Roll No. ....

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

Question Booklet Number

M. Sc. (Biochemistry) (Fourth Semester)

EXAMINATION, July, 2022

BIOINFORMATICS

Paper Code				
BCH	4	0	0	2

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)

(Only for Rough Work)

1. Expand DDBJ :
   - (A) DNA Data Bank of Japan
   - (B) DNA Database of Japan
   - (C) DNA Domain Bank of Japan
   - (D) Data Domain Bank of Japan

2. What is the size limitation for email attachment ?
   - (A) 25 MB
   - (B) 250 MB
   - (C) 500 MB
   - (D) 1000 MB

3. Profile analysis is used for :
   - (A) Multiple sequence alignment
   - (B) Protein modelling
   - (C) Structure prediction
   - (D) Sequence retrieval

4. PubMed is :
   - (A) A search engine for journal references
   - (B) Repository of protein sequences
   - (C) Database of nucleotide sequences
   - (D) None of the above

5. The following tool(s) will be helpful for preparing virtual library :
   - (A) Google scholar
   - (B) PubMed
   - (C) Science Direct
   - (D) All of the above

6. SwissProt is operated by :
   - (A) University of Geneva
   - (B) University of California
   - (C) University of Stanford
   - (D) NCBI

7. Which of the following is an example for analysing structure of macromolecules ?
   - (A) DDBJ
   - (B) PDB
   - (C) NCBI
   - (D) None of the above

8. Journal search can be done using :
   - (A) Science direct
   - (B) Pubmed
   - (C) Web of science
   - (D) All of the above

9. Types of molecular markers include :

(A) VNTR

(B) RAPD

(C) RFLP

(D) All of the above

10. Expand RAPD :

(A) Rapid Amplification of Polymorphic DNA

(B) Random Amplified Polymorphic DNA

(C) Regular Amplified Polymorphic DNA

(D) Rare Amplification of Polymorphic DNA

11. Methods of proteomic analysis include :

(A) iTRAQ

(B) 2-DE

(C) Both (A) and (B)

(D) None of the above

12. iTRAQ stands for :

(A) Isobaric Tags for Relative and Absolute Quantitation

(B) Isometric Tags for Relative and Absolute Quantitation

(C) Isotopic Tags for Relative and Absolute Quantitation

(D) None of the above

13. Ramachandran plot is used for :

(A) Analysing the angles of amino acids in a polypeptide

(B) Analysing protein-protein interaction

(C) Analysing quaternary structure of protein

(D) Analysing protein-ligand interaction

14. According to IUPAC, purines are indicated by the symbol :

(A) R

(B) Y

(C) K

(D) M

15. FASTA sequences are preceded with :

(A) <

(B) >

(C) =

(D) :

16. UPGMA protocol is used for generation of :

(A) Phylogenetic tree

(B) Secondary structures

(C) Heat maps

(D) None of the above

17. EMBL is :

(A) European Molecular Biology Laboratory

(B) Located at Germany

(C) (A) and (B) are true

(D) None of the above

18. Ac/Ds elements are :

(A) Molecular markers

(B) Primer sequences

(C) Transposons

(D) Peptide fragments

19. Which of these is incorrect for stop codon ?

(A) Amber

(B) Umbel

(C) Opal

(D) Ochre

20. The statistical packages among the following are :

(A) SPSS

(B) Sigma

(C) R

(D) All of the above

21. Text based format to represent a nucleotide or amino acid is ....

(A) BLAST

(B) FASTA

(C) Multiple sequence alignment

(D) PROSITE

22. Which of the following is incorrect about ENTREZ ?

(A) It provides a series of forms that can be filled out to retrieve a Medline reference related to the molecular biology sequence databases.

(B) It provides a series of forms that can be filled out to retrieve a DNA or protein sequence.

(C) It is a resource prepared only by the staff of the National Centre for Biotechnology Information.

(D) One straightforward way to access the sequence databases is through ENTREZ.

23. Which of the following is not the objective to perform sequence comparison ?

(A) To find the common motifs present in both sequences

(B) To study the physical properties of molecules

(C) To study evolutionary relationships

(D) To observe patterns of conservation

24. Which of the following is untrue about homology modelling ?

(A) It doesn't involve the evolutionary distances anywhere.

(B) 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.

(C) Homology modelling predicts protein structures based on sequence homology with known structures.

(D) It is also known as comparative modelling.

25. 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

26. The term '*in vitro*' refers to :

(A) Within the lab

(B) Within the cell

(C) Within the glass

(D) Outside the glass

27. The laboratory work using computers and associated with web-based analysis is referred to as :

(A) In silico

(B) Dry lab

(C) Wet lab

(D) Pure lab

28. Analysing or comparing entire genome of organism :

(A) Genomics

(B) Proteomics

(C) Pharmacogenomics

(D) Metabalomics

29. Which of the following is a mail client ?

(A) PINE

(B) Google

(C) Eudora

(D) All of the above

30. Types of FTP include :

(A) FTPES

(B) FTPS

(C) SFTP

(D) All of the above

31. Bioinformatics deals with :

(A) Application of statistical tools for analysis of biological data

(B) Application of information technology tools for analysis of biological data

(C) Application of biophysical techniques for analysis of biological data

(D) Entrepreneurial application of biological research

32. Degeneracy of genetic code explains :

(A) Each amino acid is coded by multiple codons

(B) Each codon codes for single amino acid

(C) Triplet codon is without any gaps

(D) Genetic code is universal

33. Identify an operating system :

(A) Windows 10

(B) Linux

(C) Unix

(D) All of the above

34. The extension used for file transfer protocol :

(A) .doc

(B) .xls

(C) .ftp

(D) .ptx

35. NCBI stands for :

(A) National Center for Bioinformatics

(B) National Center for Biotechnology Information

(C) National Center for Biology Information

(D) National Center for Biomedical Information

36. Which of the following is useful for construction of phylogenetic tree ?

(A) Dendrogram

(B) Cladogram

(C) Phylogram

(D) All of the above

37. 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 or system.

(D) All of the above

38. Regarding structural proteomics which of the following is true ?

(A) Structure domain is an element of proteins overall structure and often folds independent of rest of protein chain.

(B) Ribbon and Cartoon Diagram of protein structure gives information about various secondary structures that occurs in protein.

(C) Structure proteomics include the analysis of protein structure at large scale.

(D) All of the above

39. The database useful for homology modelling of proteins :

(A) BLAST

(B) EMBL

(C) SwissMODEL

(D) DDBJ

40. Which of the following statements is true ?

(A) Multiple Sequence Alignment (MSA) is useful to know the conserved regions of genes.

(B) Alignment can be done for both genes and protein sequences.

(C) Multalin is useful in performing the sequence alignment.

(D) All of the above

41. Central dogma of molecular biology refers to :

(A) DNA $\rightarrow$ *c*DNA $\rightarrow$ Protein

(B) DNA $\rightarrow$ RNA $\rightarrow$ Protein

(C) Protein $\rightarrow$ RNA $\rightarrow$ DNA

(D) RNA $\rightarrow$ DNA $\rightarrow$ Protein

42. The software tool used for sequence alignment :

(A) C++

(B) PRISM

(C) HTML

(D) CLUSTALW

43. BLASTx is useful for :

(A) Translated nucleotide to protein

(B) Protein to translated nucleotide

(C) Protein to protein

(D) Nucleotide to nucleotide

44. FASTA format is used to represent :

(A) Nucleotide or amino acid sequences in standard format

(B) Diagrammatic representation of protein structures

(C) Phylogenetic tree

(D) Sugar moieties in a glycoprotein

45. All are sequence alignment tools, except :

(A) Rasmol

(B) BLAST

(C) MultAlin

(D) CLUSTAL W

46. The sequence alignment tool provided by NCBI is :

(A) Chime

(B) BLAST

(C) Multalin

(D) CLUSTALW

47. The procedure of aligning many sequences simultaneously :

(A) Multiple Sequence Alignment

(B) Pairwise alignment

(C) Global alignment

(D) Local alignment

48. Nucleotide sequence databases include :

(A) PDB

(B) ExPASY

(C) SWISSPROT

(D) GenBank

49. SwissProt is :

(A) Protein database

(B) Nucleotide database

(C) UniProt consortium

(D) Both (A) and (C)

50. Incorrect statement for BLOSUM :

(A) BLOSUM is substitution matrix

(B) Rely on substitution sequences

(C) Rely on conserved sequences

(D) Do not measure the evolutionary distance

51. MEGA 7 is :

(A) Molecular Evolutionary Genetics Analysis

(B) Creates dendrogram

(C) Useful for phylogenetic relationship

(D) All of the above

52. WWW is :

(A) World Wide Web

(B) World Wired Web

(C) World War Web

(D) World Wild Web

53. CENSOR program is used to find :

(A) Multiple sequence alignment

(B) Repetitive elements

(C) SNP

(D) Protein modelling

54. Transposons :

(A) can transfer genetic information form one position to another position in the genome.

(B) can operate through DNA or RNA sequences.

(C) are important factor for evolution.

(D) All of the above

55. Which of the following tools is used to find repetitive sequences ?

(A) Repbase

(B) CENSOR

(C) Dfam

(D) All of the above

56. GCG software tool is useful for :

(A) Analysis of gene and protein sequences

(B) Performing GO annotation

(C) Identifying SNPs

(D) Analyzing repetitive sequences

57. Which of the following is a feature of database ?

(A) To deposit and store data

(B) To retrieve data

(C) To analyse and interpret data

(D) All of the above

58. Which of the following is a nucleotide database ?

(A) EMBL

(B) Pfam

(C) Swiss-Prot

(D) Uni-Prot

59. Which of the following databases is useful for whole genome sequences ?

(A) Ensembl

(B) Expasy

(C) SwillProt

(D) UniProt

60. How many different open reading frames are possible in an *m*RNA strand ?

(A) 2

(B) 3

(C) 4

(D) 5

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 Ⓐ ● Ⓒ Ⓓ
   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 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 Ⓐ ● Ⓒ Ⓓ
   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।