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Molecular Basis of Inheritance — CBSE Class 12 Biology Chapter Test

FREE CHAPTER TEST · CLASS XII · BIOLOGY (044) · PATTERN OF THE CBSE SAMPLE QUESTION PAPER 2026-27

TIME ALLOWED	MAXIMUM MARKS	QUESTIONS	NAME / ROLL NO.
1½ hours	37	17 (A 8 · B 3 · C 3 · D 1 · E 2)	

GENERAL INSTRUCTIONS

Read the following instructions very carefully and strictly follow them:

1. This question paper contains 17 questions. All questions are compulsory.
2. This question paper is divided into five sections: A, B, C, D and E.
3. Section A (Q1–8) contains 6 multiple choice questions and 2 assertion-reason based questions of 1 mark each.
4. Section B (Q9–11) contains short answer questions of 2 marks each.
5. Section C (Q12–14) contains short answer questions of 3 marks each.
6. Section D (Q15) contains case-based questions of 4 marks each, with sub-parts of 1, 2 and 1 marks.
7. Section E (Q16–17) contains long answer questions of 5 marks each.
8. There is no overall choice. However, an internal choice has been provided in 2 questions in Section B, 1 question in Section D, 2 questions in Section E. Attempt only one of the alternatives in such questions.
9. Draw neat, labelled diagrams wherever necessary.
10. This chapter test follows the section structure, question types and marks per question of the CBSE Class XII Biology (044) Sample Question Paper 2026-27, at about half the length of the 70-mark board paper: 37 marks in 1½ hours.
11. The answer key and the marking scheme are at the end of this booklet. Attempt the paper in 1½ hours before you look at them.

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Chapter: Molecular Basis of Inheritance · **Topics:** Structure and packaging of DNA · The search for the genetic material · Replication · Transcription · Genetic code and translation · Regulation (lac operon), HGP and DNA fingerprinting

SECTION A

This section comprises 8 questions of 1 mark each: 6 multiple choice questions (MCQs) and 2 assertion-reason based questions.

1. A double-stranded DNA molecule contains 20 % adenine. Its cytosine content is 1

(A) 20 %
(B) 30 %
(C) 40 %
(D) 60 %

2. In eukaryotes, RNA polymerase III transcribes 1

(A) tRNA, 5S rRNA and snRNAs
(B) mRNA (hnRNA)
(C) the 28S, 18S and 5.8S rRNAs
(D) only the genes of mitochondria

3. The distance between two consecutive base pairs in the DNA double helix is 1

(A) 3.4 nm
(B) 0.034 nm
(C) 34 nm
(D) 0.34 nm

4. The template strand of a short stretch of DNA reads 3′-TACGGA-5′. The mRNA transcribed from it is 1

(A) 5′-UACGGA-3′
(B) 5′-ATGCCT-3′
(C) 5′-AUGCCU-3′
(D) 3′-AUGCCU-5′

5. Which of the following nitrogenous bases is a purine? 1

(A) Adenine
(B) Cytosine
(C) Thymine
(D) Uracil

6. In eukaryotes, the removal of introns and the joining of exons in a defined order is called 1

(A) capping
(B) tailing
(C) translation
(D) splicing

7. **Assertion (A):** RNA is chemically more reactive than DNA. 1
Reason (R): RNA is double-stranded in all organisms.

(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

8. **Assertion (A):** In bacteria, translation can begin before the transcription of an mRNA is complete. 1
Reason (R): The DNA of E. coli has about 4.6×10^6 base pairs.

(A) Both A and R are true and R is the correct explanation of A.
(B) Both A and R are true but R is not the correct explanation of A.
(C) A is true but R is false.
(D) A is false but R is true.

SECTION B

This section comprises 3 short answer questions of 2 marks each.

9. (a) Describe the structure of a nucleosome. 2

OR

(b) Distinguish between euchromatin and heterochromatin.

10. (a) What did the Hershey-Chase experiment prove? Briefly state how. 2

OR

(b) Describe Griffith's experiment with Streptococcus pneumoniae and state his conclusion.

11. Write the sequence of amino acids coded by the mRNA 5′-AUG UUU GGC UAA-3′. Why does the chain stop there? 2

SECTION C

This section comprises 3 short answer questions of 3 marks each.

12. Describe the Meselson and Stahl experiment, and state what it proved. What would be found after one and after two generations in ^{14}N medium? 3

13. Describe a transcription unit in bacteria, and the roles of the sigma and rho factors. 3

14. State six salient features of the genetic code. 3

SECTION D

This section comprises 1 case-based question of 4 marks, with sub-parts of 1, 2 and 1 marks.

15. A crime has been committed and blood is found at the scene. The police collect blood samples from three suspects. A forensic laboratory compares the DNA from the crime scene with the DNA of the suspects using DNA fingerprinting, and finds that the band pattern of one suspect exactly matches that of the sample from the scene.

(I) What is the basis of DNA fingerprinting? [1]

(II) List the main steps involved in DNA fingerprinting. [2]

(III) Who developed the technique of DNA fingerprinting? [1]

OR

(III) Which kind of DNA sequence is used as the probe in DNA fingerprinting? [1]

SECTION E

This section comprises 2 long answer questions of 5 marks each.

16. (a) Describe the lac operon of E. coli, and explain how it is switched on in the presence of lactose and off in its absence. 5

OR

(b) State two goals of the Human Genome Project, and any three salient features of the human genome revealed by it.

17. (a) Describe the process of translation in prokaryotes. 5

OR

(b) Describe the replication of DNA, explaining the continuous and discontinuous synthesis on the two strands.

END OF THE QUESTION PAPER

ANSWER KEY — SECTION A

Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8
(B)	(A)	(D)	(C)	(A)	(D)	(C)	(B)

MARKING SCHEME AND WORKED SOLUTIONS

Marks for each step are shown in brackets, as in the CBSE marking scheme. Any correct alternative method earns full marks.

Q1. Answer (B). A = T = 20 %, so G + C = 60 % and C = 30 %.

Q2. Answer (A). RNA polymerase I transcribes the 28S, 18S and 5.8S rRNAs, II the precursor of mRNA (hnRNA), and III tRNA, 5S rRNA and snRNAs.

Q3. Answer (D). 0.34 nm (3.4 nm per complete turn of about 10 base pairs).

Q4. Answer (C). Complementary to the template, with U for T, written 5′→3′: AUGCCU.

Q5. Answer (A). Adenine and guanine are purines; cytosine, thymine and uracil are pyrimidines.

Q6. Answer (D). In splicing the introns of the hnRNA are removed and the exons joined; capping adds methyl guanosine triphosphate at the 5′ end and tailing adds adenylate residues at the 3′ end.

Q7. Answer (C). The 2′-OH group in every nucleotide of RNA makes it reactive and easily degraded, so A is true. Most RNA is single-stranded, so R is false. Answer C.

Q8. Answer (B). Both are true. Translation can start early because bacterial mRNA needs no processing and both processes take place in the cytoplasm; the size of the genome does not explain it. Answer B.

Q9. (2 marks) Answer: (a) histone octamer + ~200 bp DNA; (b) loose/active vs dense/inactive.
(a) Positively charged histone proteins (rich in lysine and arginine) form a unit of eight molecules, the histone octamer. [1] The negatively charged DNA is wrapped around the octamer; a nucleosome contains about 200 bp of DNA; nucleosomes along the chromatin look like 'beads on a string' under the electron microscope. [1]
OR (b) Euchromatin is loosely packed, stains light and is transcriptionally active. [1] Heterochromatin is densely packed, stains dark and is inactive. [1]

Q10. (2 marks) Answer: (a) DNA is the genetic material; (b) transforming principle.
(a) DNA, not protein, is the genetic material. [1] Phages grown with radioactive phosphorus (DNA labelled) and with radioactive sulphur (protein labelled) were allowed to infect bacteria; after blending and centrifuging, the bacteria infected by phages with labelled DNA were radioactive, while those infected by phages with labelled protein were not: only DNA entered the bacteria. [1]
OR (b) S strain (virulent) injected into mice killed them; R strain did not; heat-killed S strain did not; but heat-killed S + live R killed the mice, and live S bacteria were recovered. [1] Some 'transforming principle' from the dead S strain had transformed R into S (later shown to be DNA by Avery, MacLeod and McCarty). [1]

Q11. (2 marks) Answer: Met–Phe–Gly; UAA is a stop codon.
Met – Phe – Gly. [1]
UAA is a stop (nonsense) codon; it codes for no amino acid, so a release factor ends translation. [1]

Q12. (3 marks) Answer: all hybrid; 50 % hybrid + 50 % light; semiconservative.
E. coli were grown in $^{15}NH_4Cl$ for many generations, so ^{15}N was incorporated into their DNA (heavy DNA); they were then transferred to $^{14}NH_4Cl$, and DNA was extracted at intervals and separated by density in a caesium chloride gradient. [1]
After one generation (about 20 min) all the DNA was hybrid (intermediate density); after two generations (about 40 min) half was hybrid and half light. [1]
This proves that DNA replicates semiconservatively: each daughter molecule has one old (parental) strand and one new strand. [1]

Q13. (3 marks) Answer: promoter, structural gene, terminator; σ initiates, ρ terminates.
A transcription unit has three regions: a promoter, the structural gene and a terminator. [1] The promoter, upstream of the structural gene, is the binding site for RNA polymerase; the terminator, downstream, marks the end of transcription. [1] The sigma (σ) factor associates with RNA polymerase and helps it start (initiation); the rho (ρ) factor associates with it at the terminator and helps end transcription (termination). [1]

Q14. (3 marks) Answer: triplet, 61 + 3, unambiguous, degenerate, comma-less, universal, AUG start.
Any six [3]: the codon is a triplet; 61 codons code for amino acids and 3 (UAA, UAG, UGA) are stop codons; one codon codes for only one amino acid (unambiguous and specific); some amino acids are coded by more than one codon (degenerate); the code is read in a contiguous fashion, without punctuation; it is nearly universal; AUG codes for methionine and also acts as the start codon.

Q15. (4 marks) Answer: (I) polymorphism in VNTRs; (II) isolation → restriction digestion → electrophoresis → blotting → hybridisation → autoradiography; (III) Alec Jeffreys, or VNTR.
(I) DNA polymorphism: differences in repetitive DNA (satellite DNA, especially VNTRs — variable number tandem repeats), which differ in copy number from person to person. [1]
(II) Isolation of DNA; digestion with restriction endonucleases; separation of the fragments by electrophoresis; transfer (blotting) to a membrane such as nylon or nitrocellulose (Southern blotting); [1] hybridisation with a labelled VNTR probe; detection of the hybridised fragments by autoradiography. [1]
(III) Alec Jeffreys. [1]
OR (III) A VNTR (minisatellite) sequence. [1]

Q16. (5 marks) Answer: (a) i, p, o, z, y, a; repressor bound/inactivated; (b) goals and features of the HGP.
(a) The lac operon has a regulatory gene (i), a promoter (p), an operator (o) and three structural genes: z (β-galactosidase, which hydrolyses lactose into glucose and galactose), y (permease, which increases the permeability of the cell to lactose) and a (transacetylase). [2] The i gene produces the repressor protein all the time. [½] Without lactose the repressor binds the operator and prevents RNA polymerase from transcribing the structural genes: the operon is switched off. [1] With lactose (the inducer) the repressor is inactivated by binding the inducer, so it cannot bind the operator; RNA polymerase transcribes the genes and the enzymes are made. [1] This regulation by the repressor is negative regulation. [½]
OR (b) Goals (any two): identify all the estimated 20,000–25,000 genes in human DNA; determine the sequence of the 3 billion base pairs; store the information in databases and improve tools for data analysis; address the ethical, legal and social issues. [2] Salient features (any three): the human genome contains 3164.7 million bases; the average gene has 3000 bases, the largest (dystrophin) 2.4 million; the functions of over 50 % of the discovered genes are unknown; less than 2 % of the genome codes for proteins; repeated sequences make up a large part; chromosome 1 has the most genes (2968) and the Y the fewest (231); about 1.4 million single-base DNA differences (SNPs) were identified. [3]

Q17. (5 marks) Answer: (a) charging, initiation (AUG), elongation, termination; (b) origin, fork, 5′→3′, leading and lagging (Okazaki, ligase).

(a) Charging of tRNA: amino acids are activated in the presence of ATP and linked to their specific tRNAs (aminoacylation). [1] Initiation: the small subunit of the ribosome binds the mRNA; the initiator tRNA carrying methionine pairs with the start codon AUG, and the large subunit joins; the ribosome has two sites for tRNAs. [1½] Elongation: charged tRNAs come in according to the codons; peptide bonds form between adjacent amino acids (catalysed by the 23S rRNA, a ribozyme) and the ribosome moves along the mRNA codon by codon. [1½] Termination: at a stop codon, a release factor binds and the polypeptide is released. [½] The mRNA also has untranslated regions (UTRs) before the start codon and after the stop codon, needed for efficient translation. [½]

OR (b) Replication starts at an origin of replication; the strands separate there to form a replication fork. [1] DNA-dependent DNA polymerase uses each strand as a template and polymerises nucleotides only in the 5′→3′ direction (using deoxyribonucleoside triphosphates as substrate and energy source). [1½] On the template with 3′→5′ polarity replication is continuous (leading strand); on the other it is discontinuous, in short Okazaki fragments (lagging strand), which are joined by DNA ligase. [1½] Each new molecule has one parental and one new strand: semiconservative replication. [1]

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