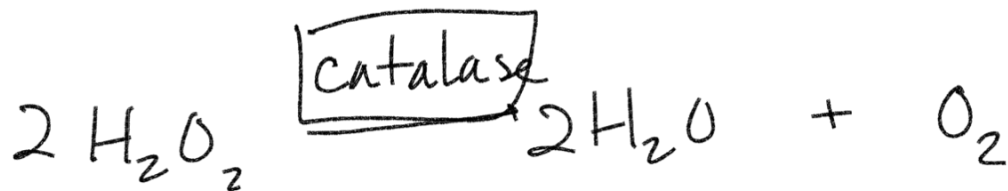


T-GB General Biology Week 8 10/24

Hydrogen Peroxide  $H_2O_2$  (toxic)

Free radical  $\rightarrow$  rogue electrons  
molecular damage



hydrogen peroxide                      water                      oxygen

catalase is an enzyme  $\rightarrow$  protein  
that breaks down hydrogen peroxide.

Enzymes Function based on their shape

Bacteria do not have peroxisomes, they die in the presence of  $H_2O_2$ .

peroxisomes — organelle found in our cells that eliminates hydrogen peroxide.

protein denaturation  $\rightarrow$  protein/enzyme loses its shape  $\rightarrow$  loses functionality.

①

hydroxyl carbonyl nonpolar methyl

Atoms: C, H, O

Fat/lipid

The diagram shows a chemical structure of a lipid molecule. On the left, a hydroxyl group (H-O) is circled in red and labeled "hydroxyl". It is connected to a carbonyl group (C=O), which is also circled in red and labeled "carbonyl". The carbonyl carbon is part of a long hydrocarbon chain. The chain consists of several carbon atoms, each bonded to hydrogen atoms. The end of the chain is a methyl group (CH3), which is enclosed in a red box and labeled "methyl". Above the chain, the word "nonpolar" is written, indicating the nature of the hydrocarbon tail. At the bottom, the text "Atoms: C, H, O" lists the elements present, and "Fat/lipid" identifies the molecule.



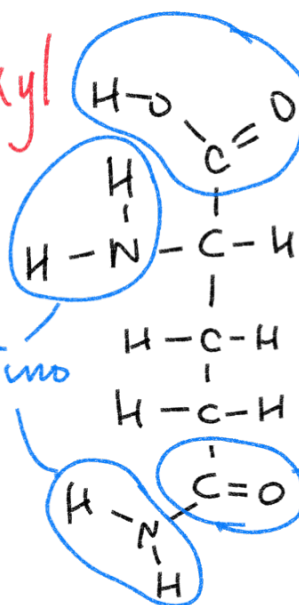
Atoms: C, H, O Fat/lipid methyl

carboxyl  - carboxyl

2.)

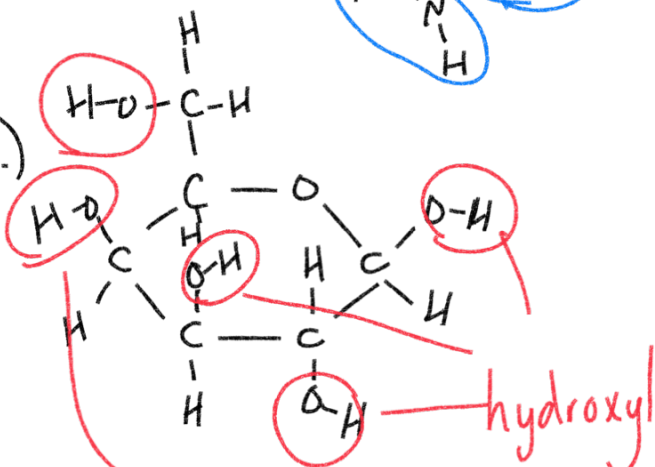
amino  
acid

amino



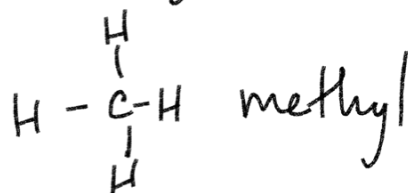
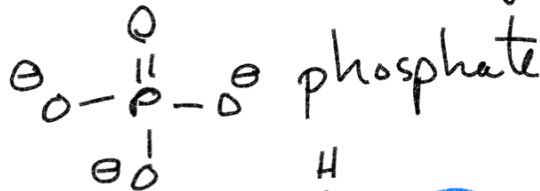
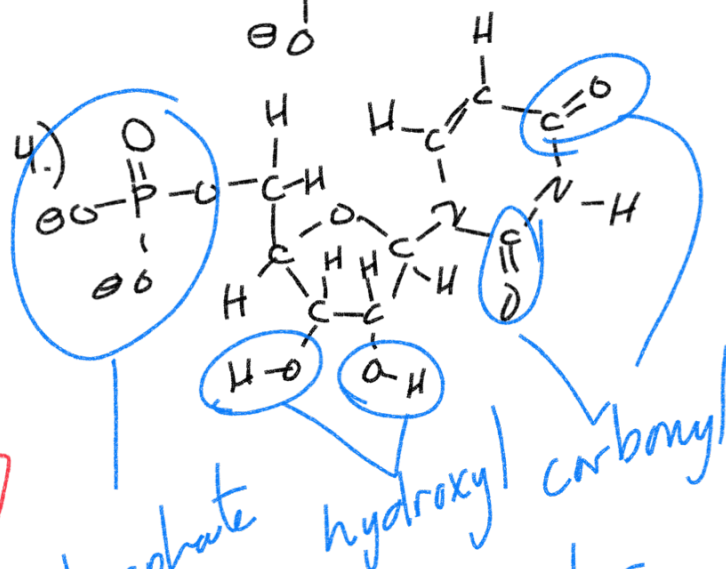
carbonyl

3.)



hydroxyl  
polar

carbohydrate - sugar

 $\text{C}=\text{O}$  carbonyl $\text{C}(=\text{O})\text{OH}$  carboxyl
$$\begin{array}{c} \text{H} - \text{N} - \text{H} \\ | \\ \text{H} \end{array} \text{ amino}$$
$$\begin{array}{c} \text{H} \\ | \\ \text{S}-\text{H} \end{array} \text{ sulfhydryl}$$
~~4.)~~

phosphate

hydroxy

polar

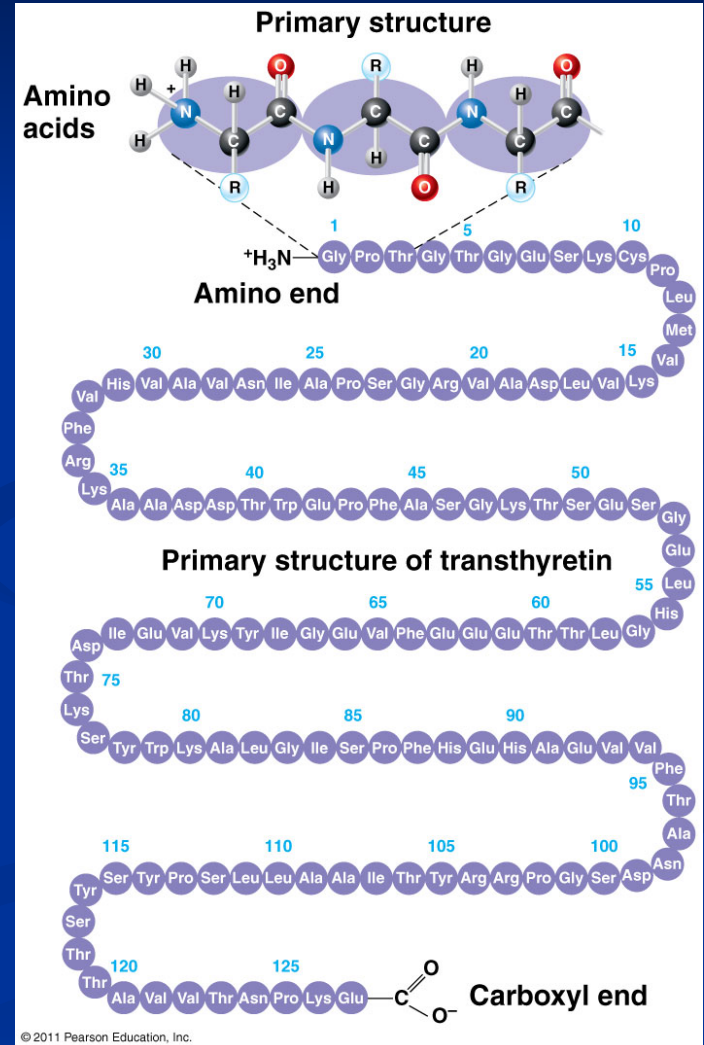
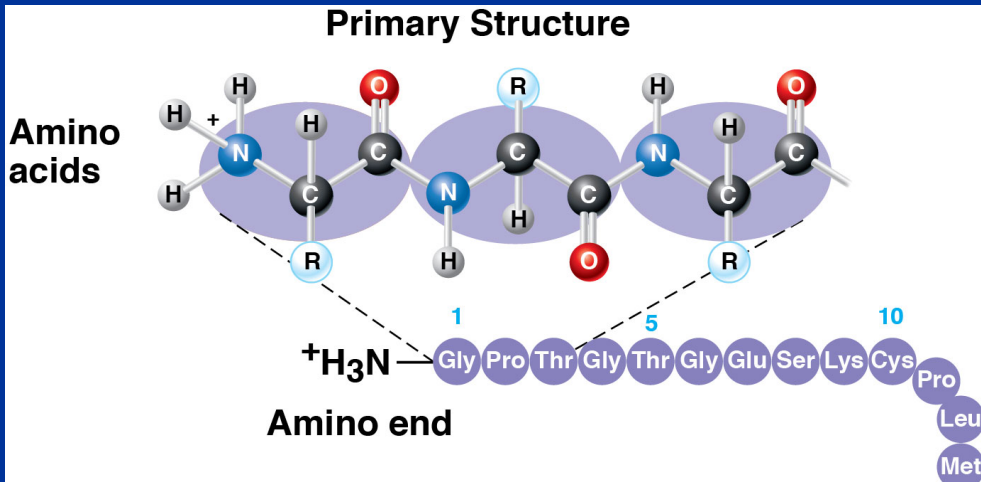
nucleic acid

# Four Levels of Protein Structure

# Primary

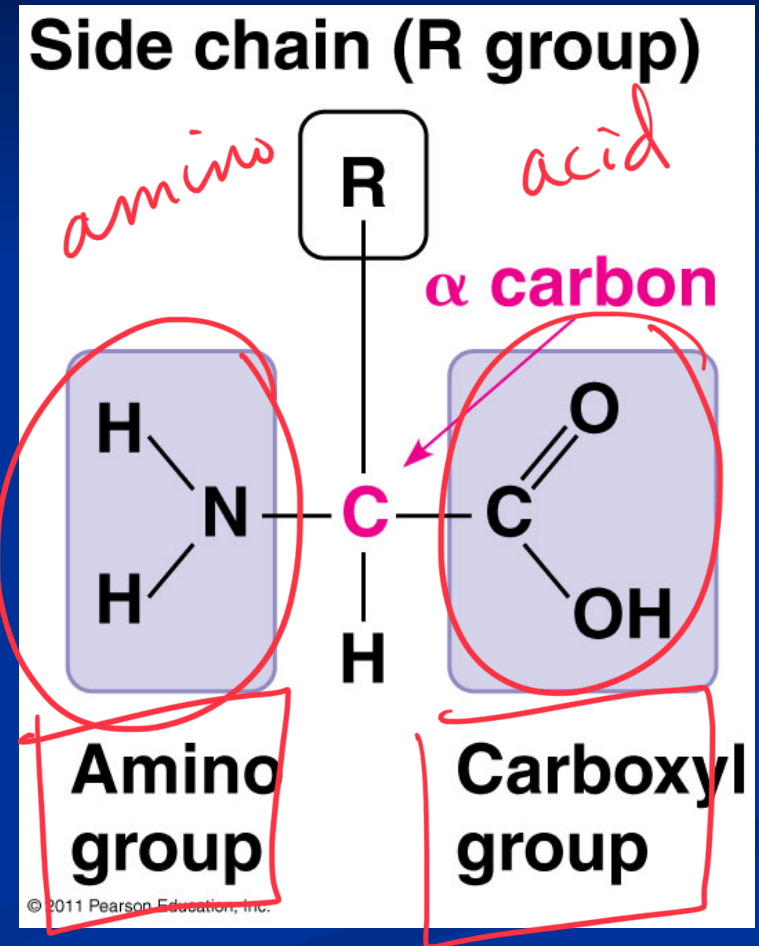
- **Amino acid** (AA) sequence
- 20 different AA's
- **peptide bonds** link AA's

sequence of amino acids



# Amino Acid

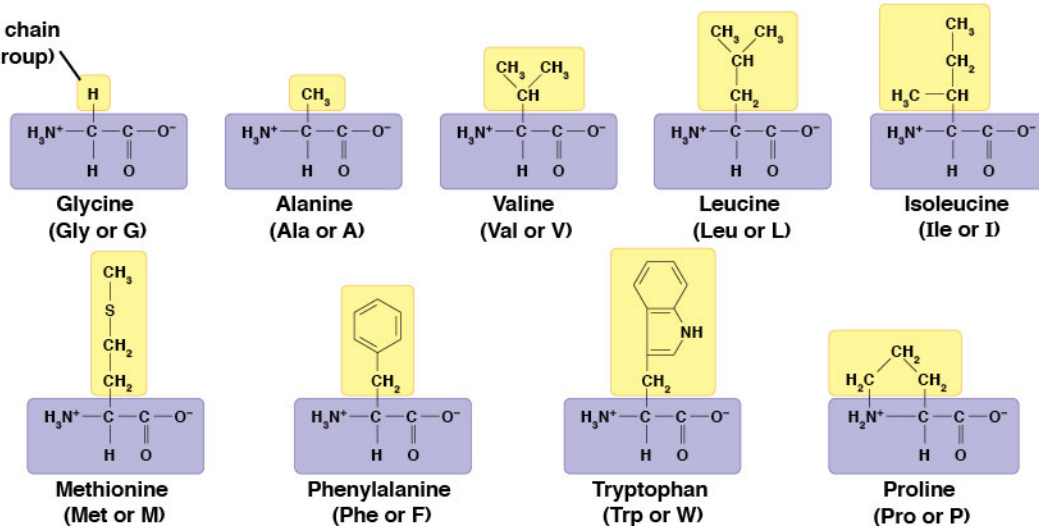
- **R group** = side chains
- Properties:
  - hydrophobic
  - hydrophilic
  - ionic (acids & bases)
- “amino” :  $\text{-NH}_2$
- “acid” :  $\text{-COOH}$



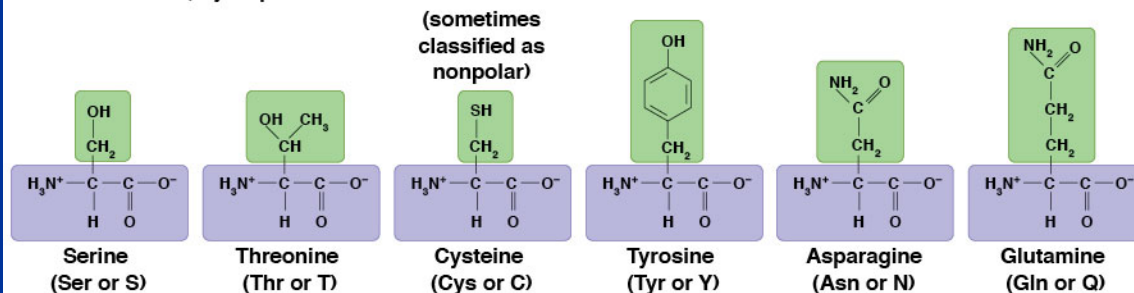


## Nonpolar side chains; hydrophobic

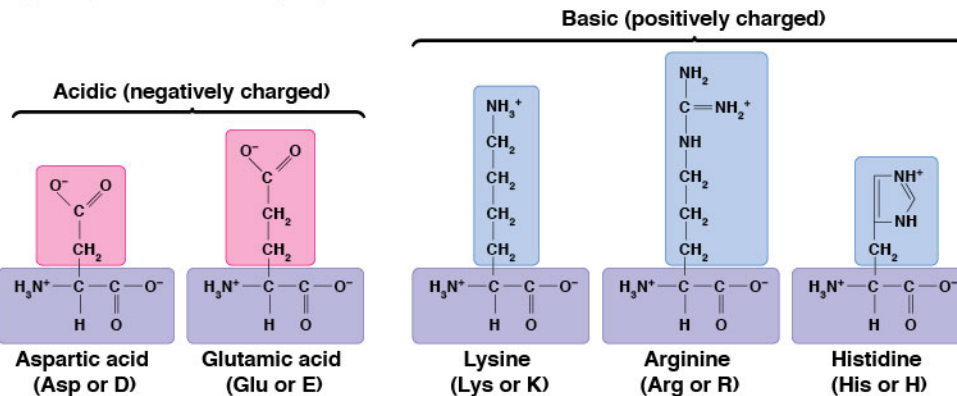
Side chain  
(R group)

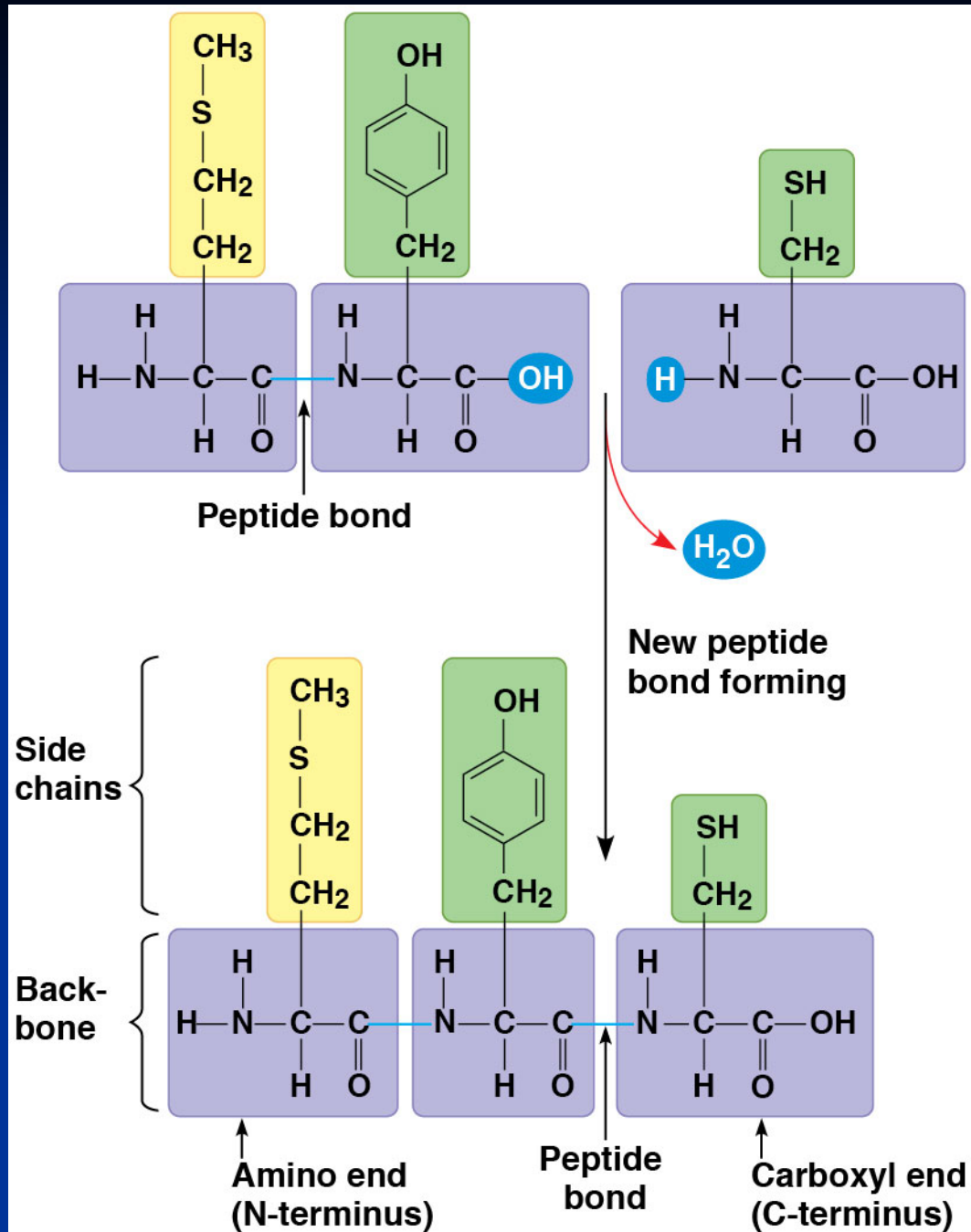


## Polar side chains; hydrophilic

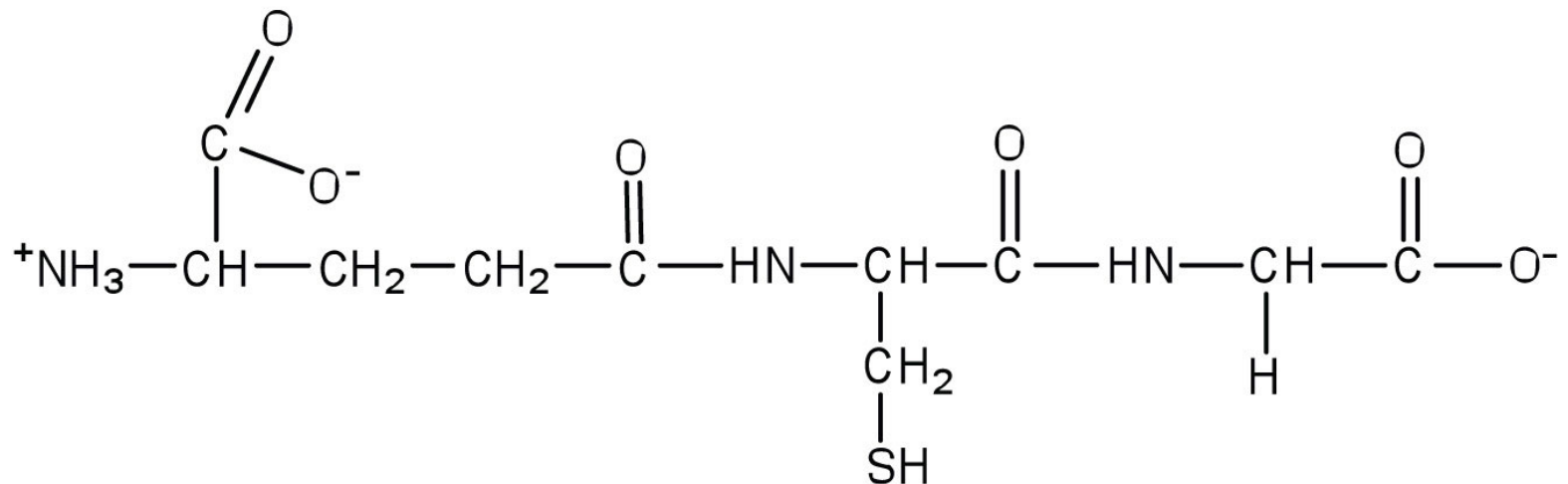
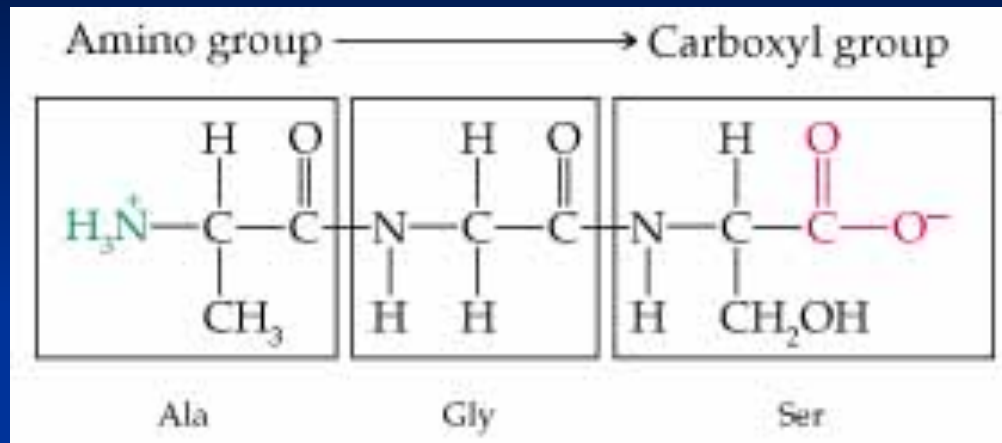


## Electrically charged side chains; hydrophilic



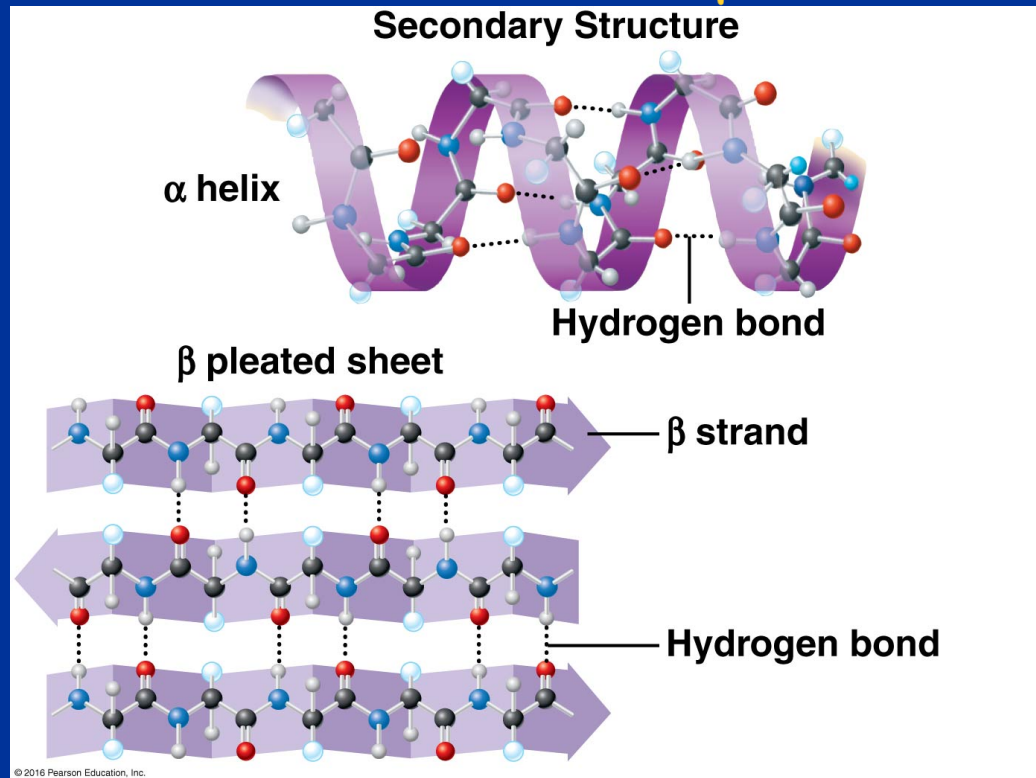


# Peptide Bonds



# Four Levels of Protein Structure (continued)

2. Secondary motifs or patterns familiar arrangement
- Gains 3-D shape (folds, coils) by **H-bonding**
  - Alpha ( $\alpha$ ) helix, Beta ( $\beta$ ) pleated sheet inside the protein



$\alpha$ -helix  
↑  
alpha

beta-sheet

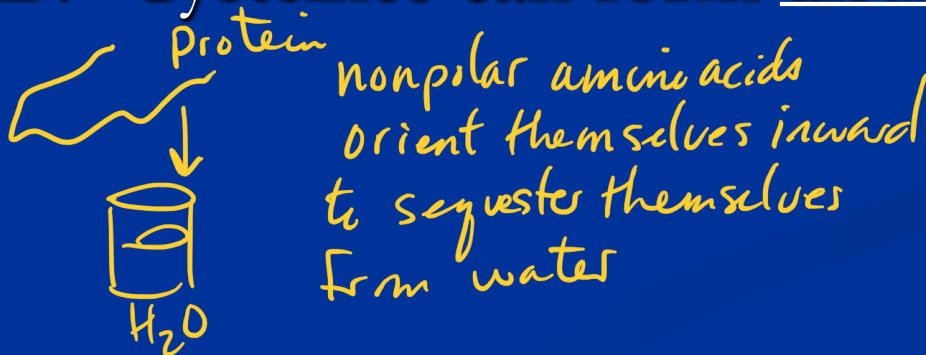


Hydrogen  
Bonding  
within the  
molecules  
internal

# Basic Principles of Protein Folding

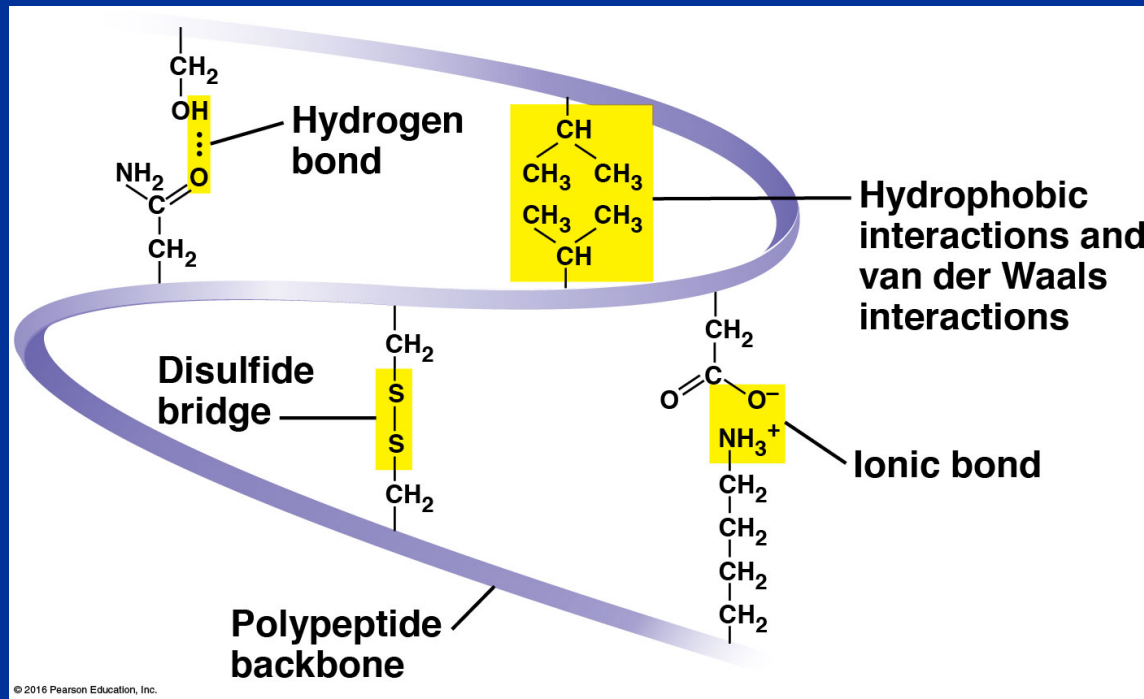
1Cnm!!

- A. Hydrophobic AA buried in interior of protein (hydrophobic interactions)
- B. Hydrophilic AA exposed on surface of protein (hydrogen bonds)
- C. Acidic + Basic AA form salt bridges (ionic bonds).
- D. Cysteines can form disulfide bonds.



## Four Levels of Protein Structure (continued)

3. Tertiary → shape of protein → gives it functionality
- Bonding between side chains (R groups) of amino acids
  - H bonds, ionic bonds, disulfide bridges, hydrophobic interactions, van der Waals interactions



entire of  
piece of  
music  
for a  
french  
horn.

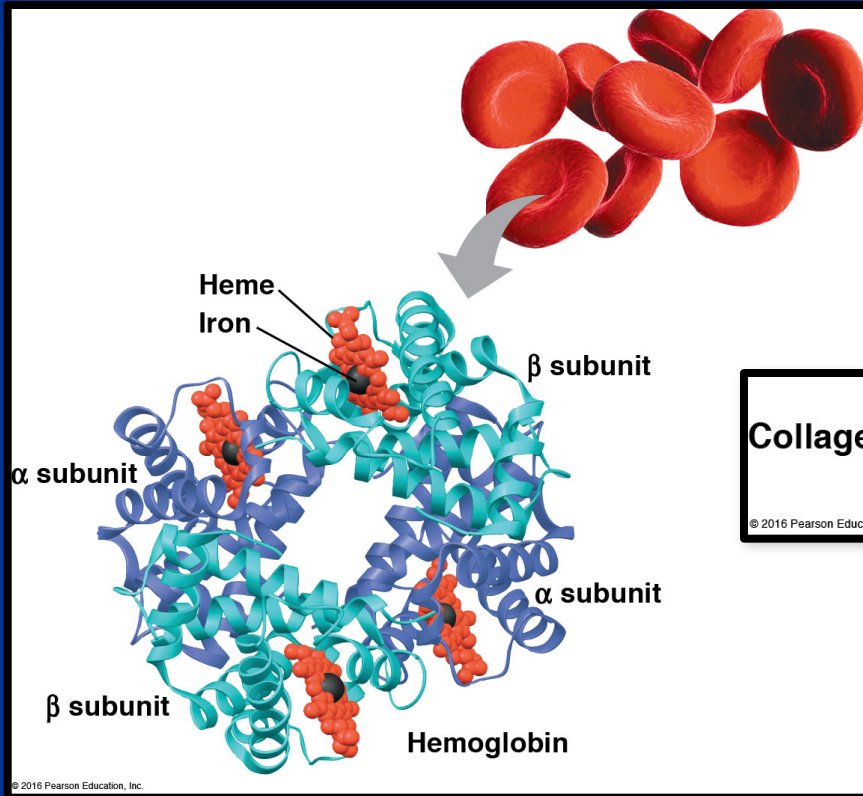


# Four Levels of Protein Structure (continued)

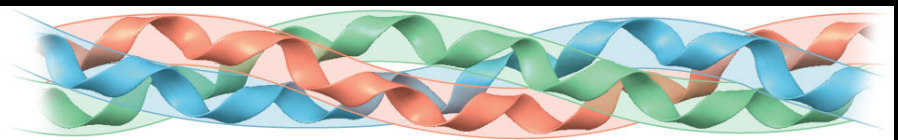
## 4. Quaternary

- 2+ polypeptides bond together

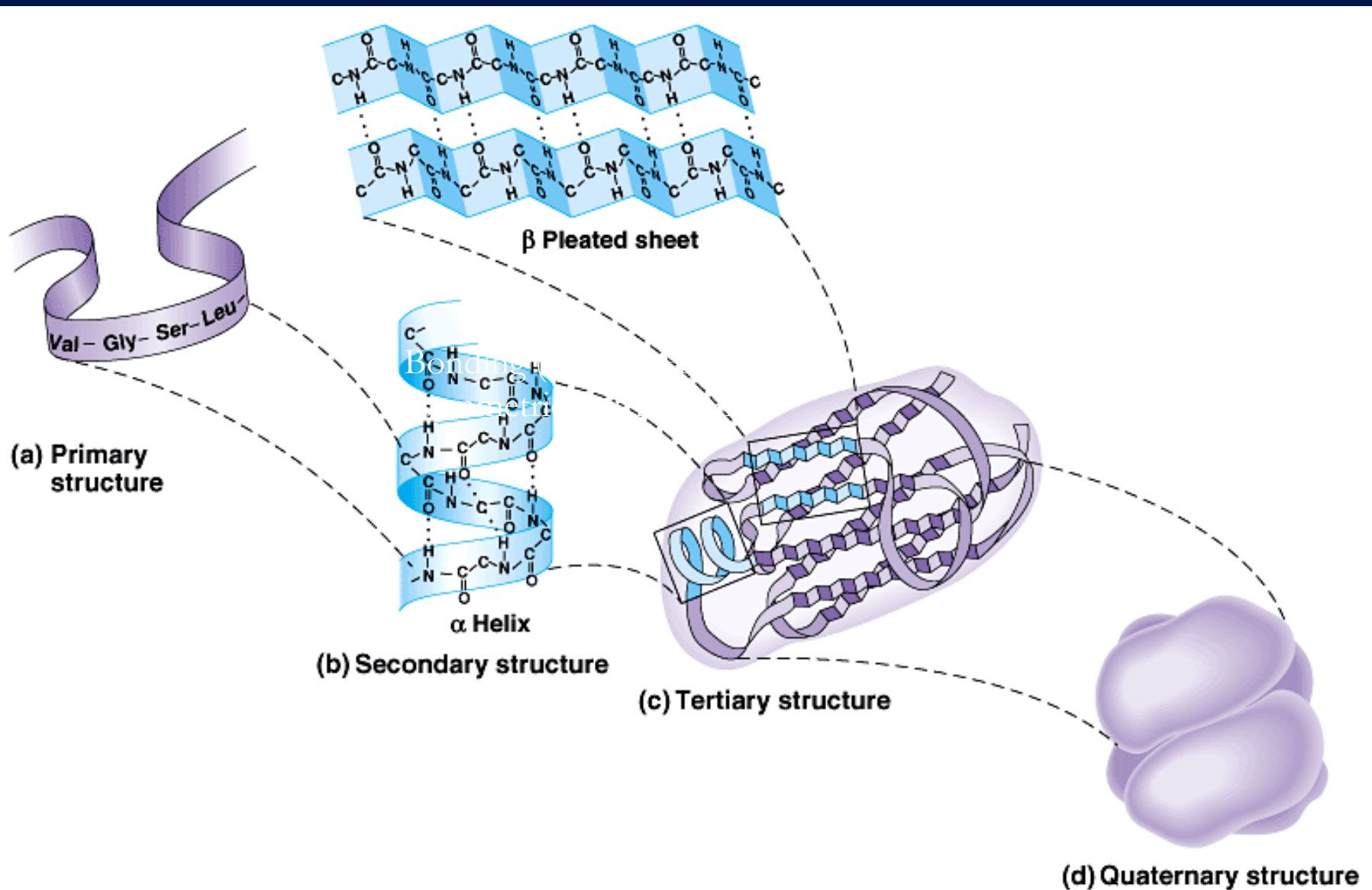
assembly of  
functional  
proteins/polypeptides  
orchestra



Collagen

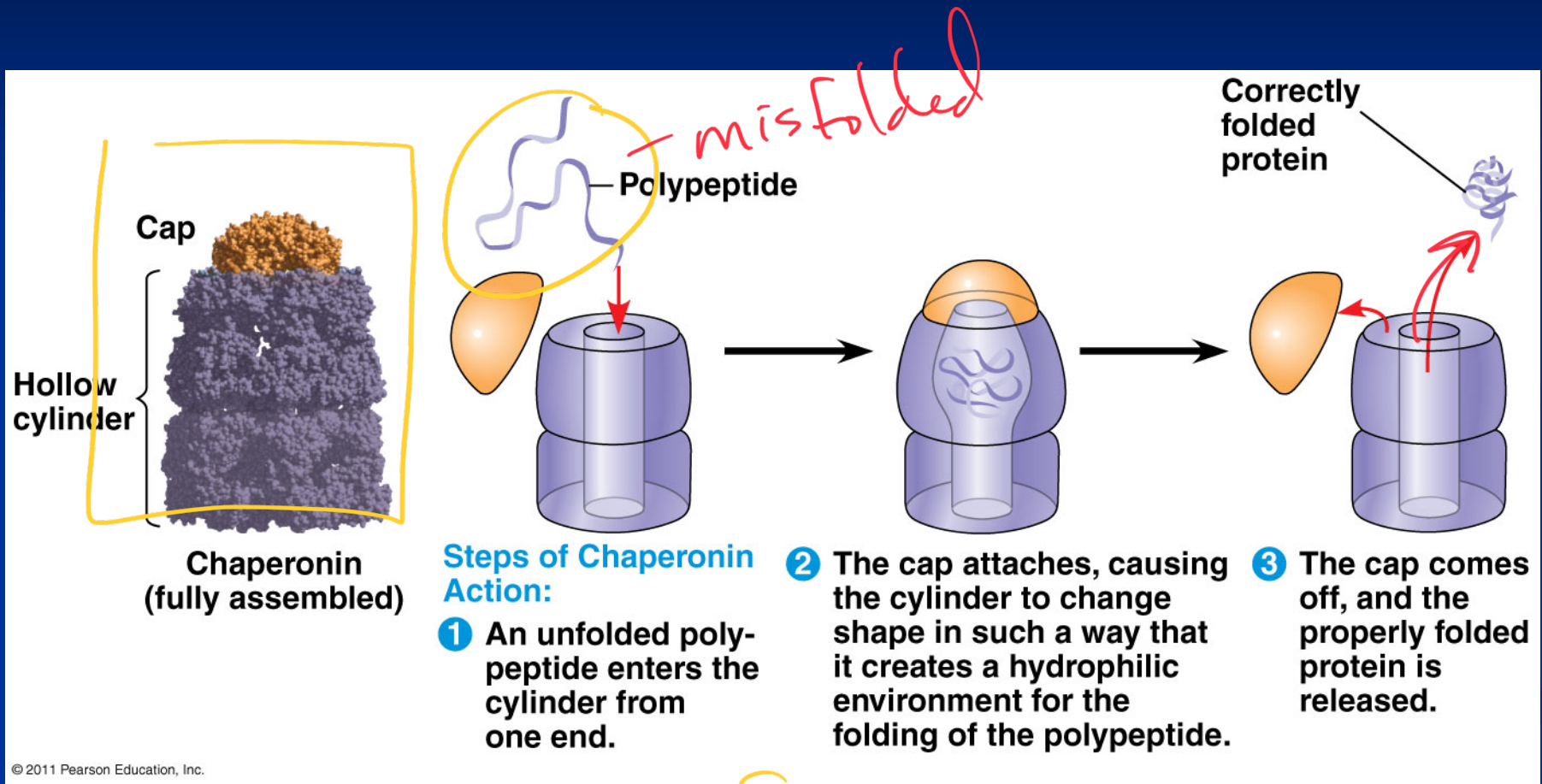


monomer  
amino acids  $\rightarrow$  polymer  
polypeptides  $\rightarrow$  protein



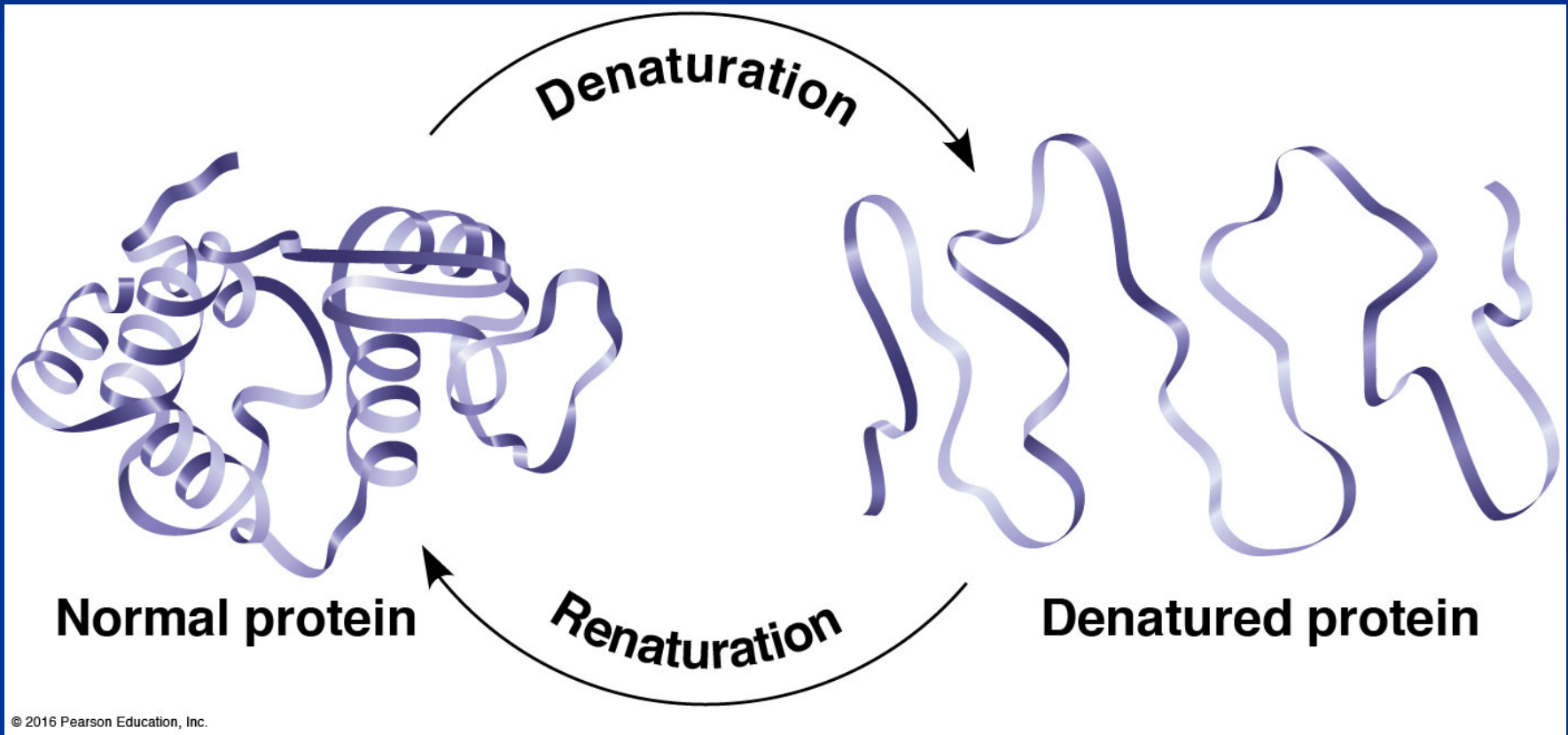
# Chaperonins assist in proper folding of proteins

heat-shock protein



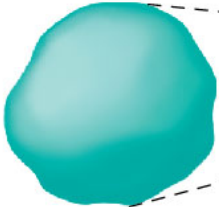
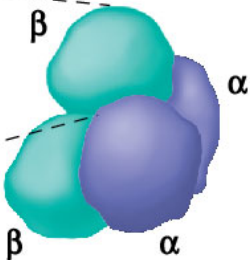
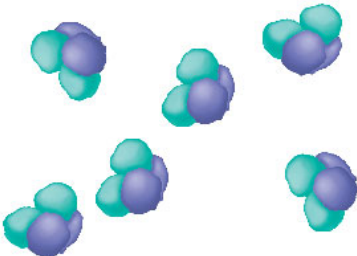
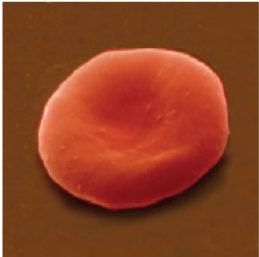
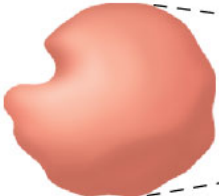
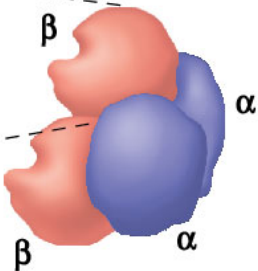
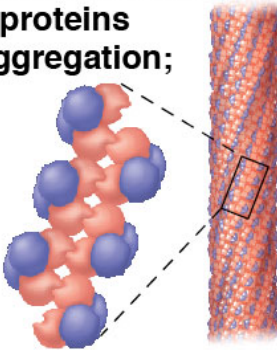

Shape = function

- Protein **structure and function** are sensitive to chemical and physical conditions
- Unfolds or **denatures** if pH and **temperature** are not optimal

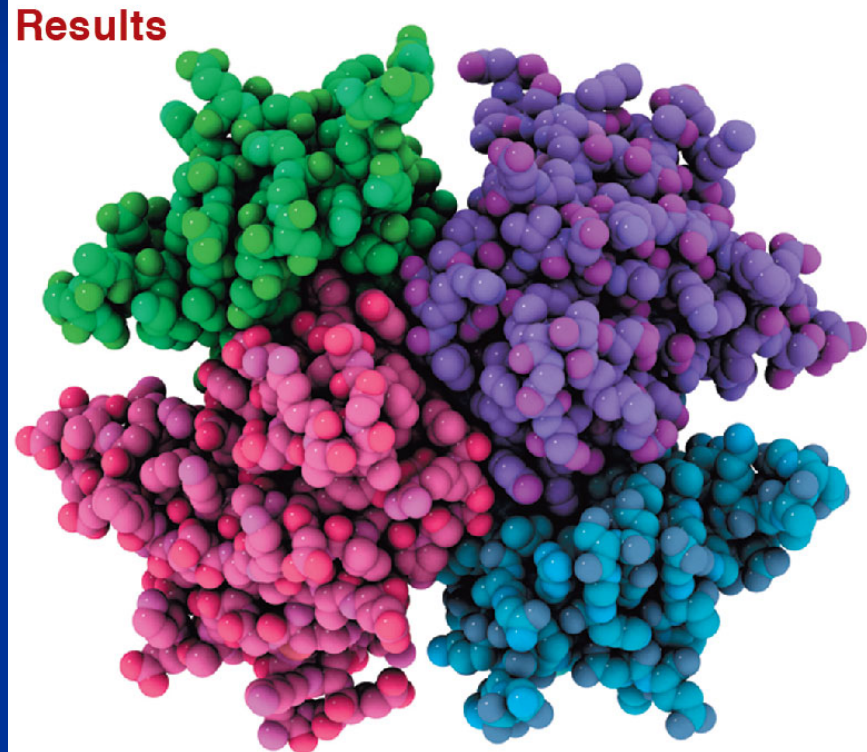
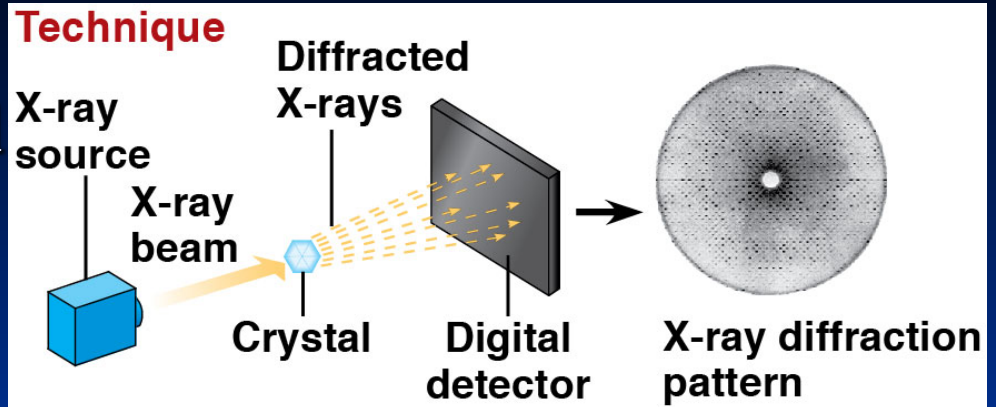




# change in **structure** = change in **function**

	Primary Structure	Secondary and Tertiary Structures	Quaternary Structure	Function	Red Blood Cell Shape
<b>Normal</b>	1 Val 2 His 3 Leu 4 Thr 5 Pro 6 Glu 7 Glu	<b>Normal <math>\beta</math> subunit</b> 	<b>Normal hemoglobin</b> 	Proteins do not associate; each carries oxygen. 	Normal red blood cells are full of individual hemoglobin proteins.  5 $\mu\text{m}$
<b>Sickle-cell</b>	1 Val 2 His 3 Leu 4 Thr 5 Pro 6 <b>Val</b> 7 Glu	<b>Sickle-cell <math>\beta</math> subunit</b> 	<b>Sickle-cell hemoglobin</b> 	Hydrophobic interactions between proteins lead to aggregation; oxygen carrying capacity reduced. 	Fibers of abnormal hemoglobin deform red blood cell into sickle shape.  5 $\mu\text{m}$

X-ray crystallography used  
to determine the 3-D  
structure of proteins





# Genomics: Analysis of genes and genomes

