<u>April 21, 2004</u>

FINAL EXAMINATION

PAPER NO: <u>567</u> LOCATION: <u>Frank Kennedy Brown Gym</u>

PAGE NO: <u>1 of 4</u>

DEPARTMENT & COURSE NO: <u>Chemistry 2.463</u> TIME: <u>3</u> HOURS

EXAMINATION: Biochemistry of Proteins

EXAMINER: J. O'Neil

<u>Section 1</u>: You must answer <u>all</u> of the following questions in Section 1. As a guide you can spend up to 2 hours and 20 minutes on this part of the exam. Wherever possible **use diagrams** to enhance your answers.

Marks

- 10 1a Explain the two modern methods for converting protein molecules to gas-phase ions, as the first step in mass measurement by mass spectrometry. For each method, give the name (and abbreviation), a brief but clear explanation of how the method works, and what the resulting mass spectrum for a single pure protein looks like.
- 5 1b In the mass spectrum for a single pure protein shown in the Figure, the measured mass/charge ratios for the two peaks labelled A and B are 877.7 and 905.1, respectively. The peaks are cations, and their charges are the result of the attachment of different numbers of protons. From the information given, calculate the molecular mass of the protein, and determine what charges should be assigned to peaks A and B.



- 10 2 Explain the concept of the tandem mass spectrometry (MS/MS) experiment, and outline how it can be used to obtain amino acid sequence information from individual peptides in a tryptic digest of a protein.
- 6 3 Draw the chemical structure of the tripeptide Phe-Ala-Leu at pH 5 and label <u>all</u> the dihedral angles with Greek letters or names.
- 8 4 Name and describe the four levels of protein structure.
- 10 5 Define the backbone dihedral angle ω . Explain the difference between *cis* and *trans* Xxx-Pro. Describe the kinetics of isomerization of Pro amide bonds and the relevance of this to the folding of proteins.
- 8 6 What structural features of Gly, Ser, and Pro make them well suited for turn structures?

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- 10 7 Describe in detail the two types of helical packing in the RNA binding protein ROP.
- 12 8 Identify the following structures. Describe the main features of each using examples wherever possible.



- 6 9 The first high-resolution protein structure was solved in 1960 by the research group of John Kendrew. The protein was myoglobin extracted from the muscles of the sperm whale. These animals' muscles need lots of myoglobin to store O_2 for deep dives in the ocean. Knowing the positions of all the atoms revealed a puzzle about how the protein works. Explain both the puzzle and how is was solved.
- 2 10 What is the range of distances that atoms in proteins move during conformational changes?
- 8 11 Explain the concept of fluorescence and how fluorescence spectra are acquired. How can fluorescence be used to monitor protein folding?
- 6 12 Discuss the problem of determining the hydrophobicity and hydrophilicity of amino acid side-chains using model compounds.

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13 Discuss the significance of the following reaction:



- 4 14 How many different conformations can a 10 amino acid peptide form if each amino acid can adopt 6 different conformations? What is the Levinthal Paradox?
- 6 15 What two key discoveries about the folding of proteins were made by the research group of Christian Anfinsen?
- Section 2: Answer <u>1</u> of the following questions in Section 2. You can spend about 25 min. on this question.
- 20 16 With the use of the following diagrams discuss the structure and function of the photosynthetic reaction centre from *Rhodopseudomonas viridis*.



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17 With the use of the following diagrams discuss the structure and function of the E. 20 *coli* OmpF porin.

A







Section 3: Answer <u>1</u> of the following questions in Section 2. You can spend about 12 min. on this question.

- Using examples, discuss the potential value of high-resolution protein structures 10 18 to the pharmaceutical industry.
- Cells have evolved a number of mechanisms to assist protein folding. Describe 3 10 19 such mechanisms and name the factors involved in the process.

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