

E-BOOK SEARCH

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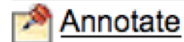
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Unit Two



Annotate

Proteins



MP3 Tutor

Protein Structure and Function

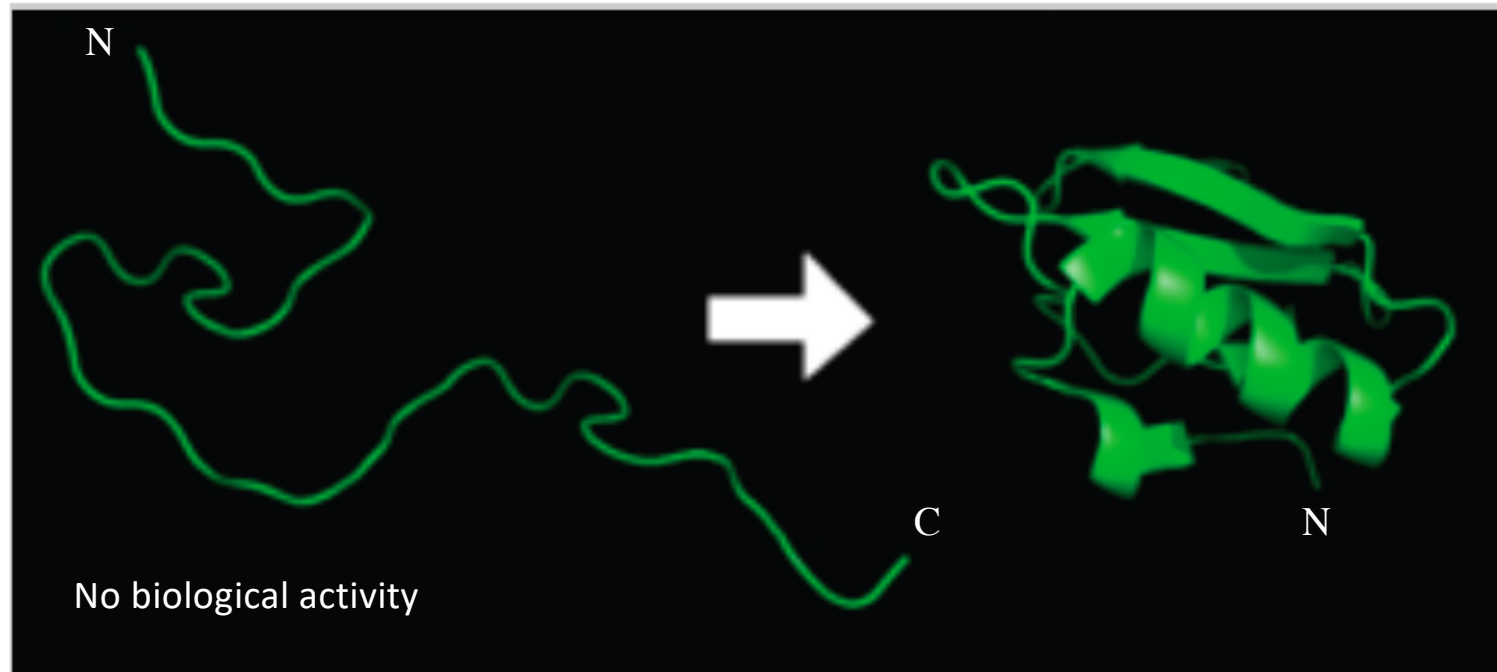
Proteins are the most elaborate of life's molecules. A **protein** is a polymer constructed from amino acid monomers. Your body has tens of thousands of different kinds of proteins, and each kind of protein has a unique three-dimensional shape that corresponds to a specific function. Proteins perform most of the tasks the body needs to function. **Figure 3.19** surveys the functions of four types of proteins: structural proteins, storage proteins, contractile proteins, and transport proteins. Other types of proteins include defensive proteins, such as antibodies of the immune system, and signal proteins, which convey messages from one cell to another. Enzymes (such as lactase), another important type of protein, change the rate of a chemical reaction without being changed in the process (as you will see in Chapter 5). Now let's take a look at the architecture of proteins.



(Click image to enlarge)

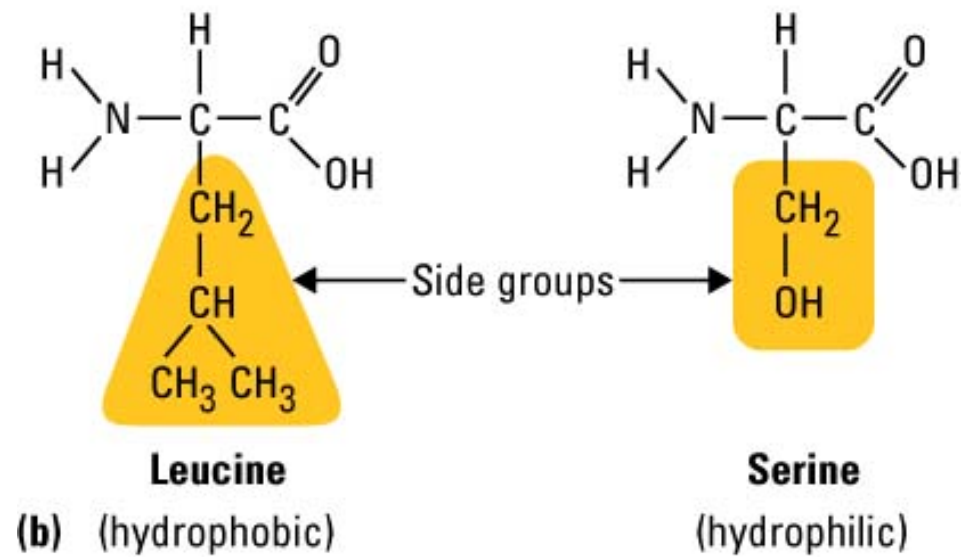
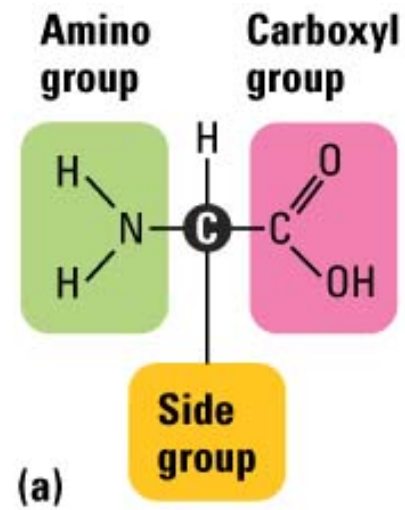
Figure 3.19 Some functions of proteins.

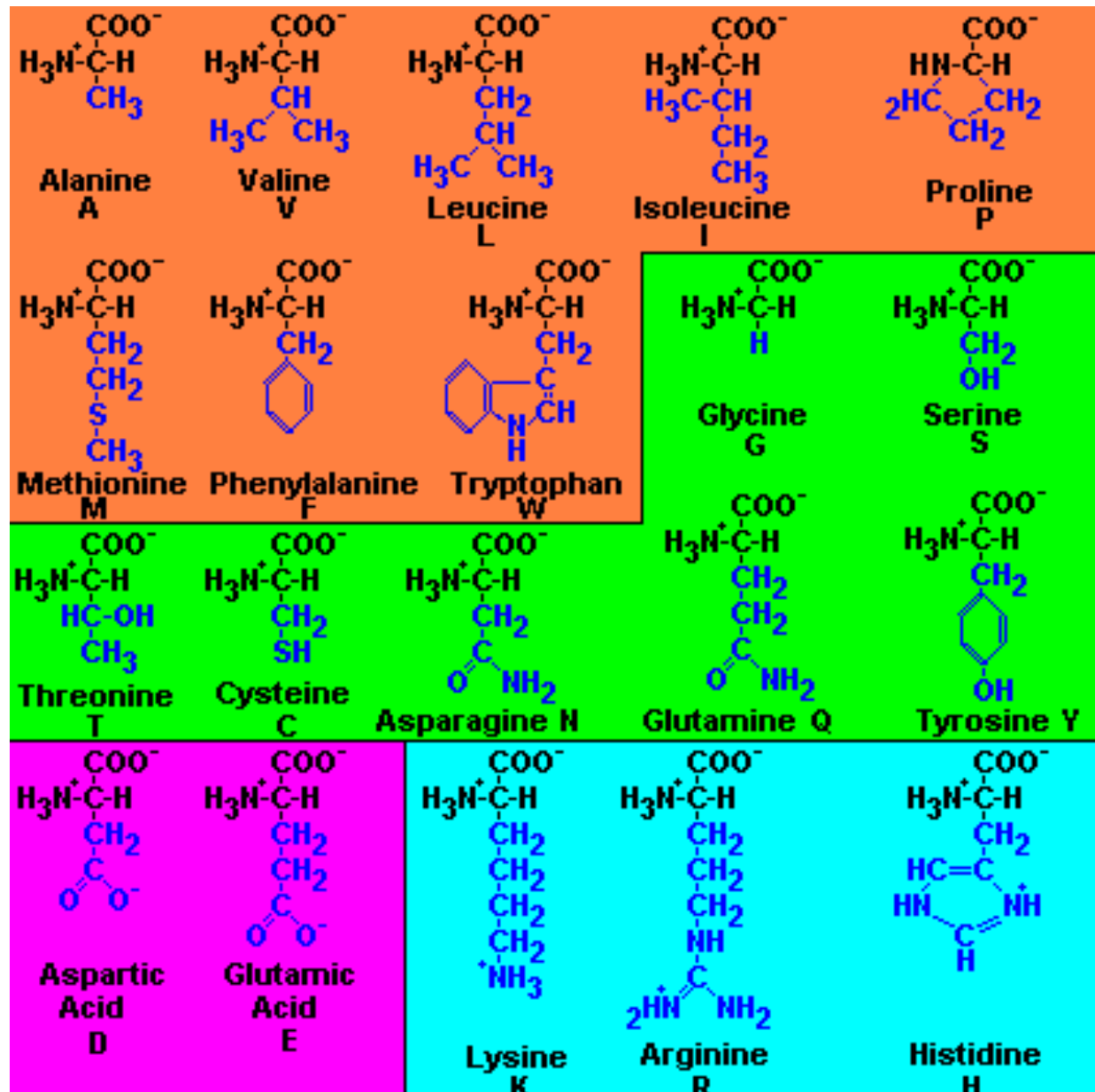
Proteins are long polymers of aminoacids.



Protein before and after folding.

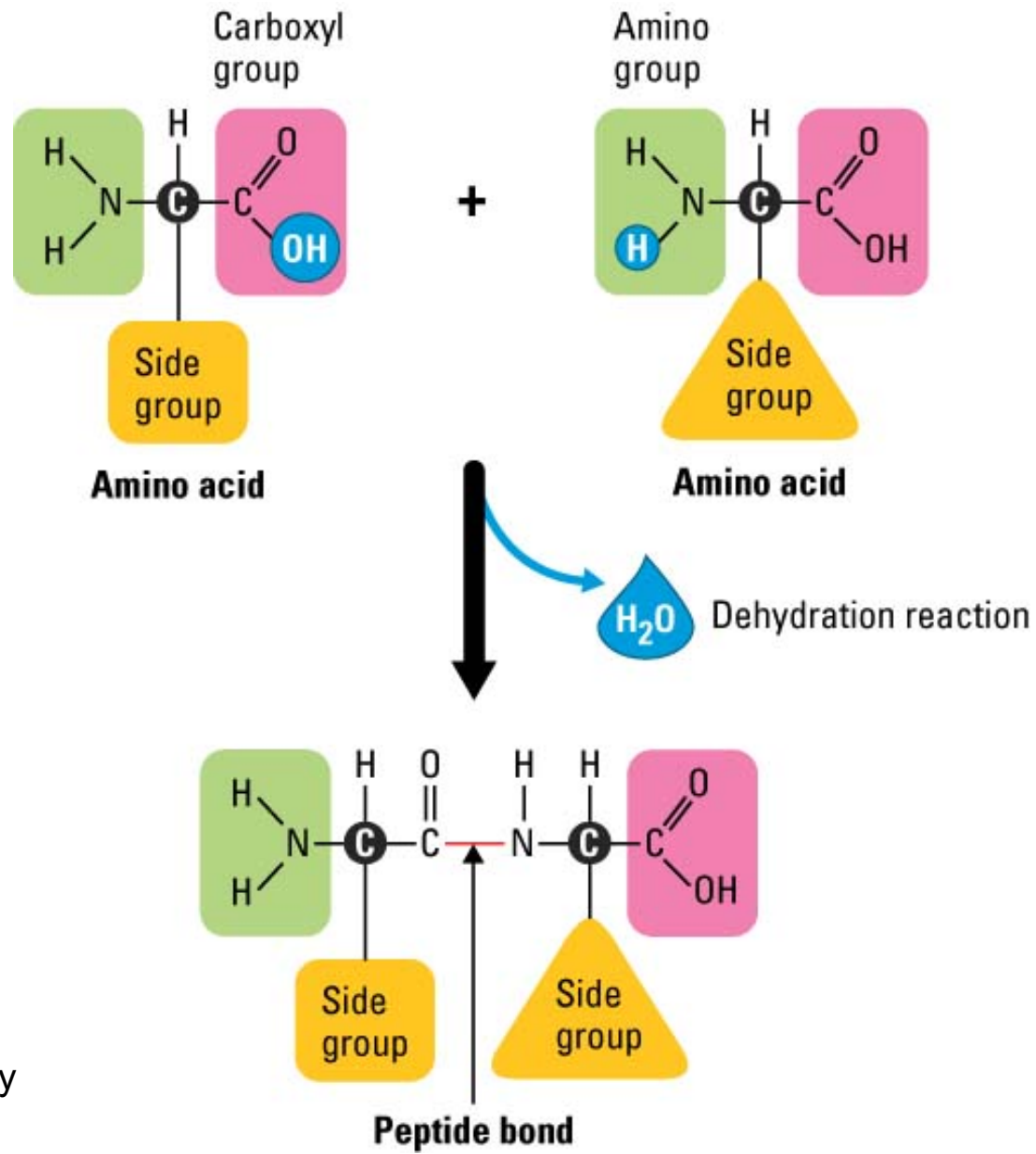
Only correctly folded proteins
Have a biological activity





The 20 amino acids used for protein synthesis

These amino acids have been separated according to the chemical properties of their side chains



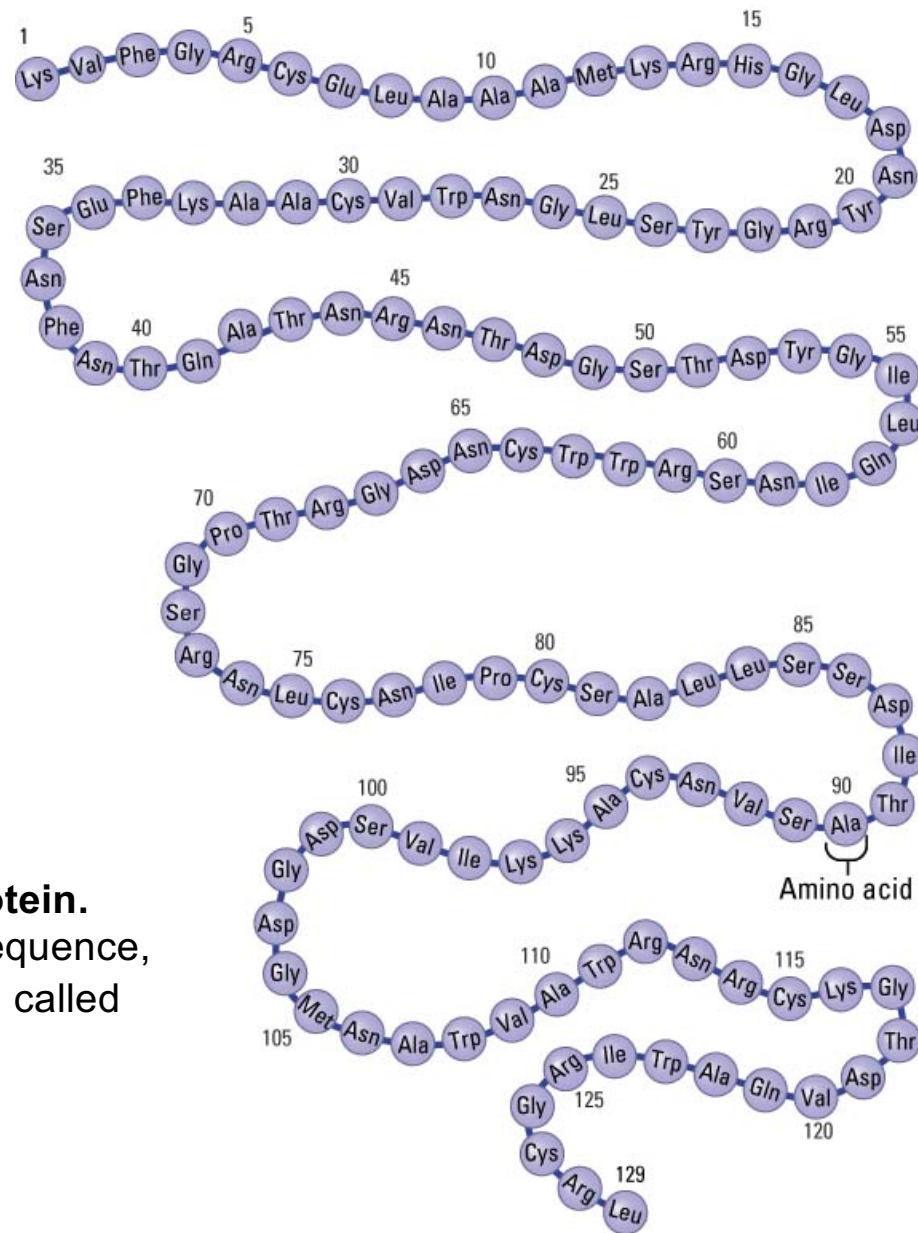
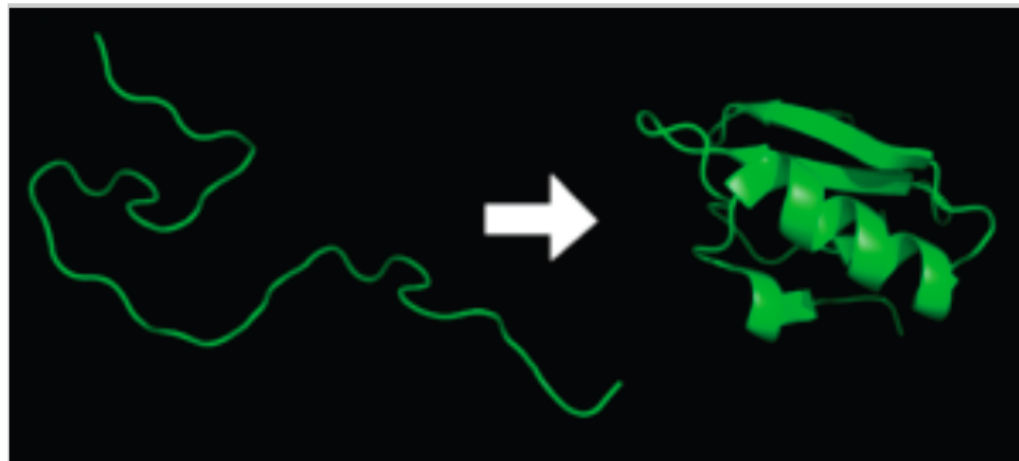


Figure 3.22
The primary structure of a protein.
 This is the unique amino acid sequence, or primary structure, of a protein called lysozyme.

Protein structure

- **Secondary structure** is the local spatial arrangement of a polypeptide's backbone atoms **without regard to the conformations of its side chains.**
- **Tertiary structure** refers to the three-dimensional structure of an entire polypeptide, **including that of its side chains.**
- Many proteins are composed of two or more polypeptide chains, loosely referred to as subunits. A protein's **quaternary structure** refers to the spatial arrangement of its subunits.

Side chains
are not shown



Protein before and after folding.

Folding of a polypeptidic chain

secondary structure:

structure produced by *regular repeated interactions* between atoms of the *backbone*.

→ α helix

→ β sheet



Hydrogen bond :

- donor
- acceptor

Which ones are the closest possible acceptor/donor ?

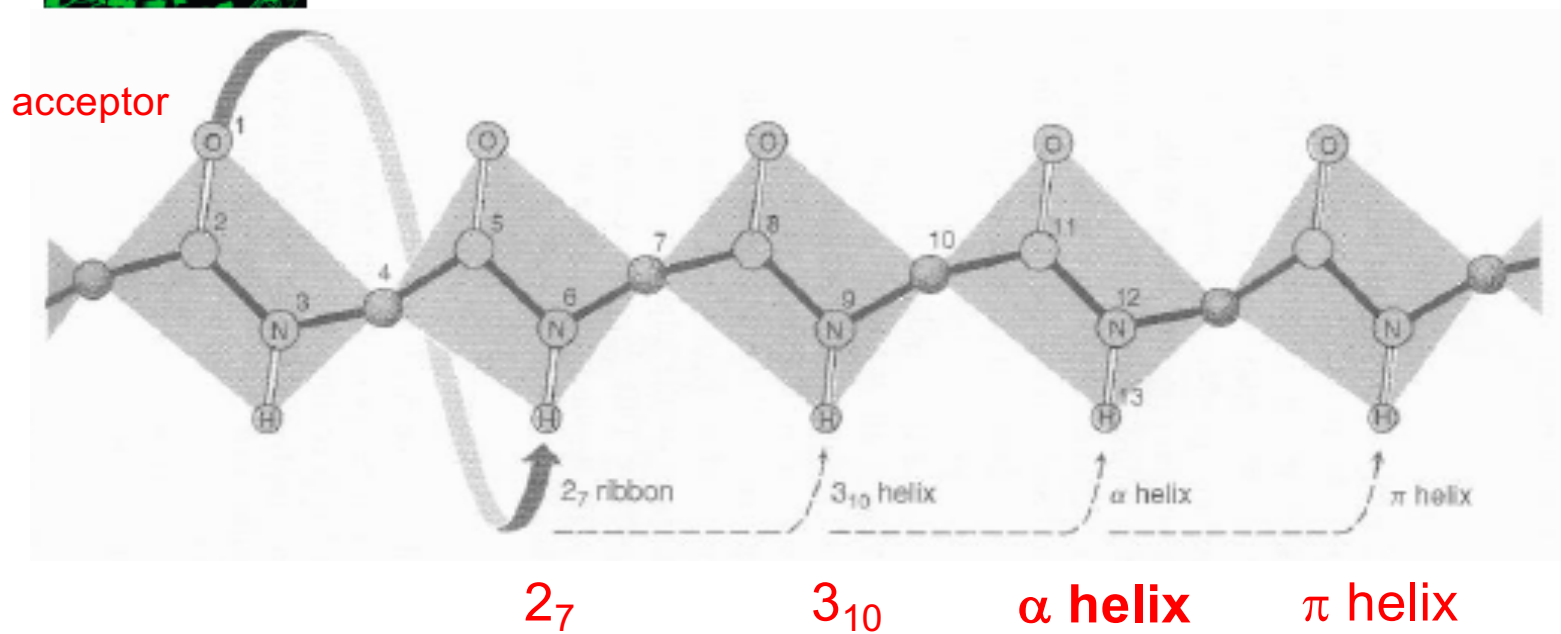
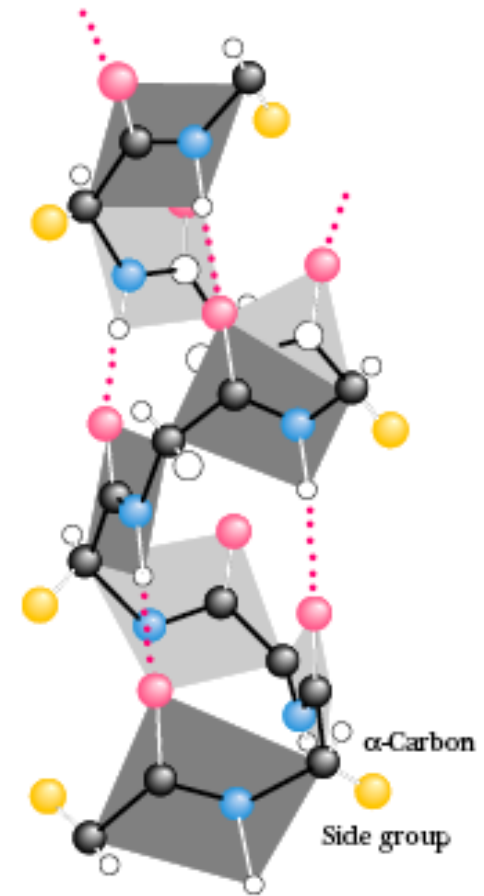


Fig 2-28



Linus Pauling and a model of the alpha helix.(1963)

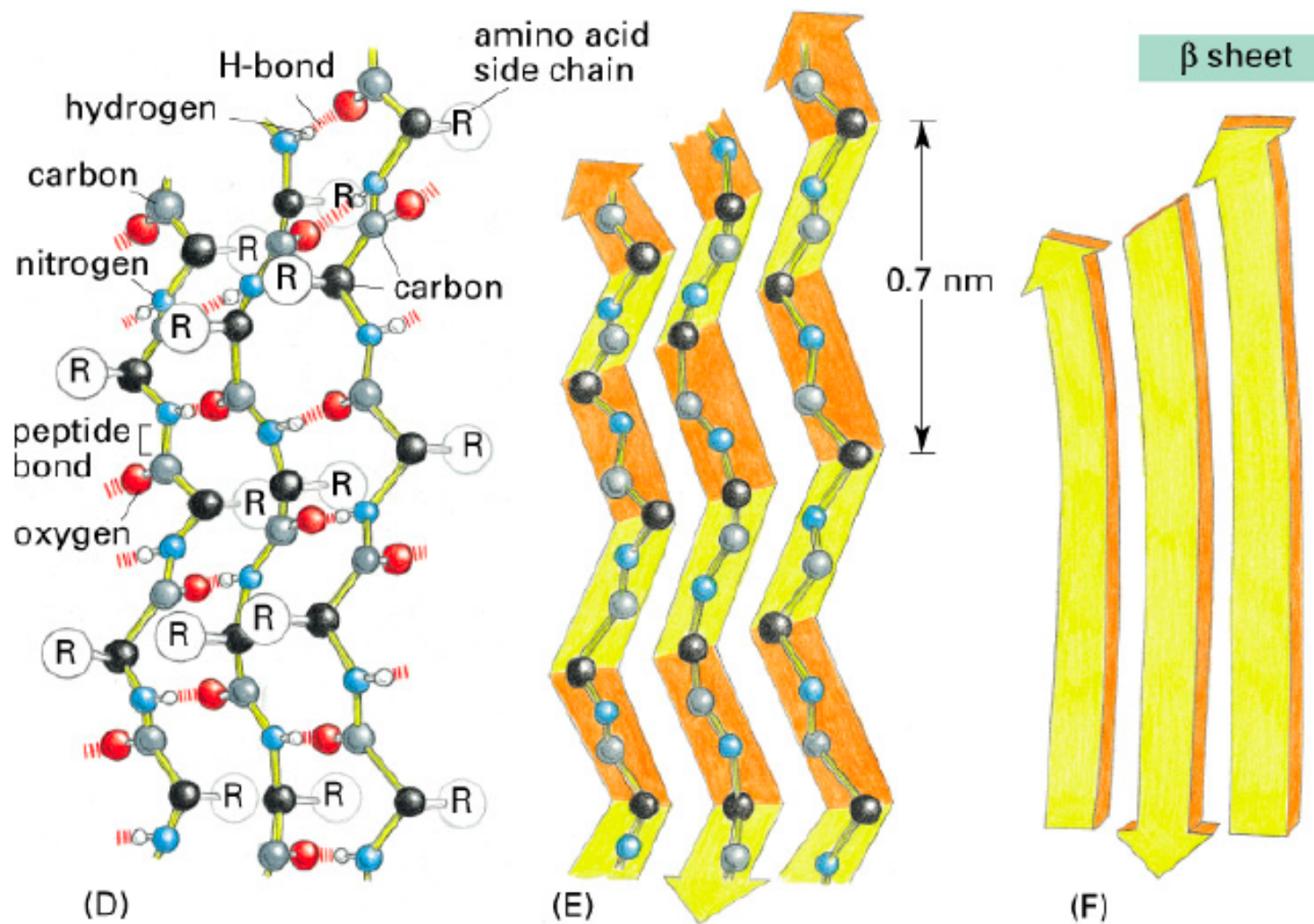


Figure 3-9 part 2 of 2. Molecular Biology of the Cell, 4th Edition.

Secondary structure

β -sheet: parallel or anti-parallel

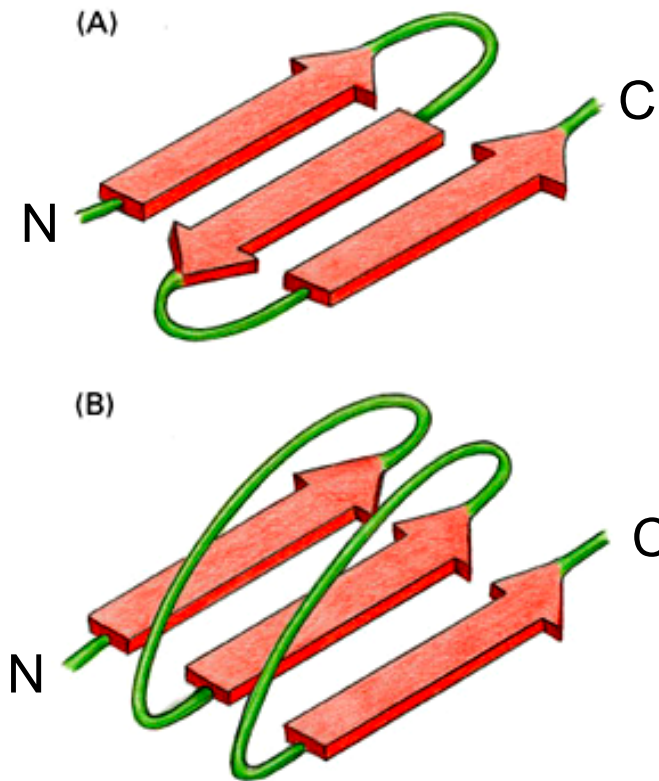


Figure 4-17 Essential Cell Biology, 2/e. (© 2004 Garland Science)

Secondary structure

Several strands (at least 2) make a sheet

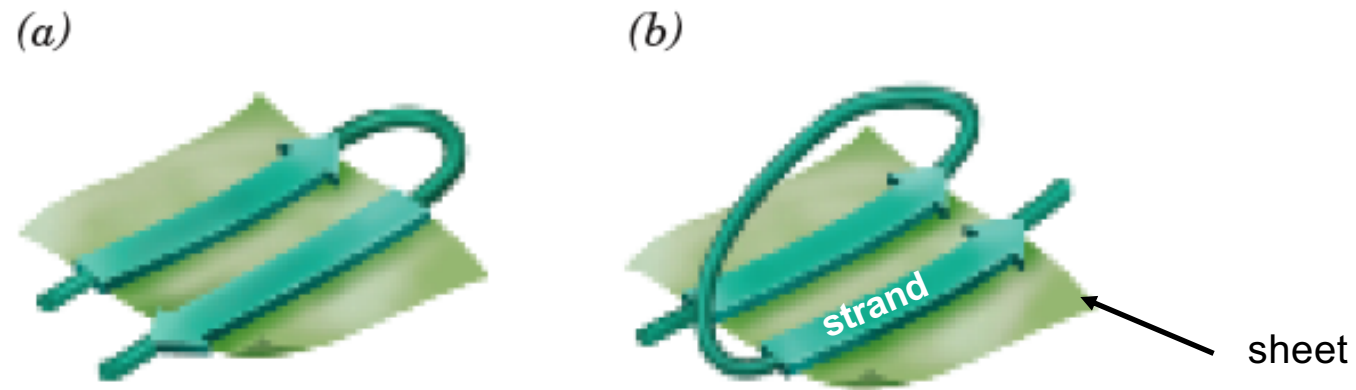
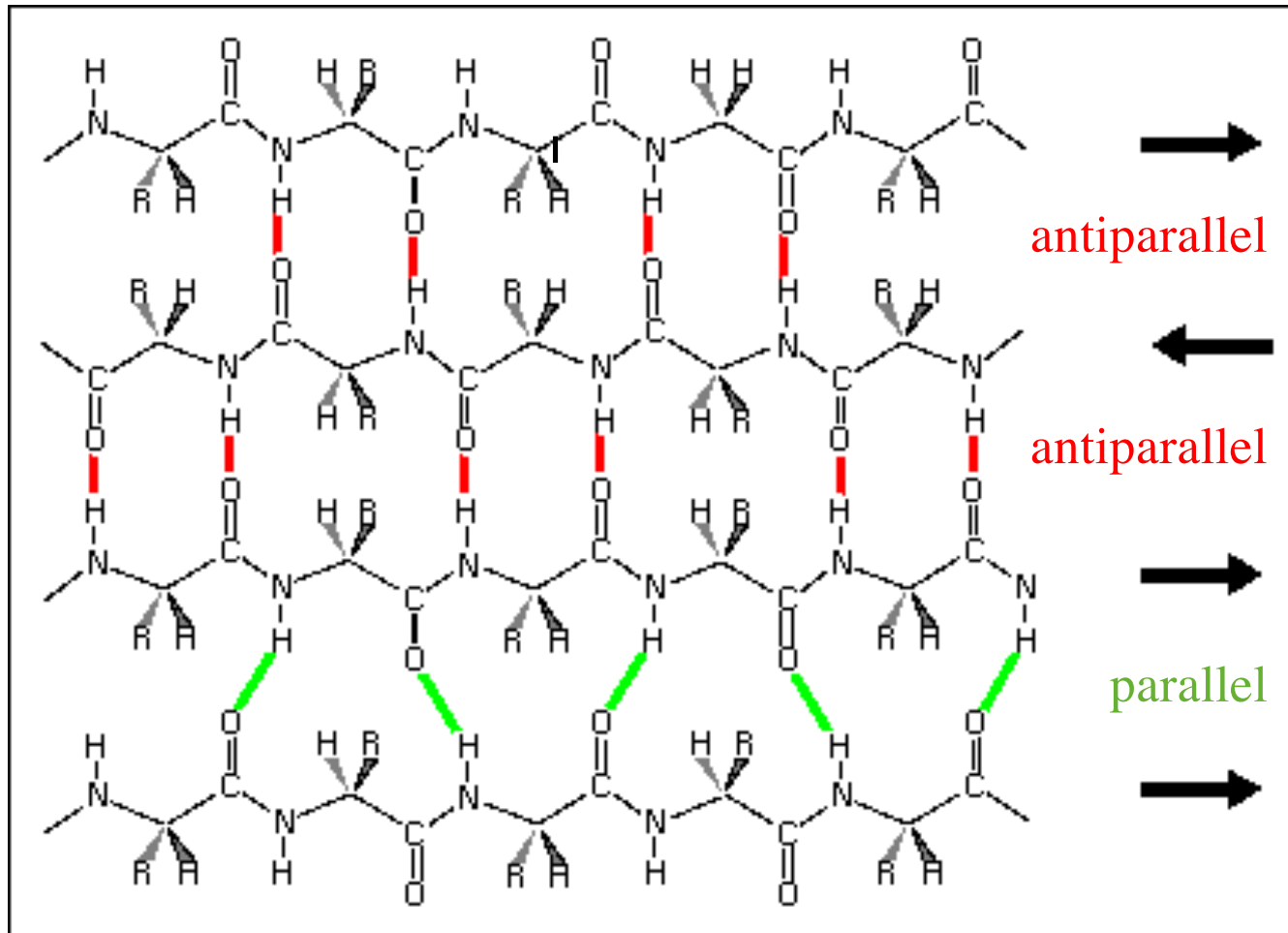


Figure 6-13 Connections between adjacent strands in β sheets. (a) Antiparallel strands may be connected by a small loop. (b) Parallel strands require a more extensive crossover connection. [After Richardson, J.S., *Adv. Protein Chem.* **34**, 196 (1981).]

Hydrogen bonds geometry :
anti-parallel β -sheets are more stable.



Directionality of the hydrogen bond

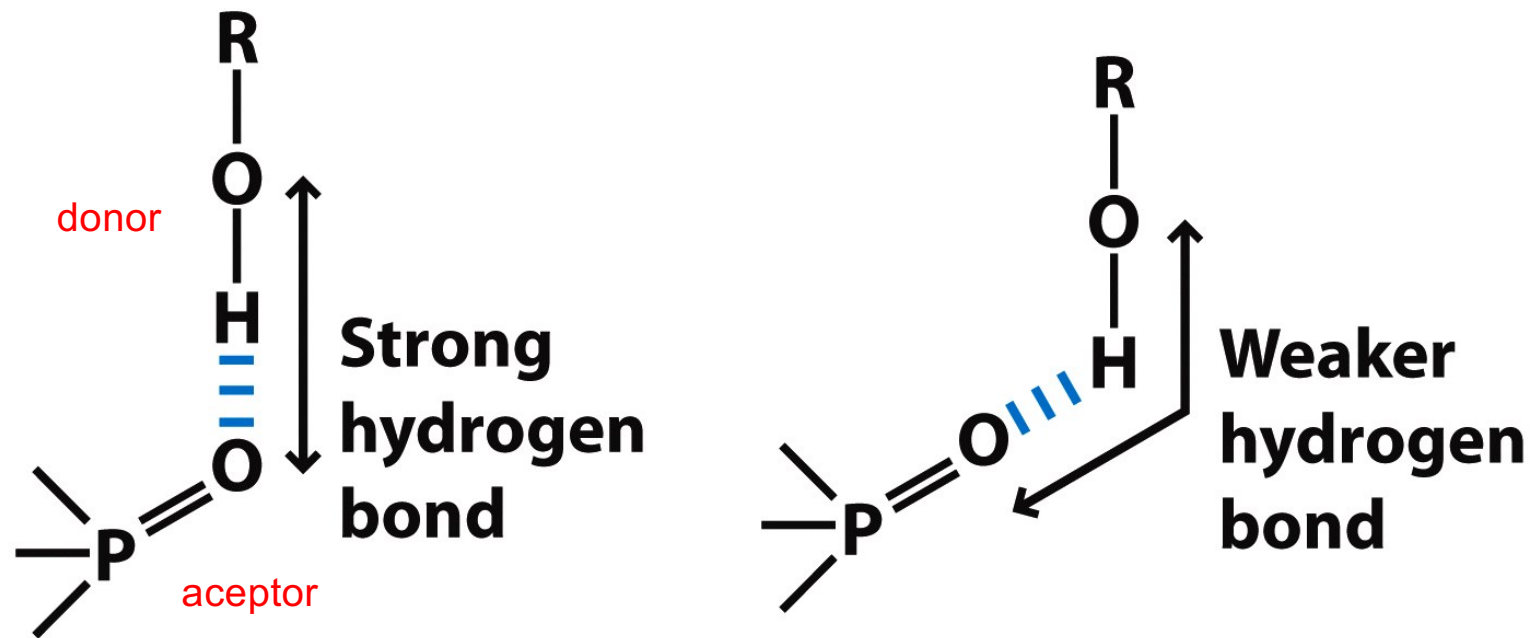
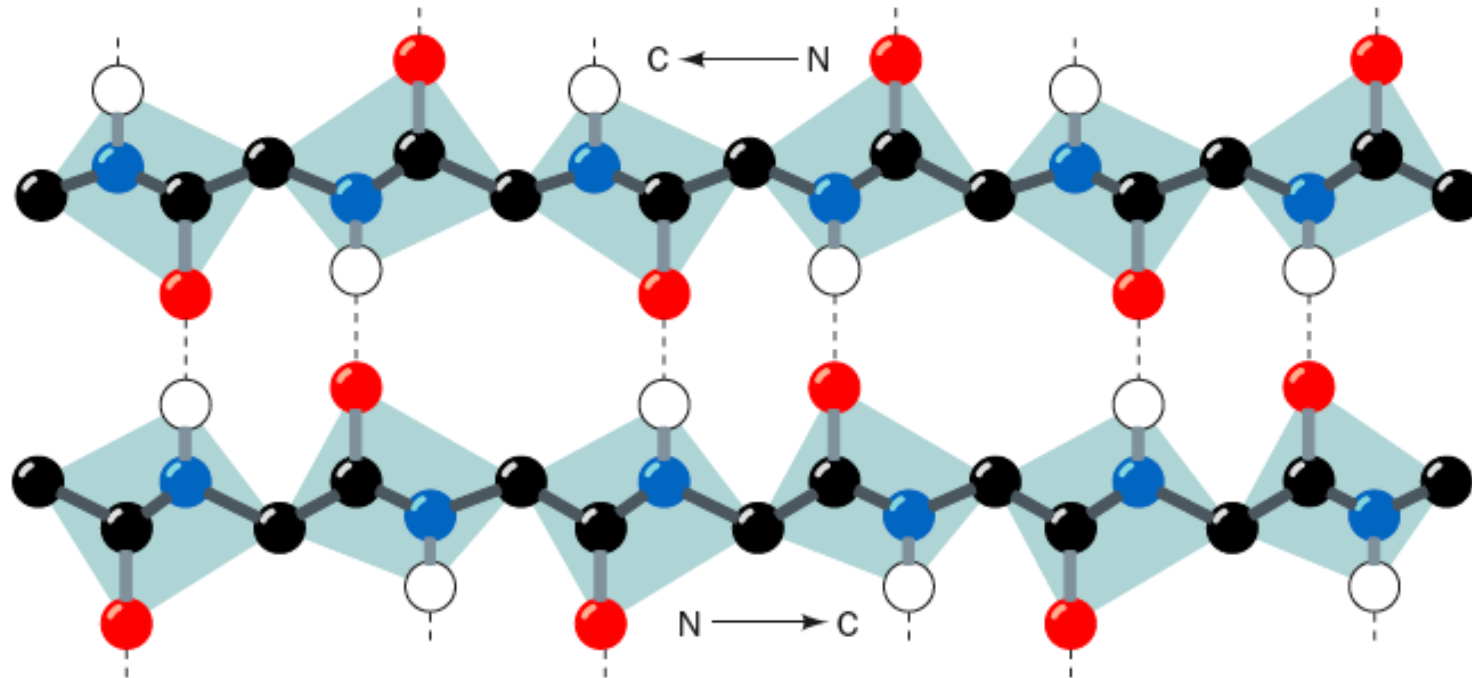


Figure 2-5
Lehninger Principles of Biochemistry, Fifth Edition
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The attraction between the partial electric charges is greatest when the three atoms involved in the bond (in this case O, H, and O) lie in a straight line. When the hydrogen-bonded moieties are structurally constrained (when they are parts of a single protein molecule, for example), this ideal geometry may not be possible and the resulting hydrogen bond is weaker.

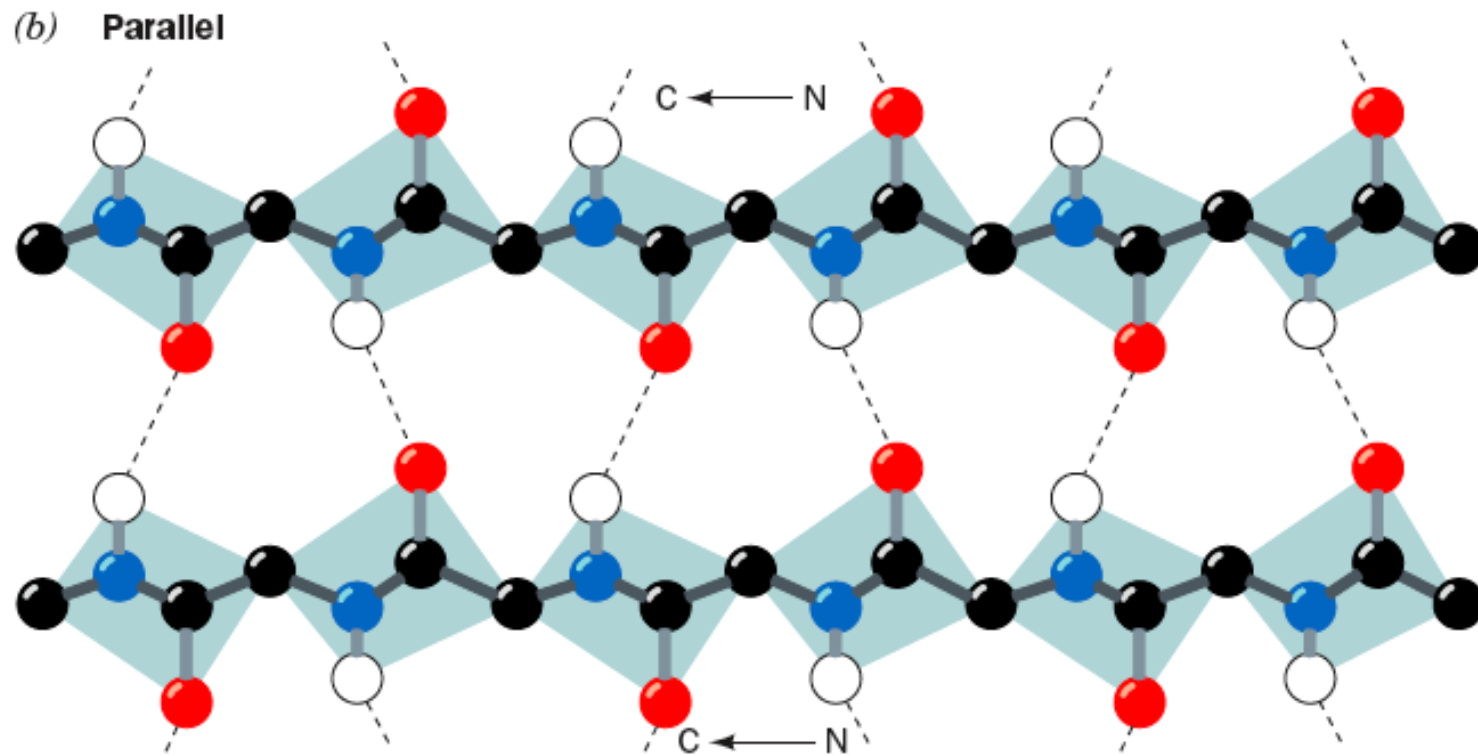
β -sheets

(a) **Antiparallel**



Voet & Voet

β -sheets



Voet & Voet

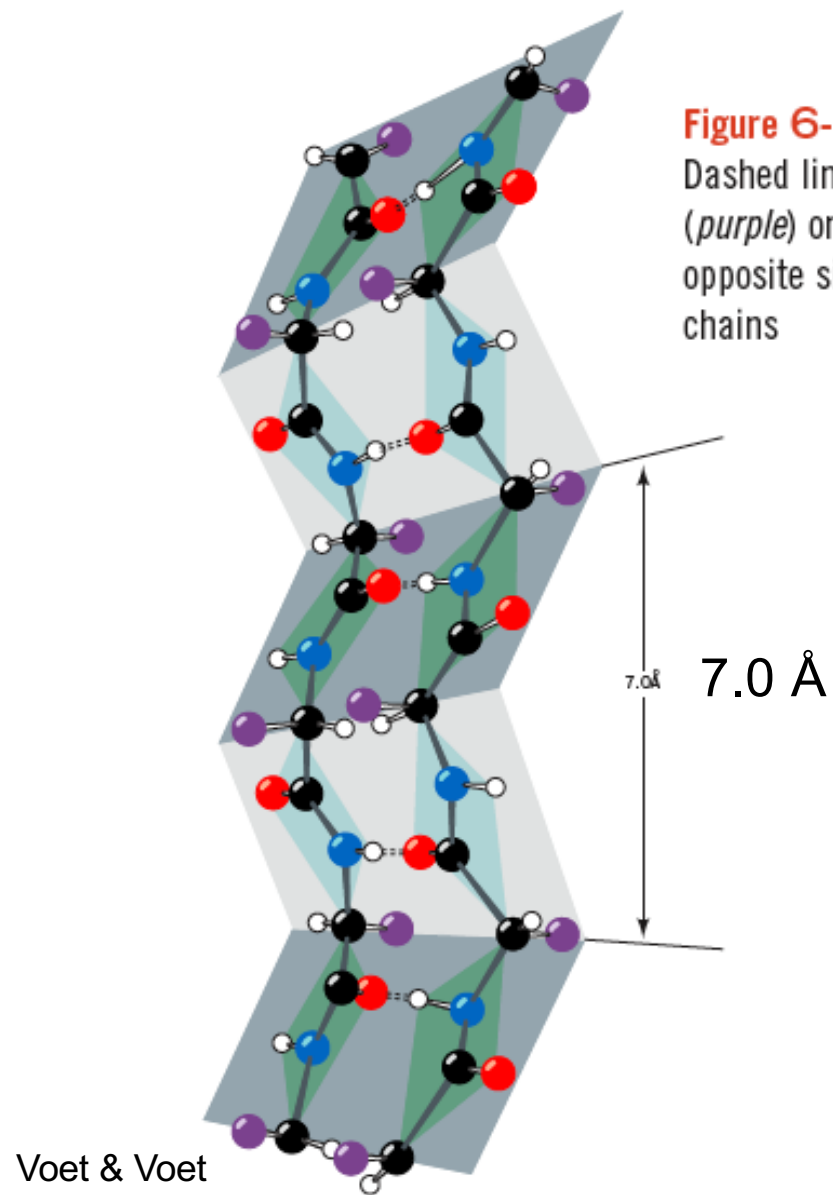


Figure 6-10 Pleated appearance of a β sheet. Dashed lines indicate hydrogen bonds. The R groups (*purple*) on each polypeptide chain alternately extend to opposite sides of the sheet and are in register on adjacent chains

β -sheet : feuillet plissé

antiparallel

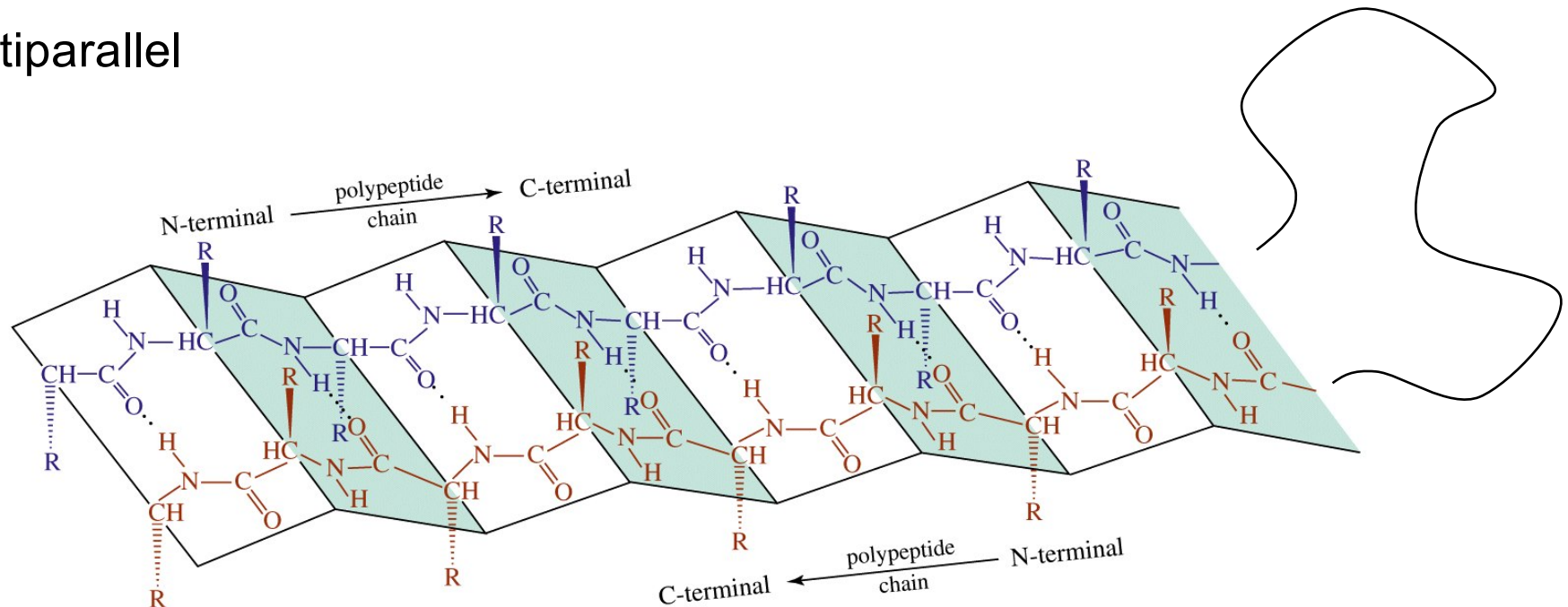


Figure 4-7 Concepts in Biochemistry, 3/e
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Human hemoglobin

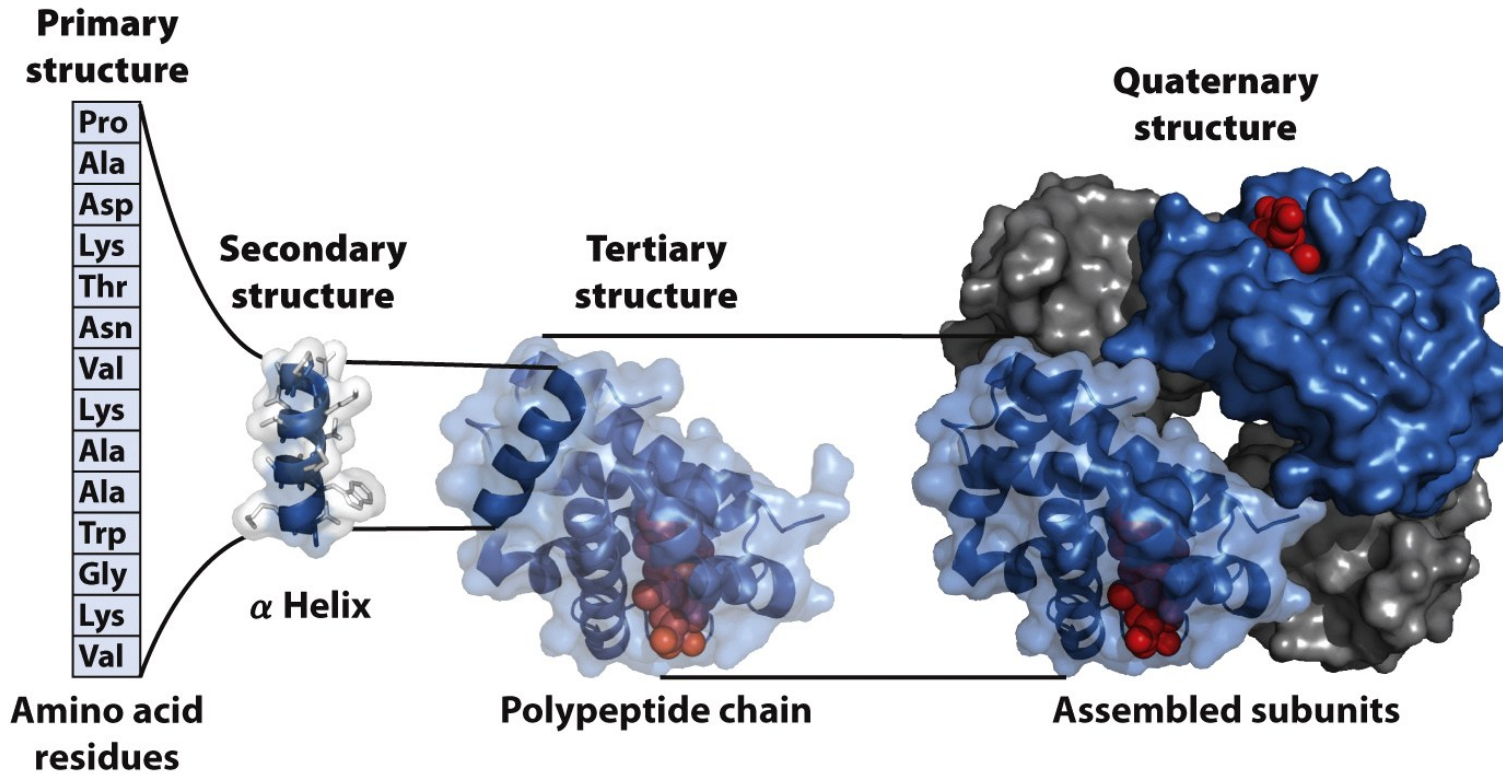
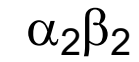


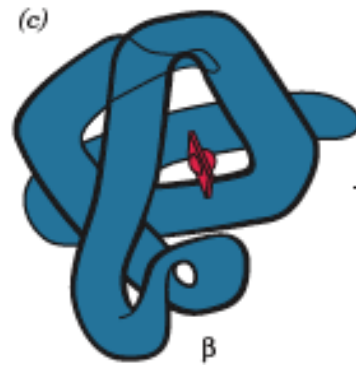
Figure 3-23

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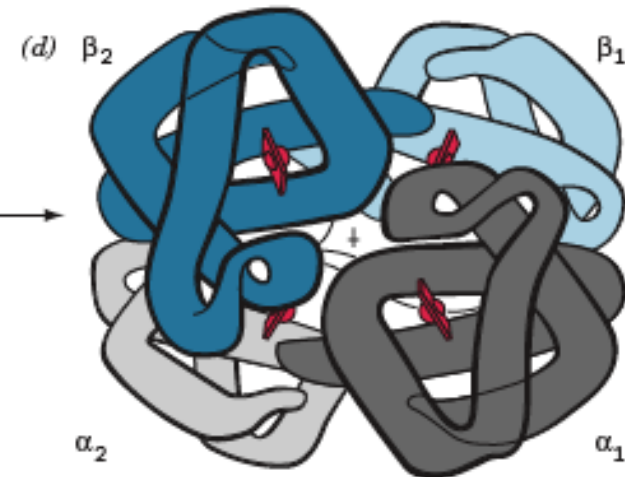
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Example : hemoglobin

(a) – Lys – Ala – His – Gly – Lys – Lys – Val – Leu – Gly – Ala –
 Primary structure (amino acid sequence in a polypeptide chain)



Tertiary structure:
 one complete protein chain
 (β chain of hemoglobin)

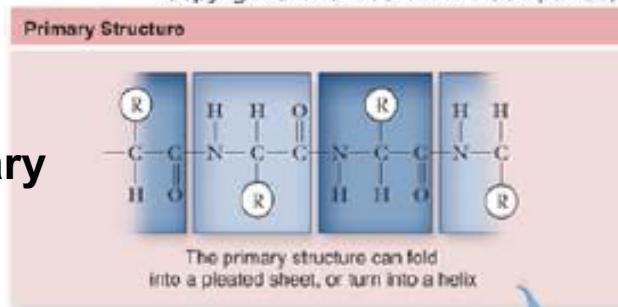


Quaternary structure:
 the four separate chains
 of hemoglobin assembled
 into an oligomeric protein

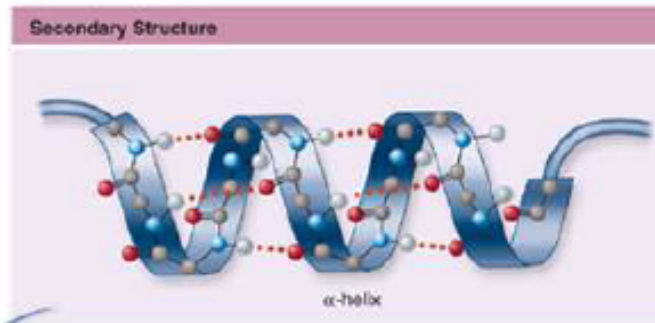
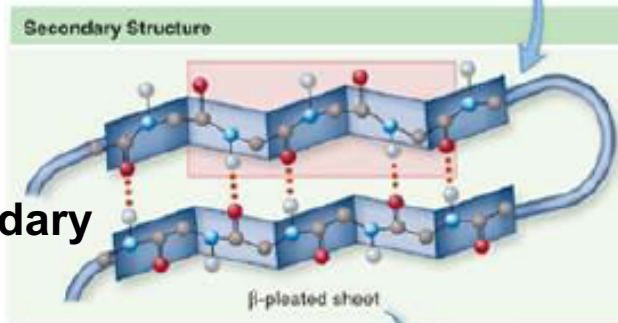
Example : hemoglobin

Protein structure

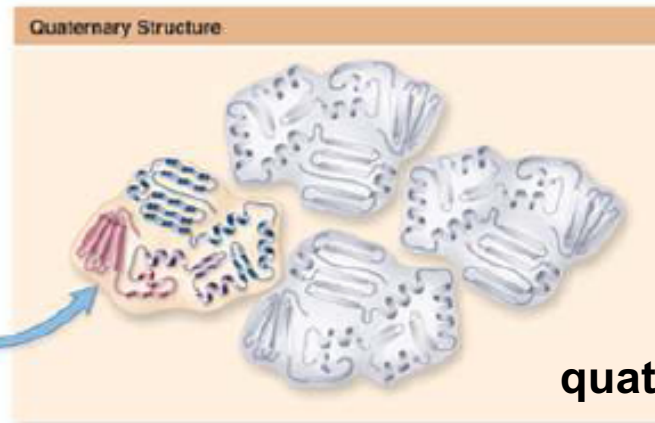
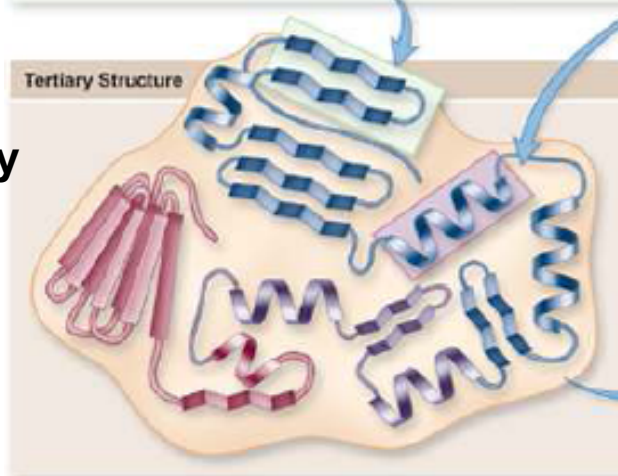
primary



secondary



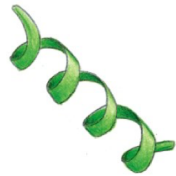
tertiary



quaternary

This protein has

3 α helices



and

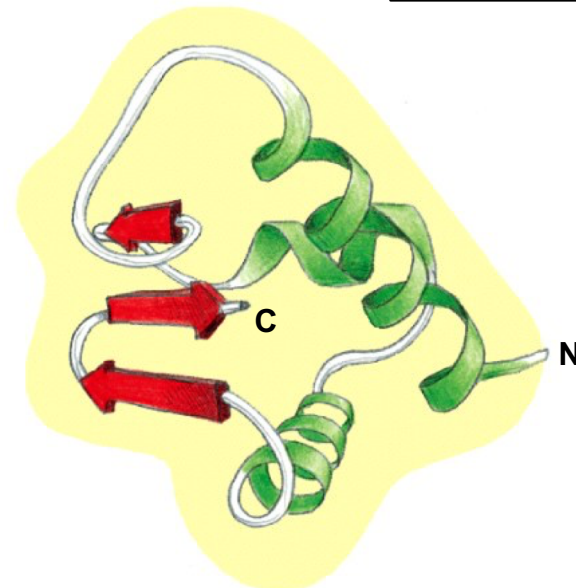
1 β sheet



made of

3 β strands.

Tertiary structure



Proteins can be

- soluble in the cytosol
- embedded in a membrane

**Membrane
bilayer**

Red blood cell
cytoplasm

Soluble protein :
hemoglobin

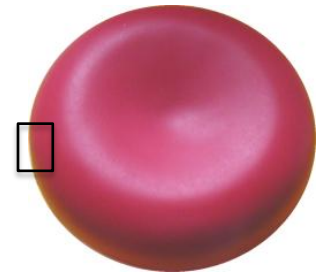
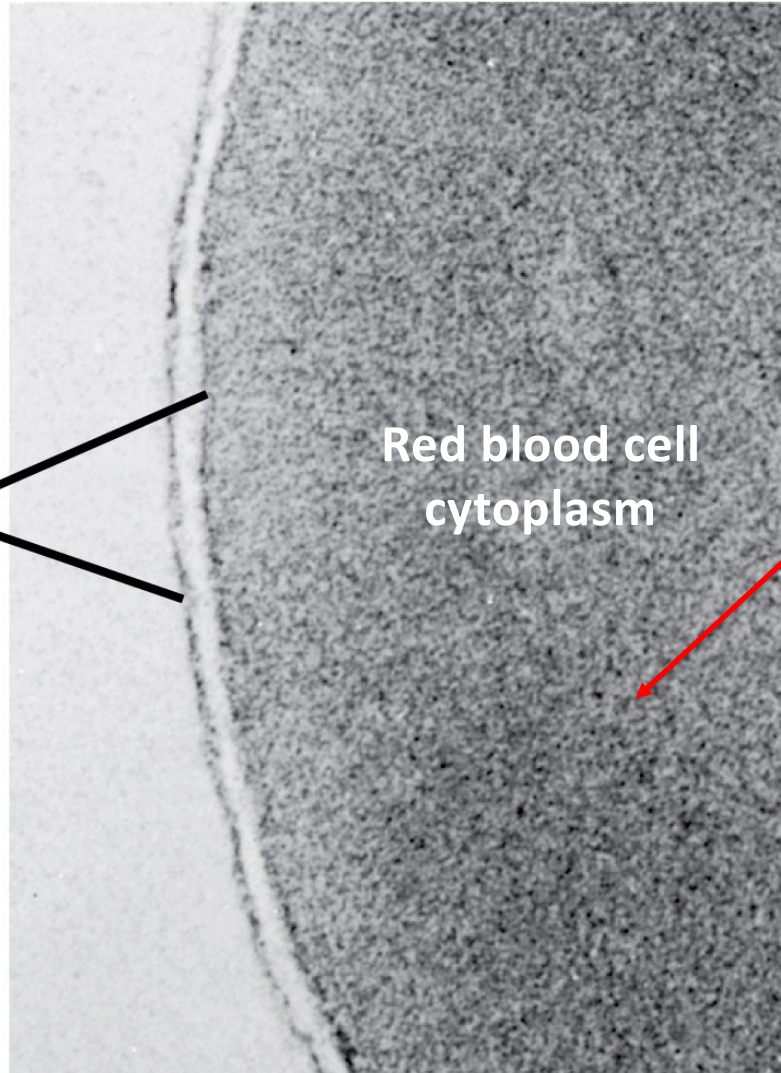


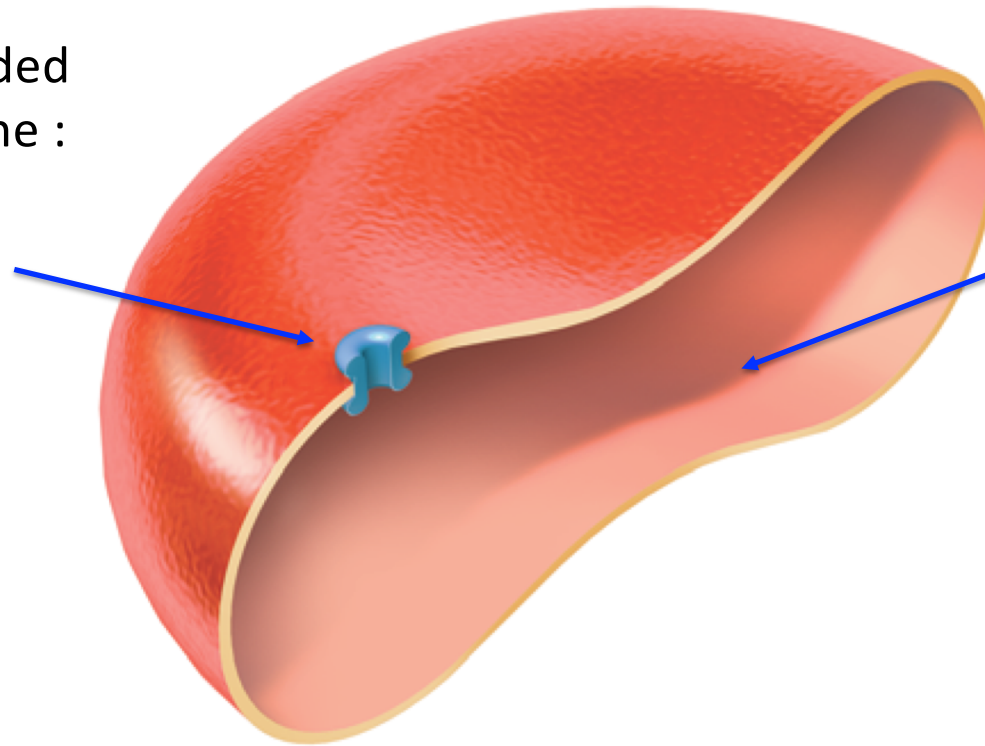
Figure 11-1

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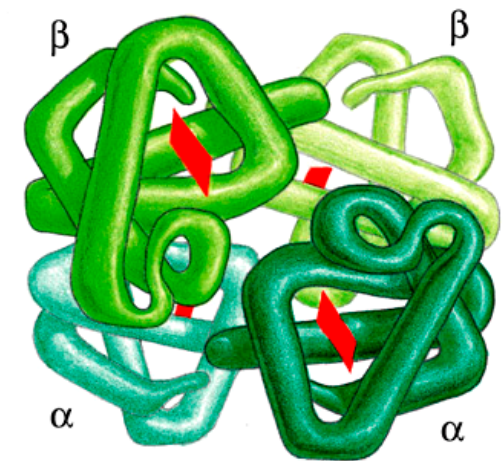
Protein embedded
in the membrane :

Aquaporin 1



Protein soluble
in the cytosol :

Hemoglobin



**Proteins often composed of several subunits:
-> either of identical subunits**

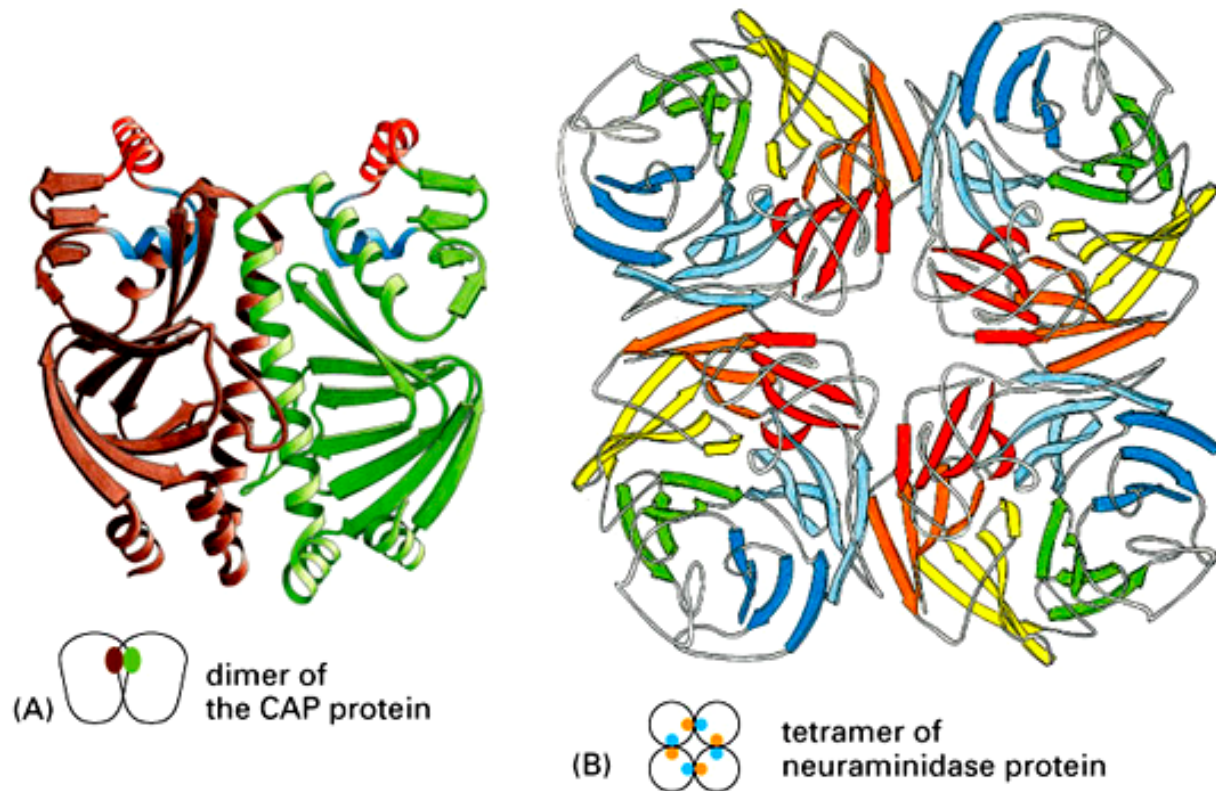
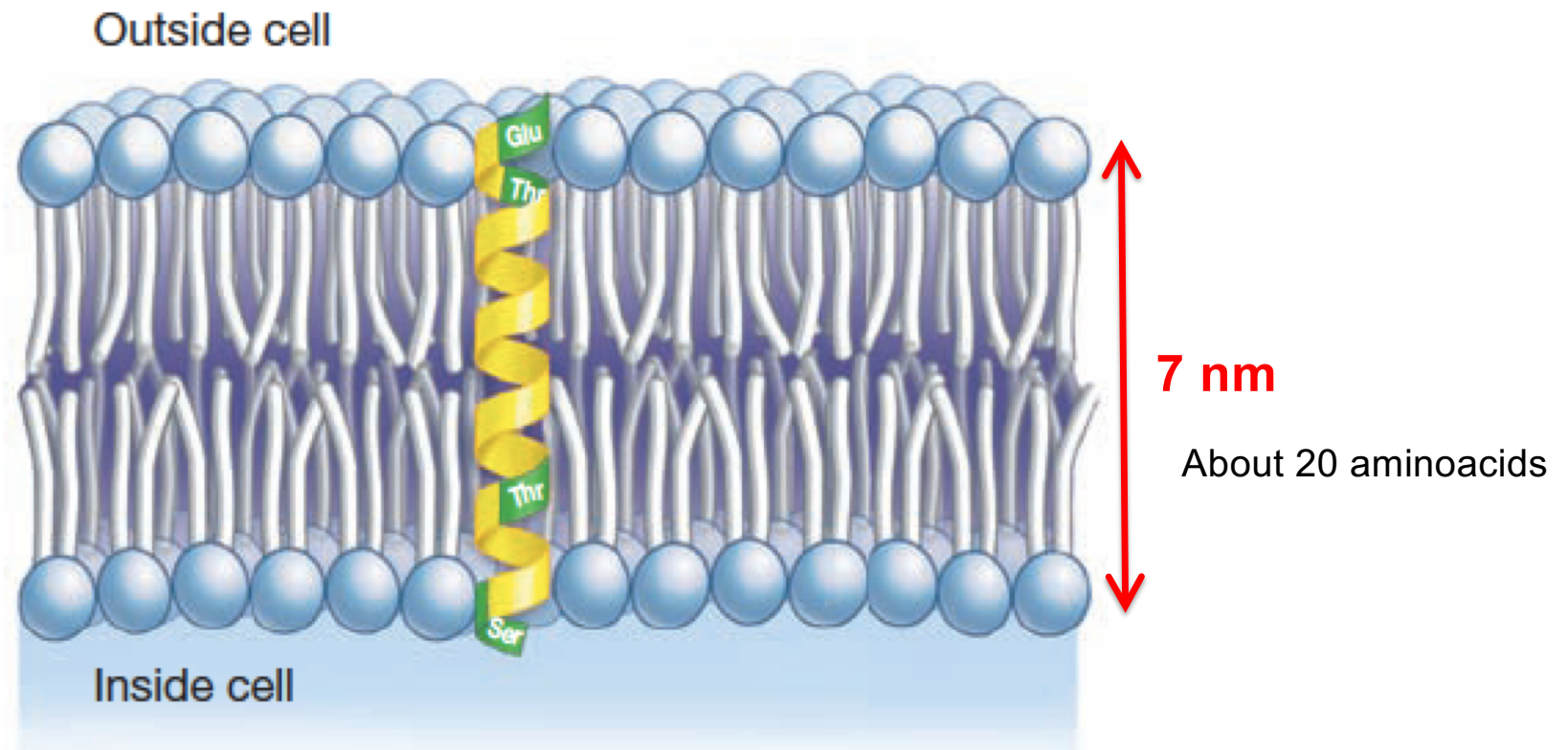


Figure 4-22 Essential Cell Biology, 2/e. (© 2004 Garland Science)

Transmembrane domain :



Always an α helix .

Bacteriorhodopsin :

Protein with 7 TM

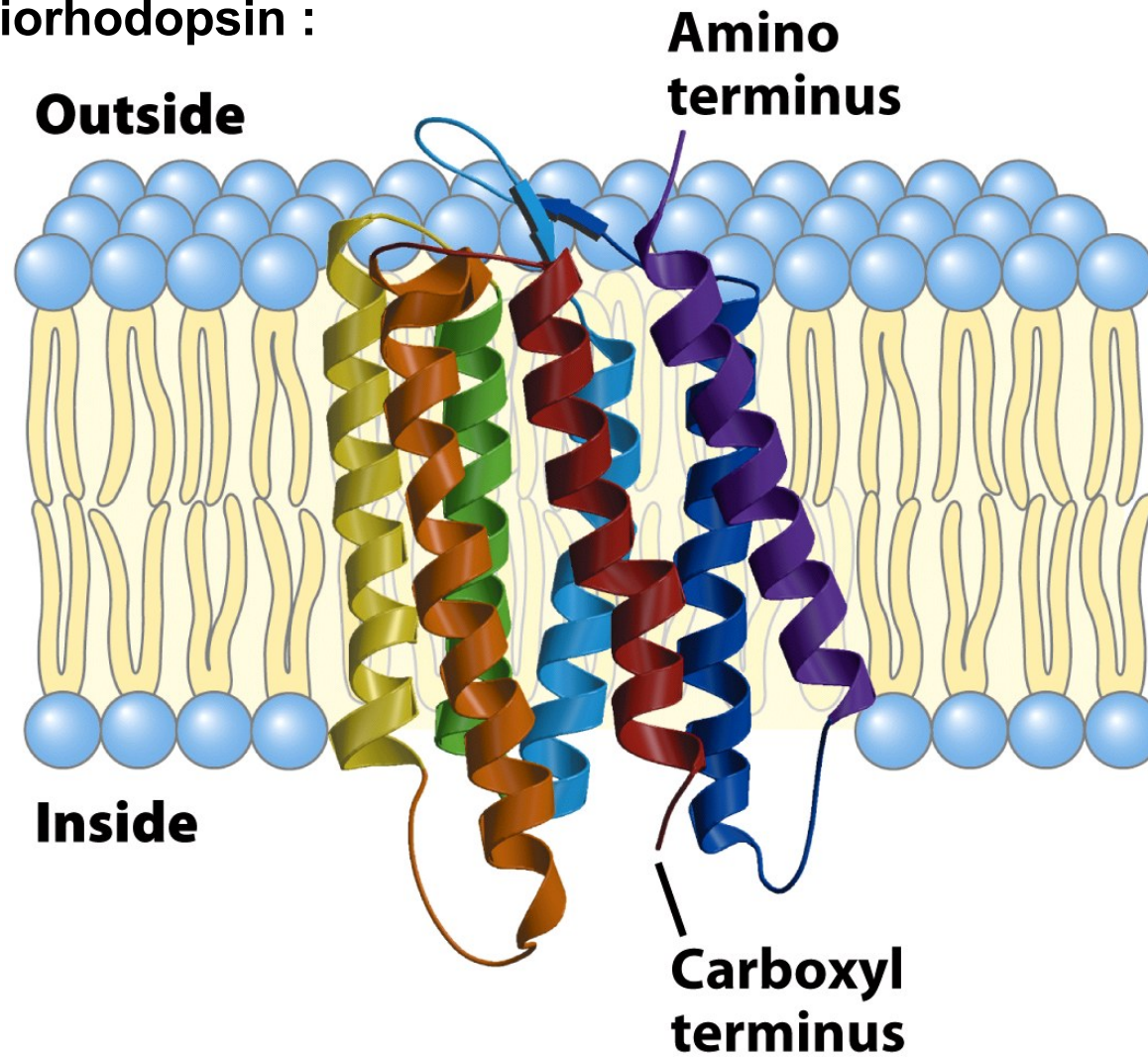
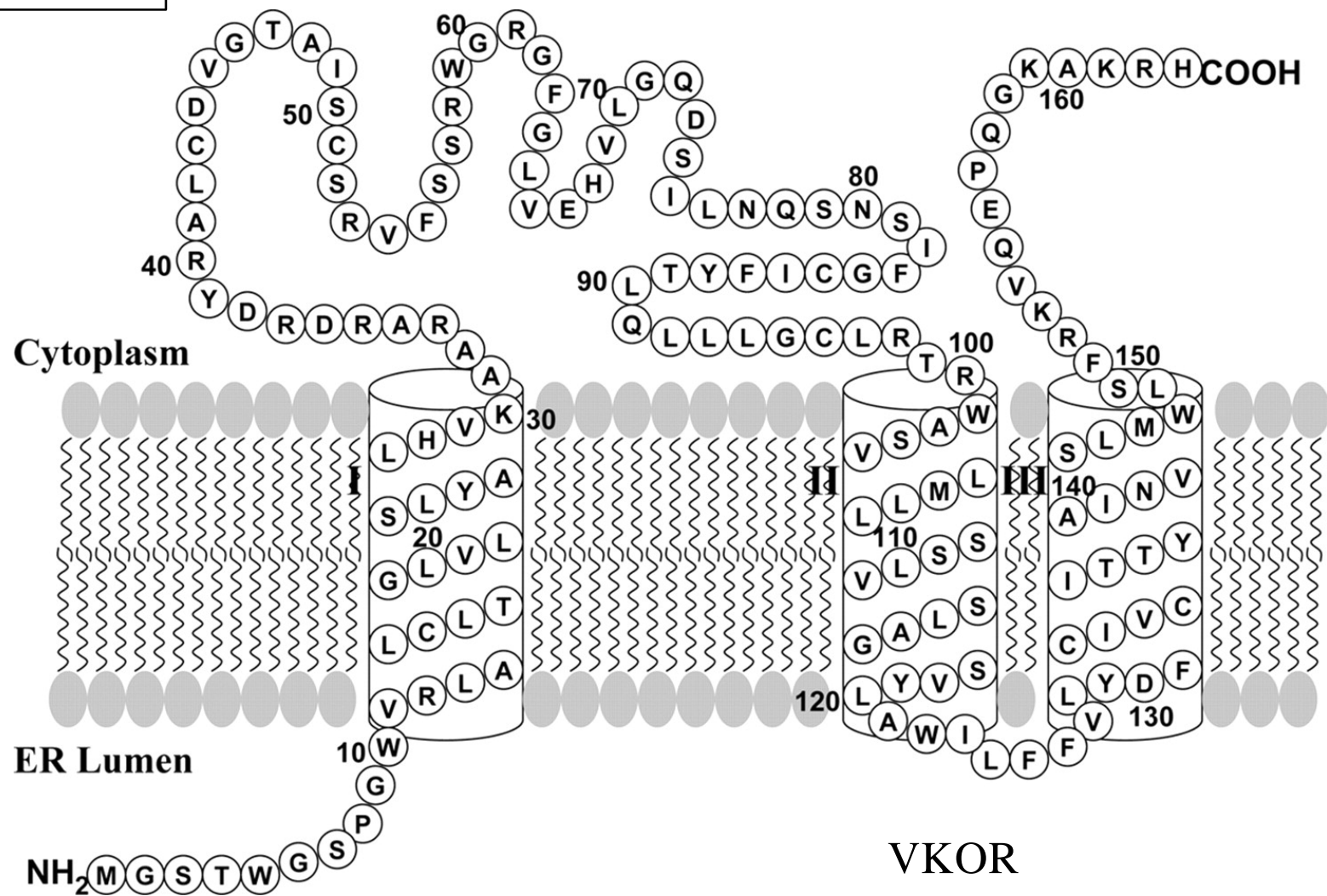


Figure 11-9
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Protein with 3 TM



Proposed structure of GLUT1

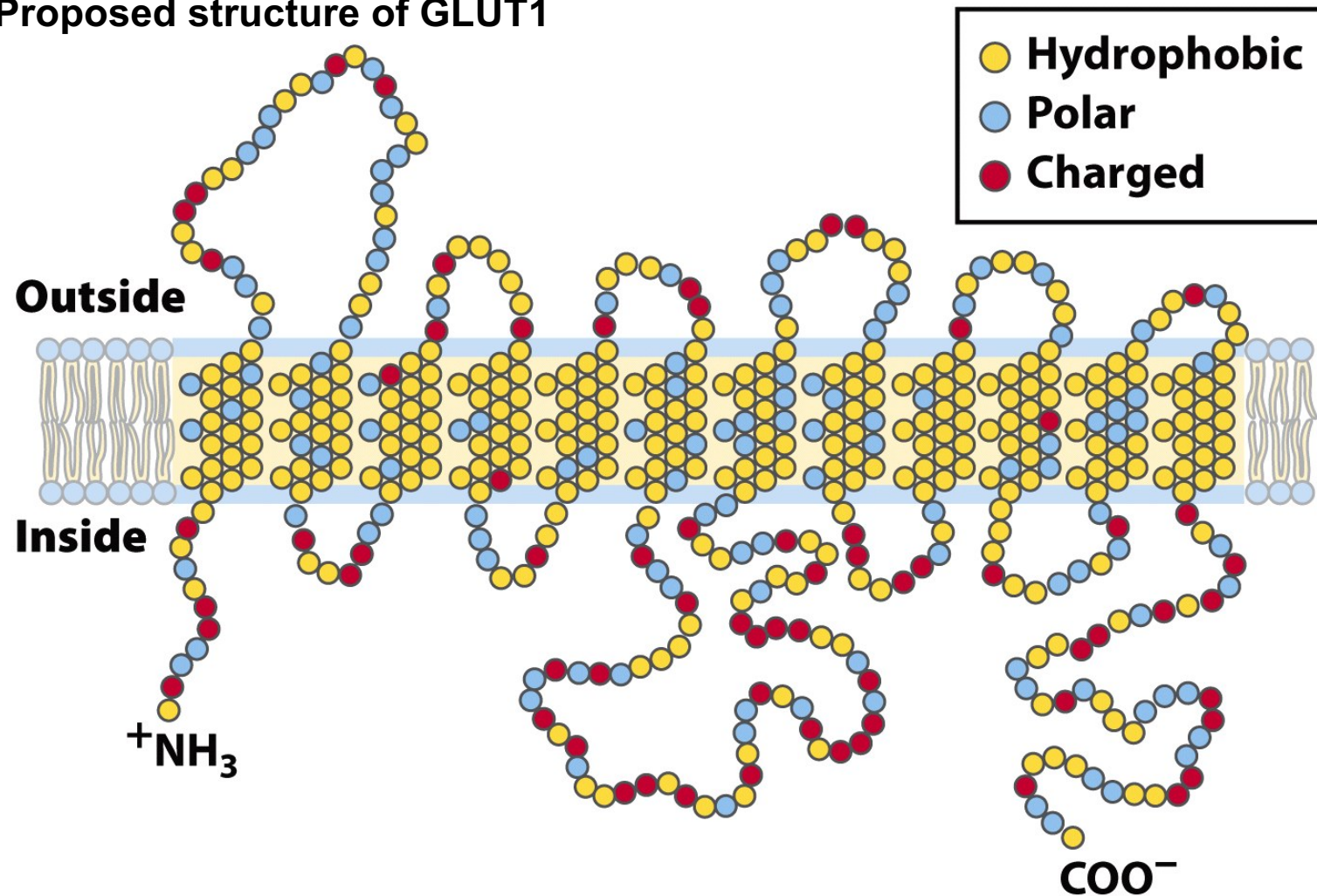


Figure 11-29a
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Hydropathy scale

Quantitative scale

Table 6-2 Hydropathy Scale for Amino Acid Side Chains

Side Chain	Hydropathy
Ile	4.5
Val	4.2
Leu	3.8
Phe	2.8
Cys	2.5
Met	1.9
Ala	1.8
Gly	-0.4
Thr	-0.7
Ser	-0.8
Trp	-0.9
Tyr	-1.3
Pro	-1.6
His	-3.2
Glu	-3.5
Gln	-3.5
Asp	-3.5
Asn	-3.5
Lys	-3.9
Arg	-4.5

Source: Kyte, J. and Doolittle, R.F., *J. Mol. Biol.* **157**, 110 (1982).

Hydropathy scale

Table 1.2 A hydrophobicity scale for amino acids

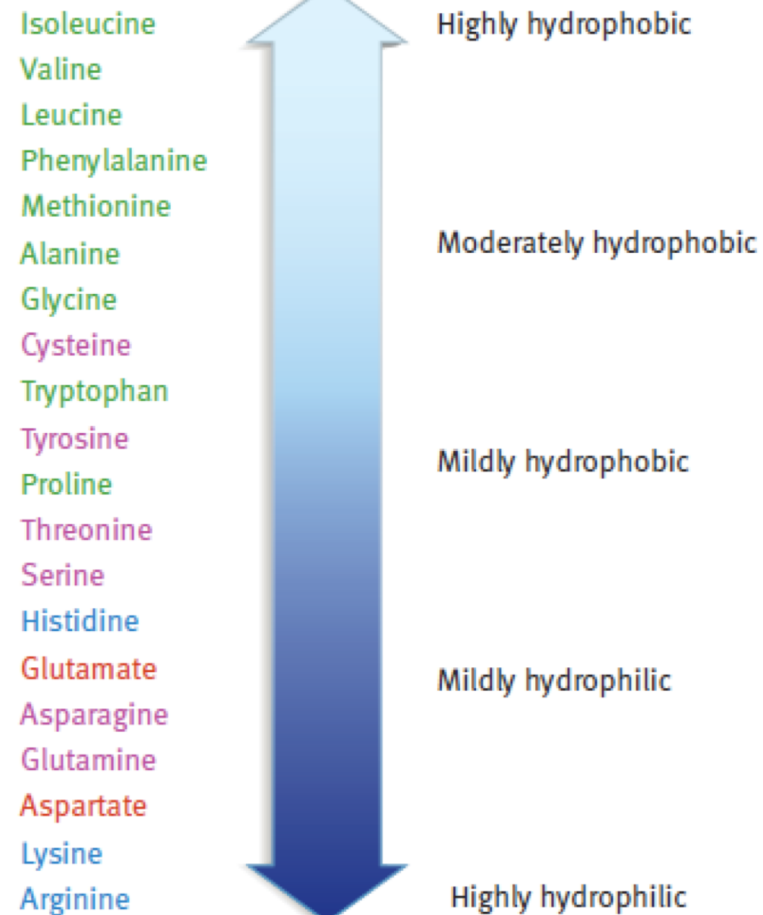
Amino acid	Transfer free energy (kJ mol ⁻¹)
Phe (F)	15.5
Met (M)	14.2
Ile (I)	13.0
Leu (L)	11.7
Val (V)	10.9
Cys (C)	8.4
Trp (W)	7.9
Ala (A)	6.7
Thr (T)	5.0
Gly (G)	4.2
Ser (S)	2.5
Pro (P)	-0.8
Tyr (Y)	-2.9
His (H)	-12.5
Gln (Q)	-17.1
Asn (N)	-20.1
Glu (E)	-34.3
Lys (K)	-36.8
Asp (D)	-38.5
Arg (R)	-51.4

Hydropathy scale

Purely qualitative

TABLE 3.1 **How Amino Acids Interact with Water**

20 amino acids are ranked according to how likely they are to interact with water. Color codes are based on Figure 3.3.



Transbilayer disposition of glycophorin in an erythrocyte

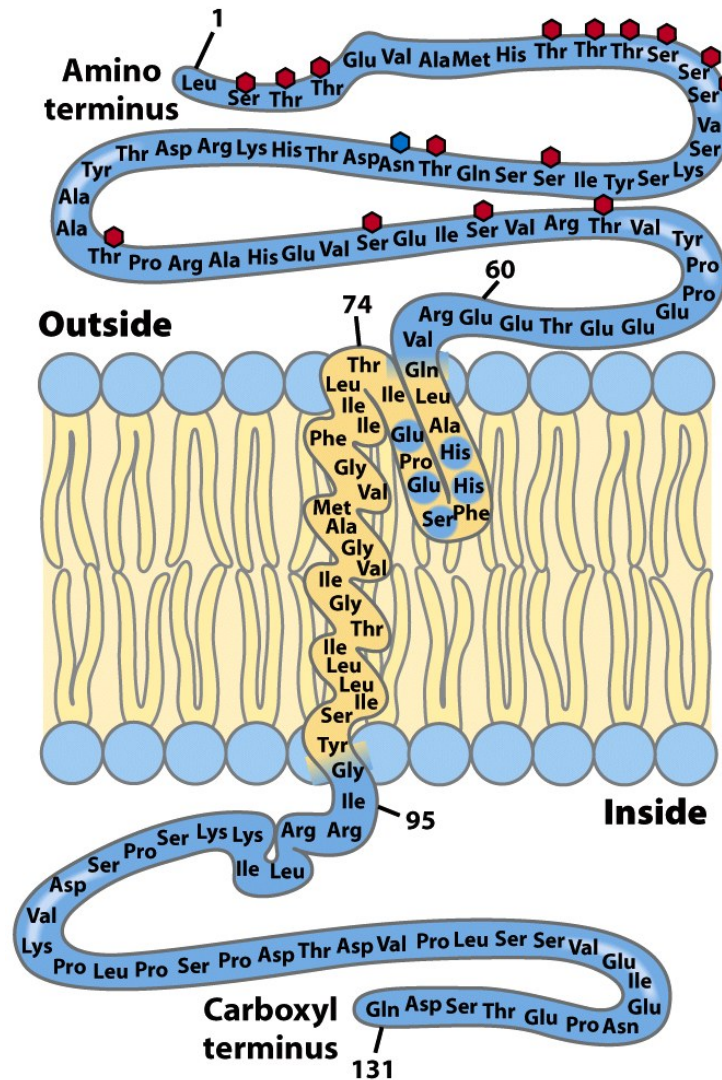


Figure 11-7
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Hydropathy profile

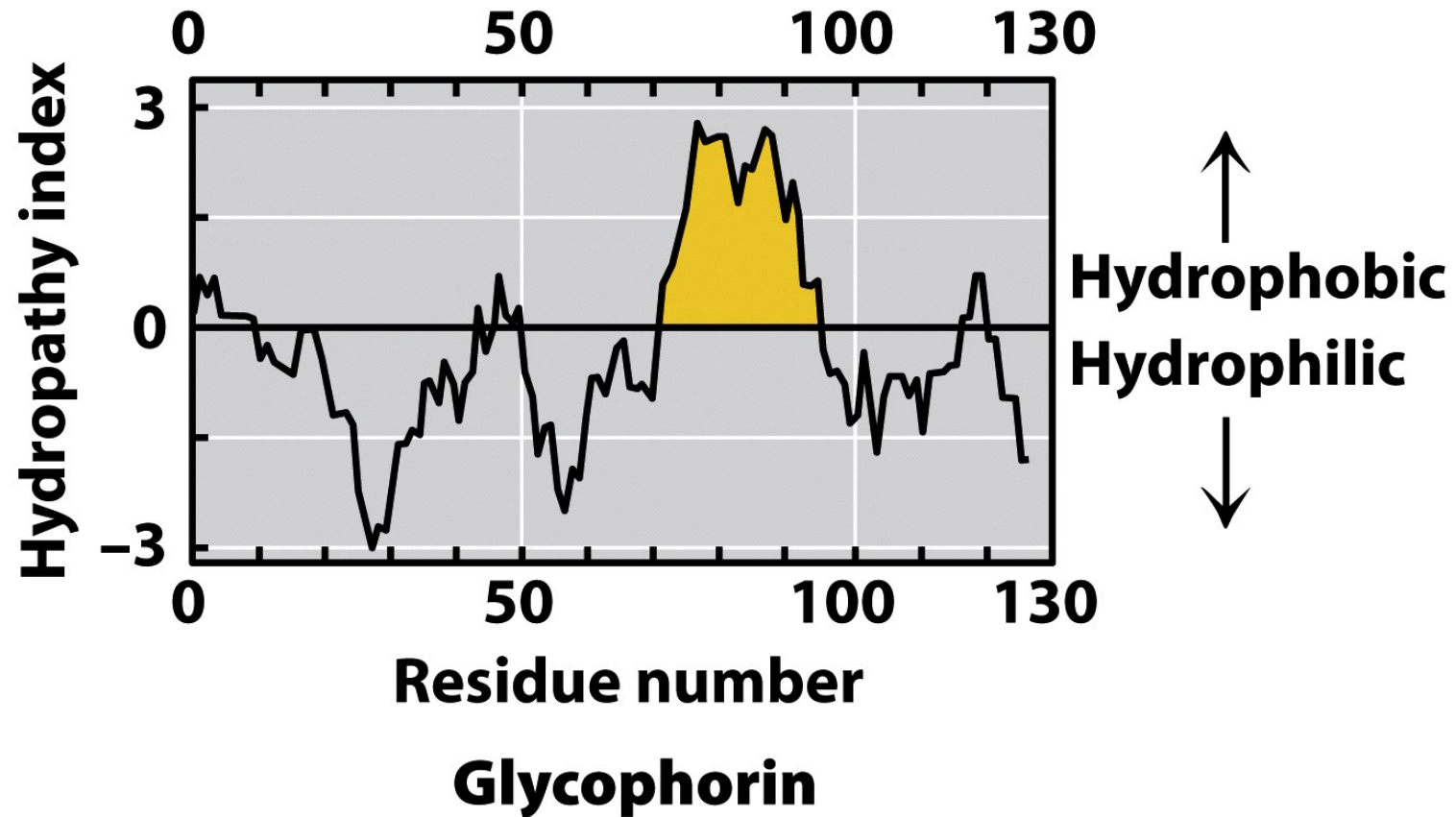
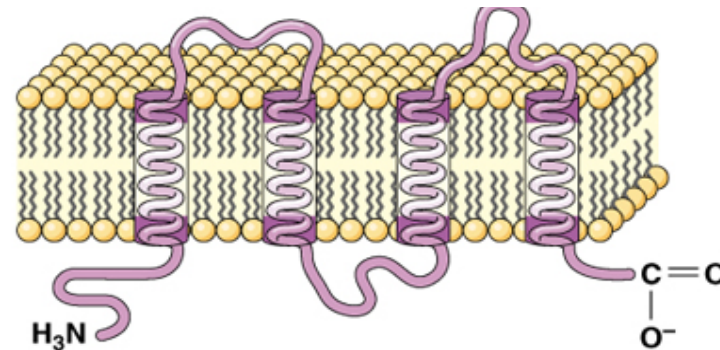
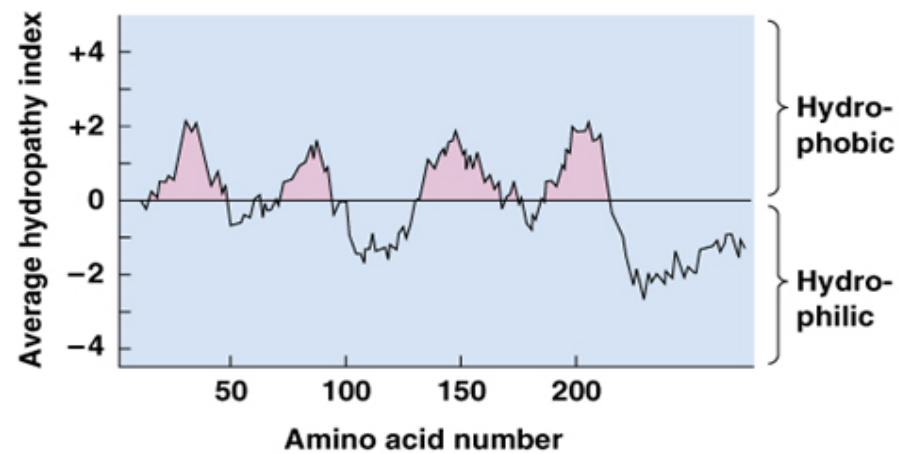


Figure 11-11a
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Hydropathy profile

Textbook examples are oversimplified.



(b)

Example of **connexin**: 4 positive peaks from hydropathy analysis predicts the protein has 4 transmembrane domains.

Hydropathy profile

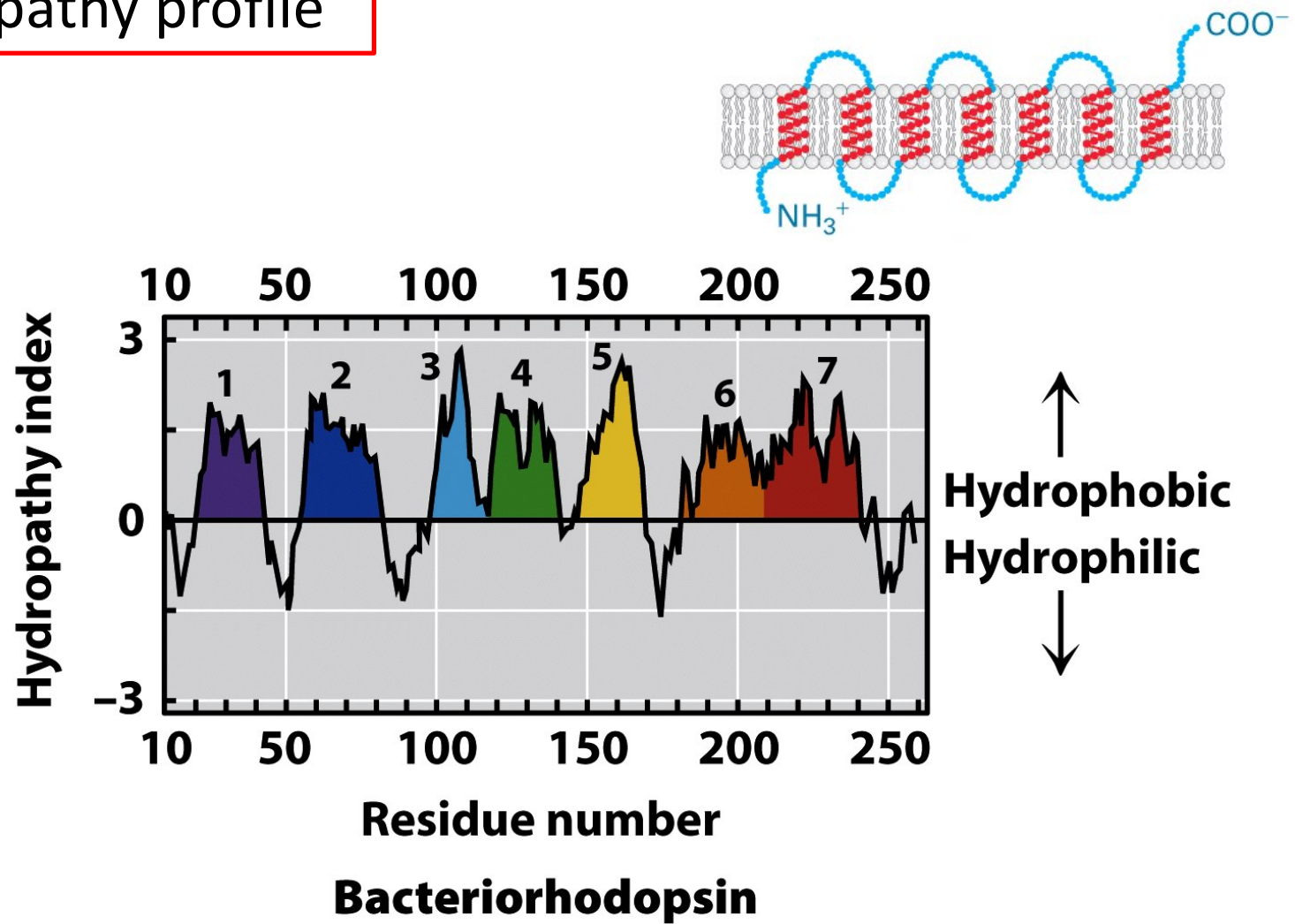


Figure 11-11b
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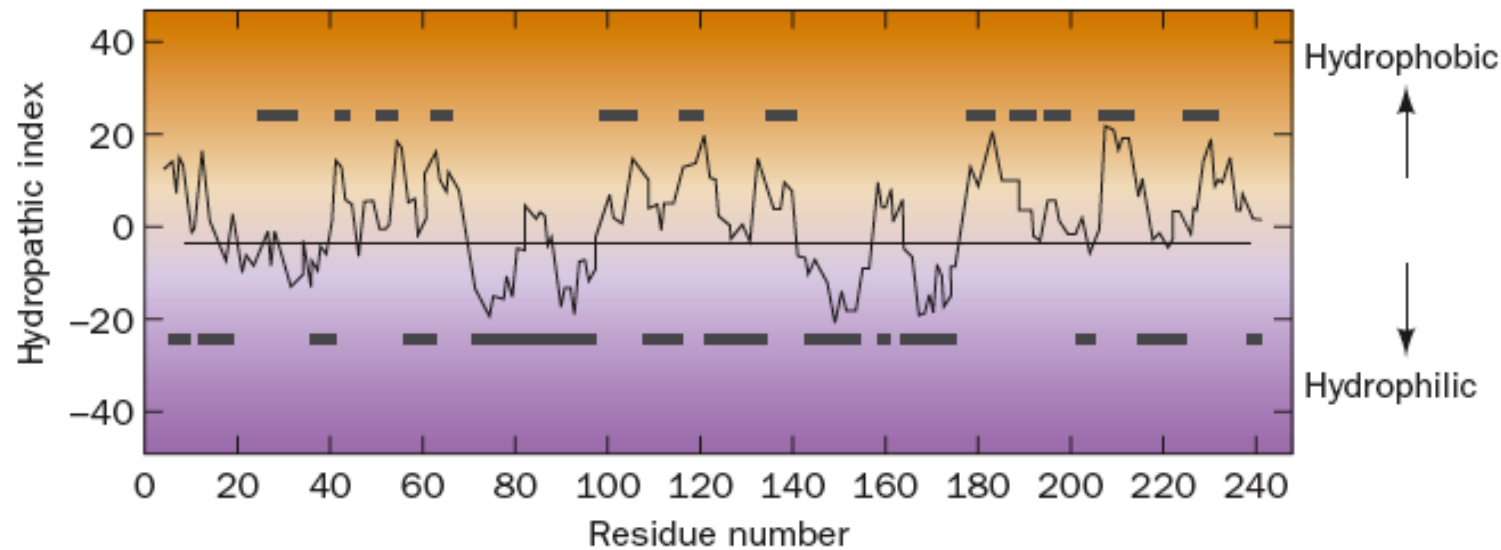
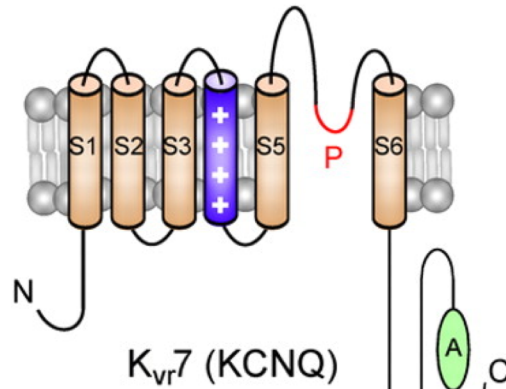
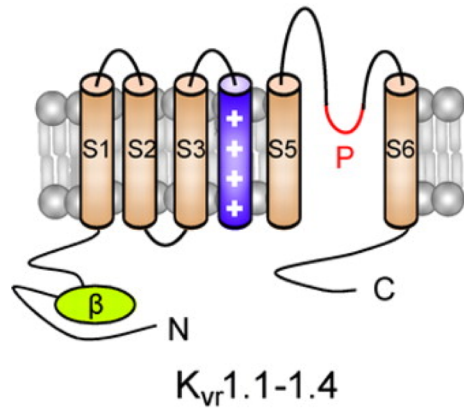
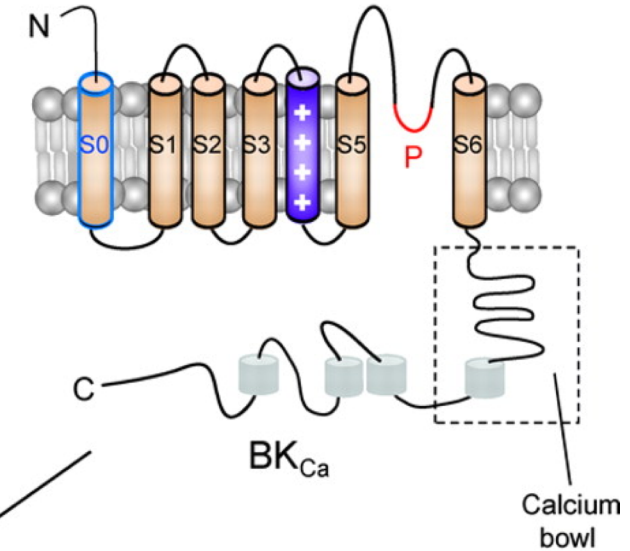


Figure 6-35 A hydropathic index plot for bovine chymotrypsinogen. The sum of the hydropathies of nine consecutive residues is plotted versus residue sequence number. A large positive hydropathic index indicates a hydrophobic region of the polypeptide, whereas a large negative value indicates a hydrophilic region. The upper bars denote the protein's interior regions, as determined by X-ray crystallography, and the lower bars denote the protein's exterior regions. [After Kyte, J. and Doolittle, R.F., *J. Mol. Biol.* **157**, 111 (1982).]

Voltage-gated K⁺ channels (K_{ir})

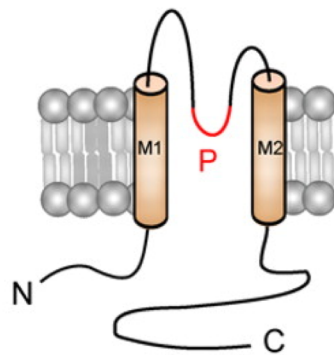


Calcium-activated K⁺ channels (K_{Ca})

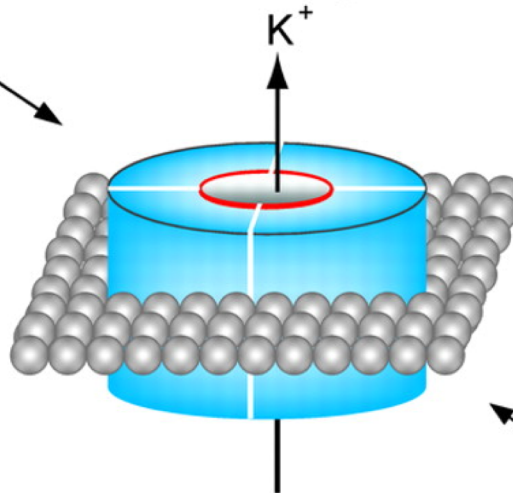


4 families

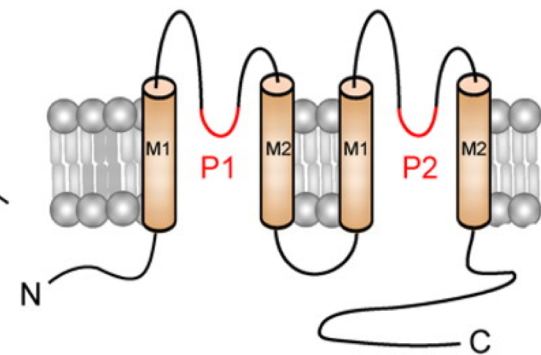
(75 genes)



Inward rectifier K⁺ channels (K_{ir})



Hyperpolarization
decrease cell excitability



"Leak" or background K⁺ channels