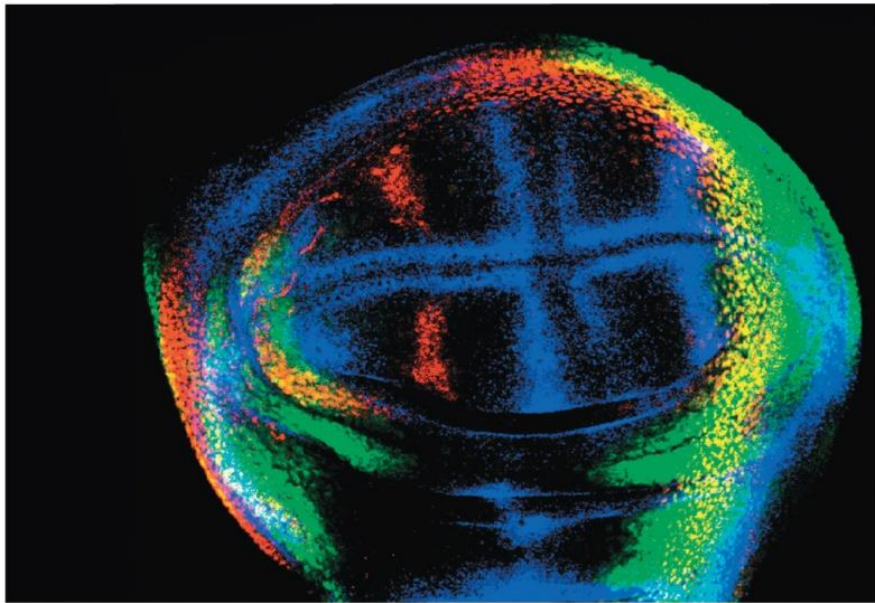


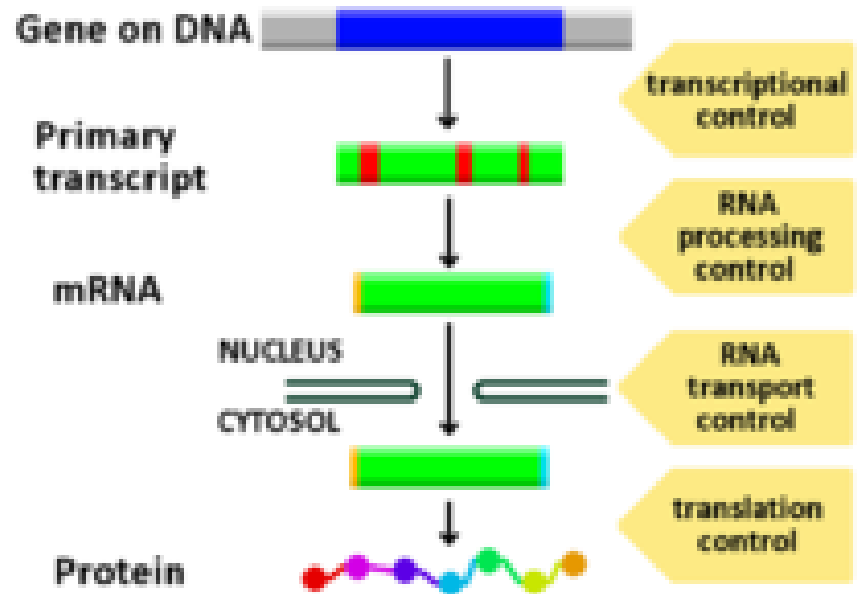
NOTES: CH 18 – part 1

Regulation of Gene Expression:

Prokaryotes vs. Eukaryotes



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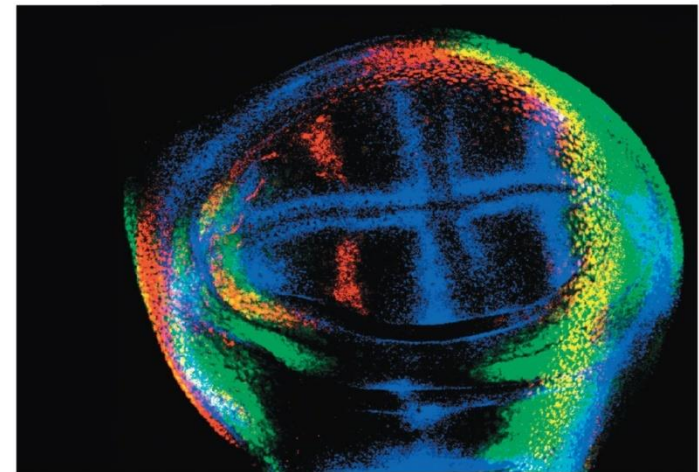


Regulation of Gene Expression:

- Both prokaryotes & eukaryotes must alter their patterns of gene expression in response to changes in environmental conditions;
- Multicellular eukaryotes must also develop and maintain multiple cell types
 - each cell type contains the **same genome** but expresses a **different subset of genes**...*how is this accomplished??*

Regulation of Gene Expression:

- Gene expression in both eukaryotes & prokaryotes is often regulated at the stage of TRANSCRIPTION (DNA → mRNA)
- we now know that RNA molecules play many roles in regulating gene expression

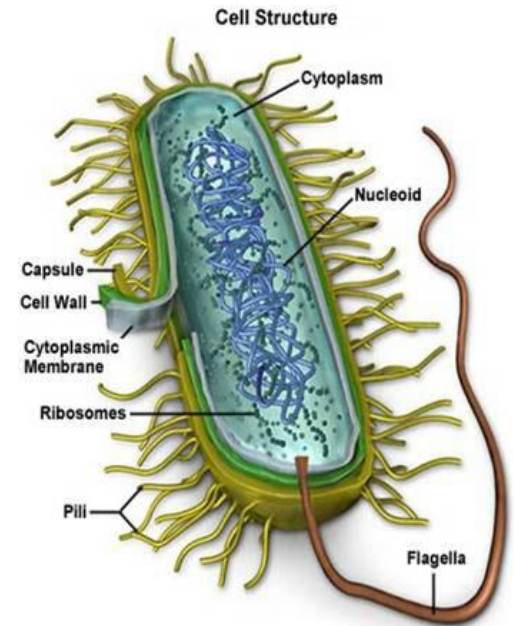


18.1: BACTERIA

- bacterial cells that can conserve resources and energy have a selective advantage over cells that are unable to do so...
- thus, natural selection has **avored** bacteria that express **ONLY** the genes whose products are needed by the cell at any given moment...

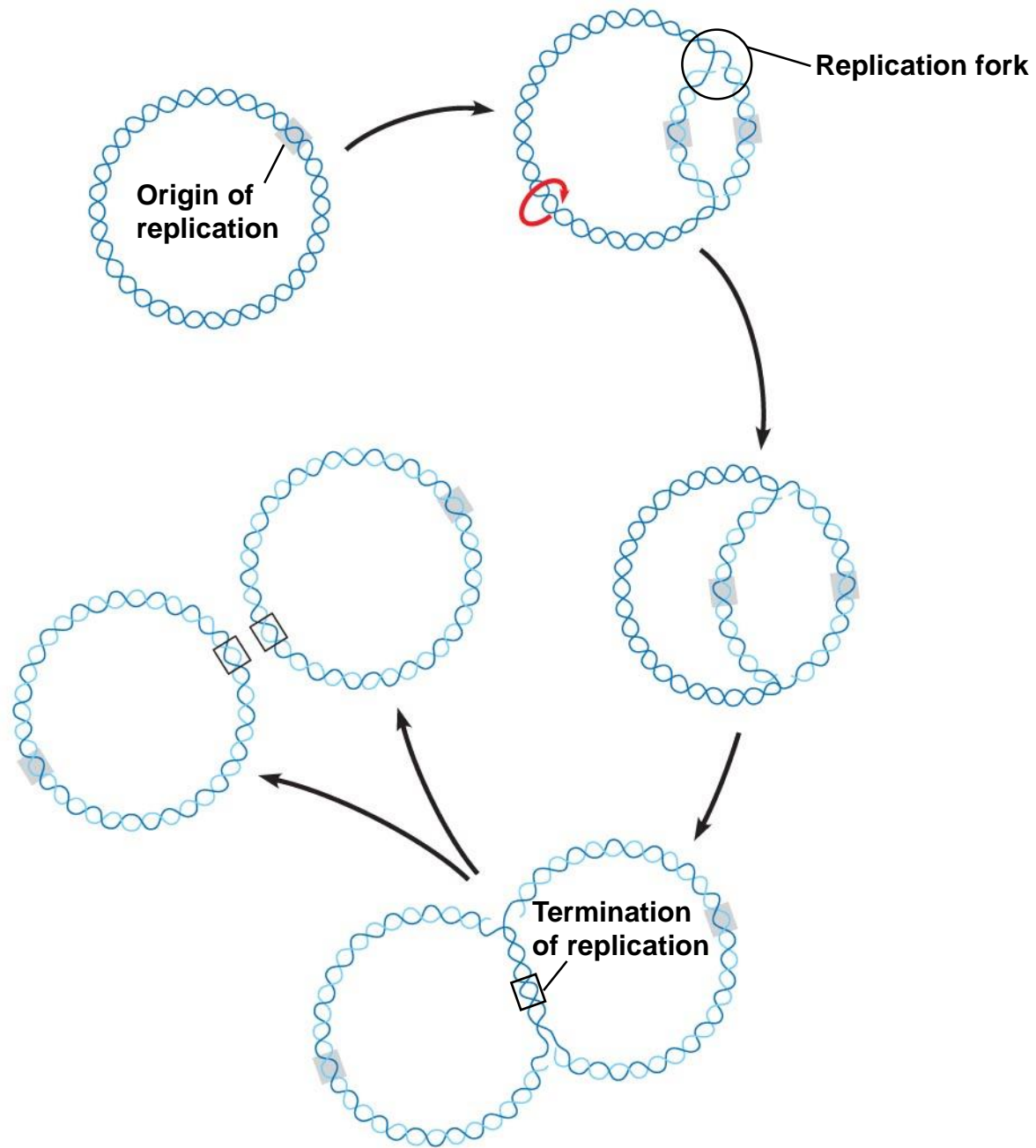
Rapid reproduction, mutation, and genetic recombination contribute to the genetic diversity of bacteria

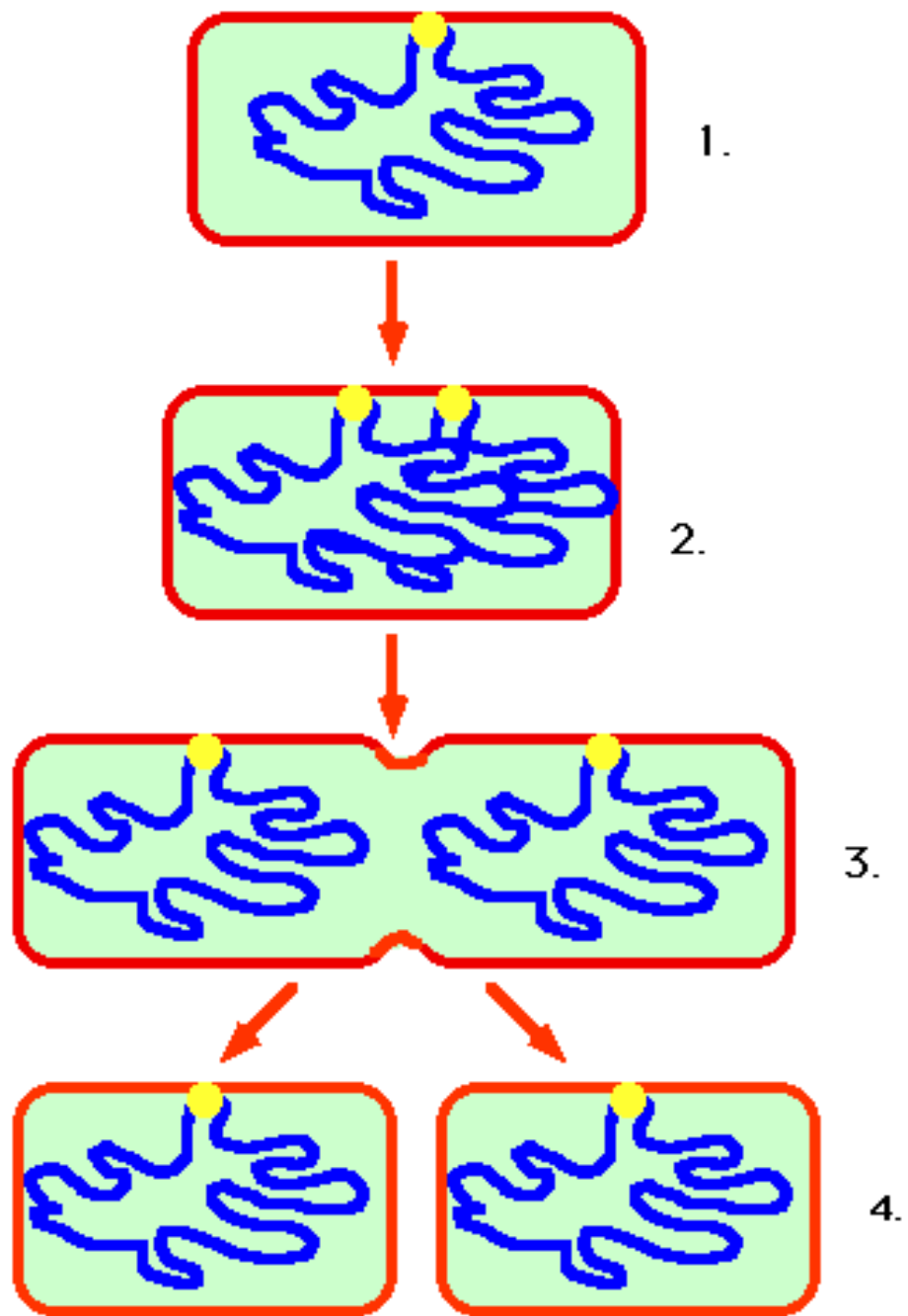
- Bacteria allow researchers to investigate molecular genetics in the simplest true organisms
- The well-studied intestinal bacterium *Escherichia coli* (*E. coli*) is “the laboratory rat of molecular biology”



The Bacterial Genome and Its Replication:

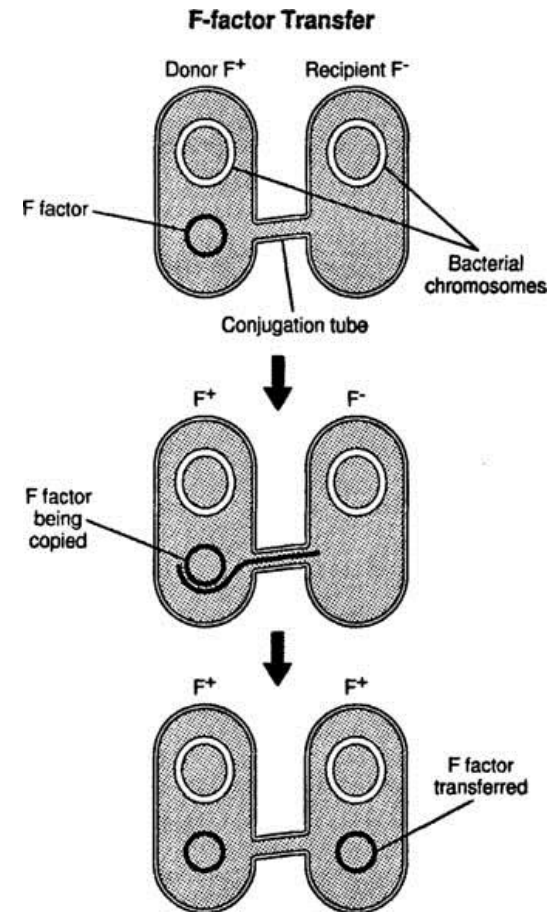
- The bacterial chromosome is usually a circular DNA molecule with few associated proteins
- Many bacteria also have **PLASMIDS**, smaller circular DNA molecules that can replicate independently of the chromosome
- Bacterial cells divide by **BINARY FISSION**, which is preceded by replication of the chromosome





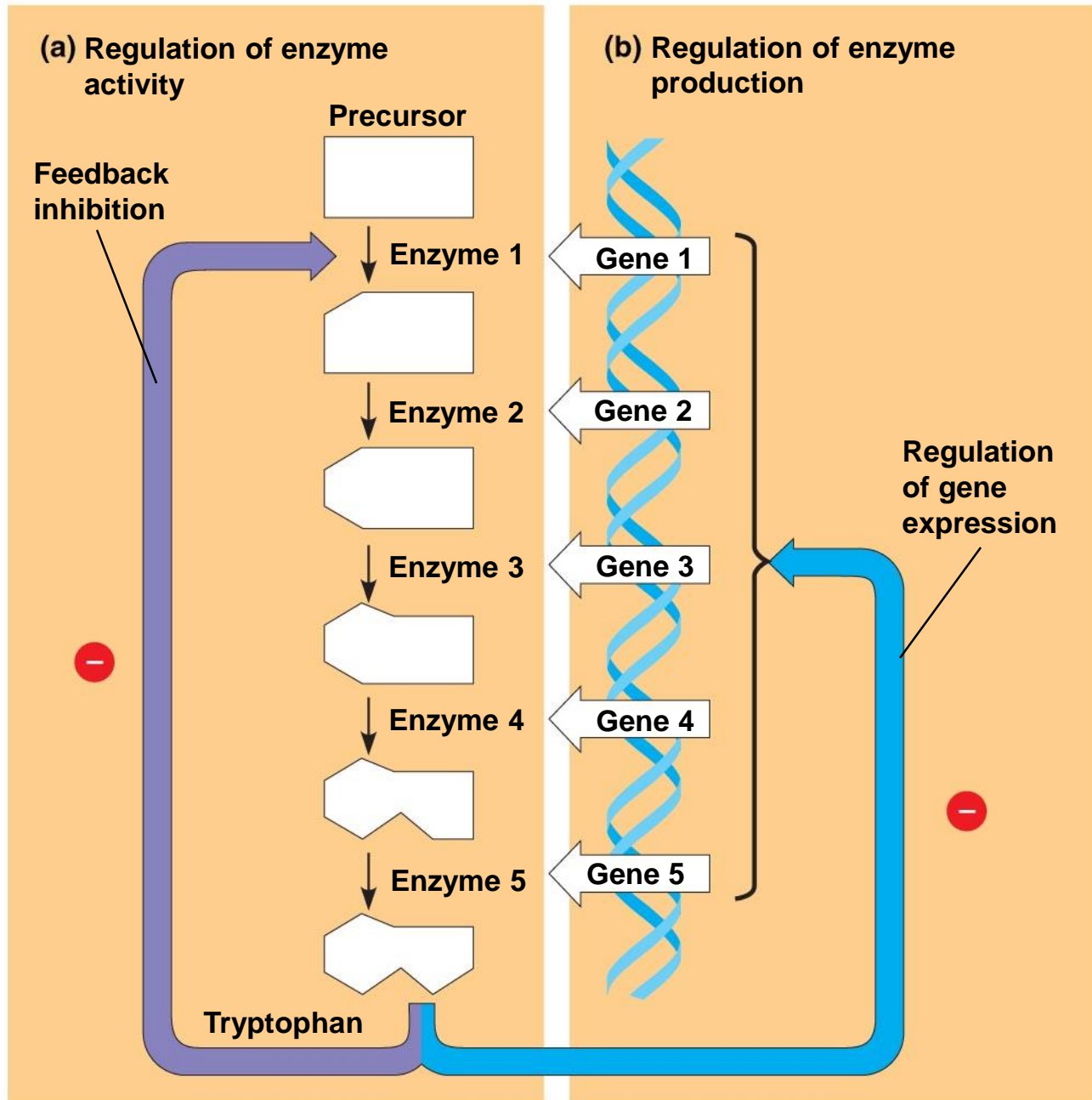
Mutation and Genetic Recombination as Sources of Genetic Variation

- Since bacteria can reproduce rapidly, new mutations quickly increase genetic diversity
- More genetic diversity arises by recombination of DNA from two different bacterial cells



Individual bacteria respond to environmental change by regulating their gene expression

- A bacterium can tune its metabolism to the changing environment and food sources
- This metabolic control occurs on two levels:
 - 1) Adjusting activity of metabolic enzymes
 - 2) Regulating genes that encode metabolic enzymes

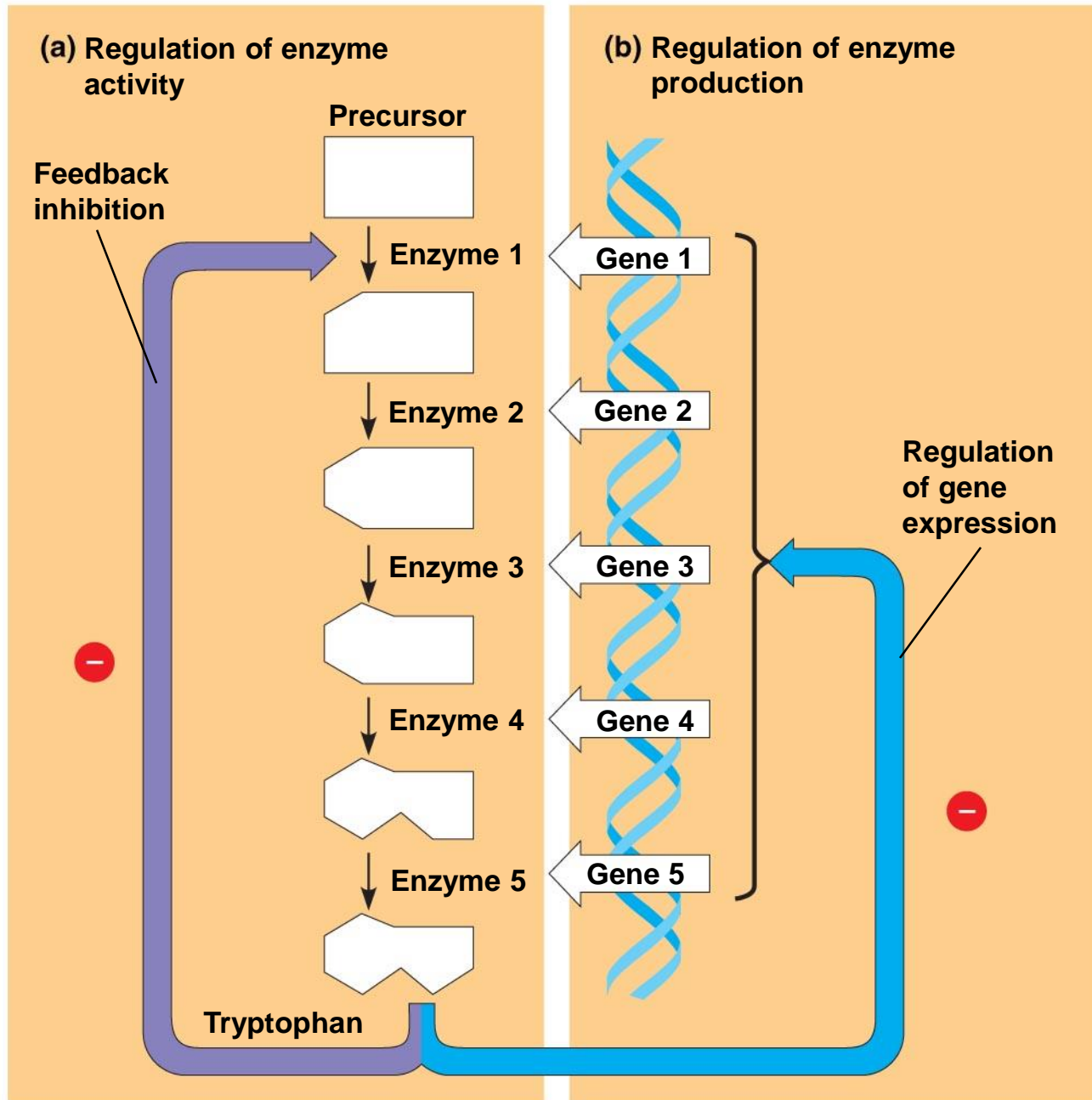


EXAMPLE:

- consider an individual *E. coli* cell living in the constantly-changing environment of a human colon...it depends on the eating habits of its host!!
- if, for example, the environment is lacking in the amino acid tryptophan, which it needs to survive, the cell responds by activating a metabolic pathway that makes tryptophan from another compound...

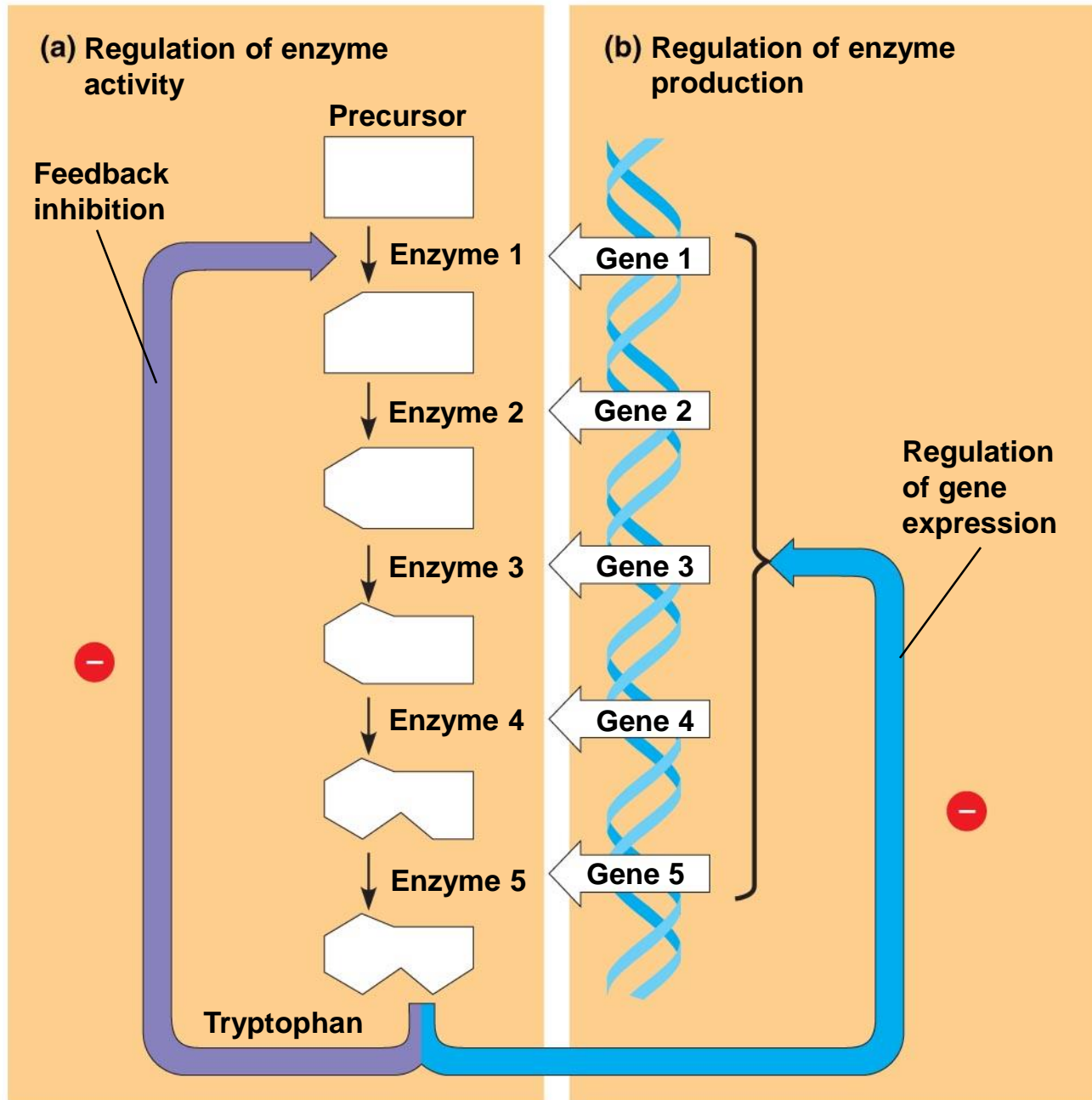
EXAMPLE:

- later, if the human host eats a tryptophan-rich meal, the bacterial cell stops producing tryptophan, thus saving itself from wasting resources to produce a substance that is readily available from its surroundings...
- this is one example of how bacteria respond and fine-tune their metabolism to a changing environment!



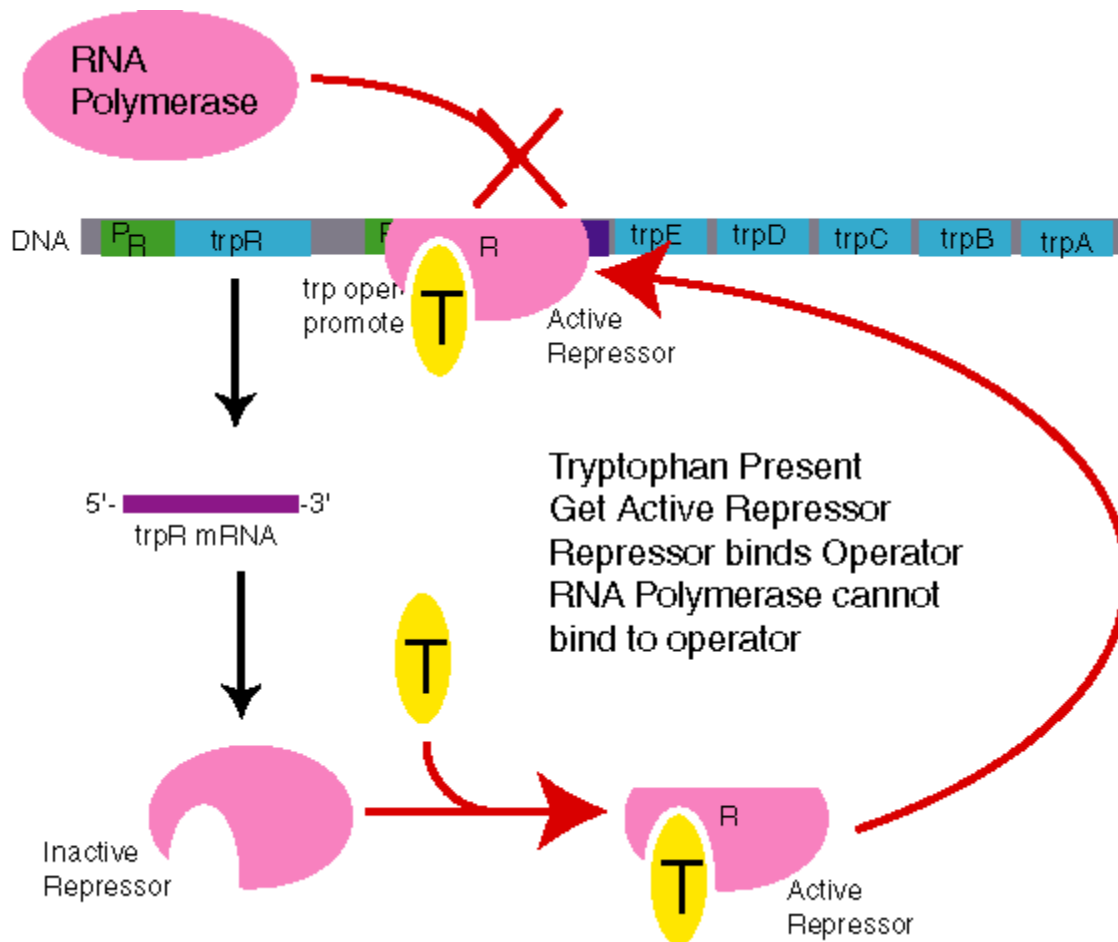
Individual bacteria respond to environmental change by regulating their gene expression

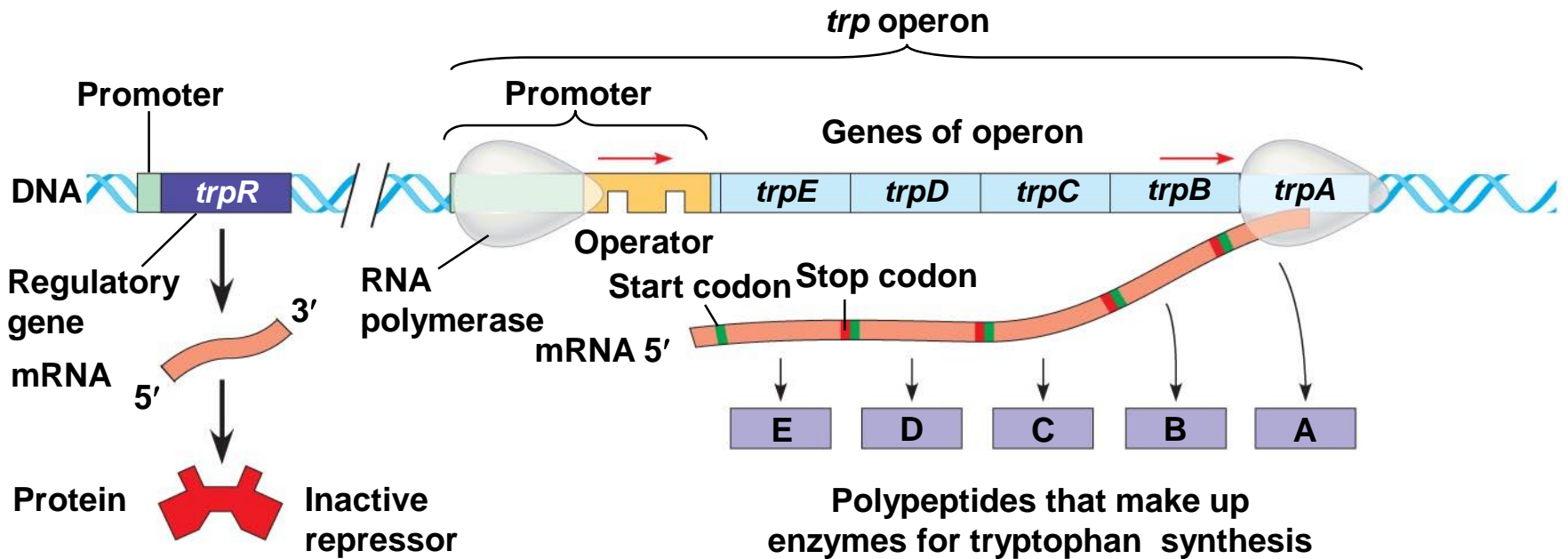
- A bacterium can tune its metabolism to the changing environment and food sources
- This metabolic control occurs on two levels:
 - 1) Adjusting activity of metabolic enzymes
(**Allosteric regulation**; short-term feedback inhibition)
 - 2) Regulating genes that encode metabolic enzymes (***occurs at the level of transcription!...how?...OPERONS!!***)



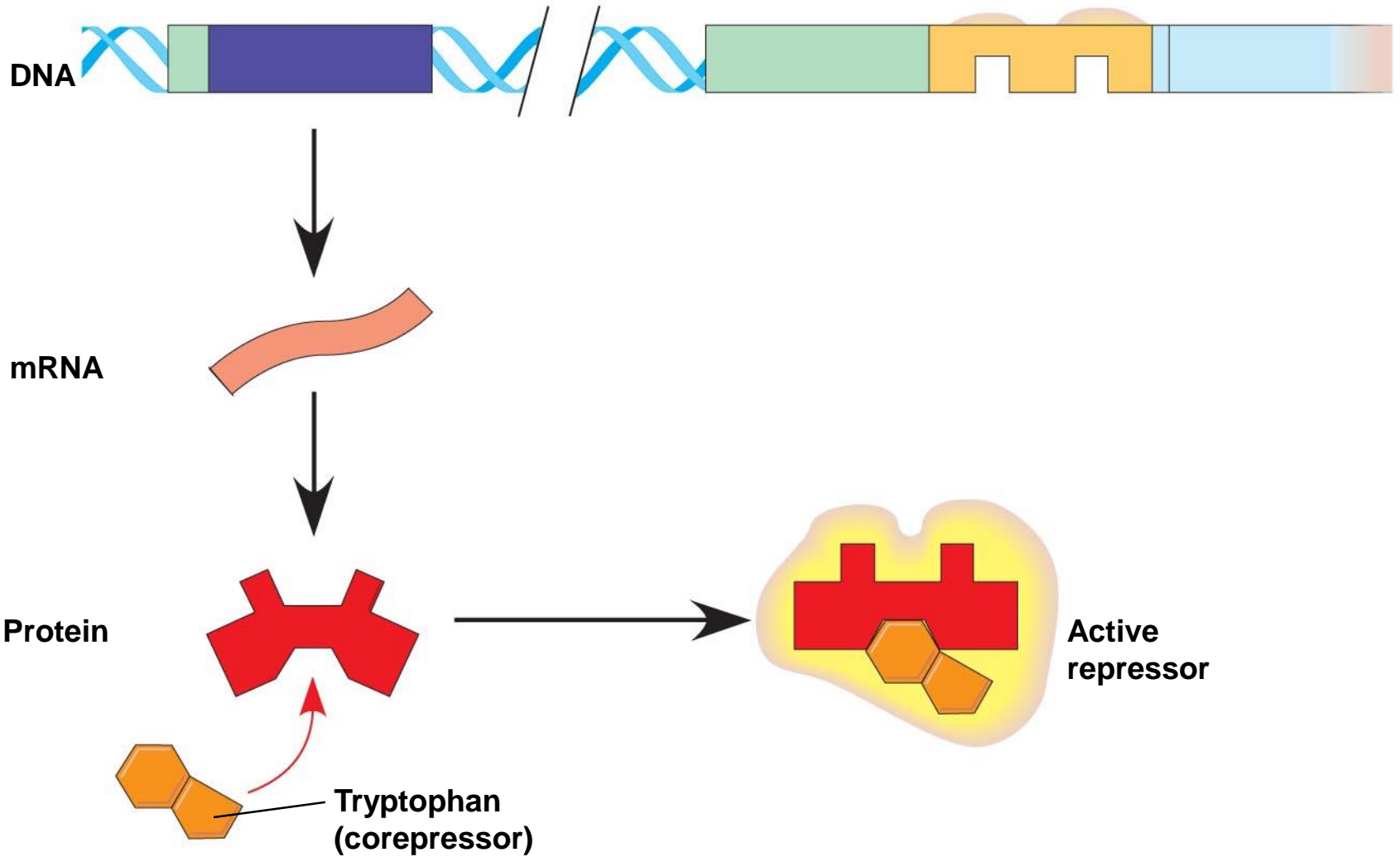
Operons: The Basic Concept

- In bacteria, genes are often clustered into operons, composed of:
 - An **OPERATOR**, an “on-off” switch
 - A **PROMOTER**
 - **GENES** for metabolic enzymes
- An operon can be switched off by a protein called a **REPRESSOR**
- A **corepressor** is a small molecule that cooperates with a repressor to switch an operon off



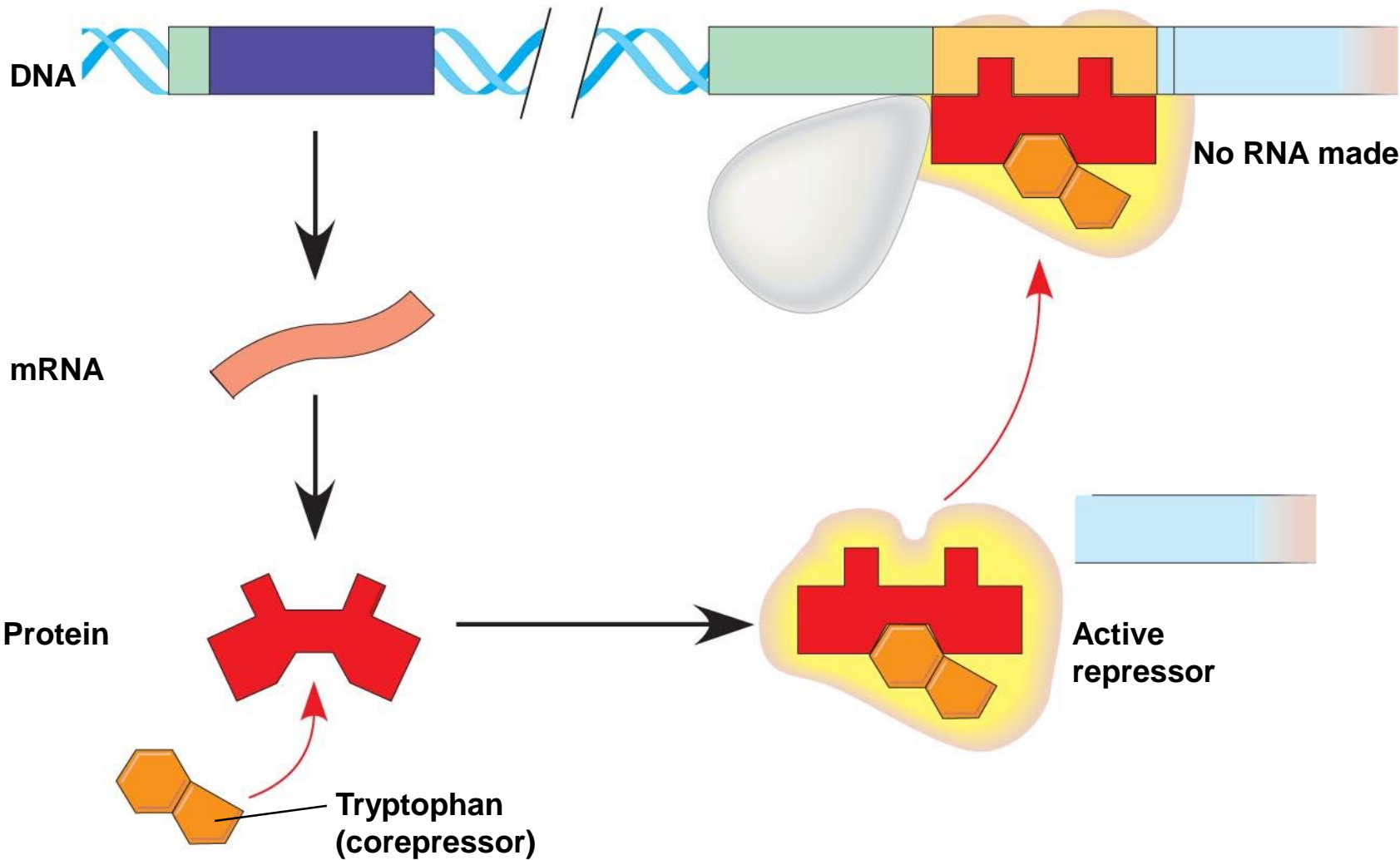


(a) Tryptophan absent, repressor inactive, operon on



(b) Tryptophan present, repressor active, operon off

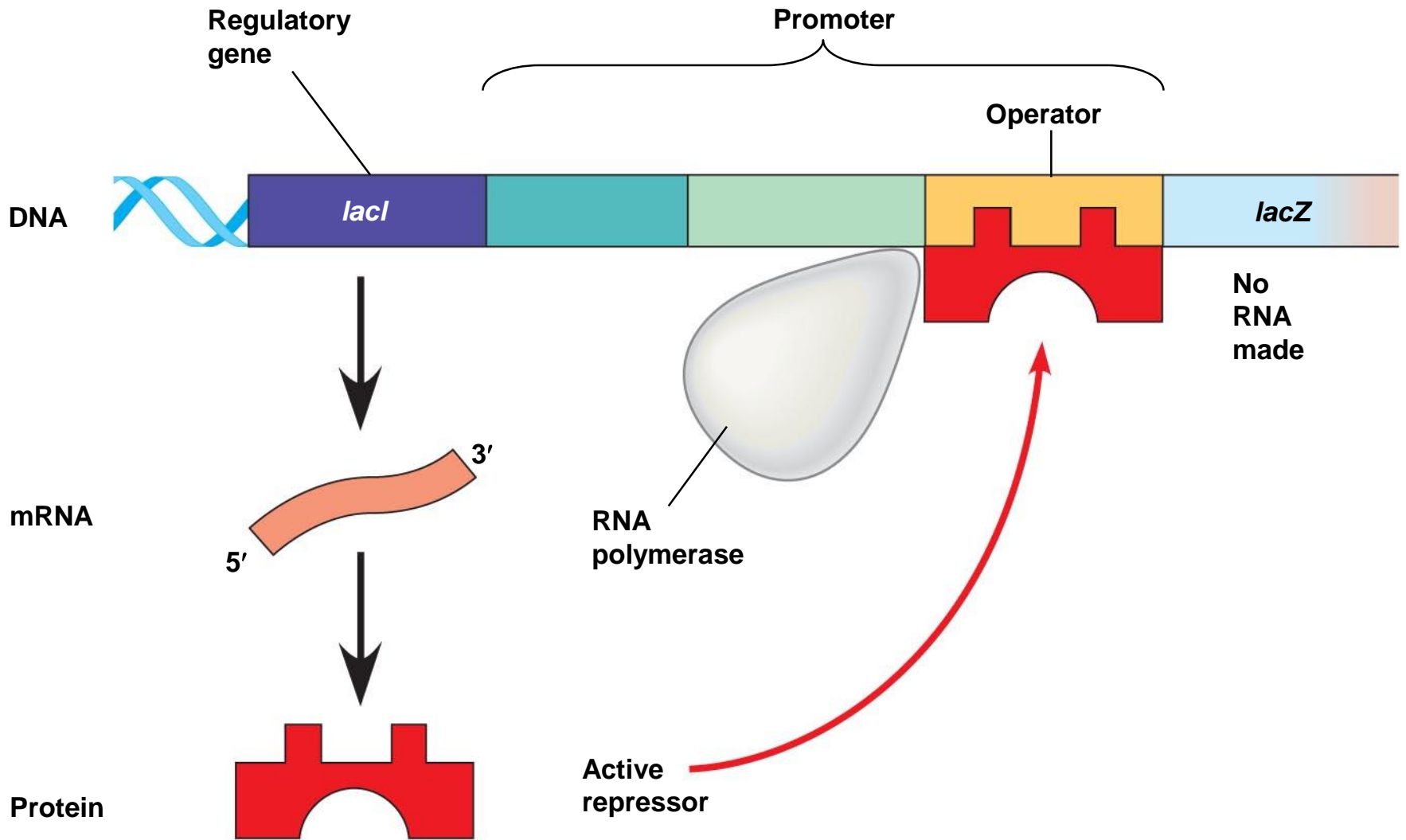
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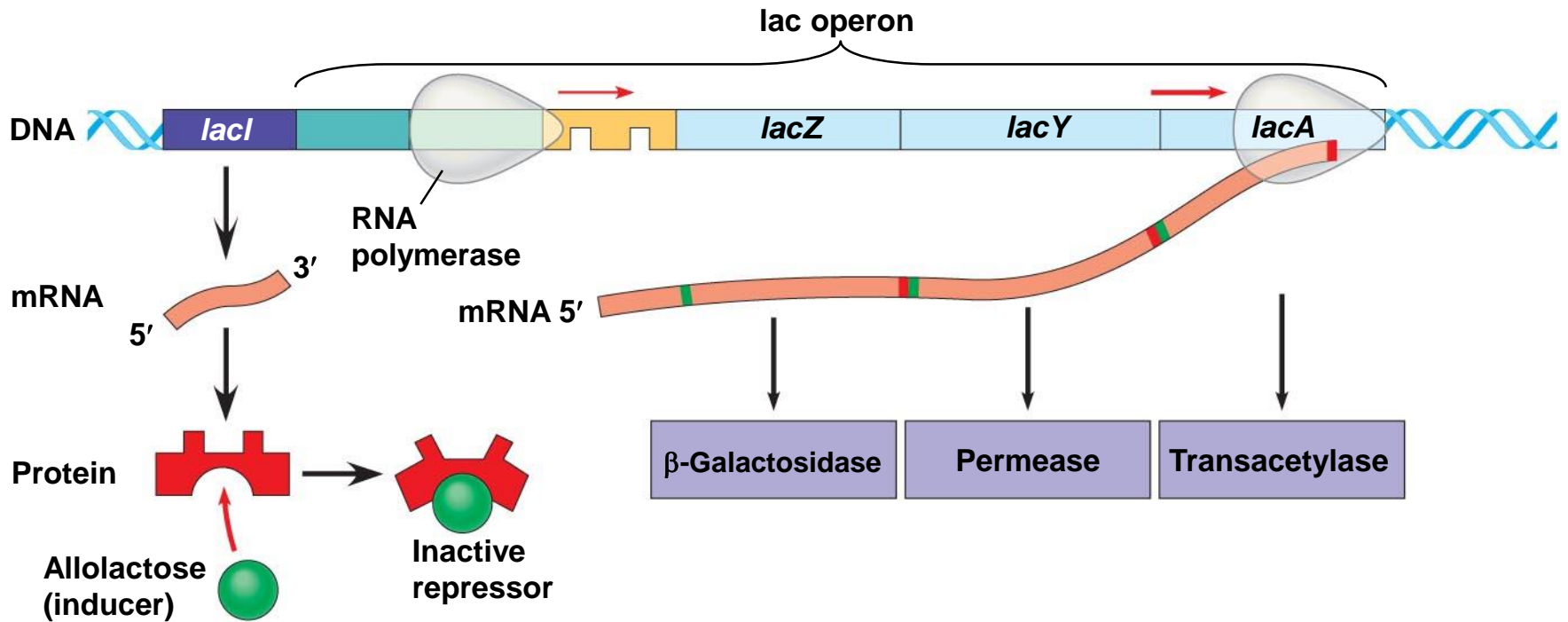
(b) Tryptophan present, repressor active, operon off

Repressible and Inducible Operons: Two Types of Negative Gene Regulation

- A **repressible operon** is one that is usually on; binding of a **REPRESSOR** to the operator shuts off transcription
- The ***trp* operon** is a repressible operon
- An **inducible operon** is one that is usually off; a molecule called an **INDUCER** inactivates the repressor and turns on transcription
- The classic example of an inducible operon is the ***lac* operon**, which contains genes coding for enzymes used in hydrolysis and metabolism of lactose (disaccharide; “milk sugar”)



(a) Lactose absent, repressor active, operon off



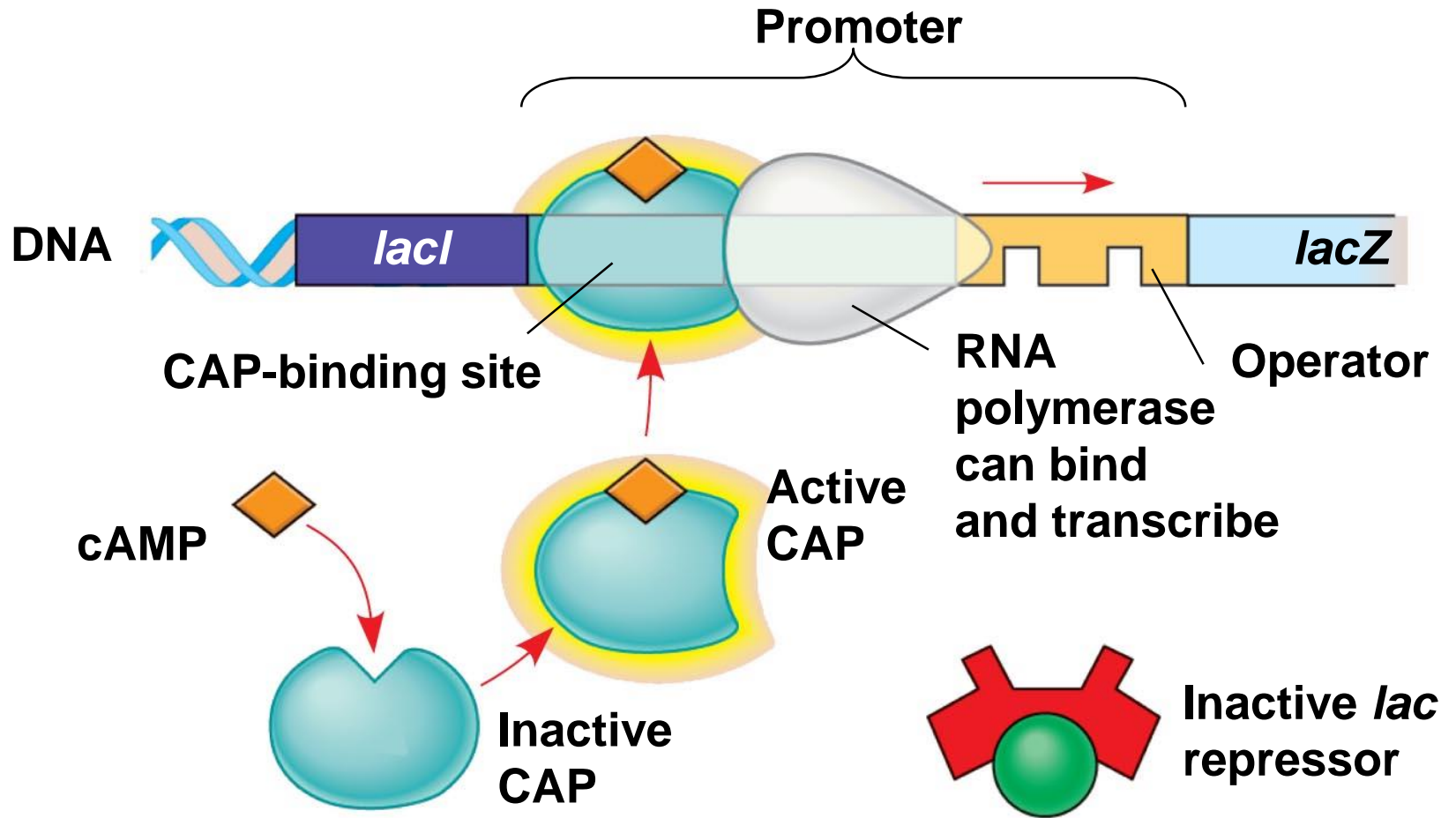
(b) Lactose present, repressor inactive, operon on

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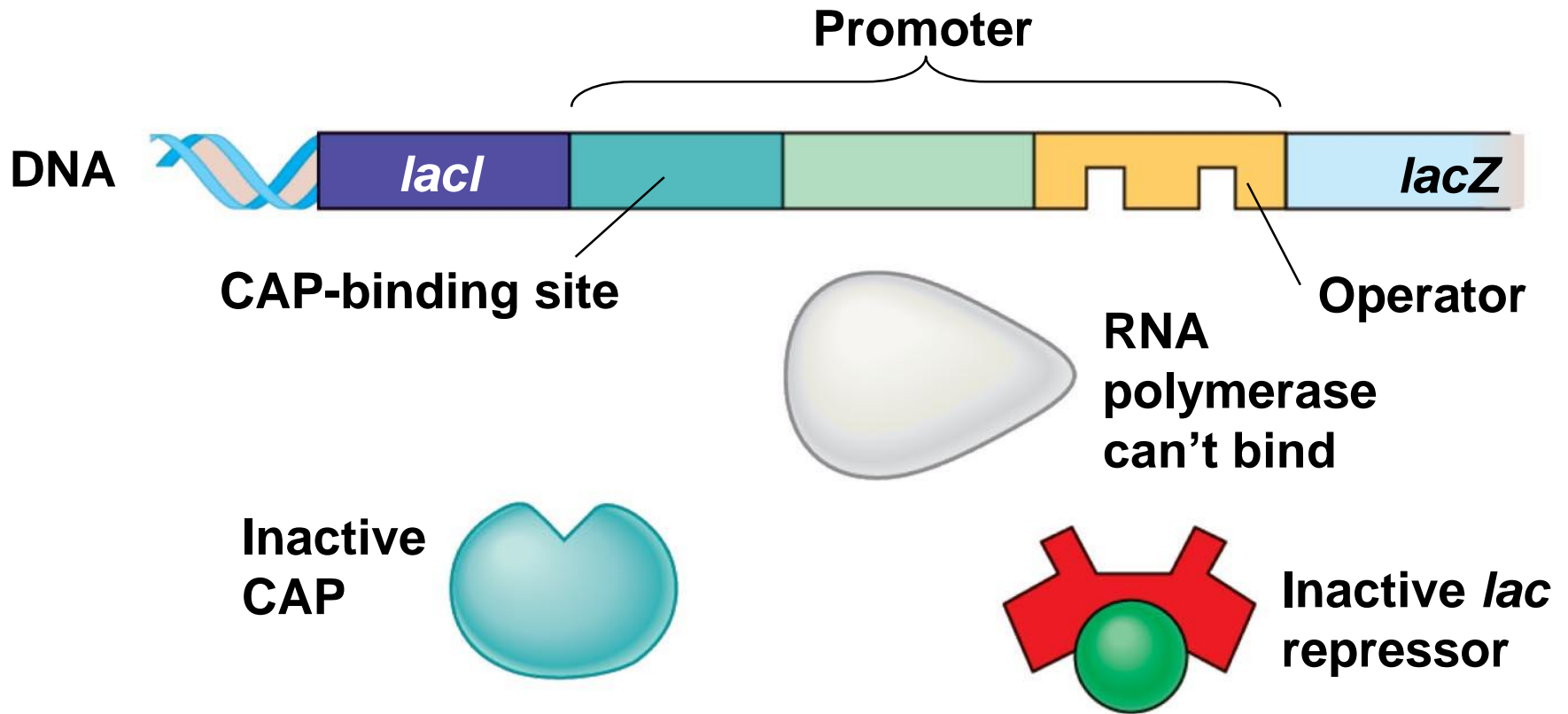
- Inducible enzymes usually function in **catabolic pathways**
- Repressible enzymes usually function in **anabolic pathways**
- Regulation of **both** the *trp* and *lac* operons involves ***negative*** control of genes because operons are **switched off by the active form of the repressor**

Positive Gene Regulation

- Some operons are also subject to *positive* control through a stimulatory activator protein, such as **catabolite activator protein (CAP)**
- When glucose (a preferred food source of *E. coli*) is scarce, the ***lac* operon** is activated by the binding of CAP (so the enzymes to break down lactose are produced)
- When glucose levels increase, CAP detaches from the ***lac* operon**, turning it off

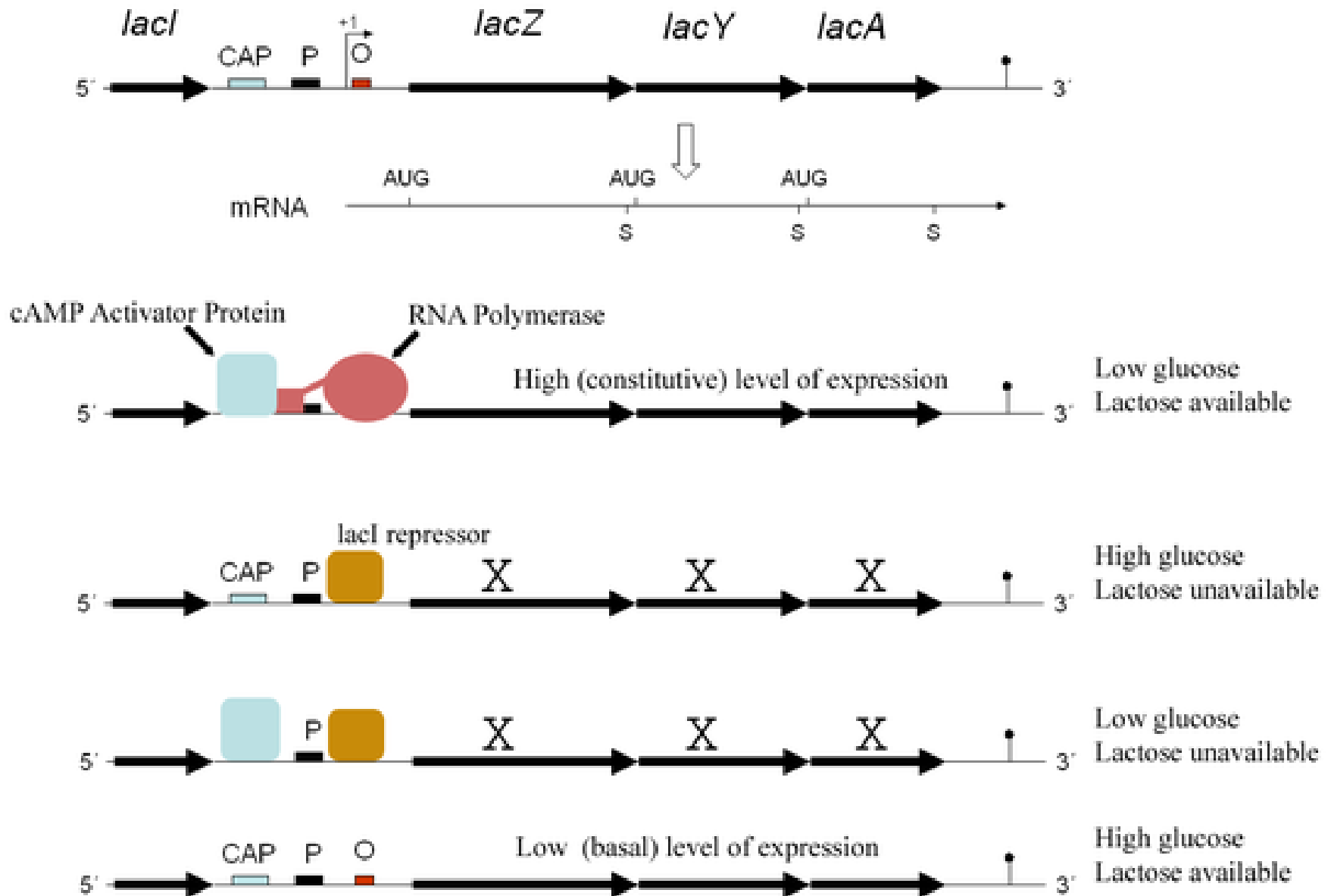


(a) Lactose present, glucose scarce (cAMP level high): abundant *lac* mRNA synthesized



(b) Lactose present, glucose present (cAMP level low): little *lac* mRNA synthesized

The *lac* Operon and its Control Elements



18.2: Eukaryotic Gene Expression

- a typical human cell might express about 20% of its protein-coding genes at any given time;
- specialized cells (muscle, nerve cells) express an even smaller fraction;
- almost all cells contain an identical genome...however, the subset of genes expressed in each cell type is unique...
- ***DIFFERENTIAL GENE EXPRESSION!***

18.2: Eukaryotic Gene Expression

- when gene expression proceeds abnormally, serious imbalances and diseases, including cancer, can arise
- as in prokaryotes, much of the regulation of gene expression in eukaryotes occurs at the transcription stage...
- however, the greater complexity of eukaryotic cell structure & function provides opportunities for regulating gene expression at many additional stages (**see fig. 18.6**)

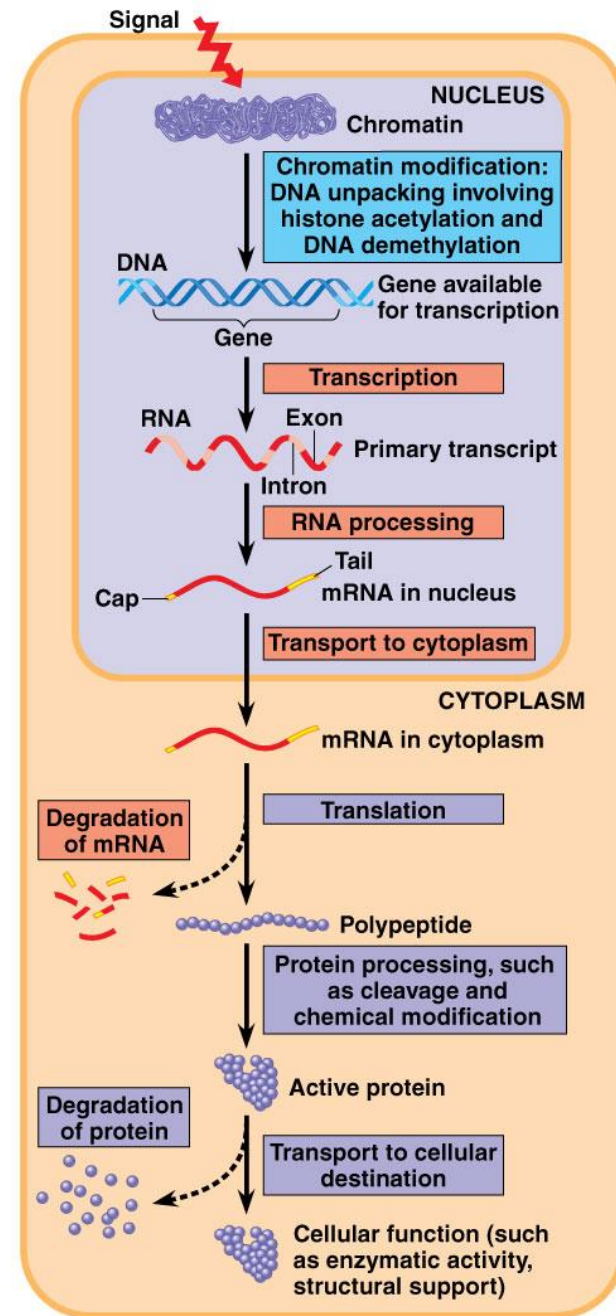
18.2: Eukaryotic Gene Expression

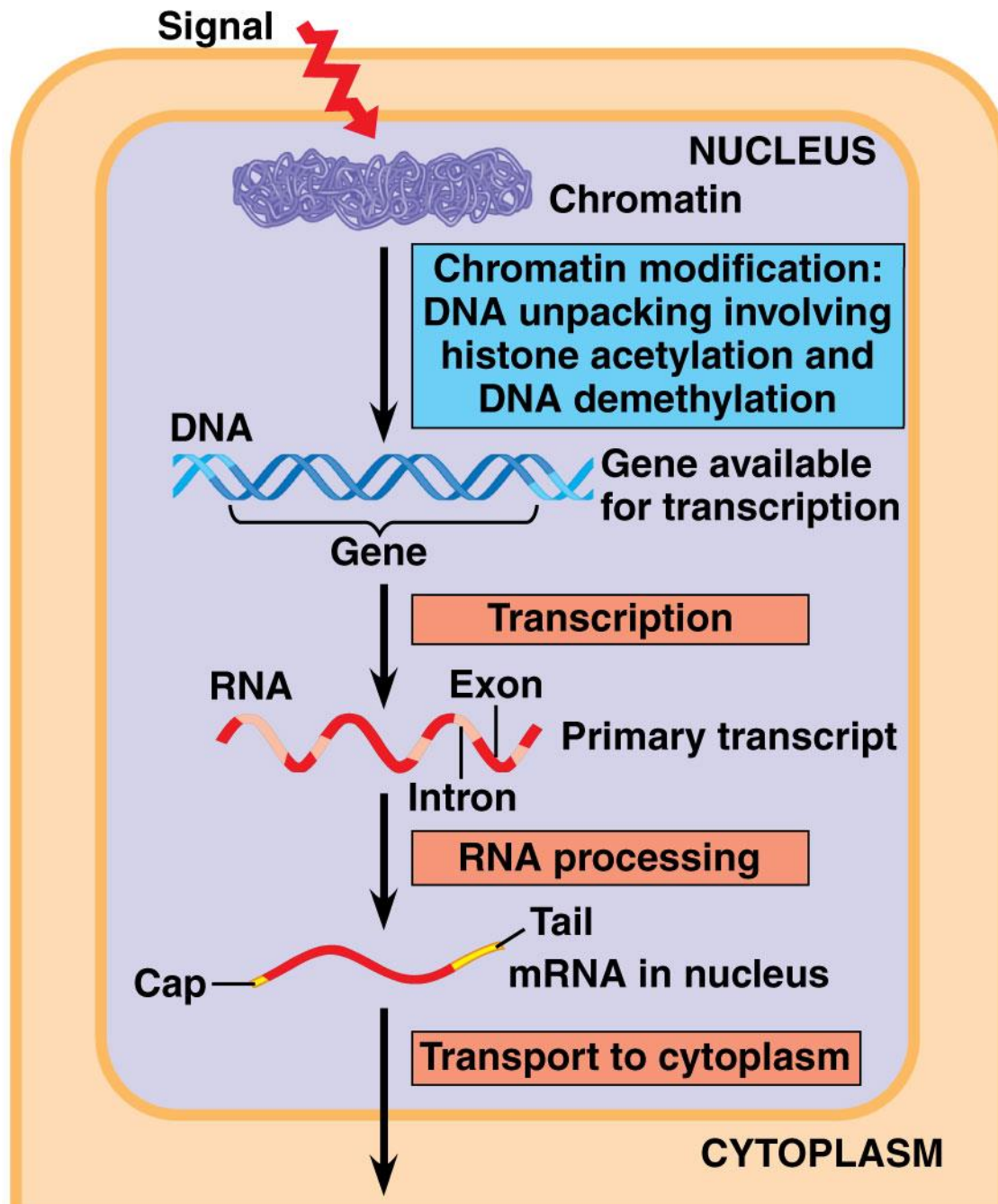
- eukaryotic gene expression is regulated at many stages:
 - 1) **regulation of chromatin structure**
 - 2) **regulation of transcription initiation**
 - 3) **post-transcriptional regulation**

1) regulation of chromatin structure

2) regulation of transcription initiation

3) post-transcriptional regulation





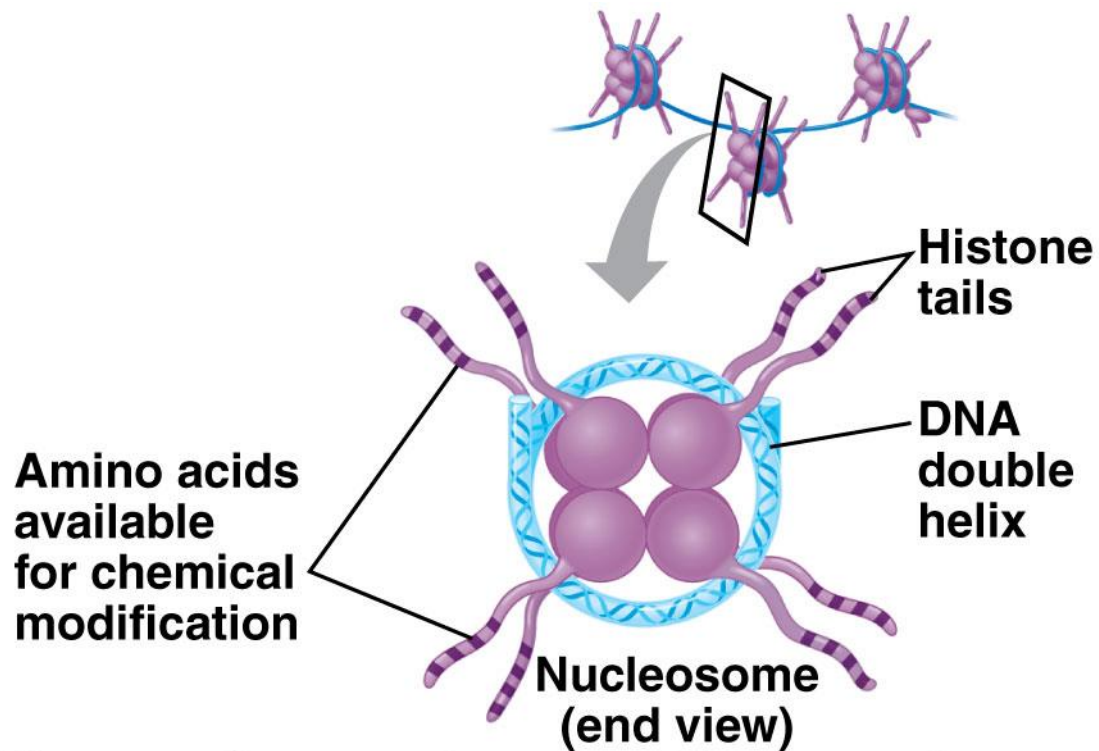
1) regulation of chromatin structure

- recall that the DNA in eukaryotic cells is packaged with proteins (**HISTONES**) into an elaborate complex known as **CHROMATIN**
- ***HOW the DNA is packed / coiled regulates how it genes are expressed!***

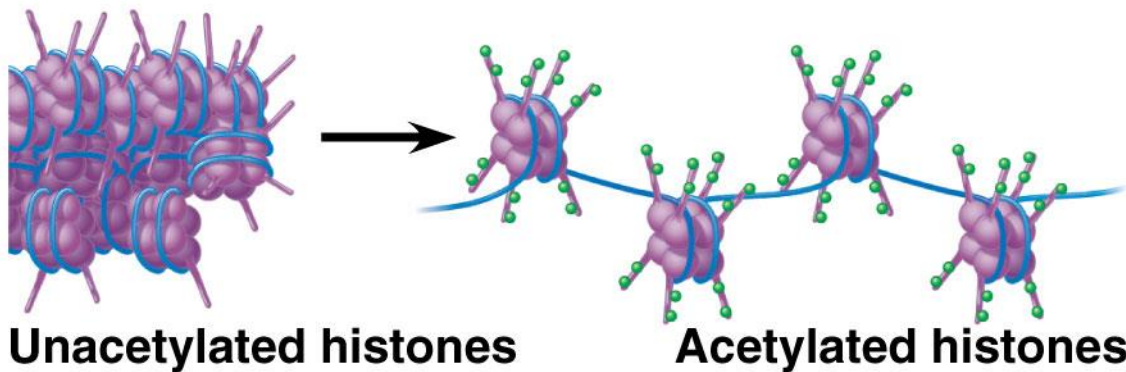
1) regulation of chromatin structure

- examples of chromatin modifications:

A) Histone Modifications: chemical groups (i.e. acetyl groups, methyl groups) can be added to amino acids in the histone structure to alter chromatin folding:
-make the chromatin fold “tighter” (**harder to transcribe**) or “looser” (**easier to transcribe**)



(a) Histone tails protrude outward from a nucleosome



(b) Acetylation of histone tails promotes loose chromatin structure that permits transcription

1) regulation of chromatin structure

- examples of chromatin modifications:

B) DNA Methylation: enzymes add methyl groups (CH_3) to certain bases in DNA (usually cytosine)...typically inactivates these segments of DNA

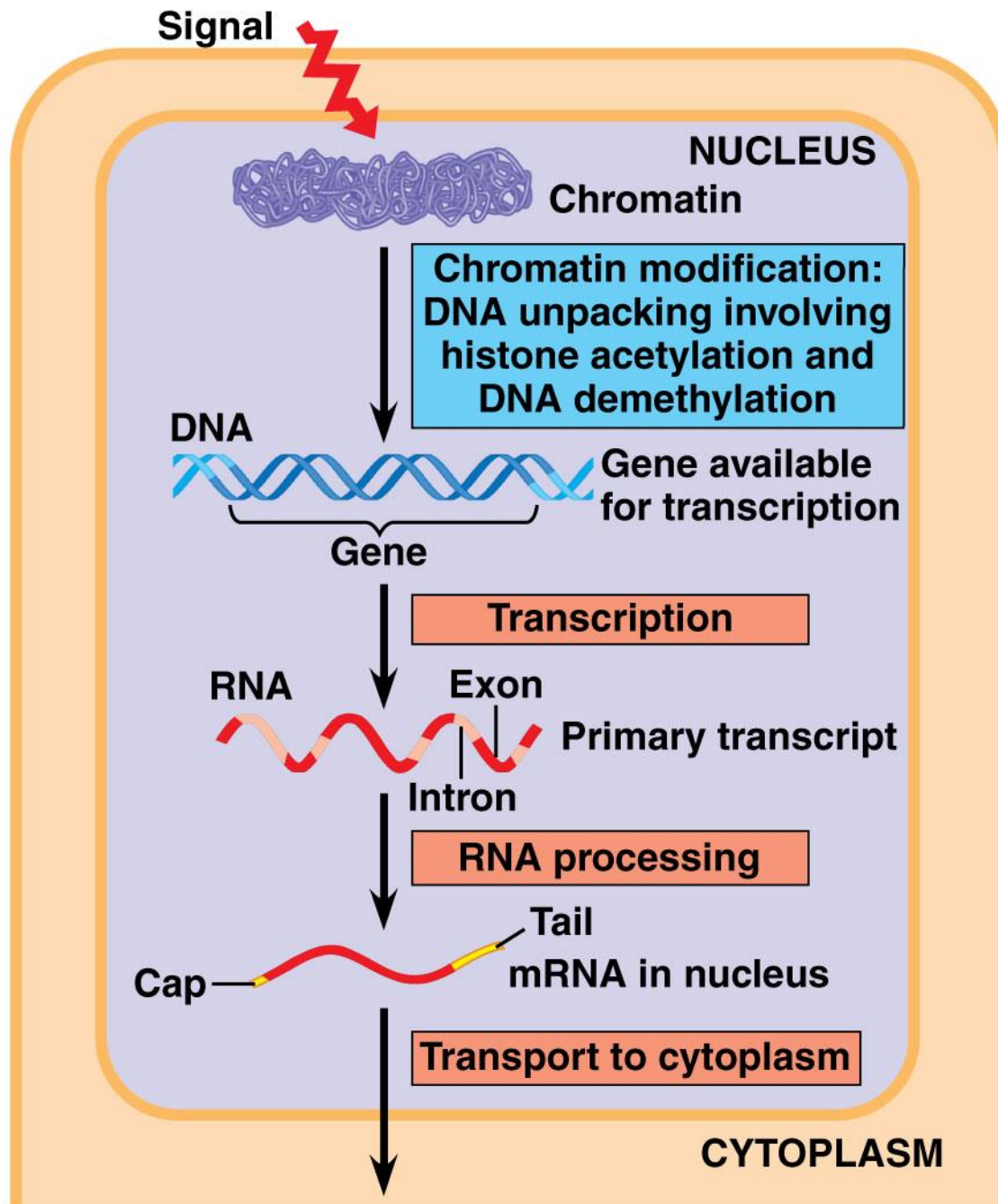
-evidence: individual genes are more heavily methylated in cells in which they are NOT expressed...removal of these methyl groups can turn some of these genes on!

1) regulation of chromatin structure

- examples of chromatin modifications:

C) Epigenetic Inheritance: inheritance of traits transmitted by mechanisms not directly involved with the DNA nucleotide sequence (i.e. histone modifications & DNA methylation!)

-these are modifications that can typically be reversed!

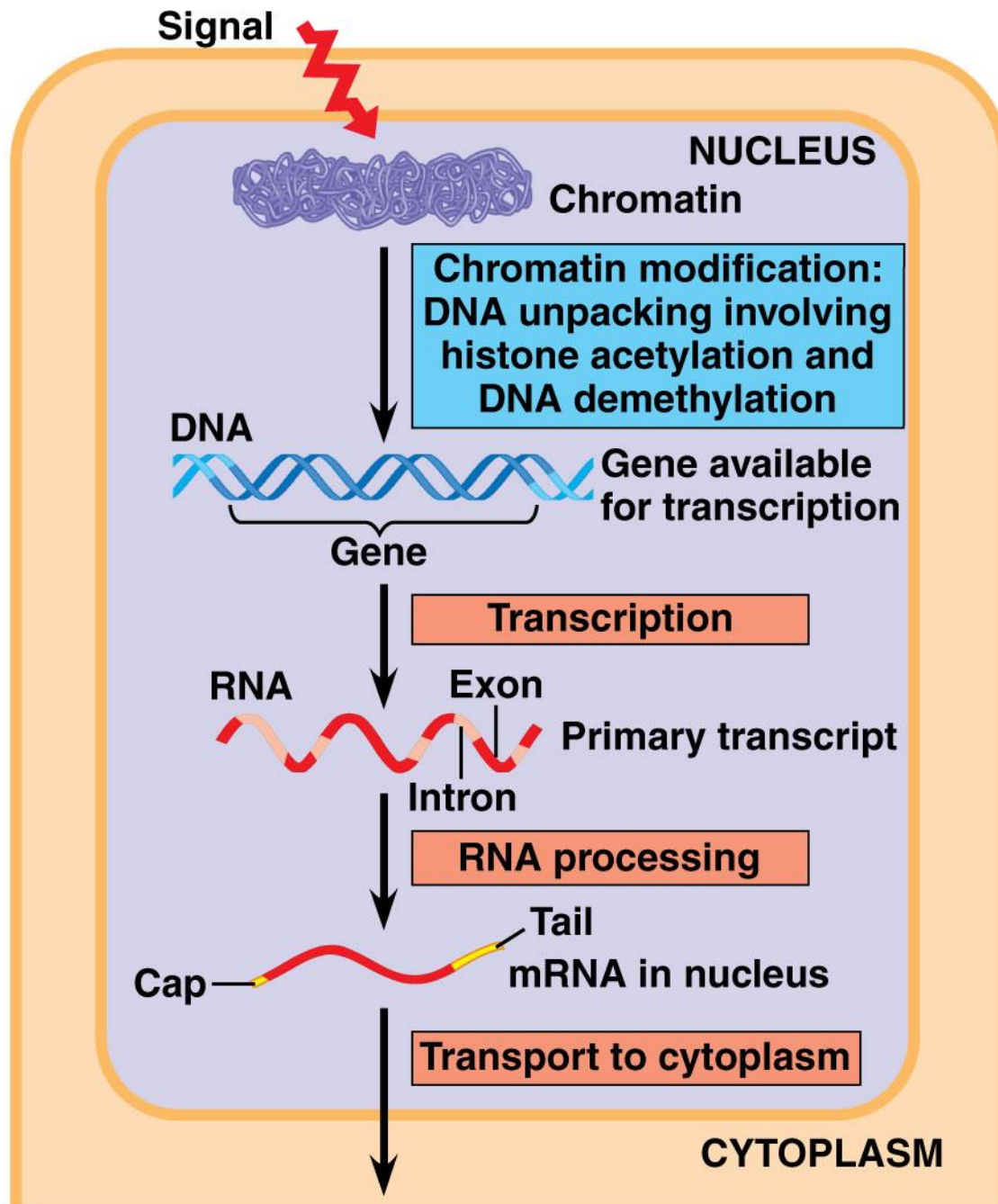


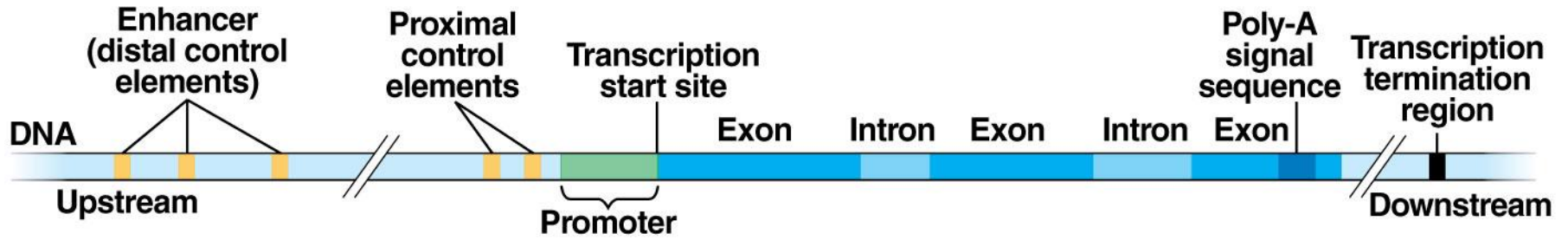
2) regulation of transcription initiation

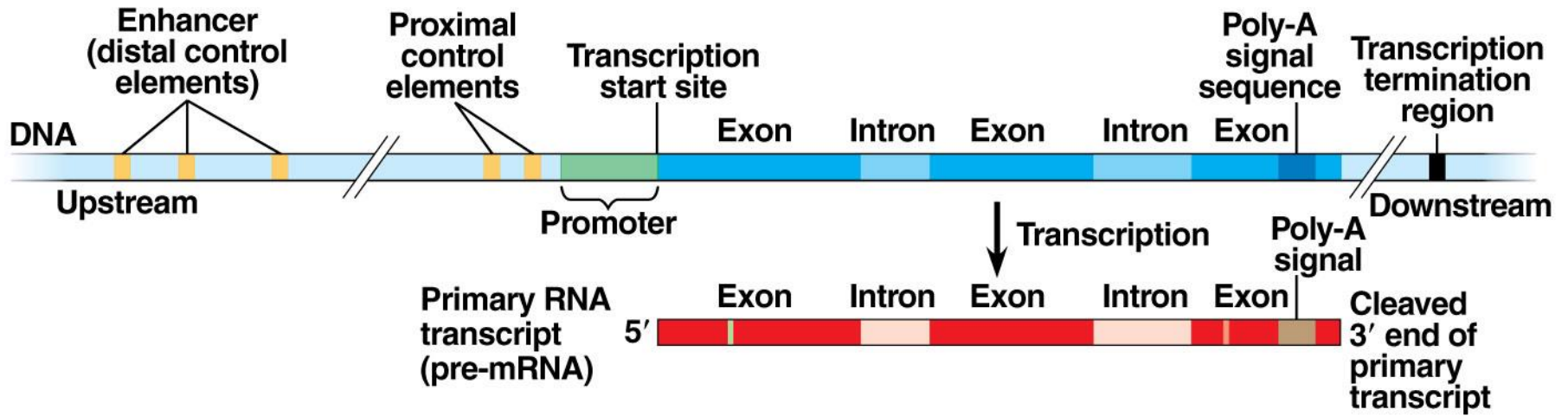
- most eukaryotic genes have multiple **control elements** – segments of noncoding DNA that serve as binding sites for proteins known as **TRANSCRIPTION FACTORS**, which in turn regulate transcription

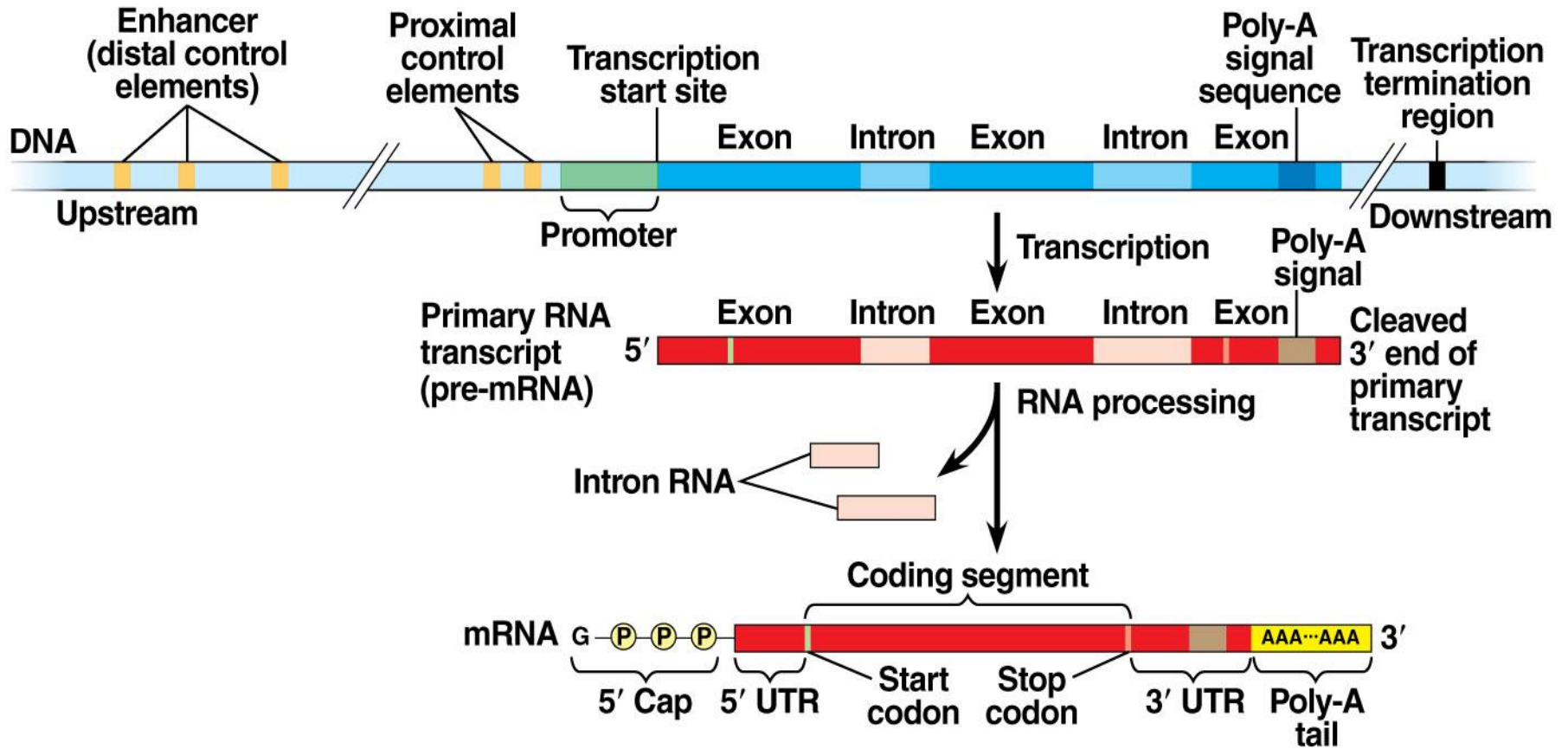
2) regulation of transcription initiation

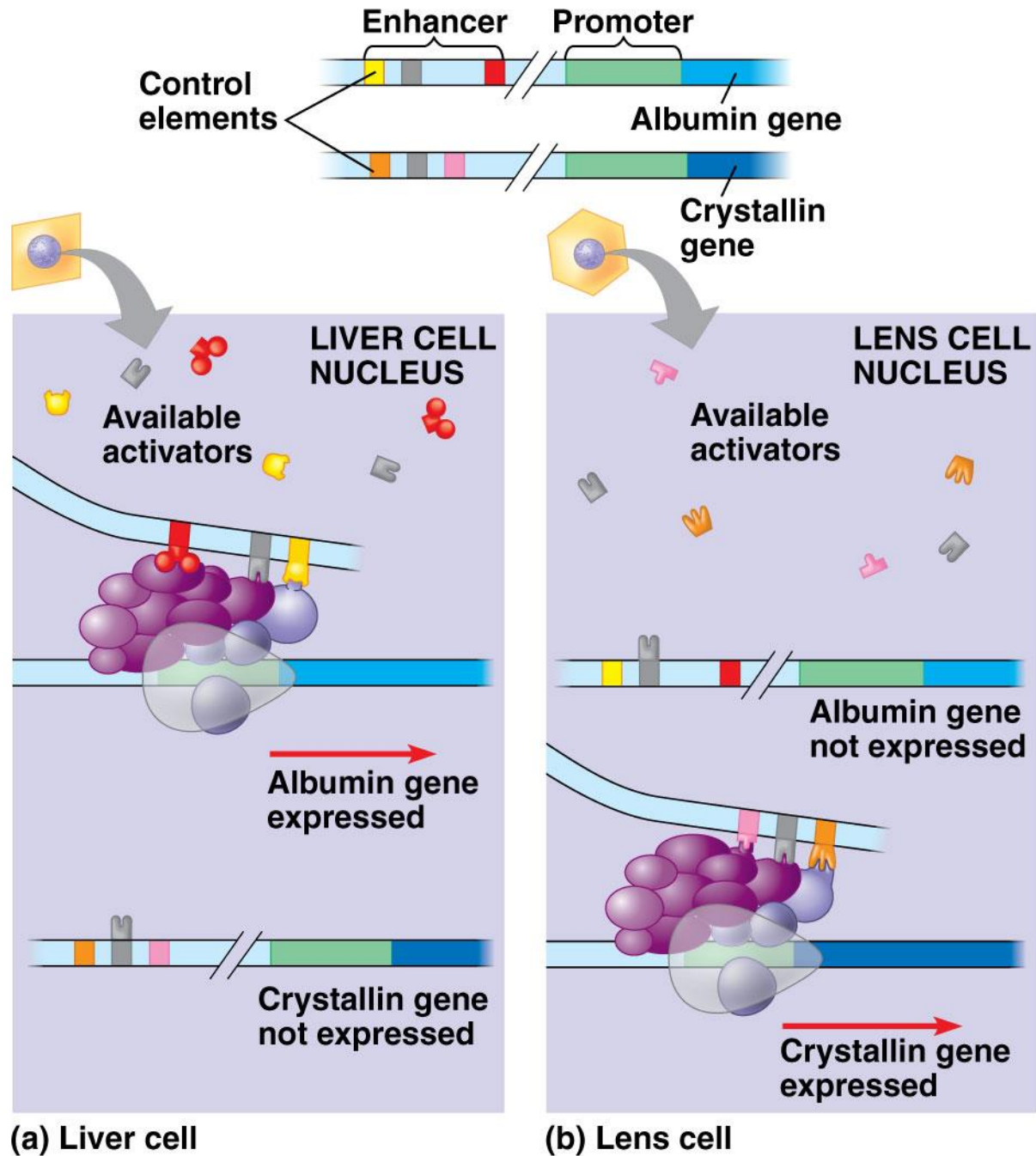
- as we saw in CH 11 (Cell Signaling), **signaling molecules (i.e. steroid or non-steroid hormones)** can cause the activation of one or more transcription factors, turning “on” the transcription of one or more genes











(a) Liver cell

(b) Lens cell

3) post-transcriptional regulation

- transcription alone does not constitute gene expression...the expression of a protein-coding gene is ultimately measured by the amount of functional protein it makes!

3) post-transcriptional regulation

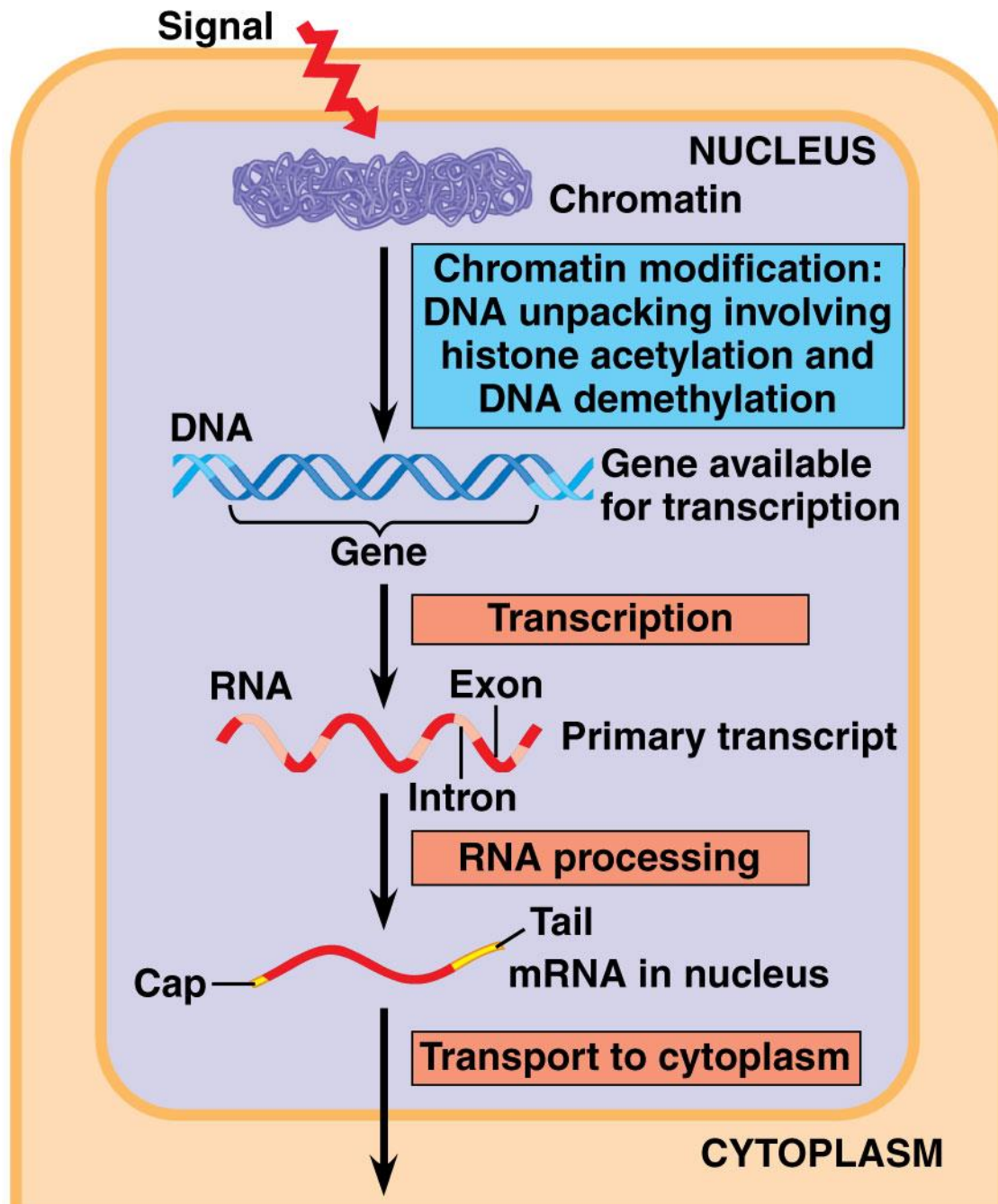
- much happens between the synthesis of mRNA and the activity of the protein in the cell:

A) RNA Processing

B) mRNA Degradation

C) Initiation of Translation

D) Protein Processing and Degradation

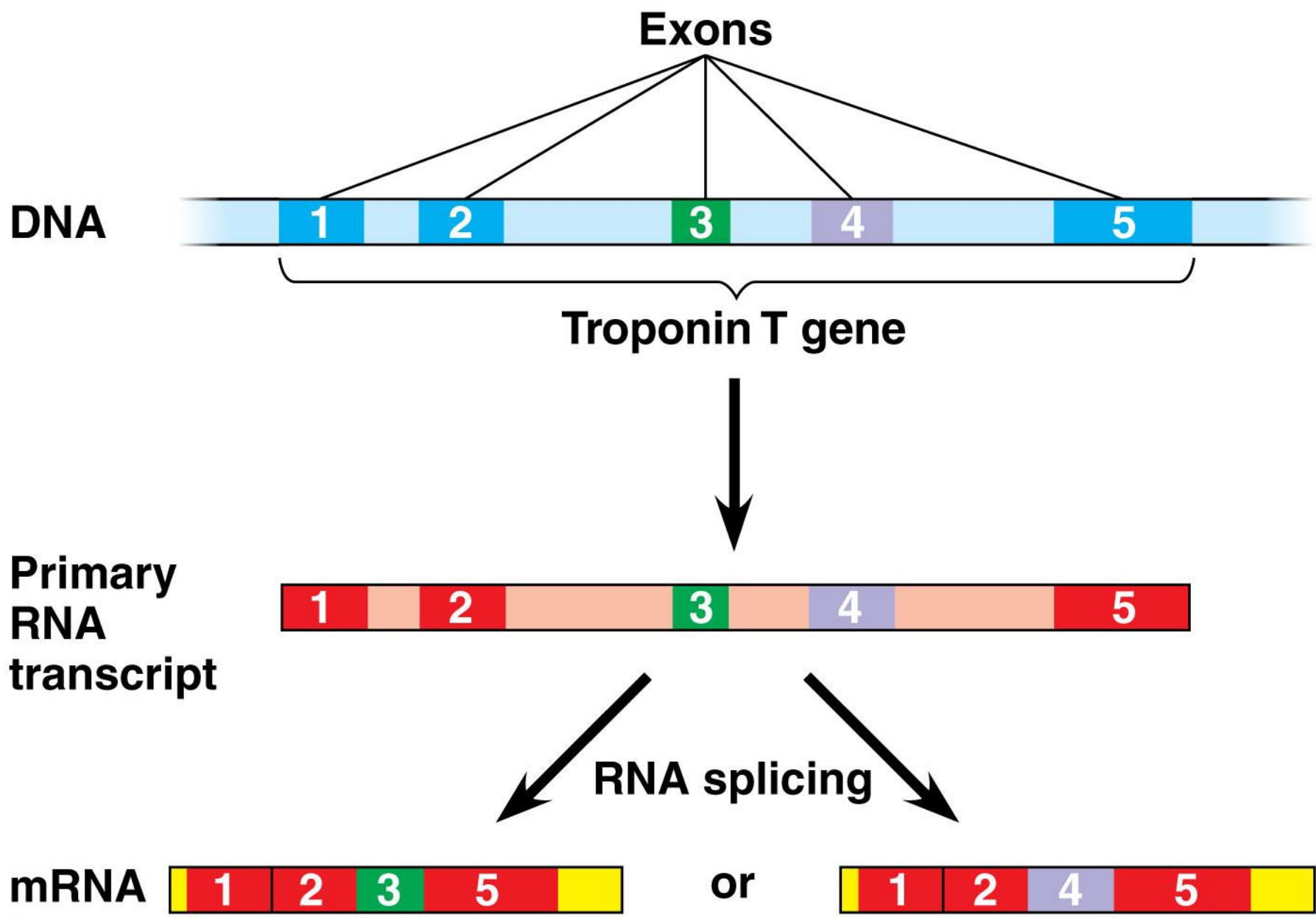


A) RNA Processing

- we've already discussed: 5' cap, 3' poly-A tail, and removal of introns (**exons remain**)

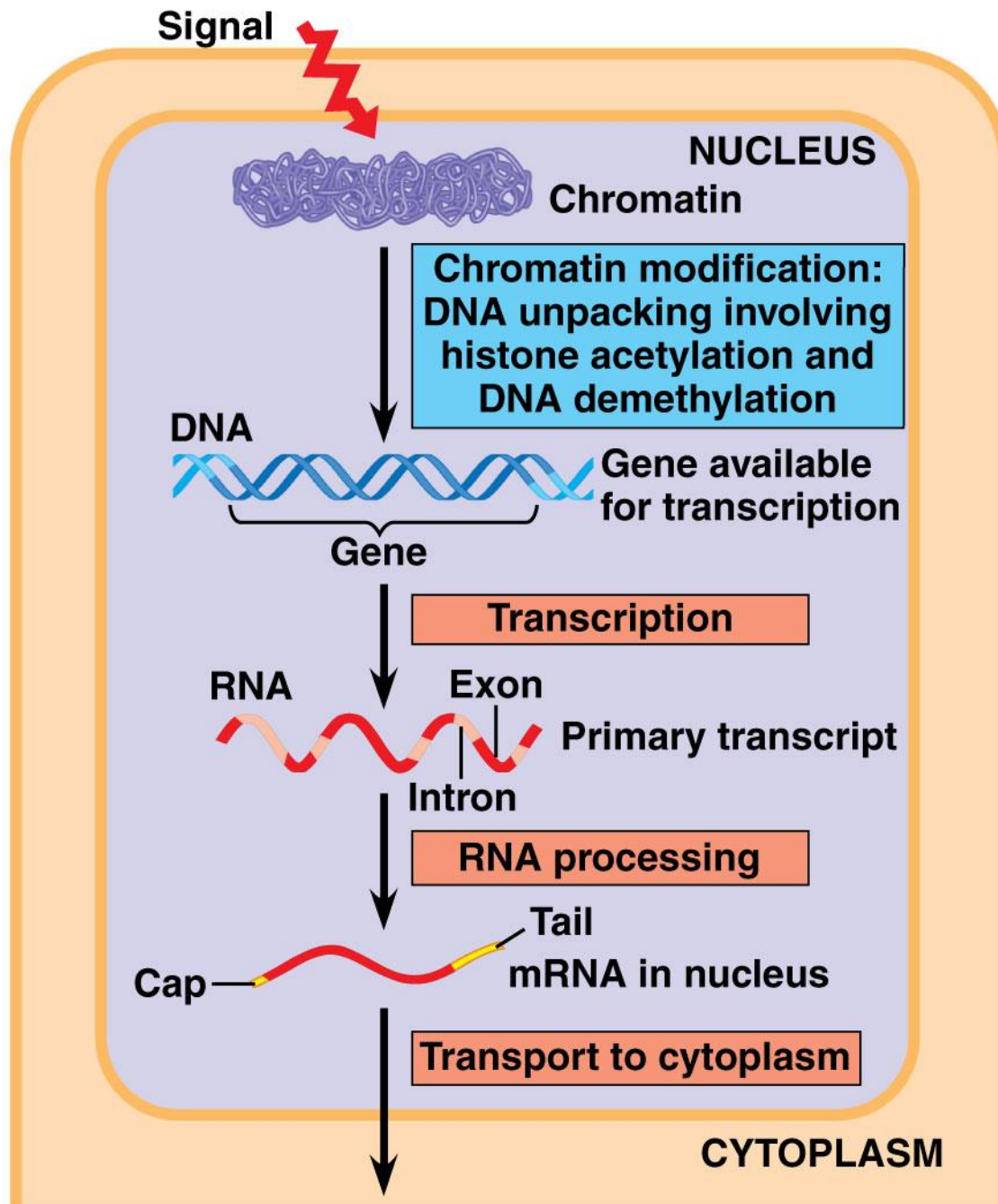
A) RNA Processing

- **alternative RNA splicing**: different mRNA molecules can be made from the same primary transcript! (depending on which RNA segments are treated as exons & which as introns)
- example**: researchers have found 1 *Drosophila* gene with enough alternatively spliced exons to produce **19,000 membrane proteins** that have different extracellular domains!!!



B) mRNA Degradation

- the lifespan of mRNA molecules in the cytoplasm is important in determining the pattern of protein synthesis
- **bacterial mRNA** molecules are typically degraded by enzymes within a few minutes
- **eukaryotic mRNAs** are typically more stable...can last for hours, days, weeks...
(i.e. mRNAs for hemoglobin polypeptides are long-lived!)



C) Initiation of Translation

- there are regulatory proteins that can bind to specific sequences at the 5' or 3' end of mRNA & prevent the attachment of ribosomes

CYTOPLASM

mRNA in cytoplasm

Degradation of mRNA

Translation



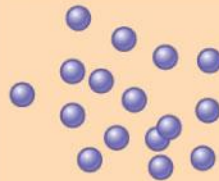
Polypeptide

Protein processing, such as cleavage and chemical modification

Active protein

Degradation of protein

Transport to cellular destination



Cellular function (such as enzymatic activity, structural support)

D) Protein Processing and Degradation

- most polypeptides require some processing before they are functional
 - phosphate groups added / removed
 - transported to target destination (i.e. cell surface)
 - proper folding or combining with other polypeptides to form quaternary structure...
- **regulation can occur at any of these steps!**

CYTOPLASM

mRNA in cytoplasm

Degradation of mRNA

Translation



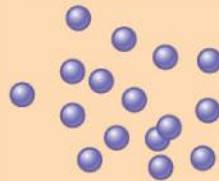
Polypeptide

Protein processing, such as cleavage and chemical modification

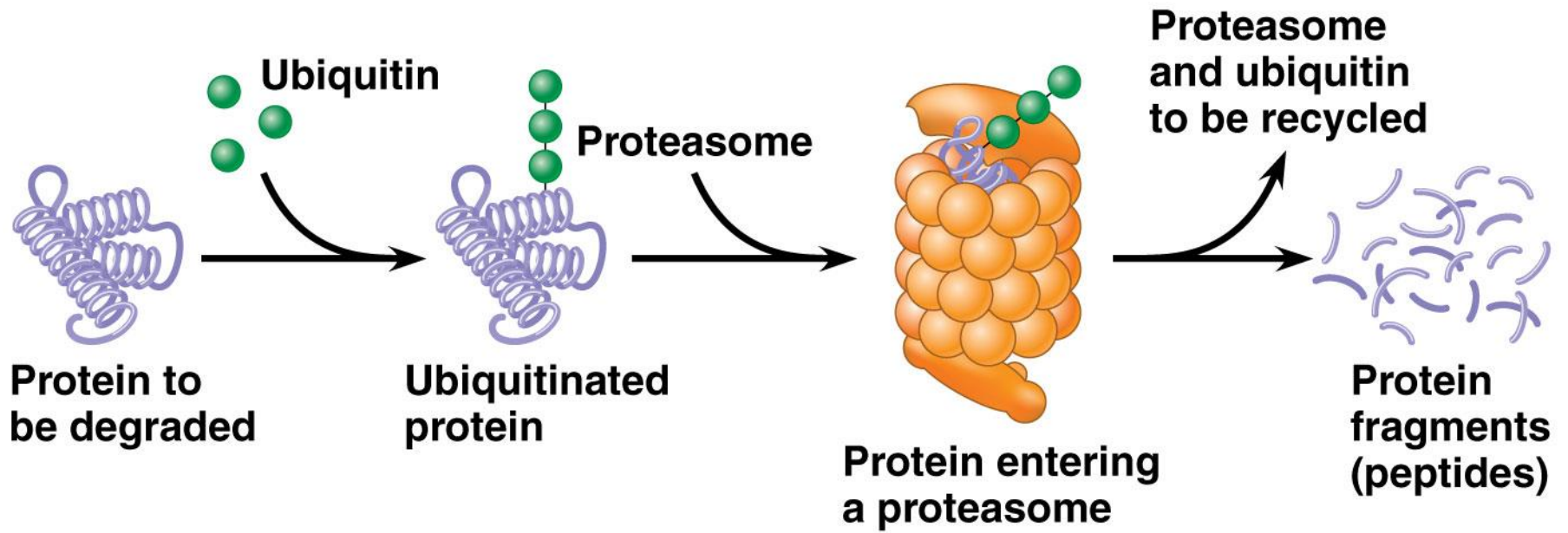
Active protein

Degradation of protein

Transport to cellular destination



Cellular function (such as enzymatic activity, structural support)



18.3: Noncoding RNAs play multiple roles in controlling gene expression

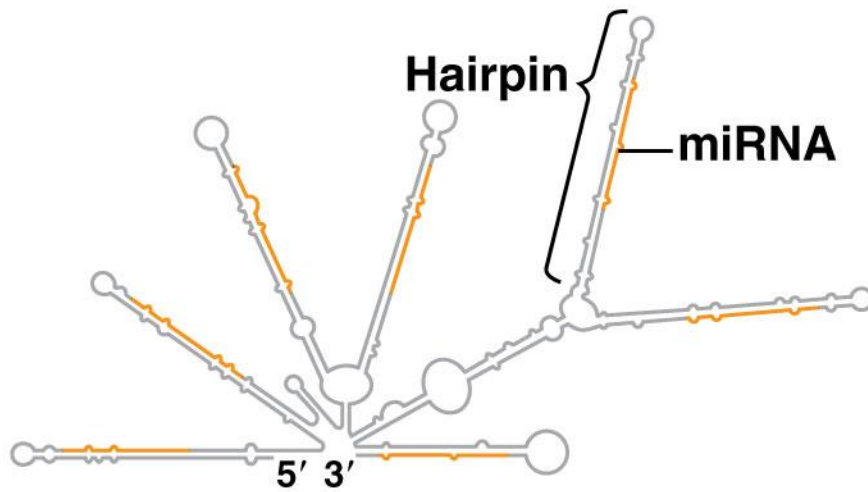
- genome sequencing has shown that protein-coding DNA only accounts for 1.5% of the human genome (& other eukaryotes)
- a small fraction of the non-protein coding DNA consists of genes for rRNAs and tRNAs

18.3: Noncoding RNAs play multiple roles in controlling gene expression

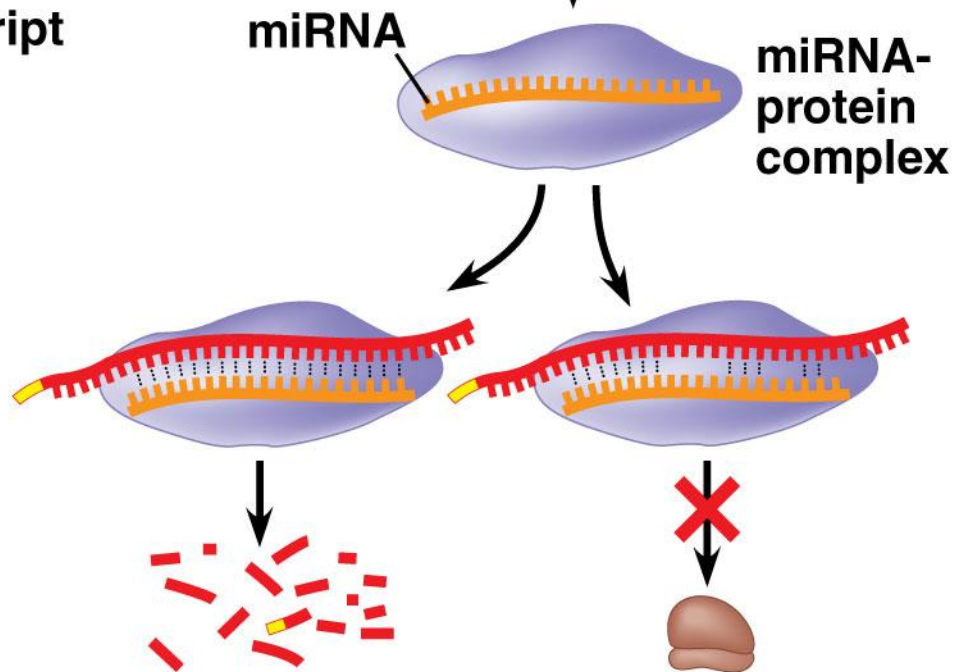
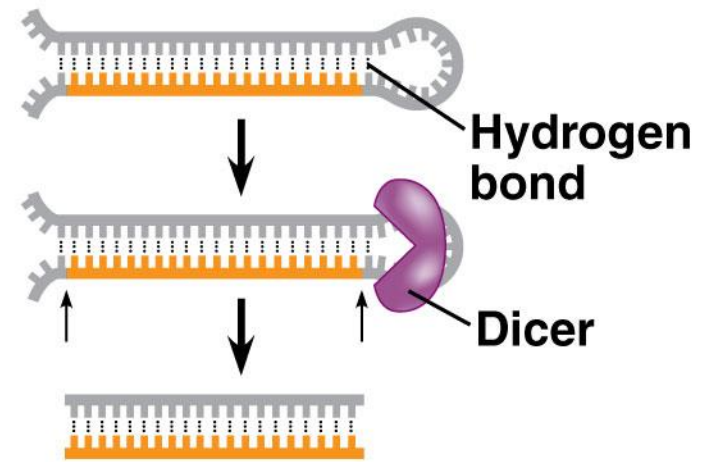
- until recently, researchers assumed that most of the remaining DNA was untranscribed... "junk" DNA
- however, new research suggests that a significant amount of the genome may be transcribed into non-protein-coding RNAs that are involved in regulation of gene expression!!
 - **noncoding RNAs** (ncRNAs)
 - **microRNAs** (miRNAs)
 - **RNA interference** (RNAi)
 - **small interfering RNAs** (siRNAs)

microRNAs (miRNAs)

- small, single-stranded RNA molecules
- capable of binding to complementary sequences in mRNA
- typically, a miRNA forms a complex with 1 or more proteins; this complex then binds with a mRNA
- the result is the mRNA is either degraded or translation of it is blocked



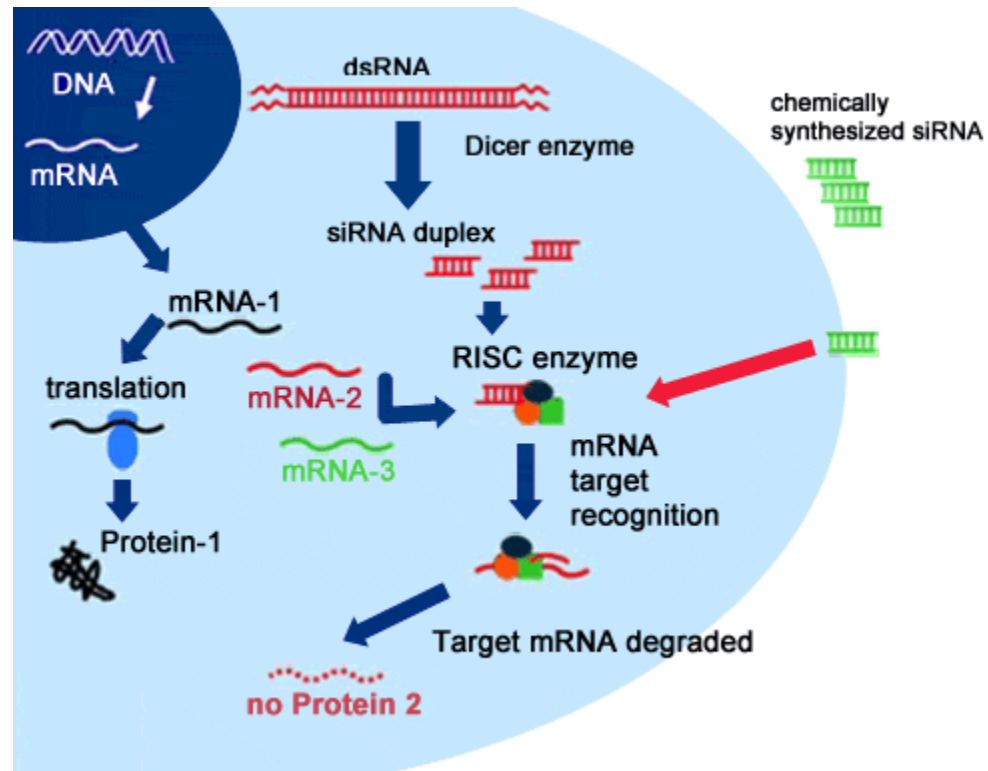
(a) Primary miRNA transcript



(b) Generation and function of miRNAs

RNA interference (RNAi)

- **small interfering RNAs (siRNAs)**, similar to miRNAs, can associate with the same proteins as miRNAs and block expression of a gene with the same sequence as the RNA...



LINK to RNA interference video!