MOLECULAR BASIS OF INHERITANCE

BIOLOGY

Matrix-Match Type

This section contain(s) 0 question(s). Each question contains Statements given in 2 columns which have to be matched. Statements (A, B, C, D) in **columns I** have to be matched with Statements (p, q, r, s) in **columns II**.

1. Match the codons with their respective amino acids and choose the correct answer.

			Co	olumn-I				Column- II
	(A)	UUU					(1)	Serine
	(B)	GGG					(2)	Methionine
	(C)	UCU					(3)	Phenylalanine
	(D)	CCC					(4)	Glycine
	(E)	AUG					(5)	Proline
	COD	DES :						
		Α	В	С	D	E	Ŷ	
	a)	3	4	1	5	C_2)		
	b)	3	1	4	5	2		
	c)	3	4	5	1	2		
	d)	2	4	1	5	2		
	e)	2	4	1	3	2		
2.	Mate	ch the foll	owing colu	imns				
		A.	Co	olumn-I				Column- II
	(A)	RNA dige	esting enzy	/mes			(1)	Lipase
	(B)	Protein o	ligesting e	nzymes			(2)	DNase
C	(C)	DNA dig	esting enzy	ymes			(3)	Protease
•	(D)	Fat diges	sting enzyr	nes			(4)	RNase
	COD	ES :						
		Α	В	С	D			
	a)	3	4	2	1			

	b)	1	2	4	3		
	c)	4	3	2	1		
	d)	1	2	3	4		
3.	Mat	ch the follo	wing colu	umns			
			Co	olumn-I			Column- II
	(A)	Segment	of DNA co	oding for p	oolypeptide	(1)	Recon
	(B)	Segment	of DNA go	oes for rec	combination	(2)	Muton
	(C)	Segment	of DNA go	oes for mu	itation	(3)	Cistron
	COD	DES :					
		Α	В	С	D		
	a)	1	2	3			
	b)	3	2	1			
	c)	3	1	2			27
4	d) Mot	1 ch the follo	3 wing colu	2			
4.	маю	ch the follo		olumn-I		$\langle \rangle$	Column- II
	(A)	Splicing		Juiiii-i	SC.	(1)	<i>Lac</i> operon
		Okazaki fi	ragment			(2)	Lagging strand
		Jacob and		6		(3)	Lactose
		Inducer		$\langle X \rangle$	>	(4)	Removal of introns
		DES :	C	$\mathbf{\mathbf{\hat{b}}}$			
		Α	В	С	D		
	a)	1	2	3	4		
	b)	4	2	1	3		
	c)	4	2	3	1		
5	d)	2	4	3	1		
5.	Iden	ntify the cor	rect mat	ch betwee	en the codons a	ind coding	g functions.

(A)	AUG	(1)	Phenylalanine
(B)	UAA	(2)	Methionine

						(2)	Turnetenher
		UUU				(3)	Tryptophan
		UGG				(4)	Termination
	COD						
		Α	В	С	D		
	a)	1	4	2	3		
	b)	2	4	1	3		
	c)	4	3	2	1		
	d)	4	1	3	2		
6.		-	wer with			-	r column I with their function listed in column II. of the two columns. Column- II
	(A)	Structural	gene			(1)	Binding site for repressor protein
	(B)	Operator g	gene			(2)	Codes for repressor protein
	(C)	Promoter	gene			(3)	Induces lactose transport from the medium
	(D)	Regulator	gene			(4)	Codes for enzyme proteins
						(5)	Binding site for RNA polymerase
	COD	DES :				CV	
		Α	В	С	D		
	a)	2	5	1	3	Y	
	b)	3	4	5	1		
	c)	4	1	5	2		
	d)	5	4	2	1		
7.	Mate	ch the follow	wing col	umns			
		2	C	olumn-I			Column- II
	(A)	5' AUG 3'				(1)	Segment of DNA
	(B)	RNA with	introns	and exon		(2)	Chromatin
5	(C)	Gene				(3)	<i>hn</i> RNA
	(D)	Nucleoson	nes			(4)	Initiation codon
	COD	DES :					
		Α	В	С	D		
	a)	4	3	1	2		
	-						

	1.)	4	2	1	2		
	b)	4	2	1	3		
	c)	2	1	4	3		
	d)	2	3	1	4		
8.	Mato	ch the follow					
			C	olumn-I			Column- II
	(A)	Terminatio	on (Trar	slation)		(1)	Aminoacyl <i>t</i> RNA synthesis
	(B)	Translatio	n			(2)	Okazaki fragments
	(C)	Transcript	tion			(3)	GTP dependent release factor
	(D)	DNA replic	cation			(4)	RNA polymerase
	COD	ES :					
		Α	В	С	D		10
	a)	3	1	4	2		
	b)	2	3	1	4		
	c)	4	3	1	2	7	ST.
	d)	2	1	3	4		
9.	Mato	ch the follow	wing col	umns and o	choose th	ne correct optio	n.
			C	olumn-I			Column- II
	(A)	<i>t</i> RNA			3	(1)	Linking of amino acids
	(B)	<i>m</i> RNA				(2)	Transferof genetic information
	(C)	<i>r</i> RNA		\sim		(3)	Nucleolarorganising region
	(D)	Peptidyl tr	ransfera	se		(4)	Transfer of amino acid from cytoplasm to
	COD	ES:					ribosome
		A	В	С	D		
	a)	4	2	3	1		
	b)	1	4	3	2		
C	-) c)	1	2	3	4		
	d)	1	3	2	4		
10.		ch the follow			•		
10.	matt	101100		olumn-I			Column- II
	(1)	7-0000				(1)	
	(A)	z-gene				(1)	Transacetylase

	(B)	y-gene					(2)	Permease
	(C)	a-gene					(3)	B-galactosides
	COD	ES:						
		Α	В	С	D			
	a)	1	2	3				
	b)	3	2	1				
	c)	1	3	2				
	d)	3	1	2				
11.	Mato	ch the follow	ving col	umns				
			C	olumn-I				Column- II
	(A)	F. Mieschei	r				(1)	DNA double helix
	(B)	Griffith					(2)	Nuclein
	(C)	Hershey an	nd Chas	e			(3)	Streptococcus pneumoniae
	(D)	Watson and	d Crick				(4)	Bacteriophage
	(E)	Wilkins and	d Franl	din			(5)	X-ray diffraction studies
	COD	ES:			(
		Α	В	C	D	E		
	a)	5	4	3	1	2		
	b)	1	4	3	2	2		
	c)	2	3	4	1	2		
	d)	1	3	4	2	2		
12.	Mato	ch the follow	ving col	umns				
		0	C	olumn-I				Column- II
	(A)	Southern B	Blotting				(1)	Protein
	(B)	Northern E	Blotting				(2)	DNA
5	(C)	Western Bl	lotting				(3)	RNA
	COD	ES:						
		Α	В	С	D			
	a)	3	1	2				
	b)	3	2	1				

	c)	1	2	3				
	d)	1	3	2				
13.	Mate	ch the follow	wing col	umns				
			C	olumn-I				Column- II
	(A)	Topoisom	erase				(1)	Relaxes the DNA from its super-coiled nature
	(B)	DNA gyras	se				(2)	Relieves strain of unwinding by DNA helicase;
	(C)	DNA ligas	e				(3)	this is a specific type of topoisomerase Re-anneals the semiconservative strands and
		-						joins Okazaki fragments of the lagging strand
	(D)	Primase					(4)	Provides a starting point of RNA (or DNA) for DNA polymerase to begin synthesis of the new
	(E)	Telomeras	20				(5)	DNA strand Lengthens telomeric DNA by adding repetitive
		reionieru					(5)	nucleotide sequence to the ends of eukaryotic
	COD	ES:						chromosomes
		Α	В	C	D	E		Ar.
	a)	1	2	5	4	3	7	
	b)	1	2	3	5	3	Ç.,	
	c)	5	4	3	2	3	Y	
	d)	1	2	3	4	3		
14.	Mate	ch the follow	wing col	umns				
			С	olumn-I				Column- II
	(A)	Sigma fact	or	<u>A</u>			(1)	5'-3'
	(B)	Capping	C	Š.			(2)	Initiation
	(C)	Tailing					(3)	5' end
	(D)	Coding str	and				(4)	3' end
	COD	DES :						
	\mathcal{A}	А	В	C	D			
6	a)	2	4	5	1			
	b)	1	2	3	4			
	c)	4	3	1	2			
	d)	5	3	2	1			

15. Match the given enzymes with their respective function in DNA replication

Column-I

- (A) DNA helicase
- (B) DNA polymerase
- (C) DNA clam
- (D) Single-Strand Binding (SSB) Proteins

CODES:

	Α	В	С	D
a)	1	2	4	3
b)	3	4	1	2
c)	4	3	2	1
d)	1	2	3	4

Column- II

- (1) A protein which prevents DNA polymerase-III form dissociating from the DNA parent strand
- (2) Bind to ssDNA and prevent the DNA double helix from re-annealing after DNA helicase unwinds it thus maintaining the strand separation
- (3) Also known as helix destabilizing enzyme. Unwinds the DNA double helix at the replication fork
- (4) Builds a new duplex DNA strands by adding nucleotides in the 5' to 3' direction. Also performs proofreading and error correction

16. Some of the inhibitors of bacterial protein synthesis and their effect are listed in Column I and Column II below. Match them and choose the correct option from answer key.

Column-I

- (A) Chloramphenicol
- (B) Erythromycin
- (C) Neomycin
- **(D)** Streptomycin
- (E) Tetracycline

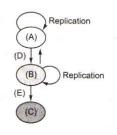
CODES :

	1	A	В	С	D	Ε
	a)	1	2	3	5	4
C	b)	3	1	5	4	4
	c)	2	3	4	1	4
	d)	4	5	4	3	4
	e)	5	4	1	2	4

Column- II

- (1) Inhibits binding of aminoacyl *t*RNA to ribosome
- (2) Inhibits interaction between *t*RNA and *m*RNA
- (3) Inhibits initation of translation
- (4) Inhibits peptidyltransferase activity
- (5) Inhibits translocation of *m*RNA along ribosomes

17. The diaram represents the 'central dogma' of molecular biology. Choose the correct combination of labeling.



Column-I

Column- II

CODES :

	Α	В	С	D	Ε
a)	protein	rna	dna	transla tio	transcri pt
b)	rna	dna	protei n	transcr ipt	transcri pt
c)	transcri pt	transla tio	transla tio	dna	transcri pt
d)	dna	rna	protei n	transla tio	transcri pt
e)	dna	rna	protei n	transcr ipt	transcri pt

18. Match the following columns

Column-I

- **(A)** AUG
- **(B)** UAA
- (C) Operon model
- (D) Jumping gene

CODES :

		Α	В	C	D
	a)	1	2	3	4
	b)	4	1	3	2
C	c)	4	3	1	2
	d)	2	3	1	4

19. Match the following columns

Column-I

(A) Exon

Column- II

- (1) Jacob and Monod
- (2) Transposons
- (3) Chain terminating codon
- (4) Methionine

Column- II

(1) Coding sequence

(B) Intron (2) Non-coding sequence (C) Genetic code (3) Triplet bases on *m*RNA **(D)** DNA packaging (4) Nucleosome **CODES**: A В С D a) 1 3 2 4 2 b) 1 4 3 1 2 3 c) 4 d) 4 1 2 3 20. Match the enzyme in column I with its function in column II and choose the correct option. Column- II Column-I (1) Joining of DNA fragments (A) β-galactosidase Peptide bond formation (B) Permease (2) (3) Hydrolysis of lactose (C) Ligase (D) Ribozyme (4) Increases permeability to β -galactosidase

CODES:

a)

b)

c)

d)

A

2

3

2

1

B

1

2

4

2

С

4

D

3

4

3

3

MOLECULAR BASIS OF INHERITANCE

BIOLOGY

						: ANS	SWER	KEY	:				
1) 5) 9) 13) 17)	a c a d d	2) 6) 10) 14) 18)	c c b a c	3) 7) 11) 15) 19)	c a c d c	4) 8) 12) 16) 20)	b a b d b					<u> </u>	5
										G	2		
								A					
				4		R	, c						
			Ć										
5		8	Y										

MOLECULAR BASIS OF INHERITANCE

BIOLOGY

		: HIN	TS AND	SO]	LUTIONS :				
1	(a)								
	UUU– Phenylala	JUU— Phenylalanine GGG—Glycine		7	(a)5' AUG 3'Initiation codonRNA with intron and exonhnRNA				
	GGG-Glycine								
	UCU-Serine				Gene Nucleosome	Chromatin Segment of DNA	A		
	CCC-Proline			8 (a) Termination – GTP release factor					
	AUG-Methionin	e			ease factor				
2	(c)				Translation – Amino a	cyl <i>t</i> RNA synthesis			
-	A. RNA digesting enzymes – RNase B. Protein digesting enzymes – Protease C. DNA digesting enzymes – DNase				Transcription – RNA polymerase DNA replication – Okazaki fragments (a)				
				9					
	D. Fat digesting enzymes – Lipase				Column I	Column II			
с С	0 0	enzymes – Lipase			<i>t</i> RNA	Transfer of			
3	(c)		D			amino acid from			
		uton term given by the	e Benzer to	S.	X Y	cytoplasm to			
	describe the gene					ribosome			
		of DNA codes for poly		\mathbf{S}	<i>m</i> RNA	Transfer of			
	-	of DNA goes for recomb		Y		genetic			
	Muton Segment of	of DNA goes for mutati	on			information			
4	(b)				<i>r</i> RNA	Nucleolar			
	Splicing – Removal of introns					organising			
	Okazaki fragment – Lagging strand					region			
	Jacob and Monod – <i>Lac</i> operon				Peptidyltransferase	Linking of amino acids			
	Inducer – Lactose					ammo actus			
5	(c)								
0	AUG–Methionine								
	nou metholim	Add-Metholinie			(b)				
	UAA-Terminatio	AA-Termination			Structural (Lac operor	n) genes Secretion			
	UUU–Phenylalanine			Z-genes	- β-galactosic	laco			
				0	- Permease	lase			
					Y-gene		000		
	UGG–Tryptophan				A-gene	- Transacety	lase		
6	(c)				Lac operon consists of the following parts				
0	Column I Column II			(i) Structural Genes They transcribes the <i>m</i> RNA for polypeptide synthesis. An operon has one or					
						-			
	Structural	Codes for enzyme			more structural genes	=	has		
	gene Operator gone	proteins Binding site for			three structural genes				
	Operator gene	repressor protein			Z-gene Encodes β -gala	ctosidase (for hydrol	yzing		
	Promoter	Binding site for			lactose or galactose)				
	gene	RNA polymerase			Y-gene Encodes perme	ease (for allowing the	entry		
	Regulator	Codes for repressor			of lactose)				
	gene	protein			A-gene Encodes transa	acetylase (for metabo	lizing		
		-			the toxic thiogalactosi	- ,	_		

	entry by lactose	2)				pol	ymerase III	
	(ii) Operator Ge	e ne It is gene which di	rectly			fro	m dissociating	
	•••	thesis of <i>m</i> RNA over	-			fro	m the DNA	
	genes. It is switched off by the presence of a repressor					-	ent strand	
					Single-strand		d to ssDNA	
					Binding	-	event the DNA	
	(iii) Promoter Gene It functions as the recognition		(SSB)			uble helix from		
		polymerase, provided			proteins		annealing after	
	operator gene is switched on. RNA polymerase					A helicase		
	binds at this site						winds it thus	× •
	(iv) Regulatory	Gene (lac i-gene) in la	<i>ac</i> operon, it				intaining the	XV
	is called <i>i</i> -gene as it produces inhibitor or						and separation axes the DNA	
	repressor. The repressor binds to the operator				Tanaisamana			
	gene and stops the working of operon				Topoisomera		m its super- led nature	Y
	(v) Inducer It is the substrate that prevents the				se		ieves strain of	
	repressor from binding to the operator, so that						winding by	
							A helicase; this	
11	transcription ca	in de started			DNA gyrase is a top Re		specific type of	
11	(c)	• .					oisomerase	
	F Miescher – Nu						anneals the	
	Griffith – <i>Strept</i>	ococcus pneumonia					emiconservative	
	Hershey and Chase – Bacteriophage					sta	nds and joins	
	Watson and Crie	ck – DNA double helix	C		DNA ligase	Oka	azaki fragments	
	Wilkins and Fra	nklin – X-ray diffracti	on studies		of		he lagging	
12	(b)						and	
	Technique	Used for			XY		ovides a	
	Southern blottin	ng – DNA					rting point of	
	Northern blotti	-		\mathbf{x}	Drimago		A (or DNA) for	
	Western blottin	-	C		Primase		a polymerase Degin synthesis	
13	(d)						the new DNA	
15	A-1, B-2, C-3, D-	1 6 5					and	
14		4, Ľ-5	$\langle \rangle$				ngthens	
14	(a)						omeric DNA by	
	0	nitiation of transcript	lon			ado	ling repetitive	
	Capping – 3' end				Telomerase nucleo		cleotide	
	Tailing – 5' end of RNA					seq	sequences to the	
	-	5'-3' strand of DNA					ls of eukaryotic	
15	(d)						omosomes	
	Enzyme	Enzyme Function in DNA		16	(d)			
		Replication			Column I		Column II	
	DNA helicase	Also known as			Chlorampheni	col	Inhibits	
		helix destabilising					peptidyltransfera	a
		enzyme. Unwinds					se activity	
	N K Y	the DNA double			Erythromycin		Inhibits	
	helix at the replication forkDNABuilds a new					translocation of		
					mRNA along			
							ribosomes	
	polymerase duplex DNA strand by adding nucleotides in the 5' to 3' direction. Also performs proofreading and error correction			Neomycin		Inhibits		
						peptidyltransfera	a	
				Streptomycin Tetracycline		se activity		
						Inhibits initation of translation		
						Inhibits binding		
				i cu acyclille		of		
	DNA clamp	A protein, which					aminoacyl <i>t</i> RNA	
	prevents DNA					to ribosome		
				•	•			

17 **(d)**

Central dogma is the flow of information from DNA to *m*RNA and then to protein. It was originally formulated by **Crick**.

Central dogma of modern biology is shown as:

 $DAN \xrightarrow{Transcription} RNA \xrightarrow{Translation} Proteins$

18 **(c)**

A Transposable Element (TE) is a DNA sequence that can change its position within the genome, sometimes creating or reversing the mutations and altering the cell's genome size. Transposition often results in the duplication of the TE Barbara McClintock's discovery of these jumping genes earned her a Nobel Prize in 1983.

Transposable Elements (TEs) represents one of the several types of mobile genetic elements. TEs are assigned to one or two classes according to their mechanism of transposition, which can be described as either copy and paste (class I TEs) or cut and paste (class II TEs)

19 **(c)**

Exon coding (functional) part of DNA or RNA **Intron** non-coding (non-function) part of DNA or RNA

Genetic codes Triplet bases or *m*RNA DNA packaging Nucleosomal model

20 **(b)**

 β -galactosidase (β -gal), coded by z-structural genes, is primarily responsible for the hydrolysis of the disaccharide, lactose into its monomeric units, galactose and glucose.