3 Protein Structure and Function

Section 3.1

1. Which of the following is defined as the tertiary structure of a protein?
a. the primary amino acid sequence
b. structural domains such as a DNA-binding domain
c. folded structures such as an α helix
d. structural features such as a turn

Ans: b
Question Type: Multiple Choice
Chapter: 3
Blooms: Understanding
Difficulty: Easy

2. Monomeric proteins do not contain a:
a. primary structure.
b. secondary structure.
c. tertiary structure.
d. quaternary structure.

Ans: d
Question Type: Multiple Choice
Chapter: 3
Blooms: Understanding
Difficulty: Easy

3. Which of the following is NOT part of a zinc-finger motif?
a. zinc ion
b. proline residue
c. cysteine residue
d. histidine residue

Ans: b
Question Type: Multiple Choice
Chapter: 3
Blooms: Remembering
Difficulty: Easy

4. Describe the types of bonds/interactions that hold together or stabilize the primary, secondary, tertiary, and quaternary structures of proteins.

Ans: The primary structure of a protein is linked by covalent peptide bonds. The secondary structure is stabilized by hydrogen bonds between atoms of the peptide backbone. The tertiary structure is stabilized by hydrophobic

interactions between the nonpolar side groups and hydrogen bonds between polar side groups. The quaternary structure is held together by noncovalent bonds between protein subunits.
Question Type: Essay
Chapter: 3
Blooms: Understanding
Difficulty: Easy

5. Many proteins contain one or more motifs built from particular combinations of secondary structure. Describe the three common structural motifs discussed in this chapter.

Ans: The three structural motifs described in this chapter include the coiled coil motif, the helix-loop-helix motif, and the zinc finger motif. The coiled-coil motif consists of two or more α helices wrapped around one another. The helix-loop-helix motif consists of two helices connected by a loop that contains certain hydrophilic residues at invariant positions in the loop. The zinc-finger motif consists of an α helix and two β strands held together by a zinc ion in a fingerlike bundle.
Question Type: Essay
Chapter: 3
Application
Difficulty: Moderate

6. What types of bonds are apt to be more common in the nonaqueous, interior environment of a protein than in the aqueous, surface environment of a protein?

Ans: Proteins are arranged so that hydrophilic amino acids are on the surface of the protein and hydrophobic amino acids are in the interior. Hence, hydrogen bonding and ionic interactions with water are particularly common at the protein surface; hydrophobic interactions are more common in the protein interior.
Question Type: Essay
Chapter: 3
Blooms: Applying
Difficulty: Moderate

7. There are many important roles for the dynamic nature of proteins in a cell. Which of the following is NOT likely to describe one such reason?
a. A protein's structure determines its function.
b. Other molecules could be needed to allow proteins to fold into their active (ordered) conformation.
c. Quaternary structures are usually very transient (occur for short periods of time).
d. Proteins are crucial for many cell functions.

Ans: c
Question Type: Multiple Choice
Chapter: 3
Blooms: Applying
Difficulty: Moderate

9. You are studying an oligopeptide composed of eight amino acids. The four amino acids nearest the C terminus are nonpolar. The two amino acids nearest the N terminus are charged. The middle two amino acids are polar. Which amino acid is likely to be labeled as number 2?
a. threonine
b. phenylalanine
c. glutamine
d. lysine

Ans: d
Question Type: Multiple Choice
Chapter: 3

Blooms: Applying
Difficulty: Moderate

10. A protein containing several proline residues is:
a. not likely to form quarternary structures.
b. likely to be an integral membrane protein.
c. not likely to form alpha helices.
d. likely to be found in beta turns.

Ans: c
Question Type: Multiple Choice
Chapter: 3
Blooms: Remembering
Difficulty: Moderate

11. Which of the following is true about protein folding?
a. Amino acids cluster in the primary sequence so that all the hydrophobic amino acids are near each other to facilitate folding into the hydrophobic core of the tertiary structure.
b.All known proteins have well-ordered conformations.
c.Amino acids with hydrophobic, nonpolar side chains stabilize the tertiary structure through hydrogen bonding with water molecules surrounding the proteins.
d.Elements from the secondary structure are maintained in the tertiary structure.

Ans: d
Question Type: Multiple Choice
Chapter: 3
Blooms: Understanding
Difficulty: Moderate

12. When comparing domains and structural motifs, which of the following is NOT true?
a.Motifs are found in secondary structures, while domains are found in tertiary structures.
b.Helices are observed in motifs and domains.
c.Structural domains appear in different proteins with similar functions, while structural motifs have been less conserved over evolution.
d.A domain may be repeated in the same protein, but multiple copies of the same motif are rare.

Ans: c
Question Type: Multiple Choice
Chapter: 3
Blooms: Understanding
Difficulty: Moderate

13. You disrupt all hydrogen bonds in a protein. What level of structure will be preserved?
a. secondary structure
b. primary structure
c. tertiary structure
d. quaternary structure

Ans: b
Question Type: Multiple Choice
Chapter: 3
Blooms: Understanding
Difficulty: Easy

14. Two proteins that have a similar function:
a. will share similar amino acid sequences if they are homologs.

b. must have similar amino acid sequences.
c. will have identical primary structures.
d. belong in families together.

Ans: a
Question Type: Multiple Choice
Chapter: 3
Blooms: Remembering
Difficulty: Moderate

Section 3.2

15. All the following statements about molecular chaperones are true EXCEPT:
a. they play a role in the proper folding of proteins.
b. they are located in every cellular compartment.
c. they are found only in mammals.
d. they bind a wide range of proteins.

Ans: c
Question Type: Multiple Choice
Chapter 3.2
Blooms: Understanding
Difficulty: Easy

16. Hsp90 family members are present in all organisms EXCEPT:
a. archaea.
b. bacteria.
c. fungi.
d. plants.

Ans: a
Question Type: Multiple Choice
Chapter 3.2
Blooms: Remembering
Difficulty: Easy

17. Describe the mechanism by which the bacterial chaperonin GroEL promotes protein folding.

Ans: The bacterial chaperonin GroEL forms a barrel-shaped complex of 14 identical subunits. A partially folded or misfolded polypeptide is inserted into the GroEL barrel, where it binds to the inner wall and folds into its native conformation. In an ATP-dependent step, the GroEL barrel expands to a more open state, which results in release of the folded protein.
Question Type: Essay
Chapter 3.2
Blooms: Understanding
Difficulty: Moderate

18. What role does aberrant protein folding play in the development of a disease such as Alzheimer's disease?

Ans: Misfolding of a protein marks it for degradation by proteolytic cleavage. In Alzheimer's disease, misfolding and subsequent proteolytic degradation of the amyloid precursor protein generates a short fragment called β-amyloid protein, which changes from an α-helical to a β-sheet conformation. This aberrant structure aggregates into highly stable filaments called amyloid plaques that accumulate in the brains of Alzheimer's patients.
Question Type: Essay
Chapter 3.2
Blooms: Understanding

Difficulty: Easy

19. Which of the following does NOT impose limits on protein folding?
a. ability of side chains to form hydrogen and ionic bonds
b. backbone sequence of the polypeptide
c. rotations of the planes around the peptide bonds
d. size of side chains

Ans: b
Question Type: Multiple Choice
Chapter 3.2
Blooms: Remembering
Difficulty: Easy

20. Eggs are protein-rich foods. An uncooked egg can catalyze a reaction that breaks down bacterial cell walls. After cooking, this activity is almost abolished. This is likely because:
a. the enzyme became denatured.
b. bacteria can grow on cooked eggs.
c. the cell membranes were liquefied.
d. cooking sped up chemical reactions.

Ans: a
Question Type: Multiple Choice
Section 3.2
Blooms: Understanding
Difficulty: Moderate

21. The correct order for molecular chaperone–mediated protein folding is:
I – exchange of ATP for ADP on chaperone
II – chaperone undergoes conformational change, which affects protein folding
III – chaperone binds to exposed hydrophobic residues on unfolded protein
IV – folded protein is released
a. I, II, III, IV
b. III, II, I, IV
c. III, I, II, IV
d. II, III, I, IV

Ans: b
Question Type: Multiple Choice
Section 3.2
Blooms: Understanding
Difficulty: Easy

Section 3.3

22. All the following statements about enzymes are true EXCEPT:
a. they function in an aqueous environment.
b. they lower the activation energy of a reaction.
c. they increase the rate of a reaction.
d. a single enzyme typically reacts with many different substrates.

Ans: d
Question Type: Multiple Choice
Chapter 3.3
Blooms: Understanding
Difficulty: Easy

23. The K_m for an enzyme-catalyzed reaction:
a. determines the shape of the kinetics curve.
b. determines the V_{max} for the reaction.
c. is a measure of the affinity of the substrate for the enzyme.
d. is a measure of the rate of the reaction.

Ans: c
Question Type: Multiple Choice
Chapter 3.3
Blooms: Understanding
Difficulty: Moderate

24. For an enzyme-catalyzed reaction, doubling the concentration of enzyme will:
a. double the V_{max}.
b. halve the V_{max}.
c. double the K_m.
d. halve the K_m.

Ans: a
Question Type: Multiple Choice
Chapter 3.3
Application
Difficulty: Easy

25. A small molecule that binds directly to the active site of an enzyme and disrupts its catalytic reaction is called:
a. an allosteric inhibitor.
b. a competitive inhibitor.
c. a noncompetitive inhibitor.
d. RNAi.

Ans: b
Question Type: Multiple Choice
Chapter 3.3
Blooms: Remembering
Difficulty: Easy

26. Changes in the conformational shape of an enzyme that diminish the size of its ligand-binding pocket are likely to affect an enzyme's:
a. specificity.
b. affinity.
c. epitope.
d.specificity and affinity.

Ans:d
Question Type: Multiple Choice
Section 3.3
Blooms: Remembering
Difficulty: Easy

27. Which of the following is true about enzymes?
a.The catalytic site is responsible for substrate specificity.
b.Reactions catalyzed by enzymes give the products more free energy than reactions that occur spontaneously.
c.The rate of an enzymatic reaction is always proportional to the concentration of the substrate .

d.Enzymes increase reaction rates by lowering the activation energy needed to reach the transition state.

Ans: d
Question Type: Multiple Choice
Section 3.3
Blooms: Understanding
Difficulty: Moderate

Section 3.4

28. Which of the following plays a role in the degradation of proteins?
a. RNAi
b. ubiquitin
c. proteasome
d. b and c

Ans: d
Multiple select
Chapter 3.4
Blooms: Understanding
Difficulty: Easy

29. Which of the following modifications marks a protein for degradation in proteasomes?
a. phosphorylation
b. ubiquitinylation
c. acetylation
d. glycosylation

Ans: b
Question Type: Multiple Choice
Chapter 3.4
Blooms: Remembering
Difficulty: Easy

30. Protein self-splicing:
a. is autocatalytic.
b. occurs in all eukaryotes.
c. is an ATP-dependent process.
d. is autocatalytic and occurs in all eukaryotes.

Ans: a
Question Type: Multiple Choice
Chapter 3.4
Blooms: Remembering
Difficulty: Easy

31. Proteases that attack selected peptide bonds within a polypeptide chain are synthesized and secreted as inactive forms called:
a. carboxypeptidases.
b. aminopeptidases.
c. zymogens.
d. none of the above

Ans: c
Question Type: Multiple Choice
Chapter 3.4

Blooms: Remembering
Difficulty: Easy

32. Which of the following is a mechanism for regulating protein activity?
a. proteolytic processing
b. phosphorylation/dephosphorylation
c. ligand binding
d. all of the above

Ans: d
Question Type: Multiple Choice
Chapter 3.4
Blooms: Understanding
Difficulty: Easy

33. Protein kinase A is converted from an inactive state to an active state by binding:
a. ATP.
b. calcium.
c. cAMP.
d. ATP and cAMP.

Ans: c
Question Type: Multiple Choice
Chapter 3.4
Blooms: Remembering
Difficulty: Easy

34. Kinases, which are responsible for the activation or inactivation of a number of proteins, add phosphate groups onto:
a. tryptophan residues.
b. serine residues.
c. cysteine residues.
d. tryptophan and cysteine residues.

Ans: b
Question Type: Multiple Choice
Chapter 3.4
Blooms: Remembering
Difficulty: Easy

35. The conversion of inactive chymotrypsinogen to active chymotrypsin is an example of:
a. proteolytic activation.
b. positive cooperativity.
c. allostery.
d. ligand-induced activation.

Ans: a
Question Type: Multiple Choice
Chapter 3.4
Blooms: Understanding
Difficulty: Easy

36. Describe the general mechanism by which a multisubunit protein can be activated by binding an allosteric effector molecule.

Ans: A multisubunit protein often contains both regulatory and catalytic subunits. In the absence of the allosteric effector molecule, the active site of the enzyme is masked by the regulatory subunit. Upon binding the allosteric effector molecule, a conformational change occurs, which relievesthe suppressionby the regulatory subuniton the catalytic subunit.
Question Type: Essay
Chapter 3.4
Blooms: Understanding
Difficulty: Difficult

37. What is positive cooperativity?

Ans: The activity of a protein can be modulated by binding a ligand. Cooperativity describes a phenomenon in which the binding of one ligand molecule affects the binding of subsequent ligand molecules. This allows a protein molecule to respond more efficiently to small changes in ligand concentration. In positive cooperativity, the binding of one ligand molecule enhances the binding of subsequent ligand molecules.
Question Type: Essay
Chapter 3.4
Blooms: Understanding
Difficulty: Moderate

38. A misfolded protein targeted to the proteasome will undergo:
a. unfolding using energy released by ATPases.
b. entry into the proteasome through the narrow channel in the beta channel.
c. death by a thousand cuts in the alpha subunit rings.
d. complete cleavage into its amino acid monomers.

Ans: a
Question Type: Multiple Choice
Section 3.4
Blooms: Remembering
Difficulty: Easy

39. Modification of proteins by ubiquitin and ubiquitin-like E3ligases can stimulate all of the following EXCEPT:
a. recognition of intracellular viruses.
b. regulation of the cell cycle.
c. mRNA stability.
d. nuclear import.

Ans: c
Question Type: Multiple Choice
Section 3.4
Blooms: Remembering
Difficulty: Moderate

40. GTPases serve in many signal transduction pathways and the presence of GTP or GDP dictates whether the pathway is on or off, respectively. Which of the following statements is true regarding guanine nucleotide exchange factors (GEF) and their role in these signaling pathways?
a. They hydrolyze GTP into GDP and P_i.
b. They decrease the GTPase activity of the G-protein.
c. They catalyze the dissociation of GDP on the G-protein to therefore promote the replacement of GTP.
d. none of the above

Ans: c
Question Type: Multiple Choice
Section 3.4

Blooms: Remembering
Difficulty: Moderate

Section 3.5

41. Which of the following methods can separate proteins based on their mass?
a. centrifugation
b. ion exchange chromatography
c. SDS polyacrylamide gel electrophoresis
d. centrifugation and SDS polyacrylamide gel electrophoresis

Ans: d
Question Type: Multiple Choice
Chapter 3.5
Blooms: Understanding
Difficulty: Moderate

42.In two-dimensional gel electrophoresis, proteins are first resolved by _____ and then by _____.
a. IEF; SDS-PAGE
b. SDS-PAGE; affinity chromatography
c. SDS-PAGE; ion exchange
d. IEF; gel filtration

Ans: a
Question Type: Multiple Choice
Chapter 3.5
Blooms: Remembering
Difficulty: Easy

43. Gel filtration chromatography separates proteins on the basis of their:
a. charge.
b. mass.
c. affinity for a ligand.
d. mass and charge.

Ans: b
Question Type: Multiple Choice
Chapter 3.5
Blooms: Remembering
Difficulty: Easy

44. Starting with 1 mCi (milliCurie) of a phosphorus-32-labeled compound, how long would it take until only 0.125 mCi remains?
a. 14.3 days
b. 28.6 days
c. 42.9 days
d. 57.2 days

Ans: c
Question Type: Multiple Choice
Chapter 3.5
Application
Difficulty: Moderate

45. Western blotting is a method for detecting:
a. DNA.

b. RNA.
c. protein.
d. carbohydrate.

Ans: c
Question Type: Multiple Choice
Chapter 3.5
Blooms: Remembering
Difficulty: Easy

46. What is the basis for separation of proteins by two-dimensional gel electrophoresis? Why is this better for resolving a mixture of proteins?

Ans: In the first dimension, proteins are separated by isoelectric focusing, which separates proteins on the basis of their charge. In the second dimension, the proteins that have been separated by charge are further separated by their molecular weight (mass). The advantage of the two-dimensional technique is its ability to separate proteins more effectively. For example, two proteins with the same molecular weight could not be separated by one-dimensional SDS polyacrylamide gel electrophoresis. However, if these proteins differed in charge, then the two-dimensional gel would be able to separate these proteins into unique spots.
Question Type: Essay
Chapter 3.5
Application
Difficulty: Moderate

47. How can gel filtration chromatography separate proteins based on their mass?

Ans: In gel filtration chromatography, a column of porous beads made from acrylamide, dextran, or agarose is poured into a column. Proteins flow around the spherical beads. Because the surface of the beads contains large depressions, smaller proteins will penetrate into the depressions more easily than larger proteins and thus will travel more slowly through the column than larger proteins.
Question Type: Essay
Chapter 3.5
Blooms: Understanding
Difficulty: Easy

48. What is Western blotting? How can this technique be used to detect proteins?

Ans: Western blotting or immunoblotting is a method for identifying proteins separated on a gel using a specific antibody. The proteins are first separated by molecular weight using polyacrylamide gel electrophoresis and then transferred from the gel to a membrane. The membrane is incubated with a primary antibody specific for the desired protein. After unbound antibody is washed away, the presence of the bound primary antibody is detected using a secondary enzyme-linked antibody. The presence of the antibody-enzyme complex can then be detected using a chromogenic substrate.
Question Type: Essay
Chapter 3.5
Blooms: Understanding
Difficulty: Easy

49. A chunk of tissue is treated so that each cell's membrane is broken open to release the contents inside, and then subjected to differential centrifugation. Which of the following is true at the end of the centrifugation?

a. Depending on the speed of the centrifugation, the proteasome is more likely to be in the supernatant than a chaperone.
b. Proteins of similar density will be found in the same fraction (either pellet or supernatant).

c. The pellet contains the least dense material.
d. The pellet will contain a purified protein for further analysis.

Ans: b
Question Type: Multiple Choice
Section 3.5
Application
Difficulty: Moderate

Section 3.6

50. Medical researchers are developing new clinical tests that detect and analyze the expression of multiple proteins and protein complexes in the hope that they might improve diagnosis of diseases such as early stage cancers. What techniques might researchers use in these studies?

Ans: They might use protein separation techniques such as two-dimensional gel electrophoresis and high-throughput LC-MS/MS (liquid chromatography/mass spectroscopy) to separate and identify proteins and protein fragments on a global scale.
Question Type: Essay
Chapter 3.6
Blooms: Understanding
Difficulty: Easy

51. Proteomics allows researchers to:
a. examine where a protein is located within the cytosol of a cell.
b. compare thousands of samples from different people in the same experiment.
c. examine which proteins differ in abundance between a normal sample and a disease sample.
d. use antibodies to label specific proteins on an SDS-PAGE gel.

Ans: c
Section 3.6
Application
Difficulty: Moderate

52. Mass spectrometry techniques are used in proteomics for all of the following purposes EXCEPT:

a. identification of thousands of proteins' amino acid sequences within a single cell.
b. characterization of proteolyticallydigested pieces of proteins from the sample.
c. identification of all the protein complexes present in certain yeast species.
d. identification of proteins within each organelle in liver tissue.

Ans: a
Question Type: Multiple Choice
Section 3.6
Blooms: Understanding
Difficulty: Easy