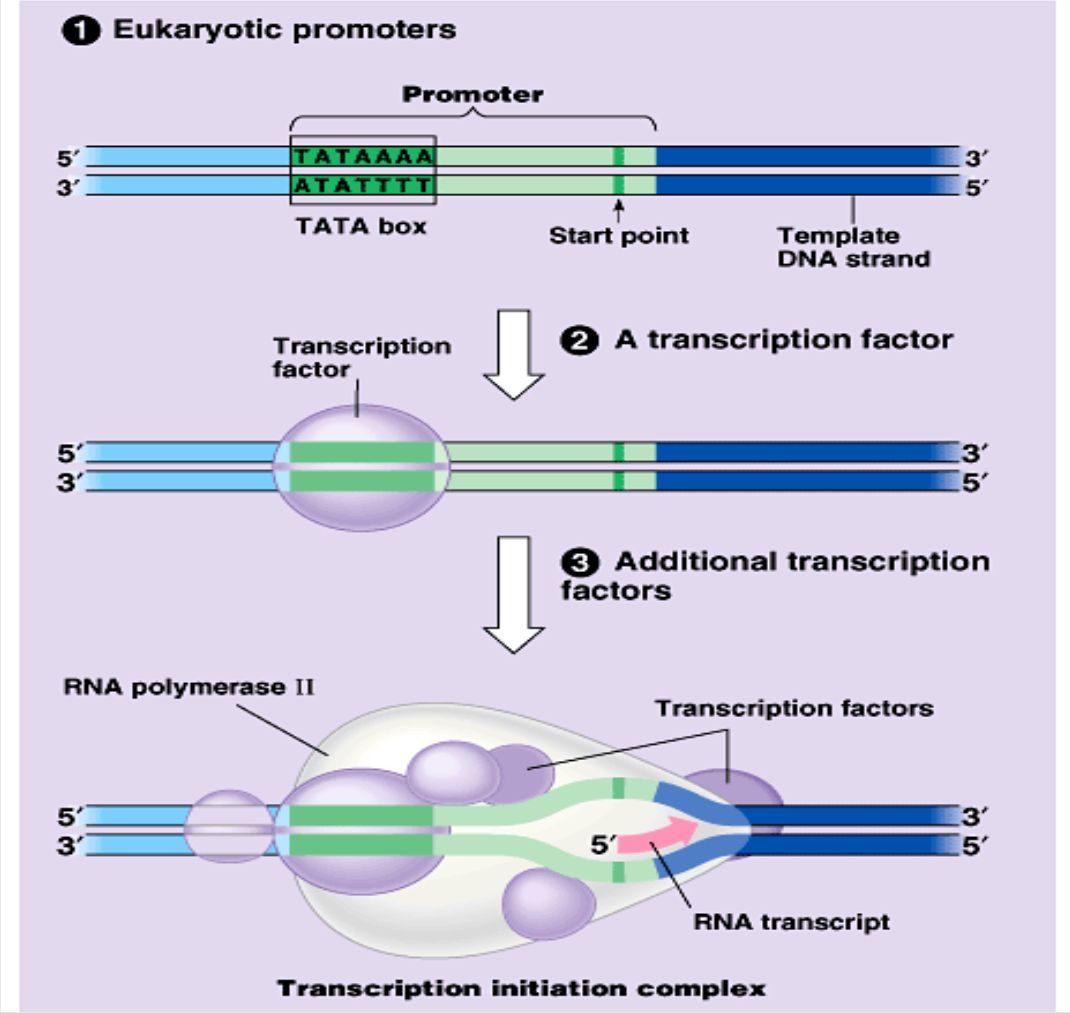
Aim: How is DNA transcribed in eukaryotes?

Initiation of eukaryote transcription

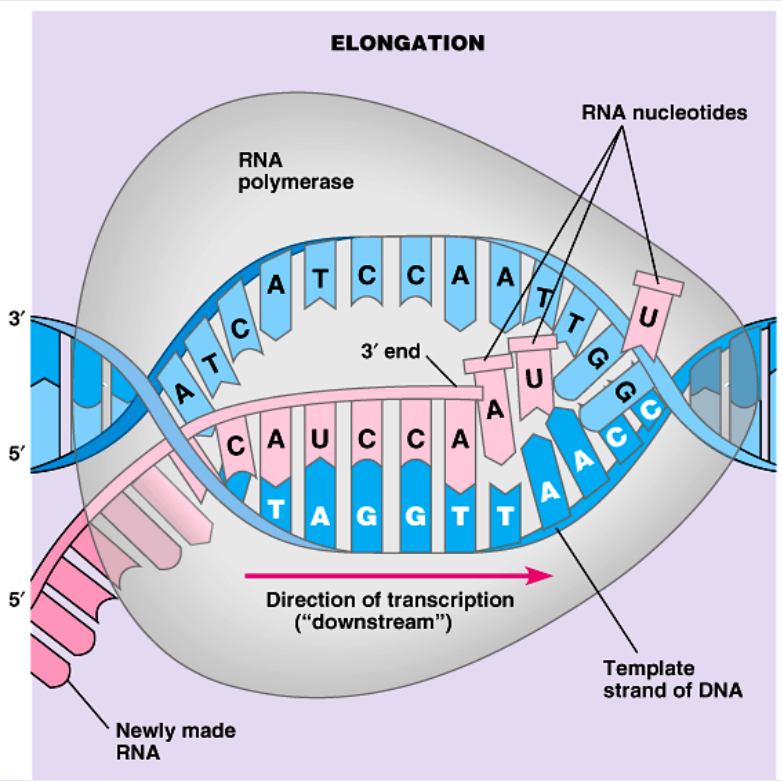
- DNA transcription in eukaryotes is much more complex than in prokaryotes.
- Before RNA polymerase can bind to DNA promoter sites, a special group of proteins called *transcription factors* must bind first.
- Transcription factors + RNA polymerase make up a *transcription initiation sequence(complex)'*
- Promoter DNA includes 3' ATATTT….5'

Initiation of eukaryote transcription



Elongation of eukaryote transcription

- Depending on the type of RNA being synthesized, an RNA polymerase moves along the DNA strand in a 3’ to 5’ direction, adding complimentary RNA nucleotides.

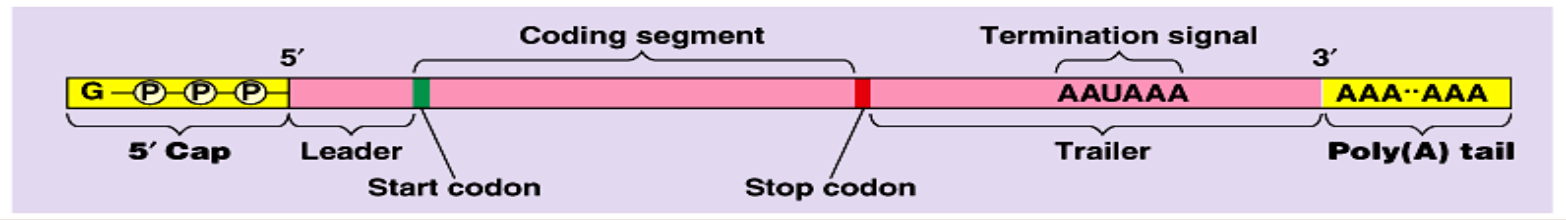


Elongation of eukaryote transcription

- Transcription continues hundreds of nucleotides past the termination signal, AAUAAA.
- Enzymes finally cut the new RNA strand about 10 – 35 base units beyond the termination signal.
- More than one RNA polymerase may transcribe the DNA at a time. This creates many mRNA molecules.
- Eukayrotic RNA is first processed into a rough draft called the primary transcript or pre-mRNA. This is edited and capped before leaving the nucleus.

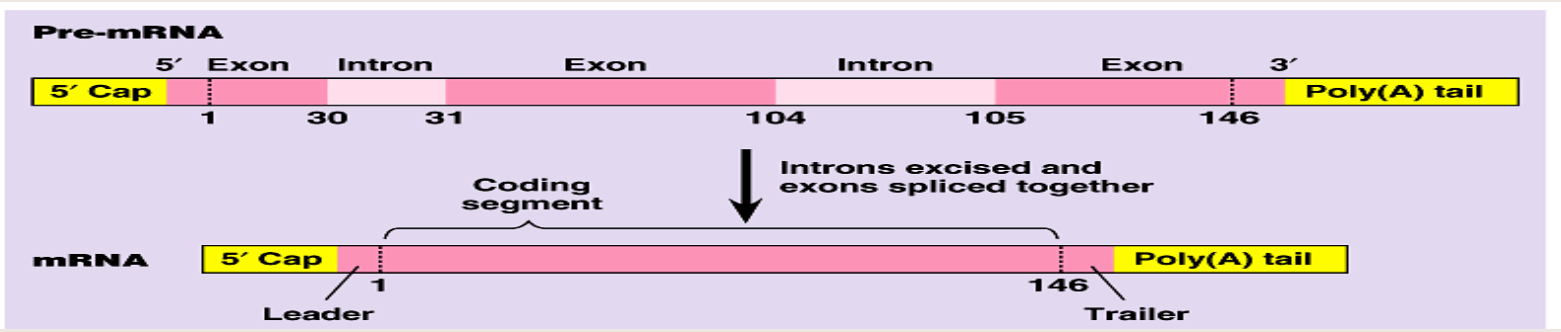
How is the primary transcript modified?

- The ends of the RNA are capped.
- 1) A 5’ CAP = 7 methyl guanasine is added to the 5’ end of the new RNA.
- 2) polyadenine tail is added to the 3’ end of the new RNA. (50 to 250 adenines)
- Both caps protect the RNA from being hydrolyzed by enzymes. They act as attachment sites for ribosomes during translation. The poly A tail helps the RNA leave the nucleus.



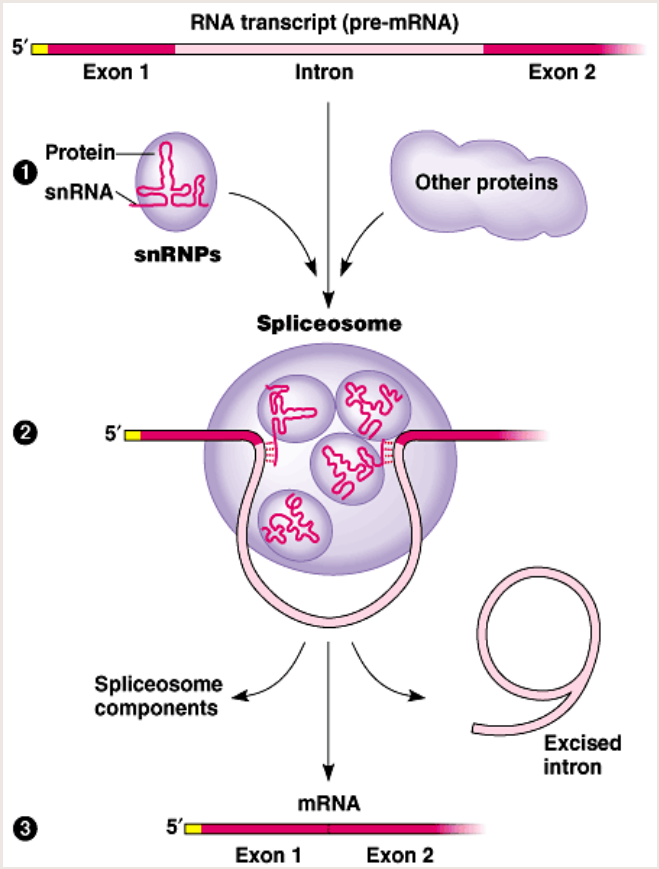
How is the primary transcript modified?

- Exons contain RNA code necessary to make a polypeptide product. Introns are non-code sequences of RNA that must be removed.
- Discovered by Philip Sharp and Richard Roberts who won the Nobel Prize in 1993
- Introns must be removed before RNA can leave the nucleus.

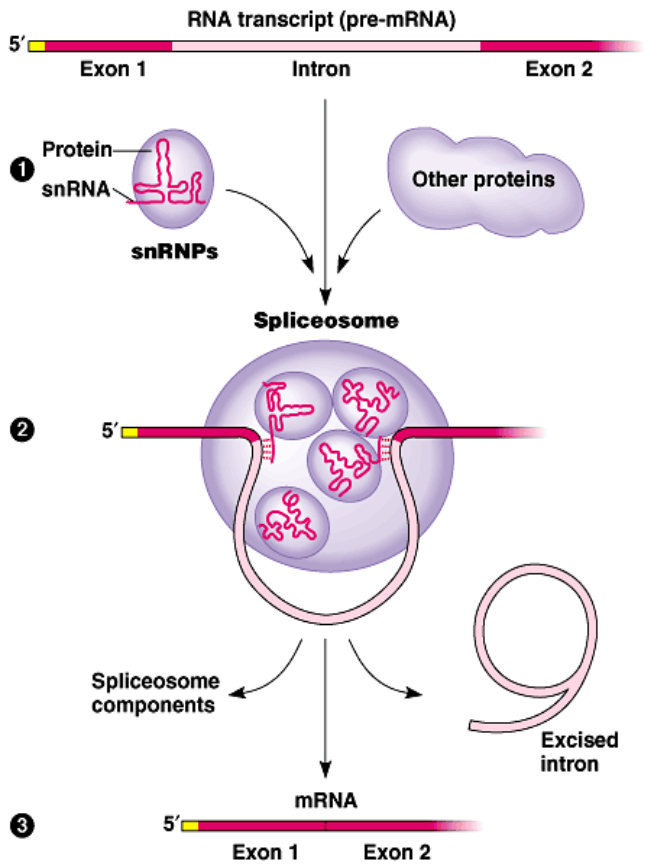


RNA splicing

- RNA splicing removes introns and joins exons to create an mRNA molecule with a continuous coding sequence.
- This splicing is accomplished by a **spliceosome**



RNA splicing

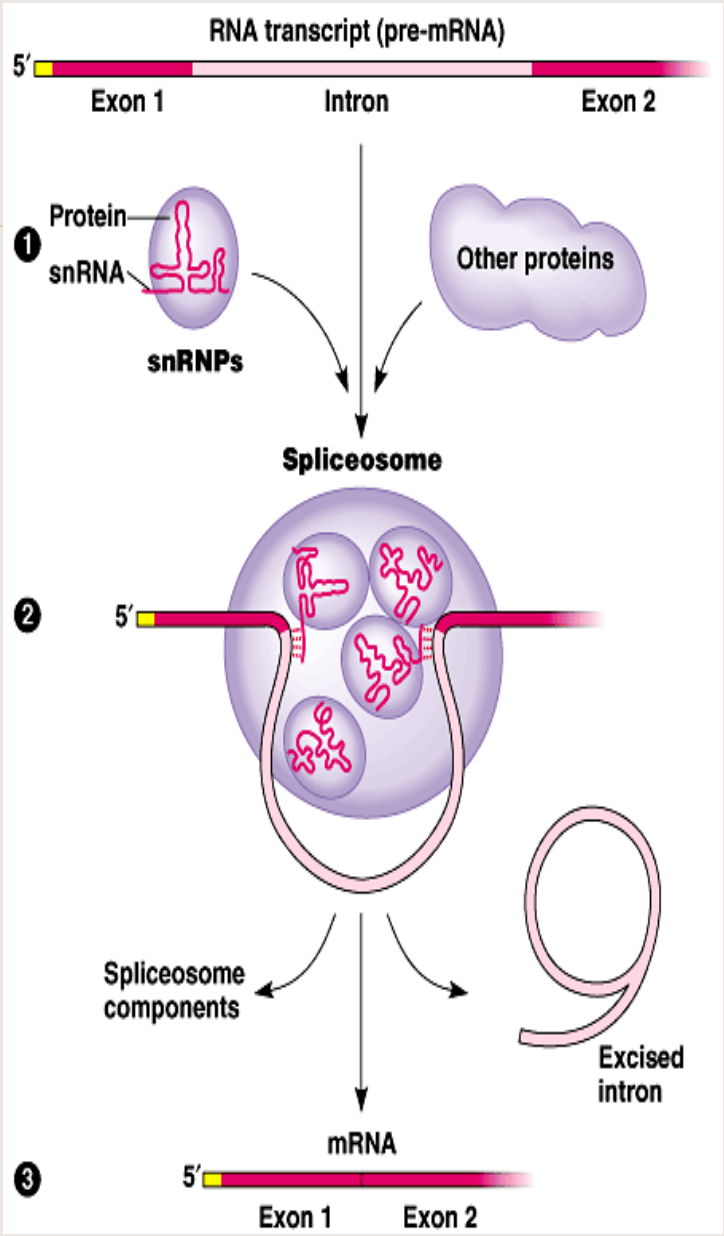


- spliceosomes consist of a variety of proteins and several *small nuclear ribonucleoproteins* (*snRNPs*).
- Each snRNP has several protein molecules and a *small nuclear RNA molecule* (*snRNA*).
  - Each is about 150 nucleotides long.

(1) Pre-mRNA combines with snRNPs and other proteins to form a spliceosome.

(2) Within the spliceosome, snRNA base-pairs with nucleotides at the ends of the intron.

(3) The RNA transcript is cut to release the intron, and the exons are spliced together; the spliceosome then comes apart, releasing mRNA, which now contains only exons.



- In this process, the snRNA acts as a **ribozyme,** an RNA molecule that functions as an enzyme.
- RNA splicing appears to have several functions.
  - First, at least some introns contain sequences that control gene activity in some way.
  - Splicing itself may regulate the passage of mRNA from the nucleus to the cytoplasm.
  - One clear benefit of split genes is to enable a one gene to encode for more than one polypeptide.