BIRKBECK COLLEGE

(University of London)

Advanced Certificate in the Principles of Protein Structure

Date: Wednesday 19th September 2007

Time: 3 hours

Start time as per instructions to local exam centre

Students will be expected to answer 6 of the 10 short questions in section A, and 4 of the 8 long questions in section B. They will be advised to spend 1 hour on section A and 2 hours on section B.

Short questions are worth 6 marks.

Long questions are worth 18 marks.

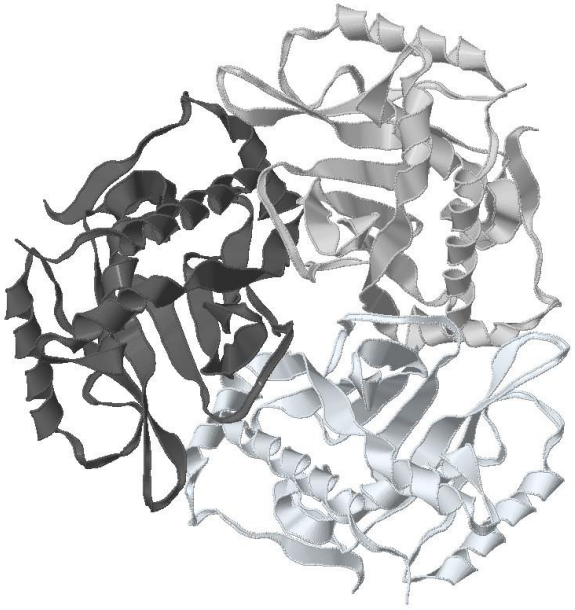
Section A: Short Questions

Six questions only to be attempted from section A

(Suggested time 10 minutes on each)

A1. Describe the Rossmann fold. What is its primary binding function?

A2. From this topology diagram of the enzyme chloramphenicol acetyltransferase below, describe its quaternary structure and comment on the symmetry.



A3. Describe the structure and function of a protein that binds in the major groove of B-DNA.

Section A: Continued

A4. What are the principal types of information held in the databases Prosite and Pfam? Which of these databases would you use to find all potential post-translational modification sites in a protein, and why?

A5. Draw the structure of a G-protein coupled receptor. Where in the cell is it found? Briefly describe its mechanism of action.

A6. Draw or describe the folds of the MHC Class I and Class II molecules, clearly illustrating the main structural differences between these proteins.

A7. Name two sugar-binding proteins that are important drug targets against influenza. Outline the structural features of one of them.

A8. The Pro23His mutation in human rhodopsin causes blindness;

i) Draw the side chains for both Pro and His {2 marks}.

ii) Illustrate the positions of the Phi and Psi angles along the polypeptide backbone. What is the likely affect on the backbone flexibility with this mutation {2 marks}.

iii) What changes occur in the chemistry of this position with the substitution of Pro with His {2 marks}?

Section A: Continued

A9. Illustrate the following;

i) A polypeptide in which all the amino acids have typical phi and psi values around -60 degrees and -50 degrees, respectively {2 marks}.

ii) The polypeptide conformation that has typical values of phi = -140 degrees and psi = +130 degrees {2 marks}.

iii) A reverse turn. What is the main difference between the type I and II turn {2 marks}?

A10. Define the following briefly {1 mark for each part};

i) Plagiarism

ii) Patents

iii) Peer review

iv) Copyright

v) PDF

vi) URL

Section B: Long Questions

Four questions only to be attempted from section B
(Suggested time 30 minutes on each)

B11. Discuss the roles of sequence repeats, domains and gene duplication in protein structure.

B12. Explain the difference between cyclic, dihedral and higher symmetries in protein quaternary structure. Indicate the kinds of protein functions that are associated with higher symmetries.

B13. Outline the range of protein molecules that are involved in detecting and processing abnormal proteins in humans. Why might a missense point mutation lead to a protein folding disease?

B14. Indicate for each of the following single letter codes for the 20 L-amino acids normally found in proteins;

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

i) The three letter abbreviation {1% for each, 20% maximum}

ii) The amino acid name {1% for each, 20% maximum}

iii) The chemical nature of the amino acid {1% for each, 20% maximum}

iv) The structure of the side chain {2% for each, 40% maximum}

Section B: Continued

B15. Explain in detail why proteins that are found in the outer membrane of Gram negative bacteria cannot be identified using the same simple bioinformatics tools as other transmembrane proteins. Name one of these proteins; draw and describe its structure, and describe its function and mechanism of action in detail.

B16. Draw and describe in detail the structure of the immunoglobulin fold, naming one type of supersecondary structure (motif) that is found in this structure. Name three different proteins that contain at least one immunoglobulin domain, and describe the structure, function and role played in the immune system by each.

B17. Compare and contrast the tertiary structure and catalytic function of chymotrpsin and HIV proteinase.

B18. Describe the molecular geometry of the polypeptide chain and how its geometric properties can explain the ways in which it folds into a three-dimensional conformation.