

Structure of Ribonucleic acids (RNAs)

LESSON III

RNA

- RNA contains ribose instead of deoxyribose as the sugar moiety.
- RNA is very unstable compared to DNA and is a single stranded polymer of ribonucleotides of adenine, guanine, cytosine and uracil.
- It is found in nucleus, nucleolus, cytoplasm and mitochondria.

- It is mainly of four types:
 - Messenger RNA (mRNA),
 - Transfer RNA (tRNA),
 - Ribosomal RNA (rRNA)
 - Small nuclear RNA (SnRNA).
 - SnRNA is used in mRNA splicing and gene regulation.

- Other than these forms, there are ribozymes, catalytic RNA enzymes that cut and splice RNA molecules and aid formation of peptide bonds during protein synthesis in the ribosome.
- The different forms of RNA differ in: gene of origin, function, size, post transcriptional structural modification and half-life.
- By intrachain base complementation, RNAs can form secondary and tertiary structures, e.g., hairpins, stem-loops and pseudoknots giving rise to possible structural domains.

- Single mammalian cell contains a total of approximately 1×10^{-5} μg of RNA;
 - 80 -85% is ribosomal RNA (rRNA) 28S, 18S and 5S subunits;
 - 15 -20% is composed of a variety of low molecular weight species, i.e., tRNA and SnRNAs; and 1 -5% mRNA.
- The rRNAs and tRNAs are of defined size and sequence and therefore relatively homogenous.
- The mRNA is highly heterogeneous with respect to both size (~ 100 -14,000 nucleotides) and sequence

Messenger RNA (mRNA)

- Is the single stranded coding nucleic acid that acts to transfer the genetic codes from the nucleus to the cytosol for proteins synthesis.
- Actually they carry the transcript of the nucleotide sequences corresponding to the sequence of amino acids in the protein they code for.
- Constituting 1-5% of the total cellular RNA content

- The **mRNA** is highly **heterogeneous** with respect to size (~100 -14,000 nucleotides); half-life/stability and sequence except for the 3'-terminus, which in eukaryotic cells mostly carries a **poly-adenylic acid (poly A) sequence**.
- This is why the initial single-stranded blue scripts and intermediate processing products of mRNAs are called **heterogeneous nuclear RNAs(hnRNAs)**.
- These thousands of types of intermediary mRNA forms constitutes less than **0.1%** of the total cellular RNA and ranges from **0.5 -500 kb** in size, thus, they may be 5 times larger than their mature mRNA forms.

- **Eukaryotic mRNA post transcriptional modifications**

1. The translation-non-functional, internal sequences, i.e., the **introns are removed.**

2. **A polyadenylate tail** (up to 250 bases) is added at the 3'-end.

1. The poly A tail marks the mRNA for **transportation** to the cytoplasm

2. Protects it from degradation by **3'-exonuclease.**

3. The polyA tail is used to **purify mRNA** from other RNAs by attachment to a stationary phase **oligo-deoxythymidine polymers.**

3. **7-methyl-guanosine triphosphate-2-o-methylribonucleotide cap** is added at the **5'-end of mRNA.**

1. This cap directs the **initiation of translation**

2. protects the mRNA from degradation by 5'-exonuclease.

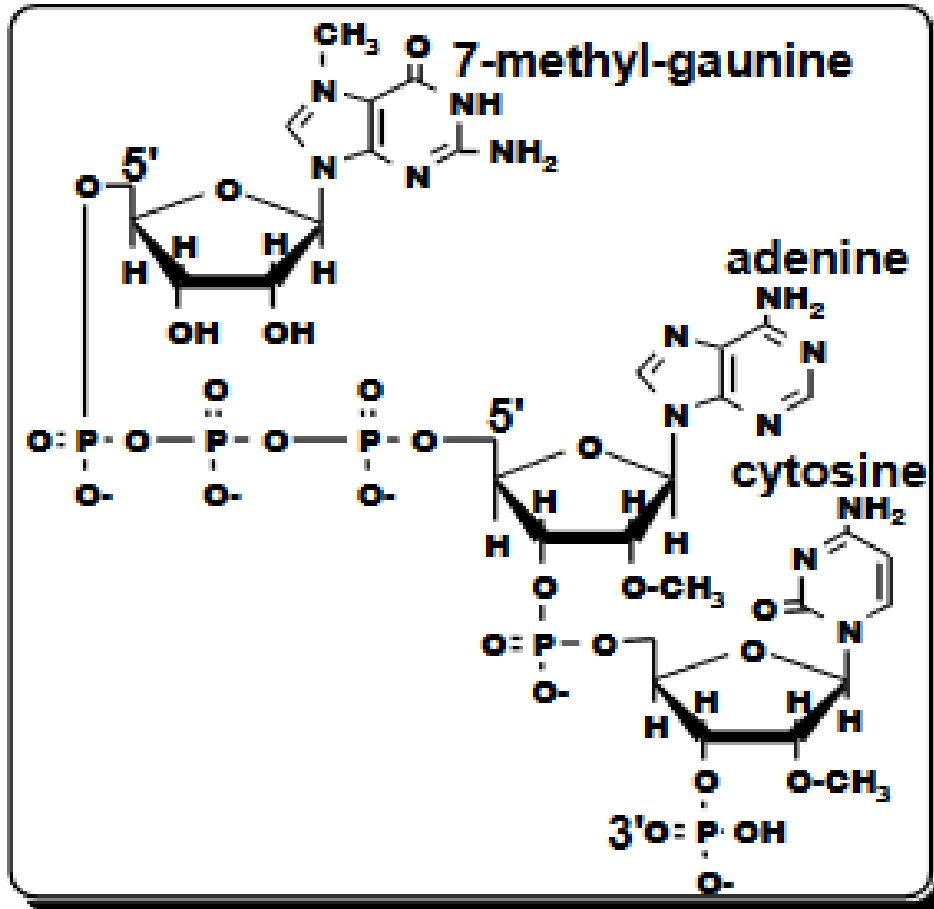
Post-transcriptional modification of RNA

- **Processing of mRNA**

- crude transcript of mRNA- **pre-mRNA** or **heterogeneous nuclear RNA (hnRNA)**

- **Capping:**

- It is the prompt addition of **7-methyl guanosine triphosphate** to the 5'-end of hnRNA by a specific enzyme called **guanylate transferase** after its transcription.
 - The cap is attached by 5' to 5' triphosphate linkage.



- It enhances subsequent hnRNA processing and the translation of mRNA and protects mRNA from the action of 5' 3' **exonucleases** and **phosphatases**, therefore controlling its half-life

- Mature mRNA still has 5'-and 3'-terminal **untranslated** regions (UTR) that contain sequences that control **rate of mRNA translation** and **mRNA half-life**.



Transfer RNA (tRNA):

- The tRNA is the **simplest** and **smallest non-coding** RNA, having only **74 -95 nucleotides** length
- Constituting ~5% of the total cellular RNA.
- it is transcribed from specific genes in the nucleus.
- The post-transcriptional modifications
 - Removal of introns
 - Modifications of its bases.
 - A 3'-ACC nucleotide sequence is added at the acceptor arm.

- Characterized by the presence of several inter-chain hydrogen bonds that give it a clover-leaf like shape

A.The D loop and arm: The loop contains an unusual nitrogen base, i.e., Dehydrouridine (DHU).

- The loop is important for proper recognition of a given tRNA by its amino-acyl-tRNA synthetase.

B.The TΨC loop and arm: The loop contains an unusual nitrogen base known as **Pseudouridine** (Ψ).The “**Thymine-Pseudouridine-Cytosine**” sequence is characteristics to the loop.

- The arm is involved in binding of amino-acyl-tRNA to ribosome.

- A. Anticodon arm:** The loop carries the “anticodon” triplet sequence that recognizes a specific codon of the “Code” on the mRNA molecule.
- B. The variable loop:** This is an extra loop hanging between T Ψ C and the anticodon arms and vary in size from one tRNA to the other.
- C. The 3'-ACC-amino acid acceptor end:** It carries a specific amino acid to be transferred into the ribosomes for protein synthesis. Therefore, each amino acid has at least one tRNA, i.e., there are 33 types of tRNA in cytoplasm and only 22 types in mitochondria. D-loop

Ribosomal RNA (rRNA):

- The **rRNAs** are the types of **non-coding RNA** found in the **ribosomes**, in association with the proteins.
 - The nucleoprotein assembly acts as the proteins synthetic machinery in the cytosol.
- **Polysomes** are assemblies of several ribosomes connected to one mRNA.
- The **highly methylated rRNA** molecules are assembled in the nucleolus with specific ribosomal proteins into **ribosomes**.
- The rRNAs constitutes ~80% of the total RNA content.

- They are classified according to their rate of floatation during centrifugation in NaCl solution in **Svedberg units (S)** into; **5S**, **16S** and **23S** in prokaryotes and mitochondria (120, 1700, and 3700 nucleotides, respectively).
- The 5S, 5.8S, 18S and 28S rRNAs exist in eukaryotes that are 120, 160, 1900 and 4800 nucleotides in length, respectively.
- **Eukaryotic ribosome is 80S in size and is formed of two subunits; 60S and 40S.**
 - 60S subunit is composed of ~50 protein molecules and 5S, 5.8S and 28S rRNAs.
 - The 40S subunit is composed of ~35 protein molecules and 18S rRNA.
- **Prokaryotic ribosome is 70S in size and formed of 50S and 30S subunits.**
 - The 50S is formed of ~34 protein molecules and 23S and 5S rRNA.
 - The 30S subunit is formed of ~21 proteins and 16S rRNA .

Small/Stable nuclear RNA (snRNA):

- They are large number of non-coding small discrete highly conserved and stable RNA species, found in nucleus and/or cytoplasm complexed in ribonucleoprotein complexes.
- They range from 90 -300 nucleotides and are present in 100,000 -1,000,000copies per cell constituting less than 1% of the total cellular RNA content.
- SnRNAs are a subset that is involved in mRNA processing and gene regulation with about 30 types.
 - Examples, U1, 2, 4, 5, 6 are involved in introns removal.
 - U7 may be involved in production of the correct 3'-end of histone mRNA that lacks polyA tail.
 - U4 and 6 may also be required for polyA tail processing

Small Nucleolar RNAs (snoRNAs):

- They are similar to the snRNAs but function mainly in the Nucleolar organizer area for rRNA posttranscriptional modifications including methylation and conversion of uridine into pseudouridine formation.
- They may have more than 200 types and their size range is 70-100 nucleotides constituting less than 1% of the total cellular RNA content.
- They are transcribed from specific genes and from introns of other genes.

Small cytoplasmic RNAs (scRNAs)

- They are tens of types of non-coding small RNAs (90-330 nucleotides)
- Constituting less than 1% of the total cellular RNA content that are located in the cytoplasm.
- They function in protein synthesis and transport mainly as a major part of the signal recognition particle that temporarily interrupts protein synthesis to direct the nascent polypeptide sequence into endoplasmic reticulum after which the synthesis resumes.

Telomeric RNA (telRNA)

- It is one type of non-coding RNA component in the ribonucleo-protein reverse transcriptase (RNA-dependent DNA polymerase) complex responsible for synthesis and maintenance of the telomere that stabilizes the ends of chromosomes and determines the replicative ability of cells.
- The telRNA molecule functions as a template for its own enzyme to synthesize species-specific telomere.
- Human telRNA is one type of 450 nucleotide in size out of which 5-CCCUAA-3, is reverse transcribed into the 5-TTAGGG-3 telomeric repeat.
- It constitutes very small % of the total cellular RNA content.
- **Read about other types of RNA**

RNA Synthesis (Transcription)

- The transcription unit (i.e., a gene) is a sequence (stretch) of DNA, which consists of:
 - 1. The regulatory gene response sequences (enhancer/silencer),*
 - 2. The basal rate controlling sequence (the promoter),*
 - 3. The transcription initiation start point,*
 - 4. the gene proper, and*
 - 5. The transcription termination sequence.*
- **Between genes or islands of related genes** there are **insulator sequences** that separate the coordinately regulated gene(s) so as regulatory sequences would work only on these isolated gene(s)

1. The gene enhancer/silencer,

- Are **cis-acting response sequences** that regulate the rate of gene expression through specific binding into transacting basal transcription machinery regulatory proteins.

2. The gene promoter region or transcription initiator sequence up-stream the gene proper.

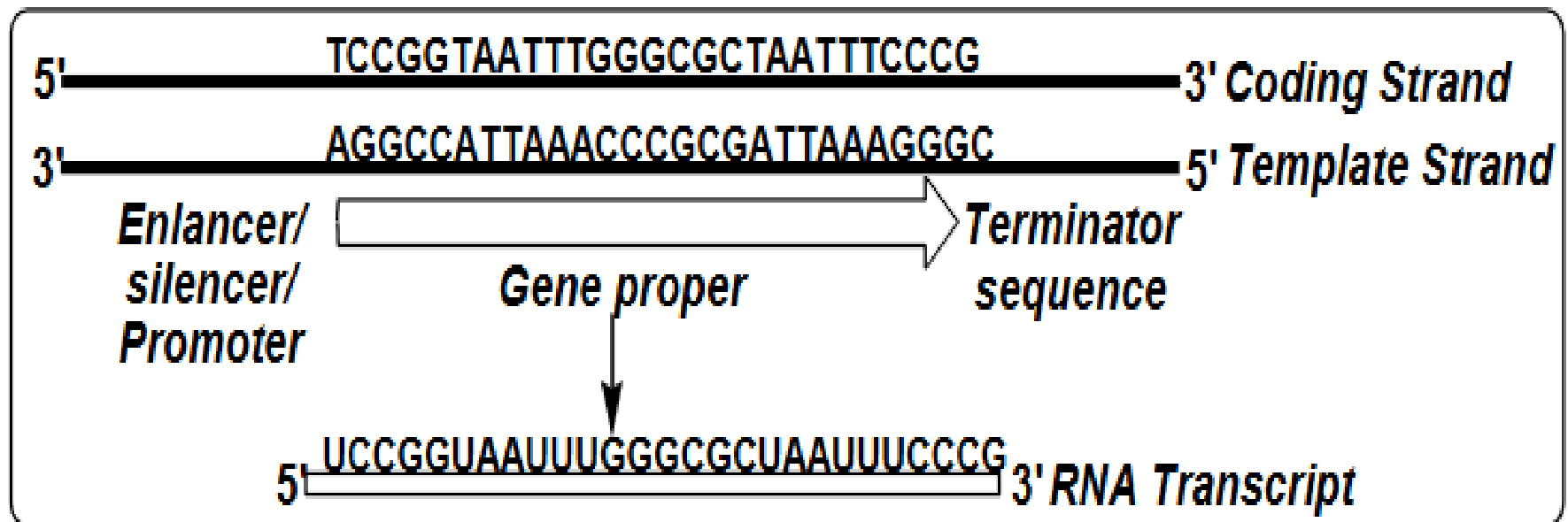
- The promoter provides the region of binding of the RNA polymerase.

3. Transcribed region or gene proper

- The DNA sequence that is copied as **hnRNA** or other types of RNAs that is mostly composed of **introns** and **exons** in eukaryotes, but intron-containing genes are very rare in prokaryotes.

4. Termination region,

- A regulatory DNA sequence downstream the gene proper of some genes, at which the RNA polymerase



Structure and function of the gene promoter

- It is transcription initiator sequence and works in the same orientation of the gene reading frame (3' → 5') and is located in a close continuity with the gene proper
- RNA polymerase binds DNA template at the gene promoter to initiate the basal (**unregulated**) **rate of transcription**.
- Some promoters are weak and others are strong, with a rate of transcription that is much faster; nevertheless there are certain **promoterless** genes.
- One gene may also have more than one promoter to be used differentially according to tissue specific needs.

Characteristics of prokaryotic promoter

- It is simpler than eukaryotic promoter and is formed of three parts:

1. Pribnow or TATA box:

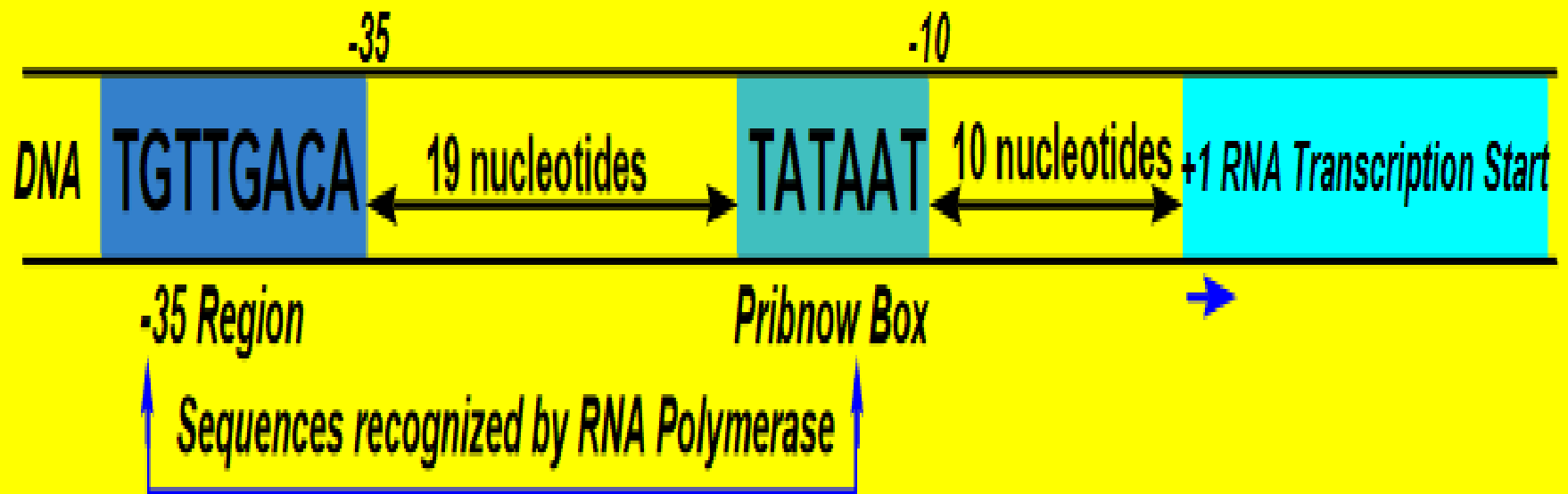
- It is a 6 bp stretch; **5'-TATAAT-3'** located 10 nucleotide upstreams the transcription **start site**.

2. The spacer stretches

- Nucleotides of about **10 bp** in between the **transcription start** and **Pribnow** box and about 19 nucleotides in between the **Pribnow box** and **the -35 region**.

3. The -35 region:

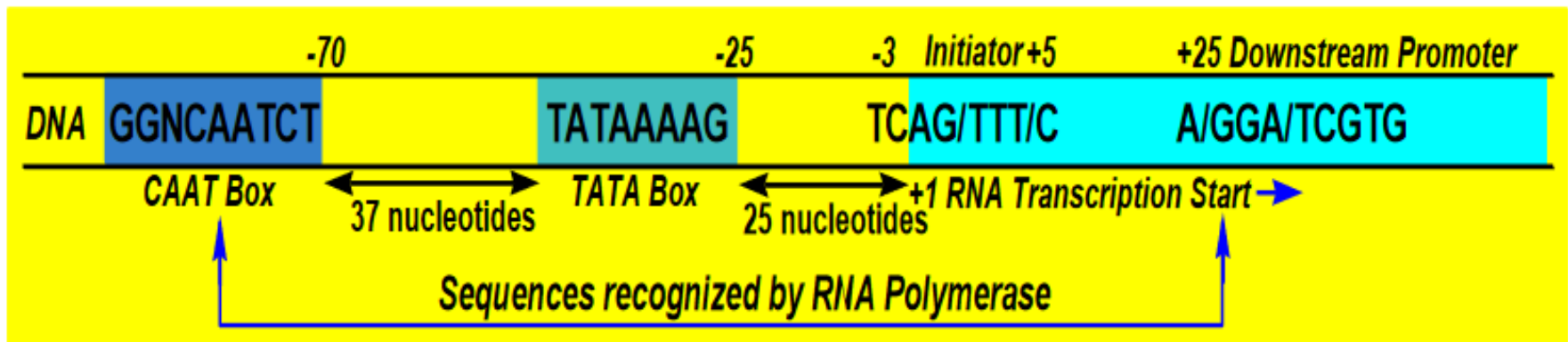
- It is a stretch of 8 nucleotides; **5'-TGTTGACA-3'** located about **35 nucleotide** upstream the **transcription start site**. Both **Pribnow** box and the **-35** region are recognized by RNA polymerases



Eukaryotic Promoter:

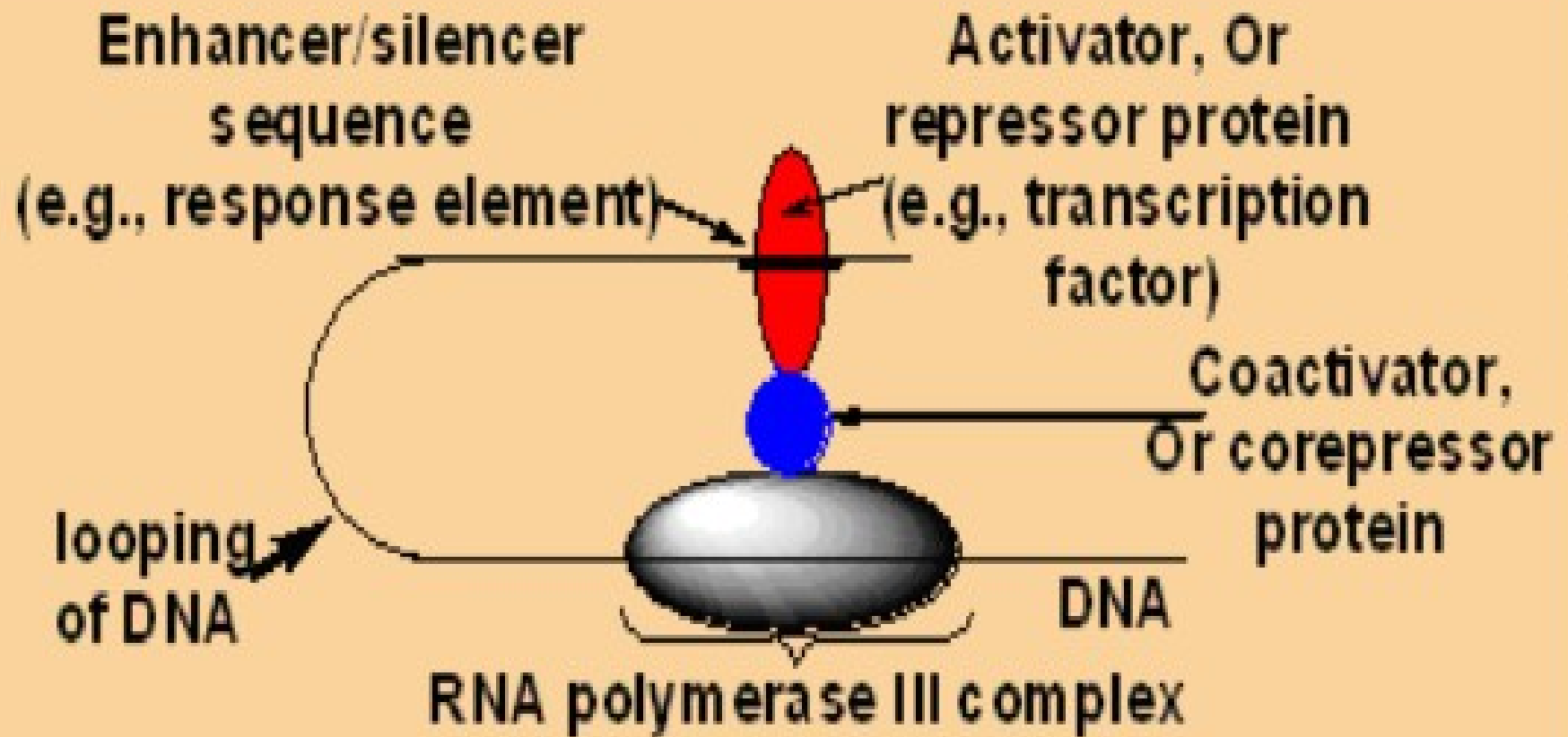
- **Hogness or TATA box:**
- It is an 8bp stretch of DNA, e.g., **5'-TATAAAAG-3'** located 25-30 nucleotides **upstreams** the transcription start site.
- *~30% of the eukaryotic genes do not have TATA box and instead they have **initiator sequence** that spans the transcription start site -3 to +5, e.g., **TCAG/TTT/C**.*
- *~30% of the stronger genes have both **TATA** and **initiator sequences**.*
- *Still ~25% of the genes have initiator sequence and a downstream promoter sequence (A/GGA/TCGTG, 25 bp downstream **transcription start** site).*
- The remaining ~15% of the genes contain the three elements.
 - These elements determine where transcription starts through the binding of the TATA binding protein (TBP) and its associating factors (TAFs) that form the **TFIID complex** to recruit the RNA polymerase.

- **Specific trans-activating proteins** bind these elements by their DNA-binding domain and interact with basal transcription machinery through their **trans-activation domains**.
- They control the **frequency** of **transcription initiation** for the basal rate of expression.
 - Depending on their type, they are less rigid in their orientation dependency than the TATA box group



Gene response elements (Enhancer or Silencer):

- The response elements may **activate transcription** above the basal rate, therefore, are called **Enhancer elements** or **suppress** transcription below the basal rate, therefore, are called **Silencer/Repressor elements**.
- They mediate responses to various signals including **hormones, environmental changes** and **toxins such as dioxin**.
- **Transcription factors** are activator or suppressor proteins that bind at these elements and interact with RNA polymerases directly or indirectly through co-activator or corepressor proteins to increase or decrease rate of transcription.
- Tens of these elements may work on one gene with the transcription factors binding to them in a cooperative, agonistic, synergistic or antagonistic fashion.



In Prokaryotes	In Eukaryotes
A single type of RNA polymerase that is responsible for synthesis of all types of RNA	There are three types of RNA polymerases; each is specific for the synthesis of a specific type of RNA.
Products of RNA polymerase require slight or no modification after transcription.	Mostly require extensive post-transcriptional modifications particularly in mRNA.
The holoenzyme is formed of five subunits: two identical α subunits, two similar but not identical $\beta\beta'$ the catalytic subunits and a regulatory σ subunit ($\alpha_2\beta\beta'\sigma$). The core part of the enzyme is formed of the four $\alpha_2\beta\beta'$ subunits.	They are much complex in structure and are formed of 2 large (homologous to $\beta\beta'$) and up to 14 small subunits. The three types of RNA polymerases are: • <u>RNA polymerase I</u>: Responsible for synthesis of the large RNA molecules (rRNA). It is insensitive to α-amanitin (a mushroom peptide toxin that prevent polymerase translocation). • <u>RNA polymerase II</u>: Responsible for synthesis of mRNA and some snRNA. It is sensitive to low concentration of α-amanitin. • <u>RNA polymerase III</u>: Responsible for synthesis of small RNA molecules, i.e., tRNA, 5S rRNA and snRNA. It is sensitive to high concentration of α-amanitin.

Initiation

- Initiation of transcription occurs on a single strand of a transcription unit (a gene) that is called **template (non-coding or non-sense)** strand that is complementary to the RNA, and it never occurs in the other strand, **non-template, coding or sense strand**.

- The template strand is read in 3' to 5' so that the synthesized RNA will be formed in 5' to 3'.
- Which DNA strand is the template and which is the coding, differs from one gene to the other but is always the strand that contains the **prompter sequence** read in 3' to 5' direction.
- RNA polymerase recognizes the promoter region by the help of **the σ (sigma) factor** that then recruits the core enzyme ($\sigma_2\beta\beta'$)for tight binding into DNA.

- There are several types to σ factors that recognize different promoters to differentially control gene transcription according to the growth and environmental conditions of the bacterium.
- The core enzyme unwinds 17-20 bp nucleotides to separate the two strands (~ 60 bp in eukaryotes, from -30 to $+30$), i.e., the transcription bubble.
- This requires **unwindase**, disruption of the nucleosome structure and the participation of **topoisomerases**.

- The enzyme complex then searches for the transcription initiation site (an open reading frame starting at TAC).
- This process requires participation of **topoisomerases**.
- The synthesized RNA always starts with a purine that enters at the initiation site of the enzyme.
- This 5'-purine ribonucleotide at the 5' end retains its **triphosphate** and **stays in mature mRNA**.

- When the second nucleotide enters at the elongation site of the enzyme it forms a **phosphodiester bond** between 3'-OH group of ribose of the first nucleotide and the 5'-OH of the phosphate group on C5 of ribose of the second nucleotide.
- While on the promoter, the polymerase synthesizes 10 -20 nucleotide stretch of RNA

Elongation

- The σ Factor is released before elongation starts leading to core enzyme conformational change that enables its translocation to clear the promoter.
- The four ribonucleotides triphosphate; ATP, GTP, CTP and UTP continue to enter into the polymerization (or elongation) site of β unit with the release of a pyrophosphate (PPi) each time a new nucleotide is added to the growing RNA chain.

Elongation

- **Pyrophosphatases hydrolyze** P_{PPi} into 2 P_i to ensure irreversibility of the polymerization.
- The RNA polymerase continues transcription from 3' towards 5' end of the template strand according to the base pairing rule in an anti-parallel manner.
- Elongation continues through the termination sequence.

Termination of transcription

- At the completion of the transcription of a gene, the elongation has to be terminated. The termination takes place in **two ways** .
 1. **rho (ρ) factor dependent or**
 2. **rho (ρ) factor independent:**
- **rho-dependent termination:**
 - The rho(ρ)factor is an ATP-dependent **RNA-stimulated helicase** that recognizes and binds the termination sequence (~40 bp) in the template DNA, then; it **disassembles the enzyme/RNA/DNA complex**.
 - The termination sequence may occur hundreds of **base-pairs downstream** the site at which poly(A) tail is added in mRNA.

- An RNA endonuclease cleaves the primary RNA transcript at 15 -31 bases 3" of the cleavage consensus sequence, i.e.,AAUAAA.The poly(A) tail is added to this new 3" end.
- **rho-independent termination:**
- RNA polymerase stops transcription when the synthesized complete RNA molecule takes its three-dimensional form with the formation of specific secondary structures such as **a hairpin** followed by an **oligo-U sequence**.
- This structure pauses the RNA polymerase and then disassembly of the transcription machinery.

Processing of tRNA:

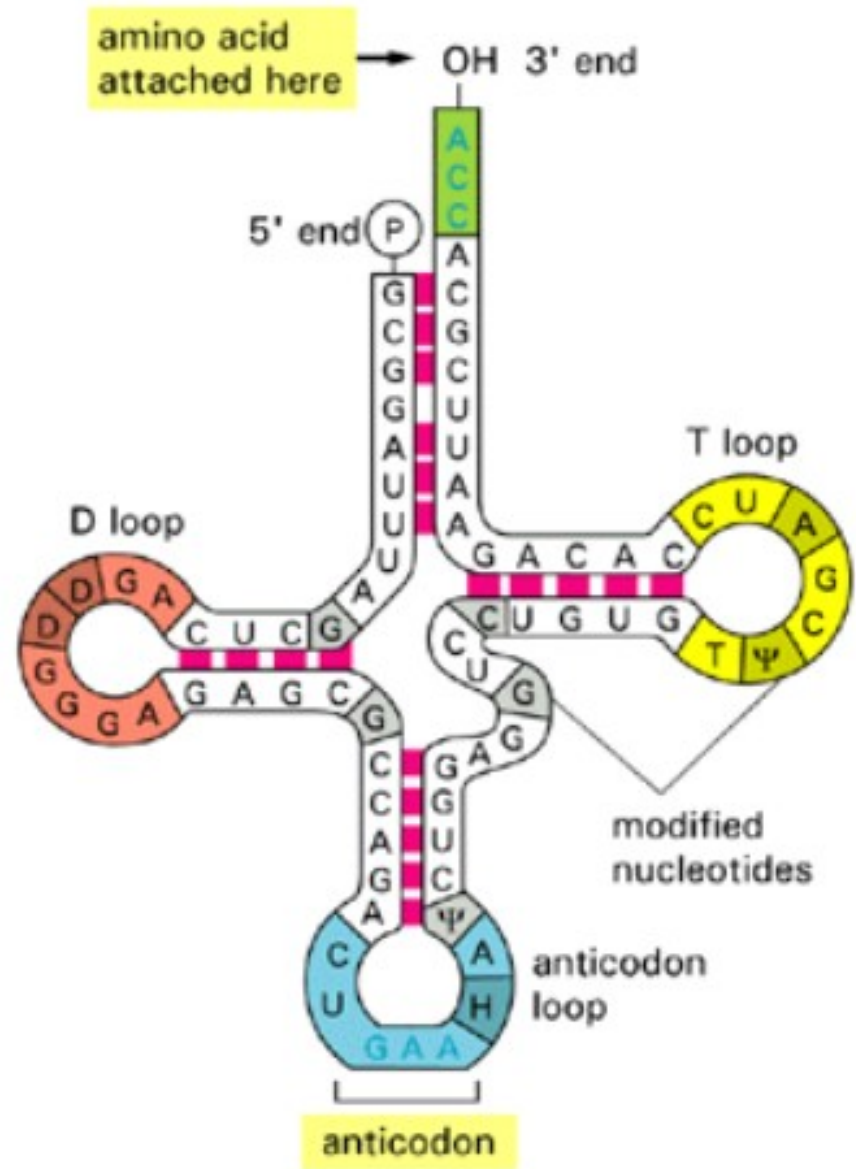
- **Cleavage:**

- Primary tRNA transcript is a large precursor containing **more than one tRNA**.
- It is processed by the action of specific class of **ribonucleases**, folds into its **clover-leaf shape**, where **introns** are removed by specific splicing **endonucleases** and 5'-and 3'-extra sequences are removed.

- **Nucleotide modification:**

- The tRNA nucleotides are modified by **methylation, deamination, alkylation, reduction and glycosylation**.

- **Acceptor terminus:**
 - The 3'-terminal UU of the tRNAs are replaced by the characteristic amino acceptor - CCA terminus by the enzyme **nucleotidyl transferase**.



- **Processing of ribosomal RNA:**
 - There are hundreds of copies of rRNA genes to provide the enormous number (10⁷) of ribosomes required for each cell.
 - A large 45S precursor intron-less molecule is cleaved by specific **endonucleases** and **exonucleases** into 5.8S, 18S, and 28S rRNAs.
 - The 5S rRNA is transcribed from a separate gene

Major differences between prokaryotic and eukaryotic mRNA

	<i>Prokaryote</i>	<i>Eukaryotes</i>
<i>Half-life.</i>	<i>Short</i>	<i>Long</i>
<i>Number of cistron.</i>	<i>Polycistronic</i>	<i>Monocistronic</i>
<i>Presence of introns and their splicing.</i>	<i>No</i>	<i>Yes</i>
<i>Separation of translation from transcription.</i>	<i>No</i>	<i>Yes</i>
<i>Translation during transcription and their regulatory interaction.</i>	<i>Yes</i>	<i>No</i>
<i>Posttranscriptional processing of mRNA; capping/tailing/editing.</i>	<i>No</i>	<i>Yes</i>
<i>Processing of large precursor rRNA and tRNA into smaller units.</i>	<i>Yes</i>	<i>Yes</i>

Regulation of gene expression

- Some of the genes products are required at all times during the life of the cells
- Enzymes of central metabolic pathways, are expressed at a more or less constant level in almost all the cells of an organism.
- Such genes are called as **housekeeping genes** and this constant expression of a gene is called **constitutive gene expression**.

Regulation

- The expression of other genes that respond to the metabolic, endocrine or environmental factors changes as per the existence and balance of these stimuli.
- The cellular levels of products of these genes rise and fall in response to molecular signals; this is called as **regulated gene expression**.
- Gene products that increase in concentration under particular molecular circumstances are referred to as **inducible**; the process of increasing their expression is **induction**.

Regulation ...

- The gene expression is controlled at least at five levels:
 - A. At epigenetic level.**
 - B. Gene rearrangement.**
 - C. Utilization of alternative promoters.**
 - D. At transcription level.**
 - E. At post transcription level.**

A. Epigenetic control of gene expression

- An epigenetic control is a change in the genome that does not involve a change in the DNA sequence but is heritable by cell **progeny**.
- Gene expression is regulated by epigenetic factors such as:
- **The spatial cell-cell and cell-matrix contact.**
 - Contact inhibition of cell proliferation and change of the nature of cell differentiation on specific extracellular matrix are examples.

- **Methylation at cytosine of specific 5'-CpG-3'** islands of the promoter region of genes is a very important regulatory mechanism.
 - **Hypomethylation** activates, whereas,
 - **Hypermethylation** (by DNA methyltransferases) silence gene expression through interaction with **histone deacetylases**.

- The preferential expression of a particular gene exclusively from the allele contributed by one parent is called **parental imprinting**.
- **Chromatin remodeling:**
 - Nucleosome and higher chromosome organization and function may vary with modification of the **nucleoproteins**.
 - **Core Histones**; H3 and H4 proteins are susceptible to acetylated(by histone **acetyl transferases**)or deacetylated(by histone deacetylases) at their amino terminal lysine to recruit coactivators and induce transcription or **corepressors** and suppress transcription, respectively.
 - Histones are also susceptible to methylation/demethylation.

B. Gene rearrangement:

- The number of copies and position of the different genes helps in controlling their expression
- **Chromosomal recombination (cross-over)**
 - is are combination between homologous **metaphase chromosomes** during meiosis or between sister chromatids during mitosis.
 - With **equal reciprocal** exchange of genetic material, it has no pathological consequences.
 - **Unequal reciprocal** exchange of genetic material results in diseases due deletion/insertion mutation,

- **Differential rearrangement:**

- A number of genes exist as multiple copies and recombination of “xth” copy of „X” gene with “yth” copy of „Y” gene results in the production of the functional protein.
- This kind of rearrangement is the basis for the diversity and polymorphism of proteins like immunoglobulins, e.g., **the VL and CL genes** for a single immunoglobulin molecule are widely separated in the germ line genome.

- **Transposition:**

- Transposons are **small mobile DNA** elements that have the capability of changing their position in the genome.
- They are also called as the jumping genes.
- They may affect the function of the neighboring sequences and may transfer flanking sequences of DNA that profoundly affect development

- **Gene conversion**

- is due to recombination of similar DNA sequences on homologous or non-homologous chromosomes.
 - They become similar in these Chromosomes due to elimination of any mismatched sequences leading to genetic change and allelic loss.

- **Integration of oncogenic viruses:**

- **Gene amplification**

C. Utilization of alternative promoters

- This is a type of regulation of **tissue-specific gene expression** that is achieved by usage of different elements of the promoter or usage of different promoters.
- A good example of alternative promoter usage is the **glucokinase** gene in the **liver and β -cells of pancreas**.
- In both, the gene consists of 10 exons.
- In liver, the utilized promoter is **close to exon 1** and during splicing both promoter and exon 1 sequences are removed.
- In β -cells, the utilized promoter is **far upstream exon 1** and during splicing exon 1 is joined to other exons of the gene and is not removed.
- ***This gives differential control of rate of transcription and function for the produced protein.***

D. Transcriptional control of gene expression

- Each differentiated cell has the capacity to synthesize certain types of protein in suitable amounts through differential regulation of gene expression.
- Regulation of gene expression can be illustrated by the Lac-Operon in E.Coli as the simplest model for regulation of gene expression, since regulation of other genes in E.Coli or eukaryotes are far more complex.
- Operon is a coordinated unit of gene expression (Lac = lactose-metabolizing enzymes, Oper = operation, and On = is on).
- Lac-Operon is formed of two genes along with their regulatory sequences.

The two states of Lac-Operon (Repression and induction) are:

- **Repression:**

- When E. coli is grown in presence of glucose, whether lactose or other sugars are present or not, transcription of the Lac-gene is repressed and hence lactose is not metabolized.
- Repression is mediated by **Lac repressor**, which binds as a tetramer to the operator sequence preventing the binding of RNA polymerase to the promoter and prevents the transcription of the Lac-gene.
- The repressor is a negative regulator, and its binding site acts as a silencer sequence on expression of the Operon.

- **Induction (or derepression):**

- When glucose is absent, the Lac-gene is induced, i.e., expression rate of the Operon is increased.
- Starvation of the bacterium of glucose leads to increase of cAMP that binds and activates the DNA binding of the cAMP Receptor Protein (CRP) or **Catabolite gene Activator Protein (CAP)**.
- The CAP binds to the CAP binding sequence of DNA up-stream the promoter to facilitate binding of RNA polymerase to the promoter to induce transcription of the Lac-gene at a low level (about 50 fold).

E. Post-Transcriptional control of gene expression:

- Control of RNA processing (e.g., capping, tailing, editing),
- RNA transport and rate of translation(e.g., proteins utilized in iron absorption, transport and storage) and
- half-life are other mechanisms for regulate levels of gene expression.
- Alternative splicing of mRNA to generate different mRNAs and hence different proteins from same mRNA is a tissue-specific adaptive and developmental control mechanism that is achieved by:

Read

- **Prokaryote transcription**
- **Transcription in Eukaryotes**