Roll No. .....

Question Booklet Number

O. M. R. Serial No.

M. Sc. (Biochemistry) (Fourth Semester) EXAMINATION, 2025-26

(Old Syllabus Effective from 2022)

(Only Back Paper Students)

OMICS TECHNOLOGIES

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.

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।

(Remaining instructions on the last page) **(शेष निर्देश अन्तिम पृष्ठ पर)**

(Only for Rough Work)

1. Comparative genomics between crop varieties helps in :

(A) Estimating crop weight

(B) Enhancing mechanical threshing

(C) Increasing chlorophyll levels only

(D) Identifying genes for stress resistance

2. Nutrigenomics combines knowledge from :

(A) Metabolomics and plant breeding

(B) Genomics and nutrition

(C) Transcriptomics and fertilizers

(D) Hydrology and proteomics

3. Future agriculture could greatly benefit from :

(A) Soil mineral removal

(B) Increased manual labor

(C) Traditional breeding only

(D) Genome-edited crops for climate resilience

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

(A) DNA probes

(B) DNA polymerase

(C) DNA microarrays

(D) DNA fingerprinting

5. 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

6. In Sanger sequencing, the chain termination is caused by :

(A) ddNTPs

(B) dNTPs

(C) RNA primers

(D) Restriction enzymes

7. In Sanger sequencing, ddNTPs differ from dNTPs by lacking :

(A) 5′ phosphate group

(B) 3′ hydroxyl group

(C) Nitrogenous base

(D) Deoxyribose sugar

8. Maxam-Gilbert sequencing is based on :

(A) Chain elongation

(B) PCR amplification

(C) Fluorescent dye labeling

(D) DNA chemical cleavage

9. Maxam-Gilbert sequencing mainly uses :
   (A) ddNTPs
   (B) Radioactive labeling
   (C) Fluorescent dyes
   (D) Pyrophosphate detection

10. Pyrosequencing detects :
   (A) Radioactive signals
   (B) Electrical current
   (C) Light emission
   (D) Heat production

11. Which enzyme is responsible for converting pyrophosphate to ATP in pyrosequencing ?
   (A) DNA polymerase
   (B) Luciferase
   (C) Sulfurylase
   (D) Kinase

12. A key limitation of pyrosequencing is :
   (A) Limited read length
   (B) High cost per base
   (C) Very slow reaction
   (D) Cannot detect AT bases

13. Shotgun sequencing is primarily used for :
   (A) Short, known DNA sequences
   (B) Targeted DNA sequencing
   (C) Whole genome sequencing
   (D) Single protein sequencing

14. A major requirement after shotgun sequencing is :
   (A) DNA hybridization
   (B) Sequence assembly
   (C) RNA extraction
   (D) Sanger sequencing

15. What is a major advantage of shotgun sequencing ?
   (A) Requires prior sequence knowledge
   (B) Only useful for small DNA molecules
   (C) Highly error-prone
   (D) Fast and suitable for large genomes

16. A major strength of Illumina sequencing is :
   (A) Extremely long reads (up to 10 million bp)
   (B) Very low error rates and high throughput
   (C) Use of radioactive materials
   (D) Manual data analysis

17. In Illumina sequencing, DNA fragments are attached to :
   (A) Agar plates
   (B) Beads in oil droplets
   (C) A sequencing flow cell surface
   (D) Magnetic beads

18. Illumina sequencing detects nucleotides via :

(A) Radioactive signals

(B) Electrical current

(C) Fluorescent dyes

(D) Mass spectrometry

19. Which method is not considered Next-Generation Sequencing (NGS) ?

(A) Illumina sequencing

(B) Pyrosequencing

(C) Sanger sequencing

(D) Ion Torrent sequencing

20. In Illumina sequencing, a "bridge amplification" refers to :

(A) Amplifying DNA on a solid surface

(B) Connecting different DNA strands

(C) Copying RNA

(D) Restriction fragment mapping

21. Which sequencing platform is best suited for large-scale human genome projects today ?

(A) Maxam-Gilbert sequencing

(B) Sanger sequencing

(C) Illumina sequencing

(D) Southern blotting

22. In whole-genome shotgun sequencing, what is the primary method used to assemble the sequence ?

(A) Blotting

(B) Sequence alignment algorithms

(C) Amplification

(D) Restriction digestion

23. Which of the following best describes "scaffolding" in genome assembly ?

(A) Aligning reads to a reference genome

(B) Annotating genes

(C) Deleting low-quality reads

(D) Linking contigs together using paired-end information

24. What is a "contig" in genome sequencing ?

(A) A database of annotated genes

(B) A continuous sequence without gaps

(C) A restriction map of a chromosome

(D) A functional gene array

25. Which tool is widely used for de novo genome assembly ?

(A) BLAST

(B) BWA

(C) SPAdes

(D) FastQC

26. Which technique uses fluorescent probes to map physical locations of genes on chromosomes ?

(A) RFLP

(B) PCR

(C) FISH

(D) RAPD

27. A physical map measures distances between DNA elements in :

(A) Centibases

(B) Base pairs

(C) Kilodaltons

(D) Megahertz

28. Which vector is commonly used for creating very large-insert genomic libraries ?

(A) Plasmid

(B) Cosmid

(C) BAC

(D) Phagemid

29. A genomic library ideally contains :

(A) Random fragments covering the entire genome

(B) Only coding sequences

(C) Only non-coding regions

(D) Chromosome-specific DNA only

30. Which step comes first in creating a genomic library ?

(A) PCR amplification

(B) Cloning into vectors

(C) Screening the library

(D) Fragmenting the genome

31. The term "coverage" in a genomic library refers to :

(A) Number of unique genes

(B) Number of times the genome is represented

(C) Number of exons

(D) Number of vectors used

32. Which property is MOST important for a vector used in a genomic library ?

(A) Small insert size

(B) Ability to replicate independently

(C) High transformation efficiency for large inserts

(D) Antibiotic resistance

33. Which assembly strategy reconstructs genome sequences without a reference ?

(A) Reference-guided assembly

(B) Hybrid assembly

(C) De novo assembly

(D) Alignment assembly

34. In De Bruijn graph-based assembly, nodes represent :

(A) Genes

(B) k-mers

(C) Exons

(D) Mutations

35. What does "ab initio" gene prediction rely on ?

(A) Experimental RNA data

(B) Statistical models and gene structure rules

(C) Homology to known proteins

(D) DNA microarrays

36. The functional annotation of a gene typically involves :

(A) Predicting the protein it encodes

(B) Determining its exact chromosomal position

(C) Mapping its restriction sites

(D) All of the above

37. Which database provides functional annotation for many organisms' genomes ?

(A) UniProt

(B) NCBI SRA

(C) KEGG

(D) GEO

38. Which term describes non-functional sequences in the genome resembling functional genes ?

(A) Orthologs

(B) Pseudogenes

(C) Paralogs

(D) Haplotypes

39. "Orthologous genes" are :

(A) Duplicated within the same genome

(B) Genes sharing identical promoters

(C) Unrelated genes with similar function

(D) Homologous genes in different species

40. Comparative genomics primarily helps in :

(A) Building protein structures

(B) Identifying conserved sequences across species

(C) Producing synthetic genomes

(D) Increasing mutation rates

41. Which technique involves silencing a gene to study its function ?

(A) RNA interference

(B) PCR

(C) CRISPR amplification

(D) RFLP

42. The "transcriptome" represents :

(A) All DNA in a genome

(B) All non-coding RNAs

(C) All proteins encoded by a genome

(D) All RNA transcripts at a given time

43. Which technique provides a comprehensive analysis of all RNA molecules in a cell ?

(A) PCR

(B) RNA-Seq

(C) Southern blot

(D) FISH

44. What is the first step in RNA-Seq library preparation ?

(A) cDNA synthesis

(B) RNA fragmentation

(C) Reverse transcription

(D) RNA extraction

45. What is "differential gene expression" analysis ?

(A) Identifying proteins in the cell

(B) Comparing expression levels between different conditions

(C) Sequencing DNA

(D) Deleting genes one by one

46. In forward genetics, the workflow begins with :

(A) Known gene → mutant phenotype

(B) Random mutant → identifying the gene

(C) Sequencing known genes

(D) Silencing a target gene

47. CRISPR-Cas9 can be used to :

(A) Knock in mutations

(B) Knock out genes

(C) Edit specific sequences

(D) All of the above

48. RNA interference primarily functions by :

(A) Activating transcription

(B) Degrading target mRNA

(C) Repairing DNA

(D) Producing new proteins

49. siRNAs guide the RNA-induced silencing complex (RISC) to :

(A) Inhibit DNA replication

(B) Promote translation

(C) Degrade complementary mRNA

(D) Activate splicing

50. Which organism was RNA interference first discovered in ?

(A) *Arabidopsis thaliana*

(B) *Drosophila melanogaster*

(C) *Caenorhabditis elegans*

(D) *Homo sapiens*

51. Proteomics mainly deals with the study of :

(A) DNA

(B) RNA

(C) Proteins

(D) Carbohydrates

52. Proteomics does not typically involve :

(A) Protein identification

(B) Protein quantification

(C) DNA cloning

(D) Study of protein modifications

53. Yeast two-hybrid assay is used to detect :

(A) Protein-DNA interactions

(B) Protein-protein interactions

(C) DNA replication

(D) RNA transcription

54. A common reporter gene used in yeast two-hybrid screening is :

(A) GFP

(B) LacZ

(C) Luciferase

(D) All of the above

55. In yeast two-hybrid, the bait protein is fused with :

(A) Activation domain

(B) DNA-binding domain

(C) Reporter gene

(D) Ligand domain

56. SDS-PAGE separates proteins based on :

(A) Shape

(B) Charge

(C) Size

(D) pH

57. The gel used in SDS-PAGE is made from :

(A) Agarose

(B) Cellulose

(C) Polyacrylamide

(D) Starch

58. Which dye is used for tracking during electrophoresis ?

(A) Coomassie Brilliant Blue

(B) Bromophenol Blue

(C) Ethidium Bromide

(D) DAPI

59. A common stain for proteins in SDS-PAGE gels is :

(A) Ethidium bromide

(B) Alcian Blue

(C) Methylene Blue

(D) Coomassie Brilliant Blue

60. Mass spectrometry measures :

(A) Protein solubility

(B) Protein mass-to-charge ratio

(C) Protein size only

(D) Protein color

61. In MALDI, proteins are :

(A) Crystallized

(B) Ionized with a laser

(C) Renatured

(D) Ligated

62. TOF in mass spectrometry stands for :

(A) Transfer of Force

(B) Total Organic Fraction

(C) Time of Flight

(D) Thermal Optical Force

63. ESI stands for :

(A) Electron Shock Ionization

(B) Energy Spread Isolation

(C) Electromagnetic Spectrum Ionization

(D) Electrospray Ionization

64. Which is a common detector in mass spectrometry ?

(A) Photomultiplier tube

(B) Electron multiplier

(C) Microchannel plate

(D) Both (B) and (C)

65. MS/MS analysis involves :

(A) Single ion analysis

(B) Fragmentation of ions

(C) Neutral atom detection

(D) Direct fluorescence reading

66. TAP tagging is used for :

(A) Protein purification

(B) Protein sequencing

(C) RNA extraction

(D) DNA editing

67. TAP stands for :

(A) Tandem Affinity Purification

(B) Target Affinity Purification

(C) Total Absorption Process

(D) Two-phase Affinity Purification

68. TAP tag includes :

(A) His-tag

(B) Protein A and Calmodulin-binding domain

(C) Only FLAG tag

(D) GST and Myc tag

69. TAP tagging is particularly useful for studying :

(A) RNA splicing

(B) DNA arrays

(C) Metabolites

(D) Protein complexes

70. MS/MS sequencing determines :

(A) RNA structure

(B) Peptide sequence

(C) DNA structure

(D) Cell membrane composition

71. Tandem affinity purification generally yields :

(A) Highly pure proteins

(B) Denatured proteins

(C) Low amounts of proteins

(D) Fragmented proteins

72. The purpose of using two affinity steps in TAP is :

(A) Faster purification

(B) Greater specificity

(C) Protein fragmentation

(D) Denaturation

73. Trypsin cleaves at :

(A) Arginine and Lysine residues

(B) Tyrosine residues

(C) Histidine residues

(D) Cysteine residues

74. In MALDI, what is mixed with the sample ?

(A) Buffer

(B) Matrix

(C) Enzyme

(D) Detergent

75. Which proteomics approach is used to compare protein expression under different conditions ?

(A) Structural proteomics

(B) Functional proteomics

(C) Comparative proteomics

(D) Genomics

76. In yeast two-hybrid, non-interacting proteins :

(A) Activate the reporter gene

(B) Do not activate the reporter gene

(C) Bind together strongly

(D) Cause cell death

77. Which of the following is a databank exclusively for proteins ?

(A) EMBL

(B) GenBank

(C) DDBJ

(D) PDB

78. Metabolomics is the comprehensive study of :

(A) DNA

(B) RNA

(C) Proteins

(D) Metabolites

79. Secondary metabolites often function as :

(A) Structural proteins

(B) Enzyme cofactors

(C) Defense compounds

(D) Ribosomal RNAs

80. Which technique is most commonly used in metabolomics ?

(A) PCR and RNAseq

(B) Mass spectrometry and NMR

(C) Northern and Southern blot

(D) DNA and peptide sequencing

81. GC-MS combines :

(A) Genomic cloning with mass spectrometry

(B) Gas chromatography with mass spectrometry

(C) Gel electrophoresis with MS

(D) Gene clipping and MS

82. A common limitation of GC-MS is :

(A) It can only analyze volatile compounds

(B) It requires DNA probes

(C) It cannot detect metabolites

(D) It degrades proteins

83. In metabolomics, untargeted analysis refers to :

(A) Measuring specific metabolites

(B) Isolation of primary metabolites

(C) Enrichment of metabolites

(D) Global profiling of all metabolites

84. The first step in a typical metabolomics workflow is :

(A) Data analysis

(B) Metabolite extraction

(C) Solvent selection

(D) None of the above

85. Identify the metabolome database :

(A) HMDB

(B) GenBank

(C) PDB

(D) UniProt

86. Nutrigenomics aims to understand :

(A) How diet affects gene expression

(B) How genes replicate

(C) How proteins degrade

(D) How metabolites oxidize

87. Nutrigenomics can help in :

(A) Treating genetic disorders

(B) Designing personalized diets

(C) Studying bacterial infections

(D) Enhancing gel electrophoresis

88. CRISPR-Cas9 is a tool primarily used for :

(A) Protein purification

(B) Genome editing

(C) Metabolite profiling

(D) Carbohydrate analysis

89. Genomic selection in agriculture mainly aims to :

(A) Improve disease resistance in crops

(B) Increase mechanical harvesting

(C) Enhance photosynthesis visualization

(D) Improve pesticide spraying techniques

90. Gene therapy in human health focuses on :

(A) Protein degradation

(B) Correcting defective genes

(C) Metabolite storage

(D) Removing blood clots

91. Genomic studies have contributed to which infectious disease breakthrough ?

(A) Vaccine for tetanus

(B) Discovery of penicillin

(C) Synthesis of insulin

(D) Treatment for COVID-19

92. In agriculture, “Golden Rice” was developed through :

(A) Proteomics

(B) Genomic engineering

(C) Enzyme kinetics

(D) Environmental DNA sampling

93. Proteomics aids in understanding :

(A) RNA secondary structure

(B) DNA folding patterns

(C) Protein functions in diseases

(D) Lipid biosynthesis only

94. Proteomics can assist in agriculture by :

(A) Enhancing crop flavor only

(B) Promoting only GMO crops

(C) Increasing polyploidy

(D) Identifying proteins related to drought resistance

95. In precision medicine, proteomics allows :

(A) Disease gene identification

(B) Customized drug therapies based on patient proteins

(C) Plant growth optimization

(D) Atmospheric studies

96. Genome sequencing primarily aims to determine the :

(A) Protein structure

(B) DNA sequence

(C) RNA expression level

(D) Gene regulation pattern

97. Which of the following is a high-throughput sequencing technique ?

(A) Sanger sequencing

(B) Illumina sequencing

(C) Maxam-Gilbert sequencing

(D) All of the above

98. Which of the following methods involves random breaking of DNA into small fragments ?

(A) Sanger sequencing

(B) PCR

(C) Maxam-Gilbert sequencing

(D) Shotgun sequencing

99. Next-Generation Sequencing (NGS) platforms are characterized by :

(A) Manual reading of sequences

(B) Low throughput

(C) Parallel sequencing of millions of fragments

(D) Sequencing one DNA fragment at a time

100. Sanger sequencing is also known as :

(A) Chain termination method

(B) Chemical cleavage method

(C) Pyrosequencing

(D) Hybridization sequencing

(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 (A) ● (C) (D)
Q. 2 (A) (B) ● (D)
Q. 3 (A) ● (C) (D)

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 (A) ● (C) (D)
प्रश्न 2 (A) (B) ● (D)
प्रश्न 3 (A) ● (C) (D)

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।