Name : .....

Roll No. : .....

Invigilator's Signature : .....

CS/B.SC(H),MICRO.BIO/BT/MOL-BIO/GENETICS/SEM-5/DPB-501/2012-13

2012
DNA TYPING, PROTEOMICS AND BEYOND

Time Allotted : 3 Hours *Full Marks :* 70

The figures in the margin indicate full marks.

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

GROUP – A

(Multiple Choice Type Questions)

1. Choose the correct alternatives for any *ten* of the following : 10 × 1 = 10

   i) The example of one metabolic pathway database is

      a) KEGG b) SWISS

      c) BLISS d) OMIMM.

   ii) Transcriptome are the

      a) Whole genome b) Whole set of RNA

      c) Total set of exons d) Whole set of protein.

   iii) Number of base pairs in hypervariable region 1 of *mt*DNA control region is

      a) 268 b) 342

      c) 400 d) 500.

iv) DYS-390 is a
   a) Single locus VNTR marker
   b) Multilocus VNTR marker
   c) STR marker
   d) None of these.

v) LINEs are more frequent in
   a) Human b) Birds
   c) Frogs d) none of these.

vi) The size of the core sequence of microsatellie is
   a) 2-4 bp b) 5-50 bp
   c) 10-100 bp d) 100-1000 bp.

vii) ESI is
   a) Electro Spray Ionisation
   b) Electron Spark Ionization
   c) Electron Spark Initiation
   d) None of these.

viii) Cellular proteomics is the branch of proteomics whose goal is
   a) about the analysis of whole genome
   b) to map the location of proteins and protein-protein interactions in whole cells during key cell events
   c) about the transcriptional regulation control
   d) none of these.

ix) One disadvantage of metabolomics is
   a) high risk of false positive data
   b) highly qualified expertise required
   c) unavailability of biomarkers
   d) problem of collecting body fluid.

x) Protein array includes interactions of

a) protein ligand b) protein drug

c) protein antibody d) all of these.

xi) To identify the location of labelled proteins, the technique used is

a) chromatography b) FRET

c) NMR d) X-ray tomography.

xii) Analyser used in Tandem mass can be

a) TOF b) magnetic analyzer

c) quadrupole d) all of these.

GROUP – B

(Short Answer Type Questions)

Answer any *three* of the following. 3 × 5 = 15

2. What is the full form of RAPD ? Describe how it can be used as genetic fingerprint. 1 + 4

3. Describe the process of protein array. 5

4. Write down the use of SNP mapping. 5

5. Describe any PCR based DNA typing technique. 5

6. Write a short note on mitochondrial DNA (*mt*DNA) analysis. 5

GROUP – C

(Long Answer Type Questions)

Answer any *three* of the following. 3 × 15 = 45

7. Write short notes on the following :

   a) STR

   b) VNTR

   c) Satellite DNA.

8. What is DNA typing ? Discuss the characteristic features of DNA polymorphisms. What is SNP ? Write down the limitations of metabolomics. What are the key applications of metabolomics ? 2 + 3 + 2 + 4 + 4

9. What is repetitive DNA ? How does it differ from unique DNA ? Classify repetitive DNA and describe each class with suitable example. 2 + 2 + 4 + 7

10. Write the procedure of Transcriptome analysis. Point out the application of proteomics. What is nuclear proteome ? Name one database used in forensic science laboratory.

    6 + 5 + 2 + 2

11. Write down the significance of colors in obligo-nucleotide microarray. Define synonymous, missence, frame-shift SNPs. What are the limitations of metabolomics. What is biochemical network. Explain briefly.