

(n) (n+4)  
 C=O ... H-N  
 Hydrogen bond

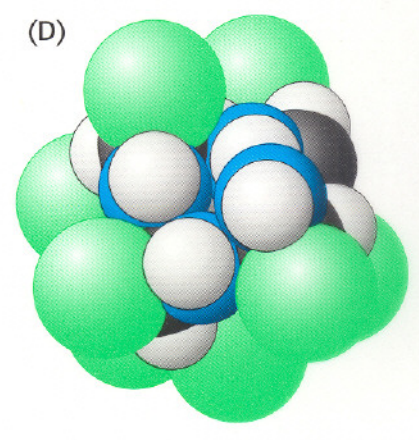
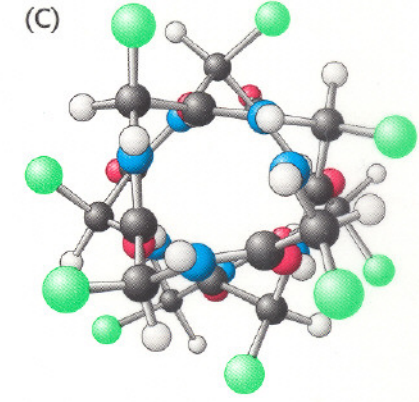
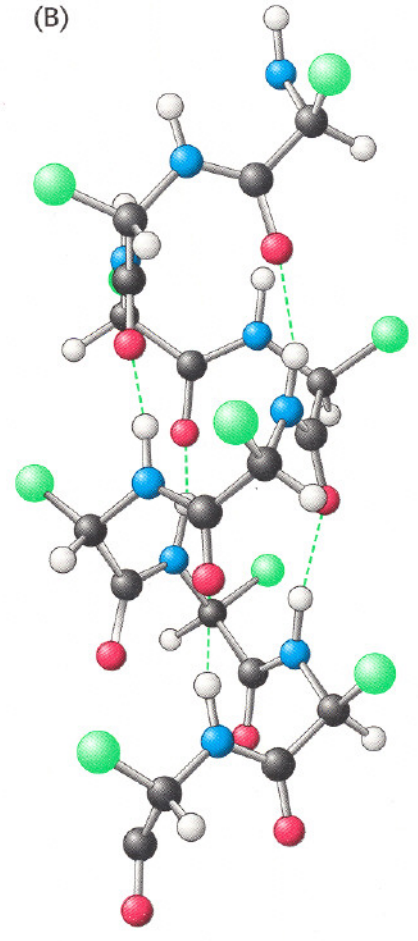
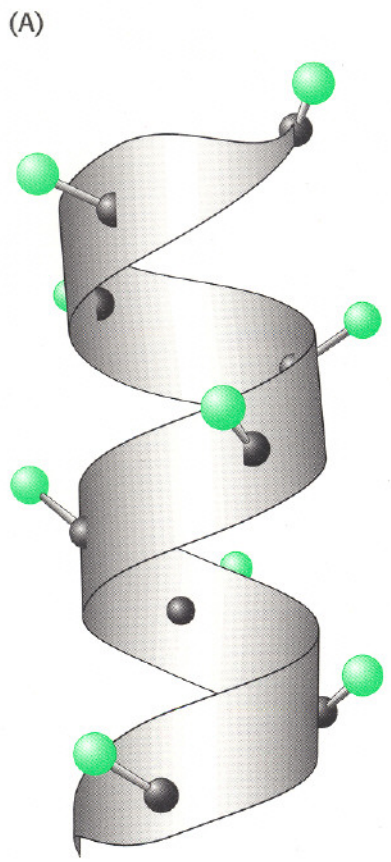
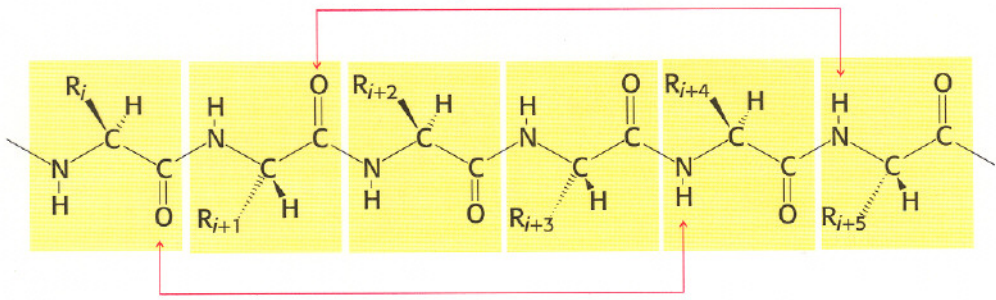


Figure 3-29, 3-30  
 Stryer, Tymoczko, & Berg, BIOCHEMISTRY, Fifth Edition.  
 Copyright © 2002 by W. H. Freeman and Company.

## **POLYPEPTIDE CHAINS CAN FOLD INTO REGULAR STRUCTURES SUCH AS THE HELIX**

**Can a polypeptide chain fold into a regularly repeating structure?**

- **In 1951, Pauling and Corey proposed two periodic polypeptide structures, called the helix and the pleated sheet.**

### **Features of the $\alpha$ - helix:**

- **rod-like structure**
- **the tightly coiled polypeptide main chain forms the inner part of the rod**
- **the side chains extend outward in a helical array**
- **the helix is stabilized by hydrogen bonds between the NH and CO groups of the main chain**
- **there are 3.6 amino acid residues per turn of helix**
- **the screw sense of the  $\alpha$ - helix found in proteins is right-handed**

**The  $\alpha$ - helical content of proteins ranges widely, from nearly none to almost 100%**



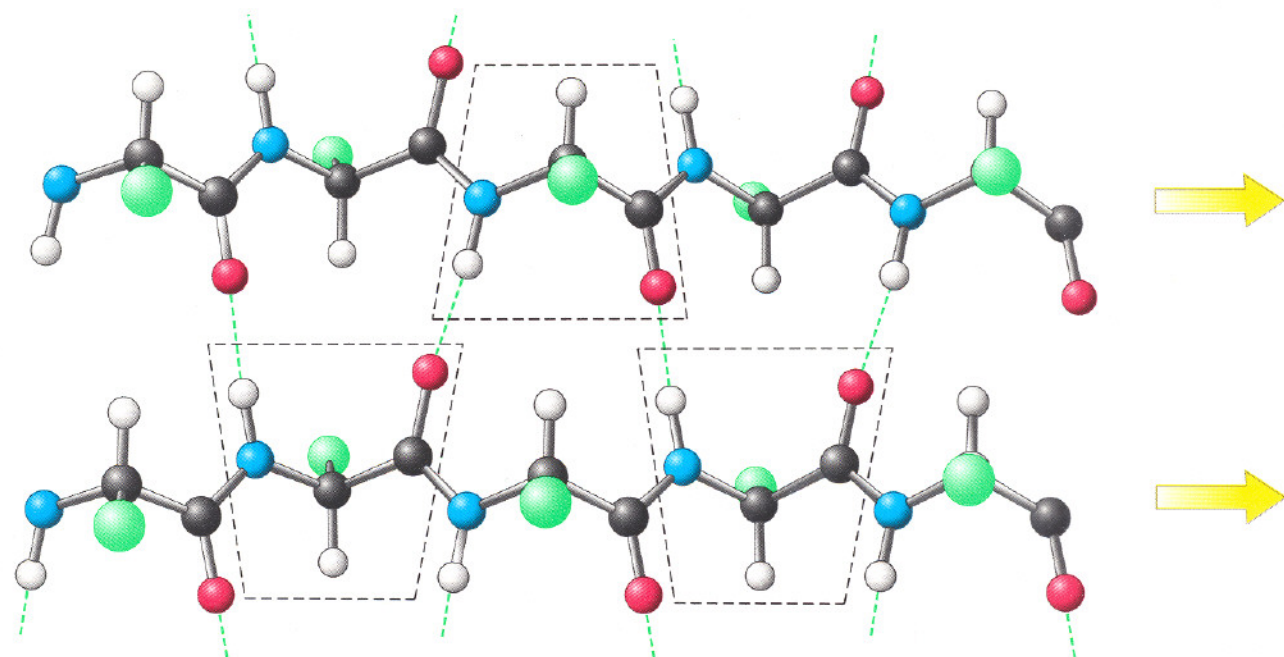
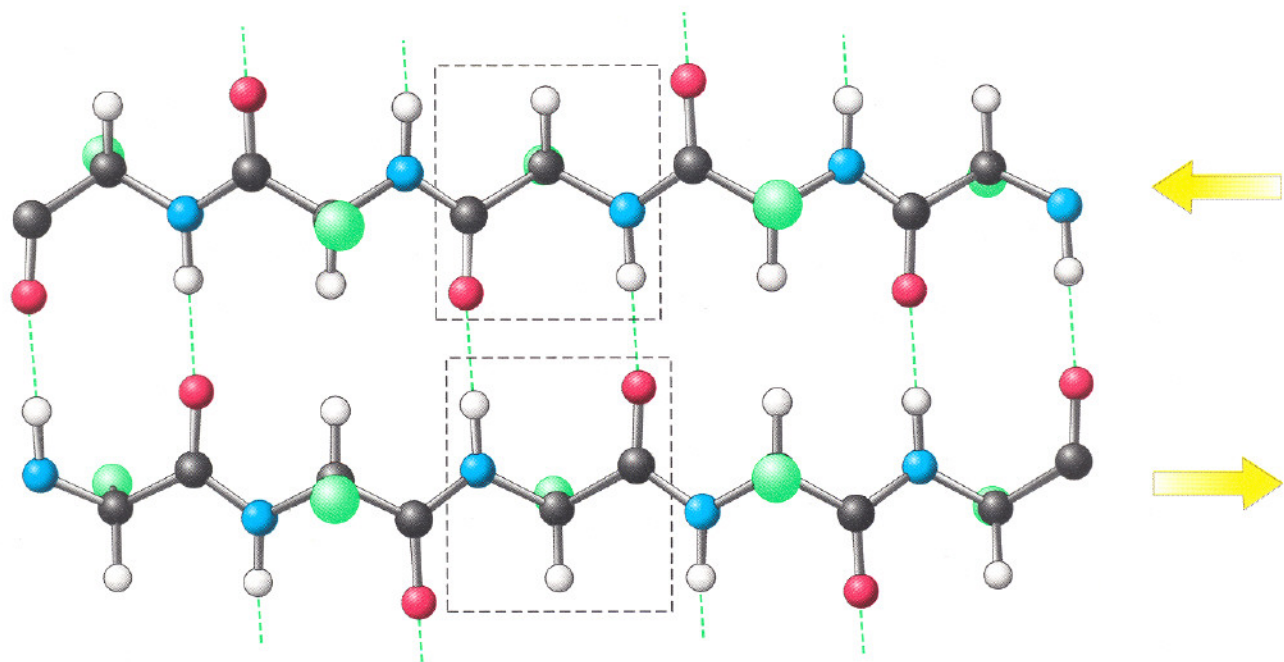
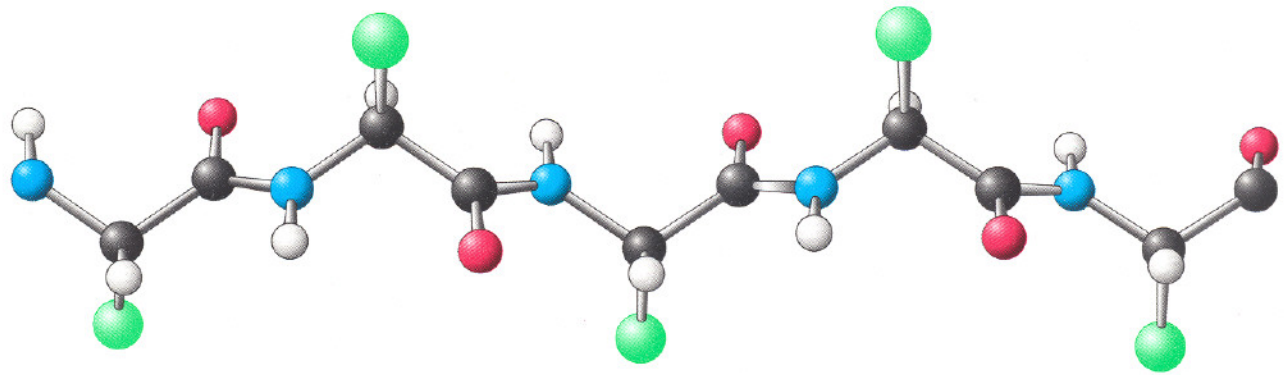


Figure 3-36, 3-37, 3-38  
 Stryer, Tymoczko, & Berg, BIOCHEMISTRY, Fifth Edition.  
 Copyright © 2002 by W. H. Freeman and Company.

## **$\beta$ PLEATED SHEETS ARE STABILIZED BY HYDROGEN BONDING BETWEEN $\beta$ STRANDS**

**The  $\beta$  Pleated Sheet Differs Markedly from the Rod- like  $\alpha$ -helix**

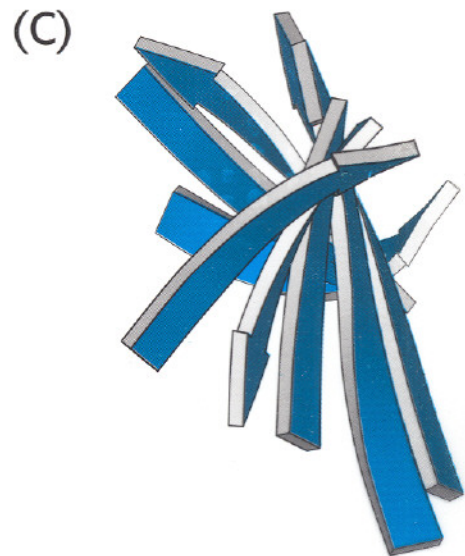
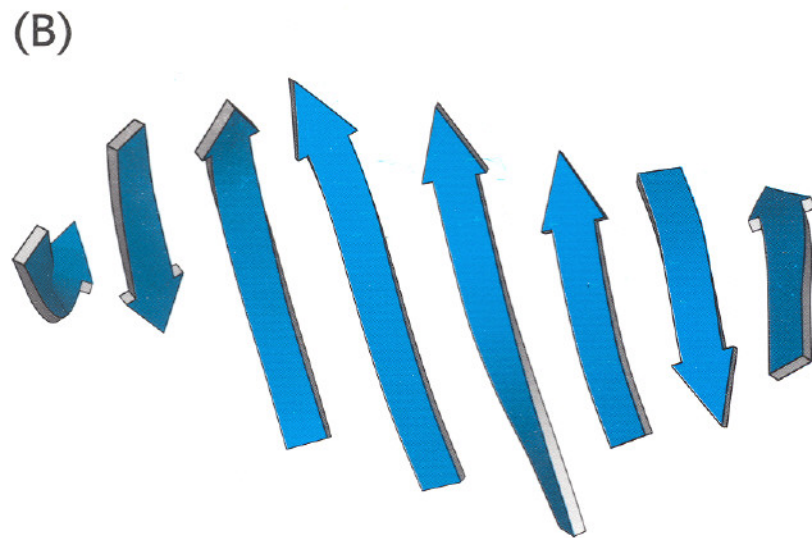
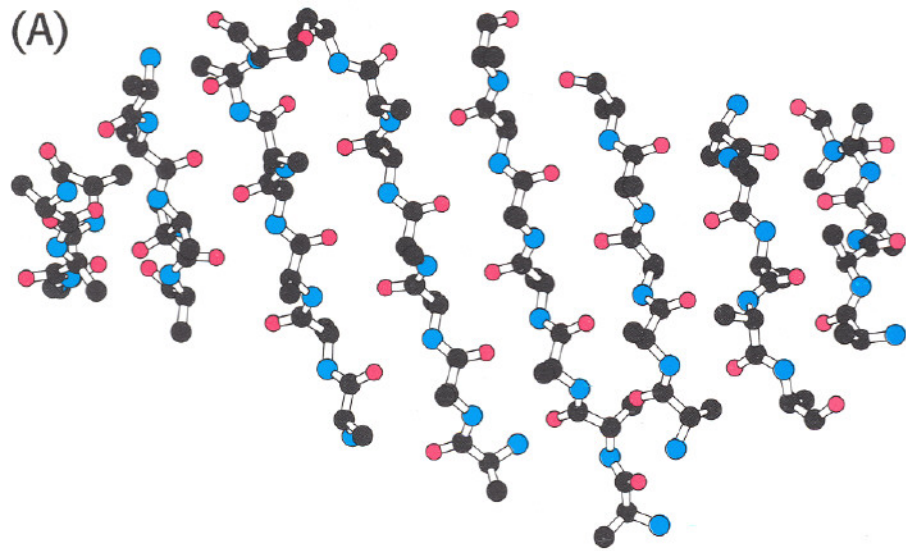
- **The polypeptide chain (called  $\beta$  strand is almost fully extended rather than tightly coiled as in the  $\alpha$ -helix**
- **The axial distance between adjacent amino acids is 3.5 Å, in contrast with 1.5 Å for the  $\alpha$ -helix**
- **The  $\beta$  pleated sheet is stabilized by hydrogen bonds between NH and CO groups in different polypeptide chains, whereas in the helix the hydrogen bonds are in the same strand**

### **TWO TYPES OF $\beta$ PLEATED SHEET STRUCTURES:**

- 1. Parallel sheet: when the adjacent chains run in the same direction**
- 2. Anti-parallel sheet: when the adjacent chains run in opposite directions**

### **POLYPEPTIDE CHAINS CAN REVERSE DIRECTIONS BY MAKING HAIRPIN TURNS**

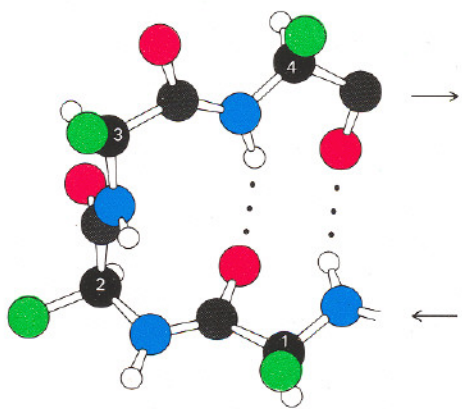
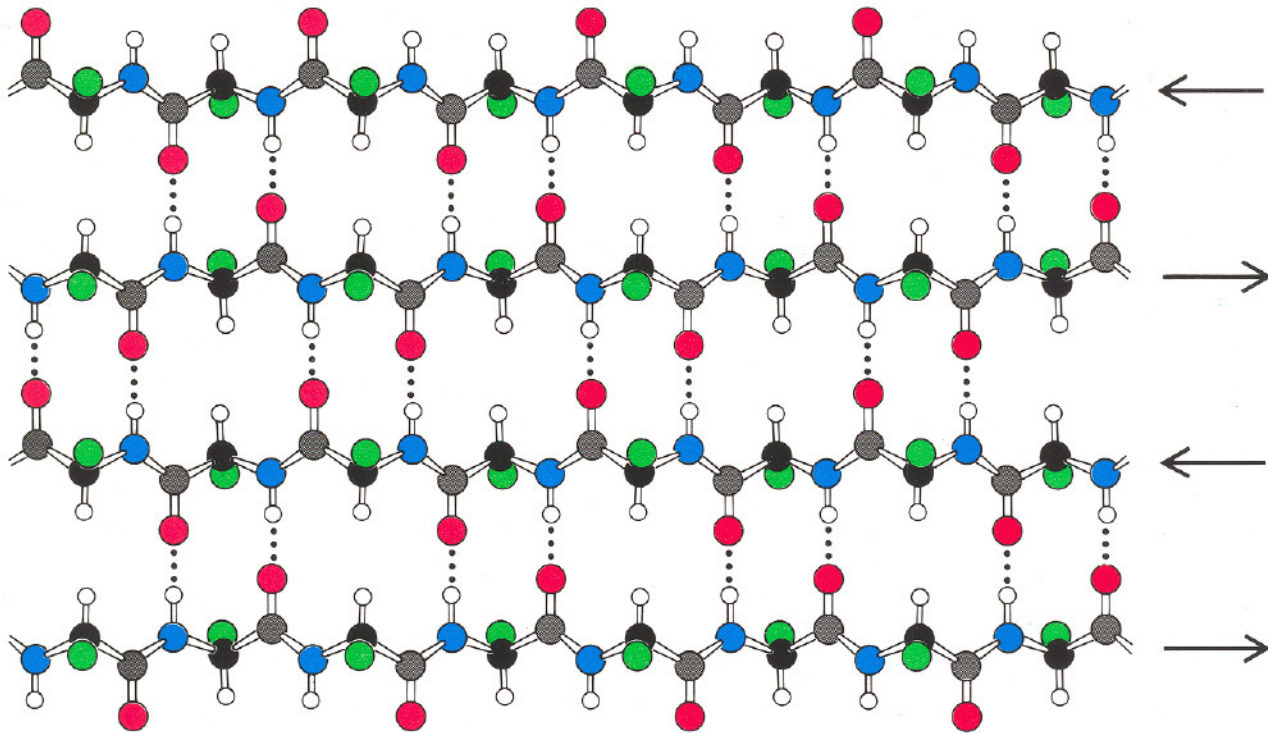
**Most proteins have compact, globular shapes owing to reversals in the direction of their polypeptide chains, accomplished by a common structural element called the  $\beta$  TURN**



*A twisted  $\beta$  sheet*

Figure 3-40  
Stryer, Tymoczko, & Berg, BIOCHEMISTRY, Fifth Edition.  
Copyright © 2002 by W. H. Freeman and Company.





Figures 2-36 and 2-37, page 31

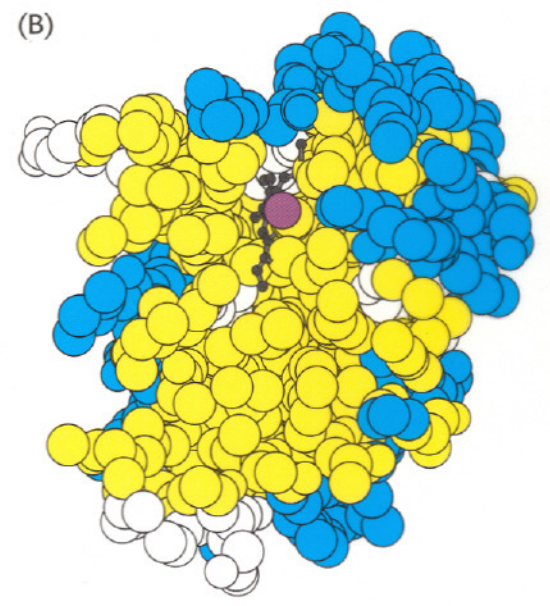
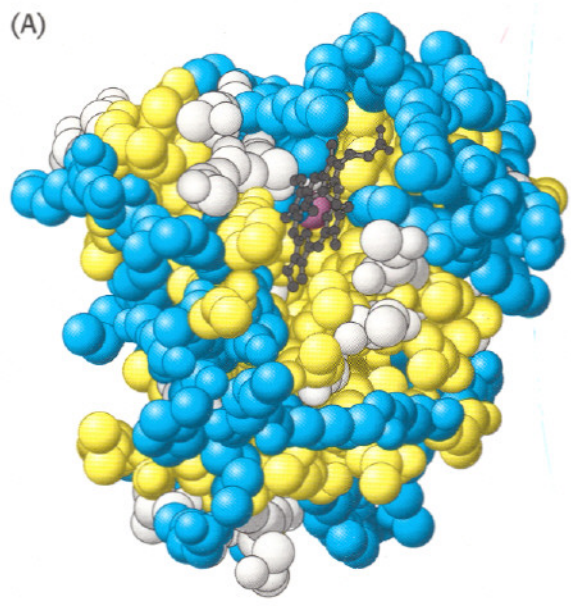
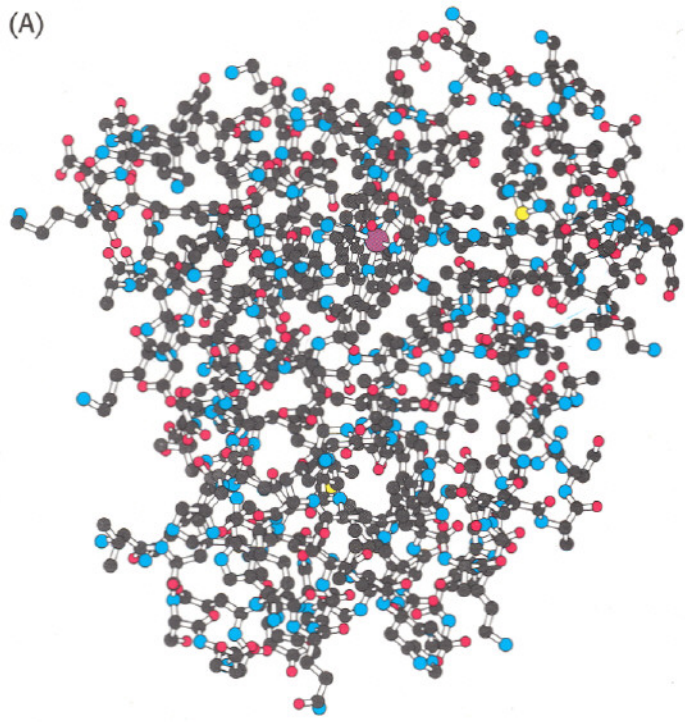
# WATER-SOLUBLE PROTEINS FOLD INTO COMPACT STRUCTURES WITH NONPOLAR CORES

e.g.:

## MYOGLOBIN

- Single polypeptide chain of 153 amino acids (mass= 18kd)
- It is the oxygen carrier in muscle. The capacity to bind oxygen depends on the presence of heme (a nonpolypeptide prosthetic group) consisting of protoporphyrin and a central iron atom
- It is extremely compact (overall dimensions: 45 x 35 x 25 Å)
- It is built primarily of  $\alpha$ - helices (eight); the rest of the chain forms <sup>turns</sup> between helices
- The interior consists almost entirely of nonpolar residues, whereas, the outside of myoglobin consists of both polar and nonpolar residues

The contrasting distribution of polar and nonpolar residues reveals a key facet of protein architecture: In an aqueous environment, protein folding is driven by the strong tendency of hydrophobic residues to be excluded from water.



3D structure of myoglobin  
Distribution of aa in myoglobin



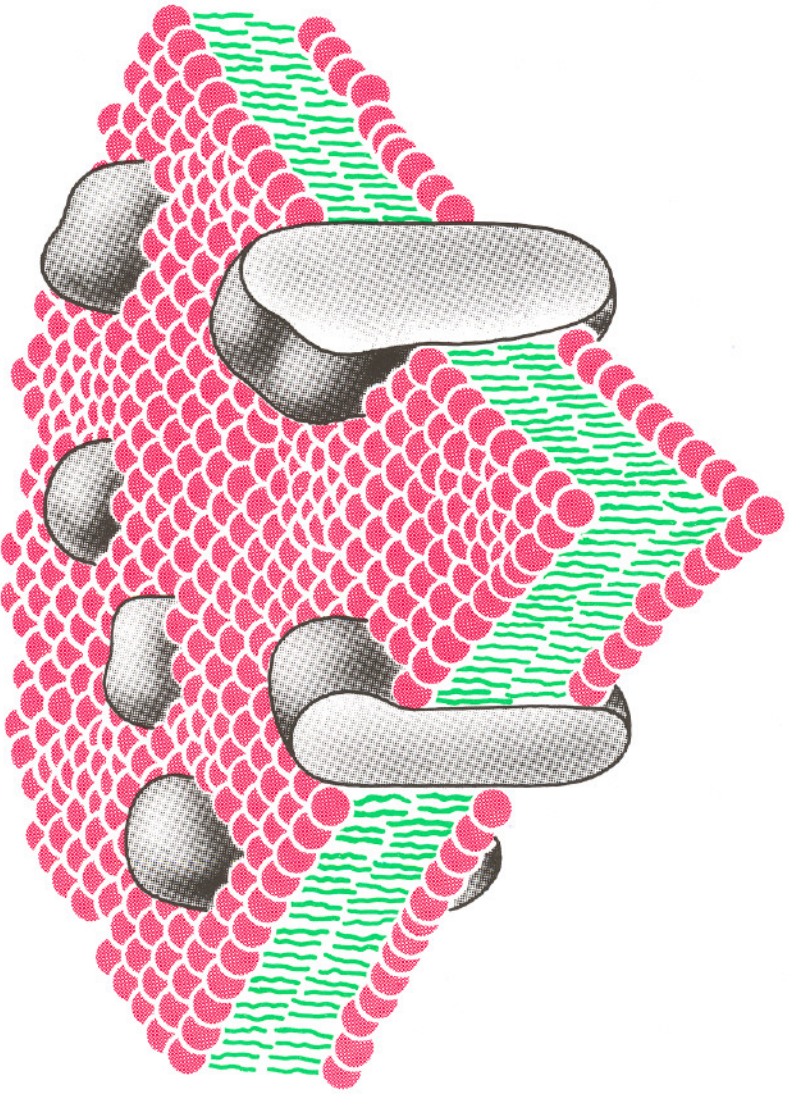
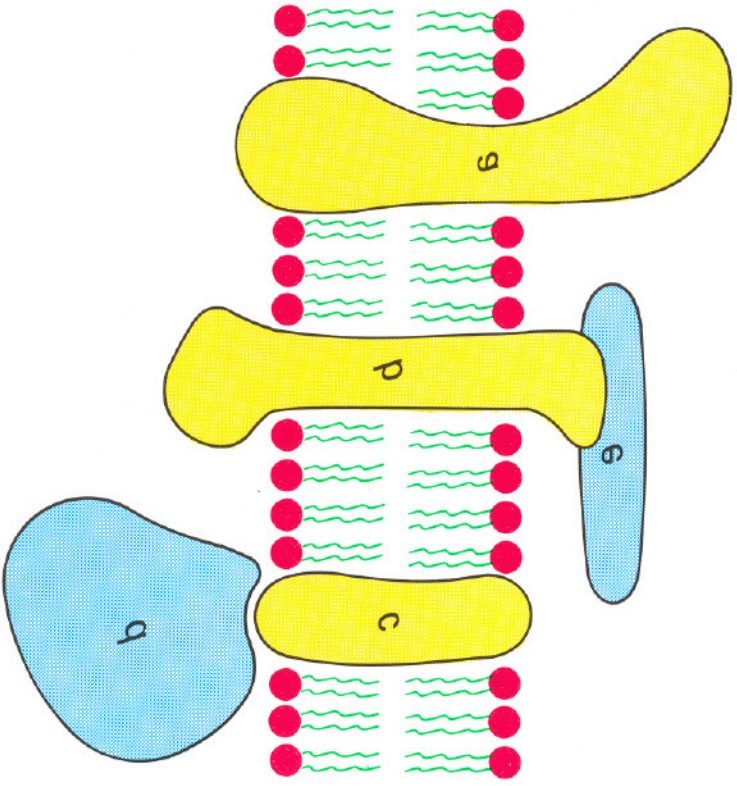
## **RIBONUCLEASE A (pancreatic enzyme that hydrolyzes RNA):**

- A single polypeptide chain of 124 residues
- Folded mainly into <sup>*β-*</sup>strands
- Contains a tightly packed, highly nonpolar interior
- Its structure, is further stabilized by four disulfide bonds

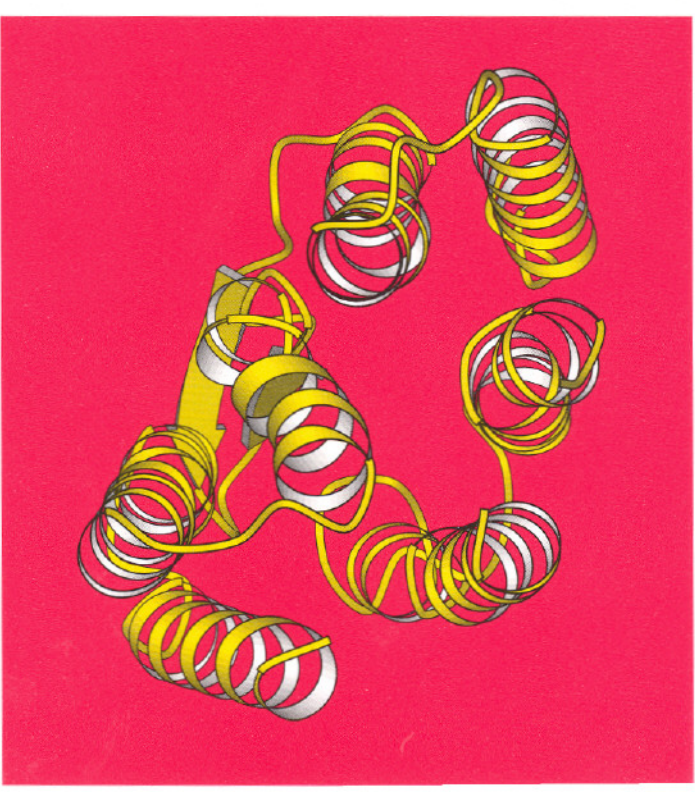
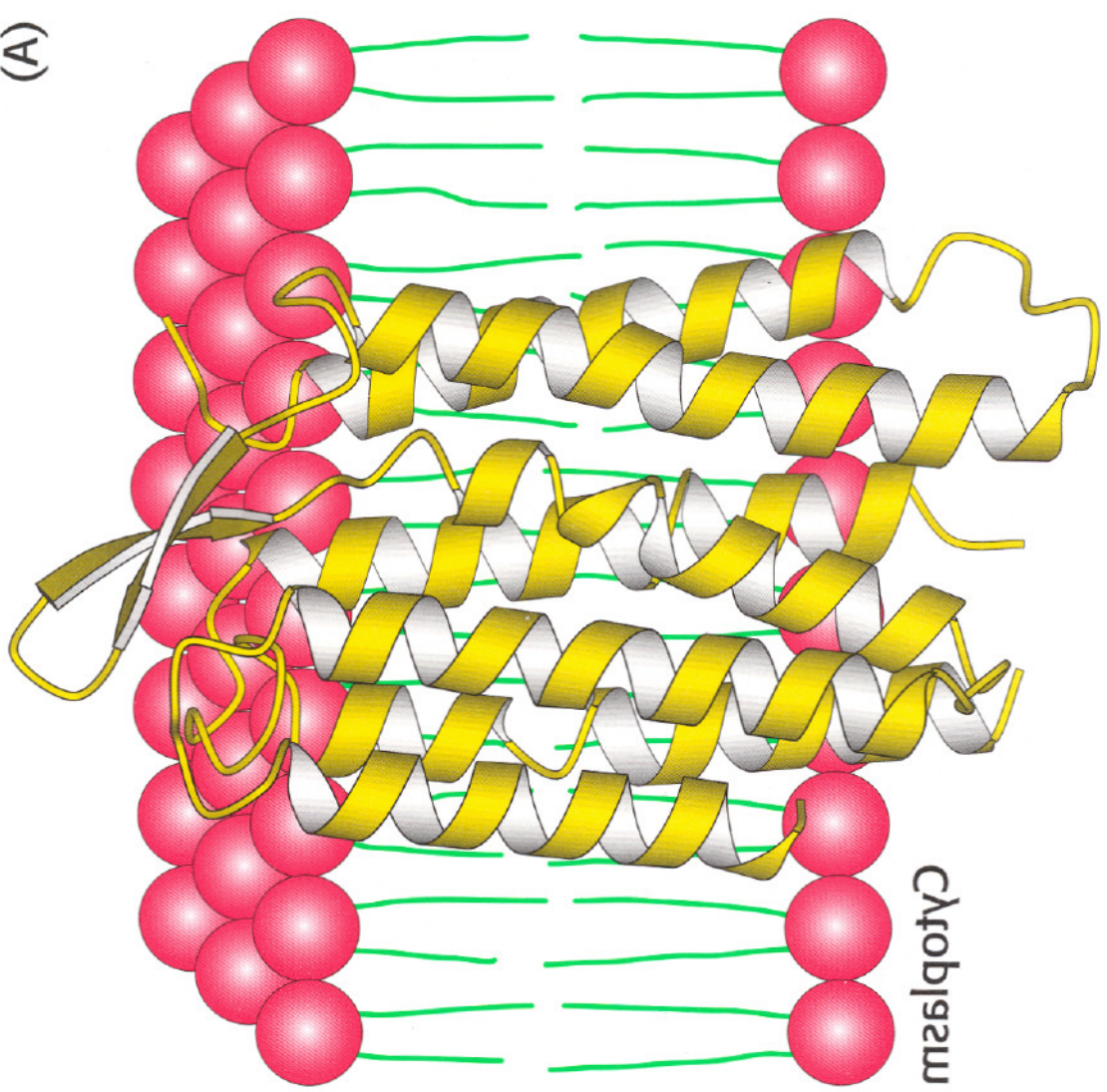
## **INTEGRAL MEMBRANE PROTEINS:**

- Proteins that span biological membranes
- These proteins are designed differently from soluble proteins

Figure 11-56, page 512; Figure 11-35, page 518

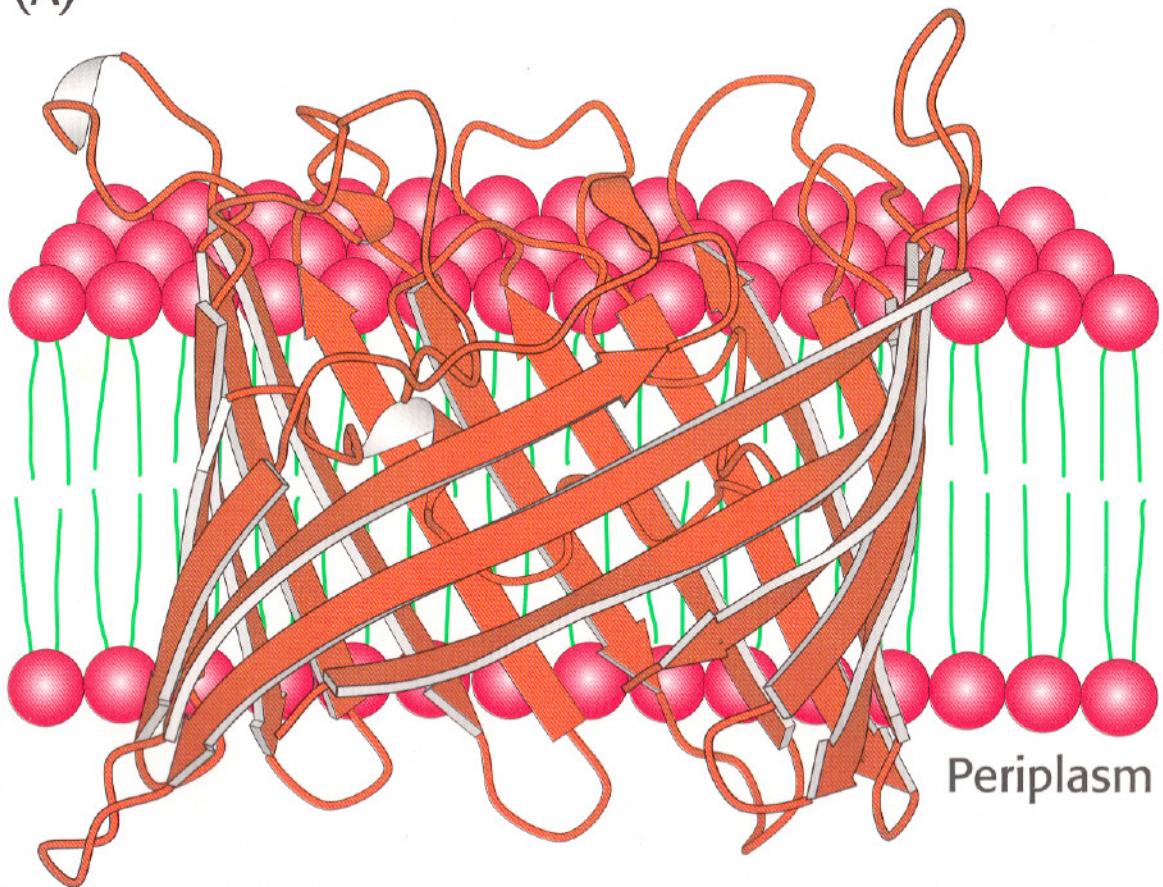








(A)



(B)



Figure 12-20  
Stryer, Tymoczko, & Berg, BIOCHEMISTRY, Fifth Edition.  
Copyright © 2002 by W. H. Freeman and Company.

Protein	Molecular Weight	Residues	Cysteine
	Molecular	Number of	Number of
Albumin (human)	51,000	585	1
Gamma globulin (E. coli)	213,000	2,238	1
Bovine serum albumin (E. coli)	420,000	4,128	2
Hexokinase (yeast)	105,000	225	5
Serum albumin (human)	68,200	608	1
Hemoglobin (human)	64,500	574	4
Cytochrome c (bovine)	13,000	104	1
Cytochrome c (human)	13,000	104	1

Molecular Data on Some Proteins

used to determine the amounts of these amino acids in solution. The isoelectric point of a protein is the pH at which the protein carries no net electrical charge. The isoelectric point of a protein is determined by the relative numbers of acidic and basic residues. Note that standard procedures for the acid hydrolysis of

acid amino	Total	
	104	542
Asp	3	53
Thr	4	4
Leu	1	8
Val	8	53
Met	1	58
Pro	1	9
Phe	4	9
Met	5	5
Phe	18	14
Leu	9	13
Ile	9	10
His	3	5
Glu	14	53
Gln	9	2
Arg	3	10
Cys	5	10
Asp	3	8
Val	2	12
Arg	5	4
His	9	55

Amino Acid Composition of Two Proteins\*

acid amino	Cytochrome c	Cytochrome c
	Bovine	Bovine
	per molecule of protein	
	Number of residues	



# **THE AMINO SEQUENCE OF A PROTEIN SPECIFIES ITS THREE-DIMENSIONAL STRUCTURE**

## **“Protein Sequence Specifies Conformation”**

**Studies of Christian Anfinsen on the role of denaturing agents on the structure and enzymatic activity of ribonuclease (1964)**

## **SPECIFIC BINDING AND TRANSMISSION OF STRUCTURAL CHANGES ARE AT THE HEART OF PROTEIN ACTION**

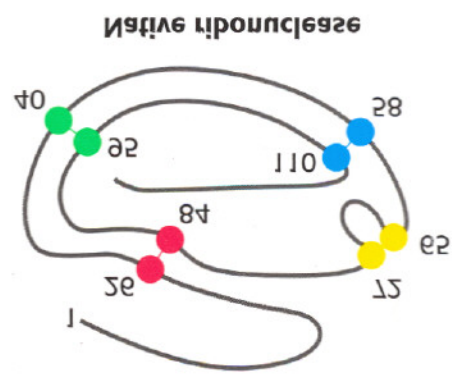
**The first step in the action of a protein is its binding of another molecule**

**Proteins as a class of macromolecules are unique in being able to recognize and interact with highly diverse molecule e.g.**

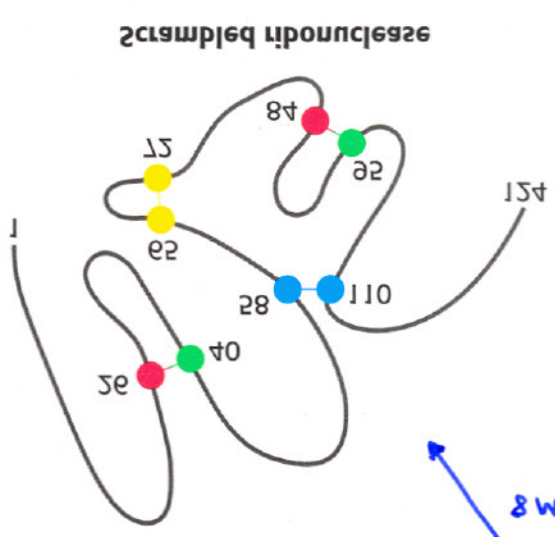
- ◆ **myoglobin binds a heme group**
- ◆ **some proteins can bind to DNA sequences**
- ◆ **enzymates bind to substrate to catalyze reactions**

**The activity of some protein molecules is controlled by an allosteric mechanism.**

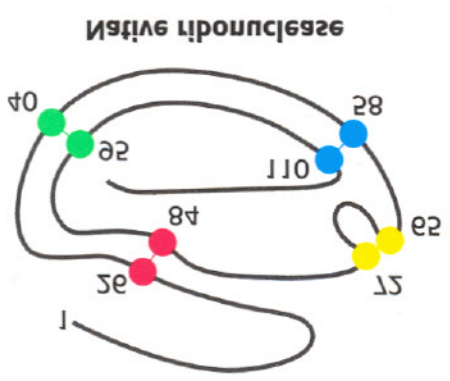




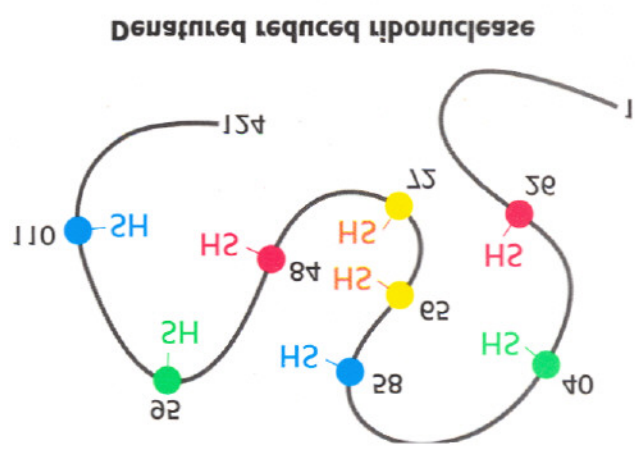
β-mercaptoethanol  
 110000



8 M urea



β-mercaptoethanol  
 8 M urea and



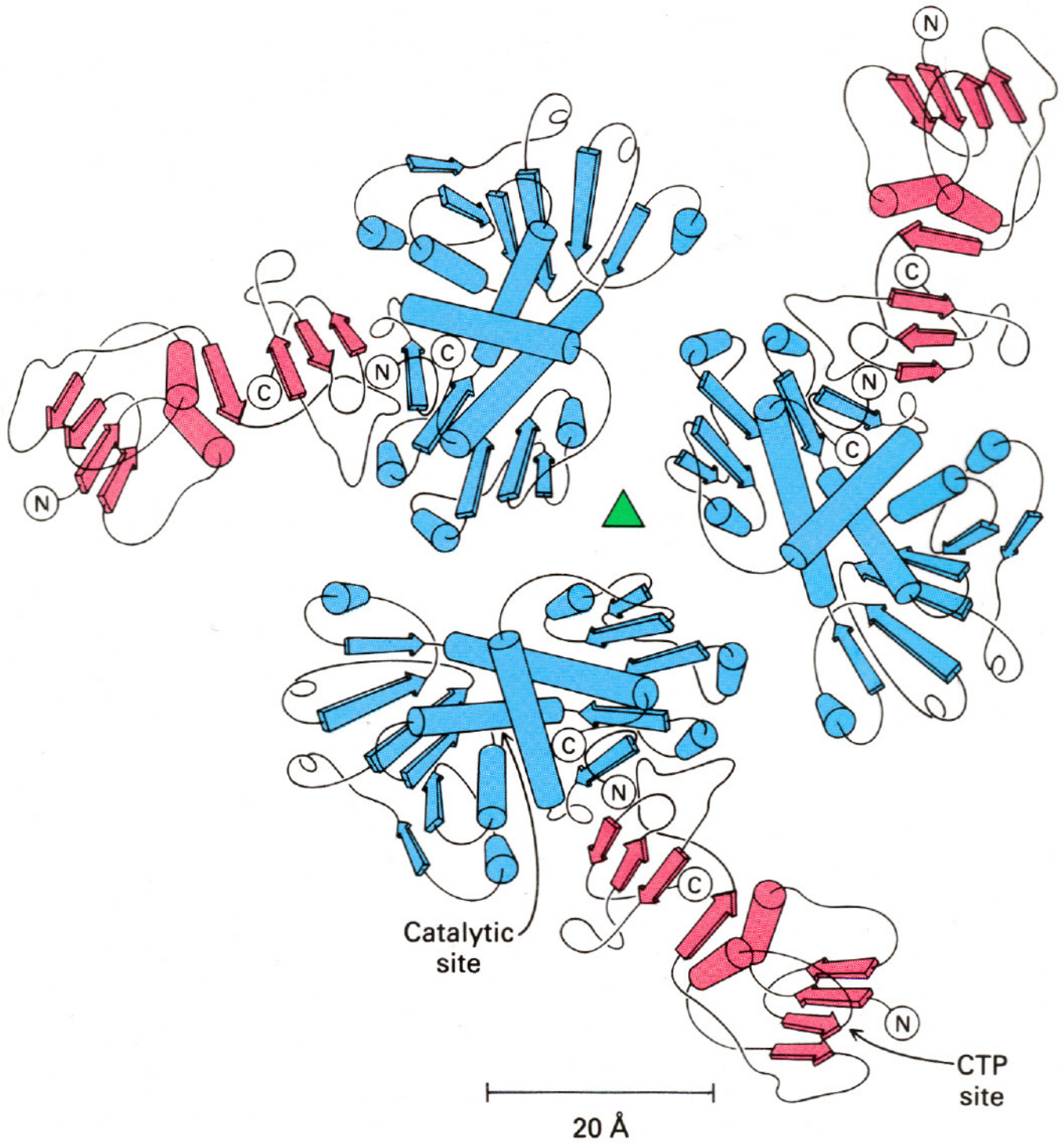
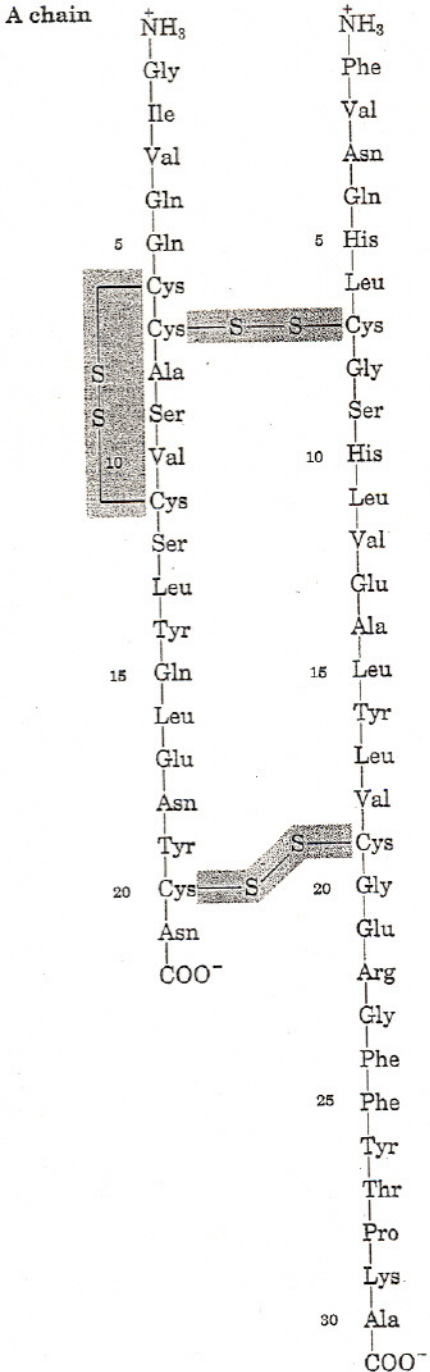


Figure 10-5, page 240



**figure 5-24**

**Amino acid sequence of bovine insulin.** The two polypeptide chains are joined by disulfide cross-linkages. The A chain is identical in human, pig, dog, rabbit, and sperm whale insulins. The B chains of the cow, pig, dog, goat, and horse are identical. Such identities between similar proteins of different species are discussed in Box 5-2.

**table 5-4**

Conjugated Proteins		
Class	Prosthetic group(s)	Example
Lipoproteins	Lipids	$\beta_1$ -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