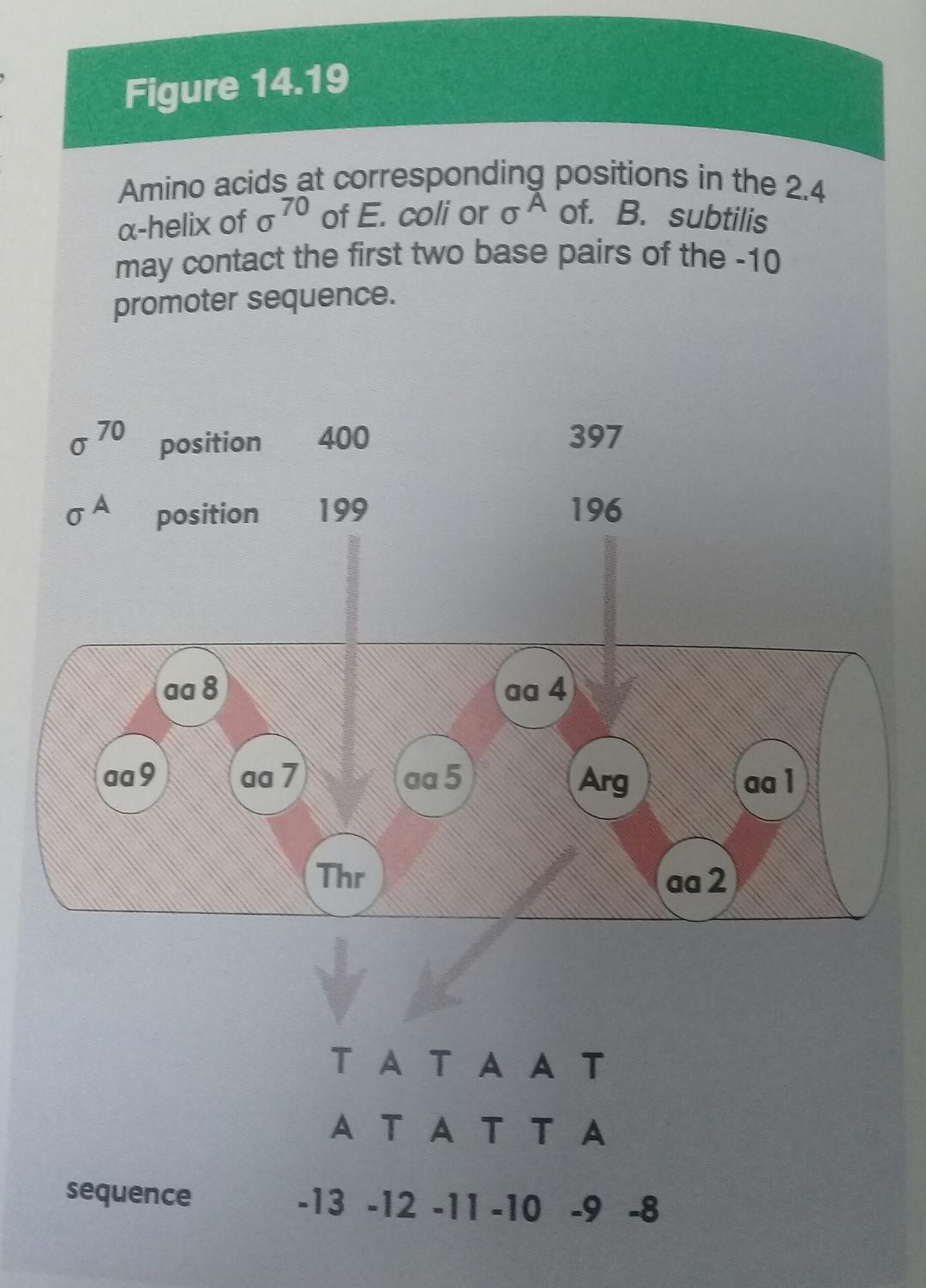
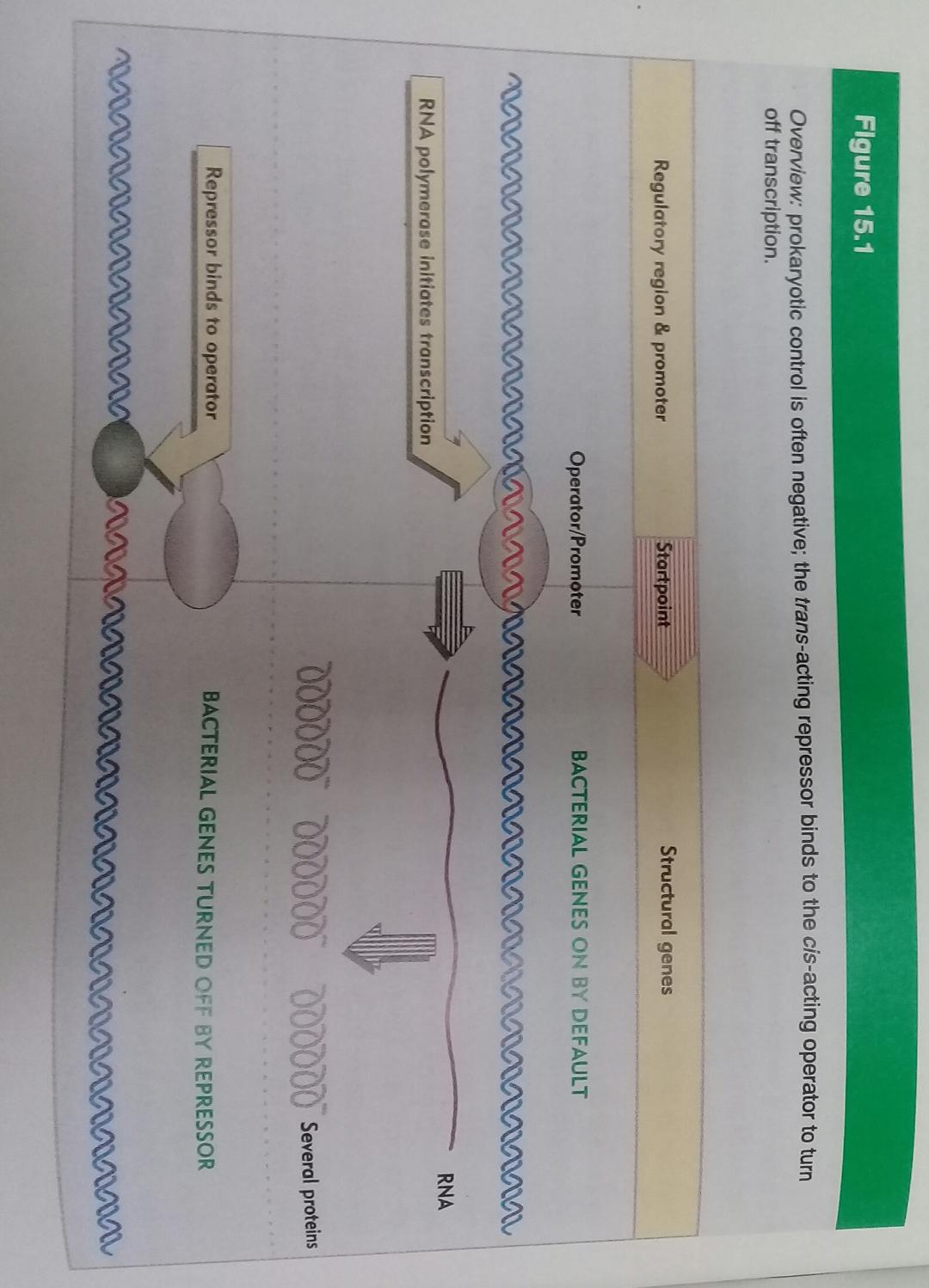
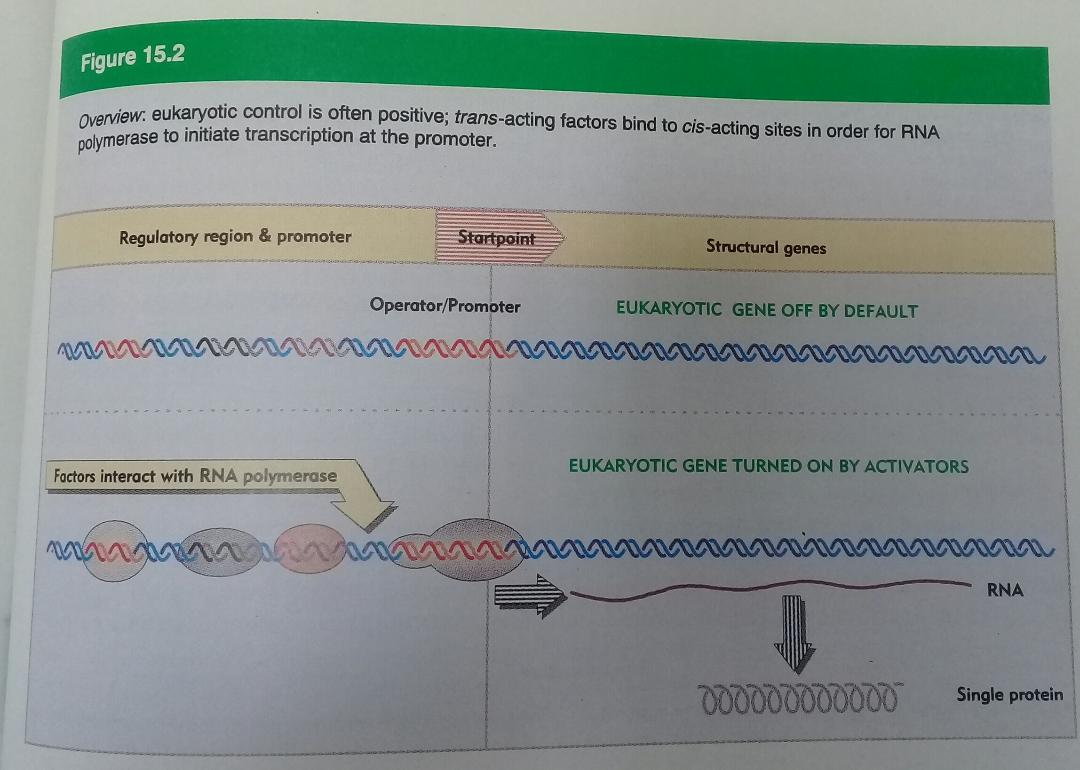
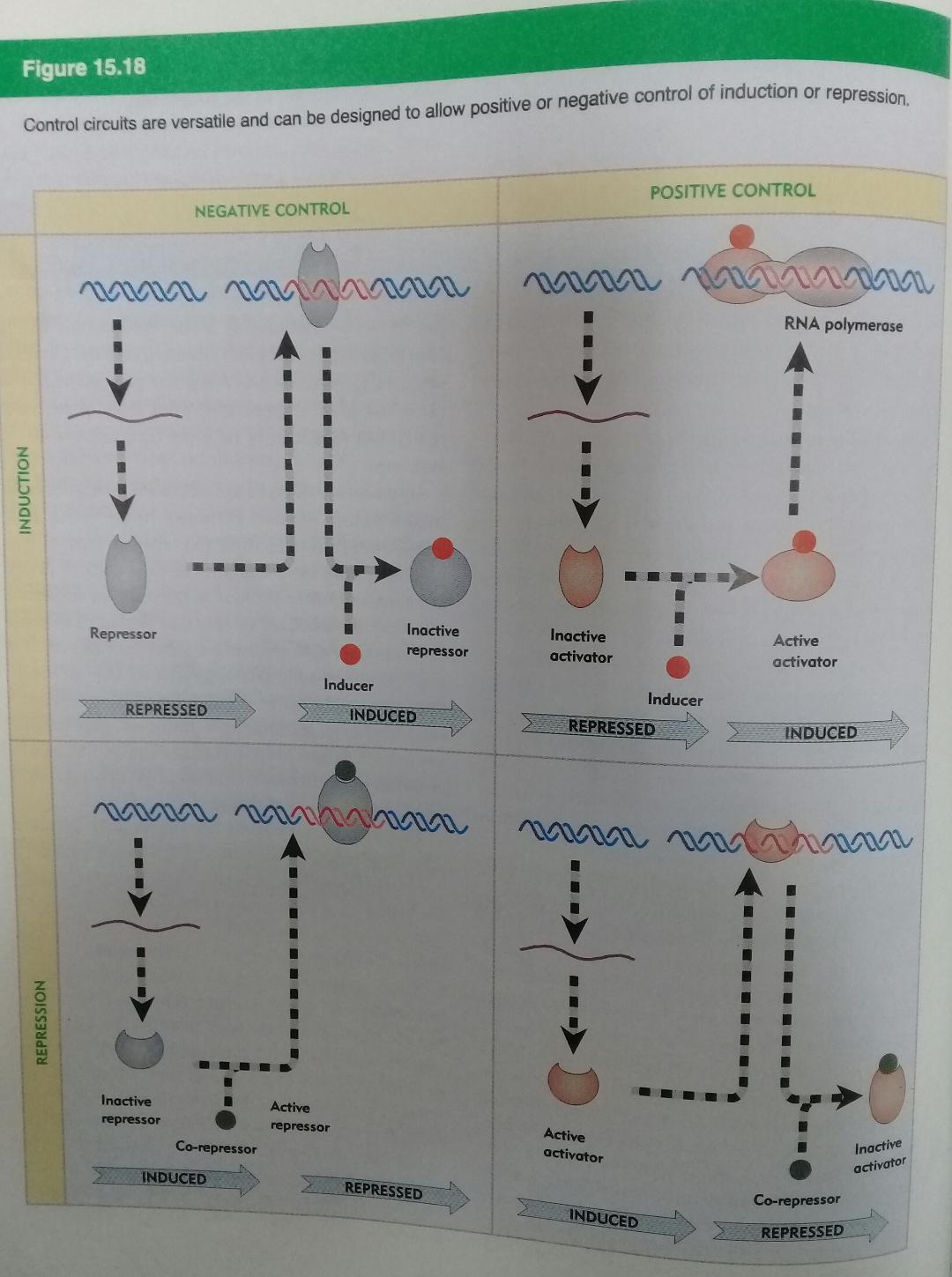
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**Transcription Is Regulated at Several Levels**

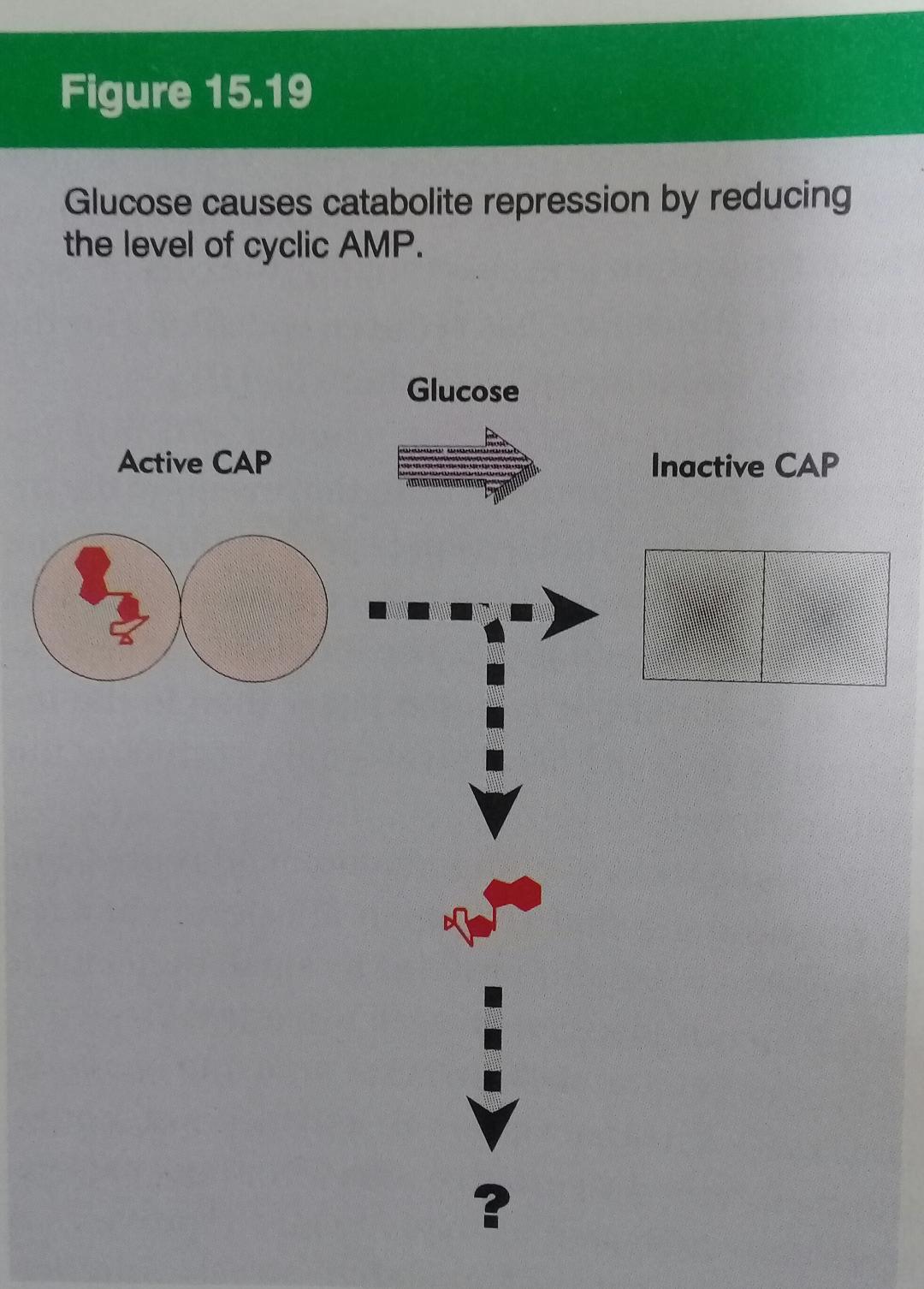
* Regulation can occur at any step in transcription, including elongation and termination.
* The binding of proteins to sequences both near to and distant from the promoter can also affect levels of gene expression.
* Protein binding can *activate* transcription by facilitating either RNA polymerase binding or steps further along in the initiation process, or it can *repress* transcription by blocking the activity of the polymerase.
* **Repressors** are proteins that block the synthesis of RNA at specific genes.

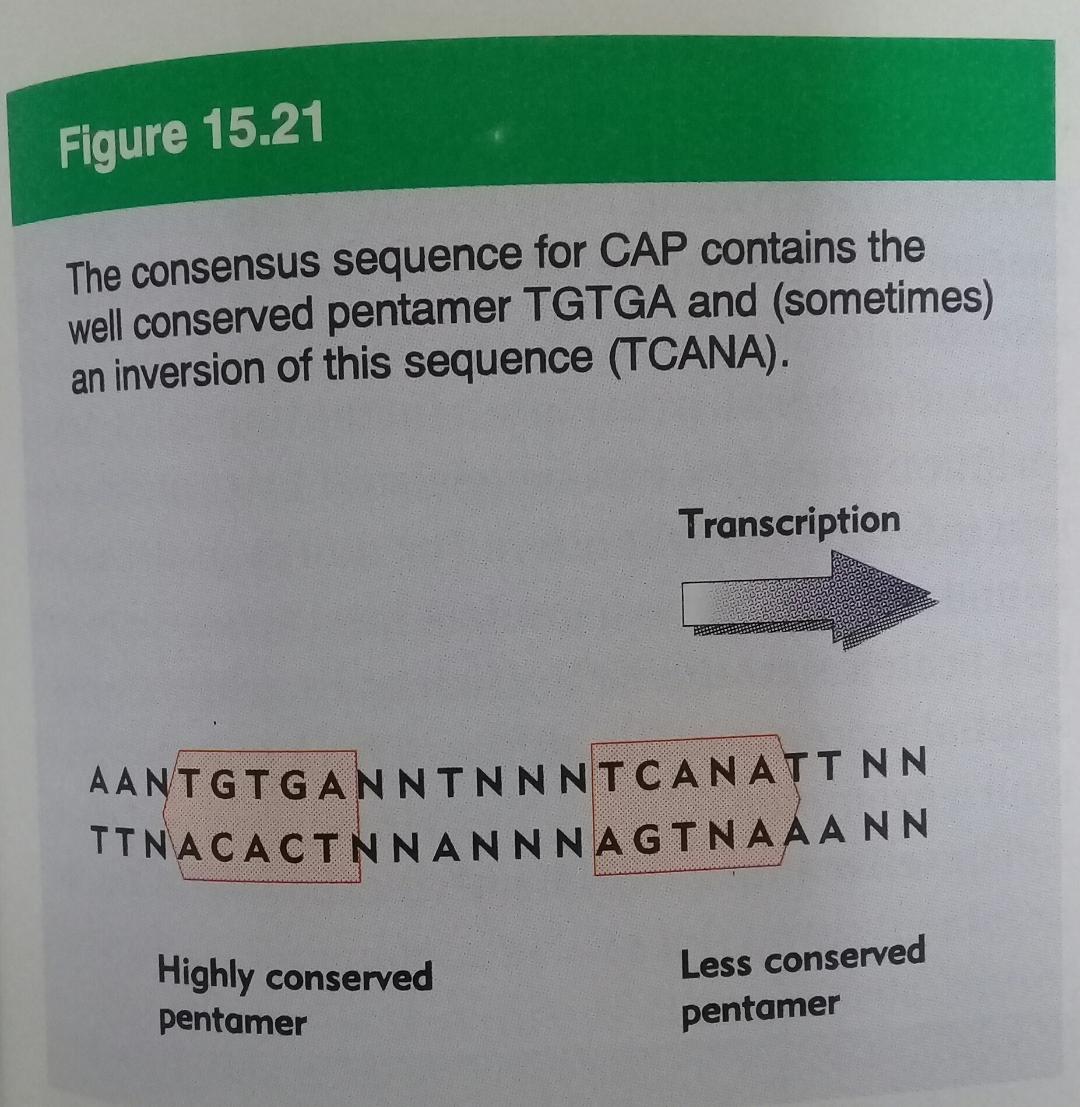
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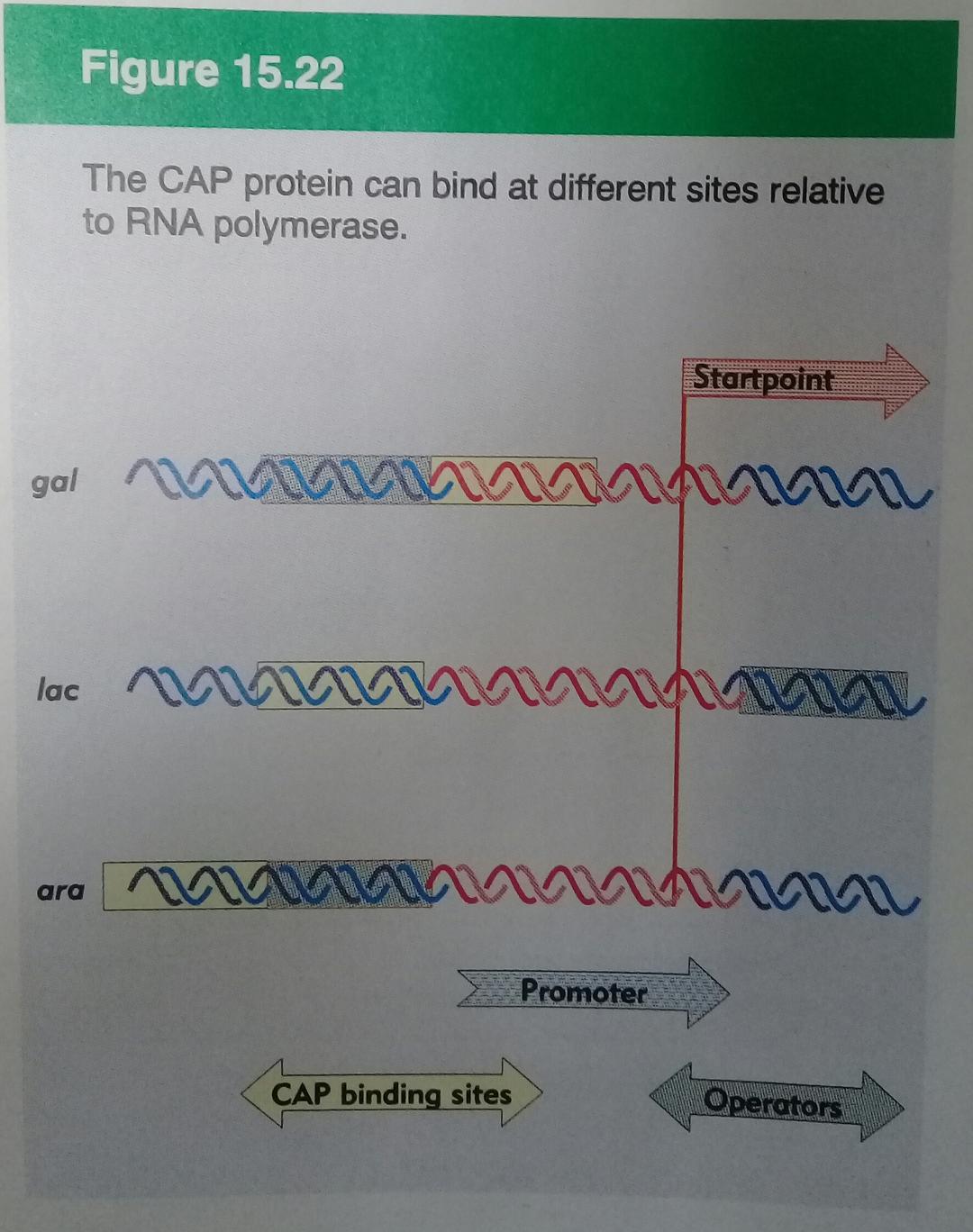


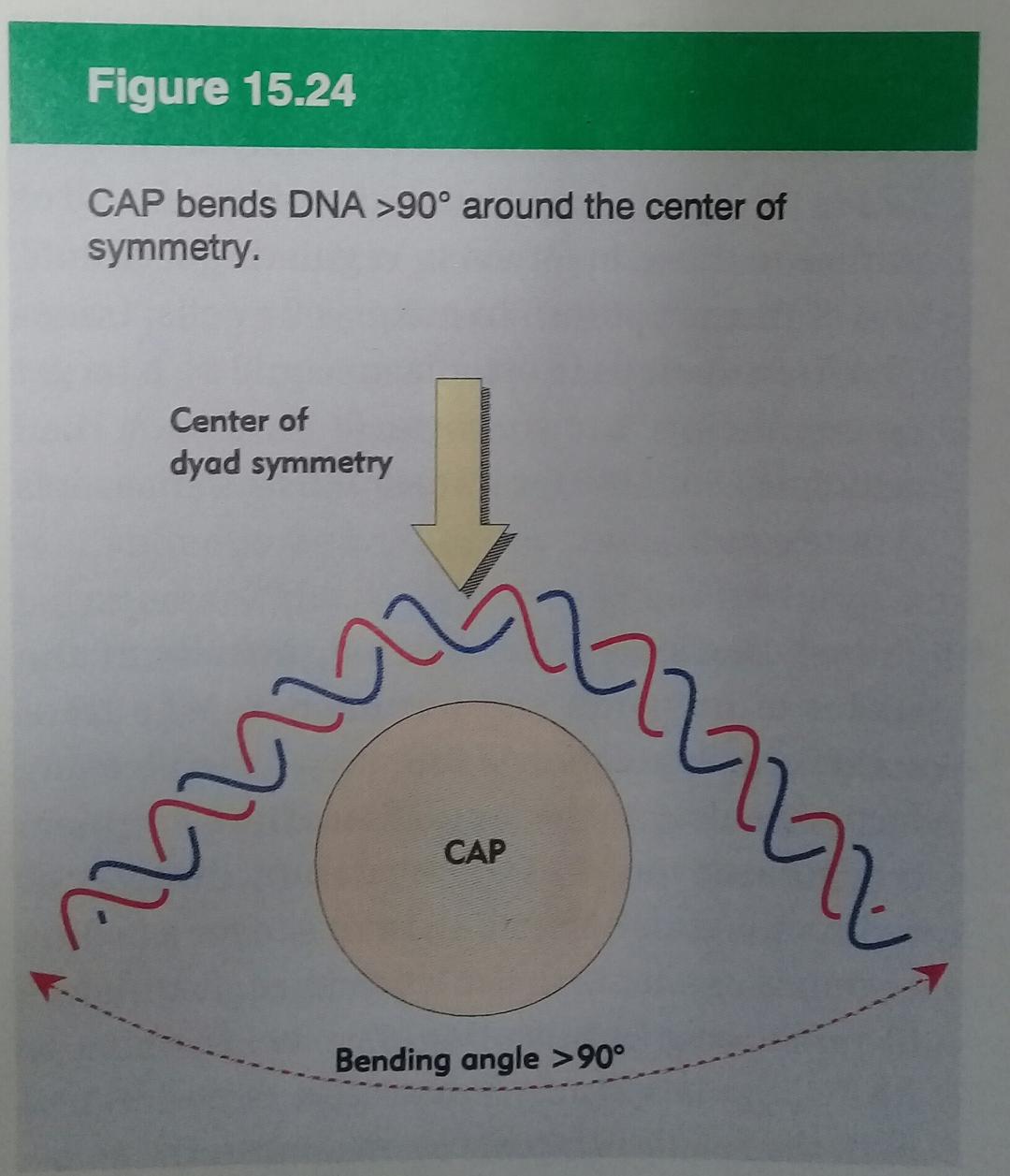
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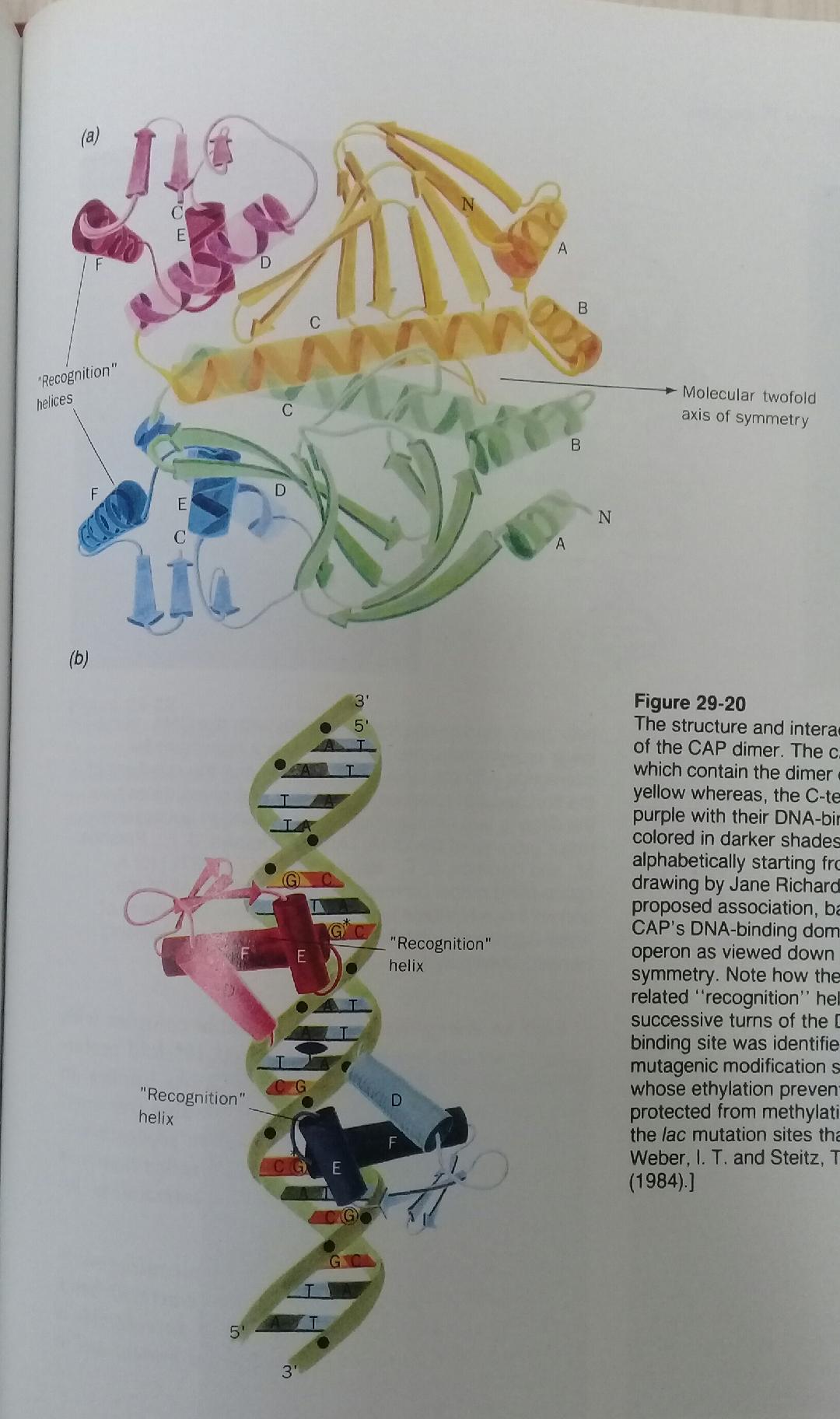
* In *E. coli*, one protein that activates transcription is the **cAMP receptor protein (CRP)**, **(CAP, catabolite activator protein),** which increases the transcription of genes coding for enzymes.





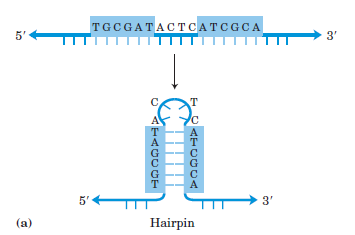




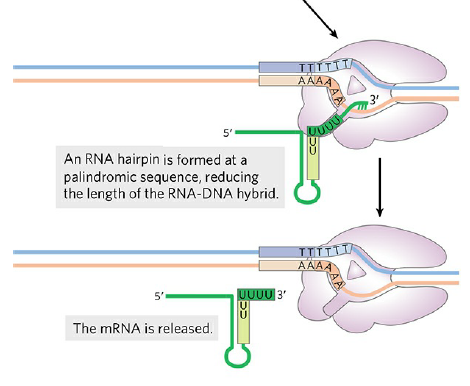
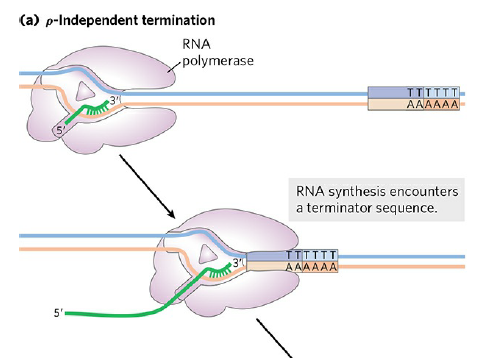
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**Specific Sequences Signal Termination of RNA Synthesis**

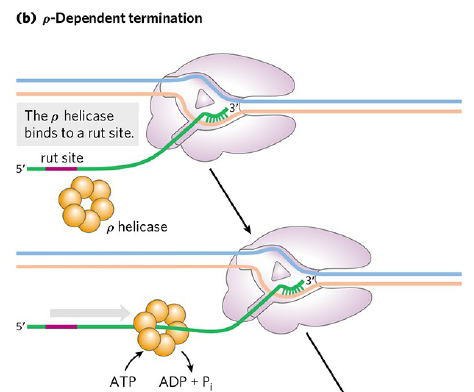
* *E. coli* has at least two classes of termination signals: one class relies on a protein factor called  (rho) and the other is -independent.
* Most  -independent terminators have two distinguishing features.
* The first is a region that produces an RNA transcript with self-complementary sequences, permitting the formation of a hairpin structure centered 15 to 20 nucleotides before the projected end of the RNA strand **(Fig. 8–19a)**.

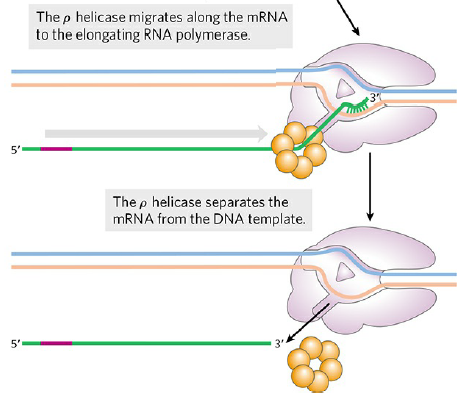


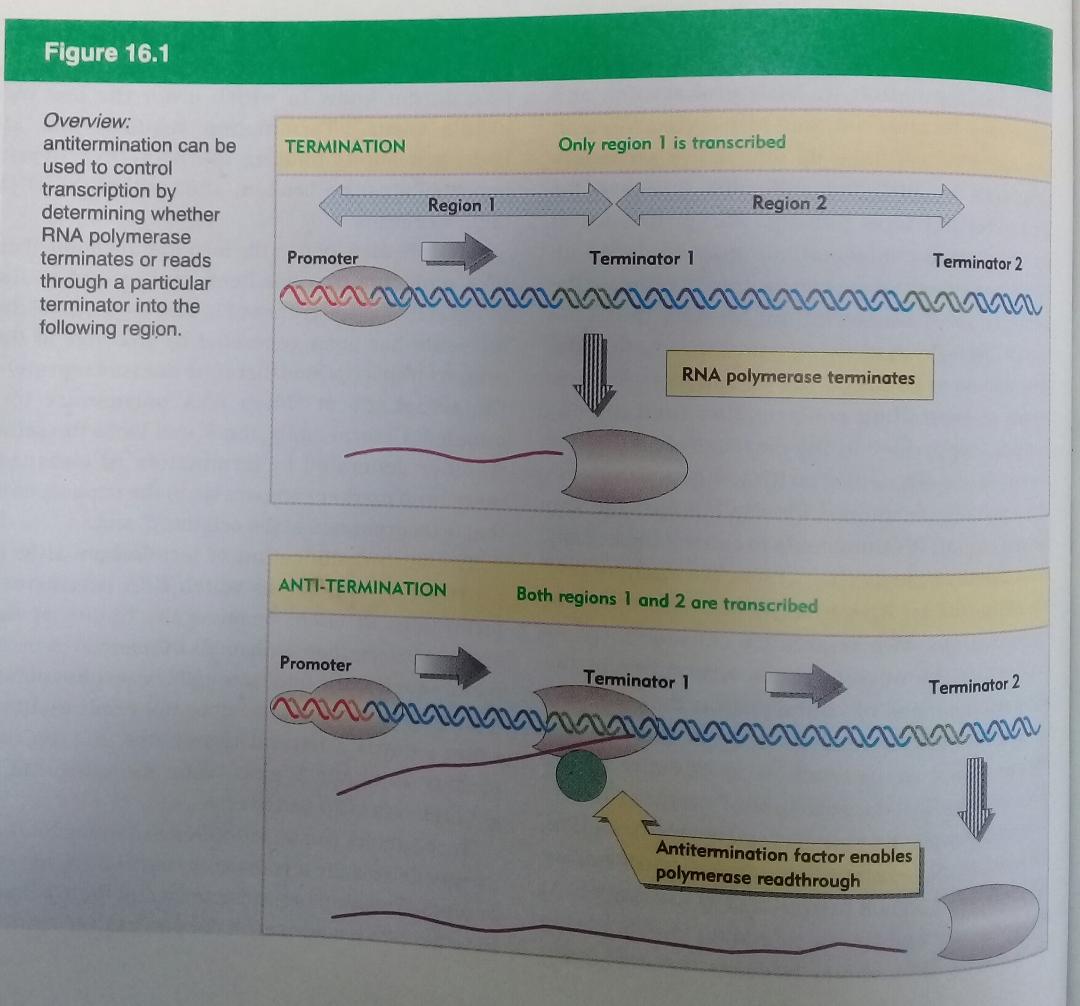
* The second feature is a highly conserved string of three A residues in the template strand that are transcribed into U residues near the 3’ end of the hairpin **(Fig. 26–7a)**.
* When a polymerase arrives at a termination site with this structure, it pauses.
* Formation of the hairpin structure in the RNA disrupts several A=U base pairs in the RNA-DNA hybrid segment and may disrupt important interactions between RNA and the RNA polymerase, facilitating dissociation of the transcript.

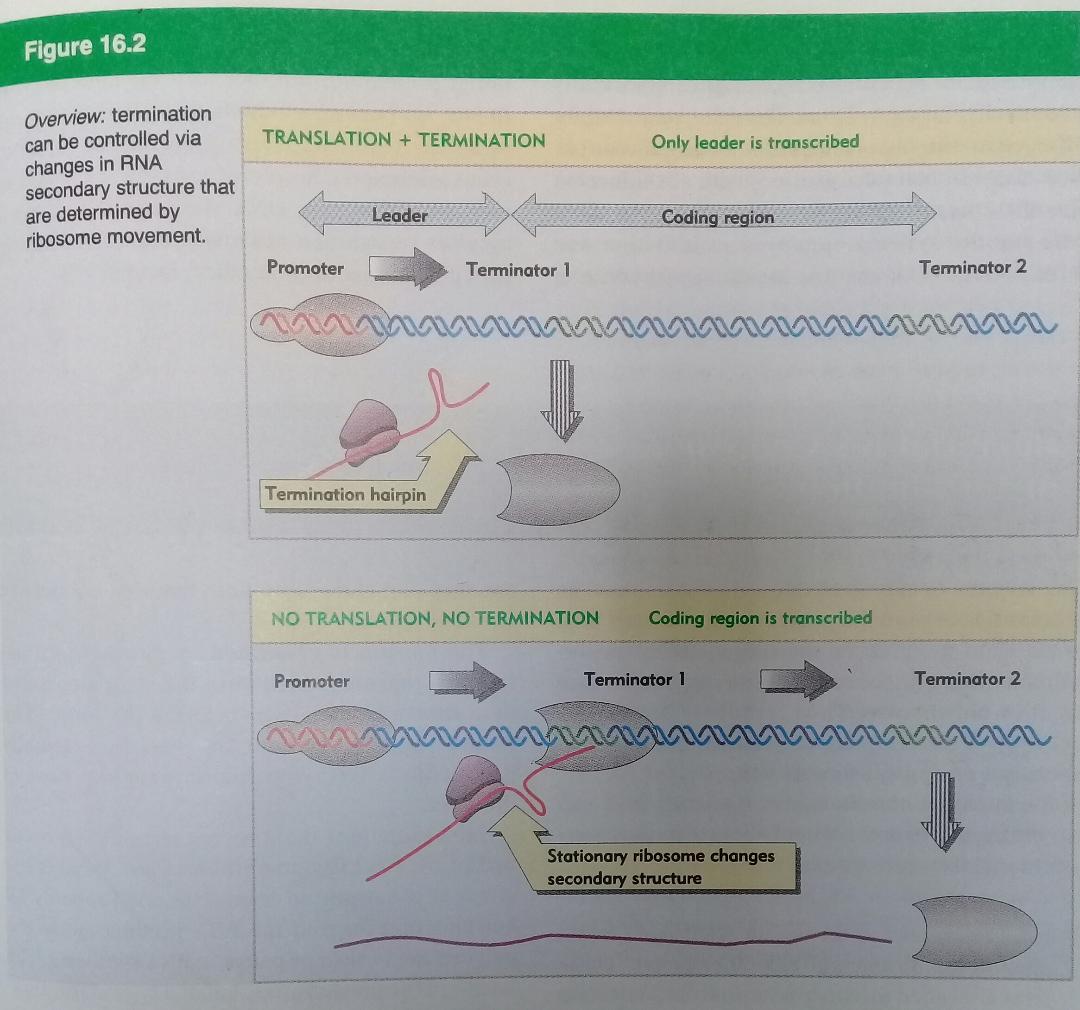


* The -dependent terminators lack the sequence of repeated A residues in the template strand but usually include a CA-rich sequence called a *rut* (rho utilization) element **(Fig. 26–7b)**.
* The protein associates with the RNA at specific binding sites and migrates in the 5’  3’ direction until it reaches the transcription complex that is paused at a termination site.
* Here it contributes to release of the RNA transcript.

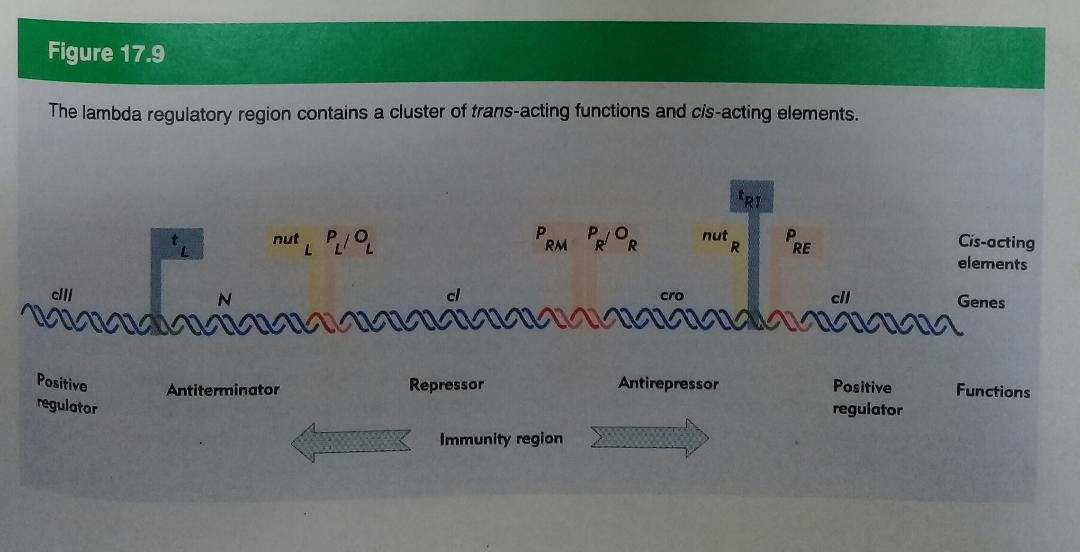


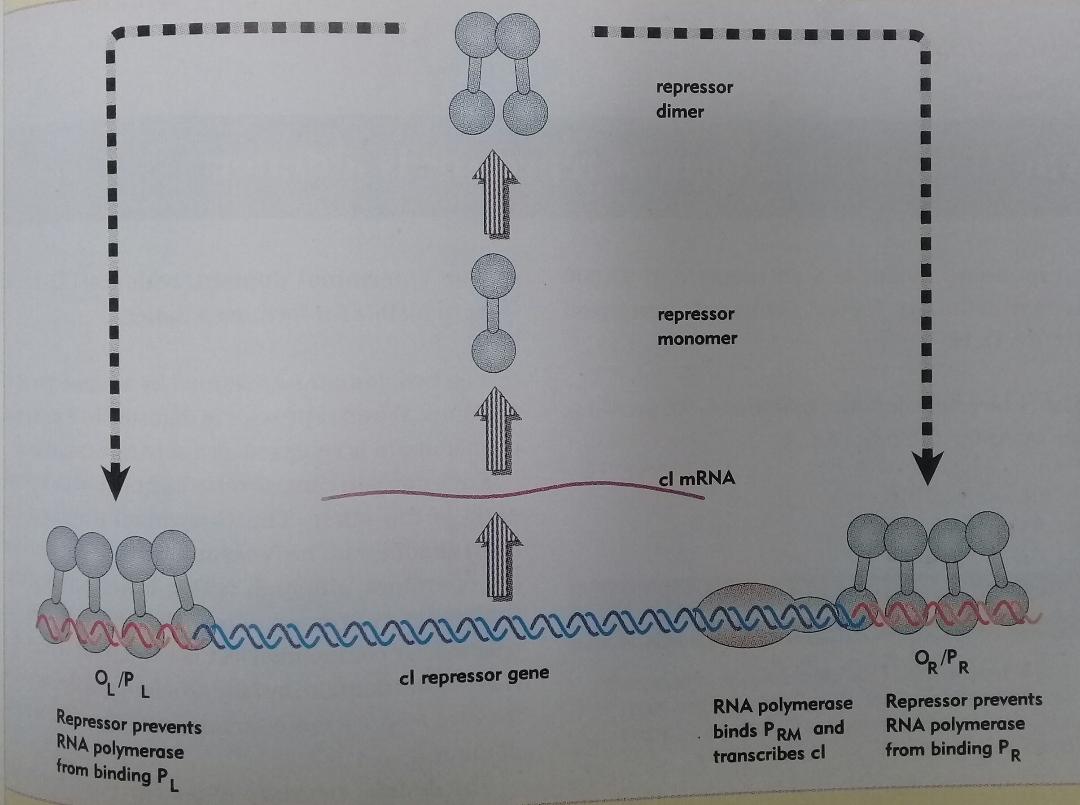


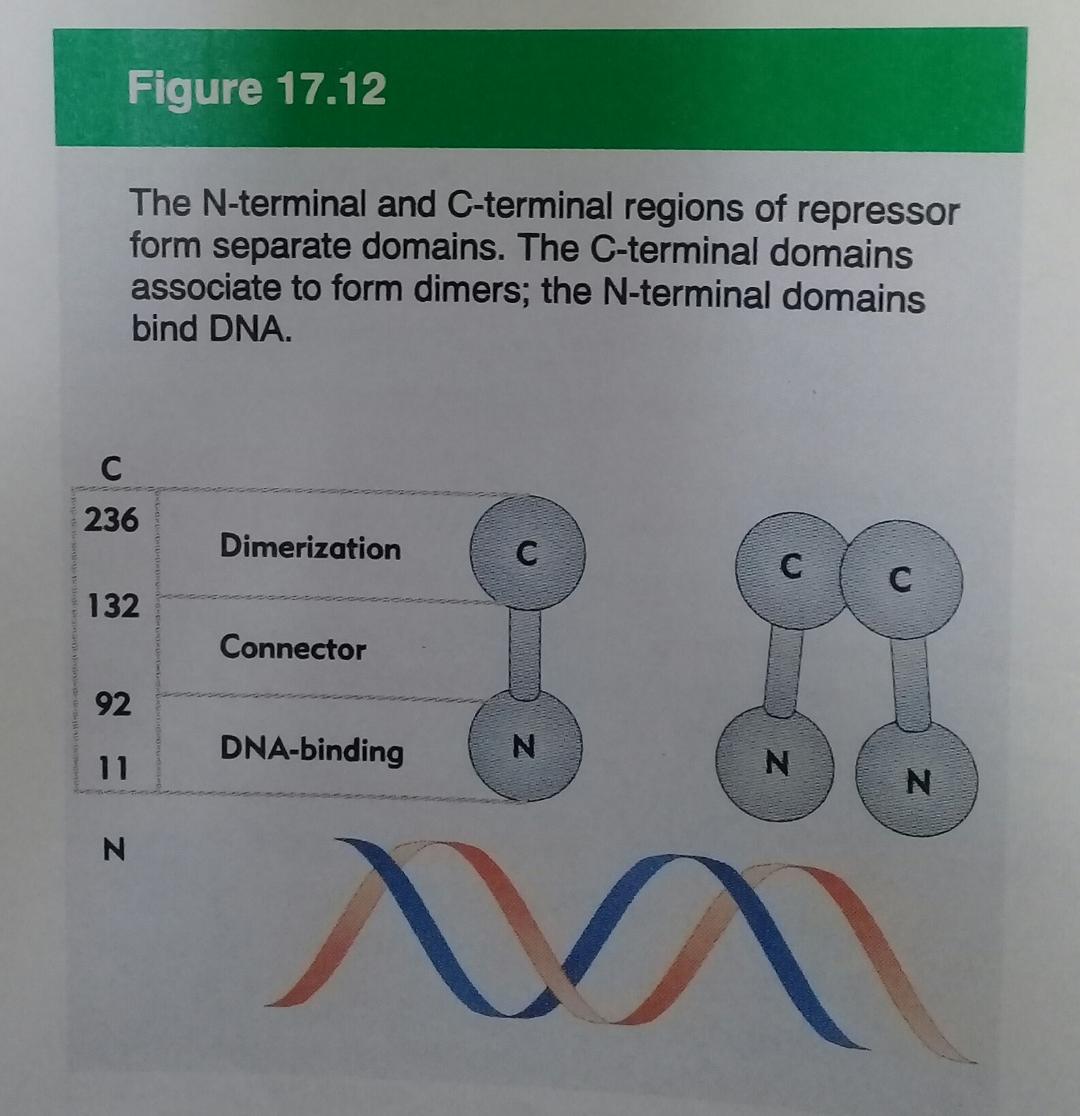


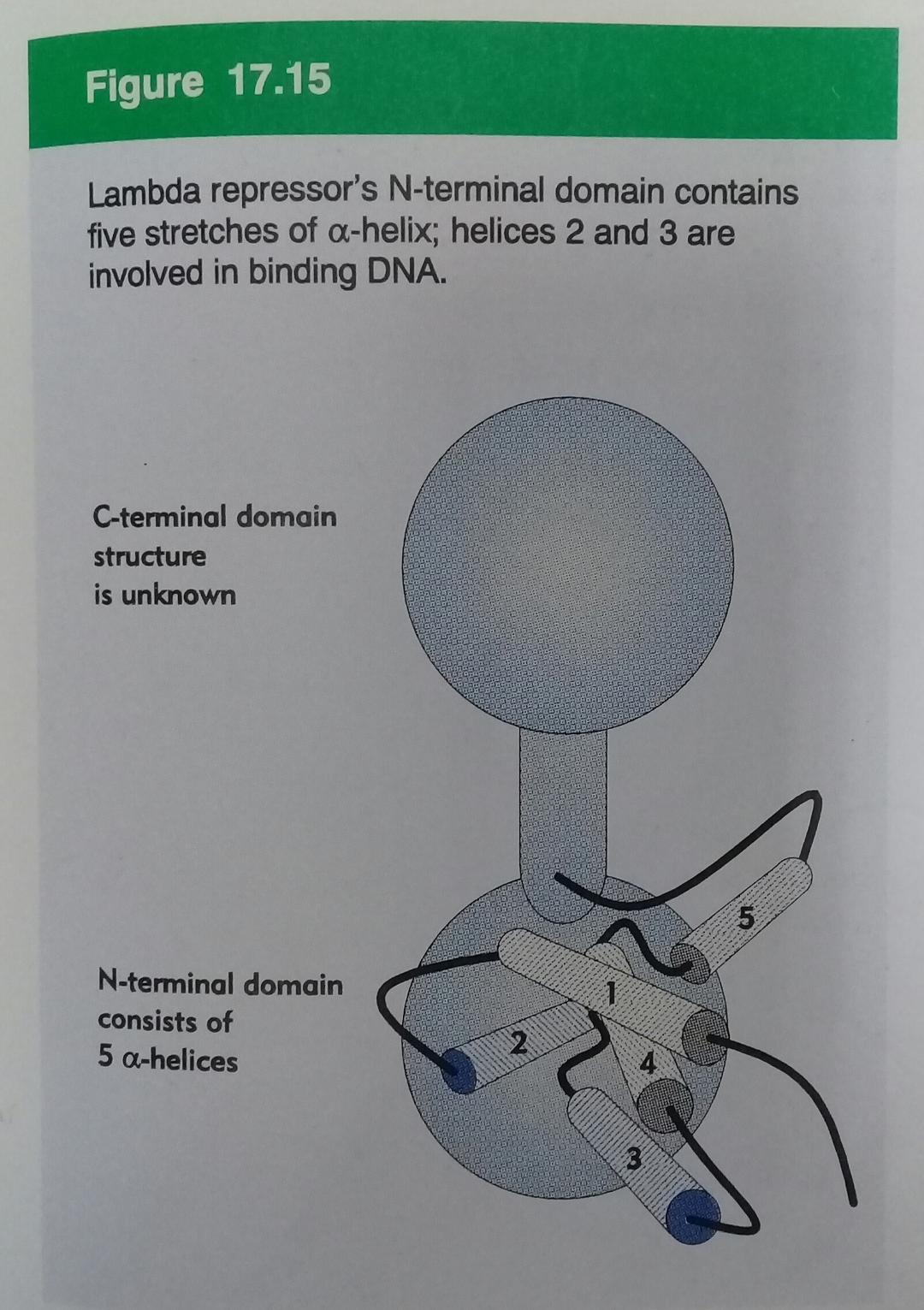
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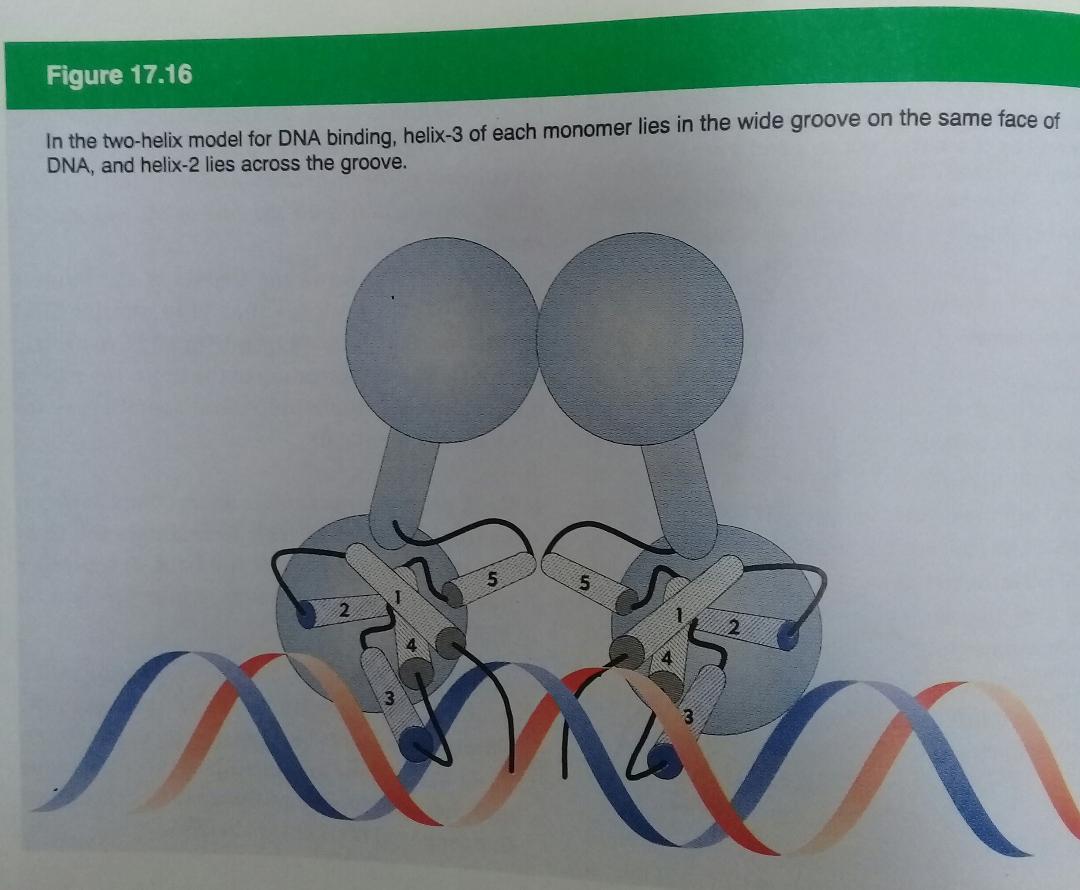
**Lambda DNA**

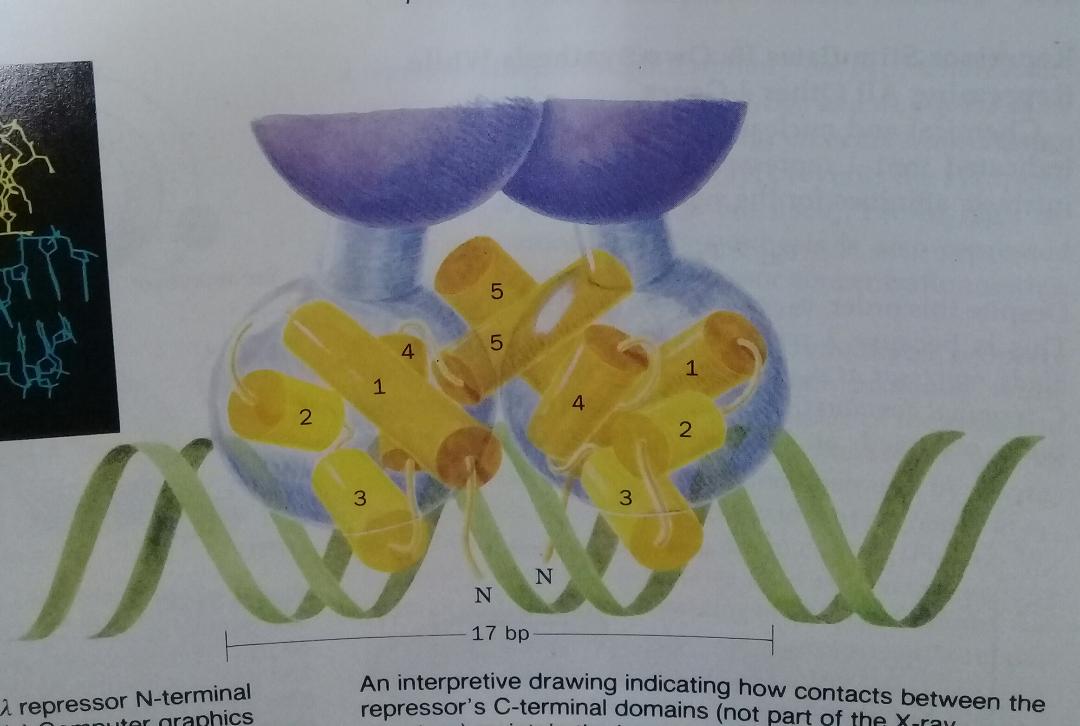
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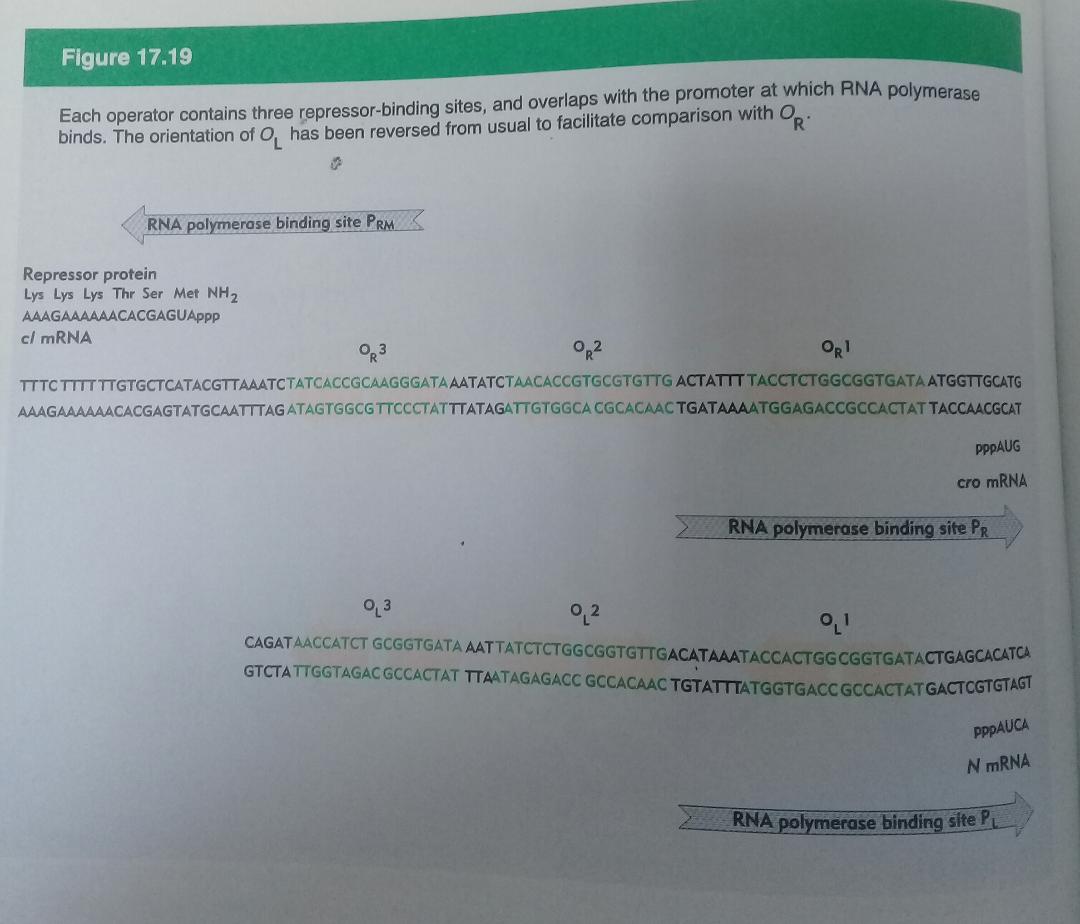
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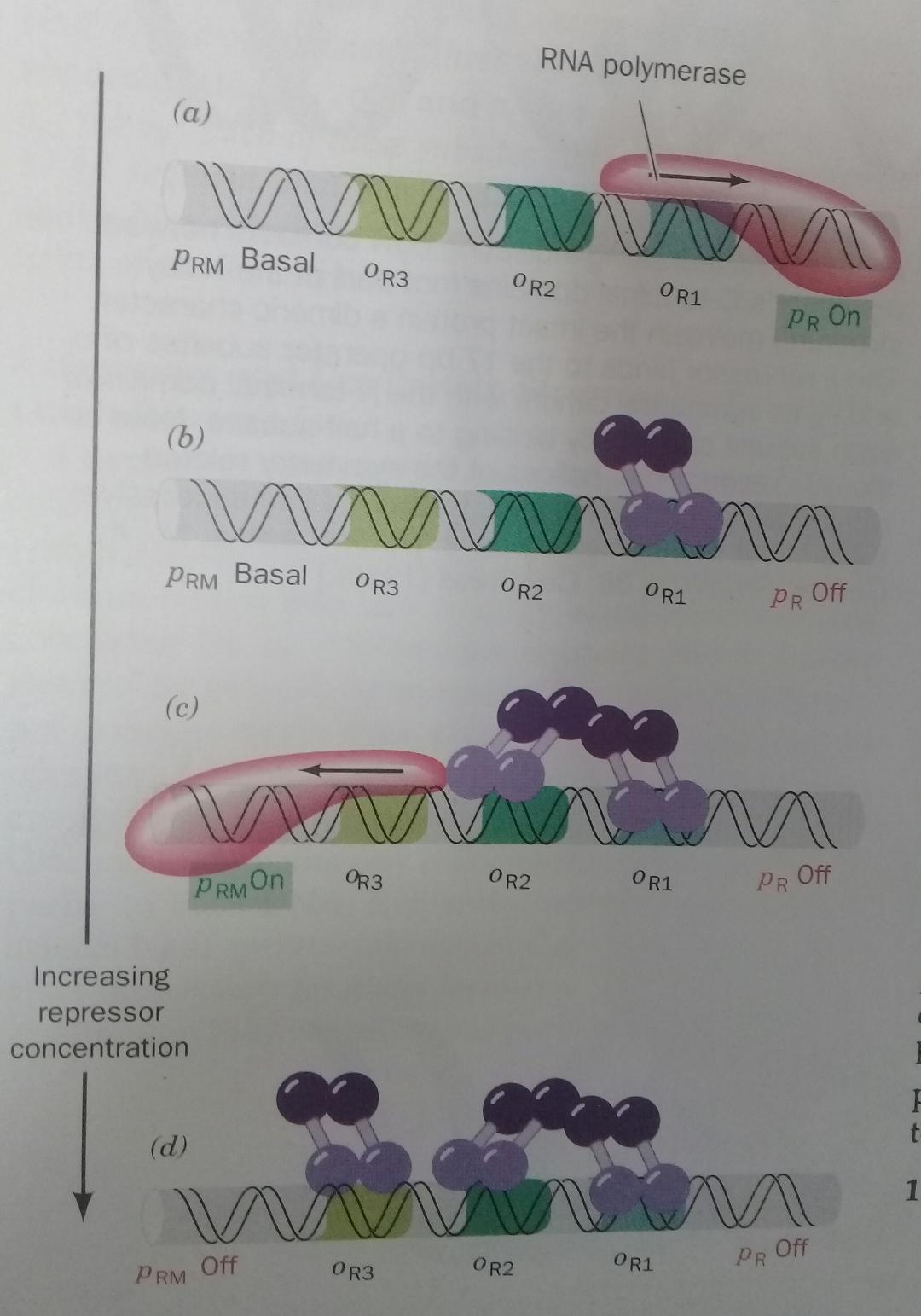
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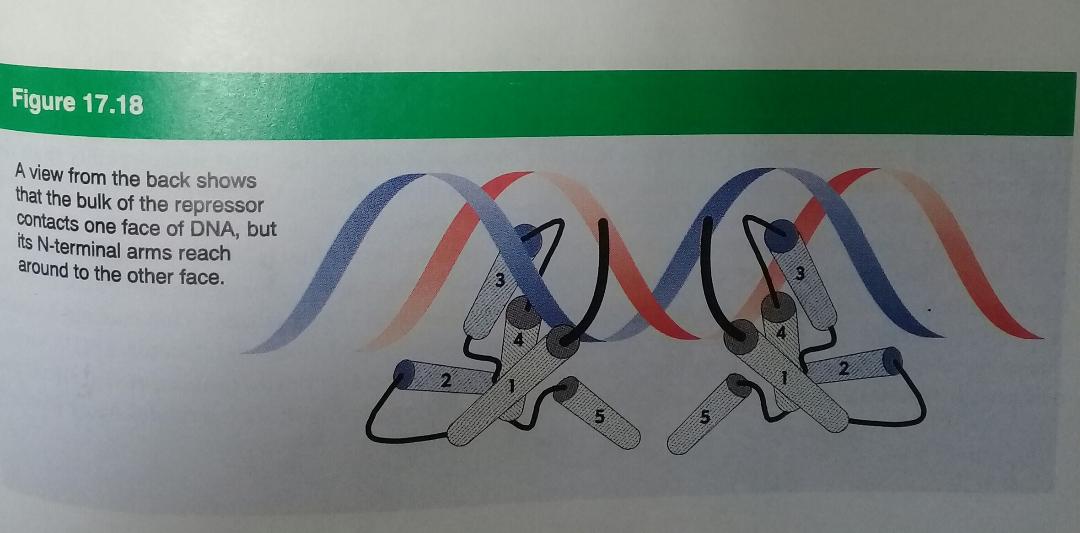
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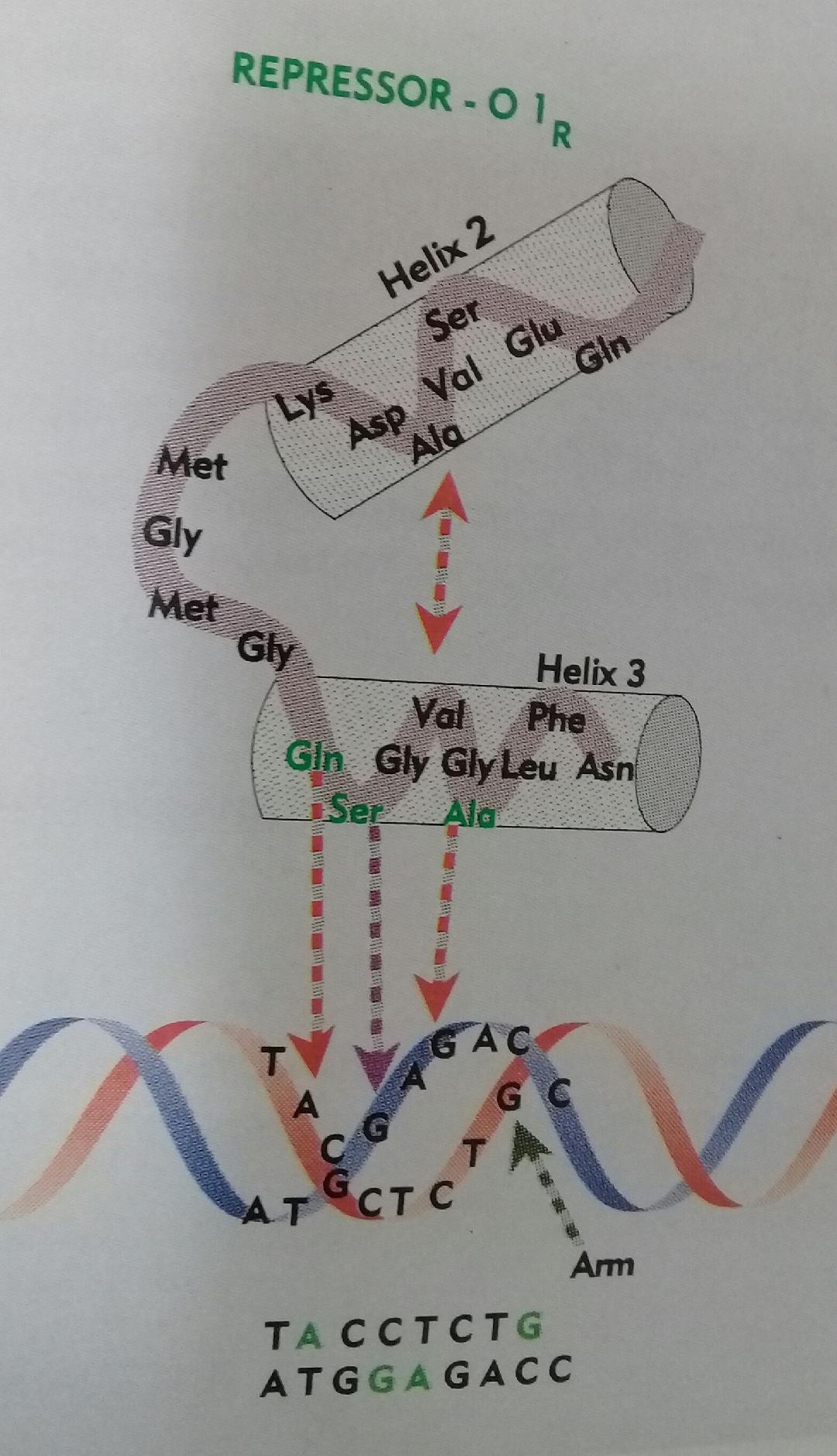
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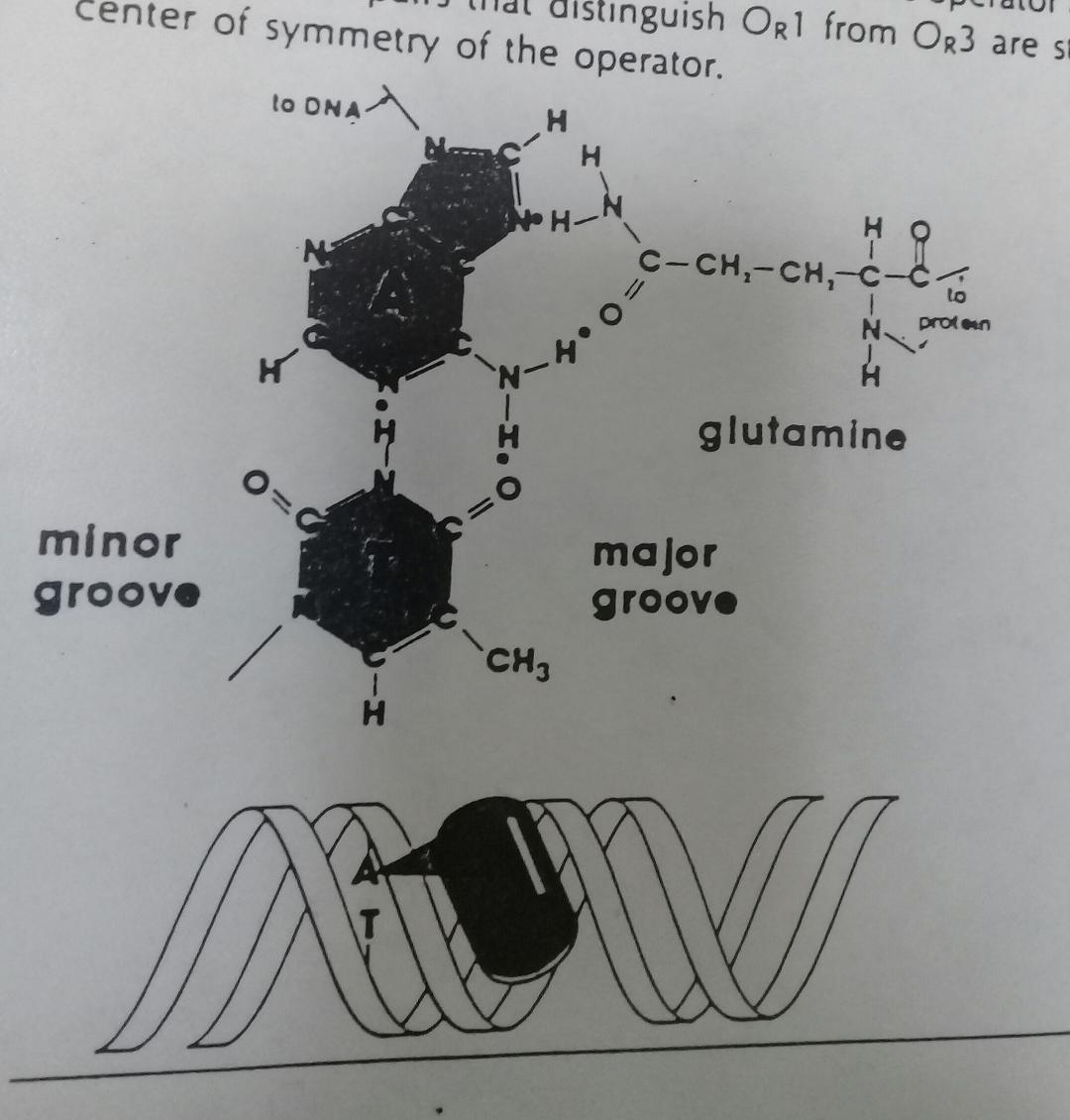
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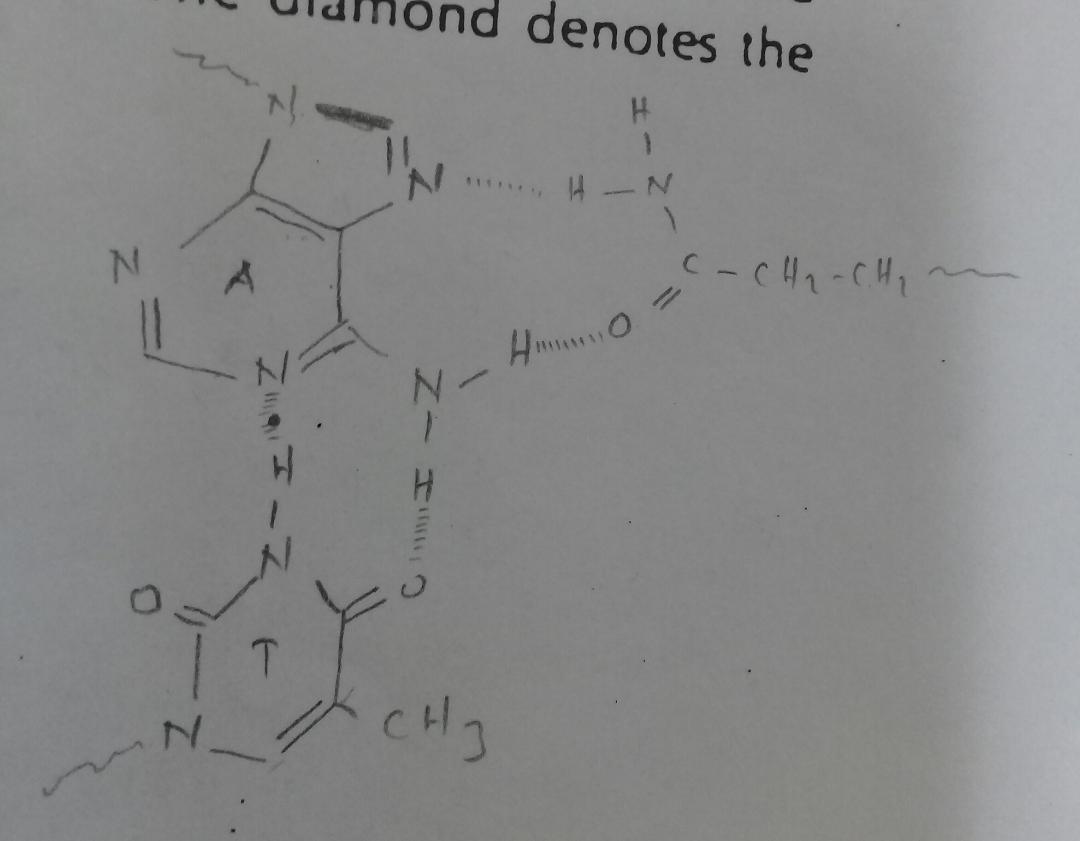
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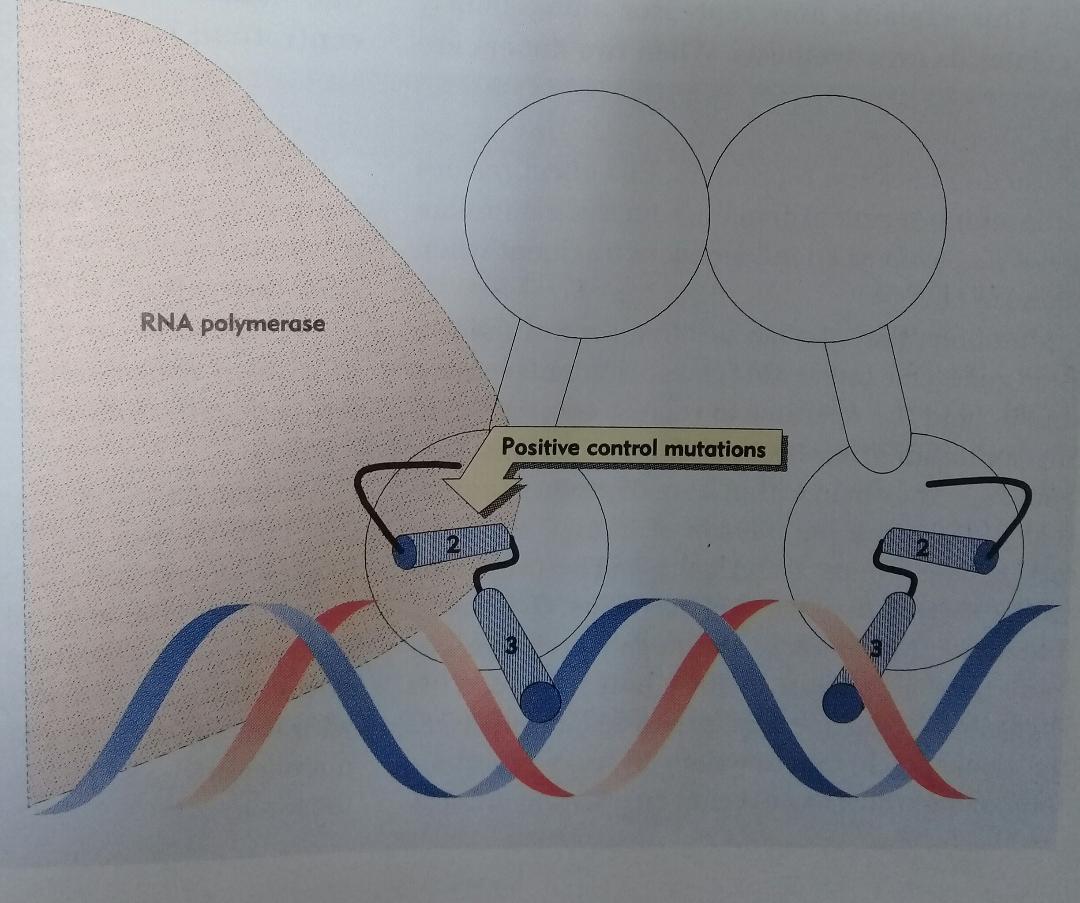
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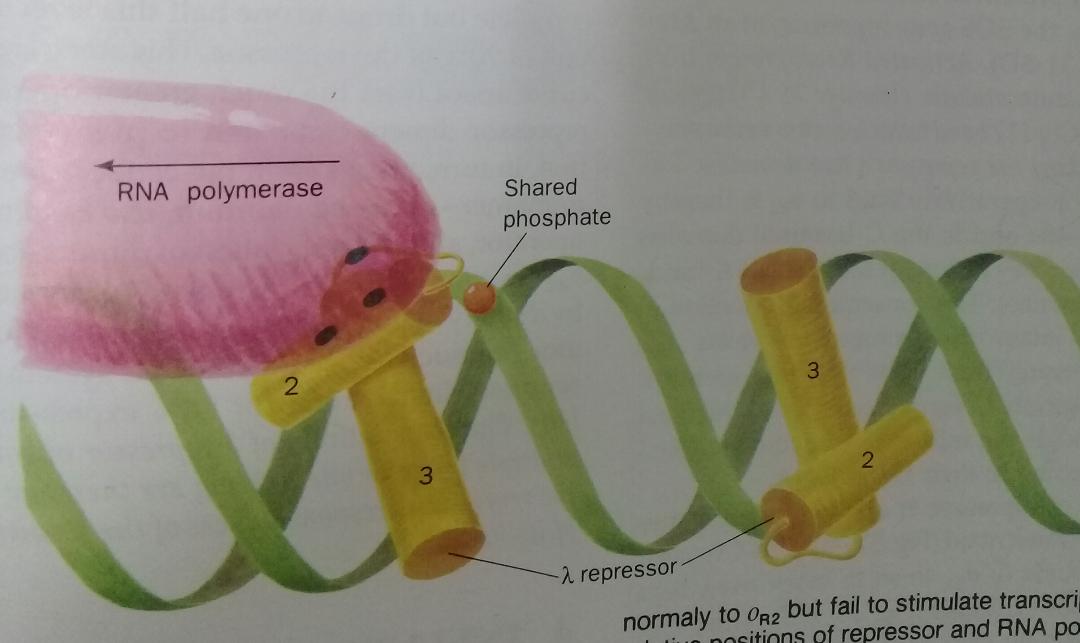
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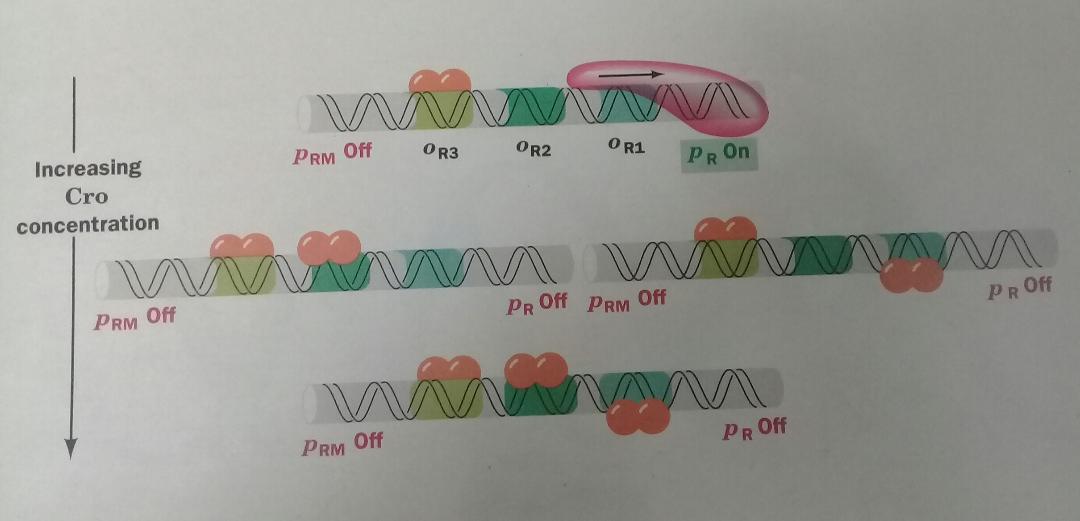
* Lysine residues in the arm make contacts with G residues in the major groove and also with the phosphate backbone. The interaction between arm and DNA contributes heavily to DNA binding.

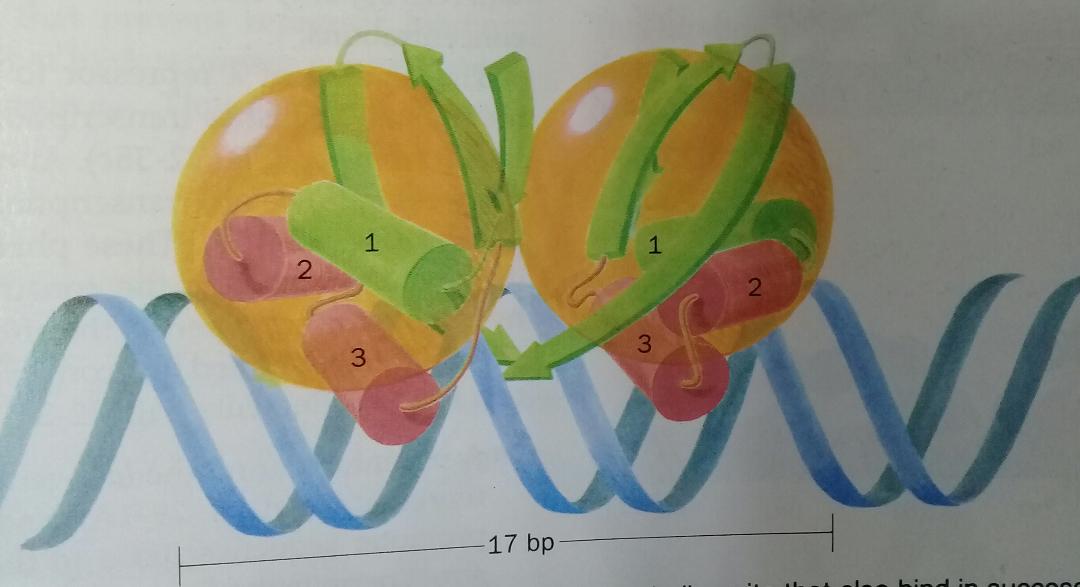


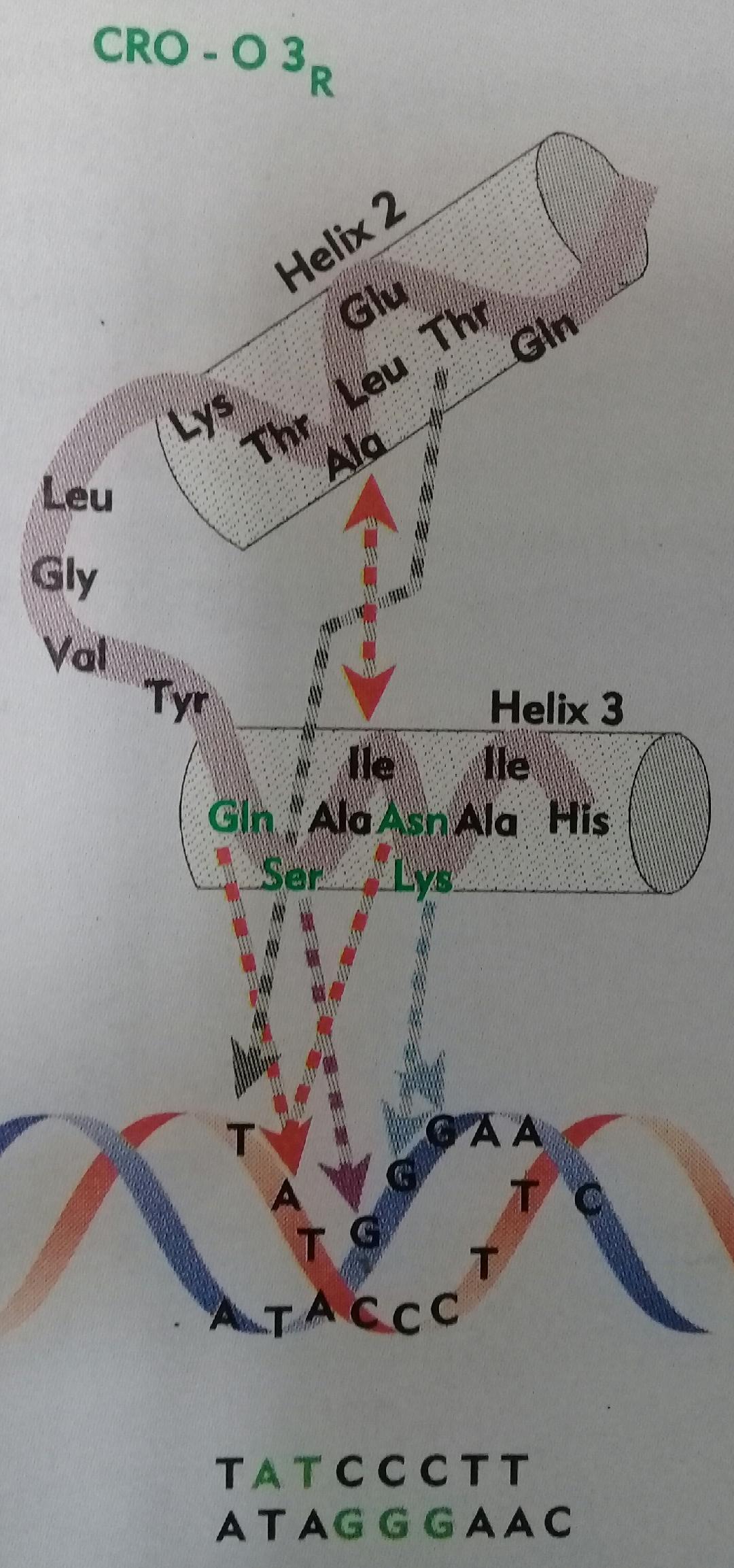


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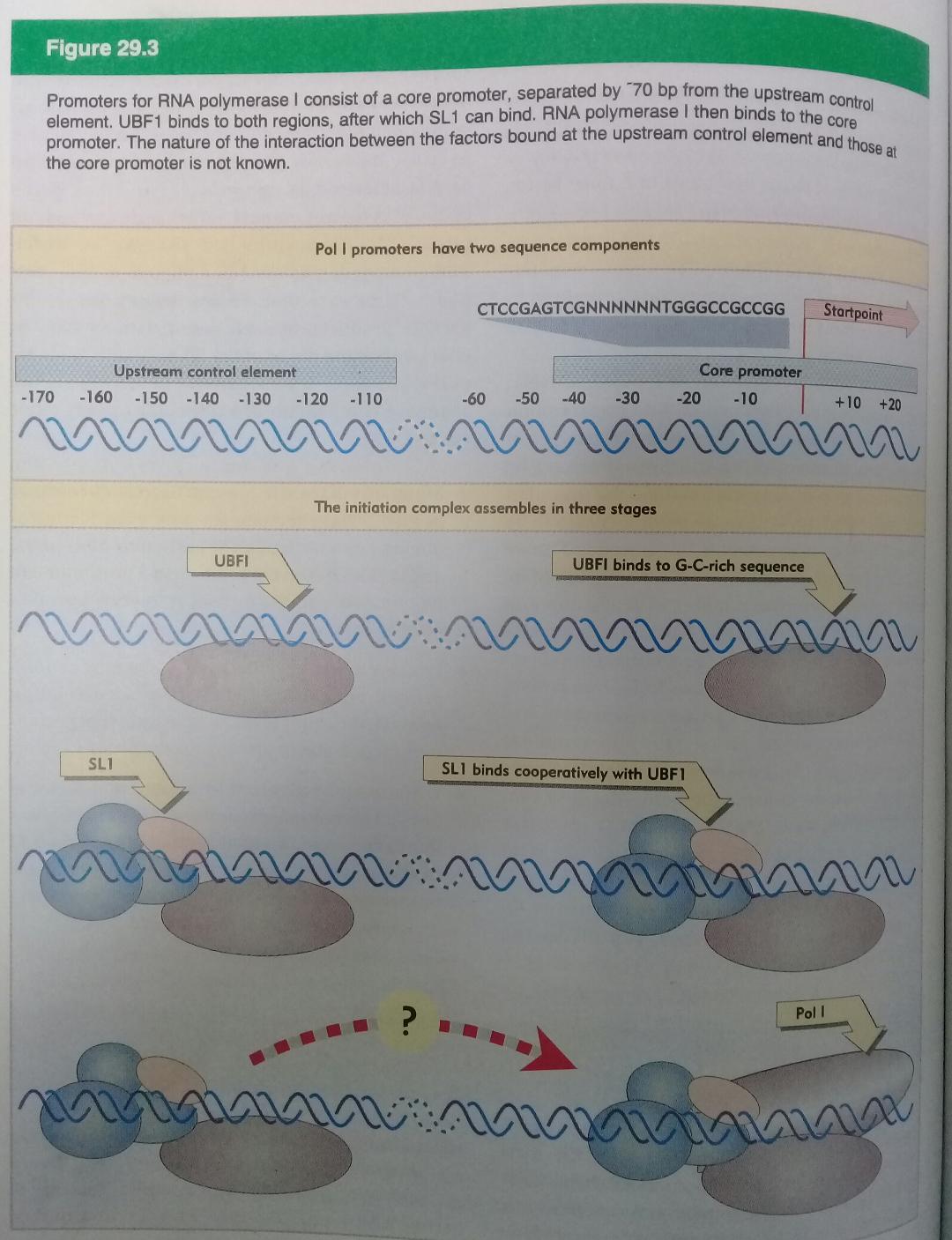
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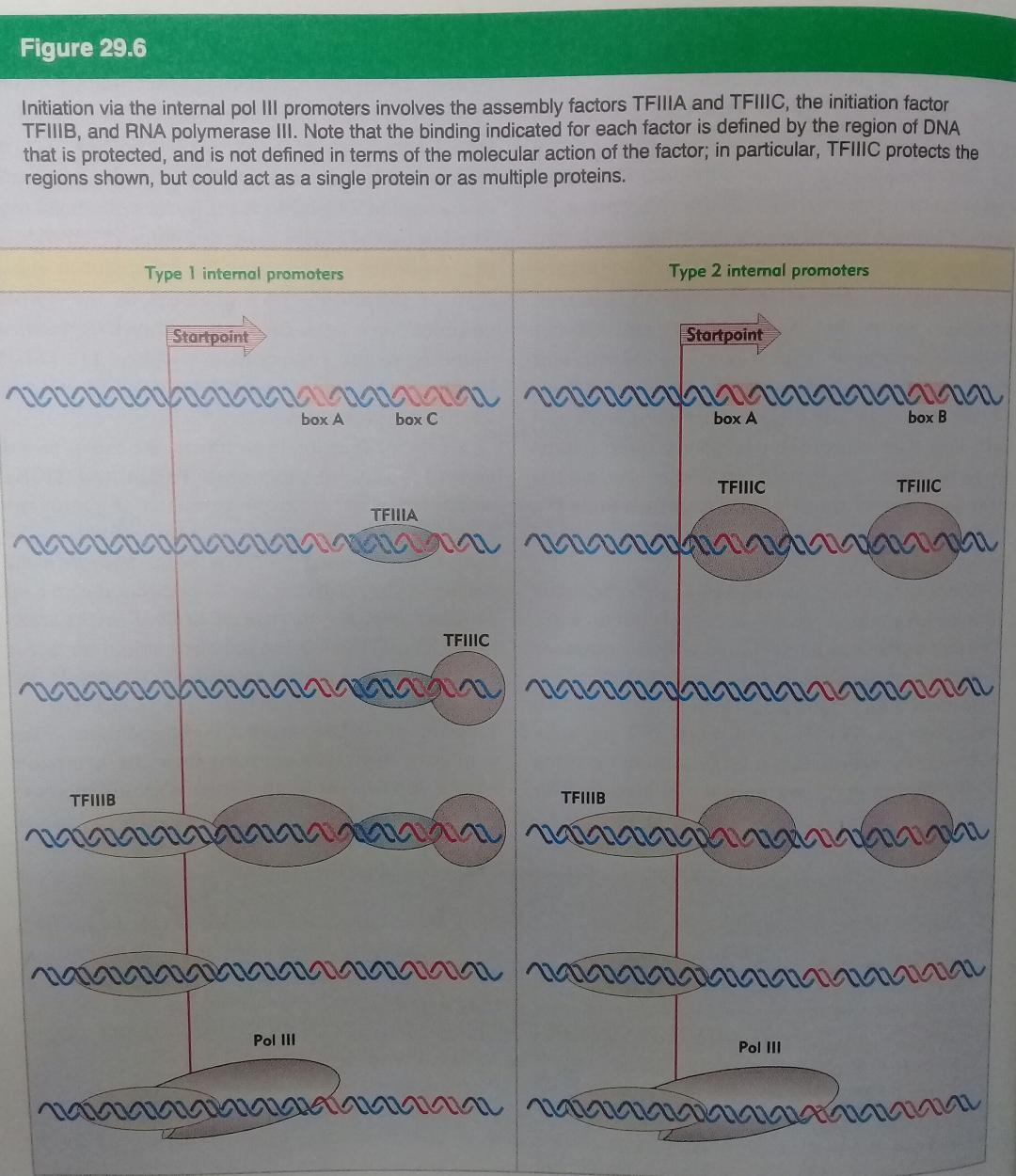
**Eukaryotic Cells Have Three Kinds of Nuclear RNA Polymerases**

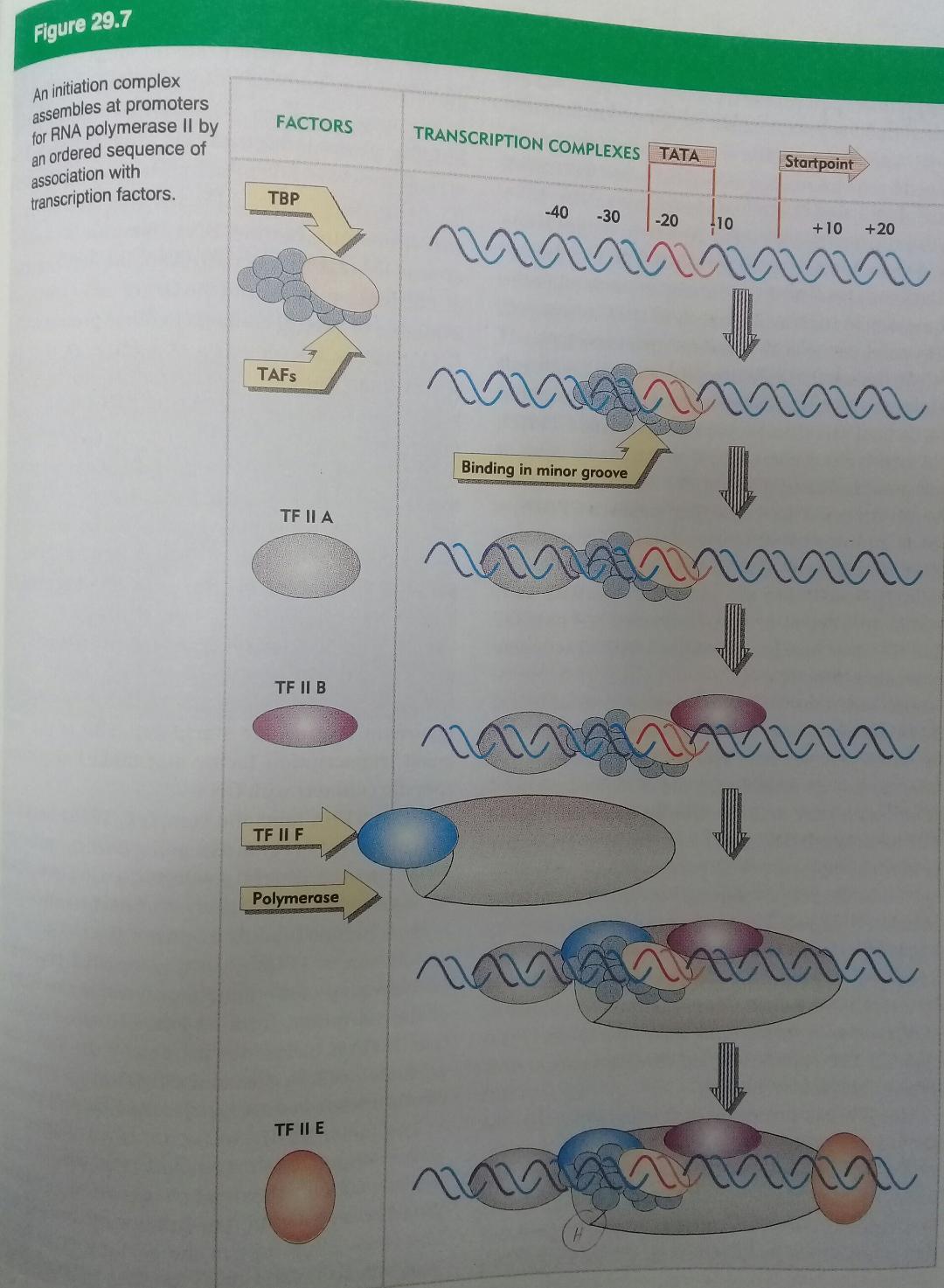
* RNA polymerases are designated RNA Pol I, RNA Pol II and RNA Pol III.
* RNA Pol I is responsible for the synthesis of rRNAs (5.8S, 18S and 28S rRNAs).
* RNA Pol II is responsible for the synthesis of mRNAs.
* RNA Pol III is responsible for the synthesis of tRNAs and 5S rRNA.

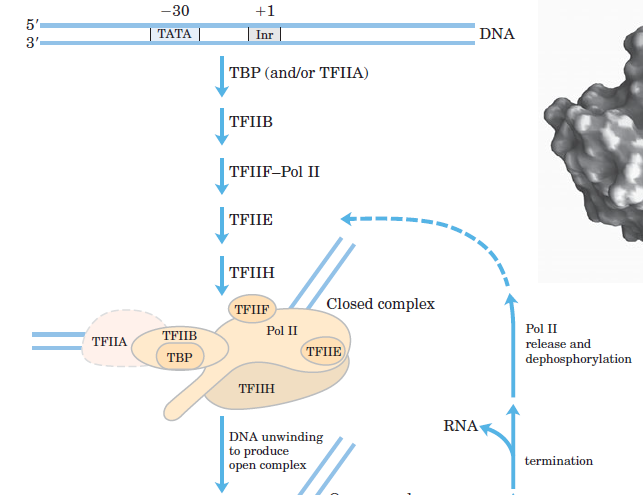
**RNA Polymerases Require Many Other Protein Factors for Its Activity**

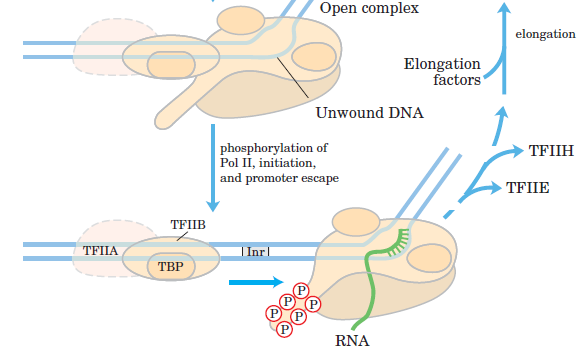
* The other proteins are called **general** **transcription factors**.
* Transcription factors are required for initiation of transcription at the RNA polymerase promoters.
* Activation factors are also required.

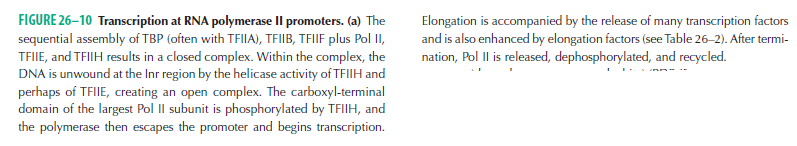


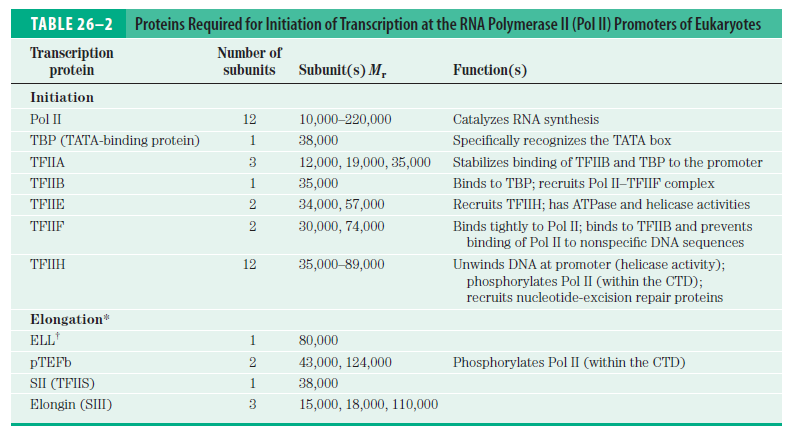


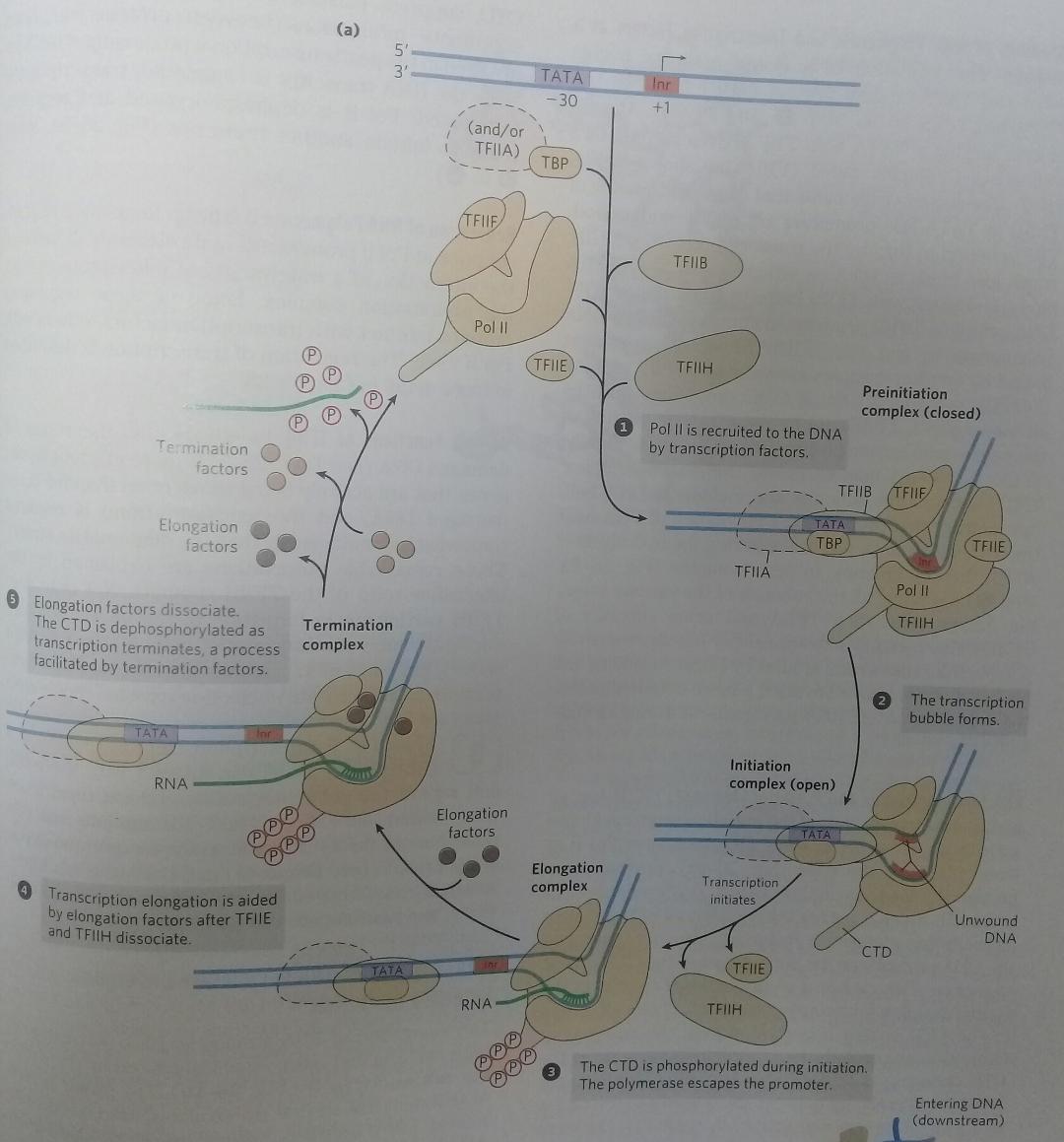


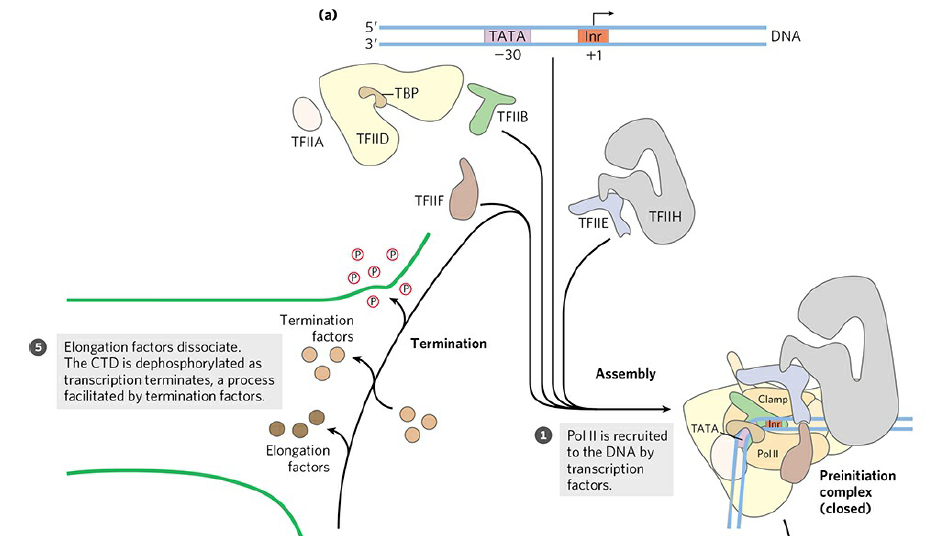


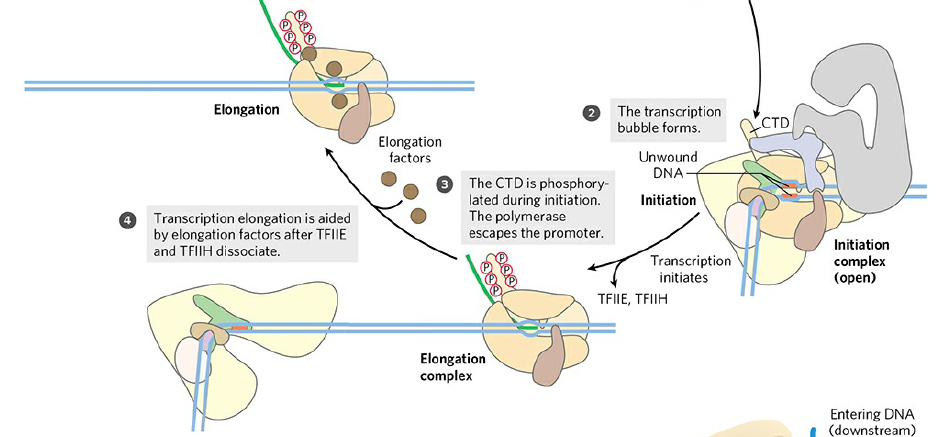


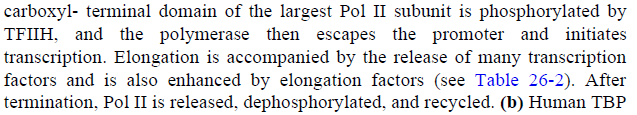
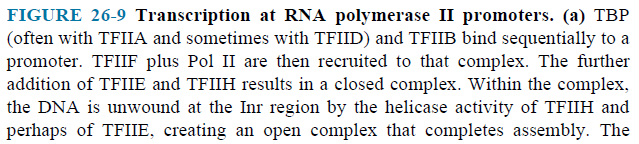




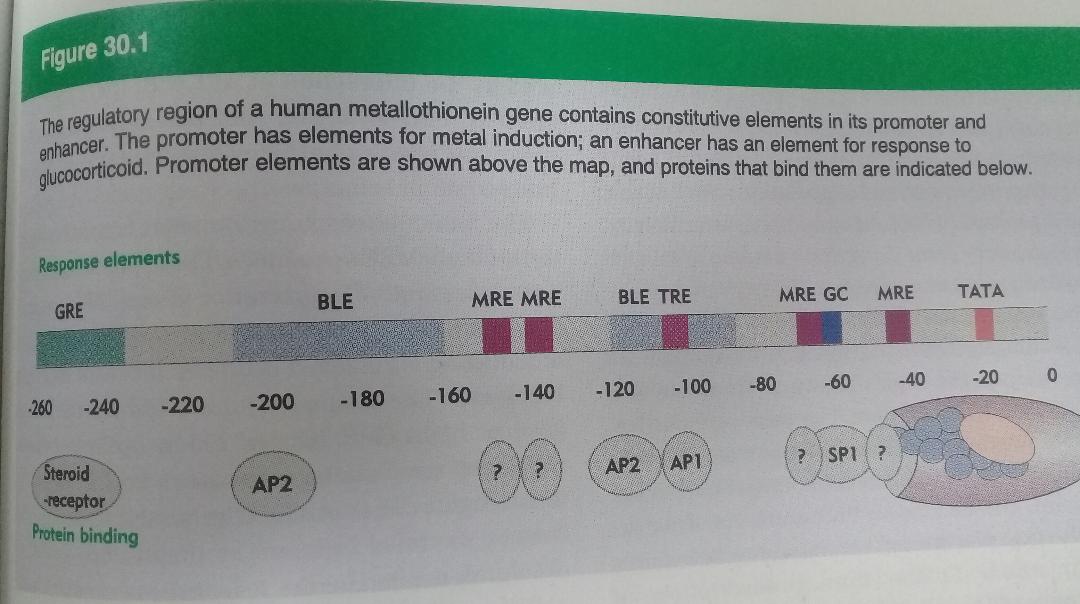








**Metallothionein (MT) Geninin Organizasyonu**

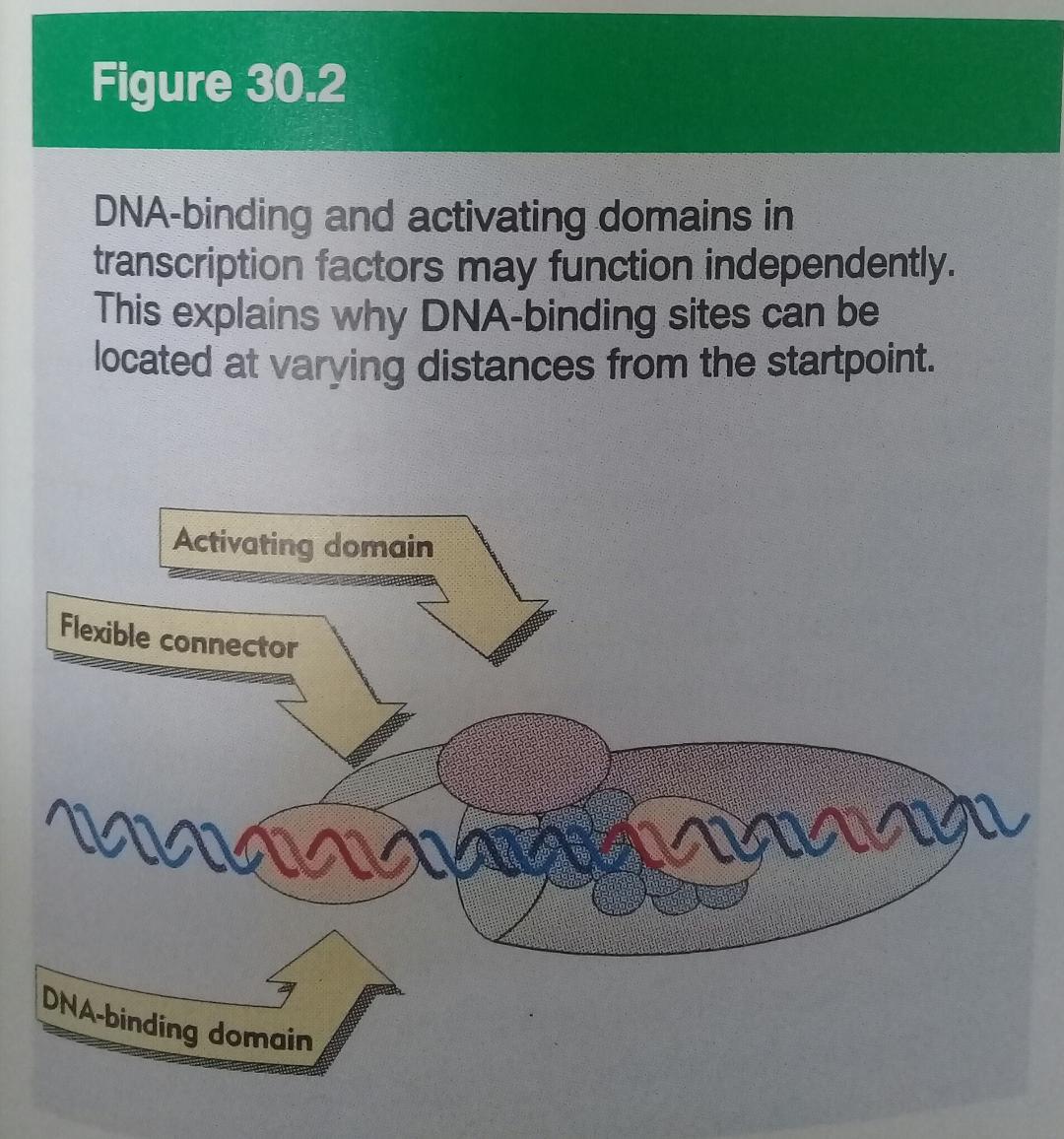


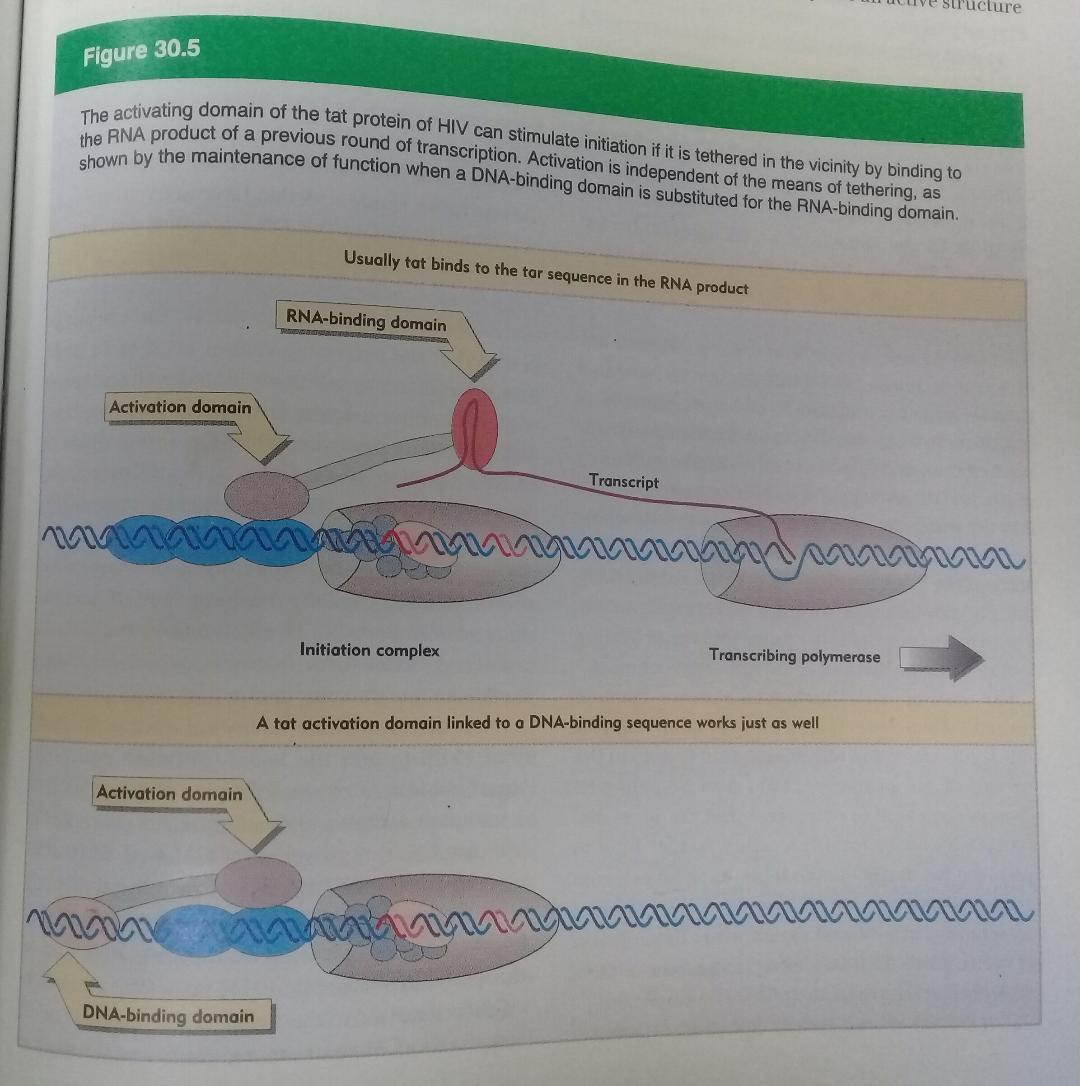
MT proteini hücreyi ağır metallerden korumaktadır. Metale bağlanıp fazlasının hücreden dışarı atmaktadır.

Cd ve glukokortikoidler vasıtasıyla gen uyarılır ve aktivasyon başlar.

MRE : Metallere cevap veren element

**Transkripsiyon Faktörleri DNA’ya Bağlanır ve Bağımsız Bölgeler Vasıtasıyla Transkripsiyonu Aktive Eder**

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tat proteini tar dizisine bağlanarak başlangıcı hızlandırır ve uyarır.

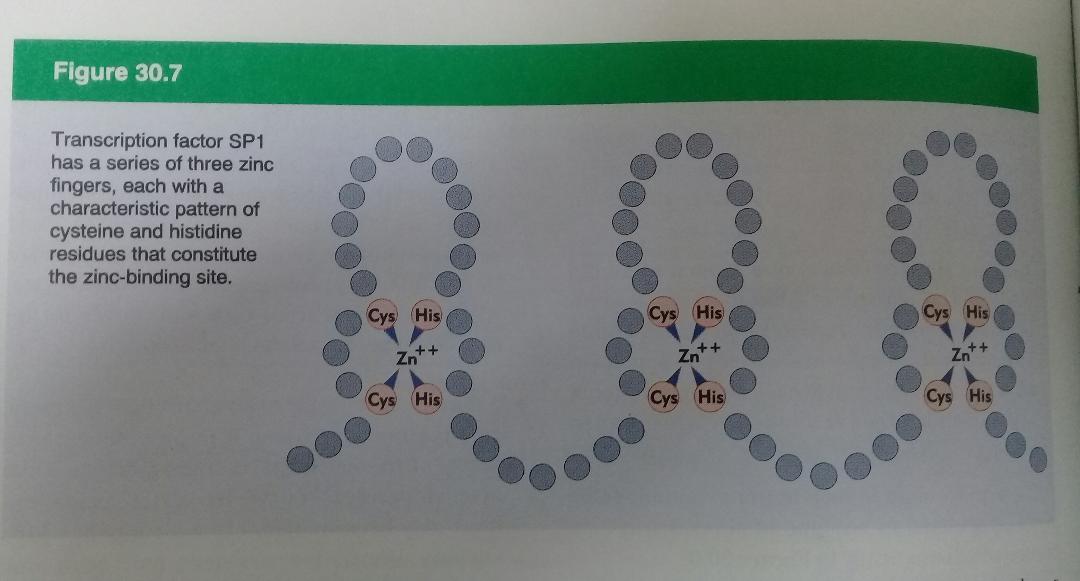
**Proteinlerin DNA’ya Bağlanma Modelleri**

Proteinlerin küçük bir parçası bu işi görmeye yetebilir.

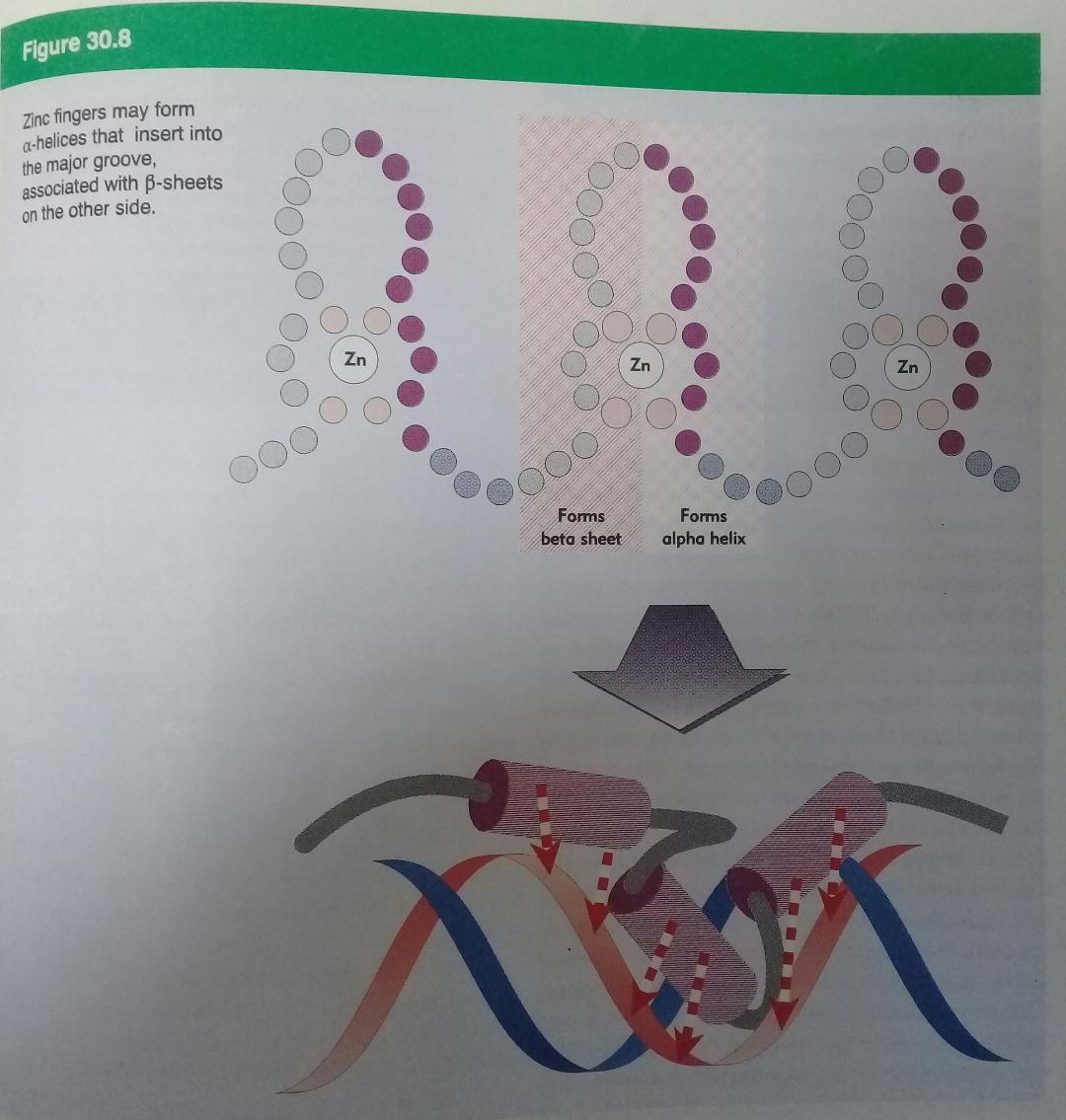
1. Helix-turn-helix modeli : Repressor ve cro proteinleri gibi
2. Zinc fingers (Çinko parmak) modeli

Cys - X2-4 – Cys – X3 – Phe – X5 – Leu – X2 – His- X3 – His

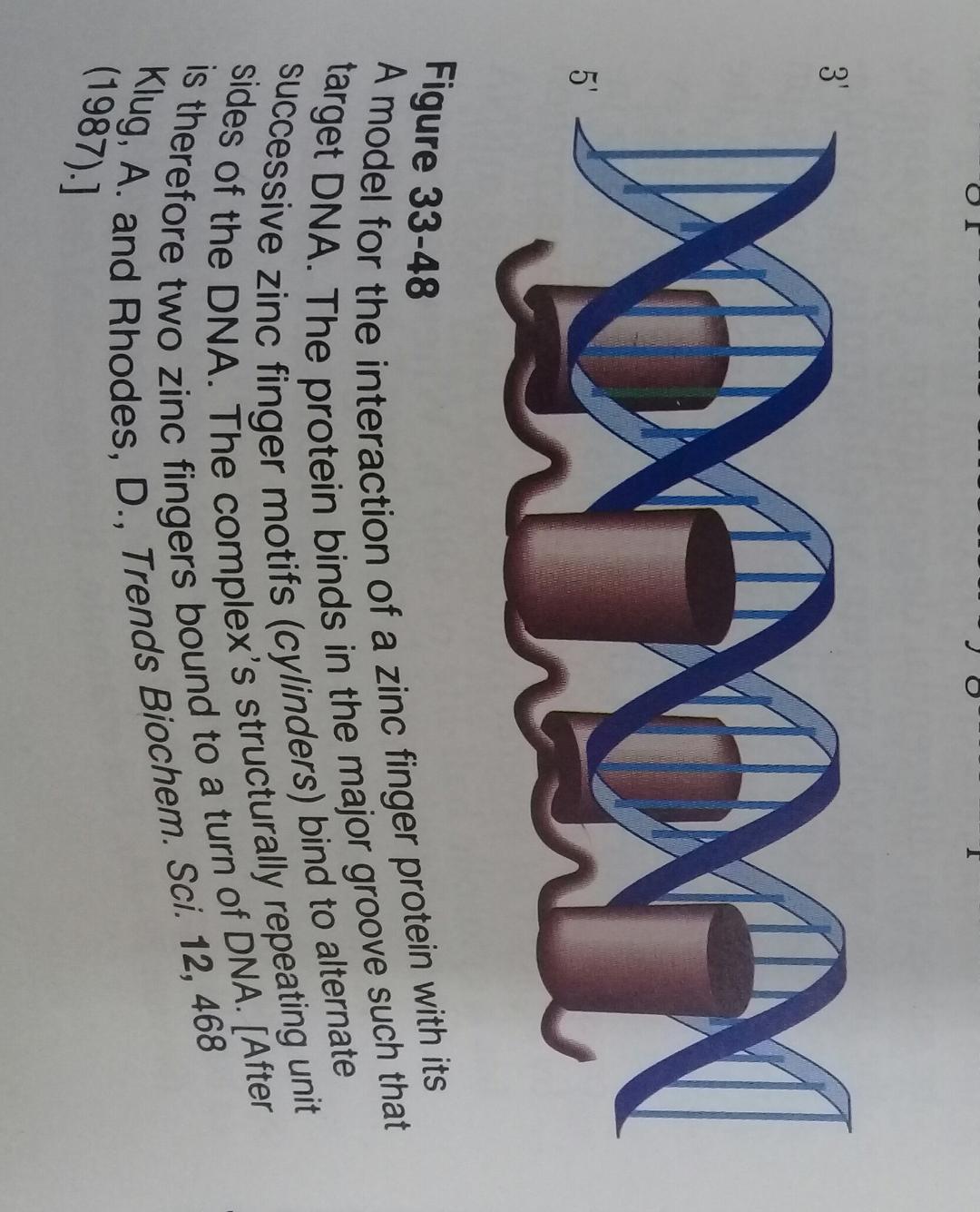
Bu motif Cys2 / His2 olarak tanımlanır.



TFIIIA 5S RNA’nın transkripsiyonunda rol alır. 9 tane finger vardır.



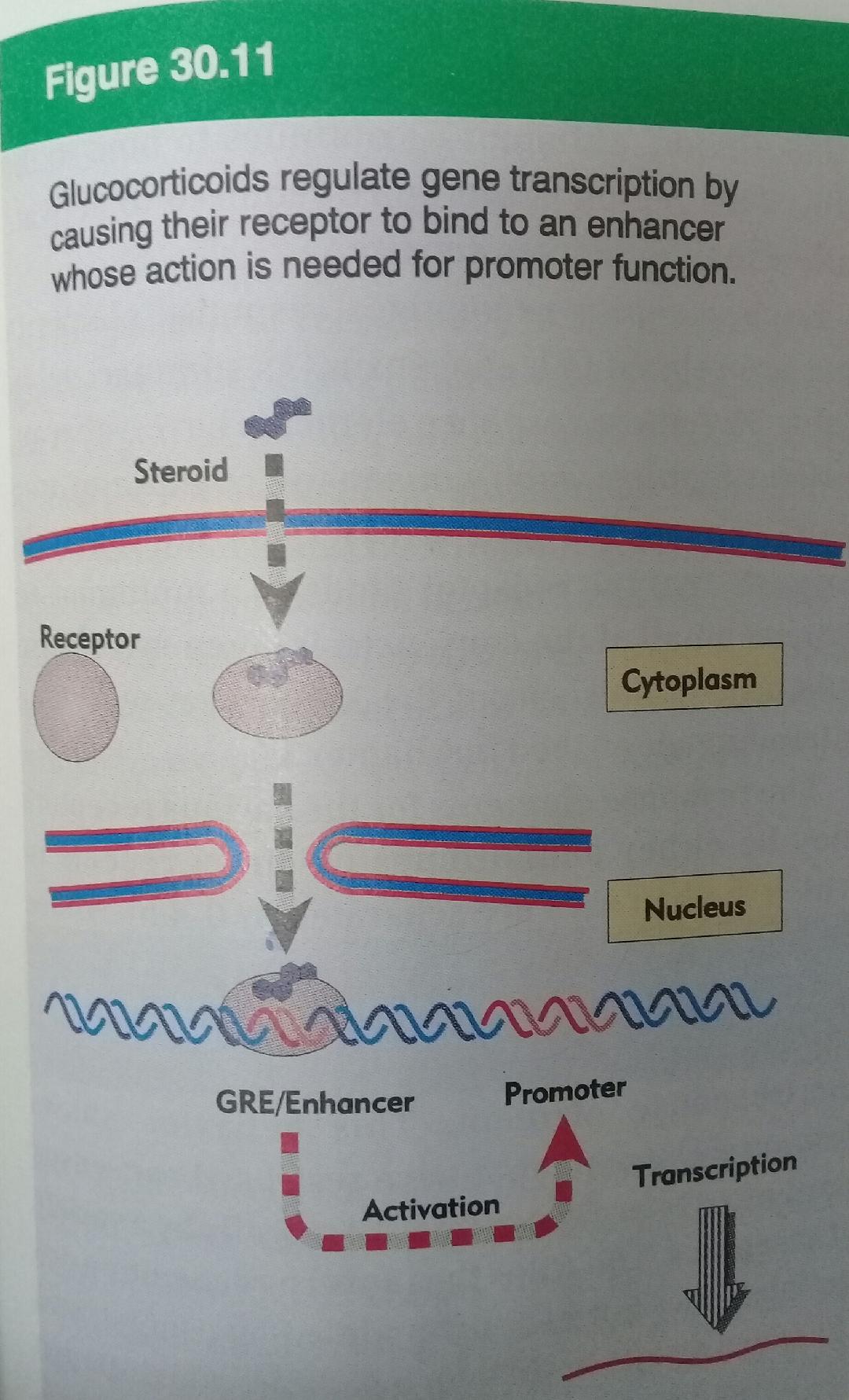
Her bir helix 2 yerden DNA’ya bağlanır. 3 helix büyük oyuğa sığmaktadır.



1. Steroid reseptörleri modeli : Farklı çinko parmak modeline sahipler.

Cys – X2– Cys – X1-3 – Cys – X2 – Cys

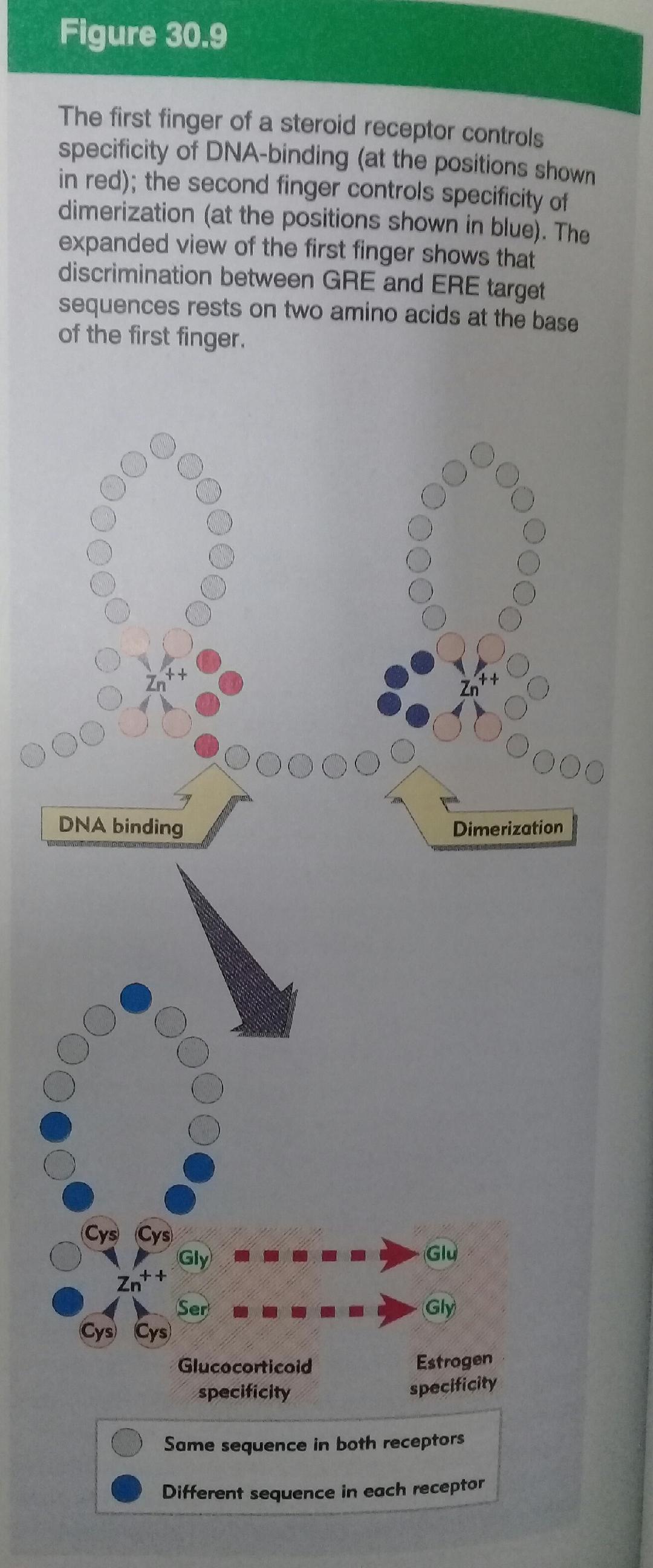
Bu motif Cys2 / Cys2 olarak tanımlanır.



Steroid reseptörleri

hormonu bağlama, DNA’ya bağlanma ve transkripsiyonu aktive etme bölgelerine sahiptir.

Glukokortikoid ve östrojen reseptörleri 2 finger bulundurur.

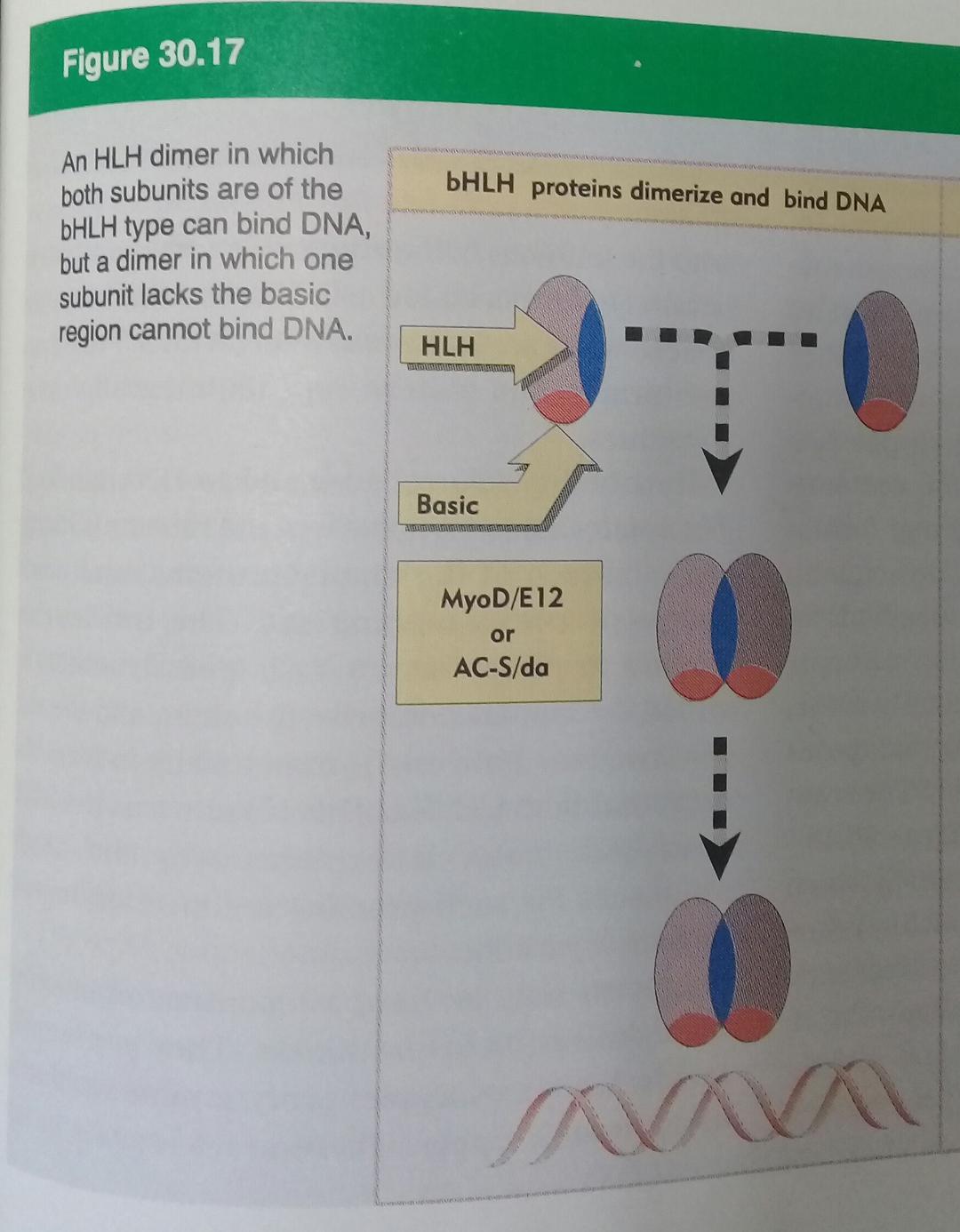


1. Helix-loop-helix modeli : Dimer yapıdadır.

Bir helix’de hidrofobik residüler diğerinde pozitif yüklü rezidüler vardır.

Hidrofobik rezidüler dimerleşmeyi sağlar.

Yüklü rezidüler iyonik etkileşme ile DNA’ya bağlanmayı sağlar.



1. Lösin fermuar (zipper) modeli

