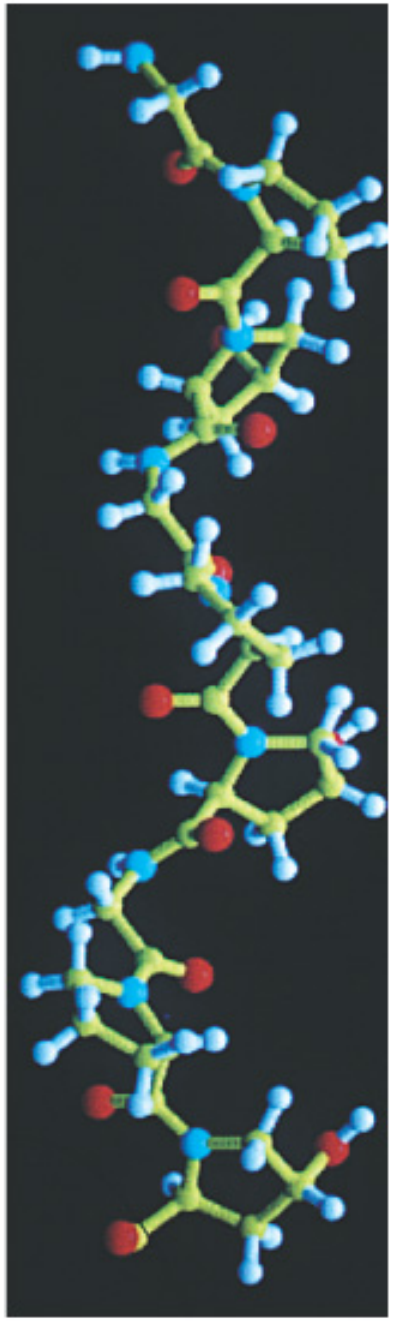


(a)

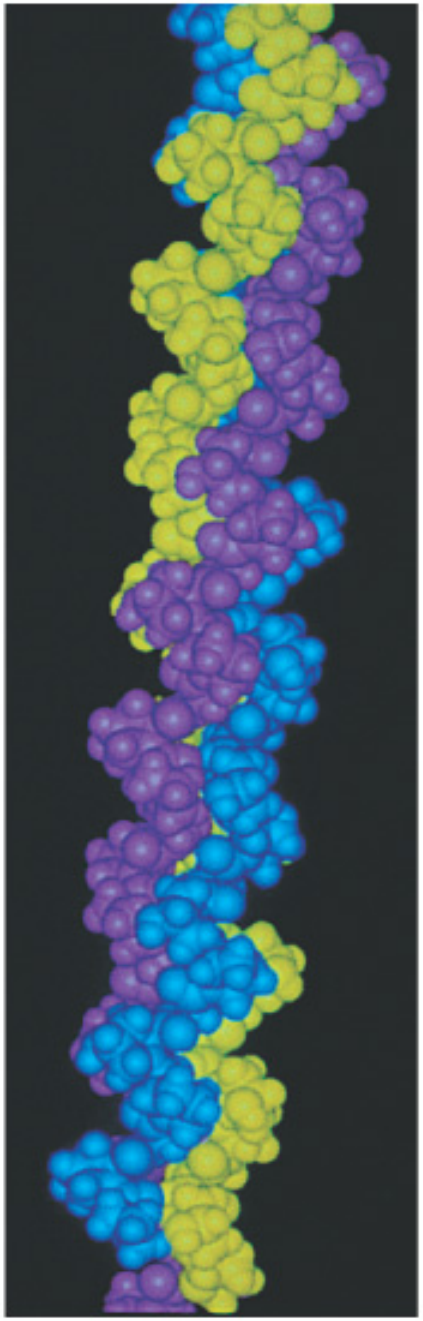


(b)

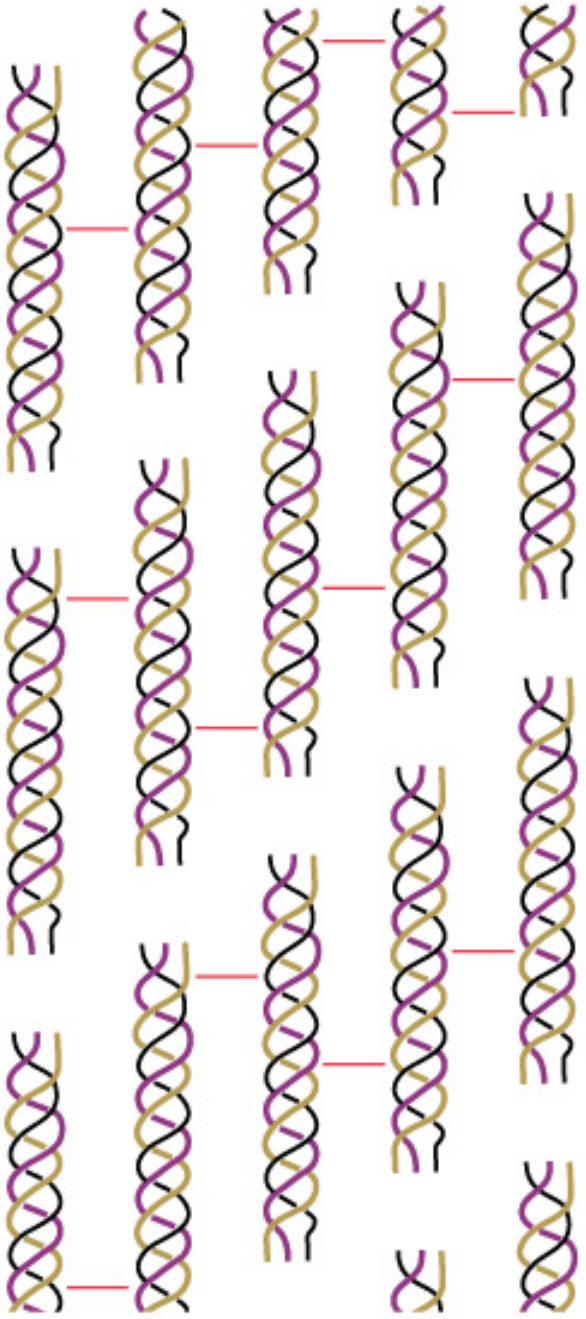




(a)



(b)

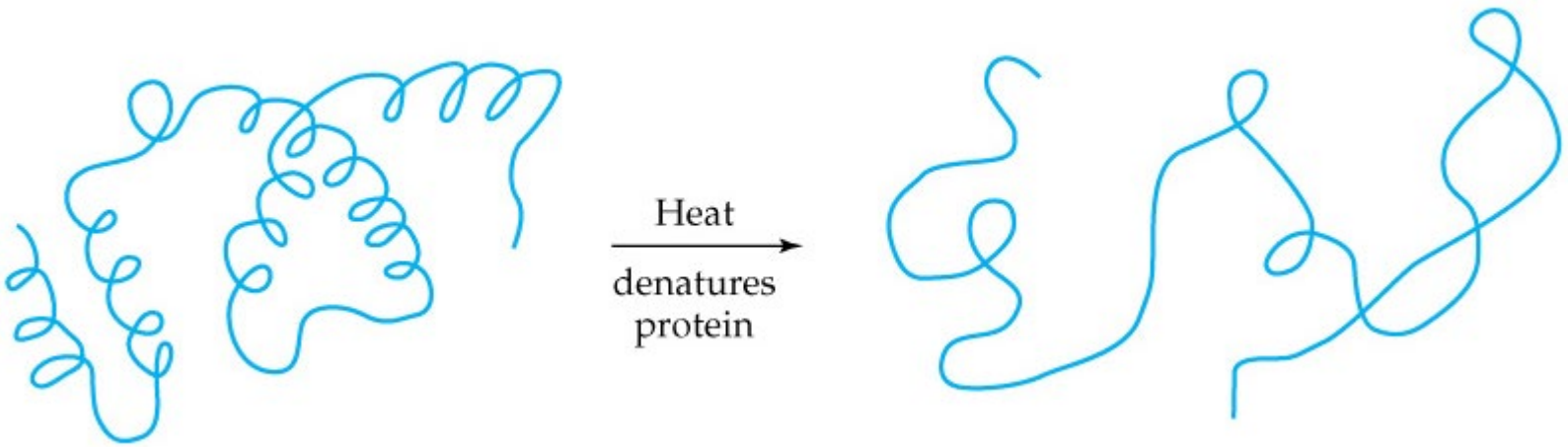


(c)

Chemical Properties of Proteins

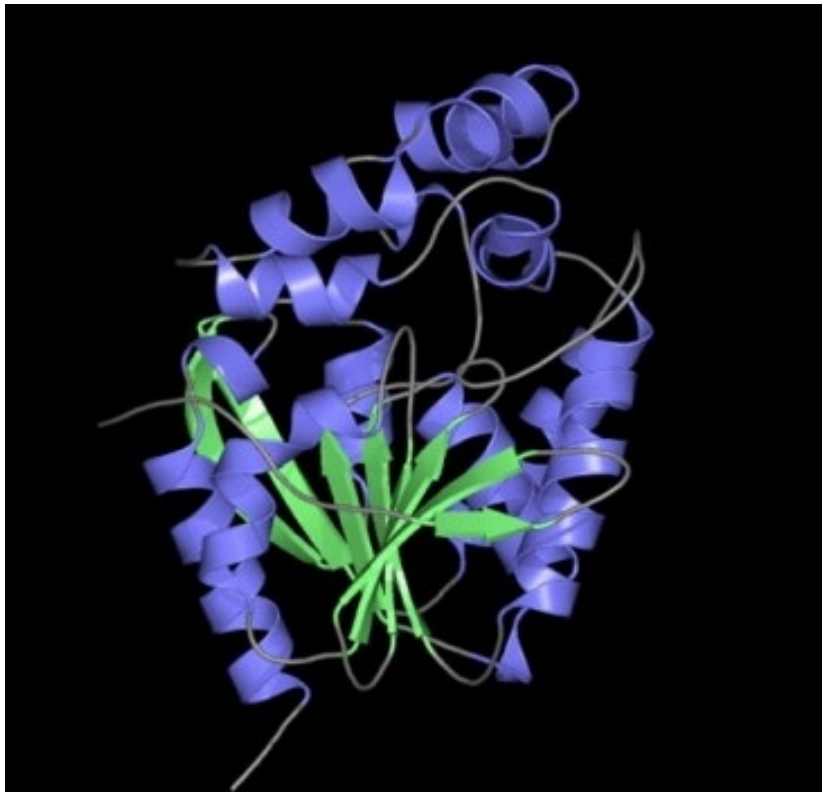
- *Protein hydrolysis:* In protein hydrolysis, peptide bonds are hydrolyzed to yield amino acids. This is reverse of protein formation.

- *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

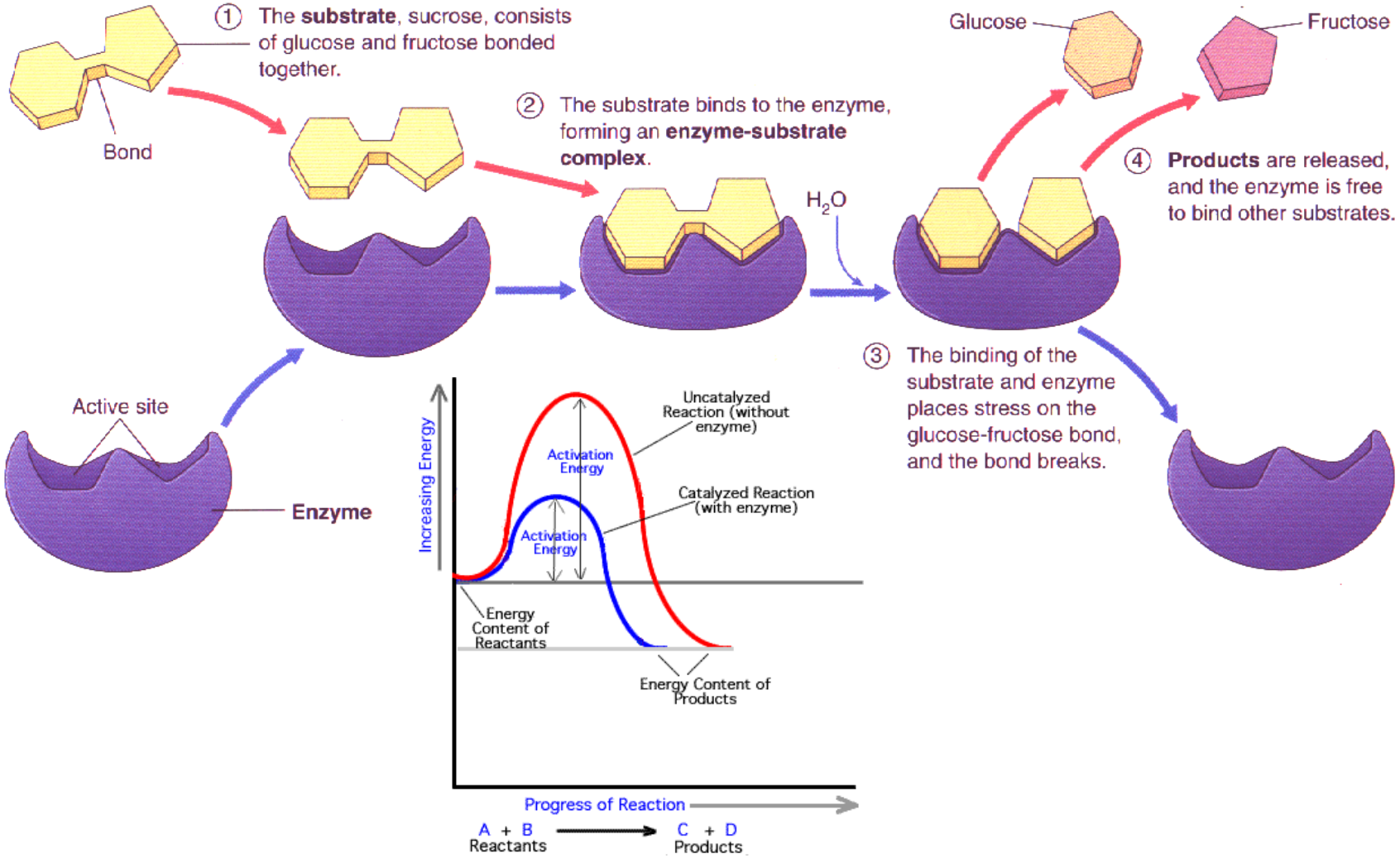


Catalysis by Enzymes

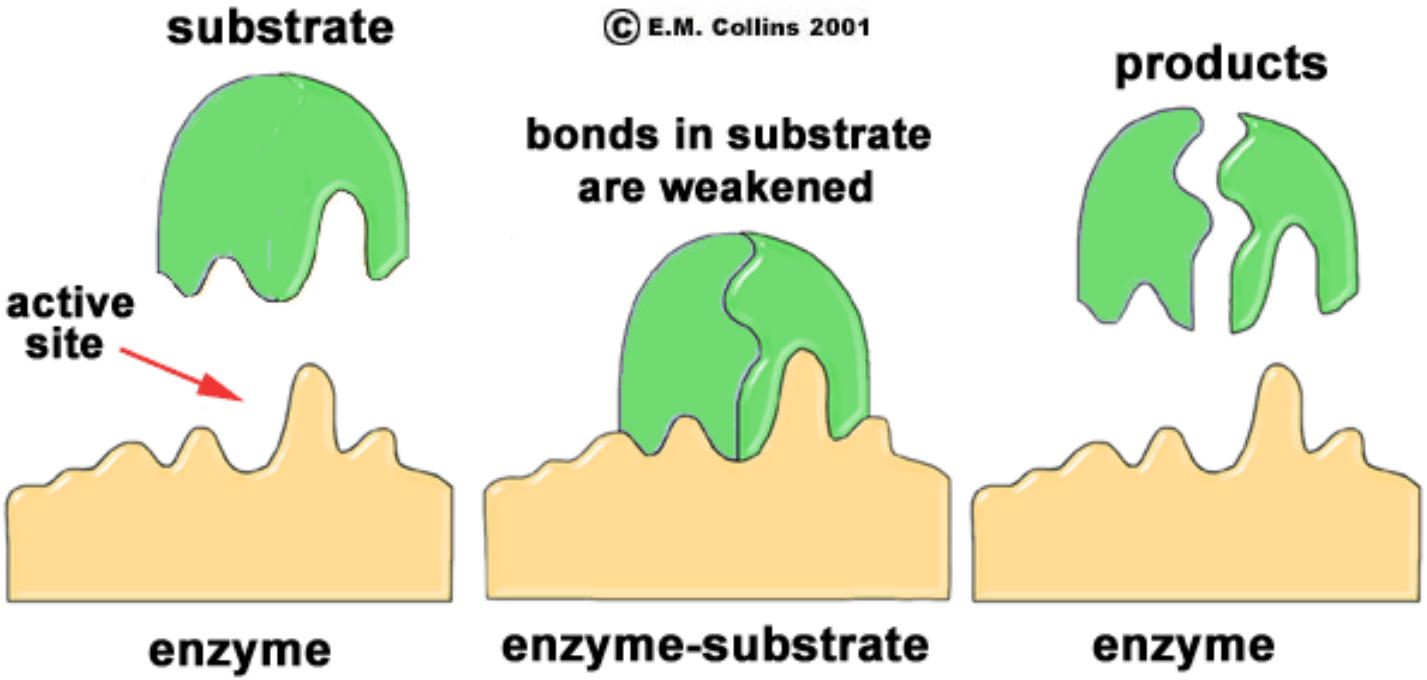
- ***Enzyme*** A protein that acts as a catalyst for a biochemical reaction.



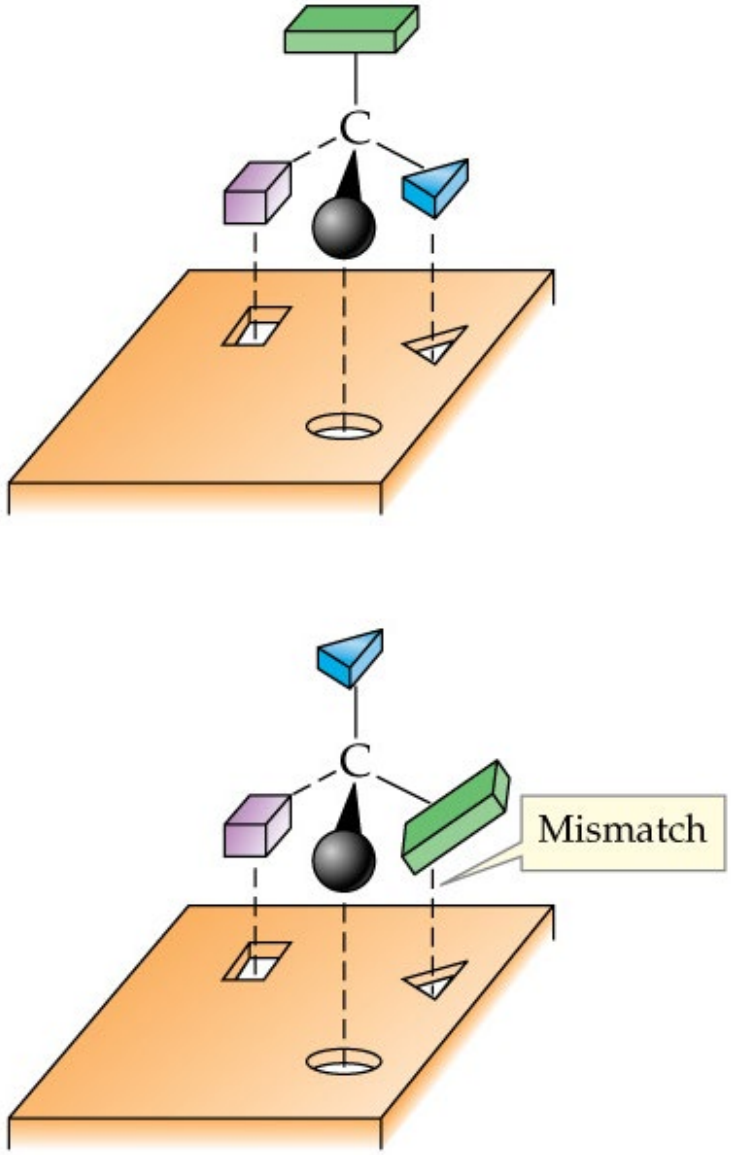
Enzymatic Reaction



Specificity



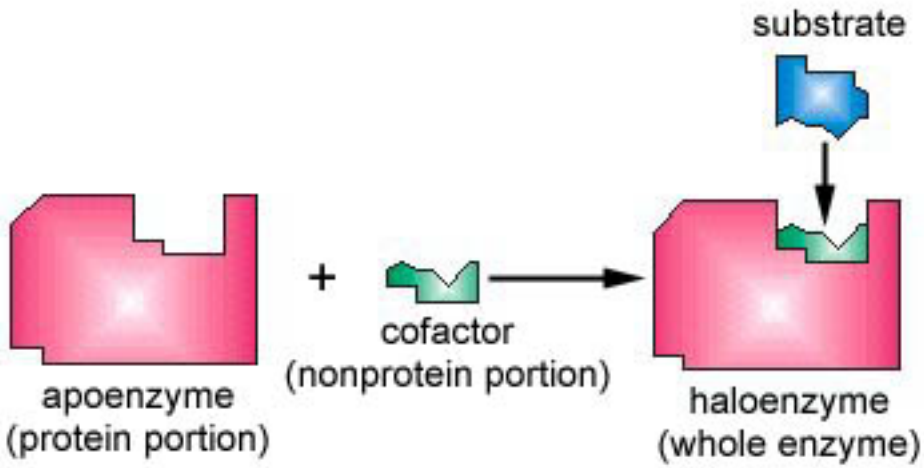
The specificity of an enzyme for one of two enantiomers is a matter of fit. One enantiomer fits better into the active site of the enzyme than the other enantiomer. Enzyme catalyzes reaction of the enantiomer that fits better into the active site of the enzyme.

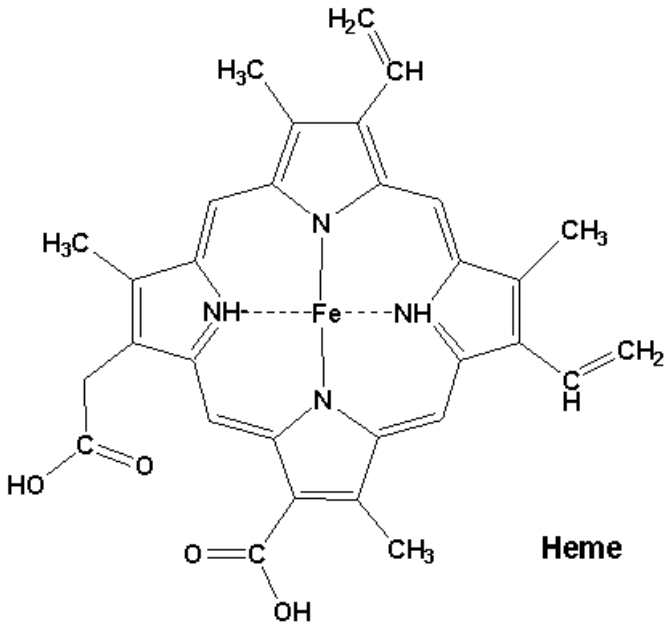


Enzyme Cofactors

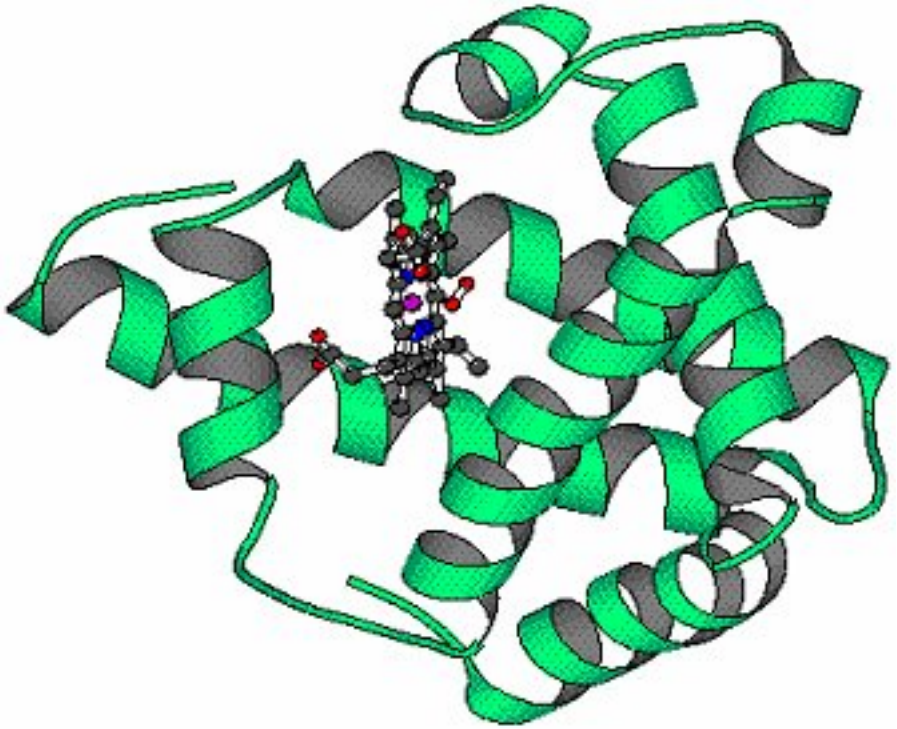
- Many enzymes are conjugated proteins that require nonprotein portions known as ***cofactors***.
- Some cofactors are metal ions, others are nonprotein organic molecules called ***coenzymes***.
- An enzyme may require a metal-ion, a coenzyme, or both to function.

Cofactor





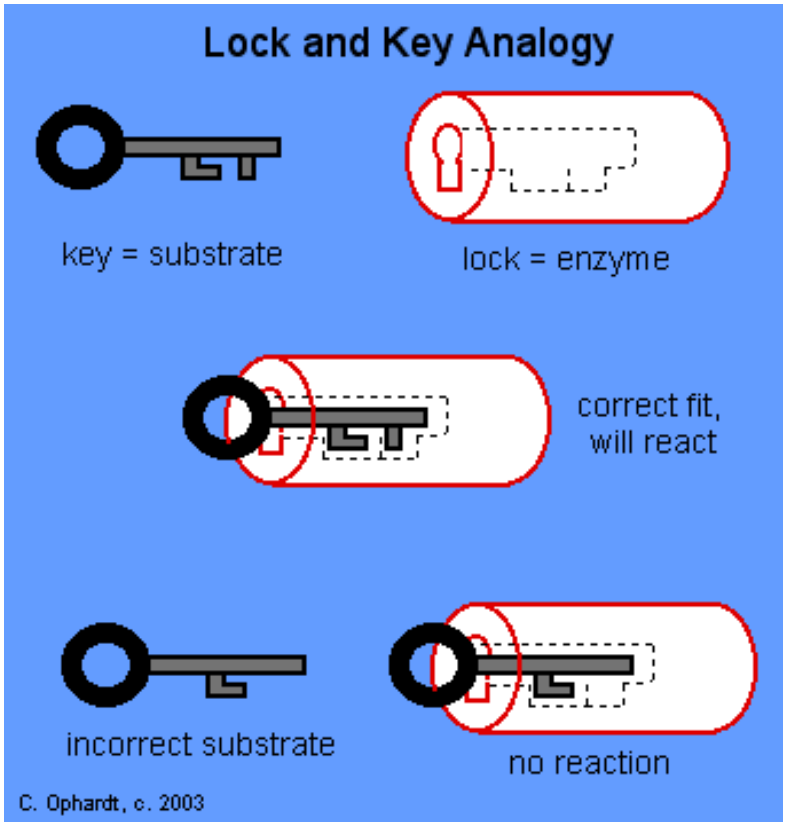
Heme

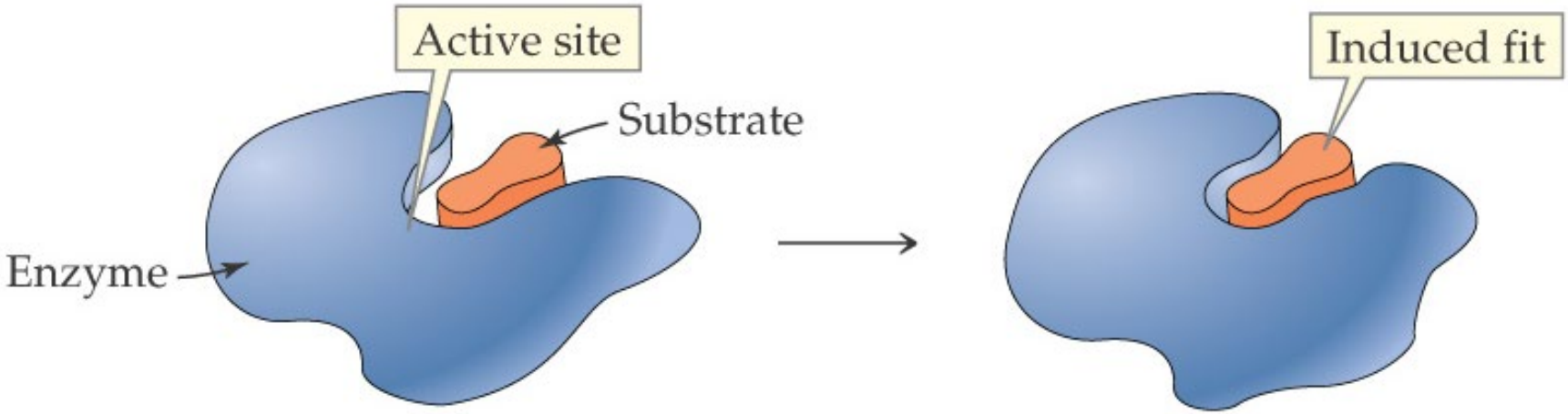


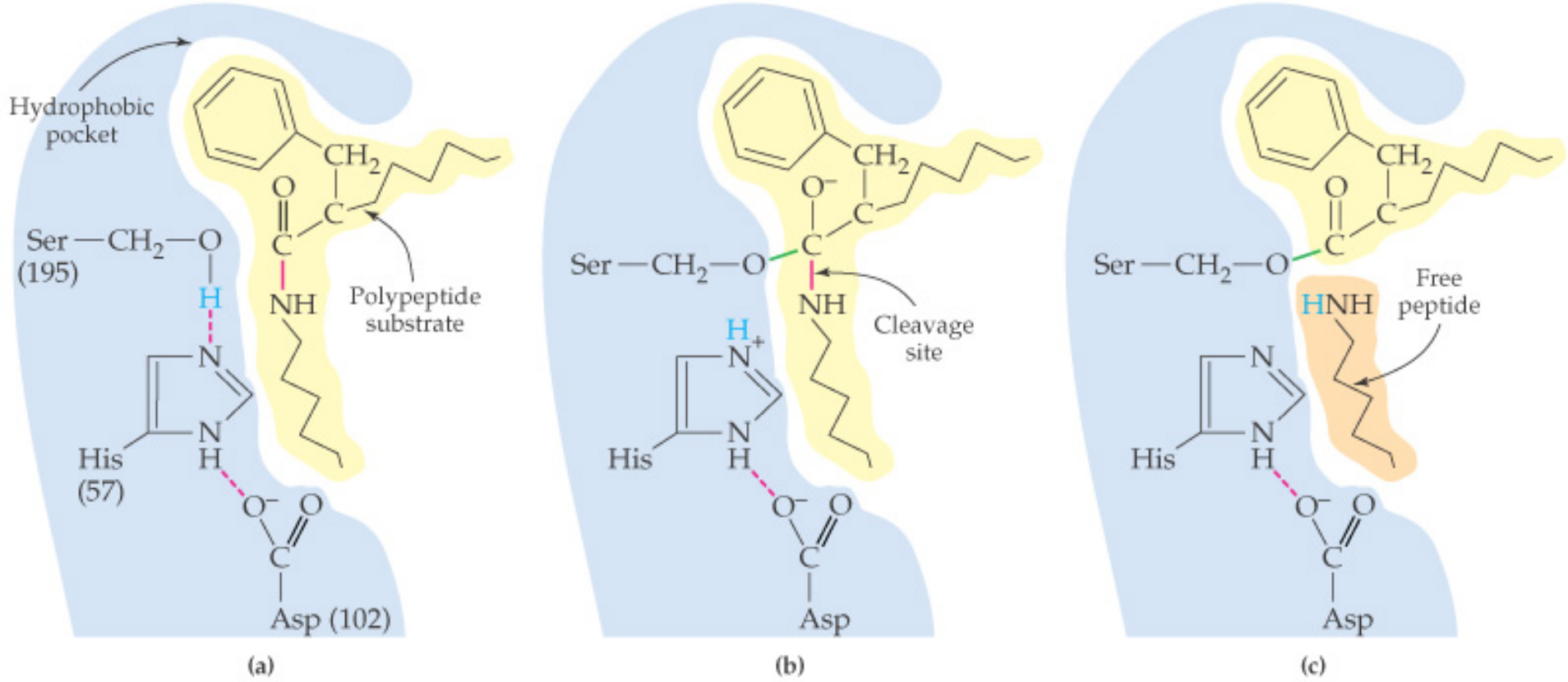
- Cofactors provide additional chemically active functional groups which are not present in the side chains of amino acids that made up the enzyme.
- Metal ions may anchor a substrate in the active site or may participate in the catalyzed reaction.

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)
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.

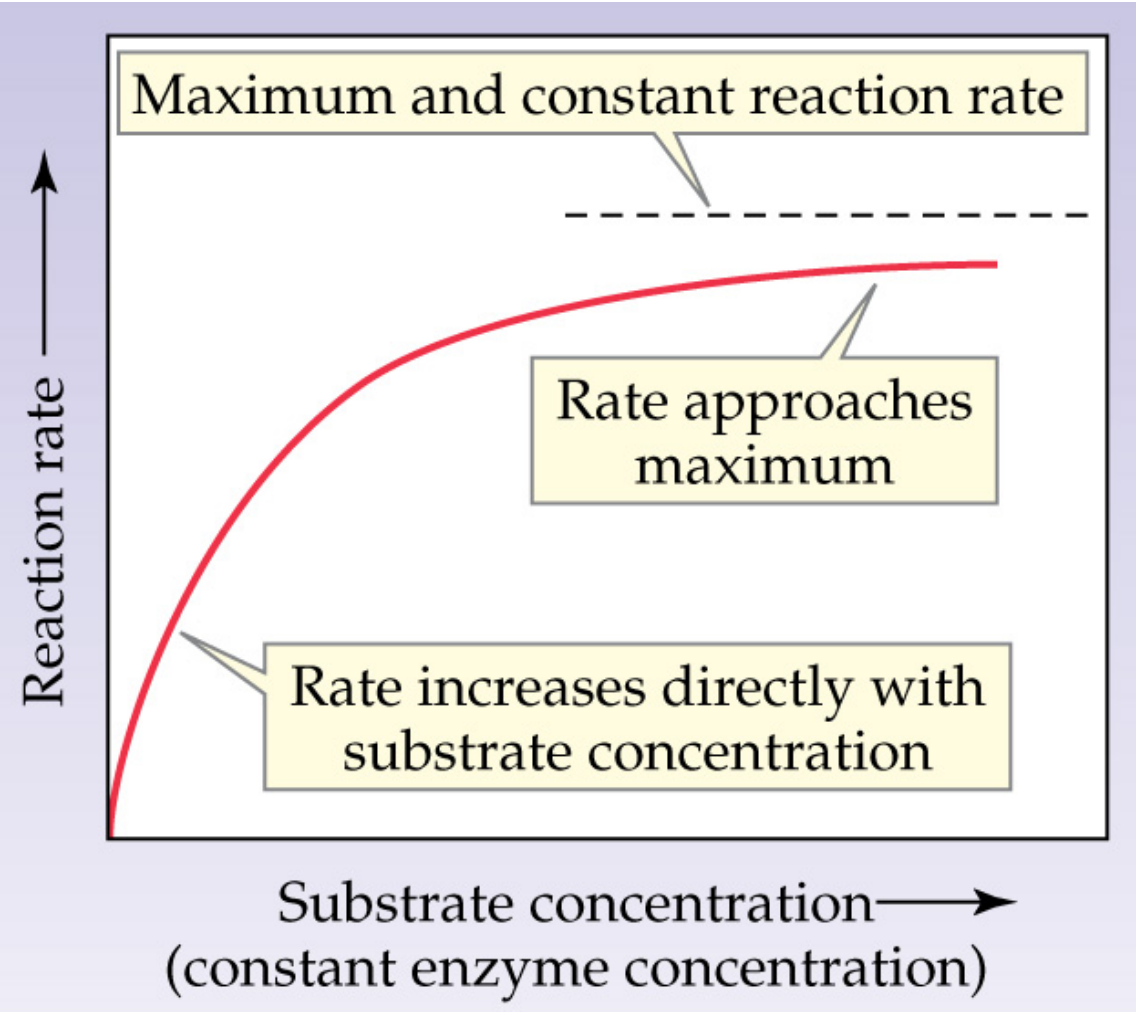
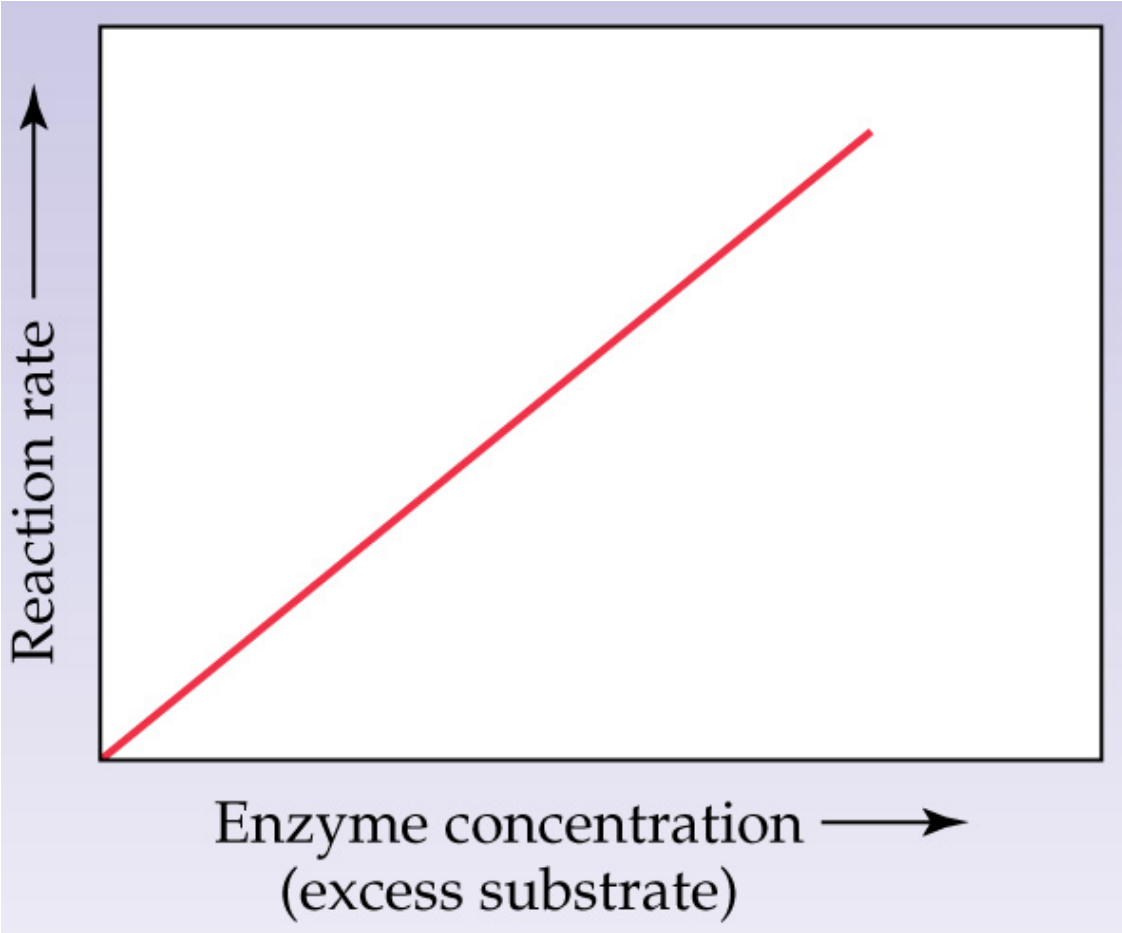


Fig 19.5 Change of reaction rate with substrate concentration when enzyme concentration is constant.

- *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.

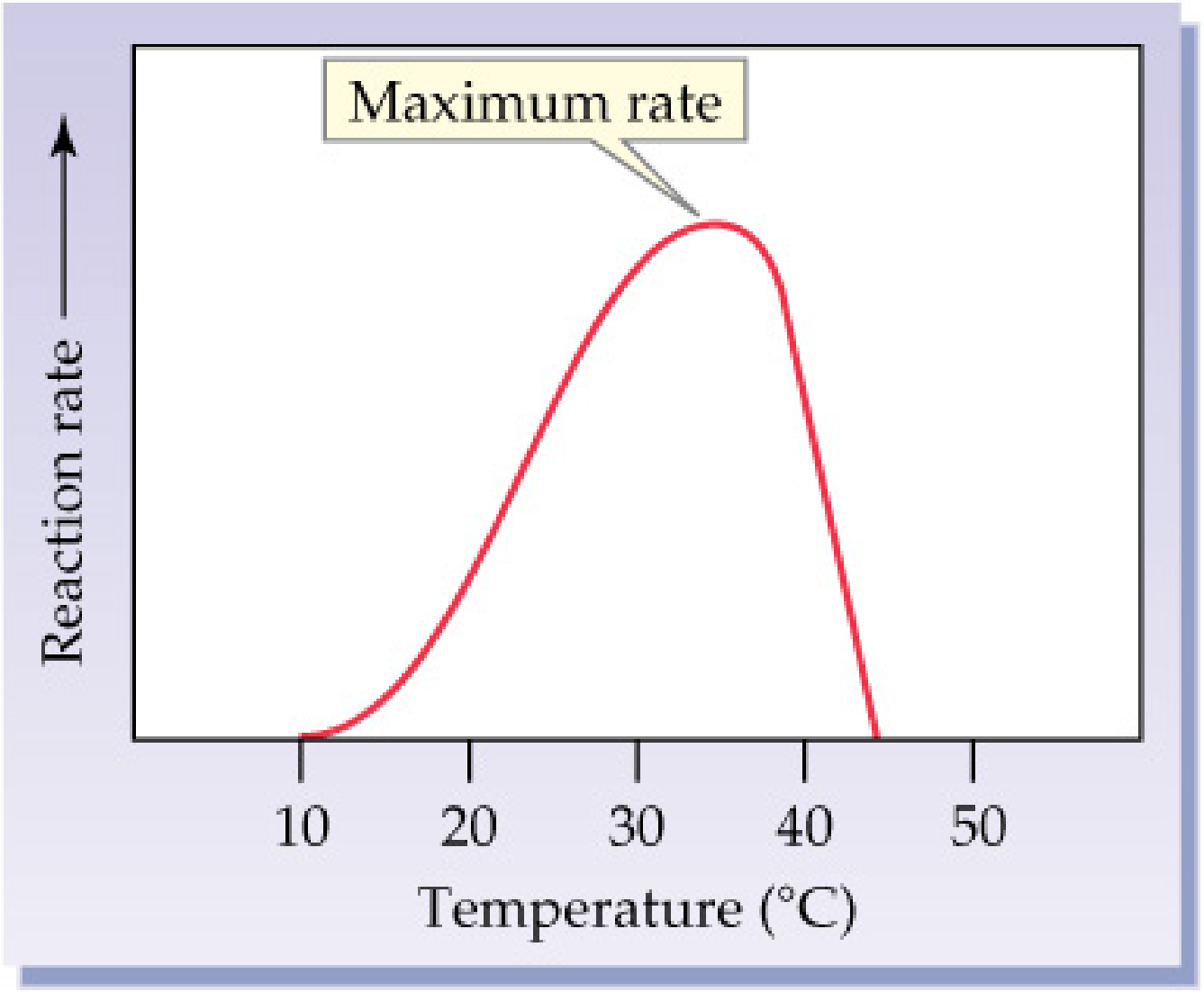
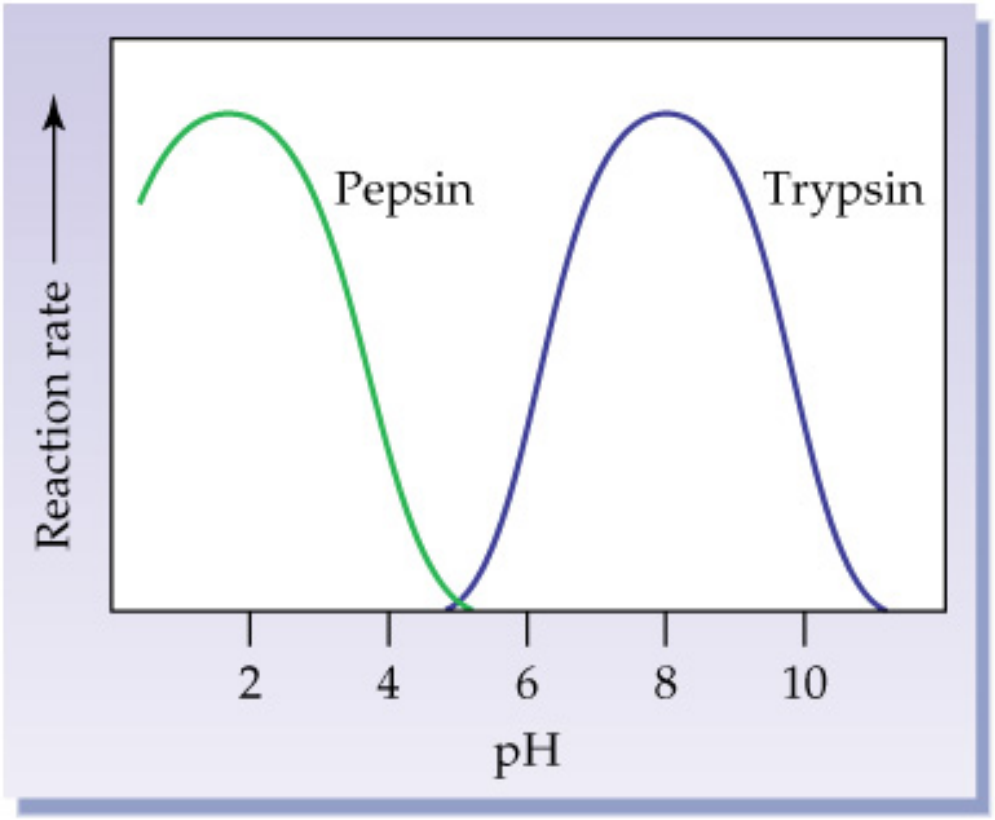


Fig 19.7 (a) Effect of temperature on reaction rate

- 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.

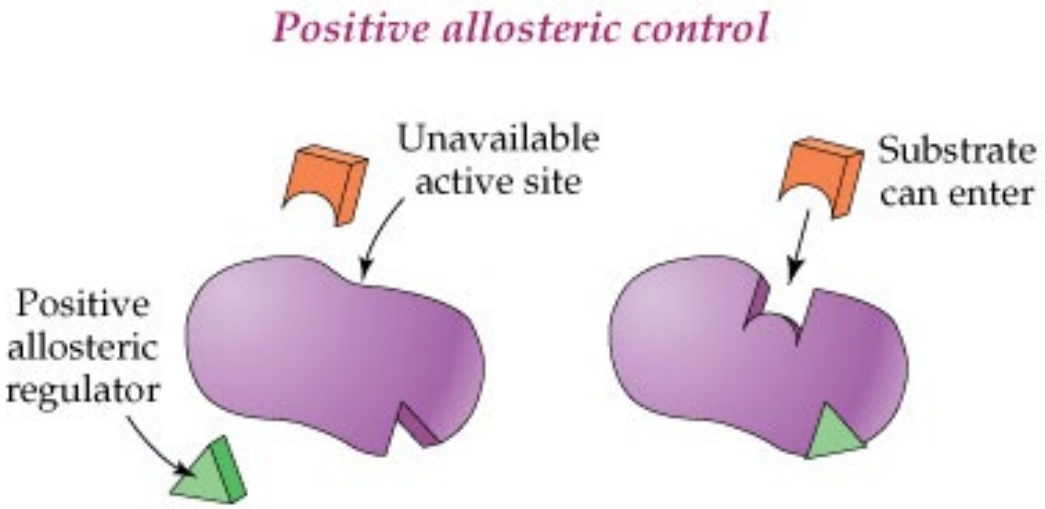


19.7 Enzyme Regulation: Feedback and Allosteric Control

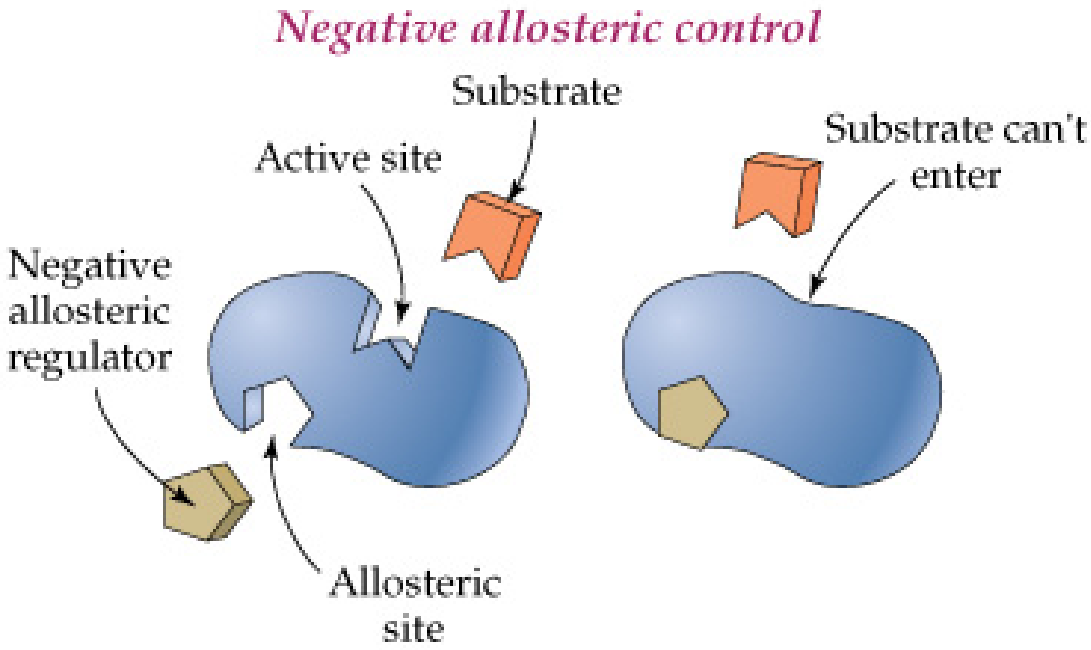
- Concentration of thousands of different chemicals vary continuously in living organisms which requires regulation of enzyme activity.
- Any process that starts or increase the activity of an enzyme is ***activation.***
- Any process that stops or slows the activity of an enzyme is ***inhibition.***

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.

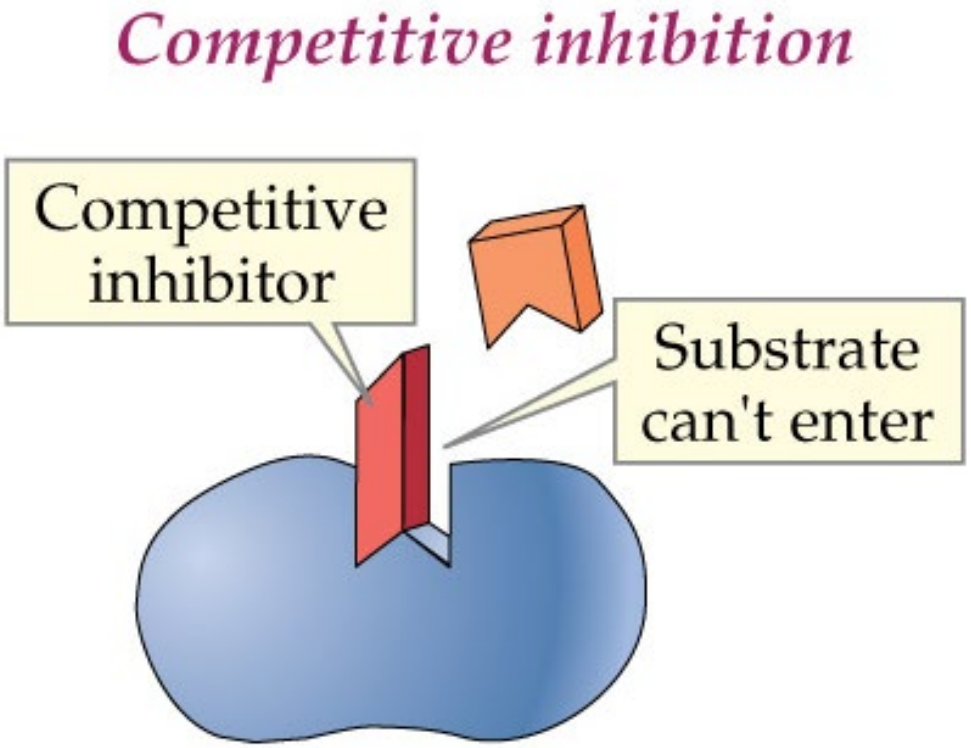


A negative regulator changes the activity site so that the enzyme becomes less effective catalyst and rate slows down.

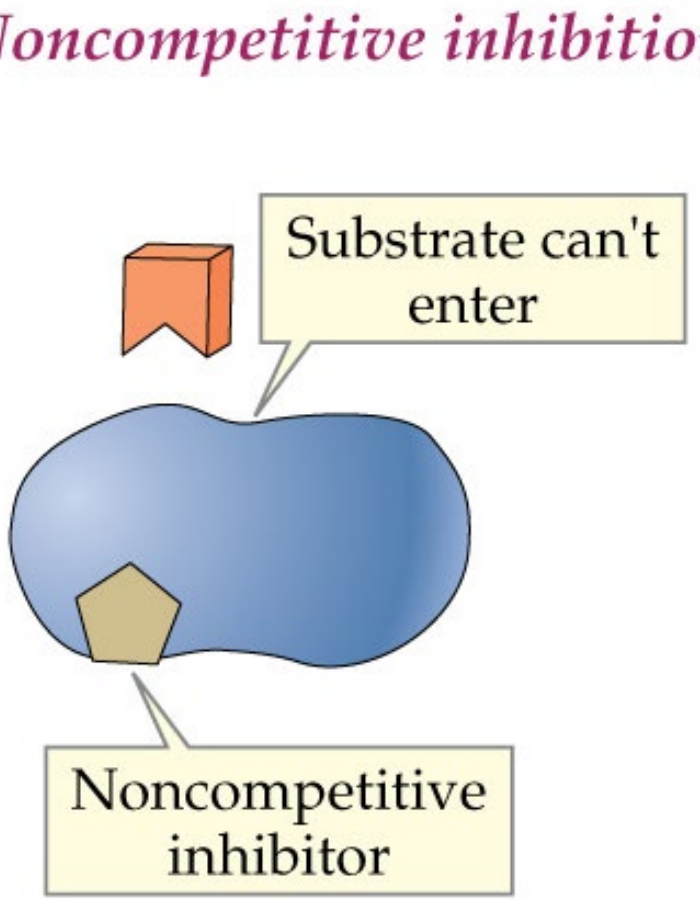
19.8 Enzyme Regulation: Inhibition

- 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.

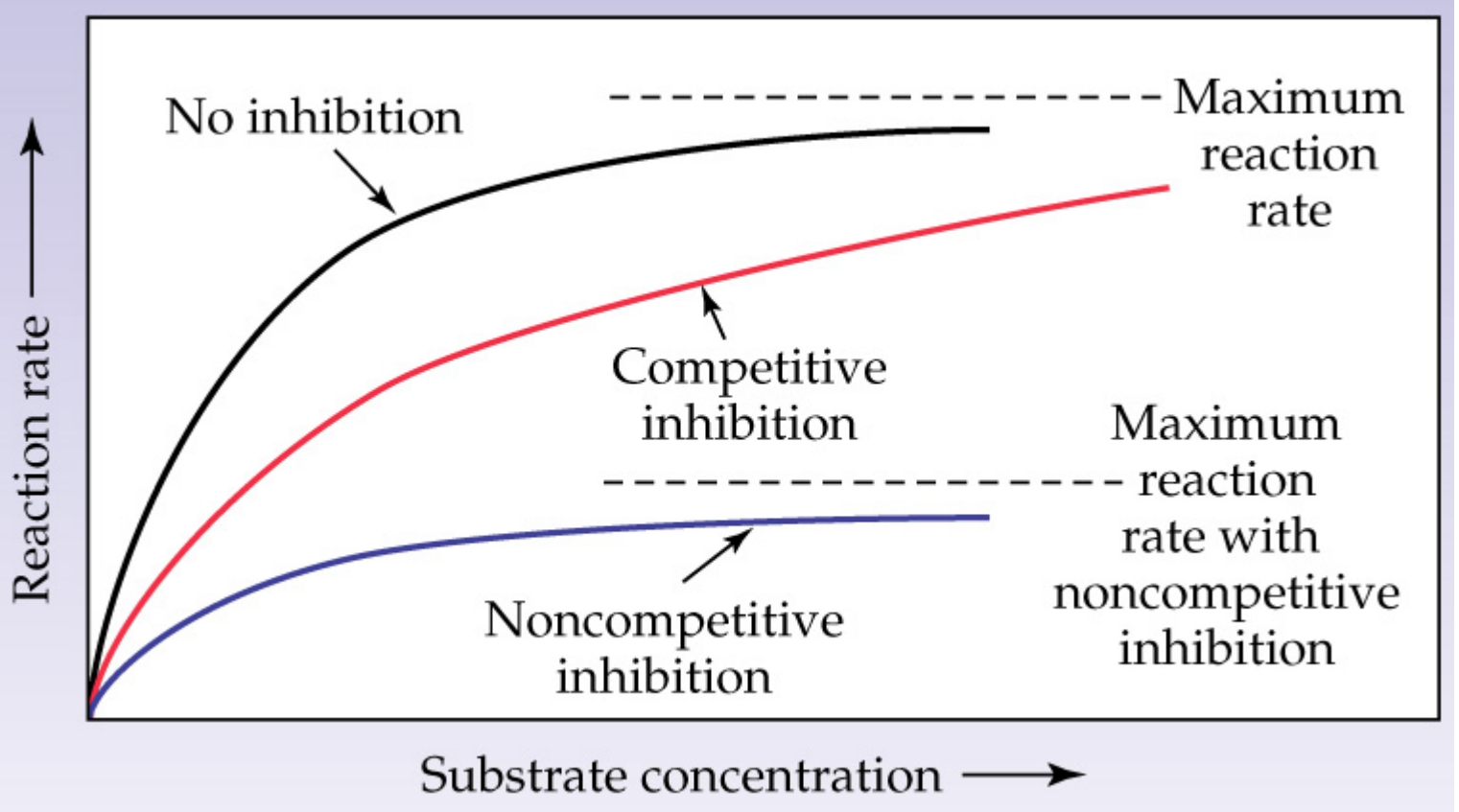
- Inhibitions are further classified as:
- *Competitive inhibition if* the inhibitor binds to the active site.

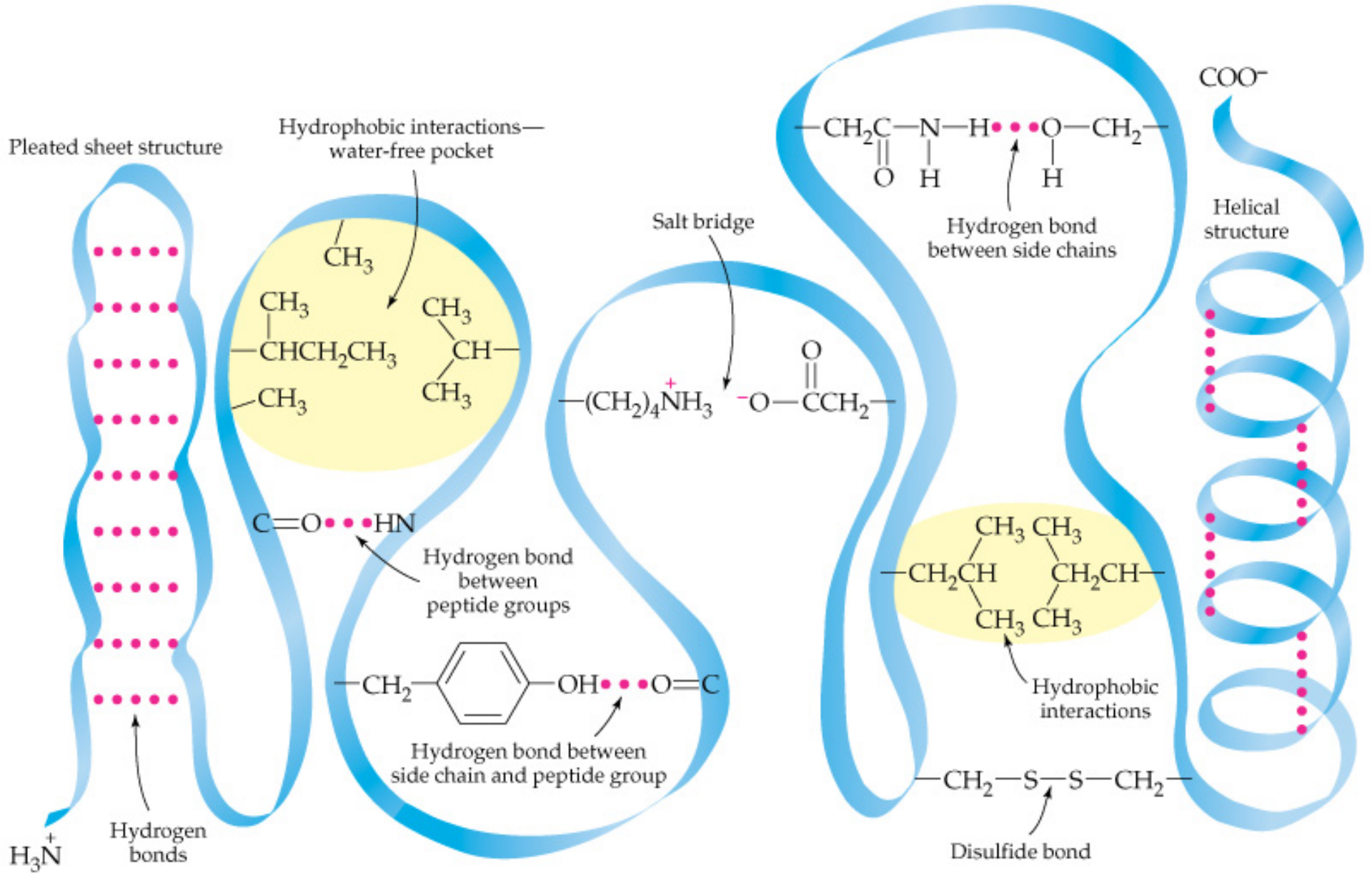


- *Noncompetitive inhibition,* if the inhibitor binds elsewhere and not to the active site.



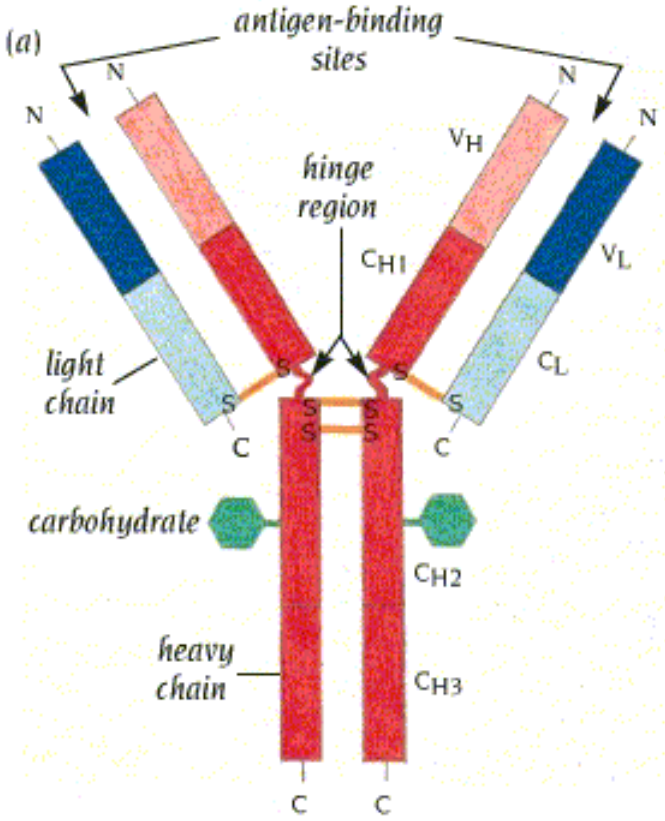
•The rates of enzyme catalyzed reactions with or without a competitive inhibitor are shown in the Fig 19.9 below.

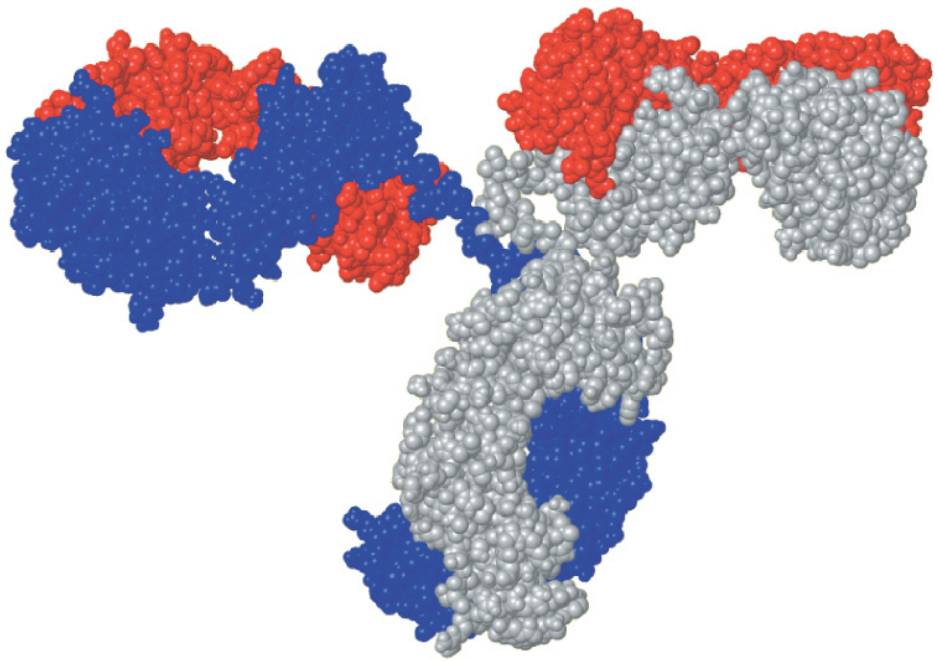



Pleated sheet structure
Hydrophobic interactions—
water-free pocket
Salt bridge
Hydrogen bond
between side chains
Helical
structure
Hydrogen bond
between
peptide groups
Hydrogen bond between
side chain and peptide group
Hydrophobic
interactions
Hydrogen
bonds
Disulfide bond

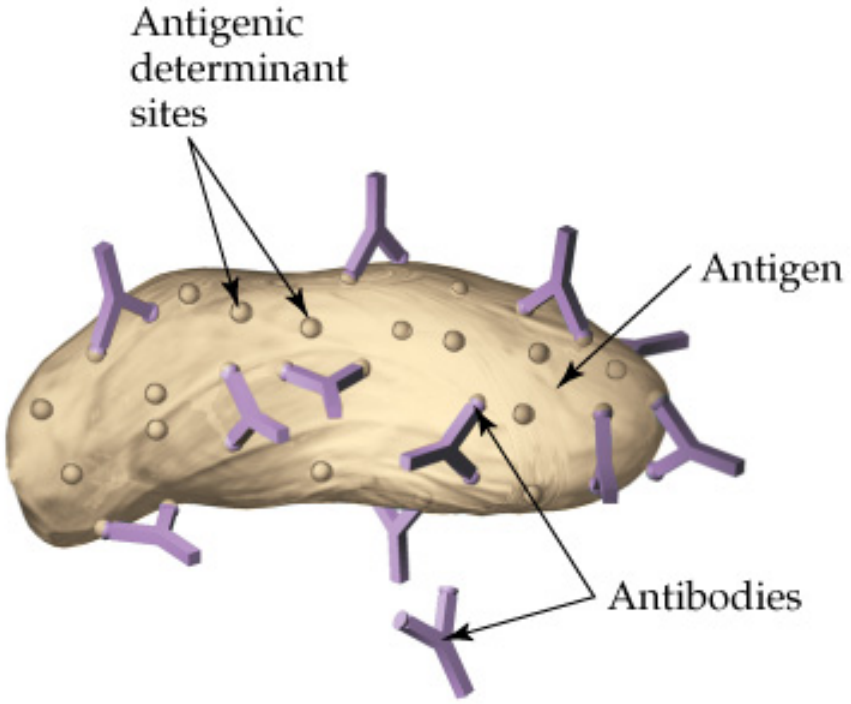
Shape-Determining Interactions in Proteins

- 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.

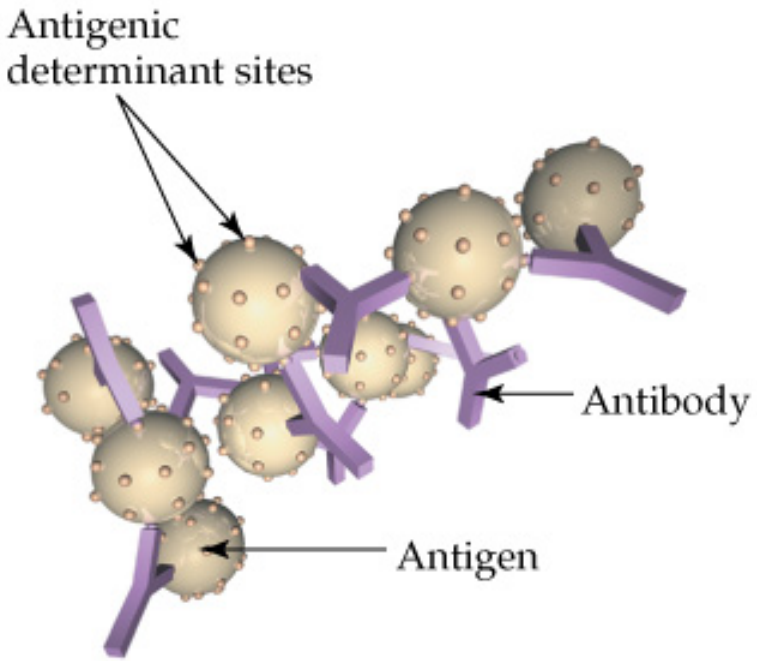

(a)
antigen-binding sites
N
N
N
N
VH
VL
hinge region
CH1
CL
light chain
S
S
S
S
S
S
S
S
C
C
carbohydrate
CH2
heavy chain
CH3
C
C



(b)

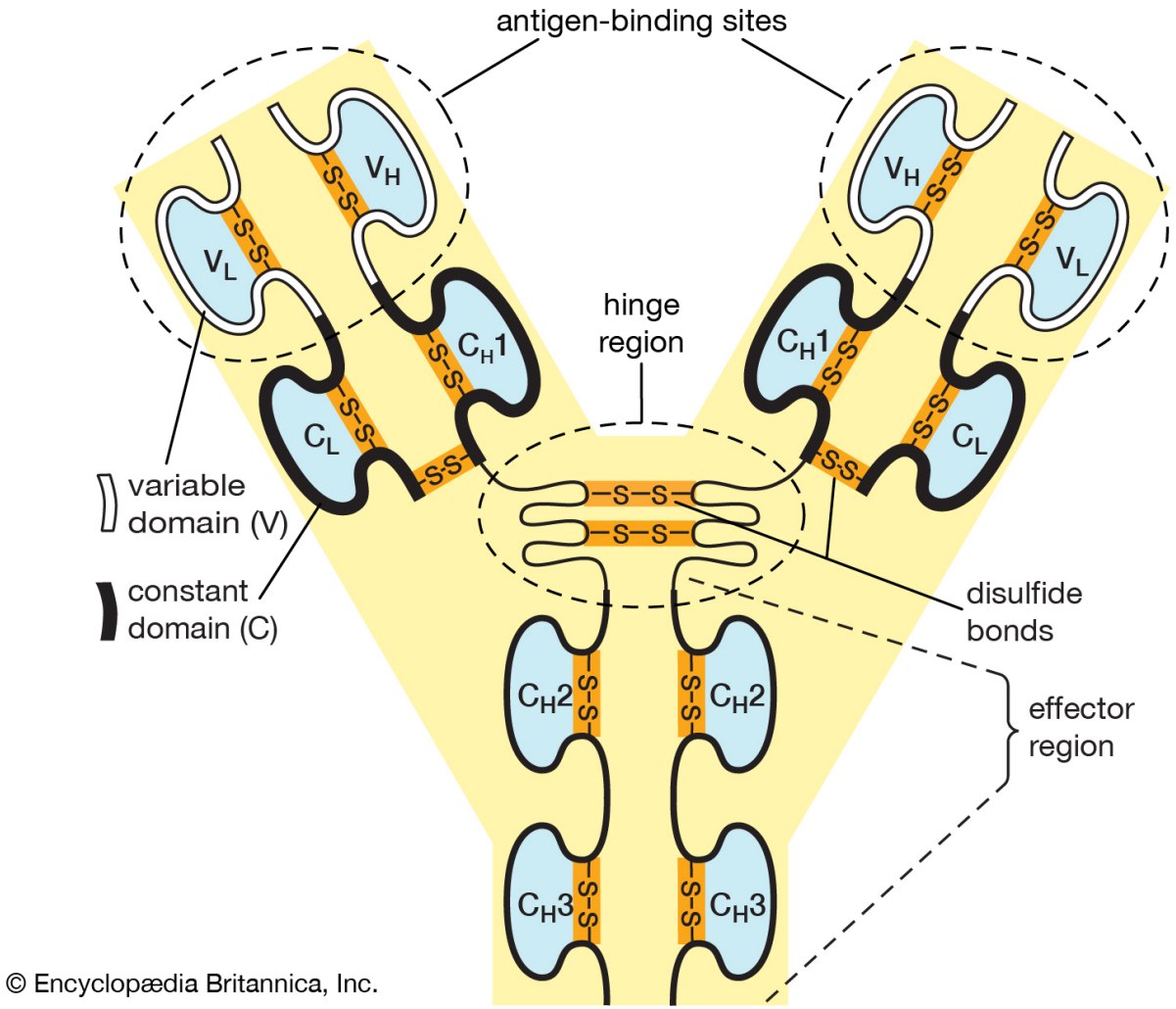

Antigenic determinant sites
Antigen
Antibodies

(a)


Antigenic determinant sites
Antibody
Antigen

(b)

Antibody


antigen-binding sites
V_H
V_L
C_H1
C_L
hinge region
variable domain (V)
constant domain (C)
disulfide bonds
C_H2
C_H3
effector region
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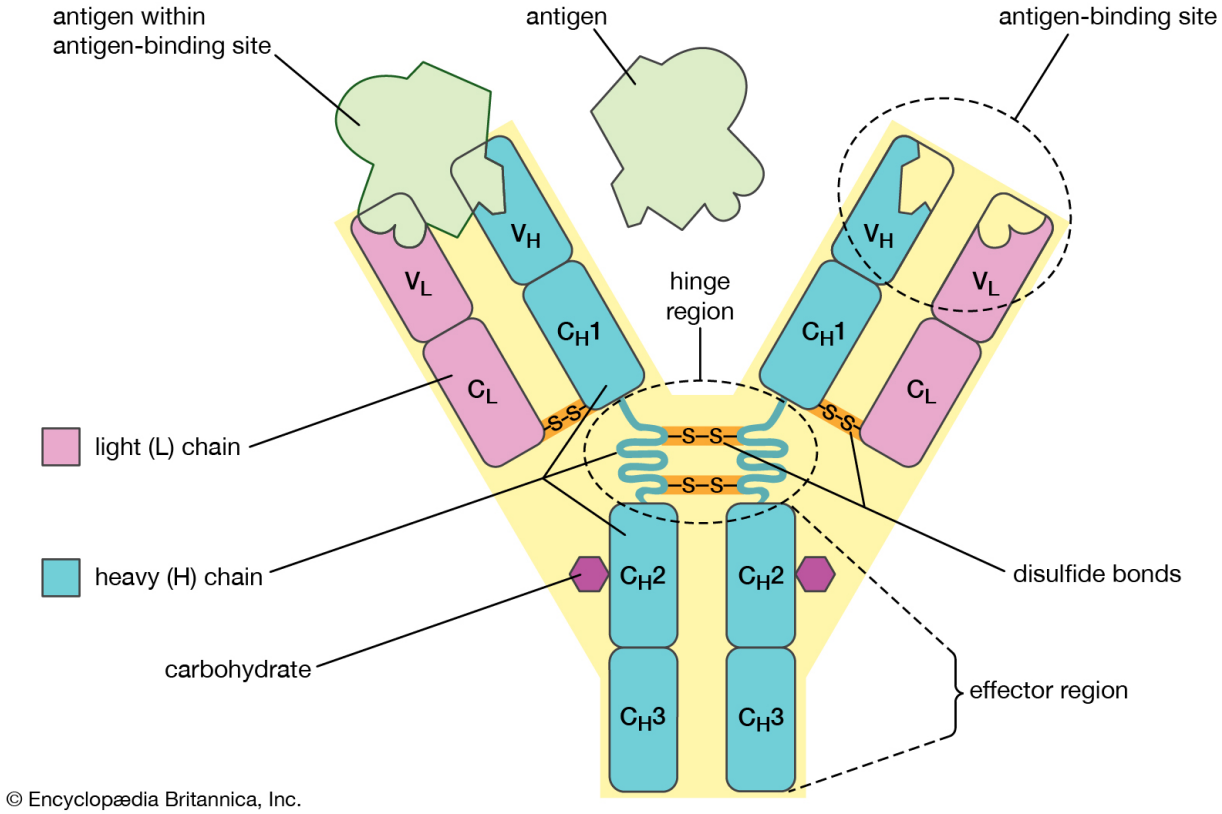
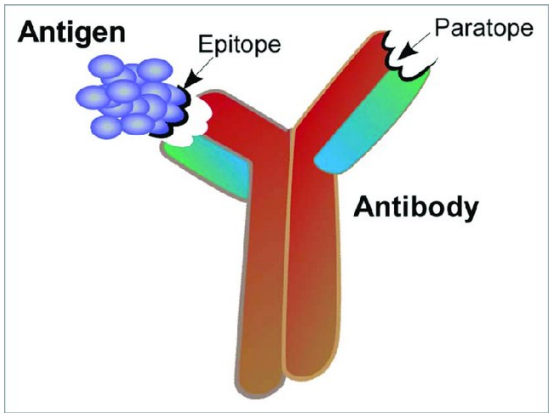
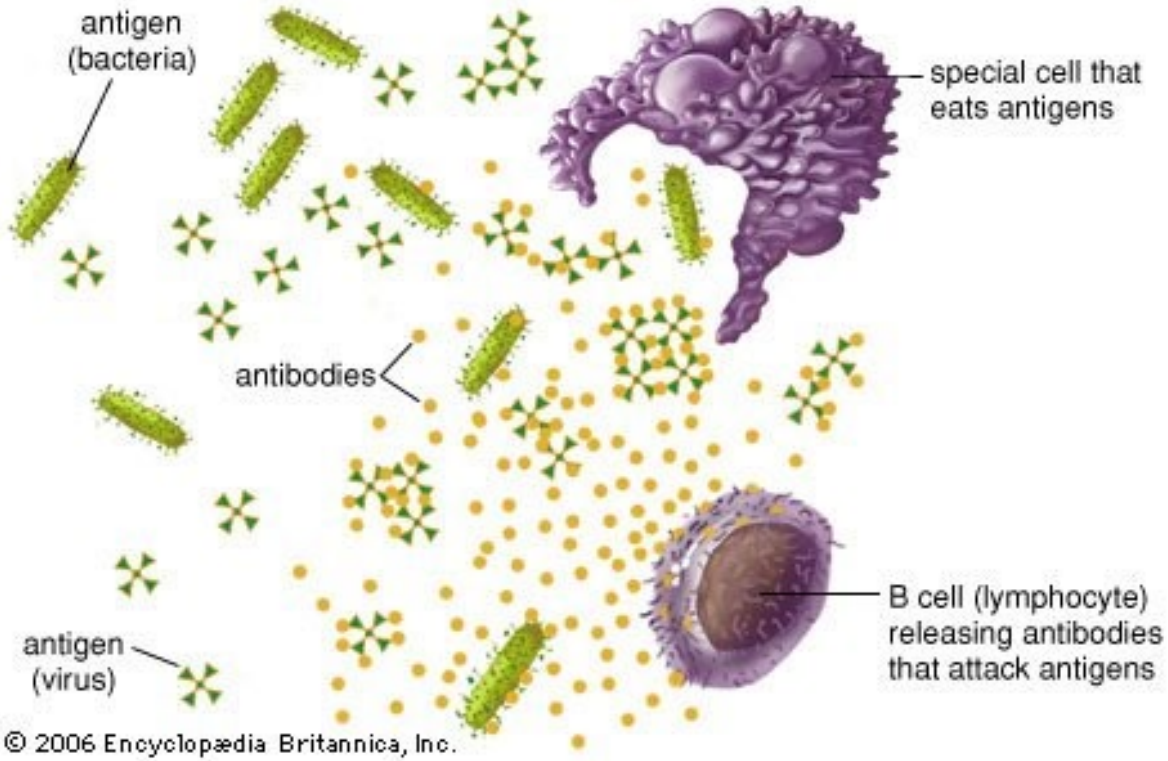
Antibody Binding Sites






antigen
(bacteria)
special cell that
eats antigens
antibodies
B cell (lymphocyte)
releasing antibodies
that attack antigens
antigen
(virus)
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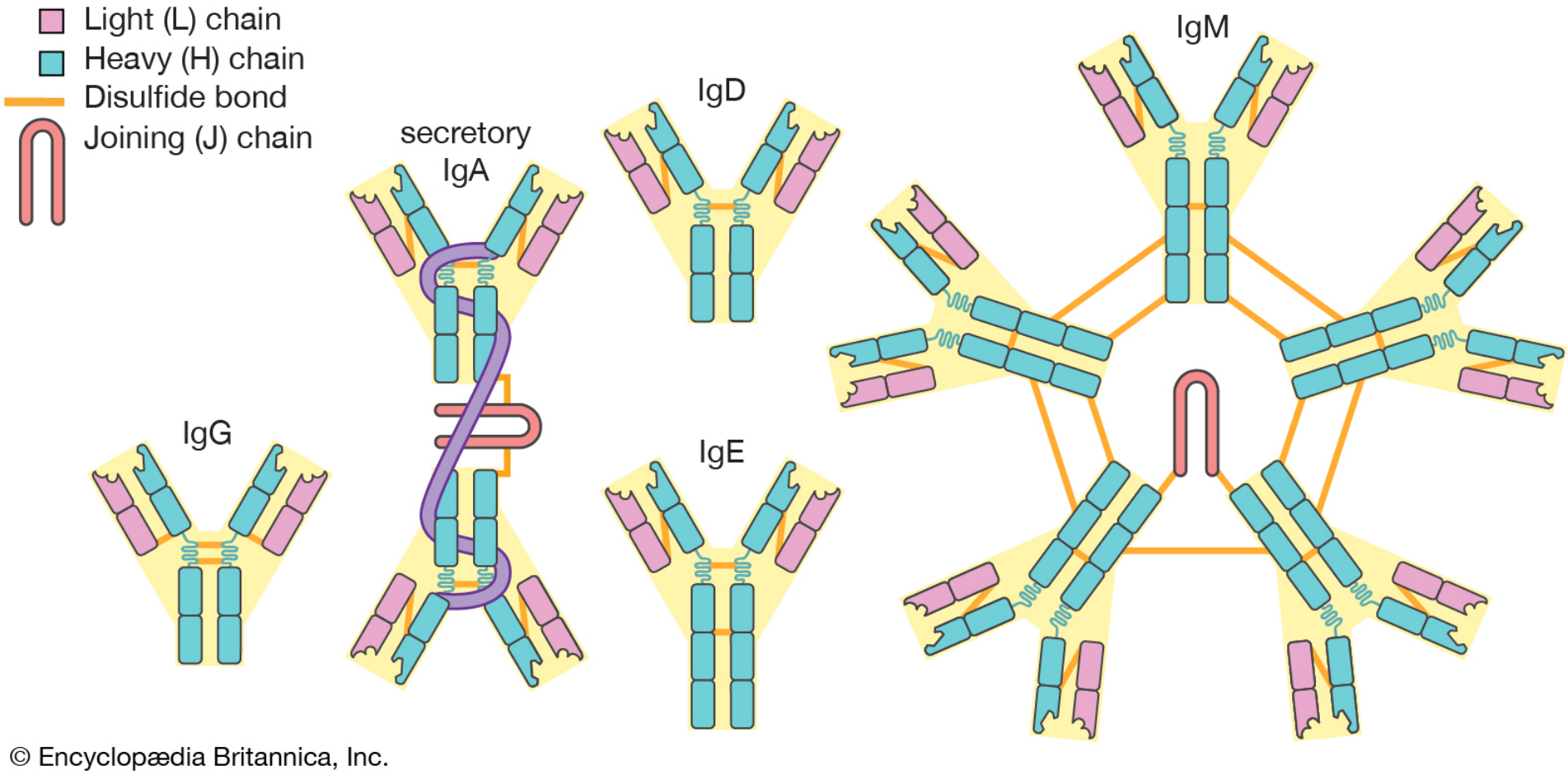
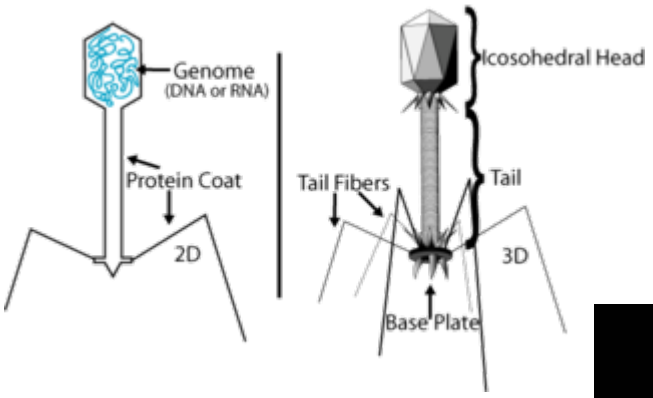
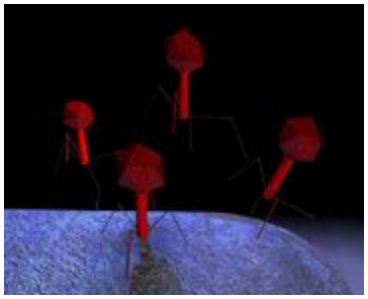
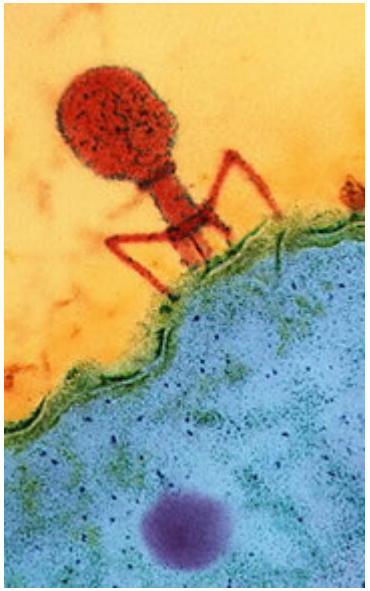
Different Types of Antibodies

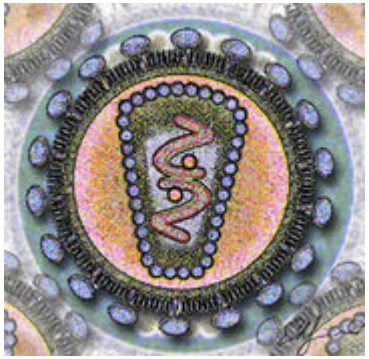


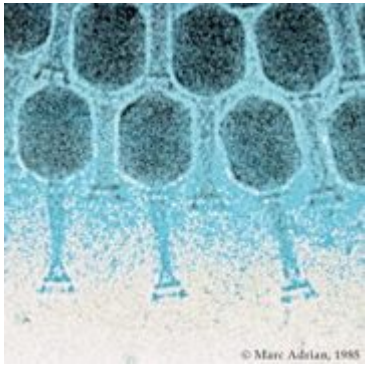
Virus


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

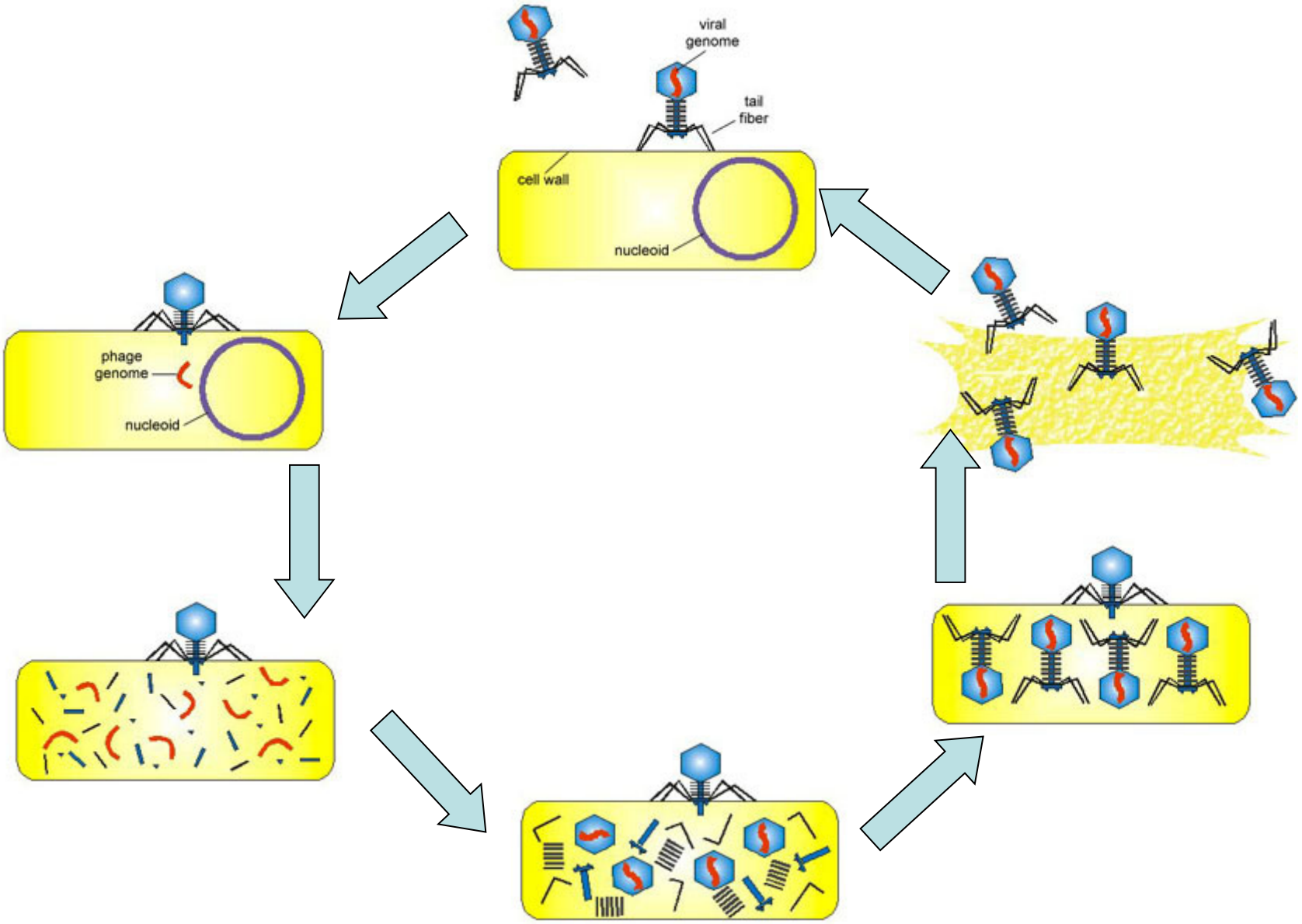




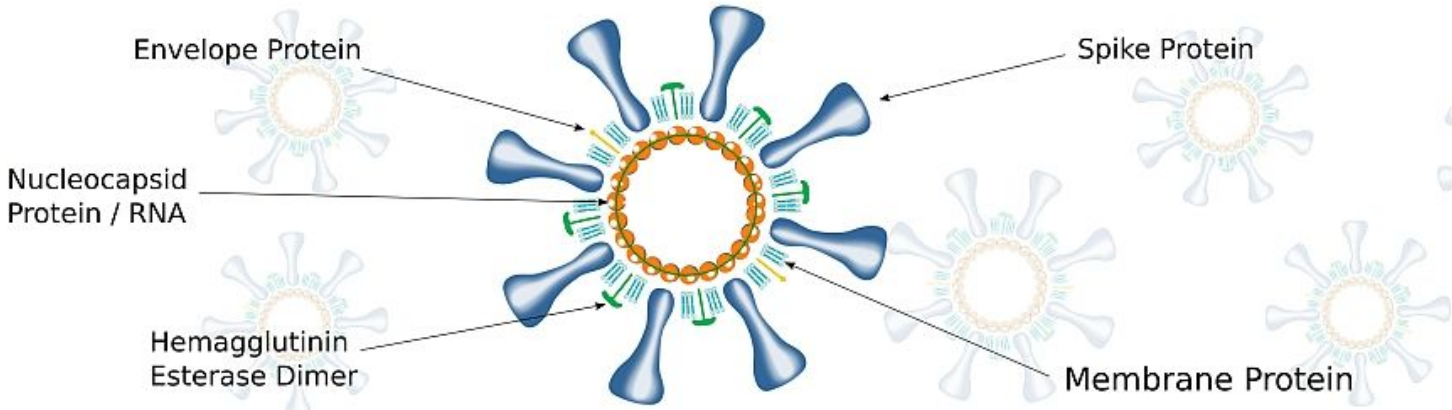


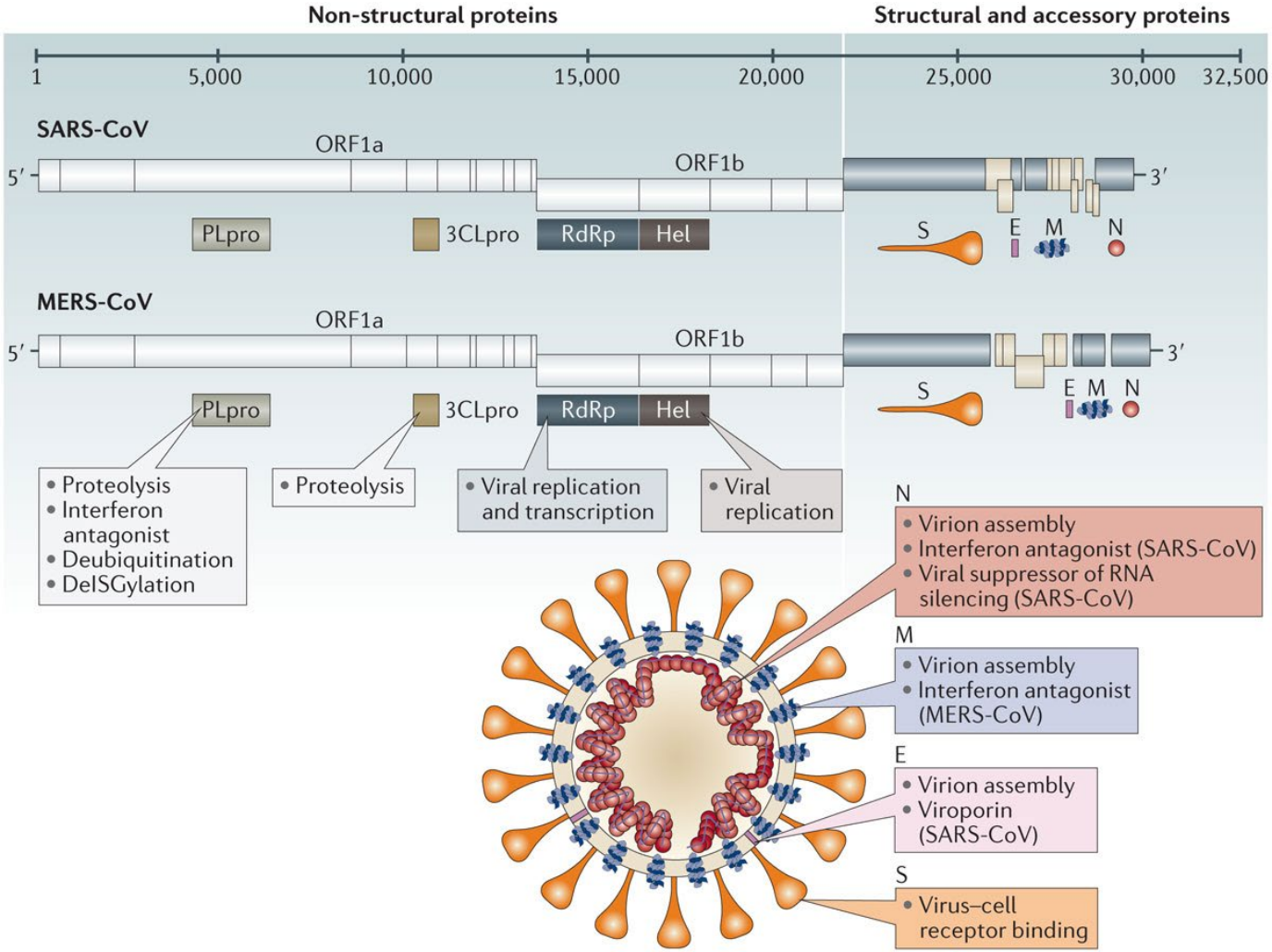

© Marc Adelan, 1985

Virus Reproduction



SARS-CoV-2

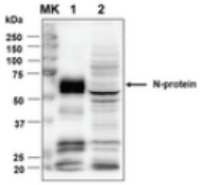

Envelope Protein
Spike Protein
Nucleocapsid
Protein / RNA
Hemagglutinin
Esterase Dimer
Membrane Protein


Non-structural proteins
Structural and accessory proteins
1
5,000
10,000
15,000
20,000
25,000
30,000
32,500
SARS-CoV
ORF1a
ORF1b
5′
3′
PLpro
3CLpro
RdRp
Hel
S
E
M
N
MERS-CoV
ORF1a
ORF1b
5′
3′
PLpro
3CLpro
RdRp
Hel
S
E
M
N
• Proteolysis
• Interferon antagonist
• Deubiquitination
• DelSGylation
• Proteolysis
• Viral replication and transcription
• Viral replication
N
• Virion assembly
• Interferon antagonist (SARS-CoV)
• Viral suppressor of RNA silencing (SARS-CoV)
M
• Virion assembly
• Interferon antagonist (MERS-CoV)
E
• Virion assembly
• Viroporin (SARS-CoV)
S
• Virus–cell receptor binding

COVID-19 Antibodies

Monoclonal & Polyclonal Antibodies to SARS-CoV-2

The antibodies available below have been validated to bind to proteins from SARS-CoV-2 (COVID-19), but were developed originally to target proteins from SARS-CoV-1, the virus responsible for the 2003 outbreak. We are currently developing monoclonal mouse and polyclonal rabbit antibodies specific to SARS-CoV-2 spike and nucleocapsid proteins. The polyclonal antibodies will be available in May. The monoclonal antibodies will be available sometime between July - August.



Rabbit Anti-SARS-CoV-2 Nucleocapsid Protein

Rabbit Anti-SARS-CoV-2 Coronavirus Nucleocapsid Protein

CODE: 128-10165-1

$1,450.00

SELECT SIZE ADD TO COMPARISON LIST

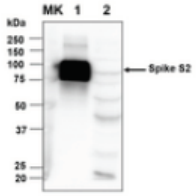
Mouse Anti-SARS-CoV-2 Nucleocapsid Protein

Mouse Anti-SARS-CoV-2 Coronavirus Nucleocapsid protein

CODE: 128-10166-1

$1,450.00

SELECT SIZE ADD TO COMPARISON LIST



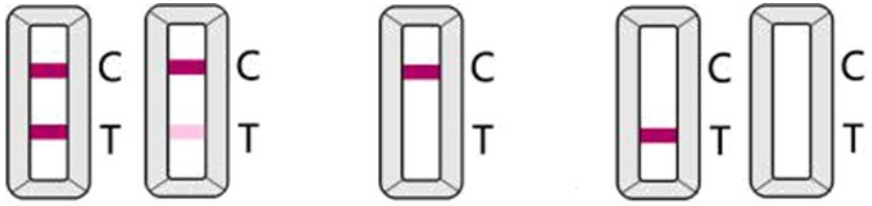
Rabbit Anti-SARS-CoV-2 Spike Protein

Rabbit Anti-SARS-Associated Coronavirus (COVID-19) Spike Protein

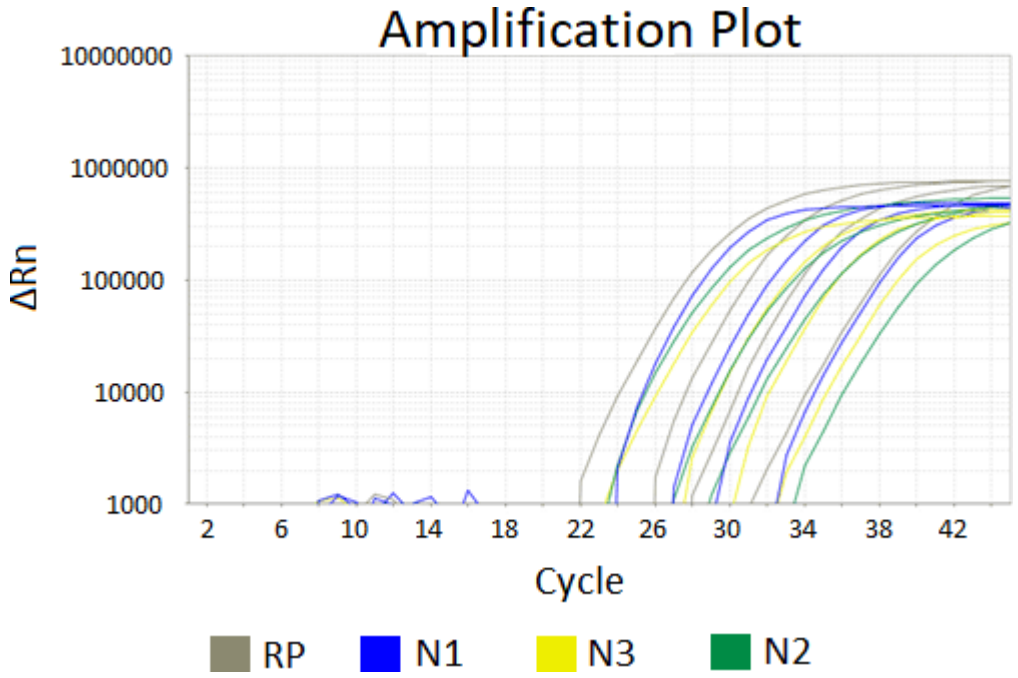
CODE: 128-10168-1

$1,450.00

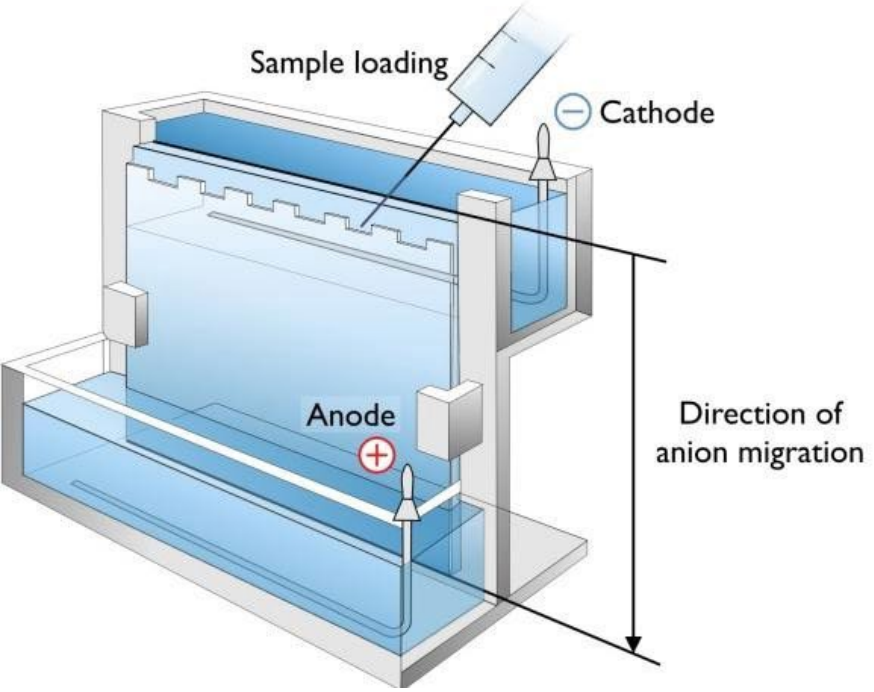
Fast Screening Kit

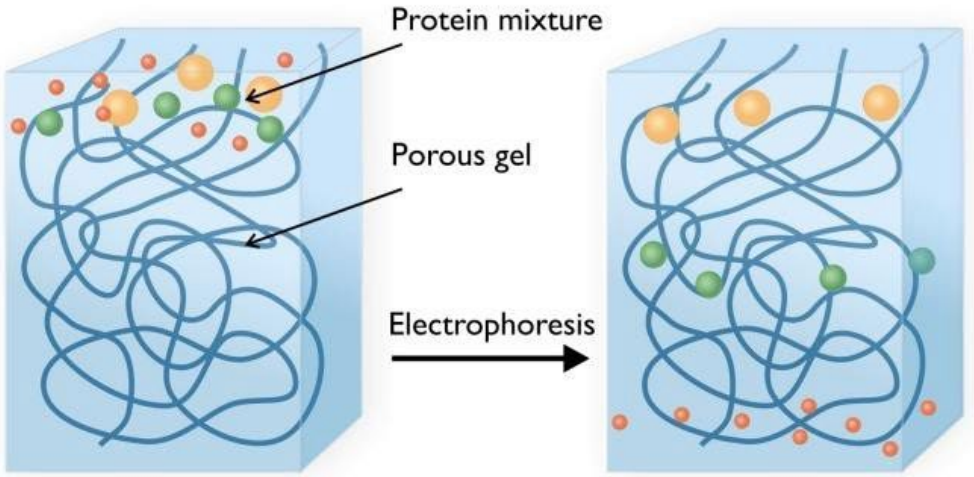


Real-time RT PCR

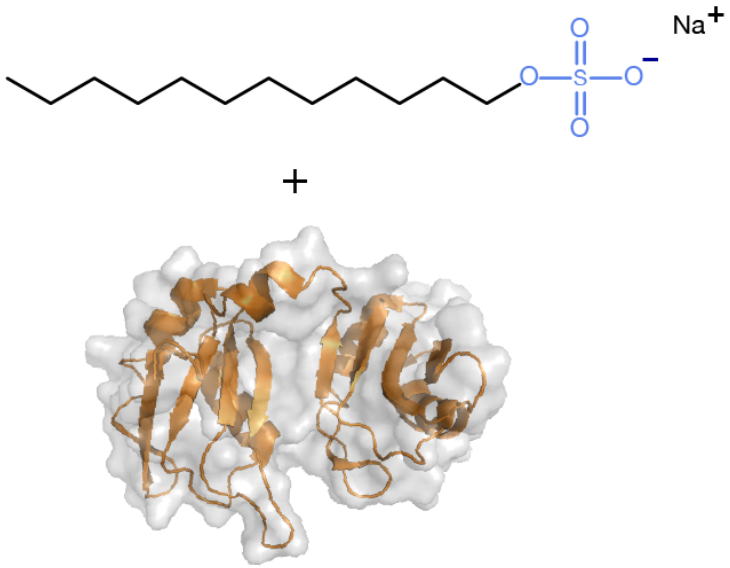


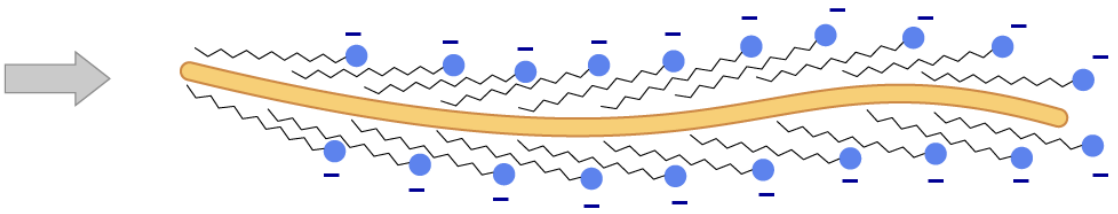
Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE)



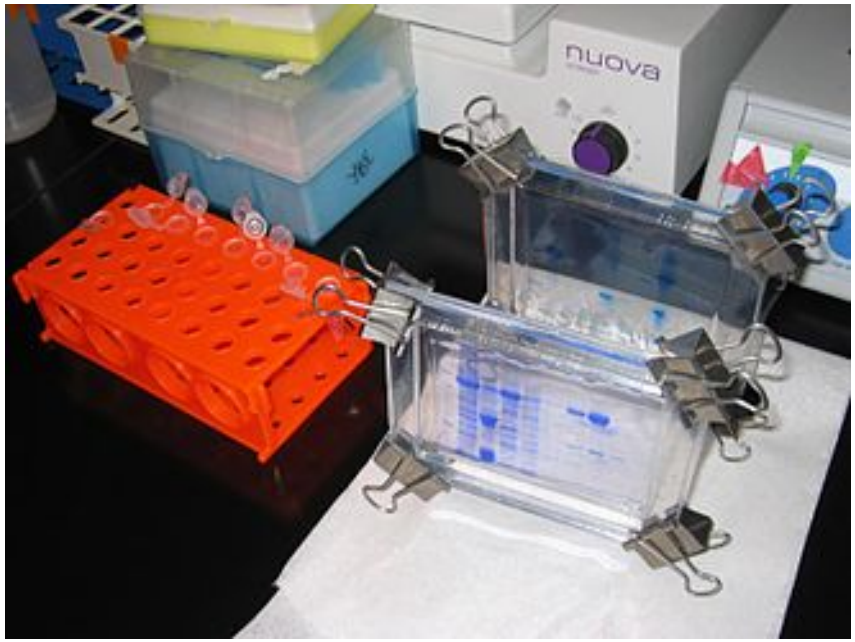


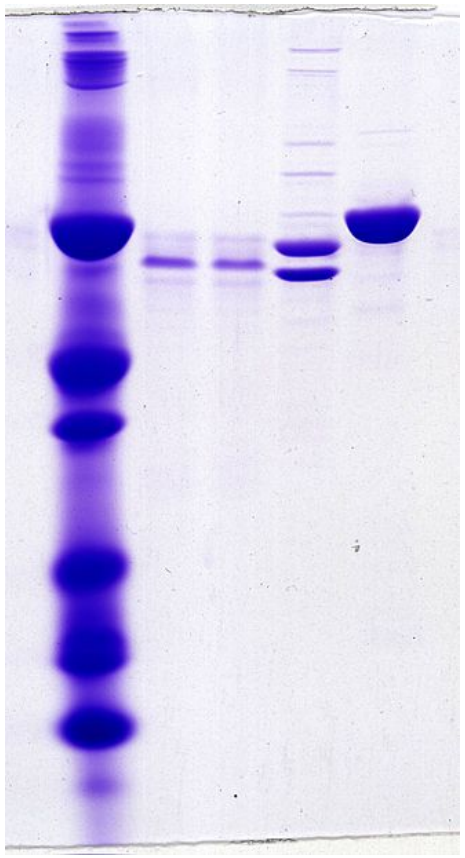
Protein Denature



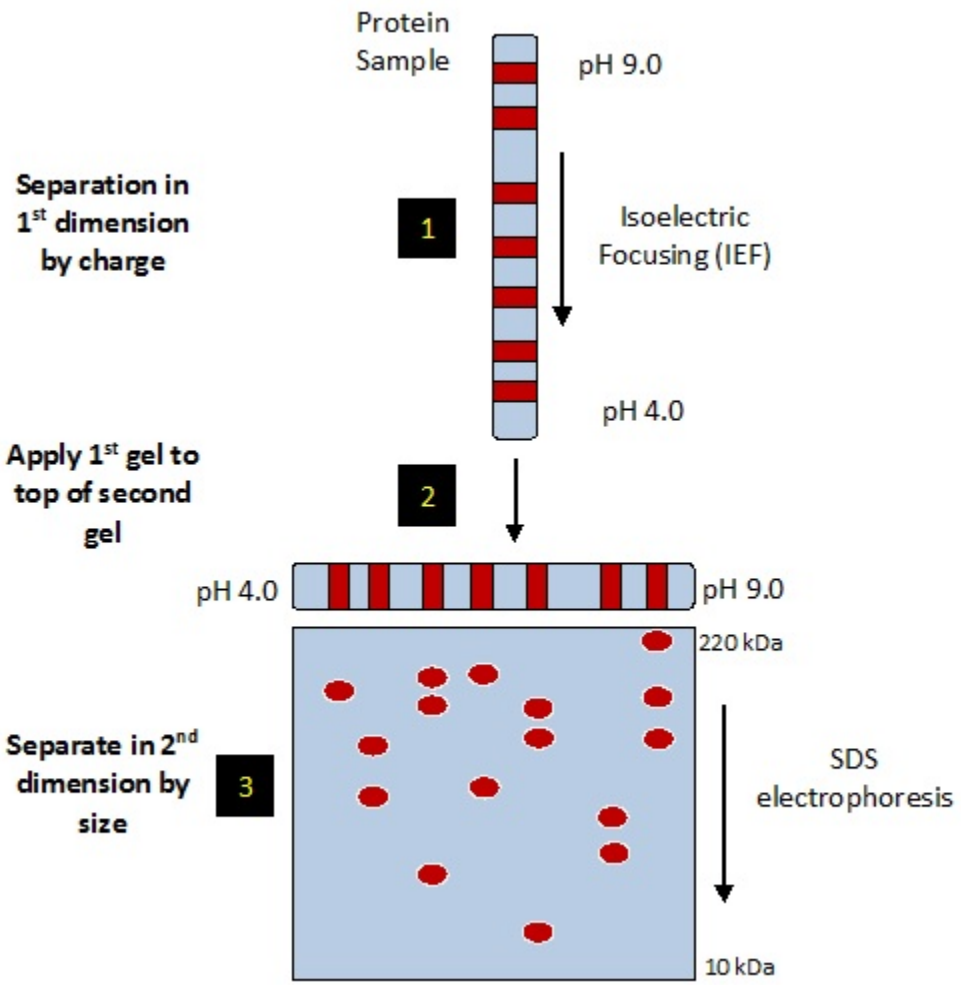


SDS-PAGE

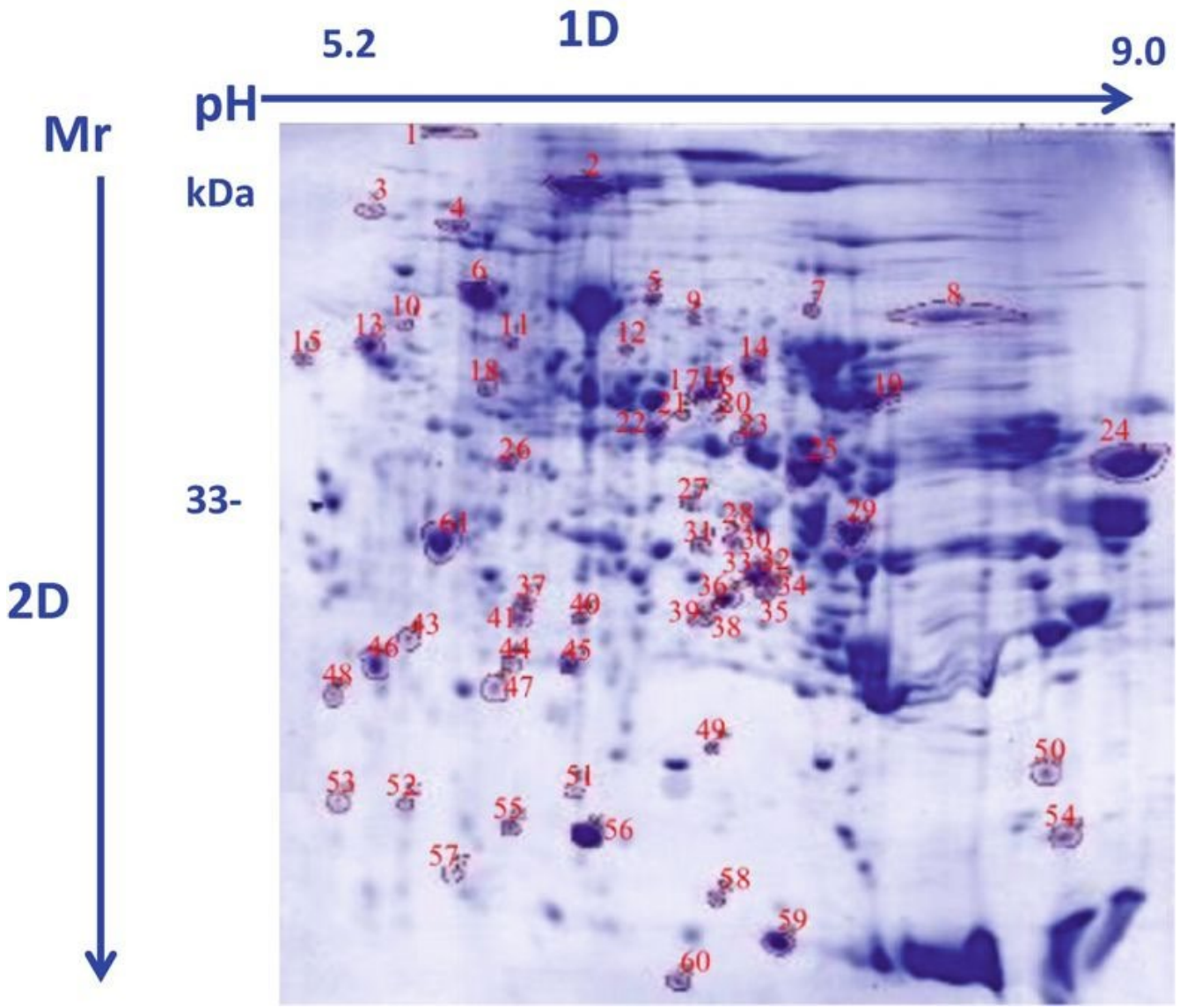


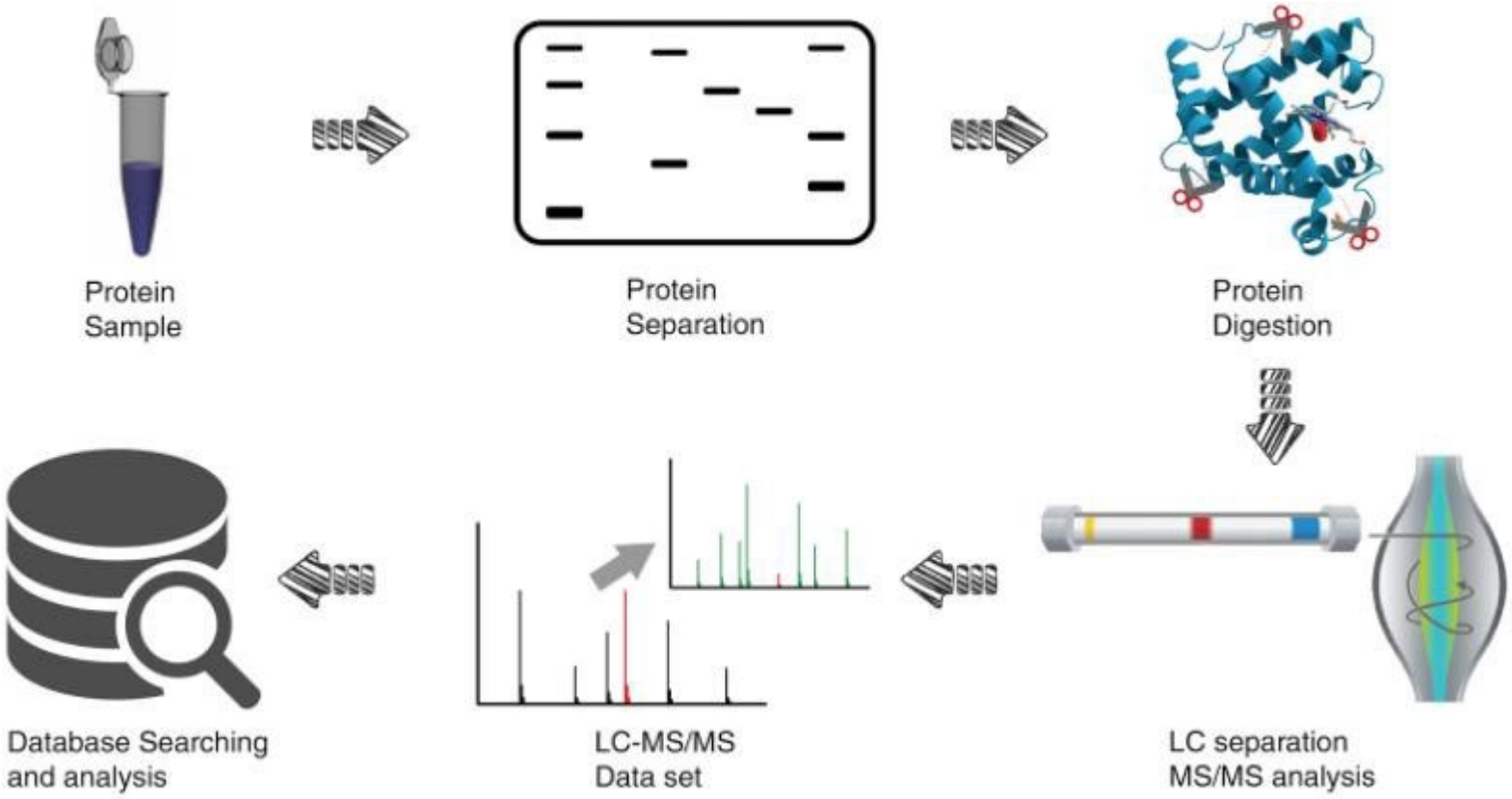


2D PAGE


Protein Sample
pH 9.0
Separation in 1st dimension by charge
1
Isoelectric Focusing (IEF)
pH 4.0
Apply 1st gel to top of second gel
2
pH 4.0
pH 9.0
220 kDa
Separate in 2nd dimension by size
3
SDS electrophoresis
10 kDa

2D PAGE



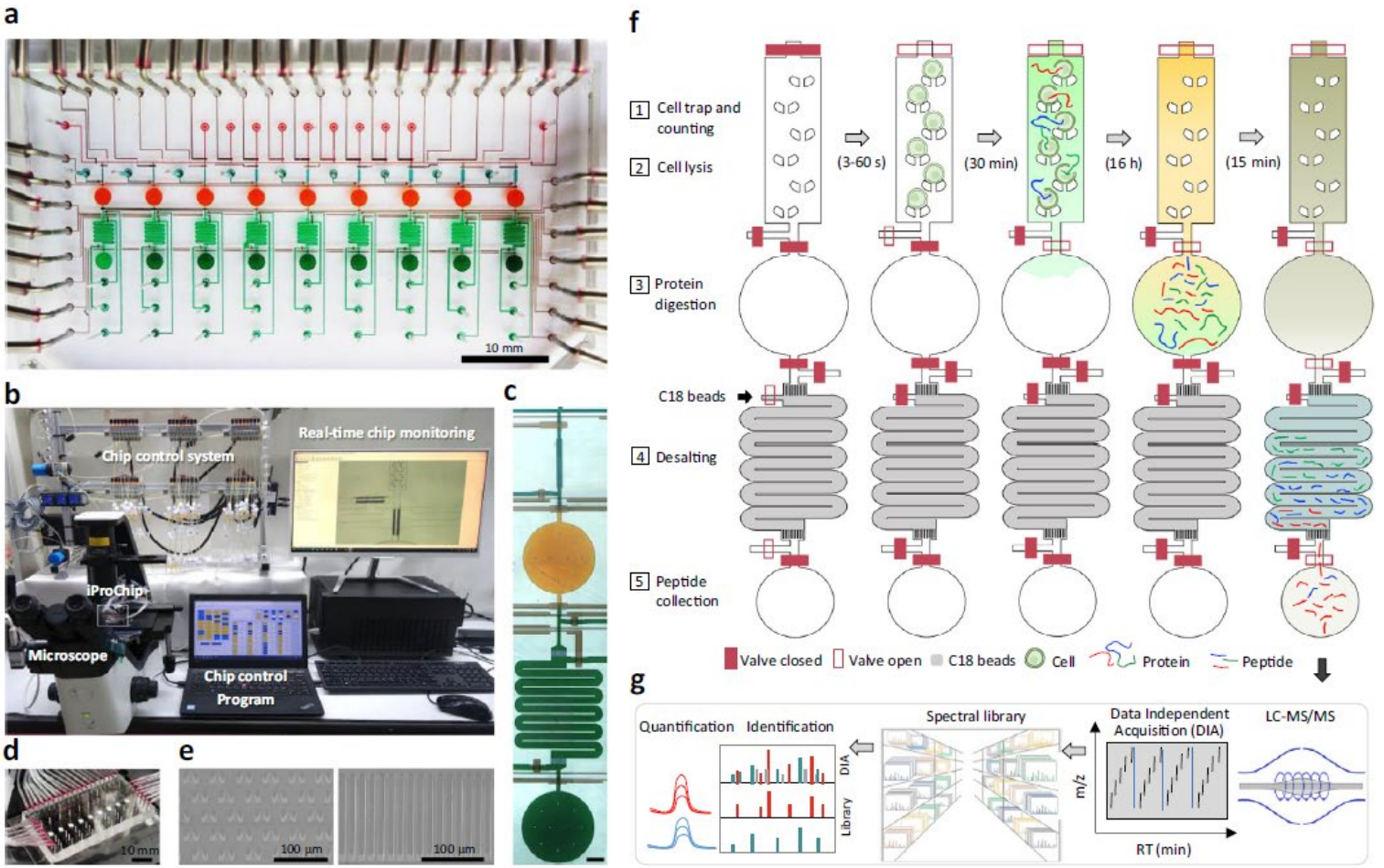

Protein
Sample
Protein
Separation
Protein
Digestion
Database Searching
and analysis
LC-MS/MS
Data set
LC separation
MS/MS analysis

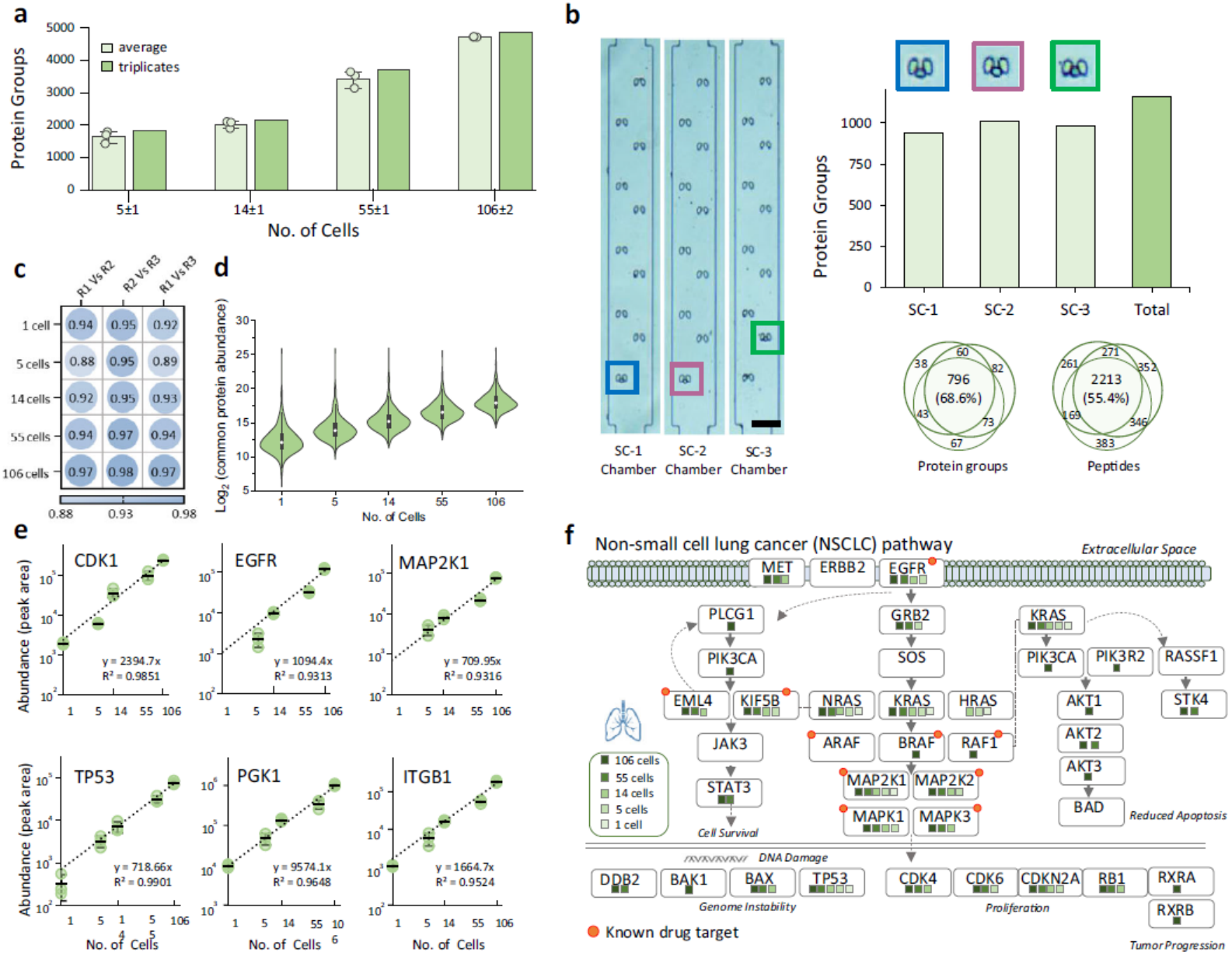
ARTICLE

https://doi.org/10.1038/s41467-021-27778-4 OPEN

Streamlined single-cell proteomics by an integrated microfluidic chip and data-independent acquisition mass spectrometry

Sofani Tafesse Gebreyesus[1,2,3,9], Asad Ali Siyal[1,4,5,9], Reta Birhanu Kitata[1], Eric Sheng-Wen Chen[1], Bayarmaa Enkhbayar[4,6], Takashi Angata[6], Kuo-I Lin[7], Yu-Ju Chen[1,3,4,8✉] & Hsiung-Lin Tu[1,2,4,8✉]




a
Protein Groups
average
triplicates
No. of Cells
5±1
14±1
55±1
106±2
b
SC-1 Chamber
SC-2 Chamber
SC-3 Chamber
Protein Groups
SC-1
SC-2
SC-3
Total
796 (68.6%)
2213 (55.4%)
Protein groups
Peptides
c
R1 Vs R2
R2 Vs R3
R1 Vs R3
1 cell
5 cells
14 cells
55 cells
106 cells
d
Log2 (common protein abundance)
No. of Cells
e
CDK1
EGFR
MAP2K1
TP53
PGK1
ITGB1
Abundance (peak area)
No. of Cells
f
Non-small cell lung cancer (NSCLC) pathway
Extracellular Space
MET
ERBB2
EGFR
PLCG1
GRB2
KRAS
PIK3CA
SOS
PIK3CA
PIK3R2
RASSF1
EML4
KIF5B
NRAS
KRAS
HRAS
AKT1
STK4
JAK3
ARAF
BRAF
RAF1
AKT2
AKT3
STAT3
MAP2K1
MAP2K2
BAD
MAPK1
MAPK3
Reduced Apoptosis
Cell Survival
DNA Damage
DDB2
BAK1
BAX
TP53
CDK4
CDK6
CDKN2A
RB1
RXRA
RXRB
Genome Instability
Proliferation
Tumor Progression
Known drug target