

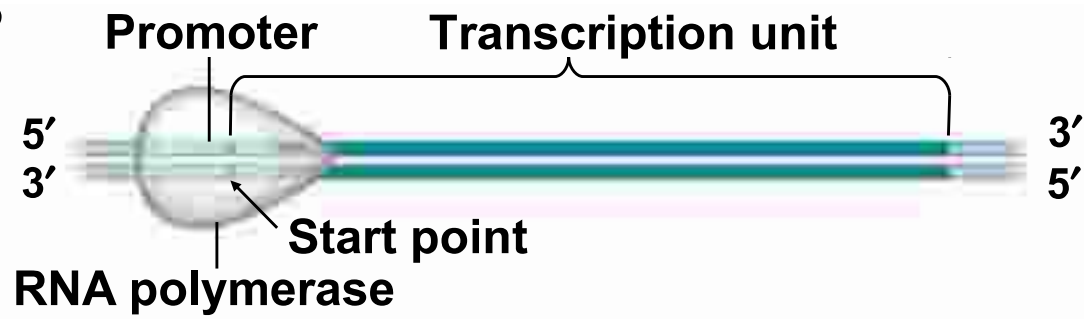
Molecular Components of Transcription

- RNA synthesis is catalyzed by **RNA polymerase**, which pries the DNA strands apart and hooks together the RNA nucleotides
- RNA synthesis follows the same base-pairing rules as DNA, **except uracil substitutes for thymine**
- The DNA sequence where RNA polymerase attaches is called the **promoter**; in prokaryotes, the sequence signaling the end of transcription is called **the terminator**
- The stretch of DNA that is transcribed is called a transcription unit

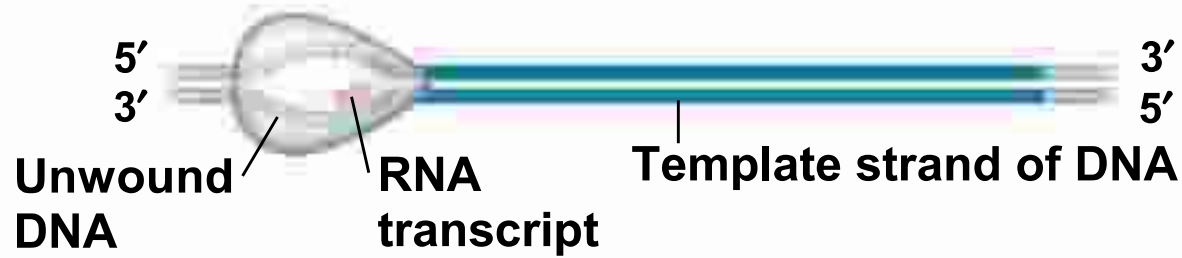
Synthesis of an RNA Transcript

- The three stages of transcription:
 - Initiation
 - Elongation
 - Termination

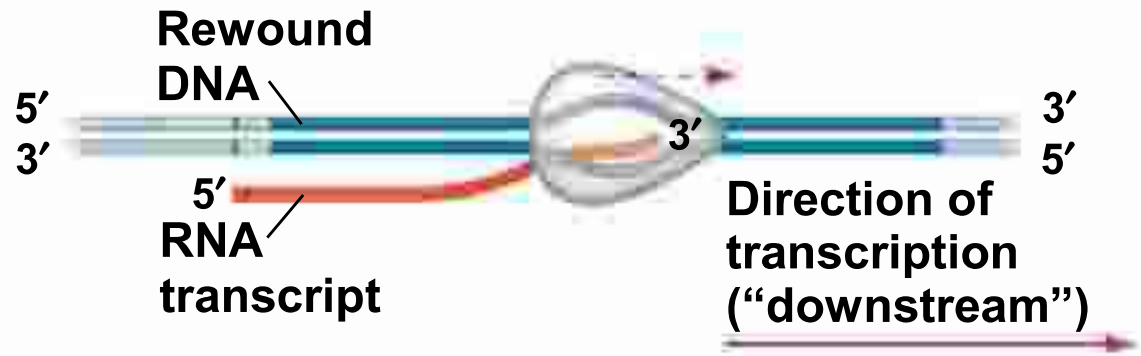
Figure 17.7-3



1 Initiation



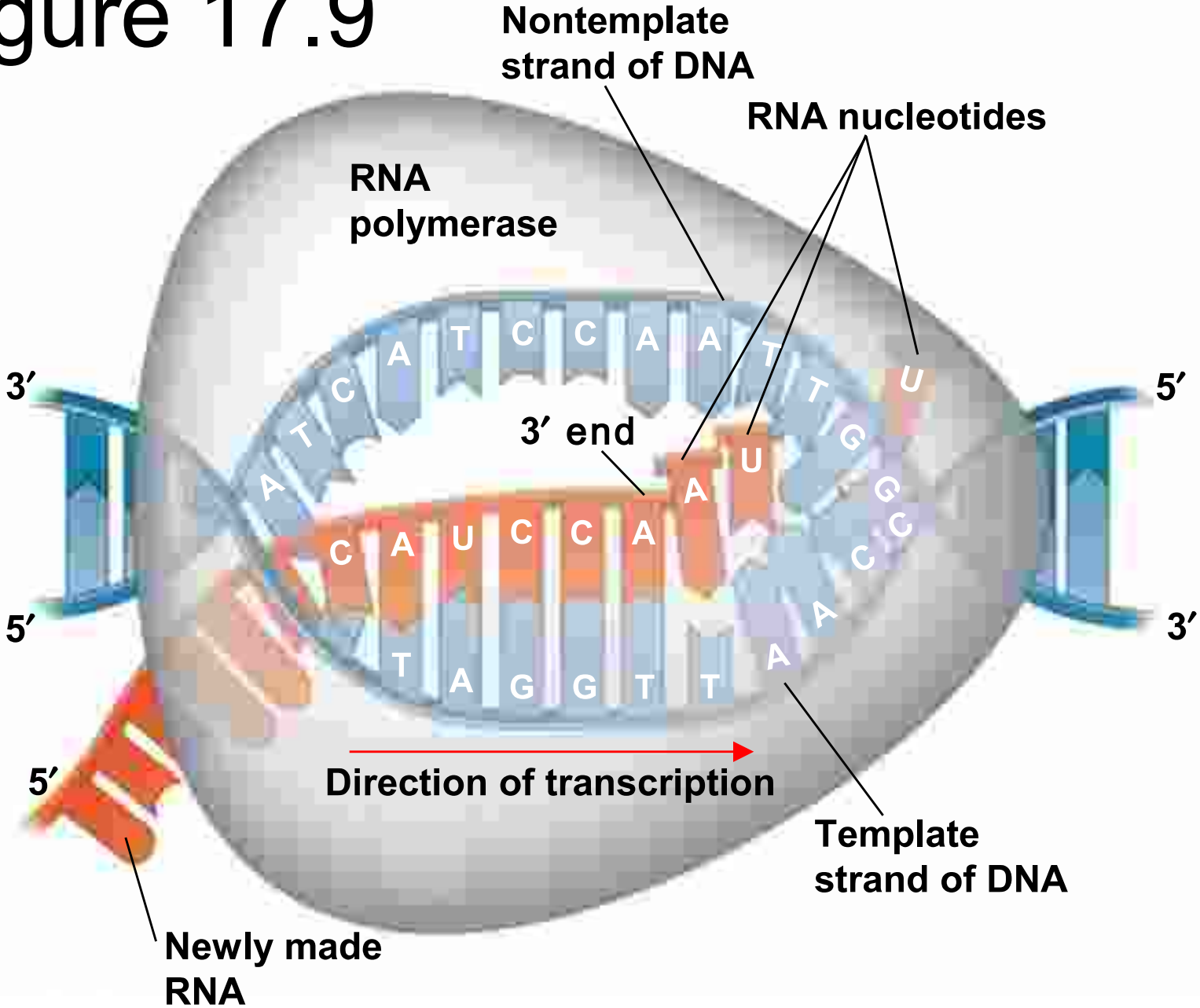
2 Elongation



3 Termination

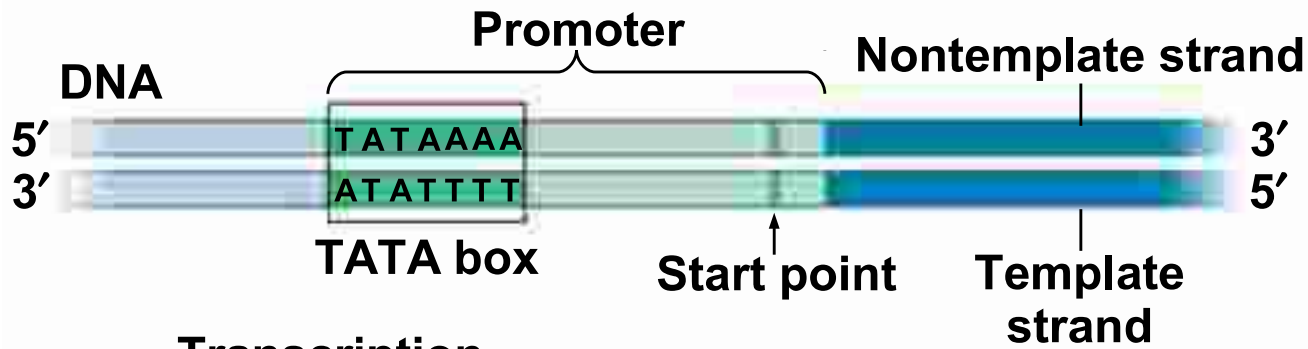


Figure 17.9

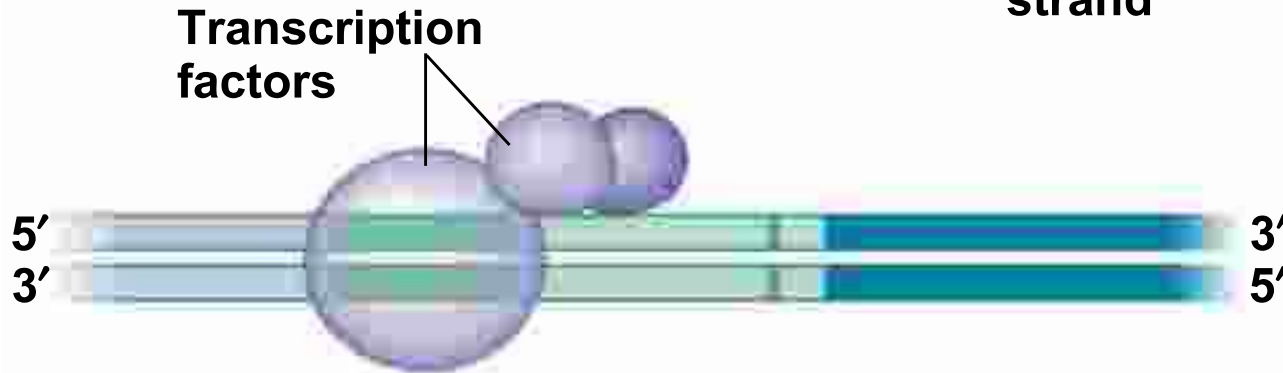


RNA Polymerase Binding and Initiation of Transcription

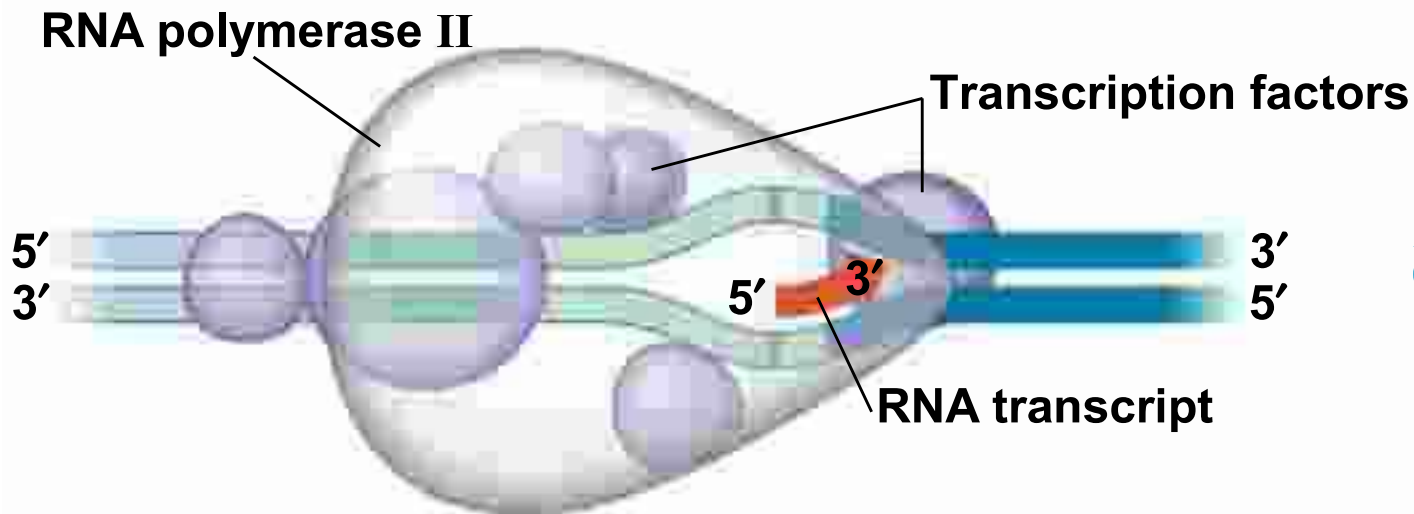
- Promoters signal the initiation of RNA synthesis
- **Transcription factors** mediate the binding of RNA polymerase and initiation of transcription in eukaryotes
- The completed assembly of transcription factors and RNA polymerase II bound to a promoter is called a **transcription initiation complex**
- A promoter called a **TATA box** is crucial in forming the initiation complex in eukaryotes



1 A eukaryotic promoter



2 Several transcription factors bind to DNA.



3 Transcription initiation complex forms.

Transcription initiation complex

Elongation of the RNA Strand

- As RNA polymerase moves along the DNA, it untwists the double helix, 10 to 20 bases at a time
- Transcription progresses at a rate of 40 nucleotides per second in eukaryotes
- A gene can be transcribed simultaneously by several RNA polymerases

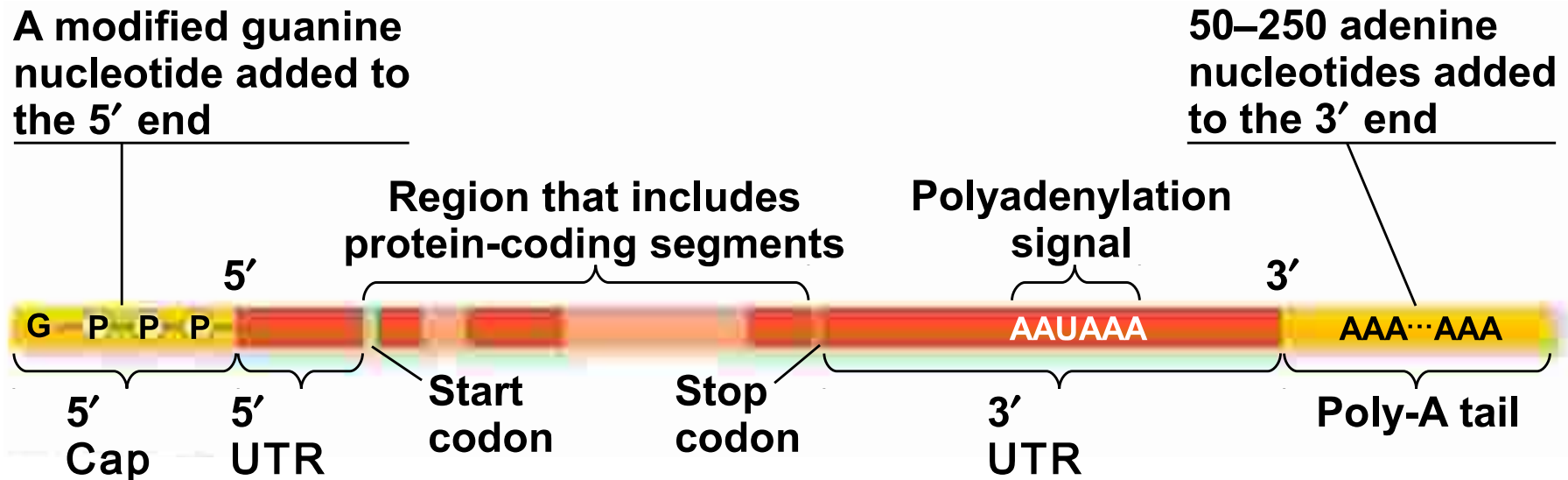
Termination of Transcription

- The mechanisms of termination are different in prokaryotes and eukaryotes
- In prokaryotes, the polymerase stops transcription at the end of the terminator
- In eukaryotes, RNA polymerase II transcribes the polyadenylation signal sequence; the RNA transcript is released 10–35 nucleotides past this polyadenylation sequence

Concept 17.3: **Eukaryotic** cells modify RNA after transcription

- Enzymes in the eukaryotic nucleus modify pre-mRNA (**RNA processing**) before the messages are dispatched to the cytoplasm
- During RNA processing, both ends of the primary transcript are usually altered (**5' cap and 3' polyA tail addition**)
- Also, usually some interior parts of the molecule are cut out, and the other parts spliced together (**RNA splicing**)

Figure 17.10



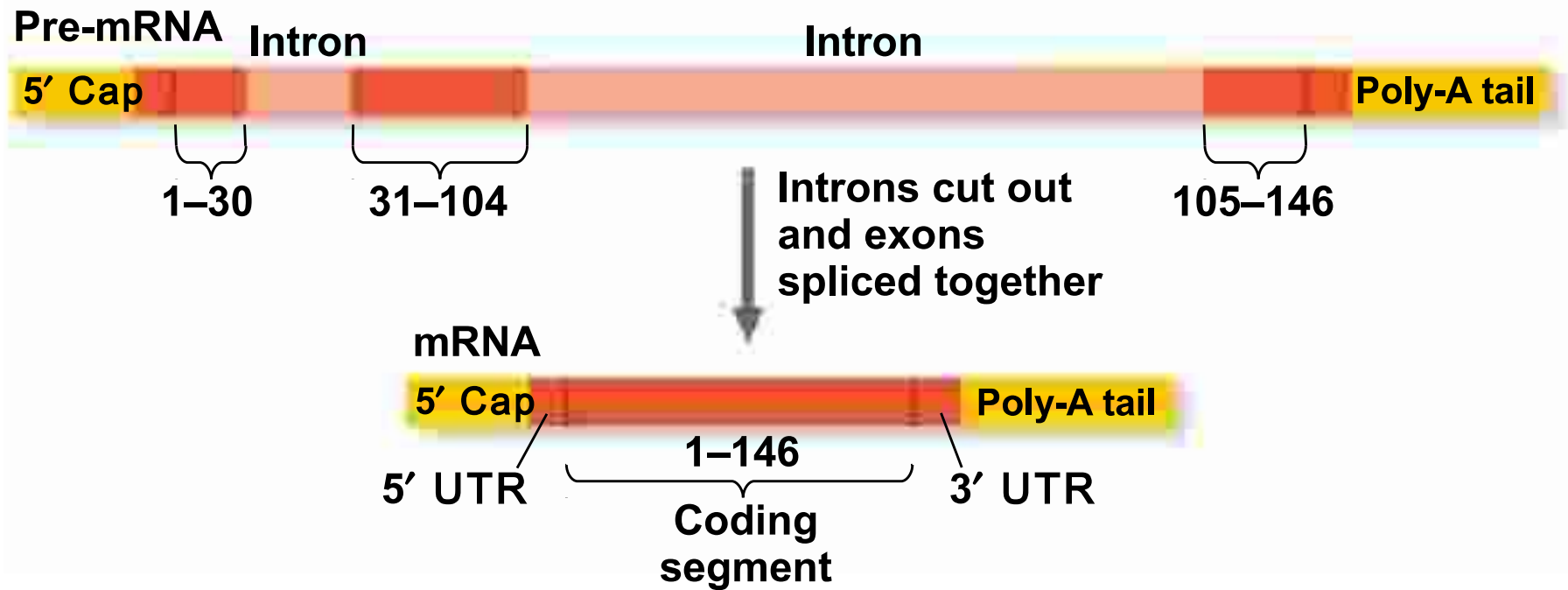
These modifications share several functions:

- They seem to facilitate the export of mRNA
- They protect mRNA from hydrolytic enzymes

Split Genes and RNA Splicing

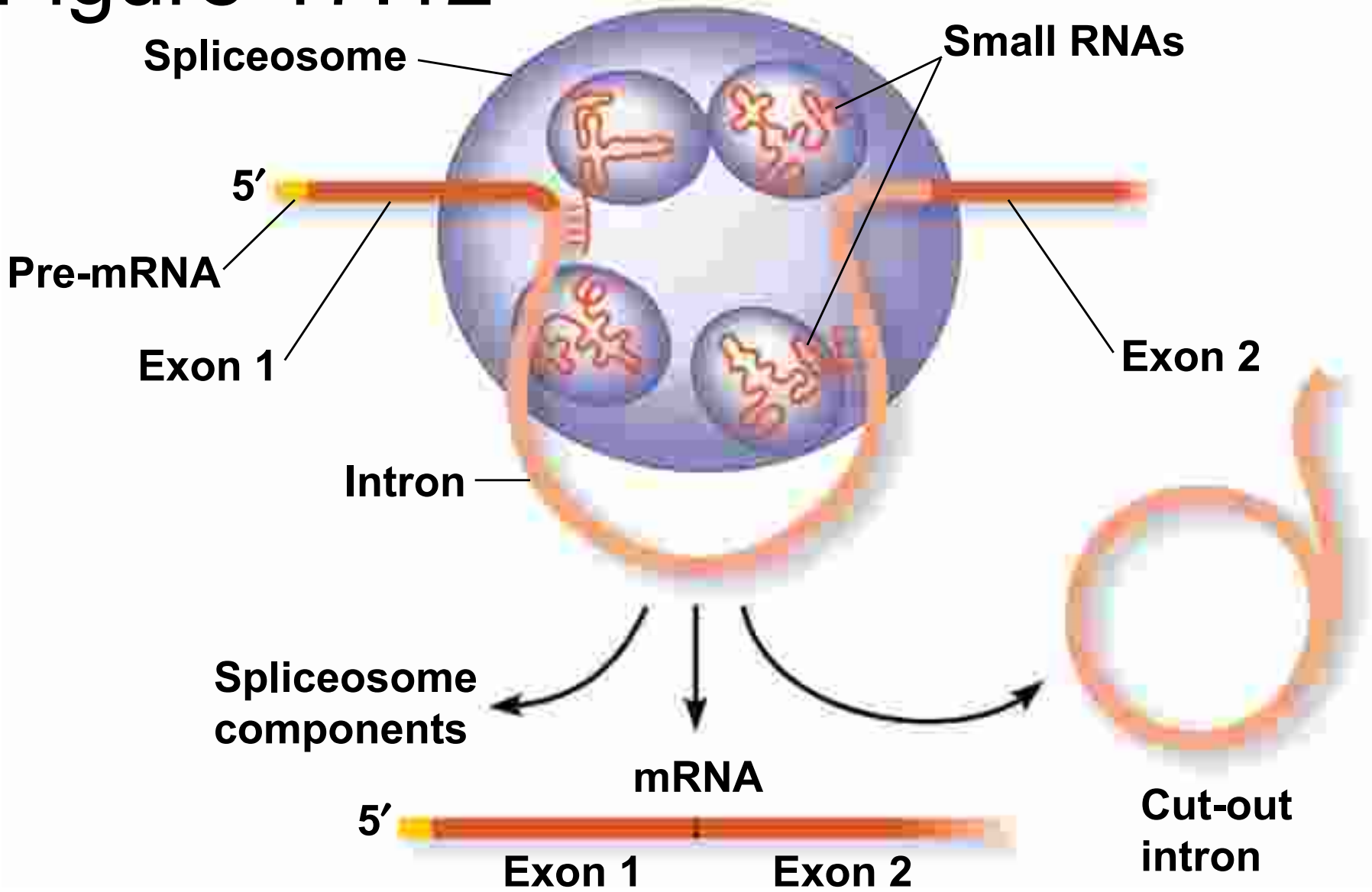
- Most eukaryotic genes and their RNA transcripts have long noncoding stretches of nucleotides that lie between coding regions
- These noncoding regions are called intervening sequences, or **introns**
- The other regions are called **exons** because they are eventually expressed, usually translated into amino acid sequences
- **RNA splicing removes introns and joins exons**, creating an mRNA molecule with a continuous coding sequence

Figure 17.11



- In some cases, RNA splicing is carried out by **spliceosomes**
- Spliceosomes consist of a variety of proteins and several small nuclear ribonucleoproteins (snRNPs) that recognize the splice sites

Figure 17.12



Ribozymes

- **Ribozymes** are catalytic RNA molecules
- Here they function as enzymes that can splice RNA
- The discovery of ribozymes rendered obsolete the belief that all biological catalysts were proteins

- Three properties of RNA enable it to function as an enzyme
 - It can form a three-dimensional structure because of its ability to base-pair with itself
 - Some bases in RNA contain functional groups that may participate in catalysis
 - RNA may hydrogen-bond with other nucleic acid molecules

The Functional and Evolutionary Importance of Introns

- Some introns contain sequences that may regulate gene expression
- Some genes can encode more than one kind of polypeptide, depending on which segments are treated as exons during splicing
- This is called **alternative RNA splicing**
- Consequently, the number of different proteins an organism can produce is much greater than its number of genes

- Proteins often have a modular architecture consisting of discrete regions called domains
- In many cases, different exons code for the different domains in a protein

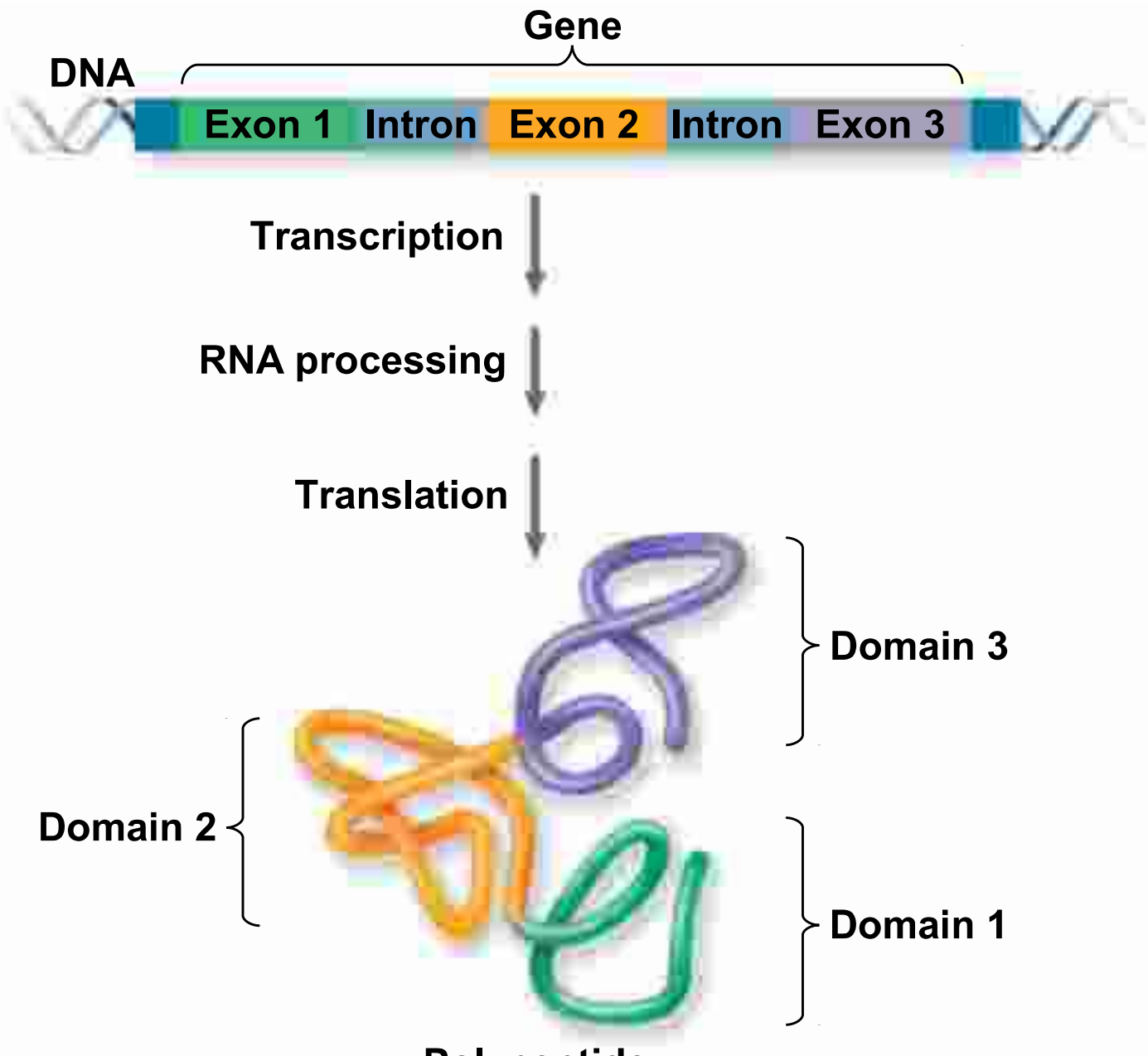


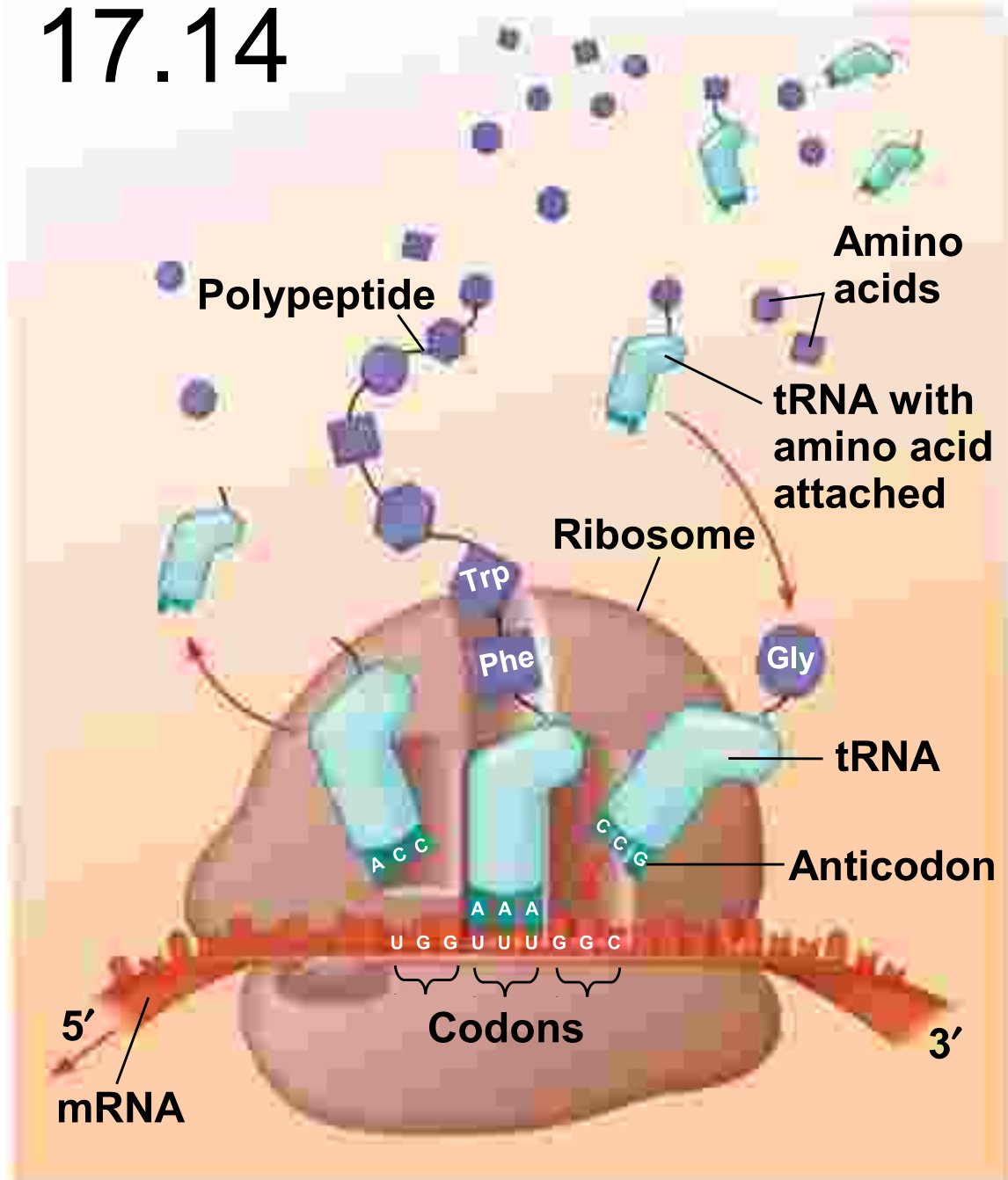
Figure 17.13

Polypeptide

Molecular Components of Translation

- A cell translates an mRNA message into protein with the help of transfer RNA (tRNA) & ribosomes
- tRNAs transfer amino acids to the growing polypeptide in a ribosome
- Molecules of tRNA are not identical:
 - Each carries a specific amino acid on one end
 - Each has an anticodon on the other end; the anticodon base-pairs with a complementary codon on mRNA

Figure 17.14

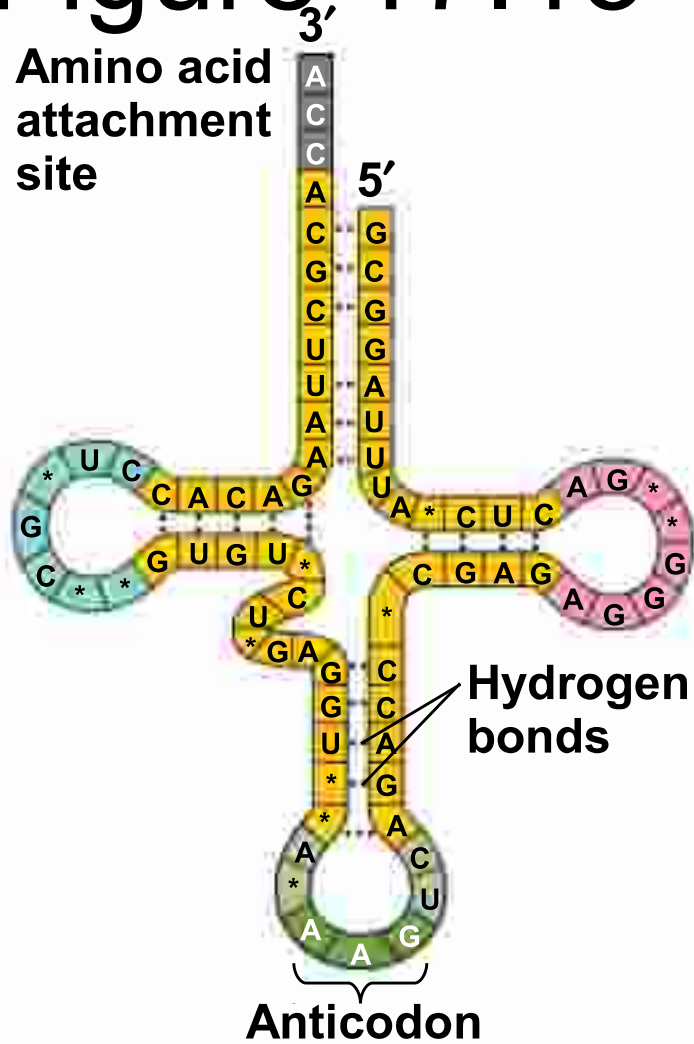


The Structure and Function of Transfer RNA

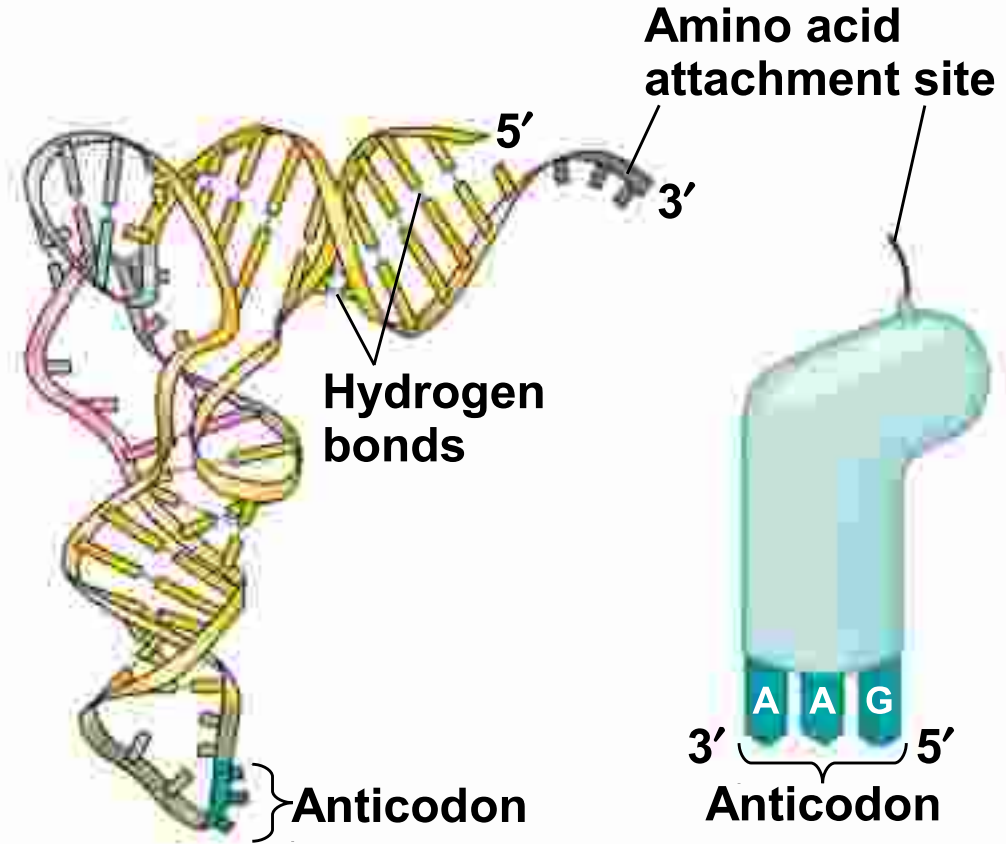
- A tRNA molecule consists of a single RNA strand that is only about 80 nucleotides long
- Flattened into one plane to reveal its base pairing, a tRNA molecule looks like a cloverleaf
- Amino acid at one end of sock and anticodon at the other
- Because of hydrogen bonds, tRNA actually twists and folds into a three-dimensional molecule
- tRNA is roughly L-shaped

Figure 17.15

Amino acid attachment site



(a) Two-dimensional structure



(b) Three-dimensional structure

(c) Symbol used in this book

- Accurate translation requires two steps:
 - First step: a correct match between a tRNA and an amino acid, done by the enzyme **aminoacyl-tRNA synthetase**
 - Second step: a correct match between the tRNA anticodon and an mRNA codon

Flexible pairing at the third base of a codon is called **wobble** and allows some tRNAs to bind to more than one codon

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