HW4: Chapter 4: 1, 4, 7, 10, 15, 16

① C-N bond in peptides 1.32 Å
Typical C-N bond length 1.49 Å
Typical C=N bond length 1.27 Å

a) It's length suggests that the peptide bond has partial double bond character

b) The planarity suggests it has partial sp^2 hybridization which means that there is no rotation around the bond

④ Poly Glu: α helix @ pH 3
Random @ pH 7

The α-helix is held together by bonds b/w the Carbonyl oxygen and amide hydrogen, BUT the side chains of the amino acids project out from the helical axis.

Poly lys: Random coil @ <pH 8.5
α-helix @ >pH 8.5

The side chain pKas are determining the secondary structural state of each polymer by electrostatic repulsion

The side chains of poly Glu are ionized @ pH values above 4, The side chains of poly Lys are ionized @ pH values less than 8.5-9

When the side chains are ionized, they repel each other and disrupt the secondary structure. Conversely, when the side chains are not charged, there is no repulsion and the polymers are α-helical!

(7) a) β-turns: Type I: Proline in Position 2
X-P-X-X

Type II: Glycine in Position 3
X-X-G-X

β-turns might be in residues:

4-7	Type II
6-9	Type I
18-21	Type I
19-22	Type II

b) Disulfide bridges occur b/w Cys residues

Possible Disulfide bonds: Cys^{13} - Cys^{24}

(7) Asp : Exterior
Ile : Interior
Thr : Interior or Exterior
Ala : Interior
Gln : Exterior
Lys : Exterior

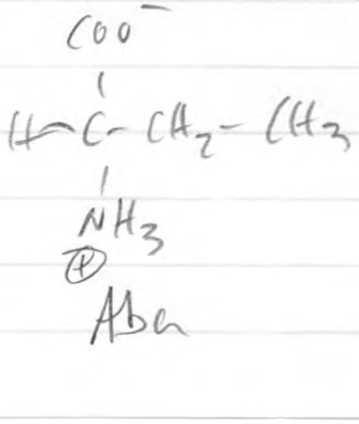
- Charged residues (Asp, Lys) may also be found in salt bridges in the interior of the protein.

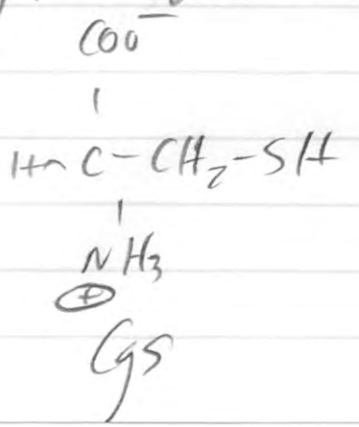
(12) Protein b is entirely α-helical, so it is likely found in the Ramachandran plot in (D)

Protein a is mostly β-sheet so its Ramachandran plot is likely (C).

(13) you got this. No answers needed (It is NF-Kappa B or p65)

(16) a) The Aba is roughly the same size as Cys so that is one reason why it might have worked.





The Aba would be unable to form a disulfide bond, so that is one reason it might not have worked.

b) i) Aba is chemically different from Cys with respect to polarity, so it might disrupt the "normal" hydrophobic core by folding away from solvent. Cys is hydrophilic and is solvent accessible

ii) Aba cannot form disulfide bonds and they may be needed for the protein to fold properly

iii) The cytosol is different than the buffer used, so the protein may misfold because of a solution problem

c) Disulfide bonds are not important in maintaining the structure of HIV protease

d) For situation 1: with the exception of chirality, everything else is the same if D-amino acids are used

Against situation 1: Chirality is freaking important!!! It determines the handedness of the 2° structures among other things.

For situation 2: Since the chiralities are opposite, the D-amino acid based protein should fold in the opposite manner

Against situation 2: Chirality is only one part of protein folding so the D-amino acid based protein might fold only slightly completely different.

Situation 3 is a catch all situation. you could use any of the above arguments for or against it.

c) Model 1 is supported by the data

f) Evans Blue is achiral so it doesn't matter to the enzyme (its chirality doesn't matter)

g) No because chymotrypsin recognizes L-amino acids not D-amino acids

h) Who knows? There is no way to predict

Crossword 4

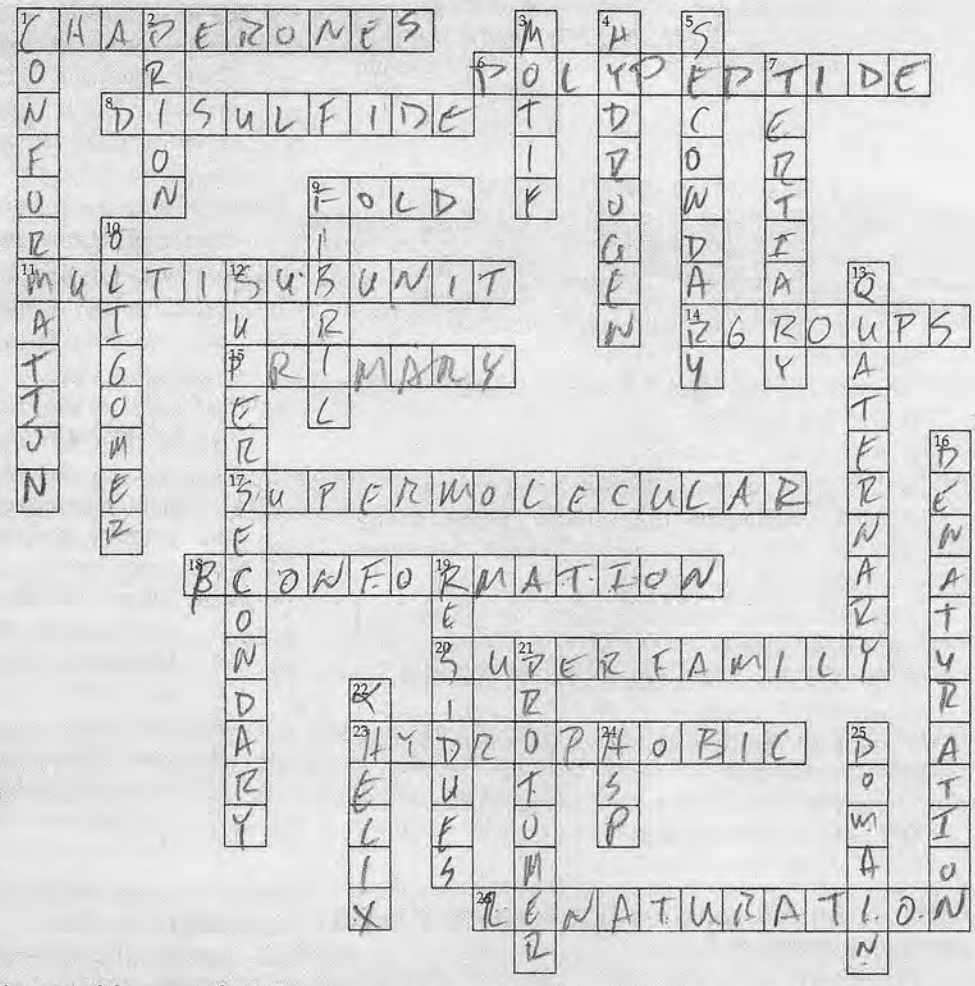
SELF-TEST

Do You Know the Terms?

ACROSS

1. Cellular agents that assist in protein folding at elevated temperatures.
6. Covalently linked amino acids with a single amino terminus and a single carboxyl terminus is called a(n) _____.
8. Bonds that occur between cysteine residues in proteins.
9. Also called a "motif."
11. Hemoglobin is a(n) _____ protein because it has two or more polypeptide chains.
14. They protrude in opposite directions from the zigzag structure of the β conformation. (2 words)

15. GCKKGGLVCAH for example; _____ structure.
17. Muscle fibers are an example of a(n) _____ complex.
18. Protein secondary structure that extends 0.35 nm per amino acid residue.
20. Though unrelated based on their amino acid sequences, proteins that belong to a(n) _____ have related structural features.
23. The noncovalent interactions that are thought to be the driving force behind the formation of a "molten globule."
26. An example is the re-formation of disulfide bonds during permanent waving.



DOWN

1. A native protein is in its functional _____.
2. An example of protein misfolding that has lethal consequences.
3. A stable arrangement of a few secondary structures.
4. α helices are stabilized by _____ bonds between the carbonyl oxygen and the amino hydrogen.
5. A β turn is an example of _____ structure.
7. Disrupting the hydrophobic interactions of a single-subunit protein would have the greatest effect on the _____ structure of that protein.
9. An example of a supramolecular assembly is the collagen _____.
10. α-keratin is referred to as a supramolecular complex of protein subunits; hemoglobin with only four subunits is referred to as a(n) _____.
12. The saddle conformation is a(n) _____ structure.
13. Myoglobin is to tertiary as hemoglobin is to _____.
16. Roasting a chicken results in the permanent _____ of myosin and actin proteins in the muscle cells.
19. Individual amino acids when polymerized in a protein.
21. The $\alpha\beta$ subunits in hemoglobin compose a single _____; the intact hemoglobin tetramer contains two of these.
22. Protein secondary structure that extends 0.15 nm per amino acid residue.
24. This class of proteins binds to and shields hydrophobic portions of unfolded polypeptides in cells. These proteins also are denatured by elevated temperatures.
25. Refers to the portion of a protein that is often composed of noncontiguous amino acid sequences and is usually defined on the basis of its contribution to protein function.