E. coli maintains its plasma membrane fluidity constant.

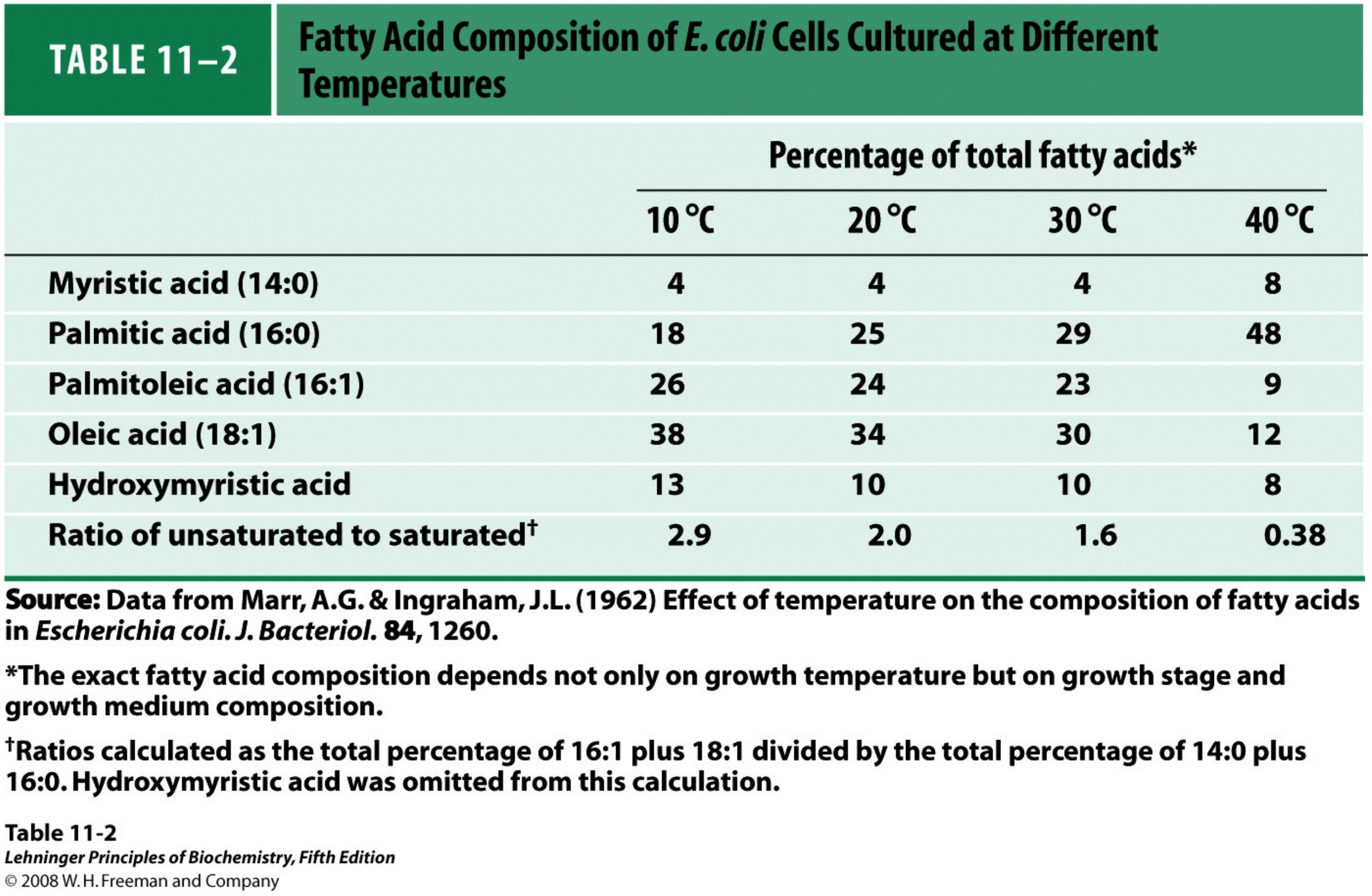

TABLE 11–2 **Fatty Acid Composition of *E. coli* Cells Cultured at Different Temperatures**

	Percentage of total fatty acids*			
	10 °C	20 °C	30 °C	40 °C
Myristic acid (14:0)	4	4	4	8
Palmitic acid (16:0)	18	25	29	48
Palmitoleic acid (16:1)	26	24	23	9
Oleic acid (18:1)	38	34	30	12
Hydroxymyristic acid	13	10	10	8
Ratio of unsaturated to saturated†	2.9	2.0	1.6	0.38

Source: Data from Marr, A.G. & Ingraham, J.L. (1962) Effect of temperature on the composition of fatty acids in *Escherichia coli*. *J. Bacteriol.* **84**, 1260.

*The exact fatty acid composition depends not only on growth temperature but on growth stage and growth medium composition.

†Ratios calculated as the total percentage of 16:1 plus 18:1 divided by the total percentage of 14:0 plus 16:0. Hydroxymyristic acid was omitted from this calculation.

Table 11-2
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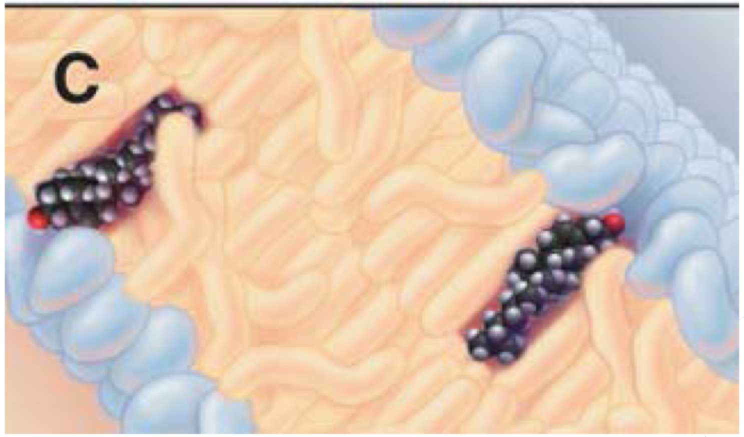
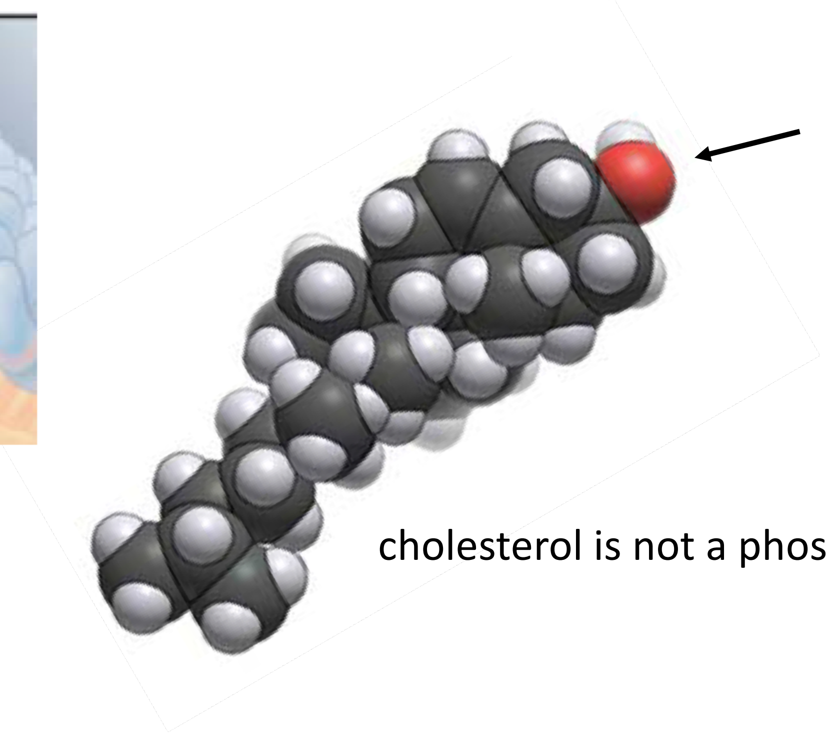
Cholesterol is present in cell membrane:

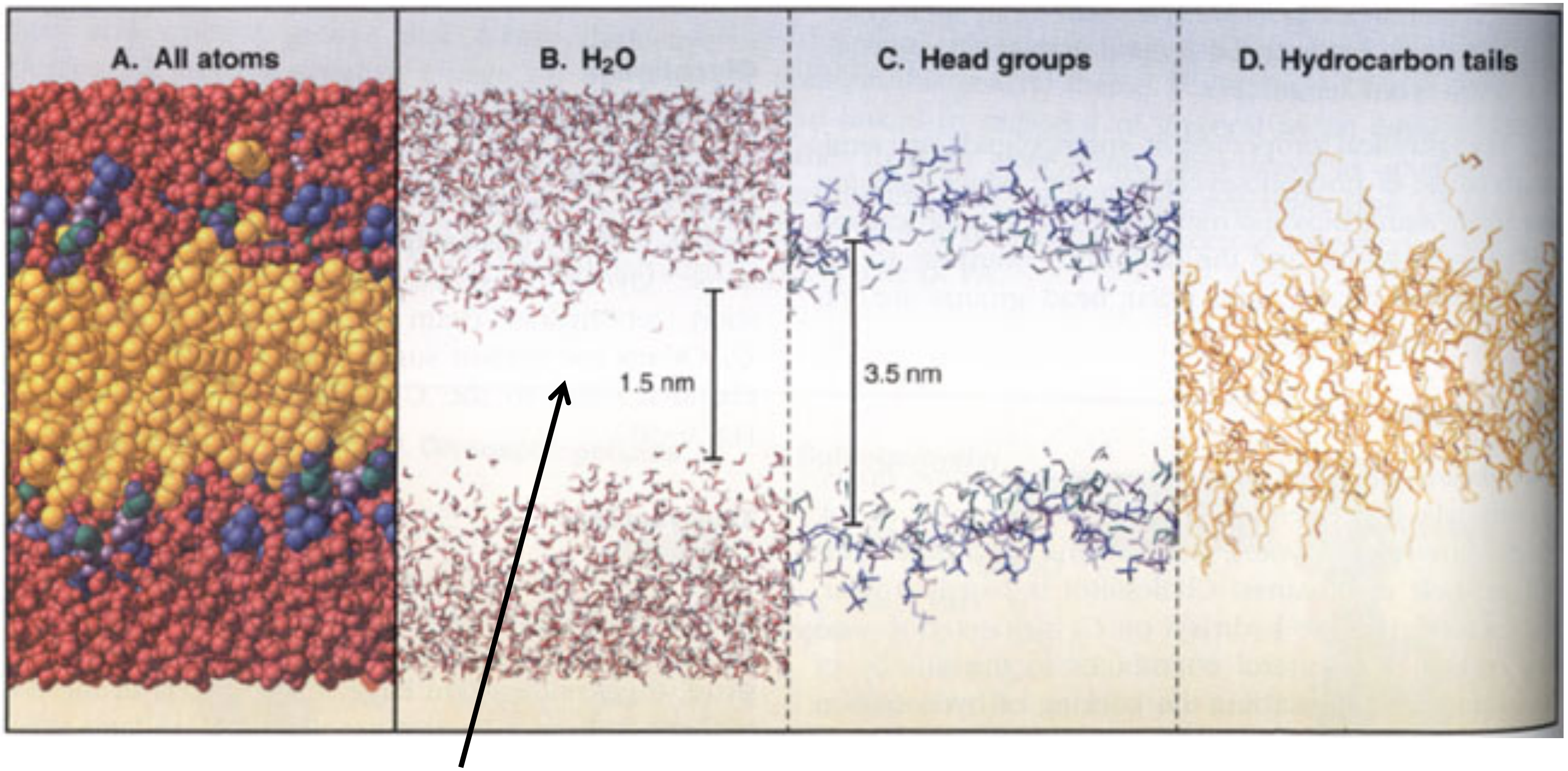




cholesterol is not a phospholipid

Cholesterol influences the Tm.

Structure of the plasma membrane

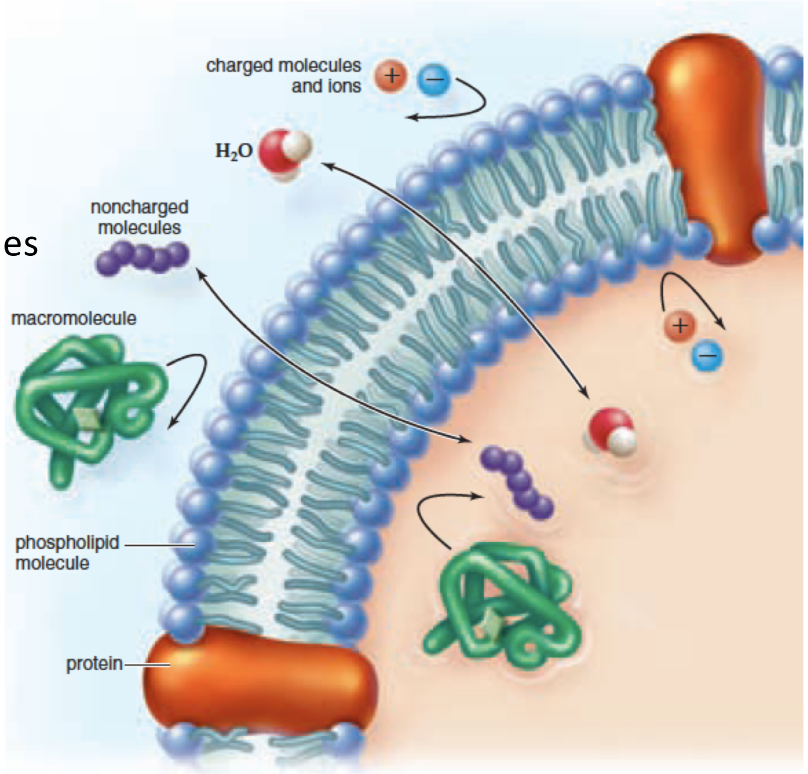


No water molecule is shown in the middle of the membrane;
this could suggest that the plasma membrane is not permeable to water

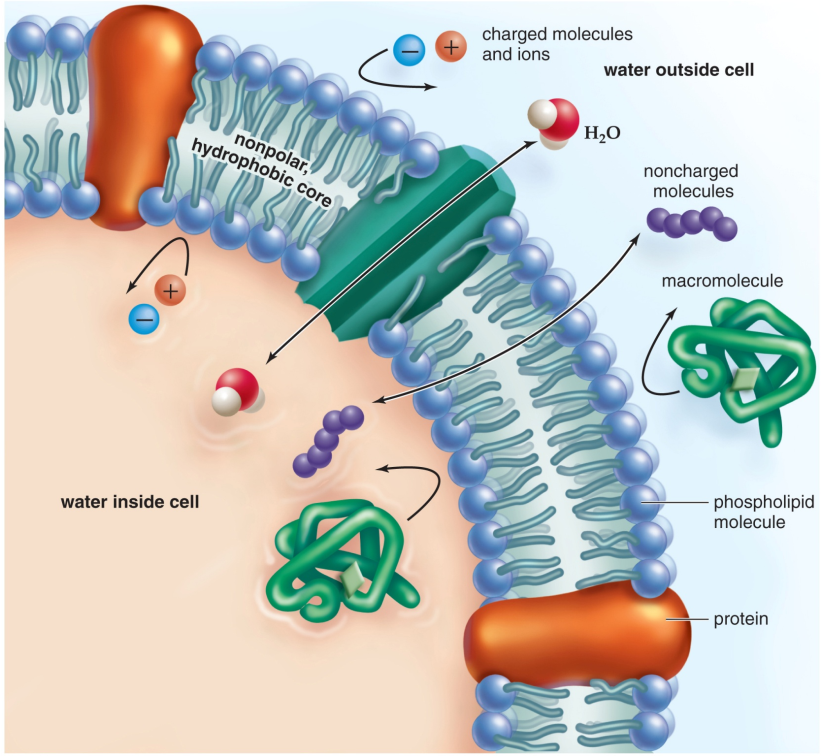
Textbooks provide confusing information about permeability to water.

Steroid hormones

protein



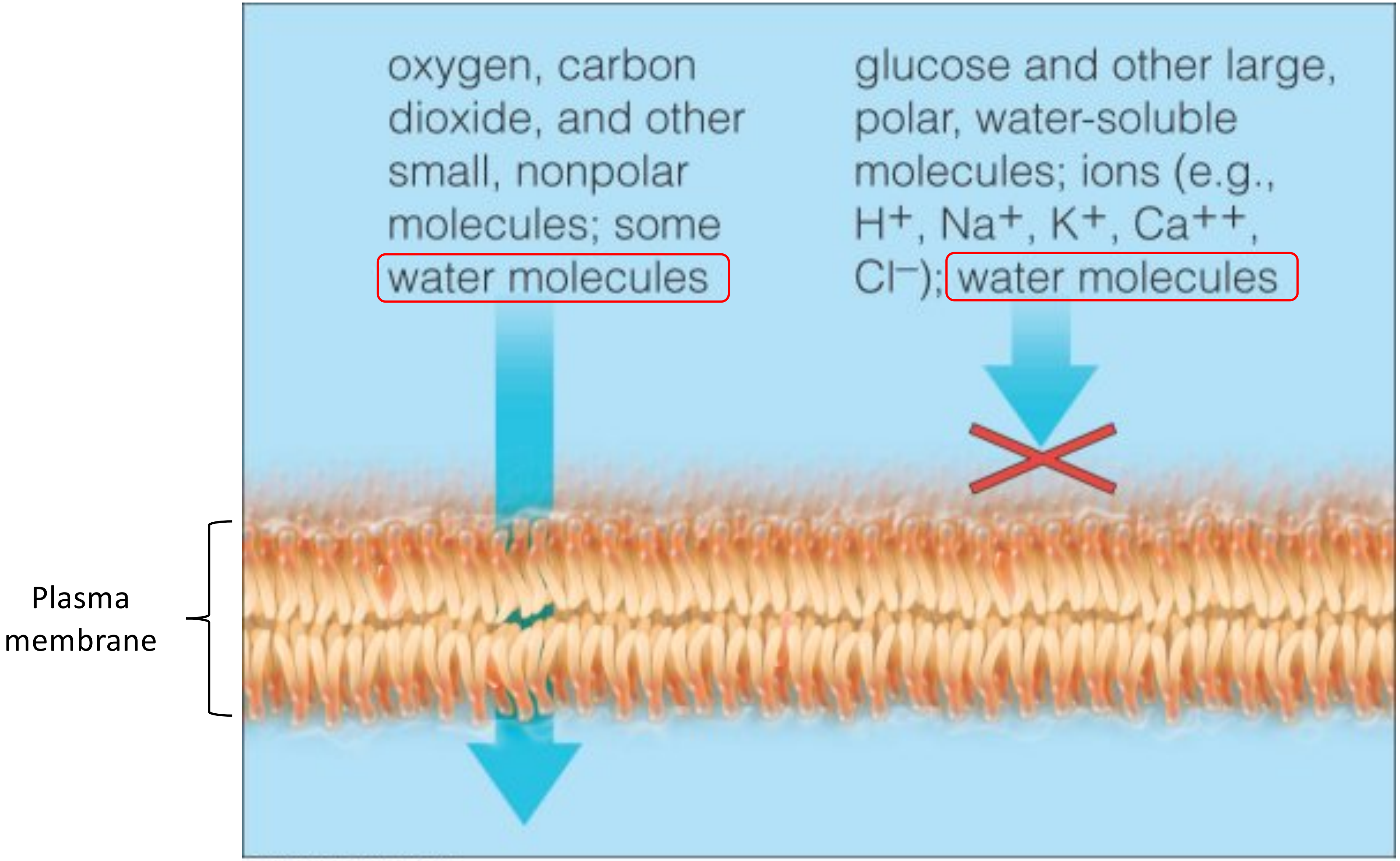
13th edition



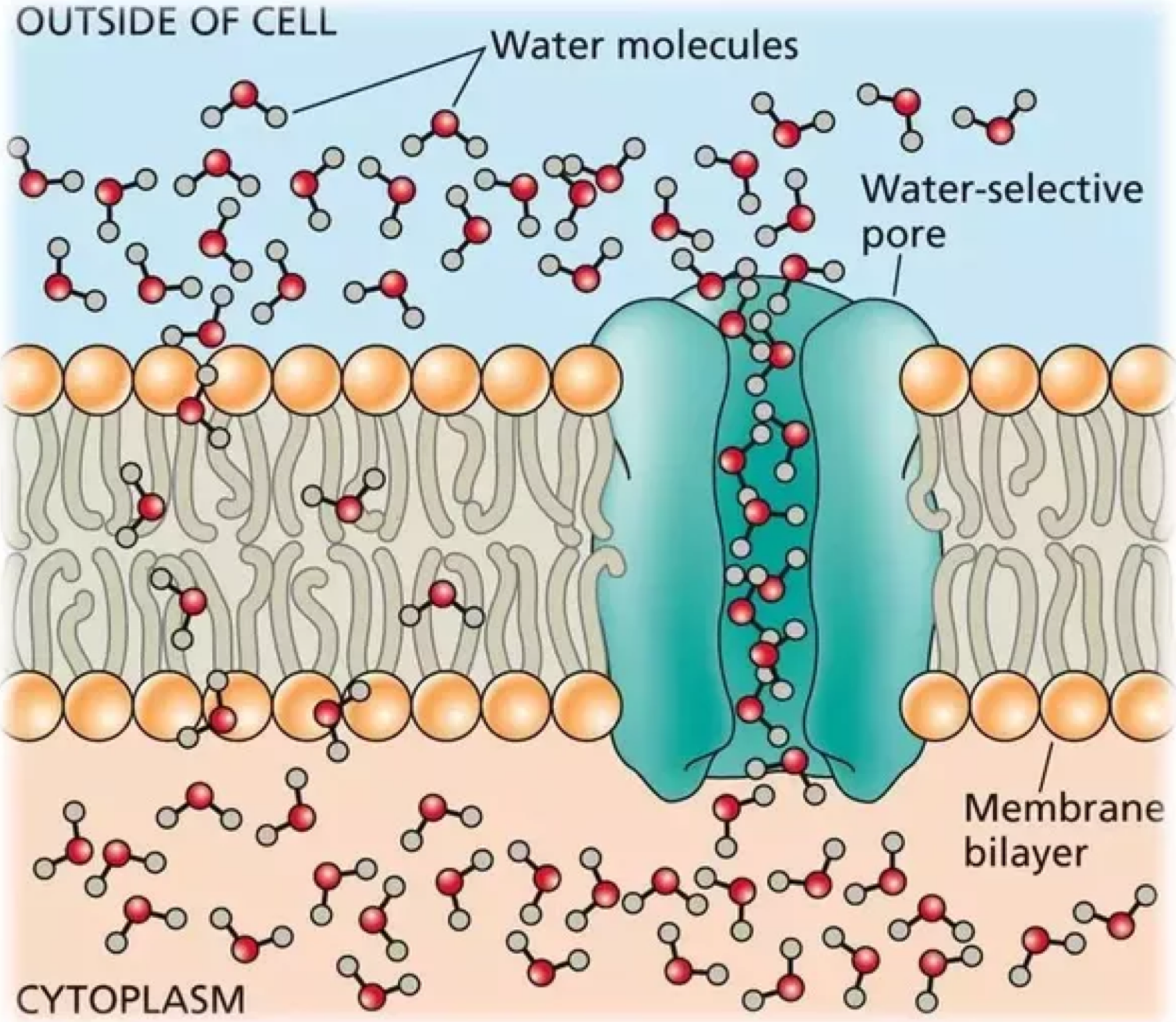
14th edition

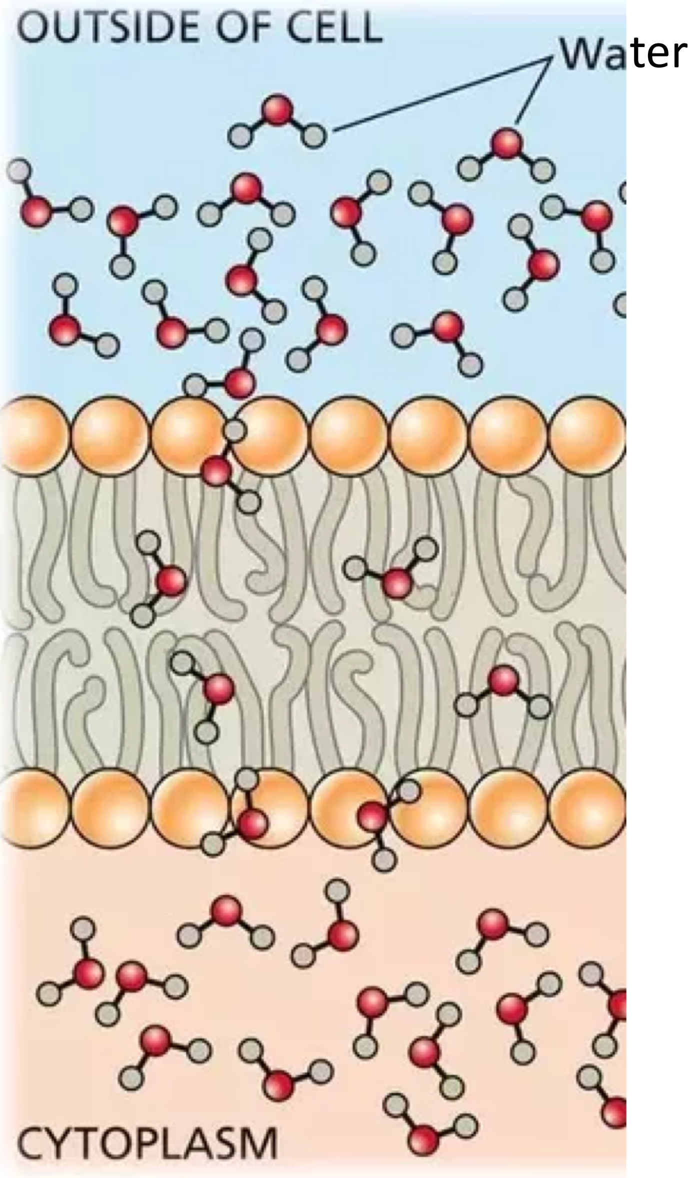
Sylvia Mader : Inquiry into life

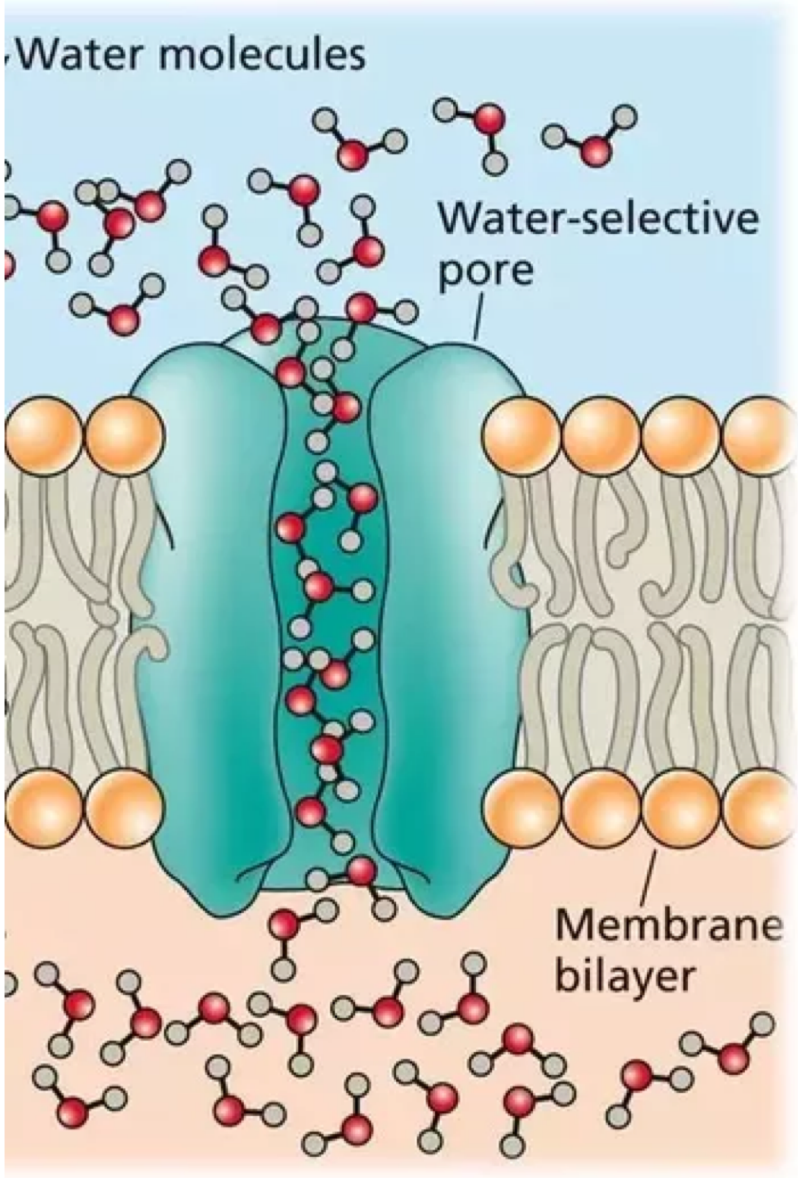
Selective permeability of plasma membrane.



? ? ?


OUTSIDE OF CELL
Water molecules
Water-selective pore
Membrane bilayer
CYTOPLASM


OUTSIDE OF CELL
Water
CYTOPLASM


Water molecules
Water-selective pore
Membrane bilayer

aquaporin

Proteins can be
- soluble in the cytosol
- embedded in a membrane

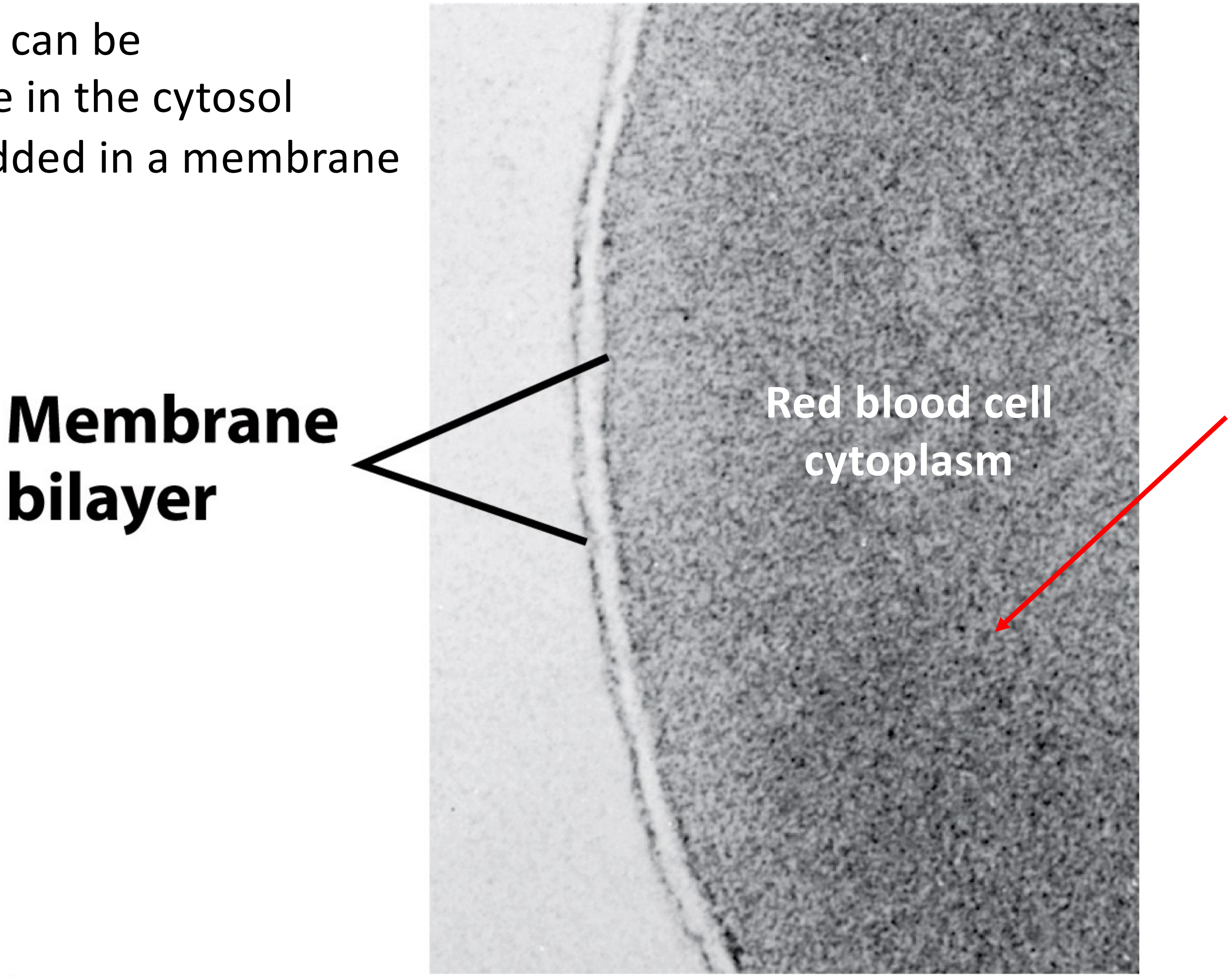


Figure 11-1
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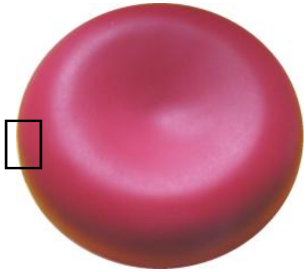
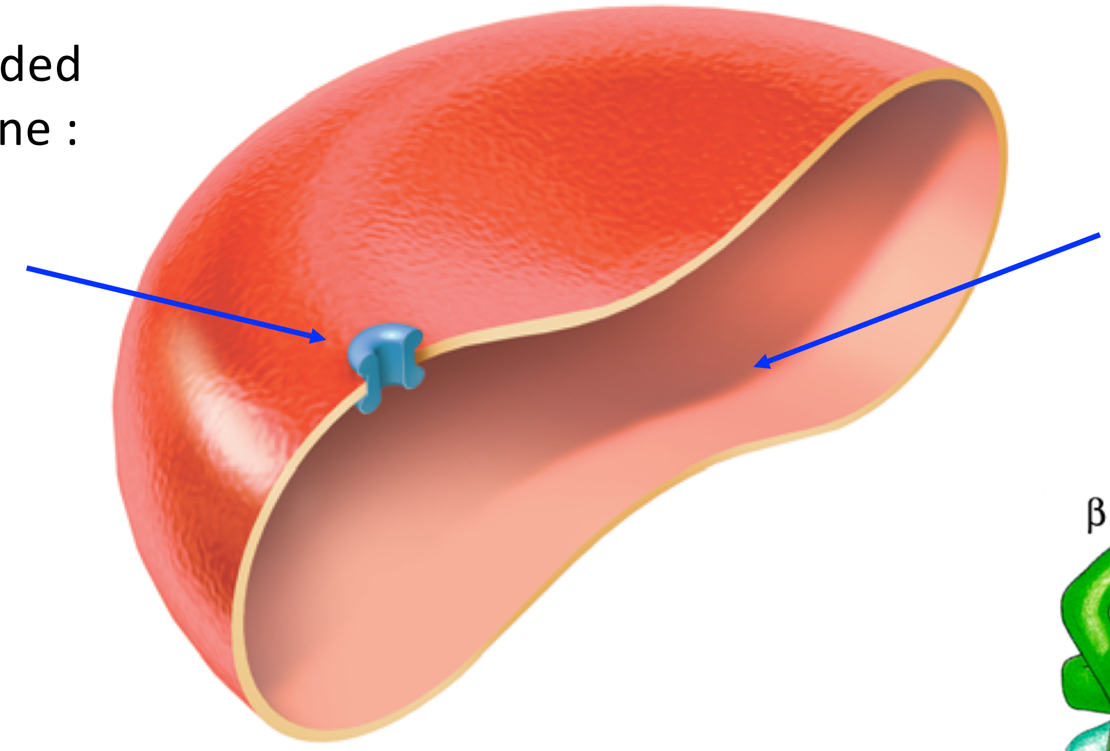


Soluble protein :

hemoglobin

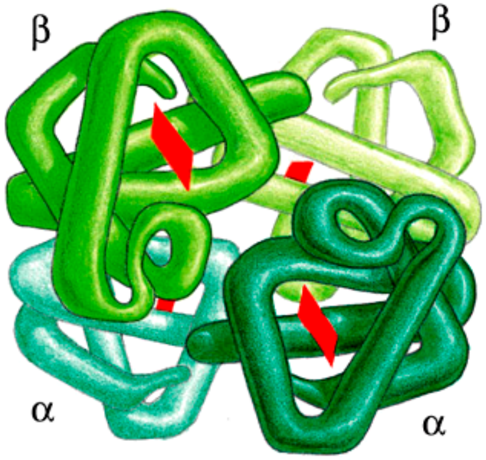
Protein embedded
in the membrane :

Aquaporin 1

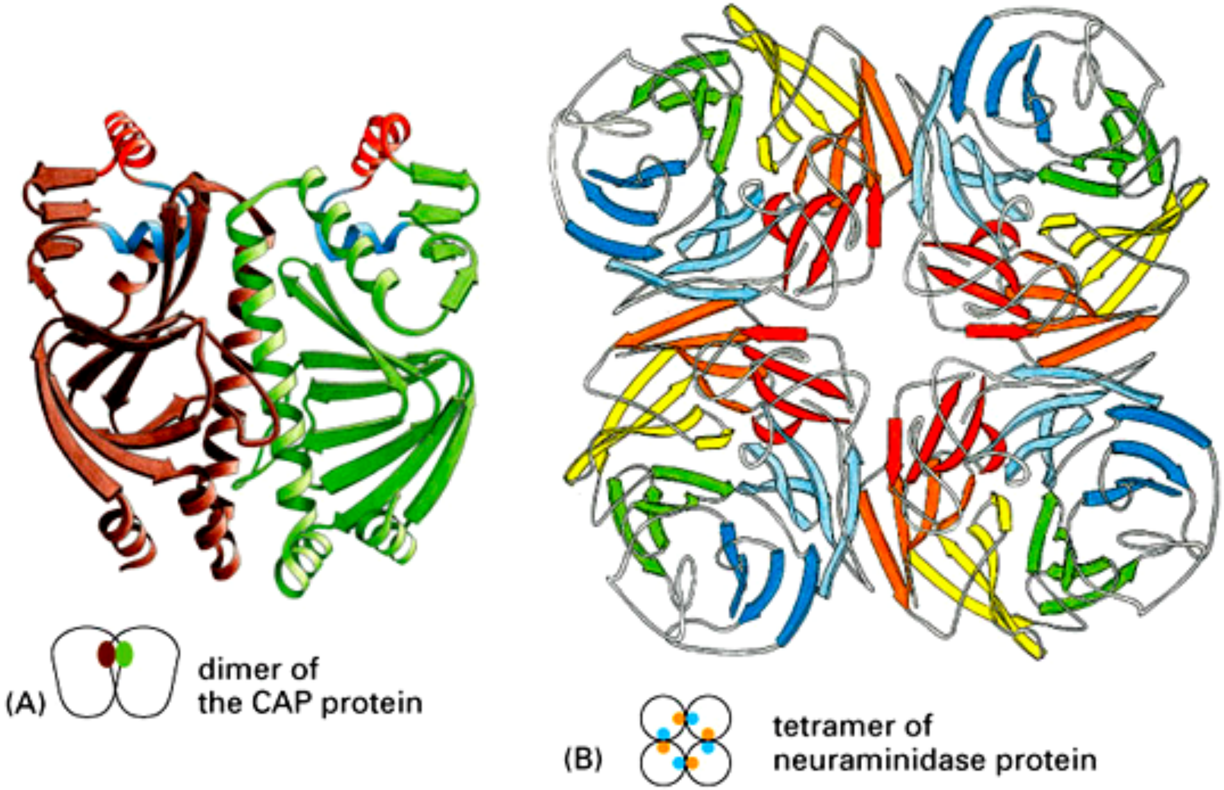


Protein soluble
in the cytosol :

Hemoglobin



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



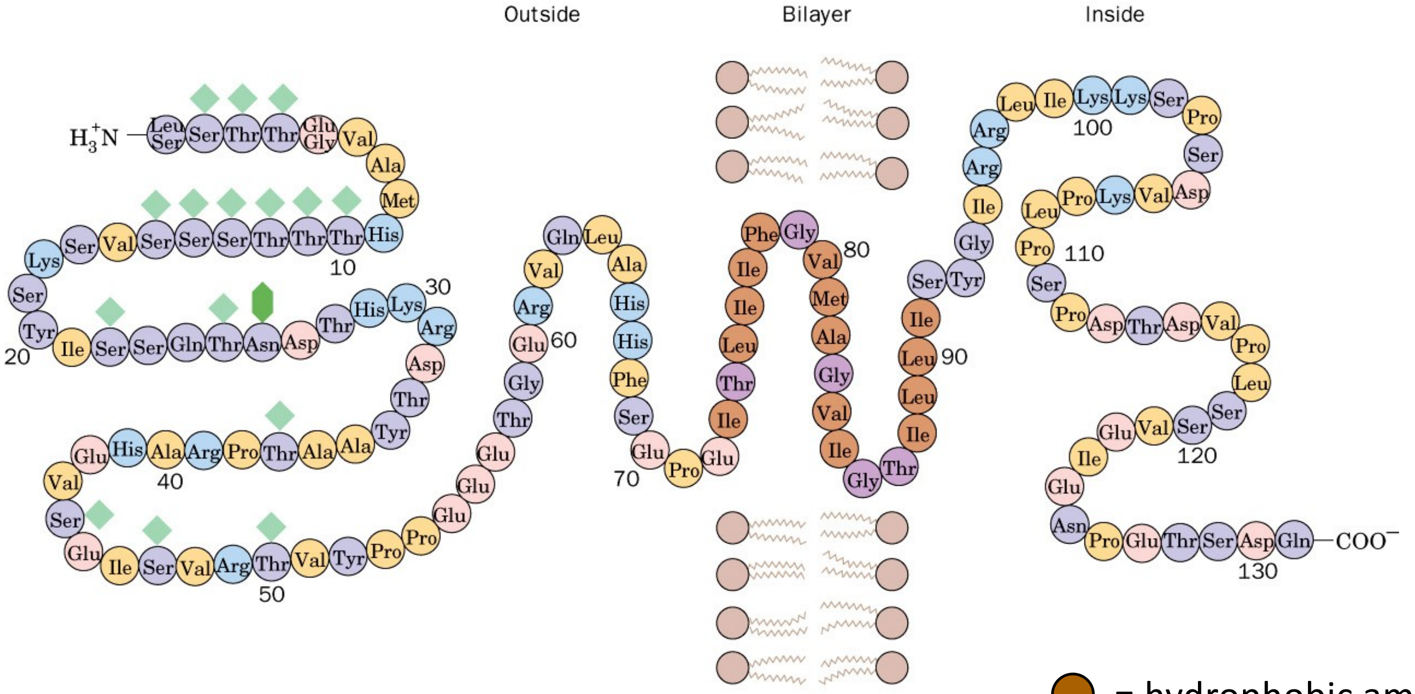
(A) dimer of the CAP protein

(B) tetramer of neuraminidase protein

homotetramer

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

A protein is a chain of **amino acids**.



● = hydrophobic amino acids

The transmembrane part is an **α-helix**

E-BOOK SEARCH
Search for:
GO

Annotate

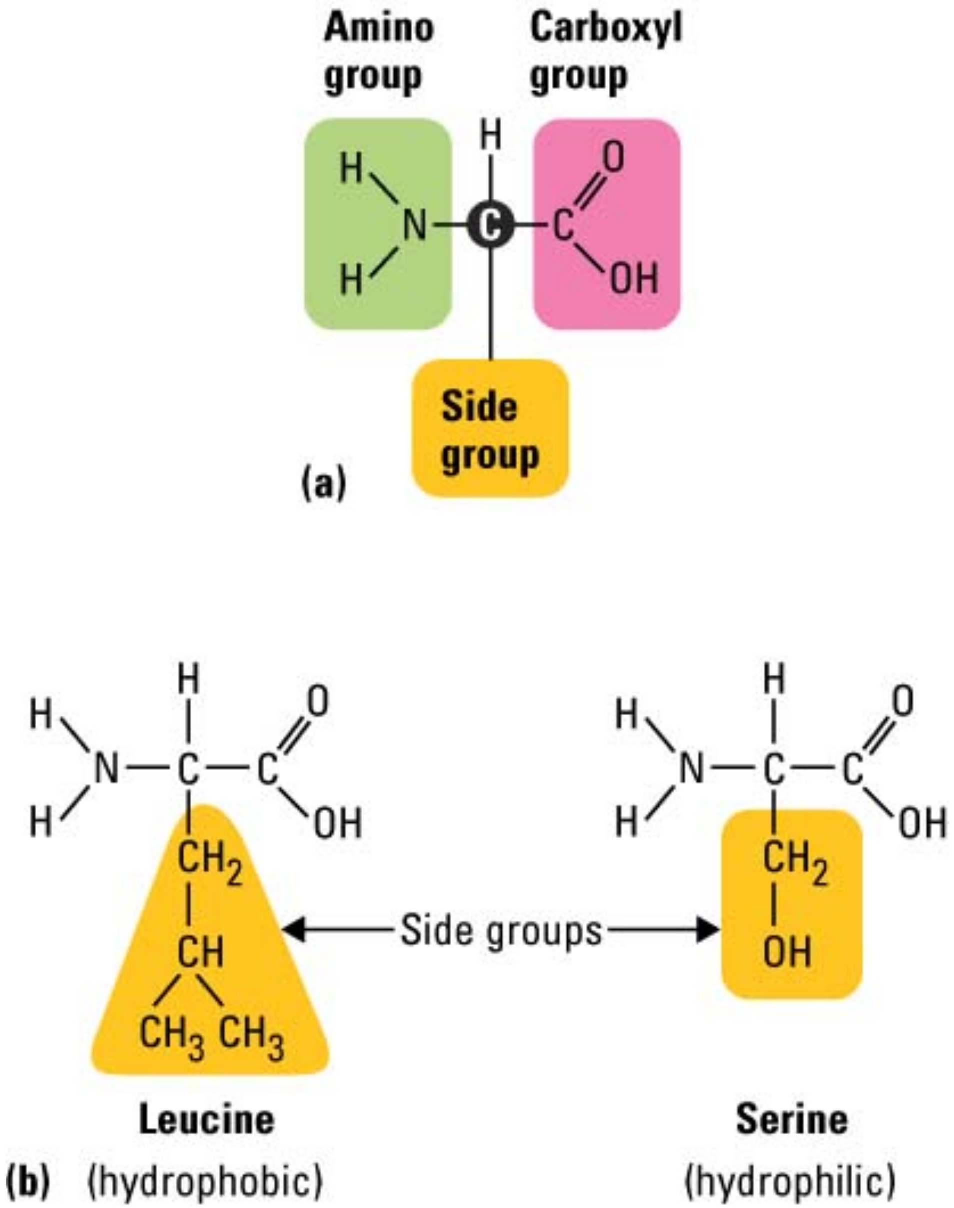
Proteins

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.



Side chains can be hydrophilic or hydrophobic

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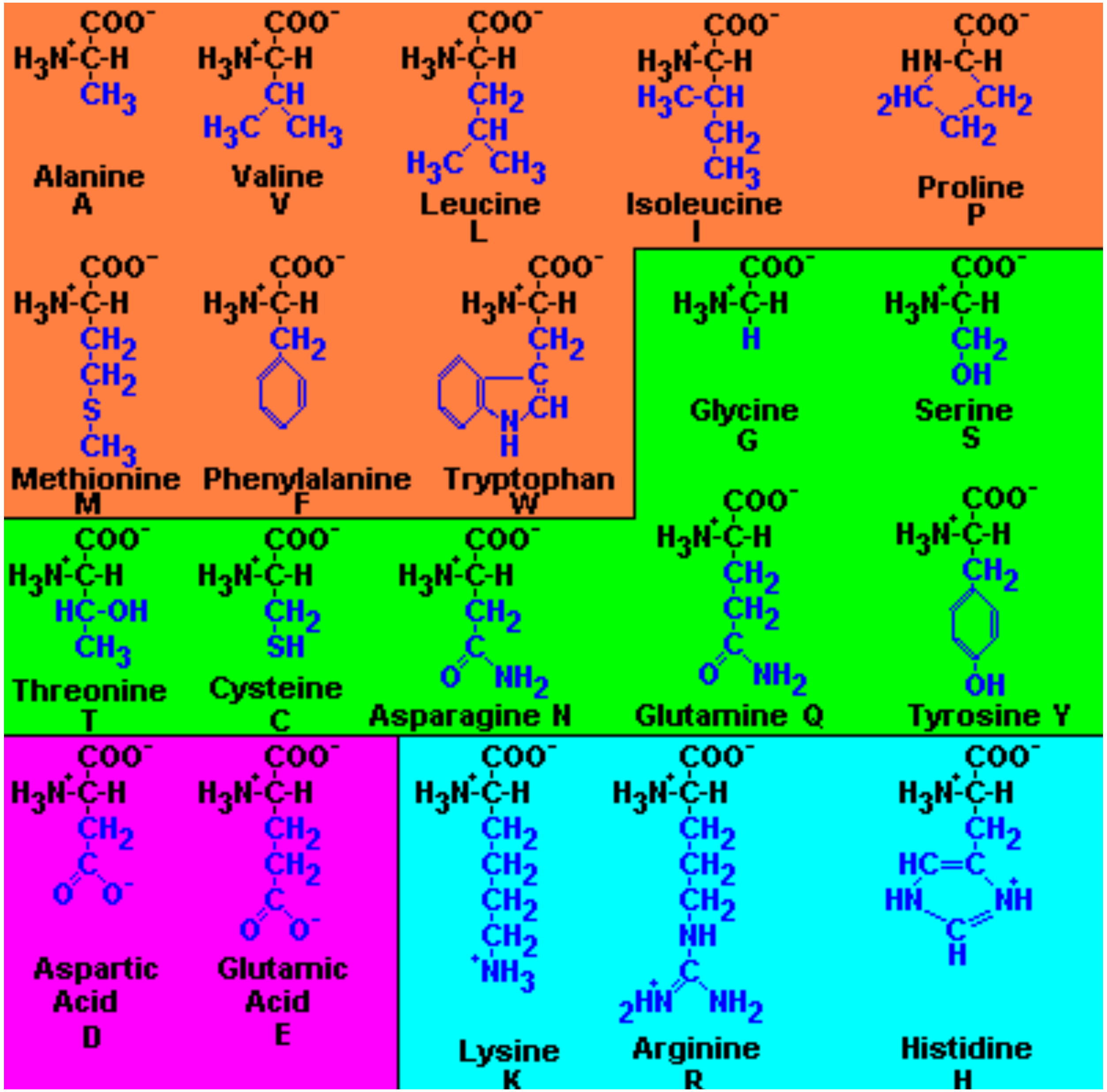
The 20 amino acids used for protein synthesis

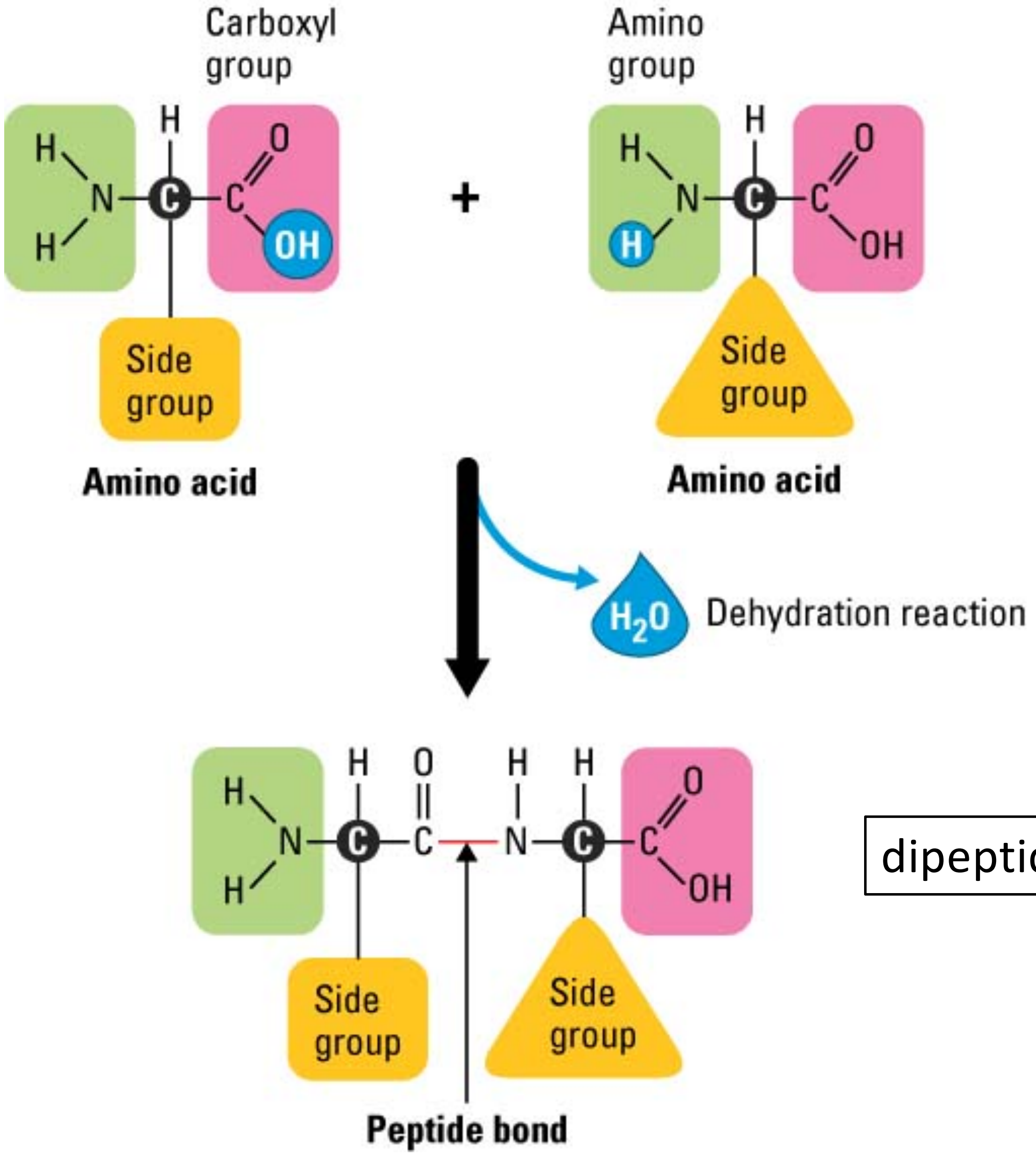
non polar

polar

charged



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



dipeptide

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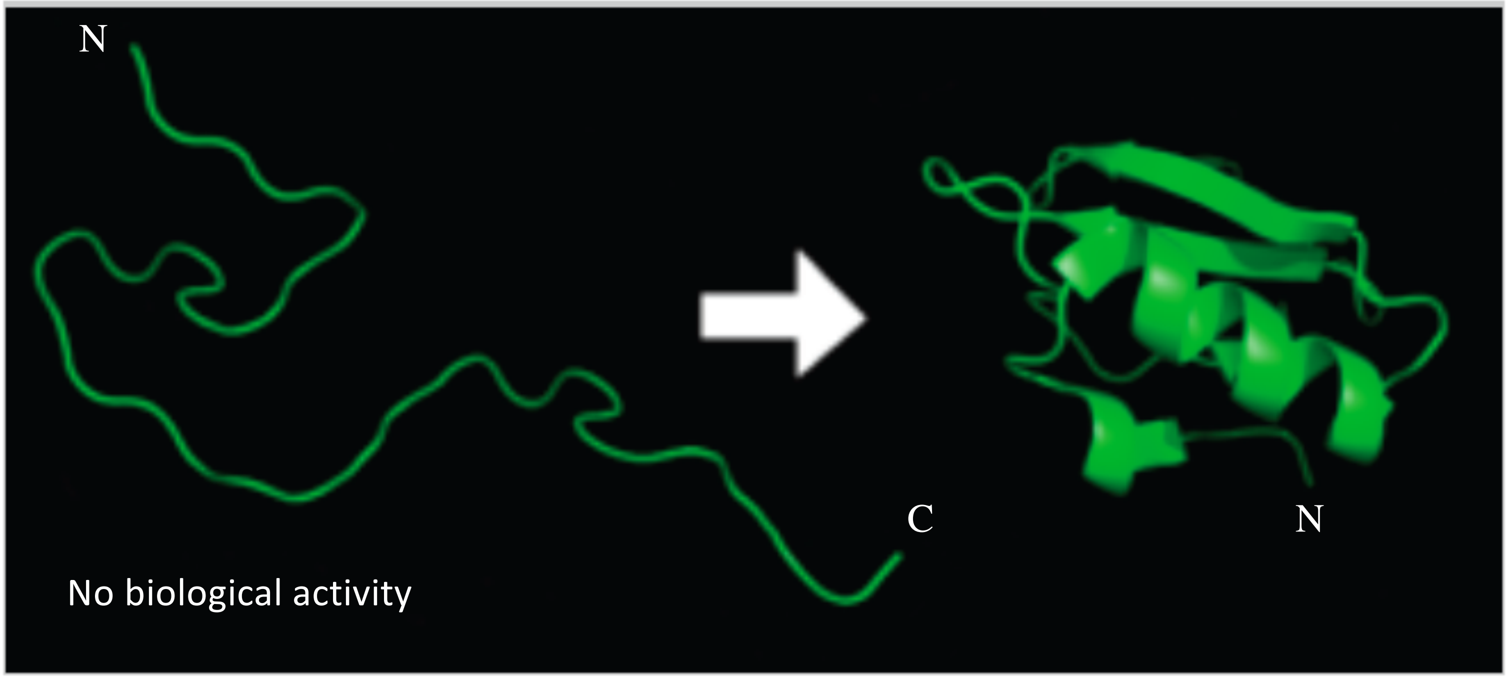
Proteins are long polymers of amino acids.



Protein before and after folding.

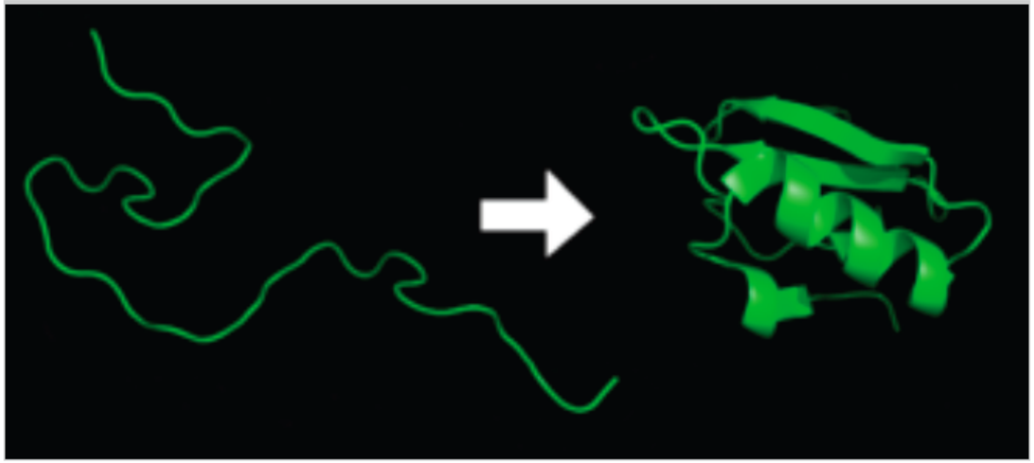
Only correctly folded proteins
Have a biological activity

http://en.wikipedia.org/wiki/Protein_folding

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.

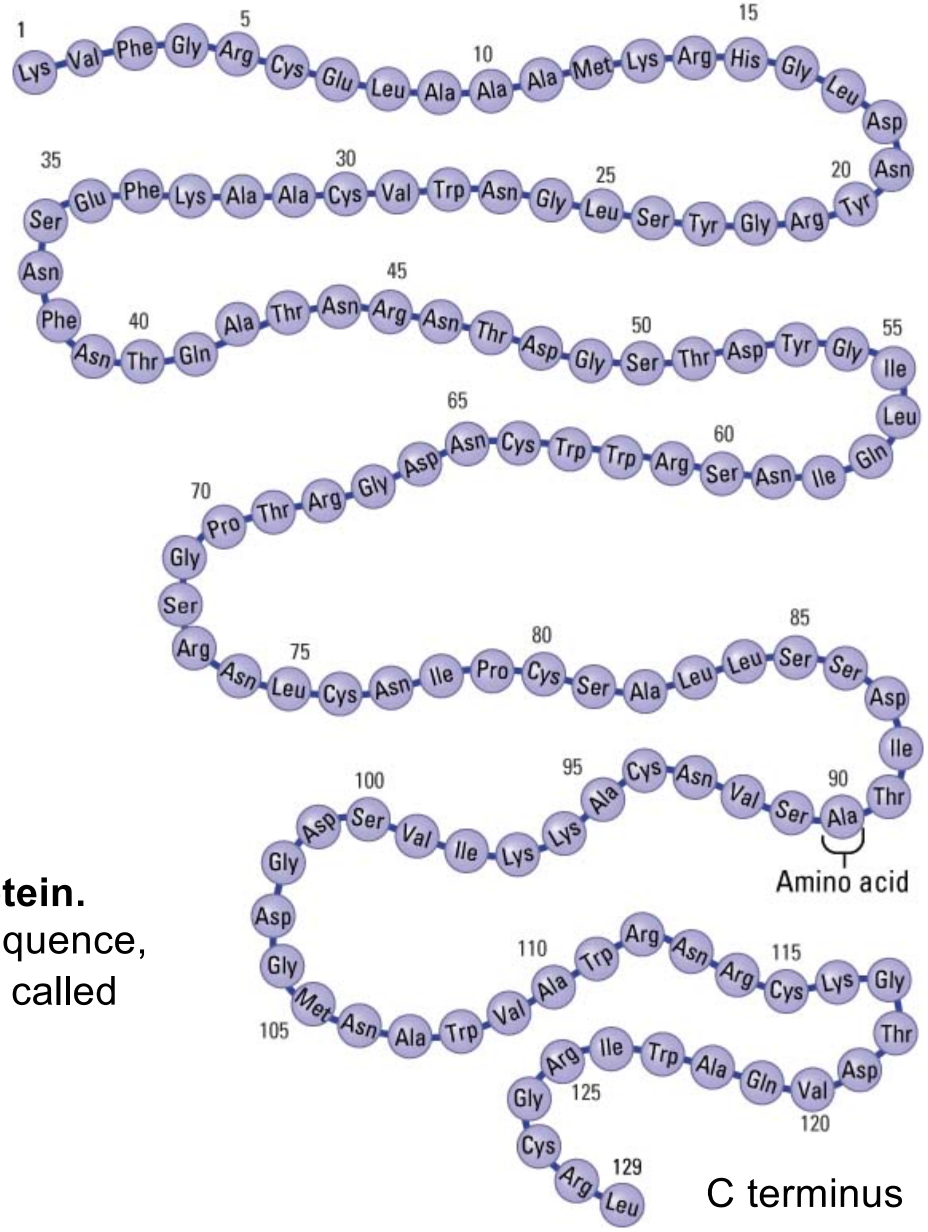
Side chains
are not shown



Protein before and after folding.

N terminus

Convention :
numbering starts at the
N-terminus



C terminus

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

Campbell Essential Biology

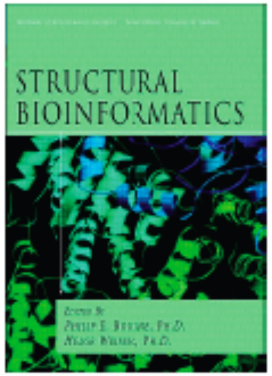
Folding of a polypeptidic chain

secondary structure:

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

→ α helix

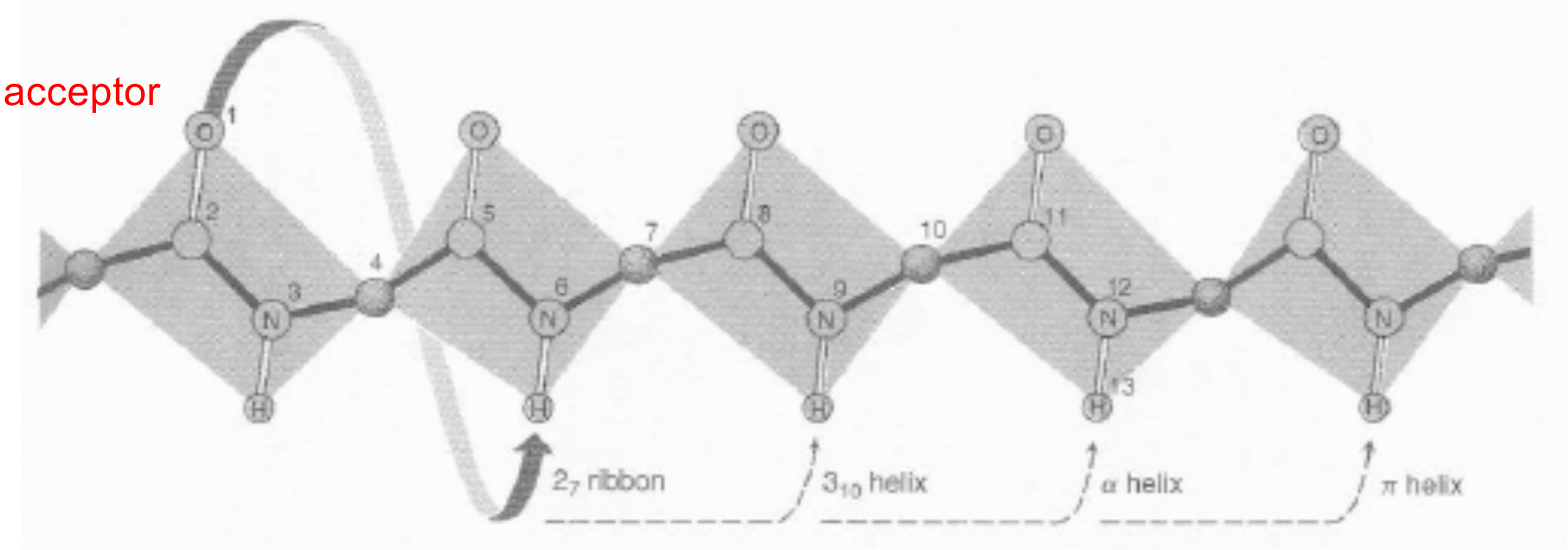
→ β sheet



Hydrogen bond :

- donor
- acceptor

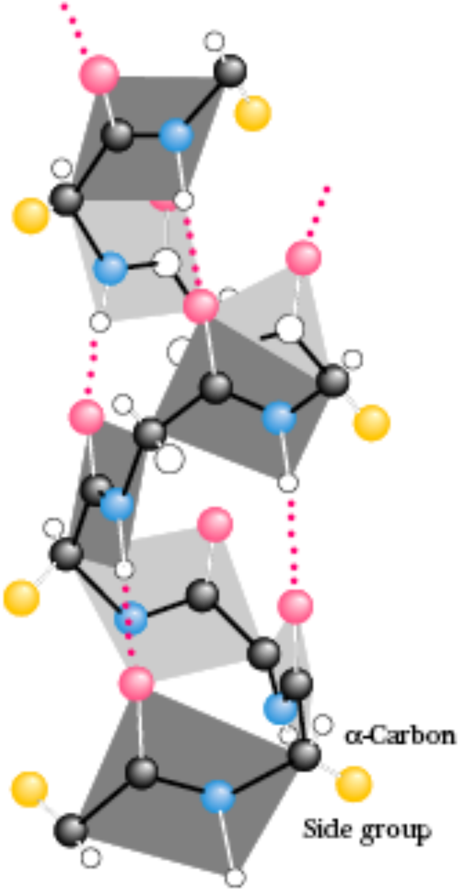
Which ones are the closest possible acceptor/donor ?



acceptor

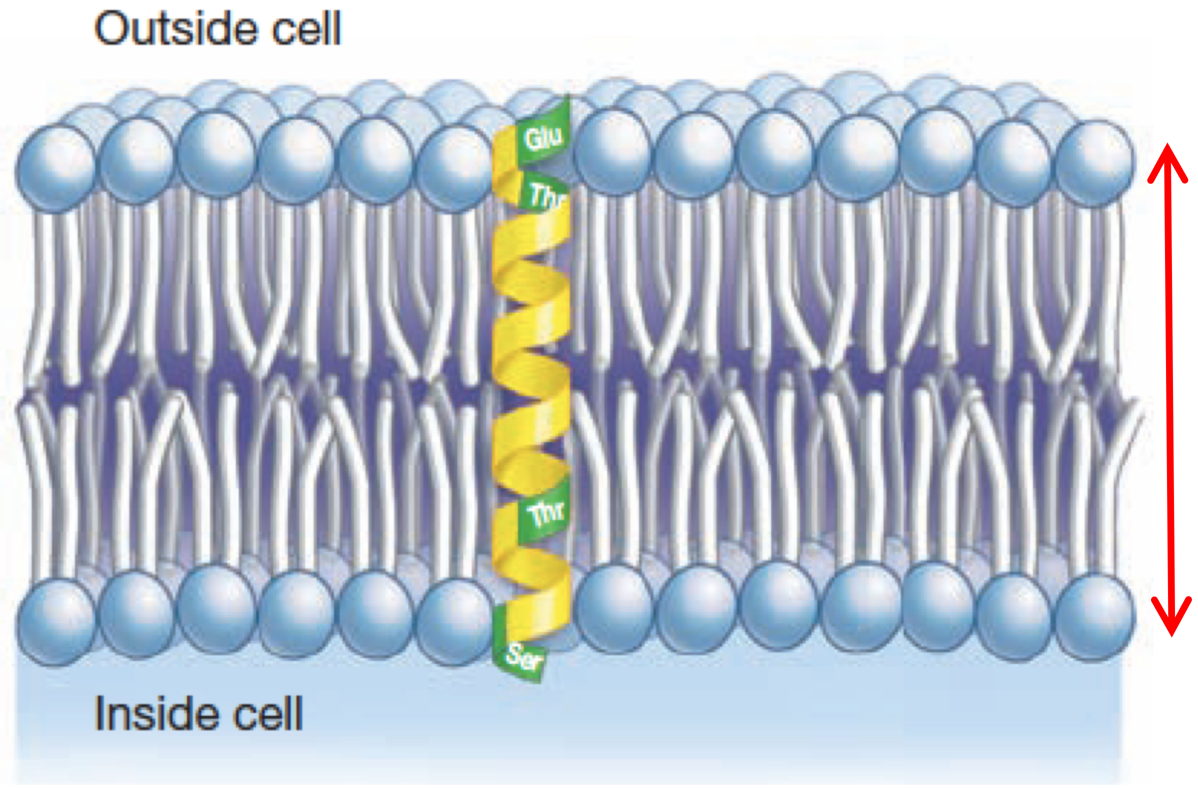
2_7 3_{10} **α helix** π helix

Fig 2-28



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

Transmembrane domain :



7 nm

About 20 amino acids

Always an α helix .

Bacteriorhodopsin :

Protein with 7 TM

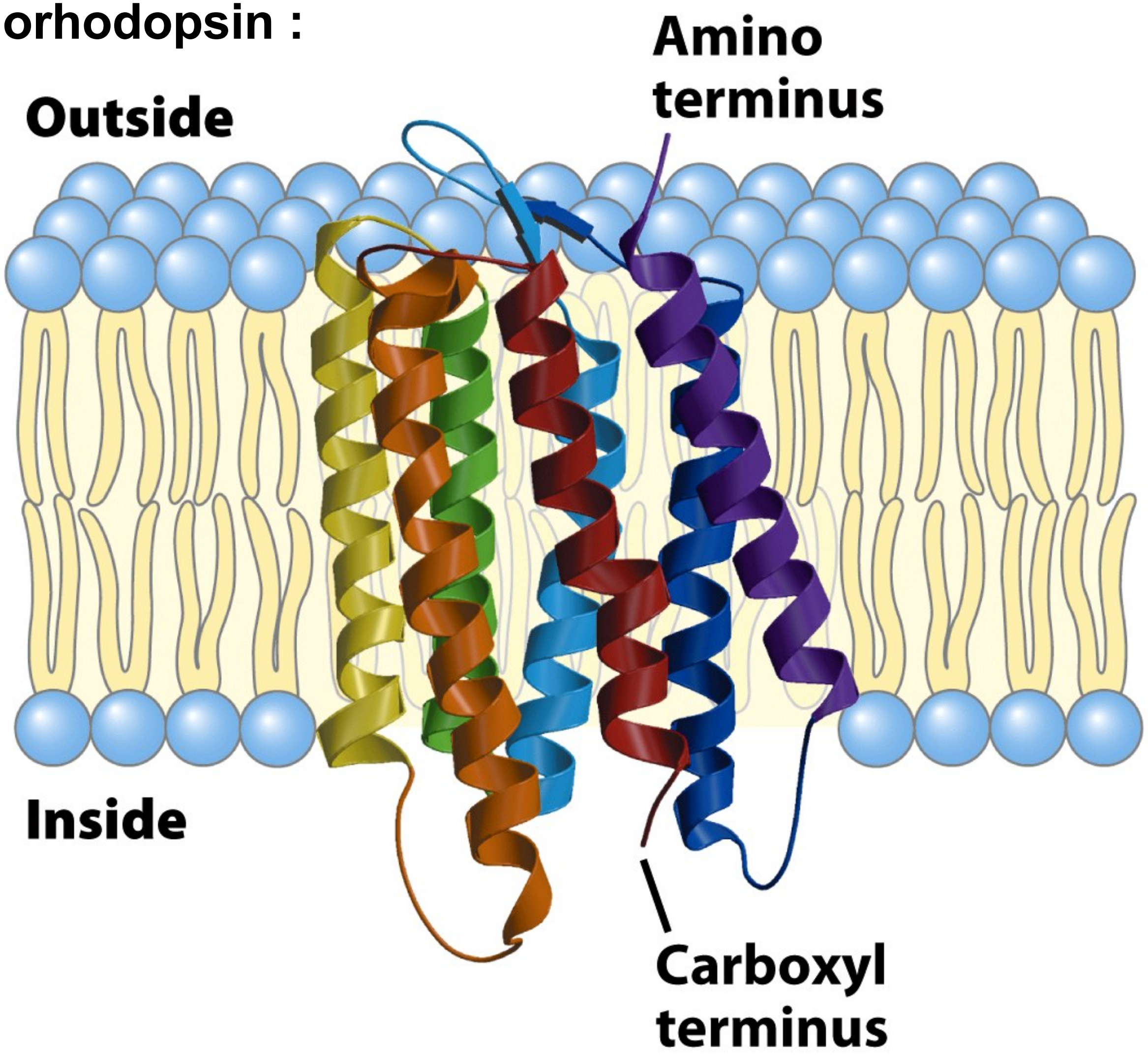
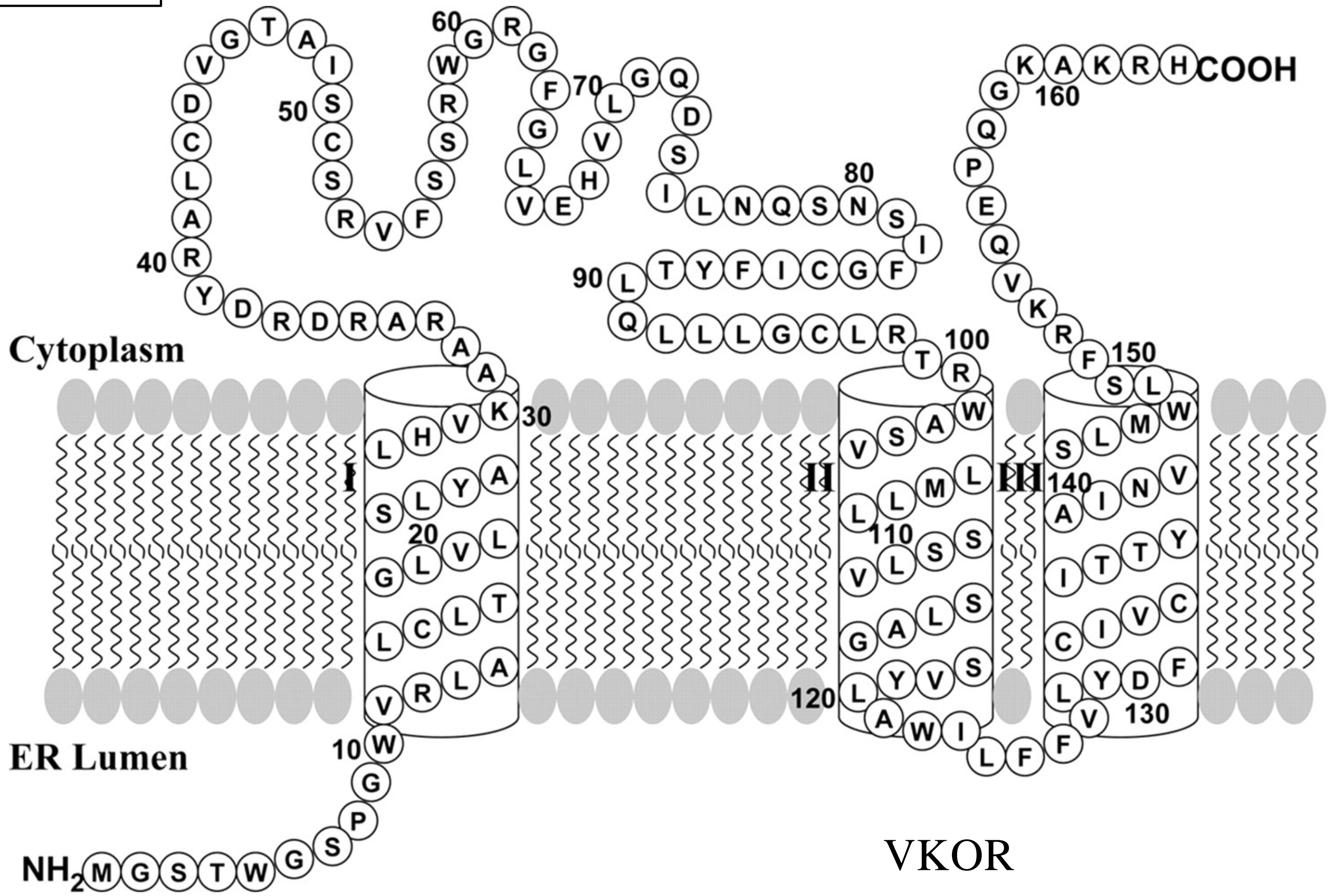


Figure 11-9
Lehninger Principles of Biochemistry, Fifth Edition

Protein with 3 TM



VKOR

Proposed structure of GLUT1 (12 TM)

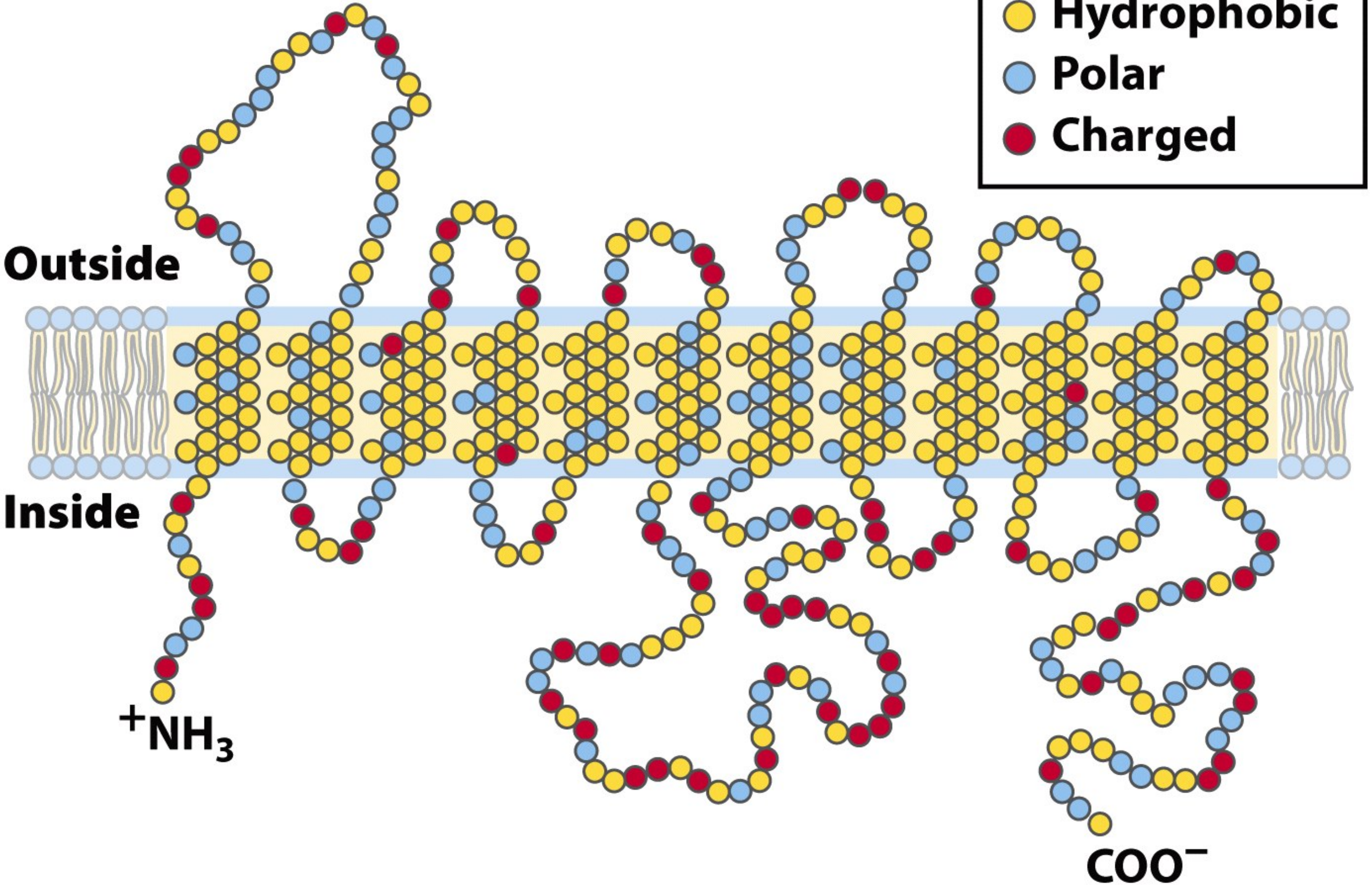
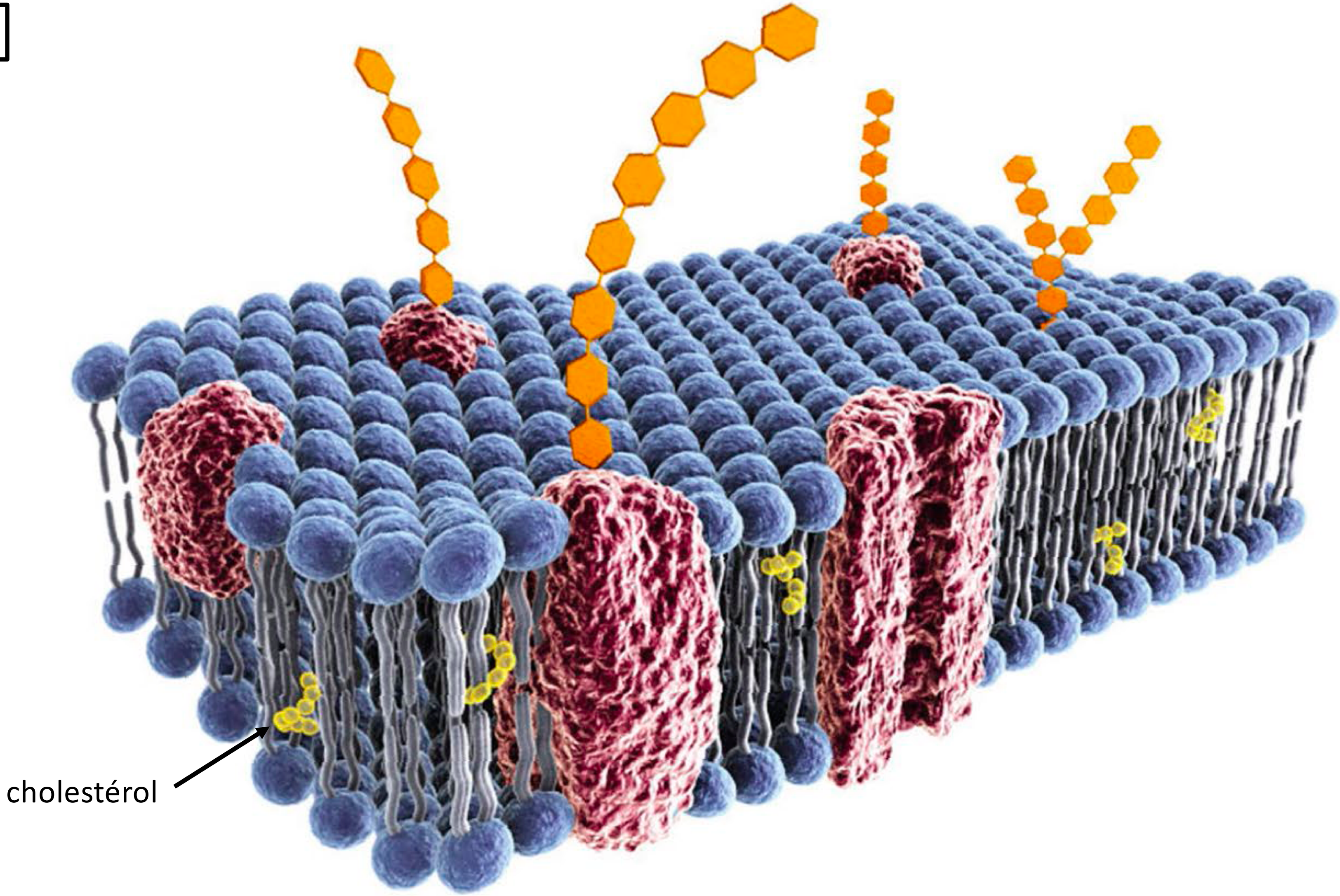


Figure 11-29a
Lehninger Principles of Biochemistry, Fifth Edition

Membrane



Hydropathy scale

Quantitative scale

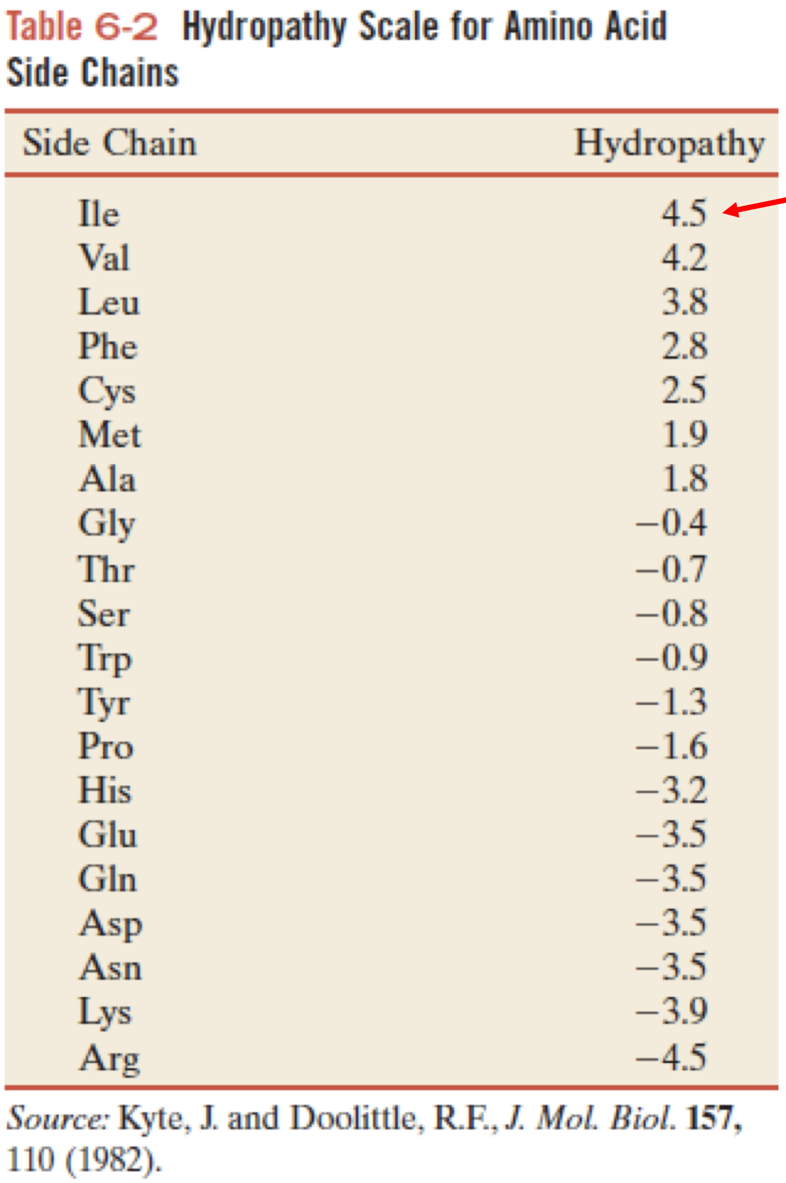


Table 6-2 **Hydropathy Scale for Amino Acid Side Chains**

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).

How does one get experimentally such a number ?

Hydropathy scale

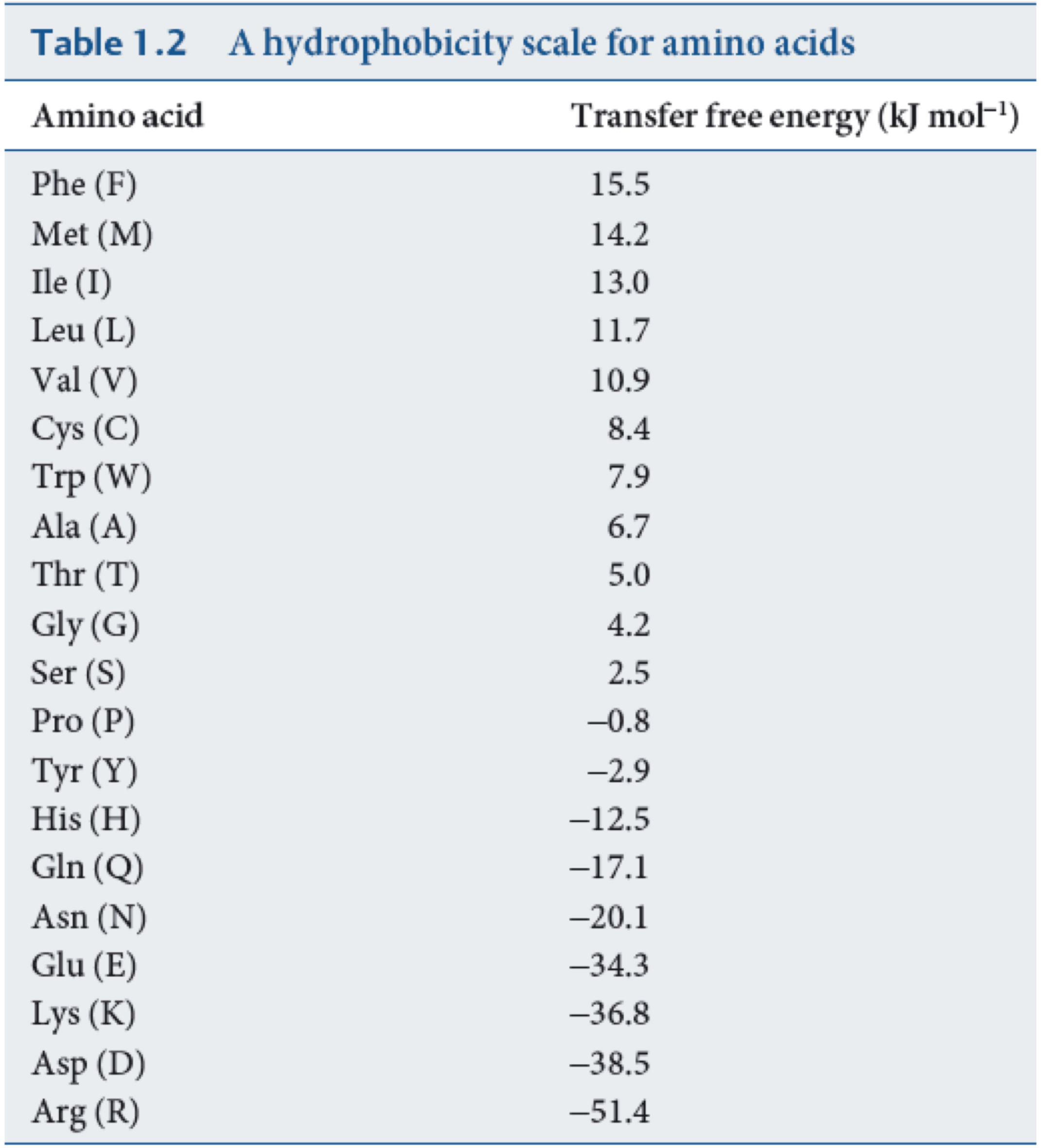


Table 1.2 A hydrophobicity scale for amino acids

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

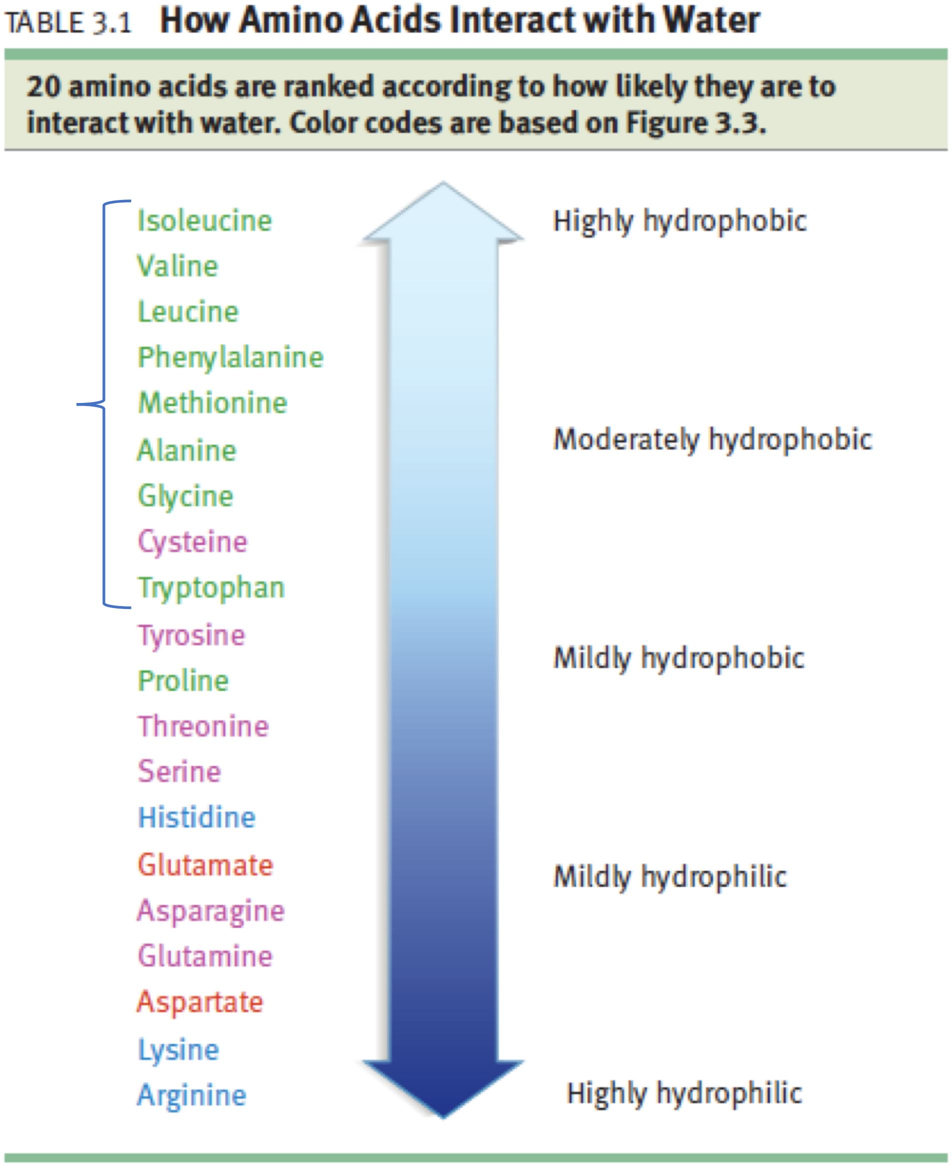


TABLE 3.1 **How Amino Acids Interact with Water**

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

Isoleucine
Valine
Leucine
Phenylalanine
Methionine
Alanine
Glycine
Cysteine
Tryptophan
Tyrosine
Proline
Threonine
Serine
Histidine
Glutamate
Asparagine
Glutamine
Aspartate
Lysine
Arginine

Highly hydrophobic
Moderately hydrophobic
Mildly hydrophobic
Mildly hydrophilic
Highly hydrophilic

Transbilayer disposition of glycophorin in an erythrocyte

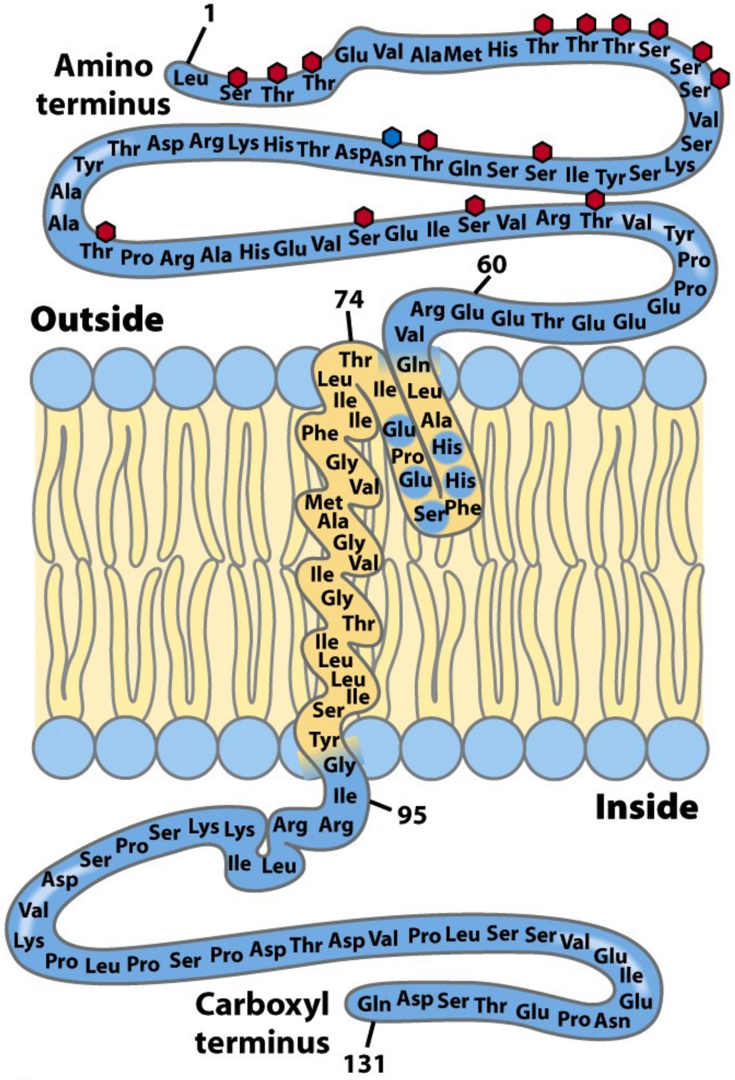


Figure 11-7

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Hydropathy profile

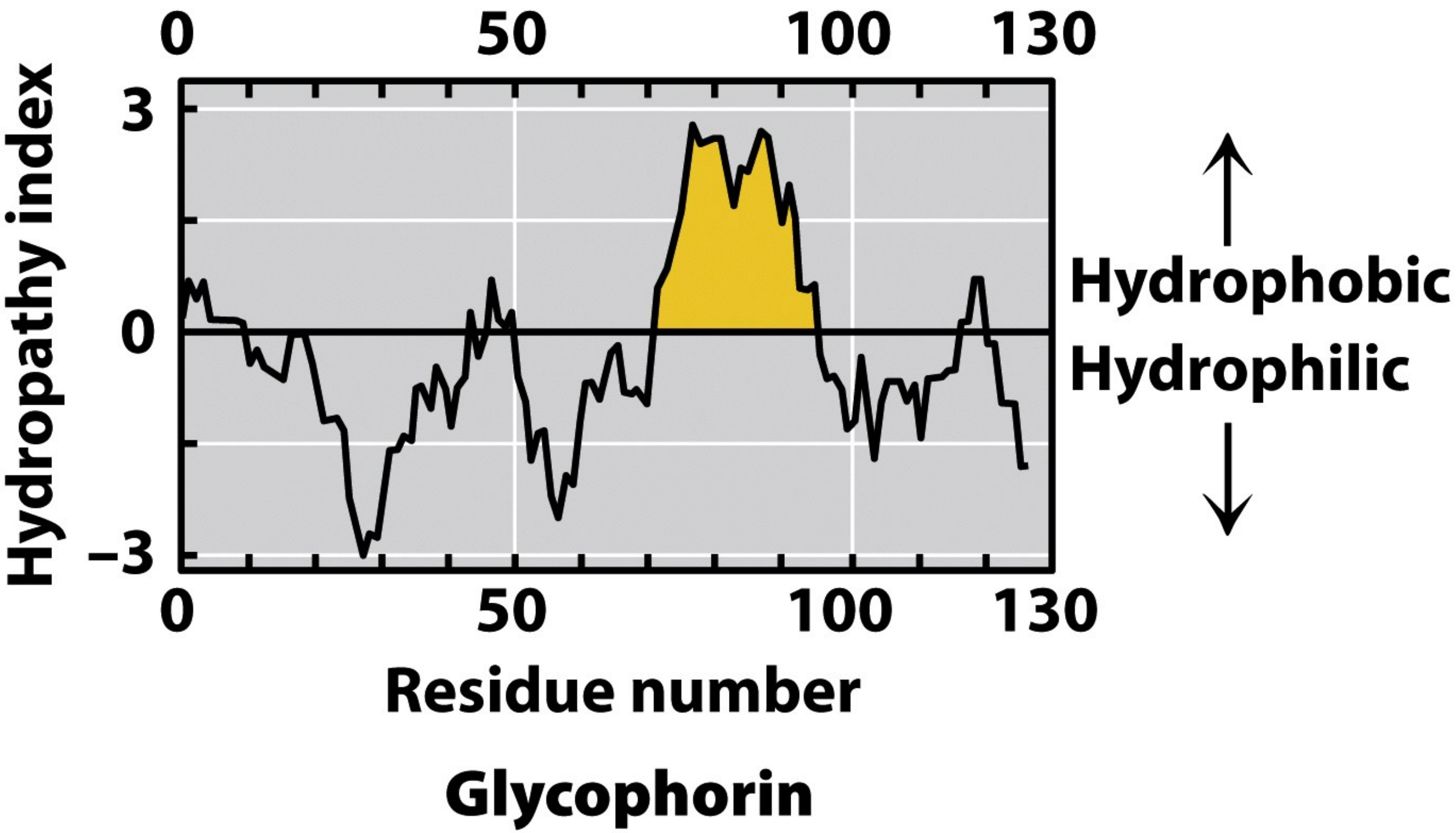
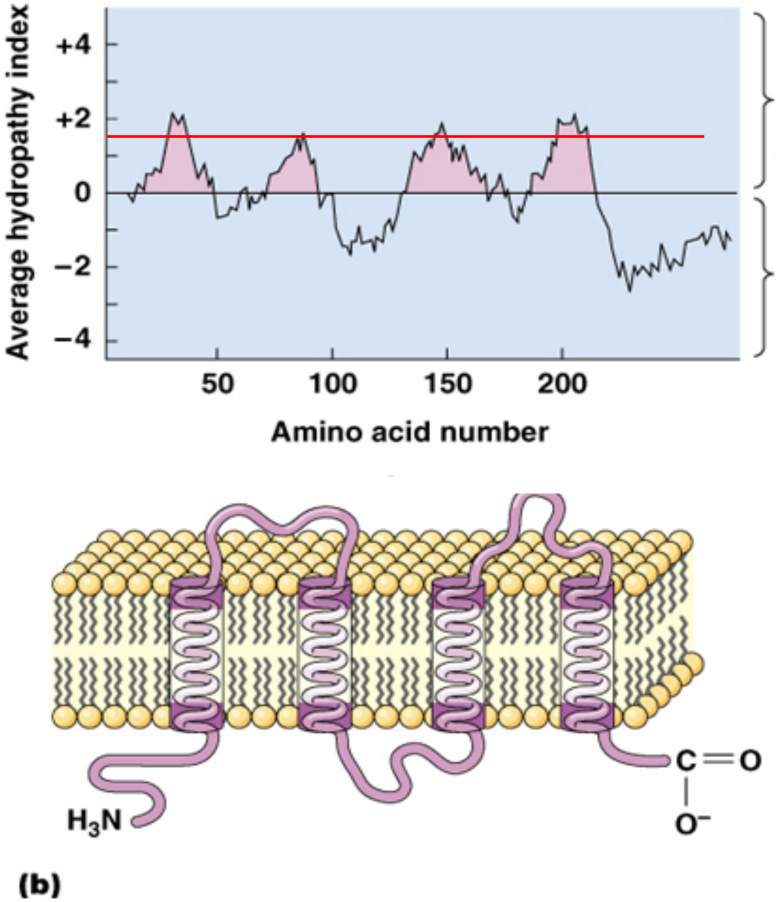


Figure 11-11a

Lehninger Principles of Biochemistry, Fifth Edition

Hydropathy profile

Textbook examples are oversimplified.



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

Hydropathy profile

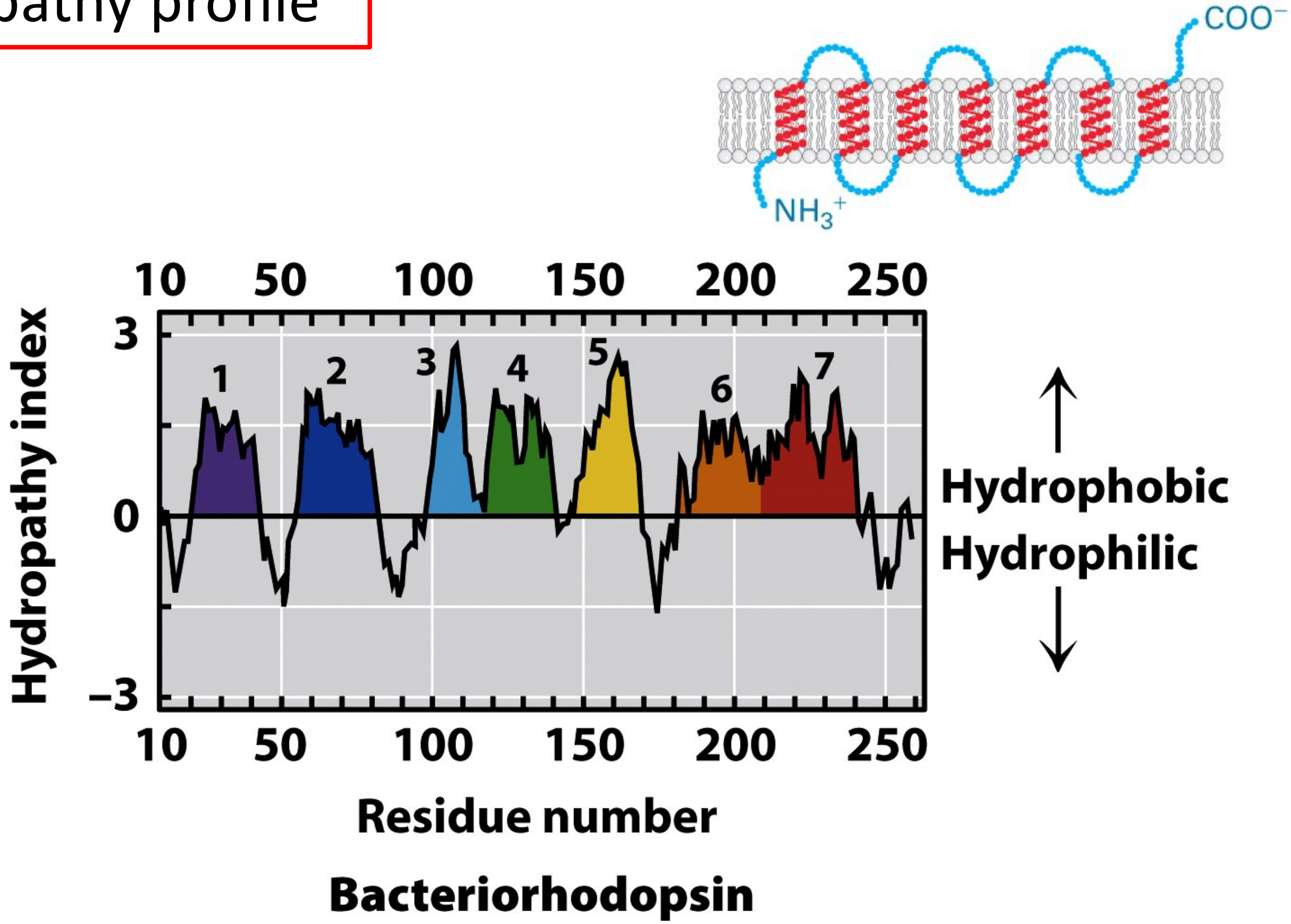


Figure 11-11b
Lehninger Principles of Biochemistry, Fifth Edition

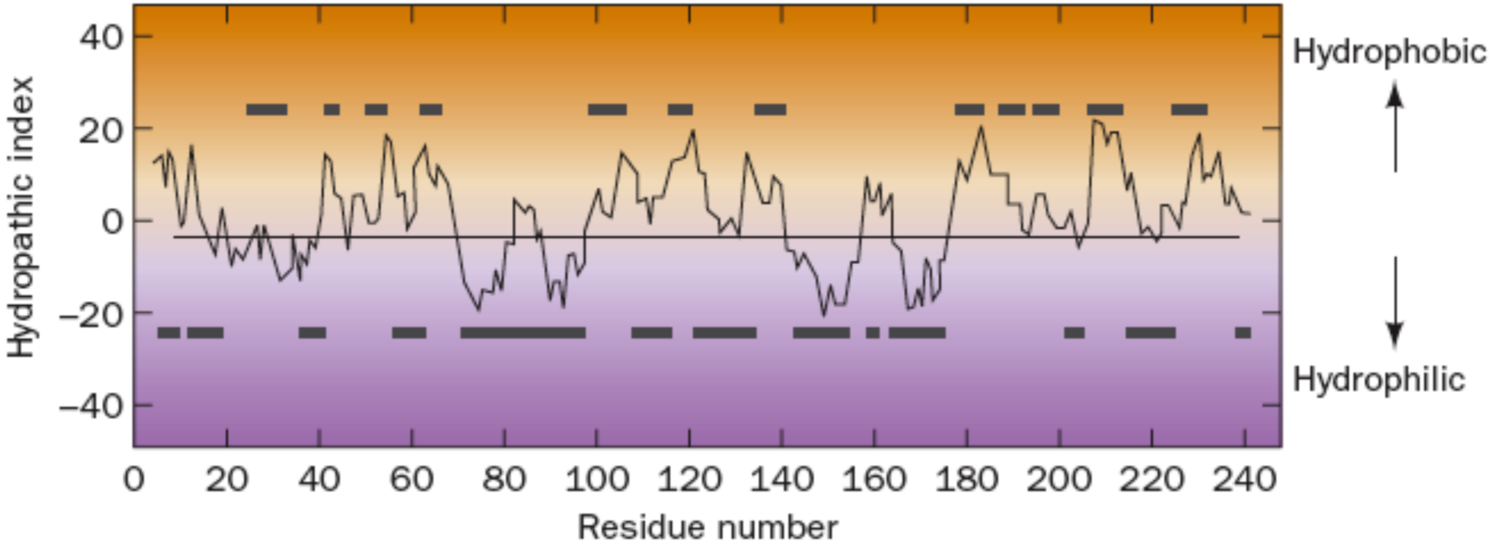
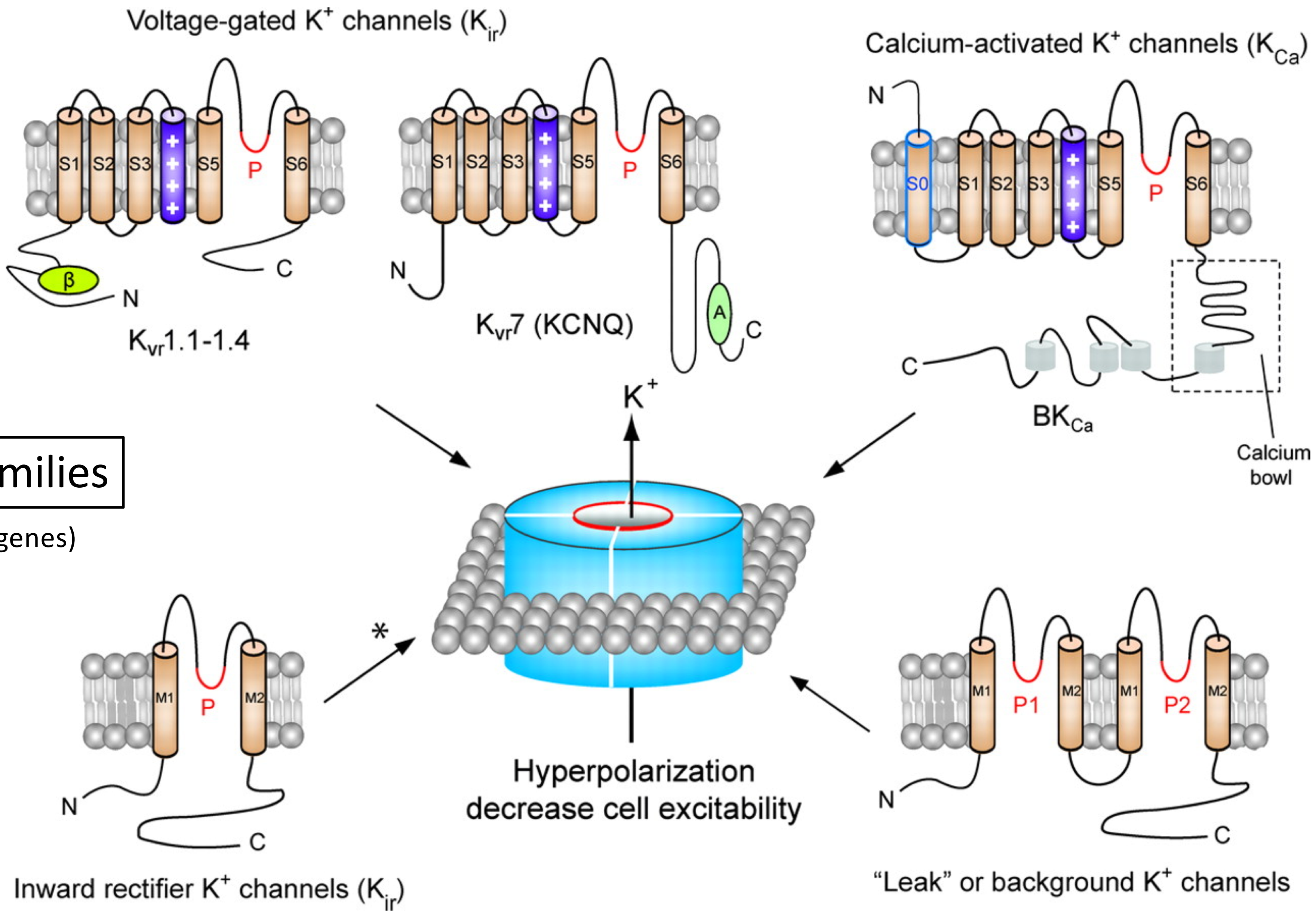


Figure 6-35 **A hydropathic index plot for bovine chymotrypsinogen.** The sum of the hydropathies of nine consecutive residues is plotted versus residue sequence number. A large positive hydropathic index indicates a hydrophobic region of the polypeptide, whereas a large negative value indicates a hydrophilic 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).]

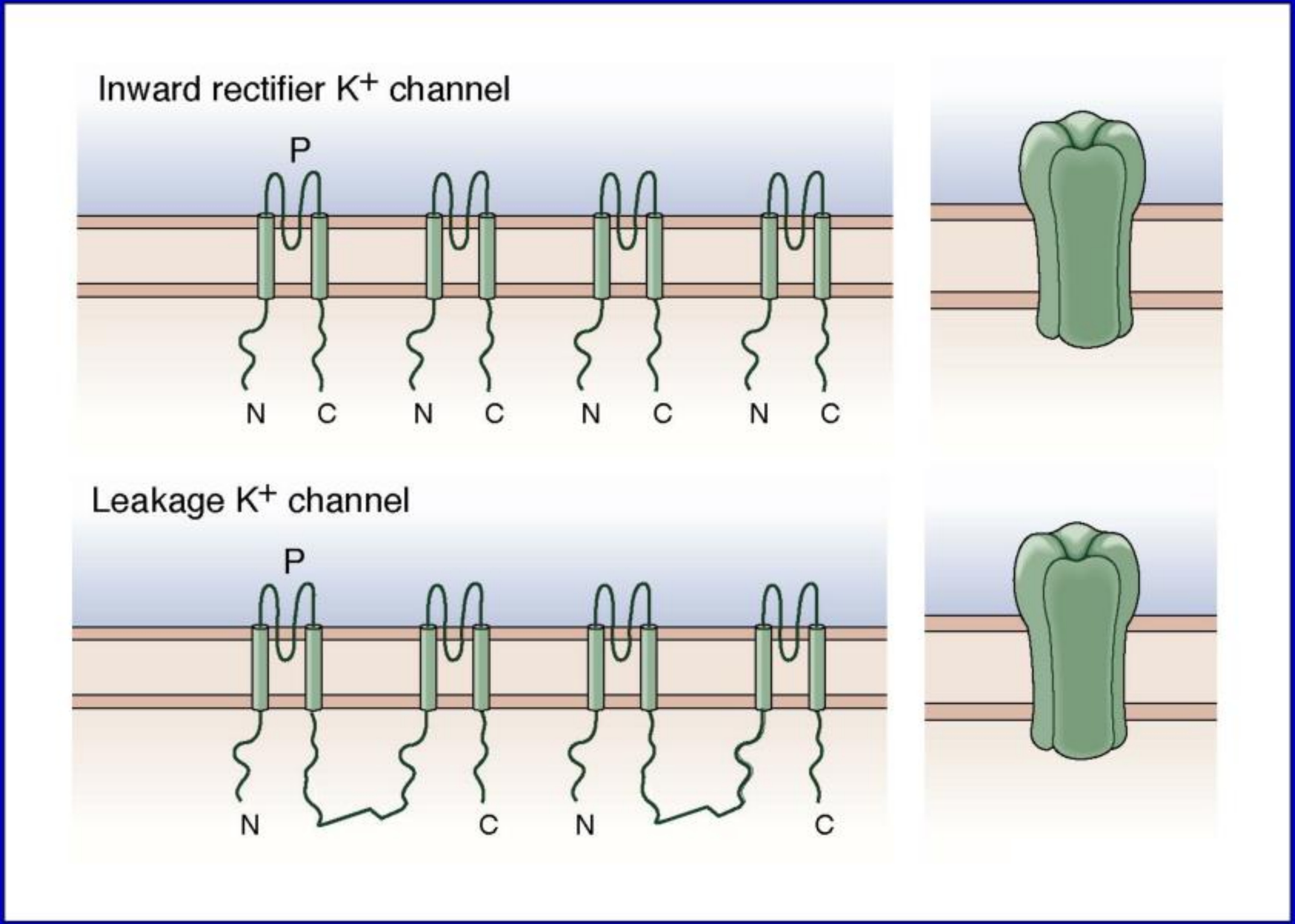
Voet & Voet



4 families

(75 genes)

Leakage K⁺ Channels Are Dimers of Subunits With Two P-Loops Each



tetramer

4 x 2 = 8 TM

dimer

2 x 4 = 8 TM

Leakage channels are “almost always ” open

Potassium leakage

Ion channels

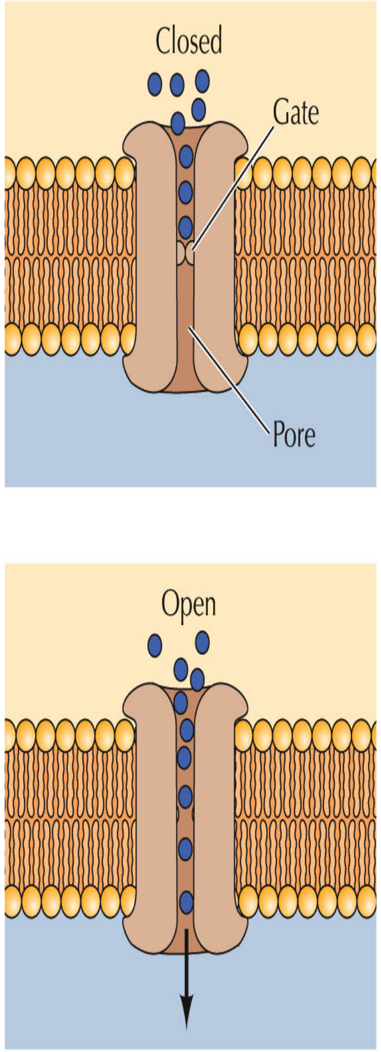
Ions **never** diffuse through the plasma membrane

- **Porins** permit the free passage of ions and small polar molecules through the outer membranes of bacteria.
- **Ion channels** mediate the passage of ions across plasma membranes.

◊ **Ligand-gated channels** open in response to the binding of neurotransmitters or other signaling molecules.

◊ **Voltage-gated channels** open in response to changes in electric potential across the plasma membrane.

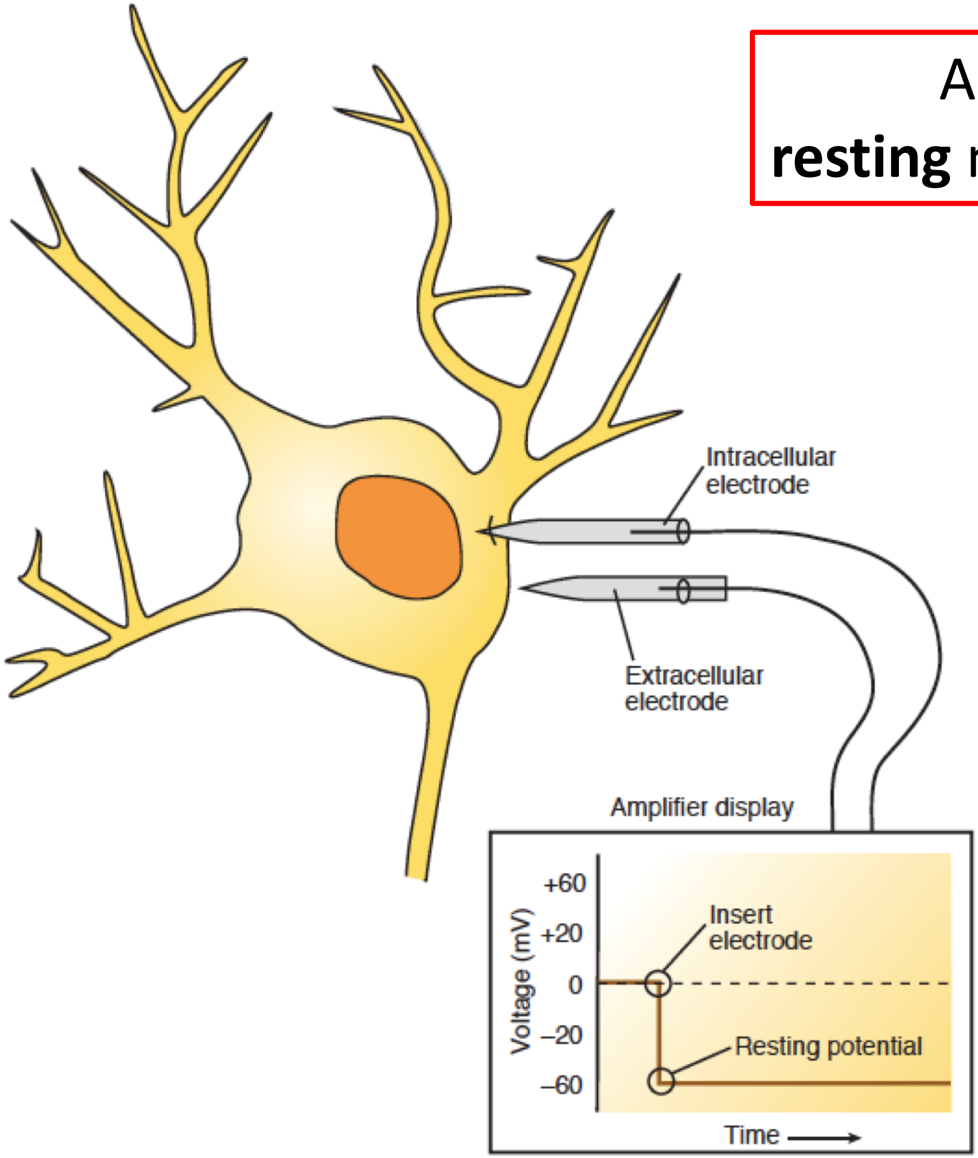
Leakage channels are “almost always ” open

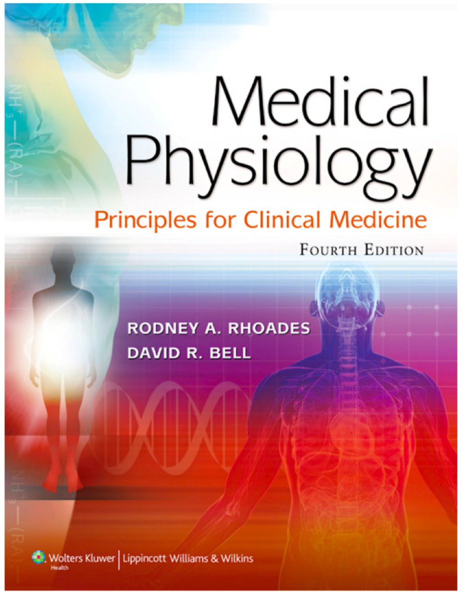


THE CELL, Fourth Edition, Figure 13.18 © 2006 ASM Press and Sinauer Associates, Inc.

Membrane potential

All cells have a
resting membrane potential

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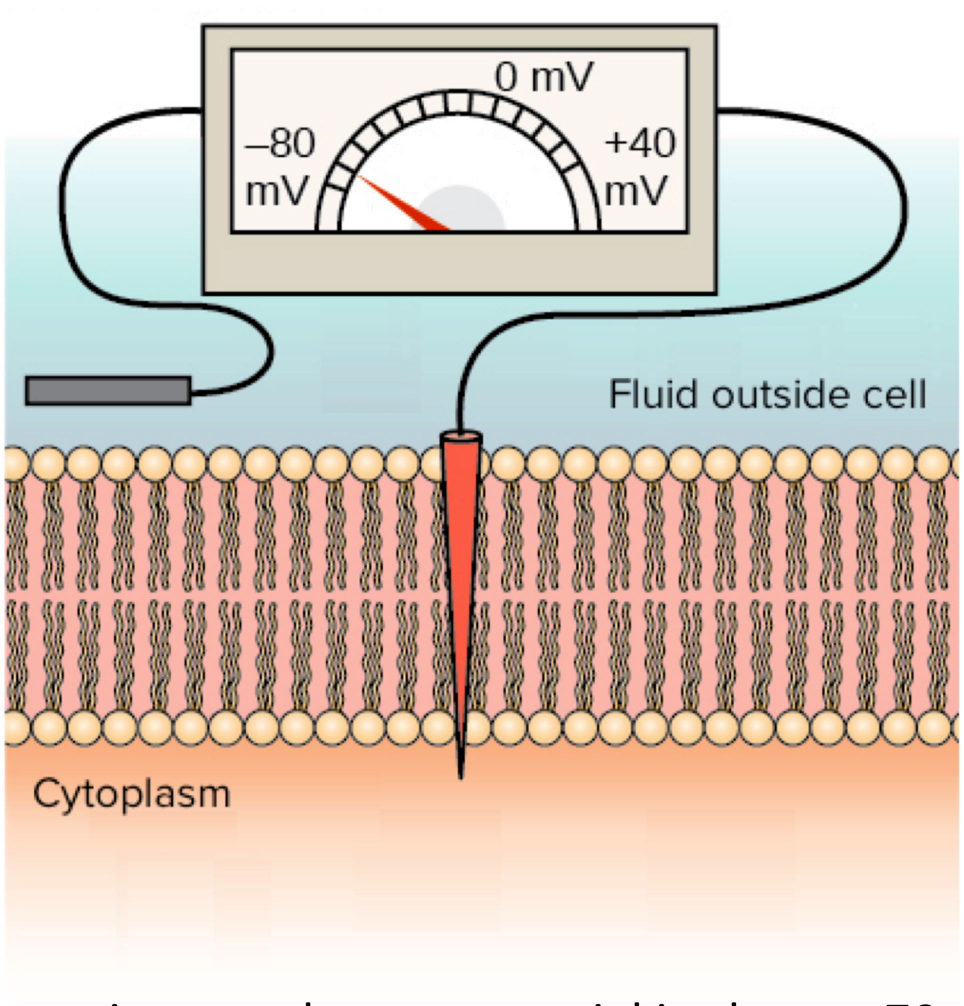
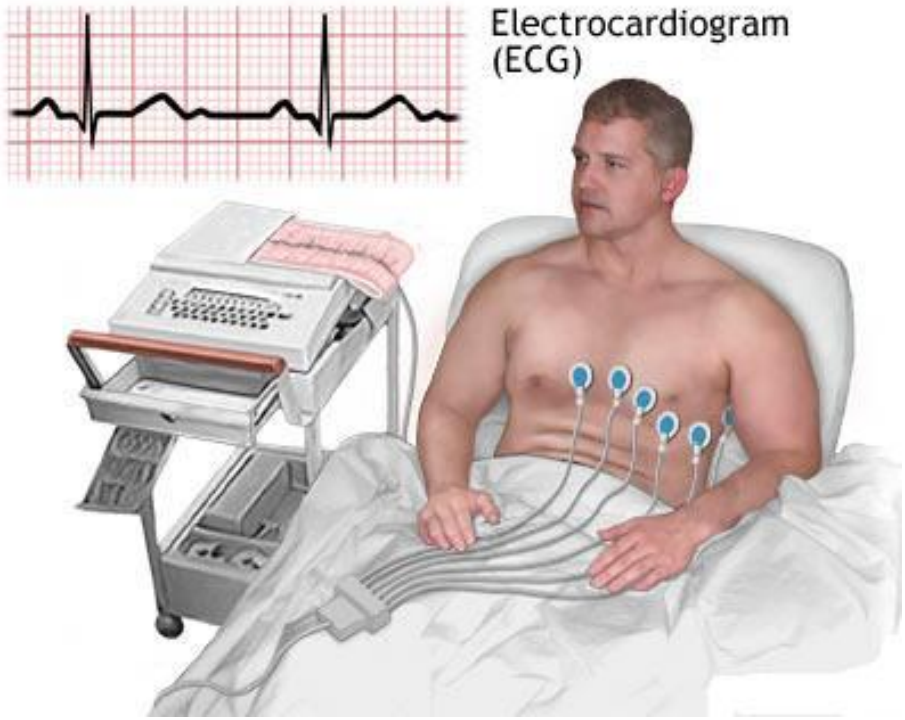
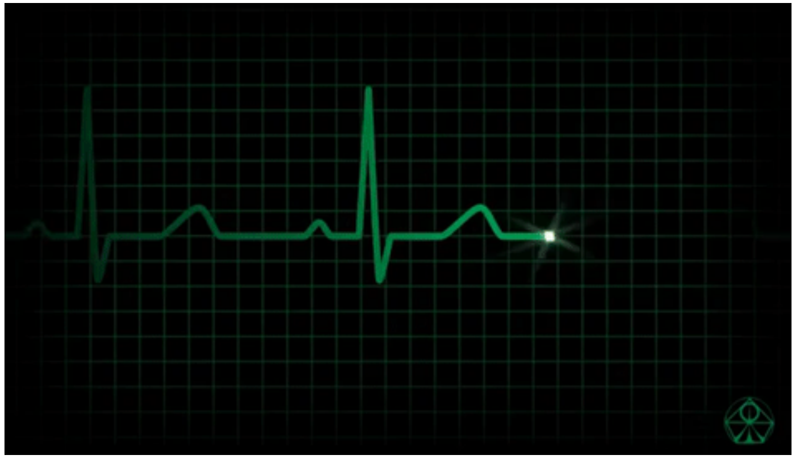
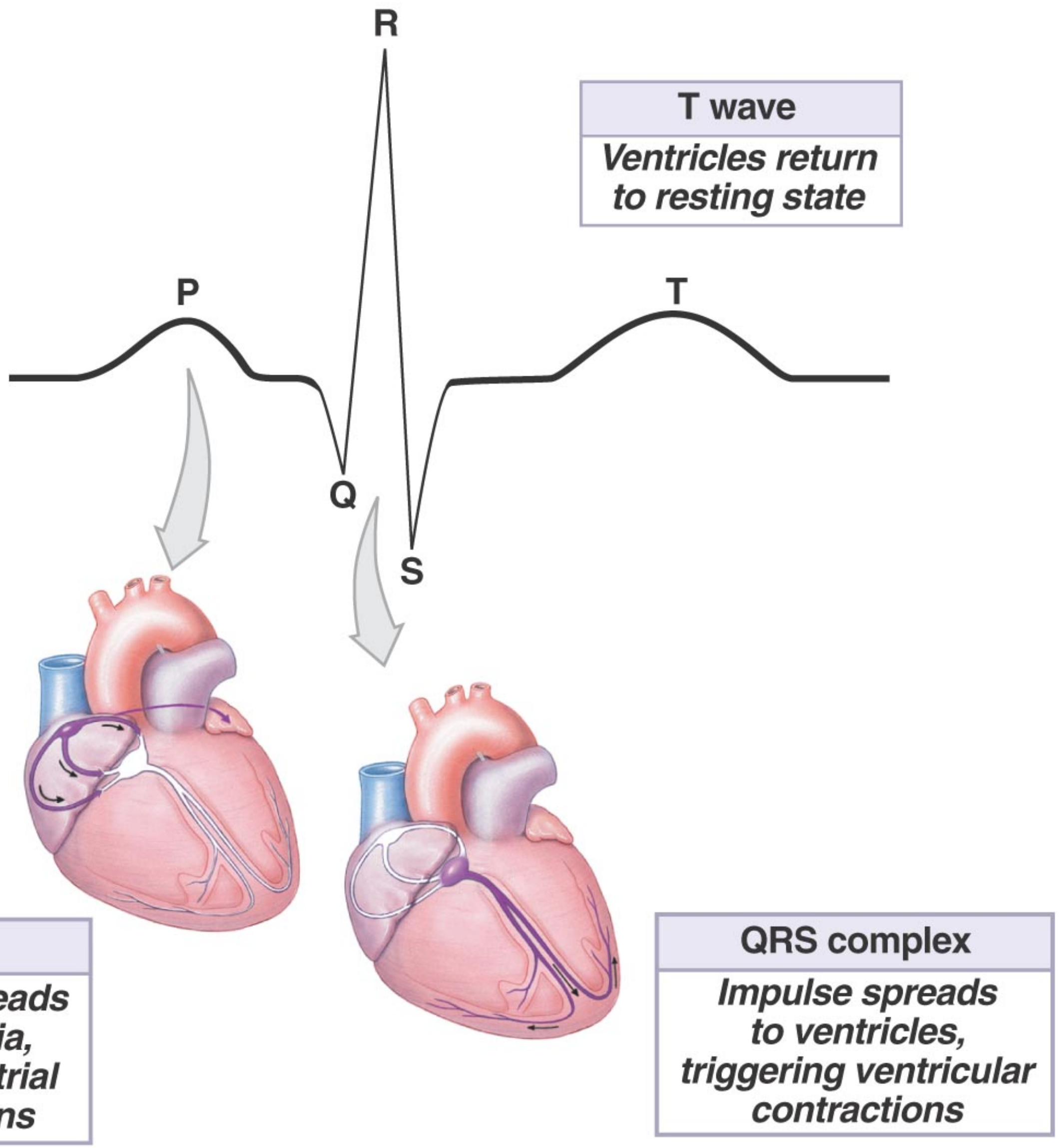
Health



The resting membrane potential is about – 70 mV.







T wave

Ventricles return to resting state

P wave

Impulse spreads across atria, triggering atrial contractions

QRS complex

Impulse spreads to ventricles, triggering ventricular contractions

EEG : Electro Encephalo Graphy

(a)

(b)

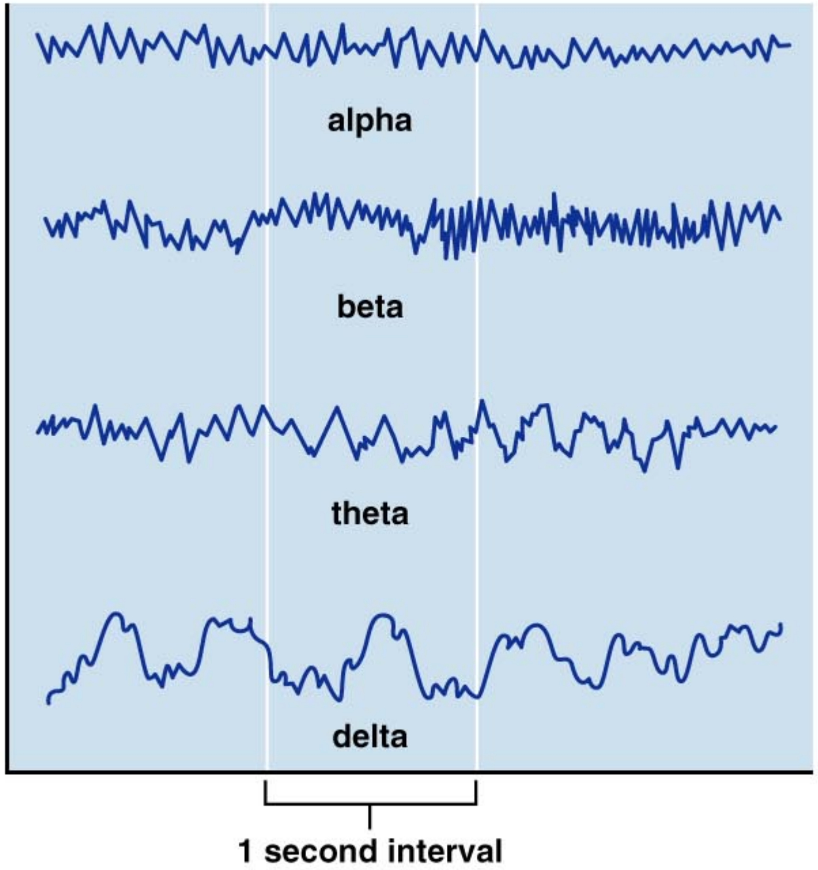
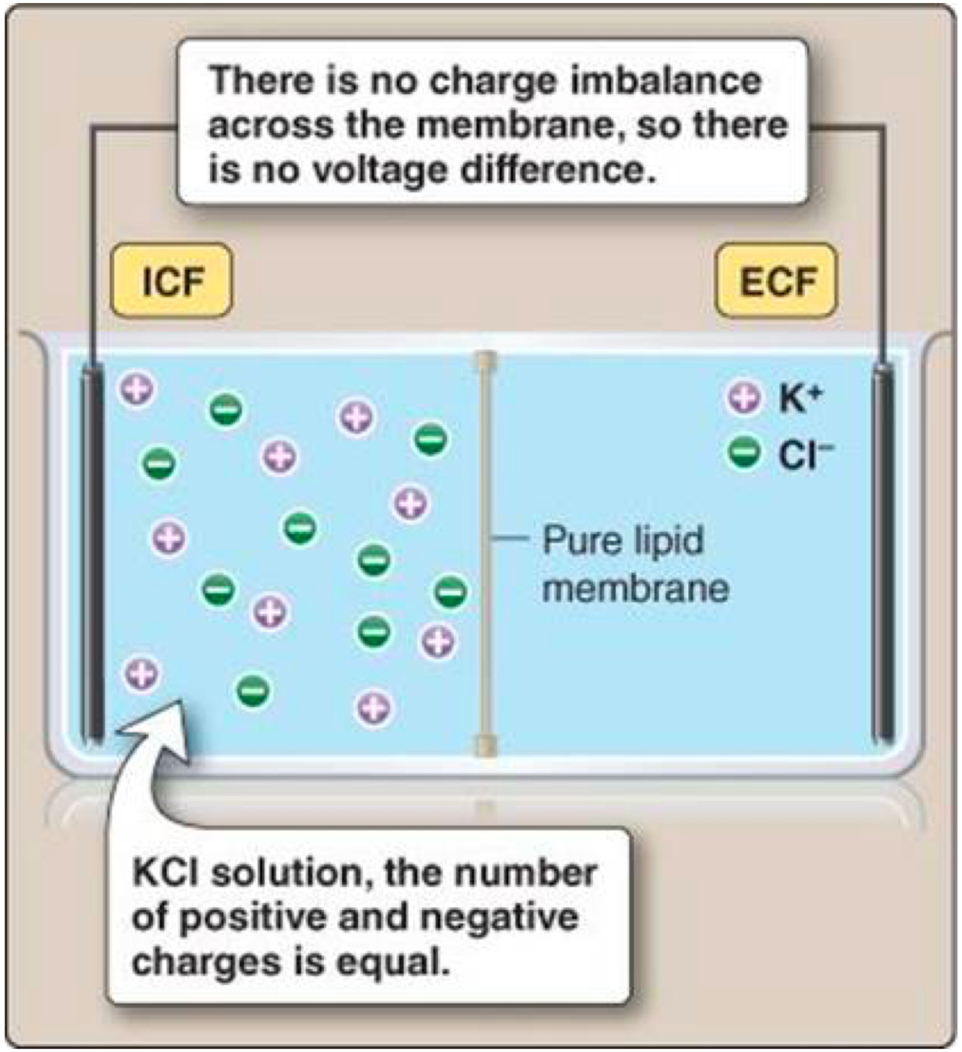
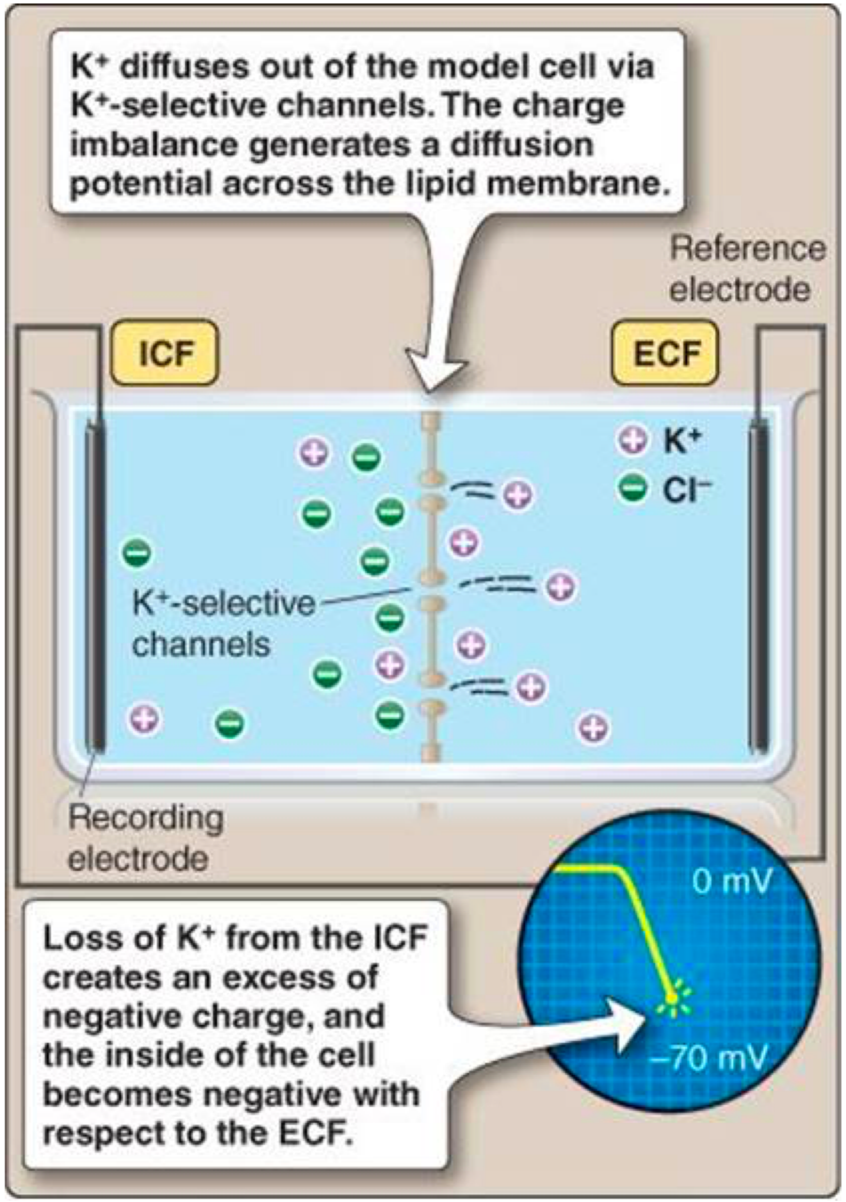


Figure 12.20



There is no charge imbalance across the membrane, so there is no voltage difference.

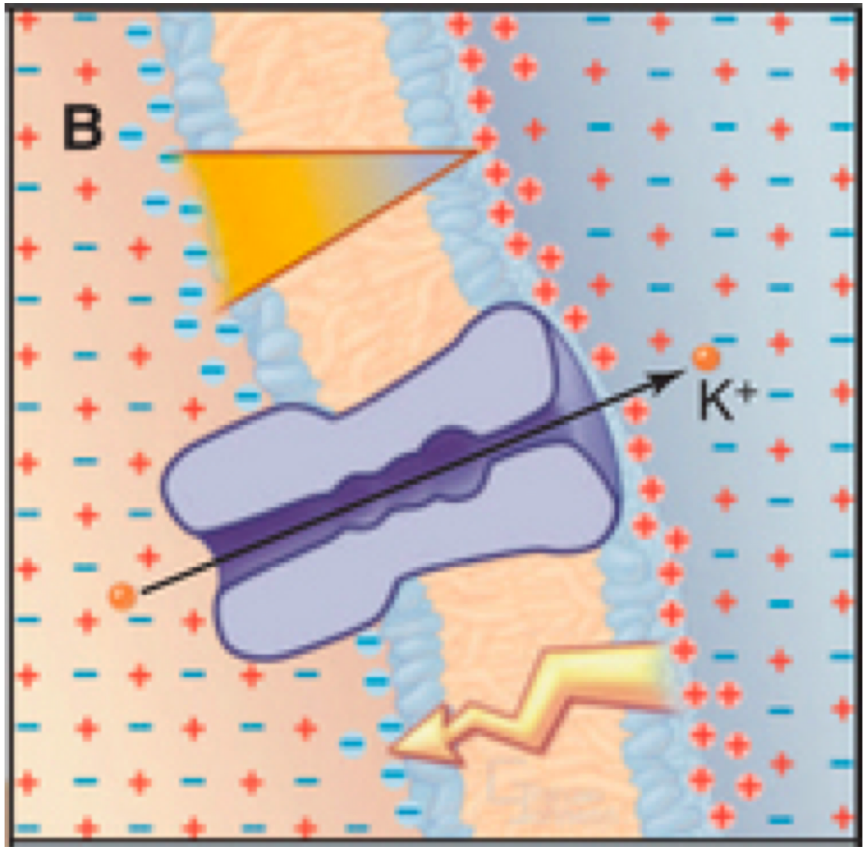
KCl solution, the number of positive and negative charges is equal.



K^+ diffuses out of the model cell via K^+-selective channels. The charge imbalance generates a diffusion potential across the lipid membrane.

Loss of K^+ from the ICF creates an excess of negative charge, and the inside of the cell becomes negative with respect to the ECF.

Potassium channels play a key role in resting membrane potential.

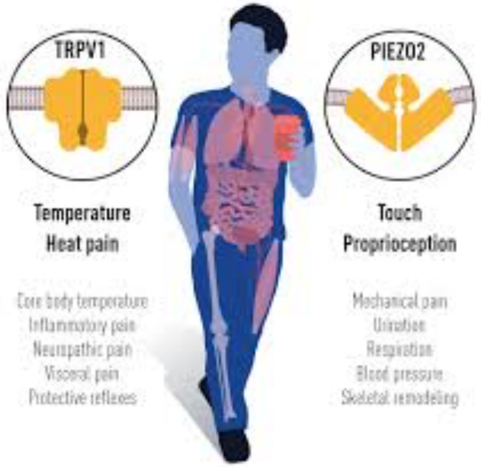


The triangle represents the **concentration difference** of K+ across the membrane.

The zigzag arrow represents the **membrane potential**, negative inside.

Note the electrical neutrality everywhere except very close to the cell membrane.

Nobel prize 2021 for Medicine :



To researchers who discovered ions channels