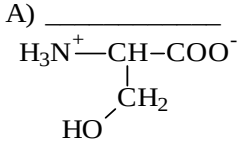
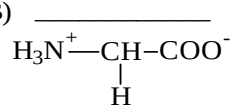
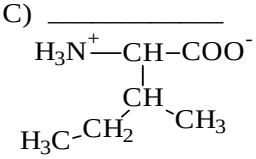
Spring '05 **CH370 / CH387D** Name _____
Hackert **Exam I**

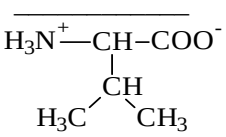
1. Identify each **amino acid** by its **three <u>and</u> one letter codes** (e.g. **Ala / A**, etc.) and each **N base, nucleoside** or **nucleotide** by its **full name** in the blanks **ABOVE** the structures (26 pts).

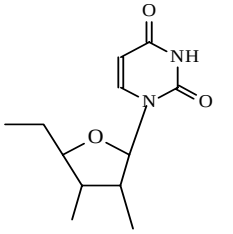
(26)

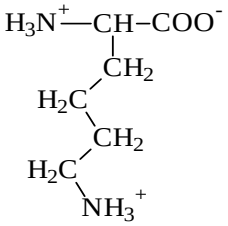
A) _____ 

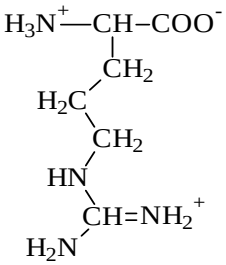
B) _____ 

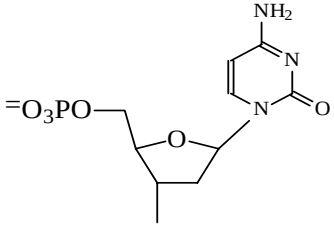
C) _____ 

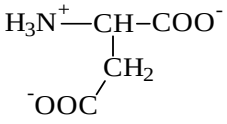
D) _____ 

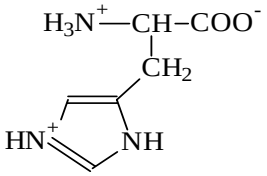
E) _____ 

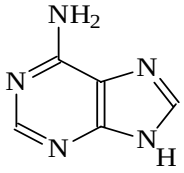
F) _____ 

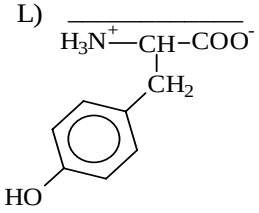
G) _____ 

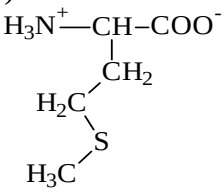
H) _____ 

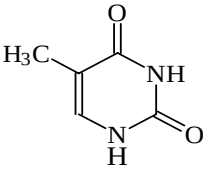
I) _____ 

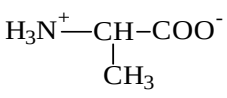
J) _____ 

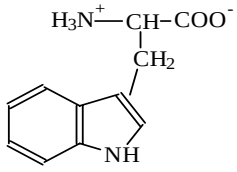
K) _____ 

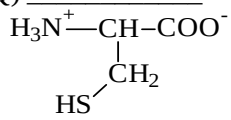
L) _____ 

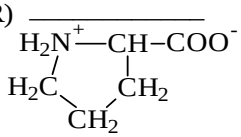
M) _____ 

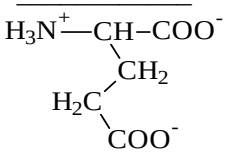
N) _____ 

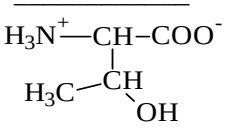
O) _____ 

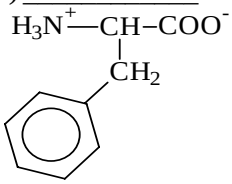
P) _____ 

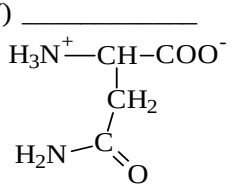
Q) _____ 

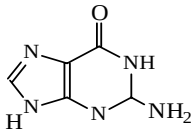
R) _____ 

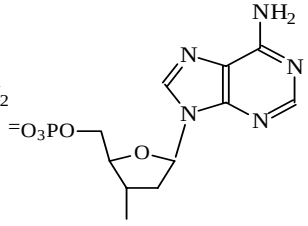
S) _____ 

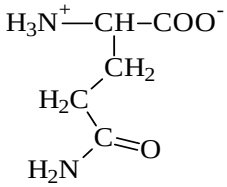
T) _____ 

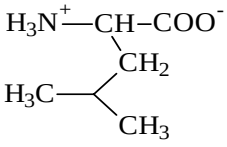
U) _____ 

V) _____ 

W) _____ 

X) _____ 

Y) _____ 

Z) _____ 

2. a) Which **one** amino acid is primarily responsible for the adsorption by proteins at 280 nm?
(2)

_____

b) Identify the 3-letter code of **one** amino acid for the approx. pKa's listed for their side chains.
(5) 4: ____ 6: ____ 8: ____ 10: ____ 12: ____

3. You are trying to purify a mixture of the following two polypeptides:

RAMACHANDRAN and **TEAMLEADER**

a) Estimate the charge of each peptide at pH 14.

(4) **RAMACHANDRAN** _____

TEAMLEADER _____

b) Estimate (± 1 pH) the isoelectric point of each peptide.

(4) **RAMACHANDRAN** _____

TEAMLEADER _____

Describe how you could take advantage the charge properties resulting from the amino acid content of these peptides to separate them. Recommend a chromatography method and conditions (pH, etc.) for their separation.

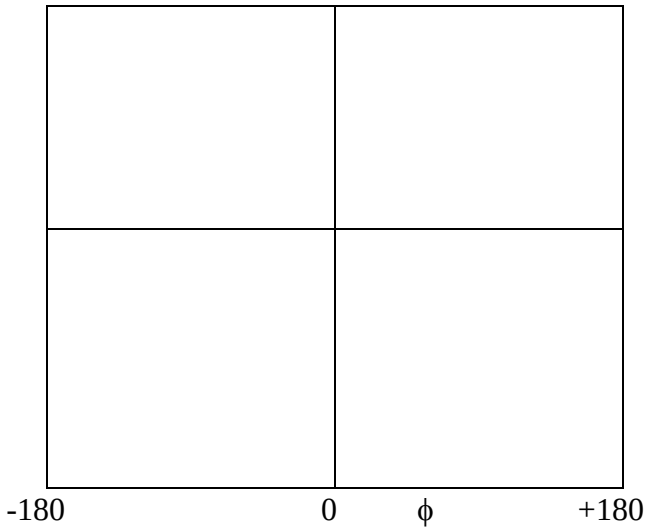
(4)

4. Define the difference between a folding "**domain**" and a "**motif**". Name one example of each.
(6)

5. Draw the structure of the dipeptide glycylglycine in a conformation that has a value of phi $\varphi = 180^o$ and psi $\psi = 0^o$ with the peptide bond in a trans ($\omega = 180^o$) configuration. In what type of protein structure would you expect to find this conformation to be present?
(6)

6. A common method of evaluating the stereochemistry of a protein structural model is to compute a _____ plot? Draw a circle on the plot below the approximate regions for β-sheet and right handed α-helix.

(6)



7. You are modeling the X-ray structure of an AMP-dependent enzyme and are stuck having to work with a low-resolution (poor) electron density map. You can make out some features that appear to be helices and sheets, but the resolution is too poor to tell the direction of the polypeptide chain. However, the electron density for the phosphate of the AMP moiety shows up strong in the map, and appears to be positioned at one end of a helix. How does this information help you assign the direction of the polypeptide chain for that helix? Why does the phosphate prefer that binding location?

(5)

8. Some oligomeric proteins are known to "fall apart" when stored in the cold and are more stable in solution at room temperature. Speculate on what types of non-covalent forces might dominate oligomer formation for such systems and explain this in terms of Gibb's free energy.

(5)

9. You have the following amino acid sequence from a protein that you believe is part of a "smart hormone" that recognizes DNA. P-Y-V-N-V-K-L-P-G-R-S-D-E-Q-L-K-N-L-V-S-E-V-T-D-A-V-E. You want to search for homologues to find out more about the properties of this protein's relatives. You use your web browser to go to the __ __ __ __ site that is a well known bioinformatics site providing access to many sequence databases. You search for homologues using the _____ routine and obtain the following results.

(2)

			E - score
1.	gi[1042879] HUMAN PROTEIN	482	2e-85
2.	gi[2346879] HYPOTHETICAL PROTEIN Mus	123	4e-18
3.	gi[5310428] UNKNOWN PROTEIN FROM 2D-PAGE	79	7e-13
4.	gi[2385419] Y531 protein [Methanobacterium]	55	1.45

a) What can you conclude from the search results? Are there any significant homologues?

(3)

b) Aligning up the amino acid sequences gives the following results:

```
                    1        5          10         15         20         25

  1. gi[1042879] P-Y-V-K-V-Q-L-P-G-P-S-D-E-Q-L-K-N-L-V-R-E-V-T-D-A-V-E
  2. gi[2346879] P-F-L-S-L-R-L-P-G-P-S-N-E-Q-L-K-N-L-V-R-E-L-S-E-A-V-E
  3. gi[5310428] P-F-I-N-V-K-L-P-G-P-S-S-E-Q-L-K-D-I-V-R-E-I-T-Q-A-V-E
  4. gi[2385419] P-I-V-N-V-I-T-G-G-D-V-A-H-E-S-P-L-V-S-M-V-I-K-A-D-V-A
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The protein is believed to bind non-specifically to the phosphate backbone of nucleic acids, place an (*****) **above those residues most likely to be involved in this binding**. Why?

(4)

10. Name four general properties of proteins whose differences can be exploited to separate and purify proteins. Also, name one technique based on each of these properties.

(8)

A) _____ -_____

B) _____ -_____

C) _____ -_____

D) _____ -_____

11. A classmate asks for you help. They are having trouble understanding the use of dideoxy nucleotides and how that relates to the Maxam-Gilbert method of DNA sequencing. Explain their misunderstanding by contrasting the difference between the Maxam-Gilbert and Sanger methods of DNA sequencing.

(5)

Consider the following nucleic acid sample: 5'-ATGCCTTAGCT-3' used as the template in a dideoxy sequencing experiment by an undergraduate assistant. On the "gel" below, draw the expected gel pattern that *would occur if* the student used 5'-primer with a fluorescent label, but forgot to add the dideoxy CTP to that reaction mixture.

(5) [DNA polymerase I + 4 dNTPs + ddATP ddTTP ddCTP ddGTP]