Question Booklet Code

A

21MBL1S1LP

M.Sc. I Semester Degree Examination, April/May - 2023
Skill Enhancement Courses (SEC)
MICROBIOLOGY
MBSEC1 : Bioinformatics for Microbiology

Time : 1 Hour   Maximum Marks : 30

INSTRUCTIONS TO CANDIDATES

1. The Question Paper will be given in the form of a Question Booklet. There will be four/two/one versions of Question Booklets with Question Booklet Code viz. **A**, **B**, **C** & **D** / **A** & **B** / **A**.

2. The Question Booklet Serial Number is printed on the top right margin of the facing sheet. If your Question Booklet is un-numbered, please get it replaced by new Question Booklet with same Code.

3. Immediately after the commencement of the examination, the candidate should check that the Question Booklet supplied to him contains all the 30 questions in serial order. The Question Booklet does not have unprinted or torn or missing pages and if so he/she should bring it to the notice of the Invigilator and get it replaced by a complete booklet with same Code. This is most important.

4. A blank sheet of paper is attached to the Question Booklet. This may be used for Rough Work.

5. **Please read carefully all the instructions on the top of the Answer Sheet before marking your answers.**

6. Each question is provided with four choices **(A)**, **(B)**, **(C)** and **(D)** having one correct answer. Choose the correct answer and darken the bubble corresponding to the question number using **Black Ball-Point Pen** in the OMR Answer Sheet.

7. No candidate will be allowed to leave the examination hall till the end of the session and without handing over his/her Answer Sheet to the Invigilator.

8. Strict compliance of instructions is essential. Any malpractice or attempt to commit any kind of malpractice in the Examination will result in the disqualification of the candidate.

9. First fifteen minutes is provided to fill the general information of the Student. Eg. Student Name, Student ID, etc. in the OMR Answer Sheet.

10. Without the instruction of the Invigilator do not open the Question Paper Booklet Seal.

1. The first molecular biology server expasy was in the year _____.

(A) 1992   (B) 1993   (C) 1994   (D) 1995

2. Molecular simulation refers to :

(A) Computer programme used to study the movement of atoms and molecules

(B) Computer programme used for interaction of proteins with water molecule

(C) Wet lab methodology for validation

(D) (A) and (B) only

3. The term genome was adapted in _____.

(A) Johanson 1909   (B) Valter 1920

(C) Hans Winkler 1920   (D) Hooke 1922

4. Which of the following scientists created the first Bioinformatics database ?

(A) Dayhoff   (B) Pearson

(C) Richard Durbin   (D) Michael. J. Dunn

5. MALDI toff MS refers to :

(A) Matrix assisted laser desorption ionization-time of Flight mass spectrometry

(B) Matrix assisted laser desorption ionization-time of Flow mass spectrometry

(C) Matrix associated laser desorption ionization-time of Flow mass spectrometry

(D) None of the above

6. Which of the following is a protein sequence database ?

(A) DDBJ   (B) EMBL   (C) Genbank   (D) PIR

A

7. DNA Microarray is used to study :

(A) Protein expression   (B) Gene expression

(C) RNA expression   (D) All the above

8. DDBJ refers to :

(A) DNA data bank of Japan

(B) DNA data base of Jackson Wiley

(C) DNA data bank of European Union

(D) None of the above

9. What is the deposition of cDNA into the inert structure called ?

(A) DNA probes   (B) DNA polymerase

(C) DNA microarrays   (D) DNA fingerprinting

10. The first secondary database developed was :

(A) PRINTS   (B) PROSITE   (C) PDB   (D) PIR

11. Which of the following is a nucleotide sequence database ?

(A) EMBL   (B) SWISS PROT   (C) PROSITE   (D) TREMBL

12. Which of the following statements concerning the PILEUP Programme is false ?

(A) It is the MSA programme, which is part of the Genetics Computer Group's sequence analysis software suite.

(B) It has been owned by Oxford Communications since 1997 and is commonly used due to its popularity and availability.

(C) The Needleman-Wunsch dynamic programming approach is used to align the sequences pair by pair.

(D) It employs a method for MSA that is fundamentally opposite to CLUSTALW.

13. BLOSUM matrices are used for :

(A) Multiple sequence alignment   (B) Pairwise sequence alignment

(C) Phylogenetic analysis   (D) All of the above

A

14. Which of the following is / are secondary biological databases ?

(1) DDBJ   (2) PDB

(3) Swiss PROT/UNIPROT   (4) OMIM

(A) (1) and (4) only   (B) (1), (3) and (4) only

(C) (1), (2), (3) and (4)   (D) (2) only

15. In Genomics and proteomics, the data normalization will be done :

(A) To avoid the error and noise   (B) To remove normal data

(C) To remove sample data   (D) For adjustment of data

16. Primer 3 is used for :

(A) Designing of DNA probe   (B) Designing of primers

(C) Designing of oligomer   (D) All the above

17. Which of the following are not Bioinformatics Applications ?

(A) Data storage and management

(B) Understand the relationship between organisms

(C) Drug designing

(D) None of the above

18. Analysis or comparing entire genome of species ?

(A) Bioinformatics   (B) Genomics

(C) Proteomics   (D) Pharmacogenomics

19. Auto Doc is used to dock :

(A) Ligands   (B) Bacteria   (C) Peptides   (D) Virus

A

20. Which is not a protein database ?

(A) PRINTS   (B) Swissport   (C) MHCpep   (D) PubMed

21. Which of the following are not the applications of bioinformatics ?

(A) Drug designing

(B) Data storage and management

(C) Understand the relationships between organisms

(D) None of the above

22. Which of the following are similarity search tool ?

(A) Fasta   (B) RasMol   (C) EMBOSS   (D) PROSPECT

23. ClustalW refers to :

(A) Alignment tool   (B) Alignment tool for protein

(C) Multiple alignment tool   (D) All the above

24. In terms of protein structural comparison, which of the following statements is incorrect ?

(A) Finding distant protein homologs requires a comparative method.

(B) The conservation of protein structures is substantially higher than that of sequences.

(C) The conservation of protein structures is substantially lower than that of protein sequences.

(D) Proteins can have similar structures even though their sequences aren't identical

25. Tool used for restriction enzymes selection, which among the following is not correct ?

(A) NEB cutter v 2   (B) Nib cutter

(C) Web cutter   (D) Restriction mapper V 3

26. The algorithm used in alignment of DNA sequences is :

(A) BLAST   (B) Multialign

(C) Needleman Wunsch   (D) CLUSTAL

27. KEGG database is maintained from :

(A) Japan (B) Europe (C) USA (D) Russia

28. Size of the E.coli genome :

(A) 4.5 to 5.5 Mb (B) 2.5 to 3.5 Mb (C) 8.5 to 9.5 Mb (D) 18 to 20 Mb

29. Schrödinger is used for :

(A) Molecular modeling (B) Chemical bond studies

(C) Protein-ligand interaction (D) (A) and (C)

30. _____ is the NIH genetic sequence database, a collection of all publicly available DNA sequences.

(A) NCBI (B) GenBank (C) EXPASY (D) Both of (A) & (B)

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SPACE FOR ROUGH WORK

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