### BIRLA INSTITUTE OF TECHNOLOGY AND SCIENCE PILANI, HYDERABAD CAMPUS rDNA Technology (BIO F311) 2022-23 I SEM; Quiz1 (Closed book) Total Marks: 20

	Date 03-10-22 Time 11:10 AM to 11:30AM Duration: 30mins	
<b>Student Name:</b>		(A)
Student ID:		$(\Lambda)$

Write your answers legibly in the space given below. No overwriting is allowed.

### Section A: Short answer type Total 12 M

**Student ID:** 

1. Draw <u>nucleotide</u> structure of adenine and <u>nucleoside</u> structure of Uracil. (Note: Need to draw chemical structure of sugar base and phosphate with proper valency. No need to draw details of purine / pyrimidine structure) 2M

Nucleotide structure of Adenine	<u>Nucleoside</u> structure of Uracil

2. Complete the table 1.5 M

Category	Example	Function
DNA-dependent DNA		
polymerase copies DNA into		
DNA,		
RNA-dependent DNA		
polymerase copies RNA into		
DNA,		
DNA-dependent RNA		
polymerase transcribes DNA into		
RNA.		

3. Akshat and Umang are isolating nucleic acids from a animal cells in rDNA laboratory. There are two separate bottles labelled extraction solution A (EXA) and B (EXB) respectively. Akshat started isolation with A solution while Umang used solution B. After the isolation when both of them performed spectrophotometric measurements they found the following results.

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	Concentration	260/260	260/230
Samples extracted with	700 ng/µl	1.8	1.5
EXA			
Samples extracted with	700 ng/µl	2.0	2.0
EXB			

Answer the followings

a`	)Identif	y the	nucleic	acid	extracted	by	Akshat and	Umang	resp	ectivel	y. (	0.5N	V

- b) Which property of the buffer lead to different results? Justify your answer with explanation. 1M
- c) Which one of the extracted nucleic acid is more pure and why do you think so? 0.5M

Ans. a.	
Ans. b.	
Ans c.	

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4.	Using Sanger's dideoxy chain termination method, a particular exonic region of a protein
	coding gene was sequenced for two individuals referred to as Subject 1 and Subject 2. The figure
	below shows a segment of the autoradiogram corresponding to a small window of the DNA sequence

Subject 1						Subje	ct 2	
Α	Т	G	С		Α	Т	G	С
								_
	_					_		
						_		
		_					—	
			_		_			
		_					_	
			_					—
		_					—	
	—					_		
					<b> </b> —			

Can you predict the sequence of Subject 1 and Subject 2? 1M

From the sequence what are the features can you identify at the sequence level and at the protein level. Justify with your answer. (3M)

Subject 1	
Sequence	
Subject 2 Sequence	
Sequence	
Features:	

5. During Sanger sequencing Durjoy forget one of the fluorescent labelled ddGTP and sequenced a genes from wild type cells and cancer type cell respectively. Cancer type cell has two point mutations (see below).

Wild type : ATCTGCCGT Cancer cell: ATCTCCATT

- a. After Sequencing what will be the different length product(s) from two different cell type. 1.5M
- b. Could you able to identify the point mutation? Justify your answer 1M

	Wild type	Cancer cells
Ans	Products	Products
a.		

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Ans	Justification:						
b							
Ü							

### Section B. MCQ with one or more correct answers and Fill the blanks (Note: No partial marking for multiple answer questions.) Shade/mark the box with only correct answer (Total 8M).

S No	a	b	c	d	S No	a	b	С	d
i					vii				
ii					viii				
iii					ix				
iv					X				
V					xi				
vi					xii				

- i. If 5' cgcgcgtta 3' this is the non-template strand then mRNA sequence will be \_\_\_\_\_\_. (0.5M)
- ii. Uridine 5' triphosphate and 2' deoxythymidine 5' triphosphate differs to each other due to (1M)
  - a) Difference in the attachment of phosphate bonds in the Sugar backbone
  - b) Difference in one methyl group in nitrogenous base
  - c) Difference in oxygen in the sugar backbone
  - d) Difference in the number of hydroxyl group
- iii. Genomic DNA differs from the complementary DNA(cDNA) in having (0.5M)
  - a. 5'cap with no introns
  - b. sequences between genes
  - c. noncoding regions with poly A tail
  - d. both have identical sequences

### iv. Southern differs from northern blot (0.5M)

- a. In southern RNA and in northern DNA probes are utilised
- b. Southern gives information of the gene while northern can give information of gene expression.
- c. Southern is can also detect protein expression but norther cannot.
- d. Both procedure can be coupled to Chemiluminescence based detection.
- v. Kriti wants to make 30 copies of a particular human gene beta actin. She extracted DNA from skin cells and used the DNA to perform polymerase chain reaction /PCR. How many minimum cycles of the reaction will it be required? (0.5M)
  - a. 8
  - b. 4
  - c. 5
  - d. 6

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- Vi. Kriti made 30 copies of a particular human gene beta actin after isolating DNA from skin cells. But Akshaya made the 30 copies of the same from the RNA of the same cells after using reverse transcription followed by PCR. The PCR amplified products obtained were run separately in DNA gels. Actin Gene amplified by Akshaya is smaller in size (base pair length) than by Kriti. This is due to (0.5M)
  - a. An insertion mutation in the DNA sequence
  - b. A nonsense mutation in the DNA sequence
  - c. Splicing
  - d. PCR amplification failure
- vii. \_\_\_\_\_\_, a nucleic acid can be self-replicating with catalytic activity. (0.5M)
- viii. What would happen to DNA molecules treated with restriction endonuclease? (0.5M)
  - a. All the nitrogenous bases would get separated from the deoxyribose sugars.
  - b. The phosphodiester bonds between deoxyribose sugars would be broken.
  - c. The hydrogen bonds between A-T and G-C would break and two strands of the double helix would separate.
  - d. All the nitrogenous bases would get separated from the ribose sugars.
- ix. After sequencing of the actin, it was found that "TACGTACGTACGTAAGTAATC" is the sequence of the non-coding template strand of the DNA. Estimate the number of hydrogen bonds that may exist in the double stranded form of DNA from the sequence. (1 M)
  - a. 26
  - b. 24
  - c. 50
  - d. 100
- x. Klenow fragment has (1M)
  - a. DNA polymerase activity 3' to 5'
  - b. Exonuclease activity 5' to 3'
  - c. Exonuclease activity 5' to 3'
  - d. Used for radioactive labelling
- xi. "Nested fragments" (0.5M)
  - a. Are Product of nested PCR
  - b. Are generated during fragmentation resulting in overlapping DNA sequence
  - c. Used to derive sequence information during sanger sequencing
  - d. Product from conventional PCR with "nest" sequence
- xii. Choose the statement(s) which are **NOT TRUE** for Real time PCR (1M)
  - a. It can detect Realtime concentration of mRNA only.
  - b. It involves radioactive probe based dye
  - c. It measures only end point product amount
  - d. For a primer efficiency of 2, the optimal slope of the standard curve will be -3.32.