

# Information Processing: Gene Expression



## Regulating gene expression

The processes of transcription and translation described so far tell us what steps are involved in the copying of information from a gene (DNA) into RNA and the synthesis of a protein directed by the sequence of the transcript (Figure 7.102). These steps are required for gene expression, the process by which information in DNA directs the production of the proteins needed by the cell.

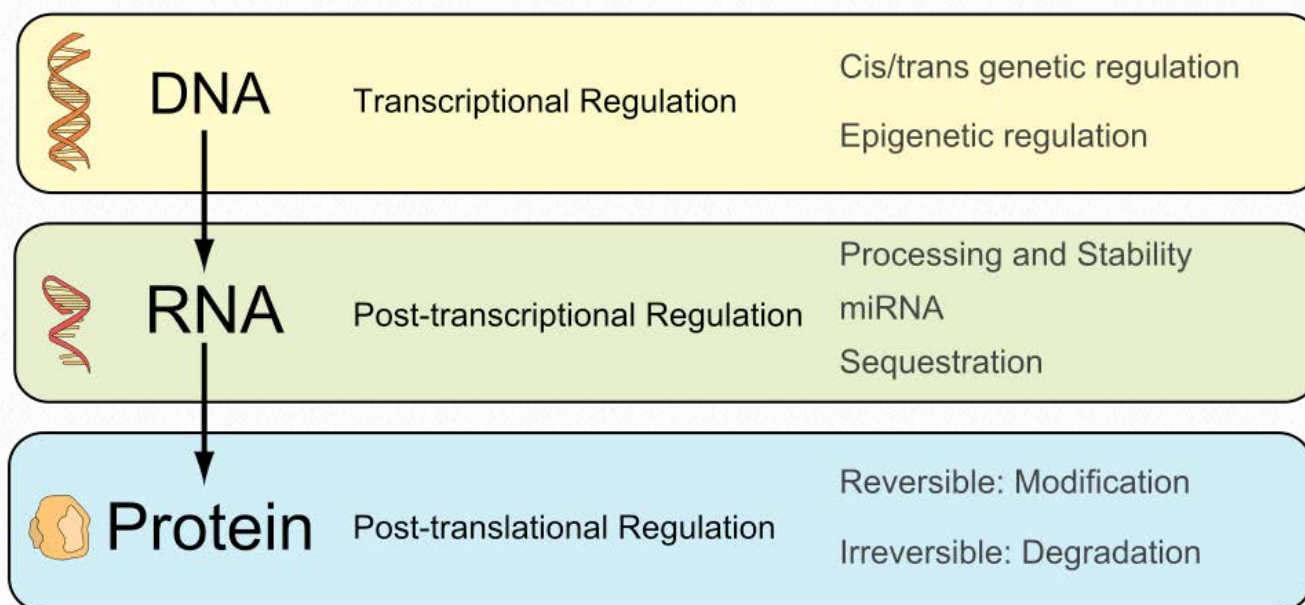
But what determines whether a

gene is expressed at a given time? Cells do not, as we know, express all of their genes all of the time. Some genes are expressed in particular cell types but not others, while others may be expressed at specific stages of development. Cells must also be able alter their patterns of gene expression in response to internal and external cues, controlling the production of proteins as needed, to

meet their changing needs. Regulating gene expression is, therefore, crucial. Given that there are multiple steps involved in gene ex-

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**Figure 7.102 - Multiple levels of control of gene expression** Wikipedia

What are these regulatory sequences and what proteins bind them? In addition to the promoter sequences required for transcription initiation, genes have additional *cis* regulatory sequences (sequences of DNA on the same DNA

pression, there are several different points at which the process could be regulated. Not surprisingly, many regulatory mechanisms are known, each acting at a different stage in the path from DNA to protein.

### Regulation of transcription

The first step in gene expression is transcription, so regulation of transcription is an obvious way to affect whether a gene is expressed and to what extent.

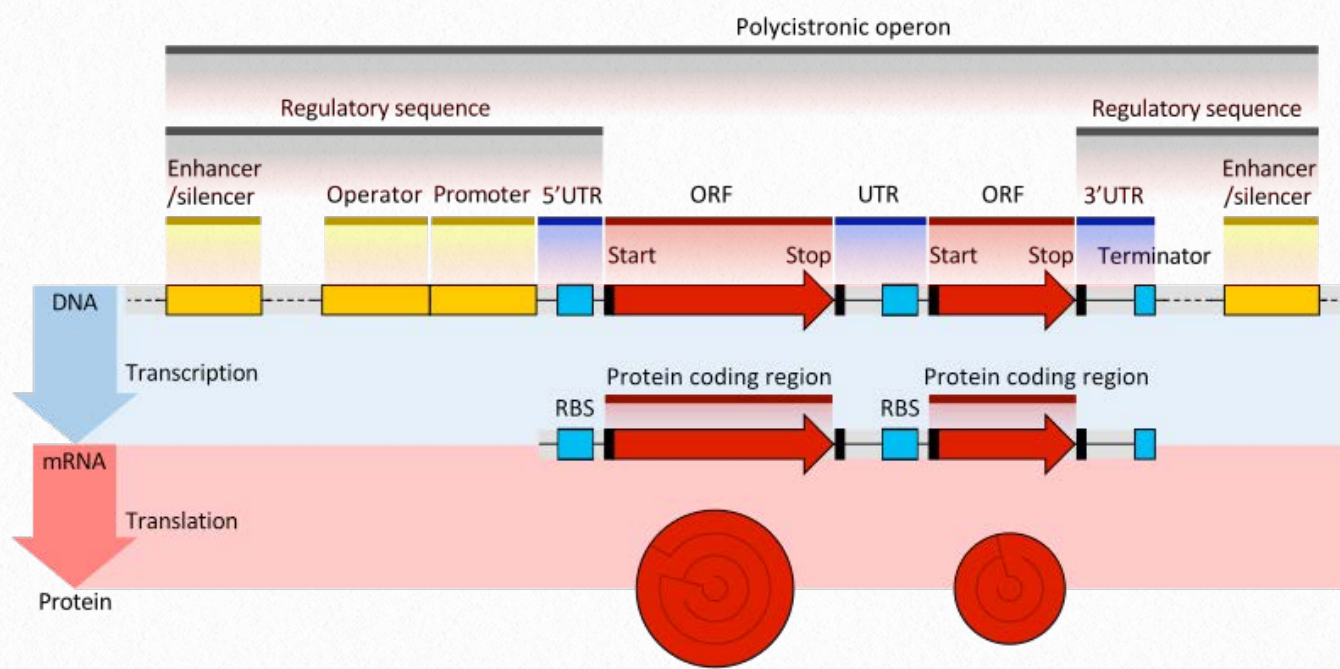
What are the molecular switches that turn transcription on or off? Although there are additional factors that affect transcription, such as the accessibility of a gene to the transcriptional machinery, the basic mechanism by which transcription is regulated depends on highly specific interactions between transcription regulating proteins and regulatory sequences on DNA.

molecule as the gene) that control when a gene is transcribed. Regulatory sequences are bound tightly and specifically by transcriptional regulators, proteins that can recognize DNA sequences and bind to them. The binding of such proteins to the DNA can regulate transcription by preventing or increasing transcription from a particular promoter.

### Transcriptional regulation in prokaryotes

Let us first consider some examples from prokaryotes. In bacteria, genes are often clustered in groups, such that genes that need to be expressed at the same time are next to each other and all of them are controlled as a single unit by the same promoter. Groups of genes that are coordinately regulated by a single promoter are referred to as operons. The entire set of genes in an operon can be controlled through the action of DNA binding proteins



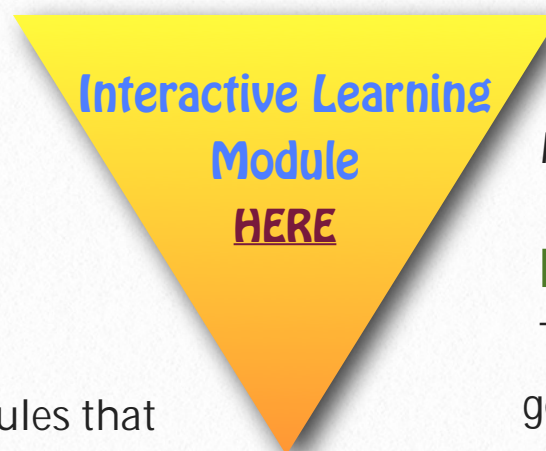


**Figure 7.103 - Prokaryotic genes organized in an operon**

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available, and lactose is present, the bacteria will take up lactose and break it down for energy. Since the proteins for taking up and breaking down lactose are only needed when glucose is absent and lactose is available, the bacterial cells need a way to express the genes of

that act as either repressors (preventing transcription of the genes) or activators (increasing transcription of the genes). The binding of these proteins to their DNA targets is allosterically controlled by the binding of specific small molecules that signal the state of the cell.



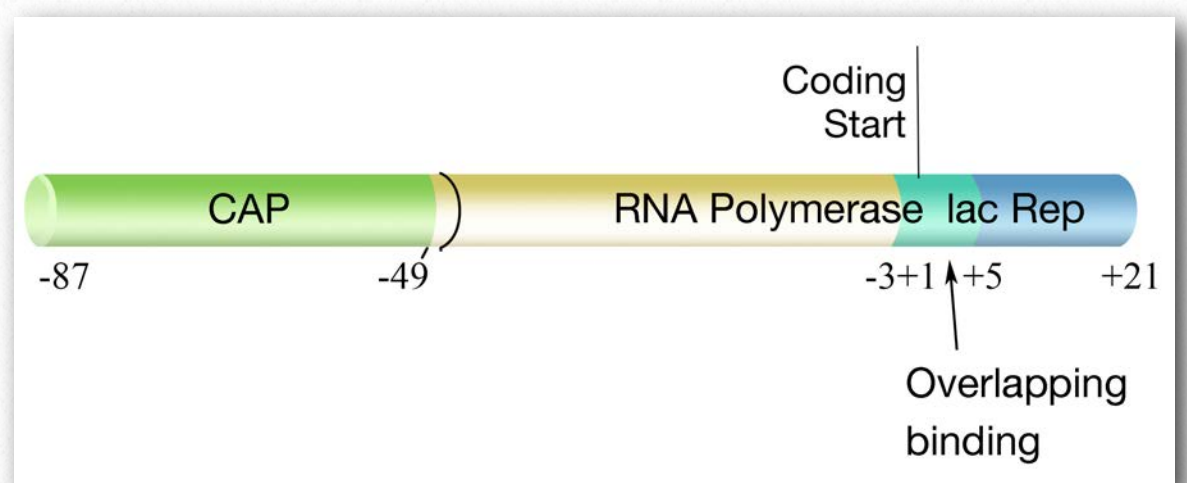
the *lac* operon only under those conditions. The default state of the *lac* operon is OFF.

### Removing a repressor

Transcription of the *lac* cluster of genes is primarily controlled by a repressor protein that binds to a region of the

### Induction of the *lac* operon

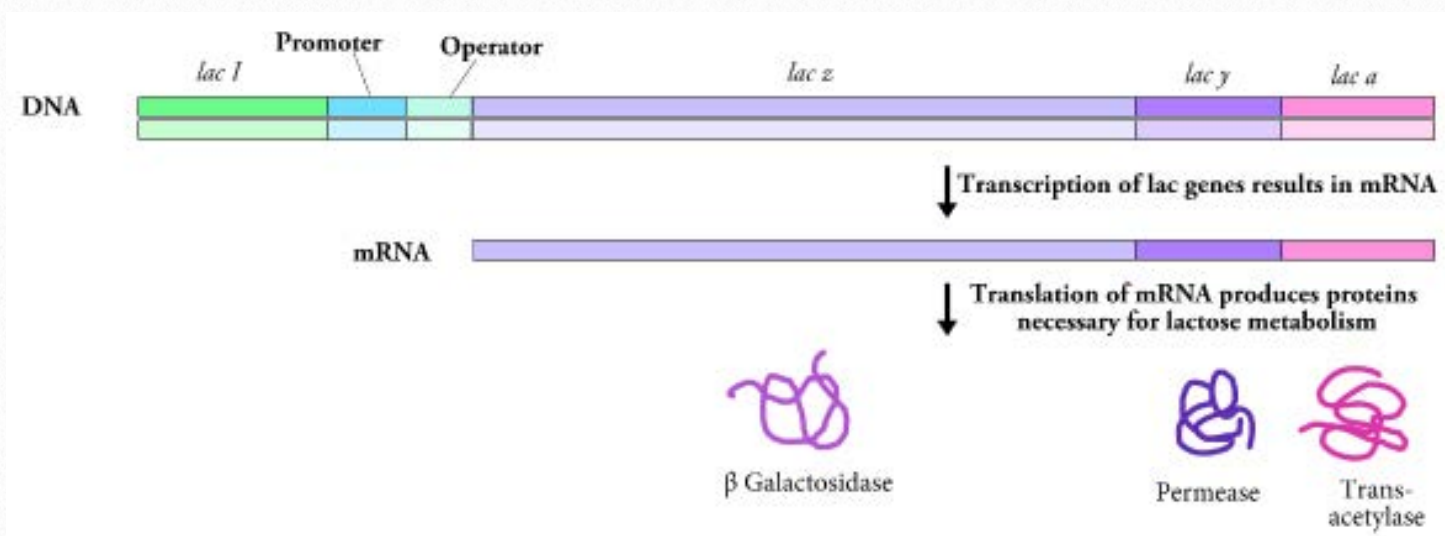
The *lac* operon is one such group of coordinately regulated genes that encode proteins needed for the uptake and breakdown of the sugar lactose. *E.coli* cells preferentially use glucose for their energy needs, but if glucose is un-



**Figure 7.104 - Protein binding sites in the *lac* regulatory region**

Image by Martha Baker





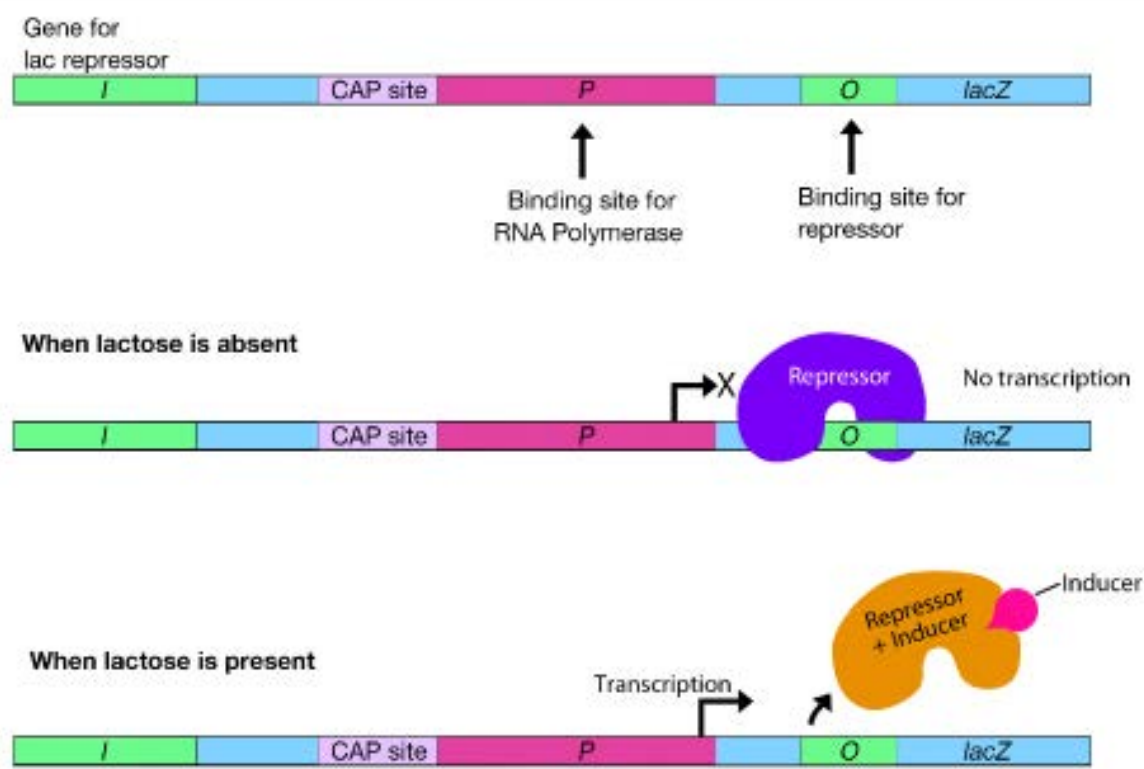
**Figure 7.105 - Lac operon structure and products**

Image by Martha Baker

How is the repressor removed? When the sugar lactose is present, a small amount of it is taken up by the cells and converted to an isomeric form, allolactose (Figure

DNA just downstream of the -10 sequence of the *lac* promoter (Figure 7.104). Recall that the promoter is where the RNA polymerase must bind to begin transcription. The location on the DNA where the lac repressor is bound is called the operator (Figure 7.105). When the repressor is bound at this position, it physically blocks the RNA polymerase from transcribing the genes, just as a vehicle blocking your driveway would prevent you from pulling out. Obviously, if you want to leave, the vehicle that is blocking your path must be removed. Likewise, in order for transcription to occur, the repressor must be removed from the operator to clear the path for RNA polymerase (Figure 7.106).

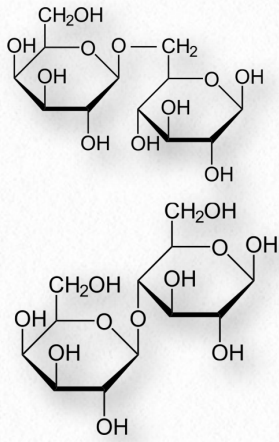
7.107). Allolactose binds to the repressor, changing its conformation so that it no longer binds to the operator. When the repressor is no longer bound to the operator, the "road-block" in front of the RNA polymerase is re-



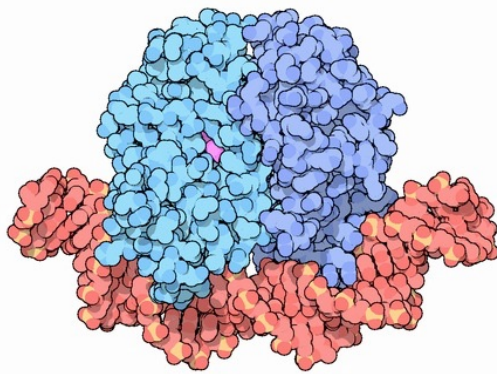
**Figure 7.106 - Lac operon in the absence (middle) and presence (bottom) of inducer**

Image by Martha Baker





**Figure 7.107 - Allolactose (top) and lactose (bottom)**



**Figure 7.108 - CAP (blue) bound to the DNA adjacent to the lac promoter (orange). cAMP shown in pink.**

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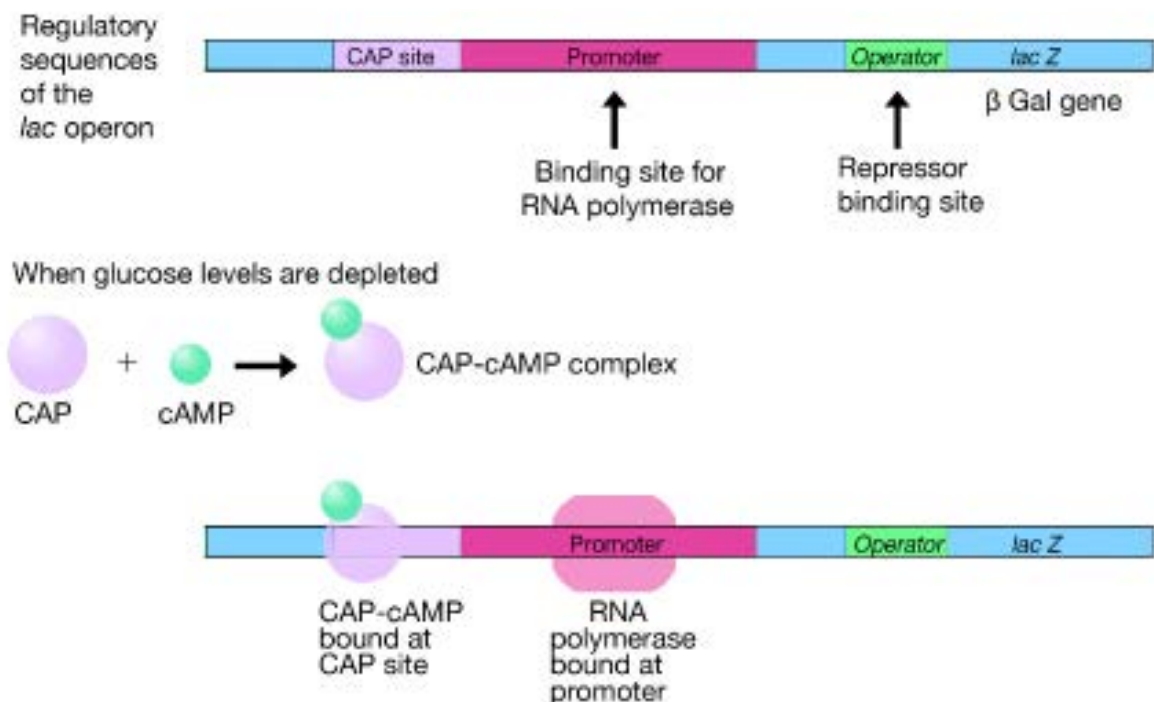
els affect the expression of the *lac* genes? We noted earlier that if glucose was present, lactose would not be used. A second level of control is exerted by a protein called Catabolite Activator Protein (CAP - [Figure 7.108](#)). CAP (also sometimes called CBP or cAMP binding protein) binds to a site adjacent to the promoter and is necessary to recruit RNA polymerase to bind the *lac* promoter.

moved, permitting the transcription of the genes of the *lac* operon

What makes this an especially effective control system is that the genes of the *lac* operon encode proteins that enable the break down of lactose. Turning on these genes requires lactose to be present. Once the lactose has been broken down, the lac repressor binds to the operator once more and the *lac* genes are no longer expressed. This allows the genes to be expressed only when they are needed.

### cAMP binding

CAP binds to its site only when glucose levels are low. Low glucose levels are linked to the activation of an enzyme, adenylate cyclase, that makes the molecule cyclic AMP



**Figure 7.109 - Lac operon in the presence (top) and absence (bottom) of glucose**

Image by Martha Baker

### Recruiting RNA polymerase

But how do glucose lev-



(cAMP). The binding of cAMP to the CAP causes a conformational change in CAP that allows it to bind to the CAP-binding site. When CAP is bound at this site, it is able to recruit RNA polymerase to bind at the promoter, and begin transcription.

The combination of CAP binding and the lac repressor dissociating from the operator when lactose levels are high ensures transcription of the lac operon just when it is most needed. The binding of CAP may be thought of as a green light for the RNA polymerase, while the removal of lac repressor is like the lifting of a barricade in front of it. When both conditions are met, the RNA polymerase transcribes the downstream genes.

### Control of the *trp* operon by repression

The *lac* operon we have just described is a set of genes that are expressed only under the specific conditions of glucose depletion and lactose availability. Other genes may be expressed *unless* a particular condition is met.

For these genes, the default state is ON.

An example of this is the *trp* operon, which encodes enzymes necessary for the synthesis of the amino acid tryptophan. These genes are constitutively expressed (always on), except when tryptophan is available from the cell's surroundings, making its synthesis unnecessary. Under conditions where tryptophan is abundant in the environment, the *trp* genes can be turned off. This is achieved by a repressor protein that will bind to the operator only in the presence of tryptophan (Figure 7.110). Binding of tryptophan to the repressor causes binding of the repressor to the operator. Be-

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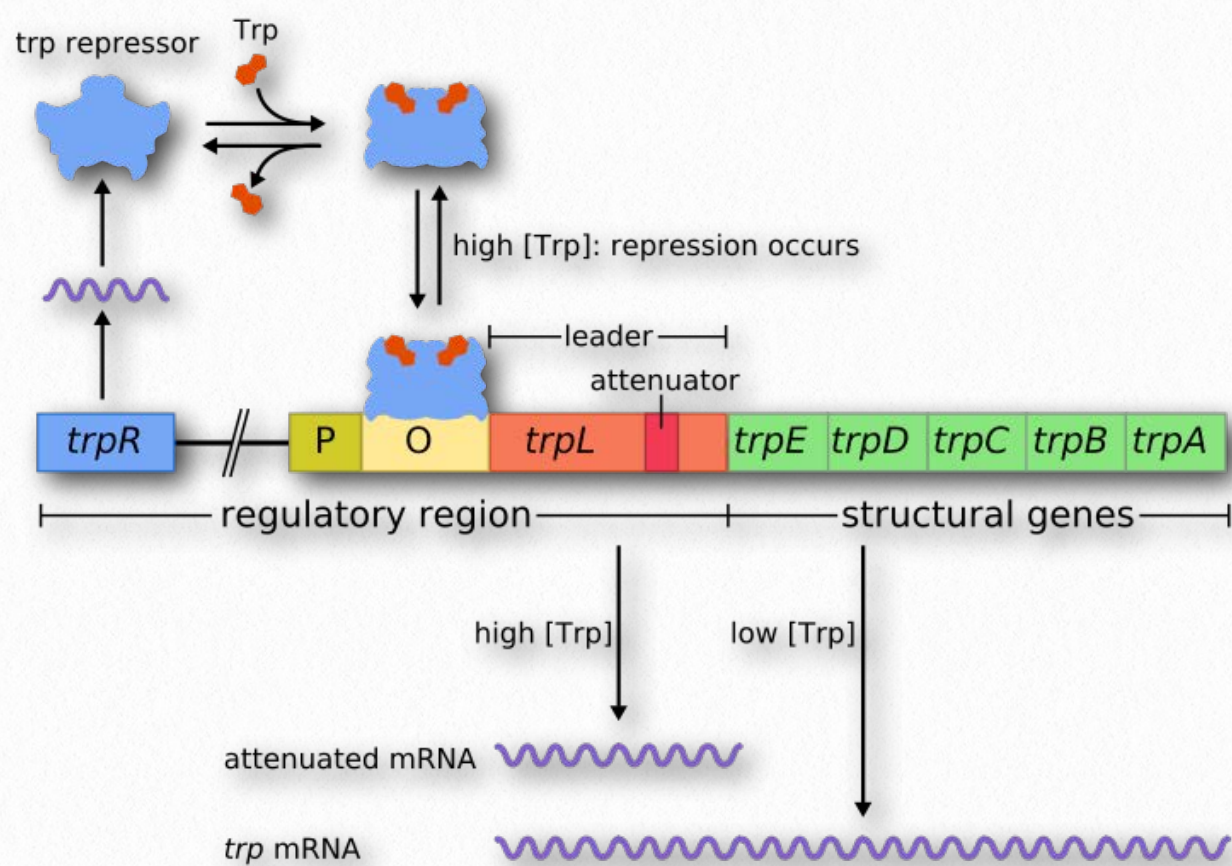


Figure 7.110 - Structure and regulation of the *trp* operon

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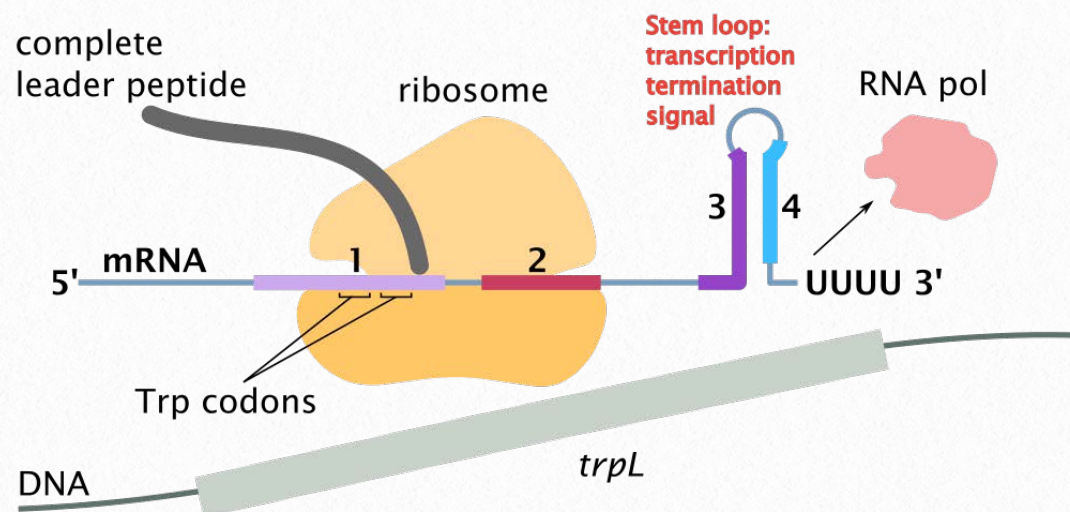


## Attenuation

Another mechanism that regulates the expression of the *trp* operon is attenuation. Attenuation is a process by which the expression of an operon is controlled by termination of transcription before the first gene of the operon (Figure 7.111).

In the *trp* operon, this functions as follows: Transcription begins some distance upstream of the first gene in the operon, producing what is termed a 5' leader sequence. This leader sequence contains an intrinsic terminator that can form a hairpin structure that stops tran-

### High level of tryptophan



### Low level of tryptophan

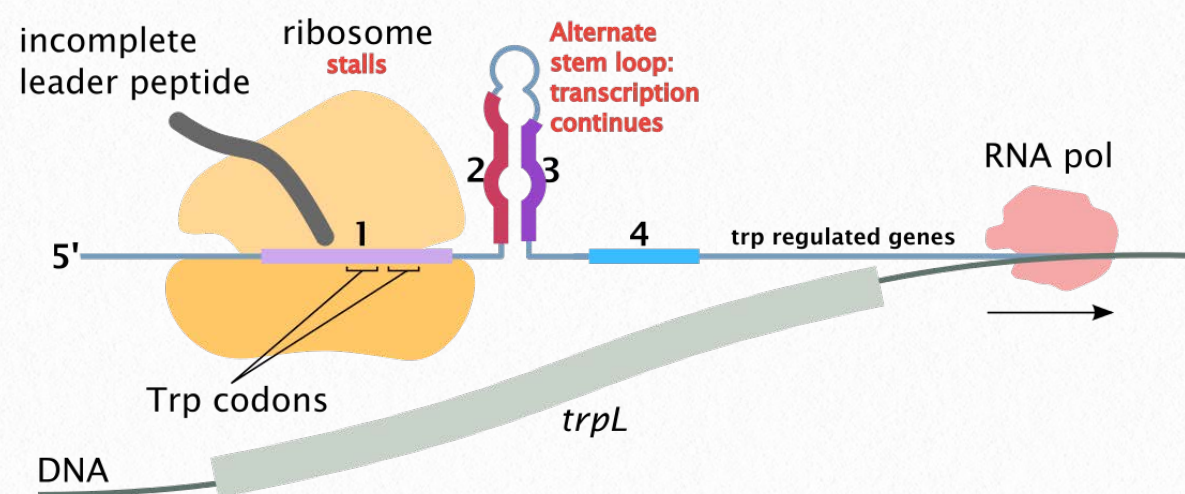


Figure 7.111 - Attenuation in regulation of the *trp* operon

Wikipedia

cause it acts together with the repressor to turn off the *trp* genes, tryptophan is called a co-repressor.

scription when high levels of tryptophan are available to the cells. It can also form a different structure that permits continued tran-

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XX AUG AAA GCA AUU UUC GUA CUG AAA GGU UGG UGG CGC ACU UCC UGA -XX
MET LYS ALA ILE PHE VAL LEU LYS GLY TRP TRP ARG THR SER STOP
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Figure 7.112 - Sequence of the leader region of the *trp* operon



scription of the genes in the operon when tryptophan levels are low. How does the level of tryptophan influence which of these two structures are formed?

Recall that the 5' end of the RNA is the first part of the transcript to be made and that in bacteria translation is linked to transcription, so the 5' end of the RNA begins to be translated before the entire transcript is made. It turns out that the 5' leader sequence of the *trp* operon mRNA encodes a short peptide that contains two tryptophan codons. If there is plenty of tryptophan available, the leader sequence will be easily translated. Under these conditions, the leader sequence is able to form the termination hair-

pin, preventing the transcription of the downstream *trp* genes.

If, however, levels of tryptophan are low, then the ribosome stalls as it attempts to translate the leader sequence. Under these conditions, the leader sequence adopts a different conformation that permits continued transcription of the genes of the *trp* operon.

## Riboswitches

Similar in concept to the attenuation of the *trp* operon described above, but not dependent on translation, is a control mechanism called a riboswitch (Figure 7.113). Riboswitches are typically found in the 5'UTR

of messenger RNAs (i.e., they are part of the sequence of the RNA).

These sequences can control transcription of the downstream genes based on the conformation they adopt. One conformation allows continued transcription, while the other terminates it. So, what determines which conformation they adopt?

## Features

Riboswitches have two characteristic features that are important for their function. One is a region of the sequence called an aptamer, which folds into a three-dimensional shape that can bind a small effector molecule. The other is an adjacent region of the

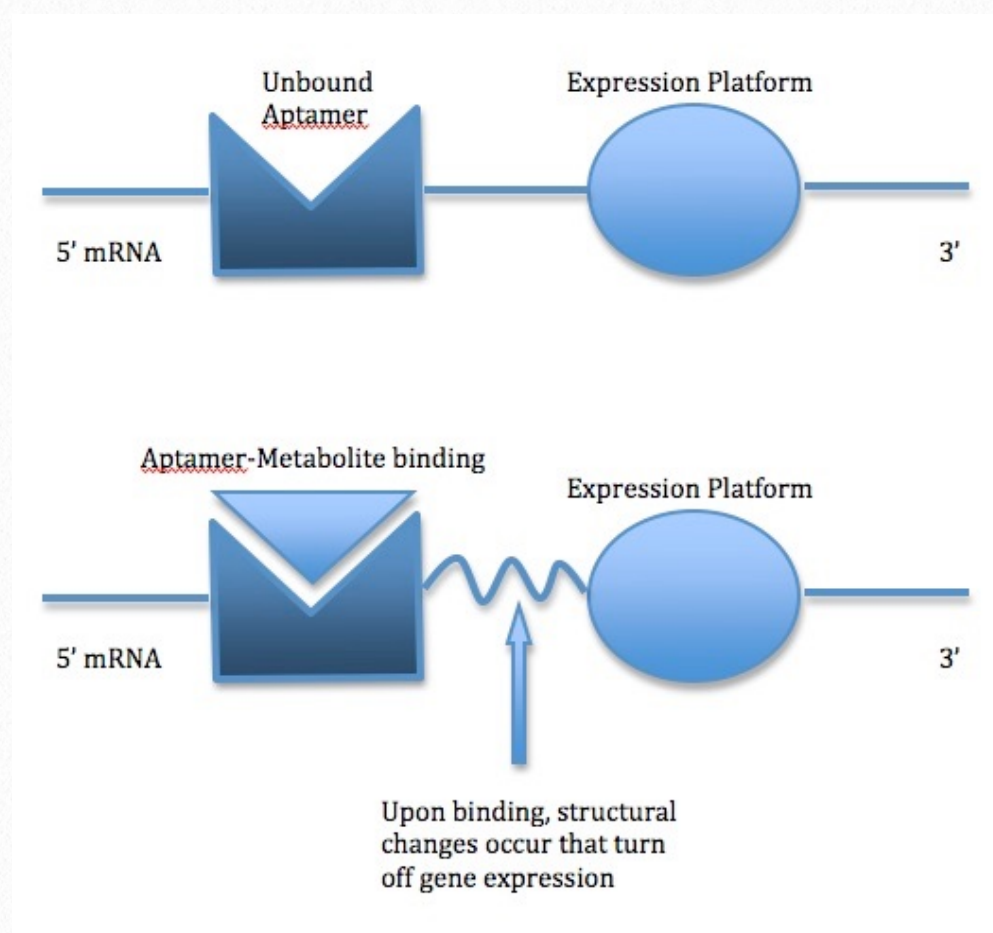
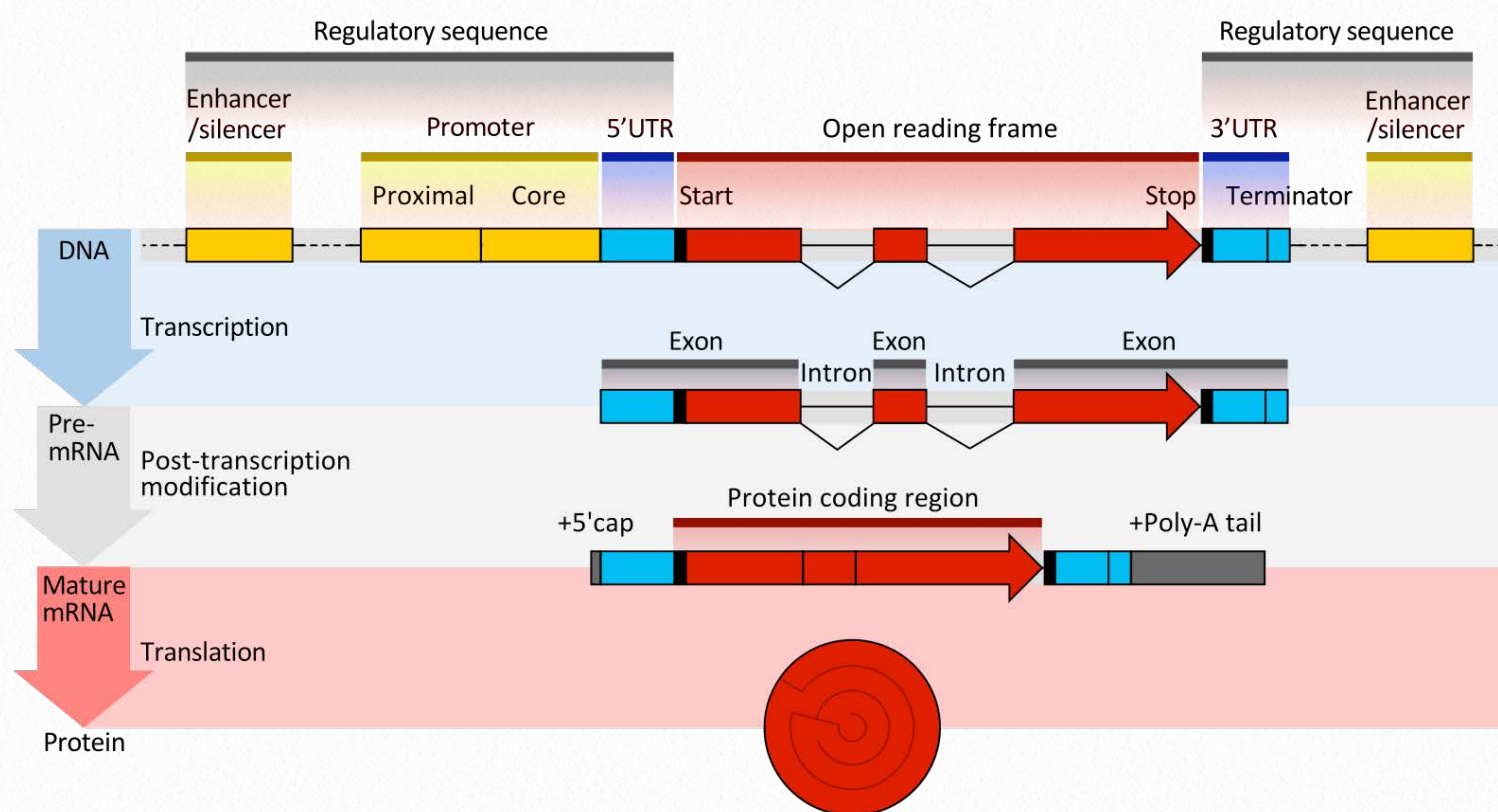


Figure 7.113 - Riboswitch features





**Figure 7.114 - Regulatory sequences for a eukaryotic gene**

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RNA, called the expression platform, that can fold into different conformations depending on whether or not the aptamer is bound to the effector.

An example of a riboswitch found in bacteria is the guanine riboswitch, which controls the expression of genes required for purine biosynthesis. The aptamer region of this riboswitch binds to the effector, guanine, when levels of the base are high. The binding of the guanine triggers a change in the folding of the downstream expression platform, causing it to adopt a conformation that terminates transcription of the genes needed for the synthesis of guanine. In the absence of guanine, the expression platform assumes a different conformation that allows

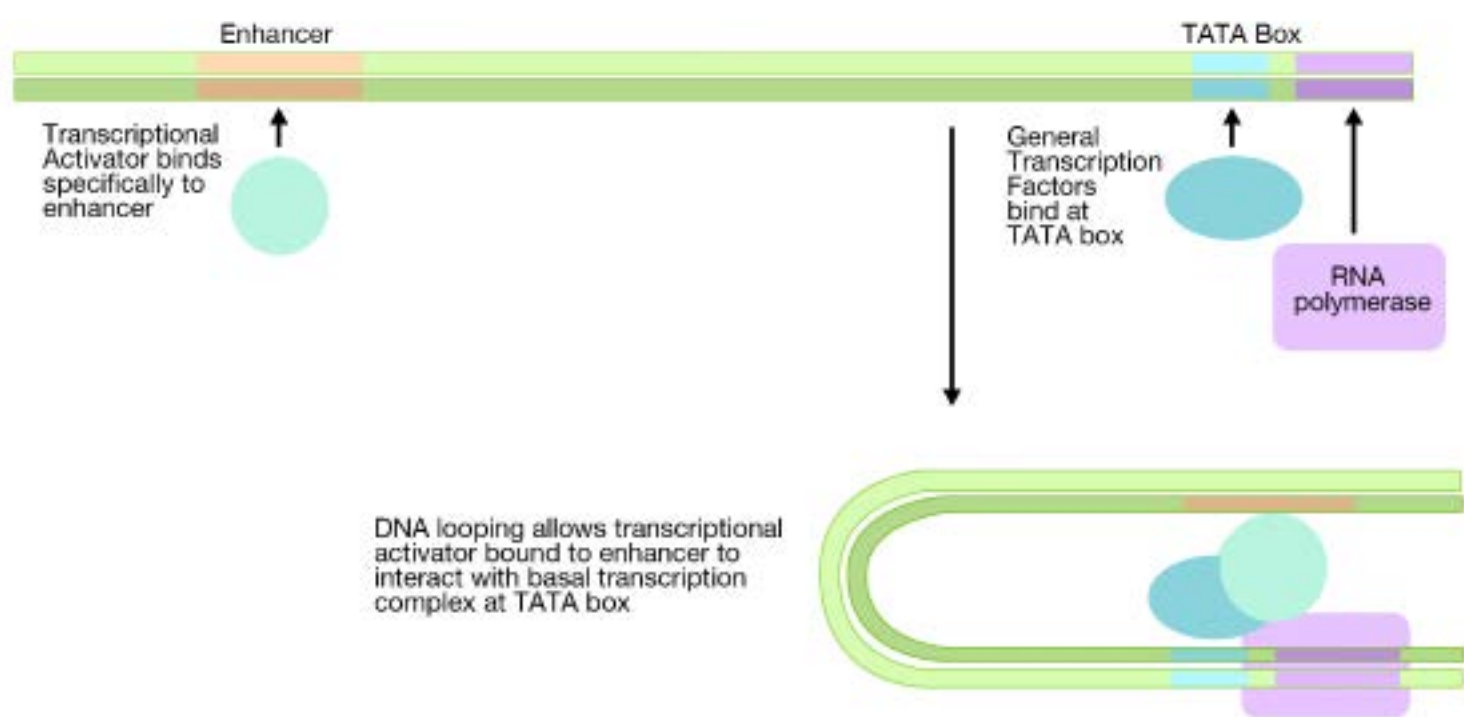
transcription of the purine biosynthesis genes. Thus, levels of guanine can be sensed and the genes needed for its synthesis can be expressed as needed.

### Regulation of transcription in eukaryotes

Transcription in eukaryotes is also regulated by the binding of proteins to specific DNA sequences, but with some differences from the simple schemes outlined above.

For most eukaryotic genes, general transcription factors and RNA polymerase (i.e., the transcription initiation complex) are necessary but not sufficient for high levels of transcription. Promoter-proximal DNA sequences like the CAAT box and GC





**Figure 7.115 - DNA looping allows contact between activator bound at a distant enhancer and the basal transcription complex**

Image by Martha Baker

box bind proteins that interact with the transcription initiation complex, influencing its formation (Figure 7.114).

### Distant regulatory sequences

Additional regulatory sequences called enhancers and the proteins that bind to them are needed to achieve high levels of transcription. Enhancers are short DNA sequences that regulate the transcription of genes, but may be located at a distance from the gene they control (although they are on the same DNA molecule as the gene). Often enhancers are many kilobases away on the DNA, either upstream or downstream of the gene. As the name suggests, enhancers can enhance (increase) transcription of a particular gene. How can a DNA sequence far from

the gene being transcribed affect the level of transcription?

### Transcriptional activators

Enhancers work by binding proteins (transcriptional activators) that can, in turn, interact with the proteins bound at the promoter. The enhancer region of the DNA, with its associated transcriptional activator(s) can come in contact with the transcription initiation complex that is bound at a distant site by looping of the DNA (Figure 7.115). This allows the protein bound at the enhancer to make contact with the proteins in the basal transcription complex. The interaction of the activator with the transcription initiation complex may be direct, or it may be through a “middle-man”, a protein complex called mediator.



# transcription factors of eukaryotic cells

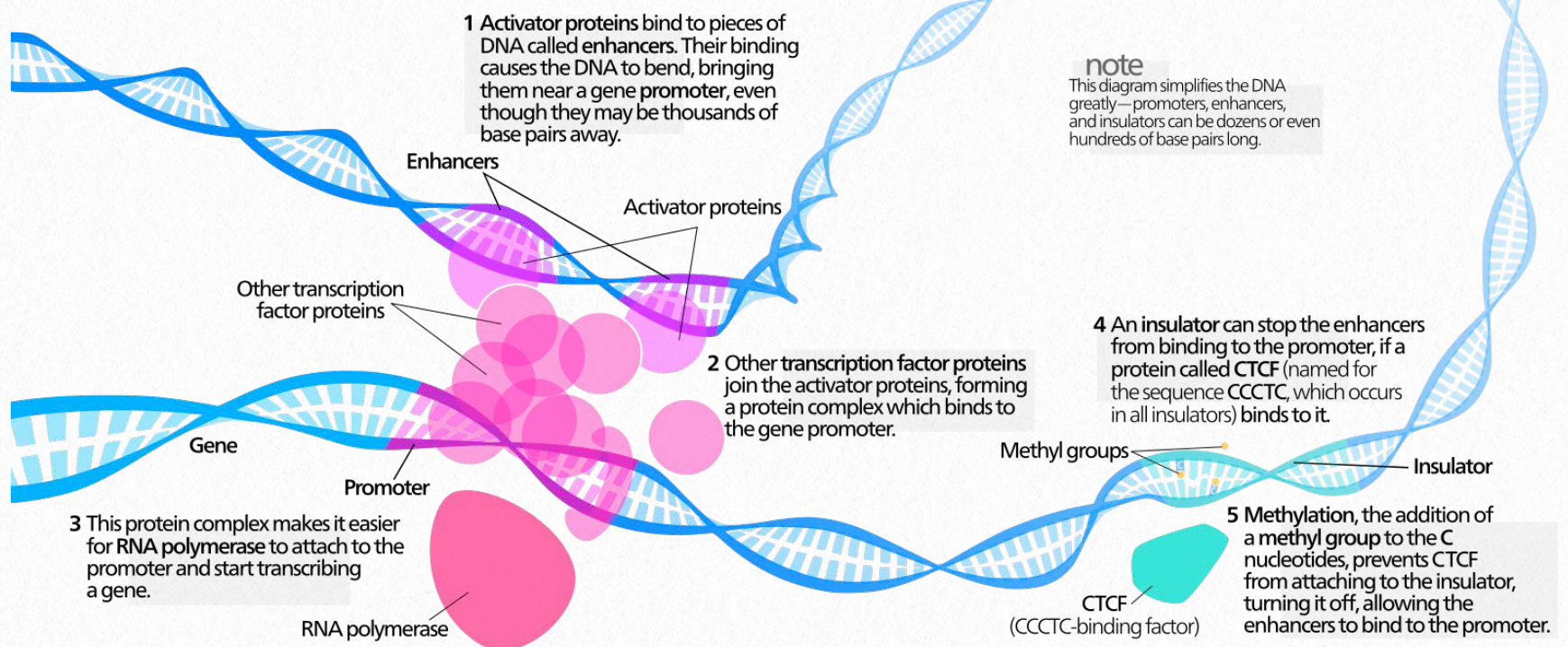


Figure 7.116 - Transcription factors in regulation of eukaryotic transcription

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One effect of this interaction is to assist in recruiting proteins necessary for transcription, like the general transcription factors and RNA polymerase to the promoter, increasing the frequency and efficiency of formation of the transcription initiation complex. There is also evidence that at some promoters, following assembly of the transcription initiation complex, the RNA polymerase remains stalled at the promoter. In such cases, the interaction with the transcription initiation complex of an activator bound to an enhancer could play a role in facilitating the transition of the RNA polymerase to the elongation phase of transcription.

## Chromatin remodeling proteins

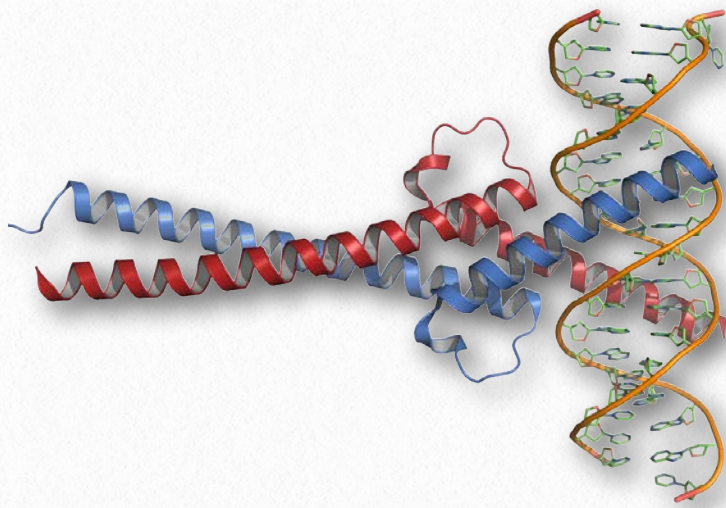
Another mechanism by which activators bound at the enhancer can affect transcription is by recruiting to the promoter proteins that can modify the structure of that region of the chromosome. In eukaryotes, DNA is packaged with proteins to form chromatin. When the DNA is tightly associated with these proteins, it is difficult to access for transcription. So proteins that can make the DNA more accessible to the transcription machinery can also play a role in the extent to which transcription occurs.

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## Silencers

In addition to enhancers, there are also negative regulatory se-





**Figure 7.117 - Binding of c-myc protein to its target DNA sequence**

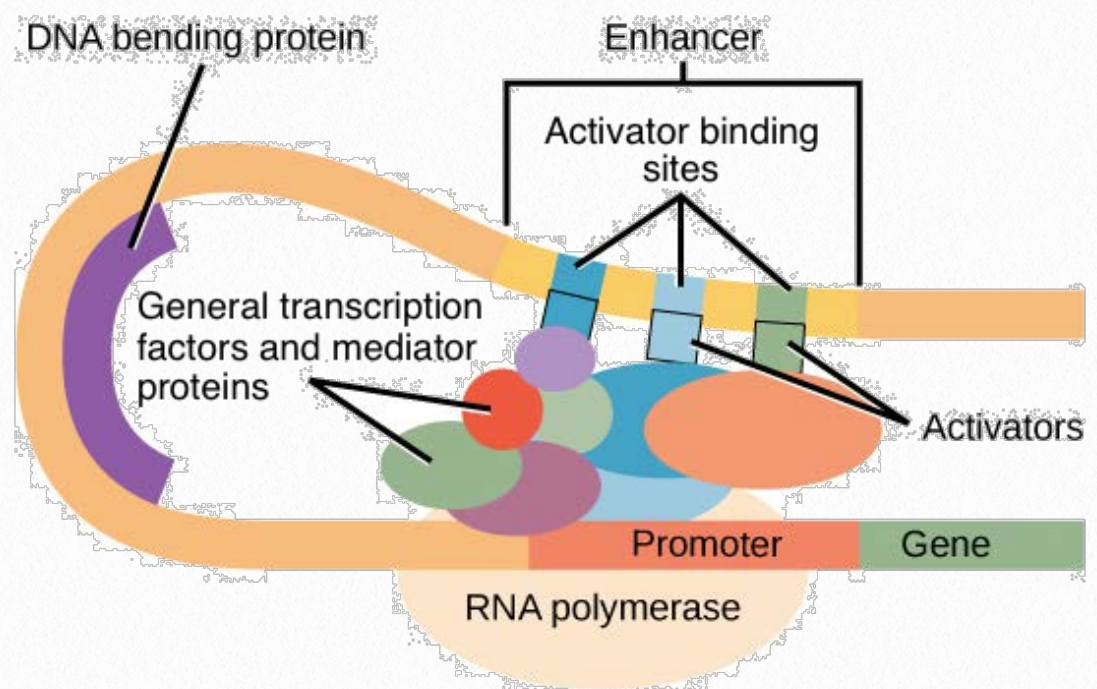
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quences called silencers. Such regulatory sequences bind to transcriptional repressor proteins. Like the transcriptional activators, these repressors work by interacting with the transcription initiation complex. In the case of repressors, the effect they have on the transcription initiation complex is to reduce transcription.

### DNA binding proteins

Transcriptional activators and repressors are modular proteins- they have a part that binds DNA and a part that activates or represses transcription by interacting with the transcription initiation complex (Figure 7.118). The DNA binding domain is the part of the protein that confers specificity for determining which gene(s) will be activated or repressed. The activation domain is

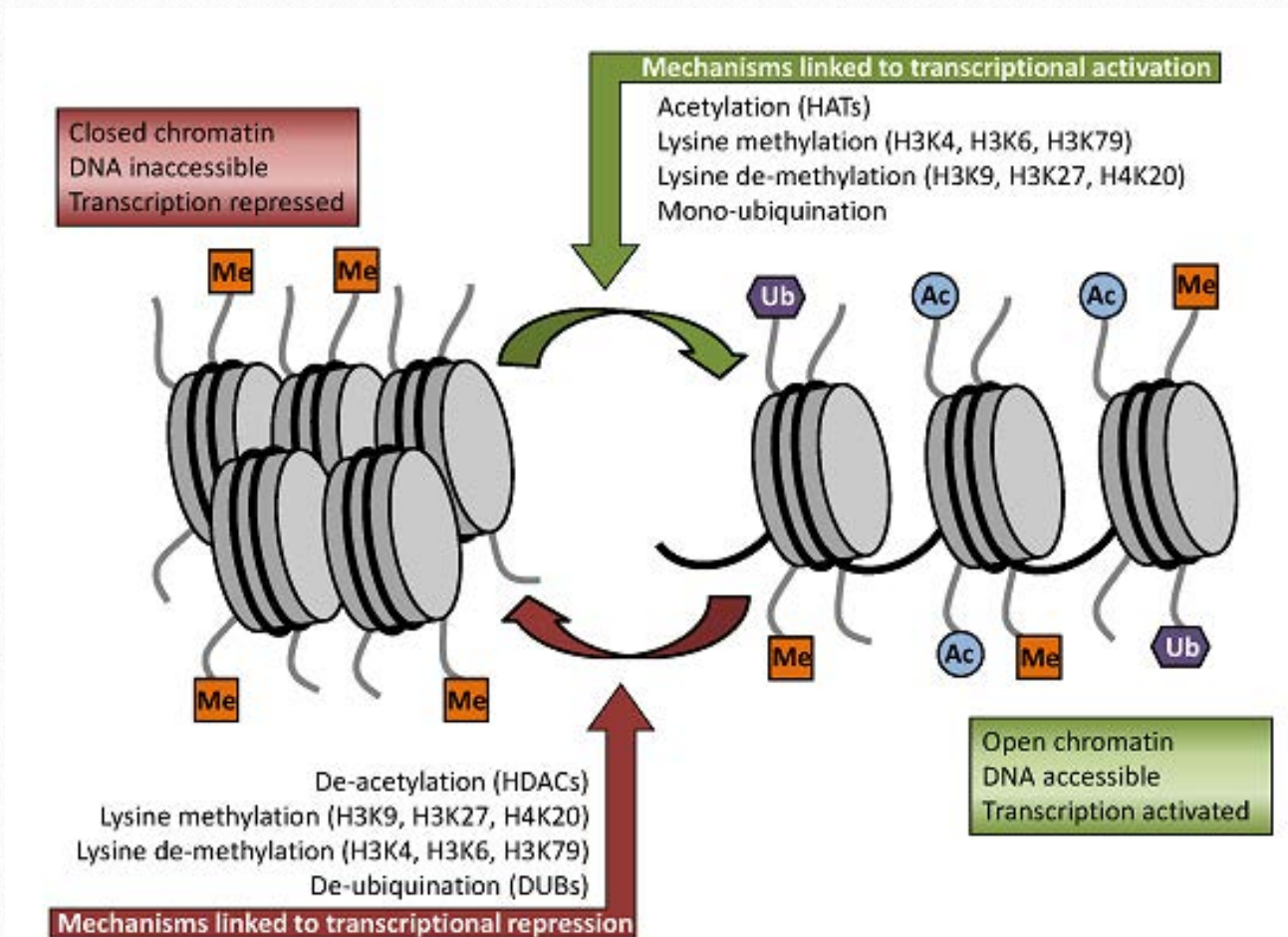
the part of the protein that stimulates or represses transcription. The DNA binding domains of transcriptional activators form characteristic structures that recognize their target DNA sequences by making contacts with bases, usually in the major groove of the DNA helix. It is possible to engineer hybrid transcription factors that combine the DNA binding domain of one activator with the activation domain of another. Such proteins retain the specificity dictated by the DNA binding domain. Truncated transcription factors can also be generated that have their DNA binding domain but lack the activation domain. Such transcription factors can be useful tools in studying transcriptional regulation because their DNA binding domains can compete with the endogenous



**Figure 7.118 Activators bound at multiple sites can regulate transcription from a given promoter**

OpenStax





**Figure 7.119 - Transcriptional activation (right) and deactivation (left) by histone modification**

Wikipedia

transcription factors for regulatory binding sites without increasing transcription from the target promoters.

### Multiple factors

The description above may suggest that each gene in eukaryotes is controlled by the binding of a single transcriptional activator or repressor to a particular enhancer or silencer site. However, it turns out that the transcription of any given gene may be simultaneously regulated by a combination of proteins, both activators and repressors, bound at multiple regulatory sites on the DNA, all of which interact with the transcription initiation complex. The combi-

natorial nature of such regulation provides great versatility, with different combinations of regulatory elements and proteins working together in response to a wide variety of conditions and signals.

The mechanisms described so far have focused on the sequence elements in DNA that regulate transcription through the activa-

tor and repressor proteins bound to them. Following transcription, alternative splicing (see [HERE](#)) and editing of the transcripts can also modify the proteins that are produced by the cell. We will now examine some of the other ways in which gene expression is modulated in cells.

First, we will consider some so-called epigenetic mechanisms that affect gene expression. The term epigenetics derives from epi (above, or on top of) and genetic (of genes) and refers to the fact that these mechanisms act in addition to, or overlaid on, the information in the gene sequences. Two such epigenetic mechanisms are the covalent modifications of his-



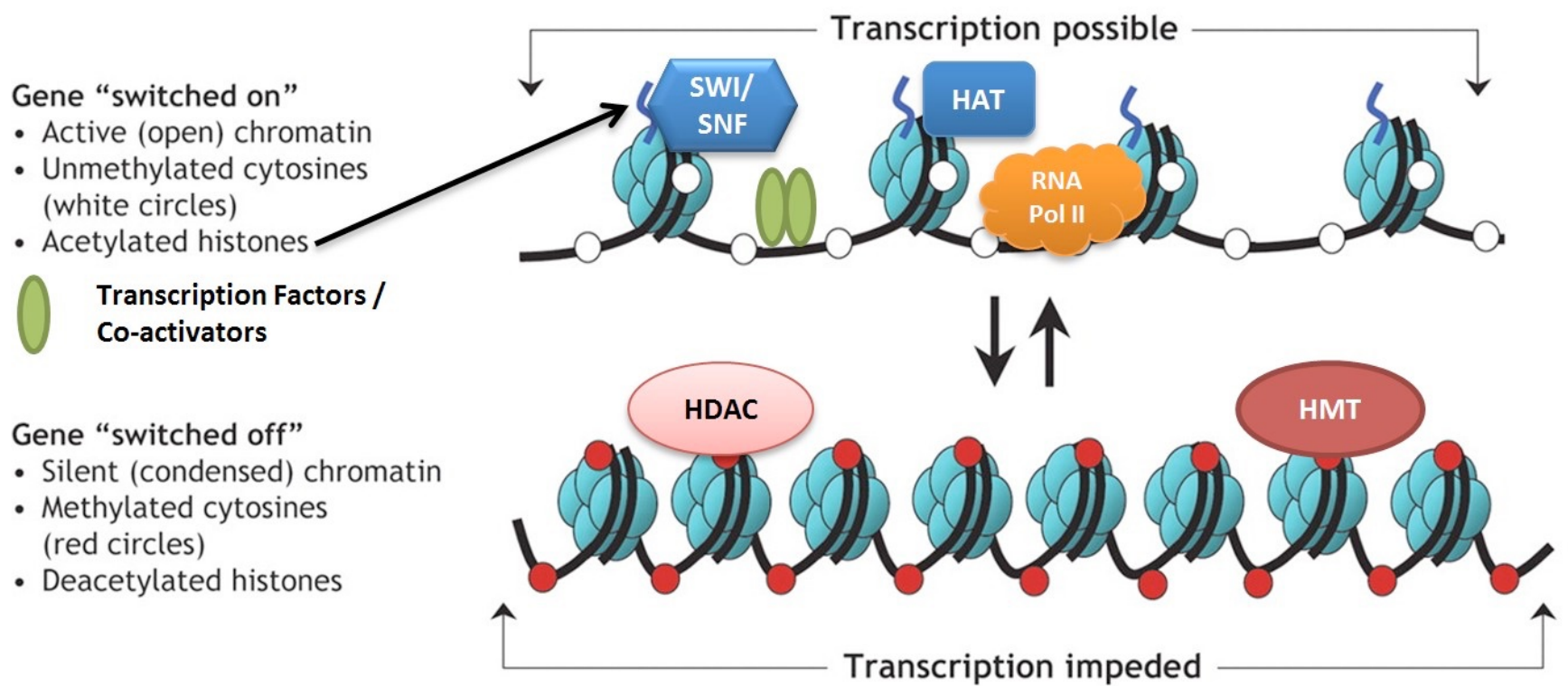


Figure 7.120 - Chromatin configuration affects transcription

Wikipedia

tones in chromatin and the methylation of DNA sequences.

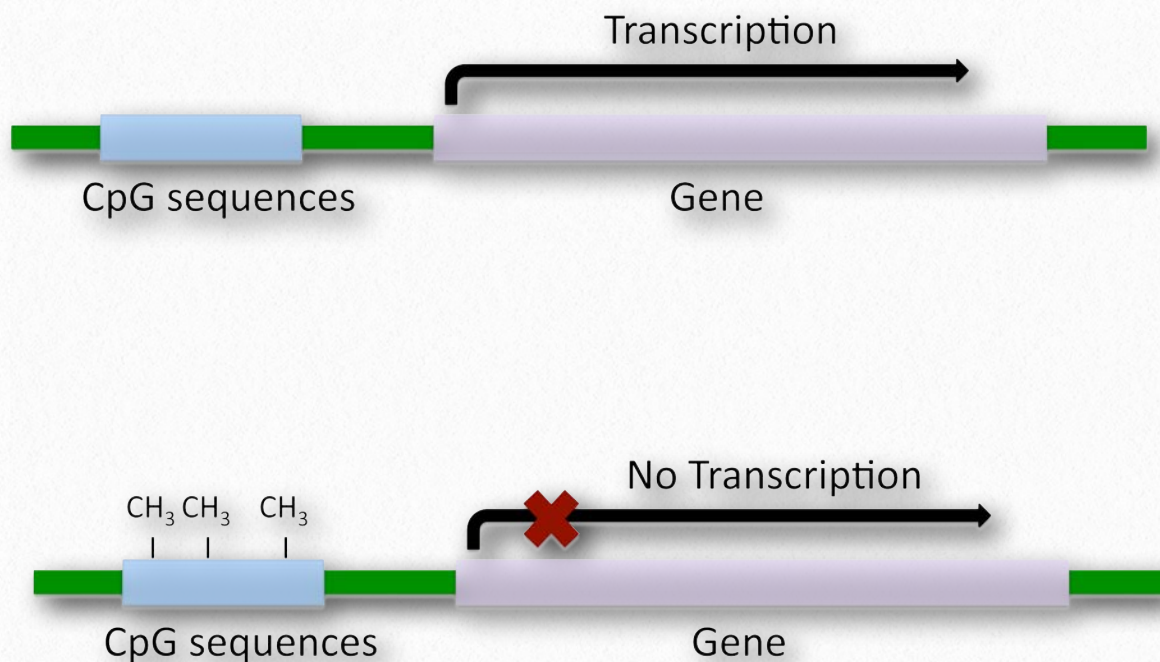
## Histone modification

As noted earlier, transcription in eukaryotes is complicated by the fact that the DNA is packaged with histones to make chromatin. This means that for a gene to be transcribed, the relevant regions of the chromatin must be opened up to allow access to the RNA polymerase and transcription factors. This provides another potential point of control of gene expression. Chromatin remodeling factors, mentioned earlier, assist in reorganizing the nucleosome structure at regions that need to be made accessible.



But what determines that a given region of the chromatin will be acted upon by the remodeling complexes? Transcriptional activator proteins bound at enhancers, sometimes work by recruiting histone modifying enzymes to the promoter region. An example of such a modifying enzyme is histone acetyl transferase (HAT) that works to acetylate specific amino acid residues in the tails of the histones forming the nucleosome core (Figures 7.119 & 7.120). Acetylation of histones is thought to be responsible for loosening the interaction between histones and the DNA in nucleosomes and helps to make the DNA more readily accessible for transcription. The opposite effect may be achieved if the enzymes recruited are histone deacetylases





**Figure 7.121 - Inactivation of transcription by CpG methylation**

Image by Indira Rajagopal

(HDAC) which remove acetyl groups from the tails of the histones in the nucleosome, and lead to tighter packing of the chromatin.

### Writers, readers and erasers

In addition to the histone acetyl transferases and the deacetylases, other enzymes may add or remove methyl groups, phosphate groups, and other chemical moieties to specific amino acid side chains on the histone tails. The patterns of these covalent modifications, sometimes called the histone code, are established by the so-called "writers", or enzymes, such as histone methyltransferases, that add the chemical groups on to the histone tails. Yet other enzymes, like the histone demethylases, may act as "erasers," removing the

chemical groups added by the "writers." The histone code is interpreted by "readers," proteins that bind to specific combinations of the modifications and assist in either silencing the expression of genes in the vicinity or making the region more transcriptionally active.

### DNA methylation

Gene expression can also be regulated by methylation

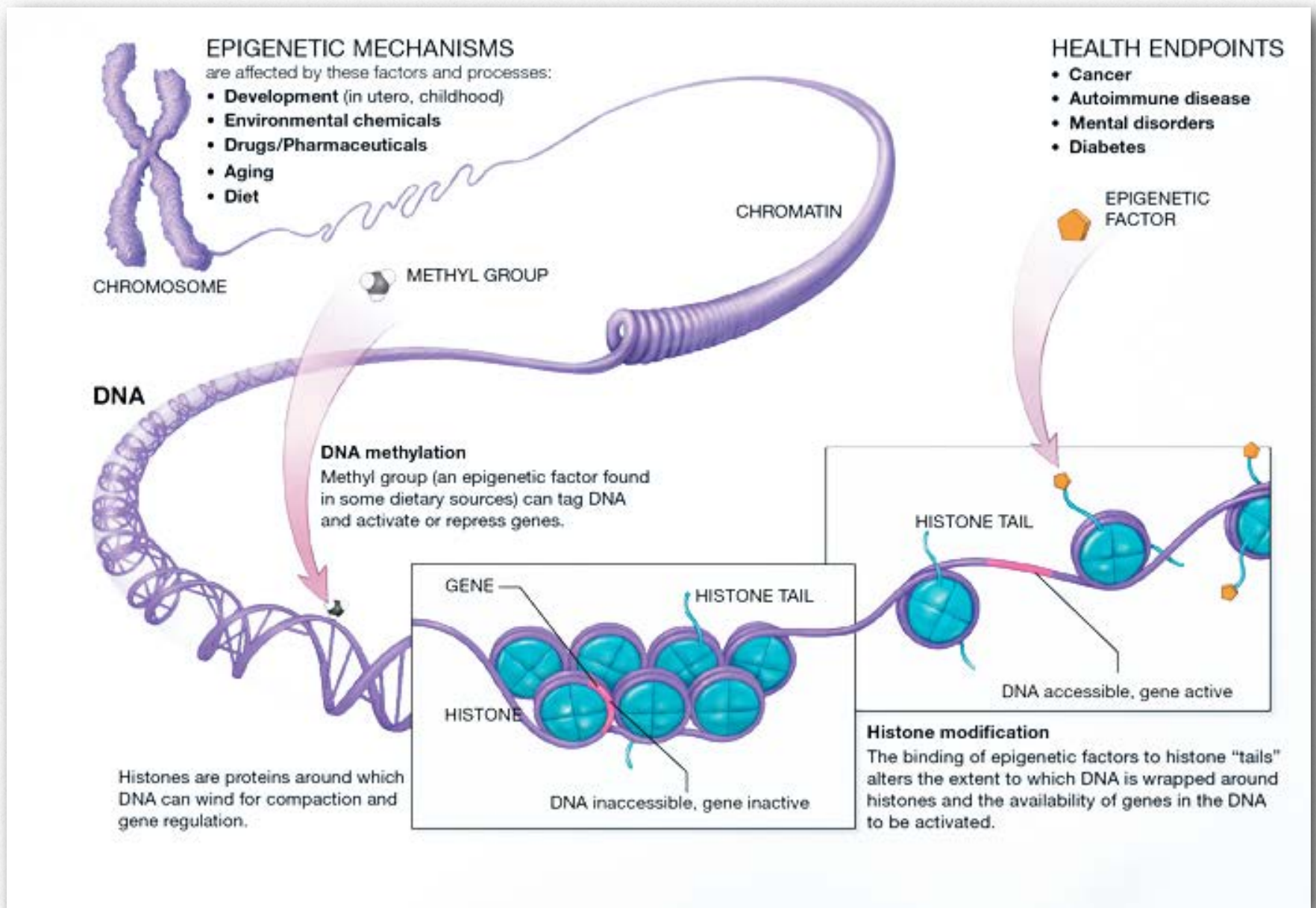
of the other component of chromatin - DNA. Enzymes called DNA methyltransferases (DNMTs) catalyze the covalent addition of a methyl group to C<sub>5</sub> of cytosines in DNA. Patterns of cytosine methylation vary in different organisms, with methylation concentrated in some parts of the genome in some groups and scattered throughout the genome in others. In vertebrates, the cytosines that are methylated are generally next to a guanine (the CG dinucleotide is commonly abbreviated as CpG). Methylation of

DNA seems to correlate with gene silencing while demethylation is associated with increased transcription ([Figure 7.121](#)).

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How does methylation of the DNA at CpG sites regulate gene expression? Although the extent of DNA methylation near promoters





**Figure 7.122 - Epigenetic changes through histone and DNA modification**

has been observed to correlate with gene silencing, it is not clear how exactly methylation brings about this effect. It has been suggested that methylation could block the binding of proteins necessary for transcription. Methylation at enhancer sites might also prevent the binding of transcriptional activators to them.

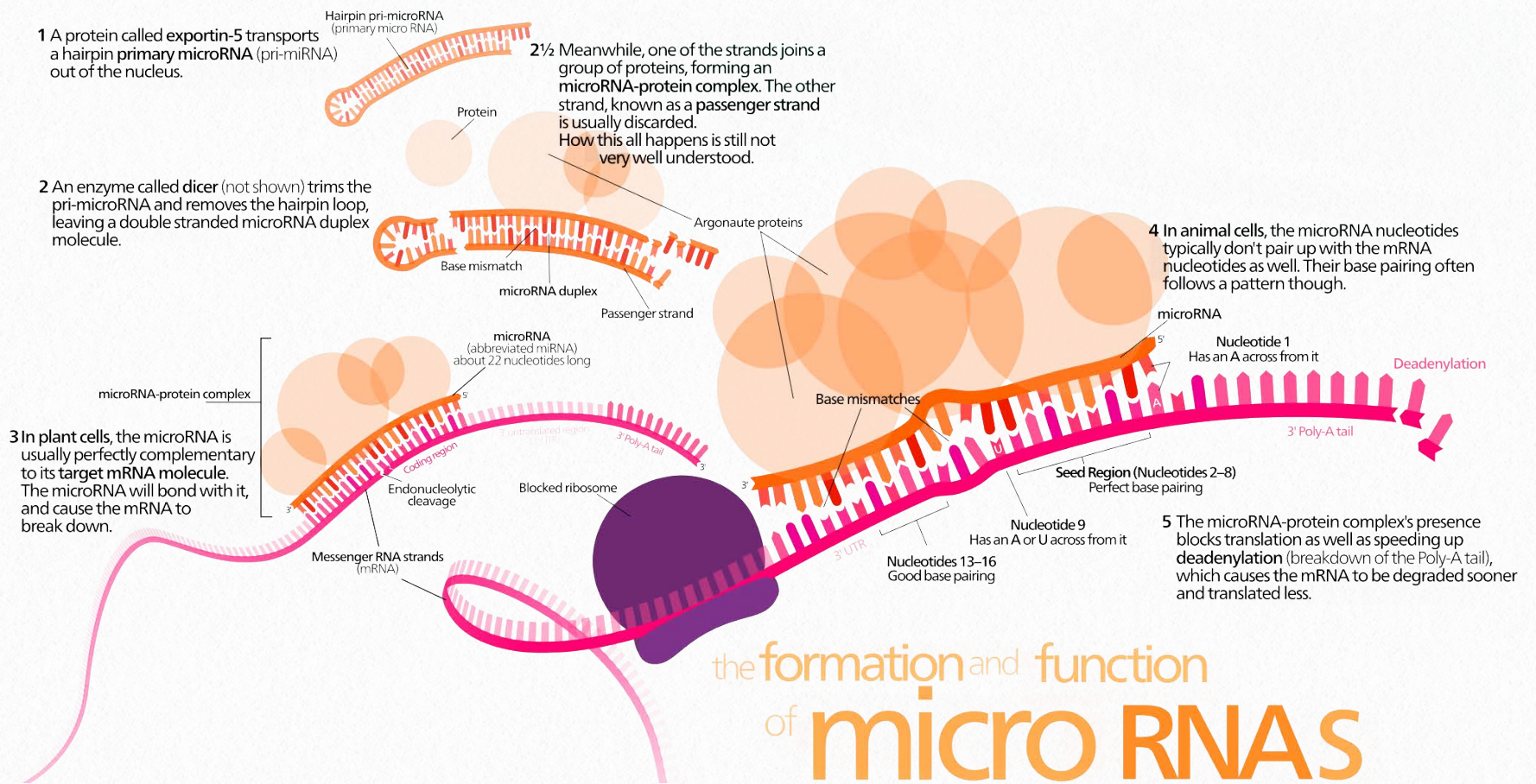
Another interesting observation is that certain proteins that bind to methylated CpG sites also seem to interact with histone deacetylases. As noted above, histones deacetylases

remove acetyl groups from histones, and promote tighter packing of chromatin and transcriptional silencing. Thus, methylation on DNA likely works in combination with histone modification to affect gene expression.

### Regulatory RNAs

One of the most unexpected discoveries in the past few decades has been the role that RNAs play in regulating gene expression. The classic view that RNA either encoded proteins (mRNA) or assisted in their synthesis (rRNA





**Figure 7.123 - miRNAs function in the regulation of gene expression**

Wikipedia

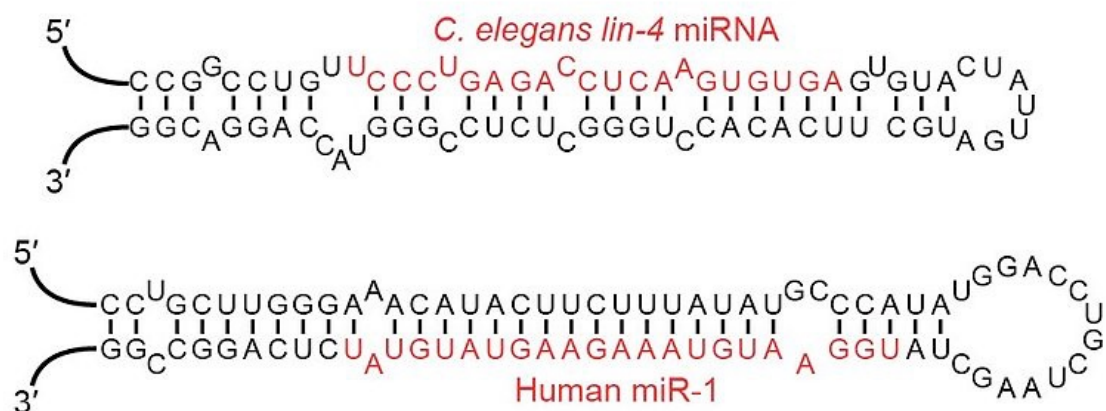
and tRNA) is now known to be a vast underestimate of the various ways in which RNAs function in gene expression. It is now clear that regulatory RNAs have widespread and significant effects on gene expression, a realization that has revolutionized our understanding of gene regulation.

What are some of the ways in which regulatory RNAs function to modulate the expression of genes?

## Small regulatory RNAs

MicroRNAs (miRNAs) and Short Interfering

RNAs (siRNAs) are small, non-coding RNAs that act at the post-transcriptional level to regulate gene expression (Figure 7.123 & 7.124). These RNAs appear to silence genes by base-pairing with target mRNAs and marking them for degradation, or by



**Figure 7.124 Pre-miRNA hairpin structures with the mature guide miRNAs shown in red**

Wikipedia



blocking their translation. The functional forms of both miRNAs and siRNAs are from 20-30 nucleotides long and are derived by processing from longer primary transcripts. Mature miRNAs and siRNAs work in association with a class of proteins called Argonaute proteins to form a gene silencing complex.

MicroRNAs are transcribed from specific genes by RNA polymerase II. The primary transcript, known as a pri-miRNA folds on itself to form double-stranded hairpin structures that are cleaved by an RNase in the nucleus called Drosha. The products of Drosha cleavage, double-stranded RNAs of roughly 60-70 nucleotides known as pre-miRNAs, are exported to the cytoplasm, where they are further processed into the small 20-30 nucleotide lengths of mature double-stranded miRNAs by an enzyme known as Dicer. The RNA duplexes of miRNAs are not perfectly matched, and have loops and mismatches (Figure 7.124).

siRNAs also derive from double-stranded

RNAs, but these may arise from either endogenous or exogenous sources (such as viruses). These double-stranded RNAs are processed in the cytoplasm by the same enzyme, Dicer, that generates the mature miRNAs, to produce the small, 20-30 nucleotide double-stranded RNAs.

In contrast to miRNAs, the mature siRNAs are perfectly base-paired along their lengths.

### RISC assembly

Both miRNAs and siRNAs then are assembled with Argonaute proteins to form a silencing complex called RISC (RNA-induced silencing complex). Recall that both miRNAs

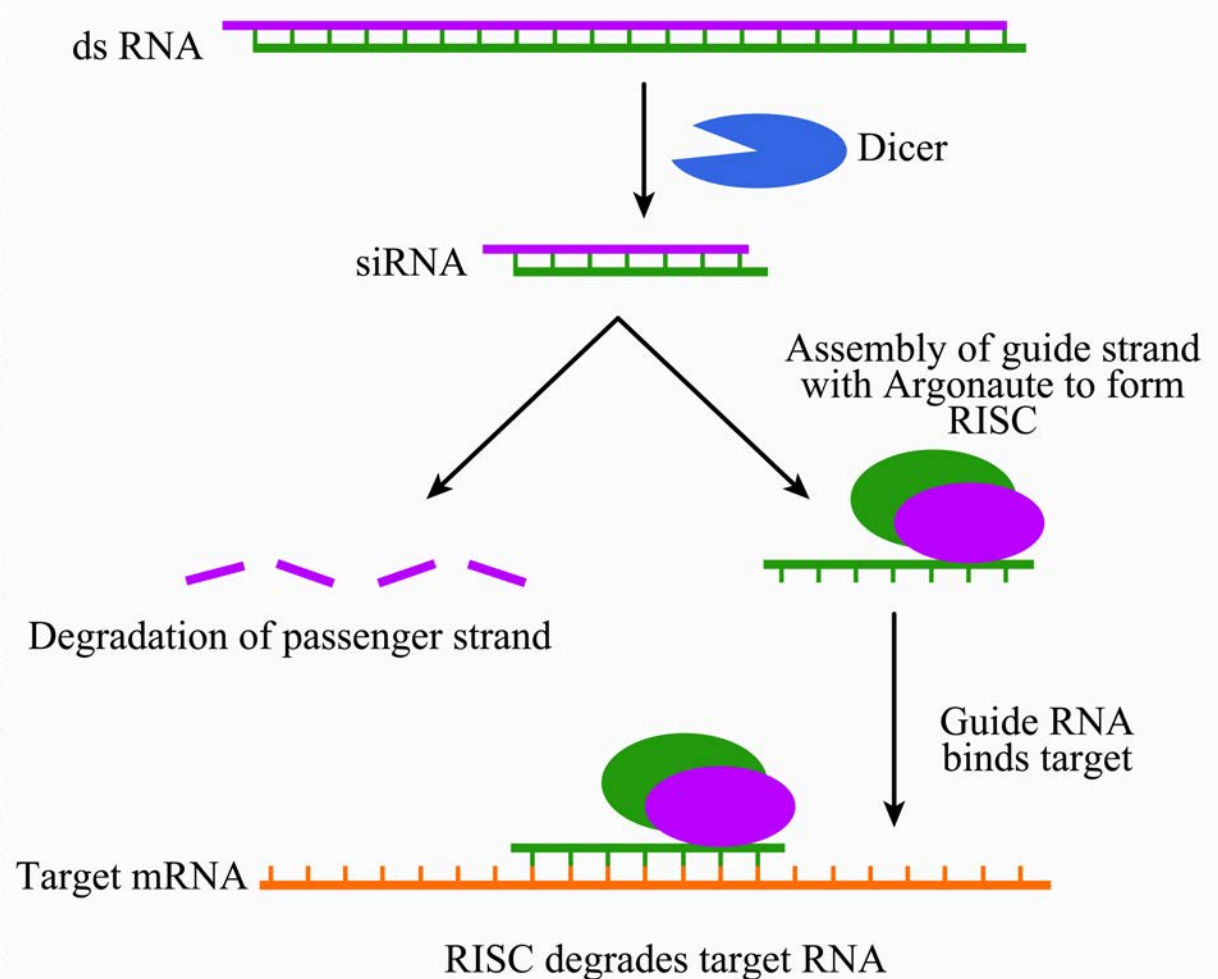
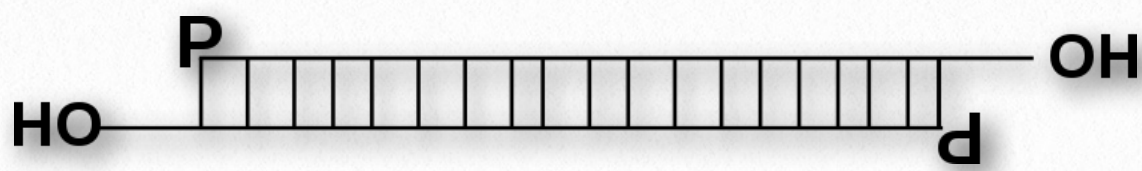


Figure 7.125 - Gene silencing by siRNA

Image by Pehr Jacobson





**Figure 7.126 - Processed siRNA duplex with perfect base-pairing, 5' phosphates and two bases overhanging at each 3' end**

and siRNAs are, at this point double-stranded. One strand of the RNA is referred to as the guide RNA, while the other is called the passenger RNA.

During the process of loading the RNA onto the Argonaute protein, the guide strand of the RNA remains associated with the protein, while the passenger strand is removed. The guide RNA associated with the Argonaute protein is the functional gene silencing complex (Figure 7.125).

Sequence specific base-pairing of the guide RNA with an mRNA leads to either the degradation of the mRNA by the Argonaute protein (in the case of the siRNAs) or in suppression of translation of the mRNA (for miRNAs). The extent to which these processes play a role in regulating gene expression is impressive. The expression of at least a third of all human genes has already been shown to be modulated by miRNAs, demonstrating clearly that these RNAs play a major role in gene regulation.

## Long noncoding RNAs

Long noncoding RNAs (lncRNAs) are RNAs of greater than 200 nucleotides that do not code for proteins. Some of these RNAs are derived from intron sequences, while others, transcribed from intergenic regions form a subset of

lncRNAs called lincRNAs (long intergenic noncoding RNAs). Yet other lncRNAs are produced as antisense transcripts of coding genes. An astounding 30,000 transcripts in humans are thought to be lncRNAs, but little is known of their function. From the few lncRNAs that have been intensively studied, it is evident that they do not all function in the same way. However, they appear to affect gene expression in a variety of ways including modification of chromatin structure, regulation of splicing, or serving as structural scaffolds for the assembly of nucleoprotein complexes. Additional mechanisms will doubtless be uncovered as these fascinating RNAs are investigated in years to come.

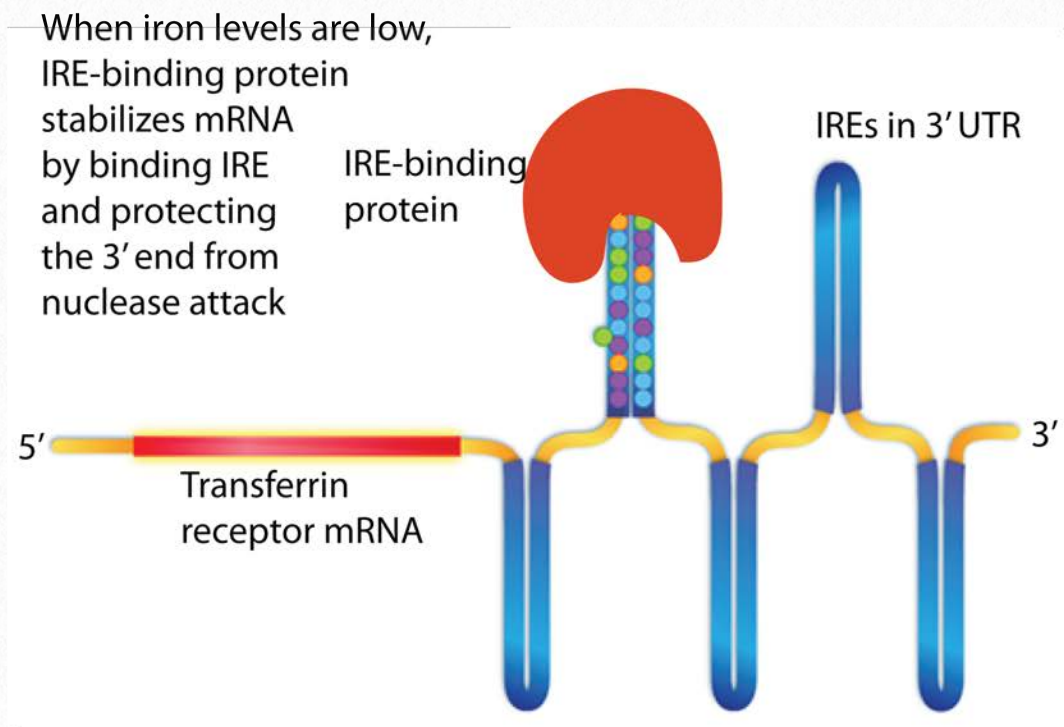
## Regulation of translation

The synthesis of proteins is dependent on the availability of the mRNAs encoding them. If an mRNA is blocked at its 5' end, it cannot be translated. The rate of degradation of an mRNA will influence how long it is around to direct the synthesis of the protein it codes for. Gene expression can also, there-

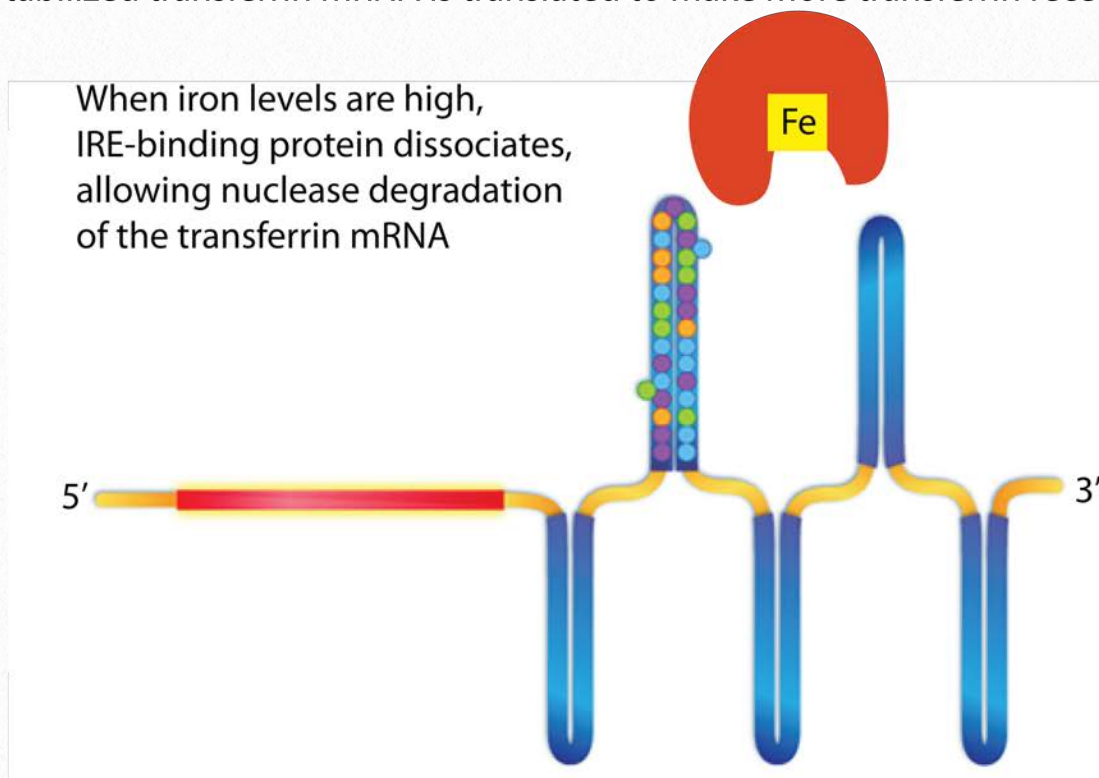








Stabilized transferrin mRNA is translated to make more transferrin receptor



Degradation of transferrin mRNA results in less transferrin receptor made

**Figure 7.128 -Regulation of transferrin receptor mRNA translation**

Image by Aleia Kim

## Gene expression is controlled at many steps

As can be seen from the examples in this section, regulation of gene expression in eukaryotic cells is a function of multiple mechanisms that act at different stages in the flow of information from DNA to protein, responding to the internal state of the cell as well as external conditions and signals.

mRNA. At times when iron levels are low, the IRE-binding protein remains bound to the 3' UTR of the mRNA, stabilizing it and permitting more transferrin receptor to be made by translation.



Graphic images in this book were products of the work of several talented students.  
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# God Bless These Complexes

To the tune of "God Bless America"

**Metabolic Melodies** Website [HERE](#)

All information in  
Cells' DNA  
Just increases  
With pieces  
Mixed and matched in the mRNAs

Linking exons  
All together  
Using snurps in  
Complex-ES

God bless the spliceosomes  
And trans-crip-tomes  
(*slow and loud*) God bless the spliceosomes  
And my ge-nome

Your blueprint info is  
In DNA  
Since you need it  
Proofread it  
Or you'll mutate the mRNA

You can translate  
All the codons  
With the cells' gen-  
et-ic code

God bless the ribosomes  
They translate code  
(*slow and loud*) God bless the ribosomes  
And proteomes

Recording by David Simmons  
Lyrics by Kevin Ahern



# The Book of Life

To the tune of "The Look of Love"

**Metabolic Melodies** Website [HERE](#)

The book of life - the stuff of dreams  
Is everywhere, it seems

The book of life, is biochemistry and  
Its words fill every day  
Just what it says is written in the DNA

I just want to get to know it  
How the info's coded  
What are all the secrets?  
Ribosomes can read it  
Goodness knows it's needed

And so its alphabet's  
In codon forms  
For ribosome bookworms

They read it right  
A protein's function to its sequence corresponds  
It's not just randomly created peptide bonds

What a marvel of creation, how they do translation  
Of m-R-N-A chains,  
Using bits of glycine  
Proline and some lysine  
Translate the code

*Instrumental*

I just marvel at the knowledge  
That I got in college  
To learn all the secrets  
Double helix spaces  
Complementary bases

Pyrimidines  
Paired to purines  
The book of life

*Recording by Carol Adriane Smith  
Lyrics by Kevin Ahern*