Q. Code: 271067

Reg. No. | | | | | | | | | | | | | | |

B.E / B.TECH. DEGREE EXAMINATION, MAY 2023

Sixth Semester

BT18602 – GENETIC ENGINEERING AND GENOMICS

(Biotechnology)

(Regulation 2018 / Regulation 2018A)

TIME: 3 HOURS **MAX. MARKS: 100**

CO 1 Explain the methodology to be followed for cloning commercially important genes and for the production of recombinant proteins

CO 2 Categorize the different methodology to be followed for constructing genomic and cDNA library and to screen them.

CO 3 Make use of gene sequencing techniques, site directed mutagenesis and different PCR techniques to amplify and quantify gene expression.

CO 4 Utilize whole genome sequencing and mapping.

CO 5 Apply Microarray, SAGE, TOGA techniques.

PART- A (10 x 2 = 20 Marks)

(Answer all Questions)

		CO	RBT LEVEL
1.	Differentiate a gene cloning from whole organism cloning.	**1**	**4**
2.	Identify the most useful type of restriction enzyme (Type 1,2,3) useful in gene cloning and describe the reason for selecting it.	**1**	**4**
3.	List the properties of a radioactive probe.	**2**	**2**
4.	What is the role of S1 nuclease?	**2**	**2**
5.	Define Asymmetric PCR.	**3**	**2**
6.	Differentiate absolute and relative quantification of gene expression.	**3**	**4**
7.	Identify any 4 techniques that are helpful in the genome assembly.	**4**	**3**
8.	Define Sequence tagged site.	**4**	**2**
9.	Compare the types of microarray.	**5**	**4**
10.	What is proteogenomics?	**5**	**2**

PART- B (5 x 14 = 70 Marks)

			Marks	CO	RBT LEVEL
11. (a)	**(i)**	Describe in detail about any 2 cloning vectors used to clone the gene of your interest.	**(4)**	**1**	**2**
	(ii)	Explain the role of Restriction and modification system in the bacteria.	**(10)**	**1**	**2**
		(OR)			
(b)	**(i)**	Elaborate in detail about the Cre-Lox P based vector.	**(7)**	**1**	**2**
	(ii)	Explain the principle of blue white screening.	**(7)**	**1**	**2**

12. (a)	**(i)**	Illustrate the stepwise procedure involved in the construction of genomic DNA library.	**(7)**	**2**	**3**
	(ii)	Describe in detail about the steps involved in creating first strand cDNA using different primers.	**(7)**	**2**	**3**
		(OR)			
(b)	**(i)**	Exemplify the technique of functional complementation used to find the gene related to deafness in mice.	**(4)**	**2**	**3**
	(ii)	Describe the methodology used to identify the full-length mRNA/Cdna.	**(10)**	**2**	**3**
13. (a)	**(i)**	Compare chemical method and enzymatic method of DNA sequencing.	**(7)**	**3**	**3**
	(ii)	Discuss about the following PCR types. (a) Nested PCR (b) Assembly PCR.	**(7)**	**3**	**3**
		(OR)			
(b)	**(i)**	Describe about the usage of DNA binding dyes and probes in real time PCR for quantifying gene expression.	**(7)**	**3**	**3**
	(ii)	Explain the principle of error prone PCR, degenerate primers and nucleotide analogs used to create mutation.	**(7)**	**3**	**3**
14. (a)	**(i)**	Explain the techniques of hierarchical sequencing and shotgun sequencing in the elucidation of human genome.	**(14)**	**4**	**4**
		(OR)			
(b)	**(i)**	Discuss in detail about physical and genetic mapping techniques to order the fragmented DNA.	**(14)**	**4**	**4**
15. (a)	**(i)**	Justify that subtractive hybridization is used to detect the deleted genes and uniquely expressed genes.	**(7)**	**5**	**3**
	(ii)	Describe about the list of steps involved in measuring gene expression using microarray.	**(7)**	**5**	**3**
		(OR)			
(b)	**(i)**	Illustrate the principle of SAGE and its application in finding genes expressed.	**(7)**	**5**	**3**
	(ii)	Describe the steps in the yeast two hybrid system to find the physically interacting proteins.	**(7)**	**5**	**3**

PART- C (1 x 10 = 10 Marks)

(Q.No.16 is compulsory)

		Marks	CO	RBT LEVEL
16.	Distinguish the illumina sequencing and pyro sequencing and compute the pyrogram of the following sequence. 5'-GATTCCGATTTCCA-3'	**(10)**	**3**	**5**

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