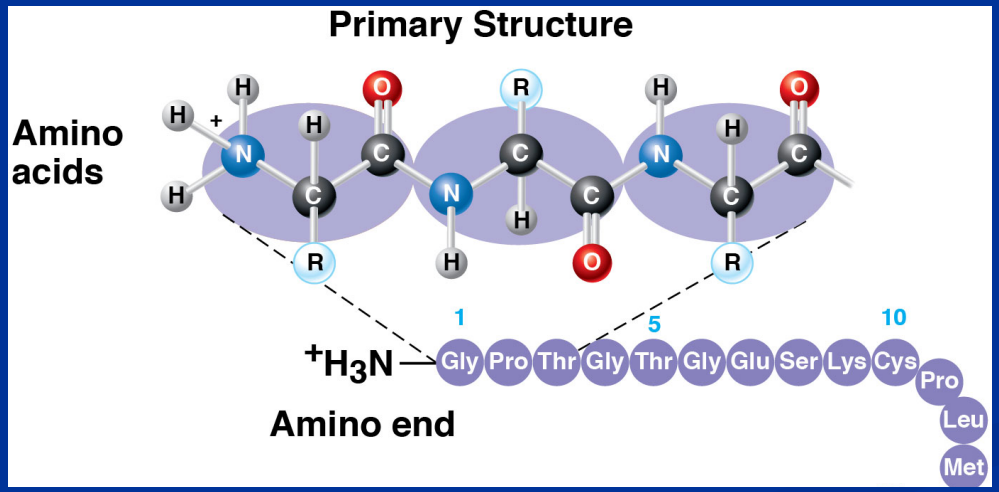
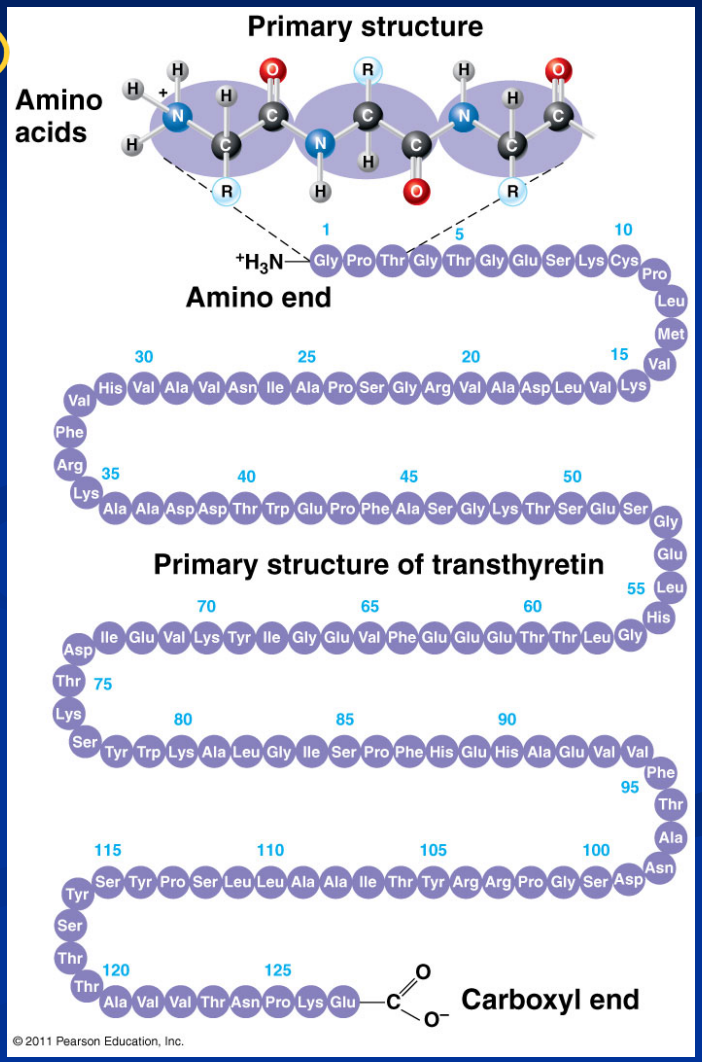
Four Levels of Protein Structure

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

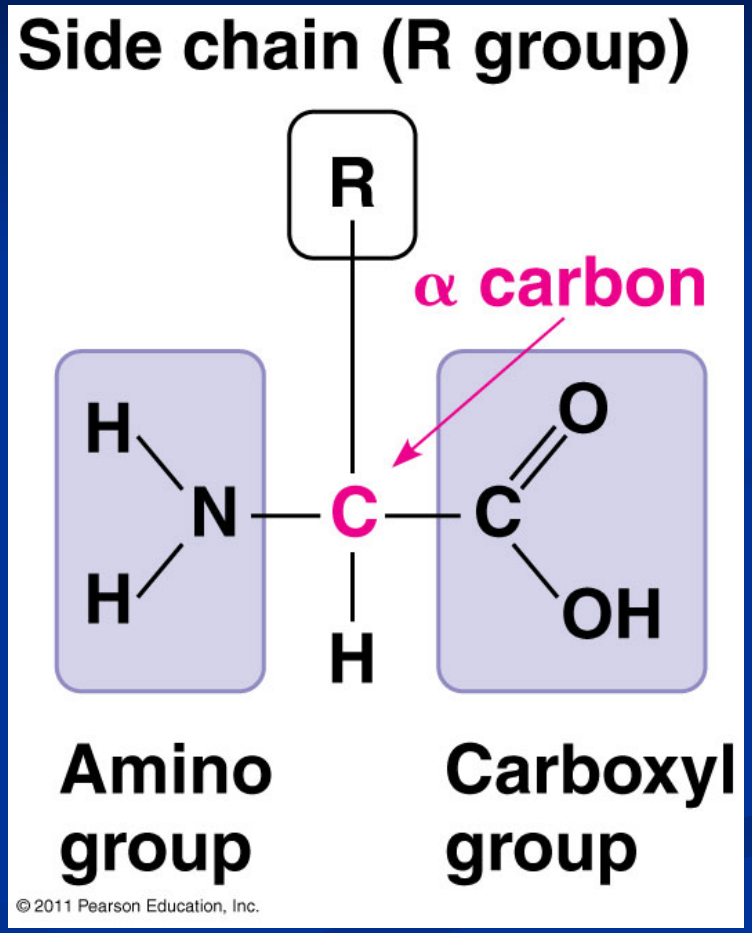
music notes

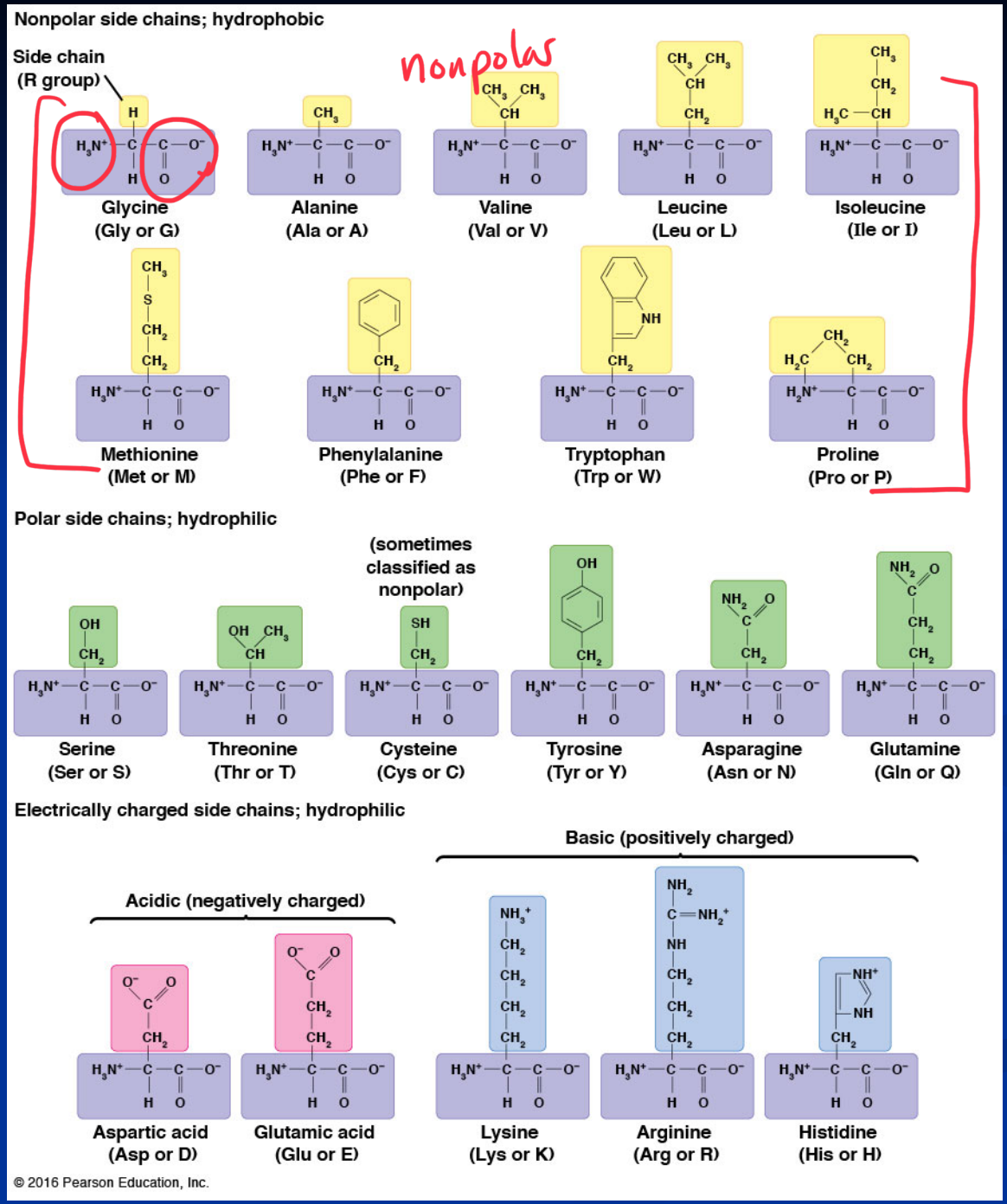


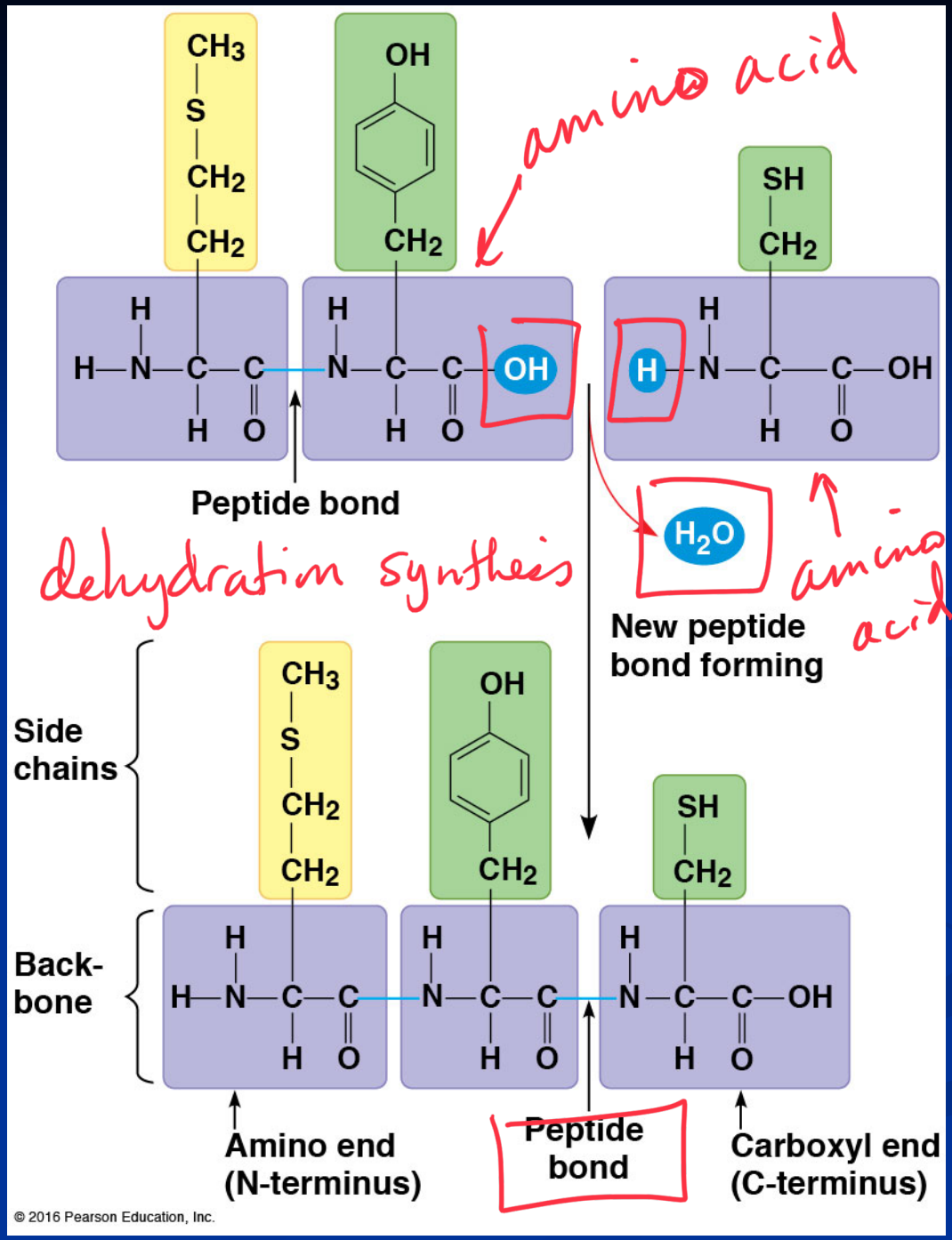


Amino Acid

- **R group** = side chains
- Properties:
  - hydrophobic
  - hydrophilic
  - ionic (acids & bases)
- "amino" : $-NH_2$
- "acid" : -COOH

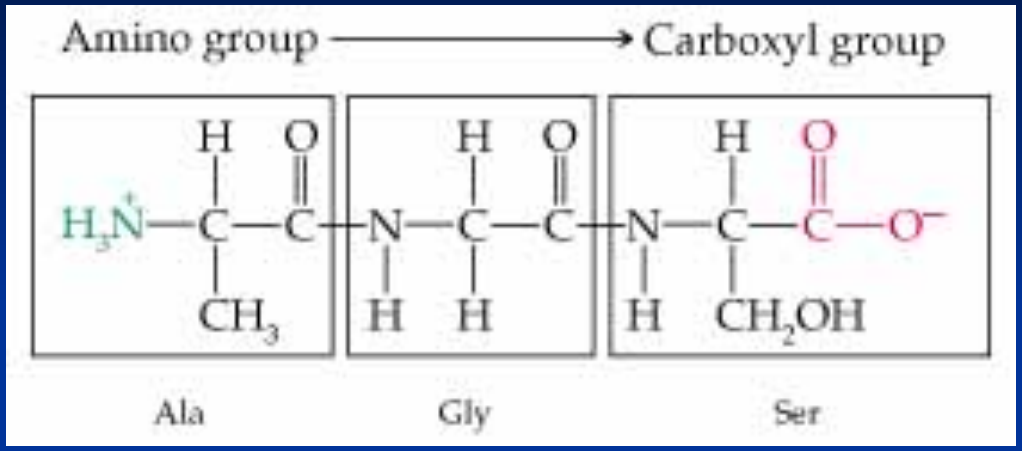


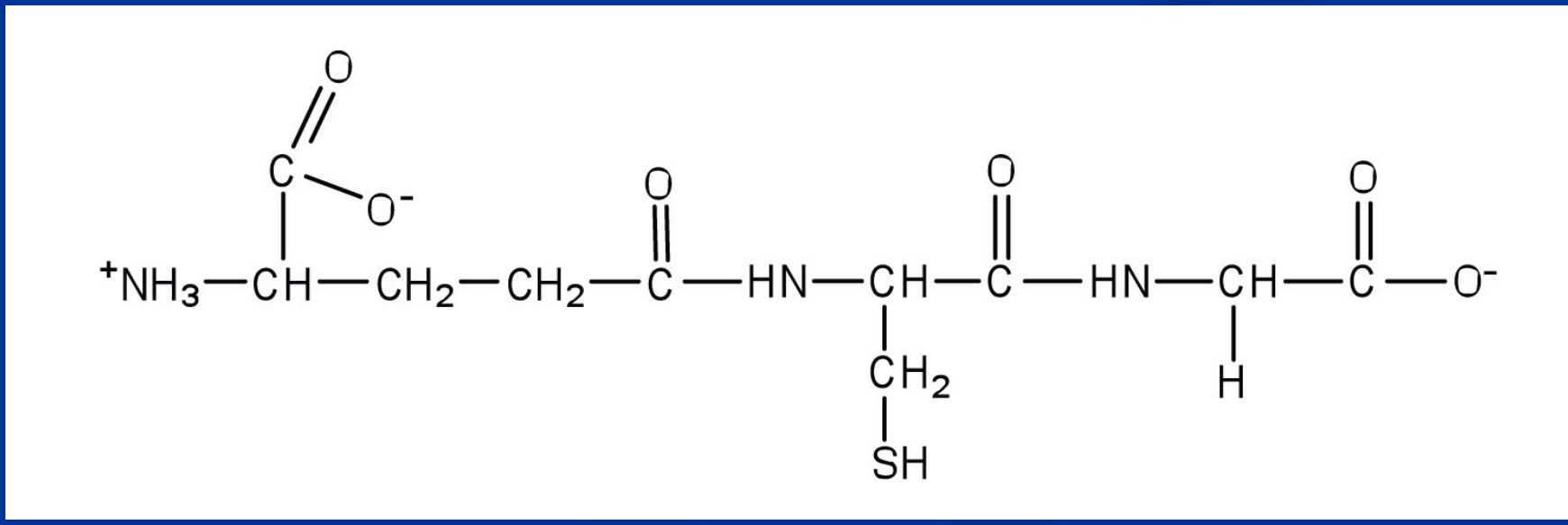




polypeptide

Peptide Bonds





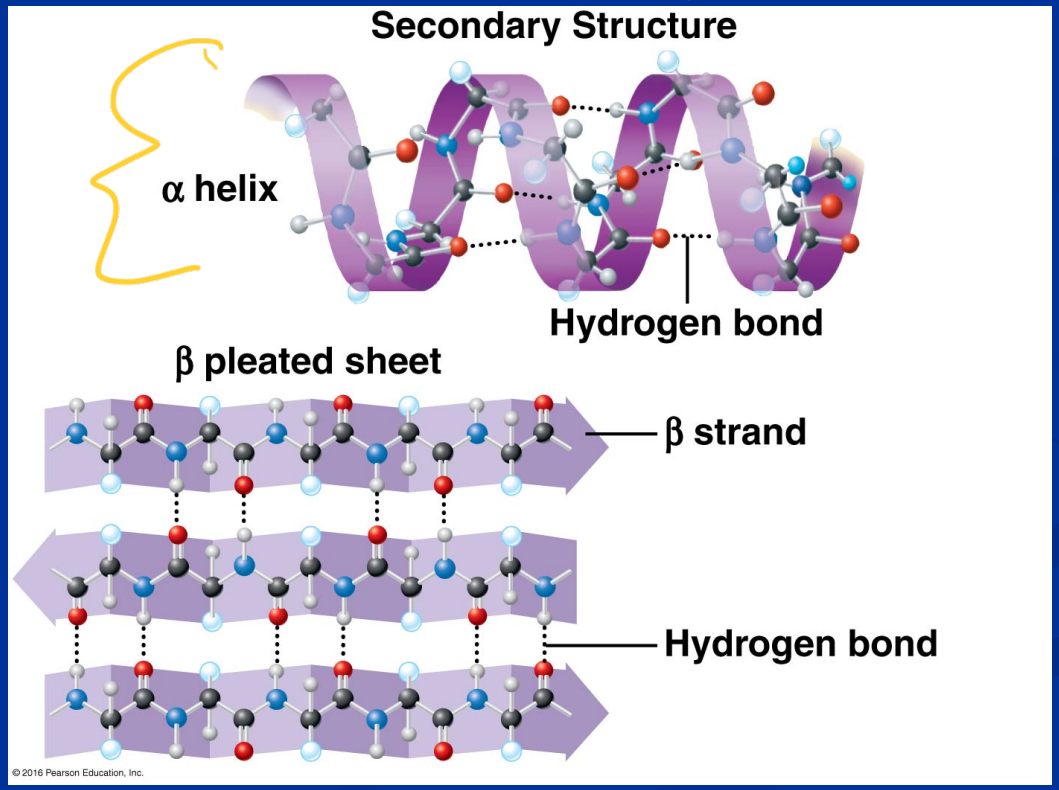
melody

Four Levels of Protein Structure (continued)

2. Secondary

patterns and motifs

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



of nonpolar amino acids in the interior of the protein

Basic Principles of Protein Folding

Know this

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 <u>disulfide bonds</u>.

sheet music for one instrument

Four Levels of Protein Structure (continued)

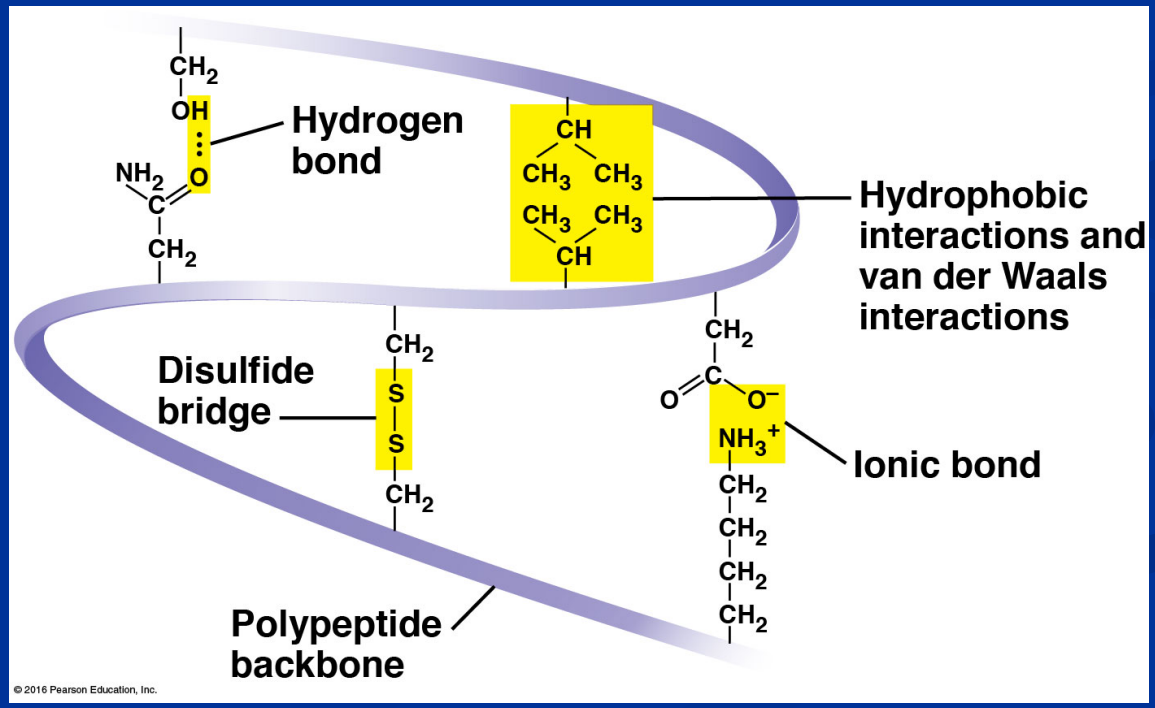
in orchestra

3. Tertiary

3-D model/structure

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

structure → function



Four Levels of Protein Structure (continued)

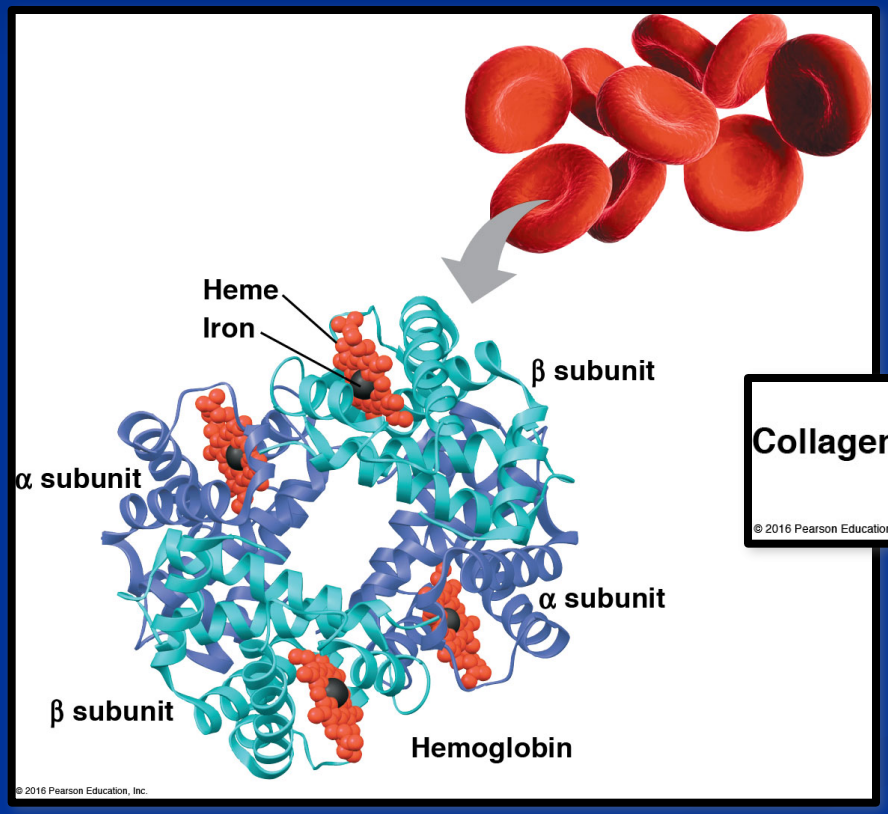
4. Quaternary

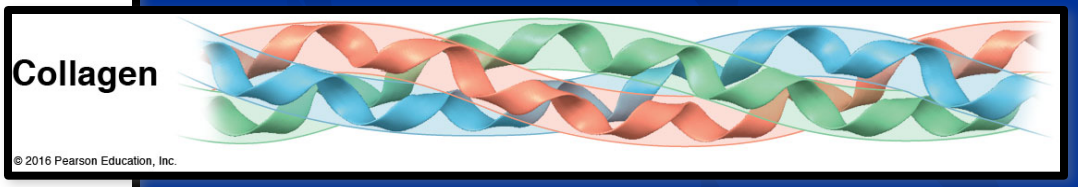
whole orchestra

- **2+ polypeptides** bond together

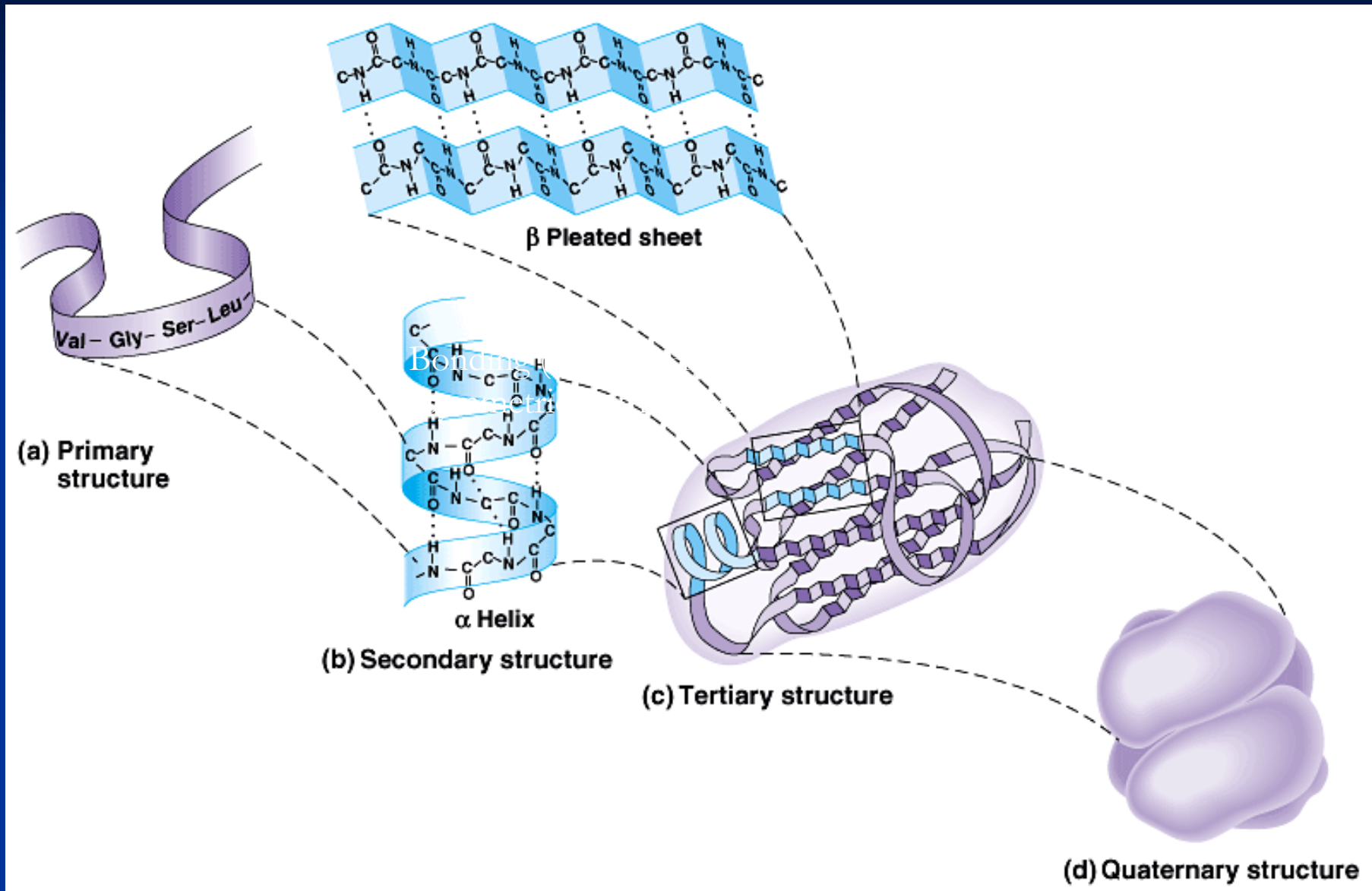
music for every instrument.

multiple polypeptides structures come together to form one functional protein

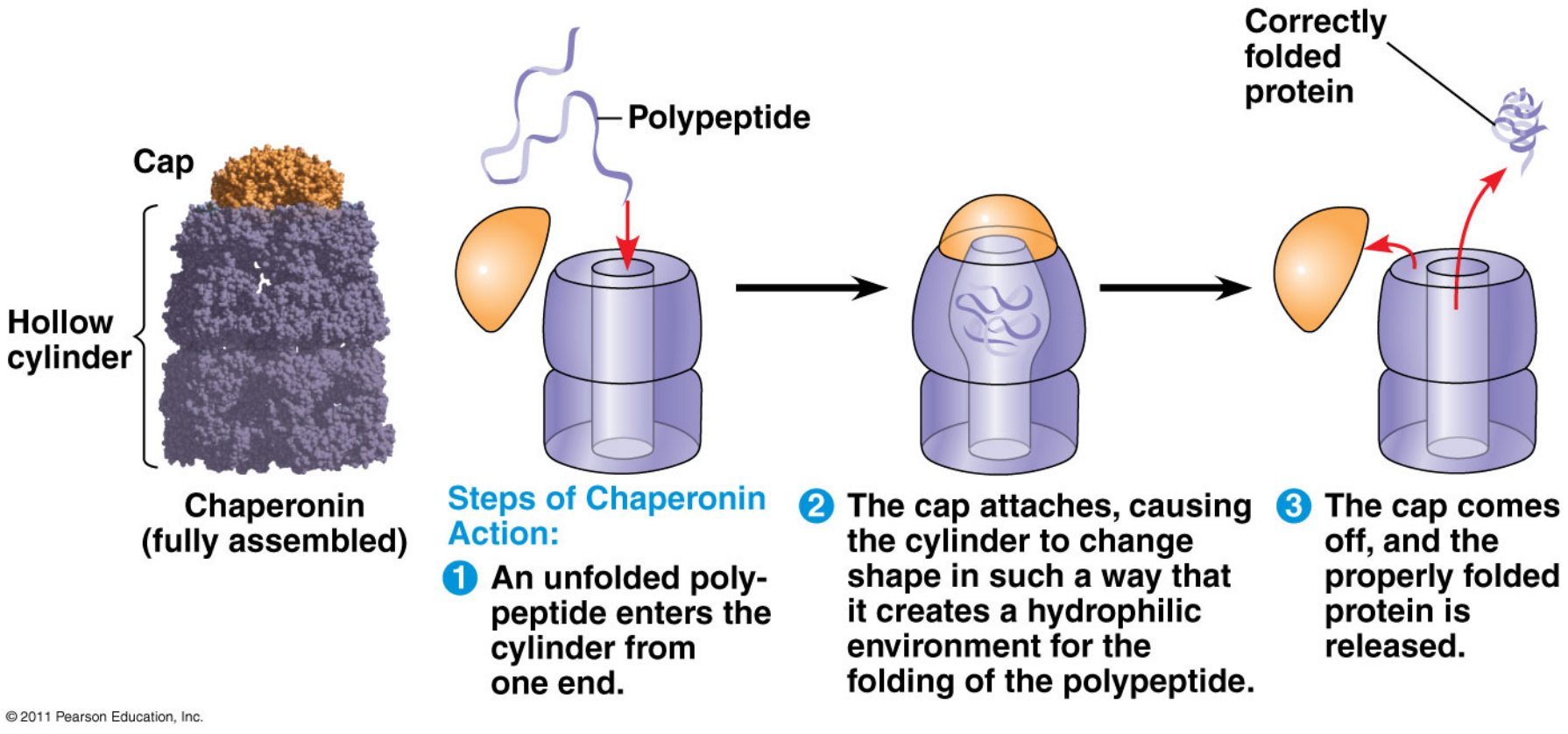




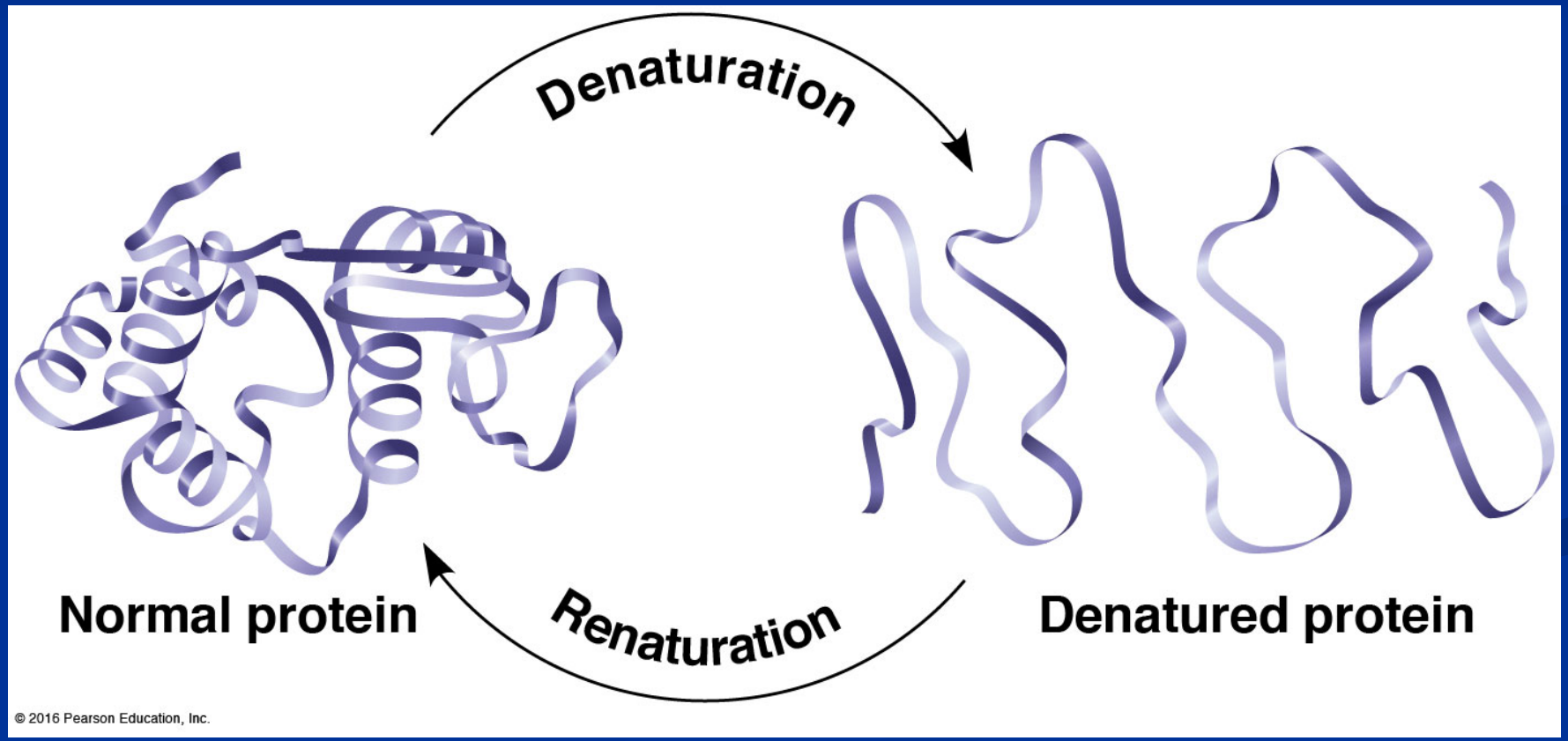
amino acids → polypeptides → protein



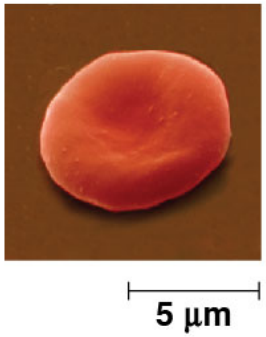
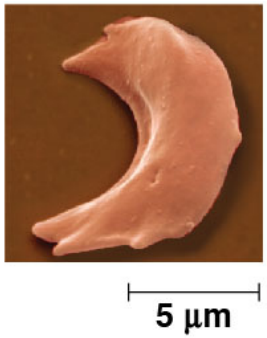
Chaperonins assist in proper folding of proteins



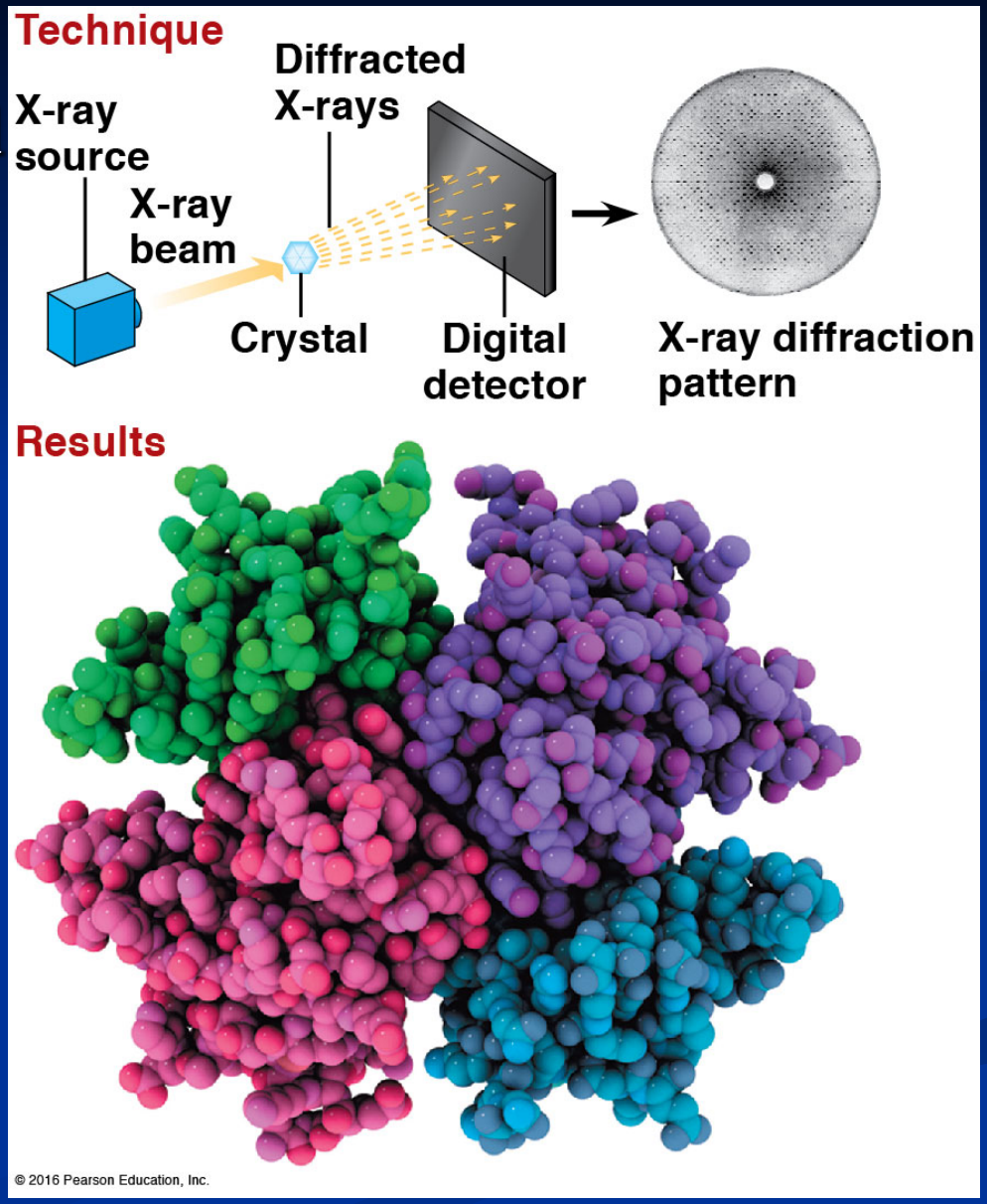
- Protein **structure and function** are sensitive to chemical and physical conditions
- Unfolds or **denatures** if **pH** and **temperature** are not optimal



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 β α β α	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 β α β α	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



Genomics: Analysis of genes and genomes