THE UNIVERSITY OF MANITOBA

April 22, 2006 FINAL EXAMINATION

PAPER NO: 718 LOCATION: E2-330 EIT Complex PAGE NO: 1 of 5

DEPARTMENT & COURSE NO: Chemistry 2.463 TIME: 3 HOURS

EXAMINATION: Biochemistry of Proteins EXAMINER: J. O'Neil

Section 1: *You must answer all of the following questions in* Section 1. *As a guide you can spend up to 2 hours and 35 minutes on this part of the exam. Wherever possible* ***use diagrams*** *to enhance your answers.*

Marks

5 1. What important insight was gained by studying the structure and function of synthetic all *D*- and all *L*-HIV-1 protease?

6 2. Draw the chemical structure of the tripeptide Tyr-Lys-Met at pH 7 and label all the dihedral angles with Greek letters or names.

8 3. What information did V. N. Ramachandran use to construct his Plot? Draw a Ramachandran Plot and label the locations of the right- and left-handed α-helices, parallel and antiparallel β-sheets, the right-hand 3_{10} helix, and the collagen triple helix.

8 4. Give a definition of the helical structural parameters ***pitch, rise,*** and ***repeat***. Then use your definitions to compare and contrast the α-helix and 3_{10}-helix.

3 5. Describe the "globin fold".

8 6a. Making use of the following equation, explain the principles behind the simulation of protein molecular dynamics.

$$E = \sum_{bonds} \frac{a_i}{2}(l_i - l_{i0})^2 + \sum_{angles} \frac{b_i}{2}(\theta_i - \theta_{i0})^2 + \sum_{torsions} \frac{Vn}{2}(1 + \cos(n\omega - \gamma)) + \sum_{i=1}^{N} \sum_{i \neq j}^{N} 4\varepsilon_{ij}\left[\left(\frac{\sigma_{ij}}{r_{ij}}\right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}}\right)^{6}\right] + \frac{1}{2}\sum_{i=1}^{N} \sum_{i \neq j}^{N} \frac{q_i q_j}{r_{ij}}$$

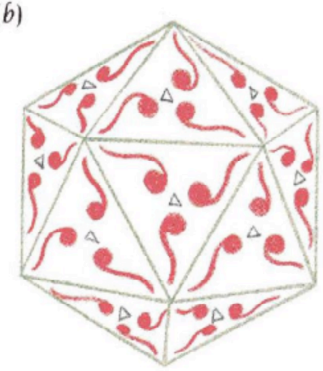
4 6b. What has been learned about protein dynamics from such simulations?

4 7. Using diagrams show a possible folding pathway for the 4-strand Greek Key β–sheet.

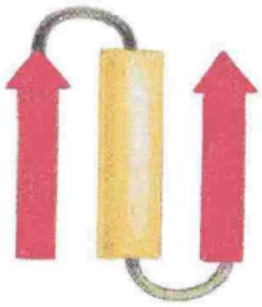
Marks

4 8. Explain the significance of the following structure:

(*b*)



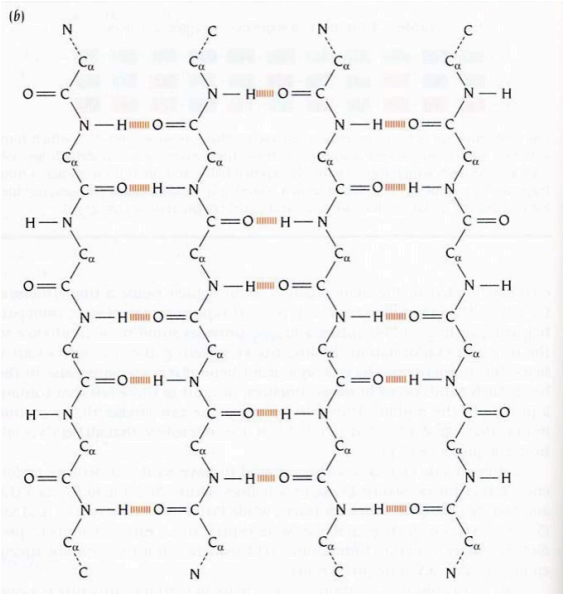
8 9. The structural motif shown below is the basis for the formation of both an open-twisted-sheet and a closed barrel structure. Explain how this is possible and name one enzyme or class of enzyme from each structural class.



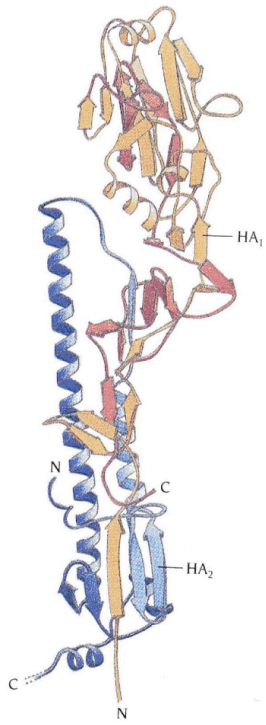
Marks

12 10. Identify the following structures. Describe the main features of each using examples wherever possible.

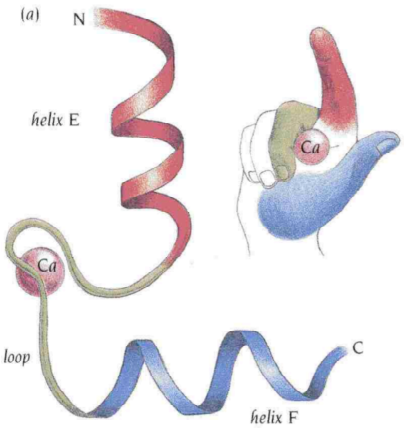
A



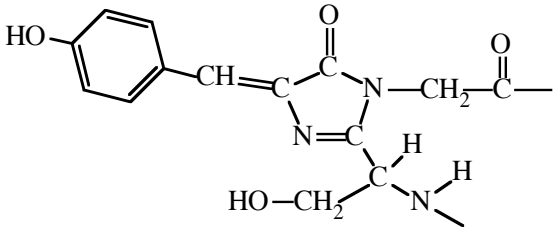
B



C



D



Marks

7 11. Explain the principles and uses of FRET (Fluorescence Resonance Energy Transfer).

6 12. Discuss the problem of determining the hydrophobicity and hydrophilicity of amino acid side-chains using model compounds.

8 13. Name 1 water-soluble protein and 1 integral membrane protein that form a 4-helix bundle. Describe the structures of each of the proteins you named.

2 14. What feature of β-sheet packing do the integral membrane protein ***porin*** and the water-soluble ***retinol-binding protein*** share.

6 15. Explain the role of the Proline Isomerase in assisting the folding of proteins. Be sure to include a diagram of the structure of Proline in your answer.

12 16. Describe helix formation in poly-*L*-Glutamic acid. Explain why the ***helix ←→ coil*** transition is highly cooperative in long homopolymers.

6 17. Draw and label a 3-dimensional folding funnel. Outline the main features of protein folding that are illustrated in folding funnels.

3 18. What is a cation-π interaction?

Marks

Section 2: *Answer **1** of the following questions in* Section 2. *You can spend about 25 min. on this question.*

20 19. In general, peptides shorter than about 25 amino acids do not fold into a stable tertiary conformation. In amino acid homopolymers hundreds of residues in length, a single α-helix forms by a highly cooperative folding mechanism. In proteins, short helices with fewer than 5 turns are commonplace. Describe the features of protein structure that contribute to stabilization of short helices in proteins.

20 20. Explain the different mechanisms by which helices pack together in proteins. Give examples of each.

20 21. Interactions between electromagnetic radiation and proteins can provide useful information about protein structure, dynamics, folding, and function. Describe the theory and application of ultraviolet and visible absorption and fluorescence spectroscopies, circular dichroism spectropolarimetry, and X-ray diffraction to proteins.

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