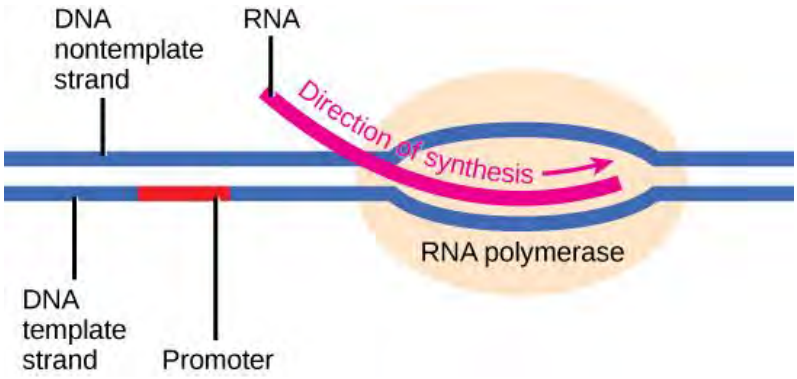

Figure 10.23 The initiation of transcription begins when DNA is unwound, forming a transcription bubble. Enzymes and other proteins involved in transcription bind at the promoter. (credit: Fowler et al. / Concepts of Biology OpenStax)

Elongation

Transcription always proceeds from one of the two DNA strands, which is called the template strand. The mRNA is complementary to the template strand and is almost identical to the other DNA strand, called the non-template strand. The two big exceptions are that RNA nucleotides contain the sugar ribose while DNA nucleotides contain the sugar deoxyribose, and that RNA contains the nitrogenous base uracil (U) instead of the thymine (T) found in DNA. During elongation, an enzyme called **RNA polymerase** proceeds along the DNA template adding RNA nucleotides by base pairing with the DNA template in a manner similar to DNA replication. As elongation proceeds, the DNA is continuously unwound ahead of the enzyme and then rewound behind it (Figure 10.24).

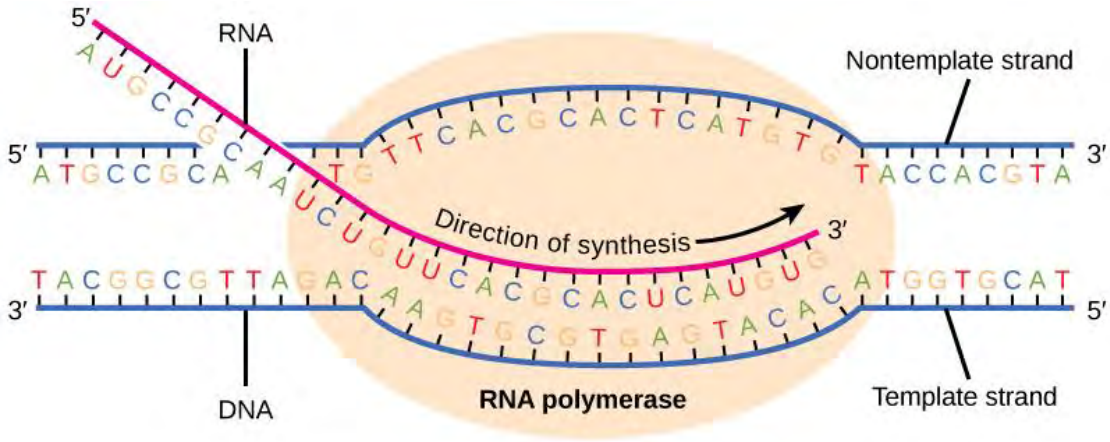

Figure 10.24 During elongation, RNA polymerase tracks along the DNA template, synthesizes mRNA in the 5' to 3' direction, and unwinds then rewinds the DNA as it is read. (credit: Fowler et al. / Concepts of Biology OpenStax)

Termination

When the polymerase has reached the end of the gene, the RNA polymerase needs to be instructed to dissociate, or separate, from the DNA template strand. Once the RNA polymerase

dissociates, the newly made mRNA transcript is released. Depending on the gene being transcribed, there are two kinds of termination signals, but both involve repeated nucleotide sequences in the DNA template. These repeated sequences cause the RNA polymerase to stall, separate from the DNA template, and free the newly synthesized mRNA.

At the end of termination, the process of transcription is complete. In a prokaryotic cell, by the time termination occurs, the mRNA is already being used to synthesize numerous copies of the encoded protein. This is possible because prokaryotic cells do not have their DNA enclosed in membrane bound nuclei. As soon as the mRNA is partially synthesized, ribosomes attach and begin generating the protein (Figure 10.25). Because of their nucleus, this is not possible for eukaryotic cells. Once the mRNA has been synthesized and undergoes modifications it must first be moved out of the nucleus and into the cytoplasm before translation can begin. This prevents simultaneous transcription and translation in eukaryotic cells.

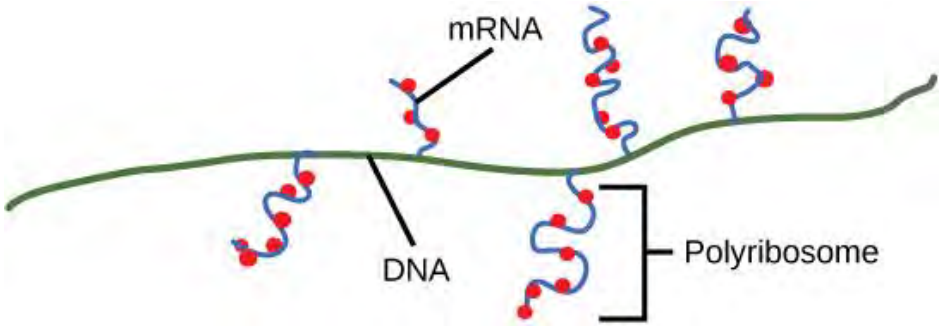

Figure 10.25 Multiple polymerases can transcribe a single bacterial gene while numerous ribosomes concurrently translate the mRNA transcripts into polypeptides. (credit: Fowler et al. / Concepts of Biology OpenStax)

CONCEPTS IN ACTION – Observe transcription at this site.

Eukaryotic RNA Processing

The newly transcribed eukaryotic mRNAs are referred to as primary transcripts. These primary transcripts must undergo several processing steps before they can be transferred from the nucleus to the cytoplasm and then translated into a protein. The additional steps involved in eukaryotic mRNA maturation create a molecule that is much more stable than a prokaryotic mRNA. For example, eukaryotic mRNAs last for several hours, whereas the typical prokaryotic mRNA lasts no more than five seconds.

The mRNA transcript is first coated in RNA-stabilizing proteins to prevent it from degrading while it is processed and exported out of the nucleus. This occurs while the mRNA transcript is still being synthesized and involves adding a special nucleotide “cap” to the 5' end of the growing transcript (Figure 10.26). In addition to preventing degradation, factors involved in protein synthesis recognize the cap to help initiate translation by ribosomes.

Once elongation is complete, an enzyme then adds a string of approximately 200 adenine nucleotides to the 3' end, called the poly-A tail (Figure 10.26). This modification further protects the mRNA transcript from degradation and signals that the mRNA transcript is ready to be exported to the cytoplasm.

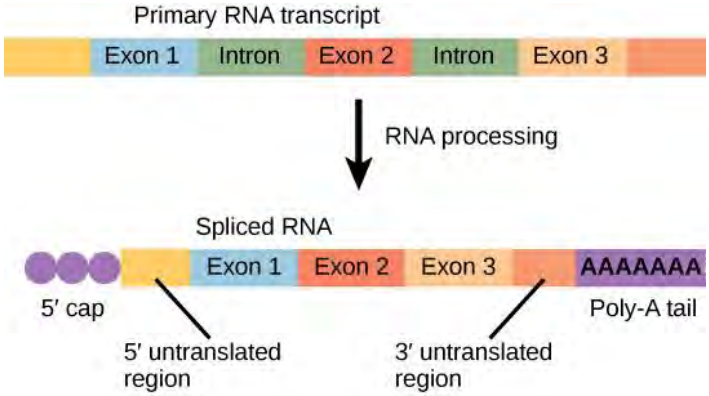

Figure 10.26 Eukaryotic mRNA contains introns that must be spliced out. A 5' cap and 3' tail are also added. (credit: Fowler et al. / Concepts of Biology OpenStax)

Eukaryotic DNA, and thus complementary mRNA, contains long non-coding regions that do not code for amino acids. Their function is still not well understood, but the process called **splicing** removes these non-coding regions, called **introns**, from the mRNA transcript (Figure 10.27). The non-coding regions are called introns because they are *int*ervening sequences. The coding regions are called **exons**; *ex*-on signifies that they are *ex*pressed.

A **spliceosome**, a structure composed of various proteins and other molecules, attaches to the mRNA transcript and "splices" or cuts out the non-coding, introns. The remaining exons are pasted together to form the mature mRNA which will then be transported to the cytoplasm.

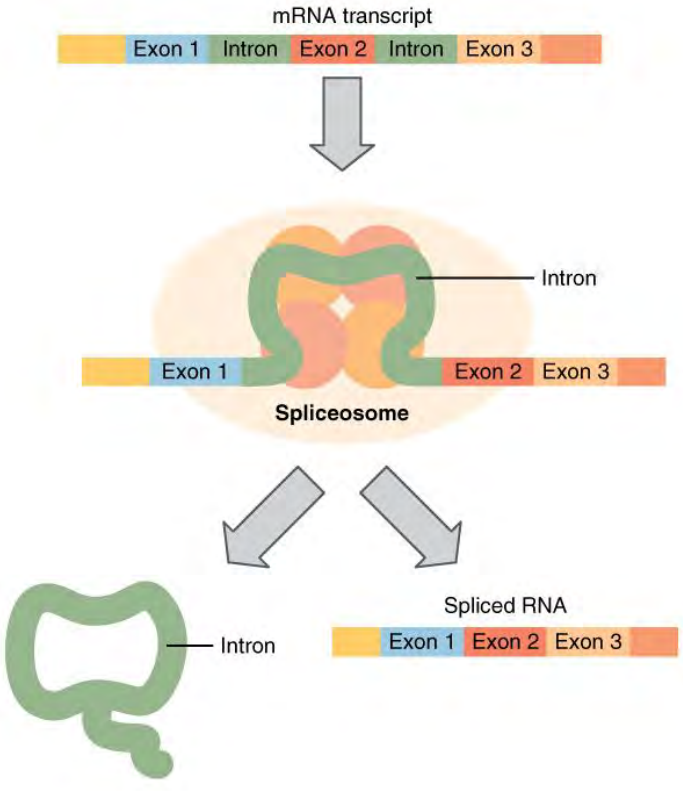

Figure 10.27 Splicing DNA in the nucleus, a structure called a spliceosome cuts out introns (noncoding regions) within a pre-mRNA transcript and reconnects the exons. (credit: Betts et al. / Anatomy and Physiology OpenStax)