Prokaryotic transcription termination

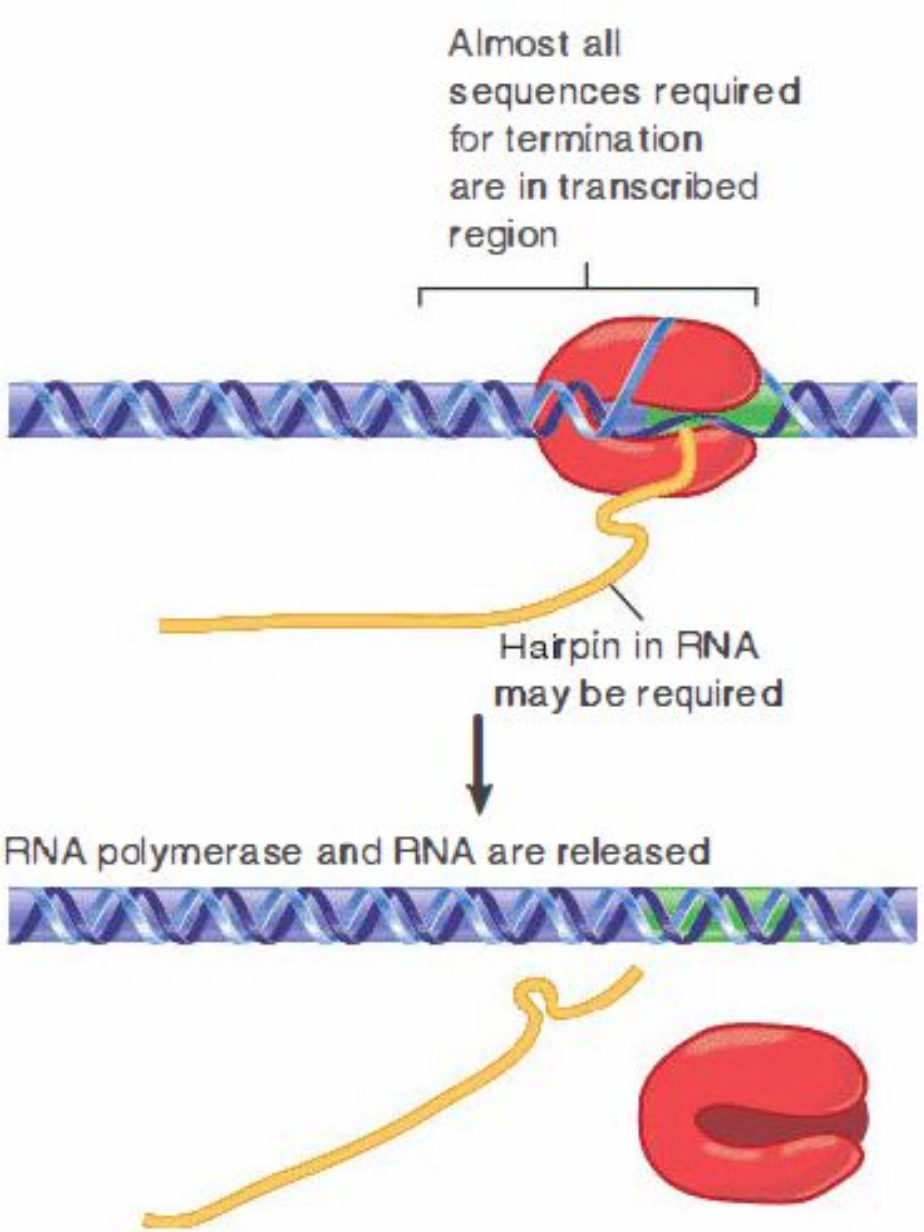
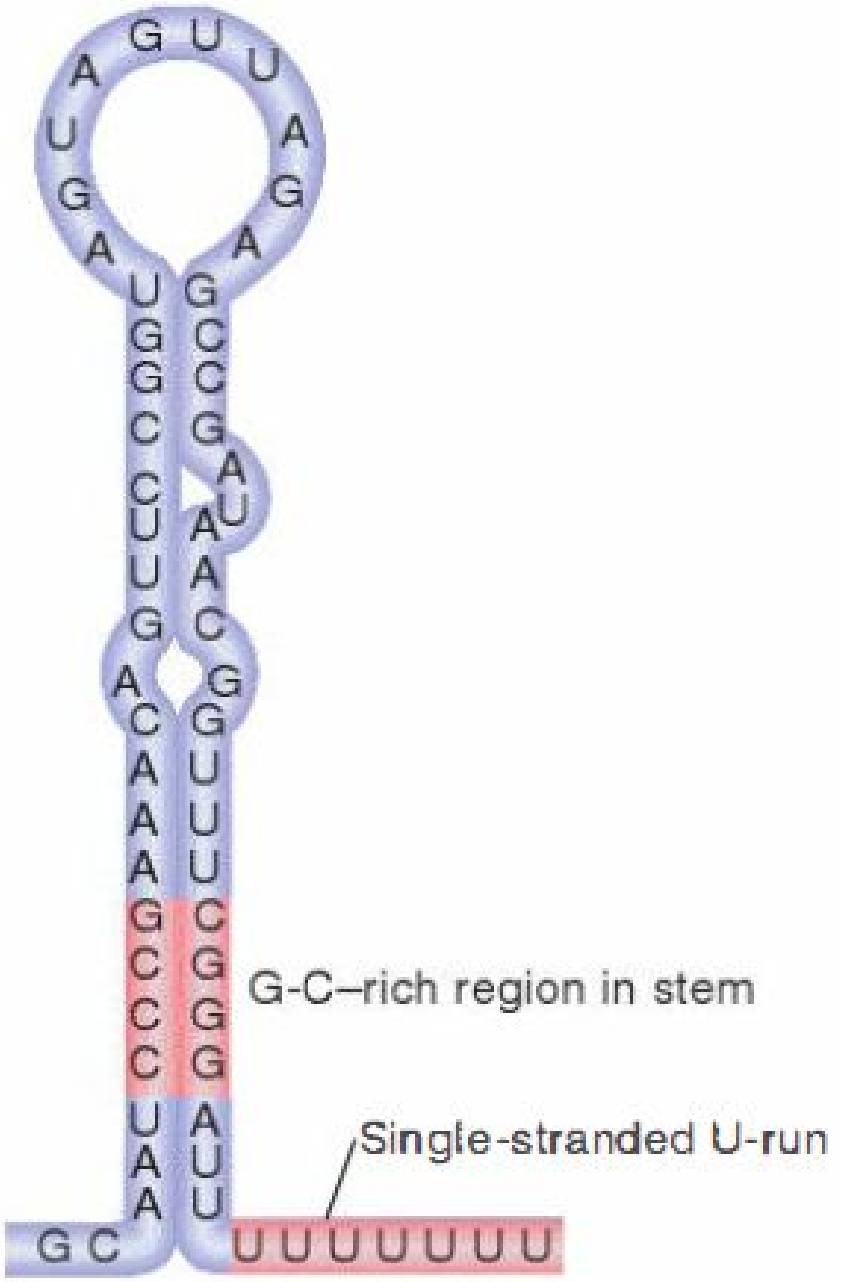


FIGURE 19.28 The DNA sequences required for termination are located upstream of the terminator sequence. Formation of a hairpin in the RNA may be necessary.

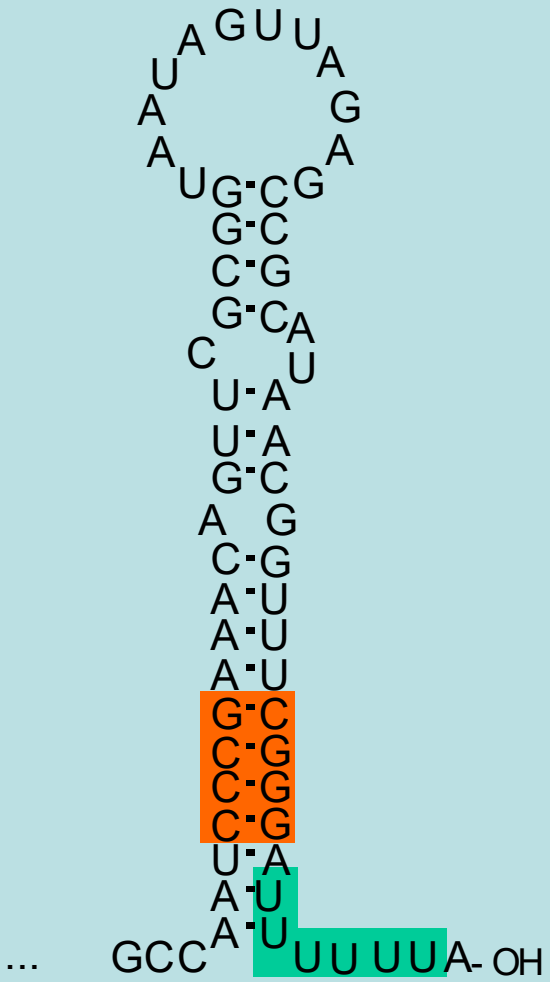
FIGURE 19.29

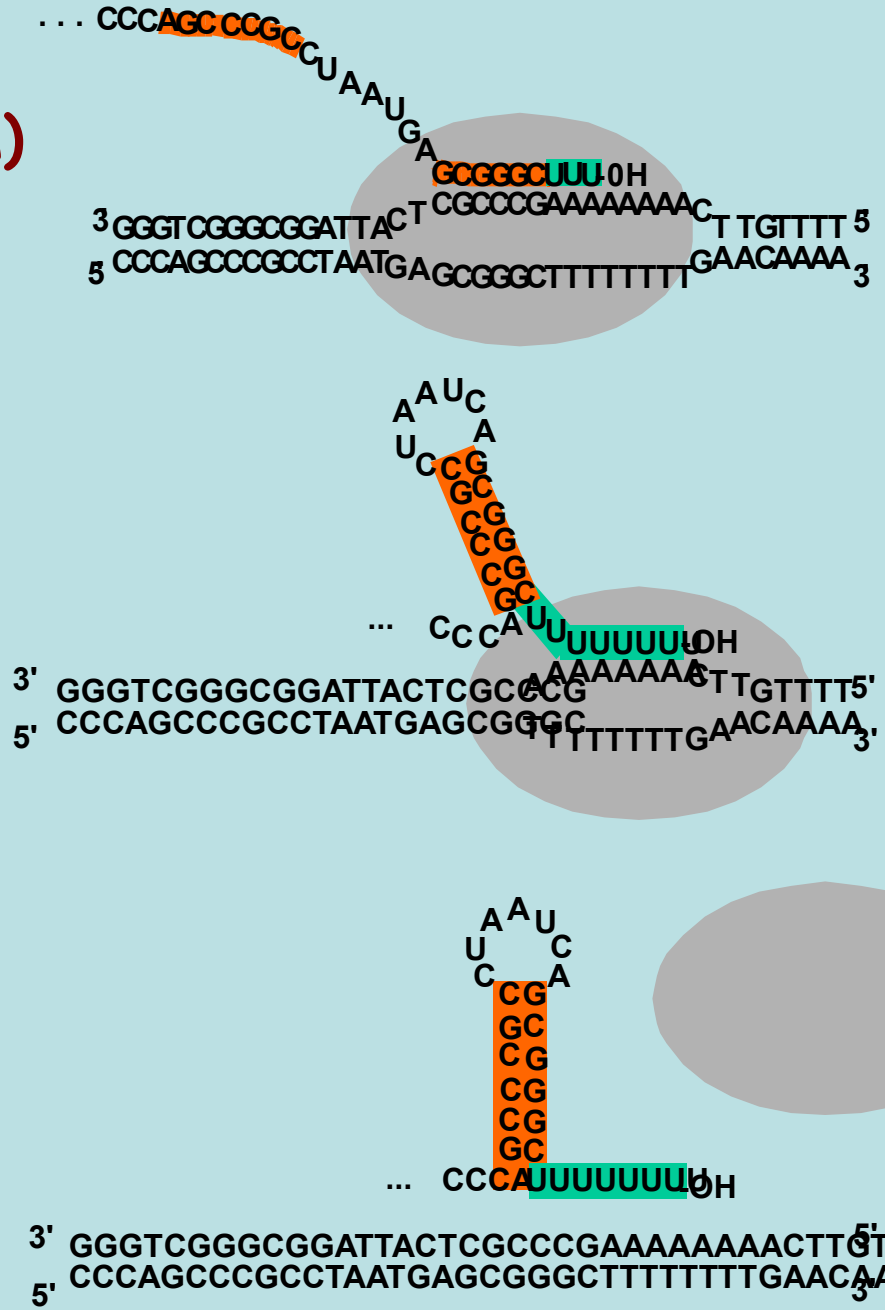
Intrinsic terminators

include palindromic regions that form hairpins varying in length from 7 to 20 bp. The stem-loop structure includes a G-C-rich region and is followed by a run of U residues.



Intrinsic terminator
(rho independent termination)





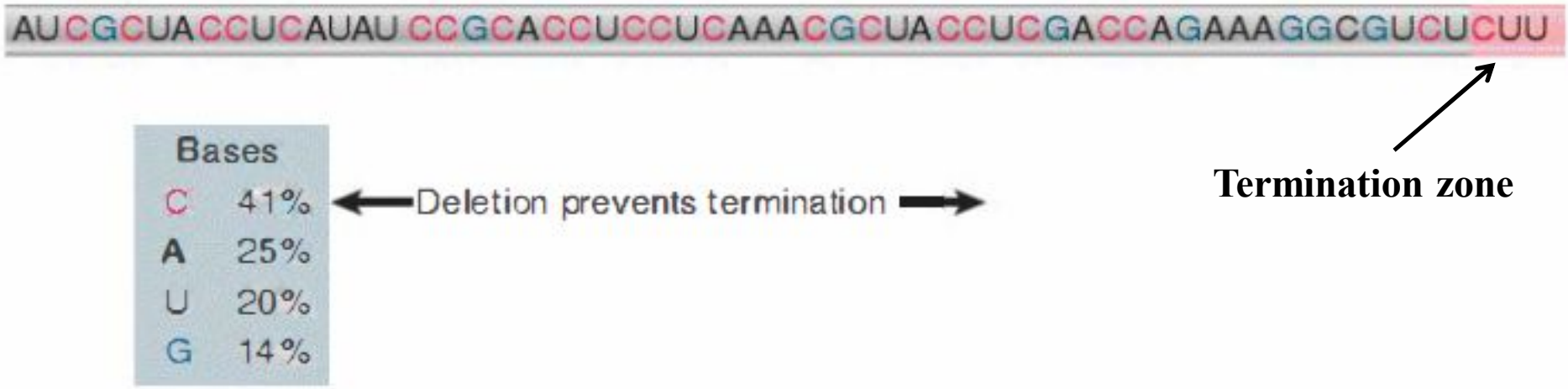


FIGURE 19.31

A rut site has a sequence rich in C and poor in G preceding the actual site(s) of termination.
The sequence corresponds to the 3' end of the RNA.

After binding to the rut site, rho uses its helicase activity, driven by ATP hydrolysis, to translocate along RNA until it reaches the RNA polymerase. It then may utilize its helicase activity to unwind the duplex structure and/or interact with RNA polymerase to help release RNA.

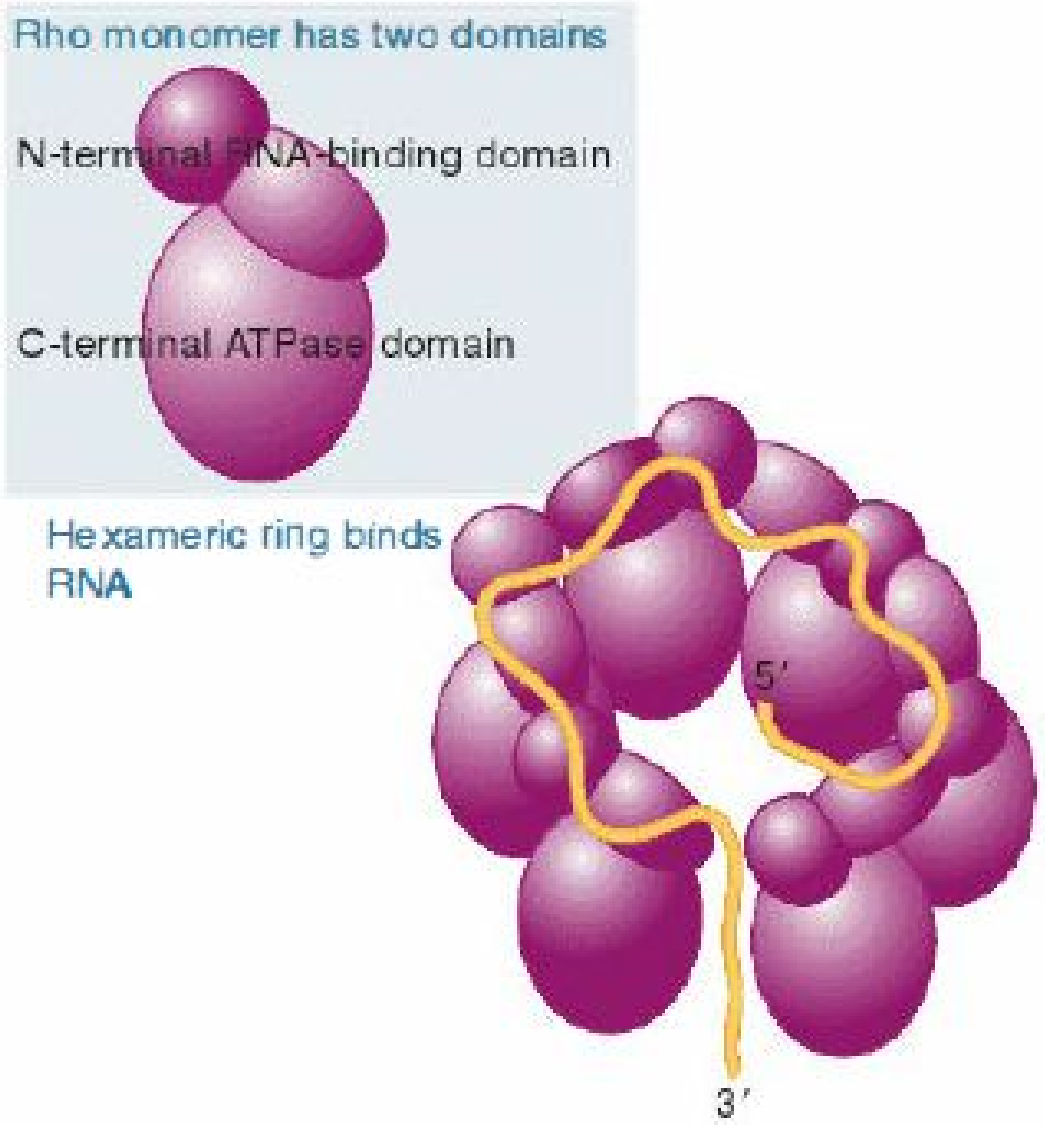


FIGURE 19.32 Rho has an N-terminal, RNA-binding domain and a C-terminal ATPase domain. A hexamer in the form of a gapped ring binds RNA along the exterior of the N-terminal domains. The 5′ end of the RNA is bound by a secondary binding site in the interior of the hexamer.

Internal Rho dependent terminator

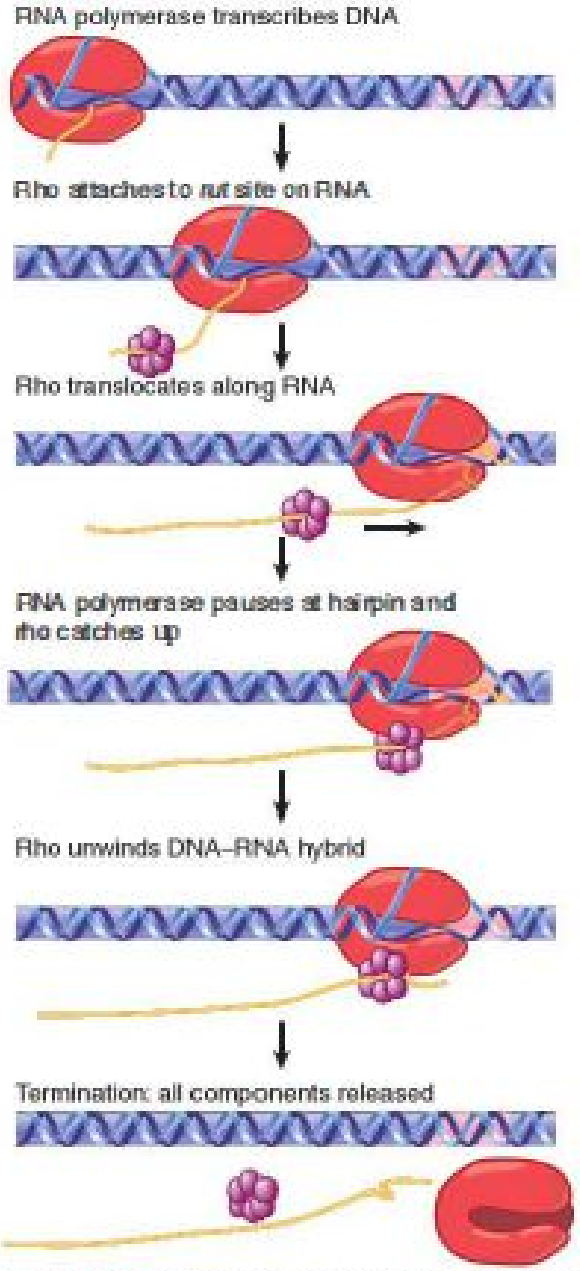


FIGURE 19.30 Rho factor binds to RNA at a *rut* site and translocates along RNA until it reaches the RNA–DNA hybrid in RNA polymerase, where it releases the RNA from the DNA.

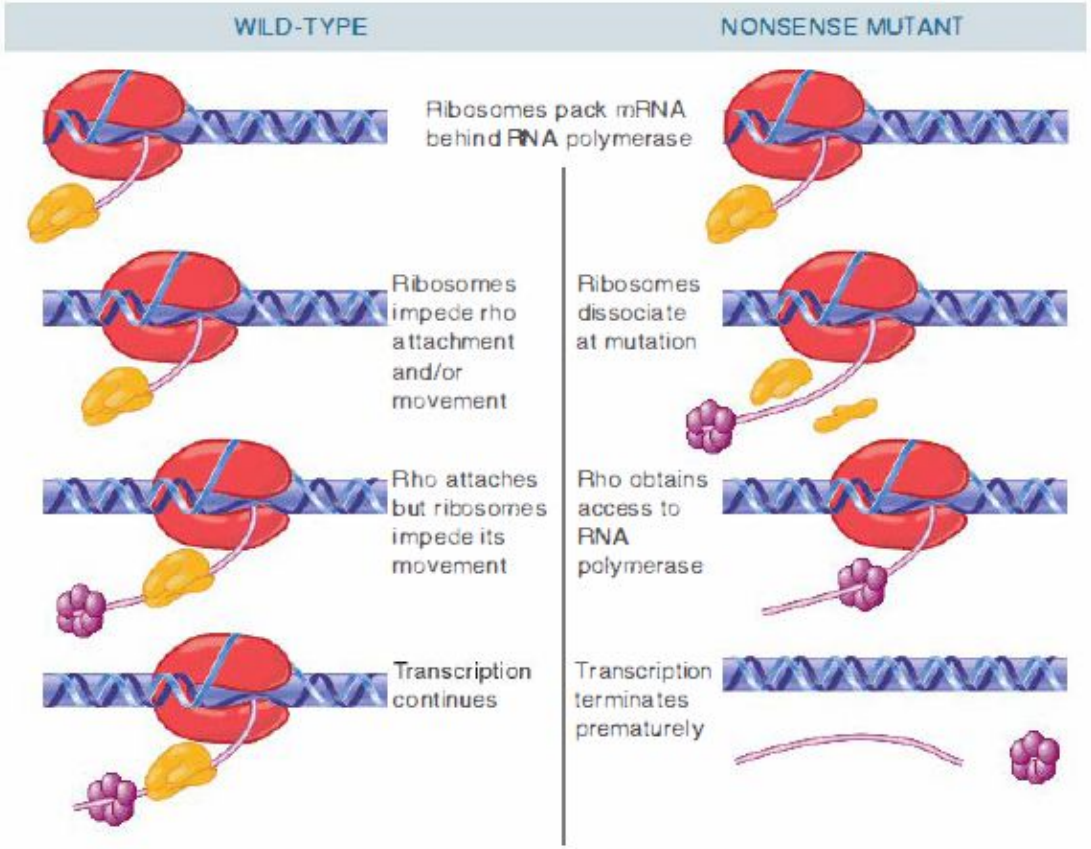


FIGURE 19.33 The action of rho factor may create a link between transcription and translation when a rho-dependent terminator lies soon after a nonsense mutation.

Antitermination

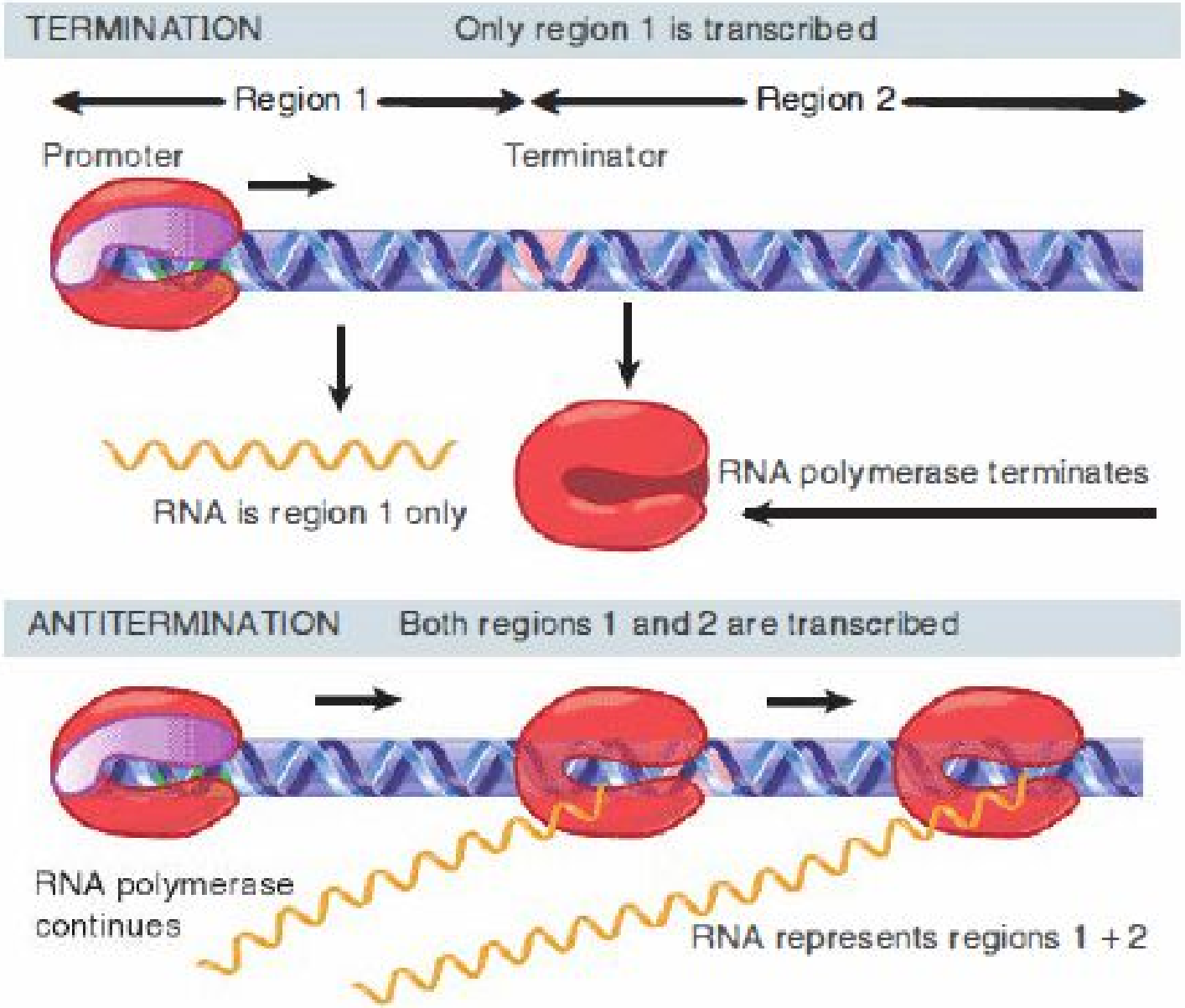
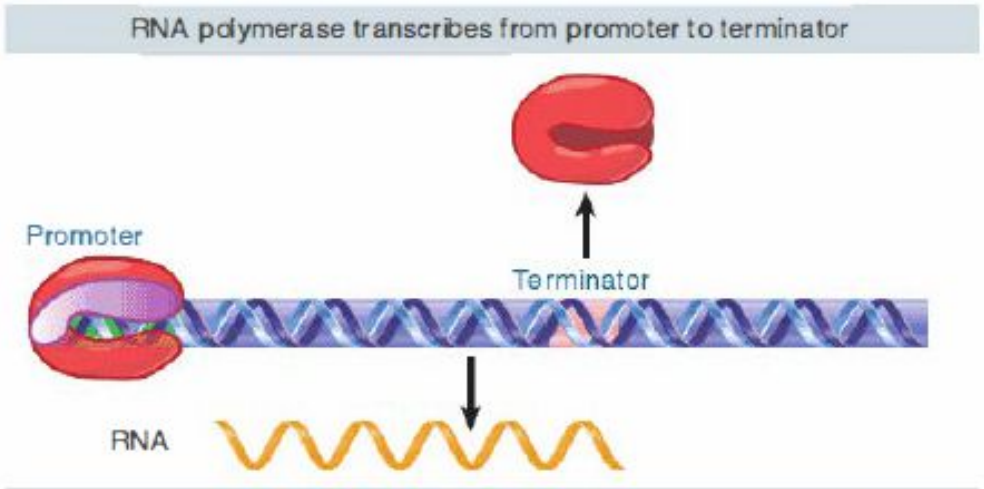


FIGURE 19.44 Antitermination can control transcription by determining whether RNA polymerase terminates or reads through a particular terminator into the following region.

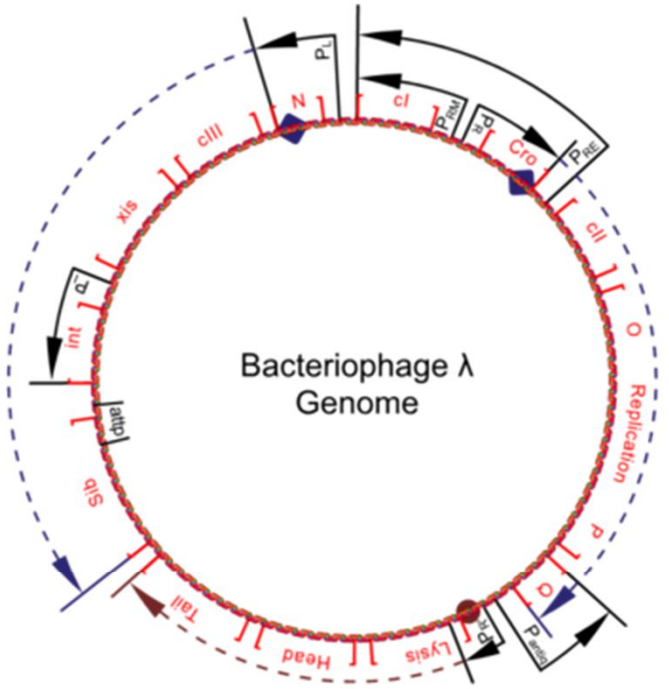
λ phage antitermination system

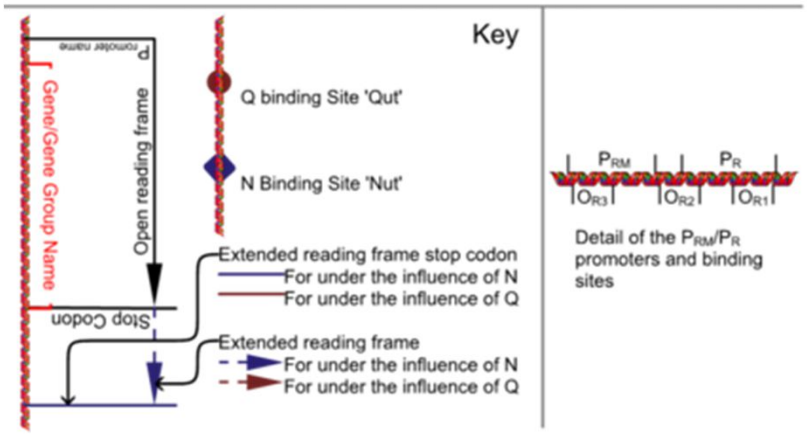


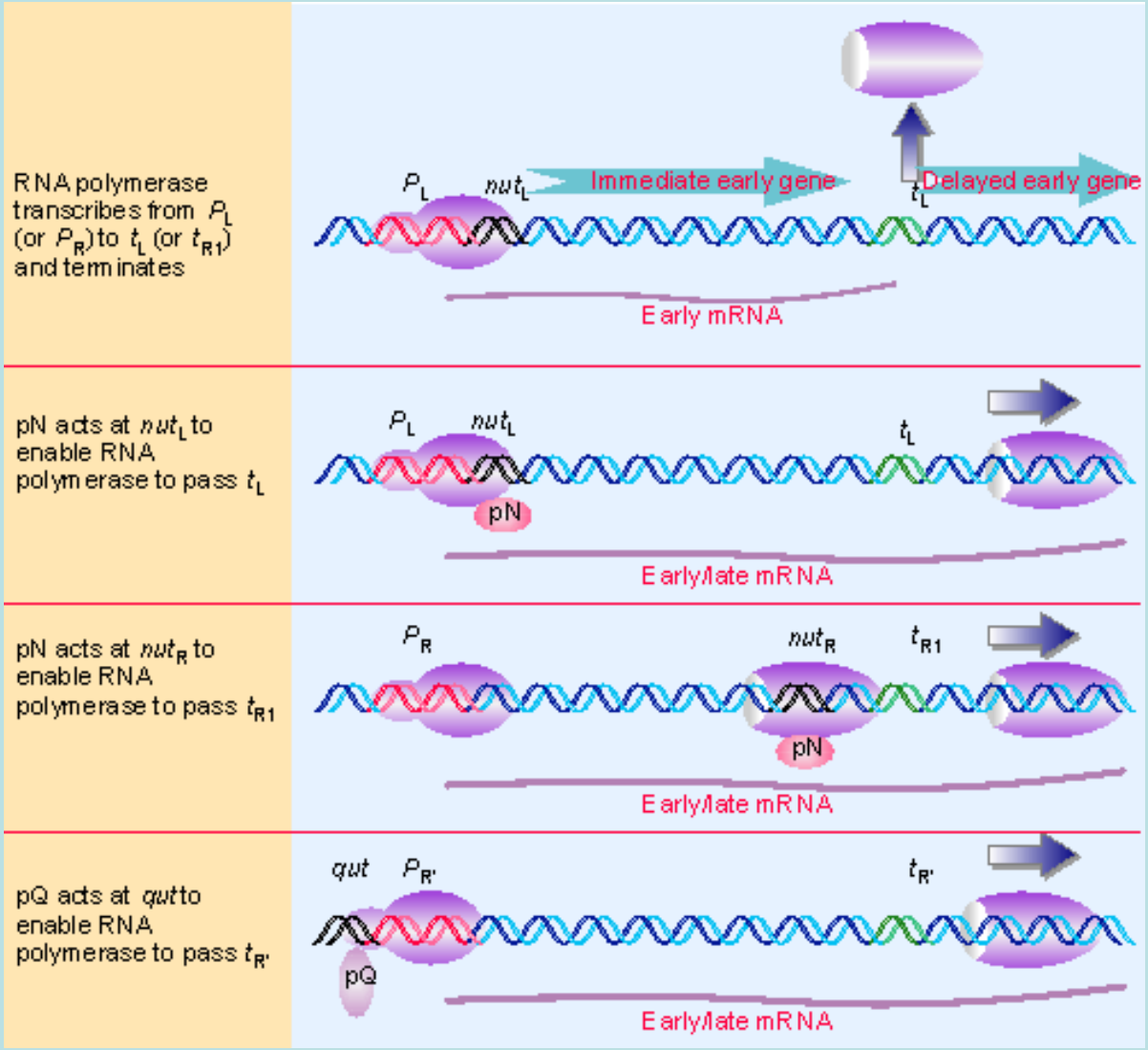
Antitermination proteins act on specific terminators

Transcription unit	Promoter	Terminator	Antitermination Protein
Immediate early	P_L	t_L	pN
Immediate early	P_{R1}	t_{R1}	pN
Late	$P_{R'}$	$t_{R'}$	pQ

FIGURE 19.45 An antitermination protein can act on RNA polymerase to enable it to read through a specific terminator.

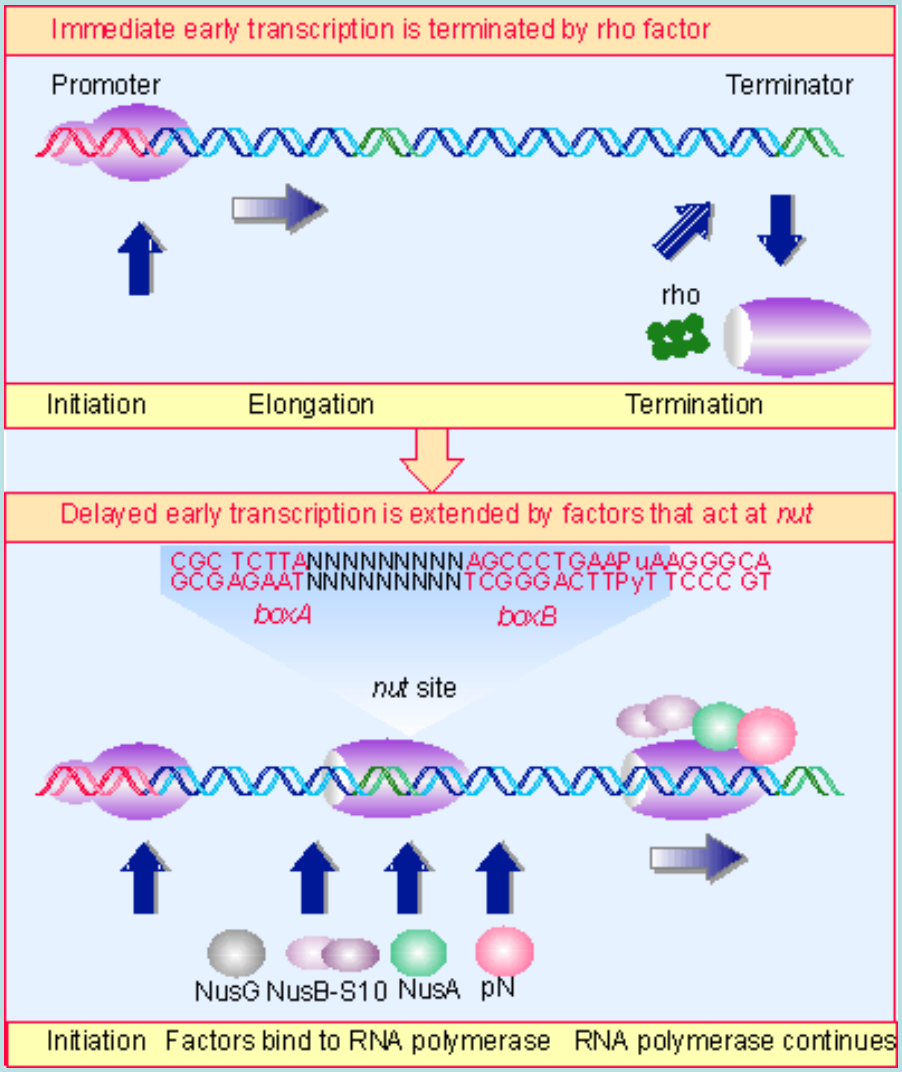




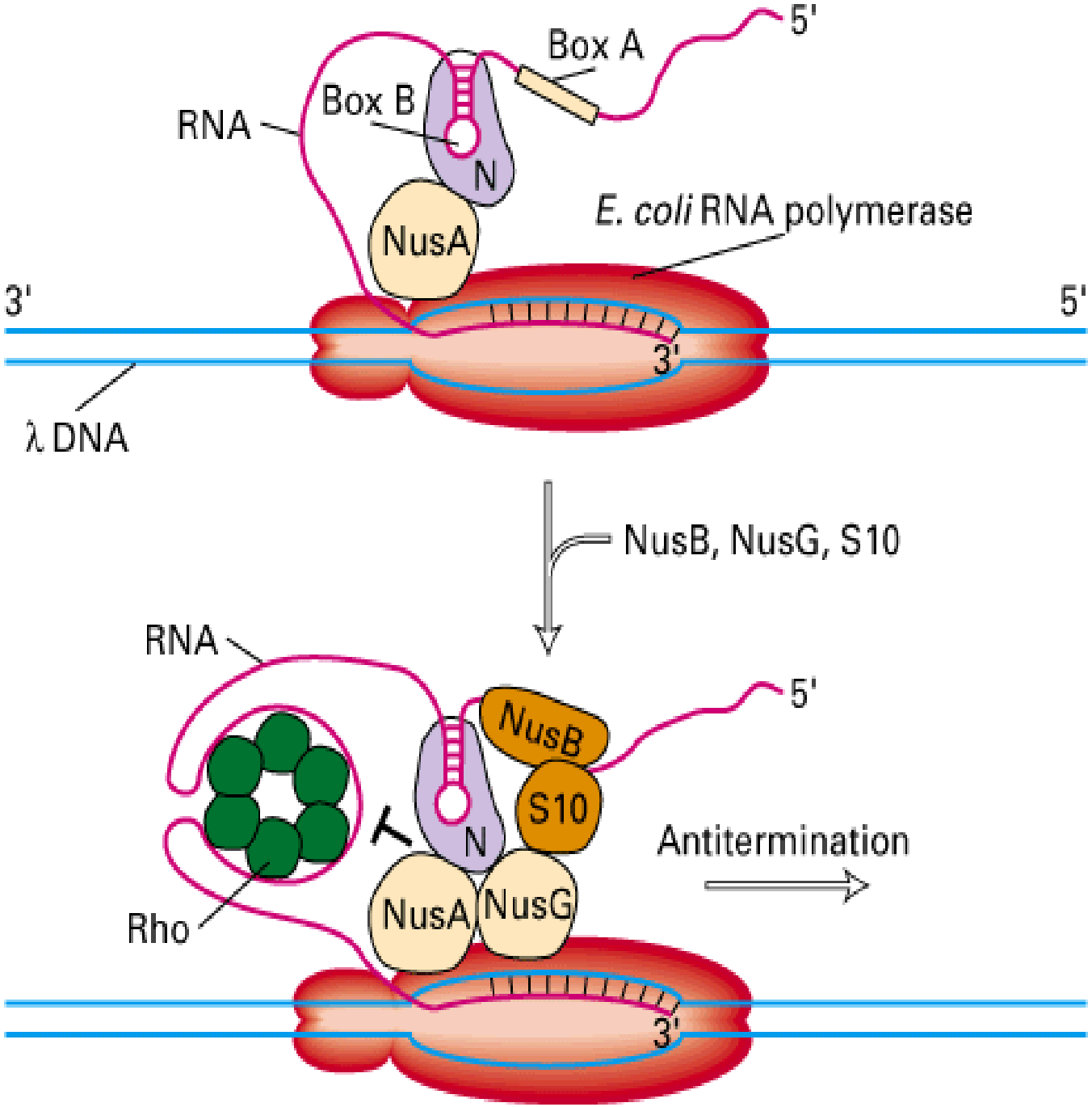


A juggernaut is a term used to describe a literal or metaphorical force regarded as unstoppable.
The word is derived from the Sanskrit जगन्नाथ Jagannātha (meaning "Lord of the Universe") which is one of the many names of Krishna from the ancient Vedic scriptures of India.

Host RNA polymerase transcribes lambda genes and terminates at t sites. pN allows it to read through terminators in the L and R1 units; pQ allows it to read through the R¢F terminator.
The sites at which pN acts (nut) and at which pQ acts (qut) are located at different relative positions in the transcription units.



Ancillary factors bind to RNA polymerase as it passes certain sites. The nut site consists of two sequences. NusB-S10 join core enzyme as it passes boxA. Then NusA and pN protein bind as polymerase passes boxB. The presence of pN allows the enzyme to read through the terminator, producing a joint mRNA that contains immediate early sequences joined to delayed early sequences.


Box A
5'
Box B
RNA
N
NusA
E. coli RNA polymerase
3'
5'
3'
λ DNA
NusB, NusG, S10
RNA
5'
NusB
S10
N
λ
Antitermination
NusA
NusG
Rho
3'

Attenuation

REGULATORY SYSTEM FOR BACTERIAL OPERONES BASED ON TRANSCRIPTION TERMINATION

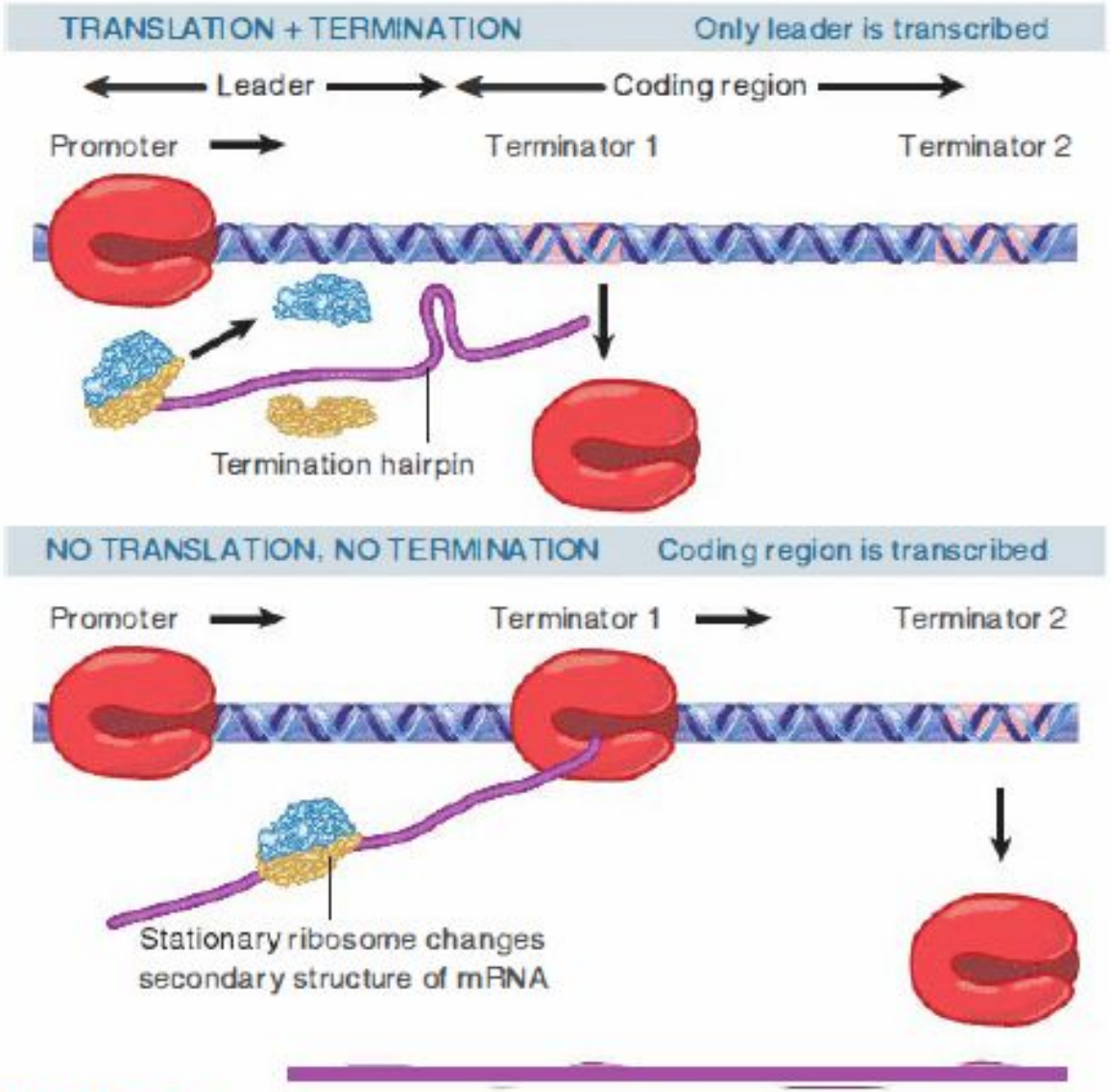
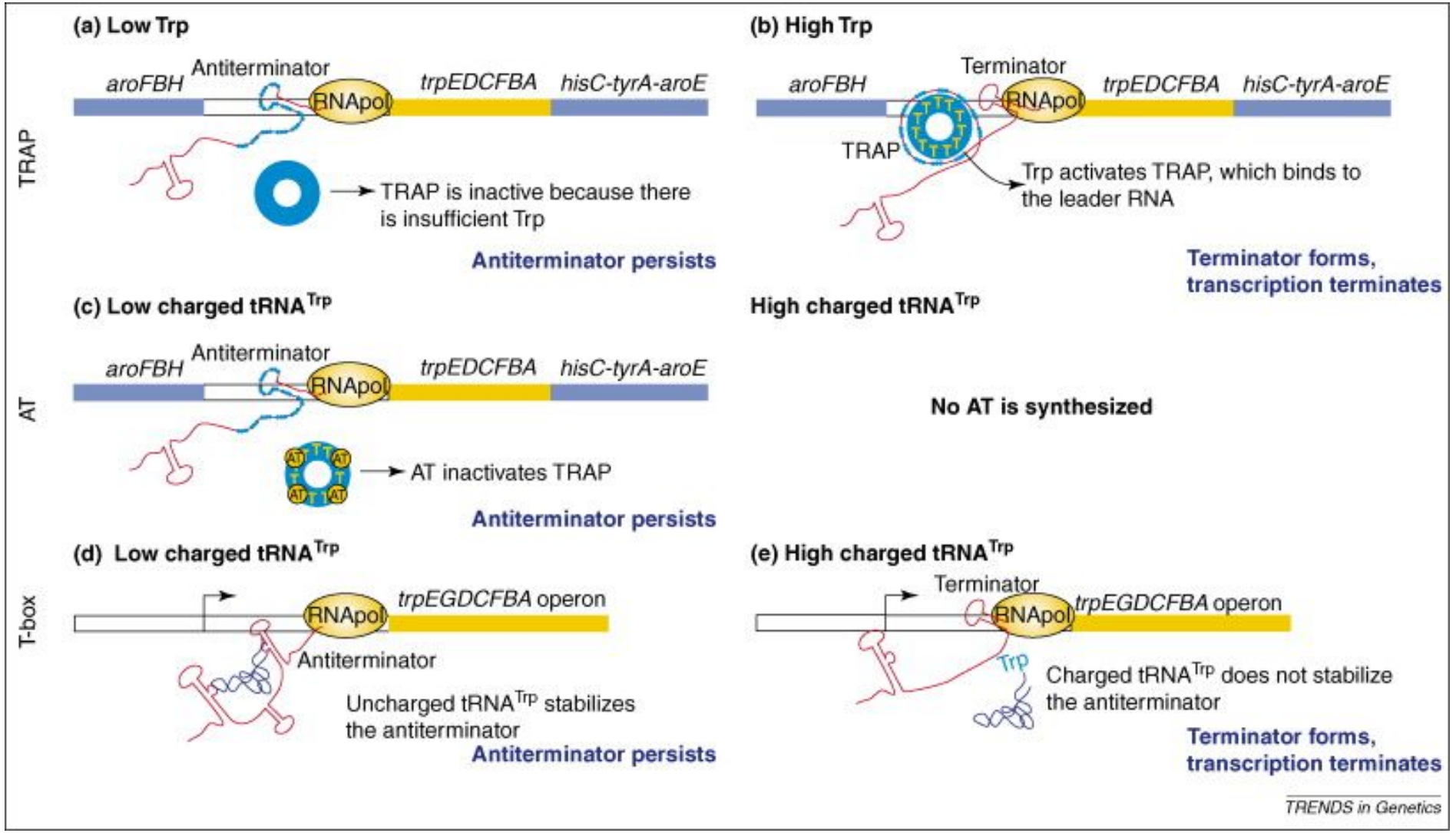


FIGURE 26.33 Termination can be controlled via changes in RNA secondary structure that are determined by ribosome movement.

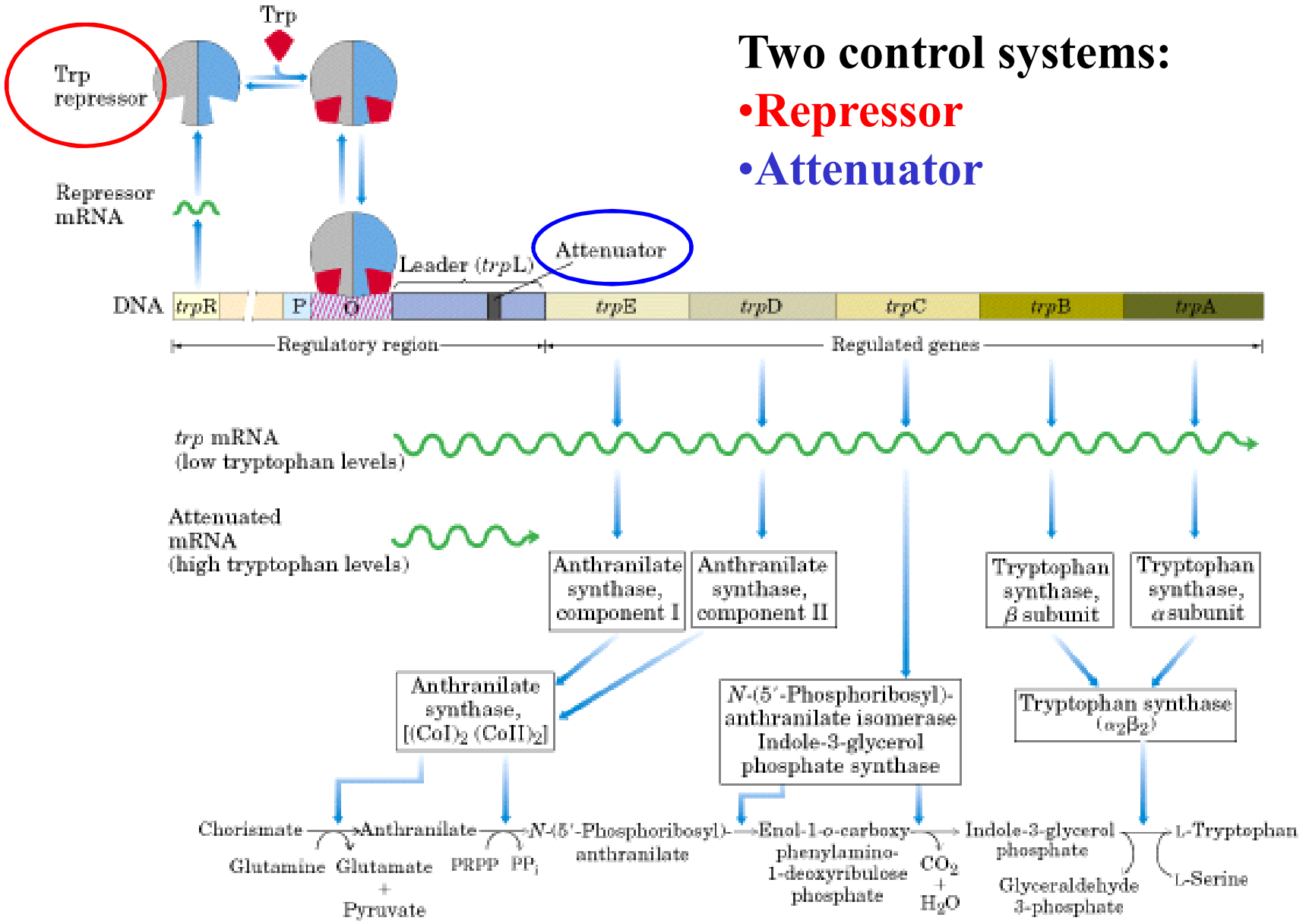
Attenuator: a terminator sequence at which attenuation occurs. Attenuation is the regulation of bacterial operons by controlling termination of transcription at a site located before the first structural gene.

In *B. subtilis* the presence of tryptophan promote the early transcription termination at the beginning of the *trp* operon.

TRAP: Trp RNA-binding Attenuation Protein



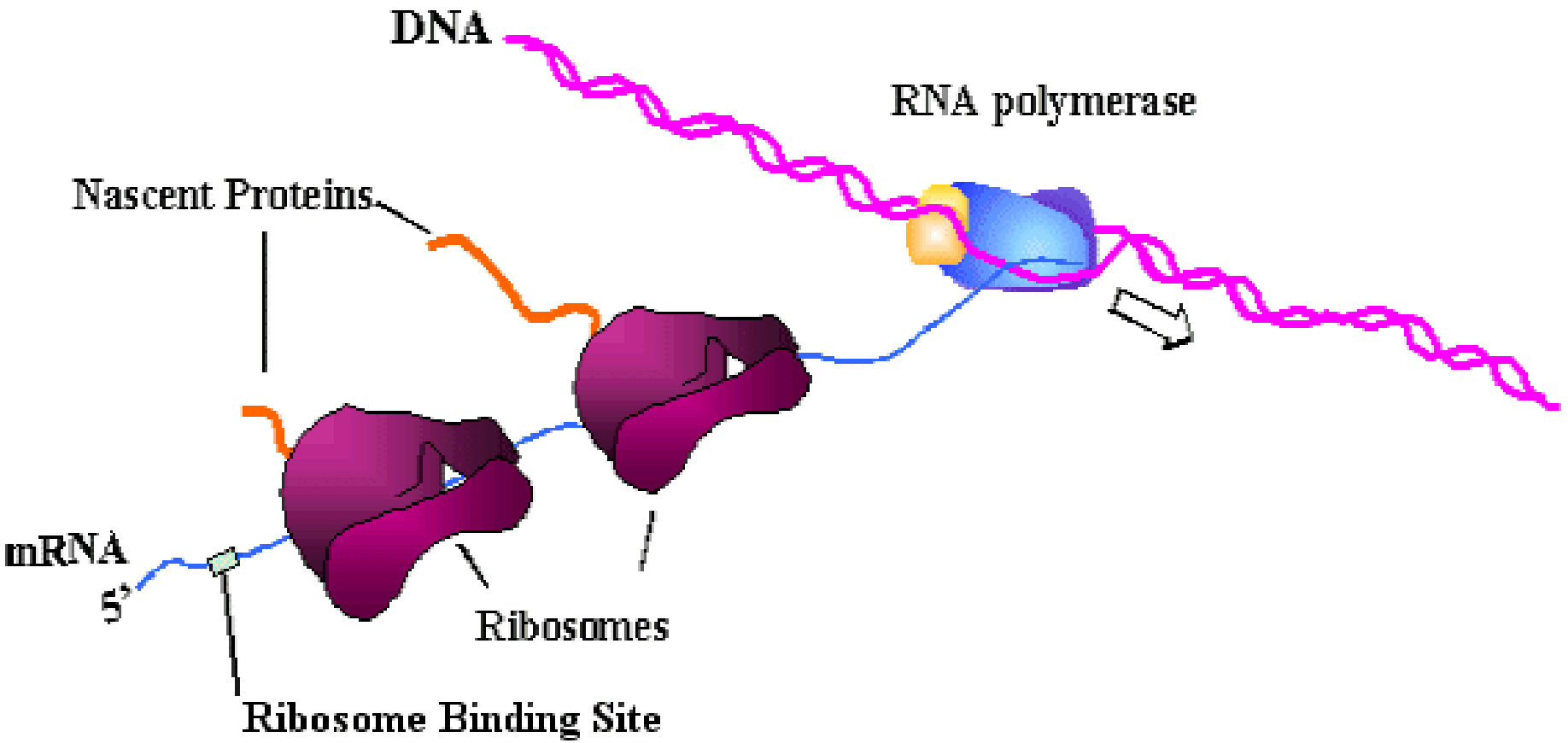
Trp operon in *E. coli*



Two control systems:

- **Repressor**
- **Attenuator**

Transcription and translation are coupled in bacteria



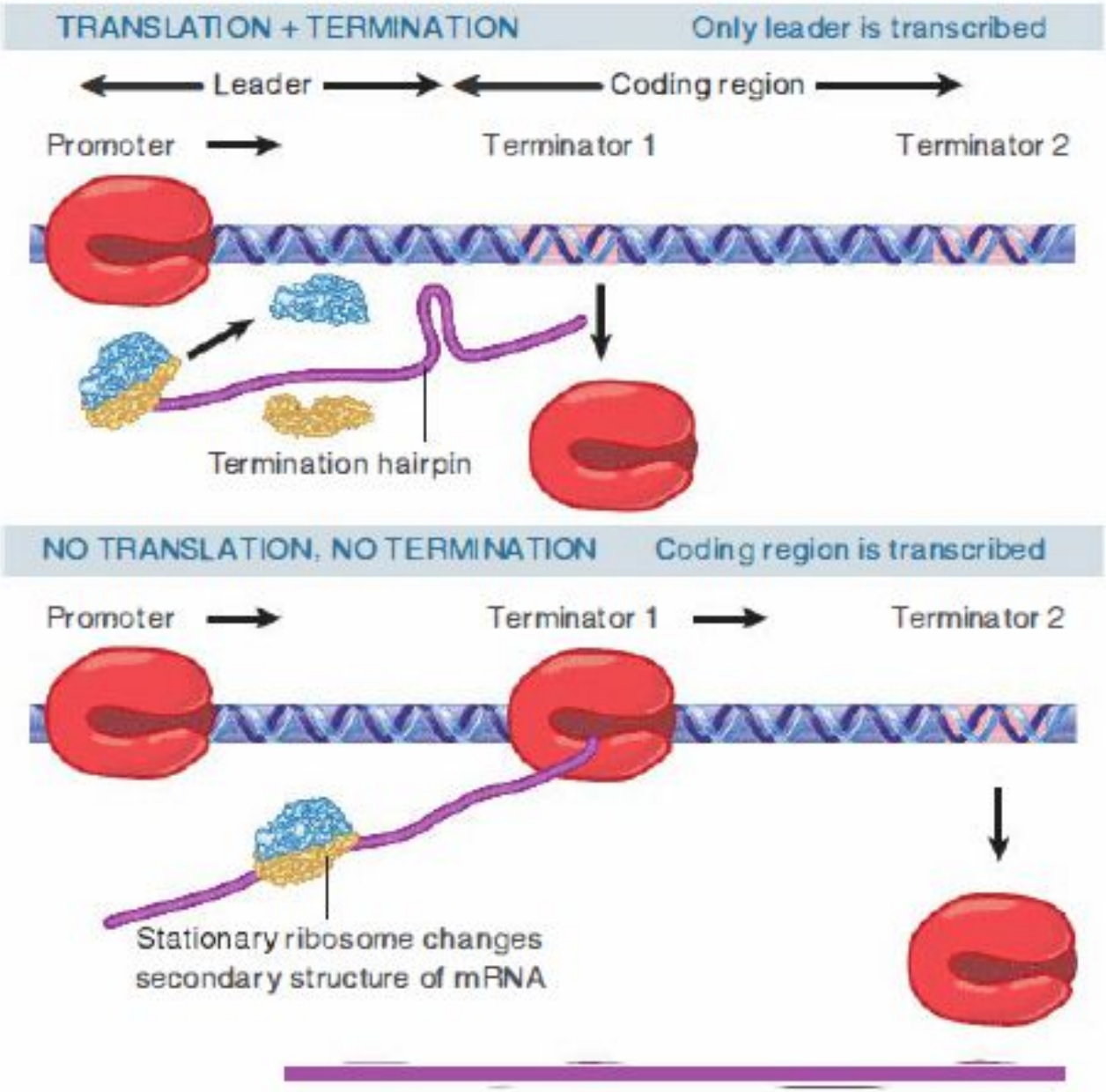


FIGURE 26.33 Termination can be controlled via changes in RNA secondary structure that are determined by ribosome movement.

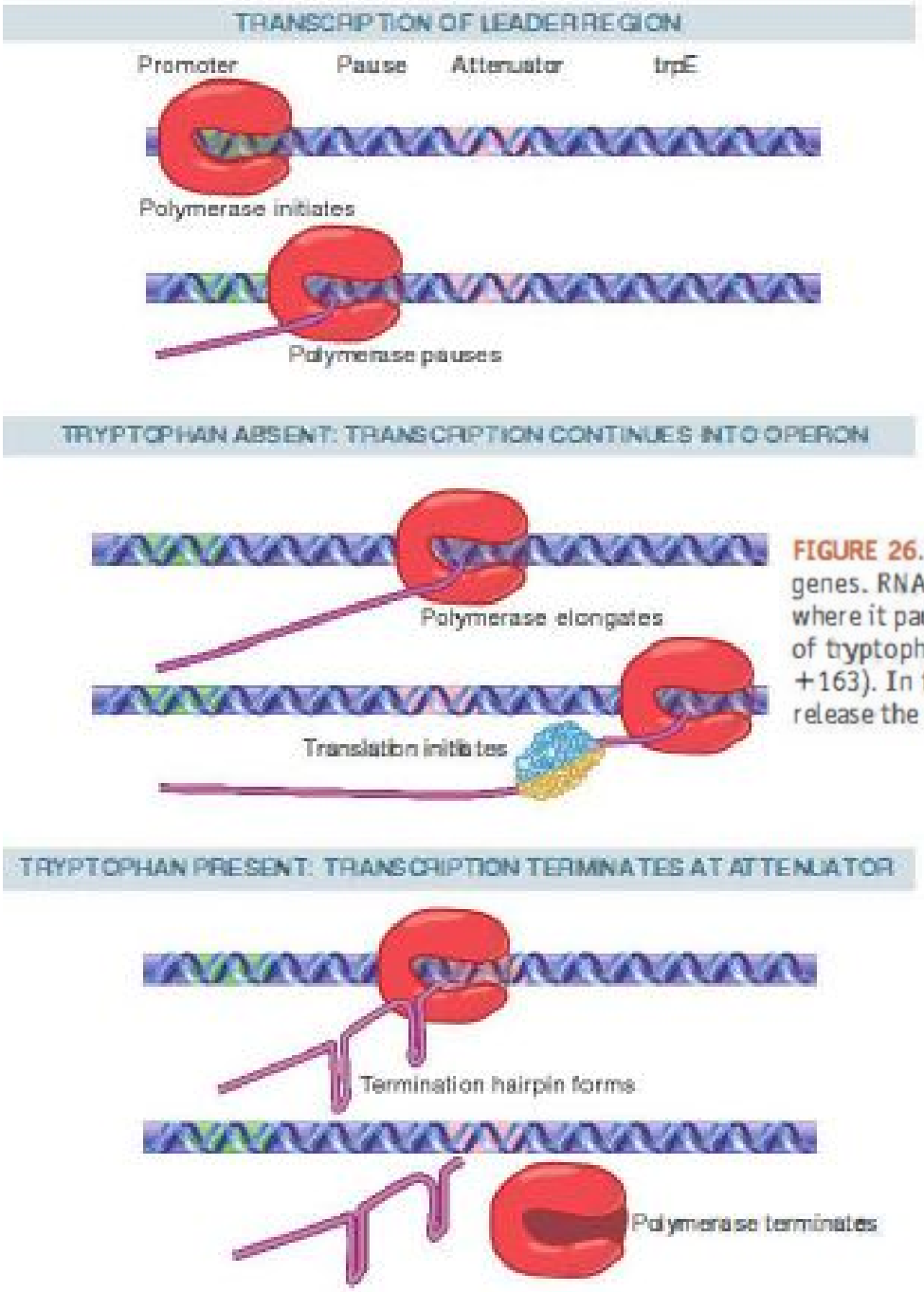


FIGURE 26.34 An attenuator controls the progression of RNA polymerase into the *trp* genes. RNA polymerase initiates at the promoter and then proceeds to position 90, where it pauses before proceeding to the attenuator at position 140. In the absence of tryptophan, the polymerase continues into the structural genes (*trpE* starts at +163). In the presence of tryptophan there is ~90% probability of termination to release the 140-base leader RNA.

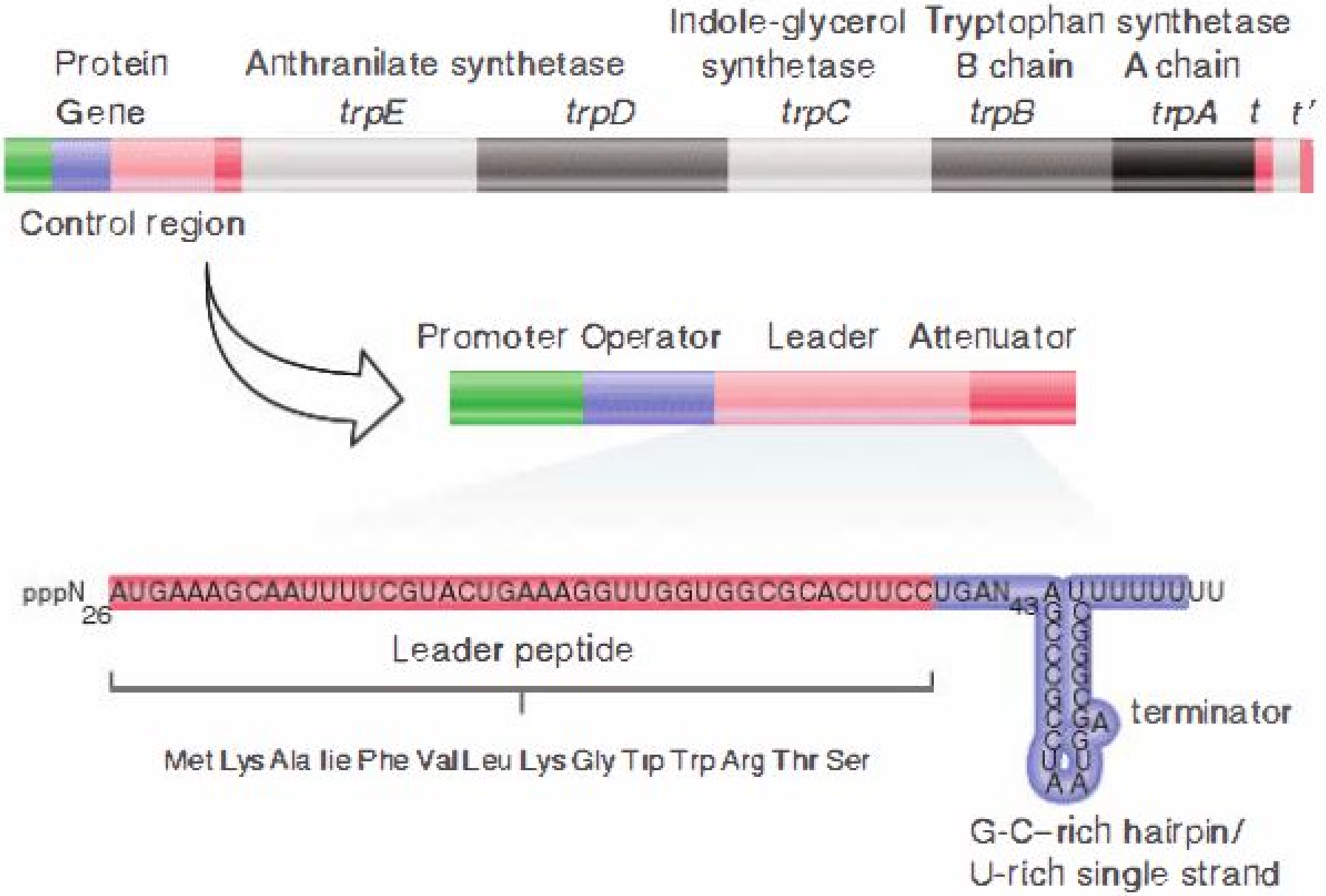


FIGURE 26.35 The *trp* operon has a short sequence coding for a leader peptide that is located between the operator and the attenuator.

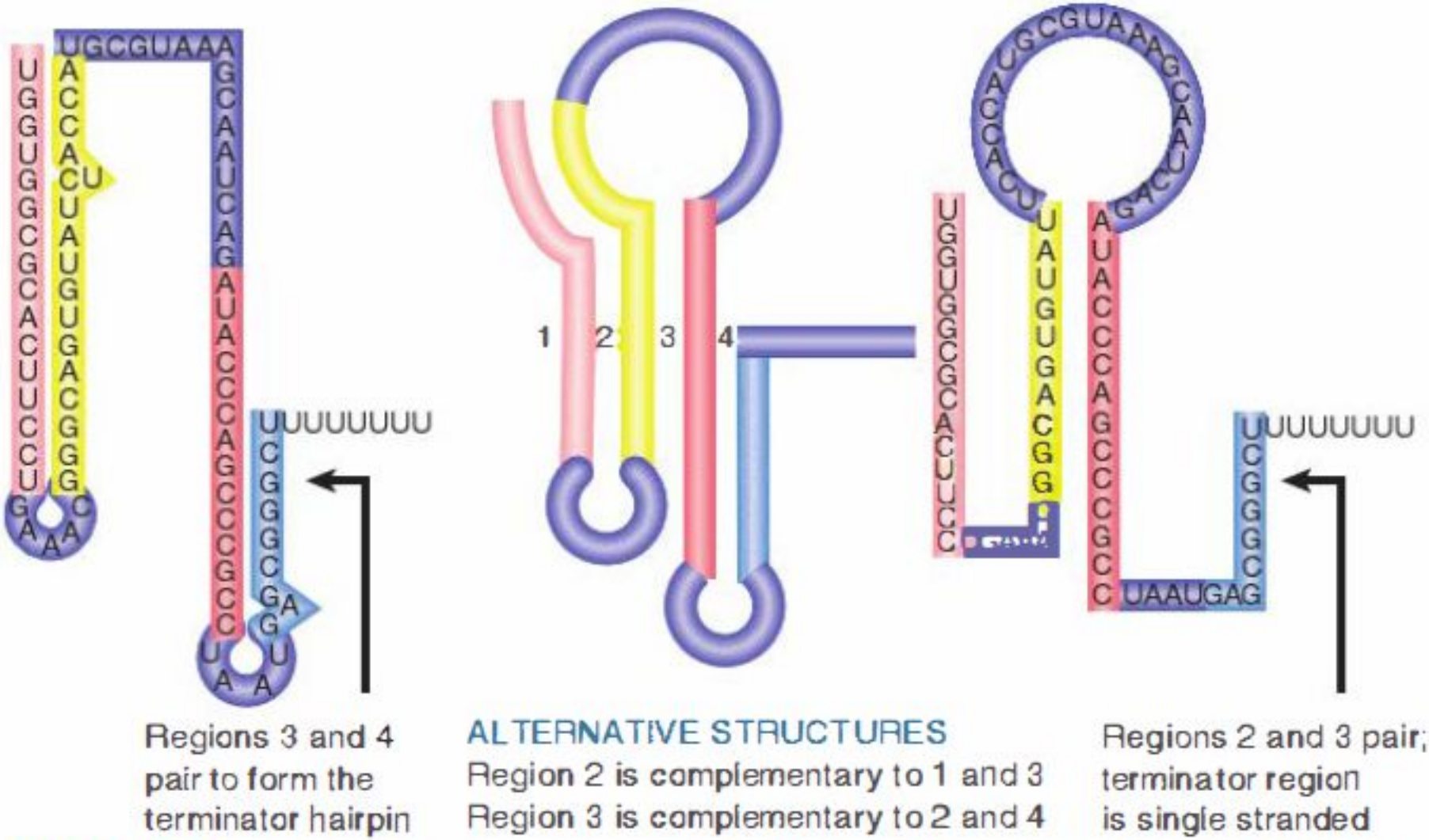


FIGURE 26.36 The *trp* leader region can exist in alternative base-paired conformations. The center shows the four regions that can base pair. Region 1 is complementary to region 2, which is complementary to region 3, which is complementary to region 4. On the left is the conformation produced when region 1 pairs with region 2 and region 3 pairs with region 4. On the right is the conformation when region 2 pairs with region 3, leaving regions 1 and 4 unpaired.

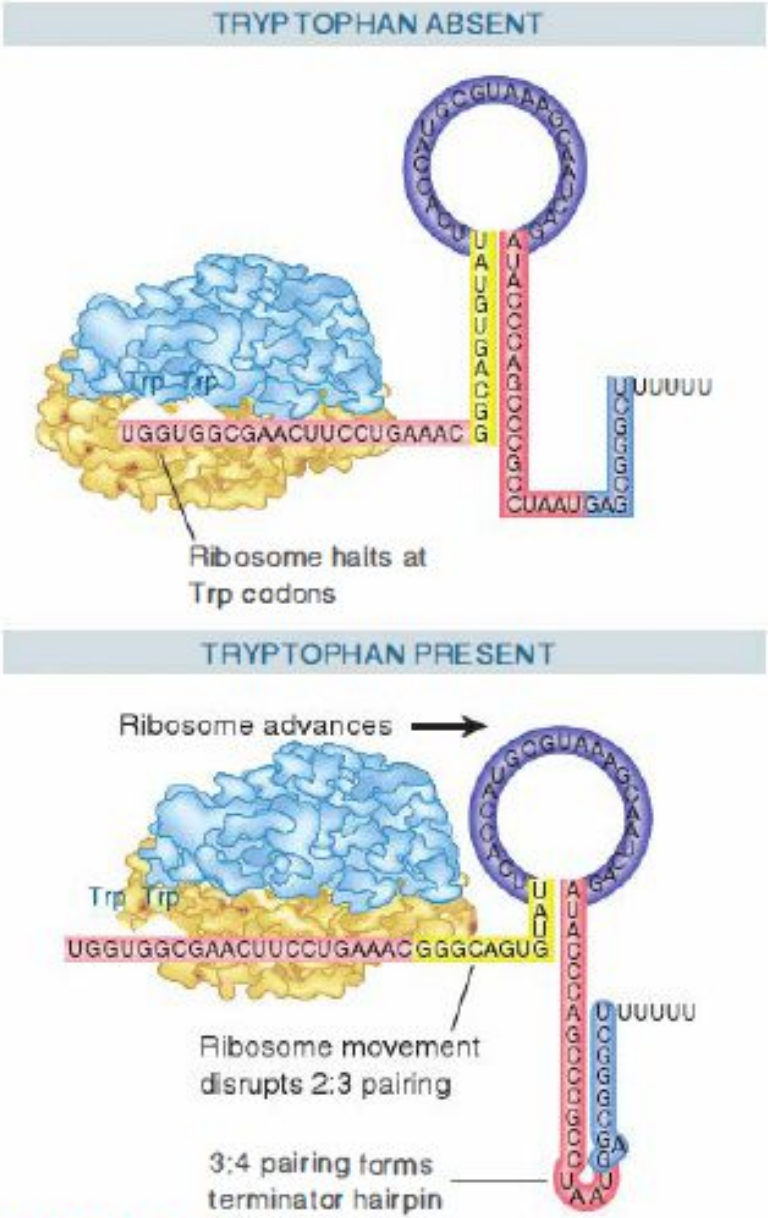


FIGURE 26.37 The alternatives for RNA polymerase at the attenuator depend on the location of the ribosome, which determines whether regions 3 and 4 can pair to form the terminator hairpin.

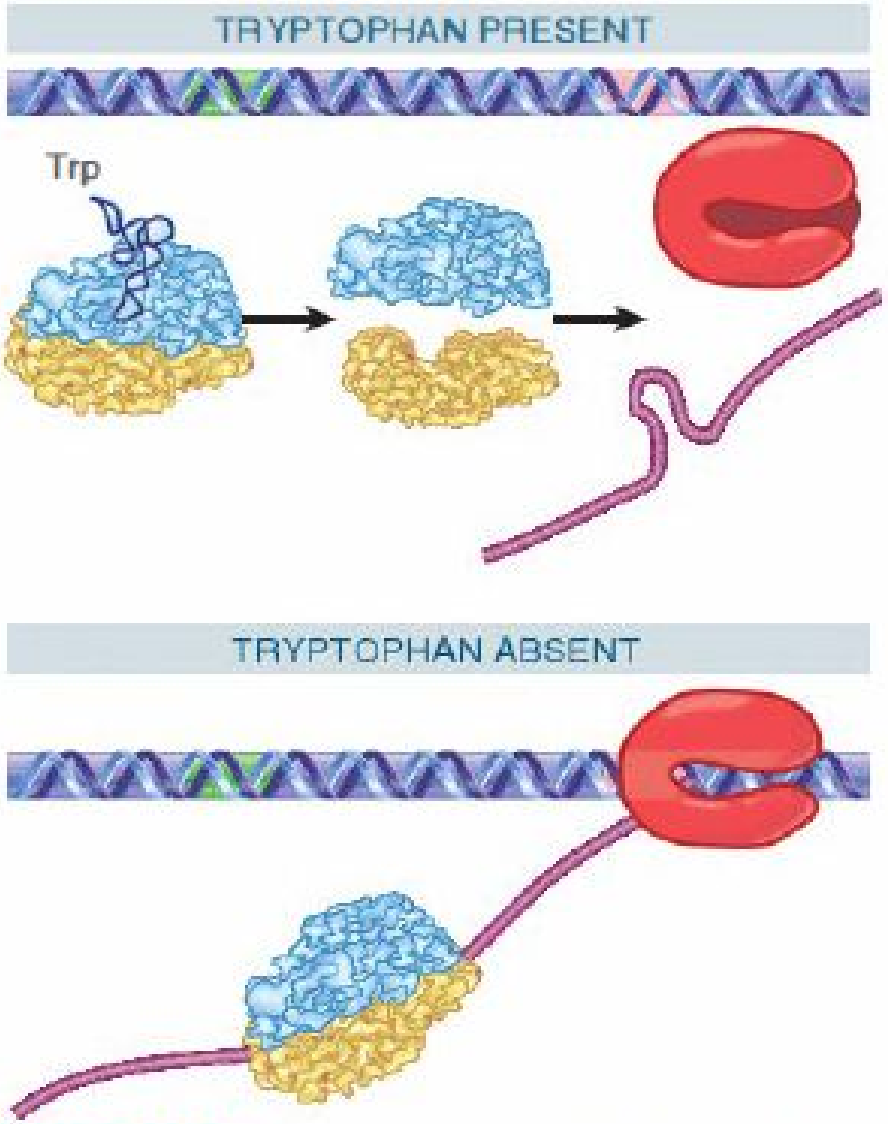


FIGURE 26.38 In the presence of tryptophan tRNA, ribosomes translate the leader peptide and are released. This allows hairpin formation, so that RNA polymerase terminates. In the absence of tryptophan tRNA, the ribosome is blocked, the termination hairpin cannot form, and RNA polymerase continues.

Leader peptides in attenuated operons with genes coding for amino acid synthesis

Tryptophan	Met Lys Ala Ile Phe Val Leu Lys Gly Trp Trp Arg Thr Ser
Threonine	Met Lys Arg Ile Ser Thr Thr Ile Thr Thr Thr Ile Thr Ile Thr Thr Gly Asn Gly Ala Gly
Histidine	Met Thr Arg Val Gln Phe Lys His His His His His His Pro Asp
Phenylalanine	Met Lys His Ile Pro Phe Phe Phe Ala Phe Phe Phe Thr Phe Pro