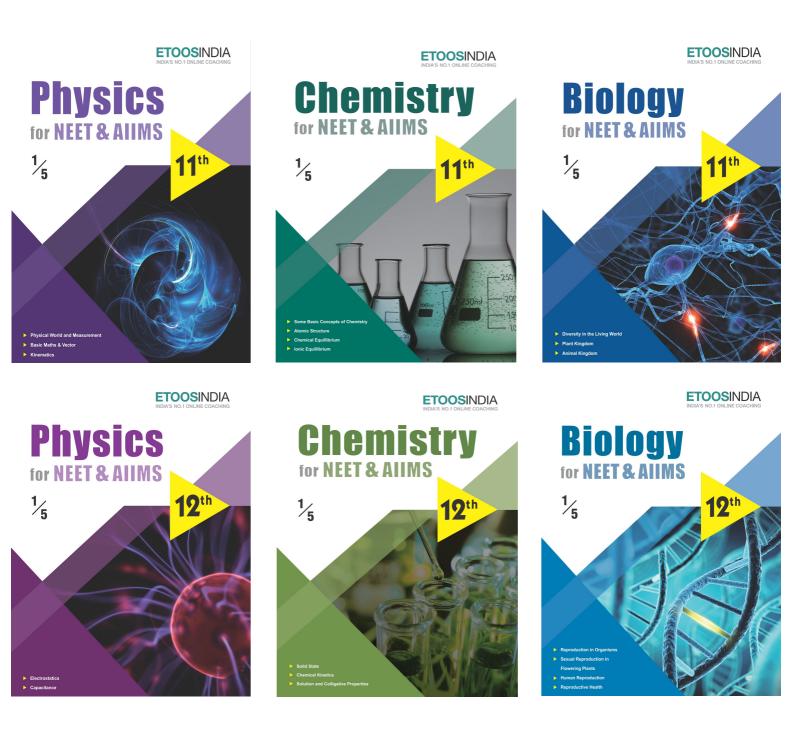
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# CHAPTER

# MOLECULAR BASIS OF INHERITANCE

"One of the deepest functions of a living organisms is to look ahead... to produce future".

"FRANCOIS JACOB (1920-2013)"

# INTRODUCTION

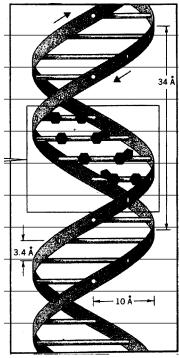
n previous chapter, you have learnt the inheritance patterns and genetic basis of such patterns. Factors/Genes were first detected and analyzed by Mendel and subsequently many other scientists, by following their patterns of transmission from generation to generation. Over the next hundred years, the nature of the putative genetic material was investigated culminating in the realisation that DNAdexyribonucleic acid-is the genetic material at least for the majority of various organisms. This is the substance which controls the inheritance of traits from one generation to the next and it is also able to express its effect through the formation and functioning of traits.

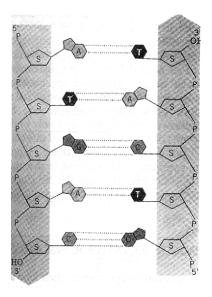
Nucleic acid is of two types in all living system i.e., deoxyribonucleic acis (DNA) and ribonucleic acid (RNA). DNA is a genetic material in all organism except some viruses. RNA is a genetic material in riboviruses. In others, RNA also functions as messenger which carry genetic information, an adapter for picking up amino acids, structural and catalytic molecule in some cases.

## **Molecular Basis of Inheritance**

#### DNA

- Discovered by Meischer. DNA was first identified by Friedrich Mrischer in 1869. He named it as Nuclein. Altmann found these substances to be acidic in nature and hence named it as nucleic acid.
- In DNA pentose sugar is deoxyribose sugar and four types of nitrogen bases A,T,G,C
- Wilkins and Franklin studied DNA molecule with the help of X-Ray crystallography.





- With the help of this study, **Watson** and **Crick** (1953) proposed a double helix molel for DNA. For this model Watson, Crick and Wilkins were awarded by Noble Prize in 1962.
- According to this model, DNA is composed of two polynucleotide chains.
- Both polynucleotide chains are complementary and antiparallel to each other.
- In both strand of DNA direction of phosphodiester bond is opposite. i.e. If direction of phosphodiester bond in one strand is 3'-5' then it is 5'-3' in another strand.
- Both strand of DNA held together by hydrogen bonds. These hydrogen bonds are present between nitrogen bases of both strand.
- Adenine binds to thymine by two hydrogen bonds and cytosine binds to guanine by three hydrogen bonds.
- Chargaff's equivalency rule In a double stranded DNA amount of purine nucleotides is equals to amount of pyrimidine nucleotides.

Purine = Pyrimidine  

$$[A] + [G] = [T] + [C]$$

$$\frac{[A] + [G]}{[T] + [C]} = 1$$

• Base ratio =  $\frac{A + T}{G + C}$  = constant for a given species.

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Types of DNA :-

On the basis of direction of twisting, there are two types of DNA.

1. Left handed DNA :-

Anticlockwise twisting e.g. Z-DNA - discovered by Rich. Phosphate and sugar backbone is zig-zag. Units of Z-DNA are dinucleotides (purine and pyrimidine in alternate order)

Helix length  $-5.6 \text{ A}^{\circ}$ Diameter  $-18.4 \text{ A}^{\circ}$ No. of base pairs -12 (6 dimers) Distance between 2 base - pairs  $-3.75 \text{ A}^{\circ}$ 

2. Right Handed DNA-

Clockwise twisting e.g. The DNA for which Watson and Crick proposed model was 'B' DNA.

DNA	Helix Length	No. of base pairs	Distance between two pairs	Diameter
'A'	28 A <sup>0</sup>	11 pairs	2.56 Å <sup>0</sup>	23 A <sup>0</sup>
'B'	34 A <sup>0</sup>	10 pairs	3.4 A <sup>0</sup>	$20A^0$
'C'	31 A <sup>0</sup>	9.33 pairs	3.32 A <sup>0</sup>	19 A <sup>0</sup>
'D'	24.24 A <sup>0</sup>	8 pairs	3.03 A <sup>0</sup>	19 A <sup>0</sup>

• Palindromic DNA – Wilson and Thomas

	<b>&gt;</b>		
CC	GG T A	CC	GG
GG	CC AT	GG	CC

Sequence of nucleotides same from both ends.

## ETOOS KEY POINTS

DNA molecule is Dextrorotatory while RNA molecule is Laevorotatory.

C – value = Total amount of DNA in a haploid genome of organism

#### Packaging of DNA Helix -

Taken the distance between two consecutive base pairs as  $0.34 \text{ nm} (0.34 \times 10^{-9} \text{ m})$ , if the length of DNA double helix in a typical mammalian cell is calculated (simply by multiplying the total number of bp with distance between two consecutive bp, that is  $6.6 \times 10^9 \text{ bp} \times 0.34 \times 10^{-9} \text{ m / bp}$ ), it comes out of be approximately 2.2 metres. A length that is far greater than the dimension of a typical nucleus (approximately  $10^{-6m}$ ). How is such a long polymer packaged in a cell? If the length of E. coli DNA is 1.36 mm, can you calculate the number of base pairs in E.coli?

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Etoos Tips & Formulas

#### 1. GENE EXPRESSION

- $\rightarrow$  One gene-one enzyme hypothesis was given by Beadle & Tatum.
- $\rightarrow$  According to this, each gene produces a particular type of enzyme.
- $\rightarrow$  They worked on Neurospora crassa.
- $\rightarrow$  Prototroph : It is the wild type Neurospora which can easily grow on minimal nutrient medium.
- $\rightarrow$  Auxotroph : These are the nutritional mutants which are unable to grow on minimal nutrient medium.
- $\rightarrow$  Later on one gene-one enzyme hypothesis has been modified into one gene-one polypeptide hypothesis.

#### 2. REGUIATION OF GENE EXPRESSION

- → The 'ON' or 'OFF' mechanism of non-constitutive genes, as per requirement is called gene regulation.'
- $\rightarrow$  In 1961, F.Jacob and J. Monad proposed Operon model for the regulation of gene action in £. coli.
- $\rightarrow$  An operon is a part of DNA, which acts as single regulated unit having one or more structural genes, one operator gene, one promotor gene and one regulator gene.
- $\rightarrow$  Operons are of two types :-
- (i) Inducible operon (e.g. Lac operon)
- (ii) Repressible operon (e.g. Tryptophan operon)
- $\rightarrow$  In lac operon, a polycistronic structural gene in regulated by a common promoter and regulatory genes.
- $\rightarrow$  Lactose is the substrate for the enzyme  $\beta$ -galactosidase and it regulates switching on & off the operon. Hence it is called inducer.
- → A very low level of expression of lac operon has to be present in the cell all the time, otherwise lactose cannot enter the cells.
- $\rightarrow$  The repressor of the operon is synthesised (all the time constitutively) from the i-gene.
- → Glucose or galactose cannot act as inducers for lac operon. The lac operon would be expressed in the presence of lactose till the level of glucose remain low in cell.
- $\rightarrow$  Regulation of lac operon by repressor is referred to as negative regulation.

#### **The Lac Operon**

In eukaryotes, the regulation could be exerted at

- (i) transcriptional level (formation of primary transcript)
- (ii) processing level (regulation of splicing)
- (iii) transport of mRNA from nucleus to the cytoplasm
- (iv) translational level

#### 3. HUMANGENETICS

- → Study of inheritance of genetic characters and aspects like genetic improvements among humans is known as human genetics.
- → In human direct genetical studies are not possible. For this different indirect methods are used. Pedigree analysis one such important method.
- $\rightarrow$  Study of the family history for the inheritance of particular trait in several generation of a family is called the pedigree analysis.

#### 4. POPULATION GENETICS:

- $\rightarrow$  Study of gene frequency in a population is called population genetics.
- $\rightarrow$  Gene frequency : It is the proportion of different alleles of a gene in a population.
- $\rightarrow$  Hardy-Weinberg law :
- $\rightarrow$  In a large, randomly mating population, the frequency of a gene remain constant from generation to generation when factors like selection, mutation & migration are absent.
- $\rightarrow$  According to this law, p + q = 1

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	SOLVED E	XAM	PLE
Ex.1 Sol.	<ul> <li>Which site of a t-RNA molecule hydrogen bonds to a m-RNA molecule</li> <li>(A) Codon</li> <li>(B) Anticodon</li> <li>(C) 5' end of the t-RNA molecule</li> <li>(D) 3' end of the t-RNA molecule</li> <li>(B) : Anticodon arm is responsible for recognizing and binding codons in the m-RNA.</li> </ul>	Ex.7 Sol.	Nucleotides are building blocks of nucleic acids. Each nucleotide is a composite molecules formed by (A) (Base-sugar)n (B) Base-sugar-OH (C) Base-sugar-phosphate (D) Sugar-phosphate (C) : Nucleotides are the building blocks or mono- meric units. Each nucleotide contain Nitrogen bases (Purines and pyrimidines), pentose sugar (5c) and phosphoric acid.
Ex.2	Removal of introns and joining the exons in a defined order in a transcription unit is called(A) Splicing(B) Tailing(C) Transformation(D) Capping	Ex.8	Which one of the following also acts as a catalyst in a bacterial cell(A) 23 sr RNA(B) 5 sr RNA(C) sn RNA(D) hn RNA
Sol.	(A) : Spliceosomes cut introns from hn-RNA and exons are joined by RNA ligase. It is called splicing.	Sol.	(A) : 23 S rRNA is catalytic RNA.
Ex.3	Semiconservative model of DNA replication was proposed by which workers in eukaryotes (A) Taylor, Woods and Hughes, 1957 (B) Messelson and Stahl, 1957 (C) Nirenberg and Khorana, 1967 (D) Watson and Crick, 1952	Ex.9	<ul> <li>Read the following four statements (A - D)</li> <li>A. In transcription, adenosine pairs with uracil</li> <li>B. Regulation of lac operon by repressor is referred to as positive regulation</li> <li>C. The human genome has approximately 50,000 genes</li> <li>D. haemophilia is a sex-linked recessive disease</li> </ul>
Sol.	(B)		How many of the above statements are right
Ex.4	In the double helix model of DNA, how far is each base pair from the next base pair (A) 3.4 nm (B) 0.34 nm (C) 2.0 nm (D) 34 nm	Sol.	<ul> <li>(A) Two</li> <li>(B) Three</li> <li>(C) Four</li> <li>(D) One</li> <li>(A) : Regulation of lac operon by repressor is referred as negative regulation. Human genome has approximately 30000 genes.</li> </ul>
Sol.	(E) 0.034 nm (B)	Ex.10	A triplet codon means
Ex.5	If the DNA codons are ATG ATG ATG and a cy- tosine base is inserted at the begining, which of the following will result (A) A non-sense mutation	Sol.	<ul> <li>(A) A sequence of three nitrogen bases on mRNA</li> <li>(B) A sequence of three nitrogen bases in tRNA</li> <li>(C) A sequence of three bases in rRNA</li> <li>(D) The presence of only three bases in mRNA</li> <li>(A)</li> </ul>
	<ul><li>(B) CA TGA TGA TG</li><li>(C) CAT GAT GAT G</li><li>(D) C ATG ATG ATG</li></ul>	Ex.11	The one aspect which is not a salient feature of genetic code, is its being
Sol.	(C)		<ul><li>(A) Specific</li><li>(B) Degenerate</li><li>(C) Ambiguous</li><li>(D) Universal</li></ul>
Ex.6	The chemical knives of DNA are	Sol.	(C)
	Or Enzyme that cleaves nucleic acids within the poly- nucleotide chain is known as (A) Ligases (B) Polymerases (C) Endonucleases (D) Transcriptase	Ex.12 Sol.	<ul> <li>Which one-of the following is not a part of a transcription unit in DNA</li> <li>(A) The inducer</li> <li>(B) A terminator</li> <li>(C) A promoter</li> <li>(D) The structural gene</li> <li>(A) : Transcription unit consists of promoter, structure</li> </ul>
Sol.	(C) : Endonucleases enzymes cut DNA at specific desired place so it is called chemical knives of DNA.		tural gene and terminator.

Ex	ercise # 1	SINGLE OB.	JECTIV	VE NI	EET LEVEL
of pe	sea urchin DNA, which is f the bases were shown ercentages of the other t e present in this DNA are	n to be cytosine. The hree bases expected to	6.	The enzyme that brea (A) Helicase (C) Ligase	aks H <sub>2</sub> bonds in DNA is (B) Topoisomerase (D) Polymerase
(A (E	A) G 17%, A 16.5%, T 32.5 B) G 17%, A 33%, T 33% C) G 8.5%, A 50%, T 24.5%	5%	7.	Exon part of m-RNA: (A) Protein (C) Phospholipid	s has code for (B) Lipid (D) Carbohydrate
2. W ar to	)) G 34%, A 24.5%, T 24.5 /hich of the following R mino acid (from amino aci ribosome during proteir or	NAs picks up specific d pool) in the cytoplasm a synthesis	8.	pairing we have postu	our notice that the specificated immediately suggests chanism for genetic materia (B) Archibold Garrod (D) Waston and Crick
cl (A		<ul><li>a structure resembling</li><li>(B) mRNA</li><li>(D) All of these</li></ul>	9.	DNA elements, which called (A) Exons (B) Introns	n can switch their position, a
СС	ead the following states prect option . Nitrogenous base is link	ted to the pentose sugar		<ul><li>(C) Cistrons</li><li>(D) Transposons/Jun</li></ul>	1 00
С	<ul> <li>through a N-glycosidie</li> <li>Phosphate group is a nucleoside through ph</li> <li>Two nucleosides are li glycosidic linkage</li> <li>Negatively charged DI</li> </ul>	linked to 5'-OH of a nosphoester linkage nked through 3'-5' N-	10.	-	quence where EcoRI cuts i or ing plaindromic sequence (B) GAATTC CAAGTT
	positively charged hi nucleosome . The chromatin that is m	stone octamer to form ore densely packed and	44	(C) GCTTAA TAAGCT	(D) GTTCAA CTTAAG
(I	stains dark is called eu A) A, B and C alone are w B) D alone is wrong	rong	11.	(A) Kornberg (C) Waston and Crick	(B) Okazaki (D) Jacob and Mono
(I	<ul> <li>C) C and E alone are wron</li> <li>O) A alone is wrong</li> <li>E) A, B and D alone are wrong</li> </ul>	-	12.	What is false about t (A) It binds with an a (B) It has five double	mino acid at it 5' end
tv (A	he substance that acts as c vo generation is A) Ribonucleic acid	onnecting link between		anticodon on me (D) It looks like clove	one end which recognizes t essenger RNA r leaf in the three dimension
(0	<ul> <li>3) Deoxyribonucleic acid</li> <li>C) Nucleoplasm</li> <li>D) Ribonucleic acid + Dec</li> </ul>	oxyribonucleic acid	13.	structure c-DNA can be formed (A) Transaminase	d by
ul	which one of the followi traviolet light by hetero ases)			(B) DNA ligase	DNA polymerase (Reven
· · · · · · · · · · · · · · · · · · ·	/	(B) 26 nm (D) 260 nm		( <b>D</b> ) DNA dependent l	DNA polymerase

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#### **MOLECULAR BASIS OF INHERITANCE**

	Exercise # 2 SINGLE OB.	JECTI	VE AII	MS LEVEL
1.	In prokaryotes, the process of replication is catalysed by the following enzymes. Identify which of the enzymes is best coordinate with the role (A) Helicase– Joins the ends of DNA segments	8.	DNA is acidic due to (A) Sugar (C) Purine	(B) Phosphoric acid (D) Pyrimidine
	<ul> <li>(B) DNA polymerase I – Synthesis DNA</li> <li>(C) DNA polymerase II – Erases primer and fills gaps</li> <li>(D) Primase – Synthesis RNA primers</li> </ul>	9.	RNA is not found in (A) Chromosome (C) Nucleous	<ul><li>(B) Plasmmaalemma</li><li>(D) Ribosome</li></ul>
2.	<ul> <li>(b) Frindse "Synthesis Reverprinters"</li> <li>The eukaryotic differs from the prokaryotic genome because</li> <li>(A) Repetitive sequences are present in eukaryotes.</li> <li>(B) Genes in the former case are organized into operons</li> <li>(C) The DNA is complexed with with histones in prokaryotes</li> <li>(D) The DNA is circular and single stranded in</li> </ul>	10.		sential genes cleosomes n of repetitive DNA
3.	prokaryotes The double helix model of Waston and Crick is		<ul><li>(A) Parallel</li><li>(C) Antiparallel</li></ul>	<ul><li>(B) Discontinuous</li><li>(D) Semiconservative</li></ul>
	known as (A) C-DNA (B) B-DNA (C) Z-DNA (D) D-DNA	12.	e	nisms, guanine constitutes at percentage of the bases
4.	<ul><li>Find out the wrong statement</li><li>(A) Mobile genetic elements, transposons were visualized by Barbara McClintock</li></ul>		<ul> <li>(A) 0%</li> <li>(C) 20%</li> <li>(E) 40%</li> </ul>	<ul><li>(B) 10%</li><li>(D) 30%</li></ul>
	<ul> <li>(B) Udder cell, a somatic cell is used to produce the cloned sheep nuclear transplantation method</li> <li>(C) In pedigree analysis, a person immediately</li> </ul>	13.	Base composition in R1 (A) $A+T=G+C$ (C) $A+U=G+C$	NA is (B) $A+G=T+C$ (D) $A+G=U+C$
	<ul> <li>affected by an action is called propositus</li> <li>(D) Dr. Ian Wilmut produced a cloned sheep called Dolly</li> <li>(E) DNA ligase are used to cleave a DNA molecule</li> </ul>	14.	Left handed DNA amor (A) DNA (C) C DNA	ng following is (B) A DNA (D) B DNA
5.	<ul><li>Who among the following did not provide experimental proof for the semiconservative model of DNA replication</li><li>(A) Meselson &amp; Stahl</li><li>(B) Cairns</li></ul>	15.	Which of the following b from RNA (A) A–DNA (C) C–DNA	<ul> <li>(B) B – DNA</li> <li>(D) Z–DNA</li> </ul>
6.	(C) Waston & Crick (D) Taylor mRNA carries the genetic information from DNA to the	16.	of which, in one of th (methyl guanosine trip	additional processing. Out em an unusual nucleotide phosphate) is added to the
7.	<ul> <li>Which of the following is the site of translation of the mRNA</li> <li>(A) Chloroplasts</li> <li>(B) Ribosomes</li> <li>(C) Mitochondria</li> <li>(D) Lysosomes</li> <li>During DNA replication in prokaryotes DNA is anchored</li> <li>(A) Chromosome</li> <li>(B) Mesosome</li> <li>(C) Nucleolus</li> <li>(D) Ribosome</li> </ul>	17.	-	<ul> <li>(B) Tailing</li> <li>(D) Termination</li> <li>A molecule has the sequence which of the following could e DNA molecule</li> <li>(B)5'GUACCGAUGC3'</li> </ul>

I.       Match the following         Column - I       Column - I         A, tRNA       1. I inking of amino acids         B, mRNA       2. Transfer of genetic information         C, rRNA       3. Nucleolar organising region         D. Peptidyl transferase       4. Transfer of amino acid from cytoplasm of ribosome         A       B       C         (A)4       2       3       1         (B)1       4       3       2         (D)1       3       2       4         2.       Identify the correct match between the codons and coding functions       Column - I         Column -1       Column - II       AAUG       1. Phenylalanine         B. UAA       2. Methify the correct match between the codons and coding functions       Column - II         C. UUU       3. Tryptophan       DUGG       4. Termination         (A)A - 1, B - 4, C - 2, D - 3       (B)A - 2, B - 4, C - 1, D - 3       (C)A - 2, B - 3, C - 4, D - 1         3.       Match the following.	]	Exercise # 3	PAR	RT - 1 MATRIX MATCH COLUMN
A. RNA       1. Linking of amino acids         B. mRNA       2. Transfer of genetic information         C. rRNA       3. Nucleolar organising region         D. Peptidyl transferase       4. Transfer of amino acid from cytoplasm of ribosome         A       B       C         D. Peptidyl transferase       4. Transfer of amino acid from cytoplasm of ribosome         A       B       C         (A)4       2       3         (B)1       4       3       2         (O)1       2       3       4         (D)1       3       2       4         2.       Identify the correct match between the codons and coding functions:       Column -1         Column -1       Column - II       A.AUG         A. AUG       1. Phenylalanine       B.UAA         B. UAG       2. Methionine       C.UUU         C.UUU       3. Tryptophan       D.UGG         Match the following:       Column -1I       Column -1         Column -1       Column -1       A.VITR         A.VITR       P. Largest gene       B. Bulk DNA         D.Satellite       S.Splicing       (A)A-R; B-S; C-P; D -Q         (A) A-R; B -S; C -P; D -Q       (B) A -Q; B -S; C -P; D -R       (D) A - S; B -P	1.	Match the following		
B.mRNA       2. Transfer of genetic information         C.rRNA       3. Nucleolar organising region         D. Peptidyl transferase       4. Transfer of amino acid from cytoplasm of ribosome         A       B       C         D. (A)4       2       3       1         (B)1       4       3       2         (D)1       3       2       4         2.       Identify the correct match between the codins and coding functions       Column -1         Column -1       Column -1       Column -1         AAUG       I. Phenylalanine       B. UAA         B. UAA       2. Methionine       C. UUU       3. Tryptophan         D.UGG       4. Tramsfer of genetic information       (A)A - 1, B - 4, C - 2, D - 3         (C) A - 4, B - 3, C - 2, D - 1       (D) A - 4, B - 1, C - 3, D - 2       (P) (P) A - 2, B - 3, C - 4, D - 1         3.       Match the following.       Column - II         Column -1       Column -1       A.VNTR       P. Largest gene         B. Introns and Exons       Q. DNA fingerprinting       C Dystrophin         D.Satellite       S. Splicing       (A) A - R; B - S; C - P; D - Q         (A) A - R; B - S; C - P; D - Q       (B) A - Q; B - S; C - P; D - R       (C) A - Q; B - P; C - S; D - R		Column - I		Column - II
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		A. tRNA		1. Linking of amino acids
D. Peptidyl transferase4. Transfer of amino acid from cytoplasm of ribosomeABCD(A) 4231(B) 1432(C) 1234(D) 13242.Identify the correct match between the codons and coding functions Column -1Column -11AAUG1PhenylalanineB. UAA2MethionineC. UUU3. TryptophanD.UGG4. Termination(A) A - 1, B - 4, C - 2, D - 3(D) A - 4, B - 1, C - 3, D - 2(C) A - 4, B - 3, C - 2, D - 1(D) A - 4, B - 1, C - 3, D - 2(P) A - 2, B - 3, C - 4, D - 1Column - 113.Match the following.Column -1Column -11A.VNTRP. Largest geneB. Introns and ExonsQ. DNA fingerprintingC. DystrophinR. Sulli NAD. SatelliteS. Splicing(A) A - R, B - S, C - P, D - Q(B) A - Q, B - S, C - P, D - R(C) A - Q, B - P, C - S, D - R(D) A - 4, B - 3, C - 2, D - 3(C) A - Q, B - P, C - S, D - R(D) A - 3, B - P, C - Q, D - R4.Match the following in column - I with column - II and choose the correct combinationColumn -1A.VITRA. Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD.DNA replication4. RNA polymerase(A) A - 1; B - 3; C - 4; D - 2(D) A - 4; B - 2; C - 1; D - 3		B. mRNA		2. Transfer of genetic information
ABCD(A) 4231(B) 1432(C) 1234(D) 13242.Identify the correct match between the codons and coding functions Column -1Column -1A.AUG1PhenylalanineB. UAA2. MethionineC. UUU3. TryptophanD.UGG4. Termination(A) A - 1, B - 4, C - 2, D - 3(B) A - 2, B - 4, C - 1, D - 3(C) A - 4, B - 3, C - 2, D - 1(D) A - 4, B - 1, C - 3, D - 2(F) A - 2, B - 3, C - 4, D - 1(D) A - 4, B - 1, C - 3, D - 23.Match the following.Column - IIColumn -1Column -1A.VNTRP. Largest geneB. Introns and ExonsQ. DNA fingerprintingC. DystrophinR. Bulk DNAD. SatelliteS. Splicing(A) A - R; B - S; C - P; D - Q(B) A - Q; B - S; C - P; D - R(C) A - Q; B - P; C - S; D - R(D) A - S; B - P; C - Q; D - R4.Match the following in column - I with column - II and choose the correct combinationColumn -1Column -1IA.Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD.DNA replication4. RNA polymerase(A) A - 1; B - 3; C - 1; D - 4(D) A - 1; B - 2; C - 1; D - 3		C. rRNA		3. Nucleolar organising region
(A) 4 2 3 1 (B) 1 (B) 1 4 3 2 3 (C) 1 (C) 1 2 3 4 (D) 1 3 2 4 2. Identify the correct match between the codons and coding functions Column -1 Column - II A AUG 1. Phenylalanine B. UAA 2. Methionine C. UUU 3. Tryptophan D. UCG 4. Termination (A) A - 1, B - 4, C - 2, D - 3 (C) A - 4, B - 3, C - 2, D - 1 (D) A - 4, B - 1, C - 3, D - 2 (E) A - 2, B - 3, C - 4, D - 1 3. Match the following. Column - 1 A VNTR P. Largest gene B. Introns and Exons Q. DNA fingerprinting C. Dystrophin R. Bulk DNA D. Satellite S. Splicing (A) A - R; B - S; C - P; D - Q (C) A - Q; B - P; C - S; D - R (C) A - Q; B - P; C - S; D - R (C) A - Q; B - P; C - S; D - R 4. Match the following in column - I with column - II and choose the correct combination Column - 1 A Termination 1. Aminoacyl synthetase B. Translation 2. Okazaki fragments C. Transcription 3. GTP dependent release factor D. DNA replication 4. RNA polymerase (A) A - 1; B - 3; C - 1; D - 4 (C) A - 2; B - 1; C - 4; D - 2 (D) A - 4; B - 2; C - 1; D - 3 (C) A - 3; B - 1; C - 4; D - 2 (D) A - 4; B - 2; C - 1; D - 3		D. Peptidyl transferase		4. Transfer of amino acid from cytoplasm of ribosome
(B) 1432(C) 1234(D) 13242.Identify the correct match between the codons and coding functionsColumn -1Column - IIA.AUG1. PhenylalanineB. UAA2. MethionineC. UUU3. TryptophanD.UCG4. Termination(A) A - 1, B - 4, C - 2, D - 3(B) A - 2, B - 4, C - 1, D - 3(C) A - 4, B - 3, C - 2, D - 1(D) A - 4, B - 1, C - 3, D - 2(F) A - 2, B - 3, C - 4, D - 1(D) A - 4, B - 1, C - 3, D - 23.Match the following.Column - IColumn - IIA. VNTRP. Largest geneB. Introns and ExonsQ. DNA fingerprintingC. DystrophinR. Bulk DNAD. SatelliteS. Splicing(A) A - R; B - S; C - P; D - Q(B) A - Q; B - S; C - P; D - R(C) A - Q; B - P; C - S; D - R(D) A - S; B - P; C - Q; D - R4.Match the following in column - I with column - II and choose the correct combinationColumn - IColumn - IIA. Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD. DNA replication4. RNA polymerase(A) A - 1; B - 3; C - 1; D - 4(B) A - 1; B - 4; C - 2; D - 3(C) A - 3; B - 1; C - 4; D - 2(D) A - 4; B - 2; C - 1; D - 3		Α	В	C D
(C) 1234(D) 13242.Identify the correct match between the codons and coding functions Column - IColumn - II $AAUG$ I. PhenylalanineB. UAA2. MethionineC. UUU3. TryptophanD.UGG4. Termination(A) A - 1, B - 4, C - 2, D - 3(B) A - 2, B - 4, C - 1, D - 3(C) A + B - 3, C - 2, D - 1(D) A - 4, B - 1, C - 3, D - 2(E) A - 2, B - 3, C - 4, D - 1Column - IIA. VNTRP. Largest geneB. Introns and ExonsQ. DNA fingerprintingC. DystrophinR. Bulk DNAD. SatelliteS. Splicing(A) A - R; B - S; C - P; D - Q(B) A - Q; B - S; C - P; D - R(C) A - Q; B - P; C - S; D - R(D) A - S; B - P; C - Q; D - R4.Match the following in column - I with column - II and choose the correct combinationColumn - IColumn - IIA. Termination1. Aminoacyl synthetaseB. Transation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD. DA rigBication4. RNA polymerase(A) A - 1; B - 3; C - 1; D - 4(B) A - 1; B - 4; C - 2; D - 3(C) A - 3; B - 1; C - 4; D - 2(D) A - 4; B - 2; C - 1; D - 3		(A) 4	2	3 1
(D) 1 3 2 4 (D) 1 3 2 4 . Identify the correct match between the codons and coding functions Column -1 Column -I A.AUG 1. Phenylalanine B. UAA 2. Methionine C. UUU 3. Tryptophan D.UGG 4. Termination (A) A - 1, B - 4, C - 2, D - 3 (C) A - 4, B - 3, C - 2, D - 1 (D) A - 4, B - 3, C - 2, D - 1 (D) A - 4, B - 3, C - 2, D - 1 (D) A - 4, B - 3, C - 2, D - 1 (D) A - 4, B - 3, C - 2, D - 1 (D) A - 4, B - 3, C - 2, D - 1 (D) A - 4, B - 3, C - 2, D - 1 (D) A - 4, B - 3, C - 2, D - 1 (D) A - 4, B - 3, C - 3, D - 2 (E) A - 2, B - 3, C - 4, D - 1 3. Match the following. Column -1 Column - I A.VNTR P. Largest gene B. Introns and Exons Q. DNA fingerprinting C. Dystrophin R. Bulk DNA D. Satellite S. Splicing (A) A - R; B - S; C - P; D - Q (D) A - C; B - S; C - P; D - R (C) A - 0; B - P; C - S; D - R (D) A - S; B - P; C - 0; D - R 4. Match the following in column - I with column - I and choose the correct combination Column -1 Column - I A. Termination 1. Aminosey I synthetase B. Transatiption 2. Okazaki fingments C. Transcription 3. GTP dependent release factor D.DNA replication 4. RNA polymerase (A) A - 1; B - 3; C - 1; D - 4 (D) A - 1; B - 4; C - 2; D - 3 (D) A - 4; B - 1; C - 4; D - 2 (D) A - 4; B - 2; C - 1; D - 3		(B) 1	4	3 2
<ol> <li>Identify the correct match between the codons and coding functions         <ul> <li>Column - I</li> <li>Column - II</li> </ul> </li> <li>A.AUG         <ul> <li>I. Phenylalanine</li> <li>B. UAA</li> <li>Methionine</li> <li>C. UUU</li> <li>Tryptophan</li> <li>D.UGG</li> <li>A. Termination</li> <li>(A) A - 1, B - 4, C - 2, D - 3</li> <li>(B) A - 2, B - 4, C - 1, D - 3</li> <li>(C) A - 4, B - 3, C - 2, D - 1</li> <li>(D) A - 4, B - 3, C - 2, D - 1</li> <li>(D) A - 4, B - 1, C - 3, D - 2</li> <li>(E) A - 2, B - 3, C - 4, D - 1</li> </ul> </li> <li>Match the following.         <ul> <li>Column - I</li> <li>Column - I</li> <li>Column - I</li> <li>A.VNTR</li> <li>P. Largest gene</li> <li>B. Introns and Exons</li> <li>Q. DNA fingerprinting</li> <li>C. Dystrophin</li> <li>R. Bulk DNA</li> <li>D. Satellite</li> <li>S. Splicing</li> <li>(A) A - R; B - S; C - P; D - Q</li> <li>(B) A - Q; B - S; C - P; D - R</li> <li>(C) A - Q; B - P, C - S; D - R</li> <li>(D) A - S; B - P; C - Q; D - R</li> </ul> </li> <li>Match the following in column - I with column - II and choose the correct combination</li> <li>Column - 1</li> <li>Column - 1I</li> <li>A. Termination</li> <li>A. Aminoacyl synthetase</li> <li>B. Translation</li> <li>C. Okazaki fragments</li> <li>C. Transcription</li> <li>A. GTP dependent release factor</li> <li>D. DNA replication</li> <li>A. RNA polymerase</li> <li>(A) A - 1; B - 3; C - 1; D - 4</li> <li>(B) A - 1; B - 4; C - 2; D - 3</li> <li>(C) A - 3; B</li></ol>		(C) 1	2	3 4
Column - IColumn - IIA.AUG1. PhenylalanineB. UAA2. MethionineC. UUU3. TryptophanD.UGG4. Termination(A) A - 1, B - 4, C - 2, D - 3(B) A - 2, B - 4, C - 1, D - 3(C) A - 4, B - 3, C - 2, D - 1(D) A - 4, B - 1, C - 3, D - 2(F) A - 2, B - 3, C - 4, D - 1(D) A - 4, B - 1, C - 3, D - 23.Match the following.Column - 1Column - IIA.VNTRP. Largest geneB. Introns and ExonsQ. DNA fingerprintingC. DystrophinR. Bulk DNAD. SatelliteS. Splicing(A) A - R; B - S; C - P; D - Q(B) A - 2; B - S; C - P; D - R(C) A - Q; B - P; C - S; D - R(D) A - S; B - P; C - Q; D - R4.Match the following in column - I with column - II and choose the correct combinationColumn - 1Column - IIA. Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD. DNA replication4. RNA polymerase(A) A - 1; B - 3; C - 1; D - 4(B) A - 1; B - 4; C - 2; D - 3(C) A - 3; B - 1; C - 4; D - 2(D) A - 4; B - 2; C - 1; D - 3		(D) 1	3	2 4
A.AUG1. PhenylalanineB. UAA2. MethionineC. UUU3. TryptophanD.UGG4. Termination $(A) A - 1, B - 4, C - 2, D - 3$ $(B) A - 2, B - 4, C - 1, D - 3$ $(C) A - 4, B - 3, C - 2, D - 1$ $(D) A - 4, B - 1, C - 3, D - 2$ $(F) A - 2, B - 3, C - 4, D - 1$ $(D) A - 4, B - 1, C - 3, D - 2$ <b>3.</b> Match the following.Column -1Column - IIA.VNTRP. Largest geneB. Introns and ExonsQ. DNA fingerprintingC. DystrophinR. Bulk DNAD. SatelliteS. Splicing $(A) A - R; B - S; C - P; D - Q$ $(B) A - Q; B - S; C - P; D - R$ $(C) A - Q; B - P; C - S; D - R$ $(D) A - S; B - P; C - Q; D - R$ <b>4.</b> Match the following in column - I with column - II and choose the correct combinationColumn -1Column - IIA. Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD. DNA replication4. RNA polymerase $(A) A - 1; B - 3; C - 1; D - 4$ $(B) A - 1; B - 4; C - 2; D - 3$	2.	Identify the correct mat	ch between the co	odons and coding functions
B. UAA2. MethonineC. UUU3. TryptophanD.UGG4. Termination(A) A-1, B-4, C-2, D-3(B) A-2, B-4, C-1, D-3(C) A-4, B-3, C-2, D-1(D) A-4, B-1, C-3, D-2(E) A-2, B-3, C-4, D-1(D) A-4, B-1, C-3, D-23.Match the following.Column -1Column -IIA. VNTRP. Largest geneB. Introns and ExonsQ. DNA fingerprintingC. DystrophinR. Bulk DNAD. SatelliteS. Splicing(A) A- R; B-S; C-P; D-Q(B) A-Q; B-S; C-P; D-R(C) A-Q; B-P; C-S; D-R(D) A-S; B-P; C-Q; D-R4.Match the following in column - I with column - II and choose the correct combinationColumn -1Column -IIA. Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD. DNA replication4. RNA polymerase(A) A-1; B-3; C-1; D-4(B) A-1; B-4; C-2; D-3(C) A-3; B-1; C-4; D-2(D) A-4; B-2; C-1; D-3		Column - I		Column - II
C. UUU3. Tryptophan $D.UGG$ 4. Termination $(A) A-1, B-4, C-2, D-3$ $(B) A-2, B-4, C-1, D-3$ $(C) A-4, B-3, C-2, D-1$ $(D) A-4, B-1, C-3, D-2$ $(E) A-2, B-3, C-4, D-1$ $(D) A-4, B-1, C-3, D-2$ <b>3.</b> Match the following.Column-IColumn - II $A. VNTR$ $P.$ Largest gene $B.$ Introns and Exons $Q.$ DNA fingerprinting $C.$ Dystrophin $R.$ Bulk DNA $D.$ Satellite $S.$ Splicing $(A) A-R; B-S; C-P; D-Q$ $(B) A-Q; B-S; C-P; D-R$ $(C) A-Q; B-P; C-S; D-R$ $(D) A-S; B-P; C-Q; D-R$ <b>4.</b> Match the following in column - I with column - II and choose the correct combinationColumn-IColumn - II $A.$ Termination1. Aminoacyl synthetase $B.$ Translation2. Okazaki fragments $C.$ Transcription3. GTP dependent release factor $D. DNA$ replication4. RNA polymerase $(A) A-1; B-3; C-1; D-4$ $(B) A-1; B-4; C-2; D-3$ $(C) A-3; B-1; C-4; D-2$ $(D) A-4; B-2; C-1; D-3$		A.AUG		1. Phenylalanine
D.UGG4. Termination(A) A-1, B-4, C-2, D-3(B) A-2, B-4, C-1, D-3(C) A-4, B-3, C-2, D-1(D) A-4, B-1, C-3, D-2(E) A-2, B-3, C-4, D-1(D) A-4, B-1, C-3, D-23. Match the following.Column - IIA. VNTRP. Largest geneB. Introns and ExonsQ. DNA fingerprintingC. DystrophinR. Bulk DNAD. SatelliteS. Splicing(A) A- R; B-S; C-P; D-Q(B) A-Q; B-S; C-P; D-R(C) A-Q; B-P; C-S; D-R(D) A-S; B-P; C-Q; D-R4.Match the following in column - I with column - II and choose the correct combinationColumn - IColumn - IIA. Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD. DNA replication4. RNA polymerase(A) A-1; B-3; C-1; D-4(B) A-1; B-4; C-2; D-3(C) A-3; B-1; C-4; D-2(D) A-4; B-2; C-1; D-3		B. UAA		2. Methionine
(A) $A - 1, B - 4, C - 2, D - 3$ (C) $A - 4, B - 3, C - 2, D - 1$ (D) $A - 4, B - 1, C - 3, D - 2$ (E) $A - 2, B - 3, C - 4, D - 1$ 3.Match the following. Column - I A. VNTRColumn - II P. Largest gene B. Introns and Exons C. DystrophinB. Introns and ExonsQ. DNA fingerprinting C. DystrophinR. Bulk DNA S. Splicing (A) $A - R; B - S; C - P; D - Q$ (C) $A - Q; B - P; C - S; D - R$ 4.Match the following in column - I with column - II and choose the correct combination Column - I A. TerminationColumn - II A. Termination4.Match the following in column - I with column - II and choose the correct combination Column - I A. TerminationColumn - II A. Termination4.Match the following in column - I with column - II and choose the correct combination Column - I A. TerminationColumn - II A. Termination4.Match the following in column - I with column - II and choose the correct combination Column - I A. TerminationColumn - II A. Termination5.C. Transcription3. GTP dependent release factor B. Translation2. Okazaki fragments A. P. 2; D - 3 (C) $A - 3; B - 1; C - 4; D - 2$		C. UUU		3. Tryptophan
(C) $A - 4, B - 3, C - 2, D - 1$ (D) $A - 4, B - 1, C - 3, D - 2$ (E) $A - 2, B - 3, C - 4, D - 1$ (D) $A - 4, B - 1, C - 3, D - 2$ 3. Match the following.Column - I $A \cdot VNTR$ P. Largest geneB. Introns and ExonsQ. DNA fingerprintingC. DystrophinR. Bulk DNAD. SatelliteS. Splicing(A) $A - R; B - S; C - P; D - Q$ (B) $A - Q; B - S; C - P; D - R$ (C) $A - Q; B - P; C - S; D - R$ (D) $A - S; B - P; C - Q; D - R$ 4. Match the following in column - I with column - II and choose the correct combinationColumn - IColumn - IIA. Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD. DNA replication4. RNA polymerase(A) $A - 1; B - 3; C - 1; D - 4$ (B) $A - 1; B - 4; C - 2; D - 3$ (C) $A - 3; B - 1; C - 4; D - 2$ (D) $A - 4; B - 2; C - 1; D - 3$		D. UGG		4. Termination
<ul> <li>(E) A-2, B-3, C-4, D-1</li> <li>3. Match the following.</li> <li>Column - I</li> <li>A. VNTR</li> <li>P. Largest gene</li> <li>B. Introns and Exons</li> <li>Q. DNA fingerprinting</li> <li>C. Dystrophin</li> <li>R. Bulk DNA</li> <li>D. Satellite</li> <li>S. Splicing</li> <li>(A) A-R; B-S; C-P; D-Q</li> <li>(B) A-Q; B-S; C-P; D-R</li> <li>(C) A-Q; B-P; C-S; D-R</li> <li>(D) A-S; B-P; C-Q; D-R</li> </ul> 4. Match the following in column - I with column - II and choose the correct combination Column - I <ul> <li>Column - I</li> <li>Column - II</li> <li>A. Termination</li> <li>I. Aminoacyl synthetase</li> <li>B. Translation</li> <li>C. Transcription</li> <li>J. GTP dependent release factor</li> <li>D. DNA replication</li> <li>(A) A-1; B-3; C-1; D-4</li> <li>(B) A-1; B-4; C-2; D-3</li> <li>(C) A-3; B-1; C-4; D-2</li> <li>(D) A-4; B-2; C-1; D-3</li> </ul>		(A) A - 1, B - 4, C - 2, D -	3	<b>(B)</b> A - 2, B - 4, C - 1, D - 3
<ul> <li>3. Match the following.</li> <li>Column - I</li> <li>A. VNTR</li> <li>P. Largest gene</li> <li>B. Introns and Exons</li> <li>Q. DNA fingerprinting</li> <li>C. Dystrophin</li> <li>R. Bulk DNA</li> <li>D. Satellite</li> <li>S. Splicing</li> <li>(A) A - R; B - S; C - P; D - Q</li> <li>(B) A - Q; B - S; C - P; D - R</li> <li>(C) A - Q; B - P; C - S; D - R</li> <li>(D) A - S; B - P; C - Q; D - R</li> <li>4. Match the following in column - I with column - II and choose the correct combination</li> <li>Column - I</li> <li>Column - I</li> <li>A. Termination</li> <li>B. Translation</li> <li>C. Transcription</li> <li>G. GTP dependent release factor</li> <li>D. DNA replication</li> <li>(A A - 1; B - 3; C - 1; D - 4</li> <li>(B) A - 1; B - 4; C - 2; D - 3</li> </ul>		(C) A - 4, B - 3, C - 2, D -	1	(D) A - 4, B - 1, C - 3, D - 2
Column - IColumn - IIA. VNTRP. Largest geneB. Introns and ExonsQ. DNA fingerprintingC. DystrophinR. Bulk DNAD. SatelliteS. Splicing(A) A - R; B - S; C - P; D - Q(B) A - Q; B - S; C - P; D - R(C) A - Q; B - P; C - S; D - R(D) A - S; B - P; C - Q; D - R4.Match the following in column - I with column - II and choose the correct combinationColumn - IColumn - IIA. Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD. DNA replication4. RNA polymerase(A) A - 1; B - 3; C - 1; D - 4(B) A - 1; B - 4; C - 2; D - 3(C) A - 3; B - 1; C - 4; D - 2(D) A - 4; B - 2; C - 1; D - 3		(E) A-2, B-3, C-4, D-	1	
Column - IColumn - IIA. VNTRP. Largest geneB. Introns and ExonsQ. DNA fingerprintingC. DystrophinR. Bulk DNAD. SatelliteS. Splicing(A) A - R; B - S; C - P; D - Q(B) A - Q; B - S; C - P; D - R(C) A - Q; B - P; C - S; D - R(D) A - S; B - P; C - Q; D - R4.Match the following in column - I with column - II and choose the correct combinationColumn - IColumn - IIA. Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD. DNA replication4. RNA polymerase(A) A - 1; B - 3; C - 1; D - 4(B) A - 1; B - 4; C - 2; D - 3(C) A - 3; B - 1; C - 4; D - 2(D) A - 4; B - 2; C - 1; D - 3	3.	Match the following.		
<ul> <li>B. Introns and Exons</li> <li>Q. DNA fingerprinting</li> <li>C. Dystrophin</li> <li>R. Bulk DNA</li> <li>D. Satellite</li> <li>S. Splicing</li> <li>(A) A - R; B - S; C - P; D - Q</li> <li>(B) A - Q; B - S; C - P; D - R</li> <li>(C) A - Q; B - P; C - S; D - R</li> <li>(D) A - S; B - P; C - Q; D - R</li> </ul> 4. Match the following in column - I with column - II and choose the correct combination Column - I <ul> <li>Column - I</li> <li>Column - II</li> <li>A. Termination</li> <li>I. Aminoacyl synthetase</li> <li>B. Translation</li> <li>C. Transcription</li> <li>GTP dependent release factor</li> <li>D. DNA replication</li> <li>(A) A - 1; B - 3; C - 1; D - 4</li> <li>(B) A - 1; B - 4; C - 2; D - 3</li> </ul>		-		Column - II
<ul> <li>B. Introns and Exons</li> <li>Q. DNA fingerprinting</li> <li>C. Dystrophin</li> <li>R. Bulk DNA</li> <li>D. Satellite</li> <li>S. Splicing</li> <li>(A) A-R; B-S; C-P; D-Q</li> <li>(B) A-Q; B-S; C-P; D-R</li> <li>(C) A-Q; B-P; C-S; D-R</li> <li>(D) A-S; B-P; C-Q; D-R</li> </ul> 4. Match the following in column - I with column - II and choose the correct combination Column - I <ul> <li>Column - I</li> <li>Column - II</li> <li>A. Termination</li> <li>I. Aminoacyl synthetase</li> <li>B. Translation</li> <li>C. Transcription</li> <li>J. GTP dependent release factor</li> <li>D. DNA replication</li> <li>(A) A-1; B-3; C-1; D-4</li> <li>(B) A-1; B-4; C-2; D-3</li> <li>(C) A-3; B-1; C-4; D-2</li> <li>(D) A-4; B-2; C-1; D-3</li> </ul>		A. VNTR		P. Largest gene
<ul> <li>A. A R; B - S; C - P; D - Q</li> <li>(B) A - Q; B - S; C - P; D - R</li> <li>(C) A - Q; B - P; C - S; D - R</li> <li>(D) A - S; B - P; C - Q; D - R</li> </ul> 4. Match the following in column - I with column - II and choose the correct combination Column - I <ul> <li>Column - I</li> <li>A. Termination</li> <li>B. Translation</li> <li>C. Transcription</li> <li>C. Transcription<th></th><th>B. Introns and Exons</th><th></th><th>Q. DNA fingerprinting</th></li></ul>		B. Introns and Exons		Q. DNA fingerprinting
<ul> <li>(A) A-R; B-S; C-P; D-Q</li> <li>(B) A-Q; B-S; C-P; D-R</li> <li>(C) A-Q; B-P; C-S; D-R</li> <li>(D) A-S; B-P; C-Q; D-R</li> </ul> 4. Match the following in column - I with column - II and choose the correct combination Column - I <ul> <li>A. Termination</li> <li>B. Translation</li> <li>C. Transcription</li> <li>B. Transcription</li> <li>C. Transcription</li> <li>D. DNA replication</li> <li>(D) A-1; B-4; C-2; D-3</li> <li>(C) A-3; B-1; C-4; D-2</li> <li>(D) A-4; B-2; C-1; D-3</li> </ul>		C. Dystrophin		R. Bulk DNA
<ul> <li>(C) A - Q; B - P; C - S; D - R</li> <li>(D) A - S; B - P; C - Q; D - R</li> <li>4. Match the following in column - I with column - II and choose the correct combination Column - I <ul> <li>A. Termination</li> <li>B. Translation</li> <li>C. Transcription</li> <li>DNA replication</li> <li>(A) A - 1; B - 3; C - 1; D - 4</li> <li>(B) A - 1; B - 4; C - 2; D - 3</li> <li>(C) A - 3; B - 1; C - 4; D - 2</li> <li>(D) A - S; B - P; C - Q; D - R</li> </ul> </li> </ul>		<b>D.</b> Satellite		S. Splicing
<ul> <li>4. Match the following in column - I with column - II and choose the correct combination</li> <li>Column - I</li> <li>A. Termination</li> <li>B. Translation</li> <li>C. Transcription</li> <li>DNA replication</li> <li>(A) A-1; B-3; C-1; D-4</li> <li>(B) A-1; B-4; C-2; D-3</li> <li>(C) A-3; B-1; C-4; D-2</li> <li>(D) A-4; B-2; C-1; D-3</li> </ul>		(A) A - R; B - S; C - P; D	- Q	<b>(B)</b> A - Q; B - S; C - P; D - R
Column - IColumn - IIA. Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD. DNA replication4. RNA polymerase(A) A-1; B-3; C-1; D-4(B) A-1; B-4; C-2; D-3(C) A-3; B-1; C-4; D-2(D) A-4; B-2; C-1; D-3		$(\mathbb{C})$ A - Q; B - P; C - S; D	- R	<b>(D)</b> A - S; B - P; C - Q; D - R
Column - IColumn - IIA. Termination1. Aminoacyl synthetaseB. Translation2. Okazaki fragmentsC. Transcription3. GTP dependent release factorD. DNA replication4. RNA polymerase(A) A-1; B-3; C-1; D-4(B) A-1; B-4; C-2; D-3(C) A-3; B-1; C-4; D-2(D) A-4; B-2; C-1; D-3	4.	Match the following in c	column - I with co	olumn - II and choose the correct combination
B. Translation       2. Okazaki fragments         C. Transcription       3. GTP dependent release factor         D. DNA replication       4. RNA polymerase         (A) A-1; B-3; C-1; D-4       (B) A-1; B-4; C-2; D-3         (C) A-3; B-1; C-4; D-2       (D) A-4; B-2; C-1; D-3		e		
B. Translation       2. Okazaki fragments         C. Transcription       3. GTP dependent release factor         D. DNA replication       4. RNA polymerase         (A) A-1; B-3; C-1; D-4       (B) A-1; B-4; C-2; D-3         (C) A-3; B-1; C-4; D-2       (D) A-4; B-2; C-1; D-3				1. Aminoacyl synthetase
C. Transcription       3. GTP dependent release factor         D. DNA replication       4. RNA polymerase         (A) A- 1; B - 3; C - 1; D - 4       (B) A- 1; B - 4; C - 2; D - 3         (C) A- 3; B- 1; C - 4; D - 2       (D) A- 4; B - 2; C - 1; D - 3		<b>B.</b> Translation		
<b>D.</b> DNA replication <b>4.</b> RNA polymerase(A) A-1; B-3; C-1; D-4(B) A-1; B-4; C-2; D-3(C) A-3; B-1; C-4; D-2(D) A-4; B-2; C-1; D-3				e
(A) $A - 1; B - 3; C - 1; D - 4$ (B) $A - 1; B - 4; C - 2; D - 3$ (C) $A - 3; B - 1; C - 4; D - 2$ (D) $A - 4; B - 2; C - 1; D - 3$		-		
(C) $A-3; B-1; C-4; D-2$ (D) $A-4; B-2; C-1; D-3$		-	4	

### **MOLECULAR BASIS OF INHERITANCE**

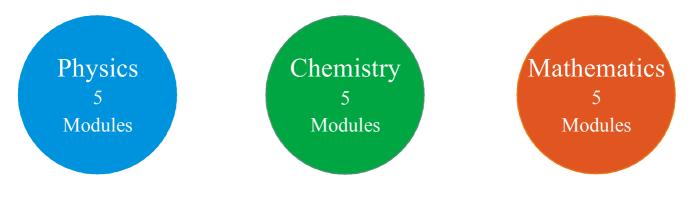
	Exercise # 4	PART - 1		PREVIOUS YEAR (	NEET/AIPMT)
1.	rate. Each of these serves mation of new strand. S called	NA, its two strands sepa- s as a templete for the for- uch type of replication is [CBSE AIPMT 2000]	7.	In negative operon (A) co-repressor binds v (B) co-repressor does no (C) co-repressor binds v (D) cAMP has negative	ot bind with repressor vith inducer
	<ul><li>(A) non-conservative</li><li>(C) flexible</li></ul>	<ul><li>(B) semi-conservative</li><li>(D) conservative</li></ul>	8.	the phylogeny ?	e following is used to know [CBSE AIPMT 2001]
2.	'Signal hypothesis' for tory type of proteins wa	the biosynthesis of secre- s proposed by [CBSE AIPMT 2000]	9.	(A) mRNA (C) tRNA In E. coli, during lactose	(B) rRNA (D) DNA metabolism repressor binds
	(A) Camillo Golgi (C) Baltimore	<ul><li>(B) Blobel and Sabatini</li><li>(D) Sheeler and Bianchi</li></ul>		to (A) regulator gene (C) structural gene	[CBSE AIPMT 2002] (B) operator gene (D) promoter gene
3.	Due to discovery of which the evolution was termed		10.	coli and proposed Oper cept applicable for	ed lactose metabolism in E. ron concept. Operon con- [CBSE AIPMT 2002]
	(A) mRNA, tRNA, rRNA (B) In some viruses, RNA	• •		<ul> <li>(A) all prokaryotes</li> <li>(B) all prokaryotes and</li> <li>(C) all prokaryotes and a</li> </ul>	•
	<ul><li>(C) Some RNAs have en</li><li>(D) RNA is not found in a</li></ul>	zymatic property	11.	( <b>D</b> ) all prokaryotes and In a DNA percentage of	some protozoans
4.		was placed in a medium ymidine for five minutes.		percentage of guanine ? (A) 20% (C) 30%	
	-	cate in a normal medium. observation shall be cor- [CBSE AIPMT 2001]	12.	?	rect bacterial transduction [CBSE AIPMT 2002]
	<ul><li>(A) Both the strands of D</li><li>(B) One strand radioactive</li></ul>	NA will be radioactive		another bacteria thi (B) Transfer of genes fr	om one bacteria to another
	(C) Each strand half radi (D) None is radioactive	oactive		bacteria by conjuga (C) Bacteria obtained its (D) Bacteria obtained	
5.	Gene and cistron wor synonymosuly because	ds are sometimes used [CBSE AIPMT 2001]	13.		bryonal cell/somatic cell is
	<ul><li>(A) one cistron contains</li><li>(B) one gene contains m</li></ul>			formation of organism v	[CBSE AIPMT 2002]
	<ul><li>(C) one gene contains of</li><li>(D) one gene contains no</li></ul>			donor cell (B) Organism will have	extra-nuclear genes of the extra-nuclear genes of re-
6.	In which direction mRN template ?	A is synthesised on DNA [CBSE AIPMT 2001]		cipient cell (C) Organism will have donor and recipient	extra-nuclear genes of both cell
	(A) $5' \rightarrow 3'$ (C) both (A) and (B)	(B) $3' \rightarrow 5'$ (D) any of above		-	nuclear genes of recepient

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		MO	OCK TEST					
1.	Beads on string like st division	ructures of A are seen in	B, which further condense	e to form chromosomes in C stage of cel				
	Α	В	С					
	(A) Chromonema	Chromatin	Metaphase					
	(B) Chromatin	Chromatid	Metaphase					
	(C) Chromonema	Chromosome	Anaphase					
	(D) Chromonema	Chromatid	Anaphase					
2.	Microsatellites are							
	(A) Repetitive DNA se	equences	(B) ESTs					
	(C) YAC		(D) BAC					
	(E) UTR							
3.	In the DNA molecule							
	(A) The proportion of	adenine in relation to thy	mine varies with the organ	nism				
	(B) There are two stran	nds which run antiparalle	el-one in 5' $\rightarrow$ 3' direction	and other in $3 \rightarrow 5$				
	(C) The total amount	of purine nucleotides and	pyrimidine nucleotieds is	s not always equal				
	(D) There are two stran	nds which run parallel in	the 5' $\rightarrow$ 3' direction					
		important concept in the	genetic implication of DN	S. Fill in the blanks A to C.				
4.	The diagram shows an	The diagram shows an important concept in the genetic implication of DNS. Fill in the blanks A to C. $\overrightarrow{DNA} \xrightarrow{A} mRNA \xrightarrow{B} Proposed by \xrightarrow{C} C$						
4.	-							
4.	-							
4.	(A) A-Transcription, B	A $\xrightarrow{B}$ Proposed by $\xrightarrow{P}$ B - Translation, C-Francis	roposed by C Crick (B) A-Translation,	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff				
4. 5.	(A) A-Transcription, B $(C) A-Transcription, B$	B → Proposed by $\xrightarrow{P}$ B - Translation, C-Francis B - Replication, C-James V	Crick (B) A-Translation, Vatson (D) A-Translation,	B - Extension, C-Rosalind Frankline				
	(A) A-Transcription, B $(C) A-Transcription, B$	B → Proposed by $\xrightarrow{P}$ B - Translation, C-Francis B - Replication, C-James V	Crick (B) A-Translation, Vatson (D) A-Translation,	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff				
	(A) A-Transcription, E $(C) A-Transcription, E$ If the total of adenine a $(A) 45%$ $(E) 40%$	A B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5%	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25%	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe				
5.	(A) A-Transcription, E $(C) A-Transcription, E$ If the total of adenine a $(A) 45%$ $(E) 40%$ Read the following sta	A → Proposed by B - Translation, C-Francis B - Replication, C-James W and thymine in a double s (B) 27.5%	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5%				
5.	(A) A-Transcription, E $(C) A-Transcription, E$ If the total of adenine a $(A) 45 %$ $(E) 40%$ Read the following state A. Nitrogenous base in	A B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% atements and choose the s linked to the pentose su	<pre>troposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25%</pre>	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5%				
5.	A (A) A-Transcription, B (C) A-Transcription, B (C) A-Transcription, B If the total of adenine a (A) 45 % (E) 40% Read the following sta A. Nitrogenous base is B. Phosphate group is	B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% atements and choose the s linked to the pentose su s linked to 5' -OH of a nu	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option gar through a N-glycosidi cleoside through phospho	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5%				
5.	A (A) A-Transcription, E (C) A-Transcription, E If the total of adenine a (A) 45 % (E) 40% Read the following sta A. Nitrogenous base is B. Phosphate group is C. Two nucleoside are	B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% atements and choose the s linked to the pentose su b linked to 5' -OH of a nu- linked through 3'-5' N-g	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option gar through a N-glycosidi cleoside through phospho lycosidic linkage	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5% ic linkage. ester linkage				
5.	A (A) A-Transcription, E (C) A-Transcription, E (C) A-Transcription, E If the total of adenine a (A) 45 % (E) 40% Read the following sta A. Nitrogenous base is B. Phosphate group is C. Two nucleoside are D. Negatively charged	B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% Atements and choose the s linked to the pentose su b linked to 5' -OH of a nu- linked through 3'-5' N-g d DNA is wrapped around	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option gar through a N-glycosidi cleoside through phospho lycosidic linkage d positively charged histor	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5% ic linkage. ester linkage ne octamer to form nucleosome.				
5.	A (A) A-Transcription, E (C) A-Transcription, E If the total of adenine a (A) 45 % (E) 40% Read the following sta A. Nitrogenous base is B. Phosphate group is C. Two nucleoside are D. Negatively charged E. The chromatin that	B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% atements and choose the s linked to the pentose su s linked to 5' -OH of a nu- linked through 3'-5' N-g d DNA is wrapped around is more densely packed a	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option gar through a N-glycosidi cleoside through phospho lycosidic linkage l positively charged histor and stains dark is called eu-	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5% ic linkage. ester linkage ne octamer to form nucleosome. chromatin.				
5.	<ul> <li>A mRNA</li> <li>(A) A-Transcription, E</li> <li>(C) A-Transcription, E</li> <li>If the total of adenine a</li> <li>(A) 45 %</li> <li>(E) 40%</li> <li>Read the following state A. Nitrogenous base is</li> <li>B. Phosphate group is</li> <li>C. Two nucleoside are</li> <li>D. Negatively charged</li> <li>E. The chromatin that</li> <li>(A) A,B and C alone a</li> </ul>	A B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% Atements and choose the s linked to the pentose su s linked to 5' -OH of a nu- linked through 3'-5' N-g d DNA is wrapped around is more densely packed are re wrong	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option gar through a N-glycosidi cleoside through phospho lycosidic linkage d positively charged histor ind stains dark is called eur (B) D alone is wro	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5% ic linkage. ester linkage ne octamer to form nucleosome. chromatin. ng				
5.	<ul> <li>A mRNA</li> <li>(A) A-Transcription, E</li> <li>(C) A-Transcription, E</li> <li>If the total of adenine a</li> <li>(A) 45 %</li> <li>(E) 40%</li> <li>Read the following state</li> <li>A. Nitrogenous base is</li> <li>B. Phosphate group is</li> <li>C. Two nucleoside are</li> <li>D. Negatively charged</li> <li>E. The chromatin that</li> <li>(A) A,B and C alone are</li> <li>(C) C and E alone are</li> </ul>	B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% atements and choose the s linked to the pentose su b linked to 5' -OH of a nu- linked through 3'-5' N-g d DNA is wrapped around is more densely packed a re wrong wrong	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option gar through a N-glycosidi cleoside through phospho lycosidic linkage l positively charged histor and stains dark is called eu-	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5% ic linkage. ester linkage ne octamer to form nucleosome. chromatin. ng				
5.	<ul> <li>A mRNA</li> <li>(A) A-Transcription, E</li> <li>(C) A-Transcription, E</li> <li>If the total of adenine a</li> <li>(A) 45 %</li> <li>(E) 40%</li> <li>Read the following sta</li> <li>A. Nitrogenous base is</li> <li>B. Phosphate group is</li> <li>C. Two nucleoside are</li> <li>D. Negatively charged</li> <li>E. The chromatin that</li> <li>(A) A,B and C alone a</li> </ul>	B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% atements and choose the s linked to the pentose su b linked to 5' -OH of a nu- linked through 3'-5' N-g d DNA is wrapped around is more densely packed a re wrong wrong	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option gar through a N-glycosidi cleoside through phospho lycosidic linkage d positively charged histor ind stains dark is called eur (B) D alone is wro	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5% ic linkage. ester linkage ne octamer to form nucleosome. chromatin. ng				
5.	(A) A-Transcription, B $(A) A-Transcription, B$ $(C) A-Transcription, E$ If the total of adenine a $(A) 45 %$ $(E) 40%$ Read the following state A. Nitrogenous base in B. Phosphate group is C. Two nucleoside are D. Negatively charged E. The chromatin that $(A) A, B and C alone are (C) C and E alone are (E) A, B and D alone are The result of which of$	B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% atements and choose the s linked to the pentose su s linked to 5' -OH of a nu- linked through 3'-5' N-g d DNA is wrapped around is more densely packed a re wrong wrong re wrong.	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option gar through a N-glycosidi cleoside through phospho lycosidic linkage l positively charged histor ind stains dark is called eu (B) D alone is wrom (D) A lone is wrom	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5% ic linkage. ester linkage ne octamer to form nucleosome. chromatin. ng				
5.	<ul> <li>A mRNA</li> <li>(A) A-Transcription, E</li> <li>(C) A-Transcription, E</li> <li>If the total of adenine a</li> <li>(A) 45 %</li> <li>(E) 40%</li> <li>Read the following state A. Nitrogenous base is</li> <li>B. Phosphate group is</li> <li>C. Two nucleoside are</li> <li>D. Negatively charged</li> <li>E. The chromatin that</li> <li>(A) A,B and C alone are</li> <li>(C) C and E alone are</li> <li>(E) A,B and D alone are</li> <li>The result of which of proved conclusively the</li> </ul>	B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% atements and choose the s linked to the pentose su s linked to 5' -OH of a nu- linked through 3'-5' N-g d DNA is wrapped around is more densely packed a re wrong wrong re wrong. 'the following reaction ex	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option gar through a N-glycosidi cleoside through phospho lycosidic linkage d positively charged histor ind stains dark is called eu (B) D alone is wron (D) A lone is wron periments carrid out by Ar aterial ?	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5% ic linkage. ester linkage ne octamer to form nucleosome. chromatin. ng g				
5.	(A) A-Transcription, B $(A) A-Transcription, B$ $(C) A-Transcription, E$ If the total of adenine a $(A) 45 %$ $(E) 40%$ Read the following state A. Nitrogenous base in B. Phosphate group is C. Two nucleoside are D. Negatively charged E. The chromatin that $(A) A, B and C alone are (C) C and E alone are (E) A, B and D alone are The result of which of proved conclusively th (A) Live `R' strain + D$	B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V and thymine in a double s (B) 27.5% A - Translation, C-James V a - Transl	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option gar through a N-glycosidi cleoside through phospho lycosidic linkage 1 positively charged histor ind stains dark is called eu- (B) D alone is wrom (D) A lone is wrom the periments carrid out by Ar- aterial ? Nase	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5% ic linkage. ester linkage ne octamer to form nucleosome. chromatin. ng g				
5.	(A) A-Transcription, B (A) A-Transcription, B (C) A-Transcription, B If the total of adenine a (A) 45 % (E) 40% Read the following state A. Nitrogenous base in B. Phosphate group is C. Two nucleoside are D. Negatively charged E. The chromatin that (A) A,B and C alone are (C) C and E alone are of (E) A,B and D alone are The result of which of proved conclusively th (A) Live 'R' strain + D (B) Live 'R' strain + D	B → Proposed by B - Translation, C-Francis B - Replication, C-James V and thymine in a double s (B) 27.5% atements and choose the s linked to the pentose su b linked to 5' -OH of a nu- linked through 3'-5' N-g d DNA is wrapped around is more densely packed a re wrong wrong re wrong. The following reaction ex- hat DNA is the genetic mark NA from 'S' strain + RNA	roposed by C Crick (B) A-Translation, Vatson (D) A-Translation, standed DNA is 55 %, the (C) 25% correct option gar through a N-glycosidi cleoside through phospho lycosidic linkage d positively charged histor ind stains dark is called eu- (B) D alone is wron; (D) A lone is wron; experiments carrid out by Ar- aterial ? A ase A ase	B - Extension, C-Rosalind Frankline B- Transcription, C-Ervin Chargaff amount of guanine is this DNA willbe (D) 22.5% ic linkage. ester linkage ne octamer to form nucleosome. chromatin. ng g				

# 11<sup>th</sup> Class Modules Chapter Details



#### PHYSICS

#### CHEMISTRY

#### **Module-1**

- 1. Physical World & Measurements
- 2. Basic Maths & Vector
- 3. Kinematics

#### Module-2

- 1. Law of Motion & Friction
- 2. Work, Energy & Power

#### Module-3

- **1.** Motion of system of
- particles & Rigid Body
- 2. Gravitation

#### Module-4

- 1. Mechanical Properties of Matter
- 2. Thermal Properties of Matter

#### Module-5

- 1. Oscillations
- 2. Waves

#### Module-1(PC)

- 1. Some Basic Conceps of Chemistry
- 2. Atomic Structure
- 3. Chemical Equilibrium
- **4.** Ionic Equilibrium

#### Module-2(PC)

- 1. Thermodynamics & Thermochemistry
- 2. Redox Reaction
- **3.** States Of Matter (Gaseous & Liquid)

#### Module-3(IC)

- 1. Periodic Table
- 2. Chemical Bonding
- 3. Hydrogen & Its Compounds
- 4. S-Block

#### Module-4(OC)

- 1. Nomenclature of
- Organic Compounds
- 2. Isomerism
- 3. General Organic Chemistry

#### Module-5(OC)

- 1. Reaction Mechanism
- 2. Hydrocarbon
- **3.** Aromatic Hydrocarbon
- 4. Environmental Chemistry & Analysis Of Organic Compounds

#### BIOLOGY

#### Module-1

- 1. Diversity in the Living World
- 2. Plant Kingdom
- 3. Animal Kingdom

#### Module-2

- 1. Morphology in Flowering Plants
- **2.** Anatomy of Flowering Plants
- **3.** Structural Organization in Animals

#### Module-3

- 1. Cell: The Unit of Life
- 2. Biomolecules
- 3. Cell Cycle & Cell Division
- 4. Transport in Plants
- 5. Mineral Nutrition

#### Module-4

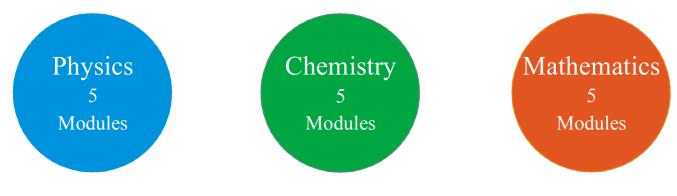
- 1. Photosynthesis in Higher Plants
- 2. Respiration in Plants
- 3. Plant Growth and Development
- 4. Digestion & Absorption
- 5. Breathing & Exchange of Gases

#### Module-5

- Body Fluids & Its Circulation
   Excretory Products & Their Elimination
- **3.** Locomotion & Its Movement
- 4. Neural Control & Coordination
- **5.** Chemical Coordination and Integration

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# 12<sup>th</sup> Class Modules Chapter Details



### PHYSICS

#### **Module-1**

- 1. Electrostatics
- 2. Capacitance

#### Module-2

- 1. Current Electricity
- 2. Magnetic Effect of Current and Magnetism

#### Module-3

- 1. Electromagnetic Induction
- 2. Alternating Current

#### **Module-4**

- 1. Geometrical Optics
- 2. Wave Optics

#### Module-5

- 1. Modern Physics
- 2. Nuclear Physics
- 3. Solids & Semiconductor Devices
- 4. Electromagnetic Waves

## CHEMISTRY

#### Module-1(PC)

- 1. Solid State
- 2. Chemical Kinetics
- **3.** Solutions and Colligative Properties

#### Module-2(PC)

- 1. Electrochemistry
- 2. Surface Chemistry

#### Module-3(IC)

- 1. P-Block Elements
- 2. Transition Elements (d & f block)
- 3. Co-ordination Compound
- 4. Metallurgy

#### Module-4(OC)

- 1. HaloAlkanes & HaloArenes
- Alcohol, Phenol & Ether
   Aldehyde, Ketone &
- Carboxylic Acid

#### Module-5(OC)

- 1. Nitrogen & Its Derivatives
- 2. Biomolecules & Polymers
- 3. Chemistry in Everyday Life

## BIOLOGY

#### Module-1

- 1. Reproduction in Organisms
- 2. Sexual Reproduction in
- Flowering Plants
- 3. Human Reproduction
- 4. Reproductive Health

#### Module-2

- **1.** Principles of Inheritance and Variation
- 2. Molecular Basis of Inheritance
- **3.** Evolution

#### Module-3

- 1. Human Health and Disease
- 2. Strategies for Enhancement in
- Food Production
- 3. Microbes in Human Welfare

#### Module-4

- **1.** Biotechnology: Principles and Processes
- 2. Biotechnology and Its
- Applications
- 3. Organisms and Populations

#### Module-5

- 1. Ecosystem
- 2. Biodiversity and Conservation
- 3. Environmental Issues

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