RNA **پردازش**
(RNA processing)

زیست شناسی مولکولی

منابع : بیوشیمی لنینجر، ژنوم ۳

- Primary transcript
- تغییرات روی RNA اولیه (RNA processing)
- تکامل RNA در پروکاریوتها و یوکاریوت ها

پردازش tRNA و rRNA در پروکاریوتها

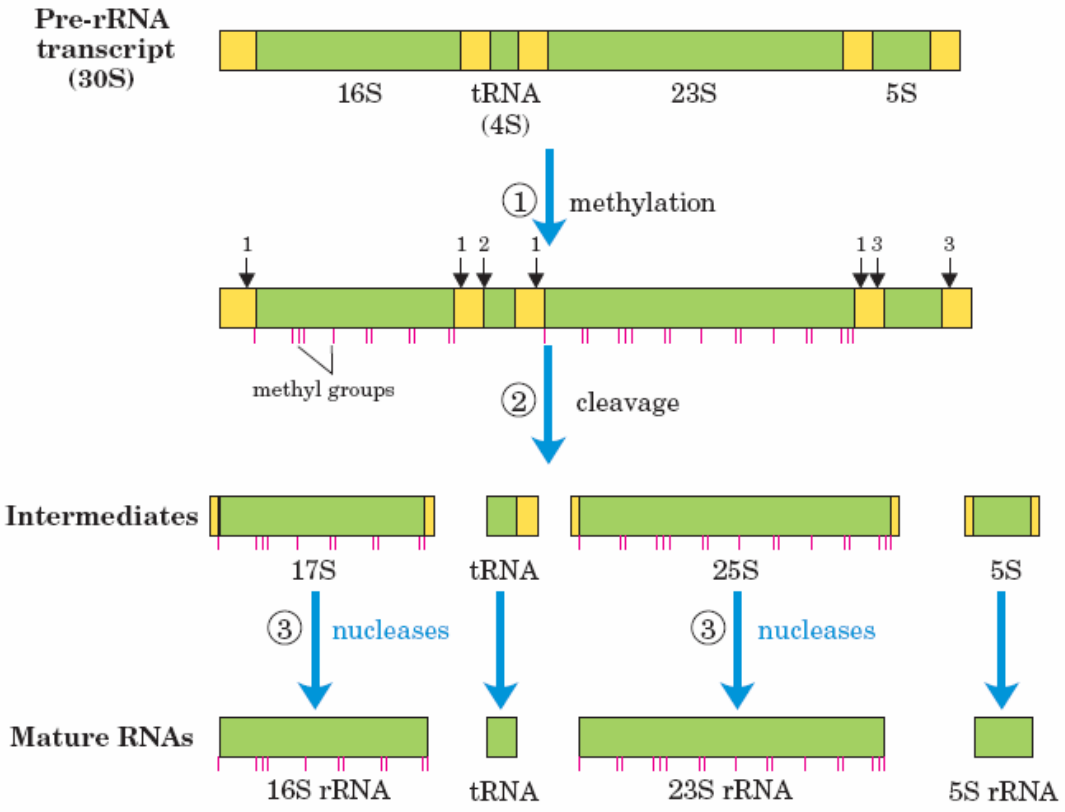
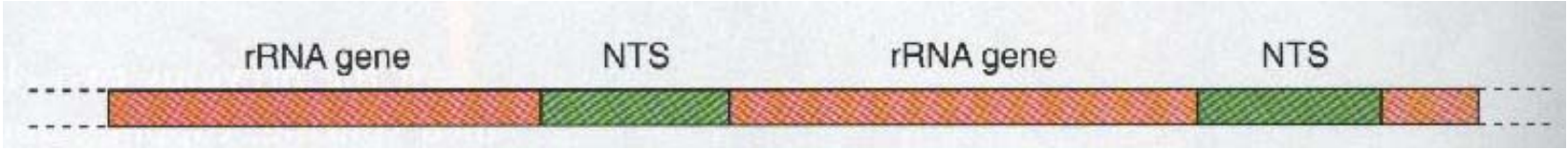
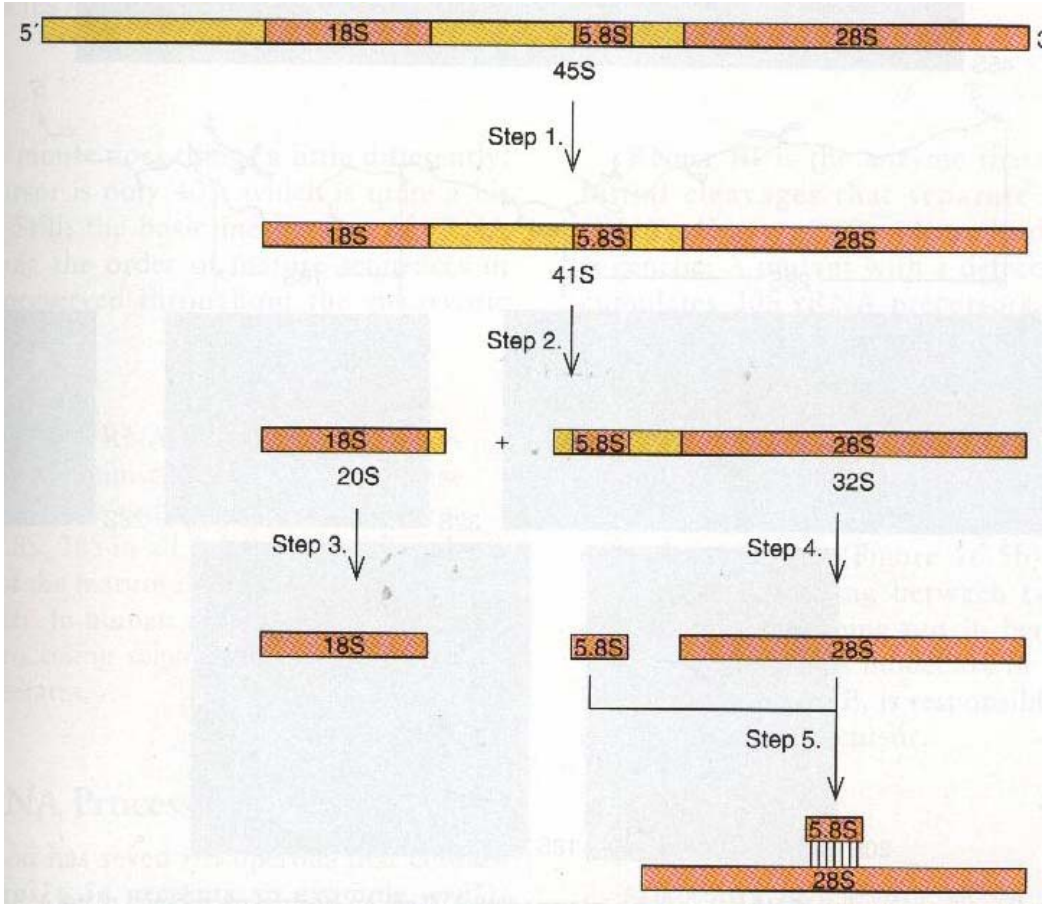
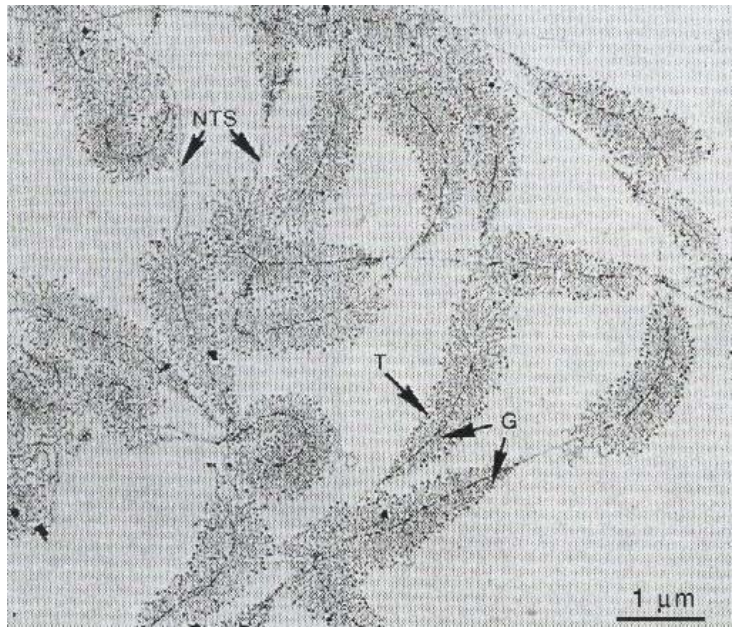


FIGURE 26–21 Processing of pre-rRNA transcripts in bacteria. ① Before cleavage, the 30S RNA precursor is methylated at specific bases. ② Cleavage liberates precursors of rRNAs and tRNA(s). Cleavage at the points labeled 1, 2, and 3 is carried out by the enzymes RNase III, RNase P, and RNase E, respectively. As discussed later in the text, RNase P is a ribozyme. ③ The final 16S, 23S, and 5S rRNA products result from the action of a variety of specific nucleases. The seven copies of the gene for pre-rRNA in the *E. coli* chromosome differ in the number, location, and identity of tRNAs included in the primary transcript. Some copies of the gene have additional tRNA gene segments between the 16S and 23S rRNA segments and at the far 3′ end of the primary transcript.

تکامل rRNA در یوکاریوت ها



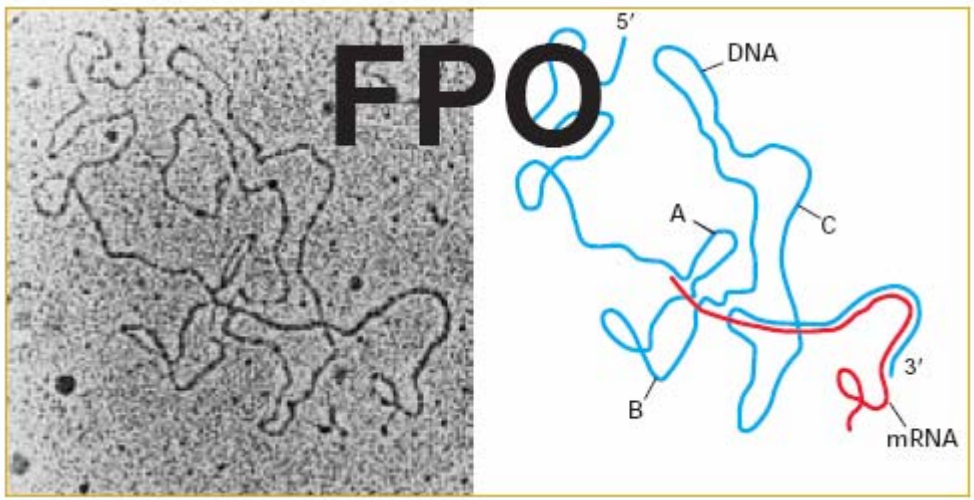




- Processing
- اینترون و اگزون
- Splicing

در mRNA یوکاریوتی:

- اگزون ها ۱۰۰ تا ۲۰۰ نوکلئوتید (کمتر از ۱۰۰۰)
- اینترون ها ۵۰ تا ۲۰۰۰۰ نوکلئوتید



kb. (b) Electron micrograph (*left*) and schematic drawing (*right*) of hybrid between an *Eco*RI A fragment and hexon mRNA. The loops marked A, B, and C correspond to the introns indicated in (a). Since these intron sequences in the viral genomic DNA are not present in mature hexon mRNA, they loop out between the exon sequences that hybridize to their complementary sequences in the mRNA. [Micrograph from S. M. Berget et al., 1977, *Proc. Natl. Acad. Sci. USA* **74**:3171; courtesy of P. A. Sharp.]

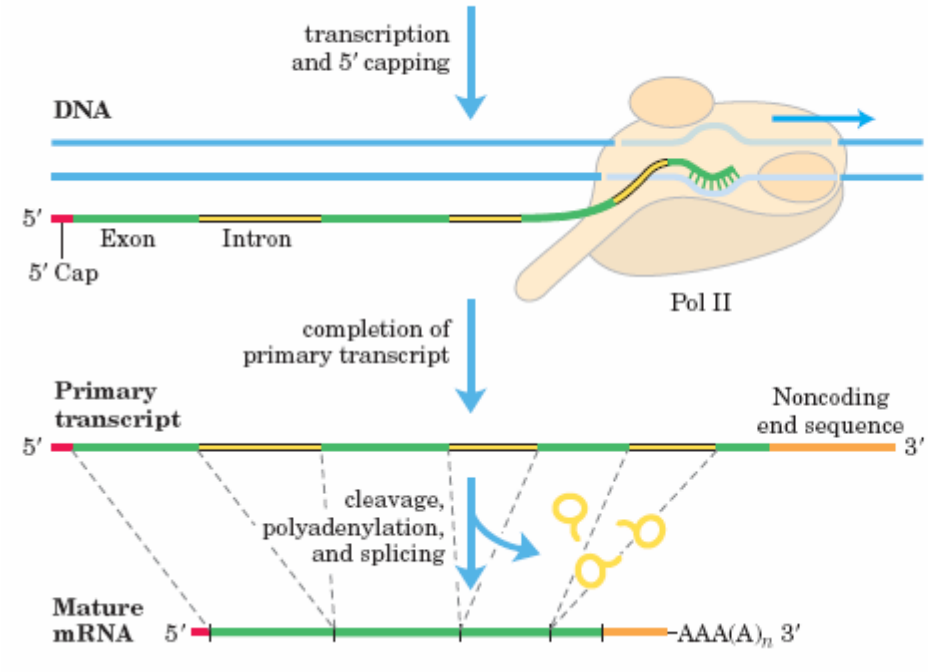


FIGURE 26–11 Formation of the primary transcript and its processing during maturation of mRNA in a eukaryotic cell. The 5′ cap (red) is added before synthesis of the primary transcript is complete. A noncoding sequence following the last exon is shown in orange. Splicing can occur either before or after the cleavage and polyadenylation steps. All the processes shown here take place within the nucleus.

گروه I

Group I introns are found in some nuclear, mitochondrial, and chloroplast genes coding for **rRNAs**, **mRNAs**, and **tRNAs**.

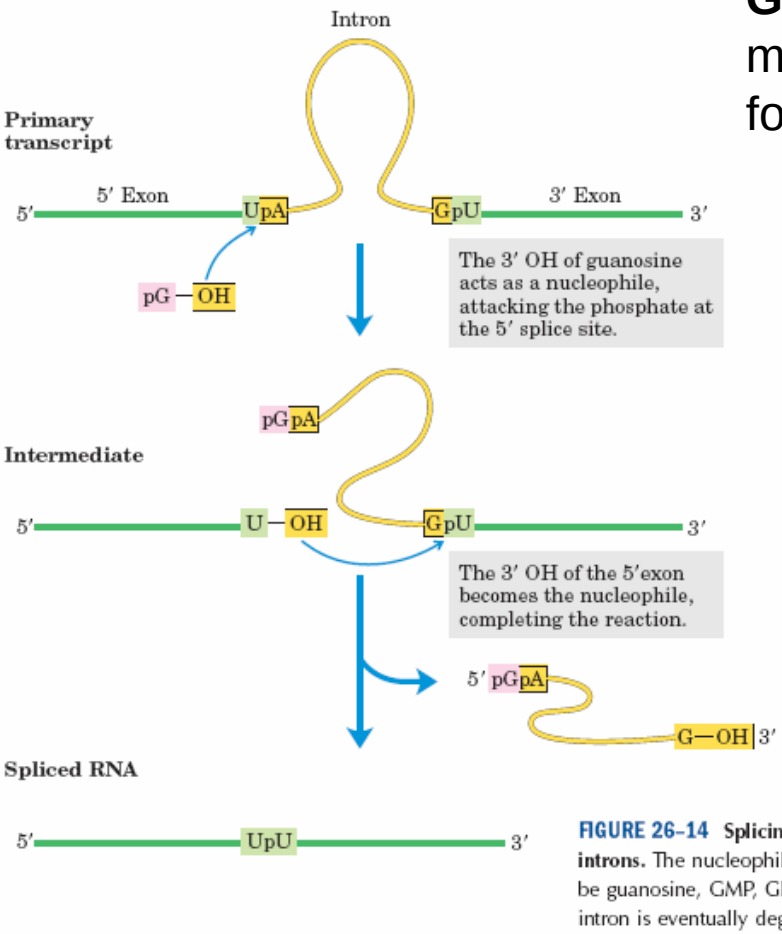


FIGURE 26–14 Splicing mechanism of group I introns. The nucleophile in the first step may be guanosine, GMP, GDP, or GTP. The spliced intron is eventually degraded.

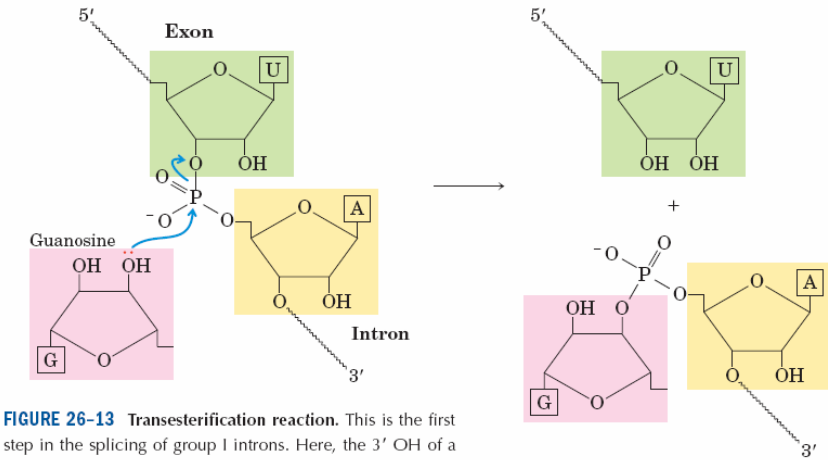


FIGURE 26–13 Transesterification reaction. This is the first step in the splicing of group I introns. Here, the 3′ OH of a guanosine molecule acts as nucleophile.

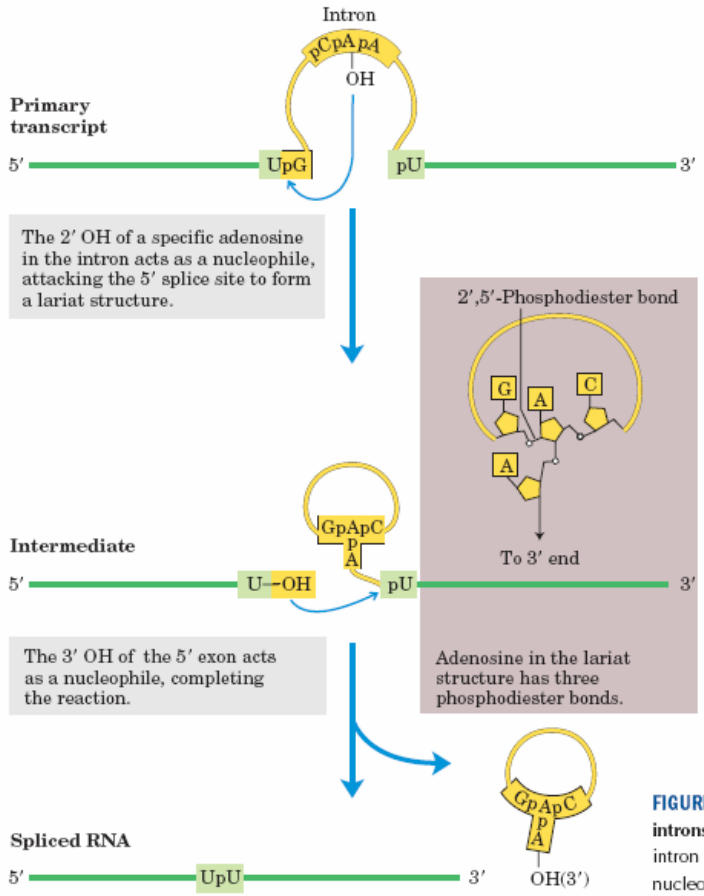
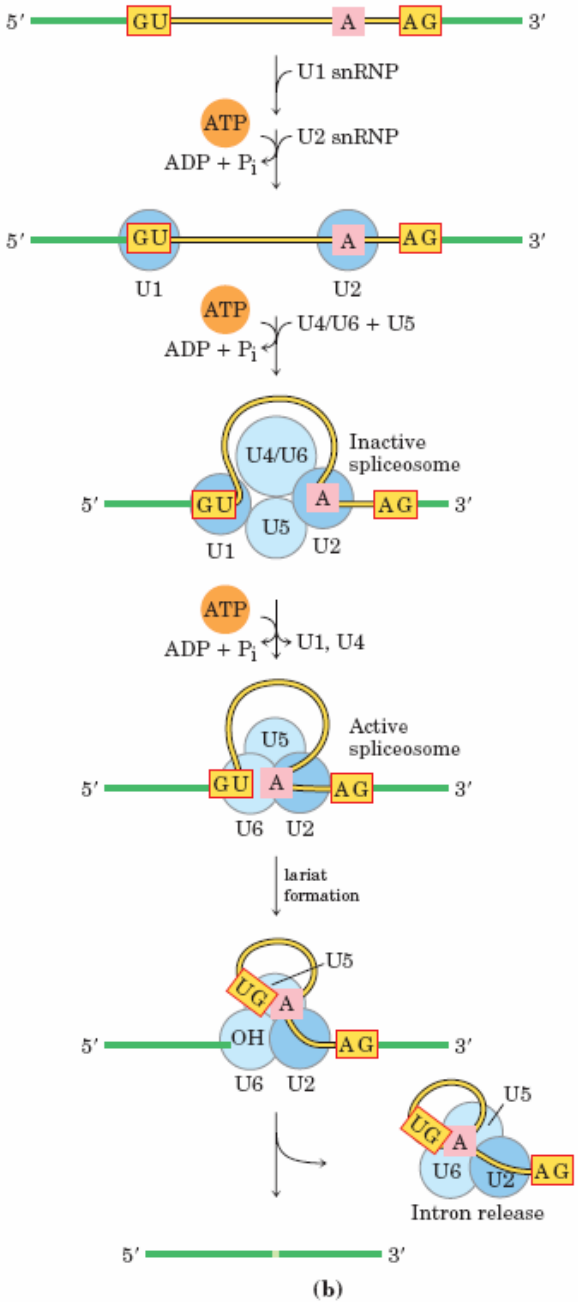
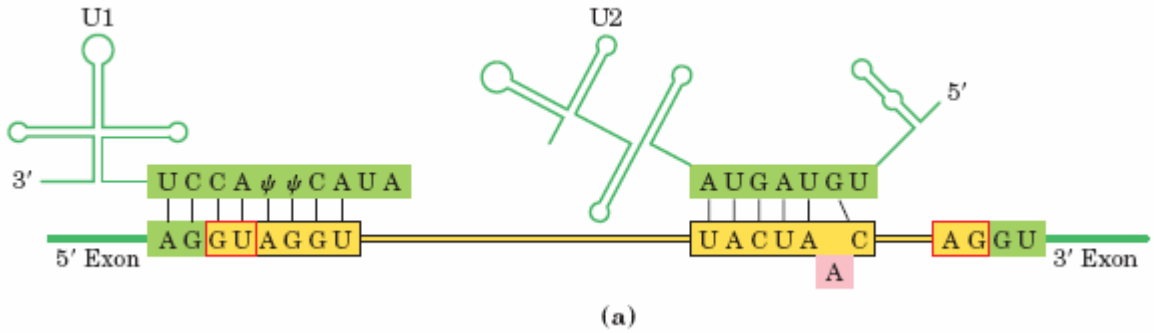


FIGURE 26–15 Splicing mechanism of group II introns. The chemistry is similar to that of group I intron splicing, except for the identity of the nucleophile in the first step and formation of a lariatlike intermediate, in which one branch is a 2′,5′-phosphodiester bond.

Group II introns are generally found in the primary transcripts of mitochondrial or chloroplast **mRNAs** in fungi, algae, and plants.

اینترون های کلاس III





Nuclear mRNA

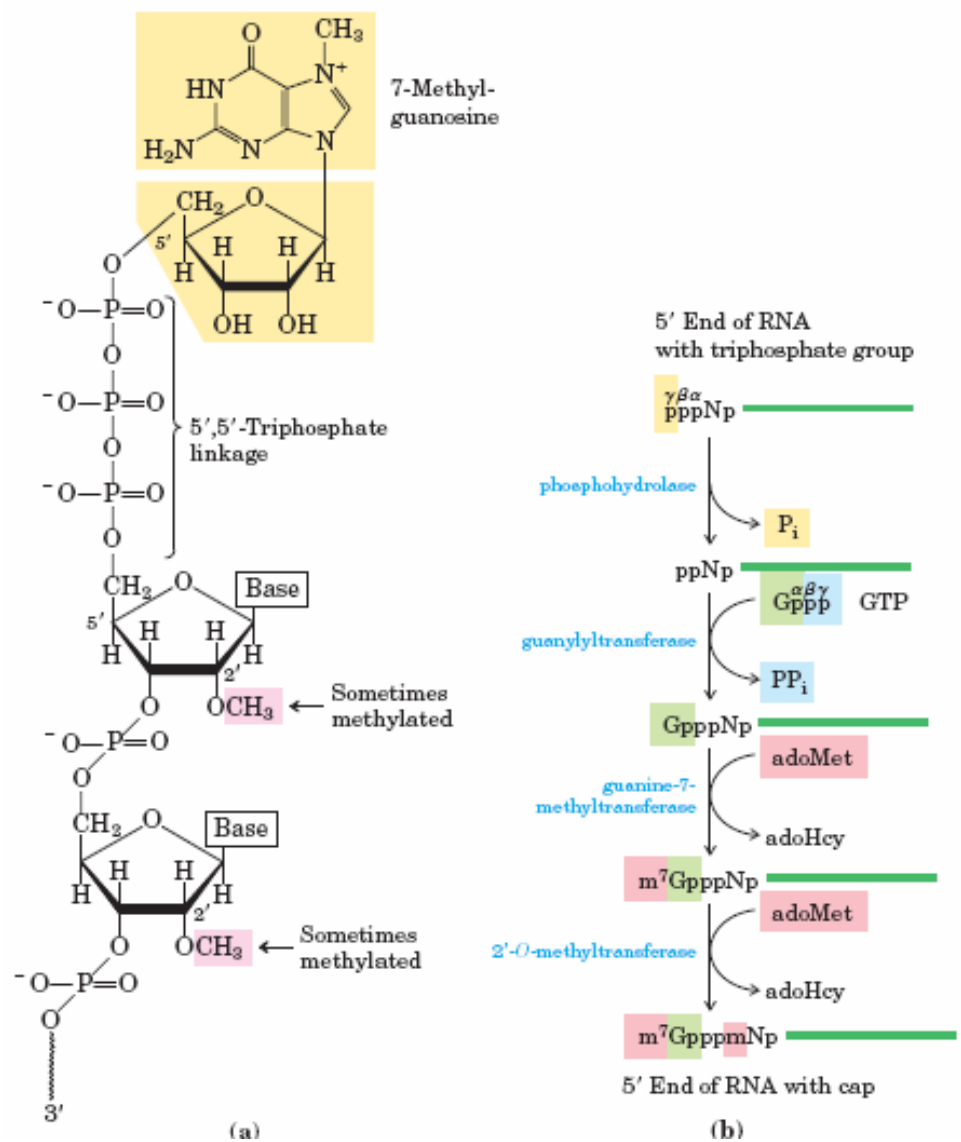
FIGURE 26–16 Splicing mechanism in mRNA primary transcripts. **(a)** RNA pairing interactions in the formation of spliceosome complexes. The U1 snRNA has a sequence near its 5′ end that is complementary to the splice site at the 5′ end of the intron. Base pairing of U1 to this region of the primary transcript helps define the 5′ splice site during spliceosome assembly (Ψ is pseudouridine; see Fig. 26–24). U2 is paired to the intron at a position encompassing the A residue (shaded pink) that becomes the nucleophile during the splicing reaction. Base pairing of U2 snRNA causes a bulge that displaces and helps to activate the adenylate, whose 2′ OH will form the lariat structure through a 2′,5′-phosphodiester bond.

(b) Assembly of spliceosomes. The U1 and U2 snRNPs bind, then the remaining snRNPs (the U4/U6 complex and U5) bind to form an inactive spliceosome. Internal rearrangements convert this species to an active spliceosome in which U1 and U4 have been expelled and U6 is paired with both the 5′ splice site and U2. This is followed by the catalytic steps, which parallel those of the splicing of group II introns (see Fig. 26–15).

اینترون های کلاس IV

- Found in certain tRNAs
- Requires ATP and an endonuclease.

5’ cap


7-Methyl-guanosine
5′,5′-Triphosphate linkage
Base
Sometimes methylated
Base
Sometimes methylated
3′
(a)
5′ End of RNA with triphosphate group
pppNp
phosphohydrolase
Pi
ppNp
GTP
guanylyltransferase
PPi
GpppNp
adoMet
guanine-7-methyltransferase
adoHcy
m7GpppNp
adoMet
2′-O-methyltransferase
adoHcy
m7GpppmNp
5′ End of RNA with cap
(b)

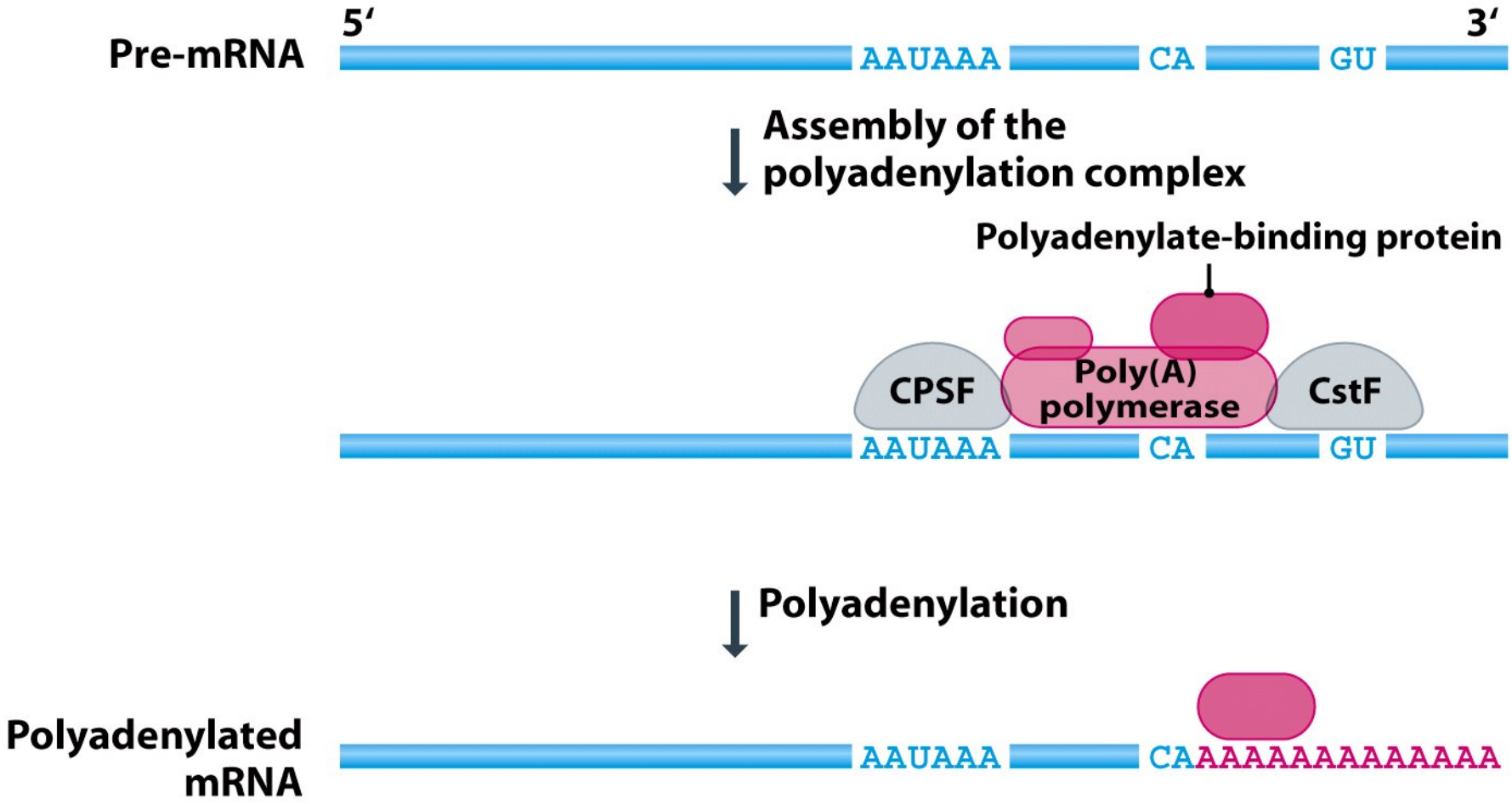


Figure 12.22 *Genomes 3* (© Garland Science 2007)

3’ poly A

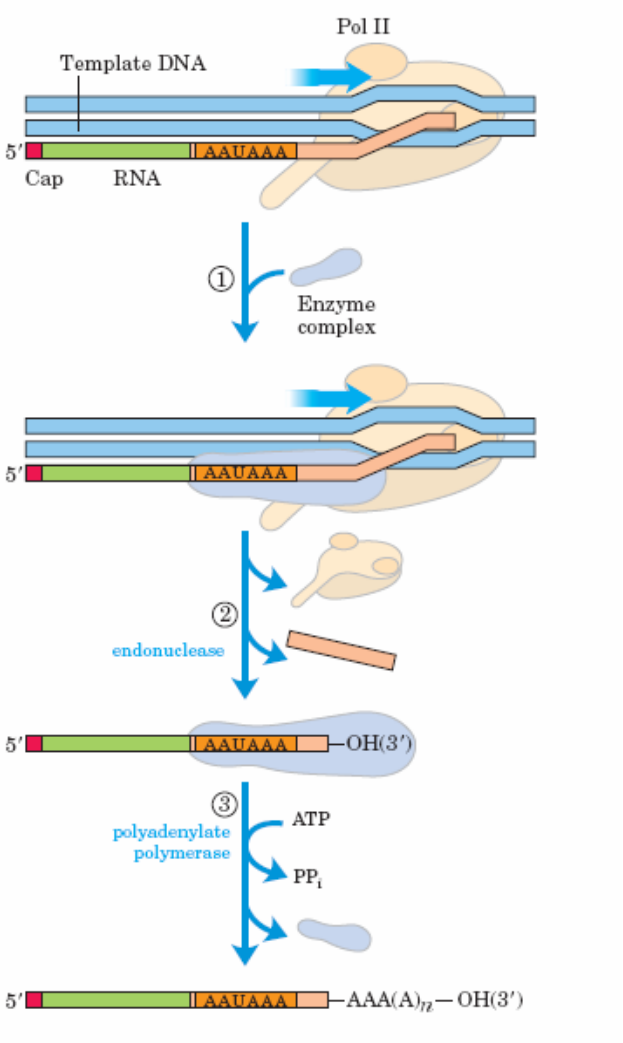


FIGURE 26–17 Addition of the poly(A) tail to the primary RNA transcript of eukaryotes. Pol II synthesizes RNA beyond the segment of the transcript containing the cleavage signal sequences, including the highly conserved upstream sequence (5′)AAUAAA. ① The cleavage signal sequence is bound by an enzyme complex that includes an endonuclease, a polyadenylate polymerase, and several other multisubunit proteins involved in sequence recognition, stimulation of cleavage, and regulation of the length of the poly(A) tail. ② The RNA is cleaved by the endonuclease at a point 10 to 30 nucleotides 3′ to (downstream of) the sequence AAUAAA. ③ The polyadenylate polymerase synthesizes a poly(A) tail 80 to 250 nucleotides long, beginning at the cleavage site.

پیرایش

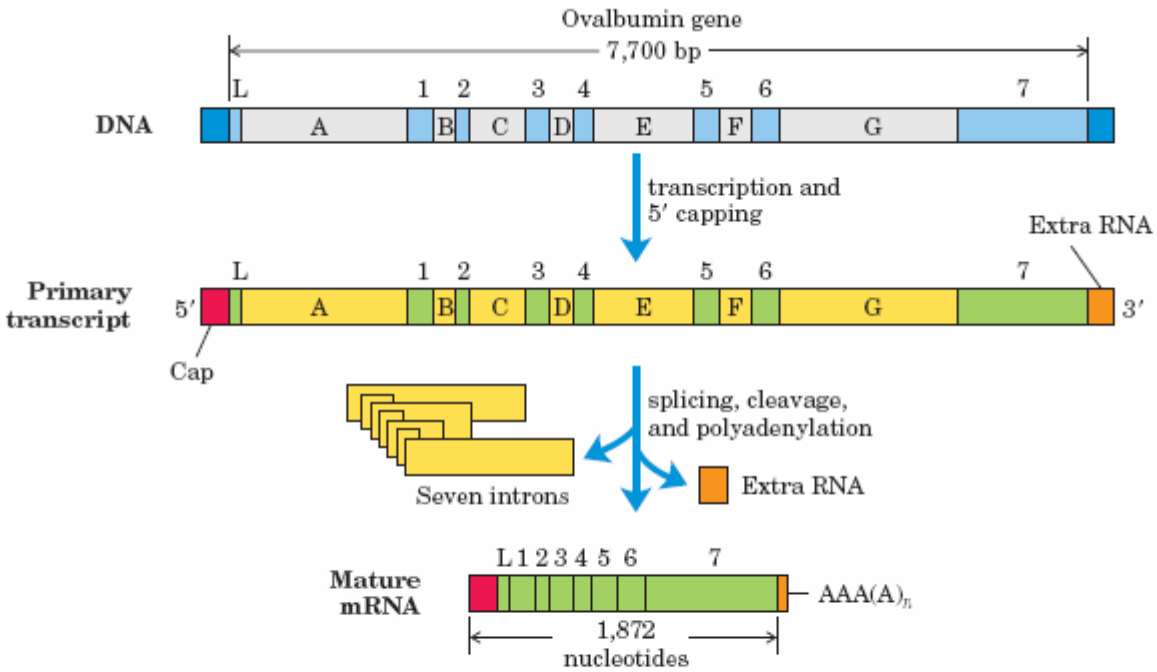
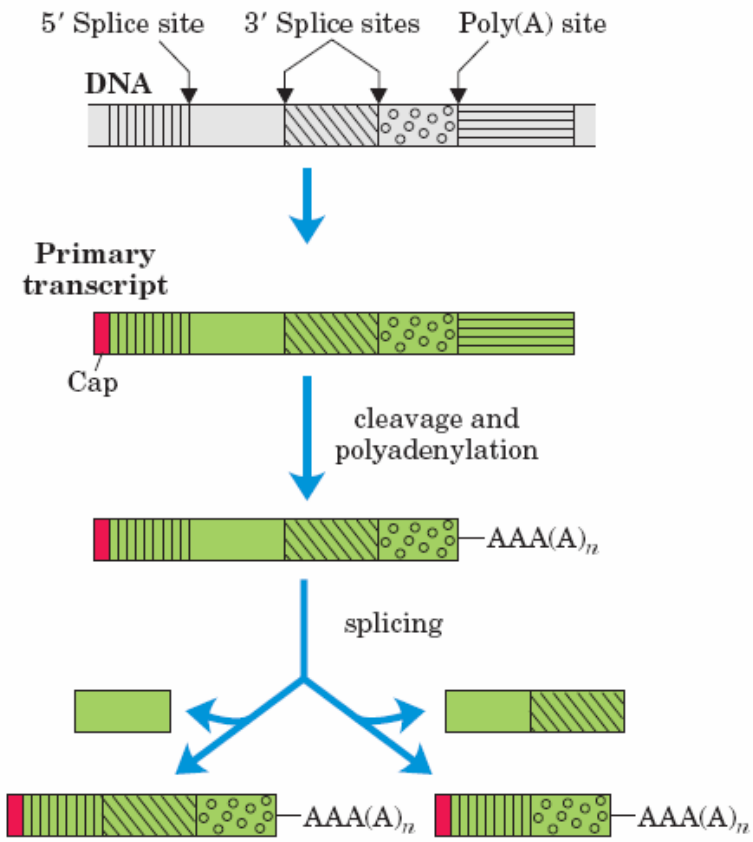


FIGURE 26–18 Overview of the processing of a eukaryotic mRNA. The ovalbumin gene, shown here, has introns A to G and exons 1 to 7 and L (L encodes a signal peptide sequence that targets the protein for export from the cell; see Fig. 27–34). About three-quarters of the RNA is removed during processing. Pol II extends the primary transcript well beyond the cleavage and polyadenylation site ("extra RNA") before terminating transcription. Termination signals for Pol II have not yet been defined.

Animation

Alternative splicing



(b) Alternative splicing patterns. Two different 3′ splice sites are shown. In both mechanisms, different mature mRNAs are produced from the same primary transcript.

Alternative splicing

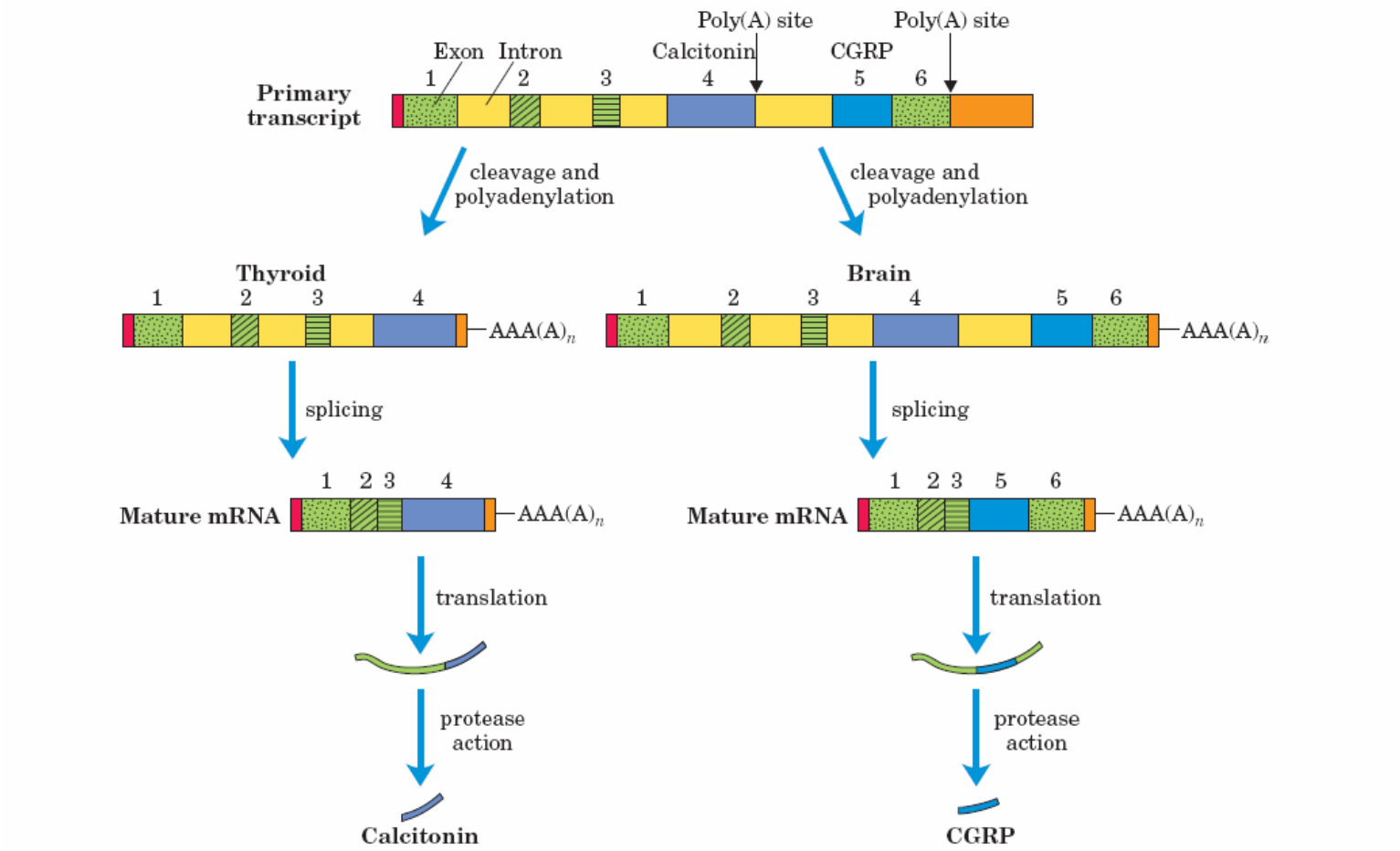
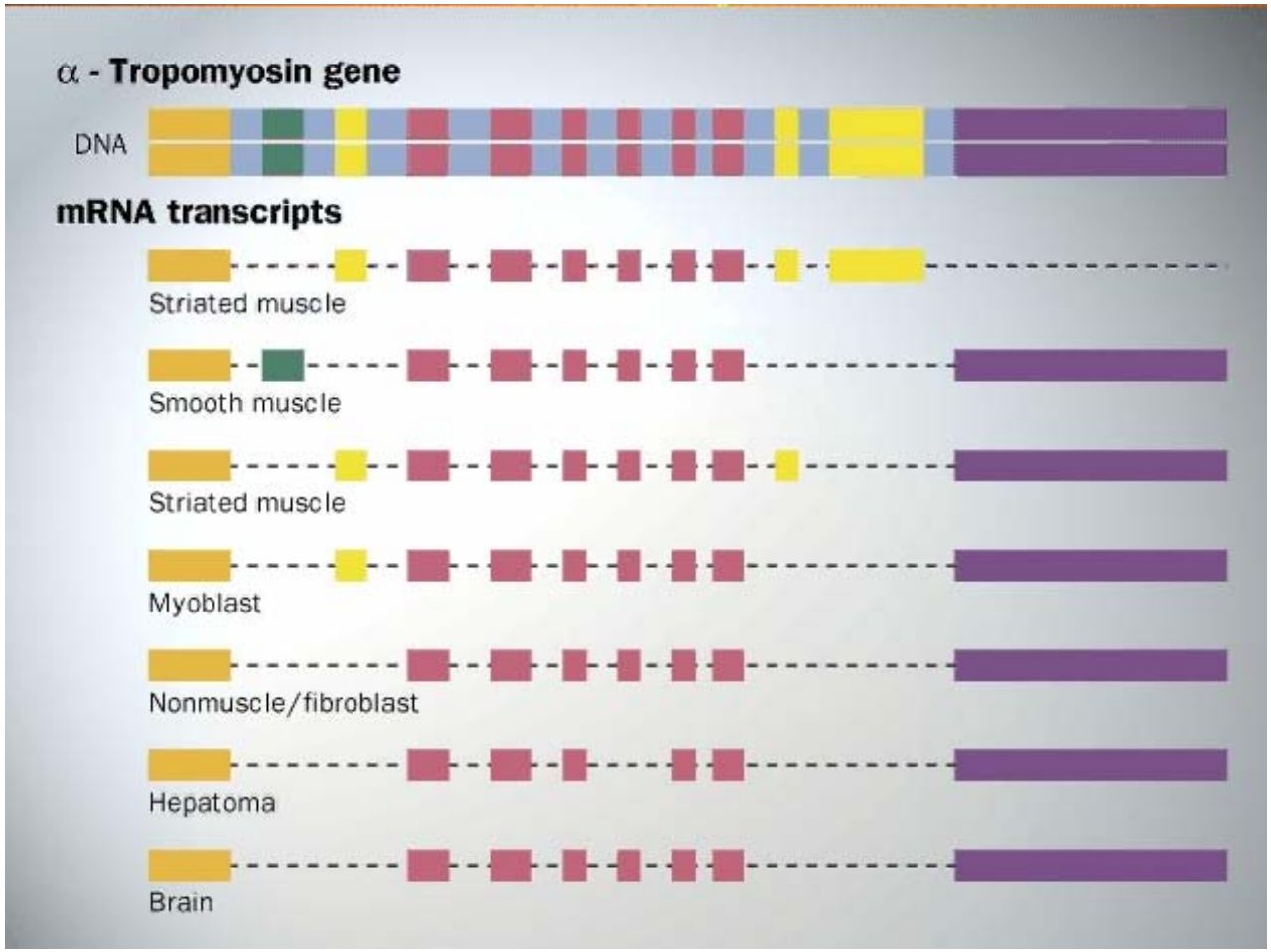


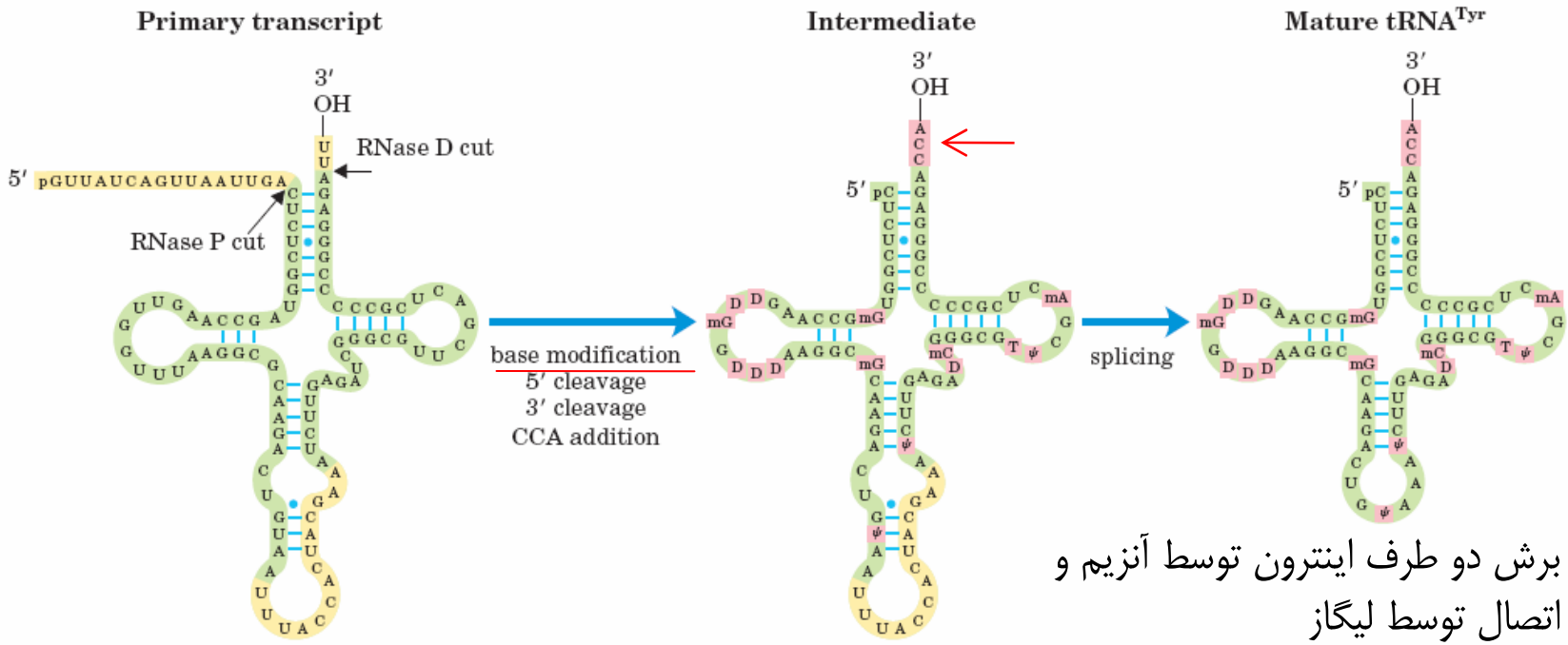
FIGURE 26–20 Alternative processing of the calcitonin gene transcript in rats. The primary transcript has two poly(A) sites; one predominates in the brain, the other in the thyroid. In the brain, splicing eliminates the calcitonin exon (exon 4); in the thyroid, this exon is retained. The resulting peptides are processed further to yield the final hormone products: calcitonin-gene-related peptide (CGRP) in the brain and calcitonin in the thyroid.

Alternative splicing



پردازش tRNA در یوکاریوت ها

تعدادی از tRNA های یوکاریوتی دارای اینترون هستند.



برش دو طرف اینترون توسط آنزیم و اتصال توسط لیگاز

FIGURE 26–23 **Processing of *t*RNAs in bacteria and eukaryotes.** The yeast $tRNA^{Tyr}$ (the tRNA specific for tyrosine binding; see Chapter 27) is used to illustrate the important steps. The nucleotide sequences shown in yellow are removed from the primary transcript. The ends are processed first, the 5′ end before the 3′ end. CCA is then added to the 3′ end, a necessary step in processing eukaryotic tRNAs and those bacterial tRNAs that lack this sequence in the primary transcript. While the ends are being processed, specific bases in the rest of the transcript are modified (see Fig. 26–24). For the eukaryotic tRNA shown here, the final step is splicing of the 14-nucleotide intron. Introns are found in some eukaryotic tRNAs but not in bacterial tRNAs.