BIRKBECK COLLEGE
(University of London)

SCHOOL OF BIOLOGICAL SCIENCES

M.Sc. EXAMINATION FOR INTERNAL STUDENTS ON:

Postgraduate Certificate in Principles of Protein Structure
MSc Structural Molecular Biology

CRYS024D7

PRINCIPLES OF PROTEIN STRUCTURE

Thursday 20 August 2015

Duration of examination: 3 hours

10.00 – 13.00

Students will be required to answer 8 out of 12 questions.

All questions carry equal marks.

Each question must start on a new page and the question number written at the top of each sheet.

The exam papers have not been prior-disclosed.

1. Answer all parts;

   a) Using alanine as an example, describe the difference between the L- and D- forms for amino acids. [2 marks]

   b) Name the only non-chiral amino acid and what are the conformational effects? [2 marks]

   c) Indicate which two amino acids have chiral side-chains. [2 marks]

   d) Show how a peptide bond formed? [2 marks]

   e) What is the difference between a *trans* and *cis* peptide bond ? [2 marks]

2. Answer both parts;

   a) What is a hydrogen bond? [2 marks]

   b) Indicate the torsion angles as defined in a polypeptide. [2 marks]

   c) On a Ramachandran plot show the secondary structure regions for both beta sheets and alpha helix. Also show on your figure where a left handed alpha helix region is located. [6 marks]

3. Compare and contrast the detailed structural features of a standard alpha helix with the various forms of beta structure that occur in protein. [10 marks]

4. Answer all parts, Draw the following;

   a) A beta turn. [2.5 marks]

   b) A beta-alpha-beta motif . [2.5 marks]

   c) A four helix bundle. [2.5 marks]

   d) A Greek Key motif. [2.5 marks]

5. How can you model alpha helix packing? [10 marks]

6. Answer both parts;

   a) Discuss plagiarism and scientific fraud. [5 marks]

   b) What key points are important to consider when publishing a scientific paper? [5 marks]

7. Answer all parts;

   a) Explain in detail how the bioinformatics program BLAST can be used to select protein sequences that are likely to be homologous to a test sequence. Describe the results that are obtained from a BLAST run and explain how they should be interpreted; include in your explanation a precise definition of the term 'E-value'. [8 marks]

   b) Explain why it is not always possible to tell whether two sequences are homologous from BLAST alone. What other programs might you use if the results are ambiguous? [2 marks]

8. Answer all parts;

   a) Describe the structure and function of each of the three main types of RNA that are involved in the process of protein transcription. [6 marks]

   b) Briefly describe the process of protein synthesis at the molecular level, making reference where relevant to each of these types of RNA. [4 marks]

9. Answer both parts;

a) Explain in detail, making reference to the electronic structure of atoms, how each of the following types of 'non-bonded' interactions that are found in proteins arises.
[2 marks for each, total of 8 marks]

i. Van der Waals interactions

ii. Hydrogen bonds

iii. Ion pairs

iv. Aromatic-aromatic interactions

b) Which of these types of interaction cannot be made by the side chain of the amino acid tryptophan? Give a reason for your choice.
[2 marks]

10. Answer all parts;

a) Explain briefly, using diagrams if you prefer, the structural difference between the monosaccharides glucose and galactose. [2 marks]

b) Describe how a sugar-binding site in a protein can distinguish between these structures in order to favour the binding of one monosaccharide over the other. [2 marks]

c) Describe the structure of the influenza protein haemagglutinin and explain how it uses interactions with a simple sugar to bind to cells in the human respiratory tract. [6 marks]

11. Answer all parts;

a) Explain the function and role of the secretion systems found in the membranes of Gram negative bacteria. Why do Gram positive bacteria not require such complex systems? [3 marks]

b) Describe in detail the structure of the type IV secretion system and explain how a conformational change causes the system to become functional [6 marks].

c) Explain briefly how this system is involved in infectious disease. [1 mark].

12. Answer all parts;

a) Describe in detail, or draw, the structure of an immunoglobulin constant domain. What are the main differences between this structure and that of a variable domain? [4 marks]

b) Draw a schematic diagram showing the structure of the immunoglobulin IgG molecule. [6 marks total]

Indicate the following on your diagram;

i. Each constant and each variable domain.

ii. The location of the antigen binding sites.

iii. The N- and C-termini of each chain.

iv. Approximate locations for a carbohydrate-binding region and at least one disulphide bond.