(*University of Choice*)

MASINDE MULIRO UNIVERSITY OF SCIENCE AND TECHNOLOGY (MMUST)

(MAIN CAMPUS)

UNIVERSITY EXAMINATIONS (MAIN EXAM) 2022/2023 ACADEMIC YEAR

THIRD YEAR SECOND SEMESTER EXAMINATIONS

FOR THE DIPLOMA OF MEDICAL BIOTECHNOLOGY

COURSE CODE: BBD 324

COURSE TITLE: PROTEOMICS AND GENOMICS

DATE: 24TH APRIL 2023 **TIME: 11.00 AM – 1.00PM**

INSTRUCTIONS TO CANDIDATES

This paper is divided into three sections, **A B** and **C,** carrying respectively: Multiple Choice Questions (**MCQs**), Short Answer Questions (**SAQs**) and Long Answer Questions (**LAQs**). **Answer all questions**. **DO NOT WRITE ON THE QUESTION PAPER.**

TIME: 2 Hours

MMUST observes ZERO tolerance to examination cheating

This Paper Consists of 4 Printed Pages. Please Turn Over

SECTION A: Multiple Choice Questions (20 Marks)

1. The collection of proteins that can be produced by a given species is:
A)   Considered that species' genetic complement.
B)   Correlated with the size of the organism.
C)   Called the proteome.
D)   All of these

2. A cDNA library:
A) Can also be called an expressed sequence tag (EST) library.
B) Consists of coding sequences from genes that are expressed.
C) Is specific to the set of conditions under which the original mRNA was generated.
D) All of these.

3.   A cluster analysis is the study of groups of genes that seem to be regulated together.
A)   True
B)   False

4. The two most common processes that lead to production of multiple functional proteins from the same DNA sequence are:
A)   RNA editing and alternative splicing.
B)   Protein folding and posttranslational covalent modifications.
C)   Alternative splicing and posttranslational covalent modifications.
D)   Posttranslational covalent modification and transcriptional regulation.

5. Which of the following statements regarding the proteome is the most correct?
A)   A large proportion of the proteome is expressed by each cell of a species.
B)   Levels of gene expression at the mRNA level generally correlate highly with levels of functional protein.
C)   The proteins produced by a specific cell depend on cell type and environmental conditions.
D)   All of the above.

6. If computers were not able to access the entire genomic sequence of an organism, which of the following techniques might allow determination of the gene sequence that encodes a particular protein?
A)   PCR amplification of related gene sequences.
B)   Hybridization of a genomic library with a degenerate probe.
C)   Production of synthetic peptides.
D)   All of these.

.7. Which of the following pieces of information would not be required for a computer program to determine exon/intron structure of a gene?
A)   A table correlating codons to amino acids.
B)   The nucleotide sequence of the mRNa.
C)   Splice site signals for the species under study.
D)   All of these pieces of information would be required.

8. You have cloned a new gene from your favorite species of experimental organism, which has had very few genes cloned so far. Which of the following techniques would you expect to provide information about the function of this gene?
A)   Comparison of regulatory sequences to other DNA sequences in this organism.
B)   Comparison of regulatory sequences to DNA sequences from other organisms.
C)   Comparison of the gene sequence to other DNA sequences in this organism.
D)   Comparison of the gene sequence to DNA sequences from other organisms..

9. Why might you want to search a database for a protein motif?
A)   A specific motif may impart a specific function to the molecule. You could then identify groups of proteins that may have similar functions.
B)   Presence of a specific motif in several proteins indicates that they are likely to be all from the same species.
C)   Absence of a specific motif from one of a pair of otherwise similar proteins indicates that they are produced by alternative splicing of the same gene.
D)   All of the above.
10. Which of these would not be an example of sequence element?
A)   A recognition site for binding of a particular transcription factor.
B)   A restriction endonuclease cut site.
C)   An open reading frame.
D)   A stop codon.
11. Homologous genes:
A)   Would be expected to have very similar sequences in related organisms.
B)   Would be expected to be more similar in distantly related organisms than in organisms that are closely related.
C)   May have become similar to each other by random mutation.
D)   All of these.
12. A multiple sequence alignment of related genes can identify amino acids required for protein function.
A)   True
B)   False
13. RNA does not contain a base of?
A) Adenine
B) Uracil
C) Thymine
D) Cytosine
14. A process which a protein assumes its functional shape is?
A. Denaturing
B. Folding
C. Synthesis
D. Hydrolysis
15. The study of the full complement of proteins expressed by a genome s called
A. Proteomics
B. Genomics
C. Protein formation
D. Proteome
16. The effect of protein on an entire organism is described in?
A. Phenotypic function
B. Cellular function
C. Molecular function
D. None of the above

17. Polymerase can be defined as _____
    A. an enzyme used to synthesize a new DNA or RNA strand on the basis of pre-existing strand or at times without a pre-existing strand
    B. an enzyme used for removal of nucleotides from the DNA or RNA strand
    C. an enzyme which can synthesize only a new DNA strand, not an RNA strand
    D. an enzyme which can synthesize either a new DNA or an RNA strand but only when a strand is there
18. The Laboratory Work is Done using the Computers and Computer-Generated Models Offline Generally is referred to as _____?

    A. Dry lab
    B. Wet lab
    C. Insilico
    D. All of the above

19. All are sequence alignment tools except

    A. Rasmol
    B. BLAST
    C. FASTA
    D. Clustal W

20. The science of collecting and analyzing complex biological data such as genetic codes is known as…?

    A. Bioinformatics
    B. Histology
    C. Microbiology
    D. Entomology

SECTION B: Short Answer Questions (40 Marks).
1. Describe the mode replication in eukaryotes [8 Marks].
2. State the key applications of karyotyping in cytogenetics and medicine [8 Marks].
3. Describe the posttranscriptional modifications [8 Marks].
4. Describe the structure of prokaryotic chromosome [8 Marks].
5. Discuss the main types of chromosomes [8 Marks].

SECTION C: Long Answer Questions (60 Marks).
1. Describe in detail gene expression in eukaryotes   [20 Marks].
2. Explain the concept and methodology of genomics [20 Marks].
3. Write notes on
a) Structural proteomics.
b) Computational approach to understand protein - protein interactions. [20 Marks].