

**17U617**

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Name: .....

Reg. No.....

**SIXTH SEMESTER B.Sc. DEGREE EXAMINATION, APRIL 2020**

(CUCBCSS-UG)

(Regular/Supplementary/Improvement)

**CC15U ZO6 B12 - MOLECULAR BIOLOGY AND BIOINFORMATICS**

Zoology - Core Course

(2015 Admission onwards)

Time: Three Hours

Maximum: 80 Marks

A. Answer *all* questions. Each question carries 1 mark.

1. Name the codon for tryptophan.
2. Expand the abbreviation PAM
3. Name the database search engine developed by NCBI
4. The organism used by Griffith to prove bacterial transformation.
5. The enhancers that also used to inhibit transcription is known as.
6. The complete set of mRNA in an organism is known as.
7. Give an example for primary biological database.
8. The scientist who got Nobel prize for his contributions to understanding the genetic code
9. Who coined the term bioinformatics?
10. Give an example for retrovirus.

**(10 x 1 = 10 Marks)**

B. Answer any *ten* questions in *two or three* sentences. Each question carries 2 marks.

11. Define operon.
12. What are housekeeping genes?
13. What are the main features of Genbank?
14. What are cryptic genes?
15. What is Swiss Prot?
16. What is splicesome?
17. Give a short account on MIPS.
18. What are hnRNAs?
19. What is SRS?
20. What is KEGG?
21. Differentiate between cistron and recon.
22. Expand the abbreviation BLAST and PIR.

**(10 x 2 = 20 Marks)**

C. Answer any *five* questions in not more than a paragraph each. Each question carries 6 marks.

23. What are microarrays? How microarray is useful in biological research?

24. What is genomics. Distinguish between structural and functional genomics.

25. Explain wobble hypothesis.

26. Explain the tools, applications and significance of metabolomics.

27. Write notes on a) jumping genes b) pseudogenes c) Satellite DNA

28. What are the features provided in the NCBI web page?

29. What are the major protein components of the eukaryotic chromosomes? What are their functions?

30. What do you understand by sequence alignment? Explain different types of alignments used in sequence analysis.

**(5 x 6 = 30 Marks)**

D. Write essays on any *two* of the following. Each question carries 10 marks.

31. Explain the various steps used in FASTA search.

32. Differentiate between lytic and lysogenic cycle of phages.

33. Give a detailed account of nucleotide sequence database.

34. Describe post translational modification and targeting of proteins.

**(2 x 10 = 20 Marks)**

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