

Reg. No. :

D 704

Q.P. Code : [D 07 PBI 04]

(For the candidates admitted from 2007 onwards)

M.Sc. DEGREE EXAMINATION, DECEMBER 2009.

First Year

Part III — Bioinformatics

MOLECULAR INTERACTIONS

Time : Three hours

Maximum : 100 marks

Answer any FIVE questions out of EIGHT.

(5 × 20 = 100)

Each carries 20 marks.

1. Describe the theories of atomic and molecular orbitals.
2. Enumerate different kinds of isomers. Give examples. Mention the significance of these isomers to the biological system.
3. Explain the importance of H-bonding and van der Waals forces in biomolecules.
4. Discuss the molecular interaction in the architecture of biomembranes.

5. (a) Draw and describe the stereochemical structure of proteins.

(b) Explain the topological structure of nucleic acids.

6. How ultraviolet spectroscopy and CD are used in the structural elucidation of macromolecules?

7. Explain the molecular interaction between

(a) Protein and carbohydrates

(b) DNA and drug.

8. Comment on the different levels of organization of biomolecules. Add a note on the chiro-optical properties.
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D 702

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M.Sc. DEGREE EXAMINATION, DECEMBER 2009.

First Year

Bioinformatics

FUNDAMENTALS OF BIOLOGICAL SYSTEMS

Time : Three hours

Maximum : 100 marks

Answer any FIVE questions.

All questions carry equal marks.

(5 × 20 = 100)

1. Discuss elaborately the structure and characteristics features of prokaryotic and eukaryotic cells.
2. Explain in detail the transport of materials across plasma membrane.
3. Describe the structural organisation of protein and write a note on the contributions of G.N. Ramachandran.
4. Write in detail the structure of monosaccharides.

5. What do you know about dark reaction and give special focus on C_3 pathway and its significance?

6. What are allosteric enzymes and write its properties and mechanism?

7. Explain elaborately the genetic significance of meiosis.

8. What do you mean by lactose operon? How does it function?

Reg. No. :

D 703

Q.P. Code : [D 07 PBI 021]

(For the candidates admitted from 2007 onwards)

M.Sc. DEGREE EXAMINATION, DECEMBER 2009.

First Year

Bioinformatics

COMPUTATIONAL METHODS FOR SEQUENCE ANALYSIS

Time : Three hours

Maximum : 100 marks

Answer any FIVE of the following.

(5 × 20 = 100)

1. Discuss the fundamental applications of bioinformatics to varied field of biological sciences.
2. Comment on the role of pairwise alignment techniques and its implications.
3. How has the rooted and unrooted tree analysis helped the study of evolutionary behaviors? Cite examples.

4. Mention the infrastructure based on which the genome sequencing among eukaryotes are analysed.

5. What do you understand by secondary structural predictions? How will you apply this to biological field for better understanding?

6. Describe in detail the role of data retrieval systems in the frontiers of bioinformatics.

7. Compare the validation of sequence alignment methods through structural data analysis.

8. How will you conduct an analysis for the predication of regulatory regions among normal and abnormal genomic systems?



Q. P. CODE: DO

(For candidates admitted from 2007 onwards)
M. Sc. Degree Examinations, December-2009

First Semester

Bioinformatics

PROGRAMMING IN C AND PERL

Time: Three hours

Maximum : 100 marks

Carefully read the questions.

Write the program code wherever necessary.

Answer any FIVE questions.

All questions carry equal marks.

(5 x 20 = 100)

1. a) Explain in detail about keywords and identifiers in C.
b) Discuss about the data types and qualifiers for data types in C.
2. Discuss the concepts of looping structures in C:
 - a) The while statement
 - b) do-while statement
 - c) for statement
3. Define user defined function. Explain the use of recursive function with an example in C program.
4. How one-dimensional and two-dimensional arrays are defined in C. Write a C program to find the product of two matrices.
5. Write a 'C' program to find the total and average mark of a student using structure.
6. Write the C program for a file named DATA contains a series of integer numbers. Code a program to read these numbers and then write all 'odd' numbers to a file to be called ODD and all 'even' numbers to a file to be called EVEN.

7. a) Write about associative arrays in Perl.
b) Briefly explain subroutine in Perl.
 8. Explain about regular expression in perl. Discuss in detail with text and string processing using regular expression.
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