

1. What is the process by which information is transferred from a DNA to an mRNA? **Transcription** (2 marks)
2. What is the process by which polypeptide molecules are made from an mRNA? **Translation** (2 marks)

Sequence	Type of BLAST search chosen and why (2 marks each)	What is the protein (coded for by the gene for a nucleic acid sequence) and in what biological process is it involved? (2 marks each)
A	Nucleotide. The sequence was comprised of exclusively DNA nucleotides (A, T, G, and C).	'The complete DNA polymerase protein'. As the specified polymerases is vague, only III and I will be discussed. DNA Polymerase III constructs a complementary DNA strand either in Okazaki fragments when primed or as a constant stream. DNA polymerase I replaces Okazaki fragment RNA-based primers with DNA nucleotides. Both polymerases are involved in the DNA transcription process (Urry et. al; 2021:1426)
B	Nucleotide. The sequence was comprised of exclusively DNA nucleotides (A, T, G, and C).	'RNA polymerase II, I, and III subunit H'. Subunit 'H' seems to refer to the RPABC3 subunit (NCBI; 2020 section FEATURES:CDS). All RNA polymerases (RNAs) are involved in the transcription of DNA to RNA, with RNA polymerase II being a primary focus. RNAs untwist the DNA double helix and forms a complementary RNA strand going from the 3' to the 5' end (Urry et. al; 2021:1466-1467). Each RNA Polymerase produces different type of RNA, I being rRNA, II being primarily mRNA, and III being primarily tRNA (Cramer et. al; 2008).
C	Protein. The given sequence is comprised of the shortened names for amino acids/polypeptides. It was figured out in part by learnt knowledge and process of elimination, being fully confirmed by utilising Berkeley Library (2023) resources.	Tyrosyl-tRNA synthetase, also known as TyrRS, is responsible for the activation and the stabilisation of tyrosine joining tRNA (Bedouille; 2000-2013)
D	Protein. The given sequence is comprised of the shortened names for amino acids/polypeptides (Berkeley Library; 2023).	Histone H2A variant, isoform B, or H2A.B. The following description is a composite of H2A.B and H2A.B.1 through to H2A.B.3 as the roles are similar and for the sake of clarity. Like all histones, H2A.B allows DNA (chromatin) to be tightly compressed. Furthermore, it is necessary for converting spermatids to fully-fledged sperm through processes in spermatogenesis like the facilitation of RNA splicing by holding RNA within the spermatids. It is also believed to assist with the elongation phase of transcription (Jiang; 2020).

Sequence	Organism scientific name (in correct binomial format) (1 mark)	Is the organism a prokaryote or a eukaryote? (1 mark)	Stop codon (written in cDNA format) (write N/A for protein sequences) (1 mark)	Number of nucleotides in coding sequence (write N/A for protein sequences) (1 mark)	Number of amino acids in translated sequence (1 mark)
A	<i>Thermus aquaticus</i>	Bacteria - Prokaryote	TGA	1..2499, so <u>2499</u> nucleotides. (2496 excluding STOP release factor, <u>2499</u> is my answer though)	2499 nucleotides ÷ 3 nucleotides per codon = <u>833</u> amino acids.
B	<i>Ailuropoda melanoleuca</i> (giant panda)	Animal – Eukaryote	TGA	18..470, so <u>453</u> nucleotides. (450 excluding STOP release factor, <u>453</u> is my answer though)	453 nucleotides ÷ 3 nucleotides per codon = <u>151</u> amino acids.
C	<i>Staphylococcus aureus</i>	Bacteria (-coccus is a bacteria shape) - Prokaryote	N/A	<u>N/A</u> (421 * 3 = 1263 nucleotides, assuming a STOP release factor)	1..421, so <u>421</u> amino acids. Interestingly, there are two START acids (mm) at the start, but that does not affect the count.
D	<i>Drosophila melanogaster</i> (fruit fly)	Insect - Eukaryote	N/A	<u>N/A</u> (141 * 3 = 423 nucleotides, assuming a STOP release factor)	1..141, so <u>141</u> amino acids.

(any underlined text is my actual answer)

References

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Berkeley Library; (August 28 2023); [NCBI Bioinformatics Resources: An Introduction: BLAST: Compare & identify sequences](#); The Regents of the University of California; accessed 16 September 2023

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NCBI (National Center for Biotechnology Information); (2020); [DNA-directed RNA polymerases I, II, and III subunit RPABC3 \[Ailuropoda melanoleuca\]](#); NCBI; United States Government; accessed 16 September 2023

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