

CLASS : XIth
DATE :

SUBJECT : BIOLOGY
DPP No. : 4

Topic :-MOLECULAR BASIS OF INHERITANCE

1. Match the following
- | | | | |
|--------------------|------------------------------------|-------------|-----------------------|
| (A) tRNA | 1. Linking of amino acids | | |
| (B) mRNA | 2. Transfer of genetic information | | |
| (C) rRNA | 3. Nucleolar organising region | | |
| (D) Peptidyl Codes | 4. Transfer of amino acid from | transferase | cytoplasm of ribosome |
- | | A | B | C | D |
|-----|---|---|---|---|
| (A) | 4 | 2 | 3 | 1 |
| (B) | 1 | 4 | 3 | 2 |
| (C) | 1 | 2 | 3 | 4 |
| (D) | 1 | 3 | 2 | 4 |
2. If percentage of cytosine is 18%, then percentage of adenine will be
(A) 32% (B) 64% (C) 36% (D) 23%
3. DNA nucleotides are attached by
(A) Hydrogen bond (B) Covalent bond (C) Van der waals bond (D) Electrovalent Bond
4. During Meselson and Stahl's experiments, heavy DNA was distinguished from normal DNA by centrifugation in
(A) CsOH gradient (B) $^{14}\text{NH}_4\text{Cl}$ (C) $^{15}\text{NH}_4\text{Cl}$ (D) $^{35}\text{SO}_2$
(E) CsCl gradient
5. Consider the following statements
(A) r-RNA provides the template for synthesis of proteins
(B) t-RNA brings amino acids and reads the genetic code
(C) RNA polymerase binds to promoter and initiates transcription
(D) A segment of DNA coding for polypeptide is called intron
(A) (A) and (C) are correct (B) (A) and (B) are correct
(C) (A), (B) and (C) are correct (D) (B) and (C) are correct
(E) (A),(B) and (D) are correct
6. Locations or sites in the human DNA where single base DNA differences occurs are called
(A) Repetitive DNA (B) VNTR (C) SNP (D) SSCP
(E) Expressed sequence tags
7. Strand X in the figure shows a small part of a nucleic acid molecule
- Which pair of the following strands are complementary to strand X
- (A) 1 and 3 (B) 2 and 4 (C) 1 and 2 (D) 3 and 4

8. If the total amount of adenine and thymine in a double-stranded DNA is 45%, the amount of guanine in this DNA will be
 (A) 22.5% (B) 27.5% (C) 45% (D) 55%
9. The 3' – 5' phosphodiester linkages inside a polynucleotide chain serve to join
 (A) One DNA strand with the other DNA strand
 (B) One nucleoside with another nucleoside
 (C) One nucleotide with another nucleoside
 (D) One nitrogenous base with pentose sugar
10. Match the following
- | | | | |
|-------------------------|---|---|---|
| Column - I | | Column - II | |
| A. tRNA | | 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 |
| (A) 4 | 2 | 3 | 1 |
| (B) 1 | 4 | 3 | 2 |
| (C) 1 | 2 | 3 | 4 |
| (D) 1 | 3 | 2 | 4 |
11. 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 | |
| (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 | | | |
12. Match the following.
- | | | | |
|--------------------------------|--|--------------------------------|--|
| Column - I | | Column - 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 | |
13. Match the following in column - I with column - II and choose the correct combination
- | | | | |
|--------------------------------|--|---------------------------------|--|
| Column - I | | Column - II | |
| 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 | | (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 - 4; C - 1; D - 3 | | | |

14. Match the enzyme in column I with its function in column II and select the correct option
- | | |
|--------------------------------|--|
| Column - I | Column - II |
| A. β -galactosidase | 1. Joining of DNA fragments |
| B. Permease | 2. Peptide bond formation |
| C. Ligase | 3. Hydrolysis of lactose |
| D. Ribozyme | 4. Increase permeability to β -galactosidase |
| (A) A - 2; B - 1; C - 4; D - 3 | (B) A - 3; B - 4; C - 1; D - 2 |
| (C) A - 2; B - 4; C - 1; D - 3 | (D) A - 1; B - 2; C - 4; D - 3 |
| (E) A - 3; B - 1; C - 4; D - 2 | |
15. Match Column - I with Column - II and select the correct option from the codes given below.
- | | |
|---|---|
| Column - I | Column - II |
| A. F. Meischer | i. DNA double helix |
| B. Griffith | ii. Nuclein |
| C. Hershey and chase | iii. S. pneumoniase |
| D. Watson and Crick | iv. Bacteriophages |
| E. Wilkins and Franklin | v. X-ray diffraction studies |
| (A) A - ii; B - iii; C - iv; D - i; E - v | (B) A - v; B - iv; C - iii; D - i; E - ii |
| (C) A - i; B - iii; C - iv; D - ii; E - v | (D) A - i; B - iv; C - iii; D - ii; E - v |
16. Match Column - I with Column - II and select the correct option from the codes given below.
- | | |
|------------------------------------|-----------------------------------|
| Column - I | Column - II |
| A. Sigma factor | i. 5' - 3' |
| B. Capping | ii. Intiation |
| C. Tailing | iii. Termination |
| D. Coding strand | iv. 5' end |
| E. Colour blindness | v. 3' end |
| (A) A - iii; B - v; C - iv; D - ii | (B) A - ii; B - iv; C - v; D - i |
| (C) A - ii; B - v; C - iv; D - iii | (D) A - iii; B - v; C - iv; D - i |
17. Match Column - I with Column - II and select the correct option from the codes given below.
- | | |
|---|---|
| Column - I | Column - II |
| (Codons) | (Translated amino acid) |
| A. UUU | (i) Serine |
| B. GGG | (ii) Methionine |
| C. UCU | (iii) Phenylalanine |
| D. CCC | (iv) Glycine |
| E. AUG | (v) Proline |
| (A) A - (iii), B - (iv), C - (i), D - (v), E - (ii) | (B) A - (ii), B - (i), C - (iv), D - (v), E - (ii) |
| (C) A - (iii), B - (iv), C - (v), D - (i), E - (ii) | (D) A - (ii), B - (iv), C - (i), D - (v), E - (iii) |
18. Match Column - I with Column - II and select the correct option from the codes given below.
- | | |
|----------------------------------|----------------------------------|
| Column - I | Column - II |
| A. Translation | (i) Aminoacyl tRNA synthetase |
| B. Transcription | (ii) Okazaki fragments |
| C. DNA replication | (iii) RNA polymerase |
| (A) A - (ii), B - (i), C - (iii) | (B) A - (i), B - (iii), C - (ii) |
| (C) A - (iii), B - (i), C - (ii) | (D) A - (ii), B - (iii), C - (i) |

19. Match Column - I with Column - II and select the correct option from the codes given below.
- | Column - I | Column - II |
|------------------------|--|
| A. Griffith | (i) Lac operon |
| B. Hershey and Chase | (ii) Semi-conservative DNA replication |
| C. Messelson and Stahl | (iii) Transduction |
| D. Jacob and Monod | (iv) Transformation |
- (A) A - (iv), B - (iii), C - (ii), D - (i)
(B) A - (iii), B - (iv), C - (ii), D - (i)
(C) A - (iv), B - (ii), C - (iii), D - (i)
(D) A - (ii), B - (i), C - (iii), D - (iv)
20. Match Column - I with Column - II and select the correct option from the codes given below.
- | Column - I | Column - II |
|--------------------|--|
| A. Operator site | (i) Binding site for RNA polymerase |
| B. Promoter site | (ii) Binding site for repressor molecule |
| C. Regulator gene | (iii) Codes for protein/ enzyme |
| D. Structural gene | (iv) Codes for repressor molecule |
- (A) A - (ii), B - (i), C - (iii), D - (iv)
(B) A - (ii), B - (i), C - (iv), D - (iii)
(C) A - (iv), B - (iii), C - (i), D - (ii)
(D) A - (ii), B - (iii), C - (i), D - (iv)

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