

BIOS 452/CHEM 452

Second Exam

Fall, 2010

12:00-12:55pm, Wednesday, November 3, 2010

Name: Answer Key

UIN: _____

Circle Discussion Section:

Mon	8
Tue	9:30
Wed	9
Thu	9:30
Fri	9
Fri	11

General Instruction

- * Do not turn the page until you are told to do so.
- * You may take the exam with you only after 12:35pm.
- * No calculators allowed. **For calculations and graphing, show all your work!!!**
- * The exam is total 9 pages (including cover page), 31 questions grouped into 13 for 55 minutes.
- * Read the question carefully to the end.

Pay attention to units.

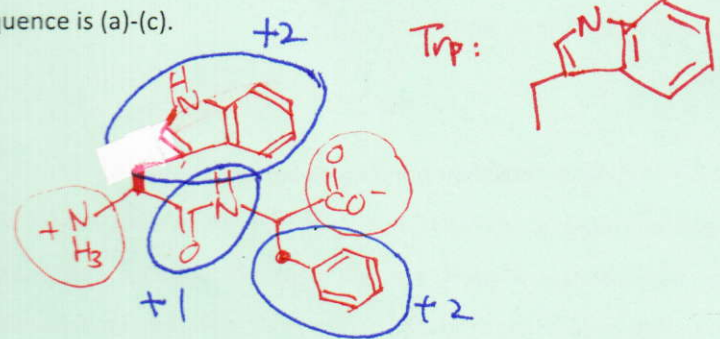
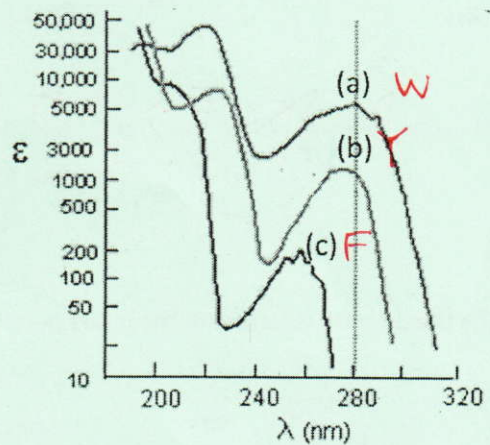
Remember that X-ray structures do not show hydrogen atoms.

1. (4 pts) Circle amino acid(s) whose side chain(s) can be hydrogen bond donors at a neutral pH.

Tyrosine Glycine Glutamate Cysteine Proline

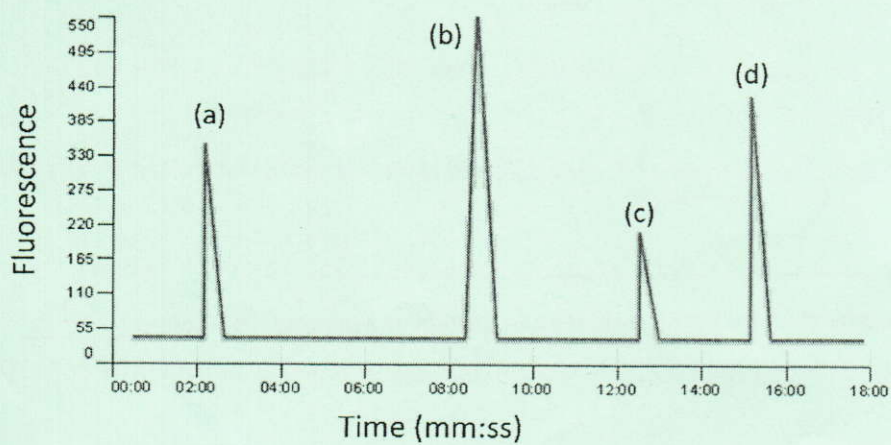
* -2 for incorrect answer.

2. (5 pts) The figure on the right shows UV absorption spectra of amino acids, (a), (b) and (c) in their free forms. Draw the complete chemical structure of a dipeptide of which the sequence is (a)-(c).



* Side chains must show -CH₂-

3. A mixture of free amino acids consisting of K, R, M, D were derivatized with o-phthalaldehyde in the presence of 2-mercaptoethanol and were subsequently separate by reverse-phase HPLC.



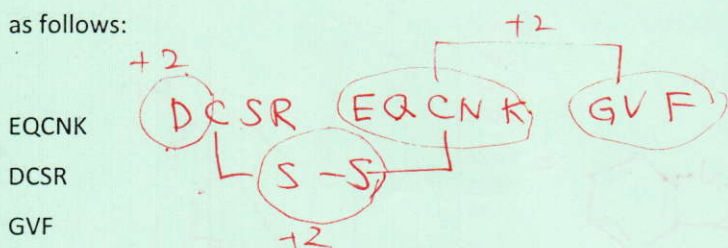
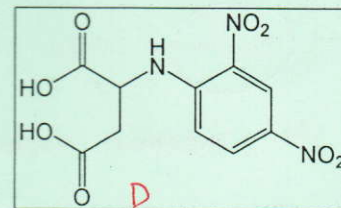
(1) (4 pts) Match the peaks with the corresponding amino acid: (a) D ; (b) R ; (c) M ; (d) K.

* If order is correct for ≥ 2, give 1 for each correct a.a.

(2) (2 pts) To elute the bound derivatives from the column as above, one should (increase) decrease - Circle one the ratio of acetonitrile (CH₃CN) to water in the mobile phase.

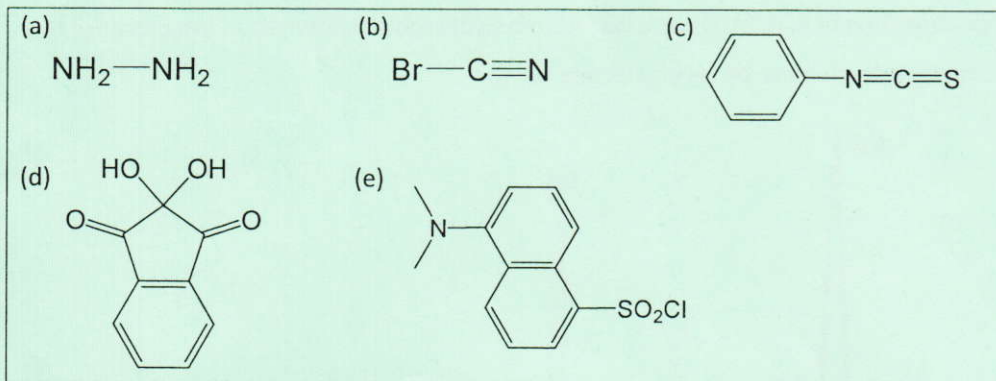
4. (6 pts) When a single polypeptide Z was treated with Sanger's reagent followed by acid hydrolysis, it gave an α -amino derivative shown on the right.

When peptide Z was treated with trypsin, it yielded two fragments. When subsequently treated with dithiothreitol (DTT), two fragments were further split into three. The sequences of the resulting three fragments are determined and they are as follows:



Describe the primary structure of the intact peptide Z including any covalent bond involving side chains.

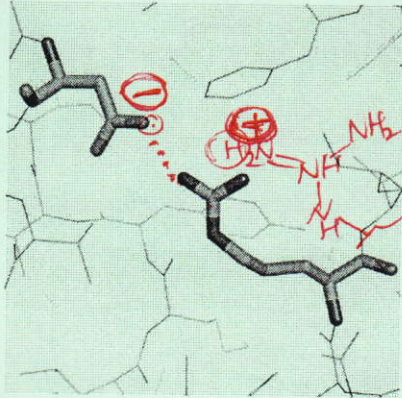
5. Choose one from below.



(1) (3 pts) You want to determine the sequence of the first 5 residues of a protein or a peptide. Compound C best suits this purpose.

(2) (3 pts) Compound a can be used to selectively determine the C-terminal residue of a protein.

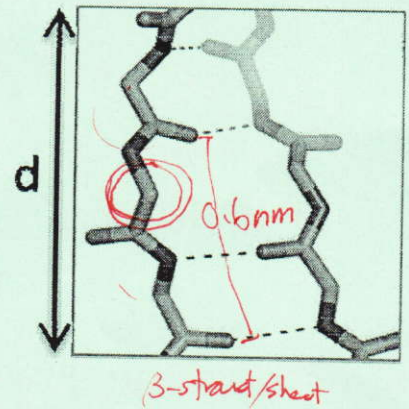
6. The figure shows a portion of a protein structure determined by X-ray at pH 8. Two residues that interact with each other inside the protein core are highlighted in a stick representation. Oxygen is in red, nitrogen in blue and carbon in green.



(1) (2 pts) The interaction between the two highlighted residues is a (van der Waals interaction, hydrogen bond, salt bond, metal-ligand bond – Circle one).

(2) (2 pts) The strength of this interaction would (decrease, increase, remain the same – Circle one) on the surface of the protein.

7. This figure shows a segment of a protein structure determined by X-ray crystallography. Only backbone atoms are shown in a stick model. Hydrogen bonds are in dotted lines. Oxygen is in red, nitrogen in blue, and carbon in green.



(1) (3 pts) Which (phi, psi) pair is closest to those of the residues shown in the figure?

(-90, -90) (-90, 90) (90, -90) (90, 90)



(2) (3 pts) Which of the following is most enriched with the type of protein scaffold shown in the figure?

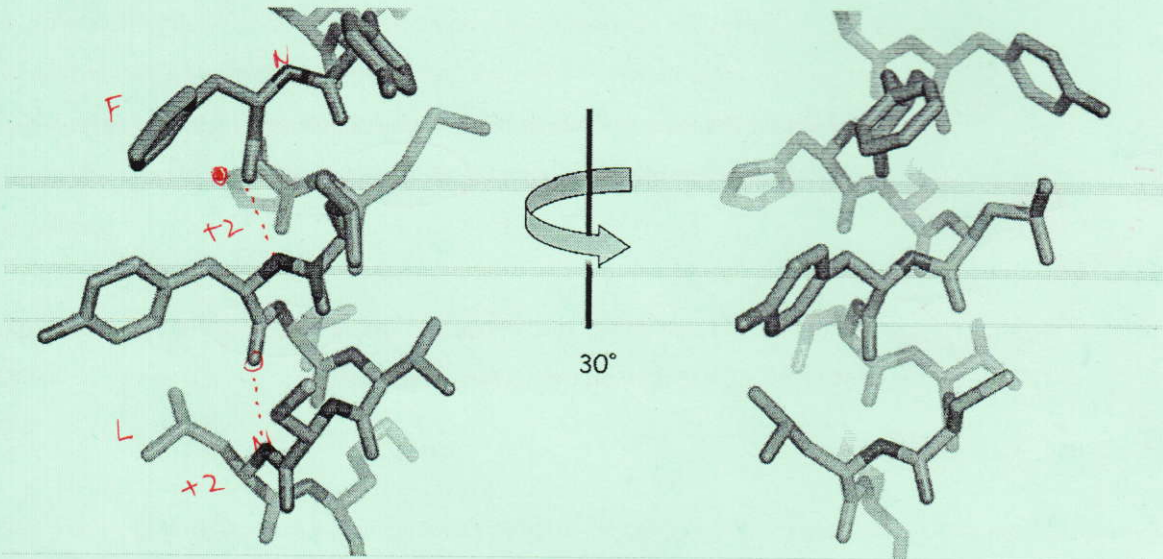
Tendon Hair Silk Red blood Wool

(3) (3 pts) Which of the following is closest to the distance indicated as "d" in the figure?

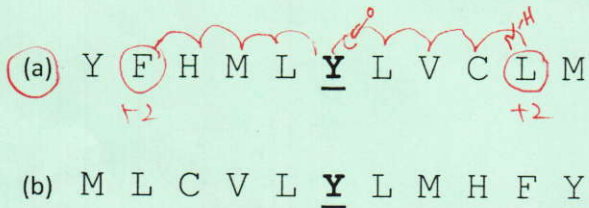
1×10^{-12} m 1×10^{-11} m 1×10^{-10} m 1×10^{-9} m 1×10^{-8} m 1×10^{-7} m 1×10^{-6} m

10 nm

8. This is a portion of a protein structure determined by X-ray in a stick representation. Oxygen is in red, nitrogen in blue, sulfur in yellow and carbon in green.



(1) (3 pts) What is the amino acid sequence of this protein segment? ((a), (b) - Circle one)



(2) (4 pts) On your answer for (1), circle the TWO residues that form hydrogen bonds with the backbone atoms of the underlined residue, Y.

(3) (4 pts) On one of the figures, draw lines between atoms indicating the TWO hydrogen bonds that the backbone of the underlined residue Y makes.

(4) (3 pts) When you transfer this protein segment from a non-polar to a polar environment, it will result in an (decrease, increase +1 - Circle one) in ΔG and an (decrease, increase +1 - Circle one) in ΔS .

Thus, the segment is likely to (exposed outside of, embedded inside of - Circle one) of a protein due to this thermodynamic effect. +1

9. (4 pts) Which of the following statement(s) is/are NOT true?

(a) The tertiary structure of a protein can be predicted from a known 3D structure of a protein with a similar primary structure.

+2 (b) The secondary structures of a protein cannot be predicted without a known 3D structure of a homologous protein.

(c) Collagen structure is stabilized by hydrogen bonds, van der Waals interactions and covalent crosslinks between side chains.

+2 (d) When curly hair is converted into straight hair using β -mercaptoethanol during a "permanent wave (perm)" process, the constituent protein changes its secondary structure to a more extended form.

10. (1) (4 pts) Hemoglobin is a conjugated protein. It contains a complex of a protoporphyrin and Fe^{2+} which is called a Heme. Such non-amino acid component of a conjugated protein is called a Prosthetic group.

+2

+2

(2) (4 pts) CO_2 is a (Substrate, Allosteric effector, Competitive inhibitor - Circle one) for hemoglobin.

And CO is a (Substrate, Allosteric effector, Competitive inhibitor - Circle one) for hemoglobin.

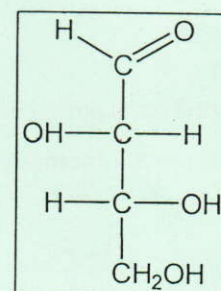
+2

(3) (3 pts) Myoglobin has a molecular weight of 17,000 g/mole. Estimate the molecular weight of hemoglobin in kilodalton (kDa). Show your reasoning.

$$17. \text{ kDa} * 4 \text{ subunits/Hb} = 68 \text{ kDa}$$

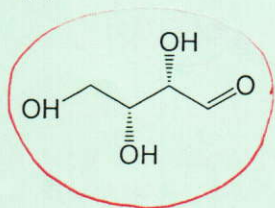
11. (5 pts) The monosaccharide drawn in a Fisher representation on the right is a

(D, L - Circle one) - (aldose, ketose - Circle one) and also is a (triose, tetrose, pentose - Circle one).

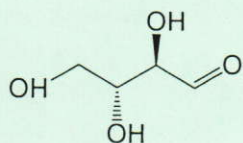


(2) (Bonus 3 pts) Choose the appropriate chemical structure for the monosaccharide.

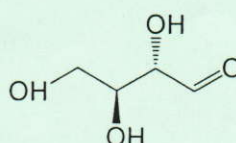
(a)



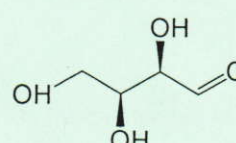
(b)



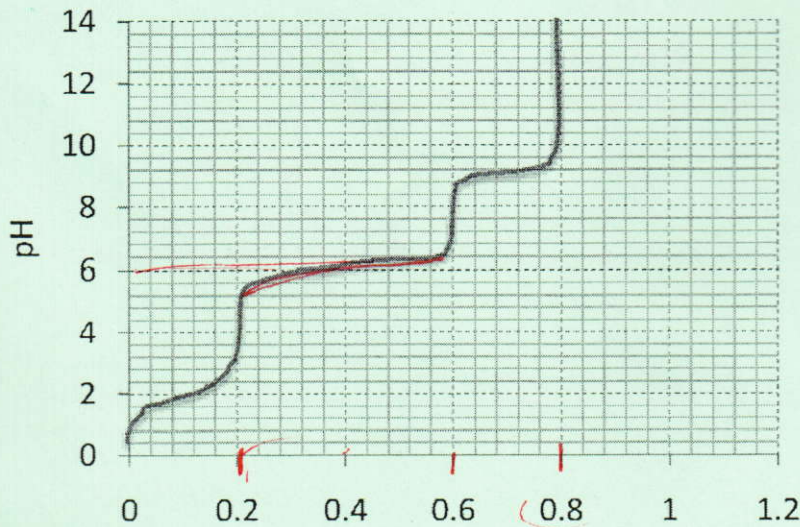
(c)



(d)



13. Following is a titration curve of a peptide sample. The molecular weight of the peptide is 1.1 kDa.



OH⁻ added to sample (mmole) \Rightarrow equivalence point.

(1) (3 pts) This peptide consists of approximately (1, 2, 10, 20, 100, 200 - Circle one) residues.

$$\frac{1.1 \text{ kDa}}{110 \text{ Da/aa}} = \frac{1100}{110} = 10$$

(2) (3 pts) Circle amino acid residue(s) that the peptide MUST contain.

W Y G S H

e.g. If calculated as $\frac{9+6}{2} = 7.5$ (+3)

(3) (6 pts) What is the pI of this peptide? Show all your work.



2: $\text{H}_{\text{is}} = \text{pKa} = 6$

2: Calculating charges
Partial

pI = 8.0

Q2

				0	
pH=9	-1	0	0	+0.5	-0.5
		0	0	+1	← pI
pH=6	-1	+0.5	+0.5	+1	+1
	-1	+1	+1		
	-0.5				
	0				

(4) (Bonus 3 pts) Given the total volume of the sample during titration was 100 mL, what is the concentration of the peptide in this sample in molarity (M) ?

(+) $\frac{0.2 \text{ mmole}}{0.1 \text{ L}} = 2 \text{ mM} = 0.002 \text{ M}$