Figure 10.20 Control circuits are versatile and can be designed to allow positive or negative control of induction or repression.

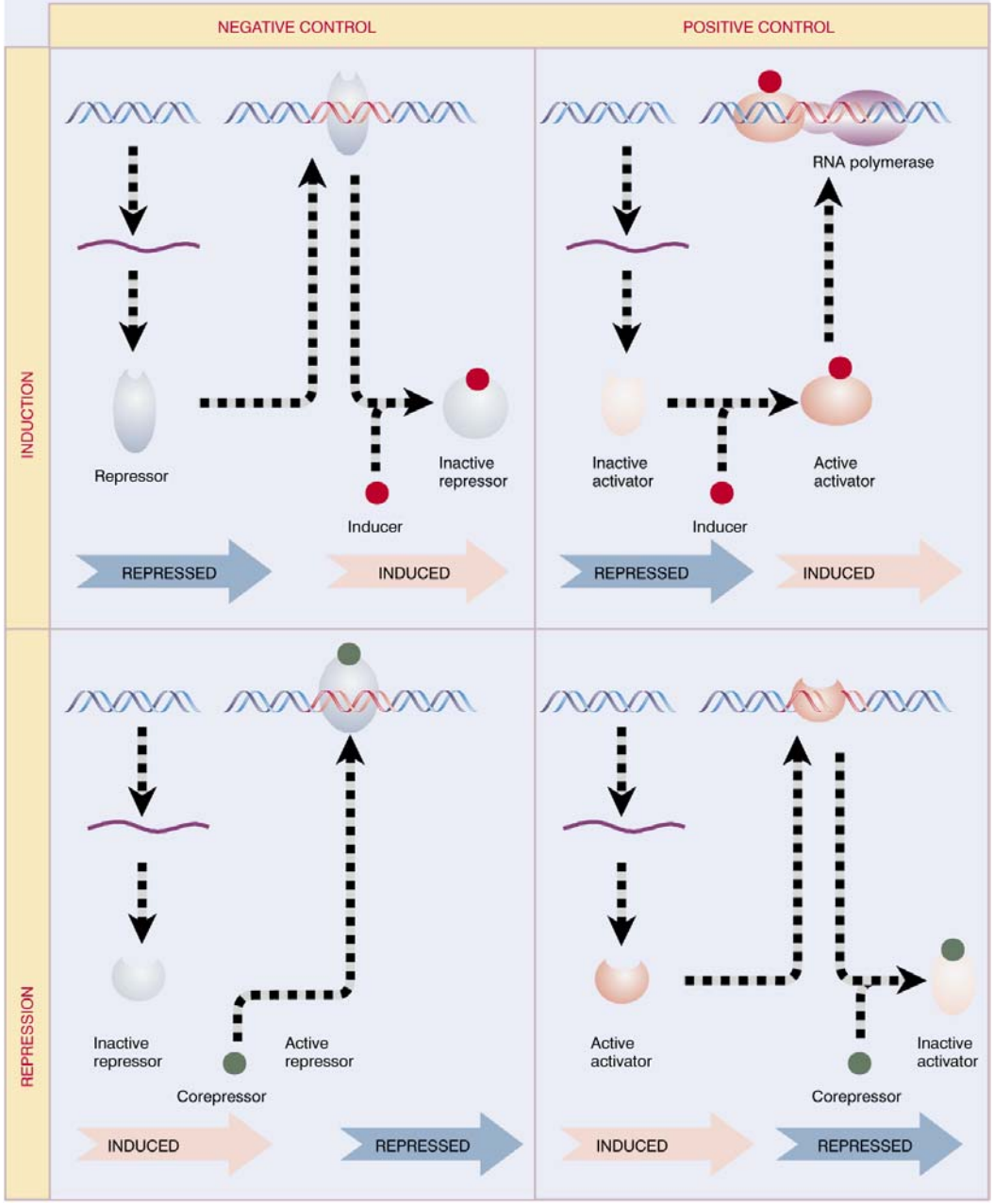


Figure 10.1 *Overview*: in negative control, a *trans*-acting repressor binds to the *cis*-acting operator to turn off transcription. In prokaryotes, multiple genes are controlled coordinately.

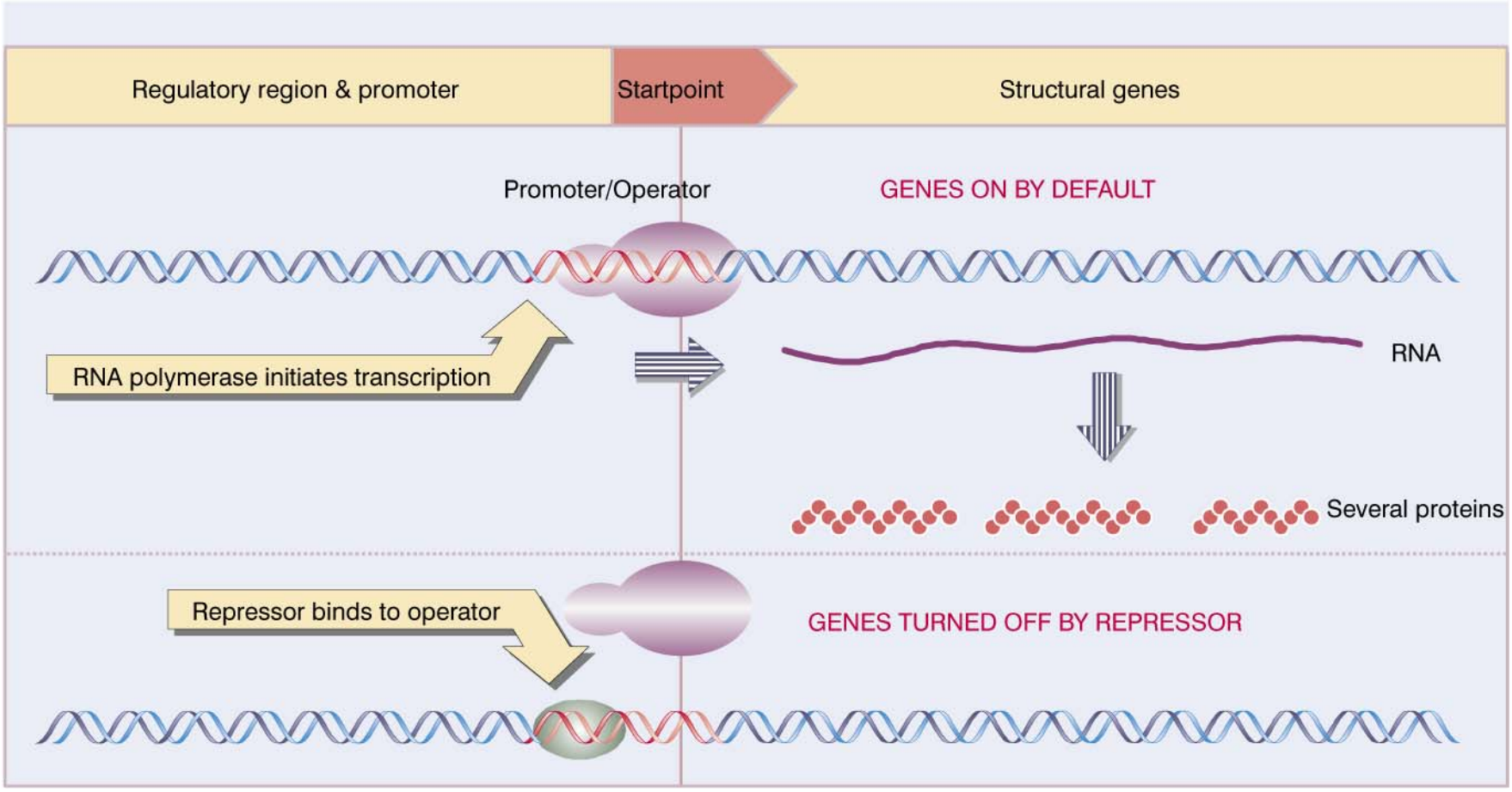


Figure 10.2 *Overview*: in positive control, *trans*-acting factors must bind to *cis*-acting sites in order for RNA polymerase to initiate transcription at the promoter. In a eukaryotic system, a structural gene is controlled individually.

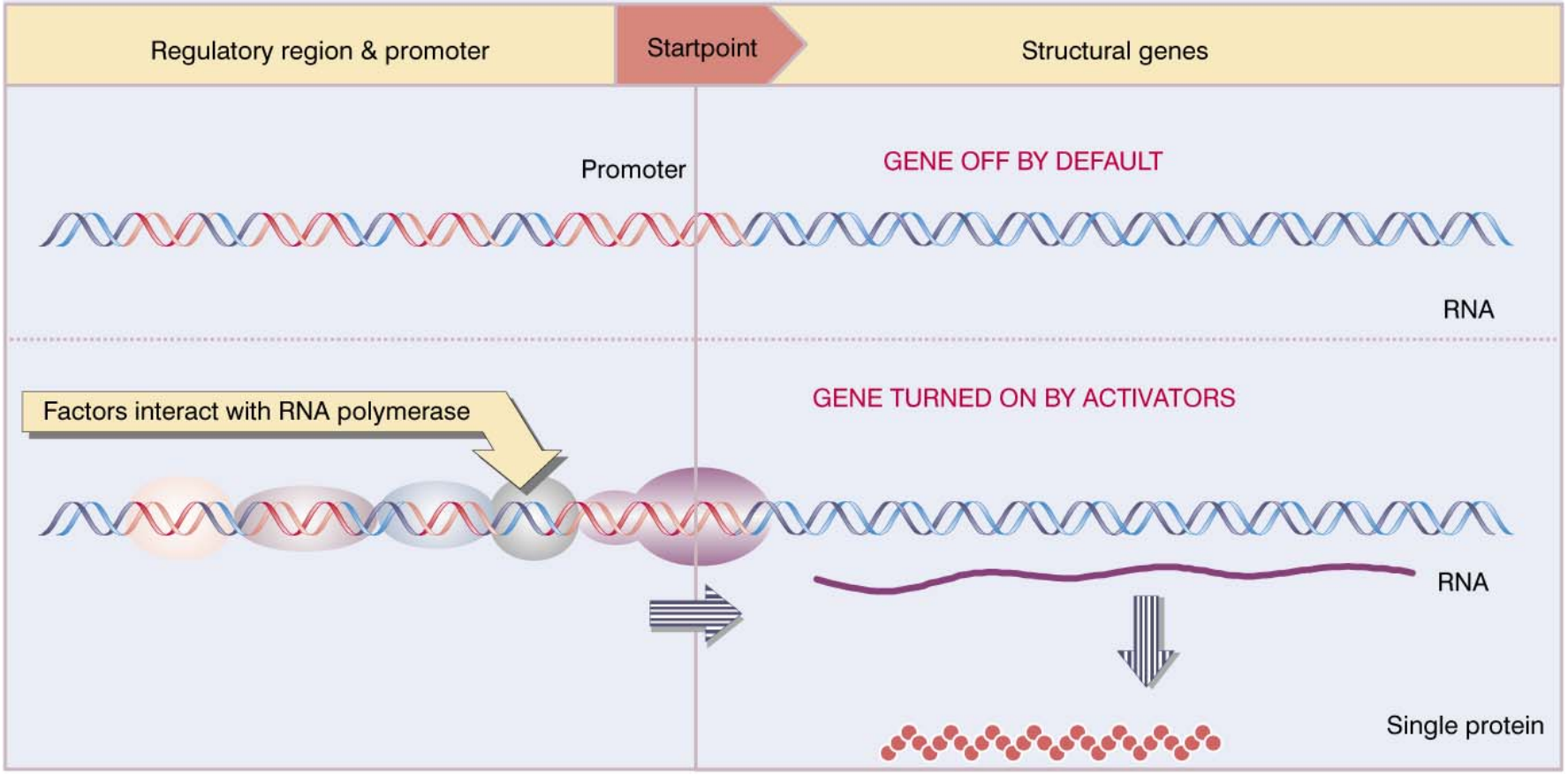


Figure 10.3 The *lac* operon occupies ~6000 bp of DNA. At the left the *lacI* gene has its own promoter and terminator. The end of the *lacI* region is adjacent to the promoter, P. The operator, *O*, occupies the first 26 bp of the long *lacZ* gene, followed by the *lacY* and *lacA* genes and a terminator.

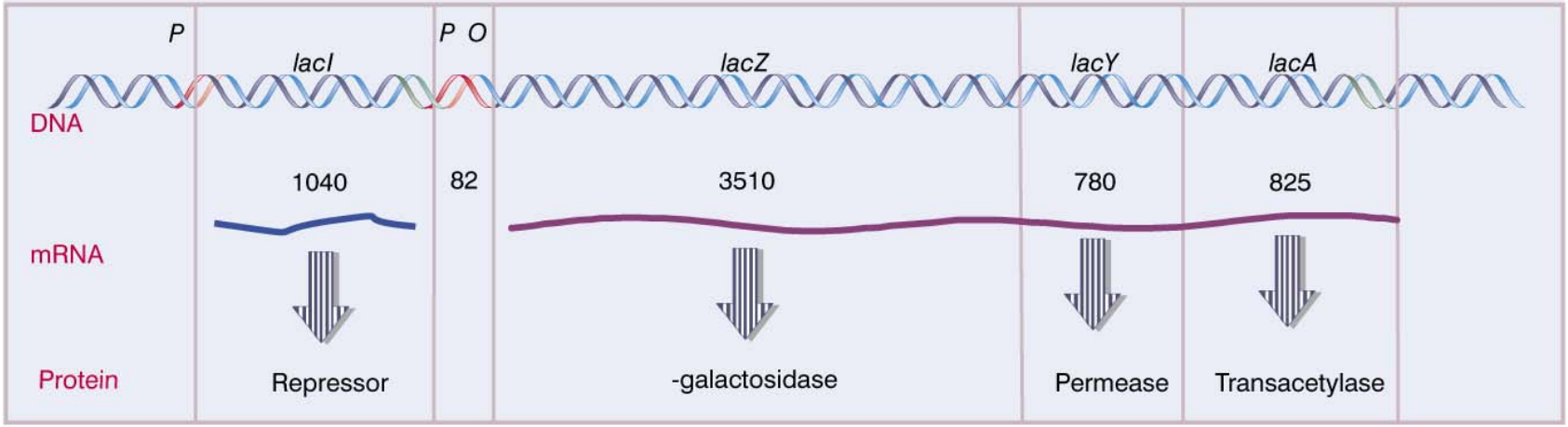


Figure 10.4 Repressor and RNA polymerase bind at sites that overlap around the startpoint of the *lac* operon.

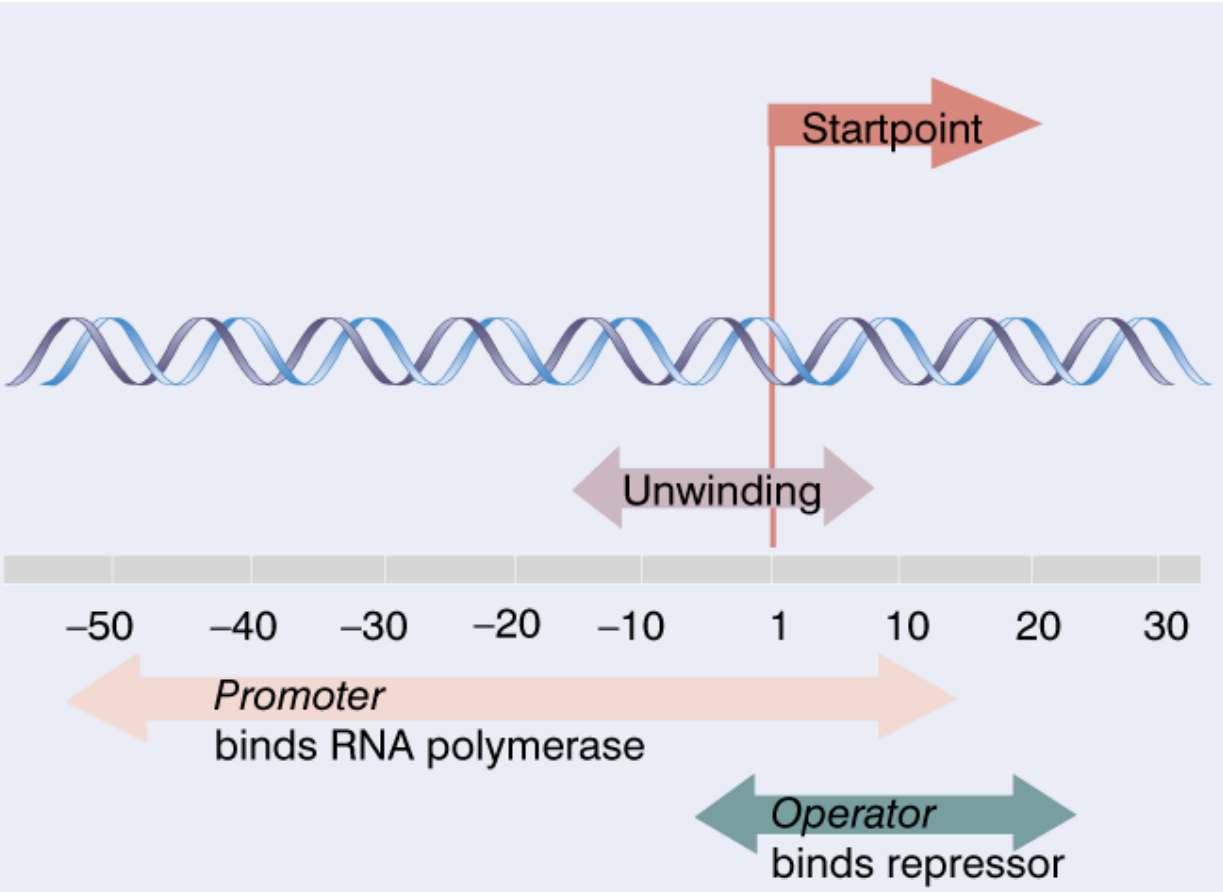


Figure 10.5 Addition of inducer results in rapid induction of *lac* mRNA, and is followed after a short lag by synthesis of the enzymes; removal of inducer is followed by rapid cessation of synthesis.

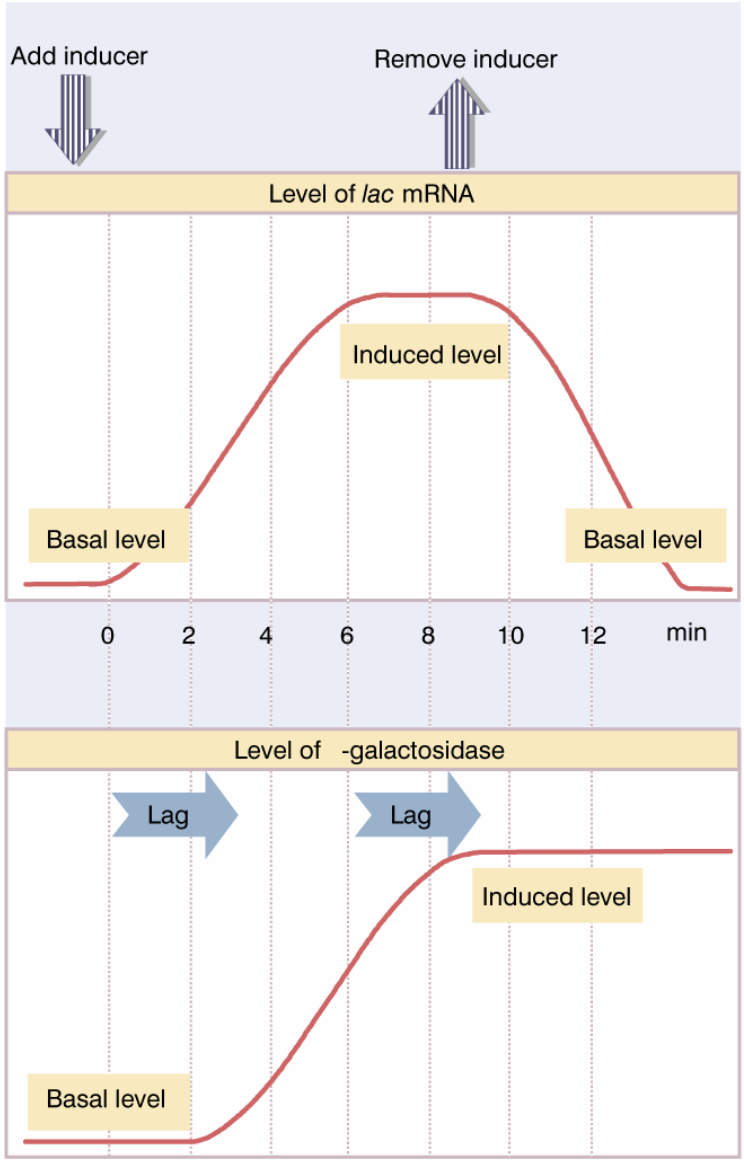


Figure 10.6 Repressor maintains the *lac* operon in the inactive condition by binding to the operator; addition of inducer releases the repressor, and thereby allows RNA polymerase to initiate transcription.

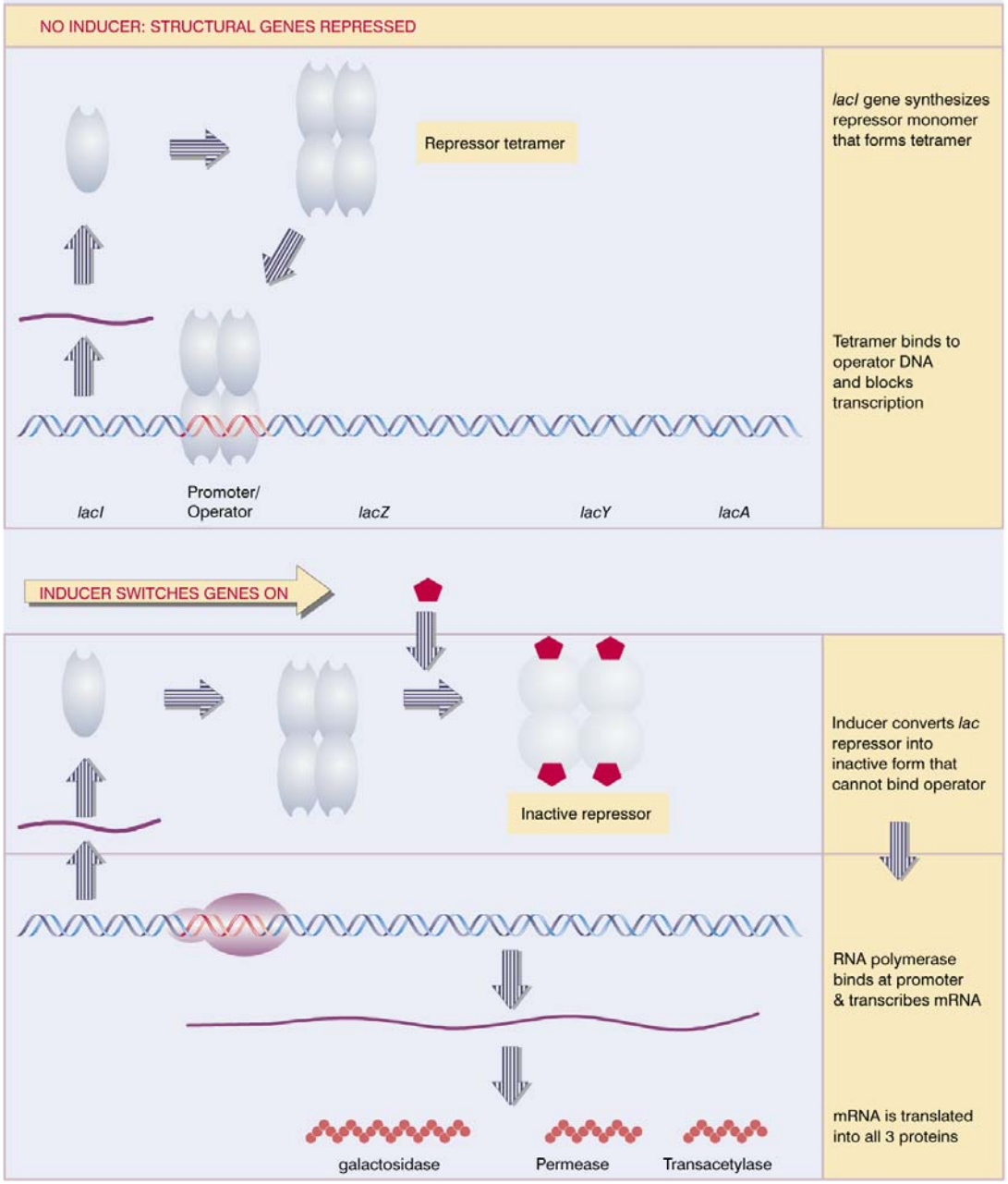


Figure 10.7
Operator mutations are constitutive because the operator is unable to bind repressor protein; this allows RNA polymerase to have unrestrained access to the promoter. The O^c mutations are *cis*-acting, because they affect only the contiguous set of structural genes.

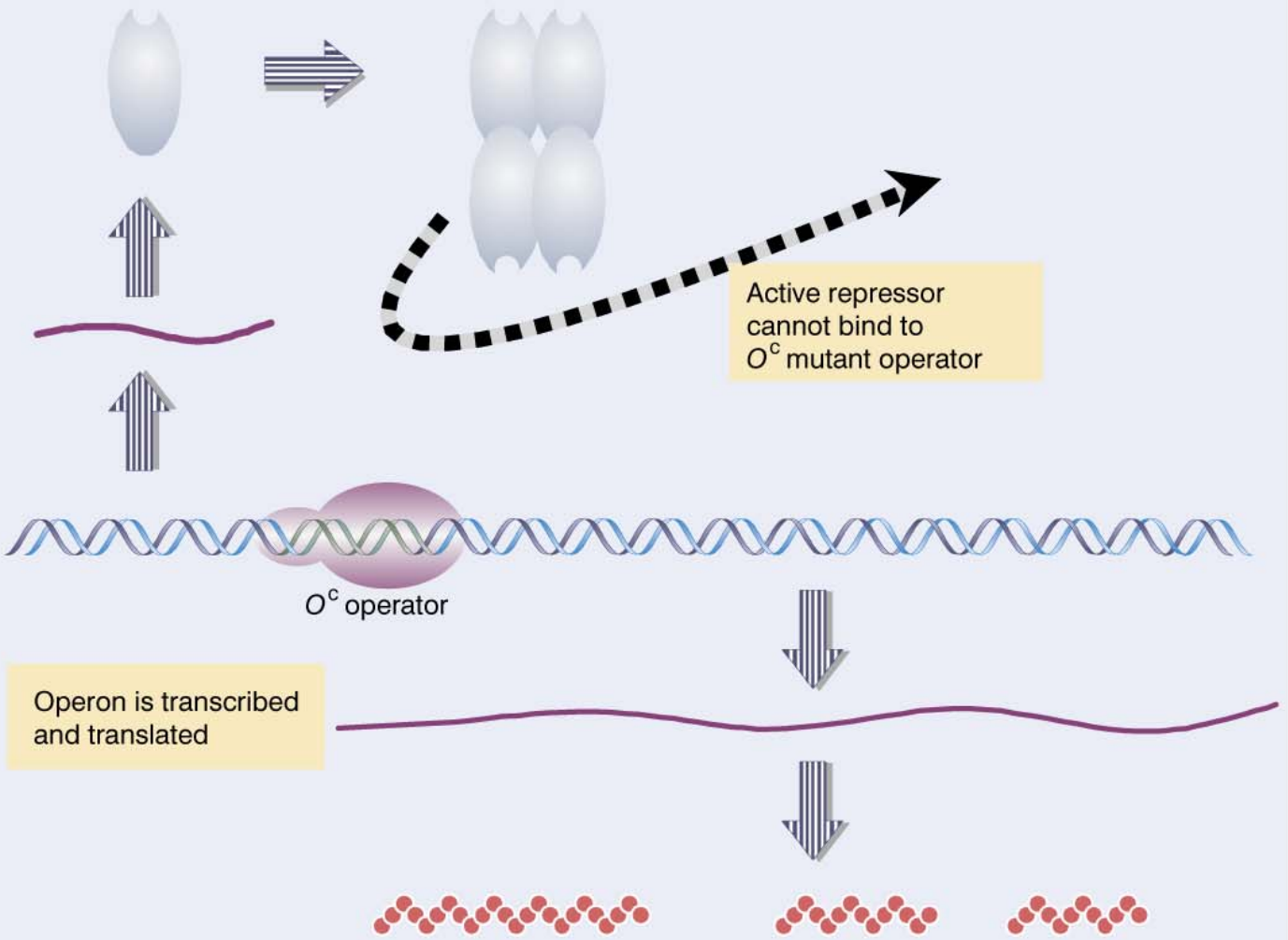


Figure 10.8
Mutations that inactivate the *lacI* gene cause the operon to be constitutively expressed, because the mutant repressor protein cannot bind to the operator.

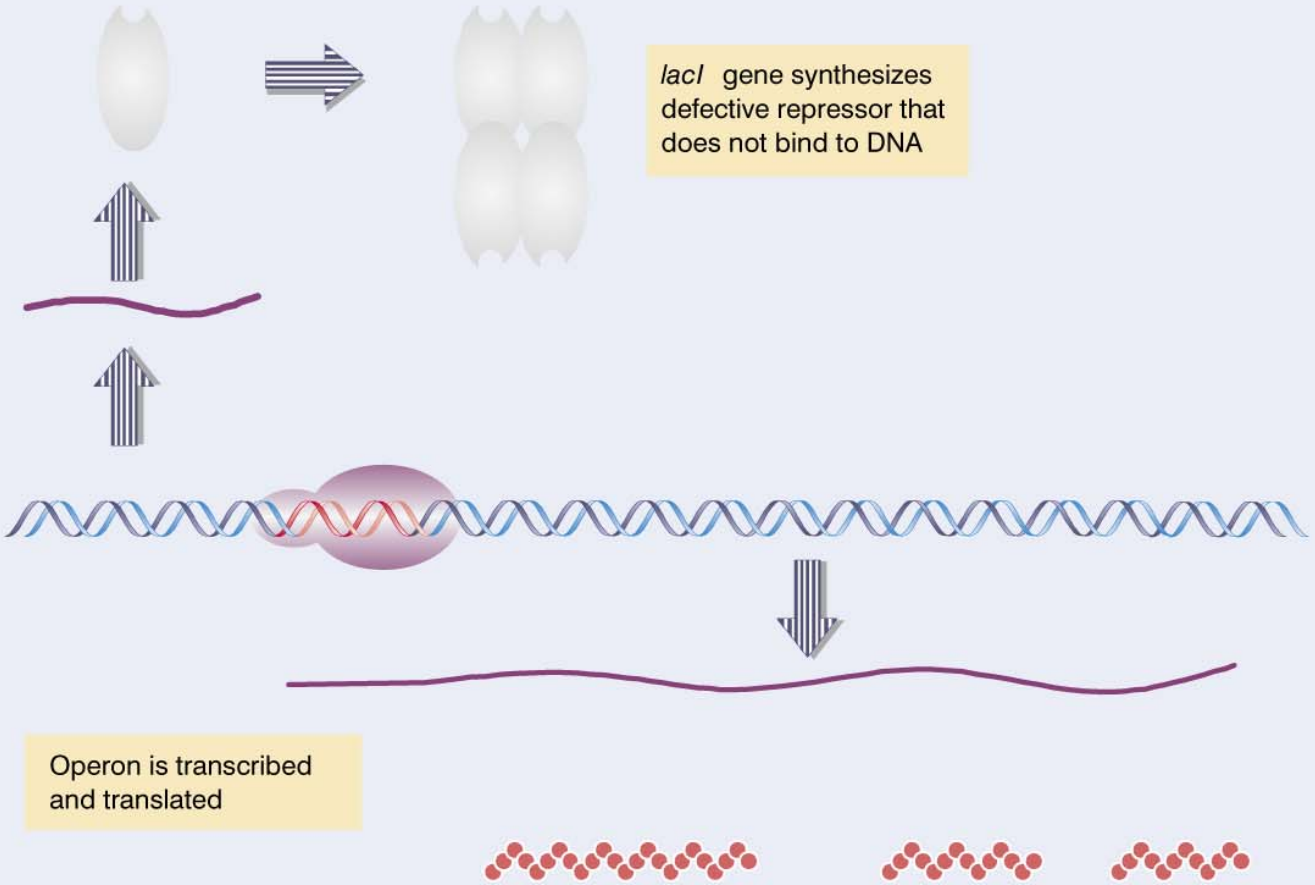


Figure 10.10 The *lac* operator has a symmetrical sequence. The sequence is numbered relative to the startpoint for transcription at +1. The regions of dyad symmetry are indicated by the shaded blocks.

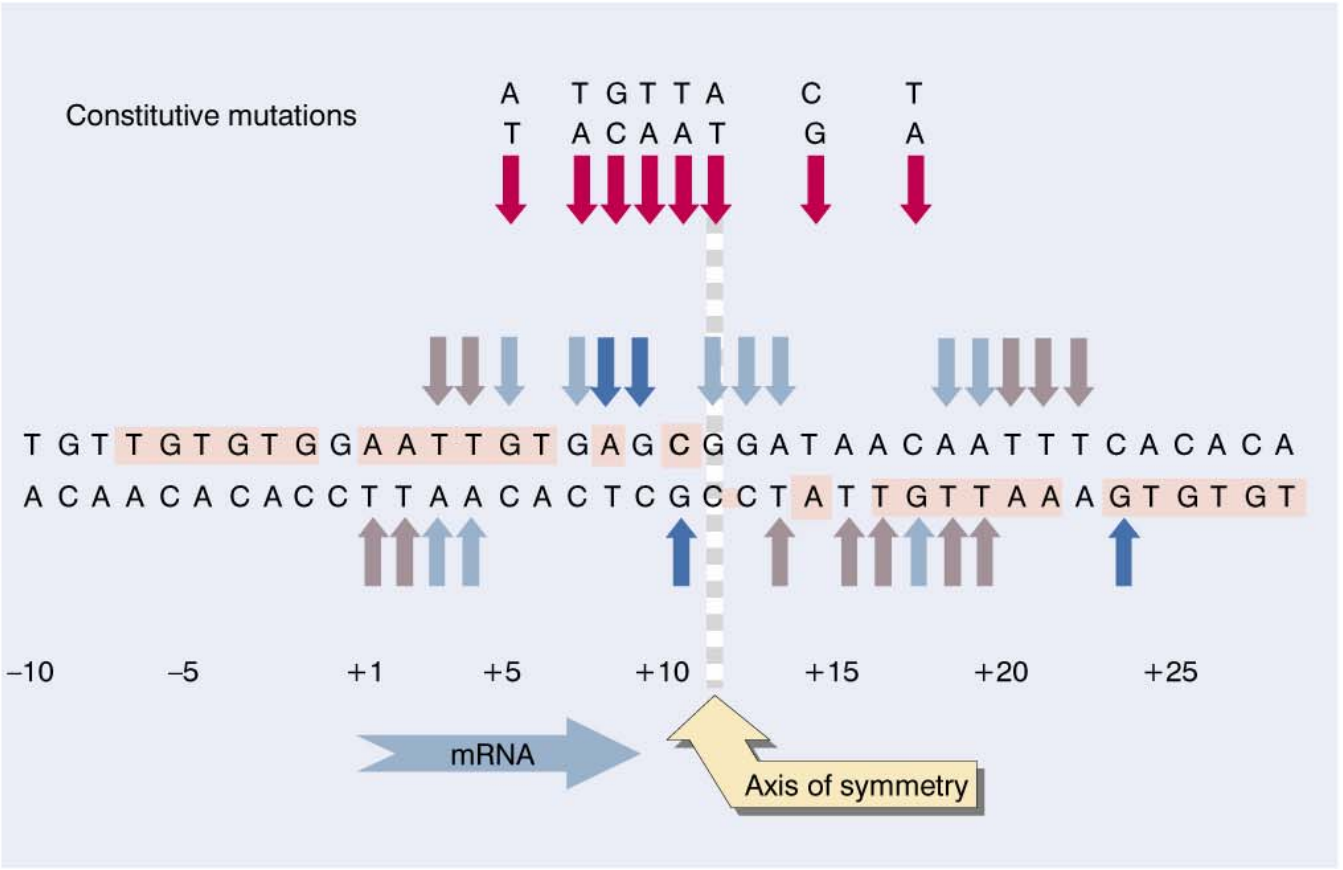


Figure 10.11 Does the inducer bind to free repressor to upset an equilibrium (left) or directly to repressor bound at the operator (right)?

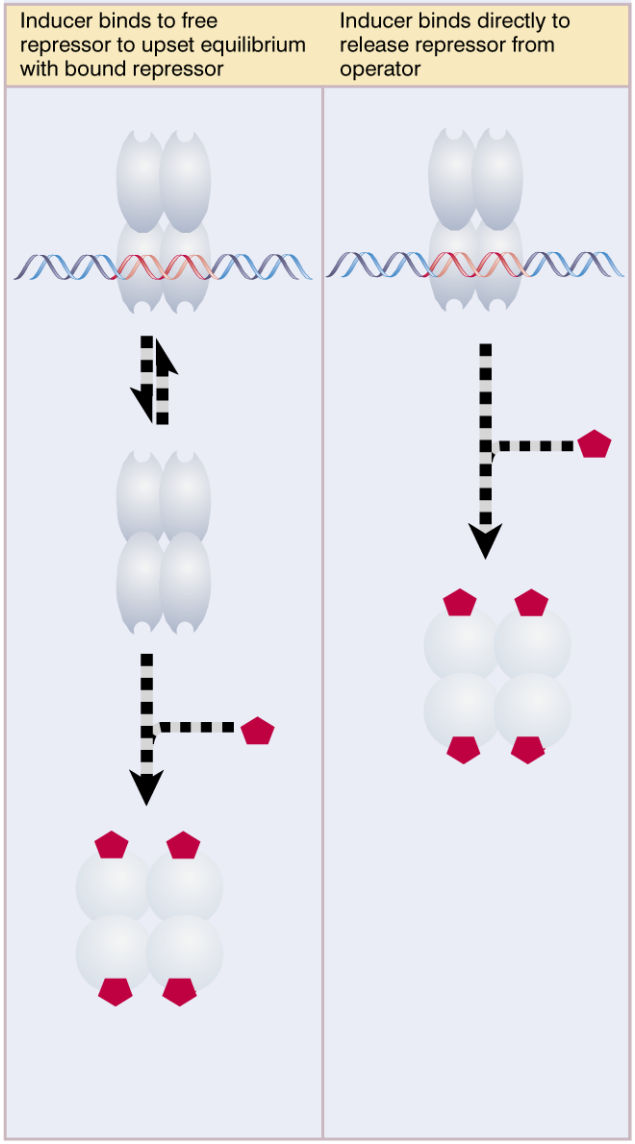


Figure 10.16 Lac repressor binds strongly and specifically to its operator, but is released by inducer. All equilibrium constants are in M^{-1}.

DNA	Repressor	Repressor + inducer
Operator	2×10^{13}	2×10^{10}
Other DNA	2×10^{6}	2×10^{6}
Specificity	10^{7}	10^{4}

Figure 10.17 Virtually all the repressor in the cell is bound to DNA.

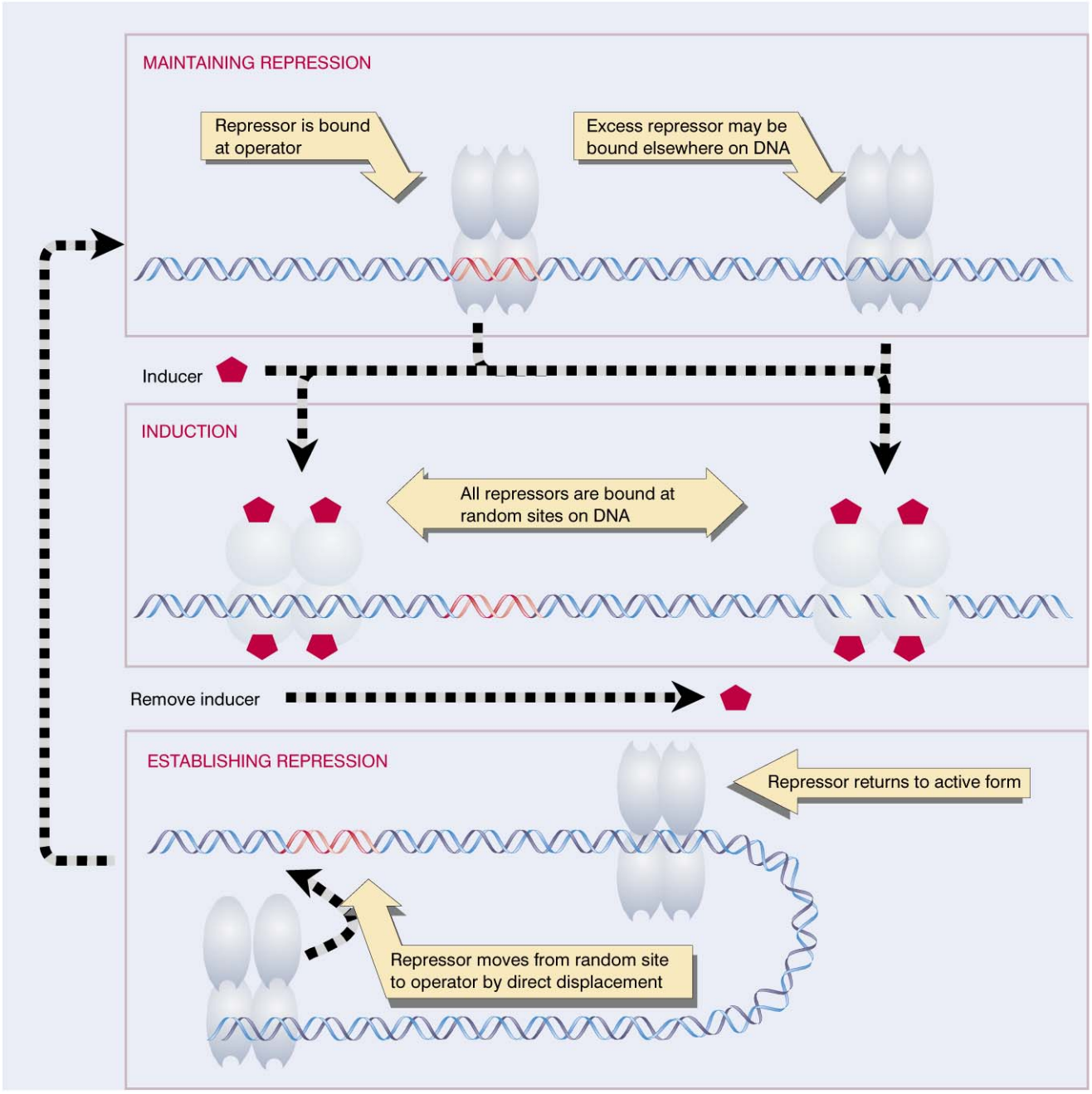


Figure 10.18 The *trp* repressor recognizes operators at three loci. Conserved bases are shown in red. The location of the mRNA varies, as indicated by the red arrows.

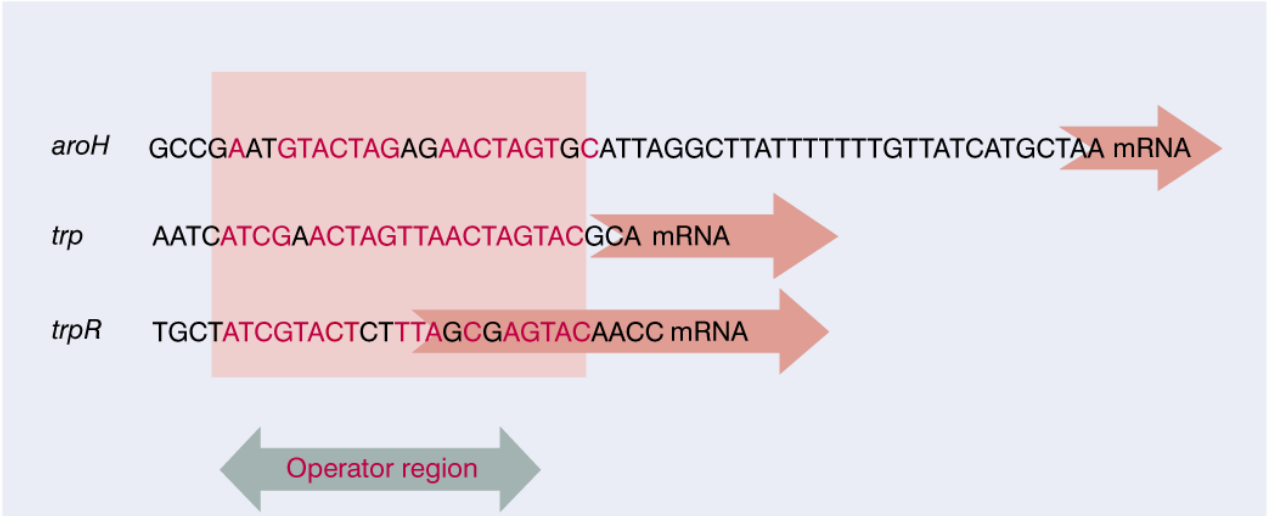


Figure 10.19 Operators may lie at various positions relative to the promoter.

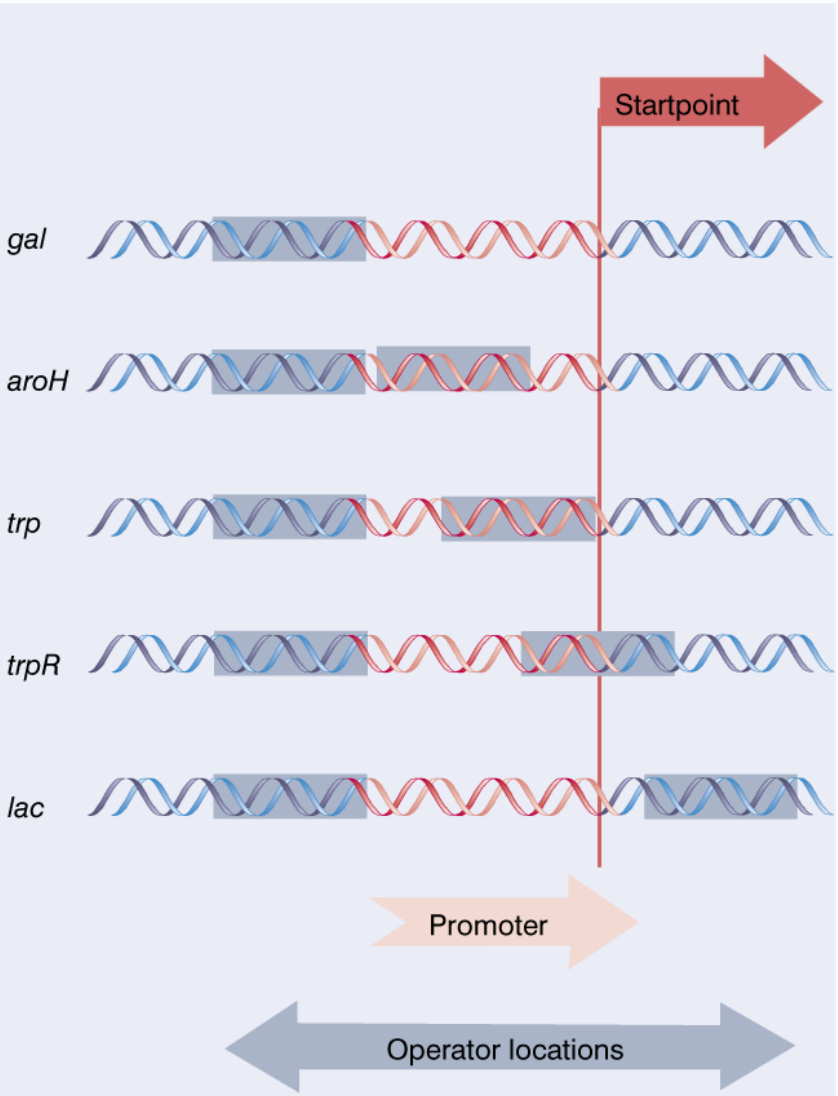


Figure 10.20 Control circuits are versatile and can be designed to allow positive or negative control of induction or repression.

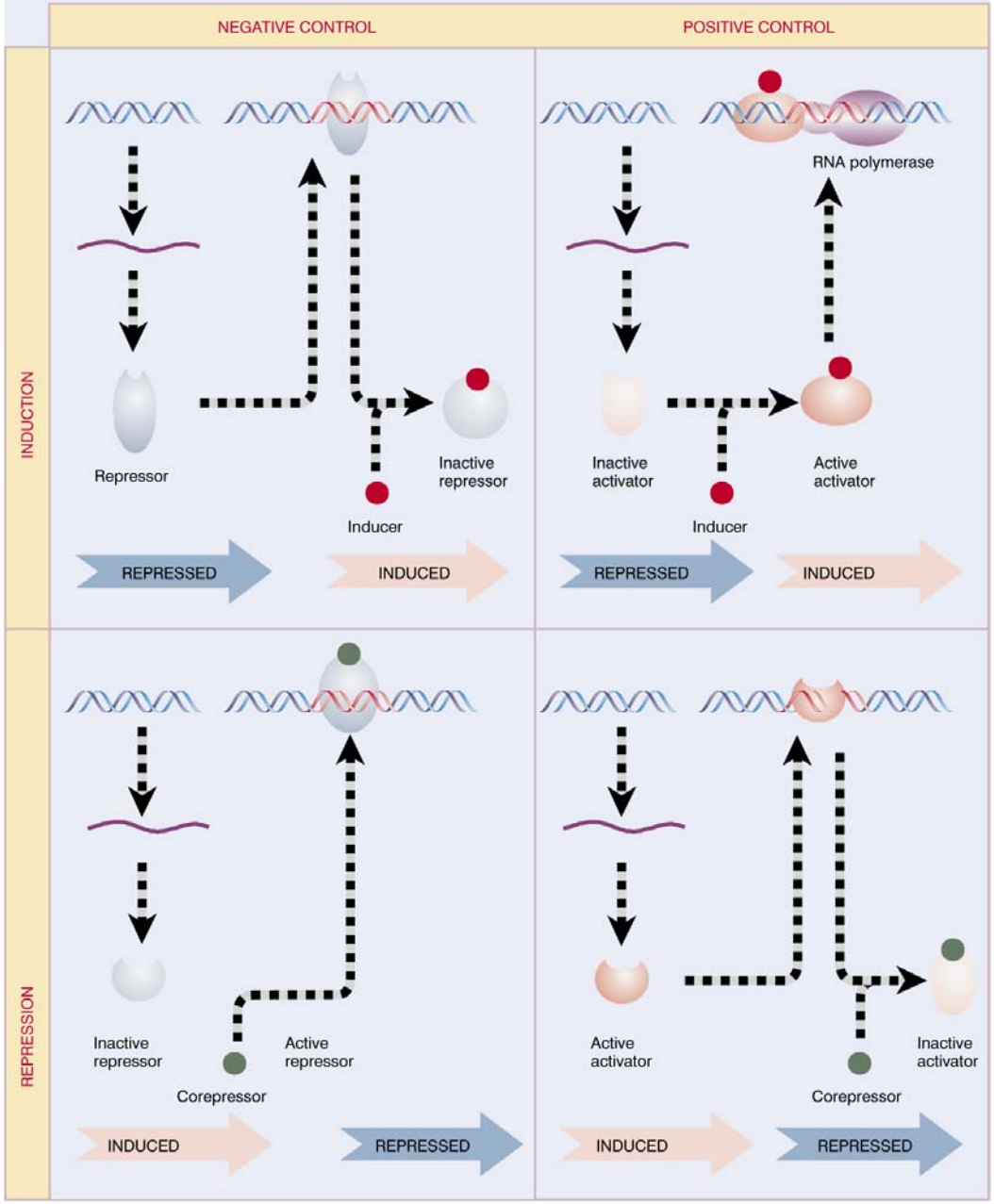


Figure 10.22 Glucose causes catabolite repression by reducing the level of cyclic AMP.

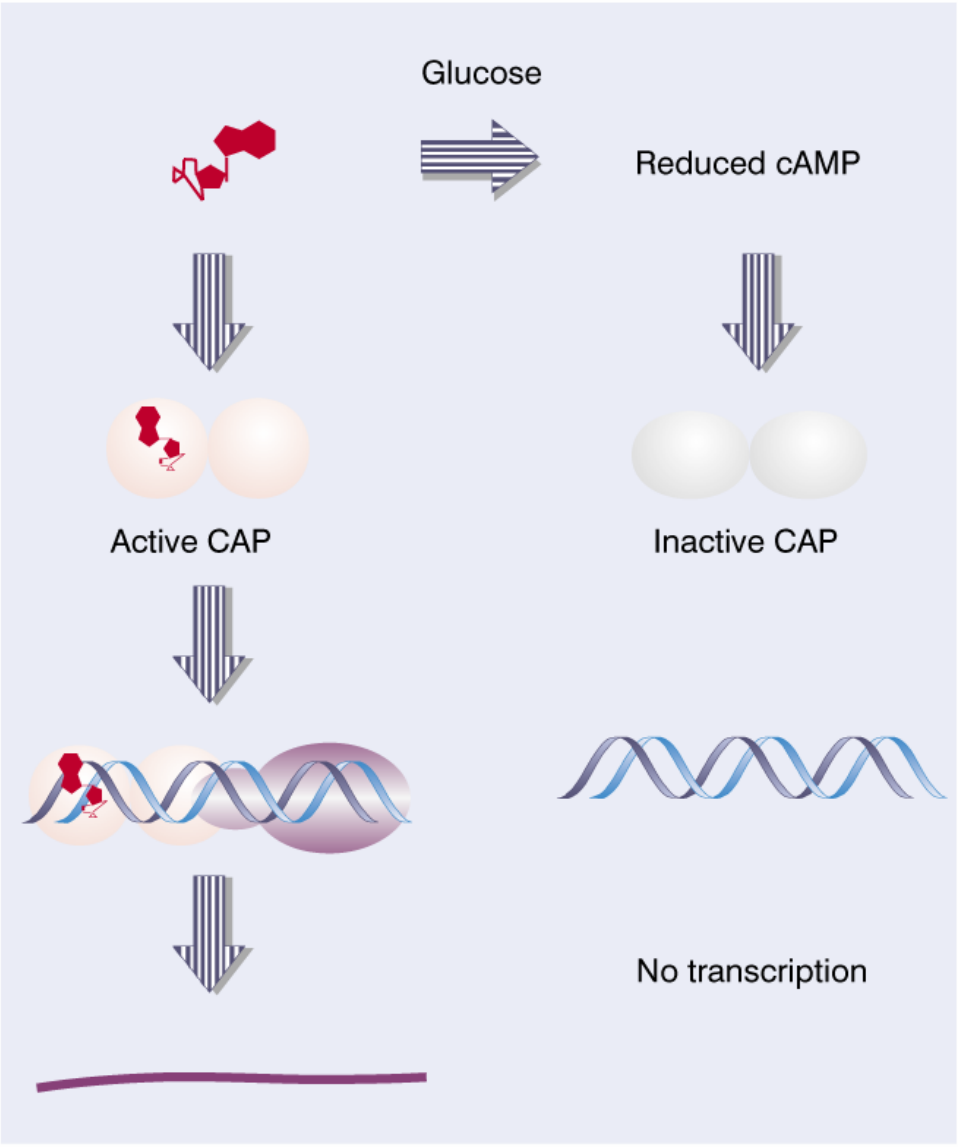


Figure 10.23 The consensus sequence for CAP contains the well-conserved pentamer TGTGA and (sometimes) an inversion of this sequence (TCANA).

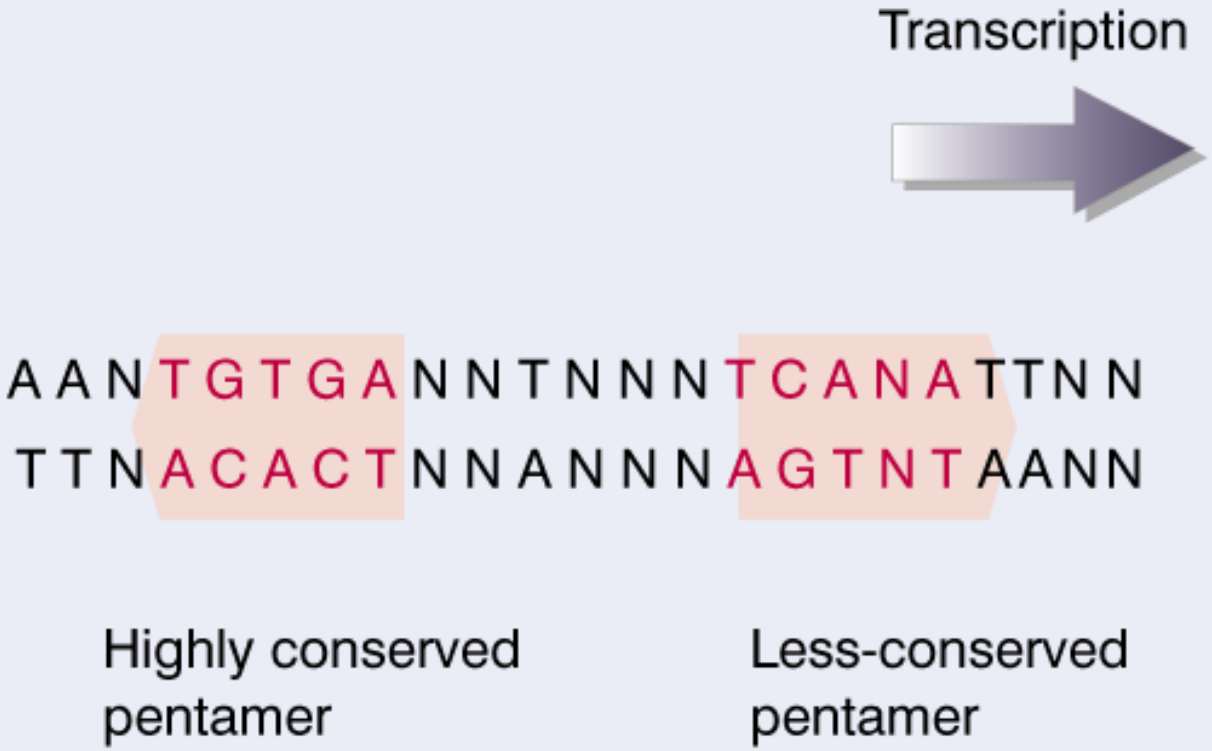


Figure 10.24 The CAP protein can bind at different sites relative to RNA polymerase.

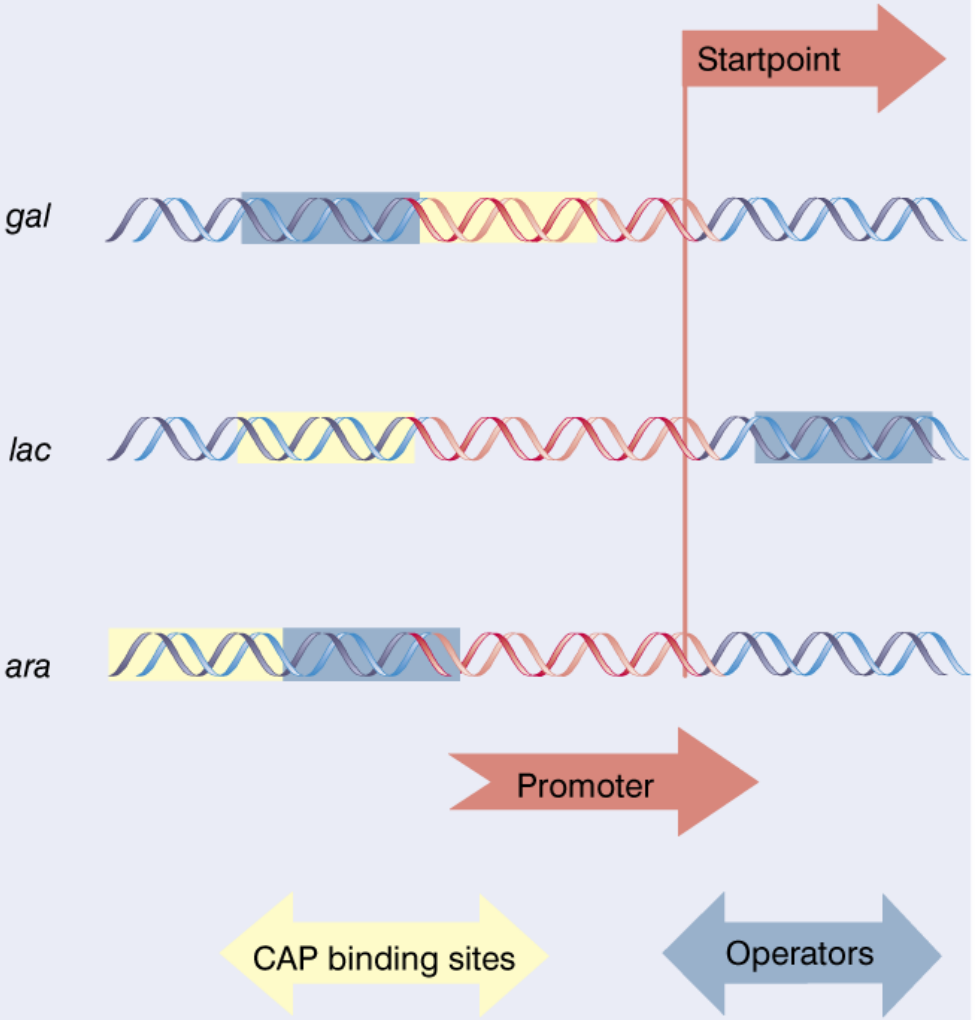
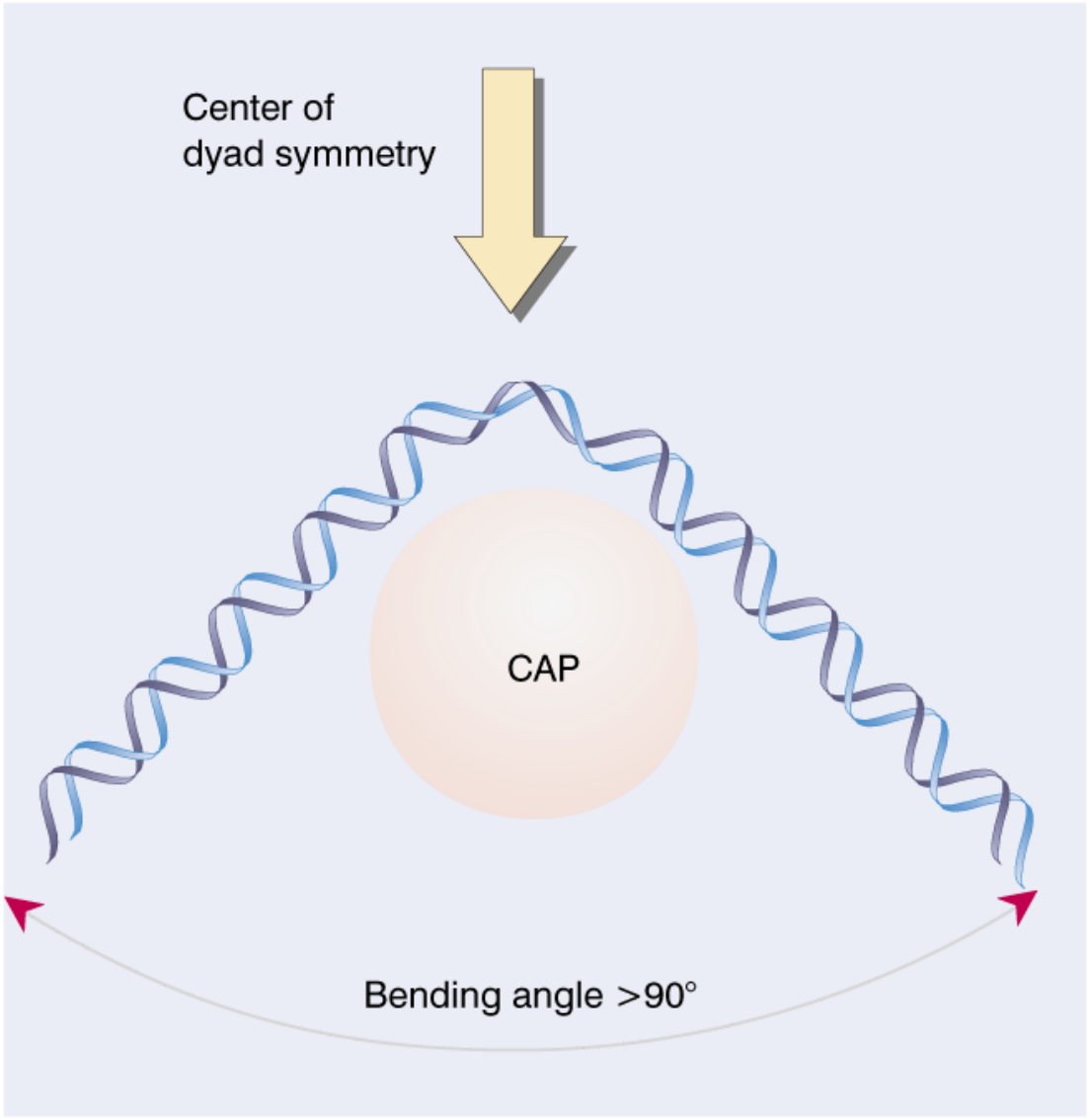


Figure 10.26 CAP bends DNA >90° around the center of symmetry.



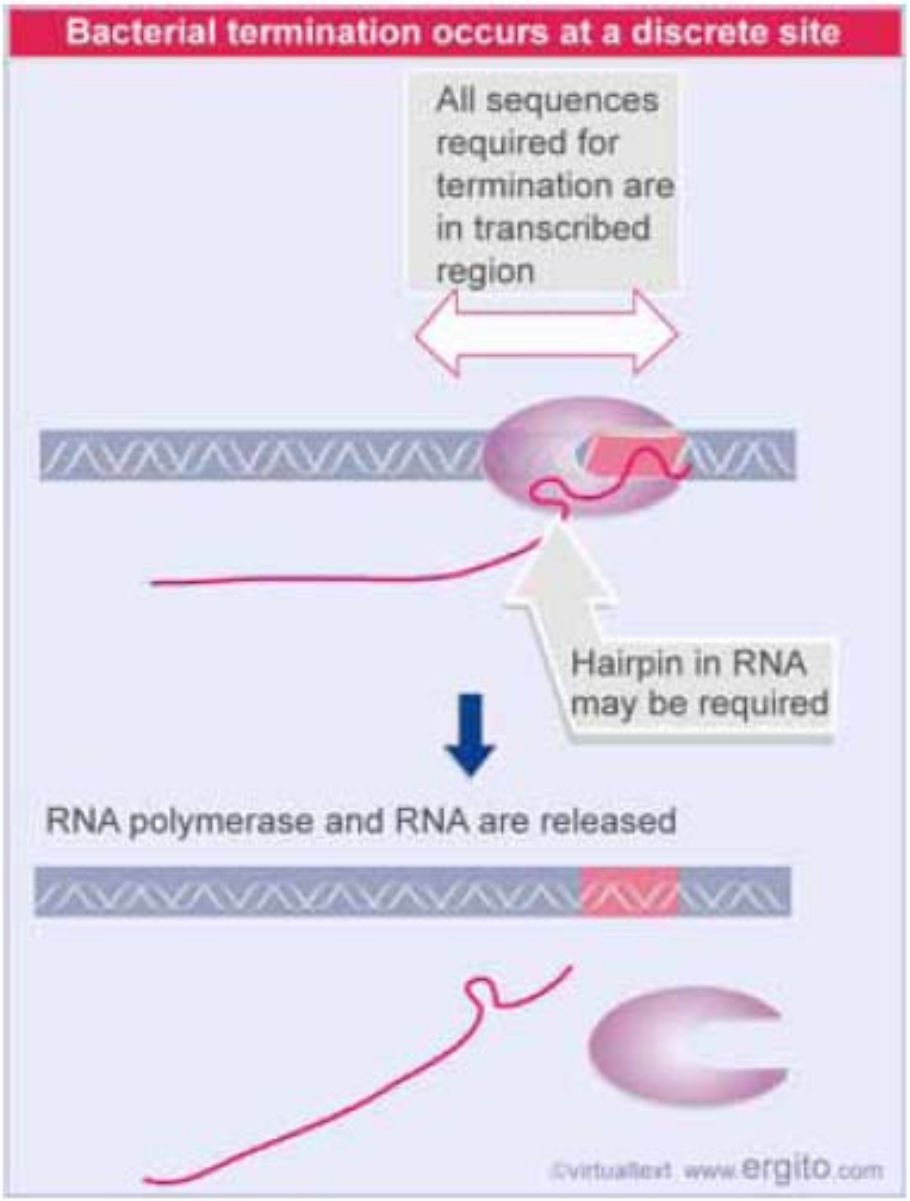


Figure 9.45 The DNA sequences required for termination are located prior to the terminator sequence. Formation of a hairpin in the RNA may be necessary.

Figure 9.27 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.

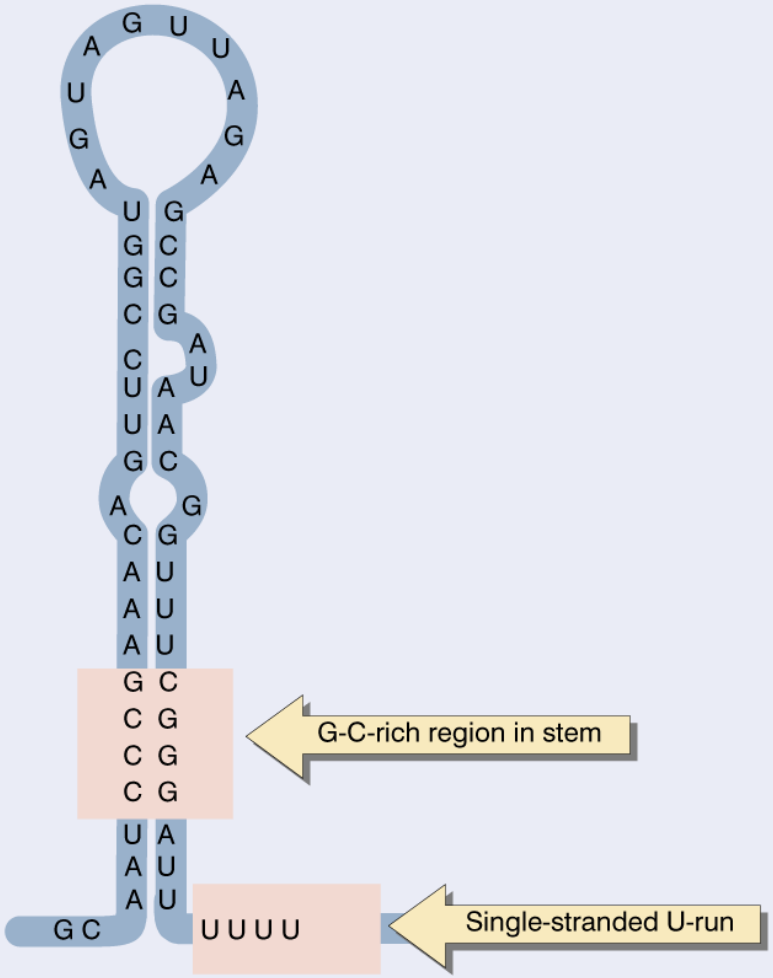
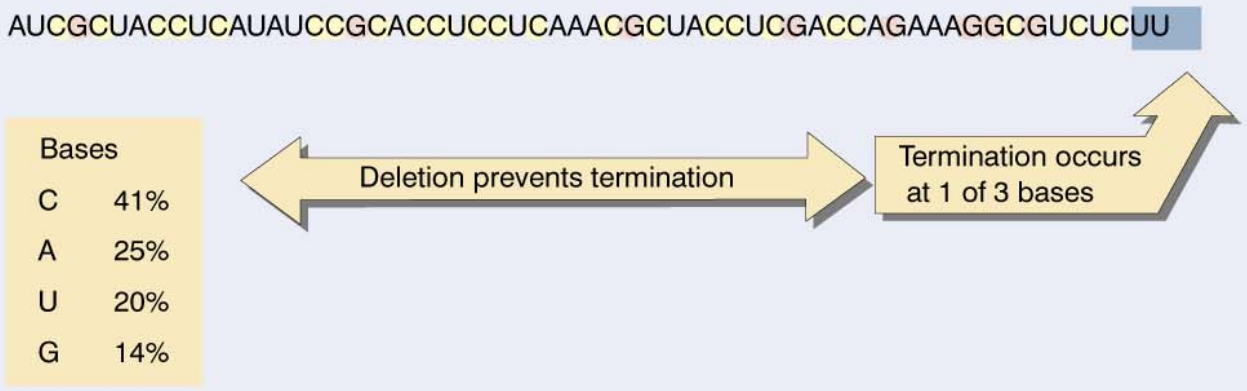


Figure 9.28 A rho-dependent terminator has a sequence rich in C and poor in G preceding the actual site(s) of termination.



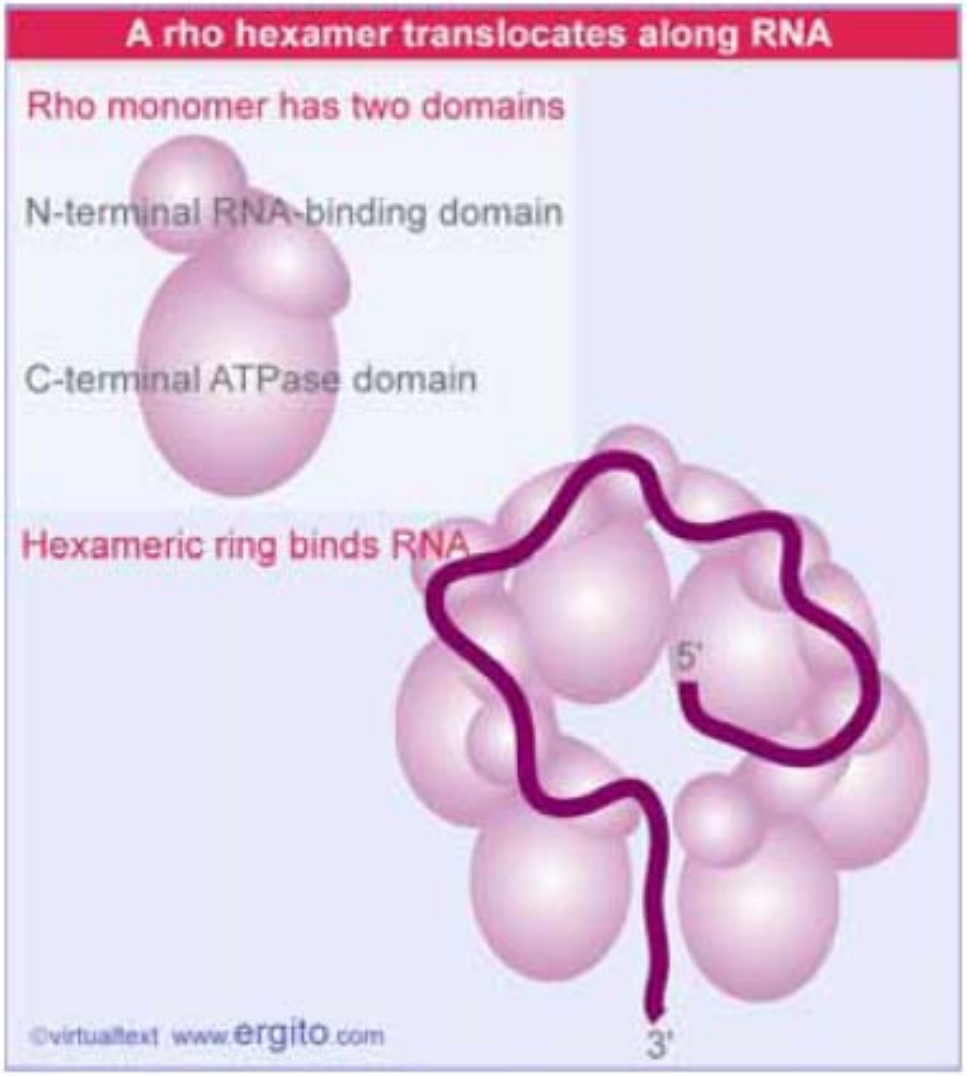


Figure 9.48 Rho has an N-terminal RNA-binding domain and a C-terminal ATPase domain. A hexamer in the form of a gapped ring binds RNA along the exterior of the N-terminal domains. The 5&#; end of the RNA is bound by a secondary binding site in the interior of the hexamer.

Figure 9.29 Rho factor pursues RNA polymerase along the RNA and can cause termination when it catches the enzyme pausing at a rho-dependent terminator.

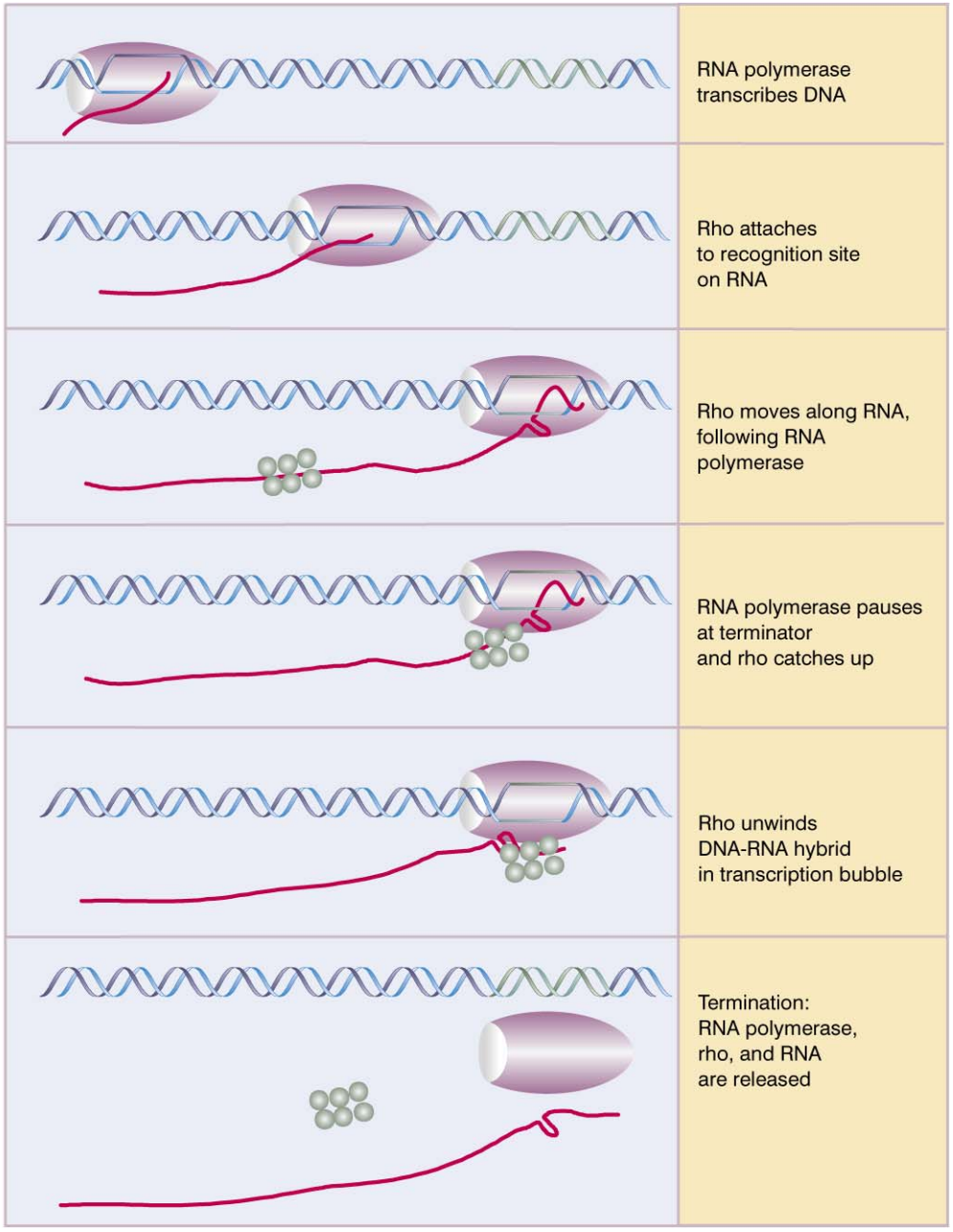


Figure 9.30 The action of rho factor may create a link between transcription and translation when a rho-dependent terminator lies soon after a nonsense mutation.

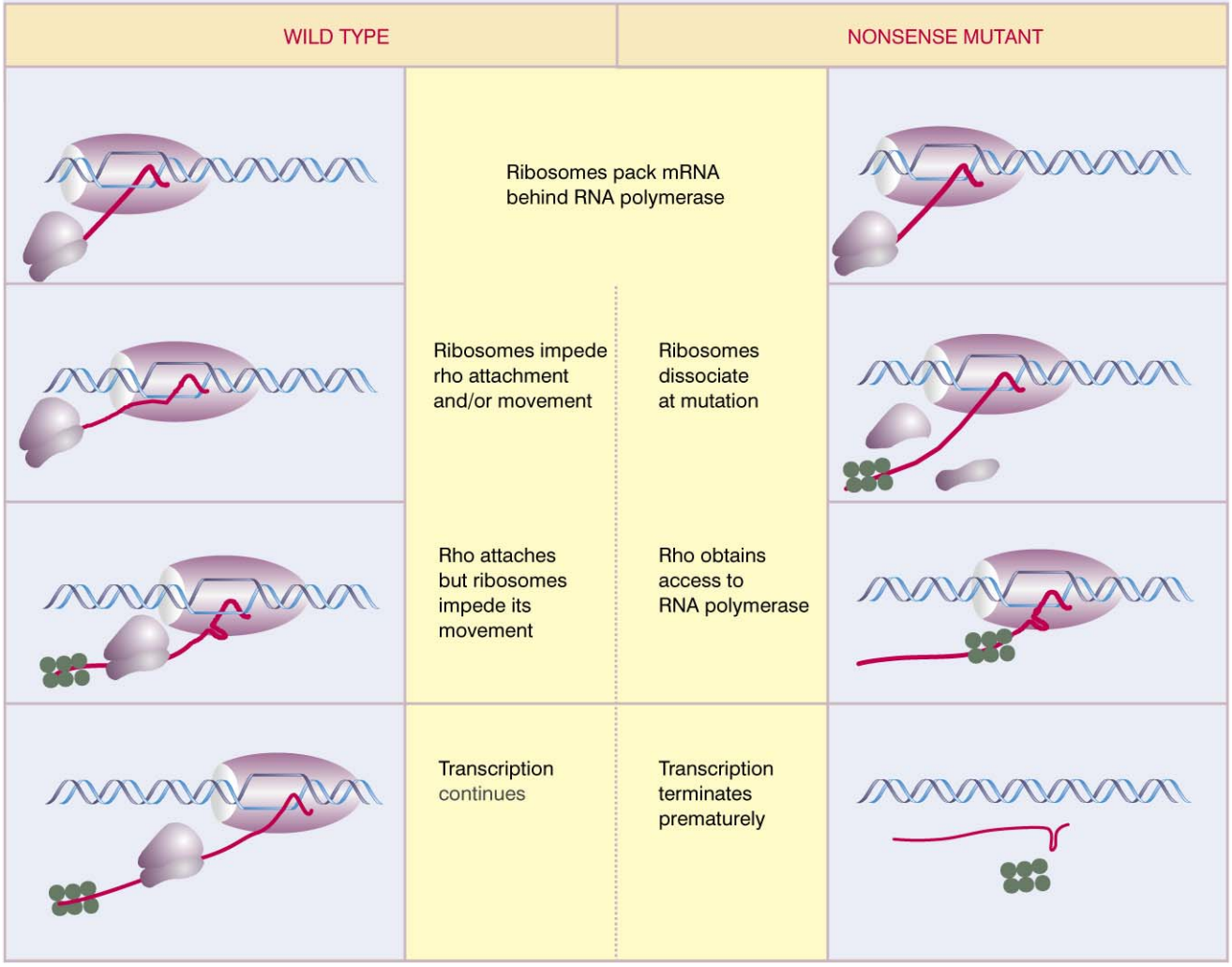


Figure 9.31
Antitermination can be used to control transcription by determining whether RNA polymerase terminates or reads through a particular terminator into the following region.

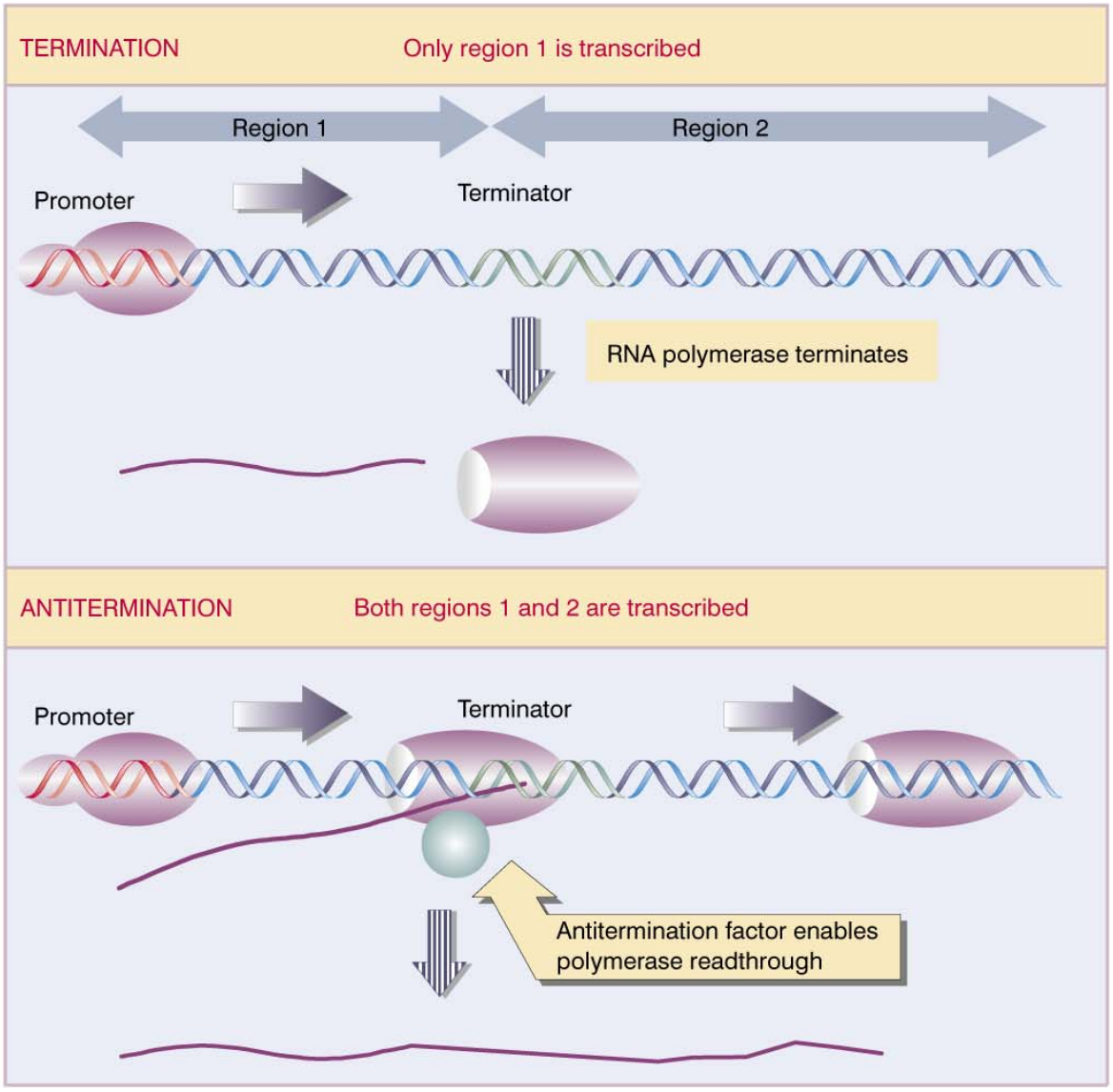


Figure 9.32 Switches in transcriptional specificity can be controlled at initiation or termination.

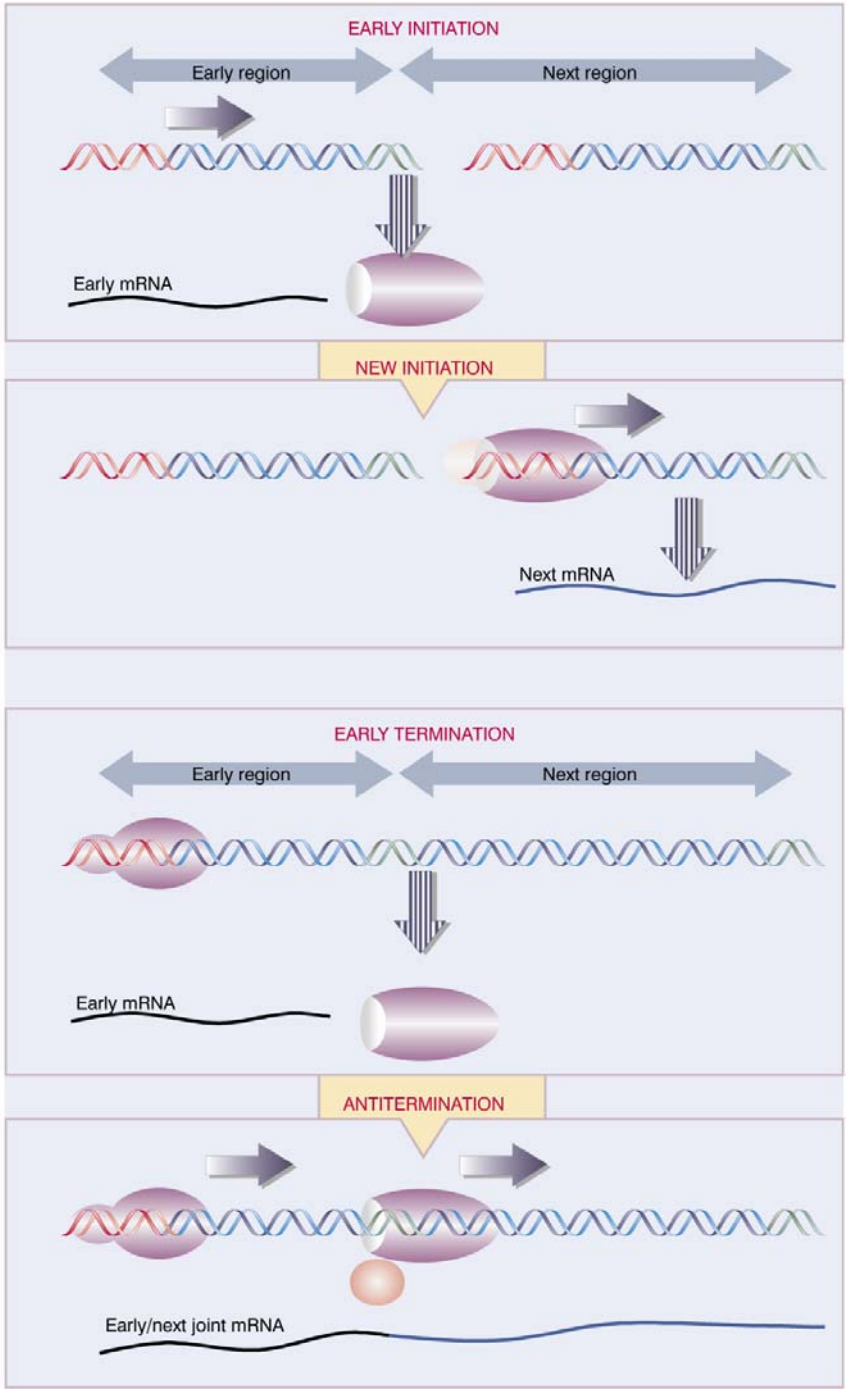
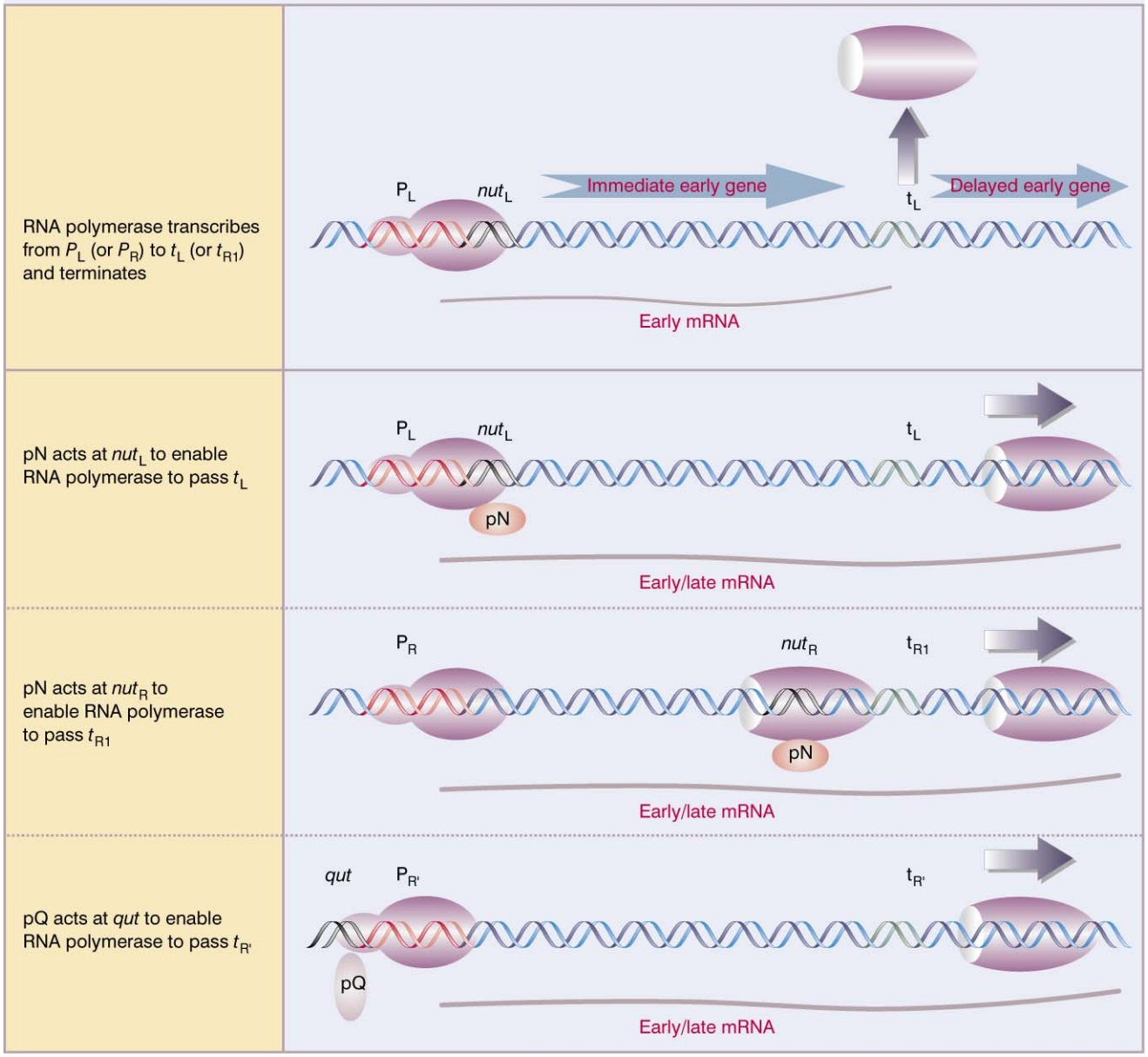


Figure 9.33 Host RNA polymerase transcribes lambda genes and terminates at *t* sites. pN allows it to read through terminators in the L and R1 units; pQ allows it to read through the R' terminator. The sites at which pN acts (*nut*) and at which pQ acts (*qut*) are located at different relative positions in the transcription units.



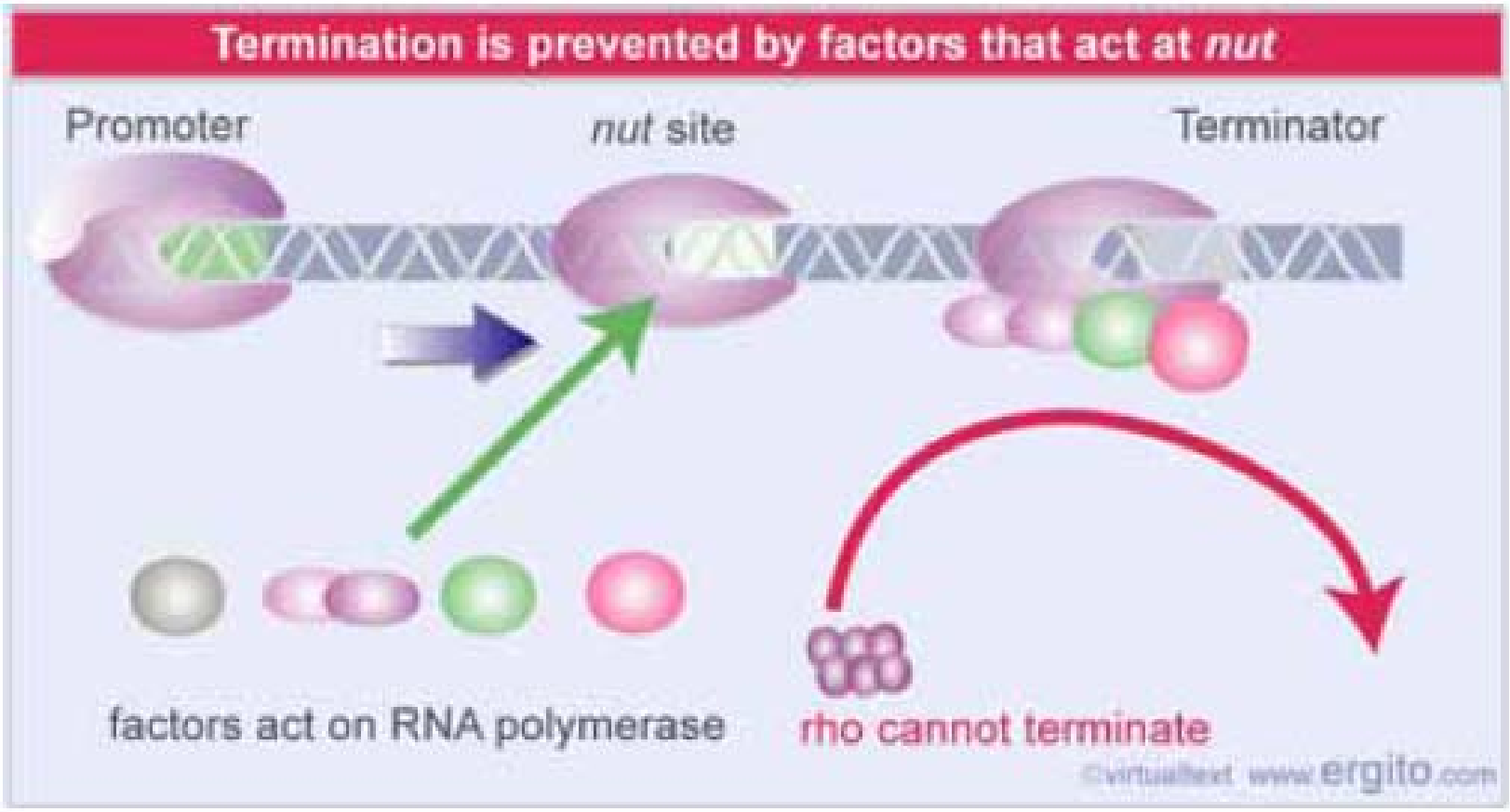


Figure 9.54 Ancillary factors bind to RNA polymerase as it passes the *nut* site. They prevent rho from causing termination when the polymerase reaches the terminator.

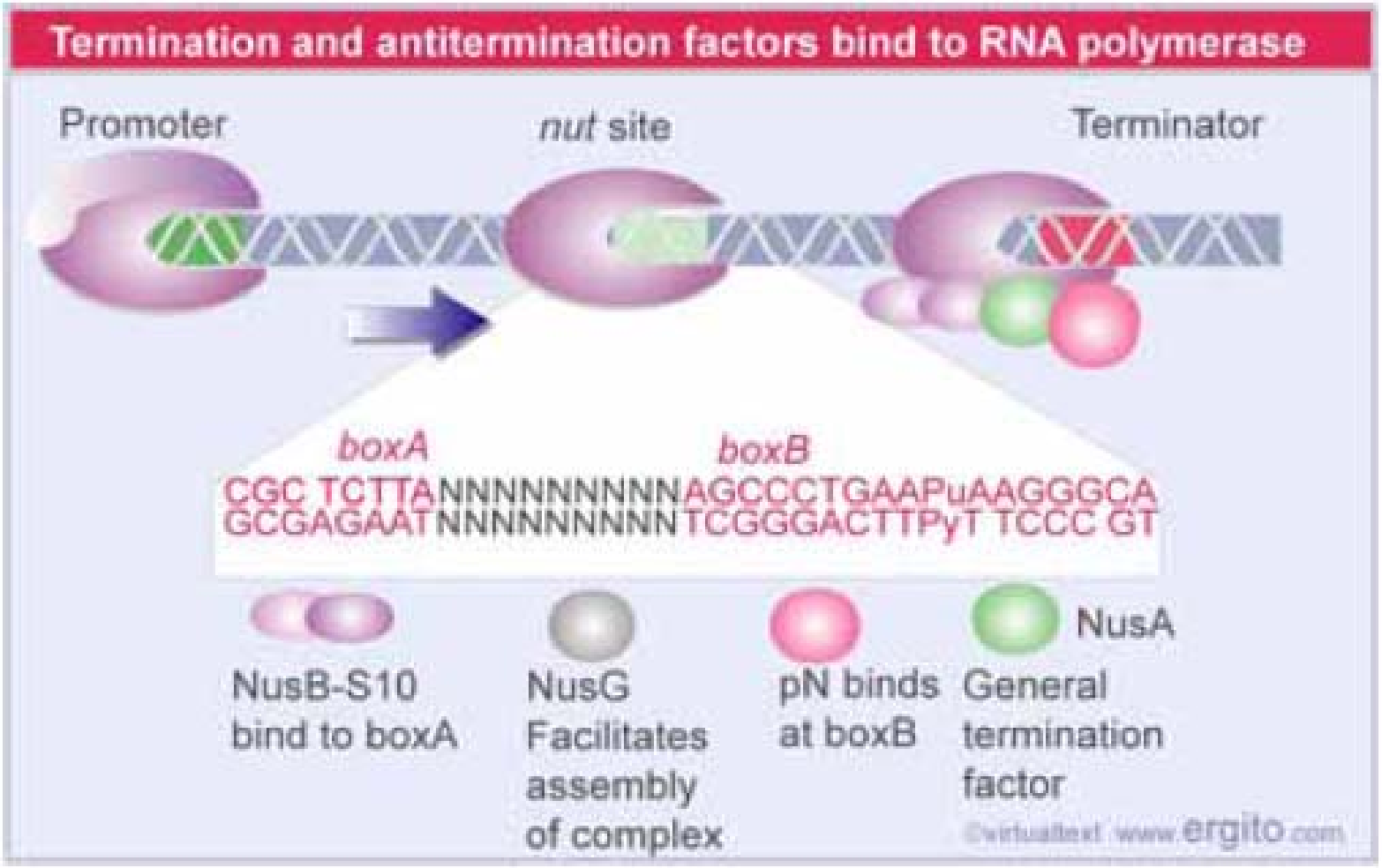


Figure 9.55 Ancillary factors bind to RNA polymerase as it passes certain sites. The *nut* site consists of two sequences. NusB-S10 join core enzyme as it passes *boxA*. Then NusA and pN protein bind as polymerase passes *boxB*. The presence of pN allows the enzyme to read through the terminator, producing a joint mRNA that contains immediate early sequences joined to delayed early sequences.

Figure 9.35 RNA polymerase may alternate between initiation-competent and termination-competent forms as sigma and Nus factors alternatively replace one another on the core enzyme.