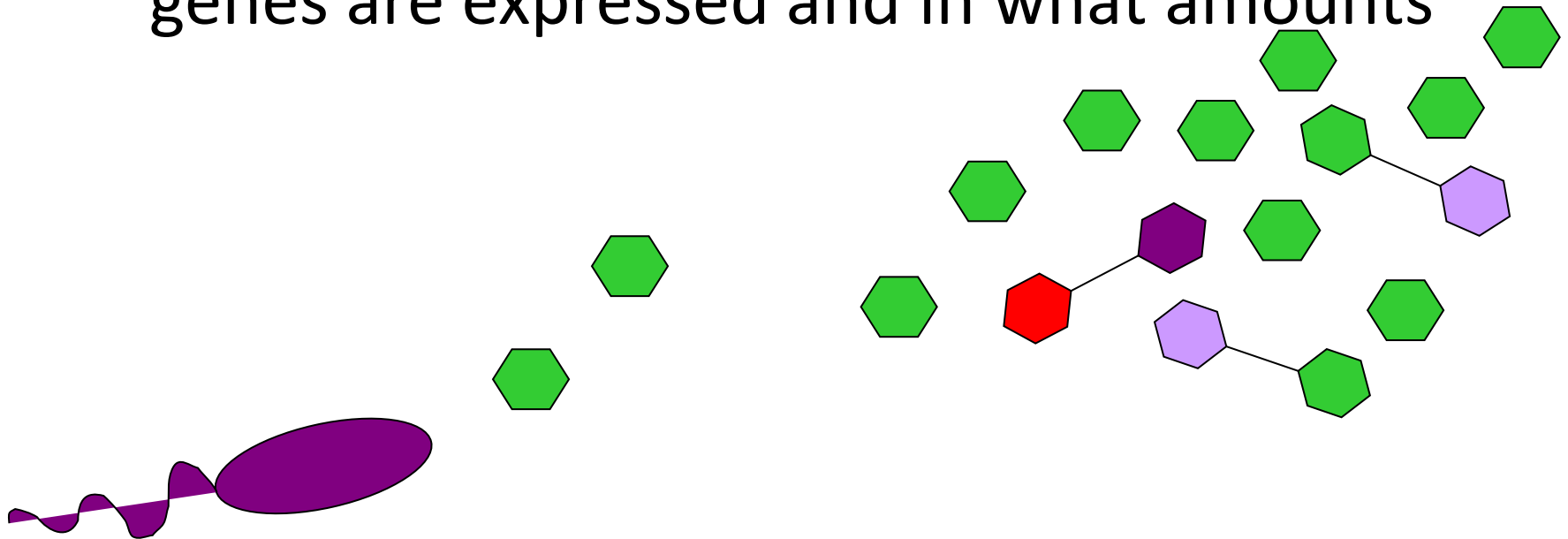


Regulation of Gene Expression in Bacteria

Transcription

- Cells are extremely selective about which genes are expressed and in what amounts



A bacterium will sense its environment and move towards nutrients

Which genes will the bacteria need to express to break down all of these sugars to make ATP. ?

Will some genes be constitutively expressed?

Will some gene expression be regulated – turned on & off?

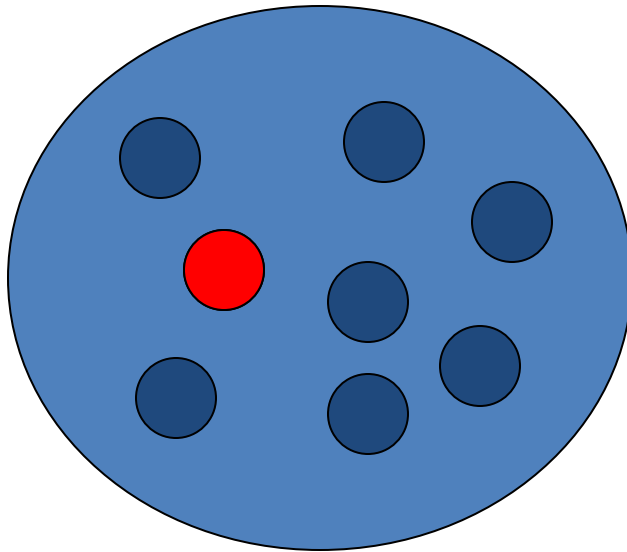
Metabolizing Lactose – A Model System

- B-galactosidase is a bacterial enzyme which is at high levels in the cell when lactose is present
- Jacques Monod & Francois Jacob hypothesized the lactose might be an inducer
 - A molecule which can stimulate gene expression

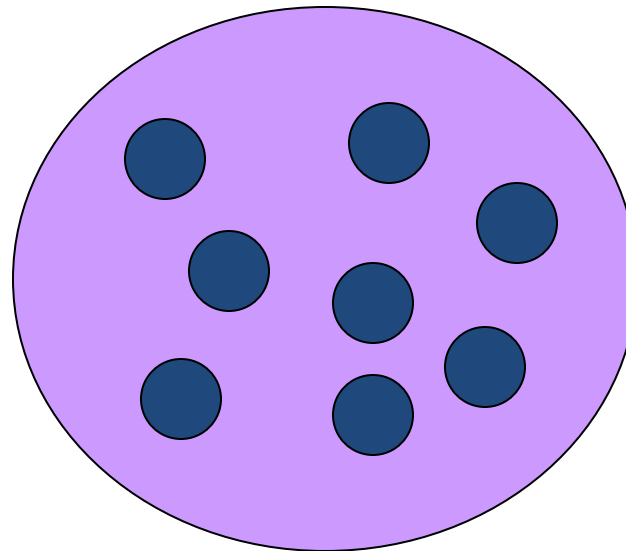
Identifying the Genes Involved

- Monod and Jacob performed a *genetic screen*
- **Step 1**
 - Generate a large pool of random mutants
 - X-rays, UV light, or chemicals
- **Step 2**
 - Screen the mutants to find individuals with defects in the biochemical pathway you are studying

Replica Plating



Master Plate - Glucose



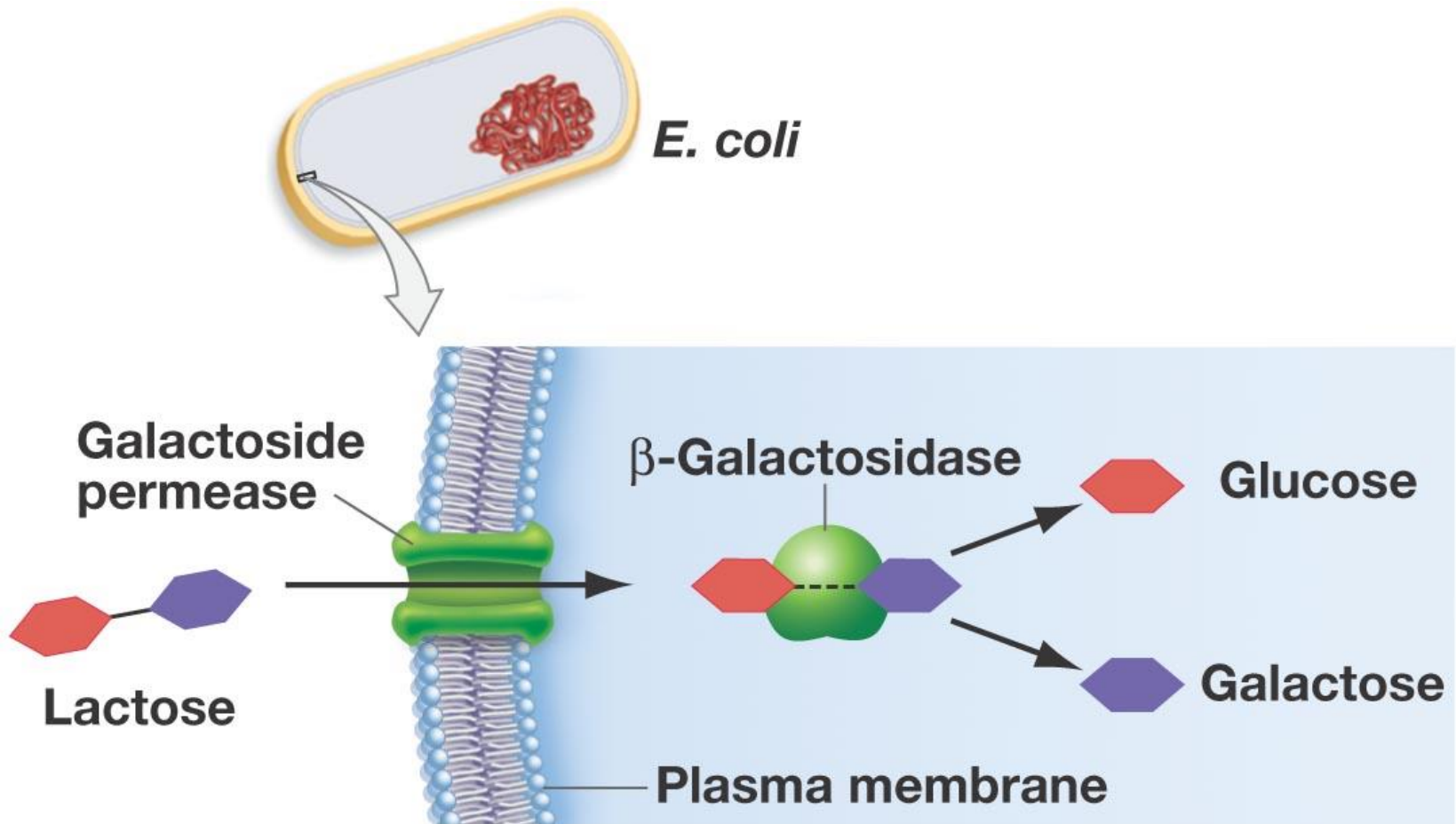
Replica Plate - Lactose

This technique ensures that the position of the bacteria is the same on both plates. When one colony does not grow on the lactose plate but does grow on the master plate then this colony has some biochemical defects in the metabolism of lactose. This colony will be isolated and characterized

Three Distinct Types of Mutants in Lactose Metabolism of *E. coli*

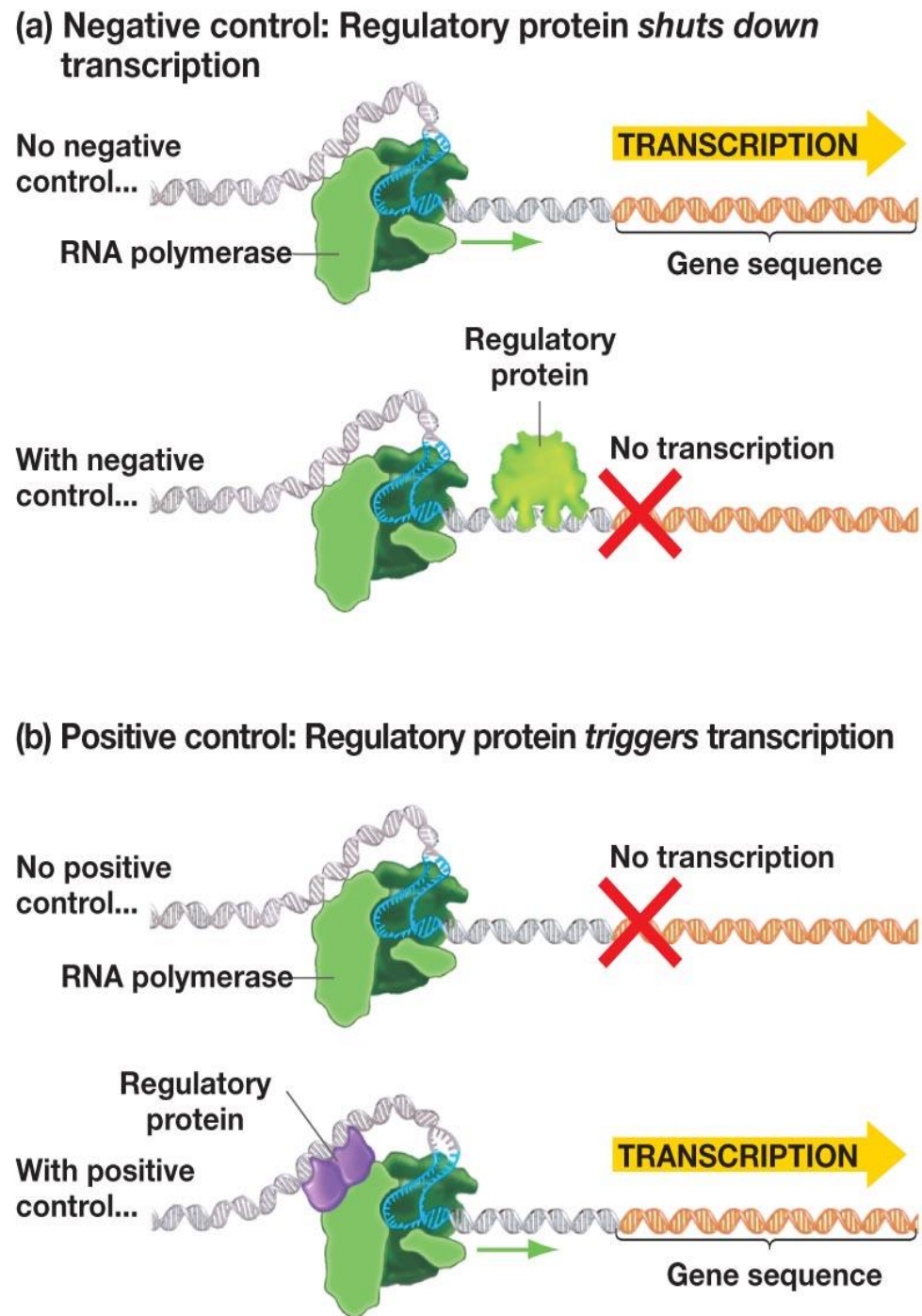
Mutant Phenotype	Interpretation	Inferred Genotype
Cells cannot cleave indicator molecule	β -galactosidase defective	<i>lacZ</i> ⁻
Lactose does not accumulate inside cells	Membrane protein for transport defective (galactoside permease)	<i>lacY</i> ⁻
Indicator molecule is cleaved even if lactose is absent	Constitutive expression of <i>lacZ</i> ⁻ and <i>lacY</i> ⁻ Regulatory gene is defective.	<i>lacI</i> ⁻

Critical Proteins for Lactose Metabolism



Transcription Regulation

- Repression
 - Transcription factors and regulatory proteins bind to DNA and block transcription
- Induction
 - Transcription factors and regulatory proteins bind to DNA and allow transcription



The *lac* Operon

- Jacob and Monod summarized their results in 1961 with a comprehensive model of negative control
- They coined the term ***operon*** for a set of coordinately regulated bacterial genes that are transcribed together into one mRNA

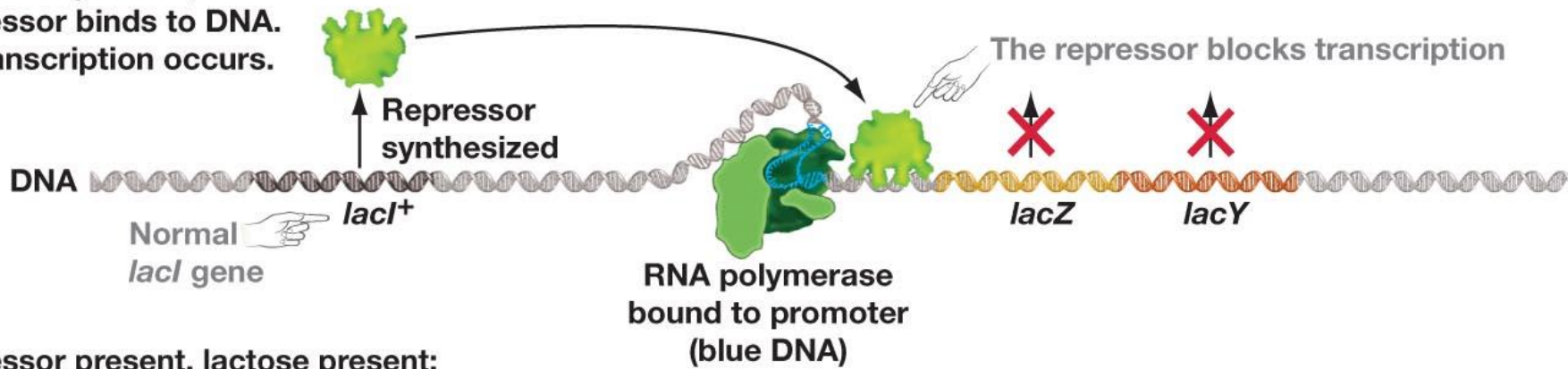


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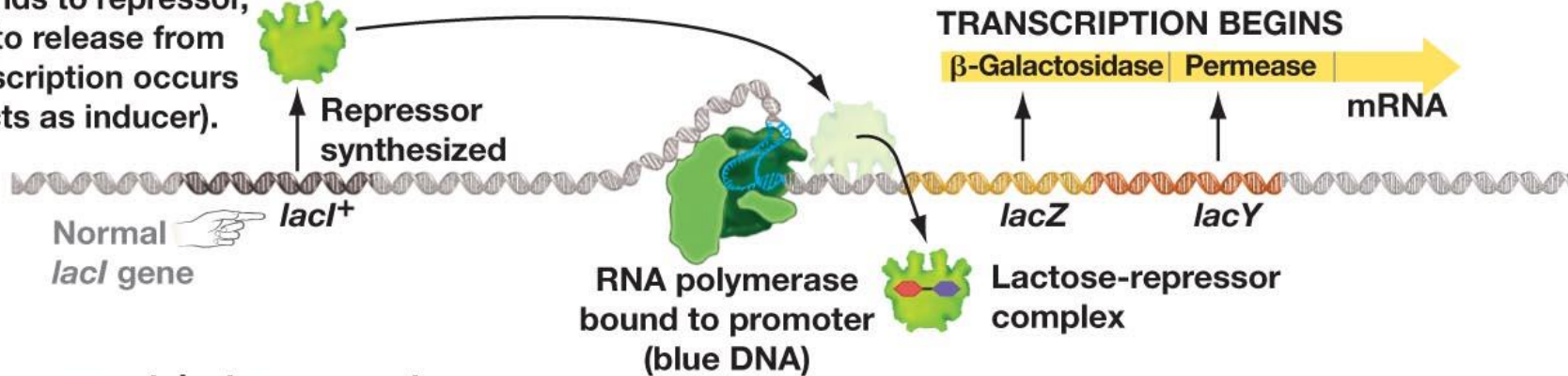
Polycistronic mRNA



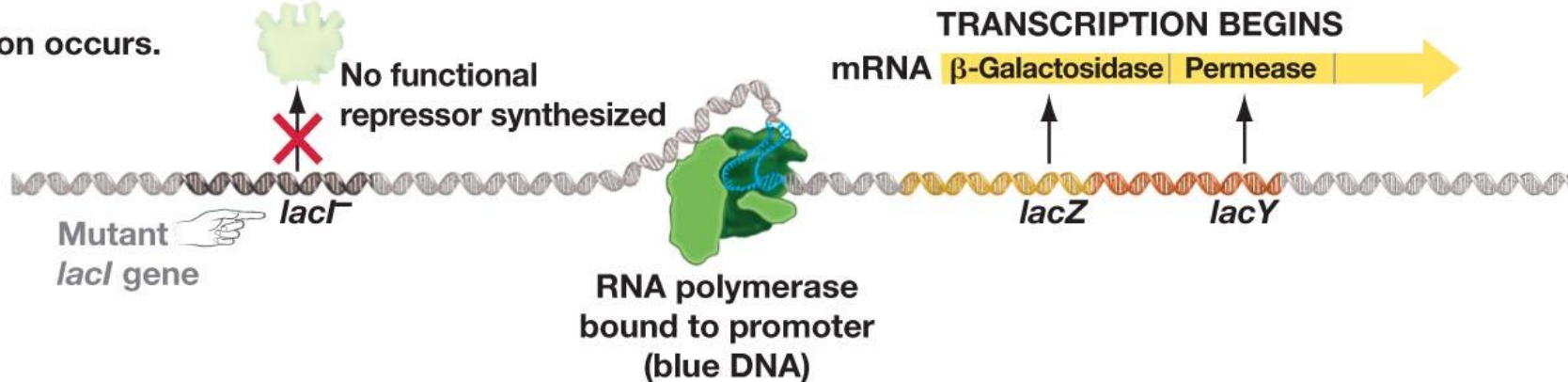
(a) Repressor present, lactose absent:
Repressor binds to DNA.
No transcription occurs.



(b) Repressor present, lactose present:
Lactose binds to repressor,
causing it to release from
DNA. Transcription occurs
(lactose acts as inducer).



(c) No repressor present, lactose present
or absent:
Transcription occurs.

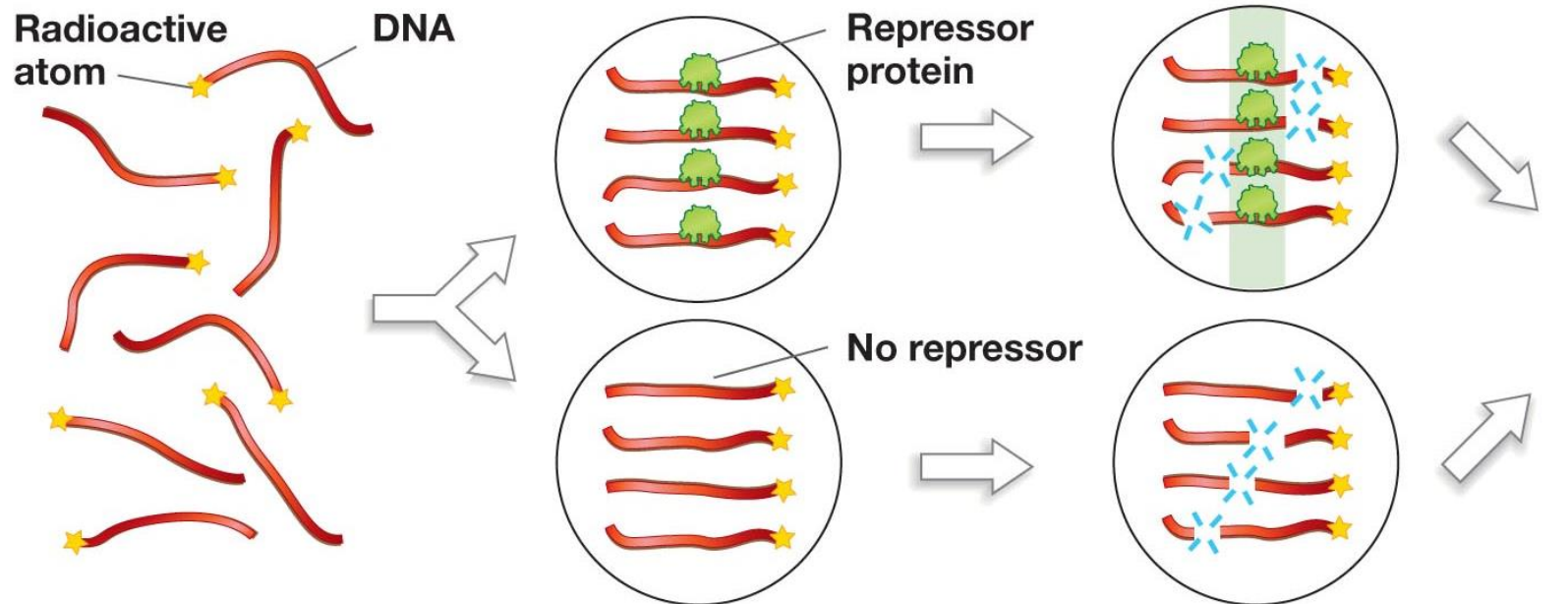


The Jacob-Monod Model

- *lacZ*, *lacY*, and *lacA* genes are adjacent and are transcribed into one mRNA initiated from a single promoter
 - Coordinated gene expression
- Repressor protein is encoded by *lacI*, binds to operator and prevents transcription of *lacZ*, *lacY* and *lacA*
 - *lacI* is expressed constitutively
- Lactose is the inducer and binds to repressor
 - Allosteric regulation of repressor

DNA Footprinting

In 1967, six years after the Jacob and Monod paper Walter Gilbert confirmed the hypothesis of Jacob and Monod by fully characterizing the operator



1. Generate fragments from the DNA region of interest, such as the *lac* operon of *E. coli*. Attach a label to end of fragments.

2. Divide fragments into two samples. Add repressor protein to one sample. The repressor will bind to the operator.

3. Cut fragments with nuclease to produce fragments of different lengths. Repressor protects operator DNA from nuclease cleavage.

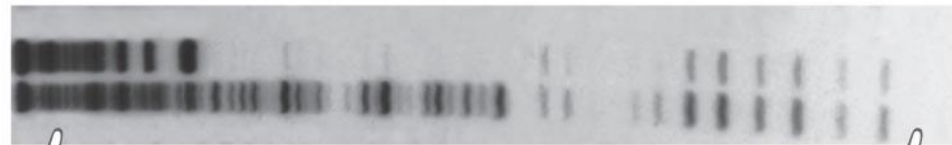
DNA Footprinting

- These experiments showed that the repressor interacted physically with the DNA sequences of the operator
- The operator was not a protein or a mRNA molecule

DNA FOOTPRINTING

"Footprint"

No cuts occurred in the DNA region protected by the repressor.
This region must be the operator.



Largest fragments
(cut far from label)

Smallest fragments
(cut close to label)

4. Load fragments into two lanes in a gel. Sort by size via electrophoresis. (The fragments with a label will be visible.)

A DNA sequencing reaction can be used to determine the sequence of the "footprint."

Importance of *lac* operon

- Confirmed the presence of regulatory sequences of DNA
- Confirmed the presence of regulatory DNA binding proteins
- Post translational modification (binding of lactose to an existing protein)-the activity of existing protein is altered as the environment changes.

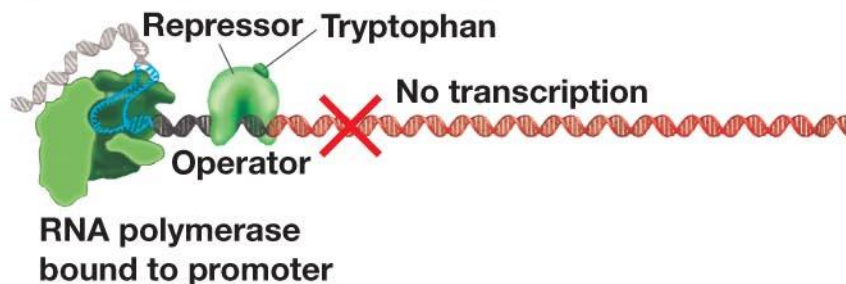
Other Operons

- The *lac* operon system is an ***inducible system***
 - This means that the genes under control of this promoter are always “OFF” and must be regulated “ON”
 - Many other genes in *E. coli* are regulated by an inducible system
- However further work has shown that ***repressible systems*** also exist in *E. coli*
 - This means that the genes under control of this promoter are always “ON” and must be regulated “OFF”

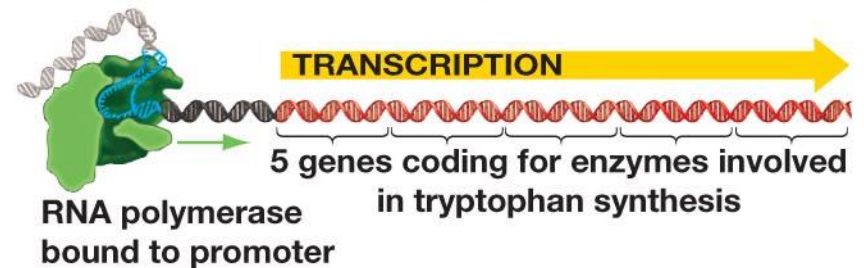
trp Operon

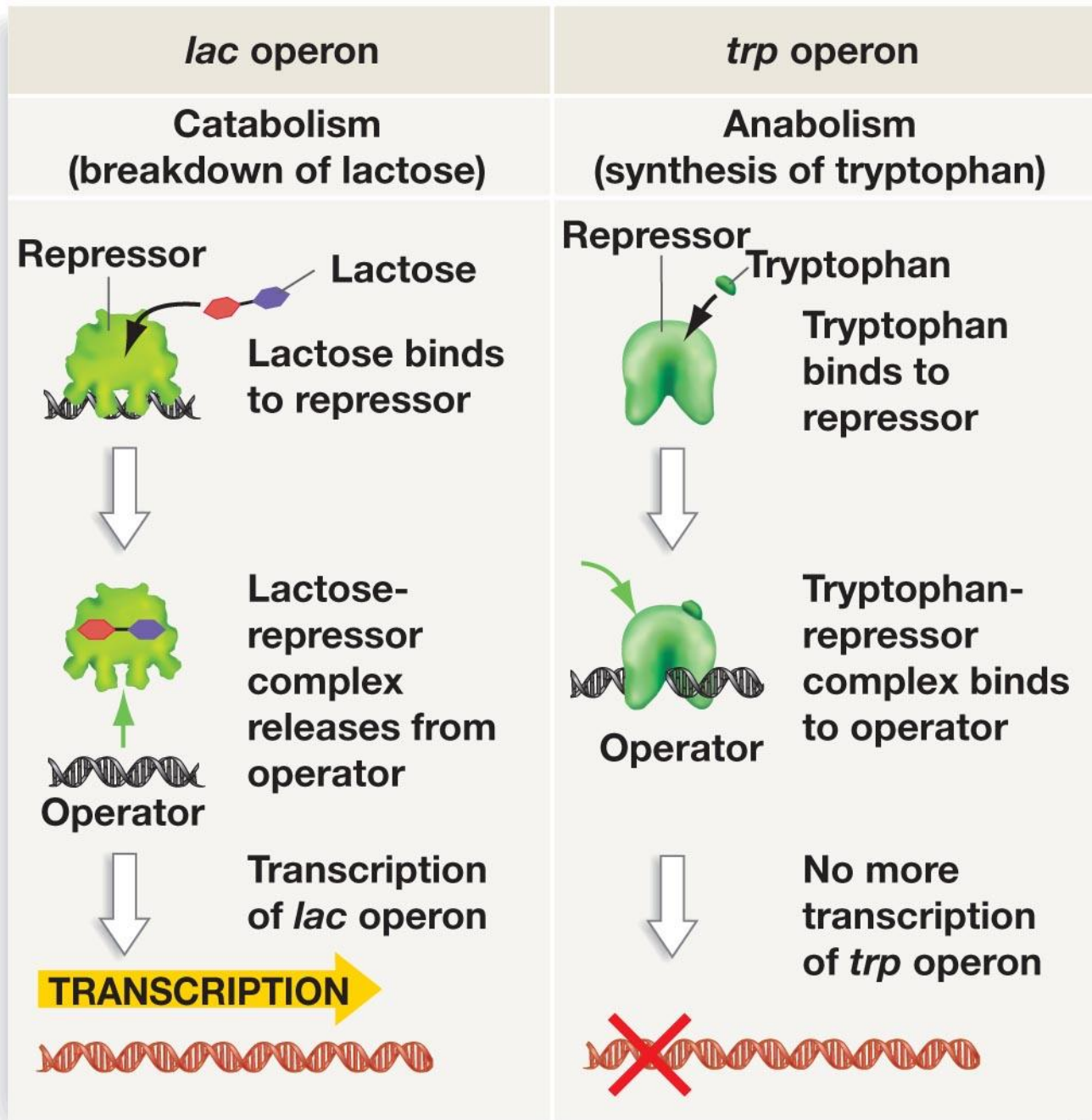
- The *trp* operon codes for an enzymes needed for the synthesis of tryptophan
- This is an anabolic pathway as opposed to the catabolic pathway for the *lac* operon
- Bacterial cells should have the *trp* operon “ON” in the absence of tryptophan and “OFF” in the presence of tryptophan

(a) When tryptophan is present, transcription is blocked.



(b) When tryptophan is absent, transcription occurs.





Catabolite Repression

- Glucose is the preferred fuel source for bacterial cells
- In the presence of both glucose and lactose very little β -galactosidase is present
- How can this result be explained?
 - Lactose is present so the repressor is not bound to the operator transcription should occur?

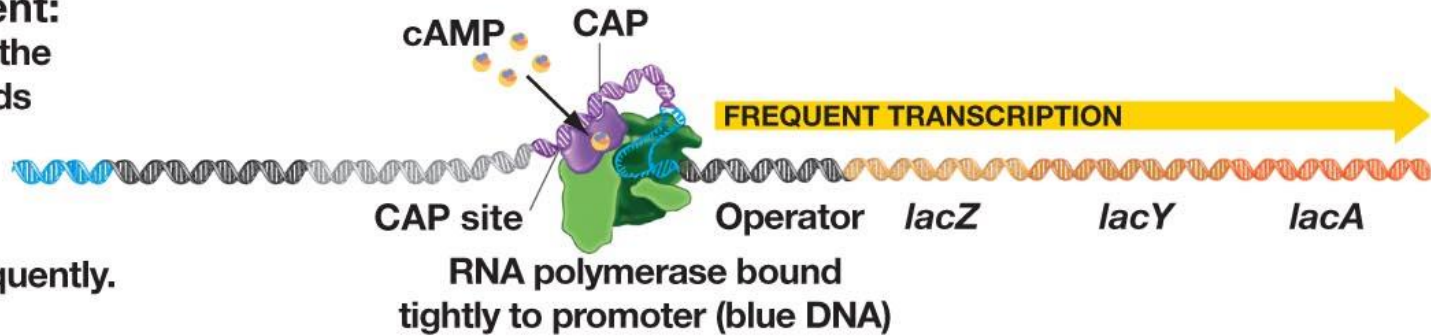
Promoter Strength

- Not all promoters are created equal
- Strong promoters
 - RNA polymerase and sigma strongly bind to promoter and initiate transcription without additional factors
- Weak promoters
 - Additional factors are necessary to for the promoter to strongly bind to RNA polymerase

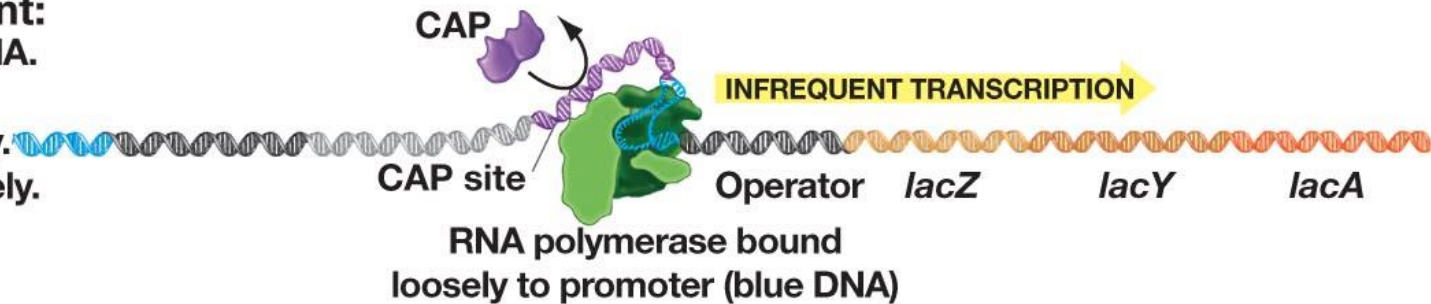
lac Promoter

- *lac* promoter is a weak promoter
 - *lac* promoter has an additional regulatory DNA sequence known as the CAP binding site
 - Catabolite activator protein
- CAP binding greatly **increases the strength** of the *lac* promoter
 - CAP can only bind when its allosteric molecule cAMP is present
- How this all works ???????

(a) When cAMP is present:
cAMP binds to CAP and the
cAMP-CAP complex binds
to DNA at the CAP site.
RNA polymerase binds
the promoter efficiently.
Transcription occurs frequently.



(b) When cAMP is absent:
CAP does not bind to DNA.
RNA polymerase binds
the promoter inefficiently.
Transcription occurs rarely.

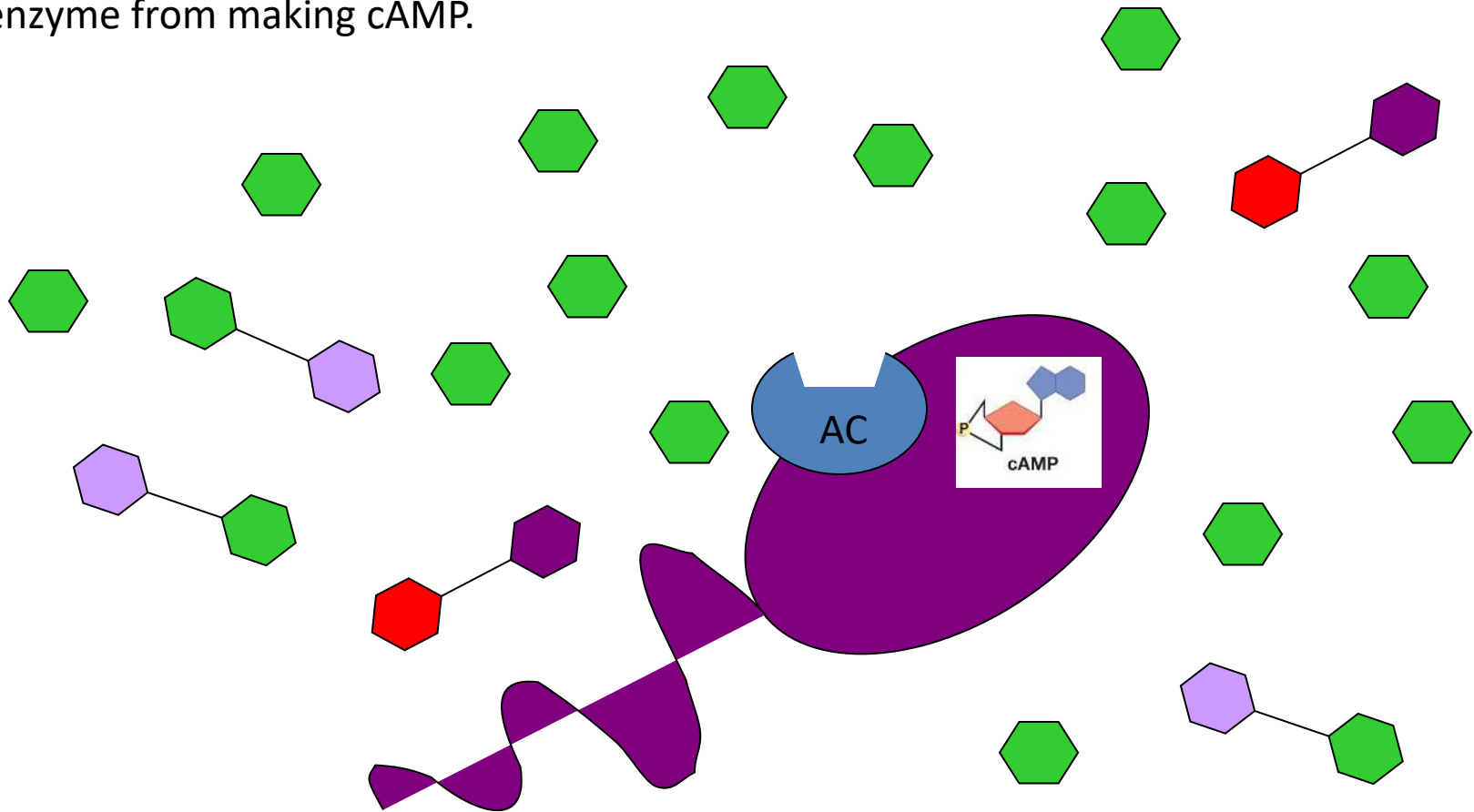


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But how does a bacteria cell decide when to make cAMP?

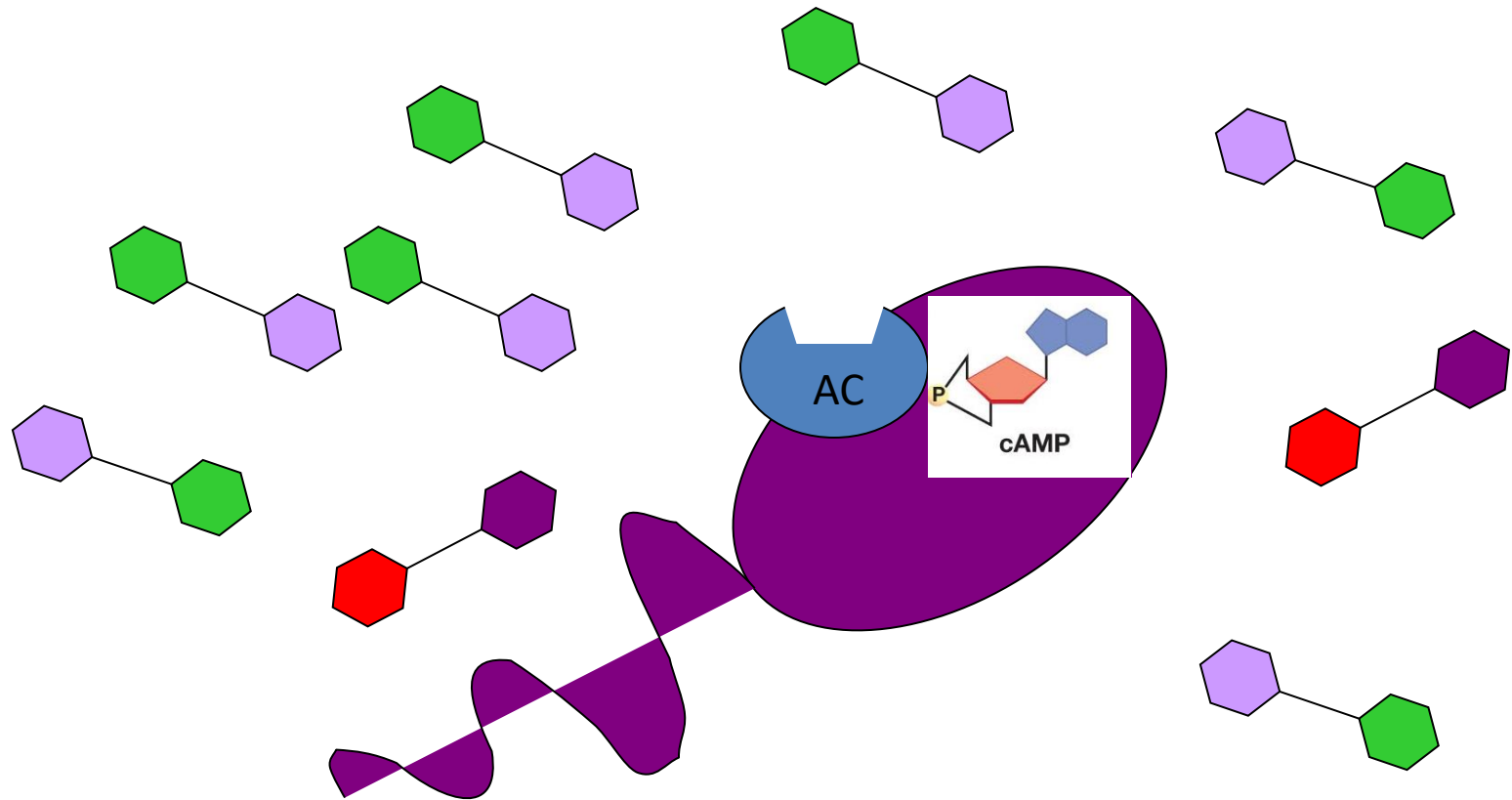
Blocking Production of cAMP

In the original example the bacteria has many sugars to choose from. Glucose is known to be the fuel source of choice. Under these conditions glucose levels outside the cell will bind to **adenylyl cyclase** and inhibit this enzyme from making cAMP.

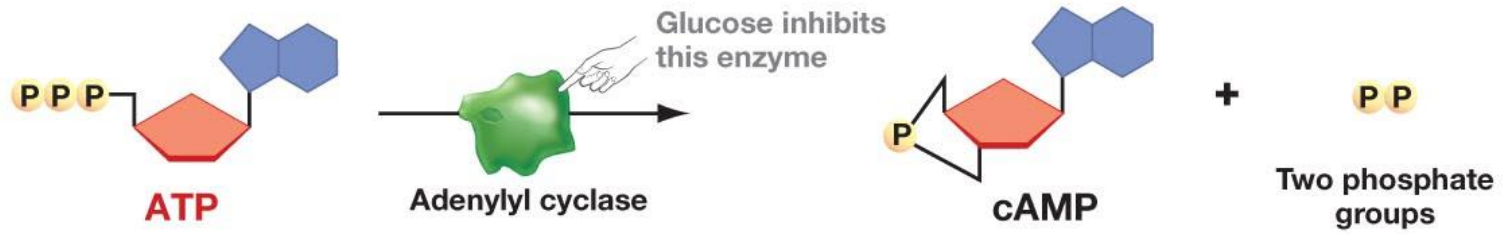


Production of cAMP

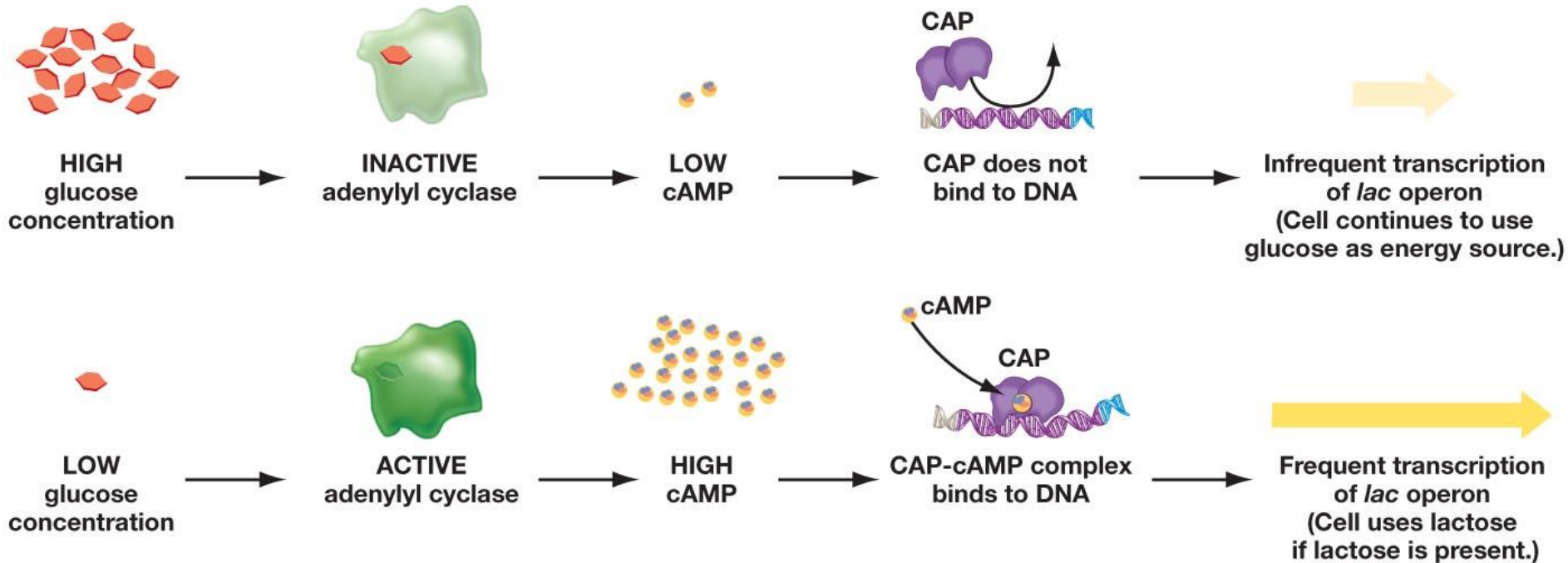
However, if environmental conditions change then no glucose will bind to adenylyl cyclase. Therefore, cAMP levels will increase and if lactose is present the lac operon will be turned “ON”. However, if no lactose is present the repressor will still be bound to the operator and no transcription will occur.



(a) Glucose inhibits the activity of the enzyme adenylyl cyclase, which catalyzes production of cAMP from ATP.

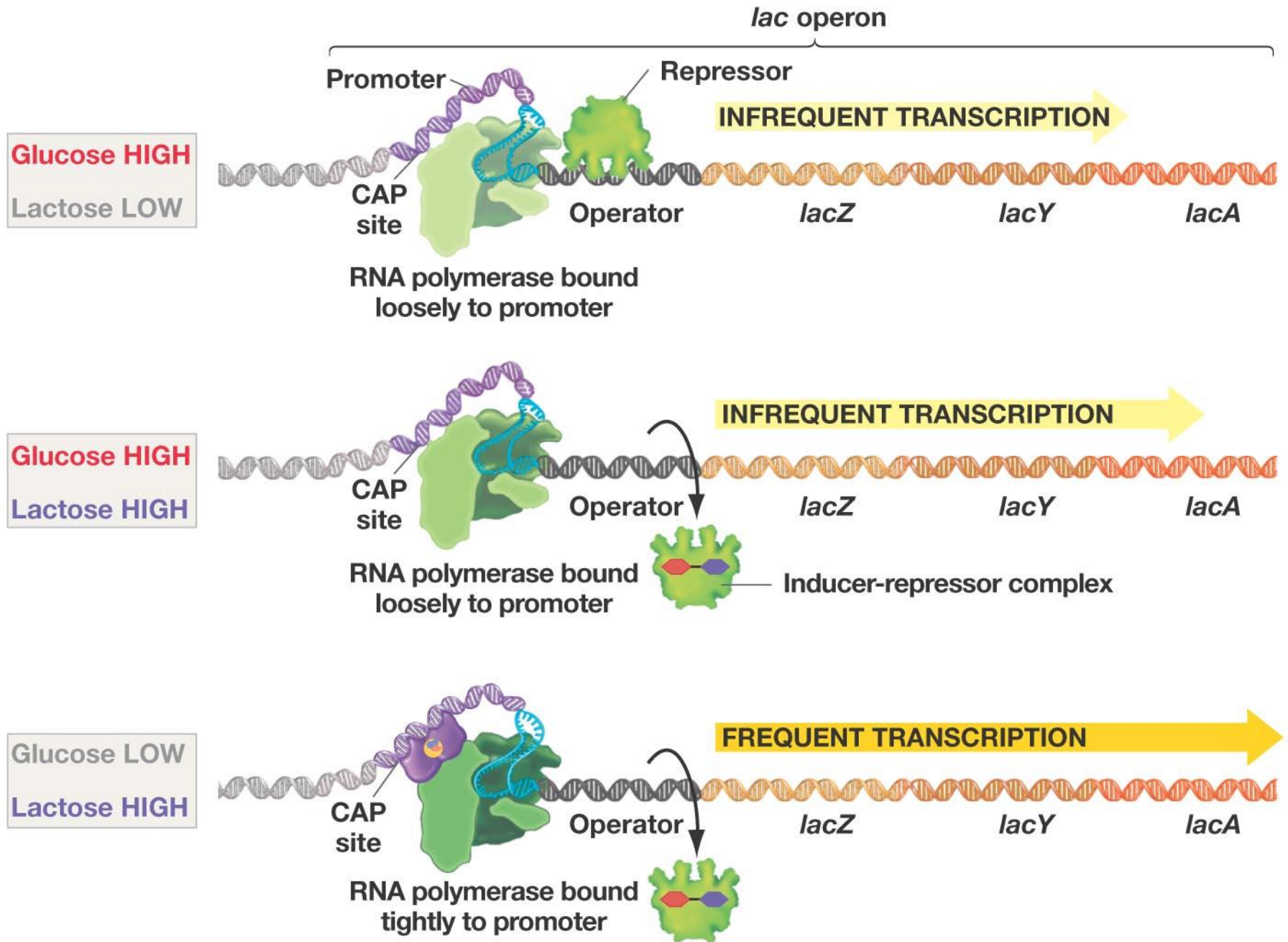


(b) The amount of cAMP and the rate of transcription of the *lac* operon are inversely related to the concentration of glucose.



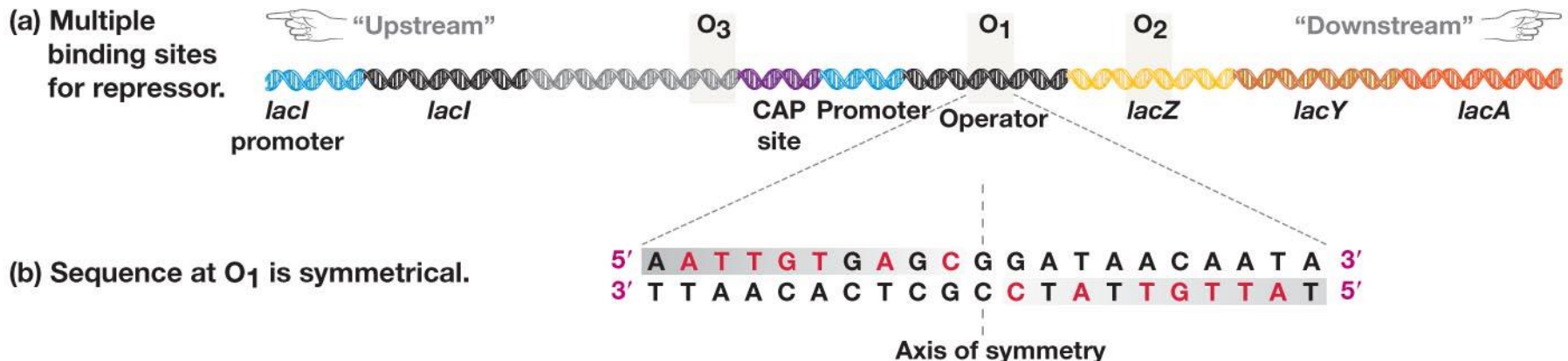
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CAP-cAMP system influences many genes in addition to the *lac* operon. Cap sites are found adjacent to the promoters for several operons that are required for the metabolism of sugars other than glucose



Characterization of the Operator

- The sequences of many DNA regulatory elements have **dyad symmetry**
- These sequences are now known to interact with specific amino acid sequences in the DNA binding protein



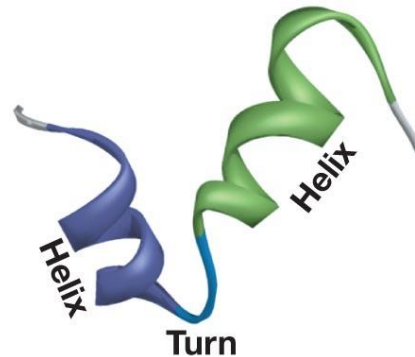
Characterization of DNA Binding Proteins

- Most DNA binding proteins have distinct domains which are characterized by specific motifs
 - Each domain has a specific job
 - Bind to DNA
 - Bind to inducer
 - Each motif is a specific 3D structure
 - Helix turn helix
 - Leucine zipper
 - Barrel motif

Helix Turn Helix

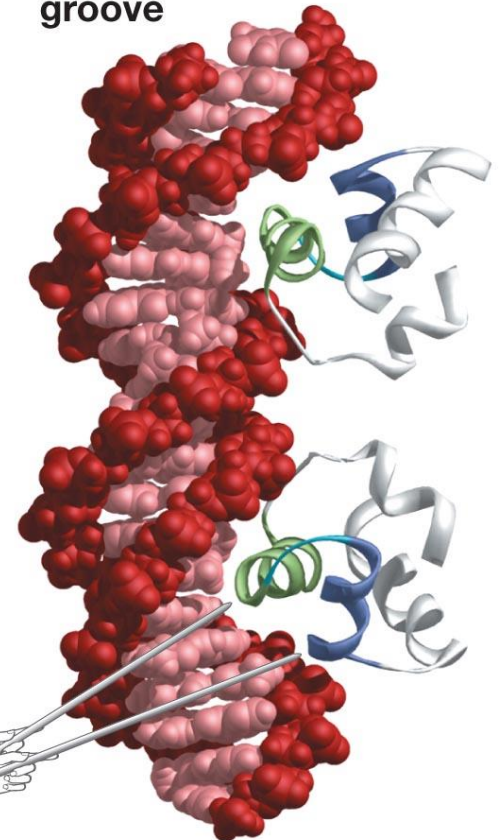
- One helix interacts with sugar phosphate backbone
- One helix interacts with base pairs in the major groove
 - Recognition sequence

(a) Helix-turn-helix motif in DNA-binding protein



(b) Recognition sequence of helix-turn-helix motif binds to DNA sequences in major groove

Interactions between amino acids in helix-turn-helix and bases in DNA



Recognition Sequence

- The amino acid sequences of recognition sequences vary
- Each regulatory protein has a unique recognition sequence and a unique regulatory sequence of DNA
- As with many DNA regulatory proteins, binding of the allosteric molecule causes a conformational change in structure
 - Cause the protein to bind
 - Cause the protein to fall off

(b) Interaction of inducer and repressor

