Roll No. .....

Question Booklet Number

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

M. Sc. (Microbiology) (Fourth Semester)

EXAMINATION, July, 2022

(Elective)

MICROBIAL GENOMICS & PROTEOMICS & BIOINFORMATICS

Paper Code					
MIC	4	0	0	3	(B)

Questions Booklet Series
C

Time : 1:30 Hours] [*Maximum Marks : 100*

Instructions to the Examinee :

1. Do not open the booklet unless you are asked to do so.
2. The booklet contains 60 questions. Examinee is required to answer any 50 questions in the OMR Answer-Sheet provided and not in the question booklet. If more than 50 questions are attempted by student, then the first attempted 50 questions will be considered for evaluation. 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 60 प्रश्न हैं। परीक्षार्थी को किन्हीं 50 प्रश्नों को केवल दी गई OMR आन्सर-शीट पर ही हल करना है, प्रश्न-पुस्तिका पर नहीं। यदि छात्र द्वारा 50 से अधिक प्रश्नों को हल किया जाता है तो प्रारम्भिक हल किये हुए 50 उत्तरों को ही मूल्यांकन हेतु सम्मिलित किया जाएगा। 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)

1. Biological literature databases include :

(A) PubMed

(B) PDB

(C) PROSITE

(D) PDS

2. Short read, massively parallel sequencing technique is referred to as :

(A) Next Generation Sequencing

(B) First Generation Sequencing

(C) Third Generation Sequencing

(D) None of the above

3. Technique which detects pyrophosphate release, using light signal (bioluminescence), after nucleotides are incorporated by polymerase to a new strand of DNA is known as :

(A) Illumina Sequencing

(B) Ion Torrent Sequencing

(C) Roche 454 Pyrosequencing

(D) All of the above

4. Which of the following can be used as an analyser in Mass Spectrometry ?

(A) Electron Multiplier

(B) Laser

(C) Microchannel Plate

(D) Time of Flight

5. It involves the chemical or enzymatic treatment of a protein resulting in the formation of peptide fragments followed by separation and identification of the fragments in a reproducible manner is known as :

(A) Real Time PCR

(B) Southern Blotting

(C) Peptide Mass Fingerprinting

(D) Chromosome walking

6. In enzymatic amino acid sequence determination, trypsin cleaves peptides on the C terminal side of :

(A) Ala and Ser

(B) Cys and Glu

(C) Lys and Arg

(D) All of the above

7. Analytical technique used to measure mass-to-charge ration of charged particles for elucidation of chemical nature of peptides is :

(A) Mass Spectroscopy

(B) Ion Torrent

(C) Real Time PCR

(D) Microarray

8. Which of the following is untrue regarding affinity purification of proteins ?

(A) Affinity chromatography separates proteins on the basis of an interaction between a protein and a specific ligand.

(B) The binding of the protein to a ligand attached to a matrix cannot be reversed by either competition or by decreasing the affinity with pH and/or ionic strength.

(C) Protein A (ligand), which can be utilized to purify immunoglobulin G antibodies (target protein) .

(D) His-tag, GST-tag can be used as affinity tags.

9. Which of the following is an example of Restriction Enzyme Finder ?

(A) NEBcutter

(B) Restriction Mapper

(C) Webcutter 2.0

(D) All of the above

10. Which of the following tools are useful in gene prediction ?

(A) Glimmer

(B) GeneParser

(C) GeneMark

(D) All of the above

11. Which of the following vectors are useful for human genome sequencing project ?

(A) HAC

(B) Phage vectors

(C) CMV vectors

(D) BAC

12. A method to determine the tertiary structure of protein in the absence of experimentally solved structure of a similar/homologous protein is known as :

(A) Ab initio method

(B) Homology based method

(C) Threading

(D) All of the above

13. The process of deriving the structural and functional information of a protein or

gene from a raw data set using different analysis is known as :

(A) Genome editing

(B) Genome annotation

(C) Genome filling

(D) All of the above

14. Which of the following is a feature of Next Generation Sequencing ?

(A) High Throughput Technology

(B) Massive Parallel Processing

(C) Emulsion PCR

(D) All of the above

15. PRIMER-BLAST :

(A) allows users to sequence primers

(B) to check the specificity of non-existing primers

(C) allows users to design new target-specific primers in one step as well as to check the specificity of pre-existing primers

(D) None of the above

16. A fully automated protein structure homology-modelling server, accessible via the Expasy web server is :

(A) SWISSMODEL

(B) PDB

(C) RasMol

(D) Jmol

17. Which of the following is an example of NGS technology ?

(A) Illumina Sequencing

(B) Solid Sequencing

(C) Roche Pyrosequencing

(D) All of the above

18. The following can be used for conducting a BLAST search :

(A) FASTA sequence

(B) Genbank accession number

(C) Upload file

(D) All of the above

19. A genomic library is :

(A) a database where the sequence of an organism's genome is stored.

(B) a collection of many clones possessing different DNA fragments from the same organisms inserted in vectors.

(C) a book that describes how to isolate DNA from a particular organism.

(D) a place where the information of the genetic organization of organisms are kept.

20. Partial Sequencing of complementary DNA deposited in biological databases are known as :

(A) Expressed Sequence Tags (EST)

(B) Expressed RNA sequences

(C) Expression of Sequence Terminal

(D) None of the above

21. In Sanger's DNA sequencing reaction, chain termination is obtained by :

(A) Chemicals for base specific cleavage

(B) ddNTPs

(C) dNTPs

(D) ^{32}P

22. Which of the following is untrue about Shotgun Sequencing ?

(A) When DNA fragments derived from different chromosomal regions have repeats of the same sequence, they will appear to overlap.

(B) Contigs are assembled into scaffold.

(C) A large number of reads are then assembled by computer.

(D) There is no requirement of creating a genomic library.

23. Which step is not included in Illumina NGS ?

(A) Emulsion PCR

(B) Library preparation

(C) Bridge PCR and cluster generation

(D) Sequencing, alignment and data analysis

24. Field of biological research involving comparison of complete genome sequences of different species is known as :

(A) Functional Genomics

(B) Structural Genomics

(C) Comparative Genomics

(D) Pharmacogenomics

25. Whole-exome sequencing is a widely used next-generation sequencing (NGS) method that involves sequencing :

(A) the protein-coding regions of the genome.

(B) the non-protein-coding regions of the genome

(C) the RNA complement of genome

(D) All of the above

26. Orthologs or orthologous genes are :

(A) genes in different species that originated by vertical descent from a single gene of the last common ancestor.

(B) genes in same species that originated by vertical descent from a single gene of the last common ancestor.

(C) genes in same species by gene duplication event.

(D) genes in different species that differ in sequence and functional domains.

27. Amplification of DNA molecules in physically separated picoliter-volume water-in-oil droplets is known as :

(A) Western Blotting

(B) Emulsion PCR

(C) Reverse Transcriptase

(D) All of the above

28. ORF finder is not a :

(A) protein structure database.

(B) Graphical analysis tool.

(C) Tool that identifies all open reading frames using the standard or alternative genetic codes.

(D) Finds all open reading frames of a selectable minimum size in a nucleotide sequence.

29. GWAS stands for :

(A) Genome Wide Association Studies

(B) Gene Wide Association Studies

(C) Genetic Way Application Scope

(D) All of the above

30. Model Organism Databases :

(A) Generate, source and collate Species specific information

(B) Generate, source and collate Phylum specific information

(C) Generate, source and collate Order specific information

(D) Generate, source and collate Kingdom information

31. Genome refers to :

(A) Total DNA and RNA of an organism

(B) Complete DNA content of an organism

(C) Complementary DNA content of an organism

(D) Entire genes of an organism

32. The term ‘genome’ was coined by :

(A) Craig Venter

(B) Wilkinson

(C) Watson and Crick

(D) Hans Winkler

33. Father of Genomics is :

(A) Fred Sanger

(B) Craig Venter

(C) Tom Roderick

(D) All of the above

34. First completed genome sequencing project is :

(A) *E. coli*

(B) Phi X 174

(C) Tobacco Mosaic Virus

(D) Haemophilus influenza

35. Variation between individuals due to single base change are referred to as :

(A) EST

(B) SNP

(C) ACE

(D) Gene

36. Which of the following is a Nucleotide Sequence Database ?

(A) SWISSPROT

(B) PROSITE

(C) SCOP

(D) EMBL

37. Clustal W is a :

(A) Search Engine

(B) Protein Structure Prediction Tool

(C) Multiple Sequence Analysis Tool

(D) RNA Structural Database

38. Alignment procedure that tries to align entire sequence is :

(A) Global alignment

(B) Pairwise alignment

(C) Multiple sequence alignment

(D) Local alignment

39. Which of the following is a protein structure database ?

(A) Genbank

(B) DDBJ

(C) PDB

(D) BLAST

40. Banklt are sequence submission tools for :

(A) NCBI

(B) DDBJ

(C) EBI

(D) Swissbank

41. Which of the following is a sequence retrieval tool for NCBI ?

(A) ExPASY

(B) Entrez

(C) PIR

(D) SRS

42. Stepwise method of solving problems in Computer Science is known as :

(A) Tabulate

(B) Project

(C) Procedure

(D) Algorithm

43. Bioinformatics applications include :

(A) Biological database storage

(B) Provide software tools for understanding relationships between organisms

(C) Database management

(D) All of the above

44. Which of the following is true about Proteomics ?

(A) Proteomics has enabled the identification of ever increasing numbers of protein.

(B) Proteomics generally refers to the large-scale experimental analysis of proteins and proteomes.

(C) Proteome is the entire set of proteins that is produced or modified by an organism.

(D) All of the above

45. Size of *Escherichia coli* genome is approximately :

(A) 4.6×10^6 bp

(B) 4.6×10^6 Kbp

(C) 4.6×10^6 Mbp

(D) 4.6×10^3 bp

46. Structural genomics refers to :

(A) Study of physical nature of genome

(B) Study of expression of genome

(C) Both of the above

(D) None of the above

47. The study of how genes and intergenic regions of the genome contribute to different functions of biological processes :

(A) Functional Genomics

(B) Comparative Genomics

(C) Structural Genomics

(D) Proteomics

48. Genome wide gene expression analysis can be performed using :

(A) Microarrays

(B) Affinity Chromatography

(C) Northern Blotting

(D) PCR

49. For Microarray experiment comparing gene expression between two samples of the same yeast strain grown in hot *vs.* cold temperatures. Which best describes the experimental conditions ?

(A) Total yeast RNA is spotted on the array, total RNA samples from hot and cold yeast are labelled and hybridized to the slide.

(B) Total DNA from hot and cold yeast is spotted on the array, total yeast DNA is labelled and hybridized to the slide.

(C) Hot and cold yeast cDNA is spotted on the array, total yeast RNA is labelled and hybridized to the slide.

(D) Total yeast DNA is spotted on the array, hot and cold yeast cDNA is labelled and hybridized to the slide.

50. RNA sequencing methods have which of the following advantage over Microarray ?

(A) Offers Single Nucleotide Resolution

(B) Knowledge of genome not required

(C) Dynamic range of expression levels

(D) All of the above

51. Human genome is approximately :

(A) 3 billion base pairs

(B) 9 billion base pairs

(C) 3 million base pairs

(D) 4.2 million base pairs

52. The initiation of FASTA sequence has the following symbol :

(A) >

(B) <

(C) /

(D) #

53. BLAST programme was developed by :

(A) Altschul

(B) Venter

(C) Watson

(D) Dayhoff

54. Which of the following diseases is not a variant of BLAST ?

(A) BLASTn

(B) BLASTp

(C) TBLASTXN

(D) Mega BLAST

55. Databases that are part of International Nucleotide Sequence Database Collboration are :

(A) DDBJ, NCBI, EMBL

(B) SWISSPROT, NCBI, EMBL

(C) DDBJ, PDB, EMBL

(D) STS, NCBI, EMBL

56. Which of the following is a primary nucleotide database ?

(A) RefSeq

(B) GenBank

(C) OMIM

(D) BLAST

57. BLAST stands for :

(A) Basic Level Alignment Search Tool

(B) Beginners Level Alignment Search Tool

(C) Basic Level Alignment Scopus Tool

(D) Basic Local Alignment Search Tool

58. What is E value of BLAST search ?

(A) Expectation value

(B) Expression value

(C) Experience value

(D) Expo value

59. BLASTx searches for :

(A) protein database using a translated nucleotide query

(B) nucleotide database using a nucleotide query

(C) protein database using a nucleotide query

(D) nucleotide database using a translated nucleotide query

60. Full form of NCBI is :

(A) National Center for Biological Information

(B) National Center for Biotechnology Information

(C) National Complex for Biological Sciences

(D) National Complex for Biotechnology Sciences

4. Four alternative answers are mentioned for each question as—A, B, C & D in the booklet. The candidate has to choose the most correct/appropriate 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 ny 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 सबसे सही अथवा सबसे उपयुक्त 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।