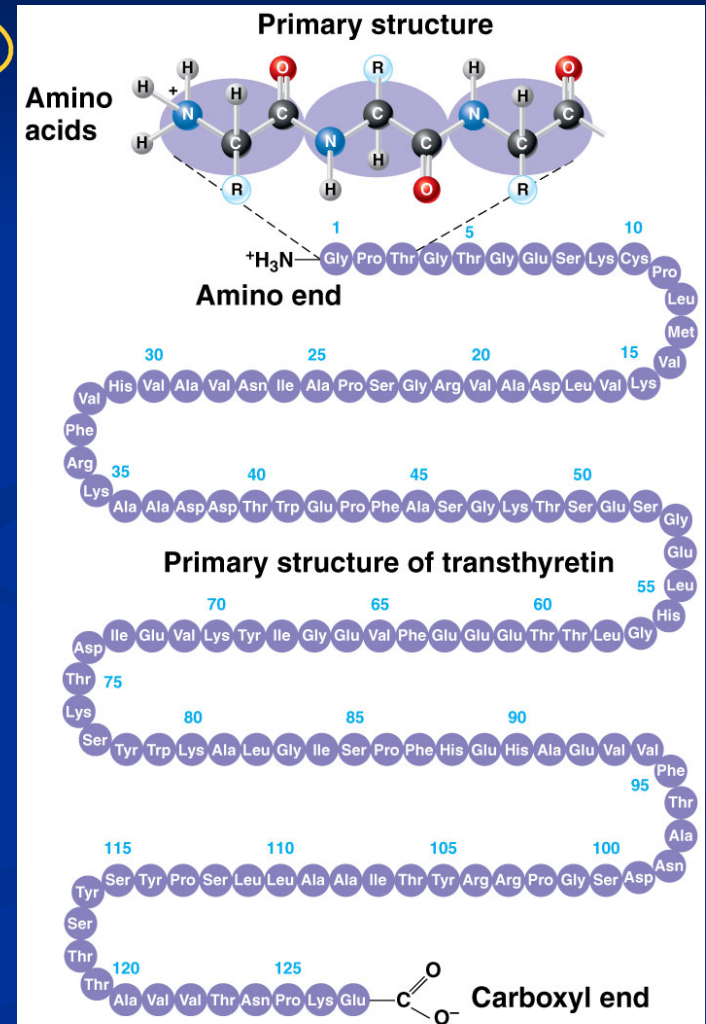
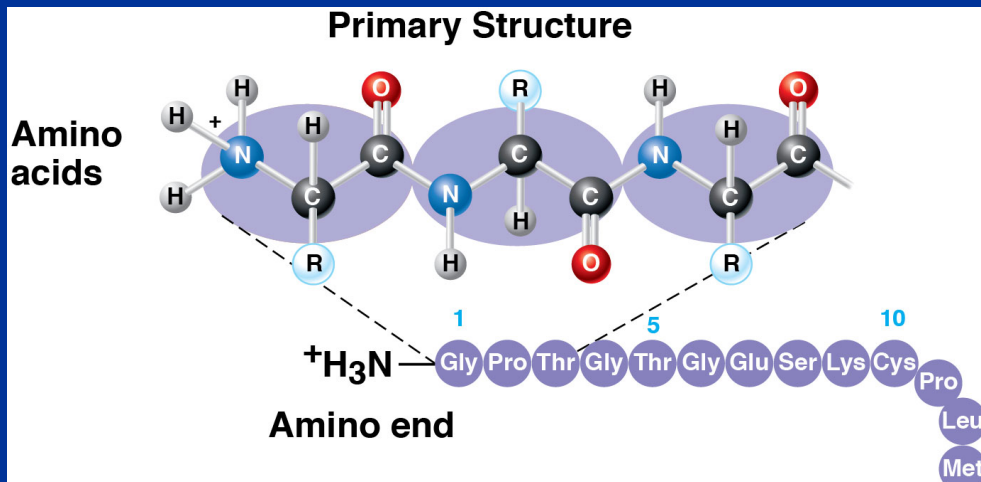


Four Levels of Protein Structure

1. Primary

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

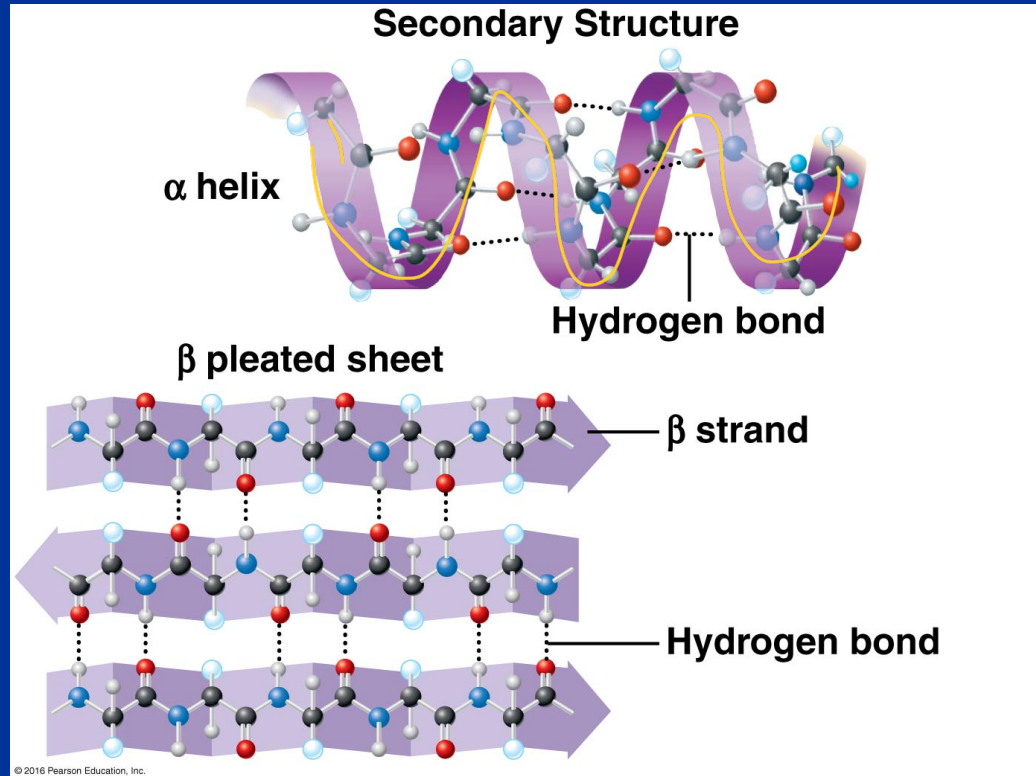


Four Levels of Protein Structure (continued)

2. Secondary

repeating patterns

- Gains 3-D shape (folds, coils) by **H-bonding**
- **Alpha (α) helix, Beta (β) pleated sheet**



Result of hydrogen bonding in the nonpolar interior of protein.

involves amino and carboxyl groups

Basic Principles of Protein Folding

- 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.



amino acid

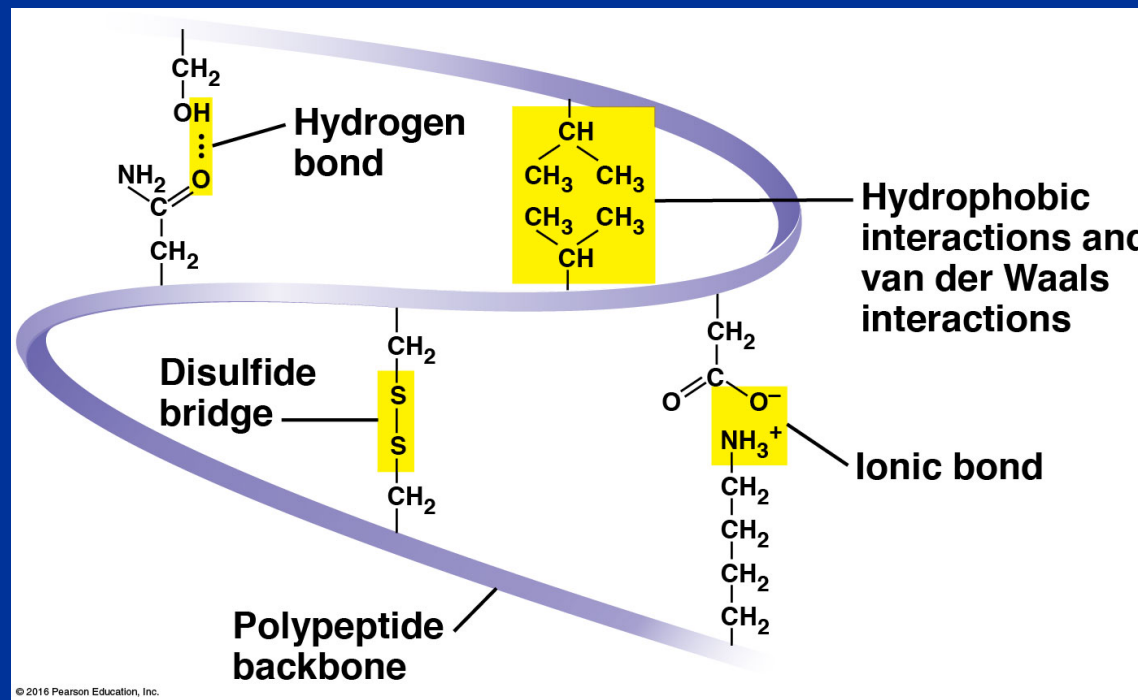


polar amino acid monomers go outward, nonpolar go inward — water leaves interior — protein collapses to functional form.

Four Levels of Protein Structure (continued)

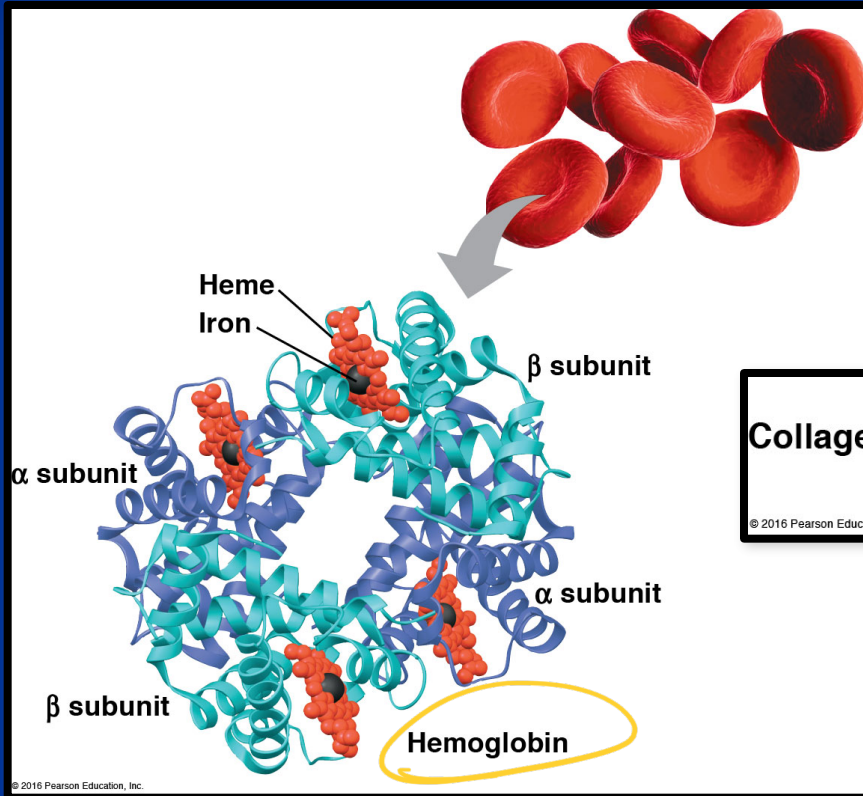
3. Tertiary 3-D structure → shape

- Bonding between **side chains** (R groups) of amino acids
- H bonds, ionic bonds, disulfide bridges, hydrophobic interactions, van der Waals interactions



Four Levels of Protein Structure (continued)

4. Quaternary *multiple polypeptide chains*
- **2+ polypeptides** bond together *come together*

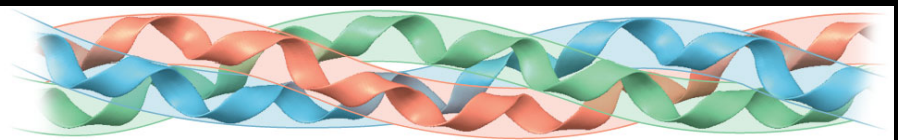


adult

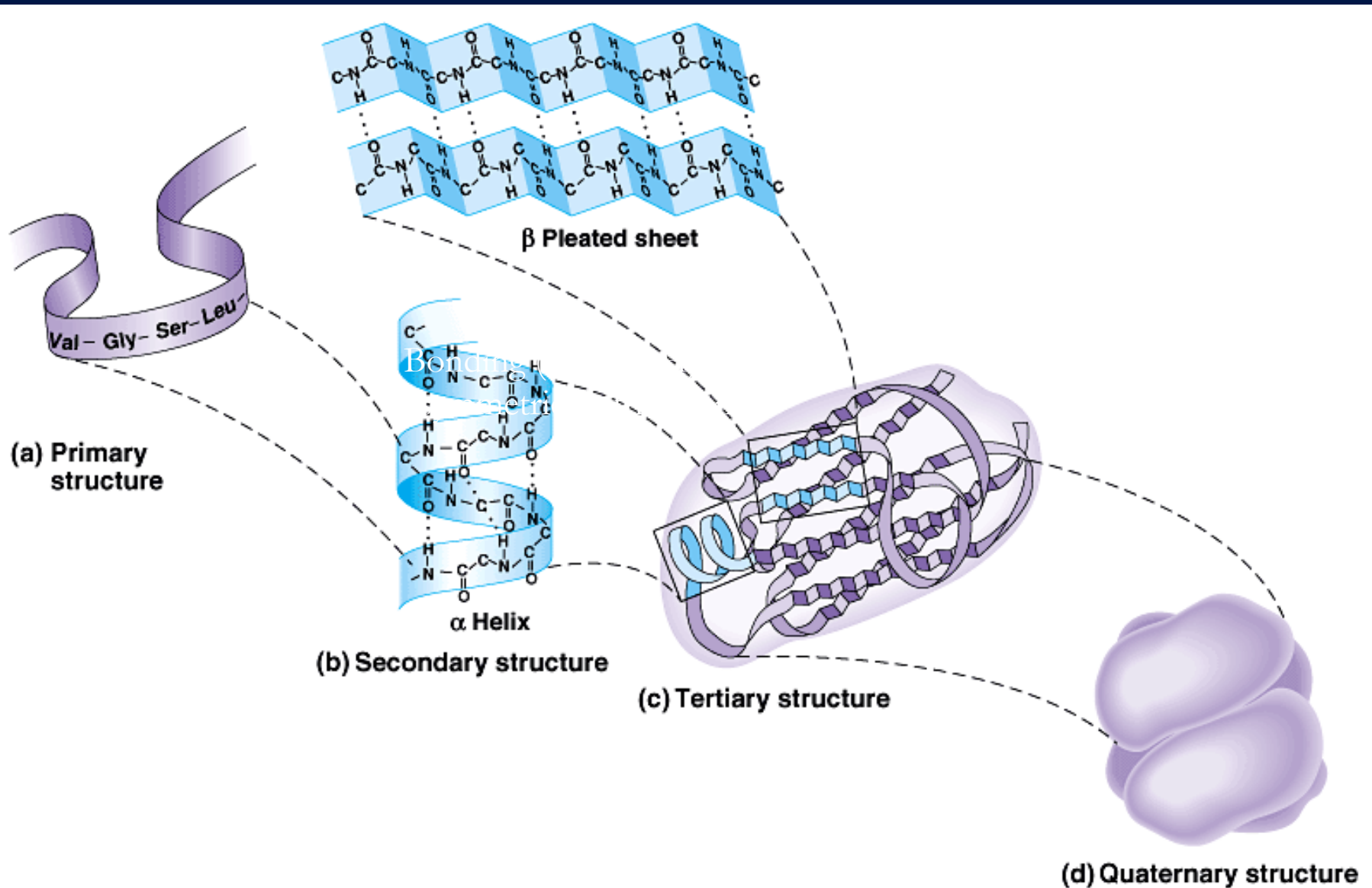


fetal

Collagen



amino acids → polypeptides → protein



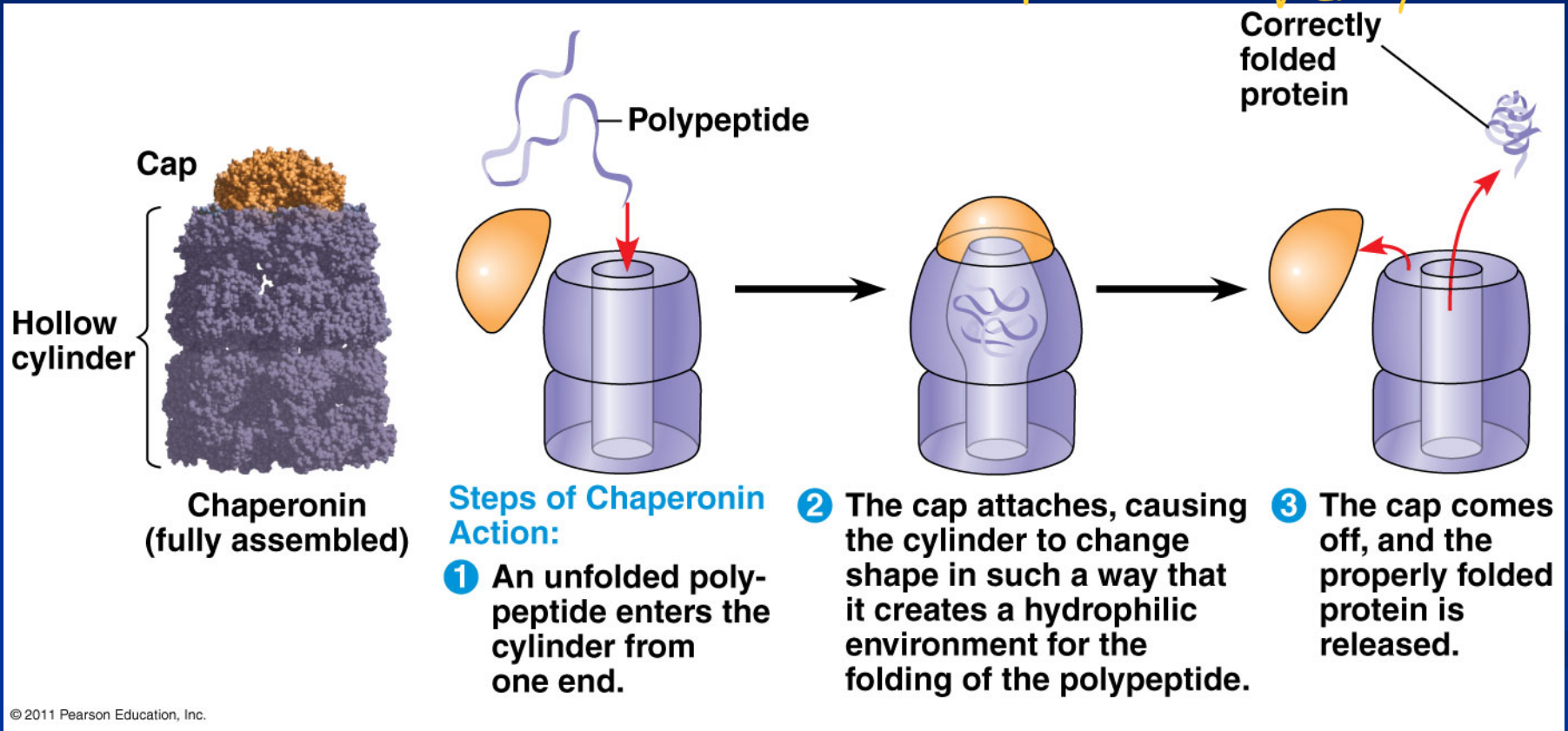
refold misfolded (denatured) proteins

Chaperonins assist in proper folding of

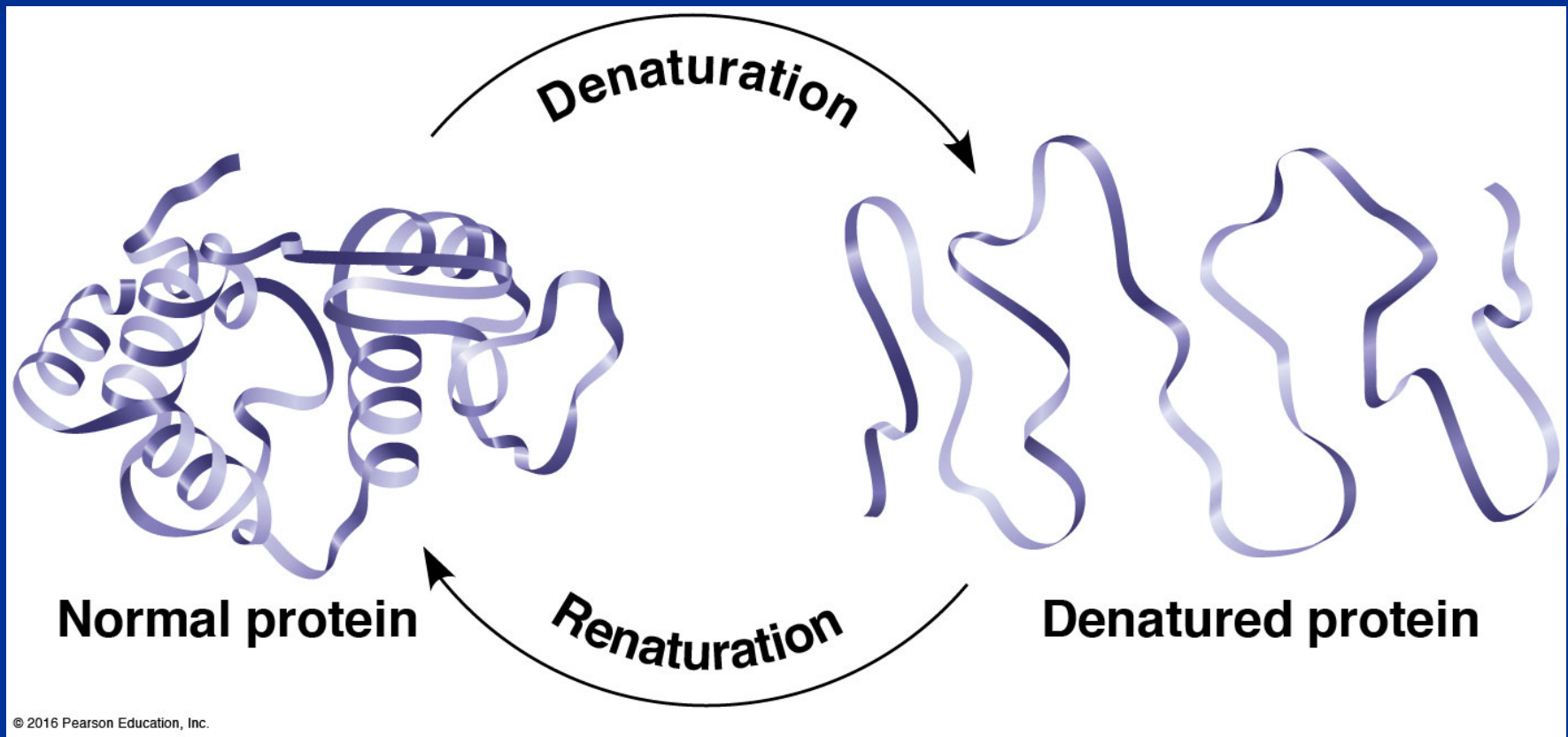
proteins

heat shock protein (hsp)

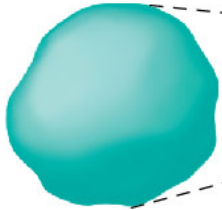
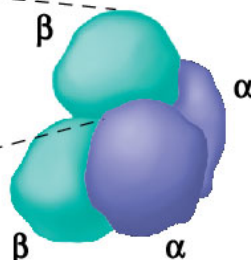
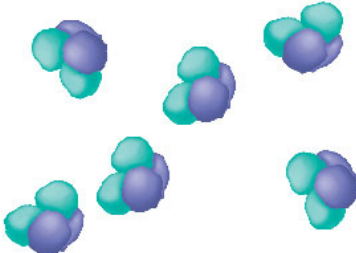
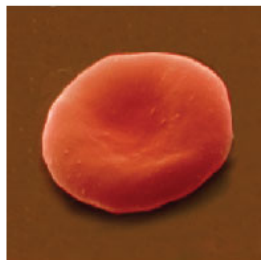
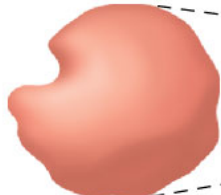
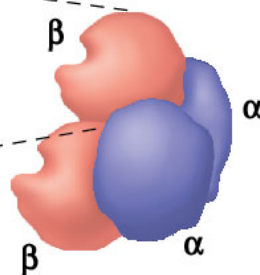
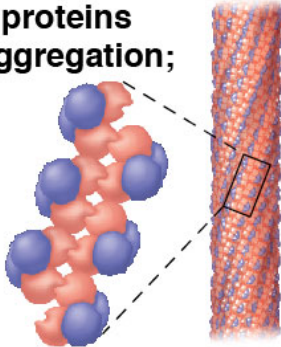
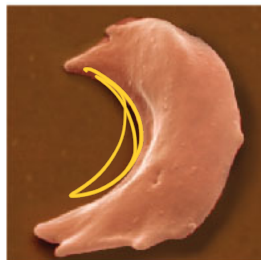
denatured protein → misfolded protein. occur due to heat, acid...



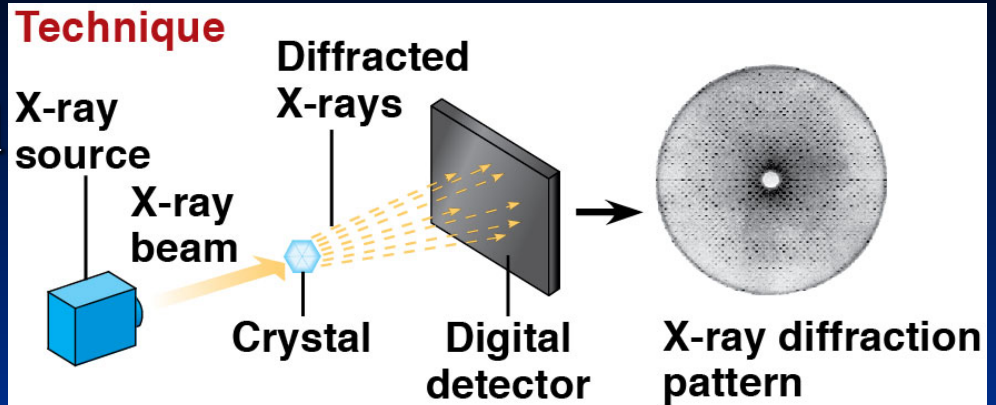
- Protein **structure and function** are sensitive to chemical and physical conditions
- Unfolds or **denatures** if **pH** and **temperature** are not optimal



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

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

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



Results



Genomics: Analysis of genes and genomes

