UNIVERSITY OF JOHANNESBURG

FACULTY	: Science	
DEPARTMENT	: Biochemistry	
CAMPUS	: APK	
MODULE	: BIC8X02	PROTEIN BIOCHEMISTRY
SEMESTER	: First	
EXAM	: June 2019	

DATE	: 27 May 2019	**SESSION**	: 08:30-11:30
ASSESSOR(S)	: PROF L BORNMAN DR G KOORSEN		
MODERATOR	: DR P MOTSHWENE		
DURATION	: 3 HOURS	**MARKS**	: 100

NUMBER OF PAGES: 6 PAGES

INSTRUCTIONS:

1. Answer ALL THE QUESTIONS.
2. Number your answers clearly

QUESTION 1 **[12]**

1.1. Spectroscopic techniques are often employed in the study of proteins. In all spectroscopic methods, proteins are excited by electromagnetic radiation, after which the proteins relax to the ground state. Name five energy transfer processes by which a protein can return to the ground state. (5)

1.2. FRET and FRAP are examples of spectroscopic techniques often used in the study of protein structure and function.

1.2.1. Compare the two techniques in terms of the reversibility of the photochemical processes involved. (2)

1.2.2. Provide a diagram that illustrates the path of energy and relative energy levels between a FRET donor and acceptor pair. (5)

QUESTION 2 **[15]**

2.1. Draw the chemical structure of the tripeptide His-Pro-Lys (assuming the peptide preceding Pro is in the *cis* conformation). (6)

2.2. How many angles of internal rotation are there in a lysine *side-chain*? (1)

2.3. Consider the structure of *acylphosphatase* projected onto the screen.

2.3.1. Identify the supersecondary structures that occur in the protein. (2)

2.3.2. Draw a topology diagram for acylphosphatase. (6)

QUESTION 3 **[7]**

The accessible surface area (ASA in Å^2) of small, globular (spherical) monomeric proteins varies with molecular weight *M* according to the relationship:

$$ASA = 1.11M^{2/3}$$

If the amino acid sequence of these proteins is placed on a polypeptide with an extended conformation, the ASA is higher, and is given by:

$$ASA_{\text{extended conformation}} = 1.45M$$

3.1. Explain why the ASA of a native protein varies with the 2/3rd power of *M*, whereas an extended polypeptide varies linearly with *M*. (2)

3.2. Derive a formula that relates the portion of the ASA in the extended chain that is buried when a protein adopts the native conformation, to the *M* of the protein? (2)

3.3. What is the expected buried surface area per residue for(in Å^2/residue) a monomeric protein of 100 residues (assume the average *M* per residue is 110 g/mol) ? (3)

QUESTION 4 **[15]**

Experimental methods and computational methods are used to determine and predict the structure of proteins. Write an essay on this topic, giving examples of the experimental and computational methods that are most often used for protein structure determination as well as discussing the advantages and disadvantages of each. (15)

<u>QUESTIONS 5 TO 9 SHOULD BE ANSWERED IN A DIFFERENT COLOUR ANSWER BOOK</u>

QUESTION 5 **[10]**

You have isolated from yeast a novel protein with enzymatic activity, of which you determined the amino acid and nucleotide sequence. Give the acronym and full name for the databases you could use to do the following and what you need to access the database or to perform the task:

5.1 Submit the nucleotide sequence to a database.

5.2 Identify homologues.

5.3 You have identified a mammalian homologue, serine palmitoyltransferase (**SPT**; EC 2.3.1.50). Where can you browse vertebrate genomes for SPT?

5.4 Gain knowledge of molecular functions and biological process in which the SPT is involved.

5.5 You solved the three dimensional structure of your yeast novel protein by X-ray crystallography. Where will you submit the structure to and what do you need to do so.

5.6 Analyse multiple sequence alignments to your protein of interest and draw phylogenetic trees to understand evolutionary relationships.

5.7 Obtain metabolic pathways in which SPT functions.

5.8 Investigate the protein structure classification of SPT.

5.9 Gain knowledge of SPT post-translational modifications, interaction with other molecules, and subcellular location.

5.10 Obtain enzyme classification for SPT and the reaction it catalyses.

QUESTION 6 **[10]**

Proteins of the immune system are examples of proteins with partners. Compare and contrast antibody and class II protein of the major histocompatibility complex (MHC) in terms of the following:

6.1 Domain structure (2)

6.2 Function (2)

6.3 Cell of origin and type of immunity (2)

6.4 Specificity and 'self', non-self' distinction (2)

6.5 Origin of molecular partner recognized (2)

QUESTION 7 **[10]**

7.1 Discuss the evolutionary relationships between proteins, by using the globin family of proteins in humans and horses, referring to, and defining homologues,

orthologues and paralogues. Give examples of these between and within these two species (use a phylogenetic tree). (5)

7.2 Comment on the measurability of homology and similarity and its implication for statements on homology. (2)

7.3 Compare and contrast divergent and convergent protein evolution by referring to evolution of structural features, sequence and function. Give an example for each. (2)

7.4 Which tool on the internet could you use to draw phylogenetics relationships between proteins and what input do you need? (1)

QUESTION 8 **[10]**

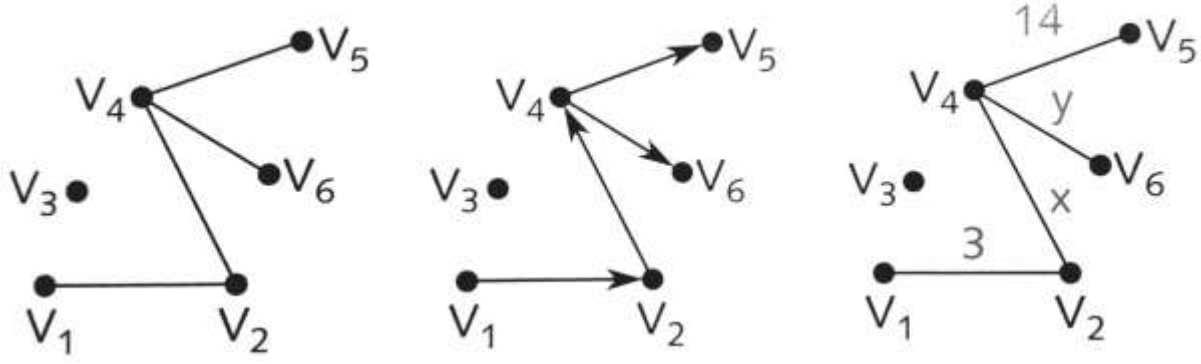
8.1 Describe three steps in a common scenario for protein folding. (3)

8.2 Define molten globule. (1)

8.3 Describe the operational cycle of the chaperonin system GroEL-GroES that catalyses protein folding. You may use a diagram or write out the answer in words. (6)

QUESTION 9 **[11]**

Graphs are abstract representations of networks, commonly used in systems biology. They show the connectivity of the network. Consider the following graph types:



(i) **(ii)** **(iii)**

9.1 Distinguish between graphs (i), (ii) and (iii) regarding labelling and direction. (3)

9.2 What is the density of connections of the graph in (i)? (2)

9.3 Would you consider the graphs shown above to represent small world networks? Motivate your answer by referring to the definition of a small world network. (2)

9.4 Biological networks need to be robust. What is the main source of robustness in biological networks? Discuss two ways in which the source mentioned above can lead to robustness. (4)

TOTAL: 100 MARKS