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Detailed mark scheme

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Designed to test your ability and thoroughly prepare you

Level: SL IB in Biology

Subject: Biology Topic: IB SL Biology Type: Topic Question



All International Baccalaureate IB Topic Questions SL Biology

BIOLOGY

SL - IB

Key skills



Question 1.

The nucleotide base sequence and the associated sequence of four amino acids can be seen below:

AGG ACA CCT GGA Serine Tyrosine Glycine Proline

The table shows the mRNA codons and their associated amino acids.

| | | Second Letter | | | | | |
|--------------|---|------------------------------|-----------------|---------------------------------------|----------------------------------|------------------|-----|
| | | U | С | Α | G | | |
| First Letter | U | UUU Phe UUC Leu UUG Leu | UCU UCC UCA UCG | UAU Tyr UAC TYP UAA - STOP UAG - STOP | UGU Cys UGC STOP GGU - Trp | U C A G | |
| | c | CUU - CUC CUA CUG - | CCU CCC CCA CCG | CAU His CAC GIN CAG | CGU CGC CGA CGG | O > O C | ICE |
| | A | AUU IIIe AUA AUG – Met | ACU ACC ACA ACG | AAU Asn AAC AAA Lys | AGU Ser AGC AGA Arg | O V O O | |
| | G | GUU - GUC GUA GUG - | GCU GCC Ala | GAU Asp GAC GAA GIU | GGU GGC GGA GGG | U C A | |

A single mutation occurred in the original base sequence of the DNA which resulted in only one amino acid from the sequence being produced.



Which of the following would represent the correct nucleotide base sequence which was found in the DNA after the mutation occurred?

- A. AGT ACA CCT GGA
- B. AGG ACT CCT GGA
- C. AGG ACC CCT GGA
- D. AGG ACA UGA GGA

[1 mark]



Question 2.

In a gene editing experiment using CRISPR-Cas9, a researcher introduces a double-strand break in a specific gene. Which of the following repair mechanisms could result in a gene knock-out?

- A. Non-homologous end joining (NHEJ)
- B. Homologous recombination (HR)
- C. Base excision repair (BER)
- D. Nucleotide excision repair (NER)

[1 mark]



Question 3.

A researcher is studying a new gene-editing technique that uses an engineered nuclease to create specific double-strand breaks in the DNA. The researcher finds that the technique exhibits higher precision and fewer off-target effects compared to traditional CRISPR-Cas9. Which technique is the researcher most likely using?

- A. TALENs (Transcription Activator-Like Effector Nucleases)
- B. ZFNs (Zinc Finger Nucleases)
- C. Meganucleases
- D. RNA-guided endonucleases



[1 mark]

