

**BENG 100 Frontiers of Biomedical Engineering**  
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**Chapter 4**

**SUMMARY**

- Linear polymers of amino acids are polypeptide chains. A protein can be composed of one or more polypeptide chains.
- There are 20 different amino acids; each with its unique chemical properties conferred by the side chain. The amino acids can be placed into broad categories: polar, nonpolar, acidic, and basic.
- There are four levels of structure for proteins. The amino acid sequence is the primary structure, the local domains are the secondary structure, the overall three-dimensional shape is the tertiary structure, and the formation of a complex with other polypeptide chains is the quaternary structure.
- All the information necessary for a protein to fold properly into its tertiary structure is contained in the primary amino acid sequence.
- Non-covalent interactions such as hydrogen bonding or the hydrophobic/hydrophilic forces hold a protein in its native form. Covalent disulfide bonds can be formed between two cysteine amino acids located at different regions of the polypeptide chain.
- The three-dimensional protein structure can be determined experimentally using NMR spectroscopy or X-ray crystallography.
- Proteins are often modified after translation by the addition of chemical groups to certain amino acids.
- Proteins can also be processed via proteolytic cleavage of the polypeptide chain into smaller segments.
- Proteins have diverse functions such as maintaining cell structure, transporting small molecules, facilitating cell communication, protecting against foreign invaders, and catalyzing chemical reactions.
- Enzymes catalyze chemical reactions by lowering the activation energy of a reaction.

## KEY CONCEPTS AND DEFINITIONS

alpha ( $\alpha$ ) helix – a common secondary structure of proteins in which the linear sequence of amino acids is folded into a right-handed spiral stabilized by hydrogen bonds between carboxyl and amide groups in the backbone; a coiled secondary structure of a polypeptide chain formed by hydrogen bonding between amino acids separated by four residues.

acetylation - the addition of one or more acetyl groups to a protein; the formation of an acetyl derivative..

activation energy - the input of energy required to (overcome the barrier to) initiate a chemical reaction. By reducing the activation energy, an enzyme increases the rate of a reaction.

active site - the region of an enzyme that binds substrates and catalyzes an enzymatic reaction.

acylation - the addition of one or more acyl groups to a protein.

beta ( $\beta$ ) sheet - a planar secondary structure of proteins that is created by hydrogen bonding between the backbone atoms in two different polypeptide chains or segments of a single folded chain; a sheet-like secondary structure of a polypeptide chain, formed by hydrogen bonding between amino acids located in different regions of the polypeptide.

affinity – a measure of the degree to which an substance tends to bind to another.

antibody – a specialized immune protein, which helps fight infection by neutralizing pathogens and tagging them for destruction.

catalyst – a substance that increases the rate of a reaction without itself undergoing any chemical change.

dimer – a compound formed by two molecules of a simpler compound; a polymer formed from two molecules of a monomer.

disulfide bond (-S-S-) - covalent linkage formed between two sulfhydryl groups on cysteines. For extracellular proteins, disulfide bonding is a common way of joining two proteins together or linking different parts of the same protein. Formed in the endoplasmic reticulum of eukaryotic cells.

enzyme – a biological substance produced by living organisms to increase the rate of a biochemical reaction.

glycosylation - the addition of one or more sugars to a protein or lipid molecule.

hydrophobic effect - tendency of nonpolar groups to cluster so as to shield themselves

from contact with an aqueous environment.

ion channel – a transmembrane protein that transports ions, which are otherwise impermeable to the cells.

ligand - any molecule, other than an enzyme substrate, that binds tightly and specifically to a macromolecule, usually a protein, forming a macromolecule-ligand complex

Lineweaver-Burke plot - Graphical model used to determine the maximum reaction rate,  $V_{max}$ , and Michaelis constant,  $K_M$ . The linear graph is obtained by taking the reciprocal of both sides of the Michaelis-Menten Equation.

Michaelis constant ( $K_M$ ) - The value equal to the substrate concentration at which the enzyme reaction proceeds at half of the maximum velocity.

Michaelis-Menten equation - Is an equation that describes the velocity of a given reaction developed from a simple model of enzyme substrate kinetics.

nascent proteins – a protein that has not yet achieved its functional final folding pattern.

N-myristoylation - the addition of myristic acid (a 14-carbon fatty acid) to the N-terminal glycine residue of a polypeptide chain.

nuclear magnetic resonance (NMR) spectroscopy - technique in which the magnetic nucleus of an atom is aligned with an external magnetic field and disturbing this alignment via the use of an electromagnetic field. The response of this disturbance is interpreted and gives information concerning physical, chemical, electronic and structural information of compounds.

peptide bond - covalent bond that links adjacent amino acid residues in proteins; formed by a condensation reaction between the amino group of one amino acid and the carboxyl group of another with the release of a water molecule

phosphorylation - reaction in which a phosphate group becomes covalently coupled to another molecule

post-translational modification - the enzyme-catalyzed change to a protein made after it is synthesized.

protease - enzyme such as trypsin that degrades proteins by hydrolyzing some of their peptide bonds.

protease inhibitor – a substance that functions by inhibiting the actions of a protease.

proteome – the complete set of proteins present in the cell.

proteomics – a branch of molecular biology concerned with determining the proteome

proteolysis - degradation of polypeptide chains.

receptor transmembrane protein – a transmembrane protein that has an extracellular domain that binds to molecules called ligands.

sequence homology analysis - comparison of an unknown primary amino acid sequence to a database of known primary amino acid sequences in an attempt to identify functional capabilities of the unknown amino acid.

substrate - molecule on which an enzyme acts.

transition state – the structure that forms transiently in the course of a chemical reaction and has the highest free energy of any reaction intermediate. Its formation is a rate limiting step in the reaction.

turnover number ( $k_{cat}$ ) - a rate constant that is equal to the number of substrate molecules processed per enzyme molecule each second

x-ray crystallography - technique for determining the three-dimensional structure of macromolecules (particularly proteins and nucleic acids) by passing x-rays through a crystal of the purified molecules and analyzing the diffraction pattern of discrete spots that results; a method in which the diffraction pattern of X rays is used to determine the arrangement of individual atoms within a molecule.

## QUESTIONS

1. Describe the varying levels of structure for proteins. How do scientists experimentally determine the protein structure?
2. What is remarkable about post-translational modification of proteins?
3. Describe the hydrophobic effect and how it contributes to an energetically favorable protein folding reaction.
4. Describe the difference between the lock and key model and the induced fit model; then give a reason why the induced fit model may be more appropriate in describing enzyme mechanism.
5. Describe some ways that drugs might act as enzyme inhibitors.
6. Using a biochemistry textbook, or on-line resources, determine which of the following proteins has quaternary structure:  $\alpha$ -chymotrypsin, hemoglobin, insulin, myoglobin, and trypsin.