

Proteins

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

MCC BP Based on work by K. Foglia www.kfoglia.com



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

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Amino acids

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

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

Based on work by K. Foglia
www.kimunity.com

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?

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Polar amino acids

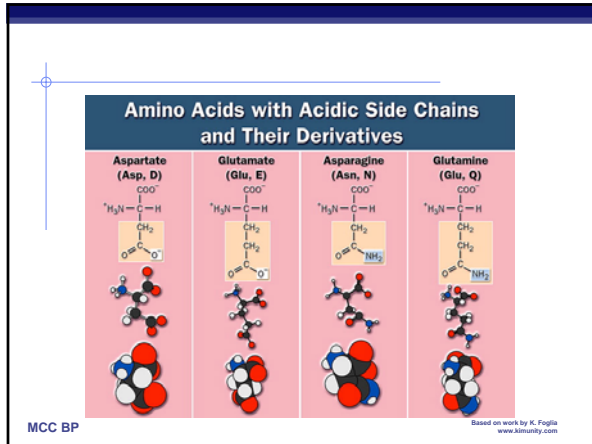
- polar or charged & hydrophilic

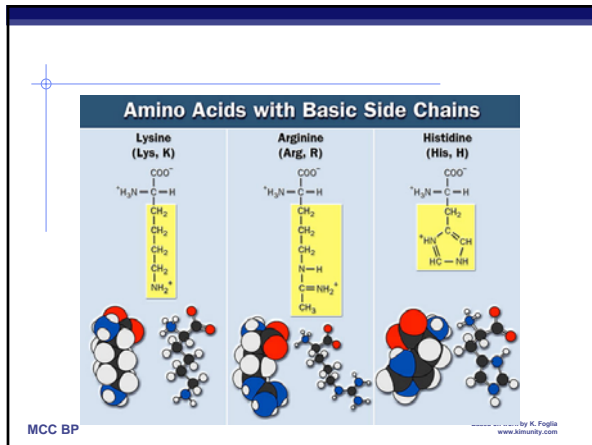
Serine (Ser)	Threonine (Thr)	Cysteine (Cys)	Tyrosine (Tyr)	Asparagine (Asn)	Glutamine (Gln)
Acidic			Basic		
Aspartic acid (Asp)	Glutamic acid (Glu)	Lysine (Lys)	Arginine (Arg)	Histidine (His)	

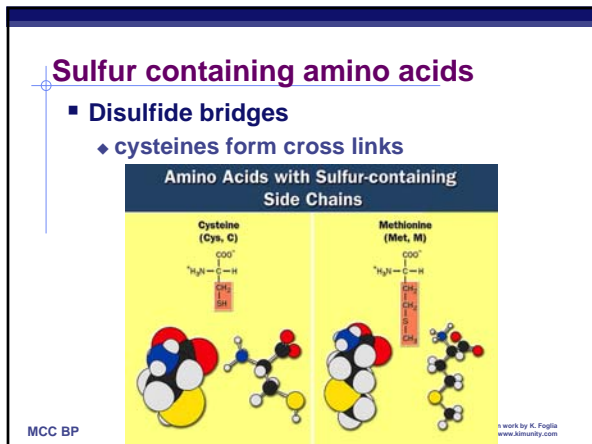
Why are these polar & hydrophilic?

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Building proteins

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

Peptide bond

peptide bond

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www.kimunity.com

Building proteins

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

Side chains

Backbone

Peptide bond

Amino end (N-terminus)

Carboxyl end (C-terminus)

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Protein structure & function

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

hemoglobin

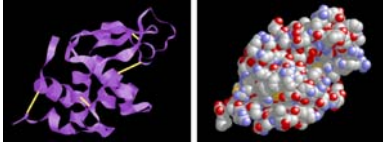
pepsin

collagen

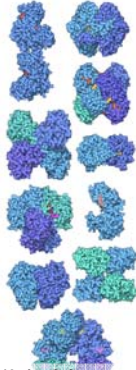
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Protein structure & function

- 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

"Let's go to the video tape!"
(play movie here)


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!



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Sickle cell anemia



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

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

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

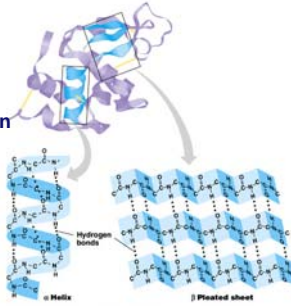
Val | His | Leu | Thr | Pro | Val | Glu | ...
1 2 3 4 5 6 7

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Secondary (2°) structure

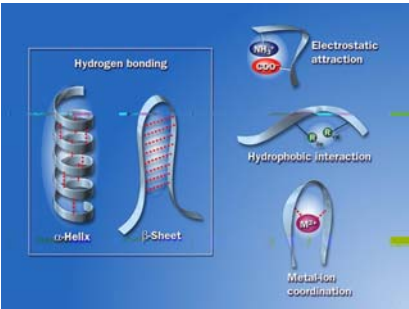
- “Local folding”
 - ◆ Folding along short sections of polypeptide
 - interaction between adjacent amino acids
 - H bonds between R groups
 - α-helix
 - β-pleated sheet



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Secondary (2°) structure

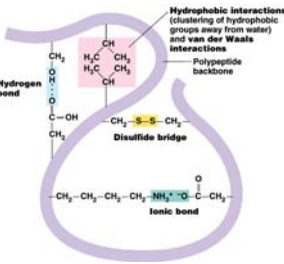


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Tertiary (3°) structure

- “Whole molecule folding”
 - ◆ determined by interactions between R groups
 - hydrophobic interactions
 - ◆ effect of water in cell
 - anchored by disulfide bridges (H & ionic bonds)



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Quaternary (4°) structure

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

collagen = skin & tendons

hemoglobin

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Protein structure (review)

aa sequence peptide bonds determined by DNA

R groups H bonds

R groups hydrophobic interactions, disulfide bridges

multiple polypeptides hydrophobic interactions

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Chaperonin proteins

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

1 An unfolded polypeptide enters the cylinder from one end.

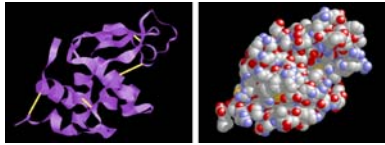
2 The cap attaches to that end, causing the cylinder to change shape in such a way that it creates a hydrophilic environment for the folding of the polypeptide.

3 The cap comes off, and the properly folded protein is released.

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Protein models

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

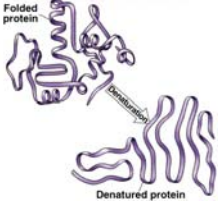


lysozyme

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Denature a protein

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



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Let's build some Proteins!



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