

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.

	Column-I	Column-II
(A)	UUU	(1) Serine
(B)	GGG	(2) Methionine
(C)	UCU	(3) Phenylalanine
(D)	CCC	(4) Glycine
(E)	AUG	(5) Proline

CODES :

	A	B	C	D	E
a)	3	4	1	5	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. Match the following columns

	Column-I	Column-II
(A)	RNA digesting enzymes	(1) Lipase
(B)	Protein digesting enzymes	(2) DNase
(C)	DNA digesting enzymes	(3) Protease
(D)	Fat digesting enzymes	(4) RNase

CODES :

	A	B	C	D
a)	3	4	2	1

- b) 1 2 4 3
 c) 4 3 2 1
 d) 1 2 3 4

3. Match the following columns

Column-I

Column- II

- | | |
|---|-------------|
| (A) Segment of DNA coding for polypeptide | (1) Recon |
| (B) Segment of DNA goes for recombination | (2) Muton |
| (C) Segment of DNA goes for mutation | (3) Cistron |

CODES :

- | | A | B | C | D |
|----|----------|----------|----------|----------|
| a) | 1 | 2 | 3 | |
| b) | 3 | 2 | 1 | |
| c) | 3 | 1 | 2 | |
| d) | 1 | 3 | 2 | |

4. Match the following columns

Column-I

Column- II

- | | |
|----------------------|------------------------|
| (A) Splicing | (1) <i>Lac</i> operon |
| (B) Okazaki fragment | (2) Lagging strand |
| (C) Jacob and Monod | (3) Lactose |
| (D) Inducer | (4) Removal of introns |

CODES :

- | | A | B | C | D |
|----|----------|----------|----------|----------|
| a) | 1 | 2 | 3 | 4 |
| b) | 4 | 2 | 1 | 3 |
| c) | 4 | 2 | 3 | 1 |
| d) | 2 | 4 | 3 | 1 |

5. Identify the correct match between the codons and coding functions.

Column-I

Column- II

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

(C) UUU

(3) Tryptophan

(D) UGG

(4) Termination

CODES :

	A	B	C	D
a)	1	4	2	3
b)	2	4	1	3
c)	4	3	2	1
d)	4	1	3	2

6. Match the components of 'LacOperon' of *E.coli* given under column I with their function listed in column II. Choose the answer with correct combination of alphabets of the two columns.

Column-I

Column- II

(A) Structural gene

(1) Binding site for repressor protein

(B) Operator 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

CODES :

	A	B	C	D
a)	2	5	1	3
b)	3	4	5	1
c)	4	1	5	2
d)	5	4	2	1

7. Match the following columns

Column-I

Column- II

(A) 5' AUG 3'

(1) Segment of DNA

(B) RNA with introns and exon

(2) Chromatin

(C) Gene

(3) *hn*RNA

(D) Nucleosomes

(4) Initiation codon

CODES :

	A	B	C	D
a)	4	3	1	2

- b) 4 2 1 3
 c) 2 1 4 3
 d) 2 3 1 4

8. Match the following columns

Column-I	Column- II
(A) Termination (Translation)	(1) Aminoacyl <i>t</i> RNA synthesis
(B) Translation	(2) Okazaki fragments
(C) Transcription	(3) GTP dependent release factor
(D) DNA replication	(4) RNA polymerase

CODES :

	A	B	C	D
a)	3	1	4	2
b)	2	3	1	4
c)	4	3	1	2
d)	2	1	3	4

9. Match the following columns and choose the correct option.

Column-I	Column- II
(A) <i>t</i> RNA	(1) Linking of amino acids
(B) <i>m</i> RNA	(2) Transfer of genetic information
(C) <i>r</i> RNA	(3) Nucleolar organising region
(D) Peptidyl transferase	(4) Transfer of amino acid from cytoplasm to ribosome

CODES :

	A	B	C	D
a)	4	2	3	1
b)	1	4	3	2
c)	1	2	3	4
d)	1	3	2	4

10. Match the following columns

Column-I	Column- II
(A) <i>z</i> -gene	(1) Transacetylase

(B) y-gene

(2) Permease

(C) a-gene

(3) B-galactosides

CODES :

	A	B	C	D
a)	1	2	3	
b)	3	2	1	
c)	1	3	2	
d)	3	1	2	

11. Match the following columns

Column-I

Column- II

(A) F. Miescher

(1) DNA double helix

(B) Griffith

(2) Nuclein

(C) Hershey and Chase

(3) *Streptococcus pneumoniae*

(D) Watson and Crick

(4) Bacteriophage

(E) Wilkins and Franklin

(5) X-ray diffraction studies

CODES :

	A	B	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. Match the following columns

Column-I

Column- II

(A) Southern Blotting

(1) Protein

(B) Northern Blotting

(2) DNA

(C) Western Blotting

(3) RNA

CODES :

	A	B	C	D
a)	3	1	2	
b)	3	2	1	

- c) 1 2 3
 d) 1 3 2

13. Match the following columns

Column-I	Column- II
(A) Topoisomerase	(1) Relaxes the DNA from its super-coiled nature
(B) DNA gyrase	(2) Relieves strain of unwinding by DNA helicase; this is a specific type of topoisomerase
(C) DNA ligase	(3) 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 DNA strand
(E) Telomerase	(5) Lengthens telomeric DNA by adding repetitive nucleotide sequence to the ends of eukaryotic chromosomes

CODES :

	A	B	C	D	E
a)	1	2	5	4	3
b)	1	2	3	5	3
c)	5	4	3	2	3
d)	1	2	3	4	3

14. Match the following columns

Column-I	Column- II
(A) Sigma factor	(1) 5'-3'
(B) Capping	(2) Initiation
(C) Tailing	(3) 5' end
(D) Coding strand	(4) 3' end

CODES :

	A	B	C	D
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

Column- II

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

CODES :

	A	B	C	D
a)	1	2	4	3
b)	3	4	1	2
c)	4	3	2	1
d)	1	2	3	4

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

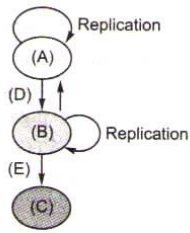
Column- II

- | | |
|---------------------|--|
| (A) Chloramphenicol | (1) Inhibits binding of aminoacyl <i>tRNA</i> to ribosome |
| (B) Erythromycin | (2) Inhibits interaction between <i>tRNA</i> and <i>mRNA</i> |
| (C) Neomycin | (3) Inhibits initiation of translation |
| (D) Streptomycin | (4) Inhibits peptidyltransferase activity |
| (E) Tetracycline | (5) Inhibits translocation of <i>mRNA</i> along ribosomes |

CODES :

	A	B	C	D	E
a)	1	2	3	5	4
b)	3	1	5	4	4
c)	2	3	4	1	4
d)	4	5	4	3	4
e)	5	4	1	2	4

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



Column-I

Column- II

CODES :

	A	B	C	D	E
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

Column- II

(A) AUG	(1) Jacob and Monod
(B) UAA	(2) Transposons
(C) Operon model	(3) Chain terminating codon
(D) Jumping gene	(4) Methionine

CODES :

	A	B	C	D
a)	1	2	3	4
b)	4	1	3	2
c)	4	3	1	2
d)	2	3	1	4

19. Match the following columns

Column-I

Column- II

(A) Exon	(1) Coding sequence
-----------------	----------------------------

- (B) Intron
- (C) Genetic code
- (D) DNA packaging

- (2) Non-coding sequence
- (3) Triplet bases on *mRNA*
- (4) Nucleosome

CODES :

	A	B	C	D
a)	1	3	2	4
b)	1	4	2	3
c)	1	2	3	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-I

Column- II

- (A) β -galactosidase
- (B) Permease
- (C) Ligase
- (D) Ribozyme

- (1) Joining of DNA fragments
- (2) Peptide bond formation
- (3) Hydrolysis of lactose
- (4) Increases permeability to β -galactosidase

CODES :

	A	B	C	D
a)	2	1	4	3
b)	3	2	1	4
c)	2	4	1	3
d)	1	2	4	3

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BIOLOGY

: ANSWER KEY :

1)	a	2)	c	3)	c	4)	b
5)	c	6)	c	7)	a	8)	a
9)	a	10)	b	11)	c	12)	b
13)	d	14)	a	15)	d	16)	d
17)	d	18)	c	19)	c	20)	b

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entry by lactose)

(ii) **Operator Gene** It is gene which directly controls the synthesis of mRNA over structural genes. It is switched off by the presence of a repressor

(iii) **Promoter Gene** It functions as the recognition centre for RNA-polymerase, provided the operator gene is switched on. RNA polymerase binds at this site

(iv) **Regulatory Gene** (*lac i*-gene) in *lac* operon, it is called *i*-gene as it produces inhibitor or repressor. The repressor binds to the operator gene and stops the working of operon

(v) **Inducer** It is the substrate that prevents the repressor from binding to the operator, so that transcription can be started

11 (c)

F Miescher – Nuclein

Griffith – *Streptococcus pneumonia*

Hershey and Chase – Bacteriophage

Watson and Crick – DNA double helix

Wilkins and Franklin – X-ray diffraction studies

12 (b)

Technique **Used for**

Southern blotting – DNA

Northern blotting – RNA

Western blotting – Protein

13 (d)

A-1, B-2, C-3, D-4, E-5

14 (a)

Sigma factor – Initiation of transcription

Capping – 3' end of RNA

Tailing – 5' end of RNA

Coding strand – 5'-3' strand of DNA

15 (d)

Enzyme	Function in DNA Replication
DNA helicase	Also known as helix destabilising enzyme. Unwinds the DNA double helix at the replication fork
DNA polymerase	Builds a new duplex DNA strand by adding nucleotides in the 5' to 3' direction. Also performs proofreading and error correction
DNA clamp	A protein, which prevents DNA

Single-strand Binding (SSB) proteins	polymerase III from dissociating from the DNA parent strand Bind to ssDNA prevent the DNA double helix from re-annealing after DNA helicase unwinds it thus maintaining the strand separation Relaxes the DNA from its super-coiled nature
Topoisomerase	Relieves strain of unwinding by DNA helicase; this is a specific type of topoisomerase Re-anneals the semiconservative stands and joins Okazaki fragments of the lagging strand
DNA gyrase	Provides a starting point of RNA (or DNA) for DNA polymerase to begin synthesis of the new DNA strand
DNA ligase	Lengthens telomeric DNA by adding repetitive nucleotide sequences to the ends of eukaryotic chromosomes
Primase	
Telomerase	

16 (d)

Column I	Column II
Chloramphenicol	Inhibits peptidyltransferase activity
Erythromycin	Inhibits translocation of mRNA along ribosomes
Neomycin	Inhibits peptidyltransferase activity
Streptomycin	Inhibits initiation of translation
Tetracycline	Inhibits binding of aminoacyl-tRNA to ribosome

17 **(d)**
Central dogma is the flow of information from DNA to *mRNA* and then to protein. It was originally formulated by **Crick**.

Central dogma of modern biology is shown as:



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 *mRNA*

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.