

Chem 464 Biochemistry

Multiple choice (4 points apiece):

1. Two amino acids of the standard 20 contain sulfur atoms. They are:
 - A) cysteine and serine.
 - B) cysteine and threonine.
 - C) methionine and cysteine
 - D) methionine and serine
 - E) threonine and serine.
2. The peptide alanylglutamylglycylalanylleucine has:
 - A) a disulfide bridge.
 - B) five peptide bonds.
 - C) four peptide bonds.
 - D) no free carboxyl group.
 - E) two free amino groups.
3. In a mixture of the five proteins listed below, which should elute second in size-exclusion (gel-filtration) chromatography?

A) cytochrome <i>c</i>	$M_r = 13,000$
B) immunoglobulin G	$M_r = 145,000$
C) ribonuclease A	$M_r = 13,700$
D) RNA polymerase	$M_r = 450,000$
E) serum albumin	$M_r = 68,500$
4. In an α helix, the R groups on the amino acid residues:
 - A) alternate between the outside and the inside of the helix.
 - B) are found on the outside of the helix spiral.
 - C) cause only right-handed helices to form.
 - D) generate the hydrogen bonds that form the helix.
 - E) stack within the interior of the helix.
5. An α helix would be destabilized most by:
 - A) an electric dipole spanning several peptide bonds throughout the helix.
 - B) interactions between neighboring Asp and Arg residues.
 - C) interactions between two adjacent hydrophobic Val residues.
 - D) the presence of an Arg residue near the carboxyl terminus of the helix.
 - E) the presence of two Lys residues near the amino terminus of the helix.
6. Amino acid residues commonly found in the middle of β turn are:
 - A) Ala and Gly.
 - B) hydrophobic.
 - C) Pro and Gly.
 - D) those with ionized R-groups.
 - E) two Cys.
7. Which of the following statements concerning protein domains is true?
 - A) They are a form of secondary structure.
 - B) They are examples of structural motifs.
 - C) They consist of separate polypeptide chains (subunits).
 - D) They have been found only in prokaryotic proteins.
 - E) They may retain their correct shape even when separated from the rest of the protein.

8A. (2 points) Glycine is occasionally used as a buffer. Given that the pK_a of one functional group on glycine is 2.34, and the pK_a of the other functional group is 9.60, at what pH's would glycine be a good buffer?

1.34-3.34, 8.6-10.6

8B. (2 points) Draw the structure of glycine in its fully protonated form.

8C. (6 points) If I mix .5 moles of glycine in the fully protonated state with .3 moles of NaOH in .5 L of water, what is the pH of this solution?

Reaction Table

	$\text{Hgly} + \text{OH}^- \rightarrow \text{Gly} + \text{H}_2\text{O}$			
	.5	.3	0	-
Rxn	-.3	-.3	+.3	-
Net	.2	0	.3	

$$X = 2.34 + \log (.3/.2) = 2.58$$

9. (10 points) There are three different methods used to describe the conformation around the chiral center on the C_α of an amino acid. Briefly describe these three systems and give the proper designation of the biologically active conformation of alanine in each system.

D, L system. The Fischer system. Based on chemical conversion to D or L glyceraldehyde
All natural amino acids are in the L configuration

+,- or d,l system. Based on whether the compound rotates plane polarized light to the left (levorotatory - *l*) or the right (dextroatory, -*d*) Some amino acids are + here, some are -, so there is now way you would know.

R/S system. Based on assigning priority numbers to substituent groups around the chiral C. We did not go into this so again there is no way you would know the correct answer

9. (20 points) *Fill in the following table:*

Name	Asparagine	Glutamic Acid	Cysteine
3 letter abbreviation	ASN	GLU	CYS
1 letter abbreviation	N	E	C
Structure			
side chain pK _a (if ionizable)		4.25	8.18
General classification (nonpolar, polar, etc)	Polar	Charged/Acid	Polar

Longer questions:

10. (10 points) Assume that you have just isolated a protein from a fungi that seems to be a new kind of antibiotic. Describe the different chemical tests and experiments you will have to do to determine the sequence of the protein.

Determine Molecular weight - Mass Spec, SDS Gel Electrophoresis or Gel Permeation Chromatography

Determine Amino acid composition - Hydrolyze protein in 6M HCL for > 24 Hrs separate and quantify AA's by HPLC (Actually a little more complicated need to do both acid and base hydrolysis, and need to do a couple of different hydrolysis times)

Determine N Terminal AA by treatment with FDNB followed by hydrolysis and identification of N terminal modified AA with HPLC

Cleavage of protein into at least two sets of overlapping peptides using CNBr and proteases like Trypsin

Isolation of the above peptides and sequencing of these peptides using the Edman degradation.

Use the overlapping segments to piece together the entire sequence.

11. (10 points) How is the triple helix of collagen similar to or different than the single helix of α -keratin

Triple Helix - Found in the fibrous protein collagen made up of three strands of protein. Each strand is in a left-handed extended helix with 3 residues / turn. The individual strands are supertwisted around each other in a right-handed coiled coil. Tight interaction between the coils insures aht $>1/3$ of the residues are glycine. There is also a large amount of Alanine (11%) and Proline or Hydroxyproline (21%). Unusual Lysine cross-links are used to bridge between fibrils

α -keratin - uses 2 right handed α -helices wrapped around each other in a left handed coiled coil. In this structure the helices are separate and not intertwined. A single right handed helix with 3.6 residues per turn, and each turn is a distance of about 5.4\AA . Side chains of the Amino Acids are on the outside of the helix, so almost any AA can be found in a helix. The two exceptions are Proline and Glycine. Proline's ring structure is not easily accommodated into the helix, and glycine structural flexibility tend to break the helix. Standard Cystine cross-links are used to bridge between fibrils

12. (10 points) Describe the two different models currently used to explain how proteins fold.

Hierarchic Folding Model - Helices and sheets fold first. These units then fold against each other to form super-secondary structures. The super-secondary structures then aggregate together to form larger domains and then these coalesce to form the completed protein.

Molten Globule Model - The hydrophobic force makes a the hydrophobic core of the proteins collapse first with little or no internal structure. Helices and sheets then form in this core, but the actual helices that form first may not be the same as those found in the native protein. These nascent structures form, dissolve, and reform ad the protein goes to a lower energy state, and eventually the native structure emerges as the lowest energy state.

