RW-6519 **502201**

M.Sc. DEGREE EXAMINATION APRIL 2011

Bioinformatics

GENETICS AND MOLECULAR BIOLOGY

(CBCS—2010 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** the questions.

All questions carry equal marks.

1. Nucleotide.

2. Promoter.

3. Structural genes.

4. Prophage.

5. CDKs.

6. Example for alkylating agents.

7. Tn10.

8. Eugenics.

9. CVS.

10. Anti-codon.

Part B (5 × 5 = 25)

Answer **all** questions choosing **either** (a) **or** (b)

All questions carry equal marks.

11. (a) Explain Theta replication model with a neat diagram.

(*Or*)

(b) Describe post translational modification.

12. (a) Write a note on Trp operon.

(*Or*)

(b) .Draw and explain in brief about λ– phage.

13. (a) Give an account about the various types of mutants.

(*Or*)

(b) Explain briefly Heat shock response

14. (a) Write short notes on *Hfr* strains.

(*Or*)

(b) Short notes on Recombinational repair mechanism.

15. (a) Give an account on Etiology of cancer.

(*Or*)

(b) Write short notes on Prenatal diagnosis.

Part C (3 × 10 = 30)

Answer any **three** questions.

All questions carry equal marks.

16. Describe in detail about the Gene regulations in eukaryotes.

17. Compare and contrast on lysis and lysogeny cycle.

18. Describe the various DNA repair mechanism with neat sketch.

19. What are transposable elements ? Comment on its mechanisms.

20. Describe in detail about Cell cycle regulation.

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RW-6520 **502202**

M.Sc. DEGREE EXAMINATION APRIL 2011

Bioinformatics

BIOLOGICAL DATABASES

(CBCS—2010 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** the questions.

All questions carry equal marks.

1. Name any *two* secondary database.

2. Popular sequence formats.

3. Genomic viewers.

4. MMDB.

5. Information retrieval system-Entrez

6. Genetic linkage map.

7. UCSC.

8. MINT.

9. Protein folding.

10. DNA marker.

Part B (5 × 5 = 25)

Answer **all** questions choosing **either** (a) **or** (b)

All questions carry equal marks.

11. (a) Explain in brief about Uniprot.

(*Or*)

(b) Explain the primary nucleotide databases.

12. (a) Write a detailed account on protein structural viewers.

(*Or*)

(b) Discuss in short about structure similarity searching.

13. (a) Give a short account on sequence retrieval system with examples.

(*Or*)

(b) Explain the importance of MESH terms in retrieving data from PUBMED

14. (a) Describe the unique features of nucleic acid sequence analysis.

(*Or*)

(b) Write short notes on genomic databases.

15. (a) Comment on genome mapping element.

(*Or*)

(b) Write brief account on 'Ensemble'.

Part C (3 × 10 = 30)

Answer any **three** questions.

All questions carry equal marks.

16. Give a detailed account on protein sequence databases with suitable examples.

17. Explain in detail about PDB and MMDB with suitable illustrations.

18. Write a detailed account on information retrieval system with examples.

19. Discuss in detail about human genome project add a note on its current developments.

20. Write an account on protein structure prediction with suitable examples.

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RW-6521 **502203**

M.Sc. DEGREE EXAMINATION, APRIL 2011

Bioinformatics

ALGORITHMS FOR COMPUTATIONAL BIOLOGY

(CBCS—2010 onwards)

Time : 3 Hours Maximum : 75 Marks

Section A (10 × 2 = 20)

Answer **all** the questions.

All questions carry equal marks.

1. Designing algorithms.

2. Bubble sort.

3. Connected components.

4. Prim's Algorithm

5. Forests.

6. Ancestors and descendants.

7. Iteration method.

8. Divide and conquer.

9. Dynamic programming.

10. Red-black trees.

Section B (5 × 5 = 25)

Answer **all** questions choosing **either** (a) **or** (b)

All questions carry equal marks.

11. (a) List out the applications of Binary search trees.

(*Or*)

(b) Discuss about Time and Complexity algorithms and its property.

12. (a) Give short note on relation matrices with example.

(*Or*)

(b) Describe about string matching with any two example.

13. (a) Describe about colouring of graphs with suitable example.

(*Or*)

(b) Give detail note on insertion and deletion in trees.

14. (a) Write the features of sets in computing algorithm.

(*Or*)

(b) Differentiate asymptomatic notation and standard notation

15. (a) Give an account on Backtracking algorithms.

(*Or*)

(b) Write a comment on Red-black trees with properties.

Section C (3 × 10 = 30)

Answer any **three** questions.

All questions carry equal marks.

16. Explain in detail about Fibonacci search.

17. Explain the following :

    (a) Knuth-Morris-Pratt algorithm.

    (b) Boyer-Moore algorithm.

18. What are All-pair shortest paths and explain it with Floyd-Warshall algorithm.

19. Give an account on backtracking algorithms along with any two examples.

20. Explain about Binary search trees and its applications.

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RW-6522 **502204**

M.Sc. DEGREE EXAMINATION, APRIL 2011

Bioinformatics

LAB III : SEQUENCE ANALYSIS

(CBCS—2010 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

All questions carry equal marks

1. Define blastp

2. Define dot plot

3. What is an alpha helix?

4. What are the uses of Rasmol?

5. List the software used for secondary structure prediction.

6. What is a MMDB?

7. Define phylogenetic analysis

8. What are the uses of Pfam Database?

9. Define Expressed sequence tag

10. What are the uses of structural databases?

Part B (5 × 5 = 25)

Answer **all** questions. Choosing either (a) or (b)

All questions carry equal marks

11. (a) Write short notes' on sequence alignment?

(*Or*)

(b) Explain how is dot plot analysis performed?

12. (a) Differenciate global and local alignment methods?

(*Or*)

(b) What are the conserved sequences? What are the advantages of MSA over pair-wise comparisons?

13. (a) Define different FASTA programs and its applications.

(*Or*)

(b) What are the databases used in phylogenetic analysis?

14. (a) Write short notes on CATH and SCOP databases

(*Or*)

(b) What are the methods used in primer design?

15. (a) What are the tools used for protein identification?

(*Or*)

(b) Write short notes on OMIM

Part C (3 × 10 = 30)

Answer any **three** questions

All questions carry equal marks

16. Explain in details about protein secondary structure predition methods.

17. Write down short summary on PSI-BLAST and its applications.

18. State the role of Smith-Waterman algorithm in alignment techniques.

19. Describe varous PAM matrices and its uses in sequence alignment.

20. Write short notes on

    (a) PROSITE

    (b) BLOCKS

    (c) PFAM

    (d) Interpro

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RW-6523 **502205**

M.Sc. DEGREE EXAMINATION, APRIL 2011

Bioinformatics

LAB IV : MYSOL AND PERL PROGRAMMING

(CBCS—2010 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

All questions carry equal marks

1. Define : Database

2. Write a syntax to delete a table.

3. What are the advantages of MYSQL over others?

4. What are the operators available in MYSQL?

5. Define : arrays.

6. What are the heirarchy of operators?

7. Define : Regular expressions.

8. Define : Patterns.

9. What is Database manipulation?

10. Define : Process management.

Part B (5 × 5 = 25)

Answer **all** questions. Choosing either (a) or (b)

All questions carry equal marks

11. (a) Write a SQL program to create and delete database.

(*Or*)

(b) Write a SQL statement to create a student table.

12. (a) Differentiate sorting and grouping.

(*Or*)

(b) Explain about math functions.

13. (a) Explain about literal representation.

(*Or*)

(b) Explain array manipulation functions.

14. (a) Write short notes on split and join function.

(*Or*)

(b) Write short notes on substitution.

15. (a) Explain random access databases.

(*Or*)

(b) Explain the uses of BIOPERL

Part C (3 × 10 = 30)

Answer any **three** questions

All questions carry equal marks

16. Explain string operators in detail with example.

17. Explain about the use of indexes and security management in MYSQL.

18. Explain the various control structures of PERL.

19. Explain the concept of regular expression. Give example.

20. What is object oriented PERL. Give example.

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RW-6524 **502504**

M.Sc. DEGREE EXAMINATION, APRIL 2011

Bioinformatics

Elective : IMMUNOINFORMATICS

(CBCS—2010 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

All questions carry equal marks

1. Adaptive immunity

2. Antigen presenting cells

3. TCR complex

4. Immunogenomics

5. HLA

6. Viral Bioinformatics

7. MHC supertypes

8. Reverse immunology

9. Cytotoxic T cell epitope

10. MHC class II epitopes

Part B (5 × 5 = 25)

Answer **all** questions. Choosing either (a) or (b)

All questions carry equal marks

11. (a) Describe the primary structure of an antitody molecule with a neatly labelled diagram.

(*Or*)

(b) Explain a suitable design to humanize antibody and add a note on its clinical applications.

12. (a) Describe the structure of BCR with a neat diagram.

(*Or*)

(b) How do antibodies neutralize toxins?

13. (a) Explain the guidelines applicable for designing a vaccine.

(*Or*)

(b) Write a short note on HLA nomenclature.

14. (a) Explain any one mathematical model for HIV and host immune responses.

(*Or*)

(b) Elucidate any two causes for MHC polymorphism.

15. (a) Explain the application of homology modelling to predict 3D structure of immunoglobulin.

(*Or*)

(b) Give a brief account on databases available for prediction of MHC ligands.

Part C (3 × 10 = 30)

Answer any **three** questions

All questions carry equal marks

16. Give a detailed account on processing and presentation of antigens by endocytic pathway.

17. What are epitopes and affinity maturation? Explain their immunologic significance.

18. Explain various types of vaccines. Add a note on their preparation and clinical applications.

19. Discuss the computational views of host and viral pathogens.

20. Elaborate the applications of data bases currently used for prediction of epitopic structures.

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RW-6525 **502401**

M.Sc. DEGREE EXAMINATION, APRIL 2011

Bioinformatics

DRUG DESIGN AND PHARMACOGENOMICS

(CBCS—2008 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.
All questions carry equal marks.

1. Aromatase inhibitors.

2. Epitome.

3. MDI.

4. 3D database

5. Molecular docking

6. Dipole moment.

7. Topological indices.

8. Cluster analysis.

9. 3D QSARS.

10. Umbrella sampling.

Part B (5 × 5 = 25)

Answer **all** questions by choosing **either** (a) **or** (b).
All questions carry equal marks.

11. (a) Write a gene based drug targets.

(*Or*)

(b) How will you predict epitomes on Genomic scale ?

12. (a) Write a brief account on molecular simulations.

(*Or*)

(b) Enumerate the steps involved in designing a therapeutic drug.

13. (a) List out the applications of 3D database searching and docking.

(*Or*)

(b) How will you derive 3D pharmacophore for therapeutic target ?

14. (a) Comment on genetic algorithms.

(*Or*)

(b) How will you incorporate additional geometric features into a 3D pharmacore ?

15. (a) Give short notes on active site prediction.

(*Or*)

(b) Write briefly about ParDOCK.

Part C (3 × 10 = 30)

Answer any **three** questions.
All questions carry equal marks.

16. Explain in detail about the pharmacogenetic targets of cancer.

17. Write in detail about the topological indices.

18. Write in detail about the neural networks and its applications in QSAR studies.

19. Give a detailed account on the structure based methods to identify lead compounds.

20. Write in detail about the tools available for drug discovery.

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RW-6526 **502402**

M.Sc. DEGREE EXAMINATION, APRIL 2011

Bioinformatics

BIOINFORMATICS IN AGRICULTURE, MEDICINE AND ENVIRONMENT

(CBCS—2008 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

All questions carry equal marks.

1. ASIP.

2. PLEXdb.

3. Preventive medicine.

4. Pharmacogenetics.

5. miRNA.

6. Adenoviral vectors.

7. Differentiate somatic cell and germ line gene therapy.

8. Fuel cells.

9. Multidrug tolerance.

10. Horizontal gene transfer.

Part B (5 × 5 = 25)

Answer **all** questions, choosing **either** (a) **or** (b)

All questions carry equal marks.

11. (a) Give an account on prot4EST.

(*Or*)

(b) Write short notes on ESTminer.

12. (a) Describe in detail the Somatic cell gene therapy with one example.

(*Or*)

(b) Write brief note on adenoviral vector.

13. (a) Discuss the applications of personalized medicine.

(*Or*)

(b) Give a brief account on pharmacogenomics.

14. (a) Discuss in detail about alternative energy sources.

(*Or*)

(b) Comment on Microbes and Climate change.

15. (a) Write short notes on biotechnological applications of microbes.

(*Or*)

(b) Enumerate the reality of bioweapon creation.

Part C (3 × 10 = 30)

Answer any **three** of the following.

All questions carry equal marks.

16. Elaborate on the EST visualization tools.

17. Discuss in detail about Gene testing.

18. Write a brief account on fundamental and Applications of Gene therapy.

19. Enumerate and describe the concepts of Super bugs.

20. Describe in detail the metagenomics and applications.

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RW-6527 **502102**

M.Sc. DEGREE EXAMINATION, APRIL 2011

Bioinformatics

FUNDAMENTALS OF COMPUTING

(CBCS—2010 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.
All questions carry equal marks.

1. Specify the role of main memory.

2. What is meant by real time processing ?

3. Mention the difference between hardware and software.

4. Mention any four features of windows OS.

5. What is the difference between a router and a switch ?

6. Name any two internet programming languages.

7. What is ISDN ? Name any two ISDN services.

8. Mention the difference between a webpage and a website.

9. Define the term authentication.

10. What is a plain text ? How it is differing from a cipher text ?

Part B (5 × 5 = 25)

Answer **all** questions by choosing **either** (a) **or** (b).
All questions carry equal marks.

11. (a) What are peripheral devices ? Explain.

(*Or*)

(b) Compare online and offline processing methods.

12. (a) What is an algorithm ? Explain its use.

(*Or*)

(b) List the features of Unix OS.

13. (a) Define the following terms :

(i) Protocol

(ii) VPN

(iii) Open systems

(*Or*)

(b) What are satellite links ? Specify their role.

14. (a) Mention the various internet resources.

(*Or*)

(b) Explain the role of Java.

15. (a) Explain the need for Data security.

(*Or*)

(b) What are threats to security.

Part C

(3 × 10 = 30)

Answer any **three** questions.
All questions carry equal marks.

16. Explain the structure of a digital computer and discuss its working.

17. What is software ? Explain different types of software.

18. Explain the characteristics of any two communication links.

19. Discuss the characteristics on Internet Browsers.

20. Write short note on :

(i) Access control

(ii) Mobile computing.

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RW-6528 **502103**

M.Sc. DEGREE EXAMINATION, APRIL 2011

Bioinformatics

CELL BIOLOGY

(CBCS—2010 Onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** the questions.

All questions carry equal marks.

1. Membrane asymmetry.

2. Cyclins.

3. Autophagy.

4. Calvincycle.

5. Polyadenylation.

6. Membrane lipids.

7. Photo chemistry.

8. Glycocalycas.

9. Davidson–Danielle model.

10. Tight junction.

Part B (5 × 5 = 25)

Answer **all** the questions.

All questions carry equal marks.

11. (a) Give an account on the role of different regulators in cell cycle progression.

(*Or*)

(b) Comment on the three dimensional organization and functions of cytoskeletons.

12. (a) Write the salient features of nucleosomes.

(*Or*)

(b) Explain the relationship between ER and golgi apparatus in cell secretion.

13. (a) Discuss cell junctions.

(*Or*)

(b) Give an account on golgi complex system in protein trafficking.

14. (a) Enumerate the structure and function of proteosomes.

(*Or*)

(b) Discuss nuclear cytoplasm interactions.

15. (a) Write an account on cloning vectors.

(*Or*)

(b) Comment on "Pace Maker".

Part C (3 × 10 = 30)

Answer any **three** questions.

All questions carry equal marks.

16. Write an essay on fluid-mosaik model of plasma membrane.

17. Give an elaborate account on the role of mitochondria in energy metabolism.

18. Give a detailed note on the cellular differentiation in plants and animals.

19. Elaborate on the classification and cellular functions of chaperons.

20. Comment on the theories regarding tumour formation.

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RW-6529 **502104**

M.Sc. DEGREE EXAMINATION, APRIL 2011

BioInformatics

LAB: I : ANALYTICAL AND INSTRUMENTATIONS METHODS

(CBCS—2010 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

All questions carry equal marks.

1. Define : monochromator

2. Define : Lambert's law.

3. State : Michaelis–Menten equation.

4. Comment on the role of pH on enzyme activity.

5. Two advantages of glass electrode of pH meter.

6. What is meant by solvent front ?

7. Define down stream processing ?

8. Two fungal species for enzyme production.

9. Comment on Monomer.

10. What is coomasie brilliant blue ?

Part B (5 × 5 = 25)

Answer **all** questions, choosing **either** (a) **or** (b)

All questions carry equal marks.

11. (a) Describe the basic components of a colorimeter.

(*Or*)

(b) List out the applications of colorimeter and spectrophotometer.

12. (a) Narrate the significance of optimum temperature for enzyme activity.

(*Or*)

(b) Write down the procedure for the determination of Vmax for an enzyme.

13. (a) Write about the hydrogen electrode of a pH meter.

(*Or*)

(b) Enumerate the factors affecting the buffer capacity.

14. (a) Describe the principle of ion exchange chromatography.

(*Or*)

(b) Write about the cation exchanger and anion exchanger.

15. (a) Write the applications of radio labeling.

(*Or*)

(b) Describe the silver staining of DNA

Part C (3 × 10 = 30)

Answer any **three** questions.

All questions carry equal marks.

16. Elaborate the carbohydrate determination by DNSA method.

17. How do you assay ALP and Lipases ? Explain. Add a note on their clinical significance.

18. Describe separation of amino acids by 2D paper chromatography.

19. Give a detailed account on down stream processing.

20. Elaborate about the separation of DNA by agarose gel electrophoresis.

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RW-6530 **502105**

M.Sc. DEGREE EXAMINATION, APRIL 2011

Bioinformatics

Lab II : PROGRAMMING IN C

(CBCS—2010 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

All questions carry equal marks.

1. What are keywords in C ? Give examples.

2. Write the syntax 'switch-case' statement.

3. Define function prototype.

4. Discuss about the C preprocessor.

5. How to initialize single and two dimensional array in C.

6. How to declare a structure in C.

7. What is Raster algorithm ?

8. Define Gouraud and phong shading.

9. Name any two applications 'C' in bioinformatics data processing.

10. Discuss pair-vise alignment.

Part B (5 × 5 = 25)

Answer **all** the questions choosing **either** 'a' **or** 'b'.

All questions carry equal marks.

11. (a) Write a C program to convert the given temperature in Fahrenheit to Centigrade scale.

(*Or*)

(b) Write a C program to arrange the given set of n values in the ascending order.

12. (a) Write a C program for passing array as arguments.

(*Or*)

(b) Explain the advantages of Pointers in C.

13. (a) What are the advantages of structures in C ?

(*Or*)

(b) What is a union ? How does a union differ from a structure ?

14. (a) Write a C program to draw any two geometric objects.

(*Or*)

(b) Discuss about the Scalable Vector Graphics (SVG).

15. (a) Explain with suitable examples the applications of C programming in Bioinformatics.

(*Or*)

(b) Write a C program to obtain the six ORF of a DNA sequences.

Part C

(3 × 10 = 30)

Answer any **three** questions.
All questions carry equal marks.

16. Write a C program to swap two values using pointers.

17. Write a C program to compute the percentage of A + T and G + C content of a given DNA sequence.

18. Write a C program to find the percentage of hydrophobic amino acid present in the given protein sequences.

19. Write a C program to get a lowercase protein sequence file and store it in an another file with uppercase.

20. Write a C program to find the reverse complement of a given oligo-nucleotide sequence.

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RW-6531 **502302**

M.Sc. DEGREE EXAMINATION, APRIL 2011

Bioinformatics

COMPARATIVE FUNCTIONAL GENOMICS

(CBCS—2008 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.
All questions carry equal marks.

1. Orthologs and Paralogs.

2. Physical mapping.

3. Automated sequencing.

4. Eukaryotic genome.

5. Micro arrays.

6. Name any two genome databases.

7. Gene arrangements.

8. Metabolic pathways.

9. Transposons.

10. Repetitive sequence.

Part B (5 × 5 = 25)

Answer **all** questions by choosing **either** (a) **or** (b).
All questions carry equal marks.

11. (a) Explain in detail about genomic alignments.

(*Or*)

(b) Give an account on genome databases with its application.

12. (a) Discuss about gene knock-out analysis along with its importance.

(*Or*)

(b) Write a short note on genome annotation.

13. (a) Write a detail note on SNP with related database.

(*Or*)

(b) Explain the following algorithms : BLASTZ, LAGAN.

14. (a) Write a short note on comparative genomics.

(*Or*)

(b) Enumerate the applications of metabolic pathway.

15. (a) Compare the SAGE with DNA-microarrays.

(*Or*)

(b) Discuss the applications of comparitive genomics in evolution.

Part C (3 × 10 = 30)

Answer any **three** questions.
All questions carry equal marks.

16. Explain in detail about eukaryotic genome anatomy.

17. Give a detail account on genome mapping and its types

18. Explain about manual and automated method in genome sequencing.

19. Comment on antisense RNA and its mechanism in translation.

20. Explain the methods involved in the gene prediction.

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RW-6532 **502503**

M.Sc. DEGREE EXAMINATION, APRIL 2011

Bioinformatics

Elective II : IMMUNOLOGY FOR BIOINFORMATICS.

(CBCS—2008 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

All questions carry equal marks

1. Antigen presenting cell

2. Fc fragment

3. B-cell receptor

4. Autoimmune diseases

5. mIgM

6. Vaccines

7. Immunogenomics

8. Reverse immunology

9. MHC supertypes

10. T-Cell Epitopes

Part B (5 × 5 = 25)

Answer **all** questions. Choosing **either** (a) **or** (b)

All questions carry equal marks

11. (a) Explain the functional features of innate immunity.

(*Or*)

(b) Highlight the scientific reasons for humanization of antibodies.

12. (a) Describe the structure of T-Cell receptor complex.

(*Or*)

(b) Write a shortnote on the importance of MHC molecules.

13. (a) What are polytope vaccines? Explain their applications.

(*Or*)

(b) Elucidate any two mechanisms of interaction between antigen and antibody.

14. (a) How do peptides bind on the MHC molecules?

(*Or*)

(b) What are superantigens? Explain their immunologic significance.

15. (a) Give a short account on databases for antibody sequence and structure.

(*Or*)

(b) How will you predict MHC class I epitopes?

Part C (3 × 10 = 30)

Answer any **three** questions

All questions carry equal marks

16. Explain the process of presentation of exogenous antigens.

17. Give an account on contemporary challenges to the immune system.

18. Discuss the availability of various tools and servers to study the nature of B-Cell epitopes.

19. Highlight the significance of vaccine design and web-based tool essential for the design.

20. Write an essay on the methods for prediction of 3D structure of antibody.

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RW-6783 502503

M.Sc. DEGREE EXAMINATION APRIL 2011

Bioinformatics

BIOINFORMATICS IN AGRICULTURE, MEDICINE, BIODIVERSITY AND ENVIRONMENT

(CBCS—2010 onwards)

Time : 3 Hours Maximum : 75 Marks

Section A (10 × 2 = 20)

Answer **all** the questions.

All questions carry equal marks.

1. What is EST ?

2. List any *four* plant genome database.

3. Define personalized medicine.

4. Define the term Gene testing.

5. Define biodiversity.

6. What is Metadatabase ?

7. Expand :

   (a) SOFC.

   (b) MCFC.

8. List out any *two* Resistant microbes.

9. What is meant by ortholog ?

10. What is MEGAN ?

Section B (5 × 5 = 25)

Answer **all** questions choosing **either** (a) **or** (b)

All questions carry equal marks.

11. (a) Write a short note on Insect resistance.

(*Or*)

(b) Describe *At*GDB.

12. (a) Explain the application of Bioinformatics in cancer detection ?

(*Or*)

(b) Explain the concept of Gene therapy and list out its applications ?

13. (a) Explain virtual library.

(*Or*)

(b) Describe species diversity ?

14. (a) Explain alternative energy sources.

(*Or*)

(b) What is fuel cells and explain its various types.

15. (a) Discuss on Bioweapon creation.

(*Or*)

(b) Describe UPGMA ?

Section C (3 × 10 = 30)

Answer any **three** questions.

All questions carry equal marks.

16. Describe comparative genetics with reference to plant genomes.

17. Write a detailed note on pharmacogenomics.

18. Explain the scope and various types of Biodiversity.

19. Write a detail note on waste cleanup.

20. Detail on Metagenomics.

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