

Syllabus for Admission for the PhD programme in RMRIMS for the Academic Year 2024-2025 for Calcutta University

There are two part of the syllabus, part 'A' and part 'B'. Part 'A' is compulsory. Those who qualify part 'A' will be evaluated for part 'B'

Part A

This part is common to all the candidates appearing for pre Ph.D. registration test. There will be 50 objective type questions in Part 'A' of written test paper (One mark each; Total 50 marks, Time: one hour, no negative marking).

Topics

1. Questions will be asked from general awareness of science and its interface with society, aptitude of scientific and quantitative reasoning to evaluate the creativity, analytical ability and research aptitude of candidates.
2. Computer application. Tools of artificial intelligence.

Part B

The candidate has to answer all the objective type questions (One mark each. Total 100 marks, Time: 2 ½ hours. For each incorrect answer, a negative marking of 0.25 marks will be applied).

GROUP-A: LIFE SCIENCES:

1. Structure of atoms, molecules and chemical bonds. Structure and function of carbohydrates, lipids, proteins, nucleic acids and vitamins. Stabilizing interactions (electrostatic, hydrogen bonding, hydrophobic interaction etc.). Principles of biophysical chemistry, pH, buffer. Bioenergetics, glycolysis, oxidative phosphorylation. Principles of catalysis, enzymes and enzyme kinetics, enzyme assay, enzyme regulation.
2. Cellular Organization: Structure of membrane and function, lipid bilayer and membrane protein diffusion, osmosis, ion channels, ion pumps. Structure and function of nucleus, mitochondria, Golgi bodies and plastids. Organization of gene and chromosomes, structure of chromatin and chromosomes, heterochromatin, euchromatin. Cell division and cell cycle.
3. Bio molecules and their process: DNA replication and recombination. RNA synthesis and processing. Protein synthesis and post transcriptional modification.
4. Cellular communication and signalling: Host parasite interaction. Cell surface receptors. Signal Transduction Pathways and its regulation. Cells and molecules involved in innate and adaptive immunity, antigens, antigenicity and immunogenicity. Epitopes, structure and function of antibody, generation of antibody diversity, monoclonal antibodies, antigen-antibody interactions, MHC molecules, antigen processing and presentation, activation and differentiation of B and T cells, B and T cell receptors. Hypersensitivity and autoimmunity. Vaccine.
5. Photosynthesis, respiration and photorespiration, nitrogen metabolism, plant hormones. Structure, function and mechanisms of action of phytochromes, stomatal movement, photoperiodism and biological clocks. Blood and circulation, blood group and blood coagulation, cardiovascular system, respiration, central and peripheral nervous system, physiology of excretion, kidney, waste elimination, regulation of water balance, blood volume, blood pressure, electrolyte balance, acid-base balance, thermoregulation, digestion and absorption of food, endocrine glands, hormones and diseases.
6. Mendelian principles, deviation from Mendelian inheritance, concept of gene, allele, multiple alleles, pseudoallele, extensions of Mendelian principles, incomplete dominance, gene interactions, linkage and crossing over. Extra chromosomal inheritance. Microbial genetics, transformation, conjugation, transduction and sex-duction. Structural and numerical alterations of chromosomes, deletion, duplication, inversion, translocation, ploidy and their genetic implications.
7. Concepts of species and hierarchical taxa, biological nomenclature, classical and quantitative methods of taxonomy of plants, animals and microorganisms, structural organization of unicellular, colonial and multicellular forms.

8. The Environment, biotic and abiotic interactions, ecological niche, population growth curves, species interactions, interspecific competition, herbivory, carnivory, pollination, symbiosis, community structure, species diversity, succession, concept of climax, energy flow and mineral cycling (CNP), biomes.
9. Sterilization; Media preparation; Plant and animal tissue/cell culture; Drug sensitivity assay; Fermentation.
10. Methods for isolation and purification of nucleic acids and proteins, gel electrophoresis, isoelectric focusing, HPLC, FPLC, molecular cloning of DNA/RNA in bacterial systems, expression of recombinant proteins, isolation of specific nucleic acid sequences, generation of genomic and cDNA libraries, in vitro mutagenesis and deletion techniques, gene knock out in bacterial and eukaryotic organisms, protein sequencing, detection of post-translation modification of proteins, DNA sequencing, micro array, RFLP, RAPD and AFLP, ELISA, RIA, western blot, immunoprecipitation, flow cytometry and immunofluorescence microscopy. Analysis of biomolecules using UV/visible spectroscopy, fluorescence spectroscopy, staining techniques, different types of microscopy, immunohistochemistry. Quality Control, Good Clinical Practice (GCP), Good Laboratory practice (GLP).
11. Measures of central tendency and dispersal; probability, sampling distribution, confidence interval, errors, levels of significance, regression and correlation, t-test, analysis of variance, X² test.
12. Nucleic acid and protein sequence databases, data mining methods for DNA and protein sequence analysis, web-based tools for sequence searches, motif analysis and presentation, multiple sequence alignments. Molecular modeling: Energy minimization, conformational analysis, global conformational analysis, approaches and problems; minimum conformations. Protein Ligand docking, QSAR, methods for protein-ligand docking, applications; Screening small molecule databases, docking of combinatorial libraries, input data, analyzing docking results software accessibility; Flexidock, creating input structures, Ligand proposition, binding pockets, flexible bonds, genetic algorithm, scoring. Protein folding and model generation; secondary structure prediction, analyzing secondary structure; protein loop searching, concept of homology modeling, homologous sequence identification; Align structure; Construction of variable and conserved region, topology fingerprint approach, alignment algorithm analysis, crystallographic databases.