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O.M.R. Serial No. | | | | | | | | |

Question Booklet Number

B.Sc. (SEM.-VI) (NEP) (SUPPLE.) EXAMINATION, 2024-25

BIOTECHNOLOGY

(Genomics and Proteomics)

(BBT-6002)

Paper Code							
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Question Booklet Series

A

Time : 1 : 30 Hours **Max. 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.
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 :

(Remaining instructions on 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, उसे तुरन्त बदल लें।
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 उत्तर-पत्रक में सम्बन्धित प्रश्न संख्या में निम्न प्रकार भरना है :

(शेष निर्देश अन्तिम पृष्ठ पर)

1. What is the distinguishing feature of Maxam-Gilbert sequencing?
   (A) Uses chemical cleavage of DNA at specific bases
   (B) Uses chain termination by dideoxynucleotides
   (C) Sequencing by synthesis method
   (D) Sequencing via fluorescent dye labeling

2. Which radioactive isotope is commonly used to label DNA in Maxam-Gilbert sequencing?
   (A) Carbon-14
   (B) Phosphorus-32
   (C) Sulfur-35
   (D) Iodine-131

3. What is the purpose of using chemicals like dimethyl sulfate and hydrazine in Maxam-Gilbert sequencing?
   (A) To fluorescently tag nucleotides
   (B) To amplify DNA segments
   (C) To inhibit DNA polymerase
   (D) To cleave DNA at specific bases

4. In Sanger sequencing, what terminates the DNA chain elongation?
   (A) Normal dNTPs
   (B) DNA ligase
   (C) Dideoxynucleotides (ddNTPs)
   (D) RNA primers

5. Which enzyme catalyzes DNA synthesis in Sanger sequencing?
   (A) DNA ligase
   (B) DNA polymerase I (Klenow fragment)
   (C) RNA polymerase
   (D) Reverse transcriptase

6. Pyrosequencing primarily detects which molecule to infer DNA sequences?
   (A) Fluorescent dyes
   (B) Radioactive decay
   (C) Optical density
   (D) Pyrophosphate release

7. What light-producing enzyme is used in pyrosequencing?
   (A) Luciferase
   (B) ATP synthase
   (C) DNA polymerase
   (D) Amylase

8. Shotgun sequencing involves :
   (A) Using chemical cleavage for sequencing
   (B) Sequence by synthesis using fluorescently labeled nucleotides
   (C) Sequencing DNA protected by proteins
   (D) Sequencing short random DNA fragments and assembling them

9. Hierarchical sequencing is characterized by:

(A) Cloning large DNA fragments and sequencing sub-fragments methodically

(B) Random fragment sequencing

(C) Using only maxam-Gilbert method

(D) Sequencing RNA instead of DNA

10. Which software is commonly used in genome assembly?

(A) BLAST

(B) CAP3

(C) ClustalW

(D) GeneMapper

11. Pyrosequencing detects DNA synthesis in real-time by measuring:

(A) Incorporation of nucleotides by fluorescent tagging

(B) Radioactive labeling decay

(C) DNA melting curve

(D) Release of pyrophosphate and subsequent light emission

12. Which chemical is used to cleave DNA at guanine bases in Maxam-Gilbert sequencing?

(A) Piperidine

(B) Hydrazine

(C) Dimethyl sulfate

(D) Hydroxylamine

13. The primary disadvantage of Maxam-Gilbert sequencing is:

(A) Radioactive waste and hazardous chemicals

(B) High throughput and automation

(C) Low cost and simplicity

(D) Requirement of cloning DNA

14. Which of the following is an automated DNA sequencing technique?

(A) Sanger sequencing with fluorescent ddNTPs

(B) Maxam-Gilbert chemical sequencing

(C) Manual gel electrophoresis only

(D) Northern blotting

15. What is the role of a primer in Sanger sequencing?

(A) Terminate DNA synthesis

(B) Label DNA fragments for detection

(C) Bind specifically to the DNA template to initiate replication

(D) Cleave DNA strands at specific sites

16. How many different dideoxynucleotides are used in Sanger sequencing to terminate synthesis?

(A) Two

(B) Four

(C) One

(D) Eight

17. Which of the following is not used in pyrosequencing?

(A) DNA polymerase

(B) Luciferase

(C) Pyrophosphatase

(D) Taq polymerase

18. In shotgun sequencing, genome assembly relies heavily on:

(A) Overlapping sequences (contigs) to reconstruct the entire genome

(B) Chemical cleavage patterns

(C) Protein binding profiles

(D) RNA transcription data

19. Electrophoretic separation in Maxam-Gilbert sequencing is used to:

(A) Label DNA fragments with fluorescence

(B) Amplify DNA regions

(C) Bind primers to DNA templates

(D) Sort DNA fragments by size for sequence interpretation

20. What is a major advantage of hierarchical sequencing over shotgun sequencing?

(A) More controlled assembly by ordering large clones first

(B) Faster but less accurate

(C) Uses chemical cleavage methods only

(D) Requires no computational tools

21. Which nucleotide is missing a hydroxyl group at the 3' position in dideoxynucleotides?

(A) Adenine

(B) Thymine

(C) Both are missing 3' OH in dideoxynucleotides

(D) Cytosine

22. What is the main reason pyrosequencing produces light during nucleotide incorporation?

(A) ATP is converted to light directly

(B) Sequencing dye emits light

(C) Luciferase catalyzes light-emitting reaction using ATP produced from pyrophosphate

(D) DNA polymerase fluoresces on nucleotide addition

23. The first genome to be fully sequenced using shotgun sequencing was:

(A) Human genome

(B) Bacteriophage PhiX174

(C) Yeast genome

(D) Rice genome

24. Which part of DNA acts as the starting point for genomic library construction in hierarchical sequencing?

(A) Random DNA fragments

(B) Large clone inserts like BACs or YACs

(C) Only exons of genes

(D) Protein coding sequences

25. What is the main limitation of Sanger sequencing compared to NGS methods?

(A) Lower read length accuracy

(B) Higher throughput

(C) More time-consuming and lower throughput

(D) Uses chemical cleavage

26. Which of the following is a web-based server for genome analysis?

(A) BLAST

(B) CLUSTALW

(C) FASTA

(D) ENSEMBL

27. UCSC Genome Browser is used to:

(A) Analyze protein sequences

(B) Perform DNA synthesis

(C) Clone DNA fragments

(D) Visualize genomic data and annotation tracks

28. NCBI Genome database mainly provides:

(A) Protein 3D structures

(B) Whole genome sequences and annotations

(C) Microarray expression data

(D) Chromosomal metaphase images

29. VISTA is a tool used for :

(A) Comparative genomics and alignment of genomic sequences

(B) Protein structure prediction

(C) RNA sequencing data analysis

(D) Phylogenetic tree construction

30. Which organism's genome is commonly used as a model for human genome studies?

(A) *Saccharomyces cerevisiae*

(B) *Drosophila melanogaster*

(C) *Mus musculus*

(D) All of the above

31. Genome browsers facilitate the visualization of :

(A) DNA microarray spots

(B) Electron microscopy images

(C) Protein gel electrophoresis results

(D) Functional annotations on genome assemblies

32. ENSEMBL stores genome data primarily from :

(A) Bacterial genomes only

(B) Vertebrate genomes including human

(C) Viral genomes only

(D) Mitochondrial genomes only

33. Which tool helps in aligning multiple genomic sequences for comparative studies?

(A) VISTA

(B) BLAST

(C) FASTQ

(D) MAQ

34. UCSC Genome Browser displays information as :

(A) Text files only

(B) Three-dimensional protein models

(C) Raw sequence chromatograms

(D) Graphical tracks aligned to chromosomes

35. What is a primary challenge in genome data management?

(A) Genome annotation errors

(B) Sequencing cost only

(C) Large data volume and storage

(D) Lack of sequencing methods

36. What type of map is the 'physical map' in genomics?

(A) Chromosomal landmarks visualized microscopically

(B) DNA fragment-based map with measured distances

(C) Protein interaction maps

(D) Metabolic pathway map

37. Which database is part of NCBI that contains genome sequences?

(A) GenBank

(B) UniProt

(C) PDB

(D) RefSeq

38. Which software is used for genome assembly from sequencing data?

(A) CAP3

(B) BLAST

(C) PubMed

(D) RASMOL

39. ENSEMBL genome browser is developed by :

(A) NCBI

(B) UCSC

(C) JGI

(D) EMBL-EBI

40. The UCSC Genome Browser can display :

(A) Transcriptome and regulatory elements

(B) Only protein sequences

(C) Only bacterial genomes

(D) Only mitochondrial DNA

41. What is the advantage of web-based genome browsers?

(A) Require no internet access

(B) Provide graphical visualization and annotation access anywhere

(C) Only downloadable offline tools

(D) Only for DNA sequencing

42. Which of the following is not a feature available at ENSEMBL?

(A) Gene prediction

(B) Comparative genomics

(C) Protein 3D structure prediction

(D) Variation data browser

43. What kind of data does the UCSC genome browser support integration of?

(A) DNA sequences only

(B) Protein crystal structures only

(C) Gene expression, epigenetics, variation and regulatory elements

(D) Viral genome sequences only

44. What is a key use of model organism genomes?

(A) Studying human diseases and gene function

(B) Industrial fermentation

(C) Plant breeding only

(D) Synthetic biology exclusively

45. What does VISTA primarily focus on displaying?

(A) Variations in single nucleotides

(B) Sequence conservation across multiple species

(C) Protein motifs

(D) Metabolic pathways

46. Which of the following terms describes web platforms like NCBI or UCSC Genome Browser?

(A) Offline genome analysis tools

(B) Protein purification software

(C) DNA sequencing machines

(D) Integrated genome databases and browsers

47. Managing genome data typically requires:

(A) Only wet-lab experiments

(B) High-performance computing and storage resources

(C) No computational skills

(D) Only manual sequence analysis

48. What major format is used for storing genome sequences?

(A) PDF

(B) CSV

(C) TIFF

(D) FASTA

49. Which database provides annotated human genome data?

(A) NCBI RefSeq

(B) Protein Data Bank

(C) KEGG

(D) Reactome

50. UCSC Genome Browser date and feature tracks can be customized for :

(A) Specific tissue types

(B) Different species and genome builds

(C) Only bacterial genomes

(D) None of the above

51. The linear sequence of amino acids in a polypeptide refers to which protein structure?

(A) Quaternary

(B) Tertiary

(C) Secondary

(D) Primary

52. What is the main bond responsible for holding together the primary structure of proteins?

(A) Disulfide bond

(B) Hydrogen bond

(C) Van der Waals interaction

(D) Peptide bond

53. The secondary structure of proteins is stabilized mainly by :

(A) Hydrophobic interactions

(B) Hydrogen bonds

(C) Ionic bonds

(D) Peptide bonds

54. Which of the following represents a secondary structure in proteins?

(A) Alpha-helix

(B) Beta-pleated sheet

(C) Both A and B

(D) None of the above

55. The tertiary structure of proteins is maintained by :

(A) Peptide bonds

(B) Disulfide and hydrogen bonds

(C) Only hydrophobic interactions

(D) Only ionic bonds

56. The quaternary structure of a protein involves :

(A) Linear sequence of amino acids

(B) 3D folding of a single polypeptide

(C) Association of multiple polypeptide chains

(D) Peptide bond formation

57. Which is not a property of a protein's secondary structure?

(A) Hydrogen bonding

(B) Disulfide bond formation

(C) Alpha-helix

(D) Beta-sheet

58. Which technique separates proteins based on molecular weight?

(A) Ion exchange chromatography

(B) Gel filtration (size exclusion)

(C) Thin-layer chromatography

(D) SDS-PAGE

59. What does SDS do in SDS-PAGE?

(A) Stains the protein

(B) Reduces disulfide bonds only

(C) Imparts a uniform negative charge and denatures proteins

(D) None of the above

60. The purpose of ß-mercaptoethanol in sample buffer is to :

(A) Impart negative charge

(B) Break hydrophobic interactions

(C) Stain proteins

(D) Reduce disulfide bonds

61. In gel filtration chromatography, proteins are separated based on :

(A) Size

(B) Charge

(C) Hydrophobicity

(D) pH optima

62. Which interaction stabilizes protein tertiary structure?

(A) Peptide bond

(B) Hydrogen bond

(C) Hydrophobic interaction

(D) Both B and C

63. The denaturation of proteins usually involves:

(A) Loss of tertiary structure

(B) Loss of primary structure

(C) Loss of peptide bonds

(D) Loss of amino acid sequence

64. Which method is used to determine the amino acid sequence from the N-terminus of a polypeptide?

(A) Sanger sequencing

(B) Edman degradation

(C) Gel electrophoresis

(D) X-ray crystallography

65. What chemical reacts with the N-terminal amino acid during Edman degradation?
(A) Phenylisothiocyanate
(B) Ninhydrin
(C) Biuret reagent
(D) Coomassie blue

66. What is the main feature of a protein's quaternary structure?
(A) Covalent bonds among amino acids
(B) Single polypeptide structure
(C) Assembly of multiple subunits
(D) Beta-sheet formation

67. Van der Waals interactions in proteins are:
(A) Short-range attractions between uncharged atoms
(B) Main bonds of primary structure
(C) Found only in DNA
(D) Only between disulfide bridges

68. The smallest unit of protein that maintains a functional structure is:
(A) Subunit
(B) Monomer
(C) Domain
(D) Alpha-helix

69. Which is not a true statement about hydrogen bonds in proteins?
(A) Stabilize secondary structure
(B) Involve electrostatic attraction
(C) Found in ß-sheets
(D) Form only between side chains

70. Native PAGE separates proteins based on:
(A) Size only
(B) Sequence only
(C) Only hydrophilicity
(D) Charge and size

71. A protein's isoelectric point is :
(A) pH at which it is least soluble
(B) Always at pH 7.0
(C) pH at which its net charge is zero
(D) None of the above

72. The Edman degradation method cannot be used if:
(A) Protein is larger than 50 residues
(B) The N-terminus is blocked
(C) Disulfide bonds are present
(D) The protein contains proline

73. Which is a hydrophobic amino acid?
(A) Lysine
(B) Glutamate
(C) Phenylalanine
(D) Serine

74. The function of the hydrophobic effect in protein folding is to :
(A) Stabilize alpha helices
(B) Form salt bridges
(C) Enhance hydrogen bonding
(D) Drive nonpolar residues to the protein core

75. Chemical degradation of proteins by strong acids like HCl provides :

(A) Peptide sequence

(B) Amino acid composition

(C) Protein structure

(D) C-terminal residue

76. What is the primary goal of proteomics?

(A) Analysis of nucleic acid sequences

(B) Analysis of carbohydrate structures

(C) Analysis of protein composition, function, and interactions

(D) Analysis of lipid membranes

77. Which technique is commonly used to separate complex mixtures of proteins in proteomics?

(A) PCR

(B) Southern blotting

(C) ELISA

(D) 2D-PAGE

78. In 2D-PAGE, proteins are separated by :

(A) First by molecular weight, then by charge

(B) First by charge, then by molecular weight

(C) Only by molecular weight

(D) Only by hydrophobicity

79. What is the function of a reducing agent during sample preparation for proteomics?

(A) Maintains protein tertiary structure

(B) Promotes DNA replication

(C) Breaks disulfide bonds

(D) Stains protein bands

80. Which compound is most commonly used for protein solubilization in 2D-PAGE?

(A) Sodium dodecyl sulfate (SDS)

(B) Phenol-chloroform

(C) Agarose

(D) Formaldehyde

81. What aspect of 2D-PAGE contributes to its high resolution?

(A) Large pore size

(B) Sequential separation by isoelectric point and size

(C) Use of restriction enzymes

(D) Single-dimension separation

82. Which is not a step in mass spectrometry-based protein identification?

(A) Ionization of peptides

(B) Detection of mass-to-charge ratios

(C) Hybridization of DNA

(D) Database matching of peptide masses

83. MALDI-TOF is a type of :

(A) Protein staining method

(B) DNA sequencing platform

(C) Mass spectrometry method

(D) RNA labeling technique

84. What is “de novo sequencing” in mass spectrometry?

(A) Sequencing of new DNA

(B) Determination of protein sequence directly from spectral data

(C) Protein identification using antibody binding

(D) mRNA quantification by RT-PCR

85. Which factor is critical for reproducibility of 2D-PAGE?

(A) Consistent sample loading

(B) Staining all proteins with silver

(C) Use of agarose gel only

(D) Presence of DNA

86. Electrospray ionization (ESI) is particularly useful for :

(A) Generating large protein crystals

(B) Sequencing DNA

(C) Visualizing cell organelles

(D) Ionizing proteins and peptides for mass spectrometry

87. Which instrument analyzes mass-to-charge ratio (m/z) of peptides in proteomics?

(A) Spectrophotometer

(B) Mass spectrometer

(C) PCR cycler

(D) Microarray scanner

88. Why is sample preparation critical for reliable proteome analysis?

(A) It increases gel thickness

(B) Allows RNA extraction

(C) Ensures proteins are solubilized, reduced, and dispersed for analysis

(D) Causes protein denaturation only

89. Resolution of 2D-PAGE refers to:

(A) The ability to distinguish separate protein spots

(B) Speed of gel run

(C) Cost of chemicals

(D) Incubation temperature

90. What is the role of dithiothreitol (DTT) in protein analysis?

(A) Promotes protein folding

(B) Prevents aggregation by reducing disulfide bonds

(C) Forms peptide bonds

(D) Increases pH of the buffer

91 Sample solubilization helps to:

(A) Preserve nucleic acid structure

(B) Keep proteins in solution and prevent aggregation

(C) Synthesize ATP

(D) Initiate gene transcription

92. Which mass spectrometry method is typically used for high-throughput protein identification?

(A) Thin-layer chromatography

(B) Triple-quadrupole MS

(C) Liquid chromatography-tandem mass spectrometry (LC-MS/MS)

(D) Northern blot

93. How does 2D-PAGE improve over 1D-PAGE for complex samples?

(A) Lower cost

(B) Better separation of proteins with similar size but different charge

(C) No separation by charge

(D) Does not require stains

94. What is a main application of mass spectrometry in proteomics?

(A) Protein sequencing and identification

(B) Gene splicing

(C) Imaging tissue sections

(D) Phospholipid analysis only

95. A common stain for visualizing 2D-PAGE protein spots is :

(A) Ethidium bromide

(B) Coomassie brilliant blue

(C) Silver stain

(D) Both (B) and (C)

96. What is the most common reason for poor reproducibility in 2D-PAGE?

(A) Use of excessive voltage

(B) Inconsistent sample preparation or gel conditions

(C) Use of mass spectrometry

(D) Protein folding errors

97. Mass spectrometers typically output :

(A) Chromatograms

(B) RT-PCR curves

(C) Spectra showing m/z values

(D) pH titration graphs

98. Which step is crucial in de novo sequencing of proteins by mass spectrometry?

(A) Peptide fragmentation and analysis of resultant ions

(B) RNA extraction

(C) Carbohydrate quantification

(D) DNA denaturation

99. 2D-PAGE can separate proteins based on differences in :

(A) Both isoelectric point and size

(B) Only peptide bonds

(C) Only DNA content

(D) Only charge

100. Mass spectrometry-based methods are limited in protein analysis by :

(A) Requirement for specialized instrumentation and expertise

(B) Inability to analyze RNA

(C) No need for separation

(D) Only qualitative results

Rough Work / रफ कार्य

Example :

Question :

Q.1 Ⓐ ● Ⓒ Ⓓ

Q.2 Ⓐ Ⓑ ● Ⓓ

Q.3 Ⓐ ● Ⓒ Ⓓ

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 & 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.

उदाहरण :

प्रश्न :

प्रश्न 1 Ⓐ ● Ⓒ Ⓓ

प्रश्न 2 Ⓐ Ⓑ ● Ⓓ

प्रश्न 3 Ⓐ ● Ⓒ Ⓓ

5. प्रत्येक प्रश्न के अंक समान हैं। आपके जितने उत्तर सही होंगे, उन्हीं के अनुसार अंक प्रदान किये जायेंगे।

6. सभी उत्तर केवल ओ०एम०आर० 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. ओ०एम०आर० 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 में, रफ-कार्य के लिए दिए खाली पेज पर ही किया जाना चाहिए।

11. परीक्षा-कक्ष में लॉग-बुक, कैल्कुलेटर, 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।

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