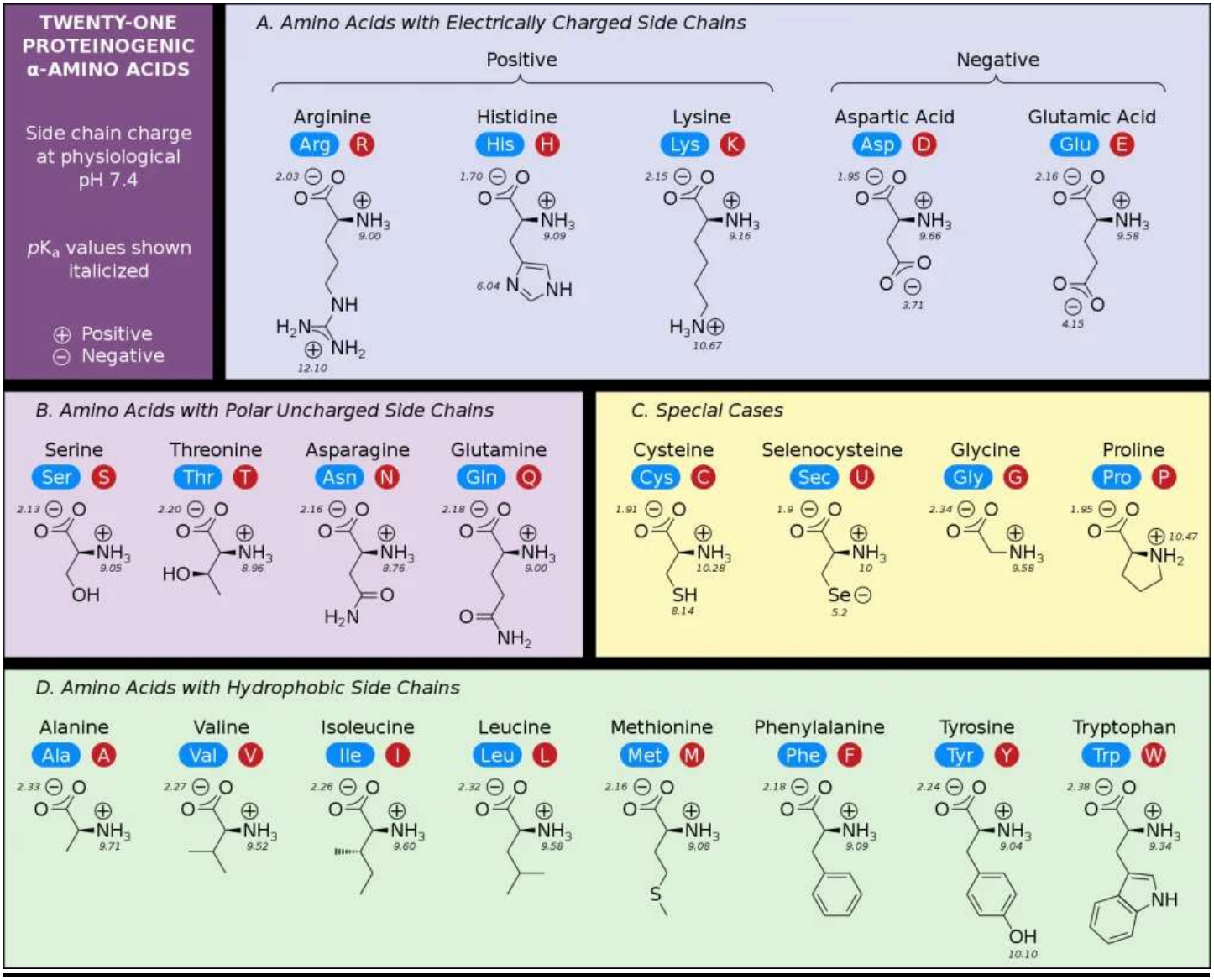


Protein Conformation

The four atoms of the peptide bond and the two consecutive α-carbons lie in a single plane. The H and the O atoms are *trans* to each other (Fig. 2-1). The peptide bond is rigid, but the planes can rotate about the α-carbon atoms. The distance between consecutive α-carbon atoms remains 3.6 Å. Thus, a fully extended polypeptide chain of 1000amino acid residues is 3600 Å long.

Source: Biochemical Calculations - How to Solve Mathematical Problems in General Biochemistry, Second Edition, Irwin H. Segel, pg.101

The linear polypeptide chain can assume a number of different secondary structures, depending on the nature of the R-groups present. One common structure is called the α-helix (Fig. 2-2). This is a right-handed helix with 3.6 amino acid residues per turn. (A right-handed helix can be visualized by making a fist with your right hand, with the thumb extended. Your thumb points in the direction that the helix progresses, while your other fingers indicate the rotation of the helix. Thus, a right-handed helix progresses upward while coiling counter-clockwise.) The α-helix has a pitch of 5.4 Å. That is, for each turn, the helix rises 5.4 Å along the axis. The α-helix is stabilized by intrachain hydrogen bonds between the —C═O of each peptide bond and the —NH of the peptide bond four residues away. (If the H is called atom number 1, the hydrogen-bonded oxygen is the 13th atom along the chain. Thus, the coil is designated a 3.6_{13} helix.) The α-helix is prevented from forming by two or more consecutive residues with like charges (e.g., lysine, glutamate) or by two or more consecutive residues with bulky R-groups that branch at the β-carbon (e.g., isoleucine, threonine, valine). In these cases, the polypeptide chain may assume a random coil structure. Proline cannot participate in forming an α-helix because the nitrogen atom is in a rigid ring. Thus, no rotation about the α-carbon is possible. Also, there are no hydrogen atoms on the nitrogen of a proline residue, so no intrachain hydrogen bonds can form. Successive serine residues disrupt the α-helix because of the tendency of the OH groups to hydrogen bond strongly to water. Stretches of proline and serine coil into helical arrangements other than an α-helix.

Repeating sequences of amino acids with small, compact R-groups (e.g., glycine, alanine) tend to form the β, or pleated sheet, structure, which consists of parallel (Fig. 2-3*a*) or antiparallel (Fig. 2-3*b*) polypeptide chains linked by interchain hydrogen bonds. Silk is an example of the antiparallel sheet.

Most nonfibrous proteins have a very precise and compact three-dimensional or tertiary structure formed when the α-helix and random coil of the polypeptide chain bends, twists, and folds over and back upon itself. The tertiary structure is stabilized by interactions of amino acid R-groups (Fig. 2-4*a*), and thus, is dictated by the primary structure. The biochemical function of a protein is intimately tied to its tertiary structure. That is, to function in a certain way, a protein must have the correct tertiary structure. Stated conversely: only one specific tertiary structure will permit a protein to serve optimally a specific function (see also Figs. 4-3 and 4-4).

Many proteins have still another order of structural complexity—a quaternary structure formed by the noncovalent association of tertiary-structured subunits (Fig. 2-4*b*). Often, only the quaternary structured protein (dimer, tetramer, and so on) shows full activity.

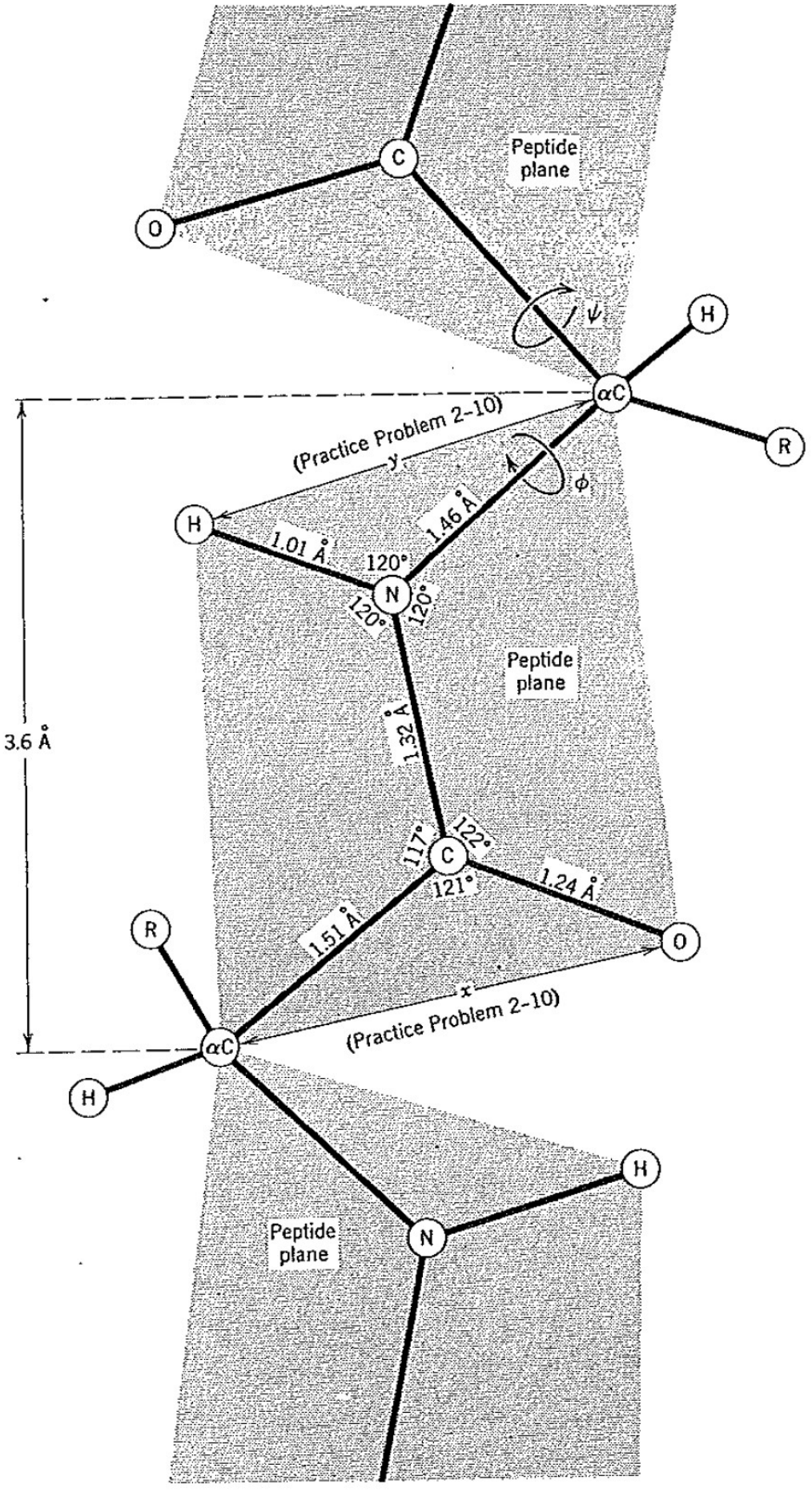
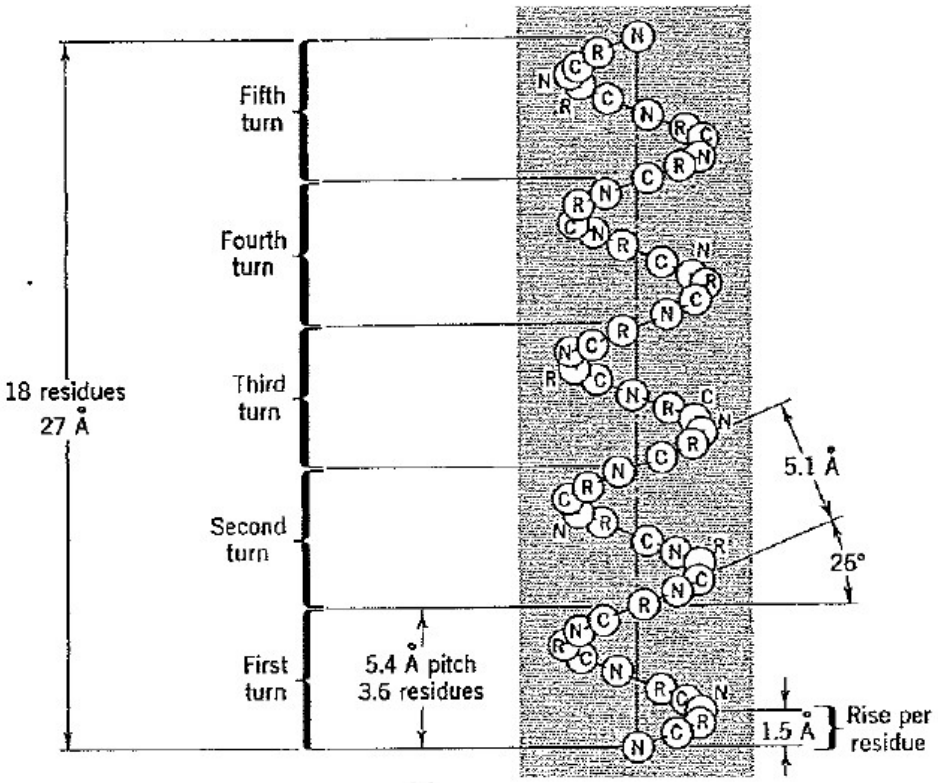
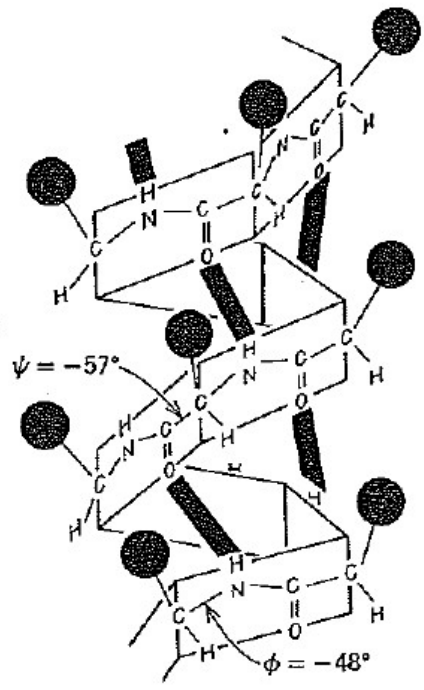


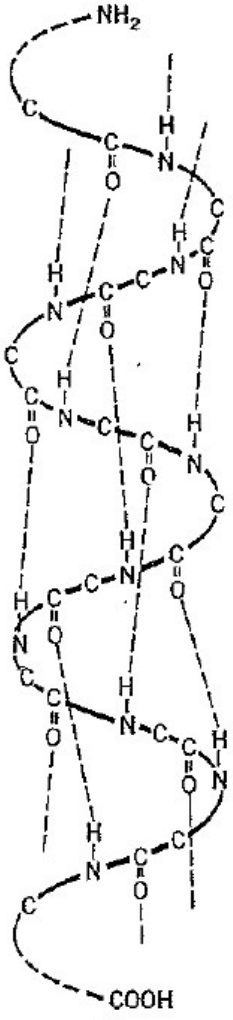
Figure 2-1 The peptide bond is rigid and fixed in a plane. The planes can rotate about the α-carbons. The rotation is described by the angles ϕ and ψ.


Fifth turn
Fourth turn
Third turn
Second turn
First turn
18 residues
27 Å
5.4 Å pitch
3.6 residues
5.1 Å
26°
1.5 Å
Rise per residue

(a)


ψ = −57°
φ = −48°

(b)


NH2
COOH

(c)

Figure 2-2 Three representations of the α-helix. The helix rises 1.5 Å per residue and completes a turn every 3.6 residues to yield a pitch of 5.4 Å. When the NH_2 terminus is placed at the top, each —C=O is hydrogen-bonded to an —NH four residues (but three peptide planes) below. (*a*) Redrawn from from E. E. Conn and P. K. Stumpf, *Outlines of Biochemistry.* Wiley (1972). R represents the α-carbon. (*b*) Redrawn from R. Barker, *Organic Chemistry of Biological Molecules.* Prentice-Hall (1971). (*c*) Redrawn from K. D. Kopple, *Peptides and Amino Acids.* Benjamin (1966). For clarity, the R-groups on the α-carbons are not shown.

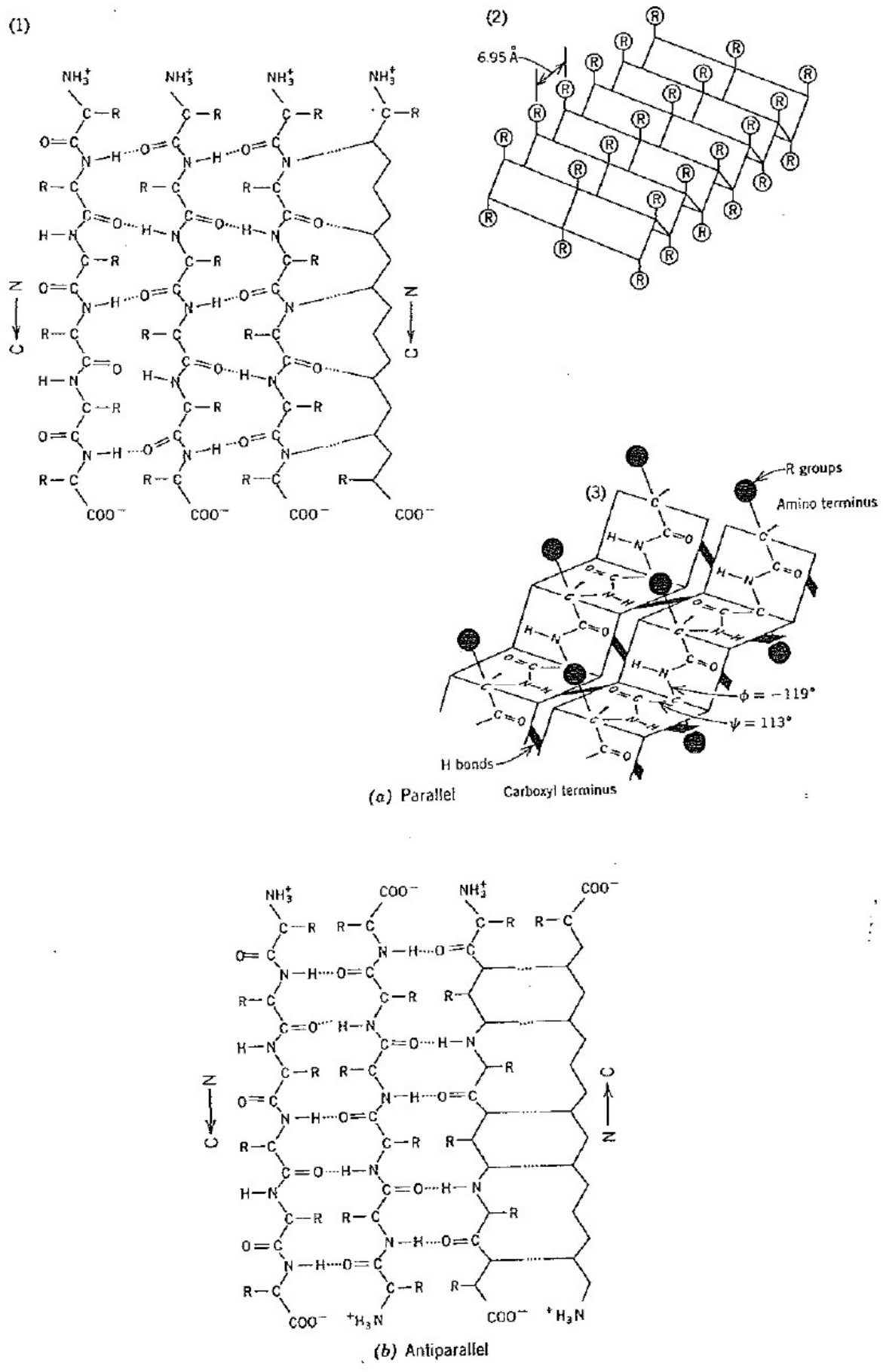
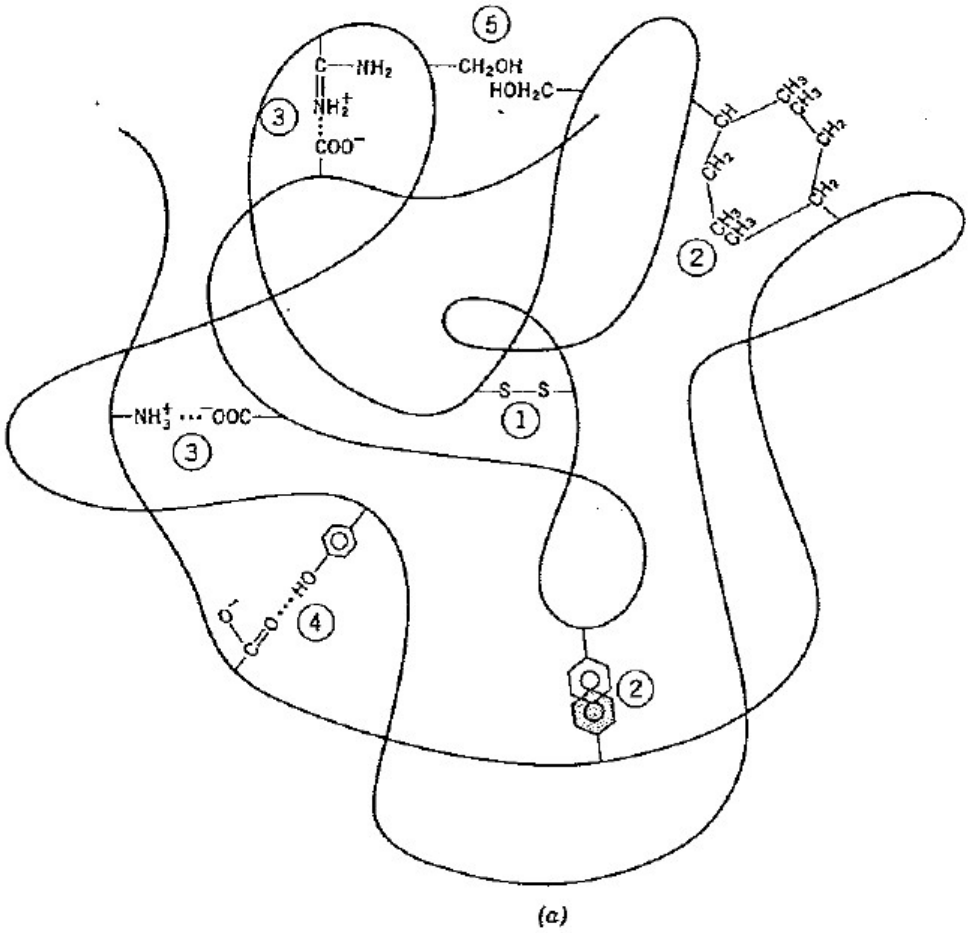
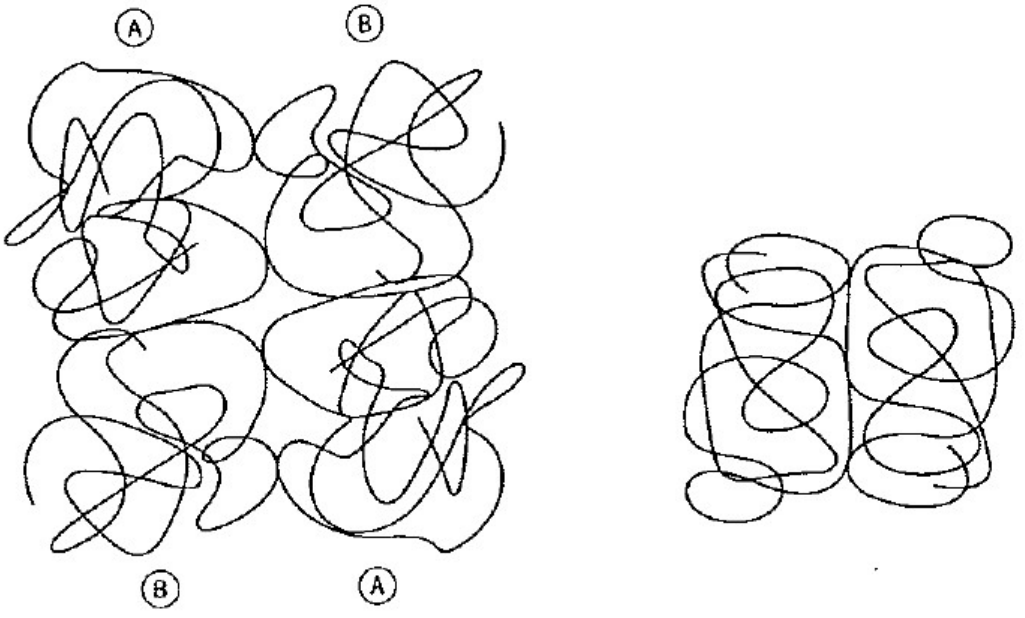


Figure 2-3 (*a*) Three representations of the parallel β-structure. Representation 3 is redra from Barker (1971). (*b*) Antiparallel β-structure.



(a)



Tetramer
(composed of two different subunits)

(b)

Dimer
(composed of identical subunits)

Figure 2-4 (*a*) The tertiary structure of a protein is stabilized by (1) covalent disulfide bonds formed by the oxidation of two cysteine residues; (2) hydrophobic interactions; (3) ionic interactions (salt linkages); (4) hydrogen bonds; and (5) dipole–dipole interactions. (*b*) The association of tertiary-structured subunits to form a dimer and a tetramer (quaternary structures). The subunits of an oligomer are not always identical.