2021

Molecular Biology and Biotechnology

[HONOURS]

Paper : VIII

Full Marks : 80 Time : 4 Hours

The figures in the right-hand margin indicate marks.

Candidates are required to give their answers in their own words as far as practicable.

Use separate answer script for each GROUP.

GROUP-A

(Marks : 50)

1. Answer any **two** questions: 1×2=2

   a) What is Pribnow box?

   b) RAPD is a –

      i) Restriction digestion based technique

      ii) DNA sequencing based technique

      iii) PCR based technique

      iv) All of these

   c) Name one gaseous mutagenic agent.

   d) What is gene kissing?

2. Answer any **five** questions: 2×5=10

   a) What is the difference between chromosome walking and chromosome jumping?

   b) Schematically represent the workflow of 2-D gel electrophoresis.

   c) Why SNP array technology is considered as a powerful genomic analysis tool?

   d) Why photoreactivation is not regarded as a universal DNA repair system?

   e) Why P^{53} has been widely regarded as "the guardian of the genome"?

   f) What is the biological significance of intron?

   g) What are the "hallmarks" (traits/characters) of cancer?

   h) What were the primary goals of HGP (Human genone project)?

3. Answer any **three** questions: 6×3=18

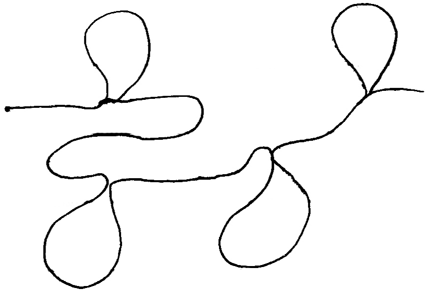
   a) Write two characteristic features of apoptosing cell. With suitable diagram illustrate the extrinsic (receptor mediated) apoptosis pathway. 1+5=6

   b) What is expression proteomics? Write a brief note on application of proteomics. 2+4=6

   c) Cite two examples of second messenger. What is the role of G protein in a signaling pathway? 2+4=6

d) What is transcription bubble? How can enhance affect the transcription of a gene that is thousand of nucleotide away from the promoter? 2+4=6

e) DNA from a eukaryotic gene was isolated, denatured and hybridized to a mRNA transcribed from a gene. This hybridized structure was observed using electron microscope. The following structure was observed.



How many introns are there in this gene? What is lariat structure? Explain the role of guide RNAs in RNA editing. 2+2+2=6

f) Deamination of guanine by nitrous acid is not mutagenic - explain why? Schematically represent the base excision repair pathway. 2+4=6

4. Answer any **two** questions: 10×2=20

a) What is DNA fingerprinting? Describe how RFLPs can be used in gene mapping. Compare between RFLP and RAPD. 1+6+3=10

b) Differentiate between gene and genome. What was the name of sequence method which was proposed by Craig Venter? Differentiate between structural proteomics and functional proteomics.Write a brief note on compartive proteomics. 2+1+4+3=10

c) With suitable diagram describe the "Holiday model" for homologous recombination of DNA. Write down the role of RecA (recA gene product) in the SOS repair and homologous recombination. 7+3=10

d) Define proto-oncogene and tumor suppressor gene. What is philadelphia chromosome? Explain how philadelphia chromosome is formed and causes and CML cancer? Enumerate the Knudson's two-hit hypothesis for the occurrence of retinoblastoma. 2+1+3+4=10

GROUP-B

(Marks : 30)

5. A) Select the correct answer from the following options : 1×4=4

   i) DDBJ is

      a) Tool

      b) Software

      c) Protein sequence based Database

      d) Nucleotide sequence based Database

   ii) Maximum parsimony method will be used to generate phylogenetic tree when the sequences are

      a) Less similar

      b) Moderately similar

      c) Highly similar

      d) None of the above

   iii) BLAST is a

      a) Database

      b) Format

      c) Tool

      d) All

   iv) PIR is

      a) Format

      b) Database of Protein sequences

      c) Tool

      d) None of the above

   B) Mention **true** or **false** for (i); (ii) and fill in the blanks in (iii) and (iv): 1×4=4

   i) WiFi stands for _____

   ii) URL of NCBI is _______

   iii) PDB is a software.

   iv) UPGMA is a database.

6. Answer any **two**: 2×2=4

   i) What is the difference between phylogram and cladogram?

   ii) What is drug?

   iii) What are the features of FASTA format?

   iv) What are the differences between local and global alignment?

7. Answer any **two**: 4×2=8

   i) What are PAM and BLOSUM?

ii) Write about the algorithm of FASTA search tool.

iii) How many rooted and unrooted trees are possible using 7 taxa?

8. Answer any **two**: 5×2=10

i) Write a short note with example on SW algorithm.

ii) How will you use microarray chip for the determination of a disease responsible protein / gene to develop a new drug?

iii) What is the role of Bioinformatics in Biotechnology?