

Chem 464

Biochemistry

Multiple choice (4 points apiece):

- A true statement about hydrophobic interactions is that they:
 - are the driving force in the formation of micelles of amphipathic compounds in water.
 - do not contribute to the structure of water-soluble proteins.
 - have bonding energies of approximately 20–40 Kjoule per mole.
 - involve the ability of water to denature proteins.
 - primarily involve the effect of polar solutes on the entropy of aqueous systems.
- In which reaction below does water *not* participate as a reactant (rather than as a product)?
 - Conversion of an acid anhydride to two acids.
 - Conversion of an ester to an acid and an alcohol.
 - Conversion of ATP to ADP.
 - Photosynthesis
 - Production of gaseous carbon dioxide from bicarbonate.
- Of the 20 standard amino acids, only _____ is not optically active. The reason is that its side chain _____ .
 - alanine; is a simple methyl group
 - glycine; is a hydrogen atom
 - glycine; is unbranched
 - lysine; contains only nitrogen
 - proline; forms a covalent bond with the amino group
- The uncommon amino acid selenocysteine has an R group with the structure $\text{—CH}_2\text{—SeH}$ ($\text{p}K_{\text{a}} \approx 5$). In an aqueous solution, $\text{pH} = 7.0$, selenocysteine would:
 - be a fully ionized zwitterion with no net charge.

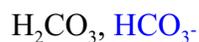
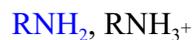
The above answer is the one given in the text. I think it is wrong. If you had this question wrong, and you can tell me what is wrong with their answer I will give you 4 points, but you have to promise not to tell anybody else!

 - be found in proteins as D-selenocysteine.
 - never be found in a protein.
 - be nonionic.
 - not be optically active.
- 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	$M_r = 68,500$
- In the _____ helix the hydrogen bonds:
 - are roughly parallel to the axis of the helix.
 - are roughly perpendicular to the axis of the helix.
 - occur mainly between electronegative atoms of the R groups.
 - occur only between some of the amino acids of the helix.
 - occur only near the amino and carboxyl termini of the helix.
- Determining the precise spacing of atoms within a large protein is possible only through the use of:
 - electron microscopy.
 - light microscopy.
 - molecular model building.
 - Ramachandran plots.
 - x-ray diffraction.

Longer questions (70 points total)

8. (10 points) Which is the conjugated base in each of the pairs below?



9. (10 points) Aspirin is a weak acid with a pKa of 3.5. It is absorbed in the blood through the cells lining the stomach and the small intestine. Highly charged molecules pass through this lining slowly, but neutral molecules pass through the lining more quickly. Given that the pH of the stomach is about 1.5 and the pH of the small intestine is about 6, is aspirin absorbed into the bloodstream more in the stomach or the small intestine. Justify your answer.

Since this is a simple weak acid, when you are 1 pH unit **below** the pKa you will be fully protonated and have **no charge** (COOH). At 1 pH unit **above** the pKa you will be fully protonated, and will be in the COO⁻ **charged** form.

The pH of the stomach is so low that aspirin will be fully protonated, neutral and will pass quickly through the lining. The pH of the small intestine is much higher, so the aspirin will be in the COO⁻ charged form and will not pass through the lining.

10. (20 points) *Fill in the following table:*

Name	Threonine	Tyrosine	Aspartic Acid
3 letter abbreviation	THR	TYR	ASP
1 letter abbreviation	T	Y	D
Structure			
side chain pK _a (if ionizable)	-	10.07	3.65
General classification (nonpolar, polar, etc)	Polar	Aromatic or polar	Acidic

11. (6 points minimum) In class we talked about different ways to cleave a protein at specific sites. Name as many of these site specific methods as you can, and state where they cleave the peptide backbone (bonus points for more than three chemicals or enzymes). Why is it important to be able to cleave a protein at different sites (4 points) ?

There are eight or more enzymes or reactions listed in your text for cleaving proteins at specific linkages I gave 2 points for each enzyme and correct cleavage point.

The importance of being able to cleave at different specific sites is that it allows you to overlap fragments so you can reconstruct the entire protein's sequence.

12. (10 points) In class we talked about three types of fibrous proteins. Name these three protein types and tell how the structures observed in these proteins are similar to, or different than, structures observed in globular proteins.

α - Keratin - observed in hair-wool, nails, claws, quill horn, hooves, outer layer of skin. Part of broad family of intermediate filament (IF) proteins. It is composed of 2 right handed alpha helices twisted around each other like rope. The α helix part of this structure is observed in globular proteins, but the higher level structure of twisting helices around each other is not.

Silk Fibroin - Mostly Ala & Gly in antiparallel sheet. Ala's lock together on one side and gly on other. Does not stretch because the backbone is fully extended, but is flexible because sheets are held together by weak van der Waals interaction instead of covalent crosslinks. This structure is observed in globular proteins.

Collagen - A strong structure that cannot be stretched. Used for tendons & cartilage. Composed of three very extended polypeptide strands that are wrapped around each other in a left-handed helix. In this triple helix the 3rd residue of each strand is in close contact on inside on the inside of the structure, so it must be the very small side chain of glycine. This structure also requires many prolines to make some tight kinks to the overall composition is 35% gly, 21% pro & Hypro, 11% ala. This structure is never observed in globular proteins.

13. (10 points) What different enzymes does a cell have to help proteins fold up properly? (Name the enzyme and tell what it does.)

Chaperone Proteins

The Hsp70 a family of chaperonenes, also called DNA K DNA J in E coli

About 70,000 MW. Abundant in cells stressed by high temp (Why they are called Heat Shock Proteins). They bind to exposed hydrophobic regions of Misfolded proteins, even while the proteins are still being synthesizes on the ribosome.

Prevents aggregation hydrophobic protein regions with other hydrophobic proteins that would start denaturation and precipitation

Chaperonins

Large molecular complex built to hold protein in till it folds right. Proper folding of proteins is linked to large changes of structure in chaperonin proteins and hydrolysis of ATP, but actual mechanism is still unknown

Isomerases

Protein disulfide isomerase

Shuffles incorrect disulfides

Peptide prolyl cis-trans isomerase

Changes between cis and trans proline