BIOL 112: Unit 2 Practice Questions & Answers – PART I

This document contains some questions for you to practice. The questions are grouped by topic along with the learning objectives associated with each of the topics. We encourage you to use the learning objectives to guide your studying; ask yourself if you could answer each objective if it was in the form of a question. There are different levels of questions provided:

1. **Study questions**: these are questions on your direct knowledge of the topics, so essentially 'drills' on the basics – practice to make sure you get the fundamentals. Work with these questions first to build up your skills.
2. **Exam-type questions, of which there are two types:**
    a. **Multiple choice:** these are the types of questions you are likely to see on the exam – various levels of application of the fundamental knowledge and skills for each topic area.
    b. **Open response questions (ORQs):** a few examples to give you an idea of the kinds of short answer questions you will see on the exams.

Nucleic Acids - Structure, DNA assembly and organization

Nucleic acids are one of the four major macromolecules in cells. This topic focuses on the structure, assembly and organization of DNA highlighting some key structural comparisons to RNA.

Nucleic Acids – Genomes

This topic deals with all the heritable genetic information of a cell or organism as a whole, and introduces how the structural sequence of the genome dictates observable characteristics.

Study questions:

1. What interactions serve to stabilize/hold DNA together in its secondary structure? Explain how this stabilizes DNA in its aqueous environment.
   Hydrogen bonds between strands (base pairing), stacking interactions (mostly ID-ID) above and below in the same strand. The stacking interactions allow for the hydrophobic surfaces to be excluded from water, allowing water to have more motional freedom and thereby increasing stability.
2. By convention how is the directionality of a DNA molecule written?
   5' to 3'

3. By convention how is the directionality of a protein molecule written?
   N to C

4. Which linkage forms the backbone of a nucleic acid?
    A. A base-phosphate linkage
    B. A Sugar-phosphate linkage
    C. A sugar-base-phosphate linkage
    D. A sugar-base linkage

5. In describing DNA or RNA, you will see the term 5' to 3' (verbally, this is "5-prime to 3-prime"). The terms 5' and 3' apply to which of the statement(s) below? Choose all that apply.
    A. One of the two DNA strands.
    B. The sequence of the bases in the DNA or RNA.
    C. The direction of the strands.
    D. Particular carbon atoms on the ribose or deoxyribose ring.
    E. The linkage between the ribose ring and the base.

Exam Type Questions:

6. In a bacterium, 14% of the DNA nucleotides were found to be Thymine. What proportions of the bases would be Guanine?
   - A. 28% G
   - B. **36% G**
   - C. 14% G
   - D. 58% G
   - E. Cannot be determined.

7. In normal double-stranded DNA, purines base pair with only certain types of pyrimidines. This is because…
   - A. a purine-purine pair would be too small, and a pyrimidine-pyrimidine pair would be too large
   - B. the number of A must equal the number of T and the number of G must equal the number of C
   - C. the strongest stacking interactions are found between purines and pyrimidines, making the DNA more stable
   - D. purine-pyrimidine pairs maximize the number of hydrogen bonds, making the DNA more stable.
   - E. **all Watson-Crick purine-pyrimidine base pairs have the same geometries**

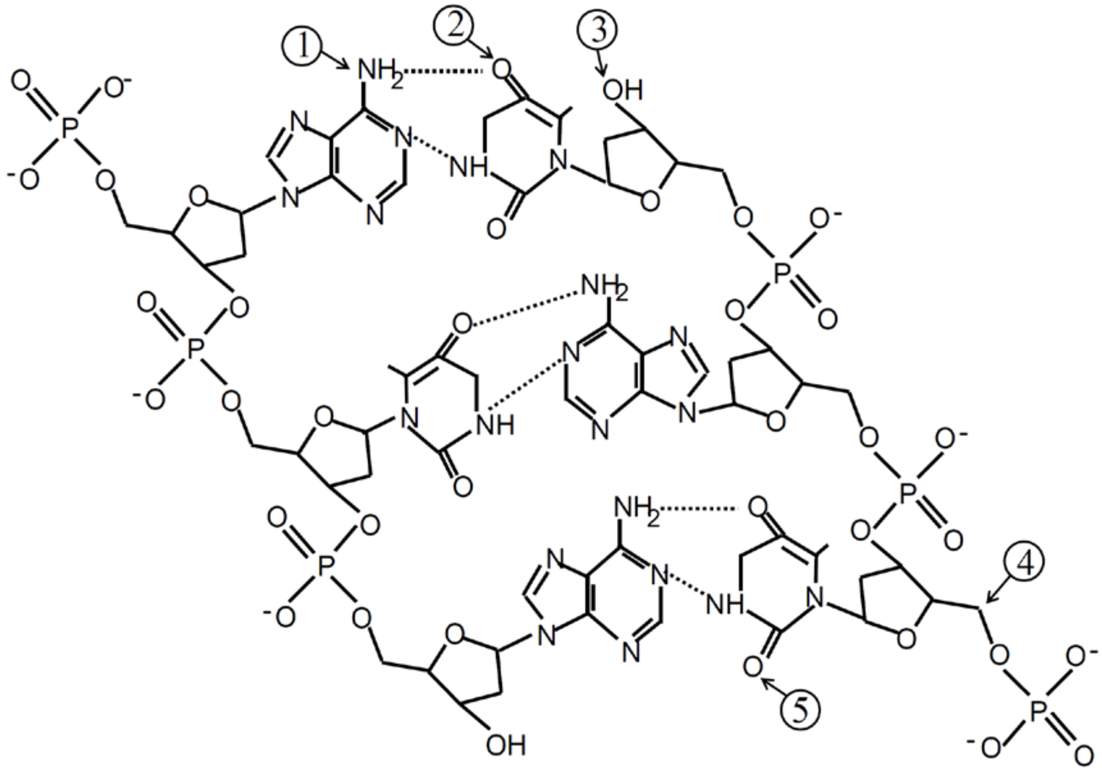
8. You are comparing the genetic material of two species. Species A has 100 million base pairs in one of its skin cells. Species B has 96 million base pairs in one of its skin cells.
   From this data, you can conclude that:
   - A. **The genome of species A is larger than the genome of species B.**
   - B. Species A has more genes than species B.
   - C. The genome of species B is larger than the genome of species A.
   - D. Species B has more genes than species A.
   - E. More than one of the above can be concluded based on this data.
   - F. None of the above can be concluded based on this information.

9. From a series of experiments, you determine the following information.

Species	Amount of DNA in a cell (base pairs)	Number of base-pairs that code for proteins
A	8,000,000	8,000
B	200,000,000	19,000
C	19,000,000	500,000

   Based on the information shown, which statement is true? The genome …
   - A. of species A is the largest.
   - B. **of species B is the largest.**
   - C. of species C is the largest.
   - D. of species B contains the most genes.

10. Two strands of a short DNA molecule with 3 base pairs are shown below. The dotted lines indicate hydrogen bonds. Five atoms are labelled from 1 to 5. Indicate which label correctly points to one of the 5′ ends of one of the DNA strands.



A. 1
B. 2
C. 3
D. **4**
E. 5

11. DNA is double stranded and the two strands are said to run in an antiparallel fashion. The term antiparallel refers to which observation?

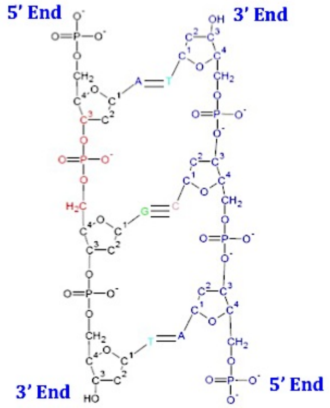
A. One strand of DNA is identical to the other but is simply the mirror image
B. One strand of DNA is complimentary to the other but they both run in the same direction from 5’ to 3’
C. One strand of DNA runs 5’ to 3’ while the other strand runs in the opposite direction from 3’ to 5’

12. Anti-parallel stands of DNA form complementary base pairing by hydrogen bonds. Which of the following statements is false regarding base pairing?

A. Adenine always base pairs with thymine while guanine forms three hydrogen bonds with cytosine.
B. A purine will always base pair with a pyrimidine to correctly align the bases to maintain a uniform DNA double helix.
C. One set of the complimentary base pairs has stronger interactions via H bonds.
D. Adenine is always linked to a thymine by a phosphodiester bond.

ORQ Style Questions

13 Label the ends of the two strands of DNA below to indicate their directionality.
Assuming this small segment of DNA was part of a larger segment of DNA not shown, indicate where a new nucleotide would be added if either of these strands were extended further.



A new nucleotide would be added to the 3' end of the strand with a free OH group.

Topic:
Biological Information flow

This topic describes the major functions of DNA as the hereditary genetic material that can be copied and inherited; DNA is transcribed to generate an RNA molecule, and that a subset of RNA called messenger RNA are read/translated into proteins.

Transcription

This topic describes the general mechanisms of how DNA is transcribed to generate an RNA molecule. We will compare and contrast this process in both bacteria and eukaryotes.

Study questions:

1. Transcription is the process of copying DNA to RNA
2. Translation is the synthesis of protein from mRNA.
3. **Transcription comparison:**

Compare/contrast…	**Eukaryotes**	**Bacteria**
Chromosome structure	Contains histones (nucleosomes)	Does not contain histones
Site of transcription	Nucleus	Cytoplasm
What is the promoter structure?	TATA box, 25 bp upstream	-35 box and -10 box
What are the proteins involved contacting the promoter?	General/basal transcription factors	Sigma
Is splicing (removal of introns) required?	Yes	No
Capping and tailing of mRNA?	Yes	No
Site of translation	Cytoplasm	Cytoplasm
Can translation occur while transcription is still occurring?	No	Yes

4. **Transcript initiation and processing comparison:**

Compare and contrast	**Eukaryotes**	**Bacteria**
Splicing (yes or no)	Yes	No
Site of initiation for transcription (promoter structure)	TATA box	-35 and -10 box
RNA has 5'cap (yes or no)	yes	no
RNA has 3' poly A tail (yes or no)	yes	no

Exam Type Questions:

5. Transcription factors only bind specific DNA sequences. What part of the DNA molecule would you predict is most important for **specific** interactions between a transcription factor like Sigma and the promoter sequence it binds?
   - A. Deoxyribose
   - B. The phosphate group
   - C. The bases
   - D. The major and minor grooves

6. The following is a list of components of a gene that can be identified by looking at nucleic acid sequences. For a bacterial gene, which of these is NOT coded in RNA?
   - A. Promoter
   - B. Ribosome binding site
   - C. Start codon
   - D. Stop codon
   - E. Terminator

7. What determines where the *E. coli* RNA Polymerase initiates transcription?
   - A. The binding of the RNA Pol to the single unique origin of transcription downstream on the *E. coli* chromosome.
   - **B. The binding of the sigma subunit to the consensus sequences upstream of the transcription start site.**
   - C. The binding of the sigma subunit to the consensus sequences downstream of the transcription start site.
   - D. At the RNA stem loop that forms at a consensus sequence 5' of the transcription start site.
   - E. RNA Pol initiates transcription at the first AUG codon of each gene.

8. What features of a DNA binding protein are required to recognize the correct binding site on DNA?
   - **1.** They can make specific ionic interactions with the phosphodiester backbone of the DNA only at that sequence.
   - **2.** They make specific non-covalent interactions with the exposed bases of the DNA only at that sequence.
   - **3.** Part of their 3D structure is the right size/ shape/charge/polarity to interact with the major and minor grooves of that sequence of DNA.
     - A. 1 and 2
     - B. 2 and 3
     - C. 1 and 3
     - D. 3 only
     - E. All

9. You have found that a particular protein binds to a specific sequence of bases in the DNA of a bacterial cell. There are six possible sequences for this binding site.

The sequences where it binds are shown at right:

Which of the following is the consensus base in position 4?

Position 123456
TAGTCA
AAGACA
TTAAGA
TGTCAT
CTGAAC
TAATCA
TCGGCA
TTTACA

A. **A**
B. G
C. C
D. T
E. There is no consensus.

10. Which of the following describes the comparison of typical bacterial and eukaryotic mRNAs?
   A. Eukaryotic mRNAs have 5’ untranslated regions, but bacterial mRNAs do not.
   B. **Eukaryotic mRNAs are spliced before translation but bacterial mRNAs are not**.
   C. Eukaryotic mRNAs have several open reading frames, but bacterial mRNAs have only one.
   D. Bacterial RNA polymerases are the same as RNA polymerases in eukaryotes.
   E. Eukaryotic mRNAs can accommodate several ribosomes, but bacterial mRNAs cannot.

11. The fact that translation is not simultaneous with transcription in eukaryotes is primarily due to:

   A. the fact that introns are spliced from eukaryotic mRNAs before translation.
   B. the fact that eukaryotic mRNAs need a polyA tail to be translated.
   C. the fact that eukaryotic mRNAs need a 5' cap to be translated.
   D. **the fact that the processed mRNA needs to be exported to the cytoplasm for translation**.
   E. the fact that the DNA must be decondensed in the nucleus before transcription.

12. Which of the following components come together to form the initiation complex so that transcription can begin in eukaryotic cells?

   1. Sigma factor.
   2. General transcription factors.
   3. RNA Polymerase.
   4. TATA Binding Protein.

   A. 1 and 3
   B. 1, 2, 3
   C. 2, 3, 4
   D. 2 and 3 only
   E. 3 and 4 only

13. Which of the following statements about alternative splicing are true?
   1) introns are spliced out and exons are joined together.
   2) exons are spliced out and introns are joined together.
   3) is a form of post-translational control of gene expression.
   4) reduces the number of genes needed to express different proteins.

   A. 2 only.

B. 1, 3 and 4.
C. 3 and 4.
D. **1 and 4.**
E. 1 and 3.

14. What would happen to an mRNA strand in a eukaryotic cell if during RNA processing the poly A tail is not added? CHOOSE ALL THAT APPLY
    A. Nothing. The tail is just a way to mark the 3’ ends of the mRNA strand.
    B. The mRNA strand would not be able to leave the nucleus as the tail is necessary to pass through the nuclear membrane.
    C. **The mRNA strand would no longer be protected by the poly A tail and would be more easily degraded by ribonucleases**.
    D. The mRNA strand would be transported into the mitochondria where poly A tails are not required from translation.
    E. The mRNA would be translated in the nucleus.

15. An intron is ________________________; and an exon is typically __________________.
    A. RNA that is removed during the processing of an mRNA molecule and leaves the nucleus; part of an intact, mature mRNA that stays in the nucleus.
    B. a peptide sequence that is spliced out post-transcriptionally; a peptide sequence spliced out post-translationally.
    C. RNA that is removed during the processing of an mRNA molecule and degraded in the nucleus; part of an intact, mature mRNA that leaves the nucleus.
    D. part of a tRNA that binds to the codon during translation; part of mRNA that has the ORF.
    E. part of an rRNA that becomes part of the ribosomes; part of the mRNA that has the ORF.

ORQ Style Questions

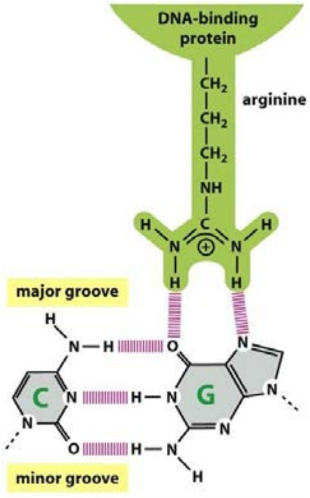
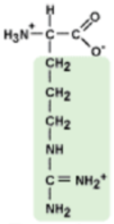


Figure 7-25 Molecular Biology of the Cell 5/e (© Garland Science 2008)

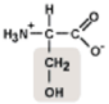
16. Shown at right is the interaction between an amino acid side chain (Arginine) in the bacterial DNA-binding protein, sigma, and a nucleotide base (guanine) within the promoter of a gene.

If Arginine were replaced with by Serine in the protein (both shown below) **predict** what would be the effect on the protein-DNA binding. See next page…

Arginine

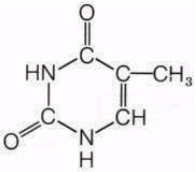


Serine



Could this replacement have an effect on transcription of this gene? **Explain** your reasoning for your prediction.

If Serine were in the protein there would be a substantial decrease in R-group size, and there would be no possibility for ionic bonds, decreasing the strength and frequency of protein-DNA binding. This would likely result in less frequent transcription.



Thymine (T)
(in DNA)

Compared to the original situation: In the DNA sequence, if guanine were replaced by thym (shown at right), **predict** what would be the effect on the protein-DNA binding.
Could this replacement have an effect on transcription of this gene?
Explain your reasoning for your prediction.

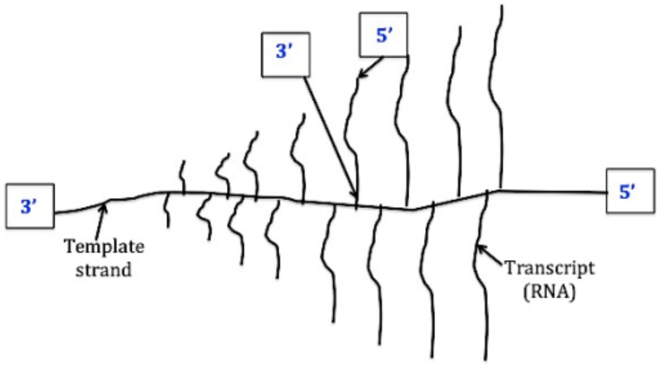
With a base substitution, different non-covalent interactions will be possible between the protein and the side of the base. This could also perturb the regular structure of the DNA. For both of these reasons, it is likely that the frequency of protein-DNA binding will decrease. This would likely result in less frequent transcription

17. **The diagram below represents part of a genome of a bacterial cell.** The light blue lines represent double stranded DNA. The boxed areas represent two different genes (gene 1, gene 2) that code for two different proteins. Recall in BIOL 112, a "gene" is defined as the DNA sequence from the promoter to the terminator.

For each statement, indicate true or false (T or F).

T or F?	Statement
T	a. The direction of transcription for both gene 1 and gene 2 is 3' –> 5' on the template strand.
T	b. The template strand for gene 2 is represented by the bottom strand.
F	c. The +1 site (start of transcription) for gene 2 is downstream of its "T" (terminator).
T	d. For gene 2, the top strand sequence is identical to its mRNA except T's will be U's.
F	e. If the two genes above (gene 1, gene 2) were being transcribed simultaneously, the RNA polymerases would be moving towards each other (convergent).
F	f. The coding strand for gene 1 is the top strand (5' –> 3')
T	g. When considering the direction of transcription for gene 1, the promoter for gene 2 (P2) is upstream from the promoter (P1) for gene 1.
F	h. The top strand will always be the coding strand for all genes in this bacterium.
T	*i.* The -10 box of the promoter sequence for gene 1 will be located closer to the 3' end of the bottom strand than its 5' end.
T	j. The +1 site for gene 2 can be found upstream of T2 considering direction of transcription for gene 2.
F	k. Both genes would share a ribosomal binding site.
T	l. The template strand for gene 1 is represented by the top strand.
T	m. For both genes 1 and 2, movement of RNA polymerase depends on the orientation of two different consensus sequences (-35 box and -10 box) on the promoter.

18. The cartoon below represents the process of transcription as observed in an electron micrograph. On the diagram below indicate the directionality (5' or 3') in the boxes against the structure.



Template strand (DNA) read 3' to 5'; transcript (RNA) synthesized 5' to 3'

19. Which is which? In transcription, which structural elements of a gene correspond to a typical bacteria vs. eukaryotes? What is the function of each?

Gene structure	Bacterial Gene? √	Eukaryotic Gene? √	Description and Function
Promoter	√	√	Binds the RNA Polymerase
Introns		√	Sequence that are cut out in RNA processing/splicing
Stop codon			Does not function in transcription, only TRANSLATION! Codes for the end of protein synthesis.
5' CAP		√	Added to mRNA once the 5' end is synthesized .
TATA box		√	sequence on Euk promoter, TBP/general transcription factors bind here
-10 and -35 box	√		sequence on Bac promoter, sigma binds here
Template strand	√	√	DNA strand that Codes for the mRNA
Transcription start site	√ (+1 site)	√	First base that is transcribed into mRNA Bac = ~10 bases from -10 box Euk = ~25 bases from TATA box
Terminator	√ (hairpin)	√	Terminates transcription – Bac = hairpin loop, Euk – multiple repeat sequences
+1 site	√	√	First base that is transcribed into mRNA
Start codon			Does not function in transcription, only TRANSLATION!
Exons		√	Coding regions that may be spliced out or kept in a mRNA transcript.
Ribosomal binding site			Does not function in transcription, only TRANSLATION!
Non-template /coding	√	√	Opposite strand of the template but often used to read the code! (Same sequence as the mRNA except with T's instead of U's.
Poly A tail		√	Added after mRNA made in Euk.

Translation

Study Questions:

1. How is translation initiated in bacteria? What part of the mRNA transcript does the ribosome bind to? How does this differ in Eukaryotes?

2. What specific sequence or region leads to transcription termination and translation termination?

The terminator sequence mediates transcription termination.
Translation is terminated by the stop codon.

3. If a given tRNA has an anticodon of 5’-ACU-3’, what is the mRNA codon, what is the template strand DNA sequence, and which amino acid does it carry? (3points)
   mRNA: 5’- AGU-3’ or 3’-UGA-5’
   template strand: 5’-ACT-3’ or 3’-TCA-5’
   Amino acid: Ser

Exam Type Questions:

4. Given that there are 61 codons for the 20 amino acids, which of the following is good evidence for the wobble hypothesis?
   A. The genetic code is a triplet.
   B. There are three different termination codons but only one start codon.
   C. The tRNAs are the main translators of protein synthesis.
   D. Wobble controls the number of proteins translated from each mRNA.
   E. **The fewer than 60 different types of tRNA in a cell.**

5. The DNA sequence below (the template strand) is part of the coding region of a gene. What would be the sequence of amino acids for this portion of DNA? (the reading frame is indicated by the vertical lines)

   3' – ACG|ATT|CTT|TGC - 5'

   A. N - alanine - lysine - asparagine - arginine - C
   B. N - cysteine - asparagine - valine - serine - C
   C. N - threonine - isoleucine - leucine - cysteine - C
   D. **N - cysteine – C**
   E. More information is needed to answer this question.

6. A region of DNA is transcribed and the mRNA is translated into a sequence of amino acids. The sequence of amino acids that is encoded by this strand is:

   NH_2 - serine - alanine - lysine - leucine - COOH.

   What is/are the possible sequence(s) of the corresponding template DNA?

   1. 3′-CAATTTAGCAGA-5′
   2. 3′-AGTCGGTTCGAT-5′
   3. 3′-AGACGATTTAAC-5′
   4. 3′-GTTAAATCGTCT-5′
   5. 3′-TCTGCTAAATTG-5′
   6. 3′-AGACGATTCGAC-5′

   A. 1 only
   B. 4 only
   C. 1, 4 and 5 only
   D. 2 and 3 only
   E. **2, 3, and 6 only**

7. Shown below is a portion of an mRNA stretch, starting at the start codon:
   AUG GGG AGU AAA UUU

   The DNA encoding this region would be correctly written as:

   A. 3′ ATGGGGAGTAAATTT 5′
   5′ TACCCCTCATTTAAA 3′

   B. **5′ ATGGGGAGTAAATTT 3′**
   3′ TACCCCTCATTTAAA 5′

   C. 5′ TTTAAATGAGGGGAT 3′
   3′ AAATTTACTCCCCTA 5′

   D. 3′ TTTAAATGAGGGGAT 5′
   5′ AAATTTACTCCCCTA 3′

8. What is the function of aminoacyl-tRNA synthetases?
   A. They catalyze the folding of the tRNA into a cloverleaf structure.
   B. They catalyze the modification of the bases in tRNAs.
   C. They catalyze the correct alignment of the mRNA codon with a tRNA anticodon.
   D. They catalyze peptide-bond formation between two amino acids.
   E. **They catalyze the covalent attachment of an amino acid to the correct tRNA.**

9. Which of the following statements about translation in bacteria are TRUE?
    1. Proteins called initiation factors contribute to the interaction between the RNA in ribosome small subunit at the 5’ cap.
    2. An internal sequence in the mRNA specifies where the ribosome binds.
    3. Complementary sequences in the tRNAs translate mRNA sequence into protein sequence .
    4. Some regions of the mRNA are removed before translation.
    5. A release factor ends protein synthesis by binding to the stop codon and to trigger the release of the polypeptide chain.

        A. 1, 2 and 3.
        B. 1, 3 and 4.
        C. 2 and 4.
        D. 2, 3 and 5.
        E. 2, 3, 4 and 5.

10. Cells use a two-step process (transcription and translation) to synthesize proteins from the information carried in the DNA, instead of directly translating information in the DNA to proteins. Which of the following statements could explain why this two-step process might benefit the cell?
    1) There are more places to control protein synthesis.
    2) More proteins can be produced in a given time period.
    3) Resolves the problem of the ribosomes being too large to interact with DNA.
    4) DNA does not need to have the sequence for the ribosome binding sites (RBS).
        A. **1 and 2.**
        B. 2 and 3.
        C. 3 and 4.
        D. 1, 2 and 3.
        E. 2, 3 and 4.

11. The following nucleotide sequence encodes the C terminus region of a wild type (also called “native” or “normal”) protein. The stop codon is underlined.

Native: 5'-GCCTCT**A**AAATCAGGAGAACACACTAA-3'
3’-CGGAGA**T**TTTAGTCCTCTTGTGTGATT-5'

The highlighted bases are mutated to the form below:

Mutant: 5'-GCCTCT**T**AAATCAGGAGAACACACTAA-3'
3’-CGGAGA**A**TTTAGTCCTCTTGTGTGATT-5'

Predict the consequence of this base change from A to T on the protein produced.
    a. **The mutation would result in a shorter protein**.
    b. The mutation would result in a different amino acid being inserted into the protein.
    c. The mutation would result in a longer protein.
    d. The mutation would not change the amino acid sequence of the protein.
    e. The mutation would change all the amino acid sequence in this region.

ORQ-Style Questions

12. Not all mutations in a protein coding region cause a change in phenotype. Explain giving 2 examples.
Example: If say a silent mutation will result in no change in phenotype then you must add that there is no change in the polypeptide and/or no change in the shape and function of the protein.
If you use base-substitution mutations for both examples then you must explain 2 different ways this can result in no change in phenotype.
Some examples…The genetic code is degenerate – some amino acids have more than one codon and a mutation in a codon can result in the same amino acid and no change in the protein.
Amino acid substitutions of similar types might not lead to a change in protein function or the substitution is present in the polypeptide chain that does not change the protein shape (folding) or function.

13. Each of the statements below is false. Re-write the statements to make them factually correct. You must re-write the statements for full points. Examples of changes we were looking for:

A. The nitrogenous base thymine is present in DNA and RNA, while uracil is present only in RNA. (F)
The nitrogenous base thymine is present in DNA while uracil is present in RNA in place of thymine.

B. A hydrogen atom is present on the 3' carbon of the ribose of DNA nucleotides, whereas a hydroxyl group is present at the same position on RNA nucleotides. (F)
A hydrogen atom is present on the 2' carbon the ribose of DNA nucleotides, whereas a hydroxyl group is present at the same position on RNA nucleotides.

C. Ribosomes transcribe RNA and RNA polymerase translates RNA.

Ribosomes translate RNA and RNA polymerase transcribes RNA.

14. The antibiotic called streptomycin is known to bind to the ribosome. Streptomycin distorts the ribosome structure so the ribosome does not stabilize the correct codon-anticodon base pairs. Instead, the ribosome stabilizes incorrect codon-anticodon base pairs.

Consider a ribosome where streptomycin is present during translation. Compared to normal translation, do you predict that the proteins being translated by the streptomycin-bound ribosome will have: ***(circle one)***

fewer mistakes **the same number of mistakes** **more mistakes**

Explain your choice in one short sentence.
Students should state the result when the ribosome stabilizes the wrong codon-anti-codon:
Eg The wrong tRNA will be able to H-bond (or recognize) the mRNA in the ribosome and this may add the wrong amino acid.
Therefore, mistakes will be observed due to incorrect amino acids in the protein's polypeptide sequence.

NOTE: Zero points for only re-stating "ribosome stabilizes incorrect codon-anticodon base pairs" as this is information given in the question.

15. The following DNA sequence is part of a transcribed region of a gene, and has a start codon in one of the strands only:

    5′ GCGTAATTGCCGCATTTCAATAA 3′
    3′ CGCATTAACGGCGTAAAGTTATT 5′

    a. Which is the template strand? TOP
    b. Which is the coding strand? BOTTOM
    c. Write out the mRNA sequence that will be synthesized from this sequence.
    5’-UUAUUGAAAUGCGGCAAUUACGC-3’
    d. Translate the mRNA sequence to protein: N-Met-Arg-Gln-Leu-Arg-C
    e. In the above sequence, if the underlined cytosine on the top strand is changed to G, what would happen to the product of transcription, and what would happen to the product of translation?
    The transcript would contain a C instead of a G at that position. No change to the protein product as the codons 5’-CGG-3’ and 5’-GGC-3’ both code for Argenine.

    f. What is meant when we say the genetic code is redundant? Explain with an example of a specific codon.
    Redundant: More than one codon can specify the addition of the same amino acid. E.g. Tyrosine has at least two codons. Or, the above example with Argenine.