QUESTION BANK
INTRODUCTION TO COMPUTATIONAL BIOLOGY
UNIT – 3
STRUCTURE BIOLOGY

CHOOSE THE BEST ANSWER

1.   In the protein synthesis, tRNA carrying initiating amino acid enters in which site of ribosome?

    a)   A site
    b)   **P site**
    c)   anticodon
    d)   recognition site

2.   What is the E site of ribosome

    a)   site where eukaryotic mRNA is processed
    b)   no specific role
    c)   site where endonuclease restricts ribosome
    d)   **site where tRNA exits the prokaryotic ribosome**

3.   Following is an initiation codon for protein synthesis

    a)   **AUG**
    b)   AAU
    c)   UAA
    d)   GUA

4.   Termination codons for protein synthesis are

    a)   AUU, AUG and GUU
    b)   **UAA, UAG and UGA**
    c)   UAU, UAG and UUA
    d)   AAA, UUU and UGA

5.   Formation of RNA over the template of DNA is

    a)   replication
    b)   duplication
    c)   **transcription**
    d)   transversion

6.   In polypeptide synthesis, amino acids are brought over ribosome-mRNA complex by

    a)   rRNA
    b)   **tRNA**
    c)   DNA
    d)   nucleotides

7. tRNA attaches amino acid at its

   a) **3'-end**
   b) 5'-end
   c) anticodon
   d) loop

8. AUG initiation codon occurs over

   a) 3' end of mRNA
   b) **5' end of mRNA**
   c) short arm of tRNA
   d) long arm of tRNA

9. A codon is read in

   a) **5' ⟶ 3' direction**
   b) 3' ⟶ 5' direction
   c) bi direction
   d) non-specific direction

10. Following are the **coding** regions of DNA or RNA

    a) introns
    b) **exons**
    c) segment
    d) fragment

11. Transcription results in

    a) amino acid chain
    b) **messenger RNA**
    c) complementary DNA
    d) Okazaki fragments

12. Immediately after transcription

    a) **a methylated guanine cap is added to the 5' end of the transcript**
    b) a methylated guanine cap is added to the 3' end of the transcript
    c) both a and b
    d) a poly adenylation signal is added

13. tRNA molecule consists of a single polynucleotide chain folded to

    a) 3 arms
    b) **5 arms**
    c) 4 arms
    d) 2 arms

14. Which is required for protein synthesis?

   a) tRNA
   b) mRNA
   c) rRNA
   d) **all the above**

15. Which of the following amino acid starts the protein synthesis?

   a) glycine
   b) proline
   c) thymine
   d) **methionine**

16. On the ribosome, mRNA binds

   a) between the subunits
   b) to the large subunit
   c) **to the small subunit**
   d) none of these

17. Which site of the tRNA molecule binds to the mRNA molecule?

   a) **anticodon**
   b) codon
   c) amino acid
   d) 5' end

18. Beta pleated sheets are examples of protein's

   a) primary structure
   b) **secondary structure**
   c) tertiary structure
   d) quaternary structure

19. Alpha right-handed helix contains

   a) 2.6 amino acid residues per turn
   b) 4.6 amino acid residues per turn
   c) **3.6 amino acid residues per turn**
   d) 5.6 amino acid residues per turn

20.   Following is the one that provide stability to alpha helix

      a)   phosphodiester bond
      b)   nitrogen bond
      c)   **hydrogen bond**
      d)   covalent bond

21.   The distance between the two amino acids in an alpha helix is

      a)   3.5 angstrom
      b)   **1.5 angstrom**
      c)   2.5 angstrom
      d)   1.0 angstrom

22.   Alpha helix is

      a)   always right-handedly twisted only
      b)   always left-handedly twisted only
      c)   **right-handedly or left-handedly twisted**
      d)   not having twist in any direction

23.   First four and last four amino acids are not bonded by a hydrogen bond in

      a)   beta-pleated sheet
      b)   **alpha helix**
      c)   both in alpha-helix and beta-pleated sheets
      d)   none of the secondary structures

24.   Following is the more stable form of beta-pleated sheet

      a)   parallel beta-pleated sheet
      b)   **anti-parallel beta-pleated sheet**
      c)   both parallel and anti-parallel beta-pleated sheets
      d)   none of the above

25.   The distance between the two amino acids in a beta-pleated sheet is

      a)   **3.5 angstrom**
      b)   1.5 angstrom
      c)   2.5 angstrom
      d)   1.0 angstrom

26. Identify the correct statement/s

    i)   Alpha helix is a fully extended form of amino acids and the most common one is left-handed helix
    ii)   Parallel form of beta-pleated sheet is more stable than Anti-parallel one
    iii)   Alpha helix is an inflexible rod-like structure and can either be twisted right-handedly or left-handedly
    iv)   Beta-pleated sheet is arranged only in parallel direction

    a)   both i and ii
    b)   **only iii**
    c)   both iii and iv
    d)   all the above

27. Secondary structure

    a)   is a linear form
    b)   **is formed by the folding of primary structure**
    c)   is an extended form of amino acids
    d)   is formed by chemical interactions

28. In the beta-pleated sheets

    a)   chains lie in a flat plane
    b)   **polypeptide chain segments are lined up sideways**
    c)   no specific arrangement is seen
    d)   chemical interactions occur

29. Fully collinear hydrogen bonds are present in

    a)   parallel beta-pleated sheets
    b)   **anti-parallel beta-pleated sheets**
    c)   both in parallel and anti-parallel beta-pleated sheets
    d)   alpha helix

30. Enormous diversity of protein molecules is due to

    a)   **sequence of amino acids**
    b)   bonds
    c)   amino group of amino acids
    d)   all the above

31. Following is a type of protein that is responsible for osmotic balance

    a)   actin
    b)   **serum albumin**
    c)   keratin
    d)   insulin

32. Which of the following protein plays a role in protection mechanism?

    a)   collagen
    b)   protease
    c)   **antibodies**
    d)   oxytocin

33. Proteins that involve in muscle functioning

    a)   proton pump and Anion channels
    b)   lac repressor
    c)   vasopressin
    d)   **actin and myosin**

34. Long rod-shaped proteins are

    a)   globular proteins
    b)   water Soluble
    c)   **fibrous proteins**
    d)   physically soft proteins

35. Following protein is not involved in transport of substances

    a)   **insulin**
    b)   haemoglobin
    c)   myoglobin
    d)   cytochrome

36. Lac repressor is involved in

    a)   muscle functioning
    b)   **gene regulation**
    c)   metabolism
    d)   osmotic balance

37. Following proteins work as stored resources

    a)   insulin, vasopressin, oxytocin
    b)   **ferritin, casein, cytochrome**
    c)   protease, kinase, polymerase
    d)   haemoglobin, myoglobin, cytochrome

38. Following is a structural database

    a)   Gen Bank
    b)   DDBJ
    c)   **PDB**
    d)   All the above

39. Organized collection of structured information or data stored electronically is a

    a) storage system
    b) **database**
    c) filing
    d) resource

40. NCBI created in

    a) **1988**
    b) 1987
    c) 1986
    d) 1985

41. Experimentally derived data like sequence of nucleotide/protein or macromolecular structure is

    a) secondary database
    b) **primary database**
    c) databank
    d) array

42. Data derived from analysing primary data

    a) **secondary database**
    b) array
    c) databank
    d) information

43. Identifying the proteins in a complex and to characterize protein-protein interactions is possible by

    a) **structural proteomics**
    b) sequencing
    c) expression proteomics
    d) functional proteomics

44. Thomas Roder is related to the following term

    a) structure
    b) sequence
    c) **genomics**
    d) function

45. Creating high-resolution genetic, physical or transcript maps is possible with

    a) **structural genomics**
    b) sequence
    c) functional genomics
    d) none of the above

46. Reconstruction of the genome to determine the biological function of genes and the interactions between genes is

    a) sequence
    b) **functional genomics**
    c) structural interpretation
    d) data analysis

47. The resources available from the NCBI gives us information

    a) only on sequence level
    b) only on structural level
    c) **on gene, sequence, structure, genome levels**
    d) only on gene level sequences

48. RasMol is a tool for

    a) predicting the functional groups
    b) **visualisation of molecules**
    c) characterisation of the structure
    d) representing the sequence

49. The aim of RasMol is to

    a) analyze the conformational changes
    b) predict the mutation
    c) **display, teaching, and generation of public quality images**
    d) interpret nature

50. The representation of the molecule through RasMol involves

    a) black and white images
    b) **variety of colour schemes**
    c) only texts
    d) none of the above

51. RasMol

    a) is not supported by windows and other operating systems
    b) **runs in Microsoft Windows, Apple Macintosh, UNIX and VMS**
    c) is not user-friendly
    d) do not generate quality images

52. Input file format/s that supports RasMol is/are

    a) Protein Data Bank
    b) Tripos Associates' Alchemy
    c) XYZ (XMol) format and CHARMm format
    d) **all the above**

53. Representations of molecule in RasMol can be

    a) macromolecular ribbons and wireframe bonds
    b) hydrogen bonding and dreiding stick bonds
    c) dot Surface
    d) **all the above**

54. RasMol is created by

    a) **Roger Sayle**
    b) John Holland
    c) Thomas Roder
    d) James Watson

55. The displayed molecule in RasMol

    a) cannot be translated
    b) cannot be zoomed
    c) cannot be rotated
    d) **can be rotated, translated, and zoomed**

56. The image can be written out

    a) PostScript format
    b) GIF format
    c) PPM format
    d) **all the above**

57. The command line in RasMol is

    a) "help <topic>"
    b) "help <topic> <subtopic>"
    c) "topic <help> <subtopic>"
    d) **both a and b**

58. Drug designing and designing of novel enzymes can be made possible by

   a) knowing the sequence of macromolecules
   b) **predicting the structure of protein**
   c) predicting only the primary structure
   d) only the R group

59. The prediction of secondary structure can

   a) only reveal the arrangement of amino acids
   b) only reveal the information on the conformation
   c) **reveal the arrangement of amino acids and the conformation**
   d) only determine the sequence of amino acids

60. Three-dimensional arrangement of atoms in a protein can be visualised by

   a) primary structure of the protein
   b) amino acid arrangement in the protein
   c) **secondary structure prediction algorithms**
   d) both a and b

61. More insight on the function of the protein is possible by

   a) predicting the sequence of the protein
   b) **predicting the structure of the protein**
   c) predicting the number of amino acids in the polypeptide
   d) none of the above

62. Chou-Fasman and GOR methods are examples of

   a) representation of amino acid sequences
   b) **protein Secondary Structure Prediction algorithms**
   c) representation of disulphide bonds
   d) determining the backbone of the molecule

63. Protein Secondary Structure Prediction (PSSP) plays a vital role in

   a) food industry
   b) textile industry
   c) leather manufacture
   d) **pharmaceutical industry**

64. Structure of protein is

   a) simple arrangement of amino acids in a chain
   b) two-dimensional arrangement of amino acids
   c) **three-dimensional arrangement of atoms in the amino acids**
   d) simple and do not reveal any data on conformation

65. Following are the type/s of secondary structure

    a) alpha helix
    b) linear arrangement
    c) beta-pleated sheet
    d) **both a and c**

66. Along with the information on predominate states, helix, sheet and random coils, secondary structure prediction algorithms provide data on multiple sequence alignment

    a) **True**
    b) False

67. Statistical approach based on calculation of statistical propensities of each residuum to form an alpha-helix or beta-strand is

    a) **Chow-Fasman algorithm**
    b) Garinier Osguthorpe Robson (GOR)
    c) both a and b
    d) none

68. Which one of the following is an information theory-based method?

    a) Chow-Fasman algorithm
    b) **Garinier Osguthorpe Robson (GOR)**
    c) both a and b
    d) none

69. The resources available from the NCBI gives us information

    a) only on sequence level
    b) only on structural level
    c) **on gene, sequence, structure, genome levels**
    d) only on gene level sequences

70. X-ray crystallography and NMR spectroscopy are the methods that can determine

    a) protein sequence
    b) **structural information of a protein**
    c) protein length
    d) all the above

71. Changes in the secondary structure of proteins leads to the following disease/s

    a) Spongiform encephalopathy
    b) Amyloidosis
    c) **both a and b**
    d) none

Answer the following (4 marks) – Draw diagrams wherever necessary

1) Write a note on secondary structure of the protein.
2) Write a note on structural databases.
3) Write a note on protein visualizing tools.
4) Write a note on function of the proteins.
5) Write a note on secondary structure prediction algorithms.
6) Write a note on RNA editing.

Answer the following (12 marks) – Draw diagrams wherever necessary

1) Illustrate protein synthesis.
2) Explain secondary structure and function of the protein.
2) Explain transcription.
3) Explain translation.
4) Write a note on protein visualizing tools and secondary structure prediction algorithms.