

S.No. 7107

P 16 BC 42

(For candidates admitted from 2016–2017 onwards)

M.Sc. DEGREE EXAMINATION, APRIL 2018.

Biochemistry

BIOINFORMATICS

Time : Three hours

Maximum : 75 marks

SECTION A — (10 × 2 = 20)

Answer ALL questions.

1. Expand PSSM. PSSM used by BLIMPS is also called.
2. Name two participating databases, among which the International Nucleotide sequence data base collection (INSDC) Operators.
3. Expand CASP.
4. What are the secondary levels of a protein structures?
5. Name the global alignment algorithm.
6. What does BLAST represent?



7. What does scop contain?
8. List few protein modeling tools.
9. List any two genome based data bases.
10. What are the methods to sequence genomes?

SECTION B — (5 × 5 = 25)

Answer ALL questions, choosing either (a) or (b).

11. (a) What is CDD? What are the different methods of searching in CDD?

Or

- (b) Brief uses of tools in Bioinformatics for sequence.

12. (a) Give a brief note on Rama Chandran Map.

Or

- (b) What is homology modeling?

13. (a) How does Blosum matrix help in bioinformatic analysis?

Or

- (b) Write a note on Smith Waterman algorithm.



14. (a) Write the steps involved in homology modeling using Swiss PDB views.

Or

(b) Brief about scope database.

15. (a) Give notes on few features about which information can be obtained from a genome database.

Or

(b) List five bioinformatics tools that can be used in drug discovery.

SECTION C — (3 × 10 = 30)

Answer any THREE questions.

16. Write about five database integrated to NCB.

17. What are the different levels of differentiation of protein structures?

18. How can BLAST be used to query databases?

19. Explain Five display commands in RASMOL.

20. Explain how CYTOSCAPE is used in Bioinformatic analysis.



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(b) Brief about scope database.

15. (a) Give notes on few features about which information can be obtained from a genome database.

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