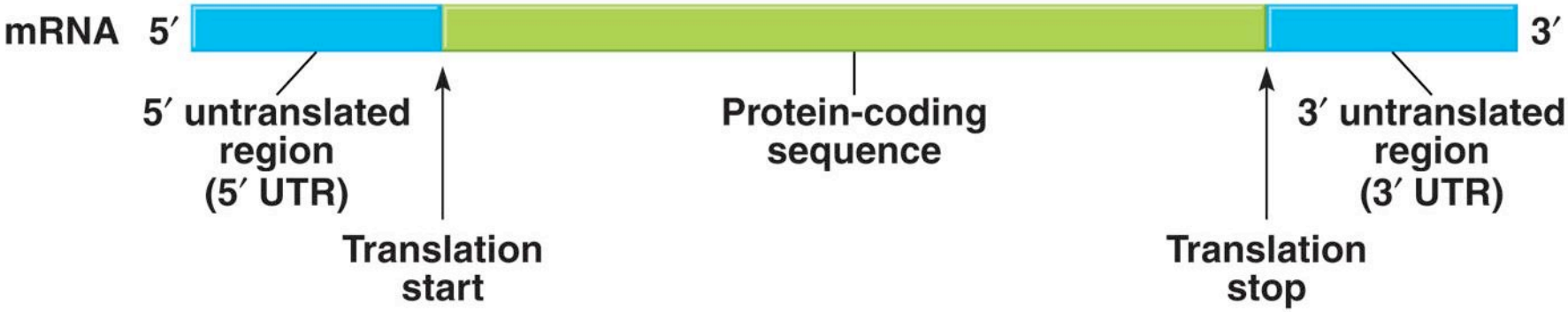
RNA Processing: Eukaryotic mRNAs



- Eukaryotic mRNAs have three main parts (Figure 13.8):
  - 5′ untranslated region (5′ UTR),
    - varies in length.
  - The coding sequence
    - specifies the amino acid sequence of the protein that will be produced during translation.
    - It varies in length according to the size of the protein that it encodes.
  - 3′ untranslated region (3′ UTR),
    - also varies in length and contains information influencing the stability of the mRNA.

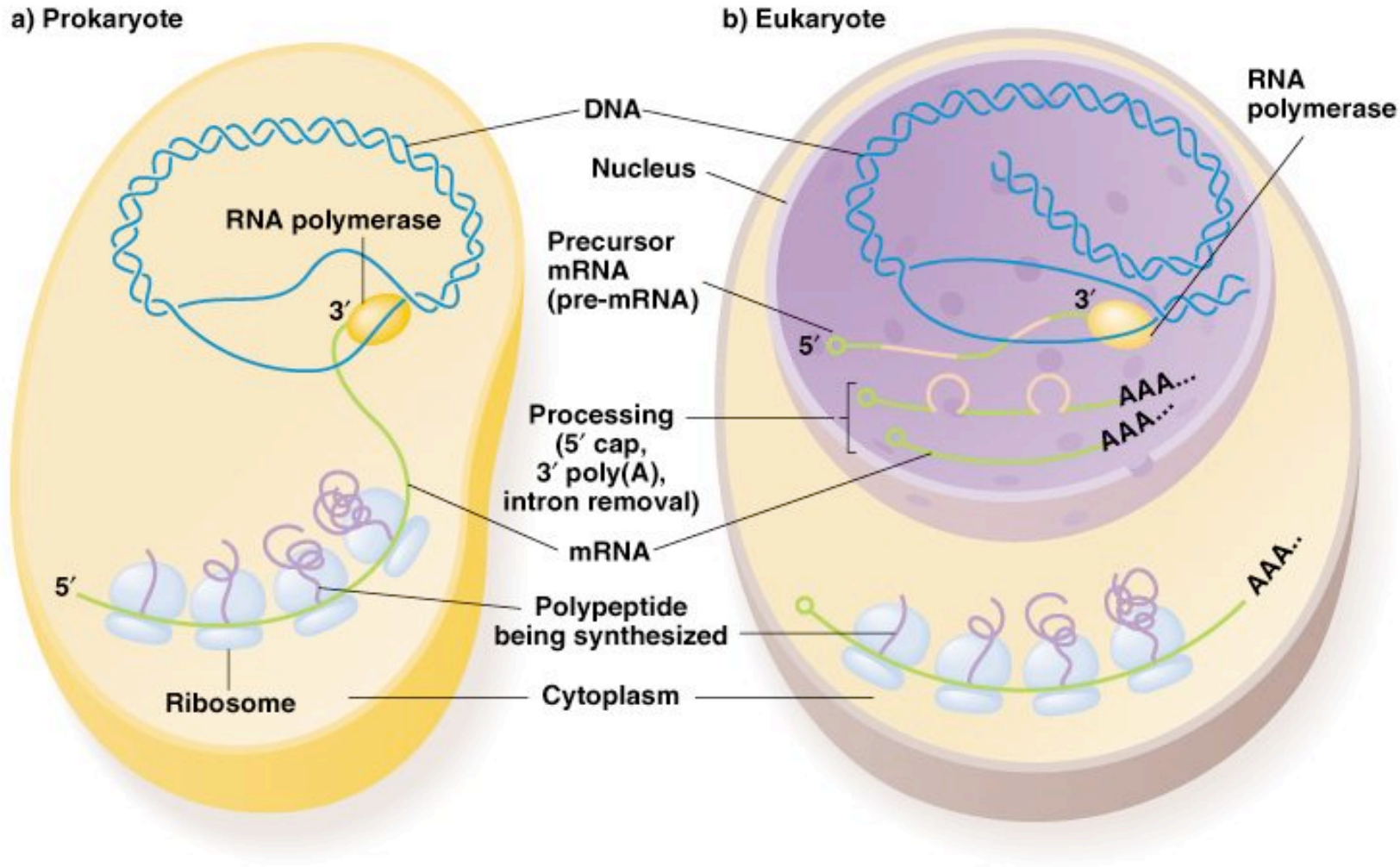
RNA Processing

- In prokaryotes, no RNA processing is necessary:
  - the nascent RNA is usually the mRNA.

- In eukaryotes, the nascent RNA is called primary transcript-RNA
  - needs to be processed
  - and transported to the cytoplasm for translation to occur.

- The processing steps are:
  - Addition of a 5' 7-methyl guanosine cap (capping).
  - Addition of a poly-A tail at the 3' end (polyadenylation)
  - RNA splicing to remove intervening sequences (remove introns).

Fig. 13.9
Processes for synthesis of functional mRNA in prokaryotes and eukaryotes



Eukaryotic RNA Processing: Capping

- When the RNA chain is about 30 nucleotides long, the 5' ends are modified by the addition of a guanine group in the opposite orientation:
  - involves a 5'-5' triphosphate linkage.
  - Happens before transcription is finished = co-transcriptionally
- Methyl transferases then add methyl groups in the 7 position to that and a couple more nucleotides.
- The caps are recognized by the translation machinery.
- They protect the growing RNA chain from degradation by nucleases.

Eukaryotic RNA Processing: Capping

Co-transcriptional capping

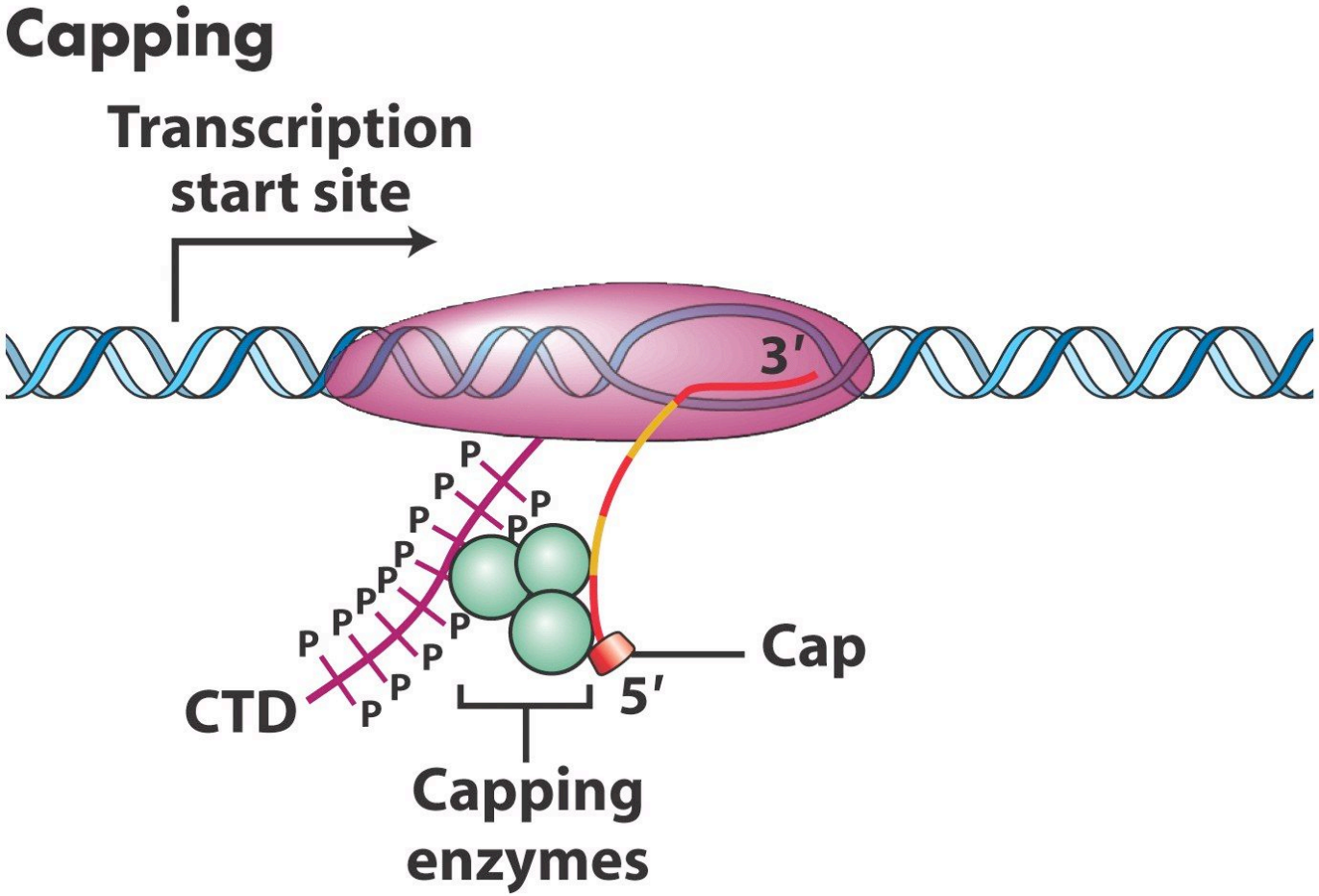
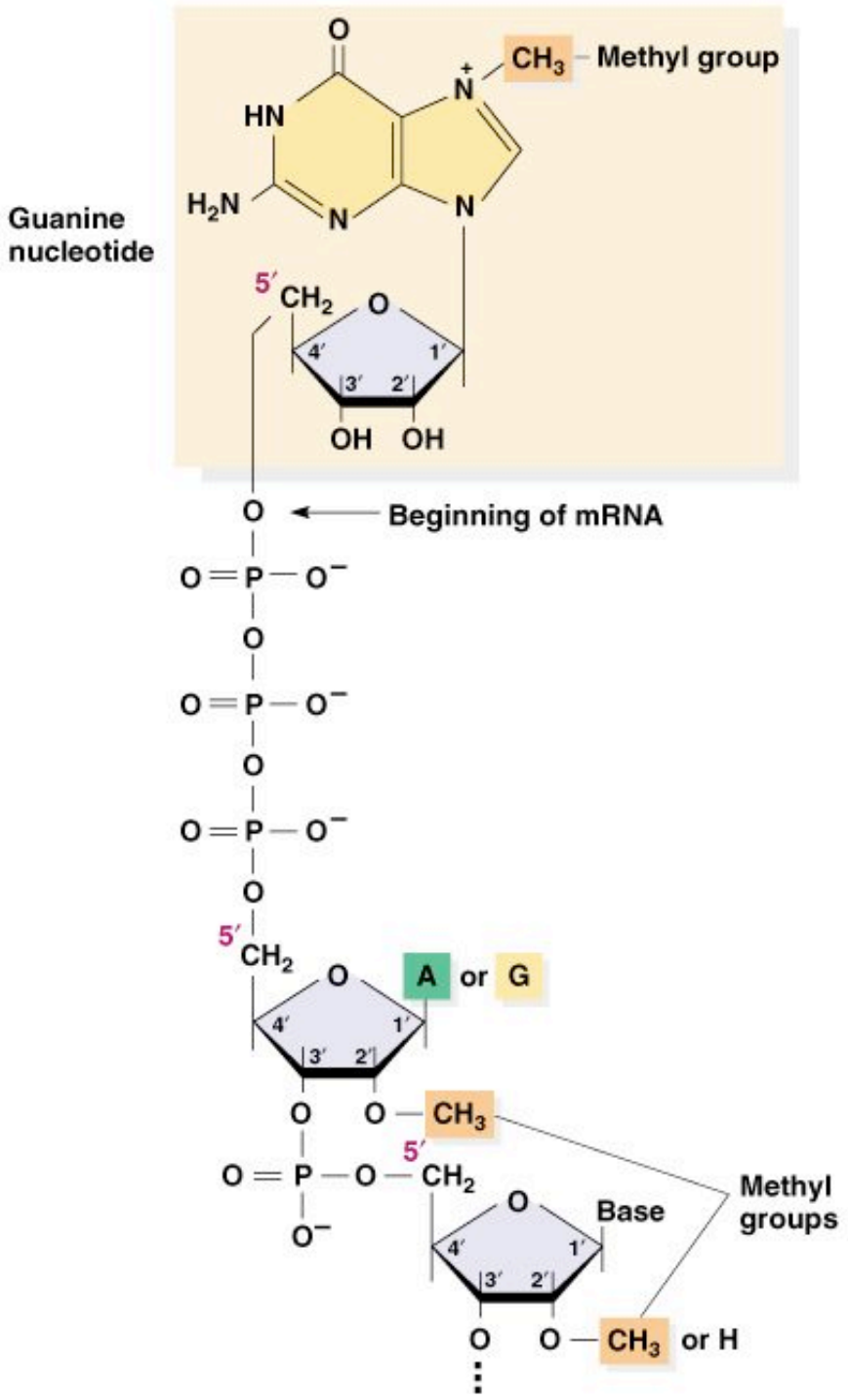


Fig. 13.10

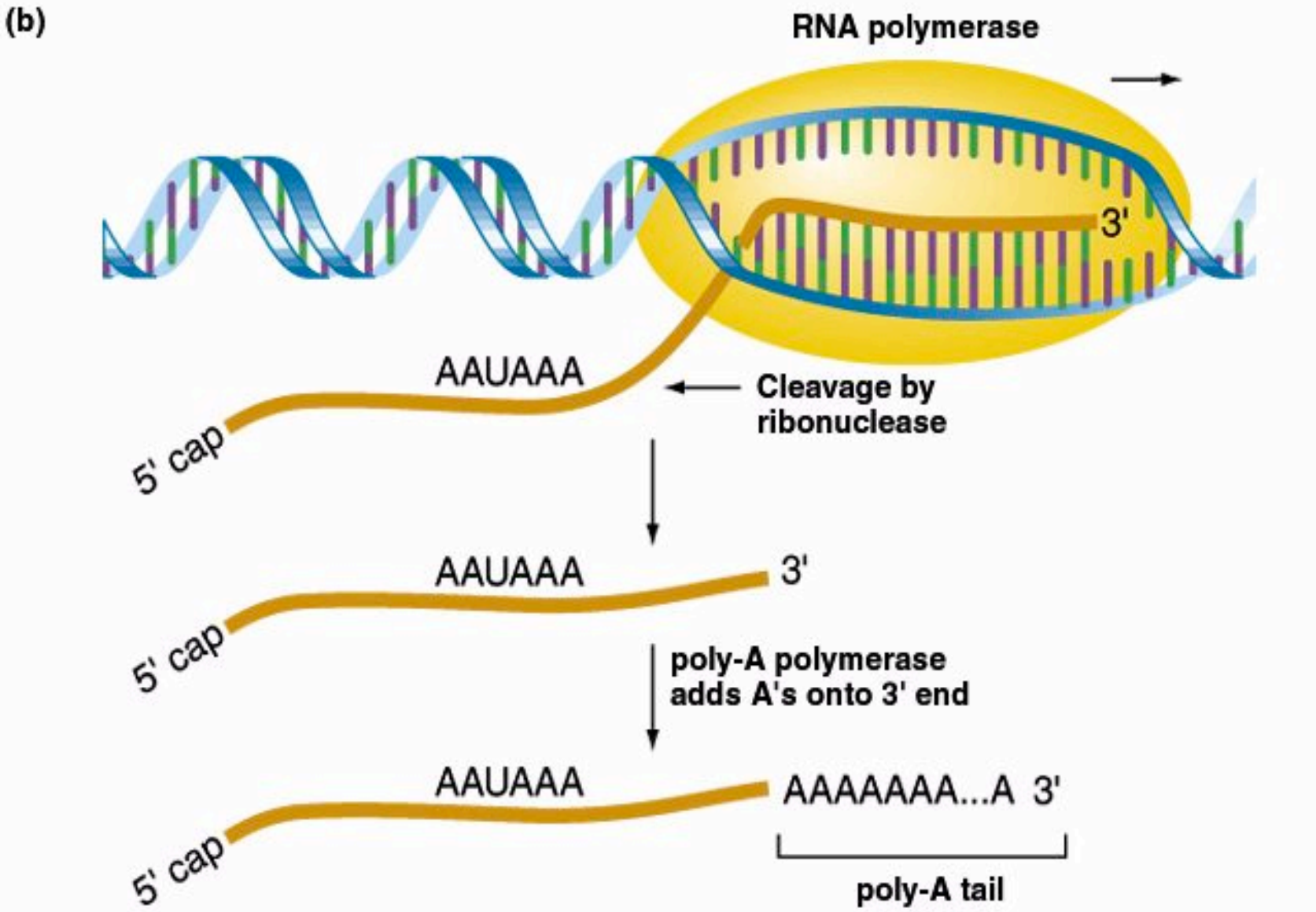
Cap structure at the 5′ end of a eukaryotic mRNA



Eukaryotic RNA Processing: Polyadenylation

- nascent RNA is cleaved downstream from the AAUAAA conserved sequence.
  - By ribonuclease
- The enzyme poly(A) polymerase adds adenine ribonucleotides
  - up to 200 bases long at the 3' end of the RNA.
- The poly(A) tail
  - enhances the stability of eukaryotic mRNA and
  - regulates its transport to the cytoplasmic compartment.

The ends of eukaryotic mRNAs

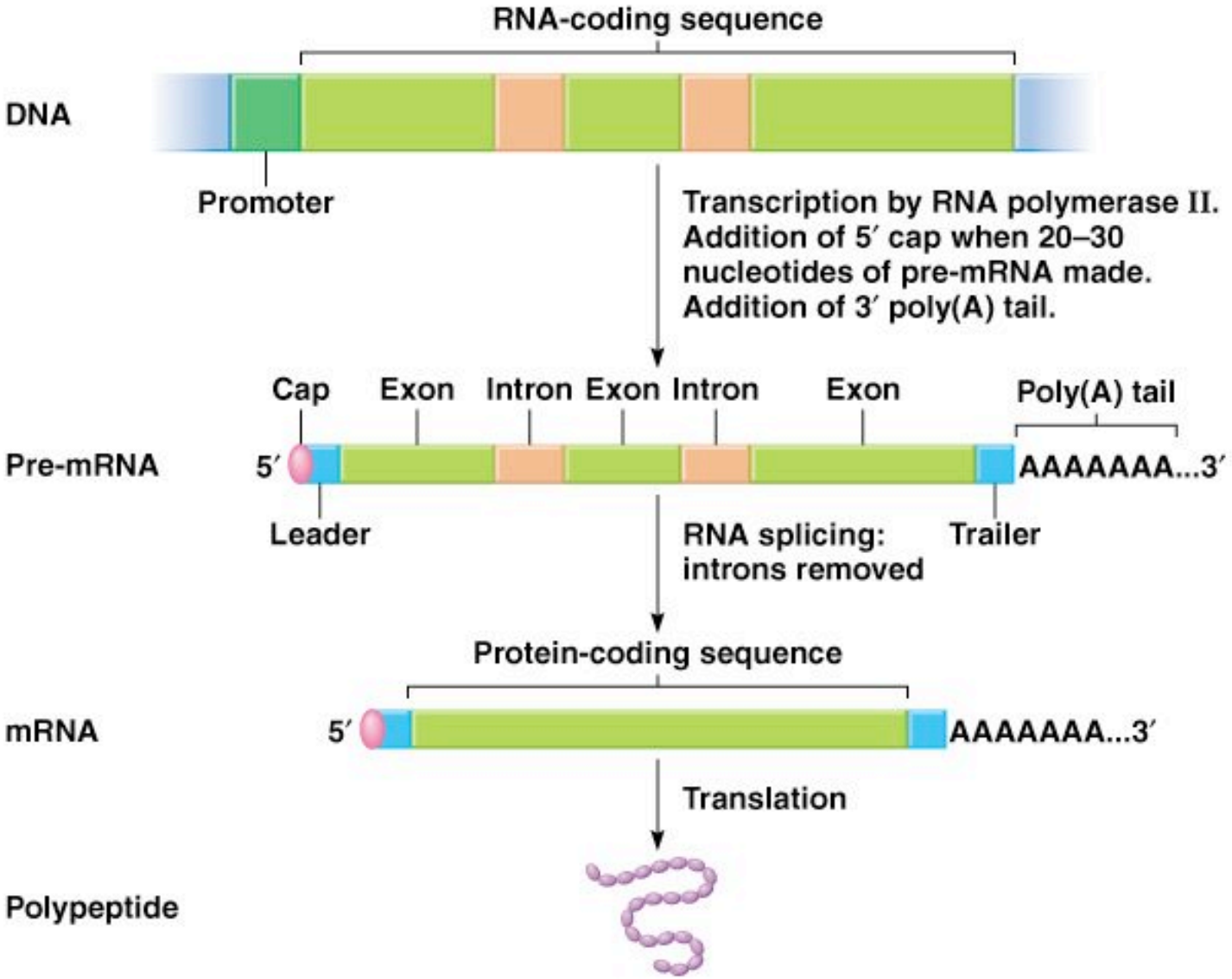


Eukaryotic RNA Processing: RNA splicing

(RNA is called hnRNA - Heteronuclear RNA before splicing occurs)

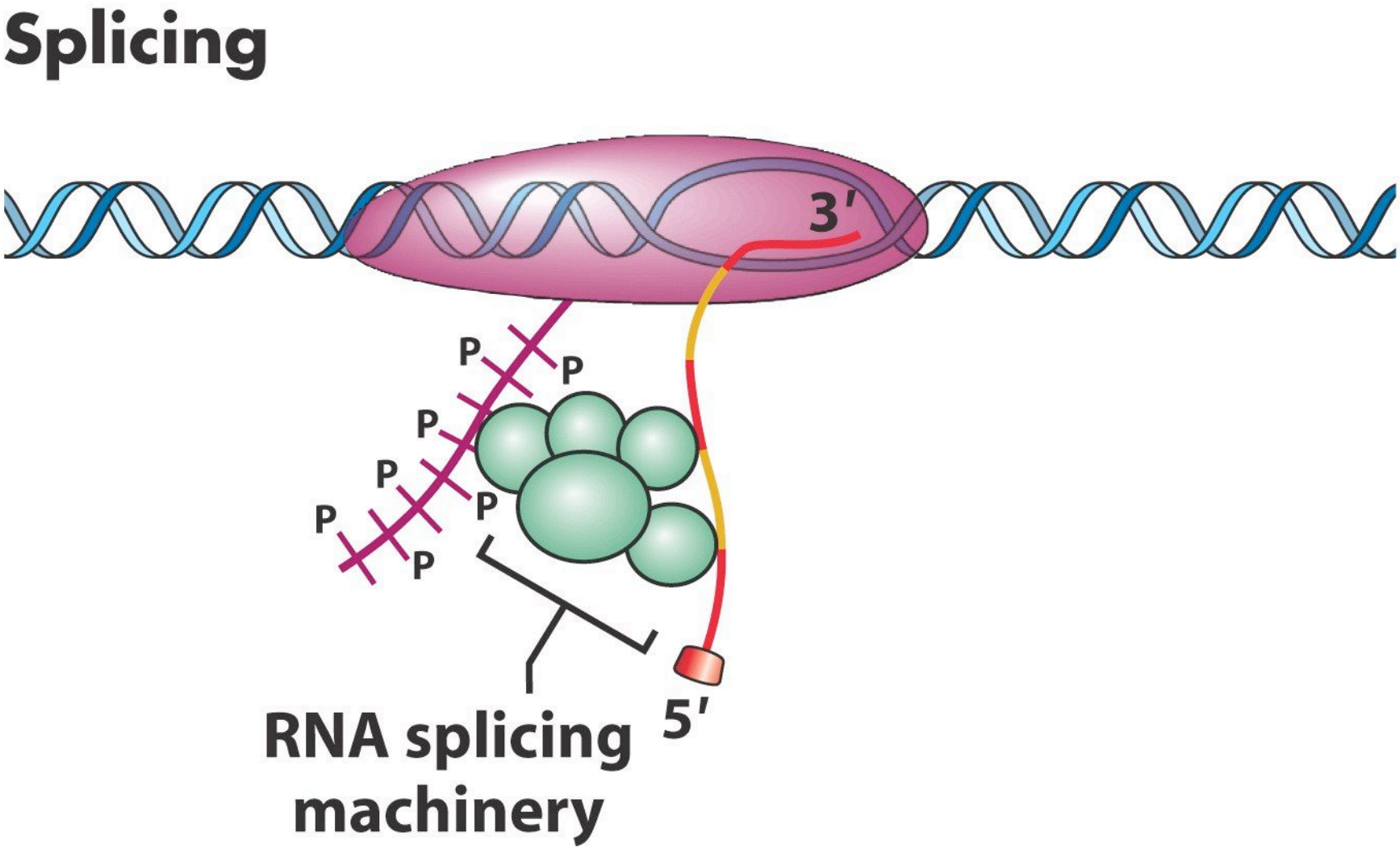
- Splicing is:
  - The mechanism by which introns are removed.
- Introns are intervening sequences - not expressed in proteins
- Exons are retained in the mature mRNA molecules.
  - expressing sequences
- Exon and intron lengths and numbers vary in various genes:
  - extreme example is dystrophin gene:
    - Gene size: 2500 Kb
    - mRNA size: 14kb
    - Exons: 79

Fig. 13.11 General sequence of steps in the formation of eukaryotic mRNA



Eukaryotic RNA Processing:

Co-transcriptional splicing



Introns

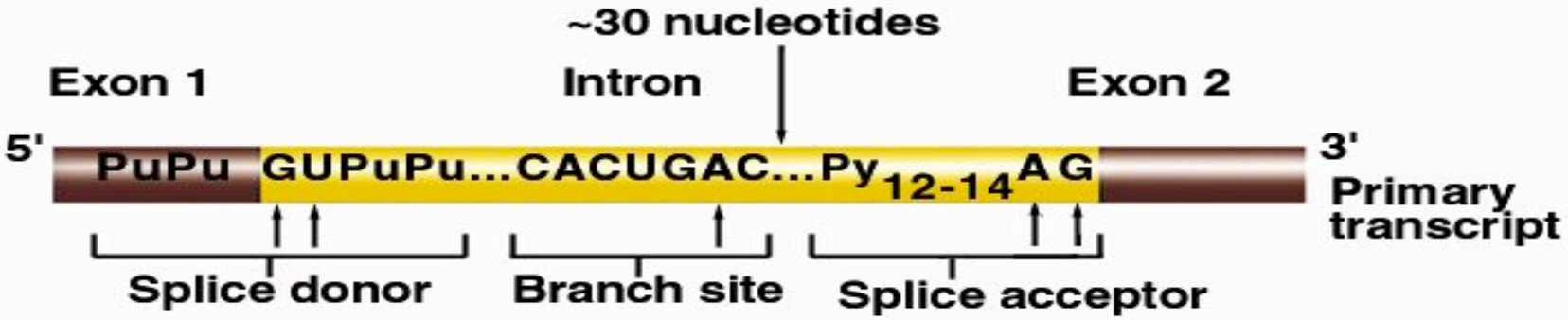
- Begin with 5’-GU
- End with AG-3’
- but mRNA splicing signals involve more than just these two small sequences.

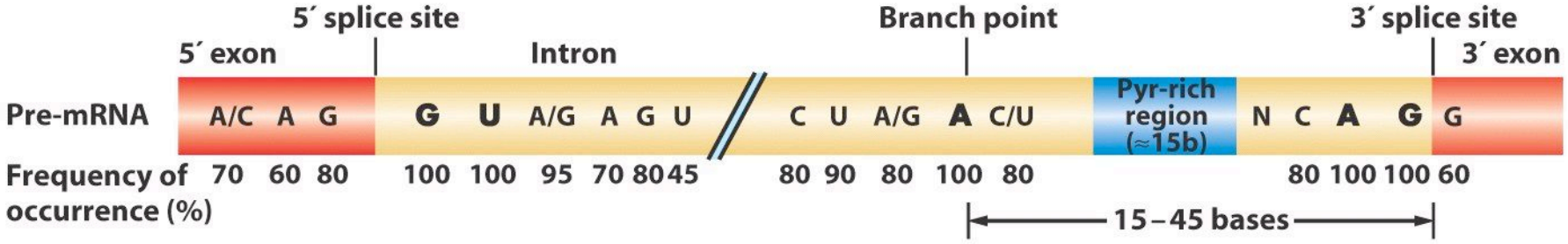
Mechanism of Splicing

- There is an intranuclear protein/RNA complex called the splicosome that ensures proper splicing.
- Three types of short sequences dictate the precise cutting of the intron/exon boundaries - called splice junctions.
  - **Splice donor**: 5' end of intron: **exon-G-U**
  - **Splice Acceptor**: 3' end of intron: **A-G-exon**
  - **Branch site**: within the intron, about 30 nucleotides upstream of the splice acceptor, has an AT rich region with at least one A.
- Two sequential cuts:
  - splice donor site is cleaved,
  - attaches to the branch site to form a lariat or loop structure,
  - then the splice acceptor site is cleaved.
- The intron degrades, the two exons are ligated.

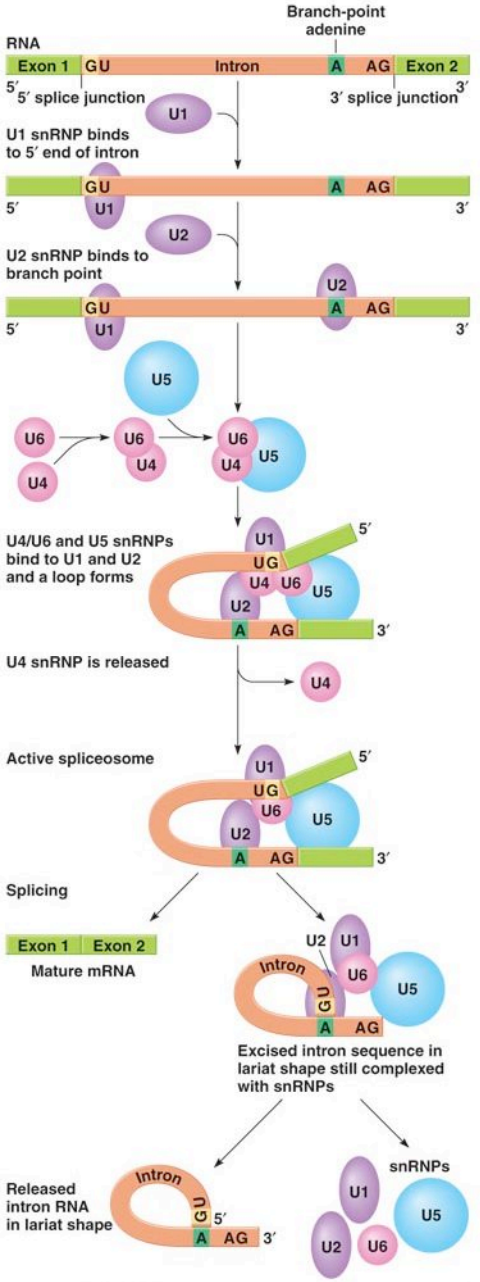
Mechanism of splicing

Short sequences dictate the sites of splicing





Mechanism of Splicing



Question

- Why is the mRNA not equal in length to the DNA it was transcribed from?
  - 1) the mRNA was longer because it has a Poly A tail
  - 2) The mRNA was longer because it contains only introns
  - 3) The DNA was shorter because it does not have the Methylated cap
  - 4) The mRNA was shorter because of Intron splicing

Question

- Which nucleotides signal the 5’ end of an intron splice site?
  - 1. AT
  - 2. GU
  - 3. AG
  - 4. GG

Homework Problems

Chapter 13

22, 23

- DON'T forget to take the online QUIZ!!
- DON'T forget to submit the online iActivity
  - "transcription"