NAME Key

CHEM 527 First exam, Spring 2008

1. Where appropriate, show work to receive full credit.
2. This exam contains 7 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. PLEASE write *clearly.* If we cannot read it .... it is wrong.
8. Finally the little boxes at the bottom of the pages are for grading – not for your initials – thanks!

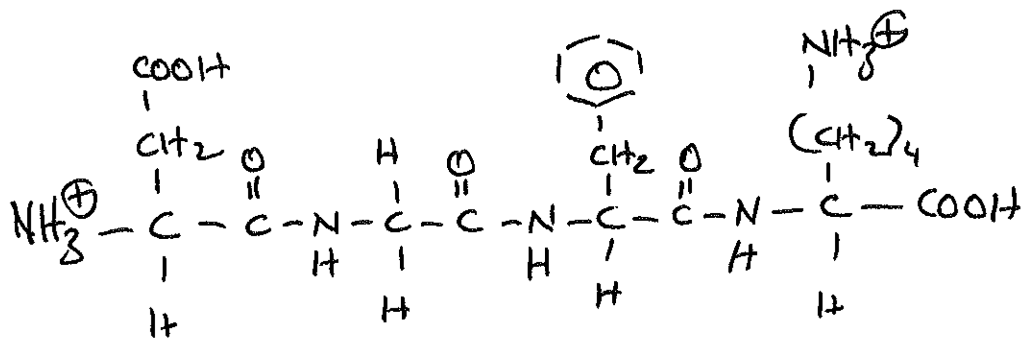
Use the following atomic weights; H = 1; C = 12; N = 14; O = 16; S = 32

Table of amino acid pK values

Name	pK αCOOH	pK αNH	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 (14 pts.)

In the space below draw the peptide: ASP-GLY-PHE-LYS in the form that predominates at pH 1 (use the pK table on page 1 – ignore any changes in pK that might come by incorporating the amino acids into a peptide).



8 pts
-1 ea
sig. error

Suppose you have 0.2 moles of this (protonated) form of the peptide. How much KOH would you need to get to the following pH values:

From the original form to pH 2.2 ___0.1___ 2

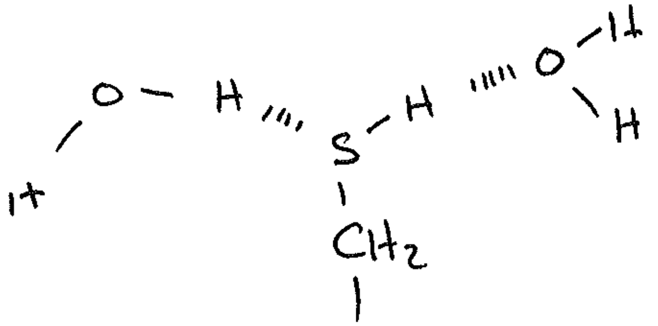
From the original form to pH 3.9 ___0.3___ 2

A 0.2 M solution of this peptide will have the best buffering capacity/ability (with the smallest change in pH upon the addition of 0.001 M HCl) at only one pH range.

It is: pH = ___8.8___ **to** pH = ___11___ 9.8, 10 2

Question 2. (3 pts) Draw a correct representation of a hydrogen bond between the **side chain** of a protonated cysteine and water ... just the **side chain** should be drawn.

3



(one or other)

Question 3 (27 pts) The following are parts of aligned peptides for several enzymes called QSOX (their species origin is denoted by the Hs or Mm designation at the left of the aligned sequences)

3

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HsQSOX1      CGHCIAFAPTWKALAEDVKAWR
MmQSOX1      CGHCIAFAPTWKELANDVKDWR
GgQSOX1      CGHCIHFAPTWRALAEDVREWR
HsQSOX1b     CGHCIAFAPTWKALAEDVKAWR
MmQSOX1b     CGHCIAFAPTWKELANDVKDWR
CeQSOX       CGACIGYAPTFKKFAKQLEKWA
DmQSOX       CGHCRRFAPTYKSVAEHLLPWS
TbQSOX       CGACRRYASTFSKFAGGLKVEH
AtQSOX       CPACRNYKPHYEKVARLFNGAD
```

2

a. Give the three letter abbreviations for

-YASTF- TYR ALA SER THR PHE 5

examples for completing the next two parts: ACDEFGHIKLMNPQRSTVWY

b. Carefully **circle** in the **top row above** (HsQSOX1) **invariant** amino acid(s) in this alignment.

c. Carefully **place a square or squares** in the <u>**bottom row**</u> (AtQSOX) to identify conserved aromatic amino acid position(s) in this alignmen.

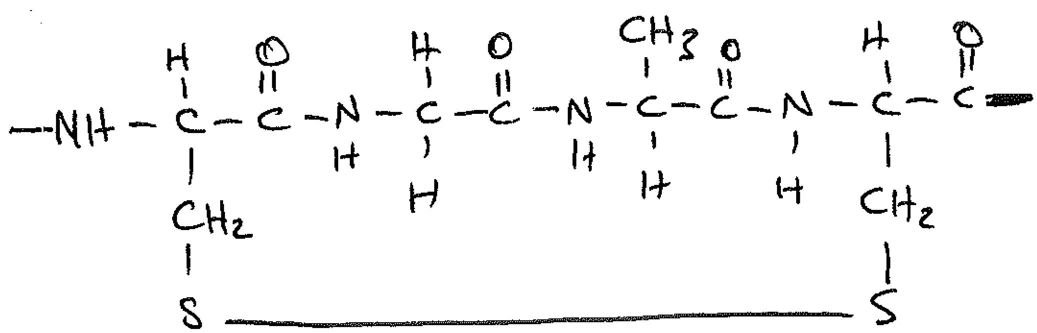
d. In human **HsQSOX1** write down the shortest peptide that would result after *trypsin* treatment of this 22 residue peptide.

AWR 2

e. In mouse **MmQSOX1** write down the shortest peptide that would result after *chymotrypsin* treatment of this 22 residue peptide.

[redacted] R 2

f. In the trypanosome **TbQSOX** peptide a disulfide is present. Draw the disulfide in the space provided with all the intervening amino acids in the peptide (show all atoms).



7

-1 each error

g. Draw and name the structure of a chemical reducing agent that should be able to reduce this disulfide

Name beta mercaptoethanol

H-O-CH$_2$-CH$_2$-SH

(2)

h. And draw and name the structure of a compound commonly used to alkylate cysteine side chains

Name sodium iodoacetate

$I-CH_2-\overset{O}{\overset{\|}{C}}-O^{\ominus} Na^{\oplus}$

or $I-CH_2-COOH$

(2)

etc.

i. What is the charge of the worm CeQSOX peptide at pH 1?

+5

(2)

Question 4 (18 pts). Short problems. Most of the credit goes for the correct numerical answer.

(3)

a. The pH of a solution is 5.5. What is the hydroxide ion concentration?

$pH = 5.5 \quad [H^+] = 3.162 \times 10^{-6}\,M$

$[OH^-][H^+] = 10^{-14} \quad$ so $[OH^-] = \dfrac{10^{-14}}{3.162 \times 10^{-6}}$

$[OH^-] = 3.16 \times 10^{-9}$ M

b. You have a buffer (pK 7.2) made by adding the acid and the conjugate base components to give final concentrations of 0.15 and 0.10 M respectively. The total volume was 1L.

i) what is the pH of the mixture

7.02 pH

(3)

$pH = 7.2 + \log\left(\dfrac{0.1}{0.15}\right)$

ii) what is the pH after adding 1 mL of 10 M KOH to the buffer

7.095 pH

(3)

1mL, 10M $\equiv$ .01 moles

So new HA amount in moles = .15 − .01 = .14 moles

new A .. .. .. = .10 + .01 = .11 mol

$pH = 7.2 + \log \dfrac{.11}{.14}$

iii) now calculate what is the pH when 1 mL of 10 M KOH is added to 1L of water (instead of the buffer)

12 pH

(3)

.01 moles/L $\equiv$ .01 M $OH^{\ominus}$ so $H^+ = \dfrac{10^{-14}}{.01} = 10^{-12}$

$-\log 10^{-12} = 12$

c. How much 0.2 M acetic acid (pK 4.7) would you need to add to 10 mL of 0.1 M potassium hydroxide to make a buffer with a pH of 5.4?

10mL of .1M KOH ≡ .001 moles $^{\ominus}$OH

vol = 5.998 mL (3)

when add acetic acid acetate ≡ .001 moles

so

$5.4 = 4.7 + \log \frac{.001}{x}$ So $\frac{.001}{x} = 5.012$ ($x = 1.995 \times 10^{-4}$ moles).

So total acetic acid in moles $= 1.1995 \times 10^{-3}$ moles so vol = 5.998 mL

d. What is the pH of a solution of 0.5 M formic acid (pK 3.7)? pH = 2.00

$pK = -\log K_{eq}$ so $K_{eq} = 1.995 \times 10^{-4} = \frac{[H^+]^2}{.5}$ ($[A^-] = [H^+]$) (3)

$H^+ = 9.988 \times 10^{-3}$ M so pH = 2.00

Question 5 (9 pts.) A polypeptide chain has the following sequence repeat pattern. The molecular weight of the chain is 10,000 Da (Daltons).

FDDFDDDFDDFDDDFDDFDDDFDDFDDDFDDFDDDFDDFDDDFDDFDDDFDDFDDD....*etc*

a. Over what pH range would you expect this chain to be alpha-helical? Circle your range:

1 2 3 4 5 6 7 8 9 10 11 12 13 14 (2)

accept 4

b. Explain your answer in one line:

(1)

Protonation of many carboxylate side chains allow helix formation avoiding charge repulsion

Now ... the molecular weight of the protein in solution indicates that it is in equilibium between a monomer and a dimer – MW 10,000 and 20,000 respectively)

c. At what pH would you there to be half monomer and half dimer at ~ 3.9 (2)

d. Explain your answer in one line: (any reasonable answer for ½ protonation)

at pK of asp side chain one might expect to see half coiled coil (1)

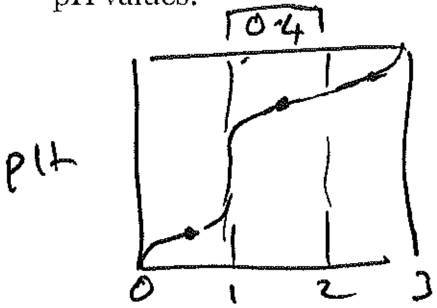
e. In brief, describe the likely molecular structure of the dimer. ***BE SPECIFIC*** (2)

what is the structure likely to be: Coiled coil (because of the pseudo repeat)

why? pseudo repeat with underlined hydrophobic residues

(1)

Question 6 (10 pts). You have 0.4 moles of cysteine hydrochloride salt (all protonated) in 500 mL of water. How much moles of KOH would you need to get this original solution to the following pH values:



pH 1.8 0.2 (2)

~~pH 5.9~~ 0.4 ignore

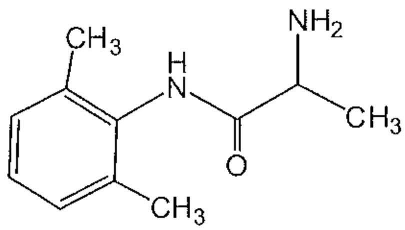
pH 8.3 0.6 (2)

pH 10.8 1.0 (2)

Cysteine would not be a good buffer at which of the following pH values. Circle as many as apply:

1.8 5.9 8.3 10.8 (2)

Question 7 (6 pts) Predict the pH values at which the absorption of this heart medication across biological membranes will be



tocainide (cardiac depressant) pK 7.9

a. 10% of the maximal rate **pH** 6.9 (2)

b. 50% of the maximal rate **pH** 7.9 (2)

c. 90% of the maximal rate **pH** 8.9 (2)

Question 8 (6 pts) Draw chemically correct, complete and clear depictions of the equilibria which describe the reactions involved when carbon dioxide dissolves in pure water.

$$CO_2 + H_2O \rightleftharpoons H_2CO_3 \rightleftharpoons H^+ + HCO_3^-$$ (4)

b. When 10 mM Tris buffer (an amine containing buffer), pH 9.0, is exposed to air it does not maintain the pH very well. Explain this carefully. Be specific.

(2) CO_2 dissolving in water generates H^+ via dissociation of carbonic acid (as above). Continual dissolution gives progressively lower pH

lea.

Question 9 (11 pts.) ~~Fill in the~~ blanks with not more than three legible words. Incorrect spelling may be penalized.

a. glycosylation and disulfide bond formation are example of post-translational modification

b. an organ that relies on surfactants for function lung (gastrointestine)

c. These trees lead to evolutionary relationships phylogenetic

d. the two most abundant unmodified amino acids in collagen (put one here) glycine

e. and the other one here .... proline

f. a *chemical* reagent useful for fragmenting proteins and large peptides cyanogen bromide

g. a cage of water surrounding hydrophobic molecules clathrate

h. Brittle bone disease (Osteogenesis imperfecta) reflects a single GLY to SER mutation

i. This helix type has a H-bond between the i^{th} and $i+4^{th}$ amino acid alpha helix

j. The word that best describes this exam over

the end of Exam #1