TOTAL PAGES: 3

**22BTU520N**

**PSG COLLEGE OF ARTS & SCIENCE**
(AUTONOMOUS)

**BSc DEGREE EXAMINATION DECEMBER 2025**
(Fifth Semester)

Branch – **BIOTECHNOLOGY**

**GENOMICS AND PROTEOMICS**

Time: Three Hours Maximum: 75 Marks

**SECTION-A (10 Marks)**
Answer **ALL** questions
**ALL** questions carry **EQUAL** marks (10 × 1 = 10)

| Module No. | Question No. | Question | K Level | CO |
|---|---|---|---|---|
| 1 | 1 | Which of the following non-coding repetitive sequences are typically shorter than 500 bp and are not autonomous in their replication?<br>a. LINEs b. SINEs<br>c. Pseudogenes, d. Satellites | K1 | CO1 |
| | 2 | What is the primary purpose of gene annotation in structural genomics?<br>a. To compare genomes of different species,<br>b. To physically map genes on a chromosome,<br>c. To assign functional and structural information to raw DNA sequences,<br>d. To determine the order of DNA fragments | K1 | CO1 |
| 2 | 3 | The sequencing technology that involves mapping large-insert clones (like BACs) before fragmentation is known as:<br>a. Whole-Genome Shotgun b. NGS<br>c. Hierarchical Shotgun Sequencing d. Pyrosequencing | K2 | CO2 |
| | 4 | Distinguish the key difference between orthologs and paralogs.<br>a. Orthologs arise from gene duplication, paralogs from speciation.<br>b. Orthologs are non-coding; paralogs are coding. c. Orthologs are within a species; paralogs are across species.<br>d. Orthologs arise from speciation; paralogs arise from gene duplication. | K2 | CO2 |
| 3 | 5 | In a typical 2D-Electrophoresis experiment, which property is used to separate proteins in the first dimension ?<br>a. Molecular Weight b. Hydrophobicity<br>c. Isoelectric Point (pI) d. Charge Density | K2 | CO3 |
| | 6 | Outline the principle that allows Mass Spectrometry to identify an unknown protein or peptide.<br>a. Measuring the speed of the protein in an electric field.<br>b. Determining the mass-to-charge ratio (m/z) of ionized peptides and matching it to a database.<br>c. Separating proteins based on gel matrix migration.<br>d. Using antibodies to detect specific protein sequences. | K2 | CO3 |
| 4 | 7 | The specialized area of proteomics focused on determining the three-dimensional atomic structure of proteins is called_____.<br>a Functional Proteomics b. Differential Proteomics<br>c. Structural Proteomics d. Expression Proteomics | K2 | CO4 |
| | 8 | Summarize the main difference in application between Protein Microarrays and DNA Microarrays.<br>a. DNA microarrays study protein function; protein microarrays study gene expression.<br>b. Protein microarrays study protein binding/function; DNA microarrays study mRNA expression.<br>c. DNA microarrays are used for sequencing; protein microarrays for quantification.<br>d. Protein microarrays use fluorescent labels; DNA microarrays use radioisotopes. | K2 | CO4 |

**Cont...**

| | | | | |
|---|---|---|---|---|
| 5 | 9 | Personalized Medicine primarily relies on information derived from which field of study?<br>a. Systems Biology b. Pharmacogenomics<br>c. Epidemiology d. Metabolomics | K2 | CO5 |
| | 10 | Explain the core purpose of High Throughput Screening (HTS) in the context of drug discovery.<br>a. To validate the safety of clinical drug candidates.<br>b. To determine the 3D structure of a drug target protein.<br>c. To rapidly screen large chemical libraries for compounds that modulates a specific biological target.<br>d. To analyze all metabolites in a cell. | K2 | CO4 |

## SECTION - B (35 Marks)

Answer **ALL** questions

**ALL** questions carry **EQUAL** Marks (5 × 7 = 35)

| Module No. | Question No. | Question | K Level | CO |
|---|---|---|---|---|
| 1 | 11.a. | Illustrate the procedure for RFLP (Restriction Fragment Length Polymorphism) as a DNA marker tool. | K4 | CO1 |
| | | (OR) | | |
| | 11.b. | Compare and contrast the characteristics of SINEs (Short Interspersed Nuclear Elements) and LINEs (Long Interspersed Nuclear Elements). | | |
| 2 | 12.a. | Solve the process of hierarchical shotgun sequencing, highlighting its key steps and advantages over whole-genome shotgun sequencing. | K4 | CO2 |
| | | (OR) | | |
| | 12.b. | Apply the concepts of orthologs and paralogs to categorize gene relationships across different species and within the same species | | |
| 3 | 13.a. | Analyze the steps involved in a Yeast Two-Hybrid System and infer how it is used to identify protein-protein interactions. | K3 | CO3 |
| | | (OR) | | |
| | 13.b. | Examine the process of MALDI-TOF Mass Spectrometry and determine how it is specifically used for protein identification. | | |
| 4 | 14.a. | Analyze the data output from a c-DNA microarray experiment and interpret the results to understand gene expression profiling. | K3 | CO4 |
| | | (OR) | | |
| | 14.b. | Examine the field of Metabolomics and outline how it complements Genomics and Proteomics studies. | | |
| 5 | 15.a. | Model the path of a drug from gene target identification using pharmacogenomics to the development of a personalized medicine. | K3 | CO5 |
| | | (OR) | | |
| | 15.b. | Relate the concept of personalized medicine to the outcomes of pharmacogenomic studies in drug development. | | |

Cont...

## SECTION -C (30 Marks)

Answer **ANY THREE** questions
**ALL** questions carry **EQUAL** Marks (3 × 10 = 30)

| Module No. | Question No. | Question | K Level | CO |
|---|---|---|---|---|
| 1 | 16 | Analyze the different types of DNA Polymorphisms (RFLP, SNP, AFLP) and examine their significance as genetic markers in physical and genetic mapping. | K5 | CO1 |
| 2 | 17 | Examine the Human Genome Project (HGP), outlining its goals, initial procedures, and major outcomes that transformed modern biology. | K4 | CO2 |
| 3 | 18 | Analyze the process of 2D-Electrophoresis (Isoelectric Focusing and SDS-PAGE) and its limitations, and interpret why it is often coupled with Mass Spectrometry (LC/MS-MS) for comprehensive protein analysis. | K5 | CO3 |
| 4 | 19 | Analyze the use of Microarrays in proteomics. Compare and contrast different microarray types (protein and peptide) and determine their applications in drug discovery. | K4 | CO4 |
| 5 | 20 | Examine the role of Pharmacogenomics in High Throughput Screening (HTS) for drug discovery. Interpret how identifying gene targets using HTS contributes to developing safer and more effective drugs. | K4 | CO5 |

Z-Z-Z END