Roll No. ....

Question Booklet Number

O. M. R. Serial No.

M. Sc. (Microbiology) (Fourth Semester)
EXAMINATION, 2025-26
(Old Syllabus Effective From 2022)
(Only Back Paper Students)
MICROBIAL GENOMICS, PROTEOMICS AND BIOINFORMATICS

Paper Code							
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Questions Booklet Series

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Time : 1:30 Hours]

[*Maximum Marks : 75*

Instructions to the Examinee :

1. Do not open the booklet unless you are asked to do so.

2. The booklet contains 100 questions. Examinee is required to answer 75 questions in the OMR Answer-Sheet provided and not in the question booklet. All questions carry equal marks.

3. Examine the Booklet and the OMR Answer-Sheet very carefully before you proceed. Faulty question booklet due to missing or duplicate pages/questions or having any other discrepancy should be got immediately replaced.

(Remaining instructions on the last page)

परीक्षार्थियों के लिए निर्देश :

1. प्रश्न-पुस्तिका को तब तक न खोलें जब तक आपसे कहा न जाए।

2. प्रश्न-पुस्तिका में 100 प्रश्न हैं। परीक्षार्थी को 75 प्रश्नों को केवल दी गई OMR आन्सर-शीट पर ही हल करना है, प्रश्न-पुस्तिका पर नहीं। सभी प्रश्नों के अंक समान हैं।

3. प्रश्नों के उत्तर अंकित करने से पूर्व प्रश्न-पुस्तिका तथा OMR आन्सर-शीट को सावधानीपूर्वक देख लें। दोषपूर्ण प्रश्न-पुस्तिका जिसमें कुछ भाग छपने से छूट गए हों या प्रश्न एक से अधिक बार छप गए हों या उसमें किसी अन्य प्रकार की कमी हो, तो उसे तुरन्त बदल लें।

(शेष निर्देश अन्तिम पृष्ठ पर)

1. What is the primary focus of transcriptomics in bioinformatics ?
   (A) Studying gene expression patterns
   (B) Analyzing protein structures
   (C) Examining DNA sequences
   (D) Investing metabolic pathways

2. What type of data does bioinformatics primarily analyze ?
   (A) Ecological relationships
   (B) Chemical reactions in cells
   (C) Biological sequences and structures
   (D) Physical properties of organisms

3. Which bioinformatics technique predicts the three-dimensional structure of proteins ?
   (A) Sequence alignment
   (B) Homology modeling
   (C) Phylogenetic analysis
   (D) Polymerase Chain Reaction (PCR)

4. Full form of BLAST is :
   (A) Beginners Local Alignment Search Tool
   (B) Beginners Logical Alignment Search Tool
   (C) Basic Local Alignment Search Tool
   (D) Beginners Local Alignment Software Tool

5. Which of the following is a databank exclusively for proteins ?
   (A) EMBL
   (B) GenBank
   (C) DDBJ
   (D) PDB

6. Which of the following is not a sequence alignment tool ?
   (A) BLASTn
   (B) BLAST_X
   (C) RAMSOL
   (D) CLUSTAL

7. What is the purpose of a phylogenetic tree in bioinformatics ?
   (A) To visualize evolutionary relationship between organisms
   (B) To study ecological niche
   (C) To analyse metabolic pathways
   (D) To predict protein interactions

8. The lab work using computers and related web-based analysis is referred as :
   (A) *In vitro*
   (B) *In silico*
   (C) *In vivo*
   (D) All of the above

9. What is PDB ?

(A) Planning Database

(B) Protein Data Bank

(C) Producer Database

(D) None of the above

10. What is primary focus of metagenomics ?

(A) Study of individual genomes

(B) Investigating genetic material recovered directly from environmental samples

(C) Determining protein structures in a community

(D) Analyzing genetic mutation within a population

11. Which of the following statements is incorrect ?

(A) PDB is a worldwide central repository of structural information of biological macromolecules.

(B) PDB is currently managed by the Research Collaboratory for Structural Bioinformatics (RCSB).

(C) PDB website provides a number of services for structure submission and data searching and retrieval.

(D) PDB is currently managed by the NCBI.

12. 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

(C) May have become similar to each other by random mutation

(D) All of the above

13. How many potential open reading frames are present in a DNA sequence ?

(A) One

(B) Two

(C) Three

(D) Six

14. 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) RNA editing and base modification

15. 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 the above

16. Which of the following is untrue about Ab initio prediction ?

(A) The limited knowledge of protein folding forms the basis of ab initio prediction

(B) The ab initio prediction method attempts to produce all-atom protein models based on sequence information alone without the aid of known protein structures

(C) The ab initio prediction method attempts to produce all-atom protein models based on sequence information alone with some aid of known protein structures

(D) The perceived advantage of this method is that predictions are not restricted by known folds and that novel protein folds can be identified

17. Wallace rule is used to :

(A) Identify the active site of an enzyme

(B) Calculate the melting temperature of primers

(C) Predict the secondary structure of RNA

(D) Predict the primary structure of proteins

18. Which of the following is favored for primer design ?

(A) The melting temperature should be different for both the primers

(B) Primers should be long in length

(C) Primers should not be complementary to each other

(D) Matching should be of whole primer to the template

19. Which of the following is true about homology modeling ?

(A) Homology modeling predicts protein structures based on sequence homology with known structures

(B) It is also known as comparative modeling

(C) The principle behind it is that if two proteins share a high enough sequence similarity, they are likely to have very similar three-dimensional structures

(D) All of the above

20. What is the number of amino acids present in a Hemoglobin molecule, if each α chain and β chain contains 141 and 146 amino acids respectively in it ?

(A) 428

(B) 292

(C) 282

(D) 574

21. A library that contains at least one copy of all the sequences represented in the genome is :

(A) Chromosome - specific library

(B) Genomic library

(C) cDNA library

(D) Expression library

22. A DNA sequence is having two ends, 5' and 3'. Which of the following statements is correct regarding the nature of the ends ?

(A) The 5' end is having hydroxyl group

(B) The 5' end is having phosphate group

(C) The 3' end is having phosphate group

(D) Any group can be present at any end

23. β-pleated sheets are the examples of :

(A) Primary structure

(B) Secondary structure

(C) Tertiary structure

(D) Quaternary structure

24. Which among the following is not a technique to determine the structure of a protein ?

(A) X-ray crystallography

(B) NMR spectroscopy

(C) Cryoelectron microscopy

(D) Mass spectrometry

25. Which of the following is a structural database ?

(A) BLAST

(B) FASTA

(C) VAST

(D) PDB

26. A protein molecule contains amino acid residues and not amino acids because when a peptide bond is formed .... is lost.

(A) Nitrogen molecule

(B) Hydrogen molecule

(C) Oxygen molecule

(D) Water molecule

27. In metal chelate affinity chromatography, divalent cations such as Zn^{2+} or Ni^{+2} is attached on the electrophoretic matrix and it binds to :

(A) Trp tag
(B) Ala tag
(C) Gly tag
(D) His tag

28. Cutting DNA at each restriction sites creates multiple :

(A) Restriction enzymes
(B) Restriction fragments
(C) Genomic libraries
(D) Single stranded RNA

29. Which of the following method is used to map an unknown segment of DNA by breaking it into pieces and then identifying the locations of the breakpoints ?

(A) Southern blotting
(B) PCR
(C) Restriction mapping
(D) Western blotting

30. Which of the following is related to the primary structure of proteins ?

(A) Alpha helix
(B) Beta-sheets
(C) Loops
(D) Amino acid sequence

31. Which one of the following is used for sequencing of peptides ?

(A) X-ray crystallography
(B) Spectrophotometry
(C) NMR spectroscopy
(D) Mass spectrometry

32. Binary number system uses :

(A) 0 to 9
(B) 0 and 1
(C) A to F
(D) 0 to 7

33. FASTA format stores :

(A) Images
(B) Chemical structures
(C) Sequences
(D) Pathways

34. Which of the following represents the two-dimensional structure of proteins ?

(A) Quaternary
(B) Tertiary
(C) Secondary
(D) Primary

35. The structure formed by joining the amino acids by a peptide bond is called .... structure of a protein.

(A) Quaternary
(B) Tertiary
(C) Secondary
(D) Primary

36. Which of the following technique made it possible to shorten the laborious procedure of protein purification ?

(A) Precipitation

(B) Column chromatography

(C) Adsorption

(D) Affinity chromatography

37. Restriction endonucleases are enzymes :

(A) Capable of restricting protein synthesis

(B) Capable of cutting DNA molecules

(C) Capable of adding nucleotides to the 3'end of DNA

(D) Capable of joining DNA molecules

38. Which of the following affinity tag is an 8 amino acid residue peptide that can be a target of monoclonal antibody ?

(A) S-tag

(B) Myc tag

(C) His-tag

(D) Flag-peptide

39. Which mass analyzer is most frequently used with MALDI ?

(A) Magnetic sector

(B) Quadrupole

(C) Ion trap

(D) TOF

40. Which of the following is incorrect regarding pair wise sequence alignment ?

(A) The most fundamental process in this type of comparison is sequence alignment.

(B) It is an important first step toward structural and functional analysis of newly determined sequences.

(C) This is the process by which sequences are compared by searching for common character patterns and establishing residue-residue correspondence among related sequences.

(D) It is the process of aligning multiple sequences.

41. Which of the following is the first completed and published gene sequence ?

(A) ΦX174

(B) T4 phage

(C) M13 phage

(D) Lambda phage

42. The stepwise method for solving problems in computer science is called :

(A) Flowchart

(B) Algorithm

(C) Procedure

(D) Sequential design

43. The computational methodology that tries to find the best matching between two molecules, a receptor and ligand are called ?

(A) Molecular fitting
(B) Molecular matching
(C) Molecular docking
(D) Molecule affinity checking

44. The process of finding the relative location of genes on a chromosome is called :

(A) Gene tracking
(B) Genome walking
(C) Genome mapping
(D) Chromosome walking

45. Proteomics refers to the study of :

(A) Set of proteins in a specific region of the cell
(B) Biomolecules
(C) Set of proteins
(D) The entire set of expressed proteins in the cell

46. The bioinformatics tool, MEGA, stands for :

(A) Microbial Evolutionary Genomic Analysis
(B) Molecular Evolutionary Genetics Analysis
(C) Microbial Evolutionary Genomic Algorithm
(D) Molecular Evolutionary Genomic Application

47. 16S ribosomal RNA sequencing used to identify :

(A) Fungi
(B) Virus
(C) Bacteria
(D) Plant

48. RNA fold web server predicts the structure of :

(A) Secondary structure of RNA
(B) Secondary structure of protein
(C) Tertiary structure of ribonucleotide reductase
(D) Ribozymes

49. Which of the following is untrue about DNA sequencing ?

(A) It is now routinely carried out using the Sanger method.
(B) This doesn't make use of DNA polymerases.
(C) This involves the synthesis of DNA chains of varying length.
(D) The DNA synthesis is stopped by adding dideoxynucleotides.

50. Which of the following is not a commonly used NGS platform ?

(A) PacBio
(B) Illumina
(C) Oxford nanopore
(D) Sanger

51. The identification of drugs through the genomic study is called :

(A) Genomics
(B) Pharmacogenomics
(C) Pharmacogenetics
(D) Cheminformatics

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

(A) DNA probes
(B) DNA polymerase
(C) DNA microarrays
(D) DNA fingerprinting

53. Which of the following tools is used for the identification of motifs ?

(A) BLAST
(B) COPIA
(C) PROSPECT
(D) Pattern hunter

54. The human genome contains approximately :

(A) 6 billion base pairs
(B) 5 billion base pairs
(C) 3 billion base pairs
(D) 4 billion base pairs

55. Which of the following is an example of Homology and similarity tool ?

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

56. In splicing event :

(A) Introns are removed and exons are joined together
(B) Exons are removed and Introns are joined together
(C) Both exons and introns are removed
(D) None of the above

57. An operon is defined as :

(A) A related set of genes each having different promoters and are present differently.
(B) A set of genes which are present together but are controlled by different promoters.
(C) A set of genes which are present together and are controlled by the same promoter.
(D) A set of genes which are not present together but controlled by the same promoter.

58. The complete set of genetic information in an organism is called :

(A) Gene
(B) Genome
(C) Genomics
(D) Proteome

59. The *Escherichia coli* genome varies in size from :

(A) 1 to 2.5 Mb
(B) 4.5 to 5.5 Mb
(C) 45 to 55 Mb
(D) 450 to 550 Mb

60. Proteomics is crucial in identifying :

(A) mRNA molecules
(B) Protein biomarkers
(C) DNA mutations
(D) RNA transcripts

61. Which of the following information is obtained by microarray analysis ?

(A) Which genes are expressed at a particular stage of the cell cycle
(B) Which genes are expressed at a particular stage of developmental cycle of an organism
(C) Genes that respond to a given environmental signal to the same extent
(D) All of the above

62. Gene identification in prokaryotic organisms is simplified by their lacking.

(A) Exons
(B) Introns
(C) Coding segments
(D) Useful nucleotide sequences

63. Screening the predicted protein sequences against .... library confirms the prediction and expression of the gene.

(A) Expressed sequence tag (EST)
(B) Tags
(C) Palindromes
(D) Proteomes

64. Which of the following information sequence comparisons do not provide ?

(A) Gene relationships
(B) Function history
(C) Evolutionary history
(D) Gene locations

65. The use of genomics in cancer research helps in :

(A) General vaccination programs
(B) Targeted therapy development
(C) Radiation development
(D) Colorimetric testing

66. The dideoxy method of sequencing is also known as :

(A) Maxam and Gilbert method
(B) Sanger sequencing
(C) Pyrosequencing
(D) Autosequencing

67. What is the role of bioinformatics in next generation sequencing (NGS) data analysis ?

(A) Clonal amplification of DNA fragments
(B) Sequencing of DNA fragments
(C) Generation of DNA libraries
(D) Assembling sequencing reads and analyzing data

68. Which of the following is the first and the most important step in the polymerase chain reaction ?

(A) Annealing

(B) Primer extension

(C) Denaturation

(D) None of the above

69. DNA fingerprinting was developed by :

(A) Francis Crick

(B) Alec Jeffrey

(C) James Watson

(D) Nathan, Arber and Smith

70. Phage display is a potent and versatile method for studying :

(A) Protein-DNA interaction

(B) Post-translation modification

(C) Protein-protein interaction

(D) Protein-RNA intercation

71. Which of the following is the basic requirement of a PCR reaction ?

(A) Primers

(B) Template DNA

(C) A heat-stable DNA polymerase

(D) All of the above

72. Which of the following can be used to identify the genetic disorders ?

(A) Centrifugation

(B) PCR

(C) RIA

(D) Chromatography

73. The .... E-Value, the more significant the hit.

(A) Lower

(B) Higher

(C) Average

(D) Superior

74. PAM stands for :

(A) Percent Altered Mutation

(B) Point Accepted Mutation

(C) Percent Accepted Mutation

(D) Probable Altered Mutation

75. What does the term "gap penalty" refer to in sequence alignment ?

(A) The number of mismatches in the alignment

(B) The type of nucleotide presents in the sequence

(C) The length of the sequence

(D) The cost of introducing gaps in the alignment

76. MBP (Maltose binding protein) -tagged fusion proteins are eluted using :

(A) Sucrose

(B) Maltose

(C) Glucose

(D) Amylose

77. Which technique uses restriction enzyme digestion followed by agarose gel electrophoresis to generate a banding pattern for comparison to another sample processed in the same way ?

(A) qPCR

(B) RT-PCR

(C) RFLP

(D) 454 sequencing

78. FTP stands for :

(A) First transfer process

(B) File transfer protocol

(C) File transfer program

(D) None of the above

79. Which is the default scoring matrix used in BLAST ?

(A) PAM62

(B) BLOSUM 62

(C) BLOSUM 60

(D) BLOSUM 80

80. What is the role of bioinformatics in proteomics ?

(A) Predicting protein functions and pathways

(B) Sequencing analysis of proteins

(C) Analyzing protein structures

(D) All of the above

81. The alignment method suitable for finding out conserved patterns in DNA or protein sequence is :

(A) Multiple sequence alignment

(B) Pairwise alignment

(C) Global alignment

(D) Local alignment

82. Full form of HTML is :

(A) Hyper Text Markup Language

(B) Hyper Text Manipulation Language

(C) Hyper Text Managing Links

(D) Hyper Text Manipulating Links

83. GenBank, the nucleic acid sequence database is maintained by :

(A) Brookhaven laboratory

(B) DDBJ

(C) EMBL

(D) NCBI

84. Which one of the following tool compares protein sequence against translated nucleotide databases ?

(A) blastp

(B) blastx

(C) tblastn

(D) tblastx

85. Which one of the following tool compares translated nucleotide query sequence against protein databases ?

(A) blastp

(B) blastx

(C) blastn

(D) tblastx

86. Which one of the following tool compares protein sequences against protein databases ?

(A) blastp

(B) blastx

(C) blastn

(D) tblastx

87. Which one of the following tool compares nucleotide sequences against DNA databases ?

(A) blastn

(B) tblastx

(C) blastp

(D) tblastn

88. Which one of the following is a bibliographic database ?

(A) PubMed

(B) PIR

(C) Entrez

(D) EBI

89. Which one of the following is a primary protein database ?

(A) SWISS-PROT

(B) DDBJ

(C) EMBL

(D) NCBI

90. Which tool is used for multiple sequence alignment ?

(A) Phyre2

(B) BLASTn

(C) MEME

(D) CLUSTALW

91. Homology is a measure of :

(A) Sequence similarity

(B) Gene expression

(C) Protein function

(D) Species diversity

92. Which programming language is commonly used in bioinformatics ?

(A) HTML
(B) Java
(C) Python
(D) C++

93. Which of the following is a sequence alignment tool ?

(A) BLAST
(B) PRINT
(C) PROSITE
(D) PIR

94. Submission to GenBank are made using :

(A) Banklt and Sequin
(B) Banklt and Bankin
(C) Sequin and Bankin
(D) Entrez

95. CLUSTALW is a more recent version of CLUSTAL with the W standing for :

(A) Weakening
(B) Winding
(C) Weighting
(D) Wiping

96. Which of the following is the brain of the computer ?

(A) Central Processing Unit
(B) Memory
(C) Arithmetic and Logic unit
(D) Control unit

97. Which of the following is wrong about EMBL data library format ?

(A) EMBL maintains DNA and protein sequence databases
(B) As with GenBank entries, a large amount of information describing each sequence entry is given
(C) Sequence entry includes literature references and information about the function of the sequence, but not locations of mRNAs and coding regions
(D) Information is organized into fields, each with an identifier, shown as the first text on each line

98. The Smith-Waterman Algorithm is used for :

(A) Local alignment
(B) Global alignment
(C) Both (A) and (B)
(D) None of the above

99. The Needleman-Wunsch algorithm is widely used for optimal :

(A) Local alignment
(B) Global alignment
(C) Both (A) and (B)
(D) None of the above

100. The initiation of the FASTA format has .... symbol .

(A) >
(B) <
(C) /
(D) *

(Only for Rough Work)

4. Four alternative answers are mentioned for each question as—A, B, C & D in the booklet. The candidate has to choose the correct answer and mark the same in the OMR Answer-Sheet as per the direction :

Example :

Question :

Q. 1 Ⓐ ● Ⓒ Ⓓ
Q. 2 Ⓐ Ⓑ ● Ⓓ
Q. 3 Ⓐ ● Ⓒ Ⓓ

Illegible answers with cutting and over-writing or half filled circle will be cancelled.

5. Each question carries equal marks. Marks will be awarded according to the number of correct answers you have.
6. All answers are to be given on OMR Answer Sheet only. Answers given anywhere other than the place specified in the answer sheet will not be considered valid.
7. Before writing anything on the OMR Answer Sheet, all the instructions given in it should be read carefully.
8. After the completion of the examination candidates should leave the examination hall only after providing their OMR Answer Sheet to the invigilator. Candidate can carry their Question Booklet.
9. There will be no negative marking.
10. Rough work, if any, should be done on the blank pages provided for the purpose in the booklet.
11. To bring and use of log-book, calculator, pager and cellular phone in examination hall is prohibited.
12. In case of any difference found in English and Hindi version of the question, the English version of the question will be held authentic.

Impt. : On opening the question booklet, first check that all the pages of the question booklet are printed properly. If there is any discrepancy in the question Booklet, then after showing it to the invigilator, get another question Booklet of the same series.

4. प्रश्न-पुस्तिका में प्रत्येक प्रश्न के चार सम्भावित उत्तर—A, B, C एवं D हैं। परीक्षार्थी को उन चारों विकल्पों में से सही उत्तर छाँटना है। उत्तर को OMR आन्सर-शीट में सम्बन्धित प्रश्न संख्या में निम्न प्रकार भरना है :

उदाहरण :

प्रश्न :

प्रश्न 1 Ⓐ ● Ⓒ Ⓓ
प्रश्न 2 Ⓐ Ⓑ ● Ⓓ
प्रश्न 3 Ⓐ ● Ⓒ Ⓓ

अपठनीय उत्तर या ऐसे उत्तर जिन्हें काटा या बदला गया है, या गोले में आधा भरकर दिया गया, उन्हें निरस्त कर दिया जाएगा।

5. प्रत्येक प्रश्न के अंक समान हैं। आपके जितने उत्तर सही होंगे, उन्हीं के अनुसार अंक प्रदान किये जायेंगे।
6. सभी उत्तर केवल ओ. एम. आर. उत्तर-पत्रक (OMR Answer Sheet) पर ही दिये जाने हैं। उत्तर-पत्रक में निर्धारित स्थान के अलावा अन्यत्र कहीं पर दिया गया उत्तर मान्य नहीं होगा।
7. ओ. एम. आर. उत्तर-पत्रक (OMR Answer Sheet) पर कुछ भी लिखने से पूर्व उसमें दिये गये सभी अनुदेशों को सावधानीपूर्वक पढ़ लिया जाये।
8. परीक्षा समाप्ति के उपरान्त परीक्षार्थी कक्ष निरीक्षक को अपनी OMR Answer Sheet उपलब्ध कराने के बाद ही परीक्षा कक्ष से प्रस्थान करें। परीक्षार्थी अपने साथ प्रश्न-पुस्तिका ले जा सकते हैं।
9. निगेटिव मार्किंग नहीं है।
10. कोई भी रफ कार्य, प्रश्न-पुस्तिका के अन्त में, रफ-कार्य के लिए दिए खाली पेज पर ही किया जाना चाहिए।
11. परीक्षा-कक्ष में लॉग-बुक, कैलकुलेटर, पेजर तथा सेल्युलर फोन ले जाना तथा उसका उपयोग करना वर्जित है।
12. प्रश्न के हिन्दी एवं अंग्रेजी रूपान्तरण में भिन्नता होने की दशा में प्रश्न का अंग्रेजी रूपान्तरण ही मान्य होगा।

महत्वपूर्ण : प्रश्नपुस्तिका खोलने पर प्रथमतः जाँच कर देख लें कि प्रश्न-पुस्तिका के सभी पृष्ठ भलीभाँति छपे हुए हैं। यदि प्रश्नपुस्तिका में कोई कमी हो, तो कक्षनिरीक्षक को दिखाकर उसी सिरीज की दूसरी प्रश्न-पुस्तिका प्राप्त कर लें।