Review

TYPES OF RNA

Four distinct types of RNA are known; ribosomal (rRNA), transfer (tRNA), messenger (mRNA), and micro (miRNA), each with its own distinctive structure and function.

A. Ribosomal RNA

rRNA accounts for approximately 80% of total RNA in the cell and associates with proteins to form ribosomes. Ribosomes are important during protein synthesis

B. Transfer RNA

tRNA is the smallest of the three RNAs. It functions in the protein synthesis by virtue of its ability to carry the appropriate amino acid and also provide a mechanism by which nucleotide information can be translated to amino acid information through its anticodon.

C. Messenger RNA

mRNA carries genetic information from DNA to cytosol for translation. About 5% of the total RNA within a cell is mRNA. It carries specific information necessary for the synthesis of different proteins.

D. MicroRNA

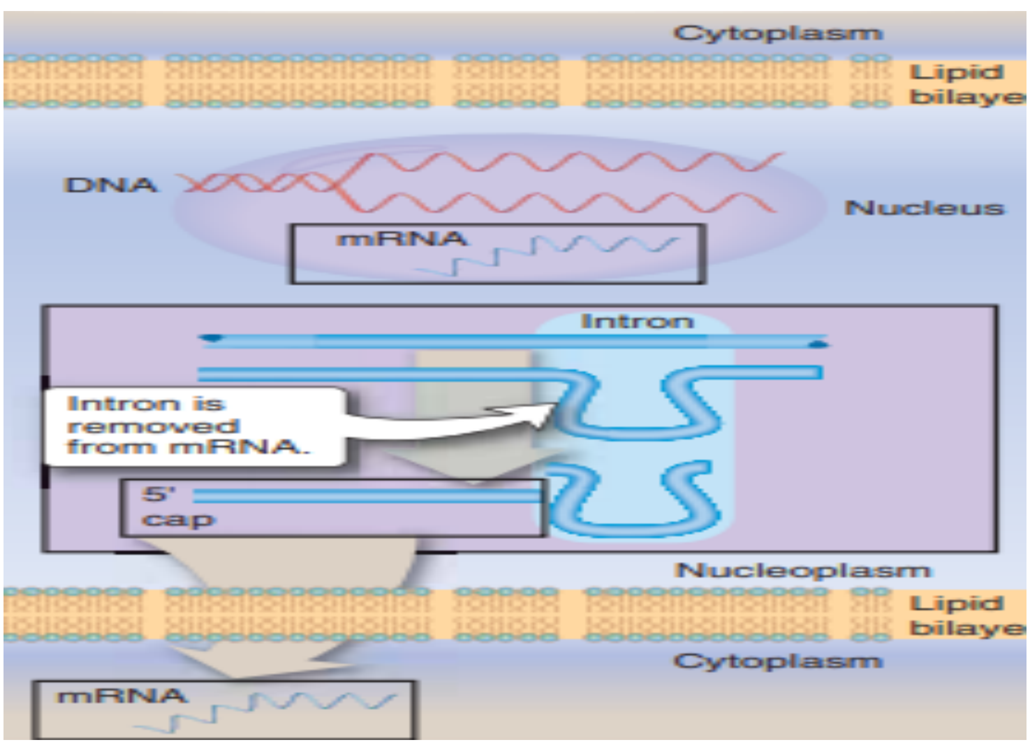
miRNAs, like the other RNA molecules, are encoded by genes and are single-stranded RNA molecules about 21 to 23 nucleotides in length. These newly discovered molecules are transcribed but not translated. They function in regulating gene expression by their ability to bind mRNA and to down-regulate the gene expression

Post transcriptional modification

Gene transcription produces an RNA that is larger than the mRNA found in the cytoplasm for translation. This larger RNA, called the primary transcript or heterogeneous nuclear RNA (hnRNA), contains segments of transcribed introns. The intron segments are removed and the exons are joined at specifc sites, called donor and acceptor sequences, to form the mature mRNA by a mechanism of RNA processing

A. Addition of a 5′ cap

Almost immediately after the initiation of RNA synthesis, the 5′ end of RNA is capped by a methyl guanosine residue, which protects it from degradation (by 5′ exonucleases) during elongation of the RNA chain. The cap also helps the transcript bind to the ribosome during protein synthesis.

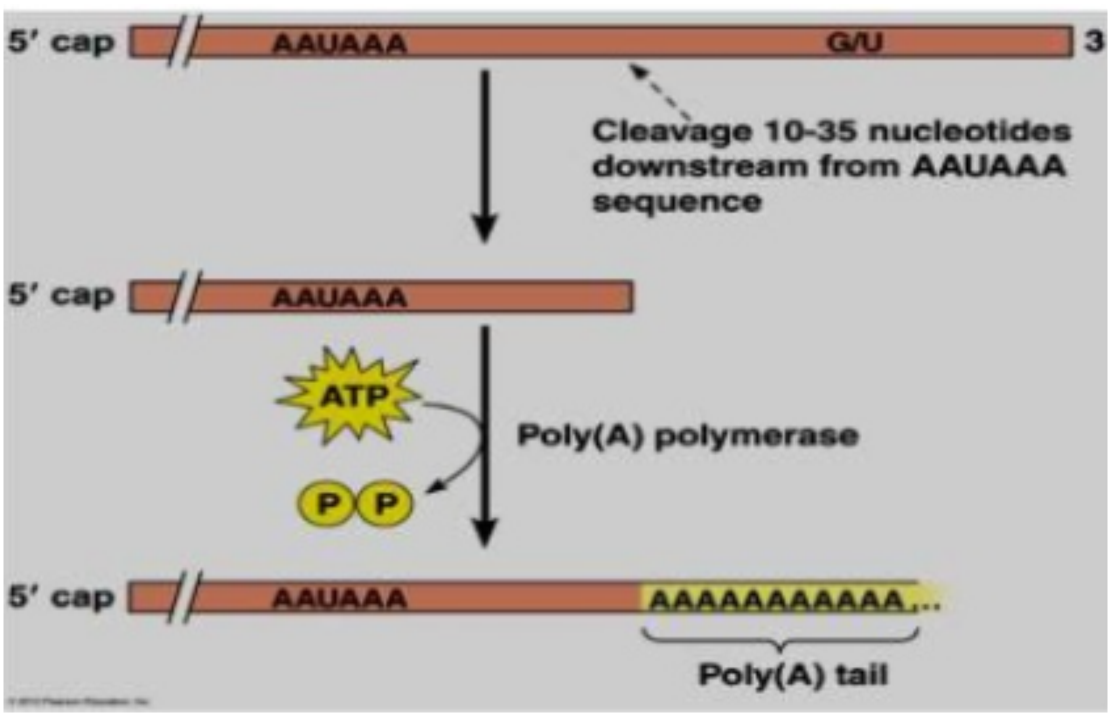


mRNA is transcribed and processed in the nucleus.

B. Addition of a poly(A) tail

The primary transcripts contain a highly conserved AAUAAA consensus sequence, known as a polyadenylation signal, near their 3′ end. The polyadenylation site is recognized by a specific endonuclease that cleaves the RNA approximately 20 nucleotides downstream.

The newly created 3′ terminus, however, serves as a primer for enzymatic addition by poly(A) polymerase of up to 250 adenine nucleotides . The poly(A) tail appears to protect the 3' end of mRNA from 3' 5' exonuclease attack.

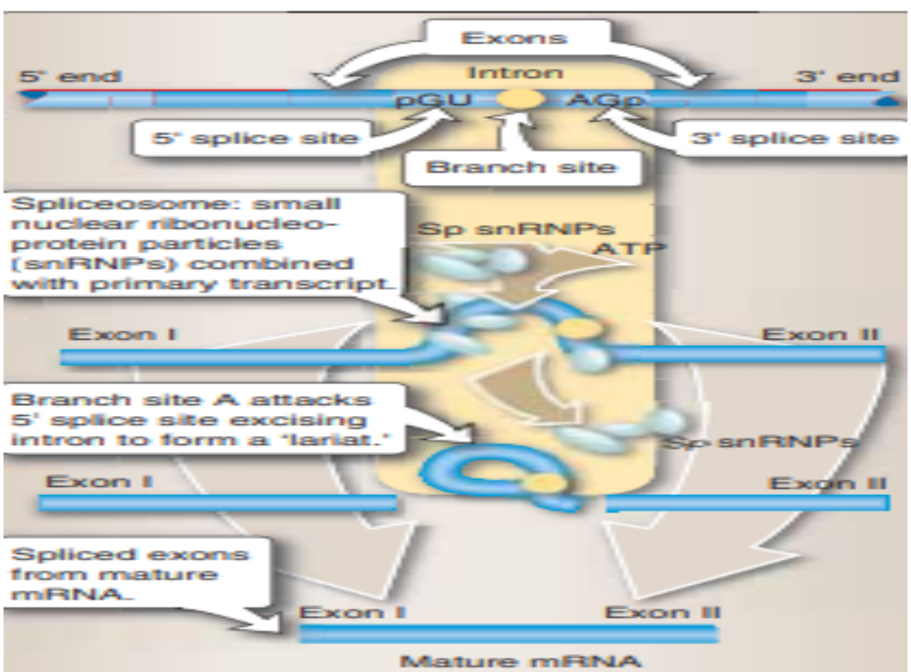


RNA processing reactions.

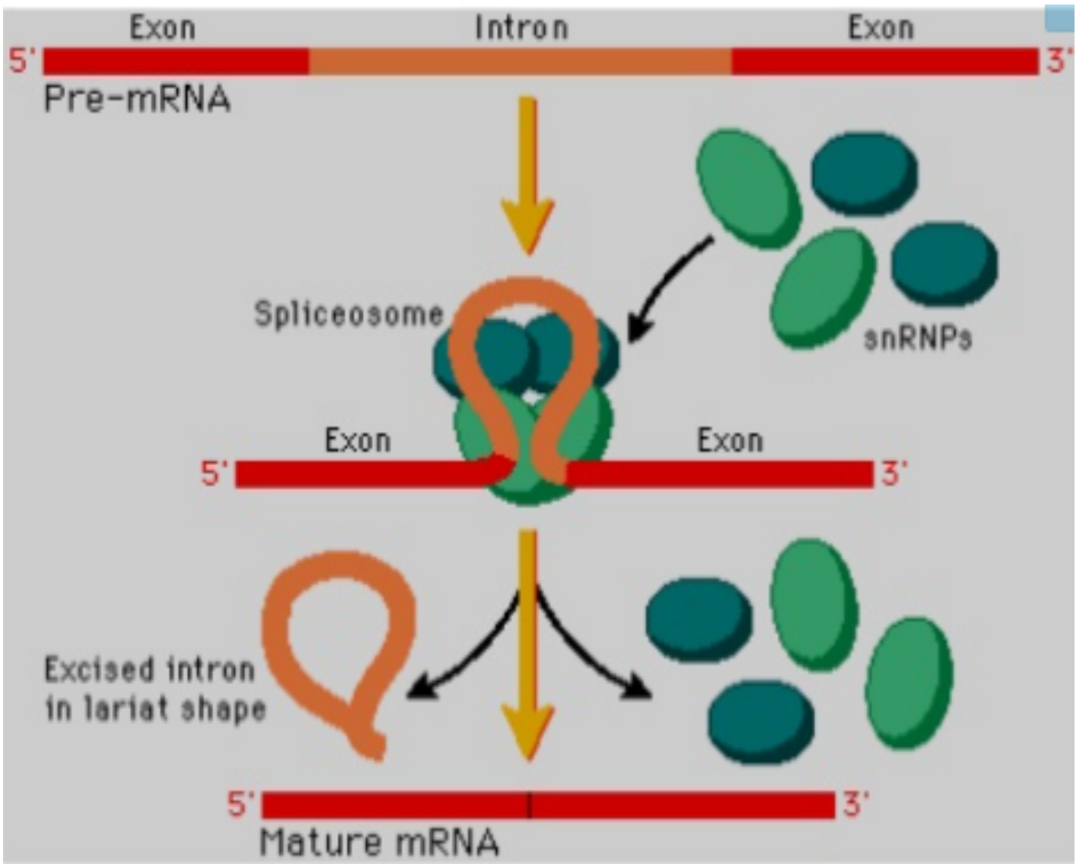
C. Intron removal

Splice site sequences, which indicate the beginning (GU) and ending (AG) of each intron, are found within the primary RNA transcript. Introns are removed and exons are spliced (joined) together to form the mature mRNA. aspecial structure called the spliceosome converts the primary transcript into mRNA.

Introns are the RNA sequences which do not code for the proteins. These introns are removed from the primary transcript in the nucleus, exons (coding sequences) are ligated to form the mRNA molecule, and the mRNA molecule is transported to the cytoplasm. The molecular machine that accomplishes the task of splicing is known as the spliceosome. Small nuclear RNA molecules that recognize splice sites in the pre- mRNA sequence. The excised intron is released as a "lariat" structure, which is degraded. The mature RNA molecule now leaves the nucleus by passing into the cytoplasm through the pores in the nuclear membrane.



mRNA splicing.


Exon
Intron
Exon
5'
3'
Pre-mRNA
Spliceosome
snRNPs
Exon
Exon
5'
3'
Excised intron
in lariat shape
5'
3'
Mature mRNA