



## Dr.G.R.Damodaran College of Science

(Autonomous, affiliated to the Bharathiar University, recognized by the UGC) Re-accredited at the 'A' Grade Level by the NAAC and ISO 9001:2008 Certified CRISL rated 'A' (TN) for MBA and MIB Programmes

I MSC [2017-2019]

SEMESTER I

ELECTIVE I: COMPUTATIONAL BIOLOGY AND OMICS-158U1

Multiple Choice Questions.

1. Who coined the term Bioinformatics and when?

- A. Paulien Hogeweg, 1979.
- B. Dr Margaret Oakley Dayhoff, 1976.
- C. Robert Ledley, 1978.
- D. David W Mount, 1977.

ANSWER: A

2. Which one of the following is not a primary nucleic acid database?

- A. GenBank.
- B. DDBJ.
- C. EMBL.
- D. TREMBL.

ANSWER: D

3. Which one of the following is a primary protein database?

- A. SWISS-PROT.
- B. EMBL.
- C. DDBJ.
- D. NCBI.

ANSWER: A

4. \_\_\_\_\_ is a secondary database. .

- A. DDBJ.
- B. PROSITE.
- C. NRDB.
- D. OWL.

ANSWER: B

5. \_\_\_\_\_ is a composite database.

- A. PROSITE.
- B. DDBJ.
- C. NRDB.
- D. EMBL.

ANSWER: C

6. \_\_\_\_\_ is a primary protein structure database.

- A. PDB.
- B. PubChem.
- C. ChemBank.
- D. SCOP.

ANSWER: A

7. Which one of the following is a secondary protein structure database?

- A. PubChem.
- B. PDB.
- C. ChemBank.
- D. SCOP.

ANSWER: D

8. FASTA format starts with \_\_\_\_\_ symbol.

- A. /.
- B. \*.
- C. >.
- D. #.

ANSWER: C

9. Which one of the following is a complementary DNA database?

- A. Swiss-Prot.
- B. GenBank.
- C. UniSTS.
- D. NRDB.

ANSWER: C

10. \_\_\_\_\_ is a bibliographic database.

- A. PubMed.
- B. Entrez.
- C. PIR.
- D. EBI.

ANSWER: A

11. Which one of the following is a life science search engine?

- A. PubMed
- B. Entrez
- C. Mozilla.
- D. EBI.

ANSWER: B

12. \_\_\_\_\_ is a biomedical literature database which is used to retrieve full text content.

- A. Entrez
- B. Pubmed
- C. PubMed central
- D. Medscape

ANSWER: C

13. Entrez, a life science search engine used to search across databases is maintained by \_\_\_\_\_.

- A. SWISS-PROT.
- B. EMBL.
- C. DDBJ.
- D. NCBI.

ANSWER: D

14. Which Boolean operator find documents that contain terms on both sides of the operator?

- A. AND.
- B. OR.
- C. NOT.

D. ALL THREE

ANSWER: A

15. Which Boolean operator find documents those contain either any one term?

- A. NOT
- B. OR
- C. AND.
- D. AND, NOT.

ANSWER: B

16. Which Boolean operator finds documents that contain the term on the left but not the term on the right of the operator?

- A. OR.
- B. AND.
- C. NOT.
- D. AND, NOT.

ANSWER: C

17. \_\_\_\_\_ is a similarity search tool.

- A. BLAST.
- B. CLUSTALW.
- C. CLUSTALX.
- D. RASMOL.

ANSWER: A

18. What is the input sequence format in BLAST?

- A. GenBank.
- B. EMBL.
- C. FASTA.
- D. PIR.

ANSWER: C

19. \_\_\_\_\_ compares protein sequence against protein databases.

- A. blastp.
- B. blastn.
- C. blastx.
- D. tblastx.

ANSWER: A

20. The \_\_\_\_\_ tool compares nucleotide sequence against DNA databases.

- A. blastn.
- B. blastp.
- C. tblastx.
- D. tblastn.

ANSWER: A

21. The \_\_\_\_\_ tool compares translated nucleotide query sequence against protein databases.

- A. blastp.
- B. tblastn.
- C. blastx
- D. tblastx.

ANSWER: C

22. The \_\_\_\_\_ tool compares protein sequence against translated nucleotide databases.

- A. blastp.
- B. tblastx.
- C. blastn.
- D. tblastn.

ANSWER: D

23. The \_\_\_\_\_ tool compares translated nucleotide query sequence against translated nucleotide databases.

- A. blastp.
- B. blastn.
- C. tblastx.
- D. tblastn.

ANSWER: C

24. The \_\_\_\_\_ the E-value, the more significant the hit.

- A. lower.
- B. higher.
- C. average.
- D. superior.

ANSWER: A

25. PIR was established by \_\_\_\_\_.

- A. NBRF.
- B. NCBI.
- C. SIB.
- D. DDBJ.

ANSWER: A

26. Swiss-Prot is maintained by \_\_\_\_\_.

- A. NCBI.
- B. NBRF.
- C. SIB.
- D. DDBJ.

ANSWER: C

27. ExPASy stands for \_\_\_\_\_.

- A. Expert Protein Analysis Server.
- B. Exponential Protein Analysis Server.
- C. Expert Protein Analysis System.
- D. Exponential Protein Analysis System.

ANSWER: C

28. EST stands for \_\_\_\_\_.

- A. Expressed Sequence Tag.
- B. Expressed Site Tag.
- C. Expressed Structure Tag.
- D. Expressed Symbol Tag.

ANSWER: A

29. SNP stands for \_\_\_\_\_.

- A. Small Nucleic Polymorphism.
- B. Single Nucleic Polymorphism.
- C. Single Nucleotide Polymorphism.
- D. Small Nucleotide Polymorphism.

ANSWER: C

30. What is PROSITE?

- A. A database of protein structures.
- B. A database of protein sequences.
- C. A database of protein motifs.
- D. option a and b.

ANSWER: C

31. Which area is considered to be the well-conserved regions in multiple sequence alignments?

- A. Reflect areas of structural importance.
- B. Reflect areas of functional importance.
- C. Reflect areas of both functional and structural importance.
- D. Reflect areas likely to be of functional and/or structural importance.

ANSWER: B

32. In PROSITE, the term PATTERN indicates that the entry describes a \_\_\_\_\_.

- A. block.
- B. profile.
- C. regular expression.
- D. fuzzy regular expression.

ANSWER: C

33. When searching the BLOCKS and PRINTS databases, a match is judged significant, when?

- A. Single motif is matched.
- B. Two motifs are matched.
- C. The E-value is above  $e^{-4}$ .
- D. A combined E-value above a given threshold is reported for a multiple-motif match.

ANSWER: D

34. InterPro is an \_\_\_\_\_ database.

- A. integrated protein family.
- B. integrated protein sequence.
- C. integrated protein structure
- D. integrated protein interaction.

ANSWER: A

35. Which alignment contains more than two sequences?

- A. Multiple sequence.
- B. Pairwise sequence.
- C. Global.
- D. Local.

ANSWER: A

36. The most commonly used algorithms that produce multiple alignments are derived from the progressive alignment method of \_\_\_\_\_ and \_\_\_\_\_.

- A. Krogh and Eddy.
- B. Baldi and Birney.
- C. Da-Fei Feng and Russell Doolittle.
- D. Schultz and Ponting.

ANSWER: C

37. The family that consists of related genes within an organism is called \_\_\_\_\_.

- A. orthologs.

- B. zologs.
- C. paralogs.
- D. xenologs.

ANSWER: C

38. The family that consists of related genes in another organism is called\_\_\_\_\_.

- A. orthologs.
- B. zologs.
- C. paralogs.
- D. xenologs.

ANSWER: A

39. \_\_\_\_\_ characterizes a protein family are defined by the existence of a multiple sequence alignment of a group of homologous sequences.

- A. Domains.
- B. DNA.
- C. Proteins.
- D. RNA.

ANSWER: A

40. ClustalW program accepts the input sequences only in the \_\_\_\_\_ format.

- A. genbank.
- B. embl.
- C. pdb.
- D. fasta.

ANSWER: D

41. When you are comparing two sequences of same or different organisms, what is the type of the alignment?

- A. Global.
- B. Local.
- C. Pairwise sequence.
- D. Multiple sequence.

ANSWER: C

42. When you are comparing two or more than two sequences of same or different organisms, what is the type of the alignment?

- A. Global.
- B. Pairwise sequence.
- C. Local.
- D. Multiple sequence.

ANSWER: D

43. Which alignment is useful to detect the highly similar sequences?

- A. Pairwise sequence.
- B. Local.
- C. Global.
- D. Multiple sequence.

ANSWER: C

44. Which alignment is useful to detect the highly conserved regions?

- A. Local.
- B. Global.
- C. Pairwise sequence.

D. Multiple sequence.

ANSWER: A

45. The optimal alignment of two similar sequences is usually that \_\_\_\_\_ number of matches and \_\_\_\_\_ the number of gaps.

- A. minimize, maximize.
- B. maximize, minimize.
- C. degrade, upgrade.
- D. upgrade, degrade.

ANSWER: B

46. Multiple sequence alignment method is called as \_\_\_\_\_ alignment method.

- A. global.
- B. local.
- C. progressive.
- D. non-progressive.

ANSWER: C

47. Which branching diagram is assumed to be an estimate of a phylogeny when branching lengths are proportional to the amount of inferred evolutionary change?

- A. Phylogram.
- B. Cladogram.
- C. A guide tree.
- D. Cardiogram.

ANSWER: A

48. Pfam-A and Pfam-B is automatically generated from the \_\_\_\_\_ database.

- A. SMART.
- B. PRINTS.
- C. PROSITE.
- D. PRODOM.

ANSWER: D

49. Which database of Pfam is having high quality data?

- A. Pfam-A.
- B. Pfam-B.
- C. Pfam-C.
- D. Pfam-D.

ANSWER: A

50. Which database of Pfam is having low quality data?

- A. Pfam-D.
- B. Pfam-B.
- C. Pfam-A.
- D. Pfam-C.

ANSWER: B

51. SMART stands for \_\_\_\_\_.

- A. Simple Molecular Architecture Research Tool.
- B. Simple Molecular Alignment Research Tool.
- C. Simple Modular Architecture Research Tool.
- D. Simple Modular Alignment Research Tool.

ANSWER: C

52. CDD stands for \_\_\_\_\_.

- A. Conserved Domain Database.
- B. Conserved Dictionary Database.
- C. Conserved Domain Dictionary.
- D. Conserved Dictionary Database.

ANSWER: A

53. Which BLAST program is used by conserved domain database?

- A. BLASTN.
- B. BLASTP.
- C. SNP-BLAST.
- D. PSI-BLAST.

ANSWER: D

54. Which BLAST is related to RPS (Reverse Position Specific) BLAST?

- A. PHI-BLAST.
- B. PSI-BLAST.
- C. BLASTN.
- D. TBLASTX.

ANSWER: B

55. PopSet stands for \_\_\_\_\_.

- A. Population Set.
- B. Population Study Sets.
- C. Population Data Study Sets.
- D. Population Study Data Sets.

ANSWER: D

56. Dot-matrix representations denote the sequences \_\_\_\_\_.

- A. as the coordinates of a two-dimensional graph.
- B. are represented in the form of trees.
- C. as the coordinates of a 3D graph.
- D. not represented as graph.

ANSWER: A

57. Which algorithm is used by local alignment?

- A. Needleman and Wunsch.
- B. PAM.
- C. Smith-Waterman.
- D. All the above.

ANSWER: C

58. Which algorithm is used by global alignment?

- A. Needleman and Wunsch.
- B. Smith-Waterman.
- C. BLAST.
- D. PAM .

ANSWER: A

59. SRS is \_\_\_\_\_.

- A. a website for sequence similarity searches.
- B. a website specialized in mapping mutations related to human disease.
- C. a website that indexes many biological databases and is searchable by keywords.
- D. a website for protein family database searches.



ANSWER: C

60. If a mismatch occurs in the sequence alignment of two protein sequences, there occurs \_\_\_\_\_.
- A. gap.
  - B. deletion.
  - C. insertion.
  - D. transition.

ANSWER: A

61. Gene duplication results in \_\_\_\_\_.
- A. orthologs.
  - B. paralogs.
  - C. xenologs.
  - D. zoologs.

ANSWER: B

62. Speciation event results in \_\_\_\_\_.
- A. zoologs.
  - B. paralogs.
  - C. xenologs.
  - D. orthologs.

ANSWER: D

63. The paired dot in the sequence alignment represents \_\_\_\_\_.
- A. conserved substitutions.
  - B. semi-conserved substitutions.
  - C. gaps.
  - D. identity.

ANSWER: A

64. Single dot in the sequence alignment represents \_\_\_\_\_.
- A. identity.
  - B. semi-conserved substitutions.
  - C. conserved substitutions.
  - D. gaps.

ANSWER: B

65. BLAST2 compares \_\_\_\_\_ number of sequences.
- A. two.
  - B. three.
  - C. four.
  - D. five.

ANSWER: A

66. Two principal ways to construct guide tree in progressive alignment is \_\_\_\_\_.
- A. UPGMA and Neighbor joining method.
  - B. Maximum Parsimony.
  - C. Maximum Likelihood.
  - D. all the above.

ANSWER: A

67. An asterisk mark indicated above the sequences to mark every \_\_\_\_\_ base pairs.
- A. 5.
  - B. 10.

- C. 15.
- D. 20.

ANSWER: B

68. Which method of multiple sequence alignment uses genetic recombination?

- A. Progressive.
- B. Dynamic Programming.
- C. Genetic Algorithm.
- D. Hidden Markov Model.

ANSWER: C

69. What is the Twilight Zone?

- A. Where alignments appear plausible and are statistically significant.
- B. Where alignments may appear plausible to the eye, but are no longer statistically significant.
- C. Where alignments neither appear plausible nor statistically significant.
- D. Where alignments share 30% identity.

ANSWER: C

70. What kind of information present in the middle portion of the BLAST result?

- A. General description about the sequence, database and the type of BLAST program.
- B. Graphical color coded summary of the similar sequences.
- C. Description line of the similar sequences.
- D. Pairwise alignments of the query and the target sequences.

ANSWER: B

71. A term used to classify protein domains according to their secondary structural content and organization is \_\_\_\_\_.

- A. class.
- B. architecture.
- C. taxonomy.
- D. homologs.

ANSWER: A

72. Hydropathy plots are usually used to predict \_\_\_\_\_.

- A. beta secondary structure.
- B. transmembrane domains.
- C. alpha secondary structure.
- D. tertiary structure.

ANSWER: B

73. Databases such as CATH and SCOP are used to identify \_\_\_\_\_.

- A. the structural family to which a protein belongs.
- B. the generic family to which a protein belongs.
- C. homologous proteins.
- D. analogous proteins.

ANSWER: A

74. Coordinates for known protein structures are housed in?

- A. CATH.
- B. SCOP.
- C. PDBsum.
- D. PDB.

ANSWER: D

75. With homology modeling, if there are minor errors in the template, the model will be?

- A. Very good.
- B. Just as good as the template is unable.
- C. Built using current modeling programs.
- D. Completely wrong.

ANSWER: B

76. Homology modeling is a procedure whereby?

- A. Due to low sequence similarity between proteins of unknown and known structure, the structure is predicted from first principles.
- 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.

ANSWER: C

77. 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.
- 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.

ANSWER: D

78. With homology modeling, if there are major errors in the template, the model will be?

- A. Very good.
- B. Just as good as the template is unable.
- C. rejected.
- D. Completely wrong.

ANSWER: B

79. Which is a repository for the 3-dimensional structure data for large biomolecules?

- A. NCBI.
- B. EMBL.
- C. Swiss-Prot.
- D. PDB.

ANSWER: D

80. How many methods are there to predict 3-dimensional structure of a protein?

- A. 1.
- B. 3.
- C. 7.
- D. 5.

ANSWER: B

81. Which symbol represents the termination line of the PDB file?

- A. //.
- B. #.
- C. MASTER.

D. END.

ANSWER: D

82. Which of the following is the distance based method?

- A. UPGMA.
- B. Maximum parsimony.
- C. Maximum likelihood.
- D. Neighbor-Joining.

ANSWER: D

83. PDBID is a \_\_\_\_\_ representation.

- A. SMILES.
- B. ROSDAL.
- C. WLN.
- D. ALPHANUMERIC.

ANSWER: D

84. Which server is used to deposit the protein structures in PDB?

- A. ClustalW.
- B. ClustalX.
- C. ExPASy.
- D. ADIT.

ANSWER: D

85. Which one of the following method predicts the protein structure based on fold recognition?

- A. Comparative modeling.
- B. Threading.
- C. Abinitio.
- D. Homology modeling.

ANSWER: B

86. SCOP stands for \_\_\_\_\_.

- A. Similar Classification of Proteins.
- B. Structural Classification of Proteins.
- C. Similar Characterization of Proteins.
- D. Similar Classification of Proteins.

ANSWER: B

87. DDD stands for \_\_\_\_\_.

- A. Dali Domain Dictionary.
- B. Distance Matrix Alignment Server.
- C. Distance Matrix Domain Dictionary.
- D. Distance Domain Dictionary.

ANSWER: A

88. Template based protein modeling techniques is called as \_\_\_\_\_.

- A. comparative modeling.
- B. surface modeling.
- C. threading.
- D. abinitio prediction.

ANSWER: A

89. Which of these methods is a distance-based method in tree construction?

- A. Unweighted pair group method with arithmetic mean.

- B. Jukes-Cantor.
- C. Minimum evolution.
- D. Maximum parsimony.

ANSWER: A

90. Which one of the following is not a character-based method in tree construction?

- A. Maximum parsimony.
- B. Minimum likelihood.
- C. Minimum evolution method.
- D. Neighbor joining.

ANSWER: D

91. A tree representation of a family showing the relationships between members and pattern of inheritance of a given trait is known as \_\_\_\_\_.

- A. pedigree.
- B. physical Map.
- C. genetic map.
- D. population studies.

ANSWER: A

92. The study of evolutionary relationships is \_\_\_\_\_.

- A. Phylogenics.
- B. Molecular Evolution.
- C. Cladogenesis.
- D. Cladistics.

ANSWER: A

93. A bifurcating branch point in the phylogenetic tree is known as \_\_\_\_\_.

- A. node.
- B. clade.
- C. branch.
- D. taxon.

ANSWER: A

94. Expand UPGMA.

- A. Unweighted Pair Group Method with Arithmetic Mean.
- B. Unweighted Pair Group Method with All Mean.
- C. Upreulated Gene Method with Arithmetic Mean.
- D. Unregulated Genome Method with All Mean.

ANSWER: A

95. Single substitution in the nucleotide sequence is called \_\_\_\_\_.

- A. single substitution.
- B. simple substitution.
- C. single nucleotide polymorphism.
- D. simple nucleotide polymorphism.

ANSWER: C

96. One of the most common errors in making and analyzing phylogenetic tree is \_\_\_\_\_.

- A. using a bad multiple sequence alignment as input.
- B. trying to infer the evolutionary relationship of genes or proteins in the tree.
- C. trying to infer the age at which genes or proteins diverged from each other.
- D. assuming that clades are monophyletic.

ANSWER: A

97. Which one of the following tool can be used to generate neighbor joining trees with or without bootstrap values?

- A. ClustalX.
- B. BLAST.
- C. Swiss-PDB viewer.
- D. ChemSketch.

ANSWER: A

98. Which one of the following tools can be used for both modeling the protein and structure visualization?

- A. Swiss-PDB Viewer.
- B. QMol.
- C. RasMol.
- D. ChemSketch.

ANSWER: A

99. Homology modeling can be done using \_\_\_\_\_.

- A. Swiss-PDB Viewer.
- B. QMol.
- C. Raswin.
- D. Babel.

ANSWER: A

100. Energy minimization of a modeled protein can be done using \_\_\_\_\_.

- A. ChemSketch.
- B. Moldraw.
- C. RasMol.
- D. Swiss-PDB Viewer.

ANSWER: D

101. Which tool can be used for viewing molecular structures and animating molecular trajectories?

- A. Chimera.
- B. QMol.
- C. Arguslab.
- D. ChemSketch.

ANSWER: B

102. Which one of the following is actually based on MolView?

- A. Raswin.
- B. QMol.
- C. RasMol.
- D. Moldraw.

ANSWER: B

103. Molecular phylogeny can be performed with \_\_\_\_\_ sequences.

- A. only DNA.
- B. only RNA.
- C. only protein.
- D. DNA, RNA and protein.

ANSWER: D

104. Which one of the following is a command based offline tool for molecular structural visualization?

- A. Swiss-PDB Viewer.

- B. RasMol.
- C. QMol.
- D. PyMol.

ANSWER: B

105. A phylogenetic tree that explicitly represents number of character changes through its branch lengths is \_\_\_\_\_.

- A. dendogram.
- B. cladogram.
- C. phylogram.
- D. chronogram.

ANSWER: C

106. Which of the following is the character based method?

- A. UPGMA.
- B. Maximum Parsimony and Maximum Likelihood.
- C. Maximum Likelihood and Neighbor-Joining.
- D. Neighbor-Joining.

ANSWER: B

107. Which of the following model account for nucleotide substitutions?

- A. Jukes-Cantor.
- B. Kimuras.
- C. Complex.
- D. Option a, b and c.

ANSWER: D

108. Which one of the following is an experimental method to determine the three-dimensional structure of the protein?

- A. Threading.
- B. X-ray crystallography.
- C. Homology modeling.
- D. Abinitio method.

ANSWER: B

109. Which one of the following is a computational method to predict the three-dimensional structure of the protein?

- A. X-ray crystallography.
- B. NMR.
- C. UV Spectroscopy.
- D. Threading.

ANSWER: D

110. Homology modeling is also called as \_\_\_\_\_.

- A. comparative modeling.
- B. abinitio prediction.
- C. threading.
- D. surface modeling.

ANSWER: A

111. Which one of the following tool uses comparative modeling method to predict the three-dimensional structure of a protein?

- A. Rosetta.
- B. Threader.

- C. CASP.
  - D. Modeller.
- ANSWER: D

112. Which one of the following tool is used to predict the three-dimensional structure of a protein?

- A. AutoDock.
- B. Gromacs.
- C. ChemSketch.
- D. Modeller.

ANSWER: D

113. Which is a repository for the 3-dimensional structure data for large biomolecules?

- A. NCBI.
- B. EMBL.
- C. Swiss-Prot.
- D. PDB.

ANSWER: D

114. Which technique is used to amplify a single or a few copies of piece of DNA across several orders of magnitude, generating thousands to millions of copies of a particular DNA sequence?

- A. Polymerase chain reaction.
- B. DNA replication.
- C. Ligation.
- D. DNA sequencing.

ANSWER: A

115. Which field deals with the study of influence of genetic variation on drug response in patients by correlating gene expression or single-nucleotide polymorphisms with a drug's efficacy or toxicity?

- A. Pharmacogenomics.
- B. Toxicogenomics.
- C. Metagenomics.
- D. Pharmacokinetics

ANSWER: A

116. Which field of science that deals with the collection, interpretation, and storage of information about gene and protein activity within particular cell or tissue of an organism in response to toxic substances?

- A. Pharmacogenomics.
- B. Toxicogenomics.
- C. Metagenomics.
- D. Pharmacokinetics.

ANSWER: B

117. The first step in the drug discovery process is \_\_\_\_\_. Answer: A.

- A. target identification.
- B. target isolation and purification.
- C. target structure determination.
- D. analyzing the targets structure for potential ligand binding site

ANSWER: A

118. In phase I of the clinical trials the safety of the new drug is examined and the dosage is determined by administering the compound to \_\_\_\_\_ healthy volunteers.

- A. 10-100.
- B. 20-100.



C. 10-50.

D. 20-50.

ANSWER: B

119. In phase II of the clinical trials the safety, efficacy and investigation of toxicity of the new drug is examined and the dosage is determined by administering the compound to \_\_\_\_\_ healthy volunteers.

A. 50-300.

B. 100-300.

C. 150-300.

D. 200-300.

ANSWER: B

120. Number of patients to be tested in phase III clinical trials \_\_\_\_\_.

A. More than 1000.

B. More than 2000.

C. Less than 1000.

D. Less than 500.

ANSWER: A

121. Mechanism of action of receptor is \_\_\_\_\_.

A. agonist and antagonist.

B. reversible and irreversible.

C. blockers and openers.

D. alkylating agents.

ANSWER: A

122. Mechanism of action of an enzyme is \_\_\_\_\_.

A. agonist and antagonist.

B. reversible and irreversible.

C. blockers and openers.

D. alkylating agents.

ANSWER: B

123. Mechanism of action of ion channel is \_\_\_\_\_.

A. agonist and antagonist.

B. reversible and irreversible.

C. blockers and openers.

D. alkylating agents.

ANSWER: C

124. Mechanism of action of DNA is \_\_\_\_\_.

A. agonist and antagonist.

B. reversible and irreversible.

C. blockers and openers.

D. alkylating agents.

ANSWER: D

125. is the process by which a drug enters the bloodstream without being chemically altered.

A. Absorption.

B. Distribution.

C. Excretion.

D. Metabolism.

ANSWER: A

126. \_\_\_\_\_ is the process that involves the delivery of the drug to the tissues.

- A. Absorption.
- B. Distribution.
- C. Excretion.
- D. Metabolism.

ANSWER: B

127. \_\_\_\_\_ have a profound effect upon the speed and efficiency with which the drug acts.

- A. Absorption.
- B. Distribution.
- C. Excretion.
- D. Routes of drug administration.

ANSWER: D

128. \_\_\_\_\_ is the process that excretes the drug through the kidney.

- A. Absorption.
- B. Distribution.
- C. Excretion.
- D. Metabolism.

ANSWER: C

129. \_\_\_\_\_ algorithm can be applied to the generation of combinatorial libraries.

- A. Morgan.
- B. Generic.
- C. Genetic.
- D. High-throughput.

ANSWER: C

130. \_\_\_\_\_ number of rules are there under the Lipinkis Rule of Five.

- A. Three.
- B. Four.
- C. Five.
- D. Two.

ANSWER: B

131. CNS active drugs crosses the \_\_\_\_\_.

- A. BB.
- B. BBB.
- C. CC.
- D. CCC.

ANSWER: B

132. Which one of the following program can be used for de novo design?

- A. LigandFit.
- B. Gold.
- C. Fred .
- D. SPROUT.

ANSWER: D

133. \_\_\_\_\_ number of years will take to come out with a single drug.

- A. 10-15.
- B. 11-15.
- C. 12-15.

D. 15-18

ANSWER: C

134. The development of drug costs upto \_\_\_\_\_.

- A. Euro500.
- B. Euro600.
- C. Euro700.
- D. Euro800.

ANSWER: D

135. \_\_\_\_\_ is placing a drug directly into the blood stream.

- A. Intravascular.
- B. Intramuscular.
- C. Subcutaneous.
- D. Inhalation.

ANSWER: A

136. \_\_\_\_\_ is endogenous catalysts converting one or several substrates into one or several products.

- A. Substrate.
- B. Enzyme.
- C. Receptor.
- D. Transporter.

ANSWER: B

137. \_\_\_\_\_ is membrane-bound or soluble protein or protein complexes exerting a physiological effect after binding of a ligand.

- A. Antagonist.
- B. Agonist.
- C. Receptor.
- D. Transporter.

ANSWER: C

138. \_\_\_\_\_ is a receptor ligand mediating a receptor response.

- A. Antagonist.
- B. Agonist.
- C. Substrate.
- D. Transporter.

ANSWER: B

139. \_\_\_\_\_ is the second step in the drug discovery process.

- A. Target identification.
- B. Target validation.
- C. Lead Finding.
- D. Lead optimization.

ANSWER: B

140. \_\_\_\_\_ is the third step in the drug discovery process.

- A. Target identification.
- B. Target validation.
- C. Lead Finding.
- D. Lead optimization.

ANSWER: C

141. \_\_\_\_\_ is the fourth step in the drug discovery process.

- A. Target identification.
- B. Target validation.
- C. Lead Finding.
- D. Lead optimization.

ANSWER: D

142. \_\_\_\_\_ is the fifth step in the drug discovery process.

- A. Lead Optimization.
- B. Preclinical trials.
- C. Clinical trials.
- D. Drug approval.

ANSWER: B

143. \_\_\_\_\_ is the sixth step in the drug discovery process.

- A. Lead Optimization.
- B. Preclinical trials.
- C. Clinical trials.
- D. Drug approval.

ANSWER: C

144. \_\_\_\_\_ is the seventh step in the drug discovery process.

- A. Lead Optimization.
- B. Preclinical trials.
- C. Clinical trials.
- D. Drug approval.

ANSWER: D

145. \_\_\_\_\_ approves drug.

- A. NCBI.
- B. EMBL.
- C. DDBJ.
- D. FDA.

ANSWER: D

146. The screening of compound using computer is called as \_\_\_\_\_ screening.

- A. In silico.
- B. In vitro.
- C. In vivo.
- D. Ex vivo.

ANSWER: A

147. Ligand and protein structure is unknown.

- A. High throughput screening.
- B. Quantitative structure activity relationship.
- C. De novo-design.
- D. Structure based design.

ANSWER: A

148. Ligand and protein structure is known, \_\_\_\_\_ is used.

- A. high throughput screening.
- B. quantitative structure activity relationship.
- C. de novo-design.
- D. structure based design.

ANSWER: D

149. In Lipinski's rule of five, the molecular weight of the drug should be less than \_\_\_\_\_ daltons.

- A. 200.
- B. 300.
- C. 400.
- D. 500.

ANSWER: D

150. Fitting a ligand from a 3D structure database into the binding site of a target protein is called \_\_\_\_\_.

- A. modeling.
- B. docking.
- C. threading.
- D. comparative modeling.

ANSWER: B

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