Part B - Modeling Transcription: How is RNA modified?  

Name: ____________________

Essential Question: What are the three ways that mRNA is modified after transcription?

Build the model:

Continuing on with learning about transcription, use your model from PART A to investigate and record the ways that mRNA is modified before it leaves the nucleus to proceed with the final phase of protein synthesis; translation.

With a partner:
1. Use mRNA segment from PART A: Remove the termination sequence and then, add the "second part of mRNA".
2. You should now have a transcribed molecule of RNA that is complementary to the hemoglobin gene DNA transcription unit.

   NOTE: the termination sequence does not get translated during protein synthesis in the cytoplasm.

   Draw the transcribed nucleotide sequence of the mRNA molecule below. Label the 5' and 3' ends.

   5' __________________________________________________________ 3'

   2. Read the following paragraph on two of the ways that mRNA is modified after transcription.

   Each end of a mRNA molecule is modified in a particular way. The 5' end, the end made first during transcription, is immediately capped off with a modified form of a guanine (G) nucleotide (G-triphosphate). This 5' cap has at least two important functions. First, it helps protect the mRNA from degradation by hydrolytic enzymes. Second, after the mRNA reaches the cytoplasm, the 5' cap functions as part of an "attach here" sign for ribosomes. The other end of an mRNA molecule, the 3' end, is also modified before the message exits the nucleus. At the 3' end, an enzyme makes a poly(A) tail consisting of some 50 to 250 adenine nucleotides. Like the 5' cap, the poly(A) tail inhibits degradation of the RNA and probably helps ribosomes attach to it. The poly(A) tail also seems to facilitate the export of mRNA from the nucleus.

   After reading: (1) make the changes to your model mRNA molecule to reflect this information.
   (2) re-draw the modified mRNA below.

   5' __________________________________________________________ 3'

   3. Read the following paragraph on third way that mRNA is modified after transcription.

   The most remarkable stage of RNA processing in the eukaryotic nucleus is the removal of a large portion of the RNA molecule that is initially synthesized—a cut-and-paste job called RNA splicing. The average length of a transcription unit along a eukaryotic DNA molecule is about 8,000 nucleotides, so the primary RNA transcript is also that long. But it takes only about 1,200 nucleotides to code for an average-sized protein of 400 amino acids. (Remember, each amino acid is encoded by a triplet of nucleotides.) This means that most eukaryotic genes and their RNA transcripts have long noncoding stretches of nucleotides, regions that are not translated. Even more surprising is that most of these noncoding sequences are interspersed between coding segments of the gene and thus between coding segments of the pre-mRNA. In other words, the sequence of DNA nucleotides that codes for a eukaryotic polypeptide is not continuous. The noncoding segments of nucleic acid that lie between coding regions are called introns.

   The other regions are called exons, because they are eventually expressed, usually by being translated into amino acid sequences. You may find it helpful to think of exons as DNA that exits the nucleus.

   In making a primary transcript from a gene, RNA polymerase transcribes both introns and exons from the DNA, but the mRNA molecule that enters the cytoplasm is an shortened version. The introns are cut out from the molecule and the exons are joined together to form an mRNA molecule with a continuous coding sequence. This is the process of RNA splicing. Particles called small nuclear ribonucleoproteins, or snRNPs (pronounced "snurps"), recognize these splice sites. As the name implies, snRNPs are located in the cell nucleus and are composed of RNA and protein molecules. Several different snRNPs join with additional proteins to form an even larger assembly called a spliceosome. The spliceosome interacts with the splice sites at the ends of an intron. It cuts at specific points to release the intron, then immediately joins together the two exons that flank the intron.

   4. Your model has actually been spliced already. The sketch you made in step 2 is of mRNA that consists of continuous exons spliced together after having the sections of introns cut out.

   As a final step you will draw what the original mRNA would have looked like with stretches of introns interspersed between the stretches exon nucleotide segments, before RNA splicing occurred. The sequence of the genome that contains the hemoglobin gene consists of nucleotides 62,137 - 63,660. The first nucleotide in your segment is 62137. Make up the combination of nucleotides in the introns (A,G,C,U).

<table>
<thead>
<tr>
<th>Exon #1</th>
<th>Intron #1</th>
<th>Exon #2</th>
<th>Intron #2</th>
<th>Exon #3</th>
</tr>
</thead>
<tbody>
<tr>
<td>↓ mRNA nucleotide sequence ↓</td>
<td></td>
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Questions:
1. List and briefly summarize the three ways that mRNA is modified after transcription.

2. Draw a cartoon that shows a mRNA that has not been spliced labeling the exons and introns and the process of splicing. Be sure to include snRNPs and spliceosome.

Take the quiz
1. In eukaryotic cells, transcription cannot begin until:
   - a. the two DNA strands have completely separated and exposed the promoter.
   - b. the appropriate transcription factors have bound to the promoter.
   - c. the 5’ caps are removed from the mRNA.
   - d. the DNA introns are removed from the template.
   - e. DNA nucleases have isolated the transcription unit from the noncoding DNA

2. Which of the following is not true of a codon?
   - a. It consists of three nucleotides.
   - b. It may code for the same amino acid as another codon does.
   - c. It never codes for more than one amino acid.
   - d. It relates to both DNA and RNA.
   - e. It is the basic unit of the genetic code.

3. Which of the following is not true of RNA processing?
   - a. Exons are excised and hydrolyzed before mRNA moves out of the nucleus.
   - b. The presence of introns may facilitate crossing over between regions of a gene that code for polypeptide domains.
   - c. Ribozymes may function in RNA splicing.
   - d. RNA splicing may be catalyzed by spliceosomes.
   - e. A primary transcript is often much longer than the final RNA molecule that leaves the nucleus.

8. Using the genetic code table identify a possible 5’ 3’ sequence of nucleotides in the DNA template strand for an mRNA coding for the polypeptide sequence Phe-Pro-Lys.
   - a. UUU-GGG-AAA
   - b. GAA-CCC-CTT
   - c. AAA-ACC-TTT
   - d. CTT-CGG-GAA
   - e. AAA-CCC-UUU

HW: p. 249 # 1, 3 - 6, 10