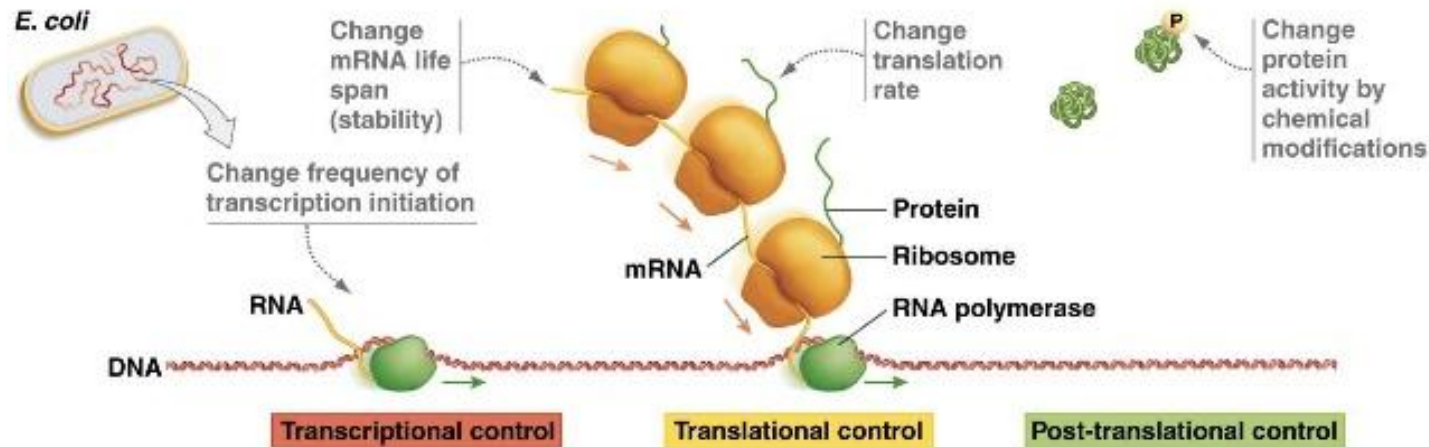


Gene Expression

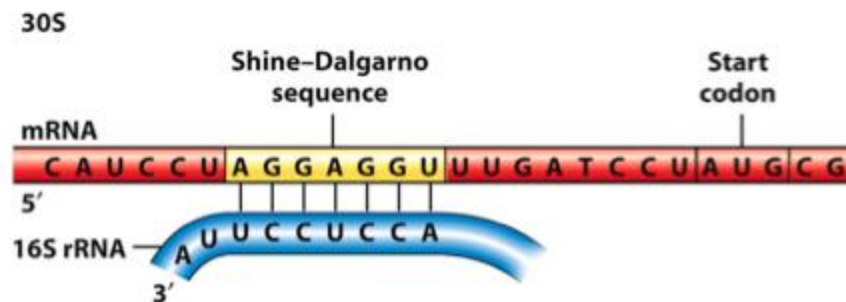
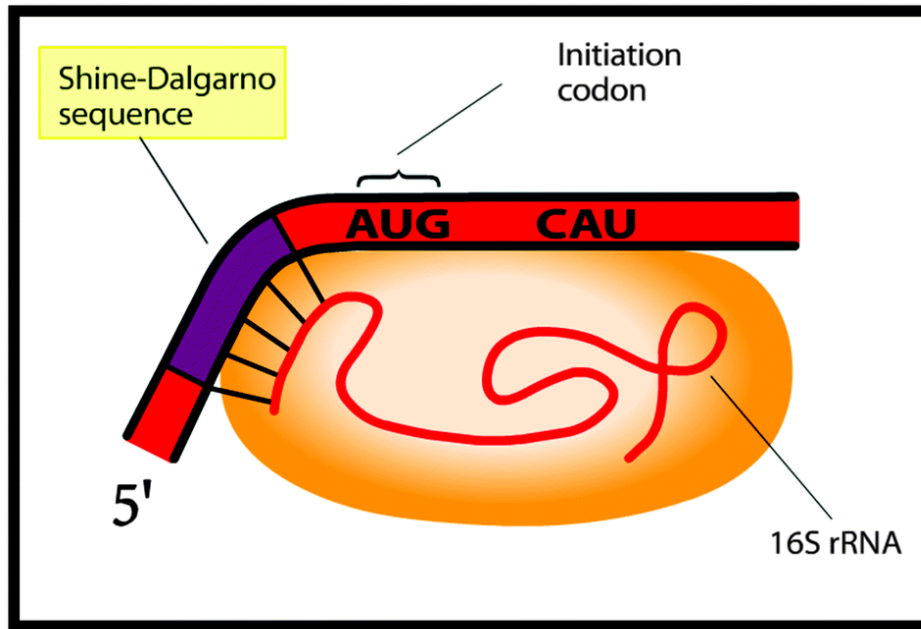
Regulation of Gene Expression



- Gene expression can be regulated:
 - During transcription (transcriptional control).
 - During translation (translational control).
 - After translation (post-translational control).

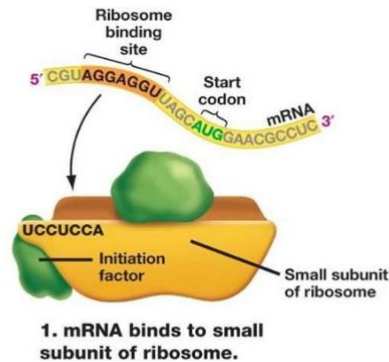
Translational control in prokaryotes

- In prokaryotes translation begins with binding of ribosome to a specific sequence in the messenger RNA - Shine-Dalgarno (SD) Sequence. SD is a ribosomal binding site generally located around 8 bases upstream of the start codon AUG. The six-base consensus sequence is AGGAGG. It is complementary to a specific region of 16S ribosomal RNA.



Translation initiation in bacteria

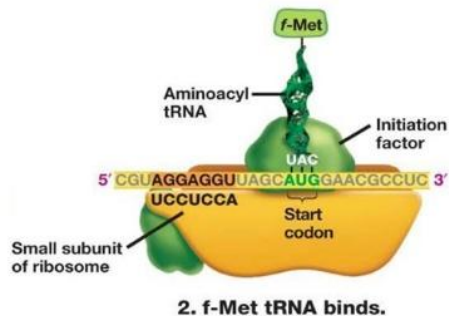
Shine-Dalgarno sequence



Translation initiation in bacteria

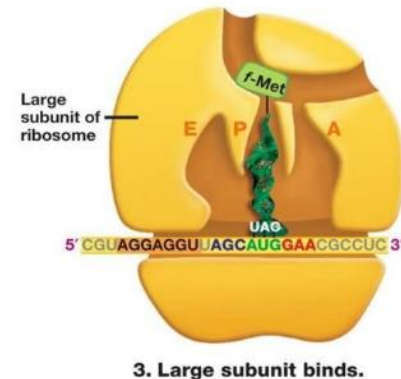
Initiator tRNA in bacteria

1. The initiator tRNA (fMet-tRNA) gets carried to the complex (30S ribosome + IF1 + IF3) by initiation factor IF2 using GTP.



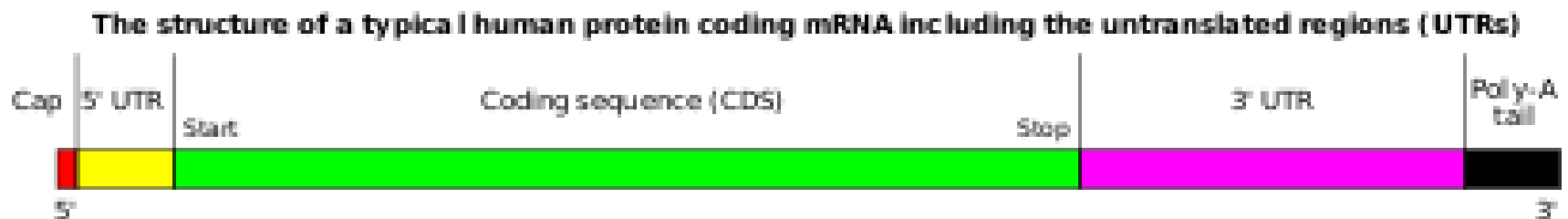
Translation initiation in bacteria

- The initiation factors (IF1 and IF3) get released and the resulting complex is called **the initiation complex**.



In eukaryotes messenger RNA undergoes several steps of post-transcriptional modification

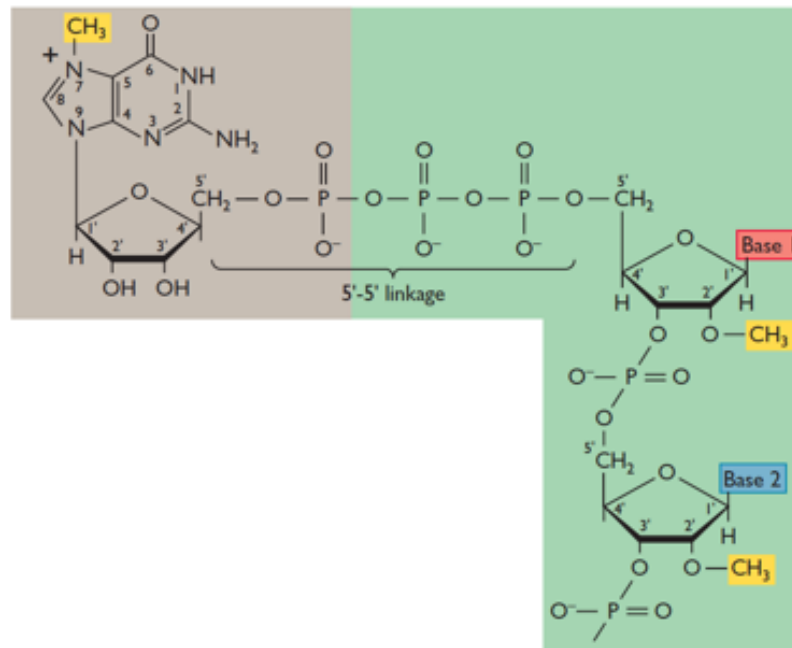
- Post-transcriptional modification is the process in eukaryotic cells where primary transcript RNA is converted into mature RNA.
- The process includes three major steps: addition of a 5' cap, addition of a 3' poly-adenylation tail, and splicing.



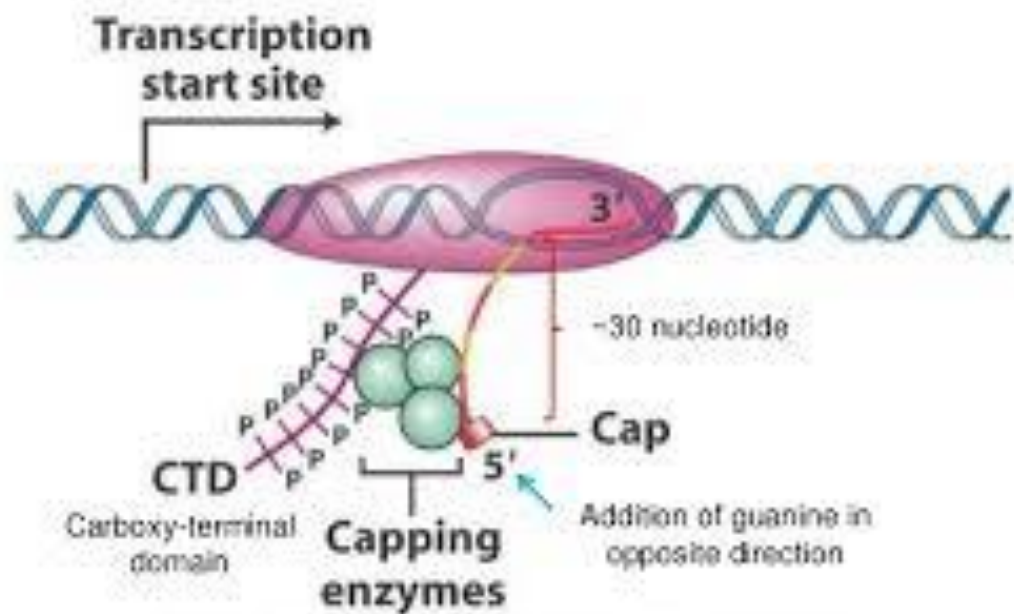
5'-capping

- the five-prime cap (5' cap) is a specially altered nucleotide on the 5' end of precursor messenger RNA.

5'-cap structure

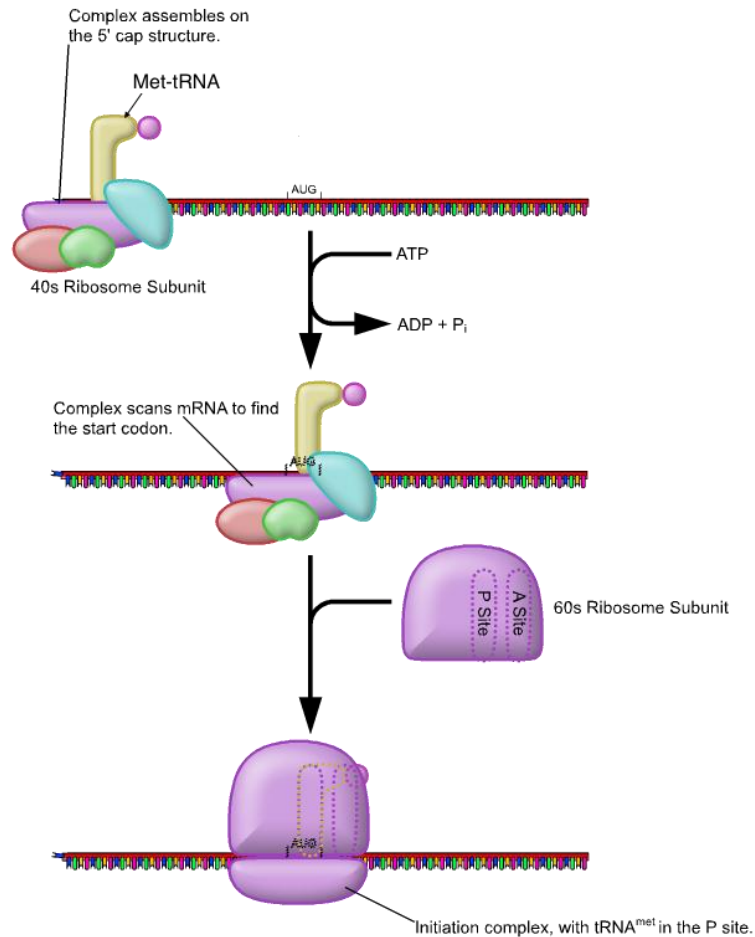


Co-transcriptional capping

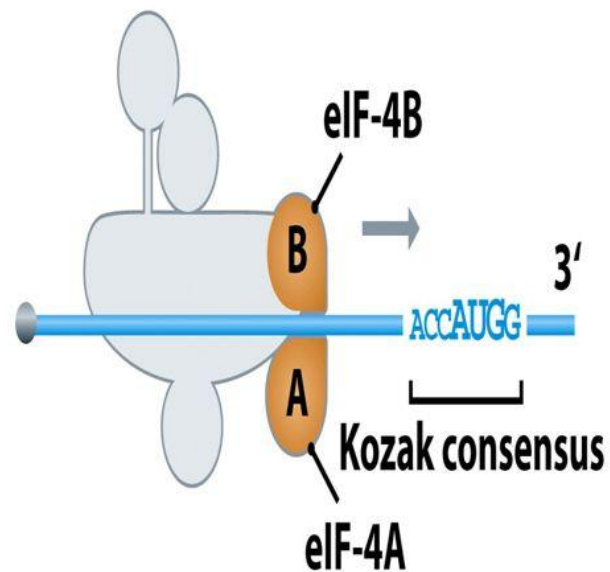


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Translation pre-initiation complex binds to 5'cap of mRNA



Scanning



13-2. (Cont.) Translation initiation in eukaryote.

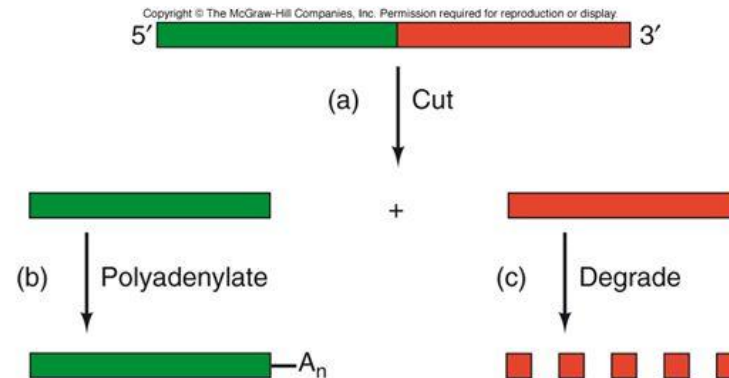
Preinitiation complex scans along mRNA until it reaches the initiation codon (a few tens or hundreds nt downstream & located within **Kozak consensus** sequence); large subunits then attach.

3' polyadenylation

- Polyadenylation is the addition of a poly(A) tail to a messenger RNA. The poly(A) tail consists of multiple adenosine monophosphates.
- The poly(A) tail is important for the nuclear export, translation, and stability of mRNA.

Basic Mechanism of Polyadenylation

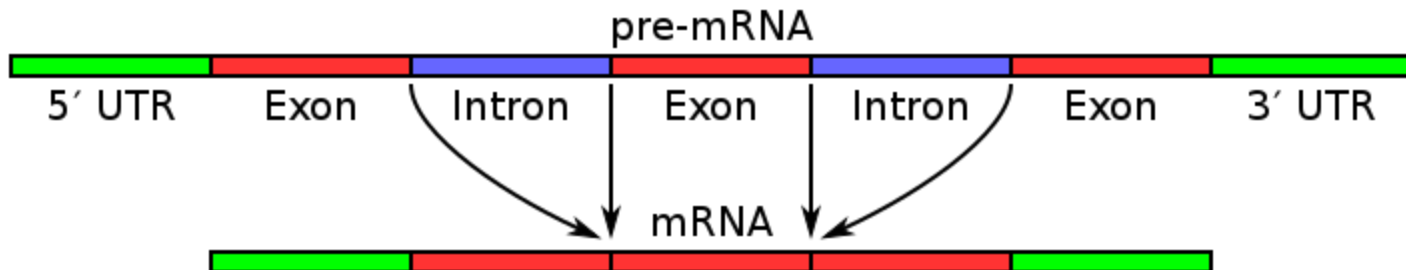
- Transcription of eukaryotic genes extends beyond the polyadenylation site



- The transcript is:
 - Cleaved
 - Polyadenylated at 3'-end created by cleavage

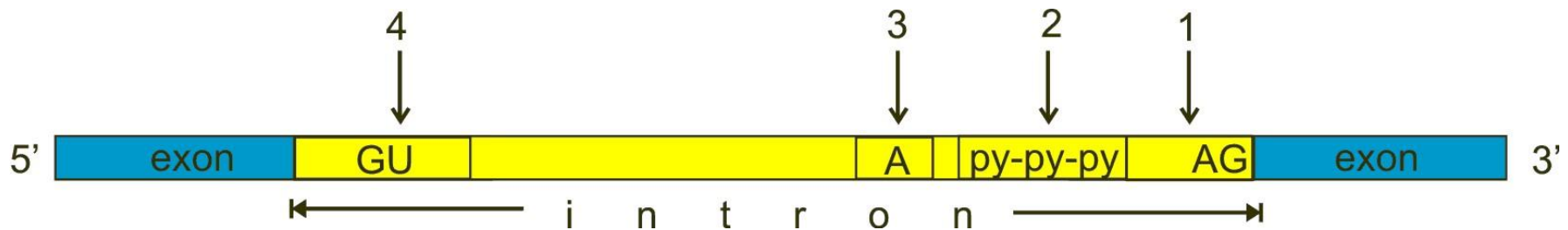
Splicing of RNA

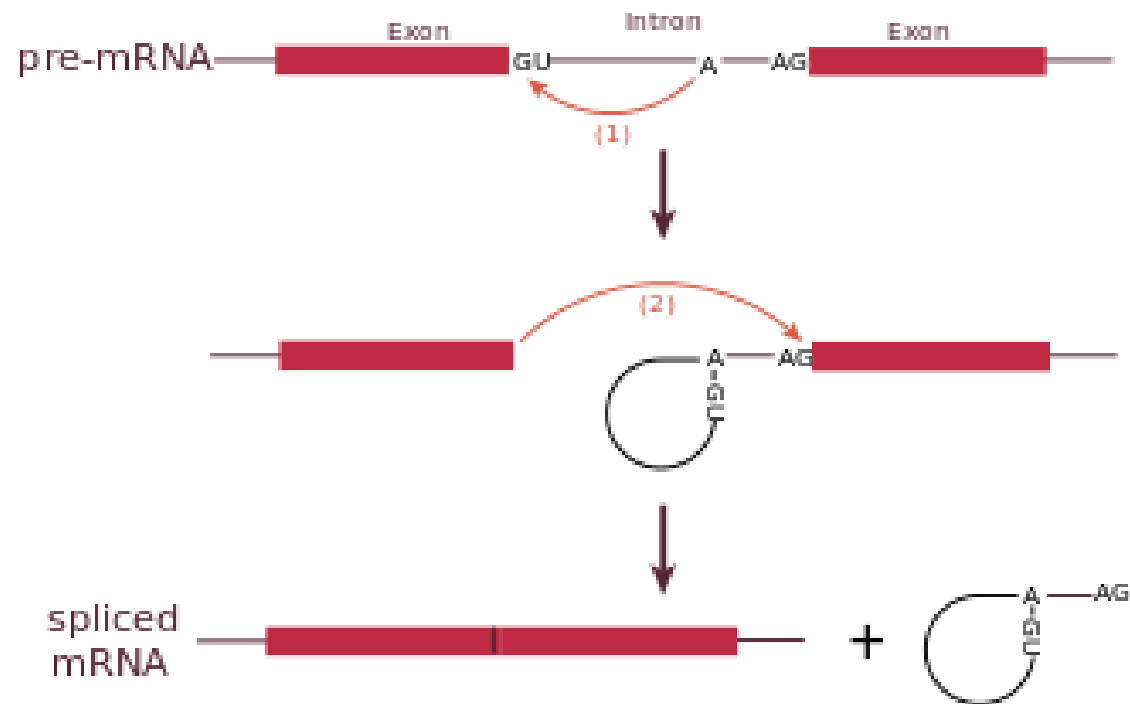
- Eukaryotic genes are often interrupted. They contain sections of DNA called exons, which are expressed as RNA and protein, interrupted by sections of DNA called introns, which are not expressed.
- Introns are removed by a process called RNA splicing during maturation of the final RNA product.



- Introns often reside within the sequence of eukaryotic protein-coding genes. Within the intron, a donor site (5' end of the intron), a branch site (near the 3' end of the intron) and an acceptor site (3' end of the intron) are required for splicing.
- The splice donor site includes an almost invariant sequence GU at the 5' end of the intron
- The splice acceptor site at the 3' end of the intron terminates the intron with an almost invariant AG sequence.

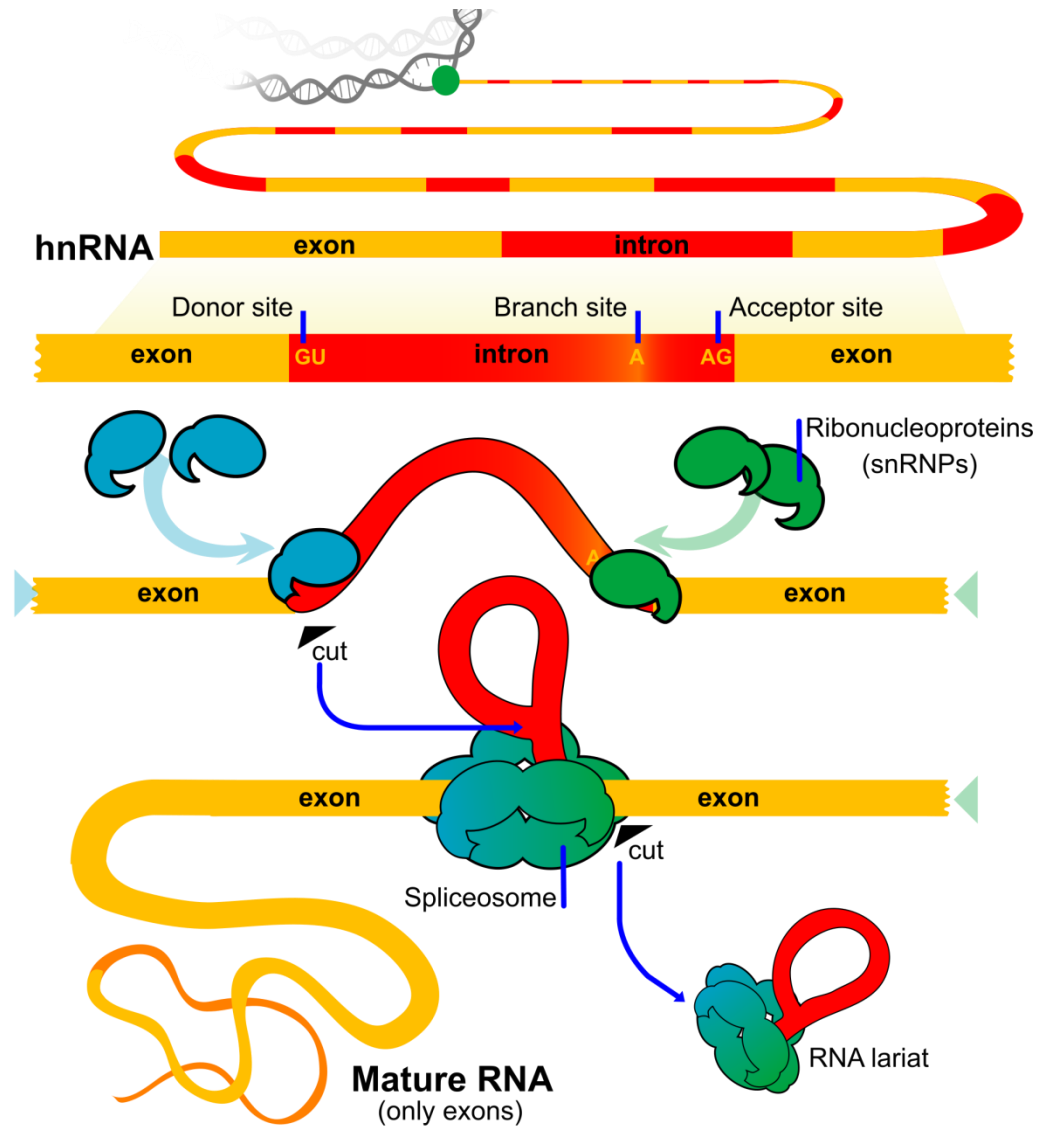
- Upstream (5'-ward) from the AG there is a region high in pyrimidines (C and U), or polypyrimidine tract
- Further upstream from the polypyrimidine tract is the branchpoint, which includes an adenine nucleotide involved in lariat formation.





Spliceosome

- Splicing is catalyzed by the **spliceosome**, a large RNA-protein complex composed of five small nuclear ribonucleoproteins (snRNPs). Assembly and activity of the spliceosome occurs during transcription of the pre-mRNA. The RNA components of snRNPs interact with the intron and are involved in catalysis.



Self-splicing introns

- Self-splicing occurs for rare introns that form a ***ribozyme***, performing the functions of the spliceosome by RNA alone.

