Chapter 5

1. Nitrate reductase is a dimer (2 Mo/240,000 M_r).
2. Phe-Asp-Tyr-Met-Leu-Met-Lys.
3. Ser-Glu-Tyr-Arg-Lys-Lys-Phe-Met-Asn-Pro.
4. The ionic character of proteins A, B, and C is A>C>B at the pH used in the ion exchange column. Assuming all three proteins have a similar globular shape, their sizes are C>A>B. Protein C is a flavin-binding protein; proteins A and B are not.
5. The protein may consist of two polypeptide chains linked together through disulfide bridges.
6. Gly-Arg-Lys-Trp-Met-Tyr-Arg-Phe.
7. Actually, there are four possible sequences: NIGIRVIA, GINIRVIA, VIRNIGIA, and, of course, VIRGINIA.
8. Gly-Trp-Arg-Met-Tyr-Lys-Gly-Pro.
9. Leu-Met-Cys-Val-Tyr-Arg-Cys-Gly-Pro.

   S———S
10. Alanine, attached to a solid-phase matrix via its α-carboxyl group, is reacted with diisopropylcarbodiimide-activated lysine. Both the α-amino and ϵ-amino groups of the lysine must be blocked with 9-fluorenyl-methoxycarbonyl (Fmoc) groups. To add leucine to Lys-Ala to form a linear tripeptide, precautions must be taken to prevent the incoming Leu α-carboxyl group from reacting inappropriately with the Lys ϵ-amino group instead of the Lys α-amino group.
11. Bovine ribonuclease; *Neurospora crassa* NADPH–nitrite reductase
12. The mass of the myoglobin chain is calculated to be 16,947 ± 1 daltons.
13. Unlike any amino acid side chain, the phosphate group (or more appropriately, the phosphoryl group) bears two equivalents of negative charge at physiological pH. Furthermore, replacing an H atom on an S, T, or Y side chain with a phosphoryl group introduces a very bulky substituent into the protein structure where none existed before.
14. Compound Z the ligand with the strongest affinity for the protein.
15. A graph of ν versus [L] reveals that at $\nu = 0.5$, [L] = K_D = 2.4 m*M*.
16. Percent Saturation of Protein with Ligands A and B

Ligand concentration (m*M*)	Ligand A (K_D = 0.3 m*M*)	Ligand B (K_D = 1 m*M*)
0.1	0.25	0.091
0.2	0.4	0.167
0.5	0.625	0.33
1	0.77	0.5
2	0.87	0.67

    More B is required to achieve the same degree of saturation as any given concentration of A. K_D and affinity are inversely related.
17. IRS-1 has 1242 amino acids. Its average molecular mass is 131,590.97. The amino acid sequence of the tryptic peptide of IRS-1 of mass of 1741.9629 is LNSEAAAVVLQLMNIR. The sequence of the tryptic fragment containing the SHPTP-2 site is LCGAAGGLENGLNYIDLDLVK.
18. Nucleophilic attack by the hydroxyl O of the active-site serine on the carbonyl carbon of a peptide bond.
19. a. Amino acid changes in mutant hemoglobins that appear on the surface of the folded globin chains may affect quaternary structure.
    b. Amino acid substitutions on the surface on the quaternary hemoglobin structure that create hydrophobic patches might lead to polymerization. Such amino acids would include all of the hydrophobic amino acids.
20. a. They refer to the sedimentation coefficients of these two subunits.
    b. The ribosomal subunits are quaternary complexes of protein and rRNA. The larger the S value, the larger the rRNA is and the more protein molecules the ribosomal subunit has.

Think-Pair-Share Question:

Digestion order 4:

1. Chymotrypsin: QVDGL MRTSEQMKNSRV	Edman degradation : QM
2. Trypsin: QVDGL MR TSEQMK NSR V	Edman degradation : QMTNV
3. St. Protease: QVD GL MR TSE QMK NSR V	Edman degradation : QGMTNV

Digestion order 5:

1. St. Protease: QVD GLMR-TSE QMKNSRV	Edman degradation : QG
2. Trypsin: QVD GLMR TSE QMK NSR V	Edman degradation : QGTNV
3. Chymotrypsin: QVD GL MR TSE QMK NSR V	Edman degradation : QGMTNV

The order of endopeptidase treatment did not affect the final results.

Chapter 6

1. The central rod domain of keratin is composed of distorted α-helices, with 3.6 residues per turn, but a pitch of 0.51 nm, compared with 0.54 nm for a true α-helix.

   (0.51 nm/turn)(312 residues)/(3.6 residues/turn) = 44.2 nm = 442 Å.

   For an α-helix, the length would be:

   (0.54 nm/turn)(312 residues)/(3.6 residues/turn) = 46.8 nm = 468 Å.

   The distance between residues is 0.347 nm for antiparallel β-sheets and 0.325 nm for parallel β-sheets. So 312 residues of antiparallel β-sheet amount to 1083 Å and 312 residues of parallel β-sheet amount to 1014 Å.
2. The collagen helix has 3.3 residues per turn and 0.29 nm per residue, or 0.96 nm/turn. Then:

   (4 in/year)(2.54 cm/in)(10^7 nm/cm)/(0.96 nm/turn) = 1.06×10^8 turns/year.

   (1.06×10^8 turns/year)(1 year/365 days)(1 day/24 hours)(1 hour/60 minutes) = 201 turns/minute.
3. **Asp:** The ionizable carboxyl can participate in ionic and hydrogen bonds. Hydrophobic and van der Waals interactions are negligible.

   Leu: The leucine side chain does not participate in hydrogen bonds or ionic bonds, but it will participate in hydrophobic and van der Waals interactions.

   Tyr: The phenolic hydroxyl of tyrosine, with a relatively high pK_a, will participate in ionic bonds only at high pH but can both donate and accept hydrogen bonds. Uncharged tyrosine is capable of