Roll No. ....

O. M. R. Serial No.

Question Booklet Number

M. Sc. (Biotechnology) (Second Semester)

EXAMINATION, July, 2022

COMPUTATIONAL BIOLOGY & BIOINFORMATICS

Paper Code				
MBT	2	0	0	4

Questions Booklet Series

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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.

(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 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।

(शेष निर्देश अन्तिम पृष्ठ पर)

(Only for Rough Work)

1. Ramachandran plot can be used to predict which of the following structures ?
   - (A) Quaternary structure
   - (B) Secondary structure
   - (C) Primary structure
   - (D) Tertiary structure

2. Homology modelling includes :
   - (A) sequence alignment
   - (B) database searches
   - (C) structure evaluation to generate a structure
   - (D) All of the above

3. Threading is a procedure whereby :
   - (A) due to low sequence similarity between proteins of unknown and known structure, the structure is predicted from first principles (*i.e., ab. initio*).
   - (B) due to high sequence similarity between proteins of unknown and known structure, the same function is assumed for both.
   - (C) due to high sequence similarity between proteins of unknown and known structure, the structure of the latter is used as a template to model the former.
   - (D) a protein of unknown structure is compared against a library of fold templates to find the best match.

4. Which of the following approaches is considered under the 'Ligand based drug designing' ?
   - (A) Molecular docking
   - (B) Pharmacophore modelling
   - (C) QSAR modelling
   - (D) Both (B) and (C)

5. Which one is the application of bioinformatics ?
   - (A) Design of primers
   - (B) Grouping of proteins into families
   - (C) Reconstructing genes from EST sequences
   - (D) All of the above

6. Which of the following methods is used for virtual screening ?
   - (A) ADMET analyses
   - (B) QSAR modelling
   - (C) Pharmacophore modelling
   - (D) All of the above

7. Computer aided drug design includes :
   - (A) Structure based drug design
   - (B) Ligand based drug design
   - (C) Lead molecule optimization
   - (D) All of the above

8. What is meant by molecular docking ?

(A) The process by which two different structures are compared by molecular modelling.

(B) The process by which a lead compound is simplified by removing excess functional groups.

(C) The process by which drugs are fitted into their target binding sites using molecular modelling.

(D) The process by which a pharmacophore is identified.

9. Which of the following is key concepts of protein-ligand interaction ?

(A) Ligand binding plays an important role in regulation of biological function.

(B) Ligand binding may lead to the conformational changes in proteins.

(C) This concept is used for drug design.

(D) All of the above

10. Key concept of protein-ligand interaction is :

(A) Ligand binding plays an important role in regulation of biological function.

(B) Ligand binding may leads to the conformational changes in proteins.

(C) Ligand binding is transient in nature.

(D) All of the above

11. The main advantages of drug discovery through CADD are :

(A) It is useful in high-throughput drug design.

(B) It is helps in optimization of lead compounds.

(C) It time and cost efficient method of drug design

(D) All of the above

12. The protein-ligand complex is :

(A) reversible non-covalent interaction between protein and ligand

(B) irreversible non-covalent interaction between protein and ligand

(C) irreversible covalent interaction between protein and ligand

(D) None of the above

13. Understanding Pharmacodynamics is an important part of drug discovery, it is associated with which of the following ?

(A) Drug Absorption

(B) Drug Distribution

(C) Drug Metabolism and Drug Excretion

(D) All of the above

14. Which of the following is protein visualization software ?

(A) David Bioinformatics

(B) PyMol

(C) AutoDock

(D) STRING

15. Which of the following is molecular docking software ?

(A) PANTHER

(B) GeneMania

(C) AutoDock

(D) STRING

16. The application of information technology tools for analysis of biological data is termed as :

(A) Biostatistics

(B) Biophysics

(C) Bioinformatics

(D) Biomedical Science

17. Central dogma of molecular biology refers to :

(A) DNA $\rightarrow$ cDNA $\rightarrow$ Protein

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

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

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

18. The biosynthesis of 21 amino acids from four nitrogen bases can be better explained by :

(A) Genetic code

(B) Codon-Anticodon interaction

(C) Open reading frame

(D) All of the above

19. Identify an operating system :

(A) Windows 10

(B) Linux

(C) Unix

(D) All of the above

20. The extension used for file transfer protocol :

(A) .doc

(B) .xls

(C) .ftp

(D) .ptx

21. 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

22. A phylogenetic diagram can be rooted or unrooted.

(A) True

(B) False

(C) Can be true or false

(D) Cannot say

23. 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

24. Which of the following databases is relevant to structure proteomics ?

(A) UniProt

(B) PDB

(C) SwissProt

(D) All of the above

25. Which of the following statements is incorrect ?

(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) Using MSA a nucleotide sequence can be aligned with an amino acid sequence.

26. The software tool used for sequence alignment is :
   (A) C++
   (B) PRISM
   (C) HTML
   (D) CLUSTAL W

27. Nucleotide BLAST from a protein sequence can be done using :
   (A) BLASTn
   (B) tBLASTn
   (C) BLASTx
   (D) None of the above

28. 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

29. Types of FTP include :
   (A) FTPES
   (B) FTPS
   (C) SFTP
   (D) All of the above

30. All are sequence alignment tools, except :
   (A) RasMol
   (B) BLAST
   (C) MultAlin
   (D) CLUSTAL W

31. The sequence alignment tool provided by NCBI is :
   (A) Chime
   (B) BLAST
   (C) MultAlin
   (D) CLUSTAL W

32. A SNP is an example of :
   (A) Frameshift mutation
   (B) Transpositional control
   (C) Genetic regulation
   (D) A genetic marker

33. WWW is :
   (A) World Wide Web
   (B) World Wired Web
   (C) World War Web
   (D) World Wild Web

34. The procedure of aligning many sequences simultaneously :
   (A) Multiple sequence alignment
   (B) Pairwise alignment
   (C) Global alignment
   (D) Local alignment

35. Nucleotide sequence databases include :

(A) NCBI

(B) ExPASY

(C) SWISSPROT

(D) PROSITE

36. SwissProt is :

(A) Protein database

(B) Nucleotide database

(C) UniProt consortium

(D) Both (A) and (C)

37. Phylogenetic relationship is shown with :

(A) Dendrogram

(B) A tree

(C) Branches

(D) None of the above

38. MEGA 7 is :

(A) Molecular Evolutionary Genetics Analysis

(B) Creates dendrogram

(C) Phylogenetic relationship

(D) All of the above

39. 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 an important factor for evolution.

(D) All of the above

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

(A) Repbase

(B) CENSOR

(C) Dfam

(D) All of the above

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

(A) To deposit and store data

(B) To retrieve data

(C) To analyze and interpret data

(D) All of the above

42. Which of the following is not a protein database ?

(A) EMBL

(B) Pfam

(C) SwissProt

(D) UniProt

43. DDBJ is a database operated from :

(A) U. S. A.

(B) China

(C) India

(D) Japan

44. What is the size limitation for e-mail attachment ?

(A) 25 MB

(B) 250 MB

(C) 500 MB

(D) 1000 MB

45. Profile analysis is used for :

(A) Multiple sequence alignment

(B) Protein modelling

(C) Structure prediction

(D) Sequence retrieval

46. Which of the following steps is not a stage of microarray analysis ?

(A) Hybridization

(B) Array fabrication

(C) Genomic DNA sequencing

(D) Scanning

47. The short DNA fragments that are placed onto a microarrav are called :

(A) Probes

(B) Markers

(C) mRNA

(D) Test sequences

48. What is hybridization in microarray ?

(A) The transformation of one strand into DNA into another.

(B) Using an enzyme to make a complementary strand of DNA from mRNA.

(C) The binding of complementary strands of DNA.

(D) Using an enzyme to make a complementary strand of mRNA from DNA.

49. Which of the following steps is true about microarray ?

(A) A microarray is a multiplex lab-on-a-chip. Its purpose is to simultaneously detect the expression of thousands of genes from a sample.

(B) Microarray is a spectrophotometer-based test.

(C) Microarray detect differential expression of proteins.

(D) None of the above

50. Which of the following is true regarding “clustering” ?

(A) Clustering is the process of grouping several objects into a number of groups or clusters.

(B) The clustering of gene expression data has been proven to be useful in making known the natural structure inherent in gene expression data.

(C) Both (A) and (B)

(D) None of the Above

51. ‘PCA’ stands for which of the following ?

(A) Primary Chemical Analysis

(B) Principal Component Analysis

(C) Priority Chiral Annotation

(D) Protein Chemistry Analysis

52. Which of the following techniques is used for determining protein structure ?

(A) X-ray crystallography

(B) NMR

(C) 2D Gel Electrophoresis

(D) Both (A) and (B)

53. Which of the following is associated with proteomics study ?

(A) High-throughput protein expression

(B) Protein-Protein interaction

(C) Post-translational Protein Modification

(D) All of the above

54. Which of the following laws is the working principle of X-ray crystallography ?

(A) Pasteur’s law

(B) Ohm’s law

(C) Bragg’s law

(D) None of the above

55. ‘NMR’ stands for :

(A) Nuclues Mitochondria Repair

(B) Nucluear Magnetic Resonance

(C) Nuclear Magnetic Reversal

(D) None of the above

56. Which of the following is true about PDB (Protein Data Bank) ?

(A) Information about the 3D shapes of proteins

(B) Resources for research and education in structural biology

(C) It includes steps in protein synthesis

(D) Both (A) and (B)

57. NMR is the study of absorbtion of .... by nuclei in magnetic field.

(A) Radioactive radiation

(B) Microwaves

(C) Radio Frequency radiation

(D) IR radiation

58. Differential expressed genes derived from microarray :

(A) is valuable source to study disease mechanism.

(B) can be used to find cellular pathways.

(C) differential expression of a particular gene is derived by comparing its expression with a housekeeping gene.

(D) All of the above

59. Which of the following come under Genomics ?

(A) DNA sequencing methods

(B) Bioinformatics to assemble genome sequence

(C) Cell biology

(D) Both (A) and (B)

60. Regarding protein structure 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 occur in protein.

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

(D) All of the above

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।