Molecular Basis of Inheritance

Standard difficulty · 20 questions · 40 marks · Time: 42 minutes

Name: _____ Date: _____ Score: ____ / 40

Show your working for Sections B and C. Answers are on the last page — try every question first!

Section A — Choose the correct answer — 8 × 1 = 8 marks

1. The double-helix model of DNA was proposed by:

(a) Griffith **(b)** Hershey and Chase
(c) Meselson and Stahl **(d)** Watson and Crick (1953)

2. The template strand of a gene reads 5′-TCATTTGCCCAT-3′. The mRNA transcribed from this gene reads:

(a) 5′-AUGGGCAAAUGA-3′ **(b)** 5′-UACCCGUUUACU-3′
(c) 5′-ATGGGCAAATGA-3′ **(d)** 5′-AGUAAACGGGUA-3′

3. The mRNA 5′-AUGUUUAAGUAA-3′ is translated. The polypeptide formed is:

(a) Met–Phe–Lys–Stop **(b)** Lys–Phe–Met
(c) Phe–Lys **(d)** Met–Phe–Lys

4. The genome of rice has 3.9×10^8 base pairs. Its length as a stretched double helix is about: (0.34 nm per base pair)

(a) 0.0663 m **(b)** 132.6 m **(c)** 1.326×10^{-4} m **(d)** 0.1326 m

5. E. coli grown for many generations in ^{15}N is moved to ^{14}N. After 3 generations, the fraction of DNA molecules that are hybrid ($^{15}N^{14}N$) is:

(a) 1/4 **(b)** 1/2 **(c)** 0 **(d)** 1

6. If each nucleosome, with its linker, takes up about 200 base pairs, a stretch of 26,000 base pairs of DNA forms about how many nucleosomes?

(a) 65 **(b)** 260 **(c)** 3,250 **(d)** 130

7. Which of these adds nucleotides in the 5′ → 3′ direction during replication?

(a) DNA polymerase **(b)** Aminoacyl-tRNA synthetase
(c) Lactose (allolactose) **(d)** RNA polymerase III

8. Assertion (A): The codons UUA and UUC code for different amino acids.
Reason (R): Every codon that starts with the same two bases codes for the same amino acid.

(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 — Short answer — 8 × 2 = 16 marks

9. What is the central dogma of molecular biology?

10. Translate the mRNA 5′-UAUGAUUCGAUCCCGUGGCUGA-3′. How many amino acids does the polypeptide have?

11. The mRNA 5′-AUGACUGCGGCUGAGUGA-3′ changes to 5′-AUGACUGCGGCUGCGUGA-3′ by a point mutation. Give both polypeptides and say what kind of mutation this is.

12. One strand of a DNA segment is 5′-GCCATTAACCTC-3′. Write the other strand and find the number of hydrogen bonds between them.

13. One ^{15}N-labelled DNA molecule replicates 3 times in a ^{14}N medium. How many DNA molecules are formed, and how many of them are hybrid and how many light?

14. Why must the genetic code be a triplet code? How many bases of mRNA, including the stop codon, code for a polypeptide of 340 amino acids?

15. The mouse haploid genome has about 2.7×10^9 base pairs. Find the length of this DNA. (0.34 nm per base pair)

16. In the lac operon, what are the roles of the promoter and the operator?

Section C — Word problems — 4 × 4 = 16 marks

17. Describe the double-helix model of DNA.

18. The coding strand of a gene reads 5′-ATGACGCGTAGACCATGA-3′. Write (a) the template strand, (b) the mRNA, (c) the polypeptide, (d) the number of amino acids.

19. Describe the Meselson–Stahl experiment. If 50 molecules of ^{15}N DNA replicate for 6 generations in ^{14}N, how many molecules form, and what fraction of the DNA is hybrid and what fraction is light? What would these fractions be if replication were conservative?

20. The mRNA 5′-AUGAUCGCGGGUCGUUAG-3′ gains an extra C after the sixth base. Give the normal and the mutant polypeptides, name the kind of mutation, and explain why it is usually more harmful than a substitution.

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Answer key

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Q	Answer	Working
1	**(d) Watson and Crick (1953)**	—
2	**(a) 5′-AUGGGCAAAUGA-3′**	the mRNA is complementary to the template strand and runs antiparallel to it
3	**(d) Met–Phe–Lys**	AUG Met, UUU Phe, AAG Lys, UAA stop
4	**(d) 0.1326 m**	length = number of base pairs × 0.34 × 10^{-9} m
5	**(a) 1/4**	semi-conservative: always 2 hybrid molecules out of 2^3
6	**(d) 130**	the histone octamer and linker hold about 200 bp
7	**(a) DNA polymerase**	—
8	**(c) A is true, but R is false.**	A is true: UUA = Leu, UUC = Phe. R is false.
9	**Genetic information flows from DNA to RNA (transcription) and from RNA to protein (translation). In some viruses information flows from RNA to DNA (reverse transcription).**	—
10	**Met–Ile–Arg–Ser–Arg–Gly; 6 amino acids**	start at AUG, read in triplets, stop at UGA
11	**normal: Met–Thr–Ala–Ala–Glu; mutant: Met–Thr–Ala–Ala–Ala; a base substitution that changes one amino acid (a missense mutation, like the one in sickle-cell anaemia)**	codon 5: GAG → GCG
12	**3′-CGGTAATTGGAG-5′; 30**	A–T: 2 hydrogen bonds; G–C: 3
13	**8 molecules: 2 hybrid ($^{15}N^{14}N$) and 6 light ($^{14}N^{14}N$)**	semi-conservative replication keeps each pair of old strands in two molecules
14	**There are 20 amino acids; a doublet code would give only 4^2 = 16 codons, a triplet gives 4^3 = 64, enough for all; (340 + 1) × 3 = 1,023 bases**	—
15	**0.918 m**	2.7 × 10^9 × 0.34 × 10^{-9} m
16	**The promoter is the site where RNA polymerase binds; the operator is the site where the repressor binds**	—
17	**Two polynucleotide chains wind round each other in a right-handed helix with the sugar–phosphate backbone outside and bases inside. The chains are antiparallel (5′ → 3′ and 3′ → 5′). Bases pair by hydrogen bonds: A with T (two bonds) and G with C (three), so**	—

Q	Answer	Working
	a purine always faces a pyrimidine and the width is uniform. The pitch is 3.4 nm with about 10 base pairs per turn, 0.34 nm apart.	
18	**(a) 3′-TACTGCGCATCTGGTACT-5′; (b) 5′-AUGACGCGUAGACCAUGA-3′; (c) Met–Thr–Arg–Arg–Pro; (d) 5**	mRNA = coding strand with U for T; translation from AUG to the stop codon
19	**3,200 molecules. E. coli was grown in $^{15}NH_4Cl$, moved to $^{14}NH_4Cl$, and the DNA separated by density in CsCl. Semi-conservative: hybrid 1/32, light 31/32. Conservative: no hybrid DNA at all; heavy 1/64 and light 63/64**	—
20	**normal: Met–Ile–Ala–Gly–Arg; mutant (reading frame shifted): Met–Ile–Arg–Gly–Ser–Leu; a frameshift (insertion) mutation, which changes every codon after it and often gives a non-functional protein**	read the mutant in triplets from AUG

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