STUDY GUIDE - *Ch. 17.3 - Eukaryotic Cells Modify RNA After Transcription* **NAME:** _____

- **PHYSICALLY PRINT OUT this PDF and HANDWRITE (with a black or blue pen) your answers directly on this PDF.** *Typed or digitally-written work is **not** accepted. Do **not** answer questions on separate paper.*
- **Importantly, study guides are NOT GROUP PROJECTS!!!** *You, and you alone, are to answer the questions as you **read** your assigned textbook. You are **not** to share answers with other students. You are **not** to copy any answers from any other source, including the internet.*
- **Get in the habit of writing LEGIBLY, neatly, and in a medium-sized font.** *AP essay readers and I will skip grading anything that cannot be easily read so start perfecting your handwriting, and don't write so large you can't add all the relevant details and key elaborations in the space provided.*
- **SCAN physical documents in color and with good resolution. Then, upload your final work as PDFs to Archie.** *Avoid uploading dark, shaded, washed-out, sideways, or upside-down scans of homework. Keep completed physical study guides organized in your biology binder to use as future study and review tools.*
- **READ FOR UNDERSTANDING and not merely to complete an assignment.** ***First**, read a section quickly to get an overview of the topic covered. Then, read it a **second** time slowly, paraphrasing each paragraph **out loud** and analyzing every figure. Finally, read it a **third** time as you answer the study guide questions if assigned and start building your memory. Try to write answers out in your own words, when possible, and try to purposefully and accurately use all new terminology introduced.*

NOTE: In prokaryotes, the primary transcript (produced in the **cytoplasm**) **IS** the **mRNA** that ribosomes will translate into a polypeptide for the building of a protein. This isn't the case in Eukaryotes, where the primary transcript made, the **pre-mRNA**, is **NOT** the final transcript, the mRNA, that will be translated by ribosomes in the cytoplasm.

Let's learn exactly how eukaryotic cells modify the RNA after DNA transcription and before RNA Translation starts.

1. The modification of pre-mRNA to make mRNA which occurs in **EUKARYOTES** (but not bacteria) is called **RNA Processing**, which involves making changes to the beginning, ending, and middle of the pre-mRNA initial transcript. Where does RNA Processing occur in the cell?

2. **Eukaryotes modify pre-mRNA before the final mRNA is ready to be sent to the cytoplasm for translation**. What three alterations occur during **RNA processing**? Name the addition or the event, and describe the details of what changes are made or what takes place. *Describe what happens during each modification **and** where in the pre-mRNA transcript the modification occurs.*

   1. Name of modification (at 5′ end of the pre-mRNA transcript) = _____

   Description of modification and/or process =

   2. Name of modification (at 3′ end of the pre-mRNA transcript) = _____

   Description of modification and/or process =

   3. Name of modification (in the middle of the pre-mRNA transcript) = _____

   Description of modification and/or process =

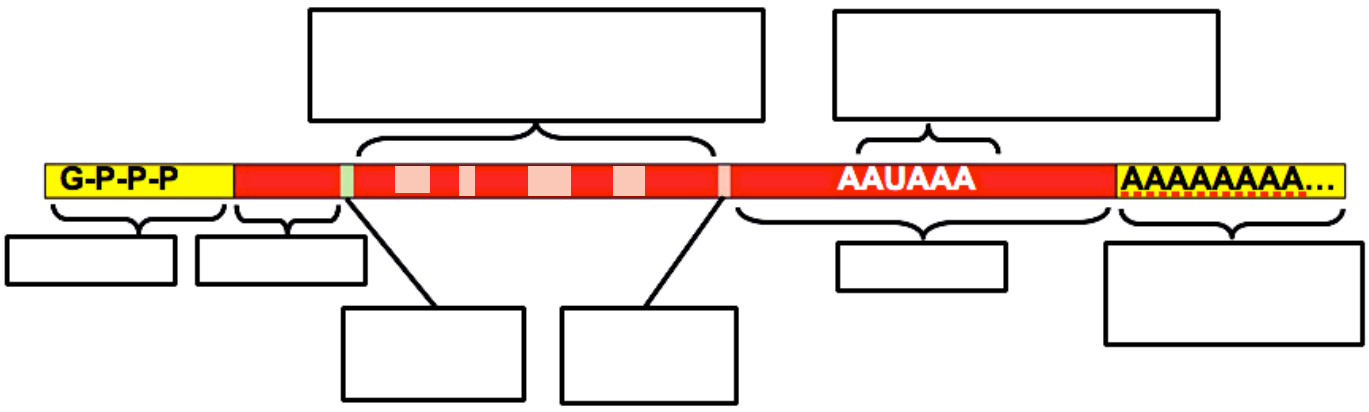
3. a. *Think:* Study **Figure 17.11**. Based on what you learned about all the parts of a gene in **Ch.17 Section 1** and which parts of the processed mRNA shown in Figure 17.11 are **NOT** found in the original DNA, draw below, as large as possible and horizontally, the DNA that would correspond to the mRNA shown in Figure 17.11.

Draw two horizontal, parallel lines representing the two strands of the DNA molecule of the chromosome. Label all parts of your drawing, make sure your DNA gene contain a **Promoter region**, the **Transcription Start Point**, the **Polyadenylation Sequence**, which helps with the termination of transcription. Make sure your Polyadenylation Sequence in the DNA is complimentary and antiparallel to what it should end up being in the pre-mRNA that would be transcribed from your DNA gene.

Finally, make sure you have also labeled correctly the **5′ and 3′ ends** of your two DNA strands *(remembering again that RNA polymerase can only build RNA in the 5′ to 3′ direction)* and have also labeled the **template and coding (non-template) DNA strands of the gene**.

b. Next, draw the pre-mRNA below that results immediately following DNA transcription by RNA Polymerase, and prior to any RNA processing. Label the 5′ and 3′ ends, the 5′ and 3′ UTRs, the region with the coding sequences that ribosomes will eventually translate into a protein (polypeptide of a protein), and the Polyadenylation Sequence.

c. Finally, label the figure below, showing what the pre-mRNA looks like following **partial RNA Processing,** after the **5′ Cap and 3′ Poly-A Tail have been added**.



4. What are **the three important roles** of the **5′ cap** and **poly-A tail** added to the ends of the mRNA transcript?

   1.

   2.

   3.

5. **Remember exons EXit the nucleus so the majority of them are referred to as coding sequences both in the pre-mRNA and final mRNA as well as in the original DNA gene's transcription unit** *(these **coding SEQUENCES** are NOT to be confused with the non-template, **coding STRAND** of the DNA double helix, the DNA strand that isn't transcribed during DNA transcription)!* **Remember too that introns stay IN the nucleus and so can be referred to as intervening or noncoding sequences.**

   Distinguish between **introns** and **exons** with regards to **how they influence the primary structure of the protein** (the amino acid sequence in the polypeptide) the ribosome will build.

   Introns =

   Exons =

6. a. What are the **5′ and 3′ UTRs**?

   b. Do the nucleotides that make up the UTRs code for amino acids in the polypeptide the ribosome will build?

   c. What is their **function** (especially that of the **5′ UTR**)?

   c. Are the UTRs considered intronic or exonic DNA (and after transcription) pre-mRNA sequences?

7. a. Read your text and **study Figure 17.12 & 17.13**. Explain **what happens during the part of RNA Processing known as RNA Splicing** again?

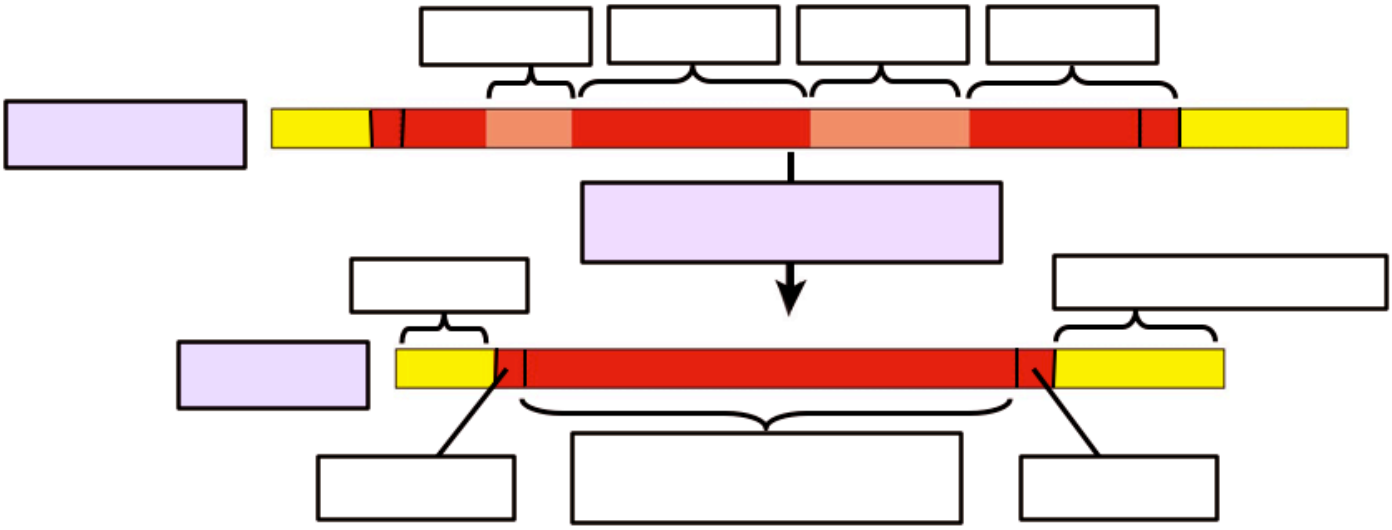
   b. The **spliceosome is the large complex of macromolecules that removes introns, degrades introns, and splices together exons in the pre-mRNA.** Which two types of macromolecules are **spliceosomes made up of**?

c. Though not mentioned in your textbook, the RNA involved in the structure of the spliceosome is called **small nuclear RNA or snRNA**. SnRNAs associate with proteins to form smaller complexes known **snRNPs**. SnRNPs bind to the start and ending regions of introns in the pre-mRNA. Then, the individual snRNPs all are brought together, causing the intron to loop out *(form a lariat),* the entire complex of snRNPs together now called a **spliceosome** *(the body that does splicing).*

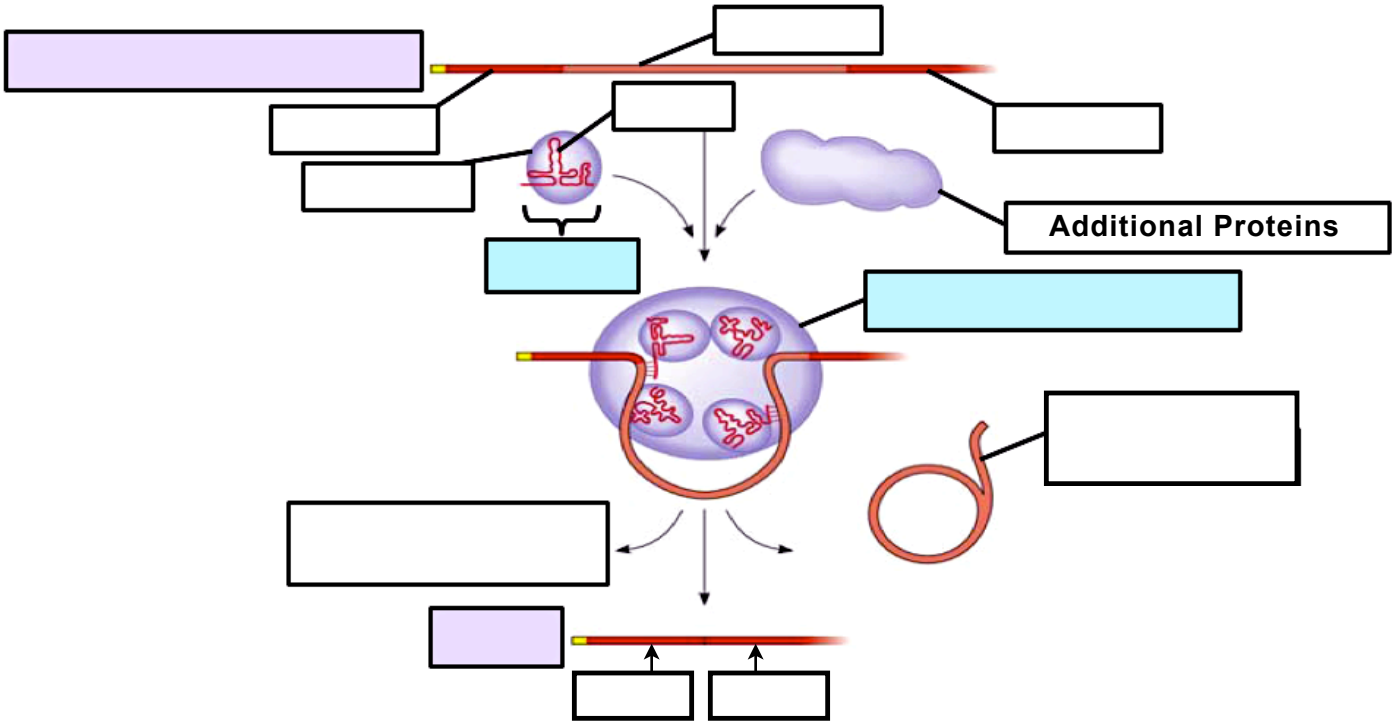
RNA splicing involved doing **hydrolysis** reactions to break the phosphodiester covalent bonds connecting the introns to the exons in the pre-mRNA RNA. It also involves doing **dehydration synthesis** reactions when building phosphodiester covalent bonds to connect the exons together. (*Notice that the introns are **NOT** removed from the DNA gene itself).*

What is so interesting about the **role of the small nuclear RNA** that make up the snRPS that make up the entire spliceosome?

8. a. Once you feel you understand RNA Splicing well and have studied carefully Figure 17.12, test your memory by trying to label the diagram below showing the the results of **RNA Splicing in Eukaryotes.**



b. Now let's see if you understood the **make up and action of Spliceosomes** by trying to label the diagram below. Check yourself for accuracy when you're done.



9. Variations in how RNA Splicing happens can be found in different species. In some organisms, proteins aren't involved at all in the structure of the spliceosome, only snRNA molecules being present. In other organisms, even the snRNA molecules are missing, the intronic RNA itself acting as the catalyst in the removal of introns and splicing together of exons during RNA Splicing.

   a. What are **ribozymes**?

   b. What commonly held **idea was rendered obsolete** by the discovery of ribozymes?

   c. What are **three properties of RNA that allow it to function as an enzyme**? *This is important to understand as scientists currently think RNA catalysts (ribozymes) **evolved first**, prior to protein catalysts (enzymes) in the history of life on Earth.*

      1.

      2.

      3.

10. Now that you understand the idea of DNA transcript and RNA Processing in Eukaryotes well. Think carefully about the following questions. Review the information you just read through i you are not sure until you are positive of your answers. *AP Free Response Questions like asking these types of questions.*

   a. Do you expect the **pre-mRNA** to be close in nucleotide length to the **transcriptional unit** of the gene **in the DNA**? *Why or why not?*

   b. Do you expect the **pre-mRNA** to be close in nucleotide length to the **entire gene** - promoter and transpirational unit combined - **in the DNA**? *Why or why not?*

   c. Do you expect the **mRNA** sequence to be close in nucleotide length to the **transpirational unit of the gene in the DNA in PROKARYOTES**? *Why or why not?*

   d. Do you expect the **mRNA** sequence to be close in nucleotide length to the **transpirational unit of the gene in the DNA in EUKARYOTES**? *Why or why not?* (**FYI:** Though the illustrations in your textbook (like Figure 17.12) show very few introns in the transcriptional unit of a Eukaryotic gene. In reality, **introns make up 40%, on average, of the transcriptional unit of a gene,** the **average length of a Eukaryotic transcriptional unit being around 27,000 nucleotides or base-pairs long**. In higher-level eukaryotes, intronic sequences may make up 10x more DNA than exonic sequences do. Remember too that the **5' GTP cap is one nucleotide long** and the **Poly-A tail tens to be between 50-250 nucleotides long**.)

e. Would you find **complimentary nucleotides in the DNA template of the gene for the 5′ (methylated) GTP Cap**? *Why or why not?*

f. Would you find **complimentary nucleotides in the DNA template of the gene for the 3′ Poly-A Tail**? *Why or why not?*

g. Would you find **complimentary nucleotides in the DNA template of the gene for the introns in pre-mRNA**? *Why or why not?*

h. Would you find **complimentary nucleotides in the DNA template of the gene for the exons in pre-mRNA and mRNA**? *Why or why not?*

i. Would you find **complimentary nucleotides in the DNA template of the gene for the 5′ UTR in the pre-mRNA and mRNA**? *Why or why not?*

j. Would you find **complimentary nucleotides in the DNA template of the gene for the 3′ UTR in the pre-mRNA and mRNA**? *Why or why not?*

k. Based on what you learned in **Ch.17 Section 1** about our **genetic code** *(and how nucleotides in mRNA code for the amino acids),* why is it that the **average mRNA is a few thousands bases/nucleotides long** (*after* RNA Processing edits out several tens of thousands of nucleotides that were copied from the original DNA gene), but the t**ypical Eukaryotic protein is only a few hundreds of amino acids long**?

11. a. It turns out, not all exons have to be left in the final mRNA. What occurs during **alternative RNA splicing** of identical pre-mRNA transcripts of the same gene?

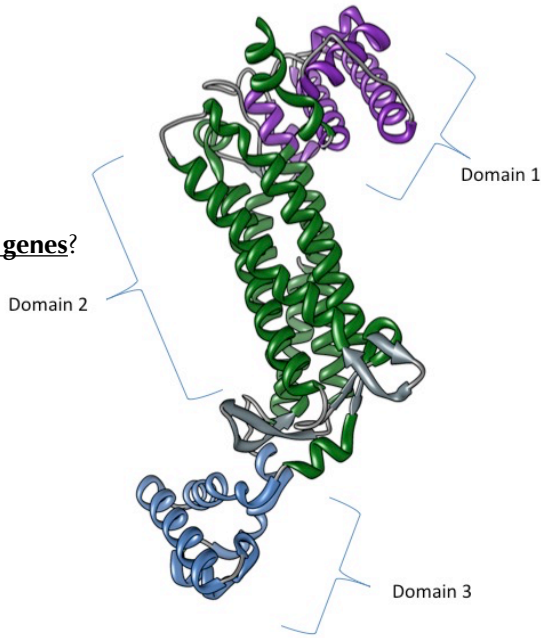
b. Why is it important?

c. Assume a gene has a total of 9 exons. Two alternates for exon 3 and three alternates for exon 5 exist among these 9 total exons. During RNA Splicing, one of the two possibilities for exon 3 will be treated as an "intron" (and removed from the pre-mRNA) while the other is treated as an exon. Similarly, two of the three possibilities for exon 5 will be treated as "introns" while the other option is treated as an exon. Six total exons always end up in the final transcript (mRNA) of this gene, including one version of exon 3 and one version of exam 5. How many different polypeptides could be made from this one gene through **Alternative Splicing**.

12. a. What are **domains** of a protein?

b. what are some **examples of domains of a protein**?

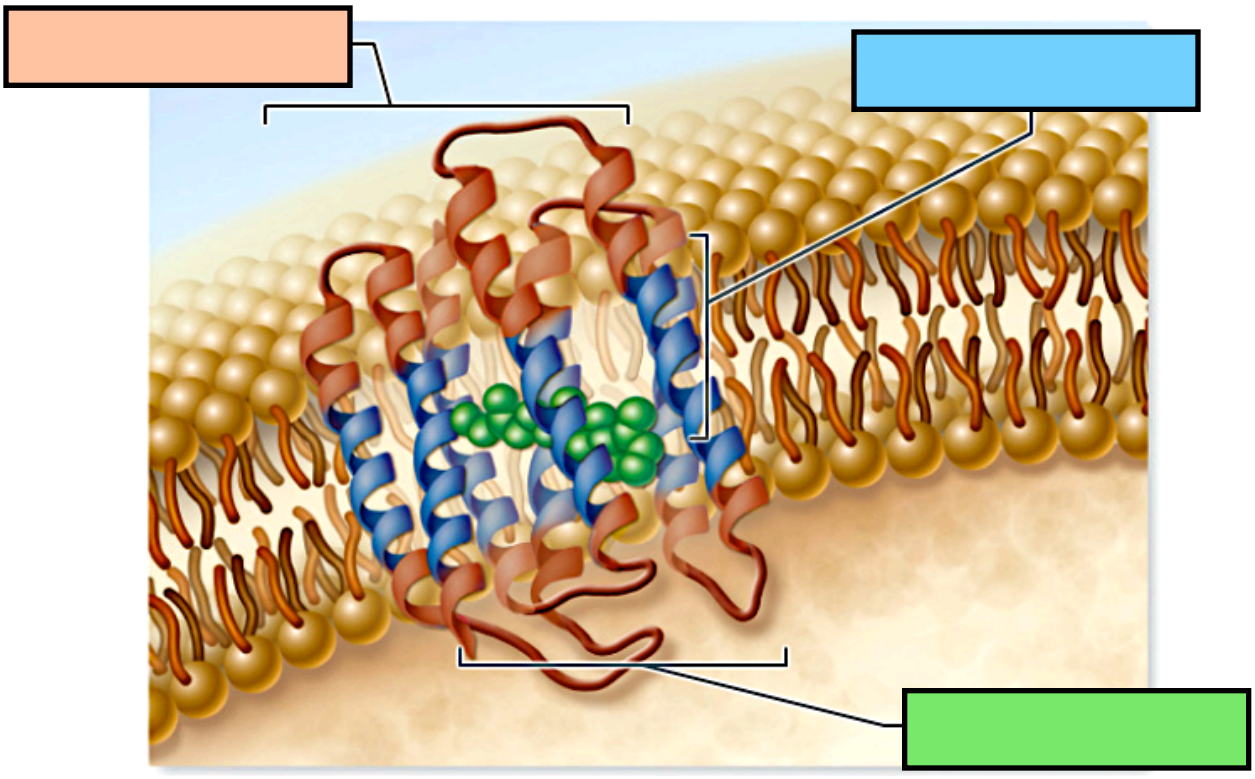
c. Review Figure 17.14. How do protein **domains correlate to exons in the genes**?



d. The image below is of a transmembrane protein with three domains highlighted in different colors. This transmembrane protein lacks quaternary structure. **(Review the levels of protein folding in Ch.5!!!).** Changes in the DNA sequences (mutations) of the transcriptional unit of the gene that encodes the instructions ribosomes use to build the polypeptide that then folds up to form this transmembrane protein, with its three functional domains, would potentially alter the primary structure of the polypeptide. **Altering primary structure** (the polypeptides amino acid sequence), **could alter secondary and/or tertiary structure of this protein. Alteration of protein folding** (not to mention the fact that some amino acids and their R groups may now be missing, added, or replaced with amino acids containing R groups that have **different chemical properties**) **can, therefore, alter a domain's (and thus the protein's) ability to carry out its function.**

Label the three domains of this transmembrane protein. *(The options are found at the top of the image).*

Transmembrane domain | Cytoplasmic domain | Extracellular domain



13. a. What is **exon shuffling**?

b. How does **exon shuffling** occur?

c. What may be the evolutionary **benefit of exon shuffling**?

14. Given that there are about 20,000 human protein-coding genes, how can humans make 75,000 to 100,000 type of final proteins. *(Besides what you learned in question #11 above, remember that a polypeptide is built from a gene and that proteins can be made up of one or more polypeptides)*

15. What would be the effect of treating a cell with an agent that removed the methylated 5′ GTP cap from the Eukaryotic mRNA? *(Check your answers by going to the Ch.17.3* ***Concept Check Question #3*** *in Appendix A of your textbook)*