

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)
 - storage (bean seed proteins)

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

$$\begin{array}{c}
 \text{H} & & \text{O} \\
 | & & || \\
 \text{H}-\text{N}-\text{C}-\text{C}-\text{OH} \\
 | & & | \\
 \text{H} & & \text{R}
 \end{array}$$

Nonpolar amino acids

- nonpolar & hydrophobic

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

Why are these nonpolar & hydrophobic?

Polar amino acids

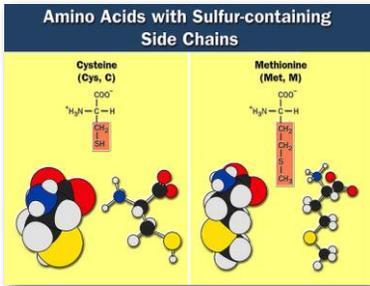
- polar or charged & hydrophilic

| | | | | | |
|---------------------|---------------------|----------------|----------------|------------------|-----------------|
| | | | | | |
| Serine (Ser) | Threonine (Thr) | Cysteine (Cys) | Tyrosine (Tyr) | Asparagine (Asn) | Glutamine (Gln) |
| Acidic | | | Basic | | |
| | | | | | |
| Aspartic acid (Asp) | Glutamic acid (Glu) | Lysine (Lys) | Arginine (Arg) | Histidine (His) | |

Why are these polar & hydrophilic?

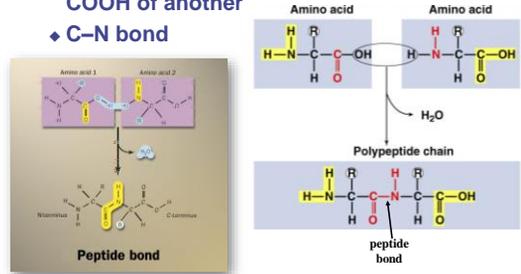
Sulfur containing amino acids

- Disulfide bridges
 - cysteines form cross links



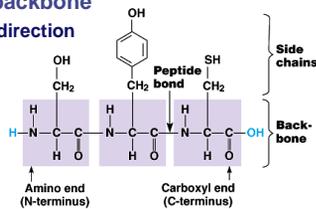
Building proteins

- Peptide bonds: dehydration synthesis
 - linking NH₂ of 1 amino acid to COOH of another
 - C-N bond



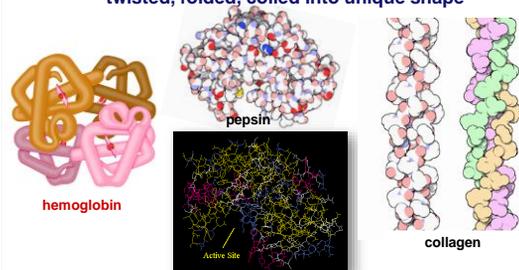
Building proteins

- Polypeptide chains
 - N-terminal = NH₂ end
 - C-terminal = COOH end
 - repeated sequence (N-C-C) is the polypeptide backbone
 - grow in one direction



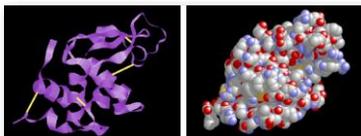
Protein structure & function

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



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

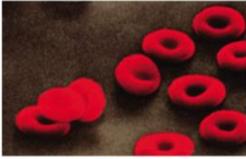
the 10 glycolytic enzymes used to breakdown glucose to make ATP

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!



Primary (1°) structure: Sickle cell anemia



10 μm

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



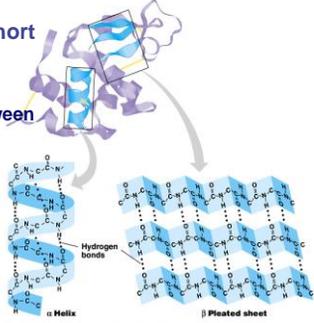
10 μm

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

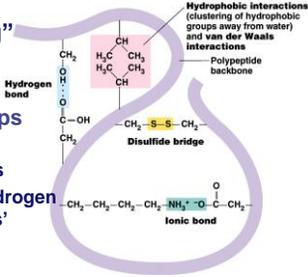
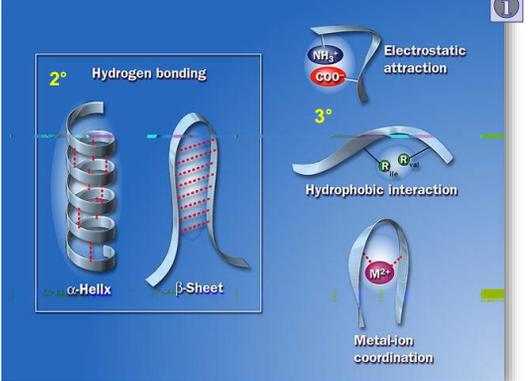
Secondary (2°) structure

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



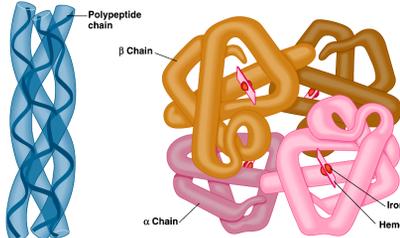
Tertiary (3°) structure

- “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

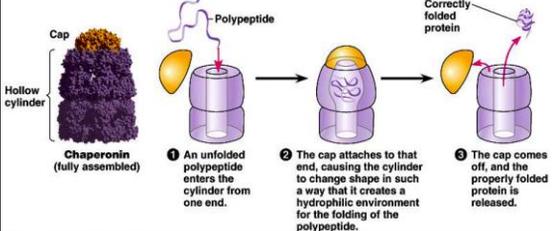
- Joins together more than 1 polypeptide chain
 - ♦ only then is it a functional protein



(a) Collagen (b) Hemoglobin

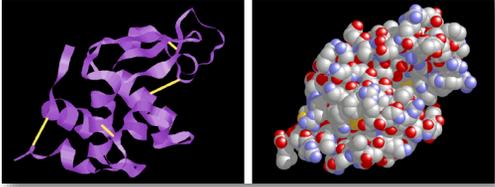
Chaperonin proteins

- 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)

1° aa sequence peptide bonds; determined by DNA

2° backbone H bonds

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

4° multiple polypeptides hydrophobic interactions, ionic bonds

(a) Primary structure
(b) Secondary structure
(c) Tertiary structure
(d) Quaternary structure

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!

