Term Test-1

Answer all questions in the Exam Booklets. Put your name and student number on all exam booklets. You may use a calculator, and draw **structures** and **diagrams** where appropriate.

The total number of marks is 43, and you have 50 minutes to complete the exam, so spend about 1 minute per mark i.e. 8 min. for an 8-mark question etc.

Answer question 1. It is worth 6 marks.

1. Draw the chemical structure at pH 7 of the following peptide:

Name all of the products of cyanogen bromide treatment of the peptide above.

Answer question 2 OR question 3. Each is worth 15 marks.

- 2. Outline a protocol for amino acid analysis of a protein and describe in chemical detail peptide hydrolysis by strong acid. Explain the problem that arises in amino acid analysis when a protein contains β-branched dipeptides and present a solution to the problem.
- 3. Explain the chemical reactivity of the amino acid Cys, give some examples, and describe the role of this chemistry in the folding of proteins.

Answer question 4. It is worth 6 marks.

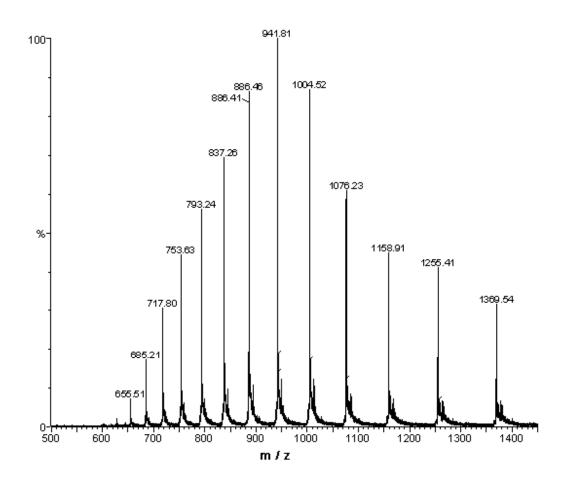
4. Explain how Immobilized Metal Affinity Chelate Chromatography can be used to purify proteins.

Answer question 5. It is worth 6 marks.

5. Give a definition of the "hydrodynamic particle". Briefly, but clearly, explain the difference between sedimentation velocity and sedimentation equilibrium analysis of proteins emphasizing the information obtained from each method.

Answer question 6. It is worth 6 marks.

6. From the data given in the mass spetrum below calculate the mass of the protein. For full marks show your calculations. What method was used to introduce the protein into the mass spetrometer?



Answer question 7. It is worth 4 marks.

7. With the use of the following equation explain how time-of-flight mass spectrometry measures the masses of proteins: $\frac{m}{z} = \frac{2Vt^2}{L^2}$