LECTURES 11 & 12 – Proteins

QUESTIONS TO TRY FOR PRACTICE

1) Which is not a role proteins play in organisms?
A) store genetic information
B) movement and shape changes
C) chemical signaling
D) structural support

2) Three important functions of proteins are cell
A) wall composition, cushioning, and membrane fluidity.
B) movement, signaling, and reaction catalysis.
C) information coding, conversion, and transfer.

3) Which of the following is not a major functional class of proteins?
A) hereditary proteins
B) enzymes
C) motility proteins
D) regulatory proteins
E) structural proteins

4) An amino acid has an R-group that is negatively charged at cellular pH. Which of the following categories would best describe it?
A) acidic
B) basic
C) uncharged and polar
D) nonpolar

5) An amino acid has an R-group that is positively charged at cellular pH. Which of the following categories would best describe it?
A) acidic
B) basic
C) uncharged and polar
D) nonpolar

6) An amino acid has an R-group that is composed of only carbon and hydrogen atoms. Which of the following categories would best describe it?
A) acidic
B) basic
C) uncharged and polar
D) nonpolar

7) An amino acid has an R-group that does not have a positive or a negative charge but has an oxygen atom. Which of the following categories would best describe it?
A) acidic
B) basic
C) uncharged and polar
D) nonpolar

8) Which of the following statements about the peptide-bonded backbone is correct?
A) Both ends of the backbone have a free carboxyl group.
B) Both ends of the backbone have a free amino group.
C) The orientation of the side chains in the backbone does not allow them to interact with each other or water.
D) One end of the backbone has a free amino group while the other has a free carboxyl group.
E) Interactions only take place between C=O and N—H groups in the different peptide-bonded backbones.

9) Which of the following statements about peptides is correct?
A) As a whole, the structure of the peptide-bonded backbone is flexible.
B) The peptide bond is capable of rotating.
C) Joining two amino acids together through a peptide bond results in the formation of a carboxyl group.
D) A peptide bond is formed by a condensation reaction between two carboxyl groups.
E) A peptide bond is formed by a condensation reaction between the carboxyl and amino group of the same amino acid.

10) Which one of the following is not a component of each monomer used to make proteins?
A) a phosphorous atom, P
B) an amino functional group, NH_2
C) a side chain, R
D) a carboxyl group, COOH

11) Amino acid side chains (R groups) with what characteristic(s) dissolve best in water?
A) small sizes and simple structures
B) at least one ring structure
C) polarity or charged structures
D) the presence of sulfur

12) Why are polymerization reactions endergonic?
A) They reduce entropy.
B) They release heat, making the reactant monomers move faster.
C) Because the condensation and hydrolysis reactions are equally spontaneous.
D) Because polymers are energetically more stable and have lower potential energy than monomers do.

13) At the pH found in cells (about 7.0), what happens to the amino group on an amino acid?
A) It acts as a base and gains a proton, giving it a positive charge.
B) It acts as an acid and loses a proton, giving it a negative charge.
C) It is reduced and tends to act as an electron donor in redox reactions.
D) It remains neutral, like water, and does not have a charge.

14) At the pH found in cells (about 7.0), what happens to the carboxyl group on an amino acid?
A) It acts as a base and gains a proton, giving it a positive charge.
B) It acts as an acid and loses a proton, giving it a negative charge.
C) It is oxidized and tends to act as an electron acceptor in redox reactions.
D) It remains neutral, like water, and does not have a charge.

15) How does the structure of an amino acid enable it to play its most important roles in cells?
A) It can serve a wide variety of functions in a cell, because it contains the atoms most commonly found in organisms (C, H, N, and O).
B) Because both carboxyl and amino groups are present, polymerization is exergonic. In addition, the presence of a side chain makes the molecule water soluble.
C) The presence of carboxyl and amino groups gives it the ability to form peptide bonds, and its side chain gives it unique chemical properties.
D) Because each amino acid contains a variety of functional groups, they can participate in a wide variety of chemical reactions.

16) Which of the following involves an increase in entropy?
A) hydrolysis
B) condensation
C) polymerization
D) chemical evolution

17) In solution, why do hydrolysis reactions occur more readily than condensation reactions?
A) Hydrolysis increases entropy and is exothermic.
B) Hydrolysis raises G, or Gibbs free energy.
C) Hydrolysis decreases entropy and is exothermic.
D) Hydrolysis increases entropy and is endothermic.

18) Suppose you discovered a new amino acid. Its R-group contains only hydrogen and carbon atoms. Predict the behavior of this amino acid.
A) It is hydrophobic.
B) It is hydrophilic.
C) Relative to the amino acids found in organisms, its interactions with water will be intermediate.
D) Relative to the amino acids found in organisms, its interactions with water will be very high.

19) A peptide bond is
A) an ionic bond, not a covalent one.
B) a triple covalent bond.
C) a particularly stable, planar covalent bond.
D) a particularly unstable covalent bond.

20) When polymerization of a protein is complete, but the protein is still completely linear, what is the highest level of structure that has been completed?
A) primary
B) secondary
C) tertiary
D) quaternary

21) Which of the following best describes primary structure in proteins?
A) It is the number of amino acids present in the complete protein.
B) It is the number of peptide bonds in the complete protein.
C) It is the sequence of amino acids in the complete protein.
D) It is the number of α-helices and β-pleated sheets in the complete protein.

22) You are studying a protein that is shaped like a doughnut. The shape is a function of which level(s) of protein structure?
A) primary only
B) secondary only
C) tertiary only
D) secondary and tertiary only
E) primary, secondary, and tertiary

23) An enzyme has a total of four active sites. When you denature the molecule and study its composition, you find that each active site occurs on a different polypeptide. Which of the following hypotheses does this observation support?
A) The enzyme is subject to allosteric regulation.
B) The enzyme requires a cofactor to function normally.
C) The protein's structure is affected by temperature and pH.
D) The protein has quaternary structure.

24) Which of the following observations is the strongest argument in favor of the hypothesis that protein structure and function are correlated?
A) Proteins function best at certain temperatures.
B) Proteins have four distinct levels of structure and many functions.
C) Enzymes tend to be globular in shape.
D) Denatured (unfolded) proteins do not function normally.

25) You've just sequenced a new protein found in mice and observe that sulfur-containing cysteine residues occur at regular intervals. What is the significance of this finding?
A) Cysteine residues are required for the formation of α-helices and β-pleated sheets.
B) It will be important to include cysteine in the diet of the mice.
C) Cysteine residues are involved in disulfide bridges that help form tertiary structure.
D) Cysteine causes bends, or angles, to occur in the tertiary structure of proteins.

26) Interactions between side chains (R-groups) in a polypeptide are most important in stabilizing which of the following?
A) the primary structure of a protein
B) an α-helix
C) a β-sheet
D) the tertiary structure of a protein
E) the secondary structure of a protein

27) Recent technological advances have made it more feasible than ever to work out the three-dimensional structure of proteins. There is intense interest in this research field, called structural biology. Why?
A) Understanding structure should help us understand function.
B) Understanding structure can help in the design of drugs that alter the function of certain proteins.
C) Solving a protein's 3-D structure can lead to a better understanding of how the molecule works–for example, by identifying the active site and determining if there are regulatory sites.
D) All of the above apply.

28) What type of interaction is directly responsible for the formation of secondary structure?
A) peptide bonds between adjacent amino acids
B) peptide bonds between nonadjacent amino acids
C) hydrogen bonds between sections of the polypeptide backbone
D) hydrogen bonds between side chains of amino acids

29) A series of hydrophobic side chains will congregate together as a protein folds in an aqueous solution and be stabilized by
A) disulfide bonds.
B) van der Waals interaction.
C) hydrogen bonds.
D) quaternary structure bonds.

30) If the primary structure of a protein is incorrect
A) the secondary structure will be correct.
B) the tertiary structure will be correct.
C) any quaternary structure will be correct.
D) any higher-level folding of the protein will be incorrect.

31) You have isolated a previously unstudied protein, identified its complete structure in detail, and determined that it catalyzes the breakdown of a large substrate. You notice it has two binding sites. One of these is large, apparently the bonding site for the large substrate; the other is small, possibly a binding site for a regulatory molecule. What do these findings tell you about the mechanism of this protein?
A) It is probably a structural protein that is involved in cell-to-cell adhesion.
B) It is probably an enzyme that works through allosteric regulation.
C) It is probably an enzyme that works through competitive inhibition.
D) It is probably a cell membrane transport protein, like an ion channel.
E) It is probably a structural protein found in cartilage or skeletal tissue.

32) Consider the HIV enzyme called protease. The amino acid residues at the active site are highly hydrophobic. In designing a drug that would bind to the active site and jam it, researchers should use which type of molecule?
A) hydrophobic
B) polar
C) charged
D) acidic

33) When, and by whom, was the lock-and-key model of enzyme specificity developed?
A) 1894 by Fischer
B) 1894 by Miller
C) 1936 by Fischer
D) 1956 by Fischer
E) 1974 by Haldane and Oparin

34) Which one of the following is not a component of each monomer used to make proteins?
A) an iron atom, Fe
B) an amino functional group, NH_2
C) a side chain, R
D) a carboxyl group, COOH

Refer to the following paragraph and Figure 3.1 to answer the following question(s).

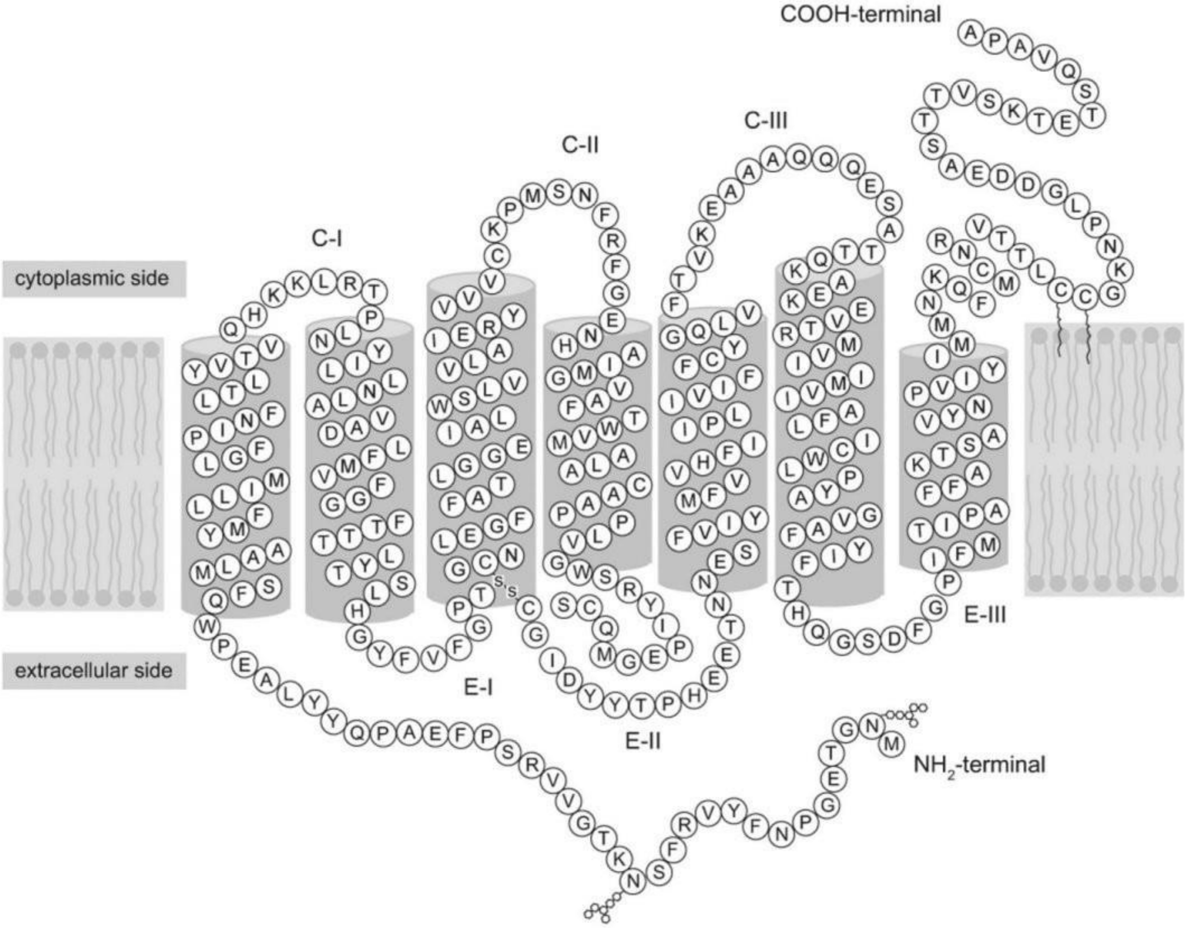

Figure 3.1

Since structure correlates so well with function, biochemists are constantly looking for new ways to probe the complex structure of proteins in order to understand what they do and how they do it. One of the most powerful techniques in existence today is X-ray crystallography. The main difficulty with this technique is getting the protein to crystallize. Once crystallized, the protein is bombarded with X-rays to create a pattern that can be analyzed mathematically to determine the three-dimensional structure of the protein. This analysis has been performed by Krzysztof Palczewski on the protein rhodopsin, which is a light-sensitive protein found in species ranging from ancient bacteria (archaea) to humans. The structure (schematically shown above, where each letter represents an amino acid) is characterized by a single polypeptide chain with several α-helical segments that loop back and forth across the cell membrane. Another notable feature is the disulfide bond (-S-S-) that can be seen at the bottom of the third transmembrane segment. [Figure adapted from K. Palczewski et al., Science 289 (2000): 739.]

35) How many times does the protein in Figure 3.1 cross the cell membrane?
A) 1
B) 3
C) 4
D) 7

36) If you were reading off the sequence of amino acids in Figure 3.1 to a biologist friend, what should the first three letters be?
A) M-N-G
B) A-P-A
C) It doesn't matter, since the protein has no polarity or directionality.

37) Identify the location of the disulfide bond in Figure 3.1. What is the name of the amino acids that are forming this bond?
A) cytosine
B) aspartic acid
C) cysteine
D) glycine

38) What is the location of the C-terminus of the protein in Figure 3.1?
A) extracellular
B) cytoplasm
C) embedded within the membrane
D) nucleus

39) Refer to Figure 3.1. Which level of structure is being maintained by the disulfide bond?
A) primary
B) secondary
C) tertiary
D) quaternary

40) The aquaporin family of proteins plays a major role in the transport of water all over the body. During the folding process of these proteins, α-helices start forming as
A) part of the primary structure of the protein.
B) part of the secondary structure of the protein.
C) part of the tertiary structure of the protein.
D) part of the quaternary structure of the protein.