

## **5' Untranslated Region (5' UTR)**

**Location:** Upstream of the coding sequence (before the start codon).

### **Function:**

- Regulates translation initiation.
- May contain ribosome binding sites and secondary structures that influence translation efficiency.
- Plays a role in mRNA stability and localization.

### **Features:**

- Can include upstream open reading frames (uORFs).
- Often interacts with proteins and small RNAs for regulation.

## **Coding Sequence (CDS)**

**Location:** Between the start codon (AUG) and stop codon.

### **Function:**

- Encodes the actual protein.
- Translated by ribosomes into amino acid chains.

### **Features:**

- Defines the primary structure of the protein.
- Its sequence determines protein folding, function, and interactions.

### 3' Untranslated Region (3' UTR)

**Location:** Downstream of the stop codon.

**Function:**

- Regulates mRNA stability, translation efficiency, and localization.
- Contains binding sites for microRNAs and RNA-binding proteins.

### Exons

- **Definition:** Coding regions of a gene that remain in the mature mRNA after splicing.
- **Function:**
  - Encode proteins.
  - Determine the amino acid sequence of the final protein.
- **Location:** Found in both DNA and RNA; retained in mature mRNA.
- **Expression:** Translated into proteins during gene expression.
- **Conservation:** Highly conserved across species due to their functional importance.

**Mutation Impact:** Mutations can directly affect protein structure and function, potentially leading to disease.

## Introns

**Definition:** Non-coding regions of a gene that are removed during RNA splicing.

**Function:**

- Regulate gene expression.
- Allow for alternative splicing, increasing protein diversity.

**Location:** Present in DNA and pre-mRNA; removed from mature mRNA.

**Expression:** Not translated into proteins.

**Conservation:** Less conserved; vary widely among species.

**Mutation Impact:** Can affect splicing accuracy or regulation, potentially leading to misexpression

## Enhancer Features

**Function:** Increase transcription of specific genes.

**Location:** Can be far upstream or downstream from the gene they regulate—sometimes over 1 million base pairs away.

**Binding:** Serve as docking sites for transcription factors (activator proteins).

**Action:** Help recruit RNA polymerase to the promoter via looping mechanisms.

**Flexibility:** Can function regardless of orientation or distance from the gene.

**Activity:** Often transcribed into non-coding enhancer RNAs (eRNAs), which may further regulate gene expression.

## Silencer Features

**Function:** Decrease or suppress transcription of specific genes.

**Location:** Like enhancers, they can be located upstream, downstream, or within introns of the target gene.

**Binding:** Attract repressor proteins that inhibit transcription.

**Mechanism:** Block activator binding or interfere with transcription machinery.

**Role in Disease:** Malfunctioning silencers can lead to inappropriate gene activation, contributing to disorders like cancer

## Key Features in a Gene Sequence

Feature	Location	Function
<b>Promoter</b>	Upstream of the gene	Initiates transcription by binding RNA polymerase and transcription factors
<b>5' UTR</b>	Before the start codon	Regulates translation initiation and mRNA stability
<b>Start Codon (AUG)</b>	Beginning of CDS	Signals the start of protein synthesis
<b>CDS (Coding Sequence)</b>	Between start and stop codons	Encodes the amino acid sequence of the protein
<b>Exons</b>	Within CDS and UTRs	Retained in mature mRNA; may be translated or regulatory
<b>Introns</b>	Between exons	Removed during RNA splicing; may regulate gene expression
<b>Stop Codon</b>	End of CDS	Signals termination of translation
<b>3' UTR</b>	After the stop codon	Influences mRNA stability, localization, and translation efficiency
<b>Enhancers</b>	Upstream/downstream	Increase transcription rate from a distance
<b>Silencers</b>	Upstream/downstream	Suppress transcription from a distance
<b>Polyadenylation Signal</b>	Near 3' end of gene	Signals addition of poly-A tail to mRNA