

MCB 102: Discussion 4 Problem Set Answers

Chapter 4:

1) Pauling and Corey's studies of the peptide bond showed that:

- A) at pH 7, many different peptide bond conformations are equally probable.
- B) peptide bonds are essentially planar, with no rotation about the C—N axis.
- C) peptide bonds in proteins are unusual, and unlike those in small model compounds.
- D) peptide bond structure is extraordinarily complex.
- E) primary structure of all proteins is similar, although the secondary and tertiary structure may differ greatly.

Page: 118; Ans: B

2) In an aqueous solution, protein conformation is determined by two major factors. One is the formation of the maximum number of hydrogen bonds. The other is the:

- A) formation of the maximum number of hydrophilic interactions.
- B) maximization of ionic interactions.
- C) minimization of entropy by the formation of a water solvent shell around the protein.
- D) placement of hydrophobic amino acid residues within the interior of the protein.
- E) placement of polar amino acid residues around the exterior of the protein.

Page: 118 ; Ans: D

3) In the α helix the hydrogen bonds:

- A) are roughly parallel to the axis of the helix.
- B) are roughly perpendicular to the axis of the helix.
- C) occur mainly between electronegative atoms of the R groups.
- D) occur only between some of the amino acids of the helix.
- E) occur only near the amino and carboxyl termini of the helix.

Pages: 120–121; Ans: A

4) Thr and/or Leu residues tend to disrupt an α helix when they occur next to each other in a protein because:

- A) an amino acids like Thr is highly hydrophobic.
- B) covalent interactions may occur between the Thr side chains.
- C) electrostatic repulsion occurs between the Thr side chains.
- D) steric hindrance occurs between the bulky Thr side chains.
- E) the R group of Thr can form a hydrogen bond.

Page: 121; Ans: D

5) A D-amino acid would interrupt an α helix made of L-amino acids. Another naturally occurring hindrance to the formation of an α helix is the presence of:

- A) a negatively charged Arg residue.
- B) a nonpolar residue near the carboxyl terminus.
- C) a positively charged Lys residue.
- D) a Pro residue.
- E) two Ala residues side by side.

Page: 122; Ans: D

6) The major reason that antiparallel β -stranded protein structures are more stable than parallel β -stranded structures is that the latter:

- A) are in a slightly less extended configuration than antiparallel strands.
- B) do not have as many disulfide crosslinks between adjacent strands.
- C) do not stack in sheets as well as antiparallel strands.
- D) have fewer lateral hydrogen bonds than antiparallel strands.
- E) have weaker hydrogen bonds laterally between adjacent strands.

Page: 123; Ans: E

7) Proteins often have regions that show specific, coherent patterns of folding or function. These regions are called:

- A) domains.
- B) oligomers.
- C) peptides.
- D) sites.
- E) subunits.

Page: 140; Ans: A

8) The structural classification of proteins (based on motifs) is based primarily on their:

- A) amino acid sequence.
- B) evolutionary relationships.
- C) function.
- D) secondary structure content and arrangement.
- E) subunit content and arrangement.

Page: 141; Ans: D

9) Experiments on denaturation and renaturation after the reduction and reoxidation of the —S—S— bonds in the enzyme ribonuclease (RNase) have shown that:

- A) folding of denatured RNase into the native, active conformation, requires the input of energy in the form of heat.
- B) native ribonuclease does not have a unique secondary and tertiary structure.
- C) the completely unfolded enzyme, with all —S—S— bonds broken, is still enzymatically active.
- D) the enzyme, dissolved in water, is thermodynamically stable relative to the mixture of amino acids whose residues are contained in RNase.

- E) the primary sequence of RNase is sufficient to determine its specific secondary and tertiary structure.

Page: 148; Ans: E

10) Which of the following is *not* known to be involved in the process of *assisted* folding of proteins?

- A) Chaperonins
- B) Disulfide interchange
- C) Heat shock proteins
- D) Peptide bond hydrolysis
- E) Peptide bond isomerization

Pages: 151–153; Ans: D

11) Any given protein is characterized by a unique amino acid sequence (primary structure) and three-dimensional (tertiary) structure. How are these related?

Ans: The three-dimensional structure is determined by the amino acid sequence. This means that the amino acid sequence contains all of the information that is required for the polypeptide chain to fold up into a discrete three-dimensional shape.

12) When a polypeptide is in its native conformation, there are weak interactions between its R groups. However, when it is denatured there are similar interactions between the protein groups and water. What then accounts for the greater stability of the native conformation?

Ans: In the unfolded polypeptide, there are ordered solvation shells of water around the protein groups. The number of water molecules involved in such ordered shells is reduced when the protein folds, resulting in higher entropy. Hence, the lower free energy of the native conformation. **See Pages: 117–118**

13) Draw the hydrogen bonding typically found between two residues in an α helix.

Ans: Hydrogen bonds occur between every carbonyl oxygen in the polypeptide backbone and the peptide —NH of the fourth amino acid residue toward the amino terminus of the chain. (See Fig. 4-2, p. 119.)

14) How does one determine the three-dimensional structure of a protein? Your answer should be more than the name of a technique.

Ans: The protein is crystallized, and the crystal structure is determined by x-ray diffraction. The pattern of diffracted x-rays yields, by Fourier transformation, the three-dimensional distribution of electron density. By matching electron density with the known sequence of amino acids in the protein, each region of electron density is identified as a single atom. Sometimes, the three-dimensional structure of a small protein or peptide can be determined in solution by sophisticated analysis of the NMR spectrum of the polypeptide. This technique can also reveal dynamic aspects of protein structure such as conformational changes. Computer analysis of two-dimensional NMR spectra can be used to generate a picture of the three-dimensional structure of a protein.

15) Draw a $\beta\alpha\beta$ loop, and describe what is found in the interior of the loop.

Ans: Hydrophobic amino acid residues are usually found in the interior of the loop; these help stabilize the arrangement through hydrophobic interactions. (See Fig. 4-20, p. 140.)

16) Explain (succinctly) the theoretical and/or experimental arguments in support of this statement: “The primary sequence of a protein determines its three-dimensional shape and thus its function.”

Ans: Anfinsen showed that a completely denatured enzyme (ribonuclease) could fold spontaneously into its native, enzymatically active form with only the primary sequence to guide it. **See Page: 148**

17) What are two mechanisms by which “chaperone” proteins assist in the correct folding of polypeptides?

Ans: Chaperones protect unfolded polypeptides from aggregation by binding to hydrophobic regions. They can also provide a microenvironment that promotes correct folding.

Chapter 5

18) When oxygen binds to a heme-containing protein, the two open coordination bonds of Fe^{2+} are occupied by:

- A) one O atom and one amino acid atom.
- B) one O_2 molecule and one amino acid atom.
- C) one O_2 molecule and one heme atom.
- D) two O atoms.
- E) two O_2 molecules.

Pages: 158–159; Ans: B

19) Myoglobin and the subunits of hemoglobin have:

- A) no obvious structural relationship.
- B) very different primary and tertiary structures.
- C) very similar primary and tertiary structures.
- D) very similar primary structures, but different tertiary structures.
- E) very similar tertiary structures, but different primary structures.

Page: 163 ; Ans: E

20) In hemoglobin, the transition from T state to R state (low to high affinity) is triggered by:

- A) Fe^{2+} binding.
- B) heme binding.
- C) oxygen binding.
- D) subunit association.

E) subunit dissociation.

Page: 165 ; Ans: C

21) The fundamental cause of sickle-cell disease is a change in the structure of:

- A) blood.
- B) capillaries.
- C) hemoglobin.
- D) red cells.
- E) the heart.

Page: 173; Ans: C

22) An individual molecular structure within an antigen to which an individual antibody binds is as a(n):

- A) antigen.
- B) epitope.
- C) Fab region.
- D) Fc region
- E) MHC site.

Page: 175; Ans: B

23) The proteins of the Major Histocompatibility Complex (MHC) bind and display:

- A) antigen fragments.
- B) B cell fragments.
- C) immunoglobulin fragments.
- D) macrophage fragments.
- E) T cell fragments.

Page: 176 ; Ans: A

24) Explain why most multicellular organisms use an iron-containing protein for oxygen binding rather than free Fe^{2+} . Your answer should include an explanation of (a) the role of heme and (b) the role of the protein itself.

Ans: (a) Binding of free Fe^{2+} to oxygen would result in the formation of reactive oxygen species that can damage biological structures. Heme-bound iron is less reactive in this regard. (b) Binding of oxygen to free heme can result in irreversible oxidation of the Fe^{2+} to Fe^{3+} that does not bind oxygen. The environment of the heme group in proteins helps to prevent this from occurring.

25) Explain why the structure of myoglobin makes it function well as an oxygen-storage protein whereas the structure of hemoglobin makes it function well as an oxygen-transport protein.

Ans: The hyperbolic binding of oxygen to the single binding site of myoglobin results in a high affinity even at the relatively low partial pressures of O_2 that occur in tissues. In

contrast, the cooperative (sigmoidal) binding of O₂ to the multiple binding sites of hemoglobin results in high affinity at high partial pressures such as occur in the lungs, but lower affinity in the tissues. This permits hemoglobin to bind O₂ in the lungs and release it in the tissues. **See Pages 161 & 166.**

26) a) What is the effect of pH on the binding of oxygen to hemoglobin (the Bohr Effect)?

(b) Briefly describe the mechanism of this effect.

Ans: (a) The affinity decreases with decreasing pH. (b) At lower pH (i.e., higher H⁺ concentration) there is increasing protonation of protein residues such as histidine, which stabilizes the low affinity conformation of the protein subunits. **Pages: 161, 166**

27) Describe briefly the basic structure of an IgG protein molecule.

Ans: An IgG protein contains two copies of a large polypeptide (heavy chain) and two copies of a small polypeptide (light chain). β structure contributes significantly to the tertiary structure of domains of both chains. Disulfide bonds link the heavy chains to one another and to the light chains. The chains are arranged in a Y-shaped structure where the two arms are linked to the base by a protease sensitive (“hinge”) region. **See Page 178.**

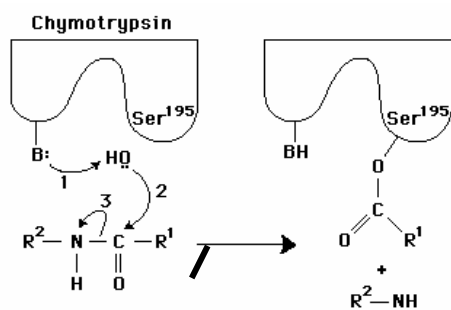
Chapter 6

28) Which one of the following statements is true of enzyme catalysts?

- A) Their catalytic activity is independent of pH.
- B) They are generally equally active on D and L isomers of a given substrate.
- C) They can increase the equilibrium constant for a given reaction by a thousand fold or more.
- D) They can increase the reaction rate for a given reaction by a thousand fold or more.
- E) To be effective, they must be present at the same concentration as their substrate.

Pages: 194-196; Ans:D

29) In the following diagram of the first step in the reaction catalyzed by the protease chymotrypsin, the process of general base catalysis is illustrated by the number _____, and the process of covalent catalysis is illustrated by the number _____.



A) 1; 2

- B) 1; 3
- C) 2; 3
- D) 2; 3
- E) 3; 2

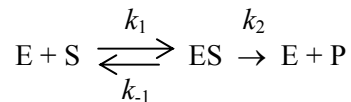
Pages: 200-201; Ans: A

30) The benefit of measuring the *initial* rate of a reaction V_0 is that at the beginning of a reaction:

- A) [ES] can be measured accurately.
- B) changes in [S] are negligible, so [S] can be treated as a constant.
- C) changes in K_m are negligible, so K_m can be treated as a constant.
- D) $V_0 = V_{\max}$.
- E) varying [S] has no effect on V_0 .

Page: 202; Ans: B

31) Michaelis and Menten assumed that the overall reaction for an enzyme-catalyzed reaction could be written as



Using this reaction, the rate of breakdown of the enzyme-substrate complex can be described by the expression:

- A) $k_1 ([E_t] - [ES])$.
- B) $k_1 ([E_t] - [ES])[S]$.
- C) $k_2 [ES]$.
- D) $k_{-1} [ES] + k_2 [ES]$.
- E) $k_{-1} [ES]$.

Page: 204; Ans: D

32) An enzyme-catalyzed reaction was carried out with the substrate concentration initially a thousand times greater than the K_m for that substrate. After 9 minutes, 1% of the substrate had been converted to product, and the amount of product formed in the reaction mixture was 12 μmol . If, in a separate experiment, one-third as much enzyme and twice as much substrate had been combined, how long would it take for the same amount (12 μmol) of product to be formed?

- A) 1.5 min
- B) 13.5 min
- C) 27 min
- D) 3 min
- E) 6 min

Pages: 204-207; Ans: C

33) The following data were obtained in a study of an enzyme known to follow Michaelis-Menten kinetics:

V_0 ($\mu\text{mol}/\text{min}$)	Substrate added (mmol/L)
217	0.8
325	2
433	4
488	6
647	1,000

The K_m for this enzyme is approximately:

- A) 1 mM.
- B) 1,000 mM.
- C) 2 mM.
- D) 4 mM.
- E) 6 mM.

Page: 205 ; Ans: C

34) The double-reciprocal transformation of the Michaelis-Menten equation, also called the Lineweaver-Burk plot, is given by

$$1/V_0 = K_m/(V_{\max}[S]) + 1/V_{\max}.$$

To determine K_m from a double-reciprocal plot, you would:

- A) multiply the reciprocal of the x-axis intercept by -1 .
- B) multiply the reciprocal of the y-axis intercept by -1 .
- C) take the reciprocal of the x-axis intercept.
- D) take the reciprocal of the y-axis intercept.
- E) take the x-axis intercept where $V_0 = 1/2 V_{\max}$.

Page: 206 ; Ans: A

35) In competitive inhibition, an inhibitor:

- A) binds at several different sites on an enzyme.
- B) binds covalently to the enzyme.
- C) binds *only* to the ES complex.
- D) binds reversibly at the active site.
- E) lowers the characteristic V_{\max} of the enzyme.

Pages: 209-210 ; Ans: D

36) V_{\max} for an enzyme-catalyzed reaction:

- A) generally increases when pH increases.
- B) increases in the presence of a competitive inhibitor.
- C) is limited only by the amount of substrate supplied.

- D) is twice the rate observed when the concentration of substrate is equal to the K_m .
E) is unchanged in the presence of a uncompetitive inhibitor.

Pages: 209-212; Ans: D

37) The difference in (standard) free energy content, ΔG° , between substrate S and product P may vary considerably among different reactions. What is the significance of these differences?

Ans: The difference in free energy content between substrate (or reactant) and product for each reaction reflects the relative amounts of each compound present at equilibrium. The greater the difference in free energy, the greater the difference in amounts of each compound at equilibrium. **See Page 194.**

38) Why does pH affect the activity of an enzyme?

Ans: The state of ionization of several amino acid side chains is affected by pH, and the activity of many enzymes requires that certain of the amino acid residue side chains be in a specific ionization state. (See Fig 6-20, p. 215.)