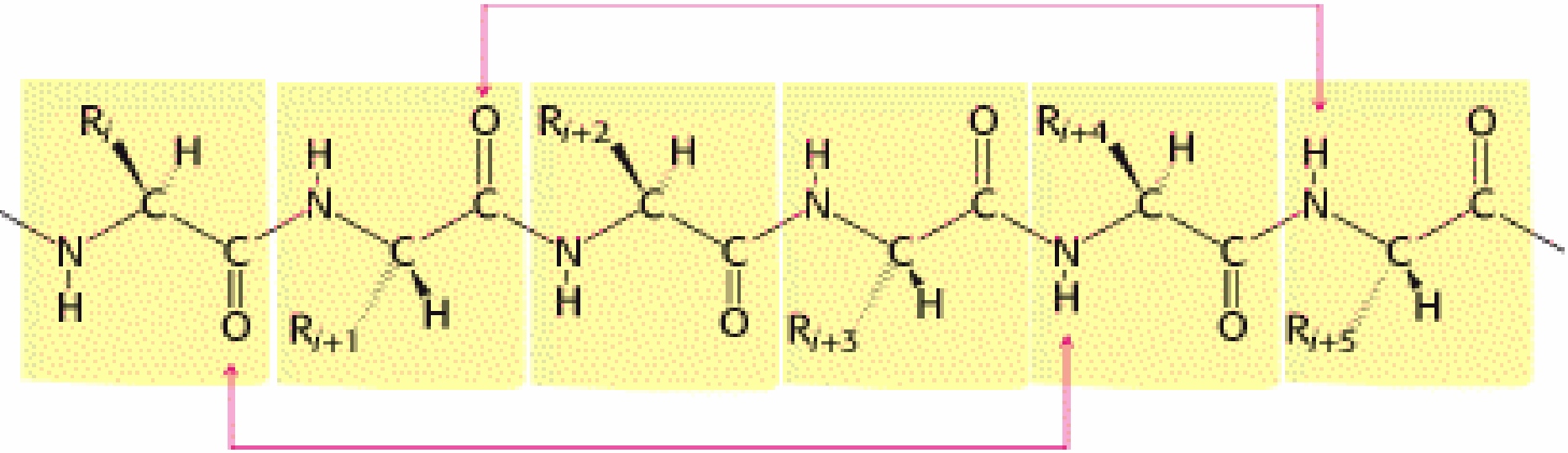
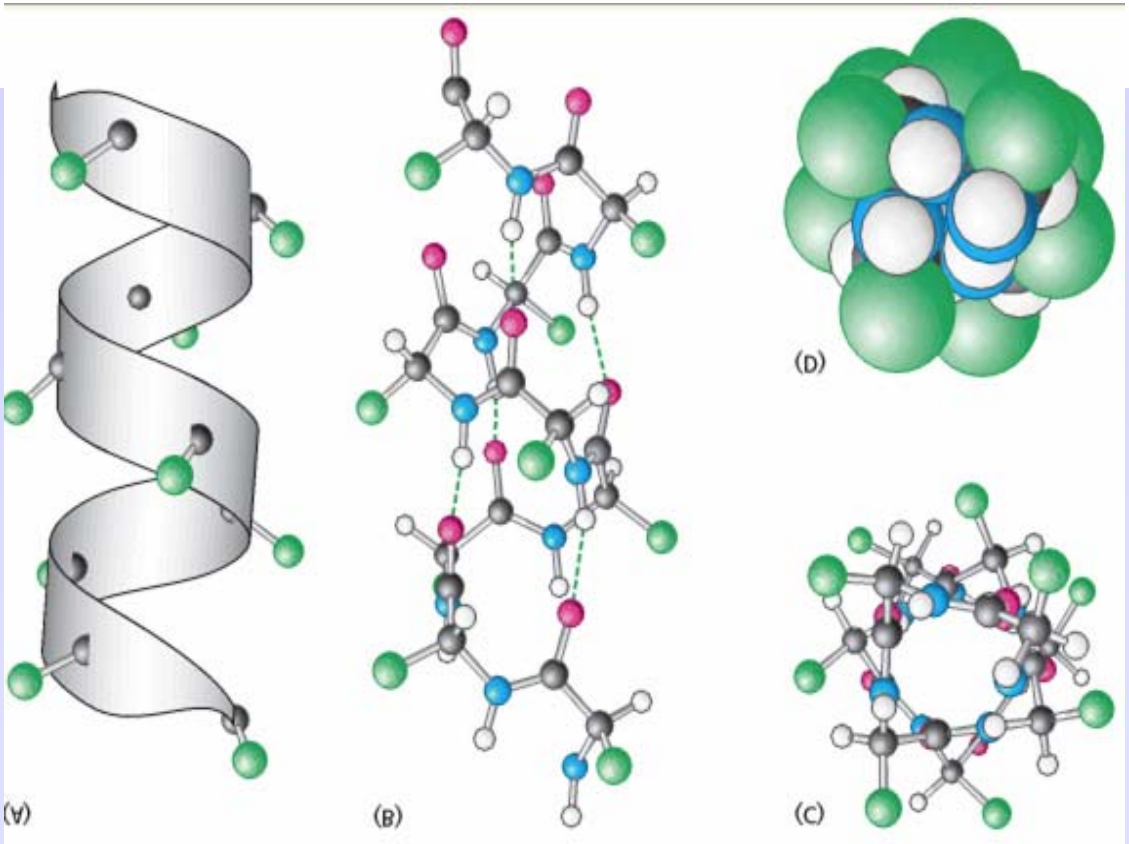
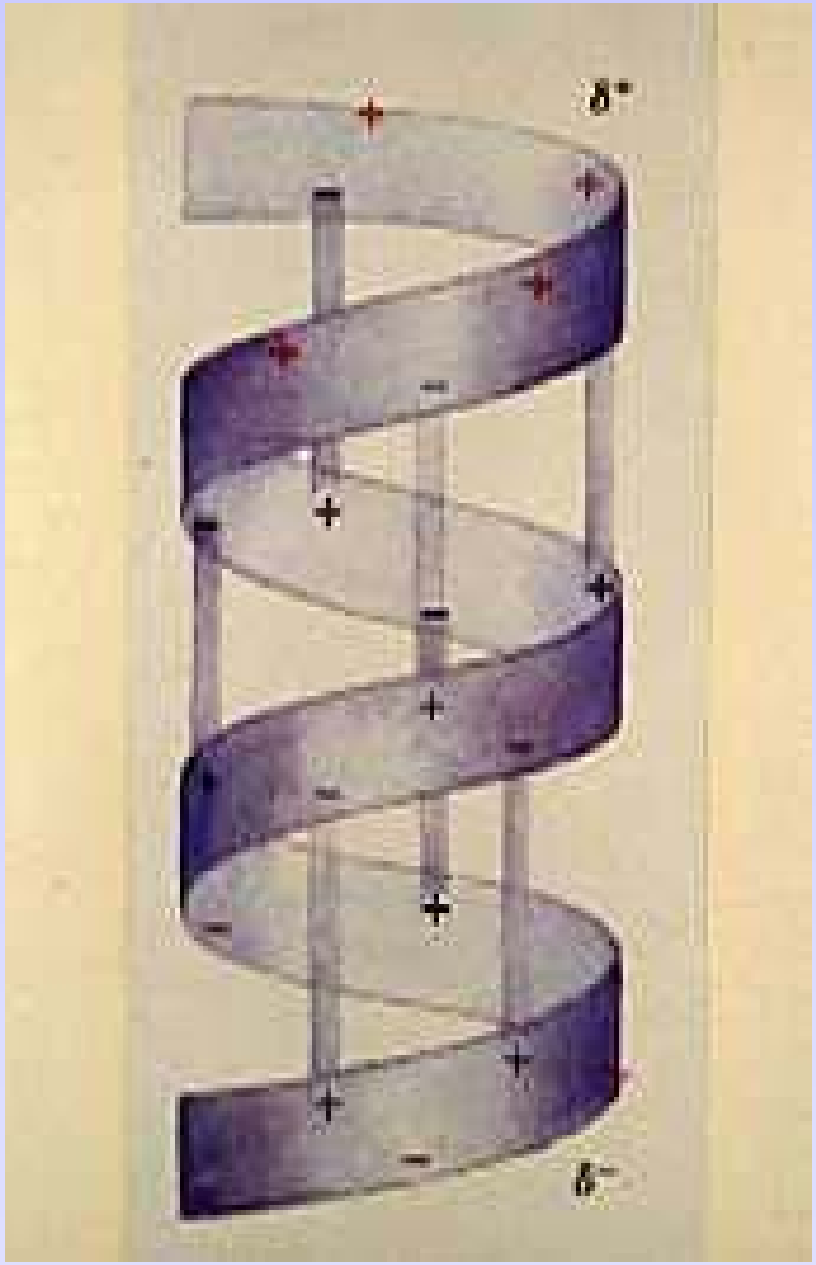
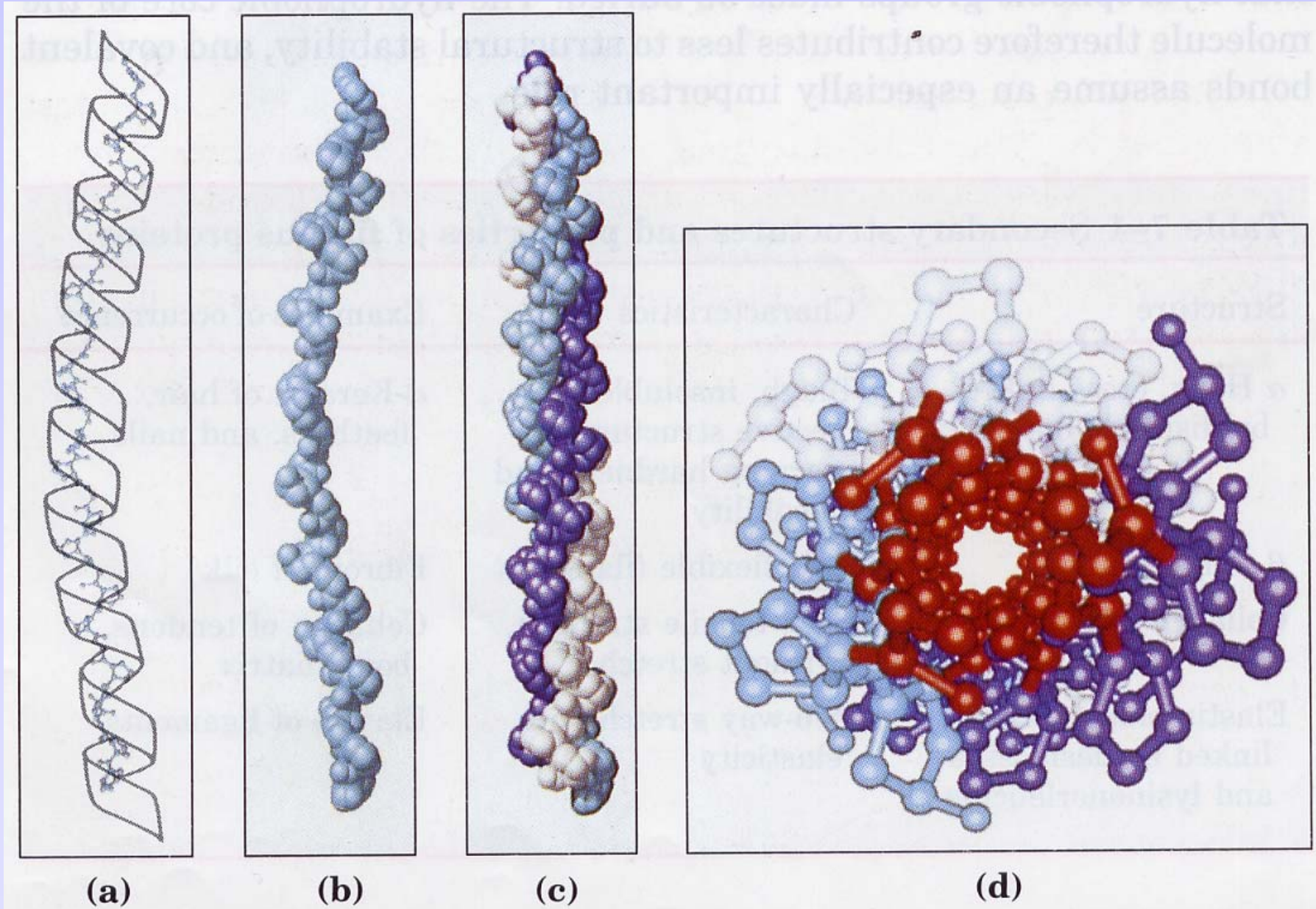
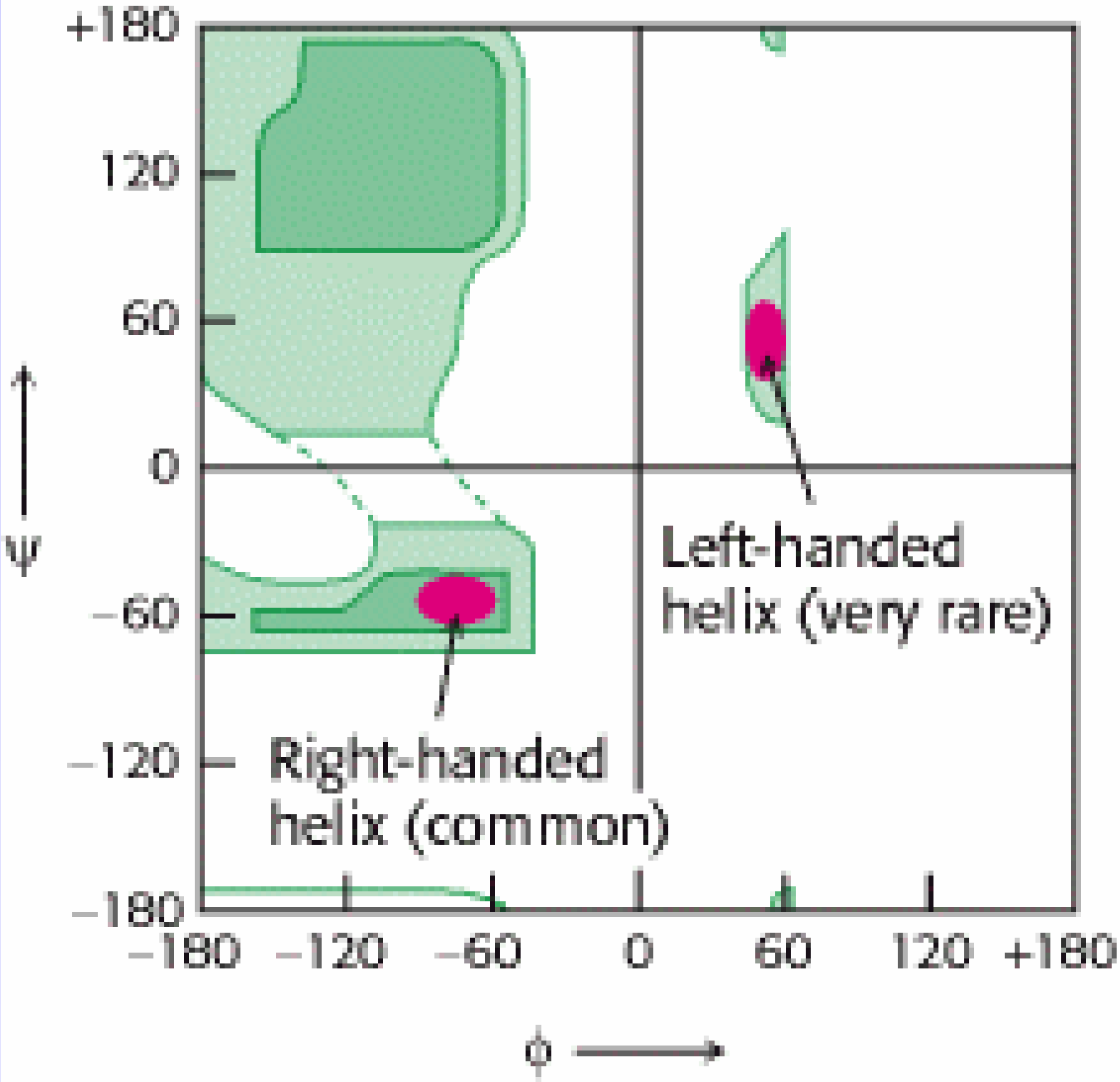
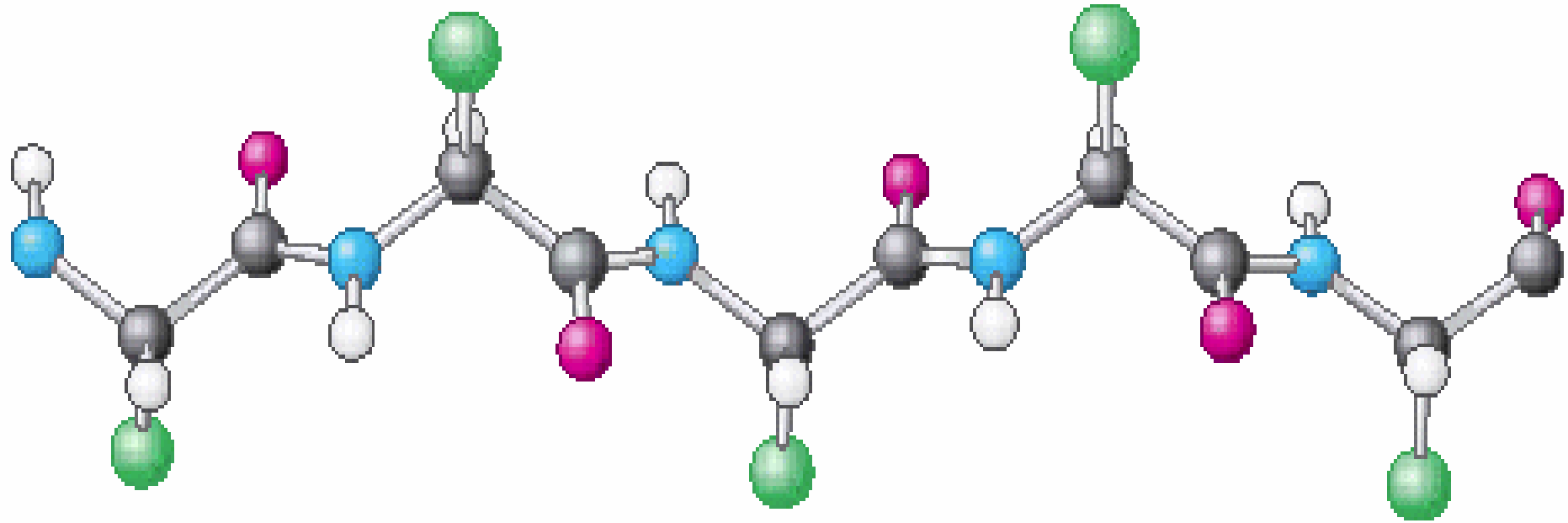

R
H
C
N
H
C
O
O
H
N
C
H
R
O
C
N
H
C
O
R
H
C
N
H
C
O
R
H
C
N
H
C
O
R
H
C
N
H
C
O

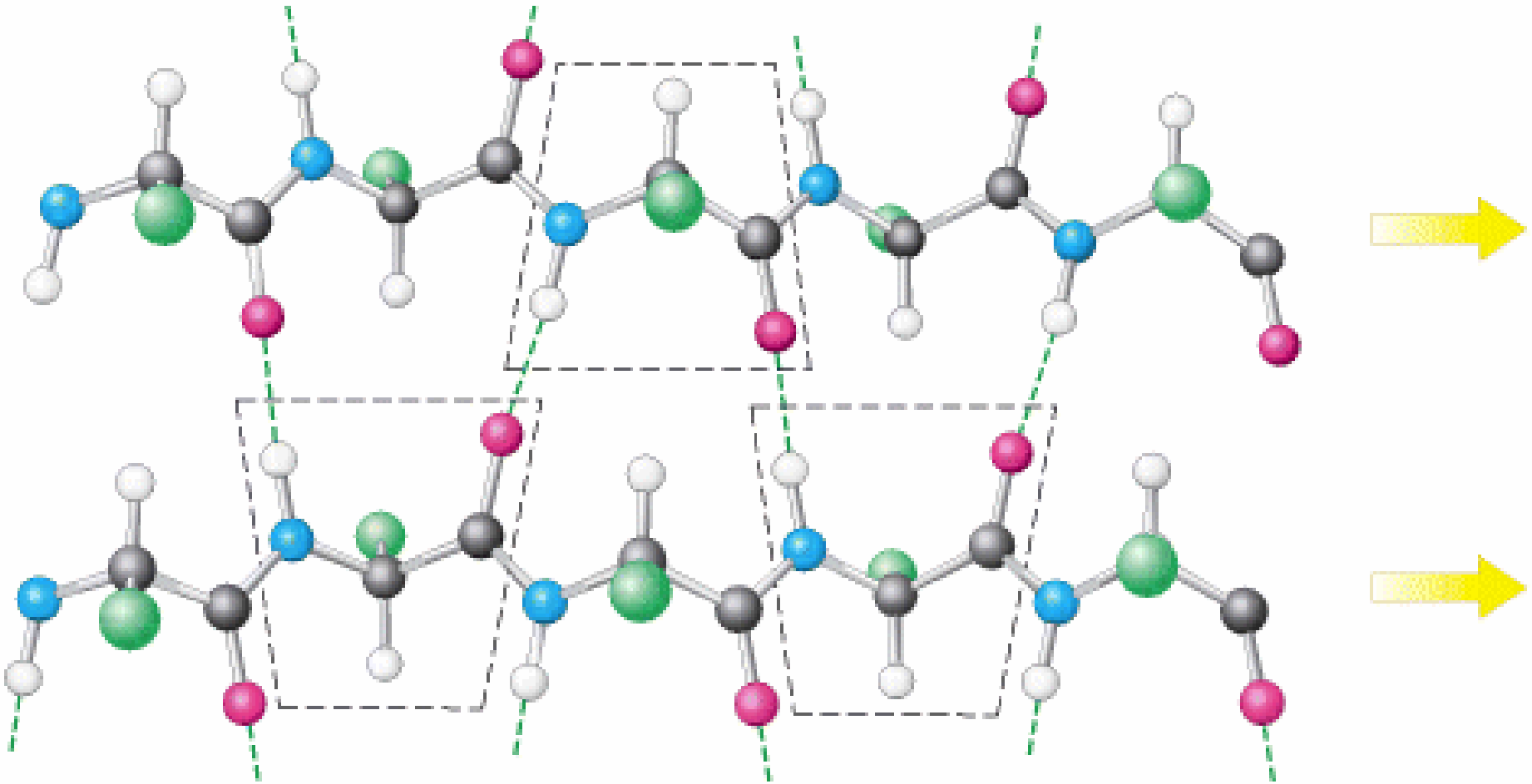

(A)
(B)
(C)
(D)

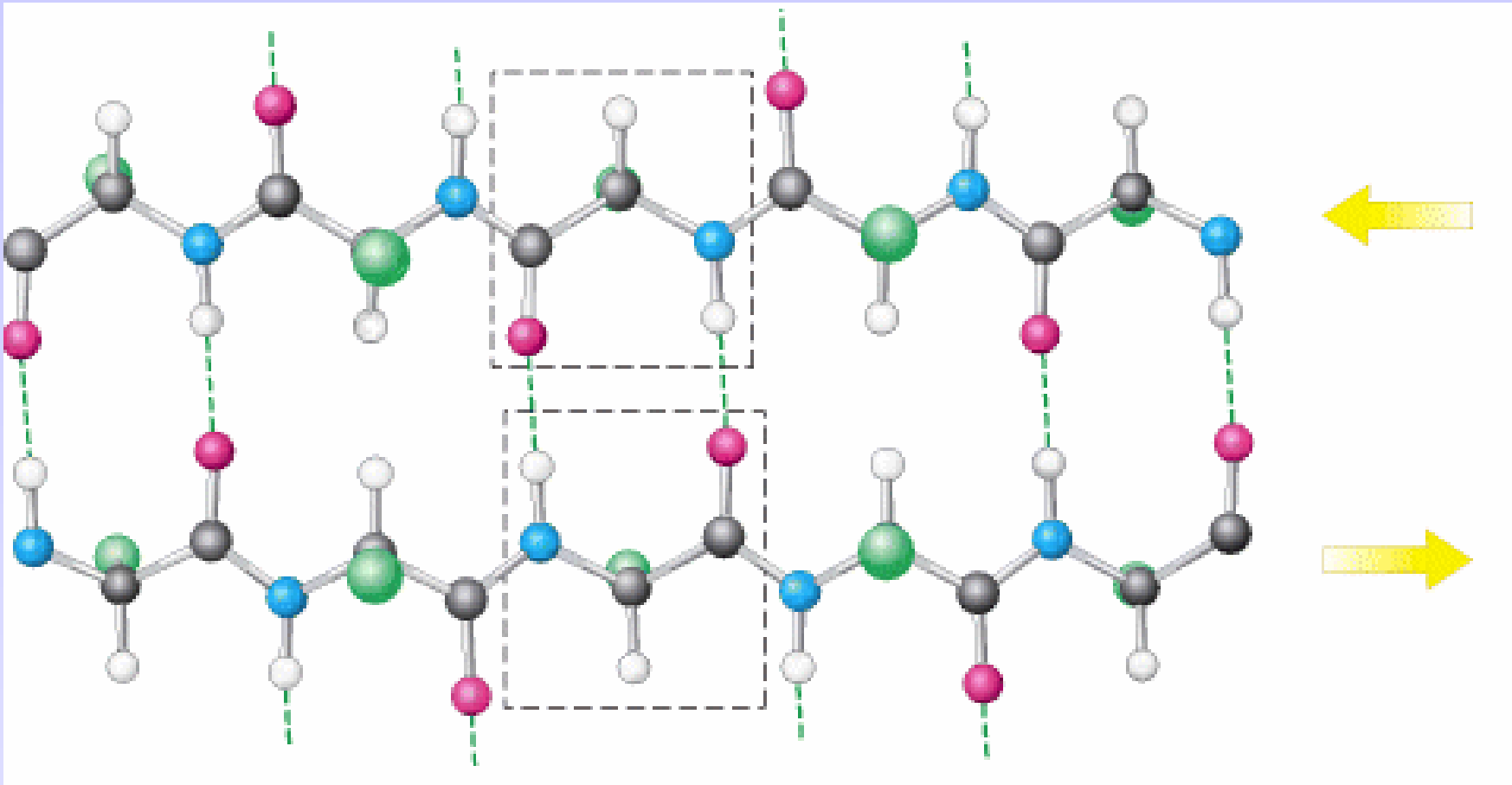

δ+
δ−

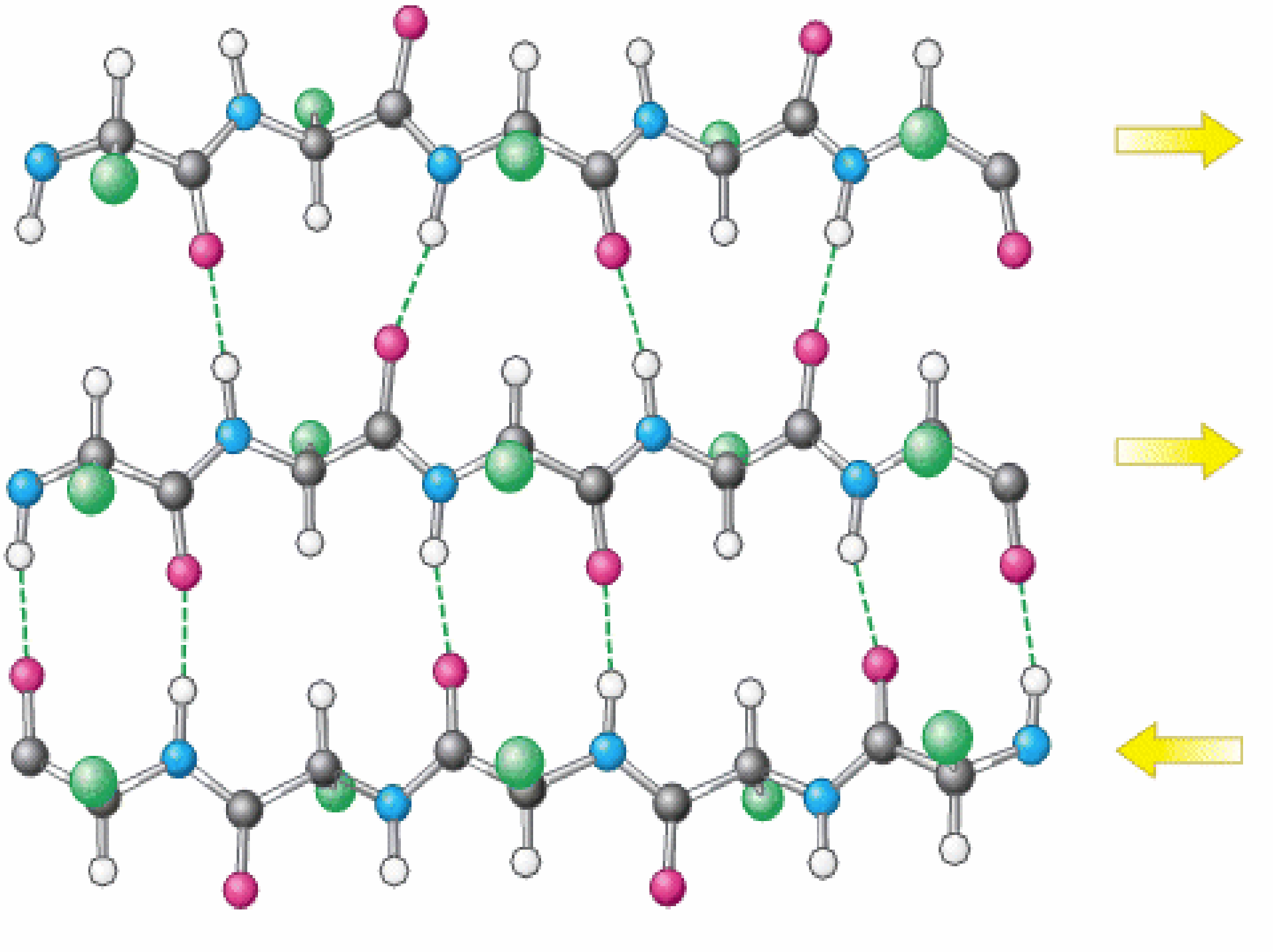

(a)
(b)
(c)
(d)

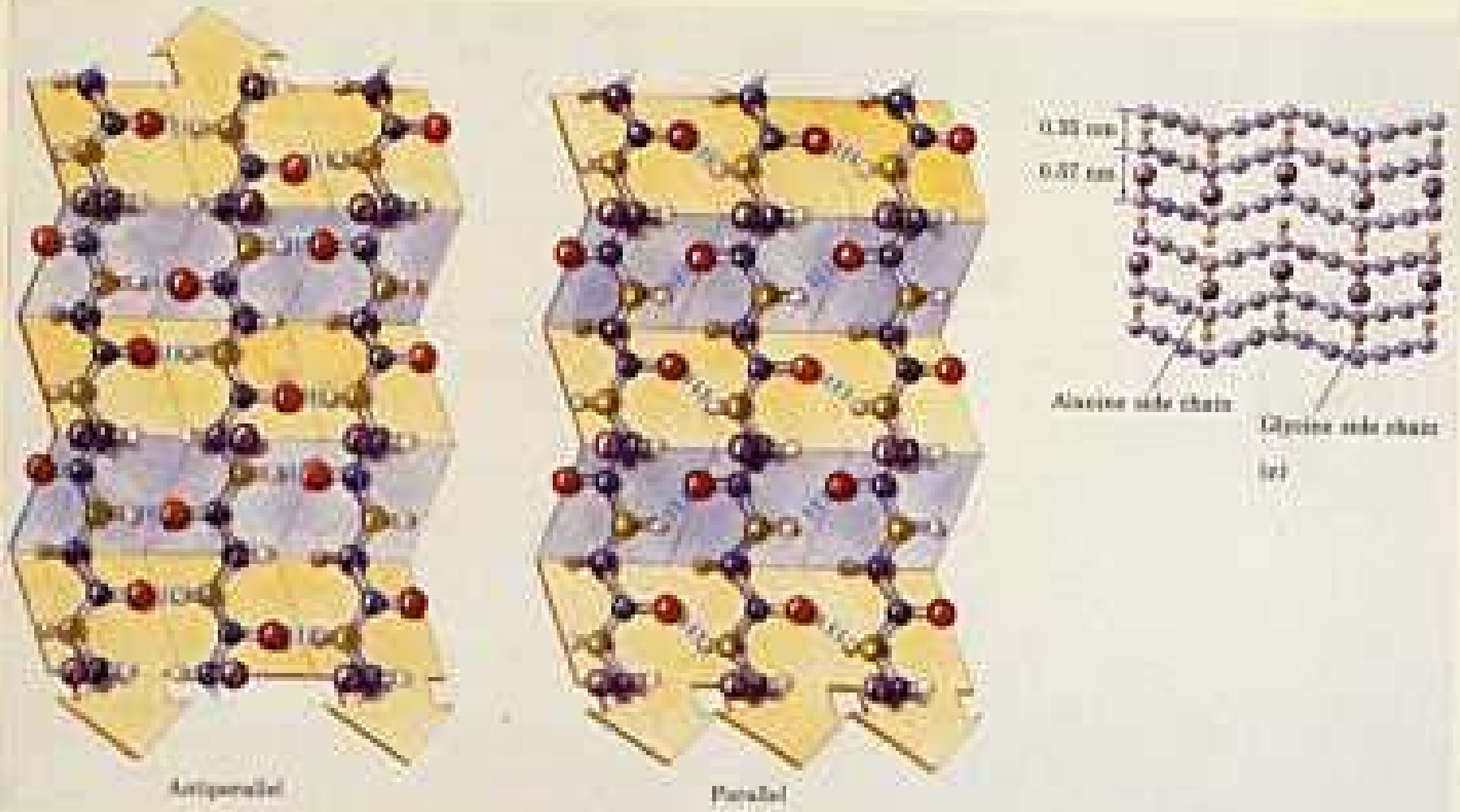

+180
120
60
0
−60
−120
−180
ψ
−180
−120
−60
0
60
120
+180
ϕ
Left-handed
helix (very rare)
Right-handed
helix (common)

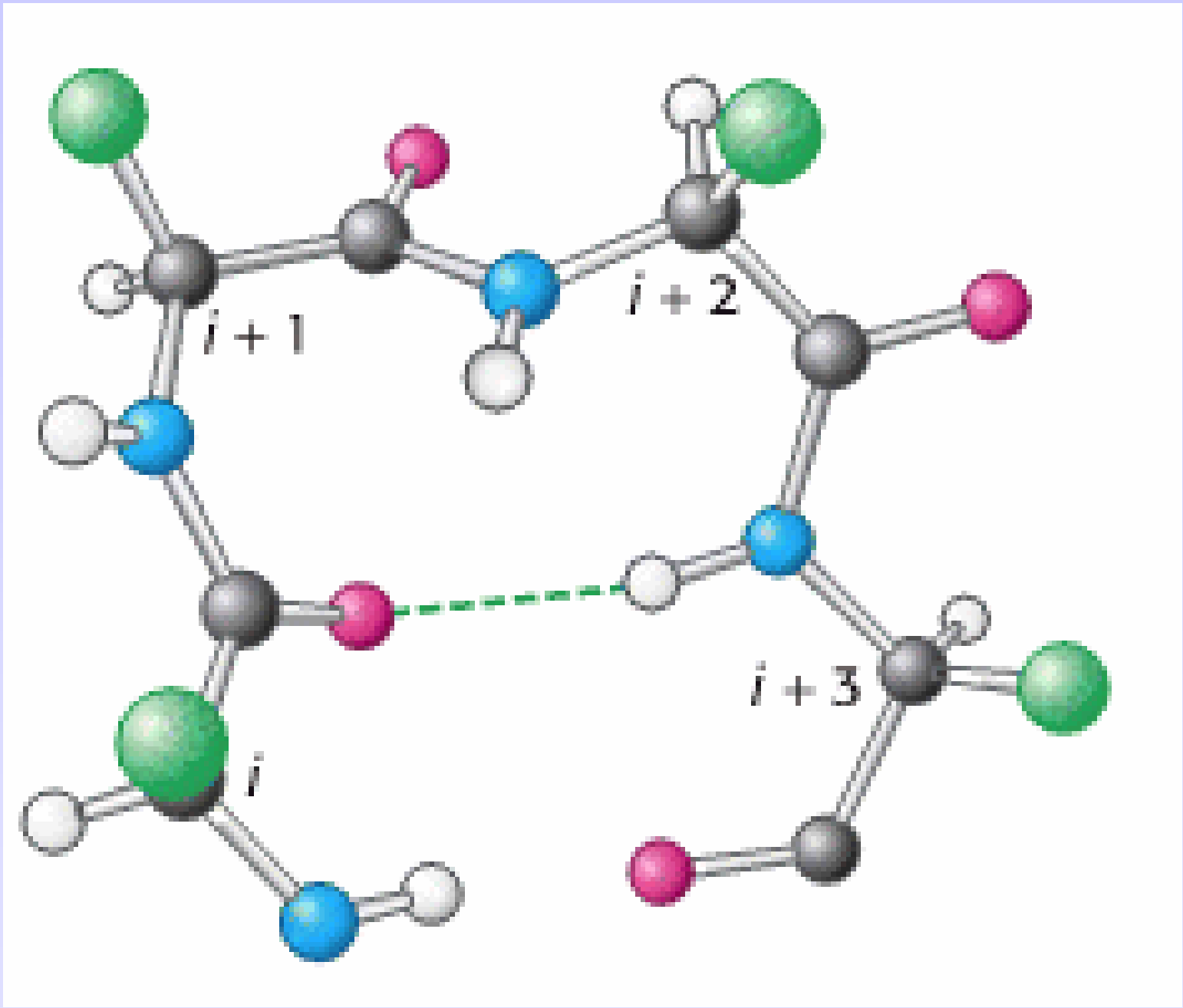


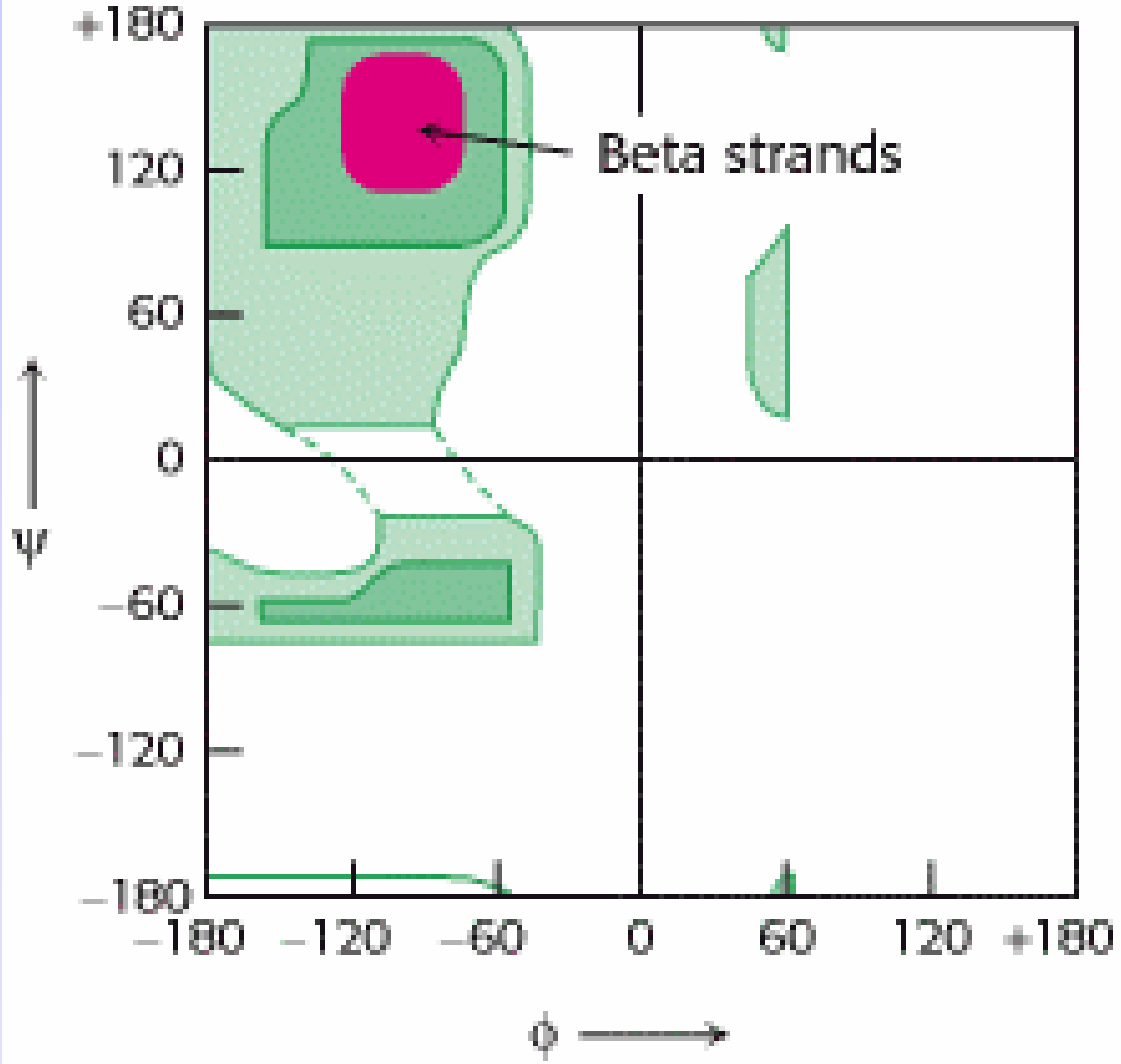







0.35 nm
0.57 nm
Alanine side chain
Glycine side chain
(c)
Antiparallel
Parallel


i + 1
i + 2
i + 3
i


+180
120
60
0
−60
−120
−180
ψ
Beta strands
−180
−120
−60
0
60
120
+180
ϕ

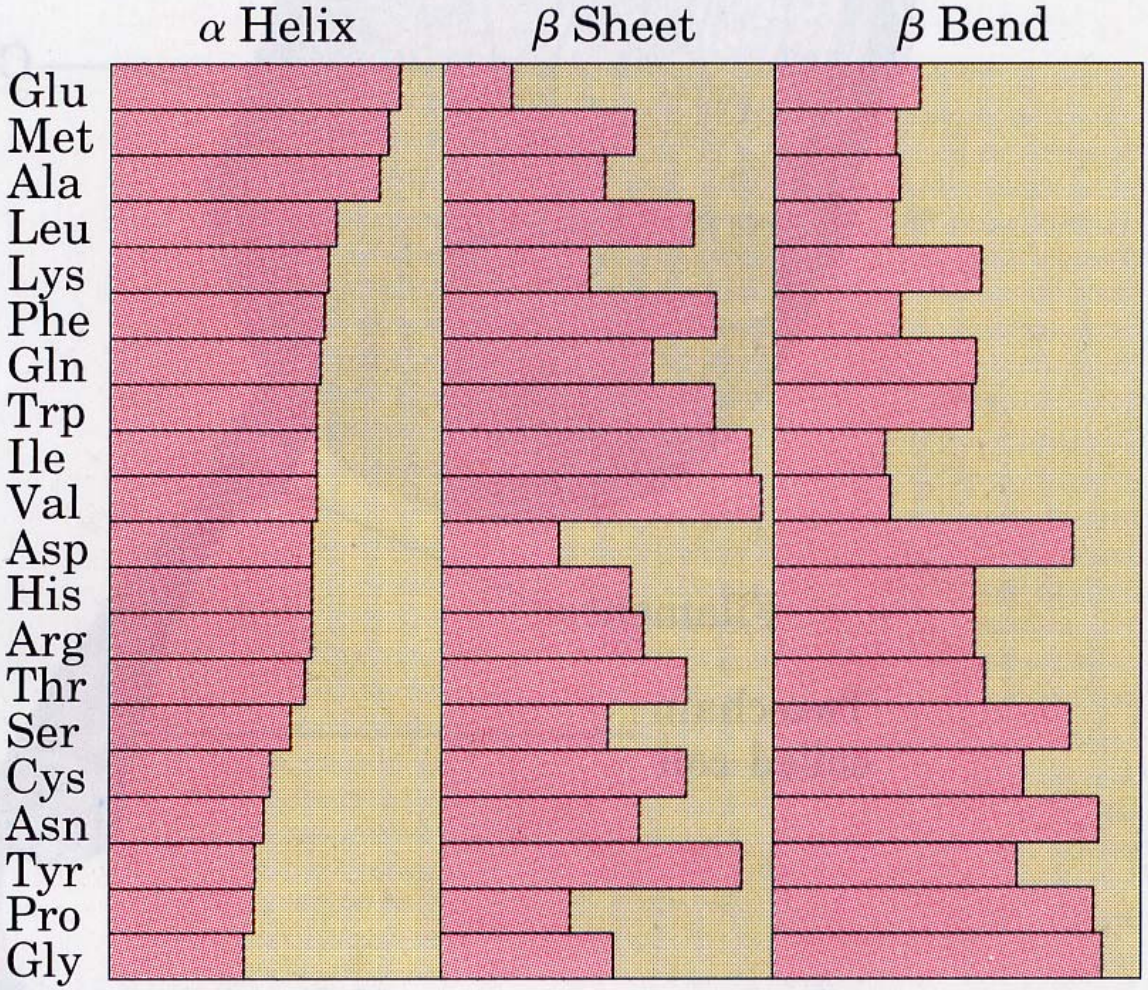


Figure 7–12 Relative probabilities that a given amino acid will occur in the three common types of secondary structure.

Table 7–1 Secondary structures and properties of fibrous proteins

Structure	Characteristics	Examples of occurrence
α Helix, cross-linked by disulfide bonds	Tough, insoluble protective structures of varying hardness and flexibility	α-Keratin of hair, feathers, and nails
β Conformation	Soft, flexible filaments	Fibroin of silk
Collagen triple helix	High tensile strength, without stretch	Collagen of tendons, bone matrix
Elastin chains cross-linked by desmosine and lysinonorleucine	Two-way stretch with elasticity	Elastin of ligaments

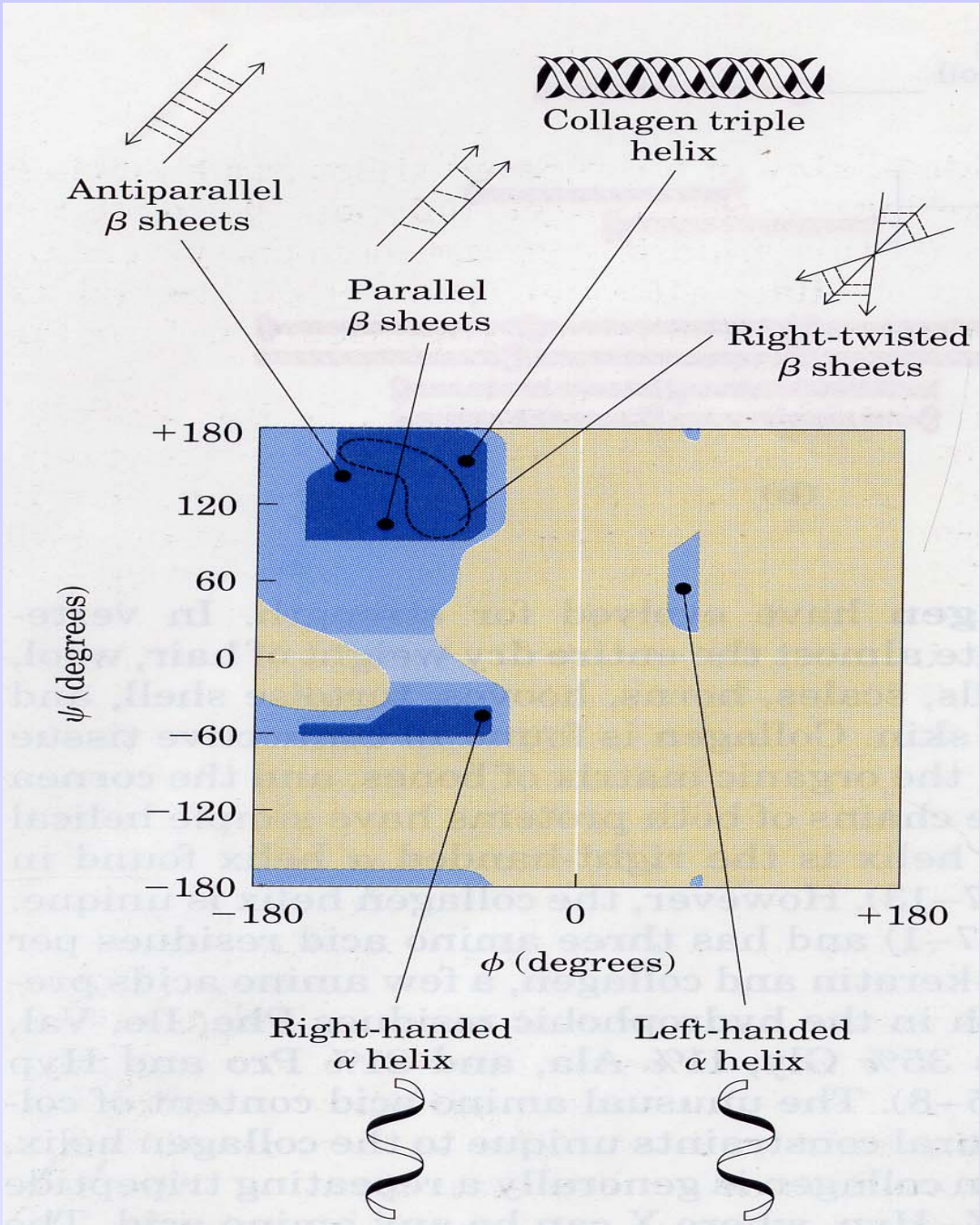

Antiparallel
β sheets
Parallel
β sheets
Collagen triple
helix
Right-twisted
β sheets
+180
120
60
0
−60
−120
−180
ψ (degrees)
−180
0
+180
ϕ (degrees)
Right-handed
α helix
Left-handed
α helix

Table 6–2 Amino acid composition of two proteins

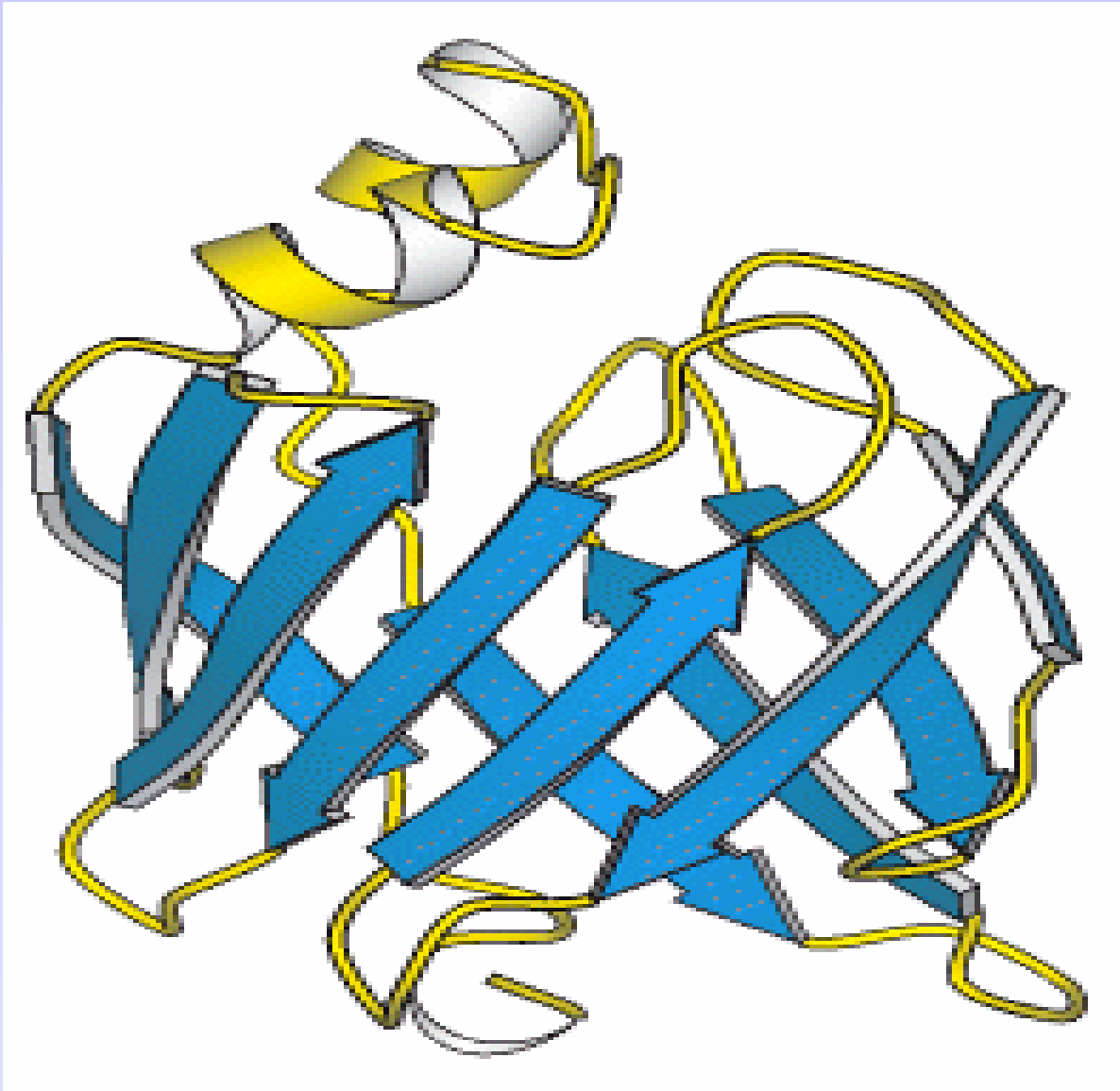
Amino acid	Number of residues per molecule of protein: Human cytochrome *c*	Number of residues per molecule of protein: Bovine chymotrypsinogen
Ala	6	22
Arg	2	4
Asn	5	15
Asp	3	8
Cys	2	10
Gln	2	10
Glu	8	5
Gly	13	23
His	3	2
Ile	8	10
Leu	6	19
Lys	18	14
Met	3	2
Phe	3	6
Pro	4	9
Ser	2	28
Thr	7	23
Trp	1	8
Tyr	5	4
Val	3	23
Total	104	245

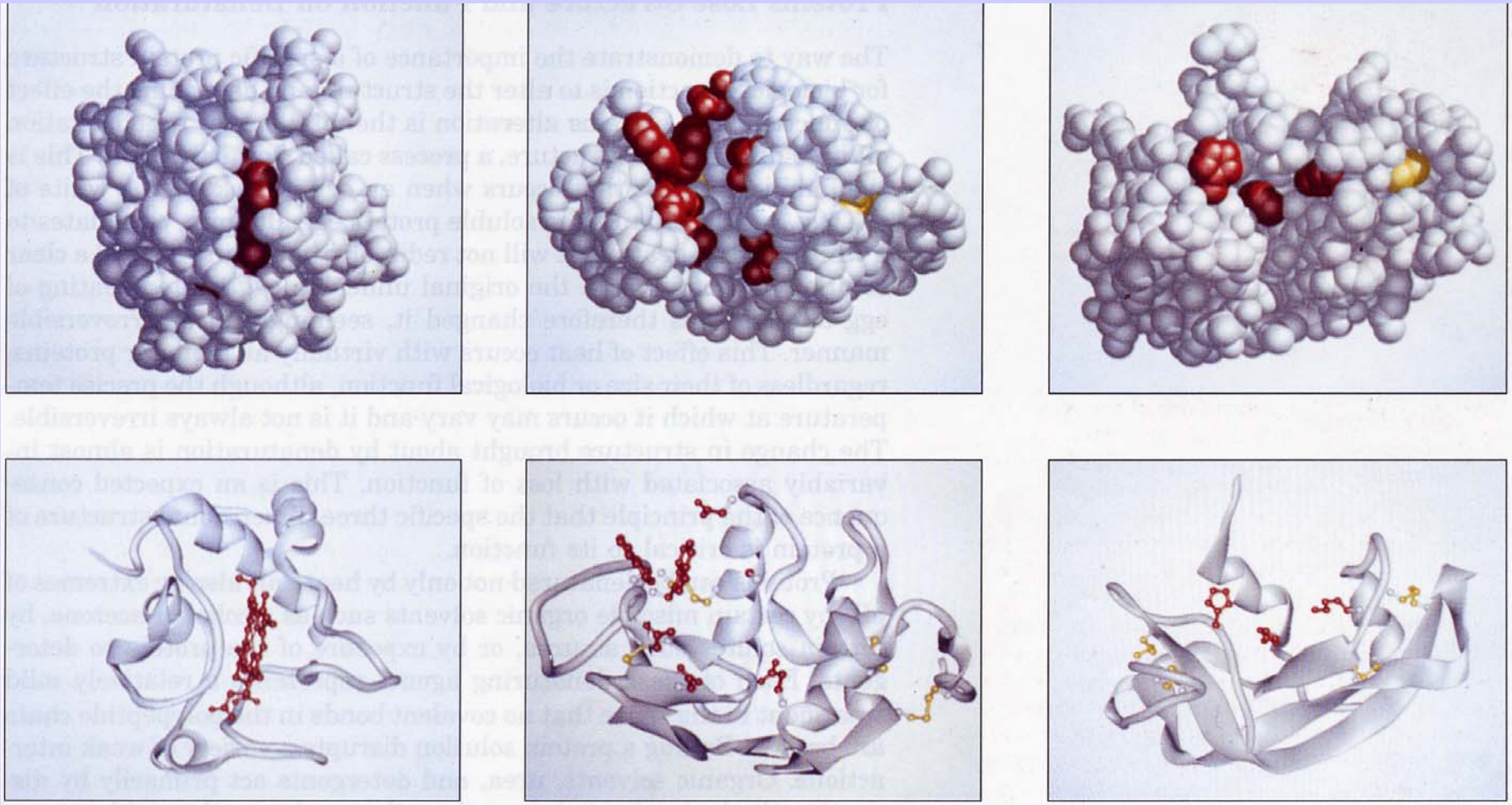
Table 6–1 Molecular data on some proteins

	Molecular weight	Number of residues	Number of polypeptide chains
Insulin (bovine)	5,733	51	2
Cytochrome *c* (human)	13,000	104	1
Ribonuclease A (bovine pancreas)	13,700	124	1
Lysozyme (egg white)	13,930	129	1
Myoglobin (equine heart)	16,890	153	1
Chymotrypsin (bovine pancreas)	21,600	241	3
Chymotrypsinogen (bovine)	22,000	245	1
Hemoglobin (human)	64,500	574	4
Serum albumin (human)	68,500	~550	1
Hexokinase (yeast)	102,000	~800	2
Immunoglobulin G (human)	145,000	~1,320	4
RNA polymerase (*E. coli*)	450,000	~4,100	5
Apolipoprotein B (human)	513,000	4,536	1
Glutamate dehydrogenase (bovine liver)	1,000,000	~8,300	~40

Table 7–2 Approximate amounts of α helix and β conformation in some single-chain proteins*

Protein (total residues)	Residues (%)	
	α Helix	β Conformation
Myoglobin (153)	78	0
Cytochrome *c* (104)	39	0
Lysozyme (129)	40	12
Ribonuclease (124)	26	35
Chymotrypsin (247)	14	45
Carboxy-peptidase (307)	38	17

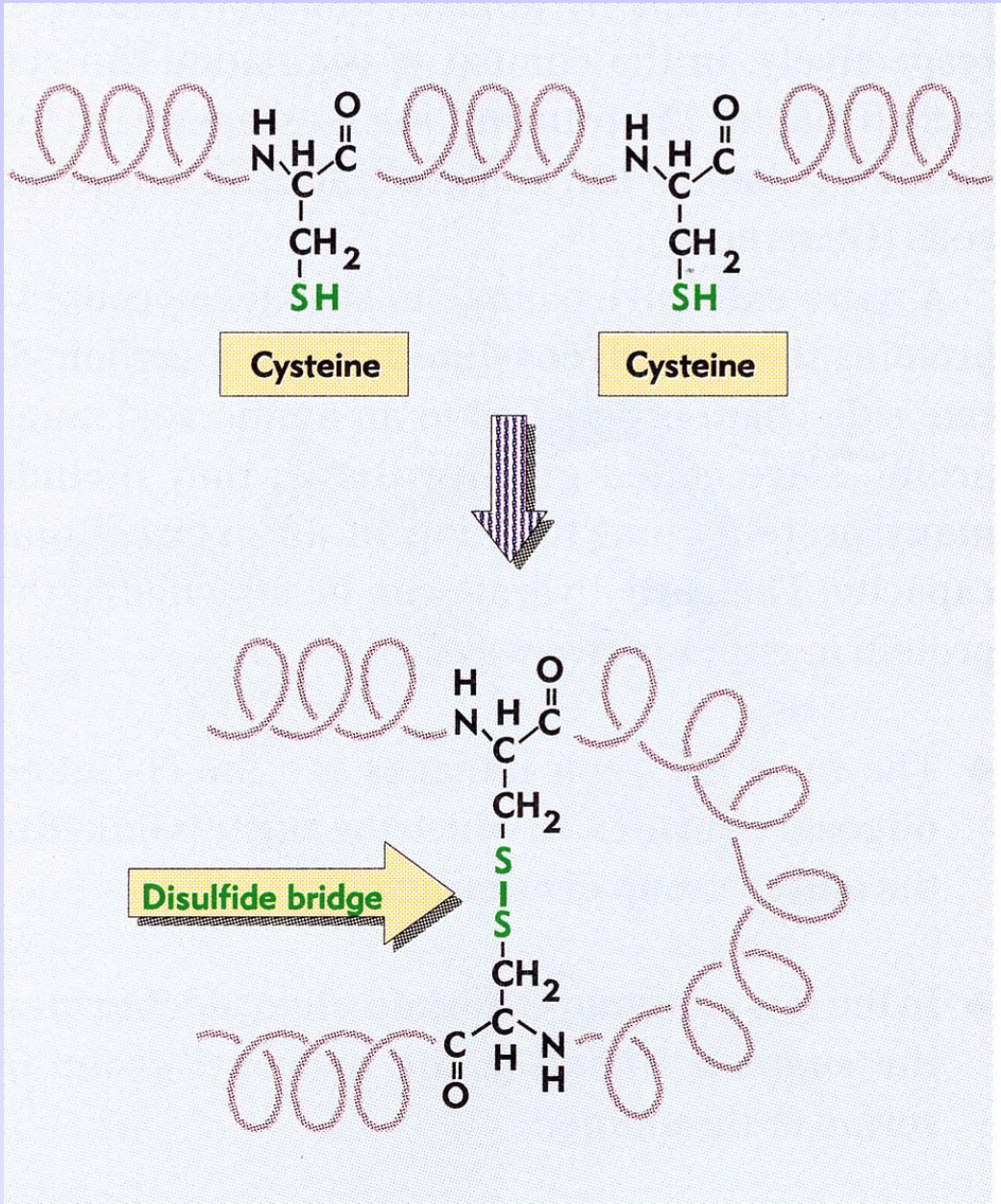


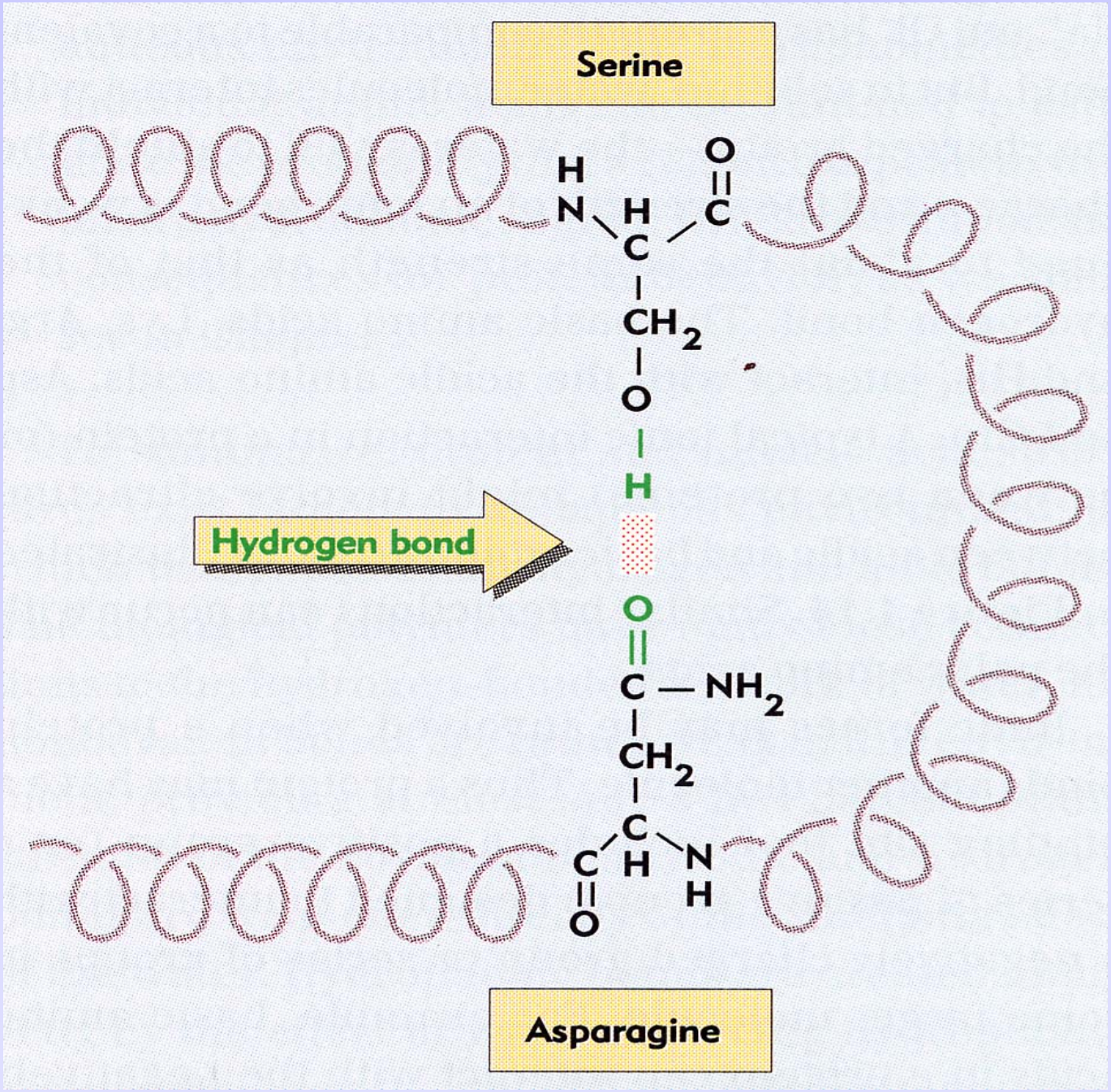


Cytochrome *c* **Lysozyme** **Ribonuclease**

Covalent and noncovalent bonds differ greatly in strength.

Type of Bond	Strength (kcal/mol)		
Covalent	-50	to	-100
Ionic	-80	or	-1
Hydrogen	-3	to	-6
Van der Waals	-0.5	to	-1
Hydrophobic	-0.5	to	-3


Cysteine
Cysteine
Disulfide bridge


Serine
Hydrogen bond
Asparagine

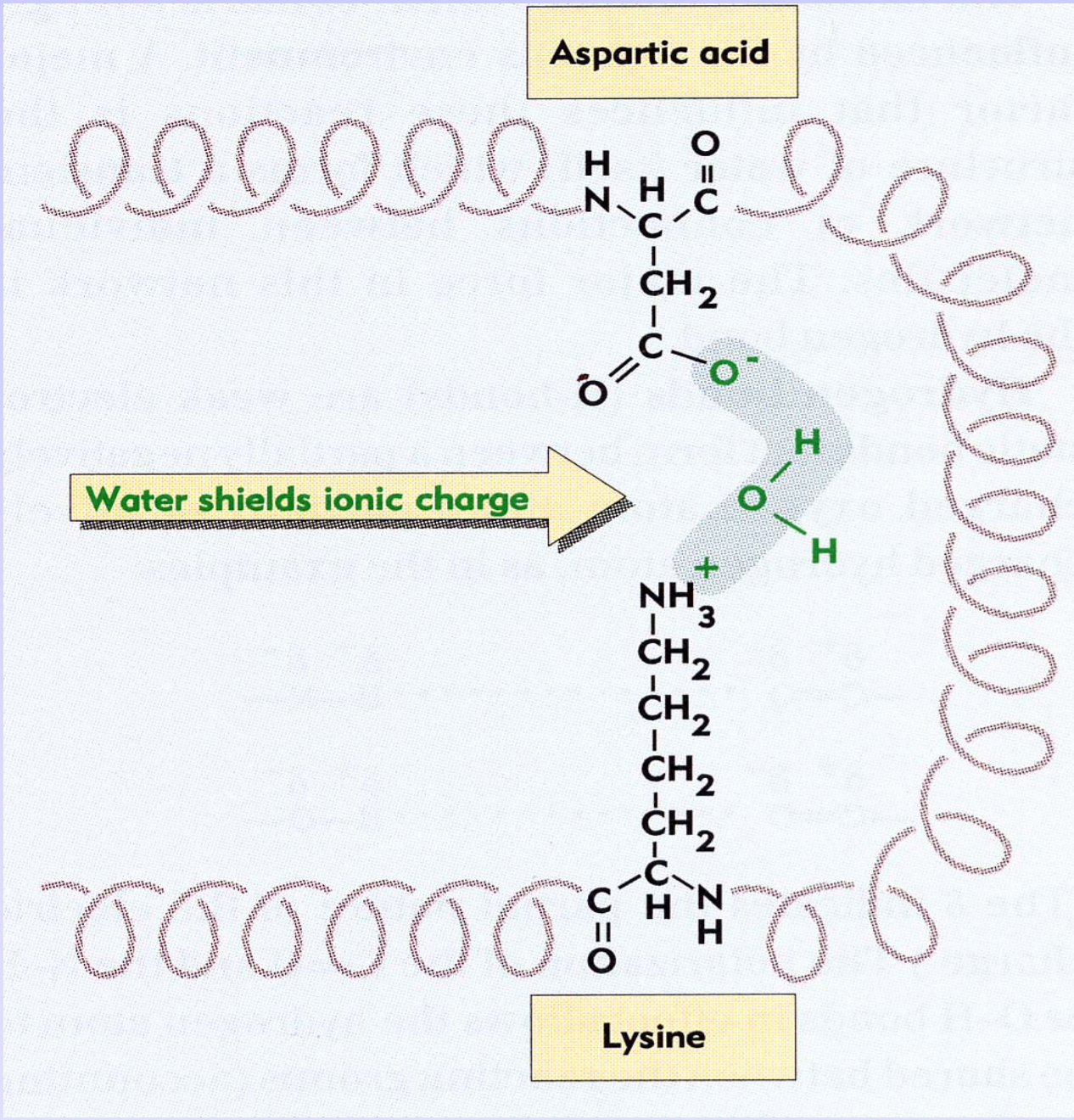
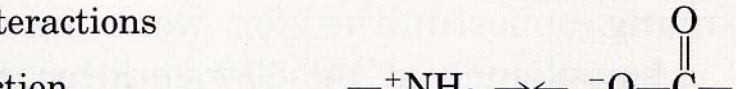
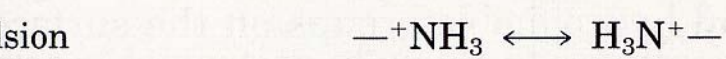
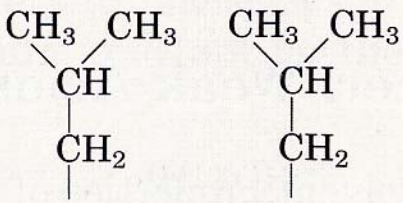
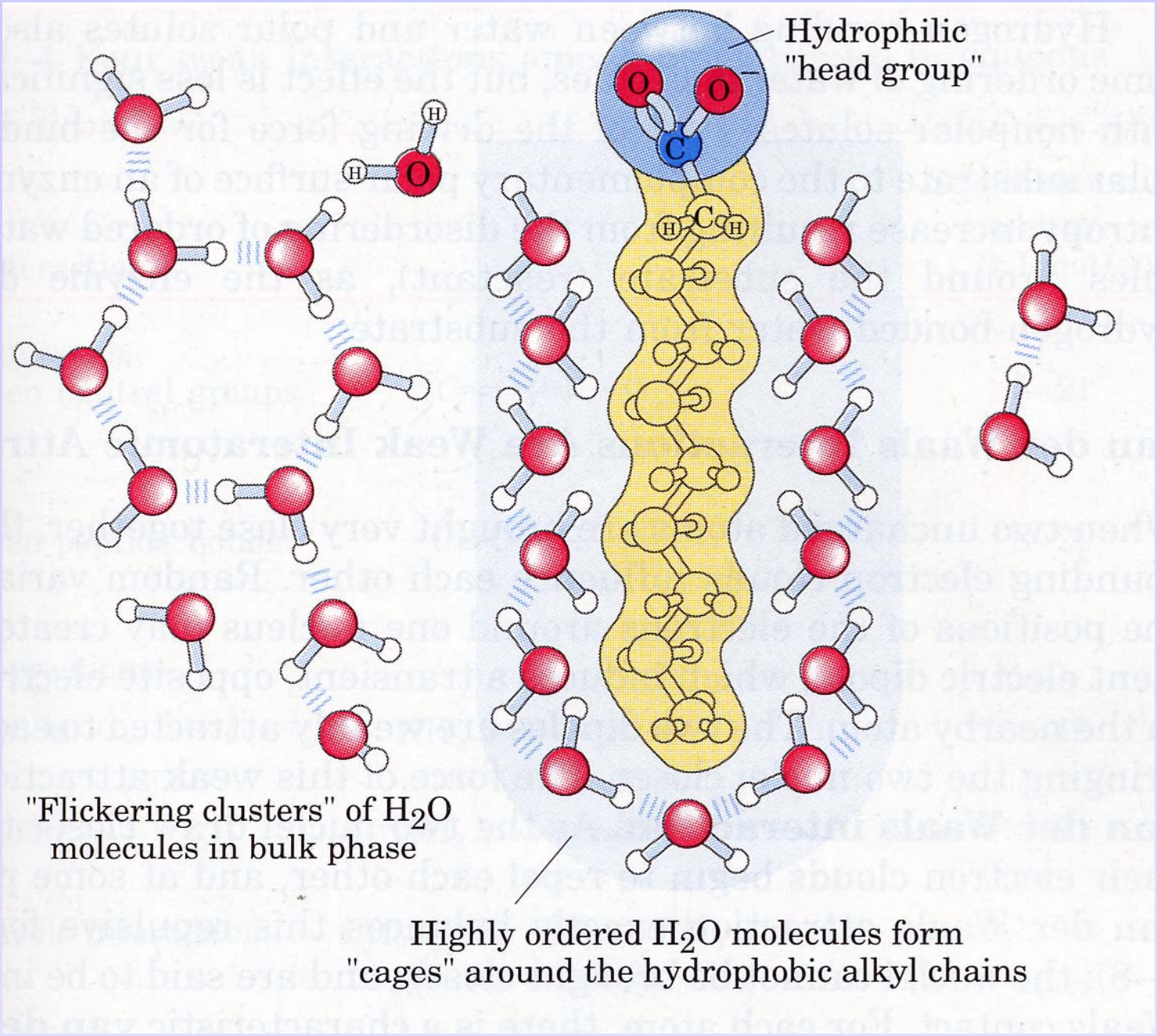
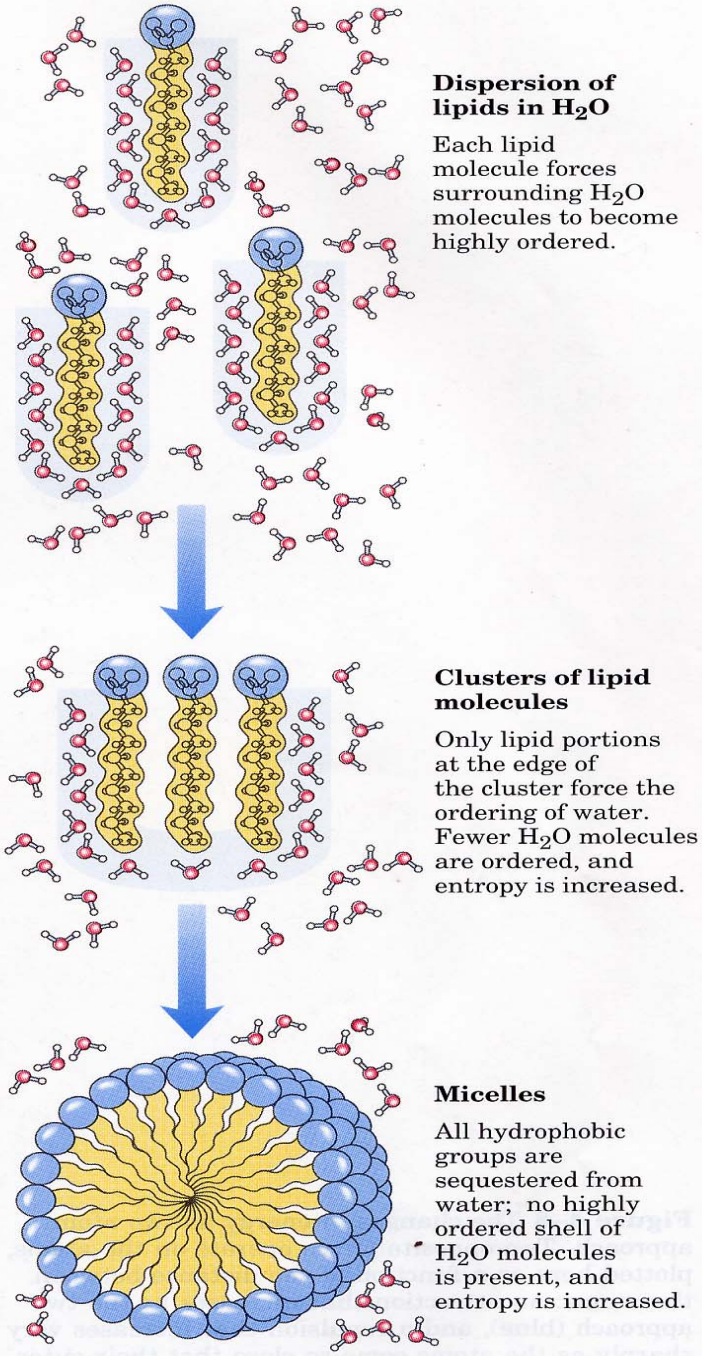

Aspartic acid
Water shields ionic charge
Lysine

Table 4–4 Four weak interactions among biomolecules in aqueous solvent

Weak interaction		Stabilization energy (kJ/mol)
Hydrogen bonds		
Between neutral groups		8–21
Between peptide bonds		8–21
Ionic interactions		
Attraction		42
Repulsion		≈−21
Hydrophobic interactions		4–8
van der Waals interactions	Any two atoms in close proximity	4


Hydrophilic
"head group"
O
O
C
H
C
H
H
H
O
"Flickering clusters" of H_2O
molecules in bulk phase
Highly ordered H_2O molecules form
"cages" around the hydrophobic alkyl chains



Dispersion of lipids in H_2O

Each lipid molecule forces surrounding H_2O molecules to become highly ordered.

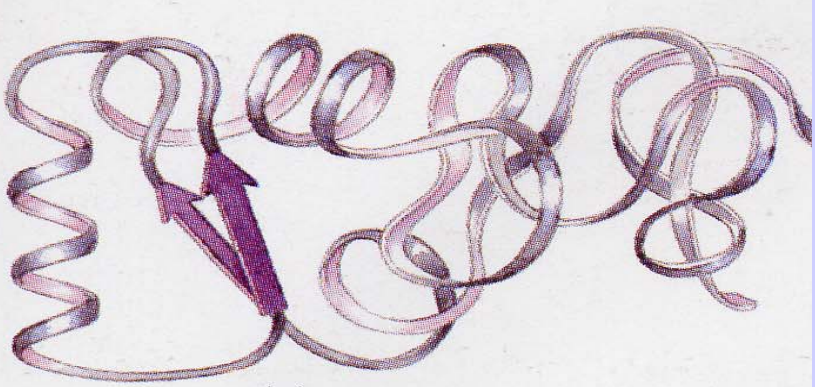
Clusters of lipid molecules

Only lipid portions at the edge of the cluster force the ordering of water. Fewer H_2O molecules are ordered, and entropy is increased.

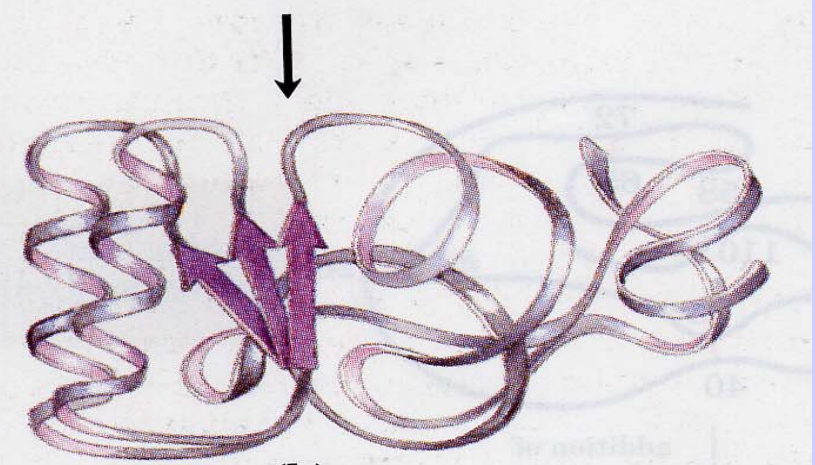
Micelles

All hydrophobic groups are sequestered from water; no highly ordered shell of H_2O molecules is present, and entropy is increased.

(b)

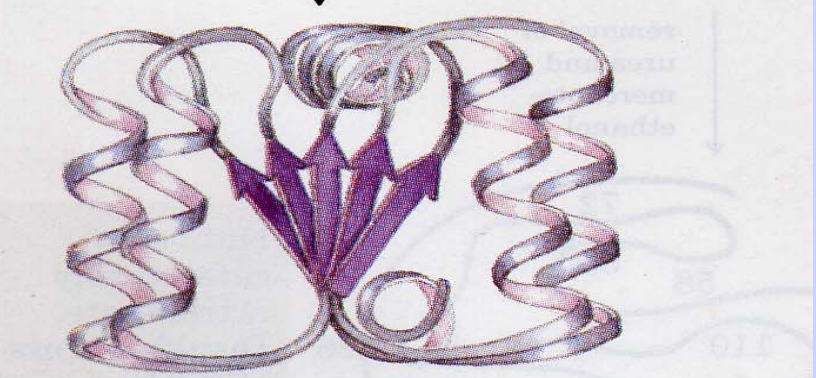


(a)

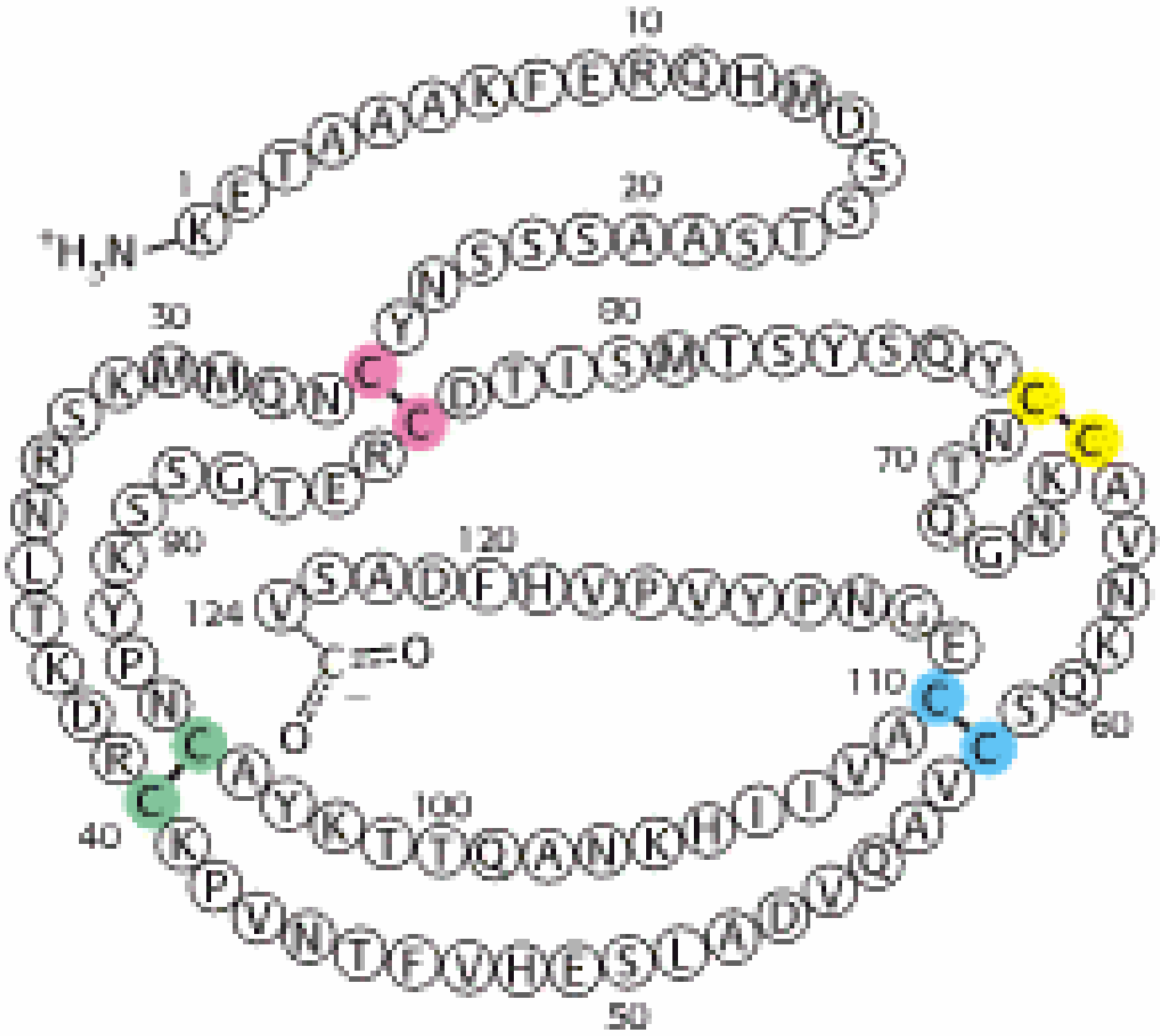


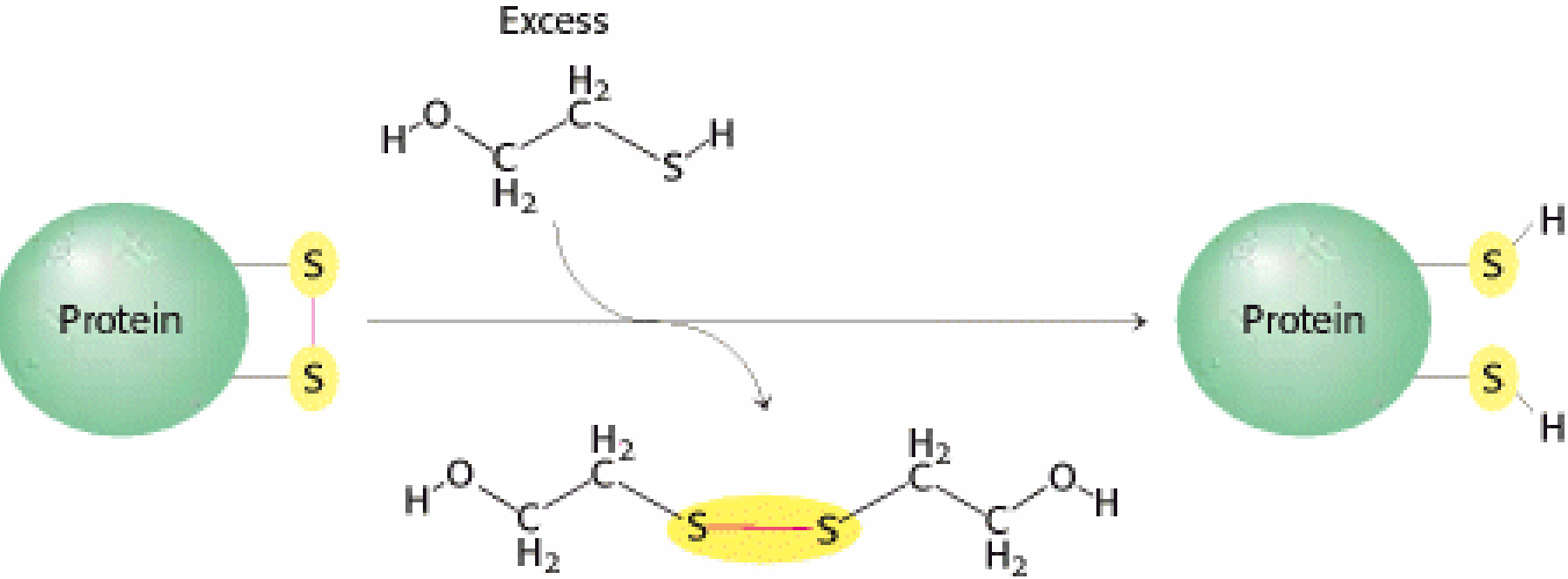
(b)

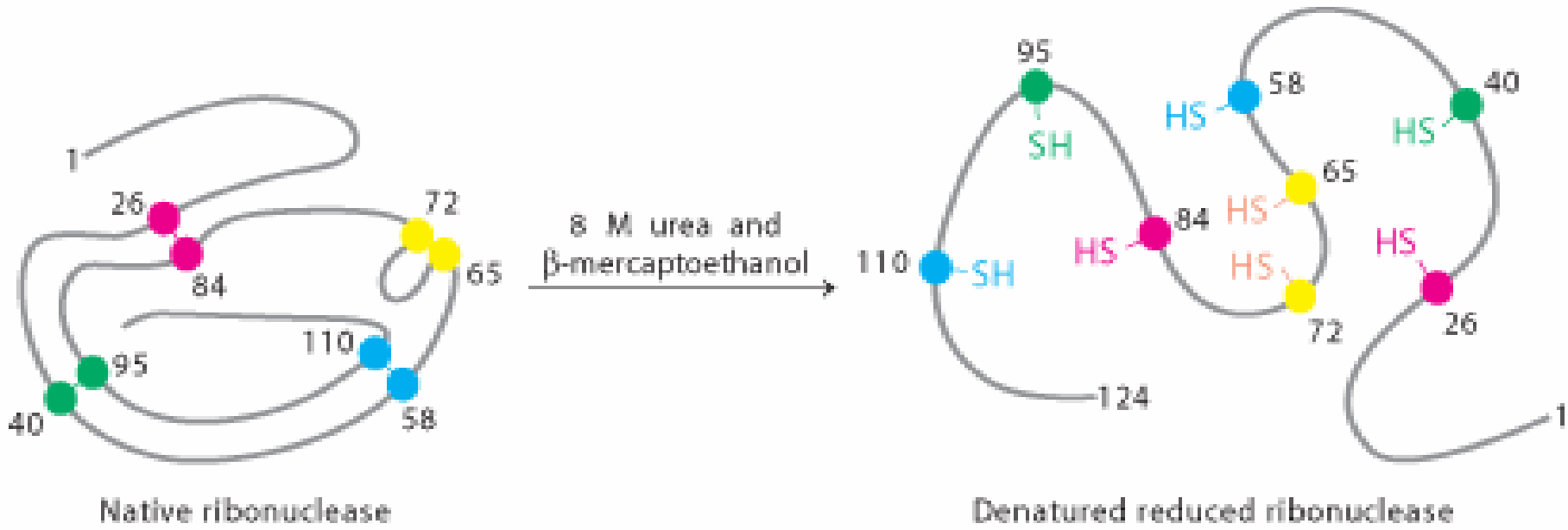
(c)

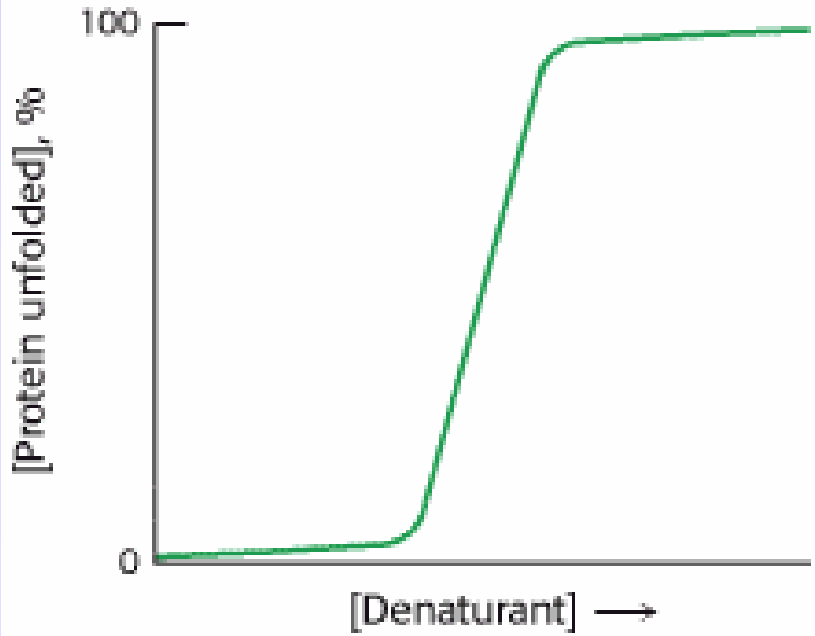


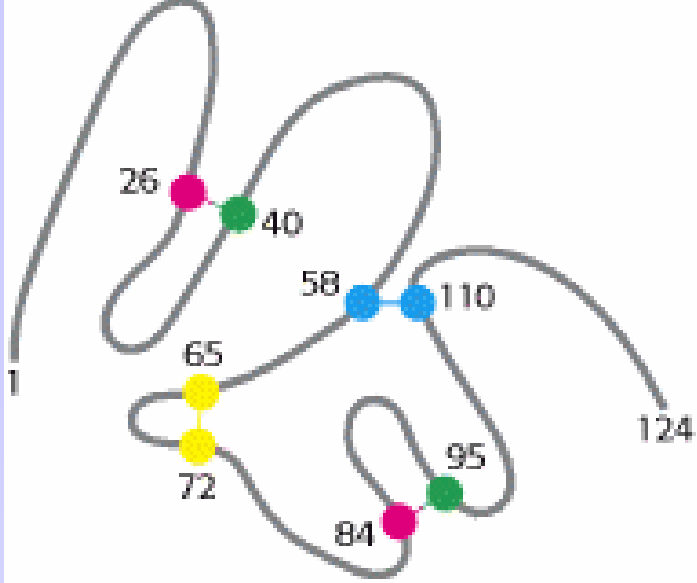
(d)


10
20
30
80
70
120
124
90
110
60
40
100
50
1
$^{+}H_3N$


Excess
Protein
S
S
H
O
C
H2
S
H
Protein
S
H
S
H

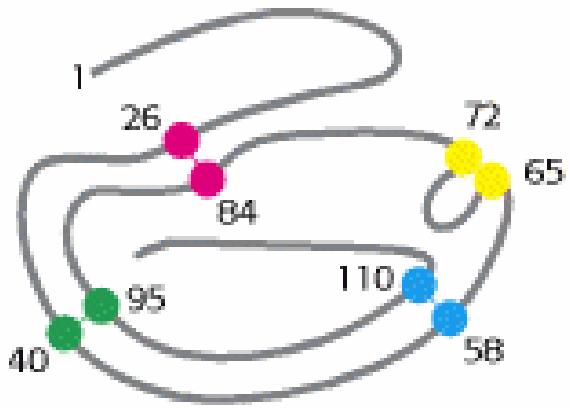

1
26
84
72
65
110
95
40
58
8 M urea and
β-mercaptoethanol
95
SH
110
SH
HS
58
HS
84
HS
65
HS
HS
72
HS
40
HS
26
124
1
Native ribonuclease
Denatured reduced ribonuclease


100
0
[Protein unfolded], %
[Denaturant] ⟶



Scrambled ribonuclease

Trace of
β-mercaptoethanol



Native ribonuclease

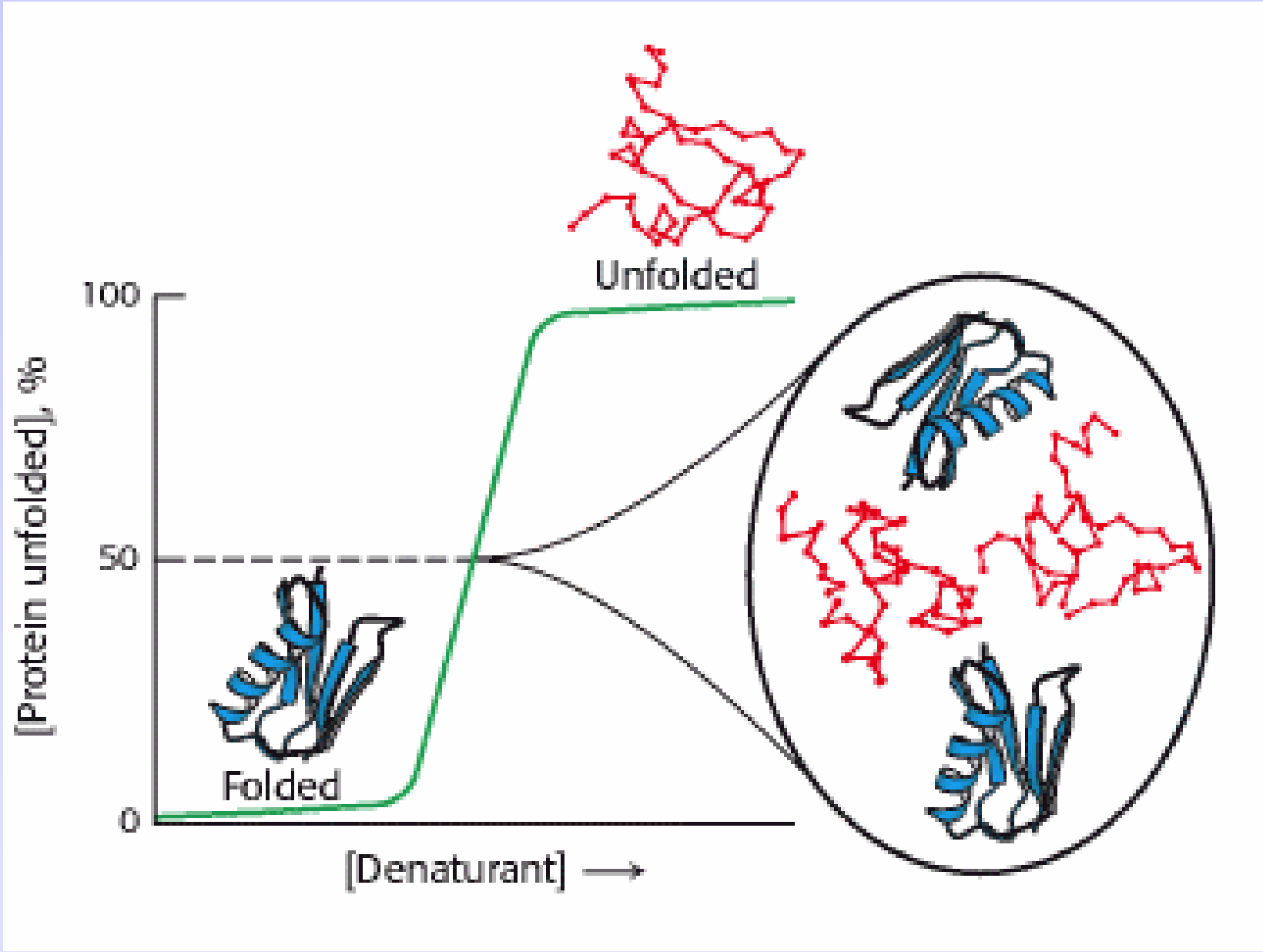
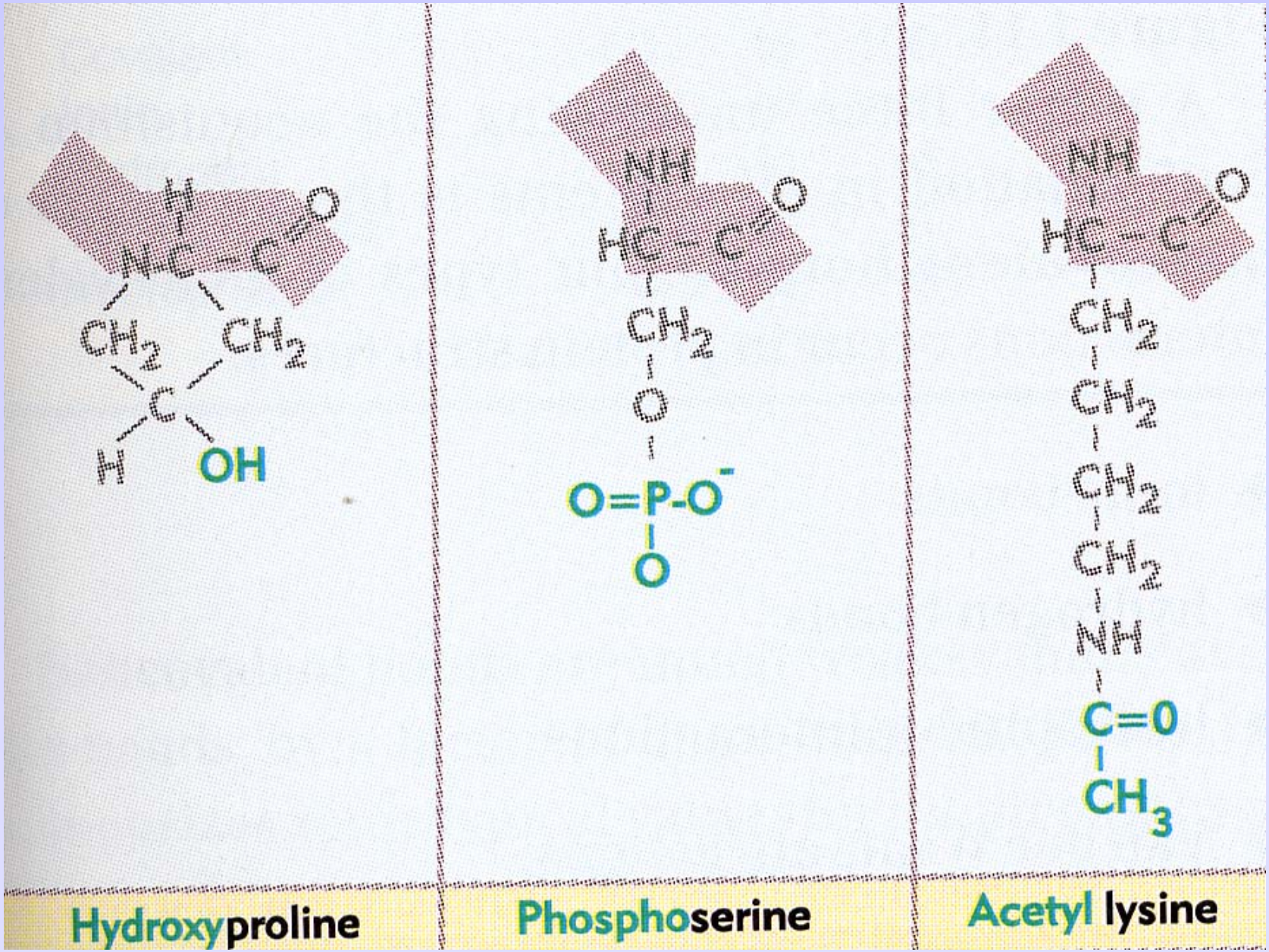
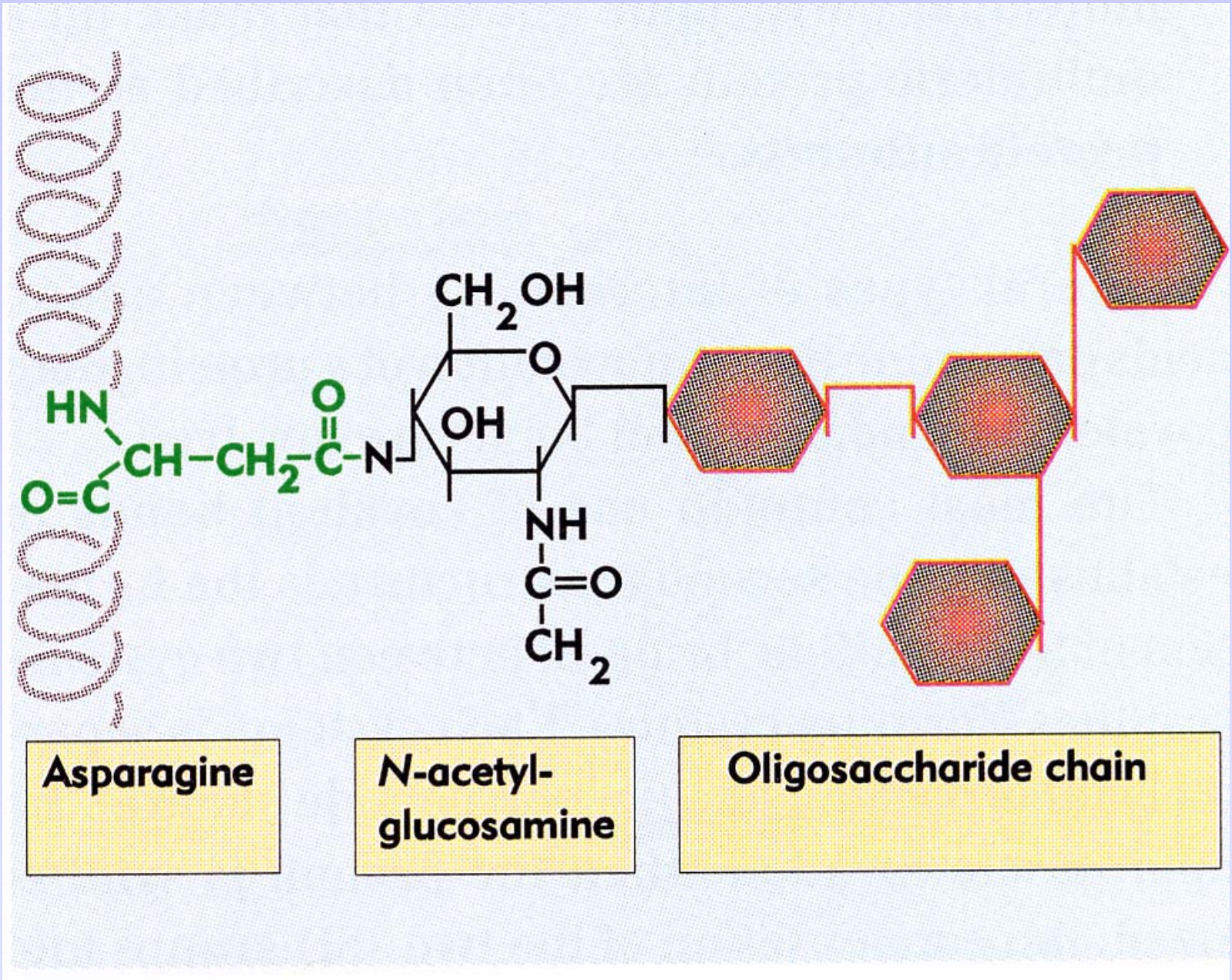
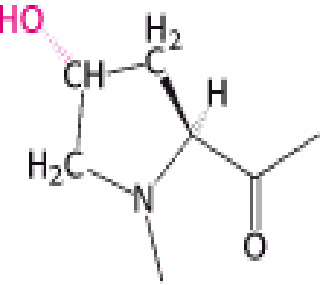

Unfolded
100
50
0
[Protein unfolded], %
Folded
[Denaturant]

Table 6–3 Conjugated proteins

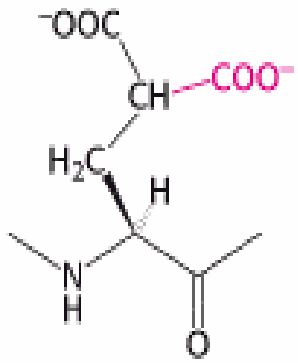
Class	Prosthetic group	Example
Lipoproteins	Lipids	β_1-Lipoprotein of blood
Glycoproteins	Carbohydrates	Immunoglobulin G
Phosphoproteins	Phosphate groups	Casein of milk
Hemoproteins	Heme (iron porphyrin)	Hemoglobin
Flavoproteins	Flavin nucleotides	Succinate dehydrogenase
Metalloproteins	Iron	Ferritin
	Zinc	Alcohol dehydrogenase
	Calcium	Calmodulin
	Molybdenum	Dinitrogenase
	Copper	Plastocyanin


Hydroxyproline
Phosphoserine
Acetyl lysine

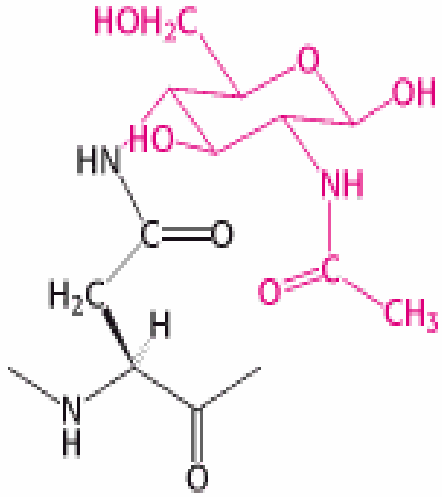

HN
CH–CH2–C–N
O=C
O
CH2OH
O
OH
NH
C=O
CH2
Asparagine
N-acetyl-glucosamine
Oligosaccharide chain



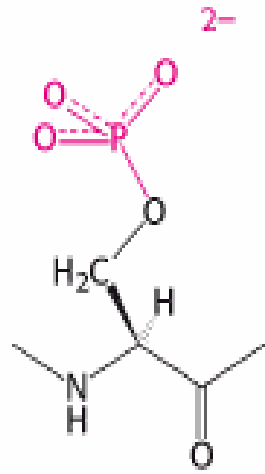
Hydroxyproline



γ-Carboxyglutamate



Carbohydrate–asparagine adduct



Phosphoserine

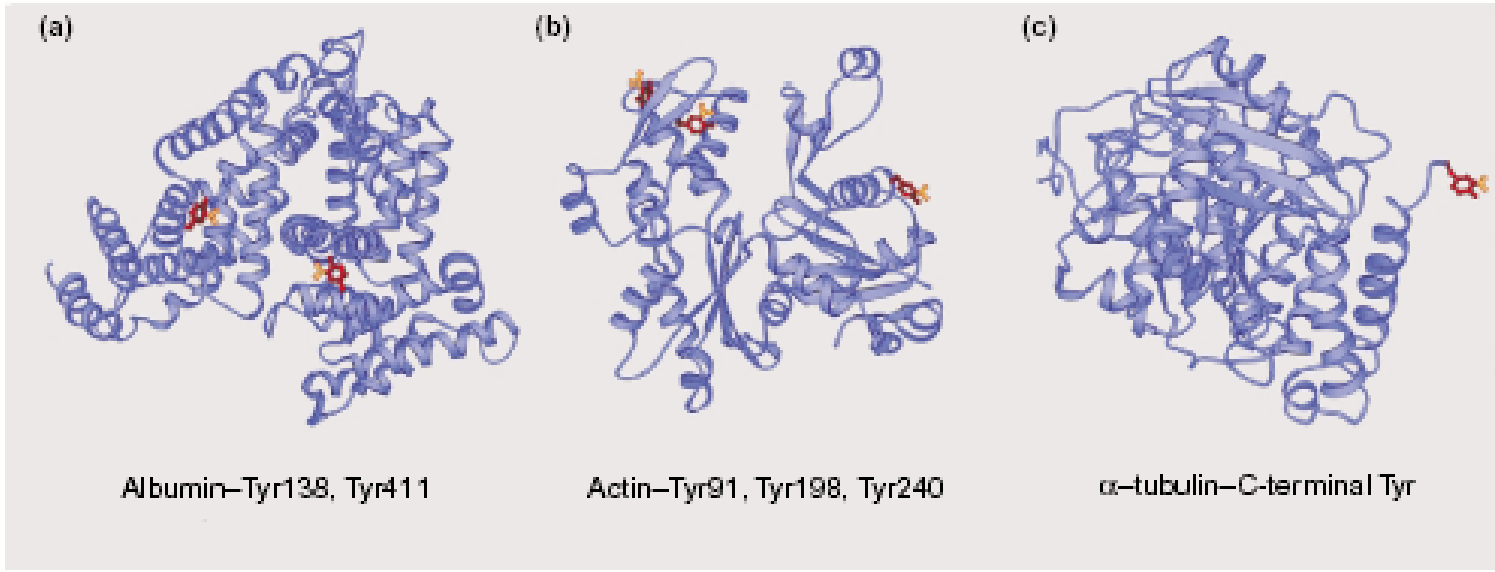
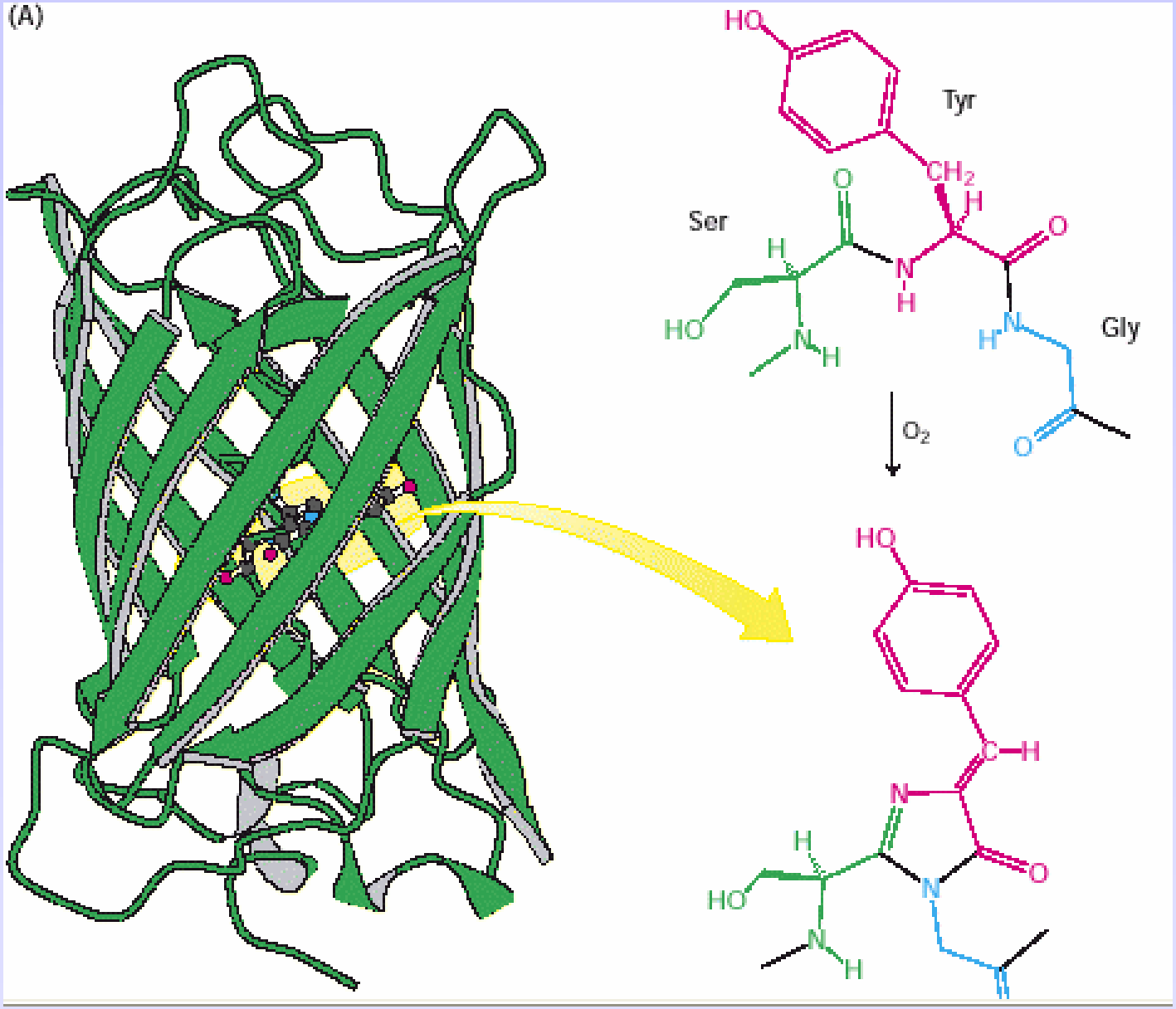
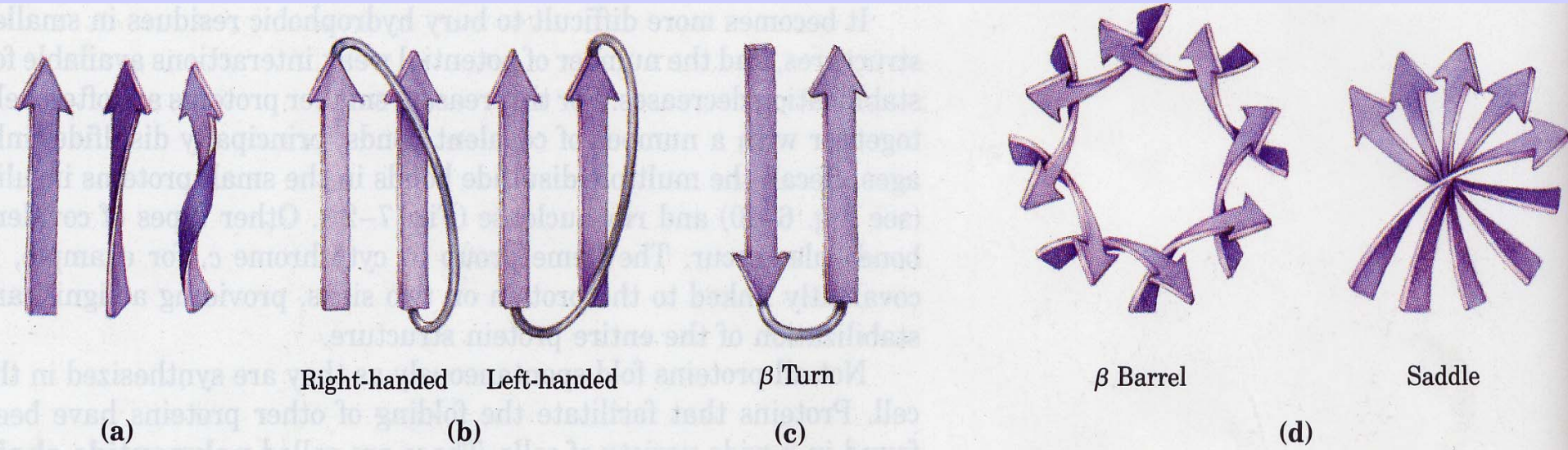
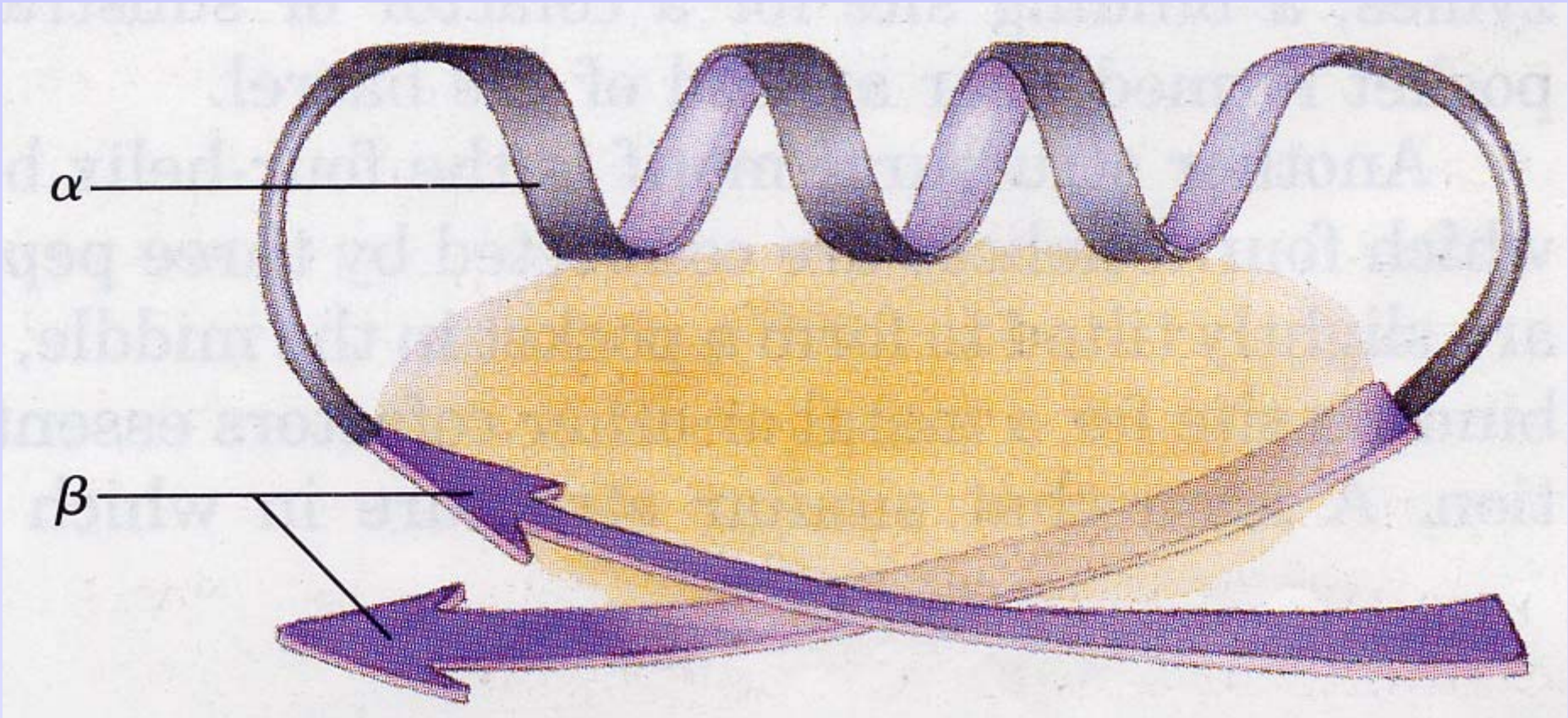
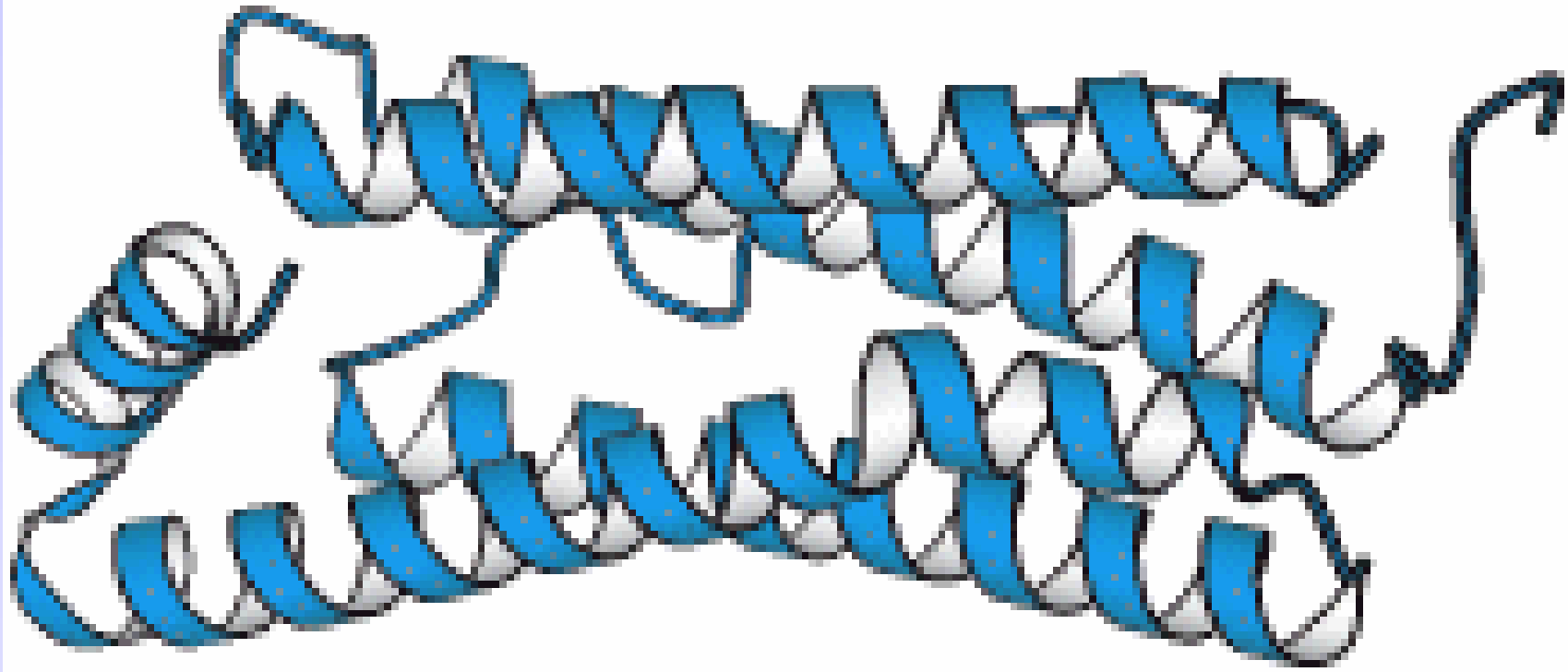


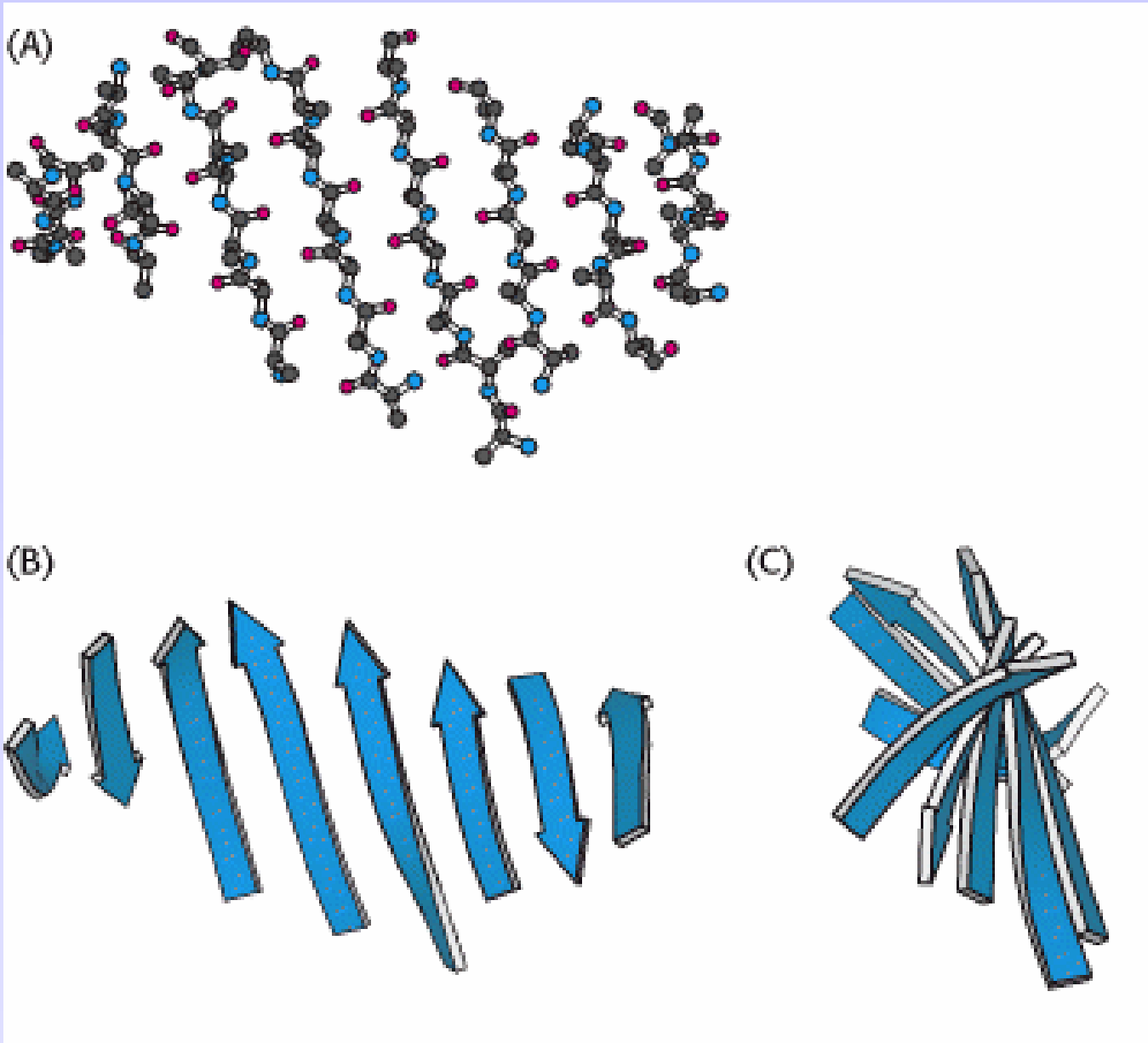
Figure 2. Protein tyrosine nitration. Ribbon structures showing the specific positions of 3-nitrotyrosine (NO_2Tyr) in **(a)** human albumin (PDB 1AO6), **(b)** rabbit actin (PDB 1J6Z), and **(c)** pig α-tubulin (PDB 1TUB). Tyrosine residues are shown in red and NO_2 groups are shown in yellow.


(A)
HO
Tyr
CH2
H
O
Ser
H
HO
N
H
O
N
H
N
H
Gly
O2
O
HO
C
H
N
H
HO
N
O
N
H

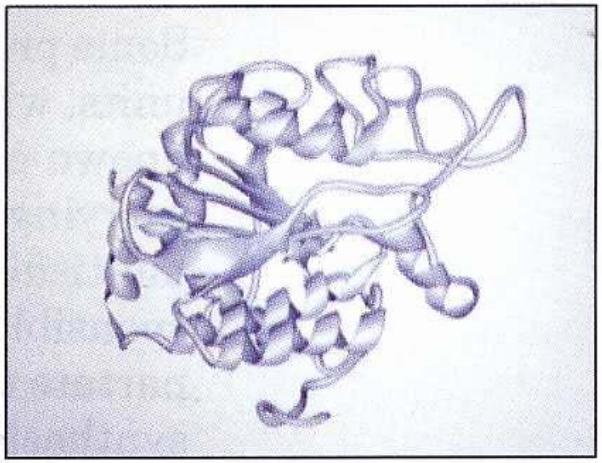

Right-handed
Left-handed
β Turn
β Barrel
Saddle
(a)
(b)
(c)
(d)


α
β



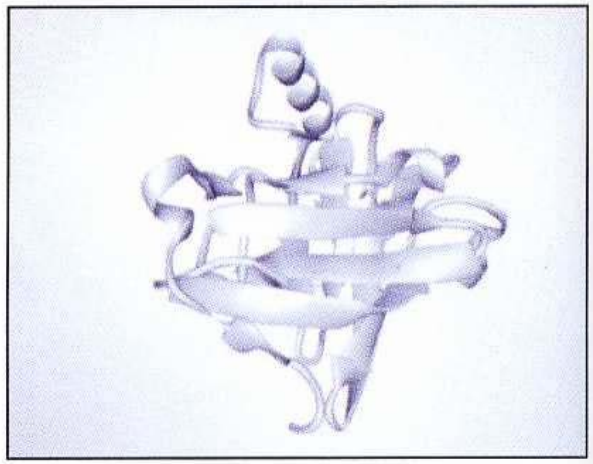

(A)
(B)
(C)

$\alpha\beta$ with saddle at core

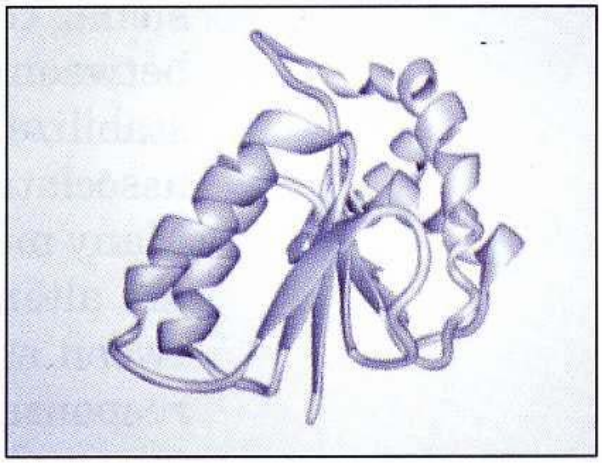


Carboxypeptidase

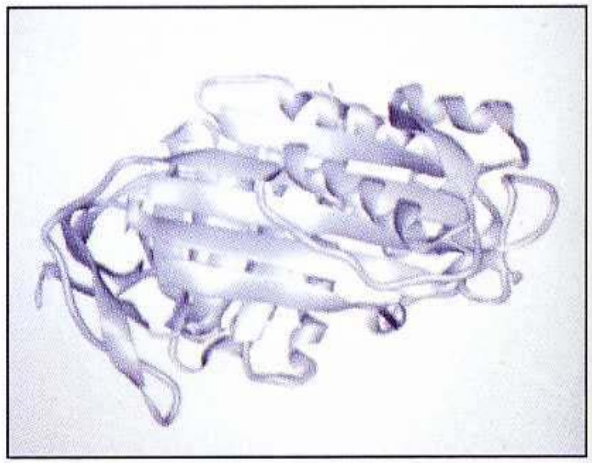
β–β Sandwich



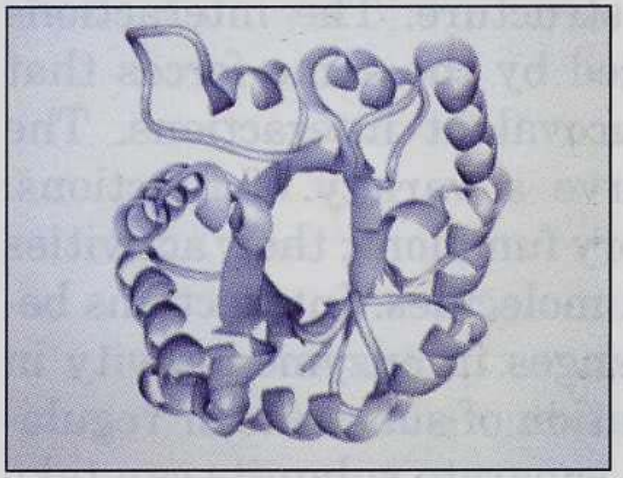
Insecticyanin



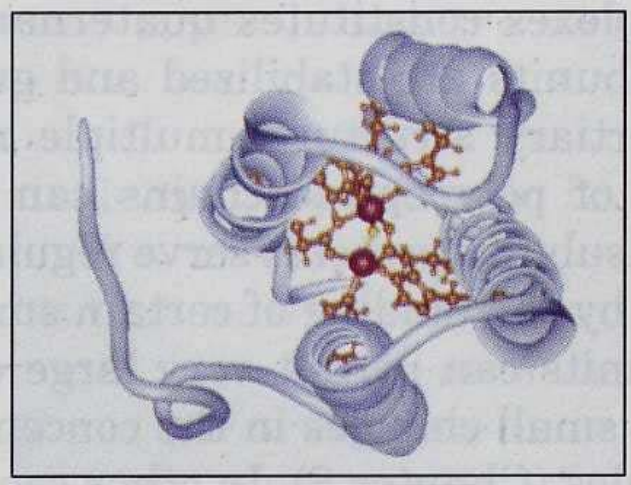
Lactate
dehydrogenase
domain 1



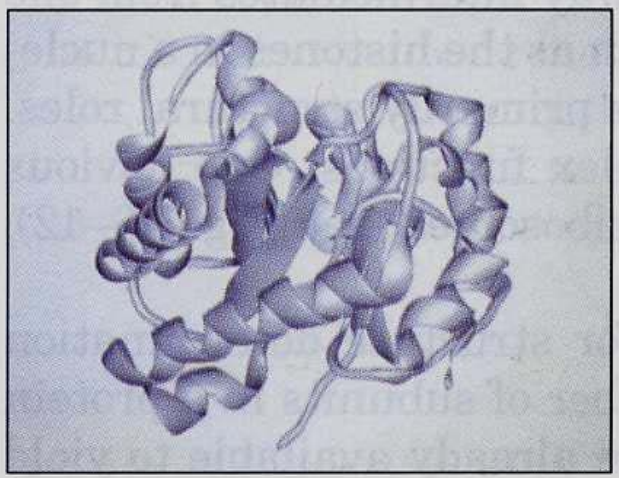
α_1-Antitrypsin



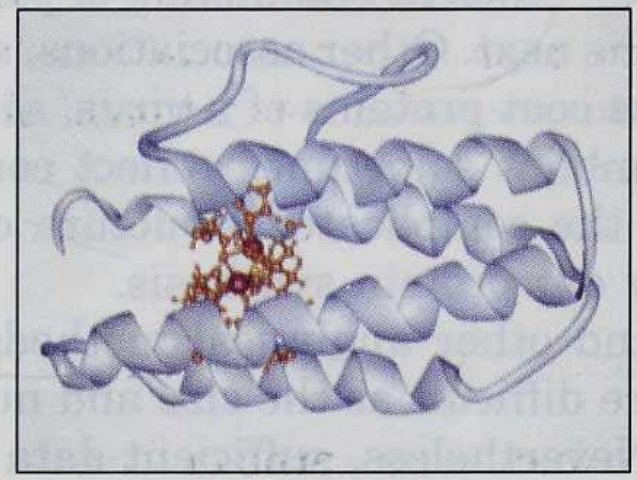
Triose phosphate
isomerase
(top view)



Myohemerythrin
(top view)

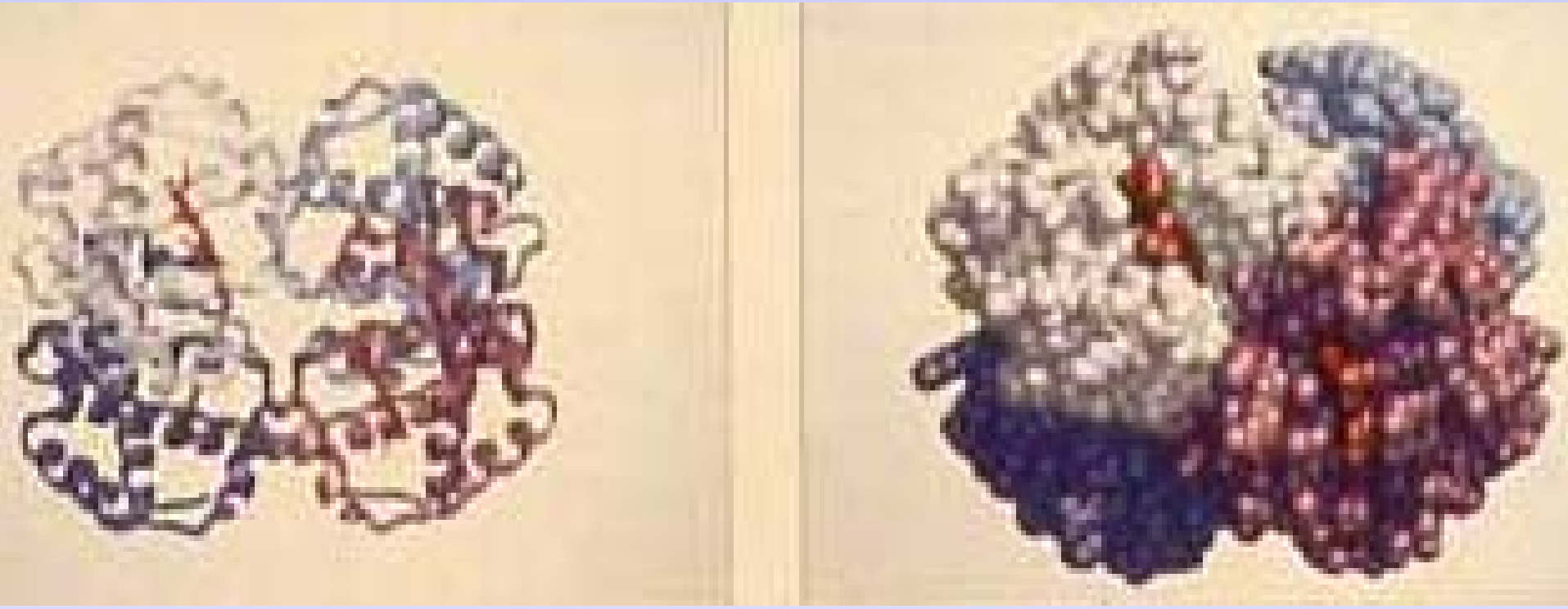


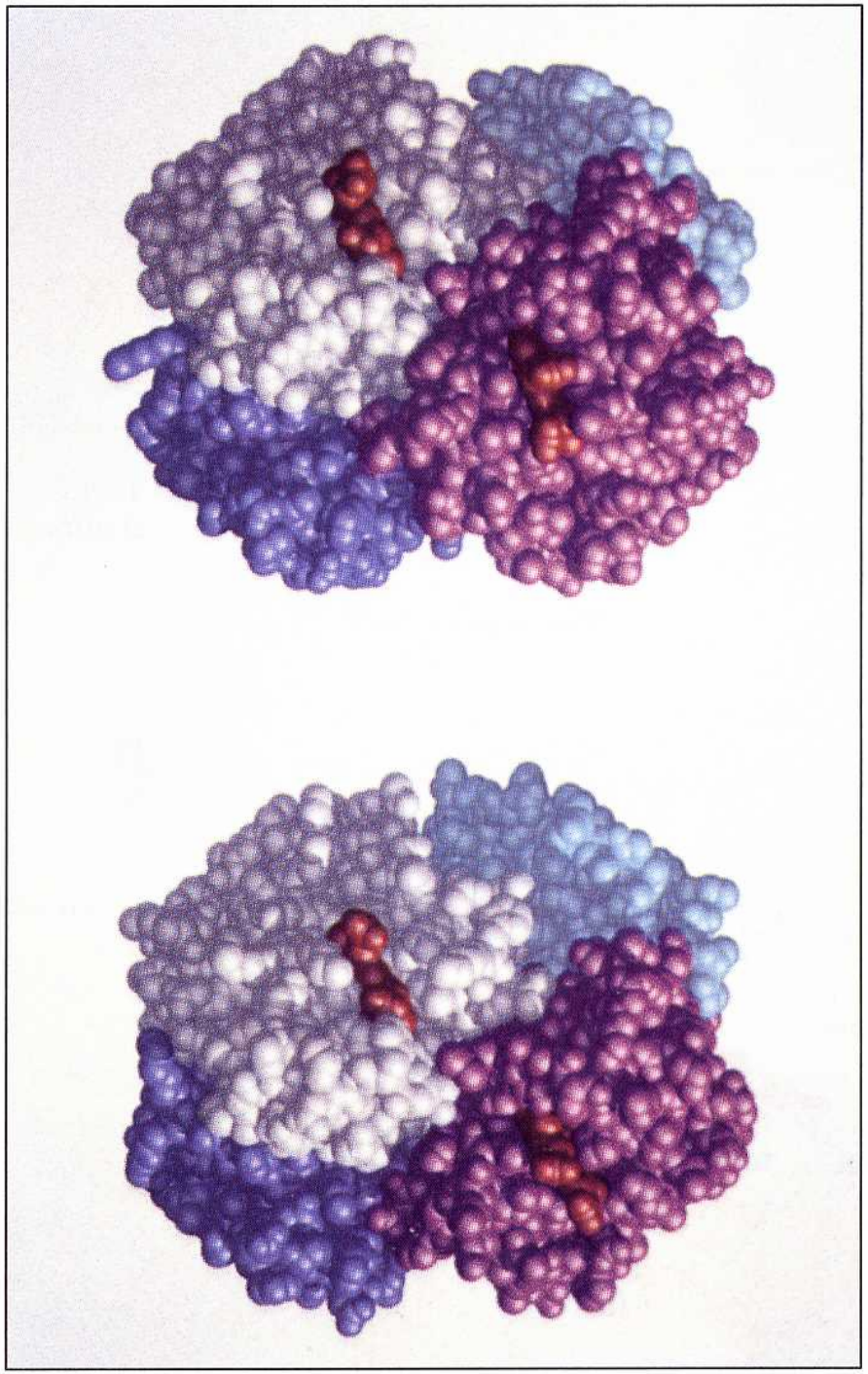
Triose phosphate
isomerase
(side view)

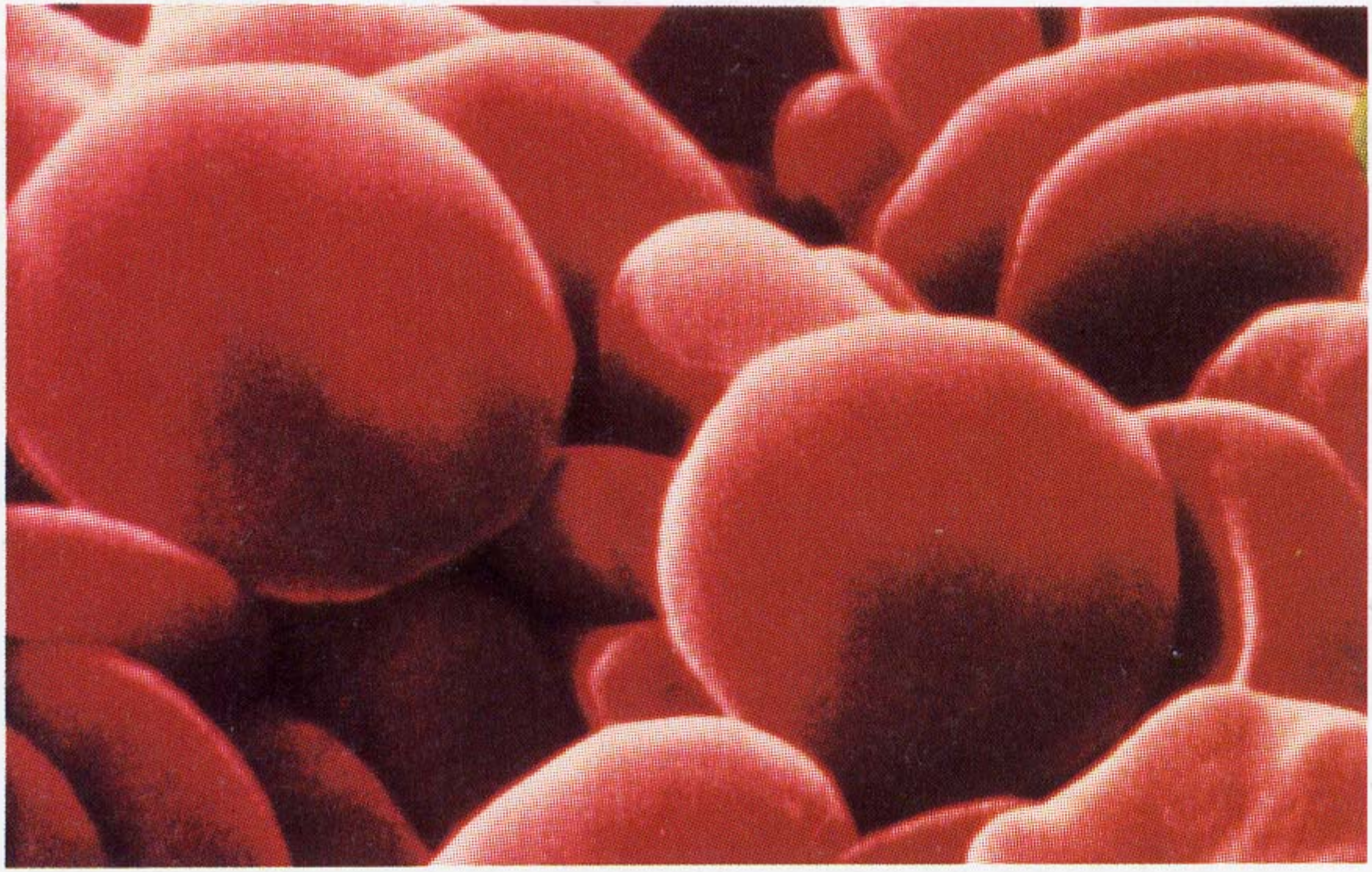


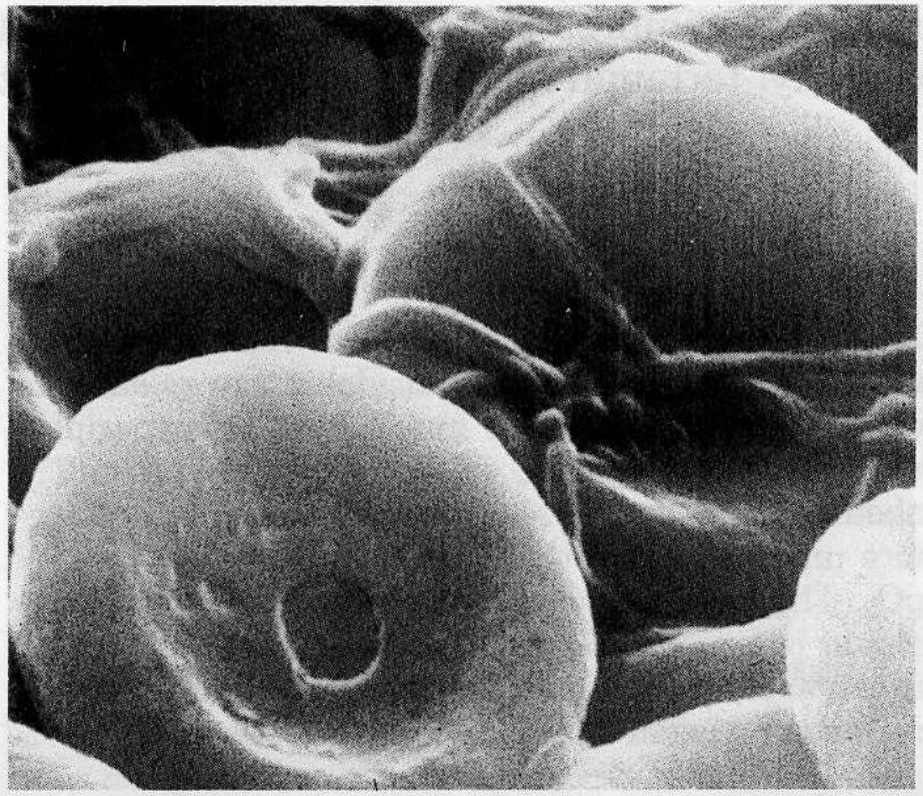
Myohemerythrin
(side view)

(a) **(b)**

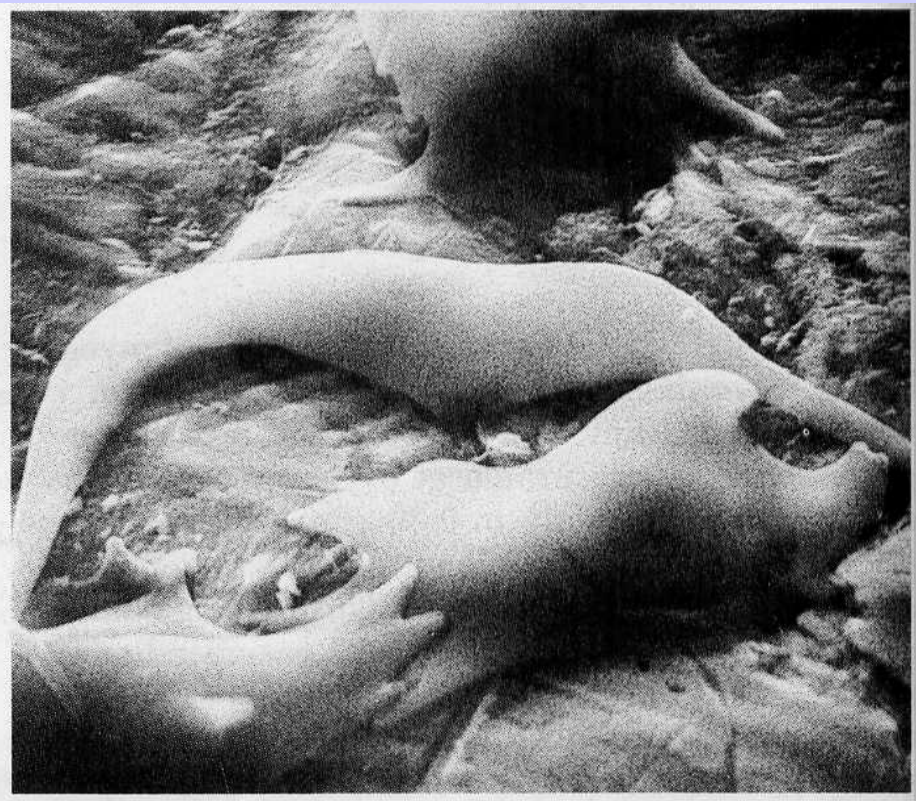




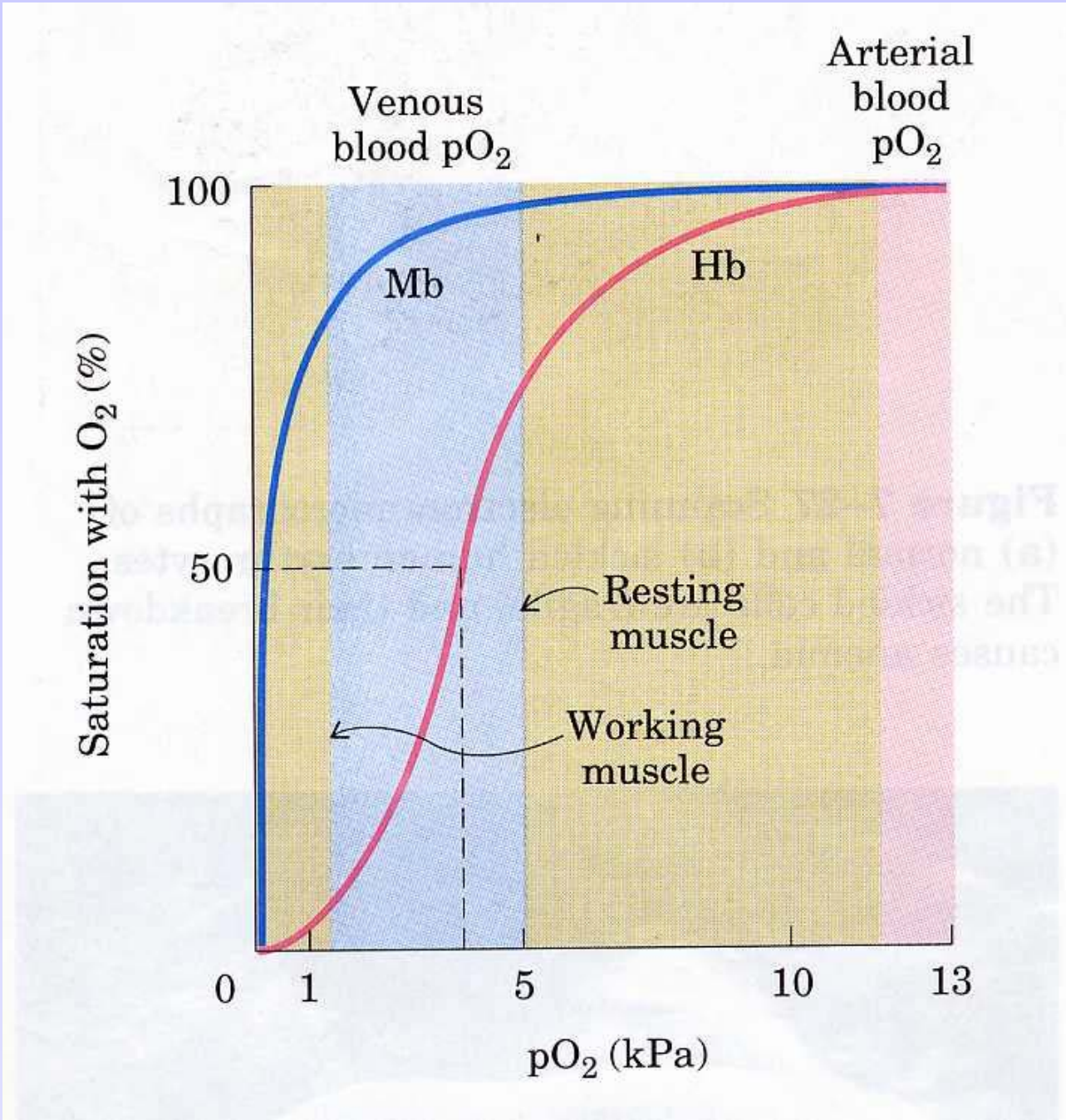




(a)



(b)


Arterial blood pO_2
Venous blood pO_2
100
Mb
Hb
Saturation with O_2 (%)
50
Resting muscle
Working muscle
0
1
5
10
13
pO_2 (kPa)