Unit 2: Genome and Information flow from DNA to Proteins: Answers

Learning Objectives - Genomes and DNA Structure

- Discuss the diversity in genome sizes among organisms and if genome size is a good predictor of biological (organismal) complexity.
- Compare genome structure and arrangement in bacterial cells versus eukaryote cells.
- Explain the terms genotype and phenotype.
- Discuss in general terms the biological role of DNA as an information molecule for storage and transmitting genetic information.
- Describe and recognize the structural components of nucleic acids, including the monomers, the directionality, and the reason for the directionality.
- Label a schematic diagram of double stranded DNA to show the 3’ and 5’ ends, including the chemical group found at each 3’ and 5’ position.
- Know and apply the Chargaff’s (Watson & Crick) base pair rules.

1. **What interactions serve to stabilize/hold DNA together in its secondary/tertiary structure? Explain how this stabilizes DNA in its aqueous environment.**

2. **By convention how is the directionality of a DNA molecule written?**

3. **By convention how is the directionality of a protein molecule written?**

4. **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.

5. **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

6. **In a bacterium, 14% of the DNA nucleotides were found to be Thymine. What proportions of the other bases would you expect to be present in this particular DNA?**
   a. 28% G, 28% C, 28% A
   b. 36% G, 36% C, 14% A
   c. 14% G, 58% C, 14% A
   d. 58% G, 14% C, 28% A
   e. Cannot be determined.

7. **In normal double-stranded DNA, why are purines base-paired with pyrimidines?**
   a. Because a purine-purine pair would be too small, and a pyrimidine-pyrimidine pair would be too large
   b. Because the number of A must equal the number of T and the number of G must equal the number of C
   c. Because the strongest stacking interactions are found between purines and pyrimidines, making the DNA more stable
   d. Because purine-pyrimidine pairs maximize the number of hydrogen bonds, making the DNA more stable.
   e. Because 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 more compact than the genome of species A.
   d. Species B has more genes than species A.

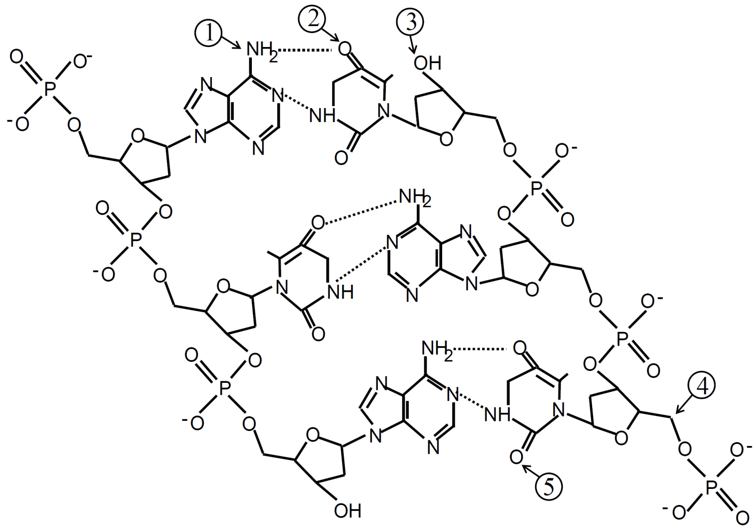
9. From a series of experiments, you determine the following information.

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 hereditary genetic material...

a. of species A is the largest.
b. of species B is the largest.
c. of species C is the smallest.
d. of species B contains the most protein coding genes.
e. More than one of the above can be concluded based on this information.

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

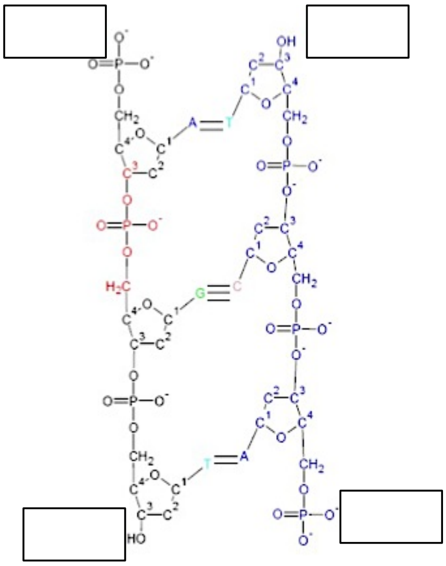
11. DNA is double stranded and the two strands are said to run in an antiparallel fashion. The term <u>antiparallel</u> refers to the observation that:

1. One strand of DNA is identical to the other but is simply the mirror image
2. One strand of DNA is complimentary to the other and they both run in the 5’ to 3’ direction.
3. One strand of DNA runs 5’ to 3’ while the other strand runs in the opposite direction from 3’ to 5’
   - A. 1 only
   - B. 2 only
   - C. 3 only
   - D. 1 and 2 only
   - E. 1 and 3 only

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.

13a. Label the ends of the two strands of DNA below to indicate their directionality (2 points)



13b. Indicate where a new nucleotide would be added if either of these strands were extended further. (1 point)

Learning Objectives - Polymerase Chain Reactions (PCR)

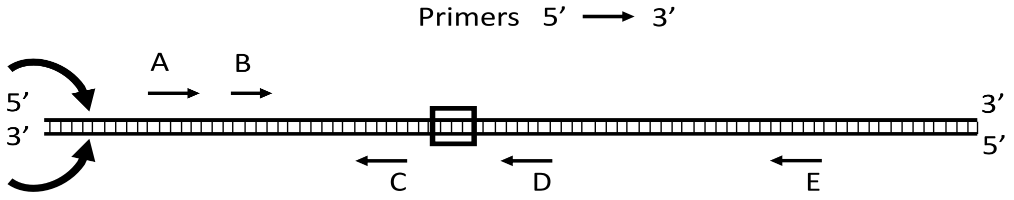
- Describe the process of polymerase chain reaction amplification of DNA including the role of each step.
- List the components needed (in a test tube) to start a PCR amplification experiment.
- Recognize the four deoxyribonucleotide triphosphates (dNTPs) used in DNA synthesis (dATP, dGTP, dCTP, dTTP)
- Predict at which ends for the DNA strands dNTPs will be added during DNA synthesis.
- Define DNA denaturation ("melting") and renaturation ("annealing"), and explain what role these play in the replication of DNA.
- Describe what is happening at each of the first 3 steps of a PCR experiment
- Predict what primers would be needed to amplify a given piece of double stranded DNA.
- Predict the products of an amplification reaction given locations of primers on a DNA.
- Discuss uses for the PCR reaction in biology and society.

1. **Compare and contrast DNA replication in cells and DNA amplification by PCR.**

2. **Below is the gene of interest that you wish to amplify by PCR. Design the primer pair (5bp each) to amplify this sequence. Indicate the 5' and 3' ends of the primers.**

5'-CCTTCTCGAGTTCCGTCCAGTTAAGCGTGACAGTCCCAGTGTACCCACAA-3'

3.



In the PCR reaction you add the template, dNTPs and the DNA polymerase.

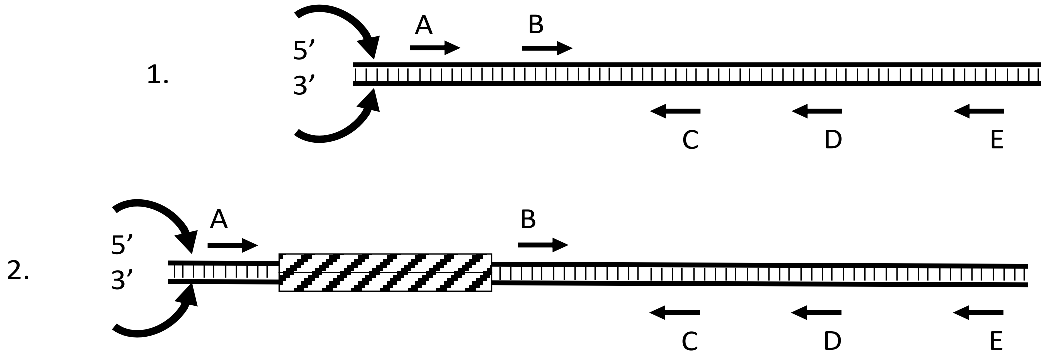
Q1. If you use primer A, adding which of the other primers will produce the smallest DNA product?

Q2. If you use primer B, adding which of the other primers will not product an amplified product?

Q3. Assume you amplified some DNA with primers B and D. If you want to use the amplified DNA as a template and primer C as one of the primers, what could be the primer other?

4.

Assume that DNA templates 1 and 2 are the same EXCEPT 2 has extra DNA sequences in between A and B.



You compare the amplified products you get using the two templates and primer D and one other primer.

Q1. Adding which second primer would give you different size products from template 1 versus template 2?

Q2. Adding which second primer would give you products that are not different from the two templates?

DNA Replication

- Explain the semi-conservative model of replication.
- Explain the logistics of the process of DNA replication including how the cell solves the problems of:
  - Separating the DNA strands.
  - Replicating both strands simultaneously in the 5' to 3' direction.
  - Synthesizing primers and providing primers for the leading and the lagging strands during replication (DNA synthesis).
  - Replicating the ends of the DNA.
- Distinguish between, and label the leading and the lagging strands of DNA in a replication fork.
- Explain what an Okazaki fragment is and its role in replication.
- Compare and contrast DNA replication in vitro (PCR) and in vivo (in cells).
- Describe and compare origins of replication in bacterial cells and eukaryotic cells.
- Explain how the ends of eukaryotic chromosomes are extended by telomerase and why this is necessary and important.
- List examples of DNA-protein interactions during DNA replication (DNA Polymerase, helicase, RNA primase, DNA ligase, telomerase).
- List the types of non-covalent interactions that enable interactions between DNA and DNA-binding proteins.

1. **Which of the following statements about DNA synthesis is true?**

   A. Nucleotides are added in a random fashion to single-stranded DNA
   B. DNA polymerase adds dNTP monomers in the 3' to 5' direction
   C. Primers are short sequences that allow the initiation of DNA synthesis by DNA Pol.
   D. As DNA polymerase moves along the template strand, each new nucleotide provides a 5' hydroxyl group for the next reaction to occur.

2. **Put the following steps of DNA replication on the lagging strand in chronological order.**

   A. Single-stranded binding proteins attach to the DNA strands.
   B. Hydrogen bonds between base-pairs of the DNA strands are broken.
   C. Primase binds to the single strand DNA.
   D. DNA polymerase elongates the primer.
   E. A short RNA primer is created.

3. **What is an advantage that bacteria have due to their circular DNA?**
   - A. They don't need to deal with Okazaki fragments.
   - B. The length of their DNA is not decreasing with each cell division
   - C. They don't need to unwind their DNA during replication.
   - D. They only need to replicate one of the strands.
   - E. They are quicker with their DNA replication.

4. **How does telomerase prevent the linear chromosome from shortening during replication?**

5. **The leading strand is the daughter strand that has its ____ end pointed toward the replication fork and is therefore synthesized ______.**
   - a. 3'; discontinuously
   - b. 3'; continuously
   - c. 5'; discontinuously
   - d. 5'; continuously
   - e. 5'; away from the fork

6. **What catalyzes DNA synthesis?**
   - A. DNA polymerase
   - B. RNA polymerase
   - C. Ligase
   - D. Primase
   - E. Gyrase

7. **Which of the following choices describes the function of DNA Polymerase?**
   - A. Opens up double-stranded DNA to make it single stranded.
   - B. Re-winds the old and new strand together after replication.
   - C. Catalyzes the linking of dATP, dCTP, dGTP and dTTP in a specific order, using single stranded DNA as a template.
   - D. Fuses intermediate length DNA segments into longer segments.

8. **A defect occurs during replication where DNA replication proceeds without the RNA primers being removed and replaced with DNA. Which enzyme is most likely to be defective in this system?**

   A. RNA primase
   B. helicase
   C. single strand binding protein
   D. a DNA polymerase
   E. DNA ligase

9. **In a DNA double helix an adenine of one strand always pairs with a(n)______ of the complementary strand, and a guanine of one strand always pairs with a(n)______ of the complementary strand.**

   A. guanine...adenine
   B. cytosine...uracil
   C. cytosine...thymine
   D. uracil...cytosine
   E. thymine...cytosine

10. **After DNA replication is complete,_________.**

    A. Each new DNA double helix consists of two new strands
    B. One DNA double helix consists of two old strands and one double helix consists of two new strands.
    C. There are four double helices
    D. Each of the four DNA strands consist of some old strand parts and some new strand parts.
    E. Each new double helix consists of one old DNA strand and one new DNA strand.

11. **An old DNA strand is used as a _____________ for the assembly of a new DNA strand.**

    A. Primer
    B. Complement
    C. Model
    D. Source of nucleotides
    E. Template

12. **When we say that DNA replication is semiconservative, we mean that:**

   A. only half of an organism's DNA is replicated during each cell division.
   B. when DNA is replicated, each new double helix contains one parental strand and one newly synthesized daughter strand.
   C. when DNA is replicated, one double helix contains both parental strands and one contains two newly synthesized daughter strands.
   D. parental DNA stays in the parent cell and daughter DNA ends up in the daughter cell.

13. **Describe three major challenges faced by both bacteria and eukaryotic cells in replicating their DNA, and how the challenges are overcome. Name one challenge faced by eukaryotes but not bacterial, and how they overcome this challenge.**

Errors and Repair during and after DNA replication

- Describe the origin of mutations through errors in replication.
- Describe mechanisms that cells have for correcting errors during replication (proofreading by DNA Polymerase), and why this is important for cells.
- Describe mechanisms that cells have for correcting errors after replication (e.g. mismatch, base excision, nucleotide excision repair).

1. **One of the DNA replication proteins/enzymes is altered in a way that it results in an increased rate of mismatched bases in the newly synthesized DNA strand. Which function is most likely to be disrupted?**

   A. the unwinding function of helicase
   B. the winding stress relief function of topoisomerase II
   C. the fragment joining function of DNA ligase
   D. the proofreading function of DNA polymerase
   E. the strand separation function of single-stranded binding protein

2. **Compare and contrast nucleotide excision repair and mismatch repair.**

DNA Mutations and their consequences

1 . **Which types of mutation could lead to the introduction of a new stop codon in a gene?**

A. Base pair substitutions
B. Insertions
C. Deletions

2. **The following is a partial sequence of the coding strand of a gene. The first base shown at the 5' end is the +1 site. A mutated form of this gene is shown below, including three point mutations (bold/underlined):**

Original gene: 5'- AAGGAGGUTTTGGCATGTTATATCATCGTTTGGGGGATGAGTAT-3'

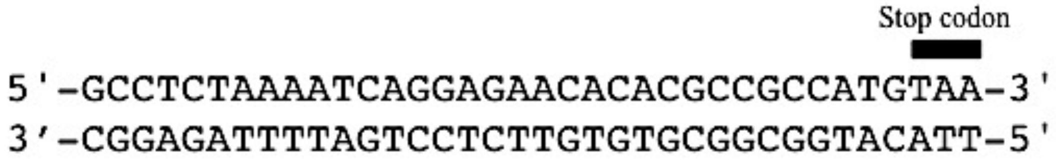
Mutant gene: 5'- AAGGAGGUTTTGGCATGTTATA**A**CATCGTTT**A**G**C**GGATGAGTAT-3'

A. **Of the three point mutations, which is a missense mutation? Explain your reasoning.**

B. **When this mutant gene is expressed, there is no functional protein product. Which point mutation is likely to be the reason for this phenotype? Explain your reasoning.**

3. **Why do mutations always spontaneously occur during growth of a population of cells?**

4. The following nucleotide sequence encodes the C terminus region of a Wild type protein.



5'-GCCTCTAAAATCAGGAGAACACACGCCGCCATGTAA-3'
3'-CGGAGATTTTAGTCCTCTTGTGTGCGGCGGTACATT-5'

In the mutant form of this gene in this region, a single base is changed from A to T as shown below:

5'-GCCTCTAA-'3 changed to 5'-GCCTCTTA-3' – Note: only the coding strand is shown here, but a corresponding complementary base mutation is on the template strand too.

Using the *genetic code table in the textbook for this,* 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.

Biological Information flow

- Describe the biological information flow from DNA to proteins in cells, and the role of transcription and translation in this process.
- Distinguish between the processes of replication, transcription, and translation.
- Describe the role of RNA molecules as a link between genes and proteins.

1. Transcription is the process of copying____ to_______

2. ________is the synthesis of _______from mRNA.

3. Compare and contrast the processes of DNA replication and transcription

4. Choose the *BEST* answer that explains the stable nature of double-stranded DNA structure compared to an RNA structure.

A. The sugar-phosphate backbone provides greater stability to DNA structure.
B. The H-bonds between complementary bases of the two strands is the reason for stability in DNA.
C. The strands are twisted around each other and can't get apart and this fact holds DNA in a stable manner.
D. Stacking interactions between neighboring bases of the same strands and H-bonds between complementary bases of the two strands make DNA more stable.
E. Covalent bonds between the nucleotides of the two strands in DNA are strongest bonds, making DNA structurally more stable than RNA.

Transcription

- Draw the structure of transcription units (a gene) in both bacteria and eukaryotes, clearly differentiating between regulatory and coding regions.
- Explain what a promoter of a gene (transcription unit) is.
- Identify a general promoter region on of a transcription unit (gene).
- Compare how proteins involved in transcription in bacteria and eukaryotes recognize a promoter.
- Define consensus sequences and their role in transcriptional control.
- Determine the consensus sequence from a simple data set.
- Explain the difference between the template strand and the non-template (coding) strand in DNA.
- Describe the role of RNA polymerase in transcription, and initiation of transcription.
- Compare and contrast the transcription units in bacteria and eukaryotes.
- Transcribe a mature mRNA from a transcription unit on a genomic DNA.

Transcription comparison:

Compare/contrast…	**Eukaryotes**	**Bacteria**
Chromosome structure		
Site of transcription		
How many RNA polymerase?		
What is the promoter feature?		
What are the proteins involved contacting the promoter?		
Is splicing (removal of introns) required?		

Capping and tailing of mRNA?		
Site of translation		
Can translation occur while transcription is still occurring?		

Transcript processing comparison:

Compare and contrast	**Eukaryotes**	**Bacteria**
Type of RNA polymerase		
Splicing (yes or no)		
RNA has 5’cap (yes or no)		
RNA has 3’ poly A tail (yes or no)		

1. **Which of the following *correctly* 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.

2. **The following is a list of regulatory sites that are partly identified by looking at nucleic acid sequences. Which of them are found in RNA as well as DNA?**

   1) Promoter
   2) Ribosome binding site
   3) Start codon

   a. 1 only.
   b. 2 and 3.
   c. 1 and 2.
   d. 1 and 3.
   e. All of the above

3. **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.

4. **What would happen to an mRNA in a eukaryotic cell if during RNA processing the poly A tail is not added?**
    a. Nothing. The tail is just a way to mark the 3' ends of the mRNA strand.
    b. The mRNA strand would circularize
    c. The mRNA strand would not 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.

5. **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 in the promoter 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 hairpin structure 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.

6. **How do DNA-binding proteins (such as sigma or transcription factors) specifically recognize the correct binding site on DNA? (Choose any/all that are true)**
    a. They make ionic interactions with the phosphodiester backbone of the DNA at the binding site.
    b. Part of their tertiary structure is similar (in size, shape, and charge/polarity) to the major or minor groove of that DNA sequence
    c. They interact with the major and minor groves of the DNA by binding to a specific sequence of bases
    d. They make specific covalent interactions with the DNA
    e. They interfere with the base-pair hydrogen bonds and stacking interactions to stabilize the DNA.

7. An intron is ______________________; and an exon is ________________.

a. Encodes for RNA that is removed during the processing of an mRNA molecule and leaves the nucleus; encodes for part of a 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. Encodes for RNA that is removed during the processing of an mRNA molecule and degraded in the nucleus; encodes part of a 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.

8. 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:

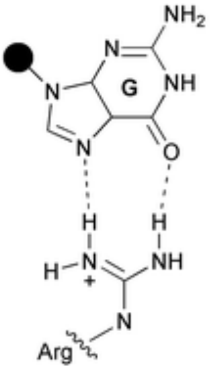
Position	**123456**
	TAGTCA
	AAGACA
	TTAAGA
	TGTCAT
	CTGAAC
	TAATCA
	TCGGCA
	TTTACA

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

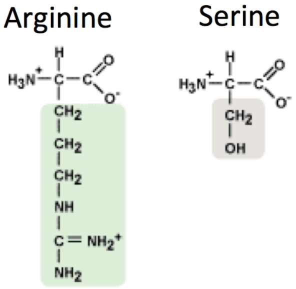
a. A
b. G
c. C
d. T
e. There is no consensus.

9. **Shown below is the interaction between an amino acid side chain (Arginine) in the sigma protein, and a nucleotide base (guanine) within the promoter of a gene.**

(To simplify the diagram, the other strand of DNA is present but is not shown, and the phosphodiester backbone is represented as the black circle. The protein backbone is represented as the squiggled line at the bottom, and only the end of the amino acid chain is shown.)



a. **If Arginine were replaced with by Serine in the protein (both 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.**



b. **Compared to the original situation: In the DNA sequence, if guanine were replaced by thymine (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.**

10. 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).

True/False statements:

T or F?	**Statement**
	a. During transcription, the transcript is synthesized 3' -> 5'for both gene 1 and gene 2
	b. The template strand for gene 2 is represented by the bottom strand.
	c. The +1 site (start of transcription) for gene 2 is downstream of its "T" (terminator).
	d. For gene 2, the top strand sequence is identical to its mRNA except T's will be U's.
	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. The coding strand for gene 1 is the top strand (5' –> 3')
	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.
	h. The top strand will always be the coding strand for all genes in this bacterium.
	i. The +1 site for gene 2 can be found upstream of T2.
	j. Both genes would share a ribosomal binding site.
	k. The template strand for gene 1 is represented by the top strand.
	l. For both genes 1 and 2, movement of RNA polymerase depends on the orientation of two different consequences sequences (-35 box and -10 box) on the promoter.

11. Polymerase comparison:

	DNA polymerase	RNA polymerase
Are primers required?		
Type of nucleotide required		
Direction of movement		
Process starts at which end:		

Types of RNA

- Compare and contrast the major types of RNA molecules: rRNA, tRNA, mRNA (and miRNA, siRNA).
- Compare the types of RNA polymerases found in bacteria and eukaryotes.
- List the various eukaryotic mRNA processing events – 5'-capping, splicing, and poly-adenylation (polyA tails).

1. Which of the following *distinguishes* bacterial mRNAs from human mRNAs?

A. Human mRNAs have 5' untranslated regions, but bacterial mRNAs do not.
B. Human mRNAs undergo splicing before translation but bacterial mRNAs do not.
C. Human mRNAs have several open reading frames, but bacterial mRNAs have only one.
D. Human mRNAs are transcribed by many RNA Pols but bacterial mRNAs by one RNA Pol.
E. Human mRNAs have several ribosomes binding to them, but bacterial mRNAs do not.

Translation

- List RNAs involved in the process of translation, and describe their roles.
- Explain the features of the genetic code as universal, redundant (degenerate) and non-overlapping.
- Explain the function of amino acyl tRNA synthetase enzymes and why they are described as "the translators" of the genetic information.
- Explain what is meant by "wobble" in tRNA binding.
- List the general components of a ribosome.
- Describe the general events in the three-step process of translation (initiation, elongation, and termination) and the directionality of translation.
- Compare translation initiation in bacteria and eukaryotes- Shine-Dalgarno sequence (ribosome binding site or rbs) versus 5' cap.
- Predict the anticodon of a tRNA for a given amino acid using the codon table.
- Translate a stretch of DNA coding sequence into its polypeptide sequence by identifying the correct Start and Stop codon for the translatable sequence.
- Identify the different types of mutations (point mutations, insertion/deletion mutations).
- Predict the effects of mutations in different locations (the genome, transcription units/gene, coding regions, non-coding regions, regulatory regions etc.).
- Predict the effect of different types of mutations on the protein.
- Predict the effect of different types of mutations on the genotype and phenotype of a cell.

1. **Given the following DNA sequence, with a start codon in one of the strands only:**

   5’ GCGTAATTGCCGCATTTCAATAA 3’
   3’ CGCATTAACGGCGTAAAGTTATT 5’
   *

   A. Which is the template strand?
   B. Which is the coding strand?
   C. Write out the mRNA sequence transcribed from it.

   D. Translate the mRNA sequence to protein:

   E. In the above sequence, if the nucleotide on the bottom strand with * is changed to G, what would happen to the product of transcription, and what would happen to the product of translation?

2. **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**AAATCAGGAGAACACACGCCGCCATGTAA-3'
   3’-CGGAGA**T**TTTAGTCCTCTTGTGTGCGGCGGTACATT-5'

   The highlighted bases are mutated to the form below:

   Mutant: 5'-GCCTCT**T**AAATCAGGAGAACACACGCCGCCATGTAA-3'
   3’-CGGAGA**A**TTTAGTCCTCTTGTGTGCGGCGGTACATT-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.

3. **Interaction between which two macromolecules sets the translation frame in bacteria?**
   - A. The ribosome and the tRNA.
   - B. The mRNA and the tRNA.
   - C. The ribosome and the rRNA.
   - D. The ribosome and the mRNA.
   - E. The tRNA and the initiation amino acid methionine.

4. **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.

5. **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

6. 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.

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. 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.

9. What is meant when we say the genetic code is redundant? Explain with an example of a specific codon.

10. **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.

11. **Which of the following describes what happens *during* peptide bond formation on the ribosome?**

A. The amino acid attached to the tRNA in the P site is transferred to the amino acid attached to the tRNA in the E site.
B. The amino acid attached to the tRNA in the P site is transferred to the amino acid attached to the tRNA in the A site.
C. The amino acid attached to the tRNA in the p site is covalently linked to the amino acid attached to the tRNA in the E site.
D. The amino acid attached to the tRNA in the P site is covalently linked to the amino acid attached to the tRNA in the A site.

12. **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 and the ribosomal binding site on the mRNA.
2) Initiation factors mediate the interaction between the N-formylmethionine aminoacyl tRNA and the AUG codon on the mRNA.
3) During elongation, tRNAs enter at the A site, move to the P site, then exit from the E site.
4) The RNA in the ribosome catalyzes formation of peptide bonds.
5) A release factor ends protein synthesis by binding to the stop codon and preventing the ribosomes from moving on the mRNA anymore.

a. 1, 3 and 5.
b. 1, 3 and 4.
c. 2 and 4.
d. 2, 3 and 5.
e. 2, 3, 4 and 5.

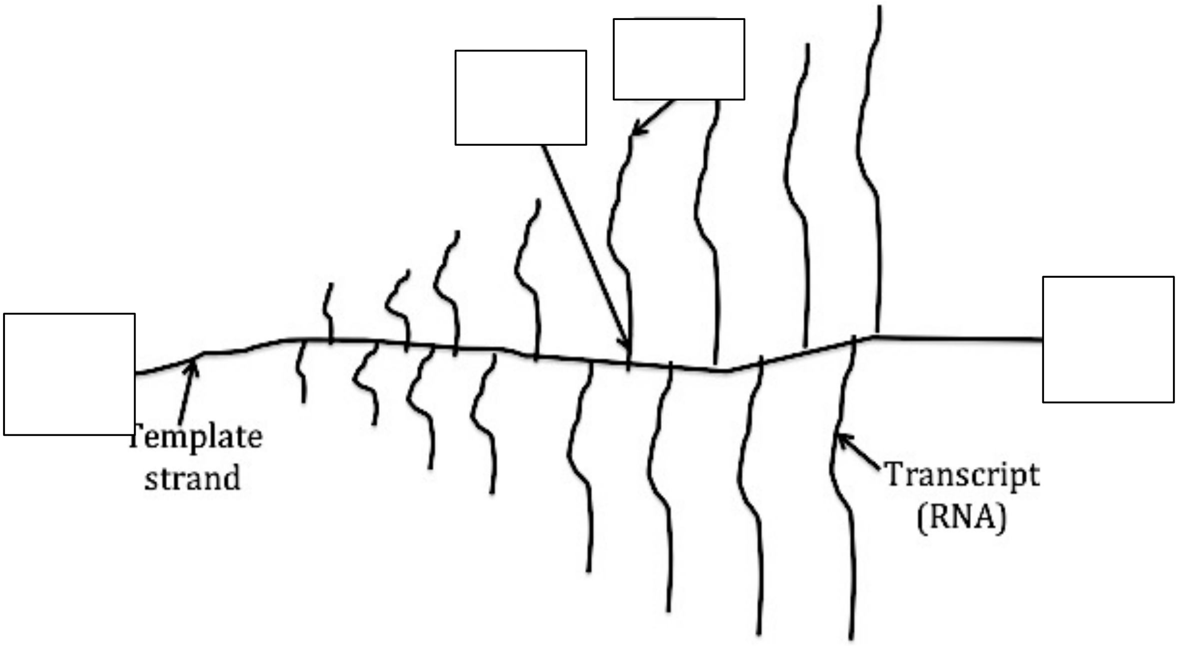
13. Cells use a two-step process (transcription and translation) to synthesize proteins from the information carried in the DNA, instead of directly translating information in the DNA to proteins. Which of the following features result from the two-step process?

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.

14. The cartoon below represents the process of transcription and translation as observed in an electron micrograph.

On the diagram below indicate the directionality (5' or 3') in the boxes against the structure.



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

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

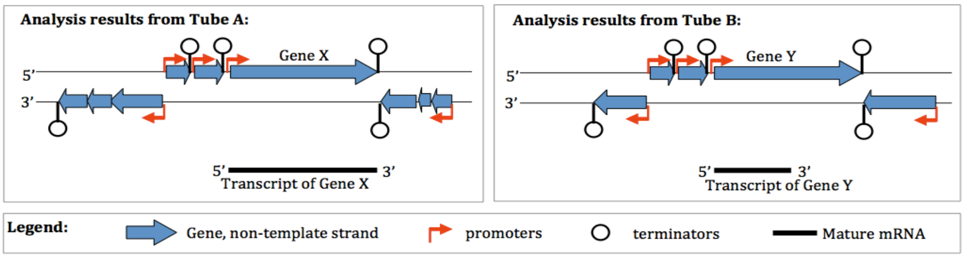
A. introns being spliced from eukaryotic mRNAs before translation.
B. the eukaryotic mRNAs needing a polyA tail to be translated.
C. the eukaryotic mRNAs needing a 5' cap to be translated.
D. the processed mRNA needing to be exported to the cytoplasm for translation.
E. the DNA needing to be decondensed in the nucleus before transcription.

17. 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)

Additional Open response Qs for practice:

Q1. You are visiting your cousin Vinny in Victoria where he has a job in a research laboratory studying two rainforest species: a species of frog, and a species of bacteria. Vinny is investigating the DNA sequences from both species – the samples are sent for analysis in one tube each. Unfortunately, the labels got mixed up, so Vinny does not know which tube contained which DNA sample.

Vinny shows you the analysis results he got using a computer program that finds coding regions on the DNA, and also one example of an mRNA molecule that will be transcribed (shown below). Both diagrams are on the same scale.



From this analysis, you tell Vinny that he can certainly figure out which DNA sample (frog or bacteria) was in which tube.

(a) Tube A contained DNA from which species?

Explain how you reached your conclusion (1 point)

(b) Tube B contained DNA from which species?

Explain how you reached your conclusion.

Q2. (2 points) Not all mutations in a <u>protein coding region</u> cause a change in phenotype. Explain giving 2 examples.

Q3. (3 points) Each of the statements below is false. Re-write the statements to make them factually correct.

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

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)

C. The DNA and RNA molecules in a cell are copied by replication before a cell divides. (F)

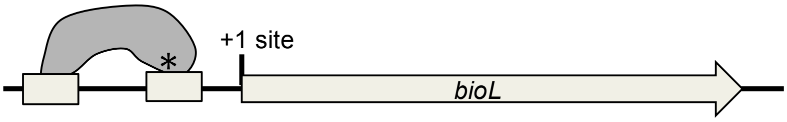
Q4. (2 points) The antibiotic called streptomycin is known to bind to the ribosome. Streptomycin distorts the ribosome structure so the ribosome does not stabilize the correct codon-anticodon base pairs. Instead, the ribosome stabilizes incorrect codon-anticodon base pairs

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)***

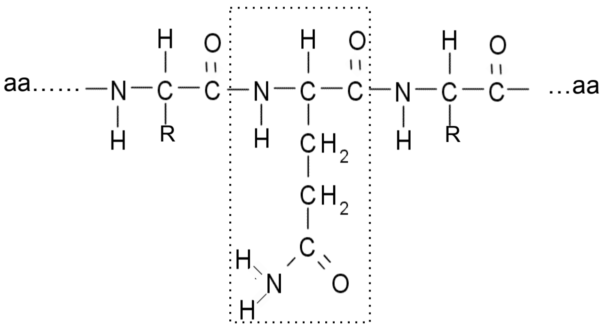
<u>fewer</u> mistakes　　the <u>same number of</u> mistakes　　<u>more</u> mistakes

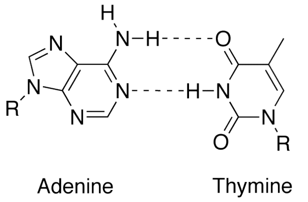
Explain your choice in one short sentence.

Q5. Experimental evidence has shown that a single <u>glutamine</u> amino acid residue (*) near the C-terminal end of the sigma factor protein (dark grey) is critical for its interaction with the TATAAT regulatory region of bacterial promoters, as shown in the diagram for gene *bioL* below.



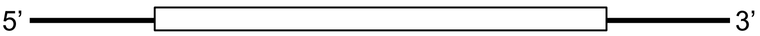
a. Shown below is a portion of the sigma polypeptide chain including the critical glutamine (boxed region). Indicate, by drawing lines on the diagram, <u>TWO</u> possible H-bonds that can form between atoms in the glutamine side chain and atoms in an adenine-thymine base pair. Note the sugar phosphate backbone is not shown, but its position is denoted 'R.'



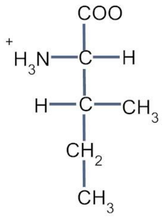


b. The diagram below represents the resulting mRNA transcript from gene *bioL*. Label on the diagram the following structures (use the abbreviations in brackets to label): (3 marks total - 0.5 marks for each correct label)

- Untranslated regions (UTR)
- Protein coding region (PC)
- Termination sequence (T)
- Ribosome binding site (RBS)
- Start codon (Start)
- Stop codon (Stop)



c. Predict what would be the effect of an amino acid substitution that replaced glutamine with isoleucine (shown below) on the amount of *bioL* gene expression in the bacterial cell. Briefly explain why.



Q6. In 1-2 statements, explain a major difference between how RNA polymerases and DNA polymerases function? (1 mark)