Roll No.----------

प्रश्नपुस्तिका क्रमांक
Question Booklet No.

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

K-1374

B.Sc. (Biotech.) (Sixth Semester) Examination, 2025-26

(NEP)

(BBT6002)

GENOMIC AND PROTEOMICS

Paper Code
BBT6002

(To be filled in the OMR Sheet)

प्रश्नपुस्तिका सीरीज
Question Booklet Series
B

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 हो या उसमें किसी अन्य प्रकार की कमी हो, तो उसे तुरन्त बदल लें।

(शेष निर्देश अन्तिम पृष्ठ पर)

1. Which functional group is missing in a ddNTP compared to a standard dNTP?

   (A) 5'-Phosphate

   (B) 2'-Hydrogen

   (C) 3'-Hydroxyl (-OH)

   (D) Nitrogenous base

2. ddNTPs prevent the addition of the next nucleotide because:

   (A) They lack a 3'-hydroxyl group

   (B) They are too large

   (C) They are radioactive

   (D) They destroy the polymerase

3. In modern automated sequencing, ddNTPs are typically labeled with:

   (A) Radioactive Phosphorus

   (B) Fluorescent dyes

   (C) Heavy metals

   (D) Biotin

4. How are DNA fragments separated in the chain-termination method?

   (A) Centrifugation

   (B) Gel electrophoresis

   (C) Precipitation

   (D) Filtration

5. What is the purpose of radioactive or fluorescent labels in sequencing?

   (A) To make the DNA heavier.

   (B) To bind the primer to the template.

   (C) To stop the reaction.

   (D) To allow the detection and visualization of fragments.

6. How do ddNTPs help determine the DNA sequence?

(A) They create fragments of different lengths ending in a known base.

(B) They color-code the entire strand

(C) They prevent the DNA from folding.

(D) They act as a template for RNA

7. What is a key advantage of using Taq DNA polymerase in sequencing?

(A) It works at room temperature

(B) It is resistant to heat during the denaturation steps

(C) It does not require a primer

(D) It can sequence RNA directly

8. Taq polymerase creates new DNA strands using a mix of dNTPs and:

(A) RNA

(B) Lipids

(C) Proteins

(D) ddNTPs

9. In which direction does Taq polymerase synthesize a new DNA strand?

(A) 3’ to 5’

(B) 5’ to 3’

(C) Both directions

(D) It depends on the primer

10. Which step is NOT part of the Whole Genome Shotgun (WGS) strategy?

(A) Breaking the genome into random fragments

(B) Sequencing every fragment

(C) PCR amplification of one specific gene only

(D) Reassembling fragments using computers

11. What is the main advantage of NGS over Sanger sequencing?

(A) It produces longer individual reads

(B) It has much higher throughput (sequencing millions of bits at once)

(C) It does not require any computer analysis

(D) It uses radioactive isotopes

12. What is "Library Preparation" in the context of NGS?

(A) Building a room to store data

(B) Preparing DNA/RNA samples for the sequencing machine.

(C) Training scientists to read the data

(D) Buying books about genetics.

13. What is "De novo assembly"?

(A) Comparing a sequence to a known reference.

(B) Measuring the amount of RNA

(C) Identifying the function of a protein.

(D) Piecing together short reads into a long sequence without a reference.

14. Which of these is NOT a common use for NGS?

(A) Sequencing whole genomes.

(B) Studying all microbial DNA in an environment (metagenomics).

(C) Performing a single standard PCR to see a band on a gel.

(D) Profiling gene expression (RNA-seq).

15. Which of these steps is NOT usually involved in WGS?

(A) Fragmenting the DNA

(B) Cloning or amplifying fragments

(C) Using gel electrophoresis to read the sequence manually

(D) Computer-based assembly

16. Why is “random fragmentation” used in shotgun sequencing?

(A) To destroy the DNA

(B) To ensure there are overlapping regions for assembly

(C) To make the DNA easier to see

(D) To stop the polymerase

17. Which technology is a leader in whole genome shotgun sequencing?

(A) Maxam-Gilbert

(B) Microscopy

(C) Northern Blotting

(D) Illumina

18. What is a key benefit of Pyrosequencing compared to Sanger?

(A) It provides real-time detection of nucleotide incorporation

(B) It is much slower and more careful

(C) It uses large radioactive labels

(D) It requires manual gel reading

19. Where does Pyrosequencing often struggle with accuracy?

(A) In the middle of a gene

(B) In regions with repetitive sequences (homopolymers)

(C) In short DNA fragments

(D) In bacterial DNA

20. A limitation of Pyrosequencing is:

(A) It cannot detect SNPs.

(B) It has lower accuracy in GC-rich regions.

(C) It is too expensive for any research.

(D) It only works on RNA

21. What is NOT a goal of sequence comparison?

(A) Finding motifs and patterns

(B) Understanding evolutionary relationships

(C) Studying physical properties like boiling point

(D) Predicting gene function

22. In a Genetic Algorithm, what does “mutation” mean?

(A) The sequence stays exactly the same

(B) The sequence is changed to explore new possibilities

(C) Gaps are removed from the alignment

(D) The computer is turned off

23. Which of these is NOT a version of the BLAST tool?

(A) BLASTN

(B) BLASTP

(C) TBLASTNX

(D) BLASTX

24. The study of how genes affect a person’s response to drugs is:

(A) Pharmacogenomics

(B) Proteomics

(C) Metagenomics

(D) Structural Genomics

25. What is the primary use of the VISTA tool?

(A) To predict protein folding

(B) For comparative genomic analysis between species

(C) To design primers

(D) To edit DNA sequences

26. In genome browsers, “CDS” stands for:

(A) Conserved DNA Site

(B) Complete DNA Strand

(C) Coding DNA Sequence

(D) Cellular Delivery System

27. The process of building longer continuous sequences from small reads is:

(A) Gene annotation

(B) Contig assembly

(C) DNA denaturation

(D) Protein synthesis

28. Why is contig assembly important in genomics?

(A) It labels the introns

(B) It measures the weight of the nucleus

(C) It translates DNA into protein

(D) It allows for the reconstruction of a genome without a reference

29. What is an “Open Reading Frame” (ORF)?

(A) A piece of DNA that cannot be read

(B) A sequence that potentially codes for a protein.

(C) The space between two genes.

(D) A type of mutation.

30. Finding ORFs is useful because they:

(A) Are always junk DNA

(B) May represent actual genes that encode proteins

(C) Tell us the age of the organism

(D) Stop the sequencing machine

31. Which is NOT a step in using the NCBI ORF Finder?

(A) Pasting your sequence

(B) Selecting the genetic code

(C) Identifying the promoter and enhancer regions

(D) Setting the minimum ORF length

32. Structural Genomics primarily focuses on:

(A) The 3D shapes of proteins and DNA

(B) The speed of DNA replication

(C) The cost of sequencing

(D) The history of genetics

33. Metagenomics is the study of:

(A) One single gene

(B) The collective genetic material from an environmental community

(C) The structure of the ribosome

(D) Human ancestry only

34. Cancer genomics aims to:

(A) Sequence the genomes of healthy people only

(B) Stop DNA from mutating at all

(C) Clone dinosaurs

(D) Study genomic changes associated with cancer development

35. What is the goal of Functional Genomics?

(A) To find the weight of a chromosome

(B) To assign biological functions to genes and non-coding elements

(C) To name all the species in the world

(D) To synthesize new life

36. Which technique is used in Functional Genomics to study gene expression?

(A) RNA-seq

(B) X-ray crystallography

(C) Gram staining

(D) NMR

37. How does Functional Genomics help in medicine?

(A) By identifying genes and pathways involved in diseases

(B) By measuring blood pressure

(C) By predicting the weather

(D) By improving computer speeds

38. Which method is used to see what happens when a gene's expression is stopped?

(A) Gene knockout or knockdown

(B) PCR

(C) DNA fingerprinting

(D) Southern Blotting

39. What is the main force that causes a polypeptide to fold into a 3D shape?

(A) Hydrogen bonds

(B) Hydrophobic interactions

(C) Ionic bonds

(D) Metal ions

40. What is the role of hydrogen bonds in a protein?

(A) They provide structural support for the shape

(B) They are only for decoration

(C) They break the protein apart

(D) They carry oxygen

41. Which interaction helps stabilize the final folded protein?

(A) Gravity

(B) Van der Waals interactions

(C) Light energy

(D) Atmospheric pressure

42. Functional groups on amino acids are important because they:

(A) Change the color of the protein

(B) Regulate protein activity and interactions

(C) Make the protein heavy

(D) Stop the protein from moving

43. Why is pH sensitivity important for proteins?

(A) It changes the taste

(B) It has no importance

(C) It changes the DNA sequence

(D) It affects the stability and conformation of the protein

44. How do physical interactions assist in “ligand binding”?

(A) They repel the ligand

(B) They mediate complementary binding between the protein and ligand

(C) They turn the ligand into DNA

(D) They dissolve the ligand

45. Allosteric regulation is possible because interactions between distant parts:

(A) Break the protein

(B) Change the amino acid sequence

(C) Make the protein bigger

(D) Induce shape changes that affect the protein’s activity

46. The “first dimension” of 2D-PAGE separates by:

(A) Weight

(B) Charge (pI)

(C) Color

(D) Age

47. The “second dimension” of 2D-PAGE separates by:

(A) Charge

(B) Solubility

(C) Molecular Weight

(D) Length of time

48. SDS is used in electrophoresis to:

(A) Keep proteins in their native shape

(B) Give proteins a uniform negative charge

(C) Bind the DNA to the gel

(D) Increase the temperature

49. Dideoxynucleotides (ddNTPs) are called “chain terminators” because they:

(A) Start the DNA chain

(B) Are very expensive

(C) Kill the bacteria

(D) Lack the group needed to add the next nucleotide

50. In bioinformatics, BLAST is used to:

(A) Edit genes

(B) Find regions of similarity between biological sequences

(C) Print posters of DNA

(D) Store samples in a freezer

51. Which of the following is FALSE regarding Differential In-Gel Electrophoresis (DIGE) ?

(A) Proteins are mixed before running the 2D gel

(B) Differentially expressed proteins cannot be visualized on the same gel

(C) It detects expression differences similarly to fluorescent DNA microarrays

(D) Control and experimental samples are tagged with different fluorescent dyes

52. What is the core principle of SDS-PAGE?

(A) Reducing proteins with a chemical agent

(B) Applying a positive charge to proteins using detergents

(C) Separating proteins based on natural charge density

(D) Denaturing proteins and providing a uniform negative charge

53. Which statement about 2D-PAGE is incorrect?

(A) Some proteins may not stain or separate effectively

(B) Gels can be digitized for computer-based image analysis

(C) Membrane proteins are mostly hydrophilic and easy to dissolve

(D) A major challenge is the separation of hydrophobic membrane proteins

54. What is the most common stain used to see protein bands after SDS-PAGE?

(A) Ethidium bromide

(B) Coomassie Brilliant Blue

(C) Hematoxylin

(D) Silver nitrate

55. In 2D electrophoresis, what does the "second dimension" separate by?

(A) Net charge

(B) Isoelectric point

(C) Molecular weight (Size)

(D) Hydrophobicity

56. Which of these is NOT a typical use for 2-D Gel Electrophoresis?

(A) Preparing samples for Mass Spectrometry

(B) Identifying potential disease biomarkers

(C) Determining the total protein concentration in a liquid sample

(D) Comparing protein expression between two different cell types

57. Polyacrylamide gels are formed by polymerizing acrylamide with:

(A) N, N — acrylamide

(B) N — methyleneacrylamide

(C) N, N — methylene bisacrylamide

(D) Bis-polyacrylamide

58. In a "Native" PAGE setup, the migration rate is primarily determined by:

(A) Size only

(B) Net charge

(C) Protein length

(D) Denaturation state

59. How are proteins visualized specifically after a Native PAGE run?

(A) Staining with Coomassie Brilliant Blue

(B) Western Blotting

(C) Ethidium bromide staining

(D) UV shadowing

60. What is the main factor used by Isoelectric Focusing (IEF) to separate proteins?

(A) Molecular weight

(B) Total mass

(C) Net charge

(D) Solubility

61. At what point do proteins stop migrating during an IEF procedure?

(A) When they reach the anode

(B) When they reach their isoelectric point (pI)

(C) When they reach the cathode

(D) When the gel pores become too small

62. Which component is essential for generating the pH gradient in IEF?

(A) Strong acids

(B) Ampholyte buffers

(C) SDS detergent

(D) Beta-mercaptoethanol

63. What is the standard gel matrix used for IEF?

(A) Agarose

(B) . Starch

(C) Polyacrylamide

(D) Silica

64. In 2D-PAGE, which dimension involves separation by isoelectric point?

(A) First dimension

(B) Second dimension

(C) Both dimensions

(D) Neither dimension

65. What is the primary objective of the IEF step in a 2D-PAGE workflow?

(A) To separate proteins by size

(B) To separate proteins by their pI

(C) To quantify protein concentration

(D) To identify protein interactions

66. During which step of 2D-PAGE are disulfide bonds reduced and alkylated?

(A) Rehydration

(B) First dimension run

(C) Equilibration

(D) Staining

67. What is a significant drawback of 2D-PAGE for proteomics research?

(A) High resolution

(B) Inability to detect charge

(C) Limited dynamic range and sensitivity

(D) Automation is too easy

68. What is a major benefit of the SDS-PAGE technique?

(A) It keeps proteins in their native state

(B) It is highly compatible with Western blotting

(C) It separates proteins solely by charge

(D) It requires no specialized equipment

69. Identify a limitation of SDS-PAGE.

(A) It is very difficult to reproduce

(B) It cannot handle denatured proteins

(C) It is difficult to accurately quantify protein abundance

(D) It only works for very large proteins

70. In which scenario is SDS-PAGE used to ensure the removal of contaminants?

(A) DNA sequencing

(B) Protein purification

(C) Drug metabolic testing

(D) Cell imaging

71. Why are molecular weight markers included in an electrophoresis run?

(A) To keep the pH stable

(B) To provide a reference for estimating protein size

(C) To ensure the current is flowing

(D) To stain the other proteins

72. What is the core principle of Gel Filtration Chromatography?

(A) Separation by charge

(B) Separation by size and shape

(C) Separation by affinity

(D) Separation by boiling point

73. Which molecules exit the column first in Gel Filtration?

(A) Smallest molecules

(B) Medium molecules

(C) Largest molecules

(D) Highly charged molecules

74. The stationary phase in Gel Filtration is typically made of:

(A) Liquid solvent

(B) Cross-linked polymers

(C) Metal beads

(D) Paper strips

75. How is the exit of molecules usually monitored in Gel Filtration?

(A) Refractive index detection

(B) Visible color change

(C) Weighing the tubes

(D) pH changes

76. Gel Filtration Chromatography is also frequently called:

(A) Ion Exchange Chromatography

(B) Size Exclusion Chromatography (SEC)

(C) HPLC

(D) Affinity Chromatography

77. What is a critical step in de novo peptide sequencing?

(A) Comparing data to a known genome library

(B) Calculating the total mass of the cell

(C) Inferring sequences from fragmentation patterns

(D) Identifying the DNA promoter

78. What is "Selected Reaction Monitoring" (SRM) specifically used for?

(A) Finding every protein in a sample

(B) Quantifying and comparing a specific targeted protein

(C) Sequencing an unknown organism

(D) Measuring DNA mutations

79. Which ionization method is preferred for large biomolecules like proteins?

(A) Electron Impact (EI)

(B) Flame Ionization

(C) Chemical Ionization

(D) MALDI

80. What is the goal of de novo sequencing?

(A) To match a peptide to a database

(B) To determine the sequence without prior info or databases

(C) To identify the 3D structure of a protein

(D) To find the mRNA sequence

81. Which mass analyzer calculates mass based on the time an ion takes to travel?

(A) Quadrupole

(B) Ion Trap

(C) Time-of-Flight (TOF)

(D) Magnetic Sector

82. Which technique is the "gold standard" for protein ID and characterization?

(A) PCR

(B) Mass Spectrometry (MS)

(C) NMR

(D) Northern Blotting

83. What is the primary advantage of protein microarrays?

(A) High-throughput screening of interactions

(B) Slow, detailed analysis of one protein

(C) Measuring DNA length

(D) Separating isotopes

84. In de novo sequencing, which process interprets spectra to find the sequence?

(A) Ionization

(B) Sequence reconstruction

(C) Sample preparation

(D) Elution

85. Why are "ion series" (like b and y ions) important in Mass Spectrometry?

(A) They stabilize the protein

(B) They help identify characteristic fragment ions

(C) They indicate the color of the protein

(D) They determine the protein's solubility

86. How is protein abundance compared between different 2D gel samples?

(A) By measuring the width of the gel

(B) By weighing the dried gel

(C) By counting the number of proteins

(D) By comparing the intensity of the spots

87. What is the study of all proteins expressed by a genome called?

(A) Genomics

(B) Proteomics

(C) Metabolomics

(D) Transcriptomics

88. Which question can Proteomics answer?

(A) Does the gene have a mutation?

(B) What is the melting temperature of this DNA?

(C) How many exons are in this gene?

(D) Which proteins are in the Golgi apparatus of a mouse liver?

89. Proteomics is widely used in "Biomarker Discovery" to:

(A) Map the human genome.

(B) Find proteins that indicate a specific disease.

(C) Synthesize new DNA

(D) Track bird migration.

90. What is the main benefit of using 2D gels for complex protein mixtures?

(A) It is the fastest method available.

(B) It only requires a small amount of salt

(C) High resolution and separation efficiency.

(D) It works best for small peptides.

91. In Sanger sequencing, what must happen to the DNA after synthesis?

(A) It must be frozen.

(B) It must be denatured (made single-stranded).

(C) It must be circularized

(D) It must be stained with iodine.

92. How many different dNTPs (standard nucleotides) are used in Sanger sequencing?

(A) 1

(B) 2

(C) 3

(D) 4

93. To start DNA synthesis, a _____ is needed, which is usually _____

(A) Catalyst; biological

(B) Primer; chemically synthesized

(C) Template; radioactive

(D) Ligase; an enzyme

94. The "Chain-Termination" method (Sanger) depends on which enzyme?

(A) DNA Ligase

(B) RNA Polymerase

(C) DNA Polymerase

(D) Restriction Endonuclease

95. What chemical principle does the Maxam-Gilbert method use?

(A) Enzymatic synthesis

(B) Base-specific chemical cleavage

(C) Light-based synthesis

(D) Heat-driven fragmentation

96. What was the first organism to have its whole genome sequenced?

(A) E. coli

(B) Homo sapiens

(C) Saccharomyces cerevisiae

(D) Haemophilus influenzae

97. Why are ddNTPs (dideoxynucleotides) added to a Sanger sequencing reaction?

(A) To speed up the reaction

(B) To stop DNA synthesis at specific nucleotides

(C) To prevent DNA from denaturing

(D) To act as a primer

98. What is the role of the "Sequenase" enzyme?

(A) To break DNA

(B) To transcribe RNA

(C) To join two DNA strands

(D) To incorporate labeled nucleotides during sequencing.

99. Which sequencing method is most associated with the use of ddNTPs?

(A) Maxam-Gilbert

(B) Sanger method

(C) NGS

(D) Shotgun sequencing

100. What is the primary role of ddNTPs in the Sanger method?

(A) DNA repair

(B) Chain termination

(C) Primer binding

(D) Strand separation

******

Rough Work / रफ कार्य

4. Four alternative answers are mentioned for each question as – A, B, C & D in the question 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 एक 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, उत्तर 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।