Transcription & Modifications Activity

1. Cut out strips of DNA and tape them in order into one long strand of DNA. This is the template strand. (*DO NOT cut off empty boxes*)

2. Cut out blank strips of mRNA and tape them in order into one long strand

Draw a transcription factor, label the promoter region and transcription unit & take a picture.

3. Write the appropriate RNA nucleotides that would be transcribed from the template strand of DNA onto the paper strand of **pre-mRNA**. Remember that the promoter region is NOT transcribed.

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:

4. Make the changes to your model mRNA to reflect this information.

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. 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 a 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 flanked the intron.

5. Make the changes to your model mRNA to reflect this information. (The introns are the shaded regions).

6. Now your mRNA is ready to leave the nucleus ☺

Take a picture