

Subject: Zoology
 Paper name: **Biotechnology and Bioinformatics**
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Put a tick (✓) mark against the correct answer in the corresponding brackets

1. Integrated tool for conducting automatic and manual sequence alignment, inferring phylogenetic trees, mining web-based databases
 - (a) BLAST ()
 - (b) NCBI ()
 - (c) EMBL ()
 - (d) MEGA ()

2. Which of the following terms best describes the procedure in which DNA fragments are separated on an agarose gel, transferred onto a nylon membrane, and screened with a labeled hybridization probe?
 - (a) dot blotting ()
 - (b) Southern blotting ()
 - (c) Northern blotting ()
 - (d) Western blotting ()

3. Restriction enzymes capable of making internal cuts in a DNA molecule is called
 - (a) restriction exonuclease ()
 - (b) restriction endonuclease ()
 - (c) Molecular cutter ()
 - (d) Protein knife ()

4. DNA Ligase, T4 The catalytic activity of the enzyme requires the presence of
 - (a) ATP and Mg⁺⁺
 - (b) CTP and Ca⁺⁺
 - (c) NADP and Mn ions
 - (d) Non of the above

5. Which of the following statements are true regarding PCR
 - a) billions of copies of desired DNA can be synthesized from DNA ()
 - b) Automated PCR machines are called thermal cyclers ()
 - c) A thermostable DNA polymerase is required ()
 - d) all of these ()

6. Gene therapy is the technique of cure inherit diseases by
 - (a) Repairing the faulty gene ()
 - (b) Introducing the correct copy of the gene ()
 - (c) Adding new copies of the gene ()

(d) All the above ()

7. URL of NCBI

- (a) <https://www.ebi.ac.uk/> ()
- (b) <https://www.ncbi.edu.in/> ()
- (c) <https://www.ncbi.com/> ()
- (d) <https://www.ncbi.nlm.nih.gov/> ()

8. Basic BLAST programme search translated nucleotide databases using protein query

- (a) BLAST (P) ()
- (b) BLAST (N) ()
- (c) BLAST(X) ()
- (d) BLAST(q) ()

9. 30 million citations for biomedical literature citations and abstracts include the fields of biomedicine and health, covering portions of the life sciences

- (a) MEGA ()
- (b) Pubmed ()
- (c) ENTREZ ()
- (d) FASTA ()

10. Applying the techniques of genetics and molecular biology to the genetic mapping and DNA sequencing of sets of genes or the complete genomes of selected organisms

- (a) Proteomics ()
- (b) Data Bases ()
- (c) cDNA Library ()
- (d) Genomics ()

11. Analytical technique used to detect specific proteins in a sample of tissue homogenate or extract.

- (a) Southern Blotting ()
- (b) Northern Blotting ()
- (c) Eastern Blotting ()
- (d) Western Blotting * ()

12. Restriction endonuclease is an enzyme that cuts DNA at or near specific recognition nucleotide sequences known as restriction sites

- (a) EcoRI ()
- (b) BamHI ()
- (c) HinIII ()
- (d) All the above* ()

13. Which of the following cut the DNA from specific places

- (a) Ecoli restriction endonuclease II* ()
- (b) DNA ligase ()

- (c) Exonuclease ()
- (d) Akaline Phosphatase ()

14. Data base retrieval tools are

- (a) ENTREZ, BROWSER, LOCUS LINK* ()
- (b) Introducing the correct copy of the gene ()
- (c) Adding new copies of genes ()
- (d) All the above ()

15. BLAST

- (a) BASIC LOCAL ALIGNMENT SEARCH TOOLS* ()
- (b) BASIC LOGARITHM ALIGNMENT SEARCH TOOLS ()
- (c) BASIC LOGICAL ALOGARITHM SECONDARY TOOLS ()
- (d) Non of the Above ()

16. The term Bioinformatics was coined by

- (a) Frank Tetkaia ()
- (b) Poulis Lewis ()
- (c) Paulien Hogeweg* ()
- (d) All of the above ()

17. RNA interference helps in

- (a) Cell proliferation
- (b) Micropropagation
- (c) Cell defence
- (d) Cell differentiation

18. Restriction enzymes are enzymes

- a) capable of cutting DNA molecule
- b) capable of adding nucleotides to the 3'OH end
- c) capable of restricting protein synthesise
- d) capable of joining DNA molecules

19. Which of the following are true regarding restriction enzyme

- (a) restriction enzyme are used to cut DNA molecule
- (b) restriction enzyme are used to construct restriction maps
- (c) restriction enzyme are used in RFLP
- (d) d) all of these

20. The PCR technique was developed by

- (a) Kary Mullis
- (b) Kohler
- (c) Milstein
- (d) Altman

21. PCR is a
- DNA degradation technique
 - DNA amplification technique
 - DNA sequencing technique
 - all of these
22. Which of the following statements are true regarding PCR
- billions of copies of desired DNA can be synthesized from microgram quantities of DNA
 - Automated PCR machines are called thermal cyclers
 - A thermostable DNA polymerase is required
 - all of these
23. *Thermus aquaticus* is the source of
- Taq polymerase
 - Vent polymerase
 - both a and b
 - primase enzyme
24. All the following are thermostable polymerases except
- Taq polymerase
 - Vent polymerase
 - DNA polymerase III
 - pfu polymerase
26. The first step of PCR is
- denaturation
 - annealing
 - primer extension
 - none of these
27. Genetic engineering involves the treatment of genetic disorders like sickle cell anemia, Duchenne muscular dystrophy
- Genetic Engineering in agriculture
 - Genetic Engineering in Medicines
 - Both a & b
 - all the above
28. Pubmed comprises more than 29 million citations for biomedical literature from
- MEDLINE
 - Pubmed
 - ClinVar
 - All the above
29. PCR is used in
- site specific recombination
 - site directed mutagenesis

- c) both a and b
d) site specific translocation
30. Reverse transcriptase PCR uses
a) mRNA as a template to form cDNA
b) RNA as a template to form DNA
c) DNA as a template to form ssDNA
d) all of these
31. Two bacteria most useful in genetic engineering are
a) Rhizobium and Azobacter
b) Nitrosomonas and Klebsilla
c) Escherichia and Agrobacterium
d) Rhizobium and Diplococcus
32. The travel of gene expression and gene activation can be measured using which of the following?
a) Reporter gene
b) Marker gene
c) Gene sequences
d) Promoter element
33. Application of embryo culture is in
a) clonal propagation
b) Production of alkaloids
c) Production of soma clonal variation
d) overcoming hybridisation barrier
34. The uptake of plasmid DNA into the bacterial cell is facilitated by the presence of --- in the medium
a) Calcium Chloride
b) Potassium chloride
c) Magnesium chloride
d) none of these
35. DNA molecules, identical except for different numbers of super helical turns are called
a) Chain isomers
b) Topoisomers
c) Helical isomers
d) Geometrical isomers
36. Margaret Dayhoff developed the first protein sequence database called
a) SWISS PROT
b) PDB
c) Atlas of protein sequence and structure
d) Protein sequence databank
37. NCBI was established in
a) 1988
b) 1989

- c) 1990
d) 1991
38. Application of bioinformatics include
a) data storage and management
b) drug designing
c) understand relationships between organisms
d) all of the above
39. Proteomics is the study of
a) set of proteins
b) set of proteins in a specific region of the cell
c) entire set of expressed proteins in a cell
d) none of these
40. The process of finding $\beta^\circ z$ /relative location of genes on a chromosome is called
a) gene tracing
b) genome mapping
c) genome walking
d) chromosome walking
- 41 Catalyzes the linkage between two free ends of double-stranded DNA chains by forming a phosphodiester bond
(a) Ligans
(b) DNA Fragments
(c) DNA ligase
(d) All the above
- 42 DNA is produced from fully transcribed mRNA found in the
(a) Nucleus
(b) Nucleolus
(c) Cytoplasm
(d) All the above
- 43 produce proteins that kill certain insects with alkaline digestive tracts
(a) Bt
(b) Bc
(c) Tdn
(d) All the above
- 44 Determining the nucleotide sequencing of all the DNA in a genome is called
(a) Gene mapping
(b) Gene splicing
(c) Genome sequencing
(d) All the above
- 45 locate specific sequences in restriction fragments that have been separated by gel electrophoresis

- (a) Southern Blot Technique
- (b) Northern Blot technique
- (c) Eastern Blot technique
- (d) Western Blot technique

46 computer software for conducting statistical analysis of molecular evolution and for constructing phylogenetic trees

- (a) MEGA
- (b) EMBL
- (c) FASTA
- (d) BLAST

47 A collection of genomics, functional genomics, and genetics studies and links to their resulting datasets.

- (a) GeneBank
- (b) Gene Library
- (c) Genome size
- (d) All the above

48. A resource to provide a public, tracked record of reported relationships between human variation and observed health status with supporting evidence.

- (a) PubMed
- (b) Bookshelf
- (c) NIH
- (d) ClinVar

49 citations and abstracts include the fields of biomedicine and health, covering portions of the life sciences, behavioral sciences, chemical sciences, and bioengineering.

- (a) Pubmed
- (b) Bookshelf
- (c) PDBe
- (d) EMBL

50. European resource for the collection, organisation and dissemination of data on biological macromolecular structures

- (a) PDBe
- (b) BLAST
- (c) NCBI
- (d) EMBL

51. Be also works actively with the

- (a) X-ray crystallography,
- (b) Nuclear Magnetic Resonance (NMR)
- (c) cryo-Electron Microscopy (EM)
- (d) all the above

- 52 Branch of biotechnology concerned with applying the techniques of molecular biology, biochemistry, and interactions of the proteins produced by the genes
- (a) Proteomics
 - (b) Genomics
 - (c) Bionic
 - (d) All the above
53. the software that interacts with end users, applications, and the database itself to capture and analyze the data.
- (a) DBMS
 - (b) IBMS
 - (c) Data Bank
 - (d) all the above
54. Software that manages computer hardware and software resources and provides common services for computer programs
- (a) Bioinformatics
 - (b) Genomic
 - (c) Proteomics
 - (d) all the above
- 55 A collection of nucleotide sequences from several sources, including GenBank, RefSeq,
- (a) RNA Data bases
 - (b) ClinVar
 - (c) Nucleotide Data bases
 - (d) All the above
56. The BLAST program was developed in _____
- a) 1992
 - b) 1995
 - c) 1990
 - d) 1991
57. The final step involves pairwise alignment by extending from the words in both directions while counting the alignment score using the same
- (a) substitution matrix.
 - (b) Genomic matrix
 - (c) Extra cellular fluid
 - (d) All tha above
- 58 Which of the following is not a variant of BLAST?
- a) BLASTN
 - b) BLASTP
 - c) BLASTX
 - d) TBLASTNX

59. Which of the following is not a correct about BLAST?
- The BLAST web server has been designed in such away as to simplify the task of program selection.
 - The programs are organized based on the type of query sequences
 - The programs are organized based on the type of nucleotide sequences, or nucleotide sequence to be translated
 - BLAST is not based on heuristic searching methods
60. Which of the following is a mismatch?
- Polymerase – Taq polymerase
 - Template – double stranded DNA
 - Primer – oligonucleotide
 - Synthesis – 5' to 3' direction
- 61 Primer used for the process of polymerase chain reaction are
- Single stranded DNA oligonucleotide
 - Double stranded DNA oligonucleotide
 - Single stranded RNA oligonucleotide
 - Double stranded RNA oligonucleotide
- 62 Polymerase used for PCR is extracted from
- Escherichia coli*
 - Homo sapiens*
 - Thermus aquaticus*
 - Saccharomyces cerevisiae*
- 63 How many DNA duplex is obtained from one DNA duplex after 4 cycles of PCR?
- 4
 - 8
 - 16
 - 32
- 64 At what temperature do denaturation of DNA double helix takes place?
- 60°
 - 54°
 - 74°
 - 94°
- 65 At what temperature do annealing of DNA and primer takes place?
- 42°
 - 54°
 - 74°
 - 96°
- 66 The type of DNA amplification where the region of DNA amplified lies on either side of a known segment
- RT – PCR
 - Anchored – PCR
 - Inverse – PCR
 - Nested – PCR

- 67 Primer complementary to regions used in inverse PCR is
- (a) 3' end of unknown region
 - (b) 5' end of unknown region
 - (c) 3' end of known region
 - (d) 5' end of known region
- 68 With respect to target DNA used in inverted PCR which of the following is not true?
- (a) Restricted segment
 - (b) Blunt ended segment
 - (c) Intact known segment
 - (d) Flanked unknown segment flanked on either side
- 69 Which of the following is not required for DNA sequencing?
- (a) Restriction digestion
 - (b) Electrophoresis
 - (c) Cloning
 - (d) Polymerase chain reaction
70. The first bioinformatics database was created by
- (a) Richard Durbin
 - (b) Dayhoff
 - (c) Michael J.Dunn
 - (d) Pearson
- 71 SWISSPROT protein sequence database began in
- (a) 1985
 - (b) 1986
 - (c) 1987
 - (d) 1988
- 72 An example of Homology & similarity tool?
- (a) PROSPECT
 - (b) EMBOSS
 - (c) RASMOL
 - (d) BLAST
- 73 Deposition of cDNA into inert structure is
- (a) DNA fingerprinting
 - (b) DNA polymerase
 - (c) DNA probes
 - (d) DNA microarrays
- 74 Analysing or comparing entire genome of species
- (a) Bioinformatics
 - (b) Genomics
 - (c) Proteomics
 - (d) Pharmacogenomics

75 Which of the following is a nucleotide sequence data base?

- (a) EMBL
- (b) SWISS PROT
- (c) PROSITE
- (d) TREMBL

B. Fill up the blanks [15 (3 from each unit)]

1. _____ banks are a type of biorepository which preserve genetic material
- 2 DNA Finger printing) technique was developed by _____ in 1985 (UK)
- 3 The most common enzymes used in PCR is Thermostable enzyme called _____
- 4 P** _____ are commonly constructed to figure out the evolutionary relationship among species
- 5** _____ Search protein database using a translated nucleotide query
- 6** _____ is stored as a file or a set of files on magnetic disk or tape, optical disk, or some other secondary storage device
- 7** _____ is the field of science in which biology, computer science, and information technology merge to form a single discipline.
- 8 The term Bioinformatics was coined by _____ in 1979
- 9 the Human Genome Project was started in the year of _____
- 10.** PDBe participates regularly in _____ roadshows
- 11 PDBe collaboration with Worldwide _____ (wwPDB)
12. Full form of PDBe-KB is Proten Data Bank in Europe _____
- 13 _____ is a method widely used to rapidly make millions to billions of copies of a specific DNA sample
14. _____ is a free search engine accessing primarily the MEDLINE database of references and abstracts on life sciences and biomedical topics.
15. _____ refers to the direct **manipulation** of DNA to alter an organism's characteristics (phenotype) in a particular way

Key Answers

A. Multiple choice questions [replace x]

1. d) 2. b) 3. b) 4. a) 5. d) 6. d) 7. d)
8. b) 9. b) 10. d) 11. d) 12. d) 13. a) 14. a)
15. a) 16. c) 17. d) 18. a) 19. d) 20. a) 21. d)
22. d) 23. a) 24. c) 25. b) 26. a) 27. b) 28. a)
29. b) 30. a) 31. c) 32. b) 33. d) 34. a) 35. b)
36. c) 37. a) 38. d) 39. c) 40. b) 41. c) 42. a)
43. a) 44. c) 45. a) 46. a) 47. a) 48. d) 49. a)
50. a) 51. d) 52. a) 53. a) 54. a) 55. c) 56. a)
57. a) 58. d) 59. d) 60. b) 61. a) 62. c) 63. c)
64. d) 65. d) 66. c) 67. c) 68. b) 69. c) 70. a)
71. c) 72. d) 73. d) 74. b) 75. d)

B. Fill up the blanks

1. Gene
2. Alee Jeffrays
3. Tag Polymerase
4. Phylogenetic trees
5. Blastx
6. database
7. Bioinformatics
8. Paulien Hogeweg
9. 1991
10. EMBL-EBI
11. Protein Data Bank
12. Knowledge bank
13. Polymerase chain reaction (PCR)
14. PubMed
15. Genetic Engineering