Molecular Biology (6)

Transcription-Regulation

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Second semester, 2020-2021

Resources

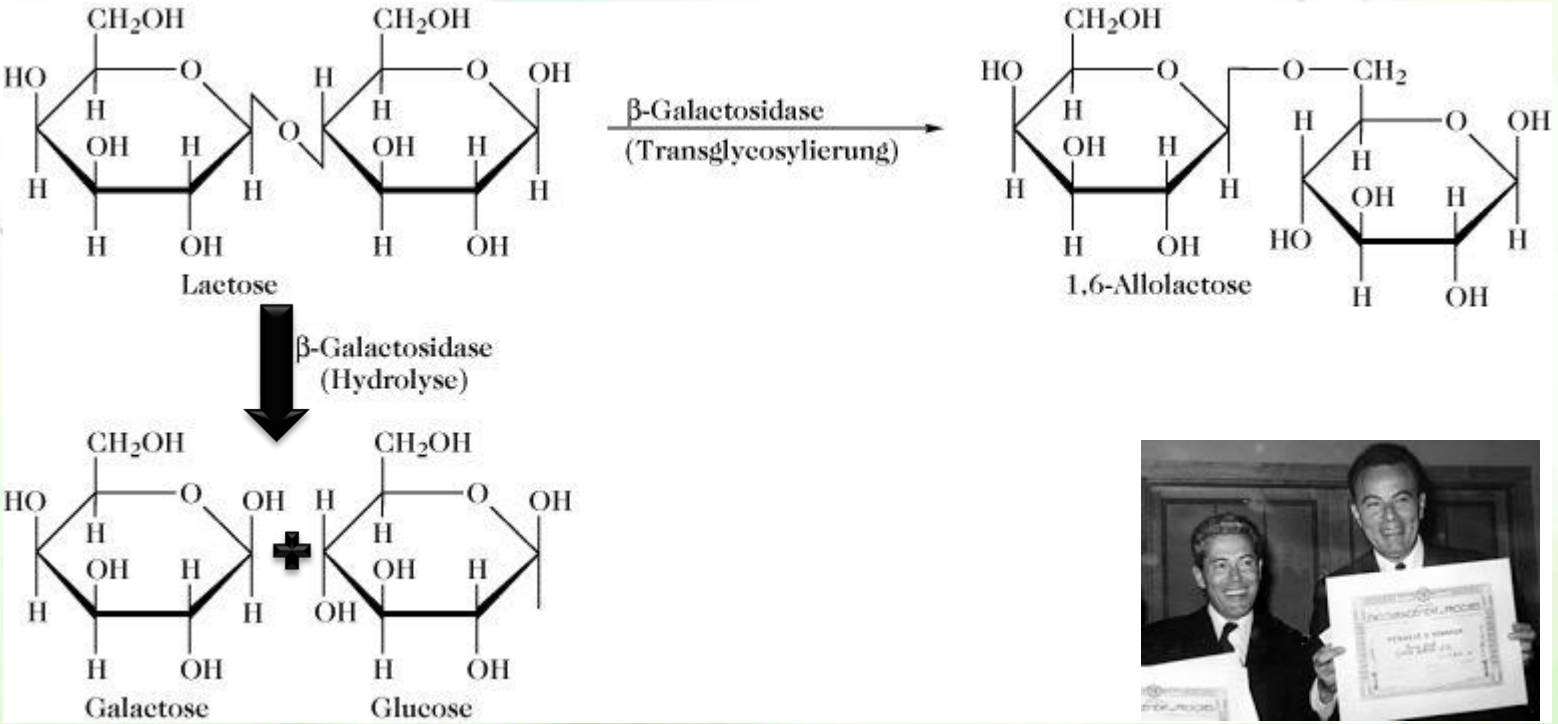
- This lecture
- Cooper, Chapter 8

Regulation of transcription in prokaryotes

The lac operon

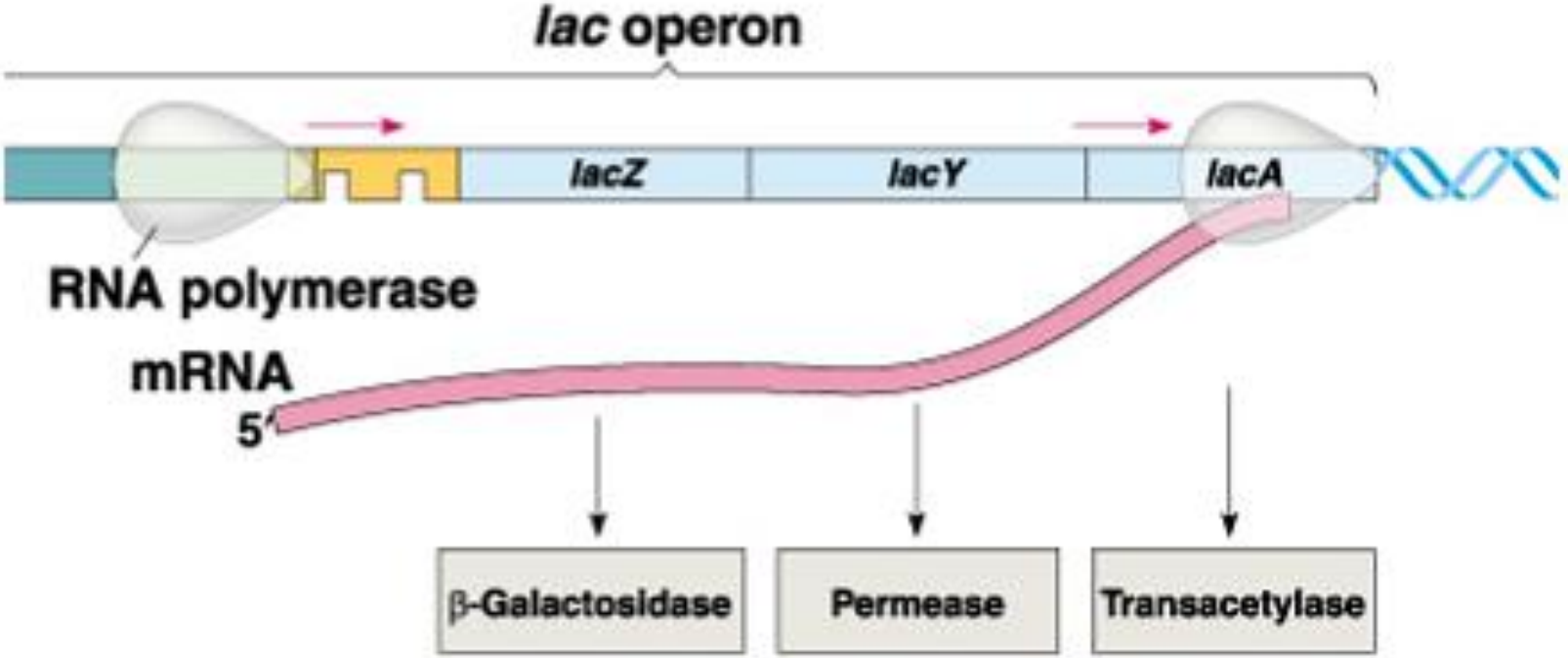
Metabolism of lactose

- In the 1950s, pioneering experiments were carried out by François Jacob and Jacques Monod who studied regulation of gene transcription in E. coli by analyzing the expression of enzymes involved in the metabolism of lactose.

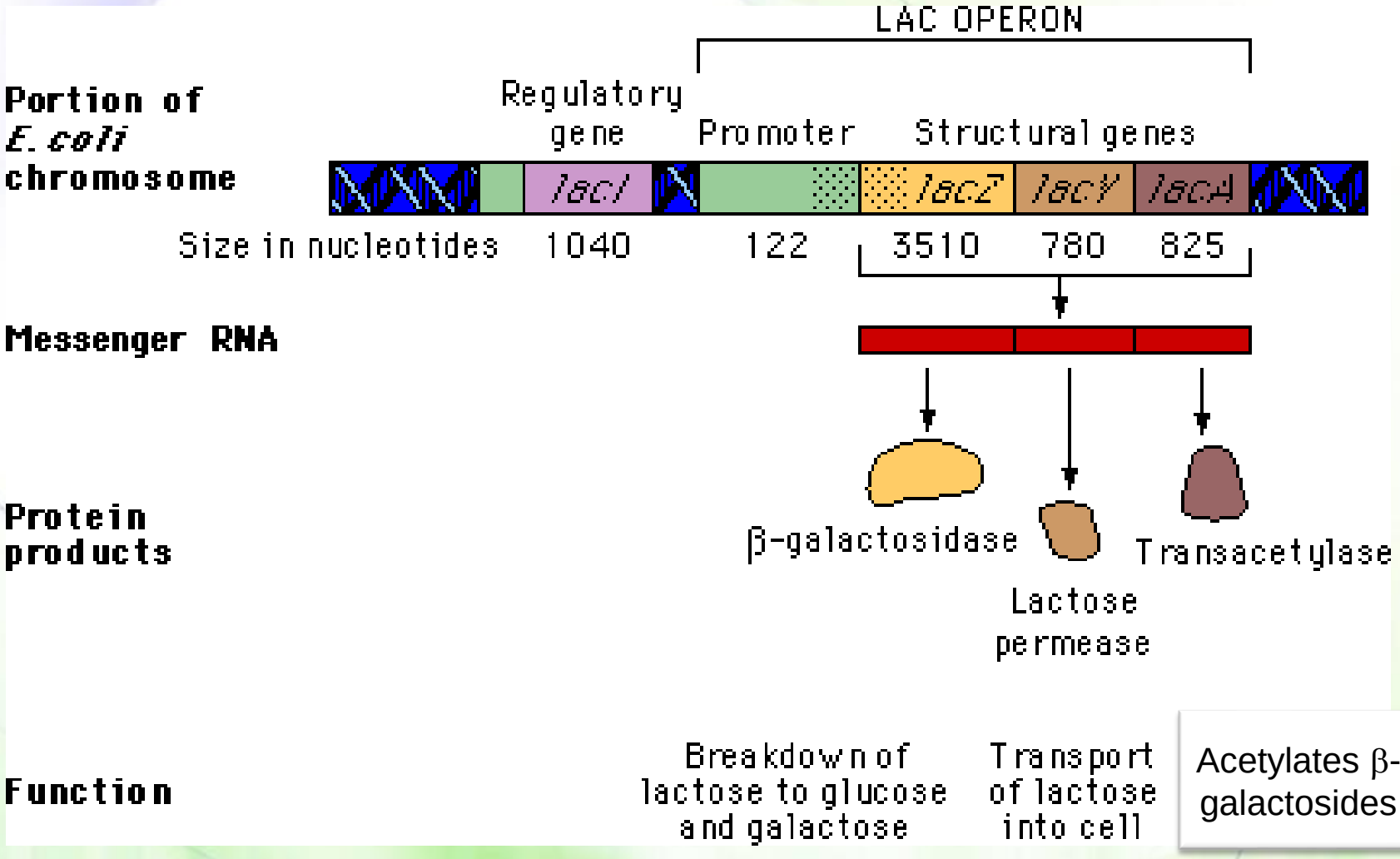


The lac operon

- A cluster of genes transcribed from one promoter producing a polycistronic mRNA that is used to make proteins that are totally different in structure and function, but they participate in the same pathway (purpose).

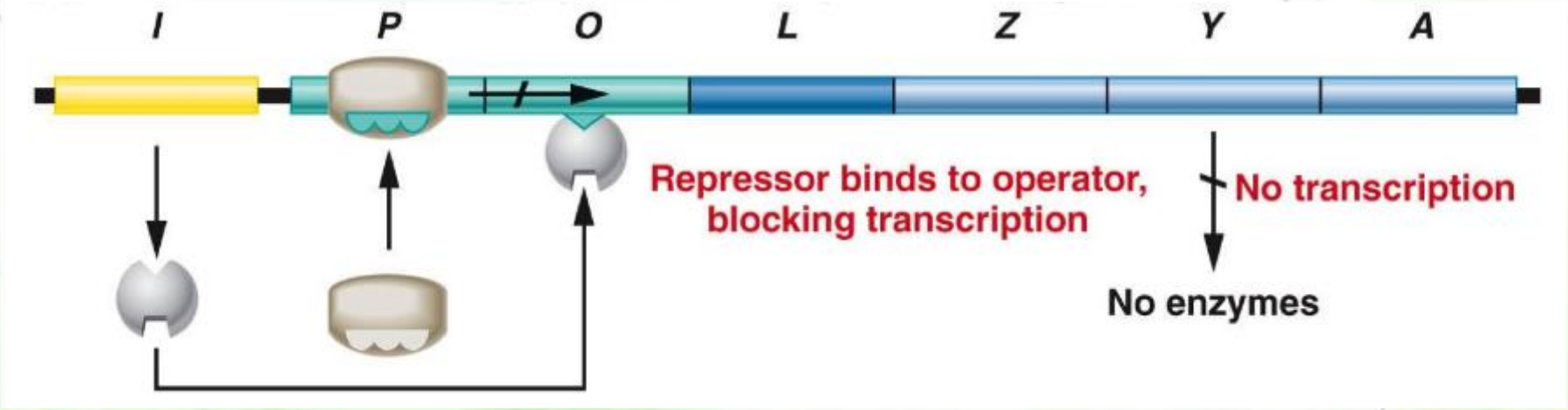


Components of the lac operon

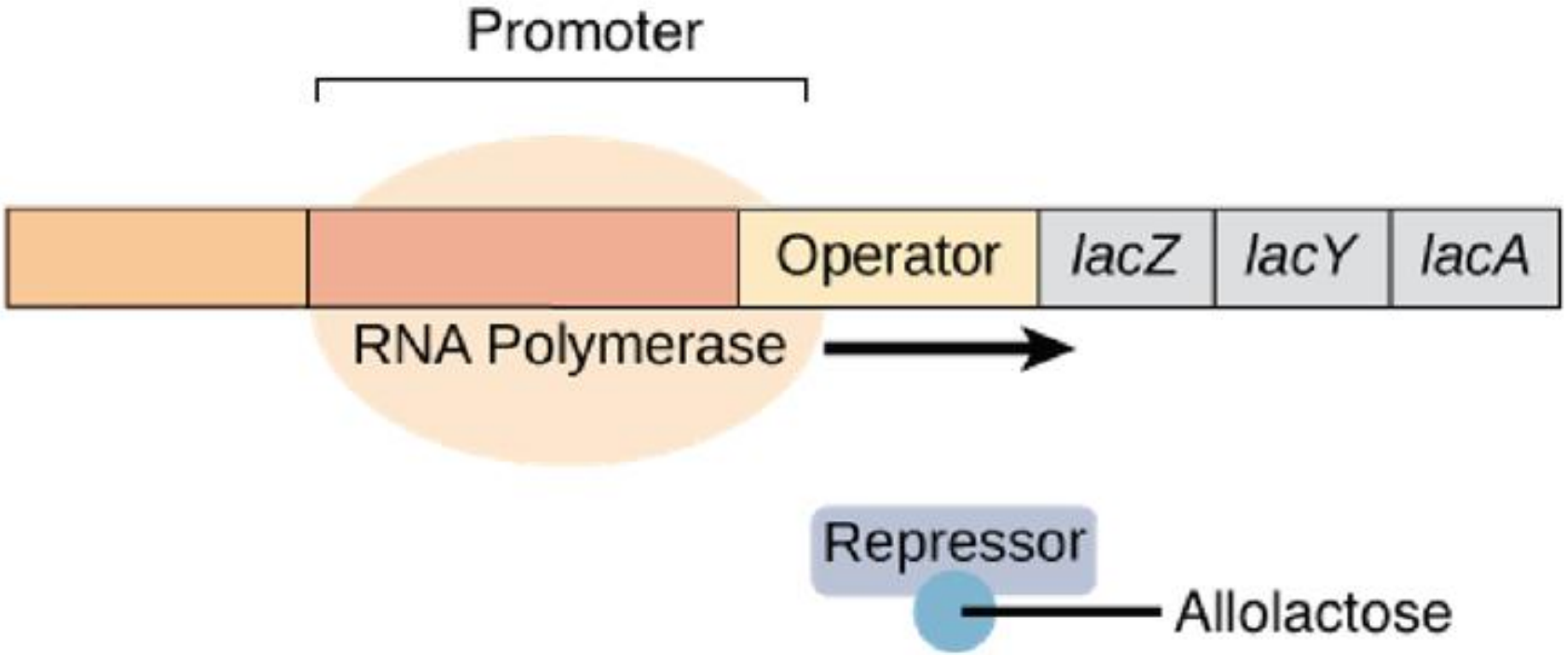


The operator

- The promoter region includes the operator region, which is a binding site of a protein called the lac repressor.
- The lac repressor blocks transcription by preventing the RNA polymerase from binding to the promoter.

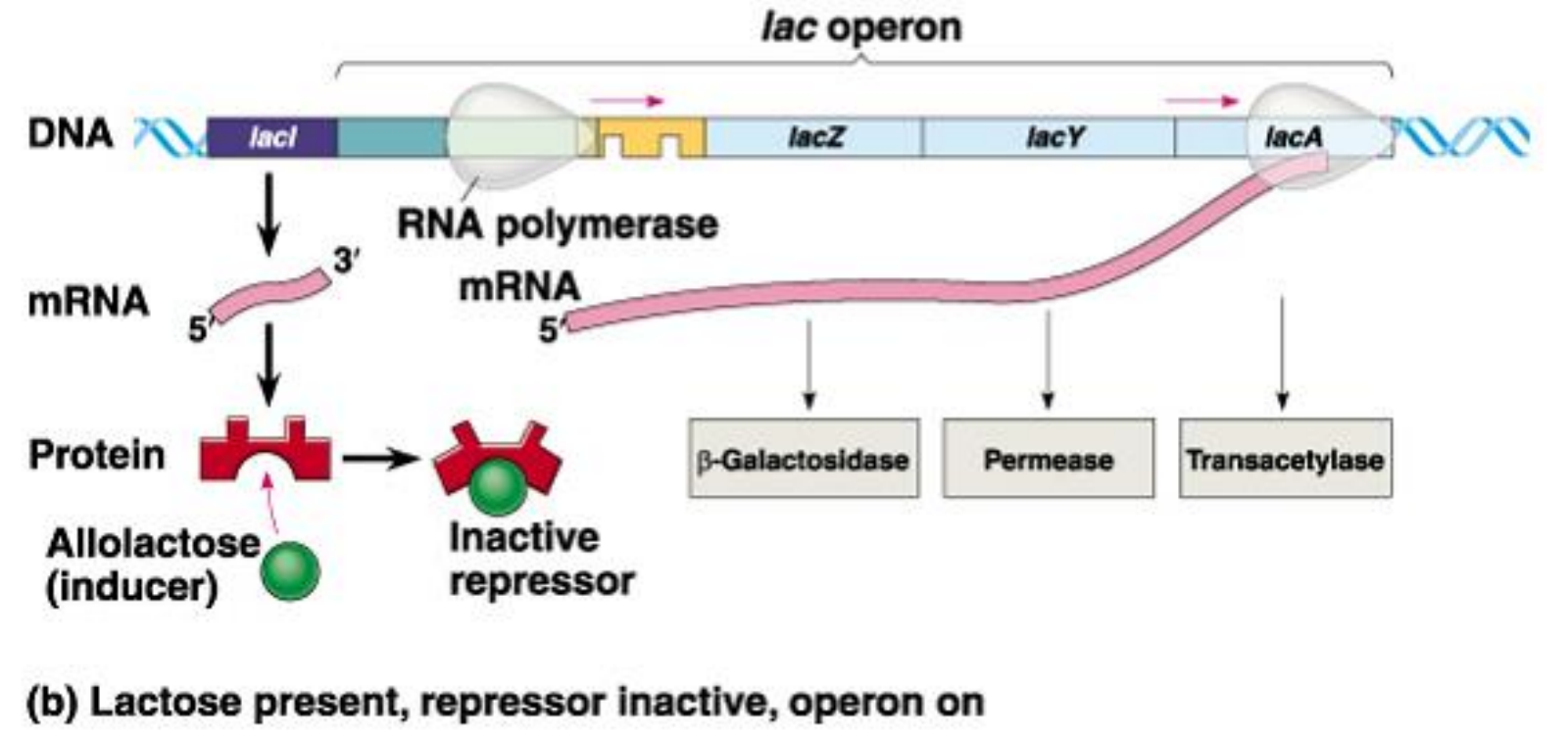


The role of allolactose



Regulation by lactose (positive)

- Lactose binds to the repressor, thereby preventing it from binding to the operator DNA and activating transcription.
- This is known as positive regulation.

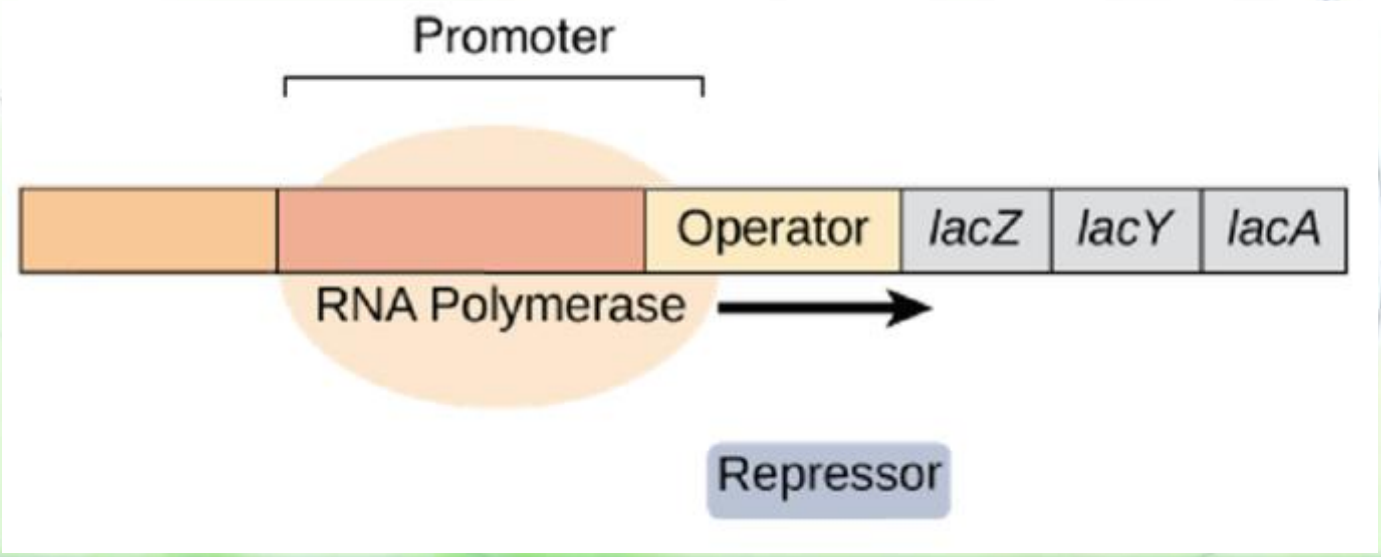


(b) Lactose present, repressor inactive, operon on

Wait...

- So, we need lactose to make β-galactosidase, but we need β-galactosidase to make allolactose. Which one comes first?

- ANSWER: some promoters are leaky.



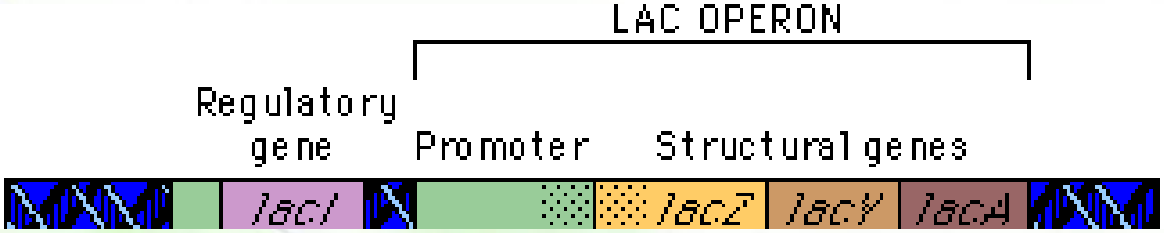
Cis vs. trans regulatory elements

- DNA regulatory sequences like the operator are called **cis-acting elements** because they affect the expression of only genes linked on the same DNA molecule or close-by.
  - Mention other examples of cis-acting elements.

- Proteins (*usually*) like the repressor are called **transacting factors** because they can affect the expression of genes located on other chromosomes within the cell. They are produced from **trans-acting elements**.
  - Mention other examples of trans-acting elements.

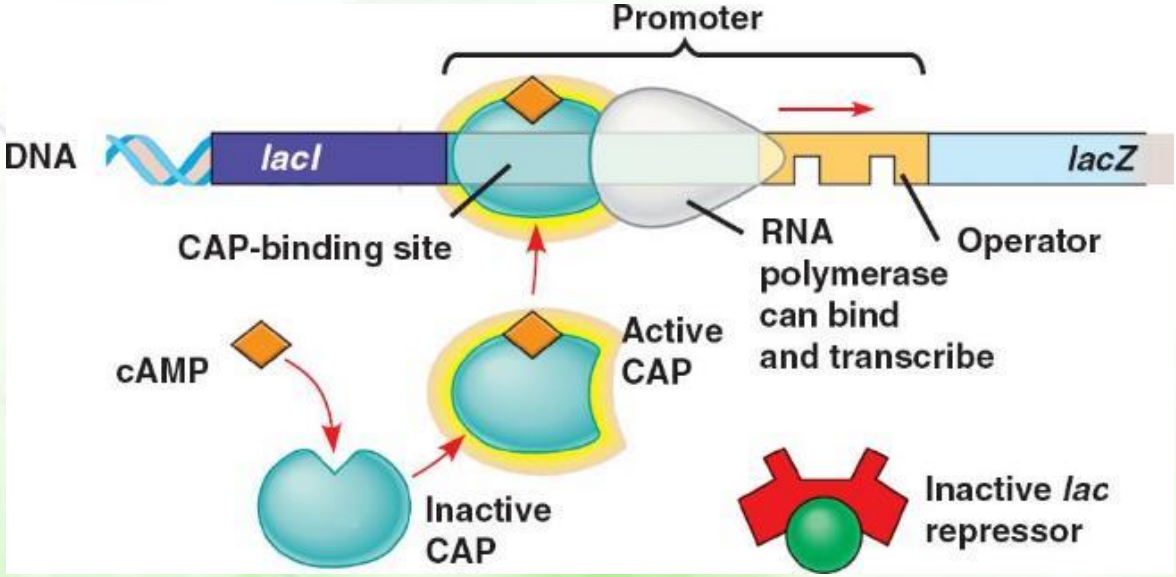
Effect of mutations

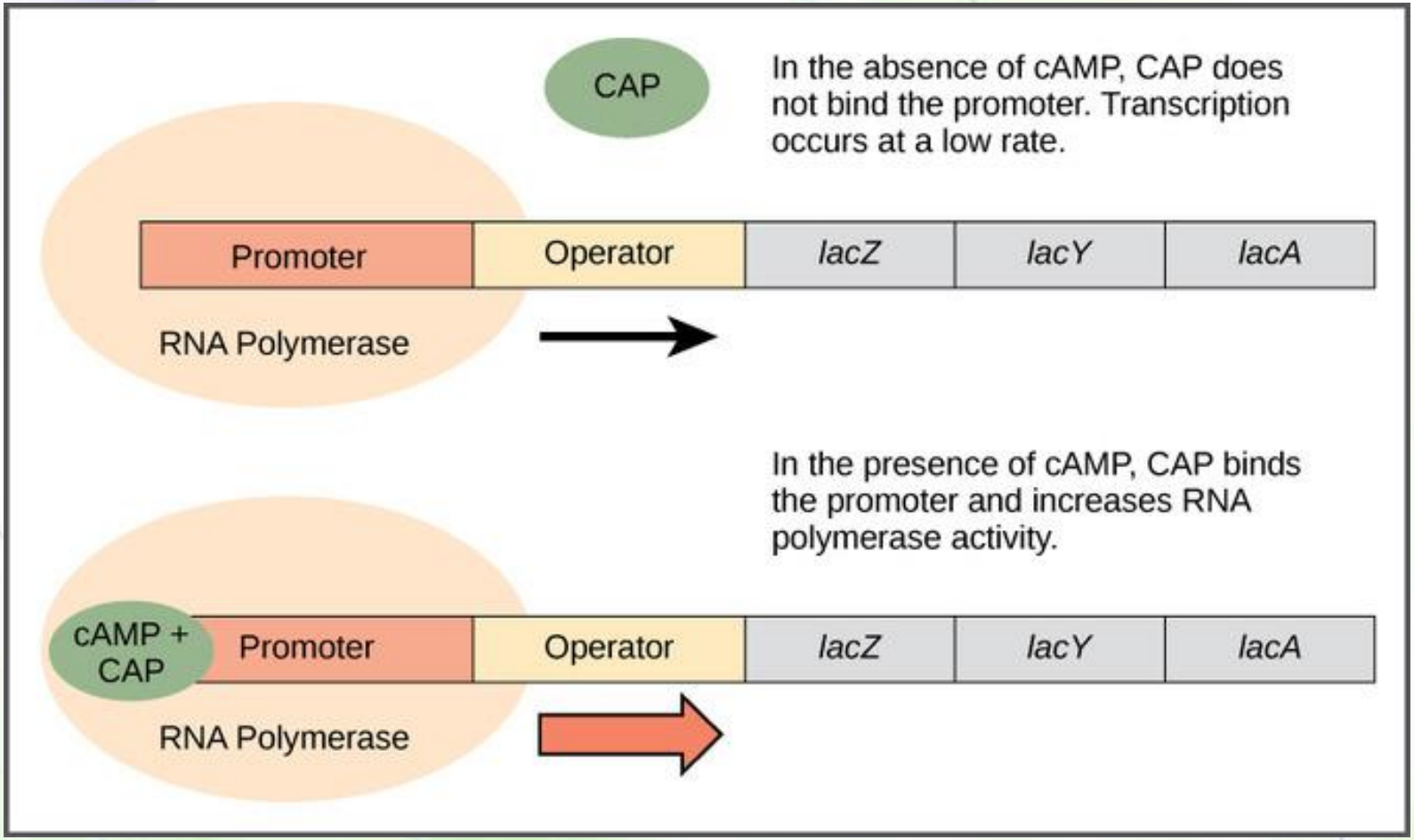
- Some mutations result in **constitutive** expression (always on).
  - Mention examples.
- Other mutations cause **non-inducible** or **repressed** expression (always off).
  - Mention examples



Another level of regulation

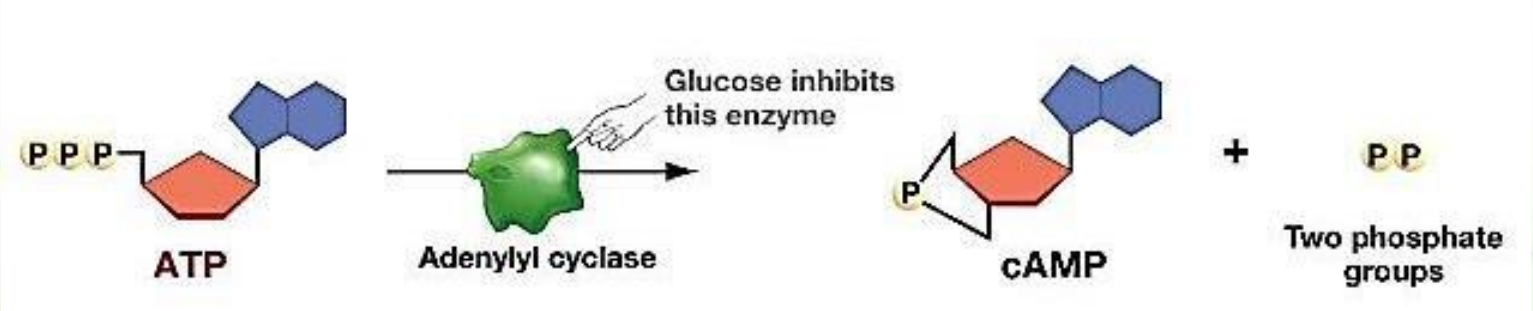
- Another regulator is cAMP, which binds to a protein known as catabolite activator protein (CAP) and stimulates its binding to regulatory sequences upstream of the promoter.
- CAP interacts with the RNA polymerase to facilitate the binding of the polymerase to the promoter (P).




CAP
In the absence of cAMP, CAP does not bind the promoter. Transcription occurs at a low rate.
Promoter
Operator
lacZ
lacY
lacA
RNA Polymerase
In the presence of cAMP, CAP binds the promoter and increases RNA polymerase activity.
cAMP + CAP
Promoter
Operator
lacZ
lacY
lacA
RNA Polymerase

Regulation by glucose (negative)

- The ability of CAP to bind to the promoter is influenced by how much cAMP is in the cell is produced by adenylyl cyclase, which is inhibited by high level of glucose.
- Glucose is preferentially utilized by bacterial cells and it represses the lac operon even in the presence of the normal inducer (lactose).
- This is known as negative regulation.



Glucose repression

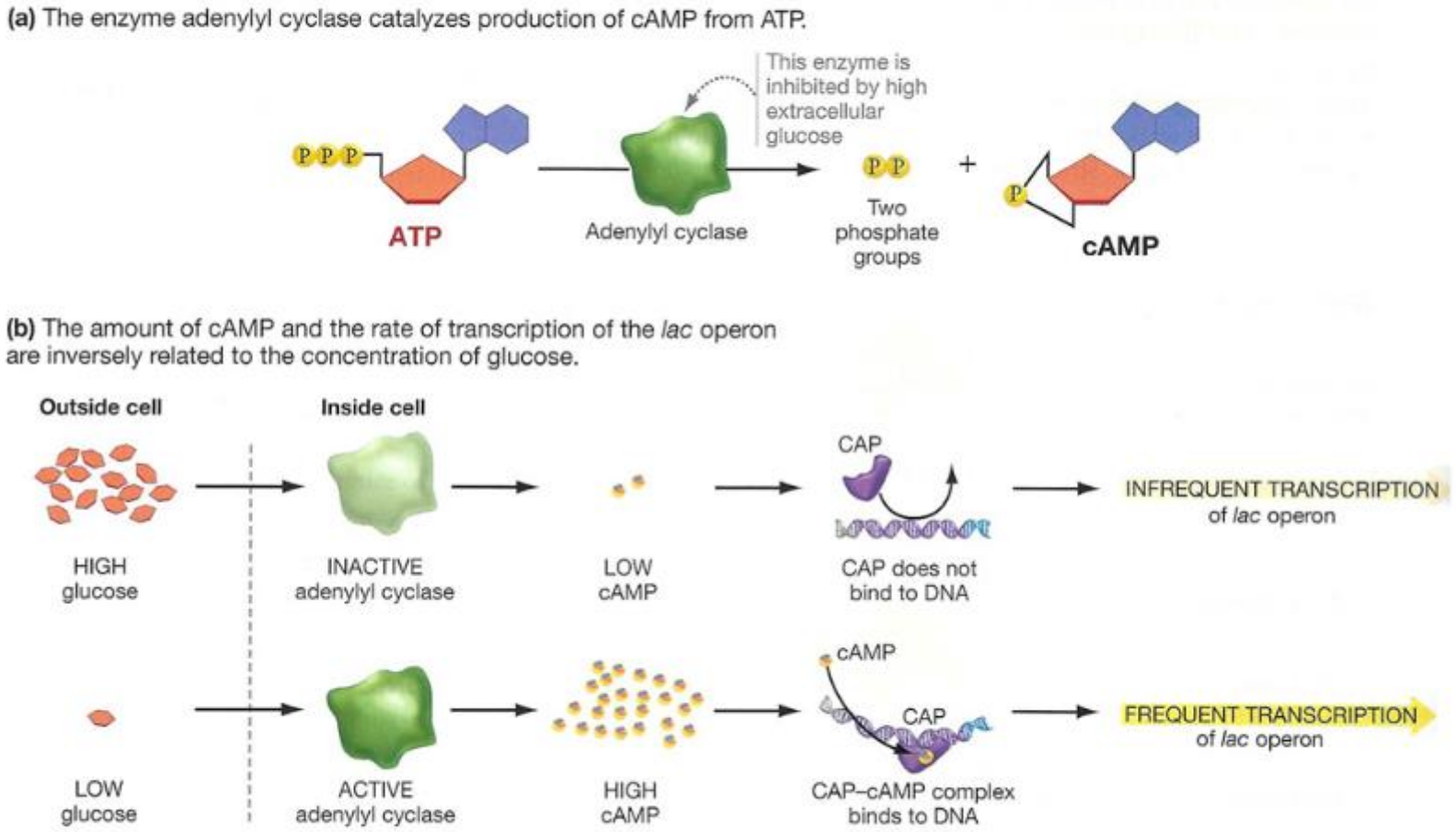
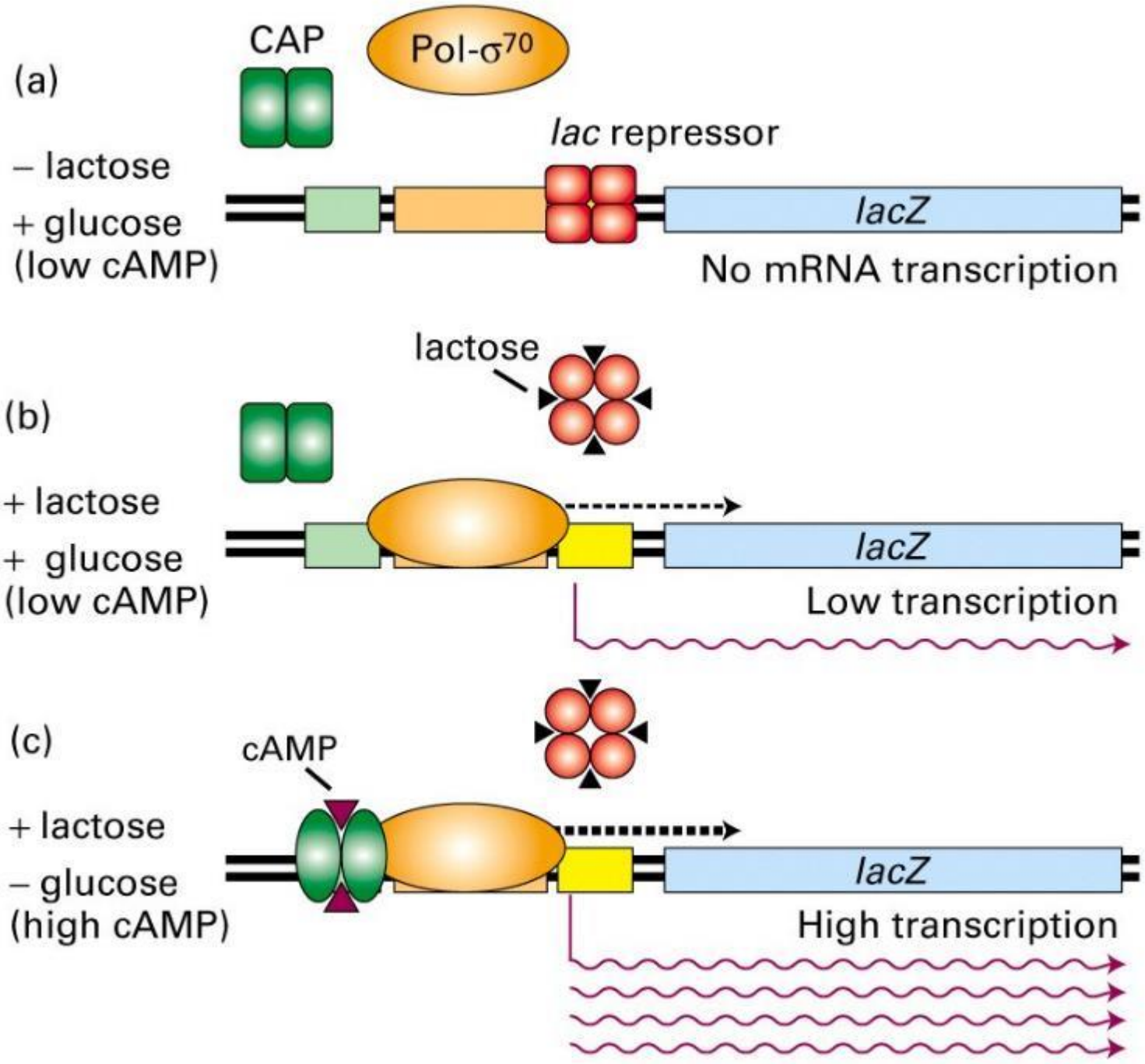


FIGURE 17.11 Cyclic AMP (cAMP) Is Synthesized When Glucose Levels Are Low.


CAP
Pol-σ70
(a)
lac repressor
– lactose
+ glucose
(low cAMP)
lacZ
No mRNA transcription
lactose
(b)
+ lactose
+ glucose
(low cAMP)
lacZ
Low transcription
(c)
cAMP
+ lactose
– glucose
(high cAMP)
lacZ
High transcription

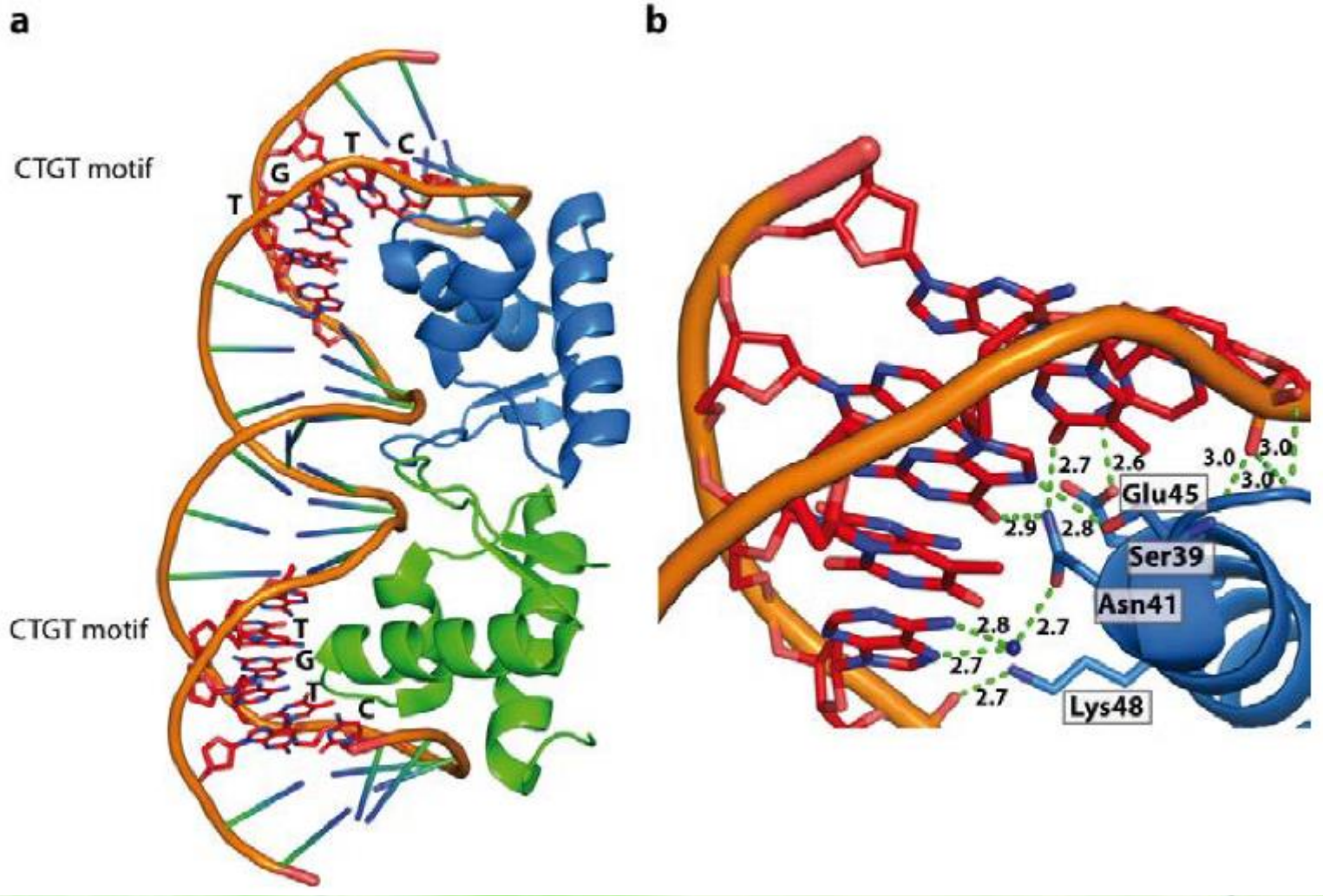
Take-home message

- Gene expression is regulated by regulatory proteins that would ultimately:
  - Guide the RNA polymerase (or other regulatory proteins) to the promoter
  - Strengthen/stabilize the RNA polymerase (or other regulatory proteins) binding to the promoter
  - Activate the RNA polymerase (or other regulatory proteins)
  - Create the open promoter complex for the RNA polymerase (or other regulatory proteins)

OR the opposite of the above in case of repressors.

  - All of the above effects are mediated via modulating non-covalent interactions between the amino acids of proteins and specific sequences of DNA.

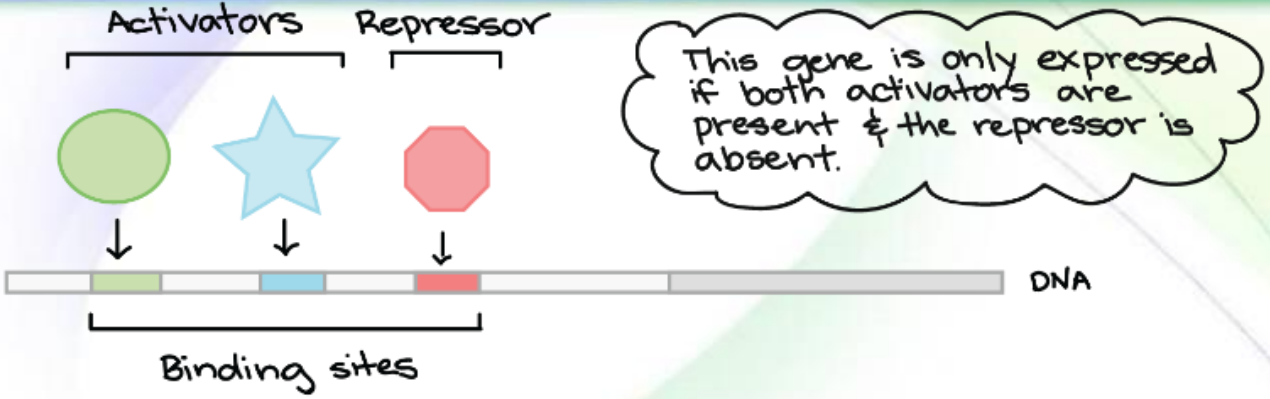
How do proteins recognize/interact with DNA sequences specifically?

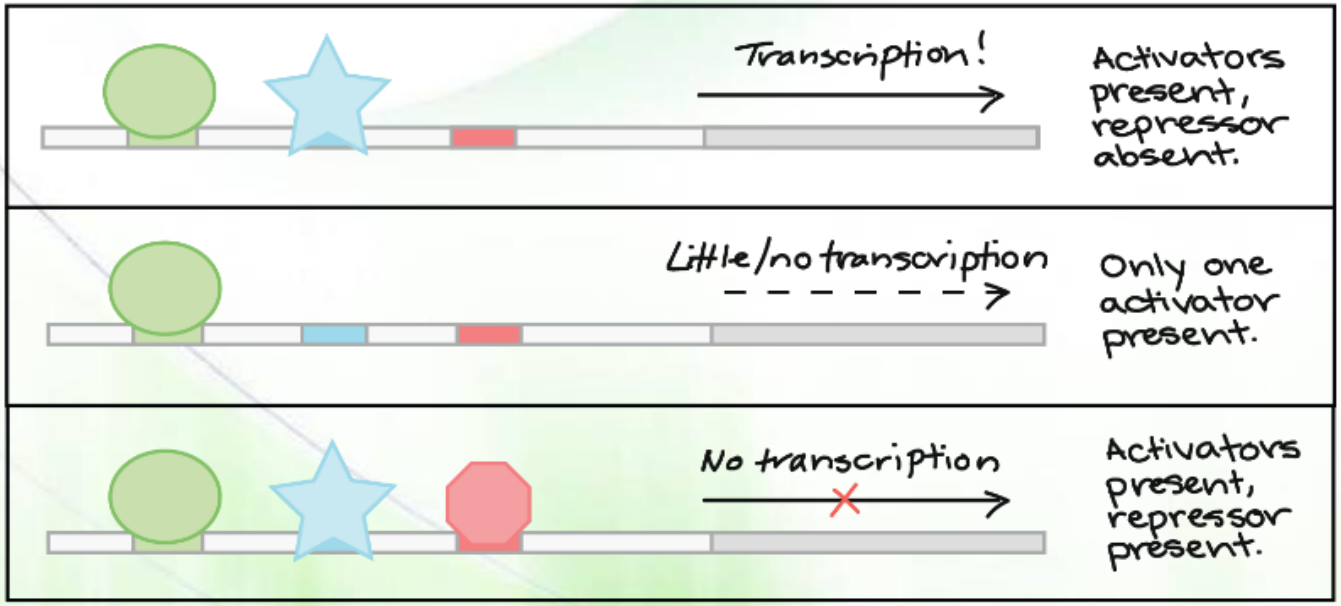


Regulation of transcription in eukaryotes

Regulatory mechanisms

- Although the control of gene expression is far more complex in eukaryotes than in bacteria, the same basic principles apply.
- Transcription in eukaryotic cells is controlled by:
  - Cis-acting elements
    - Promoters, proximal promoter elements, enhancers, and silencers
  - Trans-acting factors
    - transcriptional regulatory proteins (activators, repressors)
      - DNA and chromatin structural modification
      - DNA chemical modification (example: methylation of cytosine)
  - Noncoding RNA molecules


Activators
Repressor
This gene is only expressed if both activators are present & the repressor is absent.
DNA
Binding sites


Transcription!
Activators present, repressor absent.
Little/no transcription
Only one activator present.
No transcription
Activators present, repressor present.

How do TFs regulate gene expression?

- Transcription factors cause epigenetic/epigenomic changes in DNA and chromatin.

- What is epigenetics?
  - Epi: “above” or “in addition to”
  - It indicates genetic alterations in gene expression without a change in DNA sequence.
    - Chromatin packaging
    - Chemical modification of histones
    - Chemical modification of DNA

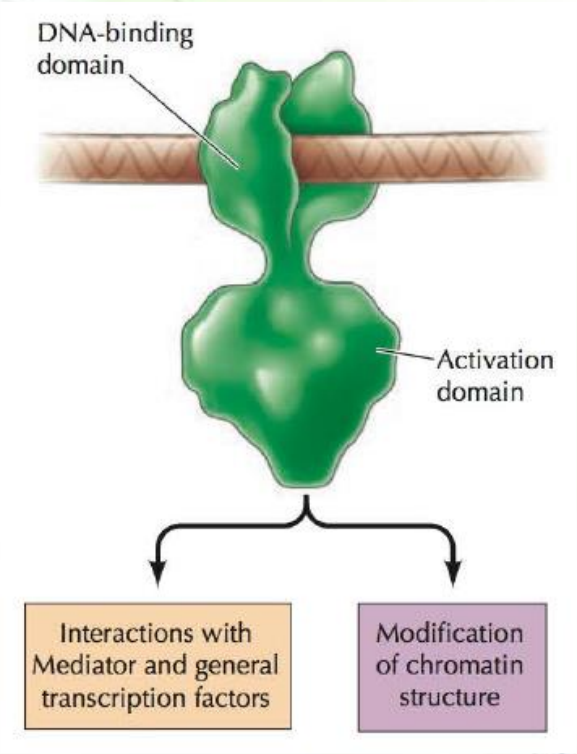
General structure of TFs

- Positive transcription factors have at least two domains:
  - DNA-binding domain
  - Activation domain

- A three-dimensional structure that is part of a protein's structure. It forms independently of the rest of the protein and usually has a function.
  - In other words, it can be separated from the protein and till be functional

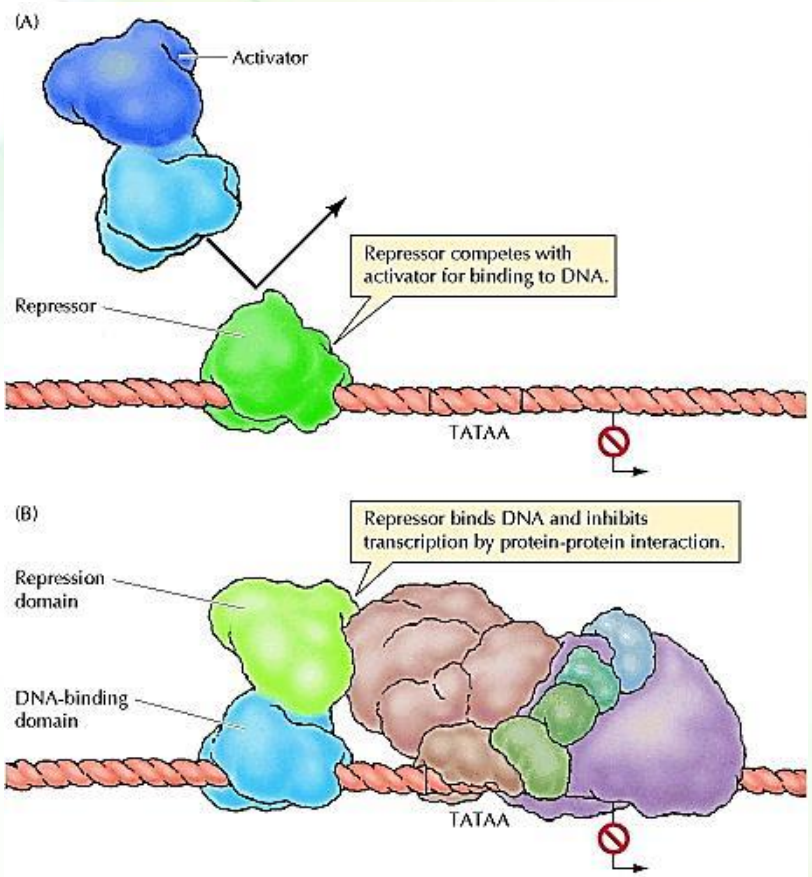
The activation domains

- Activation domains stimulate transcription by
  - interacting with general transcription factors and facilitating the assembly of a transcription complex on the promoter,
  - modifying the chromatin.



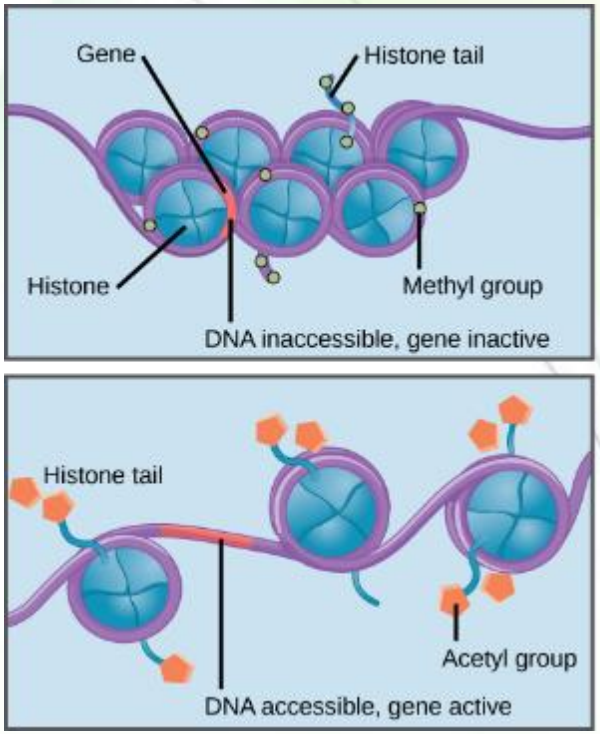
Eukaryotic repressors

- Repressors bind to specific DNA sequences and inhibit transcription.
- Repressors may have
  - both DNA-binding and protein-binding domains
  - DNA-binding domains, but not protein-interaction domains



Modulation of chromosomal structure

- The packaging of eukaryotic DNA in chromatin has important consequences in terms of its availability as a template for transcription
  - Actively transcribed genes are found in loose chromatin (euchromatin)
  - Inactive genes are located in highly packed heterochromatin.
- Regulatory proteins switch between the two structures of chromatin.

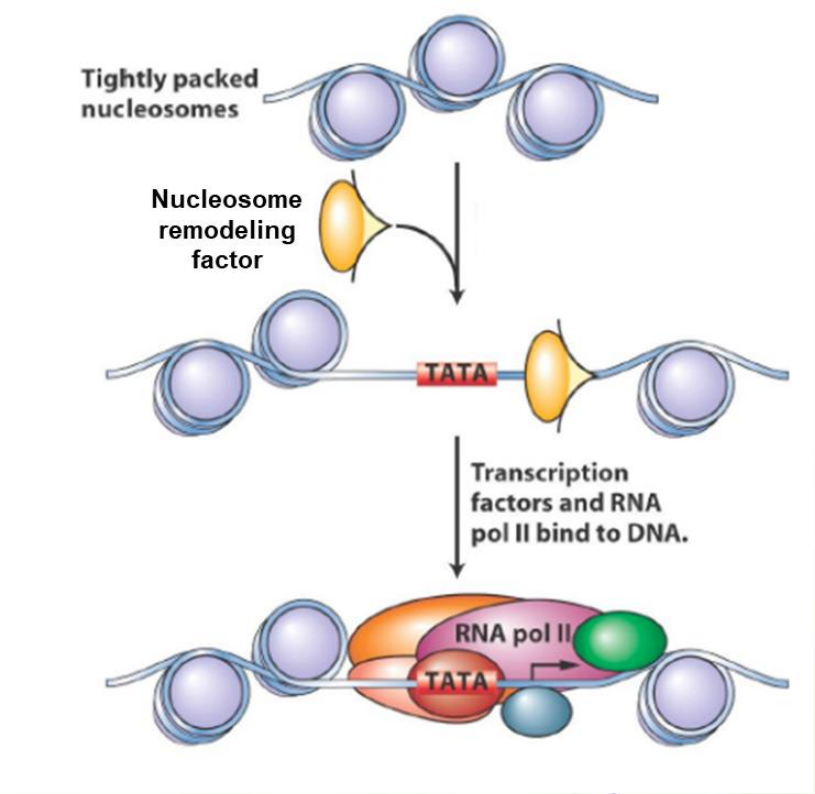


Methylation of DNA and histones causes nucleosomes to pack tightly together. Transcription factors cannot bind the DNA, and genes are not expressed.

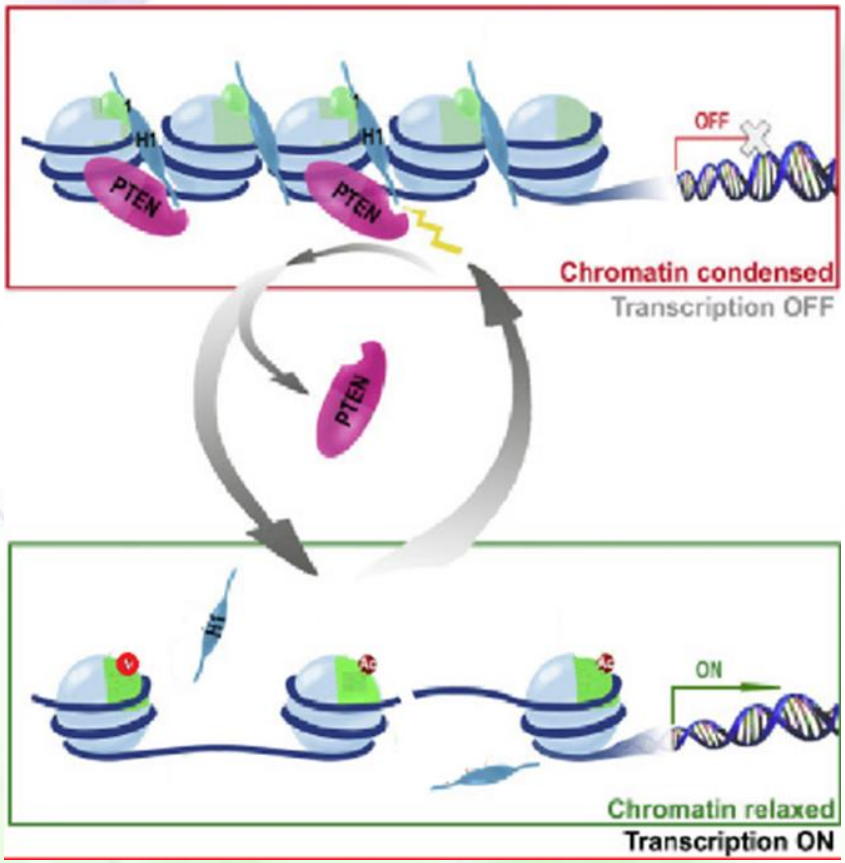
Histone acetylation results in loose packing of nucleosomes. Transcription factors can bind the DNA and genes are expressed.

Chromatin remodeling factors

- They facilitate the binding of transcription factors by
  - Removing histones from DNA
  - Repositioning nucleosomes making DNA accessible
  - Altering nucleosome structure allowing protein binding to DNA
- Chromatin remodeling factors can be associated with transcriptional activators and repressors.



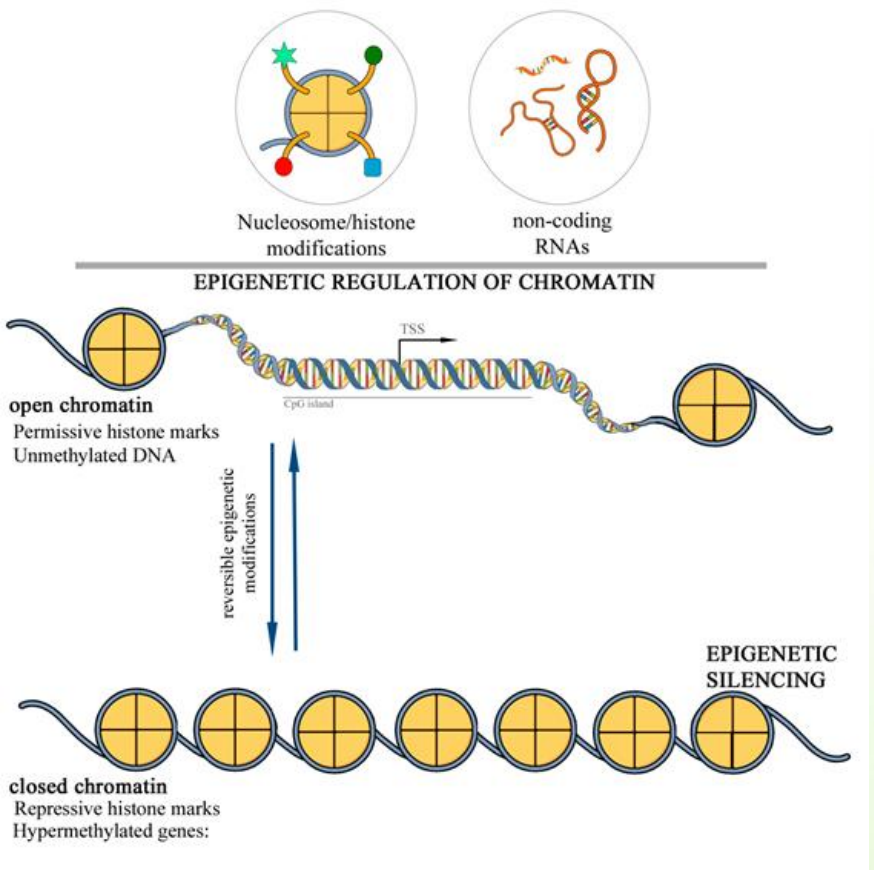
Changing nucleosome structure by histone 1



- Transcriptional regulatory proteins either release Histone 1 (H1) from DNA or facilitate its binding.

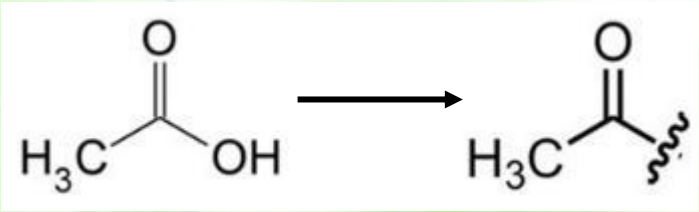
How else are chromosomal structures altered?

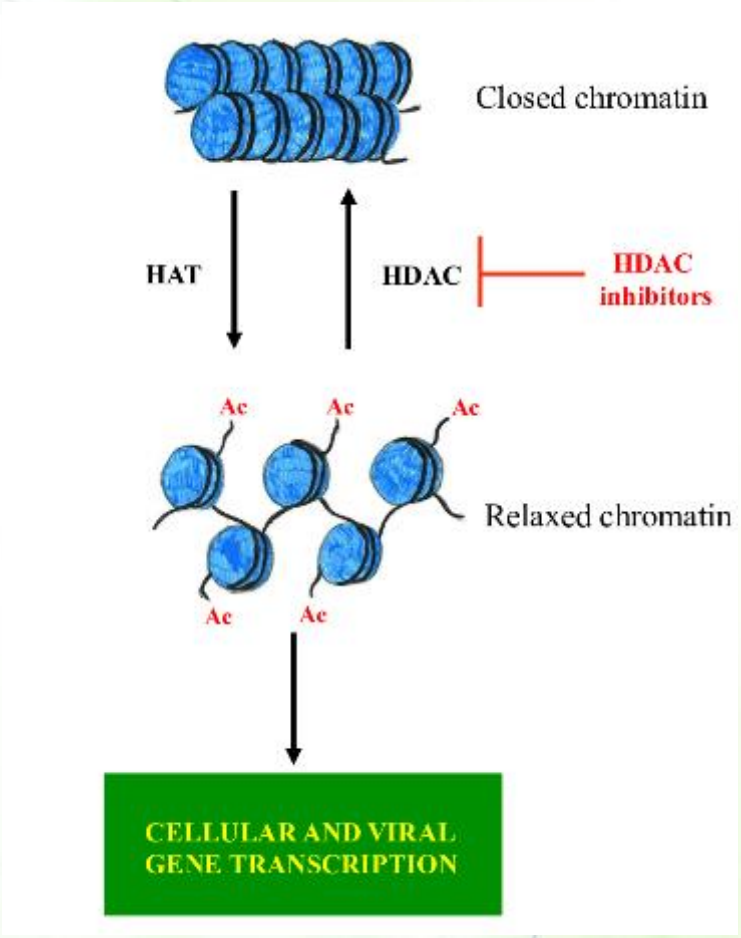
- Change of compactness of the chromatin by:
  - Chemical modification of histones
    - Acetylation, methylation, and phosphorylation
  - Binding of noncoding RNAs to DNA



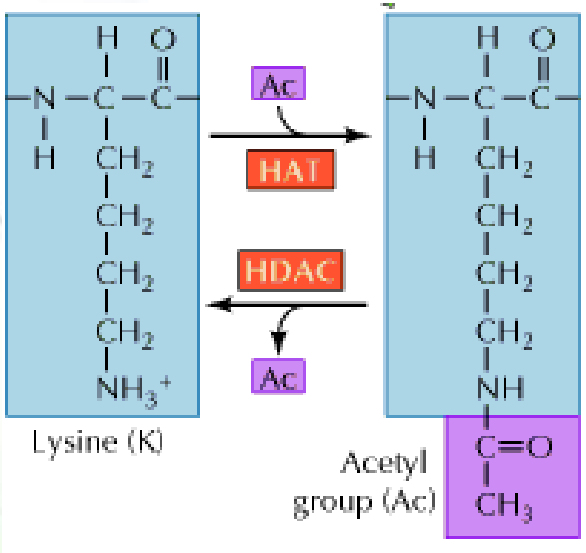
Histone acetylation

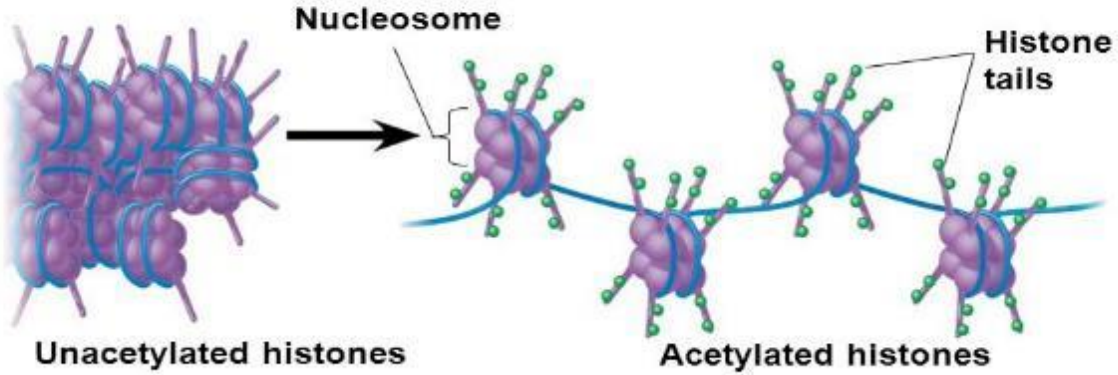
- The core histones (H2A, H2B, H3, and H4) have two domains (internal 3-dimensional structures):
  - A histone-fold, which is involved in interactions with other histones and in wrapping DNA around the nucleosome core particle.
  - An amino-terminal tail, which extends outside of the nucleosome, and is rich in lysine.





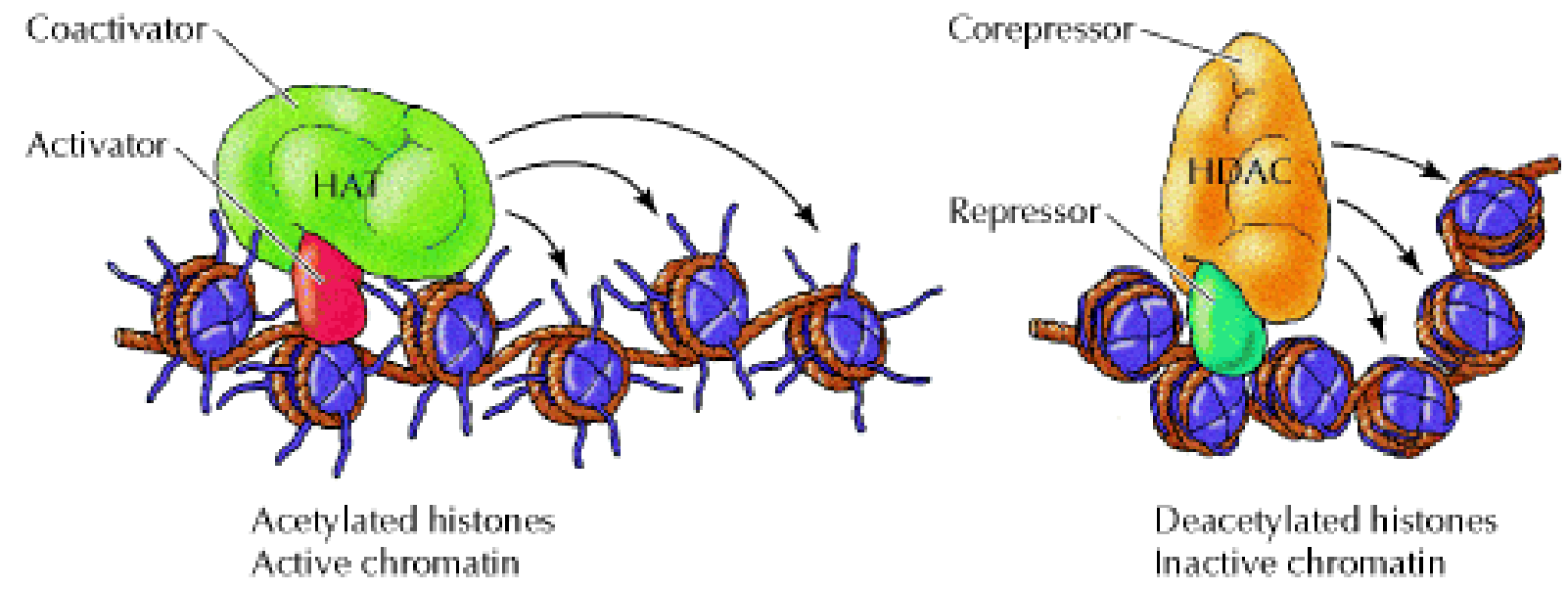
In **histone acetylation**, acetyl groups are attached to positively charged lysines in histone tails. This generally loosens chromatin structure, promoting the initiation of transcription.





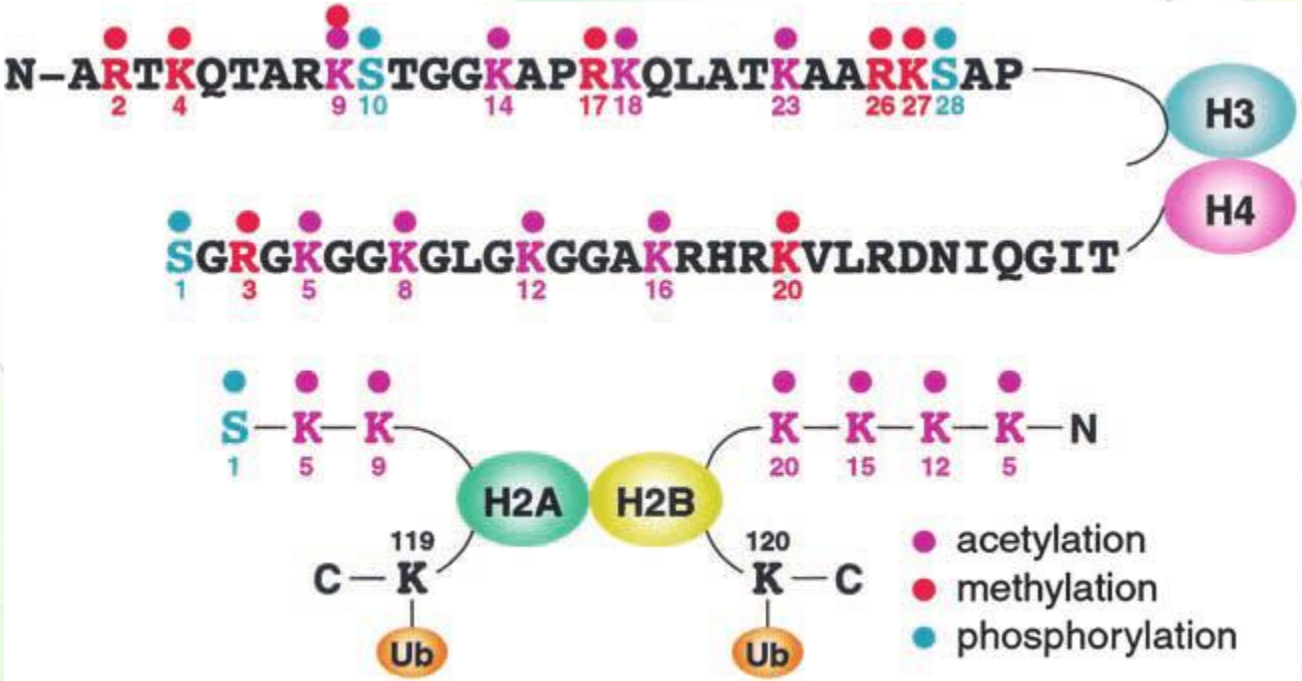
Enzymatic association

- Transcriptional activators and repressors are associated with histone acetyltransferases and deacetylases, respectively
  - TFIID associates with histone acetyltransferases.



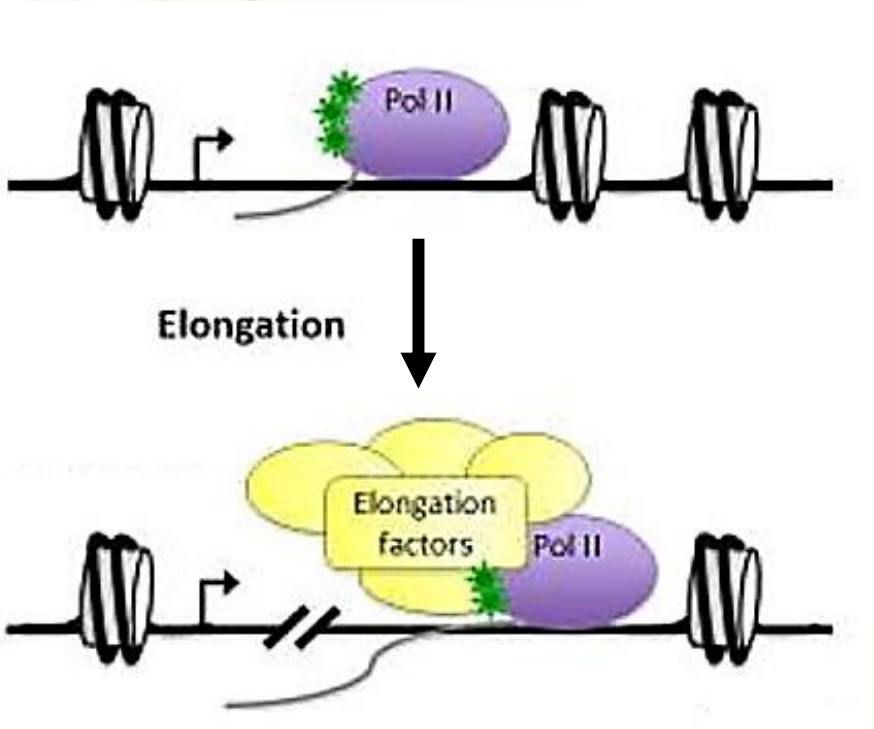
Other modifications of histones

- Histone can also be methylated or phosphorylated.
- Effect is dependent on sites of modification.



Again, the challenge of chromatin

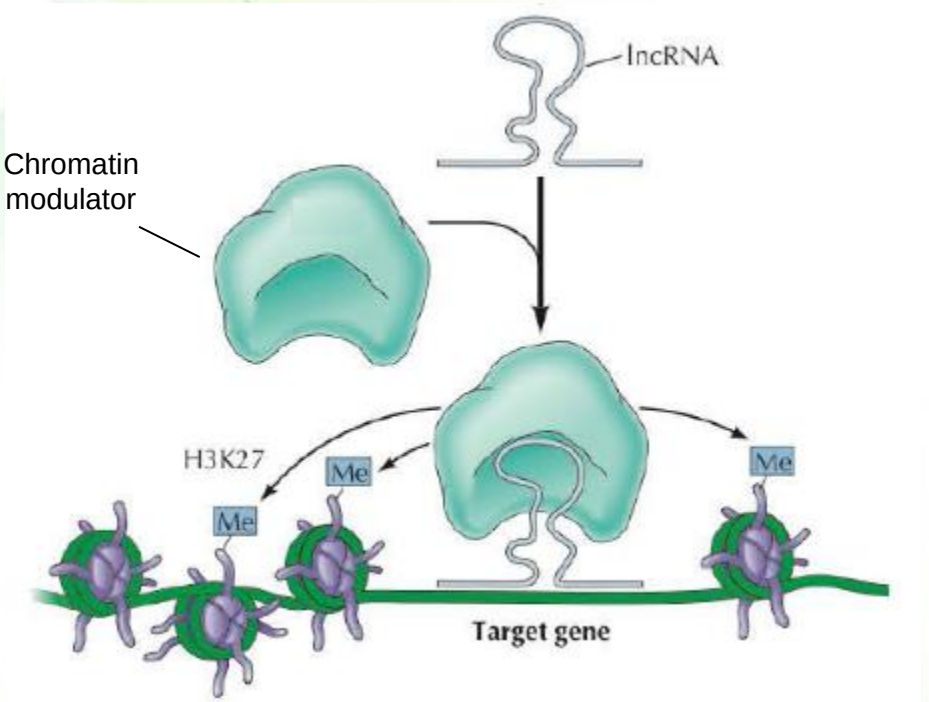
- Chromatin is still a challenge to RNA polymerase II during transcription.
- Elongation factors associate with the phosphorylated C-terminal tail of RNA polymerase II when RNA elongation is initiated.

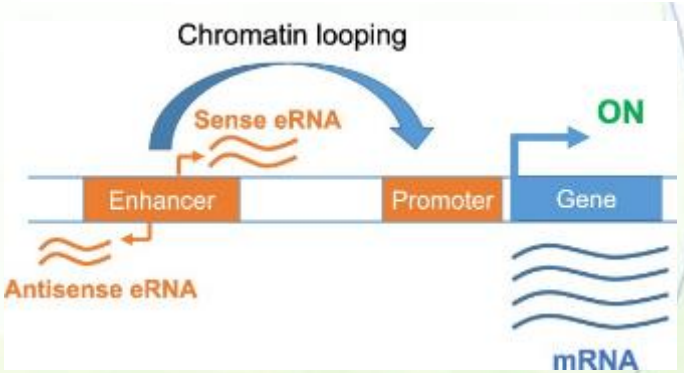


- These elongation factors include both histone modifying enzymes (e.g., histone acetylases) and chromatin remodeling factors that transiently displace nucleosomes during transcription.

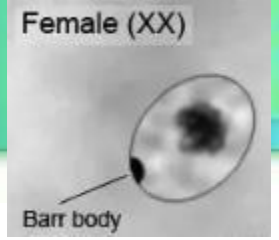
Role of noncoding RNAs

- More than 50,000 long noncoding RNAs (lncRNA), which are >200 nucleotides long, are encoded by the human genome.
- LncRNAs can be homologous to certain DNA sequences and form complexes with chromatin and DNA modifiers to repress gene expression via chromatin condensation and histone methylation.
- Other lncRNAs can complex with general or specialized transcription factors (e.g. TFIIB), mediator, or RNA processing proteins.
- Some enhancers can be transcribed into eRNA that can regulate transcription of adjacent genes.

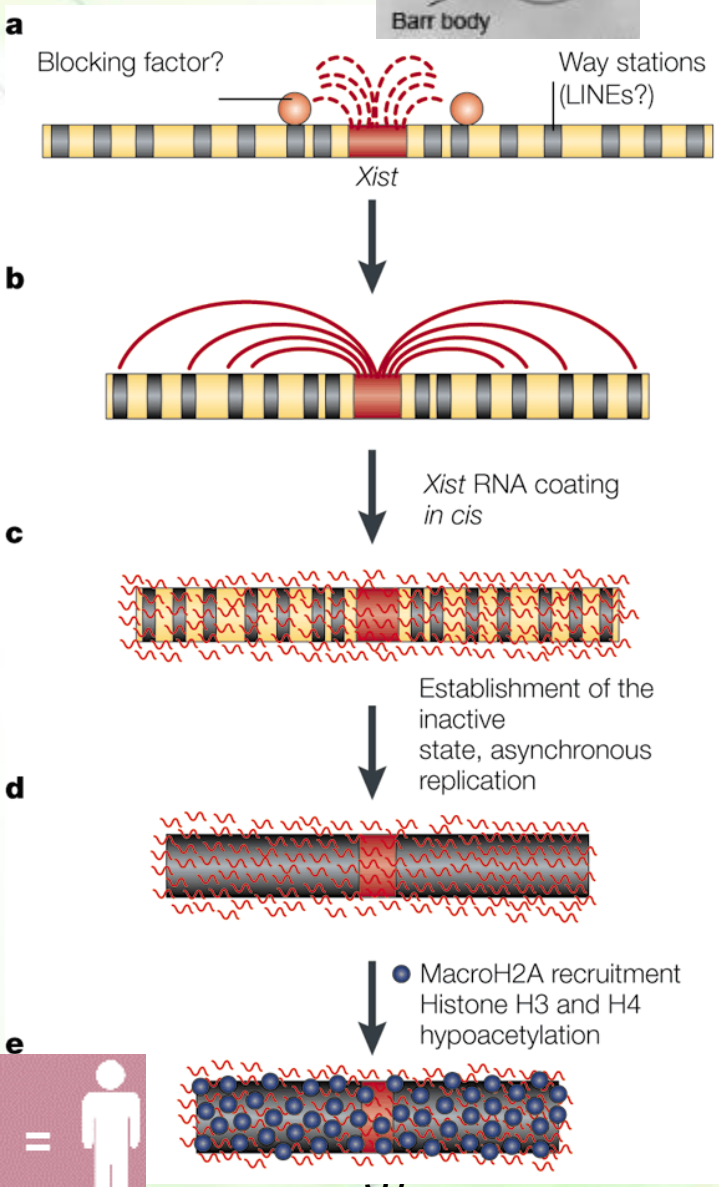


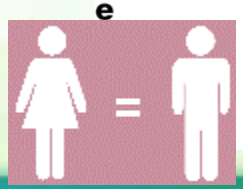


X chromosome inactivation

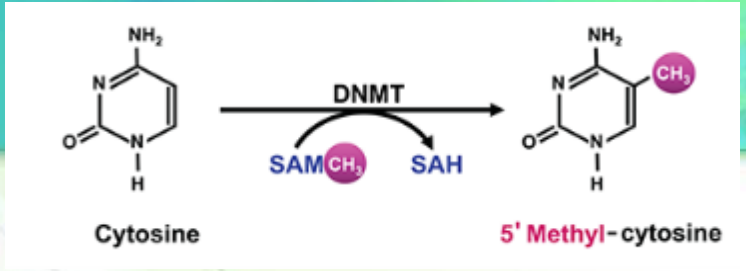


- LncRNA can act in cis or trans.
- A long noncoding RNA (lncRNA) is transcribed from *Xist* gene located on one of the two X chromosomes in females.
- The Xist RNA coats the X chromosome and promotes the recruitment of a protein complex that methylates histone 3 leading to chromosomal condensation.
- This results in X-chromosome inactivation in a phenomenon called dosage compensation to equate number (and activity) of X chromosomes between males and females.

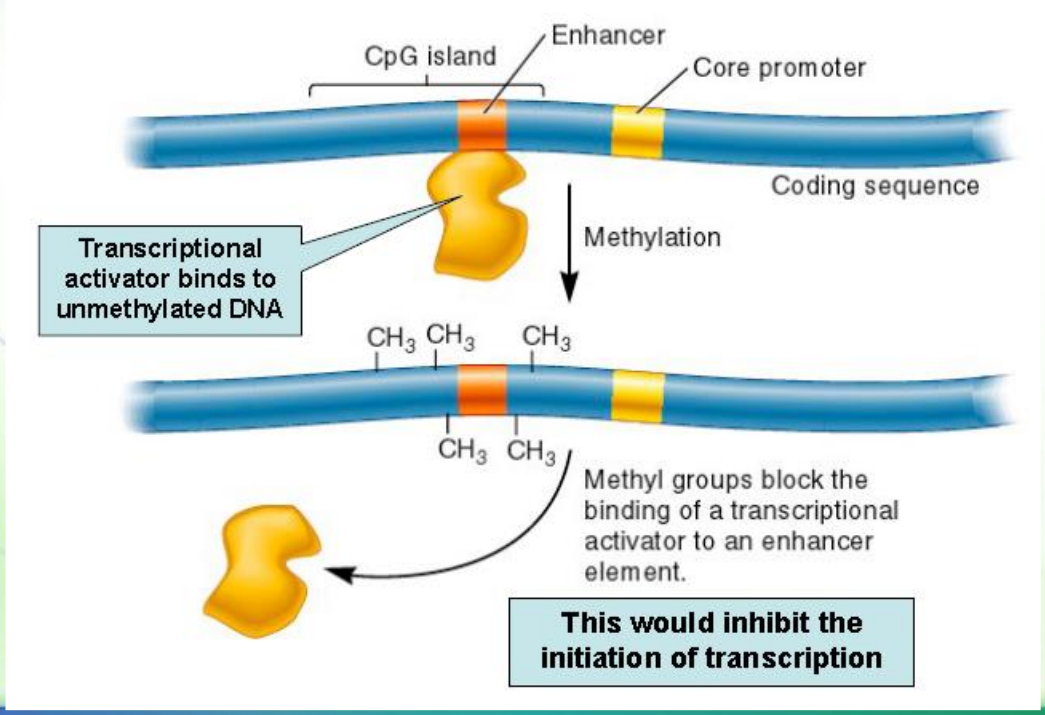




DNA methylation

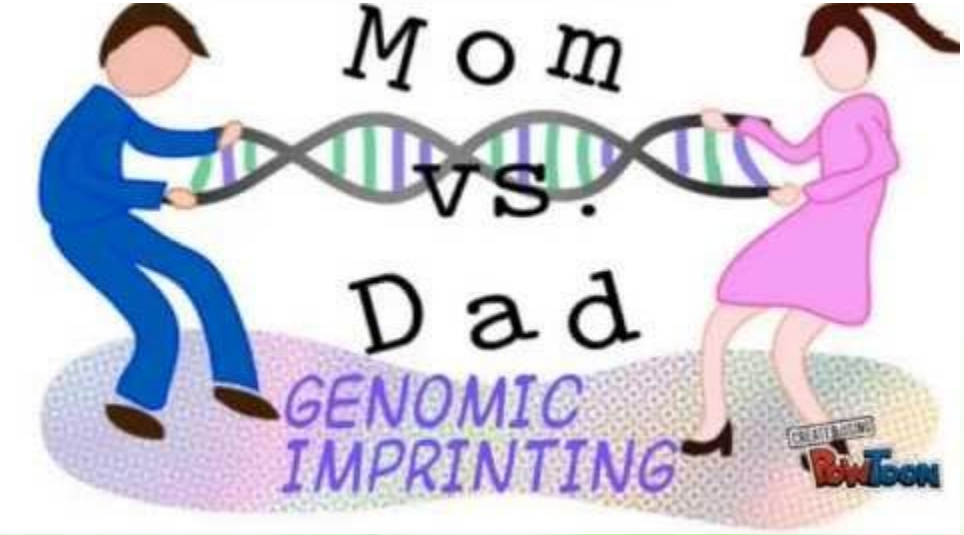


- Cytosine residues can be methylated groups at the 5’-carbon position specifically at CG sequences (called CpG isalnds near promoters).
- DNA methylation reduces gene transcription by blocking of activator binding to DNA and inducing heterochromatin formation.



Genetic imprinting

- Methylation is maintained following replication and is inherited.
- Methylation is a mechanism of genomic imprinting (either the paternal gene or the maternal gene is active).



Identical twins have the exact same genetic information

But their epigenomes become increasingly different over time

- Epigenetic changes can cause dramatic differences between twins, including many cases where one twin develops a disease and the other does not.

The power of epigenetics

- Non-sequence dependent inheritance

Epigenetics is significant and heritable

PNAS

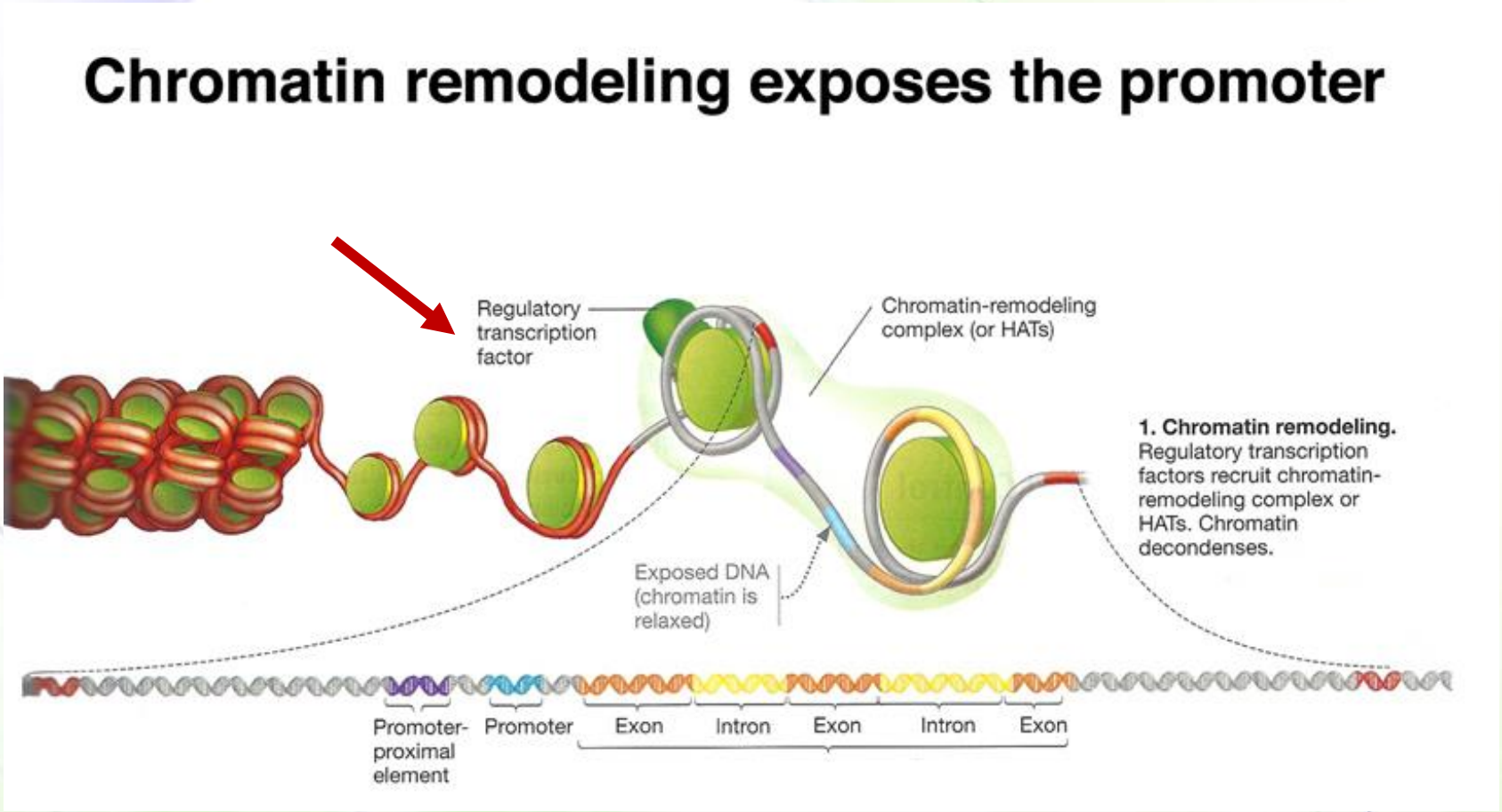
Stress-induced gene expression and behavior are controlled by DNA methylation and methyl donor availability in the dentate gyrus

Emily A. Saunderson[a,1], Helen Spiers[b], Karen R. Mifsud[a], Maria Gutierrez-Mecinas[a,2], Alexandra F. Trollope[a,3], Abeera Shaikh[a], Jonathan Mill[b,c], and Johannes M. H. M. Reul[a,4]

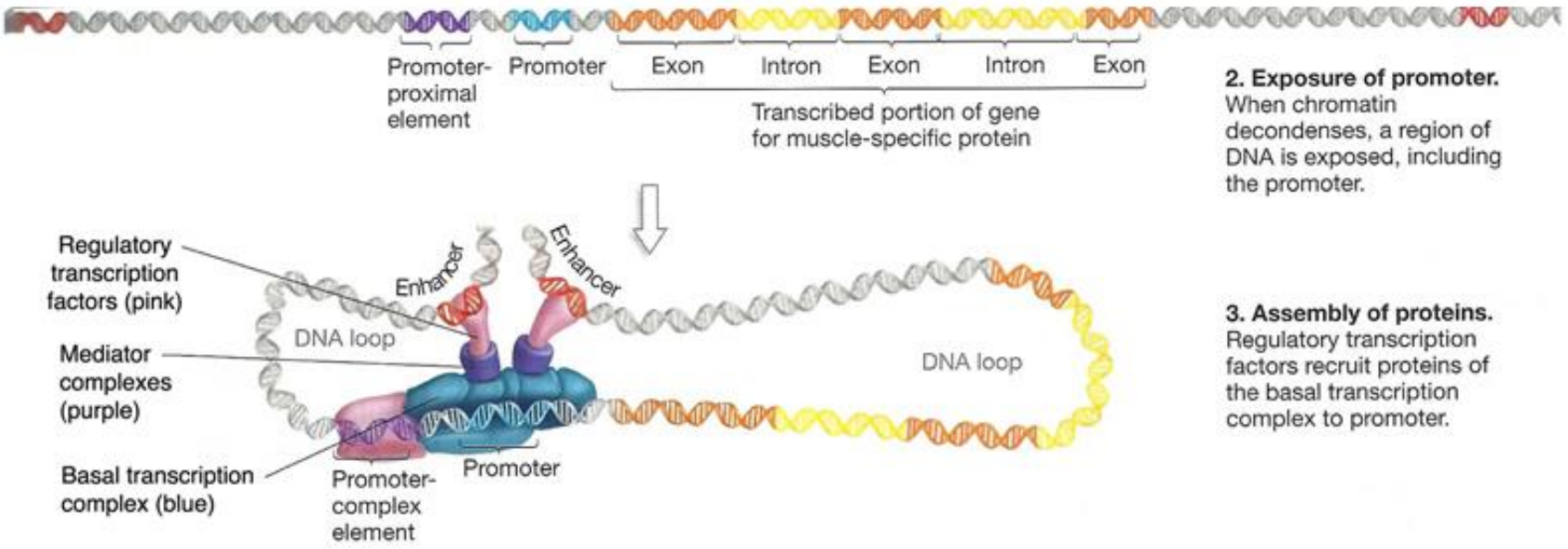
[a]Neuro-Epigenetics Research Group, University of Bristol, Bristol BS1 3NY, United Kingdom; [b]Institute of Psychiatry, King's College London, London United Kingdom; and [c]University of Exeter Medical School, University of Exeter, Exeter EX2 5DW, United Kingdom

A scenario

A little more detailed process



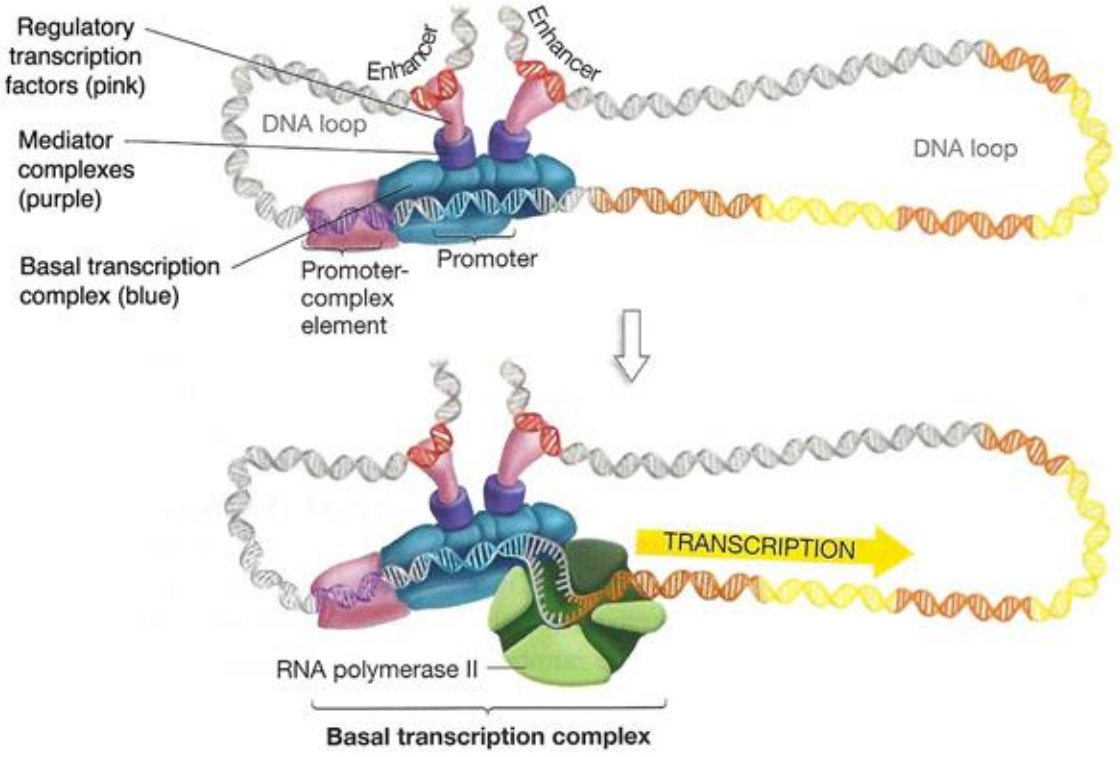
Assembly of basal transcription complex



2. Exposure of promoter. When chromatin decondenses, a region of DNA is exposed, including the promoter.

3. Assembly of proteins. Regulatory transcription factors recruit proteins of the basal transcription complex to promoter.

RNA polymerase joins transcription complex



3. Assembly of proteins. Regulatory transcription factors recruit proteins of the basal transcription complex to promoter.

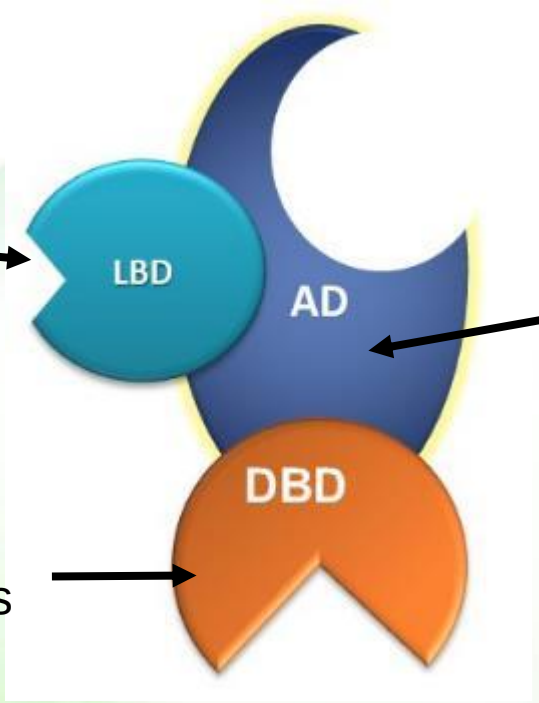
4. Attachment of RNA polymerase. RNA polymerase II completes the basal transcription complex; transcription begins.

Example

Nuclear steroid receptor

General structure of SNRs

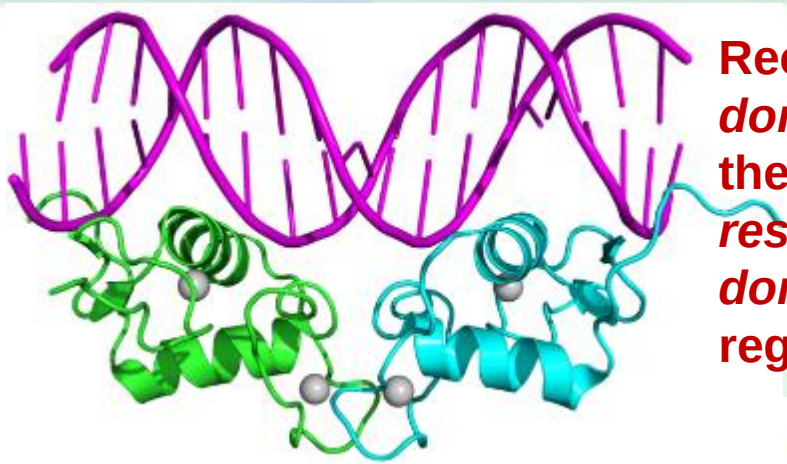
Ligand-binding domain: binds to steroid hormones



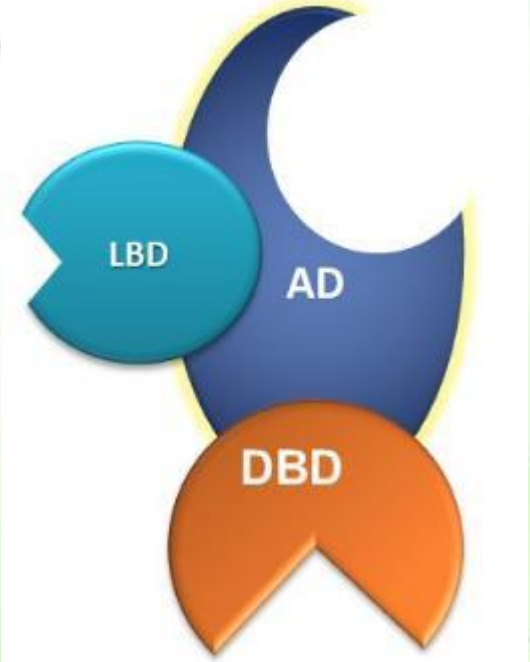
Activation domain: binds to transcriptional regulatory proteins known as co-activators and co-repressors

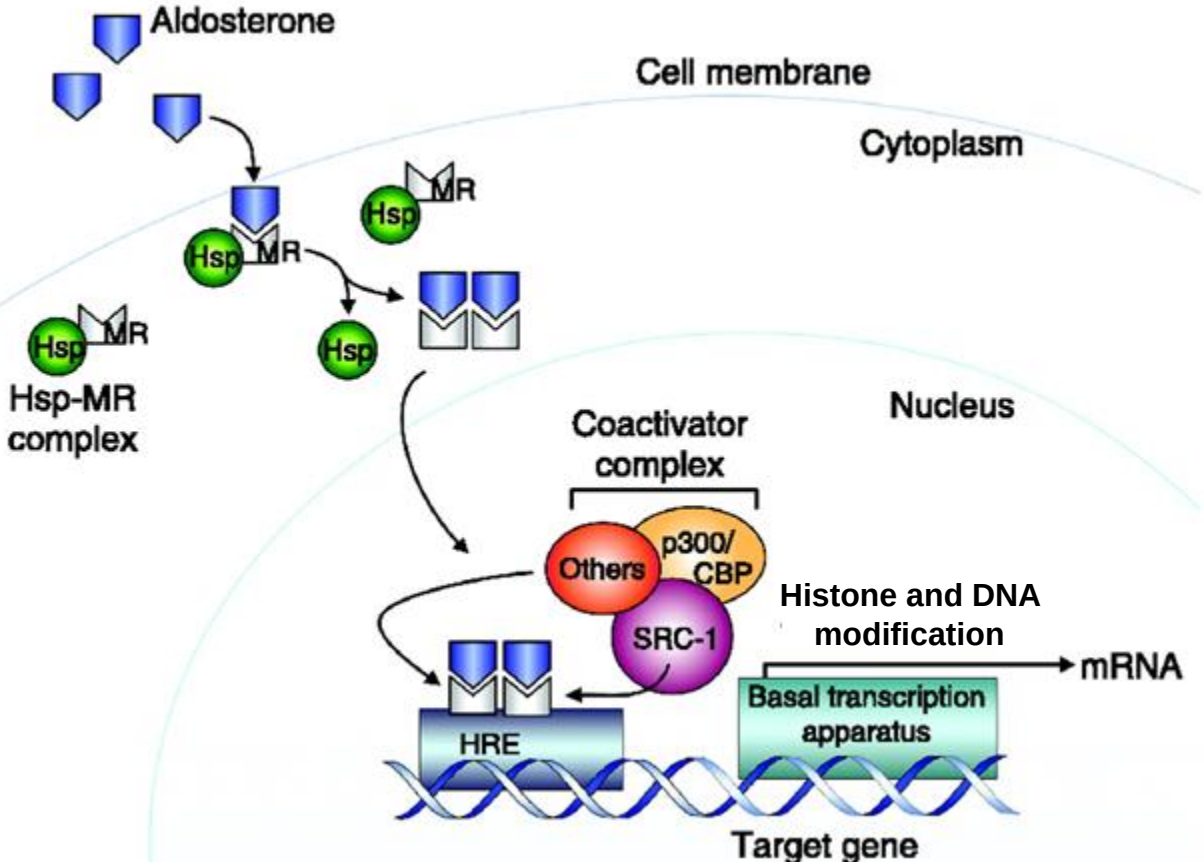
DNA-binding domain: binds to DNA elements

Steroid hormone receptors

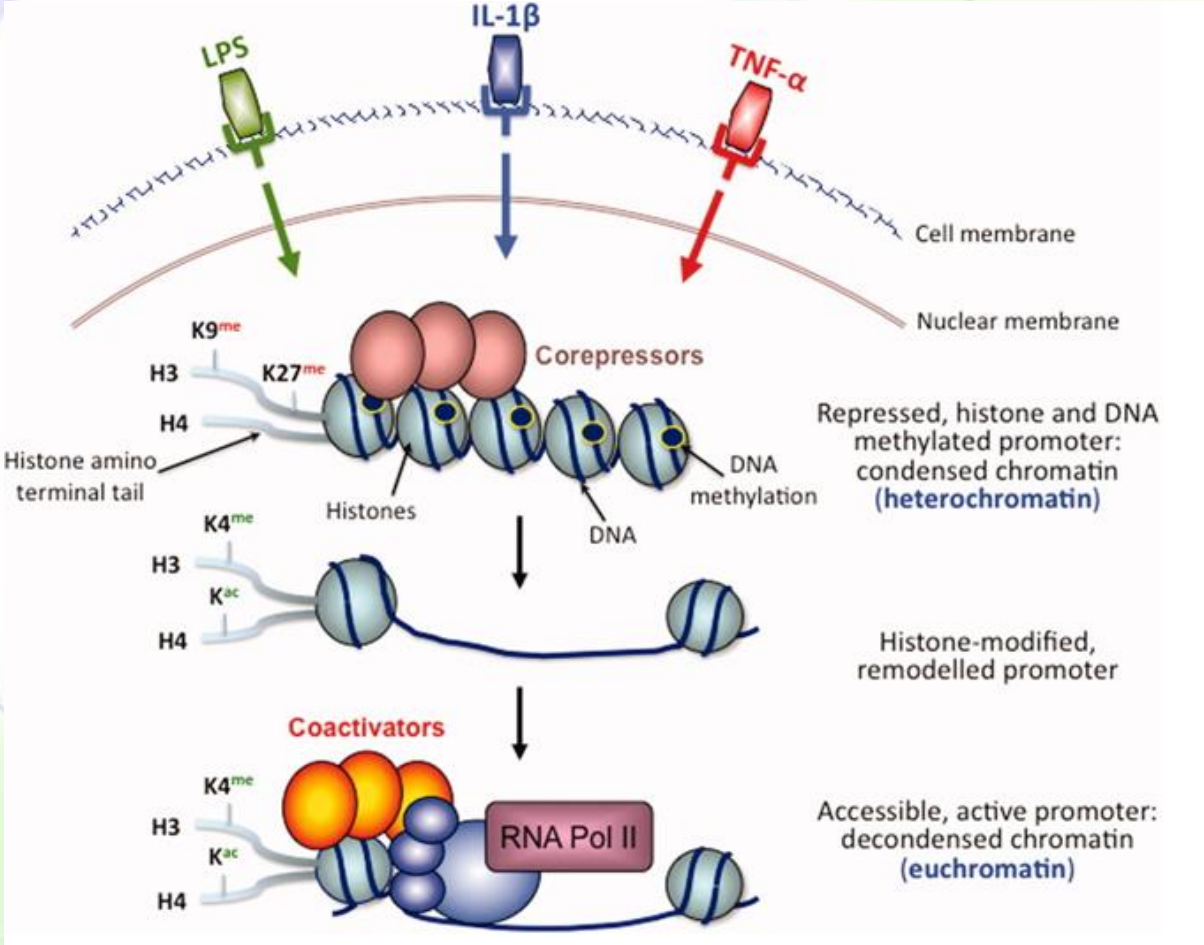


Receptors bind steroid hormones at *ligand-binding domain*, then translocate into the nucleus where they bind specific DNA sequences called *hormone response element (PPE)* via *their DNA-binding domain*, and recruit and bind transcriptional regulatory proteins using their *activation domain*.





Also, linking outside to inside



Co-repressors can also bind