**Section 1:** You must answer <u>all</u> of the following questions in Section 1. As a guide, you can spend up to 2 hours and 30 minutes on this part of the exam. Wherever possible **use diagrams and structures** to enhance your answers.

Marks

- 10 1. Describe the results of a study in which synthetic *D* and *L*-snow flea antifreeze protein were produced.
- *10* 2. Describe protein structure determination by X-ray diffraction.
- 5 3. Briefly describe the hydrophobic effect and its importance to protein folding.
- 8 4. Name and briefly describe the 4 levels of protein structure.
- 10 5. Draw the chemical structure of the tetrapeptide Trp–Ile–Phe–Val at pH 7. Label the backbone and side-chain dihedral angles that describe the conformation of the phenylalanine.

Give a definition of the  $\phi$  dihedral angle. Such a short peptide will exist in dynamic equilibrium between many different conformations. What do you think is the most stable conformation for the

backbone of this peptide at pH 7? Explain your reasoning.

- 4 6. Explain the structural feature of the peptide bond that makes it possible to describe the conformation of a polypeptide using two bond angles only.
- 2 7. Describe the H-bonding in a  $\pi$ -helix.
- 6 8. Which amino acids are most frequently found in turn structures? What structural features in these residues promote turn formation?
- 9. With the use of the following diagrams, name and describe 3 different ways that α-helices can pack. It will be helpful to add diagrams of your own.



- 10 10. Describe the structure and function of neuraminidase and comment on pharmaceutical interest in this protein.
- 8 11. What is the purpose of a hydropathy plot? Briefly describe how to construct a hydropathy plot. Use a properly labeled sketch to illustrate your answer.
- 3 12. Which protein structures are easier to design  $\alpha$ -helical or  $\beta$ -sheet? Why?
- *3* 13. What is a molten globule?
- 4 14. Molecular dynamics simulations of proteins calculate atomic trajectories over very small periods of time. What is that period of time? Some small proteins fold very rapidly. About how long does it take for a small protein to fold? Using your answers above calculate the number of separate trajectories that must be calculated to simulate the folding of a small, fast-folding protein.

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## Marks

16 15. Identify the following structures. Describe the main features of each using examples wherever possible.



- 4 16. Briefly explain what is ROSETTA and how does it work?
- 4 17. What two important discoveries about protein folding were made by Christan Anfinson and his coworkers?
- 10 18. With the use of the following figure explain how the GroE chaperonin complex functions.



6 19. Proteome analysis suggests that 33% of eukaryotic proteins contain segments of 30 residues or longer that are natively unfolded.
What information forms the basis of such predictions?

Section 2: Answer Question 20. You can spend about 20 min. on this question.

Marks

15 20. With the use of the appropriate diagrams discuss the structure and function of the enzyme cycloxygenase (also known as prostaglandin synthase) <u>OR</u> the E. coli OmpF porin.





<u>C</u>

D







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