Chapter 3.2 Proteins

Proteins

- **Most structurally & functionally diverse group of biomolecules**
- **Functions:**
  - **involved in almost everything**
    - **enzymes**
    - **structure (keratin, collagen)**
    - **carriers & transport (membrane channels)**
    - **receptors & binding (defense)**
    - **contraction (actin & myosin)**
    - **signaling (hormones)**

Proteins

- **Structure:**
  - **monomer = amino acids**
    - **20 different amino acids**
  - **polymer = polypeptide**
    - **protein can be 1 or more polypeptide chains folded & bonded together**
    - **large & complex molecules**
    - **complex 3-D shape**

Amino acids

- **Structure:**
  - **central carbon**
  - **amino group**
  - **carboxyl group (acid)**
  - **R group (side chain)**
    - **variable group**
    - **confers unique chemical properties of the amino acid**

Nonpolar amino acids

- **nonpolar & hydrophobic side chains**

Nonpolar: Glycine (Gly), Alanine (Ala), Valine (Val), Leucine (Leu), Isoleucine (Ile), Methionine (Met), Phenylalanine (Phe), Tryptophan (Trp), Proline (Pro)

Why are these considered nonpolar & hydrophobic?

Polar amino acids

- **polar or charged & hydrophilic side chains**

Polar: Serine (Ser), Threonine (Thr), Cysteine (Cys), Tyrosine (Tyr), Asparagine (Asn), Glutamine (Gln)

Electrically charged — Acidic: Aspartic acid (Asp), Glutamic acid (Glu); Basic: Lysine (Lys), Arginine (Arg), Histidine (His)

**Why are these considered polar & hydrophillic?**

Sulfur containing amino acids

- **Disulfide bridges**
  - ◆ cysteines form cross links

Amino Acids with Sulfur-containing Side Chains

Cysteine (Cys, C)   Methionine (Met, M)
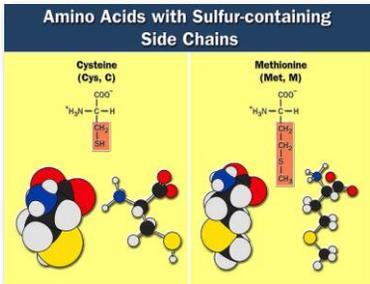
Building proteins

- **Peptide bonds: dehydration synthesis**
 - ◆ linking NH_2 of 1 amino acid to COOH of another
  - ◆ C–N bond

Peptide bond

Amino acid   Amino acid

H_2O

Polypeptide chain
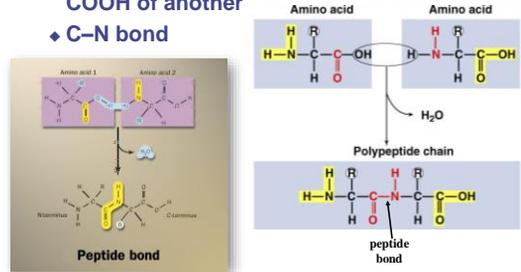
peptide bond

Building proteins

- **Polypeptide chains**
  - ◆ N-terminal = NH_2 end **(BEGINNING)**
  - ◆ C-terminal = COOH end **(END)**
  - ◆ repeated sequence (N-C-C) is the polypeptide backbone
    - ▪ grow in one direction

Side chains

Peptide bond

Back-bone

Amino end (N-terminus)   Carboxyl end (C-terminus)
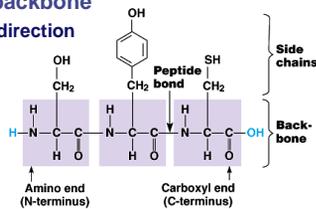
Protein structure & function

- **function depends on structure**
  - ◆ 3-D structure
    - ▪ twisted, folded, coiled into unique shape

hemoglobin   pepsin   collagen

Active Site
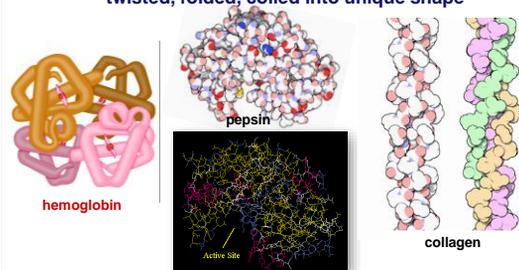
Protein structure & function

- **function depends on structure**
  - ◆ all starts with the __order of amino acids__
    - ▪ what determines that order of amino acids?
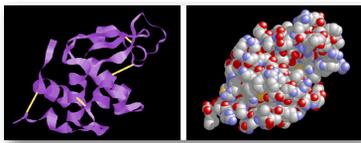
lysozyme: enzyme in tears & mucus that kills bacteria
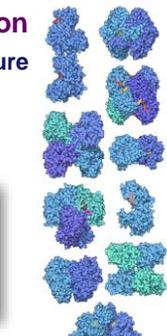
the 10 glycolytic enzymes used to breakdown glucose to make ATP

Primary (1°) structure

- __Order__ of amino acids in chain
  - ◆ __amino acid sequence determined by DNA__
  - ◆ slight change in amino acid sequence can affect protein's structure & it's function
    - ▪ even just one amino acid change can make all the difference!

Tell 'em about the Colonie Youth in a lineup!

Primary (1°) structure: Sickle cell anemia
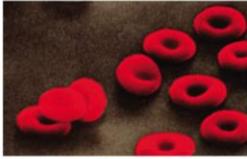
| Val | His | Leu | Thr | Pro | Glu | Glu | · · · |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | |

(a) Normal red blood cells and the primary structure of normal hemoglobin

| Val | His | Leu | Thr | Pro | Val | Glu | · · · |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | |

(b) Sickled red blood cells and the primary structure of sickle-cell hemoglobin

Secondary (2°) structure

- **"Local folding"**
  - **folding along short sections of polypeptide**
    - interaction between adjacent amino acids
    - H bonds on backbone
    - α-helix
    - β-pleated sheet

α Helix   β Pleated sheet
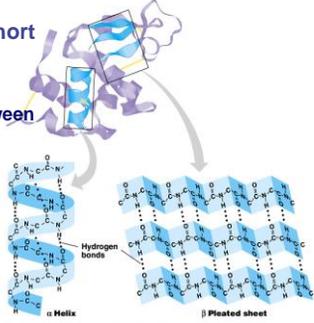
Tertiary (3°) structure

- **"Global (whole molecule) folding"**
  - **determined by interactions between R groups**
    - anchored by disulfide bridges
    - stabilized by hydrogen and ionic 'bonds'
    - hydrophobic interactions
      - effect of water in cell
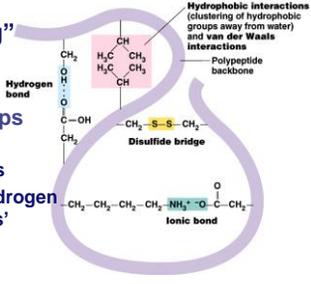
Quaternary (4°) structure

- **Joins together more than 1 polypeptide chain**
  - **only then is it a functional protein**

(a) Collagen   (b) Hemoglobin
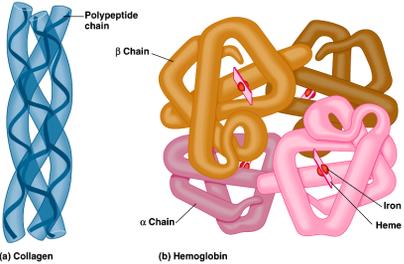
Chaperonin proteins

- **Guide protein folding**
  - **provide shelter for folding polypeptides**
  - **keep the new protein segregated from cytoplasmic influences**
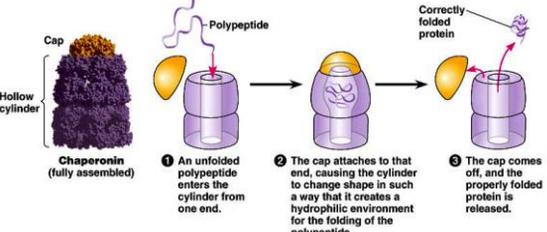
Protein models

- **Protein structure visualized by**
  - **X-ray crystallography**
  - **extrapolating from amino acid sequence**
  - **computer modelling**

lysozyme

Protein structure (review)

3°   **R groups**
hydrophobic interactions, disulfide bridges, ionic bonds

β Pleated sheet

α Helix

(a) Primary structure

(b) Secondary structure

(c) Tertiary structure

(d) Quaternary structure

4° multiple **polypeptides** hydrophobic interactions, ionic bonds

1° **aa sequence** peptide bonds; determined by DNA

2° backbone H bonds

Denature a protein

- **Disrupt 3° structure**
  - pH
  - temperature
  - salt
  - ◆ unravel or **denature** protein
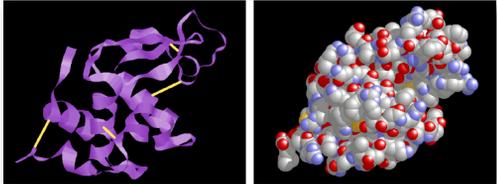 - ◆ disrupts H bonds, ionic bonds & disulfide bridges
- **Some proteins can return to their functional shape after denaturation, many cannot!**

Folded protein

Denaturation

Denatured protein