Lac Operon Review

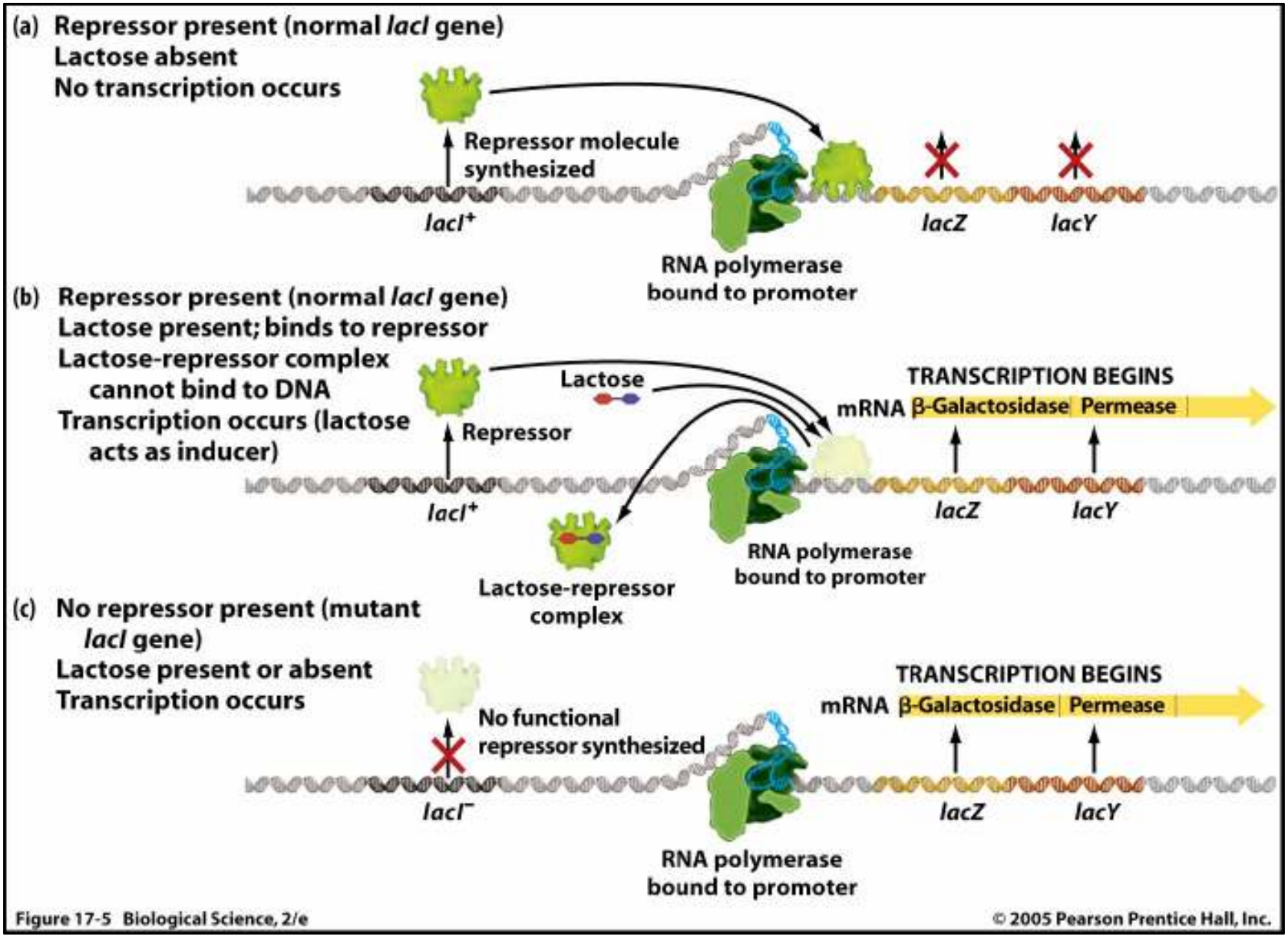
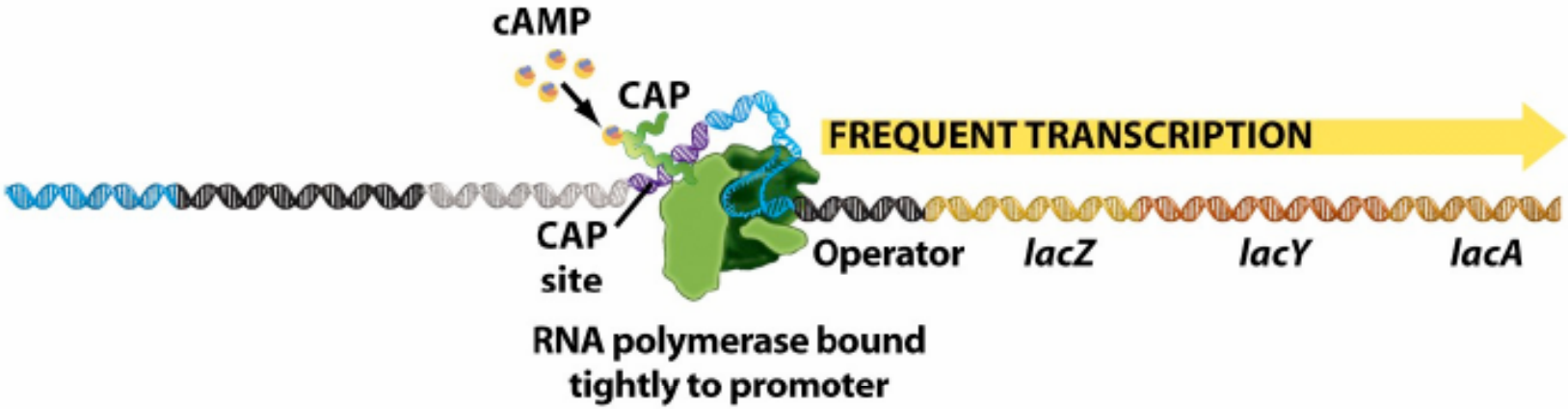


Figure 17-5 Biological Science, 2/e

(a) When cAMP is present, it binds to CAP. The cAMP-CAP complex binds to DNA at the CAP site and increases binding of RNA polymerase to promoter. Transcription occurs frequently.



(b) When cAMP is absent, CAP does not bind to DNA. RNA polymerase does not bind the promoter efficiently, and transcription occurs rarely.

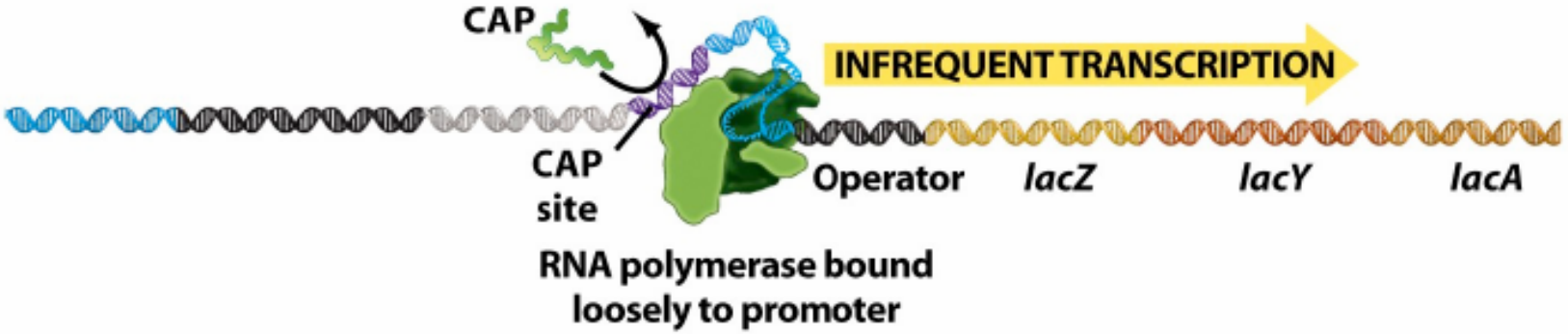


Figure 17-8 Biological Science, 2/e

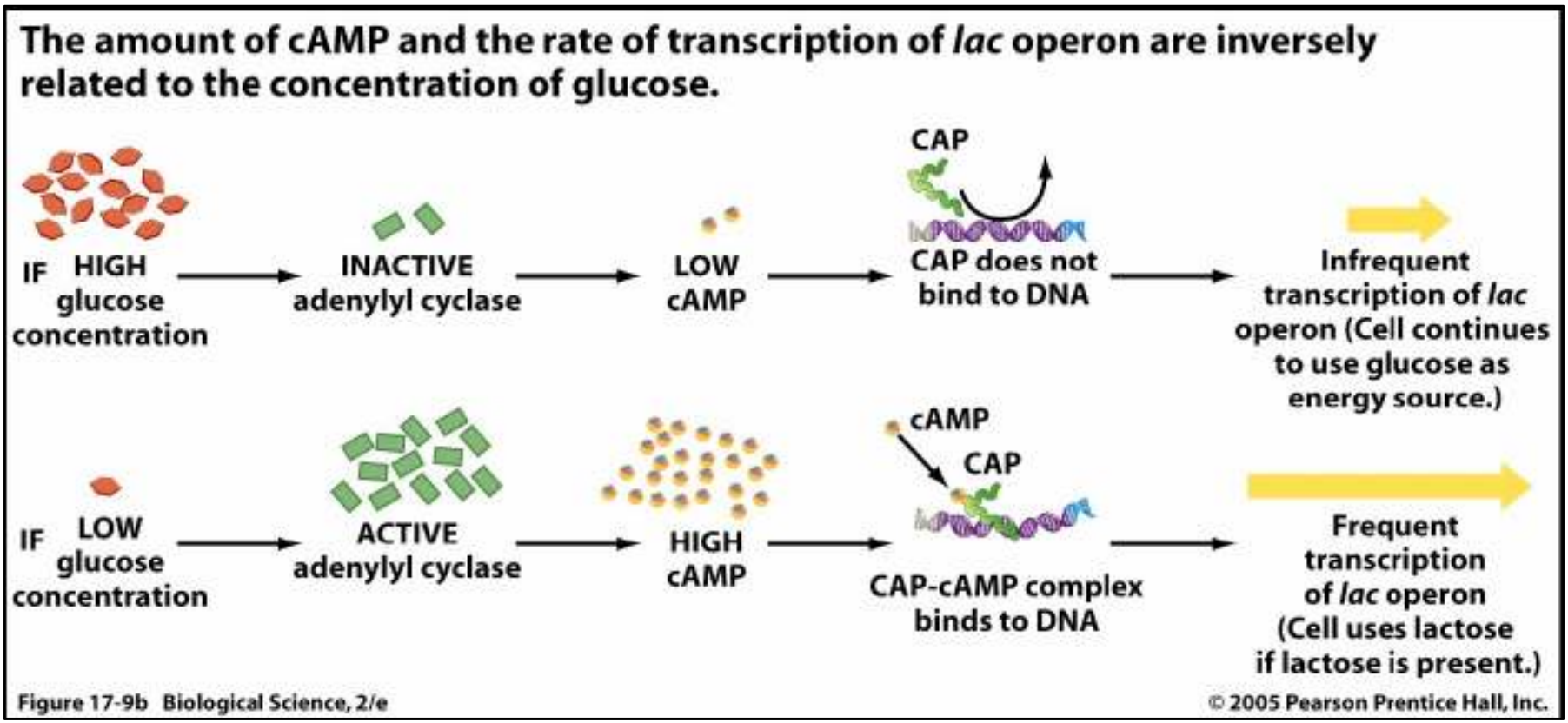


Figure 17-9b Biological Science, 2/e

Which of the following experiments would help you to determine whether the ß-galactosidase gene is induced by lactose or glucose?

a. Measure the amount of ß-galactosidase produced by *E. coli* grown on a glucose plate

b. Measure the amount of ß-galactosidase produced by *E. coli* grown on a glucose + lactose plate

c. Measure the amount of ß-galactosidase produced by *E. coli* grown on a glucose plate, a lactose plate, and a glucose + lactose plate

d. Measure the amount of ß-galactosidase produced by *E. coli* grown on a lactose plate

In a normal system, if no lactose were present, where would RNA polymerase initiate transcription on the DNA shown in the figure below?

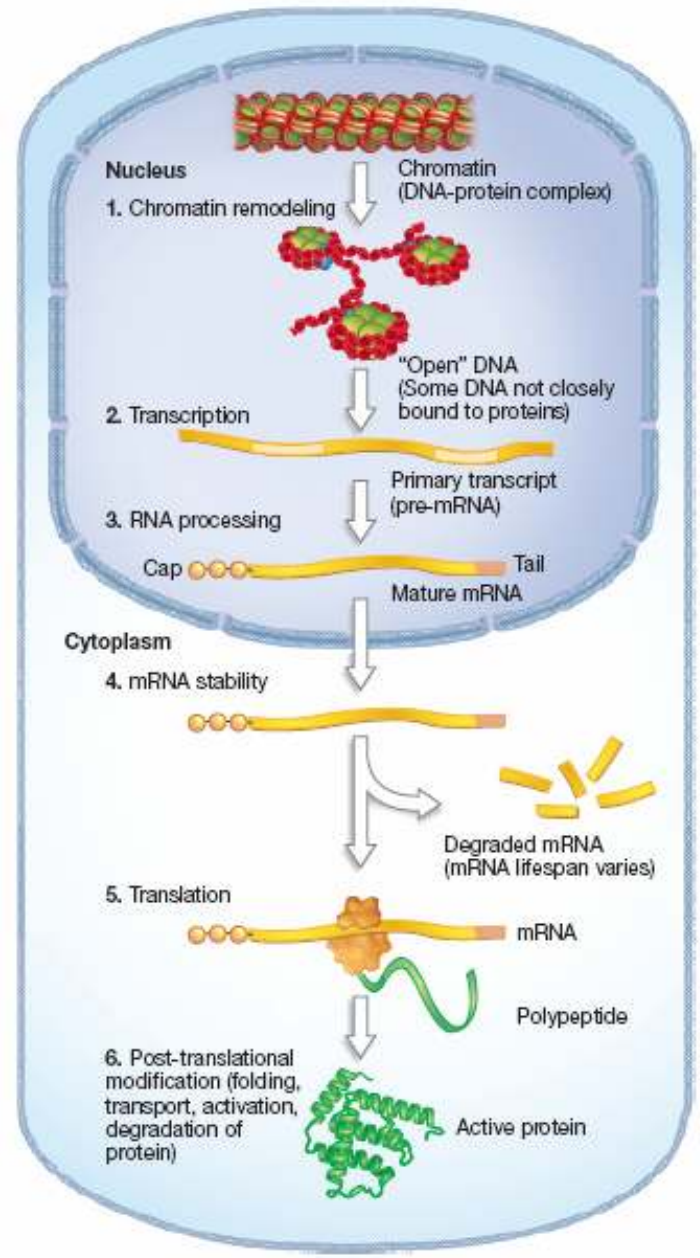
a. *lac* operon promoter
b. *lac* operon operator
c. *lacI* promoter
d. lacI

A hypothetical bacterium isolated from a Martian sea uses a silica-based sugar called silicose as its main energy source. Which of the following would be the most efficient type of control for the production of silicase, the enzyme used to metabolize silicose?

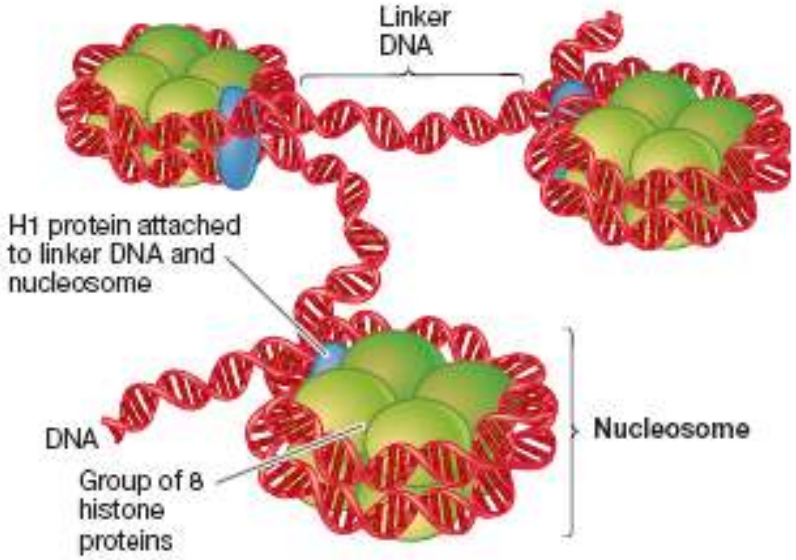
a. Constitutive transcription of silicase gene
b. Negative control of transcription of silicase gene
c. Catabolite repression transcription of silicase gene
d. Inducible operon in control of transcription of silicase gene

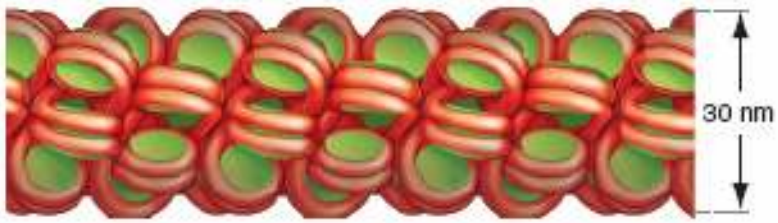
CONTROL

At all steps in gene expressoin!

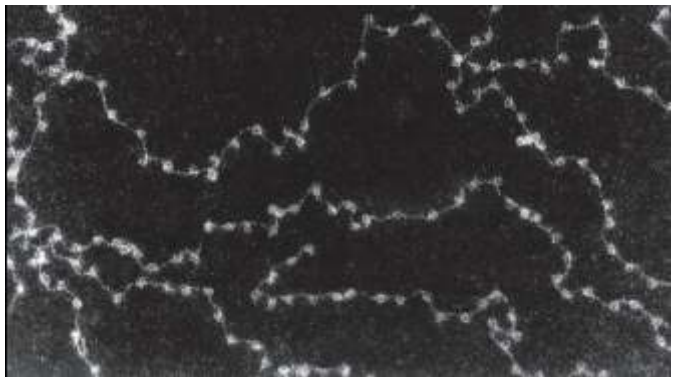


DNA has a (-) charge, Histone proteins are (+)
So, DNA wraps around 8 histones with linkers

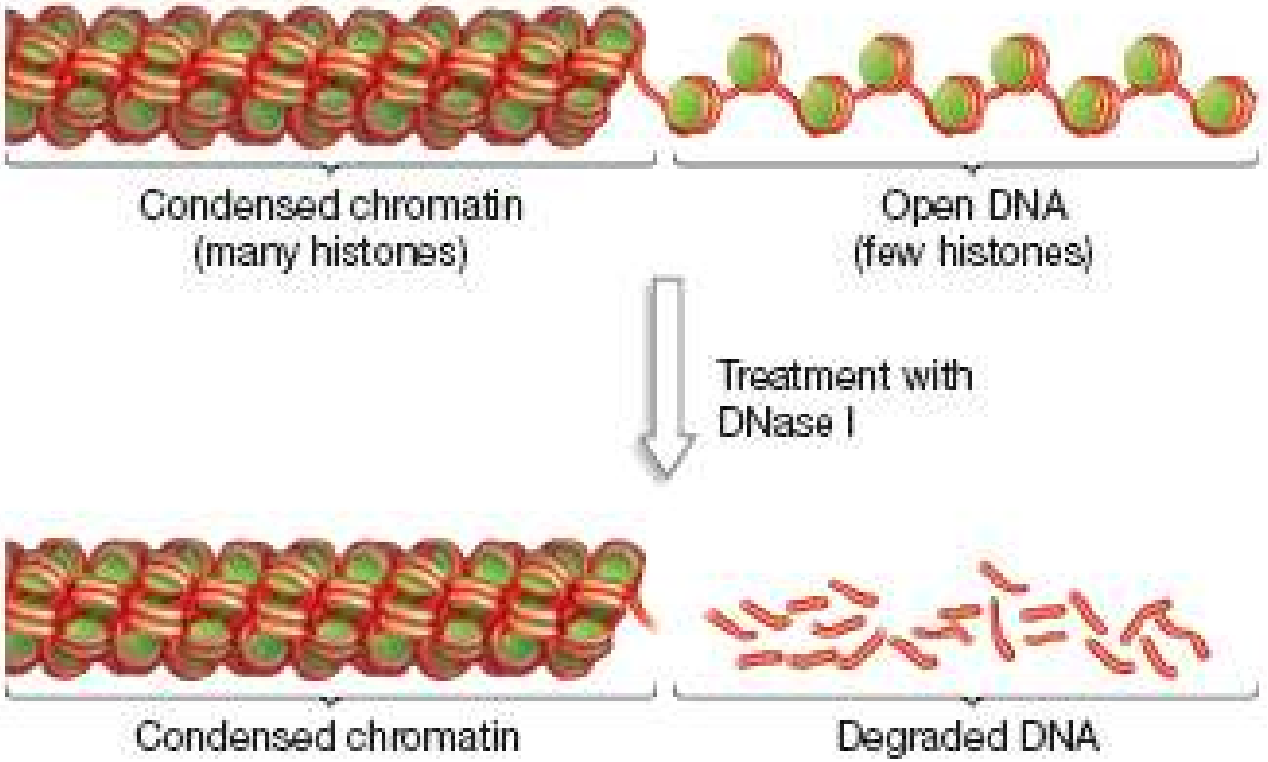


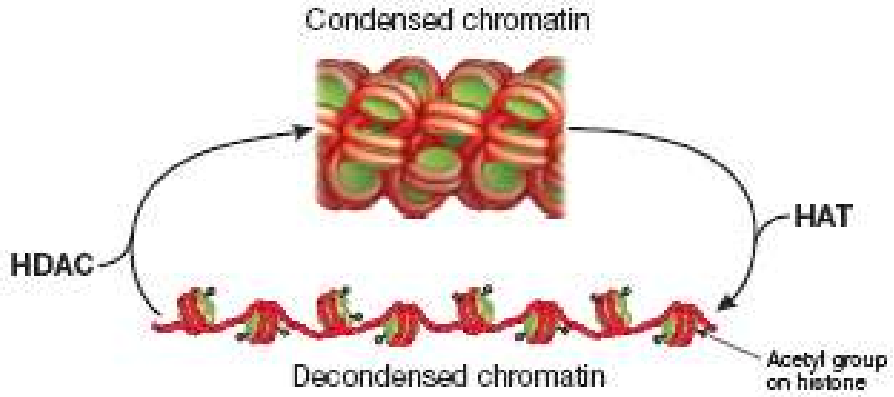


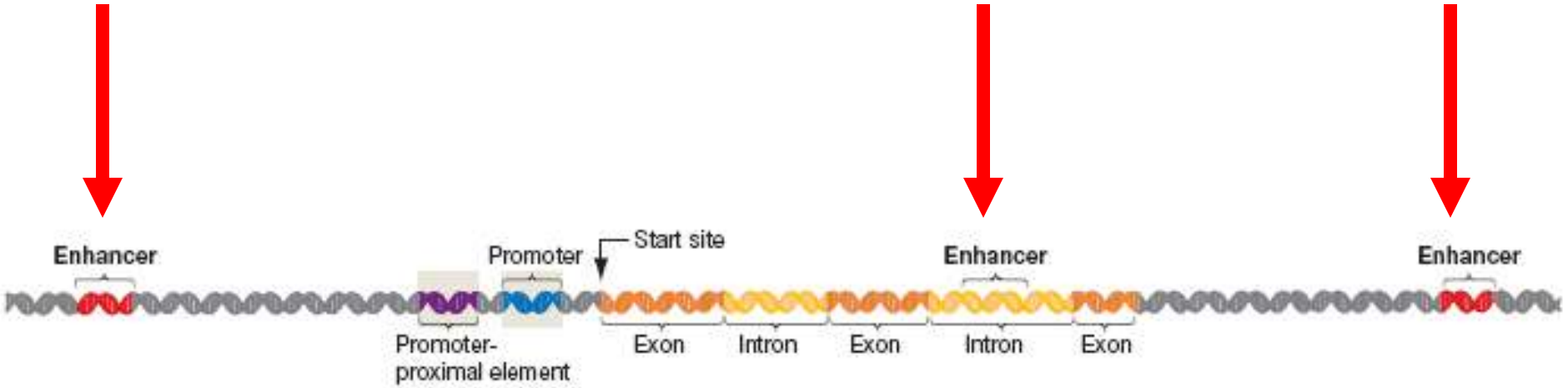
H1 linkers interact

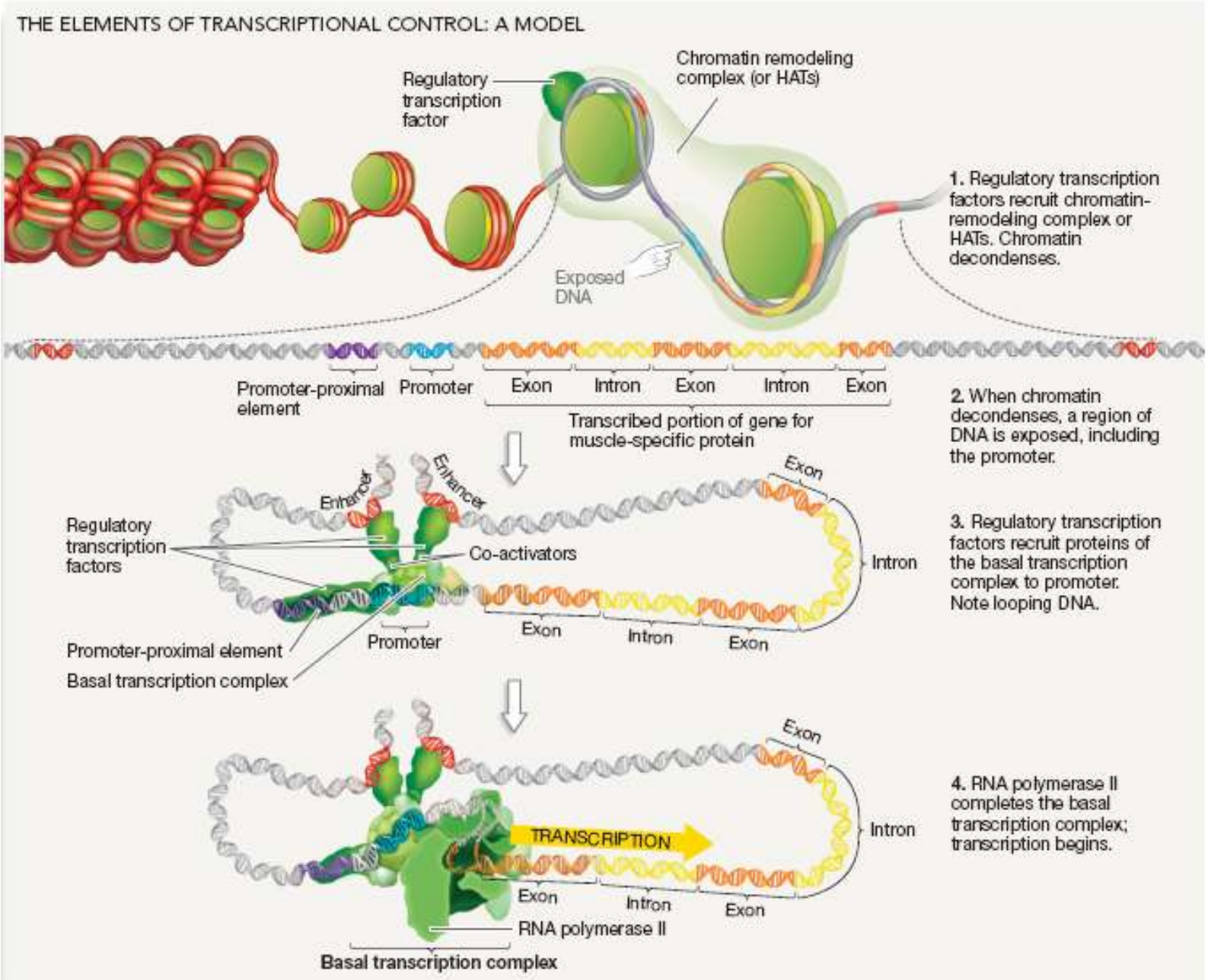


Looks like beads on a string!

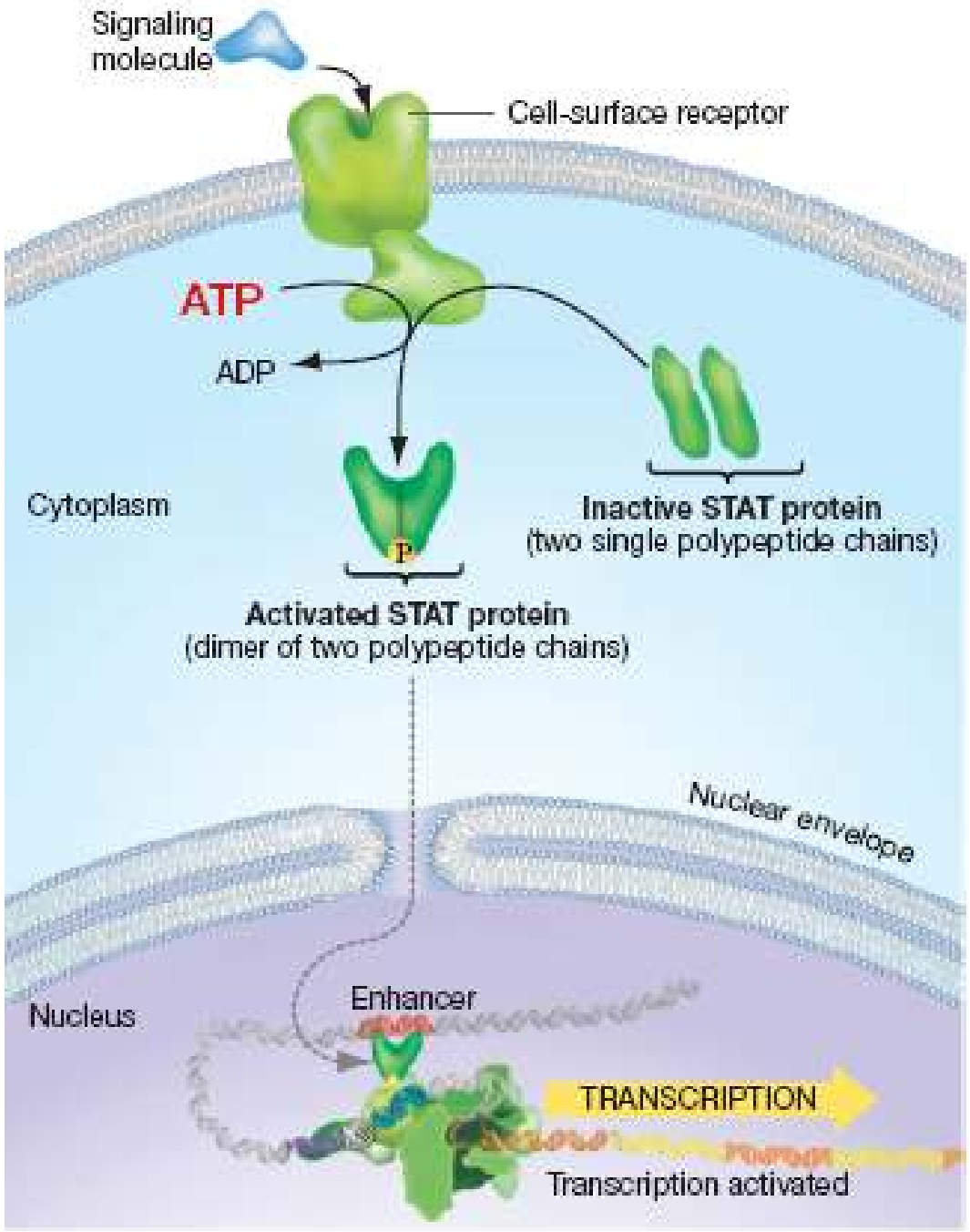

Condensed chromatin
(many histones)
Open DNA
(few histones)
Treatment with
DNase I
Condensed chromatin
Degraded DNA

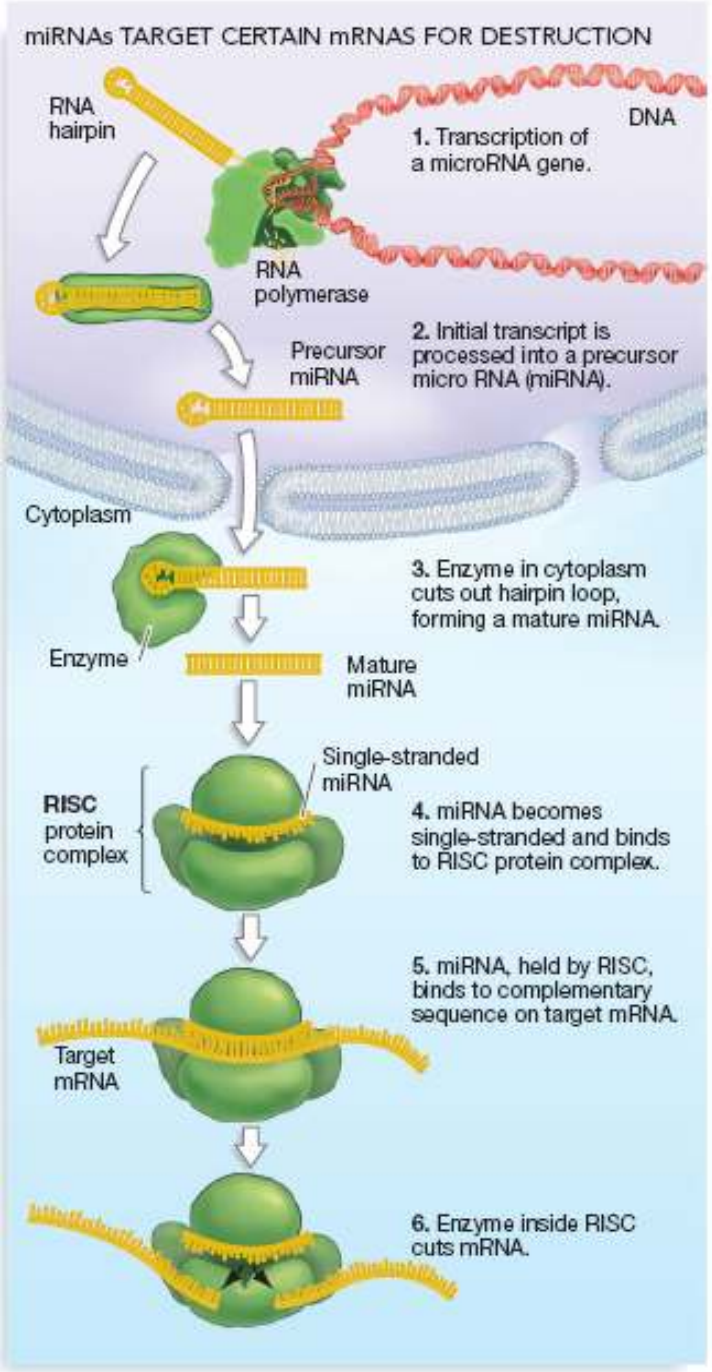

Condensed chromatin
HAT
HDAC
Decondensed chromatin
Acetyl group
on histone


Enhancer
Promoter
Start site
Enhancer
Enhancer
Promoter-
proximal element
Exon
Intron
Exon
Intron
Exon


THE ELEMENTS OF TRANSCRIPTIONAL CONTROL: A MODEL
Regulatory transcription factor
Chromatin remodeling complex (or HATs)
Exposed DNA
1. Regulatory transcription factors recruit chromatin-remodeling complex or HATs. Chromatin decondenses.
Promoter-proximal element
Promoter
Exon
Intron
Exon
Intron
Exon
Transcribed portion of gene for muscle-specific protein
2. When chromatin decondenses, a region of DNA is exposed, including the promoter.
Enhancer
Enhancer
Regulatory transcription factors
Co-activators
Promoter-proximal element
Promoter
Basal transcription complex
Exon
Intron
Exon
Intron
Exon
3. Regulatory transcription factors recruit proteins of the basal transcription complex to promoter. Note looping DNA.
TRANSCRIPTION
Exon
Intron
Exon
Intron
Exon
RNA polymerase II
Basal transcription complex
4. RNA polymerase II completes the basal transcription complex; transcription begins.

Signal Transduction Pathway

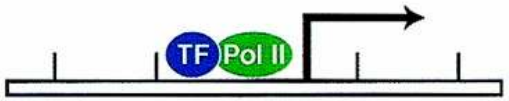



miRNAs TARGET CERTAIN mRNAS FOR DESTRUCTION
RNA hairpin
DNA
1. Transcription of a microRNA gene.
RNA polymerase
Precursor miRNA
2. Initial transcript is processed into a precursor micro RNA (miRNA).
Cytoplasm
3. Enzyme in cytoplasm cuts out hairpin loop, forming a mature miRNA.
Enzyme
Mature miRNA
Single-stranded miRNA
RISC protein complex
4. miRNA becomes single-stranded and binds to RISC protein complex.
5. miRNA, held by RISC, binds to complementary sequence on target mRNA.
Target mRNA
6. Enzyme inside RISC cuts mRNA.

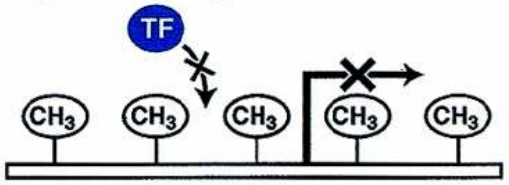
DNA Methylation and Transcriptional Repression

1. Direct interference with transcription activator factor binding

a. Active transcription



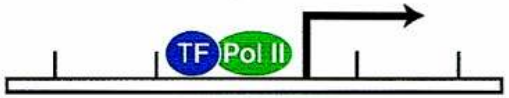
b. Repression by inhibition of TF binding



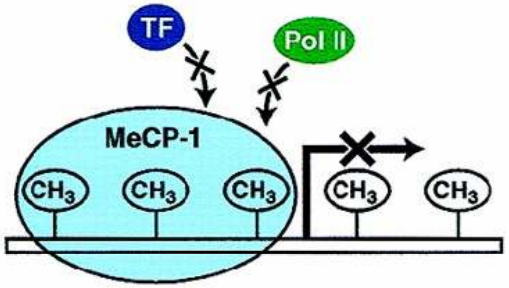
Examples: Methylation sensitive TF: *AP-2, E2F, NFkB*
Methylation insensitive TF: *Sp1*

2. Specific transcriptional repressors

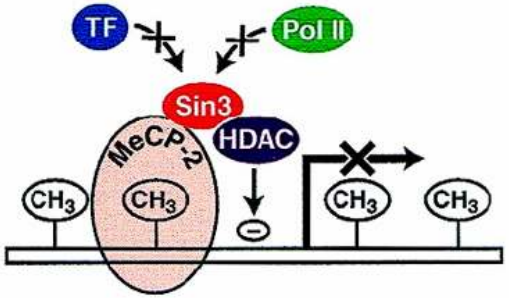
a. Active transcription



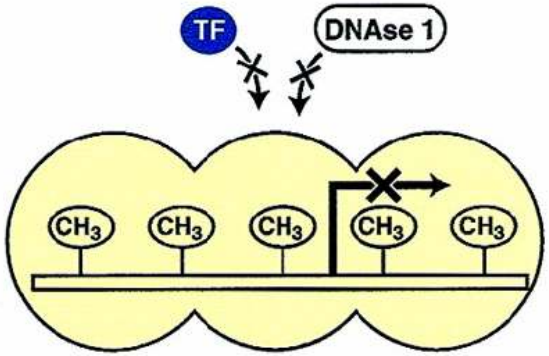
b. Repression by MeCP-1



c. Repression by MeCP-2



3. Inactive chromatin structure formation



methylated CpG: 

unmethylated CpG: