

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
 TEST -3 EXAMINATIONS- May 2018
 B.Tech/Vth Semester

COURSE CODE: 15B11BI411 MAX. MARKS: 35
 COURSE NAME: Genetic Engineering and Genomics
 COURSE CREDITS: 04 MAX. TIME: 2Hr

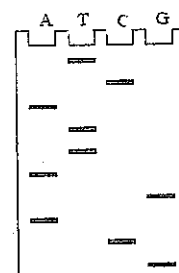
Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means.

Q.1 Briefly answer following questions. 1.5x6=9.0 (CO II, CO III) (20 min.)

- How it is ensured that a progressive ladder of DNA fragments is synthesized in PCR reaction carried in sanger's sequencing?
- Explain strategy for computational gene prediction?
- What is the principle of pyrosequencing? Mention the reactions and enzymes used
- Why it is preferable to have cDNA library of eukaryotes rather than genomic library and vice versa?
- What are different essential elements of an expression vectors?
- How mRNA is isolated from Total RNA preparation?

Q.2 Attempt any four of following. 2.5x4=10 (CO III) (40 min.)

- Calculate the minimum number of clones required in a gene library of *D. melanogaster*? Given genome size 1.2×10^5 KB, fragment size 700KB, desired probability of finding the fragment 0.99.
- How second strand of cDNA is synthesized?
- The DNA band profile generated after electrophoresis of products synthesized by dideoxy chain termination method is shown. Deduce the nucleotide sequence of the parental DNA fragment. Do not forget to mention the direction of chain.
- What do you mean by Genome Annotation? What all databases used for genome annotation
- Briefly discuss the modification in original sanger's method of DNA sequences which led in following automations. i) automatic base calling ii) Conducting all nucleotide based termination in single PCR tube iii) Replacement of gel electrophoresis



Q.3 1+2+1+2= 6 (COIV) (20 min.)

What do you understand by the term 'molecular marker'? Why are molecular DNA based markers preferred over morphological and biochemical markers? What is the difference between dominant and co-dominant markers? Explain following terms: VNTR, SNP, CDS, Contig

Q.4 5 (COII, COIII COIV) (20 min.)

How whole genomes are sequenced given the fact that DNA is sequenced in very small reads compared to genome size? Discuss one of approach of whole genome sequence in details along with its advantages and limitations

Q.5 5 (COII) (20 min.)

Discuss the typical components yeast artificial chromosome vector. How cloning and selection is done using these vectors?