

Model Answers: Medium

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The correct answer is **D** because:

- The number of **thymine** (T) bases on one strand **equals** the number of **adenine** (A) bases on the other strand as these bases are **complementary**.
- The number of **guanine** (G) bases on one strand **equals** the number of **cytosine** (C) bases on the other strand as these bases are complementary.
- Therefore, on one strand of DNA the number of nucleotides on strand 1 of the DNA is: $30 \text{ A} + 30 \text{ T} + 22 \text{ G} + 38 \text{ C} = \mathbf{120 \text{ total}}$
- RNA polymerase will produce an mRNA molecule complementary to the template strand of DNA so the **mRNA** will also have 120 nucleotides.
- 3 nucleotide bases form a **codon** which codes for one **amino acid**, therefore the number of amino acids coded for by 120 nucleotide is:
 $120 \div 3 = \mathbf{40 \text{ amino acids}}$

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The correct answer is **B** because protein synthesis occurs in the following steps:

1. **Transcription**

- DNA helicase unwinds the DNA double helix.
- RNA polymerase binds to the start of the gene then moves along the template strand assembling free RNA nucleotides that are complementary to bases in the DNA.
- RNA nucleotides are joined by phosphodiester bonds to produce a messenger RNA – a complementary copy of the template strand.

2. **Translation**

- mRNA leaves the nucleus and binds to a ribosome.
- The ribosome moves along the mRNA displaying codons to tRNA.
- Each tRNA molecule has a 3 base anti-codon which is complementary to an mRNA codon. They carry an amino acid specific to the codon and therefore act as adapters between nucleic acid and protein.

3. **Peptide bonding**

- When the correct amino acid is brought to the ribosome, the ribosome catalyses the formation of a peptide bond between amino acids
- This forms a chain – the **primary structure** of a protein (polypeptide).

4. **Hydrogen bonding**

- Hydrogen bonds form between the main chain amino acids in the polypeptide which forms a secondary structure.
- The secondary structure is usually either an alpha-helix or a beta-sheet

The correct answer is **C** because:

- **mRNA** contains a **start** and **stop codon** to signal to the ribosome the beginning and end of the **coding sequence**.
- There is a small section before and after the coding sequence to protect it from degradation.
- No tRNAs have an **anti-codon** complementary to a stop codon and this therefore signals the end of the protein coding sequence.

A is incorrect as	the mRNA molecule has a small section of non-coding nucleotides before and after the coding sequence to protect the coding sequence from degradation. Therefore, the protein would be too long if the ribosome reached the end before it stopped translating.
B is incorrect as	tRNA are in large supply in the cytoplasm, where translation takes place, and the cell is synthesising many different proteins on different ribosomes at the same time. Therefore, tRNA supply will not stop translation.
D is incorrect as	RNA polymerase is only found in the nucleus , and ribosomes are only found in the cytoplasm . RNA polymerase never makes contact with the peptide chain and is only used in the transcription stage of protein synthesis, not translation.

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The correct answer is **D** because:

- The tRNA **anticodon** is the same **triplet** seen in DNA (both are **complementary** to the **mRNA** strand).
- However, remember that RNA molecules contain **uracil** (U) and DNA molecules contain **thymine** (T).

The DNA codes for the amino acids are:

- **Alanine** is GCT or GCG, therefore only **B** or **D** can be correct.
- **Valine** is GTA or GTC, therefore either **B** or **D** could be correct.
- **Lysine** is AAA or AAG, therefore either **B** or **D** could be correct.
- **Serine** is TCG or TCA, therefore only **D** is correct.

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The correct answer is **C** because

DNA replication:

- Occurs in the **nucleus**.
- **Two double stranded DNA** molecules are produced from one double stranded DNA molecule.
- **DNA polymerase** assembles free DNA nucleotides into two new chains each of which is **complementary** to an original DNA strand.
- The two newly produced DNA strands are **hybrids**: one chain of each is from the original DNA molecule and the other is newly synthesized. This is called **semi-conservative** replication.

Transcription:

- Occurs in the **nucleus**.
- Is the production of a **messenger RNA** chain, which is complementary to the template strand of DNA, by **RNA polymerase**.

Translation:

- **mRNA** binds to the ribosome in the **cytoplasm**.
- The **ribosome** holds the mRNA so that **tRNA** molecules can bind and their amino acids can be linked by peptide bonds into a polypeptide.

A is incorrect as	transcription occurs in the nucleus, not the cytoplasm.
B is incorrect as	translation produces a polypeptide not mRNA. mRNA is produced in transcription.
D is incorrect as	RNA polymerase is only used in the transcription stage of protein synthesis, not translation.

The correct answer is **B** because:

- **Genes** are sequences in DNA that code for a **protein** (polypeptide).
- Within DNA they include a transcription initiation site, a translation initiation site, the coding exon sequences, the non-coding intron sequences, and a termination section.

A is incorrect as	there is no protein section of DNA .
C is incorrect as	exons is a part of a gene that codes for the polypeptide. However, it cannot enable protein synthesis on its own as it requires other areas of the gene for this.
D is incorrect as	a triplet or 'codon' codes for one amino acid within a polypeptide, not a whole polypeptide .

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The correct answer is **D** because:

- A **silent** mutation is a change in the nucleotide sequence which results in the **same amino acid sequence**.
- This is possible because some amino acids can be coded for by up to four different triplet codon sequences.
- Silent mutations are often a change in the 2nd or 3rd base in the codon, rather than the first.
- For example, valine is coded for by GUU, GUC, GUA, GUG – therefore as long as the first two nucleotides in the codon are guanine and uracil valine will be inserted into the polypeptide.

A is incorrect as	silent mutations do not always create recessive genotypes.
B is incorrect as	substitution mutations also do not result in a frame shift however some substitution mutations can cause the amino acid sequence to change.
C is incorrect as	if the exact amino acid changes it is not classed as a silent mutation, however it is possible that the function of the protein will not be greatly affected. For example, aspartic acid instead of glutamic acid – the functional groups are the same but they are slightly different sizes which may impact structure and function.

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The correct answer is **C** as **DNA transcription** is the process of making a copy of the DNA code in RNA for protein synthesis - it does not involve the enzymes DNA ligase or DNA polymerase

- **RNA polymerase** is used to produce **messenger RNA** which then moves out of the nucleus to a ribosome for protein synthesis so it is needed for transcription
- **Helicase** unwinds the DNA double helix and breaks the hydrogen bonds between complementary base pairs for transcription or replication so it is required

DNA ligase catalyses the formation of **phosphodiester bonds** between separate DNA nucleotides during **DNA replication**.

DNA polymerase is required for **DNA replication** as it assembles free nucleotides to form new complementary strands of DNA.