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Level: HL IB in Biology

Subject: Biology

Topic: IB HL Biology

Type: Mark Scheme

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All International Baccalaureate IB Topic Questions HL Biology

BIOLOGY

HL - IB

Key skills

Answer 1

The correct answer is B because:

- There is a total of 19 base pairs per chain (this is stated in the question).
- 19 total bases – 8 T – 3 G – 4 C = 4 A bases
- In any one piece of DNA:
 - The amount of adenine = amount of thymine
 - The amount of cytosine = the amount of guanine

Remember that the bases are complementary, so the no. of A on strand 1 = the no. of T on strand 2 and no. of C on strand 1 = no. of G on strand 2

Thus, on strand 1 there would be:

- 4 thymine that bond with the 4 adenine on strand 2
- 4 guanine that bond with the 4 cytosine on strand 2
- 3 cytosine that bond with the 3 guanine on strand 2

	Number of nucleotide bases			
	A	T	G	C
Strand 1	8	4	4	3
Strand 2	4	8	3	4

Answer 2

The correct answer is A because in every nucleotide there is one phosphate group, one pentose sugar, and one base. Therefore, there would be an equal ratio of pentose sugars to phosphates (1:1).

Thymine and adenine are complementary bases and therefore they will appear in equal numbers in a DNA molecule.

B is incorrect because each nucleotide contains one pentose and one phosphate so their ratio in the overall polymer must also be 1:1.

C and D are both incorrect because the sugars in DNA are pentose (5-carbon) not hexose, which are 6-carbon. Both statements also claim inaccurate information about ratios of bases because T does not base pair with C and G does not base pair with A.

Answer 3

The correct answer is D. The orientation of the whole nucleotide (including sugar, phosphate and base) is flipped on the sense strand versus the antisense strand. Therefore, the DNA code runs in opposite directions on the two strands.

A is incorrect because all the sugars in DNA are deoxyribose; ribose sugars feature in RNA.

B and C are incorrect because they only state that part of the nucleotides on the opposite strand are inverted, when in fact the whole chain of nucleotides inverts.

Answer 4

The correct answer is C because a nucleotide angle of 36 degrees would mean that 10 base pairs would equal one whole turn of 360°.



A. $\frac{360^\circ}{5} = 72^\circ$ [too large]

B. $\frac{360^\circ}{8} = 45^\circ$ [too large]

C. $\frac{360^\circ}{10} = 36^\circ$ [correct] [1 mark]

D. $\frac{360^\circ}{12} = 30^\circ$ [too small]

Answer 5

The correct answer is C because:

- The circle shapes depict phosphate groups (Z).
- The pentagon shapes depict ribose sugars (Y).
- Adenine is already shown; X has a complementary shape to adenine and is therefore
- W is therefore guanine and the other unlabelled base is cytosine.

Answer 6

The correct answer is C because the complementary bases pairs are adenine with thymine and cytosine with guanine. The ratios of complementary base pairs should be equal:

- Thymine in human liver = 10% so W (Adenine) = 10%
- Guanine in mouse bone marrow = 26% so X (Cytosine) = 26%
- Cytosine in sunflower leaf = 39% so Y (Guanine) = 39%
- Adenine in human liver = 30% so Z (Thymine) = 30%

These values are percentages and therefore each row must add to 100!

Answer 7

The correct answer is C.

The mistakes are:

1. In the final base pair, cytosine (C) and guanine are complementary; however, adenine (A) is shown to pair with guanine.
2. On the whole of the right strand: the phosphates are bound on the wrong side of the deoxyribose sugars. Phosphate always binds to the opposite side to the base.
3. The strands should run in antiparallel directions (one goes 3' to 5' and the other 5' to 3').

Answer 8

The correct answer is C.

A is incorrect because one of the sugars is depicted with a hexagon, which implies a hexose sugar. All sugars in DNA (and RNA) are pentose so should be drawn with a pentagon.

B is incorrect because the covalent bonds are shown from each sugar's 2-carbon atom to the phosphate groups; this should be from the 3-carbon atoms.

D is incorrect because the bases are shown bonded to the 2-carbon atoms of the pentose sugars; this should be bonded to the 1-carbon atoms.

Answer 9

The correct answer is A because statement III describes the degenerate code, which allows the 64 combinations of 4 bases in a triplet to code for the 20 amino acids, with a wide scope for different codons to code for the same amino acid.

Statement I is incorrect because some base sequences are never transcribed. Other bases are part of genes that are only expressed for a short part of an organism's life eg. fetal haemoglobin.

Statement II is incorrect because a single base will only ever be part of (maximum) one gene and the code is non-overlapping.

Statement IV is incorrect because mutations occur during every cell cycle, so an organism's genome changes slightly throughout its life.

Answer 10

The correct answer is B because the nucleosome consists of a strand of DNA coiled around a core of eight histone proteins to form a bead-like structure. This helps to supercoil the DNA, resulting in a compact structure that saves space within the nucleus

- Option A is incorrect because although nucleosomes do contain histone proteins they also help supercoil DNA
- Option C is incorrect as prokaryotes such as bacteria do not possess nucleosomes, their DNA is referred to as 'naked DNA'
- Option D is incorrect as although nucleosomes are basic units that aggregate together to form chromatin, they don't specifically contain chromatin

Answer 11

The correct answer is A: Hershey and Chase took advantage of the chemical differences between DNA and proteins. DNA does not contain sulphur and protein does not contain phosphorus. As the virus inserts its DNA (and not protein) into the bacteria only bacteria containing the ^{32}P labelled was radioactive.

- Option B is incorrect because bacteria infected by the ^{32}P labelled virus were found in the pellet after centrifugation
- Option C is incorrect because only the protein coat of the virus contained ^{35}S and this was not inserted into the bacteria
- Option D is incorrect because prior to centrifugation, Hershey and Chase removed any viral protein coat (containing ^{35}S) from infected bacteria by agitation - this was detected in the supernatant

Answer 12

The correct answer is B because molecular visualisation software can be used for all of these activities and many more not listed.

C and D are incorrect as IV is not a true statement. BLAST (Basic Local Alignment Search Tool) is usually used to compare an unknown DNA sequence with all known gene sequences. Although some molecular visualisation software can now integrate with other software to identify unknown DNA sequences it is not its primary use.



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