Take notes while watching the following video tutorials to prepare for the

"Proteins Part 1 Activity".

Proteins & Enzymes Part 1: Amino Acids

The building blocks of proteins are α -amino acids, small molecules that contain a carboxylic acid and an amino group. The amino group and the carboxylic acid group are bonded to the same carbon. This shared carbon is called the α carbon.

Amino Acid at Physiological pH Amino acids are always ionized at pH 7.4.

Zwitterion:

Essential Amino Acids: amino acids that can NOT be produced by the body There are 20 different amino acids found in proteins which differ only in the side chain (R group).



Note the omission of α from amino acids. Everyone is "supposed to know".

Acidic R Groups and Amino Acid Nomenclature

Remember the acid/base chemistry of carboxylic acids and amines.

Label the following reactants and products using the names: Aspartic acid; glutamic acid; aspartate; glutamate.



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Proteins and Enzymes Part 3: An Overview of Protein Structure Protein: A polypeptide with a specific biological function Levels of Structure of Proteins



Proteins and Enzymes Part 4: The Primary Structure of Proteins

The primary structure of proteins is the amino acid sequence.

Peptides: two or more amino acids bonded together The amine group of one amino acid and the acid group of another can undergo an acyl group transfer reaction to form an amide bond (peptide bond). The new molecule is called a dipeptide. More reactions lead to tripeptides, tetrapeptides, etc. and finally polypeptides. Polypeptides are always written with the N-terminus on the left and the C-terminus on the right.

The acyl transfer reaction (synthetic dehydration) of threonine (Thr) and valine (Val) to make a dipeptide is shown below.



Draw the neutral forms of each amino acid to help you recognize the synthetic dehydration reaction.

Draw an arrow to the peptide bond connecting threonine to valine. Circle the part of the dipeptide that originated from threonine. Circle the part of the dipeptide that originated from valine. What is the relationship between Val-Thr and Thr-Val? Tripeptides - Use the tripeptide below to answer the following questions.

Draw an arrow to each peptide bond.

Circle the 3 side chains (R groups) in the following tripeptide.

Classify each R group as nonpolar, polar, acidic, or basic.

Label the N-terminus and C-terminus

Write the peptide sequence.



Draw the bond-line structure for the tripeptide Glu-Ser-Cys at physiological pH.

Proteins and Enzymes Part 5: Secondary Structure

Secondary Structure: regular folding patterns in localized regions of the polypeptide backbone.

Secondary structure is held in place by H-bonds between backbone carbonyls & amino groups.

- α-helix: the polypeptide backbone twists so that H-bonds form between
 C=O and an N-H group 4 residues (amino acids) further along in
 the sequence
- β-sheet: the polypeptide backbone is extended and H-bonds form between the C=O and N-H groups on adjacent strands. In parallel sheets, the primary sequence of both stands proceeds in the same directions. In anti-parallel sheets, the primary sequences proceed in opposite directions.



Secondary Structure distinguishes the different types of Fibrous Proteins.

Fibrous Proteins - primarily found in structural proteins

- ♦ water insoluble
- small fibrils twist into larger bundles
- the # of disulfide bonds affects hardness, flexibility & stretchiness
- α -helix: wool, hair & fingernails
- β-sheets: silk & spider webs (small R groups allow close stacking)

Collagen is an example of a fibrous protein. Note the 3 α -helixes.



Other Important Fibrous Proteins

Fibrous Protein	Occurrence and Function
	Found in skin, wool, feathers, hooves,
keratins	silk, finger nails
	Found in animal hide, tendons, bone,
collagens	eye cornea, & other connective tissue
elastins	Found in blood vessels & ligaments where the ability to stretch is important
myosins	Found in muscle tissue
fibrin	Found in blood clots

Proteins and Enzymes Part 6: Tertiary Structure

Tertiary structure – stabilized in 5 ways by R groups (side chains) that can be quite far apart along the amino acid backbone and may include nonpeptide organic molecules or metal ions

1. Covalent bonds - disulfide bonds form between cysteine residues



- 2. H-bonding
 - polar groups on side chains (R groups)
 - side chains with peptide back bone
- 3. Salt Bridges electrostatic interactions between ionized side chains
- 4. Hydrophobic (London/Dispersion) Interactions Globular proteins usually turn their polar groups outward toward the aqueous body fluids while the nonpolar side chains (R groups) move inward – away from the water. While the interaction is weak, it usually acts over large surface areas. Collectively, the interactions are strong enough to stabilize some 3° structures.
- 5. Metal-Ion Coordination

Trace minerals (metal cations) form bridges btwn anionic side chains

Classify the 3° interactions below.



Identify the 2° & 3° structures in the protein segment shown below.



Tertiary Structure and Globular Proteins

Tertiary structures make use of H-bonding, but the most important force holding globular proteins in place is the hydrophobic effect – a process by which the water solvent attracts the polar amino acids to the outside of the protein and "squeezes" the nonpolar amino acids into the center of the globular protein.



Globular Protein	Occurrence and Function
insulin	Regulatory hormone for glucose metabolism
ribonuclease	Enzyme that catalyzes RNA hydrolysis
Immunoglobulin	Proteins involved in immune response
Hemoglobin	Protein involved in O_2 transport
Albumins	Blood transport protein

Other Important Globular Proteins

Proteins and Enzymes Part 7: Quaternary Structure

Quaternary Structure – the way two or more polypeptide chains are held together by noncovalent interactions to form a single 3–D protein

Example: Hemoglobin consists of four polypeptide subunits, each containing a heme group that binds an O₂ molecule



What is the difference between a polypeptide and a protein?

Denaturation

An active protein must be in its native conformation. The primary structure is composed of amino acids connected with covalent peptide bonds that are not easily broken. However, the secondary, tertiary, & quaternary structures are held together with weaker, noncovalent interactions. These structures can be disturbed by heat, agitation, drastic pH changes, detergents, salts, organic solvents, etc. in a process called denaturing.

Denatured proteins are often said to be unfolded and are no longer able to perform their intended function. Some proteins can spontaneously refold, but most denaturations are essentially irreversible and deactivate the protein.



About half of the 223 amino acid residues of the digestive enzyme trypsin are hydrophobic. Describe where in the tertiary structure you would expect to find these residues.

Describe where in the tertiary structure you would expect the polar amino acid residues in trypsin to be located.

Suppose a polypeptide containing 150 amino acid residues is synthesized in the laboratory. Why is it not correct to call this polypeptide a protein?

What part(s) of the protein structure is(are) affected by hydrolysis?