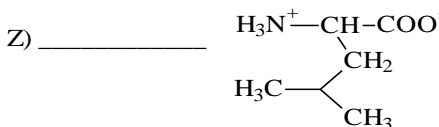
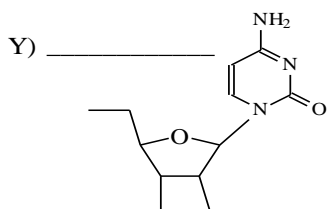
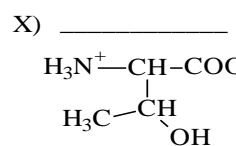
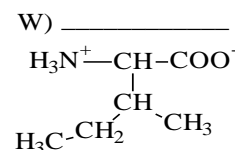
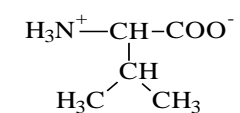
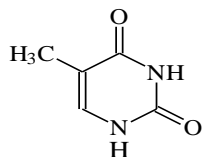
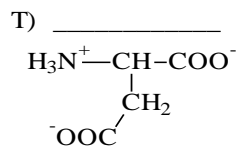
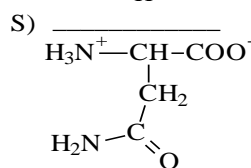
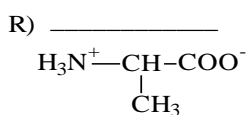
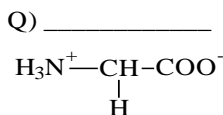
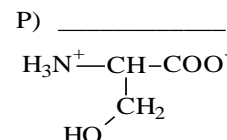
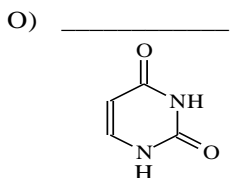
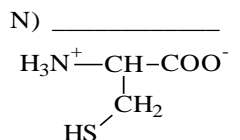
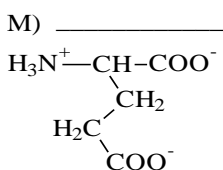
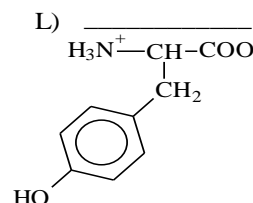
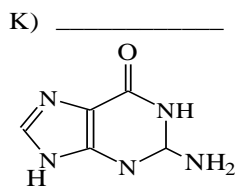
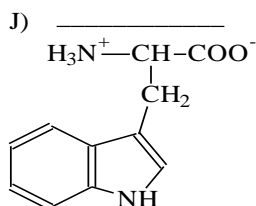
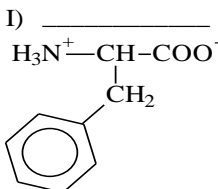
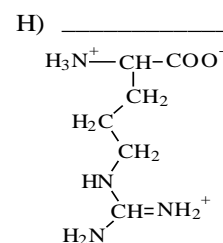
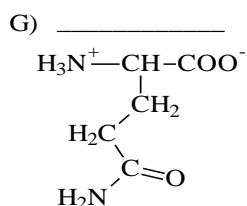
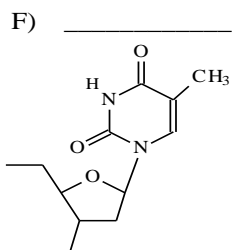
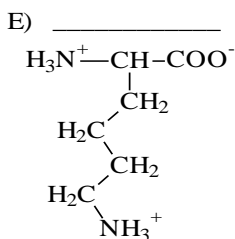
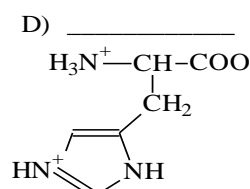
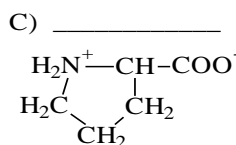
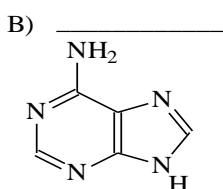
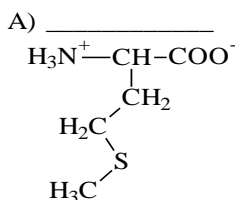


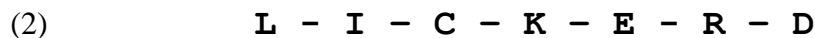
Given: $c = 3.0 \times 10^{10}$ cm/sec; $k = 1.38 \times 10^{-23}$ J/K; $h = 6.63 \times 10^{-34}$ J-sec; $N_0 = 6.02 \times 10^{23}$ /m
 $|E(1\%) \times MW| = |10 \times \epsilon|$; $\text{Eff.} = 1 / (1 + (R/R_0)^6)$; $E = h\nu$

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

(26)



2. Consider the following oligopeptide: **(circle all residues with titratable protons)**



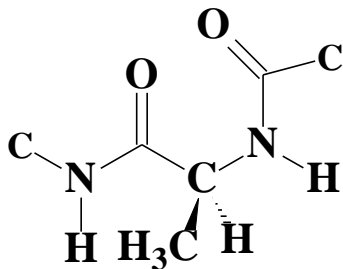
a) What is the net charge on this oligopeptide at very low pH (pH = 1.0)? _____
(2)

c) What is the approximate pI for this oligopeptide? _____ **(show your work)**
(4)

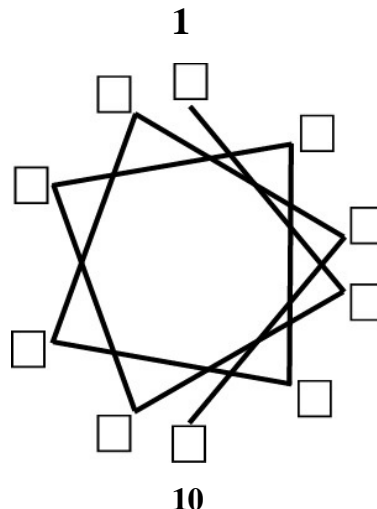
3. **Recognition of Terms:** Match each of the first six terms with the phrase that best describes it. Define the last two terms.

- | | |
|--------------------------|--|
| (6) ___ domain | a) arrangement of subunits |
| ___ ClustalW | b) multiple sequence alignments |
| ___ Homology | c) independent folding unit with a subunit |
| ___ quaternary structure | d) covalent structure |
| ___ BLAST | e) sequence comparison algorithm / search sequence databases |
| ___ Blosum62 | f) substitution matrix |
| | g) similarity attributed to descent from a common ancestor |

4. Consider the alanyl residue below. Label the bond rotation angles phi ϕ and psi ψ , and determine what those values are for this residue: $\phi =$ _____; $\psi =$ _____ (Watch direction!)
(4)



5. Write an amino acid sequence for a decamer that would fold into an alpha helix with the right side of the helix hydrophobic and the left side hydrophilic in nature. Use the helical wheel to illustrate the validity of your sequence.



(3)
1 _____ 10

6. For the 5-step enzyme purification shown, **answer** the questions below:

Step	Protein (mg/mL)	Volume (mL)	Total Activity (units)	Specific Activity
1. Crude extract	2.8	235	28,550	43.4
2. Salt ppt	7.2	48	21,750	
3. Ion exchange Chrom	5.8	32	15,250	
4. Affinity Chrom.	2.0	25	12,000	
5. Gel filtration	1.5	30	11,600	

- (2) a) Which step (#) exploited the differences in charge? _____
- (2) b) Which step (#) exploited the differences in size? _____
- (2) c) Complete the purification table by filling in the remaining blanks. _____
- (3) d) What is the overall percentage “yield” for this purification scheme? _____
- (2) e) Which step (#) of the purification produced the largest % increase in specific activity? _____
- (2) f) Which step (#) of the purification produced the smallest % increase in specific activity? _____

7. Consider a “gel filtration” column that is 150 cm in length and 2.50 cm in diameter. It is packed with spherical beads that are 0.13 mm in diameter with a V_o that is 33% of V_{tot} . The column is calibrated with trypsin inhibitor (~21.5 kD) and β -galactosidase (~116 kD) which gave V_e/V_o values of 2.63 and 1.44, respectively. An unknown protein is then eluted from the column.

- a) Calculate the **partition coefficients** for the **two standard** proteins (show work).
 trypsin inhibitor _____ β -galactosidase _____
- (4)
- b) **If** an unknown protein had a **partition coefficient** that was exactly the **average** of the two calculated for the **two standards**, what would be the best estimate for the molecular weight for the unknown protein? _____ (show work)
- (4)

8. Light and Energy: Calculate the frequency and energy in **kJ/mole** of visible light of wavelength = 500 nm (Show work - Draw a Box around your answer).

(5)

12. Briefly describe the basis of the Maxam-Gilbert method of DNA sequencing.
(4)

13. 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 a primer with a 5' - fluorescent label, but forgot to add the dideoxy GTP to that reaction mixture.
(4)

DNA polymerase I + 4 dNTPs + ddATP ddTTP ddCTP ddGTP

A T C G



(Please sign your name on the back of your exam in a manner that you can recognize it when it is returned.)