

BIOS 452/CHEM 452

Second Exam

Fall, 2010

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

Name: Study Points

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.

* What is the magnitude of

- one ionic bond (salt bridge) "
- one VdW interaction "
- one hydrogen bond in kcal/mol ?
- one covalent bond "

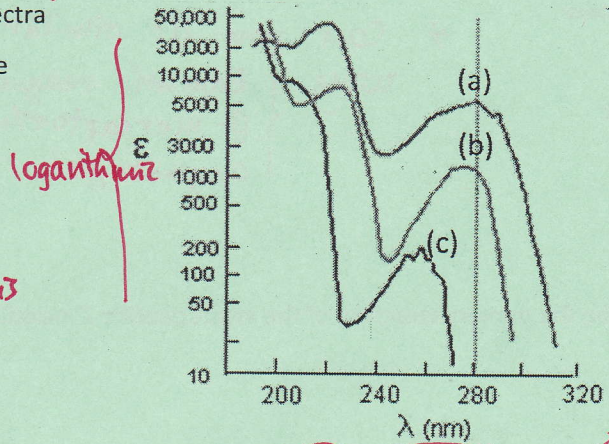
1. (4 pts) Circle amino acid(s) whose side chain(s) can be hydrogen bond donors at a neutral pH.

Tyrosine Glycine Glutamate Cysteine Proline

* Try distinguishing Hydrogen bond donors & acceptors in every amino acid.

* Anything related to hydrogen bond is "Very important" b/c H-bond is one of the major ways biomolecules can form specific interactions w/ each other.

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).

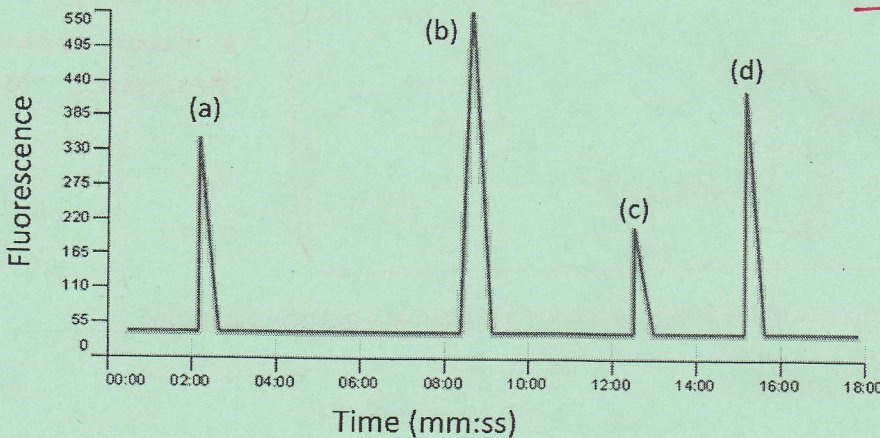


logarithmic

UV range wavelength

* Know all (a), (b), (c) ?
 * Pay attention to the scale of Y axis & numbers in X axis.

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.



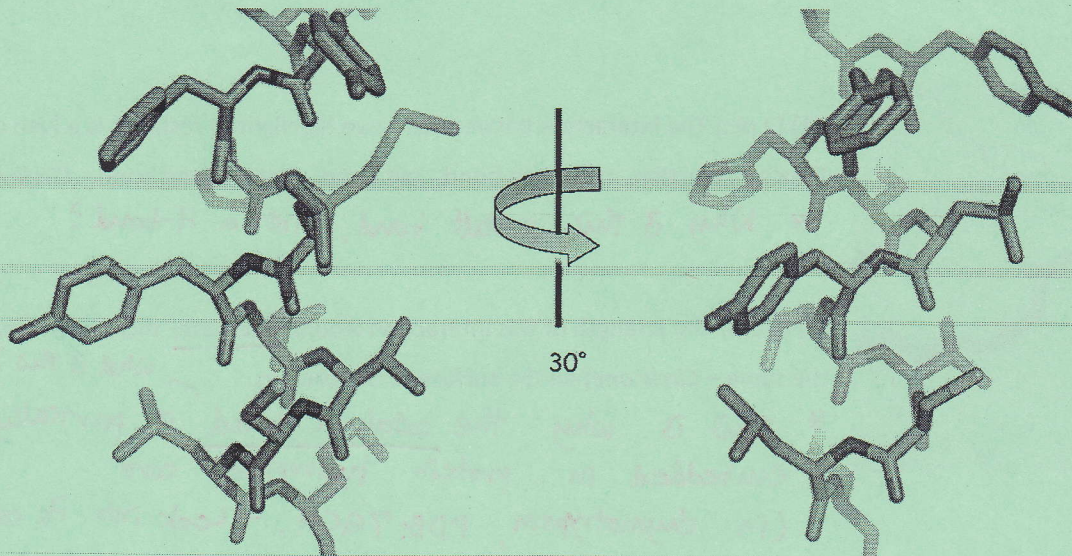
* Know how to do similar problem for ion-exchange chromatography?

(1) (4 pts) Match the peaks with the corresponding amino acid: (a) ____ ; (b) ____ ; (c) ____ ; (d) ____ .

(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.

How about ion-exchange?
 How do you elute the bound molecules?

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)

* Recognize amino acids by its 3-D structures.

(a) Y F H M L Y L V C L M

* Distinguish N-ter & C-ter of a peptide segment in 3D.

(b) M L C V L Y L M H F Y

(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.

* Know H-bond rules that makes up the 2° structures.

(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.

* Know this on 3D structure.

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

* Is a transmembrane helix an amphipathic helix?

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* What does "amphipathic" helix mean?

→ the α -helix that spans across lipid bilayer membrane

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.
- (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.
- (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.

* Can you explain why & why not of (a) - (d) ?

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

(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.

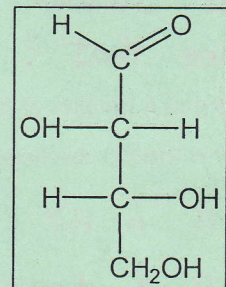
(3) (3 pts) Myoglobin has a molecular weight of 17,000 g/mole. Estimate the molecular weight of hemoglobin in kilodalton (kDa). Show your reasoning.

* What does it mean to say

myoglobin is homologous to hemoglobin ?

"Da"; Please at least know this even if you can't do anything else.
"Da = g/mole", "kDa = 1,000 Da".

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).



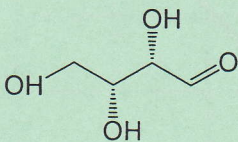
Distinguish D & L in Carbs, protein & Lipids ?

(part of nucleic acid)

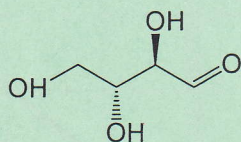
Freely convert different ways to describe same structures

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

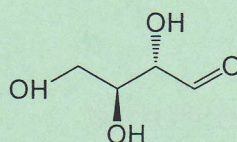
(a)



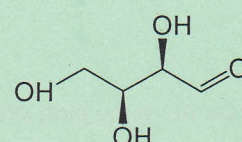
(b)



(c)



(d)



* This type of question can be applied to any protein binding to anything.

12. Consider an oxygen binding protein X with a P_{50} value of 100 mmHg and a Hill coefficient of 1.

(1) (3 pts) Calculate the ratio of the concentration of oxygen-bound X to the concentration of total X at 25 mmHg.

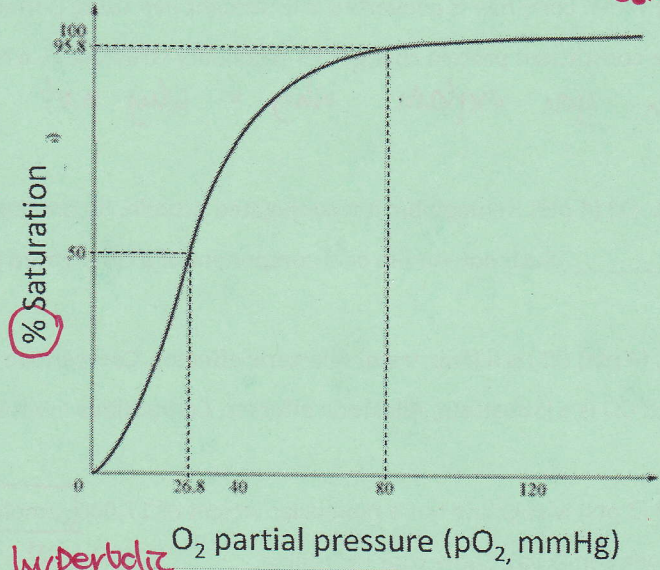
* P_{50} is like K_d . Why? How?

* High P_{50} / K_d means weak binding - Why? Express in curve/plot.
 " Low P_{50} / K_d means tight binding

(2) (5 pts) An oxygen binding curve of hemoglobin is

shown on the right. On the same plot, sketch the

binding curve of Protein X.



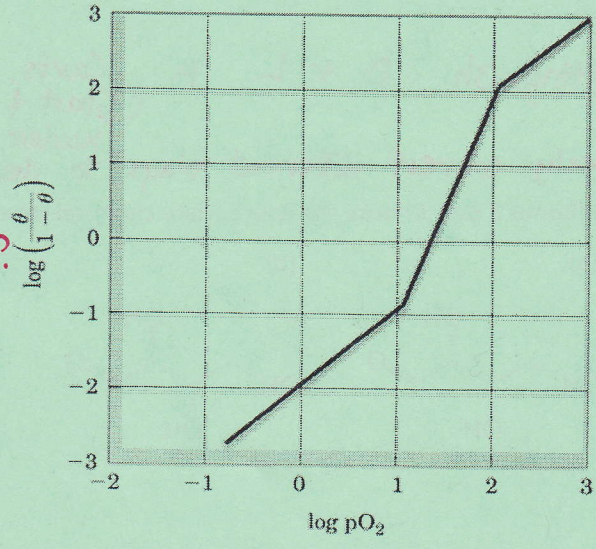
* Please at least know the distinction between a hyperbolic & a sigmoidal curve.

(3) (3 pts) Protein X binds to oxygen (stronger than, weaker than, the same as - Circle one) hemoglobin does.

* You can determine P_{50} looking at a hyperbolic O_2 partial pressure (pO₂, mmHg) curve of % saturation vs binding molecule's concentration.

This is similar to how you can determine K_M in V_o vs $[S]$ plot. You see that?

(4) (3 pts) A Hill plot of hemoglobin is shown on the right. What is the Hill coefficient of hemoglobin?

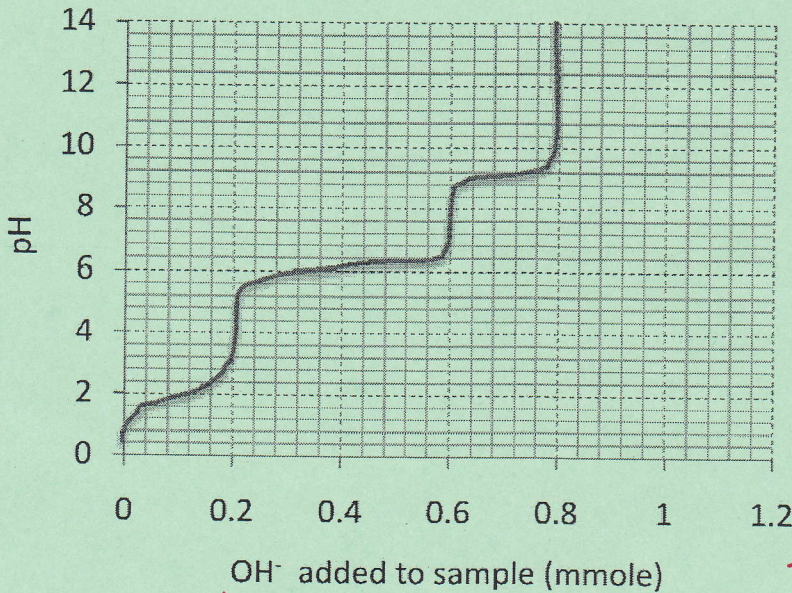


* What is a Hill coefficient?

* What is a cooperative binding? / Not cooperative binding?

(5) (Bonus 3 pts) On the same plot, sketch the Hill plot of Protein X.

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



* What is the flat part?
* What is the steep part?

OH⁻ added to sample (mmole)
↳ Usually you saw the x axis
in "Equivalents [OH⁻]"

→ * Can you find equivalence points?

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

- * M.W. of an amino acid $\sim 110 \text{ Da} = 0.11 \text{ kDa}$
 - * M.W. of a nucleotide pair $\sim 660 \text{ Da} = 0.66 \text{ kDa}$
 - * M.W. of a single nucleotide $\sim \frac{660}{2} \text{ Da} = 0.33 \text{ kDa}$
- (2) (3 pts) Circle amino acid residue(s) that the peptide MUST contain. } ON average.

W Y G S H

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

* Please practice w/ other peptide w/ different composition
For certain, there will be a question of a pI.

(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)?

* Why figuring out pI is important / useful?

E.g. How will you use this info for ion-exchange chromatography?