Birkbeck College

University of London

School of Crystallography

Advanced Certificate in Principles of Protein Structure

Date: Thursday 26th September 2002

Time: 14.00 - 17.00

Answer four questions.

1. The following is a list of the single letter codes for the twenty L-amino acids normally found in living organisms:

   A C D E F G H I K L M N P Q R S T V W Y

   For each one indicate:

   a) the three-letter code

   b) the amino acid name

   c)the general chemical nature of the amino acid side chain (R)

   Draw the structures of E, A, Y, P and G. Very briefly indicate why P and G are important in terms of protein folding?

2. Describe the arrangement of genes and mechanism of their control within the lac operon.

3. Compare and contrast the three principle forms of RNA found in living organisms.

4. Illustrate the secondary and tertiary structural elements in gamma crystallin. Briefly how is this different to the TIM barrel fold.

5. Illustrate in detail the structure and hydrogen bonding interactions found in the following:

   a)alpha helix

   b)parallel and anti-parallel beta pleated sheet

   c)type I and type II turn

   Show on a Ramachandran plot the expected positions for an alpha helix and beta sheet. Which single amino acid can be located anywhere on the plot and why?

6. Describe, with the aid of diagrams, the structure and function of DNA.

7. Illustrate the different levels of structural complexity in proteins using the small polypeptide hormone insulin as an example.

8. Give an overview of the non-covalent interactions acting on protein macromolecules.

Chose four of these molecular forces and discuss their important for determining protein folds and macromolecular associations in detail.

9. Describe the tertiary structure, active site and specificity of the serine protease superfamily. How do the active sites ofchymotrypsin, trypsin and elastase alter their specificity.

10.Describe the type of information that is contained in databases of protein motifs and domains, and explain why one such database is not sufficient. What type of database would be most appropriate to identify putative phosphorylation sites in a protein, and why ?

11.(a) Describe in detail a procedure for determining, from a protein sequence, whether that protein traverses a cell or organelle membrane. If found, which are the transmembrane segments?

(b)There is one class of membrane proteins that cannot be distinguished using most general tools for determining transmembrane segments. What type of secondary structure characterises these proteins? Name, and roughly sketch, one example of this class.

12.Discuss, in detail, three different experimental methods to analyse the structure of a globular 30 KDa protein. Indicate the requirements needed to apply each method and the type of information that may be obtained by each technique.

13.The structure and function of metalloproteins are of critical importance for many living processes. Illustrate this using the iron carrying protein responsible for oxygen transport within the red corpuscles of the blood stream.