Before beginning this chapter, review and fully understand the following terms from the lecture on Cells:

- DNA
- Gene
- Codon and stop codon
- Genetic code
- Transcription
- RNA Polymerase enzyme
- messenger RNA (mRNA)
- Translation
- Ribosome
- transfer RNA (tRNA)
- Anticodon

Figs 17.3, 17.4, 17.5, and17.26

Template strand

The strand of the gene that is transcribed (that RNA Polymerase makes a complementary mRNA to)

- The RNA Polymerase enzyme always moves along the template strand 3' to 5'
- The mRNA is always assembled 5' to 3'

Figs 17.6 and 17.7

Non-template strand

The strand of the gene that is not transcribed

Figs 17.6 and 17.7

Transcription in Prokaryotes:

Promoter

A special nucleotide sequence in the gene that RNA Polymerase binds to begin transcription

- The promoter is located several nucleotides upstream of the gene's first codon

Fig 17.7

Terminator

A special nucleotide sequence in the mRNA that causes RNA Polymerase to detach from the template DNA and end transcription

- The terminator is located several nucleotides downstream of the translated region (the codons)

Transcription in Eukaryotes:

Starting transcription

- RNA Polymerase II (RNA Pol II) = The enzyme that transcribes mRNAs in eukaryotes

  √ Eukaryotes have two enzymes (RNA Polymerase I and RNA Polymerase III) that transcribe RNAs that are not translated into proteins (such as ribosomal RNA and transfer RNA)

- The promoter is located several nucleotides upstream of the gene's first codon

  √ The TATA box = A nucleotide sequence found in many eukaryotic promoters

- RNA Pol II does **not** bind directly to the promoter sequence

  √ RNA Pol II attaches to transcription factors (proteins that do bind to the promoter sequence)

Fig 17.8

Ending transcription

- The Poly-Adenylation signal (Poly-A signal) = A sequence in the mRNA (AAUAAA) that signals the end of transcription

  √ The poly-adenylation signal is found downstream of the translated region (downstream of the last codon)

  √ Enzymes in the nucleus cut the mRNA free from RNA Pol II a few nucleotides downstream of the poly-A signal

Fig 17.9

Pre-mRNA (the primary transcript)

The mRNA as it exists right after transcription

- The pre-mRNA is as long as and complementary to the transcribed region of the gene's template strand

- Eukaryotes process (modify) the mRNA in three ways before it leaves the nucleus

  √ Addition of a 5' cap

  √ Addition of a poly-adenosine tail

  √ Removal of introns

Figs 17.9 and 17.10

The 5’ cap

A modified Guanine (G) nucleotide added to the 5’ end of the mRNA

Fig 17.9

The poly-adenosine (poly-A) tail

50 – 250 adenosine (A) nucleotides added to the 3’ end of the mRNA a few nucleotides downstream of the poly-A signal

- The poly-A tail and the 5’ cap both serve three functions:

  √ They promote export of the mRNA from nucleus to cytoplasm

  √ They protect the mRNA from degrading enzymes in the cytoplasm

  √ They help the ribosome bind to the mRNA

Fig 17.9

Introns

Regions of the primary transcript that are spliced out before it exits the nucleus

- Because introns are removed from the transcript, they do not exit the nucleus and therefore are not translated into proteins
- Introns are located between exons (the non-removed regions)
- Prokaryotic genes do **not** contain introns

Exons

The regions of the primary transcript that are not spliced out

- In the primary transcript, the exons are separated from each other by introns
- After the introns are removed from the primary transcript, the exons are joined together to make the mature mRNA

  √ The mature mRNA is simply the joined-together exons

- Because the mature mRNA is made only of exons (not introns), it is the exons (not the introns) that are translated into protein when the mature mRNA exits the nucleus and binds to a ribosome

RNA splicing

Cutting out the introns from the primary transcript and joining together the exons (done before the mRNA leaves the nucleus)

- There are short nucleotide sequences at the exon/intron junctions that mark the beginning and end of the intron

    √ These sequences serve as splice sites for removing the intron

- Several snRNPs (small nuclear ribonucleoproteins) bind to the splice sites

- The spliceosome = All the snRNPs and several other proteins together at the intron's splice site

    - The spliceosome joins the upstream exon to the downstream exon

    - It then cuts out the intron

It is not fully understood why eukaryotic genes contain introns, but some explanations are:

- It allows more than one protein to be made from the gene through the process of alternative splicing

  √ Alternative splicing = When an exon has the option of being spliced to one or the other of two downstream exons

- It may facilitate the creation of new genes by the occasional mixing together of exons from different genes

  √ Exons usually correspond to functional domains of the protein

  - Functional domain = A region with a specific function, such as an active site, a hydrophobic transmembrane domain, an allosteric site, etc.

  √ Mixing exons from different genes creates a protein with a new mixture of functional domains

Figs 17.10, 17.11, 17.12, and 19.8

Overview of mRNA structure:

The processed mRNA that exits the nucleus contains (from 5' to 3'):

1) The 5' cap

2) The first exon

- The first exon contains the first codons
  - AUG (the codon for the amino acid methionine) is always the starting codon
- The first exon also contains a short 5' untranslated region (5' UTR) upstream of the start codon
  - The ribosome scans along the 5' UTR until it finds the start codon to begin translation

3) Other exons (spliced together)

4) The last exon

- The last exon contains the final codons
  - The last codon is always a stop codon (UGA, UAG, or UAA) which signals the ribosome to stop translation
- The last exon also contains a 3' UTR downstream of the stop codon
  - The 3' UTR contains the polyadenylation signal

5) The poly-A tail

- The poly-A tail begins a few nucleotides downstream of the poly-A signal

Fig 17.10