Biochemistry of Proteins CHEM 4630   **February 11, 2014**

Term Test-1

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

The total number of marks is 55 and you have 75 minutes to complete the exam.
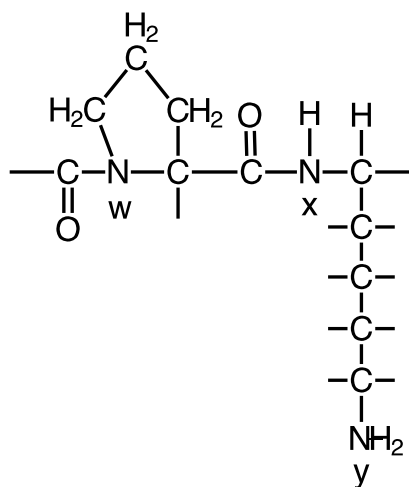
Answer question 1. It is worth 6 marks.

1. The peptide shown below was treated with DMSO in HCl. Following partial neutralization it was treated with CNBr in 90% formic acid. Draw the chemical structure at pH 7 of **one** of the peptides that result from this treatment.

Thr-His-Ala-Trp-Met-Pro-Arg

Answer question 2. It is worth 2 marks.

2. In the following peptide fragment, 3 N atoms are labeled w, x, and y. Indicate the order of protonation of the atoms in strongly acidic solution.

Answer question 3 OR question 4. Each is worth 15 marks.

3. Outline a protocol for amino acid analysis of a protein and describe in chemical detail peptide hydrolysis by strong acid. What problem arises in amino acid analysis of proteins containing tryptophan? What can be done about this?

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

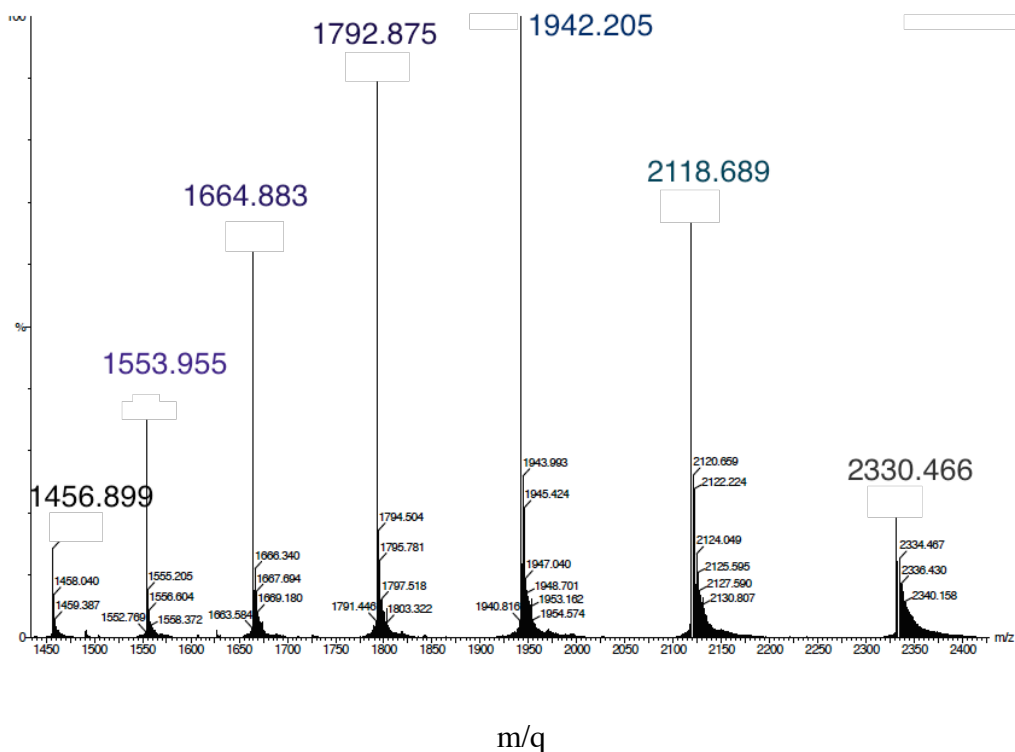**Answer question 5.   It is worth 8 marks.**

5. What is the advantage of colloidal silica compared to polymers such as acrylamide and dextran as resin particles in HPLC?
    Explain how reverse phase chromatography can be used to separate a mixture of proteins, peptides or amino acids.

Answer question 6 <u>OR</u> question 7. Each is worth 8 marks.

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

7. Describe a chemical method for determining the oxidized and reduced Cys content of a protein.

Answer question 8. It is worth 10 marks.

8. Below is shown the mass spectrum of a protein. Name the method that was used to introduce the protein into the vacuum of the mass spectrometer.
    Explain this method of introducing proteins into a mass spectrometer.
    The spectrum contains 7 major peaks labeled by their mass-to-charge ratio. From the mass/charge ratios of two of the peaks calculate the molecular weight of the protein **showing your calculations**.
    Near each of the major labeled major peaks in the spectrum are smaller peaks – what is their origin?

m/q

Answer question 9. It is worth 6 marks.

9. Define proteomics.
    Explain how the SILAC method can be used to quantify proteins in cells.

Bonus Question: 2 marks maximum

10. Describe one of the evolutionary processes by which circularly permuted proteins may arise.