3 Protein Structure and Function

PART A: Linking Concepts and Facts

3.1 *Hierarchical Structure of Proteins*

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

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

Ans: d

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

3.2 *Protein Folding*

4. 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

5. Hsp90 family members are present in all organisms except

a. Archaea
b. Bacteria
c. Fungi
d. Plants

Ans: a

3.3 *Protein Binding and Enzyme Catalysis*

6. 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. They typically react with many different substrates.

Ans: d

7. 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

8. 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

9. 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

3.4 *Regulating Protein Function*

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

Ans: d

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

Ans: b

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

Ans: a

13. 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

14. 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: e

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

Ans: c

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

Ans: b

17. 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

3.5 *Purifying, Detecting, and Characterizing Proteins*

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

Ans: d

19. 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

20. 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

21. 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

22. Western blotting is a method for detecting
a. DNA.
b. RNA.
c. protein.
d. carbohydrate.

Ans: c

PART B: Testing on the Concepts

3.1 *Hierarchical Structure of Proteins*

23. 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.

24. 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.

3.2 *Protein Folding*

25. 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.

26. 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.

3.4 *Regulating Protein Function*

27. 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 releases suppression of the catalytic subunit by the regulatory subunit.

28. What is positive cooperativity?

Ans: The activity of proteins can be modulated by binding of 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.

3.5 *Purifying, Detecting, and Characterizing Proteins*

29. 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, which have been separated by charge, are then 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.

30. 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.

31. 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 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 with a secondary enzyme-linked antibody. The presence of the antibody-enzyme complex can then be detected using a chromogenic substrate.

3.6 Proteomics

32. 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.