# **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 45, 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 8 marks.

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

Name all of the products of acid hydrolysis of the peptide above.

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

- 2. Describe in chemical detail the main steps of an Edman degradation indicating the role and importance of pH, buffers, and organic solvents.
- 3. 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.

#### Answer question 4. It is worth 8 marks.

4. With the use of the following equation describe sedimentation velocity analysis of proteins. Be sure to describe how the method works and what is measured.

$$\frac{dr}{dt} = \frac{M_r (1 - \bar{v}\rho)\omega^2 r}{N \cdot f}$$

## Answer question 5. It is worth 4 marks.

5. Briefly explain how a Fourier transform ion cyclotron resonance mass spectrometer works. What is the main advantage of this type of mass spectrometer.

# Answer question 6. It is worth 10 marks.

6. Compare and contrast solid-, liquid-, and gas-phase protein sequencing.

Bonus Question: 5 marks maximum

7. Name the protein that has the largest number of knots in its backbone. What is its function? What is the connection between its function and its knotted backbone?