NAME

CHEM 527 First exam, Fall 2006

NOTES:

- 1. Where appropriate, show work to receive full credit.
- 2. This exam contains 10 pages.
- 3. Pace yourself you may want to do the easiest questions first.
- 4. Note the point value of questions varies widely adjust your answers accordingly.
- 5. Please give concise answers unfocused, rambling, answers often receive less credit than a few short phrases. If there isn't much space allotted a short answer is appropriate.
- 6. Some questions have more data than needed to tackle the problem.
- 7. FINALLY PLEASE write *clearly*. If we cannot read it it is wrong.

Table of amino acid pK values

Name	ρΚ αCOOH	ρΚ αΝΗ	pK (-R)
Alanine	2.3	9.7	-
Arginine	2.2	9.0	12.5
Asparagine	2.0	9.0	-
Aspartic acid	2.1	9.8	3.9
Cysteine	1.8	10.8	8.3
Glutamine	2.2	9.1	-
Glutamic acid	2.2	9.7	4.2
Glycine	2.3	9.6	-
Histidine	1.8	9.2	6.0
Isoleucine	2.4	9.7	-
Leucine	2.4	9.6	-
Lysine	2.2	9.0	10.0
Methionine	2.3	9.2	-
Phenylalanine	1.8	9.1	-
Proline	2.0	10.6	-
Serine	2.2	9.2	-
Threonine	2.6	10.4	-
Tryptophan	2.4	9.4	-
Tyrosine	2.2	9.1	10.1
Valine	2.3	9.6	-

Question 1 (15 pts). Short problems. Most of the credit goes for the correct numerical answer.

a. The pH of a solution is 3.3. What is the hydroxide ion concentration?

[OH⁻] = _____ M

b. Aspirin (pK 3.5), a weak carboxylic acid, is dissolved in water to give a solution with a pH of 2.5. What concentration of aspirin was used?

[aspirin] = _____M

c. You add 0.19 moles of KOH to 0.5 L of 0.4 M formic acid (pK 3.7). What is the pH of the mixture?

pH = _____

d. A 100 residue protein with 5 disulfide bridges is reduced and then disulfides are allowed to reform under denaturing conditions. How many possible disulfide combinations are possible?

Number _____

e. you add 0.25 moles of $K^+ H_2 PO_4^-$ to 0.5 moles of $K^+_2 HPO_4^{2-}$ in 1 L of water. The pK of the phosphate species here is 7.2. What is the pH of the mixture?

pH = _____

Figure 2 (13 pts) The figure below depicts the crystal structure of "WIND". WIND is a protein involved in the development of multicellular organisms. WIND is a dimer of identical subunits. Answer the questions as directed.



a. In the chain starting with an A (the N-terminus) what is the term for sections A-B and C-D?

b. Suppose **A-B** and **C-D** were also obtained as separate folded proteins (by expressing the fragments in bacteria). After denaturation in 8 M urea, which would you expect to fold fastest.

Circle:

A-B or C-D

Why? (one phrase on one line):

- **c.** Draw the chemical structure of urea $\dots \rightarrow$
- d. The protein fragments (A-B and C-D) were found to differ in molecular weight when evaluated separately on gel-filtration in buffer. Which is likely to be a dimer. Circle one:

A-B or C-D or insufficient information

e. How many amino acids would you expect between positions E and F?

f. How many H-bonds are likely to stabilize the structure between E and F _____

g. What amino acid is likely to be at position G **h.** Is **H** (in the figure on the previous page) an N-terminus or a C-terminus? **Circle one**: C-terminus N-terminus cannot say/insufficient information i. The two segments labeled H and I are: circle all appropriate answers Parallel beta stands Antiparallel beta strands Coiled coil **Triple helix** _____ Question 3 (10 pts) You have 0.2 mol of arginine (shown) in this NH_2 particular ionic form dissolved in 1 L of water. Answer the (+)following questions first circling the reagent (KOH or HCI) and then the amount you will need to get from the form shown to the $= NH_2$ indicated pH. NH CH_2 a. From original solution to a pH of 2.2 _____ mol of ĊH₂ KOH HCI (circle one) or CH₂ Θ H₂N-·ĆH**b.** From original solution to a pH of 9.0 _____ mol of KOH HCI or c. From original solution to a pH of 12.5 _____ mol of KOH HCI or **d.** From the original solution to a pH of 5.6 mol *of* KOH HCI or e. Circle the charge on arginine at pH 1 \rightarrow 2 1 0 -2 -1 f. Circle the charge on arginine at pH 14 \rightarrow 2 1 0 -1 -2

Question 4 (8 pts.) Draw the peptide cys-asp-gly-lys in the form that predominates at pH 6.0. Depict every atom in your drawing.

Question 5 (21 pts) Give the 3-letter abbreviation for the sequence: NEWTS

b. what is the electrical charge on NEWTS (assume the same side chain pK values as in the Table on first page. **E has a side chain of** $-CH_2-COOH$)

at pH 12 _____

c. NEWTS is attacked by a proteolytic enzyme, named

d. List the LARGEST fragment formed in "c"

a. _____

e. How special is the **NEWTS** sequence? How many possible peptides of 5 amino acids could be synthesized if you could pick from 20 amino acids at every position (*i.e.* NNNNN is one of the sequences).

#_____

f. would this sequence often occur by chance in a protein of 500 amino acid resides? Circle one:

yes no insufficient information

g. below is a sequence of an **envelope glycoprotein from Human immunodeficiency virus 1** Inspect the sequence shown below (a single chain of 180 amino acids) and answer the following questions.

1 IKPVVSTQLLLNGSLAEEEIIIRTENITNNAKIIIVQLNESITITCTRPYQSQKRGSHIG

LGRAYYTTRIQGNIKQIHCNISEIGWNRTLQQVAKKLRDLYNTTKIIFKPSSGGDPEITT

HSFNCGEEFFFCNTSGLFNNNEWTSNSTSVTSTSTGVNEDTIILPCRIKQIINMWQGVGK 180

i. clearly underline the **newts** sequence in the protein above.

ii. what are the **maximum number of disulfide bonds** that could form in a **monomer** of this protein?

..... disulfides per **monomer** (a number from 0 - 10)

iii. if this envelope glycoprotein were a **dimer**, what is the maximum number of disulfide bonds that could form in the **dimer**

..... disulfides per dimer (a number from 0 - 20)

iv.	In the <u>top line of sequence</u> (residues 1-60) give the first
	4 amino acids of the largest tryptic peptide
	(assume that the protein was reduced/alkylated first

v. In <u>the entire sequence</u> write below the **shortest** fragment generated on CNBr treatment of the envelope glycoprotein

Question 6 (6 pts) A buffer, pK 8.5, was being used at a concentration of 5 mM to maintain a protein solution at pH 8.9. The solution was stored exposed to air at 4 $^{\circ}$ C and the pH kept on dropping (... it was pH = 8.2 after 2 days).

Explain why (one line) - with appropriate chemical equations. In addition to using chemical notation please also give the chemical names for the compounds you draw.

Why:_____

Question 7 (7 pts) Maximum of one line of text per answer. Please write legibly.

a. What is a significant disadvantage of peptide sequencing by mass spectrometry (apart from the cost of the instrument!).

b. Name a program you might use to see if the amino acid sequence SLYSPSDPLELLGADTAERRLL is found in the chicken (and its translated genome).

c. Identify the amino acid change in a mutation that causes brittle bone disease(s) (*osteogenesis imperfecta*)

The mutation from amino acid ______ to _____

And the molecular reason that this mutation is harmful/fatal:

Question 8 (9 pts) Referring to the graphs below, deduce the schematic structure of the proteins A-C. Using the sample answer for the amount of detail required, show the quaternary structural arrangement including disulfide linkages (if appropriate). The triangles on the graph to the right indicate the behavior of proteins A-C.





Question 9 (6 pts) The structure of the analgesic lidocaine hydrochloride is shown (pK 7.9).

Predict the approximate pH values that would ensure a rate of absorption across a biological membrane that is:



a. 10% of the maximal rate pH _____

b. 90% of the maximal rate pH _____

half of the maximal rate

pH____

Question 10 (5 pts) Using the table answer the following questions.

overall MW (native MW)	рІ	#subunits
160,000	7	8
40,000	11	5
39,000	8	3
20,000	3	2
	overall MW (native MW) 160,000 40,000 39,000 20,000	overall MW (native MW)pl160,000740,0001139,000820,0003

In the spaces provided put proteins A-D as appropriate, (you can use an answer multiple times). None of the proteins contains disulfide bridges.

The protein sticking tightest to an anion exchange (+ charged resin) at pH 7	
The protein sticking tightest to a cation exchange resin (at pH 7)	
The protein running fastest on SDS-PAGE	
The protein running slowest on gel filtration in non-denaturing conditions	
The protein with the largest proportion of ARG+LYS (compared to ASP+GLU)	

Extra work space here - (not graded).



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